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Doctor of Philosophy

Cardioprotective effects of metformin or sappanone A
on alleviating left ventricular diastolic dysfunction
in a rat myocardial I/R injury model

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of the University of Ulsan
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A Dissertation

Submitted to
the Graduate School of the University of Ulsan
In partial Fulfillment of the Requirements
for the Degree of

Doctor of Philosophy

by

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February 2021

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Abstract

The increased incidence of myocardial infarction (MI) has emerged globally as a leading cause of cardiovascular morbidity and mortality. In the development of new drugs, the evaluation of cardiac function is important factor in the withdrawal of drug candidates. In addition, as life expectancy increases, the prevalence of metabolic syndrome is gradually increasing, and metabolic syndromes such as diabetes, abdominal obesity, dyslipidemia, and hypertension are the main causes of cardiovascular disease. The aim of this study was to establish a rat myocardial ischemia and reperfusion (I/R) injury model similar to human acute MI and investigate cardiac function commonly referred to as left ventricular (LV) function including LV systolic and diastolic function using echocardiographic evaluation.

Male Sprague-Dawley rats, 8-9-week-old, were ligated and reperfused the left anterior descending coronary artery (LAD) for 30 minutes under ventilation. Echocardiography was performed under anesthesia after the induction of MI according to the experimental plan. Among the echocardiographic indices, EF and FS represent the left ventricular systolic function in three-dimensional and two-dimensional meanings respectively. To assess the left ventricular diastolic function, the values of peak velocity of the transmitral flow at early filling (E), the early diastolic mitral annular velocity (E') at the medial mitral annulus, and E/E' ratio were measured. In the preliminary study, the EF and FS values of rats with MI were significantly decreased compared with those of the sham group at 2 hours and on day 1 ($P<0.01$). However, the significantly decreased E' and increased E/E' values of MI group were shown compared with those of sham group during the entire experimental period. These results indicate that, unlike left ventricular systolic function, left ventricular diastolic function does not recover at the early phase of rat myocardial I/R injury model. Moreover, this acute myocardial infarction animal model and echocardiographic assessment of cardiac function show the importance of the left ventricular diastolic function, which is currently highlighted in patients with heart failure in human. In this study, in a rat myocardial I/R injury model, we can evaluate the efficacy study of candidates for new drug development especially using echocardiographic evaluation of left ventricular diastolic function, and applied metformin and saipanone A.

Metformin, dimethyl biguanide as a first-line treatment for type II diabetes, significantly improved left ventricular systolic function including EF and FS values on days 3 and 7 after MI surgery. In addition, metformin resulted in recovery of left ventricular diastolic function in the early phase of rat ischemic reperfusion injury in this model. It was also possible to confirm the cardioprotective effect of metformin in histopathological results, in line with echocardiographic results.

Sappanone A, isolated from heartwood *Caesalpinia sappan*, homoisoflavanone, has proven anti-inflammatory effects with cells and LPS-induced bone loss mouse model. Sappanone A administration significantly attenuated left ventricular systolic and diastolic dysfunction in a rat myocardial I/R injury model in the early phase of MI. Also, myocardial infarct size, serum cardiac marker assay, histopathological assessment of inflammatory cells infiltration of rat hearts, transcriptome analysis of rat left ventricles showed that 50 mg/kg sappanone A has a cardioprotective effect.

Therefore, this rat myocardial I/R injury model using multimodal assessment of cardiac function including echocardiographic evaluation of left ventricular systolic and diastolic function, serum cardiac marker, myocardial infarct size, histopathologic evaluation, and mRNA sequencing can be widely used in translational research and in the development of new heart failure-related drugs.

Keywords: acute myocardial infarction; rat myocardial ischemia/reperfusion injury model; left ventricular diastolic dysfunction; echocardiography; metformin; sappanone A

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Abbreviations

MI	myocardial infarction
AMI	acute myocardial infarction
LV	left ventricular
ECG	electrocardiogram
I/R	ischemia/reperfusion
NO	nitric oxide
iNOS	inducible nitric oxide synthase
COX-2	cyclooxygenase-2
LPS	lipopolysaccharide
HO	heme oxydase
Nrf2	nuclear factor E2 related factor 2
BMMs	bone marrow macrophages
LAD	left anterior descending
TTC	triphenyltetrazolium chloride
PSSAX	parasternal short axis
EF	ejection fraction
FS	fractional shortening
SV	stroke volume
CO	cardiac output
PWD	pulse wave doppler
TDI	tissue doppler imaging
E	transmitral flow at early filling
E'	Early diastolic mitral annular velocity at the medial mitral annulus
LVIDd	left ventricular internal diameter at diastole
LVIDs	left ventricular internal diameter at systole
IVSd	interventricular septal thickness at diastole
IVSs	interventricular septal thickness at systole
LVPWd	left ventricular posterior wall thickness at diastole
LVPWs	left ventricular posterior wall thickness at systole
DEG	differentially expressed gene
GOBP	gene ontology biological process

Introduction

Myocardial infarction (MI) is one of the leading causes of increased cardiovascular mortality and morbidity globally and acute myocardial infarction (AMI) is strongly related to metabolic syndrome such as diabetes mellitus, visceral obesity, dyslipidemia, hypertension, insulin resistance (1). MI is characterized by an interruption of the blood supply to a part of the heart especially the left ventricle (LV), causing ischemic damage to the heart muscle (2, 3). Myocardial dysfunction can be detected by echocardiography which is a well-established diagnostic tool for non-invasive and accurate evaluation of cardiac anatomy and hemodynamic function in clinical practice (4). In addition, echocardiography in the ischemic state occurs prior to the appearance of the chest pain or electrocardiogram (ECG) changes (5). In clinical practice, the best indicator of prognosis in MI patients is left ventricular function (6), and the patients with left ventricular diastolic dysfunction have poorer surgical outcomes including heart failure or cardiac death than those of the patients with only left ventricular systolic dysfunction in the perioperative period (7, 8).

In cardiovascular research, there are two types of myocardial infarction animal model such as permanent or transient model of rat myocardial infarction model. Transient rat myocardial infarction model known as rat myocardial ischemia reperfusion (I/R) injury model is the most commonly used animal model for acute myocardial infarction (AMI) due to the similarity to those in the patients with heart disease (9). Recent scientific and technological advancements in echocardiography devices allow through echocardiographic assessment even in small laboratory animals with a rapid heart rate of above 300 beats per minute for the accurate evaluation of cardiac function in rodents as a basic research tool (10-12). In addition, a rat myocardial ischemia/reperfusion (I/R) injury model has recently widely used for the mechanism studies to evaluate new drugs or stem cell therapies (13-16). Previous echocardiographic studies for the evaluation of MI animal models have focused on a relatively late phase of MI as myocardial remodeling is the main subject in MI studies (11, 12, 14, 17). However, I/R injury is a common cause of AMI, and since therapeutic strategies for the prevention of myocardial I/R injury can improve clinical outcomes in patients, it is necessary to assess cardiac function, including left ventricular systolic and diastolic function in the early phase after MI.

In this study, a multi-mode evaluation of myocardial I/R injury, mainly including echocardiographic evaluation of left ventricular diastolic dysfunction in particular in a rat myocardial I/R injury model, was used to evaluate the efficacy studies of new drug development candidates, and metformin and sappanone A were applied.

Metformin is a first-line anti-diabetic agent as directed by the guidelines of the American Diabetes Association (ADA) and the European Association for the Study of Diabetes (EASD) (18). In the clinical studies, the cardio-protective action of metformin cannot be entirely attributed to its anti-hyperglycemic actions (19, 20), and a previous study showed the non-glycemic effects of metformin, such as the potential to improve cardiovascular clinical outcomes, anticancer effects, and longevity (21). In addition, the previous short term mechanism study of metformin was conducted in a rat isoproterenol-induced myocardial infarction model (22). Moreover, since myocardial I/R injury is a common cause of AMI, it is necessary to apply the efficacy study of metformin in a rat myocardial I/R injury model in an early stage of MI and assess the left ventricular diastolic function using echocardiography. Also, the further studies of mechanistic analysis using mRNA sequencing, myocardial infarct size, histopathology were conducted to show the effectiveness of metformin on rat hearts.

Sappanone A, a homoisoflavanone, is a small class of natural products isolated from the heartwood *Caesalpinia sappan* and is known for its anti-inflammatory properties that inhibit nitric oxide (NO) production and the expression of inducible nitric oxide synthase (iNOS and cyclooxygenase-2 (COX-2) using lipopolysaccharide (LPS)-stimulated RAW264.7 cells (23). Also, in the same RAW264.7 cells, sappanone A induces heme oxygenase (HO)-1 protein and simultaneously increases nuclear translocation of the nuclear factor-E2-related factor 2 (Nrf2) and the expression of Nrf2 target genes, including NAD(p)H:quinone oxidoreductase 1 (NQO1) (24). In addition, sappanone A showed inhibitory effect of RANKL-induced osteoclast production in mouse bone marrow macrophages (BMMs), and suppressed inflammation-induced bone loss in a mouse model (25). Myocardial infarction is also inflammation-related disease due to ischemia, and we found that despite its anti-inflammatory effect, there is no evaluation of sappanone A's cardiovascular protective effects *in vivo*. Therefore, in this study, the cardiovascular protective effective of sappanone A on left ventricular systolic and diastolic dysfunction was mainly performed using echocardiography in a rat myocardial I/R injury model. To evaluate the effectiveness of sappanone A in a rat myocardial I/R injury model, we assessed left ventricular function via echocardiography, determined left ventricular infarct size, performed serum cardiac marker

analysis, histopathological examination of rat hearts, and mechanism analysis using mRNA sequencing of left ventricles in rats.

In summary, the purpose of this study was to perform an efficacy assessment of metformin and saipanone A in a rat myocardial I/R injury model induced by transient ligation of the left anterior descending (LAD) artery to determine these cardiovascular protective effects in the early stage of MI and left ventricular dysfunction.

The thesis is composed of three chapters, and the first chapter (Chapter . Preliminary study) explains the background of the establishment of human AMI animal model called rat myocardial ischemia / reperfusion injury model, and methods for evaluating left ventricular systolic and diastolic function using echocardiography. Chapter (Efficacy study of metformin) investigated the efficacy study of metformin in a rat myocardial I/R injury model using echocardiography and its cardioprotective effects on left ventricular diastolic dysfunction at the early stage of MI. Chapter (Efficacy study of saipanone A) conducted efficacy study of saipanone A in a rat myocardial I/R injury model to show the anti-inflammatory effect on early stage of left ventricular dysfunction using echocardiography.

In order to evaluate those efficacy studies, evaluation methods included ultrasound-based assessment of left ventricular systolic and diastolic function, myocardial infarct size using 1% 2,3,5-triphenyltetrazolium chloride (TTC) staining, serum chemistry of cardiac markers, histopathological analysis using hematoxylin and eosin staining and Masson's trichrome staining, and mRNA sequencing data analysis. These results will provide further understanding of the effects of metformin and saipanone A on the development of AMI and help future MI patients in the early stage of cardiovascular disease development.

Chapter □. Preliminary study

1. Materials and Methods

1. 1. Animals

Sprague Dawley rats were purchased from Koatech (Kyungki, South Korea). All rats were housed 3 per cage at the beginning of the study and were fed an autoclaved pellet diet (SAFE + 40RMM; SAFE Diets, Augy, France) *ad libitum*. For the entire experimental period, including the 7-day acclimatization period, animals were housed under the following conditions. Environmental conditions were maintained at a temperature of 22 ± 1 °C, the relative humidity of 50 ± 10 %, 12 h light/dark cycles, illumination at 150-300 Lux, and 10-20 times per hour ventilation. These conditions were monitored every hour for 24 hours and remained within acceptable ranges throughout the study.

1.2. Study design

Sprague Dawley rats (8-week-old adult males, mean weight: 277.40 ± 9.48 g) were randomly divided into sham group (n=15) and myocardial I/R injury group (n=18). All animal experiments were conducted in accordance with the Daegu-Gyeongbuk Medical Innovation Foundation guidelines for the care and use of laboratory animals and approved by the Institutional Animal Care and Use Committee of Daegu-Gyeongbuk Medical Innovation Foundation (DGMIF-16091201-00). A preliminary study was conducted to establish a rat myocardial ischemia reperfusion injury model with 30 % of ischemic lesions and echocardiographic methods to assess left ventricular systolic and diastolic function.



Figure 1. Study design for preliminary study.

1.3. Rat myocardial ischemia/reperfusion injury model

Animals were anesthetized with pentobarbital (60 mg/kg, IP). After anesthetization, rats were intubated and ventilated using a ventilator (Harvard Apparatus Inspira, MA, USA), maintained at a tidal volume of 3.0 mL/kg and a respiratory rate of 60 breaths/min. Intraoperatively, rats were placed on a heated plate and monitored by ECG and a rat myocardial I/R injury model induced a ligation of the left anterior descending (LAD) coronary artery for 30 min.

A 3-cm transverse incision was made in the left fourth intercostal space and a thoracic retractor was placed within the incision. The pericardium was opened to expose the left anterior descending coronary artery (LAD) ligated between the pulmonary cone and the left auricle using 6-0 silk (Figure 2A). MI was confirmed by cyanosis of the apical region of the heart (the paleness of the apical region of the left ventricle) with the elevation of the S-T segment of electrocardiogram (Figure 2B). After 30 min of ischemia through snaring (Figure 2A), the suture of the polyethylene tube was unscrewed to allow reperfusion. The intercostal space was closed with 3-0 white silk suture and the skin incision was closed with 4-0 nylon suture. Remove air using a 21G needle to maintain negative pressure in the chest cavity. After confirming the recovery of peripheral reflexes, extubation and weaning are performed. The sham group were through the same surgical procedure without ligation.

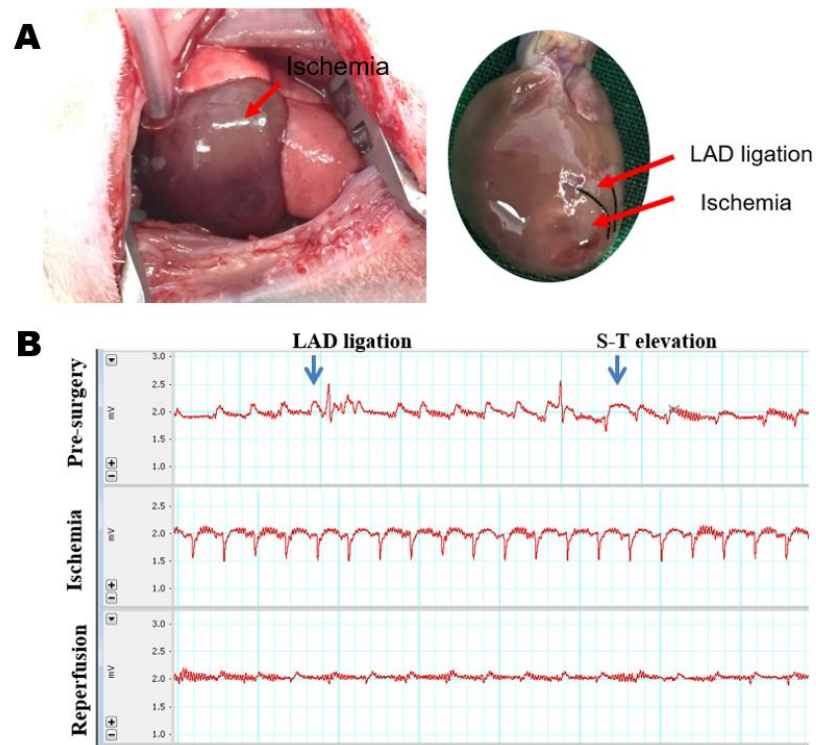


Figure 2 Establishment of rat myocardial I/R injury model. Representative photograph of rat heart (A) and ECG changes (B).

1.4. Echocardiographic analysis

Echocardiography was performed using Vevo2100 (Visual Sonics Inc., ON, Canada) at 2 hours, 1, 3, 7 days after MI induction. Rats were anesthetized with pentobarbital sodium (60 mg/kg, IP) and monitored by ECG in a supine position and body temperature was maintained at 37°C. Echocardiographic parameters follow the American Society of Echocardiography guidelines (1). Image of the left ventricular parasternal short-axis (PSSAX) view at the level of papillary muscle for evaluation of left ventricular systolic function (Figure 3A). In the parasternal short axis (PSSAX) view, images of regional wall motion abnormalities in the LAD area were obtained to detect wall thickness and internal diameters during left ventricular systolic and diastolic phase. In addition, the posterior wall of the left ventricle, the interventricular septum thicknesses, and the left ventricular internal diameter at the diastolic and systolic phase were measured. Ejection fraction (EF), fractional shortening (FS), stroke volume (SV), and cardiac output (CO) were also measured for left ventricular systolic function. To evaluate left ventricular diastolic function, images of apical four-chamber views (Figure 3B) were obtained and E' , E/A , and E/E' were calculated using B-mode, M-mode, Doppler color flow, pulsed wave Doppler, and tissue Doppler.

1.5. Statistical analysis

Values are expressed as mean \pm standard deviation (SD). Statistical analysis was performed using SPSS version 19 (SPSS, Inc., IL, USA). The results for each group were compared with a two-sample t-test and a repeated measure two-factor analysis. Multiple comparisons were performed with Bonferroni correction. The difference was considered statistically significant at $p < 0.05$.

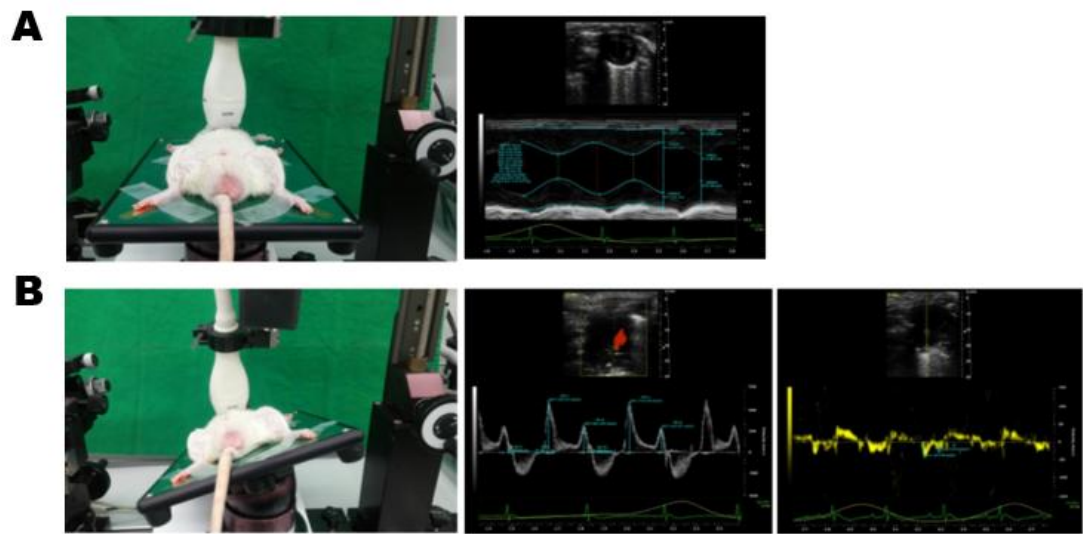


Figure 3. Representative images of echocardiographic evaluation. Positioning for echocardiographic evaluation for left ventricular systolic function using M-mode at parasternal short axis view **(A)** and left ventricular diastolic function using PWD and TDI mode at Apical 4 chamber view **(B)**.

2. Results

2.1. Echocardiographic results

To determine the optimal assessment of left ventricular systolic and diastolic function, echocardiographic data were obtained from M-mode tracings, pulse wave doppler, and tissue doppler imaging (Figure 4) and were summarized in Table 1.

EF and FS, the indices reflecting left ventricular systolic function, were significantly reduced ($P<0.01$) in the MI group compared to the sham group at 2 hours and 1 day. To evaluate left ventricular diastolic function, we measured the peak velocity of the transmitral flow at early filling (E), the early diastolic mitral annular velocity (E') at the medial mitral annulus, and the E/E' ratio, which exhibits relatively high reproducibility in human. The E' values were significantly decreased and the E/E' values were significantly increased in the MI group compared to the sham group ($P<0.01$).

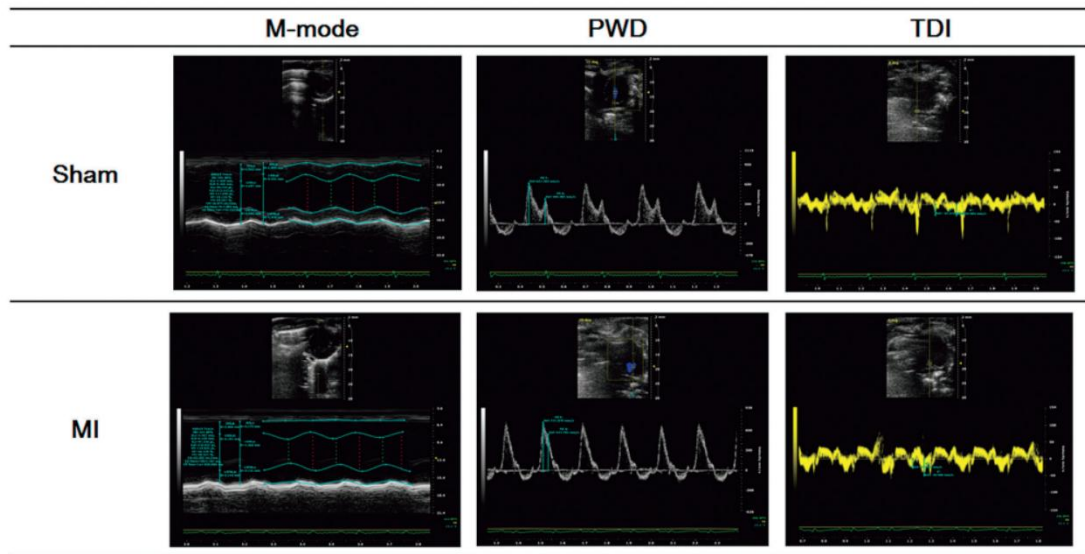


Figure 4. Representative echocardiographic images of rat hearts. Images of the mitral inflow velocity profile determined by pulsed wave doppler mode and tissue doppler mode on day 3. The E' value was significantly decreased and the E/E' value was significantly increased in the MI group compared to the sham group contrary to the similarity of EF and FS values between groups on day 3. PWD: pulse wave doppler; and TDI: tissue doppler imaging.

Table 1. Cardiac function measured by echocardiography of preliminary study

Cardiac function	2 hours		Day 1		Day 3		Day 7	
	Sham	MI	Sham	MI	Sham	MI	Sham	MI
EF (%)	68.82 ± 4.37 ^{ff}	53.71 ± 4.22 ^{**}	56.76 ± 3.18	52.26 ± 3.72 ^{**}	57.39 ± 3.43	54.78 ± 4.27	58.51 ± 3.88	55.91 ± 4.21
FS (%)	39.33 ± 3.50 ^{ff}	28.47 ± 2.67 ^{**}	30.60 ± 2.18	27.59 ± 2.80 ^{**}	31.13 ± 2.36	29.36 ± 2.80	31.99 ± 2.62	30.23 ± 2.81
SV (μl)	110.34 ± 15.32	107.95 ± 13.48	127.87 ± 18.82	124.15 ± 29.90	146.71 ± 19.08	138.14 ± 19.07	159.07 ± 27.52	162.98 ± 23.79
CO (mL/min)	46.52 ± 6.07	46.60 ± 9.45	55.65 ± 7.88	60.21 ± 18.96	57.97 ± 7.87	70.27 ± 32.71	62.61 ± 8.48	62.07 ± 11.55
LVIDd (mm)	5.59 ± 0.43	6.22 ± 0.44 ^{**}	6.44 ± 0.56	6.75 ± 0.67	6.91 ± 0.45	6.89 ± 0.49	7.05 ± 0.59	7.33 ± 0.49
LVIDs (mm)	3.53 ± 0.42	4.46 ± 0.46 ^{**}	4.56 ± 0.50	4.86 ± 0.51	4.78 ± 0.41	4.92 ± 0.51	4.86 ± 0.53	5.14 ± 0.55
IVSd (mm)	1.89 ± 0.30	1.83 ± 0.25	1.79 ± 0.24	1.83 ± 0.19	1.83 ± 0.32	1.79 ± 0.23	1.78 ± 0.24	1.78 ± 0.16
IVSs (mm)	2.75 ± 0.52	2.52 ± 0.32	2.45 ± 0.43	2.48 ± 0.24	2.52 ± 0.35	2.47 ± 0.42	2.54 ± 0.27	2.54 ± 0.32
LVPWd (mm)	2.30 ± 0.31	2.30 ± 0.28	2.07 ± 0.30	1.99 ± 0.22	1.94 ± 0.17	1.94 ± 0.17	1.88 ± 0.37	1.87 ± 0.13
LVPWs (mm)	3.08 ± 0.34	2.96 ± 0.41	2.65 ± 0.41	2.67 ± 0.17	2.63 ± 0.30	2.70 ± 0.20	2.51 ± 0.52	2.64 ± 0.17
E'	35.03 ± 3.88	28.26 ± 2.37 ^{**}	33.47 ± 3.56	27.36 ± 2.83 ^{**}	32.75 ± 3.89	27.64 ± 3.56 ^{**}	34.08 ± 2.52	26.75 ± 1.78 ^{**}
E/A	1.50 ± 0.25	1.55 ± 0.16	1.51 ± 0.24	1.39 ± 0.27	1.40 ± 0.19	1.50 ± 0.18	1.34 ± 0.20	1.42 ± 0.28
E/E'	21.16 ± 0.85	26.71 ± 0.92 ^{**ff}	20.99 ± 1.10	26.49 ± 0.93 ^{**ff}	21.20 ± 1.18	25.88 ± 0.94 ^{**}	20.86 ± 0.66	25.35 ± 0.85 ^{**}

EF: ejection fraction; FS: fractional shortening; SV: stroke volume; CO: cardiac output; LVIDd: left ventricular internal diameter at diastole; LVIDs: left ventricular internal diameter at systole; IVSd: interventricular septal thickness at diastole; IVSs: interventricular septal thickness at systole; LVPWd: left ventricular posterior wall thickness at diastole; LVPWs: left ventricular posterior wall thickness at systole; E': early diastolic tissue Doppler velocity; E/A: the ratio of the early E to late (A) ventricular filling velocities; and E/E': the ratio of the early E to early diastolic tissue Doppler velocities. ** indicates a significant difference compared to rats of the sham group by two sample t-test ($P < 0.01$). ^{ff} indicates a significant difference by multiple comparison with Bonferroni correction ($P < 0.01$).

3. Discussion

In this study, rat myocardial ischemia reperfusion (I/R) injury model was established and the main evaluation methods for the left ventricular systolic diastolic dysfunction was echocardiography. Significant decreases in ejection fraction (EF) and fractional shortening (FS) after myocardial infarction (MI) indicate MI induction as typical ischemic changes that have been reported. (11, 26)

Cardiovascular disease remains the most important health concerns in developed countries and continues to be a major issue in prevention. In addition, acute myocardial infarction (AMI) remains one of the leading causes of increased cardiovascular morbidity and mortality worldwide (1, 3). Metabolic syndrome causes abnormal endothelial function, increased vascular inflammation, and dyslipidemia along with insulin resistance and hyperglycemia, all of which act as factors aggravating cardiovascular disease. Therefore, metabolic syndrome patients are known to have a high risk of cardiovascular disease and a high mortality rate (27). Abdominal obesity and intrinsic factors play the most important role in the induction of insulin resistance, chronic inflammation, progression to metabolic syndrome, which is due to various factors such as cytokines and inflammatory cells, resulting in dysfunction of vascular endothelial cells, dyslipidemia, and hyperglycemia. It also causes clotting disorders and inflammatory reactions, leading to atherosclerosis and cardiovascular disease. Currently, obesity is changing like a pandemic that is spreading across the country, and more than a quarter of the population is affected in the United States. A recent study published in Korea also reported that obesity increased the mortality from cardiovascular disease (28). Moreover, as major risk factors for vascular disease such as diabetes and hypercholesterolemia increase, the incidence of ischemic heart disease may increase sooner or later, especially in South Korea (29-31). Not all metabolic syndromes have the same risk, it is considered inflammation of endothelial cells as the most important requirement, and the inflammatory biomarker hsCRP may be helpful as a risk factor predicting cardiovascular disease in metabolic syndrome. An increase in hsCRP can lead to an exacerbation of cardiovascular disease in patients with metabolic syndrome and is combined with a decrease in systemic fibrinolytic ability and hyperinsulinemia in human (32).

In human MI patients, left ventricular diastolic dysfunction during acute MI is one of the important indicators of poor surgical outcomes and recurrences (7). Echocardiography is useful for detecting LV dysfunction and is the best prognostic indicator for human MI patients (4, 6). In clinical cases, patients with LV diastolic dysfunction or diastolic heart failure with

normal EF make up nearly one-third of elderly patients undergoing surgery. Patients with poor ventricular diastolic function tend to have worse postoperative outcomes than patients with poor ventricular systolic function alone. In the current study, even in rodents, recent technological advances have made it possible to use echocardiography for an accurate assessment of cardiac function (10-12).

As an animal model of transient myocardial infarction, the rat myocardial I/R injury model is the most commonly used animal model for AMI, and this model is widely used in the study of *in vivo* mechanisms with high reproducibility of animal models. In this study, the rat myocardial I/R injury model was successfully induced by transient ligation of LAD. Using echocardiography, rats in the MI group found that EF and FS values decreased, E' values decreased and E/E' ratio increased, reflecting LV systolic dysfunction, indicating LV diastolic dysfunction similar to human MI.

Transmitral inflow (E) occurs during the rapid filling phase in early diastole with sensitivity to preload and reduced early diastolic mitral annular velocity (E') usually the earliest manifestation of diastolic dysfunction in human with its less sensitivity to preload and decreases at all stages of diastolic dysfunction (5). In addition, E' reflects the myocardial velocity (33), not blood flow velocity, and indicates early active diastolic relaxation of the left ventricle, but is not compliant. The E' and E/E' values reflect the global function of the LV and are relatively independent of LV systolic function, heart rhythm abnormalities, and LV hypertrophy (34, 35), so the E/E' ratio is an acceptable reflection of mean left atrial pressure and, thus, LV filling pressure (36). Furthermore, in humans, an increase in LV filling pressure is a key indicator of poor outcomes such as mortality, morbidity, and length of stay in the ICU/hospital (8, 37). Therefore, evaluation of left ventricular diastolic function is important in patients with myocardial infarction, and by confirming this, it becomes a good indicator for predicting the prognosis and evaluating the efficacy of the development of new drug effective for heart disease.

Chapter . Efficacy study of metformin

1. Materials and Methods

1. 1. Animals

Sprague Dawley rats were purchased from Koatech (Kyungki, South Korea); all rats were housed three per cage and fed an autoclaved pellet diet (SAFE + 40RMM; SAFE Diets, Augy, France) *ad libitum*. The environmental conditions were maintained using a temperature of 22 ± 1 °C, relative humidity of 50 ± 10 %, a 12-hour light/dark cycles, lighting of 150-300 Lux, ventilation 10-20 times per hour. These conditions were monitored every hour for 24 hours and maintained within acceptable range throughout the study.

1. 2. Study design

Sprague Dawley rats (8-week-old adult males, mean weight: 287.90 ± 6.62 g) were randomly divided into 4 groups (6 rats/group) as follows: A) Sham group, B) MI group, C) Sham+MET group, D) MI+MET group. The rats in groups A and B received reverse osmosis (RO) drinking water, and the rats in groups C and D were treated with 200 mg/kg metformin (Sigma-Aldrich, St Louis, MO, USA, Figure 5) dissolved in RO drinking water by daily oral administration for 11 days (3 days before the surgery to 7 days post-surgery). The study design (Figure 6) was approved by the Institutional Animal Care and Use Committee of Daegu-Gyeongbuk Medical Innovation Foundation (DGMIF-19022001-00).

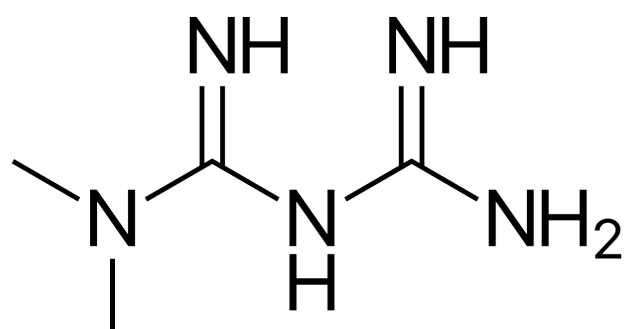


Figure 5. Chemical structure of metformin.

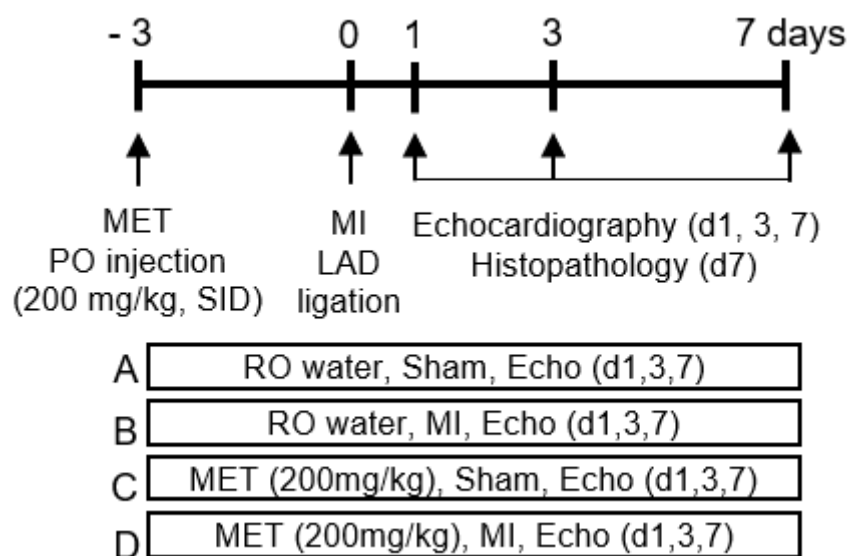


Figure 6. Study design for the efficacy study of metformin.

1.3. Rat myocardial ischemia/reperfusion injury model

Animals were anesthetized with alfaxalone (50 mg/kg, IP) and xylazine (5 mg/kg, IP). After anesthesia, rats were intubated and ventilated using a respirator (Harvard Apparatus VentElite, MA, USA) and maintained at a tidal volume of 3.0 mL/kg and a respiratory rate of 60 breaths/min. Intraoperatively, the rats were placed on a heating plate at 37°C and monitored by ECG and the rat myocardial I/R injury model was induced by ligation of the left anterior descending (LAD) coronary artery for 30 min.

1.4. Echocardiographic analysis

Echocardiography was performed using Vevo2100 (Visual Sonics Inc., ON, Canada) on 1, 3, and 7 days after MI induction. Rats were anesthetized with alfaxalone (50 mg/kg, IP) and xylazine (5 mg/kg, IP), monitored by ECG and maintained body temperature at 37°C in the supine position. Echocardiographic parameters follow the American Society of Echocardiography guidelines. As described preliminary study, left ventricular systolic and diastolic function was evaluated by echocardiography using B-mode, M-mode, Dopper color flow, pulsed wave Doppler, and tissue Doppler.

1.5. Myocardial infarct size

After echocardiographic evaluation on day 7 after MI surgery, the rats were euthanized under isoflurane anesthesia and their hearts were excised. Following reperfusion with 0.9% normal saline, the hearts were sectioned into 2 mm transverse slices and the slices were immersed in 1 % solution of 2,3,5-triphenyltetrazolium chloride (TTC, Sigma, St. Louis, MO, USA) at 37 °C for 15 min in the dark. The images of these slices were obtained using a digital camera. The infarct area and total area of the left ventricles were analyzed by the Image J software (National Institutes of Health, Bethesda, MA, USA).

1.6. Histopathological analysis

After echocardiography on day 7 after MI surgery, the rats were euthanized under isoflurane anesthesia and their hearts were excised. For the histopathological analysis, the heart tissues were fixed in 10% neutral buffered formalin (BBC Biochemicals, Mount Vernon, WA, USA). Samples were prepared from formalin fixed tissue for histopathological analysis by fixation, dehydration, and staining using a tissue processor (Thermo Fisher Scientific, Inc., Runcorn, UK). Paraffin-embedded tissue blocks were cut to a thickness of 4 μm and mounted on glass slides. Staining was performed using an autostainer (Dako Coverstainer; Agilent, Santa Clara, CA, USA) with hematoxylin (YD-Diagnostics, Kyungki, Korea) and eosin (BBC Biochemicals, Mount Vernon, WA, USA). After staining, all slides including short axis area with papillary muscle and apex area of the left ventricle were scanned with a slide scanner (Pannoramic SCAN II; 3DHISTECH, Budapest, Hungary) and captured with a slide viewer (CaseViewer; 3DHISTECH). Histopathological examination was performed in a blinded manner by two investigators.

In addition, to assess fibrosis, tissue sections were stained using a Masson's trichrome staining kit according to the manufacturer's instructions (ScyTek Laboratories, West Logan, UT, USA). After staining, the slides were scanned with a slide scanner (Pannoramic SCAN II; 3DHISTECH, Budapest, Hungary) and captured with a slide viewer (CaseViewer; 3DHISTECH). Morphometric analysis of fibrosis was performed using Image J software (National Institutes of Health, Bethesda, MA, USA). In the MT staining, red and blue were designated, and the blue area (collagen fiber) was measured by comparing it with the total red area.

1.7. mRNA sequencing and data analysis

Total RNA was obtained from left ventricular tissues of three rat groups (Sham group, MI group, and MI + MET group) using Trizol reagent (Invitrogen Life Technologies, Grand Island, NY) for RNA sequencing. Total RNA integrity was analyzed using an Agilent Bioanalyzer. RNA integrity values for all of the samples were greater than 7. Poly (A) mRNA isolation from total RNA and fragmentation was performed using the Illumina TruSeq Stranded mRNA sample prep kit according to the manufacturer's instructions. Adaptor ligated libraries were sequenced using an Illumina NovaSeq 6000 (Bioneer, Korea). In each condition, mRNA-sequencing analysis was performed on two biological replicates obtained from independent rats. The resulting read sequences for each sample were aligned to the *Rattus_norvegicus* reference genome (Rnor_6.0) with the default parameters (38) using STAR software (version 2.7). After alignment, HTseq was used to calculate the number of reads mapped to the gene features (GTF file of Rnor_6.0.90) (39). The read counts for the samples in each condition were then normalized using the TMM (trimmed mean of M-values) normalization of the edgeR package (40) and converted to log₂-values.

1.8. Identification of differentially expressed genes (DEGs)

A previously reported statistical hypothesis test was performed to identify DEGs between three conditions (41). Briefly, for each gene, T-statistic values were calculated using Student's t-test in two comparisons (MI group versus Sham group or MI + MET group versus MI group). In each comparison, the empirical distribution of T-statistic values for the null hypothesis (i.e., the genes are not differentially expressed) was estimated by performing all possible combinations of random permutations of the samples. Using the estimated empirical distributions, adjusted P-values for Student's t-test for each gene were computed. Finally, DEGs were identified as having adjusted p -values ≤ 0.05 and absolute log₂-fold-changes ≥ 0.58 (1.5-fold). To identify cellular processes represented by DEGs, an enrichment analysis of GOBPs was performed using DAVID software (42) and the GOBPs with a P-value < 0.05 were selected as the processes enriched by DEGs.

1.9. Statistical analysis

Values are expressed as mean \pm standard deviation (SD). ANOVA with Tukey's multiple comparisons analyses were performed by using GraphPad Prism 6 (GraphPad Software Inc., La Jolla, CA, USA). The fold changes in biomarker expression levels are expressed compared to those at the baseline or vehicle control. $P < 0.05$ was considered statistically significant.

2. Results

2.1. Body weight and heart changes

Total body weight changes (%) over 7 days are shown in Figure 7A and 7B. The weight difference between the MI group and the MI+MET group (induced MI) was lower than that of the Sham and Sham+MET groups on day 7. In particular, there were significant differences between groups MI and the Sham+MET versus Sham group ($p < 0.05$ and $p < 0.01$, respectively). As can be seen in Figures 7C and 7D, as a result of evaluating heart weight changes on day 6 and heart weight/body weight (%) on day 7, relative heart weight (%) was highest in the MI+MET group, and significant differences were seen between Sham+MET group and MI group ($p < 0.01$).

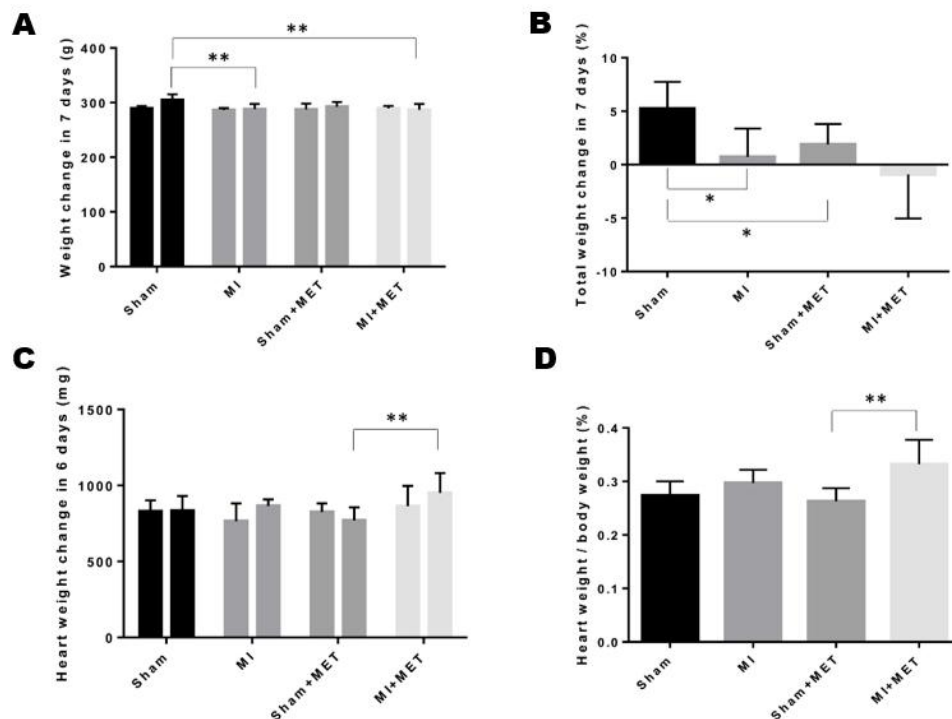


Figure 7. Body weight and heart changes. (A) Body weight change and **(B)** Differences in total body weight change in 7 days. **(C)** Heart weight change in 6 days. **(D)** Relative heart weight/body weight (%) on day 7.

* indicates a statistically significant difference compared with the Sham group by two-sample *t*-test ($p < 0.05$). ** indicates a statistically significant difference compared with the Sham group ($p < 0.01$) by two-tailed unpaired *t*-test (B, D) and Tukey's multiple comparisons test (A, C).

MET: metformin; and MI: myocardial infarction.

2.2. Echocardiographic results

Echocardiographic results are summarized in Figure 8 and Table 2. Representative echocardiographic images are shown in Figure 9. The EF and FS values (reflecting LV systolic function) in the MI group decreased significantly compared to the values in the Sham group during the entire experiment. Metformin administration improved left ventricular systolic function, and the rats in MI+MET group showed a significant increase in EF and FS values on day 3 and 7 compared to the MI group. The E' value of the medial annulus (reflecting early active diastolic relaxation of the LV, an indicator of left ventricular diastolic dysfunction) decreased significantly in the MI group compared to the Sham group over the entire experimental period. This means that left ventricular diastolic dysfunction did not recover 7 days after MI surgery. However, in the Sham+MET and MI+MET groups, the E' values were significantly different until day 3, but not on day 7. This means that metformin administration restored some of the left ventricular diastolic function by day 7. In addition, the E/E' ratio reflects the left atrial pressure to indicate the left ventricular filling pressure, and the elevated value is an important indicator of poor prognosis in humans. In this experiment, the E/E' ratio varied significantly by day 7 in the Sham and MI groups, which means that left ventricular diastolic dysfunction did not recover during the entire experiment. The difference between the MI group and the MI+MET group showed the effect of metformin administration and was significant throughout the experiment. In addition, the comparison of group Sham+MET and MI+MET showed no significant differences between the Sham and MI groups during the study period. This indicates that metformin administration can prevent left ventricular diastolic dysfunction due to MI, especially in the early phase.

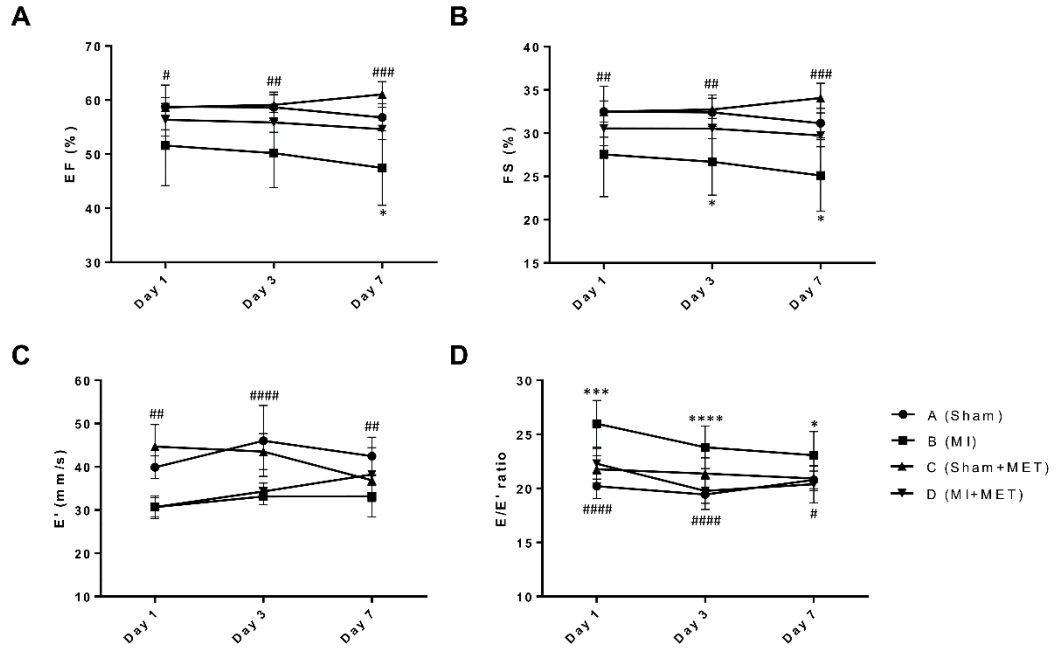


Figure 8. Echocardiographic results. (A) Ejection fraction, EF; (B) Fractional shortening, FS; (C) Early relaxation velocity on tissue doppler, E'; (D) E/E' ratio of diastolic function. EF and FS determined by M-mode imaging reflects LV systolic dysfunction; the E' and E/E' ratio determined by pulse wave doppler and tissue doppler imaging reflects LV diastolic dysfunction.

* $p < 0.05$, *** $p < 0.001$, ***** $p < 0.0001$ between group B and D; # $p < 0.05$, ## $p < 0.01$, ### $p < 0.001$, #### $p < 0.0001$ between group A and D by Dunnett's multiple comparisons test.

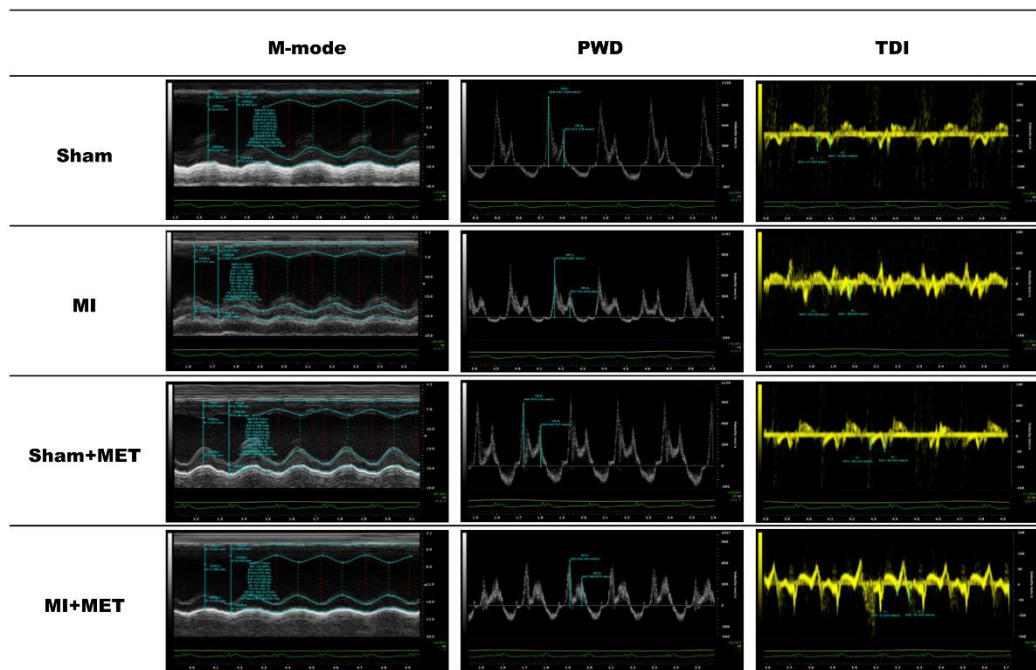


Figure 9. Representative echocardiographic imaging of rat hearts. Metformin administration significantly improved LV diastolic function on day 3 after MI surgery.

PWD: Pulse Wave Doppler; and TDI: Tissue Doppler Imaging.

Table 2. Cardiac function measured by echocardiography of metformin efficacy study

Cardiac function	Day 1				Day 3				Day 7			
	Sham	MI	Sham +MET	MI+M ET	Sham	MI	Sham +MET	MI+M ET	Sham	MI	Sham +MET	MI +MET
EF, %	58.79 ± 1.65	51.60 ± 7.43	58.64 ± 4.14	56.36 ± 3.01	58.65 ± 2.38	50.17 ± 6.37	59.12 ± 2.37	55.86 ± 1.82	56.79 ± 2.52	47.44 ± 6.92	61.04 ± 2.39	54.63 ± 1.91
FS, %	32.52 ± 1.22	27.55 ± 4.90	32.48 ± 2.94	30.56 ± 2.00	32.41 ± 1.65	26.70 ± 3.86	32.73 ± 1.70	30.54 ± 1.18	31.16 ± 1.71	25.11 ± 4.13	34.70 ± 1.72	29.73 ± 1.31
SV, µl	237.16 ± 25.70	162.13 ± 20.91	162.97 ± 13.01	163.64 ± 14.13	228.59 ± 19.43	185.49 ± 22.62	227.65 ± 2037	218.79 ± 18.72	235.95 ± 24.19	208.30 ± 21.03	222.30 ± 26.28	247.02 ± 29.44
CO, mL/min	62.42 ± 7.03	50.42 ± 13.71	63.80 ± 9.31	55.77 ± 7.38	60.82 ± 7.43	48.30 ± 8.02	63.81 ± 5.59	69.43 ± 10.22	60.58 ± 6.73	63.23 ± 23.69	56.10 ± 9.15	63.17 ± 8.30
LVIDd, mm	8.38 ± 0.31	7.60 ± 0.53	8.50 ± 0.35	7.36 ± 0.33	8.33 ± 0.41	8.30 ± 0.56	8.36 ± 0.39	8.38 ± 0.32	8.58 ± 0.54	8.81 ± 0.85	8.08 ± 0.52	8.92 ± 0.39
LVIDs, mm	5.70 ± 0.31	5.46 ± 0.73	5.89 ± 0.51	5.11 ± 0.49	5.60 ± 0.36	6.00 ± 0.84	5.73 ± 0.28	5.82 ± 0.29	5.92 ± 0.58	6.74 ± 0.91	5.53 ± 0.43	6.35 ± 0.34
IVSd, mm	1.44 ± 0.17	1.51 ± 0.16	1.41 ± 0.16	1.68 ± 0.24	1.39 ± 0.13	1.29 ± 0.05	1.37 ± 0.15	1.47 ± 0.24	1.40 ± 0.21	1.49 ± 0.50	1.38 ± 0.12	1.45 ± 0.15
IVSs, mm	2.30 ± 0.24	1.98 ± 0.22	2.18 ± 0.15	2.48 ± 0.30	2.22 ± 0.24	1.94 ± 0.28	2.32 ± 0.24	2.44 ± 0.43	2.33 ± 0.32	2.10 ± 0.37	2.21 ± 0.22	2.26 ± 0.44
LVPWd, mm	1.58 ± 0.17	1.60 ± 0.17	1.58 ± 0.15	1.83 ± 0.09	1.50 ± 0.09	1.56 ± 0.04	1.53 ± 0.11	1.66 ± 0.14	1.53 ± 0.15	1.63 ± 0.14	1.57 ± 0.09	1.64 ± 0.09
LVPWs, mm	2.36 ± 0.19	2.27 ± 0.19	2.33 ± 0.19	2.56 ± 0.18	2.50 ± 0.19	2.23 ± 0.17	2.29 ± 0.18	2.49 ± 0.16	2.27 ± 0.25	2.11 ± 0.18	2.39 ± 0.20	2.41 ± 0.12
E', mm/s	39.90 ± 2.63	30.67 ± 2.24	44.70 ± 5.09	30.67 ± 2.59	46.00 ± 8.18	33.14 ± 1.89	43.53 ± 4.14	34.31 ± 1.91	42.49 ± 4.35	33.20 ± 4.78	36.91 ± 1.27	38.21 ± 6.22
E/A	1.69 ± 0.25	1.92 ± 0.24	2.08 ± 0.80	1.46 ± 0.26	2.16 ± 0.66	2.34 ± 0.41	1.69 ± 0.29	1.56 ± 0.30	2.58 ± 0.90	1.81 ± 0.42	1.54 ± 0.17	2.05 ± 1.49
E/E'	20.20 ± 1.15	25.99 ± 2.15	21.77 ± 1.27	22.29 ± 1.42	19.44 ± 1.39	23.81 ± 1.97	21.37 ± 1.46	19.77 ± 1.15	20.79 ± 0.82	23.08 ± 2.18	20.93 ± 1.14	20.39 ± 1.72

EF, ejection fraction; FS, fractional shortening; SV, stroke volume; CO, cardiac output; LVIDd, left ventricular internal diameter at diastole; LVIDs, left ventricular internal diameter at systole; IVSd, interventricular septal thickness at diastole; IVSs, interventricular septal thickness at systole; LVPWd, left ventricular posterior wall thickness at diastole; LVPWs, left ventricular posterior wall thickness at systole; E', early diastolic tissue doppler velocity; E/A, the ratio of the early (E) to late (A) ventricular filling velocities; E/E', the ratio of the early (E) to early diastolic tissue Doppler velocities.

* indicates a statistically significant difference by multiple comparison with Tukey correction ($p < 0.05$). ** indicates a statistically significant difference by multiple comparison with Tukey correction ($p < 0.01$).

2.3. Myocardial infarct size

Representative gross morphology of representative cardiac tissue sections stained with 1% TTC and infarct size is shown in Figure 10. Myocardial infarct size decreases in group D (MI + MET: 24.45 ± 5.19) compared with group B (MI: 33.05 ± 6.15). However, there was no statistical significance.

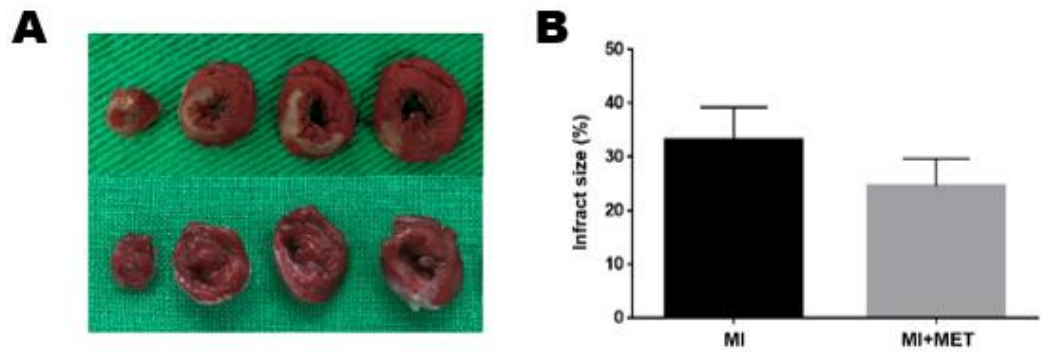


Figure 10. Protective effect of metformin on myocardial infarct size. (A) Representative gross photogram of left ventricle slices with 1% TTC staining and **(B)** Myocardial infarct size.

2.4. Histopathological results

Representative photomicrographs of tissue sections stained with hematoxylin and eosin (Figure 11A) and Masson's trichrome (Figure 11B) are shown in Figure 11. Continued coagulative necrosis, inflammatory cells infiltration and endocardial fibrosis are shown in the hematoxylin and eosin-stained slides. Masson's trichrome staining shows areas of marked fibroblast and collagen deposition. These histopathologic scores are shown in Table 3 and Table 4. In the apex area, metformin administration improved the advanced lesion with statistical significance. Figure 12A and 12B show the collagen fiber area in the LAD ligation area of the LV (parasternal SAX area with papillary muscle) and apex area. The degree of fibrosis in both the SAX and apex regions in MI group (18.42 ± 3.59 , $n = 3$; 23.72 ± 4.06 , $n = 3$, in SAX and apex, respectively) tended to be higher than that seen in MI+MET group (10.80 ± 6.61 , $n = 3$; 17.23 ± 12.49 , $n = 3$, respectively).

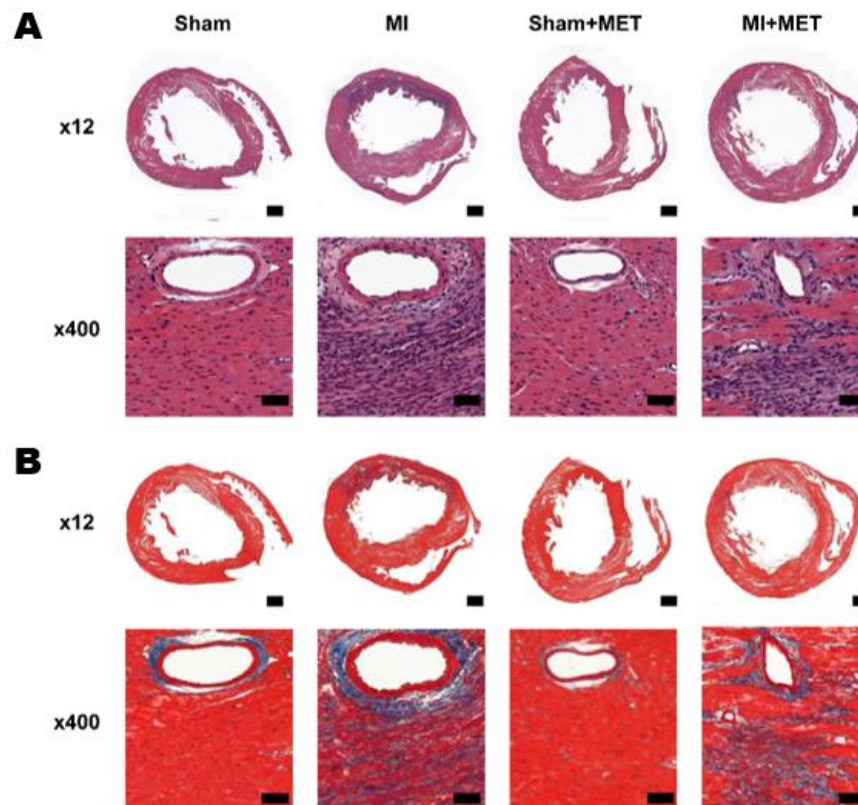


Figure 11. Representative histopathological photomicrographs of rat hearts. (A) Hematoxylin & eosin and (B) Masson's trichrome staining on day 7 (scale bar: 1000 μm , 50 μm).

Table 3. Incidence of histopathological changes in the rat hearts.

Histopathological Change	MI		MI + MET	
	Apex	SAX	Apex	SAX
Lesions (<i>n</i>)	3	3	3	3
Coagulation necrosis, myocardial	3.33 ± 0.58	3.33 ± 0.58	2.67 ± 0.58	2.67 ± 0.58
Inflammatory cells infiltration, epicardial	2.33 ± 0.58	2.67 ± 1.15	2.00 ± 1.00	1.67 ± 0.58
Inflammatory cells infiltration, myocardial	3.33 ± 0.58	3.67 ± 0.58	2.67 ± 0.58	3.33 ± 0.58
Inflammatory cells infiltration, endocardial	2.33 ± 0.58	1.67 ± 0.58	1.33 ± 0.58	1.33 ± 0.58
Fibrosis, epicardial	2.67 ± 1.15	2.33 ± 1.53	2.33 ± 1.15	2.00 ± 1.00
Fibrosis, myocardial	3.67 ± 0.58	3.67 ± 0.58	2.67 ± 0.58	2.33 ± 0.58
Fibrosis, endocardial	2.33 ± 0.58	2.00 ± 1.73	1.67 ± 1.15	1.00 ± 0.00
Total	2.86 ± 0.57	2.76 ± 0.81	* 2.19 ± 0.54	2.05 ± 0.80

Grading of histopathological changes in the rat left ventricle SAX with papillary muscle and apex area tissue. Grades 1, 2, 3 and 4 show minimal, slight, moderate, and severe pathological changes, respectively. Values are mean ± standard deviation (*n* = 3). * *p* < 0.05 indicates a statistically significant difference by two-tailed unpaired t-test compared with the MI group.

Table 4. Results of individual histopathology scoring. Grading of histopathological changes in the rat left ventricle SAX with papillary muscle and apex area tissue. Grades 1, 2, 3 and 4 show minimal, slight, moderate, and severe pathological changes, respectively.

Lesions	MI										MI+MET									
	Apex					SAX with papillary muscle					Apex					SAX with papillary muscle				
	1	2	3	AVG	SD	1	2	3	AVG	SD	1	2	3	AVG	SD	1	2	3	AVG	SD
Coagulation necrosis, myocardial	3	4	3	3.33	0.58	3	4	3	3.33	0.58	3	2	3	2.67	0.58	3	2	3	2.67	0.58
Inflammatory cells infiltration, epicardial	3	2	2	2.33	0.58	4	2	2	2.67	1.15	2	1	3	2.00	1.00	1	2	2	1.67	0.58
Inflammatory cells infiltration, myocardial	3	4	3	3.33	0.58	4	4	3	3.67	0.58	3	2	3	2.67	0.58	4	3	3	3.33	0.58
Inflammatory cells infiltration, endocardial	3	2	2	2.33	0.58	2	2	1	1.67	0.58	1	1	2	1.33	0.58	2	1	1	1.33	0.58
Fibrosis, epicardial	4	2	2	2.67	1.15	4	1	2	2.33	1.53	3	1	3	2.33	1.15	2	1	3	2.00	1.00
Fibrosis, myocardial	4	4	3	3.67	0.58	4	4	3	3.67	0.58	3	2	3	2.67	0.58	2	2	3	2.33	0.58
Fibrosis, endocardial	3	2	2	2.33	0.58	4	1	1	2.00	1.73	1	1	3	1.67	1.15	1	1	1	1.00	0.00
Total				2.86	0.57				2.76	0.81				* 2.19	0.54				2.05	0.80

* $p < 0.05$ indicates a statistically significant difference by two-tailed unpaired t-test compared with the MI group.

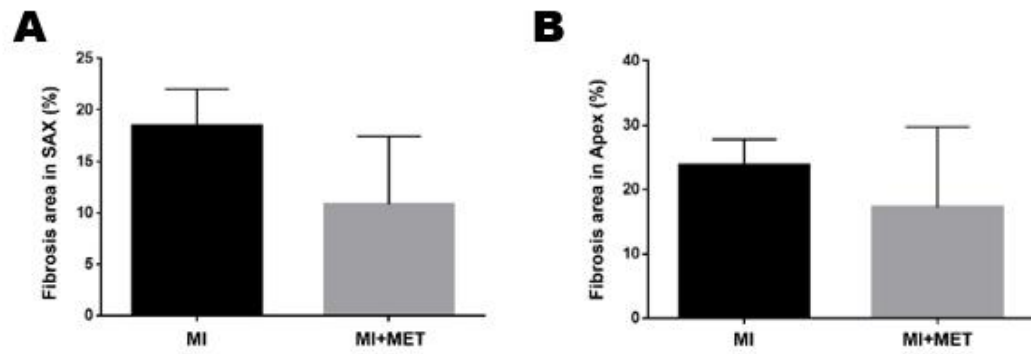


Figure 12. The degree of fibrosis. (A) Degree of fibrosis (%) in SAX (short-axis region with papillary muscle) and **(B)** Apex region (n = 3 in both groups).

2.5. mRNA sequencing and data analysis

To investigate the genes affected by metformin, gene expression profiling of groups A (Sham), B (MI) and D (MI + MET) was performed and a total of 2924 differentially expressed genes (DEGs) were identified (Materials and Methods) from the comparisons (Figure 13A and Table 5): 2501 DEGs (1332 up-regulated and 1169 down-regulated) in MI samples, compared to the Sham controls (group B versus group A); and 1026 DEGs (493 up-regulated and 533 down-regulated) in the metformin-treated MI samples, compared to MI (group D versus group B). Of the 2924 DEGs, 603 (20.6%) were shared between the two comparisons, while the other DEGs were uniquely changed in individual comparisons.

To identify reliable set of metformin-related genes, DEGs were classified into 8 clusters (C1-8) based on their differential expressions in the two comparisons (Figure 14 and Table 5). Among the clusters, C2 (359 genes) and C3 (236 genes) showed up- and down-regulation in their abundances by MI, respectively, but inhibition of the alterations by treatment of metformin (Figure 13B). C1 and C4 showed up- and down-regulation by MI, respectively, but inhibition of the alteration by treatment of metformin was not statistically significant (Figure 13B). Here, we aimed to identify potential therapeutic targets to metformin for myocardial I/R. Thus, we focused on C2 and C3.

Enrichment analysis of gene ontology biological processes (GOBPs) was performed using DAVID software to understand cellular processes represented by these two clusters (C2 and C3). The analysis showed that the genes of C2 were mainly involved in immune/inflammation responses and apoptosis (Figure 13C), whereas C3 was in glucose and fatty acid metabolism and cardiovascular system development (Figure 13D). In particular, the genes involved in immune/inflammation responses were strongly recovered from expression by metformin ($p < 0.01$) (Figure 13C and 13E).

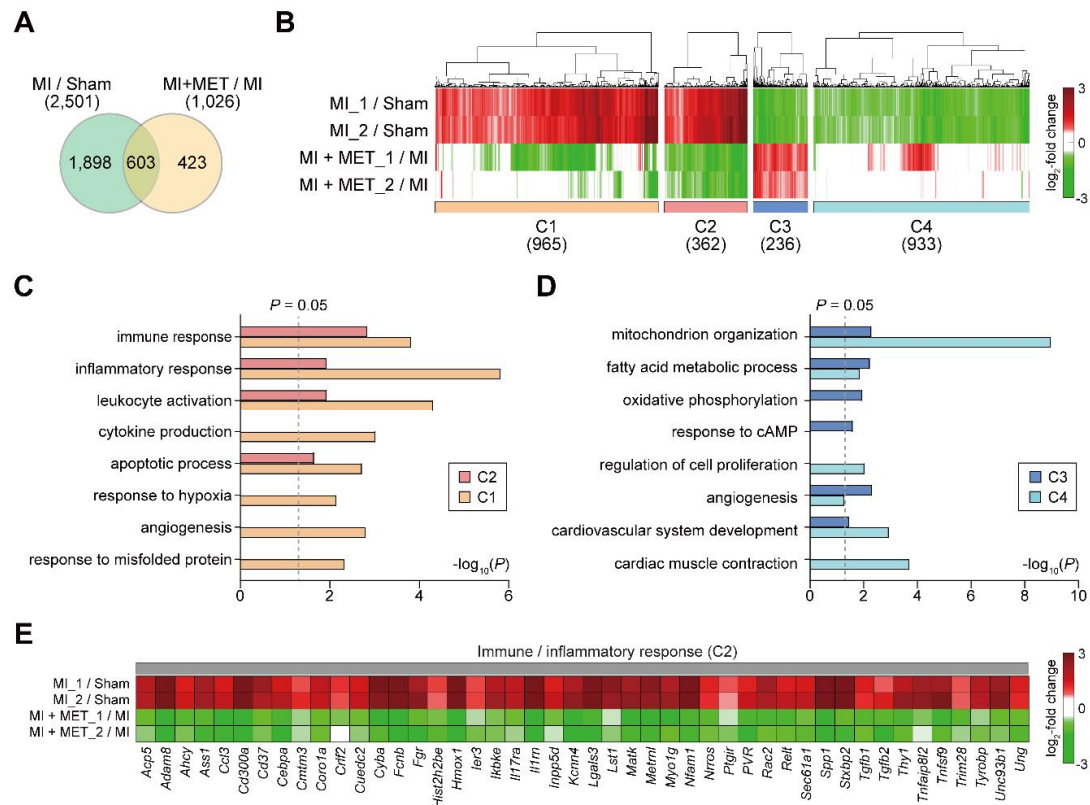


Figure 13. Cellular processes affected by metformin treatment. (A) Relationships among DEGs from the two comparisons (Group B/Group A and Group D/Group B). (B) Clusters (C1-4) of genes affected by metformin. Red and green denote up- and down-regulation, respectively. Color bar means gradient of log₂-fold-changes. Numbers of DEGs in the comparisons of clusters are denoted in parenthesis (A–B). (C–D) Cellular processes enriched by DEGs in C1-4. X-axis, –log₁₀(P) where p is the enrichment p -value calculated in DAVID software. (E) DEGs in C2 involved in the immune/inflammatory response.

Group	MI / Sham	MI+MET / MI	Number of genes
1			965
2			362
3			236
4			933
5			252
6			171
7			5
8			0
Total			2,924

Figure 14. 8 clusters of the DEGs. Colors represent the increase (red) and decrease (green) of mRNA expression levels. The number of the genes in each cluster was shown. Groups 1-4 with the four largest sizes were defined as four major groups in Figure 13B.

Table 5. 2,924 DEGs. For each DEG, gene symbol and description, adjusted P-value, log2-fold-change of mRNA levels between two comparisons are shown. The genes in cluster 1-8 are also denoted.

Ind	GeneID	Sym	Description	Clust	MI vs. Sham				MI + Met vs. MI			
					adjusted P-value	Fold-change (log ₂ -value)	Differentially expressed gene (DEG)	up/down-DEG	adjusted P-value	Fold-change (log ₂ -value)	Differentially expressed gene (DEG)	up/down-DEG
1	ENSRNOG00000023013	March3	membrane associated ring-CH-type finger 3	1	0.043952417	1.172982237	1	1	0.484174678	0.012531641	0	0
2	ENSRNOG00000029912	Septin5	septin 5	1	0.033310117	1.208480005	1	1	0.099876146	-1.318325801	0	0
3	ENSRNOG00000009736	A4galt	alpha 1,4-galactosyltransferase	1	0.043274809	1.567891043	1	1	0.188459279	-0.941216189	0	0
4	ENSRNOG00000013445	Aaas	aladin WD repeat nucleoporin	1	0.00025943	1.420930901	1	1	0.05152624	-1.05076529	0	0
5	ENSRNOG00000050057	Abca3	ATP binding cassette subfamily A member 3	1	0.021991173	1.180119251	1	1	0.14596283	-0.430361073	0	0
6	ENSRNOG00000012892	Abca4	ATP binding cassette subfamily A member 4	1	0.01177436	0.891108993	1	1	0.234929522	0.532144168	0	0
7	ENSRNOG00000002948	Abcc3	ATP binding cassette subfamily C member 3	1	0.02001724	0.8526141	1	1	0.045502862	-0.312441045	0	0
8	ENSRNOG00000011964	Abcd4	ATP binding cassette subfamily D member 4	1	0.044931522	0.70121325	1	1	0.119280601	-1.140336596	0	0
9	ENSRNOG00000001158	Abcg1	ATP binding cassette subfamily G member 1	1	0.028467278	0.77227733	1	1	0.054573885	-0.249555421	0	0
10	ENSRNOG00000017120	Abhd2	abhydrolase domain containing 2	1	0.02892435	1.318907942	1	1	0.059264602	-0.681693012	0	0
11	ENSRNOG00000022307	Acap3	ArfGAP with coiled-coil, ankyrin repeat and PH domains	1	0.030533894	0.86609367	1	1	0.114416454	-0.445289758	0	0
12	ENSRNOG000000062101	Ace	angiotensin I converting enzyme	1	0.015776153	0.885286787	1	1	0.401786935	-0.142010927	0	0
13	ENSRNOG00000013594	Acp2	acid phosphatase 2, lysosomal	1	0.015164747	0.944344224	1	1	0.022610579	-0.534699698	0	0
14	ENSRNOG00000017494	Acp6	acid phosphatase 6, lysosphosphatidic	1	0.025803324	0.714428177	1	1	0.074790773	-0.623127419	0	0
15	ENSRNOG00000058039	Acta2	actin, alpha 2, smooth muscle, aorta	1	0.010306186	2.721276066	1	1	0.074053927	-1.429082703	0	0
16	ENSRNOG00000020433	Actn4	actinin alpha 4	1	0.007222812	1.346240599	1	1	0.106280396	-0.782503711	0	0
17	ENSRNOG00000032150	Adcy2	adenylate cyclase 2	1	0.008839942	0.816965406	1	1	0.082364733	0.156187723	0	0
18	ENSRNOG00000012991	Adgra2	adhesion G protein-coupled receptor A2	1	0.009858493	1.437956329	1	1	0.141520171	-0.868314412	0	0
19	ENSRNOG00000004489	Adgre5	adhesion G protein-coupled receptor E5	1	0.027067513	0.696374714	1	1	0.126230467	-0.315364403	0	0
20	ENSRNOG00000013720	Aebp1	AE binding protein 1	1	0.017039239	1.954439287	1	1	0.101649817	-1.169941127	0	0
21	ENSRNOG00000018830	Aff3	AF4/FMR2 family, member 3	1	0.018584787	0.792374629	1	1	0.352764085	0.053581417	0	0
22	ENSRNOG00000026994	Afg3l1	AFG3(ATPase family gene 3)-like 1 (S. cerevisiae)	1	0.025318254	0.902283045	1	1	0.120018481	-0.688965686	0	0
23	ENSRNOG000000090437	Agpat1	1-acylglycerol-3-phosphate O-acyltransferase 1	1	0.045123647	0.72449244	1	1	0.146774774	-0.560234931	0	0
24	ENSRNOG00000017731	Agpat4	1-acylglycerol-3-phosphate O-acyltransferase 4	1	0.032420936	1.522005198	1	1	0.017928764	-0.54638408	0	0
25	ENSRNOG00000008619	Agtr2	angiotensin II receptor-associated protein	1	0.022897317	0.871504477	1	1	0.063311082	-0.500471391	0	0
26	ENSRNOG00000016727	Akr1a1	aldo-keto reductase family 1 member A1	1	0.005371354	0.819129421	1	1	0.006848286	-0.438813729	0	0
27	ENSRNOG00000020623	Aldh18a1	aldehyde dehydrogenase 18 family, member A1	1	0.037042867	1.811902999	1	1	0.059041307	-1.385241734	0	0
28	ENSRNOG00000001712	Alg3	ALG3, alpha-1,3- mannosyltransferase	1	0.000391008	0.846138803	1	1	0.067921316	-0.972437702	0	0
29	ENSRNOG00000010877	Alg9	ALG9, alpha-1,2-mannosyltransferase	1	0.01421433	1.030615214	1	1	0.085552307	-0.786845933	0	0
30	ENSRNOG00000024264	Amz1	archaelysin family metalloproteinase 1	1	0.002032412	1.813587347	1	1	0.135559134	-0.91156162	0	0
31	ENSRNOG00000011295	Anapc2	anaphase promoting complex subunit 2	1	0.011116751	0.87721223	1	1	0.109357286	-0.82966671	0	0
32	ENSRNOG00000010567	Angel1	angel homolog 1	1	0.027428867	0.85547154	1	1	0.177154817	-0.697291507	0	0
33	ENSRNOG00000016151	Ankrd23	ankyrin repeat domain 23	1	0.012686987	2.989176499	1	1	0.089246741	-1.621596015	0	0
34	ENSRNOG00000003186	Anks3	ankyrin repeat and sterile alpha motif domain containing	1	0.032047169	1.260790081	1	1	0.087412937	-0.790775996	0	0
35	ENSRNOG00000010362	Anxa2	annexin A2	1	0.004990828	1.891384455	1	1	0.066243914	-0.462539212	0	0
36	ENSRNOG00000018159	Anxa4	annexin A4	1	0.046775809	0.957548901	1	1	0.49043997	0.009233185	0	0
37	ENSRNOG00000007136	Anxa7	annexin A7	1	0.003398524	0.960435236	1	1	0.00791042	-0.231889942	0	0
38	ENSRNOG00000008798	Ap1b1	adaptor-related protein complex 1, beta 1 subunit	1	0.033721399	0.737233568	1	1	0.118627336	-0.695498644	0	0
39	ENSRNOG00000025819	Ap1g2	adaptor-related protein complex 1, gamma 2 subunit	1	0.01095552	1.630114159	1	1	0.058978415	-1.083826726	0	0
40	ENSRNOG00000014454	Ap1m1	adaptor-related protein complex 1, mu 1 subunit	1	0.006962416	1.216635091	1	1	0.129962781	-0.721612452	0	0

41	ENSRNOG00000001415	Ap1s1	adaptor-related protein complex 1, sigma 1 subunit	1	0.000358941	1.08893201	1	1	0.1011533	-0.735446094	0	0
42	ENSRNOG000000019534	Ap2a2	adaptor-related protein complex 2, alpha 2 subunit	1	0.008917888	0.873964835	1	1	0.011950824	-0.511064588	0	0
43	ENSRNOG00000001709	Ap2m1	adaptor-related protein complex 2, mu 1 subunit	1	0.002960899	0.784917448	1	1	0.18836694	-0.409645802	0	0
44	ENSRNOG000000018977	Ap3d1	adaptor-related protein complex 3, delta 1 subunit	1	0.037549686	0.81185992	1	1	0.10324619	-0.559901712	0	0
45	ENSRNOG000000029572	Apeh	acylaminoacyl-peptide hydrolase	1	0.023424316	0.964622935	1	1	0.128945314	-0.540351953	0	0
46	ENSRNOG000000020851	Ap1p1	amyloid beta precursor like protein 1	1	0.045107648	1.168643598	1	1	0.429292876	-0.060669424	0	0
47	ENSRNOG000000015411	Apobec1	apolipoprotein B mRNA editing enzyme catalytic subunit	1	0.014589477	1.648897545	1	1	0.208544928	0.353331495	0	0
48	ENSRNOG000000016852	Apobec3b	apolipoprotein B mRNA editing enzyme catalytic subunit	1	0.047337977	1.912505514	1	1	0.134599821	-0.576992971	0	0
49	ENSRNOG000000018454	Apoe	apolipoprotein E	1	0.008978891	3.018055762	1	1	0.096236191	-1.060497528	0	0
50	ENSRNOG000000006229	Arf1	ADP-ribosylation factor 1	1	0.001941108	0.933741629	1	1	0.142631474	-0.422444017	0	0
51	ENSRNOG000000043150	Arfgap1	ADP-ribosylation factor GTPase activating protein 1	1	0.008025791	0.739624726	1	1	0.060740845	-0.623439207	0	0
52	ENSRNOG000000013304	Arg1	arginase 1	1	0.01047514	1.582988889	1	1	0.283760775	-0.474956764	0	0
53	ENSRNOG000000031168	Arhgap15	Rho GTPase activating protein 15	1	0.029983725	0.596357308	1	1	0.171922212	0.501154396	0	0
54	ENSRNOG000000024728	Arhgap22	Rho GTPase activating protein 22	1	0.021918213	2.146186604	1	1	0.133540101	-1.038205115	0	0
55	ENSRNOG000000006946	Arhgap9	Rho GTPase activating protein 9	1	0.038391145	0.73268209	1	1	0.073738294	-0.511938198	0	0
56	ENSRNOG000000036888	Arhgdia	Rho GDP dissociation inhibitor alpha	1	0.0043437	1.684296726	1	1	0.059389283	-1.132751389	0	0
57	ENSRNOG000000020130	Arhgef1	Rho guanine nucleotide exchange factor 1	1	0.029191228	1.259334818	1	1	0.124655955	-0.798770202	0	0
58	ENSRNOG000000052354	Arhgef40	Rho guanine nucleotide exchange factor 40	1	0.001290532	0.847151119	1	1	0.139195642	-0.717301413	0	0
59	ENSRNOG000000049235	Arl16	ADP-ribosylation factor like GTPase 16	1	0.034272671	0.610373808	1	1	0.145617819	-0.363879147	0	0
60	ENSRNOG000000005988	Arl8a	ADP-ribosylation factor like GTPase 8A	1	0.012512516	0.798803479	1	1	0.104002138	-0.571028431	0	0
61	ENSRNOG000000000991	Arpc1b	actin related protein 2/3 complex, subunit 1B	1	0.015448038	2.020770659	1	1	0.052337218	-0.742073635	0	0
62	ENSRNOG000000008873	Arpc3	actin related protein 2/3 complex, subunit 3	1	0.010799807	1.371291825	1	1	0.025433556	-0.400808046	0	0
63	ENSRNOG000000030404	Armb1	arrestin, beta 1	1	0.04161382	0.729754074	1	1	0.222011861	0.202126265	0	0
64	ENSRNOG000000019308	Armb2	arrestin, beta 2	1	0.000718847	1.422068629	1	1	0.054688368	-0.545991439	0	0
65	ENSRNOG000000049714	Asap3	ArfGAP with SH3 domain, ankyrin repeat and PH domain	1	0.031927591	1.528790563	1	1	0.148140611	-0.382446131	0	0
66	ENSRNOG000000005115	Asf1b	anti-silencing function 1B histone chaperone	1	0.043438659	2.596497654	1	1	0.053979803	-1.974952728	0	0
67	ENSRNOG000000030726	Asgr2	asialoglycoprotein receptor 2	1	0.031152334	0.845788093	1	1	0.152196814	0.336909229	0	0
68	ENSRNOG000000009093	Asl	argininosuccinate lyase	1	0.035203365	1.531785234	1	1	0.122071857	-0.845899308	0	0
69	ENSRNOG000000018118	Atad3a	ATPase family, AAA domain containing 3A	1	0.012946831	1.224814468	1	1	0.078287359	-1.020366568	0	0
70	ENSRNOG000000003745	Atf3	activating transcription factor 3	1	0.041722364	1.533354377	1	1	0.069905938	-0.728661428	0	0
71	ENSRNOG000000018403	Atg4b	autophagy related 4B, cysteine peptidase	1	0.013055927	1.015645339	1	1	0.083968807	-0.736961888	0	0
72	ENSRNOG000000010776	Atp13a1	ATPase 13A1	1	0.002678022	1.479161143	1	1	0.122293359	-0.932737563	0	0
73	ENSRNOG000000008052	Atp13a2	ATPase 13A2	1	0.042550307	1.127080645	1	1	0.108677388	-1.637132562	0	0
74	ENSRNOG000000006542	Atp6v0c	ATPase H+ transporting V0 subunit C	1	0.045048479	1.162695873	1	1	0.083088821	-1.063295053	0	0
75	ENSRNOG000000017235	Atp6v0d1	ATPase H+ transporting V0 subunit D1	1	0.027154817	0.723549033	1	1	0.074799945	-0.607299941	0	0
76	ENSRNOG000000007842	Aup1	ancient ubiquitous protein 1	1	0.007245293	0.843862474	1	1	0.100574029	-0.723503798	0	0
77	ENSRNOG000000008283	B4galt5	beta-1,4-galactosyltransferase 5	1	0.042445762	1.264552894	1	1	0.372943935	-0.069077732	0	0
78	ENSRNOG0000000021886	B4galt7	beta-1,4-galactosyltransferase 7	1	0.034883249	1.46173115	1	1	0.065684505	-1.279067376	0	0
79	ENSRNOG000000021147	Bad	BCL2-associated agonist of cell death	1	0.015126957	1.382153889	1	1	0.108095304	-0.83458404	0	0
80	ENSRNOG000000000485	Bak1	BCL2-antagonist/killer 1	1	0.01706834	1.235880002	1	1	0.120358527	-0.811569601	0	0
81	ENSRNOG000000020876	Bax	BCL2 associated X, apoptosis regulator	1	0.030959934	1.377327634	1	1	0.103711813	-0.878487125	0	0
82	ENSRNOG000000019253	Bcar1	BCAR1, Cas family scaffolding protein	1	0.020304117	1.49728076	1	1	0.070125302	-1.353318754	0	0
83	ENSRNOG000000020486	Bcl2l12	BCL2 like 12	1	0.039471623	1.566223126	1	1	0.219682849	-0.337418267	0	0
84	ENSRNOG000000013165	Bet1l	Bet1 golgi vesicular membrane trafficking protein-like	1	0.045353286	0.990961011	1	1	0.057307496	-0.270958304	0	0
85	ENSRNOG000000012852	Bin1	bridging integrator 1	1	0.01259458	0.849910187	1	1	0.101335149	-0.794901104	0	0

86	ENSRNOG00000018023	Bin3	bridging integrator 3	1	0.007754224	0.817335952	1	1	0.078478105	-0.415802628	0	0
87	ENSRNOG00000011778	Blvra	biliverdin reductase A	1	0.023611751	1.171964445	1	1	0.106399007	-0.392878002	0	0
88	ENSRNOG00000021773	Bop1	block of proliferation 1	1	0.025124198	1.306444767	1	1	0.101448935	-1.238286725	0	0
89	ENSRNOG00000028841	Brpf3	bromodomain and PHD finger containing, 3	1	0.040078339	0.862555914	1	1	0.070018481	-0.944553103	0	0
90	ENSRNOG00000019856	Btd	biotinidase	1	0.00728598	1.074006886	1	1	0.105823323	-0.876277394	0	0
91	ENSRNOG000000049121	Bysl	bystin-like	1	0.028901041	1.215059283	1	1	0.062482794	-0.845802753	0	0
92	ENSRNOG00000007613	C1qtnf5	C1q and TNF related 5	1	0.033887458	1.214960118	1	1	0.101909799	-0.556328399	0	0
93	ENSRNOG000000051235	C2	complement C2	1	0.048805188	1.993735705	1	1	0.128054617	0.449943154	0	0
94	ENSRNOG000000046834	C3	complement C3	1	0.036213089	2.015565957	1	1	0.08810882	0.963240853	0	0
95	ENSRNOG000000047800	C5ar1	complement C5a receptor 1	1	0.028114889	2.30612937	1	1	0.111623819	-0.649532257	0	0
96	ENSRNOG000000049028	C5ar2	complement component 5a receptor 2	1	0.013337425	1.07880371	1	1	0.132661265	0.667359399	0	0
97	ENSRNOG000000039852	Cactin	cactin, spliceosome C complex subunit	1	0.029971884	1.328402552	1	1	0.120650783	-0.861671033	0	0
98	ENSRNOG000000020325	Calhm2	calcium homeostasis modulator family member 2	1	0.018107303	0.852356099	1	1	0.059746155	-0.171313976	0	0
99	ENSRNOG000000038202	Calml4	calmodulin-like 4	1	0.0237054	0.733561094	1	1	0.377467968	0.108021909	0	0
100	ENSRNOG000000003239	Cant1	calcium activated nucleotidase 1	1	0.005621543	1.173577421	1	1	0.08890311	-0.826521334	0	0
101	ENSRNOG000000013658	Capg	capping actin protein, gelsolin like	1	0.002597062	1.950071998	1	1	0.06293828	-1.023796898	0	0
102	ENSRNOG000000045623	Capn10	calpain 10	1	0.039670492	1.240306227	1	1	0.107735673	-1.107469384	0	0
103	ENSRNOG000000017073	Car9	carbonic anhydrase 9	1	0.034389077	1.185979615	1	1	0.490880988	-0.014712188	0	0
104	ENSRNOG000000031129	Carm1	coactivator-associated arginine methyltransferase 1	1	0.019708986	0.716312301	1	1	0.095236329	-0.89915267	0	0
105	ENSRNOG000000012944	Casp9	caspase 9	1	0.041805958	1.233040365	1	1	0.121218875	-0.858989858	0	0
106	ENSRNOG000000001701	Cbr3	carbonyl reductase 3	1	0.032234191	1.278406031	1	1	0.166857251	-0.27486345	0	0
107	ENSRNOG000000018295	Coar2	cell cycle and apoptosis regulator 2	1	0.043795049	0.618301177	1	1	0.143312254	-0.488058105	0	0
108	ENSRNOG000000011799	Ccdc159	coiled-coil domain containing 159	1	0.000484242	1.168868521	1	1	0.072693331	-0.87533777	0	0
109	ENSRNOG000000002052	Ccdc80	coiled-coil domain containing 80	1	0.012423833	0.903849039	1	1	0.105799807	0.314282109	0	0
110	ENSRNOG000000020925	Ccdc86	coiled-coil domain containing 86	1	0.048095993	0.975174551	1	1	0.107019309	-0.810802366	0	0
111	ENSRNOG000000029768	Col12	chemokine (C-C motif) ligand 12	1	0.048367561	1.617906926	1	1	0.318104062	-0.483365122	0	0
112	ENSRNOG000000007159	Col2	C-C motif chemokine ligand 2	1	0.021125991	2.683120777	1	1	0.124451279	-1.301599381	0	0
113	ENSRNOG000000000239	Col7	C-C motif chemokine ligand 7	1	0.015551203	2.965080095	1	1	0.070888421	-1.122320256	0	0
114	ENSRNOG000000028548	Col9	chemokine (C-C motif) ligand 9	1	0.002097924	1.108743593	1	1	0.05418047	-0.875127367	0	0
115	ENSRNOG000000007483	Conf	cyolin F	1	0.048028895	2.354885976	1	1	0.065239225	-1.83429902	0	0
116	ENSRNOG000000006715	Cor1	C-C motif chemokine receptor 1	1	0.016405903	1.445200719	1	1	0.128845597	0.462816155	0	0
117	ENSRNOG000000047816	Cos	copper chaperone for superoxide dismutase	1	0.041948279	1.769942339	1	1	0.121704158	-1.035139096	0	0
118	ENSRNOG000000017819	Cd14	CD14 molecule	1	0.008824909	2.570478514	1	1	0.117525964	-0.455100014	0	0
119	ENSRNOG000000024000	Cd22	CD22 molecule	1	0.022805475	1.446214688	1	1	0.052491276	-0.840419189	0	0
120	ENSRNOG000000036728	Cd300lb	CD300 molecule-like family member b	1	0.025628509	3.212129478	1	1	0.058683471	-1.522707834	0	0
121	ENSRNOG000000042825	Cd300le	CD300 molecule-like family member E	1	0.044121371	2.283261786	1	1	0.127027171	-0.510702743	0	0
122	ENSRNOG000000037331	Cd33	CD33 molecule	1	0.023579477	3.436795169	1	1	0.071592994	-1.172455447	0	0
123	ENSRNOG000000007650	Cd63	CD63 molecule	1	0.000212951	1.34689998	1	1	0.069773878	-0.350611362	0	0
124	ENSRNOG000000000047	Cd82	CD82 molecule	1	0.00710682	1.904377237	1	1	0.032252258	-0.562341156	0	0
125	ENSRNOG000000028415	Cdc20	cell division cycle 20	1	0.036900785	2.808831918	1	1	0.067143714	-2.148721947	0	0
126	ENSRNOG000000060538	Cdc42se1	CDC42 small effector 1	1	0.001988001	1.109640623	1	1	0.068724364	-0.845938768	0	0
127	ENSRNOG000000000632	Cdk1	cyclin-dependent kinase 1	1	0.042423419	2.82786744	1	1	0.102953176	-1.885269013	0	0
128	ENSRNOG000000025602	Cdk4	cyclin-dependent kinase 4	1	0.003988348	1.199556896	1	1	0.076950279	-0.859093717	0	0
129	ENSRNOG000000022261	Cenpu	centromere protein U	1	0.042942418	2.488828013	1	1	0.06760851	-1.646383608	0	0
130	ENSRNOG000000028604	Cercam	cerebral endothelial cell adhesion molecule	1	0.015977657	1.36596515	1	1	0.114408888	-0.843670249	0	0

131	ENSRNOG00000019141	Ch25h	cholesterol 25-hydroxylase	1	0.009265016	2.064593091	1	1	0.257804082	-0.11098622	0	0
132	ENSRNOG000000060248	Chohd6	coiled-coil-helix-coiled-coil-helix domain containing 6	1	0.021512447	1.988457212	1	1	0.088941176	-1.550538512	0	0
133	ENSRNOG00000004014	Chmp6	charged multivesicular body protein 6	1	0.021200331	0.659408109	1	1	0.142817737	-0.573463008	0	0
134	ENSRNOG000000008885	Chst11	carbohydrate sulfotransferase 11	1	0.017302531	0.807654489	1	1	0.117414178	-0.364722323	0	0
135	ENSRNOG000000001252	Chst12	carbohydrate sulfotransferase 12	1	0.016880629	1.739617291	1	1	0.084617957	-0.588019707	0	0
136	ENSRNOG000000047734	Chst2	carbohydrate sulfotransferase 2	1	0.015147783	0.9845124	1	1	0.064175367	-0.728145371	0	0
137	ENSRNOG000000047246	Chtf8	chromosome transmission fidelity factor 8	1	0.03270271	0.854176507	1	1	0.042531274	-0.555018213	0	0
138	ENSRNOG000000012638	Ciao1	cytosolic iron-sulfur assembly component 1	1	0.011281291	0.622571644	1	1	0.038518585	-0.391778001	0	0
139	ENSRNOG000000033498	Cib1	calcium and integrin binding 1	1	0.013711882	1.804175042	1	1	0.102752914	-0.528762586	0	0
140	ENSRNOG000000002659	Ciita	class II, major histocompatibility complex, transactivator	1	0.034567685	1.159823446	1	1	0.174765395	-0.497415849	0	0
141	ENSRNOG000000018715	Clec10a	C-type lectin domain containing 10A	1	0.023285429	1.347274768	1	1	0.019413006	0.509610981	0	0
142	ENSRNOG000000030012	Clec4a2	C-type lectin domain family 4, member A2	1	0.0160451	3.113676754	1	1	0.283928764	-0.697419944	0	0
143	ENSRNOG000000010018	Clec4a3	C-type lectin domain family 4, member A3	1	0.045149438	2.070520134	1	1	0.469646607	0.058758436	0	0
144	ENSRNOG000000010181	Clec4d	C-type lectin domain family 4, member D	1	0.019453141	2.836307502	1	1	0.444592097	0.170014512	0	0
145	ENSRNOG000000007164	Cln6	CLN6, transmembrane ER protein	1	0.016379008	0.69171796	1	1	0.105078615	-0.507401075	0	0
146	ENSRNOG000000012565	Cln8	CLN8, transmembrane ER and ERGIC protein	1	0.045331494	0.693996328	1	1	0.082839184	-0.478832903	0	0
147	ENSRNOG000000014635	Clta	clathrin, light chain A	1	0.010246742	1.067344531	1	1	0.165868635	-0.373189874	0	0
148	ENSRNOG000000013178	Cmip	c-Maf-inducing protein	1	0.021803738	0.704867984	1	1	0.411565409	-0.079423113	0	0
149	ENSRNOG000000027739	Cndp1	carnosine dipeptidase 1	1	0.032620785	1.461615888	1	1	0.391342321	0.067944206	0	0
150	ENSRNOG000000027736	Cnn1	calponin 1	1	0.036623819	3.163006209	1	1	0.057228329	-1.966494005	0	0
151	ENSRNOG000000043044	Cnn2	calponin 2	1	0.01737825	1.814666077	1	1	0.057254672	-0.909912151	0	0
152	ENSRNOG000000053234	Cnot3	CCR4-NOT transcription complex, subunit 3	1	0.034666851	0.729037686	1	1	0.070752707	-0.55865504	0	0
153	ENSRNOG000000017496	Cnp	2',3'-cyclic nucleotide 3' phosphodiesterase	1	0.027698779	1.259714106	1	1	0.313204676	-0.129104981	0	0
154	ENSRNOG000000003549	Cnpy2	canopy FGF signaling regulator 2	1	0.015063789	0.60872977	1	1	0.241269016	0.064502197	0	0
155	ENSRNOG000000008270	Cntrb	centriole, centriole duplication and spindle assembly protein	1	0.035745949	1.072464922	1	1	0.085819185	-0.950344154	0	0
156	ENSRNOG000000002795	Cog1	component of oligomeric golgi complex 1	1	0.008115992	0.763355376	1	1	0.087704779	-0.735417207	0	0
157	ENSRNOG000000001229	Col18a1	collagen type XVIII alpha 1 chain	1	0.008659954	2.159728642	1	1	0.056512172	-0.999516995	0	0
158	ENSRNOG000000001249	Col8a1	collagen type VI alpha 1 chain	1	0.037804427	1.267715029	1	1	0.110294669	-0.877583379	0	0
159	ENSRNOG000000039668	Col8a1	collagen type VIII alpha 1 chain	1	0.025252327	2.115621008	1	1	0.073162816	-0.851230017	0	0
160	ENSRNOG000000023317	Colgalt1	collagen beta(1-O)galactosyltransferase 1	1	0.032773878	0.751981186	1	1	0.047226881	-0.414797795	0	0
161	ENSRNOG000000019615	Colq	collagen like tail subunit of asymmetric acetylcholinesterase	1	0.041421695	0.945274492	1	1	0.345447693	-0.212193972	0	0
162	ENSRNOG000000004755	Comm9	COMM domain containing 9	1	0.023955038	1.661485698	1	1	0.109970892	-0.702357886	0	0
163	ENSRNOG000000013968	Comtd1	catechol-O-methyltransferase domain containing 1	1	0.010370043	0.812760662	1	1	0.155187091	-0.152468392	0	0
164	ENSRNOG000000020178	Cope	coatamer protein complex, subunit epsilon	1	0.009436866	1.636387681	1	1	0.125699952	-1.028121874	0	0
165	ENSRNOG000000021828	Coro1b	coronin 1B	1	0.010683539	1.263059625	1	1	0.082901938	-0.565512569	0	0
166	ENSRNOG000000000897	Coro1c	coronin 1C	1	0.022412247	1.057098369	1	1	0.061619888	-0.626446472	0	0
167	ENSRNOG000000004146	Coro7	coronin 7	1	0.029401559	1.660627	1	1	0.082407696	-1.120403481	0	0
168	ENSRNOG000000038616	Cox8b2	cytochrome c oxidase subunit 8B2	1	0.021551755	0.610454745	1	1	0.293911592	-0.175963623	0	0
169	ENSRNOG000000030705	Cpsf1	cleavage and polyadenylation specific factor 1	1	0.030710296	0.754962024	1	1	0.121545893	-1.040649052	0	0
170	ENSRNOG000000000985	Cpsf4	cleavage and polyadenylation specific factor 4	1	0.026534584	0.771365666	1	1	0.147162127	-0.488425512	0	0
171	ENSRNOG000000026163	Cpt1c	carmitine palmitoyltransferase 1c	1	0.039586925	0.668721559	1	1	0.128789483	-0.80740684	0	0
172	ENSRNOG000000021220	Cpxm1	carboxypeptidase X (M14 family), member 1	1	0.038978829	0.953969705	1	1	0.108052893	-0.479399566	0	0
173	ENSRNOG000000004659	Crd2	cysteine-rich with EGF-like domains 2	1	0.028783394	1.472362402	1	1	0.059592304	-0.77821347	0	0
174	ENSRNOG000000008334	Croc	ciliary rootlet coiled-coil, rootletin	1	0.042820633	0.973202297	1	1	0.06196814	-0.566793869	0	0
175	ENSRNOG000000022421	Crtc1	CREB regulated transcription coactivator 1	1	0.003596304	0.860893915	1	1	0.073708434	-0.535552886	0	0

176	ENSRNOG00000011975	Crto3	CREB regulated transcription coactivator 3	1	0.009946762	0.977304429	1	1	0.142209365	-0.789794265	0	0
177	ENSRNOG00000018859	Csf1	colony stimulating factor 1	1	0.027296188	0.777345188	1	1	0.064561961	-0.303933074	0	0
178	ENSRNOG00000018414	Csf1r	colony stimulating factor 1 receptor	1	0.029326253	1.663211925	1	1	0.18566223	-0.374446884	0	0
179	ENSRNOG000000000187	Csf2rb	colony stimulating factor 2 receptor beta common subunit	1	0.021883871	1.976481144	1	1	0.498705262	-0.000973012	0	0
180	ENSRNOG00000008759	Csf3r	colony stimulating factor 3 receptor	1	0.041471485	3.258019937	1	1	0.084482932	-1.141435134	0	0
181	ENSRNOG00000019374	Csk	C-terminal Src kinase	1	0.002574581	1.588430803	1	1	0.061726226	-1.005648343	0	0
182	ENSRNOG00000003772	Csrp2	cysteine and glycine-rich protein 2	1	0.040693469	1.761224312	1	1	0.448979174	-0.059700696	0	0
183	ENSRNOG000000006767	Cst7	cystatin F	1	0.005706779	1.502807739	1	1	0.095745259	-0.624905424	0	0
184	ENSRNOG00000001201	Cstb	cystatin B	1	0.042873043	0.768167945	1	1	0.263979657	-0.230013193	0	0
185	ENSRNOG00000005357	Ctcl1	CST telomere replication complex component 1	1	0.00117454	0.623437549	1	1	0.085706227	-0.588401487	0	0
186	ENSRNOG000000054129	Ctla4	cytotoxic T-lymphocyte-associated protein 4	1	0.02853417	0.846989564	1	1	0.191655748	-0.128893479	0	0
187	ENSRNOG00000012021	Ctnnb1	catenin, beta like 1	1	0.018105648	0.981917574	1	1	0.085483139	-0.615582682	0	0
188	ENSRNOG00000010331	Ctsb	cathepsin B	1	0.03914668	1.334067019	1	1	0.061752086	-0.688302451	0	0
189	ENSRNOG000000021155	Ctsk	cathepsin K	1	0.000381353	1.424578193	1	1	0.265652989	-0.17226352	0	0
190	ENSRNOG000000050697	Ctsz	cathepsin Z	1	0.022550859	2.769874229	1	1	0.063700779	-1.039489679	0	0
191	ENSRNOG000000020743	Cyp2s1	cytochrome P450, family 2, subfamily s, polypeptide 1	1	0.022325633	0.901296635	1	1	0.046770774	-0.515596782	0	0
192	ENSRNOG000000007679	Cyth4	cytohesin 4	1	0.022440659	1.821452846	1	1	0.059234536	-0.700075237	0	0
193	ENSRNOG000000053945	Daam2	dishevelled associated activator of morphogenesis 2	1	0.001898352	0.658478471	1	1	0.078859954	-0.962441148	0	0
194	ENSRNOG000000009090	Dad1	defender against cell death 1	1	0.009273961	1.262168406	1	1	0.034319081	-0.472790171	0	0
195	ENSRNOG000000027264	Dagla	diacylglycerol lipase, alpha	1	0.005921661	1.65752298	1	1	0.101757327	-0.756342431	0	0
196	ENSRNOG000000001079	Daglb	diacylglycerol lipase, beta	1	0.022785187	1.203868783	1	1	0.071378043	-0.815140102	0	0
197	ENSRNOG00000010747	Dap	death-associated protein	1	0.021752155	0.859415324	1	1	0.143691883	-0.257639638	0	0
198	ENSRNOG00000012378	Dbln1	drebrin-like	1	0.017112751	1.131558856	1	1	0.128034205	-0.768107198	0	0
199	ENSRNOG000000021882	Deakd	dephospho-CoA kinase domain containing	1	0.024212951	1.148583167	1	1	0.097754569	-1.172773869	0	0
200	ENSRNOG000000057078	Ddit4	DNA-damage-inducible transcript 4	1	0.036334873	0.718026226	1	1	0.211362113	0.838030044	0	0
201	ENSRNOG00000015079	Ddost	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	1	0.00612909	1.171685074	1	1	0.059493897	-0.783170891	0	0
202	ENSRNOG000000080154	Ddx23	DEAD-box helicase 23	1	0.017431074	0.928030704	1	1	0.195110061	-0.503335073	0	0
203	ENSRNOG00000013040	Ddx31	DEAD-box helicase 31	1	0.020975381	0.698478584	1	1	0.055464451	-0.870806632	0	0
204	ENSRNOG00000012771	Ddx41	DEAD-box helicase 41	1	0.014352941	1.771687199	1	1	0.153024067	-0.503255078	0	0
205	ENSRNOG000000004670	Ddx56	DEAD-box helicase 56	1	0.042753052	0.922234414	1	1	0.084845666	-1.064001077	0	0
206	ENSRNOG000000003779	Dedd	death effector domain-containing	1	0.018238466	0.797806124	1	1	0.185050824	-0.514117159	0	0
207	ENSRNOG000000005052	Def6	DEF6 guanine nucleotide exchange factor	1	0.032244121	0.800956464	1	1	0.059401834	-0.668883421	0	0
208	ENSRNOG000000029868	Dennd6b	DENN domain containing 6B	1	0.00733908	1.20894446	1	1	0.137245156	-1.009454438	0	0
209	ENSRNOG000000019810	Des	desmin	1	0.039997104	1.097027347	1	1	0.133538584	-0.963007897	0	0
210	ENSRNOG000000061814	Dgor2	DiGeorge syndrome critical region gene 2	1	0.030798979	0.827960857	1	1	0.255920281	-0.271851819	0	0
211	ENSRNOG000000006787	Dhcr24	24-dehydrocholesterol reductase	1	0.018226743	1.84185929	1	1	0.052432729	-1.695877648	0	0
212	ENSRNOG000000005380	Dhrs7b	dehydrogenase/reductase 7B	1	0.023621819	0.852122843	1	1	0.011639197	-0.386893716	0	0
213	ENSRNOG000000043212	Dip2a	disco-interacting protein 2 homolog A	1	0.02404648	0.834206221	1	1	0.070376526	-0.526195458	0	0
214	ENSRNOG000000005783	Dlg5	discs large MAGUK scaffold protein 5	1	0.013013034	0.763893716	1	1	0.144980829	-0.655889049	0	0
215	ENSRNOG0000000030408	Dnajb12	DnaJ heat shock protein family (Hsp40) member B12	1	0.032693469	0.75770857	1	1	0.089244121	-0.546896105	0	0
216	ENSRNOG000000007649	Dnm2	dynamin 2	1	0.025239639	0.700289576	1	1	0.147013172	-0.72419761	0	0
217	ENSRNOG000000018397	Dnph1	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	1	0.003808703	1.78598322	1	1	0.114881181	-0.978874343	0	0
218	ENSRNOG00000017863	Dolpp1	dolichyl-diphosphatase 1	1	0.018015309	1.19014852	1	1	0.050373078	-0.706888702	0	0
219	ENSRNOG000000017241	Dpod	deleted in primary ciliary dyskinesia	1	0.011067237	0.642061353	1	1	0.13309558	-0.166711482	0	0
220	ENSRNOG000000049110	Dpm2	dolichyl-phosphate mannosyltransferase subunit 2, regulated	1	0.009144473	2.330237251	1	1	0.056601407	-1.153320984	0	0

221	ENSRNOG00000031485	Dpp3	dipeptidylpeptidase 3	1	0.025678919	1.327688795	1	1	0.115234122	-0.548529058	0	0
222	ENSRNOG00000012640	Dpp7	dipeptidylpeptidase 7	1	0.004528929	1.87120612	1	1	0.079418523	-0.862053795	0	0
223	ENSRNOG00000001881	Dscr3	DSCR3 arrestin fold containing	1	0.038953314	0.600094026	1	1	0.302632439	-0.056830889	0	0
224	ENSRNOG000000001432	Dbx2	deltex E3 ubiquitin ligase 2	1	0.027131094	1.391722886	1	1	0.28463437	-0.402468691	0	0
225	ENSRNOG00000018904	Dtymk	deoxythymidylate kinase	1	0.034222054	0.978580501	1	1	0.05771402	-0.508262841	0	0
226	ENSRNOG00000018005	Duoxa1	dual oxidase maturation factor 1	1	5.02E-05	1.431585588	1	1	0.172696504	-0.508993678	0	0
227	ENSRNOG00000030091	Dusp14	dual specificity phosphatase 14	1	0.035087513	0.912378631	1	1	0.065958003	-0.761074107	0	0
228	ENSRNOG000000011222	Dynl1	dynein light chain LC8-type 1	1	0.024085373	0.620927345	1	1	0.061324943	-0.290975411	0	0
229	ENSRNOG00000018207	Dynl1	dynein light chain Tctex-type 1	1	0.003136611	1.408364597	1	1	0.211132405	-0.208057865	0	0
230	ENSRNOG00000004870	Dyrk3	dual specificity tyrosine phosphorylation regulated kinase	1	0.001594924	1.02458853	1	1	0.07386263	-0.73379114	0	0
231	ENSRNOG00000015708	E2f4	E2F transcription factor 4	1	0.012692918	0.805573565	1	1	0.091402248	-0.66605467	0	0
232	ENSRNOG00000014241	Ece1	endothelin converting enzyme 1	1	0.049790359	0.804819273	1	1	0.32592035	0.224670332	0	0
233	ENSRNOG000000024025	Ecd4	enhancer of mRNA decapping 4	1	0.047836701	0.98427898	1	1	0.129901662	-0.836476203	0	0
234	ENSRNOG000000009439	Eef1a1	eukaryotic translation elongation factor 1 alpha 1	1	0.008946869	0.885922041	1	1	0.395062547	-0.035639307	0	0
235	ENSRNOG000000024186	Eef1b2	eukaryotic translation elongation factor 1 beta 2	1	0.037178815	0.74672409	1	1	0.43117916	0.043519352	0	0
236	ENSRNOG000000021838	Eef1d	eukaryotic translation elongation factor 1 delta	1	0.004091028	1.666332522	1	1	0.083108337	-0.781657278	0	0
237	ENSRNOG000000020286	Eef2	eukaryotic translation elongation factor 2	1	0.02189118	1.36412079	1	1	0.18185139	-0.691290656	0	0
238	ENSRNOG00000012954	Eefsec	eukaryotic elongation factor, selenocysteine-tRNA-spec	1	0.022371009	1.298444322	1	1	0.067083444	-1.130543515	0	0
239	ENSRNOG000000020588	Efn4	ephrin A4	1	0.029875595	0.687987657	1	1	0.12108027	-0.264806252	0	0
240	ENSRNOG00000002818	Eftud2	elongation factor Tu GTP binding domain containing 2	1	0.013023929	0.780223806	1	1	0.09971884	-0.587168287	0	0
241	ENSRNOG000000001039	Eif2b1	eukaryotic translation initiation factor 2B subunit alpha	1	0.011338253	0.795038802	1	1	0.016097717	-0.466122503	0	0
242	ENSRNOG000000006467	Eif2b2	eukaryotic translation initiation factor 2B subunit beta	1	0.00801062	1.258788009	1	1	0.066976691	-0.94835412	0	0
243	ENSRNOG000000005804	Eif3d	eukaryotic translation initiation factor 3, subunit D	1	0.013924143	0.767766479	1	1	0.099279636	-0.628087682	0	0
244	ENSRNOG000000020819	Eif3g	eukaryotic translation initiation factor 3, subunit G	1	0.048481896	0.777373259	1	1	0.141974485	-0.49769478	0	0
245	ENSRNOG000000020495	Eif3k	eukaryotic translation initiation factor 3, subunit K	1	0.011105579	1.210780309	1	1	0.141394387	-0.508065985	0	0
246	ENSRNOG00000016478	Eif5a	eukaryotic translation initiation factor 5A	1	0.014399007	0.856634876	1	1	0.083666437	-0.557589395	0	0
247	ENSRNOG000000049497	Eif6	eukaryotic translation initiation factor 6	1	0.039903869	1.409487643	1	1	0.13021102	-0.755114757	0	0
248	ENSRNOG000000009285	Eipr1	EARP complex and GARP complex interacting protein 1	1	0.004426867	1.266158159	1	1	0.068003103	-0.49981847	0	0
249	ENSRNOG000000014284	Elof1	elongation factor 1 homolog	1	0.007410385	1.057920356	1	1	0.072392863	-0.753762187	0	0
250	ENSRNOG000000006329	Emb	embigin	1	0.042984208	2.87729665	1	1	0.123679884	-1.683047087	0	0
251	ENSRNOG00000019532	Emc10	ER membrane protein complex subunit 10	1	0.029791876	1.468011263	1	1	0.135282808	-0.997892798	0	0
252	ENSRNOG00000017854	Emc8	ER membrane protein complex subunit 8	1	0.037613544	0.876244024	1	1	0.04418185	-0.496402634	0	0
253	ENSRNOG00000012828	Emg1	EMG1 N1-specific pseudouridine methyltransferase	1	0.000918557	0.675774244	1	1	0.045498449	-0.251834425	0	0
254	ENSRNOG000000008246	Emilin1	elastin microfibril interfacier 1	1	0.032529894	3.453417882	1	1	0.124742569	-1.678289709	0	0
255	ENSRNOG00000014837	Emilin2	elastin microfibril interfacier 2	1	0.009081856	1.044313998	1	1	0.052418661	0.544896949	0	0
256	ENSRNOG000000030127	Eml2	echinoderm microtubule associated protein like 2	1	0.02686794	0.981133057	1	1	0.12456472	-0.612264968	0	0
257	ENSRNOG00000019873	Eml3	echinoderm microtubule associated protein like 3	1	0.004167437	0.850061292	1	1	0.076595683	-0.840848335	0	0
258	ENSRNOG000000021104	Emp3	epithelial membrane protein 3	1	0.015144473	2.671369321	1	1	0.072773671	-1.104462139	0	0
259	ENSRNOG00000017895	Eno1	enolase 1	1	0.027024087	1.441508377	1	1	0.076487828	-1.059344109	0	0
260	ENSRNOG00000013791	Enpp3	ectonucleotide pyrophosphatase/phosphodiesterase 3	1	0.024742707	0.805005985	1	1	0.461856355	-0.032668998	0	0
261	ENSRNOG00000004964	ErbB3	erb-b2 receptor tyrosine kinase 3	1	0.045183918	0.871995594	1	1	0.138412937	-0.538794748	0	0
262	ENSRNOG000000008781	Erg28	ergosterol biosynthesis 28 homolog	1	0.041045997	0.900512128	1	1	0.300510654	-0.097835052	0	0
263	ENSRNOG00000003508	Ergic1	endoplasmic reticulum-golgi intermediate compartment 1	1	0.037941245	1.158378382	1	1	0.275533549	-0.362139899	0	0
264	ENSRNOG000000031085	Ergic3	ERGIC and golgi 3	1	0.009984967	1.305771686	1	1	0.120692021	-0.547218231	0	0
265	ENSRNOG00000010259	Esrrb	estrogen-related receptor beta	1	0.025659058	0.97743216	1	1	0.195925384	-0.733495137	0	0

266	ENSRNOG00000019982	Ethe1	ETHE1, persulfide dioxygenase	1	0.030774154	1.222053229	1	1	0.058168954	-0.617970367	0	0
267	ENSRNOG00000024818	Eva1b	eva-1 homolog B	1	0.035253982	0.736065345	1	1	0.030337218	-0.457152954	0	0
268	ENSRNOG00000006037	Exosc7	exosome component 7	1	0.015714089	1.165855451	1	1	0.037446452	-0.301324921	0	0
269	ENSRNOG000000008944	Ext2	exostosin glycosyltransferase 2	1	0.008573202	1.023894126	1	1	0.050676367	-0.444730137	0	0
270	ENSRNOG000000022393	Faap24	Fanconi anemia core complex associated protein 24	1	0.019166678	0.81480019	1	1	0.049775119	-0.300701616	0	0
271	ENSRNOG000000020480	Fads1	fatty acid desaturase 1	1	0.03185532	0.714237823	1	1	0.089105717	-0.25178316	0	0
272	ENSRNOG000000020385	Fads3	fatty acid desaturase 3	1	0.040885456	1.044821645	1	1	0.104806358	-1.149399208	0	0
273	ENSRNOG000000013223	Fah	fumarylacetoacetate hydrolase	1	0.009961382	1.919801889	1	1	0.059071926	-0.28093644	0	0
274	ENSRNOG000000050946	Fam110a	family with sequence similarity 110, member A	1	0.007224467	1.40730414	1	1	0.055807062	-1.171513383	0	0
275	ENSRNOG000000049425	Fam167b	family with sequence similarity 167, member B	1	0.02104379	0.88644824	1	1	0.074167644	-0.879689965	0	0
276	ENSRNOG000000039528	Fam32a	family with sequence similarity 32, member A	1	0.030525343	0.676690452	1	1	0.116702365	-0.267775437	0	0
277	ENSRNOG000000022582	Fam58b	family with sequence similarity 58, member B	1	0.000604924	0.690128003	1	1	0.293890918	-0.243675467	0	0
278	ENSRNOG000000003149	Farsa	phenylalanyl-tRNA synthetase, alpha subunit	1	0.029157713	1.449891898	1	1	0.065258258	-0.890264886	0	0
279	ENSRNOG000000008577	Fbf1	Fas binding factor 1	1	0.042889732	0.874207903	1	1	0.115328184	-0.945332276	0	0
280	ENSRNOG000000007338	Fbln2	fibulin 2	1	0.006506448	2.276549269	1	1	0.092347493	-0.513081873	0	0
281	ENSRNOG000000007302	Fbn1	fibrillin 1	1	0.039169437	1.526386509	1	1	0.103188952	-0.587020695	0	0
282	ENSRNOG000000017597	Fbp1	fructose-bisphosphatase 1	1	0.028257086	0.753154851	1	1	0.195165506	0.183413023	0	0
283	ENSRNOG000000025497	Fbx06	F-box and leucine-rich repeat protein 6	1	0.009317288	1.990311589	1	1	0.078784084	-1.099424668	0	0
284	ENSRNOG000000046211	Fbxw4	F-box and WD repeat domain containing 4	1	0.043022964	0.934006828	1	1	0.05351493	-0.789039002	0	0
285	ENSRNOG000000024159	Fcer1g	Fc fragment of IgE receptor Ig	1	0.023512861	1.709814001	1	1	0.276102476	-0.269972355	0	0
286	ENSRNOG000000021199	Fcgr1a	Fc fragment of IgG receptor Ia	1	0.01481222	2.197044647	1	1	0.365547824	-0.123281244	0	0
287	ENSRNOG000000046663	Fcgr2a	Fc fragment of IgG, low affinity IIa, receptor	1	0.012276119	3.952745226	1	1	0.05010282	-1.275008234	0	0
288	ENSRNOG000000046452	Fcgr2b	Fc fragment of IgG receptor IIb	1	0.013297014	2.40873809	1	1	0.445683746	0.188781049	0	0
289	ENSRNOG000000003136	Fcrla	Fc receptor-like A	1	0.010996483	1.417177654	1	1	0.084417075	-0.912470042	0	0
290	ENSRNOG000000011683	Fes	FES proto-oncogene, tyrosine kinase	1	0.000547135	1.612265761	1	1	0.05456141	-1.341777461	0	0
291	ENSRNOG000000000528	Fgd2	FYVE, RhoGEF and PH domain containing 2	1	0.000297359	1.765903646	1	1	0.037241156	-0.32153091	0	0
292	ENSRNOG000000054625	Fhod1	formin homology 2 domain containing 1	1	0.022830839	1.223975812	1	1	0.075126198	-1.535126663	0	0
293	ENSRNOG000000004899	Fibin	fin bud initiation factor homolog (zebrafish)	1	0.023413971	1.384974821	1	1	0.059227019	-0.543085705	0	0
294	ENSRNOG000000021153	Fkbp2	FK506 binding protein 2	1	0.009561134	1.7082819	1	1	0.096925109	-0.791242209	0	0
295	ENSRNOG000000014288	Fn1	fibronectin 1	1	0.038227295	2.543781418	1	1	0.327751327	-0.46505529	0	0
296	ENSRNOG000000019890	Folr2	folate receptor beta	1	0.008123716	2.621828874	1	1	0.088118888	-0.440194529	0	0
297	ENSRNOG000000047446	Foxc2	forkhead box C2	1	0.015266395	1.466971837	1	1	0.033828426	-0.549154002	0	0
298	ENSRNOG000000020843	Ftl1	ferritin light chain 1	1	0.002662575	2.978705415	1	1	0.050529688	-1.531216017	0	0
299	ENSRNOG000000009325	Fuca1	alpha-L-fucosidase 1	1	0.004158196	1.555135046	1	1	0.06513206	-0.393827198	0	0
300	ENSRNOG000000016469	Fxyd2	FXYD domain-containing ion transport regulator 2	1	0.035270809	1.884722234	1	1	0.245578926	-0.359563795	0	0
301	ENSRNOG000000004169	Fzr1	fizzy and cell division cycle 20 related 1	1	0.039540997	2.162668813	1	1	0.068737122	-1.176845688	0	0
302	ENSRNOG000000021105	Gabpb2	GA binding protein transcription factor, beta subunit 2	1	0.027199841	0.631581974	1	1	0.343995862	0.062271205	0	0
303	ENSRNOG000000019822	Gadd45b	growth arrest and DNA-damage-inducible, beta	1	0.008081374	1.10519682	1	1	0.112751672	-0.591054296	0	0
304	ENSRNOG000000004589	Gaint16	polypeptide N-acetylglucosaminyltransferase 16	1	0.044444383	0.970238874	1	1	0.132668299	-0.058098406	0	0
305	ENSRNOG000000001528	Gap43	growth associated protein 43	1	0.041408179	1.158350389	1	1	0.220721261	0.221571812	0	0
306	ENSRNOG000000026989	Gapt	Grb2-binding adaptor protein, transmembrane	1	0.043237432	0.592019434	1	1	0.031044962	0.448647038	0	0
307	ENSRNOG000000049361	Gas7	growth arrest specific 7	1	0.044028274	0.857709709	1	1	0.05261051	0.430174392	0	0
308	ENSRNOG000000007810	Gdf6	growth differentiation factor 6	1	0.003257017	1.789809348	1	1	0.14642135	-1.01960549	0	0
309	ENSRNOG000000049772	Gemin7	gem (nuclear organelle) associated protein 7	1	0.047749535	1.385125002	1	1	0.160891249	-0.575713599	0	0
310	ENSRNOG000000013370	Gfer	growth factor, augmentor of liver regeneration	1	0.022302462	0.789131267	1	1	0.036596717	-0.480978117	0	0

311	ENSRNOG00000018908	Ghdc	GH3 domain containing	1	0.007997655	1.849122857	1	1	0.151660092	-0.86664648	0	0
312	ENSRNOG00000003864	Gipc1	GIPC PDZ domain containing family, member 1	1	0.001853527	0.997858138	1	1	0.058710296	-0.988952582	0	0
313	ENSRNOG00000011513	Gla	galactosidase, alpha	1	0.035164471	0.855849477	1	1	0.386999241	-0.081977717	0	0
314	ENSRNOG000000026644	Glipr1	GLI pathogenesis-related 1	1	0.034502586	1.885867774	1	1	0.303300945	-0.370806281	0	0
315	ENSRNOG00000014838	Glipr2	GLI pathogenesis-related 2	1	0.047069581	1.426851433	1	1	0.147921661	-0.223044526	0	0
316	ENSRNOG00000012183	Glrax	glutaredoxin	1	0.042382181	0.901582752	1	1	0.33794159	-0.159003316	0	0
317	ENSRNOG00000011192	Gltg	glycolipid transfer protein	1	0.008941314	0.885169844	1	1	0.193245018	-0.272116115	0	0
318	ENSRNOG00000019838	Gmfg	glia maturation factor, gamma	1	0.030355424	1.478070954	1	1	0.302306875	-0.180759213	0	0
319	ENSRNOG00000018782	Gmnn	geminin, DNA replication inhibitor	1	0.045063789	2.260562569	1	1	0.228778636	-0.78332841	0	0
320	ENSRNOG00000005378	Gna15	G protein subunit alpha 15	1	0.044711123	1.337311912	1	1	0.091147024	-0.735765031	0	0
321	ENSRNOG00000016592	Gna12	G protein subunit alpha i2	1	0.011918826	0.715154856	1	1	0.209765395	-0.352999505	0	0
322	ENSRNOG00000019570	Gng3	G protein subunit gamma 3	1	0.035287084	0.661963954	1	1	0.154035101	-0.396120705	0	0
323	ENSRNOG000000029280	Gpaa1	glycosylphosphatidylinositol anchor attachment 1	1	0.03584539	1.33127743	1	1	0.126309013	-1.158633966	0	0
324	ENSRNOG00000004941	Gpn1	GPN-loop GTPase 1	1	0.011809117	0.729842081	1	1	0.036663196	-0.476357402	0	0
325	ENSRNOG000000046128	Gpr108	G protein-coupled receptor 108	1	0.024982001	1.095750147	1	1	0.143543756	-0.555103405	0	0
326	ENSRNOG00000005971	Gpr176	G protein-coupled receptor 176	1	0.002859389	1.174631242	1	1	0.055246121	-0.846757704	0	0
327	ENSRNOG000000012628	Gpr18	G protein-coupled receptor 18	1	0.038466175	0.83006422	1	1	0.422238466	-0.080593144	0	0
328	ENSRNOG000000021586	Gpr39	G protein-coupled receptor 39	1	0.029441832	2.523391051	1	1	0.087759672	-0.939782482	0	0
329	ENSRNOG000000000095	Gpr89b	G protein-coupled receptor 89b	1	0.04341011	0.619141869	1	1	0.048045445	-0.380100617	0	0
330	ENSRNOG000000008412	Gprc5a	G protein-coupled receptor, class C, group 5, member A	1	0.024072133	1.56183252	1	1	0.459866423	-0.080849503	0	0
331	ENSRNOG000000046698	Gps1	G protein pathway suppressor 1	1	0.029780291	1.121272682	1	1	0.139362596	-0.620248907	0	0
332	ENSRNOG000000009751	Gpx7	glutathione peroxidase 7	1	0.005325584	1.811240442	1	1	0.047692642	-0.571313842	0	0
333	ENSRNOG000000021108	Gramd1a	GRAM domain containing 1A	1	0.030853458	0.715467674	1	1	0.056335218	-0.887479345	0	0
334	ENSRNOG000000029941	Grina	glutamate ionotropic receptor NMDA type subunit associated	1	0.049831322	1.58961943	1	1	0.143866768	-0.790751711	0	0
335	ENSRNOG000000018985	Grk2	G protein-coupled receptor kinase 2	1	0.019754086	0.672341906	1	1	0.172380319	-0.376858234	0	0
336	ENSRNOG00000014615	Grk6	G protein-coupled receptor kinase 6	1	0.011532722	0.93860107	1	1	0.180689401	-0.308981964	0	0
337	ENSRNOG000000021031	Gn	granulin precursor	1	0.021294669	1.599288168	1	1	0.057040273	-0.907788433	0	0
338	ENSRNOG000000021058	Gnwd1	glutamate-rich WD repeat containing 1	1	0.045203503	0.943947052	1	1	0.109856906	-0.722750282	0	0
339	ENSRNOG000000029728	Gstm1	glutathione S-transferase mu 1	1	0.047599062	0.958518421	1	1	0.425798635	0.051883221	0	0
340	ENSRNOG000000049771	Gstt1	glutathione S-transferase theta 1	1	0.048144266	1.225998768	1	1	0.229027446	-0.380055243	0	0
341	ENSRNOG000000047134	Gtf2f1	general transcription factor IIF subunit 1	1	0.017109441	1.385902126	1	1	0.074471071	-0.916618418	0	0
342	ENSRNOG000000050016	Gtf3a	general transcription factor III A	1	0.017238259	1.023021766	1	1	0.167148679	-0.619291286	0	0
343	ENSRNOG000000052275	H2afv	H2A histone family, member V	1	0.006849735	0.613339551	1	1	0.453392387	-0.019702106	0	0
344	ENSRNOG000000011523	H2afy	H2A histone family, member Y	1	0.002883249	0.945604918	1	1	0.034536584	-0.570819461	0	0
345	ENSRNOG00000010306	H2afz	H2A histone family, member Z	1	0.034575547	0.928491225	1	1	0.222356458	-0.379724719	0	0
346	ENSRNOG00000010994	Has1	hyaluronan synthase 1	1	0.04476243	1.633918518	1	1	0.478308599	0.055476783	0	0
347	ENSRNOG00000004854	Has2	hyaluronan synthase 2	1	0.017645404	1.758075959	1	1	0.463218192	-0.035721581	0	0
348	ENSRNOG000000024266	Haus5	HAUS augmin-like complex, subunit 5	1	0.031046135	1.220292232	1	1	0.056216192	-1.011077873	0	0
349	ENSRNOG000000053510	Hofc2	host cell factor C2	1	0.018638715	0.629306087	1	1	0.021921661	-0.208869756	0	0
350	ENSRNOG000000038881	Hols1	hematopoietic cell specific Lyn substrate 1	1	0.032655955	1.868010166	1	1	0.105361216	-0.652733766	0	0
351	ENSRNOG000000000024	Hebp1	heme binding protein 1	1	0.023266395	1.529125994	1	1	0.055219019	-0.382398638	0	0
352	ENSRNOG000000018363	Hectd3	HECT domain E3 ubiquitin protein ligase 3	1	0.004905593	0.659521645	1	1	0.130485553	-0.667821233	0	0
353	ENSRNOG00000003464	Hid1	HID1 domain containing	1	0.044316254	1.202303688	1	1	0.412365768	-0.210671253	0	0
354	ENSRNOG000000007738	Hm13	histocompatibility minor 13	1	0.027646093	1.131162677	1	1	0.066377974	-0.703588416	0	0
355	ENSRNOG000000000488	Hmga1	high mobility group AT-hook 1	1	0.047791325	1.299530379	1	1	0.080179988	-0.892854744	0	0

356	ENSRNOG00000033321	Hmgb2l1	high mobility group box 2-like 1	1	0.008890897	0.617670152	1	1	0.235394593	-0.311729812	0	0
357	ENSRNOG00000020229	Homer3	homer scaffolding protein 3	1	0.011690842	0.937596874	1	1	0.168971243	-0.88661434	0	0
358	ENSRNOG00000045838	Hps1	HPS1, biogenesis of lysosomal organelles complex 3 subunit	1	0.026206193	1.607781806	1	1	0.059188539	-0.692171	0	0
359	ENSRNOG00000018433	Hps6	HPS6, biogenesis of lysosomal organelles complex 2 subunit	1	0.036977588	1.203682958	1	1	0.086481001	-1.057655576	0	0
360	ENSRNOG00000008062	Hs1bp3	HCLS1 binding protein 3	1	0.009017033	0.860625359	1	1	0.121492518	-0.56817221	0	0
361	ENSRNOG00000011193	Hsf2bp	heat shock transcription factor 2 binding protein	1	0.037730639	0.603784228	1	1	0.023384939	-0.520095539	0	0
362	ENSRNOG00000017625	Htr2b	5-hydroxytryptamine receptor 2B	1	0.022546189	2.42384897	1	1	0.068844562	-1.167698811	0	0
363	ENSRNOG00000022448	Htra2	HtrA serine peptidase 2	1	0.005341976	0.848391757	1	1	0.121672023	-0.496729956	0	0
364	ENSRNOG00000010944	Hyou1	hypoxia up-regulated 1	1	0.04336101	0.71769844	1	1	0.111719812	-0.572147292	0	0
365	ENSRNOG00000008053	Iah1	isoamyl acetate-hydrolyzing esterase 1 homolog	1	0.014161506	0.682193908	1	1	0.067646093	-0.110030852	0	0
366	ENSRNOG00000014936	Ifitm2	interferon induced transmembrane protein 2	1	0.020715537	1.562914148	1	1	0.472461279	-0.021018497	0	0
367	ENSRNOG00000015078	Ifitm3	interferon induced transmembrane protein 3	1	0.018185091	0.71835954	1	1	0.05754279	0.419752671	0	0
368	ENSRNOG000000031346	Ifi22	intraflagellar transport 22	1	0.017800152	1.549484932	1	1	0.108988966	-0.318405235	0	0
369	ENSRNOG000000033496	Igdc4	immunoglobulin superfamily, DCC subclass, member 4	1	0.031598786	0.957056015	1	1	0.187375216	-0.661253722	0	0
370	ENSRNOG00000014997	Igf2r	insulin-like growth factor 2 receptor	1	0.023822909	0.64328476	1	1	0.103590856	-0.390291988	0	0
371	ENSRNOG00000009204	Il17re	interleukin 17 receptor E	1	0.01527274	0.884349788	1	1	0.132397904	1.282555874	0	0
372	ENSRNOG000000020150	Il18bp	interleukin 18 binding protein	1	0.02797214	0.864296171	1	1	0.442087097	-0.049800492	0	0
373	ENSRNOG00000004649	Il1b	interleukin 1 beta	1	0.020982967	1.248699293	1	1	0.367767878	-0.255871673	0	0
374	ENSRNOG00000014378	Il1r2	interleukin 1 receptor type 2	1	0.016518585	2.211528333	1	1	0.178564996	-0.351813211	0	0
375	ENSRNOG00000014835	Il1r1	interleukin 1 receptor-like 1	1	0.030788085	3.061275519	1	1	0.23048914	-1.155549173	0	0
376	ENSRNOG000000023214	Il20rb	interleukin 20 receptor subunit beta	1	0.008093925	1.122252579	1	1	0.067334873	-0.593011948	0	0
377	ENSRNOG00000015441	Il4r	interleukin 4 receptor	1	0.021371078	1.866519002	1	1	0.102557134	-0.862040811	0	0
378	ENSRNOG000000020032	Impdh1	inosine monophosphate dehydrogenase 1	1	0.000632508	0.818349398	1	1	0.131857872	-0.704532471	0	0
379	ENSRNOG000000031965	Impdh2	inosine monophosphate dehydrogenase 2	1	0.02406041	0.930333644	1	1	0.048571685	-0.441254854	0	0
380	ENSRNOG000000060237	Inhb	inhibin beta B subunit	1	0.033519619	1.084633595	1	1	0.452038066	0.032315298	0	0
381	ENSRNOG00000015153	Ints3	integrator complex subunit 3	1	0.010746293	0.640022056	1	1	0.119156438	-0.575329622	0	0
382	ENSRNOG000000026005	Ints5	integrator complex subunit 5	1	0.022246742	0.98896704	1	1	0.079063789	-0.864907002	0	0
383	ENSRNOG00000019553	Ipo4	importin 4	1	0.001717813	1.89073613	1	1	0.088915592	-1.447009886	0	0
384	ENSRNOG00000014252	Irf2bp1	interferon regulatory factor 2 binding protein 1	1	0.046802014	0.613813805	1	1	0.073539342	-0.897210738	0	0
385	ENSRNOG00000017889	Irf8	interferon regulatory factor 8	1	0.035982276	0.997907474	1	1	0.11833046	-0.341862868	0	0
386	ENSRNOG00000010021	Iry1	ISY1 splicing factor homolog	1	0.02337025	0.900670234	1	1	0.03429329	-0.402586497	0	0
387	ENSRNOG000000057451	Itga5	integrin subunit alpha 5	1	0.021010137	1.33361259	1	1	0.123622509	-1.058472776	0	0
388	ENSRNOG00000001224	Itgb2	integrin subunit beta 2	1	0.031433556	3.235262394	1	1	0.150421074	-1.202410506	0	0
389	ENSRNOG00000008224	Jdp2	Jun dimerization protein 2	1	0.01732515	1.30866966	1	1	0.036032756	-0.410948713	0	0
390	ENSRNOG000000002050	Jmjd6	arginine demethylase and lysine hydroxylase	1	0.008871802	0.963760912	1	1	0.014783049	-0.553254331	0	0
391	ENSRNOG00000014626	Katnb1	katanin regulatory subunit B1	1	0.048260672	1.414171261	1	1	0.165148197	-0.837513568	0	0
392	ENSRNOG000000039544	Kond1	potassium voltage-gated channel subfamily D member 1	1	0.037274809	1.363817065	1	1	0.103239225	-0.783483979	0	0
393	ENSRNOG0000000021137	Kctd15	potassium channel tetramerization domain containing 15	1	0.046598579	1.298501161	1	1	0.055327495	-0.606849619	0	0
394	ENSRNOG0000000020231	Kctd17	potassium channel tetramerization domain containing 17	1	0.016882284	0.899307273	1	1	0.055247589	-0.598771193	0	0
395	ENSRNOG000000020880	Klhl18	kelch-like family member 18	1	0.007520861	0.844176043	1	1	0.12683077	-0.688631844	0	0
396	ENSRNOG00000001878	Klhl22	kelch-like family member 22	1	0.008805186	0.652938104	1	1	0.150191987	-0.352303014	0	0
397	ENSRNOG000000001908	Klhl6	kelch-like family member 6	1	0.017833805	1.486376919	1	1	0.114364113	-0.506629119	0	0
398	ENSRNOG000000051487	Kremen1	kringle containing transmembrane protein 1	1	0.033012896	0.913855593	1	1	0.101515206	-0.442559412	0	0
399	ENSRNOG000000020542	Krtcap2	keratinocyte associated protein 2	1	0.007431763	0.724662418	1	1	0.018703262	-0.438164358	0	0
400	ENSRNOG00000011054	Laptn5	lysosomal protein transmembrane 5	1	0.031472726	1.690552443	1	1	0.05255672	-0.839188716	0	0

401	ENSRNOG000000021856	Lat2	linker for activation of T cells family, member 2	1	0.038589615	1.240110725	1	1	0.073428798	-0.54284708	0	0
402	ENSRNOG00000001250	Lfng	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	1	0.007888973	1.342628883	1	1	0.122713399	-0.853095312	0	0
403	ENSRNOG000000009884	Lgals1	galectin 1	1	0.017222123	2.127289759	1	1	0.084977657	-0.940819926	0	0
404	ENSRNOG000000017097	Lhpp	phosphorylase phosphohistidine inorganic pyrophosphatase	1	0.015843183	0.745855532	1	1	0.241846838	-0.627154067	0	0
405	ENSRNOG000000046683	Lilrb3	leukocyte immunoglobulin like receptor B3	1	0.021858906	2.403728346	1	1	0.084474312	-1.712766975	0	0
406	ENSRNOG000000058422	Lilrb3b	leukocyte immunoglobulin-like receptor, subfamily B (with IL13R-ITAM)	1	0.042072271	1.70607234	1	1	0.44844459	-0.084813805	0	0
407	ENSRNOG000000027811	Lilrb4	leukocyte immunoglobulin like receptor B4	1	0.021640714	4.550937941	1	1	0.137906075	-2.011131936	0	0
408	ENSRNOG000000025448	Limd2	LIM domain containing 2	1	0.001353424	1.982914273	1	1	0.111535963	-0.91630036	0	0
409	ENSRNOG000000001470	Limk1	LIM domain kinase 1	1	0.018446314	0.702063133	1	1	0.180864147	-0.509377428	0	0
410	ENSRNOG000000018694	Lipg	lipase G, endothelial type	1	0.022539135	1.241953751	1	1	0.497812978	0.001418879	0	0
411	ENSRNOG000000003948	Lig1	LLGL1, scribble cell polarity complex component	1	0.028056824	1.333473481	1	1	0.199624991	-0.706716938	0	0
412	ENSRNOG000000016181	Lman2	lectin, mannose-binding 2	1	0.022910972	1.946938417	1	1	0.071383077	-1.160840486	0	0
413	ENSRNOG00000000230	Lmf1	lipase maturation factor 1	1	0.043683194	1.264394709	1	1	0.139779877	-0.971239299	0	0
414	ENSRNOG000000003045	LOC10036	ribosomal protein S20-like	1	0.037618371	0.857195352	1	1	0.291747328	-0.189321617	0	0
415	ENSRNOG000000031506	LOC10036	ferritin light chain 1-like	1	0.005618371	1.067684405	1	1	0.050092132	-0.789033303	0	0
416	ENSRNOG000000020093	LOC10036	ribosomal protein S12-like	1	0.015182953	1.06250444	1	1	0.396839184	0.083551753	0	0
417	ENSRNOG000000033152	LOC10036	ribosomal protein S18-like	1	0.030888904	2.189428738	1	1	0.063953658	-1.434851869	0	0
418	ENSRNOG000000029512	LOC10036	ribosomal protein S26-like	1	0.044915937	1.052464588	1	1	0.481199917	-0.007147816	0	0
419	ENSRNOG000000062272	LOC10036	ribosomal protein S12-like	1	0.005211916	1.510402111	1	1	0.052425005	-0.641899758	0	0
420	ENSRNOG000000018471	LOC10036	ribosomal protein S19-like	1	0.037286256	1.042814751	1	1	0.361808427	-0.075020451	0	0
421	ENSRNOG0000000021395	LOC10036	ribosomal protein S8-like	1	0.009899179	1.155636848	1	1	0.043570788	-0.361801936	0	0
422	ENSRNOG000000045885	LOC10036	40S ribosomal protein S17-like	1	0.001434246	0.939993116	1	1	0.3684008	-0.05369796	0	0
423	ENSRNOG000000022426	LOC10254	uncharacterized LOC102546884	1	0.000404662	1.645045659	1	1	0.057598177	-0.948182892	0	0
424	ENSRNOG000000059338	LOC10254	uncharacterized LOC102549714	1	0.033735329	2.48408538	1	1	0.159536928	-0.831923477	0	0
425	ENSRNOG000000046480	LOC10255	KRAB domain-containing protein ZNF747-like	1	0.039461003	0.962473258	1	1	0.117198883	-0.85402825	0	0
426	ENSRNOG000000028993	LOC10255	60S ribosomal protein L12-like	1	0.012088132	0.908619057	1	1	0.462694366	-0.020833832	0	0
427	ENSRNOG000000046031	LOC10368	antigen peptide transporter 2	1	0.034151714	0.817878953	1	1	0.468191297	-0.034361333	0	0
428	ENSRNOG000000048456	LOC10834	60S ribosomal protein L8	1	0.01415061	1.240719885	1	1	0.204951176	-0.354598483	0	0
429	ENSRNOG000000046980	LOC10834	coronin-7-like	1	0.045201848	0.757487488	1	1	0.067101303	-0.831176248	0	0
430	ENSRNOG000000002820	LOC24906	RoBo-1	1	0.017229295	2.541990006	1	1	0.202153782	-0.372983931	0	0
431	ENSRNOG000000039504	LOC38091	similar to alpha-fetoprotein	1	0.036275981	1.245080231	1	1	0.09895552	-0.890649346	0	0
432	ENSRNOG000000001289	LOC49815	hypothetical protein LOC498154	1	0.012331287	2.25103277	1	1	0.081438039	-0.947632632	0	0
433	ENSRNOG000000017857	LOC88083	similar to cullin 7	1	0.022577064	1.715284603	1	1	0.109194262	-0.861808396	0	0
434	ENSRNOG000000048881	LOC88091	similar to paired immunoglobulin-like type 2 receptor beta	1	0.027210951	2.423207778	1	1	0.211828081	-0.357207272	0	0
435	ENSRNOG000000029470	LOC88561	similar to TP53-regulating kinase (p53-related protein kinase)	1	0.041311222	0.831481279	1	1	0.121368871	-0.7952714	0	0
436	ENSRNOG000000037076	LOC88975	similar to osteoclast inhibitory lectin	1	0.03001131	3.157771497	1	1	0.102756431	-1.806366613	0	0
437	ENSRNOG000000051792	LOC88995	hypothetical protein LOC889959	1	0.004099303	0.697330494	1	1	0.494192678	0.002012666	0	0
438	ENSRNOG000000016758	Loxl2	lysyl oxidase-like 2	1	0.032417626	1.850520941	1	1	0.084268878	-0.687109116	0	0
439	ENSRNOG000000005058	Lpcat4	lysophosphatidylcholine acyltransferase 4	1	0.033583063	1.399299344	1	1	0.111374112	-0.394287344	0	0
440	ENSRNOG000000009313	Lrpap1	LDL receptor related protein associated protein 1	1	0.009840287	0.681802668	1	1	0.033907937	-0.289051889	0	0
441	ENSRNOG000000013642	Lrrc41	leucine rich repeat containing 41	1	0.009642094	0.908138963	1	1	0.089190056	-0.816720411	0	0
442	ENSRNOG000000027286	Lrrc75a	leucine rich repeat containing 75A	1	0.02504379	0.79557413	1	1	0.269618992	-0.313355024	0	0
443	ENSRNOG000000012730	Lrrk1	leucine-rich repeat kinase 1	1	0.013177988	1.030787872	1	1	0.047178401	-0.424558508	0	0
444	ENSRNOG000000025716	Lsm10	LSM10, U7 small nuclear RNA associated	1	0.023111647	0.755008597	1	1	0.069480243	-0.489702687	0	0
445	ENSRNOG000000019572	Lsm4	LSM4 homolog, U6 small nuclear RNA and mRNA degradation	1	0.013321702	1.227213787	1	1	0.061411765	-0.934546905	0	0

448	ENSRNOG00000054549	Lss	lanosterol synthase	1	0.047885284	0.711259395	1	1	0.055802993	-0.750274881	0	0
447	ENSRNOG00000019284	Ltbr	lymphotoxin beta receptor	1	0.045182283	1.54583239	1	1	0.109008889	-1.045371197	0	0
448	ENSRNOG00000000137	Ly88	lymphocyte antigen 88	1	0.041802234	1.599276729	1	1	0.385501483	0.158508145	0	0
449	ENSRNOG000000034139	Lyc2	lysozyme C type 2	1	0.036257637	2.689152705	1	1	0.157522585	-0.499341309	0	0
450	ENSRNOG00000010087	Lypla2	lysophospholipase II	1	0.035553962	1.403215409	1	1	0.113378595	-0.914283253	0	0
451	ENSRNOG00000005825	Lyz2	lysozyme 2	1	0.019178195	2.374409058	1	1	0.207874767	-0.441670325	0	0
452	ENSRNOG00000001870	Lztr1	leucine-zipper-like transcription regulator 1	1	0.032024136	0.681919545	1	1	0.110800717	-0.580714229	0	0
453	ENSRNOG00000001285	Mad1l1	mitotic arrest deficient 1 like 1	1	0.005944831	1.878916888	1	1	0.166533758	-0.98219382	0	0
454	ENSRNOG000000019463	Mad2l1bp	MAD2L1 binding protein	1	0.0370471	1.407485224	1	1	0.0543006	-0.890730576	0	0
455	ENSRNOG000000005397	Maea	macrophage erythroblast attacher	1	0.04970071	0.72397428	1	1	0.108885058	-0.525503823	0	0
456	ENSRNOG000000016037	Mafk	MAF bZIP transcription factor B	1	0.017294869	1.194614767	1	1	0.391974553	0.147894992	0	0
457	ENSRNOG000000012559	Man1b1	mannosidase, alpha, class 1B, member 1	1	0.013778291	0.748545024	1	1	0.084839873	-0.518634902	0	0
458	ENSRNOG000000023910	Man2b1	mannosidase, alpha, class 2B, member 1	1	0.012075305	0.643181392	1	1	0.123227502	-0.257603411	0	0
459	ENSRNOG000000013177	Map3k1	mitogen-activated protein kinase kinase kinase 1	1	0.033749535	1.059851274	1	1	0.168591959	-0.434072028	0	0
460	ENSRNOG000000000975	Mcoln1	mucopolin 1	1	0.026897042	0.797808538	1	1	0.100054134	-0.428083804	0	0
461	ENSRNOG000000054838	Mors1	microspherule protein 1	1	0.045433832	1.588891427	1	1	0.152711744	-1.05107132	0	0
462	ENSRNOG000000019384	Med11	mediator complex subunit 11	1	0.013892435	0.74917347	1	1	0.268888008	-0.088523076	0	0
463	ENSRNOG000000008711	Med24	mediator complex subunit 24	1	0.004415971	0.654883327	1	1	0.102202807	-0.748587064	0	0
464	ENSRNOG000000021390	Meis3	Meis homeobox 3	1	0.049104062	0.879938355	1	1	0.163891745	-0.585349284	0	0
465	ENSRNOG000000015505	Mfap5	microfibril associated protein 5	1	0.022408593	1.480050423	1	1	0.128251778	0.291885089	0	0
466	ENSRNOG000000012534	Mfsd10	major facilitator superfamily domain containing 10	1	0.02887418	1.750391187	1	1	0.063584513	-1.449910517	0	0
467	ENSRNOG000000024780	MGC9521	hypothetical LOC287798	1	0.049208468	0.721125318	1	1	0.092248052	-0.399491005	0	0
468	ENSRNOG000000007743	Mgst1	microsomal glutathione S-transferase 1	1	0.008815958	1.182854142	1	1	0.412518033	0.028408933	0	0
469	ENSRNOG000000000307	Mical1	microtubule associated monooxygenase, calponin and L	1	0.009077443	1.262314804	1	1	0.072840358	-1.101231088	0	0
470	ENSRNOG000000016244	Mical2	microtubule associated monooxygenase, calponin and L	1	0.019884285	0.756273346	1	1	0.088951521	-0.387493549	0	0
471	ENSRNOG000000022533	Mical2	MICAL-like 2	1	0.016336391	1.221738558	1	1	0.054990345	-1.133860892	0	0
472	ENSRNOG000000017513	Miga2	mitoguardin 2	1	0.026992897	1.357114038	1	1	0.133994988	-1.088184447	0	0
473	ENSRNOG000000040350	Mir675	microRNA 675	1	0.018480934	1.387914416	1	1	0.44142935	0.124287694	0	0
474	ENSRNOG000000006778	Mmp19	matrix metalloproteinase 19	1	0.038095442	1.533778313	1	1	0.09223888	-0.38286238	0	0
475	ENSRNOG000000015113	Mocoos	molybdenum cofactor sulfuryase	1	0.01988692	0.732515246	1	1	0.207058548	-0.153876561	0	0
476	ENSRNOG000000011784	Mocs1	molybdenum cofactor synthesis 1	1	0.003458858	1.399383174	1	1	0.089599752	-0.783878551	0	0
477	ENSRNOG000000007850	Mok	MOK protein kinase	1	0.007233846	1.316038522	1	1	0.025720088	-0.482423431	0	0
478	ENSRNOG000000001398	Mospd3	motile sperm domain containing 3	1	0.002080981	1.704951406	1	1	0.073549135	-1.20722434	0	0
479	ENSRNOG000000019394	Mpv17l2	MPV17 mitochondrial inner membrane protein like 2	1	0.02235832	1.860956267	1	1	0.099615475	-0.892822867	0	0
480	ENSRNOG000000018085	Mpz2	myelin protein zero-like 2	1	0.010807688	0.783459983	1	1	0.117818428	1.208320883	0	0
481	ENSRNOG000000008548	Mrc2	mannose receptor, C type 2	1	0.029157581	1.772568011	1	1	0.150551134	-0.905055094	0	0
482	ENSRNOG000000013428	Mrgprf	MAS related GPR family member F	1	0.039155389	0.936829389	1	1	0.383228881	-0.123880418	0	0
483	ENSRNOG000000033685	Mrgprx2	MAS related GPR family member X2	1	0.038800221	1.59777838	1	1	0.125942211	-1.248840428	0	0
484	ENSRNOG000000028211	Mri1	methylthioninose-1-phosphate isomerase 1	1	0.008443831	1.218880738	1	1	0.115847321	-1.139040509	0	0
485	ENSRNOG000000039297	Mrip52	mitochondrial ribosomal protein L52	1	0.044378802	0.867017987	1	1	0.114908351	-0.519849615	0	0
486	ENSRNOG0000000050395	Ms4a6bl	membrane-spanning 4-domains, subfamily A, member 6	1	0.044501758	1.276848887	1	1	0.402251088	-0.128037214	0	0
487	ENSRNOG000000012779	Msr1	macrophage scavenger receptor 1	1	0.035120888	3.794168398	1	1	0.205291428	-1.072138967	0	0
488	ENSRNOG000000059919	Mtg2	mitochondrial ribosome-associated GTPase 2	1	0.048250803	0.880750127	1	1	0.265841735	-0.333805874	0	0
489	ENSRNOG000000020817	Mus81	MUS81 structure-specific endonuclease subunit	1	0.039855734	1.32821659	1	1	0.100218881	-1.047381478	0	0
490	ENSRNOG000000017369	Mustn1	musculoskeletal, embryonic nuclear protein 1	1	0.008812234	0.870154343	1	1	0.126261018	-0.223574027	0	0

491	ENSRNOG00000017887	Mutyh	mutY DNA glycosylase	1	0.005551065	0.800572921	1	1	0.056815875	-1.197049385	0	0
492	ENSRNOG00000017949	Mvb12a	multivesicular body subunit 12A	1	0.034162747	1.900881501	1	1	0.098257982	-0.892960213	0	0
493	ENSRNOG00000020182	Mvp	major vault protein	1	0.046156955	1.520361934	1	1	0.1670962	-0.842229806	0	0
494	ENSRNOG00000019244	Mxra8	matrix remodeling associated 8	1	0.012913178	0.715877486	1	1	0.279346804	-0.056984409	0	0
495	ENSRNOG00000015236	Mybbp1a	MYB binding protein 1a	1	0.032078477	0.845897823	1	1	0.081840701	-0.726881916	0	0
496	ENSRNOG00000019627	Mybpc2	myosin binding protein C, fast-type	1	0.022292807	3.359841486	1	1	0.103297635	-1.998884881	0	0
497	ENSRNOG00000013634	Myd88	myeloid differentiation primary response 88	1	0.03638356	0.927568891	1	1	0.074066893	-0.369417495	0	0
498	ENSRNOG00000046883	Mydgf	myeloid-derived growth factor	1	0.009141301	1.572176999	1	1	0.079847252	-0.862048873	0	0
499	ENSRNOG00000016983	Myh7	myosin heavy chain 7	1	0.047343769	2.359131069	1	1	0.294873388	-0.425285718	0	0
500	ENSRNOG000000054140	Myh8	myosin light chain 8	1	0.007333149	1.313190943	1	1	0.034670023	-0.531547311	0	0
501	ENSRNOG00000017645	Myh9	myosin light chain, phosphorylatable, fast skeletal muscle	1	0.004443694	0.783397794	1	1	0.007365078	-0.335976917	0	0
502	ENSRNOG000000059219	Myo15a	myosin XVA	1	0.008950693	0.984731312	1	1	0.050839818	-0.548513631	0	0
503	ENSRNOG000000008409	Myo1f	myosin IF	1	0.044224122	2.43615078	1	1	0.06030991	-1.178865642	0	0
504	ENSRNOG00000016256	Myo9b	myosin IXb	1	0.018605751	1.266881466	1	1	0.062982208	-1.039152702	0	0
505	ENSRNOG000000028274	Myrf	myelin regulatory factor	1	0.019716847	2.473023061	1	1	0.228770085	-0.572847048	0	0
506	ENSRNOG000000002273	Naaa	N-acyl ethanolamine acid amidase	1	0.004493069	1.136006916	1	1	0.188373767	-0.117184962	0	0
507	ENSRNOG000000002884	Naoa1	nucleus accumbens associated 1	1	0.021445693	1.011885305	1	1	0.163372733	-0.904204563	0	0
508	ENSRNOG000000020736	Nadsyn1	NAD synthetase 1	1	0.026037377	1.202476567	1	1	0.002205572	-0.508173549	0	0
509	ENSRNOG000000008064	Naga	alpha-N-acetylglucosaminidase	1	0.035065858	0.726328881	1	1	0.094848424	-0.643468319	0	0
510	ENSRNOG000000032381	Naglu	N-acetyl-alpha-glucosaminidase	1	0.001875457	0.764320055	1	1	0.085830908	-0.918035667	0	0
511	ENSRNOG000000019854	Napsa	napsin A aspartic peptidase	1	0.010469485	2.732407787	1	1	0.151388456	-0.750860745	0	0
512	ENSRNOG000000003264	Nat9	N-acetyltransferase 9	1	0.029298255	1.206072398	1	1	0.099180057	-0.602039481	0	0
513	ENSRNOG000000008425	Nav1	neuron navigator 1	1	0.004891249	1.333526742	1	1	0.210048273	-0.404620101	0	0
514	ENSRNOG000000031890	Ncam1	neural cell adhesion molecule 1	1	0.006049579	3.184311829	1	1	0.114205986	-1.275955125	0	0
515	ENSRNOG000000006940	Ncf4	neutrophil cytosolic factor 4	1	0.001369637	2.893591149	1	1	0.06787594	-0.814910775	0	0
516	ENSRNOG000000031816	Nckipd	NCK interacting protein with SH3 domain	1	0.033345424	0.848880199	1	1	0.078940901	-0.82381836	0	0
517	ENSRNOG000000019014	Ndst1	N-deacetylase and N-sulfotransferase 1	1	0.018208951	0.920114857	1	1	0.478519619	-0.041845876	0	0
518	ENSRNOG000000016708	Necab3	N-terminal EF-hand calcium binding protein 3	1	0.04354348	2.095367442	1	1	0.057085649	-1.256386734	0	0
519	ENSRNOG000000008427	Necap2	NECAP endocytosis associated 2	1	0.008613889	1.283747407	1	1	0.082958072	-0.836426101	0	0
520	ENSRNOG000000015474	Nelfa	negative elongation factor complex member A	1	0.030623543	0.67276841	1	1	0.032983794	-0.57134036	0	0
521	ENSRNOG000000009377	Nelfb	negative elongation factor complex member B	1	0.019675471	0.955059437	1	1	0.166947383	-0.768029235	0	0
522	ENSRNOG000000000420	Nelfe	negative elongation factor complex member E	1	0.029219502	1.837036749	1	1	0.095283429	-1.087282154	0	0
523	ENSRNOG000000019907	Nfkbie	NFKB inhibitor epsilon	1	0.019104338	0.932758475	1	1	0.057791325	-0.430076037	0	0
524	ENSRNOG000000016571	Ngf	nerve growth factor	1	0.049879319	0.856068708	1	1	0.141097786	-0.580108935	0	0
525	ENSRNOG000000011445	Nkain1	Sodium/potassium transporting ATPase interacting 1	1	0.037539894	1.407429091	1	1	0.14916123	-0.639976067	0	0
526	ENSRNOG000000015430	Nlgn2	neuroligin 2	1	0.009886766	0.88391373	1	1	0.15647714	-0.421538189	0	0
527	ENSRNOG000000020721	Nme6	NME/NM23 nucleoside diphosphate kinase 6	1	0.037403903	0.802044782	1	1	0.150022136	-0.277896899	0	0
528	ENSRNOG000000005930	Nnmt	nicotinamide N-methyltransferase	1	0.022580374	1.403386918	1	1	0.20649769	-0.298705321	0	0
529	ENSRNOG000000010209	Nol12	nucleolar protein 12	1	0.045713951	1.482084749	1	1	0.088817613	-0.953265781	0	0
530	ENSRNOG000000020321	Nop9	NOP9 nucleolar protein	1	0.048139852	0.692182637	1	1	0.051457348	-0.584709298	0	0
531	ENSRNOG000000012062	Npc2	NPC intracellular cholesterol transporter 2	1	0.024926895	0.926534422	1	1	0.098230467	-0.203022217	0	0
532	ENSRNOG000000008176	Nppa	natriuretic peptide A	1	0.049371905	3.844987264	1	1	0.181013172	-1.035273097	0	0
533	ENSRNOG000000013172	Nr1h3	nuclear receptor subfamily 1, group H, member 3	1	0.040991794	1.478566583	1	1	0.165807544	-0.649501683	0	0
534	ENSRNOG000000008752	Nrf1	nuclear respiratory factor 1	1	0.009198538	0.84663968	1	1	0.094203365	-0.578854573	0	0
535	ENSRNOG000000001450	Nsun5	NOP2/Sun RNA methyltransferase family member 5	1	0.013972692	1.311709328	1	1	0.072033722	-0.877183752	0	0

538	ENSRNOG00000000034	Nuak2	NUAK family kinase 2	1	0.000248121	0.90832442	1	1	0.34469078	0.088037473	0	0
537	ENSRNOG000000002574	Nubp1	nucleotide binding protein 1	1	0.014252258	1.122100048	1	1	0.200423488	-0.477177841	0	0
538	ENSRNOG00000015090	Nubp2	nucleotide binding protein 2	1	0.038728384	1.348861786	1	1	0.143195573	-0.461798878	0	0
539	ENSRNOG0000000020889	Nuob1	nucleobindin 1	1	0.038713806	1.149453509	1	1	0.182652162	-0.591259559	0	0
540	ENSRNOG000000002188	Nudt9	nudix hydrolase 9	1	0.04111413	0.919515833	1	1	0.117310737	-0.64351058	0	0
541	ENSRNOG0000000020887	Numb1	NUMB-like, endocytic adaptor protein	1	0.026585892	1.299048948	1	1	0.214234949	-0.781805096	0	0
542	ENSRNOG0000000025185	Nup188	nucleoporin 188	1	0.001812703	1.04045792	1	1	0.061958761	-0.876187924	0	0
543	ENSRNOG0000000005390	Nup210	nucleoporin 210	1	0.042355288	1.084576078	1	1	0.086391973	-0.936636251	0	0
544	ENSRNOG0000000055790	Nup210l	nucleoporin 210-like	1	0.037580305	0.78236835	1	1	0.064912558	-0.333640375	0	0
545	ENSRNOG0000000023393	Nup214	nucleoporin 214	1	0.049229157	0.585042647	1	1	0.094330253	-0.88490548	0	0
546	ENSRNOG000000008178	Nxn	nucleoredoxin	1	0.024601338	1.392723689	1	1	0.088835404	-0.50348165	0	0
547	ENSRNOG0000000004700	Nxt1	nuclear transport factor 2-like export factor 1	1	0.009238949	1.133889004	1	1	0.039362596	-0.478989489	0	0
548	ENSRNOG0000000048431	Nynrin	NYN domain and retroviral integrase containing	1	0.007127371	0.727149019	1	1	0.05995035	-0.245492828	0	0
549	ENSRNOG0000000009243	Oaf	out at first homolog	1	0.046382318	1.381988573	1	1	0.37320502	-0.238337121	0	0
550	ENSRNOG0000000002196	Ociad2	OciA domain containing 2	1	0.013960892	2.132472976	1	1	0.149005034	-0.357185452	0	0
551	ENSRNOG0000000052140	Ogg1	8-oxoguanine DNA glycosylase	1	0.021652989	0.642419821	1	1	0.035151921	-0.324342228	0	0
552	ENSRNOG0000000056219	Olr1	oxidized low density lipoprotein receptor 1	1	0.025926488	2.372087817	1	1	0.452394731	-0.202374579	0	0
553	ENSRNOG0000000011781	Oplah	5-oxoprolinase (ATP-hydrolysing)	1	0.026324529	1.477462917	1	1	0.124998828	-0.991419025	0	0
554	ENSRNOG0000000001427	Orai2	ORAI calcium release-activated calcium modulator 2	1	0.024804772	1.826382217	1	1	0.029050962	-0.525867953	0	0
555	ENSRNOG0000000008841	Orc1	origin recognition complex, subunit 1	1	0.04702986	2.498588648	1	1	0.079129784	-1.963378804	0	0
556	ENSRNOG0000000007886	Orm1	orosomucoid 1	1	0.033140887	1.575339864	1	1	0.225060685	0.194134686	0	0
557	ENSRNOG0000000025570	Os9	OS9, endoplasmic reticulum lectin	1	0.014813875	0.878487734	1	1	0.332827322	-0.14818818	0	0
558	ENSRNOG0000000055716	Oscar	osteoclast associated, immunoglobulin-like receptor	1	0.015227364	1.063588469	1	1	0.071039032	-0.666834418	0	0
559	ENSRNOG0000000004210	Osr1	odd-skipped related transcription factor 1	1	0.015004758	1.202789401	1	1	0.290224398	0.151900103	0	0
560	ENSRNOG0000000001300	P2rx4	purinergic receptor P2X 4	1	0.037875595	1.379818787	1	1	0.156515964	-0.209418995	0	0
561	ENSRNOG0000000019270	P2ry6	pyrimidinergic receptor P2Y6	1	0.025021033	1.216198011	1	1	0.044222123	-0.500339547	0	0
562	ENSRNOG0000000016071	P3h3	prolyl 3-hydroxylase 3	1	0.013872712	1.749076375	1	1	0.100467899	-0.904985389	0	0
563	ENSRNOG0000000015787	P3h4	prolyl 3-hydroxylase family member 4 (non-enzymatic)	1	0.004364251	1.500831817	1	1	0.140408524	-0.818260813	0	0
564	ENSRNOG0000000007574	Padi2	peptidyl arginine deiminase 2	1	0.045329839	0.7111384559	1	1	0.135277153	-0.381533473	0	0
565	ENSRNOG0000000018838	Paox	polyamine oxidase	1	0.025516999	0.909587875	1	1	0.104330529	-0.519004829	0	0
566	ENSRNOG0000000011311	Papss1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	1	0.037438659	0.983530884	1	1	0.080687884	-0.563117855	0	0
567	ENSRNOG0000000012830	Paqr8	progesterin and adipoQ receptor family member 8	1	0.027012896	1.085038803	1	1	0.147808441	-0.523275528	0	0
568	ENSRNOG00000000021221	Pced1a	PC-esterase domain containing 1A	1	0.026781739	0.908488107	1	1	0.053338942	-0.898091228	0	0
569	ENSRNOG0000000020742	Pcnx3	pecanex homolog 3	1	0.020711123	1.747954969	1	1	0.082758775	-1.373222319	0	0
570	ENSRNOG0000000010832	Pdgfrl	platelet-derived growth factor receptor-like	1	0.003316185	1.509227543	1	1	0.298437694	-0.127710824	0	0
571	ENSRNOG0000000013653	Pdlim7	PDZ and LIM domain 7	1	0.019768844	2.015713107	1	1	0.089622026	-1.092629364	0	0
572	ENSRNOG0000000013972	Pef1	penta-EF hand domain containing 1	1	0.022110061	1.229738631	1	1	0.140390594	-0.730281318	0	0
573	ENSRNOG0000000028015	Pf4	platelet factor 4	1	0.033238122	2.13088855	1	1	0.177880023	-0.410334276	0	0
574	ENSRNOG0000000001214	Pfkl	phosphofructokinase, liver type	1	0.042653058	1.696442988	1	1	0.107515551	-1.026220889	0	0
575	ENSRNOG0000000003975	Pfn1	profilin 1	1	0.024184953	0.956436847	1	1	0.063189092	-0.714058942	0	0
576	ENSRNOG0000000014783	Pgghg	protein-glucosylgalactosylhydroxyllysine glucosidase	1	0.016860782	0.89072014	1	1	0.0588036	-0.681697724	0	0
577	ENSRNOG0000000002949	Pgs1	phosphatidylglycerophosphate synthase 1	1	0.026109923	1.435528829	1	1	0.113889883	-0.890206914	0	0
578	ENSRNOG0000000009088	Phlda3	pleckstrin homology-like domain, family A, member 3	1	0.009832425	1.505416211	1	1	0.186356113	-0.626178971	0	0
579	ENSRNOG0000000016794	Phyhd1	phytanoyl-CoA dioxygenase domain containing 1	1	0.021311222	1.021117874	1	1	0.12852424	-0.453128048	0	0
580	ENSRNOG0000000011386	Pigs	phosphatidylinositol glycan anchor biosynthesis, class S	1	0.020651955	0.894835171	1	1	0.07808227	-0.641150064	0	0

581	ENSRNOG00000014690	Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	1	0.032167713	0.755497317	1	1	0.079500724	-0.611799452	0	0
582	ENSRNOG00000034228	Pik3c2g	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit	1	0.02752486	2.279236561	1	1	0.08849831	0.308054395	0	0
583	ENSRNOG00000016846	Pik3cd	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit	1	0.016816909	1.44405926	1	1	0.062335425	-1.064836714	0	0
584	ENSRNOG00000054954	Pirb	paired Ig-like receptor B	1	0.019117164	1.320691384	1	1	0.38847597	-0.307250416	0	0
585	ENSRNOG00000000811	Pkib	cAMP-dependent protein kinase inhibitor beta	1	0.016001379	1.732265579	1	1	0.063780498	-0.562299485	0	0
586	ENSRNOG00000011329	Pkm	pyruvate kinase M1/2	1	0.048915523	1.098440096	1	1	0.147319771	-0.779918439	0	0
587	ENSRNOG00000019859	Pla2g15	phospholipase A2, group XV	1	0.000401214	1.133345094	1	1	0.010848148	-0.303690108	0	0
588	ENSRNOG00000016826	Pla2g2d	phospholipase A2, group IID	1	0.020800772	0.84280456	1	1	0.303439694	0.128053016	0	0
589	ENSRNOG00000002217	Plac8	placenta-specific 8	1	0.00808924	2.109492329	1	1	0.119906972	0.567338218	0	0
590	ENSRNOG00000001385	Plbd2	phospholipase B domain containing 2	1	0.034964209	1.522696561	1	1	0.21421702	-0.617337697	0	0
591	ENSRNOG000000021150	Plcb3	phospholipase C beta 3	1	0.002705882	1.517582674	1	1	0.137840839	-0.66408752	0	0
592	ENSRNOG000000019604	Pld2	phospholipase D2	1	0.027901938	0.848815352	1	1	0.112218675	-0.30322889	0	0
593	ENSRNOG00000028566	Pld4	phospholipase D family, member 4	1	0.024718709	1.469442191	1	1	0.241451624	-0.297750443	0	0
594	ENSRNOG00000030266	Plekkg2	pleckstrin homology and RhoGEF domain containing G2	1	0.016241383	0.627602537	1	1	0.078456865	-1.130282201	0	0
595	ENSRNOG00000006670	Plekkg3	pleckstrin homology and RhoGEF domain containing G3	1	0.035237708	0.856679317	1	1	0.137840852	-0.374176695	0	0
596	ENSRNOG00000001417	Plod3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	1	0.002480243	1.649573913	1	1	0.073822564	-0.963605574	0	0
597	ENSRNOG000000039496	Plp2	proteolipid protein 2	1	0.042935798	1.712839123	1	1	0.079621199	-0.933347148	0	0
598	ENSRNOG00000000177	Plpp2	phospholipid phosphatase 2	1	0.001254948	1.048823791	1	1	0.276553548	-0.27001943	0	0
599	ENSRNOG000000016488	Pltp	phospholipid transfer protein	1	0.026737053	1.359802723	1	1	0.438072823	-0.093797588	0	0
600	ENSRNOG000000008400	Pml	promyelocytic leukemia	1	0.042827391	1.06413162	1	1	0.267813392	0.304363831	0	0
601	ENSRNOG000000005358	Pmm1	phosphomannomutase 1	1	0.025683608	1.329998712	1	1	0.095571892	-0.534380542	0	0
602	ENSRNOG000000020318	Pnkp	polynucleotide kinase 3'-phosphatase	1	0.042494725	1.242102466	1	1	0.178573822	-0.793760057	0	0
603	ENSRNOG000000009982	Pnp	purine nucleoside phosphorylase	1	0.041404317	1.239954506	1	1	0.143099579	-0.337798148	0	0
604	ENSRNOG000000010104	Pofut1	protein O-fucosyltransferase 1	1	0.043721123	0.826265171	1	1	0.157489346	-0.269378042	0	0
605	ENSRNOG000000001228	Pofut2	protein O-fucosyltransferase 2	1	0.028402593	1.057919181	1	1	0.154833322	-0.732882491	0	0
606	ENSRNOG000000019681	Pold1	DNA polymerase delta 1, catalytic subunit	1	0.017376595	1.996497091	1	1	0.06197414	-1.603124492	0	0
607	ENSRNOG000000000954	Polr1d	RNA polymerase I subunit D	1	0.005602648	0.583679171	1	1	0.154157231	0.0555689764	0	0
608	ENSRNOG000000004471	Polr3h	RNA polymerase III subunit H	1	0.018094752	1.162079592	1	1	0.040480382	-0.529867261	0	0
609	ENSRNOG000000023455	Pomgnt1	protein O-linked mannose N-acetylglucosaminyltransferase 1	1	0.01261844	0.803346577	1	1	0.093720502	-0.792495731	0	0
610	ENSRNOG000000010477	Pomt1	protein-O-mannosyltransferase 1	1	0.03802193	0.953405077	1	1	0.097805669	-0.775070531	0	0
611	ENSRNOG000000009096	Pon3	paraoxonase 3	1	0.022891249	0.602799094	1	1	0.062168609	1.015079804	0	0
612	ENSRNOG000000012660	Postn	perlecan	1	0.041449417	4.56645271	1	1	0.210945866	-1.06222886	0	0
613	ENSRNOG000000020608	Ppan	peter pan homolog (Drosophila)	1	0.001959727	1.810492185	1	1	0.06183408	-1.301124297	0	0
614	ENSRNOG000000016781	Ppib	peptidylprolyl isomerase B	1	0.00151893	1.35015104	1	1	0.007306117	-0.474209989	0	0
615	ENSRNOG000000000523	Ppil1	peptidylprolyl isomerase like 1	1	0.023059375	0.948793624	1	1	0.120745535	-0.790470408	0	0
616	ENSRNOG000000021151	Ppp1r14b	protein phosphatase 1, regulatory (inhibitor) subunit 14B	1	0.008427557	1.57803305	1	1	0.05069609	-0.801737479	0	0
617	ENSRNOG000000018561	Pprc1	peroxisome proliferator-activated receptor gamma, coactivator 1	1	0.017080063	0.964853813	1	1	0.056073995	-0.901791504	0	0
618	ENSRNOG0000000007141	Preb	prolactin regulatory element binding	1	0.014638439	1.030817649	1	1	0.154118337	-0.610700422	0	0
619	ENSRNOG000000008952	Prex1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac	1	0.028215571	0.934683802	1	1	0.13221633	-0.995535871	0	0
620	ENSRNOG000000016346	Prkod	protein kinase C, delta	1	0.021985104	1.260175802	1	1	0.080877802	-0.604251227	0	0
621	ENSRNOG000000013380	Prkcs	protein kinase C substrate 80K-H	1	0.002701055	1.209578941	1	1	0.060593132	-0.984287478	0	0
622	ENSRNOG000000001297	Prmt2	protein arginine methyltransferase 2	1	0.019007517	0.965507453	1	1	0.115940211	-0.290914834	0	0
623	ENSRNOG000000061039	Prpf31	pre-mRNA processing factor 31	1	0.009040766	0.92644907	1	1	0.06806103	-0.472636606	0	0
624	ENSRNOG0000000052880	Prph	peripherin	1	0.036619681	1.250850172	1	1	0.277420868	0.317744759	0	0
625	ENSRNOG000000016433	Prrc1	proline-rich coiled-coil 1	1	0.008658299	1.563362329	1	1	0.051403283	-0.989172215	0	0

626	ENSRNOG00000019494	Psmb10	proteasome subunit beta 10	1	0.02188318	1.509886571	1	1	0.235926281	-0.457883945	0	0
627	ENSRNOG00000000456	Psmb8	proteasome subunit beta 8	1	0.034984484	1.49238941	1	1	0.464447486	-0.04721725	0	0
628	ENSRNOG00000000459	Psmb9	proteasome subunit beta 9	1	0.005807186	0.955351688	1	1	0.133400662	0.558433538	0	0
629	ENSRNOG00000000925	PspH	phosphoserine phosphatase	1	0.000173092	1.294598686	1	1	0.001781256	-0.531017132	0	0
630	ENSRNOG00000002525	Ptgs2	prostaglandin-endoperoxide synthase 2	1	0.041277567	1.500237572	1	1	0.381158334	-0.168977945	0	0
631	ENSRNOG000000027839	Prk2b	protein tyrosine kinase 2 beta	1	0.010031998	0.990903096	1	1	0.378529343	-0.031087997	0	0
632	ENSRNOG00000018457	Ptpa	protein phosphatase 2 phosphatase activator	1	0.005347493	1.401548713	1	1	0.098014827	-0.963711996	0	0
633	ENSRNOG000000014294	Ptpn6	protein tyrosine phosphatase, non-receptor type 6	1	0.035532584	1.959464062	1	1	0.111967382	-0.689690474	0	0
634	ENSRNOG00000019977	Ptpnf	protein tyrosine phosphatase, receptor type, F	1	0.020086891	1.518886439	1	1	0.179774981	-0.263222277	0	0
635	ENSRNOG00000006231	Ptpro	protein tyrosine phosphatase, receptor type, O	1	0.044439632	1.268441021	1	1	0.338011103	0.218464165	0	0
636	ENSRNOG00000001223	Pttg1ip	PTTG1 interacting protein	1	0.008888353	0.642218678	1	1	0.108775257	-0.400576028	0	0
637	ENSRNOG00000001210	Pwp2	PWP2, small subunit processome component	1	0.00794759	1.224260613	1	1	0.089828426	-0.976253434	0	0
638	ENSRNOG000000036649	Pwpp2b	PWPP domain containing 2B	1	0.04146514	1.680169592	1	1	0.194491897	-0.524987707	0	0
639	ENSRNOG00000019675	Pycard	PYD and CARD domain containing	1	0.010413902	1.275155622	1	1	0.380860217	-0.061561654	0	0
640	ENSRNOG000000036882	Pycr1	pyrroline-5-carboxylate reductase 1	1	0.041030274	2.066673435	1	1	0.061190056	-1.162593945	0	0
641	ENSRNOG000000054724	Pycr3	pyrroline-5-carboxylate reductase 3	1	0.025465692	1.032377987	1	1	0.131579408	-0.573294388	0	0
642	ENSRNOG00000006388	Pylg	glycogen phosphorylase L	1	0.035461279	1.46849222	1	1	0.169252327	-0.523368687	0	0
643	ENSRNOG000000058130	Pym1	PYM homolog 1, exon junction complex associated factor	1	0.019118819	0.698078797	1	1	0.048176195	-0.330161688	0	0
644	ENSRNOG00000015413	Qpotl	glutamyl-peptide cyclotransferase-like	1	0.024780774	0.618718958	1	1	0.010956417	-0.316791881	0	0
645	ENSRNOG000000058940	Rab11fip1	RAB11 family interacting protein 1	1	0.043402662	1.208380422	1	1	0.375885125	-0.208599223	0	0
646	ENSRNOG000000016733	Rab13	RAB13, member RAS oncogene family	1	0.04498738	1.364249326	1	1	0.098073926	-0.531834294	0	0
647	ENSRNOG000000020349	Rab31l1	RAB3A interacting protein-like 1	1	0.042327702	1.700948639	1	1	0.161611958	-0.667794806	0	0
648	ENSRNOG000000018568	Rab5c	RAB5C, member RAS oncogene family	1	0.001562375	1.113841257	1	1	0.109999104	-0.555742661	0	0
649	ENSRNOG000000039754	Rab7b	Rab7b, member RAS oncogene family	1	0.043317151	1.54778076	1	1	0.140071719	-0.547734099	0	0
650	ENSRNOG000000014621	Rab8a	RAB8A, member RAS oncogene family	1	0.031880423	0.979523739	1	1	0.044451624	-0.416950945	0	0
651	ENSRNOG00000018591	Rabepk	Rab9 effector protein with kelch motifs	1	0.018416799	1.069870653	1	1	0.252385146	-0.25323493	0	0
652	ENSRNOG000000052620	Rack1	receptor for activated C kinase 1	1	0.002801324	1.344089817	1	1	0.102993931	-0.352510187	0	0
653	ENSRNOG000000024456	Radil	Rap associating with DIL domain	1	0.042315289	0.637380931	1	1	0.358756913	0.273809101	0	0
654	ENSRNOG000000060615	Rai1	retinoic acid induced 1	1	0.049981932	1.542424135	1	1	0.156252534	-0.888156396	0	0
655	ENSRNOG00000001884	Ranbp1	RAN binding protein 1	1	0.045855044	0.962033968	1	1	0.061442176	-0.905796768	0	0
656	ENSRNOG000000037853	Rarres1	retinoic acid receptor responder 1	1	0.019325564	1.217488339	1	1	0.217467554	0.294144161	0	0
657	ENSRNOG000000017671	Rasa3	RAS p21 protein activator 3	1	0.039068892	0.771496688	1	1	0.081541618	-0.416885419	0	0
658	ENSRNOG000000021261	Rassf2	Ras association domain family member 2	1	0.047139783	0.938164549	1	1	0.446120612	0.041181834	0	0
659	ENSRNOG000000020710	Raver1	ribonucleoprotein, PTB-binding 1	1	0.043422661	0.849955845	1	1	0.075042756	-1.180872142	0	0
660	ENSRNOG000000024278	Rbm42	RNA binding motif protein 42	1	0.044637611	1.111508266	1	1	0.181240052	-0.907314593	0	0
661	ENSRNOG00000002408	Rbm47	RNA binding motif protein 47	1	0.001885125	0.973149832	1	1	0.134995724	-0.374774992	0	0
662	ENSRNOG000000025881	Rbms3	RNA binding motif, single stranded interacting protein 3	1	0.002598717	1.255556356	1	1	0.056854217	-0.464084885	0	0
663	ENSRNOG000000015491	Rcl1	RNA terminal phosphate cyclase-like 1	1	0.008848079	1.259529735	1	1	0.084083787	-0.78062561	0	0
664	ENSRNOG000000043007	Rcn3	reticulocalbin 3	1	0.009116888	2.403711382	1	1	0.090416316	-1.249349597	0	0
665	ENSRNOG000000018586	Retreg2	reticulophagy regulator family member 2	1	0.037488449	0.659202656	1	1	0.151885387	-0.474740727	0	0
666	ENSRNOG00000001457	Rfc2	replication factor C subunit 2	1	0.013285429	1.664979585	1	1	0.055402455	-0.993128547	0	0
667	ENSRNOG000000031269	RGD1304	similar to CG9646-PA	1	0.009765947	1.16401567	1	1	0.078479691	-0.646796739	0	0
668	ENSRNOG000000025796	RGD1306	hypothetical LOC304854	1	0.032582718	1.106871705	1	1	0.122672367	-0.734350681	0	0
669	ENSRNOG000000042230	RGD1307	similar to RIKEN cDNA B430306N03 gene	1	0.010609199	1.322989058	1	1	0.299106406	-0.225288221	0	0
670	ENSRNOG000000029146	RGD1308	similar to 1700123O20Rik protein	1	0.015391352	0.694461586	1	1	0.375388387	-0.043158306	0	0

671	ENSRNOG00000025245	RGD1311	similar to RIKEN cDNA 1810055G02	1	0.017040894	1.442119054	1	1	0.085252052	-0.820076411	0	0
672	ENSRNOG000000027271	RGD1359	Ribosomal_L22 domain containing protein RGD1359290	1	0.00728267	1.162791537	1	1	0.241848838	0.122702256	0	0
673	ENSRNOG00000042421	RGD1559	RGD1559909	1	0.033135094	1.174906924	1	1	0.135810082	-0.47234547	0	0
674	ENSRNOG000000001787	RGD1562	RGD1562339	1	0.017568099	0.819073923	1	1	0.198016206	-0.130501186	0	0
675	ENSRNOG000000029670	RGD1564	similar to 60S ribosomal protein L23a	1	0.025967884	1.479492908	1	1	0.092700917	-0.244803038	0	0
676	ENSRNOG000000019701	RGD1597	uncharacterized protein LOC690349	1	0.007952141	0.77609144	1	1	0.097050203	-0.227008419	0	0
677	ENSRNOG00000015616	Rgs14	regulator of G-protein signaling 14	1	0.003241983	1.336626559	1	1	0.173975036	-0.866241371	0	0
678	ENSRNOG000000027032	Rhbdd3	rhomboid domain containing 3	1	0.025584029	0.627728467	1	1	0.125538239	-0.619143003	0	0
679	ENSRNOG00000012630	Rhoc	ras homolog family member C	1	0.029378684	1.293400899	1	1	0.117746224	-0.705168885	0	0
680	ENSRNOG000000046548	Rhox5	Rhox homeobox family member 5	1	0.002878698	1.133065446	1	1	0.178235294	-0.366606177	0	0
681	ENSRNOG000000007062	Rin3	Ras and Rab interactor 3	1	0.005758017	1.857530929	1	1	0.169961451	-0.849632388	0	0
682	ENSRNOG000000020465	Ripk3	receptor-interacting serine-threonine kinase 3	1	0.040469899	2.241159197	1	1	0.072555341	-1.238387841	0	0
683	ENSRNOG000000011690	Rmdn3	regulator of microtubule dynamics 3	1	0.001772154	0.913711498	1	1	0.361886491	0.107550821	0	0
684	ENSRNOG000000008584	Rnaseh1	ribonuclease H1	1	0.047326667	0.65195894	1	1	0.064273912	-0.156613863	0	0
685	ENSRNOG000000020700	Rnaseh2c	ribonuclease H2, subunit C	1	0.025303358	0.667811982	1	1	0.161029929	-0.69278806	0	0
686	ENSRNOG000000020175	Rnf121	ring finger protein 121	1	0.047392042	0.780267274	1	1	0.072401078	-0.339988465	0	0
687	ENSRNOG000000009028	Rnf126	ring finger protein 126	1	0.045016895	0.950582797	1	1	0.103967451	-0.832468945	0	0
688	ENSRNOG000000000123	Rnf19b	ring finger protein 19B	1	0.03932846	0.897728934	1	1	0.171272188	-0.423795378	0	0
689	ENSRNOG000000016416	Rnh1	ribonuclease/angiogenin inhibitor 1	1	0.00074519	1.607408578	1	1	0.061944142	-0.775599077	0	0
690	ENSRNOG000000005483	Rpap1	RNA polymerase II associated protein 1	1	0.040380683	0.593906714	1	1	0.13597807	-0.986620121	0	0
691	ENSRNOG000000005675	Rpl10	ribosomal protein L10	1	0.005569547	0.674811627	1	1	0.088906627	0.082787056	0	0
692	ENSRNOG000000000505	Rpl10a	ribosomal protein L10A	1	0.004578374	1.552143895	1	1	0.098963858	-0.499810314	0	0
693	ENSRNOG000000026260	Rpl11	ribosomal protein L11	1	0.002374319	0.77194944	1	1	0.139330667	0.080546775	0	0
694	ENSRNOG000000016220	Rpl12	ribosomal protein L12	1	0.023985932	1.005102717	1	1	0.39752355	-0.054053311	0	0
695	ENSRNOG000000015335	Rpl13	ribosomal protein L13	1	0.014808772	1.397816304	1	1	0.063592649	-0.580717378	0	0
696	ENSRNOG000000019007	Rpl14	ribosomal protein L14	1	0.00043928	0.727511454	1	1	0.470888897	0.007692581	0	0
697	ENSRNOG000000008140	Rpl15	ribosomal protein L15	1	0.044326736	0.793121104	1	1	0.084247155	-0.247888145	0	0
698	ENSRNOG000000021035	Rpl18	ribosomal protein L18	1	0.013543894	1.490218953	1	1	0.099819047	-0.522531007	0	0
699	ENSRNOG000000018795	Rpl18a	ribosomal protein L18A	1	0.030089373	1.772270327	1	1	0.208857803	-0.355208207	0	0
700	ENSRNOG000000004741	Rpl19	ribosomal protein L19	1	0.037616716	1.539003188	1	1	0.253341563	-0.269667969	0	0
701	ENSRNOG000000011104	Rpl22	ribosomal protein L22	1	0.035923867	0.594840351	1	1	0.195915454	0.097235907	0	0
702	ENSRNOG000000020674	Rpl27	ribosomal protein L27	1	0.020148679	0.850338842	1	1	0.308298807	-0.110169175	0	0
703	ENSRNOG000000017127	Rpl28	ribosomal protein L28	1	0.041538032	2.142923016	1	1	0.179587339	-0.785264903	0	0
704	ENSRNOG000000016896	Rpl3	ribosomal protein L3	1	0.002300393	1.721820681	1	1	0.027550721	-0.341604668	0	0
705	ENSRNOG000000010748	Rpl32	ribosomal protein L32	1	0.001639749	0.643139098	1	1	0.005851045	0.121755419	0	0
706	ENSRNOG000000016387	Rpl34	ribosomal protein L34	1	0.015527067	1.492478984	1	1	0.245184677	-0.268084701	0	0
707	ENSRNOG000000014272	Rpl35	ribosomal protein L35	1	0.030120681	1.532586369	1	1	0.259957313	-0.251665321	0	0
708	ENSRNOG000000042233	Rpl41	ribosomal protein L41	1	0.000370181	0.721596611	1	1	0.01099035	0.092689517	0	0
709	ENSRNOG000000016269	Rpl71i	ribosomal protein L7-like 1	1	0.006247845	0.625068759	1	1	0.131966968	-0.128769838	0	0
710	ENSRNOG000000048523	Rpl8	ribosomal protein L8	1	0.011807462	1.232946636	1	1	0.202525757	-0.35917752	0	0
711	ENSRNOG000000001148	Rplp0	ribosomal protein lateral stalk subunit P0	1	0.019465554	1.598563263	1	1	0.143038411	-0.609811173	0	0
712	ENSRNOG000000007492	Rpn2	ribophorin II	1	0.027982898	0.954537131	1	1	0.036094338	-0.554636448	0	0
713	ENSRNOG000000000490	Rps10	ribosomal protein S10	1	0.01438163	1.126107356	1	1	0.263861182	-0.192172092	0	0
714	ENSRNOG000000016411	Rps12	ribosomal protein S12	1	0.036856217	1.05266504	1	1	0.273595959	-0.142755448	0	0
715	ENSRNOG000000019578	Rps16	ribosomal protein S16	1	0.021188401	1.041084238	1	1	0.156643128	-0.255470532	0	0

716	ENSRNOG000000028505	Rps18	ribosomal protein S18	1	0.010264809	1.739601762	1	1	0.245241087	-0.316224067	0	0
717	ENSRNOG000000037897	Rps19	ribosomal protein S19	1	0.036454589	0.684655744	1	1	0.055851596	-0.465231828	0	0
718	ENSRNOG000000048199	Rps19	ribosomal protein S19	1	0.036192283	1.236270772	1	1	0.062963382	-0.49768675	0	0
719	ENSRNOG000000014179	Rps2	ribosomal protein S2	1	0.037711054	1.156033642	1	1	0.122389697	-0.595794312	0	0
720	ENSRNOG000000008555	Rps20	ribosomal protein S20	1	0.026780084	0.893377823	1	1	0.126888353	0.14554789	0	0
721	ENSRNOG000000050473	Rps27l	ribosomal protein S27-like	1	0.007904558	1.024578109	1	1	0.479108475	0.01607663	0	0
722	ENSRNOG000000042886	Rps28	ribosomal protein S28	1	0.030159299	1.729153868	1	1	0.247891663	-0.337583865	0	0
723	ENSRNOG000000017418	Rps3	ribosomal protein S3	1	0.005966347	1.062724308	1	1	0.479615682	0.007355358	0	0
724	ENSRNOG000000019453	Rps5	ribosomal protein S5	1	0.018251293	2.116833789	1	1	0.159770499	-0.543788016	0	0
725	ENSRNOG000000021117	Rps8ka4	ribosomal protein S8 kinase A4	1	0.025319909	0.7914893	1	1	0.060719881	-0.536058942	0	0
726	ENSRNOG000000008551	Rps7	ribosomal protein S7	1	0.013940142	0.720694188	1	1	0.046932418	0.23378086	0	0
727	ENSRNOG000000054626	Rps8	ribosomal protein S8	1	0.004036963	0.949911711	1	1	0.287324736	-0.078553906	0	0
728	ENSRNOG000000005890	Rps9	ribosomal protein S9	1	0.014655817	1.431628511	1	1	0.149920281	-0.430060037	0	0
729	ENSRNOG000000018645	Rpsa	ribosomal protein SA	1	0.028111854	1.288110911	1	1	0.095837115	-0.499917084	0	0
730	ENSRNOG000000023639	Rpsd1	RNA pseudouridylation synthase domain containing 1	1	0.022307427	1.308648113	1	1	0.134002758	-0.734332318	0	0
731	ENSRNOG000000005958	Rrbp1	ribosome binding protein 1	1	0.040658575	0.928981409	1	1	0.056078822	-0.514117273	0	0
732	ENSRNOG0000000048495	Rrp12	ribosomal RNA processing 12 homolog	1	0.011356734	1.696343062	1	1	0.054960554	-1.372757795	0	0
733	ENSRNOG000000017836	Rrp36	ribosomal RNA processing 36	1	0.022268395	0.757932498	1	1	0.227835749	-0.372298245	0	0
734	ENSRNOG000000022896	Rrp7a	ribosomal RNA processing 7 homolog A	1	0.01141604	0.621539025	1	1	0.318740501	-0.257075112	0	0
735	ENSRNOG000000017595	Rsu1	Ras suppressor protein 1	1	0.010484656	0.717367381	1	1	0.180772912	-0.04157359	0	0
736	ENSRNOG000000004813	Rtob	RNA 2',3'-cyclic phosphate and 5'-OH ligase	1	0.001666644	0.672067406	1	1	0.067273498	-0.334722621	0	0
737	ENSRNOG000000013195	Ruvb1l	RuvB-like AAA ATPase 1	1	0.034101234	0.955420841	1	1	0.01147778	-0.502709059	0	0
738	ENSRNOG000000020793	Ruvb1l2	RuvB-like AAA ATPase 2	1	0.047144335	1.342333221	1	1	0.081015378	-1.187064016	0	0
739	ENSRNOG000000023226	S100a10	S100 calcium binding protein A10	1	0.047907179	0.763261111	1	1	0.096897883	0.428139381	0	0
740	ENSRNOG000000011821	S100a4	S100 calcium-binding protein A4	1	0.006780222	2.860778948	1	1	0.08582284	-0.831717129	0	0
741	ENSRNOG000000011847	S100a6	S100 calcium binding protein A6	1	0.00969009	1.674759193	1	1	0.242764292	-0.120356403	0	0
742	ENSRNOG000000011557	S100a8	S100 calcium binding protein A8	1	0.025108958	2.367930603	1	1	0.410085098	-0.06578846	0	0
743	ENSRNOG000000011483	S100a9	S100 calcium binding protein A9	1	0.010985725	2.739740359	1	1	0.288134818	-0.187246809	0	0
744	ENSRNOG000000020653	S1pr2	sphingosine-1-phosphate receptor 2	1	0.014367009	0.77355082	1	1	0.034382456	-0.422112292	0	0
745	ENSRNOG000000020901	S1pr5	sphingosine-1-phosphate receptor 5	1	0.025332736	0.696806528	1	1	0.207808096	-0.138209043	0	0
746	ENSRNOG000000008558	Sapod1	suppressor APC domain containing 1	1	0.02380291	1.293158054	1	1	0.070039721	-0.736204061	0	0
747	ENSRNOG000000020255	Sars	seryl-tRNA synthetase	1	0.043900145	0.672579964	1	1	0.108229019	-0.352643992	0	0
748	ENSRNOG000000000702	Sart3	squamous cell carcinoma antigen recognized by T-cells 3	1	0.012030756	0.724621592	1	1	0.150105096	-0.531614935	0	0
749	ENSRNOG000000013987	Sbno2	strawberry notch homolog 2	1	0.02388718	2.152520427	1	1	0.121183367	-1.230440185	0	0
750	ENSRNOG000000002888	Scarf2	scavenger receptor class F, member 2	1	0.034414316	1.532700792	1	1	0.058900421	-1.170799928	0	0
751	ENSRNOG000000013552	Sod	stearoyl-CoA desaturase	1	0.040740087	1.376998317	1	1	0.335618509	-0.490921027	0	0
752	ENSRNOG000000002358	Soxep1	serine carboxypeptidase 1	1	0.021547342	1.104093388	1	1	0.234922557	-0.13056447	0	0
753	ENSRNOG000000023668	Soxyl1	SCY1 like pseudokinase 1	1	0.032902283	1.447003181	1	1	0.113572788	-0.94456067	0	0
754	ENSRNOG000000059947	Sdc1	syndecan 1	1	0.028131577	2.680026041	1	1	0.064805393	-1.494436904	0	0
755	ENSRNOG000000014297	Sdc4	syndecan 4	1	0.013658644	0.953884818	1	1	0.466991449	-0.037379228	0	0
756	ENSRNOG000000012121	Sdf2	stromal cell derived factor 2	1	0.011341976	0.644636003	1	1	0.38005441	-0.011136598	0	0
757	ENSRNOG000000001859	Sdf2l1	stromal cell-derived factor 2-like 1	1	0.026935108	1.776265692	1	1	0.095043238	-0.815966981	0	0
758	ENSRNOG000000004672	Sec14l2	SEC14-like lipid binding 2	1	0.010989035	0.683910825	1	1	0.038444659	0.352211261	0	0
759	ENSRNOG000000047873	Sec22c	SEC22 homolog C, vesicle trafficking protein	1	0.044647955	0.967660843	1	1	0.075769947	-0.551533366	0	0
760	ENSRNOG000000008345	Sec51b	Sec51 translocase beta subunit	1	0.026796221	1.62049846	1	1	0.099677471	-0.706700783	0	0

761	ENSRNOG00000002794	Selp	selectin P	1	0.015912282	2.579996797	1	1	0.244982485	-0.565615835	0	0
762	ENSRNOG000000021101	Sema6c	semaphorin 6C	1	0.009910765	1.120156064	1	1	0.127673816	-0.712622312	0	0
763	ENSRNOG000000012989	Serinc2	serine incorporator 2	1	0.014578788	2.110941452	1	1	0.065090959	-1.840858991	0	0
764	ENSRNOG000000010478	Serpin3n	serine (or cysteine) peptidase inhibitor, clade A, member	1	0.015453693	4.165267142	1	1	0.495132612	-0.010596721	0	0
765	ENSRNOG000000016581	Serpinb1a	serpin family B member 1A	1	0.023926764	3.239301612	1	1	0.288045997	-0.427094021	0	0
766	ENSRNOG000000015967	Sh3bgr3	SH3 domain binding glutamate-rich protein like 3	1	0.009555893	1.781781398	1	1	0.050428522	-1.467310781	0	0
767	ENSRNOG000000009360	Sh3bp1	SH3-domain binding protein 1	1	0.005018413	1.588540272	1	1	0.08141404	-1.156268258	0	0
768	ENSRNOG000000049683	Sh3gl1	SH3 domain containing GRB2 like 1, endophilin A2	1	0.020268257	1.530324327	1	1	0.090413558	-0.929038832	0	0
769	ENSRNOG000000020353	Sh3pxd2a	SH3 and PX domains 2A	1	0.020738984	0.910777452	1	1	0.463559479	0.038981107	0	0
770	ENSRNOG000000004063	Sh3pxd2b	SH3 and PX domains 2B	1	0.019896283	1.990401919	1	1	0.053800186	-0.756270573	0	0
771	ENSRNOG000000020882	Shkbp1	Shkbp1 binding protein 1	1	0.018754017	1.043700621	1	1	0.120588994	-0.954848757	0	0
772	ENSRNOG000000005433	Shq1	SHQ1, H/ACA ribonucleoprotein assembly factor	1	0.036115716	0.62746383	1	1	0.112710227	-0.274244578	0	0
773	ENSRNOG000000017871	Sid2	SID1 transmembrane family, member 2	1	0.047769257	0.897788762	1	1	0.108190194	-0.781404859	0	0
774	ENSRNOG000000014604	Sigmar1	sigma non-opioid intracellular receptor 1	1	1.43E-05	1.487372828	1	1	0.102289704	-0.525177178	0	0
775	ENSRNOG000000048622	Sin3b	SIN3 transcription regulator family member B	1	0.000321219	0.72434893	1	1	0.10933046	-0.488770172	0	0
776	ENSRNOG000000004783	Sirpa	signal-regulatory protein alpha	1	0.045699193	1.122685454	1	1	0.062928626	-0.663137816	0	0
777	ENSRNOG000000028640	Siva1	SIVA1, apoptosis-inducing factor	1	0.045900834	1.37799727	1	1	0.058171988	-0.738201615	0	0
778	ENSRNOG0000000055340	Ski	SKI proto-oncogene	1	0.004272947	1.040413201	1	1	0.126692021	-0.580471103	0	0
779	ENSRNOG000000038286	Slamf6	SLAM family member 6	1	0.023951727	2.224703279	1	1	0.082924143	-1.543827336	0	0
780	ENSRNOG000000008045	Slamf9	SLAM family member 9	1	0.048082201	2.46722748	1	1	0.4243026	-0.132093752	0	0
781	ENSRNOG0000000060580	Slc10a3	solute carrier family 10, member 3	1	0.000372802	0.651767574	1	1	0.012683815	-0.399149376	0	0
782	ENSRNOG000000021644	Slc15a3	solute carrier family 15 member 3	1	0.020994	1.643278155	1	1	0.082220881	-0.955134544	0	0
783	ENSRNOG000000017072	Slc16a14	solute carrier family 16, member 14	1	0.004387284	0.740857062	1	1	0.166395007	-0.323119373	0	0
784	ENSRNOG000000010275	Slc17a9	solute carrier family 17 member 9	1	0.01051693	1.754388921	1	1	0.181357355	-0.480839904	0	0
785	ENSRNOG000000039980	Slc25a5	solute carrier family 25 member 5	1	0.00653086	0.658119205	1	1	0.033740639	-0.249803738	0	0
786	ENSRNOG000000030537	Slc26a11	solute carrier family 26 member 11	1	0.024582167	0.916106488	1	1	0.172346866	-0.797099014	0	0
787	ENSRNOG000000015421	Slc27a3	solute carrier family 27 member 3	1	0.018204813	1.223300956	1	1	0.094633749	-1.021303873	0	0
788	ENSRNOG000000014369	Slc27a4	solute carrier family 27 member 4	1	0.026801752	1.677158994	1	1	0.075246948	-1.298339185	0	0
789	ENSRNOG000000000568	Slc29a3	solute carrier family 29 member 3	1	0.005144749	1.212034011	1	1	0.133827805	-0.496384916	0	0
790	ENSRNOG000000005302	Slc2a9	solute carrier family 2 member 9	1	0.002884904	0.74217267	1	1	0.186299083	-0.097251494	0	0
791	ENSRNOG000000002908	Slc35a4	solute carrier family 35, member A4	1	0.010633749	0.754486935	1	1	0.087133094	-0.708892547	0	0
792	ENSRNOG000000004510	Slc35b1	solute carrier family 35, member B1	1	0.015927729	0.725628204	1	1	0.013867251	-0.361213762	0	0
793	ENSRNOG000000019900	Slc35b2	solute carrier family 35 member B2	1	0.004788084	1.860954132	1	1	0.064446521	-1.439508731	0	0
794	ENSRNOG000000018649	Slc35c2	solute carrier family 35 member C2	1	0.015403903	1.411179908	1	1	0.165921592	-0.872319884	0	0
795	ENSRNOG000000012287	Slc35e1	solute carrier family 35, member E1	1	0.009296738	1.857413398	1	1	0.088287704	-0.990107024	0	0
796	ENSRNOG000000012356	Slc36a1	solute carrier family 36 member 1	1	0.030892214	1.021409015	1	1	0.086541963	-0.844847393	0	0
797	ENSRNOG000000004604	Slc38a10	solute carrier family 38, member 10	1	0.000168954	1.823824377	1	1	0.102408455	-1.046137625	0	0
798	ENSRNOG000000012007	Slc38a7	solute carrier family 38, member 7	1	0.027187918	1.433095664	1	1	0.054843735	-1.350256139	0	0
799	ENSRNOG000000011981	Slc39a13	solute carrier family 39 member 13	1	0.008124405	1.348986274	1	1	0.063833736	-1.152849244	0	0
800	ENSRNOG000000045524	Slc39a3	solute carrier family 39 member 3	1	0.04771533	0.935853686	1	1	0.170082408	-0.428623274	0	0
801	ENSRNOG000000008713	Slc41a2	solute carrier family 41 member 2	1	0.039639749	2.339086082	1	1	0.093404248	-1.113862184	0	0
802	ENSRNOG000000014347	Slc4a2	solute carrier family 4 member 2	1	0.004025515	1.381815083	1	1	0.060138811	-1.010828841	0	0
803	ENSRNOG000000010210	Slc7a11	solute carrier family 7 member 11	1	0.016407558	1.467671228	1	1	0.12253486	-1.075896492	0	0
804	ENSRNOG000000010296	Slc7a7	solute carrier family 7 member 7	1	0.027772429	1.553155844	1	1	0.050559961	-0.996647545	0	0
805	ENSRNOG000000008554	Slc9a9	solute carrier family 9 member A9	1	0.032661196	0.735437931	1	1	0.024138749	0.467850981	0	0

806	ENSRNOG00000009005	Sloc2a1	solute carrier organic anion transporter family, member 2	1	0.015376733	1.96702004	1	1	0.083701469	-0.409327738	0	0
807	ENSRNOG00000046899	Slpi	secretory leukocyte peptidase inhibitor	1	0.00343397	1.536416048	1	1	0.071709875	0.76555883	0	0
808	ENSRNOG00000029508	Slpi2	antileukoprotease-like 2	1	0.023072618	1.82854799	1	1	0.184075098	0.207618399	0	0
809	ENSRNOG00000024445	Slx4	SLX4 structure-specific endonuclease subunit	1	0.041736984	0.669485186	1	1	0.080904558	-0.808039042	0	0
810	ENSRNOG00000019596	Smg9	SMG9 nonsense mediated mRNA decay factor	1	0.037472588	1.795601794	1	1	0.074846714	-1.443128185	0	0
811	ENSRNOG00000008332	Smo	smoothened, frizzled class receptor	1	0.017742087	0.863314287	1	1	0.055731329	-0.327564072	0	0
812	ENSRNOG00000000257	Smpd3	sphingomyelin phosphodiesterase 3	1	0.042456382	0.885270895	1	1	0.287703538	0.231408082	0	0
813	ENSRNOG000000037299	Smpd5	sphingomyelin phosphodiesterase 5	1	0.0487485	0.64762704	1	1	0.215107303	-0.126819321	0	0
814	ENSRNOG000000031173	Snd1	staphylococcal nuclease and tudor domain containing 1	1	0.042922695	1.105738628	1	1	0.069996621	-0.733666841	0	0
815	ENSRNOG00000001080	Snmp35	small nuclear ribonucleoprotein U11/U12 subunit 35	1	0.043749121	0.925729306	1	1	0.142276802	-0.610532124	0	0
816	ENSRNOG000000015844	Snrd2	small nuclear ribonucleoprotein D2 polypeptide	1	0.008837184	0.787694544	1	1	0.325205227	-0.190641815	0	0
817	ENSRNOG000000050410	Snrd3	small nuclear ribonucleoprotein D3 polypeptide	1	0.000833046	0.583702284	1	1	0.077624095	-0.144477985	0	0
818	ENSRNOG000000016507	Snrg	small nuclear ribonucleoprotein polypeptide G	1	0.042862147	0.671565186	1	1	0.493635198	0.004728216	0	0
819	ENSRNOG000000014202	Snx20	sorting nexin 20	1	0.023329012	2.324326384	1	1	0.07503586	-0.789934376	0	0
820	ENSRNOG000000001258	Snx8	sorting nexin 8	1	0.004442038	1.884242729	1	1	0.056712227	-1.655420731	0	0
821	ENSRNOG000000053240	Soga1	suppressor of glucose, autophagy associated 1	1	0.016880492	1.065134674	1	1	0.164740225	-0.412735006	0	0
822	ENSRNOG000000010626	Sphk1	sphingosine kinase 1	1	0.012624371	1.681245714	1	1	0.16561975	-0.859777588	0	0
823	ENSRNOG000000012811	Spint1	serine peptidase inhibitor, Kunitz type 1	1	0.049133853	0.962264458	1	1	0.074202055	-0.491498167	0	0
824	ENSRNOG000000020636	Spint2	serine peptidase inhibitor, Kunitz type, 2	1	0.032124819	1.616638902	1	1	0.38275581	-0.134712848	0	0
825	ENSRNOG000000058003	Spon1	spodion 1	1	0.026338873	1.199527507	1	1	0.228260189	-0.230867017	0	0
826	ENSRNOG000000025711	Sput1	SPOUT domain containing methyltransferase 1	1	0.032268395	1.225250108	1	1	0.080267913	-0.821184787	0	0
827	ENSRNOG000000051915	Spre3	sprouty-related, EVH1 domain containing 3	1	0.014142059	0.6490849	1	1	0.009045169	-0.456232067	0	0
828	ENSRNOG000000010793	Spry3	SPRY domain containing 3	1	0.026111579	1.202609044	1	1	0.152892835	-0.596720911	0	0
829	ENSRNOG00000003463	Sreb1	sterol regulatory element binding transcription factor 1	1	0.039475071	1.544641135	1	1	0.104120474	-1.188220985	0	0
830	ENSRNOG000000003715	Srxp2	sushi-repeat-containing protein, X-linked 2	1	0.045264877	2.019380047	1	1	0.115899593	-1.092217068	0	0
831	ENSRNOG000000016887	Ssc5d	scavenger receptor cysteine rich family member with 5	1	0.006474312	1.389145201	1	1	0.121355286	-1.035126878	0	0
832	ENSRNOG000000018878	Ssh3	slingshot protein phosphatase 3	1	0.005661816	0.947326444	1	1	0.057825874	-0.464550199	0	0
833	ENSRNOG000000053172	Ssr4	signal sequence receptor subunit 4	1	0.004712227	1.608913596	1	1	0.040275153	-0.441557086	0	0
834	ENSRNOG000000018434	Stab1	stabilin 1	1	0.016566995	2.090895393	1	1	0.150621543	-1.347159399	0	0
835	ENSRNOG000000042044	Stard3	StAR-related lipid transfer domain containing 3	1	0.023406248	1.074884351	1	1	0.077396455	-0.942042687	0	0
836	ENSRNOG000000025052	Stard5	StAR-related lipid transfer domain containing 5	1	0.03047776	1.188806849	1	1	0.07901393	-0.380379374	0	0
837	ENSRNOG000000004217	Stk10	serine/threonine kinase 10	1	0.0493988	1.364906688	1	1	0.223263844	-0.401214736	0	0
838	ENSRNOG000000008530	Stom1	stomatin like 1	1	0.009569133	1.09914831	1	1	0.100709744	-0.65517145	0	0
839	ENSRNOG000000015670	Stx7	syntaxin 7	1	0.010795531	0.593856177	1	1	0.156088753	0.056330942	0	0
840	ENSRNOG000000009922	Sumf2	sulfatase modifying factor 2	1	0.031944969	1.508357487	1	1	0.059271774	-0.420329727	0	0
841	ENSRNOG000000032840	Sumo4	small ubiquitin-like modifier 4	1	0.020504517	0.771463562	1	1	0.07788318	-0.215977894	0	0
842	ENSRNOG000000012160	Syk	spleen associated tyrosine kinase	1	0.035440314	2.143994788	1	1	0.0688563	-0.949046472	0	0
843	ENSRNOG000000014353	Sympk	sympkin	1	0.005063789	1.451468127	1	1	0.095489759	-1.182694705	0	0
844	ENSRNOG000000000483	Syngap1	synaptic Ras GTPase activating protein 1	1	0.011818771	1.137249938	1	1	0.151382801	-0.642820773	0	0
845	ENSRNOG000000019780	Syp12	synaptophysin-like 2	1	0.045844838	1.225872405	1	1	0.183949452	-1.039988121	0	0
846	ENSRNOG000000004229	Tac3	tachykinin 3	1	0.021255775	1.228452309	1	1	0.050068203	-0.784469433	0	0
847	ENSRNOG000000019178	Taf10	TATA-box binding protein associated factor 10	1	0.01859127	0.721078426	1	1	0.128787325	-0.546690642	0	0
848	ENSRNOG000000001355	Taf6	TATA-box binding protein associated factor 6	1	0.02105372	0.805292985	1	1	0.131758086	-0.442459158	0	0
849	ENSRNOG000000019419	Taf6l	TATA-box binding protein associated factor 6 like	1	0.00792897	1.009909889	1	1	0.080624095	-0.864562038	0	0
850	ENSRNOG000000008301	Tagln2	transgelin 2	1	0.005469416	1.078473244	1	1	0.033872905	-0.403681975	0	0

851	ENSRNOG00000019357	Tax1bp3	Tax1 binding protein 3	1	0.01653348	0.787195452	1	1	0.104165299	-0.473488027	0	0
852	ENSRNOG00000006394	Tbc1d10a	TBC1 domain family, member 10a	1	0.021418861	1.016778607	1	1	0.217925522	-0.49000357	0	0
853	ENSRNOG00000005786	Tbc1d20	TBC1 domain family, member 20	1	0.029505985	1.137151315	1	1	0.078673609	-0.739081954	0	0
854	ENSRNOG000000017057	Tbc1d22a	TBC1 domain family, member 22a	1	0.005665284	0.59551787	1	1	0.113830632	-0.395924674	0	0
855	ENSRNOG000000052204	Tbc1d24	TBC1 domain family, member 24	1	0.030661196	1.020377951	1	1	0.054618578	-0.879193681	0	0
856	ENSRNOG00000005303	Tbc1d25	TBC1 domain family, member 25	1	0.002312668	0.874641744	1	1	0.155922557	-0.860243144	0	0
857	ENSRNOG00000013429	Tbl3	transducin (beta)-like 3	1	0.021222398	1.886359442	1	1	0.050010827	-1.300856949	0	0
858	ENSRNOG000000023850	Tbrg1	transforming growth factor beta regulator 1	1	0.007919888	1.703280363	1	1	0.082297152	-0.80009182	0	0
859	ENSRNOG00000007918	Tbxas1	thromboxane A synthase 1	1	0.033854217	2.625317114	1	1	0.116317151	-0.708919118	0	0
860	ENSRNOG00000004280	Ton2	transcobalamin 2	1	0.03168347	1.049161698	1	1	0.170720502	-0.5545082	0	0
861	ENSRNOG000000042576	Top11l1	t-complex 11 like 1	1	0.019824012	1.15457781	1	1	0.203375422	-0.480205883	0	0
862	ENSRNOG00000002278	Tec	tec protein tyrosine kinase	1	0.038140956	0.656651729	1	1	0.052025102	-0.80481313	0	0
863	ENSRNOG000000021904	Tecpr2	tectonin beta-propeller repeat containing 2	1	0.019498793	1.210515434	1	1	0.11211082	-0.656612758	0	0
864	ENSRNOG000000060307	Ten1	TEN1 CST complex subunit	1	0.028722157	1.444594345	1	1	0.10082615	-0.273541754	0	0
865	ENSRNOG000000051952	Tes	testin LIM domain protein	1	0.038908075	1.283594669	1	1	0.06078829	-0.830460643	0	0
866	ENSRNOG00000013712	Tex261	testis expressed 261	1	0.030287704	1.018534126	1	1	0.098406731	-0.613480655	0	0
867	ENSRNOG000000030625	Tf	transferrin	1	0.016560513	1.007521071	1	1	2.13778E-06	0.406257783	0	0
868	ENSRNOG000000056098	Tfpt	TCF3 fusion partner	1	0.029807737	0.999213212	1	1	0.047719881	-0.472566522	0	0
869	ENSRNOG000000019985	Tgfb11	transforming growth factor beta 1 induced transcript 1	1	0.013703193	1.690217566	1	1	0.051355975	-1.178807753	0	0
870	ENSRNOG000000009887	Tgfb3	transforming growth factor, beta 3	1	0.011369147	0.858748716	1	1	0.374562582	0.063731392	0	0
871	ENSRNOG000000012216	Tgfb1	transforming growth factor, beta induced	1	0.025335632	1.184115308	1	1	0.087577822	-0.609839479	0	0
872	ENSRNOG000000013285	Tgfb2	transforming growth factor, beta receptor 2	1	0.040929315	1.071260799	1	1	0.489045238	-0.013028406	0	0
873	ENSRNOG000000037967	Thap7	THAP domain containing 7	1	0.048035032	1.188373401	1	1	0.168854288	-0.841101371	0	0
874	ENSRNOG000000059903	Thbs3	thrombospondin 3	1	0.03897276	1.005910057	1	1	0.103312944	-0.219878022	0	0
875	ENSRNOG000000000104	Thoc3	THO complex 3	1	0.012564375	0.888898418	1	1	0.065417895	-0.607808018	0	0
876	ENSRNOG00000003497	Thoc6	THO complex 6	1	0.042981725	1.180512459	1	1	0.125005103	-0.746800856	0	0
877	ENSRNOG000000018630	Tln1	talin 1	1	0.023630646	1.064006185	1	1	0.099865802	-0.766573479	0	0
878	ENSRNOG000000009822	Tlr2	toll-like receptor 2	1	0.041554376	1.948092554	1	1	0.315917937	-0.383041983	0	0
879	ENSRNOG000000016437	Tm4sf4	transmembrane 4 L six family member 4	1	0.017081719	0.700348031	1	1	0.167331839	1.484194231	0	0
880	ENSRNOG000000055679	Tmbim6	transmembrane BAX inhibitor motif containing 6	1	0.026827391	0.600385391	1	1	0.073970071	-0.293988043	0	0
881	ENSRNOG000000007901	Tmed10	transmembrane p24 trafficking protein 10	1	0.026817185	0.756738243	1	1	0.126381422	-0.233846243	0	0
882	ENSRNOG000000013889	Tmed3	transmembrane p24 trafficking protein 3	1	0.021892835	1.562373773	1	1	0.070917178	-0.450151644	0	0
883	ENSRNOG000000002434	Tmem100	transmembrane protein 100	1	0.015758775	1.096743271	1	1	0.230397973	0.250858086	0	0
884	ENSRNOG0000000001441	Tmem120	transmembrane protein 120A	1	0.008414888	0.80499683	1	1	0.095259568	-0.514029412	0	0
885	ENSRNOG0000000023708	Tmem176	transmembrane protein 176A	1	0.002742018	1.429751879	1	1	0.188444797	0.064690722	0	0
886	ENSRNOG000000008465	Tmem176	transmembrane protein 176B	1	0.01452355	1.331099827	1	1	0.05023226	0.338105725	0	0
887	ENSRNOG000000022802	Tmem184	transmembrane protein 184B	1	0.002893466	0.677536244	1	1	0.10701882	-0.580968294	0	0
888	ENSRNOG0000000015974	Tmem208	transmembrane protein 208	1	0.047985794	1.841258356	1	1	0.068052962	-0.79200794	0	0
889	ENSRNOG0000000028083	Tmem35b	transmembrane protein 35B	1	0.004705055	1.160294008	1	1	0.331417282	-0.192853279	0	0
890	ENSRNOG000000003075	Tmem39a	transmembrane protein 39a	1	0.033125026	1.256693031	1	1	0.059564858	-0.693905697	0	0
891	ENSRNOG000000007519	Tmem43	transmembrane protein 43	1	0.017803462	0.992438417	1	1	0.158822633	-0.20616942	0	0
892	ENSRNOG0000000017279	Tmem50a	transmembrane protein 50A	1	0.026451969	0.870158929	1	1	0.182833322	-0.207309371	0	0
893	ENSRNOG000000010204	Tmem9	transmembrane protein 9	1	0.002043032	1.440473252	1	1	0.087081994	-0.973338744	0	0
894	ENSRNOG0000000022857	Tmem97	transmembrane protein 97	1	0.042623819	2.729838551	1	1	0.082093925	-1.549542575	0	0
895	ENSRNOG0000000042499	Tmsb10	thymosin, beta 10	1	0.010913316	0.914070423	1	1	0.043129577	-0.383551222	0	0

896	ENSRNOG00000058645	Tnc	tenascin C	1	0.01943328	6.081539034	1	1	0.09312675	-3.147682753	0	0
897	ENSRNOG00000050792	Tnfrsf11b	TNF alpha induced protein 8	1	0.013614647	1.491957458	1	1	0.457225088	-0.047293198	0	0
898	ENSRNOG00000008336	Tnfrsf11a	TNF receptor superfamily member 11B	1	0.013000621	2.082831773	1	1	0.406122888	0.18841513	0	0
899	ENSRNOG000000031312	Tnfrsf11a	TNF receptor superfamily member 1A	1	0.009304738	0.979741552	1	1	0.033123371	-0.512754778	0	0
900	ENSRNOG000000014464	Tnfrsf13b	TNF superfamily member 13b	1	0.020362596	0.904612891	1	1	0.365181298	0.039531552	0	0
901	ENSRNOG000000026807	Tnfrsf18	TNF superfamily member 18	1	0.020552238	1.698688414	1	1	0.200255775	-0.751808934	0	0
902	ENSRNOG000000006894	Tor1a	torsin family 1, member A	1	0.036262741	0.837416025	1	1	0.067294118	-0.488023954	0	0
903	ENSRNOG000000008435	Tor1b	torsin family 1, member B	1	0.004658575	0.795292291	1	1	0.021104682	-0.427089651	0	0
904	ENSRNOG000000009369	Tor4a	torsin family 4, member A	1	0.031230674	1.057057799	1	1	0.063241018	-0.540427882	0	0
905	ENSRNOG000000015122	Tpd52l2	tumor protein D52-like 2	1	0.034702572	0.591567331	1	1	0.261962072	-0.043467624	0	0
906	ENSRNOG000000048914	Traf1	TNF receptor-associated factor 1	1	0.022046893	0.685741273	1	1	0.059214882	-0.298431363	0	0
907	ENSRNOG000000003131	Traf7	TNF receptor associated factor 7	1	0.01544059	0.768629733	1	1	0.091957106	-0.634624909	0	0
908	ENSRNOG000000037627	Trappo1	trafficking protein particle complex 1	1	0.038659817	0.640999462	1	1	0.381557962	-0.064187086	0	0
909	ENSRNOG000000014581	Trappo2l	trafficking protein particle complex 2-like	1	0.001797807	0.887886259	1	1	0.094441418	-0.363895528	0	0
910	ENSRNOG000000022859	Trem1	triggering receptor expressed on myeloid cells 1	1	0.031002689	2.728929456	1	1	0.116656989	-1.30847889	0	0
911	ENSRNOG000000011824	Trh	thyrotropin releasing hormone	1	0.025187228	1.589501957	1	1	0.095202193	0.927975918	0	0
912	ENSRNOG000000048580	Trp6	thyroid hormone receptor interactor 6	1	0.018957865	2.214019395	1	1	0.055085856	-1.399890498	0	0
913	ENSRNOG000000018122	Tspan17	tetraspanin 17	1	0.036878146	1.771380574	1	1	0.184191849	-0.392921096	0	0
914	ENSRNOG000000032777	Tsco4	tumor suppressing subtransferable candidate 4	1	0.020173092	1.43277542	1	1	0.147120957	-0.825142289	0	0
915	ENSRNOG000000009020	Tsta3	tissue specific transplantation antigen P35B	1	0.026688504	1.223014095	1	1	0.119067168	-0.391164369	0	0
916	ENSRNOG000000014879	Ttc7a	tetratricopeptide repeat domain 7A	1	0.038027033	0.89428795	1	1	0.101483553	-0.594177176	0	0
917	ENSRNOG000000010141	Ttl1	tubulin tyrosine ligase like 1	1	0.022419833	0.904504528	1	1	0.303529963	-0.116101409	0	0
918	ENSRNOG000000017445	Tubb2b	tubulin, beta 2B class IIb	1	0.009046549	2.150040914	1	1	0.060099924	-1.352678366	0	0
919	ENSRNOG000000020213	Tubg1	tubulin, gamma 1	1	0.013594787	1.273915235	1	1	0.091143369	-1.242588063	0	0
920	ENSRNOG000000006494	Tubg2	tubulin, gamma 2	1	0.01799269	0.771208004	1	1	0.186506448	-0.447700617	0	0
921	ENSRNOG000000048242	Txlna	taxilin alpha	1	0.021504862	1.037271335	1	1	0.096725467	-0.645374152	0	0
922	ENSRNOG000000012081	Txn1	thioredoxin 1	1	0.021042135	0.635469329	1	1	0.424845942	0.034222642	0	0
923	ENSRNOG000000032948	Tyk2	tyrosine kinase 2	1	0.011435487	0.618044197	1	1	0.026979243	-0.571980477	0	0
924	ENSRNOG000000024352	Tyrw1	tRNA-yW synthesizing protein 1 homolog	1	0.022318047	1.23511748	1	1	0.14868147	-0.47907026	0	0
925	ENSRNOG000000045860	U2af1	U2 small nuclear RNA auxiliary factor 1	1	0.016831943	0.839998371	1	1	0.065736225	-0.60323854	0	0
926	ENSRNOG000000015914	U2af2	U2 small nuclear RNA auxiliary factor 2	1	0.014023033	1.127727152	1	1	0.091923798	-0.799243148	0	0
927	ENSRNOG000000016930	Ube2s	ubiquitin-conjugating enzyme E2S	1	0.015811185	1.065332247	1	1	0.079357217	-0.88630819	0	0
928	ENSRNOG000000048411	Uhrf1	ubiquitin-like with PHD and ring finger domains 1	1	0.028447279	2.18826172	1	1	0.07291111	-2.021150981	0	0
929	ENSRNOG0000000001797	Umps	uridine monophosphate synthetase	1	0.011020068	1.220817084	1	1	0.010671678	-0.441525231	0	0
930	ENSRNOG000000021725	Unc119b	unc-119 lipid binding chaperone B	1	0.046604786	0.632414805	1	1	0.12499469	-0.348479943	0	0
931	ENSRNOG000000012357	Unc45a	unc-45 myosin chaperone A	1	0.044865595	1.190682825	1	1	0.151792497	-0.813055108	0	0
932	ENSRNOG000000026636	Urm1	ubiquitin related modifier 1	1	0.044919523	0.64949746	1	1	0.043550514	-0.53860715	0	0
933	ENSRNOG000000004255	Usf1	upstream transcription factor 1	1	0.027885939	0.7604381	1	1	0.359242742	-0.144283416	0	0
934	ENSRNOG000000012748	Vamp8	vesicle-associated membrane protein 8	1	0.02950762	1.248670232	1	1	0.199198814	-0.238125748	0	0
935	ENSRNOG000000010457	Vash1	vasohibin 1	1	0.040493207	0.845934433	1	1	0.093688022	-0.760033485	0	0
936	ENSRNOG0000000050430	Vav1	vav guanine nucleotide exchange factor 1	1	0.036437763	2.667884371	1	1	0.061509068	-1.377208881	0	0
937	ENSRNOG000000003587	Vegf1	vascular endothelial growth factor D	1	0.022190883	0.985701033	1	1	0.093378733	-0.891556296	0	0
938	ENSRNOG000000028774	Vgll3	vestigial-like family member 3	1	0.042787118	1.177072777	1	1	0.122358872	-0.560507619	0	0
939	ENSRNOG0000000050828	Vkorc1	vitamin K epoxide reductase complex, subunit 1	1	0.009075788	0.889034308	1	1	0.069845183	-0.182455656	0	0
940	ENSRNOG000000021222	Vps16	VPS16 CORVET/HOPS core subunit	1	0.008674712	0.792321447	1	1	0.09218578	-0.626991456	0	0

941	ENSRNOG000000013889	Vps18	VPS18 CORVET/HOPS core subunit	1	0.014271981	1.692398768	1	1	0.068508034	-1.015968081	0	0
942	ENSRNOG000000021081	Vps72	vacuolar protein sorting 72 homolog	1	0.042027998	1.036005149	1	1	0.067748638	-0.980446527	0	0
943	ENSRNOG00000000569	Vsir	V-set immunoregulatory receptor	1	0.002913178	1.652910874	1	1	0.089831598	-0.406473951	0	0
944	ENSRNOG000000029662	Wdfy4	WDFY family member 4	1	0.039492173	1.527532483	1	1	0.064746638	-1.044378921	0	0
945	ENSRNOG000000031171	Wdr46	WD repeat domain 46	1	0.028576098	1.7096334	1	1	0.11448907	-0.968940465	0	0
946	ENSRNOG000000042878	Wdr74	WD repeat domain 74	1	0.025558927	0.839978084	1	1	0.122352803	-0.413861746	0	0
947	ENSRNOG000000030243	Wdr81	WD repeat domain 81	1	0.037827184	1.495462768	1	1	0.093102269	-0.949955409	0	0
948	ENSRNOG000000010421	Wdr91	WD repeat domain 91	1	0.020570168	1.614817184	1	1	0.063612234	-0.668776656	0	0
949	ENSRNOG000000012084	Xpnpep1	X-prolyl aminopeptidase 1	1	8.22E-05	1.159260747	1	1	0.090174471	-0.539748757	0	0
950	ENSRNOG00000001881	YdjC	YdjC chitinoglycosaccharide deacetylase homolog	1	0.008459141	1.051798091	1	1	0.156065858	-0.163387559	0	0
951	ENSRNOG000000010512	Yip1	Yip1 domain family, member 1	1	0.026944211	0.9022954	1	1	0.131535342	-0.228601135	0	0
952	ENSRNOG000000018998	Yip3	Yip1 domain family, member 3	1	0.015280463	1.054360259	1	1	0.135056893	-0.702489759	0	0
953	ENSRNOG000000009595	Zbtb48	zinc finger and BTB domain containing 48	1	0.047515482	1.362654625	1	1	0.072584305	-1.152566603	0	0
954	ENSRNOG000000032917	Zfand2a	zinc finger AN1-type containing 2A	1	0.033622923	0.674762425	1	1	0.090880505	-0.427311538	0	0
955	ENSRNOG000000018839	Zfand2b	zinc finger AN1-type containing 2B	1	0.045547893	1.408528983	1	1	0.141807393	-1.059571985	0	0
956	ENSRNOG000000025140	Zfat	zinc finger and AT hook domain containing	1	0.025055238	1.314184817	1	1	0.179800497	-0.203939749	0	0
957	ENSRNOG000000017290	Zfp335	zinc finger protein 335	1	0.017144335	1.157514909	1	1	0.102882491	-0.893199123	0	0
958	ENSRNOG000000018272	Zfp511	zinc finger protein 511	1	0.033032205	0.699046045	1	1	0.108150265	-0.31579191	0	0
959	ENSRNOG000000016258	Zfp516	zinc finger protein 516	1	0.021132336	1.020087976	1	1	0.022393076	-0.546870315	0	0
960	ENSRNOG000000016683	Zfp668	zinc finger protein 668	1	0.011294118	1.173575745	1	1	0.094536101	-0.695788665	0	0
961	ENSRNOG000000050180	Zfp1	zinc finger protein-like 1	1	0.010008965	1.389489487	1	1	0.091405972	-0.929451075	0	0
962	ENSRNOG000000012528	Zfyve19	zinc finger FYVE-type containing 19	1	0.013323357	1.131551239	1	1	0.147919178	-0.920311432	0	0
963	ENSRNOG000000010119	Zmat3	zinc finger, matrin type 3	1	0.029338804	0.964841229	1	1	0.138251707	-0.403614085	0	0
964	ENSRNOG000000007752	Zmynd19	zinc finger, MYND-type containing 19	1	0.020904351	0.904368229	1	1	0.058002345	-0.629048991	0	0
965	ENSRNOG000000017354	Zyx	zyxin	1	0.034640232	1.758342322	1	1	0.147332943	-0.977252498	0	0
966	ENSRNOG000000005935	A3galt2	alpha 1,3-galactosyltransferase 2	2	0.007124336	1.771643621	1	1	0.010533618	-1.181068286	1	-1
967	ENSRNOG000000000967	Aacs	acetoacetyl-CoA synthetase	2	0.037032756	1.656849783	1	1	0.02413868	-1.205449365	1	-1
968	ENSRNOG000000018883	Abcc10	ATP binding cassette subfamily C member 10	2	0.026751948	0.979994876	1	1	0.037039308	-0.807088016	1	-1
969	ENSRNOG000000036934	Abhd12	abhydrolase domain containing 12	2	0.02547976	1.268881905	1	1	0.026587959	-0.856233466	1	-1
970	ENSRNOG000000009199	Aocs	1-aminocyclopropane-1-carboxylate synthase homolog	2	0.043753396	0.676507217	1	1	0.00379829	-0.632695631	1	-1
971	ENSRNOG0000000046261	Acp5	acid phosphatase 5, tartrate resistant	2	0.008745604	1.883977897	1	1	0.022648093	-0.839722237	1	-1
972	ENSRNOG000000034254	Actb	actin, beta	2	0.008380525	1.648793437	1	1	0.01863175	-1.043544067	1	-1
973	ENSRNOG000000036701	Actg1	actin, gamma 1	2	0.003995724	2.129054473	1	1	0.031446797	-1.341296555	1	-1
974	ENSRNOG000000056756	Actn1	actinin, alpha 1	2	0.030006344	2.174549569	1	1	0.049783049	-1.044378398	1	-1
975	ENSRNOG000000021242	Adam33	ADAM metalloproteinase domain 33	2	0.000362182	1.000388033	1	1	0.005100476	-0.849230313	1	-1
976	ENSRNOG000000017897	Adam8	ADAM metalloproteinase domain 8	2	0.038288394	3.769622938	1	1	0.035957727	-3.106457827	1	-1
977	ENSRNOG000000003538	Adamts4	ADAM metalloproteinase with thrombospondin type 1 motif 4	2	0.04043859	2.547726471	1	1	0.031915109	-1.984978517	1	-1
978	ENSRNOG000000005574	Adamts8	ADAM metalloproteinase with thrombospondin type 1 motif 8	2	0.005146404	2.055085239	1	1	0.002606234	-1.570694002	1	-1
979	ENSRNOG0000000054033	Adap1	ArfGAP with dual PH domains 1	2	0.047684298	1.736003188	1	1	0.025193366	-1.713931287	1	-1
980	ENSRNOG000000017777	Ahoc	adenosylhomocysteinease	2	0.004532101	1.411264554	1	1	0.032184539	-0.987145214	1	-1
981	ENSRNOG000000009734	Akr1b8	aldo-keto reductase family 1, member B8	2	0.02958458	2.734533947	1	1	0.041878353	-0.753871288	1	-1
982	ENSRNOG000000017512	Aldh3b1	aldehyde dehydrogenase 3 family, member B1	2	0.004388939	1.636511168	1	1	0.011989794	-1.236335981	1	-1
983	ENSRNOG000000014645	Aldh7a1	aldehyde dehydrogenase 7 family, member A1	2	0.029600855	0.692276385	1	1	0.048578926	-0.836118978	1	-1
984	ENSRNOG000000002883	Alg1	ALG1, chitobiosylidiphosphodolichol beta-mannosyltransferase 1	2	0.00733646	1.333991785	1	1	0.021205089	-0.932054316	1	-1
985	ENSRNOG000000036887	Alyref	Aly/REF export factor	2	0.02704048	0.741936676	1	1	0.024424591	-0.678813352	1	-1

986	ENSRNOG00000008480	Amdhd2	amidohydrolase domain containing 2	2	0.024795889	2.161725883	1	1	0.022420247	-1.729180545	1	-1
987	ENSRNOG00000019240	Ampd2	adenosine monophosphate deaminase 2	2	0.041801807	0.933423743	1	1	0.048759672	-0.781617276	1	-1
988	ENSRNOG00000019938	Anapc15	anaphase promoting complex subunit 15	2	0.001361561	1.758239865	1	1	0.016871678	-0.823377288	1	-1
989	ENSRNOG000000007545	Angptl4	angiopoietin-like 4	2	0.036203158	3.213143777	1	1	0.035403007	-1.757496493	1	-1
990	ENSRNOG00000015885	Ap2s1	adaptor-related protein complex 2, sigma 1 subunit	2	0.002786588	1.263688144	1	1	0.036114544	-0.754911088	1	-1
991	ENSRNOG000000026114	Ap5b1	adaptor-related protein complex 5, beta 1 subunit	2	0.007298945	0.782693342	1	1	0.039572788	-0.623678248	1	-1
992	ENSRNOG000000054775	Arf3	ADP-ribosylation factor 3	2	0.008090201	2.098168538	1	1	0.026897317	-1.02648333	1	-1
993	ENSRNOG000000046472	Arfgap3	ADP-ribosylation factor GTPase activating protein 3	2	0.005165575	1.620636344	1	1	0.038052824	-0.783272958	1	-1
994	ENSRNOG000000028569	Arhgap27	Rho GTPase activating protein 27	2	0.005901862	1.229754722	1	1	0.025918419	-0.962148333	1	-1
995	ENSRNOG000000058545	Arhgap4	Rho GTPase activating protein 4	2	0.012697055	1.642235723	1	1	0.041189643	-0.987915794	1	-1
996	ENSRNOG000000013220	Arhgap45	Rho GTPase activating protein 45	2	0.006564927	2.261384081	1	1	0.019630853	-1.022299895	1	-1
997	ENSRNOG000000050334	Arhgef25	Rho guanine nucleotide exchange factor 25	2	0.048393904	0.951533092	1	1	0.032880354	-0.847361647	1	-1
998	ENSRNOG000000014653	Arh11	ADP-ribosylation factor like GTPase 11	2	0.008273498	3.319584157	1	1	0.04197214	-0.932291571	1	-1
999	ENSRNOG000000037707	Armox8	armadillo repeat containing, X-linked 8	2	0.038982139	1.155511901	1	1	0.014335701	-0.803688323	1	-1
1000	ENSRNOG000000014448	Arntl	aryl hydrocarbon receptor nuclear translocator-like	2	0.014798704	2.218155174	1	1	0.043662368	-0.816909984	1	-1
1001	ENSRNOG000000007622	Arndc1	arrestin domain containing 1	2	0.001443782	1.140216037	1	1	0.018909682	-1.080018173	1	-1
1002	ENSRNOG000000026060	Arsi	arylsulfatase family, member 1	2	0.0004459	2.357180418	1	1	0.029290945	-0.933126506	1	-1
1003	ENSRNOG000000008837	Ass1	argininosuccinate synthase 1	2	0.009266871	2.219891146	1	1	0.004139921	-1.278844392	1	-1
1004	ENSRNOG000000007486	Atg7	autophagy related 7	2	0.016334736	1.500452933	1	1	0.01091173	-0.808031743	1	-1
1005	ENSRNOG000000004049	Baiap2	BAI1-associated protein 2	2	0.001274671	1.585728138	1	1	0.044765464	-1.274661986	1	-1
1006	ENSRNOG000000015514	Bcat1	branched chain amino acid transaminase 1	2	0.02544059	2.890627476	1	1	0.044405282	-1.469598289	1	-1
1007	ENSRNOG000000010890	Bmp1	bone morphogenetic protein 1	2	0.049954141	1.255043176	1	1	0.046799186	-1.080568473	1	-1
1008	ENSRNOG000000033700	Bud23	BUD23, rRNA methyltransferase and ribosome maturati	2	0.04025943	0.74902495	1	1	0.043382663	-1.030316106	1	-1
1009	ENSRNOG000000026474	Cad	carbamoyl-phosphate synthetase 2, aspartate transcarb	2	0.00417847	1.438395147	1	1	0.008810358	-1.337485057	1	-1
1010	ENSRNOG0000000021560	Cass4	Cas scaffolding protein family member 4	2	0.029693263	1.067824286	1	1	0.025980348	-0.985852032	1	-1
1011	ENSRNOG000000010846	Ccdc22	coiled-coil domain containing 22	2	0.019105993	0.704313555	1	1	0.019111096	-0.93599075	1	-1
1012	ENSRNOG000000024931	Ccdc88b	coiled-coil domain containing 88B	2	0.042829046	1.133418804	1	1	0.048158955	-0.877947004	1	-1
1013	ENSRNOG000000050233	Cohor1	coiled-coil alpha-helical rod protein 1	2	0.022040411	1.551441853	1	1	0.008621061	-1.326451186	1	-1
1014	ENSRNOG000000011205	Col3	C-C motif chemokine ligand 3	2	0.010116682	1.488721529	1	1	0.005468106	-1.524103489	1	-1
1015	ENSRNOG0000000057058	Cd300a	Cd300a molecule	2	0.010149921	3.407992026	1	1	0.020530101	-1.626972907	1	-1
1016	ENSRNOG000000020699	Cd37	CD37 molecule	2	0.014068409	2.148248819	1	1	0.031595614	-0.870325908	1	-1
1017	ENSRNOG000000016825	Cd3eap	CD3e molecule associated protein	2	0.021899731	1.455499508	1	1	0.016495414	-1.237018483	1	-1
1018	ENSRNOG000000037563	Cd68	Cd68 molecule	2	0.032324943	3.36324422	1	1	0.042152817	-1.746211938	1	-1
1019	ENSRNOG000000018616	Cdc42ep5	CDC42 effector protein 5	2	0.042595821	1.245055509	1	1	0.018893111	-0.59725467	1	-1
1020	ENSRNOG000000005410	Cdca7l	cell division cycle associated 7 like	2	0.037369285	2.349131874	1	1	0.042154748	-1.533987451	1	-1
1021	ENSRNOG000000025815	Cdr2l	cerebellar degeneration-related protein 2-like	2	0.034415971	0.922504492	1	1	0.036499897	-0.716575005	1	-1
1022	ENSRNOG000000013970	Cdt1	chromatin licensing and DNA replication factor 1	2	0.037675809	1.163870445	1	1	0.027276257	-1.175856809	1	-1
1023	ENSRNOG000000010918	Cebpa	CCAAT/enhancer binding protein alpha	2	0.024662713	1.630736501	1	1	0.015881803	-1.405120491	1	-1
1024	ENSRNOG000000019340	Cep250	centrosomal protein 250	2	0.002783256	0.708611697	1	1	0.047787187	-0.708692914	1	-1
1025	ENSRNOG000000007923	Cgref1	cell growth regulator with EF hand domain 1	2	0.005079236	2.162591757	1	1	0.007220192	-1.045668308	1	-1
1026	ENSRNOG000000011143	Cit	citron rho-interacting serine/threonine kinase	2	0.01403848	1.965547057	1	1	0.020120199	-1.129407189	1	-1
1027	ENSRNOG000000008016	Ckap4	cytoskeleton-associated protein 4	2	0.034361768	1.472223905	1	1	0.027528033	-1.20765826	1	-1
1028	ENSRNOG000000029682	Clic1	chloride intracellular channel 1	2	0.007721812	1.877514276	1	1	0.028189642	-0.704466727	1	-1
1029	ENSRNOG000000010691	Cmtm3	CKLF-like MARVEL transmembrane domain containing 3	2	0.036204813	1.043063857	1	1	0.027069995	-0.62892887	1	-1
1030	ENSRNOG000000015591	Cndp2	carnosin dipeptidase 2	2	0.029217847	1.443623801	1	1	0.047851114	-0.736428899	1	-1

1031	ENSRNOG000000031475	Col16a1	collagen type XVI alpha 1 chain	2	0.003178539	2.651047701	1	1	0.026997311	-1.53358214	1	-1
1032	ENSRNOG000000003897	Col1a1	collagen type I alpha 1 chain	2	0.029420454	2.068839123	1	1	0.024948831	-1.516388928	1	-1
1033	ENSRNOG000000007657	Col27a1	collagen type XXVII alpha 1 chain	2	0.037780568	1.002901732	1	1	0.008955934	-1.086152232	1	-1
1034	ENSRNOG000000008749	Col5a1	collagen type V alpha 1 chain	2	0.018805324	1.722431405	1	1	0.049296876	-1.040176482	1	-1
1035	ENSRNOG0000000020525	Col5a3	collagen type V alpha 3 chain	2	0.026501896	1.783259122	1	1	0.026275981	-1.424374214	1	-1
1036	ENSRNOG000000001889	Comt	catechol-O-methyltransferase	2	0.005680022	1.611692582	1	1	0.00781422	-0.972763669	1	-1
1037	ENSRNOG000000010474	Copg1	coatamer protein complex, subunit gamma 1	2	0.02212937	1.049108563	1	1	0.037350321	-0.714748071	1	-1
1038	ENSRNOG0000000018723	Cops7b	COP9 signalosome subunit 7B	2	0.021878215	0.776021206	1	1	0.008808165	-0.705637106	1	-1
1039	ENSRNOG000000019430	Coro1a	coronin 1A	2	0.013247086	1.66401846	1	1	0.003301014	-0.978199459	1	-1
1040	ENSRNOG000000016257	Cot1	coactosin-like F-actin binding protein 1	2	0.007836149	2.874373374	1	1	0.010711675	-1.72790007	1	-1
1041	ENSRNOG000000049828	Crif2	cytokine receptor-like factor 2	2	0.008726295	1.015825184	1	1	0.048376181	-0.596374495	1	-1
1042	ENSRNOG000000008937	Csrp1	cysteine and glycine-rich protein 1	2	0.003480312	1.516075476	1	1	0.027928695	-0.816469794	1	-1
1043	ENSRNOG000000015036	Ctgf	connective tissue growth factor	2	0.001489828	1.74704211	1	1	0.017294118	-0.884623279	1	-1
1044	ENSRNOG0000000020206	Ctsd	cathepsin D	2	0.019846218	1.530077989	1	1	0.025157024	-1.186280509	1	-1
1045	ENSRNOG000000019574	Cuedc2	CUE domain containing 2	2	0.01695883	1.520183506	1	1	0.022929453	-0.79403403	1	-1
1046	ENSRNOG000000013014	Cyba	cytochrome b-245 alpha chain	2	0.01239818	2.950817926	1	1	0.028372802	-1.418886539	1	-1
1047	ENSRNOG000000014350	Cyr61	cysteine-rich, angiogenic inducer, 61	2	0.014091994	1.594166497	1	1	0.008528377	-1.147406784	1	-1
1048	ENSRNOG000000008551	Dcaf15	DBF1 and CUL4 associated factor 15	2	0.008644645	2.090344272	1	1	0.048925315	-1.384914712	1	-1
1049	ENSRNOG000000017850	Dctpp1	dCTP pyrophosphatase 1	2	0.03651624	2.316363165	1	1	0.037780153	-1.540065152	1	-1
1050	ENSRNOG000000004373	Ddx39a	DEAD-box helicase 39A	2	0.008077374	1.546039762	1	1	0.003222398	-1.162478113	1	-1
1051	ENSRNOG0000000037480	Ddx51	DEAD-box helicase 51	2	0.036890283	0.709249301	1	1	0.016229846	-0.86394482	1	-1
1052	ENSRNOG0000000026705	Dgki	diacylglycerol kinase, iota	2	0.017498855	0.764776223	1	1	0.007812578	-0.594561512	1	-1
1053	ENSRNOG0000000020776	Dhcr7	7-dehydrocholesterol reductase	2	0.012366182	1.246229122	1	1	0.034516881	-0.815040262	1	-1
1054	ENSRNOG000000015063	Dhohd	dihydroorotate dehydrogenase (quinone)	2	0.00500793	0.847137498	1	1	0.035805407	-0.905279968	1	-1
1055	ENSRNOG000000018526	Dlg4	discs large MAGUK scaffold protein 4	2	0.001116337	1.177369481	1	1	0.034604096	-0.837854612	1	-1
1056	ENSRNOG0000000053498	Dnajc22	DnaJ heat shock protein family (Hsp40) member C22	2	0.018599821	1.984847621	1	1	0.016898917	-1.052653702	1	-1
1057	ENSRNOG0000000023830	Dnase2	deoxyribonuclease 2, lysosomal	2	0.011820426	1.837992609	1	1	0.031042983	-0.828088054	1	-1
1058	ENSRNOG000000013196	Dok5	docking protein 5	2	0.032226329	0.735205508	1	1	0.006902834	-1.224543742	1	-1
1059	ENSRNOG0000000020587	Efemp2	EGF-containing fibulin-like extracellular matrix protein 2	2	0.001993931	2.571777448	1	1	0.043741121	-1.511655943	1	-1
1060	ENSRNOG000000013783	Efh2	EF-hand domain family, member D2	2	0.016432246	1.808092852	1	1	0.03216123	-0.823181822	1	-1
1061	ENSRNOG0000000042029	Efs	embryonal Fyn-associated substrate	2	0.032304807	1.233601058	1	1	0.036472519	-0.801349184	1	-1
1062	ENSRNOG000000000640	Egr2	early growth response 2	2	0.022151438	1.826927828	1	1	0.014018757	-1.182879321	1	-1
1063	ENSRNOG000000017753	Erc2	ERCC excision repair 2, TFIIH core complex helicase subunit	2	0.002448797	1.262745435	1	1	0.020294118	-1.036228305	1	-1
1064	ENSRNOG0000000001348	Erp29	endoplasmic reticulum protein 29	2	0.034405765	1.832202407	1	1	0.041698917	-1.253099495	1	-1
1065	ENSRNOG0000000060753	Esyt1	extended synaptotagmin 1	2	0.015750776	1.460629752	1	1	0.036251017	-1.020889842	1	-1
1066	ENSRNOG0000000049075	Fabp5	fatty acid binding protein 5	2	0.048531136	0.936496383	1	1	0.028567616	-0.900307834	1	-1
1067	ENSRNOG000000015845	Fam129b	family with sequence similarity 129, member B	2	0.004163023	2.25204134	1	1	0.021049652	-1.455504975	1	-1
1068	ENSRNOG0000000001314	Fam20c	FAM20C, golgi associated secretory pathway kinase	2	0.007851872	1.833992247	1	1	0.01085601	-1.352784395	1	-1
1069	ENSRNOG000000016706	Fanca	Fanconi anemia, complementation group A	2	0.030051307	2.363030207	1	1	0.047262603	-1.42844963	1	-1
1070	ENSRNOG000000011203	Farp1	FERM, ARH/RhoGEF and pleckstrin domain protein 1	2	0.003532446	0.610890042	1	1	0.036852148	-0.635180998	1	-1
1071	ENSRNOG000000019229	Fbl	fibrillarin	2	0.009535342	1.201563179	1	1	0.028484242	-0.954400288	1	-1
1072	ENSRNOG000000008815	Fbxo46	F-box protein 46	2	0.035468037	0.779478519	1	1	0.010619543	-0.725463731	1	-1
1073	ENSRNOG000000009342	Fcnb	ficollin B	2	0.011952141	3.08864989	1	1	0.012442383	-1.892932164	1	-1
1074	ENSRNOG0000000021161	Fermt3	fermitin family member 3	2	0.004234053	3.210292529	1	1	0.024719537	-1.844187026	1	-1
1075	ENSRNOG000000009912	Fgr	FGR proto-oncogene, Src family tyrosine kinase	2	0.026649197	2.408231946	1	1	0.031032481	-1.296164077	1	-1

1076	ENSRNOG00000015941	Fkbp10	FK506 binding protein 10	2	0.014955796	1.782670818	1	1	0.036508999	-1.087204875	1	-1
1077	ENSRNOG00000024663	Fkbp15	FK506 binding protein 15	2	0.021201986	0.985085819	1	1	0.025888146	-0.78663859	1	-1
1078	ENSRNOG000000054890	Flna	filamin A	2	0.019535342	1.402444641	1	1	0.023124267	-0.877040437	1	-1
1079	ENSRNOG000000005888	Fsfp1	fibrous sheath interacting protein 1	2	0.024187573	1.902951391	1	1	0.032422316	-1.091207935	1	-1
1080	ENSRNOG00000011631	Fst	folistatin	2	0.011793394	2.281133583	1	1	0.02672064	-1.276508852	1	-1
1081	ENSRNOG000000009311	Fstl3	folistatin like 3	2	0.031305585	0.935997435	1	1	0.008434522	-1.400080066	1	-1
1082	ENSRNOG00000004776	Ftsj1	FtsJ RNA methyltransferase homolog 1	2	0.0283477	0.611755159	1	1	0.023667885	-0.581897125	1	-1
1083	ENSRNOG0000000059453	Fuk	fuok kinase	2	0.021086132	0.670068892	1	1	0.018380732	-0.870268986	1	-1
1084	ENSRNOG00000021062	Fxyd5	FXD domain-containing ion transport regulator 5	2	0.015091787	2.360205147	1	1	0.031650162	-1.31966113	1	-1
1085	ENSRNOG000000009712	Gale	UDP-galactose-4-epimerase	2	0.00591242	2.121174993	1	1	0.018432039	-1.386286624	1	-1
1086	ENSRNOG000000006359	Galk1	galactokinase 1	2	0.019722088	1.999723565	1	1	0.023273498	-1.499098162	1	-1
1087	ENSRNOG000000014461	Galsn	galactosamine (N-acetyl)-6-sulfatase	2	0.044423557	1.705233308	1	1	0.035800979	-1.134754287	1	-1
1088	ENSRNOG000000008091	Gins1	GINS complex subunit 1	2	0.029182401	1.80875412	1	1	0.033330322	-1.284520635	1	-1
1089	ENSRNOG000000017575	Gins2	GINS complex subunit 2	2	0.009479346	2.111371478	1	1	0.043298255	-0.948320875	1	-1
1090	ENSRNOG000000019281	Gimp	glycosylated lysosomal membrane protein	2	0.01286532	1.8127276	1	1	0.012223226	-1.298401047	1	-1
1091	ENSRNOG000000037229	Gmpb	GDP-mannose pyrophosphorylase B	2	0.020279153	1.882264494	1	1	0.015384387	-1.181633743	1	-1
1092	ENSRNOG000000007083	Gpn2	GPN-loop GTPase 2	2	0.017859734	0.785420281	1	1	0.03431487	-0.793897152	1	-1
1093	ENSRNOG000000008816	Gpnmb	glycoprotein nmb	2	0.02085139	4.995718252	1	1	0.046821667	-2.671884036	1	-1
1094	ENSRNOG000000018964	Gss	glutathione synthetase	2	0.009227777	0.851014856	1	1	0.031546445	-0.639402535	1	-1
1095	ENSRNOG000000016148	Gtse1	G-2 and S-phase expressed 1	2	0.009735053	2.943129971	1	1	0.01649831	-1.780154319	1	-1
1096	ENSRNOG000000039284	Haus4	HAUS augmin-like complex, subunit 4	2	0.036088959	2.009843754	1	1	0.026300393	-1.444174542	1	-1
1097	ENSRNOG000000018846	Hbegf	heparin-binding EGF-like growth factor	2	0.030113234	1.04530709	1	1	0.036846355	-1.354055438	1	-1
1098	ENSRNOG000000009499	Hinf1	histone H4 transcription factor	2	0.028856631	0.737902504	1	1	0.037255086	-0.688849803	1	-1
1099	ENSRNOG000000045753	Hist2h2be	histone cluster 2 H2B family member E	2	0.021057858	0.90592514	1	1	0.028595683	-1.004815301	1	-1
1100	ENSRNOG0000000026235	Hk3	hexokinase 3	2	0.024274464	4.255844143	1	1	0.021334873	-3.180332394	1	-1
1101	ENSRNOG000000014117	Hmox1	heme oxygenase 1	2	0.00502255	3.758868894	1	1	0.012939659	-2.162788531	1	-1
1102	ENSRNOG000000003682	Hook2	hook microtubule-tethering protein 2	2	0.014781188	1.073047323	1	1	0.031053445	-0.994327264	1	-1
1103	ENSRNOG000000005492	Hpcal1	hippocalcin-like 1	2	0.01335301	0.890638893	1	1	0.027229915	-0.813707381	1	-1
1104	ENSRNOG000000022189	Htatip2	HIV-1 Tat interactive protein 2	2	0.031090132	2.123459191	1	1	0.031447824	-0.990651172	1	-1
1105	ENSRNOG0000000026124	Id3	inhibitor of DNA binding 3, HLH protein	2	0.00915661	1.561095467	1	1	0.009797117	-1.230581128	1	-1
1106	ENSRNOG000000000827	Ier3	immediate early response 3	2	0.019454796	0.978967811	1	1	0.016148541	-0.684841154	1	-1
1107	ENSRNOG000000019387	Ifi30	IFI30, lysosomal thiol reductase	2	0.002025378	1.998826314	1	1	0.006584649	-0.979936292	1	-1
1108	ENSRNOG000000004273	Ifitm1	interferon induced transmembrane protein 1	2	0.003169437	1.833397695	1	1	0.023138542	-0.675423683	1	-1
1109	ENSRNOG000000006440	Ifit27	intraflagellar transport 27	2	0.008507413	1.098678476	1	1	0.010646852	-0.635116605	1	-1
1110	ENSRNOG000000007604	Igsf8	immunoglobulin superfamily, member 8	2	0.045019792	1.365551733	1	1	0.021819323	-1.172185376	1	-1
1111	ENSRNOG0000000025100	Ikbke	inhibitor of nuclear factor kappa B kinase subunit epsilon	2	0.022952348	2.051942614	1	1	0.039357148	-0.785142259	1	-1
1112	ENSRNOG000000011153	Il17ra	interleukin 17 receptor A	2	0.000992897	1.760092741	1	1	0.017787878	-0.771890564	1	-1
1113	ENSRNOG000000005871	Il1rn	interleukin 1 receptor antagonist	2	2.37E-05	3.972188923	1	1	0.034364596	-2.450716737	1	-1
1114	ENSRNOG000000017020	Inpp5d	inositol polyphosphate-5-phosphatase D	2	0.012270602	1.460188843	1	1	0.043259637	-0.715585927	1	-1
1115	ENSRNOG000000007437	Irf5	interferon regulatory factor 5	2	0.046392111	2.238020697	1	1	0.029690435	-0.924033196	1	-1
1116	ENSRNOG000000012208	Itgb7	integrin subunit beta 7	2	0.009438521	1.804269417	1	1	0.049628301	-0.889322156	1	-1
1117	ENSRNOG000000022438	Jmjd4	jumonji domain containing 4	2	0.014269499	0.851128357	1	1	0.00292304	-0.740640933	1	-1
1118	ENSRNOG000000019440	Konn4	potassium calcium-activated channel subfamily N member 4	2	0.035054962	2.251993341	1	1	0.011102062	-1.960518843	1	-1
1119	ENSRNOG000000001083	Kdelr2	KDEL endoplasmic reticulum protein retention receptor 2	2	0.03076974	1.412673907	1	1	0.040604303	-0.855202349	1	-1
1120	ENSRNOG000000008471	Kif21b	kinesin family member 21B	2	0.030831115	1.191113342	1	1	0.001782912	-0.746329529	1	-1

1121	ENSRNOG00000000479	Kifc1	kinesin family member C1	2	0.04384208	2.279699205	1	1	0.027014137	-1.638106209	1	-1
1122	ENSRNOG000000033694	Kif16	Kruppel-like factor 16	2	0.017830908	1.111608889	1	1	0.01635501	-0.698257629	1	-1
1123	ENSRNOG000000016422	Kih36	kelch-like family member 36	2	0.041758224	0.846566729	1	1	0.024609061	-0.846418442	1	-1
1124	ENSRNOG000000004132	Lasp1	LIM and SH3 protein 1	2	0.026629046	0.960832662	1	1	0.037070892	-0.614688476	1	-1
1125	ENSRNOG000000010645	Lgals3	galectin 3	2	0.015258534	3.332233124	1	1	0.033025171	-1.556639984	1	-1
1126	ENSRNOG000000007089	Lgmn	legumain	2	0.011388594	1.982209137	1	1	0.015517344	-1.205818508	1	-1
1127	ENSRNOG000000042776	Lins1	lines homolog 1	2	0.01102988	0.874908352	1	1	0.012278395	-0.81750629	1	-1
1128	ENSRNOG000000002520	Litaf	lipopolysaccharide-induced TNF factor	2	0.016597062	1.220912186	1	1	0.018066961	-0.927240552	1	-1
1129	ENSRNOG0000000025742	Lmn2	lamin B2	2	0.008926419	1.022420909	1	1	0.001737328	-1.122776782	1	-1
1130	ENSRNOG000000007436	LOC10014	hypothetical protein LOC100158225	2	0.03627074	1.872032205	1	1	0.021165437	-1.170414948	1	-1
1131	ENSRNOG000000053452	LOC10036	actin, gamma 1 propeptide-like	2	0.004654024	1.327128068	1	1	0.017025929	-1.10412972	1	-1
1132	ENSRNOG000000050554	LOC10036	rCG47764-like	2	0.046992207	0.837749159	1	1	0.0242515	-0.72262102	1	-1
1133	ENSRNOG000000029529	LOC10256	endothelin-converting enzyme 2-like	2	0.036228674	1.412499268	1	1	0.01990311	-1.203168465	1	-1
1134	ENSRNOG000000057834	LOC10256	uncharacterized LOC102553018	2	0.04070802	1.115232221	1	1	0.014914696	-0.972252882	1	-1
1135	ENSRNOG000000018747	LOC10256	engulfment and cell motility protein 2-like	2	0.010081374	1.196314605	1	1	0.04820902	-1.08687888	1	-1
1136	ENSRNOG000000023005	LOC88132	hypothetical protein LOC881325	2	0.018289359	2.377237009	1	1	0.033109923	-1.12793597	1	-1
1137	ENSRNOG000000033256	LOC89114	hypothetical protein LOC891141	2	0.034409075	2.581787538	1	1	0.047308875	-1.1671353	1	-1
1138	ENSRNOG000000008680	Loxd1	lysyl oxidase-like 1	2	0.008851803	2.135250983	1	1	0.023518999	-0.88725977	1	-1
1139	ENSRNOG0000000061373	Loxd3	lysyl oxidase-like 3	2	0.048803531	1.011429388	1	1	0.019504586	-0.79047277	1	-1
1140	ENSRNOG000000022585	Lrrc25	leucine rich repeat containing 25	2	0.025177574	2.40724194	1	1	0.032755051	-1.474773885	1	-1
1141	ENSRNOG000000003524	Lrrc59	leucine rich repeat containing 59	2	0.027720019	1.274621302	1	1	0.013692159	-1.118382108	1	-1
1142	ENSRNOG000000001429	Lrrwd1	leucine-rich repeats and WD repeat domain containing 1	2	0.010543411	1.616295335	1	1	0.030218261	-0.967310626	1	-1
1143	ENSRNOG0000000048725	Lsm2	LSM2 homolog, U6 small nuclear RNA and mRNA degra	2	0.032184283	1.099378806	1	1	0.013961865	-1.176365867	1	-1
1144	ENSRNOG000000020300	Lsp1	lymphocyte-specific protein 1	2	0.004800906	2.232062029	1	1	0.02097276	-0.897728404	1	-1
1145	ENSRNOG000000000855	Lst1	leukocyte specific transcript 1	2	0.005641818	2.495120642	1	1	0.030919681	-0.616800588	1	-1
1146	ENSRNOG000000012094	Ltpb2	latent transforming growth factor beta binding protein 2	2	0.008721054	4.372275331	1	1	0.012385629	-3.273026982	1	-1
1147	ENSRNOG000000002950	Lyl1	LYL1, basic helix-loop-helix family member	2	0.020893042	1.477670122	1	1	0.030624371	-0.596969495	1	-1
1148	ENSRNOG000000006756	Maged1	MAGE family member D1	2	0.027889801	1.178966949	1	1	0.026467892	-0.942490878	1	-1
1149	ENSRNOG000000002449	Maged2	MAGE family member D2	2	0.007334804	1.398635873	1	1	0.008971657	-0.821552055	1	-1
1150	ENSRNOG000000020505	Map4k1	mitogen activated protein kinase kinase kinase kinase 1	2	0.019720433	1.299116284	1	1	0.034459692	-0.8769665	1	-1
1151	ENSRNOG0000000027204	Map6	microtubule-associated protein 6	2	0.008535273	1.068065587	1	1	0.026718916	-1.089132402	1	-1
1152	ENSRNOG000000011351	Mat1a	methionine adenosyltransferase 1A	2	0.049711806	0.789714555	1	1	0.034466589	-0.893095191	1	-1
1153	ENSRNOG000000020431	Matk	megakaryocyte-associated tyrosine kinase	2	0.012556651	2.360367078	1	1	0.032055169	-1.68085186	1	-1
1154	ENSRNOG000000016316	Mcm2	minichromosome maintenance complex component 2	2	0.014397352	2.007135322	1	1	0.009036204	-1.482858444	1	-1
1155	ENSRNOG000000012543	Mcm3	minichromosome maintenance complex component 3	2	0.0322535	2.279674083	1	1	0.028378595	-1.76462748	1	-1
1156	ENSRNOG000000001349	Mcm7	minichromosome maintenance complex component 7	2	0.045780153	1.266616247	1	1	0.036761258	-1.033968649	1	-1
1157	ENSRNOG000000009433	Mcob	mitochondrial calcium uniporter dominant negative beta s	2	0.036477898	2.45978871	1	1	0.035145093	-1.123088186	1	-1
1158	ENSRNOG0000000046202	Metrl	meteorin-like, glial cell differentiation regulator	2	0.005973243	2.545153116	1	1	0.008792359	-1.540176704	1	-1
1159	ENSRNOG000000012832	Mfsd5	major facilitator superfamily domain containing 5	2	0.025017585	1.112720924	1	1	0.02881815	-0.686033972	1	-1
1160	ENSRNOG000000043436	Micu1	mitochondrial calcium uptake 1	2	0.003196469	0.648344479	1	1	0.041093511	-0.592837384	1	-1
1161	ENSRNOG000000030187	Mmp12	matrix metalloproteinase 12	2	0.039184608	5.284890181	1	1	0.03353948	-4.551620863	1	-1
1162	ENSRNOG000000017477	Mmp23	matrix metalloproteinase 23	2	0.01765892	1.618109968	1	1	0.001434936	-1.22887697	1	-1
1163	ENSRNOG000000009907	Mmp8	matrix metalloproteinase 8	2	0.03518778	1.580553914	1	1	0.022407075	-1.336834323	1	-1
1164	ENSRNOG000000018971	Mob3a	MOB kinase activator 3A	2	0.013257568	1.615677017	1	1	0.021843114	-1.170325977	1	-1
1165	ENSRNOG000000017979	Mrt4	MRT4 homolog, ribosome maturation factor	2	0.001163506	1.285901273	1	1	0.028802979	-0.78755328	1	-1

1166	ENSRNOG00000007540	Msc	musculin	2	0.048159299	1.323770058	1	1	0.040853458	-0.841301828	1	-1
1167	ENSRNOG00000007805	Myb2	MYB proto-oncogene like 2	2	0.029897248	2.943394059	1	1	0.022676229	-2.733281207	1	-1
1168	ENSRNOG000000020248	Myi9	myosin light chain 9	2	0.010645335	1.202080502	1	1	0.047988986	-0.944071405	1	-1
1169	ENSRNOG000000059140	Myo1g	myosin IG	2	0.04392235	2.117670154	1	1	0.037849183	-1.223570105	1	-1
1170	ENSRNOG000000013641	Myo7a	myosin VIIA	2	0.049347831	1.715895892	1	1	0.028201296	-1.300841806	1	-1
1171	ENSRNOG000000013911	Nagk	N-acetylglucosamine kinase	2	0.0410962	1.376496514	1	1	0.041426867	-0.91467441	1	-1
1172	ENSRNOG000000008945	Nans	N-acetylneuraminase synthase	2	0.018409213	1.348297051	1	1	0.026941886	-0.7280983	1	-1
1173	ENSRNOG000000010897	Nek6	NIMA-related kinase 6	2	0.049055927	1.576322047	1	1	0.040907937	-0.922087942	1	-1
1174	ENSRNOG000000022975	Nfam1	NFAT activating protein with ITAM motif 1	2	0.0106012	3.352825961	1	1	0.027932074	-1.325502667	1	-1
1175	ENSRNOG000000017146	Nfat1	nuclear factor of activated T-cells 1	2	0.011170816	1.128867495	1	1	0.036291497	-0.59827811	1	-1
1176	ENSRNOG000000002693	Nme1	NME/NM23 nucleoside diphosphate kinase 1	2	0.011880422	1.753214677	1	1	0.02253879	-1.019735546	1	-1
1177	ENSRNOG0000000021890	Nob1	NIN1/PSMD8 binding protein 1 homolog	2	0.00735079	0.791002179	1	1	0.043485484	-0.596493758	1	-1
1178	ENSRNOG000000018453	Nop2	NOP2 nucleolar protein	2	0.034595883	1.218175286	1	1	0.042811461	-0.853623845	1	-1
1179	ENSRNOG000000017622	Npm3	nucleophosmin/nucleoplasm, 3	2	0.010537066	1.520934198	1	1	0.045488656	-0.972888919	1	-1
1180	ENSRNOG000000016156	Nptxr	neuronal pentraxin receptor	2	0.034718847	1.828168233	1	1	0.01873588	-1.910446417	1	-1
1181	ENSRNOG0000000001752	Nrros	negative regulator of reactive oxygen species	2	0.006421764	1.216428995	1	1	0.017724364	-1.018884378	1	-1
1182	ENSRNOG000000018358	Nt5dc2	5'-nucleotidase domain containing 2	2	0.027224191	2.847988554	1	1	0.008188953	-1.852916206	1	-1
1183	ENSRNOG000000001260	Nudt1	nudix hydrolase 1	2	0.008183298	0.725422952	1	1	0.017774016	-0.586499815	1	-1
1184	ENSRNOG000000018564	Nup93	nucleoporin 93	2	0.016934694	1.207135341	1	1	0.016494035	-0.810578871	1	-1
1185	ENSRNOG000000003018	Olfml2b	olfactomedin-like 2B	2	0.027817116	1.28583051	1	1	0.015430453	-0.95666239	1	-1
1186	ENSRNOG0000000020481	Pafah1b3	platelet-activating factor acetylhydrolase 1b, catalytic s	2	0.004425212	1.306892976	1	1	0.00234839	-0.940679881	1	-1
1187	ENSRNOG0000000052084	Parvg	parvin, gamma	2	0.025355493	2.654881624	1	1	0.049337839	-1.130850823	1	-1
1188	ENSRNOG0000000025001	Pcolce	procollagen C-endopeptidase enhancer	2	0.008181091	2.621781502	1	1	0.014151093	-1.449167345	1	-1
1189	ENSRNOG0000000050197	Pdia8	protein disulfide isomerase family A, member 8	2	0.015489139	1.609380085	1	1	0.024263706	-0.697991168	1	-1
1190	ENSRNOG0000000004515	Pes1	pescadillo ribosomal biogenesis factor 1	2	0.002976622	1.177263008	1	1	0.049267775	-0.658087837	1	-1
1191	ENSRNOG000000017163	Pfkip	phosphofructokinase, platelet	2	0.003801393	1.10304354	1	1	0.043019171	-0.819567955	1	-1
1192	ENSRNOG000000019328	Phgdh	phosphoglycerate dehydrogenase	2	0.018294187	2.43470105	1	1	0.041056341	-1.486847688	1	-1
1193	ENSRNOG0000000056788	Piezo1	piezo-type mechanosensitive ion channel component 1	2	0.009677264	2.135261786	1	1	0.015642438	-0.896834534	1	-1
1194	ENSRNOG0000000020634	Pih1d1	PIH1 domain containing 1	2	0.015790083	1.543925637	1	1	0.049312116	-1.142148016	1	-1
1195	ENSRNOG000000004885	Pkd11i	polycystin 1 like 1, transient receptor potential channel i	2	0.042883525	0.839504447	1	1	0.02698338	-0.730502767	1	-1
1196	ENSRNOG000000010516	Plau	plasminogen activator, urokinase	2	0.037264189	2.430568894	1	1	0.040845597	-1.522538765	1	-1
1197	ENSRNOG000000037931	Plaur	plasminogen activator, urokinase receptor	2	0.027775802	2.157748494	1	1	0.040200883	-1.868843969	1	-1
1198	ENSRNOG0000000058337	Plob2	phospholipase C, beta 2	2	0.038085787	1.721844141	1	1	0.041171367	-1.103935659	1	-1
1199	ENSRNOG000000018390	Plid3	phospholipase D family, member 3	2	0.003629819	3.894294158	1	1	0.010941886	-2.204599665	1	-1
1200	ENSRNOG000000007060	Plin2	perilipin 2	2	0.013367768	1.325505587	1	1	0.038734984	-0.634834193	1	-1
1201	ENSRNOG000000017003	Plxna1	plexin A1	2	0.02246052	1.278943186	1	1	0.027481896	-0.827246315	1	-1
1202	ENSRNOG000000007133	Plxnb2	plexin B2	2	0.009942073	1.852323254	1	1	0.03832515	-0.969820819	1	-1
1203	ENSRNOG000000019620	Pmf1	polyamine-modulated factor 1	2	0.034283705	1.760341086	1	1	0.031676298	-1.222880572	1	-1
1204	ENSRNOG000000037295	Poc1a	POC1 centriolar protein A	2	0.00829322	1.383002698	1	1	0.016083305	-1.290534178	1	-1
1205	ENSRNOG000000025310	Pop7	POP7 homolog, ribonuclease P/MRP subunit	2	0.001077719	1.073891393	1	1	0.003850631	-0.582770711	1	-1
1206	ENSRNOG000000013733	Ppp4r1	protein phosphatase 4, regulatory subunit 1	2	0.041957796	0.621134695	1	1	0.03210351	-0.704943693	1	-1
1207	ENSRNOG000000016410	Preli1	PREL1 domain containing 1	2	0.009728846	1.826356647	1	1	0.0408507	-1.124082954	1	-1
1208	ENSRNOG000000042094	Prn13	proline rich 13	2	0.003896297	1.792899035	1	1	0.013880629	-0.642594997	1	-1
1209	ENSRNOG0000000025184	Prss35	protease, serine, 35	2	0.032594166	3.44007284	1	1	0.035063306	-2.828582626	1	-1
1210	ENSRNOG000000016413	Pstpip1	proline-serine-threonine phosphatase-interacting protein 1	2	0.006929039	2.163882082	1	1	0.040909523	-0.94730908	1	-1

1211	ENSRNOG00000010448	Ptbp1	polypyrimidine tract binding protein 1	2	0.014385786	1.103288473	1	1	0.017548514	-0.859161034	1	-1
1212	ENSRNOG00000016756	Ptgir	prostaglandin I2 receptor	2	0.032148817	0.767324028	1	1	0.025557617	-0.62516591	1	-1
1213	ENSRNOG00000039976	Ptk7	protein tyrosine kinase 7	2	0.000110889	2.606778501	1	1	0.022000896	-1.840983762	1	-1
1214	ENSRNOG00000037500	Pus1	pseudouridylylate synthase 1	2	0.049485966	1.059615921	1	1	0.038056341	-1.08023968	1	-1
1215	ENSRNOG00000019202	PVR	poliovirus receptor	2	0.019904896	1.442533434	1	1	0.009292945	-1.39695465	1	-1
1216	ENSRNOG00000007364	Rab15	RAB15, member RAS oncogene family	2	0.002515964	2.686363624	1	1	0.002145645	-1.921880031	1	-1
1217	ENSRNOG00000023375	Rab34	RAB34, member RAS oncogene family	2	0.001932143	0.979525545	1	1	0.022447417	-0.640858985	1	-1
1218	ENSRNOG000000001500	Rab4b	RAB4B, member RAS oncogene family	2	0.024936901	1.423028901	1	1	0.045425212	-0.995243975	1	-1
1219	ENSRNOG000000007350	Rac2	Rac family small GTPase 2	2	0.01043859	2.157035144	1	1	0.023793738	-1.109856974	1	-1
1220	ENSRNOG000000000938	Ran	RAN, member RAS oncogene family	2	0.006996897	1.040460793	1	1	0.014445555	-0.668027998	1	-1
1221	ENSRNOG000000031789	Rangap1	RAN GTPase activating protein 1	2	0.002989725	1.876940438	1	1	0.017007655	-1.328902187	1	-1
1222	ENSRNOG000000033744	Rasgrp4	RAS guanyl releasing protein 4	2	0.01838025	1.193258988	1	1	0.020225502	-1.026337224	1	-1
1223	ENSRNOG000000001397	Rbm19	RNA binding motif protein 19	2	0.024375284	1.053053196	1	1	0.045181918	-1.028898967	1	-1
1224	ENSRNOG00000013794	Rbp1	retinol binding protein 1	2	0.028733605	2.31423329	1	1	0.008949383	-0.820074624	1	-1
1225	ENSRNOG00000019488	Roe1	Ras converting CAAX endopeptidase 1	2	0.037602648	0.981363241	1	1	0.016666023	-0.917084886	1	-1
1226	ENSRNOG000000032448	Recl4	Recl4 like helicase 4	2	0.021177574	2.26109764	1	1	0.005983449	-1.647201856	1	-1
1227	ENSRNOG000000005107	Recl5	Recl5 like helicase 5	2	0.036139301	0.667243819	1	1	0.011588787	-0.741443732	1	-1
1228	ENSRNOG000000025075	Relt	REL, TNF receptor	2	0.013818771	1.517886119	1	1	0.017969795	-1.174380889	1	-1
1229	ENSRNOG000000054765	Renbp	renin binding protein	2	9.60E-05	1.303224157	1	1	0.036203503	-0.636492035	1	-1
1230	ENSRNOG00000001088	Rfc3	replication factor C subunit 3	2	0.02256934	1.654537045	1	1	0.016802772	-0.932642179	1	-1
1231	ENSRNOG000000020144	RGD1310	similar to cDNA sequence BC017158	2	0.028165644	0.948048583	1	1	0.003922557	-0.857287487	1	-1
1232	ENSRNOG000000048771	RGD1559	similar to immunoglobulin superfamily, member 7	2	0.016508103	4.385827274	1	1	0.024578581	-1.599555056	1	-1
1233	ENSRNOG000000016193	RGD1562	RGD1562114	2	0.013088408	1.3136016	1	1	0.042155575	-0.671458966	1	-1
1234	ENSRNOG00000018547	Rgs19	regulator of G-protein signaling 19	2	0.001539894	1.689166029	1	1	0.028888904	-0.907197346	1	-1
1235	ENSRNOG000000011459	Rhbf2	rhomboid 5 homolog 2	2	0.039424591	1.499722022	1	1	0.028095028	-0.893123201	1	-1
1236	ENSRNOG00000019220	Rhod	ras homolog family member D	2	0.041851045	0.962768829	1	1	0.015711882	-0.838748236	1	-1
1237	ENSRNOG000000020393	Rhog	ras homolog family member G	2	0.010903938	0.617041809	1	1	0.013629474	-0.630429155	1	-1
1238	ENSRNOG000000059857	Rnd1	Rho family GTPase 1	2	0.019725122	2.995352741	1	1	0.028597959	-1.890237009	1	-1
1239	ENSRNOG000000053232	Ror2	receptor tyrosine kinase-like orphan receptor 2	2	0.016028136	1.145950331	1	1	0.019311703	-1.260217949	1	-1
1240	ENSRNOG000000042411	Rps6ka1	ribosomal protein S6 kinase A1	2	0.032635818	1.620767456	1	1	0.009134749	-0.759038069	1	-1
1241	ENSRNOG000000003767	Rps6kc1	ribosomal protein S6 kinase C1	2	0.030499628	0.652567351	1	1	0.038972002	-0.599369283	1	-1
1242	ENSRNOG000000012927	Rrp9	ribosomal RNA processing 9, U3 small nucleolar RNA bi	2	0.034040549	1.283681313	1	1	0.046101441	-1.256292249	1	-1
1243	ENSRNOG000000010105	S100a11	S100 calcium binding protein A11	2	0.002044687	2.028681074	1	1	0.003680298	-1.04261389	1	-1
1244	ENSRNOG000000019136	Scamp2	secretory carrier membrane protein 2	2	0.018410868	0.943370719	1	1	0.04829598	-0.740008351	1	-1
1245	ENSRNOG000000000981	Scarb1	scavenger receptor class B, member 1	2	0.008148541	1.514978048	1	1	0.034287015	-1.25277484	1	-1
1246	ENSRNOG000000010628	Sec13	SEC13 homolog, nuclear pore and COPII coat complex c	2	0.032238053	1.275268003	1	1	0.048276602	-0.701432229	1	-1
1247	ENSRNOG000000013743	Sec61a1	Sec61 translocon alpha 1 subunit	2	0.020010088	1.542412954	1	1	0.028088477	-1.01969222	1	-1
1248	ENSRNOG0000000061231	Selenom	selenoprotein M	2	0.01360251	1.073543374	1	1	0.014463485	-0.806366665	1	-1
1249	ENSRNOG00000016831	Serpinh1	serpin family H member 1	2	0.007088408	1.495719764	1	1	0.014866906	-0.830410955	1	-1
1250	ENSRNOG00000001699	Setd4	SET domain containing 4	2	0.021722226	0.673889803	1	1	0.009446728	-0.82643382	1	-1
1251	ENSRNOG000000013747	Sh3bp2	SH3-domain binding protein 2	2	0.027137853	2.150648606	1	1	0.044766292	-1.060833401	1	-1
1252	ENSRNOG000000036683	Sirt7	sirtuin 7	2	0.000895387	1.800782455	1	1	0.018463899	-1.285894911	1	-1
1253	ENSRNOG000000036677	Slc16a3	solute carrier family 16 member 3	2	0.00178236	2.040860391	1	1	0.036890766	-1.363357273	1	-1
1254	ENSRNOG000000015948	Slc1a5	solute carrier family 1 member 5	2	0.016640645	1.75771025	1	1	0.009272671	-1.696513992	1	-1
1255	ENSRNOG000000009459	Slc35f6	solute carrier family 35, member F6	2	0.027612165	0.988627268	1	1	0.012213089	-0.916952211	1	-1

1256	ENSRNOG000000039390	Slc37a2	solute carrier family 37 member 2	2	0.032506034	2.601374659	1	1	0.034643404	-1.850529292	1	-1
1257	ENSRNOG00000000465	Slc39a7	solute carrier family 39 member 7	2	0.020808841	1.276899878	1	1	0.041702296	-0.968922315	1	-1
1258	ENSRNOG000000018487	Slc3a2	solute carrier family 3 member 2	2	0.008916213	1.282093889	1	1	0.027339701	-0.792952484	1	-1
1259	ENSRNOG000000025220	Slc6a16	solute carrier family 6, member 16	2	0.015487484	0.747421211	1	1	0.001423281	-0.739585808	1	-1
1260	ENSRNOG000000018824	Slc7a5	solute carrier family 7 member 5	2	0.005930763	2.363688995	1	1	0.0201533	-1.703483718	1	-1
1261	ENSRNOG000000014311	Slc7a8	solute carrier family 7 member 8	2	0.03528612	2.596821183	1	1	0.038983883	-1.631714624	1	-1
1262	ENSRNOG000000001383	Slc8b1	solute carrier family 8 member B1	2	0.022867802	1.802399513	1	1	0.042421902	-1.170763519	1	-1
1263	ENSRNOG000000003232	Slc9a3r1	SLC9A3 regulator 1	2	0.011025722	1.616804048	1	1	0.030011447	-0.977051345	1	-1
1264	ENSRNOG000000009594	Snail	snail family transcriptional repressor 1	2	0.003307634	2.131895728	1	1	0.013375009	-1.657024962	1	-1
1265	ENSRNOG000000001501	Snrpa	small nuclear ribonucleoprotein polypeptide A	2	0.00454548	2.011597101	1	1	0.027857803	-1.50188777	1	-1
1266	ENSRNOG000000012172	Spi1	Spi-1 proto-oncogene	2	0.00744528	2.090836508	1	1	0.018395904	-0.878851127	1	-1
1267	ENSRNOG000000004351	Spp1	secreted phosphoprotein 1	2	0.0007485	8.748467132	1	1	0.019769188	-4.615888571	1	-1
1268	ENSRNOG000000019940	Ssr2	signal sequence receptor subunit 2	2	0.004998828	1.72522406	1	1	0.012355424	-0.697624339	1	-1
1269	ENSRNOG000000004805	Stac2	SH3 and cysteine rich domain 2	2	0.018127577	0.84028997	1	1	0.014698159	-0.642839509	1	-1
1270	ENSRNOG000000029165	Stx1a	syntaxin 1A	2	0.008542445	0.831900282	1	1	0.015101441	-0.696931523	1	-1
1271	ENSRNOG000000000994	Stxbp2	syntaxin binding protein 2	2	0.007253845	3.211408888	1	1	0.023716916	-1.235293241	1	-1
1272	ENSRNOG000000021182	Sv2a	synaptic vesicle glycoprotein 2a	2	0.031650093	0.797130193	1	1	0.039890973	-0.731004014	1	-1
1273	ENSRNOG000000019306	Syt12	synaptotagmin 12	2	0.004862561	1.224335871	1	1	0.010571547	-1.222532378	1	-1
1274	ENSRNOG000000017628	Tagln	transgelin	2	0.014503551	3.340790333	1	1	0.041973728	-1.841732761	1	-1
1275	ENSRNOG000000018367	Taldo1	transaldolase 1	2	0.004433487	1.498957347	1	1	0.025255362	-0.915899007	1	-1
1276	ENSRNOG000000023348	Tbc1d2	TBC1 domain family, member 2	2	0.011522929	1.739263479	1	1	0.019045169	-1.261106876	1	-1
1277	ENSRNOG000000016288	Toea2	transcription elongation factor A2	2	0.005456727	0.843730896	1	1	0.005872492	-0.587459625	1	-1
1278	ENSRNOG000000017220	Toirg1	T-cell immune regulator 1, ATPase H+ transporting V0 subunit	2	0.012497345	2.317098922	1	1	0.02755741	-1.634955636	1	-1
1279	ENSRNOG000000026108	Toof1	treacle ribosome biogenesis factor 1	2	0.005091235	1.377199587	1	1	0.048538928	-1.128121544	1	-1
1280	ENSRNOG000000005153	Todc1	tubulin epsilon and delta complex 1	2	0.00084408	1.928728557	1	1	0.003030825	-0.975720406	1	-1
1281	ENSRNOG000000025327	Tert	telomerase reverse transcriptase	2	0.035365837	0.631764526	1	1	0.013357906	-0.637774383	1	-1
1282	ENSRNOG000000019222	Tfdp1	transcription factor Dp-1	2	0.035335494	1.06763668	1	1	0.041161782	-0.825308107	1	-1
1283	ENSRNOG000000020652	Tgfb1	transforming growth factor, beta 1	2	0.01277967	1.23672687	1	1	0.042442245	-1.072891486	1	-1
1284	ENSRNOG000000002418	Tgfb2	transforming growth factor, beta 2	2	0.042910696	1.058891171	1	1	0.043776222	-1.343936942	1	-1
1285	ENSRNOG000000012471	Thbs4	thrombospondin 4	2	0.001936418	3.749211754	1	1	0.017264671	-2.718010072	1	-1
1286	ENSRNOG000000008604	Thy1	Thy-1 cell surface antigen	2	0.030347148	2.113308796	1	1	0.043693331	-1.183286747	1	-1
1287	ENSRNOG000000010208	Timp1	TIMP metalloproteinase inhibitor 1	2	0.001844838	3.694235177	1	1	0.026742707	-0.891220746	1	-1
1288	ENSRNOG0000000047314	Tk1	thymidine kinase 1	2	0.035147921	2.805705859	1	1	0.045493414	-1.948795158	1	-1
1289	ENSRNOG000000016084	Tkt	transketolase	2	2.83E-05	2.185940847	1	1	0.03495159	-1.387123502	1	-1
1290	ENSRNOG000000001757	Tm4sf19	transmembrane 4 L six family member 19	2	0.01916061	2.700917979	1	1	0.048393766	-1.986822548	1	-1
1291	ENSRNOG000000021882	Tmed9	transmembrane p24 trafficking protein 9	2	0.002767809	1.516057535	1	1	0.012282601	-0.881693618	1	-1
1292	ENSRNOG0000000025689	Tmem104	transmembrane protein 104	2	0.005712709	1.524435507	1	1	0.022736294	-1.258061673	1	-1
1293	ENSRNOG000000010081	Tmem144	transmembrane protein 144	2	0.034423695	0.590244999	1	1	0.015896828	-0.745710902	1	-1
1294	ENSRNOG000000008812	Tmem214	transmembrane protein 214	2	0.015661403	1.210147127	1	1	0.040140404	-1.102027399	1	-1
1295	ENSRNOG0000000047114	Tmem37	transmembrane protein 37	2	0.011927453	2.046055805	1	1	0.003487277	-1.046952785	1	-1
1296	ENSRNOG0000000021100	Tnfrsf8	TNF alpha induced protein 8 like 2	2	0.004346459	2.401915122	1	1	0.043511551	-0.603440425	1	-1
1297	ENSRNOG000000003546	Tnfrsf12a	TNF receptor superfamily member 12A	2	0.009864285	3.112740974	1	1	0.016932143	-1.74266835	1	-1
1298	ENSRNOG0000000045595	Tnfrsf9	TNF superfamily member 9	2	0.021728984	2.568206793	1	1	0.040284118	-1.29105828	1	-1
1299	ENSRNOG000000017561	Toe1	target of EGR1, member 1 (nuclear)	2	0.020390318	0.62913898	1	1	0.019643818	-0.58818243	1	-1
1300	ENSRNOG000000014703	Tonsl	tonsoku-like, DNA repair protein	2	0.025713675	1.735895857	1	1	0.022250328	-1.410748806	1	-1

1301	ENSRNOG00000022514	Tor2a	torsin family 2, member A	2	0.003716847	1.585039571	1	1	0.0370942	-1.079096198	1	-1
1302	ENSRNOG00000013387	Tpon2	two pore segment channel 2	2	0.021905388	0.914712087	1	1	0.019089581	-0.904948355	1	-1
1303	ENSRNOG00000016731	Tpm2	tropomyosin 2	2	0.004995655	2.034328104	1	1	0.002774981	-1.932352744	1	-1
1304	ENSRNOG00000013169	Traf4	Tnf receptor associated factor 4	2	0.033434798	0.817856422	1	1	0.022497207	-0.879980518	1	-1
1305	ENSRNOG00000013578	Trem2	triggering receptor expressed on myeloid cells 2	2	0.01497014	3.0319514	1	1	0.03433377	-1.27449166	1	-1
1306	ENSRNOG000000027487	Trim28	tripartite motif-containing 28	2	0.004355562	0.843049708	1	1	0.046604185	-0.923649115	1	-1
1307	ENSRNOG000000002914	Trmt1	tRNA methyltransferase 1	2	0.020539135	1.094696311	1	1	0.03990111	-1.059755374	1	-1
1308	ENSRNOG000000001885	Trmt2a	tRNA methyltransferase 2 homolog A	2	0.013008068	0.807756135	1	1	0.035738639	-0.580115118	1	-1
1309	ENSRNOG000000003104	Trpv2	transient receptor potential cation channel, subfamily V,	2	0.025280877	3.125809231	1	1	0.025515758	-2.114081442	1	-1
1310	ENSRNOG000000027784	Tasku	tsukushi, small leucine rich proteoglycan	2	0.031070961	1.731679888	1	1	0.020173988	-0.812288585	1	-1
1311	ENSRNOG000000022623	Ttl12	tubulin tyrosine ligase like 12	2	0.039469968	1.771344217	1	1	0.044242259	-1.022942924	1	-1
1312	ENSRNOG000000006728	Tuba1a	tubulin, alpha 1A	2	0.008445487	1.092246521	1	1	0.004749052	-0.998128887	1	-1
1313	ENSRNOG0000000053468	Tuba1b	tubulin, alpha 1B	2	0.00298007	1.570573179	1	1	0.012119509	-1.088649647	1	-1
1314	ENSRNOG000000021438	Tuba1c	tubulin, alpha 1C	2	0.004679677	3.192833897	1	1	0.009345562	-1.824228742	1	-1
1315	ENSRNOG000000017558	Tubb2a	tubulin, beta 2A class IIa	2	0.007365837	1.709905909	1	1	0.009002889	-0.867883842	1	-1
1316	ENSRNOG000000010170	Tubb4b	tubulin, beta 4B class IVb	2	0.001688159	1.324609746	1	1	0.039325771	-1.4602435	1	-1
1317	ENSRNOG0000000061216	Tubb5	tubulin, beta 5 class I	2	0.021058203	1.87485163	1	1	0.013982898	-1.431442262	1	-1
1318	ENSRNOG000000018371	Tubb6	tubulin, beta 6 class V	2	0.013072478	2.531116239	1	1	0.024639286	-1.675674634	1	-1
1319	ENSRNOG000000013469	Txndc5	thioredoxin domain containing 5	2	0.019596028	1.083320347	1	1	0.027623267	-0.830910021	1	-1
1320	ENSRNOG000000020845	Tyrbp	Tyrosine protein tyrosine kinase binding protein	2	0.00528267	1.841177816	1	1	0.017567892	-0.72938615	1	-1
1321	ENSRNOG000000009575	UbiA1	UbiA prenyltransferase domain containing 1	2	0.036175436	0.691056037	1	1	0.028803807	-0.779333015	1	-1
1322	ENSRNOG000000017703	Unc93b1	unc-93 homolog B1, TLR signaling regulator	2	0.007908282	2.495446949	1	1	0.033809737	-0.876724737	1	-1
1323	ENSRNOG000000000692	Ung	uracil-DNA glycosylase	2	0.005449279	1.276614414	1	1	0.005800979	-1.12984558	1	-1
1324	ENSRNOG000000020684	Vat1	vesicle amine transport 1	2	8.79E-05	1.417114002	1	1	0.036731191	-0.766637819	1	-1
1325	ENSRNOG000000020006	Wdr90	WD repeat domain 90	2	0.011405007	1.647914019	1	1	0.025189918	-1.513604223	1	-1
1326	ENSRNOG000000007213	Yars	tyrosyl-tRNA synthetase	2	0.007309013	1.018533172	1	1	0.03563506	-0.854811672	1	-1
1327	ENSRNOG000000015791	Zdhc12	zinc finger, DHHC-type containing 12	2	0.030610717	1.424303275	1	1	0.020945176	-1.089574897	1	-1
1328	ENSRNOG000000013692	Abhd18	abhydrolase domain containing 18	3	0.0296032	-1.018198285	1	-1	0.048435694	0.896145187	1	1
1329	ENSRNOG000000012966	Acadl	acyl-CoA dehydrogenase, long chain	3	0.02144128	-1.16541145	1	-1	0.032322116	0.637579179	1	1
1330	ENSRNOG000000020624	Acadsb	acyl-CoA dehydrogenase, short/branched chain	3	0.006361216	-1.290142424	1	-1	0.029155438	0.959320912	1	1
1331	ENSRNOG000000018415	Acat13	acyl-CoA thioesterase 13	3	0.034294325	-0.823908288	1	-1	0.037421695	0.613844947	1	1
1332	ENSRNOG000000026745	Acsf8	acyl-CoA synthetase long-chain family member 6	3	0.021418937	-1.640757087	1	-1	0.042238811	1.139381999	1	1
1333	ENSRNOG000000004448	Acsf3	acyl-CoA synthetase short-chain family member 3	3	0.010988208	-1.166381586	1	-1	0.005389697	0.6492414	1	1
1334	ENSRNOG0000000007875	Acr6	ARF6 actin-related protein 6 homolog	3	0.009706779	-0.712018905	1	-1	0.032664437	0.894056052	1	1
1335	ENSRNOG000000011154	Adgrf5	adhesion G protein-coupled receptor F5	3	0.009894076	-1.55480841	1	-1	0.009775802	1.14491782	1	1
1336	ENSRNOG000000057569	Ahnak	AHNAK nucleoprotein	3	0.010366044	-0.803553116	1	-1	0.009051996	0.888928431	1	1
1337	ENSRNOG000000017672	Akr1c14	aldo-keto reductase family 1, member C14	3	0.039012206	-1.368734161	1	-1	0.033965933	1.016066839	1	1
1338	ENSRNOG000000011419	Aldh6a1	aldehyde dehydrogenase 6 family, member A1	3	0.016270464	-1.328209034	1	-1	0.028878422	0.895575695	1	1
1339	ENSRNOG000000005765	Ap4s1	adaptor-related protein complex 4, sigma 1 subunit	3	0.01021033	-1.137294086	1	-1	0.032170678	0.819835697	1	1
1340	ENSRNOG000000007830	Apol1	apolipoprotein L domain containing 1	3	0.032063582	-1.031092188	1	-1	0.016255362	0.949688703	1	1
1341	ENSRNOG0000000045649	Armd3	arrestin domain containing 3	3	0.005382939	-0.874228843	1	-1	0.00106372	1.227466783	1	1
1342	ENSRNOG0000000001551	Atp5j	ATP synthase, H+ transporting, mitochondrial Fo complex	3	0.025655472	-0.93294227	1	-1	0.042307634	0.781534959	1	1
1343	ENSRNOG000000017123	B2m	beta-2 microglobulin	3	0.01144528	-0.865343723	1	-1	0.021712709	0.923800494	1	1
1344	ENSRNOG000000011376	Bbaf1	basal body orientation factor 1	3	0.003189849	-1.131084805	1	-1	0.016569616	0.910388025	1	1
1345	ENSRNOG000000007636	Cadps2	calcium dependent secretion activator 2	3	0.01578898	-1.345807163	1	-1	0.004744569	0.951888899	1	1

1346	ENSRNOG00000016322	Camk2n1	calcium/calmodulin-dependent protein kinase II inhibitor 1	3	0.028881594	-1.168569542	1	-1	0.001713054	1.557086285	1	1
1347	ENSRNOG000000025895	Cavin2	caveolae associated protein 2	3	0.038212399	-0.774040033	1	-1	0.019324805	0.700253163	1	1
1348	ENSRNOG000000021381	Cdc68	coiled-coil domain containing 68	3	0.040928695	-1.256491968	1	-1	0.022288671	1.186182101	1	1
1349	ENSRNOG000000003256	Cgng1	cyclin G1	3	0.009021171	-1.152548747	1	-1	0.021890021	0.747426236	1	1
1350	ENSRNOG000000002089	Cgng2	cyclin G2	3	0.0306994	-1.045522168	1	-1	0.010987518	1.000445716	1	1
1351	ENSRNOG000000002125	Cgng3	cyclin G3	3	0.035696159	-0.627409936	1	-1	0.003096131	0.611783836	1	1
1352	ENSRNOG000000002141	Cd200	Cd200 molecule	3	0.032096545	-0.788853829	1	-1	0.037596097	0.895950896	1	1
1353	ENSRNOG000000016112	Cd274	CD274 molecule	3	0.045775878	-1.189882395	1	-1	0.019280327	0.963207831	1	1
1354	ENSRNOG000000040108	Cd36	CD36 molecule	3	0.018736363	-0.879890906	1	-1	0.035904972	0.854667109	1	1
1355	ENSRNOG000000056783	Cd69	Cd69 molecule	3	0.008445487	-1.185254977	1	-1	0.001008482	1.915521708	1	1
1356	ENSRNOG000000012209	Cdad1	cytidine and dCMP deaminase domain containing 1	3	0.001520999	-0.769955518	1	-1	0.046797807	0.899464089	1	1
1357	ENSRNOG000000013211	Chchd3	coiled-coil-helix-coiled-coil-helix domain containing 3	3	0.008598166	-0.881877126	1	-1	0.026754086	0.685319396	1	1
1358	ENSRNOG000000058271	Chpt1	choline phosphotransferase 1	3	0.011175643	-1.534884097	1	-1	0.016104751	0.90641231	1	1
1359	ENSRNOG000000046972	Chrm2	cholinergic receptor, muscarinic 2	3	0.042120957	-0.934118193	1	-1	0.021438797	0.593121855	1	1
1360	ENSRNOG000000018286	Chna1	cholinergic receptor nicotinic alpha 1 subunit	3	0.017467071	-2.188277086	1	-1	0.011233156	2.254854625	1	1
1361	ENSRNOG000000006460	Clec1a	C-type lectin domain family 1, member A	3	0.008023447	-1.714844912	1	-1	0.00895814	0.899756889	1	1
1362	ENSRNOG000000059538	Clec2g	C-type lectin domain family 2, member G	3	0.035240604	-0.849883714	1	-1	0.026565133	1.20969526	1	1
1363	ENSRNOG000000011260	Cmb1	carboxymethylglutaminase homolog	3	0.023087235	-1.473597512	1	-1	0.041858699	0.925493858	1	1
1364	ENSRNOG000000018102	Coa5	cytochrome C oxidase assembly factor 5	3	0.018857458	-1.130720112	1	-1	0.036813737	0.603858931	1	1
1365	ENSRNOG000000027016	Cob1l1	cordon-bleu WH2 repeat protein-like 1	3	0.01723757	-1.263583493	1	-1	0.007761258	0.670798441	1	1
1366	ENSRNOG000000014851	Col4a3	collagen type IV alpha 4 chain	3	0.039170678	-1.123041331	1	-1	0.039123233	0.803427192	1	1
1367	ENSRNOG000000018951	Col4a5	collagen type IV alpha 5 chain	3	0.040308255	-0.824733413	1	-1	0.018890352	0.644296735	1	1
1368	ENSRNOG000000009974	Coq3	coenzyme Q3 methyltransferase	3	0.035200607	-0.776422241	1	-1	0.047688092	0.618958522	1	1
1369	ENSRNOG000000054689	Cox7b	cytochrome c oxidase subunit 7B	3	0.047651748	-0.798423579	1	-1	0.029245293	0.8848283	1	1
1370	ENSRNOG0000000021840	Cpep1	cadherin-like and PC-esterase domain containing 1	3	0.034928281	-1.054990976	1	-1	0.03148107	1.288317223	1	1
1371	ENSRNOG000000006534	Crbn	cereblin	3	0.000920488	-0.988174213	1	-1	0.04436432	0.858734486	1	1
1372	ENSRNOG0000000020769	Crebrf	CREB3 regulatory factor	3	0.018852907	-1.267629611	1	-1	0.030340459	1.192946187	1	1
1373	ENSRNOG0000000061058	Csde1	cold shock domain containing E1, RNA binding	3	0.003503758	-1.080030024	1	-1	0.033500517	0.643046467	1	1
1374	ENSRNOG0000000039971	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	3	0.043928695	-0.619665233	1	-1	0.003312737	1.202129455	1	1
1375	ENSRNOG000000010593	Ctnna1	catenin alpha-like 1	3	0.006796979	-1.152369318	1	-1	0.012436797	0.644037497	1	1
1376	ENSRNOG000000010452	Cyca	cytochrome c, somatic	3	0.019135508	-1.179482946	1	-1	0.041162954	0.849504216	1	1
1377	ENSRNOG000000001544	Cypr1	cysteine and tyrosine rich 1	3	0.042572512	-1.577716514	1	-1	0.047643128	0.859797029	1	1
1378	ENSRNOG000000008834	Dach1	dachshund family transcription factor 1	3	0.029180746	-1.569764648	1	-1	0.030940901	1.004303866	1	1
1379	ENSRNOG000000015029	Dab1	dihydrolipoamide branched chain transacylase E2	3	0.001369009	-1.157938446	1	-1	0.009783532	0.606103838	1	1
1380	ENSRNOG000000009083	Dnajc15	DnaJ heat shock protein family (Hsp40) member C15	3	0.032999931	-1.08020546	1	-1	0.048596717	0.921486675	1	1
1381	ENSRNOG000000002026	Dnajc28	DnaJ heat shock protein family (Hsp40) member C28	3	0.00610813	-1.140408855	1	-1	0.024387146	0.913782069	1	1
1382	ENSRNOG000000003977	Dusp1	dual specificity phosphatase 1	3	0.014430453	-0.912292643	1	-1	0.024108131	0.837554412	1	1
1383	ENSRNOG0000000042201	Efab2	EF-hand calcium binding domain 2	3	0.032315427	-1.15053698	1	-1	0.035811392	1.143843961	1	1
1384	ENSRNOG000000014648	Efnb2	ephrin B2	3	0.034820081	-1.422113444	1	-1	0.04276774	1.182802167	1	1
1385	ENSRNOG000000001770	Ehahd1	enoyl-CoA hydratase and 3-hydroxyacyl CoA dehydrogenase	3	0.006771395	-0.988079688	1	-1	0.008027653	0.602901348	1	1
1386	ENSRNOG000000016459	Eif3j	eukaryotic translation initiation factor 3, subunit J	3	0.00596152	-1.212657131	1	-1	0.03683146	0.604298539	1	1
1387	ENSRNOG0000000001815	Eif4a2	eukaryotic translation initiation factor 4A2	3	0.013656713	-0.992783066	1	-1	0.04736294	0.878844565	1	1
1388	ENSRNOG000000022910	Emon	endomucin	3	0.0005481	-1.309211157	1	-1	0.041713054	0.913700458	1	1
1389	ENSRNOG000000010174	Enpp4	ectonucleotide pyrophosphatase/phosphodiesterase 4	3	0.00411213	-1.018573318	1	-1	0.003031929	1.20552909	1	1
1390	ENSRNOG000000009538	Etfdh	electron transfer flavoprotein dehydrogenase	3	0.009300876	-1.158431047	1	-1	0.025582787	0.839122972	1	1

1391	ENSRNOG00000015848	Etfrf1	electron transfer flavoprotein regulatory factor 1	3	0.002145845	-0.866294286	1	-1	0.037701193	0.967588284	1	1
1392	ENSRNOG00000002285	Fam122b	family with sequence similarity 122B	3	0.003495621	-0.896306335	1	-1	0.001989173	0.64208134	1	1
1393	ENSRNOG000000011925	Fam83b	family with sequence similarity 83, member B	3	0.002298324	-2.061443346	1	-1	0.030899593	0.737586535	1	1
1394	ENSRNOG000000009549	Fbxo3	F-box protein 3	3	0.014384525	-1.17275327	1	-1	0.039446935	0.734662665	1	1
1395	ENSRNOG000000006738	Fbxo32	F-box protein 32	3	0.014758017	-1.383798255	1	-1	0.023352183	0.736619844	1	1
1396	ENSRNOG000000001931	Fgf12	fibroblast growth factor 12	3	0.029364871	-1.712210105	1	-1	0.032514447	1.191537482	1	1
1397	ENSRNOG000000000940	Flt1	FMS-related tyrosine kinase 1	3	0.009202952	-1.071678543	1	-1	0.036424522	0.666674552	1	1
1398	ENSRNOG000000008754	Fltv2	feline leukemia virus subgroup C cellular receptor family	3	0.036230191	-0.735274822	1	-1	0.046501758	0.621525267	1	1
1399	ENSRNOG000000034191	Fmo1	flavin containing monooxygenase 1	3	0.000963658	-1.280014291	1	-1	0.024888008	0.917210113	1	1
1400	ENSRNOG000000003470	Fundc1	FUN14 domain containing 1	3	0.00223888	-1.017888008	1	-1	0.035505275	0.852566435	1	1
1401	ENSRNOG000000016848	Fzd4	frizzled class receptor 4	3	0.00022495	-1.249018017	1	-1	0.000895938	0.931519578	1	1
1402	ENSRNOG000000034084	Ggt	gamma-glutamyl cyclotransferase	3	0.017661403	-0.972361285	1	-1	0.040238397	0.641835754	1	1
1403	ENSRNOG000000015654	Ghr	growth hormone receptor	3	0.004478864	-1.026116721	1	-1	0.013189711	0.718994426	1	1
1404	ENSRNOG000000008369	Gimap4	GTPase, IMAP family member 4	3	0.028576512	-1.600177243	1	-1	0.024878078	1.069240411	1	1
1405	ENSRNOG000000002169	Gimap8	GTPase, IMAP family member 8	3	0.02604248	-1.609327542	1	-1	0.013537756	0.767882994	1	1
1406	ENSRNOG0000000053201	Gpcpd1	glycerophosphocholine phosphodiesterase 1	3	0.014535411	-1.807481042	1	-1	0.024905662	0.973325339	1	1
1407	ENSRNOG0000000023657	Gprn3	GPRIN family member 3	3	0.024202193	-1.40330188	1	-1	0.018848079	0.650581606	1	1
1408	ENSRNOG000000004550	Gvin1	GTPase, very large interferon inducible 1	3	0.047839321	-1.604598202	1	-1	0.022951245	1.655517888	1	1
1409	ENSRNOG000000049976	Gzmb	granzyme B	3	0.008555134	-1.430398736	1	-1	0.009022826	1.640037871	1	1
1410	ENSRNOG000000025910	Hccs	holocytochrome c synthase	3	0.02209889	-0.92099189	1	-1	0.040896145	0.82637194	1	1
1411	ENSRNOG000000013257	Hecw2	HECT, C2 and WW domain containing E3 ubiquitin prote	3	0.00959258	-1.110484875	1	-1	0.001470312	0.983883114	1	1
1412	ENSRNOG000000028557	Hibch	3-hydroxyisobutyryl-CoA hydrolase	3	0.00194028	-1.182917839	1	-1	0.048468451	0.768491909	1	1
1413	ENSRNOG000000007034	Hipk2	homeodomain interacting protein kinase 2	3	0.000455141	-1.233316168	1	-1	0.017339632	0.851851712	1	1
1414	ENSRNOG000000001711	Hrasl	HRAS-like suppressor	3	0.041931867	-1.004764783	1	-1	0.022073857	0.841103993	1	1
1415	ENSRNOG000000016692	Hsd12	hydroxysteroid dehydrogenase like 2	3	0.028544928	-0.879577603	1	-1	0.041837322	0.763542881	1	1
1416	ENSRNOG000000017206	Igf1bp5	insulin-like growth factor binding protein 5	3	0.016903248	-1.196808509	1	-1	0.011627336	0.798069607	1	1
1417	ENSRNOG000000007270	Il12rb2	interleukin 12 receptor subunit beta 2	3	0.037897524	-1.106715307	1	-1	0.01824288	1.149204876	1	1
1418	ENSRNOG000000003439	Il15	interleukin 15	3	0.043844976	-0.863558992	1	-1	0.027154334	0.933729559	1	1
1419	ENSRNOG000000014066	Jade1	jade family PHD finger 1	3	0.022285222	-0.96804291	1	-1	0.016377698	0.80062959	1	1
1420	ENSRNOG000000028149	Kans1l1	KAT8 regulatory NSL complex subunit 1-like	3	0.008735122	-1.473712571	1	-1	0.023657265	0.939734681	1	1
1421	ENSRNOG000000018285	Kona2	potassium voltage-gated channel subfamily A member 2	3	0.023010137	-1.648155672	1	-1	0.049544583	0.622802642	1	1
1422	ENSRNOG000000027843	Kir3dl1	killer cell immunoglobulin-like receptor, three domains, lo	3	0.046124129	-1.144476564	1	-1	0.031712916	1.29769869	1	1
1423	ENSRNOG000000014215	Klf9	Kruppel-like factor 9	3	0.008755948	-1.54088129	1	-1	0.017594718	1.014207852	1	1
1424	ENSRNOG000000033372	Klhl24	kelch-like family member 24	3	0.003116613	-1.145877046	1	-1	0.02346514	0.806705327	1	1
1425	ENSRNOG000000005215	Klhl4	kelch-like family member 4	3	0.038271705	-1.721433201	1	-1	0.007596924	1.160024496	1	1
1426	ENSRNOG000000010453	Klhl7	kelch-like family member 7	3	0.012422729	-0.861473655	1	-1	0.022272395	0.691194408	1	1
1427	ENSRNOG000000007310	Klrb1b	killer cell lectin-like receptor subfamily B member 1B	3	0.041209572	-0.741759243	1	-1	0.013285084	0.710053082	1	1
1428	ENSRNOG0000000060246	Klrd1	killer cell lectin like receptor D1	3	0.009349976	-1.367628103	1	-1	0.034142128	1.499523179	1	1
1429	ENSRNOG0000000058714	Klre1	killer cell lectin-like receptor, family E, member 1	3	0.020464796	-1.297925062	1	-1	0.025848838	1.406234842	1	1
1430	ENSRNOG000000014918	Klrg1	killer cell lectin like receptor G1	3	0.043165713	-0.959973725	1	-1	0.016109854	0.910521897	1	1
1431	ENSRNOG0000000052803	Klr1	killer cell lectin-like receptor family I member 1	3	0.026302048	-1.071359307	1	-1	0.022158955	1.475049228	1	1
1432	ENSRNOG000000028996	Krt1	keratin 1	3	0.02359589	-1.257522885	1	-1	0.011662644	0.640934848	1	1
1433	ENSRNOG000000005484	Lgalsl	galectin-like	3	0.003998621	-0.988010324	1	-1	0.014735673	0.761809376	1	1
1434	ENSRNOG000000011696	Lifr	LIF receptor alpha	3	0.036793463	-1.127112438	1	-1	0.007604372	1.318768252	1	1
1435	ENSRNOG000000032443	Lmod3	leiomod 3	3	0.03863306	-1.206157622	1	-1	0.03934039	0.721460187	1	1

1436	ENSRNOG00000013738	LOC1001	glutaredoxin-like protein	3	0.028684229	-1.234733255	1	-1	0.022771395	0.923703782	1	1
1437	ENSRNOG00000032885	LOC10036	cytochrome c, somatic-like	3	0.013784153	-0.85381957	1	-1	0.034402455	0.946102617	1	1
1438	ENSRNOG00000046338	LOC10096	zinc finger protein 60-like	3	0.047438896	-0.922215458	1	-1	0.007184884	0.854473903	1	1
1439	ENSRNOG000000060019	LOC10369	uncharacterized LOC103692984	3	0.042103027	-0.983371216	1	-1	0.025113785	0.741708012	1	1
1440	ENSRNOG00000042889	LOC10369	up-regulated during skeletal muscle growth protein 5	3	0.027931591	-1.055459947	1	-1	0.049710985	1.088514351	1	1
1441	ENSRNOG00000033402	LOC50111	similar to Glutathione S-transferase A1 (GTH1) (HA subu	3	0.014814565	-1.314640807	1	-1	0.018147231	1.80408842	1	1
1442	ENSRNOG00000015117	Lrrc39	leucine rich repeat containing 39	3	0.023635198	-1.237807285	1	-1	0.028070823	1.051521979	1	1
1443	ENSRNOG000000026196	Lrrd1	leucine-rich repeats and death domain containing 1	3	0.040768775	-1.253280651	1	-1	0.03044859	0.927551083	1	1
1444	ENSRNOG00000008802	Lrrn1	leucine rich repeat neuronal 1	3	0.01562306	-1.683704031	1	-1	0.03757927	0.711005815	1	1
1445	ENSRNOG000000039110	Lsmem1	leucine-rich single-pass membrane protein 1	3	0.001096478	-1.424595519	1	-1	0.045399697	0.705192394	1	1
1446	ENSRNOG00000005176	Map7d2	MAP7 domain containing 2	3	0.004522998	-0.769798559	1	-1	0.041194056	0.878850328	1	1
1447	ENSRNOG00000003177	Mat2b	methionine adenosyltransferase 2B	3	0.019391214	-0.584108628	1	-1	0.021204607	0.806198547	1	1
1448	ENSRNOG000000016327	Mcee	methylmalonyl CoA epimerase	3	0.012509068	-0.758510652	1	-1	0.014512654	0.645813163	1	1
1449	ENSRNOG000000013282	Mctp1	multiple C2 and transmembrane domain containing 1	3	0.022127715	-0.763608093	1	-1	0.018178264	0.697837331	1	1
1450	ENSRNOG00000004926	Mett15	methyltransferase like 15	3	0.036292532	-0.88336549	1	-1	0.027571271	0.744853426	1	1
1451	ENSRNOG000000061337	Mindy2	MINDY lysine 48 deubiquitinase 2	3	0.010482036	-1.286973645	1	-1	0.022237363	0.869827079	1	1
1452	ENSRNOG000000012827	Mif1	myeloid leukemia factor 1	3	0.00660762	-1.239158364	1	-1	0.039198814	0.897669153	1	1
1453	ENSRNOG00000005934	Milp	muscular LMNA-interacting protein	3	0.023773533	-0.969176236	1	-1	0.023226812	0.753169068	1	1
1454	ENSRNOG000000018760	Mpp7	membrane palmitoylated protein 7	3	0.010292945	-0.96221576	1	-1	0.01140742	0.926635938	1	1
1455	ENSRNOG000000028982	Mrgprb3	MAS-related GPR, member B3	3	0.037224487	-0.889687588	1	-1	0.024537825	1.085876939	1	1
1456	ENSRNOG000000011639	Mrp47	mitochondrial ribosomal protein L47	3	0.002449624	-0.989274827	1	-1	0.026571961	0.940463004	1	1
1457	ENSRNOG000000061213	Mrps36	mitochondrial ribosomal protein S36	3	0.023133991	-1.057683721	1	-1	0.035067682	0.801848811	1	1
1458	ENSRNOG000000021294	Mstn	myostatin	3	0.002420799	-1.501199976	1	-1	0.010645955	0.824244539	1	1
1459	ENSRNOG00000006978	Mterf2	mitochondrial transcription termination factor 2	3	0.00097345	-1.182519636	1	-1	0.027957244	0.756561802	1	1
1460	ENSRNOG000000010655	Mtp	microsomal triglyceride transfer protein	3	0.016019861	-1.029886076	1	-1	0.045029239	0.685974499	1	1
1461	ENSRNOG000000050843	Mut	methylmalonyl CoA mutase	3	0.000248948	-1.428623505	1	-1	0.022258741	0.770749145	1	1
1462	ENSRNOG000000009754	Nampt	nicotinamide phosphoribosyltransferase	3	0.025916557	-1.072566071	1	-1	0.020123164	1.051764128	1	1
1463	ENSRNOG000000029087	Nap113	nucleosome assembly protein 1-like 3	3	0.023923591	-1.059808773	1	-1	0.039666299	0.677132827	1	1
1464	ENSRNOG000000011476	Nars2	asparaginyl-tRNA synthetase 2, mitochondrial	3	0.004750569	-1.336662231	1	-1	0.005877664	0.692841594	1	1
1465	ENSRNOG00000005512	Ndufa4	NDUFA4, mitochondrial complex associated	3	0.0452515	-0.943532664	1	-1	0.035679057	0.846799596	1	1
1466	ENSRNOG000000038218	Ndufc1	NADH:ubiquinone oxidoreductase subunit C1	3	0.015503758	-1.056814431	1	-1	0.04736825	0.790315014	1	1
1467	ENSRNOG000000011849	Ndufs1	NADH:ubiquinone oxidoreductase core subunit S1	3	0.005715882	-1.357721124	1	-1	0.022531067	0.747528653	1	1
1468	ENSRNOG000000011383	Ndufs4	NADH:ubiquinone oxidoreductase subunit S4	3	0.026118475	-1.082476247	1	-1	0.045927729	0.704653071	1	1
1469	ENSRNOG000000049452	Neb1	nebulin	3	0.01118185	-1.097276125	1	-1	0.012294325	0.763737445	1	1
1470	ENSRNOG000000047788	NEWGEN	osteoglycin	3	0.016571547	-1.119957052	1	-1	0.038298324	0.989406796	1	1
1471	ENSRNOG000000006966	Nfia	nuclear factor I/A	3	0.011274395	-0.930512004	1	-1	0.002013585	0.726284572	1	1
1472	ENSRNOG000000009795	Nfib	nuclear factor I/B	3	0.037475071	-0.987467833	1	-1	0.029130474	0.777208656	1	1
1473	ENSRNOG000000017820	Nqo2	N-ribosylhydronicotinamide:quinone reductase 2	3	0.004922005	-0.950726678	1	-1	0.046722502	0.90926167	1	1
1474	ENSRNOG00000005981	Nt5c3a	5'-nucleotidase, cytosolic IIIA	3	0.009845114	-0.961434013	1	-1	0.024207986	0.713808192	1	1
1475	ENSRNOG000000022576	Nudt12	nudix hydrolase 12	3	0.003605407	-1.369177964	1	-1	0.002439694	0.604231969	1	1
1476	ENSRNOG000000027730	Nxpe1	neuraxophilin and PC-esterase domain family, member 1	3	0.004884768	-1.574505641	1	-1	0.004454934	1.10167875	1	1
1477	ENSRNOG000000043094	Oxct1	3-oxoacid CoA transferase 1	3	0.021146473	-1.508523233	1	-1	0.040071168	0.75862075	1	1
1478	ENSRNOG000000056487	Oxr1	oxidation resistance 1	3	0.023045445	-1.099478346	1	-1	0.047567754	0.829983093	1	1
1479	ENSRNOG000000019934	Paip2	poly(A) binding protein interacting protein 2	3	0.000889594	-0.837836496	1	-1	0.036942694	0.701157571	1	1
1480	ENSRNOG000000013306	Podh20	protocadherin 20	3	0.012228398	-1.478259194	1	-1	0.003870699	1.048322667	1	1

1481	ENSRNOG00000039489	Podhb19	protocadherin beta 19	3	0.020231984	-0.851751786	1	-1	0.00203717	0.871728687	1	1
1482	ENSRNOG00000005730	Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase	3	0.001020481	-1.19370824	1	-1	0.03431053	0.895535848	1	1
1483	ENSRNOG00000025383	Pdha1	pyruvate dehydrogenase E1 alpha 1 subunit	3	0.012348045	-1.025272187	1	-1	0.027028688	0.701515596	1	1
1484	ENSRNOG000000001517	Pdk1	pyruvate dehydrogenase kinase 1	3	0.010677808	-1.248468301	1	-1	0.02135832	0.70198359	1	1
1485	ENSRNOG000000057116	Pex19	peroxisomal biogenesis factor 19	3	0.027028619	-1.034380518	1	-1	0.036302462	0.596293888	1	1
1486	ENSRNOG000000008858	Pigy	phosphatidylinositol glycan anchor biosynthesis, class Y	3	0.007213985	-1.188800307	1	-1	0.038855527	0.911619675	1	1
1487	ENSRNOG000000000665	Pitpnb	phosphatidylinositol transfer protein, beta	3	0.017474933	-0.805065215	1	-1	0.013662989	0.768199099	1	1
1488	ENSRNOG000000012095	Pkia	cAMP-dependent protein kinase inhibitor alpha	3	0.00843128	-1.004428214	1	-1	0.011014896	0.712403515	1	1
1489	ENSRNOG000000033119	Plob4	phospholipase C, beta 4	3	0.005785118	-1.339827104	1	-1	0.003879528	0.59909188	1	1
1490	ENSRNOG000000000413	Pln	phospholamban	3	0.020794428	-1.000183675	1	-1	0.022164747	0.822610528	1	1
1491	ENSRNOG000000006102	Pole4	DNA polymerase epsilon 4, accessory subunit	3	0.012549341	-0.775690454	1	-1	0.049526446	0.860097765	1	1
1492	ENSRNOG000000004473	Ppargc1a	PPARG coactivator 1 alpha	3	0.024830288	-1.354150704	1	-1	0.025814854	0.836132758	1	1
1493	ENSRNOG0000000043186	Ppilb	peptidylprolyl isomerase like 6	3	0.000824495	-0.838135923	1	-1	0.005213227	0.742157101	1	1
1494	ENSRNOG000000008893	Ppm1k	protein phosphatase, Mg2+/Mn2+ dependent, 1K	3	0.016997173	-1.044137109	1	-1	0.024762837	0.853174873	1	1
1495	ENSRNOG000000016368	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c	3	0.012202331	-1.293728812	1	-1	0.029886422	0.860259347	1	1
1496	ENSRNOG000000059350	Ppp1r3a	protein phosphatase 1, regulatory subunit 3A	3	0.002890435	-1.685298233	1	-1	0.047755741	0.838827893	1	1
1497	ENSRNOG0000000054052	Ppp4r4	protein phosphatase 4, regulatory subunit 4	3	0.013390801	-0.879101885	1	-1	0.029388387	0.692220438	1	1
1498	ENSRNOG000000010958	Prdx3	peroxiredoxin 3	3	0.042702021	-0.953420819	1	-1	0.038894283	0.730654828	1	1
1499	ENSRNOG000000005391	Prex2	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac	3	0.003809688	-1.094847911	1	-1	0.007537342	0.876206225	1	1
1500	ENSRNOG000000003098	Prom1	prominin 1	3	0.008874285	-1.659989584	1	-1	0.045857044	0.715272552	1	1
1501	ENSRNOG0000000055293	Ptpnb	protein tyrosine phosphatase, receptor type, B	3	0.015647059	-0.956369454	1	-1	0.01903979	1.165697737	1	1
1502	ENSRNOG000000019295	Rab12	RAB12, member RAS oncogene family	3	0.009633818	-0.854007242	1	-1	0.008627474	0.859284139	1	1
1503	ENSRNOG000000017074	Rab28	RAB28, member RAS oncogene family	3	0.008452383	-1.059730837	1	-1	0.029326738	0.820906351	1	1
1504	ENSRNOG000000046256	Ralgapa1	Ral GTPase activating protein catalytic alpha subunit 1	3	0.012629612	-1.132913175	1	-1	0.046812289	0.879204717	1	1
1505	ENSRNOG0000000032463	Rap1a	RAP1A, member of RAS oncogene family	3	0.014118888	-0.883231596	1	-1	0.040095304	0.712321341	1	1
1506	ENSRNOG000000001516	Rapgef4	Rap guanine nucleotide exchange factor 4	3	0.031776981	-1.019502328	1	-1	0.00298945	0.724130205	1	1
1507	ENSRNOG000000005271	Rapgef5	Rap guanine nucleotide exchange factor 5	3	0.030931798	-1.257827099	1	-1	0.034722847	0.842968714	1	1
1508	ENSRNOG000000038957	RGD1305	similar to CDNA sequence BC023105	3	0.00987325	-2.143239044	1	-1	0.001103185	3.331347583	1	1
1509	ENSRNOG000000039871	RGD1306	similar to HT021	3	0.002968071	-0.671681705	1	-1	0.020349355	0.807074399	1	1
1510	ENSRNOG000000015523	RGD1308	similar to expressed sequence AW209491	3	0.013794911	-0.595824254	1	-1	0.048552583	0.696903009	1	1
1511	ENSRNOG0000000046779	RGD1309	similar to apolipoprotein L2; apolipoprotein L-II	3	0.015674091	-1.016868251	1	-1	0.034222874	0.742535843	1	1
1512	ENSRNOG000000002322	RGD1310	similar to hypothetical protein FLJ14146	3	0.036834839	-0.927357298	1	-1	0.032722985	0.734554961	1	1
1513	ENSRNOG0000000028651	RGD1566	similar to Hypothetical protein A430033K04	3	0.033311772	-0.750837414	1	-1	0.02858969	0.993230495	1	1
1514	ENSRNOG0000000007949	Rgn	regucalcin	3	0.037089718	-0.794511472	1	-1	0.00251362	1.118891009	1	1
1515	ENSRNOG000000002730	Rgs5	regulator of G-protein signaling 5	3	9.88E-05	-0.836883729	1	-1	0.011108337	0.630021848	1	1
1516	ENSRNOG0000000057589	Rnf111l	ring finger protein 11-like 1	3	0.000792911	-0.781328067	1	-1	0.002028688	0.636592044	1	1
1517	ENSRNOG0000000007331	Rragd	Ras-related GTP binding D	3	0.029154679	-1.432819631	1	-1	0.002188877	0.959729363	1	1
1518	ENSRNOG0000000013683	S1pr1	sphingosine-1-phosphate receptor 1	3	0.006223985	-1.096713103	1	-1	0.019905593	0.894882065	1	1
1519	ENSRNOG0000000028087	Sdhaf4	succinate dehydrogenase complex assembly factor 4	3	0.008384525	-0.590124096	1	-1	0.00869478	0.758549312	1	1
1520	ENSRNOG000000016420	Serpincb2b	serine (or cysteine) peptidase inhibitor, clade B, member	3	0.021425005	-1.045870767	1	-1	0.011722571	0.841732864	1	1
1521	ENSRNOG000000005828	Skip1	S-phase kinase-associated protein 1	3	0.014361492	-0.876916948	1	-1	0.044373216	0.681478526	1	1
1522	ENSRNOG0000000020305	S1p2a2	solute carrier family 15 member 2	3	0.048442728	-0.879373434	1	-1	0.021314481	1.388285952	1	1
1523	ENSRNOG000000004901	S1c4a1ap	solute carrier family 4 member 1 adaptor protein	3	0.027049721	-0.729985149	1	-1	0.017760017	0.882896216	1	1
1524	ENSRNOG0000000021719	S1fn5	schlafen family member 5	3	0.031510103	-1.534743642	1	-1	0.017611268	1.685992448	1	1
1525	ENSRNOG000000004188	Snx13	sorting nexin 13	3	0.031329012	-0.923087496	1	-1	0.049381148	0.625397688	1	1

1526	ENSRNOG00000020514	Sox6	SRY box 6	3	0.009079374	-0.636162348	1	-1	0.026087787	0.588643899	1	1
1527	ENSRNOG00000015137	Spata8l	spermatogenesis associated 8-like	3	0.000167023	-1.173974172	1	-1	0.002416178	0.700394982	1	1
1528	ENSRNOG00000015095	Spryd7	SPRY domain containing 7	3	0.022022205	-1.123157796	1	-1	0.00987063	0.767755081	1	1
1529	ENSRNOG00000000394	Srgn	serglycin	3	0.013976691	-0.748959573	1	-1	0.012748155	0.851909876	1	1
1530	ENSRNOG00000014002	St7l	suppression of tumorigenicity 7-like	3	0.007163506	-0.808083956	1	-1	0.047704158	0.793299675	1	1
1531	ENSRNOG00000014079	Stat1	signal transducer and activator of transcription 1	3	0.026499276	-0.717240008	1	-1	0.003719812	1.305164191	1	1
1532	ENSRNOG00000017481	Sucla2	succinate-CoA ligase ADP-forming beta subunit	3	0.006151438	-1.506802476	1	-1	0.039163437	0.906382417	1	1
1533	ENSRNOG000000037137	Svip	small VCP interacting protein	3	0.019631612	-0.835417944	1	-1	0.03413668	0.753759224	1	1
1534	ENSRNOG00000006399	Synj2bp	synaptotagmin 2 binding protein	3	0.004407972	-1.279711756	1	-1	0.019261913	0.807890406	1	1
1535	ENSRNOG00000004493	Tasp1	taspace 1	3	0.011111647	-1.070240046	1	-1	0.039319909	0.711106273	1	1
1536	ENSRNOG00000008587	Tek	TEK receptor tyrosine kinase	3	0.033461279	-0.807244201	1	-1	0.00830791	1.053382382	1	1
1537	ENSRNOG00000002695	Tfb2m	transcription factor B2, mitochondrial	3	0.00363437	-1.173305725	1	-1	0.043728639	0.731758057	1	1
1538	ENSRNOG00000006649	Thrb	thyroid hormone receptor beta	3	0.011628991	-1.176004012	1	-1	0.045983863	0.816122883	1	1
1539	ENSRNOG00000004303	Timp3	TIMP metalloproteinase inhibitor 3	3	0.020679539	-0.970938387	1	-1	0.019890214	0.887467864	1	1
1540	ENSRNOG00000013239	Tle4	transducin-like enhancer of split 4	3	0.047055927	-0.594668088	1	-1	0.030301703	0.800620249	1	1
1541	ENSRNOG000000022748	Tmem126	transmembrane protein 126A	3	0.047512309	-1.131890902	1	-1	0.046909248	1.073413984	1	1
1542	ENSRNOG00000006608	Tmem70	transmembrane protein 70	3	0.016716364	-1.258890522	1	-1	0.033386939	0.781077306	1	1
1543	ENSRNOG00000013269	Tnfsf10	TNF superfamily member 10	3	0.034429826	-1.862512846	1	-1	0.00501993	1.630194145	1	1
1544	ENSRNOG00000004103	Trappo8b	trafficking protein particle complex 8B	3	0.018779946	-0.925290826	1	-1	0.041119509	0.702901579	1	1
1545	ENSRNOG00000012609	Trdn	triadin	3	0.009499759	-1.324133244	1	-1	0.035556927	0.891343552	1	1
1546	ENSRNOG000000003980	Ttc1	tetratricopeptide repeat domain 1	3	0.026040825	-0.680293724	1	-1	0.018294049	0.583937523	1	1
1547	ENSRNOG00000004971	Txlng	taxilin gamma	3	0.027901386	-0.993583843	1	-1	0.015101096	0.712281026	1	1
1548	ENSRNOG00000006334	Txndc16	thioredoxin domain containing 16	3	0.047169437	-0.689784233	1	-1	0.022793463	0.699170016	1	1
1549	ENSRNOG00000000921	Ubi3	ubiquitin-like 3	3	0.040991242	-0.719935985	1	-1	0.029672919	0.822832533	1	1
1550	ENSRNOG000000008616	Ubr3	ubiquitin protein ligase E3 component n-recognin 3	3	0.021688967	-1.097996374	1	-1	0.048953314	0.804103271	1	1
1551	ENSRNOG00000004950	Ubxn2a	UBX domain protein 2A	3	0.010766844	-0.975355131	1	-1	0.04932384	0.940058262	1	1
1552	ENSRNOG00000008079	Ugp2	UDP-glucose pyrophosphorylase 2	3	0.022726433	-1.239441359	1	-1	0.043515964	0.729440408	1	1
1553	ENSRNOG000000036742	Uqorc2	ubiquinol cytochrome c reductase core protein 2	3	0.023271085	-1.099008389	1	-1	0.028009723	0.816771363	1	1
1554	ENSRNOG000000020296	Usmg5	up-regulated during skeletal muscle growth 5 homolog (m	3	0.036650852	-1.058559453	1	-1	0.039889249	1.079256132	1	1
1555	ENSRNOG000000004009	Xpnpep2	X-prolyl aminopeptidase 2	3	0.038146473	-1.734615123	1	-1	0.048415902	0.870889187	1	1
1556	ENSRNOG000000026742	Ypel5	yippee-like 5	3	0.000456796	-0.783651099	1	-1	0.049975036	0.834514659	1	1
1557	ENSRNOG000000056716	Zbtb20	zinc finger and BTB domain containing 20	3	0.022002069	-1.386649603	1	-1	0.018346459	0.941843988	1	1
1558	ENSRNOG00000003803	Zdhc17	zinc finger, DHHC-type containing 17	3	0.028081512	-1.190799196	1	-1	0.048155851	0.767794497	1	1
1559	ENSRNOG000000013565	Zfp507	zinc finger protein 507	3	0.036276671	-0.983492504	1	-1	0.041782085	0.803893358	1	1
1560	ENSRNOG000000022391	Zfp711	zinc finger protein 711	3	0.023168333	-1.734808921	1	-1	0.046316875	0.741419365	1	1
1561	ENSRNOG000000033351	Zfp869	zinc finger protein 869	3	0.025891042	-0.782753787	1	-1	0.046042135	0.60806624	1	1
1562	ENSRNOG000000030416	Zfp870	zinc finger protein 870	3	0.012749741	-0.78130599	1	-1	0.019247017	0.888895806	1	1
1563	ENSRNOG000000024135	Zmat1	zinc finger, matrin-type 1	3	0.036146128	-1.110171693	1	-1	0.049854562	0.858835476	1	1
1564	ENSRNOG000000017396	March5	membrane associated ring-CH-type finger 5	4	0.037041583	-0.728343506	1	-1	0.098776667	0.453462333	0	0
1565	ENSRNOG000000011066	March6	membrane associated ring-CH-type finger 6	4	0.027611061	-0.888781616	1	-1	0.108265223	0.308363858	0	0
1566	ENSRNOG000000002790	Abcb7	ATP binding cassette subfamily B member 7	4	0.030223019	-1.140640352	1	-1	0.082870905	0.8108252	0	0
1567	ENSRNOG000000036960	Aboc9	ATP binding cassette subfamily C member 9	4	0.031849666	-0.925010328	1	-1	0.125815875	0.178372502	0	0
1568	ENSRNOG000000011929	Abod3	ATP binding cassette subfamily D member 3	4	0.007581132	-0.850034643	1	-1	0.016483622	0.320278577	0	0
1569	ENSRNOG000000031665	Ace2	angiotensin I converting enzyme 2	4	0.019208806	-0.88270375	1	-1	0.424485001	0.049967618	0	0
1570	ENSRNOG000000008755	Acox1	acyl-CoA oxidase 1	4	0.02580291	-0.804032774	1	-1	0.027838149	0.438807913	0	0

1571	ENSRNOG00000010633	Aos1	acyl-CoA synthetase long-chain family member 1	4	0.024537342	-1.050739417	1	-1	0.122804772	0.242489117	0	0
1572	ENSRNOG00000012166	Adal	adenosine deaminase-like	4	0.031998828	-0.612995159	1	-1	0.378890904	0.14022458	0	0
1573	ENSRNOG00000038275	Adam4	a disintegrin and metalloprotease domain 4	4	0.018967933	-0.793522458	1	-1	0.268087304	0.251560318	0	0
1574	ENSRNOG00000032860	Adgrl2	adhesion G protein-coupled receptor L2	4	0.030530446	-0.717640783	1	-1	0.474788428	-0.012085673	0	0
1575	ENSRNOG00000033940	Adgrl4	adhesion G protein-coupled receptor L4	4	0.029448176	-1.250436873	1	-1	0.055254051	0.627851474	0	0
1576	ENSRNOG00000012325	Adk	adenosine kinase	4	0.046264671	-0.819051811	1	-1	0.150481415	0.254138992	0	0
1577	ENSRNOG00000013887	Adra2b	adrenoceptor alpha 2B	4	0.007945797	-0.830651405	1	-1	0.247746224	-0.177573571	0	0
1578	ENSRNOG00000023753	Afdn	afadin, adherens junction formation factor	4	9.60E-05	-0.874547344	1	-1	0.003147507	0.472641491	0	0
1579	ENSRNOG00000017965	Afg3l2	AFG3 like matrix AAA peptidase subunit 2	4	0.007242259	-0.707039548	1	-1	0.459371492	-0.011964367	0	0
1580	ENSRNOG00000010397	Agl3	ATP/GTP binding protein-like 3	4	0.040513068	-0.600221096	1	-1	0.145733329	0.409698988	0	0
1581	ENSRNOG00000016214	Agl	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	4	0.000980898	-1.132300948	1	-1	0.008655886	0.523531349	0	0
1582	ENSRNOG00000020205	Agrn	agrin	4	0.044354872	-0.68367441	1	-1	0.206328667	0.239771371	0	0
1583	ENSRNOG00000018651	Agtbp1	ATP/GTP binding protein 1	4	0.004536377	-1.199528479	1	-1	0.005417833	0.529741577	0	0
1584	ENSRNOG00000008067	Aifm1	apoptosis inducing factor, mitochondria associated 1	4	0.010856493	-0.869036066	1	-1	0.054029239	0.396454485	0	0
1585	ENSRNOG00000045738	Ak4	adenylate kinase 4	4	0.04449169	-0.704267372	1	-1	0.050698228	0.380506971	0	0
1586	ENSRNOG00000004841	Akap6	A-kinase anchoring protein 6	4	0.003830922	-1.0961508	1	-1	0.07332315	0.306328675	0	0
1587	ENSRNOG00000013202	Akap7	A-kinase anchoring protein 7	4	6.95E-05	-0.933741999	1	-1	0.007682505	0.236117638	0	0
1588	ENSRNOG00000026319	Akap9	A-kinase anchoring protein 9	4	0.039085858	-0.814817285	1	-1	0.221454885	0.214961316	0	0
1589	ENSRNOG00000008288	Akirin2	akirin 2	4	0.036641473	-0.712613528	1	-1	0.088278533	0.228997012	0	0
1590	ENSRNOG00000011076	Ank2	ankyrin 2	4	0.02213668	-1.109710378	1	-1	0.176899731	0.258325114	0	0
1591	ENSRNOG000000053288	Ank3	ankyrin 3	4	0.019999882	-0.659644756	1	-1	0.233143232	-0.351935293	0	0
1592	ENSRNOG00000005623	Ankmy2	ankyrin repeat and MYND domain containing 2	4	0.030302738	-0.805617868	1	-1	0.068862492	0.372235499	0	0
1593	ENSRNOG00000012733	Ankrd12	ankyrin repeat domain 12	4	0.024300945	-1.099305531	1	-1	0.068274947	0.567435213	0	0
1594	ENSRNOG00000011340	Ankrd13c	ankyrin repeat domain 13C	4	0.007316737	-0.720926825	1	-1	0.250117302	0.23416859	0	0
1595	ENSRNOG00000006841	Ano4	anoctamin 4	4	0.012194469	-2.263662232	1	-1	0.102061582	-0.36320889	0	0
1596	ENSRNOG00000049873	Ap1s3	adaptor related protein complex 1 sigma 3 subunit	4	0.027434246	-0.839639709	1	-1	0.086180332	0.663275815	0	0
1597	ENSRNOG00000020423	Apc	APC, WNT signaling pathway regulator	4	0.0458523	-0.697374414	1	-1	0.182513551	0.241509467	0	0
1598	ENSRNOG00000003984	Apln	apelin	4	0.009808427	-2.205582813	1	-1	0.145058272	0.540166336	0	0
1599	ENSRNOG000000046918	Apoo	apolipoprotein O	4	0.016767395	-1.330918825	1	-1	0.050221916	1.017101729	0	0
1600	ENSRNOG000000004512	Apool	apolipoprotein O-like	4	0.004827805	-0.977048787	1	-1	0.072699262	0.794941542	0	0
1601	ENSRNOG00000011648	Aqp1	aquaporin 1	4	0.039834908	-0.786892854	1	-1	0.073729605	0.59954225	0	0
1602	ENSRNOG000000056826	Arap2	ArfGAP with RhoGAP domain, ankyrin repeat and PH do	4	0.02893566	-1.405775101	1	-1	0.103825943	0.498797557	0	0
1603	ENSRNOG00000024142	Arglu1	arginine and glutamate rich 1	4	0.01161382	-0.914442452	1	-1	0.350472036	0.105889968	0	0
1604	ENSRNOG00000017791	Arhgap12	Rho GTPase activating protein 12	4	0.049462244	-0.589792918	1	-1	0.102632439	0.660169793	0	0
1605	ENSRNOG00000008659	Arhgap21	Rho GTPase activating protein 21	4	0.019218399	-0.864890507	1	-1	0.401516102	0.050830596	0	0
1606	ENSRNOG00000004696	Arhgap5	Rho GTPase activating protein 5	4	0.021905248	-1.34499537	1	-1	0.087550859	0.854035322	0	0
1607	ENSRNOG00000049751	Anid4b	AT-rich interaction domain 4B	4	0.048181643	-0.830975715	1	-1	0.094605475	0.585433879	0	0
1608	ENSRNOG00000009887	Arih1	ariadne RBR E3 ubiquitin protein ligase 1	4	0.02802455	-0.748822208	1	-1	0.150886766	0.356395973	0	0
1609	ENSRNOG000000055880	Ari8b	ADP-ribosylation factor like GTPase 8B	4	0.02188594	-0.738634389	1	-1	0.224450038	0.212001301	0	0
1610	ENSRNOG00000014521	Armcd8	armadillo repeat containing 8	4	0.009767326	-0.853468707	1	-1	0.037937522	0.407268367	0	0
1611	ENSRNOG00000019489	Armt1	acidic residue methyltransferase 1	4	0.002320116	-0.687244291	1	-1	0.078357424	0.298435746	0	0
1612	ENSRNOG00000014317	Arpc5l	actin related protein 2/3 complex, subunit 5-like	4	0.036367561	-0.661115612	1	-1	0.123663471	0.2159738	0	0
1613	ENSRNOG00000026937	Arsk	arylsulfatase family, member K	4	0.001316737	-0.654212929	1	-1	0.111389354	0.697373426	0	0
1614	ENSRNOG00000012196	Asah2	N-acylsphingosine amidohydrolase 2	4	0.008205503	-0.900171227	1	-1	0.489559058	-0.006238851	0	0
1615	ENSRNOG000000061519	Asap2	ArfGAP with SH3 domain, ankyrin repeat and PH domain	4	0.007230536	-0.601986096	1	-1	0.270596097	0.172974323	0	0

1616	ENSRNOG000000006365	Asb15	ankyrin repeat and SOCS box containing 15	4	0.003826633	-1.026193407	1	-1	0.103232536	0.238872193	0	0
1617	ENSRNOG0000000032471	Asb3	ankyrin repeat and SOCS box-containing 3	4	0.005323771	-1.118721751	1	-1	0.071723329	0.740956942	0	0
1618	ENSRNOG000000000415	Asf1a	anti-silencing function 1A histone chaperone	4	0.013423212	-0.600384552	1	-1	0.189979243	0.274718354	0	0
1619	ENSRNOG0000000020386	Asf1	ASH1 like histone lysine methyltransferase	4	0.025233294	-0.97096141	1	-1	0.056916971	0.483008596	0	0
1620	ENSRNOG0000000020202	Asrg1	asparaginase like 1	4	0.049192745	-0.662868915	1	-1	0.23898338	0.133544779	0	0
1621	ENSRNOG0000000010861	Atad1	ATPase family, AAA domain containing 1	4	0.001027102	-0.715182633	1	-1	0.098763671	0.487465276	0	0
1622	ENSRNOG0000000016342	Atg10	autophagy related 10	4	0.008986691	-0.836118604	1	-1	0.06611875	0.516902075	0	0
1623	ENSRNOG000000000157	Atg12	autophagy related 12	4	0.004437763	-0.688357992	1	-1	0.146488104	0.414665948	0	0
1624	ENSRNOG0000000052116	Atp11b	ATPase phospholipid transporting 11B (putative)	4	0.03063568	-0.87128443	1	-1	0.069446728	0.538618009	0	0
1625	ENSRNOG0000000007290	Atp1a2	ATPase Na+/K+ transporting subunit alpha 2	4	0.023294256	-1.211644977	1	-1	0.44787594	-0.045406493	0	0
1626	ENSRNOG0000000001285	Atp2a2	ATPase sarcolemmal/endoplasmic reticulum Ca2+ trans	4	0.024792221	-0.955240276	1	-1	0.11271795	0.316569601	0	0
1627	ENSRNOG0000000046299	Atp5f1	ATP synthase, H+ transporting, mitochondrial Fo comple	4	0.01138818	-1.009778575	1	-1	0.111853045	0.3656212	0	0
1628	ENSRNOG0000000001596	Atp5g3	ATP synthase, H+ transporting, mitochondrial Fo comple	4	0.030129784	-1.046789562	1	-1	0.048097924	0.584430811	0	0
1629	ENSRNOG0000000003626	Atp5h	ATP synthase, H+ transporting, mitochondrial Fo comple	4	0.019814909	-0.793338406	1	-1	0.02112875	0.555969998	0	0
1630	ENSRNOG0000000010169	Atpaf1	ATP synthase mitochondrial F1 complex assembly facto	4	0.000383974	-1.365841256	1	-1	0.028142197	0.49569786	0	0
1631	ENSRNOG0000000056703	Atrx	ATRX, chromatin remodeler	4	0.045159506	-0.909608848	1	-1	0.105893056	0.55858682	0	0
1632	ENSRNOG0000000005333	Azin1	antizyme inhibitor 1	4	0.02256672	-0.68618186	1	-1	0.239835046	0.248585572	0	0
1633	ENSRNOG0000000016855	B3galnt2	beta-1,3-N-acetyl/galactosaminyltransferase 2	4	0.03024219	-0.699081283	1	-1	0.047725053	0.309897679	0	0
1634	ENSRNOG0000000004697	Baalc	BAALC, MAP3K1 and KLF4 binding	4	0.009919316	-0.626518979	1	-1	0.208420592	0.366302035	0	0
1635	ENSRNOG0000000056984	Baz2b	bromodomain adjacent to zinc finger domain, 2B	4	0.038265637	-0.785947509	1	-1	0.235278119	0.132631578	0	0
1636	ENSRNOG0000000007884	Bcap29	B-cell receptor-associated protein 29	4	0.023686366	-0.767800472	1	-1	0.085217571	0.605087302	0	0
1637	ENSRNOG0000000009826	Bche	butyrylcholinesterase	4	0.003202952	-1.359954622	1	-1	0.03966223	0.556794423	0	0
1638	ENSRNOG0000000037149	Bcl2l15	BCL2-like 15	4	0.039464175	-1.23912525	1	-1	0.198252396	-0.251458003	0	0
1639	ENSRNOG0000000059566	Bcl6b	B-cell CLL/lymphoma 6B	4	0.02006634	-1.619090995	1	-1	0.028562513	-0.319908743	0	0
1640	ENSRNOG0000000048961	Bhlhe41	basic helix-loop-helix family, member e41	4	0.010391697	-0.967082608	1	-1	0.229295566	-0.243168887	0	0
1641	ENSRNOG0000000037160	Bloc1s6	biogenesis of lysosomal organelles complex 1 subunit 6	4	0.006299428	-0.607727814	1	-1	0.074749603	0.40319659	0	0
1642	ENSRNOG0000000016585	Bmi1	BMI1 proto-oncogene, polycomb ring finger	4	0.028796221	-0.814436595	1	-1	0.173915937	0.256318792	0	0
1643	ENSRNOG0000000009820	Bnip3l	BCL2 interacting protein 3 like	4	0.014085925	-0.616647112	1	-1	0.104452727	0.546993	0	0
1644	ENSRNOG0000000010957	Braf	B-Raf proto-oncogene, serine/threonine kinase	4	0.040234742	-0.812595994	1	-1	0.140065099	0.21711393	0	0
1645	ENSRNOG0000000052963	Brox	BRO1 domain and CAAX motif containing	4	0.017518102	-0.607364529	1	-1	0.224094131	0.207409411	0	0
1646	ENSRNOG000000001632	Brwd1	bromodomain and WD repeat domain containing 1	4	0.022140128	-0.82658467	1	-1	0.422620785	0.03829404	0	0
1647	ENSRNOG0000000019529	Btdb1	BTB domain containing 1	4	0.002975381	-1.136883105	1	-1	0.032972416	0.508120026	0	0
1648	ENSRNOG0000000014341	Btdb10	BTB domain containing 10	4	0.011692849	-0.607187623	1	-1	0.088642438	0.229712729	0	0
1649	ENSRNOG0000000018378	Caonb2	calcium voltage-gated channel auxiliary subunit beta 2	4	0.010779257	-0.707110106	1	-1	0.088873802	0.146469176	0	0
1650	ENSRNOG0000000057852	Caong6	calcium voltage-gated channel auxiliary subunit gamma	4	0.00635501	-1.252774325	1	-1	0.485502172	-0.046223017	0	0
1651	ENSRNOG0000000011589	Camk2d	calcium/calmodulin-dependent protein kinase II delta	4	0.000189504	-0.92494968	1	-1	0.035071099	0.321607929	0	0
1652	ENSRNOG0000000008741	Camsap2	calmodulin regulated spectrin-associated protein family,	4	0.029078884	-0.603480711	1	-1	0.144325978	0.333604342	0	0
1653	ENSRNOG0000000018602	Camta1	calmodulin binding transcription activator 1	4	0.004818978	-0.601391316	1	-1	0.097105579	0.169326858	0	0
1654	ENSRNOG0000000019273	Capn7	calpain 7	4	0.031975726	-0.692862127	1	-1	0.13738087	0.414546917	0	0
1655	ENSRNOG0000000056207	Capza2	capping actin protein of muscle Z-line alpha subunit 2	4	0.017280188	-0.782923994	1	-1	0.081954141	0.653057972	0	0
1656	ENSRNOG0000000056216	Casp7	caspase 7	4	0.045440177	-0.602323571	1	-1	0.110742845	0.212519048	0	0
1657	ENSRNOG0000000016243	Casq2	calsequestrin 2	4	0.037152748	-0.734400903	1	-1	0.149391973	0.184206061	0	0
1658	ENSRNOG0000000008364	Cat	catalase	4	0.02898338	-0.801594403	1	-1	0.046422109	0.45296411	0	0
1659	ENSRNOG0000000056836	Cav1	caveolin 1	4	0.011990759	-1.39835261	1	-1	0.050772429	0.672843424	0	0
1660	ENSRNOG0000000057713	Cav2	caveolin 2	4	0.028589615	-1.511580875	1	-1	0.052189575	0.961150303	0	0

1661	ENSRNOG00000019778	Cavin1	caveolae associated protein 1	4	0.047657541	-0.647822614	1	-1	0.09684077	0.341516464	0	0
1662	ENSRNOG00000008027	Cavin4	caveolae associated protein 4	4	0.018324118	-1.062866192	1	-1	0.434946831	0.027032068	0	0
1663	ENSRNOG00000024411	Cbr4	carbonyl reductase 4	4	0.005467899	-0.780950704	1	-1	0.085456727	0.415181518	0	0
1664	ENSRNOG000000059715	Co2d2a	coiled-coil and C2 domain containing 2A	4	0.007849528	-0.936615895	1	-1	0.014963727	0.233600272	0	0
1665	ENSRNOG00000009322	Codo126	coiled-coil domain containing 126	4	0.015013861	-0.747981206	1	-1	0.205642921	0.316747334	0	0
1666	ENSRNOG000000012580	Codo141	coiled-coil domain containing 141	4	0.003569133	-0.856800159	1	-1	0.021800152	0.492488462	0	0
1667	ENSRNOG000000010906	Col5	C-C motif chemokine ligand 5	4	0.028669747	-1.44640074	1	-1	0.080780705	0.730771349	0	0
1668	ENSRNOG000000017113	Cont2	cyclin T2	4	0.015850631	-0.787891609	1	-1	0.130144197	-0.158587801	0	0
1669	ENSRNOG000000053428	Copg1	cell cycle progression 1	4	0.02140942	-0.810675727	1	-1	0.040077581	0.409053638	0	0
1670	ENSRNOG000000025332	Cd109	CD109 molecule	4	0.013401145	-1.845577675	1	-1	0.119885389	-0.319746913	0	0
1671	ENSRNOG000000015821	Cd2	Cd2 molecule	4	0.045043514	-0.940383546	1	-1	0.065486587	0.21667634	0	0
1672	ENSRNOG000000000321	Cd24	CD24 molecule	4	0.027112199	-1.112861522	1	-1	0.109394593	1.328554171	0	0
1673	ENSRNOG000000010283	Cd28	CD28 molecule	4	0.038431005	-0.906842641	1	-1	0.205305565	0.296051073	0	0
1674	ENSRNOG000000023030	Cd96	CD96 molecule	4	0.006758568	-1.118718053	1	-1	0.127624991	0.398799546	0	0
1675	ENSRNOG000000010967	Cdc37i1	cell division cycle 37-like 1	4	0.00221833	-0.820964008	1	-1	0.037891387	0.545903175	0	0
1676	ENSRNOG000000032138	Cdc42ep3	CDC42 effector protein 3	4	0.030434591	-0.591892003	1	-1	0.353833749	0.07260128	0	0
1677	ENSRNOG000000013324	Cdh5	cadherin 5	4	0.025877864	-1.173744826	1	-1	0.168139715	0.438145455	0	0
1678	ENSRNOG000000000583	Cdk19	cyclin-dependent kinase 19	4	0.040163989	-0.803918358	1	-1	0.078788911	0.327559695	0	0
1679	ENSRNOG000000003742	Cdk15	cyclin-dependent kinase-like 5	4	0.032840356	-1.424439822	1	-1	0.105038273	0.675930257	0	0
1680	ENSRNOG000000007249	Cdkn1b	cyclin-dependent kinase inhibitor 1B	4	0.025801545	-0.89983624	1	-1	0.036056548	0.451574318	0	0
1681	ENSRNOG000000021265	Cds2	CDP-diacylglycerol synthase 2	4	0.006668919	-1.002552304	1	-1	0.172056686	0.332123858	0	0
1682	ENSRNOG000000024924	Cep19	centrosomal protein 19	4	0.014173229	-0.642294519	1	-1	0.019779463	0.422355788	0	0
1683	ENSRNOG000000007859	Cep83	centrosomal protein 83	4	0.004093097	-1.155565913	1	-1	0.080141783	0.630395909	0	0
1684	ENSRNOG00000001072	Cers4	ceramide synthase 4	4	0.017424453	-0.691139557	1	-1	0.063900697	0.287634058	0	0
1685	ENSRNOG000000059593	Cetn2	centrin 2	4	0.003857251	-0.790975028	1	-1	0.096172809	0.67067717	0	0
1686	ENSRNOG000000003901	Cfap36	cilia and flagella associated protein 36	4	0.019744845	-0.810254525	1	-1	0.129948073	0.513590134	0	0
1687	ENSRNOG000000032192	Cfap97	cilia and flagella associated protein 97	4	0.045271085	-0.720085084	1	-1	0.13403979	0.535224719	0	0
1688	ENSRNOG000000045892	Cfil2	cofilin 2	4	0.001600579	-0.592194809	1	-1	0.079952693	0.440698845	0	0
1689	ENSRNOG0000000051180	Chohd2	coiled-coil-helix-coiled-coil-helix domain containing 2	4	0.035728915	-0.982580698	1	-1	0.038953107	0.401986956	0	0
1690	ENSRNOG000000040257	Chmp2b	charged multivesicular body protein 2B	4	0.024337494	-0.79273832	1	-1	0.07549638	0.488359969	0	0
1691	ENSRNOG000000017939	Chn1	chimerin 1	4	0.014313358	-1.147375918	1	-1	0.03936494	0.401676691	0	0
1692	ENSRNOG000000004258	Chst7	carbohydrate sulfotransferase 7	4	0.029354665	-1.08028782	1	-1	0.084240397	0.362021856	0	0
1693	ENSRNOG000000012760	Chtop	chromatin target of PRMT1	4	0.00122895	-0.635813628	1	-1	0.19990973	0.210597845	0	0
1694	ENSRNOG000000018719	Cir1	corepressor interacting with RBPJ, 1	4	0.009516033	-0.729066339	1	-1	0.12823357	0.464310591	0	0
1695	ENSRNOG000000056940	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich ca	4	0.000704917	-1.177529987	1	-1	0.004215089	0.575539742	0	0
1696	ENSRNOG000000003533	Clon4	chloride voltage-gated channel 4	4	0.008382043	-1.155130818	1	-1	0.004238328	0.316206641	0	0
1697	ENSRNOG0000000047218	Clic5	chloride intracellular channel 5	4	0.011880423	-0.705155107	1	-1	0.158243087	0.16817908	0	0
1698	ENSRNOG0000000008806	Clip4	CAP-GLY domain containing linker protein family, memb	4	0.011595476	-1.101146084	1	-1	0.184858079	0.373986343	0	0
1699	ENSRNOG000000025768	Clk1	CDC-like kinase 1	4	0.041505689	-0.706386077	1	-1	0.121239363	0.70815198	0	0
1700	ENSRNOG000000003714	Clk4	CDC-like kinase 4	4	0.036948624	-0.727930809	1	-1	0.1751453	0.468507822	0	0
1701	ENSRNOG000000030225	Clpx	caseinolytic mitochondrial matrix peptidase chaperone s	4	0.005229432	-1.047445889	1	-1	0.043028138	0.475637422	0	0
1702	ENSRNOG000000011201	Cmlt8	CKLF-like MARVEL transmembrane domain containing 8	4	0.016144956	-1.049042498	1	-1	0.407947728	0.102522419	0	0
1703	ENSRNOG000000010239	Cnbp	CCHC-type zinc finger, nucleic acid binding protein	4	0.028360527	-0.589167429	1	-1	0.114187782	0.396137248	0	0
1704	ENSRNOG000000001171	Coq5	coenzyme Q5, methyltransferase	4	0.04188278	-0.741701043	1	-1	0.137843183	0.184561338	0	0
1705	ENSRNOG000000017230	Cox15	COX15 cytochrome c oxidase assembly homolog	4	0.046161782	-0.694153947	1	-1	0.121777464	0.261574952	0	0

1706	ENSRNOG00000004553	Cox20	COX20 cytochrome C oxidase assembly factor	4	0.03088575	-0.88542872	1	-1	0.0544519	0.752349634	0	0
1707	ENSRNOG000000018818	Cox5a	cytochrome c oxidase subunit 5A	4	0.008648576	-1.128815217	1	-1	0.025515828	0.443113558	0	0
1708	ENSRNOG00000001181	Cpa3	carboxypeptidase A3	4	0.03212937	-0.824051819	1	-1	0.11336232	0.789729332	0	0
1709	ENSRNOG000000020689	Cpeb3	cytoplasmic polyadenylation element binding protein 3	4	0.049031515	-0.914978402	1	-1	0.498849472	0.0024182	0	0
1710	ENSRNOG000000020688	Cpsf7	cleavage and polyadenylation specific factor 7	4	0.047594924	-0.84722995	1	-1	0.253081443	-0.124612556	0	0
1711	ENSRNOG000000017108	Csnk1a1	casein kinase 1, alpha 1	4	0.01814468	-0.611780234	1	-1	0.180846838	0.337835334	0	0
1712	ENSRNOG000000005276	Csnk2a1	casein kinase 2 alpha 1	4	0.001143094	-0.646830131	1	-1	0.000264602	0.520859886	0	0
1713	ENSRNOG000000050289	Cstf2t	cleavage stimulation factor subunit 2, tau variant	4	0.027759603	-0.862338428	1	-1	0.051343425	0.360188824	0	0
1714	ENSRNOG000000018962	Ctf1	cardiotrophin 1	4	0.027937522	-0.802147531	1	-1	0.267181574	0.151570501	0	0
1715	ENSRNOG000000061845	Cttnbp2	cortactin binding protein 2	4	0.044210468	-1.216821438	1	-1	0.102776222	0.615562043	0	0
1716	ENSRNOG000000015633	Cul3	cullin 3	4	0.000822164	-0.981306943	1	-1	0.127311703	0.383277604	0	0
1717	ENSRNOG000000008039	Cul5	cullin 5	4	0.031062885	-1.195751439	1	-1	0.091776567	0.790079484	0	0
1718	ENSRNOG000000017298	CutC	CutC copper transporter	4	0.026282739	-0.866315938	1	-1	0.044095718	0.499673917	0	0
1719	ENSRNOG000000024372	Cwf19i2	CWF19-like 2, cell cycle control (S. pombe)	4	0.018677195	-0.919146907	1	-1	0.080835046	0.908244619	0	0
1720	ENSRNOG000000001557	Cxadr	CXADR, Ig-like cell adhesion molecule	4	0.04836563	-0.625058712	1	-1	0.284148266	0.071154455	0	0
1721	ENSRNOG000000013589	Cxcl12	C-X-C motif chemokine ligand 12	4	0.026477346	-0.898030615	1	-1	0.494803324	-0.003228629	0	0
1722	ENSRNOG000000045784	Cxxc4	CXXC finger protein 4	4	0.038863251	-1.217708935	1	-1	0.183848769	0.27883101	0	0
1723	ENSRNOG000000011142	Cyb5b	cytochrome b5 type B	4	0.00904117	-0.97287838	1	-1	0.059574788	0.280028134	0	0
1724	ENSRNOG000000006785	Dcaf8	DDB1 and CUL4 associated factor 8	4	0.004881732	-0.631964237	1	-1	0.330394111	0.095436957	0	0
1725	ENSRNOG000000059605	Ddn	dendrin	4	0.012688508	-2.289358984	1	-1	0.196720088	-0.231138785	0	0
1726	ENSRNOG000000011063	Dennd1b	DENN domain containing 1B	4	0.006651817	-0.921317227	1	-1	0.01979698	0.557843465	0	0
1727	ENSRNOG000000018716	Dennd2c	DENN domain containing 2C	4	0.042748224	-1.133394071	1	-1	0.103790566	0.333831516	0	0
1728	ENSRNOG000000011636	Dennd6a	DENN domain containing 6A	4	0.027470381	-0.928918795	1	-1	0.115492035	0.511007056	0	0
1729	ENSRNOG000000004328	Deptor	DEP domain containing MTOR-interacting protein	4	0.021736708	-0.821837846	1	-1	0.065487415	0.346212399	0	0
1730	ENSRNOG000000002338	Dgke	diacylglycerol kinase epsilon	4	0.012456106	-1.405057979	1	-1	0.231760154	0.275803728	0	0
1731	ENSRNOG000000011617	Dguok	deoxyguanosine kinase	4	0.04924488	-0.786432924	1	-1	0.052836494	0.453256704	0	0
1732	ENSRNOG000000015288	Dip2c	disco-interacting protein 2 homolog C	4	0.006501207	-1.079620812	1	-1	0.116522585	0.38401017	0	0
1733	ENSRNOG000000009994	Dlat	dihydrolipoamide S-acetyltransferase	4	0.013256465	-1.167234778	1	-1	0.083251224	0.232088831	0	0
1734	ENSRNOG000000006364	Dld	dihydrolipoamide dehydrogenase	4	0.01120571	-1.293513979	1	-1	0.051757327	0.801002876	0	0
1735	ENSRNOG000000046366	Dmd	dystrophin	4	0.005548307	-1.307877649	1	-1	0.034236811	0.484988767	0	0
1736	ENSRNOG000000024093	Dmrt1	DMRT-like family A1	4	0.044754982	-1.534703532	1	-1	0.340006896	0.050536879	0	0
1737	ENSRNOG000000024671	Dmxd1	Dmx-like 1	4	0.028108882	-1.150712717	1	-1	0.086864078	0.742365014	0	0
1738	ENSRNOG000000048363	Dnah5	dynein, axonemal, heavy chain 5	4	0.032244121	-1.494044625	1	-1	0.483309082	0.010804422	0	0
1739	ENSRNOG000000016251	Dnaj2	DnaJ heat shock protein family (Hsp40) member A2	4	0.002329081	-0.608901538	1	-1	0.082201986	0.236655997	0	0
1740	ENSRNOG000000013011	Dnajb4	DnaJ heat shock protein family (Hsp40) member B4	4	0.003717813	-1.144928794	1	-1	0.04634239	0.56774085	0	0
1741	ENSRNOG000000004006	Dnajb9	DnaJ heat shock protein family (Hsp40) member B9	4	0.036718433	-0.981094124	1	-1	0.174201296	0.357332207	0	0
1742	ENSRNOG000000049819	Dnajc19	DnaJ heat shock protein family (Hsp40) member C19	4	0.000942418	-0.699625325	1	-1	0.098024343	0.594226157	0	0
1743	ENSRNOG000000017876	Dnajc21	DnaJ heat shock protein family (Hsp40) member C21	4	0.003173436	-0.977093931	1	-1	0.046851321	0.378070481	0	0
1744	ENSRNOG000000003988	Dnajc27	DnaJ heat shock protein family (Hsp40) member C27	4	0.0428056	-0.902892011	1	-1	0.016888077	0.438907435	0	0
1745	ENSRNOG0000000031721	Dnajc30	DnaJ heat shock protein family (Hsp40) member C30	4	0.029493966	-0.982778245	1	-1	0.099149507	0.214310641	0	0
1746	ENSRNOG000000042333	Dnal1	dynein, axonemal, light chain 1	4	0.015944969	-0.817026115	1	-1	0.081338886	0.70359973	0	0
1747	ENSRNOG000000001813	Dnm1l	dynamitin 1-like	4	0.0253968	-0.40803543	1	-1	0.107297635	0.503345845	0	0
1748	ENSRNOG000000011969	Dock9	dedicator of cytokinesis 9	4	0.022431556	-0.830798505	1	-1	0.058748086	0.570080492	0	0
1749	ENSRNOG000000022847	Dopey1	dopey family member 1	4	0.032264809	-0.602557733	1	-1	0.1319038	0.312130589	0	0
1750	ENSRNOG000000010993	Dpm1	dolichyl-phosphate mannosyltransferase subunit 1, cata	4	0.018640508	-0.78177581	1	-1	0.087066203	0.744722485	0	0

1751	ENSRNOG00000030783	Dpp4	dipeptidylpeptidase 4	4	0.029400889	-1.465848233	1	-1	0.185108199	0.725945487	0	0
1752	ENSRNOG00000039969	Dsc2	desmocollin 2	4	0.046638163	-1.030202348	1	-1	0.199944073	0.19972015	0	0
1753	ENSRNOG00000016526	Dsg2	desmoglein 2	4	0.024757603	-0.743469887	1	-1	0.04478036	0.411297397	0	0
1754	ENSRNOG00000013928	Dsp	desmoplakin	4	0.000334322	-0.889531916	1	-1	0.218537687	0.210273661	0	0
1755	ENSRNOG00000008921	Dynl12	dynein light chain LC8-type 2	4	0.035262258	-1.070922108	1	-1	0.158954969	0.334886212	0	0
1756	ENSRNOG00000003611	Dynl13	dynein light chain LC8-type 3	4	0.01171933	-0.852997312	1	-1	0.078612165	0.735583552	0	0
1757	ENSRNOG00000001862	Dyrk1a	dual specificity tyrosine phosphorylation regulated kinase	4	0.026443142	-0.686037088	1	-1	0.194078753	0.1228014	0	0
1758	ENSRNOG000000004509	Eapp	E2F-associated phosphoprotein	4	0.016910896	-0.652879559	1	-1	0.083264878	0.573160569	0	0
1759	ENSRNOG00000016102	Ebf3	early B-cell factor 3	4	0.012118475	-0.894379595	1	-1	0.086619957	0.147498354	0	0
1760	ENSRNOG000000029549	Eci2	enoyl-CoA delta isomerase 2	4	0.017083374	-0.601473647	1	-1	0.015941176	0.516152237	0	0
1761	ENSRNOG000000039593	Ecsr	endothelial cell surface expressed chemotaxis and apoptosis	4	0.003681677	-0.815287772	1	-1	0.009791876	0.524817501	0	0
1762	ENSRNOG000000017728	Edrf1	erythroid differentiation regulatory factor 1	4	0.048085098	-0.599478018	1	-1	0.369447348	0.058534289	0	0
1763	ENSRNOG000000008917	Ehbp1	EH domain binding protein 1	4	0.007365975	-0.623617595	1	-1	0.134230536	0.249404493	0	0
1764	ENSRNOG000000008452	Eid1	EP300 interacting inhibitor of differentiation 1	4	0.042875678	-0.683781795	1	-1	0.199459072	0.308433419	0	0
1765	ENSRNOG000000033765	Eif1	eukaryotic translation initiation factor 1	4	0.018976898	-1.129828837	1	-1	0.059533549	0.601340804	0	0
1766	ENSRNOG000000010301	Eif4e3	eukaryotic translation initiation factor 4E family member	4	0.00721564	-0.752562735	1	-1	0.02792704	0.537357413	0	0
1767	ENSRNOG000000023356	Eif5b	eukaryotic translation initiation factor 5B	4	0.028872216	-0.692341048	1	-1	0.165047031	0.30162885	0	0
1768	ENSRNOG000000000113	Elac1	elaC ribonuclease Z 1	4	0.049658437	-0.79458523	1	-1	0.072493	0.432169905	0	0
1769	ENSRNOG000000010171	Elk1	ELK1, ETS transcription factor	4	0.025437694	-0.944470482	1	-1	0.128065789	0.211867851	0	0
1770	ENSRNOG000000005719	Emo4	ER membrane protein complex subunit 4	4	0.001363078	-0.701921789	1	-1	0.042463761	0.381909892	0	0
1771	ENSRNOG000000021318	Epas1	endothelial PAS domain protein 1	4	0.041658093	-0.99186529	1	-1	0.382203641	0.122379257	0	0
1772	ENSRNOG000000028050	Epb4114a	erythrocyte membrane protein band 4.1 like 4A	4	0.010870699	-1.006160366	1	-1	0.001731053	0.489209776	0	0
1773	ENSRNOG000000002538	Epb4115	erythrocyte membrane protein band 4.1 like 5	4	0.012935384	-0.790017577	1	-1	0.111382456	0.535830356	0	0
1774	ENSRNOG000000029447	Epc2	enhancer of polycomb homolog 2	4	0.044853734	-0.976874406	1	-1	0.052154127	0.628057263	0	0
1775	ENSRNOG000000006141	Epdrl	ependymin related 1	4	0.003147783	-1.033802268	1	-1	0.019639473	0.350672088	0	0
1776	ENSRNOG000000017286	Ephx2	epoxide hydrolase 2	4	0.004603269	-1.797116287	1	-1	0.098470174	0.598323678	0	0
1777	ENSRNOG000000043006	Epm2aip1	EPH2A interacting protein 1	4	0.004197366	-1.094432216	1	-1	0.085548238	0.465754666	0	0
1778	ENSRNOG000000014248	Erb4	erb-b2 receptor tyrosine kinase 4	4	0.040313771	-1.561703043	1	-1	0.157174264	0.512892261	0	0
1779	ENSRNOG000000022812	Eroc5	ERCC excision repair 5, endonuclease	4	0.006307703	-0.820265127	1	-1	0.053625405	0.466795755	0	0
1780	ENSRNOG000000019175	Eroc8l2	ERCC excision repair 8 like 2	4	0.047394249	-0.584315543	1	-1	0.099270257	0.54973073	0	0
1781	ENSRNOG000000007283	Erlec1	endoplasmic reticulum lectin 1	4	0.013460895	-0.89939045	1	-1	0.133619612	0.643439935	0	0
1782	ENSRNOG00000002609	Ero1b	endoplasmic reticulum oxidoreductase 1 beta	4	0.008674298	-0.824442487	1	-1	0.08567554	0.72781755	0	0
1783	ENSRNOG000000010797	Esm1	endothelial cell-specific molecule 1	4	0.041675195	-1.978318969	1	-1	0.191715606	0.42343049	0	0
1784	ENSRNOG000000019358	Esr1	estrogen receptor 1	4	0.041154265	-1.08890068	1	-1	0.123311772	0.230463388	0	0
1785	ENSRNOG000000002593	Esrrg	estrogen-related receptor gamma	4	0.002863127	-1.066251156	1	-1	0.119475209	0.165546895	0	0
1786	ENSRNOG000000015233	Etfa	electron transfer flavoprotein alpha subunit	4	0.036486725	-0.981853488	1	-1	0.050416454	0.761248379	0	0
1787	ENSRNOG000000008666	Etl4	enhancer trap locus 4	4	0.033083925	-1.25501043	1	-1	0.326742225	0.181212223	0	0
1788	ENSRNOG000000008941	Ets1	ETS proto-oncogene 1, transcription factor	4	0.034744638	-1.244434414	1	-1	0.027915592	0.35898707	0	0
1789	ENSRNOG000000008667	Etv1	ets variant 1	4	0.037411627	-0.735921607	1	-1	0.023278946	0.51229094	0	0
1790	ENSRNOG000000027707	Exd2	exonuclease 3'-5' domain containing 2	4	0.012389077	-0.721130287	1	-1	0.032750845	0.360090971	0	0
1791	ENSRNOG000000038601	Exoc6	exocyst complex component 6	4	0.013309289	-0.746527613	1	-1	0.088354251	0.58020018	0	0
1792	ENSRNOG000000018950	Fa2h	fatty acid 2-hydroxylase	4	0.000595821	-0.922607421	1	-1	0.349863182	0.089818601	0	0
1793	ENSRNOG000000008523	Faf1	Fas associated factor 1	4	0.024194745	-0.85116174	1	-1	0.130675264	0.28312559	0	0
1794	ENSRNOG000000014727	Fahd1	fumarylacetoacetate hydrolase domain containing 1	4	0.027085304	-1.126032898	1	-1	0.052761258	0.646479347	0	0
1795	ENSRNOG000000022086	Fam117b	family with sequence similarity 117, member B	4	0.045904558	-1.251096064	1	-1	0.055663547	0.712788343	0	0

1798	ENSRNOG00000025079	Fam128b	family with sequence similarity 128, member B	4	0.041728502	-1.245093814	1	-1	0.091556375	0.783194218	0	0
1797	ENSRNOG00000013587	Fam135a	family with sequence similarity 135, member A	4	0.028828784	-1.221303814	1	-1	0.098472728	0.530738757	0	0
1798	ENSRNOG00000019087	Fam174a	family with sequence similarity 174, member A	4	0.01888532	-0.823933318	1	-1	0.053568986	0.476303994	0	0
1799	ENSRNOG00000012389	Fam174b	family with sequence similarity 174, member B	4	0.019019792	-0.912002821	1	-1	0.051510172	0.460813898	0	0
1800	ENSRNOG00000016740	Fam210a	family with sequence similarity 210, member A	4	0.003033308	-1.157169293	1	-1	0.016049928	0.501470899	0	0
1801	ENSRNOG00000004466	Fam210b	family with sequence similarity 210, member B	4	0.021185573	-0.888152503	1	-1	0.017801117	0.476827879	0	0
1802	ENSRNOG00000015691	Fam212b	family with sequence similarity 212, member B	4	0.014013516	-1.026168681	1	-1	0.267702021	-0.142504788	0	0
1803	ENSRNOG000000058522	Fam214a	family with sequence similarity 214, member A	4	0.017122957	-0.928158027	1	-1	0.07963837	0.238298805	0	0
1804	ENSRNOG000000053607	Fam217b	family with sequence similarity 217, member B	4	0.04985883	-0.705398842	1	-1	0.16728538	-0.208869502	0	0
1805	ENSRNOG00000001728	Fam43a	family with sequence similarity 43, member A	4	0.028895938	-0.968498424	1	-1	0.048844831	0.488249498	0	0
1806	ENSRNOG000000052758	Fam49a	family with sequence similarity 49, member A	4	0.031883043	-0.863089771	1	-1	0.075979243	0.785632223	0	0
1807	ENSRNOG000000016338	Fam92a	family with sequence similarity 92 member A	4	0.029159388	-0.583941505	1	-1	0.11876443	0.503316888	0	0
1808	ENSRNOG000000024335	Fastkd1	FAST kinase domains 1	4	0.037249017	-0.848954174	1	-1	0.240214882	0.181309943	0	0
1809	ENSRNOG000000027422	Fastkd3	FAST kinase domains 3	4	0.030178128	-0.810890944	1	-1	0.351198469	0.128715148	0	0
1810	ENSRNOG000000011585	Fat3	FAT atypical cadherin 3	4	0.035306255	-0.683077283	1	-1	0.247381629	0.089096281	0	0
1811	ENSRNOG000000028335	Fat4	FAT atypical cadherin 4	4	0.02306434	-1.235863727	1	-1	0.123008344	0.275376848	0	0
1812	ENSRNOG000000013875	Fbx17	F-box and leucine-rich repeat protein 17	4	0.018116882	-0.947399479	1	-1	0.077003793	0.333445879	0	0
1813	ENSRNOG000000059334	Fbx3	F-box and leucine-rich repeat protein 3	4	0.008494587	-0.703157498	1	-1	0.043098062	0.518380952	0	0
1814	ENSRNOG000000016396	Fbxo11	F-box protein 11	4	0.017116337	-0.812825842	1	-1	0.201192194	0.285131164	0	0
1815	ENSRNOG000000002459	Fbxo40	F-box protein 40	4	0.024245087	-0.851210614	1	-1	0.474258327	-0.025998477	0	0
1816	ENSRNOG000000010502	Fbxo8	F-box protein 8	4	0.000780912	-0.811193336	1	-1	0.090910627	0.649322478	0	0
1817	ENSRNOG000000009177	Fcrla	Fc fragment of IgE receptor 1a	4	0.028989175	-0.830415089	1	-1	0.113549824	0.808585205	0	0
1818	ENSRNOG000000021314	Fdft1	farnesyl diphosphate farnesyl transferase 1	4	0.013847873	-0.899770219	1	-1	0.088067719	0.244324983	0	0
1819	ENSRNOG000000003578	Fem1c	fem-1 homolog C	4	0.040778291	-0.757126253	1	-1	0.326880229	0.149321857	0	0
1820	ENSRNOG000000013887	Fgf1	fibroblast growth factor 1	4	0.028980899	-0.749756371	1	-1	0.110168878	0.38114025	0	0
1821	ENSRNOG000000042753	Fgf13	fibroblast growth factor 13	4	0.00823819	-1.154504084	1	-1	0.022724226	0.398483555	0	0
1822	ENSRNOG0000000061530	Fgf16	fibroblast growth factor 16	4	0.039703469	-1.342880064	1	-1	0.033562168	0.521939437	0	0
1823	ENSRNOG000000011471	Fgf9	fibroblast growth factor 9	4	0.044244535	-1.054688309	1	-1	0.096742501	0.277990547	0	0
1824	ENSRNOG000000022796	Fgfbp3	fibroblast growth factor binding protein 3	4	0.019575202	-1.175283575	1	-1	0.294128888	0.238367245	0	0
1825	ENSRNOG00000001811	Fgfr1op2	FGFR1 oncogene partner 2	4	0.017022136	-0.818648938	1	-1	0.141759396	0.284387099	0	0
1826	ENSRNOG000000004829	Fkbp3	FK506 binding protein 3	4	0.011028895	-0.893843149	1	-1	0.077575547	0.701025088	0	0
1827	ENSRNOG000000028129	Fktn	fukutin	4	0.000902007	-0.897581537	1	-1	0.075119302	0.33885528	0	0
1828	ENSRNOG0000000061851	Foxj3	forkhead box J3	4	0.000860508	-0.795342392	1	-1	0.057577202	0.182834428	0	0
1829	ENSRNOG000000004709	Foxn3	forkhead box N3	4	0.017350803	-1.156832303	1	-1	0.038805631	0.525800383	0	0
1830	ENSRNOG000000013397	Foxo1	forkhead box O1	4	0.006116882	-0.722041588	1	-1	0.008420109	0.561642822	0	0
1831	ENSRNOG000000021670	Frem2	Fras1 related extracellular matrix protein 2	4	0.037092752	-1.417844079	1	-1	0.436880988	-0.057811743	0	0
1832	ENSRNOG000000009848	Frg1	FSHD region gene 1	4	0.025792586	-0.815224032	1	-1	0.095261982	0.519390871	0	0
1833	ENSRNOG0000000059878	Fsd1l	fibronectin type III and SPRY domain containing 1-like	4	0.018213365	-1.554745842	1	-1	0.087050617	0.930199478	0	0
1834	ENSRNOG000000006338	Fyco1	FYVE and coiled-coil domain containing 1	4	0.024159575	-0.998857118	1	-1	0.086245589	0.404636179	0	0
1835	ENSRNOG0000000034233	Fyrttd1	forty-two-three domain containing 1	4	0.048768016	-0.774782209	1	-1	0.087492311	0.809353084	0	0
1836	ENSRNOG000000004680	Fzd8	frizzled class receptor 8	4	0.040127184	-0.982536373	1	-1	0.087867113	0.347788522	0	0
1837	ENSRNOG000000005615	Gadd45a	growth arrest and DNA-damage-inducible, alpha	4	0.011704434	-0.803952843	1	-1	0.180855182	-0.189712177	0	0
1838	ENSRNOG000000013409	Gclm	glutamate cysteine ligase, modifier subunit	4	0.038115716	-0.838478445	1	-1	0.052071188	0.39500513	0	0
1839	ENSRNOG0000000023778	Gnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	4	0.03754279	-0.712990591	1	-1	0.189449989	0.74667649	0	0
1840	ENSRNOG000000011535	Gosh	glycine cleavage system protein H	4	0.011117854	-0.785258738	1	-1	0.11809358	0.381123324	0	0

1841	ENSRNOG00000000561	Gdpd1	glycerophosphodiester phosphodiesterase domain contain	4	0.007342528	-1.072084384	1	-1	0.145708988	0.286455882	0	0
1842	ENSRNOG000000004380	Gemin2	gem (nuclear organelle) associated protein 2	4	0.026796773	-0.651561802	1	-1	0.176771464	0.373052884	0	0
1843	ENSRNOG000000012873	Gfm1	G elongation factor, mitochondrial 1	4	0.00226743	-1.024049348	1	-1	0.009324887	0.436868483	0	0
1844	ENSRNOG0000000027880	Ggnbp2	gametogenetin binding protein 2	4	0.015250948	-0.621883721	1	-1	0.168483208	0.313148243	0	0
1845	ENSRNOG000000016787	Ggps1	geranylgeranyl diphosphate synthase 1	4	0.021513689	-0.655671218	1	-1	0.233197159	0.39674402	0	0
1846	ENSRNOG000000003847	Gid4	GID complex subunit 4	4	0.028084408	-0.941323718	1	-1	0.055509758	0.582764771	0	0
1847	ENSRNOG000000033338	Gimap6	GTPase, IMAP family member 6	4	0.032225502	-0.863411384	1	-1	0.125361079	0.357605646	0	0
1848	ENSRNOG0000000024589	Gimap9	GTPase, IMAP family member 9	4	0.041117164	-1.425845635	1	-1	0.080731536	0.949715512	0	0
1849	ENSRNOG000000051563	Giot1	gonadotropin inducible ovarian transcription factor 1	4	0.016207158	-0.763963958	1	-1	0.19857265	0.58027443	0	0
1850	ENSRNOG0000000034116	Gk	glycerol kinase	4	0.025643749	-1.086738473	1	-1	0.131516723	0.381746757	0	0
1851	ENSRNOG000000019272	Gkap1	G kinase anchoring protein 1	4	0.01854079	-0.917014837	1	-1	0.059734915	0.501650326	0	0
1852	ENSRNOG000000019296	Gnat2	G protein subunit alpha transducin 2	4	0.016924764	-1.186483104	1	-1	0.055834632	0.840384701	0	0
1853	ENSRNOG000000002509	Gnl3l	G protein nucleolar 3 like	4	0.018292689	-0.725267566	1	-1	0.051221019	0.41631935	0	0
1854	ENSRNOG000000002177	Gnpda2	glucosamine-6-phosphate deaminase 2	4	0.047724847	-0.912219384	1	-1	0.094793738	0.79239732	0	0
1855	ENSRNOG000000000408	Gopc	golgi associated PDZ and coiled-coil motif containing	4	0.033225433	-0.619324481	1	-1	0.10704579	0.409379079	0	0
1856	ENSRNOG000000015124	Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	4	0.045231088	-0.858781227	1	-1	0.187057306	0.28473892	0	0
1857	ENSRNOG0000000037595	Gppp11l	GC-rich promoter binding protein 1-like 1	4	0.006199435	-0.676111343	1	-1	0.005922626	0.259346354	0	0
1858	ENSRNOG000000033824	Gpd2	glycerol-3-phosphate dehydrogenase 2	4	0.047377008	-0.83838583	1	-1	0.358083374	-0.092134815	0	0
1859	ENSRNOG000000017528	Gpr157	G protein-coupled receptor 157	4	0.025782912	-0.930739231	1	-1	0.258967857	-0.363125294	0	0
1860	ENSRNOG000000016013	Gprc5b	G protein-coupled receptor, class C, group 5, member B	4	0.041289152	-0.813470444	1	-1	0.297747259	0.115964633	0	0
1861	ENSRNOG000000003392	Grsf1	G-rich RNA sequence binding factor 1	4	0.010302738	-1.053541326	1	-1	0.035196883	0.367103165	0	0
1862	ENSRNOG0000000056701	Gtf2a2	general transcription factor IIA, 2	4	0.049058272	-0.791344922	1	-1	0.06139618	0.733016994	0	0
1863	ENSRNOG000000012302	Gucy1a3	guanylate cyclase 1 soluble subunit alpha 3	4	0.021350941	-1.121097329	1	-1	0.123862492	0.487662657	0	0
1864	ENSRNOG000000002207	Guf1	GUF1 homolog, GTPase	4	0.005029998	-1.132591744	1	-1	0.10898807	0.562404058	0	0
1865	ENSRNOG0000000029939	Gypo	glycophorin C (Gerbich blood group)	4	0.02240342	-1.180611188	1	-1	0.064606648	0.414763072	0	0
1866	ENSRNOG000000004735	Gzf1	GDNF-inducible zinc finger protein 1	4	0.015890642	-0.677323541	1	-1	0.05221102	0.396400519	0	0
1867	ENSRNOG0000000043192	Haod1	3-hydroxyacyl-CoA dehydratase 1	4	0.002835942	-0.740758777	1	-1	0.043546445	0.244983748	0	0
1868	ENSRNOG000000018087	Hars2	histidyl-tRNA synthetase 2, mitochondrial	4	0.001397559	-0.898870875	1	-1	0.142644714	0.220240583	0	0
1869	ENSRNOG000000000604	Hdac2	histone deacetylase 2	4	0.035929798	-0.653165802	1	-1	0.419187573	0.041774029	0	0
1870	ENSRNOG0000000060972	Heca	hdc homolog, cell cycle regulator	4	0.027132612	-0.808888292	1	-1	0.051018757	0.615711026	0	0
1871	ENSRNOG000000006905	Hectd1	HECT domain E3 ubiquitin protein ligase 1	4	0.033843459	-0.709478919	1	-1	0.079319702	0.403785847	0	0
1872	ENSRNOG000000007304	Herc3	HECT and RLD domain containing E3 ubiquitin protein ligase	4	0.005313703	-0.917372351	1	-1	0.049025171	0.288098323	0	0
1873	ENSRNOG000000001720	Hes1	hes family bHLH transcription factor 1	4	0.029503758	-1.135618738	1	-1	0.461435142	0.020658184	0	0
1874	ENSRNOG000000008063	Hibadh	3-hydroxyisobutyrate dehydrogenase	4	0.014598186	-1.280380407	1	-1	0.045086822	0.548137096	0	0
1875	ENSRNOG000000019333	Hipk1	homeodomain interacting protein kinase 1	4	0.021680574	-0.867646867	1	-1	0.038804703	0.43762403	0	0
1876	ENSRNOG0000000026226	Hook1	hook microtubule-tethering protein 1	4	0.024606717	-0.992109713	1	-1	0.044126819	0.372702882	0	0
1877	ENSRNOG0000000006065	Hs3st5	heparan sulfate-glucosamine 3-sulfotransferase 5	4	0.003379077	-1.681847249	1	-1	0.128789256	0.83095788	0	0
1878	ENSRNOG0000000018019	Hspa12a	heat shock protein family A (Hsp70) member 12A	4	0.014628577	-1.063057473	1	-1	0.034589615	0.522871958	0	0
1879	ENSRNOG000000019525	Hspa9	heat shock protein family A member 9	4	0.003792842	-1.050455077	1	-1	0.021890786	0.454098813	0	0
1880	ENSRNOG000000014525	Hspd1	heat shock protein family D member 1	4	0.022341494	-1.087286386	1	-1	0.158997379	0.241432804	0	0
1881	ENSRNOG000000010277	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	4	0.023802634	-0.718028479	1	-1	0.134473416	0.149267834	0	0
1882	ENSRNOG000000007800	Igsf1	immunoglobulin superfamily, member 1	4	0.006829736	-1.330938451	1	-1	0.241161437	0.116112607	0	0
1883	ENSRNOG000000003954	Il2rg	interleukin 2 receptor subunit gamma	4	0.041455348	-0.842614629	1	-1	0.297580305	0.075343571	0	0
1884	ENSRNOG0000000020630	Il9r	interleukin 9 receptor	4	0.02105841	-0.918321998	1	-1	0.061757258	0.372686813	0	0
1885	ENSRNOG000000009097	Immt	inner membrane mitochondrial protein	4	0.024736087	-0.661346477	1	-1	0.045922005	0.303920739	0	0

1886	ENSRNOG00000045844	Impact	impact RWD domain protein	4	0.004454451	-0.862336733	1	-1	0.224640714	0.174606552	0	0
1887	ENSRNOG00000014483	Ino80	INO80 complex subunit	4	0.036646024	-0.581129563	1	-1	0.06548107	0.22326213	0	0
1888	ENSRNOG00000016532	Ino80c	INO80 complex subunit C	4	0.006411834	-0.787766979	1	-1	0.01905903	0.356336149	0	0
1889	ENSRNOG00000018382	Inpp4b	inositol polyphosphate-4-phosphatase type II B	4	0.001206537	-1.112199751	1	-1	0.121235501	0.573158756	0	0
1890	ENSRNOG00000029986	Insr	insulin receptor	4	0.027117164	-0.626506557	1	-1	0.297809737	0.099697226	0	0
1891	ENSRNOG00000038868	Iqcb1	IQ motif containing B1	4	0.018210192	-0.903534	1	-1	0.098261706	0.565910438	0	0
1892	ENSRNOG00000014083	Iqsec3	IQ motif and Sec7 domain 3	4	0.028232398	-0.725230097	1	-1	0.000627129	-0.53791357	0	0
1893	ENSRNOG00000021729	Iqub	IQ motif and ubiquitin domain containing	4	0.008752638	-1.493836624	1	-1	0.46889911	-0.016606084	0	0
1894	ENSRNOG00000005082	Irf6	interferon regulatory factor 6	4	0.039052755	-1.401946268	1	-1	0.365667126	0.17990475	0	0
1895	ENSRNOG00000012085	IscA2	iron-sulfur cluster assembly 2	4	0.005626646	-0.687220037	1	-1	0.029685608	0.511011829	0	0
1896	ENSRNOG00000006199	Ispd	isoprenoid synthase domain containing	4	0.034385904	-1.179714015	1	-1	0.123426109	0.400026944	0	0
1897	ENSRNOG00000001518	Itga6	integrin subunit alpha 6	4	0.007205848	-1.207311565	1	-1	0.060613958	0.298068362	0	0
1898	ENSRNOG00000011157	Jak1	Janus kinase 1	4	0.04738487	-0.592388878	1	-1	0.079564651	0.352439852	0	0
1899	ENSRNOG00000006110	Jph1	junctophilin 1	4	0.034703262	-0.962544946	1	-1	0.170516171	0.271074809	0	0
1900	ENSRNOG00000006185	Kansl2	KAT8 regulatory NSL complex subunit 2	4	0.038497897	-0.765957072	1	-1	0.037638852	0.350073596	0	0
1901	ENSRNOG00000022252	Kbtbd3	kelch repeat and BTB domain containing 3	4	0.010717468	-0.995951585	1	-1	0.126273705	0.650251288	0	0
1902	ENSRNOG000000015097	Kcmf1	potassium channel modulatory factor 1	4	0.038153507	-0.778228047	1	-1	0.062906696	0.356451595	0	0
1903	ENSRNOG00000019719	Kcna5	potassium voltage-gated channel subfamily A member 5	4	0.021019102	-1.122125365	1	-1	0.254237432	0.873308193	0	0
1904	ENSRNOG00000014686	Kcnd3	potassium voltage-gated channel subfamily D member 3	4	0.008114889	-1.903021985	1	-1	0.040872561	0.214395111	0	0
1905	ENSRNOG000000050450	Kcnip2	Kv channel-interacting protein 2	4	0.03100931	-1.119710838	1	-1	0.169060065	0.490319543	0	0
1906	ENSRNOG00000005369	Kcnj3	potassium voltage-gated channel subfamily J member 3	4	0.002423833	-1.17827267	1	-1	0.030047583	0.552489726	0	0
1907	ENSRNOG00000002653	Kcnk2	potassium two pore domain channel subfamily K member 2	4	0.021652438	-1.324107977	1	-1	0.391010344	0.05113945	0	0
1908	ENSRNOG00000016675	Kcnn2	potassium calcium-activated channel subfamily N member 2	4	0.003427764	-1.088635932	1	-1	0.090832287	0.074194803	0	0
1909	ENSRNOG00000012951	Kctd9	potassium channel tetramerization domain containing 9	4	0.006774429	-0.726213738	1	-1	0.109678367	0.466934564	0	0
1910	ENSRNOG000000007814	Kdm3a	lysine demethylase 3A	4	0.032643128	-0.78404292	1	-1	0.104784705	0.484985319	0	0
1911	ENSRNOG000000046829	Kdr	kinase insert domain receptor	4	0.015525412	-1.399295407	1	-1	0.314943245	0.081736776	0	0
1912	ENSRNOG00000014844	Kif21a	kinesin family member 21A	4	0.032782705	-0.672128304	1	-1	0.039490656	0.392686922	0	0
1913	ENSRNOG00000005386	Kitlg	KIT ligand	4	0.012950003	-1.778075637	1	-1	0.082189919	0.674843571	0	0
1914	ENSRNOG000000004193	Klhl12	kelch-like family member 12	4	0.0049489	-0.724593807	1	-1	0.077997242	0.175206746	0	0
1915	ENSRNOG000000007981	Klhl23	kelch-like family member 23	4	0.007428039	-0.893712183	1	-1	0.04205572	0.319338948	0	0
1916	ENSRNOG000000006224	Klhl31	kelch-like family member 31	4	0.021939452	-1.231129891	1	-1	0.095829046	0.31722745	0	0
1917	ENSRNOG000000033706	Klk14	kallikrein related-peptidase 14	4	0.046898007	-0.602454115	1	-1	0.138559065	-0.285118678	0	0
1918	ENSRNOG000000007811	Klrb1c	killer cell lectin-like receptor subfamily B member 1C	4	0.046505344	-1.200730043	1	-1	0.083241156	0.555442846	0	0
1919	ENSRNOG000000052467	Klrc2	killer cell lectin-like receptor subfamily C, member 2	4	0.007699607	-1.230532479	1	-1	0.059520999	1.253923075	0	0
1920	ENSRNOG000000021614	Kmt2e	lysine methyltransferase 2E	4	0.000170195	-0.700476787	1	-1	0.050051514	0.32586916	0	0
1921	ENSRNOG00000016790	Kmt5b	lysine methyltransferase 5B	4	0.037425971	-0.692439962	1	-1	0.04800731	0.316615259	0	0
1922	ENSRNOG000000051711	Kpna1	karyopherin subunit alpha 1	4	0.000933315	-0.84487015	1	-1	0.111259361	0.226428083	0	0
1923	ENSRNOG000000030109	Kpna5	karyopherin subunit alpha 5	4	0.019532032	-1.038162876	1	-1	0.19969009	0.354829517	0	0
1924	ENSRNOG000000007937	Krit1	KRIT1, ankyrin repeat containing	4	0.008417488	-1.101863788	1	-1	0.091421764	0.60394703	0	0
1925	ENSRNOG00000012255	Ktn1	kinectin 1	4	0.005381284	-0.899971318	1	-1	0.113989311	0.420019994	0	0
1926	ENSRNOG00000004857	L2hgdh	L-2-hydroxyglutarate dehydrogenase	4	0.015513413	-0.907845905	1	-1	0.353018895	-0.038364371	0	0
1927	ENSRNOG000000007829	Laotb2	laotamase, beta 2	4	0.008578029	-1.17764429	1	-1	0.090637404	0.750788248	0	0
1928	ENSRNOG00000011134	Lama2	laminin subunit alpha 2	4	0.00227736	-0.883589641	1	-1	0.006759672	0.386434194	0	0
1929	ENSRNOG00000013557	Lanc1	LanC like 1	4	0.001480588	-0.849150852	1	-1	0.002596097	0.530651197	0	0
1930	ENSRNOG000000038366	Larp1b	La ribonucleoprotein domain family, member 1B	4	0.010730984	-1.30443351	1	-1	0.06938156	0.53061581	0	0

1931	ENSRNOG00000015888	Larp4b	La ribonucleoprotein domain family, member 4B	4	0.049081029	-0.948017121	1	-1	0.112608924	0.377964388	0	0
1932	ENSRNOG00000005715	Lgr4	leucine-rich repeat-containing G protein-coupled receptor	4	0.020121509	-0.844288054	1	-1	0.163889871	0.214008818	0	0
1933	ENSRNOG00000014805	Lig4	DNA ligase 4	4	0.0475992	-0.871927899	1	-1	0.084405078	0.674301782	0	0
1934	ENSRNOG000000043441	Lin52	lin-52 DREAM MuvB core complex component	4	0.01340942	-0.899073084	1	-1	0.003112337	0.439343215	0	0
1935	ENSRNOG000000021213	Lix1l	limb and CNS expressed 1 like	4	0.019693125	-0.802567808	1	-1	0.059047859	0.442275574	0	0
1936	ENSRNOG000000047450	Lmo3	LIM domain only 3	4	0.032870836	-0.808072891	1	-1	0.06058327	0.214206339	0	0
1937	ENSRNOG000000060775	Lmo7	LIM domain 7	4	0.036089649	-0.945126806	1	-1	0.253839528	0.129725117	0	0
1938	ENSRNOG000000046831	Lmod2	leiomodin 2	4	0.01709358	-1.191277249	1	-1	0.184598579	0.155350091	0	0
1939	ENSRNOG000000022490	LOC10036	Cytochrome c oxidase subunit 5A, mitochondrial-like	4	0.005175919	-1.261574617	1	-1	0.106560375	0.17207502	0	0
1940	ENSRNOG000000033346	LOC10036	vasculin-like protein 1-like	4	0.039378864	-0.726994311	1	-1	0.382906972	0.060739342	0	0
1941	ENSRNOG000000057227	LOC10036	zinc finger protein 81 (HFZ20)-like	4	0.042962692	-1.206103147	1	-1	0.147155507	0.463176237	0	0
1942	ENSRNOG000000050146	LOC10091	protein FAM122B-like	4	0.008965451	-1.007190238	1	-1	0.131104407	0.307309829	0	0
1943	ENSRNOG000000049639	LOC10091	leiomodin-2-like	4	0.011706089	-1.19684481	1	-1	0.173866218	0.133484122	0	0
1944	ENSRNOG000000059683	LOC10091	RUN and FYVE domain-containing protein 2-like	4	0.032431143	-0.59719713	1	-1	0.429475691	-0.028296288	0	0
1945	ENSRNOG000000016000	LOC10091	ATP synthase subunit b, mitochondrial-like	4	0.009965933	-0.993369912	1	-1	0.111834358	0.366119784	0	0
1946	ENSRNOG000000051286	LOC10091	coiled-coil-helix-coiled-coil-helix domain-containing protein	4	0.035237984	-0.973543111	1	-1	0.037721743	0.39294937	0	0
1947	ENSRNOG000000005101	LOC10091	cutaneous T-cell lymphoma-associated antigen 5 homolog	4	0.007887732	-0.705528362	1	-1	0.39283346	-0.021512515	0	0
1948	ENSRNOG000000016391	LOC10091	AT-rich interactive domain-containing protein 4B-like	4	0.042096131	-0.933085089	1	-1	0.151631818	0.382894958	0	0
1949	ENSRNOG000000057097	LOC10255	uncharacterized LOC102550543	4	0.048677057	-0.585661887	1	-1	0.163606027	-0.195702959	0	0
1950	ENSRNOG000000047145	LOC10255	zinc finger protein 728-like	4	0.048586994	-0.816448781	1	-1	0.116837048	0.775866719	0	0
1951	ENSRNOG000000003187	LOC10255	armadillo repeat-containing X-linked protein 5-like	4	0.032933867	-1.039502197	1	-1	0.138328943	0.379136676	0	0
1952	ENSRNOG000000008112	LOC10255	zinc finger protein 598-like	4	0.014708917	-0.835459503	1	-1	0.075301841	0.728083837	0	0
1953	ENSRNOG000000010589	LOC10365	protein FAM134B	4	0.038214054	-1.003406493	1	-1	0.219547411	0.171526053	0	0
1954	ENSRNOG000000048051	LOC10365	saccharopine dehydrogenase-like oxidoreductase	4	0.040948824	-0.851821758	1	-1	0.289982346	0.103248708	0	0
1955	ENSRNOG000000040303	LOC10365	uncharacterized LOC103652531	4	0.001432867	-0.779192908	1	-1	0.080914696	0.889327572	0	0
1956	ENSRNOG000000052096	LOC10365	cytochrome c oxidase assembly protein COX11, mitochondrial	4	0.014416937	-0.898359728	1	-1	0.060994552	0.459479132	0	0
1957	ENSRNOG000000055229	LOC10834	leucyl-cystinyl aminopeptidase	4	0.038251707	-0.725768299	1	-1	0.141421419	0.132184083	0	0
1958	ENSRNOG000000051039	LOC10834	uncharacterized LOC108349594	4	0.026806427	-0.979277982	1	-1	0.118485346	0.669665098	0	0
1959	ENSRNOG000000028430	LOC25785	hippyragranin	4	0.010509482	-0.89217019	1	-1	0.038371561	0.274466101	0	0
1960	ENSRNOG000000045733	LOC29813	similar to RIKEN cDNA 2310003M01	4	0.011390939	-0.916601113	1	-1	0.052683808	0.8435227	0	0
1961	ENSRNOG000000031368	LOC49923	LRRGT00141	4	0.028815944	-0.827740002	1	-1	0.35538556	0.07835008	0	0
1962	ENSRNOG000000010594	LOC50012	similar to RIKEN cDNA 4921507P07	4	0.004485208	-0.588932882	1	-1	0.283326943	0.111914928	0	0
1963	ENSRNOG000000054488	LOC50056	similar to casein kinase 1, gamma 3 isoform 2	4	0.034401352	-0.618187933	1	-1	0.1391984	0.833821364	0	0
1964	ENSRNOG000000029292	LOC50087	Ab1-152	4	0.015259499	-0.867034899	1	-1	0.122788154	0.77611181	0	0
1965	ENSRNOG000000033654	LOC50105	Ab2-080	4	0.038696504	-0.654490284	1	-1	0.205182815	0.060404524	0	0
1966	ENSRNOG000000027623	LOC68003	hypothetical protein LOC680039	4	1.88E-05	-0.989444224	1	-1	0.000610992	0.573810572	0	0
1967	ENSRNOG000000058316	LOC68804	similar to motile sperm domain containing 1	4	0.004373078	-1.382838454	1	-1	0.065703678	0.551093464	0	0
1968	ENSRNOG000000022871	LOC69111	similar to zinc finger protein 84 (HPF2)	4	0.004624371	-0.822209052	1	-1	0.099452658	0.629038604	0	0
1969	ENSRNOG000000015577	Lpar6	lysophosphatidic acid receptor 6	4	0.026134336	-0.724545666	1	-1	0.224426729	0.416314209	0	0
1970	ENSRNOG000000004377	Lpin1	lipin 1	4	0.011383353	-0.589991163	1	-1	0.38934039	-0.142918055	0	0
1971	ENSRNOG000000012181	Lpl	lipoprotein lipase	4	0.011610096	-1.072065175	1	-1	0.019297704	0.538346979	0	0
1972	ENSRNOG000000023453	Lrba	LPS responsive beige-like anchor protein	4	0.023058134	-0.650464182	1	-1	0.014622233	0.229797017	0	0
1973	ENSRNOG000000005877	Lrpprc	leucine-rich pentatricopeptide repeat containing	4	0.004412799	-0.910265296	1	-1	0.017417971	0.409492807	0	0
1974	ENSRNOG000000028357	Lrrc14b	leucine rich repeat containing 14B	4	0.048604372	-1.059577946	1	-1	0.096614098	0.432006758	0	0
1975	ENSRNOG000000005857	Lrrc3b	leucine rich repeat containing 3B	4	0.019117716	-1.508514738	1	-1	0.115043928	0.337348894	0	0

1976	ENSRNOG00000004628	Lrrc75b	leucine rich repeat containing 75B	4	0.048409627	-0.982493624	1	-1	0.269264258	0.142037577	0	0
1977	ENSRNOG00000004048	Lrrk2	leucine-rich repeat kinase 2	4	0.036985587	-0.59825512	1	-1	0.224106682	0.231637806	0	0
1978	ENSRNOG00000006001	Luc7l2	LUC7-like 2 pre-mRNA splicing factor	4	0.047131922	-0.904203275	1	-1	0.311166264	0.141910923	0	0
1979	ENSRNOG00000002835	Luc7l3	LUC7-like 3 pre-mRNA splicing factor	4	0.039568168	-0.865455157	1	-1	0.1360451	0.590880657	0	0
1980	ENSRNOG000000051800	Ly49l2	Ly49 inhibitory receptor 2	4	0.012770154	-1.31816255	1	-1	0.116204813	0.733719368	0	0
1981	ENSRNOG000000008320	Lypla1	lysophospholipase I	4	0.00852093	-0.824349083	1	-1	0.040759327	0.498986902	0	0
1982	ENSRNOG000000043105	Lyrm2	LYR motif containing 2	4	0.026290187	-0.677852324	1	-1	0.070430108	0.484790748	0	0
1983	ENSRNOG000000045961	Lyrm7	LYR motif containing 7	4	0.027262396	-0.837584151	1	-1	0.068856424	0.403675252	0	0
1984	ENSRNOG000000019885	Magl3	membrane associated guanylate kinase, WW and PDZ d	4	0.013424867	-1.10268898	1	-1	0.011640094	0.438634057	0	0
1985	ENSRNOG000000015983	Maip1	matrix AAA peptidase interacting protein 1	4	0.005436177	-0.769464952	1	-1	0.069058341	0.422958344	0	0
1986	ENSRNOG000000002848	Maoa	monoamine oxidase A	4	0.03473788	-0.828816708	1	-1	0.236772429	0.376411494	0	0
1987	ENSRNOG000000029778	Maob	monoamine oxidase B	4	0.036831943	-1.274424453	1	-1	0.077266602	1.029226759	0	0
1988	ENSRNOG000000005724	Map3k7	mitogen activated protein kinase kinase kinase 7	4	0.005355217	-0.934733215	1	-1	0.012945314	0.232100052	0	0
1989	ENSRNOG000000002823	Mapk9	mitogen-activated protein kinase 9	4	0.01526612	-0.69176638	1	-1	0.008354389	0.396669082	0	0
1990	ENSRNOG000000016252	Mblac2	metallo-beta-lactamase domain containing 2	4	0.03578236	-1.043282567	1	-1	0.164660023	0.333200894	0	0
1991	ENSRNOG000000009715	Me1	malic enzyme 1	4	0.02708696	-0.907158014	1	-1	0.072063789	0.270474553	0	0
1992	ENSRNOG000000012645	Mecom	MDS1 and EVI1 complex locus	4	0.01939949	-0.940235368	1	-1	0.056271774	0.331666994	0	0
1993	ENSRNOG000000004844	Med30	mediator complex subunit 30	4	0.013006413	-0.74233581	1	-1	0.157638094	0.391101864	0	0
1994	ENSRNOG000000033134	Mef2c	myocyte enhancer factor 2C	4	0.021684436	-0.9859023	1	-1	0.042057031	0.234855534	0	0
1995	ENSRNOG000000004606	Meis1	Meis homeobox 1	4	0.003489968	-0.672710959	1	-1	0.21446983	0.087803786	0	0
1996	ENSRNOG000000004730	Meis2	Meis homeobox 2	4	0.019429419	-0.590909788	1	-1	0.023149162	0.249429529	0	0
1997	ENSRNOG000000011022	Mep1a	meprin A subunit alpha	4	0.009304876	-0.70285501	1	-1	0.017273085	0.336566885	0	0
1998	ENSRNOG0000000027451	Mettl25	methyltransferase like 25	4	0.035568168	-0.672588437	1	-1	0.063468244	0.307193727	0	0
1999	ENSRNOG000000011057	Mfn1	mitofusin 1	4	0.001581684	-1.099492611	1	-1	0.038886423	0.468170566	0	0
2000	ENSRNOG000000012863	Mfsd6	major facilitator superfamily domain containing 6	4	0.002646714	-0.712938782	1	-1	0.256853541	0.032129181	0	0
2001	ENSRNOG000000012729	Mfsd8	major facilitator superfamily domain containing 8	4	0.046655265	-0.847905296	1	-1	0.129352527	0.294199027	0	0
2002	ENSRNOG0000000046858	MGC1093	similar to Microsomal signal peptidase 23 kDa subunit (S	4	0.037580167	-0.677657318	1	-1	0.46771202	0.069484079	0	0
2003	ENSRNOG000000017822	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	4	0.030545618	-0.775328569	1	-1	0.12624288	0.307968587	0	0
2004	ENSRNOG000000012767	Micu3	mitochondrial calcium uptake family, member 3	4	0.003783739	-0.737026192	1	-1	0.079171988	0.61880068	0	0
2005	ENSRNOG0000000060542	Mid2	midline 2	4	0.010337356	-0.647918521	1	-1	0.08950831	0.47585165	0	0
2006	ENSRNOG000000013876	Mipep	mitochondrial intermediate peptidase	4	0.04527274	-0.764073569	1	-1	0.03833446	0.310001535	0	0
2007	ENSRNOG0000000050490	Mir3064	microRNA 3064	4	0.035615751	-1.092089204	1	-1	0.2416072	0.420904446	0	0
2008	ENSRNOG000000005619	Misp3	MISP family member 3	4	0.007063099	-0.846981233	1	-1	0.002747879	0.517704808	0	0
2009	ENSRNOG000000008658	Mitf	melanogenesis associated transcription factor	4	0.000285084	-1.222555711	1	-1	0.054859803	0.300933082	0	0
2010	ENSRNOG000000008705	Mkks	McKusick-Kaufman syndrome	4	0.008622302	-0.814209438	1	-1	0.111678022	0.579846166	0	0
2011	ENSRNOG000000017233	Mmahc	methylmalonic aciduria (cobalamin deficiency) cblC type	4	0.013574236	-0.735613462	1	-1	0.224376733	0.092317969	0	0
2012	ENSRNOG000000004740	Mmadhc	methylmalonic aciduria and homocystinuria, cblD type	4	0.019206951	-0.802112967	1	-1	0.022613475	0.486903501	0	0
2013	ENSRNOG000000002436	Mmd	monocyte to macrophage differentiation-associated	4	0.008098338	-0.771692729	1	-1	0.147810634	0.312351083	0	0
2014	ENSRNOG000000009514	Mme	membrane metallo-endopeptidase	4	0.021213985	-1.262626538	1	-1	0.082355838	1.339327687	0	0
2015	ENSRNOG000000000881	Mmg1	membrane magnesium transporter 1	4	0.010969864	-0.762922658	1	-1	0.280439487	0.187683491	0	0
2016	ENSRNOG000000010996	Mob1b	MOB kinase activator 1B	4	0.043571892	-1.044107438	1	-1	0.084668299	0.493077329	0	0
2017	ENSRNOG000000014980	Mob4	MOB family member 4, phocein	4	0.008868354	-0.698973582	1	-1	0.099041376	0.599193739	0	0
2018	ENSRNOG000000019624	Morc2	MORC family CW-type zinc finger 2	4	0.02983408	-0.599994908	1	-1	0.404357831	0.029228998	0	0
2019	ENSRNOG000000002332	Mospd1	motile sperm domain containing 1	4	0.007551203	-1.268869854	1	-1	0.056484242	0.903474044	0	0
2020	ENSRNOG000000007894	Mpdz	multiple PDZ domain crumbs cell polarity complex comp	4	0.034532653	-0.750867182	1	-1	0.032378457	0.302487955	0	0

2021	ENSRNOG00000051238	Mphosph8	M-phase phosphoprotein 8	4	0.037237018	-0.742908054	1	-1	0.263957313	0.168591601	0	0
2022	ENSRNOG00000008788	Mpp5	membrane palmitoylated protein 5	4	0.009299221	-0.7831167	1	-1	0.110645128	0.540751631	0	0
2023	ENSRNOG00000015774	Mreg	melanoregulin	4	0.004010206	-1.347243468	1	-1	0.014656162	0.565915607	0	0
2024	ENSRNOG00000004401	Mrpl13	mitochondrial ribosomal protein L13	4	0.019884837	-0.599208648	1	-1	0.039598304	0.453789492	0	0
2025	ENSRNOG00000012650	Mrpl3	mitochondrial ribosomal protein L3	4	0.014573202	-0.850274238	1	-1	0.057318668	0.247874087	0	0
2026	ENSRNOG00000008546	Mrpl35	mitochondrial ribosomal protein L35	4	0.027980967	-0.762858947	1	-1	0.077224743	0.517264364	0	0
2027	ENSRNOG00000019165	Mrpl51	mitochondrial ribosomal protein L51	4	0.008742294	-0.727775803	1	-1	0.047468588	0.372492	0	0
2028	ENSRNOG00000010363	Mrps23	mitochondrial ribosomal protein S23	4	0.036678968	-0.823288932	1	-1	0.053550721	0.36818191	0	0
2029	ENSRNOG00000012136	Mrps30	mitochondrial ribosomal protein S30	4	8.44E-05	-1.16728834	1	-1	0.105053789	0.451604349	0	0
2030	ENSRNOG00000025997	Mrrf	mitochondrial ribosome recycling factor	4	0.041854217	-0.649322593	1	-1	0.107624302	0.237191322	0	0
2031	ENSRNOG00000017767	Mrv1	murine retrovirus integration site 1 homolog	4	0.023227777	-0.659452971	1	-1	0.070586787	-0.348009606	0	0
2032	ENSRNOG00000020993	Ms4a2	membrane spanning 4-domains A2	4	0.030122336	-1.075419102	1	-1	0.088818702	0.886036289	0	0
2033	ENSRNOG00000022245	Msantd4	Myb/SANT DNA binding domain containing 4 with coiled-	4	8.61E-05	-0.845035895	1	-1	0.058981863	0.604799422	0	0
2034	ENSRNOG00000023021	Msl2	MSL complex subunit 2	4	0.045041859	-0.665513921	1	-1	0.0924439	0.303050525	0	0
2035	ENSRNOG00000004016	Msl3	MSL complex subunit 3	4	0.03680891	-0.772842024	1	-1	0.137020481	0.412747887	0	0
2036	ENSRNOG00000042688	MsrB3	methionine sulfoxide reductase B3	4	0.048194194	-0.586318466	1	-1	0.233982139	0.103984602	0	0
2037	ENSRNOG00000058658	Mtch2	mitochondrial carrier 2	4	0.021153024	-0.845035895	1	-1	0.0712064	0.607850549	0	0
2038	ENSRNOG00000007899	Mterf1	mitochondrial transcription termination factor 1	4	0.044905731	-0.749249142	1	-1	0.087940901	0.614339572	0	0
2039	ENSRNOG00000037376	Mterf4	mitochondrial transcription termination factor 4	4	0.008248121	-0.748481442	1	-1	0.018378112	0.431388476	0	0
2040	ENSRNOG00000016937	Mtfr1l	mitochondrial fission regulator 1-like	4	0.049790773	-0.81050504	1	-1	0.09926943	0.315077961	0	0
2041	ENSRNOG00000004161	Mtfr2	mitochondrial translational initiation factor 2	4	0.000936763	-1.027477273	1	-1	0.110339632	0.531522404	0	0
2042	ENSRNOG00000005923	Mtmr2	myotubularin related protein 2	4	0.02257996	-0.802797327	1	-1	0.075958417	0.445948072	0	0
2043	ENSRNOG00000016578	Mtpap	mitochondrial poly(A) polymerase	4	0.00945452	-0.829919639	1	-1	0.087586029	0.261359617	0	0
2044	ENSRNOG00000047106	Mtrf1	mitochondrial translation release factor 1	4	0.011452452	-0.580681854	1	-1	0.092123302	0.67706148	0	0
2045	ENSRNOG00000010748	Mtus1	microtubule associated scaffold protein 1	4	0.000230881	-1.001984665	1	-1	5.972E-05	0.56499887	0	0
2046	ENSRNOG0000001559	Mtx2	metaxin 2	4	0.018454885	-0.697589231	1	-1	0.100708503	0.566274591	0	0
2047	ENSRNOG00000051372	Mycn	MYCN proto-oncogene, bHLH transcription factor	4	0.013261982	-1.569628545	1	-1	0.435594856	-0.10443913	0	0
2048	ENSRNOG00000002215	Myk	myosin light chain kinase	4	0.008810841	-0.900078872	1	-1	0.096903662	0.372481953	0	0
2049	ENSRNOG00000016483	Myo16	myosin XVI	4	0.018908489	-1.764574342	1	-1	0.44611944	-0.029771473	0	0
2050	ENSRNOG00000011852	Myo6	myosin VI	4	0.00803186	-1.339417781	1	-1	0.025147024	0.507712794	0	0
2051	ENSRNOG00000018797	Myrip	myosin VIIA and Rab interacting protein	4	0.008423971	-1.130188576	1	-1	0.060709261	0.6682812	0	0
2052	ENSRNOG00000026299	Mysm1	myb-like, SWIRM and MPN domains 1	4	0.042551824	-0.669898265	1	-1	0.125192814	0.513855306	0	0
2053	ENSRNOG00000024813	Mzt1	mitotic spindle organizing protein 1	4	0.021020757	-0.709224046	1	-1	0.110814358	0.344780937	0	0
2054	ENSRNOG00000014192	Naa30	N(alpha)-acetyltransferase 30, NatC catalytic subunit	4	0.008420523	-1.227798957	1	-1	0.099921247	0.330259602	0	0
2055	ENSRNOG000000039017	Naa50	N(alpha)-acetyltransferase 50, NatE catalytic subunit	4	0.045306255	-0.602485729	1	-1	0.197626646	0.203216219	0	0
2056	ENSRNOG00000005955	Naalad2	N-acetylated alpha-linked acidic dipeptidase 2	4	0.031836011	-1.132299282	1	-1	0.063193159	0.750727646	0	0
2057	ENSRNOG000000054157	Nadk2	NAD kinase 2, mitochondrial	4	0.024218881	-0.998385034	1	-1	0.058528239	0.489123635	0	0
2058	ENSRNOG000000033133	Nae1	NEDD8 activating enzyme E1 subunit 1	4	0.005293842	-0.586147484	1	-1	0.193515689	0.501493499	0	0
2059	ENSRNOG000000026403	Naf1	nuclear assembly factor 1 ribonucleoprotein	4	0.01380291	-0.790940322	1	-1	0.18892566	0.301874745	0	0
2060	ENSRNOG00000004753	Napb	NSF attachment protein beta	4	0.03157396	-0.792071712	1	-1	0.170945038	0.296367265	0	0
2061	ENSRNOG000000021525	Nbeal1	neurobeachin-like 1	4	0.029899317	-0.881327898	1	-1	0.159633198	0.471152025	0	0
2062	ENSRNOG00000013313	Noeh1	neutral cholesterol ester hydrolase 1	4	0.005316323	-1.014317825	1	-1	0.328759051	0.031210175	0	0
2063	ENSRNOG00000017155	Nck2	NCK adaptor protein 2	4	0.026820081	-0.807515636	1	-1	0.287050755	0.058995556	0	0
2064	ENSRNOG00000004068	Ncoa1	nuclear receptor coactivator 1	4	0.000199435	-0.715670105	1	-1	0.011766154	0.261278059	0	0
2065	ENSRNOG00000018458	Ncr1	natural cytotoxicity triggering receptor 1	4	0.009693676	-1.369607594	1	-1	0.03113137	0.561476048	0	0

2068	ENSRNOG00000005008	Ndufa1	NADH:ubiquinone oxidoreductase complex assembly factor	4	0.025111923	-0.972592944	1	-1	0.017490173	0.43809791	0	0
2067	ENSRNOG00000007506	Ndufa4	NADH:ubiquinone oxidoreductase complex assembly factor	4	0.001556996	-1.063315072	1	-1	0.105772292	0.504066657	0	0
2068	ENSRNOG00000014588	Ndufb10	NADH:ubiquinone oxidoreductase subunit B10	4	0.036157231	-0.868342762	1	-1	0.380388456	-0.084889745	0	0
2069	ENSRNOG00000002616	Ndufb2	NADH:ubiquinone oxidoreductase subunit B2	4	0.023119785	-0.672605724	1	-1	0.025276188	0.424863946	0	0
2070	ENSRNOG00000012383	Ndufc2	NADH:ubiquinone oxidoreductase subunit C2	4	0.049884973	-0.822807723	1	-1	0.084304117	0.531207834	0	0
2071	ENSRNOG00000006783	Neb	nebulin	4	0.042809613	-0.580486712	1	-1	0.296525274	-0.196079616	0	0
2072	ENSRNOG00000017785	Net1	neuroepithelial cell transforming 1	4	0.006967106	-0.821775166	1	-1	0.03741673	0.383979994	0	0
2073	ENSRNOG00000012512	Nexn	nexilin (F actin binding protein)	4	0.008440521	-1.089267428	1	-1	0.059969933	0.438502171	0	0
2074	ENSRNOG00000011879	Nfat5	nuclear factor of activated T-cells 5	4	0.02226012	-0.788608228	1	-1	0.151808441	0.231505315	0	0
2075	ENSRNOG00000013553	Ngrn	neugrin, neurite outgrowth associated	4	0.016706434	-0.740612059	1	-1	0.003132749	0.507641084	0	0
2076	ENSRNOG00000008565	Nkiras1	NFkB inhibitor interacting Ras-like 1	4	0.019190283	-0.768825532	1	-1	0.01560382	0.519576137	0	0
2077	ENSRNOG000000024210	Nlrc3	NLR family, CARD domain containing 3	4	0.038499552	-0.724010938	1	-1	0.470935039	0.028505049	0	0
2078	ENSRNOG000000009310	Nmd3	NMD3 ribosome export adaptor	4	0.045208882	-0.724010938	1	-1	0.134283498	0.548399657	0	0
2079	ENSRNOG000000026842	Nnt	nicotinamide nucleotide transhydrogenase	4	0.029444314	-1.052107673	1	-1	0.088393007	0.454480547	0	0
2080	ENSRNOG000000006611	Nostrin	nitric oxide synthase trafficking	4	0.034599131	-0.94744679	1	-1	0.198945728	0.216018463	0	0
2081	ENSRNOG000000046912	Nr1d2	nuclear receptor subfamily 1, group D, member 2	4	0.020687401	-1.527462422	1	-1	0.053149024	0.844548862	0	0
2082	ENSRNOG000000006983	Nr2c1	nuclear receptor subfamily 2, group C, member 1	4	0.019822081	-0.645787983	1	-1	0.276240949	0.100695192	0	0
2083	ENSRNOG000000034007	Nr3c2	nuclear receptor subfamily 3, group C, member 2	4	0.015963037	-0.651059758	1	-1	0.225888077	0.151626244	0	0
2084	ENSRNOG000000009354	Nrarp	Notch-regulated ankyrin repeat protein	4	0.019168195	-1.168311789	1	-1	0.106429832	-0.33181307	0	0
2085	ENSRNOG000000007111	Nrdc	nardilysin convertase	4	0.011580856	-0.781088336	1	-1	0.012083649	0.215808514	0	0
2086	ENSRNOG0000000050767	Nrn1	neuritin 1	4	0.049485139	-0.788673869	1	-1	0.220880712	0.407204327	0	0
2087	ENSRNOG00000010744	Nrp1	neuropilin 1	4	0.024367581	-1.055834823	1	-1	0.059171161	0.300899665	0	0
2088	ENSRNOG000000019716	Ntf3	neurotrophin 3	4	0.024443694	-0.97610136	1	-1	0.056071099	0.617940303	0	0
2089	ENSRNOG000000031138	Ntn1	netrin G1	4	0.01496283	-1.53444149	1	-1	0.149563134	0.497202822	0	0
2090	ENSRNOG000000048053	Nudt11	nudix hydrolase 11	4	0.031205434	-1.193526468	1	-1	0.118091304	0.28918012	0	0
2091	ENSRNOG000000025239	Nudt15	nudix hydrolase 15	4	0.007307496	-0.886451148	1	-1	0.051990621	0.497156112	0	0
2092	ENSRNOG000000009094	Nudt4	nudix hydrolase 4	4	0.011489415	-1.002456081	1	-1	0.044368044	0.476979381	0	0
2093	ENSRNOG00000012679	Oard1	O-acyl-ADP-ribose deacylase 1	4	0.035105993	-0.620181295	1	-1	0.032520033	0.494791054	0	0
2094	ENSRNOG000000002205	Ociad1	OClA domain containing 1	4	0.011278946	-0.703339472	1	-1	0.116832839	0.213203428	0	0
2095	ENSRNOG00000003359	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase	4	0.011805131	-1.038316991	1	-1	0.271413006	0.125339843	0	0
2096	ENSRNOG00000018806	Olf59	olfactory receptor 59	4	0.01978636	-1.323728786	1	-1	0.102271223	0.299893767	0	0
2097	ENSRNOG00000001717	Opa1	OPA1, mitochondrial dynamin like GTPase	4	0.003982761	-0.994385437	1	-1	0.059521826	0.235688049	0	0
2098	ENSRNOG000000026573	Ophn1	oligophrenin 1	4	0.007345149	-0.798994596	1	-1	0.086177436	-0.234688881	0	0
2099	ENSRNOG00000017941	Optn	optineurin	4	0.016421074	-0.980416308	1	-1	0.081260879	0.272785446	0	0
2100	ENSRNOG000000021057	Osbp	oxysterol binding protein	4	0.003387077	-0.623023178	1	-1	0.082521757	0.158945319	0	0
2101	ENSRNOG000000054058	Osbpl1a	oxysterol binding protein-like 1A	4	0.016150197	-0.701088111	1	-1	0.039747121	0.272262693	0	0
2102	ENSRNOG00000010011	Osbpl3	oxysterol binding protein-like 3	4	0.020843252	-0.777850699	1	-1	0.106993931	0.270259654	0	0
2103	ENSRNOG00000010812	Osbpl6	oxysterol binding protein-like 6	4	0.00203117	-1.445937248	1	-1	0.019218468	0.206950922	0	0
2104	ENSRNOG00000004001	Osgepl1	O-sialoglycoprotein endopeptidase-like 1	4	0.005701124	-1.284058912	1	-1	0.058082753	0.768071835	0	0
2105	ENSRNOG000000042068	Otdub7b	OTU deubiquitinase 7B	4	0.032057513	-0.674186491	1	-1	0.159084201	0.165443955	0	0
2106	ENSRNOG00000019780	Oxnd1	oxidoreductase NAD-binding domain containing 1	4	0.020268809	-0.71858724	1	-1	0.030241983	0.179909726	0	0
2107	ENSRNOG000000005993	Oxsm	3-oxoacyl-ACP synthase, mitochondrial	4	0.04855472	-0.688523002	1	-1	0.023178264	0.388848588	0	0
2108	ENSRNOG00000014232	P2ry1	purinergic receptor P2Y1	4	0.040508103	-1.389097162	1	-1	0.120307082	0.699484824	0	0
2109	ENSRNOG00000015642	Pabpc4	poly(A) binding protein, cytoplasmic 4	4	0.014136542	-0.594762453	1	-1	0.452992759	0.025260995	0	0
2110	ENSRNOG000000002755	Pafah1b1	platelet-activating factor acetylhydrolase 1b, regulatory	4	0.025592028	-0.794992444	1	-1	0.134484932	0.373292077	0	0

2111	ENSRNOG00000058580	Paip1	poly(A) binding protein interacting protein 1	4	0.010123028	-0.817317829	1	-1	0.071808992	0.422892001	0	0
2112	ENSRNOG000000000561	Pal1	phosphatase domain containing, paladin 1	4	0.040481484	-0.734858087	1	-1	0.097914833	-0.48108916	0	0
2113	ENSRNOG00000018944	Pank1	pantothenate kinase 1	4	0.020377767	-0.948036477	1	-1	0.059296807	0.427390911	0	0
2114	ENSRNOG000000025288	Pank2	pantothenate kinase 2	4	0.015510241	-0.817044383	1	-1	0.071045928	0.143918022	0	0
2115	ENSRNOG000000024212	Papd5	poly(A) RNA polymerase D5, non-canonical	4	0.038362596	-0.72770842	1	-1	0.275798635	0.084045086	0	0
2116	ENSRNOG000000032374	Parg9	progesterone and adiponectin receptor family member 9	4	0.005628301	-1.223553181	1	-1	0.437324253	-0.042543904	0	0
2117	ENSRNOG000000011159	Parp6	poly (ADP-ribose) polymerase family, member 6	4	0.029381008	-0.668389005	1	-1	0.031772498	0.32383405	0	0
2118	ENSRNOG000000002036	Paxbp1	PAX3 and PAX7 binding protein 1	4	0.048663816	-0.787975073	1	-1	0.275886973	0.114981109	0	0
2119	ENSRNOG000000019265	Podh12	protocadherin 12	4	0.033521826	-1.325620326	1	-1	0.088358251	-0.312957996	0	0
2120	ENSRNOG000000010155	Pom1	pericentriolar material 1	4	0.028646714	-1.037541474	1	-1	0.135389628	0.574411054	0	0
2121	ENSRNOG000000017404	Pomtd2	protein-L-isoaspartate (D-aspartate) O-methyltransferase	4	0.008377215	-1.270047956	1	-1	0.060231225	0.64199083	0	0
2122	ENSRNOG000000025042	Pde3a	phosphodiesterase 3A	4	0.017067651	-0.722880482	1	-1	0.424487001	0.075025299	0	0
2123	ENSRNOG000000007895	Pdhb	pyruvate dehydrogenase E1 beta subunit	4	0.010507827	-1.173402111	1	-1	0.056093925	0.56054394	0	0
2124	ENSRNOG000000008947	Pdhx	pyruvate dehydrogenase complex, component X	4	0.047524447	-0.760245535	1	-1	0.066782291	0.391262999	0	0
2125	ENSRNOG000000016180	Pdp1	pyruvate dehydrogenase phosphatase catalytic subunit 1	4	0.026019171	-1.095630987	1	-1	0.067876009	0.836472144	0	0
2126	ENSRNOG000000022593	Pdpr	pyruvate dehydrogenase phosphatase regulatory subunit	4	0.018035722	-0.938598897	1	-1	0.258959106	0.178428007	0	0
2127	ENSRNOG000000001098	Pds5b	PDS5 cohesin associated factor B	4	0.048187022	-0.641167866	1	-1	0.117235915	0.306984523	0	0
2128	ENSRNOG000000042962	Pds2	decaprenyl diphosphate synthase subunit 2	4	0.029688159	-0.938620348	1	-1	0.055080065	0.423664551	0	0
2129	ENSRNOG000000020254	Per2	period circadian clock 2	4	0.01370471	-0.972433535	1	-1	0.111514102	0.232182282	0	0
2130	ENSRNOG000000018413	Per3	period circadian clock 3	4	0.00688518	-1.293148569	1	-1	0.248189642	0.144885478	0	0
2131	ENSRNOG000000025991	Pex1	peroxisomal biogenesis factor 1	4	0.014553755	-0.609035673	1	-1	0.100804023	0.098040534	0	0
2132	ENSRNOG000000005775	Phf14	PHD finger protein 14	4	0.00745452	-0.590210618	1	-1	0.139393145	0.252303131	0	0
2133	ENSRNOG000000005486	Phf20l1	PHD finger protein 20-like 1	4	0.036297221	-1.219624214	1	-1	0.089386526	0.651502385	0	0
2134	ENSRNOG000000003063	Phka1	phosphorylase kinase regulatory subunit alpha 1	4	0.008468657	-0.728201747	1	-1	0.086363078	0.372006408	0	0
2135	ENSRNOG0000000024101	Phkb	phosphorylase kinase regulatory subunit beta	4	0.027572443	-0.953965456	1	-1	0.037529412	0.492599278	0	0
2136	ENSRNOG000000007979	Phospho2	phosphatase, orphan 2	4	0.013804027	-0.891730355	1	-1	0.121310868	0.466895845	0	0
2137	ENSRNOG000000013517	Phtf2	putative homeodomain transcription factor 2	4	0.017615751	-0.731183427	1	-1	0.064143163	0.343432508	0	0
2138	ENSRNOG000000018044	Phyh	phytanoyl-CoA 2-hydroxylase	4	0.026070892	-1.423697708	1	-1	0.050398731	0.656342223	0	0
2139	ENSRNOG0000000056371	Pik3ca	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic	4	0.019036342	-0.756305325	1	-1	0.052973174	0.380914922	0	0
2140	ENSRNOG000000015528	Pja2	praja ring finger ubiquitin ligase 2	4	0.004346183	-0.86144251	1	-1	0.014389973	0.462608956	0	0
2141	ENSRNOG000000007753	Pla2	phospholipase A2, activating protein	4	0.043542928	-0.685995915	1	-1	0.336105096	0.160447875	0	0
2142	ENSRNOG000000008846	Plag1	PLAG1 zinc finger	4	0.039447486	-1.139832797	1	-1	0.05657065	0.615833043	0	0
2143	ENSRNOG000000004810	Plcb1	phospholipase C beta 1	4	0.004855527	-0.594011345	1	-1	0.040193642	0.306827343	0	0
2144	ENSRNOG000000014276	Plce1	phospholipase C, epsilon 1	4	0.009945935	-0.85301725	1	-1	0.066128336	0.260291499	0	0
2145	ENSRNOG000000016011	Plekha7	pleckstrin homology and RhoGEF domain containing G1	4	0.03373657	-1.031174673	1	-1	0.04291173	0.526421723	0	0
2146	ENSRNOG000000015268	Plpp6	phospholipid phosphatase 6	4	0.032595959	-0.858896296	1	-1	0.344322805	0.162021768	0	0
2147	ENSRNOG000000007324	Plxn2	plexin A2	4	0.042232398	-0.68753397	1	-1	0.087467347	0.326853325	0	0
2148	ENSRNOG000000007755	Pm20d2	peptidase M20 domain containing 2	4	0.046978277	-0.852176395	1	-1	0.048881663	0.338483691	0	0
2149	ENSRNOG000000004076	Pms1	PMS1 homolog 1, mismatch repair system component	4	0.012155024	-0.748882769	1	-1	0.092879526	0.543704512	0	0
2150	ENSRNOG000000008782	Pnir	PNN interacting serine and arginine rich protein	4	0.043423212	-0.737470144	1	-1	0.467955038	0.017069121	0	0
2151	ENSRNOG000000022268	Pnpla3	patatin-like phospholipase domain containing 3	4	0.032635267	-1.270821356	1	-1	0.144832425	-0.600796792	0	0
2152	ENSRNOG000000039091	Pnpla8	patatin-like phospholipase domain containing 8	4	0.003564168	-1.224311641	1	-1	0.051261223	0.836921953	0	0
2153	ENSRNOG000000003600	Pnpt1	polyribonucleotide nucleotidyltransferase 1	4	0.033723329	-0.975858848	1	-1	0.107400386	0.713543288	0	0
2154	ENSRNOG000000012495	Podxl	podocalyxin-like	4	0.027885387	-1.111849298	1	-1	0.032351907	0.558273434	0	0
2155	ENSRNOG000000032058	Pogk	pogo transposable element derived with KRAB domain	4	0.003215364	-0.741680315	1	-1	0.156499828	0.310715355	0	0

2156	ENSRNOG000000007548	Poli3f	RNA polymerase III subunit F	4	0.010625612	-0.727447787	1	-1	0.196723743	0.146404972	0	0
2157	ENSRNOG000000047439	Pot1b	protection of telomeres 1B	4	0.018336253	-0.898180527	1	-1	0.120700779	0.839877058	0	0
2158	ENSRNOG000000012091	Ppa2	pyrophosphatase (inorganic) 2	4	0.017304188	-1.002122828	1	-1	0.040594097	0.387493442	0	0
2159	ENSRNOG0000000021463	Ppara	peroxisome proliferator activated receptor alpha	4	0.00063306	-1.262044757	1	-1	0.230556031	0.31697642	0	0
2160	ENSRNOG000000002128	Ppat	phosphoribosyl pyrophosphate amidotransferase	4	0.048651541	-0.675896589	1	-1	0.282016137	0.109134371	0	0
2161	ENSRNOG0000000030667	Ppm1b	protein phosphatase, Mg2+/Mn2+ dependent, 1B	4	0.005588856	-0.839047037	1	-1	0.030446314	0.300778478	0	0
2162	ENSRNOG0000000046168	Ppm1l	protein phosphatase, Mg2+/Mn2+ dependent, 1L	4	0.009294256	-0.963035726	1	-1	0.047574443	0.172370438	0	0
2163	ENSRNOG0000000004612	Ppp1cb	protein phosphatase 1 catalytic subunit beta	4	0.001568995	-0.876021564	1	-1	0.089426798	0.5087141	0	0
2164	ENSRNOG0000000051440	Ppp1r12b	protein phosphatase 1, regulatory subunit 12B	4	0.029190125	-0.805759157	1	-1	0.111516378	0.254018777	0	0
2165	ENSRNOG0000000001733	Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	4	0.007387353	-0.878731236	1	-1	0.079116268	0.38282108	0	0
2166	ENSRNOG0000000022999	Ppp2r3a	protein phosphatase 2, regulatory subunit B", alpha	4	0.003392042	-1.009974448	1	-1	0.050938763	0.438801841	0	0
2167	ENSRNOG0000000009882	Ppp3ca	protein phosphatase 3 catalytic subunit alpha	4	0.010829874	-0.698524295	1	-1	0.07003779	0.199713066	0	0
2168	ENSRNOG0000000054782	Ppp3cb	protein phosphatase 3 catalytic subunit beta	4	0.001767602	-0.845773443	1	-1	0.00283346	0.482796102	0	0
2169	ENSRNOG0000000009745	Ppp3cc	protein phosphatase 3 catalytic subunit gamma	4	0.008148128	-0.783631273	1	-1	0.052163644	0.419275337	0	0
2170	ENSRNOG0000000043210	Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha	4	0.016046617	-0.835460491	1	-1	0.15884139	0.313489181	0	0
2171	ENSRNOG0000000015540	Ppp3r3	protein phosphatase 3, regulatory subunit 3	4	0.043788163	-0.592352209	1	-1	0.281637128	0.089672374	0	0
2172	ENSRNOG0000000004962	Prdm4	PR/SET domain 4	4	0.041214675	-0.639851551	1	-1	0.050791325	0.290579719	0	0
2173	ENSRNOG0000000007706	Prkaa2	protein kinase AMP-activated catalytic subunit alpha 2	4	0.020566168	-1.076112903	1	-1	0.024824495	0.469224607	0	0
2174	ENSRNOG0000000018166	Prkab2	protein kinase AMP-activated non-catalytic subunit beta	4	0.006362872	-1.357368896	1	-1	0.019363147	0.475944131	0	0
2175	ENSRNOG0000000054371	Prkcg	protein kinase C, gamma	4	0.004907386	-0.763978523	1	-1	0.471215433	-0.010204515	0	0
2176	ENSRNOG0000000004165	Prkd1	protein kinase D1	4	0.044630163	-0.776971466	1	-1	0.013178609	0.269380461	0	0
2177	ENSRNOG0000000003694	Prox1	prospero homeobox 1	4	0.036426591	-1.367462627	1	-1	0.094013881	0.421842923	0	0
2178	ENSRNOG0000000018396	Prpf18	pre-mRNA processing factor 18	4	0.002566513	-0.974062391	1	-1	0.366393904	0.039278319	0	0
2179	ENSRNOG0000000007203	Psma6	proteasome 26S subunit, ATPase 6	4	0.002775257	-0.59903725	1	-1	0.10812544	0.612283181	0	0
2180	ENSRNOG0000000003117	Psmd12	proteasome 26S subunit, non-ATPase 12	4	0.00521633	-0.580124135	1	-1	0.197422109	0.233466483	0	0
2181	ENSRNOG0000000006340	Psme4	proteasome activator subunit 4	4	0.016564513	-0.947729412	1	-1	0.147870299	0.296595723	0	0
2182	ENSRNOG0000000020605	Pstk	phosphoserine/threonine kinase	4	0.00863637	-1.470549847	1	-1	0.07130922	0.497939039	0	0
2183	ENSRNOG0000000010325	Ptger3	prostaglandin E receptor 3	4	0.049413008	-0.935202251	1	-1	0.112705262	0.4070546	0	0
2184	ENSRNOG0000000015072	Ptgr1	prostaglandin reductase 1	4	0.031953934	-0.964086781	1	-1	0.032417351	0.566452536	0	0
2185	ENSRNOG00000000038166	Ptgr2	prostaglandin reductase 2	4	0.008881181	-0.925817928	1	-1	0.014403765	0.513315694	0	0
2186	ENSRNOG0000000026564	Ptpdc1	protein tyrosine phosphatase domain containing 1	4	0.020826702	-0.67466594	1	-1	0.209207296	-0.242937248	0	0
2187	ENSRNOG0000000002625	Ptpn4	protein tyrosine phosphatase, non-receptor type 4	4	0.021245293	-1.033350494	1	-1	0.196036825	0.391972009	0	0
2188	ENSRNOG0000000005711	Ptpnd	protein tyrosine phosphatase, receptor type, D	4	0.003745535	-1.082384158	1	-1	0.027959658	0.473702761	0	0
2189	ENSRNOG0000000009419	Ptpng	protein tyrosine phosphatase, receptor type, G	4	0.008518723	-0.892769457	1	-1	0.067966209	0.511476154	0	0
2190	ENSRNOG0000000011700	Ptpnm	protein tyrosine phosphatase, receptor type, M	4	0.002862699	-0.631610595	1	-1	0.460156679	0.025088912	0	0
2191	ENSRNOG0000000006030	Ptpnz1	protein tyrosine phosphatase, receptor type Z1	4	0.029668299	-1.083286245	1	-1	0.36493959	-0.118896094	0	0
2192	ENSRNOG0000000006180	Pum2	pumilio RNA-binding family member 2	4	0.026998276	-0.733040633	1	-1	0.132635887	0.41861988	0	0
2193	ENSRNOG0000000005615	Purb	purine rich element binding protein B	4	0.013118881	-0.92243059	1	-1	0.116591063	0.305844625	0	0
2194	ENSRNOG0000000047088	Rab10	RAB10, member RAS oncogene family	4	0.037581822	-0.870087336	1	-1	0.158287153	0.296190418	0	0
2195	ENSRNOG0000000011302	Rab11a	RAB11a, member RAS oncogene family	4	0.019043514	-0.610007152	1	-1	0.182796324	0.295987351	0	0
2196	ENSRNOG0000000018901	Rab14	RAB14, member RAS oncogene family	4	0.03070271	-0.707885894	1	-1	0.197822978	0.175725978	0	0
2197	ENSRNOG0000000003923	Rab21	RAB21, member RAS oncogene family	4	0.003529963	-1.02808221	1	-1	0.059488863	0.493863942	0	0
2198	ENSRNOG0000000047960	Rab9b	RAB9B, member RAS oncogene family	4	0.010087168	-0.686282052	1	-1	0.03340542	0.543797504	0	0
2199	ENSRNOG0000000009402	Rabgap1	RAB GTPase activating protein 1	4	0.022393904	-0.75553996	1	-1	0.045864354	0.54561183	0	0
2200	ENSRNOG0000000002736	Rabgap1l	RAB GTPase activating protein 1-like	4	0.009609268	-0.744875928	1	-1	0.114493207	0.591868247	0	0

2201	ENSRNOG000000021581	Rapgef2	Rap guanine nucleotide exchange factor 2	4	0.003444452	-0.781800025	1	-1	0.038274533	0.107159208	0	0
2202	ENSRNOG000000011909	Rasa2	RAS p21 protein activator 2	4	0.018745052	-0.949236618	1	-1	0.389648838	0.067875768	0	0
2203	ENSRNOG000000032703	Rasgrp3	RAS guanyl releasing protein 3	4	0.018655127	-1.42645281	1	-1	0.088279429	0.585455758	0	0
2204	ENSRNOG000000016029	Rb1	RB transcriptional corepressor 1	4	0.009709813	-1.166702634	1	-1	0.045413558	0.513113114	0	0
2205	ENSRNOG000000008833	Rb1cc1	RB1-inducible coiled-coil 1	4	0.021319771	-1.167411655	1	-1	0.050080822	0.697711126	0	0
2206	ENSRNOG000000002827	Rbfox1	RNA binding fox-1 homolog 1	4	0.018330322	-1.353761105	1	-1	0.098885732	0.365037874	0	0
2207	ENSRNOG000000012153	Rbl2	RB transcriptional corepressor like 2	4	0.032695952	-0.71811751	1	-1	0.100143783	0.222743163	0	0
2208	ENSRNOG000000019723	Rbm12	RNA binding motif protein 12	4	0.023523757	-0.606621556	1	-1	0.043287842	0.237090774	0	0
2209	ENSRNOG000000006763	Rbm18	RNA binding motif protein 18	4	0.037065306	-0.6831654	1	-1	0.040752983	0.406125314	0	0
2210	ENSRNOG000000010350	Rcan2	regulator of calcineurin 2	4	0.028205917	-1.190445804	1	-1	0.098382387	0.395820228	0	0
2211	ENSRNOG000000046445	Rcor3	REST corepressor 3	4	0.048954693	-0.77602406	1	-1	0.189686711	0.230870897	0	0
2212	ENSRNOG0000000027919	Rdh13	retinol dehydrogenase 13	4	0.002539411	-1.003018592	1	-1	0.008677884	0.333112543	0	0
2213	ENSRNOG000000039551	Rdh14	retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	4	0.005245845	-0.43097776	1	-1	0.048525136	0.562101051	0	0
2214	ENSRNOG000000008481	Reep1	receptor accessory protein 1	4	0.04334639	-1.450025473	1	-1	0.48840811	0.011143043	0	0
2215	ENSRNOG000000000593	Rev3l	REV3 like, DNA directed polymerase zeta catalytic subu	4	0.015553134	-1.023083082	1	-1	0.059916971	0.548962739	0	0
2216	ENSRNOG000000002273	Rfk	riboflavin kinase	4	0.00846011	-0.769362858	1	-1	0.030718709	0.468295025	0	0
2217	ENSRNOG000000042492	Rfwd2	ring finger and WD repeat domain 2	4	0.002009655	-0.795901019	1	-1	0.103799393	0.41932778	0	0
2218	ENSRNOG0000000052775	RGD1305	similar to expressed sequence AW549877	4	0.024588373	-1.371141701	1	-1	0.051851665	0.808348214	0	0
2219	ENSRNOG0000000025076	RGD1306	similar to KIAA0368	4	0.00197807	-0.919325124	1	-1	0.133430453	0.314315473	0	0
2220	ENSRNOG0000000022745	RGD1308	similar to hypothetical protein FLJ11193	4	0.011632163	-0.721874653	1	-1	0.032478174	0.284928301	0	0
2221	ENSRNOG000000006973	RGD1307	similar to RIKEN cDNA C430008C19	4	0.048444383	-0.915519887	1	-1	0.064052341	0.65672781	0	0
2222	ENSRNOG000000017215	RGD1308	similar to hypothetical protein	4	0.001280601	-0.874777411	1	-1	0.020632163	0.398547593	0	0
2223	ENSRNOG000000017090	RGD1308	similar to RIKEN cDNA 4921524J17	4	0.027540721	-0.836845053	1	-1	0.062000414	0.650152955	0	0
2224	ENSRNOG000000002545	RGD1309	similar to CG4768-PA	4	0.010908351	-1.064335399	1	-1	0.130332184	0.413380453	0	0
2225	ENSRNOG000000038330	RGD1359	similar to protein C33A12.3	4	0.029909248	-0.705006426	1	-1	0.149771533	0.502756005	0	0
2226	ENSRNOG000000032042	RGD1560	similar to RIKEN cDNA 2700081O15	4	0.032594304	-0.802542735	1	-1	0.174998138	-0.142306672	0	0
2227	ENSRNOG0000000051868	RGD1561	RGD1561277	4	0.03853086	-0.657960844	1	-1	0.158110958	0.499798113	0	0
2228	ENSRNOG000000002773	Rgs4	regulator of G-protein signaling 4	4	0.019431074	-1.214230249	1	-1	0.234955451	0.391607223	0	0
2229	ENSRNOG000000008082	Rgs6	regulator of G-protein signaling 6	4	0.024437901	-1.142896752	1	-1	0.455954417	0.032120791	0	0
2230	ENSRNOG000000004093	Rhot1	ras homolog family member T1	4	0.004337908	-0.690334021	1	-1	0.120442176	0.2207299	0	0
2231	ENSRNOG000000016172	Ric1	RIC1 homolog, RAB6A GEF complex partner 1	4	0.017689283	-0.66635736	1	-1	0.008162954	0.472995353	0	0
2232	ENSRNOG000000025145	Rmdn1	regulator of microtubule dynamics 1	4	0.01930129	-1.711651416	1	-1	0.062816771	0.944902385	0	0
2233	ENSRNOG000000008082	Rmdn2	regulator of microtubule dynamics 2	4	0.038845183	-0.58555554	1	-1	0.311413902	0.168502385	0	0
2234	ENSRNOG000000019501	Rmnd1	required for meiotic nuclear division 1 homolog	4	0.014089512	-0.603885139	1	-1	0.058721261	0.429001404	0	0
2235	ENSRNOG000000007272	Rnf103	ring finger protein 103	4	0.019389837	-0.673196481	1	-1	0.193405972	0.33433119	0	0
2236	ENSRNOG000000057832	Rnf125	ring finger protein 125	4	0.046946142	-0.892580116	1	-1	0.168937591	0.402102386	0	0
2237	ENSRNOG0000000055721	Rnf128	ring finger protein 128, E3 ubiquitin protein ligase	4	0.004174471	-0.711138357	1	-1	0.399370112	-0.021537809	0	0
2238	ENSRNOG000000045637	Rnf14	ring finger protein 14	4	0.008770705	-0.975652315	1	-1	0.030348183	0.271095206	0	0
2239	ENSRNOG000000016123	Rnf144b	ring finger protein 144B	4	0.018609889	-0.616394712	1	-1	0.005691745	0.495864987	0	0
2240	ENSRNOG000000013956	Rnf38	ring finger protein 38	4	0.016926419	-0.621387216	1	-1	0.217807806	0.126189401	0	0
2241	ENSRNOG000000017310	Rnpc3	RNA-binding region (RNP1, RRM) containing 3	4	0.031071788	-0.647005743	1	-1	0.222731881	0.482612317	0	0
2242	ENSRNOG000000000406	Ros1	ROS proto-oncogene 1, receptor tyrosine kinase	4	0.008027722	-1.54206637	1	-1	0.109581132	0.111393566	0	0
2243	ENSRNOG000000008807	Rp1	RP1, axonemal microtubule associated	4	0.02043528	-1.214238725	1	-1	0.12108627	0.587622552	0	0
2244	ENSRNOG0000000053405	Rpap3	RNA polymerase II associated protein 3	4	0.018196124	-0.614031361	1	-1	0.104146888	0.350029229	0	0
2245	ENSRNOG000000003013	Rpgr	retinitis pigmentosa GTPase regulator	4	0.023642232	-0.679099229	1	-1	0.134269843	0.392631728	0	0

2246	ENSRNOG00000004362	Rps6ka5	ribosomal protein S6 kinase A5	4	0.008335563	-1.030866386	1	-1	0.052748086	0.467327382	0	0
2247	ENSRNOG000000007240	Rrs1	ribosome biogenesis regulator homolog	4	0.026806358	-0.591491489	1	-1	0.277682023	-0.066693323	0	0
2248	ENSRNOG000000019671	Rsb1	round spermatid basic protein 1	4	0.031221847	-0.806786257	1	-1	0.190498242	0.321007098	0	0
2249	ENSRNOG000000013431	Rsb1l	round spermatid basic protein 1-like	4	0.043878767	-0.9719584	1	-1	0.112188609	0.615684513	0	0
2250	ENSRNOG000000017309	Rsrp1	arginine and serine rich protein 1	4	0.037669402	-0.920358163	1	-1	0.226041721	0.261328611	0	0
2251	ENSRNOG000000017060	Ryr2	ryanodine receptor 2	4	0.007687746	-1.072688169	1	-1	0.148329977	0.328062021	0	0
2252	ENSRNOG000000006645	Ryr3	ryanodine receptor 3	4	0.006085925	-0.624740166	1	-1	0.049472381	-0.338074033	0	0
2253	ENSRNOG000000016432	Samd13	sterile alpha motif domain containing 13	4	0.047682091	-1.401960769	1	-1	0.069272326	0.868962993	0	0
2254	ENSRNOG000000006884	Scaper	S-phase cyclin A-associated protein in the ER	4	0.001925522	-0.698207316	1	-1	0.062516723	0.570770126	0	0
2255	ENSRNOG000000037984	Scopdh	saccharopine dehydrogenase (putative)	4	0.040948624	-0.851821756	1	-1	0.297969106	0.091611627	0	0
2256	ENSRNOG000000005007	Scn3a	sodium voltage-gated channel alpha subunit 3	4	0.017957244	-1.411240362	1	-1	0.313829046	0.173814615	0	0
2257	ENSRNOG000000028699	Sco1	SCO1 cytochrome c oxidase assembly protein	4	0.048685068	-0.580613499	1	-1	0.033143163	0.347163652	0	0
2258	ENSRNOG000000020646	Sdhaf2	succinate dehydrogenase complex assembly factor 2	4	0.015594511	-0.928730289	1	-1	0.036686022	0.459400096	0	0
2259	ENSRNOG000000001773	Senp2	Sumo1/sentrin/SMT3 specific peptidase 2	4	0.013413696	-0.754216504	1	-1	0.114473278	0.417033001	0	0
2260	ENSRNOG000000024336	Senp6	SUMO1/sentrin specific peptidase 6	4	0.043516999	-0.641146865	1	-1	0.141994552	0.365906228	0	0
2261	ENSRNOG000000001616	Senp7	SUMO1/sentrin specific peptidase 7	4	0.048304807	-1.104939701	1	-1	0.069773257	0.745305334	0	0
2262	ENSRNOG000000029360	Serinc1	serine incorporator 1	4	0.036785601	-0.647497375	1	-1	0.077313978	0.776167914	0	0
2263	ENSRNOG000000000302	Sesn1	sestrin 1	4	0.000743811	-0.81864589	1	-1	0.015367285	0.465634888	0	0
2264	ENSRNOG000000016216	Sft2d3	SFT2 domain containing 3	4	0.023608717	-0.730457638	1	-1	0.088742707	0.528627443	0	0
2265	ENSRNOG000000036572	Sfxn4	sideroflexin 4	4	0.002783394	-0.795808786	1	-1	0.43238618	0.044353298	0	0
2266	ENSRNOG000000037871	Sfxn5	sideroflexin 5	4	0.020552376	-0.676221103	1	-1	0.030595269	0.282124347	0	0
2267	ENSRNOG000000002135	Sgob	saroglycan, beta	4	0.006390318	-0.943926278	1	-1	0.020410248	0.350163805	0	0
2268	ENSRNOG000000006761	Sh3gl2	SH3 domain containing GRB2 like 2, endophilin A1	4	0.048134473	-0.860108997	1	-1	0.024391076	0.308492623	0	0
2269	ENSRNOG000000012957	Sh3glb1	SH3 domain -containing GRB2-like endophilin B1	4	0.005148197	-1.002090523	1	-1	0.066525895	0.51338229	0	0
2270	ENSRNOG000000004322	Sh3kbp1	SH3 domain-containing kinase-binding protein 1	4	0.034152285	-0.926419635	1	-1	0.042988002	0.539090229	0	0
2271	ENSRNOG000000002959	Shroom4	shroom family member 4	4	0.008389352	-1.094230031	1	-1	0.008075581	0.517315635	0	0
2272	ENSRNOG000000015143	Siah1	siah E3 ubiquitin protein ligase 1	4	0.011407903	-0.632632546	1	-1	0.332038963	0.05158013	0	0
2273	ENSRNOG000000007250	Six4	SIX homeobox 4	4	0.002733191	-0.959618199	1	-1	0.023442383	-0.175716211	0	0
2274	ENSRNOG000000002271	Slain2	SLAIN motif family, member 2	4	0.028223295	-0.742033494	1	-1	0.070949521	0.215949932	0	0
2275	ENSRNOG000000015971	Slc12a2	solute carrier family 12 member 2	4	0.007170678	-1.306328312	1	-1	0.056981587	0.609310612	0	0
2276	ENSRNOG000000002839	Slc19a2	solute carrier family 19 member 2	4	0.023889111	-0.892911549	1	-1	0.209494656	0.141843105	0	0
2277	ENSRNOG000000014816	Slc1a1	solute carrier family 1 member 1	4	0.018155851	-1.241933271	1	-1	0.059132129	-0.360438594	0	0
2278	ENSRNOG000000017210	Slc22a23	solute carrier family 22, member 23	4	0.045084083	-1.227057416	1	-1	0.394832356	0.09065692	0	0
2279	ENSRNOG000000008432	Slc22a5	solute carrier family 22 member 5	4	0.009292601	-0.676797029	1	-1	0.069617268	-0.176398322	0	0
2280	ENSRNOG000000020288	Slc25a20	solute carrier family 25 member 20	4	0.045976967	-0.813594108	1	-1	0.089998414	0.376894401	0	0
2281	ENSRNOG000000008931	Slc25a21	solute carrier family 25 member 21	4	0.018050479	-1.638867409	1	-1	0.056498793	0.706228276	0	0
2282	ENSRNOG000000008289	Slc25a3	solute carrier family 25 member 3	4	0.032263154	-0.885835339	1	-1	0.056616371	0.40998717	0	0
2283	ENSRNOG000000013802	Slc25a36	solute carrier family 25 member 36	4	0.015667609	-0.838493395	1	-1	0.017353631	0.560990125	0	0
2284	ENSRNOG000000017091	Slc25a46	solute carrier family 25, member 46	4	0.001594649	-1.12904383	1	-1	0.045494725	0.46540571	0	0
2285	ENSRNOG000000006878	Slc26a3	solute carrier family 26 member 3	4	0.005629957	-1.608649143	1	-1	0.145841804	1.464000111	0	0
2286	ENSRNOG000000002246	Slc30a9	solute carrier family 30 member 9	4	0.000698297	-0.921303387	1	-1	0.036862368	0.498720904	0	0
2287	ENSRNOG000000022967	Slc35d1	solute carrier family 35 member D1	4	0.043491208	-0.602260456	1	-1	0.248150817	0.091706809	0	0
2288	ENSRNOG000000000879	Slc9a6	solute carrier family 9 member A6	4	0.004964623	-0.846722976	1	-1	0.056416385	0.496840308	0	0
2289	ENSRNOG000000008966	Slc5a1	solute carrier organic anion transporter family, member 5	4	0.009268878	-0.737849674	1	-1	0.166472519	0.242064716	0	0
2290	ENSRNOG000000011307	Slmap	sarcolemma associated protein	4	0.007712158	-0.808822386	1	-1	0.090483277	0.40494708	0	0

2291	ENSRNOG00000024930	Smim19	small integral membrane protein 19	4	0.012477484	-0.616696417	1	-1	0.017647888	0.508151079	0	0
2292	ENSRNOG00000018254	Sncalp	synuclein, alpha interacting protein	4	0.048784636	-1.244288868	1	-1	0.061776774	0.678056774	0	0
2293	ENSRNOG00000058739	Snn	stannin	4	0.044039308	-0.715488545	1	-1	0.188877939	0.249942008	0	0
2294	ENSRNOG00000004050	Snrk	SNF related kinase	4	0.0123477	-0.832000256	1	-1	0.140818978	0.339928374	0	0
2295	ENSRNOG00000004821	Sntb1	syntrophin, beta 1	4	0.003754088	-1.255652165	1	-1	0.090842438	0.140204573	0	0
2296	ENSRNOG00000011348	Snx14	sorting nexin 14	4	0.029148059	-0.772482979	1	-1	0.096894421	0.583308946	0	0
2297	ENSRNOG00000038212	Socs6	suppressor of cytokine signaling 6	4	0.013544997	-0.949993906	1	-1	0.002006344	0.398384105	0	0
2298	ENSRNOG00000019048	Sod2	superoxide dismutase 2	4	0.025683608	-0.737073787	1	-1	0.032292532	0.407308965	0	0
2299	ENSRNOG00000015658	Sorbs1	sorbin and SH3 domain containing 1	4	0.008004689	-0.908485403	1	-1	0.171591883	0.27342853	0	0
2300	ENSRNOG00000007106	Sos1	SOS Ras/Rac guanine nucleotide exchange factor 1	4	0.021385422	-0.634013636	1	-1	0.442718433	0.012563556	0	0
2301	ENSRNOG00000004826	Sos2	SOS Ras/Rho guanine nucleotide exchange factor 2	4	0.027381422	-0.919904282	1	-1	0.194483139	0.153437581	0	0
2302	ENSRNOG00000012049	Sox7	SRY box 7	4	0.026910006	-1.28551041	1	-1	0.246479346	-0.172711015	0	0
2303	ENSRNOG000000002807	Sox9	SRY box 9	4	0.028095442	-0.851654162	1	-1	0.071913861	0.41350032	0	0
2304	ENSRNOG00000014084	Sp1	Sp1 transcription factor	4	0.047054272	-0.628616605	1	-1	0.103485139	0.408632788	0	0
2305	ENSRNOG00000005472	Sp4	Sp4 transcription factor	4	0.034844769	-1.288406286	1	-1	0.06861582	0.842297596	0	0
2306	ENSRNOG00000010934	Spa17	sperm autoantigenic protein 17	4	0.01773988	-0.629227432	1	-1	0.106738294	0.453287703	0	0
2307	ENSRNOG00000010078	Spag1	sperm associated antigen 1	4	0.030535825	-1.40489161	1	-1	0.269858975	-0.099088882	0	0
2308	ENSRNOG00000002749	Spag9	sperm associated antigen 9	4	0.022537342	-0.715749681	1	-1	0.107156127	0.343253242	0	0
2309	ENSRNOG00000013707	Spat13	spermatogenesis associated 13	4	0.000389904	-0.857935846	1	-1	0.01535832	0.361968875	0	0
2310	ENSRNOG00000017462	Spat5	spermatogenesis associated 5	4	0.001329288	-0.679130902	1	-1	0.093789256	0.464839081	0	0
2311	ENSRNOG00000003955	Spat7	spermatogenesis associated 7	4	0.039121302	-0.838379578	1	-1	0.052151783	0.543358706	0	0
2312	ENSRNOG00000004686	Spop	speckle type BTB/POZ protein	4	0.021611337	-0.730889656	1	-1	0.024062892	0.526970638	0	0
2313	ENSRNOG00000010058	Spry2	sprouty RTK signaling antagonist 2	4	0.015080477	-0.888967194	1	-1	0.044073305	0.496123641	0	0
2314	ENSRNOG00000003211	Srp9	signal recognition particle 9	4	0.001198262	-0.752810113	1	-1	0.09608358	0.629119108	0	0
2315	ENSRNOG00000014285	Ssh2	slingshot protein phosphatase 2	4	0.034078064	-0.652803022	1	-1	0.333992821	-0.058031502	0	0
2316	ENSRNOG00000001807	Sspn	sarcomerespan	4	0.009340735	-1.158423117	1	-1	0.030797186	0.411505741	0	0
2317	ENSRNOG00000001653	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	4	0.016885594	-1.041238036	1	-1	0.030128336	0.545352862	0	0
2318	ENSRNOG00000013479	Stard7	StAR-related lipid transfer domain containing 7	4	0.0040982	-0.889160261	1	-1	0.179064547	0.145874768	0	0
2319	ENSRNOG00000010050	Stard9	StAR-related lipid transfer domain containing 9	4	0.041366113	-0.983096098	1	-1	0.107377146	0.35416225	0	0
2320	ENSRNOG000000002956	Stim2	stromal interaction molecule 2	4	0.02202386	-0.587102031	1	-1	0.114503896	0.287798528	0	0
2321	ENSRNOG000000024808	Stk39	serine threonine kinase 39	4	0.029408937	-0.941844116	1	-1	0.044778774	0.535616853	0	0
2322	ENSRNOG00000010728	Stradb	STE20-related kinase adaptor beta	4	0.014026067	-0.846952082	1	-1	0.074772292	0.373140591	0	0
2323	ENSRNOG000000060335	Strn3	striatin 3	4	0.030333632	-0.709430482	1	-1	0.139441625	0.36697898	0	0
2324	ENSRNOG000000020392	Stxbp3	syntactin binding protein 3	4	0.000400938	-0.647981167	1	-1	0.103681539	0.502395122	0	0
2325	ENSRNOG000000050563	Sub1	SUB1 homolog, transcriptional regulator	4	0.013292325	-0.715518413	1	-1	0.074410888	0.796590369	0	0
2326	ENSRNOG00000005686	Suol2	succinate-CoA ligase, GDP-forming, beta subunit	4	0.010518585	-0.825982872	1	-1	0.018467554	0.513504218	0	0
2327	ENSRNOG000000026542	Suco	SUN domain containing ossification factor	4	0.046072409	-0.705431003	1	-1	0.205931108	0.396135083	0	0
2328	ENSRNOG000000008157	Syn2	synapsin II	4	0.048542997	-0.631473776	1	-1	0.010203227	-0.160090167	0	0
2329	ENSRNOG00000017114	Synj2	synaptojanin 2	4	0.030659265	-0.75880823	1	-1	0.48977305	-0.00841523	0	0
2330	ENSRNOG000000046139	Syt14	synaptotagmin 14	4	0.029696848	-1.503208731	1	-1	0.057194952	0.502018329	0	0
2331	ENSRNOG000000026023	Taf4b	TATA-box binding protein associated factor 4b	4	0.039997104	-0.641687513	1	-1	0.086099235	0.202709764	0	0
2332	ENSRNOG000000061102	Taf9b	TATA-box binding protein associated factor 9b	4	0.000926419	-0.975629431	1	-1	0.062656162	0.578807284	0	0
2333	ENSRNOG000000024460	Tarsl2	threonyl-tRNA synthetase-like 2	4	0.023131232	-1.04755793	1	-1	0.006296462	0.45884712	0	0
2334	ENSRNOG000000047198	Tatdn1	TatD DNase domain containing 1	4	0.040614578	-0.645433598	1	-1	0.101250672	0.635390729	0	0
2335	ENSRNOG00000003003	Tbc1d19	TBC1 domain family, member 19	4	0.008935522	-0.815180188	1	-1	0.214658851	0.317094203	0	0

2336	ENSRNOG00000009431	Tbc1d4	TBC1 domain family, member 4	4	0.008118475	-0.976931395	1	-1	0.027378181	0.216787504	0	0
2337	ENSRNOG000000011218	Tb11xr1	transducin (beta)-like 1 X-linked receptor 1	4	0.007793945	-0.615424228	1	-1	0.153902421	0.338740293	0	0
2338	ENSRNOG000000002979	Tbx19	T-box 19	4	0.004814427	-0.842433262	1	-1	0.126069512	-0.698555739	0	0
2339	ENSRNOG000000004085	Tcain	T cell activation inhibitor, mitochondrial	4	0.00923288	-0.889272381	1	-1	0.043874698	0.398995214	0	0
2340	ENSRNOG000000007587	Top11l2	t-complex 11 like 2	4	0.018581615	-1.109551624	1	-1	0.014624095	0.668801947	0	0
2341	ENSRNOG000000015488	Tead1	TEA domain transcription factor 1	4	0.037233708	-0.983366099	1	-1	0.039273638	0.666677668	0	0
2342	ENSRNOG000000001912	Teor1	trans-2,3-enoyl-CoA reductase-like	4	0.017347217	-1.804763308	1	-1	0.068149024	0.930367351	0	0
2343	ENSRNOG000000010712	Terf2ip	TERF2 interacting protein	4	0.016833874	-0.687684754	1	-1	0.078928419	0.441566255	0	0
2344	ENSRNOG000000023579	Tet2	tet methylcytosine dioxygenase 2	4	0.009009723	-0.867273976	1	-1	0.023296118	0.356879509	0	0
2345	ENSRNOG000000000613	Tfam	transcription factor A, mitochondrial	4	0.00306737	-0.698939729	1	-1	0.017313151	0.232880089	0	0
2346	ENSRNOG000000011241	Tfdp2	transcription factor Dp-2	4	0.00994428	-1.079594288	1	-1	0.066853527	0.684487229	0	0
2347	ENSRNOG000000001766	Tfrc	transferrin receptor	4	0.006674988	-1.477885017	1	-1	0.323889904	-0.230197661	0	0
2348	ENSRNOG000000020829	Them4	thioesterase superfamily member 4	4	0.025497276	-0.921549039	1	-1	0.029964692	0.449747906	0	0
2349	ENSRNOG0000000051816	Tigar	TP53 induced glycolysis regulatory phosphatase	4	0.045333977	-0.768361909	1	-1	0.056630784	0.439241478	0	0
2350	ENSRNOG000000015142	Timm21	translocase of inner mitochondrial membrane 21	4	0.011164471	-0.784991094	1	-1	0.056016757	0.52074661	0	0
2351	ENSRNOG000000009255	Timm29	translocase of inner mitochondrial membrane 29	4	0.002295152	-0.80548495	1	-1	0.093878643	0.213327163	0	0
2352	ENSRNOG000000007955	Timpe4	TIMP metalloproteinase inhibitor 4	4	0.03006303	-1.575587876	1	-1	0.301298531	0.379623565	0	0
2353	ENSRNOG000000003048	Tipri	TOR signaling pathway regulator	4	0.010159024	-0.813318858	1	-1	0.057308324	0.51962447	0	0
2354	ENSRNOG000000011077	Tjp1	tight junction protein 1	4	0.002766982	-1.036859184	1	-1	0.022961796	0.397670383	0	0
2355	ENSRNOG000000006572	Tlk1	tousled-like kinase 1	4	0.036438177	-0.722898585	1	-1	0.377861389	0.053887188	0	0
2356	ENSRNOG000000007527	Tm2d1	TM2 domain containing 1	4	0.007987449	-1.003832015	1	-1	0.066569202	0.801422498	0	0
2357	ENSRNOG000000007713	Tmcc3	transmembrane and coiled-coil domain family 3	4	0.004709882	-0.730670806	1	-1	0.020837391	0.508431871	0	0
2358	ENSRNOG000000032414	Tmem161	transmembrane protein 161B	4	0.018242466	-1.032927618	1	-1	0.111274119	0.603340415	0	0
2359	ENSRNOG000000028945	Tmem182	transmembrane protein 182	4	0.004388042	-1.136044686	1	-1	0.020888559	0.376808924	0	0
2360	ENSRNOG000000037435	Tmem196	transmembrane protein 196	4	0.007089856	-1.484317018	1	-1	0.03271133	0.548204459	0	0
2361	ENSRNOG000000009896	Tmem199	transmembrane protein 199	4	0.001610648	-0.657708941	1	-1	0.005608788	0.277672672	0	0
2362	ENSRNOG000000008757	Tmem218	transmembrane protein 218	4	0.034337356	-0.745965187	1	-1	0.009739052	0.261975646	0	0
2363	ENSRNOG000000010752	Tmem41b	transmembrane protein 41B	4	0.012989173	-0.974763509	1	-1	0.213303703	0.29765664	0	0
2364	ENSRNOG000000030418	Tmem47	transmembrane protein 47	4	0.03016785	-0.708355206	1	-1	0.158506586	0.461598727	0	0
2365	ENSRNOG000000008934	Tmem85	transmembrane protein 85	4	0.005957106	-0.980964395	1	-1	0.004643818	0.45743269	0	0
2366	ENSRNOG000000029152	Tmem89	transmembrane protein 89	4	0.008893042	-0.832196907	1	-1	0.070297773	0.684212524	0	0
2367	ENSRNOG000000005308	Tmx2	thioredoxin-related transmembrane protein 2	4	0.004031308	-0.606838256	1	-1	0.21539811	0.060416029	0	0
2368	ENSRNOG000000024852	Tmx4	thioredoxin-related transmembrane protein 4	4	0.004601614	-0.871713687	1	-1	0.195812013	0.171749008	0	0
2369	ENSRNOG000000026136	Tnfaip8	TNF alpha induced protein 8	4	0.008308944	-0.806093962	1	-1	0.023444866	0.350060763	0	0
2370	ENSRNOG000000012422	Tnik	TRAF2 and NCK interacting kinase	4	0.024697193	-1.073345902	1	-1	0.227695745	-0.152850578	0	0
2371	ENSRNOG000000002828	Tob1	transducer of ErbB-2.1	4	0.006042204	-1.121040522	1	-1	0.490547755	-0.00172141	0	0
2372	ENSRNOG0000000062108	Tomm5	translocase of outer mitochondrial membrane 5	4	0.003393697	-0.63201632	1	-1	0.146088753	0.541557723	0	0
2373	ENSRNOG000000001640	Tomm70	translocase of outer mitochondrial membrane 70	4	0.031568995	-0.67880231	1	-1	0.124516654	0.388380928	0	0
2374	ENSRNOG000000018225	Top3inp2	tumor protein p53 inducible nuclear protein 2	4	0.033436453	-0.800660256	1	-1	0.149853114	0.231327978	0	0
2375	ENSRNOG000000010881	Trak2	trafficking kinesin protein 2	4	0.018708089	-0.647534887	1	-1	0.244180332	0.08884205	0	0
2376	ENSRNOG000000005278	Trhde	thyrotropin-releasing hormone degrading enzyme	4	0.031073443	-0.962711685	1	-1	0.150243363	0.214596895	0	0
2377	ENSRNOG000000026941	Tril	TLR4 interactor with leucine-rich repeats	4	0.018190056	-0.753199274	1	-1	0.103298876	0.326843867	0	0
2378	ENSRNOG000000012354	Trim23	tripartite motif-containing 23	4	0.026962968	-0.82548398	1	-1	0.092948417	0.671087505	0	0
2379	ENSRNOG000000013251	Trim24	tripartite motif-containing 24	4	0.025585822	-0.688047828	1	-1	0.392870078	0.027685684	0	0
2380	ENSRNOG000000006432	Trmt1	tRNA nucleotidyl transferase 1	4	0.002678022	-1.000577969	1	-1	0.063794911	0.680238847	0	0

2381	ENSRNOG00000011133	Trpc4	transient receptor potential cation channel, subfamily C,	4	0.01230522	-1.091887021	1	-1	0.150783877	0.176261946	0	0
2382	ENSRNOG000000059016	Tspan12	tetraspanin 12	4	0.015799324	-1.017502613	1	-1	0.055957227	0.552622508	0	0
2383	ENSRNOG00000005046	Tspan13	tetraspanin 13	4	0.034076409	-1.202080368	1	-1	0.031230053	0.503369512	0	0
2384	ENSRNOG000000023338	Tspan2	tetraspanin 2	4	0.047698641	-1.059418855	1	-1	0.090570995	0.558962892	0	0
2385	ENSRNOG00000004411	Tspan8	tetraspanin 8	4	0.022764085	-1.445762563	1	-1	0.105753879	1.304554535	0	0
2386	ENSRNOG00000000549	Tsyp1	TSPY-like 1	4	0.015574926	-0.812570057	1	-1	0.017387008	0.421396621	0	0
2387	ENSRNOG00000011261	Ttc14	tetratricopeptide repeat domain 14	4	0.030557617	-0.88355231	1	-1	0.248039446	0.319520338	0	0
2388	ENSRNOG000000059480	Ttc30b	tetratricopeptide repeat domain 30B	4	0.002261912	-0.798824045	1	-1	0.060295773	0.597426783	0	0
2389	ENSRNOG000000049088	Ttc32	tetratricopeptide repeat domain 32	4	0.014896386	-0.729005846	1	-1	0.055987794	0.842480666	0	0
2390	ENSRNOG000000050949	Ttc39c	tetratricopeptide repeat domain 39C	4	0.012212951	-0.826877133	1	-1	0.088451141	0.223292949	0	0
2391	ENSRNOG000000025925	Txx	TXK tyrosine kinase	4	0.036901731	-0.866282626	1	-1	0.077605889	0.332154335	0	0
2392	ENSRNOG000000060021	Txnb	taxilin beta	4	0.025360182	-1.193661547	1	-1	0.045999448	0.575569273	0	0
2393	ENSRNOG00000018818	Txn1	thioredoxin-like 1	4	0.001656162	-0.81433449	1	-1	0.242530653	0.184339568	0	0
2394	ENSRNOG00000006221	Uba3	ubiquitin-like modifier activating enzyme 3	4	0.042434729	-0.614797352	1	-1	0.128493483	0.500839106	0	0
2395	ENSRNOG00000000611	Ube2d1	ubiquitin-conjugating enzyme E2D 1	4	0.039987587	-1.596406615	1	-1	0.079504172	0.7267599	0	0
2396	ENSRNOG00000013741	Ube2d3	ubiquitin-conjugating enzyme E2D 3	4	0.036036687	-0.748707405	1	-1	0.142980829	0.391256475	0	0
2397	ENSRNOG000000004544	Ube2e3	ubiquitin-conjugating enzyme E2E 3	4	0.004875802	-0.817292592	1	-1	0.072511137	0.54047751	0	0
2398	ENSRNOG00000010041	Ube2g1	ubiquitin-conjugating enzyme E2G 1	4	0.010034067	-1.107342806	1	-1	0.101372526	0.546513152	0	0
2399	ENSRNOG00000010727	Ube2r2	ubiquitin-conjugating enzyme E2R 2	4	0.002565202	-0.691257092	1	-1	0.099193228	0.206189902	0	0
2400	ENSRNOG00000015734	Ube3a	ubiquitin protein ligase E3A	4	0.032931108	-0.957369412	1	-1	0.177038549	0.480369971	0	0
2401	ENSRNOG000000026833	Ube4a	ubiquitination factor E4A	4	0.028702848	-0.645346577	1	-1	0.215844631	0.192242146	0	0
2402	ENSRNOG00000004477	Ubclp1	ubiquitin-like domain containing CTD phosphatase 1	4	0.019917109	-0.703683997	1	-1	0.09021502	0.541472032	0	0
2403	ENSRNOG00000015813	Ubr2	ubiquitin protein ligase E3 component n-recogin 2	4	0.032830701	-0.637888742	1	-1	0.289212537	0.119836228	0	0
2404	ENSRNOG000000047394	Ufd1	ubiquitin recognition factor in ER associated degradation	4	0.016583132	-0.791595529	1	-1	0.105463072	0.214485151	0	0
2405	ENSRNOG000000007831	Ufl1	Ufm1-specific ligase 1	4	0.018052134	-0.700807721	1	-1	0.192122681	0.307782636	0	0
2406	ENSRNOG000000002763	Ulk2	unc-51 like autophagy activating kinase 2	4	0.032023033	-0.676958771	1	-1	0.125304462	0.359088405	0	0
2407	ENSRNOG000000024967	Uqorb	ubiquinol-cytochrome c reductase binding protein	4	0.01627405	-1.119994733	1	-1	0.060174264	0.860273454	0	0
2408	ENSRNOG00000018281	Uqorfs1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur po	4	0.022367837	-1.15947884	1	-1	0.033989035	0.534091074	0	0
2409	ENSRNOG000000030639	Usp13	ubiquitin specific peptidase 13	4	0.034900352	-0.862147092	1	-1	0.349093787	0.0760579	0	0
2410	ENSRNOG00000008663	Usp2	ubiquitin specific peptidase 2	4	0.040999517	-0.842945313	1	-1	0.499979519	0.000189646	0	0
2411	ENSRNOG00000005802	Usp24	ubiquitin specific peptidase 24	4	0.026662575	-0.90112207	1	-1	0.145793531	0.202381258	0	0
2412	ENSRNOG00000011294	Usp33	ubiquitin specific peptidase 33	4	0.019459486	-1.110486058	1	-1	0.101957885	0.463915787	0	0
2413	ENSRNOG00000018395	Usp40	ubiquitin specific peptidase 40	4	0.010467002	-0.657465385	1	-1	0.13697145	-0.15954004	0	0
2414	ENSRNOG00000008688	Usp45	ubiquitin specific peptidase 45	4	0.022932212	-0.782265428	1	-1	0.104748293	0.503137052	0	0
2415	ENSRNOG000000026754	Usp47	ubiquitin specific peptidase 47	4	0.02945121	-0.73905062	1	-1	0.113220812	0.253570643	0	0
2416	ENSRNOG00000014860	Usp53	ubiquitin specific peptidase 53	4	0.049548514	-0.682607051	1	-1	0.085425833	0.435766898	0	0
2417	ENSRNOG000000025496	Usp7	ubiquitin specific peptidase 7	4	0.035058961	-0.716338522	1	-1	0.159262189	0.223196913	0	0
2418	ENSRNOG00000011058	Utrn	utrophin	4	0.0025441	-0.920841088	1	-1	0.003961313	0.474441656	0	0
2419	ENSRNOG00000003071	Vamp4	vesicle-associated membrane protein 4	4	0.013718226	-0.976476321	1	-1	0.101970554	0.283428271	0	0
2420	ENSRNOG00000014765	Vapa	VAMP associated protein A	4	0.018378595	-0.582287246	1	-1	0.197133784	0.236889343	0	0
2421	ENSRNOG00000013505	Vdac2	voltage-dependent anion channel 2	4	0.002781739	-0.887080789	1	-1	0.045820219	0.377890424	0	0
2422	ENSRNOG00000019277	Vdac3	voltage-dependent anion channel 3	4	0.002095442	-1.014246177	1	-1	0.054580443	0.619499352	0	0
2423	ENSRNOG00000011416	Vegfc	vascular endothelial growth factor C	4	0.025098683	-0.837892003	1	-1	0.087946555	0.778980002	0	0
2424	ENSRNOG00000012427	Veph1	ventricular zone expressed PH domain-containing 1	4	0.002742156	-1.165593329	1	-1	0.016418247	0.429957374	0	0
2425	ENSRNOG00000009819	Vezf1	vascular endothelial zinc finger 1	4	0.009165989	-0.871484557	1	-1	0.011025998	0.475585108	0	0

2426	ENSRNOG000000027491	Vldlr	very low density lipoprotein receptor	4	0.008829874	-0.835323795	1	-1	0.099913592	0.463371076	0	0
2427	ENSRNOG000000018443	Vps13d	vacuolar protein sorting 13 homolog D	4	0.038896628	-0.716233634	1	-1	0.268792842	0.137946292	0	0
2428	ENSRNOG000000051179	Vps25	vacuolar protein sorting 25 homolog	4	0.000772361	-1.081578026	1	-1	0.056265706	0.15098461	0	0
2429	ENSRNOG000000047235	Vps28b	VPS28 retromer complex component B	4	0.012158196	-0.680410476	1	-1	0.089665058	0.154138791	0	0
2430	ENSRNOG000000008975	Wasl	Wiskott-Aldrich syndrome-like	4	0.006557065	-0.980278922	1	-1	0.083009103	0.435018373	0	0
2431	ENSRNOG000000018834	Wdr37	WD repeat domain 37	4	0.019625267	-0.790812609	1	-1	0.200740914	0.15069825	0	0
2432	ENSRNOG000000010017	Wee1	WEE1 G2 checkpoint kinase	4	0.01959258	-1.101724328	1	-1	0.044603958	0.545624454	0	0
2433	ENSRNOG000000015618	Wnt5a	Wnt family member 5A	4	0.016518309	-1.496041994	1	-1	0.213040273	0.208651732	0	0
2434	ENSRNOG000000013074	Wt1	Wilms tumor 1	4	0.009121578	-1.042698071	1	-1	0.084248121	0.86545799	0	0
2435	ENSRNOG000000008328	Wwp1	WW domain containing E3 ubiquitin protein ligase 1	4	0.023415075	-0.875661011	1	-1	0.061617337	0.456189719	0	0
2436	ENSRNOG000000003749	Xk	X-linked Kx blood group	4	0.026304669	-0.984945153	1	-1	0.367507	0.061215545	0	0
2437	ENSRNOG000000009576	Xpa	XPA, DNA damage recognition and repair factor	4	0.009632163	-0.685336102	1	-1	0.051836494	0.886011053	0	0
2438	ENSRNOG000000013438	Yae1d1	Yae1 domain containing 1	4	0.006894697	-0.895634975	1	-1	0.064909179	0.705444278	0	0
2439	ENSRNOG000000004773	Yaf2	YY1 associated factor 2	4	0.015879181	-0.772742262	1	-1	0.165468106	0.354701429	0	0
2440	ENSRNOG000000025252	Yars2	tyrosyl-tRNA synthetase 2	4	0.022484932	-0.7400561	1	-1	0.110343425	0.162844334	0	0
2441	ENSRNOG000000032902	Ybox1-ps3	Y box protein 1 related, pseudogene 3	4	0.007148197	-0.94537679	1	-1	0.118806717	0.671233319	0	0
2442	ENSRNOG000000017117	Ybox2	Y box binding protein 2	4	0.00146845	-1.042359449	1	-1	0.168637818	-0.381987412	0	0
2443	ENSRNOG000000005689	Yeats4	YEATS domain containing 4	4	0.010070616	-0.872790852	1	-1	0.056434522	0.05601694	0	0
2444	ENSRNOG000000005610	Yipf4	Yip1 domain family, member 4	4	0.03682677	-0.797694653	1	-1	0.170470864	0.530369022	0	0
2445	ENSRNOG000000001996	Ythdc1	YTH domain containing 1	4	0.049112337	-0.818074866	1	-1	0.2078527	0.209814077	0	0
2446	ENSRNOG000000006441	Zbtb25	zinc finger and BTB domain containing 25	4	0.046877457	-0.927945825	1	-1	0.248780636	0.217718164	0	0
2447	ENSRNOG000000005578	Zbtb44	zinc finger and BTB domain containing 44	4	0.004384387	-0.682289761	1	-1	0.081003241	0.374507527	0	0
2448	ENSRNOG000000005256	Zc3h15	zinc finger CCHC-type containing 15	4	0.045400041	-0.71119855	1	-1	0.110738777	0.39310399	0	0
2449	ENSRNOG000000052062	Zc3h11	zinc finger CCHC-type containing 11	4	0.034861182	-0.582317413	1	-1	0.144252465	0.444297916	0	0
2450	ENSRNOG000000029064	Zc3h4	zinc finger CCHC-type containing 4	4	0.002007999	-0.764688258	1	-1	0.166180539	0.24176847	0	0
2451	ENSRNOG000000004996	Zc3h1	zinc finger CCHC-type and RNA binding motif containing	4	0.007928281	-0.949265244	1	-1	0.014105648	0.419276753	0	0
2452	ENSRNOG000000022686	Zdhc2	zinc finger, DHHC-type containing 2	4	0.024176815	-1.002751475	1	-1	0.057991311	0.63647256	0	0
2453	ENSRNOG000000018107	Zfand5	zinc finger AN1-type containing 5	4	0.008434315	-1.205810535	1	-1	0.097543273	0.42742701	0	0
2454	ENSRNOG000000013506	Zfand6	zinc finger AN1-type containing 6	4	0.004015585	-0.784786275	1	-1	0.076792428	0.520497836	0	0
2455	ENSRNOG000000031328	Zfp110	zinc finger protein 110	4	0.006099993	-0.742761819	1	-1	0.064169092	0.578956656	0	0
2456	ENSRNOG000000016417	Zfp136	zinc finger protein 136	4	0.011658368	-0.681640995	1	-1	0.073993862	0.888085272	0	0
2457	ENSRNOG000000024056	Zfp17	zinc finger protein 585B	4	0.026993862	-1.214343442	1	-1	0.13425412	0.515615831	0	0
2458	ENSRNOG000000031031	Zfp292	zinc finger protein 292	4	0.030818978	-0.947130502	1	-1	0.126791739	0.674521155	0	0
2459	ENSRNOG000000018741	Zfp318	zinc finger protein 318	4	0.013549824	-0.712160275	1	-1	0.04540742	0.287306496	0	0
2460	ENSRNOG000000019376	Zfp329	zinc finger protein 329	4	0.048471692	-0.608251156	1	-1	0.117445487	0.640740676	0	0
2461	ENSRNOG000000048101	Zfp397	zinc finger protein 397	4	0.020452521	-0.756118863	1	-1	0.14373988	0.508158294	0	0
2462	ENSRNOG000000013379	Zfp422	zinc finger protein 422	4	0.029430246	-0.648879419	1	-1	0.011615337	0.249771328	0	0
2463	ENSRNOG000000012718	Zfp451	zinc finger protein 451	4	0.020074891	-0.6821245	1	-1	0.088076684	0.257648145	0	0
2464	ENSRNOG000000017986	Zfp458	zinc finger protein 458	4	0.000291014	-0.611251359	1	-1	0.091279222	0.824058066	0	0
2465	ENSRNOG000000048394	Zfp560	zinc finger protein 560	4	0.028329219	-0.902790767	1	-1	0.198441142	0.385867291	0	0
2466	ENSRNOG000000030273	Zfp563	zinc finger protein 563	4	0.044166885	-0.606029742	1	-1	0.054849459	0.560900299	0	0
2467	ENSRNOG000000007576	Zfp597	zinc finger protein 597	4	0.013876146	-0.746707722	1	-1	0.161471419	0.052658832	0	0
2468	ENSRNOG000000019127	Zfp606	zinc finger protein 606	4	0.045801393	-1.002138596	1	-1	0.128009103	0.720521271	0	0
2469	ENSRNOG000000018971	Zfp612	zinc finger protein 612	4	0.006241639	-1.248507288	1	-1	0.010090683	0.478531593	0	0
2470	ENSRNOG000000043053	Zfp639	zinc finger protein 639	4	0.013271912	-0.603993838	1	-1	0.130341287	0.567423471	0	0

2471	ENSRNOG00000017001	Zfp852	zinc finger protein 852	4	0.040985725	-0.875484749	1	-1	0.079289084	0.372555512	0	0
2472	ENSRNOG00000033908	Zfp867	zinc finger protein 867	4	0.018314323	-1.084917273	1	-1	0.067898835	0.757152217	0	0
2473	ENSRNOG00000002713	Zfp872	zinc finger protein 872	4	0.005529888	-0.828112723	1	-1	0.173134542	-0.07889311	0	0
2474	ENSRNOG000000001317	Zfp88	zinc finger protein 88	4	0.029151507	-0.864449703	1	-1	0.107839528	0.834786475	0	0
2475	ENSRNOG00000018877	Zfp889	zinc finger protein 889	4	0.015734777	-0.785214705	1	-1	0.336246259	-0.119335615	0	0
2476	ENSRNOG00000043037	Zfp770	zinc finger protein 770	4	0.0219429	-1.021078039	1	-1	0.085432729	0.981053773	0	0
2477	ENSRNOG00000008925	Zfp788	zinc finger protein 788	4	0.032422178	-0.728857013	1	-1	0.157093028	0.46490832	0	0
2478	ENSRNOG000000028919	Zfp888	zinc finger protein 888	4	0.038954555	-0.788150811	1	-1	0.1530942	0.468142201	0	0
2479	ENSRNOG00000030517	Zfp879	zinc finger protein 879	4	0.017256485	-0.78849491	1	-1	0.148095924	0.474676342	0	0
2480	ENSRNOG00000012524	Zfp91	zinc finger protein 91	4	0.008806099	-0.978834748	1	-1	0.052479898	0.536884537	0	0
2481	ENSRNOG00000048577	Zfp955a	zinc finger protein 955A	4	5.81E-05	-1.182553221	1	-1	0.086154058	0.740895372	0	0
2482	ENSRNOG00000030410	Zfp958	zinc finger protein 958	4	0.026589339	-1.047514835	1	-1	0.17154679	-0.33327484	0	0
2483	ENSRNOG000000027183	Zfyve9	zinc finger FYVE-type containing 9	4	0.032242466	-0.80230521	1	-1	0.07400451	0.276631632	0	0
2484	ENSRNOG00000015071	Zim1	zinc finger, imprinted 1	4	0.00684387	-1.415027077	1	-1	0.007151921	0.442865428	0	0
2485	ENSRNOG00000055000	Zkscan3	zinc finger with KRAB and SCAN domains 3	4	0.006247707	-1.019259451	1	-1	0.048327288	0.195539767	0	0
2486	ENSRNOG00000004104	Zkscan7	zinc finger with KRAB and SCAN domains 7	4	0.008349789	-1.217232787	1	-1	0.348730708	0.023520763	0	0
2487	ENSRNOG00000053635	Zkscan8	zinc finger with KRAB and SCAN domains 8	4	0.005561134	-1.044986454	1	-1	0.118699607	0.52913389	0	0
2488	ENSRNOG00000008734	Zmym2	zinc finger MYM-type containing 2	4	0.033792014	-1.030274245	1	-1	0.087831184	0.731565979	0	0
2489	ENSRNOG00000013885	Zmym6	zinc finger MYM-type containing 6	4	0.023526515	-0.811029095	1	-1	0.211775395	0.24325587	0	0
2490	ENSRNOG00000014870	Zmynd11	zinc finger, MYND-type containing 11	4	0.020955382	-0.834021881	1	-1	0.061083787	0.206950092	0	0
2491	ENSRNOG000000029678	Znf354b	zinc finger protein 354B	4	0.009577684	-0.663818677	1	-1	0.192087787	0.46631446	0	0
2492	ENSRNOG00000030049	Znht6	zinc finger, HIT-type containing 6	4	0.005619888	-0.698297419	1	-1	0.315337287	0.03463792	0	0
2493	ENSRNOG00000000778	Znrd1as1	ZNRD1 antisense RNA 1	4	0.007158817	-0.768527226	1	-1	0.032682237	0.53638334	0	0
2494	ENSRNOG00000009990	Zranb2	zinc finger RANBP2-type containing 2	4	0.031075098	-0.690139107	1	-1	0.1168527	0.4287737	0	0
2495	ENSRNOG000000052959	Zscan12	zinc finger and SCAN domain containing 12	4	0.044152955	-0.836303181	1	-1	0.167687333	0.388847744	0	0
2496	ENSRNOG00000053518	Zscan26	zinc finger and SCAN domain containing 26	4	0.023967037	-0.888750512	1	-1	0.123935591	0.441301918	0	0
2497	ENSRNOG00000015783	Abca18	ATP-binding cassette, subfamily A (ABC1), member 18	5	0.854763534	-0.093837542	0	0	0.033941797	0.707390575	1	1
2498	ENSRNOG00000029370	Abhd3	abhydrolase domain containing 3	5	0.392758708	-0.233327695	0	0	0.043526584	0.668721578	1	1
2499	ENSRNOG00000058372	Ac157b	uncharacterized LOC102552783	5	0.147714916	-0.841058672	0	0	0.033355838	1.128286659	1	1
2500	ENSRNOG00000007637	Acer2	alkaline ceramidase 2	5	0.400344666	-0.405522949	0	0	0.029358734	0.842350954	1	1
2501	ENSRNOG00000011478	Ackr4	atypical chemokine receptor 4	5	0.15311413	-0.514812798	0	0	0.007970554	1.354418048	1	1
2502	ENSRNOG00000042419	Acyp2	acylphosphatase 2	5	0.064615406	-1.041113233	0	0	0.043731812	0.790621274	1	1
2503	ENSRNOG00000057794	Adamts5	ADAM metalloproteinase with thrombospondin type 1 motif 5	5	0.717273016	0.091520301	0	0	0.016213503	0.599605791	1	1
2504	ENSRNOG00000012820	Add3	adducin 3	5	0.044412385	-0.382985476	0	0	0.038023447	0.817256234	1	1
2505	ENSRNOG00000032472	Adgrg2	adhesion G protein-coupled receptor G2	5	0.074309834	-0.465713941	0	0	0.049524929	1.675532898	1	1
2506	ENSRNOG00000016306	Adgrv1	adhesion G protein-coupled receptor V1	5	0.159132474	-0.429089659	0	0	0.010410523	1.538535589	1	1
2507	ENSRNOG00000032959	Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	5	0.075833942	-0.585792238	0	0	0.02069809	1.117883508	1	1
2508	ENSRNOG00000019549	Akap12	A-kinase anchoring protein 12	5	0.17151562	-0.427049341	0	0	0.046424453	0.638828341	1	1
2509	ENSRNOG00000017531	Akr1c3	aldo-keto reductase family 1, member C3	5	0.651870216	-0.201581207	0	0	0.031223384	1.684916657	1	1
2510	ENSRNOG00000050270	Aldh1a3	aldehyde dehydrogenase 1 family, member A3	5	0.193442107	-0.897205886	0	0	0.043358596	1.651203258	1	1
2511	ENSRNOG00000012972	Alox5	arachidonate 5-lipoxygenase	5	0.660468519	-0.083174653	0	0	0.026010413	0.687241825	1	1
2512	ENSRNOG00000000585	Amd1	adenosylmethionine decarboxylase 1	5	0.084795889	-0.675591484	0	0	0.038283498	0.59113155	1	1
2513	ENSRNOG00000004712	Angptl1	angiopoietin-like 1	5	0.171126287	-0.657267484	0	0	0.03631784	1.435872685	1	1
2514	ENSRNOG000000002045	Anxa3	annexin A3	5	0.083408248	-0.915081702	0	0	0.043709882	0.982503245	1	1
2515	ENSRNOG00000005639	Ar	androgen receptor	5	0.10078105	-0.8510238	0	0	0.021812151	1.024991921	1	1

2516	ENSRNOG00000033570	Arhgap8	Rho GTPase activating protein 8	5	0.352341907	-0.133315783	0	0	0.013884629	0.736605742	1	1
2517	ENSRNOG00000014363	Arhgef3	Rho guanine nucleotide exchange factor 3	5	0.070244259	-0.636912529	0	0	0.025205779	0.648293096	1	1
2518	ENSRNOG00000011105	Arl15	ADP-ribosylation factor like GTPase 15	5	0.275463761	-0.264671994	0	0	0.033432867	0.62453666	1	1
2519	ENSRNOG00000004282	Arl4a	ADP-ribosylation factor like GTPase 4A	5	0.017811737	-0.569786899	0	0	0.006242328	1.598264943	1	1
2520	ENSRNOG00000040201	Atp6ap1l	ATPase H+ transporting accessory protein 1 like	5	0.081876146	-0.617837865	0	0	0.047217157	0.585170892	1	1
2521	ENSRNOG00000001953	Bace2	beta-site APP-cleaving enzyme 2	5	0.80124819	0.02205166	0	0	0.00522695	0.776544938	1	1
2522	ENSRNOG00000006103	Bex4	brain expressed, X-linked 4	5	0.68004886	-0.203284148	0	0	0.045770981	1.397723899	1	1
2523	ENSRNOG00000003705	Bmx	BMX non-receptor tyrosine kinase	5	0.2039429	-0.378207992	0	0	0.049124267	0.66880969	1	1
2524	ENSRNOG00000005094	C1qtnf7	C1q and TNF related 7	5	0.502888078	0.132068094	0	0	0.004282256	1.243085467	1	1
2525	ENSRNOG000000011971	C1s	complement C1s	5	0.522896145	0.254861091	0	0	0.037450452	1.338553638	1	1
2526	ENSRNOG000000061379	C7	complement C7	5	0.339934211	-0.100574988	0	0	0.004899731	0.893188711	1	1
2527	ENSRNOG000000037710	Calr4	calreticulin 4	5	0.737341838	-0.03677163	0	0	0.005130956	0.942627333	1	1
2528	ENSRNOG000000031162	Col24	C-C motif chemokine ligand 24	5	0.206317909	-0.560959611	0	0	0.020107786	1.606384526	1	1
2529	ENSRNOG00000000097	Cd160	CD160 molecule	5	0.260170195	-0.814170281	0	0	0.035487415	0.653204857	1	1
2530	ENSRNOG000000010253	Cd163	CD163 molecule	5	0.265799324	0.713780091	0	0	0.031666713	1.162527864	1	1
2531	ENSRNOG00000004698	Cd244	CD244 molecule	5	0.013700021	-0.40829977	0	0	0.02809089	0.749003983	1	1
2532	ENSRNOG000000003298	Cd247	CD247 molecule	5	0.007978346	-0.426124965	0	0	0.032801876	0.580208456	1	1
2533	ENSRNOG000000045558	Cd34	CD34 molecule	5	0.056728226	-0.527189525	0	0	0.008896642	0.79488333	1	1
2534	ENSRNOG000000042821	Cd59	CD59 molecule	5	0.087601407	-0.093886252	0	0	0.000373423	0.626541414	1	1
2535	ENSRNOG000000014515	Cdc14a	cell division cycle 14A	5	0.053785258	-1.155383522	0	0	0.015478312	0.918885743	1	1
2536	ENSRNOG0000000032490	Cdh7	cadherin 7	5	0.378281774	-0.128194237	0	0	0.017824012	1.570604877	1	1
2537	ENSRNOG000000012473	Cflar	CASP8 and FADD-like apoptosis regulator	5	0.18465361	-0.405238871	0	0	0.014279705	0.934654784	1	1
2538	ENSRNOG000000054080	Cgn1l	cingulin-like 1	5	0.75313537	-0.110081156	0	0	0.012964968	1.216135266	1	1
2539	ENSRNOG000000002267	Chic2	cysteine-rich hydrophobic domain 2	5	0.140852079	-0.315480609	0	0	0.027577822	0.641095885	1	1
2540	ENSRNOG000000051690	Clec9a	C-type lectin domain containing 9A	5	0.103073029	-0.476238928	0	0	0.014115992	0.980531553	1	1
2541	ENSRNOG000000007690	Cmpk2	cytidine/uridine monophosphate kinase 2	5	0.086998276	-1.533361463	0	0	0.025422316	1.949882236	1	1
2542	ENSRNOG000000047115	Cox16	COX16, cytochrome c oxidase assembly homolog	5	0.028202055	-0.537896121	0	0	0.047343838	0.721821406	1	1
2543	ENSRNOG000000010807	Cox6c	cytochrome c oxidase subunit 6C	5	0.116261085	-0.517000724	0	0	0.040013103	0.653814524	1	1
2544	ENSRNOG000000042903	Cox7a2	cytochrome c oxidase subunit VIIa polypeptide 2	5	0.06751162	-0.723705424	0	0	0.032440728	0.737897678	1	1
2545	ENSRNOG000000005931	Cpq	carboxypeptidase Q	5	0.258222329	0.173476043	0	0	0.012589615	1.170925814	1	1
2546	ENSRNOG000000015215	Cript	CXXC repeat containing interactor of PDZ3 domain	5	0.038750983	-0.553909772	0	0	0.048210468	0.835491538	1	1
2547	ENSRNOG000000022256	Cxcl10	C-X-C motif chemokine ligand 10	5	0.579811185	0.102521554	0	0	0.038232536	1.688268661	1	1
2548	ENSRNOG000000022242	Cxcl9	C-X-C motif chemokine ligand 9	5	0.07253086	-1.317833532	0	0	0.030431419	1.44299773	1	1
2549	ENSRNOG000000006319	Cxcr6	C-X-C motif chemokine receptor 6	5	0.198665471	-0.510619406	0	0	0.011505138	1.019467522	1	1
2550	ENSRNOG000000015205	Cyb5a	cytochrome b5 type A	5	0.020178057	-0.367877486	0	0	0.036649059	0.622962507	1	1
2551	ENSRNOG000000015076	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	5	0.548931936	-0.749015524	0	0	0.03637094	1.094413827	1	1
2552	ENSRNOG000000010519	Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1	5	0.097325978	-0.574550436	0	0	0.042490656	1.016445015	1	1
2553	ENSRNOG000000018198	Dapk1	death associated protein kinase 1	5	0.826363975	-0.034332328	0	0	0.021029308	0.601234791	1	1
2554	ENSRNOG000000044554	Dcn	decorin	5	0.229254258	-0.440135489	0	0	0.04774388	1.280006	1	1
2555	ENSRNOG000000002881	Ddr2	discoidin domain receptor tyrosine kinase 2	5	0.824096683	-0.053006283	0	0	0.022543962	0.626653772	1	1
2556	ENSRNOG000000022635	Dlg2	discs large MAGUK scaffold protein 2	5	0.509977933	-0.185888935	0	0	0.007857196	0.962970551	1	1
2557	ENSRNOG000000002947	Dpt	dermatopontin	5	0.984676505	-0.002345032	0	0	0.02512054	0.790453847	1	1
2558	ENSRNOG000000023400	Dtx3l	deltex E3 ubiquitin ligase 3L	5	0.165370526	-1.041321704	0	0	0.030845114	1.895737873	1	1
2559	ENSRNOG000000011548	Ebf2	early B-cell factor 2	5	0.094529481	-0.517687261	0	0	0.033667057	0.677590885	1	1
2560	ENSRNOG000000031716	Ecm2	extracellular matrix protein 2	5	0.072488449	-0.63604077	0	0	0.049770774	0.999621633	1	1

2561	ENSRNOG00000009773	Elovl4	ELOVL fatty acid elongase 4	5	0.499324322	-0.193814373	0	0	0.023132543	0.830745772	1	1
2562	ENSRNOG00000009512	Est	esterase D	5	0.008028895	-0.479284568	0	0	0.046803531	0.67007533	1	1
2563	ENSRNOG000000036918	Etfbkm	electron transfer flavoprotein beta subunit lysine methyl	5	0.05862844	-0.399537118	0	0	0.033827736	0.890849815	1	1
2564	ENSRNOG000000033444	F10	coagulation factor X	5	0.553265016	-0.147800141	0	0	0.01467023	1.086047754	1	1
2565	ENSRNOG000000015957	F13a1	coagulation factor XIII A1 chain	5	0.886763534	0.062244287	0	0	0.048394249	1.363036232	1	1
2566	ENSRNOG000000011800	F3	coagulation factor III, tissue factor	5	0.140691952	-1.100184451	0	0	0.044315427	1.516418922	1	1
2567	ENSRNOG000000010805	Fabp4	fatty acid binding protein 4	5	0.084477622	-0.635679107	0	0	0.025421488	0.976378969	1	1
2568	ENSRNOG000000002255	Fam162a	family with sequence similarity 162, member A	5	0.096483139	-0.531034686	0	0	0.02224419	0.852958119	1	1
2569	ENSRNOG000000016505	Fam169a	family with sequence similarity 169, member A	5	0.050665196	-1.542152509	0	0	0.031128267	1.310198788	1	1
2570	ENSRNOG000000037124	Fam227b	family with sequence similarity 227, member B	5	0.148355424	-1.397172777	0	0	0.001296188	0.702671784	1	1
2571	ENSRNOG000000002978	Faslg	Fas ligand	5	0.17891304	-0.991362162	0	0	0.045002689	0.724445501	1	1
2572	ENSRNOG000000014953	Fbxo39	F-box protein 39	5	0.12772195	-0.54755123	0	0	0.041343769	0.858966547	1	1
2573	ENSRNOG000000003620	Fmo3	flavin containing monooxygenase 3	5	0.076262327	-0.671235716	0	0	0.022687953	1.157842878	1	1
2574	ENSRNOG000000019425	Gabarapl2	GABA(A) receptor-associated protein like 2	5	0.047117992	-0.500524415	0	0	0.013197228	0.595198431	1	1
2575	ENSRNOG0000000031743	Gbp2	guanylate binding protein 2	5	0.137505689	-0.854108939	0	0	0.021198607	1.880972008	1	1
2576	ENSRNOG000000028768	Gbp4	guanylate binding protein 4	5	0.23603186	-1.311336558	0	0	0.034429832	2.576033978	1	1
2577	ENSRNOG0000000032240	Gbp5	guanylate binding protein 5	5	0.084302462	-1.344937048	0	0	0.017071443	2.196500271	1	1
2578	ENSRNOG0000000002134	Gbp6	guanylate binding protein family member 6	5	0.377496724	-0.573034544	0	0	0.043045859	1.726022724	1	1
2579	ENSRNOG0000000022110	Gcsam	germinal center-associated, signaling and motility	5	0.100993449	-0.715111541	0	0	0.038725881	1.197647021	1	1
2580	ENSRNOG000000018282	Gda	guanine deaminase	5	0.226735122	-0.410304894	0	0	0.01539418	1.543899235	1	1
2581	ENSRNOG0000000013961	Ghitm	growth hormone inducible transmembrane protein	5	0.085108751	-0.658128332	0	0	0.041258948	0.850218153	1	1
2582	ENSRNOG0000000025297	Gpr171	G protein-coupled receptor 171	5	0.439273429	-0.152851906	0	0	0.049809875	1.03211846	1	1
2583	ENSRNOG0000000047708	Gstz1	glutathione S-transferase zeta 1	5	0.05104779	-0.999843559	0	0	0.027071443	0.942758624	1	1
2584	ENSRNOG000000029876	Gucyl1a2	guanylate cyclase 1 soluble subunit alpha 2	5	0.070675126	-0.909603884	0	0	0.03816454	0.700809279	1	1
2585	ENSRNOG0000000010603	Gzma	granzyme A	5	0.169792842	-0.858014858	0	0	0.005483691	1.289154808	1	1
2586	ENSRNOG000000010661	Gzmk	granzyme K	5	0.06681622	-0.974897981	0	0	0.011937728	1.037913166	1	1
2587	ENSRNOG000000010800	Hadhb	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase	5	0.057321564	-0.78451667	0	0	0.039516792	0.876399561	1	1
2588	ENSRNOG0000000032002	Hapln1	hyaluronan and proteoglycan link protein 1	5	0.314595545	-0.691938303	0	0	0.031236742	1.571787753	1	1
2589	ENSRNOG000000010262	Hdc	histidine decarboxylase	5	0.758126198	-0.112011605	0	0	0.047136266	1.076791872	1	1
2590	ENSRNOG0000000001793	Heg1	heart development protein with EGF-like domains 1	5	0.100490311	-0.256978834	0	0	0.019882146	0.735616271	1	1
2591	ENSRNOG0000000023969	Hero6	HECT and RLD domain containing E3 ubiquitin protein ligase	5	0.071721261	-2.054814978	0	0	0.016397559	2.687106167	1	1
2592	ENSRNOG0000000021198	Hist1h2bh	histone cluster 1, H2bh	5	0.663658093	-0.050909006	0	0	0.017259086	0.606033193	1	1
2593	ENSRNOG0000000028627	Hmcn1	hemicentin 1	5	0.112676367	-0.973863557	0	0	0.035258051	1.299826717	1	1
2594	ENSRNOG0000000023614	Hsh2d	hematopoietic SH2 domain containing	5	0.225669264	-0.668669932	0	0	0.042216537	1.208179415	1	1
2595	ENSRNOG000000013042	Htr1b	5-hydroxytryptamine receptor 1B	5	0.992679677	0.003088789	0	0	0.018739811	0.671904737	1	1
2596	ENSRNOG0000000026605	Ifi272b	interferon, alpha-inducible protein 27 like 2B	5	0.492326046	0.245393732	0	0	0.002860217	2.176231495	1	1
2597	ENSRNOG0000000022218	Ifi44	interferon-induced protein 44	5	0.098595407	-1.216955595	0	0	0.029891732	2.057526833	1	1
2598	ENSRNOG0000000049994	Ifi44l	interferon-induced protein 44-like	5	0.122762292	-1.552612662	0	0	0.018515068	2.6809212	1	1
2599	ENSRNOG0000000002470	Ifi47	interferon gamma inducible protein 47	5	0.746993862	-0.137989832	0	0	0.047588925	1.358858587	1	1
2600	ENSRNOG0000000006227	Ifih1	interferon induced with helicase C domain 1	5	0.153257017	-1.063322935	0	0	0.049588029	1.439293102	1	1
2601	ENSRNOG0000000036604	Ifit2	interferon-induced protein with tetratricopeptide repeats 2	5	0.057103096	-1.894278538	0	0	0.01661422	2.28441117	1	1
2602	ENSRNOG0000000022839	Ifit3	interferon-induced protein with tetratricopeptide repeats 3	5	0.164289911	-1.437384257	0	0	0.027394111	2.831285686	1	1
2603	ENSRNOG0000000027008	Igtp	interferon gamma induced GTPase	5	0.094682582	-0.915738143	0	0	0.015202814	1.714298544	1	1
2604	ENSRNOG0000000047647	Il2ra	interleukin 2 receptor subunit alpha	5	0.731443349	-0.056117075	0	0	0.026369354	0.751552612	1	1
2605	ENSRNOG000000017414	Irf7	interferon regulatory factor 7	5	0.173392456	-0.976833996	0	0	0.028251224	2.322139213	1	1

2606	ENSRNOG00000019478	Irf9	interferon regulatory factor 9	5	0.201650845	-0.623915045	0	0	0.035358941	1.232862719	1	1
2607	ENSRNOG000000031138	Irgm	immunity-related GTPase M	5	0.132036825	-0.98626582	0	0	0.0279549	1.723006555	1	1
2608	ENSRNOG000000021802	Isg15	ISG15 ubiquitin-like modifier	5	0.455638853	-0.324432588	0	0	0.022575547	2.496959784	1	1
2609	ENSRNOG000000016271	Itn2b	integral membrane protein 2B	5	0.045486104	-0.531177846	0	0	0.011138818	0.613551508	1	1
2610	ENSRNOG000000002618	Ivns1abp	influenza virus NS1A binding protein	5	0.111496035	-0.637487061	0	0	0.018375974	0.928536127	1	1
2611	ENSRNOG000000010094	Kcnmb2	potassium calcium-activated channel subfamily M regula	5	0.416569754	-0.548861753	0	0	0.030084132	0.782488133	1	1
2612	ENSRNOG000000009145	Klf12	Kruppel-like factor 12	5	0.164244397	-0.679499638	0	0	0.035007379	0.981022992	1	1
2613	ENSRNOG000000016299	Klf4	Kruppel like factor 4	5	0.129968071	-0.415206771	0	0	0.021197021	0.856927924	1	1
2614	ENSRNOG000000046242	Klf7	Kruppel like factor 7	5	0.143016757	-0.663839125	0	0	0.033097166	0.732623097	1	1
2615	ENSRNOG000000031515	Klr1	killer cell lectin-like receptor, subfamily A, member 1	5	0.098918557	-0.461320925	0	0	0.022930625	1.338829678	1	1
2616	ENSRNOG000000030170	Krt10	keratin 10	5	0.246124681	-0.292576249	0	0	0.027937797	0.612089607	1	1
2617	ENSRNOG000000030878	Krt72	keratin 72	5	0.112614302	0.249498085	0	0	0.005342597	0.905874173	1	1
2618	ENSRNOG000000014532	Lbp	lipopolysaccharide binding protein	5	0.116909455	0.579612501	0	0	0.01958085	1.19418554	1	1
2619	ENSRNOG000000016879	Ldlrad4	low density lipoprotein receptor class A domain containin	5	0.137395076	-0.424192982	0	0	0.003203917	0.737817396	1	1
2620	ENSRNOG000000012557	Lgals5	lectin, galactose binding, soluble 5	5	0.51939618	-0.525907015	0	0	0.017817185	1.310112761	1	1
2621	ENSRNOG000000012681	Lgals9	galectin 9	5	0.152569202	-0.584780539	0	0	0.037995793	1.175795019	1	1
2622	ENSRNOG000000033583	LOC1009	zinc finger protein 709-like	5	0.013445418	-0.459648686	0	0	0.016381836	0.76384513	1	1
2623	ENSRNOG000000049893	LOC1009	interferon-inducible GTPase 1-like	5	0.515717399	-0.300905687	0	0	0.046837666	1.325257519	1	1
2624	ENSRNOG000000048302	LOC1009	interferon-inducible GTPase 1-like	5	0.035245018	-0.285181106	0	0	0.000438315	1.020440922	1	1
2625	ENSRNOG000000049229	LOC1009	proteasome maturation protein-like	5	0.972446866	-0.00698833	0	0	0.027677608	0.904458798	1	1
2626	ENSRNOG000000047782	LOC1009	apolipoprotein L3-like	5	0.081176746	-0.70299785	0	0	0.032659334	1.015490695	1	1
2627	ENSRNOG000000015428	LOC1025	mitochondrial fission factor-like	5	0.07827474	-0.653384411	0	0	0.030308393	0.733532379	1	1
2628	ENSRNOG000000003374	LOC1036	coiled-coil domain-containing protein 85A-like	5	0.239373423	-0.188799382	0	0	0.02059127	0.781483214	1	1
2629	ENSRNOG000000013484	LOC1083	glutathione S-transferase alpha-3	5	0.370335011	-0.476553223	0	0	0.037805117	1.623596625	1	1
2630	ENSRNOG000000039063	LOC6813	similar to potassium channel tetramerisation domain con	5	0.108184401	-1.001263348	0	0	0.038091028	0.676881521	1	1
2631	ENSRNOG000000014654	LOC6918	hypothetical protein LOC691807	5	0.05666023	-0.55146455	0	0	0.046170057	0.635568612	1	1
2632	ENSRNOG000000053706	Lonrf1	LON peptidase N-terminal domain and ring finger 1	5	0.102446452	-1.047540225	0	0	0.037114061	0.805404715	1	1
2633	ENSRNOG000000017538	Lrrc27	leucine rich repeat containing 27	5	0.071450245	-1.154930847	0	0	0.042273429	1.069421953	1	1
2634	ENSRNOG000000008098	Lrrc4	leucine rich repeat containing 4	5	0.727652852	0.08420872	0	0	0.011526446	0.595858579	1	1
2635	ENSRNOG000000012015	Lrrc49	leucine rich repeat containing 49	5	0.170792773	-0.386284795	0	0	0.021017999	0.631013274	1	1
2636	ENSRNOG000000021053	Lsr	lipolysis stimulated lipoprotein receptor	5	0.106896904	0.905297054	0	0	0.044729329	1.111920519	1	1
2637	ENSRNOG000000061813	Ly6c	Ly6-C antigen	5	0.393256189	-0.402465138	0	0	0.007212675	1.303931296	1	1
2638	ENSRNOG000000007091	Ly6e	lymphocyte antigen 6 family member E	5	0.273815461	-0.490266758	0	0	0.033658506	1.176762646	1	1
2639	ENSRNOG000000010642	Lysmd2	LysM domain containing 2	5	0.113610785	-0.785853696	0	0	0.03340211	0.602803444	1	1
2640	ENSRNOG000000026902	Lyve1	lymphatic vessel endothelial hyaluronan receptor 1	5	0.842998828	-0.040339645	0	0	0.021209986	1.321941572	1	1
2641	ENSRNOG000000015445	Mal	mal, T-cell differentiation protein	5	0.179340183	-0.498671818	0	0	0.034680091	0.863927275	1	1
2642	ENSRNOG000000013674	Megf10	multiple EGF-like domains 10	5	0.12487525	-1.222380469	0	0	0.007315151	0.663213302	1	1
2643	ENSRNOG000000025415	Mett11b	methyltransferase like 11B	5	0.858881043	-0.290165284	0	0	0.011960141	0.867740667	1	1
2644	ENSRNOG000000019542	MGC1088	similar to interferon-inducible GTPase	5	0.242596511	-0.970128463	0	0	0.041361354	2.239724807	1	1
2645	ENSRNOG000000033341	MGC1161	similar to RIKEN cDNA 1700001E04	5	0.419526929	-0.228712442	0	0	0.014867595	0.690617931	1	1
2646	ENSRNOG000000056325	Mocs2	molybdenum cofactor synthesis 2	5	0.06931784	-0.207830522	0	0	0.009162196	0.773710411	1	1
2647	ENSRNOG000000012415	Mpc1	mitochondrial pyruvate carrier 1	5	0.060822702	-0.880156989	0	0	0.033217916	0.736586288	1	1
2648	ENSRNOG000000025388	Mpr133	mitochondrial ribosomal protein L33	5	0.064636232	-0.393545982	0	0	0.048095855	0.73661105	1	1
2649	ENSRNOG000000042740	Mpr142	mitochondrial ribosomal protein L42	5	0.001836494	-0.50313116	0	0	0.044481553	0.599299878	1	1
2650	ENSRNOG000000002178	Mpr18c	mitochondrial ribosomal protein S18C	5	0.049667195	-0.516299481	0	0	0.039826357	0.73608735	1	1

2651	ENSRNOG00000018090	Mtmr10	myotubularin related protein 10	5	0.002510999	-0.550752287	0	0	0.000982829	0.70962316	1	1
2652	ENSRNOG00000010205	Mturn	maturin, neural progenitor differentiation regulator homolog	5	0.094459003	-0.574804259	0	0	0.032998138	1.179013933	1	1
2653	ENSRNOG0000001959	Mx1	myxovirus (influenza virus) resistance 1	5	0.279201434	-1.376307186	0	0	0.035060272	3.6177672	1	1
2654	ENSRNOG00000001963	Mx2	MX dynamin like GTPase 2	5	0.221193297	-1.206801893	0	0	0.025285773	3.119374575	1	1
2655	ENSRNOG00000017579	Myli1	myosin regulatory light chain interacting protein	5	0.001890766	-0.508683905	0	0	0.002142818	0.804068275	1	1
2656	ENSRNOG00000014104	Myo5b	myosin Vb	5	0.389175643	-0.422684496	0	0	0.048969106	1.119593153	1	1
2657	ENSRNOG000000040122	Myoz1	myozenin 1	5	0.478621336	0.335605062	0	0	0.043279636	0.97164205	1	1
2658	ENSRNOG00000014815	Myoz2	myozenin 2	5	0.056781325	-0.854429925	0	0	0.041903386	0.87370465	1	1
2659	ENSRNOG000000045689	NEWGEN	nucleolar protein 8	5	0.023809255	-0.519572247	0	0	0.003286187	0.767337242	1	1
2660	ENSRNOG00000007390	Nfkb1a	NFKB inhibitor alpha	5	0.570911937	-0.126014451	0	0	0.037750362	1.222627824	1	1
2661	ENSRNOG000000027502	Nmi	N-myc (and STAT) interactor	5	0.216883263	-0.307806195	0	0	0.025675747	0.773410808	1	1
2662	ENSRNOG00000008697	Nov	nephroblastoma overexpressed	5	0.978311013	0.004338771	0	0	0.034808151	1.419629963	1	1
2663	ENSRNOG00000010392	Nrg1	neuregulin 1	5	0.32271995	0.431100432	0	0	0.008039101	2.230352988	1	1
2664	ENSRNOG00000005700	Nsg1	neuronal vesicle trafficking associated 1	5	0.692802841	-0.136429446	0	0	0.013920695	1.068812501	1	1
2665	ENSRNOG000000027847	Nxpe2	neurexophilin and PC-esterase domain family, member 2	5	0.056704089	-1.013935121	0	0	0.024452176	1.097378237	1	1
2666	ENSRNOG00000001369	Oas1a	2'-5' oligoadenylate synthetase 1A	5	0.46760582	-0.512300143	0	0	0.036118406	2.401358884	1	1
2667	ENSRNOG000000033220	Oas1b	2-5 oligoadenylate synthetase 1B	5	0.298117095	-0.627777074	0	0	0.035238329	1.912932895	1	1
2668	ENSRNOG000000039580	Omd	osteomodulin	5	0.075680712	-1.307069745	0	0	0.0449509	2.070284083	1	1
2669	ENSRNOG000000023809	Opom1	opioid binding protein/cell adhesion molecule-like	5	0.102888022	-1.031571436	0	0	0.004389561	1.570467877	1	1
2670	ENSRNOG00000001296	P2rx7	purinergic receptor P2X 7	5	0.665147645	-0.104775677	0	0	0.009400524	0.58595312	1	1
2671	ENSRNOG000000013872	P2ry14	purinergic receptor P2Y14	5	0.117644714	-0.465631443	0	0	0.019223778	0.996035403	1	1
2672	ENSRNOG000000023483	Parp9	poly (ADP-ribose) polymerase family, member 9	5	0.222794014	-0.709525715	0	0	0.04115392	1.493815571	1	1
2673	ENSRNOG000000029244	Podhb10	protocadherin beta 10	5	0.294307585	-0.332880402	0	0	0.014202124	1.041141719	1	1
2674	ENSRNOG000000046848	PCOLCE	procollagen C-endopeptidase enhancer 2	5	0.104169781	0.455679262	0	0	0.038064892	0.781028359	1	1
2675	ENSRNOG000000012036	Posk5	proprotein convertase subtilisin/kexin type 5	5	0.170287153	-0.376531515	0	0	0.011390939	0.658212314	1	1
2676	ENSRNOG000000015473	Phactr2	phosphatase and actin regulator 2	5	0.114874974	-0.637557845	0	0	0.000342252	0.772178927	1	1
2677	ENSRNOG000000003674	Pir	pirin	5	0.015017309	-0.338197099	0	0	0.024423212	0.761561994	1	1
2678	ENSRNOG000000016945	Pla2g2a	phospholipase A2 group IIA	5	0.201994897	0.79356794	0	0	0.037255293	1.76007926	1	1
2679	ENSRNOG000000006804	Ppp1r42	protein phosphatase 1, regulatory subunit 42	5	0.824695282	-0.068273309	0	0	0.000724984	0.890269442	1	1
2680	ENSRNOG000000019330	Procr	protein C receptor	5	0.365846645	0.416104095	0	0	0.043213709	1.22052508	1	1
2681	ENSRNOG000000004483	Ptprr	protein tyrosine phosphatase, receptor type, R	5	0.126411144	-1.042765695	0	0	0.045293359	1.207358258	1	1
2682	ENSRNOG000000014135	Rab11fip4	RAB11 family interacting protein 4	5	0.19859389	-0.549146154	0	0	0.001428246	0.589967807	1	1
2683	ENSRNOG000000006698	Rab33a	RAB33A, member RAS oncogene family	5	0.228614578	-0.391285429	0	0	0.041430729	0.673728547	1	1
2684	ENSRNOG000000009008	Rab39a	RAB39A, member RAS oncogene family	5	0.125398248	-0.750636825	0	0	0.033092545	0.978871516	1	1
2685	ENSRNOG000000006579	Reg3g	regenerating family member 3 gamma	5	0.654091304	-0.130442684	0	0	0.000453555	2.921201762	1	1
2686	ENSRNOG000000014751	Ret	ret proto-oncogene	5	0.185320047	-0.908206221	0	0	0.018670023	1.133120867	1	1
2687	ENSRNOG000000014027	RGD1304	similar to 4933427D14Rik protein	5	0.062266189	-0.623782479	0	0	0.031924971	0.744615792	1	1
2688	ENSRNOG000000037567	RGD1309	similar to RIKEN cDNA B230118H07	5	0.048256534	-0.524367055	0	0	0.0283537	0.710811866	1	1
2689	ENSRNOG000000018690	Rgs17	regulator of G-protein signaling 17	5	0.72197476	-0.315436488	0	0	0.027080339	0.88952686	1	1
2690	ENSRNOG000000014859	Rnf152	ring finger protein 152	5	0.093052755	-1.194080023	0	0	0.042517757	0.9075728	1	1
2691	ENSRNOG000000027145	Rora	RAR-related orphan receptor A	5	0.19170471	-0.552589588	0	0	0.047592235	0.593569336	1	1
2692	ENSRNOG000000039829	Rpp14	ribonuclease P/MRP subunit p14	5	0.024065237	-0.479094996	0	0	0.013193849	0.692401663	1	1
2693	ENSRNOG000000007539	Rsad2	radical S-adenosyl methionine domain containing 2	5	0.06769147	-1.73835908	0	0	0.017043307	2.188105712	1	1
2694	ENSRNOG000000050210	RT1-CE10	RT1 class I, locus CE10	5	0.065922074	-1.209746292	0	0	0.021378526	0.81678498	1	1
2695	ENSRNOG000000032844	RT1-Da	RT1 class II, locus Da	5	0.162243983	0.298114431	0	0	0.020495089	0.841322631	1	1

2898	ENSRNOG00000000777	RT1-S3	RT1 class 1b, locus S3	5	0.197894904	-0.64015019	0	0	0.012133163	1.677604381	1	1
2897	ENSRNOG000000045924	RT1-T24-3	RT1 class 1, locus T24, gene 3	5	0.279769533	-0.46802283	0	0	0.018193228	1.477609564	1	1
2898	ENSRNOG000000042905	RT1-T24-4	RT1 class 1, locus T24, gene 4	5	0.124420523	-0.695587379	0	0	0.010359423	1.576791999	1	1
2899	ENSRNOG000000028895	Rtp4	receptor (chemosensory) transporter protein 4	5	0.264827391	-1.002451184	0	0	0.038805544	2.362571604	1	1
2700	ENSRNOG000000023549	Samd5	sterile alpha motif domain containing 5	5	0.052373491	-1.093004059	0	0	0.020028481	1.228447742	1	1
2701	ENSRNOG000000052444	Samd9	sterile alpha motif domain containing 9	5	0.246943797	-1.10084961	0	0	0.041990552	2.579671802	1	1
2702	ENSRNOG000000016177	Scara3	scavenger receptor class A, member 3	5	0.268591545	-0.155275086	0	0	0.015583546	1.074458482	1	1
2703	ENSRNOG000000014398	Scara5	scavenger receptor class A, member 5	5	0.704358044	-0.179644614	0	0	0.039315564	1.488702038	1	1
2704	ENSRNOG000000009278	Schp1	schwannomin interacting protein 1	5	0.064047445	-0.676424843	0	0	0.021521068	0.837888834	1	1
2705	ENSRNOG000000011283	Sdhaf3	succinate dehydrogenase complex assembly factor 3	5	0.082813599	-0.471420614	0	0	0.014098269	0.888508241	1	1
2706	ENSRNOG000000004459	Sdr9c7	short chain dehydrogenase/reductase family 9C, member 7	5	0.075112889	-0.553572919	0	0	0.003280603	0.896511814	1	1
2707	ENSRNOG000000004033	Sema6a	semaphorin 6A	5	0.05058065	-0.91380816	0	0	0.022332529	0.779756355	1	1
2708	ENSRNOG000000059073	Slamf1	signaling lymphocytic activation molecule family member 1	5	0.091048066	-0.832787474	0	0	0.038122336	0.81432959	1	1
2709	ENSRNOG000000028668	Slc28a2	solute carrier family 28 member 2	5	0.170455141	-0.429524694	0	0	0.020647059	1.049395004	1	1
2710	ENSRNOG000000061768	Slc43a3	solute carrier family 43, member 3	5	0.059406386	-0.653280783	0	0	0.007846286	1.265547563	1	1
2711	ENSRNOG000000037113	Slfn2	schlafen 2	5	0.952946555	-0.01359459	0	0	0.017831253	1.049928875	1	1
2712	ENSRNOG000000037998	Snw1	SNW domain containing 1	5	0.050715399	-0.759431325	0	0	0.04646845	0.625294593	1	1
2713	ENSRNOG000000016012	Spats2l	spermatogenesis associated, serine-rich 2-like	5	0.255216468	-0.252687117	0	0	0.01591642	0.809500733	1	1
2714	ENSRNOG000000005434	Sptbn1	spectrin, beta, non-erythrocytic 1	5	0.024124129	-0.442490441	0	0	0.041578443	0.586313083	1	1
2715	ENSRNOG000000004641	Sstr4	somatostatin receptor 4	5	0.712684782	0.105168596	0	0	0.013896786	0.692403331	1	1
2716	ENSRNOG000000011278	Stk3	serine/threonine kinase 3	5	0.008891387	-0.291114227	0	0	0.046967884	0.584346954	1	1
2717	ENSRNOG000000004198	Sxbp6	syntrophin binding protein 6	5	0.101585546	-0.764739614	0	0	0.038501896	0.890100542	1	1
2718	ENSRNOG000000009037	Sulf1	sulfatase 1	5	0.095104476	0.226147451	0	0	0.047118544	0.973463546	1	1
2719	ENSRNOG000000019342	Sult1a1	sulfotransferase family 1A member 1	5	0.103806496	-0.946723571	0	0	0.003103441	1.538001545	1	1
2720	ENSRNOG000000026951	Susd5	sushi domain containing 5	5	0.738355424	-0.09312914	0	0	0.001627681	0.91149899	1	1
2721	ENSRNOG000000018915	Tagap	T-cell activation RhoGTPase activating protein	5	0.104432522	0.732450139	0	0	0.041988897	1.04234908	1	1
2722	ENSRNOG000000002093	Tgfb3	transforming growth factor beta receptor 3	5	0.074259292	-0.732071137	0	0	0.037926764	0.728958509	1	1
2723	ENSRNOG000000013519	Tll2	tolloid-like 2	5	0.172509482	-0.712145913	0	0	0.048715951	0.814994871	1	1
2724	ENSRNOG000000032368	Tlr11	toll-like receptor 11	5	0.669990483	-0.267297542	0	0	0.028979381	0.942032279	1	1
2725	ENSRNOG000000015812	Tm4sf1	transmembrane 4 L six family member 1	5	0.033192745	-0.29901999	0	0	0.033488883	0.985530972	1	1
2726	ENSRNOG000000039464	Tmem229	transmembrane protein 229A	5	0.111795187	-0.831619649	0	0	0.047091304	1.178872587	1	1
2727	ENSRNOG000000025476	Tmem252	transmembrane protein 252	5	0.067167368	-0.94821452	0	0	0.028057444	1.259135907	1	1
2728	ENSRNOG000000025160	Tmem56	transmembrane protein 56	5	0.273026136	-0.763108809	0	0	0.045152955	1.255714972	1	1
2729	ENSRNOG000000011334	Tmem63c	transmembrane protein 63c	5	0.590133784	0.284099748	0	0	0.039929936	0.799921955	1	1
2730	ENSRNOG000000004585	Tmtc2	transmembrane and tetratricopeptide repeat containing 2	5	0.016983794	-0.566747137	0	0	0.000260879	0.615023311	1	1
2731	ENSRNOG000000050645	Tprkb	Tp53 binding protein	5	0.088933867	-0.265298668	0	0	0.034830839	0.694435499	1	1
2732	ENSRNOG000000003219	Trim16	tripartite motif-containing 16	5	0.206886422	-0.620465833	0	0	0.009300738	0.600428379	1	1
2733	ENSRNOG000000018517	Trim21	tripartite motif-containing 21	5	0.154105924	-0.96758211	0	0	0.036249845	1.387733002	1	1
2734	ENSRNOG000000017191	Trim5	tripartite motif-containing 5	5	0.085081305	-0.588611971	0	0	0.041388249	0.838925736	1	1
2735	ENSRNOG0000000056135	Tsc22d3	TSC22 domain family, member 3	5	0.082329632	-0.775794772	0	0	0.010313289	1.45478855	1	1
2736	ENSRNOG000000002928	Uap1	UDP-N-acetylglucosamine pyrophosphorylase 1	5	0.018381905	0.515722975	0	0	0.00426543	0.767757896	1	1
2737	ENSRNOG000000012550	Uqorh	ubiquinol-cytochrome c reductase hinge protein	5	0.042708841	-0.545620947	0	0	0.022273981	0.649707881	1	1
2738	ENSRNOG000000037198	Usp18	ubiquitin specific peptidase 18	5	0.17331122	-0.994497251	0	0	0.026874422	2.062157767	1	1
2739	ENSRNOG000000037371	Xaf1	XIAP associated factor 1	5	0.100448866	-0.723858	0	0	0.005140059	2.219873612	1	1
2740	ENSRNOG000000007081	Xdh	xanthine dehydrogenase	5	0.272388387	-0.135247243	0	0	0.007560306	1.193883808	1	1

2741	ENSRNOG000000037227	Yes1	YES proto-oncogene 1, Src family tyrosine kinase	5	0.080066478	-1.055306901	0	0	0.047519206	1.097004962	1	1
2742	ENSRNOG000000047924	Zbtb7c	zinc finger and BTB domain containing 7C	5	0.84218316	-0.05659162	0	0	0.042566306	1.289923356	1	1
2743	ENSRNOG000000018629	Zooch8	zinc finger CCHC-type containing 8	5	0.088325357	-0.629480417	0	0	0.035372181	0.693397542	1	1
2744	ENSRNOG000000017883	Zeb1	zinc finger E-box binding homeobox 1	5	0.077940556	-0.584010211	0	0	0.028842494	0.685413114	1	1
2745	ENSRNOG000000003215	Zfp287	zinc finger protein 287	5	0.183738915	-0.369440211	0	0	0.047826977	0.69778804	1	1
2746	ENSRNOG000000014661	Zfp385d	zinc finger protein 385D	5	0.127547479	-0.156163125	0	0	0.000886904	0.712094075	1	1
2747	ENSRNOG000000001029	Zfp655	zinc finger protein 655	5	0.059880008	-0.34089657	0	0	0.001098476	0.59413749	1	1
2748	ENSRNOG000000048910	Zfp709l1	zinc finger protein 709-like 1	5	0.0114559	-0.218709447	0	0	0.019949728	0.81182942	1	1
2749	ENSRNOG000000000054	Abhd8	abhydrolase domain containing 8	6	0.08014068	1.271144212	0	0	0.015847183	-1.413474266	1	-1
2750	ENSRNOG000000046958	Abo	ABO, alpha 1-3-N-acetylgalactosaminyltransferase and	6	0.037740432	0.576818531	0	0	0.047007586	-0.720831381	1	-1
2751	ENSRNOG000000038973	Acd	ACD, shelterin complex subunit and telomerase recruitm	6	0.101806634	0.509839871	0	0	0.049192607	-0.856922364	1	-1
2752	ENSRNOG000000053370	Adnp2	ADNP homeobox 2	6	0.072972071	0.356094407	0	0	0.028005517	-0.606601083	1	-1
2753	ENSRNOG000000059445	Aifm2	apoptosis inducing factor, mitochondria associated 2	6	0.077897938	0.397512871	0	0	0.040263568	-0.611457202	1	-1
2754	ENSRNOG000000014610	Anpep	alanine aminopeptidase, membrane	6	0.059926626	2.118635282	0	0	0.048018481	-1.521377261	1	-1
2755	ENSRNOG000000009227	Aplnr	apelin receptor	6	0.059713813	-1.543528848	0	0	0.036532584	-0.622046982	1	-1
2756	ENSRNOG000000009347	Arhgap25	Rho GTPase activating protein 25	6	0.105978346	0.958775893	0	0	0.044279015	-1.034526777	1	-1
2757	ENSRNOG000000018686	Atxn2l	ataxin 2-like	6	0.110653058	0.315342238	0	0	0.029924212	-0.614836998	1	-1
2758	ENSRNOG000000000471	B3gal4	Beta-1,3-galactosyltransferase 4	6	0.088016826	0.95595888	0	0	0.023810579	-0.814007057	1	-1
2759	ENSRNOG000000028753	B9d2	B9 domain containing 2	6	0.13729729	1.152414763	0	0	0.041274326	-0.725849262	1	-1
2760	ENSRNOG000000010428	Bahd1	bromo adjacent homology domain containing 1	6	0.092156127	0.255788567	0	0	0.021097097	-0.703383806	1	-1
2761	ENSRNOG000000050819	Birc5	baculoviral IAP repeat-containing 5	6	0.065287773	2.176765685	0	0	0.042212123	-1.722605757	1	-1
2762	ENSRNOG000000018665	Bud13	BUD13 homolog	6	0.0680491	0.576270282	0	0	0.03871884	-0.670688964	1	-1
2763	ENSRNOG000000009719	C2cd2l	C2CD2-like	6	0.015051652	0.389434412	0	0	3.55838E-05	-0.930461382	1	-1
2764	ENSRNOG000000020239	Capn15	calpain 15	6	0.089077029	0.797029543	0	0	0.028939728	-1.285938417	1	-1
2765	ENSRNOG000000010079	Car3	carbonic anhydrase 3	6	0.100086063	4.312564872	0	0	0.000478174	-3.891422934	1	-1
2766	ENSRNOG000000006930	Casq1	calsequestrin 1	6	0.71985201	0.077885887	0	0	0.029937797	-1.221495769	1	-1
2767	ENSRNOG000000001484	Castor2	cytosolic arginine sensor for mTORC1 subunit 2	6	0.081916833	0.447015707	0	0	0.011425557	-0.658008343	1	-1
2768	ENSRNOG000000049215	Cbx2	chromobox 2	6	0.061912972	0.945237356	0	0	0.049875664	-0.629816558	1	-1
2769	ENSRNOG000000009687	Ccdc120	coiled-coil domain containing 120	6	0.417852424	0.198240669	0	0	0.001754086	-0.728256091	1	-1
2770	ENSRNOG000000008319	Ccdc130	coiled-coil domain containing 130	6	0.187516171	0.47991258	0	0	0.047277222	-0.675668922	1	-1
2771	ENSRNOG000000007129	Cd8b	CD8b molecule	6	0.086401076	1.732013571	0	0	0.03978767	-1.490143943	1	-1
2772	ENSRNOG000000047427	Cdan1	codanin 1	6	0.014282877	0.427503422	0	0	0.022199848	-0.842533567	1	-1
2773	ENSRNOG000000050071	Cdc45	cell division cycle 45	6	0.062543549	1.762289733	0	0	0.033408317	-1.357860811	1	-1
2774	ENSRNOG000000008956	Cdkn2c	cyclin-dependent kinase inhibitor 2C	6	0.144554031	0.952585389	0	0	0.049075788	-0.738045816	1	-1
2775	ENSRNOG000000010950	Cep41	centrosomal protein 41	6	0.435203365	0.194257676	0	0	0.043232467	-0.694900663	1	-1
2776	ENSRNOG000000025811	Cfp	complement factor properdin	6	0.091105579	1.44345643	0	0	0.014232605	-0.646961715	1	-1
2777	ENSRNOG000000050181	Chid1	chitinase domain containing 1	6	0.089728019	0.625312102	0	0	0.034383284	-0.670182774	1	-1
2778	ENSRNOG000000010466	Chp2f	chondroitin polymerizing factor 2	6	0.026053514	0.555013461	0	0	0.0081493	-0.763626116	1	-1
2779	ENSRNOG000000029911	Cilp	cartilage intermediate layer protein	6	0.099713537	1.143750821	0	0	0.041396524	-1.318879484	1	-1
2780	ENSRNOG000000016976	Cion7	chloride voltage-gated channel 7	6	0.093733949	0.999675794	0	0	0.043285773	-1.175866267	1	-1
2781	ENSRNOG000000016315	Cnpy3	canopy FGF signaling regulator 3	6	0.054650576	1.583520148	0	0	0.048033462	-1.073839977	1	-1
2782	ENSRNOG000000010841	Col8a2	collagen type VIII alpha 2 chain	6	0.090076546	1.087740429	0	0	0.014865527	-1.096151698	1	-1
2783	ENSRNOG000000009878	Crtap	cartilage associated protein	6	0.054858424	0.769530875	0	0	0.043813668	-0.595064843	1	-1
2784	ENSRNOG000000021887	Cyb5b1d2	cytochrome b5b1 family, member D2	6	0.116852217	1.699251192	0	0	0.036282877	-0.890200168	1	-1
2785	ENSRNOG000000009481	Ddhd1	DDHD domain containing 1	6	0.156588925	-0.311588472	0	0	0.016059927	-0.63356657	1	-1

2788	ENSRNOG000000021232	Ddrgk1	DDRGK domain containing 1	6	0.108188815	0.701008713	0	0	0.044701745	-1.010580587	1	-1
2787	ENSRNOG000000020284	Dhrs1	dehydrogenase/reductase 1	6	0.051973243	0.959792017	0	0	0.025627543	-0.750352196	1	-1
2788	ENSRNOG000000018989	Dolk	dolichol kinase	6	0.40944128	0.219932792	0	0	0.032455417	-0.831380317	1	-1
2789	ENSRNOG000000032546	Dot1l	DOT1 like histone lysine methyltransferase	6	0.006252258	0.525352708	0	0	0.04780291	-1.064038704	1	-1
2790	ENSRNOG000000023303	Dpep2	dipeptidase 2	6	0.394878836	0.387909945	0	0	0.035108958	-1.012012584	1	-1
2791	ENSRNOG000000019735	Dph2	DPH2 homolog	6	0.213227639	0.234194531	0	0	0.027411075	-0.788548621	1	-1
2792	ENSRNOG000000008062	Dqx1	DEAQ box RNA-dependent ATPase 1	6	0.258251983	0.683562851	0	0	0.024465892	-1.157186222	1	-1
2793	ENSRNOG000000017915	Dvl2	dishevelled segment polarity protein 2	6	0.145243776	0.72038551	0	0	0.022207917	-0.771264853	1	-1
2794	ENSRNOG000000047741	E2f2	E2F transcription factor 2	6	0.235177022	0.374984282	0	0	0.037206331	-0.757372589	1	-1
2795	ENSRNOG000000017828	Egr3	early growth response 3	6	0.518898986	0.310854873	0	0	0.037133853	-0.844458679	1	-1
2796	ENSRNOG000000020847	Elp6	elongator acetyltransferase complex subunit 6	6	0.07683939	1.272426545	0	0	0.048987794	-0.81915038	1	-1
2797	ENSRNOG000000020792	Etv4	ets variant 4	6	0.214480381	0.851142154	0	0	0.029817118	-1.509283545	1	-1
2798	ENSRNOG000000009245	Exosc2	exosome component 2	6	0.179625881	0.507487312	0	0	0.04910089	-0.79884955	1	-1
2799	ENSRNOG000000016889	Fancc	Fanconi anemia, complementation group C	6	0.106530032	1.324072917	0	0	0.03887658	-1.122690184	1	-1
2800	ENSRNOG0000000057945	Fancg	Fanconi anemia, complementation group G	6	0.1768467	0.785714835	0	0	0.042055444	-0.771063189	1	-1
2801	ENSRNOG000000045838	Fasn	fatty acid synthase	6	0.07488463	1.467913491	0	0	0.006923109	-1.179000683	1	-1
2802	ENSRNOG000000018988	Fbx19	F-box and leucine-rich repeat protein 19	6	0.146053789	0.916470296	0	0	0.04180382	-0.828807357	1	-1
2803	ENSRNOG000000004212	Fbxw9	F-box and WD repeat domain containing 9	6	0.138813185	0.669922125	0	0	0.039389009	-0.624561518	1	-1
2804	ENSRNOG000000020531	Fen1	flap structure-specific endonuclease 1	6	0.058461485	1.290482977	0	0	0.019927315	-1.380631687	1	-1
2805	ENSRNOG000000061182	Gabre	gamma-aminobutyric acid type A receptor epsilon subunit	6	0.629918213	0.124687115	0	0	0.040497089	-0.769483806	1	-1
2806	ENSRNOG0000000061146	Gar1	GAR1 ribonucleoprotein	6	0.280881319	0.162007747	0	0	0.045088752	-0.821113451	1	-1
2807	ENSRNOG000000018441	Ggt7	gamma-glutamyltransferase 7	6	0.208658782	0.888111781	0	0	0.018752224	-0.97138815	1	-1
2808	ENSRNOG000000001891	Gnb1l	G protein subunit beta 1 like	6	0.264117923	-0.192987044	0	0	0.014466313	-0.836784897	1	-1
2809	ENSRNOG000000018989	Gpatch4	G patch domain containing 4	6	0.204138197	0.808035345	0	0	0.008614096	-0.755027778	1	-1
2810	ENSRNOG000000024751	H2afy2	H2A histone family, member Y2	6	0.266103027	0.357627181	0	0	0.009779601	-1.001440635	1	-1
2811	ENSRNOG000000052038	Haus8	HAUS augmin-like complex, subunit 8	6	0.090475691	0.885197335	0	0	0.015466726	-0.679738591	1	-1
2812	ENSRNOG000000029238	Hgh1	HGH1 homolog	6	0.059199366	0.541156921	0	0	0.028155713	-0.871281043	1	-1
2813	ENSRNOG000000029501	Hoga1	4-hydroxy-2-oxoglutarate aldolase 1	6	0.07083277	2.025024047	0	0	0.044554513	-1.762394935	1	-1
2814	ENSRNOG000000033984	Ifnlr1	interferon, lambda receptor 1	6	0.505978898	0.096140504	0	0	0.008717806	-0.955201352	1	-1
2815	ENSRNOG000000017980	Itgal	integrin subunit alpha L	6	0.074141507	0.924802463	0	0	0.047415282	-0.741363522	1	-1
2816	ENSRNOG0000000060123	Kifc2	kinesin family member C2	6	0.158802014	0.835519846	0	0	0.04503848	-0.787493412	1	-1
2817	ENSRNOG000000030281	Kik10	kallikrein related-peptidase 10	6	0.595959175	-0.167321619	0	0	0.028359286	-1.271900003	1	-1
2818	ENSRNOG000000019573	Loat	lecithin cholesterol acyltransferase	6	0.21582346	-0.225125571	0	0	0.013664437	-0.805319523	1	-1
2819	ENSRNOG000000009946	Ldlr	low density lipoprotein receptor	6	0.085718502	1.72396972	0	0	0.039220674	-2.096740735	1	-1
2820	ENSRNOG000000018842	Leng8	leukocyte receptor cluster member 8	6	0.023144749	-0.230043045	0	0	0.035347907	-0.858915496	1	-1
2821	ENSRNOG000000011032	Lhfp12	LHFPL tetraspan subfamily member 2	6	0.111484725	0.740024351	0	0	0.02697214	-1.193173712	1	-1
2822	ENSRNOG000000021028	LOC10036	zinc finger protein 687-like	6	0.105749948	0.736822797	0	0	0.024312806	-0.852979497	1	-1
2823	ENSRNOG0000000057734	LOC10096	CMRF35-like molecule-like	6	0.088686435	0.894074489	0	0	0.018072547	-0.900779403	1	-1
2824	ENSRNOG000000019351	LOC10091	chitinase domain-containing protein 1-like	6	0.103116888	0.611322904	0	0	0.040359217	-0.656193578	1	-1
2825	ENSRNOG000000057456	LOC10254	uncharacterized LOC102546883	6	0.053659058	1.153791719	0	0	0.000526171	-0.61934651	1	-1
2826	ENSRNOG000000054031	LOC10254	uncharacterized LOC102549726	6	0.068685746	0.885963931	0	0	0.024748086	-0.950545599	1	-1
2827	ENSRNOG000000019082	LOC10363	serine/threonine-protein kinase SBK1	6	0.111675471	0.681188184	0	0	0.02816081	-0.801708384	1	-1
2828	ENSRNOG000000042468	LOC88092	similar to natural cytotoxicity triggering receptor 2	6	0.088975381	0.99222192	0	0	0.04664899	-0.936735667	1	-1
2829	ENSRNOG000000045826	Lrrc45	leucine rich repeat containing 45	6	0.121456589	0.708762277	0	0	0.02942466	-0.687882008	1	-1
2830	ENSRNOG000000022753	Mast3	microtubule associated serine/threonine kinase 3	6	0.110982967	0.707442995	0	0	0.004076546	-0.986973682	1	-1

2831	ENSRNOG00000055082	Maz	MYC associated zinc finger protein	6	0.10311413	0.988729395	0	0	0.049087442	-0.917539512	1	-1
2832	ENSRNOG00000008134	Mefv	MEFV, pyrin innate immunity regulator	6	0.09583215	1.368883806	0	0	0.039861251	-0.619577648	1	-1
2833	ENSRNOG00000003088	Mrip	MRN complex interacting protein	6	0.055586235	0.80978207	0	0	0.041085099	-0.625223729	1	-1
2834	ENSRNOG00000007632	Mss51	MSS51 mitochondrial translational activator	6	0.124586442	-0.473102839	0	0	0.019675057	-0.678471929	1	-1
2835	ENSRNOG00000020357	Msto1	misato 1, mitochondrial distribution and morphology regu	6	0.171813944	0.648338848	0	0	0.044283222	-0.844267795	1	-1
2836	ENSRNOG000000025527	Mtcl1	microtubule crosslinking factor 1	6	0.3164499	0.328745924	0	0	0.031721536	-0.894672487	1	-1
2837	ENSRNOG00000008415	Nab2	Ngfi-A binding protein 2	6	0.058951245	1.590589109	0	0	0.022310806	-0.742219461	1	-1
2838	ENSRNOG000000018681	Nes	nestin	6	0.325290256	0.082516701	0	0	0.018448659	-1.519631879	1	-1
2839	ENSRNOG000000021392	Noc2l	NOC2-like nucleolar associated transcriptional repressor	6	0.073173988	0.343964623	0	0	0.027371218	-0.789609909	1	-1
2840	ENSRNOG000000048733	Nup82	nucleoporin 82	6	0.058215571	0.772288977	0	0	0.036721054	-0.707340916	1	-1
2841	ENSRNOG00000003673	Nup85	nucleoporin 85	6	0.050715537	1.175765551	0	0	0.026954762	-0.94812276	1	-1
2842	ENSRNOG000000017806	P2rx1	purinergic receptor P2X 1	6	0.259675747	0.536665515	0	0	0.012063651	-0.662904905	1	-1
2843	ENSRNOG000000018888	Pask	PAS domain containing serine/threonine kinase	6	0.08635956	1.116954286	0	0	0.025783465	-1.578598005	1	-1
2844	ENSRNOG000000012705	Pcgf2	polycomb group ring finger 2	6	0.063361148	1.191329957	0	0	0.028051721	-0.789333975	1	-1
2845	ENSRNOG000000019268	Pelp1	proline, glutamate and leucine rich protein 1	6	0.134467554	0.61315677	0	0	0.045715261	-0.780128094	1	-1
2846	ENSRNOG000000028100	Pex11g	peroxisomal biogenesis factor 11 gamma	6	0.13721895	0.484274774	0	0	0.049955796	-0.63856894	1	-1
2847	ENSRNOG000000003070	Pigl	phosphatidylinositol glycan anchor biosynthesis, class L	6	0.12562237	0.472906334	0	0	0.007656506	-0.696371205	1	-1
2848	ENSRNOG000000008040	Pimreg	PICALM interacting mitotic regulator	6	0.130391835	1.834557679	0	0	0.036575891	-2.21450209	1	-1
2849	ENSRNOG000000018484	Plk3	polo-like kinase 3	6	0.050986828	0.909369664	0	0	0.003645542	-0.952540852	1	-1
2850	ENSRNOG000000015588	Plpp5	phospholipid phosphatase 5	6	0.05597876	1.364763042	0	0	0.048488242	-1.021855662	1	-1
2851	ENSRNOG000000000977	Pnpla6	patatin-like phospholipase domain containing 6	6	0.057204607	0.973877401	0	0	0.037872492	-0.786212085	1	-1
2852	ENSRNOG000000001449	Pom121	POM121 transmembrane nucleoporin	6	0.130316806	0.465171346	0	0	0.043408179	-0.709459825	1	-1
2853	ENSRNOG000000015450	Ppp1r16a	protein phosphatase 1, regulatory subunit 16A	6	0.090579684	1.117840294	0	0	0.033656506	-1.17056813	1	-1
2854	ENSRNOG000000010574	Ptpn1	protein tyrosine phosphatase, non-receptor type 1	6	0.05046383	0.734264469	0	0	0.039247776	-0.671517017	1	-1
2855	ENSRNOG000000007158	Qtrt1	queuine tRNA-ribosyltransferase catalytic subunit 1	6	0.192224674	1.046598402	0	0	0.033468037	-0.910424025	1	-1
2856	ENSRNOG000000018729	Rad9a	RAD9 checkpoint clamp component A	6	0.066786566	0.938152394	0	0	0.000903386	-1.051022945	1	-1
2857	ENSRNOG000000045568	Rbm14	RNA binding motif protein 14	6	0.090246742	0.562531402	0	0	0.019813944	-0.836450225	1	-1
2858	ENSRNOG000000050106	Rcc1	regulator of chromosome condensation 1	6	0.052473347	1.1632717	0	0	0.021075581	-1.193991258	1	-1
2859	ENSRNOG000000006327	Rcc2	regulator of chromosome condensation 2	6	0.074644094	2.032560939	0	0	0.016643473	-1.171682408	1	-1
2860	ENSRNOG000000011373	Reep4	receptor accessory protein 4	6	0.051238873	1.025707481	0	0	0.020692987	-1.227905437	1	-1
2861	ENSRNOG000000008239	Repin1	replication initiator 1	6	0.012690987	-0.442553702	0	0	0.012107027	-0.636918534	1	-1
2862	ENSRNOG000000008113	RGD1561	similar to mKIAA1522 protein	6	0.060508379	1.052794162	0	0	0.03047776	-1.011318381	1	-1
2863	ENSRNOG000000043374	RGD1566	similar to novel protein	6	0.983800428	0.004425396	0	0	0.025158541	-0.63357865	1	-1
2864	ENSRNOG000000023814	Rimkb	ribosomal modification protein rimK-like family member 6	6	0.145377008	0.511229756	0	0	0.038328322	-0.63344608	1	-1
2865	ENSRNOG000000019474	Rsp9	radial spoke head 9 homolog	6	0.086920626	0.879746884	0	0	0.022790635	-0.992053785	1	-1
2866	ENSRNOG000000038999	RT1-A1	RT1 class Ia, locus A1	6	0.40675581	-0.16171018	0	0	0.044725743	-1.43394543	1	-1
2867	ENSRNOG000000030712	RT1-A2	RT1 class Ia, locus A2	6	0.192074891	0.23728237	0	0	0.028586787	-1.234967841	1	-1
2868	ENSRNOG0000000001704	Runt1	runt-related transcription factor 1	6	0.052813737	1.226285792	0	0	0.039019378	-0.842773278	1	-1
2869	ENSRNOG0000000001414	Serpine1	serpin family E member 1	6	0.062776774	1.779881284	0	0	0.020037653	-1.134688813	1	-1
2870	ENSRNOG000000018412	Sfi1	SFI1 centrin binding protein	6	0.00800089	0.356298233	0	0	0.000968416	-0.817403244	1	-1
2871	ENSRNOG0000000001425	Sh2b2	SH2B adaptor protein 2	6	0.06751493	1.282859915	0	0	0.046800028	-1.194605297	1	-1
2872	ENSRNOG0000000005275	Shmt1	serine hydroxymethyltransferase 1	6	0.07825019	0.674719799	0	0	0.001827253	-0.847189791	1	-1
2873	ENSRNOG000000020703	Sipa1l3	signal-induced proliferation-associated 1 like 3	6	0.09593628	0.973919487	0	0	0.013268257	-0.829017949	1	-1
2874	ENSRNOG000000000146	Six5	SIX homeobox 5	6	0.091200331	1.032353638	0	0	0.041147852	-0.962956997	1	-1
2875	ENSRNOG000000018785	Slc16a13	solute carrier family 16, member 13	6	0.227198124	0.312227754	0	0	0.043944625	-0.586037626	1	-1

2876	ENSRNOG00000038001	Slc25a1	solute carrier family 25 member 1	6	0.125894368	1.129261464	0	0	0.032259775	-0.726594294	1	-1
2877	ENSRNOG00000042387	Slc25a6	solute carrier family 25 member 6	6	0.763483206	0.041050306	0	0	0.046302293	-0.589364251	1	-1
2878	ENSRNOG00000020450	Slc28a6	solute carrier family 28 member 6	6	0.064187202	0.840419301	0	0	0.020908144	-1.193338839	1	-1
2879	ENSRNOG00000018940	Slc28a1	solute carrier family 28 member 1	6	0.522869057	0.235492788	0	0	0.04489318	-0.718667963	1	-1
2880	ENSRNOG00000054142	Slc30a2	solute carrier family 30 member 2	6	0.235332184	0.603206889	0	0	0.016808427	-0.64399896	1	-1
2881	ENSRNOG00000024801	Slc35a2	solute carrier family 35 member A2	6	0.074047859	0.854253281	0	0	0.046267499	-0.858479186	1	-1
2882	ENSRNOG00000003835	Slc43a2	solute carrier family 43 member 2	6	0.153471071	1.503105989	0	0	0.02401262	-0.974665663	1	-1
2883	ENSRNOG00000028844	Slc9a5	solute carrier family 9 member A5	6	0.846340804	0.062899229	0	0	0.014331701	-0.828578089	1	-1
2884	ENSRNOG00000023404	Slc9a2	solute carrier family 9 member B2	6	0.103185711	0.813016167	0	0	0.039786154	-0.992974096	1	-1
2885	ENSRNOG00000011162	Smco4	single-pass membrane protein with coiled-coil domains 4	6	0.090181229	1.067062887	0	0	0.02958196	-0.80647895	1	-1
2886	ENSRNOG00000015589	Smvd5	SMYD family member 5	6	0.08967725	0.835892742	0	0	0.045134473	-0.867743196	1	-1
2887	ENSRNOG00000016167	Spata2L	spermatogenesis associated 2-like	6	0.084743811	0.795269542	0	0	0.028400869	-0.632912706	1	-1
2888	ENSRNOG000000052307	Spats2	spermatogenesis associated, serine-rich 2	6	0.073017999	0.67130955	0	0	0.028948831	-0.787149216	1	-1
2889	ENSRNOG00000007400	Stebf2	sterol regulatory element binding transcription factor 2	6	0.012505896	0.3673053	0	0	0.00492635	-0.829421507	1	-1
2890	ENSRNOG00000001828	Stk38l	serine/threonine kinase 38 like	6	0.13686835	0.474257356	0	0	0.048231363	-0.60429759	1	-1
2891	ENSRNOG00000015832	Taf1c	TATA-box binding protein associated factor, RNA polymerase 1	6	0.074052824	1.03502928	0	0	0.033024343	-1.397364852	1	-1
2892	ENSRNOG00000019023	Tars	threonyl-tRNA synthetase	6	0.051902903	0.741370203	0	0	0.035831736	-0.614233557	1	-1
2893	ENSRNOG00000017349	Tbc1d10b	TBC1 domain family, member 10b	6	0.075927591	0.41554786	0	0	0.030278484	-0.782714724	1	-1
2894	ENSRNOG00000016774	Telo2	telomere maintenance 2	6	0.053305013	1.105787148	0	0	0.034624922	-1.115037116	1	-1
2895	ENSRNOG00000011387	Tet3	tet methylcytosine dioxygenase 3	6	0.198970554	0.744361426	0	0	0.04263899	-0.759331219	1	-1
2896	ENSRNOG00000001833	Tfll	Trk-fused gene	6	0.133833115	0.452708454	0	0	0.035632922	-0.65177981	1	-1
2897	ENSRNOG00000015906	Tgfb1	TGF-beta-induced factor homeobox 1	6	0.095277843	1.075486478	0	0	0.033619406	-0.616488956	1	-1
2898	ENSRNOG000000031916	Timeless	timeless circadian clock	6	0.102252121	1.316709893	0	0	0.01702386	-1.524795334	1	-1
2899	ENSRNOG000000020989	Tm7sf2	transmembrane 7 superfamily member 2	6	0.366363147	0.540031142	0	0	0.032045445	-0.591226503	1	-1
2900	ENSRNOG00000006519	Tmem107	transmembrane protein 107	6	0.061855872	1.63386444	0	0	0.00516785	-0.765886882	1	-1
2901	ENSRNOG00000017329	Tmem129	transmembrane protein 129	6	0.086120288	0.497702334	0	0	0.023701489	-0.708493084	1	-1
2902	ENSRNOG000000038607	Tmem86b	transmembrane protein 86B	6	0.954343563	-0.012414132	0	0	0.020671816	-0.830735964	1	-1
2903	ENSRNOG00000020374	Tmem8a	transmembrane protein 8A	6	0.054497483	1.780494359	0	0	0.041847459	-1.490688205	1	-1
2904	ENSRNOG00000022012	Tnfrsf18	TNF receptor superfamily member 18	6	0.055608441	0.571025902	0	0	0.033996	-0.602731299	1	-1
2905	ENSRNOG000000008145	Traf3	Tnf receptor-associated factor 3	6	0.044462037	0.466295729	0	0	0.018584029	-0.848595235	1	-1
2906	ENSRNOG00000008898	Trm54	tRNA methyltransferase 44	6	0.052555886	0.977867501	0	0	0.023155369	-0.73598802	1	-1
2907	ENSRNOG000000060703	Troap	trophinin associated protein	6	0.106852231	2.320768834	0	0	0.041067097	-2.239778507	1	-1
2908	ENSRNOG000000020188	Trpc2	transient receptor potential cation channel, subfamily C, member 2	6	0.107638301	0.788842777	0	0	0.032707951	-1.057743073	1	-1
2909	ENSRNOG000000047123	Tsfd1	thiosulfate sulfurtransferase like domain containing 1	6	0.227063789	0.259605306	0	0	0.029726915	-0.625364799	1	-1
2910	ENSRNOG000000024578	Ttyh2	tweety family member 2	6	0.10453486	1.193942628	0	0	0.033793531	-1.383528988	1	-1
2911	ENSRNOG000000000598	Tube1	tubulin, epsilon 1	6	0.062218744	1.381900438	0	0	0.049258396	-1.158953983	1	-1
2912	ENSRNOG00000013216	Ubs1	U6 snRNA biogenesis phosphodiesterase 1	6	0.08994097	0.430865972	0	0	0.014849252	-0.732311099	1	-1
2913	ENSRNOG00000003832	Vash2	vasohibin 2	6	0.041670843	-0.487882832	0	0	0.042440108	-0.782904925	1	-1
2914	ENSRNOG000000034258	Xirp2	xin actin-binding repeat containing 2	6	0.112286187	0.802674954	0	0	0.016724364	-0.992996363	1	-1
2915	ENSRNOG000000027459	Znbf45	zinc finger and BTB domain containing 45	6	0.296307289	0.111262502	0	0	0.008484794	-0.677834413	1	-1
2916	ENSRNOG00000005833	Znbf49	zinc finger and BTB domain containing 49	6	0.618823254	0.345991253	0	0	0.029543982	-0.679916172	1	-1
2917	ENSRNOG00000016631	Zfp276	zinc finger protein (C2H2 type) 276	6	0.085345287	1.273355174	0	0	0.048509827	-1.262912994	1	-1
2918	ENSRNOG00000016808	Zfp579	zinc finger protein 579	6	0.672424109	0.047525142	0	0	0.045253155	-0.98233138	1	-1
2919	ENSRNOG00000002882	Zfp692	zinc finger protein 692	6	0.25861513	0.18449056	0	0	0.038518895	-0.613842897	1	-1
2920	ENSRNOG00000023536	Adgrd1	adhesion G protein-coupled receptor D1	7	0.03104779	1.510251384	1	1	0.026170809	0.954081578	1	1
2921	ENSRNOG000000030021	Ccl8	chemokine (C-C motif) ligand 8	7	0.018289738	0.726511735	1	1	0.038062478	1.328578404	1	1
2922	ENSRNOG00000014361	Edn1	endothelin 1	7	0.047881539	0.599481987	1	1	0.010229915	0.879751255	1	1
2923	ENSRNOG00000002810	Gpi2	glutamine-fructose-6-phosphate transaminase 2	7	0.018151162	0.819385328	1	1	0.013630232	0.615334548	1	1
2924	ENSRNOG000000006151	Reg3b	regenerating family member 3 beta	7	0.047221433	4.097510033	1	1	0.039882008	2.737474548	1	1

2.6. Identification of differentially expressed genes (DEGs)

To investigate the collective association of up- and down-regulated signaling pathways, a network model was reconstructed to describe the interactions between interactions between differentially expressed genes (Figure 15A). The network has shown that metformin treatment inhibits increased inflammation and apoptosis by lowering the Tgf- β /BMP signaling pathway. Therefore, these data suggest a positive effect of metformin on myocardial I/R injury, consistent with previous results.

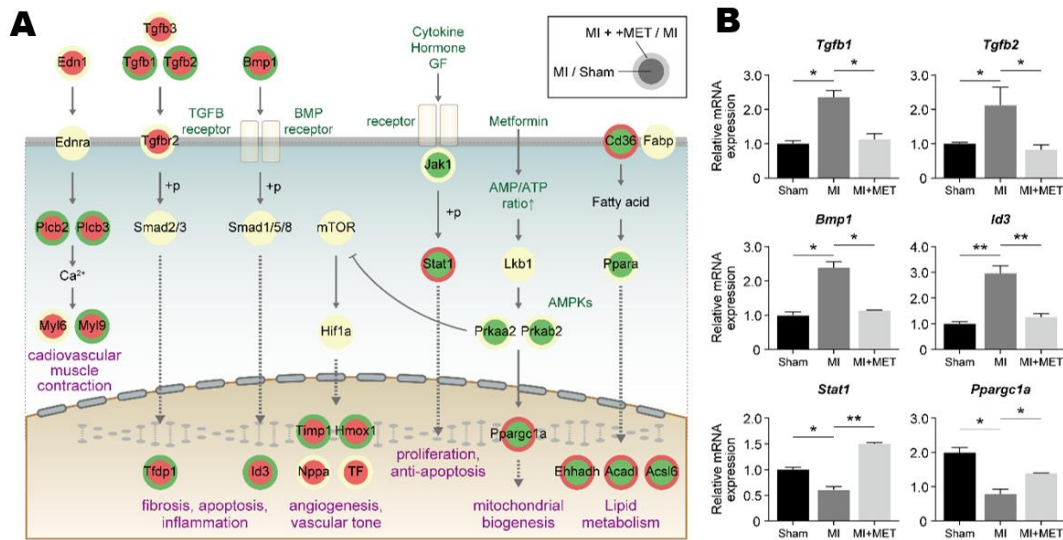


Figure 15. Network model and gene expression level from mRNA-seq.

(A) Network model describing interactions among signaling pathways. Arrows and suppression symbols, activation and inhibition in signaling. “+p”, phosphorylation. Red and green denote up- and down-regulation, respectively. (B) Gene expression levels obtained from mRNA-seq. The data are presented as mean ± SD. For each gene, all the significant differences (see Materials and Methods) from the two comparisons were indicated by an asterisk: * $p < 0.05$ and ** $p < 0.01$.

3. Discussion

In this *in vivo* rat myocardial I/R injury model, total weight changes, relative heart weight, left ventricular systolic and diastolic function using echocardiography, myocardial infarct size, histopathology, and the degree of fibrosis, mRNA sequence from left ventricles were evaluated during the study period. These data show that metformin successfully attenuated left ventricular diastolic dysfunction induced by transient LAD ligation in this animal model.

Metformin is a first-line anti-diabetic agent (18), a biguanide, which inhibits glucose production in the liver and muscle, increases glycogen synthesis, and increases activity of GLUT4 receptors, improving insulin resistance and lowering blood glucose. This study was designed to determine the effects of metformin on AMI closely associated with the metabolic syndrome (1). Previous mechanistic studies of metformin have been performed using isoproterenol-induced MI in a rat model (22), but the cardio-protective action of metformin is not entirely due to its anti-hyperglycemic actions (19, 20). With the recent development of new formulations of metformin, its efficiency and tolerability have improved, and its clinical application has expanded. In other words, it allows drug repositioning to take advantage of non-glycemic effects (43-48). Previous studies have described the non-glycemic effects of metformin, including its potential to improve cardiovascular clinical outcomes, anticancer effects, and longevity (49). In addition, the United Kingdom Prospective Diabetes Study (UKPDS) noted that intensive blood-glucose control with metformin reduced the risk of MI by 39% over a 10-year period (50), supporting promising results related to the protective effects of cardiovascular complication of diabetes mellitus of the UKPDS clinical trial (51). Other studies have shown that potential cardiovascular effects of metformin treatment are independent of glycemic control, as patients receiving intensive glycemic control with sulfonylurea or insulin did not improve cardiovascular outcomes (44, 52). In studies on longevity, metformin treatment has shown a possible effect on extending life span. In fact, the dietary restriction mechanism of metformin has long been known to increase longevity (53-56). The PRESTO clinical trial highlighted the relevance of metformin therapy, demonstrating that treatment reduced mortality and MI in diabetic patients with diabetes undergoing percutaneous coronary intervention (57). Prospective clinical trials evaluating the use of metformin in the treatment of cardiovascular disease are on the rise, and a decrease in all-cause mortality has been observed in patients with CKD and chronic HF (52), which may lead to expanded indications for metformin in disorders presently thought to be contraindications.

Previous studies on a model of myocardial I/R injury in rats have exposed metformin for a relatively long-term at least 2 weeks and have rarely tested left ventricular diastolic function using echocardiography (13-16). The current study highlighted the positive effects of metformin on acute MI. Weight loss associated with metformin treatment has been identified, and as reported in previous studies, the increased heart weight/body weight (%) in the MI-induced group reflects cardiac hypertrophy (43). Echocardiography data showed no recovery of left ventricular cardiac dysfunction in the early stages of ischemic reperfusion injury in this rat model during the experimental period, but metformin treatment significantly improved left ventricular systolic function on day 7 and significantly attenuated left ventricular diastolic dysfunction in the early stage of MI onset. E/E' values are known for reflecting an important indicator of cardiac diastolic function and poor outcomes in humans, but there are some limitations on the use of E' and E/E' , which show only the global function of LV. However, further studies are planned using the quantitative evaluation of regional function and the filling dynamics of the LV using strain, strain rate, and speckle tracking with color tissue doppler (58, 59).

In addition, the pathologic consequences of MI appear primarily in human coronary arteries and myocardium (60). The initial post-MI changes and MI lesions after MI can be classified by light microscopy over time. Previous studies have demonstrated different types of lesions in humans using hematoxylin and eosin staining, and advanced lesions have also been observed in the current rat myocardial I/R injury model. For example, persistent coagulation necrosis was observed on day 7 in MI sample from rats, which can occur in humans on days 3-7. Additionally, lesions due to macrophage phagocytosis, nuclear dust and endocardial fibrosis can occur in humans at 2-3 weeks and can be identified as complex lesions in the same rat heart sample. Masson's trichrome staining was also used to study pathologies of muscle (muscular dystrophy), heart (infarct), liver (cirrhosis), or kidney (glomerular fibrosis), to determine the degree of fibrosis in LVs to confirm the presence of connective tissue.

Moreover, despite metformin's clinical significance, there has been no systematic exploration of the alteration of the molecular signature by metformin in the rat myocardial I/R injury model. In this study, gene expression profiles of rat myocardial I/R injury mode were examined and our transcriptome profiling approach provides a list of DEGs that expands the current list identified in existing experiments. Gene ontology biological processes (GOBP) and network model can provide a molecular basis for understanding immune/inflammation and cardiovascular system alterations in myocardial I/R injury. In this study, we demonstrated

the promising positive effects of metformin on left ventricular diastolic dysfunction in a rat myocardial I/R injury model using echocardiography. These data provide a further understanding of the impact of metformin on the onset of AMI in high-risk patients.

Chapter . Efficacy study of sappanone A

1. Materials and Methods

1. 1. Animals

Sprague Dawley rats were purchased from Koatech (Kyungki, South Korea). All rats were housed three per cage and fed an autoclaved pellet diet (SAFE + 40RMM; SAFE Diets, Augy, France) *ad libitum*. The environmental conditions were maintained at a temperature of 22 ± 1 , with the relative humidity of 50 ± 10 %, using 12-hour light/dark cycles, illumination at 150-300 Lux, and ventilation 10-20 times/hour. These conditions were monitored hourly for 24 hours and maintained within acceptable range throughout the study.

1. 2. Study design

Sprague Dawley rats (8-week-old adult males, mean weight: 285.33 ± 5.09 g) were divided into four groups (eight rats/group) as follows: A) Normal group, B) MI group, C) MI + Curcumin 25 mg/kg group, D) MI + Sappanone A 50 mg/kg group (Figure 16). Rats in groups A and B received vehicle (10% dimethyl sulfoxide, DMSO, cat.co. 472301, Sigma-Aldrich, St. Louis, MO, USA and 90% polyethylene glycol, PEG400, cat.co. 91893, Sigma, St. Louis, MO, USA), and rats in groups C and D were treated with 25 mg/kg curcumin, and 50 mg/kg sappanone A dissolved in vehicle and administered orally daily for 5 days (from pre-ischemia to day 4 post-surgery). The study design (Figure 17) was approved by the Institutional Animal Care and Use Committee of Daegu-Gyeongbuk Medical Innovation Foundation (DGMIF-18041705-01).

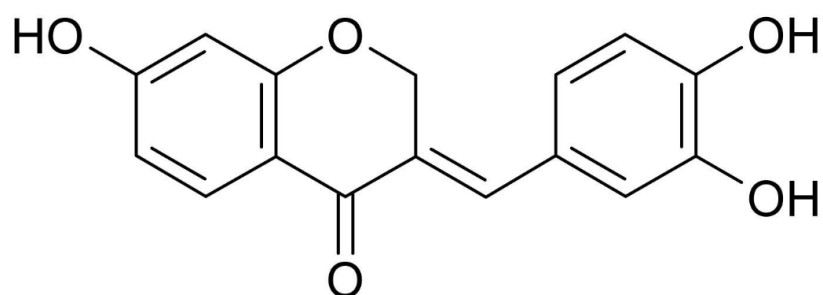


Figure 16. Chemical structure of sappanone A.

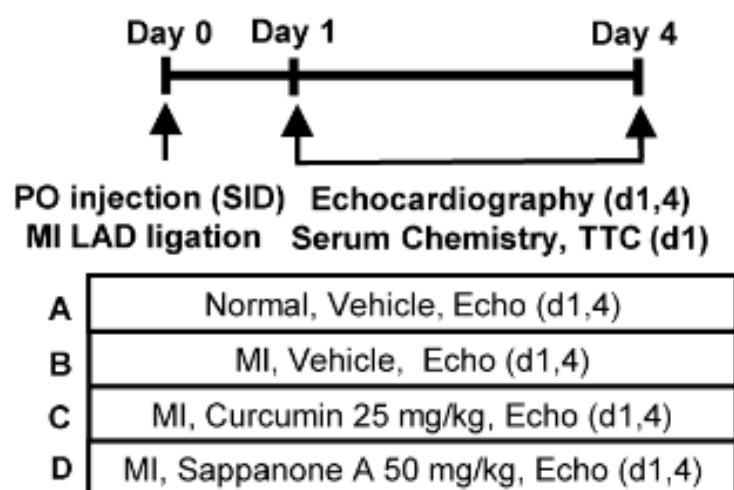


Figure 17. Study design for the efficacy study of sappanone A.

1.3. Rat myocardial ischemia/reperfusion injury model

Animals were anesthetized with alfaxalone (50 mg/kg, IP) and xylazine (5 mg/kg, IP). After anesthetization, rats were intubated and ventilated using a ventilator (Harvard Apparatus VentElite, MA, USA) and maintained at a tidal volume of 3.0 mL/kg and a respiratory rate of 60 breaths/min. During surgery, all rats were placed in a supine position on a heated plate and monitored by ECG, and the rat myocardial I/R injury model was induced by the ligation of the left anterior descending (LAD) coronary artery for 30 minutes.

1.4. Echocardiographic analysis

Echocardiography was performed on day 1 and 4 after MI surgery, using Vevo2100 (Visual Sonics Inc., ON, Canada). Rats were anesthetized with alfaxalone (50 mg/kg, IP) and xylazine (5 mg/kg, IP) and were monitored by ECG in a supine position, and maintained body temperature at 37°C. Echocardiographic parameters follow the American Society of Echocardiography guidelines (1). As described in the preliminary study, left ventricular systolic and diastolic function was evaluated by echocardiography using B-mode, M-mode, Doppler color flow, pulsed wave Doppler, and tissue Doppler.

1.5. Myocardial infarct size

On day 1 after induction of MI, rats were euthanized with 5 % isoflurane, and their hearts were excised. After reperfusion with 0.9% normal saline, 2 ml of 2 % Evans blue (Sigma, St. Louis, MO, USA) was perfused into the hearts. The hearts were then sectioned into 2 mm transverse slices and immersed in a 1% solution of 2,3,5-triphenyltetrazolium chloride (TTC, Sigma, St. Louis, MO, USA) at 37°C for 15 minutes in the dark. The infarct area, area at risk, and left ventricle area were analyzed using Image J software (National Institutes of Health, Bethesda, MA, USA) and expressed as the ratio of the area of the ischemic zone over the LV area (IA/LV).

1.6. Serum chemistry of cardiac marker

Blood samples were collected from the abdominal veins of rats on day 1 after MI surgery. For evaluation of serum chemistry parameters for cardiac markers, blood samples were placed in serum separate tubes (SST tube, cat.367989, BD Inc. USA) for at least 30 minutes at room temperature and centrifuged at 3000 rpm for 10 minutes. Serum samples were separated for use in cardiac marker assays and serum cardiac marker analysis was performed using a TBA-120FR automatic chemistry analyzer (Toshiba, Tokyo, Japan). Serum creatine kinase-MB (CK-MB), lactate dehydrogenase (LDH), and aspartate aminotransferase (AST) were measured.

1.7. Histopathological analysis

On day 4 after MI surgery, rat hearts were extracted after blood removal for histological evaluation (n=3) and fixed in 10% neutral buffered formalin (BBC Biochemicals, Mount Vernon, WA, USA). Formalin-fixed heart tissues prepared for analysis using a tissue processor (Thermo Fisher Scientific, Inc., Runcorn, UK). The paraffin-embedded tissue blocks were cut to a thickness of 4 μ m, mounted on glass slides, and then stained in hematoxylin (YD-Diagnostics, Kyungki, Korea) and eosin (BBC Biochemicals, Mount Vernon, WA, USA) using an autostainer (Dako Cover Stainer; Agilent, Santa Clara, CA, USA).

Under light microscope in H&E-stained slides, the distinction between mature lymphocytes and other three types of cells (immature lymphocyte, mature/immature monocyte) were possible to score, as shown in Figure 22 and Table 8 by three independent pathologists. However, the distinction between these three cell types (immature lymphocyte, mature/immature monocyte) was almost impossible under the microscope with H&E slide. Therefore, these three types of cells were collectively referred to mononuclear cells. As described above, the term “mixed cells” refers to a state in which lymphocytes and monocytes are mixed as shown in Table 8.

To assess fibrosis, tissue sections were stained using a Masson’s trichrome staining kit according to the manufacturer’s instructions (ScyTek Laboratories, West Logan, UT, USA). After staining, the parasternal short-axis area with papillary muscle (PM), and the medial and apex areas of the left ventricles were scanned with a slide scanner (Pannoramic SCAN II;

3DHISTECH, Budapest, Hungary) and captured by a slide viewer (Case Viewer; 3DHISTECH). Morphometric analysis of fibrosis was performed using Image J software (National Institutes of Health, Bethesda, MA, USA). In Masson's trichrome-stained sections, the blue area (collagen fiber) was measured in comparison with the total red area (left ventricle) and the results were shown in Figure 23.

1.8. mRNA sequencing and data analysis

For gene expression profiling, using Trizol reagent (Invitrogen Life Technologies, Grand Island, NY, USA), total RNAs were obtained from the LV tissues including interventricular septum of rat hearts from the four groups (normal group, MI group, MI + Curcumin group, and MI + Sappanone A group) on the day 4 after MI surgery. Total RNA integrity was analyzed using an Agilent Bioanalyzer. RNA integrity values for all samples were larger than 7. Poly (A) mRNA isolation from total RNA and fragmentation was conducted following manufacturer's instructions. The adaptor-ligated libraries were sequenced using an Illumina NovaSeq 6000 (Bioneer, Daejeon, Korea). In each condition, the mRNA-sequencing analysis was performed on two biological replicates obtained from independent rats (Table 9).

Adapter sequences (TruSeq universal and indexed adapters) were removed using Cutadapt software (version 2.7; <https://cutadapt.readthedocs.io/en/stable/>), and the remaining read sequences for each sample were aligned to the *Rattus_norvegicus* reference genome (Rnor_6.0) using TopHat2 software (version 2.1.1) with default parameters (38). After alignment, using HTseq, the number of reads mapped to the gene features (GTF file of Rnor_6.0.90) were calculated (39). Then, read counts for the samples in each condition were normalized using the TMM (trimmed mean of M-values) normalization function of the edgeR package (40).

1.9. Identification of differentially expressed genes (DEGs)

The number of reads for the gene features was converted to log₂-values after adding one (pseudo count) to the read counts. A previously reported statistical hypothesis test was performed to identify DEGs between four conditions (41). Briefly, for each gene, a T-statistic values were calculated using Student's t-test in each of the three comparisons (MI group versus normal group, MI + Curcumin group versus MI group, or MI + Sappanone A group versus MI group). In each comparison, the empirical distribution of the T-statistic value for the null

hypothesis (i.e., the genes are not differentially expressed) was estimated by performing all possible combinations of random permutations of the samples. The estimated empirical distribution was used to calculate the adjusted p values for Student's t-test for each gene. Finally, DEGs were identified as those that had adjusted p values ≤ 0.05 and absolute log2-fold-changes ≥ 0.58 (1.5-fold). Enrichment analysis of Gene Ontology Biological Processes (GOBPs) was performed using DAVID software (<https://david.ncifcrf.gov/summary.jsp>) (42) to identify cellular processes represented by the DEGs. Then, the GOBPs with p values < 0.05 were selected as the processes enriched by the DEGs. The network model was reconstructed for selected DEGs using Cytoscape software (version 3.3.0) (61). The nodes of the network model were arranged based on their locations and relationships of the corresponding genes in the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway database (62).

1.10. RT-PCR

After preparing total RNA from left ventricular tissues in rats with the same experimental conditions, cDNA was synthesized using the SuperScript™ IV First-Strand Synthesis System for RT-PCR according to the manufacturer's instructions (Invitrogen Life Technologies, Grand Island, NY, USA). PCR was performed by subjecting the samples to the following conditions: initial denaturation at 95 °C for 5 min, followed by 22~27 cycles of amplification by denaturation at 95 °C for 30 s, annealing at 57~59 °C for 30 s, extension at 72 °C for 30 s, and final extension at 72 °C for 5 min. The amplified PCR products were separated on 1.5% agarose gels and visualized by SYBR Safe staining (Invitrogen Life Technologies, Grand Island, NY, USA).

Table 11 shows the primer information used in this study and the representative bands are shown in Figure 27. Hypoxanthine-guanine phosphoribosyltransferase 1 (HPRT1) was used as a control gene for normalization, and the data were derived from four independent experiments. Densitometric analysis was performed on RNA expression patterns using ImageJ software (National Institutes of Health, Bethesda, MA, USA) and the relative values were shown in Figure 26.

1.11. Statistical analysis

Statistical significance was determined using GraphPad Prism 8 (GraphPad Software Inc., San Diego, CA, USA). All data are presented as mean \pm standard error of the mean (SEM). The results for each group were compared by one-way or two-way analysis of variance (ANOVA) with Tukey's post hoc correction. A p value <0.05 was considered statistically significant.

2. Results

2.1. Echocardiographic results

Overall, left ventricular function did not recover throughout the study period from day 1 to day 4, including systolic and diastolic function (Figure 18 and 19). EF and FS are representative values for evaluating the LV systolic function, and E' and E/E' ratio are the representative values for evaluating the LV diastolic function. LV systolic function was significantly increased in the sappanone A 50 mg/kg dose group compared to the MI+vehicle group, confirming the protective effect on systolic function. LV diastolic dysfunction did not recover in the MI+vehicle group until day 4. However, the absolute value of the E/E' ratio was significantly reduced in the curcumin-treated or sappanone A-treated groups compared to the MI+vehicle group and that means the cardioprotective effect on LV diastolic dysfunction were confirmed. In addition, sappanone A showed a higher efficacy at this dose than curcumin. In particular, the LV diastolic function was remarkably improved in relation to curcumin or sappanone A, and the E/E' ratio of the sappanone A group improved the LV diastolic function to almost normal levels. Detailed results are described in Table 6.

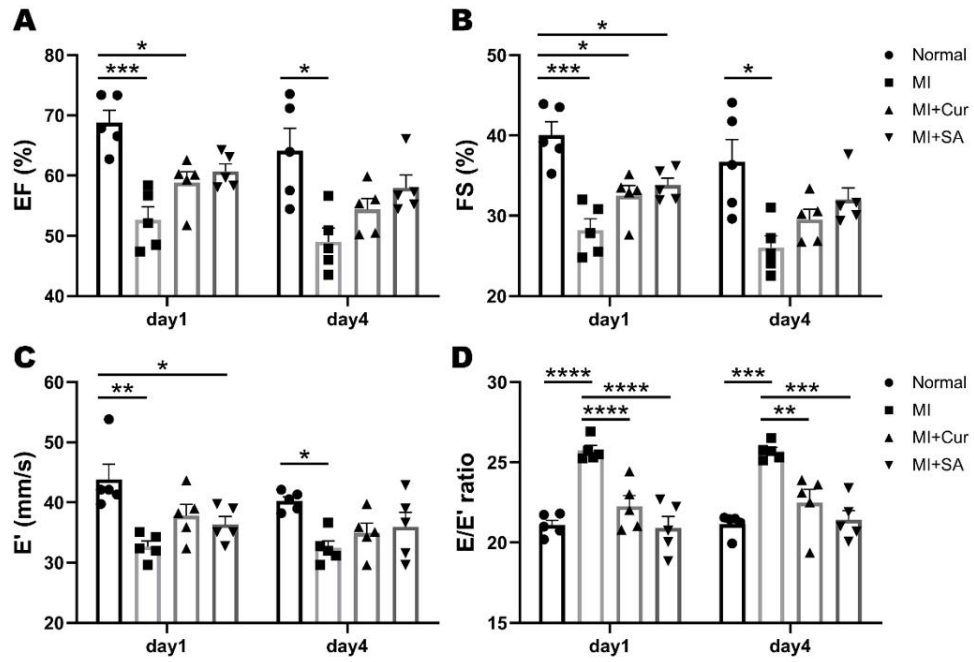


Figure 18. Echocardiographic results on day 4 after MI surgery.

Sapannone A significantly improved left ventricular (LV) systolic and diastolic function ($n = 5/\text{group}$). (A) Ejection fraction, EF; (B) Fractional shortening, FS; (C) Early relaxation velocity on tissue Doppler, E' ; (D) E/E' ratio of LV diastolic function* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$ by two-way ANOVA tests with Tukey's post hoc correction.

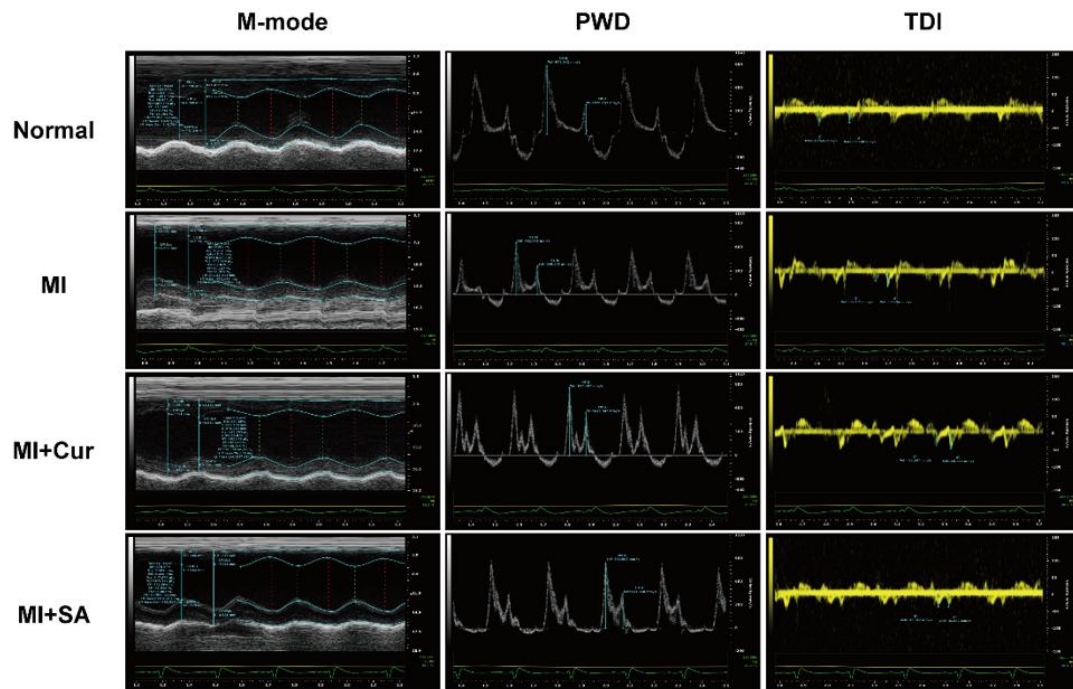


Figure 19. Representative echocardiographic imaging on day 4 after MI surgery.

PWD: Pulse Wave Doppler; and TDI: Tissue Doppler Imaging.

Table 6. Cardiac function measured by echocardiography of sappanone A efficacy study.

Cardiac function	Day 1				Day 4			
	Normal	MI	MI+Cur	MI+SA	Normal	MI	MI+Cur	MI+SA
EF, %	68.79±4.59	****52.6 3±4.85	*58.81±4.1 2	*60.68±2 .82 [#]	64.13±8. 30	***49.01 ±5.06	*54.39±4 .07	57.97±4. 70 ^{##}
FS, %	40.05±3.66	****28.2 1±3.18	**32.48±2. 85	*33.80±1 .98 [#]	36.69±6. 24	***26.03 ±3.28	*29.55±2 .80	31.99±3. 30 ^{##}
HR, BPM	256.16±2 1.28	302.19±4 8.56	303.10±20. 50	259.16±4 9.83	244.41±3 0.13	263.63±1 5.35	256.91±3 8.13	244.75±1 1.91
SV, µl	219.43±2 7.86	182.83±1 0.82	210.01±23. 71	216.28±2 1.84	233.88±2 3.15	206.55±2 2.86	224.25±2 8.84	228.74±3 8.15
CO, mL/min	55.97±6. 27	54.97±6. 07	63.39±8.80	62.82±11 .05	56.93±7. 21	54.23±5. 61	56.93±2. 95	55.90±9. 42
LVIDd, mm	7.73±0.5 3	7.90±0.2 7	7.96±0.46	8.15±0.5 2	8.18±0.7 5	8.73±0.1 5	8.63±0.2 6	8.49±0.7 1
LVIDs, mm	4.66±0.5 3	*5.66±0. 41	5.37±0.41	5.43±0.5 2	5.19±0.8 9	**6.36±0 .41	*6.13±0. 20	5.88±0.7 3
IVSd, mm	1.52±0.0 5	1.53±0.1 6	1.59±0.16	1.54±0.2 3	1.48±0.2 0	1.36±0.0 7	1.40±0.1 6	1.41±0.1 0
IVSs, mm	2.57±0.1 1	2.24±0.2 0	2.55±0.22	2.65±0.2 7	2.52±0.2 4	2.19±0.2 0	2.22±0.2 1	2.34±0.2 3
LVPWd, mm	1.66±0.1 5	1.57±0.1 2	1.70±0.09	1.98±0.5 5	1.57±0.1 7	1.62±0.2 7	1.57±0.1 6	1.66±0.1 2
LVPWs, mm	2.65±0.2 3	2.36±0.2 8	2.53±0.07	2.69±0.3 7	2.42±0.2 6	2.28±0.2 6	2.38±0.2 4	2.58±0.2 3
E', mm/s	43.82±5. 66	***32.67 ±2.14	*37.82±4.1 6	*36.33±2 .95	40.23±1. 62	**32.44± 2.62	34.93±3. 63	35.94±5. 40
E/A ratio	1.66±0.3 2	2.10±0.4 0	1.91±0.37	1.75±0.3 4	1.82±0.2 8	1.95±0.1 7	2.04±0.5 0	2.16±0.6 4
E/E' ratio	21.09±0. 68	****25.7 4±0.68	22.26±1.50 ###	20.92±1. 58####	21.14±0. 68	****25.6 9±0.54	22.50±1. 83 ^{##}	21.42±1. 29####

Values are expressed as the mean ± standard deviation. EF, ejection fraction; FS, fractional shortening; SV, stroke volume; CO, cardiac output; LVIDd, left ventricular internal diameter at diastole; LVIDs, left ventricular internal diameter at systole; IVSd, interventricular septal thickness at diastole; IVSs, interventricular septal thickness at systole; LVPWd, left ventricular posterior wall thickness at diastole; LVPWs, left ventricular posterior wall thickness at systole; E', early diastolic tissue doppler velocity; E/A, the ratio of the early (E) to late (A) ventricular filling velocities; E/E', the ratio of the early (E) to early diastolic tissue Doppler velocities. * p<0.05, ** p<0.01, *** p<0.001, **** p<0.0001 by two-way ANOVA test with Dunnett's post hoc correction for normal versus MI groups (MI, MI+Curcumin, and MI+Sappanone A, respectively). [#] p < 0.05, ^{##} p < 0.01, ^{###} p < 0.001, ^{####} p < 0.0001 for three MI groups.

2.2. Myocardial infarct size

To evaluate the cardioprotective effect of sappanone A isolated from the heartwood *C. sappan* (23), transient LAD ligation surgery and administration was performed according to the experimental design (Figure 17). In addition, Figure 20A shows representative LV slices from the treatment groups to assess LV myocardial infarct size. The infarct size of the curcumin- or sappanone A-treated groups decreased compared to the vehicle-treated MI group, and tended to alleviate myocardial infarction, and the sappanone A-treated group had statistical significance (Figure 20B and 20C). The area of each LV tissue slice was divided into four areas: parasternal short axis area with papillary muscles (SAX), proximal medial, distal medial, and apex areas. The mean and SEM values of the infarct size (%) for each slice are shown in Table 7. In particular, sappanone A treatment was associated with significantly smaller infarct sizes in the distal medial and apical regions.

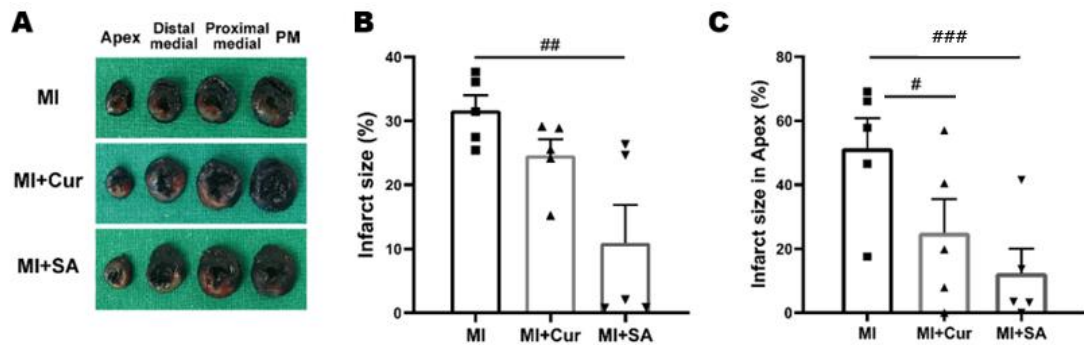


Figure 20. Positive effect of saponin A on myocardial infarct size. (A) Representative photographs of left ventricle slices of the groups and the infarct size of the left ventricles of the **(B)** total and **(C)** apex areas in each group ($n = 5/\text{group}$, right). $\# p < 0.05$ and $### p < 0.01$ by one-way ANOVA test with Tukey's post hoc correction.

Table 7. Myocardial infarct size (%) in each MI area region stained with TTC staining.

MI area region	MI	MI+Cur	MI+SA
SAX	20.52 \pm 11.54	25.68 \pm 7.45	11.53 \pm 8.35
Proximal medial	21.52 \pm 2.63	23.19 \pm 2.38	10.19 \pm 6.31
Distal medial	33.09 \pm 4.83	24.55 \pm 3.12	$\#$ 9.64 \pm 6.22
Apex	51.46 \pm 9.33	$\#$ 25.01 \pm 10.50	$###$ 12.39 \pm 7.64
Total	31.65 \pm 2.37	24.61 \pm 2.53	$###$10.94 \pm 5.95

Values are expressed as the mean \pm SEM. $\#$ ($p < 0.05$), $##$ ($p < 0.01$), and $###$ ($p < 0.001$) indicate statistically significant differences by two-way ANOVA test with Tukey's post hoc correction compared with the MI group.

2.3. Serum chemistry of cardiac markers

Serum CK-MB, LDH, and AST are important indicators in the evaluation of MI-induced models due to myocardial cell damage and rupture (63). As the results of the cardiac marker assays, serum CK-MB, LDH, and AST levels were significantly increased in the rat myocardial I/R injury model group (MI+Veh) compared to the normal control group. The curcumin or saffronone A treatment groups tended to have low CK-MB, LDH, and AST levels, while saffronone A had significantly reduced the LDH and AST levels compared to those of the MI+Veh group (Figure 21).

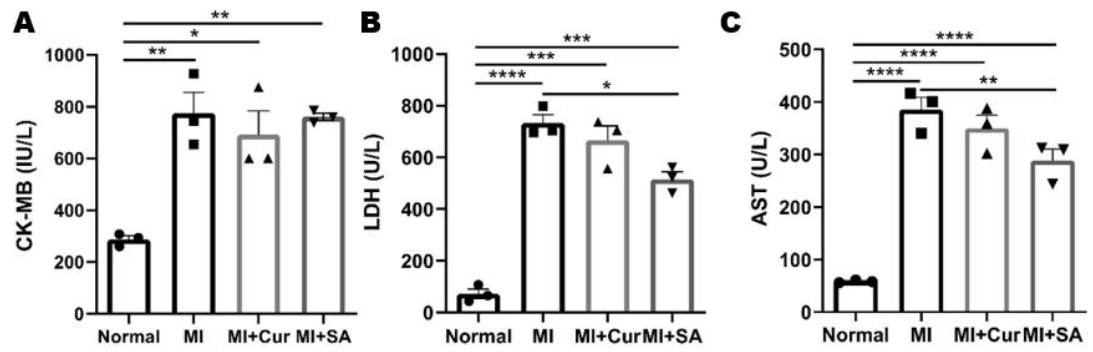


Figure 21. Serum chemistry results of cardiac markers. (A) Creatine kinase MB isozyme (CK-MB, n=3/group), (B) Lactate dehydrogenase (LDH, n=3/group), and (C) Aspartate aminotransferase (AST, n=3/group) on day 1 after MI surgery. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$ by two-way ANOVA test with Tukey's post hoc correction.

2.4. Histopathological results

Representative photomicrographs of tissue stained with hematoxylin and eosin (H&E) are shown in Figure 22 and Masson's trichrome are shown in Figures 23. In H&E-stained slide sections, inflammatory cells infiltration is indicated in epicardial, myocardial, and endocardial areas. Masson's trichrome staining revealed marked fibroblast and areas of collagen deposition. Figure 22A shows histopathological changes in the papillary muscle (PM), medial, and apex regions. Representative photomicrographs of interest with high magnification are shown in Figure 22B (x40, x400, x1500). Mixed cell (mixed state of lymphocytes and monocytes), lymphocytes (arrows) and mononuclear cells (arrow heads) are indicated in myocardial region (Top, x400) and mononuclear cells (arrow heads) with purulent (asterisk) are in endocardial region (Bottom, x400). Representative cell image of mature lymphocytes (arrows) and mononuclear cells (arrow heads) are shown in Figure 22B at high magnification (x1500). Sappanone A was associated with a marked reduction in inflammatory cells infiltration in all epicardial and the medial myocardial regions. In addition, histopathologic individual data are presented in Table 8. The degree of fibrosis in all areas of the MI+Veh group was higher than that seen in curcumin-treated or sappanone A-treated groups in the short axis with papillary muscle area (PM), sappanone A reduced the percentage of fibrosis areas compared to those of MI and curcumin treated MI with statistical significance (Figure 23).

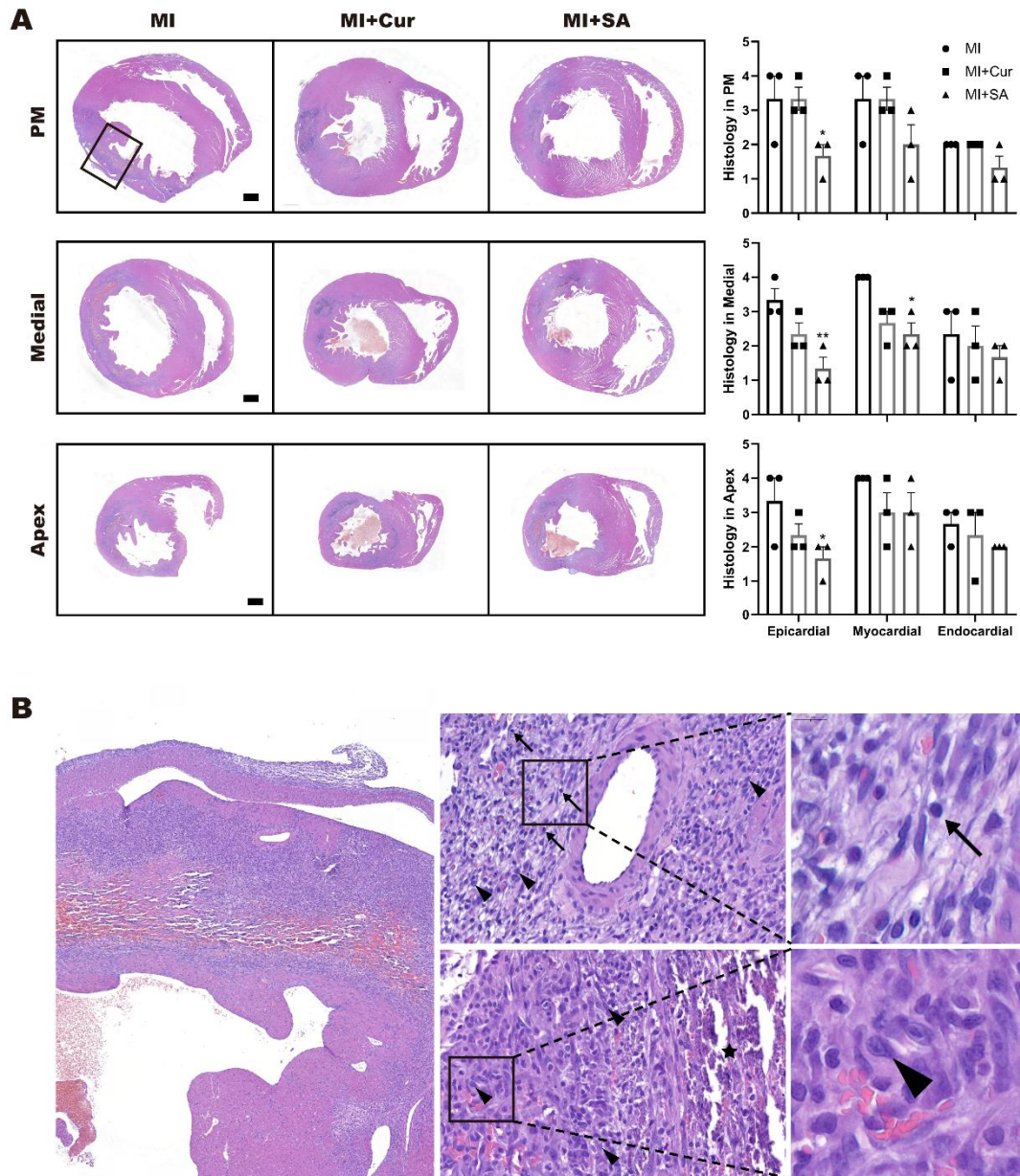


Figure 22. Histopathological images and results stained with hematoxylin and eosin. Representative photomicrographs are shown in hematoxylin and eosin and incidence of histopathological changes (**A**, x12.5) and representative H&E photomicrographs with high magnification (**B**, x40, x400, x1500). Mature lymphocyte (arrows) and mononuclear cells (arrow heads) are shown in myocardial region (Top, x400) and mononuclear cells (arrow heads) with purulent (asterisk) are shown in endocardial region (Bottom, x400). Representative cell image of lymphocyte (arrow) and mononuclear cell (arrow head) can be identified with high magnification (x1500). Grading of histopathological changes in each tissue area (papillary muscle, medial, and apex) of the rat left ventricle. Grades 1, 2, 3, and 4 show minimal, slight, moderate, and severe pathological changes, respectively. Values are mean \pm standard error of the mean (SEM, $n = 3$).

Table 8. Histopathologic individual data.

(A) Histopathologic individual data of rat heart tissues by grading. Grades 1, 2, 3, and 4 show minimal, slight, moderate, and severe pathological changes, respectively. Values are mean \pm standard deviation (SD, $n=3$).

	Animal #	Epicardial			Myocardial			Endocardial		
		PM	Medial	Apex	PM	Medial	Apex	PM	Medial	Apex
MI	1	2	3	2	2	4	4	2	1	2
	3	4	4	4	4	4	4	2	3	3
	4	4	3	4	4	4	4	2	3	3
	AVG	3.33	3.33	3.33	3.33	4.00	4.00	2.00	2.33	2.67
	SD	1.15	0.58	1.15	1.15	0.00	0.00	0.00	1.15	0.58
MI+Cur	1	3	3	3	3	3	4	2	3	3
	2	3	2	2	3	2	2	2	1	1
	5	4	2	2	4	3	3	2	2	3
	AVG	3.33	2.33	2.33	3.33	2.67	3.00	2.00	2.00	2.33
	SD	0.58	0.58	0.58	0.58	0.58	1.00	0.00	1.00	1.15
MI+SA	1	2	2	2	1	2	2	1	2	2
	4	1	1	2	3	3	4	2	2	2
	8	2	1	1	2	2	3	1	1	2
	AVG	1.67	1.33	1.67	2.00	2.33	3.00	1.33	1.67	2.00
	SD	0.58	0.58	0.58	1.00	0.58	1.00	0.58	0.58	0.00

(B) Histopathologic individual data of each cell type of inflammatory cells infiltration. Mixed cell, lymphocyte, mononuclear cell, purulent lesions were described.

	Animal #	Epicardial	Myocardial	Endocardial
MI	1-PM	mixed cell, lymphocyte and mononuclear cell	mixed cell, lymphocyte and mononuclear cell	mononuclear cell
	1-Medial	mixed cell, lymphocyte and mononuclear cell	mixed cell, lymphocyte and mononuclear cell	mononuclear cell with purulent
	1-Apex	mixed cell, lymphocyte and mononuclear cell	mononuclear cell	mononuclear cell with purulent
	3-PM	mixed cell, lymphocyte and mononuclear cell	mixed cell, lymphocyte and mononuclear cell	mononuclear cell with purulent
	3-Medial	mixed cell, lymphocyte and mononuclear cell	mixed cell, lymphocyte and mononuclear cell	mononuclear cell with purulent
	3-Apex	mononuclear cell	mononuclear cell	mononuclear cell with purulent
	4-PM	mononuclear cell	mononuclear cell	mononuclear cell with purulent
	4-Medial	mixed cell, lymphocyte and mononuclear cell	mixed cell, lymphocyte and mononuclear cell	mononuclear cell with purulent
	4-Apex	mononuclear cell	mixed cell, lymphocyte and mononuclear cell	mononuclear cell with purulent
MI+Cur	1-PM	mixed cell, lymphocyte and mononuclear cell	mononuclear cell with purulent	mononuclear cell with purulent
	1-Medial	mononuclear cell	mononuclear cell with purulent	mononuclear cell with purulent
	1-Apex	mononuclear cell	mononuclear cell with purulent	mononuclear cell with purulent
	2-PM	mixed cell, lymphocyte and mononuclear cell	mixed cell, neutrophil and mononuclear cell with purulent	mononuclear cell
	2-Medial	mixed cell, lymphocyte and mononuclear cell	mixed cell, lymphocyte and mononuclear cell	mononuclear cell
	2-Apex	mononuclear cell	mixed cell, lymphocyte and mononuclear cell	mononuclear cell
	5-PM	mononuclear cell	mononuclear cell with purulent	mononuclear cell
	5-Medial	mononuclear cell	mixed cell, lymphocyte and mononuclear cell with purulent	mononuclear cell with purulent
	5-Apex	mononuclear cell	mononuclear cell	mononuclear cell

(B) Histopathologic individual data of each cell type of inflammatory cells infiltration. Mixed cell, lymphocyte, mononuclear cell, purulent lesions were described (continued).

	Animal #	Epicardial	Myocardial	Endocardial
MI+SA	1-PM	mixed cell, lymphocyte and mononuclear cell	mononuclear cell	mononuclear cell
	1-Medial	mononuclear cell	mixed cell, lymphocyte and mononuclear cell	mononuclear cell
	1-Apex	mononuclear cell	mononuclear cell	mononuclear cell
	4-PM	mononuclear cell	mononuclear cell with purulent	mononuclear cell with purulent
	4-Medial	mononuclear cell	mononuclear cell with purulent	mononuclear cell with purulent
	4-Apex	mononuclear cell	mononuclear cell with purulent	mononuclear cell
	8-PM	mononuclear cell	mononuclear cell with purulent	mononuclear cell
	8-Medial	mononuclear cell	mononuclear cell with purulent	mononuclear cell
	8-Apex	mononuclear cell	mononuclear cell with purulent	mononuclear cell

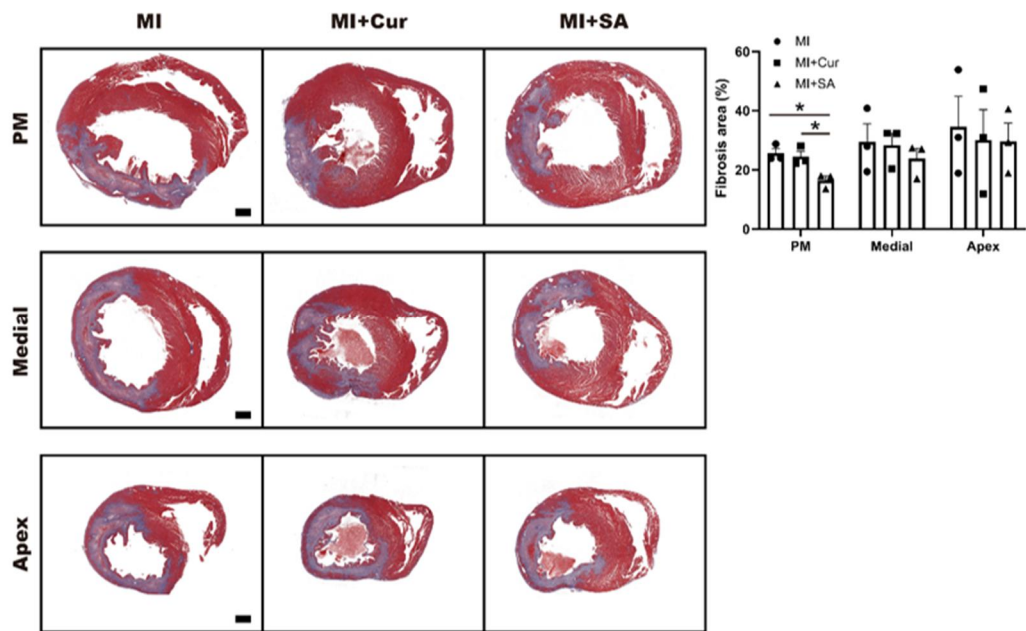


Figure 23. Histopathological images and results stained with Masson's trichrome. Representative photomicrographs in Masson's trichrome (left, x12.5) and fibrosis area percentage (right). * $p < 0.05$, indicate statistically significant differences by one-way ANOVA with Tukey's post hoc correction ($n = 3$).

2.5. mRNA sequencing and data analysis

To investigate molecular characteristics affected by saipanone A in a rat myocardial I/R injury model, we performed mRNA sequencing of left ventricle tissues from the normal group, MI group, MI + Curcumin group, and MI + Saipanone A group, and compared mRNA abundances between the different groups (Figure 24A). In MI versus normal, MI + Curcumin versus MI, and MI + Saipanone A versus MI (2163, 2020, and 793 DEGs, respectively) comparisons (Figure 24B and Table 10), a total of 3568 DEGs with false discovery rates <0.05 and fold changes >1.5 was identified (Materials and Methods). Large numbers of DEGs were identified from the MI + Saipanone A versus MI (2020 DEGs) comparison, but only 793 DEGs were identified in the MI + Curcumin versus MI comparison. In addition, among these DEGs, 883 and 392 genes were shared with the DEGs identified in the MI versus normal comparison (40.8% and 18.1% of the 2163 DEGs, respectively) (Figure 24B). These data indicate that gene expression can be significantly altered by saipanone A in a rat myocardial I/R injury model. To systematically investigate cellular processes associated with saipanone A in this rat MI model, these shared DEGs were classified into six clusters (C1-6) based on their differential expression patterns (Figure 24C).

Enrichment analysis of GOBP was performed using DAVID software to identify cellular processes represented by genes in individual clusters (42). Of the six clusters, C1/3 and C4/6 showed up- and down-regulation in abundances by MI, respectively, but saipanone A treatment suppressed these changes. GOBP enrichment analysis revealed that the genes in C1/C3 were primarily involved in immune and inflammatory responses, cytokine production, neutrophil migration, NF- κ B signaling, and apoptosis (Figure 24D), and C4/6 were involved in glucose and fatty acid metabolism, mitochondrial organization, cellular oxidant detoxification, reactive oxygen species metabolism, and cardiac muscle contraction (Figure 24E). In particular, the genes involved in inflammatory responses were strongly restored in terms of expression by saipanone A ($P < 10^{-4}$) (Figure 24F). The results showed that saipanone A affects a wide range of cellular processes.

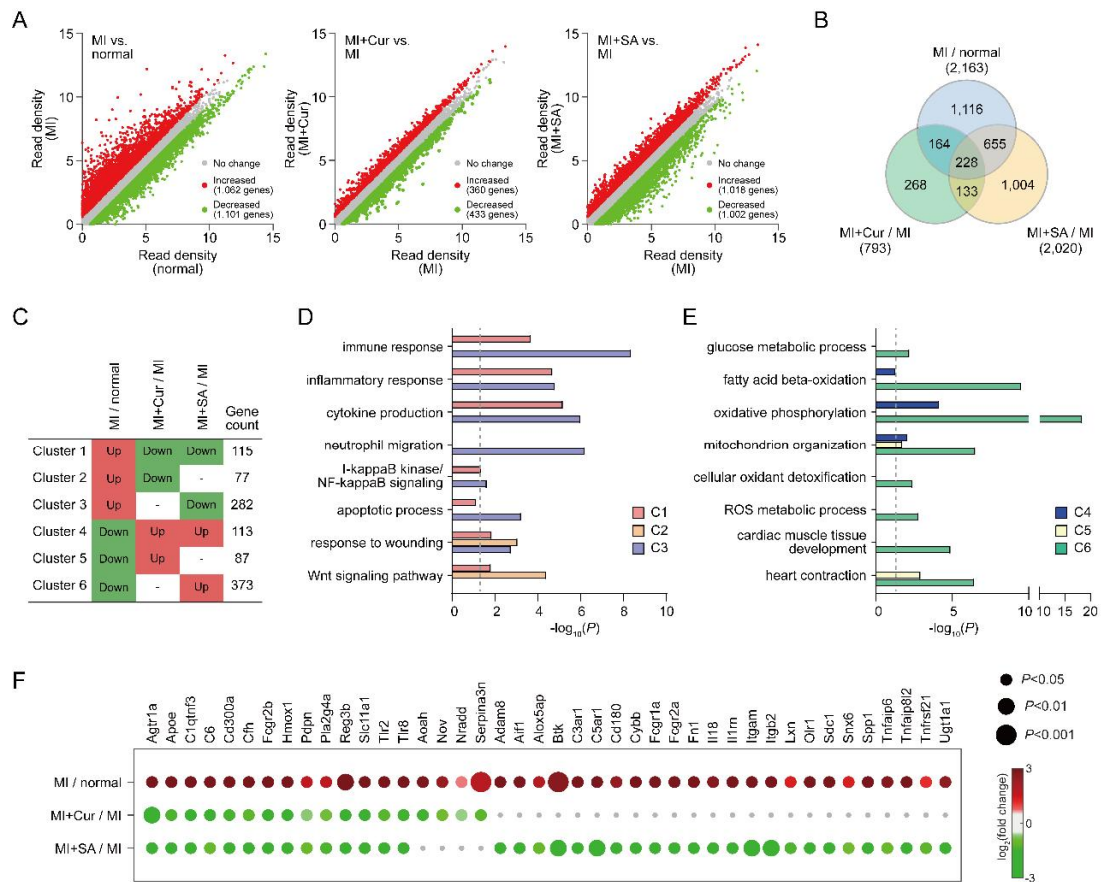


Figure 24. Cellular processes affected by sappanone A treatment. (A) Scatter plots of three comparisons (MI versus normal, MI + Curcumin versus MI, and MI + Sappanone A versus MI). **(B)** Relationships among differentially expressed genes (DEGs). **(C)** Clusters (C1-6) of the genes affected by curcumin or sappanone A. Red and green denote up- and down-regulation, respectively. The number of DEGs in each cluster is denoted. **(D, E)** Cellular processes represented by DEGs in C1-6. X-axis, $-\log_{10}(P)$ where P is the enrichment P -value calculated in DAVID software. **(F)** DEGs involved in inflammatory responses.

Table 9. mRNA seq results. UMR represents the number of reads uniquely mapped. ‘% mapped reads’ means the percentage of the mapped reads (UMR and multi-mapped reads) over the total sequenced reads. The numbers and percentages of the mapped reads to the mitochondrial genome were also shown.

Sample	Total reads	UMR	Multi-mapped reads	% mapped reads	mapped reads to the MT genome (%)
Normal_1	38,838,450	34,555,742	979,434	91.5	1,626,787 (4.2%)
Normal_2	36,005,890	31,939,265	937,963	91.3	1,508,812 (4.2%)
MI_1	45,246,188	40,746,184	1,688,407	93.8	1,242,781 (2.7%)
MI_2	34,917,396	31,272,122	931,641	92.2	1,403,589 (4.0%)
MI+Cur_1	36,082,672	31,988,882	1,062,074	91.6	1,383,980 (3.8%)
MI+Cur_2	42,613,114	37,954,412	1,424,065	92.4	1,394,025 (3.3%)
MI+SA_1	43,818,952	38,757,713	1,222,794	91.2	1,516,899 (3.5%)
MI+SA_2	44,381,526	39,266,038	1,231,531	91.2	1,555,887 (3.5%)

Table 10. 3568 DEGs from the three comparisons (MI versus normal, MI + Curcumin versus MI, and MI + Sappanone A versus MI).

Ensembl IDs, Entrez IDs, symbols, descriptions, P-values, and log₂-fold-changes of the DEGs are shown. P-values were computed as described in Materials and Methods section (This table shows the representative DEGs of each cluster among 1-6 clusters.).

GeneID	Symbol	Description	Inflammation-related genes	Cluster (1-6)	MI / normal			MI+Cur / MI			MI+SA / MI		
					adjusted p value	log ₂ (fold-change)	up/down-DEG (1: up-regulated, -1: down-regulated)	adjusted p value	log ₂ (fold-change)	up/down-DEG (1: up-regulated, -1: down-regulated)	adjusted p value	log ₂ (fold-change)	up/down-DEG (1: up-regulated, -1: down-regulated)
ENSRNOG0000000070	Tmem119	transmembrane protein 119	0	C1	0.0223926	5.130161954	1	0.041749564	-1.348706333	-1	0.032881715	-3.193422484	-1
ENSRNOG0000000081	Smpd3a	sphingomyelin phosphodiesterase, acid-like 3A	0	C1	0.028038965	2.909677814	1	0.038141263	-1.49812964	-1	0.04477969	-2.295313346	-1
ENSRNOG0000000208	Thegl	theg spermatid protein-like	0	C1	0.000136424	1.507452658	1	0.042645132	-1.318023004	-1	0.001097129	-1.536492964	-1
ENSRNOG0000000236	Itm2a	integral membrane protein 2A	0	C1	0.033558217	2.935147252	1	0.045723095	-1.249220086	-1	0.044060263	-2.324216238	-1
ENSRNOG0000000265	Pla2g4a	phospholipase A2 group IVA	1	C1	0.02164241	1.705794424	1	0.038743064	-0.888842417	-1	0.049496002	-1.345615239	-1
ENSRNOG0000000329	Creg1	cellular repressor of E1A-stimulated genes 1	0	C1	0.028780782	1.038454511	1	0.031758937	-0.971410365	-1	0.013096736	-0.664116619	-1
ENSRNOG0000000348	Mnda	myeloid cell nuclear differentiation antigen	0	C1	0.027670509	3.945393586	1	0.043032711	-1.303819323	-1	0.046797298	-2.176410661	-1
ENSRNOG0000000371	Srpx2	sushi-repeat-containing protein, X-linked 2	0	C1	0.036397259	3.837411574	1	0.040246965	-1.410856892	-1	0.036869288	-2.858325731	-1
ENSRNOG0000000395	Rgs18	regulator of G-protein signaling 18	0	C1	0.040292683	3.259778345	1	0.03805628	-1.503659286	-1	0.042061255	-2.440877225	-1
ENSRNOG0000000406	Nrcam	neuronal cell adhesion molecule	0	C1	0.034939708	3.343833895	1	0.032322335	-1.784523125	-1	0.04180483	-2.458837566	-1
ENSRNOG0000000457	Cthrc1	collagen triple helix repeat containing 1	0	C1	0.019645863	7.100597594	1	0.040757612	-1.380836547	-1	0.02719317	-3.696509266	-1
ENSRNOG0000000488	Capn6	calpain 6	0	C1	0.026304103	3.712657365	1	0.038645017	-1.472862409	-1	0.0351973	-2.992277118	-1
ENSRNOG0000000509	C1qtnf7	C1q and TNF related 7	0	C1	0.036182632	2.368544652	1	0.012489353	-0.826979474	-1	0.048253375	-1.394921023	-1
ENSRNOG0000000597	Gpr176	G protein-coupled receptor 176	0	C1	0.038099939	2.45937608	1	0.045218559	-1.26226329	-1	0.007024512	-1.626448937	-1
ENSRNOG0000000605	Sulf2	sulfatase 2	0	C1	0.023518254	1.345854935	1	0.005094851	-0.649602682	-1	0.008642024	-0.991684607	-1
ENSRNOG0000000615	Reg3b	regenerating family member 3 beta	1	C1	0.007055309	4.661947345	1	0.013913919	-3.775620517	-1	0.037504378	-2.779213562	-1
ENSRNOG0000000624	Lztf1	leucine zipper transcription factor-like 1	0	C1	0.018638705	1.073805779	1	0.009758679	-0.694628684	-1	0.023553546	-0.943692559	-1
ENSRNOG0000000673	Cdkn2b	cyclin-dependent kinase inhibitor 2B	0	C1	0.026613272	2.597955493	1	0.04637156	-1.235590265	-1	0.043935039	-2.32878767	-1
ENSRNOG0000000712	Cd8b	CD8b molecule	0	C1	0.046398065	2.934719574	1	0.040966833	-1.372891113	-1	0.04651811	-2.189786364	-1
ENSRNOG0000000781	Gdf6	growth differentiation factor 6	0	C1	2.03513E-05	3.891234228	1	0.005371016	-1.559427837	-1	0.039264628	-2.627091445	-1
ENSRNOG0000000791	Tbxas1	thromboxane A synthase 1	0	C1	0.042799753	3.20943156	1	0.045805439	-1.247908267	-1	0.042847193	-2.398234756	-1
ENSRNOG0000000830	Nanp	N-acetylneuraminic acid phosphatase	0	C1	0.00102175	1.309160307	1	0.040160021	-1.014107902	-1	0.011213789	-1.366441671	-1
ENSRNOG0000000881	Gpnmb	glycoprotein nmb	0	C1	0.012631759	5.605081144	1	0.039679191	-1.434061554	-1	0.025345552	-3.974382605	-1
ENSRNOG0000000894	Cpz	carboxypeptidase Z	0	C1	0.035698465	3.839027633	1	0.034199147	-1.655752513	-1	0.035413121	-2.977431449	-1
ENSRNOG0000000946	Sfrp2	secreted frizzled-related protein 2	0	C1	0.031907561	4.433238726	1	0.036251865	-1.56338905	-1	0.038550007	-2.68796595	-1
ENSRNOG0000000982	Tlr2	toll-like receptor 2	1	C1	0.014695123	3.392707424	1	0.046333484	-1.237982022	-1	0.049821102	-2.032348777	-1
ENSRNOG0000001007	Car3	carbonic anhydrase 3	0	C1	0.029956716	4.780156849	1	0.046453173	-1.232663526	-1	0.024837245	-4.067390521	-1
ENSRNOG0000001018	Clec4d	C-type lectin domain family 4, member D	0	C1	0.000196205	3.556417625	1	0.040274655	-1.410073576	-1	0.019893171	-2.069920452	-1
ENSRNOG0000001039	Nrg1	neuregulin 1	0	C1	0.049649336	2.741789676	1	0.048943089	-1.039224582	-1	0.045361406	-2.267567368	-1
ENSRNOG0000001066	Wisp2	WNT1 inducible signaling pathway protein 2	0	C1	0.024124167	6.069004294	1	0.011707317	-2.421343803	-1	0.022669165	-4.55662268	-1

ENSRNOG00000000156	Megf6	multiple EGF-like-domains 6	0	C2	0.000376111	1.822807295	1	0.009407666	-1.409609743	-1	0.052224561	-1.939630692	0
ENSRNOG00000000080	Msl3l2	male-specific lethal 3-like 2 (Drosophila)	0	C2	0.031774925	0.739942458	1	0.002304814	-0.778867818	-1	0.083090229	-1.141174776	0
ENSRNOG00000000090	Tps1	tyrosylprotein sulfotransferase 1	0	C2	0.002251263	1.036337092	1	0.020859466	-0.850939811	-1	0.132624355	-0.625948726	0
ENSRNOG000000001229	Col18a1	collagen type XVIII alpha 1 chain	0	C2	0.038963862	1.937343256	1	0.00250613	-0.71512137	-1	0.071801678	-1.200601555	0
ENSRNOG000000001249	Col6a1	collagen type VI alpha 1 chain	0	C2	0.043973617	1.148599755	1	0.036133895	-0.580512296	-1	0.111439834	-0.79188717	0
ENSRNOG000000001469	Ein	elastin	0	C2	0.047872205	1.590015306	1	0.041326623	-1.061185784	-1	0.088664832	-1.421559633	0
ENSRNOG000000001792	Slc12a8	solute carrier family 12, member 8	0	C2	0.000643679	0.734482336	1	0.031962834	-0.738901788	-1	0.047180495	-0.565921064	0
ENSRNOG000000002746	Fstl1	folliculin-like 1	0	C2	0.03226408	2.137770759	1	0.022451929	-0.78194852	-1	0.063880213	-1.542873433	0
ENSRNOG000000002886	Myh10	myosin heavy chain 10	0	C2	0.019601729	1.676824992	1	0.018908246	-0.956645397	-1	0.063798863	-1.459601661	0
ENSRNOG000000003587	Vegf	vascular endothelial growth factor D	0	C2	0.025818282	2.730320974	1	0.036951865	-1.439489043	-1	0.055343985	-1.80736047	0
ENSRNOG000000003736	Col5a2	collagen type V alpha 2 chain	0	C2	0.044600941	2.418666237	1	0.040113563	-0.81124472	-1	0.056835875	-1.761169356	0
ENSRNOG000000004210	Osr1	odd-skipped related transcription factor 1	0	C2	0.040189869	2.861121288	1	0.008914699	-1.596637055	-1	0.052768617	-1.913815537	0
ENSRNOG000000004229	Tac3	tachykinin 3	0	C2	0.023152912	3.048906056	1	0.005030326	-0.958437056	-1	0.051138331	-1.976505947	0
ENSRNOG000000004290	Grt10	growth factor receptor bound protein 10	0	C2	0.026540223	1.181943188	1	0.018239773	-0.813678324	-1	0.09130403	-1.014293929	0
ENSRNOG000000004624	Rnd3	Rho family GTPase 3	0	C2	0.023075963	1.055196092	1	0.003414834	-0.614772562	-1	0.110819457	-0.800365067	0
ENSRNOG000000004699	Fibin	fin bud initiation factor homolog (zebrafish)	0	C2	0.045649485	2.988295703	1	0.043917925	-1.116984799	-1	0.051522068	-1.96190971	0
ENSRNOG000000005720	Spic	Spi-C transcription factor	0	C2	0.028161182	2.442858596	1	0.040216883	-1.412954403	-1	0.053988824	-1.859169324	0
ENSRNOG000000006228	Pdia4	protein disulfide isomerase family A, member 4	0	C2	0.042143445	1.329427193	1	0.0423745	-0.749311456	-1	0.052673352	-1.022659469	0
ENSRNOG000000006553	Bnc2	basonuclin 2	0	C2	0.020629205	2.501489367	1	0.048499161	-1.045567532	-1	0.06593037	-1.48508952	0
ENSRNOG000000007271	Map3k9	mitogen-activated protein kinase kinase kinase 9	0	C2	0.042231119	1.272302817	1	0.047900374	-0.595027879	-1	0.080623929	-1.180273041	0
ENSRNOG000000008332	Smo	smoothened, frizzled class receptor	0	C2	0.035630599	1.059088969	1	0.014120532	-0.801319939	-1	0.054510421	-1.080252045	0
ENSRNOG000000008697	Nov	nephroblastoma overexpressed	1	C2	0.02406065	2.397443095	1	0.047719706	-0.900487084	-1	0.064041284	-1.539374759	0
ENSRNOG000000008749	Col5a1	collagen type V alpha 1 chain	0	C2	0.048436281	1.989482579	1	0.02775842	-0.875313599	-1	0.065149896	-1.507153845	0
ENSRNOG000000009656	Rspo1	R-spondin 1	0	C2	0.02223715	1.618667275	1	0.033439153	-0.845980137	-1	0.089923714	-1.035560457	0
ENSRNOG000000009892	Adamts15	ADAM metalloproteinase with thrombospondin type 1 motif 15	0	C2	0.047682223	1.135839618	1	0.014027616	-1.049674472	-1	0.10947123	-0.813243371	0
ENSRNOG000000010260	Dixdc1	DIX domain containing 1	0	C2	0.044142405	1.940632272	1	0.000880114	-0.944385043	-1	0.057734303	-1.327693008	0
ENSRNOG000000010311	Dzip1	DAZ interacting zinc finger protein 1	0	C2	0.014807928	1.520594329	1	0.022604207	-1.081366148	-1	0.083737294	-1.13132116	0
ENSRNOG000000010466	Chp2	chondroitin polymerizing factor 2	0	C2	0.01977572	0.82342042	1	0.02532972	-0.589265293	-1	0.081956351	-0.796797096	0
ENSRNOG000000010478	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3n	1	C2	0.000378584	1.808487487	1	0.047841008	-1.201177788	-1	0.396172802	-0.098742585	0
ENSRNOG000000010685	Tbx18	T-box18	0	C2	0.038960549	1.585508972	1	0.027278358	-0.779254941	-1	0.076916429	-1.242838449	0
ENSRNOG000000010890	Bmp1	bone morphogenetic protein 1	0	C2	0.037789414	1.375970465	1	0.023855981	-0.839716205	-1	0.073697732	-1.114731396	0
ENSRNOG000000012486	Prim2	DNA primase subunit 2	0	C2	0.017727566	1.412858434	1	0.02306104	-0.795837756	-1	0.069576894	-1.399927019	0
ENSRNOG000000012531	Ephb2	Eph receptor B2	0	C2	0.020131162	1.889451876	1	0.014819977	-1.342599818	-1	0.088508277	-1.425719743	0
ENSRNOG000000013048	Pde7a	phosphodiesterase 7A	0	C2	0.044222799	1.347261647	1	0.049768421	-0.852611847	-1	0.088792118	-1.084172842	0
ENSRNOG000000013917	Igsf10	immunoglobulin superfamily, member 10	0	C2	0.043117196	3.173544631	1	0.01073945	-1.198493581	-1	0.052764111	-1.914421668	0
ENSRNOG000000014293	Nkd1	naked cuticle homolog 1	0	C2	0.049676675	1.96285177	1	0.04922808	-1.164723835	-1	0.054100144	-1.332063164	0
ENSRNOG000000014361	Edn1	endothelin 1	0	C2	0.033174404	2.033919518	1	0.046417655	-1.234129552	-1	0.073395319	-1.312546884	0
ENSRNOG000000014883	Il1rl2	interleukin 1 receptor-like 2	0	C2	0.033081749	1.821587039	1	0.016407278	-1.108890552	-1	0.057244599	-1.751595112	0
ENSRNOG000000015505	Mfap5	microfibril associated protein 5	0	C2	0.045860303	2.592090029	1	0.035790425	-0.84188625	-1	0.058197573	-1.710225684	0
ENSRNOG000000017084	Hsd11b2	hydroxysteroid 11-beta dehydrogenase 2	0	C2	0.033078721	1.530617525	1	0.038048268	-1.505552739	-1	0.060442325	-1.645717712	0
ENSRNOG000000018251	Mrc1	mannose receptor, C type 1	0	C2	0.044252479	3.097122911	1	0.038343627	-1.484673197	-1	0.050129936	-2.016434339	0
ENSRNOG000000020151	Cdh1	cadherin 1	0	C2	0.000132922	1.579407151	1	0.04137308	-0.849199568	-1	0.082813665	-1.14645482	0
ENSRNOG000000020936	Nradd	neurotrophin receptor associated death domain	1	C2	0.031974983	0.709565632	1	0.049072138	-0.854934292	-1	0.086689605	-0.934967269	0
ENSRNOG000000020945	Msa4l	membrane spanning 4-domains A1	0	C2	0.000563378	0.824375099	1	0.024317977	-0.922416415	-1	0.079624459	-0.917401338	0
ENSRNOG000000021063	Grii2d	glutamate ionotropic receptor NMDA type subunit 2D	0	C2	0.04777338	1.176122513	1	0.019907085	-0.682215214	-1	0.059181413	-1.259476962	0
ENSRNOG000000021693	Fam149a	family with sequence similarity 149, member A	0	C2	0.003262929	1.152871126	1	0.013823719	-0.717287446	-1	0.050677677	-1.099015183	0
ENSRNOG000000022429	RGD1312005	similar to DD1	0	C2	0.000251313	1.684742082	1	0.040502234	-1.394946838	-1	0.088863219	-1.04940515	0

ENSRNOG00000000170	Slc30a4	solute carrier family 30 member 4	0	C3	0.026875776	0.780284962	1	0.168068138	-0.269590782	0	0.03520776	-0.628904534	-1
ENSRNOG00000000172	Sqor	sulfide quinone oxidoreductase	0	C3	0.02452346	0.902444303	1	0.108577427	-0.51115072	0	0.018105912	-0.685654353	-1
ENSRNOG00000000515	Mapk13	mitogen activated protein kinase 13	0	C3	0.000205719	1.69249683	1	0.082431403	-0.67329408	0	0.020805225	-1.488456575	-1
ENSRNOG00000000565	Sgpl1	sphingosine-1-phosphate lyase 1	0	C3	0.039548149	1.269229378	1	0.098480916	-0.554218216	0	0.043822913	-1.20361201	-1
ENSRNOG00000000632	Cdk1	cyclin-dependent kinase 1	0	C3	0.016188131	2.580880806	1	0.075155978	-0.739998564	0	0.049459892	-2.045072883	-1
ENSRNOG00000000816	Ppp1r18	protein phosphatase 1, regulatory subunit 18	0	C3	0.014674118	0.836951272	1	0.155287828	-0.351751515	0	0.013257308	-0.697131204	-1
ENSRNOG00000000853	Aif1	allograft inflammatory factor 1	1	C3	0.027783223	2.908047919	1	0.061155751	-0.927097168	0	0.017390729	-1.698500072	-1
ENSRNOG00000000855	Lst1	leukocyte specific transcript 1	0	C3	0.019774785	2.855726851	1	0.057231493	-0.991507095	0	0.047316162	-1.771382907	-1
ENSRNOG00000000907	Alox5ap	arachidonate 5-lipoxygenase activating protein	1	C3	0.010540689	1.833430296	1	0.08607798	-0.646508535	0	0.047134618	-1.097781195	-1
ENSRNOG00000001216	Trpm2	transient receptor potential cation channel, subfamily M	0	C3	0.00048304	1.672514359	1	0.084572719	-0.865703724	0	0.012362895	-1.111117388	-1
ENSRNOG00000001224	Itgb2	integrin subunit beta 2	1	C3	0.02105988	3.418742088	1	0.058826556	-0.959530599	0	0.007455106	-2.475677951	-1
ENSRNOG00000001348	Erp29	endoplasmic reticulum protein 29	0	C3	0.034760522	1.336922731	1	0.086079447	-0.646490922	0	0.015530214	-0.755059679	-1
ENSRNOG00000001383	Slc8b1	solute carrier family 8 member B1	0	C3	0.00596942	1.366740292	1	0.114949326	-0.479681616	0	0.042449207	-0.979907749	-1
ENSRNOG00000001514	Cdca7	cell division cycle associated 7	0	C3	0.034530402	0.821914335	1	0.17034198	-0.194114353	0	0.010920828	-1.314806654	-1
ENSRNOG00000001713	LOC100360218	interleukin 13 receptor, alpha 1-like	0	C3	0.01442257	1.148781953	1	0.116738308	-0.47098976	0	0.03983429	-0.840303106	-1
ENSRNOG00000001830	Arnt2	aryl hydrocarbon receptor nuclear translocator-like 2	0	C3	0.000108257	2.103335819	1	0.057093819	-0.754837261	0	0.04341919	-1.644384151	-1
ENSRNOG00000002396	Serpinb8	serpin family B member 8	0	C3	0.032994543	3.25881459	1	0.093263523	-0.589364476	0	0.03840942	-2.695334751	-1
ENSRNOG00000002488	Galnt10	polypeptide N-acetylgalactosaminyltransferase 10	0	C3	0.027441635	1.101424071	1	0.085288107	-0.854077393	0	0.005342116	-1.213824772	-1
ENSRNOG00000002514	Ccdc93	coiled-coil domain containing 93	0	C3	0.0185712	0.935181928	1	0.150807427	-0.365000123	0	0.045464674	-0.952162941	-1
ENSRNOG00000002520	Litaf	lipopolysaccharide-induced TNF factor	0	C3	0.048272903	1.516969246	1	0.111867797	-0.496758874	0	0.031680768	-1.123381436	-1
ENSRNOG00000002585	Cu14b	cullin 4B	0	C3	0.034741861	0.886990854	1	0.134422506	-0.392103232	0	0.023779001	-0.730888434	-1
ENSRNOG00000002662	Pbd1	polysaccharide biosynthesis domain containing 1	0	C3	0.045779421	1.243041989	1	0.113694641	-0.486715381	0	0.025206449	-0.853613821	-1
ENSRNOG00000002775	Npl	N-acetylneuraminate pyruvate lyase	0	C3	0.044651289	1.771886638	1	0.061700619	-0.920503263	0	0.013595491	-1.523596899	-1
ENSRNOG00000003104	Trpv2	transient receptor potential cation channel, subfamily V	0	C3	0.048046829	2.83478241	1	0.070318237	-0.789589525	0	0.045806954	-2.237315221	-1
ENSRNOG00000003388	Cenpf	centromere protein F	0	C3	0.022530517	2.145537232	1	0.081887284	-0.678281784	0	0.041638485	-1.869138618	-1
ENSRNOG00000003622	Cybb	cytochrome b-245 beta chain	1	C3	0.028899864	3.476904129	1	0.058965224	-0.958309385	0	0.025842181	-2.214813698	-1
ENSRNOG00000003732	Flrt2	fibronectin leucine rich transmembrane protein 2	0	C3	0.017798271	2.522857773	1	0.062583559	-0.785796991	0	0.024502556	-1.604794022	-1
ENSRNOG00000004111	Soat1	sterol O-acyltransferase 1	0	C3	0.048922347	2.779890451	1	0.08994756	-0.793672851	0	0.048895113	-2.071533082	-1
ENSRNOG00000004132	Lasp1	LIM and SH3 protein 1	0	C3	0.026853863	0.864186497	1	0.141912482	-0.388415128	0	0.004441604	-0.843910018	-1
ENSRNOG00000004217	Stk10	serine/threonine kinase 10	0	C3	0.00367841	0.623611876	1	0.10727241	-0.516326346	0	0.042835234	-0.960330027	-1
ENSRNOG00000004273	Ifitm1	interferon induced transmembrane protein 1	0	C3	0.042809129	2.588156784	1	0.054788733	-1.039431208	0	0.026718443	-1.70141875	-1
ENSRNOG00000004616	Npm1	nucleophosmin 1	0	C3	0.031217871	1.088498284	1	0.117221283	-0.468473273	0	0.024097523	-0.756350153	-1
ENSRNOG00000004659	Crel2	cysteine-rich with EGF-like domains 2	0	C3	0.02868583	0.895553017	1	0.117553233	-0.457800245	0	0.02073273	-0.66947825	-1
ENSRNOG00000004700	Nxt1	nuclear transport factor 2-like export factor 1	0	C3	0.022536231	1.032095297	1	0.100998839	-0.488888854	0	0.037213285	-0.821442534	-1
ENSRNOG00000004959	Actr2	ARP2 actin related protein 2 homolog	0	C3	0.001623074	1.035178447	1	0.134942839	-0.414098745	0	0.033212085	-0.904224886	-1
ENSRNOG00000005209	Spred1	sprouty-related, EVH1 domain containing 1	0	C3	0.049293168	0.667907536	1	0.170120015	-0.250246716	0	0.011774151	-0.749170116	-1
ENSRNOG00000005249	Snx6	sorting nexin 6	1	C3	0.027435364	1.336321823	1	0.095452563	-0.574540396	0	0.046589013	-0.919999213	-1
ENSRNOG00000005277	Ptptr	protein tyrosine phosphatase, receptor type, V	0	C3	0.030250708	4.738887421	1	0.051609993	-1.115081546	0	0.034891514	-3.007345687	-1
ENSRNOG00000005302	Slc2a9	solute carrier family 2 member 9	0	C3	0.037430277	1.371175174	1	0.095003176	-0.577490347	0	0.019939048	-1.18594149	-1
ENSRNOG00000005348	Pamr1	peptidase domain containing associated with muscle re	0	C3	0.000195615	3.30338924	1	0.053733385	-1.013321637	0	0.043620487	-2.357161662	-1
ENSRNOG00000005433	Shp1	SHQ1, H/ACA ribonucleoprotein assembly factor	0	C3	0.037327727	0.902596955	1	0.017447413	-0.234309505	0	0.037596015	-0.732157658	-1
ENSRNOG00000005679	Fap	fibroblast activation protein, alpha	0	C3	0.045540966	2.990144328	1	0.057822812	-0.979032903	0	0.048194544	-2.103550695	-1
ENSRNOG00000005772	Haod4	3-hydroxyacyl-CoA dehydratase 4	0	C3	0.035696586	2.463887673	1	0.056312622	-1.010770279	0	0.047241316	-2.148782164	-1
ENSRNOG00000005871	Il1rn	interleukin 1 receptor antagonist	1	C3	0.039937649	3.461827613	1	0.185967187	-0.361381772	0	0.043625967	-2.356774629	-1
ENSRNOG00000005988	Rbp1	ribosome binding protein 1	0	C3	2.26997E-05	0.904543748	1	0.117828004	-0.464675798	0	0.029233189	-0.703902863	-1
ENSRNOG00000006079	Psd4	plekstrin and Sec7 domain containing 4	0	C3	0.01756421	1.848988094	1	0.078879808	-0.70678629	0	0.004602176	-1.509778266	-1
ENSRNOG00000006231	Ptpro	protein tyrosine phosphatase, receptor type, O	0	C3	0.044157399	2.538729544	1	0.088885977	-0.799615404	0	0.020279198	-1.922439625	-1

ENSRNOG00000000010	Cisd1	CDGS iron sulfur domain 1	0	C4	0.043149874	-1.083490283	-1	0.046689895	0.822437792	1	0.027193603	1.239522517	1
ENSRNOG000000001182	Ndufv3	NADH:ubiquinone oxidoreductase subunit V3	0	C4	0.011402691	-1.466290538	-1	0.001884114	0.934653605	1	0.04330808	1.454319543	1
ENSRNOG000000001211	RGD1303003	homolog of zebrafish ES1	0	C4	0.030046536	-1.763202817	-1	0.036593109	0.938783489	1	0.020122559	1.454767734	1
ENSRNOG000000001551	Atp5j	ATP synthase, H+ transporting, mitochondrial Fo comp	0	C4	0.027726169	-1.11168107	-1	0.039439928	0.788874095	1	0.022955826	1.104453493	1
ENSRNOG000000001596	Atp5g3	ATP synthase, H+ transporting, mitochondrial Fo comp	0	C4	0.019751782	-1.518161502	-1	0.048426894	1.122419662	1	0.001418272	1.302233884	1
ENSRNOG000000001880	Dgcr6	DiGeorge syndrome critical region gene 6	0	C4	0.014085427	-0.864773612	-1	0.009374113	0.822793486	1	0.007798532	0.996524468	1
ENSRNOG000000001991	Atp5o	ATP synthase, H+ transporting, mitochondrial F1 comp	0	C4	0.022123542	-1.255804273	-1	0.038727578	0.867017111	1	0.030131734	1.216605013	1
ENSRNOG000000002721	Ndufb4	NADH:ubiquinone oxidoreductase subunit B4	0	C4	0.009433398	-1.128496277	-1	0.021804104	0.760971876	1	0.014119808	1.224668997	1
ENSRNOG000000002827	Rbfox1	RNA binding fox-1 homolog 1	0	C4	0.001506484	-2.563517415	-1	0.048264746	1.581744347	1	0.028499148	2.261769742	1
ENSRNOG000000003150	Mpc2	mitochondrial pyruvate carrier 2	0	C4	0.01278836	-1.310915942	-1	0.016309201	0.882423809	1	0.030813999	1.153657313	1
ENSRNOG000000003626	Atp5h	ATP synthase, H+ transporting, mitochondrial Fo comp	0	C4	0.03256565	-1.172381547	-1	0.048731449	0.807410982	1	0.0243256	1.158855213	1
ENSRNOG000000003998	Sgca	sarcoglycan, alpha	0	C4	0.013981899	-1.665969242	-1	0.027737773	1.137428925	1	0.02732927	1.555209325	1
ENSRNOG000000004608	Pam16	presequence translocase associated motor 16	0	C4	0.046779297	-0.936281962	-1	0.009583172	0.73980003	1	0.022224407	1.228350525	1
ENSRNOG000000004629	Fkbp3	FK506 binding protein 3	0	C4	0.007329687	-0.881660524	-1	0.04569696	0.826469411	1	0.020643597	0.970226279	1
ENSRNOG000000005668	Ndufa8	NADH:ubiquinone oxidoreductase subunit A8	0	C4	0.000166984	-1.199510866	-1	0.035578784	0.851283268	1	0.032955319	1.280755422	1
ENSRNOG000000005698	Ndufa5	NADH:ubiquinone oxidoreductase subunit A5	0	C4	0.039651646	-1.192330164	-1	0.025512969	0.8308704	1	0.029769301	1.155808822	1
ENSRNOG000000007235	Atp5g1	ATP synthase, H+ transporting, mitochondrial Fo comp	0	C4	0.008653768	-1.779020129	-1	0.040283908	1.192191201	1	0.019579693	1.583412862	1
ENSRNOG000000007407	Ndufa12	NADH:ubiquinone oxidoreductase subunit A12	0	C4	0.026384284	-1.295886695	-1	0.049704478	0.818906005	1	0.043139992	1.145996245	1
ENSRNOG000000007967	Sdhb	succinate dehydrogenase complex iron sulfur subunit B	0	C4	0.033683746	-1.442332496	-1	0.049056652	0.892859445	1	0.018240923	1.294287992	1
ENSRNOG000000008210	Ky	kyphoscoliosis peptidase	0	C4	0.015584496	-2.867184721	-1	0.043870866	1.738874892	1	0.034072818	2.380463259	1
ENSRNOG000000008329	Ndufb11	NADH:ubiquinone oxidoreductase subunit B11	0	C4	0.015418041	-1.451461604	-1	0.040144535	1.009217085	1	0.015112728	1.446477043	1
ENSRNOG000000008566	Mrp15	mitochondrial ribosomal protein L15	0	C4	0.024074604	-1.026650152	-1	0.02081817	0.822870716	1	0.038883864	1.035995716	1
ENSRNOG000000008569	Ndufa6	NADH:ubiquinone oxidoreductase subunit A6	0	C4	0.013914062	-1.13569883	-1	0.008674668	0.758422942	1	0.010239874	1.085016388	1
ENSRNOG000000008791	Ncs1	neuronal calcium sensor 1	0	C4	0.039254061	-1.214381285	-1	0.010473609	0.768267431	1	0.014368856	1.084277948	1
ENSRNOG000000009063	Dnajc15	DnaJ heat shock protein family (Hsp40) member C15	0	C4	0.032858114	-1.109736432	-1	0.049528971	0.755931714	1	0.031784638	1.081891745	1
ENSRNOG000000009155	Ndufs3	NADH:ubiquinone oxidoreductase core subunit S3	0	C4	0.012994567	-1.596100816	-1	0.040028391	1.045538815	1	0.016288843	1.469826435	1
ENSRNOG000000009364	Ndufb9	NADH:ubiquinone oxidoreductase subunit B9	0	C4	0.025714042	-1.25889782	-1	0.024862563	0.87090411	1	0.002925678	1.236616902	1
ENSRNOG000000009888	Timm8b	translocase of inner mitochondrial membrane 8 homolog	0	C4	0.008122192	-0.801627967	-1	0.017207382	0.609161605	1	0.038339887	0.871661549	1
ENSRNOG00000010047	Ddit4l	DNA-damage-inducible transcript 4-like	0	C4	0.013951033	-2.650904214	-1	0.047140127	1.62030634	1	0.026736794	2.108684293	1
ENSRNOG00000010092	Magi3	MAGI family member, X-linked	0	C4	0.014108491	-3.03513242	-1	0.038560665	1.966674515	1	0.002518023	2.534788803	1
ENSRNOG00000010363	Mrs23	mitochondrial ribosomal protein S23	0	C4	0.02321156	-1.052396581	-1	0.01511937	0.749484376	1	0.005667191	1.097289326	1
ENSRNOG00000010673	Eral1	Era-like 12S mitochondrial rRNA chaperone 1	0	C4	0.025841567	-0.956139404	-1	0.015369725	0.677481585	1	0.025790405	0.969112507	1
ENSRNOG00000010697	Hadh	hydroxyacyl-CoA dehydrogenase	0	C4	0.036525791	-2.384551992	-1	0.047253437	1.616701949	1	0.028128195	2.1700059	1
ENSRNOG00000010807	Cox8c	cytochrome c oxidase subunit 8C	0	C4	0.008453069	-1.029119619	-1	0.042919088	0.725118	1	0.018150478	1.043094788	1
ENSRNOG00000010819	Hspa4l	heat shock protein family A (Hsp70) member 4 like	0	C4	0.037788815	-1.042526656	-1	0.01456446	0.609769355	1	0.026087298	0.923134196	1
ENSRNOG00000010984	Anxa11	annexin A11	0	C4	0.014548867	-1.060283161	-1	0.024885792	0.650582735	1	0.012249312	1.024976078	1
ENSRNOG00000011280	Cmb1	carboxymethylenebutenolidase homolog	0	C4	0.013810504	-2.159053316	-1	0.038133953	1.541478832	1	0.01683838	2.136596875	1
ENSRNOG00000011912	Tmem38a	transmembrane protein 38a	0	C4	0.021415638	-1.635450295	-1	0.047033166	1.163544271	1	0.028886486	1.561105609	1
ENSRNOG00000011949	Ndufb5	NADH:ubiquinone oxidoreductase subunit B5	0	C4	0.022111919	-1.387352913	-1	0.034110208	0.688453115	1	0.004560888	1.321550015	1
ENSRNOG00000011994	Perp	PERP, TP53 apoptosis effector	0	C4	0.035357792	-1.988670751	-1	0.048248562	1.582834156	1	0.008384454	2.144580942	1
ENSRNOG00000012123	Fdx1	ferredoxin 1	0	C4	0.017642891	-0.916724	-1	0.049033424	0.672618972	1	0.024007734	0.988094245	1
ENSRNOG00000012410	S100a1	S100 calcium binding protein A1	0	C4	0.039195458	-1.683996502	-1	0.028958575	1.094570013	1	0.02272908	1.826760406	1
ENSRNOG00000012447	Setd6	SET domain containing 6	0	C4	0.012701036	-1.066419855	-1	0.047580333	0.949514517	1	0.048545681	0.885589749	1
ENSRNOG00000012550	Uqcrrh	ubiquinol-cytochrome c reductase hinge protein	0	C4	0.007733163	-0.789682542	-1	0.039661892	0.594879801	1	0.006921615	0.842876485	1
ENSRNOG00000013097	LOC691485	hypothetical protein LOC691485	0	C4	0.009398215	-2.4520855	-1	0.046805741	1.634931719	1	0.005330974	2.121922821	1
ENSRNOG00000013532	Pgam2	phosphoglycerate mutase 2	0	C4	0.034222812	-2.307604533	-1	0.037542909	1.527367264	1	0.020329008	1.953677471	1
ENSRNOG00000013766	Acaa2	acetyl-CoA acyltransferase 2	0	C4	0.04756562	-2.669866422	-1	0.042233035	1.811062116	1	0.011209857	2.401865437	1

ENSRNOG00000000386	Pbld1	phenazine biosynthesis-like protein domain containing 1	0	C5	0.024379821	-1.637395001	-1	0.041703446	0.684056136	1	0.083159177	1.280741356	0
ENSRNOG00000000406	Ros1	ROS proto-oncogene 1, receptor tyrosine kinase	0	C5	0.013806975	-2.158982243	-1	0.049548772	1.539569611	1	0.075121687	1.446463913	0
ENSRNOG00000000466	Hsd17b8	hydroxysteroid (17-beta) dehydrogenase 8	0	C5	0.02060601	-1.31827684	-1	0.035152923	0.913668207	1	0.077042863	1.385250522	0
ENSRNOG00000000498	Anks1a	ankyrin repeat and sterile alpha motif domain containing 1	0	C5	0.015288613	-1.649788548	-1	0.0499729	0.985038566	1	0.06341087	1.464001261	0
ENSRNOG00000000920	Phkg1	phosphorylase kinase catalytic subunit gamma 1	0	C5	0.030046206	-2.463497649	-1	0.032882515	2.256789459	1	0.057864999	2.051834659	0
ENSRNOG00000001173	Calbp1	calcium binding protein 1	0	C5	0.009057108	-2.236801868	-1	0.011085301	0.98988708	1	0.051591952	1.175137411	0
ENSRNOG00000001338	Hpd	4-hydroxyphenylpyruvate dioxygenase	0	C5	0.033689077	-1.635612106	-1	0.048049813	1.438577016	1	0.05300008	2.136534964	0
ENSRNOG00000001736	Bdh1	3-hydroxybutyrate dehydrogenase 1	0	C5	0.035652167	-1.115991696	-1	0.02158214	0.61908871	1	0.109293393	0.838012389	0
ENSRNOG00000002128	Ppat	phosphoribosyl pyrophosphate amidotransferase	0	C5	0.026851583	-0.643703387	-1	0.031955091	0.581939319	1	0.084272513	0.738736867	0
ENSRNOG00000003984	Apln	apelin	0	C5	0.010853389	-1.990506535	-1	0.008220416	1.186703419	1	0.07760388	1.207865602	0
ENSRNOG00000004206	Glnx5	glutaredoxin 5	0	C5	0.036522097	-1.330931328	-1	0.036417802	0.852592365	1	0.080541144	1.338418893	0
ENSRNOG00000004219	Dhps	deoxyhypusine synthase	0	C5	0.049074537	-1.232680424	-1	0.016115628	0.767576162	1	0.094217364	1.059627016	0
ENSRNOG00000004640	Mtfrp1	mitochondrial fission process 1	0	C5	0.023845409	-2.197658897	-1	0.009193444	1.591380303	1	0.0532585	2.152059531	0
ENSRNOG00000004726	Mapkapk2	mitogen-activated protein kinase-activated protein kinase 2	0	C5	0.032168832	-1.369921941	-1	0.039370241	0.745807777	1	0.050602962	1.260973997	0
ENSRNOG00000004980	Rangrf	RAN guanine nucleotide release factor	0	C5	0.017445967	-1.40959616	-1	0.008377855	0.905747733	1	0.077865329	1.392699945	0
ENSRNOG00000005133	Mapt	microtubule-associated protein tau	0	C5	0.034091929	-1.401573844	-1	0.049727707	0.667036502	1	0.064224014	1.132145796	0
ENSRNOG00000005530	Rps6k1	ribosomal protein S6 kinase-like 1	0	C5	0.032850278	-1.732286789	-1	0.013850794	0.731385704	1	0.092302169	1.092094438	0
ENSRNOG00000005798	Cav3	caveolin 3	0	C5	0.015857363	-1.027187154	-1	0.019186992	0.814782489	1	0.061936034	1.129247978	0
ENSRNOG00000006119	Sclt1a15	solute carrier family 7 (cationic amino acid transporter, solute)	0	C5	0.024371701	-2.200298538	-1	0.027035747	1.351780176	1	0.058774615	2.00086003	0
ENSRNOG00000006444	Fkbp4	FK506 binding protein 4	0	C5	0.04029489	-1.771608056	-1	0.032251903	1.002145591	1	0.07047878	1.576885732	0
ENSRNOG00000007387	Per1	period circadian clock 1	0	C5	0.03347685	-0.871258928	-1	0.028783069	0.816314775	1	0.064790274	1.152126718	0
ENSRNOG00000008256	Mtfrp3	mitochondrial ribosomal protein L38	0	C5	0.011388535	-1.357167968	-1	0.048117178	0.92312753	1	0.075190294	1.444670815	0
ENSRNOG00000008423	Gpr22	G protein-coupled receptor 22	0	C5	0.012161785	-1.122142609	-1	0.003473997	0.810202873	1	0.079724338	1.354781608	0
ENSRNOG00000009348	Nos3	nitric oxide synthase 3	0	C5	0.014454556	-1.872387634	-1	0.005670409	0.957755425	1	0.102356796	0.889303527	0
ENSRNOG00000009536	Pgp	phosphoglycolate phosphatase	0	C5	0.008169105	-1.062816736	-1	0.016495032	0.851222656	1	0.089878097	0.986228906	0
ENSRNOG00000010077	Smardc3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin 3	0	C5	0.03927352	-1.131511519	-1	0.018691444	0.795825467	1	0.096887613	1.011892013	0
ENSRNOG00000010259	Esrnb	estrogen-related receptor beta	0	C5	0.041941142	-1.150154239	-1	0.024103755	0.945276211	1	0.084955216	1.120115241	0
ENSRNOG00000010580	Aco7	acyl-CoA thioesterase 7	0	C5	0.038894661	-1.061381438	-1	0.033661118	0.689995346	1	0.07225521	1.122770393	0
ENSRNOG00000011189	Acy1	aminoacylase 1	0	C5	0.011731343	-1.20950513	-1	0.009007614	0.759232834	1	0.089341329	1.086214587	0
ENSRNOG00000011427	Hr	HR, lysine demethylase and nuclear receptor corepressor 1	0	C5	0.043955194	-0.754031821	-1	0.00688024	0.652279731	1	0.124548434	0.386708033	0
ENSRNOG00000011648	Aqp1	aquaporin 1	0	C5	0.021066024	-1.658899796	-1	0.026563428	0.888048901	1	0.07572421	1.348784201	0
ENSRNOG00000012049	Sox7	SRY box 7	0	C5	0.01589835	-1.810634273	-1	0.006545361	0.83615602	1	0.139626678	0.558505421	0
ENSRNOG00000012236	Hddc3	HD domain containing 3	0	C5	0.015953488	-1.082512281	-1	0.034598013	0.761321008	1	0.08973828	1.136386548	0
ENSRNOG00000012303	Apobec2	apolipoprotein B mRNA editing enzyme catalytic subunit 2	0	C5	0.017722337	-1.307859386	-1	0.038430765	0.976208317	1	0.051100406	1.37865646	0
ENSRNOG00000012369	Fam174b	family with sequence similarity 174, member B	0	C5	0.011034588	-1.540186809	-1	0.049348303	1.133489888	1	0.082931152	1.291795288	0
ENSRNOG00000012495	Podxl	podocalyxin-like 1	0	C5	0.011417611	-1.339024946	-1	0.018123629	0.854687428	1	0.113962815	0.780706287	0
ENSRNOG00000012622	Mmp15	matrix metalloproteinase 15	0	C5	0.014171984	-1.575151671	-1	0.036185314	0.858847622	1	0.058284834	1.155713875	0
ENSRNOG00000012736	Ssca1	Sjogren syndrome/scleroderma autoantigen 1	0	C5	0.033283158	-0.916399209	-1	0.022160279	0.772571103	1	0.067771661	1.070131793	0
ENSRNOG00000013364	Hey2	hes-related family bHLH transcription factor with YRPV domain 2	0	C5	0.011805159	-0.633058231	-1	0.030558782	0.611552892	1	0.156414659	0.4617961	0
ENSRNOG00000013468	Fam213b	family with sequence similarity 213, member B	0	C5	0.00773259	-1.117855439	-1	0.001602787	0.721220747	1	0.073187836	1.220509208	0
ENSRNOG00000014083	Iqsec3	IQ motif and Sec7 domain 3	0	C5	0.027844115	-1.864971487	-1	0.036482127	0.97632524	1	0.071385489	1.547282336	0
ENSRNOG00000014751	Ret	ret proto-oncogene	0	C5	0.040573793	-1.300013247	-1	0.010171635	1.151342549	1	0.100156214	0.961434789	0
ENSRNOG00000014761	Rasd2	RASD family, member 2	0	C5	0.024887393	-2.256044112	-1	0.04609627	1.633623931	1	0.055009831	2.058607134	0
ENSRNOG00000014806	Pnkd	paroxysmal nonkinesigenic dyskinesia 1	0	C5	0.008341281	-1.419542308	-1	0.007665505	0.919793154	1	0.055168436	1.268041445	0
ENSRNOG00000015206	Alad	aminolevulinic acid dehydratase	0	C5	0.011265391	-1.17876811	-1	0.02952381	0.728127532	1	0.0618469	1.041812971	0
ENSRNOG00000015479	Mtfrp34	mitochondrial ribosomal protein S34	0	C5	0.036810205	-1.179497252	-1	0.026679572	0.797519803	1	0.081594573	1.188018559	0
ENSRNOG00000015691	Fam212b	family with sequence similarity 212, member B	0	C5	0.045451574	-1.747852746	-1	0.049881918	1.192213969	1	0.07311902	1.428266254	0

ENSRNOG000000000185	Mpst	mercaptopyruvate sulfurtransferase	0	C6	0.034756466	-0.746427797	-1	0.09596335	0.378355298	0	0.013239612	0.78057717	1
ENSRNOG000000000186	Tst	thiosulfate sulfurtransferase	0	C6	0.030988079	-1.294477852	-1	0.094527444	0.805878207	0	0.033282213	1.12626214	1
ENSRNOG000000000246	Amd2	archaelysin family metalloproteinase 2	0	C6	0.021235073	-0.617023884	-1	0.177973818	0.385085307	0	0.030768122	0.558228585	1
ENSRNOG000000000302	Sesn1	sestrin 1	0	C6	0.031800454	-0.720978952	-1	0.156040779	0.388477688	0	0.017361384	0.703150694	1
ENSRNOG000000000413	Pin	phospholamban	0	C6	0.030661801	-1.343422545	-1	0.079534272	0.958079305	0	0.012384978	1.356400905	1
ENSRNOG000000000480	Phf1	PHD finger protein 1	0	C6	0.035098354	-0.846894289	-1	0.028491418	0.388369034	0	0.01962577	0.702223288	1
ENSRNOG000000000585	Amd1	adenosylmethionine decarboxylase 1	0	C6	0.036364453	-1.377654694	-1	0.085275519	0.668571594	0	0.041104994	1.125886679	1
ENSRNOG000000000588	Slc18a10	solute carrier family 18 member 10	0	C6	0.044468903	-1.143015261	-1	0.050207769	0.469645069	0	0.027763796	0.879806217	1
ENSRNOG000000000605	Hs3st5	heparan sulfate-glucosaminase 3-sulfotransferase 5	0	C6	0.026833943	-1.111520338	-1	0.081194275	0.942332398	0	0.015970838	1.08449633	1
ENSRNOG000000000658	Acoab	acetyl-CoA carboxylase beta	0	C6	0.012087541	-2.223839302	-1	0.05875991	1.304130351	0	0.003831433	1.794601983	1
ENSRNOG000000000847	Csnk2b	casein kinase 2 beta	0	C6	0.024774132	-0.682504848	-1	0.090378113	0.439313572	0	0.002022546	0.853864185	1
ENSRNOG000000001128	Tesc	tescalcin	0	C6	0.046212881	-1.429878343	-1	0.107524611	0.705601041	0	0.043636125	1.711642891	1
ENSRNOG000000001142	Prkab1	protein kinase AMP-activated non-catalytic subunit beta	0	C6	0.033577339	-0.879499177	-1	0.10958881	0.691025796	0	0.038179316	0.872855728	1
ENSRNOG000000001177	Acads	acyl-CoA dehydrogenase, C-2 to C-3 short chain	0	C6	0.033204517	-1.962551905	-1	0.068173958	1.062633054	0	0.009920727	1.807844338	1
ENSRNOG000000001205	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	0	C6	0.049468796	-1.58982012	-1	0.083598114	0.917966368	0	0.037815677	1.530128484	1
ENSRNOG000000001285	Atp2a2	ATPase sarcolemmal/endoplasmic reticulum Ca2+ trans	0	C6	0.031890018	-1.60484246	-1	0.0716382	1.06815203	0	0.004786997	1.34157693	1
ENSRNOG000000001288	Gpr146	G protein-coupled receptor 146	0	C6	0.049064408	-1.374957815	-1	0.091205505	0.835511975	0	0.015744527	1.185625984	1
ENSRNOG000000001344	Aldh2	aldehyde dehydrogenase 2 family (mitochondrial)	0	C6	0.022677858	-1.104243375	-1	0.103037811	0.534870102	0	0.004424564	0.847329873	1
ENSRNOG000000001440	Mdh2	malate dehydrogenase 2	0	C6	0.049139223	-1.497089592	-1	0.083363713	0.92108411	0	0.004515009	1.273574542	1
ENSRNOG000000001517	Pdk1	pyruvate dehydrogenase kinase 1	0	C6	0.046254165	-1.417433995	-1	0.090368384	0.844205825	0	0.043429678	1.098753261	1
ENSRNOG000000001710	Abcf3	ATP binding cassette subfamily F member 3	0	C6	0.01282422	-0.667747207	-1	0.030969157	0.357998478	0	0.003629571	0.639942932	1
ENSRNOG000000001711	Hrasl	HRAS-like suppressor	0	C6	0.023347897	-1.277317372	-1	0.10960458	0.690375517	0	0.009262882	1.292020324	1
ENSRNOG000000001770	Ehadh	enoyl-CoA hydratase and 3-hydroxyacyl CoA dehydro	0	C6	0.037916593	-1.85718889	-1	0.060240385	1.27080389	0	0.048074453	1.212409579	1
ENSRNOG000000001807	Sasn	sarcomerespan	0	C6	0.017505507	-0.949745861	-1	0.123381465	0.80073737	0	0.020937213	0.747340287	1
ENSRNOG000000001842	Mps35	mitochondrial ribosomal protein S35	0	C6	0.042987351	-1.053350651	-1	0.093738547	0.721378653	0	0.040115349	1.121978642	1
ENSRNOG000000001890	Txnd2	thioredoxin reductase 2	0	C6	0.025433534	-1.496506843	-1	0.073031359	0.795171313	0	0.040587888	1.255032538	1
ENSRNOG000000002115	Sod1	superoxide dismutase 1	0	C6	0.025773728	-0.620864591	-1	0.064209575	0.408951311	0	0.017294534	0.789428043	1
ENSRNOG000000002205	Ociad1	OciA domain containing 1	0	C6	0.02184358	-0.735506855	-1	0.124622532	0.480159857	0	0.020374885	0.720614081	1
ENSRNOG000000002256	Art3	ADP-ribosyltransferase 3	0	C6	0.031272114	-0.791898207	-1	0.0940486	0.811259063	0	0.006051252	1.101767949	1
ENSRNOG000000002459	Fbxo40	F-box protein 40	0	C6	0.048184888	-1.208350529	-1	0.085183255	0.900422058	0	0.047281426	1.07109618	1
ENSRNOG000000002516	Mtm1	myotubularin 1	0	C6	0.00830348	-1.247599176	-1	0.103867961	0.733158033	0	0.041464805	1.057717138	1
ENSRNOG000000002579	Pam1	prostate androgen-regulated mucin-like protein 1	0	C6	0.027032508	-1.292963122	-1	0.099994554	0.762801071	0	0.003265828	1.18232277	1
ENSRNOG000000002652	Rap1gap2	RAP1 GTPase activating protein 2	0	C6	0.031324118	-1.291293272	-1	0.102851744	0.741846541	0	0.024235155	1.003988235	1
ENSRNOG000000002689	Cluh	clustered mitochondria homolog	0	C6	0.044689044	-1.380518629	-1	0.097459742	0.780648978	0	0.03001704	1.11772703	1
ENSRNOG000000002713	Zfp672	zinc finger protein 672	0	C6	0.02907913	-0.972857161	-1	0.095262438	0.798886579	0	0.017113845	0.945049692	1
ENSRNOG000000002840	Atp5b	ATP synthase, H+ transporting, mitochondrial F1 comp	0	C6	0.016914494	-1.480776	-1	0.08009369	0.84527166	0	0.02651396	1.1885474	1
ENSRNOG000000003127	Spryd4	SPRY domain containing 4	0	C6	0.015360844	-0.98849293	-1	0.084687056	0.584627929	0	0.005736007	0.72174526	1
ENSRNOG000000003163	Sdhc	succinate dehydrogenase complex subunit C	0	C6	0.04304078	-1.389411205	-1	0.054378049	0.881673233	0	0.016108271	1.248249284	1
ENSRNOG000000003330	Acsf2	acyl-CoA synthetase family member 2	0	C6	0.045856651	-1.823552539	-1	0.076793435	0.98891339	0	0.008723948	1.587233044	1
ENSRNOG000000003332	Nt5f5	5'-3'-nucleotidase, mitochondrial	0	C6	0.005575149	-1.060378632	-1	0.135558823	0.538141599	0	0.044113907	0.9493416	1
ENSRNOG000000003334	Klhl21	kelch-like family member 21	0	C6	0.031217119	-1.526873659	-1	0.097747188	0.777540091	0	0.023915979	1.215181148	1
ENSRNOG000000003520	Pdx2	peroxiredoxin 2	0	C6	0.013850043	-0.758701085	-1	0.012267389	0.497636349	0	0.036052563	0.796611771	1
ENSRNOG000000003694	Prox1	prospero homeobox 1	0	C6	0.04051185	-0.995701938	-1	0.110205102	0.687091191	0	0.033167519	1.038175381	1
ENSRNOG000000003784	Rilp	Rab interacting lysosomal protein	0	C6	0.049946947	-1.283000916	-1	0.07860111	0.934120271	0	0.031851488	1.305980208	1
ENSRNOG000000003815	Slc25a11	solute carrier family 25 member 11	0	C6	0.047508556	-1.514175123	-1	0.070278266	1.086161821	0	0.005060952	1.435671796	1
ENSRNOG000000003847	Gid4	GID complex subunit 4	0	C6	0.039546899	-1.182478152	-1	0.097199639	0.672781575	0	0.03625639	1.08747096	1
ENSRNOG000000004172	Pdk2	pyruvate dehydrogenase kinase 2	0	C6	0.040034452	-1.896167182	-1	0.07287701	1.047517981	0	0.028725914	1.499694111	1

ENSRNOG00000000042	Xpr1	xenotropic and polytropic retrovirus receptor 1	0	0.008866253	1.227883478	1	0.041244031	-0.24211349	0	0.109079053	-0.819262059	0
ENSRNOG00000000075	Mtf2	metal response element binding transcription factor 2	0	0.039573895	0.587335828	1	0.180628183	-0.292211904	0	0.135001311	-0.444690178	0
ENSRNOG000000000187	Csf2rb	colony stimulating factor 2 receptor beta common subunit	0	0.035107021	2.121077373	1	0.150814595	-0.364957968	0	0.078485247	-1.248296846	0
ENSRNOG000000000239	Ccl7	C-C motif chemokine ligand 7	0	0.027715841	1.778454964	1	0.435173295	-0.052346843	0	0.214928978	-0.28230583	0
ENSRNOG000000000247	Mfsd11	major facilitator superfamily domain containing 11	0	0.011482856	0.806423885	1	0.224988966	-0.223881282	0	0.067964347	-0.553595957	0
ENSRNOG000000000257	Smpd3	sphingomyelin phosphodiesterase 3	0	0.018909696	0.953979198	1	0.083097347	-0.893019064	0	0.073224174	-1.318123348	0
ENSRNOG000000000303	Cep57i1	centrosomal protein 57-like 1	0	0.032587888	1.068876918	1	0.081393728	-0.537237543	0	0.09026609	-0.794086258	0
ENSRNOG000000000307	Mical1	microtubule associated monoxygenase, calponin and	0	0.036918517	0.952492287	1	0.108258353	-0.511319707	0	0.101424967	-0.89685768	0
ENSRNOG000000000471	B3gal4	Beta-1,3-galactosyltransferase 4	0	0.001807894	0.731028245	1	0.078144277	-0.653440275	0	0.11844068	-0.727436172	0
ENSRNOG000000000485	Bak1	BCL2-antagonist/killer 1	0	0.013802254	0.711748818	1	0.204862859	-0.252604447	0	0.006253113	-0.467203405	0
ENSRNOG000000000505	Rpl10a	ribosomal protein L10A	0	0.048784438	0.90148563	1	0.152750362	-0.358880001	0	0.038045615	-0.521096121	0
ENSRNOG000000000811	Pkib	cAMP-dependent protein kinase inhibitor beta	0	0.000322089	1.121971908	1	0.151847774	-0.361684195	0	0.139946913	-0.57841267	0
ENSRNOG000000000824	Dse	dermatan sulfate epimerase	0	0.032483448	2.294898637	1	0.059281275	-0.951564072	0	0.053851095	-1.593910171	0
ENSRNOG000000000913	Gusb	glucuronidase, beta	0	0.042987696	2.194233317	1	0.061695912	-0.920898489	0	0.053750457	-1.886120276	0
ENSRNOG000000000954	Polr1d	RNA polymerase I subunit D	0	0.025248586	0.846420126	1	0.09548845	-0.402755372	0	0.005726832	-0.51746349	0
ENSRNOG000000000994	Sxobp2	syntrophin binding protein 2	0	0.028481951	2.514100884	1	0.058752129	-0.961004958	0	0.051942421	-1.948180982	0
ENSRNOG000000001124	Rnf12	ring finger protein, transmembrane 2	0	0.001314788	0.75126704	1	0.139372822	-0.358822736	0	0.206189801	-0.305474508	0
ENSRNOG000000001138	Tao3	TAO kinase 3	0	0.002358587	0.951050454	1	0.188484912	-0.279023027	0	0.109881056	-0.771562372	0
ENSRNOG000000001201	Cstb	cystatin B	0	0.032408349	1.341677104	1	0.109194414	-0.508183518	0	0.051084877	-0.910343892	0
ENSRNOG000000001300	P2rx4	purinergic receptor P2X 4	0	0.016981929	2.226583977	1	0.057762542	-0.979890767	0	0.060741618	-1.635954359	0
ENSRNOG000000001314	Fam20c	FAM20C, golgi associated secretory pathway kinase	0	0.012413057	0.910035037	1	0.187563828	-0.280562389	0	0.105336415	-0.856832292	0
ENSRNOG000000001391	Sds1	serine dehydratase-like	0	0.00020303	0.748394573	1	0.074324429	-0.661385902	0	0.165226766	-0.395786585	0
ENSRNOG000000001417	Plod3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	0	0.017908487	0.78038096	1	0.140219383	-0.20116771	0	0.036542142	-0.50908951	0
ENSRNOG000000001425	Sh2b2	SH2B adaptor protein 2	0	0.036760761	1.968282601	1	0.130478122	-0.428361237	0	0.072307824	-1.337373485	0
ENSRNOG000000001457	Rfc2	replication factor C subunit 2	0	0.040152755	0.809780667	1	0.200691796	-0.258883048	0	0.098198322	-0.741315928	0
ENSRNOG000000001633	Trk-fused gene	Trk-fused gene	0	0.000350827	0.804325851	1	0.190393599	-0.273848593	0	0.152301743	-0.344852939	0
ENSRNOG000000001730	Acap2	ArtGAP with coiled-coil, ankyrin repeat and PH domains	0	0.016636456	0.821523196	1	0.197132533	-0.165048639	0	0.050427972	-0.755115769	0
ENSRNOG000000002057	Slc10a6	solute carrier family 10 member 6	0	0.033078465	1.991137577	1	0.054118615	-1.050744931	0	0.099613318	-0.817101985	0
ENSRNOG000000002105	Cdc7	cell division cycle 7	0	0.002347402	0.851674146	1	0.040090334	-0.472989877	0	0.068955958	-1.016105678	0
ENSRNOG000000002141	Cd200	Cd200 molecule	0	0.025647447	0.755474475	1	0.051828623	-0.348947368	0	0.129511528	-0.644692729	0
ENSRNOG000000002165	Abraxas1	abraxas 1, BRCA1 A complex subunit	0	0.035993671	0.658731801	1	0.015467802	-0.355150328	0	0.157886693	-0.379749797	0
ENSRNOG000000002180	Tbc1d1	TBC1 domain family member 1	0	0.008581944	0.717671491	1	0.151861751	-0.361638796	0	0.092174597	-0.707795699	0
ENSRNOG000000002182	44085 septin 11	septin 11	0	0.022764827	0.719305662	1	0.010558782	-0.389030522	0	0.096915585	-0.881544718	0
ENSRNOG000000002188	Hpse	heparanase	0	0.021061025	1.218914258	1	0.065456261	-0.851255882	0	0.073645229	-1.309895446	0
ENSRNOG000000002192	Rel1	RELT-like 1	0	0.008110637	0.649213134	1	0.39599133	0.067905162	0	0.133822913	-0.281464792	0
ENSRNOG000000002210	Hsd17b11	hydroxysteroid (17-beta) dehydrogenase 11	0	0.0282873	1.489500827	1	0.08294159	-0.670009628	0	0.086052563	-1.167881474	0
ENSRNOG000000002241	Hspbp1	HSPB1 associated protein 1	0	0.040146866	0.693443166	1	0.068104272	-0.393036049	0	0.204299384	-0.267649881	0
ENSRNOG000000002343	Uchl1	ubiquitin C-terminal hydrolase L1	0	0.046182515	2.942935568	1	0.060365078	-0.939333704	0	0.051585344	-1.959870015	0
ENSRNOG000000002358	Soxep1	serine carboxypeptidase 1	0	0.014118971	1.922486509	1	0.073264823	-0.757049771	0	0.064532704	-1.36781326	0
ENSRNOG000000002382	Mfap4	microfibril associated protein 4	0	0.000180713	1.130141507	1	-	-	0	-	-	0
ENSRNOG000000002389	Morf4i2	mortality factor 4 like 2	0	0.029047577	1.013410708	1	0.03393212	-0.507379942	0	0.077493774	-0.744058204	0
ENSRNOG000000002407	Pdxo1	pyridoxal-dependent decarboxylase domain containing	0	0.038948031	0.784117284	1	0.094156665	-0.36213164	0	0.128378491	-0.653460286	0
ENSRNOG000000002408	Rbm47	RNA binding motif protein 47	0	0.038865494	1.712386292	1	0.203640221	-0.254730163	0	0.075849008	-1.284423798	0
ENSRNOG000000002425	Pctp	phosphatidylcholine transfer protein	0	0.032620077	1.41792002	1	0.11970213	-0.458029642	0	0.061702058	-0.946839696	0
ENSRNOG000000002470	Ifi47	interferon gamma inducible protein 47	0	0.010213959	1.017765445	1	0.131383422	-0.426214875	0	0.003716083	-0.533109475	0
ENSRNOG000000002525	Ptgs2	prostaglandin-endoperoxide synthase 2	0	0.042134613	2.848078154	1	0.10886566	-0.452533984	0	0.058478272	-1.899427962	0
ENSRNOG000000002693	Nme1	NME/NM23 nucleoside diphosphate kinase 1	0	0.007258508	0.870631613	1	0.240413761	-0.205055871	0	0.090646218	-0.547939809	0

2.6. Identification of differentially expressed genes (DEGs)

The network model describing interactions between DEGs was reconstructed to investigate the collective actions of signaling pathways. Network models have shown that saipanone A treatment downregulates the pro-inflammatory pathways activated by MI (*Tlr*, *Tgfb*, *Tnf*, and *Ifng* signaling pathways) and the complement cascade that increases inflammation and apoptosis pathway (Figure 25).

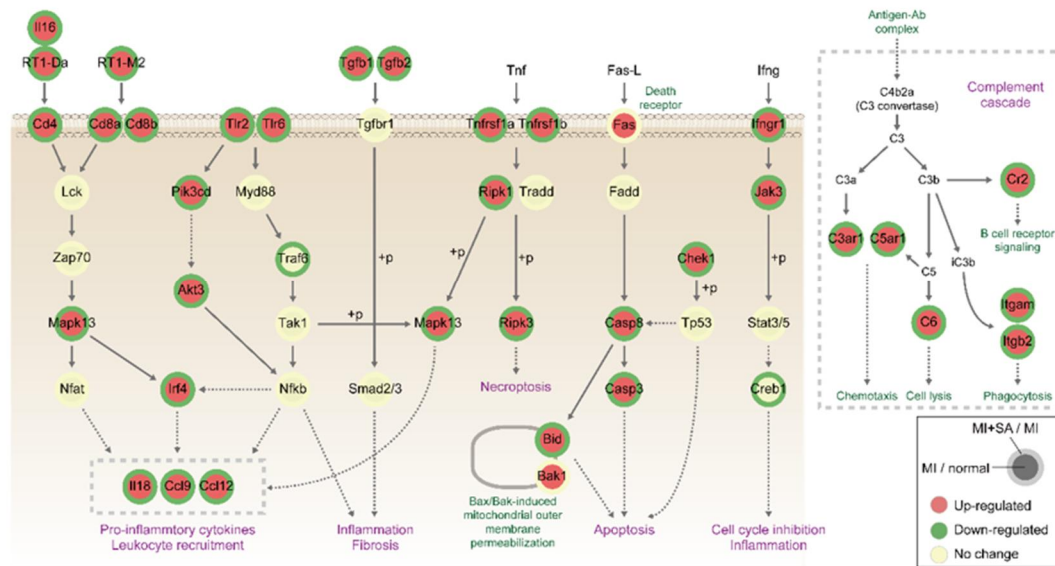


Figure 25. Inhibitory effects of sappanone A administration on the MI-related processes. Network model describing interactions among signaling pathways. Arrows, activation in signaling. “+p”, phosphorylation.

2.7. RT-PCR analysis

Downregulation of representative genes related to inflammatory responses of MI + sappanone A group (*Tgfb1*, *Tgfb2*, *Cd4*, *Cd8a*, *Il18*, *Pik3cd*, and *Tnfrsf1a*) and apoptosis (*Casp3*) were confirmed compared to the MI group (Figure 26 and 27). Thus, these results suggest that sappanone A attenuated MI-related processes including inflammation and apoptosis pathways in a rat myocardial I/R injury model.

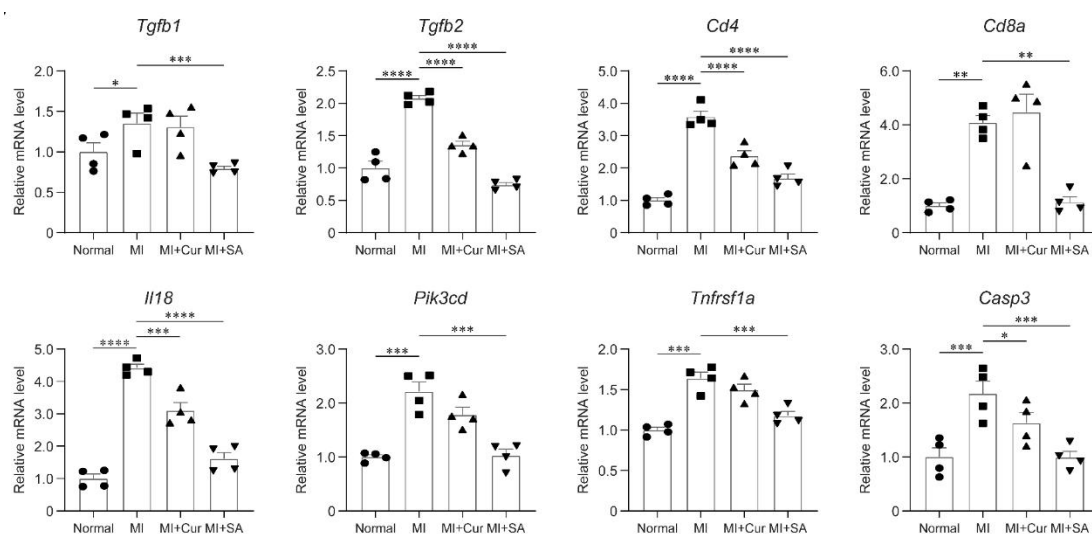


Figure 26. Confirmation of the predominant downregulation of the representative genes involved in the inflammatory responses and apoptosis by RT-PCR. The expression levels were normalized with respect to those in the control group. The normalized data are expressed as the mean \pm SEM ($n = 4$ per group). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$ by two-way ANOVA tests with Tukey's post hoc correction.

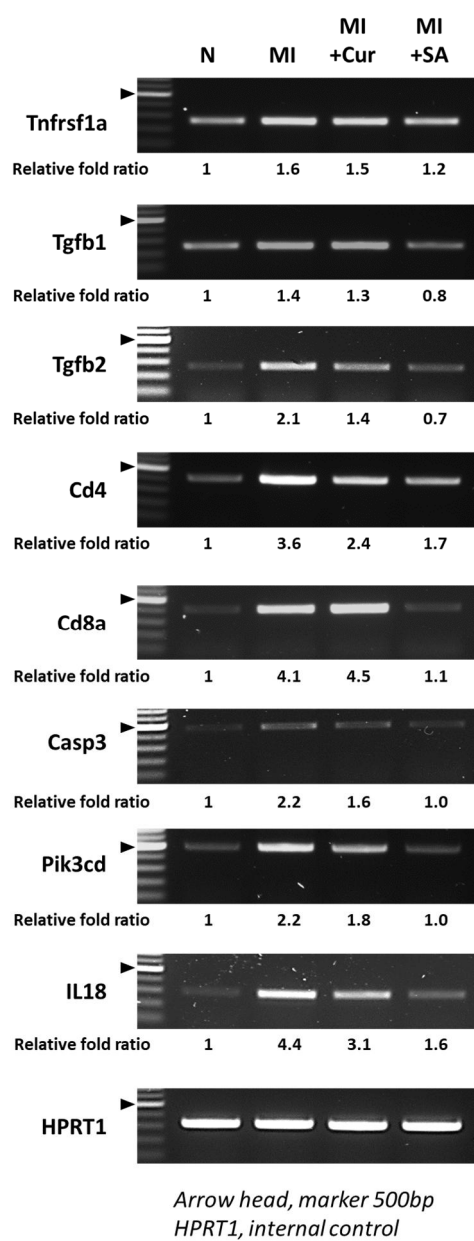


Figure 27. Validation of the DEGs involved in the inflammatory responses by RT-PCR.

Table 11. List of the primers used in sappanone A efficacy study.

Symbol	Primer direction	Primer sequence [5'→3']	Primer T _m (°C)	Annealing T _m (°C)	PCR cycles	Product size (bp)
Tnfrsf1a	forward	AAGTGCCACAAAGGAACCTAC	58.42	58	22	255
	reverse	GTCCACACACTGGAAATGCG	59.76			
Tgfb1	forward	TGACATGAACCGACCCCTCC	59.68	58	22	245
	reverse	CCAGGCTCCAAATGTAGGGG	60.11			
Tgfb2	forward	CTCAGTGGGCAGCTTTTGCT	61.18	59	27	262
	reverse	AATGTAGCGCTGGGTGGAG	60.39			
Cd4	forward	AAGGACTGGCCAGAGACTCA	60.18	58	27	397
	reverse	TTCTTGTTCTCCAGCTCGCA	59.61			
Cd8a	forward	CCTTGTCAGCCAGACCTT	59.89	59	27	399
	reverse	CAGCTTGGGTTCCTCCTGG	60.04			
Casp3	forward	GGAGCTTGGAACGCGAAGAA	60.95	59	27	473
	reverse	GGCAGTAGTCGCCTCTGAAG	60.18			
Pik3cd	forward	CATCAAGTCCCTACGGAAGC	58.06	58	27	478
	reverse	TTTGGAGTCCATGAAGGTGC	58.09			
Il18	forward	CTGATATCGACCGAACAGCC	58.23	57	27	296
	reverse	AGCATCATCTTCCTTTGGCA	58.19			
HPRT1	forward	ATACAGGCCAGACTTTGTTGGA	59.62	58	27	330
	reverse	GCTGCCTACAGGCTCATAGT	59.24			

3. Discussion

The third chapter of this study is to access cardiovascular protective effect of saffronone A in a rat myocardial I/R injury model. In this animal model, the positive effect of saffronone A on the early stage of MI was confirmed by evaluating the infarct size and serum cardiac marker (CK-MB, LDH, and AST) on day 1 after MI surgery and echocardiography the LV systolic and diastolic function using echocardiography on day 1 and 4 after induction of MI. In addition, histopathological changes (H&E and Masson Trichrome) and mRNA sequencing were analyzed to study potential changes in cellular pathways. These results demonstrated that saffronone A successfully attenuated LV dysfunction induced by LAD ligation in a rat myocardial I/R injury model.

Curcumin or saffronone A were administered daily for 5 days before ischemia from the day of surgery to 4 days after surgery, which was used to investigate the initial effects on MI, which was a relatively short exposure period compared to the previous study (64). We continued to emphasize the importance of LV diastolic and systolic dysfunction to better mimic clinical cardiac function assessment in MI patients. We found that the rats with MI had reduced EF and FS values, reflecting LV systolic dysfunction; also decreased E' value and increased E/E' values, reflecting LV diastolic dysfunction, which tends to be the same in human MI patients. Patients with acute coronary syndrome usually have increased end-diastolic filling pressure of the left ventricle, causing early aortic valve closure. Continuous reduced value in stroke volume decreases incoming blood flow to the late systolic phase (65), causing disturbances of LV diastolic function, leading to large infarctions (66). Elevation of LV filling pressure is the key indicator of poor outcomes in humans (34, 35), and the E/E' ratio can be used to evaluate LV diastolic dysfunction, given its tendency for independence from LV systolic function, heart rhythm abnormalities, and LV hypertrophy (67). Therefore, the evaluation of LV diastolic function is important for MI patients, and our echocardiographic method is a good indicator for predicting the prognosis and assessing efficacy in the development of new drugs for heart disease.

Curcumin, a natural yellow pigment, is extracted from the rhizomes of the *Curcuma longa* plant, and its cardioprotective effects have been studied in a rat chronic MI model induced via the Tgf- β /Smad-mediated signaling pathway (64). An acute myocardial I/R injury rat model was also used to study the protective effects of curcumin in relation to enhanced STAT3 phosphorylation (68). Recently, the effectiveness of curcumin nanoparticles in isoproterenol-induced MI has been demonstrated (69); however, the age and the bodyweight of rats, the

duration of ischemic of LAD ligation, and the dosage and the period of total treatment were different from our rat myocardial I/R injury model protocol. Using curcumin as a positive control, our new study is intended to identify the effects of sappanone A on acute MI.

In a previous experiment on the efficacy study of metformin, we performed a transient postoperative day sampling on day 7 after surgery, finding no difference in serum chemistry values for cardiac markers in normal and surgically induced MI model in rats on 7 days after surgery. Therefore, the time point of the sampling was needed to be changed to day 1 after surgery which was earlier than the blood-sampling time of the previous experiment; this was done to consider the time-bound effect of the enzymes in the serum, and statistically significant changes were detected in the MI group. After MI was induced, myocardial cells were damaged and ruptured, and cardiac enzymes were released into the blood. In this serum chemistry of cardiac marker study, sappanone A significantly reduced mean serum AST and LDH compared to the MI group.

In addition, the mean myocardial infarct size of the sappanone A-treated rats was significantly smaller in the distal medial and apex regions compared to those of the MI group. The pathogenic consequences of MI are commonly seen in the main coronary arteries and myocardium (60). In this study, it was confirmed that the condition progressed from acute to subchronic stage through histopathological examination of the left ventricle on the 4th day after MI surgery. Advanced lesions were rarely observed and the inflammatory cells of the lymphocyte and mononuclear cell lineages, which appear mainly seen in the sub-chronic inflammatory stage, are more distributed than neutrophils or eosinophils that appear in the acute phase. Also, on the day 4 after MI surgery, as acute lesions, the microvascular obstruction and neutrophils were rarely shown in H&E-stained slide. To assess the effect of sappanone A on microvascular occlusion and neutrophil infiltration, it was recommended to perform histopathological examinations in earlier time such as on day 1 after MI surgery. H&E-stained slide sections in each transverse cardiac region were graded for histopathologic analysis; inflammatory cells infiltration including lymphocytes and mononuclear cells, and purulent lesions. Sappanone A markedly reduced inflammatory cells infiltration in all epicardial regions and the medial myocardial region with significance, consistent with peer-review. Also, histopathological results in heart samples show that sappanone A has a greater effect on lymphocytes, but without the results of histopathological examinations of other organs such as the spleen, bone marrow, etc., there are still limitations to confirming the greater effect of sappanone A on lymphocyte based on heart results alone. Therefore, the effects of sappanone A on each cell type of inflammation and its direct/indirect relationship to MI will

be discussed in the further studies. The percentage of fibrosis area in Masson's trichrome stained slide sections, saipanone A reduced the percentage of fibrosis areas in papillary muscle area compared to those of MI and curcumin treated MI with statistical significance.

The echocardiographic results confirmed the successful establishment of our acute rat myocardial I/R injury model. The echocardiographic data showed that LV cardiac dysfunction did not recover during the early phase of ischemic-reperfusion injury in this rat model during the experimental period. However, saipanone A had cardioprotective effects against acute myocardial ischemia as left ventricular systolic and diastolic functions were significantly improved and ischemic lesions decreased. Despite some limitations to using E' and E/E' because it reflects only the global LV function, further studies using quantitative assessment in conjunction with strain speckle tracking echocardiography are planned to assess regional LV function and filling dynamics (58).

The changes of molecular signatures by saipanone A had not been systematically investigated previously using a rat myocardial I/R injury model. In this study, gene expression profiling was used to identify molecular signatures affected by saipanone A in a rat myocardial I/R injury model. Saipanone A treatment altered the mRNA expression levels of 2020 genes involved in a variety of cellular processes, including 66 genes involved in the inflammatory responses (Figure 24). These genes are likely to be involved in pathological features associated with myocardial infarction. For example, *Tgfb1* and *Tgfb2* mRNA abundances were reduced by saipanone A. The *Tgfb* family critically regulates the inflammatory responses, angiogenesis, and fibrosis under myocardial infarction (70). In addition, the network models have suggested *Tlr*, *Nfkb*, *Tnf*, *Ifng* signaling pathways associated with disease pathogenesis (71). Although the saipanone A showed potent effects in decreasing the expression of pro-inflammatory factors, the precise mechanisms of saipanone A's anti-inflammatory effects and improved heart function are not clearly understood. The pro-inflammatory factors, reduced primarily by saipanone A, may serve as a potential link of inflammation to the relief of left ventricular diastolic and systolic dysfunction (72-76). In this study, we focused on the effects of saipanone A on acute myocardial infarction and the restoration of MI-perturbed gene expression profiles (e.g., inflammation-related pathways). It can be considered valuable as an initial comparative study and additional mechanistic studies are needed to elucidate the functional link between attenuated inflammation and an improved myocardial infarction phenotypes.

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Summary

Rat myocardial I/R injury models are useful, and we especially focused on LV diastolic dysfunction with poorer surgical outcomes in human and systolic dysfunction using echocardiography. In the present study, a rat myocardial I/R injury model was successfully induced by transient LAD ligation and reperfusion using a snaring technique and area at risk was normalized by TTC/EB double staining. Histopathology of rat hearts and RNA sequencing of rat left ventricles for the mechanism study were performed. In this study, two test articles including metformin and sappanone A were evaluated after myocardial infarction surgery.

The goal of this study was to investigate cardiac function in the early phase following myocardial I/R injury in rats using echocardiography to evaluate cardioprotective effect of metformin and sappanone A. To the best of our knowledge, the current study is the first to demonstrate the promising positive effects of metformin on left ventricular diastolic dysfunction in a rat myocardial I/R injury model using echocardiography and cardiovascular protective effects of sappanone A on LV dysfunction in a rat myocardial I/R injury model using echocardiography. A rat myocardial I/R injury model is a good representation of human AMI, allowing the cardio-protective effects of metformin and sappanone A to be evaluated. These data contributed to the understanding of the effects of metformin and sappanone A on the development of AMI and provide a clear rationale for the use of these candidates for the cure for the patients in the development of heart disease.

The thesis was composed of three chapters, and the first chapter (Chapter I . Preliminary study) explained the background of the establishment of human AMI animal model called rat myocardial ischemia / reperfusion injury model, and methods for evaluating left ventricular systolic and diastolic function using echocardiography. Chapter II (Efficacy study of metformin) investigated the efficacy study of metformin in a rat myocardial I/R injury model using echocardiography and its cardioprotective effects on left ventricular diastolic dysfunction at the early stage of MI. Chapter III (Efficacy study of sappanone A) conducted efficacy study of sappanone A in a rat myocardial I/R injury model to show the anti-inflammatory effect on early stage of left ventricular dysfunction using echocardiography.

In order to evaluate those efficacy studies, evaluation methods included ultrasound-based assessment of left ventricular systolic and diastolic function, myocardial infarct size using 1% 2,3,5-triphenyltetrazolium chloride (TTC) staining, serum chemistry of cardiac markers,

histopathological analysis using hematoxylin and eosin staining and Masson's trichrome staining, and mRNA sequencing data analysis. These results will provide further understanding of the effects of metformin and saipanone A on the development of AMI and help future MI patients in the early stage of cardiovascular disease development.

국문 요약 (Summary in Korean)

심장질환은 환자의 치사율이 높은 질환이며, 특히 급성 심근 경색증 (acute myocardial infarction, AMI)는 임상경과가 빠르게 진행하고 매우 위험해 신속한 진단과 치료를 요하는 질환이다. 최근 심장 질환 평가에서는 질환의 예후를 예측함에 있어서 좌심실 수축능보다 좌심실 이완능의 중요성이 대두되고 있다. 또한 사람의 급성 심근경색 및 관동맥중재술 또는 관동맥 우회로 이식술 등으로 관동맥의 혈류가 재관류된 상황까지 반영한 랫드 심근 허혈/재관류 손상 동물모델을 질환동물모델로서 주로 사용하고 있으며, 최근 초음파영상의 발전으로 소형실험동물에서도 심장기능평가가 가능케 되었다. 본 연구는 랫드 심근 허혈/재관류 손상 동물모델을 확립하고 좌심실 수축능 및 이완능까지 평가 가능한 심장초음파 평가법을 고안하여, 실험 약물을 대상으로 좌심실 이완능을 함께 고려한 정확한 심장기능 평가법을 활용하여 심근 보호에 대한 실험 약물의 유효성을 평가하는 것을 목적으로 하였다.

메트포르민(metformin)은 바이구아니드계(biguanides) 경구용 당뇨병 치료제로서 2형 당뇨병 치료에 1차 약물로 사용되며 본 연구에서 메트포르민의 심혈관질환 예방효과를 확인하기 위하여 랫드 심근 허혈/재관류 손상 동물모델에서 경구 투여 후 심장 초음파, TTC 염색을 통한 허혈 부위 확인, H&E 염색과 Masson' s trichrome 염색을 통한 조직병리 검사를 하였다. 실험 결과, 메트포르민은 심장 이완능을 유의성 있게 향상시켰으며 허혈 부위의 크기 및 섬유화 정도는 감소하는 경향은 보였으나 유의성은 없었고, 조직병리학적 검사에서는 유두근이 위치한 부위에서는 유의성 있게 병변이 감소한 것을 확인할 수 있었다.

Sappanone A는 육두구(nutmeg-myristica fragrans) 추출물로서 항염효과가 알려지고 있으며, 랫드 심근 허혈/재관류 손상 동물모델에서 심장초음파, 심장 손상 특이 지표를 확인하기 위한 임상병리, 허혈 부위 확인, 조직병리검사를 하였다. 실험 결과, sappanone A는 심장 이완능을 유의성 있게 향상시켰고, 허혈 부위를 유의성있게 감소시켰으며, LDH와 AST를 유의성 있게 감소시켰으며, 심외막쪽 심근에서 유의성 있게 조직병리학적 병변이 감소한 것을 확인할 수 있었다. 또한 랫드 좌심실 조직에서 mRNA 전사체 분석을 통하여 sappanone A의 염증 관련 기전을 통한 효과를 확인하였다.

랫드 심근 허혈/재관류 손상 동물모델은 사람에서의 심근경색을 잘 반영한 질환 동물

모델이고, 심장 이완능 평가를 활용한 심장 초음파 평가법은 실험 약물에 대한 유효성 평가에 주요 지표가 된다. 이와 더불어 혈청 심장지표 분석, 심근 경색 허혈 부위 확인, 좌심실 조직 병리 분석, 좌심실 mRNA sequencing 분석 기법을 통한 약물 기전 확인 등을 심장 질환을 타겟으로 하는 후보물질에 대한 유효성 평가에 활용하여 좌심실 기능 평가를 다방면으로 분석하고 임상적으로 적용 가능한 물질이 도출된다면, 추후 고위험성 심장 질환을 가진 환자들에게 많은 도움이 될 것으로 판단된다.

중심단어: acute myocardial infarction; rat myocardial I/R injury model, left ventricular systolic function; left ventricular diastolic function; echocardiography