Comparative blood transcriptome analysis in idiopathic and *LRRK2* G2019S-associated Parkinson's disease

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1. Introduction

Mutations in the *LRRK2* gene are the commonest known cause of Parkinson's disease. Among the six mutations reported to date with proven pathogenicity, the G2019S mutation is the most frequent and has a worldwide distribution with higher prevalence in certain populations (Healy et al., 2008). The clinical phenotype of *LRRK2* G2019S-associated PD is clinically indistinguishable for idiopathic PD, while up to 20% of the cases might show an absence of Lewy Bodies in the pathology (Kalia LV., 2015). Whether or not similar molecular pathways are involved in the pathogenesis of idiopathic and *LRRK2* G2019S-associated PD is a hot topic of current research. *LRRK2*-associated PD constitutes a very homogeneous setting for studying and deciphering the etiopathogenic events leading to neurodegeneration in PD, a presumed heterogeneous condition. The study of the transcriptome at the genome-wide level allows, in a hypothesis-free approach, the identification of genes and pathways deregulated in a certain medical condition in a moment of the disease evolution. Blood and brain share significant gene expression similarities (Liew et al., 2006), and transcriptional profile in blood from PD patients has shown altered expression of genes involved in the pathobiological pathways known to be altered in PD (Cooper-Knock et al., 2012; Mutez et al., 2014; Scherzer et al., 2007). Our aim here was first to perform a pathway-based analysis comparing blood transcriptome between patients with idiopathic and *LRRK2* G2019S-associated PD, in order to understand whether or not common molecular pathways are involved in both conditions and second, to ascertain through the study of asymptomatic carriers of the mutation, if early variations in the blood transcriptome can be attributed to the presence of the G2019S mutation.

2. Methods

2.1. Subjects

Twenty PD patients carrying the G2019S mutation of the *LRRK2* gene (19 heterozygous and 1 homozygous; 50% female; mean age at study, 70.8 [range, 46-93] years; and mean disease duration, 10.8 years) and 20 age and sex matched idiopathic PD patients (55% female; mean age at study, 70.8 [range, 47-83] years; and mean disease duration, 7.2 years) were recruited for the study. This cohort resulted from the screening of the mutation in 400 consecutive PD patients attending the Neurology Department of the University Hospital “Marqués de Valdecilla,” in Santander, Northern Spain, between 2006 and 2011. Thirty-two PD index cases carrying the *LRRK2* G2019S mutation were identified in that study. Twenty asymptomatic carriers of the mutation matched for age and sex with PD cases (50% female; mean age at study, 71.9 [range, 60-85] years) were also recruited for this study. The characteristics of the population have been described previously (Sierra et al., 2011). All PD cases fulfilled Queen Square Brain Bank diagnostic criteria for PD. Control group consisted of 20 subjects (55% female and mean age at study, 70.6 [range, 58-85] years) free of any neurologic condition. All controls and idiopathic PD patients tested negative for *LRRK2* G2019S and R1441G mutations. Both patients and controls from these cohorts were Caucasians and came from the same geographical region in Northern Spain. We excluded PD patients or controls diagnosed of any oncologic or hematological condition and subjects with active infectious or inflammatory processes. However, we could not exclude participants suffering from common co-morbid conditions like hypertension, diabetes, or hypercholesterolemia; these conditions, nonetheless, were reported at a similar

frequency in all the compared cohorts. All study subjects gave informed consent to participate in the study, which was approved by the Ethics Committee of the University Hospital “Marqués de Valdecilla”.

2.2. Messenger RNA sequencing

Blood total RNA was extracted from each participant using TEMPUS system (Applied Biosystems). This system allows rapid RNA stabilization and long-term storage without degradation. RNA integrity was examined with the Bioanalyzer 2100 (Agilent). RNA-seq was performed at the Centro Nacional de Análisis Genómico (CNAG) in Barcelona, Spain. The libraries were prepared using the mRNA-seq sample preparation kit (Illumina Inc, Cat. # RS-100e0801) according to the manufacturer’s protocol starting with 0.5 mg of total RNA. Briefly, after poly-Aebased messenger RNA enrichment and RNA fragmentation resulting into fragments of ~~80e250~~ (250?) nucleotides, first-strand complementary DNA (cDNA) was synthesized using the random hexamers, following second-strand cDNA synthesis using RNaseH and DNA Pol I. Double-stranded cDNA was end repaired, and 3’ adenylated and the illumina adaptors were ligated. The ligation product was amplified with 15 cycles of polymerase chain reaction. Each library was sequenced using TruSeq SBS kit v3-HS, in paired-end mode, 2 ~~X~~ 76 base pair, in a fraction of a lane of a HiSeq sequencing system (Illumina, Inc) following the manufacturer’s protocol, generating minimally 20-million paired-end reads for each sample. Images from the instrument were processed using the manufacturer’s software to generate FASTQ sequence files.

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2.3. Data analysis

Data analysis was performed with the following bioinformatics analysis protocol. (1)

Alignment: the raw sequences were aligned against the hg19 reference genome with the TopHat pipeline. The number of reads per gene was calculated with Bedtools to enable further analysis. (2) Differential expression analysis: counts were imported to the statistical analysis software R, and a command script that calls to the DESeq package (with fit-only mode) performs the differential expression analysis of RNA-seq data. Multiple testing correction adjustment was performed using the Benjamini-Hochberg method. To detect gene enrichment in reactome terms or KEGG pathways, we have used...

3. Results

Comparative blood transcriptome between idiopathic and *LRRK2* G2019S-associated PD

Demographic data of the cohorts are summarized in Table 1. First, we found 696 genes with significant differential expression between PD patients carrying the *LRRK2* G2019S mutation and controls after adjusting for multiple testing (adjusted p value < 0.05) in the 23,592 human genes analyzed (Supplementary Table 1). Second, the comparison between the cohorts of idiopathic PD and controls yielded 297 differentially expressed genes (Supplementary Table 2). Fifty-eight genes showed significant differential expression in both analyses in having the expression altered in the same direction (Supplementary Table 3). The comparison between idiopathic PD and PD carriers of *LRRK2* G2019S-associated PD yielded 850 differentially expressed genes (Supplementary table 4). The top altered biological pathways in KEGG and Reactome

terms in idiopathic PD group and [PD carriers of LRRK2 G2019S-associated PD](#) group are shown in Supplementary Tables 5 and 6. Only four common altered pathways were present in both conditions: *complement and coagulation cascades* (KEGG and reactome), *cell adhesion molecules (CAMs)*, *hematopoietic cell lineage* (KEGG) and *extracellular matrix organization* (Reactome) (Table 2). The 58 genes deregulated in both idiopathic and [PD carriers of LRRK2 G2019S-associated PD](#) cohorts didn't enrich any particular KEGG or Reactome pathway, but as classified by GeneOntology, *oxygen transport* function (GO:0015671) represented by genes *HBD*, *HBG1* and *HBM* was significantly enriched (adjusted p-value = 0.02).

Changes in the transcriptome attributed to the presence of *LRRK2* G2019S mutation.

The comparison between asymptomatic carriers of the *LRRK2* G2019S mutation and controls yielded 1139 differentially expressed genes (Supplementary Table 7). The top differentially enriched pathways by these genes in KEGG and Reactome databases were *interferon alpha/beta signaling*, *O₂/CO₂ exchange in erythrocytes* and *NCAM1 interactions* (Supplementary Table 8). *Extracellular matrix organization* pathway was also among those significantly enriched. Six out of the 1139 differentially expressed genes (*DGKQ*, *TMEM175*, *MMRN1*, *SREBF1*, *PRSS53* and *SYT11*) have been reported to be associated with PD risk in GWAs studies and 279 were also found overlap with those differentially expressed in the comparison between [PD carriers of LRRK2 G2019S-associated](#) and idiopathic PD cases (Supplementary Table 9). These 279 genes [were significantly](#) enriched [in](#) sixteen KEEG pathways (Supplementary table 10) including *Parkinson's disease*, *complement and coagulation cascades*, *hematopoietic cell lineage*,

ECM-receptor interaction and transcriptional misregulation in cancer. Interestingly, we found the Gene Ontology process “nervous system development” highly enriched in these genes: We found 12 genes when we expected to find only 1.6 (P fisher = 6E-05).

4. Discussion

In this study we have shown that while there are some common genes and pathways deregulated both in idiopathic and *LRRK2* G2019S-associated PD, globally the blood transcriptomic profile differs extensively between both conditions. As shown, the

comparison between PD mutation carriers~~genetic~~ and idiopathic PD (no se puede excluir causa genética en los “idiopáticos”) yielded more than twice as many

differentially expressed genes than that observed between idiopathic PD and controls.

Also, among the 28 and 60 pathways enriched respectively (either in KEGG or Reactome databases) in idiopathic and *LRRK2* G2019S-associated PD only four were common to both conditions. Other authors have also reported a very different transcriptional profile between idiopathic and *LRRK2*-associated PD, although in these studies RNA profiling was performed on a low number of *putamen* and *locus coeruleus* samples (Botta-Orfila et al., 2012). On the contrary, very recently, Mutez et al. reported rather similar deregulated pathways in peripheral blood mononuclear cells between idiopathic and *LRRK2*-associated PD using a microarray procedure instead of RNA-seq (Mutez et al., 2014). Among the four common pathways found deregulated both in idiopathic and *LRRK2* G2019S-associated PD in our study (*cell adhesion molecules*, *complement cascades*, *hematopoietic cell lineage* and *extracellular matrix organization*) only the pathway *cell adhesion molecules* had been reported previously to be associated with PD. Mutez et al, reported this function (as classified by Geneontology) to be

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disturbed in peripheral blood mononuclear cells from *LRRK2* G2019S carriers and also Botta-Orfila et al reported similar findings in brain samples of idiopathic PD patients. Extracellular matrix (ECM) is known to regulate important processes in neuronal cell development, activity and growth, and together with cell adhesion molecules, involved in cell-cell or cell-ECM interactions, are implicated in processes related to major diseases of the central nervous system including PD (Soleman S., 2014). The complement system is an effector arm of the innate immune response and several lines of evidence suggest that innate immune system plays a role in PD pathogenesis (Huang Y., 2012). There was also some additional overlap between the pathways detected in our study and that of Botta-Orfila in idiopathic PD brains, namely *systemic lupus erythematosus* in idiopathic PD and *antigen processing and presentation*, *viral myocarditis*, *graft vs host disease*, *intestinal immune network for IgA production* and *hemostasis* in *LRRK2* G2019S-associated PD. The 58 common genes deregulated in peripheral blood of both idiopathic and *LRRK2* G2019S-associated PD did not enrich any particular pathway according to KEGG or Reactome databases. However, three of those genes (*HBD*, *HBG1* and *HBM*), related to *heme* metabolism, fell in a Gene Ontology functional category. Interestingly, those three genes were also deregulated both in idiopathic and genetic PD cases in the study of Mutez et al, in peripheral blood leukocytes. Other potentially relevant genes among those common 58 have been extensively discussed in a previous study of our group focused in the identification of individual candidate genes through the comparison of the transcriptome between manifesting and non-manifesting carriers of the *LRRK2* G2019S mutation and between idiopathic PD patients and controls (Infante J., 2015).

Despite the above reported overlap observed in the blood transcriptome between idiopathic and *LRRK2* G2019S-associated PD cases, differences seem to be greater than

similarities. Pathways related to cardiac muscle contraction were among the most enriched by genes deregulated in *LRRK2* G2019S-associated PD cases. We didn't find any explanation for that observation. As reported above a few pathways related with immunity were over-represented in both conditions while some others were enriched in just one of the conditions, namely *eukaritic translation initiation, elongation and termination, NCAM signaling, neuronal system* and *glutathione metabolism* in *LRRK2* G2019S-associated PD and *phagosome* and *transcriptional misregulation in cancer* in idiopathic PD cases.

Whether or not the presence of the *LRRK2* G2019S mutation alters the transcriptome is a matter of debate. While some studies have reported that the mutation alters significantly the expression of some mRNAs others couldn't demonstrate relevant transcriptome changes attributed to the presence of this mutation (Dorval V., 2014; Devine MJ., 2011; Nikonova E., 2012; Reinhardt P., 2013). It must be acknowledged that there is a great heterogeneity between these studies, not only in terms of the methodology used but also in the biological tissues or systems analyzed, and this hampers achieving reliable conclusions. To the best of our knowledge this is the first study applying RNA-seq technology to the study of transcriptome in *LRRK2* G2019S mutation carriers. RNA-seq allows analysis of the genomes at a higher resolution than microarray-based methods allowing the quantification of transcript levels and the sequence information. Our results suggest that the G2019S mutation of the *LRRK2* gene indeed alters the blood transcriptome *in vivo*. We compared two cohorts of *LRRK2* G2019S mutation carriers (symptomatic and asymptomatic) with two cohorts of non-carriers (symptomatic and asymptomatic): *LRRK2* G2019S-associated PD vs idiopathic PD and asymptomatic carriers of *LRRK2* G2019S mutation vs controls. The greater number of differentially expressed genes was observed between

asymptomatic carriers of the mutation and controls, yielding 1139 genes. Interestingly, six of these genes (*DGKQ*, *TMEM175*, *MMRN1*, *SREBF1*, *PRSS53* and *SYT11*) have been reported to be associated with PD risk in GWAs studies (Nalls MA., 2014; Rhodes SL., 2011; Pankratz N., 2012; Do CB., 2011). This might indicate that transcriptional changes pathogenically related with PD may be detected in peripheral blood years before the development of motor symptoms of the disease. Among those 1139 genes, 279 overlapped with those differentially expressed between *LRRK2* G2019S-associated PD and idiopathic PD cases. According to these findings, we speculate that the altered expression of these 279 genes observed in peripheral blood might be related to the presence of the *LRRK2* G2019S mutation itself. These genes enriched pathways related with immunity (*graft vs host disease*, *complement and coagulation cascades*) and Parkinson's disease (*Parkinson's disease pathway*), processes in which the *LRRK2* gene has been involved. Also, other pathways shown deregulated in our cohorts of PD cases (*ECM-receptor interaction* and *hematopoietic cell lineage*) might be affected by the presence of the G2019S mutation too, according to our results. We believe that the understanding of the biological functions of these genes and the pathways they are involved in might help in deciphering the still incompletely known biological effect of this mutation.

In summary, we found that despite some overlap, peripheral blood transcriptome differs between idiopathic and [PD carriers of *LRRK2* G2019S-associated PD](#) and [specific some of those](#) transcriptomic changes [might could](#) be attributed to the presence of the G2019S mutation. This emphasizes the notion that PD is likely a pathogenically heterogeneous condition and suggests the existence of specific mechanisms involved in *LRRK2*-associated PD.

Disclosure statement

None of the authors has conflicts of interest to declare in relation to the present research.

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Table 1. Demographic characteristics of the compared cohorts

	G2019-associated PD (n=20)	Idiopathic PD (n=20)	Non-PD G2019S carriers (n=20)	Controls (n=20)
Gender M/F	10/10	9/11	10/10	9/11
Age at study, years, mean (SD)	70.8 (11.7)	70.8 (11.4)	71.9 (7.6)	70.6 (8.8)
Disease duration, years, mean (SD)	10.8 (5.9)	7.2 (4.9)	-	-

Table 2. Common pathways (KEGG and Reactome) enriched in both idiopathic and *LRRK2* G2019S-associated PD.

KEGG pathway	Differentially expressed genes in the pathway	p-value* iPD	p-value* LRRK2-PD
Complement and coagulation cascades		0.0007	0.012
Hematopoietic cell lineage		0.001	0.001
Cell adhesion molecules (CAMs)		0.012	0.0009
Reactome term	Differentially expressed genes in the pathway	p-value* iPD	p-value* LRRK2-PD
Complement and coagulation cascades		0.003	0.002

Extracellular matrix organization		0.012	0.04
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iPD: idiopathic Parkinson's disease

* P adjusted for multiple testing (Benjamini-Hochberg)

Supplementary Table 1. Differentially expressed genes between *LRRK2* G2019S-associated PD and Controls.

Gene	Base mean G2019S PD	Base mean Controls	Fold Change Controls/PD	p-value	Adj P-value*
SNORD42A	534,903568	1,890262186	0,003533837	1,3805E-253	3,2485E-249
HBG1	647,96535	2660,159803	4,105404407	3,12686E-35	3,67891E-31
IFI27	44,00782647	217,1112768	4,933469661	1,12273E-34	8,80635E-31
AIRN	3,890279321	38,9122369	10,00242751	3,97684E-32	2,33948E-28
GAGE8	59,07321285	8,363323104	0,141575559	8,93987E-26	4,20728E-22
MYH7	29,80110393	3,390416405	0,113768148	5,12629E-25	1,72324E-21
GAGE2A	54,44194431	7,455604425	0,136945962	4,60106E-25	1,72324E-21
PCBD2	1088,077907	395,6181459	0,363593584	5,363E-24	1,57746E-20
MYH6	27,78473488	3,643929635	0,13114862	2,72292E-21	7,11923E-18
MIR3183	0,215026231	14,6170752	67,97810251	3,46591E-21	8,15564E-18
GAGE2C	39,90147788	5,301576726	0,132866676	2,1023E-20	4,49719E-17
HCN4	14,09652933	0,478877245	0,033971287	4,80103E-19	9,41443E-16
GAGE2C	33,90700463	4,456386362	0,131429668	1,97251E-18	3,5704E-15
NINL	231,9262807	86,85875076	0,37451017	2,17859E-18	3,66174E-15
GAGE2E	33,25867918	4,408679634	0,132557268	4,46551E-18	7,0052E-15
NCAPG2	705,4101772	357,6261567	0,50697618	9,35785E-17	1,37625E-13
SCARNA3	1,44833907	17,90933005	12,36542632	1,45718E-16	2,01699E-13
ACTN2	19,74778367	2,09775093	0,106227158	4,18347E-16	5,46896E-13
S100B	326,6736779	142,7504968	0,436981938	2,02629E-15	2,50951E-12
GAGE2C	26,12511314	3,350280672	0,128239853	3,35933E-15	3,95242E-12
LOC606724	1124,425136	2717,743288	2,417006878	1,12141E-14	1,25657E-11
ADARB2	822,7158309	554,5853235	0,674090983	1,71768E-14	1,83722E-11
PVRL2	343,4619301	242,1922907	0,705150322	4,07987E-14	4,17406E-11
GJC1	15,1973618	1,598130389	0,105158409	5,43911E-14	5,33282E-11
MIR4480	0,344128739	9,28309477	26,97564524	9,59244E-14	8,79165E-11
HBA2	609939,0074	1706506,271	2,797831014	9,71411E-14	8,79165E-11
LOC100287534	91,6791092	53,25428539	0,580876994	1,39366E-13	1,2146E-10
MYPN	15,4735084	1,770513161	0,114422219	2,47191E-13	2,07737E-10
HBA1	296921,4241	713558,905	2,403191037	2,67164E-13	2,1678E-10
NCAM1	1308,808313	661,4649286	0,50539481	2,9347E-13	2,30188E-10

ACTC1	8,543522512	0,254100236	0,029741858	6,694E-13	5,08118E-10
LOC728989	36,26690588	91,30077945	2,517468122	7,07823E-13	5,20493E-10
MIR632	215,2885119	94,42378547	0,438591844	1,09955E-12	7,84045E-10
HBZ	20,82704804	68,10771139	3,270156734	1,14851E-12	7,9487E-10
CASQ2	10,05833512	0,695046242	0,06910152	1,97175E-12	1,32564E-09
GAGE2D	20,85967967	2,831235221	0,135727646	2,27999E-12	1,45001E-09
GAGE2C	20,85967967	2,831235221	0,135727646	2,27999E-12	1,45001E-09
SNORA68	1025,855485	432,8831226	0,421972811	3,37111E-12	2,08752E-09
KANSL1-AS1	126,3901424	286,0559242	2,263277173	4,50435E-12	2,71774E-09
SNORD15A	6506,933708	3260,555711	0,501089431	6,02424E-12	3,45747E-09
APOD	14,83404354	1,848838149	0,124634807	5,98139E-12	3,45747E-09
SCARNA17	59,86107164	23,71686322	0,39619844	6,76974E-12	3,79283E-09
TNNT2	10,59624108	1,034244041	0,097604805	7,76944E-12	4,21675E-09
LAMA4	22,66120415	4,370566074	0,192865571	7,8848E-12	4,21675E-09
MIR3655	414,3675686	197,4191278	0,476434795	1,18083E-11	6,17468E-09
RYR2	117,6184375	48,83266815	0,415178684	1,37093E-11	7,0129E-09
TCL1A	642,0568975	1183,09882	1,842669745	1,54302E-11	7,72529E-09
NCR1	644,0030436	335,4475425	0,520878815	1,59932E-11	7,84032E-09
TRAPPC5	297,7495978	695,1919111	2,334820655	3,55296E-11	1,70622E-08
CTSE	32,9142888	95,28570404	2,894964695	4,23397E-11	1,99259E-08
KIR2DL4	80,00648185	48,76422484	0,609503427	5,79105E-11	2,67195E-08
RPL13AP6	6,29436818	23,62031573	3,752611073	8,56627E-11	3,8764E-08
GAGE12D	9,064270086	0,452863111	0,049961343	1,06819E-10	4,3337E-08
GAGE12C	9,064270086	0,452863111	0,049961343	1,06819E-10	4,3337E-08
GAGE12E	9,064270086	0,452863111	0,049961343	1,06819E-10	4,3337E-08
GAGE12G	9,064270086	0,452863111	0,049961343	1,06819E-10	4,3337E-08
GAGE6	9,064270086	0,452863111	0,049961343	1,06819E-10	4,3337E-08
GAGE12I	9,064270086	0,452863111	0,049961343	1,06819E-10	4,3337E-08
ISG15	588,4523613	1439,099811	2,445567229	1,56816E-10	6,15006E-08
GAGE12F	8,680023148	0,373534415	0,043033804	1,56553E-10	6,15006E-08
GAGE1	6,2885304	0,074459548	0,011840532	1,59462E-10	6,15133E-08
MIR4784	15,82575732	46,18242758	2,918181205	1,92665E-10	7,31225E-08
GAGE12D	9,243185444	0,569975485	0,0616644	2,74017E-10	9,48221E-08
GAGE12C	9,243185444	0,569975485	0,0616644	2,74017E-10	9,48221E-08
GAGE12E	9,243185444	0,569975485	0,0616644	2,74017E-10	9,48221E-08
GAGE12G	9,243185444	0,569975485	0,0616644	2,74017E-10	9,48221E-08
GAGE6	9,243185444	0,569975485	0,0616644	2,74017E-10	9,48221E-08
GAGE12I	9,243185444	0,569975485	0,0616644	2,74017E-10	9,48221E-08
GAGE12F	15,86120892	1,997451576	0,125933123	2,91725E-10	9,94868E-08
GOLGA8T	179,2845685	85,18725331	0,475151063	3,34336E-10	1,12389E-07
SNORD49B	1105,275125	566,785223	0,512800125	3,4335E-10	1,13794E-07
GAGE12F	8,858938507	0,490646789	0,055384377	4,22698E-10	1,38146E-07
LOC100288346	88,67510891	40,2519594	0,453926247	4,85593E-10	1,56527E-07
RAVER2	188,3449129	334,5147483	1,776075304	5,15645E-10	1,63968E-07
KIR3DX1	89,60706637	40,61292342	0,45323349	6,27672E-10	1,9693E-07
DGKK	67,10253016	31,64705409	0,471622367	7,56672E-10	2,34279E-07
CACNA1G	15,13288072	3,07977127	0,203515202	7,92329E-10	2,42134E-07
JPH2	10,67064375	1,242936041	0,116481823	8,66759E-10	2,61483E-07
MYOM2	1031,715369	692,8806633	0,671581217	1,57521E-09	4,69194E-07
SNORD49A	1006,30868	523,2986986	0,520018071	1,7018E-09	5,00564E-07

FAM154B	20,5604929	52,36719848	2,546981667	1,86132E-09	5,40725E-07
SNORD33	2231,68038	4209,145642	1,886088026	2,02927E-09	5,82326E-07
SNORA74B	219,4143172	325,4620535	1,483321862	2,34617E-09	6,65155E-07
TYRO3P	46,54360375	23,91278572	0,513771685	2,52623E-09	7,07676E-07
LRRC37A4P	612,6028885	349,2034629	0,570032348	3,01476E-09	8,34592E-07
MRGPRE	24,38748387	6,511193596	0,26698915	4,04431E-09	1,10659E-06
FBN1	105,5941589	46,86730531	0,44384373	4,62796E-09	1,25173E-06
KCNA4	6,575845152	0,434427159	0,06606408	4,77204E-09	1,27603E-06
MAPK10	9,535779513	40,47735878	4,244787616	5,07649E-09	1,34219E-06
GAGE2A	8,245181025	0,559498532	0,067857641	5,88274E-09	1,53807E-06
CTAG2	0,975701813	7,060226901	7,236049796	6,70417E-09	1,73358E-06
TMC5	497,2582258	1077,104356	2,166086553	7,05012E-09	1,78383E-06
EIF3CL	383,6958619	200,9208692	0,523646172	7,02041E-09	1,78383E-06
UNC45B	1012,23916	628,2847163	0,620688016	7,30653E-09	1,82904E-06
HLA-DQB1	2080,116311	3123,284524	1,501495137	7,83526E-09	1,94075E-06
EIF3C	386,6641921	203,3173779	0,52582417	8,54102E-09	2,09353E-06
TMTCC1	213,2637741	369,7808817	1,733913241	9,16922E-09	2,22434E-06
THBS1	2362,168157	1605,397753	0,679628903	1,15049E-08	2,76246E-06
PPP2R3B	0,078370857	4,51355665	57,59228393	1,17225E-08	2,78629E-06
EYA4	16,01599206	3,167245163	0,197755166	1,24399E-08	2,89825E-06
GAGE2D	8,946423386	0,708417628	0,079184451	1,24152E-08	2,89825E-06
USP32P2	106,5971723	190,1381816	1,783707556	2,18749E-08	5,04645E-06
HBB	4346165,029	8948544,633	2,058951875	2,33067E-08	5,27417E-06
MYL3	4,102402827	0	0	2,3321E-08	5,27417E-06
GHSR	16,53116118	3,691211797	0,223288114	2,35344E-08	5,27417E-06
KIR3DL1	447,5898954	306,9297711	0,68573883	2,47544E-08	5,49523E-06
SNORA10	3144,277974	5590,930688	1,778128631	2,53465E-08	5,53639E-06
CFD	500,4648108	840,9324719	1,680302898	2,54103E-08	5,53639E-06
MUC6	23,98682027	8,661026024	0,36107437	3,08256E-08	6,15367E-06
MIR4749	25,73301328	57,0913372	2,218602873	2,95436E-08	6,15367E-06
GAGE12D	7,406900394	0,532745711	0,071925594	3,11201E-08	6,15367E-06
GAGE12C	7,406900394	0,532745711	0,071925594	3,11201E-08	6,15367E-06
GAGE12E	7,406900394	0,532745711	0,071925594	3,11201E-08	6,15367E-06
GAGE12G	7,406900394	0,532745711	0,071925594	3,11201E-08	6,15367E-06
GAGE12H	7,406900394	0,532745711	0,071925594	3,11201E-08	6,15367E-06
GAGE12D	7,206216202	0,495515937	0,068762291	2,95961E-08	6,15367E-06
GAGE12C	7,206216202	0,495515937	0,068762291	2,95961E-08	6,15367E-06
GAGE12E	7,206216202	0,495515937	0,068762291	2,95961E-08	6,15367E-06
GAGE12H	7,206216202	0,495515937	0,068762291	2,95961E-08	6,15367E-06
BNC2	221,6644948	130,4679526	0,588582997	3,46546E-08	6,79547E-06
GAGE12D	7,625124752	0,559498532	0,073375656	3,83358E-08	7,21663E-06
GAGE12C	7,625124752	0,559498532	0,073375656	3,83358E-08	7,21663E-06
GAGE12E	7,625124752	0,559498532	0,073375656	3,83358E-08	7,21663E-06
GAGE12G	7,625124752	0,559498532	0,073375656	3,83358E-08	7,21663E-06
GAGE12H	7,625124752	0,559498532	0,073375656	3,83358E-08	7,21663E-06
HBD	1192,801806	2389,825519	2,003539487	4,2267E-08	7,89353E-06
GAGE2B	8,318939099	0,58699001	0,070560681	4,44172E-08	8,22978E-06
TDRD1	13,60171577	4,506740579	0,331336182	5,17792E-08	9,51888E-06
GAGE12B	7,223308044	0,532745711	0,073753702	5,47289E-08	9,98315E-06
TUBA3C	1,277129986	6,790404445	5,316925073	5,53456E-08	1,0018E-05

MIR3194	2,321208997	10,58566679	4,560410892	5,75406E-08	1,03358E-05
ARHGEF17	73,57270364	33,28113907	0,452357157	6,14854E-08	1,09607E-05
GAGE12B	7,441532402	0,559498532	0,07518593	6,67141E-08	1,18034E-05
MIF	191,3407519	382,0107224	1,99649431	7,0061E-08	1,2303E-05
HBQ1	113,3220424	277,4201324	2,448068588	7,48713E-08	1,30503E-05
LY6G6E	414,4433917	259,1011698	0,625178673	8,29021E-08	1,43439E-05
HOXA10	80,48140711	34,45201714	0,42807424	8,57778E-08	1,47331E-05
ADAMTS1	316,1414301	194,4604956	0,615106016	8,79661E-08	1,48916E-05
MYO18B	12,11748969	28,64392878	2,363850064	8,79552E-08	1,48916E-05
LIME1	498,1156309	953,1175823	1,913446443	9,77159E-08	1,64239E-05
HLA-DQA2	291,5707995	460,4501006	1,579205124	9,87312E-08	1,64769E-05
POLR2J3	797,9902839	463,2457152	0,580515483	1,11754E-07	1,85189E-05
WDR87	11,9476579	3,155071498	0,264074476	1,16675E-07	1,89609E-05
VPREB3	98,87287923	170,4496616	1,723927359	1,16332E-07	1,89609E-05
TSGA13	30,84460545	10,68479208	0,346407157	1,16839E-07	1,89609E-05
MIR629	30,2593284	43,26608458	1,429842858	1,27801E-07	2,05978E-05
ANP32A-IT1	97,50630052	54,13966971	0,555242784	1,32215E-07	2,11642E-05
MIR2110	38,25690981	15,27528687	0,399281775	1,35984E-07	2,16206E-05
DLG5	551,1825666	355,3355758	0,644678546	1,40333E-07	2,21622E-05
OLFM1	211,4547436	129,855208	0,614104019	1,50694E-07	2,36399E-05
GAGE2E	7,781891488	0,681664807	0,087596288	1,69218E-07	2,63306E-05
ALAS2	9442,982316	18015,53448	1,907822537	1,70084E-07	2,63306E-05
LGALS8-AS1	124,6024957	64,61927008	0,518603337	1,9559E-07	3,00812E-05
SH2D1B	2200,060192	1453,239968	0,660545549	2,01646E-07	3,08112E-05
SLFN12L	310,94536	200,9237655	0,64617065	2,58553E-07	3,92517E-05
RBP5	357,2850565	199,3641576	0,55799747	2,8533E-07	4,30391E-05
MIR611	397,0944608	219,1063039	0,551773761	3,07389E-07	4,57796E-05
WDR38	74,02591019	141,6393117	1,913374809	3,06673E-07	4,57796E-05
HOXA10-					
HOXA9	127,6823545	62,8984681	0,492616762	3,15077E-07	4,66294E-05
DRAXIN	47,72006294	26,53283414	0,556010041	3,17789E-07	4,67368E-05
ANKRD30BL	451,5523861	860,7789816	1,906266046	3,36267E-07	4,91473E-05
MIR4296	0,161387309	3,820312464	23,67170306	3,50466E-07	5,09063E-05
PDLIM3	9,644252445	1,528369027	0,158474598	3,64103E-07	5,22422E-05
MIR661	4,721554108	0,197198146	0,041765516	3,63513E-07	5,22422E-05
SEC14L5	195,4934301	126,4387414	0,646767215	3,91384E-07	5,58161E-05
RNF165	210,4561409	134,424412	0,638728865	3,95476E-07	5,60599E-05
PPP2R3B	0,35506368	4,956115943	13,95838613	4,02407E-07	5,67009E-05
DSG2	29,66156994	10,60905338	0,357669989	4,30101E-07	6,02423E-05
SNORD119	96,74511628	184,8036268	1,910211429	4,612E-07	6,4216E-05
NUAK1	117,5370787	62,52092215	0,531925098	5,06608E-07	7,01235E-05
SLC2A14	95,25736883	55,81250856	0,585912767	5,31006E-07	7,26459E-05
PGM5	209,3285771	349,0587741	1,667516107	5,29103E-07	7,26459E-05
ID3	145,5937442	236,7638444	1,626195175	5,68318E-07	7,7301E-05
SAMD11	80,22950599	153,9801397	1,919245766	5,96738E-07	8,07003E-05
ABCC13	74,25495367	142,5974838	1,920376713	6,49167E-07	8,72888E-05
PCDH1	174,0154845	119,6466505	0,687563241	6,72322E-07	8,98886E-05
ESRG	17,95825778	39,90322964	2,221998934	7,35062E-07	9,77217E-05
GPR146	299,5635562	579,8347637	1,935598479	7,67304E-07	0,000101435
LDB3	34,88439354	13,25828713	0,380063569	9,20159E-07	0,000120962

MIR1281	27,85293322	10,21690292	0,366816049	9,96569E-07	0,000126758
GAGE12D	7,133566036	0,681664807	0,09555737	9,94163E-07	0,000126758
GAGE12C	7,133566036	0,681664807	0,09555737	9,94163E-07	0,000126758
GAGE12E	7,133566036	0,681664807	0,09555737	9,94163E-07	0,000126758
GAGE12G	7,133566036	0,681664807	0,09555737	9,94163E-07	0,000126758
GAGE12H	7,133566036	0,681664807	0,09555737	9,94163E-07	0,000126758
MIR3184	21,97805113	7,62806411	0,347076457	1,03899E-06	0,000131444
CSRP3	8,800732466	1,35931648	0,154454926	1,06388E-06	0,000133873
RPLP1	12372,67189	20763,33097	1,67816064	1,09279E-06	0,000136779
PNMAL1	9,143832607	25,82670018	2,824493983	1,13216E-06	0,000140956
KRT1	785,0841782	1393,662772	1,77517623	1,3864E-06	0,000171702
MUC16	36,79962182	17,92393384	0,487068425	1,47467E-06	0,000181678
CCDC168	22,18985871	9,912728547	0,446723374	1,52181E-06	0,000186509
SLC25A39	19706,20027	35580,52165	1,805549582	1,58022E-06	0,000192664
KIF20A	104,8100166	57,68395332	0,550366799	1,66222E-06	0,000200583
GAGE12B	6,949973686	0,681664807	0,098081639	1,65628E-06	0,000200583
MIR3916	85,04846989	45,800668	0,538524303	1,72983E-06	0,000206824
GAGE12J	6,124393443	0,434700999	0,070978621	1,73152E-06	0,000206824
MIR423	22,76932077	8,383092465	0,368174903	1,75818E-06	0,000208948
PI16	228,6205808	374,3629479	1,63748577	1,8541E-06	0,000219241
PHOX2B	3,023134171	0	0	1,95194E-06	0,000229656
PDGFRB	567,5257869	385,5218827	0,679302847	2,20886E-06	0,000258591
HOXA-AS4	66,91957151	30,06203988	0,449226425	2,35413E-06	0,000274233
SNORD68	1413,328693	2400,077486	1,698173608	2,39558E-06	0,000277687
AHSP	511,0022189	970,9011171	1,899993936	2,45409E-06	0,000283074
RPLP2	10733,64122	17362,58026	1,6175853	2,54236E-06	0,000291744
SOWAHC	76,99587614	119,5597608	1,552807329	2,55404E-06	0,000291744
H1FX	764,7761316	1238,682121	1,619666292	2,56804E-06	0,000291926
NME3	141,6219707	280,717988	1,982164114	2,69727E-06	0,000303681
GAGE2E	5,994473248	0,393996661	0,065726653	2,68682E-06	0,000303681
SNORD43	1528,691364	881,413224	0,576580234	2,76243E-06	0,000309537
HELB	999,9132081	660,7641378	0,660821492	2,82464E-06	0,000315008
COL5A2	21,33614556	32,19981816	1,509167533	2,90655E-06	0,000322613
C1orf122	139,7456006	247,8535005	1,773605032	2,92938E-06	0,000323621
ELANE	56,08373025	108,5481717	1,935466332	2,94368E-06	0,000323681
SNORD45A	156,3656676	90,90014697	0,581330597	3,03371E-06	0,000332029
FLI1-AS1	662,117492	404,1754625	0,610428613	3,05747E-06	0,000333081
SCN3B	13,64207476	2,912268806	0,213476972	3,26906E-06	0,000354489
EEF1DP3	74,61189046	42,0073459	0,563011413	3,36149E-06	0,000362841
FCER2	801,8156429	1187,44572	1,480946063	3,43659E-06	0,000369253
TSPO	2114,736244	3421,635946	1,617996549	3,47219E-06	0,000370845
CA1	579,5948719	971,0778633	1,675442469	3,48293E-06	0,000370845
CCL3L1	3,308846906	10,86192274	3,282691235	3,66144E-06	0,000385662
CCL3L3	3,308846906	10,86192274	3,282691235	3,66144E-06	0,000385662
PCDHA1	17,4601956	6,823080927	0,39077918	3,67126E-06	0,000385662
LOC284889	272,445581	465,775855	1,709610606	3,68912E-06	0,000385817
GPX1	4526,335417	8385,537292	1,852610671	3,84756E-06	0,000400606
LCN8	29,79814896	55,38969855	1,858830179	3,87096E-06	0,000401267
ATP5D	355,6372858	606,1405094	1,704378404	3,97976E-06	0,000410735
EVA1B	40,66354622	80,13343585	1,970645536	4,22244E-06	0,000433879

CHCHD10	222,8143885	362,3197174	1,626105566	4,48748E-06	0,000459108
SNHG9	49,49243882	95,3311392	1,926175825	4,6749E-06	0,000475903
ITGB3	4033,486446	2961,577601	0,734247565	4,69208E-06	0,000475903
RAP1GAP	68,46703902	153,8515038	2,247088614	4,81683E-06	0,000486459
KIR2DL1	312,4878578	204,7541562	0,655238759	4,95872E-06	0,000498648
CST3	3964,044033	6242,076559	1,57467387	5,09239E-06	0,000509911
ZEB2-AS1	197,1785443	115,7773896	0,587170323	5,44672E-06	0,00054308
MRPL41	118,4467411	227,2256306	1,918378071	5,54091E-06	0,00055014
AGAP1	453,5696569	306,4079616	0,675547751	5,84562E-06	0,000577955
TMCC2	759,4543521	1377,355349	1,813611766	5,9282E-06	0,000583638
RPL23AP7	411,5111213	270,0503824	0,656240788	5,95271E-06	0,000583638
HBG2	4435,315913	10205,78248	2,301027182	6,05758E-06	0,000591456
MIR1537	3,850416795	0,092416148	0,024001596	6,13453E-06	0,000596494
SNORA52	3427,584815	5326,345982	1,553964751	6,51988E-06	0,000631356
C1orf177	111,5268355	64,66127022	0,579782166	6,73244E-06	0,000649267
GGT5	49,61861782	79,47375956	1,60169233	7,66782E-06	0,000736455
MYH1	6,635352772	1,197441425	0,180463868	7,82962E-06	0,000748938
GYLTL1B	142,7257044	232,4677616	1,628772916	8,07837E-06	0,000769604
LOC100506321	801,982595	533,8683776	0,66568574	8,38222E-06	0,000795331
KLF1	99,39353484	183,8268356	1,849484837	8,43216E-06	0,000796856
AKAP5	284,3017716	194,3702861	0,683675958	8,47834E-06	0,000798015
MUC17	15,03368577	5,9163052	0,393536575	8,90247E-06	0,000834597
C22orf32	618,0925555	978,9455013	1,583817007	9,44141E-06	0,000878125
VNN1	1240,761633	1753,841882	1,413520402	9,42208E-06	0,000878125
MZT2B	335,0236263	597,2318364	1,782655877	9,70218E-06	0,000898827
SLITRK3	2,628442615	0	0	1,01644E-05	0,000937958
HBM	545,7556078	1093,286748	2,003253346	1,03099E-05	0,000947667
BLVRB	1991,420544	3285,917997	1,650037209	1,04044E-05	0,000952631
LENG9	304,5447967	521,3657571	1,71195096	1,05847E-05	0,000965384
C16orf13	280,2338052	448,3735777	1,599998178	1,07466E-05	0,00097636
KLRC3	715,3952176	466,7253632	0,652402129	1,12223E-05	0,001015662
RBFOX2	173,8746153	302,1425066	1,737703379	1,12684E-05	0,001015929
SNORD72	2962,743558	4549,160769	1,535455459	1,21013E-05	0,00108685
C1orf21	1016,869027	710,1360985	0,69835552	1,2244E-05	0,001095489
NDUFB11	692,0982042	1052,654999	1,520961899	1,24579E-05	0,001110408
SNORA33	3214,784333	5501,94151	1,711449646	1,29876E-05	0,00115325
SNCA	3427,797843	5752,569097	1,678211307	1,35036E-05	0,001194561
CABP7	84,36587093	152,4105745	1,806543011	1,36488E-05	0,001202884
MIR643	28,44791747	12,46137551	0,438041749	1,38087E-05	0,001212436
C1orf228	326,2551217	503,8480655	1,544337643	1,39565E-05	0,001213847
CIRBP-AS1	1196,225093	753,9100356	0,630240947	1,39706E-05	0,001213847
SPDYE2	65,94496008	34,22564657	0,519003219	1,40311E-05	0,001213847
SPDYE2L	65,94496008	34,22564657	0,519003219	1,40311E-05	0,001213847
MZT2A	218,4538865	330,4828682	1,512826682	1,42084E-05	0,001224679
PCDHA2	16,04840947	6,695115736	0,417182509	1,43943E-05	0,001231727
TREML3P	235,3296536	346,4349839	1,47212635	1,43948E-05	0,001231727
SCGB3A1	4,090506492	11,54645484	2,822744533	1,48598E-05	0,001266902
PPM1L	341,0245178	219,4832159	0,64359952	1,51951E-05	0,001290816
C1orf226	17,77297194	51,2608613	2,88420313	1,64511E-05	0,001386351
GAGE4	7,083314932	0,842709393	0,118971047	1,66143E-05	0,001386351

GAGE5	7,083314932	0,842709393	0,118971047	1,66143E-05	0,001386351
GAGE12I	7,083314932	0,842709393	0,118971047	1,66143E-05	0,001386351
GAGE7	7,083314932	0,842709393	0,118971047	1,66143E-05	0,001386351
DBNDD1	78,82802534	133,2612351	1,690531186	1,68098E-05	0,001397707
TAF1L	13,45059757	4,935377147	0,366926237	1,78161E-05	0,001476165
MIR4498	45,33821982	23,63238401	0,521246403	1,78998E-05	0,001477894
KIR3DL2	429,7195045	290,7662838	0,676642044	1,80066E-05	0,001481515
CHRNA2	16,56419231	5,939146894	0,358553365	1,8588E-05	0,001524022
RPS2	19728,0753	30170,82186	1,529334281	1,96351E-05	0,001604286
COX5B	791,2924523	1214,745363	1,535140843	1,97641E-05	0,001609238
LINC00469	50,87906791	32,92440876	0,647111083	1,98908E-05	0,001613965
NTSE	278,9434901	391,504636	1,403526699	2,00949E-05	0,001624923
MYH2	6,562550736	1,49325337	0,227541611	2,05931E-05	0,001659506
SNORD54	1608,891016	2423,141485	1,506094236	2,09819E-05	0,00168507
COX8A	839,8562667	1277,775642	1,52142181	2,10618E-05	0,001685731
ERBB2	810,1592445	567,8985741	0,700971541	2,13476E-05	0,001702816
CORO2B	44,31222325	74,99209234	1,6923568	2,18453E-05	0,001730779
TXK	2417,943533	1704,415874	0,704903093	2,18343E-05	0,001730779
GSDMA	38,6117059	18,63956175	0,482743803	2,24718E-05	0,001774444
SNORD38B	2408,403119	3707,548898	1,539422063	2,30013E-05	0,00181018
DMD	77,79477666	42,30703966	0,543828795	2,34976E-05	0,001843075
PAR5	87,97995109	54,23306913	0,616425316	2,45202E-05	0,00191689
LOC147646	42,08972349	23,43158033	0,556705494	2,57632E-05	0,002007395
LOC391322	28,76904505	47,95417028	1,666866947	2,66388E-05	0,002068774
RSAD2	1564,052409	3016,094001	1,928384231	2,68227E-05	0,002076199
PTPRCAP	1687,908904	2861,181459	1,695104192	2,80384E-05	0,002163183
MIR330	53,598643	28,79643021	0,537260434	2,84017E-05	0,002184052
ZNF593	50,98639462	91,62577851	1,797063299	2,95786E-05	0,002267143
CEBPE	176,3765293	270,3008924	1,532521892	3,03106E-05	0,00231571
TSSK4	203,6182403	130,996612	0,643344191	3,05266E-05	0,002324664
B3GAT1	762,798141	561,7516161	0,736435481	3,12398E-05	0,002371302
RPL36	5204,492996	7823,821762	1,503282215	3,18663E-05	0,002411084
SNORD34	3096,487145	4677,241602	1,510499279	3,20639E-05	0,002417082
FAM156A	135,2068973	83,04389029	0,614198624	3,21511E-05	0,002417082
CAV3	5,584049723	1,06011736	0,189847407	3,34674E-05	0,002508034
ALKBH7	167,072403	273,0242896	1,63416749	3,36365E-05	0,002512701
MIR454	27,4908652	11,63153161	0,423105331	3,39684E-05	0,002529462
EFCAB4B	495,076084	330,4528887	0,667478998	3,41621E-05	0,002531096
GAGE13	4,631268545	0,382065426	0,082496928	3,4313E-05	0,002531096
GAGE2E	4,631268545	0,382065426	0,082496928	3,4313E-05	0,002531096
MUC2	7,103560703	2,033804367	0,286307734	3,52164E-05	0,002589617
KLRF1	3130,88095	2254,897879	0,720211952	3,54549E-05	0,002590964
GNL3L	2346,028637	1556,079113	0,663282233	3,53985E-05	0,002590964
OTUD7B	360,49599	240,2304033	0,666388559	3,5589E-05	0,002592707
CMKLR1	2033,195091	1410,808131	0,69388724	3,60485E-05	0,002595483
DOC2A	107,302827	194,4101087	1,811789252	3,60683E-05	0,002595483
MIR1181	269,6003532	163,7049714	0,60721349	3,60046E-05	0,002595483
SNORD100	6199,641734	10369,60917	1,67261426	3,58285E-05	0,002595483
TEX15	7,578237176	1,842835951	0,243174753	3,66093E-05	0,00262638
APRT	1140,157115	1748,544054	1,533599212	3,70701E-05	0,002651355

TREX1	624,7278525	970,744334	1,553867544	3,79971E-05	0,002706217
LRRN3	217,6231161	317,7654099	1,460163863	3,80671E-05	0,002706217
NTRK1	319,1040161	214,4695224	0,672099101	3,96048E-05	0,00280705
IL12RB2	200,6876793	157,4586156	0,784595328	4,05403E-05	0,002864725
PCDHA4	14,07205702	5,775373215	0,410414285	4,20816E-05	0,002964736
LINC00707	82,8088579	43,61891376	0,526742125	4,34466E-05	0,003036834
IGFBP2	30,25633972	59,62119215	1,97053552	4,33089E-05	0,003036834
DDX43	117,7563254	62,52500193	0,53096937	4,34921E-05	0,003036834
GFOD1	303,0923223	203,0034756	0,669774391	4,49606E-05	0,00313008
F8A2	86,84432755	137,0581313	1,578204762	4,53384E-05	0,003137815
F8A3	86,84432755	137,0581313	1,578204762	4,53384E-05	0,003137815
PLEKHG6	127,8450686	79,74559749	0,62376749	4,56115E-05	0,003147464
TESC	1485,79755	2406,482591	1,619657127	4,57941E-05	0,003150819
MIR3922	0,055441847	2,888472839	52,09914531	4,6147E-05	0,003163553
RBM38	3631,671611	6061,160432	1,668972606	4,6248E-05	0,003163553
SNORD84	377,2859466	241,9347884	0,641250464	4,67792E-05	0,003190611
RPL35	5258,471559	7575,096534	1,440551013	4,69274E-05	0,003191467
GSTP1	2315,413296	3371,027633	1,455907522	4,74576E-05	0,003199784
MIR4721	127,3163652	197,089224	1,548027417	4,74394E-05	0,003199784
KCND2	12,85061627	4,020608317	0,312872802	4,73271E-05	0,003199784
CD8B	1088,201535	1670,741368	1,535323479	4,81875E-05	0,003239715
FSTL1	216,4188838	163,1544992	0,753882916	4,91754E-05	0,003296714
CD14	7035,555643	10595,4244	1,505982603	5,01241E-05	0,003341277
PCDHA3	14,77889188	6,421140012	0,434480478	5,002E-05	0,003341277
C9orf142	533,4627495	873,5702128	1,63754679	5,12093E-05	0,003403972
MIR4709	520,1028193	808,3024344	1,554120463	5,41854E-05	0,003591652
ETV3	619,9725021	406,754869	0,656085339	5,49986E-05	0,003615005
MT1F	75,96611898	115,9205717	1,525950953	5,4818E-05	0,003615005
CLEC4G	27,50065795	46,65332418	1,696443927	5,4899E-05	0,003615005
ACCS	673,7464518	955,8025214	1,418638301	6,0986E-05	0,003997389
SULT2B1	36,30428886	18,4000025	0,506827239	6,37827E-05	0,004169087
MUC22	16,05861942	7,552123716	0,470284744	6,7384E-05	0,004392278
MIR4781	28,96825297	13,68578053	0,472440659	6,84548E-05	0,004437496
REREP3	77,01567434	49,29012794	0,640001251	6,83786E-05	0,004437496
DNAH2	24,27261322	12,65566757	0,521396994	6,95905E-05	0,004498718
SELENBP1	1294,523005	2091,397905	1,615574151	7,0722E-05	0,004559338
ARVCF	239,1673741	179,5361724	0,750671671	7,31275E-05	0,004701539
LOC100507254	15,56310145	29,82309832	1,916269608	7,49309E-05	0,004804359
CTXN2	26,22166114	54,46444667	2,077078427	7,73452E-05	0,004945678
CACNG8	253,8658261	160,9338361	0,633932651	7,75716E-05	0,004946711
PNLIPRP2	2,169697393	0	0	7,81257E-05	0,004968585
MIR140	105,0538848	61,70213009	0,587337919	7,86846E-05	0,004990638
TUBA4B	426,1694818	290,711987	0,682151114	8,04738E-05	0,005090401
ITLN1	45,35392118	87,54481965	1,930259113	8,35192E-05	0,005268875
COL3A1	6,160912561	1,610924409	0,261474967	8,6861E-05	0,005465044
FAM173A	31,76197374	64,98459061	2,045987165	8,78707E-05	0,005513826
PCDHA5	13,254306	5,600678898	0,422555425	8,84594E-05	0,005536008
SNORD80	118,6924115	178,673033	1,505345041	9,25327E-05	0,005775559
CRIP2	130,7481463	224,1180976	1,714120651	9,36527E-05	0,005830003
SNORA27	4326,73519	6907,994482	1,596583608	9,46507E-05	0,005876583

CCDC85B	55,73811656	102,8389958	1,845038945	9,75765E-05	0,006042294
ITGA2B	4142,603753	3298,887482	0,796331891	9,80738E-05	0,006057149
SEPT10	136,0655468	184,8647561	1,358644863	0,000101248	0,00623685
NR6A1	225,4299583	148,0002324	0,656524241	0,000102321	0,006286459
HYPK	731,2096114	468,4134852	0,640600832	0,000105278	0,006451297
NPAP1	5,153031147	1,153234115	0,223797234	0,000106971	0,006521085
ZNF580	668,4385609	444,8394617	0,665490425	0,000106832	0,006521085
KIR2DS4	305,5906241	287,0874641	0,939451153	0,000113046	0,006873599
LOC100505648	106,7652485	69,23682342	0,648495876	0,000115024	0,00697587
ARL14EPL	389,3511394	597,0800647	1,533525921	0,000116366	0,007039088
MROH2B	6,29640962	1,507808384	0,239471139	0,000129059	0,007786878
CHRM2	7,887100688	1,789105489	0,226839438	0,000130339	0,007844004
SCN5A	33,50574668	14,90092117	0,444727327	0,000132748	0,007968592
MMP8	385,8189654	698,9828698	1,811686134	0,000133487	0,007989846
CADM1	172,4826832	104,5275849	0,60601785	0,000133781	0,007989846
C12orf57	626,2665602	946,7796238	1,511783774	0,000135146	0,008050912
YDJC	161,356907	264,9834901	1,642219692	0,000136568	0,00809465
MIR181A2HG	57,04512272	33,38704611	0,585274332	0,00013627	0,00809465
MT2A	476,5360696	770,5328121	1,616945413	0,000137455	0,008126785
LINC00854	201,6387491	133,6675037	0,662905837	0,00013864	0,008155847
PAGE2B	28,54337259	57,17959454	2,003252922	0,000138558	0,008155847
GOLGA8S	234,6535185	158,0714709	0,673637761	0,000139367	0,008178162
PCDHA8	10,67604649	4,183985816	0,391904046	0,00013975	0,008180258
TJP1	43,69649888	69,82506614	1,597955624	0,000140864	0,008224983
A2M	122,353705	84,74394207	0,692614433	0,000142823	0,00831876
TMEM63C	311,431915	212,5827551	0,682597849	0,000146277	0,008477933
DTHD1	538,3515654	392,9436467	0,729901559	0,000146005	0,008477933
C9orf16	543,3355457	871,7653406	1,604469554	0,000147775	0,008543739
SNORA14A	9,402386029	18,1138051	1,92651153	0,000150829	0,008698911
FLNC	7,888102561	2,651402598	0,336126791	0,000155014	0,008918436
CITED4	41,96158555	67,16296406	1,600582132	0,000158658	0,009085699
MROH8	269,1653154	173,8176724	0,645765492	0,000158694	0,009085699
SNORD46	1685,946756	2299,986571	1,36421068	0,000163048	0,009289784
LINC00299	812,1649525	633,4849513	0,77999543	0,000162729	0,009289784
SNORD4B	716,4901231	1061,161755	1,481055664	0,000165179	0,009388471
LOC100506229	23,57979416	38,90656995	1,649996166	0,000168655	0,009562934
JUND	944,0500459	1452,889199	1,538995952	0,000173891	0,009789082
SFRP2	65,22740118	111,7382332	1,713056647	0,000173565	0,009789082
RHAG	69,92859006	127,5602562	1,824150267	0,000173427	0,009789082
LOC148696	62,29870408	37,82394905	0,607138617	0,000174377	0,009793007
GYPB	25,01048312	49,06982068	1,961970124	0,00017628	0,009876289
BAIAP3	687,8099222	1009,215385	1,467288203	0,000181696	0,010155574
SPN	13555,32036	9601,623745	0,708328796	0,000182282	0,010164152
MIR548W	38,630638	22,99403479	0,595227932	0,000183518	0,010165096
PDE4D	1232,161994	911,295156	0,739590379	0,000183595	0,010165096
LOC100507346	173,4557051	118,9375387	0,685694015	0,000183429	0,010165096
LOC284009	60,37605587	34,58785464	0,572873702	0,00018478	0,010206705
B3GNT8	418,2189581	662,2717291	1,583552625	0,000185563	0,010225971
AGBL4	60,26484216	92,20145962	1,529937793	0,000191372	0,010521461
F2R	2004,561018	1468,792464	0,732725245	0,000195101	0,010701473

ZBTB20	559,8176514	389,798318	0,696295154	0,000195932	0,010722027
SSR4	1204,971019	1789,254646	1,484894339	0,000198036	0,010812007
SPATA31E1	4,512842255	0,821927174	0,182130712	0,000201782	0,010991055
MAP1A	440,4764124	319,4927652	0,725334561	0,00020394	0,01108292
NAT8B	81,90961961	56,06132949	0,684429128	0,000206488	0,011160478
SELM	48,2196885	77,65107566	1,610360375	0,000206405	0,011160478
ENHO	36,19476615	56,3180221	1,555971431	0,000207264	0,011160478
LINC00278	69,07718472	40,47633987	0,585958157	0,000206981	0,011160478
LRP2	14,80980611	7,082179515	0,478208794	0,000208252	0,011188052
ZC3H13	3522,486915	2405,141867	0,682796537	0,000208804	0,01119217
GPR75	93,08152911	58,27137145	0,626025077	0,000210681	0,011248705
CHCHD2	1849,755914	2660,3201	1,438200619	0,000210815	0,011248705
ITPK1-AS1	14,03926726	4,838138387	0,344614736	0,000211672	0,011256719
F8A1	386,6163844	556,6521043	1,439804744	0,000211922	0,011256719
GSTM3	147,1653733	114,3807893	0,777226237	0,000213134	0,011295599
MS4A1	2944,452938	4109,324794	1,395615715	0,000216156	0,011430037
HOXA-AS3	21,90914666	9,649019988	0,44041058	0,000222671	0,011748156
S1PR4	2327,613137	3599,711579	1,546524859	0,000223704	0,011776227
ZBTB37	155,1816563	104,0500534	0,670504852	0,00022639	0,011891021
RPS28	4336,908025	5832,141715	1,344769518	0,000228871	0,011967912
PLCB1	604,8531885	425,1094927	0,70283087	0,000228364	0,011967912
LOXHD1	368,7373558	263,2711116	0,713980039	0,000233383	0,012176802
FAM63B	368,4136872	261,0664743	0,708623169	0,000234128	0,012188659
GP1BA	664,689184	494,5778988	0,744073938	0,000236028	0,012260445
MIR4746	395,2764867	662,6118074	1,676324876	0,000240099	0,012444418
S100A11	14898,06329	21730,20933	1,458592899	0,000241056	0,01246659
TPPP3	239,2691454	329,6374233	1,377684627	0,000242767	0,012527541
SNORD58C	1651,557637	2361,53265	1,429882068	0,000251795	0,012941544
SNORD53	56,57310624	31,25865449	0,552535587	0,00025189	0,012941544
SNORA11B	49,7850897	32,69943234	0,656811759	0,000255671	0,013107183
MORN3	184,3577879	120,7000163	0,654705275	0,000259956	0,01329789
ARRDC3-AS1	865,8497295	598,9398343	0,691736469	0,000262539	0,013400895
HCN1	12,03414112	3,926216692	0,326256494	0,000264471	0,013470298
C2orf48	64,05847498	40,93218639	0,638981593	0,000266207	0,013529415
ZFHx4	13,37274733	5,669604752	0,423967089	0,00026878	0,013630757
TBC1D16	116,5464602	167,7480647	1,439323548	0,000272158	0,013772359
PIGR	11,67621403	4,610286608	0,394844305	0,000274006	0,013836106
CLEC12B	304,8697111	448,5179496	1,471179108	0,000278667	0,014041332
C9orf84	615,0057137	435,8651129	0,708717176	0,000279813	0,014068993
SIVA1	455,5830115	708,0689342	1,55420399	0,000290614	0,01458088
FLJ14107	83,84609447	41,52349783	0,495234729	0,00029154	0,014596236
TRIM56	1379,622076	976,1907793	0,707578399	0,000301088	0,015042276
VIL1	91,89843482	67,21996406	0,731459292	0,000302841	0,015065884
PKHD1L1	257,4574116	198,7179656	0,771847912	0,000302533	0,015065884
ARSH	2,21275408	0,068493931	0,030954154	0,000306441	0,015212801
LINGO2	101,2708747	74,04904381	0,73119783	0,000308183	0,015267065
DSG4	4,036973981	0,686578908	0,170072661	0,000313318	0,015488819
MIR4505	0,545850684	3,823615668	7,004874742	0,000323267	0,015947179
SNORA78	23,69289893	43,17727922	1,822372152	0,000325377	0,016017694
ZNF841	768,1423792	548,9448476	0,71463945	0,000329301	0,016143306

SNORA72	2164,303761	3113,3725	1,438509952	0,000328855	0,016143306
LOC284757	649,2076857	468,9016062	0,722267491	0,000334932	0,016351194
MIR3140	3,504966743	0,301806445	0,086108219	0,000334365	0,016351194
LOC283177	88,32422128	62,74542434	0,71039884	0,000337083	0,01642216
STMN3	946,8266975	1411,678386	1,490957521	0,000340086	0,016534239
PCDHA6	11,95483169	5,341572345	0,446812844	0,00034153	0,016570195
SLC52A3	7,35767572	2,065000816	0,280659395	0,000345125	0,016678499
COL1A2	8,420508895	2,848526288	0,338284339	0,00034518	0,016678499
STAG3L2	422,5180861	300,9010475	0,712161343	0,00034817	0,01678852
TRPM8	18,97983364	9,020685791	0,47527739	0,000355061	0,017085768
YIF1A	266,2712423	394,9664277	1,483323638	0,000359839	0,017279502
MRS2P2	11,49375886	5,050154822	0,439382354	0,000360556	0,017279502
SLC17A4	2,758744962	0,249392362	0,090400659	0,000363439	0,017382261
LYL1	1061,7674	1680,58128	1,582814918	0,000364591	0,017401998
MALAT1	22809,3434	16430,80917	0,720354325	0,000368115	0,017499239
CRIP1	2490,260446	3383,426089	1,358663546	0,00036811	0,017499239
SNORD55	522,207037	707,2159863	1,354282758	0,000380213	0,01803789
FAM179A	543,2532184	408,4929131	0,751938321	0,000382237	0,018097422
C19orf24	272,8968541	402,6777483	1,475567571	0,000383943	0,018141687
SFT2D2	319,3834738	225,1204266	0,704859346	0,000386388	0,018183083
CD200	146,755423	201,9022085	1,375773409	0,00038791	0,018183083
DAB2	903,7589528	694,2077514	0,768133748	0,000385877	0,018183083
MIR581	0,039185429	2,109448823	53,83248066	0,0003879	0,018183083
DSEL	105,5328136	68,88783471	0,65276223	0,000404124	0,018905468
PCDHA7	10,94763175	4,72113774	0,431247401	0,000406296	0,018969363
TFDP2	1371,444826	1006,596217	0,733967709	0,000412138	0,019203998
TCTN1	703,8626134	998,6535663	1,418818882	0,000419152	0,019492238
C6orf1	426,9068181	625,9623708	1,466274007	0,000420164	0,019500755
RGS9	626,9695266	455,5709684	0,726623782	0,000422047	0,019549569
LIX1	62,28705306	96,77947343	1,553765489	0,000423129	0,019561211
SLC12A1	1462,139182	2268,258557	1,551328755	0,000425911	0,019651184
PCDHB7	1,76094723	0	0	0,000428949	0,019752631
LOC644172	8,787082836	21,03516625	2,393873671	0,000436164	0,020045649
IRS4	2,286318279	0,158657393	0,069394272	0,0004394	0,020155024
CYP4F22	122,4619687	82,77060335	0,675888231	0,000443546	0,020271174
ISYNA1	277,2741114	421,3062008	1,519457402	0,000444775	0,020271174
ZNF573	93,43342929	64,57680026	0,691153057	0,000445669	0,020271174
SLC38A11	65,10280528	105,7002672	1,623590055	0,00044517	0,020271174
C7orf50	1018,080777	1550,743194	1,52320251	0,00044624	0,020271174
HS3ST3B1	295,4021271	205,8759547	0,696934571	0,00045089	0,020442942
MIR4651	55,16476443	32,71938272	0,593121045	0,000457488	0,020702198
SCAND1	261,070012	382,618798	1,465579272	0,0004585	0,020708202
MIR5095	4801,057456	7398,577753	1,541030871	0,000462856	0,020864857
TNNI2	130,7635813	198,8011999	1,52031015	0,000466959	0,02096947
MIR5685	120,9170244	85,70112428	0,708759786	0,000466264	0,02096947
SHISA4	199,7166094	320,6036297	1,605292773	0,000473009	0,021200694
C11orf35	147,631995	222,9980004	1,510499133	0,000475505	0,021228341
MYL2	4,642920981	0,776877461	0,167325153	0,000476332	0,021228341
PPDPF	1483,253081	2037,58261	1,37372552	0,000476298	0,021228341
ZNF462	21,25112402	10,00806372	0,470942794	0,000481394	0,021413394

UNC80	14,52119675	6,409194982	0,441368235	0,000485854	0,021571001
SNORD47	168,8244584	242,3719748	1,435644912	0,000487417	0,021599648
PLEK2	119,8794357	198,5518383	1,656262704	0,000491769	0,021693274
NDN	8,9219943	17,72223957	1,986354056	0,000492113	0,021693274
UQCR11	978,2733279	1428,786632	1,460518846	0,000492296	0,021693274
TMEM256	173,8704966	263,9611784	1,518148182	0,0004939	0,021723292
FHL3	1134,587378	1529,673011	1,348219662	0,000496218	0,021784529
MIR30C1	47,62943031	60,92773662	1,279203556	0,000502818	0,021992224
RAD54L2	571,218928	408,548626	0,715222494	0,000502069	0,021992224
KCNJ13	52,33816667	32,63506324	0,623542346	0,000503939	0,022000359
PYCARD	1317,577172	1918,451285	1,45604472	0,000518391	0,022589374
SNORD83B	2905,795936	3990,625172	1,373332904	0,000521088	0,022664917
HYDIN	33,15847593	20,0562408	0,604860152	0,00053787	0,023351704
LRP3	115,5707404	176,1845135	1,524473347	0,000545304	0,023630847
MIR1184-1	50,44484617	76,70824788	1,520635976	0,000551853	0,02378325
MIR1184-2	50,44484617	76,70824788	1,520635976	0,000551853	0,02378325
MIR1184-3	50,44484617	76,70824788	1,520635976	0,000551853	0,02378325
CT45A1	1,845556846	0	0	0,000555065	0,023877935
MRPL36	143,0077622	211,255293	1,477229556	0,000557479	0,023938007
SNORA38	148,7592954	101,2546437	0,680660953	0,000559915	0,02399882
IFIT1	2626,786718	4357,285887	1,658789371	0,000562564	0,024068525
NRAP	6,402528982	1,680241883	0,262434092	0,000569695	0,024241402
CBWD3	182,4628917	123,9216438	0,679160802	0,000569334	0,024241402
CBWD5	182,4628917	123,9216438	0,679160802	0,000569334	0,024241402
TSEN34	1894,274577	2741,005454	1,446994795	0,000571841	0,024288807
COL6A5	9,78244645	3,496575201	0,357433615	0,000575945	0,024419051
DDT	304,1486215	432,6782041	1,422588082	0,000581166	0,02459608
ZDHHC12	515,0041885	754,5315199	1,465097832	0,000583089	0,024633148
PCDHA9	9,379356858	3,869776688	0,412584439	0,000584173	0,024634732
GZMK	1265,158288	1722,651137	1,361609178	0,000587188	0,024717553
ISOC2	108,5065331	163,3593667	1,505525631	0,000591329	0,024847433
CDH2	51,51395679	80,40612925	1,560861061	0,000593925	0,024896571
PF4	2026,78948	3204,23945	1,580943399	0,000595672	0,024896571
CNTNAP2	133,9178399	188,9801654	1,411164976	0,000595662	0,024896571
BCL7C	288,0901842	418,9112477	1,454097608	0,000597975	0,024948508
GOLGA8B	1215,183887	1863,341096	1,533381998	0,000602469	0,025091494
ITGAD	208,4808736	134,6726379	0,64597119	0,000603994	0,025110572
C11orf31	549,472533	797,5087569	1,451407867	0,000605525	0,025129814
VWF	362,271251	275,5111727	0,760510728	0,000612424	0,025251399
RPUSD1	268,6511654	403,6235571	1,502407616	0,000611068	0,025251399
CAPS	203,5801537	328,9756128	1,615951294	0,000610135	0,025251399
FAM196B	459,5805533	326,975885	0,711465885	0,000612747	0,025251399
LOC100129250	240,2113141	349,016732	1,452957091	0,00062002	0,025506468
VSTM2B	21,43692957	10,17758869	0,474768957	0,000621362	0,02551704
BRE-AS1	81,1697328	50,04780108	0,61658206	0,000624551	0,025603332
SYTL4	88,26775215	66,68182268	0,755449426	0,000625667	0,025604458
CLEC12A	5285,338042	7278,988606	1,377203984	0,00062676	0,025604673
CLIC3	277,5701565	231,8900003	0,835428431	0,000629459	0,025670379
PIM3	1210,503211	1676,070261	1,384606209	0,000640182	0,026062506
LLPH	1506,553729	1037,278025	0,688510476	0,000655914	0,02657798

MIR3136	50,56348342	29,88760792	0,591090762	0,000654057	0,02657798
SPARC	7654,516336	6121,660271	0,799744883	0,000656232	0,02657798
LOC100505658	83,27970744	153,2563708	1,840260677	0,000662323	0,026778572
MIR548Q	25,04366292	12,62942164	0,504296104	0,000665369	0,026855567
IRF7	1192,26435	1789,696947	1,501090717	0,00067044	0,026967731
LINC00487	8,322634981	19,67590681	2,364143911	0,000669638	0,026967731
BTBD8	27,12866253	15,11643267	0,557212603	0,000677593	0,02720896
SNORD38A	2716,015093	3791,195535	1,395866888	0,000691401	0,027716113
KCNH8	73,03172132	110,2833681	1,510074884	0,000694629	0,02779814
DPP7	1160,52347	1653,471781	1,424763759	0,000696537	0,027827204
ZNF793	217,0864837	156,5364146	0,721078586	0,000697896	0,027834221
TSSC4	429,427085	633,1159609	1,474327035	0,000705218	0,028078659
MIR5194	5,485427907	2,380002074	0,433877195	0,000706678	0,028089274
TAF15	10295,79796	7177,588567	0,697137667	0,000708077	0,02809739
MIR3978	21,02756749	12,19798277	0,58009481	0,000710153	0,028132339
CDC42EP1	110,3950328	166,4711076	1,507958314	0,000711848	0,028152097
NOG	55,73509276	85,38607434	1,531998425	0,000718676	0,02837443
LCN2	918,3170991	1565,618426	1,704877789	0,000720288	0,028390437
VKORC1	445,4326659	642,6988146	1,442864127	0,000727509	0,028627115
DDX11L1	24,43169342	16,31828102	0,667914448	0,000729931	0,028674479
TRPT1	395,4128093	576,1318039	1,457038797	0,000732401	0,028723546
YES1	404,0475216	299,7212744	0,741797087	0,000738476	0,028913612
EPB41L4A-AS1	211,292434	308,4225858	1,459695361	0,000745423	0,029137111
SLC47A1	70,81405951	45,87250957	0,647788164	0,000768232	0,029929232
CD177	433,7991888	295,2312054	0,680571133	0,00076812	0,029929232
KIAA1244	11,25011898	4,782698535	0,425124262	0,000780173	0,030344203
LOC644248	270,1569819	426,3797411	1,578266599	0,000789264	0,030647163
FBXO7	19533,89644	29293,22088	1,499609716	0,000791339	0,030677082
DUSP23	213,2174461	307,022211	1,439948825	0,000796114	0,030750895
NLRP7	86,18845742	60,69632355	0,704227983	0,000797163	0,030750895
C6orf226	35,55124938	61,40239875	1,727151642	0,000796409	0,030750895
PROS1	194,7799112	154,546886	0,793443662	0,000799569	0,030793238
MADCAM1	43,26737689	69,5537827	1,607534075	0,000804126	0,03091812
HES4	5,446203963	13,25482739	2,433773593	0,000813511	0,031187226
GALK1	292,6560037	429,6185527	1,467998426	0,000813776	0,031187226
GAS5-AS1	46,55919222	76,67501096	1,646828635	0,000822511	0,031470736
LOC390660	8,475917676	15,4446949	1,822185572	0,000823873	0,031471668
CEP78	784,7895085	617,515676	0,786855162	0,000851083	0,032458386
CBS	144,5322589	195,0097341	1,34924712	0,000855064	0,03252714
FAT1	10,81800276	5,183231091	0,479130132	0,00085565	0,03252714
MUC4	29,44807355	17,17931583	0,583376559	0,000858693	0,032590154
SNORD35A	5192,161193	7063,260073	1,360369952	0,000861135	0,032630237
TCL1B	15,4887787	30,49399534	1,968779846	0,000867794	0,032776985
MPG	692,985313	1026,34609	1,481050277	0,000866815	0,032776985
MYEOV2	292,9734611	429,17269	1,464885892	0,0008896	0,033546758
LDB2	63,60335883	42,68852994	0,671167855	0,000895111	0,033700586
GPR148	1,562503031	0	0	0,000896731	0,033707635
GLRX5	1264,681742	1908,666824	1,509207226	0,000919381	0,03450393
MYH4	5,450241654	1,938468142	0,355666458	0,000922399	0,034562041
NPHS1	3,3439336	0,662149991	0,198015293	0,000933044	0,034905337

MPL	89,04700164	67,20227318	0,754683167	0,000946682	0,03535934
SLFN5	4098,61522	3043,583234	0,742588184	0,000954775	0,035605088
UBTD1	215,9192397	299,7631601	1,388311484	0,000965979	0,035796692
SNORD58A	6304,520172	4317,834662	0,684879189	0,00096351	0,035796692
DCLK2	20,29968178	32,73474649	1,612574367	0,000965998	0,035796692
TOR2A	507,6409348	721,8412107	1,421952331	0,000961668	0,035796692
LOC100653515	57,56593333	36,0609319	0,626428337	0,00096808	0,035817434
LINC00623	163,8406407	111,1588829	0,678457325	0,000971713	0,035839144
PCSK6	509,1579564	403,8541894	0,793180553	0,000971356	0,035839144
PCDHA10	9,10552205	3,869776688	0,424992292	0,000974853	0,035898692
NAIP	2601,635904	1879,282908	0,722346623	0,000988292	0,036336719
CD226	1226,614237	962,4862204	0,784669044	0,001006903	0,036963233
MIR4685	28,01541896	52,89910854	1,88821408	0,001011111	0,037059891
TENM4	37,70855203	56,37415742	1,494996609	0,001029632	0,03768004
MIR3917	36,3240858	19,97538129	0,549921102	0,001038482	0,037886068
ISL2	159,8665481	217,0536486	1,357717741	0,001037717	0,037886068
RASSF7	278,7856921	419,0202542	1,503019222	0,00104684	0,038072929
IMPA2	1604,79159	2155,569695	1,343208495	0,001045989	0,038072929
GMEB1	645,9792082	459,3288352	0,711058234	0,001052459	0,038159328
PPP1R35	263,0640057	375,0342286	1,425638706	0,001050986	0,038159328
C10orf71	3,646619641	0,649410612	0,178085645	0,001078603	0,039047102
GP6	206,348545	163,8142897	0,793871795	0,001082684	0,039134609
MAGI3	352,7868778	255,7451294	0,724928124	0,001094209	0,03943006
MIR671	98,05712314	145,2921318	1,481709101	0,001092665	0,03943006
PCDHGA10	214,9001792	152,9855291	0,71189112	0,001098455	0,039522556
AQP10	170,7558349	125,7292238	0,736309971	0,001102421	0,039544299
HIPK2	4991,33188	3650,395642	0,731347009	0,001101231	0,039544299
MYH14	5,886525435	1,666969923	0,283184018	0,001113486	0,03988041
PITPNA-AS1	102,354905	152,0948836	1,485955984	0,001119392	0,040031029
SNORA45	4003,041023	5556,070116	1,387962323	0,001139566	0,040667559
EIF4EBP1	248,4222567	337,211067	1,357410852	0,001144105	0,040667559
TIGD5	41,58833792	73,42718536	1,765571529	0,001143516	0,040667559
SYTL5	8,442888076	4,545022071	0,538325515	0,001141625	0,040667559
FUT11	606,3253057	436,2238271	0,719455089	0,001150769	0,040842751
BOLA1	100,4119043	152,1393512	1,515152534	0,001152849	0,040849645
SNORD15B	2212,969335	2999,958223	1,355625754	0,001154435	0,040849645
LOC100652770	16,44626384	7,371888424	0,448240919	0,001178535	0,041639794
EGFL7	42,65823356	72,05141702	1,689038927	0,001184416	0,041784844
HEG1	1563,671243	1180,363011	0,754866483	0,001187006	0,041813519
ADCY1	11,27348396	5,017344871	0,44505717	0,001195049	0,042033943
TRPV3	65,97262803	49,22445784	0,746134561	0,001205815	0,042349295
PAFAH1B3	129,6756865	188,1860772	1,45120556	0,001216018	0,042644004
MYL4	991,5541088	1701,098927	1,715588602	0,001231158	0,043110677
AUTS2	936,0330164	726,6178274	0,776273715	0,001259435	0,044035321
FAM89B	1406,801184	1961,097969	1,394012169	0,001268447	0,044251942
SYNGR2	2749,963678	3653,16964	1,32844287	0,001269392	0,044251942
DLEU1	246,5483139	170,5589344	0,691787065	0,001275044	0,04438323
CPT1B	1384,326704	1903,580852	1,375095089	0,001282468	0,044575712
ABCB1	752,7940002	568,522061	0,755215983	0,001296958	0,045012855
GNG5	1465,697827	2041,122848	1,392594579	0,00130146	0,045102599

SNORD32A	7993,029538	5492,480747	0,68715882	0,001311444	0,045381744
SERPIND1	52,93169548	34,6811305	0,655205358	0,00132322	0,045722026
HSPB1	663,3946849	920,0194691	1,386835756	0,001326864	0,045780709
LRRC4C	5,124381932	11,09873198	2,165867441	0,001357201	0,046758854
SAP25	919,5150143	1365,877706	1,485432739	0,0013732	0,047240903
KRT23	2262,708597	3154,549976	1,394147696	0,001383048	0,04751021
KLRC4	400,9965726	278,9700223	0,695691787	0,001417619	0,04849914
ROMO1	184,1574309	269,2729994	1,462189161	0,001414485	0,04849914
FREM3	42,21591349	26,9192256	0,637655883	0,00142008	0,04849914
LOC100506178	18,78078452	30,29149021	1,612898023	0,00141836	0,04849914
MAP1B	17,90577542	11,21943043	0,626581657	0,001423611	0,048549259
SPATA13-AS1	35,73469957	21,06461729	0,589472349	0,001435743	0,048892133
MYO6	382,8624229	274,5459684	0,717087789	0,001441464	0,049016037
LOC100288778	553,0102196	720,1724557	1,302276939	0,001445984	0,049098761
LOC100507003	3,487861221	0,668758525	0,191738857	0,001453521	0,049283573
JTB	2066,683	2946,443221	1,425687065	0,001462519	0,049517324
MIR3607	480,7328889	657,08726	1,366844822	0,001465413	0,049544022

* P adjusted for multiple testing (Benjamini-Hochberg)

Supplementary Table 2. Differentially expressed genes between idiopathic PD and Controls.

Gene	Base mean idiopathic PD	Base mean Controls	Fold Change Controls/PD	p-value	Adj P-value*
SNORD42A	221,7101352	1,943965796	0,008768051	6,9921E-155	1,6287E-150
ADAMTS2	139,9536539	12,04524392	0,086065948	2,22429E-62	2,59064E-58
PVRL2	824,8067527	249,2350539	0,302173877	3,42158E-40	2,65674E-36
CXCL12	31,99259746	2,277019313	0,071173318	5,04011E-39	2,93511E-35
TGM2	519,0874885	178,9481756	0,34473606	7,95286E-36	3,70508E-32
C1QA	489,5665869	161,6992132	0,330290542	4,95219E-33	1,9226E-29
MIR3183	0	15,05306448	#DIV/0!	7,4199E-29	2,46913E-25
OLAH	84,8519686	19,98790776	0,235562098	2,10727E-27	6,13584E-24
C1QC	84,69090688	23,09328332	0,272677247	1,76391E-26	4,56538E-23
SCARNA3	0,70790517	18,3093115	25,86407371	3,24966E-26	7,56976E-23
APOL4	185,5808407	65,61582119	0,353570018	4,02816E-25	8,53017E-22
ANKRD22	655,6601007	277,2153009	0,422803371	1,48217E-24	2,87713E-21
SNORA68	1370,832815	444,4517861	0,32422027	5,41655E-24	9,70563E-21
VSIG4	345,4249414	127,8692566	0,370179571	1,02192E-22	1,70033E-19
GBP1P1	109,8958809	42,31278309	0,385026106	5,21069E-22	8,09186E-19
DLG2	2653,4367	6228,757319	2,347430153	1,5619E-20	2,27393E-17
C1QB	177,8288675	72,8438914	0,40962917	1,56929E-19	2,1503E-16
ANKRD30BL	392,6421315	884,5698549	2,252865355	2,91439E-19	3,77154E-16
GPR128	24,63001498	2,105545695	0,085486984	1,39078E-18	1,70509E-15
LCN8	18,22322551	57,08002291	3,132267825	3,29638E-18	3,8393E-15
DGKK	93,53210293	32,51016362	0,347582943	1,09994E-17	1,2201E-14
CFB	44,18165223	14,87676619	0,336718195	3,50781E-16	3,63708E-13
NCAPG2	711,1906593	367,8189494	0,517187543	3,59118E-16	3,63708E-13
PDE3A	2256,681347	4441,284923	1,96806028	2,87895E-15	2,79426E-12
SDC3	333,5047449	159,4409637	0,478077047	4,20667E-15	3,91961E-12
WFDC13	8,036455144	0,421325667	0,052426805	7,09232E-15	6,35417E-12
SNORA37	7,705620521	0,185293357	0,02404652	1,42548E-14	1,22982E-11
TUBA3C	0,23978728	6,946715675	28,97032606	3,67024E-14	3,05338E-11
SMIM1	80,27196699	210,6586799	2,624311922	1,41004E-13	1,1326E-10
MSR1	342,295479	181,8157594	0,531166114	1,51891E-13	1,17938E-10
OR7D2	0,92719532	10,55125961	11,37975934	2,8628E-13	2,15116E-10

MYO18B	8,790681058	29,42160796	3,346908819	2,96669E-13	2,15956E-10
TYRO3P	59,34719025	24,52330867	0,413217687	9,86291E-13	6,96202E-10
DAAM2	587,5909809	292,5738475	0,49792093	3,43225E-12	2,35149E-09
LOC644172	5,09096653	21,66226538	4,255039834	3,67386E-12	2,44511E-09
SNORA54	8,944361689	0,915849905	0,102394104	8,1575E-12	5,27836E-09
CLEC6A	109,8342895	52,71233656	0,479926049	1,04998E-11	6,48597E-09
MIR4655	5,441979534	0,070056946	0,012873431	1,05807E-11	6,48597E-09
CYP26B1	21,10833076	69,17237214	3,277017635	1,54532E-11	9,22995E-09
ALOX15B	123,1058232	53,88923839	0,437747273	3,39888E-11	1,97934E-08
MAPK10	9,631705678	41,78140686	4,337903198	5,46499E-11	3,10492E-08
MIR5690	5,929632222	0,170502292	0,028754278	5,70574E-11	3,16451E-08
ERICH1-AS1	36,89202121	15,11733191	0,409772396	6,50266E-11	3,52263E-08
IGLL5	2021,327928	1134,1416	0,561087384	7,33472E-11	3,88307E-08
SLCO5A1	14646,77319	25757,8456	1,758602066	8,87708E-11	4,59517E-08
SLC6A12	361,4399522	205,9513862	0,569808027	1,2213E-10	6,18454E-08
ITPK1-AS1	19,0494281	4,979757118	0,261412421	4,80684E-10	2,38235E-07
TPST1	691,7681996	372,6769477	0,538730962	5,18331E-10	2,51542E-07
S100B	229,9431255	146,7884956	0,638368707	6,10688E-10	2,90314E-07
CTSE	50,11025324	98,45000487	1,964667877	1,36283E-09	6,34913E-07
MYOF	1797,78813	1091,91406	0,607365263	2,37067E-09	1,08279E-06
MSLN	22,13039139	49,50997867	2,237193992	4,05745E-09	1,81758E-06
SLC1A3	114,9724585	61,34725156	0,53358215	4,48984E-09	1,97333E-06
HFM1	27253,03589	45202,83185	1,658634731	5,31609E-09	2,26258E-06
MPO	1126,888057	759,6713427	0,674132038	5,34224E-09	2,26258E-06
UGT2B11	176,5396243	335,3050726	1,899319056	6,20645E-09	2,58166E-06
SAMD4A	570,9271937	367,6346575	0,643925638	7,37175E-09	3,01259E-06
LIX1	51,21063982	99,64568767	1,945800482	8,0345E-09	3,22682E-06
TCN2	478,0268469	281,7051689	0,589308259	9,51503E-09	3,75666E-06
RRM2	244,2788488	147,6041056	0,604244315	1,58566E-08	6,15606E-06
RNASE1	60,11442164	26,68076946	0,443833089	1,86613E-08	7,12617E-06
ARHGEF17	83,90650374	34,25949007	0,408305537	2,30323E-08	8,65347E-06
CTSG	273,3621382	178,4862355	0,652929614	2,69768E-08	9,97455E-06
GBP6	96,88474291	55,01587467	0,567848693	2,98441E-08	1,08623E-05
CPA6	37,5376727	81,02821951	2,158583995	3,24463E-08	1,16277E-05
RNASE3	327,1529002	205,1699953	0,627137938	3,32277E-08	1,1637E-05
LRRC37A4P	573,5360155	358,8156626	0,625620106	3,34713E-08	1,1637E-05
FCGR1C	190,9259217	109,223132	0,572070733	3,59686E-08	1,23213E-05
ALOX15	596,0965968	967,0539855	1,622310865	4,45913E-08	1,48387E-05
PNMAL1	8,160573313	26,7642837	3,279706299	4,45293E-08	1,48387E-05
ESRG	85,54747373	41,14094782	0,48091365	4,54348E-08	1,49064E-05
KRT79	5,513474982	22,32298729	4,048805401	4,82202E-08	1,56006E-05
OVCH1	237,564303	124,1590011	0,522633239	5,78642E-08	1,84642E-05
SYCE1	39,27916082	14,88494289	0,378952671	5,97411E-08	1,88055E-05
PRSS33	275,126398	462,635469	1,681537913	6,19006E-08	1,92255E-05
HBM	653,5226699	1123,907845	1,719768719	6,72616E-08	2,06157E-05
MMP9	8168,309612	5271,745494	0,645390019	7,42027E-08	2,24478E-05
MIR617	12,96024304	4,063302862	0,313520576	7,75084E-08	2,31472E-05
ANKRD30BP3	8,405653871	1,236665215	0,147123024	8,06642E-08	2,36616E-05
JPH4	65,88005382	34,94367269	0,530413542	8,12626E-08	2,36616E-05
SIGLEC8	230,293483	383,6294237	1,665828397	1,08337E-07	3,11556E-05

FAM26F	1060,52416	683,4100615	0,64440782	1,11327E-07	3,16249E-05
IGFBP2	28,06282359	61,34459148	2,185973599	1,28555E-07	3,60792E-05
LINC00487	5,23532174	20,26181708	3,870214303	1,42417E-07	3,94937E-05
LOC441081	1867,633748	1026,609499	0,549684594	1,98165E-07	5,43065E-05
UNC45B	370,9170981	647,2699832	1,745052969	2,19388E-07	5,87406E-05
FCER2	776,6508763	1222,265229	1,573764051	2,18056E-07	5,87406E-05
KRT1	832,8838385	1433,70176	1,721370609	2,35401E-07	6,23116E-05
NPFFR1	4,743869513	0,496425485	0,104645687	2,38828E-07	6,25086E-05
RUFY4	1847,357511	1307,504944	0,707770389	2,54085E-07	6,57628E-05
GUSBP9	1362,309405	777,0409463	0,570385071	2,70087E-07	6,91362E-05
FLT3	500,1244494	288,9329613	0,577722128	2,81119E-07	7,1178E-05
GUSBP3	1384,368738	790,7209411	0,571177981	3,007E-07	7,53172E-05
ARG1	885,4882819	566,9222875	0,640236917	3,33424E-07	8,26254E-05
CORIN	205,8741779	115,7536125	0,562254158	3,38915E-07	8,3102E-05
FOLR3	1475,55212	856,0810047	0,580176731	3,47073E-07	8,42157E-05
SMA4	2819,94443	1630,375324	0,578158671	3,8221E-07	9,17855E-05
MRGPRE	16,12433527	6,69856868	0,415432238	4,26139E-07	0,000101291
OCLN	30,75974241	12,62730488	0,410514	4,39192E-07	0,000103339
LOC100506305	9,446446344	23,48881198	2,486523623	4,53134E-07	0,000105553
SLAMF8	575,3343774	372,0319581	0,646636065	4,9438E-07	0,000114021
TKTL1	259,2975939	452,8924377	1,746612573	5,13598E-07	0,000117292
SLED1	42,03987607	14,18328757	0,337377007	5,47723E-07	0,00012387
FST	10,95991638	2,293173932	0,209232794	5,85861E-07	0,000131222
ATF3	152,2693412	97,8974526	0,64292294	5,92476E-07	0,000131439
MKI67	573,0861341	402,9626641	0,703145025	6,94154E-07	0,000152544
KCNJ10	24,42180884	12,02967587	0,492579233	7,04907E-07	0,000153459
DRAXIN	50,12113742	27,2593505	0,543869351	7,45633E-07	0,000160822
LOC339975	22,43644051	7,554056974	0,336686961	7,62046E-07	0,000162854
GUSBP9	1438,310461	842,3621977	0,585660899	8,75955E-07	0,000185496
NECAB2	533,0064336	326,8336938	0,613189022	9,73424E-07	0,000203082
KANSL1-AS1	184,8211352	294,3951752	1,592865312	9,7644E-07	0,000203082
LIPM	34,28661257	18,90373362	0,551344452	1,29876E-06	0,000265381
SMA5	5262,814832	3076,992415	0,584666668	1,29141E-06	0,000265381
IGJ	2822,621967	1819,087713	0,644467355	1,42602E-06	0,000288849
PDCD1LG2	80,33206827	49,86208321	0,620699607	1,52601E-06	0,00030644
ACCS	603,2490997	984,1414489	1,631401438	1,54843E-06	0,000308284
CEACAM6	507,1154074	367,5014828	0,724690036	2,05291E-06	0,000405258
IL1R2	5397,405781	3340,025678	0,618820562	2,15189E-06	0,000417717
NXF3	15,15191007	5,830162723	0,38478071	2,13689E-06	0,000417717
NAIP	2881,618372	1932,781656	0,670727836	2,44153E-06	0,000470025
CLC	3288,88769	5002,806838	1,521124255	2,51343E-06	0,0004799
CD160	515,5731981	752,4645684	1,459471848	2,8315E-06	0,000536236
ST18	51,4781612	90,52515712	1,758515747	2,89025E-06	0,000542948
SLIT2	15,05642771	7,019639131	0,466222086	3,64217E-06	0,000678726
GRIN3A	225,2341539	153,2200221	0,68026993	4,23179E-06	0,000782345
HBG1	1580,147456	2734,573299	1,730581085	4,65451E-06	0,000853717
RMRP	5,030043869	12,68827285	2,522497454	5,03604E-06	0,000916481
CXCL10	136,5599121	91,1247675	0,66728783	5,10527E-06	0,000921878
LOC100272216	1017,087088	631,9355983	0,621319064	6,11612E-06	0,001095914
BPI	1051,154238	765,1095729	0,727875649	6,49374E-06	0,001154696

ALDH1A1	1434,167803	958,3392019	0,668219716	8,31367E-06	0,00146711
SLC38A11	62,15542274	108,9094006	1,752210761	9,3943E-06	0,001644343
SIGLEC1	897,3348438	744,0047629	0,829127241	9,45917E-06	0,001644343
ECHDC3	327,8129777	200,5878518	0,611897226	9,99354E-06	0,001724366
VAMP5	1054,179122	719,449681	0,682473847	1,02218E-05	0,001750789
MIR4779	21,04241135	10,8618217	0,516187119	1,06982E-05	0,001819005
ADARB2	702,676331	569,6706627	0,810715599	1,18143E-05	0,00197988
CD163	5603,043984	3627,447513	0,647406575	1,17625E-05	0,00197988
ART3	147,624008	101,6386901	0,688497023	1,31558E-05	0,002173418
PPP1R9A	31,65314955	55,80057626	1,762875956	1,3096E-05	0,002173418
MIR4298	1433,854443	1939,50178	1,352649001	1,39604E-05	0,00229009
MIR629	29,08388585	44,43969282	1,527983333	1,47152E-05	0,002397041
SNORA66	1022,078833	1412,245269	1,381738105	1,55455E-05	0,002514704
LOC101055625	331,5989298	197,246313	0,594833986	1,57202E-05	0,002525425
IL5RA	530,5304432	778,9519845	1,468251246	1,67389E-05	0,002670653
RUNDC3A	781,5030036	1131,125313	1,447371678	1,81405E-05	0,002874586
HJURP	53,2006014	33,90583981	0,637320611	1,93784E-05	0,003050006
GLDN	14,6641679	7,733248943	0,527356819	1,99025E-05	0,003111465
MYO16	393,3557864	277,7986859	0,706227531	2,12044E-05	0,003292898
HIST1H3E	24,99881742	12,05422368	0,482191756	2,15093E-05	0,003318128
TMTC1	260,4266403	380,3850481	1,460622645	2,23881E-05	0,003408544
GFPT2	30,45767287	15,45186021	0,507322417	2,22723E-05	0,003408544
IQSEC3	84,1176098	55,37707853	0,658329197	2,28386E-05	0,003427477
HIST1H3D	108,7719858	70,27310486	0,646058858	2,28253E-05	0,003427477
COL19A1	140,5361665	215,9107302	1,536335704	2,29538E-05	0,003427477
FAM154B	30,70860104	53,99456297	1,758287944	2,46268E-05	0,003653863
UNQ6494	87,32309496	58,58718439	0,670924277	2,51809E-05	0,003712423
CPM	514,6763526	330,2698119	0,641703879	2,5454E-05	0,003729091
CXCR2P1	1311,925043	1011,366616	0,770902745	2,60344E-05	0,003790283
PPP2R3B	1,421217887	5,088448115	3,580343422	2,83175E-05	0,004097061
CNTNAP2	125,583639	194,5092409	1,54884221	2,88068E-05	0,004142129
RSAD2	1465,159605	3112,608946	2,124416299	3,08031E-05	0,004402011
CDC20	57,79910666	36,6377281	0,633880525	3,18221E-05	0,004492516
EMID1	32,76070646	62,02700537	1,893335403	3,18123E-05	0,004492516
PPFIA4	246,2401587	373,206805	1,515621201	3,23003E-05	0,004532547
PGM5	264,304097	359,1897789	1,359001934	3,46664E-05	0,004835449
KCNH8	70,64447034	113,493858	1,606549776	3,57361E-05	0,004954984
SUSD4	155,1857972	224,3780345	1,445867074	3,70988E-05	0,005113483
STOX1	11,85674142	23,14546727	1,95209345	3,8201E-05	0,005234429
TPX2	129,0892221	89,78223697	0,695505291	3,84361E-05	0,005235855
TRPV5	194,0304253	131,4531761	0,67748744	3,93235E-05	0,005325593
TNNT1	171,4522427	114,7452368	0,669254802	4,19146E-05	0,005643693
PRSS41	40,85524013	68,65924979	1,680549412	4,23861E-05	0,005674375
EPB49	7824,878922	11473,28516	1,466257213	4,3421E-05	0,005779702
RGL3	121,0541037	72,64173694	0,600076616	4,45701E-05	0,005898948
EGR2	51,22051886	32,73372363	0,639074425	5,02932E-05	0,006508499
UNC5B	38,18821113	23,67053964	0,619838923	4,99843E-05	0,006508499
LGALS9B	41,62008515	63,97155646	1,537035694	5,01252E-05	0,006508499
POM121L9P	12,76214334	25,25874061	1,979192675	4,96415E-05	0,006508499
INHBB	74,62232055	46,54930902	0,623798733	5,31793E-05	0,00684397

BIRC5	52,22353186	33,17995766	0,635344958	5,75215E-05	0,007321887
GGT5	54,72047801	81,67718466	1,49262557	5,72242E-05	0,007321887
NFXL1	951,1208851	649,3663669	0,682737996	5,86766E-05	0,007428324
AZU1	231,8267216	169,6679204	0,731873872	6,06566E-05	0,007578422
MIR4773-1	58,78375137	37,46624961	0,637357241	6,09594E-05	0,007578422
MIR4773-2	58,78375137	37,46624961	0,637357241	6,09594E-05	0,007578422
WFDC10B	6,873824353	2,127098871	0,309449116	6,11635E-05	0,007578422
MMP8	763,7683856	721,4942279	0,944650553	6,15257E-05	0,007582962
LRRN1	185,2919716	127,9955702	0,690777745	6,24576E-05	0,007657301
PGLYRP1	1334,041855	997,6741237	0,747858187	6,34358E-05	0,007736508
PPP2R3B	1,348364764	4,633480018	3,436369846	6,75884E-05	0,008200018
RPL13AP6	10,50508191	24,34374408	2,31733025	6,89739E-05	0,008310829
MOCS1	88,03334789	53,07696092	0,602918805	6,92153E-05	0,008310829
SMOC2	8,69283199	2,850135974	0,327871973	7,8033E-05	0,00932154
CA6	239,0367468	374,4001239	1,566286895	7,97457E-05	0,009381797
VWCE	464,440205	675,8094484	1,455105396	7,91181E-05	0,009381797
KLHDC8B	629,7515687	451,9753074	0,717704139	7,96774E-05	0,009381797
RPRM	1,173205945	5,702571354	4,860673759	8,13121E-05	0,009518008
GTF2H2	102,4438666	66,68875389	0,650978493	8,22482E-05	0,009579452
MYOM2	471,8947996	712,0198546	1,508852937	8,35729E-05	0,009685308
TRPC6	47,92164412	79,19210339	1,652533106	8,68922E-05	0,010020133
DPYSL4	58,71586534	35,1797022	0,599151558	9,06207E-05	0,010347642
BEX1	32,75250812	22,12522163	0,675527552	9,03648E-05	0,010347642
ABCB4	70,83286498	108,5889287	1,533030307	9,87046E-05	0,011215727
CFH	327,9153857	239,1605052	0,729336029	0,00010362	0,011660537
ITGB4	144,5004566	99,67585286	0,68979611	0,00010324	0,011660537
ARMC9	91,05575607	55,75113902	0,612274736	0,000107355	0,012022699
RAB39A	76,76915794	51,68616662	0,673267338	0,000110307	0,01229426
FCRL1	1443,317489	2061,35296	1,428204796	0,000113136	0,012549493
FN1	116,8142714	83,01447655	0,710653549	0,000116643	0,012877187
FLJ14107	25,35698855	42,64077676	1,681618331	0,000117476	0,012908003
TOP2A	210,313781	160,7843443	0,764497426	0,000121504	0,013287861
ITLN1	58,17223724	90,20883086	1,550719641	0,000124133	0,013316649
LOC389634	638,8512129	457,5371171	0,716187287	0,000122918	0,013316649
APOBEC3B	397,7934721	272,7631758	0,685690427	0,000122559	0,013316649
GRB10	654,203081	456,3167403	0,697515425	0,000125191	0,013316649
DEFA4	715,1841109	584,2691087	0,81694923	0,000125197	0,013316649
TSIX	4239,19535	5747,736185	1,355855465	0,000123761	0,013316649
IFIT1	2495,768445	4493,372825	1,800396521	0,000126568	0,013401267
WARS	12125,31144	9186,832088	0,757657412	0,000127633	0,013452814
OLIG2	68,08597996	103,4009637	1,518682168	0,000132448	0,013897484
GBP1	6396,096646	4948,024677	0,773600674	0,000140602	0,014686912
TMEM45A	24,95631667	12,97085025	0,519742173	0,000143733	0,014946994
FAM21B	328,2320269	243,8754285	0,742997052	0,000152886	0,015828124
FAM107A	13,29533273	5,877388232	0,44206402	0,00016346	0,016847926
APCDD1	78,11871809	117,4224715	1,5031285	0,000167864	0,017225626
C9orf135	1,348583319	5,443607736	4,036537941	0,000170431	0,017412375
PTGDR2	620,3971405	881,3473494	1,420618007	0,000176604	0,017964278
TRPV4	59,29689183	38,52620926	0,649717179	0,000182522	0,018485497
LILRA3	2301,326392	1677,831608	0,729071554	0,000191149	0,019275443

TSPAN13	309,139748	429,8614032	1,390508357	0,000192535	0,019331526
MIR604	39,14572621	24,28472791	0,620367285	0,000197999	0,019794787
C1orf204	507,6799183	369,9913105	0,728788548	0,0002025	0,020158301
CEACAM8	616,0446394	530,0686142	0,860438644	0,000204759	0,02029643
SIGLEC16	209,1375107	146,7386406	0,701637119	0,000207228	0,020454086
SLAMF7	3690,7855	2778,728089	0,752882574	0,000209868	0,020627297
C2orf27A	85,89240509	143,8235519	1,674461807	0,000211366	0,020687206
TGM3	384,9976641	283,5217784	0,736424672	0,000215013	0,020956077
CD209	78,9063345	49,68148552	0,629626073	0,000217387	0,021099224
CCL3L1	5,103842615	11,19688225	2,193814171	0,000222186	0,021386748
CCL3L3	5,103842615	11,19688225	2,193814171	0,000222186	0,021386748
KLHDC7B	309,3230608	235,5754869	0,761583977	0,000223526	0,021427194
KIF18B	37,19501011	24,61054369	0,661662508	0,000227629	0,021731121
SLC5A11	13,12808334	21,85619549	1,664842836	0,000230237	0,021766231
SOWAHC	90,57372793	123,0326714	1,358370404	0,0002308	0,021766231
C2	304,7370003	221,1526856	0,725716554	0,000230176	0,021766231
SLC25A39	25472,59556	36606,47694	1,437092535	0,00023293	0,021878506
GUSBP2	216,9911123	138,6335023	0,638890233	0,000242508	0,022686678
PTH2R	40,34837264	26,94369667	0,66777654	0,000264099	0,024607689
VSTM1	588,6053912	804,3682778	1,366566276	0,000277339	0,025738362
EPB41L3	1262,79232	948,715402	0,751283791	0,000278598	0,025752667
EPPK1	42,25111826	66,30096424	1,569212058	0,000281491	0,02591719
LOC646168	5,90709693	1,615808792	0,273536868	0,000284369	0,026079126
FCRL2	554,7983042	748,9596358	1,349967421	0,000293445	0,026805906
KIF14	36,39620243	24,27659188	0,667008926	0,000297938	0,027110074
OLFML2B	83,5064334	56,56645517	0,677390386	0,000301512	0,027325743
SLC29A1	651,3151697	890,6905572	1,367526197	0,000302655	0,027325743
LTF	5176,488513	4568,873137	0,882620163	0,000313397	0,028186401
GPR84	128,0663124	96,06122591	0,750089732	0,00032194	0,02884337
TCL1B	17,37768196	31,38623713	1,806123349	0,000326211	0,02911403
SMPD3	754,714488	1046,360202	1,386431848	0,000343223	0,03039942
CACNG8	108,4023755	165,789502	1,529389934	0,000342035	0,03039942
FAM129C	966,6531703	1321,92548	1,36752821	0,000356737	0,031476671
CDT1	48,28293935	32,37128518	0,670449762	0,000362254	0,031842827
MYL4	1240,472229	1749,714785	1,410523142	0,000368923	0,032307154
EFHA2	45,29935956	77,43155763	1,709330074	0,000375393	0,03275058
GYPC	22256,07267	30608,85732	1,37530362	0,000381212	0,033134138
TESC	1733,794777	2475,996174	1,428079151	0,00039344	0,034045088
VSIG10	117,091939	156,0695905	1,332880741	0,000394616	0,034045088
MIR4315-1	83,7629661	56,37773638	0,673062799	0,00040517	0,034640561
MIR4315-2	83,7629661	56,37773638	0,673062799	0,00040517	0,034640561
SNCA	4407,508974	5921,151267	1,34342353	0,000407466	0,034640561
LHFPL2	1043,031997	764,88023	0,73332384	0,000407386	0,034640561
FCGR1A	1334,923021	988,7702964	0,740694617	0,00042418	0,035930345
CTSL1	443,0227935	346,1995471	0,781448612	0,000444964	0,037554359
CDK15	10,93147299	22,11795193	2,023327685	0,000447163	0,037603674
MYT1L	7,732314968	17,42464554	2,253483673	0,000464583	0,038928018
IFI44L	1803,521942	1794,772297	0,995148578	0,000474786	0,039640353
HIST1H2AD	38,60054691	24,79011994	0,642221987	0,000478063	0,039771467
BTNL9	29,64374166	45,85372615	1,546826533	0,00048517	0,040219073

P2RX7	946,0787033	709,3593454	0,749788937	0,00050144	0,041420346
MDGA1	272,0934198	378,323127	1,390416303	0,000514135	0,042318956
TLR7	1086,570117	840,583412	0,773611752	0,000528612	0,043357347
HBD	1707,189599	2461,155863	1,441641786	0,000552157	0,045129622
MARC1	2369,394072	1708,79673	0,721195663	0,000562174	0,045787718
AHSP	689,8924039	999,1626433	1,448287643	0,000570459	0,046139846
MIR4767	2,686366538	7,202339723	2,681071113	0,000569099	0,046139846
BCAT1	467,181096	335,6247857	0,718404038	0,000579735	0,046263538
ALOX5AP	11361,93199	8257,359873	0,726756671	0,000575981	0,046263538
LOC339822	9,997669989	23,87956895	2,388513421	0,000577569	0,046263538
OLIG1	355,6349117	472,3723432	1,328250764	0,000579933	0,046263538
STAP1	278,1032805	372,1589503	1,3382041	0,00058589	0,046579255
SLC2A14	88,18298385	57,37859123	0,650676454	0,000605685	0,047989177
XIST	5859,808694	7840,268804	1,33797351	0,000611903	0,048317521
TMC5	785,1522017	1108,383023	1,411679188	0,000614521	0,048360348

* P adjusted for multiple testing (Benjamini-Hochberg)

Supplementary Table 3. Differentially expressed genes both in idiopathic and *LRRK2* G2019S-associated PD compared to controls

Gene	Fold Change*	Fold Change**	Padj*	Padj**
ACCS	1,631401438	1,418638301	0,000308284	0,003997389
ADARB2	0,810715599	0,674090983	0,00197988	1,83722E-11
AHSP	1,448287643	1,899993936	0,046139846	0,000283074
ANKRD30BL	2,252865355	1,906266046	3,77154E-16	4,91473E-05
ARHGEF17	0,408305537	0,452357157	8,65347E-06	1,09607E-05
CCL3L1	2,193814171	3,282691235	0,021386748	0,000385662
CCL3L3	2,193814171	3,282691235	0,021386748	0,000385662
CNTNAP2	1,54884221	1,411164976	0,004142129	0,024896571
CTSE	1,964667877	2,894964695	6,34913E-07	1,99259E-08
DGKK	0,347582943	0,471622367	1,2201E-14	2,34279E-07
DRAXIN	0,543869351	0,556010041	0,000160822	4,67368E-05
FCER2	1,573764051	1,480946063	5,87406E-05	0,000369253
GGT5	1,49262557	1,60169233	0,007321887	0,000736455
HBD	1,441641786	2,003539487	0,045129622	7,89353E-06
HBG1	1,730581085	4,105404407	0,000853717	3,67891E-31
HBM	1,719768719	2,003253346	2,06157E-05	0,000947667
IFIT1	1,800396521	1,658789371	0,013401267	0,024068525
IGFBP2	2,185973599	1,97053552	3,60792E-05	0,003036834
ITLN1	1,550719641	1,930259113	0,013316649	0,005268875
ITPK1-AS1	0,261412421	0,344614736	2,38235E-07	0,011256719
KANSL1-AS1	1,592865312	2,263277173	0,000203082	2,71774E-09
KRT1	1,721370609	1,77517623	6,23116E-05	0,000171702
LCN8	3,132267825	1,858830179	3,8393E-15	0,000401267
LIX1	1,945800482	1,553765489	3,22682E-06	0,019561211
LRRC37A4P	0,625620106	0,570032348	1,1637E-05	8,34592E-07
MAPK10	4,337903198	4,244787616	3,10492E-08	1,34219E-06
MIR629	1,527983333	1,429842858	0,002397041	2,05978E-05
MRGPRE	0,415432238	0,26698915	0,000101291	1,10659E-06
MYO18B	3,346908819	2,363850064	2,15956E-10	1,48916E-05
NAIP	0,670727836	0,722346623	0,000470025	0,036336719
NCAPG2	0,517187543	0,50697618	3,63708E-13	1,37625E-13
PNMAL1	3,279706299	2,824493983	1,48387E-05	0,000140956
PVRL2	0,302173877	0,705150322	2,65674E-36	4,17406E-11
RPL13AP6	2,31733025	3,752611073	0,008310829	3,8764E-08
RSAD2	2,124416299	1,928384231	0,004402011	0,002076199

S100B	0,638368707	0,436981938	2,90314E-07	2,50951E-12
SCARNA3	25,86407371	12,36542632	7,56976E-23	2,01699E-13
SLC25A39	1,437092535	1,805549582	0,021878506	0,000192664
SLC2A14	0,650676454	0,585912767	0,047989177	7,26459E-05
SLC38A11	1,752210761	1,623590055	0,001644343	0,020271174
SNCA	1,34342353	1,678211307	0,034640561	0,001194561
SNORA68	0,32422027	0,421972811	9,70563E-21	2,08752E-09
SNORD42A	0,008768051	0,003533837	1,6287E-150	3,2485E-249
SOWAHC	1,358370404	1,552807329	0,021766231	0,000291744
TCL1B	1,806123349	1,968779846	0,02911403	0,032776985
TESC	1,428079151	1,619657127	0,034045088	0,003150819
TMC5	1,411679188	2,166086553	0,048360348	1,78383E-06
TMTC1	1,460622645	1,733913241	0,003408544	2,22434E-06
TUBA3C	28,97032606	5,316925073	3,05338E-11	1,0018E-05
TYRO3P	0,413217687	0,513771685	6,96202E-10	7,07676E-07
FAM154B	2,546981667	1,758287944	5,40725E-07	0,003653863
KCNH8	1,510074884	1,606549776	0,02779814	0,004954984
LINC00487	2,364143911	3,870214303	0,026967731	3,94937E-05
LOC644172	2,393873671	4,255039834	0,020045649	2,44511E-09
MIR3183	67,97810251	#iDIV/0!	8,15564E-18	2,46913E-25
MYL4	1,715588602	1,410523142	0,043110677	0,032307154
PGM5	1,667516107	1,359001934	7,26459E-05	0,004835449
PPP2R3B	13,95838613	3,580343422	5,67009E-05	0,004097061

P adj: adjusted for multiple testing (Benjamini-Hochberg)

* Controls/idiopathic PD

** Controls/LRRK2 G2019S-associated PD

Supplementary Table 4. Differentially expressed genes between idiopathic and *LRRK2* G2019S-associated PD.

Gene	Base mean G2019S PD	Base mean idiopathic PD	Fold Change iPD/G2019S PD	p-value	Adj P-value*
AIRN	3,958253134	59,75715431	15,09685012	5,26499E-49	1,23948E-44
ADAMTS2	16,45821669	138,6394223	8,423720801	4,79439E-36	5,64348E-32
TGM2	151,6116469	513,0162579	3,383752293	7,79327E-35	6,11564E-31
GAGE8	60,16915014	5,53429994	0,091979028	4,85723E-34	2,85872E-30
CXCL12	2,195774655	31,61616636	14,3986389	6,96316E-33	2,73211E-29
GAGE2A	55,45086791	4,957755489	0,089408077	6,21466E-33	2,73211E-29
GAGE2C	40,64308076	3,58345979	0,088169	4,13599E-27	1,39099E-23
PCBD2	1108,381598	362,5350784	0,327085075	1,91373E-25	5,63163E-22
MYH7	30,28751307	3,157111498	0,104238056	4,40525E-24	1,15232E-20
GAGE2C	34,53654731	3,156997187	0,09141033	5,40132E-24	1,27158E-20
IFI27	44,82028782	136,5808422	3,047299535	1,14357E-23	2,44744E-20
ANKRD22	255,8534051	647,7416869	2,531690702	1,90762E-23	3,66735E-20
GAGE2E	33,87475312	3,156997187	0,093196168	2,02513E-23	3,66735E-20
ESRG	18,29630151	84,4386571	4,615066988	3,92742E-23	6,60423E-20
UNC45B	1030,542447	366,7538908	0,355884313	5,70841E-23	8,95915E-20
GBP1P1	33,45962281	108,6244801	3,246434688	6,41766E-23	9,44279E-20
RYR2	119,6489329	31,49897595	0,263261654	1,70698E-20	2,36387E-17
PDE3A	5428,426379	2231,750677	0,411122952	4,79593E-20	6,27255E-17
GAGE2C	26,610068	2,416691861	0,090818703	5,6609E-20	7,01416E-17
ERICH1-AS1	9,426359943	36,53491007	3,875823785	2,38421E-19	2,80645E-16
MYOM2	1050,944179	467,3323834	0,444678597	2,72401E-19	3,05374E-16
APOL4	72,32798946	183,4046588	2,535735614	3,17405E-19	3,39652E-16
MYH6	28,24359504	3,7712993	0,133527594	3,38388E-19	3,46362E-16
VSIG4	138,5768651	341,5947376	2,465019954	1,55077E-18	1,52117E-15
C1QA	215,4174716	484,0968515	2,247249715	1,80577E-18	1,70046E-15
GAGE2D	21,24855042	1,829728008	0,086110722	3,34787E-17	2,9191E-14
GAGE2C	21,24855042	1,829728008	0,086110722	3,34787E-17	2,9191E-14
SNORD42A	545,5290992	218,833573	0,401140055	1,47561E-16	1,24067E-13
GJC1	15,44518187	1,071883194	0,069399195	8,29408E-16	6,67626E-13
NINL	236,7258304	81,2194911	0,343095179	8,50769E-16	6,67626E-13

DLG2	5642,34859	2624,883395	0,465211136	1,07914E-15	8,19523E-13
C1QC	33,47804598	83,74637581	2,501531178	3,08949E-15	2,2729E-12
C1QB	80,85338773	175,8414826	2,174818985	3,24586E-15	2,31558E-12
HCN4	14,32341967	1,032626099	0,072093545	7,44186E-15	5,15283E-12
LOC606724	1145,554034	3041,51724	2,655062223	1,05245E-14	7,07908E-12
SLED1	9,023484138	41,52254198	4,601608574	1,15298E-14	7,53986E-12
GAGE12F	16,15565758	1,320536825	0,081738352	1,26226E-14	8,03135E-12
HBG1	660,1214488	1563,395165	2,368344747	1,78534E-14	1,10607E-11
CSRP3	8,94758854	0,290350558	0,032450146	2,03833E-14	1,23042E-11
OLAH	28,68296292	83,81678919	2,9221803	3,53428E-14	2,0801E-11
APOD	15,1340243	1,392713499	0,092025325	5,23288E-14	3,0047E-11
MYPN	15,7340722	1,752888889	0,111407198	1,44483E-13	8,09861E-11
FLJ14107	85,38167465	25,08797148	0,293833209	1,65277E-13	9,04874E-11
MMP8	392,9446303	755,2273922	1,921968985	3,51426E-13	1,88029E-10
LAMA4	23,03813488	4,2997562	0,186636471	4,99133E-13	2,61124E-10
SCARNA17	60,99262943	20,64361661	0,33846084	5,14058E-13	2,63086E-10
MIR4296	0,164067964	7,091153742	43,22083085	5,55131E-13	2,78061E-10
ACTC1	8,679929978	0,386177232	0,044490823	1,59048E-12	7,80064E-10
ELANE	57,15846904	134,8215306	2,35873236	1,75579E-12	8,43568E-10
LOC728989	36,94867972	83,98495938	2,27301652	3,17785E-12	1,49626E-09
CACNG8	258,7378686	107,196095	0,414303849	3,33503E-12	1,53947E-09
MIR4655	0	5,412386458	#DIV/0!	4,67576E-12	2,11686E-09
TNNT2	10,77583041	1,084970122	0,100685523	5,82981E-12	2,58953E-09
EYA4	16,28018503	1,98817359	0,122122297	6,72838E-12	2,93332E-09
MIR4480	0,350311209	7,46725784	21,3160688	1,82811E-11	7,82497E-09
MIR3922	0,05661064	5,657600316	99,93881496	2,60913E-11	1,09686E-08
CFB	17,05957019	43,68068967	2,560480081	3,30685E-11	1,36579E-08
GAGE12F	9,022519698	0,473916548	0,052525964	3,56159E-11	1,44564E-08
JPH2	10,84676797	1,23723874	0,114065198	5,19938E-11	2,07464E-08
GAGE12D	9,414205175	0,556645128	0,059128213	5,79746E-11	2,09975E-08
GAGE12C	9,414205175	0,556645128	0,059128213	5,79746E-11	2,09975E-08
GAGE12E	9,414205175	0,556645128	0,059128213	5,79746E-11	2,09975E-08
GAGE12G	9,414205175	0,556645128	0,059128213	5,79746E-11	2,09975E-08
GAGE6	9,414205175	0,556645128	0,059128213	5,79746E-11	2,09975E-08
GAGE12I	9,414205175	0,556645128	0,059128213	5,79746E-11	2,09975E-08
LOC100506305	39,92470623	9,381483722	0,234979405	8,76097E-11	3,12501E-08
GOLGA8T	182,6737596	79,0017129	0,432474336	1,03859E-10	3,64932E-08
BNC2	225,8754588	114,1947894	0,505565279	1,40072E-10	4,84937E-08
DPYSL4	25,97404924	58,13395619	2,238155308	1,83963E-10	6,27661E-08
CASQ2	10,22012455	0,785127116	0,076821678	2,86242E-10	9,62671E-08
HLA-DQB1	2119,257638	3262,217221	1,539320733	3,08636E-10	1,02337E-07
SIGLEC1	532,9710931	887,0533908	1,664355539	3,27672E-10	1,0714E-07
GAGE12F	8,840110746	0,5802315	0,065636225	3,82259E-10	1,23276E-07
SDC3	190,1677874	329,9242909	1,73491155	3,9252E-10	1,24874E-07
GAGE12D	9,231796223	0,662960079	0,071812686	5,24248E-10	1,54273E-07
GAGE12C	9,231796223	0,662960079	0,071812686	5,24248E-10	1,54273E-07

GAGE12E	9,231796223	0,662960079	0,071812686	5,24248E-10	1,54273E-07
GAGE12G	9,231796223	0,662960079	0,071812686	5,24248E-10	1,54273E-07
GAGE6	9,231796223	0,662960079	0,071812686	5,24248E-10	1,54273E-07
GAGE12I	9,231796223	0,662960079	0,071812686	5,24248E-10	1,54273E-07
CTAG2	0,994987355	11,12989835	11,18596965	7,123E-10	2,07024E-07
GAGE2D	9,112030595	0,662960079	0,072756569	7,64741E-10	2,19555E-07
PDGFRB	578,4567731	314,3114449	0,543362027	1,06224E-09	3,01293E-07
MIR632	219,275232	100,0820842	0,456422202	1,13073E-09	3,169E-07
CXCL10	70,3816166	135,0098362	1,918254265	1,21189E-09	3,35652E-07
GAGE2A	8,398010767	0,512878232	0,061071395	1,53294E-09	4,19632E-07
IGLL5	1251,809467	1998,762404	1,596698585	1,56516E-09	4,2353E-07
TCN2	260,2876287	473,024764	1,817315584	1,6003E-09	4,28117E-07
MIR617	2,264425616	12,80898524	5,656615591	2,02072E-09	5,34514E-07
LINGO2	103,1745309	51,1562043	0,49582202	2,07435E-09	5,42603E-07
WFDC13	1,237372114	7,934826567	6,412643759	2,35135E-09	6,08302E-07
SNORD15A	6629,674373	3376,223909	0,509259387	2,97149E-09	7,6038E-07
TGM3	220,2577355	380,8197242	1,728973211	3,25732E-09	8,22105E-07
ART3	78,78457174	145,951962	1,852544969	3,28255E-09	8,22105E-07
ALOX15B	61,04711474	121,7543786	1,994432974	3,8251E-09	9,47901E-07
LIPM	15,81080192	33,87577967	2,142571885	3,86634E-09	9,48141E-07
MDGA1	476,8440764	269,0770499	0,564287286	4,09721E-09	9,94396E-07
HLA-DQA2	297,0540756	521,4517558	1,755410205	5,17278E-09	1,24263E-06
GAGE2B	8,472642703	0,662960079	0,078247142	5,28836E-09	1,25756E-06
GAGE1	6,403595494	0,315539007	0,049275287	6,0483E-09	1,42389E-06
CACNA1G	15,3935226	3,257177462	0,211594029	6,98462E-09	1,62804E-06
KCNA4	6,68641413	0,411471379	0,061538423	1,0051E-08	2,31981E-06
GAGE12D	7,766302491	0,512878232	0,06603892	1,10916E-08	2,44036E-06
GAGE12C	7,766302491	0,512878232	0,06603892	1,10916E-08	2,44036E-06
GAGE12E	7,766302491	0,512878232	0,06603892	1,10916E-08	2,44036E-06
GAGE12G	7,766302491	0,512878232	0,06603892	1,10916E-08	2,44036E-06
GAGE12H	7,766302491	0,512878232	0,06603892	1,10916E-08	2,44036E-06
SNORD49B	1126,067671	568,2699358	0,504649899	1,24598E-08	2,71601E-06
IFI44L	1172,277479	1782,494141	1,52053944	1,30506E-08	2,81868E-06
SNORD33	2273,927145	4533,073234	1,993499767	1,36244E-08	2,91586E-06
FST	1,442764162	10,84903603	7,519618461	1,52234E-08	3,22874E-06
RBFOX2	177,1429078	376,1522624	2,123439583	1,63774E-08	3,44248E-06
GAGE12D	7,543102027	0,556645128	0,073795254	1,7748E-08	3,57113E-06
GAGE12C	7,543102027	0,556645128	0,073795254	1,7748E-08	3,57113E-06
GAGE12E	7,543102027	0,556645128	0,073795254	1,7748E-08	3,57113E-06
GAGE12G	7,543102027	0,556645128	0,073795254	1,7748E-08	3,57113E-06
GAGE12H	7,543102027	0,556645128	0,073795254	1,7748E-08	3,57113E-06
COL13A1	88,09266826	43,86532652	0,497945259	1,79773E-08	3,58103E-06
MUC22	16,3551135	5,106013581	0,312196768	1,81014E-08	3,58103E-06
TRAPPC5	303,3430195	692,2307687	2,282006588	1,91115E-08	3,74935E-06
GAGE12B	7,579010931	0,512878232	0,067670866	1,99382E-08	3,87921E-06
HBZ	21,22677728	54,8433185	2,583685587	2,47005E-08	4,7664E-06

SH2D1B	2241,706602	1374,71609	0,613245323	2,53965E-08	4,86086E-06
GAGE2E	7,926479315	0,662960079	0,083638656	2,56424E-08	4,86833E-06
LINC00707	84,47706599	33,35692725	0,394863705	2,65579E-08	5,00181E-06
GAGE12B	7,355810467	0,556645128	0,075674208	3,1844E-08	5,94977E-06
GOLGA8S	239,1672771	128,6514598	0,537914138	3,41633E-08	6,28337E-06
PGLYRP1	772,0439639	1319,248677	1,708774032	3,40505E-08	6,28337E-06
KLHDC7B	179,9329898	305,9959487	1,700610595	3,4716E-08	6,33553E-06
GAGE12D	7,338891078	0,556645128	0,07584867	3,6233E-08	6,41352E-06
GAGE12C	7,338891078	0,556645128	0,07584867	3,6233E-08	6,41352E-06
GAGE12E	7,338891078	0,556645128	0,07584867	3,6233E-08	6,41352E-06
GAGE12H	7,338891078	0,556645128	0,07584867	3,6233E-08	6,41352E-06
SNORA54	1,34589008	8,891425677	6,606353529	3,88015E-08	6,76641E-06
MIR4784	16,12708327	44,35017615	2,75004323	3,86255E-08	6,76641E-06
TKTL1	385,298516	256,5519021	0,665852297	3,95785E-08	6,85115E-06
NCAM1	1333,527027	760,0858467	0,569981584	4,01793E-08	6,90438E-06
SNORD49A	1025,2215	526,9317427	0,513968682	4,32729E-08	7,3821E-06
CITED4	42,76500192	86,10835513	2,013523939	4,51801E-08	7,65201E-06
OLFM1	215,5807257	144,3808321	0,669729781	5,33107E-08	8,96458E-06
NCR1	656,1359423	367,7675111	0,560505053	6,43592E-08	1,07457E-05
FAM26F	605,3495813	1048,93145	1,732769762	6,73592E-08	1,11674E-05
MIR3655	422,0972087	220,4621941	0,522301947	7,39716E-08	1,21779E-05
TRPV4	30,58490499	58,64577691	1,917474549	7,57451E-08	1,23833E-05
LINC00299	827,4000478	537,591045	0,649735332	8,64772E-08	1,40403E-05
KIR3DX1	91,39542363	39,65212518	0,433852414	8,86396E-08	1,42928E-05
ARMC9	42,75241329	90,14114679	2,108445813	1,1347E-07	1,81722E-05
GPR128	4,644016467	24,30521435	5,233662395	1,15696E-07	1,84035E-05
MIR3140	3,568993786	0	0	1,29007E-07	2,03831E-05
PDLIM3	9,800293868	1,34091614	0,136824075	1,37787E-07	2,16252E-05
RNF165	214,3715587	126,1865552	0,58863478	1,62805E-07	2,53825E-05
FBN1	107,4483425	46,04558231	0,428536925	1,64E-07	2,54005E-05
DMD	79,13375708	32,30142638	0,408187701	1,65236E-07	2,54248E-05
ASMT	0	3,105457624	#DIV/0!	1,71702E-07	2,5922E-05
GAGE12D	7,264685118	0,662960079	0,091257924	1,75074E-07	2,5922E-05
GAGE12C	7,264685118	0,662960079	0,091257924	1,75074E-07	2,5922E-05
GAGE12E	7,264685118	0,662960079	0,091257924	1,75074E-07	2,5922E-05
GAGE12G	7,264685118	0,662960079	0,091257924	1,75074E-07	2,5922E-05
GAGE12H	7,264685118	0,662960079	0,091257924	1,75074E-07	2,5922E-05
JPH4	36,21178702	65,14768414	1,79907399	1,83332E-07	2,69751E-05
SLCO5A1	22522,97957	14490,72687	0,643375217	1,94494E-07	2,84396E-05
PPP1R9A	63,24673989	31,30163139	0,494912962	2,0561E-07	2,97531E-05
GAGE2E	6,10653345	0,349117357	0,05717112	2,06004E-07	2,97531E-05
BEX1	15,92643696	32,37948148	2,033064995	2,0884E-07	2,99788E-05
SCN1A	7,653980022	0,904961667	0,11823413	2,25309E-07	3,21468E-05
AKAP17A	0	3,039570391	#DIV/0!	2,50662E-07	3,53358E-05
AKAP17A	0	3,039570391	#DIV/0!	2,50662E-07	3,53358E-05
KCNMA1	37,02823461	68,45304433	1,848671562	2,54768E-07	3,57009E-05

MIR4749	26,20916492	58,40349827	2,228361661	2,81947E-07	3,83594E-05
LY6G6E	422,2210741	238,4149742	0,56466858	2,81529E-07	3,83594E-05
GAGE4	7,215537658	0,662960079	0,091879512	2,83516E-07	3,83594E-05
GAGE5	7,215537658	0,662960079	0,091879512	2,83516E-07	3,83594E-05
GAGE12I	7,215537658	0,662960079	0,091879512	2,83516E-07	3,83594E-05
GAGE7	7,215537658	0,662960079	0,091879512	2,83516E-07	3,83594E-05
B3GNT8	425,9641598	790,6740102	1,856198443	2,90351E-07	3,90597E-05
MIR4802	13,86325578	33,11713596	2,388842599	3,02776E-07	4,04998E-05
GAGE12B	7,077393558	0,662960079	0,093672914	3,05161E-07	4,05881E-05
OR7D2	6,661855727	0,917881176	0,137781605	3,35468E-07	4,43684E-05
BPI	660,9928396	1039,356681	1,572417458	3,4756E-07	4,57109E-05
MSR1	229,8073762	338,4500739	1,472755485	3,63533E-07	4,75461E-05
SLC1A3	63,64545326	113,6031335	1,784937142	3,8783E-07	5,04436E-05
ITGA2B	4220,662173	2613,28073	0,619163682	4,29727E-07	5,55858E-05
FAT4	76,72471525	44,04247468	0,574032429	4,42494E-07	5,69246E-05
SNORA10	3203,62369	5813,096904	1,814537994	4,85096E-07	6,2066E-05
SLAMF8	350,0165209	568,8602537	1,625238295	5,03541E-07	6,40777E-05
PROS1	198,4454038	122,7114711	0,618363886	5,29442E-07	6,69118E-05
ARG1	553,5757828	874,585197	1,579883413	5,31498E-07	6,69118E-05
GAGE12J	6,239056275	0,499199205	0,080011973	5,53709E-07	6,93373E-05
PLXNA4	242,7172699	143,2855492	0,590339325	5,85647E-07	7,29487E-05
SNORA74B	223,6017032	383,5954097	1,71552991	6,32452E-07	7,83641E-05
EVA1B	41,42248517	88,61438289	2,139282144	6,6134E-07	8,15145E-05
FN1	65,19908241	115,5314754	1,771980082	7,06683E-07	8,66497E-05
MROH7	65,74261431	34,50633896	0,524870197	7,95053E-07	9,59853E-05
ADAMTS1	322,0704746	207,7294955	0,644981493	7,88704E-07	9,59853E-05
SPARC	7797,52814	4891,226704	0,627279135	7,93325E-07	9,59853E-05
PVRL2	350,0042175	815,8550171	2,330986246	8,07092E-07	9,69417E-05
PAR5	89,57455563	42,94091114	0,479387376	8,29062E-07	9,9075E-05
FCGR1C	120,3642029	188,6823542	1,567595262	8,34055E-07	9,91683E-05
MYZAP	361,900197	242,302037	0,669527232	8,5549E-07	0,000101206
LRP2	15,08694848	4,451446938	0,295052836	8,6277E-07	0,000101557
MUC6	24,43683489	10,11384305	0,413876965	9,63526E-07	0,000112294
VNN1	1263,7982	2044,489213	1,617733918	9,61206E-07	0,000112294
SNORA37	1,794510609	7,643433599	4,259341551	1,01046E-06	0,000117183
ID3	148,3513317	252,0038103	1,698695977	1,01809E-06	0,00011749
CCDC168	22,5994949	8,112839705	0,358983231	1,08691E-06	0,000124819
SNORD119	98,57007595	195,7124183	1,985515547	1,10939E-06	0,000126783
GLOD5	9,336620664	2,016271594	0,215953038	1,13362E-06	0,000128926
MIR661	4,813395998	0,232299528	0,048261046	1,20489E-06	0,000136372
IL1R2	3082,12963	5332,389998	1,730099197	1,32832E-06	0,000149623
ATP1A4	37,43632348	18,81751833	0,502654016	1,33996E-06	0,000150216
KLRC2	273,4877979	140,332086	0,513120099	1,42664E-06	0,000159079
ITGB3	4108,898086	2644,089431	0,643503289	1,43254E-06	0,000159079
KLRF1	3189,686137	2068,953217	0,648638496	1,50378E-06	0,000166206
LOC646168	1,288138724	5,853453969	4,544117696	1,56151E-06	0,000171781

KLRC3	728,9325803	422,3077791	0,579350945	1,61376E-06	0,000176703
MRPL41	120,6914286	260,0269684	2,154477508	1,64123E-06	0,000178879
ZNF462	21,6515474	7,515139062	0,347094779	1,9804E-06	0,000214851
CES1P1	0,71290622	5,757550806	8,076168571	2,03048E-06	0,000219273
KRT77	13,20325043	5,057314016	0,383035529	2,15134E-06	0,000231264
TXK	2463,180305	1567,209538	0,636254494	2,22358E-06	0,000236866
CA1	590,2939865	1055,376768	1,787883313	2,21451E-06	0,000236866
ITGB4	80,34979142	143,0533285	1,780382077	2,45439E-06	0,000260276
LIME1	507,4581573	978,1853202	1,927617688	2,49613E-06	0,000263515
UTS2	17,68675194	33,67475046	1,903953341	2,59707E-06	0,000272948
AKAP5	289,6689972	184,6149566	0,637330741	2,69074E-06	0,000281535
MPO	745,0809292	1114,194411	1,495400523	3,00719E-06	0,000313254
MYL3	4,168838323	0,2732965	0,065556992	3,10652E-06	0,000322175
TDRD1	13,86022334	5,902836305	0,425883203	3,3397E-06	0,000343332
KIR3DL1	455,8998437	340,7061141	0,747326675	3,33126E-06	0,000343332
CD160	757,5576813	509,989017	0,673201565	3,35948E-06	0,000343864
AZU1	149,4168808	229,2285666	1,534154409	3,41847E-06	0,000348388
FLT1	63,57299164	114,7420151	1,804886196	3,50519E-06	0,000355686
KIR3DL2	438,1733119	258,8322813	0,590707545	3,54672E-06	0,000358355
WDR87	12,17104833	3,45246842	0,28366237	3,65176E-06	0,000367392
TNNT1	111,5415567	169,6289435	1,520769017	3,7893E-06	0,000379608
ASMT	0,116316382	3,132166279	26,92798911	3,8538E-06	0,000384433
MIR3115	5,219301643	13,09990588	2,5098963	4,17198E-06	0,000412676
FSTL1	220,4737256	142,7203448	0,647334935	4,17115E-06	0,000412676
NECAB2	318,8767231	527,2780048	1,653548116	4,19769E-06	0,000413481
DAAM2	342,8038436	581,2361868	1,695535793	4,24848E-06	0,00041674
MUC17	15,3110385	5,425830878	0,354373799	4,39766E-06	0,000429584
VSTM2B	21,87835435	7,039399401	0,321751777	4,60141E-06	0,00044763
HBA1	302485,2103	570531,4616	1,886146635	4,67322E-06	0,000452745
LOC100288346	90,35147365	48,11880708	0,532573572	4,72701E-06	0,000456078
ACTN2	20,06801697	6,117176276	0,30482216	5,00608E-06	0,000479253
SERPINB10	46,12574575	77,15730499	1,672760055	5,00791E-06	0,000479253
CFD	509,9860853	915,7318031	1,795601546	5,05556E-06	0,000481854
SNORD68	1440,096735	2620,254773	1,819499141	5,2127E-06	0,000492841
KCND2	13,06437408	3,069294078	0,234936175	5,19799E-06	0,000492841
MIR548Q	25,5158041	9,685668217	0,379594865	5,29164E-06	0,000498303
ST8SIA6	206,994004	126,6076587	0,611648919	5,43388E-06	0,000509526
MUC16	37,47815815	16,37248526	0,436854052	5,46278E-06	0,000509526
SPDYE2	67,18261595	34,21288667	0,509252076	5,49739E-06	0,000509526
SPDYE2L	67,18261595	34,21288667	0,509252076	5,49739E-06	0,000509526
MIR181A2HG	58,14284615	31,8215465	0,547299429	5,67513E-06	0,000523937
ANKRD30BP3	1,763450266	8,350494724	4,735316263	5,90928E-06	0,000541308
SYCE1	18,0470674	38,71005139	2,144949677	5,90365E-06	0,000541308
KIR2DL1	318,4539437	215,62428	0,67709722	6,10477E-06	0,000557048
GLDN	5,749033012	14,49514445	2,521318702	6,21794E-06	0,000564124

WDR38	75,43611262	141,2590418	1,872565233	6,23024E-06	0,000564124
CD14	7168,425194	11896,78329	1,659609045	6,44738E-06	0,000581549
LIM2	56,25917261	30,99438247	0,550921406	6,47305E-06	0,000581636
MIR3916	86,61905075	44,37166153	0,512262154	6,59762E-06	0,000590575
CA6	406,723248	236,5457754	0,58158902	6,71554E-06	0,000598853
HLA-DRB5	2871,453632	3918,355343	1,364589454	6,79603E-06	0,000603744
AKR1C3	432,1876031	295,5889747	0,683936727	7,38595E-06	0,000648718
CT47A1	2,677591144	0	0	7,60539E-06	0,000648718
CT47A10	2,677591144	0	0	7,60539E-06	0,000648718
CT47A11	2,677591144	0	0	7,60539E-06	0,000648718
CT47A12	2,677591144	0	0	7,60539E-06	0,000648718
CT47A2	2,677591144	0	0	7,60539E-06	0,000648718
CT47A3	2,677591144	0	0	7,60539E-06	0,000648718
CT47A4	2,677591144	0	0	7,60539E-06	0,000648718
CT47A5	2,677591144	0	0	7,60539E-06	0,000648718
CT47A8	2,677591144	0	0	7,60539E-06	0,000648718
CT47A9	2,677591144	0	0	7,60539E-06	0,000648718
SAMD4A	383,2176069	564,5040308	1,473063921	7,93923E-06	0,000674748
GFOD1	308,789321	191,5371771	0,62028433	8,11658E-06	0,00068734
SEC14L5	199,1444823	130,1682187	0,653637084	8,2943E-06	0,000699873
HIST1H3D	63,85069946	107,652009	1,685995767	8,38157E-06	0,00070471
BIRC5	31,81947886	51,68407452	1,624290415	8,43634E-06	0,000706791
SCN3B	13,87254756	3,683490555	0,265523729	8,55279E-06	0,000714006
SNORD45A	159,274846	88,39535833	0,554986305	8,63434E-06	0,000718267
RNASE3	221,9488882	323,5508874	1,457772058	9,13728E-06	0,000757429
KRT5	64,27003559	42,35668866	0,659042558	9,23484E-06	0,00076283
S1PR4	2371,177304	4156,416305	1,7528914	9,38919E-06	0,000772868
DDX11L1	24,89730736	12,54877033	0,504021184	9,55985E-06	0,000784174
UNC80	14,79383889	4,533509726	0,306445795	9,59669E-06	0,000784463
CCL2	7,304538281	17,93037944	2,454690324	1,02141E-05	0,000832039
ERBB2	825,5499766	543,0922742	0,657855114	1,02505E-05	0,000832125
S100A11	15175,60419	25045,69459	1,650391923	1,0955E-05	0,000886266
CHCHD10	226,9968753	379,861723	1,673422696	1,11848E-05	0,000901759
MIR5690	1,091360476	5,881154388	5,388828456	1,23742E-05	0,000994241
MIR1281	28,35359881	11,09011912	0,391136208	1,26544E-05	0,001013297
EMR4P	881,6614321	547,3107743	0,62077205	1,27101E-05	0,001014312
FCGR1A	866,609796	1319,607421	1,522723868	1,30719E-05	0,001039659
HLA-DQA1	1611,090382	2327,276684	1,444535148	1,32342E-05	0,001045499
PKHD1L1	262,2518941	175,6033779	0,66959813	1,31919E-05	0,001045499
RNASE1	31,60841107	59,60000059	1,885574079	1,34985E-05	0,001062816
CABP7	85,95755176	162,5265543	1,890776912	1,35788E-05	0,001065571
SLC12A3	53,3675081	31,34233781	0,58729251	1,46428E-05	0,00114525
KCNJ13	53,30839781	27,37172544	0,513459916	1,48374E-05	0,001156632
UGT2B11	301,9657626	174,5621024	0,578085744	1,49932E-05	0,001164532
GPR112	7,511848506	1,439453154	0,191624359	1,50377E-05	0,001164532
GBP6	60,89072287	95,76790886	1,572783248	1,52356E-05	0,001175989

DSG4	4,113436374	0,345775626	0,08406004	1,59659E-05	0,00122833
SLC6A12	247,66716	357,4727343	1,443359444	1,60962E-05	0,001230314
LPL	44,02610032	82,27016591	1,868668025	1,60825E-05	0,001230314
SI	5,157442242	0,68663236	0,13313428	1,63279E-05	0,001243983
HERC2P3	193,2236557	122,1434193	0,632134915	1,80358E-05	0,001369675
POLR2J3	812,8720199	508,5448418	0,625614893	1,81913E-05	0,001377037
CLEC6A	67,70617783	108,600868	1,604002345	1,83561E-05	0,001385065
PODN	101,6848281	63,95404284	0,628943806	1,86575E-05	0,001403309
C1orf177	113,6248401	63,45696129	0,558477893	1,8975E-05	0,00142264
CXXC11	18,23613902	39,59721427	2,171359531	1,90792E-05	0,001425913
PRSS50	8,692104911	2,715506341	0,312410673	1,94726E-05	0,001450707
SYTL5	8,599687905	3,636746256	0,422892819	1,95443E-05	0,001451456
A2M	124,6224044	78,24890912	0,627887975	2,00974E-05	0,001483466
PHOX2B	3,073883758	0,150081848	0,048824829	2,01013E-05	0,001483466
CTSG	190,015719	270,2687479	1,422349421	2,01693E-05	0,001483828
LOC100506229	24,01710791	50,2254089	2,091234676	2,04883E-05	0,001502603
DTHD1	548,4810547	374,5979592	0,682973379	2,07637E-05	0,00151807
INHBB	44,08364366	73,77484491	1,673519673	2,15301E-05	0,001569232
LRRC43	47,50371561	28,41027642	0,5980643	2,17763E-05	0,001582275
LOC100287534	93,37777198	82,88540273	0,887635258	2,25848E-05	0,001635972
CHRNA2	16,86672832	6,020501555	0,356945428	2,31326E-05	0,001670514
LRRN3	221,6662379	319,4756422	1,441246286	2,32809E-05	0,001676082
CDT1	28,79409439	47,80019751	1,660069487	2,43812E-05	0,001749944
PCDH17	7,952728202	1,999740792	0,251453431	2,46705E-05	0,001754664
RNASE6	2039,050139	3177,717009	1,558430049	2,45813E-05	0,001754664
TSPO	2154,474621	3543,024005	1,644495586	2,46153E-05	0,001754664
FLG2	8,628014343	2,474870744	0,286841288	2,58049E-05	0,001829813
MMP9	5783,359951	8077,65344	1,396705982	2,60081E-05	0,001838686
EIF3CL	390,9400529	228,8218224	0,585311791	2,78053E-05	0,001959857
MIR4721	129,7094455	212,8282777	1,64080786	2,86461E-05	0,002013093
UBTD1	219,9621686	343,6899069	1,562495538	2,90548E-05	0,0020297
SLC22A18A	85,73198745	143,9427357	1,678985172	2,90096E-05	0,0020297
S	621387,2906	1319502,658	2,123478671	3,06413E-05	0,002134191
HBA2	45395,8606	70567,10418	1,554483234	3,16154E-05	0,002195545
HLA-A	207,3944685	126,3863758	0,6094009	3,20035E-05	0,002215963
TSSK4	637,9229077	1024,854812	1,606549631	3,23202E-05	0,002231328
PANX2	12,80740145	21,75669281	1,698759338	3,24743E-05	0,002235408
KCTD4	149,6858152	109,8513901	0,73387976	3,38704E-05	0,002324714
LOC339788	393,9633041	231,854186	0,588517214	3,41754E-05	0,002338829
EIF3C	197,7023678	323,8991385	1,638316941	3,43401E-05	0,002340607
ECHDC3	13,61769349	5,089170456	0,373717506	3,44002E-05	0,002340607
ZFH4	3622,739144	5118,987286	1,4130157	3,47405E-05	0,002356945
LTF	78,42327718	49,0133358	0,62498454	3,48735E-05	0,002359171
REREP3	194,9732855	385,7523572	1,978488264	3,5543E-05	0,002397571
MIF	337,1101553	502,0066499	1,489147218	3,5967E-05	0,002419246
C1orf204					

LILRA3	1462,067969	2277,326492	1,557606446	3,7801E-05	0,002535361
B3GAT1	777,4365919	534,9950282	0,688152621	3,90457E-05	0,002611403
CHRM2	8,015370209	1,470892595	0,183509003	3,92554E-05	0,002617988
LINC00470	11,74648993	3,850719257	0,327818717	4,04725E-05	0,002691535
SULT2B1	36,99171985	17,89740012	0,48382179	4,12093E-05	0,002732814
ZNF580	680,858939	428,821613	0,629824459	4,14356E-05	0,0027401
CYP26B1	44,62478625	20,84782555	0,467180401	4,27489E-05	0,002819033
MIR611	404,5604542	236,7256662	0,585142872	4,32114E-05	0,002822274
KLRC4	408,5933264	243,5741337	0,596128517	4,3174E-05	0,002822274
GOLGA8I	21,82784746	8,516555753	0,39016929	4,30324E-05	0,002822274
CT47A1	2,943840072	0,140684915	0,047789592	4,32776E-05	0,002822274
CHIT1	96,48052195	148,9773199	1,544118096	4,35453E-05	0,002829582
BFSP1	165,014749	105,294914	0,638093956	4,38704E-05	0,002829582
CST3	4038,471941	6497,78698	1,608971679	4,38279E-05	0,002829582
MIR570	48,69871426	23,76904865	0,4880837	4,3808E-05	0,002829582
NME3	144,2818166	288,9820183	2,002899777	4,47738E-05	0,00287996
HCN1	12,23417636	3,38219053	0,276454289	4,75816E-05	0,003052225
ZMAT4	22,84545296	19,32848089	0,846053739	4,78763E-05	0,003062785
GAGE13	4,718282231	0,499199205	0,105801048	4,83991E-05	0,00307949
GAGE2E	4,718282231	0,499199205	0,105801048	4,83991E-05	0,00307949
TSEN34	1929,60144	3116,5409	1,615121566	4,86586E-05	0,00308766
LGALS8-AS1	126,8778949	71,37705114	0,562564907	4,89277E-05	0,003096388
KIR2DL4	81,48932388	71,99867083	0,883535013	4,90609E-05	0,003096492
CLU	6137,4464	4249,433412	0,692378089	4,92122E-05	0,003097734
HLA-DRB1	6023,405053	8659,102332	1,437575965	5,01502E-05	0,00314836
TMEM132A	55,21426095	102,872996	1,863159883	5,22471E-05	0,003271281
RBP5	363,7509004	221,2181624	0,608158391	5,33233E-05	0,003329808
SLFN12L	316,6206356	201,2613099	0,635654431	5,40455E-05	0,003365974
PSORS1C3	17,89191703	10,48188019	0,585844444	5,49827E-05	0,00341531
MIR4709	529,8906055	864,2714745	1,631037549	5,76456E-05	0,003571294
MIR3194	2,365356771	7,353919837	3,109010837	5,95021E-05	0,00367597
LOC339975	8,710785398	22,13887269	2,541547252	5,96475E-05	0,00367597
DSG2	30,16897821	12,98029202	0,430252955	6,0172E-05	0,003698616
MIR581	0,039930135	2,432329352	60,9146289	6,1987E-05	0,003800256
ALKBH7	170,219359	288,6753764	1,695902148	6,31541E-05	0,003861753
ARL14EPL	396,7152277	648,9218437	1,63573717	6,379E-05	0,00389053
USP32P2	108,6113918	198,3491951	1,826228279	6,41171E-05	0,003900376
NOG	56,79399698	100,5100497	1,769730166	6,47045E-05	0,003925964
ATP5D	362,3563925	623,6893777	1,721204291	6,52002E-05	0,003945871
RPS2	20100,62372	31863,02724	1,585176046	6,69341E-05	0,00404042
COX8A	855,6530332	1337,315079	1,562917477	6,71866E-05	0,004045284
CTDSPL	698,4255045	493,4519328	0,706520494	6,95503E-05	0,004176923
NLRP14	3,639087491	0,300725428	0,082637592	7,12038E-05	0,004254519
MIR3184	22,38567174	9,164064637	0,409371885	7,11486E-05	0,004254519
H1FX	779,2952393	1246,982853	1,600141757	7,19904E-05	0,004290625
KCNJ10	11,70105101	24,14382087	2,063389079	7,25331E-05	0,004312055

RPLP1	12606,95165	20651,26218	1,6380853	7,3659E-05	0,004367959
PIGR	11,90421255	4,359154023	0,366185836	8,02802E-05	0,004748635
MORN3	187,8129481	116,8403078	0,622109972	8,07745E-05	0,004765899
OR51B5	10,73887544	4,024269239	0,374738422	8,32495E-05	0,00489516
MIR423	23,1923556	9,8199985	0,423415313	8,33812E-05	0,00489516
MSLN	59,31239441	21,91171342	0,369428913	8,39709E-05	0,00491752
HYDIN	33,76243896	16,8883822	0,50021215	8,42976E-05	0,004924405
CLEC4G	28,01805462	47,89441128	1,709412446	8,5629E-05	0,004989798
LDB3	35,48890911	16,38410248	0,461668248	8,84792E-05	0,005105335
ROS1	6,858288742	1,641556003	0,239353586	8,84484E-05	0,005105335
H2AFB1	4,982612941	0,712240731	0,142945226	8,81346E-05	0,005105335
H2AFB3	4,982612941	0,712240731	0,142945226	8,81346E-05	0,005105335
HOXA10-					
HOXA9	130,2478034	72,88634611	0,559597507	9,02649E-05	0,005195641
NDUFB11	705,1487834	1079,994798	1,531584289	9,14131E-05	0,005248896
DEFA4	501,7875142	706,9219977	1,408807469	9,25719E-05	0,005302498
DRP2	11,28122415	5,111562374	0,45310352	9,28547E-05	0,005305789
C6orf25	2087,16692	1474,022486	0,706231242	9,45885E-05	0,005378753
LOC285740	9,747668278	3,128094131	0,320906913	9,44082E-05	0,005378753
MIR1262	46,84815273	74,54084425	1,591115976	9,57322E-05	0,00543067
H2AFX	121,3121083	209,7366083	1,728900859	9,59634E-05	0,005430697
LGALS9B	64,41741227	41,19348088	0,639477424	9,70067E-05	0,005476576
HOXA10	82,12765847	42,84462935	0,521683318	9,86332E-05	0,005555076
SNORD53	57,63314518	29,87055941	0,518287859	0,00010259	0,005764133
CRIP2	133,2164059	255,2138509	1,915783939	0,000103297	0,005790023
MIR4482-1	7,897547346	2,170701447	0,274857668	0,000104569	0,005847406
ADAM23	178,7084215	112,6084717	0,630124035	0,000107682	0,00600723
MIR3691	9,727990015	20,02246009	2,058231974	0,000111024	0,006179008
KIR2DS4	311,1756586	281,8986212	0,905914757	0,000111368	0,006183564
CHST13	110,5720968	180,1998723	1,629704758	0,000112437	0,006228223
MYOF	1298,152109	1778,341618	1,369902345	0,000113904	0,006294689
SAMD11	81,74547577	145,8831798	1,784602492	0,000115019	0,006341414
MIR2110	38,94929876	18,41724133	0,472851679	0,00011806	0,006493843
MYH1	6,752431132	1,724614039	0,255406387	0,000120425	0,006608505
MYO16	270,1370039	388,8127388	1,43931684	0,000121447	0,00664909
TREML1	1054,621664	764,1543027	0,724576717	0,000129086	0,007050893
G0S2	47,23086777	80,40041655	1,702285398	0,000134897	0,007351276
PCSK6	518,7131292	364,8974805	0,70346683	0,000135263	0,007352457
MT2A	485,5097415	757,3863036	1,559981683	0,000135856	0,007352457
PKHD1	15,46906857	5,688420785	0,36772872	0,000135817	0,007352457
IRF6	81,66204148	45,66255885	0,559165042	0,000137625	0,007431129
CD300LD	13,76367953	30,7857814	2,236740643	0,000141373	0,007616002
C1orf122	142,3753472	234,7774496	1,649003526	0,000143303	0,007687643
SLPI	500,9754581	688,5187034	1,374356153	0,000143356	0,007687643
TRPC6	77,44271993	47,36358283	0,611595033	0,000149281	0,007987204
RGS9	638,8589786	420,6092578	0,658375748	0,000154371	0,008240795
LRRC16B	123,3508776	91,72264938	0,74359138	0,000159819	0,008493127

GPC4	21,33046411	34,31758199	1,608853038	0,000159623	0,008493127
C2orf48	65,25942714	37,56188301	0,575577884	0,000165412	0,008770546
ZDHHC12	524,7106345	821,7875832	1,566172914	0,000170123	0,009000092
AR	31,24927405	16,34811086	0,5231517	0,0001723	0,009094832
CD8B	1108,236822	1686,668512	1,521938704	0,00017296	0,009109225
BOK	138,8540158	102,463823	0,737924808	0,000173725	0,009129106
SLC22A18	799,572639	1151,711802	1,440409221	0,000174167	0,009131934
OTOGL	7,974036158	2,023245546	0,253729166	0,000174901	0,009134161
YES1	411,643615	287,9738131	0,699570703	0,000174985	0,009134161
HOXA-AS4	68,29075172	35,97273514	0,526758518	0,000177861	0,009263711
LOC283177	90,01785344	59,15792888	0,657179955	0,000178671	0,009285368
ZNF573	95,14486428	58,51965514	0,615058475	0,000183412	0,009510786
MOCS1	48,5713733	87,08905048	1,793011903	0,000185664	0,009606371
SCN5A	34,07041665	15,82919376	0,464602295	0,000188073	0,009709706
LRG1	3292,551894	4957,875131	1,505784963	0,000191267	0,009852984
MIR330	54,59050807	30,26198407	0,554345163	0,000192744	0,009907367
NINJ1	5102,837953	7631,112748	1,495464449	0,000196669	0,010087089
TIGD5	42,37117031	81,89621837	1,932828803	0,000197225	0,010093638
PAFAH1B3	132,1185475	210,2016734	1,591008056	0,000198166	0,010119771
MPL	90,73256499	59,39793053	0,654648422	0,000200116	0,010197262
PCDHA1	17,78458021	8,739506962	0,491409235	0,000202856	0,010314525
GNLY	20492,87779	16872,32865	0,823326466	0,000204644	0,010383013
FHAD1	117,0802206	81,55594011	0,696581709	0,000209413	0,010602159
DAB2	920,6612959	665,5280921	0,722880494	0,000210416	0,010630064
FMOD	9,44257046	2,477050967	0,262328036	0,00021106	0,010639795
LGALS3BP	745,749246	1022,273811	1,370800999	0,000212394	0,010661382
LAIR2	118,8900708	79,30619543	0,667054826	0,000212279	0,010661382
GSTM2	882,4337127	665,6919845	0,754381859	0,000217097	0,010874236
NUP210L	68,35010786	38,64818908	0,565444449	0,000226237	0,011308022
ARVCF	243,6753341	184,9116932	0,758844525	0,000227201	0,011332125
LRP3	117,7241828	189,4769512	1,609498972	0,000229216	0,011408441
MALAT1	23232,86914	15752,8302	0,678040672	0,000230726	0,011435247
ECT2L	84,57448372	51,67095511	0,610952061	0,000230318	0,011435247
SYTL4	89,91349559	60,07442125	0,668135755	0,000232543	0,011501092
ANKRD61	329,7126232	216,423872	0,656401535	0,000237441	0,011718716
CAV3	5,675006889	1,059470984	0,186690696	0,000239527	0,011796971
IRS4	2,329808024	0,140184243	0,060169869	0,000243624	0,011973677
HFM1	34502,28569	26962,63473	0,78147387	0,000244967	0,012014626
MYL2	4,722726433	0,749939944	0,158793857	0,000250675	0,012268993
TNFSF11	24,8101765	14,87128216	0,599402514	0,000252238	0,01229438
HBQ1	115,4031446	232,356228	2,013430646	0,000252099	0,01229438
GPR75	94,79961832	58,31509836	0,615140645	0,000255545	0,01242984
FAM182B	11,93265305	4,397457987	0,368523074	0,000256129	0,012432542
PVALB	61,54855286	35,24638424	0,572659837	0,000262233	0,01268576
C6orf1	434,9172954	663,2500998	1,525002815	0,000262423	0,01268576
MROH2B	6,412834481	1,605961698	0,250429307	0,000267234	0,01289185

ALAS2	9620,310486	15749,00762	1,637058143	0,000269361	0,012967889
LAMA2	84,38303647	56,36245844	0,667935888	0,00027	0,01297211
NFXL1	549,2931376	940,0693523	1,711416524	0,000271737	0,013028991
RTL1	3,11057816	0,255845804	0,082250241	0,000274718	0,013145127
RAVER2	191,8728444	288,590097	1,50406952	0,000277099	0,013232189
OPLAH	132,1930757	208,2544338	1,575380803	0,000278338	0,013264455
PCDHA3	15,05314919	7,207913223	0,478830916	0,000279014	0,013269792
LCN8	30,3627947	18,0930434	0,595895193	0,00028309	0,013436493
ABLM3	718,614425	528,1833075	0,735002373	0,000286831	0,01358666
SALL4	8,011255481	2,12892392	0,265741609	0,000289931	0,013705944
PCDHA2	16,34617314	7,903584952	0,483512862	0,000297651	0,014042699
PRRT4	27,77095031	47,73202588	1,718775387	0,000300244	0,014136696
PPMIL	347,3226916	230,2684486	0,662981297	0,000305842	0,014371521
IRG1	3,252183463	7,706237585	2,369558074	0,000314131	0,014731638
HELB	1018,436315	674,6319599	0,662419387	0,000321291	0,015030019
ELOVL7	327,6785387	241,2504818	0,736241326	0,000321771	0,015030019
LOC285972	168,693562	114,7029406	0,679948536	0,000324791	0,015141041
VIL1	93,62082654	61,31446985	0,654923398	0,00032565	0,015151096
FOLR3	977,6019405	1460,111072	1,493564007	0,000330682	0,015354876
TAF1L	13,69681391	5,29218442	0,386380691	0,000332234	0,015387341
CT45A1	1,87864128	0	0	0,000332689	0,015387341
ST8SIA6-AS1	14,35223006	6,406552362	0,446380272	0,000337398	0,015544076
SNORD58A	6423,120718	4153,434143	0,646638032	0,000336837	0,015544076
RPRM	5,034830947	1,160918818	0,230577517	0,000341014	0,015654568
RP1	5,121421618	0,988978337	0,193106214	0,000341126	0,015654568
SERPING1	809,7798098	1102,705327	1,361734775	0,000342775	0,015699651
PPBP	7369,613262	5729,607013	0,77746373	0,000344019	0,015725995
NPFFR1	1,080432428	4,686965463	4,338045899	0,000346961	0,015829781
C9orf16	553,5398125	892,9511403	1,61316516	0,00035103	0,015984435
ISG15	599,4452925	934,5826909	1,559079207	0,000353572	0,016069078
MIR4779	12,91209433	20,80760388	1,611481712	0,000359432	0,016287556
EPHB4	614,4887803	855,6852067	1,39251559	0,000359763	0,016287556
OTUD7B	367,241755	243,3455628	0,662630432	0,000360489	0,016289111
GSDMA	39,3495986	19,04599488	0,484020055	0,000362235	0,016336651
GRB14	81,09238833	130,1607259	1,605091779	0,000373509	0,016812883
RPLP2	10937,37219	16879,30515	1,54326879	0,000376364	0,016875887
ZBTB20	570,3315091	391,6530401	0,686711209	0,000377059	0,016875887
PRR7-AS1	2688,715811	4081,114695	1,51786763	0,000376053	0,016875887
ELOVL3	18,00776256	31,00972824	1,722020053	0,00037808	0,016881856
CRYAB	4,080024335	0,61283101	0,150202783	0,000379339	0,016881856
NETO2	168,0732117	243,013099	1,445876452	0,000379343	0,016881856
TREX1	636,3677674	963,4582121	1,513995933	0,0003841	0,017061273
RHOG	8038,714003	12071,48343	1,50166848	0,000385099	0,017073466
OR2W5	1,709364375	0	0	0,000387283	0,01713798
TEKT4P2	1062,4752	763,817305	0,718903655	0,000399862	0,017661463
KNDC1	105,9154566	83,63979197	0,789684478	0,000404836	0,017847665

ANP32A-IT1	99,27009686	62,16447067	0,626215473	0,000407722	0,017941295
MT1E	38,9604184	63,14212173	1,620673604	0,000411149	0,018058331
FAM153A	57,963303	37,90894573	0,654016313	0,000414559	0,018174209
MYLK	857,0409808	613,6504724	0,716010653	0,000421496	0,018443955
SPATA2L	125,7965811	213,1840996	1,69467324	0,000424532	0,018542374
IFITM2	50767,23392	73963,13917	1,456907014	0,000428993	0,018702488
AATK	1878,543573	2716,935219	1,446298748	0,000429792	0,018702685
CORIN	105,0562101	203,3848259	1,935961955	0,000432482	0,018785051
FPR1	34905,16069	50489,78429	1,446484797	0,000433604	0,01879907
F3	3,927860806	9,353428114	2,381303355	0,000436169	0,018845166
PYCARD	1342,357543	2047,703282	1,525452956	0,000440569	0,018845166
MYO5B	111,7782787	81,01648603	0,724796329	0,000438717	0,018845166
SNORD34	3154,80437	4727,810494	1,49860655	0,000441071	0,018845166
VAMP5	767,0078058	1042,91842	1,359723345	0,000438298	0,018845166
DEFA1	2422,310802	3271,957033	1,350758553	0,0004404	0,018845166
DEFA1B	2422,310802	3271,957033	1,350758553	0,0004404	0,018845166
DEFA3	2422,310802	3271,957033	1,350758553	0,0004404	0,018845166
ATF3	107,0920525	150,5654931	1,405944602	0,000442734	0,018881949
VSIG2	886,1374462	668,296807	0,75416834	0,000445175	0,018951733
DTNA	27,54303469	41,33943482	1,500903415	0,000456015	0,019378171
LOC100505658	84,8600443	143,8577328	1,695235183	0,000459517	0,019491801
C19orf24	278,0636442	427,7967327	1,538484953	0,000461937	0,019559219
OR7G3	1,641298574	0	0	0,000463833	0,019604224
MAP1A	448,6413902	315,2498502	0,702676697	0,000465365	0,019633728
F8A2	88,46765577	144,6772494	1,635368861	0,000472127	0,019847882
F8A3	88,46765577	144,6772494	1,635368861	0,000472127	0,019847882
LOC349160	8,463367056	2,097223258	0,247800106	0,000480628	0,020169239
TCL1A	654,159162	936,423278	1,431491497	0,000484977	0,020243482
CIRBP-AS1	1218,806074	811,2826459	0,665637186	0,000483551	0,020243482
PCDHA4	14,33323278	6,917562665	0,482624037	0,000484532	0,020243482
TSSC4	437,5359197	690,9642609	1,579217225	0,000489084	0,020376553
LTBP1	493,2489605	354,1482849	0,71799094	0,000489896	0,020376553
RPPH1	17,15190441	8,939759456	0,521210896	0,000492502	0,020448816
USP32P1	468,7312211	342,3605143	0,730398358	0,000498003	0,020640809
DOC2A	109,3127385	190,5097379	1,742795402	0,000502174	0,020777132
HIST1H2BJ	119,6719292	79,20420023	0,661844434	0,000510303	0,021076425
PTPRCAP	1719,751715	2887,012216	1,678737803	0,000517784	0,02134793
SPINK5	4,936709938	1,114436173	0,225744714	0,000532866	0,021931329
PCDHA5	13,49937908	6,442077038	0,477212841	0,000534889	0,021976197
PTPRB	55,53288053	36,14275054	0,650835148	0,000539053	0,022108686
IL12RB2	204,3802676	157,2603771	0,769449903	0,000543162	0,022238472
APRT	1161,746662	1762,146992	1,516808311	0,000554097	0,022646796
SLC6A4	69,97647185	45,46330599	0,649694173	0,000563345	0,022984855
PRSS23	1157,036454	851,9409558	0,736312977	0,000566774	0,023084774
RPS28	4418,979621	6157,361876	1,393389969	0,000572218	0,023266239
MIR5194	5,584957924	2,949870985	0,528181416	0,000574845	0,023332747

FLJ13224	28,34203314	13,24048748	0,467167878	0,000577473	0,023399072
H3F3C	3,063192723	7,337996888	2,395538757	0,000590269	0,02383552
ANKRD36	252,971646	170,222937	0,672893345	0,000589538	0,02383552
FAM89B	1433,192339	2125,895904	1,4833291	0,000598263	0,024034669
SMCR7	121,8086277	200,6468755	1,647230408	0,000598068	0,024034669
ABCC3	1476,086941	1073,695669	0,727393244	0,000597603	0,024034669
SLITRK3	2,678624755	0,199032799	0,074304099	0,000605584	0,024287333
PDE6C	113,7939726	76,80427857	0,674941535	0,000608252	0,024352819
TUBB1	10684,35068	7949,46296	0,744028645	0,000617104	0,024665318
ACP5	622,0233268	876,0233511	1,408344853	0,000629457	0,025116408
OCLN	12,2547205	30,40309112	2,48092897	0,000635112	0,025299152
JUND	961,8777919	1524,801619	1,585234249	0,000640661	0,02543415
MIR4762	40,29331715	68,78504213	1,707107952	0,000640227	0,02543415
ANKRD30B					
L	460,0233161	388,4923107	0,844505696	0,000648969	0,025720605
EFCAB4A	68,89729857	98,37620832	1,427867425	0,000652971	0,025756478
ARRDC5	163,156318	105,5449296	0,64689453	0,000653157	0,025756478
PCDHA8	10,8740281	4,821473545	0,443393515	0,000651887	0,025756478
SELP	527,7228351	387,807522	0,734869701	0,000667172	0,026224241
FREM3	43,00357112	26,5443905	0,617260144	0,000667247	0,026224241
SORBS2	30,68512987	19,81469934	0,645742724	0,00066901	0,026249727
ISL2	162,8778868	233,5151046	1,433682062	0,000679292	0,026607668
SCARNA9L	122,7839501	75,13046175	0,611891552	0,000680393	0,026607668
LOC441081	1349,423927	1846,988332	1,368723568	0,000682865	0,026660065
STEAP3	147,9732436	212,0502567	1,433031077	0,000684409	0,026676069
HIST1H2AD	22,75795451	38,20033201	1,67854857	0,000689395	0,02682603
RARRES1	34,59884156	19,69339539	0,569192334	0,000690962	0,026842611
GLIS2	64,05554522	103,7833889	1,620209281	0,000693654	0,026902787
KIAA1377	241,2103872	172,174453	0,713793693	0,00069631	0,026961381
SMIM1	91,259664	79,38693695	0,869901701	0,000701295	0,027109815
LOC284889	277,567665	460,9555749	1,66069623	0,000703035	0,027132556
FER1L5	11,48405966	5,252674433	0,457388292	0,000705059	0,027166112
SDSL	35,34727836	56,33270708	1,593692915	0,000713774	0,027436066
S100Z	770,5056038	553,5737654	0,71845521	0,000714396	0,027436066
SNORA24	294,160984	179,9829362	0,611851829	0,000717146	0,027496819
B4GALT6	171,5957594	114,3005821	0,666103769	0,000740783	0,028356946
DOC2GP	55,46380501	35,17955426	0,634279496	0,00074861	0,028563661
SNHG5	2785,636026	1894,902043	0,680240356	0,00074787	0,028563661
SDPR	5991,193196	4568,23691	0,762492005	0,000752312	0,028658466
MYLK2	3,839894266	0,66246225	0,172520961	0,000770764	0,029313933
TRPM4	56,33038487	83,43872249	1,481238282	0,000784479	0,029787413
C16orf13	285,5209959	438,1966112	1,534726404	0,000787835	0,029866674
SNORD84	384,2967369	251,999244	0,655741305	0,000813597	0,030793728
FGFR2	71,07241882	41,61286895	0,585499546	0,000820013	0,030937108
SNORD15B	2254,805644	3237,373247	1,435765985	0,000819203	0,030937108
MIR1181	274,5453038	176,4647289	0,642752677	0,000829719	0,031253193
LOC1005056	108,7185598	68,87465057	0,633513272	0,000841101	0,03163132

PDZRN3	15,06377301	7,725006533	0,512820163	0,000845358	0,031740685
ABCG5	4,289713072	0,822852978	0,19182005	0,000858924	0,032198696
RAB27B	769,2926328	563,9778898	0,733112298	0,000861965	0,03221884
CLC	4798,615618	3252,778057	0,677857598	0,000864935	0,03221884
APOB	9,720259497	4,247376778	0,436961254	0,000864231	0,03221884
HOXA-AS3	22,33849797	10,97577863	0,491339151	0,00086287	0,03221884
PTPRZ1	6,947073177	1,974274966	0,284188019	0,000870124	0,032360906
CEACAM6	377,1910477	501,3721733	1,329226068	0,000873014	0,032417186
SNORA52	3492,788369	5143,309193	1,472551053	0,000877448	0,032530537
PDGFA	48,03759263	31,78039032	0,661573334	0,000880552	0,032594278
FAM66D	21,71570715	12,8360085	0,591093277	0,000894528	0,033059627
LOC389634	463,1601152	631,7581528	1,364016745	0,000897001	0,033099038
TRPV3	67,21750097	45,1200185	0,671254031	0,000903006	0,033218786
LOC284395	9,777221693	3,14400898	0,321564661	0,000903068	0,033218786
EEF1DP3	75,99894153	50,02641571	0,65825148	0,000904988	0,03323749
TUBBP5	29,3586012	48,06473675	1,637160313	0,000911338	0,033418571
CAMP	654,3905148	880,0689187	1,344868085	0,000913105	0,033431272
IRF7	1214,163864	1807,259213	1,488480482	0,000921075	0,033670708
NLRP7	87,80135119	64,06981924	0,729713363	0,000924366	0,033738642
MIAT	5361,554795	3942,12317	0,735257462	0,00093115	0,033926864
CLIC3	282,7627608	236,2372036	0,835460804	0,000932405	0,033926864
SIGLEC8	350,2610217	227,7577607	0,650251517	0,000934435	0,033946576
COL3A1	6,265491867	1,782358875	0,284472299	0,000935831	0,033946576
OR10A4	1,465843309	0	0	0,000942884	0,034149799
ALOX5AP	7971,654678	11237,58353	1,409692715	0,000957189	0,034561571
VNN2	22114,33809	32301,20453	1,460645324	0,000956128	0,034561571
GPR84	92,80681561	126,6828934	1,365017133	0,000959145	0,034579177
EGR2	38,13043851	50,63895144	1,328045347	0,000962592	0,034650361
RGS6	214,8902816	152,2763433	0,708623685	0,000965089	0,034687211
CLEC4E	4737,124884	7051,210526	1,488500029	0,000970663	0,034834374
SCRT2	29,25411719	16,97729384	0,580338614	0,000976524	0,034991378
TNNI1	1,998916221	0,122277572	0,061171934	0,000982324	0,035092378
FAM221B	15,85343337	8,129606265	0,512797832	0,000982131	0,035092378
CDC20	43,63549745	57,21048828	1,311099715	0,000987581	0,035226717
MIR4772	92,46840801	153,0858187	1,655547251	0,000994373	0,03541532
CCL3	168,2469838	127,0823161	0,755331913	0,001004476	0,035721094
KIFC3	423,4699368	312,9998703	0,739131265	0,001013239	0,035959561
SNAP91	6,730389291	1,905515682	0,283121169	0,001014236	0,035959561
CXCL5	572,6741255	495,9883562	0,866091786	0,001016739	0,035994085
OXER1	476,1006125	665,9116485	1,398678412	0,001025557	0,036251737
BTBD8	27,62498454	13,92934832	0,504230086	0,001027272	0,036257924
FAM173A	32,35468186	64,72905829	2,000608708	0,001037298	0,036556995
BTNL3	332,3798518	552,3584851	1,661829025	0,00104098	0,036631913
USP6	37,61207348	26,20298368	0,696664163	0,001047892	0,036820105
COL6A5	9,966150237	3,872309911	0,388546211	0,001050214	0,036846712

WHAMMP3	550,3581528	394,3182804	0,716475768	0,001056786	0,03702211
TPST1	467,3493508	684,0282776	1,463633739	0,001059866	0,037074847
ABCG1	1236,591918	1696,911399	1,372248496	0,001063986	0,037163735
HBB	4426880,026	7198358,573	1,626056846	0,001070081	0,037321271
CCNB2	38,23127078	53,44144592	1,397846444	0,001072259	0,037341886
SH3BGRL2	1260,955636	988,1942591	0,783686778	0,001100488	0,038211946
TEX15	7,722326175	2,507713661	0,324735527	0,00109974	0,038211946
LAMA3	12,98373861	5,835583303	0,449453234	0,001102633	0,038230014
RBP7	614,4599045	891,6532198	1,451117011	0,001105188	0,038262249
KIAA1755	4,648274267	1,181574532	0,254196389	0,001109107	0,038341537
EFNA1	23,52995641	40,23852642	1,710097789	0,00112016	0,038666857
MIR3654	3729,174214	5319,153709	1,426362353	0,001129349	0,038926978
COL18A1	2654,453256	3772,530307	1,421208039	0,001134913	0,039046464
LAP3	2647,133976	3251,756822	1,22840659	0,001137517	0,039046464
FLJ43663	866,5424423	625,7388034	0,722109816	0,001137791	0,039046464
KLHDC8B	449,3272381	623,1842241	1,386927324	0,001140556	0,039084387
GAA	3678,41897	5034,985337	1,368790608	0,001144195	0,039141193
CD74	61662,6535	83599,94633	1,355763036	0,001145539	0,039141193
SREBF1	1399,761809	1974,022284	1,410255853	0,001164746	0,039739777
ZNF793	221,1248425	151,2078155	0,683811976	0,001168584	0,039813024
MFAP3L	677,5630762	507,2895095	0,748697099	0,001176942	0,040039849
MCOLN3	42,76883312	25,22013664	0,589684936	0,001191443	0,040358208
ABCA4	12,40992163	6,428632164	0,518023591	0,001189759	0,040358208
GHSR	16,84254086	6,285841609	0,373212193	0,001190321	0,040358208
SAC3D1	63,81826124	104,1660814	1,632230014	0,001193647	0,04037478
SNORD75	441,1401997	292,6227164	0,663332692	0,001203088	0,04063572
CLCA1	3,428038295	0,54198656	0,158103998	0,001214096	0,040764922
YDJC	164,3928914	270,8040325	1,647297704	0,001210777	0,040764922
LHFPL2	748,5753372	1031,29577	1,377677995	0,001214388	0,040764922
CHRNA2	28,95562512	18,70320292	0,645926408	0,001212541	0,040764922
SNORA70	4573,489525	6570,219009	1,436587746	0,001215571	0,040764922
NLRP6	677,7069109	991,1873518	1,46256049	0,001224862	0,041018069
OVCH1	175,3704779	234,8522215	1,339177633	0,001226932	0,041029016
PUSL1	107,5490822	178,6087384	1,660718388	0,001392577	0,041125797
ZNF593	51,95750436	87,88635101	1,691504472	0,001266199	0,041125797
PPFIA4	339,3874895	243,5760088	0,717692951	0,001404616	0,041125797
STOX1	17,960924	11,7406155	0,653675473	0,001275318	0,041125797
TSPAN4	231,7387854	338,9047683	1,462443016	0,001254204	0,041125797
SNORD26	100,2538583	63,34280176	0,63182408	0,001314596	0,041125797
TENM4	38,39408773	53,93841952	1,404862642	0,001318849	0,041125797
SCN2B	13,42935182	5,621402799	0,418590776	0,001332601	0,041125797
AVPR1A	74,01007944	50,3750194	0,680650795	0,001233637	0,041125797
TVP23C	487,8816111	347,1102531	0,711464103	0,001293761	0,041125797
SLFN13	1486,158956	1118,713002	0,752754608	0,001360968	0,041125797
SYNGR2	2801,586784	3920,189266	1,399274614	0,001270712	0,041125797
SIGLEC12	28,04595302	44,7445481	1,595401235	0,001364545	0,041125797

COX5B	806,2016326	1184,429284	1,469147712	0,00129475	0,041125797
CDK15	22,39994588	10,81442176	0,482787852	0,001347226	0,041125797
DIP2A-IT1	22,00493525	11,35303398	0,51593126	0,001317766	0,041125797
RAB36	289,7534749	415,190877	1,432910777	0,001256087	0,041125797
NCF4	8490,684599	11981,73838	1,411162815	0,001302231	0,041125797
GUCY1A3	369,2978353	274,5565157	0,743455524	0,00139643	0,041125797
LOC100507173	27,43958299	16,57496845	0,60405322	0,001266848	0,041125797
HLA-B	131928,6208	182729,7314	1,385065123	0,001365096	0,041125797
MYCT1	94,41000874	62,42610644	0,661223394	0,001309329	0,041125797
RADIL	9,836025887	4,360918949	0,443361882	0,001398797	0,041125797
PTGS1	6332,739044	4774,617712	0,753957755	0,001392457	0,041125797
CT47A1	1,500199532	0	0	0,001406264	0,041125797
CT47A10	1,500199532	0	0	0,001406264	0,041125797
CT47A11	1,500199532	0	0	0,001406264	0,041125797
CT47A12	1,500199532	0	0	0,001406264	0,041125797
CT47A2	1,500199532	0	0	0,001406264	0,041125797
CT47A3	1,500199532	0	0	0,001406264	0,041125797
CT47A4	1,500199532	0	0	0,001406264	0,041125797
CT47A5	1,500199532	0	0	0,001406264	0,041125797
CT47A6	1,500199532	0	0	0,001406264	0,041125797
CT47A8	1,500199532	0	0	0,001406264	0,041125797
CT47A9	1,500199532	0	0	0,001406264	0,041125797
CT47A1	1,500199532	0	0	0,001406264	0,041125797
CT47A10	1,500199532	0	0	0,001406264	0,041125797
CT47A11	1,500199532	0	0	0,001406264	0,041125797
CT47A12	1,500199532	0	0	0,001406264	0,041125797
CT47A2	1,500199532	0	0	0,001406264	0,041125797
CT47A3	1,500199532	0	0	0,001406264	0,041125797
CT47A4	1,500199532	0	0	0,001406264	0,041125797
CT47A5	1,500199532	0	0	0,001406264	0,041125797
CT47A6	1,500199532	0	0	0,001406264	0,041125797
CT47A8	1,500199532	0	0	0,001406264	0,041125797
CT47A9	1,500199532	0	0	0,001406264	0,041125797
CT47A1	1,500199532	0	0	0,001406264	0,041125797
CT47A10	1,500199532	0	0	0,001406264	0,041125797
CT47A11	1,500199532	0	0	0,001406264	0,041125797
CT47A12	1,500199532	0	0	0,001406264	0,041125797
CT47A2	1,500199532	0	0	0,001406264	0,041125797
CT47A3	1,500199532	0	0	0,001406264	0,041125797
CT47A4	1,500199532	0	0	0,001406264	0,041125797
CT47A5	1,500199532	0	0	0,001406264	0,041125797
CT47A6	1,500199532	0	0	0,001406264	0,041125797
CT47A8	1,500199532	0	0	0,001406264	0,041125797
CT47A9	1,500199532	0	0	0,001406264	0,041125797
CT47A7	1,500199532	0	0	0,001406264	0,041125797
CT47A10	1,500199532	0	0	0,001406264	0,041125797

CT47A11	1,500199532	0	0	0,001406264	0,041125797
CT47A12	1,500199532	0	0	0,001406264	0,041125797
CT47A2	1,500199532	0	0	0,001406264	0,041125797
CT47A3	1,500199532	0	0	0,001406264	0,041125797
CT47A4	1,500199532	0	0	0,001406264	0,041125797
CT47A5	1,500199532	0	0	0,001406264	0,041125797
CT47A6	1,500199532	0	0	0,001406264	0,041125797
CT47A8	1,500199532	0	0	0,001406264	0,041125797
CT47A9	1,500199532	0	0	0,001406264	0,041125797
CT47A1	1,500199532	0	0	0,001406264	0,041125797
CT47A10	1,500199532	0	0	0,001406264	0,041125797
CT47A11	1,500199532	0	0	0,001406264	0,041125797
CT47A12	1,500199532	0	0	0,001406264	0,041125797
CT47A2	1,500199532	0	0	0,001406264	0,041125797
CT47A3	1,500199532	0	0	0,001406264	0,041125797
CT47A4	1,500199532	0	0	0,001406264	0,041125797
CT47A5	1,500199532	0	0	0,001406264	0,041125797
CT47A6	1,500199532	0	0	0,001406264	0,041125797
CT47A8	1,500199532	0	0	0,001406264	0,041125797
CT47A9	1,500199532	0	0	0,001406264	0,041125797
CT47A1	1,500199532	0	0	0,001406264	0,041125797
CT47A10	1,500199532	0	0	0,001406264	0,041125797
CT47A11	1,500199532	0	0	0,001406264	0,041125797
CT47A12	1,500199532	0	0	0,001406264	0,041125797
CT47A2	1,500199532	0	0	0,001406264	0,041125797
CT47A3	1,500199532	0	0	0,001406264	0,041125797
CT47A4	1,500199532	0	0	0,001406264	0,041125797
CT47A5	1,500199532	0	0	0,001406264	0,041125797
CT47A6	1,500199532	0	0	0,001406264	0,041125797
CT47A8	1,500199532	0	0	0,001406264	0,041125797
CT47A9	1,500199532	0	0	0,001406264	0,041125797
CT47A1	1,500199532	0	0	0,001406264	0,041125797
CT47A10	1,500199532	0	0	0,001406264	0,041125797
CT47A11	1,500199532	0	0	0,001406264	0,041125797
CT47A12	1,500199532	0	0	0,001406264	0,041125797
CT47A2	1,500199532	0	0	0,001406264	0,041125797
CT47A3	1,500199532	0	0	0,001406264	0,041125797
CT47A4	1,500199532	0	0	0,001406264	0,041125797
CT47A5	1,500199532	0	0	0,001406264	0,041125797
CT47A6	1,500199532	0	0	0,001406264	0,041125797
CT47A8	1,500199532	0	0	0,001406264	0,041125797
CT47A9	1,500199532	0	0	0,001406264	0,041125797
CT47A1	1,500199532	0	0	0,001406264	0,041125797
CT47A10	1,500199532	0	0	0,001406264	0,041125797
CT47A11	1,500199532	0	0	0,001406264	0,041125797
CT47A12	1,500199532	0	0	0,001406264	0,041125797
CT47A2	1,500199532	0	0	0,001406264	0,041125797
CT47A3	1,500199532	0	0	0,001406264	0,041125797
CT47A4	1,500199532	0	0	0,001406264	0,041125797
CT47A5	1,500199532	0	0	0,001406264	0,041125797
CT47A6	1,500199532	0	0	0,001406264	0,041125797
CT47A8	1,500199532	0	0	0,001406264	0,041125797
CT47A9	1,500199532	0	0	0,001406264	0,041125797
RUNDC3A	877,1537583	772,3404525	0,880507488	0,00141517	0,041334901
FAT1	11,02039029	4,379692136	0,397417153	0,001425757	0,041592517
MYLK-AS1	474,3530204	354,9285447	0,748237134	0,001457291	0,042459829
SAP25	936,5290567	1463,173576	1,562336551	0,001461371	0,0424796

OC90	1,948131269	0,086814447	0,044562935	0,001461578	0,0424796
MPDZ	9,632403506	3,376732158	0,350559666	0,001468213	0,042619828
HIST2H2BF	1511,500918	2033,124896	1,345103315	0,001474769	0,042757417
DGCR6L	410,1217358	613,5663186	1,496059011	0,001485849	0,042990592
NXF3	8,507227451	14,97074526	1,759767838	0,001486464	0,042990592
MFSD10	862,3210146	1326,509072	1,53830076	0,001489992	0,043039739
INADL	780,9911581	552,6081424	0,707572854	0,001501208	0,043308919
USH2A	17,94285442	9,060718821	0,504976444	0,00150299	0,043308919
PCDHA6	12,17594131	6,029533375	0,495200594	0,001511911	0,043512739
PBX1	363,0839361	268,0650653	0,738300538	0,001533399	0,044077274
ADORA2A	924,417975	1258,880487	1,36180875	0,001539132	0,044154568
PDE4D	1255,308506	915,8329161	0,729568	0,001539839	0,044154568
CEACAM8	480,6326629	609,1544148	1,267401202	0,00158799	0,04542461
GP6	210,1990515	155,1574154	0,738145174	0,001587175	0,04542461
ARHGEF40	3782,790287	5545,517971	1,465986098	0,001597396	0,045638225
OR6C68	1,283906889	0	0	0,001604297	0,045779822
GPBAR1	484,9051116	698,3704468	1,440220839	0,00161322	0,04597872
TAF15	10489,22633	7253,023231	0,691473613	0,001623419	0,046213468
FAT3	13,28975808	5,378306295	0,404695576	0,001628924	0,046314175
MBNL1-AS1	295,1445155	196,4684609	0,665668683	0,001659761	0,047134006
EPHA2	55,32738872	35,62376091	0,643872081	0,001669073	0,047341347
ARHGEF12	1933,515137	1486,187039	0,768645153	0,00168025	0,047601008
PCDHA7	11,15081874	5,462694198	0,489891758	0,001692522	0,047891036
SAMD14	113,4789666	79,23497115	0,698234867	0,001698816	0,048011442
PLP2	3973,803849	5373,262488	1,352171041	0,001707629	0,048202627
FBXO2	69,39469466	100,9038128	1,454056586	0,001711139	0,048243873
LRRC25	7302,068643	10207,6184	1,397907758	0,00171682	0,048346152
GPR20	37,95321685	27,48107808	0,724077703	0,001726151	0,048550829
MIR3684	40,10962985	22,82165707	0,568981991	0,001732787	0,048679313
C1orf57	638,1798911	946,1549843	1,482583512	0,001736027	0,048712213
C1orf228	332,3868464	453,8635611	1,365467876	0,00173994	0,048744184
HGD	110,7245926	84,42632069	0,762489333	0,001741307	0,048744184
SCN4B	22,80840886	10,44661818	0,458016087	0,001747641	0,04886339
MIR33B	9,304748471	19,12200397	2,055080159	0,001757526	0,04908148
GIPR	167,8947044	112,245725	0,668548335	0,001768005	0,049315596
FCAMR	3,426406908	0,674131441	0,19674588	0,001776544	0,049474514
PAGE2B	29,08134458	53,45146264	1,837998326	0,001777905	0,049474514
LY6E	2543,430741	3403,842958	1,338288046	0,001785402	0,049624485
C1orf233	69,00444365	107,1408164	1,552665462	0,001790558	0,049709099
FRA10AC1	820,5925863	576,8029063	0,702910209	0,001802176	0,0499727

* P adjusted for multiple testing (Benjamini-Hochberg)

Supplementary Table 5. Differentially enriched pathways in *LRRK2* G2019S-associated PD patients compared to controls analyzed with two different pathway databases (KEGG and Reactome).

Database	Pathway	Observed Genes in the Pathway	Genes	P-value_hyper	P-value_fisher
REACTOME	O ₂ /CO ₂ exchange in erythrocytes	6		7,14873E-10	1,43954E-06
REACTOME	Uptake of Carbon Dioxide and Release of Oxygen by Erythrocytes	6		7,14873E-10	1,43954E-06
REACTOME	Uptake of Oxygen and Release of Carbon Dioxide by Erythrocytes	6		7,14873E-10	1,43954E-06
REACTOME	Striated Muscle Contraction	8		4,69058E-08	4,0936E-06
KEGG	Cardiac muscle contraction	11		2,43274E-07	6,65992E-06
KEGG	Dilated cardiomyopathy	12		3,56534E-07	7,86789E-06
KEGG	Hypertrophic cardiomyopathy (HCM)	11		1,01335E-06	1,98969E-05
KEGG	Antigen processing and presentation	10		1,07835E-06	2,38452E-05
REACTOME	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	10		1,44495E-06	2,97679E-05
REACTOME	Platelet activation, signaling and aggregation	17		4,45797E-06	4,64529E-05
REACTOME	Muscle contraction	8		4,46599E-06	9,61369E-05
REACTOME	Platelet degranulation	10		4,79482E-06	7,45679E-05
KEGG	Viral myocarditis	9		7,14024E-06	0,000115256
REACTOME	Response to elevated platelet cytosolic Ca ²⁺	10		8,69262E-06	0,000118181
KEGG	ECM-receptor interaction	10		1,08927E-05	0,000140847
REACTOME	Platelet Adhesion to exposed collagen	4		1,1162E-05	0,000686595
REACTOME	Termination of O-glycan biosynthesis	5		1,34608E-05	0,000469511
KEGG	Focal adhesion	15		5,19385E-05	0,000381317

KEGG	Amoebiasis	10	8,2564E-05	0,000692919
KEGG	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	8	9,59411E-05	0,000946613
REACTOME	NCAM1 interactions	6	0,0001065	0,001409146
REACTOME	Hemostasis	25	0,000107058	0,001035444
KEGG	Cell adhesion molecules (CAMs)	11	0,000116686	0,00085626
KEGG	Tight junction	11	0,000116686	0,00085626
REACTOME	Formation of Fibrin Clot (Clotting Cascade)	5	0,000131323	0,002071407
KEGG	African trypanosomiasis	5	0,000186575	0,002628076
REACTOME	Integrin cell surface interactions	8	0,000278464	0,002142038
KEGG	Graft-versus-host disease	5	0,000302102	0,003655733
REACTOME	Platelet Aggregation (Plug Formation)	5	0,000302102	0,003655733
KEGG	Salmonella infection	8	0,000392701	0,002792993
REACTOME	Cell surface interactions at the vascular wall	8	0,000587005	0,003813122
REACTOME	O-linked glycosylation of mucins	6	0,000612814	0,004985154
REACTOME	Gap junction trafficking and regulation	4	0,000860536	0,009616582
KEGG	Malaria	5	0,001400794	0,010690709
KEGG	Hematopoietic cell lineage	7	0,001782106	0,009822616
REACTOME	NCAM signaling for neurite outgrowth	6	0,001876453	0,011374912
KEGG	Complement and coagulation cascades	6	0,002036564	0,012087445
REACTOME	Eukaryotic Translation Initiation	8	0,002567508	0,012049053
REACTOME	Cap-dependent Translation Initiation	8	0,002567508	0,012049053
REACTOME	Formation of a pool of free 40S subunits	7	0,003253251	0,015569148
REACTOME	Translation	9	0,004048367	0,016377543
REACTOME	Neuronal System	14	0,00520685	0,022458758
KEGG	Intestinal immune network for IgA production	4	0,005382024	0,032966004
REACTOME	L13a-mediated translational silencing of Ceruloplasmin expression	7	0,005837891	0,024387696
REACTOME	GTP hydrolysis and joining of the 60S ribosomal subunit	7	0,006163338	0,025425683
KEGG	Natural killer cell mediated cytotoxicity	8	0,006277822	0,024283634
REACTOME	Peptide chain elongation	6	0,006312539	0,028094632
REACTOME	Eukaryotic Translation	6	0,006312539	0,028094632
REACTOME	Termination	6	0,006312539	0,028094632
REACTOME	Viral mRNA Translation	6	0,006312539	0,028094632
REACTOME	SRP-dependent cotranslational protein targeting to membrane	7	0,00650232	0,026493558
REACTOME	Interferon gamma signaling	5	0,006792201	0,033117367
REACTOME	Eukaryotic Translation	6	0,007562891	0,032162899
KEGG	Elongation	6	0,007562891	0,032162899
REACTOME	Ribosome, eukaryotes	6	0,007562891	0,032162899
KEGG	Metabolism of proteins	19	0,00795002	0,047312474
REACTOME	Ribosome	6	0,008017578	0,033599835
KEGG	Nonsense Mediated Decay	6	0,008492021	0,035077784
REACTOME	Independent of the Exon Junction	6	0,008492021	0,035077784

	Complex			
	Neurotransmitter Receptor			
	Binding And Downstream			
	Transmission In The			
REACTOME	Postsynaptic Cell	8	0,009040736	0,03232745
KEGG	Glutathione metabolism	4	0,009131527	0,047359698
REACTOME	Extracellular matrix organization	6	0,009502093	0,038157993
KEGG	Adherens junction	5	0,010196511	0,044417199

Supplementary Table 6. Differentially enriched pathways in idiopathic PD patients compared to controls analyzed with two different pathway databases (KEGG and Reactome).

Database	Pathway	Observed Genes in the Pathway	Genes	p-value_hyper	p-value_fisher
REACTOME	Initial triggering of complement	5		3,13056E-08	6,31414E-06
REACTOME	Complement cascade	6		1,8302E-07	1,05171E-05
REACTOME	Classical antibody-mediated complement activation	3		5,52964E-07	0,000207659
KEGG	Staphylococcus aureus infection	7		8,41753E-07	2,22796E-05
REACTOME	Creation of C4 and C2 activators	3		4,48862E-06	0,000527476
REACTOME	Regulation of Complement cascade	3		3,36868E-05	0,001549503
KEGG	Systemic lupus erythematosus	9		3,5677E-05	0,000314136
KEGG	Complement and coagulation cascades	6		5,65106E-05	0,000681249
KEGG	Pertussis	5		0,000654748	0,005307157
KEGG	Chagas disease (American trypanosomiasis)	6		0,000675963	0,004634381
REACTOME	Degradation of the extracellular matrix	3		0,000769579	0,010576072
REACTOME	Activation of Matrix Metalloproteinases	3		0,000769579	0,010576072
REACTOME	Chemokine receptors bind chemokines	4		0,00116989	0,010114466
REACTOME	E2F mediated regulation of DNA replication	3		0,001245041	0,014468666
KEGG	Hematopoietic cell lineage	5		0,001490899	0,009859507
KEGG	Prion diseases	3		0,0015463	0,016680252
REACTOME	Immune System	24		0,001568966	0,018754112
REACTOME	Amyloids	5		0,001578546	0,010294025
REACTOME	Extracellular matrix organization	5		0,00196871	0,012163561
KEGG	Cell adhesion molecules (CAMs)	6		0,00238894	0,012442702
REACTOME	Netrin-1 signaling	3		0,002747349	0,024392004
REACTOME	Innate Immune System	13		0,003570475	0,023440926
KEGG	Transcriptional misregulation in cancer	7		0,003817116	0,016657201
KEGG	Toll-like receptor signaling pathway	5		0,004287303	0,021925712
KEGG	Phagosome	6		0,004806466	0,021526899
REACTOME	RNA Polymerase I Chain Elongation	4		0,006962029	0,036494445
KEGG	Rheumatoid arthritis	4		0,008779443	0,043156149
REACTOME	RNA Polymerase I Promoter Clearance	4		0,009589838	0,046000462

Supplementary Table 7. Differentially expressed genes between asymptomatic carriers of *LRRK2* G2019S mutation and controls.

Gene	Base mean G2019S carriers	Base mean Controls	Fold Change Controls/G2019S carriers	p-value	Adj P-value*
SNORD42A	453,9947289	1,866848334	0,004112048	2,548E-275	5,9848E-271
MSLN	7,45061115	47,76257239	6,410557661	4,8746E-39	5,72473E-35
SNORA68	1341,888151	427,5812238	0,318641478	5,07275E-35	3,97162E-31
SMIM1	57,31048925	202,1387362	3,527080973	2,82078E-29	1,65636E-25
MIR3183	0,088265004	14,44647754	163,6716352	1,28126E-25	6,01885E-22
SNORA37	13,92771141	0,177836525	0,012768539	1,63093E-24	6,38454E-21
MIR148B	0,412564987	17,10596301	41,46246909	2,52729E-24	8,48014E-21
LOC606724	1244,641957	2685,149016	2,157366624	1,58393E-21	4,65042E-18
SCARNA3	1,076912832	17,63390662	16,37449763	4,32387E-21	1,12844E-17
DEFA1	1014,998008	3058,964212	3,013763758	5,04346E-20	9,87174E-17
DEFA1B	1014,998008	3058,964212	3,013763758	5,04346E-20	9,87174E-17
DEFA3	1014,998008	3058,964212	3,013763758	5,04346E-20	9,87174E-17
HBM	449,6857084	1079,096075	2,399667267	2,26471E-19	4,09181E-16
MIF	184,5805062	377,4044982	2,044660652	8,87646E-19	1,48922E-15
SFRP1	30,76324842	6,861303108	0,223035715	5,45582E-18	8,54309E-15
SNORD15A	6491,739549	3220,551837	0,496099976	9,60272E-18	1,40968E-14
MIR3194	0,298553351	10,47039058	35,07041716	1,23352E-17	1,7043E-14
TRAPPC5	334,1723846	686,9019318	2,055531706	1,8752E-17	2,44693E-14
GAGE2A	33,71664793	7,357053366	0,218202396	7,09644E-17	8,77269E-14
GAGE8	35,7599796	8,252484099	0,230774296	8,43688E-17	9,90827E-14
HBA2	836011,2856	1685663,652	2,016316862	3,50003E-15	3,9147E-12
LIME1	505,1302872	941,5689679	1,864012101	4,61575E-15	4,92795E-12
SCARNA17	61,5511737	23,40607861	0,380270224	4,83878E-15	4,94145E-12
HBQ1	120,1928824	274,0590444	2,280160347	5,99056E-15	5,86276E-12
LOC728989	33,36317289	90,22700416	2,704389192	1,24633E-14	1,17096E-11
ISG15	619,9437305	1423,065847	2,295475826	2,43909E-14	2,20344E-11
MIR4784	17,49646177	45,6329027	2,608121762	5,59959E-14	4,87123E-11
LOC284889	252,40536	460,1547991	1,823078555	6,17423E-14	5,17929E-11
MIR632	190,5404629	93,29193137	0,489617428	6,85491E-14	5,552E-11
ANKRD30BL	440,0075021	849,586505	1,930845499	1,05568E-13	8,26524E-11
PCBD2	774,6369894	390,8710809	0,50458613	1,20362E-13	9,11957E-11
HBG1	4012,982242	2622,442988	0,653489806	2,15261E-13	1,58002E-10
GAGE2C	24,29045023	5,2317416	0,215382653	2,34374E-13	1,66817E-10
CD177	129,9232866	292,022375	2,247652307	5,70542E-13	3,94144E-10
MIR3655	371,6142877	195,0461368	0,524861781	7,42341E-13	4,98175E-10
CTAG2	0,301352494	6,985715197	23,18120918	1,01586E-12	6,62792E-10
PNMAL1	4,931214792	25,48538147	5,168175094	1,18223E-12	7,5049E-10
MZT2B	328,6501685	590,0006215	1,795223852	1,22968E-12	7,60071E-10
GAGE2E	21,15000353	4,35128822	0,205734633	1,82523E-12	1,09926E-09
GAGE2C	21,15216914	4,398372476	0,207939547	2,02076E-12	1,18659E-09
DEFA4	236,0694641	560,5958728	2,374707271	3,77688E-12	2,16369E-09
SAP25	787,4773913	1349,548233	1,713761243	5,612E-12	3,13845E-09

NME3	153,274572	277,3158087	1,809274722	8,81856E-12	4,81699E-09
KANSL1-AS1	139,3232283	282,5429255	2,027967115	1,22803E-11	6,55544E-09
C9orf142	494,8268657	862,8181717	1,743676893	1,72309E-11	8,99378E-09
C1orf226	13,93590869	50,70858906	3,638699863	2,54551E-11	1,29976E-08
ORM1	242,2647546	458,9567086	1,894442753	2,6248E-11	1,31173E-08
MRPL41	124,5316948	224,4796668	1,802590636	3,58091E-11	1,75226E-08
TMC5	567,6587457	1063,562969	1,873595673	3,83843E-11	1,81012E-08
TSGA13	31,64980252	10,55231966	0,333408705	3,85328E-11	1,81012E-08
RHPN1	115,9254593	214,9893079	1,854547821	5,66467E-11	2,60886E-08
SCGB3A1	1,78082088	11,41731628	6,411265954	6,03844E-11	2,72752E-08
MMP8	275,8792027	691,5246848	2,506621297	7,66449E-11	3,39667E-08
TUBA3C	0,513076631	6,698951454	13,05643455	8,40248E-11	3,65477E-08
TREML3P	191,3026642	342,5029647	1,790372164	1,14143E-10	4,87454E-08
FAM154B	20,94954988	51,76978287	2,471164449	1,18297E-10	4,96171E-08
MRGPRE	22,6371029	6,441969888	0,284575721	1,26265E-10	5,203E-08
EIF3CL	353,0148839	198,4887845	0,562267467	1,46735E-10	5,94226E-08
DOC2A	104,5015775	192,036126	1,837638537	1,73944E-10	6,92474E-08
GAGE2C	16,58862515	3,307005032	0,199353774	1,81561E-10	7,10751E-08
ELANE	47,37581603	107,3225048	2,265343667	1,94482E-10	7,48852E-08
EIF3C	355,2835583	200,8567234	0,565342017	2,03925E-10	7,60283E-08
LCN2	678,3367265	1548,515591	2,282812548	2,02597E-10	7,60283E-08
HBG2	5174,136771	10074,6858	1,947123983	2,32434E-10	8,53034E-08
RSAD2	1266,098374	2983,872982	2,356746555	2,71492E-10	9,81046E-08
CABP7	82,00838808	150,5931865	1,836314431	4,69974E-10	1,67254E-07
MAPK10	9,67286118	40,04328452	4,139755939	5,13708E-10	1,80089E-07
PTPRCAP	1755,54796	2826,033088	1,609772648	5,30237E-10	1,8315E-07
TREML4	272,2430382	469,5537293	1,724759363	6,42233E-10	2,1862E-07
SNORD49B	954,7849277	559,8228576	0,586333991	9,70209E-10	3,25547E-07
IFI27	96,58295479	214,7028875	2,222989428	1,49574E-09	4,94815E-07
S100B	225,0526353	141,1719039	0,627283941	1,67274E-09	5,45686E-07
RHD	528,4515904	832,2714666	1,574924708	2,051E-09	6,59915E-07
MIR611	374,6040133	216,4511329	0,577813171	2,28221E-09	7,24386E-07
TSPO	2112,719054	3380,935709	1,600277	2,54742E-09	7,97784E-07
SNORD33	2678,663463	4157,663031	1,552140867	4,30273E-09	1,32977E-06
FLJ14107	18,77082983	40,97887089	2,183114507	4,98461E-09	1,5205E-06
RPL23AP7	448,6547698	266,8636297	0,594808409	6,02762E-09	1,81509E-06
C9orf16	533,3052122	861,280076	1,614985296	6,91126E-09	2,05483E-06
FAM173A	33,31854287	64,20283514	1,926940064	7,16085E-09	2,10243E-06
S1PR4	2261,745471	3556,794717	1,572588412	7,37711E-09	2,13918E-06
SNORD49A	859,7552878	516,8618756	0,601173244	9,35503E-09	2,67964E-06
RAVER2	202,6645004	330,5560908	1,631050777	9,48996E-09	2,68555E-06
USP32P1	220,5921255	420,9908752	1,908458311	9,72436E-09	2,71912E-06
EVA1B	42,50108953	79,17986943	1,863007992	1,01711E-08	2,81057E-06
TSPAN9	2832,922963	1817,299935	0,641492889	1,10891E-08	3,02863E-06
CAPS	199,5086035	324,9512945	1,628758304	1,49538E-08	4,03718E-06
SNORD68	1556,355643	2370,829165	1,523320956	1,63972E-08	4,33266E-06
MYO18B	11,43338099	28,31707963	2,476702181	1,64172E-08	4,33266E-06
SIVA1	443,2723799	699,5634726	1,578179703	1,70968E-08	4,46187E-06
ITPK1-AS1	16,30625322	4,778948607	0,293074598	1,88789E-08	4,87283E-06
LENG9	311,3517984	514,9691588	1,653978431	1,97994E-08	5,05488E-06

TMTC1	209,5405454	365,5671849	1,744613121	2,0236E-08	5,11078E-06
MZT2A	211,0296909	326,4891247	1,54712412	2,10119E-08	5,25029E-06
IRF7	1115,331111	1768,708162	1,585814423	2,85895E-08	6,9949E-06
B3GNT8	411,3720667	654,4187429	1,590819591	2,84686E-08	6,9949E-06
C16orf13	285,7124853	442,8698163	1,550054124	3,27626E-08	7,93328E-06
SNORD119	109,206281	182,5647771	1,671742463	3,41602E-08	8,18729E-06
ITPRIPL2	1092,929278	686,1458801	0,627804465	3,89075E-08	9,2309E-06
PIDD	247,6812177	391,350123	1,580055713	3,99908E-08	9,39303E-06
HBA1	420719,4621	704809,5618	1,675248296	4,48982E-08	1,04413E-05
MUC16	35,65420415	17,7148397	0,496851357	5,15381E-08	1,18679E-05
TYRO3P	41,04918821	23,60606905	0,575067866	5,65652E-08	1,28991E-05
MUC6	21,86286964	8,551732322	0,391153241	5,96305E-08	1,34673E-05
RBFOX2	180,0299985	298,4580211	1,657823827	6,26604E-08	1,40168E-05
RBPMS2	71,95943201	40,86681858	0,567914691	6,63573E-08	1,47038E-05
GAREM	446,1958319	277,6925693	0,622355812	6,70707E-08	1,4723E-05
SLC22A18	627,1185996	977,4449398	1,558628528	7,09569E-08	1,54318E-05
EGFL7	38,93297665	71,20408329	1,828888758	7,50277E-08	1,61674E-05
SMOC1	1705,216027	1091,126402	0,639875761	7,74013E-08	1,65273E-05
CCDC85B	62,12031553	101,5966914	1,635482539	9,25937E-08	1,95932E-05
ACCS	586,3848862	944,37421	1,610502304	9,89024E-08	2,0571E-05
CRIP2	145,0075388	221,4027142	1,526835888	9,89665E-08	2,0571E-05
HELB	968,0037409	652,7899974	0,674367226	1,02875E-07	2,11958E-05
LCN8	27,1710741	54,73319619	2,01439207	1,11042E-07	2,26797E-05
TNNI2	118,3007026	196,4547247	1,660638698	1,25016E-07	2,53135E-05
PRSS50	13,88044556	4,099939704	0,295375223	1,36182E-07	2,73389E-05
RASSF7	267,9754162	413,8775579	1,54446092	1,3812E-07	2,74928E-05
SAMD11	93,96739484	152,0892946	1,618532628	1,42002E-07	2,76978E-05
TNFRSF4	54,85098559	87,60505971	1,597146501	1,41865E-07	2,76978E-05
BAIAP3	669,872098	997,3074627	1,488802811	1,42687E-07	2,76978E-05
WDR38	84,4915729	139,8926059	1,655698918	1,47176E-07	2,8335E-05
MROH6	193,3404772	298,4907232	1,543860486	1,53743E-07	2,93586E-05
PCDHA1	17,22561876	6,742547802	0,391425579	1,57354E-07	2,98058E-05
DGKK	64,02082337	31,26621936	0,488375777	1,80437E-07	3,39049E-05
ALKBH7	175,2615614	269,6897136	1,538784154	1,86705E-07	3,48042E-05
MFS10	803,5914076	1214,01237	1,510733388	1,92806E-07	3,56585E-05
G0S2	28,3482403	59,07560327	2,08392488	1,99794E-07	3,63781E-05
TKTL1	253,0952701	434,7981994	1,717923054	1,98901E-07	3,63781E-05
LY6G6E	377,0505843	256,0557955	0,679101972	2,16485E-07	3,91138E-05
AQP10	191,9410089	124,2352671	0,64725755	2,2013E-07	3,94689E-05
BRICD5	87,6241332	142,6257493	1,627699403	2,25148E-07	4,00627E-05
IFIT1	2228,248071	4309,645117	1,934095747	2,31971E-07	4,09341E-05
JUNB	2244,950831	3263,576558	1,453740774	2,33531E-07	4,09341E-05
CIRBP-AS1	1189,583457	744,7927649	0,626095429	2,56702E-07	4,46624E-05
TP53I13	313,8619287	479,2611315	1,526980776	2,90039E-07	5,00914E-05
GAGE1	3,698414062	0,073490781	0,01987089	3,07372E-07	5,26974E-05
RPLP2	11635,86392	17149,40282	1,473840098	3,13706E-07	5,30095E-05
GAGE12D	5,50273991	0,447454064	0,081314776	3,12145E-07	5,30095E-05
SNORD45A	143,6760386	89,80495796	0,62505174	3,38032E-07	5,59134E-05
C19orf60	269,3565663	411,8686519	1,529083392	3,37517E-07	5,59134E-05
SNORA33	3414,403824	5432,919964	1,591176745	3,37353E-07	5,59134E-05

LRRC37A4P	525,2933252	345,1745587	0,657108214	3,40758E-07	5,59701E-05
SPATA2L	115,7701751	183,4113793	1,584271417	3,49814E-07	5,70586E-05
SNORA10	3731,648347	5522,762584	1,479979374	3,66077E-07	5,84585E-05
GAGE12C	5,453704167	0,447454064	0,082045899	3,7333E-07	5,84585E-05
GAGE12E	5,453704167	0,447454064	0,082045899	3,7333E-07	5,84585E-05
GAGE12G	5,453704167	0,447454064	0,082045899	3,7333E-07	5,84585E-05
GAGE6	5,453704167	0,447454064	0,082045899	3,7333E-07	5,84585E-05
GAGE12I	5,453704167	0,447454064	0,082045899	3,7333E-07	5,84585E-05
ATP5D	404,7319178	598,7546307	1,479385748	3,92127E-07	6,09953E-05
MIR4691	35,77498327	62,57063303	1,749005235	4,02347E-07	6,21732E-05
RPLP1	14027,90952	20510,4875	1,46212003	4,45741E-07	6,84286E-05
CEBPD	1393,144975	2090,970335	1,500899313	4,58462E-07	6,94733E-05
GAGE2C	11,6705752	2,794029383	0,239408027	4,55965E-07	6,94733E-05
GAGE2D	11,62153946	2,794029383	0,240418181	5,0838E-07	7,65438E-05
RNU6-76	20,88398065	8,142501095	0,389892197	5,44693E-07	8,14888E-05
PCDHA2	16,0119847	6,616243973	0,413205739	5,78655E-07	8,60218E-05
MIB2	1160,30396	1711,407243	1,47496458	5,96783E-07	8,78113E-05
CEBPB	2622,229608	3943,283008	1,503790132	5,98169E-07	8,78113E-05
RHOT2	1474,091354	2152,356124	1,460123973	6,19935E-07	8,98836E-05
RMRP	3,652844207	12,20826304	3,342125299	6,1994E-07	8,98836E-05
NOC4L	256,9225882	388,0323943	1,510308599	6,34384E-07	9,14135E-05
GAGE12F	5,101717564	0,368926976	0,072314269	7,19512E-07	0,000103048
PLIN4	452,468556	686,5870296	1,517424847	7,46225E-07	0,000106226
LGALS8-AS1	103,7167874	63,85086363	0,615627086	8,28647E-07	0,000117249
SNORD100	6549,967332	10239,82616	1,563340035	8,95987E-07	0,000126018
GAGE12F	9,753302401	1,97169161	0,202156309	9,10361E-07	0,000127277
H2AFX	116,2354098	180,2077179	1,5503685	9,44193E-07	0,00013093
H1FX	858,8962743	1223,769196	1,424816049	9,47636E-07	0,00013093
C19orf77	144,8526125	235,9392249	1,62882271	9,81113E-07	0,000134762
LRG1	2648,387921	3985,641248	1,504931063	1,05352E-06	0,000143867
ISYNA1	275,3265134	416,1612684	1,511519044	1,06116E-06	0,000144073
PF4V1	272,99971	182,5770257	0,668781024	1,07957E-06	0,000145729
MUC2	8,035635281	2,009747915	0,250104422	1,09931E-06	0,000147547
CEBPE	164,4689433	267,1796495	1,624499095	1,1178E-06	0,000149176
PLCH2	329,8506016	491,4000559	1,489765529	1,13259E-06	0,000149575
NLRP6	515,3892024	769,2802124	1,492619963	1,14508E-06	0,000149575
RBFOX3	13,80245011	31,43118376	2,277217705	1,14017E-06	0,000149575
NDUFS7	481,1842851	694,2055812	1,442702105	1,14626E-06	0,000149575
TCIRG1	7547,623685	11101,5684	1,470869358	1,19029E-06	0,000153613
LMF2	1478,356433	2129,270828	1,44029598	1,18809E-06	0,000153613
MIR4749	32,47807094	56,40108232	1,736589664	1,21447E-06	0,00015503
YDJC	175,986347	261,7595742	1,48738569	1,21272E-06	0,00015503
ZNHIT2	37,69385981	63,24808176	1,677941237	1,22444E-06	0,000155458
ZEB2-AS1	180,5025506	114,3984642	0,63377755	1,27941E-06	0,000161564
PIGQ	360,0429965	532,4129891	1,478748356	1,33447E-06	0,000167616
GAGE12D	5,44148514	0,563258951	0,103511989	1,38154E-06	0,000172604
PDCD1	115,378173	183,4040977	1,589590933	1,41815E-06	0,00017624
NCF4	7208,760383	10701,88993	1,484567299	1,43034E-06	0,000176768
SLC35F1	1082,017841	717,2857922	0,66291494	1,43744E-06	0,000176768
LOC100288778	481,3494582	711,4132663	1,477955889	1,51828E-06	0,000185736

PAX8	486,6503813	866,2731257	1,780072838	1,53579E-06	0,000186904
GAGE2D	5,960655292	0,699901646	0,117420252	1,57261E-06	0,000190399
MIR4722	32,72420835	57,82625981	1,767078952	1,6255E-06	0,000192332
GAGE12C	5,392449397	0,563258951	0,104453266	1,63771E-06	0,000192332
GAGE12E	5,392449397	0,563258951	0,104453266	1,63771E-06	0,000192332
GAGE12G	5,392449397	0,563258951	0,104453266	1,63771E-06	0,000192332
GAGE6	5,392449397	0,563258951	0,104453266	1,63771E-06	0,000192332
GAGE12I	5,392449397	0,563258951	0,104453266	1,63771E-06	0,000192332
IGJ	2587,929409	1748,662249	0,675699361	1,64949E-06	0,000192753
ODF3B	593,2178885	878,9547294	1,481672664	1,70237E-06	0,000197947
MIR4637	0,045823057	3,897498093	85,05539324	1,73111E-06	0,000200297
PGLYRP1	600,5251912	957,7247373	1,594811927	1,773E-06	0,000203143
FLT4	96,57894388	151,5846627	1,569541523	1,77185E-06	0,000203143
SOCS1	69,52997761	111,3747219	1,601823065	1,79439E-06	0,000204595
IFI44L	908,3231697	1721,099136	1,894809241	1,93748E-06	0,000217739
SPSB3	1540,014902	2237,245772	1,452742937	1,92626E-06	0,000217739
ZDHHC12	509,2379558	745,5406831	1,46403204	1,93245E-06	0,000217739
ITGA2B	4318,046886	3259,879577	0,754943071	2,01427E-06	0,000225292
ITGB3	3914,429855	2926,624791	0,747650334	2,0882E-06	0,000232453
PPP1R35	252,1073941	370,5024424	1,469621483	2,13681E-06	0,000236742
SNHG9	55,856097	94,16138158	1,685785199	2,17595E-06	0,000239947
TSEN34	1850,386141	2708,663008	1,463836627	2,27423E-06	0,000249613
NCAM1	1024,530722	653,3435813	0,637700332	2,33053E-06	0,000254602
ANXA2P2	522,8847697	338,2213359	0,64683723	2,38329E-06	0,00025916
CES1	1028,448584	644,6258782	0,626794463	2,41942E-06	0,000261877
YPEL3	7008,754033	10172,08169	1,451339517	2,51404E-06	0,000270871
C1orf228	334,8273505	497,7045182	1,486451204	2,52821E-06	0,000271154
PPFIA4	227,6684865	358,2562547	1,573587369	2,77311E-06	0,000296067
HBB	5372805,875	8837969,825	1,644944938	2,8535E-06	0,000303272
C1orf122	158,5670873	244,8517892	1,544152658	3,05758E-06	0,000323498
MIR2110	30,0357796	15,09490247	0,502564031	3,22569E-06	0,000336688
FRAS1	50,31335382	27,70522143	0,550653441	3,22506E-06	0,000336688
PCDHA3	14,56008426	6,345139193	0,435790005	3,23743E-06	0,000336688
GAGE12F	5,040462794	0,484731863	0,096168126	3,23959E-06	0,000336688
LYL1	1095,479188	1660,250614	1,51554738	3,29429E-06	0,000340865
RECQL4	57,52847276	93,3257473	1,62225317	3,419E-06	0,000352217
LOC654433	397,2314222	700,9760895	1,76465418	3,48841E-06	0,000357799
IFITM3	7191,837039	10949,54707	1,522496549	3,69162E-06	0,000375363
SNORD32A	8423,859742	5424,677666	0,64396581	3,68524E-06	0,000375363
ETV3	590,0649112	401,9904842	0,681264852	3,82044E-06	0,000386787
PPP2R3B	0,693056608	4,896769799	7,065468742	3,84327E-06	0,000387428
C1orf159	140,765745	213,5308998	1,516923737	3,86557E-06	0,000388011
DPP7	1179,226917	1633,422156	1,385163561	3,91121E-06	0,000390921
GAGE12D	5,073221654	0,552920085	0,108987961	4,23288E-06	0,000421279
SNORA52	3736,93574	5261,011962	1,407841164	4,28635E-06	0,000424801
PIM3	1175,963794	1656,337351	1,408493492	4,45329E-06	0,000437652
MUC17	13,81571321	5,843794687	0,42298176	4,4361E-06	0,000437652
PCDHA4	13,52662366	5,707220531	0,421924988	4,4887E-06	0,000439295
TMEM259	2470,216071	3468,30035	1,404047359	4,70282E-06	0,000458339
LRP2	15,62609292	6,996742594	0,447760207	4,94268E-06	0,00047788

GAGE12C	5,024185912	0,552920085	0,110051677	5,00505E-06	0,00047788
GAGE12E	5,024185912	0,552920085	0,110051677	5,00505E-06	0,00047788
GAGE12G	5,024185912	0,552920085	0,110051677	5,00505E-06	0,00047788
GAGE12H	5,024185912	0,552920085	0,110051677	5,00505E-06	0,00047788
CSNK2A3	108,3997542	69,28804636	0,639190069	5,10745E-06	0,000485684
AZU1	94,55746045	162,8792146	1,722542185	5,23892E-06	0,000496176
COL9A2	286,6872844	411,636647	1,435838523	5,27077E-06	0,000497188
HBZ	38,1508487	67,27343526	1,76335357	5,53694E-06	0,000520207
LRWD1	568,0761472	833,5297198	1,467285194	5,59596E-06	0,000523657
LRRC6	390,1746215	604,7213862	1,549873705	5,63135E-06	0,000524877
COMTD1	41,1313721	69,25826957	1,683830761	5,75169E-06	0,000533975
GPX1	5610,707648	8283,175793	1,476315701	6,17761E-06	0,000571258
CYP2D7P1	89,28648816	142,2408575	1,593083796	6,40939E-06	0,000588061
NINJ1	4551,458876	6551,847292	1,439504886	6,40838E-06	0,000588061
C19orf24	281,1075149	397,7826424	1,41505517	6,47993E-06	0,00059222
MIR643	25,57090675	12,31084987	0,481439708	6,70864E-06	0,000610746
C6orf1	424,6266321	618,4065389	1,456353635	6,89425E-06	0,000625221
GAGE2A	4,926823918	0,552920085	0,112226476	6,98382E-06	0,000630908
LOC729737	5462,596395	7778,617423	1,423978061	7,10944E-06	0,000639795
ABCC13	82,52942054	140,8000584	1,706058973	7,17078E-06	0,000642853
MAGI3	367,1380805	252,6671696	0,68820747	7,46067E-06	0,000666298
DGKQ	1276,707455	1790,683386	1,402579252	7,51667E-06	0,000668756
MEGF6	1343,622434	1907,6156	1,419755693	8,12803E-06	0,000720419
C11orf35	148,0624731	220,2714018	1,487692305	8,41009E-06	0,000742617
SNORD58B	893,2889255	615,2761418	0,688776189	8,60543E-06	0,00075702
RPUSD1	285,3011683	398,7540832	1,397660183	8,74068E-06	0,000766049
GSTM1	149,9433391	222,3525163	1,482910262	8,80775E-06	0,000769057
GAGE12D	4,560554649	0,48976817	0,107392238	9,52373E-06	0,000828494
GAGE2B	5,291883819	0,579592862	0,109524865	9,57739E-06	0,000830087
SNORD84	349,9656214	239,0043721	0,682936716	9,75768E-06	0,000842605
SNORD42B	5021,83598	3485,579597	0,694084715	9,80563E-06	0,000843644
C12orf57	658,1029784	935,0347834	1,420803148	1,01074E-05	0,000864532
GAGE12B	4,797055374	0,552920085	0,115262394	1,0122E-05	0,000864532
FGF13	44,86389428	84,09866844	1,874528946	1,01673E-05	0,000865251
ANO9	953,1200588	1348,550658	1,414880156	1,0665E-05	0,000904334
MIR1249	29,65423785	19,59047644	0,660629908	1,09315E-05	0,000923594
KRT1	874,4398692	1376,972503	1,574690899	1,12995E-05	0,00093956
PANX2	577,7656975	811,0592314	1,403785713	1,11693E-05	0,00093956
GAGE12C	4,511518906	0,48976817	0,108559485	1,13205E-05	0,00093956
GAGE12E	4,511518906	0,48976817	0,108559485	1,13205E-05	0,00093956
GAGE12H	4,511518906	0,48976817	0,108559485	1,13205E-05	0,00093956
GSDMD	2070,046043	2915,771177	1,408553779	1,13654E-05	0,000939969
C9orf89	1116,363795	1589,132124	1,423489485	1,14346E-05	0,000942369
MRPL55	209,8982388	305,5854261	1,45587418	1,15382E-05	0,000947582
GAGE12D	4,657916642	0,52651356	0,113036278	1,18879E-05	0,000972904
CCDC168	19,42474803	9,789059706	0,503947834	1,19772E-05	0,000975049
DPP10	4,412591367	13,29413458	3,01277265	1,19972E-05	0,000975049
COX8A	903,853806	1262,398169	1,396684022	1,21009E-05	0,000980093
TSSC4	448,3976871	625,4252167	1,394800274	1,22066E-05	0,000981876
METRNL	574,3839053	785,4241588	1,367420207	1,21736E-05	0,000981876

SOLH	1070,534973	1517,90968	1,417898264	1,2262E-05	0,000982968
RFNG	483,2682119	695,6710933	1,439513455	1,23093E-05	0,000983402
MAP1LC3A	143,5954628	209,2499284	1,457218246	1,2453E-05	0,000991509
GNL3L	2198,219612	1537,548246	0,69945161	1,25426E-05	0,000995274
VMO1	16,18084514	33,41088609	2,064841843	1,27233E-05	0,001006208
THBS1	2121,306778	1585,806599	0,747561181	1,29224E-05	0,001018528
OLFM4	334,1237075	659,6732052	1,974338218	1,30106E-05	0,001018644
VNN1	1188,029055	1734,409448	1,459904908	1,29861E-05	0,001018644
PCDHA5	12,57275077	5,53459721	0,440205752	1,32241E-05	0,001031917
MIR3184	17,59808316	7,540556755	0,428487392	1,38716E-05	0,001078863
GAGE12C	4,6088809	0,52651356	0,114238916	1,40735E-05	0,001080256
GAGE12E	4,6088809	0,52651356	0,114238916	1,40735E-05	0,001080256
GAGE12G	4,6088809	0,52651356	0,114238916	1,40735E-05	0,001080256
GAGE12H	4,6088809	0,52651356	0,114238916	1,40735E-05	0,001080256
HLX	789,8301759	1084,786427	1,373442621	1,41347E-05	0,001081419
BRE-AS1	81,03503387	49,44618162	0,610182772	1,42365E-05	0,001085668
SNORA70B	10,85270999	2,855840807	0,263145409	1,4544E-05	0,001105534
MIR1229	39,47320552	66,15026846	1,675827123	1,50757E-05	0,001142249
FN1	127,3373296	79,68204922	0,625755616	1,52895E-05	0,001154725
SPN	13418,79435	9485,395573	0,706873906	1,58315E-05	0,00119183
KLHL11	119,7010439	78,38866286	0,654870336	1,62539E-05	0,001219717
SLC22A18AS	77,26271018	116,6258561	1,509471462	1,63729E-05	0,001223252
PROS1	207,8128294	152,6800719	0,734699933	1,64052E-05	0,001223252
NAPRT1	767,4364494	1087,403288	1,416929427	1,71452E-05	0,001274389
GABPB2	354,4276112	245,886631	0,693756985	1,79671E-05	0,001331269
RNF166	5514,666578	7791,760085	1,412915899	1,80893E-05	0,001332005
GPR112	8,726847094	2,816236691	0,322709526	1,80905E-05	0,001332005
DUSP2	388,6725451	554,3843973	1,426353377	1,85094E-05	0,001358592
C19orf25	552,6564943	767,7177586	1,389140934	1,92638E-05	0,001409558
PI16	252,082854	369,7286219	1,466694843	2,05288E-05	0,001497455
PDIA3P	489,2682723	334,4777806	0,683628593	2,09838E-05	0,001525903
C1orf233	67,3517371	101,5384765	1,507585117	2,10567E-05	0,001526479
TMEM175	672,027022	928,0832942	1,381020798	2,13315E-05	0,001541646
GALK1	300,570717	424,4820264	1,412253431	2,21208E-05	0,001593782
ADAM8	12124,94533	16805,27925	1,386008662	2,26701E-05	0,001628367
FAM229A	3,290955898	9,31531798	2,830581226	2,28136E-05	0,001633676
NCR1	493,5128778	331,3921436	0,671496446	2,31872E-05	0,001655385
OTUD7B	337,2681901	237,3440318	0,703724925	2,36163E-05	0,001680909
COL18A1	2164,725967	2916,374095	1,347225533	2,37026E-05	0,001681955
PLEKHA7	1613,336679	1138,271378	0,705538648	2,38601E-05	0,001688031
FLI1-AS1	589,2587359	399,3899228	0,677783626	2,48127E-05	0,001746023
CPT1B	1325,61714	1880,682521	1,418722242	2,48285E-05	0,001746023
SNAI3	331,9536515	472,6479062	1,423837045	2,5873E-05	0,001808643
JUND	1055,862492	1435,539815	1,359589744	2,58281E-05	0,001808643
MAP1A	449,477281	315,7524941	0,702488218	2,63462E-05	0,001836263
TTY15	116,9817276	78,40352363	0,670220258	2,66742E-05	0,001853621
MIR423	18,1816545	8,287024575	0,455790455	2,70694E-05	0,001875535
CITED4	41,43632576	66,35799101	1,601444863	2,75807E-05	0,001902615
LOC100129250	239,4783715	344,8427073	1,439974329	2,76223E-05	0,001902615
CLEC4E	3989,636332	5703,516697	1,429583105	2,828E-05	0,001942225

GAGE12B	4,381750362	0,52651356	0,120160556	2,85741E-05	0,001956702
IRS4	2,821039023	0,157054175	0,055672457	2,87363E-05	0,001962085
PCDHA8	10,16527104	4,134883771	0,406765718	2,89672E-05	0,001972122
FAM174A	332,2867994	470,2052581	1,415058494	2,91826E-05	0,001981044
MMRN1	272,047869	200,4762301	0,736915275	2,94138E-05	0,001990983
FLG2	10,05654134	4,081255611	0,405830939	2,98277E-05	0,002006608
ISOC2	113,9589814	161,3716019	1,416049879	2,99009E-05	0,002006608
OGFR	2320,024758	3152,025723	1,358617278	2,97836E-05	0,002006608
MIR4498	41,09760912	23,34931743	0,568142963	3,05996E-05	0,002047028
SNORD58A	6034,006503	4265,111896	0,706845757	3,06775E-05	0,002047028
LRCH4	5010,024616	6846,987872	1,366657531	3,09323E-05	0,002058182
COX5B	863,0537272	1199,969502	1,390376363	3,11653E-05	0,002067826
HEXDC	911,5773458	1265,520676	1,388275698	3,17386E-05	0,002094033
PRTN3	21,62749319	48,67358937	2,250542351	3,16668E-05	0,002094033
C20orf195	14,63414377	28,77415539	1,966234297	3,20022E-05	0,002105511
PNPLA2	3154,448202	4404,980857	1,396434677	3,33119E-05	0,002185558
CEACAM6	195,4143493	352,6092891	1,804418612	3,34889E-05	0,002191051
PPMIL	314,8446486	216,8799211	0,688847411	3,36724E-05	0,002196939
NDUFS8	446,3801415	612,6637707	1,372515741	3,38619E-05	0,002203178
SNORA27	4710,461261	6821,475025	1,448154362	3,46424E-05	0,002241684
PLEK2	120,2684408	196,0435139	1,630049517	3,46446E-05	0,002241684
RAVER1	1606,731832	2188,397014	1,362017587	3,56849E-05	0,002302654
SULT2B1	35,95558526	18,17704977	0,505541758	3,6099E-05	0,002322993
CST3	4639,254049	6167,956869	1,329514789	3,62696E-05	0,002327597
SEC14L5	176,4011666	124,9849378	0,708526708	3,73565E-05	0,002384317
CCR5	2089,051691	1513,928587	0,724696566	3,73336E-05	0,002384317
KIAA0754	87,67760995	56,74442446	0,647194016	3,76687E-05	0,002397733
NUDT22	492,93534	673,3429945	1,365986449	3,79815E-05	0,002411107
HLA-DQB1	2400,048399	3087,415078	1,286397007	3,81041E-05	0,002412368
ID3	166,6555853	233,8840777	1,403397776	3,83979E-05	0,002424436
GBP1P1	20,82530137	40,61443577	1,950244803	3,89334E-05	0,002451657
GALNT18	113,2782889	76,27177566	0,673313275	3,91155E-05	0,002456534
UQCR11	1010,215544	1411,44942	1,397176503	4,04536E-05	0,002533796
GMEB1	641,218934	453,8472428	0,707788274	4,18062E-05	0,00260807
ITGB2-AS1	2586,36233	3672,366448	1,419896357	4,18615E-05	0,00260807
GPAA1	916,7123178	1247,55158	1,360897586	4,25332E-05	0,002642907
LOC644172	9,230096347	20,77590035	2,250886617	4,38061E-05	0,002702402
CHCHD10	253,9073802	357,9073102	1,409597901	4,37415E-05	0,002702402
DPYSL2	3373,252107	2356,018743	0,698441346	4,38358E-05	0,002702402
RNF182	77,57415788	101,1080271	1,303372538	4,51882E-05	0,002771229
SNORD54	1740,097333	2393,355926	1,375414973	4,51511E-05	0,002771229
PCDHA7	10,79157388	4,666252266	0,43239775	4,53505E-05	0,002773939
PCDHA6	11,56623639	5,278201416	0,456345629	4,57508E-05	0,002791157
MIR661	2,627895523	0,19513613	0,074255665	4,59942E-05	0,002798737
HYPK	676,300102	462,7375606	0,684219268	4,66794E-05	0,002833088
SLC52A2	311,3292337	429,2318587	1,378707208	4,77567E-05	0,002891002
TNFRSF14	4457,302624	6057,441798	1,358992716	4,83435E-05	0,002904069
DLEU1	248,4243673	168,4809561	0,678198189	4,81516E-05	0,002904069
SELM	51,13677001	76,70304696	1,499958776	4,82806E-05	0,002904069
FMOD	0,552926448	4,30068079	7,778034146	4,93723E-05	0,002950781

UBTD1	209,2173549	296,2433894	1,415959921	4,9275E-05	0,002950781
CFH	320,4925339	229,7575477	0,716888924	4,95406E-05	0,002953322
PAR-SN	44,85243315	26,1826585	0,583751129	5,05759E-05	0,003007407
HDAC10	1070,142817	1454,515407	1,359178779	5,09677E-05	0,00301653
NCF1B	1346,158944	1868,163548	1,38777338	5,09861E-05	0,00301653
MT2A	526,7783759	761,5022257	1,445583685	5,18195E-05	0,00305047
TREX1	683,233914	959,1765546	1,403877259	5,1763E-05	0,00305047
AHNAK	119535,1436	85966,29927	0,719171757	5,41349E-05	0,003159679
PAR5	76,84142827	53,58679296	0,697368518	5,39545E-05	0,003159679
RBFOX1	5,782330676	16,5321737	2,859084793	5,40048E-05	0,003159679
FSTL1	210,223213	161,1918481	0,76676522	5,42128E-05	0,003159679
CHTF18	175,551634	247,5039506	1,409864123	5,4389E-05	0,003162102
TBC1D10C	4463,435515	6143,908049	1,37649755	5,48011E-05	0,003178191
TGM3	186,7550477	272,6261445	1,459806028	5,57039E-05	0,003222595
TMEM184A	227,6813569	320,439953	1,40740532	5,92753E-05	0,003420781
ARSA	1843,570586	2533,997306	1,374505172	5,98901E-05	0,00344779
LLPH	1434,709605	1024,807776	0,714296309	6,00667E-05	0,003449501
CORO7	4261,725889	5722,521696	1,342770944	6,16387E-05	0,003522556
MIR4721	138,1429233	194,7017913	1,40942284	6,15572E-05	0,003522556
COL17A1	35,69033739	76,88813234	2,154312286	6,19663E-05	0,003532683
UBE2D1	2730,937684	3857,969914	1,41269057	6,2342E-05	0,003545492
ITGB1	12670,64319	9373,80415	0,739804918	6,35791E-05	0,003589776
ATHL1	9396,302877	12833,85042	1,365840436	6,3508E-05	0,003589776
PALM3	6,335475872	1,72330092	0,272008126	6,35385E-05	0,003589776
DACT3-AS1	665,9276199	936,6527447	1,406538364	6,49026E-05	0,003655712
MROH8	251,3936937	171,7450278	0,683171583	6,54768E-05	0,003679231
TAF15	9896,077119	7091,012512	0,716547823	6,58302E-05	0,003690262
SYCE1	30,34235221	14,29168651	0,471014456	6,60493E-05	0,003693726
MIR4651	54,79056316	32,33162872	0,590094842	6,63932E-05	0,003704141
KREMEN1	1176,976526	1736,131629	1,475077532	6,7019E-05	0,003730193
FLYWCH1	782,4803057	1060,121571	1,354822049	6,79912E-05	0,003775358
XRCC3	886,8150667	1196,975434	1,349746389	6,84463E-05	0,003780695
FAM157A	253,8691715	378,0559837	1,489176419	6,84791E-05	0,003780695
AP5Z1	1310,559652	1765,923041	1,347457201	6,85702E-05	0,003780695
PCDHA9	9,377912516	3,824888324	0,407861378	6,90802E-05	0,003799894
NPAP1	4,700720204	1,137926314	0,242074887	7,04577E-05	0,003866614
F8A2	91,53239117	135,4829209	1,48016368	7,11561E-05	0,003886776
F8A3	91,53239117	135,4829209	1,48016368	7,11561E-05	0,003886776
MMP23A	1,922609263	6,72146828	3,496013678	7,143E-05	0,003892687
KIFC2	488,4617283	670,1802925	1,372022113	7,26959E-05	0,003952502
MIR4656	5,06543798	12,32923077	2,433991062	7,32846E-05	0,003975309
DUS1L	1240,73364	1681,208941	1,355011975	7,36589E-05	0,003986406
RAP1GAP	91,34638902	152,0330509	1,664357535	7,4838E-05	0,004031639
SNORD101	5744,744185	8478,415586	1,475856072	7,47459E-05	0,004031639
H19	74,75379691	50,04311952	0,669439167	7,52922E-05	0,004046828
LOC100505658	102,5519312	151,5034155	1,477333618	7,57658E-05	0,004062987
DBN1	481,2035402	656,5012782	1,364290209	7,83445E-05	0,004191699
SLC25A22	363,9534529	497,187862	1,366075409	7,88452E-05	0,004208902
MRS2P2	10,98997651	4,996278331	0,454621384	8,12266E-05	0,004295556
ZNF524	306,6682236	412,1422325	1,343935239	8,07573E-05	0,004295556

TRABD	1780,260862	2402,545353	1,349546802	8,08907E-05	0,004295556
MPP6	99,63685297	65,90415465	0,661443559	8,13829E-05	0,004295556
SSR4	1299,726299	1767,460585	1,359871372	8,12966E-05	0,004295556
CD7	1551,46237	2001,068784	1,289795243	8,19373E-05	0,004315117
C4orf48	10,8069801	20,71896175	1,917183299	8,21737E-05	0,004317889
ABTB1	15812,81136	21826,48377	1,38030381	8,27654E-05	0,004339272
TELO2	472,0436742	636,7254639	1,348869816	8,35652E-05	0,004371448
APRT	1288,643168	1727,167038	1,340298913	8,54189E-05	0,004458485
ZC3H13	3267,657646	2376,723447	0,727347753	8,59186E-05	0,004474626
LOC284454	1099,360955	1483,238856	1,349182768	8,74905E-05	0,004546411
MUC5B	16,00826523	7,346848633	0,458940961	8,77706E-05	0,004550896
CTSE	53,44812274	94,05871619	1,75981328	8,90105E-05	0,004583945
GOLGA8B	1244,234737	1841,008997	1,47963157	8,88288E-05	0,004583945
MPG	728,5248972	1013,870273	1,391675531	8,91886E-05	0,004583945
LINC00487	7,415844709	19,46301	2,624516932	8,91036E-05	0,004583945
SCRIB	617,4209674	824,3038865	1,335075953	9,37764E-05	0,004809213
ISG20	2949,677307	4055,304404	1,374829848	9,54428E-05	0,004856805
CHPF	58,89490405	87,68335847	1,488810618	9,49709E-05	0,004856805
TOR2A	528,1334773	713,1509468	1,350323313	9,54282E-05	0,004856805
PPP2R3B	0,878466852	4,459535726	5,076498581	9,55315E-05	0,004856805
GPR146	385,8695109	572,8875453	1,484666524	9,62464E-05	0,004882581
IFI6	1101,879667	1792,694519	1,626942191	9,64939E-05	0,00488459
TMEM120A	989,3683315	1343,828939	1,358269612	9,71141E-05	0,004905409
EXOSC4	82,48055792	119,7475368	1,451827435	9,8184E-05	0,004948811
SLC39A13	624,5094328	850,5919671	1,362016204	0,000100044	0,005031782
HELZ2	2416,487436	3447,152306	1,426513648	0,000100628	0,005050302
CARD9	485,3505652	635,2136649	1,308772896	0,000102575	0,005137057
SPPL2B	892,728174	1208,705387	1,353945604	0,000105265	0,005260541
RPS19BP1	682,8731198	939,4712477	1,375762525	0,000105798	0,005275953
ABCA7	3962,134083	5370,92701	1,355564173	0,000106442	0,005293288
GAGE2E	4,465827254	0,673495122	0,150810832	0,000106596	0,005293288
FHL3	1135,897176	1511,714514	1,330855069	0,000107091	0,00530632
PYCARD	1391,918932	1895,467354	1,361765625	0,00010731	0,00530632
UGT2B11	211,141291	322,0128842	1,525106164	0,000108045	0,005331431
MST1P2	46,25996109	73,53002711	1,589496086	0,000108942	0,005353192
CDH2	49,67893651	79,45878939	1,599446264	0,000108929	0,005353192
MIR3922	7,356952074	2,855787921	0,388175415	0,000110581	0,005411849
DPEP3	323,0928254	443,2537267	1,371908293	0,000110596	0,005411849
FGD6	410,7260282	287,6440409	0,700330686	0,000111369	0,005438342
KLHL17	169,6750585	238,0424131	1,40293108	0,000112275	0,005471178
CHST13	106,2192268	149,5457236	1,407896933	0,000112559	0,005473685
HAGHL	38,92595573	58,39189881	1,500076176	0,000112813	0,005474688
CST7	3628,419471	5105,262422	1,407021008	0,000114419	0,005541203
ZNF598	658,0791656	881,18757	1,339029734	0,000114907	0,005546556
MYL4	1157,50644	1679,519069	1,450980324	0,000115079	0,005546556
MIR1181	248,6962299	161,7294013	0,650309019	0,000115238	0,005546556
SNORD34	3468,244524	4619,860032	1,33204565	0,000119564	0,005734406
THAP7	281,8514047	378,0862969	1,341438399	0,00011963	0,005734406
STMN3	1025,346081	1394,285616	1,359819521	0,0001206	0,005769128
MICALL2	58,94917644	87,04552358	1,476619842	0,000121009	0,005776953

C22orf32	711,1365738	967,0132132	1,35981364	0,000121326	0,005780322
NUBP2	474,7934684	630,2874417	1,327498131	0,000121862	0,005794134
ZNF462	20,37268836	9,889809449	0,485444497	0,000122545	0,005814835
SLITRK3	1,804421802	0	0	0,000123326	0,005840074
SNORD53	50,30878741	30,8861557	0,613931627	0,000124119	0,005865786
LOC285740	11,36466864	3,796479193	0,334059823	0,000124769	0,005884698
S100A11	15616,77298	21473,65907	1,375038178	0,000126272	0,00593545
PRR22	12,68608439	24,76649657	1,952256962	0,000126351	0,00593545
OXER1	412,2352889	563,4239799	1,366753393	0,000127088	0,005958148
ANKRD22	173,6432538	266,198993	1,533022373	0,000127441	0,005962801
CAMP	524,5429966	905,202215	1,725696884	0,000128293	0,005990726
VCAM1	18,06276966	9,304294049	0,515108935	0,000130709	0,006041178
JTB	2124,549201	2910,839688	1,370097565	0,000130474	0,006041178
SERPING1	669,4321737	1039,753313	1,553186945	0,000131173	0,006041178
EEF1DP3	63,3778442	41,50293915	0,654849335	0,000130887	0,006041178
ELMO3	150,1683145	210,9725765	1,404907402	0,000131127	0,006041178
ALOX15	689,1818574	928,4620673	1,347194586	0,000131	0,006041178
ZNF414	132,9610024	186,0539762	1,399312376	0,000129905	0,006041178
RNPEPL1	4376,379897	5850,746936	1,336891923	0,000131722	0,006054572
RGS19	3651,975796	4876,17562	1,335215755	0,000132482	0,006077611
CXCL1	230,4115547	332,9104348	1,444851302	0,000133059	0,006092166
NDOR1	1020,638234	1386,959291	1,358913712	0,000137175	0,0062684
POLR2J3	648,3523888	457,578093	0,705755236	0,000138	0,006293868
FAM195A	172,4590953	240,371017	1,393785677	0,000140068	0,006375811
ZNF593	61,26326242	90,51486711	1,477473832	0,000141473	0,006427289
BRAT1	1045,356153	1384,477588	1,324407557	0,00014372	0,006516772
GUK1	7050,124292	10127,03357	1,436433337	0,000144836	0,006554721
COL2A1	6,226685106	2,035444804	0,326890596	0,000145562	0,006574937
TUBA4B	386,5587778	287,2324701	0,743049923	0,000145943	0,006579487
AGRN	105,3173823	164,3448616	1,560472335	0,000148956	0,006702463
IFITM2	44176,88264	61535,9248	1,392944027	0,000149973	0,006709653
CD163	4961,024308	3485,693869	0,702615761	0,000149889	0,006709653
COL5A2	56,26532687	31,82495336	0,565622829	0,000149819	0,006709653
FAT1	11,20984804	5,120897607	0,456821323	0,000150651	0,006727186
NOXA1	147,2728483	201,6149185	1,368989062	0,000152107	0,006779295
FAM63B	341,0217587	257,9958532	0,756537806	0,000152836	0,006798868
PCDHGB4	281,8827074	196,4887755	0,697058636	0,000155325	0,006896567
SMTNL1	141,3614841	212,9401838	1,506352209	0,000157889	0,006987386
LRP3	123,6647438	174,0672749	1,407573974	0,000157966	0,006987386
AHSP	610,7077157	958,7082167	1,569831512	0,000158342	0,006990841
MIR3916	66,65613122	45,25015542	0,678859613	0,000158746	0,006995556
CHRNA2	13,54524177	5,869282193	0,433309519	0,000160034	0,00703911
TRPT1	412,1354418	569,1533261	1,380986123	0,000160963	0,007066707
TCHH	12,08441369	5,609989834	0,464233514	0,000163228	0,007126192
HAPLN3	582,8371574	786,0072465	1,348588086	0,000162865	0,007126192
FASTK	945,488344	1278,249272	1,351946092	0,000163225	0,007126192
ZNF121	125,3839685	91,93277805	0,733209988	0,000167757	0,007296815
SNORD43	1045,064149	870,7984703	0,833248821	0,00016763	0,007296815
GLTPD1	261,5906609	349,8993687	1,337583565	0,000168597	0,007319812
ETV7	181,6241028	286,5849687	1,577901635	0,000170747	0,007399464

HES4	5,182742831	13,10626512	2,528827986	0,000171163	0,007403817
KRT79	8,108711047	21,40880523	2,640222978	0,000173189	0,007452259
GLIS2	55,7098695	83,86053265	1,505308366	0,000173235	0,007452259
ARSH	2,107890316	0,067776195	0,032153568	0,000173067	0,007452259
BCL7C	309,3657321	413,7748772	1,337494216	0,000175494	0,007535656
MRPL4	378,6079343	502,1098865	1,326200116	0,000176018	0,007544358
PCDHGA8	273,0986629	190,8598689	0,698867826	0,000176472	0,007550039
PI3	1516,586244	2313,580487	1,525518576	0,00017686	0,007552873
CLEC18B	24,50788281	41,86396225	1,708183549	0,00017761	0,007571138
GAGE12D	4,354830463	0,673495122	0,154654728	0,000178301	0,007586821
ANXA3	1186,332413	1745,865792	1,471649744	0,000179509	0,007616273
SNHG7	363,4002711	480,2896129	1,321654526	0,000179641	0,007616273
RBM38	4199,456068	5988,899653	1,426113181	0,000181434	0,00767843
ULK1	3255,739483	4320,573732	1,327063715	0,000182307	0,007701476
BRI3	3288,043407	4460,791333	1,356670451	0,000185172	0,007808483
TRMT2A	750,7419816	996,6172982	1,327509747	0,000185966	0,007813883
NDUFB11	768,1434486	1039,837962	1,353702833	0,000185811	0,007813883
PTOV1	2444,325849	3252,103823	1,330470659	0,000188296	0,007897659
ENTHD2	1533,589534	2058,393494	1,342206274	0,000189227	0,007922563
MIR4687	13,37191548	24,18142622	1,808374144	0,000190698	0,007955806
LOC147646	40,0859819	23,14813439	0,577462078	0,000190487	0,007955806
RHOG	7601,701067	10204,81848	1,342438802	0,000196453	0,00818135
SNORD26	95,21673411	65,07891802	0,683481939	0,000197429	0,008207441
THEM5	518,4279226	380,3715868	0,733701968	0,000198137	0,008222335
RBP7	574,0250404	792,4734727	1,38055558	0,000202507	0,008374109
PCDHGB5	268,0331364	187,7135247	0,700337008	0,000202336	0,008374109
PCDHGA9	252,6301427	176,4212675	0,698338154	0,000203278	0,008391185
C17orf97	67,35463239	42,79777501	0,635409526	0,00020364	0,008391378
DNAH2	21,14785578	12,50116416	0,591131521	0,000204766	0,00840829
ARHGAP4	6217,209701	8233,263018	1,324269795	0,000204463	0,00840829
CAPN10	668,2029348	894,0429701	1,337981208	0,000206241	0,008421223
GAGE12C	4,30579472	0,673495122	0,156415985	0,000206874	0,008421223
GAGE12E	4,30579472	0,673495122	0,156415985	0,000206874	0,008421223
GAGE12G	4,30579472	0,673495122	0,156415985	0,000206874	0,008421223
GAGE12H	4,30579472	0,673495122	0,156415985	0,000206874	0,008421223
MIR3917	33,21837208	19,7315188	0,593994153	0,000208427	0,008426897
FAM177B	65,91176483	100,2959963	1,521670624	0,000208059	0,008426897
ARL16	368,9181925	512,8377504	1,39011239	0,000207901	0,008426897
SNORA7A	3959,239043	2869,370931	0,724727883	0,000208448	0,008426897
PCSK6	512,4038235	399,0577653	0,778795448	0,000210233	0,008484459
ZNF573	90,81301416	63,78616041	0,702390081	0,000210695	0,008488531
PKD1	1017,498935	1348,30655	1,32511839	0,000212603	0,008550726
MX1	3741,896536	5907,498994	1,578744612	0,000214524	0,008613213
MMP23B	5,28477102	11,93475542	2,258329712	0,000215337	0,008631137
TMEM63C	269,1261762	210,0137421	0,780354201	0,000217595	0,008706753
RPL36	5929,973539	7727,549856	1,303133953	0,000218291	0,008719776
BPI	456,5766201	734,2002965	1,608054956	0,00021948	0,008737795
LNPEP	1394,966675	1082,634682	0,776100749	0,000219486	0,008737795
BATF2	218,5450825	327,6629565	1,499292287	0,0002201	0,008747392
PCDHA10	8,823736054	3,824888324	0,433477192	0,000220914	0,008750482

DGAT1	1671,413225	2236,342179	1,337994785	0,000220923	0,008750482
OTOF	38,46929933	66,48929607	1,728372942	0,000222899	0,008813909
MYH7	7,66131351	3,349388287	0,43718199	0,000224291	0,008854024
CEACAM8	284,7243818	508,2724224	1,785138383	0,000225868	0,008901315
HM13-AS1	877,747604	1165,894047	1,328279384	0,000230046	0,009050785
FUT11	589,5279083	431,0026085	0,731097888	0,00023192	0,009099059
MIR223	451,9151092	636,0027536	1,407350054	0,000232048	0,009099059
PCDHGB6	245,4629222	171,5223512	0,698770917	0,000233475	0,009124555
TCEAL4	463,5437159	322,1805284	0,695038067	0,000233165	0,009124555
NOTCH1	6549,998496	8731,575605	1,333065284	0,000234263	0,009140148
CD226	1231,262218	950,9014283	0,772298065	0,000237368	0,00924594
WASH7P	507,5514192	684,7337503	1,349092377	0,000240518	0,009291574
PNLIPRP2	1,689620983	0	0	0,00023982	0,009291574
EFCAB4A	64,88574805	94,6462337	1,458659822	0,000239627	0,009291574
DCXR	398,2537033	542,5132206	1,362230197	0,000239548	0,009291574
PCDHGA2	359,2698509	255,724296	0,711788911	0,000240505	0,009291574
C14orf80	167,3368207	227,7557494	1,36106177	0,000243955	0,009408878
MAN1A2	1178,002601	899,5179141	0,763595864	0,000244795	0,009425819
ATP6V0B	4368,416887	5818,033324	1,331840224	0,000247967	0,009532314
COPE	2417,308284	3173,136801	1,312673614	0,000248498	0,009537111
LOC282997	520,4342754	707,2504597	1,358962107	0,000249438	0,009557597
TMEM134	397,341235	528,1776117	1,329279635	0,000250952	0,009599924
NSUN5P2	493,9093716	690,1753973	1,397372549	0,000252533	0,009644712
SYTL1	2951,04991	3930,794467	1,33199864	0,000255341	0,009736119
LOC728392	831,5344419	1110,125195	1,335032127	0,000256005	0,009745621
MIR4781	23,89476417	13,52246849	0,565917638	0,000256621	0,009753259
PCDHGA1	363,3209386	259,1224434	0,713205367	0,000258748	0,009818213
PCDHGA3	356,714181	254,2503979	0,712756631	0,00026049	0,009868385
HBD	1489,858298	2361,027928	1,584733214	0,000261148	0,009877384
ACAP3	1072,565138	1424,735228	1,328343779	0,000261911	0,0098903
CA4	324,9937672	465,4576049	1,432204712	0,000263737	0,00994325
FLYWCH2	141,8214471	197,0284524	1,389271203	0,00026485	0,009969243
MRPL38	517,4006895	701,2159838	1,355266814	0,000266633	0,010020275
PCDHGA7	289,7854895	204,7129662	0,70642932	0,000267906	0,010052042
SMPD3	748,7695443	1004,785262	1,341915239	0,000269308	0,010083623
NDUFA11	853,6448913	1110,24368	1,300591958	0,000269606	0,010083623
ZNF80	66,15938578	99,31003606	1,501072522	0,000273013	0,010194794
GSTP1	2598,687516	3330,254342	1,281513965	0,000278748	0,010390409
LY86-AS1	378,9766426	266,6000758	0,703473633	0,000279136	0,010390409
SETBP1	590,3896034	443,0737783	0,750476932	0,000279912	0,01040279
MIR617	7,837133261	3,931019306	0,501588932	0,000283453	0,010501155
HSD3B7	72,54959527	104,8783919	1,445609607	0,000283388	0,010501155
NT5C	329,3737125	441,9219384	1,341703729	0,000283966	0,010503617
SCNN1D	65,41535993	94,80212689	1,449233437	0,000285024	0,010526183
VNN2	18776,79541	26601,71966	1,416733743	0,000287626	0,010605578
PCDHGB1	354,2185142	253,277377	0,715031448	0,00029094	0,010710979
MYBPH	80,6317538	118,2741808	1,466843709	0,000294498	0,010824992
ABHD16B	46,23274403	66,77302291	1,4442799	0,000295309	0,010837823
SCARNA9	33,432939	19,63880553	0,587408888	0,000296917	0,010879846
CXXC11	17,35810191	30,55043598	1,760010175	0,000298833	0,010933003

PCDHGA5	336,6406755	240,2120258	0,713556154	0,000299947	0,010956679
MIR1184-1	50,54376478	75,82722394	1,500229045	0,000301656	0,010967954
MIR1184-2	50,54376478	75,82722394	1,500229045	0,000301656	0,010967954
MIR1184-3	50,54376478	75,82722394	1,500229045	0,000301656	0,010967954
AURKAIP1	869,1344534	1154,447397	1,328272504	0,000307247	0,01115398
PCBP3	119,0688485	171,5015666	1,440356304	0,00030878	0,011192311
SBNO2	4211,209053	5590,104015	1,32743446	0,000309891	0,011215291
ANKRD61	320,8777889	236,5419277	0,737171396	0,000313204	0,011317741
TNFRSF17	101,7670457	69,61746805	0,684086558	0,000322114	0,011606898
CYP20A1	958,0318154	713,2697121	0,744515684	0,000322194	0,011606898
KIR3DL1	236,6923693	303,1178984	1,280640771	0,000324313	0,011647487
MITF	165,5279759	117,9716771	0,712699328	0,000324182	0,011647487
ADARB2	406,5489796	548,5508103	1,349285911	0,000326742	0,011716826
GNG5	1501,873389	2016,820708	1,342869993	0,000327294	0,011718722
C21orf2	665,7968369	875,3606617	1,314756414	0,000328954	0,011760234
TMEM132A	58,71834408	85,73463555	1,460099683	0,00033319	0,011845864
MMP25	25112,96373	33544,42876	1,335741536	0,000335102	0,011845864
GAN	68,9075875	46,00166475	0,667584898	0,000334387	0,011845864
CLEC4G	30,73810833	46,11104885	1,500126434	0,000335888	0,011845864
EGF	226,121311	175,957248	0,778154201	0,000333819	0,011845864
PCDHGA10	216,445213	151,0863211	0,698034939	0,000335685	0,011845864
F13A1	10727,18384	8390,171393	0,782141102	0,000335275	0,011845864
HOXA10- HOXA9	96,15893997	62,12492035	0,646064946	0,000332318	0,011845864
PCLO	14,35561015	6,509011075	0,45341236	0,000334605	0,011845864
PDLIM7	2997,545767	3975,268412	1,326174384	0,000337692	0,011873834
PARP10	2185,85734	2942,75688	1,346271244	0,000337393	0,011873834
CCDC78	58,24814477	86,92227655	1,492275452	0,000339661	0,011925188
GIGYF1	2903,459535	3803,771396	1,310082455	0,000342247	0,011998051
ROMO1	197,3619121	266,0106962	1,347831977	0,000342886	0,012002531
MUC22	14,02622157	7,463478706	0,532108998	0,000344138	0,012028441
MYOM2	502,0122041	684,2030064	1,362921062	0,000348942	0,012178246
LOC100873065	72,01340243	48,76596474	0,677179012	0,000350053	0,012198877
S100P	3404,799748	4637,498512	1,362047361	0,000353719	0,012308357
RPS2	23088,94651	29803,40276	1,290808255	0,000356264	0,012378598
A2M	115,3027142	83,68162053	0,72575586	0,0003595	0,012454177
TEX15	5,977361625	1,822877477	0,304963559	0,000359088	0,012454177
PRR7-AS1	2706,575453	3638,011522	1,344138224	0,000361819	0,012516053
DUSP23	223,73261	303,3471177	1,355846686	0,000363119	0,012524144
FAM193B	2667,697196	3559,437269	1,334273348	0,000362975	0,012524144
LOC284009	54,0403362	34,16570104	0,632225916	0,000364958	0,012569094
ADCY4	296,4705523	414,6944771	1,398771223	0,000367361	0,012633335
CORO7- PAM16	5155,201316	6723,165378	1,304151859	0,000371971	0,012662113
UBALD1	513,3031965	678,8451554	1,322503269	0,000370274	0,012662113
GCA	15766,05865	21563,71431	1,367730184	0,000371967	0,012662113
MIR3199-1	26,73657381	15,37417287	0,575024047	0,000371019	0,012662113
MIR3199-2	26,73657381	15,37417287	0,575024047	0,000371019	0,012662113
PCDHGA4	350,9038812	252,2951679	0,718986541	0,000371291	0,012662113
MIR671	103,4678913	143,5577882	1,387462201	0,000370276	0,012662113

LOC100131347	244,6246006	347,9499401	1,422383273	0,000374723	0,012737313
CHST7	274,0718765	378,4940276	1,381002795	0,000376638	0,012783905
HLA-DRB6	86,37175829	58,27486961	0,674698197	0,000377286	0,012787445
ACVR2B	374,0904827	273,3438031	0,730689006	0,000382894	0,012958797
GAGE12B	4,078664182	0,673495122	0,165126397	0,000383743	0,012968845
FGFR2	76,62492817	52,52130587	0,685433672	0,000386086	0,013017335
MYH2	4,891629517	1,476411895	0,301824145	0,000386286	0,013017335
LIMD2	10096,50596	13167,64456	1,304178357	0,0003899	0,013082823
MIR4746	467,8054344	654,4784741	1,399039913	0,000389506	0,013082823
MIR3153	51,54530758	32,03648691	0,621520919	0,000389047	0,013082823
MIR4489	68,8204798	96,83252721	1,407030691	0,000391673	0,013123545
CHCHD3	4524,519633	3259,105489	0,720320775	0,000395109	0,013219826
RAMP1	23,45549988	36,60575198	1,560646849	0,000397153	0,013269305
HS6ST3	1,849289866	7,08336609	3,830316825	0,000399753	0,013337227
PCDHGB3	327,8653044	235,3170805	0,717724863	0,000400953	0,013358283
PCDHGB2	345,0121695	248,90444	0,721436697	0,000412268	0,013715806
SLFN12L	254,961216	198,4755123	0,778453741	0,000414261	0,013762592
CTSG	103,1329515	171,3043519	1,661005036	0,000414911	0,013764716
NRAP	5,872596244	1,660688295	0,28278605	0,000417744	0,013839156
CCDC108	5,17144771	1,627457793	0,314700619	0,000418407	0,013841613
SNORD75	455,8774914	333,4088002	0,731356135	0,000420679	0,013897199
SYTL4	91,63768507	65,89572133	0,719089764	0,000426075	0,014055691
PSMB10	3239,181795	4201,821064	1,297185934	0,000427015	0,014066934
AGPAT2	466,7908813	617,3329993	1,32250441	0,000428239	0,014087498
ARID5A	1691,556528	2241,561385	1,325147193	0,000429925	0,014123199
EIF3A	11615,99989	8638,974865	0,743713408	0,00043161	0,014158739
HDHD3	203,7293055	276,8135442	1,358732086	0,000435357	0,014261742
SNORD72	3416,006912	4493,208041	1,315339271	0,000438151	0,014333274
RNASEK	3540,239154	4630,723338	1,30802557	0,00044214	0,014443664
NR1H2	1582,084893	2035,405691	1,286533801	0,00044323	0,014459144
ATAD3B	465,3637161	623,057621	1,338861625	0,000452456	0,014736712
LGALS9B	43,63192922	61,53899645	1,410411998	0,000452993	0,014736712
MIR4709	596,9163032	798,633802	1,337932634	0,000454032	0,014750067
SPOCD1	101,5760386	155,2083266	1,528001375	0,000457845	0,014771799
E4F1	564,7170324	747,366518	1,323435411	0,000455513	0,014771799
CEMP1	269,2009627	355,2849831	1,31977605	0,000457388	0,014771799
TRAPPC6A	371,7738464	486,632631	1,308947995	0,000457718	0,014771799
GOLIM4	395,2750974	285,7267679	0,722855474	0,000456967	0,014771799
MIR937	9,315916776	18,0413347	1,936613984	0,000470789	0,015168587
CMTM2	2794,797646	3733,036973	1,335709216	0,000475278	0,01529222
LINC00623	145,6559616	109,7912165	0,75377084	0,000480632	0,015443359
AMZ2P1	276,8230402	385,010349	1,390817573	0,000483234	0,015505733
FBXL6	344,0445688	462,3661202	1,343913441	0,000486466	0,015588155
GRIN3B	113,9837017	156,3620152	1,371792746	0,000487288	0,015593208
SOCS3	1189,650776	1592,126033	1,338313785	0,000503433	0,016066064
TIGD5	51,08358417	72,53983044	1,420022334	0,000503298	0,016066064
ZNF264	1840,257187	1381,910182	0,75093318	0,00050495	0,016092616
TAF13	255,9183224	192,9327451	0,753884065	0,000513412	0,016340125
SCAND1	299,3962774	377,9993358	1,26253853	0,000519837	0,016499892
PF4	2283,870881	3167,032802	1,386695206	0,000519482	0,016499892

C1QTNF6	146,8647533	200,9589404	1,368326545	0,000522434	0,016537651
ADAMTS2	21,36887041	11,56778216	0,541338028	0,00052241	0,016537651
MIR938	2,679073952	7,918023824	2,955507749	0,00052334	0,016544018
C1orf177	90,00639225	63,83442466	0,709221013	0,000528539	0,016685915
CHCHD2	2014,062454	2628,409643	1,305028867	0,000531809	0,016766622
INF2	861,4950349	1113,822631	1,292895009	0,000534222	0,016820107
KLRC4	367,3633595	275,6092942	0,750236209	0,00054576	0,017160388
FLJ13224	31,19201505	19,48103797	0,624552083	0,000549578	0,017234312
HES6	33,78566221	48,87966097	1,446757523	0,000549311	0,017234312
P2RX1	2275,942014	3128,380061	1,374542955	0,000553795	0,017332004
GNG10	3173,916944	4290,19006	1,351702057	0,00055417	0,017332004
CARS2	2134,033537	2846,024011	1,333636029	0,000556447	0,017380084
C20orf27	638,862299	803,4506557	1,25762728	0,000557219	0,017381082
HERC5	1068,691291	1733,952502	1,622500826	0,00055868	0,017403563
KIAA1919	141,2606318	101,5088868	0,718592898	0,000561962	0,017482589
SREBF1	1238,593544	1621,536321	1,309175499	0,000565776	0,017577958
C11orf31	598,303878	787,7704019	1,316672732	0,000568665	0,017644402
MRPL23-AS1	21,04459157	33,73377179	1,602966333	0,00057205	0,017725994
MIR4511	19,08528965	11,32147216	0,593204105	0,000573113	0,017735554
RBCK1	3394,945878	4459,888024	1,313684572	0,000576908	0,017829493
MIR3615	5,793144029	10,85579815	1,873904412	0,000581725	0,01795474
LOC390660	7,190916193	15,26406957	2,122687729	0,000588937	0,018111335
BCL3	2012,735994	2656,50583	1,319848126	0,000588006	0,018111335
CNTNAP3B	20,06827678	8,699686018	0,433504387	0,000589112	0,018111335
PCDHA11	7,43305168	3,033265029	0,408078022	0,000590895	0,018142422
BMS1P1	14,37451413	7,080885717	0,492600004	0,000595695	0,018242089
BMS1P5	14,37451413	7,080885717	0,492600004	0,000595695	0,018242089
C4BPB	4,856556909	12,24038864	2,520384063	0,000601084	0,018359256
IGSF1	4,601055789	1,307487497	0,28417119	0,000601047	0,018359256
FLJ45445	1394,985588	1821,080506	1,305447541	0,000612787	0,01869239
TSR3	588,845323	756,8369539	1,285289913	0,000614522	0,018705925
DYNLL2	3843,175684	2910,983964	0,757442335	0,000616416	0,018705925
PLIN5	509,2575125	669,5585358	1,314773998	0,000615311	0,018705925
MIR4655	2,086967129	0,067776195	0,032475928	0,000616136	0,018705925
PCP2	54,4340509	79,94841641	1,468720683	0,00061985	0,018785868
DMBT1	5,813559391	2,212245925	0,380532093	0,000621308	0,018805766
ARHGEF1	15531,15552	20102,78606	1,294352247	0,000622913	0,018806258
MYEOV2	317,4965567	423,9566349	1,335310969	0,000622925	0,018806258
RLTPR	1166,639453	1530,162708	1,31159863	0,00062413	0,01881843
GP1BB	375,5609537	540,3352574	1,43874184	0,000630513	0,018962207
LOC391322	29,70856642	47,35951979	1,594136826	0,000630141	0,018962207
SNORA25	26,75145619	44,63750709	1,66860102	0,0006416	0,019197336
PITX2	2,438868315	0,309995447	0,127106267	0,000641394	0,019197336
SPDYE2	24,59441371	13,58835225	0,552497507	0,000640973	0,019197336
SPDYE2L	24,59441371	13,58835225	0,552497507	0,000640973	0,019197336
CLU	6203,460921	5053,792503	0,814673062	0,000644475	0,019258823
SNORA78	26,21218819	42,64319941	1,626846225	0,000652447	0,019451404
SLFN5	3797,07736	3007,559846	0,792072313	0,000652576	0,019451404
HMCN1	39,21152937	25,90244462	0,66058236	0,000659414	0,0196303
TNFAIP6	698,2896984	1005,982707	1,440638046	0,000661165	0,01965752

UBE2S	156,3854162	214,6813563	1,37277095	0,000662949	0,019685653
XKR3	77,44815732	116,915962	1,509602888	0,000667801	0,019804678
PPP1R16A	136,2839799	177,252169	1,300608987	0,000674349	0,019973667
FAM98B	480,6337397	363,5328581	0,756361504	0,000680232	0,020097216
PLXDC1	309,8841452	427,524535	1,379627005	0,00067949	0,020097216
KIAA1671	642,2654987	505,6975234	0,787365232	0,000682344	0,020134303
MIR4642	22,58571096	12,85839714	0,56931558	0,000683311	0,020137529
ISL2	158,1411804	214,4914478	1,356328865	0,000685306	0,020145759
MXRA5	4,680476943	1,424723569	0,304397092	0,000684694	0,020145759
SLC19A1	1929,775195	2492,75717	1,291734486	0,000703834	0,020614942
GRIP2	306,4588478	420,0011094	1,37049758	0,000702957	0,020614942
ARL14EPL	438,9503588	589,7534054	1,343553761	0,000703899	0,020614942
TMPO-AS1	219,5404586	160,0194425	0,728883612	0,00071119	0,020776658
C17orf70	571,0455473	734,4395761	1,286131342	0,000711093	0,020776658
FOS	3228,156178	4220,938994	1,307538657	0,000723328	0,021105009
ARHGEF17	52,7248073	32,88902039	0,62378645	0,000727788	0,021183142
CXCL6	34,22384835	55,82687748	1,631227351	0,00072781	0,021183142
SLC9A7P1	198,1822435	139,0163529	0,701457156	0,000739497	0,021496663
BCAT1	436,6375885	322,4669376	0,738523082	0,000743326	0,021581253
DMBX1	1,542275548	0	0	0,00074861	0,021707834
CACTIN-AS1	288,9121233	373,8626721	1,294035944	0,000754752	0,021725023
MIR1244-1	40,88513841	60,21216342	1,472715167	0,000754006	0,021725023
MIR1244-2	40,88513841	60,21216342	1,472715167	0,000754006	0,021725023
MIR1244-3	40,88513841	60,21216342	1,472715167	0,000754006	0,021725023
SUPT20HL1	2,105594184	0,13555239	0,064377263	0,000750674	0,021725023
TMEM255A	74,52501477	53,8492958	0,722566724	0,000752358	0,021725023
GYLTL1B	169,6352439	229,6597531	1,353844566	0,000758431	0,021804194
OLFML2A	40,00485817	22,99778027	0,574874686	0,000764129	0,021941153
LOC100505865	105,8641254	73,39262933	0,693271957	0,000766272	0,021949048
PFDN6	789,9939111	583,3990829	0,738485544	0,000766273	0,021949048
FAM89B	1495,191395	1937,570371	1,295867791	0,000775331	0,022051255
PLA2G4B	779,3594765	1029,040287	1,320366683	0,000773167	0,022051255
METTL16	1098,180087	835,0593925	0,760402963	0,000774627	0,022051255
MIR636	4,777845104	10,59364612	2,217243526	0,000772302	0,022051255
TFDP2	1300,485063	994,1988586	0,764483105	0,00077459	0,022051255
LOC152217	145,4177392	194,9549705	1,340654666	0,000775474	0,022051255
IL18RAP	3404,094307	4541,223325	1,334047448	0,000776832	0,022063158
APOA2	12,74294741	5,757702626	0,451834449	0,000778791	0,022092071
NOV	414,3479496	572,479814	1,381640273	0,000780292	0,022107959
TSTD3	25,83225154	14,37462435	0,556460374	0,000787493	0,022285116
PCDHGA6	313,2205453	228,1363692	0,728356976	0,000792166	0,022390375
PPDPF	1542,700386	2012,721334	1,304674162	0,000797059	0,022501585
SLC2A4RG	784,4592157	1002,299875	1,277695328	0,000798408	0,02251262
IFIT3	5366,090056	8311,841741	1,548956811	0,000801093	0,022561238
CSF3R	93296,16352	122013,3624	1,307806857	0,000803203	0,022566544
C10orf25	79,11164397	53,55076219	0,676901143	0,000802918	0,022566544
OIP5-AS1	956,6810191	753,6942733	0,787821916	0,000810139	0,022681735
METRNL	21,02501407	32,40173471	1,541104068	0,000809232	0,022681735
PPP1R12C	2246,321406	2862,46994	1,274292242	0,000810899	0,022681735
MIR1281	19,75315204	10,09865062	0,511242489	0,000811166	0,022681735

MIR4292	103,1070044	72,26357545	0,700860003	0,000814736	0,022754475
MIR548W	34,42586295	22,70319356	0,65948074	0,000818368	0,02282878
ABCA13	113,0998539	198,261224	1,752975068	0,000820425	0,022859018
DNASE1L2	14,58663699	25,735539	1,764322991	0,000833013	0,023182236
PRR14	1492,716725	1925,002549	1,289596691	0,000839473	0,023334356
HLA-F	9477,280666	12301,22873	1,29797029	0,000843768	0,023426043
TNFRSF18	86,43059765	111,0124427	1,284411374	0,000846574	0,02346755
RNF17	6,366169417	11,45944119	1,800052817	0,000847262	0,02346755
RPSAP58	1692,889035	1271,931535	0,751337807	0,000849162	0,023492472
ZNF101	1031,007769	782,9254851	0,759378841	0,000852841	0,023538799
EPB41L4A-AS1	229,7944232	304,6378556	1,32569734	0,000852001	0,023538799
TBL3	455,5194986	578,7988022	1,270634526	0,000856853	0,023589574
AATK	1646,095153	2155,677594	1,309570465	0,000857693	0,023589574
KLF2	5583,119513	7169,515415	1,284141491	0,000855713	0,023589574
CMKLR1	1823,998013	1393,340706	0,763893763	0,000875337	0,02404669
LIPM	8,454748935	18,13865927	2,145381183	0,00087951	0,024133108
CYHR1	1604,175039	2104,205239	1,311705511	0,000881391	0,024156493
SMA4	2231,494558	1566,556876	0,702021374	0,000883851	0,024195692
SUSD3	772,6174551	1018,204837	1,317864138	0,000886455	0,024238716
LOC400680	19,9960293	33,09527729	1,655092458	0,000888372	0,024251728
MIR5095	5340,519982	7310,223748	1,368822469	0,000888996	0,024251728
PUSL1	120,9870848	159,9572485	1,322101849	0,000892829	0,024322812
UBXN6	6831,687522	9288,350597	1,359598279	0,000893673	0,024322812
LINC00351	0	1,507642501	#DIV/0!	0,00089713	0,024360461
GLDC	34,27464904	22,3742926	0,652794215	0,000896313	0,024360461
DCAF15	1217,432146	1561,714959	1,282794251	0,000902929	0,0244896
OPLAH	118,3347273	162,0153718	1,369127858	0,000904208	0,024496005
MBD6	5267,736076	6755,921514	1,282509491	0,000905303	0,024497427
ZNF890P	14,4672939	26,62585864	1,840417347	0,000909515	0,02458306
SNORD61	144,33705	102,6933544	0,711482979	0,000913494	0,02466225
SNORD80	125,2848545	176,4538654	1,408421362	0,000918907	0,024779788
NSUN5P1	706,5055523	935,7408447	1,32446354	0,000919958	0,024779788
LOC339822	9,675975225	22,88461008	2,365095978	0,000921101	0,024782161
POLD4	2146,750113	2796,002639	1,302435072	0,000934009	0,025100683
C7orf43	2214,507135	2858,602543	1,290852713	0,000940432	0,025244419
GCHFR	166,6563773	219,2692413	1,315696674	0,000943025	0,025285115
PANK3	663,5928657	520,5694871	0,784471193	0,000945253	0,025315974
FBXW5	1586,131904	2011,501364	1,268180382	0,00094862	0,025377206
CCDC144C	20,22616674	11,52210106	0,569663111	0,000954238	0,025443087
MPO	459,8720601	728,9252983	1,585061067	0,000954332	0,025443087
TREML5P	6,645405768	13,9465915	2,098681704	0,000952864	0,025443087
EXOC3L1	18,66747868	33,47800505	1,793386542	0,000955959	0,025457563
MIR548Q	22,20739996	12,47716722	0,561847278	0,000957383	0,025466617
PKHD1L1	244,5488672	196,3611473	0,802952594	0,00096621	0,025672338
FCGRT	7447,661035	9416,536424	1,264361573	0,000974717	0,0258691
RNH1	2452,690889	3023,006853	1,232526637	0,0009844	0,026086485
OXLD1	336,5195934	433,0743802	1,286921739	0,000985893	0,026086485
BASP1	7772,258649	10221,53519	1,315130601	0,00098624	0,026086485
IDO1	248,5618567	332,3170873	1,336959305	0,000993071	0,026237621

GUSBP9	1067,179636	746,6344417	0,699633329	0,000994675	0,026250468
CHKB-CPT1B	3670,019015	4821,409802	1,313728834	0,000997963	0,026278197
ARRDC3-AS1	729,6621049	591,9075585	0,811207756	0,000997896	0,026278197
TIGD3	481,3242263	614,4631271	1,276609598	0,001000901	0,026326054
LOC100506321	716,4078044	527,3030596	0,73603757	0,001006037	0,026402013
LOC100129175	1,994814774	0,152941273	0,07666941	0,001005248	0,026402013
GGT5	57,83245804	78,54168589	1,358090051	0,001018306	0,026694167
LCT	19,56524031	11,64360361	0,595116821	0,001020187	0,026713672
TSTD1	479,2076491	630,8867141	1,316520542	0,001028575	0,026903295
PLEKHA5	208,2768503	156,9173472	0,753407529	0,001031371	0,026946439
MIR181A2HG	50,65899197	32,96793582	0,65078152	0,001037351	0,027072566
DOK3	7988,19175	10418,50956	1,304238792	0,001039975	0,027110924
GPBAR1	468,45355	585,0645975	1,248927663	0,00104951	0,027329158
KRT9	3,837347189	1,039830842	0,270976482	0,001050905	0,027335178
BOLA1	111,7629128	150,2735265	1,344574176	0,001055675	0,027342274
FCGR2B	1016,571871	1330,023727	1,308342051	0,001055694	0,027342274
CEACAM3	3150,037743	4235,141622	1,344473294	0,001055835	0,027342274
F8A1	417,8264401	550,1133028	1,316607208	0,001054066	0,027342274
ATG2A	2344,596912	3019,163206	1,287710988	0,001061361	0,027455124
CMPK2	584,7663136	925,5063093	1,582694296	0,001067991	0,02759622
NOL9	1131,576624	859,58179	0,759631978	0,001069405	0,027602398
WRAP73	810,6826733	1052,510871	1,298301919	0,001077992	0,027752372
RPS26	6667,640642	8313,569786	1,246853307	0,001079783	0,027752372
HMHA1	12108,2507	15442,3856	1,275360577	0,001078908	0,027752372
HMG5	128,799796	90,51046249	0,702722095	0,001079942	0,027752372
MYO9A	605,3477808	472,22177	0,780083425	0,00108181	0,027753933
LPAR2	3033,928833	3911,857268	1,289370148	0,001082366	0,027753933
GP6	208,8949593	161,8610613	0,774844265	0,001085066	0,027792828
DNAH17	1468,188559	1921,925255	1,309045248	0,001095422	0,027966605
ZNF467	1463,242968	1900,794759	1,299028802	0,001094122	0,027966605
FOXH1	157,9633784	211,044882	1,336036771	0,001094958	0,027966605
MYH1	4,042458524	1,185059509	0,293153165	0,001097819	0,027997353
LPPR2	2596,022507	3354,045677	1,291994067	0,001101884	0,028070542
CCL26	0,185230965	2,484833655	13,41478547	0,001108869	0,028217893
SNORA75	560,3996285	418,9879034	0,747659138	0,001112211	0,028272296
HCG9	14,5241969	24,60704451	1,694210336	0,001114824	0,028308095
CASKIN1	180,7717542	229,3729833	1,26885411	0,001118654	0,028374671
BAIAP2L1	704,5210902	559,5793688	0,794269152	0,00112691	0,028553261
HGS	2446,041592	3127,609562	1,278641202	0,001129348	0,028584187
CDR1	2,215154528	0,215488619	0,097279271	0,001160837	0,029349563
CCDC154	102,2946641	140,4604478	1,373096525	0,001170362	0,029558562
C10orf71	3,463937183	0,642023202	0,185344932	0,001174691	0,029614711
PCDHGB7	192,7326921	137,6393813	0,71414652	0,001175107	0,029614711
GUSBP9	1145,501222	809,3821159	0,706574642	0,001176822	0,029626145
HOTAIRM1	1051,856775	1424,27004	1,354053207	0,00117813	0,029627333
PRSS53	165,8537971	223,5905996	1,348118665	0,001190722	0,029911962
DNMBP-AS1	210,2014319	156,9823126	0,746818474	0,001197274	0,03004442
GUSBP3	1082,914395	759,7841196	0,701610509	0,001209082	0,03030834
CCL2	6,863009561	14,43362621	2,103104488	0,001218007	0,030499529
MYH4	4,895080176	1,914616147	0,391130702	0,001219884	0,030513996

MAPK8IP3	2342,655744	2991,082026	1,276791109	0,001223811	0,030579651
KRT23	2313,639395	3118,321167	1,347799131	0,001226153	0,030605604
SPATA5	337,9377799	258,5404475	0,7650534	0,001232263	0,030725481
LINC00173	284,9969436	378,5596997	1,328293893	0,001241538	0,030923897
PADI4	4523,815356	6014,476525	1,329514149	0,001247532	0,031040292
GOLGA8T	120,5732369	84,17210784	0,698099429	0,001249344	0,031045283
RYS1	142,4716713	100,1452352	0,702913318	0,001250376	0,031045283
SIPA1	5467,213689	7007,213333	1,281679066	0,00125265	0,031068896
RPL35	6031,49273	7481,952738	1,2404811	0,001274702	0,031582484
DNAJC4	777,5592626	1007,859439	1,296183439	0,001297464	0,031977802
RPS28	4757,734175	5760,848348	1,210838634	0,001294948	0,031977802
LAMA5	64,09157626	87,23309064	1,361069515	0,001296112	0,031977802
GFOD1	267,5691	200,5904663	0,749677247	0,001292886	0,031977802
DNAJC25- GNG10	3438,447153	4563,579293	1,327221007	0,001297161	0,031977802
ARHGAP31	1194,333181	891,4095824	0,746365919	0,00129909	0,031984302
ABCC8	8,947343762	4,10794682	0,459124733	0,001303763	0,032050812
HMG20B	738,4299196	941,2986153	1,274729789	0,001304907	0,032050812
SIGLEC1	468,3965256	713,8567419	1,524043632	0,001305885	0,032050812
RNASEK- C17orf49	4674,903315	5963,89077	1,275724944	0,001309825	0,032113967
GSN	4335,23114	5546,257486	1,279345278	0,001317768	0,032275018
HNRNPA1P10	28448,48864	21514,71571	0,756269199	0,001329034	0,032483196
FAM108A1	2558,134555	3299,061224	1,289635534	0,001328605	0,032483196
GAMT	62,73794233	86,36816598	1,376649644	0,001332551	0,032535289
ATP6V0C	4076,037395	5277,955503	1,294874161	0,001337161	0,032608299
SLPI	435,3915175	612,9496131	1,407812483	0,001338317	0,032608299
COL6A1	41,91954301	60,85467109	1,451701682	0,00134436	0,03267751
GBA3	128,4125095	93,96251154	0,731723972	0,001345332	0,03267751
UPK3B	38,58367472	54,7257867	1,418366371	0,001342701	0,03267751
PCDHGA11	188,6281044	134,867058	0,714989203	0,001350797	0,03277637
FBXL16	312,840266	394,2749588	1,260307581	0,001354491	0,032832081
IMPA2	1665,5351	2130,059651	1,278904089	0,001356711	0,032851984
ZC3H12A	720,1256691	932,2920301	1,294624077	0,001360221	0,032869199
LINC00304	8,979840529	17,28136703	1,924462575	0,001358995	0,032869199
C7orf69	4,779963939	1,014070603	0,212150262	0,00136215	0,032881988
MIR4258	36,61470177	22,21173643	0,606634367	0,001368669	0,033005449
RAPGEFL1	331,4081299	435,1558256	1,313051149	0,001382705	0,033241533
SECTM1	4969,963736	6413,334569	1,290418786	0,001381529	0,033241533
ZNF658	78,66287287	55,39136849	0,704161525	0,001380721	0,033241533
HOXA9	40,7071653	25,10837269	0,616804744	0,001390427	0,033392998
MBOAT7	12397,52966	15884,91437	1,281296743	0,001399625	0,033579568
DVL1	338,0023038	418,7110231	1,238781566	0,001402058	0,033587261
IGFLR1	1159,336655	1478,101343	1,274954378	0,001402806	0,033587261
CCDC88B	7851,118953	9960,665675	1,268693766	0,001408689	0,033693769
HSPA6	4235,224639	5553,865848	1,311350948	0,001415683	0,033826612
MGRN1	3154,74257	4064,62686	1,28841792	0,001417737	0,033841256
GRINA	3883,441008	5042,701696	1,298513788	0,001421173	0,033888845
CYGB	4,290696893	8,90937967	2,076441169	0,001428527	0,034029667
LRRC4C	4,693515096	10,96108021	2,335366987	0,001441106	0,034294528

IL1R2	2473,493324	3209,223565	1,297445816	0,001443335	0,034312804
SNORD38B	2855,988684	3661,913339	1,282187622	0,001446323	0,034349066
COL1A2	6,771118213	2,815102531	0,415751497	0,001454565	0,034509921
LINC00669	4,958539281	11,40988896	2,3010585	0,001458478	0,034567849
FMN1	542,6297909	409,0464317	0,75382229	0,001462308	0,034623679
FADS2	975,1878515	726,8374239	0,745330679	0,001464541	0,034641625
NRN1L	23,53970292	36,50768301	1,550898205	0,001472854	0,034803215
NAPA-AS1	3192,302491	4209,71174	1,318707031	0,001477655	0,034881575
LOC100288346	62,34312855	39,76067559	0,63777158	0,001481589	0,034939327
IDUA	400,5435689	509,2500857	1,271397484	0,001515502	0,035703222
PUS7L	364,1194742	285,5890788	0,784327945	0,001521504	0,035808708
ANAPC11	432,7563928	552,0282323	1,275609654	0,001536252	0,036119606
ZBTB37	134,0287499	102,8296361	0,767220736	0,001540805	0,036190429
UCKL1	795,6061641	1018,809073	1,280544469	0,001544341	0,036237252
LOC728012	0	1,500332614	#iDIV/0!	0,001549599	0,036324341
FBRSL1	1466,014258	1846,548392	1,259570555	0,001566309	0,036679423
COL9A3	133,7791067	179,0981346	1,338760133	0,0015683	0,036683958
C6orf226	43,78937124	60,65044569	1,385049476	0,001569626	0,036683958
PLEKHJ1	728,6146793	917,9601823	1,259870558	0,001572876	0,036723381
ATG4D	623,2064865	801,3091072	1,285784286	0,001576448	0,036770226
TMEM192	612,2562749	460,4871554	0,752115044	0,001580612	0,03682371
ANKRD34B	64,3028943	94,74130808	1,473359934	0,001581877	0,03682371
PTGFRN	106,1014137	75,58658364	0,712399402	0,001587462	0,036917137
PP7080	324,0973554	417,7565543	1,288984767	0,001592301	0,036993051
MIR3115	12,28689858	7,790220557	0,634026602	0,001595643	0,036995001
GLB1L2	147,03502	109,5509312	0,745066932	0,001595568	0,036995001
GLYCTK	394,706529	515,3881188	1,305750174	0,00159711	0,036995001
ATOH8	70,60332937	99,98016235	1,416082828	0,001607377	0,037183906
FAM156A	112,7334999	82,04601705	0,727787367	0,001608432	0,037183906
RPL41	34315,49397	26895,02643	0,78375752	0,001633486	0,037673761
SOWAHC	90,53359672	118,1813845	1,305387048	0,001632228	0,037673761
SNORA38	130,6365663	100,0647741	0,765978293	0,001634433	0,037673761
DNAH5	11,92376673	6,65687843	0,558286536	0,001641347	0,037796038
ANO6	3650,345871	2891,082779	0,792002424	0,001644016	0,037820415
ACER3	745,3121818	581,047197	0,779602442	0,001657021	0,038082298
CACNA1H	68,73570923	95,39878997	1,387907262	0,001669688	0,038335895
FBL	4304,098063	3206,465998	0,744979773	0,001688324	0,038688146
PCDHA12	6,753925133	2,880323756	0,42646664	0,001687649	0,038688146
MIEN1	683,0036306	882,0260457	1,291392909	0,0017077	0,039094004
KIAA1549L	7,914883496	3,611639287	0,456309848	0,001719129	0,039258334
F12	47,59336715	65,83988449	1,383383619	0,001719892	0,039258334
CDC26	913,276996	685,0227664	0,750071193	0,001716861	0,039258334
ABCC12	5,00278275	1,860124891	0,371818043	0,00173175	0,039490634
MAP1S	798,0046632	992,560726	1,243803165	0,001735345	0,03953423
OR8S1	1,793037347	0,115804887	0,064585876	0,001737175	0,03953757
FHDC1	153,9587325	221,0025148	1,435465928	0,001739306	0,039547751
TNFSF13B	3201,764281	4300,21845	1,343077776	0,001742763	0,039549767
NUDT16L1	530,2130451	686,5374609	1,294833213	0,001741484	0,039549767
PLXNA2	275,7138822	389,8326733	1,413902957	0,001747708	0,039579612
TMC6	4802,200913	6140,163999	1,278614558	0,001749133	0,039579612

MIR24-2	40,72475092	56,43438581	1,385751528	0,001746981	0,039579612
CNTN5	5,78724935	13,14561382	2,271478733	0,001767349	0,039947482
PCDHGA12	176,9786387	127,612161	0,721059682	0,001768792	0,039947482
OGN	10,39099246	4,816940396	0,463568847	0,001771021	0,039959403
MIR330	42,40310465	28,45268169	0,671004681	0,001779028	0,040101536
GPR97	6792,635117	8961,730877	1,319330528	0,001800279	0,04054166
HNRNPA1	29205,8278	22264,25115	0,762322208	0,001827772	0,041049781
POLRMT	657,0154519	818,6844243	1,246065708	0,001829833	0,041049781
KIR2DL4	36,03751673	48,17747805	1,336870085	0,001829639	0,041049781
MIR486	16,39909703	10,21302216	0,622779544	0,00182792	0,041049781
CCDC17	189,1417547	243,5512742	1,2876653	0,001838293	0,041200216
IGSF8	763,8632695	969,5854027	1,269318007	0,00184037	0,041207436
C21orf7	1986,315186	2652,625251	1,33545032	0,001842252	0,041210297
PANX1	486,5248342	378,3149973	0,777586201	0,001848655	0,041314193
TMEM256	200,7560169	260,730964	1,298745453	0,001853247	0,041377431
LTF	2612,984844	4380,995312	1,676624846	0,001862557	0,041545816
INPP5E	369,8601089	478,477183	1,293670692	0,001869447	0,04165994
SLC38A10	3178,226415	4003,249422	1,259585976	0,001886154	0,041992404
TMEM86B	444,8680405	586,0095219	1,31726595	0,001891601	0,04207379
THAP3	540,5773451	684,3950793	1,266044694	0,001902489	0,042077399
ANP32A-IT1	69,87208293	53,49710065	0,765643422	0,001903764	0,042077399
WDR90	122,8223274	162,8224138	1,325674388	0,001905709	0,042077399
LINC00854	178,3003681	132,0755467	0,740747471	0,001899159	0,042077399
SMIM5	209,043074	289,7668738	1,386158691	0,001896864	0,042077399
ARHGAP33	271,9760947	359,7758918	1,322821744	0,001906095	0,042077399
KIR2DL1	166,3425241	202,2695233	1,215982049	0,001900441	0,042077399
MAMDC4	80,01960009	109,6839621	1,3707137	0,001903171	0,042077399
ALPL	7487,976898	9913,609344	1,323936956	0,001914046	0,042213245
ASPRV1	429,3887392	575,2075065	1,339596161	0,001922928	0,042369345
YBEY	420,4992689	325,6513228	0,774439688	0,001927685	0,042394634
EVC	54,9153313	39,03387067	0,710800968	0,001927295	0,042394634
TMEM55A	1395,412888	1848,368687	1,324603422	0,001935523	0,04252719
LOC100216479	29,05291154	18,76207149	0,645789716	0,00194009	0,042584945
PGAM2	992,3990761	1293,034248	1,302937779	0,001941778	0,042584945
ZNF426	184,4400002	140,5587498	0,762083874	0,001948836	0,042699863
MIR939	52,51062573	73,24078725	1,394780318	0,001951534	0,042719138
SNORD81	171,3701588	230,6247344	1,345769509	0,001956906	0,042796844
SCO2	1174,02483	1540,963424	1,312547558	0,001958765	0,042797642
APOBEC3B	202,9848726	261,9392937	1,290437511	0,001961579	0,042819298
POP7	185,3400037	238,4489159	1,286548566	0,001982413	0,043193796
GLI4	486,6258471	621,1683218	1,27648033	0,001981473	0,043193796
ARHGAP9	11524,246	14697,42069	1,275347705	0,001998917	0,043432523
CLEC11A	100,5748135	70,11327997	0,697125627	0,001998899	0,043432523
SHARPIN	1696,70842	2233,241405	1,316219911	0,001998834	0,043432523
DFFA	359,4380773	272,8648626	0,759142895	0,002003332	0,043488228
MATN1	57,51978108	81,75403335	1,421320315	0,0020104	0,043601361
FAS-AS1	27,78892598	16,56023933	0,595929448	0,002013246	0,043614152
ZNF219	163,304779	210,8078187	1,29088579	0,002014703	0,043614152
NOS1	4,460294632	1,485843019	0,333126652	0,002023378	0,043721349
R3HDM4	16372,21981	21337,58095	1,303279653	0,002023304	0,043721349

FAT3	13,46351698	7,281799739	0,540854202	0,002029122	0,043805168
CAPN12	864,2716522	1110,503037	1,284900453	0,002033364	0,043855359
RELL2	718,5738858	917,5906756	1,276960788	0,002035181	0,043855359
TYMP	5650,381103	7120,870545	1,260246064	0,002045445	0,044036135
B3GAT3	931,2999256	1181,343086	1,268488329	0,002051228	0,044120182
DNM1	95,4966159	70,36980452	0,736882704	0,002069838	0,044479741
LENG8	9527,645452	12093,12338	1,269266729	0,002079167	0,044639379
NCAPH2	1665,01719	2144,624913	1,288049712	0,002087974	0,044787522
USP18	104,1278468	165,1818475	1,586336917	0,002094777	0,044892438
TLR3	83,47063666	64,33645028	0,770767456	0,00209726	0,044904695
PHC2	10465,70796	13406,91621	1,2810329	0,002104695	0,045022846
SMIM7	1179,731267	909,0190988	0,770530649	0,002112821	0,045155544
FADS3	204,0944703	267,7714883	1,311997762	0,00211763	0,045179514
CD320	386,0744968	496,8331129	1,286884052	0,002120222	0,045179514
SNRPD3	2156,151407	1669,651808	0,774366681	0,002121637	0,045179514
ARRDC1	1952,990454	2439,075395	1,248892635	0,002119664	0,045179514
CD14	8413,39914	10470,38406	1,244489164	0,002126348	0,045238821
ZNF668	126,839567	160,8790083	1,268366112	0,002129532	0,04526556
TAF10	1536,439103	1962,691668	1,277428871	0,002133664	0,045312383
FO XK1	2343,148517	1769,925708	0,755362153	0,002138245	0,045368663
ADM5	15,36571	24,95287458	1,623932417	0,002140365	0,045372641
ENTPD2	150,7192849	101,1691737	0,671242394	0,002147695	0,04548697
DDI2	380,8818482	300,8604424	0,789904911	0,002167306	0,045860969
LRFN1	293,226809	371,0193845	1,265298306	0,002182209	0,046134766
GFRA2	91,36217777	60,3121633	0,66014367	0,002188703	0,046230436
SLC17A1	6,43090766	2,410695774	0,374860891	0,002193867	0,046297888
MPST	338,5630504	441,1888207	1,30312159	0,002199079	0,046366224
TRAF3IP1	393,7551147	294,6071531	0,748198924	0,002201973	0,046385604
DGCR6L	448,478701	557,8234664	1,243812616	0,0022087	0,046485615
LOC338799	1701,353206	2216,76765	1,302943823	0,002242834	0,047134664
TAF1L	9,635887489	4,876438639	0,506070525	0,002243552	0,047134664
NSMF	764,4883823	968,669148	1,267081581	0,002249466	0,047182385
BMX	185,2101256	260,3086507	1,405477427	0,002249841	0,047182385
SYT11	1884,820276	1505,050844	0,798511595	0,002268795	0,047537419
CLCN7	2211,767088	2729,709408	1,234175796	0,002274311	0,047610536
OSM	140,6617494	187,1000775	1,330141836	0,002278697	0,047659881
ATG16L2	23132,44847	29826,27129	1,289369404	0,002287269	0,047796605
DPYSL4	24,43181381	33,73022365	1,380586145	0,002315852	0,048307931
KRT20	2,881485967	0,499622845	0,173390692	0,002315144	0,048307931
SNORD1C	102,7432565	73,83675597	0,718653063	0,002324884	0,048355491
PCDHGC3	165,0638522	119,7417282	0,725426716	0,002326367	0,048355491
SCGB3A2	8,262460015	15,4801701	1,873554616	0,002323826	0,048355491
GAGE2E	2,882697419	0,389090278	0,134974373	0,002321464	0,048355491
SLC30A4	121,6084115	90,7027089	0,745858841	0,002341405	0,048625046
CDK2AP2	1089,302051	1349,528379	1,238892719	0,002350722	0,048775409
SLC16A3	4711,207402	5986,97617	1,270794439	0,002363697	0,04895813
ZFH X4	11,11201552	5,596278431	0,503624065	0,002363042	0,04895813
INTS1	1923,413093	2381,932505	1,238388422	0,002371713	0,049080878
SNORA11B	43,29226134	32,30385253	0,746180761	0,002375241	0,04911062
C1orf173	20,39107727	12,92407737	0,633810426	0,002380412	0,049174254

GPR179	8,662146063	3,866496284	0,446367015	0,002383834	0,049201656
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* P adjusted for multiple testing (Benjamini-Hochberg)

Supplementary Table 8. Differentially enriched pathways in asymptomatic carriers of the *LRRK2* G2019S mutation compared to controls analyzed with two different pathway databases (KEGG and Reactome).

Database	Pathway	Genes in the pathway	Genes	p-value hyper	p-value fisher
REACTOME	Interferon alpha/beta signaling	14		5,44304E-08	3,13455E-06
REACTOME	O2/CO2 exchange in erythrocytes	5		1,1239E-06	0,000252102
REACTOME	NCAM1 interactions	10		1,71061E-06	6,15761E-05
REACTOME	Formation of Fibrin Clot (Clotting Cascade)	8		5,3617E-06	0,000192376
KEGG	ECM-receptor interaction	13		1,70101E-05	0,000231128
REACTOME	Interferon Signaling	19		2,30122E-05	0,000230908
REACTOME	Platelet degranulation	12		3,07654E-05	0,000387255
REACTOME	Extracellular matrix organization	13		4,13814E-05	0,000453168
REACTOME	Latent infection of Homo sapiens with Mycobacterium tuberculosis	7		5,88446E-05	0,001126218
REACTOME	Phagosomal maturation (early endosomal stage)	7		5,88446E-05	0,001126218
REACTOME	Response to elevated platelet cytosolic Ca2+	12		5,90659E-05	0,000631698
REACTOME	Platelet activation, signaling and aggregation	21		6,94524E-05	0,000606028
REACTOME	Platelet Adhesion to exposed collagen	4		0,000140324	0,0044788
REACTOME	NCAM signaling for neurite out-growth	10		0,000172193	0,001627139
REACTOME	Common Pathway	4		0,000210488	0,005573042
REACTOME	Alpha-defensins	4		0,000210488	0,005573042
REACTOME	Termination of O-glycan biosynthesis	5		0,000254801	0,004499469
REACTOME	Immune System	62		0,000345469	0,016651656
REACTOME	Collagen formation	9		0,000405493	0,003320867
REACTOME	Collagen biosynthesis and modifying enzymes	9		0,000405493	0,003320867
REACTOME	Pantothenate and CoA biosynthesis	4		0,000583528	0,0098838
KEGG	biosynthesis	4		0,000583528	0,0098838
REACTOME	Intrinsic Pathway	4		0,000583528	0,0098838
KEGG	Phagosome	15		0,00061799	0,004332681
REACTOME	Cell surface interactions at the vascular wall	11		0,00062857	0,004019602
REACTOME	Hemostasis	34		0,000723193	0,008482539
REACTOME	Transmission across Electrical Synapses	2		0,000747407	0,031254489
REACTOME	Electric Transmission Across Gap Junctions	2		0,000747407	0,031254489
REACTOME	Acyl chain remodeling of DAG and TAG	2		0,000747407	0,031254489
REACTOME	Degradation of the extracellular matrix	5		0,001507386	0,013811432

REACTOME	Activation of Matrix Metalloproteinases	5	0,001507386	0,013811432
KEGG	Glycosaminoglycan biosynthesis - chondroitin sulfate	4	0,002073395	0,020993945
REACTOME	Interferon gamma signaling	8	0,002102755	0,012010371
REACTOME	Metabolism Regulation of Complement cascade	73	0,002273385	0,159266948
REACTOME	Cyanoamino acid metabolism	3	0,00241292	0,031070257
KEGG	Linoleic acid (LA) metabolism	2	0,002449866	0,050732045
REACTOME	African trypanosomiasis	2	0,002449866	0,050732045
KEGG	Formation of a pool of free 40S subunits	5	0,002946524	0,021422356
REACTOME	Glutathione conjugation	10	0,002983336	0,013806306
REACTOME	O-linked glycosylation of mucins	4	0,003114595	0,026957129
REACTOME	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	7	0,003123998	0,017413976
REACTOME	GRB2:SOS provides linkage to MAPK signaling for Integrins	8	0,003142336	0,016114767
REACTOME	p130Cas linkage to MAPK signaling for integrins	3	0,003178327	0,036169701
REACTOME	CRMPs in Sema3A signaling	3	0,003178327	0,036169701
REACTOME	Activation of IRF3/IRF7 mediated by TBK1/IKK epsilon	3	0,004093745	0,041670476
REACTOME	Chondroitin sulfate/dermatan sulfate metabolism	3	0,004093745	0,041670476
REACTOME	Malaria	6	0,004105349	0,023393871
KEGG	Pertussis	6	0,0046143	0,025375773
KEGG	Oxidative phosphorylation	8	0,004966722	0,022562538
KEGG	Phosphorylation of the APC/C	11	0,005020024	0,023588495
REACTOME	Conversion from APC/C:Cdc20 to APC/C:Cdh1 in late anaphase	3	0,005171735	0,047565362
REACTOME	Rheumatoid arthritis	3	0,005171735	0,047565362
KEGG	L13a-mediated translational silencing of Ceruloplasmin expression	9	0,005322664	0,022435642
REACTOME	Amoebiasis	10	0,006238667	0,03083152
KEGG	Inhibition of the proteolytic activity of APC/C required for the onset of anaphase by mitotic spindle checkpoint components	10	0,006238667	0,03083152
REACTOME	Inactivation of APC/C via direct inhibition of the APC/C complex	3	0,006424174	0,053845622
REACTOME	GTP hydrolysis and joining of the 60S ribosomal subunit	3	0,006424174	0,053845622
REACTOME	Respiratory electron transport	10	0,006676444	0,031842096
REACTOME	Metabolism of proteins	7	0,006921397	0,030846414
REACTOME	Mitotic Spindle Checkpoint	29	0,007743159	0,046322031
REACTOME	Signaling by NODAL	3	0,00786218	0,060501207
REACTOME	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	3	0,00786218	0,060501207
REACTOME	Cytokine Signaling in Immune system	8	0,008132594	0,032472131
REACTOME		20	0,008166289	0,038991105

KEGG	Antigen processing and presentation	7	0,009002171	0,037301261
REACTOME	Developmental Biology	27	0,00908043	0,051298179
REACTOME	Chondroitin sulfate biosynthesis	3	0,009496058	0,067520926
REACTOME	Integrin cell surface interactions	8	0,010198334	0,057641424
REACTOME	Eukaryotic Translation Initiation	10	0,010448608	0,040618296
REACTOME	Cap-dependent Translation Initiation	10	0,010448608	0,040618296

Supplementary Table 9. Common differentially expressed 279 genes in symptomatic and asymptomatic carriers of the G2019S mutation compared to their respective controls (idiopathic PD and healthy non-carriers)

Gene	Fold Change*	Fold Change**	Padj*	Padj**
A2M	0,72575586	0,627887975	0,012454177	0,001483466
AATK	1,309570465	1,446298748	0,023589574	0,018702685
ADAMTS2	0,541338028	8,423720801	0,016537651	5,64348E-32
AKAP17A	#iDIV/0!	#iDIV/0!	3,53358E-05	3,53358E-05
ALKBH7	1,538784154	1,695902148	3,48042E-05	0,003861753
ANKRD22	1,533022373	2,531690702	0,005962801	3,66735E-20
ANKRD30BL	1,930845499	0,844505696	8,26524E-11	0,025720605
ANKRD61	0,737171396	0,656401535	0,011317741	0,011718716
ANP32A-IT1	0,765643422	0,626215473	0,042077399	0,017941295
APRT	1,340298913	1,516808311	0,004458485	0,022646796
ARL14EPL	1,343553761	1,63573717	0,020614942	0,00389053
ASMT	#iDIV/0!	26,92798911	2,5922E-05	0,000384433
ATP5D	1,479385748	1,721204291	6,09953E-05	0,003945871
AZU1	1,722542185	1,534154409	0,000496176	0,000348388
B3GNT8	1,590819591	1,856198443	6,9949E-06	3,90597E-05
C12orf57	1,420803148	1,482583512	0,000864532	0,048712213
C16orf13	1,550054124	1,534726404	7,93328E-06	0,029866674
C19orf24	1,41505517	1,538484953	0,00059222	0,019559219
C1orf122	1,544152658	1,649003526	0,000323498	0,007687643
C1orf177	0,709221013	0,558477893	0,016685915	0,00142264
C1orf228	1,486451204	1,365467876	0,000271154	0,048744184
C1orf233	1,507585117	1,552665462	0,001526479	0,049709099
C6orf1	1,456353635	1,525002815	0,000625221	0,01268576
C9orf16	1,614985296	1,61316516	2,05483E-06	0,015984435
CABP7	1,836314431	1,890776912	1,67254E-07	0,001065571
CAMP	1,725696884	1,344868085	0,005990726	0,033431272
CCDC168	0,503947834	0,358983231	0,000975049	0,000124819
CCL2	2,103104488	2,454690324	0,030499529	0,000832039
CD14	1,244489164	1,659609045	0,045238821	0,000581549
CEACAM6	1,804418612	1,329226068	0,002191051	0,032417186
CEACAM8	1,785138383	1,267401202	0,008901315	0,04542461
CHCHD10	1,409597901	1,673422696	0,002702402	0,000901759
CHRNA2	0,433309519	0,356945428	0,00703911	0,001670514
CHST13	1,407896933	1,629704758	0,005473685	0,006228223
CIRBP-AS1	0,626095429	0,665637186	4,46624E-05	0,020243482
CITED4	1,601444863	2,013523939	0,001902615	7,65201E-06
CLEC4E	1,429583105	1,488500029	0,001942225	0,034834374
CLEC4G	1,500126434	1,709412446	0,011845864	0,004989798
CLU	0,814673062	0,692378089	0,019258823	0,003097734
COL18A1	1,347225533	1,421208039	0,001681955	0,039046464
COX5B	1,390376363	1,469147712	0,002067826	0,041125797

COX8A	1,396684022	1,562917477	0,000980093	0,004045284
CRIP2	1,526835888	1,915783939	2,0571E-05	0,005790023
CST3	1,329514789	1,608971679	0,002327597	0,002829582
CTSG	1,661005036	1,422349421	0,013764716	0,001483828
CXXC11	1,760010175	2,171359531	0,010933003	0,001425913
DEFA1	3,013763758	1,350758553	9,87174E-17	0,018845166
DEFA1B	3,013763758	1,350758553	9,87174E-17	0,018845166
DEFA3	3,013763758	1,350758553	9,87174E-17	0,018845166
DEFA4	2,374707271	1,408807469	2,16369E-09	0,005302498
DGCR6L	1,243812616	1,496059011	0,046485615	0,042990592
DOC2A	1,837638537	1,742795402	6,92474E-08	0,020777132
DPYSL4	1,380586145	2,238155308	0,048307931	6,27661E-08
EFCAB4A	1,458659822	1,427867425	0,009291574	0,025756478
EIF3C	0,565342017	0,588517214	7,60283E-08	0,002338829
EIF3CL	0,562267467	0,585311791	5,94226E-08	0,001959857
ELANE	2,265343667	2,35873236	7,48852E-08	8,43568E-10
EVA1B	1,863007992	2,139282144	2,81057E-06	8,15145E-05
F8A2	1,48016368	1,635368861	0,003886776	0,019847882
F8A3	1,48016368	1,635368861	0,003886776	0,019847882
FAM173A	1,926940064	2,000608708	2,10243E-06	0,036556995
FAT1	0,456821323	0,397417153	0,006727186	0,041592517
FAT3	0,540854202	0,404695576	0,043805168	0,046314175
FGFR2	0,685433672	0,585499546	0,013017335	0,030937108
FLG2	0,405830939	0,286841288	0,002006608	0,001829813
FLJ13224	0,624552083	0,467167878	0,017234312	0,023399072
FLJ14107	2,183114507	0,293833209	1,5205E-06	9,04874E-11
FMOD	7,778034146	0,262328036	0,002950781	0,010639795
FN1	0,625755616	1,771980082	0,001154725	8,66497E-05
FSTL1	0,76676522	0,647334935	0,003159679	0,000412676
G0S2	2,08392488	1,702285398	3,63781E-05	0,007351276
GAGE1	0,01987089	0,049275287	5,26974E-05	1,42389E-06
GAGE12B	0,115262394	0,120160556	0,000864532	0,001956702
GAGE12C	0,082045899	0,104453266	5,84585E-05	0,000192332
GAGE12D	0,081314776	0,103511989	5,30095E-05	0,000172604
GAGE12E	0,082045899	0,104453266	5,84585E-05	0,000192332
GAGE12F	0,072314269	0,202156309	0,000103048	0,000127277
GAGE12G	0,082045899	0,104453266	5,84585E-05	0,000192332
GAGE12H	0,110051677	0,108559485	0,00047788	0,00093956
GAGE12I	0,082045899	0,104453266	5,84585E-05	0,000192332
GAGE2A	0,218202396	0,089408077	8,77269E-14	2,73211E-29
GAGE2B	0,109524865	0,078247142	0,000830087	1,25756E-06
GAGE2C	0,215382653	0,207939547	1,66817E-10	1,18659E-09
GAGE2D	0,240418181	0,117420252	7,65438E-05	0,000190399
GAGE2E	0,205734633	0,150810832	1,09926E-09	0,005293288
GAGE6	0,082045899	0,104453266	5,84585E-05	0,000192332
GAGE8	0,230774296	0,091979028	9,90827E-14	2,85872E-30
GBP1P1	1,950244803	3,246434688	0,002451657	9,44279E-20
GFOD1	0,749677247	0,62028433	0,031977802	0,00068734
GLIS2	1,505308366	1,620209281	0,007452259	0,026902787
GOLGA8T	0,698099429	0,432474336	0,031045283	3,64932E-08

GP6	0,774844265	0,738145174	0,027792828	0,04542461
GPBAR1	1,248927663	1,440220839	0,027329158	0,04597872
GPR112	0,322709526	0,191624359	0,001332005	0,001164532
H1FX	1,424816049	1,600141757	0,00013093	0,004290625
H2AFX	1,5503685	1,728900859	0,00013093	0,005430697
HBA1	1,675248296	1,886146635	1,04413E-05	0,000452745
HBA2	2,016316862	2,123478671	3,9147E-12	0,002134191
HBB	1,644944938	1,626056846	0,000303272	0,037321271
HBG1	0,653489806	2,368344747	1,58002E-10	1,10607E-11
HBQ1	2,280160347	2,013430646	5,86276E-12	0,01229438
HBZ	1,76335357	2,583685587	0,000520207	4,7664E-06
HELB	0,674367226	0,662419387	2,11958E-05	0,015030019
HLA-DQB1	1,286397007	1,539320733	0,002412368	1,02337E-07
HOXA10-				
HOXA9	0,646064946	0,559597507	0,011845864	0,005195641
ID3	1,403397776	1,698695977	0,002424436	0,00011749
IFI27	2,222989428	3,047299535	4,94815E-07	2,44744E-20
IFI44L	1,894809241	1,52053944	0,000217739	2,81868E-06
IFITM2	1,392944027	1,456907014	0,006709653	0,018702488
IL1R2	1,297445816	1,730099197	0,034312804	0,000149623
IRF7	1,585814423	1,488480482	6,9949E-06	0,033670708
IRS4	0,055672457	0,060169869	0,001962085	0,011973677
ISG15	2,295475826	1,559079207	2,20344E-11	0,016069078
ISL2	1,356328865	1,433682062	0,020145759	0,026607668
ITGA2B	0,754943071	0,619163682	0,000225292	5,55858E-05
ITGB3	0,747650334	0,643503289	0,000232453	0,000159079
JUND	1,359589744	1,585234249	0,001808643	0,02543415
KIR2DL1	1,215982049	0,67709722	0,042077399	0,000557048
KIR2DL4	1,336870085	0,883535013	0,041049781	0,003096492
KIR3DL1	1,280640771	0,747326675	0,011647487	0,000343332
KLRC4	0,750236209	0,596128517	0,017160388	0,002822274
LGALS8-AS1	0,615627086	0,562564907	0,000117249	0,003096388
LGALS9B	1,410411998	0,639477424	0,014736712	0,005476576
LIME1	1,864012101	1,927617688	4,92795E-12	0,000263515
LIPM	2,145381183	2,142571885	0,024133108	9,48141E-07
LOC100288346	0,63777158	0,532573572	0,034939327	0,000456078
LOC100505658	1,477333618	1,695235183	0,004062987	0,019491801
LOC284889	1,823078555	1,66069623	5,17929E-11	0,027132556
LOC285740	0,334059823	0,320906913	0,005884698	0,005378753
LOC606724	2,157366624	2,655062223	4,65042E-18	7,07908E-12
LOC728989	2,704389192	2,27301652	1,17096E-11	1,49626E-09
LRG1	1,504931063	1,505784963	0,000143867	0,009852984
LRP2	0,447760207	0,295052836	0,00047788	0,000101557
LRP3	1,407573974	1,609498972	0,006987386	0,011408441
LTF	1,676624846	1,4130157	0,041545816	0,002356945
LY6G6E	0,679101972	0,56466858	3,91138E-05	3,83594E-05
MAP1A	0,702488218	0,702676697	0,001836263	0,019633728
MFSD10	1,510733388	1,53830076	3,56585E-05	0,043039739
MIF	2,044660652	1,978488264	1,48922E-15	0,002397571
MIR1181	0,650309019	0,642752677	0,005546556	0,031253193

MIR1281	0,511242489	0,391136208	0,022681735	0,001013297
MIR181A2HG	0,65078152	0,547299429	0,027072566	0,000523937
MIR2110	0,502564031	0,472851679	0,000336688	0,006493843
MIR3184	0,428487392	0,409371885	0,001078863	0,004254519
MIR3194	35,07041716	3,109010837	1,7043E-14	0,00367597
MIR330	0,671004681	0,554345163	0,040101536	0,009907367
MIR3916	0,678859613	0,512262154	0,006995556	0,000590575
MIR3922	0,388175415	99,93881496	0,005411849	1,09686E-08
MIR423	0,455790455	0,423415313	0,001875535	0,00489516
MIR4655	0,032475928	#DIV/0!	0,018705925	2,11686E-09
MIR4709	1,337932634	1,631037549	0,014750067	0,003571294
MIR4721	1,40942284	1,64080786	0,003522556	0,002013093
MIR4749	1,736589664	2,228361661	0,00015503	3,83594E-05
MIR4784	2,608121762	2,75004323	4,87123E-11	6,76641E-06
MIR548Q	0,561847278	0,379594865	0,025466617	0,000498303
MIR611	0,577813171	0,585142872	7,24386E-07	0,002822274
MIR617	0,501588932	5,656615591	0,010501155	5,34514E-07
MIR632	0,489617428	0,456422202	5,552E-11	3,169E-07
MIR661	0,074255665	0,048261046	0,002798737	0,000136372
MMP8	2,506621297	1,921968985	3,39667E-08	1,88029E-10
MPO	1,585061067	1,495400523	0,025443087	0,000313254
MRPL41	1,802590636	2,154477508	1,75226E-08	0,000178879
MSLN	6,410557661	0,369428913	5,72473E-35	0,00491752
MT2A	1,445583685	1,559981683	0,00305047	0,007352457
MUC16	0,496851357	0,436854052	1,18679E-05	0,000509526
MUC17	0,42298176	0,354373799	0,000437652	0,000429584
MUC22	0,532108998	0,312196768	0,012028441	3,58103E-06
MUC6	0,391153241	0,413876965	1,34673E-05	0,000112294
MYH1	0,293153165	0,255406387	0,027997353	0,006608505
MYH7	0,43718199	0,104238056	0,008854024	1,15232E-20
MYOM2	1,362921062	0,444678597	0,012178246	3,05374E-16
NCAM1	0,637700332	0,569981584	0,000254602	6,90438E-06
NCF4	1,484567299	1,411162815	0,000176768	0,041125797
NCR1	0,671496446	0,560505053	0,001655385	1,07457E-05
NDUFB11	1,353702833	1,531584289	0,007813883	0,005248896
NINJ1	1,439504886	1,495464449	0,000588061	0,010087089
NLRP6	1,492619963	1,46256049	0,000149575	0,041018069
NME3	1,809274722	2,002899777	4,81699E-09	0,00287996
OPLAH	1,369127858	1,575380803	0,024496005	0,013264455
OTUD7B	0,703724925	0,662630432	0,001680909	0,016289111
OXER1	1,366753393	1,398678412	0,005958148	0,036251737
PANX2	1,403785713	1,606549631	0,00093956	0,002231328
PAR5	0,697368518	0,479387376	0,003159679	9,9075E-05
PCBD2	0,50458613	0,327085075	9,11957E-11	5,63163E-22
PCDHA1	0,391425579	0,491409235	2,98058E-05	0,010314525
PCDHA2	0,413205739	0,483512862	8,60218E-05	0,014042699
PCDHA3	0,435790005	0,478830916	0,000336688	0,013269792
PCDHA4	0,421924988	0,482624037	0,000439295	0,020243482
PCDHA5	0,440205752	0,477212841	0,001031917	0,021976197
PCDHA6	0,456345629	0,495200594	0,002791157	0,043512739

PCDHA7	0,43239775	0,489891758	0,002773939	0,047891036
PCDHA8	0,406765718	0,443393515	0,001972122	0,025756478
PCSK6	0,778795448	0,70346683	0,008484459	0,007352457
PGLYRP1	1,594811927	1,708774032	0,000203143	6,28337E-06
PKHD1L1	0,802952594	0,66959813	0,025672338	0,001045499
POLR2J3	0,705755236	0,625614893	0,006293868	0,001377037
PPFIA4	1,573587369	0,717692951	0,000296067	0,041125797
PPM1L	0,688847411	0,662981297	0,002196939	0,014371521
PROS1	0,734699933	0,618363886	0,001223252	6,69118E-05
PRR7-AS1	1,344138224	1,51786763	0,012516053	0,016875887
PRSS50	0,295375223	0,312410673	2,73389E-05	0,001450707
PTPRCAP	1,609772648	1,678737803	1,8315E-07	0,02134793
PUSL1	1,322101849	1,660718388	0,024322812	0,041125797
PYCARD	1,361765625	1,525452956	0,00530632	0,018845166
RAVER2	1,631050777	1,50406952	2,68555E-06	0,013232189
RBFOX2	1,657823827	2,123439583	1,40168E-05	3,44248E-06
RBP7	1,38055558	1,451117011	0,008374109	0,038262249
RHOG	1,342438802	1,50166848	0,00818135	0,017073466
RPLP1	1,46212003	1,6380853	6,84286E-05	0,004367959
RPLP2	1,473840098	1,54326879	5,30095E-05	0,016875887
RPS2	1,290808255	1,585176046	0,012378598	0,00404042
RPS28	1,210838634	1,393389969	0,031977802	0,023266239
S100A11	1,375038178	1,650391923	0,00593545	0,000886266
S1PR4	1,572588412	1,7528914	2,13918E-06	0,000772868
SAMD11	1,618532628	1,784602492	2,76978E-05	0,006341414
SAP25	1,713761243	1,562336551	3,13845E-09	0,0424796
SCARNA17	0,380270224	0,33846084	4,94145E-12	2,63086E-10
SEC14L5	0,708526708	0,653637084	0,002384317	0,000699873
SERPING1	1,553186945	1,361734775	0,006041178	0,015699651
SIGLEC1	1,524043632	1,664355539	0,032050812	1,0714E-07
SLC22A18	1,558628528	1,440409221	1,54318E-05	0,009131934
SLC22A18AS	1,509471462	1,678985172	0,001223252	0,0020297
SLFN12L	0,778453741	0,635654431	0,013762592	0,003365974
SLITRK3	0	0,074304099	0,005840074	0,024287333
SLPI	1,407812483	1,374356153	0,032608299	0,007687643
SMIM1	3,527080973	0,869901701	1,65636E-25	0,027109815
SNORA10	1,479979374	1,814537994	5,84585E-05	6,2066E-05
SNORA37	0,012768539	4,259341551	6,38454E-21	0,000117183
SNORA52	1,407841164	1,472551053	0,000424801	0,032530537
SNORD119	1,671742463	1,985515547	8,18729E-06	0,000126783
SNORD15A	0,496099976	0,509259387	1,40968E-14	7,6038E-07
SNORD26	0,683481939	0,63182408	0,008207441	0,041125797
SNORD33	1,552140867	1,993499767	1,32977E-06	2,91586E-06
SNORD34	1,33204565	1,49860655	0,005734406	0,018845166
SNORD42A	0,004112048	0,401140055	5,9848E-271	1,24067E-13
SNORD45A	0,62505174	0,554986305	5,59134E-05	0,000718267
SNORD49A	0,601173244	0,513968682	2,67964E-06	7,3821E-06
SNORD49B	0,586333991	0,504649899	3,25547E-07	2,71601E-06
SNORD53	0,613931627	0,518287859	0,005865786	0,005764133
SNORD58A	0,706845757	0,646638032	0,002047028	0,015544076

SNORD68	1,523320956	1,819499141	4,33266E-06	0,000492841
SNORD75	0,731356135	0,663332692	0,013897199	0,04063572
SNORD84	0,682936716	0,655741305	0,000842605	0,030793728
SPATA2L	1,584271417	1,69467324	5,70586E-05	0,018542374
SPDYE2	0,552497507	0,509252076	0,019197336	0,000509526
SPDYE2L	0,552497507	0,509252076	0,019197336	0,000509526
SREBF1	1,309175499	1,410255853	0,017577958	0,039739777
SULT2B1	0,505541758	0,48382179	0,002322993	0,002732814
SYCE1	0,471014456	2,144949677	0,003693726	0,000541308
SYTL4	0,719089764	0,668135755	0,014055691	0,011501092
TAF15	0,716547823	0,691473613	0,003690262	0,046213468
TAF1L	0,506070525	0,386380691	0,047134664	0,015387341
TEX15	0,304963559	0,324735527	0,012454177	0,038211946
TGM3	1,459806028	1,728973211	0,003222595	8,22105E-07
TIGD5	1,420022334	1,932828803	0,016066064	0,010093638
TKTL1	1,717923054	0,665852297	3,63781E-05	6,85115E-06
TMEM132A	1,460099683	1,863159883	0,011845864	0,003271281
TRAPPC5	2,055531706	2,282006588	2,44693E-14	3,74935E-06
TREX1	1,403877259	1,513995933	0,00305047	0,017061273
TSEN34	1,463836627	1,615121566	0,000249613	0,00308766
TSPO	1,600277	1,644495586	7,97784E-07	0,001754664
TSSC4	1,394800274	1,579217225	0,000981876	0,020376553
UBTD1	1,415959921	1,562495538	0,002950781	0,0020297
UGT2B11	1,525106164	0,578085744	0,005331431	0,001164532
USP32P1	1,908458311	0,730398358	2,71912E-06	0,020640809
VNN1	1,459904908	1,617733918	0,001018644	0,000112294
VNN2	1,416733743	1,460645324	0,010605578	0,034561571
WDR38	1,655698918	1,872565233	2,8335E-05	0,000564124
YDJC	1,48738569	1,647297704	0,00015503	0,040764922
ZDHHC12	1,46403204	1,566172914	0,000217739	0,009000092
ZFHX4	0,503624065	0,373717506	0,04895813	0,002340607
ZNF462	0,485444497	0,347094779	0,005814835	0,000214851
ZNF573	0,702390081	0,615058475	0,008488531	0,009510786
ZNF593	1,477473832	1,691504472	0,006427289	0,041125797

Padj: P adjusted for multiple testing (Benjamini-Hochberg)

* Controls/Non-PD G2019S carriers

** Idiopathic PD/LRRK2 G2019S-associated PD

Supplementary Table 10. Differentially enriched pathways by the 279 common genes deregulated in symptomatic and asymptomatic carriers of the G2019S mutation compared to their respective controls (idiopathic PD and healthy non-carriers) analyzed with two different pathway databases (KEGG and Reactome).

Database	Pathway	Observed Genes in the Pathway	Genes	p-value_hyper	p- value_fisher
REACTOME	Alpha-defensins Platelet	4		3,62918E-08	1,25066E-05
REACTOME	degranulation Response to elevated platelet	7		2,42539E-06	4,39795E-05
REACTOME	cytosolic Ca2+ O2/CO2 exchange	7		3,83371E-06	6,30552E-05
REACTOME	in erythrocytes Uptake of Carbon Dioxide and Release of Oxygen by	3		2,82249E-06	0,000337393
REACTOME	Erythrocytes Uptake of Oxygen and Release of Carbon Dioxide by	3		2,82249E-06	0,000337393
REACTOME	Erythrocytes Degradation of the extracellular matrix	3		2,82249E-06	0,000337393
REACTOME	Activation of Matrix Metalloproteinases	4		1,70358E-05	0,000489654
REACTOME	Platelet activation, signaling and aggregation	4		1,70358E-05	0,000489654
REACTOME	GRB2:SOS provides linkage to MAPK signaling for	9		8,42734E-05	0,000623941
REACTOME	Integrins p130Cas linkage to MAPK signaling for	3		1,75431E-05	0,000925036
REACTOME	integrins Antigen processing and presentation	3		1,75431E-05	0,000925036
KEGG	Termination of O- glycan biosynthesis	5		0,000104447	0,001267777
REACTOME	glycan biosynthesis	3		8,83182E-05	0,002466287
KEGG	Malaria	4		0,00019124	0,002637205
REACTOME	Defensins	4		0,000210541	0,002824516
REACTOME	Interferon Signaling Extracellular matrix	7		0,000436988	0,002848075
REACTOME	organization Integrin alphaIIb	5		0,000500372	0,004161732
REACTOME	beta3 signaling O-linked glycosylation of	3		0,000202668	0,004184459
REACTOME	mucins	4		0,000423041	0,004660975

REACTOME	Formation of a pool of free 40S subunits	5	0,000626597	0,004942587
REACTOME	Interferon alpha/beta signaling	4	0,000666255	0,006473358
REACTOME	Formation of Fibrin Clot (Clotting Cascade)	3	0,000397233	0,006484292
REACTOME	Latent infection of Homo sapiens with Mycobacterium tuberculosis	3	0,000448034	0,007018174
REACTOME	Phagosomal maturation (early endosomal stage)	3	0,000448034	0,007018174
REACTOME	L13a-mediated translational silencing of Ceruloplasmin expression	5	0,001050138	0,00734117
REACTOME	Interferon gamma signaling	4	0,000821064	0,007533331
KEGG	African trypanosomiasis	3	0,000503292	0,007577425
REACTOME	GTP hydrolysis and joining of the 60S ribosomal subunit	5	0,00110219	0,007618784
REACTOME	Signal transduction by L1	3	0,00062804	0,008773116
KEGG	Graft-versus-host disease	3	0,000697962	0,009410051
REACTOME	Platelet Aggregation (Plug Formation)	3	0,000697962	0,009410051
REACTOME	Eukaryotic Translation Initiation	5	0,001523786	0,009770105
REACTOME	Cap-dependent Translation Initiation	5	0,001523786	0,009770105
REACTOME	Cytokine Signaling in Immune system	8	0,003258769	0,01409736
REACTOME	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	4	0,002023173	0,014542146
KEGG	Transcriptional misregulation in cancer	6	0,003290922	0,01587515
REACTOME	Innate Immune System	11	0,002352698	0,016523408
KEGG	ECM-receptor interaction	4	0,002490181	0,016929962
KEGG	Hematopoietic cell lineage	4	0,002490181	0,016929962
REACTOME	Peptide chain elongation	4	0,002490181	0,016929962
REACTOME	Eukaryotic Translation	4	0,002490181	0,016929962

	Termination				
	Viral mRNA				
REACTOME	Translation	4	0,002490181	0,016929962	
REACTOME	Immune System	20	0,001175027	0,017076761	
	Metabolism of				
REACTOME	proteins	11	0,002903411	0,017851013	
	Ribosome,				
KEGG	eukaryotes	4	0,002750808	0,018210615	
KEGG	Ribosome	4	0,002888239	0,018872963	
	Eukaryotic				
	Translation				
REACTOME	Elongation	4	0,002888239	0,018872963	
	Formation of the				
	ternary complex,				
	and subsequently,				
REACTOME	the 43S complex	3	0,002014213	0,01915672	
	Nonsense Mediated				
	Decay Independent				
	of the Exon Junction				
REACTOME	Complex	4	0,003177816	0,020242142	
REACTOME	Hemostasis	11	0,004523787	0,022353155	
	Cell surface				
	interactions at the				
REACTOME	vascular wall	4	0,003650405	0,022408333	
REACTOME	Translation	5	0,005150752	0,02493325	
	Translation				
	initiation complex				
REACTOME	formation	3	0,003283563	0,026680131	
	Ribosomal scanning				
	and start codon				
REACTOME	recognition	3	0,003283563	0,026680131	
KEGG	Phagosome	5	0,005672906	0,026855788	
	Activation of the				
	mRNA upon				
	binding of the cap-				
	binding complex				
	and eIFs, and				
	subsequent binding				
REACTOME	to 43S	3	0,003500577	0,027866309	
	Influenza Viral				
	RNA Transcription				
REACTOME	and Replication	4	0,005153006	0,028857524	
	Cytosolic DNA-				
KEGG	sensing pathway	3	0,004732062	0,034212494	
KEGG	Amoebiasis	4	0,006533508	0,034349075	
	Nonsense-Mediated				
REACTOME	Decay	4	0,006533508	0,034349075	
	Nonsense Mediated				
	Decay Enhanced by				
	the Exon Junction				
REACTOME	Complex	4	0,006533508	0,034349075	
	SRP-dependent				
	cotranslational				
	protein targeting to				
REACTOME	membrane	4	0,006786316	0,035319549	
	Respiratory electron				
REACTOME	transport	3	0,005903952	0,039783102	
KEGG	Viral myocarditis	3	0,006555977	0,042730684	
	Complement and				
KEGG	coagulation	3	0,00689909	0,044244603	

KEGG	cascades				
	Parkinson's disease	4	0,0093747	0,044768191	
	The citric acid				
	(TCA) cycle and				
REACTOME	respiratory electron	4	0,0093747	0,044768191	
	transport				
	Oxidative				
KEGG	phosphorylation	4	0,010030124	0,047042722	
	Immunoregulatory				
	interactions between				
	a Lymphoid and a				
REACTOME	non-Lymphoid cell	3	0,00762031	0,04735198	
REACTOME	Phase II conjugation	3	0,007998726	0,048945136	