

SYMBOL	GRA AVG	DEFINITION	log2 fold GRA over cont	fdr corrected p-val
2700060E02Rik	7434.889	RIKEN cDNA 2700060E02 gene (2700060E02Rik), .	0.383812793	0.019600657
Adipoq	16540.57	adiponectin, C1Q and collagen domain containing (Adipoq), .	0.553532957	0.00026007
Angptl4	10690.15	angiopoietin-like 4 (Angptl4), .	0.554992476	0.023729982
Apoa2	15808.75	apolipoprotein A-II (Apoa2), .	4.836632035	0.003436353
Apoc1	11171.41	apolipoprotein C-I (Apoc1), .	1.352697109	0.019850593
Apoc3	7056.521	apolipoprotein C-III (Apoc3), .	2.11585018	0.010165543
Arl6ip1	6190.104	ADP-ribosylation factor-like 6 interacting protein 1 (Arl6ip1), .	0.519922191	0.036613543
Atp5j2	8624.181	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 (Atp5j2), nuclear gene encoding mitochondrial protein, .	1.057225945	3.82645E-12
C3	11370.27		0.487977528	0.020758003
Car3	7380.525	carbonic anhydrase 3 (Car3), .	-0.547677546	0.029255726
Cdo1	11985.05	cysteine dioxygenase 1, cytosolic (Cdo1), .	0.495058901	0.001442471
Cox5b	7480.194		0.990063374	0.035321838
Dbi	9871.458	diazepam binding inhibitor (Dbi), transcript variant 2, .	0.813789354	0.005679787
Ech1	7030.994	enoyl coenzyme A hydratase 1, peroxisomal (Ech1), .	0.360116268	0.030426313
Eif4a2	9981.087	eukaryotic translation initiation factor 4A2 (Eif4a2), .	0.489787766	0.001672318
Eif4ebp1	5975.057	eukaryotic translation initiation factor 4E binding protein 1 (Eif4ebp1), .	1.010426096	1.86206E-11
Glrx5	6565.361	glutaredoxin 5 homolog (S. cerevisiae) (Glrx5), .	0.821048523	2.76383E-05
Hba-a1	21382.14	hemoglobin alpha, adult chain 1 (Hba-a1), .	0.639107199	0.00016723
Hist1h1c	6547.146	histone cluster 1, H1c (Hist1h1c), .	0.547172926	0.000331527
Hnrnpc	5455.608	heterogeneous nuclear ribonucleoprotein C (Hnrnpc), .	0.34227444	0.042315813
Iscu	6780.109	IscU iron-sulfur cluster scaffold homolog (E. coli) (Iscu), .	0.43733291	0.01778235
LOC100047184	7307.121	PREDICTED: similar to proteasome alpha7/C8 subunit (LOC100047184), .	0.492191845	0.015215741
LOC100047998	5871.141	PREDICTED: similar to ribosomal protein L37a (LOC100047998), .	0.551453634	0.036315609
LOC100048483	10236.42	PREDICTED: similar to cytochrome c oxidase subunit VIII (LOC100048483), .	0.862469058	1.26198E-07
LOC675813	18683.62	PREDICTED: similar to ribosomal protein S20 (LOC675813), misc RNA.	0.351138272	0.035006971
Ly6a	8509.603	lymphocyte antigen 6 complex, locus A (Ly6a), .	0.809901669	8.52695E-05
Mup1	16787.5	major urinary protein 1 (Mup1), .	4.832952196	8.55625E-05
Mup2	13162.77	major urinary protein 2 (Mup2), transcript variant 1, .	3.654866188	0.002167587
Ndufa13	7939.892	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 (Ndufa13), .	0.866614961	0.000131667
Ormdl3	6214.068	ORM1-like 3 (S. cerevisiae) (Ormdl3), .	0.381484342	0.030741399
Prnp	7735.496	prion protein (Prnp), .	0.513386488	0.021186241
Psmb4	5740.027	proteasome (prosome, macropain) subunit, beta type 4 (Psmb4), .	0.474052479	0.002589496
Rpl27	5785.416	ribosomal protein L27 (Rpl27), .	0.571434965	0.002661749
Rpl38	6814.514	ribosomal protein L38 (Rpl38), transcript variant 1, .	0.788813686	0.000106301
Rpl41	20970.15	ribosomal protein L41 (Rpl41), .	0.370331233	0.024813426

Rps21	8805.866	ribosomal protein S21 (Rps21), .	0.599136317	0.006741366
Rps24	6575.233	ribosomal protein S24 (Rps24), transcript variant 1, .	0.768299151	0.00407016
Rps27l	7155.128	ribosomal protein S27-like (Rps27l), .	1.128695924	2.47375E-35
Sdpr	11224.65	serum deprivation response (Sdpr), .	0.46876483	0.03076393
Serpina1b	13627.65	serine (or cysteine) peptidase inhibitor, clade A, member 1b (Serpina1b), .	5.101169313	0.023626492
Serpina1d	11026.82	serine (or cysteine) peptidase inhibitor, clade A, member 1d (Serpina1d), .	4.974476361	0.024940575
Serpina3n	11298.65	serine (or cysteine) peptidase inhibitor, clade A, member 3N (Serpina3n), .	0.77160713	0.000350761
Slc25a5	6922.466	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (Slc25a5), nuclear gene encoding mitochondrial protein, .	0.488794454	0.001740831
Sod1	9057.116	superoxide dismutase 1, soluble (Sod1), .	0.747723228	2.01141E-07
Stt3b	8844.159	STT3, subunit of the oligosaccharyltransferase complex, homolog B (<i>S. cerevisiae</i>) (Stt3b), .	0.527507598	0.000572203
Sult1a1	7679.125	sulfotransferase family 1A, phenol-preferring, member 1 (Sult1a1), .	0.717786012	2.14815E-05
Ttr	10657.89	transthyretin (Ttr), .	5.295524242	0.019791212
Txnip	10826.42	thioredoxin interacting protein (Txnip), transcript variant 1, .	0.77360439	0.002463604
Uqcr	6074.836	ubiquinol-cytochrome c reductase (6.4kD) subunit (Uqcr), .	1.069270651	8.13335E-10
Wbp2	5752.439	WW domain binding protein 2 (Wbp2), .	0.402834389	0.013331362