

S2 Table. KEGG terms enriched in each group (95% confidence intervals). Similar to **S1 Table**, except that genes with significant deviations from the 95% confidence intervals of the major axis and minor axis were divided into 4 groups.

KEGG ID	P-value*	Odds Ratio	KEGG Term
Group 1			
3010	0.00	7.51	Ribosome
3008	0.00	4.38	Ribosome biogenesis in eukaryotes
190	0.00	2.73	Oxidative phosphorylation
3013	0.00	2.07	RNA transport
3050	0.00	4.00	Proteasome
5012	0.00	2.30	Parkinson's disease
5010	0.00	2.30	Alzheimer's disease
3040	0.00	2.10	Spliceosome
5016	0.00	1.78	Huntington's disease
4260	0.00	3.06	Cardiac muscle contraction
270	0.00	3.68	Cysteine and methionine metabolism
480	0.00	3.96	Glutathione metabolism
1230	0.00	2.55	Biosynthesis of amino acids
4978	0.00	3.22	Mineral absorption
5322	0.01	2.08	Systemic lupus erythematosus
4932	0.01	1.66	Non-alcoholic fatty liver disease (NAFLD)
4140	0.01	2.97	Regulation of autophagy
1200	0.01	1.91	Carbon metabolism
330	0.02	2.63	Arginine and proline metabolism
4145	0.02	1.66	Phagosome
3060	0.04	2.41	Protein export
Group 2			
3018	0.00	3.12	RNA degradation
3040	0.00	2.15	Spliceosome
3015	0.00	2.35	mRNA surveillance pathway
3020	0.01	2.73	RNA polymerase
3013	0.01	1.60	RNA transport
900	0.02	3.37	Terpenoid backbone biosynthesis
240	0.03	1.80	Pyrimidine metabolism
4141	0.03	1.51	Protein processing in endoplasmic reticulum
4530	0.04	1.72	Tight junction
4919	0.04	1.68	Thyroid hormone signaling pathway
5100	0.05	1.81	Bacterial invasion of epithelial cells
Group 3			

5231	0.00	3.51	Choline metabolism in cancer
4070	0.00	3.51	Phosphatidylinositol signaling system
4650	0.00	3.42	Natural killer cell mediated cytotoxicity
4662	0.00	3.42	B cell receptor signaling pathway
4930	0.00	6.36	Type II diabetes mellitus
4973	0.00	6.36	Carbohydrate digestion and absorption
5160	0.00	2.80	Hepatitis C
5223	0.00	3.92	Non-small cell lung cancer
561	0.00	4.71	Glycerolipid metabolism
4015	0.00	2.19	Rap1 signaling pathway
5162	0.00	2.62	Measles
4725	0.00	2.73	Cholinergic synapse
5205	0.00	2.07	Proteoglycans in cancer
5230	0.00	2.98	Central carbon metabolism in cancer
5218	0.00	3.59	Melanoma
1100	0.00	1.41	Metabolic pathways
5213	0.00	3.07	Endometrial cancer
5214	0.00	3.07	Glioma
5221	0.00	3.18	Acute myeloid leukemia
4664	0.00	3.18	Fc epsilon RI signaling pathway
531	0.00	10.53	Glycosaminoglycan degradation
4150	0.00	2.66	mTOR signaling pathway
4012	0.00	2.66	ErbB signaling pathway
4380	0.00	2.52	Osteoclast differentiation
4919	0.00	2.14	Thyroid hormone signaling pathway
4370	0.00	3.00	VEGF signaling pathway
5200	0.01	1.66	Pathways in cancer
5144	0.01	16.83	Malaria
4014	0.01	1.92	Ras signaling pathway
4940	0.01	Inf	Type I diabetes mellitus
4210	0.01	2.63	Apoptosis
4660	0.01	2.36	T cell receptor signaling pathway
4666	0.01	2.27	Fc gamma R-mediated phagocytosis
4611	0.01	2.19	Platelet activation
5152	0.01	2.03	Tuberculosis
4810	0.01	1.79	Regulation of actin cytoskeleton
564	0.01	2.38	Glycerophospholipid metabolism
4917	0.01	2.74	Prolactin signaling pathway
5215	0.01	2.27	Prostate cancer
4960	0.01	3.38	Aldosterone-regulated sodium reabsorption
4062	0.01	1.90	Chemokine signaling pathway
5164	0.01	1.94	Influenza A
4142	0.01	1.94	Lysosome

4066	0.01	2.06	HIF-1 signaling pathway
4071	0.01	2.01	Sphingolipid signaling pathway
4720	0.01	2.59	Long-term potentiation
562	0.01	2.59	Inositol phosphate metabolism
4022	0.02	1.89	cGMP-PKG signaling pathway
5142	0.02	2.20	Chagas disease (American trypanosomiasis)
4921	0.02	1.92	Oxytocin signaling pathway
4750	0.02	2.64	Inflammatory mediator regulation of TRP channels
4914	0.02	1.91	Progesterone-mediated oocyte maturation
5212	0.02	2.49	Pancreatic cancer
4923	0.03	2.81	Regulation of lipolysis in adipocytes
4144	0.03	1.59	Endocytosis
4723	0.03	2.53	Retrograde endocannabinoid signaling
4620	0.03	2.35	Toll-like receptor signaling pathway
4640	0.04	3.16	Hematopoietic cell lineage
4974	0.04	3.16	Protein digestion and absorption
5033	0.04	Inf	Nicotine addiction
5145	0.04	1.96	Toxoplasmosis
4510	0.04	1.64	Focal adhesion
5222	0.04	2.03	Small cell lung cancer
4010	0.04	1.55	MAPK signaling pathway
4550	0.04	1.73	Signaling pathways regulating pluripotency of stem cells
5220	0.05	2.02	Chronic myeloid leukemia
4722	0.05	1.71	Neurotrophin signaling pathway
1210	0.05	4.20	2-Oxocarboxylic acid metabolism

Group 4			
4060	0.00	4.22	Cytokine-cytokine receptor interaction
4630	0.00	3.41	Jak-STAT signaling pathway
4080	0.00	5.09	Neuroactive ligand-receptor interaction
980	0.00	7.57	Metabolism of xenobiotics by cytochrome P450
5321	0.00	9.92	Inflammatory bowel disease (IBD)
310	0.00	3.70	Lysine degradation
4550	0.00	2.21	Signaling pathways regulating pluripotency of stem cells
2010	0.00	5.67	ABC transporters
4913	0.00	4.06	Ovarian steroidogenesis
534	0.00	Inf	Glycosaminoglycan biosynthesis - heparan sulfate
4020	0.01	2.28	Calcium signaling pathway
5217	0.01	4.96	Basal cell carcinoma
140	0.02	7.07	Steroid hormone biosynthesis
982	0.02	7.07	Drug metabolism - cytochrome P450

5166	0.02	1.60	HTLV-I infection
5204	0.02	3.96	Chemical carcinogenesis
5150	0.02	11.30	Staphylococcus aureus infection
4350	0.03	2.03	TGF-beta signaling pathway
4724	0.03	2.09	Glutamatergic synapse
450	0.03	4.71	Selenocompound metabolism
4916	0.04	1.94	Melanogenesis
4912	0.04	1.99	GnRH signaling pathway
4514	0.04	2.23	Cell adhesion molecules (CAMs)
5032	0.04	2.13	Morphine addiction
4610	0.04	5.65	Complement and coagulation cascades

*P values were calculated with hypergeometric test. The background gene set in the enrichment analysis is all genes in the three other groups.