Supplementary Table 4. KEGGS analysis

Cell Communication	9	O=9;E=9;R=1;P=1.02e+4
Tight junction	8	O=8;E=8;R=1;P=1.95e+4
Leukocyte transendothelial migration	8	O=8;E=8;R=1;P=1.95e+4
Glycolysis / Gluconeogenesis	8	O=8;E=8;R=1;P=1.95e+4
Complement and coagulation cascades	8	O=8;E=8;R=1;P=1.95e+4
Adherens junction	7	O=7;E=7;R=1;P=4.04e+4
Antigen processing and presentation	7	O=7;E=7;R=1;P=4.04e+4
Neurodegenerative Disorders	5	O=5;E=5;R=1;P=2.36e+5
Cell cycle	4	O=4;E=4;R=1;P=6.94e+5
Arginine and proline metabolism	4	O=4;E=4;R=1;P=6.94e+5
Nitrogen metabolism	4	O=4;E=4;R=1;P=6.94e+5
PPAR signaling pathway	4	O=4;E=4;R=1;P=6.94e+5
MAPK signaling pathway	4	O=4;E=4;R=1;P=6.94e+5
Gap junction	4	O=4;E=4;R=1;P=6.94e+5
Axon guidance	3	O=3;E=3;R=1;P=6.60e-1
Phenylalanine, tyrosine and tryptophan biosynthesis	3	O=3;E=3;R=1;P=6.60e-1
Oxidative phosphorylation	3	O=3;E=3;R=1;P=6.60e-1

O is the observed gene number in the KEGG pathway; E is the expected gene number in the KEGG pathway(Expected number of genes in a specific KEGG pathway for an interesting gene set=Total number of genes in the KEGG pathway for the reference set * Total number of genes in the interesting set / Total number of genes in the reference set); R is the ration of enrichment for the KEGG pathway (R=O/E); P is the p value indicating the significance of enrichment calculated from Fisher's exact test. It is given for the KEGG pathways with R>1. A minimum number of at least 2 genes with p<0.01 is selected for the enriched KEGG pathways. KEGG pathways with fewer genes are not reported as enriched KEGG pathways.