Table S5: Top GO term leaves in k-means clustering

Cluster	GOTERM	Description	Counts	Category	p-value
1	GO:0006888	ER to Golgi vesicle-mediated transport	11	64	3.69×10^{-8}
1	GO:0007030	Golgi organization and biogenesis	3	9	5.64×10^{-4}
1	GO:0015031	protein transport	24	635	1.46×10^{-3}
1	GO:0000184	mRNA catabolic process, nonsense-mediated decay	3	15	2.80×10^{-3}
1	GO:0006465	signal peptide processing	2	5	3.64×10^{-3}
1	GO:0043154	negative regulation of caspase activity	2	7	7.46×10^{-3}
2	GO:0006118	electron transport	30	403	3.24×10^{-5}
2	GO:0006637	acyl-CoA metabolic process	4	14	9.29×10^{-4}
2	GO:0051657	maintenance of organelle localization	2	2	1.11×10^{-3}
2	GO:0006659	phosphatidylserine biosynthetic process	2	2	1.11×10^{-3}
2	GO:0043410	positive regulation of MAPKKK cascade	3	7	1.12×10^{-2}
2	GO:0019585	glucuronate metabolic process	2	3	3.24×10^{-2}
3	GO:0007186	G-protein coupled receptor protein signaling pathway	94	606	1.32×10^{-9}
3	GO:0006813	potassium ion transport	30	154	8.06×10^{-6}

3	GO:0042472	inner ear morphogenesis	12	40	6.21 x 10^{-5}
3	GO:0001755	neural crest cell migration	8	21	1.66 x 10^{-4}
3	GO:0006814	sodium ion transport	20	104	3.02 x 10^{-4}
3	GO:0042523	positive regulation of tyrosine phosphorylation of Stat5 protein	3	3	5.68 x 10^{-4}
3	GO:0042135	neurotransmitter catabolic process	5	10	6.86 x 10^{-4}
3	GO:0007409	axonogenesis	23	137	8.45 x 10^{-4}
4	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB cascade	23	46	2.26 x 10^{-8}
4	GO:0007229	integrin-mediated signaling pathway	30	79	4.21 x 10^{-7}
4	GO:0019886	antigen presentation, exogenous peptide antigen via MHC class II	11	16	1.70 x 10^{-6}
4	GO:0019221	cytokine and chemokine mediated signaling pathway	19	42	2.64 x 10^{-6}
4	GO:0030593	neutrophil chemotaxis	10	14	3.04 x 10^{-6}
4	GO:0042535	positive regulation of tumor necrosis factor-alpha biosynthetic process	7	8	1.15 x 10^{-5}
4	GO:0045087	innate immune response	25	70	1.35 x 10^{-5}
4	GO:0007015	actin filament organization	19	48	2.77 x 10^{-5}

GO term leaves were generated based on the induced GO graph resulting from all significant GO terms ($p < 0.01$). [a]Number of differentially expressed genes in a GO term category (false discovery rate < 0.01); [b]Total number of genes in a GO term category