

Table S4 GO functional enrichment analysis

Category	GO Term	Go identifier	Count	(%)	P value	FDR
GOTERM_BP_DIRECT	inflammatory response	GO:0006954	15	53.57	5.00E-17	3.79E-14
GOTERM_BP_DIRECT	cellular response to lipopolysaccharide	GO:0071222	10	35.71	3.40E-12	1.29E-09
GOTERM_BP_DIRECT	positive regulation of angiogenesis	GO:0045766	9	32.14	4.51E-11	1.14E-08
GOTERM_CC_DIRECT	extracellular space	GO:0005615	17	60.71	1.83E-10	1.61E-08
GOTERM_BP_DIRECT	positive regulation of gene expression	GO:0010628	10	35.71	1.93E-08	3.65E-06
GOTERM_BP_DIRECT	positive regulation of interleukin-8 production	GO:0032757	6	21.43	2.86E-08	4.33E-06
GOTERM_BP_DIRECT	neutrophil chemotaxis	GO:0030593	6	21.43	9.28E-08	1.17E-05
GOTERM_MF_DIRECT	cytokine activity	GO:0005125	7	25	2.59E-07	3.06E-05
GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	GO:0032755	6	21.43	2.92E-07	3.16E-05
GOTERM_BP_DIRECT	regulation of insulin secretion	GO:0050796	5	17.86	5.25E-07	4.71E-05
GOTERM_BP_DIRECT	positive regulation of ERK1 and ERK2 cascade	GO:0070374	7	25	6.20E-07	4.71E-05
GOTERM_BP_DIRECT	positive regulation of nitric oxide biosynthetic process	GO:0045429	5	17.86	6.22E-07	4.71E-05
GOTERM_BP_DIRECT	positive regulation of leukocyte adhesion to vascular endothelial cell	GO:1904996	4	14.29	8.86E-07	6.10E-05
GOTERM_BP_DIRECT	astrocyte activation	GO:0048143	4	14.29	1.65E-06	1.04E-04
GOTERM_BP_DIRECT	positive regulation of cytokine production	GO:0001819	5	17.86	2.08E-06	1.21E-04