

**Table S2:** Significant pathways from classical enrichment-based pathway analysis method (hypergeometric enrichment test)

Pathway ID	DE Genes of Total Genes	p.value	adj. p.value
Complement and coagulation cascades	18 of 64	4.161645 e-09	1.0000 e-06
Hematopoietic cell lineage	18 of 91	1.373304 e-06	1.7200 e-04
Cholesterol metabolism	11 of 37	2.395551 e-06	2.0000 e-04
Neutrophil extracellular trap formation	24 of 165	8.412235 e-06	5.2800 e-04
Osteoclast differentiation	20 of 125	1.113291 e-05	5.5900 e-04
ECM-receptor interaction	14 of 71	2.082788 e-05	7.9000 e-04
Platelet activation	18 of 110	2.204351 e-05	7.9000 e-04
Cytokine-cytokine receptor interaction	26 of 210	6.397349 e-05	2.0070 e-03
PPAR signaling pathway	11 of 57	1.925433 e-04	5.3700 e-03
IL-17 signaling pathway	13 of 78	2.448530 e-04	6.1460 e-03
Neuroactive ligand-receptor interaction	23 of 197	3.901925 e-04	8.2720 e-03
Phagosome	18 of 137	3.954733 e-04	8.2720 e-03
Glycerolipid metabolism	9 of 50	1.226986 e-03	2.3291 e-02
JAK-STAT signaling pathway	16 of 128	1.391876 e-03	2.3291 e-02
Fat digestion and absorption	6 of 24	1.377990 e-03	2.3291 e-02
Calcium signaling pathway	20 of 185	2.310244 e-03	3.6242 e-02