

Supplement Table 2. GSEA: Enriched gene sets (Hallmark and C7).

MSigDB collection	Gene set name	NES	NOM p-val	FDR q-val
h.all.v6.2.symbols.gmt				
FABP4 high expression	HALLMARK_ANGIOGENESIS	2.150	0	0.001
	HALLMARK_APICAL_JUNCTION	2.280	0	0
	HALLMARK_COAGULATION	2.260	0	0.001
	HALLMARK_COMPLEMENT	2.190	0	0.001
	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	2.290	0	0.001
	HALLMARK_IL2_STAT5_SIGNALING	2.170	0	0.001
	HALLMARK_INFLAMMATORY_RESPONSE	2.130	0	0.001
	HALLMARK_KRAS_SIGNALING_UP	2.420	0	0
	HALLMARK_MYOGENESIS	2.220	0	0.001
	HALLMARK_UV_RESPONSE_DN	2.110	0	0.001
FABP4 low expression	HALLMARK_MYC_TARGETS_V2	-1.980	0	0.018
	HALLMARK_E2F_TARGETS	-1.840	0.027	0.044
c7.all.v6.2.symbols.gmt				
FABP4 high expression	GSE10325_CD4_TCELL_VS_MYELOID_DN	2.450	0	0
	GSE14000_4H_VS_16H_LPS_DC_TRANSLATED_RNA_UP	2.370	0	0
	GSE1460_CD4_THYMOCYTE_VS_THYMIC_STROMAL_CELL_DN	2.450	0	0
	GSE19888_ADENOSINE_A3R_ACT_VS_TCELL_MEMBRANES_ACT_IN_MAST_CELL_UP	2.360	0	0
	GSE21380_NON_TFH_VS_TFH_CD4_TCELL_UP	2.430	0	0
	GSE21774_CD62L_POS_CD56_BRIGHT_VS_CD62L_NEG_CD56_DIM_NK_CELL_UP	2.440	0	0
	GSE30971_CTRL_VS_LPS_STIM_MACROPHAGE_WBP7_KO_4H_DN	2.490	0	0
	GSE30971_WBP7_HET_VS_KO_MACROPHAGE_2H_LPS_STIM_UP	2.400	0	0
	GSE3982_DC_VS_EFF_MEMORY_CD4_TCELL_UP	2.440	0	0
	GSE6259_CD4_TCELL_VS_CD8_TCELL_UP			
	GSE18893_TCONV_VS_TREG_24H_TNF_STIM_UP			

NES: normalized enrichment score; NOM: nominal p-value; FDR: false discovery rate. Gene sets with NOM p-value less than 0.05 and FDR q-value less than 0.06 were considered as statistical significance.

Supplement Table 2. GSEA: Enriched gene sets (KEGG).

MSigDB collection	Gene set name	NES	NOM	FDR
			p-val	q-val
c2.cp.kegg.v7.4.symbols.gmt				
FABP4 high expression	KEGG_CELL_ADHESION_MOLECULES_CAMS	2.170	0	0.001
	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	2.210	0	0
	KEGG_ECM_RECEPTOR_INTERACTION	2.190	0	0
	KEGG_FOCAL_ADHESION	2.300	0	0
	KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	2.340	0	0
	KEGG_MELANOMA	2.060	0	0.005
	KEGG_PATHWAYS_IN_CANCER	2.070	0	0.005
	KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	2.140	0	0.002
	KEGG_TGF_BETA_SIGNALING_PATHWAY	2.050	0	0.005
	KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	2.050	0	0.005
FABP4 low expression	KEGG_BASE_EXCISION_REPAIR	-1.910	0.002	0.060
	KEGG_CITRATE_CYCLE_TCA_CYCLE	-1.790	0.014	0.121
	KEGG_DNA_REPLICATION	-1.680	0.047	0.182
	KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	-1.920	0	0.110
	KEGG_ONE_CARBON_POOL_BY_FOLATE	-1.700	0.018	0.186
	KEGG_PYRUVATE_METABOLISM	-1.620	0.032	0.215

NES: normalized enrichment score; NOM: nominal p-value; FDR: false discovery rate. Gene sets with NOM p-value less than 0.05 and FDR q-value less than 0.06 were considered as statistical significance.