

Supplementary Table 8: Gene Set Enrichment Analysis showing the top MSigDB pathways comparing clusters 1, 2, and 3*

	PATHWAY	FDR q-VALUE
Cluster 1 vs 2	HALLMARK_ALLOGRAFT_REJECTION	0.000
	HALLMARK_G2M_CHECKPOINT	0.000
	HALLMARK_INTERFERON_GAMMA_RESPONSE	0.000
	HALLMARK_TNFA_SIGNALING_VIA_NFKB	0.000
	REACTOME_STRIATED_MUSCLE_CONTRACTION	0.000
	HALLMARK_MITOTIC_SPINDLE	0.000
	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.000
	HALLMARK_INFLAMMATORY_RESPONSE	0.000
	REACTOME_MUSCLE_CONTRACTION	0.000
	HALLMARK_E2F_TARGETS	0.000
	HALLMARK_MYOGENESIS	0.000
	REACTOME_REGULATORY_INTERACTIONS_BETWEEN_LYMPHOID_AND_NON_LYMPHOID_CELL	0.000
	REACTOME_TCR_SIGNALING	0.000
	PID_CD8_TCR_PATHWAY	0.000
	REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	0.000
	KEGG_VIRAL_MYOCARDITIS	0.000
	KEGG_VIRAL_MYOCARDITIS	0.000
BIOCARTA_STATHMIN_PATHWAY	0.000	
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	0.000	
REACTOME_CELL_CYCLE_MITOTIC	0.000	
REACTOME_INTERFERON_GAMMA_SIGNALING	0.000	
Cluster 1 vs 3	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.000
	HALLMARK_ALLOGRAFT_REJECTION	0.000
	PID_INTEGRIN1_PATHWAY	0.000
	KEGG_ECM_RECEPTOR_INTERACTION	0.000
	KEGG_PRIMARY_IMMUNODEFICIENCY	0.000
	KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.000
	HALLMARK_INTERFERON_GAMMA_RESPONSE	0.000
	REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	0.000
	REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	0.000
	HALLMARK_INFLAMMATORY_RESPONSE	0.000
	KEGG_ALLOGRAFT_REJECTION	0.000
	REACTOME_REGULATORY_INTERACTIONS_BETWEEN_LYMPHOID_AND_NON_LYMPHOID_CELL	0.000
	ST_T_CELL_SIGNAL_TRANSDUCTION	0.000
	PID_SYNDECAN_1_PATHWAY	0.000
	KEGG_GRAFT_VERSUS_HOST_DISEASE	0.000
	NABA_COLLAGENS	0.000
	KEGG_VIRAL_MYOCARDITIS	0.000
PID_IL12_2PATHWAY	0.000	
PID_CD8_TCR_PATHWAY	0.000	
REACTOME_COLLAGEN_FORMATION	0.000	
STELLATE_CELL_PATHWAY *	0.002	

* Derived from Zhang DY, et al. Gut. 2016 Oct;65(10):1754-64

Supplementary Table 8: Gene Set Enrichment Analysis showing the top MSigDB pathways comparing clusters 1, 2, and 3* (continued)

	PATHWAY	FDR q-VALUE
Cluster 2 vs 3	PID_INTEGRIN1_PATHWAY	0.000
	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.000
	KEGG_ECM_RECEPTOR_INTERACTION	0.006
	PID_SYNDECAN_1_PATHWAY	0.012
	REACTOME_COLLAGEN_FORMATION	0.011
	NABA_BASEMENT_MEMBRANES	0.013
	NABA_CORE_MATRISOME	0.013
	NABA_COLLAGENS	0.012
	REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	0.018
	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	0.026
	REACTOME_NCAM1_INTERACTIONS	0.026
	REACTOME_TRANSLOCATION_OF_ZAP_70_TO_IMMUNOLOGICAL_SYNAPSE	0.026
	KEGG_FOCAL_ADHESION	0.029
	REACTOME_PD1_SIGNALING	0.042
	REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_CHAINS	0.053
	REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	0.052
	REACTOME_CHOLESTEROL_BIOSYNTHESIS	0.061
	BIOCARTA_TCR_ACTIVATION_PATHWAY	0.077
	NABA_ECM_GLYCOPROTEINS	0.078
	PID_INTEGRIN1_PATHWAY	0.000
STELLATE_CELL_PATHWAY *	0.000	

* Derived from Zhang DY, et al. Gut. 2016 Oct;65(10):1754-64