

**S6 Table.** Top 20 gene sets negatively associated with PD-L1 up-regulation according to gene set enrichment analysis in the discovery cohort

Gene set name	Normalized ES	Nominal p-value	FDR
KEGG_OLFACTORY_TRANSDUCTION	-1.96	<0.001	0.057
BIOCARTA_CTLA4_PATHWAY	-1.95	<0.001	0.032
REACTOME_OLFACTORY_SIGNALING_PATHWAY	-1.94	<0.001	0.024
BIOCARTA_NO2IL12_PATHWAY	-1.84	0.002	0.088
KEGG_ALLOGRAFT_REJECTION	-1.79	<0.001	0.131
PID_CD8_TCR_PATHWAY	-1.79	<0.001	0.112
REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_CHAINS	-1.77	0.002	0.132
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	-1.75	0.005	0.136
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	-1.75	0.002	0.123
PID_TCR_PATHWAY	-1.75	0.003	0.112
REACTOME_TCR_SIGNALING	-1.73	0.005	0.125
KEGG_GRAFT_VERSUS_HOST_DISEASE	-1.73	<0.001	0.118
KEGG_AUTOIMMUNE_THYROID_DISEASE	-1.72	0.003	0.123
PID_CD8_TCR_DOWNSTREAM_PATHWAY	-1.71	<0.001	0.131
REACTOME_DEFENSINS	-1.71	0.002	0.125
KEGG_ASTHMA	-1.70	0.002	0.127
BIOCARTA_IL17_PATHWAY	-1.69	0.011	0.131
PID_IL12_2PATHWAY	-1.69	0.001	0.125
REACTOME_BETA_DEFENSINS	-1.65	0.012	0.188
KEGG_TYPE_I_DIABETES_MELLITUS	-1.64	0.008	0.191

ES, enrichment score; FDR, false discovery rate; KEGG, Kyoto Encyclopedia of Genes and Genomes; PD-L1, programmed death-ligand 1.