

S5 Table. Top 30 gene sets positively 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
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	2.71	<0.0001	<0.0001
HALLMARK_HYPOXIA	2.63	<0.0001	<0.0001
PID_INTEGRIN1_PATHWAY	2.50	<0.0001	<0.0001
PID_UPA_UPAR_PATHWAY	2.46	<0.0001	<0.0001
HALLMARK_GLYCOLYSIS	2.42	<0.001	<0.0001
PID_INTEGRIN3_PATHWAY	2.27	<0.0001	2.58E-04
REACTOME_INTEGRIN_ALPHAIIIB_BETA3_SIGNALING	2.17	<0.0001	0.003
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	2.13	<0.0001	0.004
PID_INTEGRIN2_PATHWAY	2.12	<0.0001	0.004
REACTOME_COLLAGEN_FORMATION	2.10	<0.0001	0.004
PID_INTEGRIN_A9B1_PATHWAY	2.08	<0.0001	0.006
REACTOME_GLUONEOGENESIS	2.08	<0.0001	0.005
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	2.08	<0.0001	0.005
BIOCARTA_AMI_PATHWAY	2.07	<0.0001	0.005
REACTOME_GLUCOSE_METABOLISM	2.05	0.002778	0.006
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2+_	2.04	<0.0001	0.007
PID_INTEGRIN5_PATHWAY	2.04	<0.0001	0.006
BIOCARTA_INTRINSIC_PATHWAY	2.01	<0.0001	0.009
REACTOME_PLATELET_AGGREGATION_PLUGIN	2.00	<0.0001	0.009
REACTOME_GLYCOLYSIS	1.99	<0.0001	0.010
KEGG_ECM_RECEPTOR_INTERACTION	1.98	<0.0001	0.010
REACTOME_SMOOTH_MUSCLE_CONTRACTION	1.95	<0.0001	0.014
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	1.94	<0.0001	0.014
PID_HIF1_TFPATHWAY	1.94	<0.0001	0.014
HALLMARK_MTORC1_SIGNALING	1.93	<0.0001	0.014
BIOCARTA_PROTEASOME_PATHWAY	1.91	0.005666	0.019
REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC	1.90	0.005013	0.020
PID_AVB3_INTEGRIN_PATHWAY	1.89	<0.0001	0.021
PID_EPHRINB_REV_PATHWAY	1.89	<0.0001	0.021
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	1.88	<0.0001	0.024

ES, enrichment score; FDR, false discovery rate; PD-L1, programmed death-ligand 1.