

S3 Table. Top 20 gene sets positively associated with PD-L1 up-regulation according to the hypergeometric test in the discovery cohort

Gene set name	Gene set length	Overlap	Nominal p-value	FDR
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	79	7	1.48E-06	0.001
HALLMARK_MTORC1_SIGNALING	200	10	1.73E-06	0.001
HALLMARK_HYPOXIA	200	9	1.34E-05	0.006
KEGG_STARCH_AND_SUCROSE_METABOLISM	52	5	3.29E-05	0.010
REACTOME_INTEGRIN_ALPHAIIIB_BETA3_SIGNALING	27	4	3.70E-05	0.010
REACTOME_CALNEXIN_CALRETICULIN_CYCLE	11	3	5.46E-05	0.013
HALLMARK_GLYCOLYSIS	200	8	9.27E-05	0.016
REACTOME_N_GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXIN_CALRETICULIN_CYCLE	13	3	9.36E-05	0.016
SIG_PIP3_SIGNALING_IN_CARDIAC_MYOCYTES	67	5	0.000112	0.016
REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	36	4	0.000118	0.016
PID_UPA_UPAR_PATHWAY	42	4	0.000217	0.027
PID_INTEGRIN3_PATHWAY	43	4	0.000238	0.027
REACTOME_GLUCURONIDATION	18	3	0.00026	0.028
SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES	51	4	0.000462	0.046
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	25	3	0.000707	0.065
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	58	4	0.000755	0.065
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	28	3	0.000992	0.081
PID_INTEGRIN2_PATHWAY	29	3	0.001101	0.083
REACTOME_METABOLISM_OF_PROTEINS	518	11	0.001202	0.083
PID_INTEGRIN1_PATHWAY	66	4	0.001227	0.083

FDR, false discovery rate; KEGG, Kyoto Encyclopedia of Genes and Genomes; mTOR C1, phospho-mammalian target of rapamycin complex-1; PD-L1, programmed death-ligand 1; PIP3, phosphatidylinositol (3,4,5)-trisphosphate UPA, urokinase-type plasminogen activator; Upar, urokinase plasminogen activator receptor.