

**S4 Table.** Hallmark gene sets positively associated with PD-L1 up-regulation according to gene set enrichment analysis in the discovery cohort

Pathway name	Size	p-value	FDR
Glycolysis	188	<0.0001	<0.0001
Hypoxia	195	<0.0001	<0.0001
mTOR C1 signaling	192	<0.0001	0.0006
Adipogenesis	193	<0.0001	0.0220
Androgen response	98	<0.0001	<0.0001
Angiogenesis	32	<0.0001	<0.0001
Apical junction	188	<0.0001	0.0016
Apoptosis	155	<0.0001	0.0017
Cholesterol homeostasis	71	<0.0001	0.0006
Coagulation	133	<0.0001	<0.0001
Complement	191	0.004	0.0233
Epithelial mesenchymal transition	190	<0.0001	<0.0001
Oestrogen response early	195	<0.0001	<0.0001
Oestrogen response late	191	<0.0001	0.0042
Hedgehog signaling	35	0.004	0.0045
IL-2 STAT5 signaling	196	<0.0001	0.0211
Inflammatory response	199	0.002	0.0273
KRAS signaling up	195	<0.0001	0.0006
Myogenesis	193	0.002	0.0192
p53 pathway	192	<0.0001	0.0017
Protein secretion	92	0.010	0.0156
TGF-beta signaling	53	<0.0001	<0.0001
TNF-alpha signaling via NF-κB	193	<0.0001	0.0002
Unfolded protein response	106	<0.0001	0.0005
UV response	138	<0.0001	<0.0001
Xenobiotic metabolism	192	<0.0001	0.0016

FDR, false discovery rate; IL-2, interleukin-2; mTOR C1, mTOR complex 1; NF-κB, nuclear factor kappa light chain enhancer of activated B cells; PD-L1, programmed death-ligand 1; STAT5, signal transducer and activator of transcription 5; TGF-beta, transforming growth factor beta; TNF-alpha, tumor necrosis factor alpha; UV, ultraviolet.