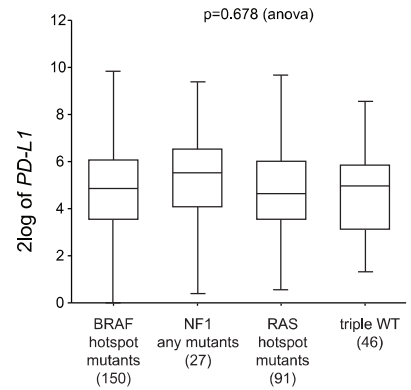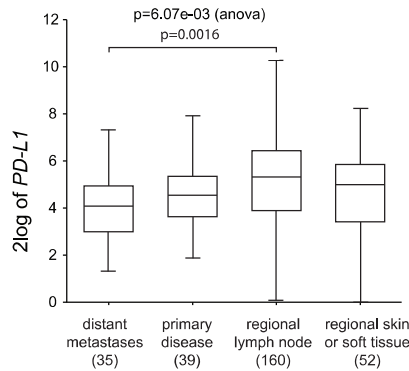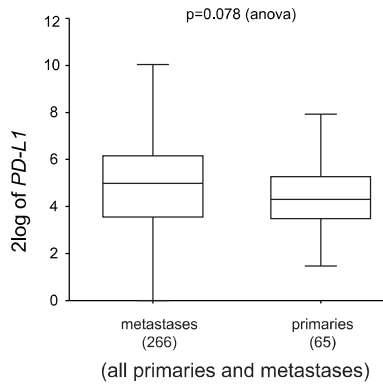S1A
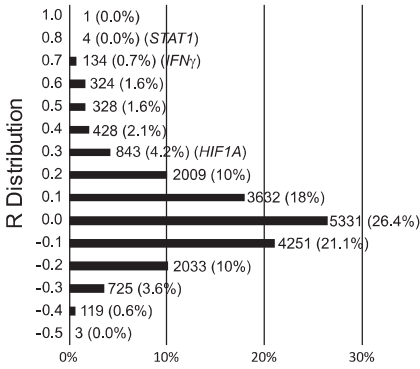
Lymphocyte score vs *PD-L1*
(R=0.423; p=1.02e-15)

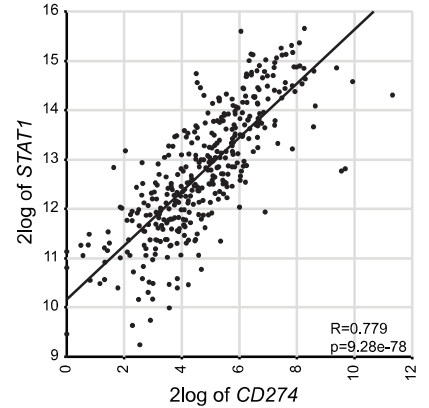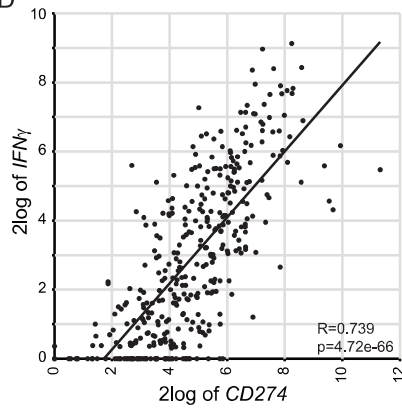p=3.5e-12
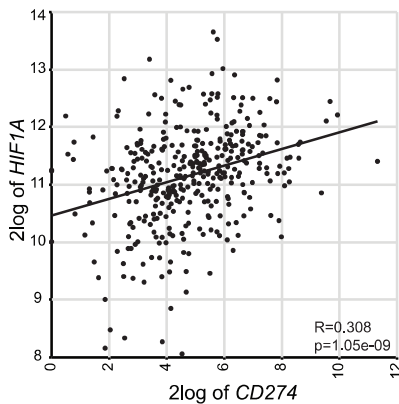p=6.3e-07
p=9.5e-03
p=2.9e-03
p=2.1e-04
p=5.6e-03

2log of *PD-L1*

p=1.0e-05
p=1.5e-07
p=9.9e-13

0 (90) 2 (77) 3 (32) 4 (36) 5 (52) 6 (42)

S1B

p=0.078 (anova)

2log of *PD-L1*

metastases (266)   primaries (65)

(all primaries and metastases)

p=6.07e-03 (anova)
p=0.0016

2log of *PD-L1*

distant metastases (35)   primary disease (39)   regional lymph node (160)   regional skin or soft tissue (52)

p=0.678 (anova)

2log of *PD-L1*

BRAF hotspot mutants (150)   NF1 any mutants (27)   RAS hotspot mutants (91)   triple WT (46)

S1C

R Distribution

1.0 1 (0.0%)
0.8 4 (0.0%) (*STAT1*)
0.7 134 (0.7%) (*IFNγ*)
0.6 324 (1.6%)
0.5 328 (1.6%)
0.4 428 (2.1%)
0.3 843 (4.2%) (*HIF1A*)
0.2 2009 (10%)
0.1 3632 (18%)
0.0 5331 (26.4%)
-0.1 4251 (21.1%)
-0.2 2033 (10%)
-0.3 725 (3.6%)
-0.4 119 (0.6%)
-0.5 3 (0.0%)

0% 10% 20% 30%

S1D

2log of *IFNγ* vs 2log of *CD274*

R=0.739
p=4.72e-66

2log of *STAT1* vs 2log of *CD274*

R=0.779
p=9.28e-78

S1E

2log of *HIF1A* vs 2log of *CD274*

R=0.308
p=1.05e-09

S1F

2log of *HIF1α* vs 2log of *BNIP3L*

R=0.377
p=3.95e-14

2log of *HIF1α* vs 2log of *PDK1*
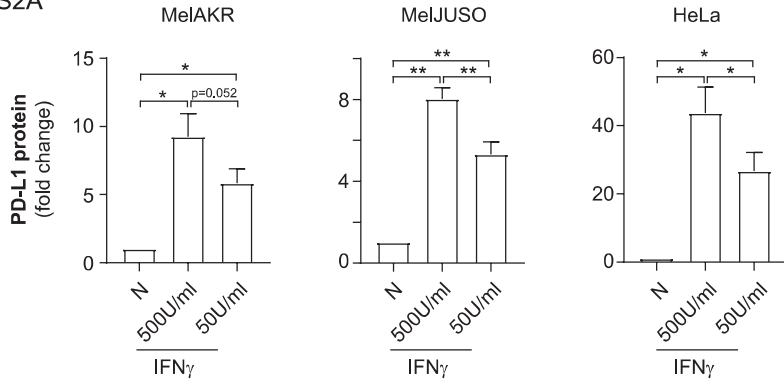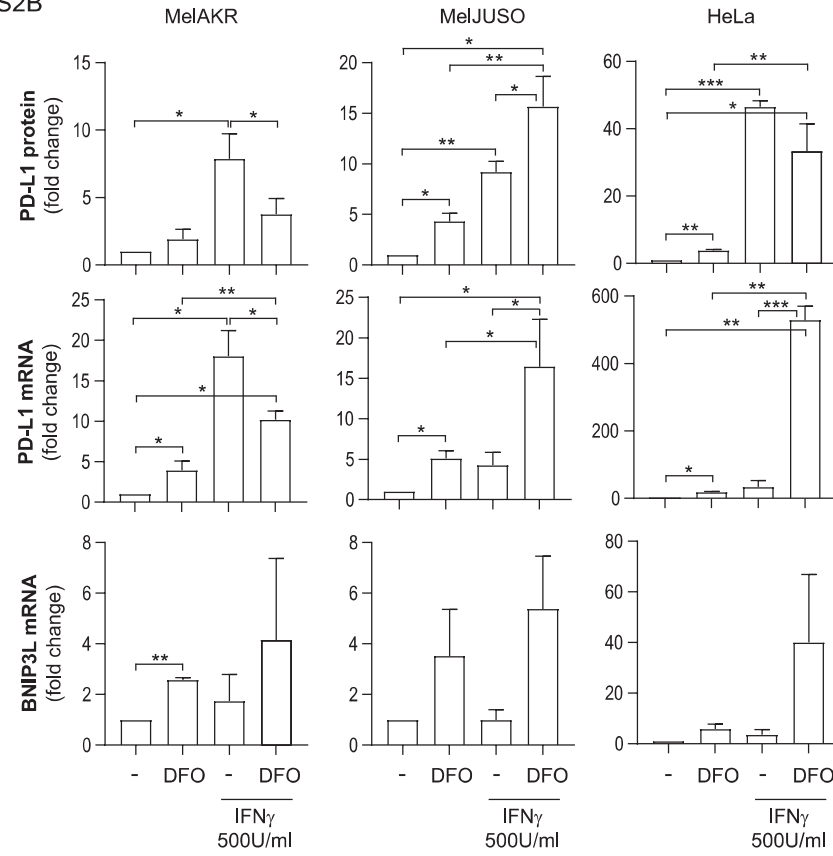
R=0.416
p=3.67e-17

Supplemental Figure S2

S2A

S2B

S2C
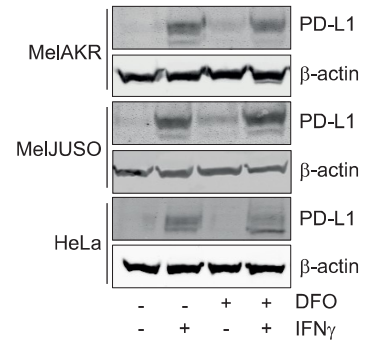
Supplemental Figure S3

S3A

Correlation *CD274* mRNA with Geneset Signature Expression	R	p-value
Melanoma cells (2018 cells)		
JAK_STAT_Signaling_Pathway (KEGG)	0.169	2.47e-14
HIF_1_signaling_pathway (KEGG)	0.119	7.79e-08
Tumor 110 (258 cells)		
JAK_STAT_Signaling_Pathway (KEGG)	0.537	1.03e-20
HIF_1_signaling_pathway (KEGG)	0.271	9.85e-06
Macrophage (420 cells)		
JAK_STAT_Signaling_Pathway (KEGG)	0.122	0.012
HIF_1_signaling_pathway (KEGG)	0.031	0.521

S3B

R=0.336
p=2.36e-11