A

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
HALLMARK_INTERFERON_ALPHA_RESPONSE	76	0.6876689	2.7127357	0.0	0.0
HALLMARK_INTERFERON_GAMMA_RESPONSE	151	0.57989234	2.596712	0.0	0.0
HALLMARK_HYPOXIA	140	0.31747052	1.3981382	0.023054754	0.29256186
HALLMARK_INFLAMMATORY_RESPONSE	101	0.32413366	1.3591833	0.04024768	0.3044521
HALLMARK_OXIDATIVE_PHOSPHORYLATION	171	0.29614064	1.3367879	0.034901366	0.2947836

B

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
HALLMARK_INTERFERON_GAMMA_RESPONSE	151	0.7310796	3.5247443	0.0	0.0
HALLMARK_INTERFERON_ALPHA_RESPONSE	76	0.7948779	3.37133	0.0	0.0
HALLMARK_ALLOGRAFT_REJECTION	115	0.5192883	2.4068158	0.0	0.0
HALLMARK_INFLAMMATORY_RESPONSE	101	0.49083138	2.2173204	0.0	0.0
HALLMARK_IL6_JAK_STAT3_SIGNALING	53	0.5114701	1.984661	0.0	6.2423653E-4
HALLMARK_IL2_STAT5_SIGNALING	134	0.36817843	1.7503326	0.0	0.006220676
HALLMARK_KRAS_SIGNALING_UP	121	0.34055185	1.5680463	0.0	0.0325136
HALLMARK_COMPLEMENT	104	0.33973402	1.5299019	0.0055658626	0.038914744
HALLMARK_HYPOXIA	140	0.3210342	1.5245386	0.0017241379	0.036534436

C

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
HALLMARK_ADIPOGENESIS	160	-0.38074797	-1.8496164	0.0	0.008797424
HALLMARK_E2F_TARGETS	180	-0.31548393	-1.5805159	0.0032051282	0.07708941

D

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
HALLMARK_E2F_TARGETS	180	-0.59575105	-3.0263436	0.0	0.0
HALLMARK_MYC_TARGETS_V1	177	-0.49817848	-2.5500927	0.0	0.0
HALLMARK_G2M_CHECKPOINT	181	-0.44648767	-2.269467	0.0	0.0
HALLMARK_MYC_TARGETS_V2	54	-0.503158	-2.0923288	0.0	2.2368421E-4
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	98	-0.3581522	-1.651485	0.0	0.01554688
HALLMARK_MTORC1_SIGNALING	185	-0.32243988	-1.6477787	0.0026041667	0.013246523
HALLMARK_DNA_REPAIR	120	-0.3372135	-1.6250446	0.0	0.014031643
HALLMARK_OXIDATIVE_PHOSPHORYLATION	171	-0.29370216	-1.4850502	0.0023584906	0.036249034
HALLMARK_CHOLESTEROL_HOMEOSTASIS	54	-0.3575968	-1.4737701	0.027972028	0.034740392

Supplemental table S4. GSEA results comparing CBX or anti-PD-1 treated CM melanomas versus non-treated CM melanomas.
(A) Gene sets with positive enrichments scores (= up in CBX treated). **(B)** Gene sets with positive enrichments scores (= up in anti-PD-1 treated). **(C)** Gene sets with negative enrichments scores (= down in CBX treated). **(D)** Gene sets with negative enrichments scores (= down in anti-PD-1 treated). NOM p-val=0.0 corresponds to p<0.001. (N)ES: (normalized) enrichments score. FDR; false discovery rate.