Supplementary

Table S1 Gene set enrichment analysis results

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
HALLMARK_APOPTOSIS	160	0.70051455	2.6257174	0	0	0
HALLMARK_COMPLEMENT	200	0.78319126	2.6200805	0	0	0
HALLMARK_IL2_STAT5_SIGNALING	199	0.7479699	2.6010416	0	0	0
HALLMARK_INFLAMMATORY_RESPONSE	200	0.8232711	2.4336164	0	0	0
HALLMARK_KRAS_SIGNALING_UP	200	0.74342144	2.4314137	0	0	0
HALLMARK_TNFA_SIGNALING_VIA_NFKB	200	0.7702892	2.4042175	0	0	0
HALLMARK_IL6_JAK_STAT3_SIGNALING	87	0.8494306	2.3989427	0	0	0
HALLMARK_ALLOGRAFT_REJECTION	200	0.873572	2.367234	0	0	0
HALLMARK_APICAL_SURFACE	44	0.68326074	2.335569	0	0	0
HALLMARK_COAGULATION	138	0.67890644	2.3255935	0	0	0
HALLMARK_P53_PATHWAY	199	0.54429597	2.2429593	0	2.18E-04	0.001
HALLMARK_PI3K_AKT_MTOR_SIGNALING	105	0.55399305	2.2292156	0	1.99E-04	0.001
HALLMARK_UV_RESPONSE_UP	158	0.49696413	2.228519	0	2.71E-04	0.002
HALLMARK_INTERFERON_GAMMA_RESPONSE	200	0.8839401	2.2202923	0	2.52E-04	0.002
HALLMARK_XENOBIOTIC_METABOLISM	200	0.5438093	2.1483989	0	3.86E-04	0.004
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	49	0.6008132	2.1454117	0	3.62E-04	0.004
HALLMARK_INTERFERON_ALPHA_RESPONSE	97	0.88612145	2.120752	0	4.69E-04	0.006
HALLMARK_HYPOXIA	200	0.5319725	2.0935123	0	5.47E-04	0.007
HALLMARK_ESTROGEN_RESPONSE_LATE	199	0.52326787	2.042317	0	9.20E-04	0.012
HALLMARK_APICAL_JUNCTION	200	0.5210891	1.9892429	0	0.00180883	0.021
HALLMARK_KRAS_SIGNALING_DN	199	0.5182481	1.9625837	0	0.002745702	0.031
HALLMARK_BILE_ACID_METABOLISM	111	0.47719282	1.7996906	0	0.014487662	0.127
HALLMARK_ESTROGEN_RESPONSE_EARLY	199	0.45337337	1.7886199	0.001968504	0.01474217	0.136
HALLMARK_HEME_METABOLISM	199	0.4446583	1.7849642	0	0.014678549	0.141
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	199	0.57943994	1.688738	0.047904193	0.032323223	0.254
HALLMARK_TGF_BETA_SIGNALING	53	0.54495263	1.654337	0.034552846	0.039072897	0.286
HALLMARK_ANDROGEN_RESPONSE	100	0.48915303	1.6522083	0.034552846	0.03813794	0.29
HALLMARK_PEROXISOME	104	0.40922758	1.6507878	0.008179959	0.03715789	0.292
HALLMARK_MTORC1_SIGNALING	200	0.42508727	1.6380237	0.050403226	0.039152853	0.311
HALLMARK_ADIPOGENESIS	200	0.35304105	1.4945569	0.066797644	0.08945501	0.508
HALLMARK_PANCREAS_BETA_CELLS	40	0.44917884	1.4772807	0.052083332	0.09640395	0.539
HALLMARK_FATTY_ACID_METABOLISM	158	0.35112223	1.4546317	0.08782435	0.104831114	0.572
HALLMARK_ANGIOGENESIS	36	0.5200693	1.4310635	0.11133201	0.113412455	0.606
HALLMARK_MYOGENESIS	200	0.3787386	1.3817526	0.103658535	0.1359807	0.67
HALLMARK_CHOLESTEROL_HOMEOSTASIS	74	0.39741302	1.3678814	0.12929294	0.14021368	0.688
HALLMARK_HEDGEHOG_SIGNALING	36	0.41040444	1.3072987	0.15238096	0.17360634	0.756
HALLMARK_UV_RESPONSE_DN	142	0.39071167	1.2472875	0.24361493	0.21259499	0.812
HALLMARK_WNT_BETA_CATENIN_SIGNALING	42	0.35652614	1.203498	0.2411215	0.2406945	0.848
HALLMARK_MITOTIC_SPINDLE	199	0.32818305	1.0717005	0.394636	0.35346884	0.917
HALLMARK_NOTCH_SIGNALING	32	0.32785797	1.0664095	0.3857143	0.35107985	0.919
HALLMARK_SPERMATOGENESIS	135	0.27206284	1.0015352	0.45418328	0.41387898	0.953
HALLMARK_GLYCOLYSIS	200	0.21274453	0.9035846	0.5714286	0.5244184	0.977
HALLMARK_PROTEIN_SECRETION	96	0.24175288	0.7521668	0.6912621	0.7269113	0.993

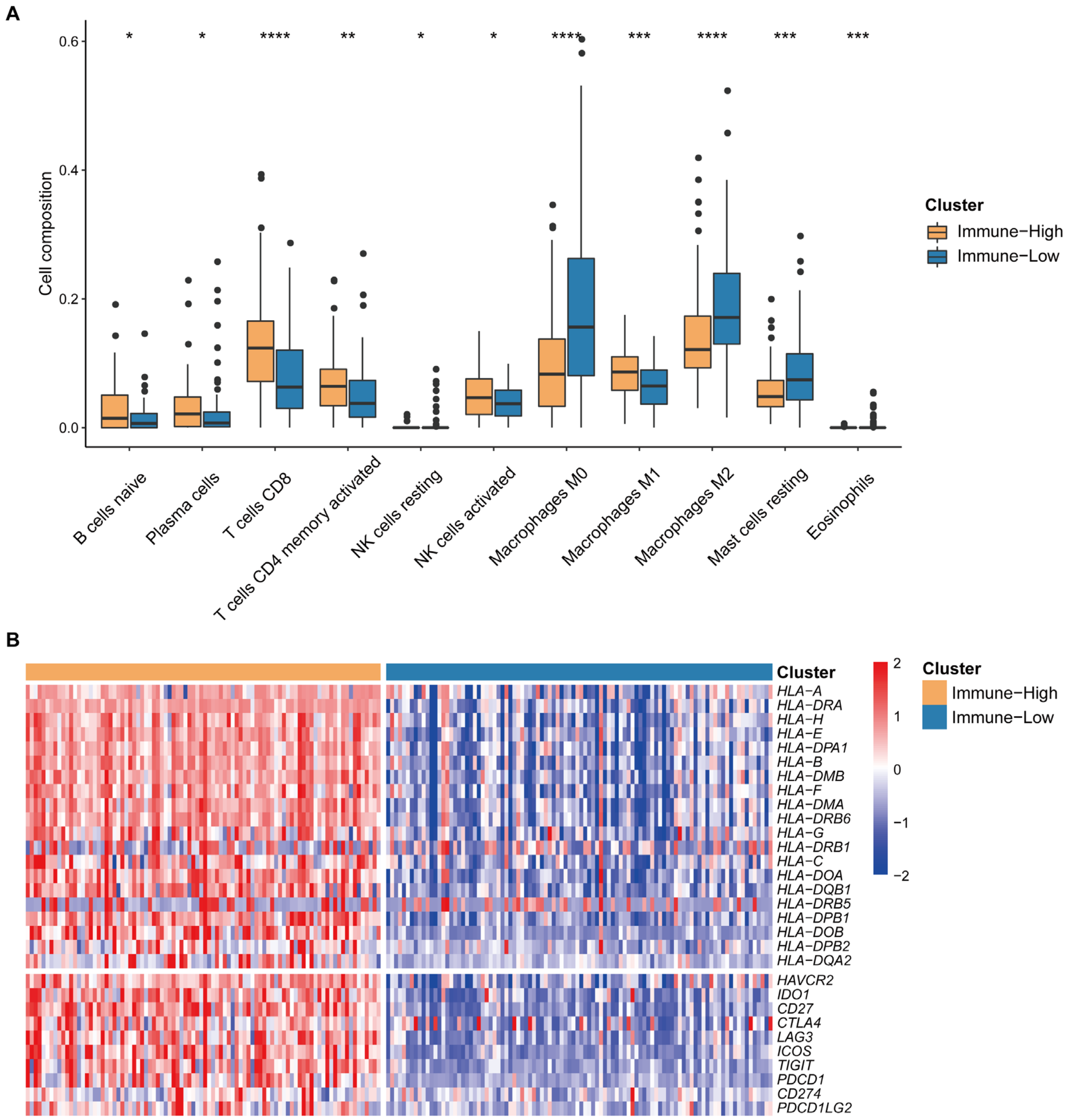

Figure S1 Immune cellular and molecular features of immune subtypes in the GSE65904 cohort. (A) Differential proportions of immune cells between the Immune-High and Immune-Low subtypes. (B) The expression of immune checkpoint molecules and MHC I/II class genes. *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$; ****, $P<0.0001$.

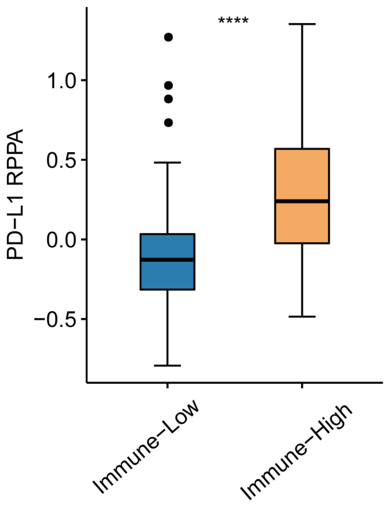

Figure S2 The comparison of the PD-L1 RPPA level in metastatic melanoma based on the immune subtypes. *, P<0.05; **, P<0.01; ***, P<0.001; ****, P<0.0001.

Table S2 Coefficient of the selected genes used in the binomial logistic regression model

Gene_Symbol	EntrezGeneID	Coefficient
BMI1	648	0.83234302
CD38	952	-5.081072919
DPP4	1803	-0.393374014
IL12RB1	3594	-0.065777101
ATG10	83734	0.671575839
MARCO	8685	-0.188629278
IKBKB	3551	0.871817474
BAX	581	0.162155814
SOCS1	8651	-1.953865493
HLA-DMB	3109	-0.576514111
PRKCE	5581	0.517669663
SPA17	53340	2.00764777
NOD1	10392	0.588443323
ILF3	3609	1.283864913
ULBP2	80328	0.552932039
PPARG	5468	0.835959749
IDO1	3620	-0.378271157
SMAD3	4088	1.371201829
TNFRSF10B	8795	0.058073446
IL12B	3593	3.558498157
HLA-DPB1	3115	-0.045606774
FCER1G	2207	-0.016552385
LAG3	3902	-0.567342322
LAMP3	27074	-0.326737527
MX1	4599	-0.007745614
CD160	11126	0.108864785
CCL23	6368	0.722310148
RPS6	6194	1.42152492
NFKB1	4790	0.185634978
TRAF6	7189	1.200688705
MASP1	5648	3.585491864
JAK3	3718	-0.512250594
MAGEA3	4102	0.252503288
CD86	942	-1.043747705
SLAMF1	6504	-0.015627253
IL21R	50615	-1.119574894
Intercept		0.9682763

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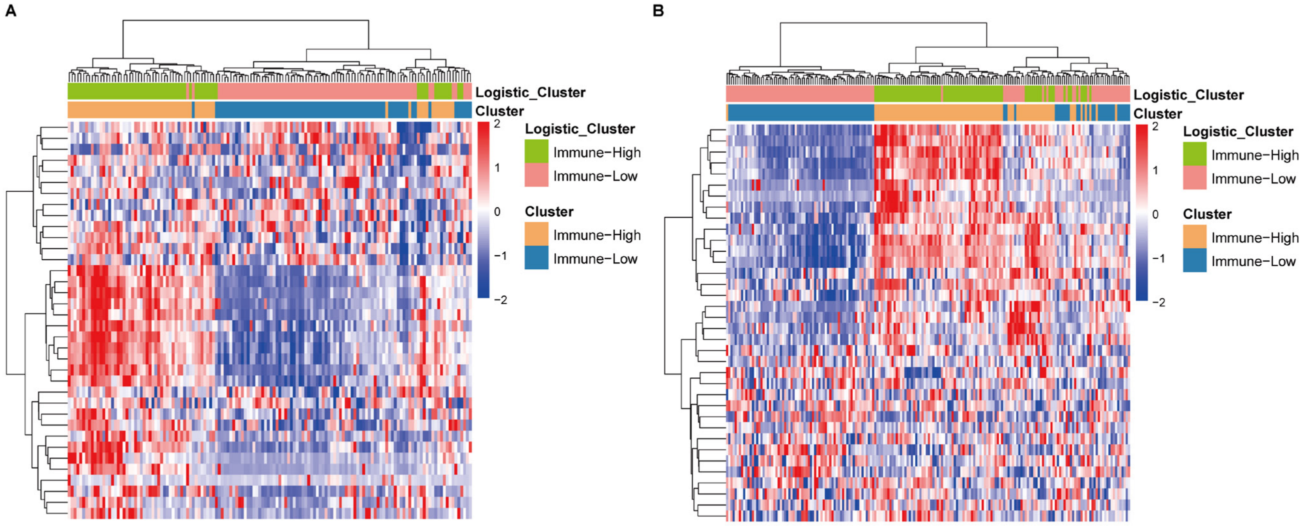

Figure S3 Heatmaps of the relative mRNA expression of the 36 genes selected by the binomial logistic regression model in TCGA training set (A) and GSE65904 cohort (B).

https://dx.doi.org/10.21037/tcr-2024-2301