

Supplementary Table 1. GSEA Pathway Enrichment Analysis in the high-TMB level group

NAME	p-val	FDR qval
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0	0.001771
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	0.001927	0.024245
KEGG_AUTOIMMUNE_THYROID_DISEASE	0.007813	0.050245
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.009881	0.05225
KEGG_GRAFT_VERSUS_HOST_DISEASE	0.00611	0.04818
KEGG_LEISHMANIA_INFECTION	0.012	0.052018
KEGG_ASTHMA	0.009843	0.051692
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	0.017751	0.062052
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	0.002041	0.05631
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.011976	0.061629
KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.015296	0.064904
KEGG_TYPE_I_DIABETES_MELLITUS	0.017787	0.060479
KEGG_VIRAL_MYOCARDITIS	0.014028	0.059515
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	0.003968	0.068157
KEGG_ALLOGRAFT_REJECTION	0.010081	0.064711
KEGG_FRUCTOSE_AND_MANNANOSE_METABOLISM	0.026157	0.0754
KEGG_P53_SIGNALING_PATHWAY	0.012024	0.078547
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	0.006048	0.078132
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.043726	0.111304
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.025641	0.111987
KEGG_APOPTOSIS	0.025948	0.115454
KEGG_PANCREATIC_CANCER	0.025263	0.118664
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.035294	0.145911
KEGG_PROTEIN_EXPORT	0.068762	0.140844
KEGG_PRION_DISEASES	0.044776	0.147001
KEGG_ONE_CARBON_POOL_BY_FOLATE	0.05336	0.144019
KEGG_CELL_CYCLE	0.08125	0.166653
KEGG_SPHINGOLIPID_METABOLISM	0.045908	0.171279
KEGG_CHEMOKINE_SIGNALING_PATHWAY	0.075547	0.169606
KEGG_OOCYTE_MEIOSIS	0.068687	0.164303
KEGG_DNA_REPLICATION	0.0998	0.169833
KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	0.070565	0.175985
KEGG_JAK_STAT_SIGNALING_PATHWAY	0.067179	0.19455
KEGG_GALACTOSE_METABOLISM	0.064777	0.19121
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	0.102161	0.186753
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE	0.10101	0.187394
KEGG_HOMOLOGOUS_RECOMBINATION	0.112016	0.19811
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	0.098837	0.235505
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	0.075547	0.250002
KEGG_ETHER_LIPID_METABOLISM	0.085066	0.245292
KEGG_VEGF_SIGNALING_PATHWAY	0.102823	0.271902

KEGG_CELL_ADHESION_MOLECULES_CAMS	0.171079	0.26877
KEGG_NUCLEOTIDE_EXCISION_REPAIR	0.191617	0.266856
KEGG_PROTEASOME	0.227545	0.277802
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	0.149897	0.278888
KEGG_GLYCOLYSIS_GLUONEOGENESIS	0.147475	0.27302
KEGG_PYRIMIDINE_METABOLISM	0.162325	0.268264
KEGG_PRIMARY_IMMUNODEFICIENCY	0.201581	0.278731
KEGG_BLADDER_CANCER	0.14557	0.274716
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	0.137331	0.2857
KEGG_MAPK_SIGNALING_PATHWAY	0.150101	0.292467
KEGG_PURINE_METABOLISM	0.151052	0.291814
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	0.167689	0.288275
KEGG_GLIOMA	0.183128	0.313611
KEGG_COLORECTAL_CANCER	0.174442	0.312966
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	0.243299	0.337829
KEGG_PROSTATE_CANCER	0.196	0.334579
KEGG_BASE_EXCISION_REPAIR	0.246063	0.335232
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	0.248062	0.338573
KEGG_INOSITOL_PHOSPHATE_METABOLISM	0.246436	0.333194
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	0.264463	0.335231
KEGG_NITROGEN_METABOLISM	0.202479	0.336377
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	0.213693	0.334495
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	0.246493	0.336135
KEGG_ARGININE_AND_PROLINE_METABOLISM	0.221328	0.334264
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	0.246377	0.332902
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.277014	0.3287
KEGG_RENAL_CELL_CARCINOMA	0.261663	0.330464
KEGG_MISMATCH_REPAIR	0.320866	0.339452
KEGG_CHRONIC_MYELOID_LEUKEMIA	0.261224	0.342027
KEGG_PATHWAYS_IN_CANCER	0.269618	0.348573
KEGG_SMALL_CELL_LUNG_CANCER	0.311508	0.382805
KEGG_ALZHEIMERS_DISEASE	0.316206	0.380826
KEGG_NON_SMALL_CELL_LUNG_CANCER	0.316116	0.391053
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	0.317365	0.403454
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	0.356275	0.408845
KEGG_LONG_TERM_POTENTIATION	0.348162	0.412247
KEGG_RNA_DEGRADATION	0.371486	0.411294
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	0.360248	0.413197
KEGG_HUNTINGTONS_DISEASE	0.391667	0.412768
KEGG_RNA_POLYMERASE	0.375746	0.416831
KEGG_TYPE_II_DIABETES_MELLITUS	0.371951	0.416821
KEGG_LONG_TERM_DEPRESSION	0.374257	0.420801
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	0.394892	0.416656
KEGG_BASAL_TRANSCRIPTION_FACTORS	0.388655	0.420075

KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	0.396414	0.425598
KEGG_BETA_ALANINE_METABOLISM	0.41483	0.424407
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	0.421505	0.444809
KEGG_PHENYLALANINE_METABOLISM	0.471774	0.478344
KEGG_PARKINSONS_DISEASE	0.484	0.483796
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	0.482255	0.479549
KEGG_LINOLEIC_ACID_METABOLISM	0.557312	0.572343
KEGG_REGULATION_OF_AUTOPHAGY	0.626953	0.587292
KEGG_O_GLYCAN_BIOSYNTHESIS	0.662028	0.662246
KEGG_SPLICEOSOME	0.612403	0.681184
KEGG_FOCAL_ADHESION	0.678647	0.755411
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	0.757576	0.795974
KEGG_OXIDATIVE_PHOSPHORYLATION	0.767396	0.848829
KEGG_ECM_RECEPTOR_INTERACTION	0.760649	0.879225

Supplementary Table 1: Overlapped genes were identified between DEGs in the different TMB level groups and the IRGs obtained from ImmPort database

Type	Gene symbol												
overlapped genes	AZGP1	CD8A	CD74	CTSB	CTSE	FCER1G	FCGRTHLA-DMA	HLA-DMB					
	HLA-DOA	HLA-DPA1	HLA-DPB1	HLA-DQA1	HLA-DQA2	HLA-DQB1							
	HLA-DRA	HLA-DRB1	HLA-DRB5	HSPA2	HSPA6	ICAM1	IFNG	KIR2DL4					
	KLRC2	CIITA	MICB	PSME1	PSME2	TAP1	TAP2	IFI30	CD209	ULBP3	ULBP2	RAET1E	
	PI3	REG3G	CXCL14	CXCL16	CXCL10	CXCL9	CXCL5	CXCL11					
	CXCL1	CXCL13	PF4	CXCL3	CCL13	DEFB1	CCL8	COLEC10	S100A8				
	S100A12	MMP12	TMSB15A	SERPIND1	S100P	S100A2	LCN12						
	S100A14	S100A16	IL6	TGFB1	PF4V1	APOBEC3G	FABP6	NOD2	RBP1				
	TLR2	PLAU	IL1B	PAEP	MUC5AC	PLTP	MX1	DDX58	LBP	R3HDML			
	OASL	CRABP1	OBP2B	RBP2	LCN15	C8G	NOX1	APOD	ORM2	PML	CYBB		
	ISG20	DUOX2	TLR3	IFIH1	LRP1	IDO1	STAT1	SOCS3	SEMG1	SOCS1			
	IRF1	IL15	APOBEC3F	RARRES3	CHIT1	ISG15	DHX58	MUC4	ELN	LYZ			
	CCL5	CST4	JUN	TLR8	GNLY	BST2	PLA2G2A	NOS2	TLR1	FGA	MSR1		
	ROBO3	SLC11A1	DMBT1	TNFRSF10A	CCL4	APOBEC3H	TMPRSS6						
	MARCO	TNFSF11	CLDN4	IL17A	APOBEC3A	IL7R	SYTL1	PTGS2	CD14				
	PROC	TRIM22	RSAD2	PDCD1	AQP9	FASLG	GBP2	CCL18	CCL26	CCL4L2			
	CCL7	CCL3	CCR5	CCL3L1	CCR1	CCL24	XCL2	CXCR4	CXCR6	IL10	PPARG		
	FGR	JAK2	CD86	HCK	OLR1	RNASE2	LYN	VAV3	RAC2	RAC3	CHP2		
	NFATC1	NFATC2	CARD11	PIK3R5	PIK3CD	CD72	LILRB3						
	FCGR2B	CX3CL1	EDN1	PROK2	SAA1	SAA2	SEMA3C	SEMA4B					
	SEMA5A	TNC	TYMP	C5AR1	CMKLR1	EDNRB	FPR1	FPR2	GPR17				
	PLXNB1	PLXNC1	PTAFR	ROBO2	ADM	AGT	AMELX	AMH					
	AREG	BMP3	BMP5	BMP7	CALCA	CCK	CD70	CHGA	CHGB	CMTM2			
	CSF1	CSF2	CSPG5	DKK1	EREG	FAM3B	FAM3D	FGF18	FGF20	FGF3			
	GCG	GDF10	GDNF	GREM2	GRP	GUCA2A	IGF2	IL17C	IL1RN	IL24			
	IL34	INHBB	INSL5	KL	LEFTY1	LEFTY2	NODAL	NRG1	NRTN				
	NTS	NUDT6	OSM	PDGFD	PDGFRL	REG1A	RETN	RETNLB					
	RLN2	SCT	SECTM1	SPP1	STC1	TAC1	TDGF1	TG	TNFSF13B	TNFSF14			
	TNFSF9	UCN2	ADRB1	AVPR1A	C3AR1	CSF1R	CSF2RB	CSF3R					
	EPOR	FGFR2	FGFR3	FGFR4	GHR	GIPR	HNF4A	IL10RA	IL12RB1	IL18R1			
	IL18RAP	IL1R2	IL21R	IL22RA1	IL23R	IL2RA	IL2RB	LGR5	MTNR1A				
	NPR3	NR112	NR4A2	NR6A1	NRP1	PRLR	PTGER1	PTGER2	RARA	S1PR2			
	SSTR5	TGFBR2	THRB	TNFRSF10D	TNFRSF11A	TNFRSF18	TNFRSF19						
	TNFRSF9	VIPR1	ITGAL	ITGB2	TYROBP	LCK	FCGR3A	FCGR3B					
	CD247	LCP2	PLCG1	FYN	HCST	CD48	CD244	PRKCG	SH2D1A	FAS			
	PRF1	CD3D	CD3E	CD3G	PTPRC	ITK	NCK2	ICOS	CTLA4	RASGRP1			

Supplementary Figure 1: Kaplan-Meier survival curves showed no statistically significant differences between the high- and low-TMB groups.

