

Table S1. The response rate to ICI immunotherapy among four subtypes.

Cohorts	Cancer type	Drug	No. of patients	Response rate	Type I (R, NR, %)	Type II (R, NR, %)	Type III (R, NR, %)	Type IV (R, NR, %)
Hugo	melanoma	anti-PD-1 (pembrolizumab and nivolumab)	26	50%	1, 0, 100%	4, 7, 36.36%	1, 1, 50%	7, 5, 58.33%
Riaz	melanoma	anti-PD-1 (nivolumab)	49	53.06%	3, 0, 100%	11, 11, 50%	1, 1, 50%	11, 11, 50%
Miao	ccRCC	anti-PD-1 (nivolumab)	33	60.6%	0, 1, 0%	9, 4, 69.23%	0, 3, 0%	11, 5, 68.75%
Snyder	urothelial cancer	anti-PD-L1 (atezolizumab)	25	36%	0, 0	2, 7, 22.22%	1, 2, 33.33%	6, 7, 46.15%
Mariathasan	urothelial cancer	anti-PD-L1 (atezolizumab)	298	22.82%	3, 5, 37.5%	21, 106, 16.54%	4, 18, 18.18%	40, 101, 28.37%

R: Responders; NR: Non-responders; %: Response rate.

Table S2. Statistical data of PD-L1 TPM, TIL (Z score) and subtypes proportion across pan-cancer.

Cancer	PD-L1 TPM		TIL (Z score)		Subtypes proportion (%)				
	x±σ	p value	x±σ	p value	Type I	Type II	Type III	Type IV	p value
UCS	1.1965±1.5641		2.5129±0.3234		0	88.24	0	11.76	<2.2e-16
ACC	1.5098±4.0215		3.2289±0.5038		0	31.58	1.32	67.11	<2.2e-16
LIHC	1.2585±1.7312		3.3436±0.3922		0	15.87	0	84.13	<2.2e-16
LAML	1.4913±2.1768		2.7441±0.3582		0	72.31	0.77	26.92	<2.2e-16
UVM	1.7863±1.901		3.2651±0.3378		0	18.57	0	81.43	<2.2e-16
UCEC	2.0186±2.9133		2.9671±0.3904		0.41	46.75	0.41	52.44	<2.2e-16
PRAD	1.5402±1.3266		3.117±0.2414		0.2	25.56	0	74.24	<2.2e-16
LGG	2.5774±4.0419		2.7171±0.2654		0.63	80.76	1.9	16.7	<2.2e-16
OV	2.2147±2.3987		2.7622±0.3614		0.29	71.97	0	27.75	<2.2e-16
READ	2.7316±3.6447		3.1745±0.3236		0.89	23.21	0.89	75	<2.2e-16
CHOL	4.1926±9.495		3.1718±0.411		0	26.47	2.94	70.59	<2.2e-16
COAD	3.6617±6.3532		3.1834±0.3787		0.95	23.17	1.9	73.97	<2.2e-16
SARC	5.5631±11.241		2.7278±0.2961		0.87	71.43	8.23	19.48	<2.2e-16
SKCM	4.975±10.2462		3.2449±0.4173		5.33	26.67	1.33	66.67	<2.2e-16
BLCA	9.3797±16.0506		3.038±0.3935		5.52	33.13	12.88	48.47	6.466e-10
BRCA	4.3186±5.3206		2.8286±0.2941		1.11	64.78	2.53	31.58	<2.2e-16
PAAD	3.6685±2.6827		2.9688±0.3212		0	48.59	1.41	50	<2.2e-16
KIRP	5.4884±7.6951	<2.2e-16	3.1708±0.3268	<2.2e-16	3.08	18.85	5	73.08	<2.2e-16
STAD	8.3054±35.2599		3.0643±0.388		3.27	32.73	4.36	59.64	<2.2e-16
MESO	10.293±19.6711		2.8601±0.321		2.9	44.93	15.94	36.23	1.703e-09
GBM	5.9626±6.9316		2.6967±0.295		0.76	72.52	7.63	19.08	<2.2e-16
ESCA	6.3593±8.6932		2.9069±0.3929		1.61	50	6.45	41.94	1.496e-15
TGCT	6.3926±7.1982		2.5819±0.2161		0	84.85	9.09	6.06	<2.2e-16
KIRC	6.0137±12.0815		3.1185±0.3061		1.38	27.17	2.17	69.29	<2.2e-16
PCPG	6.2965±5.602		3.0592±0.2854		3.37	32.02	3.37	61.24	<2.2e-16
KICH	12.264±30.428		3.3485±0.4434		7.94	11.11	3.17	77.78	<2.2e-16
LUAD	13.2727±19.7916		2.7577±0.3256		1.41	52.69	20.84	25.06	1.351e-11
THCA	7.8647±5.5019		3.1534±0.2747		7.26	18.35	3.43	70.97	<2.2e-16
CESC	15.4899±24.5242		3.0574±0.4021		13.5	21.9	16.42	48.18	1.307e-06
HNSC	14.1869±23.0509		2.9816±0.3232		9.68	30.41	16.67	43.24	6.997e-06
LUSC	19.5927±27.5279		2.5727±0.277		1.4	57.94	31.78	8.88	<2.2e-16
DLBC	24.2074±33.5574		3.0615±0.4692		7.14	4.76	30.95	57.14	1.682e-15
THYM	32.8036±28.7492		3.1237±0.2366		55.26	7.02	13.16	24.56	6.306e-12

Pan-cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as follows:

type I , PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-L1

positive with TIL negative; and type IV, PD-L1 negative with TIL positive. Abbreviations: TPM, transcripts per million reads; $\bar{x} \pm \sigma$, mean \pm standard deviation; PD-L1, programmed death ligand 1; TIL, tumor infiltrating lymphocyte; UCS, uterine carcinosarcoma; ACC, adrenocortical carcinoma; LIHC, liver hepatocellular carcinoma; LAML, acute myeloid leukemia; UVM, uveal melanoma; UCEC, uterine corpus endometrial carcinoma; PRAD, prostate adenocarcinoma; LGG, brain lower grade glioma; OV, ovarian serous cystadenocarcinoma; READ, rectum adenocarcinoma; CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; SARC, sarcoma; SKCM, skin cutaneous melanoma; BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; PAAD, pancreatic adenocarcinoma; KIRP, kidney renal papillary cell carcinoma; STAD, stomach adenocarcinoma; MESO, mesothelioma; GBM, glioblastoma multiforme; ESCA, esophageal carcinoma; TGCT, testicular germ cell tumors; KIRC, kidney renal clear cell carcinoma; PCPG, pheochromocytoma and paraganglioma; KICH, kidney chromophobe; LUAD, lung adenocarcinoma; THCA, thyroid carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; HNSC, head and neck squamous cell carcinoma; LUSC, lung squamous cell carcinoma; DLBC, lymphoid neoplasm diffuse large b-cell lymphoma; THYM, thymoma.

Table S3. Statistical data of 8 immune cell proportion across the four subtypes of tumor immune microenvironment.

Immune cell types	$\bar{x} \pm \sigma$				p value
	Type I	Type II	Type III	Type IV	
T cells	0.466±0.1833	0.2817±0.1255	0.3569±0.135	0.3582±0.134	<2.2e-16
B cells	0.0773±0.0831	0.0894±0.0944	0.0953±0.0912	0.0939±0.0963	0.0086
Macrophages	0.3067±0.1662	0.4638±0.1656	0.4054±0.1406	0.375±0.1508	<2.2e-16
DC cells	0.0622±0.0571	0.0372±0.0572	0.0497±0.0586	0.0452±0.0608	<2.2e-16
NK cells	0.0418±0.0374	0.0389±0.0357	0.0358±0.0297	0.0471±0.0384	<2.2e-16
Mast cells	0.0421±0.0409	0.0772±0.0736	0.0486±0.0413	0.0741±0.0661	<2.2e-16
Eosinophils	0.0004±0.0026	0.0033±0.0196	0.001±0.005	0.0013±0.0079	4.2e-11
Neutrophils	0.0036±0.0084	0.0085±0.0222	0.0074±0.0179	0.0053±0.017	2.1e-13

Pan-cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as follows:

type I, PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-L1 positive

with TIL negative; and type IV, PD-L1 negative with TIL positive. Abbreviations: $\bar{x} \pm \sigma$, mean \pm standard

deviation; DC cells, dendritic cells; NK cells, Natural killer cells.

Table S4. The relative proportion of 20 immune cell subtypes across the four subtypes of tumor

immune microenvironment.

Immune cell subtypes	Relative proportion (%)			
	Type I	Type II	Type III	Type IV
T cells CD8	43.56	27.44	39.43	33.81
T cells CD4 naive	3.36	1.68	0.4	1
T cells CD4 memory resting	15.03	41.49	24.86	36.15
T cells CD4 memory activated	10.3	6.03	16.04	5.16
T cells follicular helper	14.16	11.15	9.88	10.05
T cells gamma delta	1.48	1.69	1.35	2.02
T cells regulatory (Tregs)	12.11	10.53	8.05	11.82
B cells naive	50.81	61.73	55.15	56.22
B cells memory	7.46	5.64	4.5	8.4
Plasma cells	41.73	32.63	40.35	35.38
Dendritic cells resting	71.93	60.09	66.08	61.98
Dendritic cells activated	28.07	39.91	33.92	38.02
NK cells resting	36.69	36.63	50.24	25.44
NK cells activated	63.31	63.37	49.76	74.56
Mast cells resting	79.7	74.71	75.67	85.55
Mast cells activated	20.3	25.29	24.33	14.45
Monocytes	4.64	12.59	5.21	7.05
Macrophages M0	32.35	35.68	36.48	33.81
Macrophages M1	29.13	11.86	22.44	17.28
Macrophages M2	33.88	39.88	35.87	41.86

Pan-cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as follows:

type I, PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-L1

positive with TIL negative; and type IV, PD-L1 negative with TIL positive. The relative proportion

refers to the proportion of each immune cell subtype to the immune cell type which it belongs.

Table S5. Statistical data of the log2 value of TMB and the log2 value of Neoantigens across the four subtypes of tumor immune microenvironment.

Genomic factors	$\bar{x}\pm\sigma$				p value
	Type I	Type II	Type III	Type IV	
log ₂ (TMB)	0.3404±2.1294	0.6836±1.9553	1.6336±1.9317	0.4576±1.8091	<2.2e-16
log ₂ (Neoantigens)	6.2054±2.1765	6.3903±1.9487	7.3379±1.7319	6.2546±1.7246	<2.2e-16

Pan-cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as follows:

type I, PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-L1 positive with TIL negative; and type IV, PD-L1 negative with TIL positive. Abbreviations: log₂(TMB), the log₂ value of TMB; log₂(Neoantigens), the log₂ value of neoantigens; $\bar{x}\pm\sigma$, mean \pm standard deviation.

Table S6. Mutation rate of the top ten genes across the four subtypes of tumor immune

microenvironment.

Genes	Mutation rate			
	Type I	Type II	Type III	Type IV
TTN	29%	29%	46%	26%
TP53	24%	41%	51%	29%
MUC16	16%	18%	28%	16%
PIK3CA	14%	14%	— —	12%
BRAF	13%	— —	— —	— —
CSMD3	11%	13%	25%	9%
LRP1B	10%	11%	23%	9%
FAT1	10%	— —	— —	— —
GTF2I	10%	— —	— —	— —
PCLO	9%	— —	— —	— —
RYSR2	13%	13%	22%	9%
SYNE1	— —	12%	— —	9%
FLG	— —	11%	17%	— —
USH2A	— —	10%	23%	— —
ZFH4	— —	— —	20%	— —
SPTA1	— —	— —	17%	— —
APC	— —	— —	— —	9%
KMT2D	— —	— —	— —	8%

Pan-cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as follows:

type I, PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-L1

positive with TIL negative; and type IV, PD-L1 negative with TIL positive. Abbreviations: TTN, titin;

TP53, tumor protein 53; MUC16, mucin 16; PIK3CA, phosphatidylinositol-4,5-bisphosphate 3-kinase

catalytic subunit alpha; BRAF, B-Raf Proto-Oncogene; CSMD3, CUB and Sushi Multiple Domains 3;

LRP1B, LDL receptor related protein 1B; FAT1, FAT Atypical Cadherin 1; GTF2I, general transcription

factor Iii; PCLO, piccolo presynaptic cytomatrix protein; RYR2, ryanodine receptor 2; SYNE1, spectrin repeat containing nuclear envelope protein 1; FLG, filaggrin; USH2A, usherin; ZFHX4, zinc finger homeobox 4; SPTA1, spectrin alpha, erythrocytic 1; APC, adenomatous polyposis coli; KMT2D, lysine methyltransferase 2D.

Table S7. The drive gene detected of the four subtypes of tumor immune microenvironment.

Drive genes			
Type I	Type II	Type III	Type IV
GTF2I	--	--	--
BRAF	--	--	BRAF
KRAS	KRAS	KRAS	KRAS
HRAS	--	--	HRAS
CDKN2A	--	--	--
MB21D2	--	--	--
PIK3CA	--	--	--
--	IDH1	--	IDH1
--	NDUFA13	--	--
--	DGCR6L	--	--
--	S100A1	--	--
--	IAPP	--	--
--	--	SLC3A2	--
--	--	KLF3	--
--	--	GNG12	--
--	--	NRAS	NRAS
--	--	RAB9B	--
--	--	--	SH3BGRL2
--	--	--	TNP1
--	--	--	RPL22
--	--	--	MRPL22
--	--	--	CBLN3
--	--	--	PAIP2
--	--	--	SEC61B
--	--	--	DBI
--	--	--	GNA11
--	--	--	ARHGAP1
--	--	--	TVP23A

Pan-cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as follows:

type I, PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-L1

positive with TIL negative; and type IV, PD-L1 negative with TIL positive. Drive genes is detected by a

function oncodrive from R package “maftools”, which is based on algorithm oncodriveCLUST which

was originally implemented in Python. Abbreviations: GTF2I, general transcription factor Iii; BRAF, B-

Raf Proto-Oncogene; KRAS, kirsten ras; HRAS, HRas proto-oncogene; CDKN2A, cyclin dependent kinase inhibitor 2A; MB21D2, Mab-21 domain containing 2; PIK3CA, phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha; IDH1, isocitrate dehydrogenase (NADP(+)) 1; NDUFA13, NADH:ubiquinone oxidoreductase subunit A13; DGCR6L, DiGeorge syndrome critical region gene 6 like; S100A1, S100 calcium binding protein A1; IAPP, islet amyloid polypeptide; SLC3A2, solute carrier family 3 member 2; KLF3, Kruppel like factor 3; GNG12, G protein subunit gamma 12; NRAS, NRAS proto-oncogene; RAB9B, RAB9B, member RAS oncogene family; SH3BGRL2, SH3 domain binding glutamate rich protein like 2; TNP1, transition protein 1; RPL22, ribosomal protein L22; MRPL22, mitochondrial ribosomal protein L22; CBLN3, cerebellin 3 precursor; PAIP2, poly(A) binding protein interacting protein 2; SEC61B, SEC61 translocon subunit beta; DBI, diazepam binding inhibitor; GNA11, G protein subunit alpha 11; ARHGAP1, Rho GTPase activating protein 1; TVP23A, trans-golgi network vesicle protein 23 homolog A.

Table S8. Statistical data of 75 immune related genes across the four subtypes of tumor immune

microenvironment.

Genes	log10(TPM median + 1)				Amplification frequency				Deletion frequency			
	Type I	Type	Type III	Type IV	Type	Type II	Type III	Type IV	Type I	Type	Type III	Type IV
		II			I					II		IV
CD80	0.3203	0.2187	0.5281	0.1387	- 0.0138	0.0101	0.0097	-0.0098	- 0.0019	0.0043	0.0160	- 0.0062
CD28	0.4961	0.3693	0.5735	0.2757	- 0.0215	0.0081	0.0039	-0.0066	0.0184	0.0005	0.0401	- 0.0076
ICOSLG	0.1018	0.1332	0.1294	0.1010	- 0.0161	0.0093	-0.0081	-0.0063	- 0.0081	0.0036	0.0033	- 0.0033
PDCD1L G2	0.9779	0.6180	1.2218	0.4172	0.0632	-0.0060	0.1088	-0.0147	- 0.0290	0.0119	- 0.0103	- 0.0075
CD274	1.3548	0.5686	1.4731	0.5148	0.0634	-0.0057	0.1073	-0.0147	- 0.0289	0.0120	- 0.0102	- 0.0077
VTCN1	0.1741	0.5848	0.4184	0.2942	- 0.0155	0.0078	-0.0057	-0.0054	- 0.0068	0.0064	0.0290	- 0.0097
SLAMF7	1.0834	0.7382	1.3993	0.6645	- 0.0145	0.0163	0.0104	-0.0156	- 0.0073	0.0015	- 0.0005	- 0.0009
BTN3A2	1.5395	1.2574	1.4813	1.3310	0.0069	0.0064	-0.0001	-0.0064	- 0.0172	0.0063	0.0117	- 0.0064
BTN3A1	1.4734	1.2863	1.4860	1.2852	0.0071	0.0066	0.0002	-0.0067	- 0.0172	0.0063	0.0117	- 0.0064
C10orf54	1.5927	1.4480	1.5955	1.3713	- 0.0239	0.0087	0.0050	-0.0071	- 0.0070	0.0002	0.0045	- 0.0004
CD276	1.6237	1.8152	1.8457	1.6625	- 0.0032	0.0037	-0.0025	-0.0029	0.0008	0.0036	- 0.0102	- 0.0019
TNFSF9	0.8055	0.6094	1.0038	0.5845	0.0011	0.0072	0.0004	-0.0068	- 0.0241	0.0105	- 0.0135	- 0.0061
TNF	0.5080	0.4993	0.6486	0.3278	0.0102	0.0005	-0.0005	-0.0011	- 0.0183	0.0077	0.0176	- 0.0084
TNFSF4	0.5958	0.6049	0.7296	0.4572	- 0.0182	0.0127	-0.0079	-0.0094	0.0013	0.0021	- 0.0008	- 0.0020
IL1B	0.8064	0.7561	1.0571	0.5805	- 0.0198	0.0071	0.0074	-0.0063	- 0.0052	0.0029	- 0.0073	- 0.0013
CXCL9	1.9398	1.1779	2.0973	1.1652	- 0.0148	0.0154	0.0081	-0.0145	- 0.0031	0.0028	- 0.0035	- 0.0019
CXCL10	2.1239	1.4458	2.2517	1.4066	- 0.0147	0.0153	0.0083	-0.0144	- 0.0031	0.0028	- 0.0035	- 0.0019
CCL5	2.0905	1.5293	2.1492	1.5699	-	0.0025	-0.0035	-0.0012	-	0.0118	-	-

					0.0097				0.0247		0.0079	0.0081
VEGFB	2.1423	2.2064	2.1531	2.1869	0.0025	0.0134	0.0021	-0.0130	-	0.0055	-	-
									0.0109		0.0061	0.0035
CX3CL1	1.5736	1.4184	1.6616	1.4120	-	0.0019	0.0085	-0.0025	-	0.0072	-	-
					0.0065				0.0015		0.0091	0.0052
TGFB1	1.9251	1.8305	2.0088	1.6852	-	0.0051	0.0346	-0.0085	-	0.0106	0.0127	-
					0.0179				0.0262			0.0098
VEGFA	1.4662	1.4905	1.5972	1.4913	-	0.0059	0.0030	-0.0052	-	0.0052	-	-
					0.0109				0.0081		0.0031	0.0038
CD70	0.5859	0.2989	0.6044	0.3016	0.0010	0.0070	0.0020	-0.0069	-	0.0111	-	-
									0.0237		0.0131	0.0068
CD40LG	0.4312	0.2399	0.3926	0.2615	0.0105	0.0041	0.0138	-0.0066	-	0.0066	-	-
									0.0115		0.0031	0.0049
IL10	0.3088	0.2937	0.4467	0.1616	-	0.0105	-0.0047	-0.0076	-	0.0055	-	-
					0.0208				0.0044		0.0050	0.0040
IFNG	0.4397	0.0956	0.5770	0.1034	-	0.0126	0.0098	-0.0113	-	0.0039	-	-
					0.0272				0.0053		0.0004	0.0032
IL1A	0.1944	0.1882	0.6286	0.0934	-	0.0068	0.0078	-0.0061	-	0.0026	-	-
					0.0194				0.0054		0.0076	0.0010
IL12A	0.1982	0.2505	0.3109	0.1409	-	0.0084	0.0452	-0.0135	-	0.0040	0.0007	-
					0.0137				0.0041			0.0036
IFNA2	0.0000	0.0000	0.0000	0.0000	0.0047	0.0029	0.0175	-0.0055	-	0.0184	0.0227	-
									0.0074			0.0198
IFNA1	0.0000	0.0000	0.0000	0.0000	0.0048	0.0027	0.0193	-0.0057	-	0.0184	0.0241	-
									0.0094			0.0199
IL4	0.0586	0.0509	0.0404	0.0450	-	0.0008	-0.0274	0.0036	-	0.0036	0.0028	-
					0.0059				0.0119			0.0029
IL2	0.0309	0.0000	0.0382	0.0167	-	0.0054	-0.0002	-0.0049	-	0.0050	-	-
					0.0012				0.0098		0.0021	0.0037
IL13	0.0217	0.0160	0.0238	0.0098	-	0.0011	-0.0276	0.0034	-	0.0037	0.0029	-
					0.0061				0.0117			0.0030
TNFRSF18	1.1031	0.8110	1.2711	0.7118	-	0.0145	0.0041	-0.0122	-	0.0115	0.0048	-
					0.0263				0.0484			0.0081
TIGIT	0.6805	0.3483	0.8267	0.3037	-	0.0102	0.0116	-0.0099	-	0.0032	0.0102	-
					0.0187				0.0009			0.0044
PDCD1	0.9511	0.4209	0.9007	0.4105	-	0.0089	-0.0028	-0.0065	0.0285	0.0098	0.0596	-
					0.0182							0.0197
CTLA4	0.7928	0.4011	0.9165	0.3619	-	0.0080	0.0041	-0.0066	0.0180	0.0010	0.0397	-
					0.0213							0.0080
IL2RA	0.7189	0.5409	1.0712	0.3913	-	0.0131	-0.0080	-0.0105	0.0032	0.0025	0.0008	-
					0.0083							0.0027
TNFRSF4	0.9307	0.7939	0.9990	0.7702	-	0.0145	0.0041	-0.0122	-	0.0115	0.0048	-
					0.0263				0.0484			0.0081
CD27	1.2473	0.7632	1.2527	0.7593	-	0.0163	0.0054	-0.0144	-	0.0038	0.0067	-

					0.0210				0.0185		0.0032	
LAG3	1.0336	0.6141	1.1296	0.5641	- 0.0167	0.0159	0.0061	-0.0145	- 0.0241	0.0029	0.0082	- 0.0022
TNFRSF9	0.4974	0.2787	0.6772	0.2172	- 0.0276	0.0125	0.0047	-0.0104	- 0.0492	0.0112	0.0038	- 0.0075
ICOS	0.7432	0.2714	0.7143	0.2374	- 0.0209	0.0076	0.0044	-0.0062	0.0178	0.0016	0.0395	- 0.0084
BTLA	0.2973	0.1416	0.3076	0.1121	- 0.0170	0.0103	0.0099	-0.0099	- 0.0033	0.0006	0.0131	- 0.0023
KIR2DL3	0.0348	0.0119	0.0358	0.0138	- 0.0120	0.0075	0.0245	-0.0097	- 0.0218	0.0137	0.0083	- 0.0124
KIR2DL1	0.0323	0.0152	0.0376	0.0161	- 0.0120	0.0075	0.0245	-0.0097	- 0.0218	0.0137	0.0083	- 0.0124
TNFRSF1 4	1.5573	1.3036	1.4711	1.4984	- 0.0263	0.0145	0.0041	-0.0122	- 0.0484	0.0115	0.0048	- 0.0081
EDNRB	0.7013	0.8715	0.7557	0.9276	0.0052	0.0089	-0.0117	-0.0069	- 0.0172	0.0033	- 0.0093	- 0.0006
CD40	1.6639	1.2526	1.7019	1.3159	- 0.0211	0.0090	-0.0163	-0.0045	- 0.0164	0.0042	0.0092	- 0.0041
ADORA2 A	0.0857	0.0805	0.0930	0.0565	- 0.0063	0.0155	0.0078	-0.0151	- 0.0056	0.0015	0.0026	- 0.0013
TLR4	0.7458	0.9877	1.0592	0.7817	- 0.0059	0.0081	0.0002	-0.0072	- 0.0035	0.0035	- 0.0022	- 0.0027
HAVCR2	1.1448	1.1057	1.3836	0.8393	- 0.0187	0.0038	-0.0315	0.0023	- 0.0098	0.0057	0.0051	- 0.0054
ITGB2	1.7275	1.5556	1.8711	1.3055	- 0.0146	0.0081	-0.0066	-0.0056	- 0.0100	0.0034	0.0031	- 0.0029
ICAM1	1.8762	1.5580	2.0402	1.4881	- 0.0173	0.0107	-0.0060	-0.0079	- 0.0084	0.0069	- 0.0058	- 0.0050
SELP	0.5683	0.5351	0.6488	0.5996	- 0.0233	0.0112	-0.0026	-0.0084	0.0033	0.0017	0.0011	- 0.0020
HLA- DRB5	2.6365	2.1681	2.5815	2.1948	0.0102	0.0005	-0.0005	-0.0011	- 0.0183	0.0077	0.0176	- 0.0084
HLA- DQA1	1.8627	1.4800	1.9484	1.3870	0.0102	0.0005	-0.0005	-0.0011	- 0.0183	0.0077	0.0176	- 0.0084
HLA- DQB1	2.2295	1.6782	2.0907	1.6972	0.0102	0.0005	-0.0005	-0.0011	- 0.0183	0.0077	0.0176	- 0.0084
MICA	1.3878	1.3270	1.3968	1.3667	0.0102	0.0005	-0.0005	-0.0011	- 0.0183	0.0077	0.0176	- 0.0084
MICB	1.0693	0.8610	1.2010	0.7497	0.0102	0.0005	-0.0005	-0.0011	- 0.0183	0.0077	0.0176	- 0.0084
HLA- DQA2	1.7196	1.2854	1.7498	1.2424	0.0102	0.0005	-0.0005	-0.0011	- 0.0183	0.0077	0.0176	- 0.0084
HLA-	1.6699	1.0870	1.5824	1.1016	0.0102	0.0005	-0.0005	-0.0011	-	0.0077	0.0176	-

DQB2										0.0183		0.0084
HLA-B	3.5472	2.9744	3.3752	3.2447	0.0102	0.0005	-0.0005	-0.0011	-	0.0077	0.0176	-
									0.0183			0.0084
HLA-A	3.4341	2.8875	3.2356	3.1685	0.0072	0.0025	-0.0100	-0.0014	-	0.0079	0.0227	-
									0.0112			0.0099
HLA-C	3.3619	2.9029	3.2004	3.1143	0.0102	0.0005	-0.0005	-0.0011	-	0.0077	0.0176	-
									0.0183			0.0084
HLA-DRA	3.3900	3.0198	3.4367	2.9671	0.0102	0.0005	-0.0005	-0.0011	-	0.0077	0.0176	-
									0.0183			0.0084
HLA-DRB1	3.1861	2.7301	3.1601	2.7442	0.0102	0.0005	-0.0005	-0.0011	-	0.0077	0.0176	-
									0.0183			0.0084
HLA-DPB1	2.6109	2.1965	2.5544	2.1987	0.0116	0.0002	-0.0107	0.0005	-	0.0077	0.0125	-
									0.0183			0.0076
HLA-DPA1	2.3150	1.9591	2.3219	1.9226	0.0116	0.0002	-0.0107	0.0005	-	0.0080	0.0122	-
									0.0185			0.0079
IDO1	1.3350	0.7901	1.5796	0.7838	-	0.0247	0.0358	-0.0255	-	0.0044	-	-
					0.0385				0.0173		0.0076	0.0018
GZMA	1.6443	1.0393	1.6682	1.0802	-	0.0042	0.0024	-0.0037	-	0.0057	-	-
					0.0074				0.0207		0.0099	0.0024
PRF1	1.3762	0.8006	1.3650	0.8106	-	0.0082	0.0057	-0.0071	-	0.0019	0.0014	-
					0.0198				0.0067			0.0015
ARG1	0.0855	0.1031	0.0873	0.0949	0.0000	0.0094	0.0007	-0.0088	-	0.0055	-	-
									0.0227		0.0094	0.0021
HMGB1	1.9774	1.9661	1.9417	1.8891	-	0.0104	0.0012	-0.0086	-	-	0.0111	0.0016
					0.0168				0.0147	0.0024		
ENTPD1	0.9890	1.0906	1.1167	0.9566	-	0.0054	0.0040	-0.0047	-	0.0038	0.0071	-
					0.0131				0.0085			0.0040

Pan-cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as follows:

type I, PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-L1

positive with TIL negative; and type IV, PD-L1 negative with TIL positive. Amplification frequency (the

difference between the fraction of samples in which an immune gene is amplified in a particular

subtype and the amplification fraction in all samples); and the deletion frequency (as amplifications) for

75 immune genes by immune subtype. Abbreviations: log10(TPM median + 1), the log10 value of the

median of TPM plus one.

Table S9. The pathway scores of the shared pathways across the four subtypes of tumor immune microenvironment.

Pathway	Pathway score			
	Type I	Type II	Type III	Type IV
Complement and coagulation cascades	0.3925	0.0856	0.3512	0.1707
Retinol metabolism	0.3493	0.0733	0.3868	0.1906
Drug metabolism - cytochrome P450	0.3646	0.0661	0.3819	0.1874
Metabolism of xenobiotics by cytochrome P450	0.3763	0.0613	0.3882	0.1742
Chemical carcinogenesis	0.3823	0.0681	0.3812	0.1684
Steroid hormone biosynthesis	0.3608	0.0637	0.4422	0.1332
Drug metabolism - other enzymes	0.3890	0.0582	0.4255	0.1274
Ascorbate and aldarate metabolism	0.3562	0.0846	0.4158	0.1434
Glucuronate pathway	0.4071	0.0593	0.4037	0.1299
Pentose and glucuronate interconversions	0.4071	0.0593	0.4037	0.1299
Porphyrin and chlorophyll metabolism	0.4071	0.0593	0.4037	0.1299
Fat digestion and absorption	0.3525	0.0435	0.4726	0.1314
Vitamin digestion and absorption	0.3877	0.0480	0.4859	0.0784
Bile secretion	0.4251	0.1051	0.3327	0.1370
Pancreatic secretion	0.3708	0.1056	0.4237	0.0999
Protein digestion and absorption	0.3598	0.1167	0.4335	0.0901
Tyrosine metabolism	0.2231	0.0611	0.5195	0.1964
Glycolysis / Gluconeogenesis	0.3381	0.0856	0.4206	0.1557
Fatty acid degradation	0.3016	0.1124	0.4034	0.1825
Primary bile acid biosynthesis	0.3489	0.1102	0.3517	0.1891
PPAR signaling pathway	0.4308	0.0769	0.3531	0.1392
Bile acid biosynthesis, cholesterol	0.3480	0.1046	0.3550	0.1924
Linoleic acid metabolism	0.2511	0.0965	0.5003	0.1521
Arachidonic acid metabolism	0.2808	0.0708	0.5192	0.1291

Pan-cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as follows:

type I, PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-L1

positive with TIL negative; and type IV, PD-L1 negative with TIL positive.

Table S10. Statistical data of the specific gene TPM across the four subtypes of tumor immune microenvironment.

Genes	$\bar{x} \pm \sigma$				p value
	Type I	Type II	Type III	Type IV	
IFNG	3.6821±4.9707	0.9872±2.8601	6.2627±12.3615	0.9642±2.0909	<2.2e-16
TNF	5.5755±12.5646	5.4704±11.8647	8.8042±20.2282	3.2863±8.2091	<2.2e-16
IL12A	1.3549±3.1969	1.8349±3.391	1.8474±2.7986	1.0006±2.2759	<2.2e-16
IL12B	0.6232±1.457	0.4756±4.2685	1.1769±6.6174	0.2447±0.904	<2.2e-16
VEGFA	47.1882±75.8538	59.906±112.5433	55.4688±60.8448	68.5698±118.2574	1.2e-07
TGFB1	94.7305±54.7422	85.5343±71.2495	118.3545±83.4194	64.2295±60.054	<2.2e-16
IL6	13.8718±93.1519	9.7069±34.4149	23.8079±50.4288	5.3844±17.4216	<2.2e-16
IL10	1.7147±2.772	1.8251±8.8754	4.2433±15.7911	0.8615±1.6081	<2.2e-16
GZMB	40.2642±49.1587	12.0498±25.8512	57.189±96.4566	13.1238±53.808	<2.2e-16
PRF1	29.1039±28.8787	10.8678±19.7757	38.2342±53.6238	11.1715±17.645	<2.2e-16

Pan-cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as follows:

type I, PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-L1

positive with TIL negative; and type IV, PD-L1 negative with TIL positive.

Abbreviations: $\bar{x} \pm \sigma$, mean \pm standard deviation; IFNG, interferon gamma; TNF, tumor necrosis factor;

IL12A, interleukin 12A; IL12B, interleukin 12B; VEGFA, vascular endothelial growth factor A; TGFB1,

transforming growth factor beta 1; IL6, interleukin 6; IL10, interleukin 10; GZMB, granzyme B; PRF1,

perforin-1.

Table S11. Statistical data of 8 immune cell proportion across the four subtypes of tumor immune microenvironment in validation cohort from the Gene Expression Omnibus database.

Immune cell types	$\bar{x} \pm \sigma$				p value
	Type I	Type II	Type III	Type IV	
T cells	0.4328±0.0731	0.2641±0.0847	0.3544±0.0943	0.3294±0.0983	<2.2e-16
B cells	0.0429±0.0349	0.0194±0.0226	0.0237±0.0335	0.0258±0.0283	<2.2e-16
Macrophages	0.4095±0.0957	0.547±0.1239	0.5032±0.1145	0.4897±0.1215	<2.2e-16
DC cells	0.0105±0.0168	0.0101±0.0154	0.0117±0.0201	0.0111±0.0165	0.31
NK cells	0.0596±0.0251	0.0387±0.0223	0.0493±0.0274	0.0459±0.0228	<2.2e-16
Mast cells	0.0419±0.0286	0.1179±0.0726	0.0546±0.0521	0.0966±0.0619	<2.2e-16
Eosinophils	0.0±0.0	0.0±0.0006	0.0±0.0	0.0±0.0005	0.6
Neutrophils	0.0028±0.0153	0.0029±0.0094	0.003±0.0074	0.0015±0.0043	1.9e-05

Breast cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as follows:

type I, PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-L1 positive

with TIL negative; and type IV, PD-L1 negative with TIL positive. Abbreviations: $\bar{x} \pm \sigma$, mean \pm standard

deviation; DC cells, dendritic cells; NK cells, Natural killer cells.

Table S12. The relative proportion of 20 Immune cell subtypes across the four subtypes of tumor

immune microenvironment in validation cohort from the Gene Expression Omnibus database.

Immune cell subtypes	Relative proportion			
	Type I	Type II	Type III	Type IV
T cells CD8	37.8199	29.39244	34.82628	31.9061
T cells CD4 naive	0	0.005558	0	0.000943
T cells CD4 memory resting	43.69211	57.3395	48.31294	55.24973
T cells CD4 memory activated	2.000126	0.071391	1.097853	0.237152
T cells follicular helper	7.59751	7.240071	7.87873	5.852387
T cells gamma delta	0.448493	0.073389	0.466406	0.11765
T cells regulatory (Tregs)	8.441861	5.87765	7.417789	6.636037
B cells naive	74.06252	74.56335	72.51838	76.04757
B cells memory	23.2216	16.94169	20.77287	16.53687
Plasma cells	2.715881	8.494962	6.708746	7.41556
Dendritic cells resting	79.86451	90.80358	78.48169	90.61175
Dendritic cells activated	20.13549	9.196421	21.51831	9.388251
NK cells resting	0.085976	5.476928	0.98342	1.449035
NK cells activated	99.91402	94.52307	99.01658	98.55096
Mast cells resting	97.19886	93.85222	92.07631	95.20349
Mast cells activated	2.801139	6.147775	7.92369	4.796508
Monocytes	5.567441	5.912497	6.076638	6.1949
Macrophages M0	21.96947	20.33371	24.84728	17.62694
Macrophages M1	24.55563	9.010947	16.52947	13.72083
Macrophages M2	47.90746	64.74284	52.5466	62.45733

Breast cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as

follows: type I, PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-

L1 positive with TIL negative; and type IV, PD-L1 negative with TIL positive. The relative proportion

refers to the proportion of each immune cell subtype to the immune cell type which it belongs.

Table S13. Statistical data of the specific gene TPM across the four subtypes of tumor immune

microenvironment in validation cohort from the Gene Expression Omnibus database.

Genes	$\bar{x} \pm \sigma$				p value
	Type I	Type II	Type III	Type IV	
IFNG	1.3761±1.1004	0.172±0.1604	1.197±1.2829	0.155±0.1951	<2.2e-16
TNF	2.0154±2.2279	0.779±1.0797	2.2545±2.9247	0.5041±0.6719	<2.2e-16
IL12A	0.4873±0.6421	0.272±0.3575	0.6166±0.5665	0.1731±0.2657	<2.2e-16
IL12B	0.3923±0.296	0.1322±0.0892	0.3798±0.3122	0.0976±0.0867	<2.2e-16
VEGFA	23.6823±37.3677	23.1697±20.3401	37.5709±32.1312	10.9173±12.1465	<2.2e-16
TGFB1	35.7903±15.8189	36.8513±22.7435	57.1662±29.7121	20.2818±13.3514	<2.2e-16
IL6	2.2228±6.7072	1.515±2.9958	4.6579±12.2949	0.8278±2.169	<2.2e-16
IL10	0.8486±0.47	0.4593±0.3801	1.204±1.4405	0.2791±0.2449	<2.2e-16
GZMB	19.6877±12.8835	1.8425±3.0091	17.652±16.3429	2.2164±3.7294	<2.2e-16
PRF1	8.5772±5.4426	1.3393±1.1831	7.9223±6.4884	1.2897±1.3609	<2.2e-16

Breast cancer samples are divided into four groups based on PD-L1 expression and TIL Z score as

follows: type I, PD-L1 positive with TIL positive; type II, PD-L1 negative with TIL negative; type III, PD-

L1 positive with TIL negative; and type IV, PD-L1 negative with TIL positive.

Abbreviations: $\bar{x} \pm \sigma$, mean \pm standard deviation; IFNG, interferon gamma; TNF, tumor necrosis factor;

IL12A, interleukin 12A; IL12B, interleukin 12B; VEGFA, vascular endothelial growth factor A; TGFB1,

transforming growth factor beta 1; IL6, interleukin 6; IL10, interleukin 10; GZMB, granzyme B; PRF1,

perforin-1.