

**Supplementary Table S2. Characteristics of samples in TCGA according to cancer type**

Characteristic	All (N = 6,685)	BLCA (N = 407)	BRCA (N = 1,098)	CESC (N = 303)	COAD (N = 382)	GBM (N = 166)	HNSC (N = 521)	KIRC (N = 534)	LIHC (N = 373)	LUAD (N = 513)	LUSC (N = 501)	PRAD (N = 495)	SKCM (N = 468)	STAD (N = 415)	THCA (N = 509)
Age, median (IQR), yr	61 (51–70)	69 (60–76)	58 (48–67)	46 (38–56)	66 (55–75)	60 (51–69)	61 (53–69)	61 (52–70)	61 (51–69)	66 (59–73)	68 (62–73)	61 (56–66)	58 (48–71)	67 (58–73)	46 (35–58)
Gender, No. (%)															
Male	3,401 (51)	300 (74)	12 (1)	0 (0)	207 (55)	107 (65)	383 (74)	345 (65)	251 (67)	236 (46)	370 (74)	494 (100)	290 (62)	267 (64)	139 (27)
Female	3,266 (49)	106 (26)	1,085 (99)	302 (100)	170 (45)	58 (35)	137 (26)	188 (35)	121 (33)	276 (54)	130 (26)	0 (0)	177 (38)	147 (36)	369 (73)
OS, median (IQR), mo	18 (11–32)	28 (15–55)	21 (12–41)	22 (13–38)	12 (5–18)	21 (12–39)	18 (11–32)	39 (18–63)	19 (11–36)	22 (14–37)	22 (11–42)	31 (17–48)	37 (16–80)	14 (8–25)	31 (17–50)
No. of mutations, median (IQR)	50 (23–129)	168 (102–277)	33 (21–59)	82 (49–140)	53 (39–87)	36 (27–45)	102 (65–148)	14 (10–18)	82 (54–120)	157 (81–292)	219 (160–296)	37 (29–51)	279 (124–528)	118 (68–265)	16 (10–27)
No. of neoantigens, median (IQR)	11 (6–22)	25 (16–46)	7 (4–11)	15 (9–25)	--	10 (7–13)	18 (11–27)	10 (7–15)	20 (12–32)	28 (16–48)	36 (25–51)	7 (4–10)	33 (16–56)	22 (13–29)	3 (2–5)
Log2 (PD-L1 RSEM), median (IQR)	4.94 (3.73–6.15)	4.32 (3.12–6.21)	4.38 (3.55–5.27)	5.73 (4.40–7.03)	4.12 (3.23–5.30)	4.94 (4.14–5.89)	6.35 (5.25–7.47)	5.38 (4.73–6.05)	3.20 (2.37–3.98)	5.98 (4.98–6.89)	6.22 (5.22–7.59)	3.23 (2.47–3.86)	4.67 (3.52–6.00)	5.30 (4.40–6.14)	5.63 (4.50–6.44)
Log2 (CD8A RSEM), median (IQR)	7.23 (5.99–8.56)	6.37 (4.82–7.87)	7.27 (6.21–8.35)	7.73 (6.59–9.03)	6.32 (5.09–7.37)	5.40 (4.58–6.40)	7.29 (5.80–8.69)	8.70 (7.7–9.92)	6.03 (4.94–7.34)	7.95 (6.97–8.92)	7.70 (6.73–8.75)	6.66 (5.87–7.37)	7.74 (5.79–9.62)	7.83 (6.51–8.86)	6.86 (5.92–7.97)
Log2 (CYT RSEM), median (IQR)	6.65 (5.37–8.00)	6.22 (4.51–7.62)	6.13 (5.03–7.26)	7.68 (6.44–8.75)	5.22 (4.29–6.22)	5.43 (4.19–6.45)	7.37 (6.19–8.51)	8.46 (7.79–9.24)	6.05 (5.05–7.24)	7.51 (6.70–8.47)	7.39 (6.55–8.33)	5.57 (4.82–6.24)	6.86 (5.20–8.58)	7.05 (6.05–8.06)	5.88 (4.99–6.73)

Abbreviations: BLCA, bladder urothelial carcinoma; BRCA, breast cancer; CESC, cervical cancer; COAD, colon and rectal adenocarcinoma; GBM, glioblastoma multiforme; HNSC, head and neck squamous cell carcinoma; IQR, interquartile range; KIRC, kidney clear cell carcinoma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; OS, overall survival; PRAD, prostate adenocarcinoma; RSEM, RNA-Seq by Expectation Maximization; SKCM, skin cutaneous melanoma; STAD, stomach adenocarcinoma; TCGA, The Cancer Genome Atlas; THCA, thyroid carcinoma.

**Supplementary Table S3. Distribution of TMITs according to cancer type**

Cancer type	No. of cases	TMIT (PD-L1 + CD8A), No. (%)				TMIT (PD-L1 + CYT), No. (%)			
		I	II	III	IV	I	II	III	IV
BLCA	407	--	--	--	--	72 (18)	173 (43)	10 (2)	152 (37)
BRCA	1,098	--	--	--	--	291 (27)	398 (36)	40 (4)	369 (34)
CESC	303	128 (42)	52 (17)	115 (38)	8 (3)	153 (50)	46 (15)	90 (30)	14 (5)
COAD	382	71 (19)	221 (58)	25 (7)	65 (17)	64 (17)	272 (71)	32 (8)	14 (4)
KIRC	534	84 (16)	189 (35)	238 (45)	23 (4)	--	--	--	--
LIHC	373	145 (39)	70 (19)	42 (11)	116 (31)	--	--	--	--
LUAD	513	161 (31)	184 (36)	123 (24)	45 (9)	257 (50)	72 (14)	27 (5)	157 (31)
SKCM	468	--	--	--	--	175 (37)	151 (32)	12 (3)	130 (28)
STAD	415	--	--	--	--	72 (17)	258 (62)	53 (13)	32 (8)
THCA	509	--	--	--	--	331 (65)	49 (10)	51 (10)	78 (15)

Abbreviations: BLCA, bladder urothelial carcinoma; BRCA, breast cancer; CESC, cervical cancer; COAD, colon and rectal adenocarcinoma; KIRC, kidney clear cell carcinoma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; SKCM, skin cutaneous melanoma; STAD, stomach adenocarcinoma; THCA, thyroid carcinoma; TMIT, tumor microenvironment immune type.