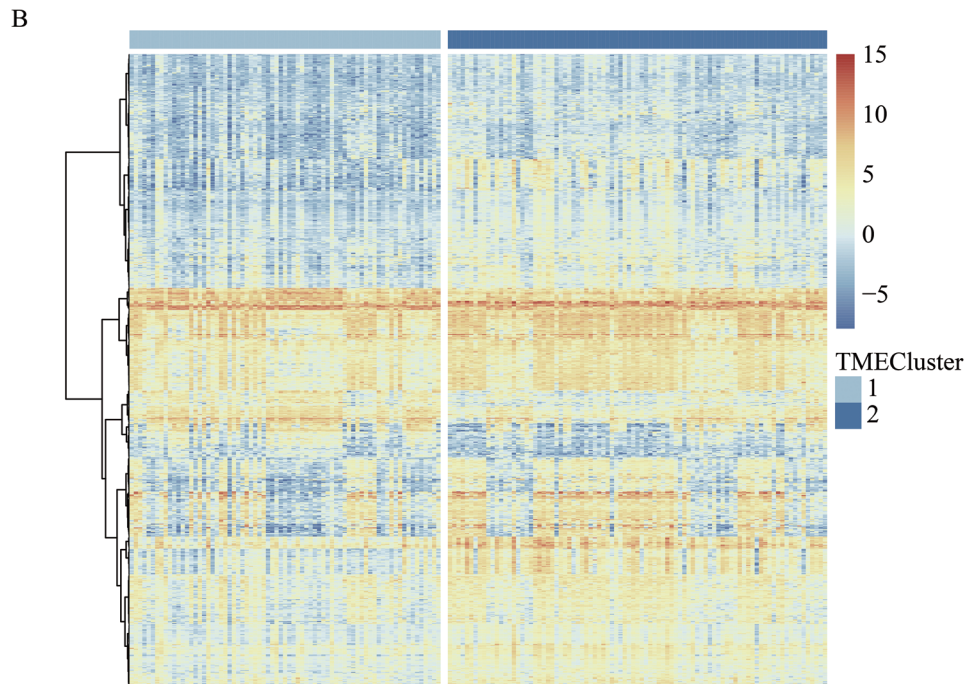
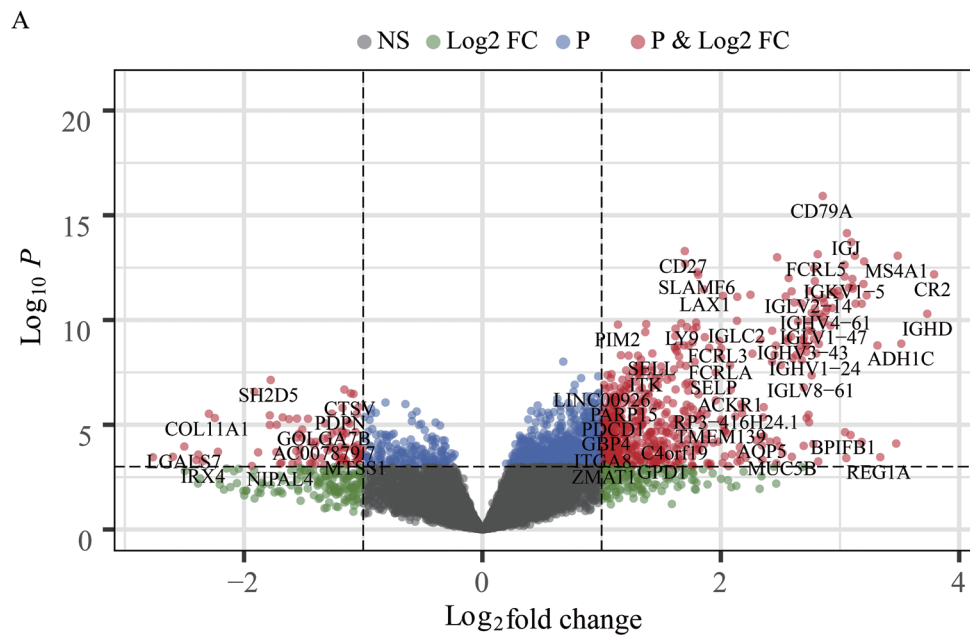
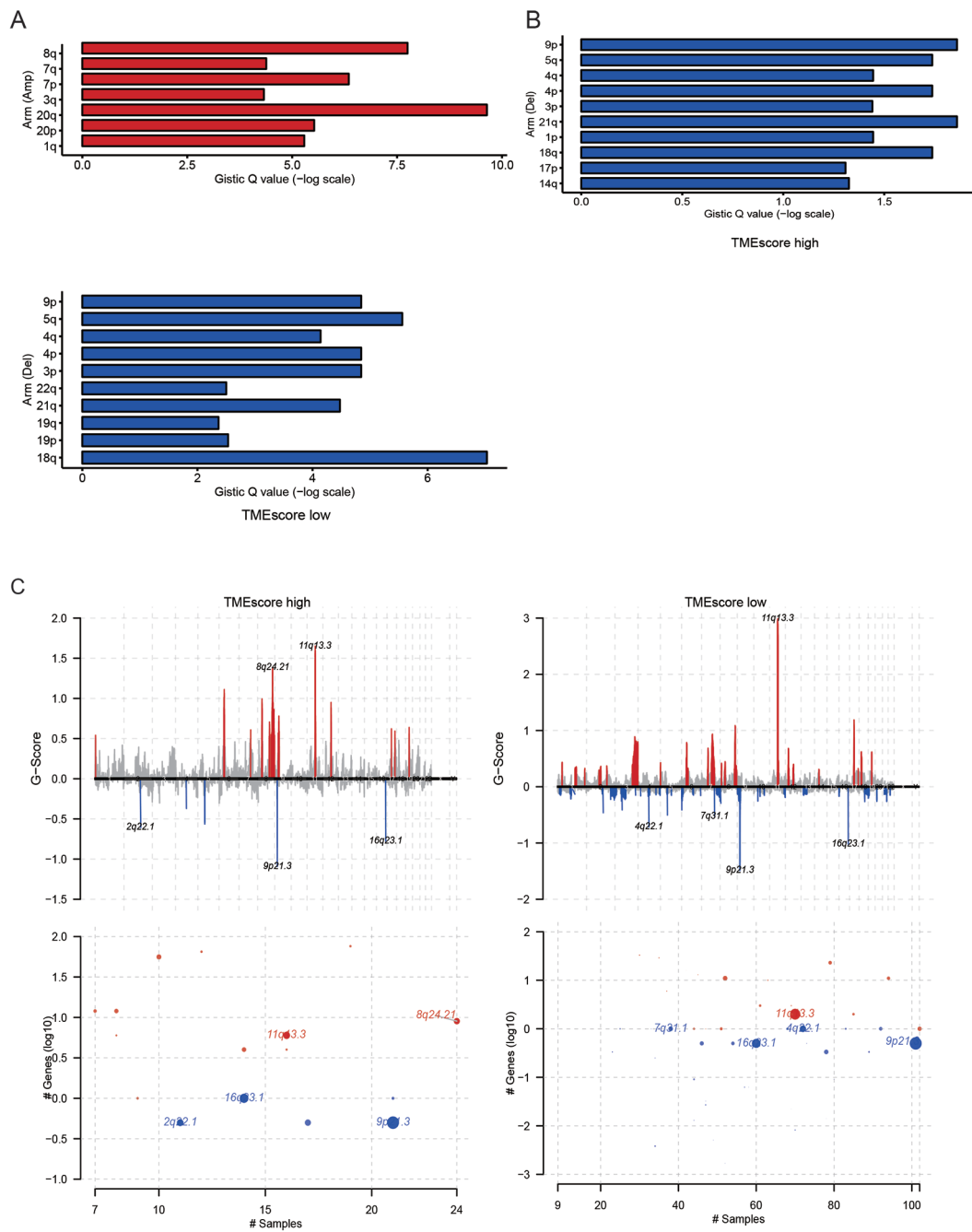


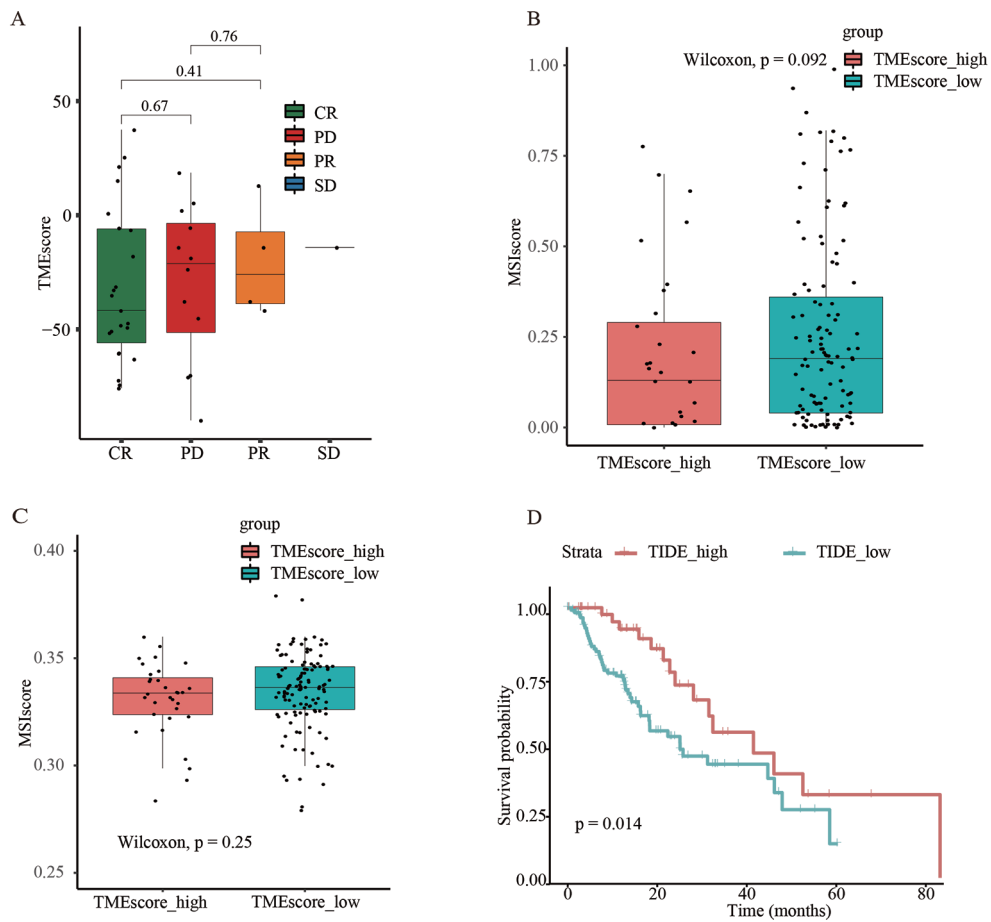
**Figure S1** TME clusters of tumor-immune cells. (A) Estimation of the optimal k value using the elbow method. (B) Consensus matrixes for K=2, displaying the clustering stability using 1,000 iterations of hierarchical clustering. (C) The proportion of tumor-immune cells in the TME cluster. (D) The distribution of tumor-immune cells in the TME cluster. TME, tumor microenvironment.



**Figure S2** DEGs in the TME cluster. (A) Volcano plot of DEGs in the TME cluster. (B) The expression values of DEGs in the TME cluster. DEG, differentially expressed gene; TME, tumor microenvironment.



**Figure S3** CNV analysis and Kaplan-Meier analysis. (A) Amplification and deletion of chromosome arm in both TME score-low. (B) Deletion of chromosome arm in both TME score-high. (C) Distribution of localized copy number amplification and deletion regions (red and blue represent amplification and deletion, respectively). CNV, copy number variation; TME, tumor microenvironment.



**Figure S4** The therapeutic benefits of the TME score. (A) The predictive value of the TME score in EC patients who received adjuvant chemotherapy. (B and C) The relationship between the TME score and MSI (Sensor score and MANTIS cohorts). (D) Kaplan-Meier curves of TIDE. TME, tumor microenvironment; EC, esophageal carcinoma; MSI, microsatellite instability; TIDE, the Tumor Immune Dysfunction and Exclusion; CR, complete response; PR, partial response; SD, stable disease; PD, progressive disease.

**Table S1** Association between immune cells and OS

Cell type	Risk	Log rank P value
Eosinophils	Negative	0.033
NK.cells.activated	Positive	0.106
Dendritic.cells.resting	Negative	0.179
T.cells.CD4.memory.activated	Negative	0.202
Mast.cells.activated	Negative	0.254
B.cells.memory	Positive	0.292
T.cells.follicular.helper	Negative	0.297
Macrophages.M1	Positive	0.306
Mast.cells.resting	Positive	0.315
Plasma.cells	Positive	0.320
Neutrophils	Negative	0.565
T.cells.gamma.delta	Positive	0.579
Monocytes	Positive	0.608
T.cells.CD4.naive	Positive	0.619
T.cells.regulatory.Tregs.	Negative	0.623
T.cells.CD8	Positive	0.629
Macrophages.M2	Negative	0.648
T.cells.CD4.memory.resting	Negative	0.655
NK.cells.resting	Negative	0.690
Macrophages.M0	Negative	0.719
B.cells.naive	Positive	0.775
Dendritic.cells.activated	Positive	0.833

OS, overall survival.

**Table S2** Signature genes positively associated with the TME

Genes
<i>IGHD, SSTR1, PKDCC, ACSL5, HOXB-AS3, PPP1R16B, DPCR1, SLC44A4, GNA14, DSC3, MECOM, PRR26, C16orf74, CHDH, DUOX2, HOMER3, SLC1A1, CTSE, ALDOB, TRHDE, CD5, SNAI2, MYRF, SHROOM3, GSDMB, BCL2L14, CLDN2, USH1C, ERN2, HABP2, CA13, WDR66, DMBT1, TMPRSS2, GPD1, AC007386.4, TJP3, SULT1B1, ZG16B, PPP1R1B, FAM221A, RP11-324O2.3, AKR7L, ADH6, GATA6, KCNK5, FUT4, TESC, VILL, S1PR5, IRF8, PIWIL4, DNAJC22, PRR15L, FA2H, C9orf152</i>

TME, tumor microenvironment.

**Table S3** Signature genes negatively associated with the TME

Genes
<i>IGJ, CAPN5, CCNI2, HID1, ATP10B, VNN2, PLEKHA6, ARHGEF38, AGT, MYO1A, KLRB1, RP11-1220K2.2, HOXB6, CES3, LGALS4, HSH2D, C4orf19, MUC5B, ARTN, BTNL8, ICA1, TMC5, IQGAP2, VSIG2, SULT1C2, SLC37A1, CDX2, TRIM31, PLS1, METTL7B, SH3BGR2, SAMD5, SMIM24, MYO15B, ADAM28, GTF2IRD2P1, KIAA1244, NCMAP, PPARG, RP3-395M20.8, SLC4A4, DDAH1, HNF4G, TOX3, AC006042.6, CTSS, PIGR, IL17RB, RAB17, OLFM4, ONECUT2, XK, SHH, SLC3A1, GATM, SPNS3, NOSTRIN, DLX2, HNF1A-AS1, GPR35, CYP3A5, PIP5K1B, RP11-739N20.2</i>

TME, tumor microenvironment.

**Table S4** Landscape of the TME in EC

	Age	Sex	Grade	OS (months)	OS status	Score	Group	TME cluster	Purity	Ploidy	TMB
TCGA-JY-A93E-01	61	Male	Stage III	25.2	0	54.21742431	High	2	0.46	3.75	147
TCGA-L5-A8NT-01	69	Male	Stage II	27.1	0	53.3347741	High	2	0.39	3.45	87
TCGA-L5-A4OU-01	81	Male	Stage II	28.98	0	48.7687703	High	2	0.42	4.14	146
TCGA-2H-A9GR-01	80	Male	Stage II	32.42	1	45.99521387	High	2	0.2	3.87	380
TCGA-2H-A9GK-01	43	Male	Stage III	7.62	1	45.73813682	High	2	0.29	3.62	153
TCGA-JY-A938-01	75	Male	Stage II	34.82	0	43.65594148	High	2	0.7	3.85	115
TCGA-JY-A6FD-01	51	Female	Stage II	67.97	0	43.03214985	High	2	0.65	3.93	114
TCGA-IG-A4P3-01	48	Male	Stage II	18.63	1	40.02176844	High	2	0.34	4.04	227
TCGA-Z6-A8JD-01	53	Male	Stage II	3.42	0	36.12807077	High	2	0.25	4.11	182
TCGA-L5-A4OH-01	71	Male	Stage I	32.59	0	29.05047095	High	2	0.62	3.08	174
TCGA-JY-A939-01	77	Male	Stage II	21.68	0	25.80574654	High	2	0.34	4.05	52
TCGA-KH-A6WC-01	82	Male	Stage I	6.27	0	25.41678036	High	2	0.61	2	26
TCGA-L5-A8NW-01	55	Male		46.06	1	23.96660129	High	2	0.4	4.4	130
TCGA-L5-A8NE-01	77	Male	Stage II	55.45	0	22.37891614	High	2	0.28	4.91	214
TCGA-LN-A49S-01	59	Male	Stage II	13.14	0	21.97945873	High	2	0.48	8.95	126
TCGA-V5-AASX-01	74	Male		8.97	0	20.61834862	High	2	0.61	3.84	267
TCGA-L5-A8NU-01	84	Male	Stage II	83.18	1	18.42952882	High	2	0.38	3.76	52
TCGA-L5-A4OG-01	79	Female	Stage I	4.7	0	17.35606076	High	2	0.5	3.85	148
TCGA-L5-A43C-01	81	Male		3.15	0	47.81625028	High	1	0.62	3.61	121
TCGA-VR-A8EY-01	44	Female	Stage II	33.67	0	45.20710463	High	1	0.74	2.35	91
TCGA-JY-A6FB-01	77	Male	Stage I	60.35	0	42.01339107	High	1	0.54	3.94	75
TCGA-IG-A5B8-01	72	Male	Stage I	0.79	1	41.79390784	High	1	0.38	3.91	231
TCGA-LN-A49U-01	62	Male	Stage II	15.34	0	37.46944181	High	1	0.57	4.17	115
TCGA-S8-A6BW-01	51	Male	Stage I	20.37	0	36.18138671	High	1	0.56	3.29	85
TCGA-L5-A88Z-01	70	Female	Stage II	7.39	0	35.72041456	High	1	0.8	1.97	59
TCGA-JY-A6FG-01	50	Male	Stage III	41.49	1	32.61960224	High	1	0.57	4.11	186
TCGA-L5-A891-01	51	Male		3.75	0	31.09107672	High	1	0.45	5.52	144
TCGA-JY-A6FH-01	53	Male	Stage II	47.34	0	30.47473299	High	1	0.22	5.53	108
TCGA-JY-A93F-01	58	Female	Stage I	24.01	0	27.08134281	High	1	0.55	4.09	84
TCGA-IG-A3QL-01	54	Male	Stage II	35.18	0	25.3023902	High	1	0.64	3.07	77
TCGA-LN-A8HZ-01	56	Male	Stage II	12.32	0	21.31145906	High	1	0.5	10.12	91
TCGA-V5-A7RC-06	55	Male		3.42	1	18.62300766	High	1	0.47	3.67	75
TCGA-IG-A97I-01	58	Male	Stage II	12.16	0	17.30201828	High	1	0.65	2	99
TCGA-IG-A625-01	60	Male	Stage III	12.81	1	16.51455926	Low	2	0.66	4.39	45

**Table S4** (continued)

Table S4 (continued)

	Age	Sex	Grade	OS (months)	OS status	Score	Group	TME cluster	Purity	Ploidy	TMB
TCGA-JY-A93D-01	51	Male	Stage III	31.54	1	15.18941367	Low	2	0.25	2.25	95
TCGA-Z6-AAPN-01	57	Male	Stage II	2.66	0	14.52304483	Low	2	0.41	3.81	330
TCGA-V5-AASV-01	67	Male	Stage II	15.34	0	12.97941016	Low	2	0.75	2.26	89
TCGA-Z6-A9VB-01	53	Male	Stage III	1.31	0	12.9078017	Low	2	0.34	7.61	81
TCGA-IG-A3YB-01	61	Male	Stage III	2.63	0	12.72295909	Low	2	0.61	4.02	65
TCGA-V5-A7RB-01	59	Male		5.29	1	12.17730994	Low	2	0.44	4.17	243
TCGA-L5-A8NV-01	75	Male	Stage II	52.53	1	11.44863349	Low	2	0.38	3.14	100
TCGA-JY-A93C-01	47	Male	Stage III	23.16	0	11.09493906	Low	2	0.55	3.16	80
TCGA-L5-A4OX-01	60	Male	Stage II	7.42	1	7.248113325	Low	2	0.65	3.87	115
TCGA-2H-A9GJ-01	57	Male	Stage I	58.51	1	6.561082013	Low	2	0.7	2.1	97
TCGA-L5-A88T-01	86	Male	Stage II	22.8	0	4.715614504	Low	2	0.45	4.01	77
TCGA-L5-A43E-01	74	Male	Stage I	30.22	0	4.53116118	Low	2	0.51	3.36	135
TCGA-L5-A893-01	71	Female	Stage I	3.02	0	3.793991204	Low	2	0.37	4.2	120
TCGA-2H-A9GL-01	74	Male	Stage III	5.91	1	3.728631352	Low	2	0.4	4.8	186
TCGA-L7-A6VZ-01	62	Male	Stage III	10.35	0	0.837002711	Low	2	0.53	8.16	98
TCGA-XP-A8T6-01	54	Male	Stage II	25.07	1	0.530405828	Low	2	0.58	3.8	71
TCGA-R6-A8W5-01	60	Male	Stage IV	15.77	1	-5.454195281	Low	2	0.2	4.15	93
TCGA-IC-A6RF-01	69	Female	Stage I	15.67	0	-5.605140944	Low	2	0.55	2.14	95
TCGA-2H-A9GO-01	58	Male	Stage IV	16.23	1	-6.066961882	Low	2	0.43	8.63	118
TCGA-IG-A8O2-01	62	Male	Stage III	4.66	1	-8.354187901	Low	2	0.61	3.2	109
TCGA-VR-AA7I-01	70	Male	Stage III	15.9	1	-10.56812262	Low	2	0.41	3.21	90
TCGA-IC-A6RE-01	59	Male	Stage II	7.69	0	-11.77930855	Low	2	0.2	4.17	462
TCGA-JY-A6FE-01	49	Male	Stage III	3.68	1	-12.74473462	Low	2	0.38	5.28	51
TCGA-L5-A4OE-01	81	Male	Stage III	23.98	1	-13.04247581	Low	2	0.49	4.6	261
TCGA-L7-A56G-01	65	Male		10.84	1	-14.06502577	Low	2	0.55	3.38	63
TCGA-L5-A4OI-01	79	Male	Stage III	19.97	0	-16.44914795	Low	2	0.66	4.33	1263
TCGA-L5-A8NG-01	77	Male	Stage III	35.94	0	-17.24047186	Low	2	0.3	7.86	118
TCGA-LN-A7HY-01	50	Male	Stage III	12.02	0	-17.91795058	Low	2	0.35	7.35	142
TCGA-L5-A8NH-01	54	Male	Stage IV	12.91	1	-23.41078436	Low	2	0.27	3.96	112
TCGA-VR-AA4D-01	53	Male	Stage II	46.16	1	-23.69132545	Low	2	0.62	3.41	77
TCGA-LN-A9FP-01	60	Female	Stage II	12.02	0	-31.30560784	Low	2	1	4.02	415
TCGA-LN-A49W-01	73	Male	Stage III	13.24	0	-32.73325872	Low	2	0.43	3.88	73
TCGA-Q9-A6FW-01	61	Male	Stage III	7.82	0	-32.85359156	Low	2	0.5	4.21	185
TCGA-LN-A8I1-01	67	Female	Stage II	13.17	0	-33.6048471	Low	2	0.63	3.46	87

Table S4 (continued)

**Table S4** (continued)

	Age	Sex	Grade	OS (months)	OS status	Score	Group	TME cluster	Purity	Ploidy	TMB
TCGA-M9-A5M8-01	58	Male	Stage II	33.08	0	-34.38105001	Low	2	0.93	2.79	65
TCGA-VR-A8EP-01	51	Male	Stage III	27.07	0	-37.48722031	Low	2	0.42	3.08	86
TCGA-V5-AASW-01	72	Male		9.26	0	-38.88859241	Low	2	0.31	6.12	117
TCGA-2H-A9GI-01	68	Male	Stage III	14.29	1	-39.75879743	Low	2	0.55	2.66	164
TCGA-L5-A4OJ-01	70	Female	Stage I	20.99	0	-39.98917851	Low	2	0.86	1.84	218
TCGA-JY-A6FA-01	51	Male	Stage II	44.71	1	-41.72588264	Low	2	0.72	2.09	106
TCGA-L5-A4OS-01	86	Female	Stage II	58.54	0	-44.40856809	Low	2	0.19	2.7	82
TCGA-LN-A4A8-01	52	Male	Stage II	15.51	0	-49.16551343	Low	2	0.71	2.03	99
TCGA-IG-A7DP-01	50	Female	Stage III	14.85	0	-50.76160756	Low	2	NA	NA	18
TCGA-2H-A9GH-01	44	Male	Stage II	31.24	1	-51.05706433	Low	2	1	8.76	106
TCGA-L5-A4OT-01	77	Male	Stage IV	4.89	1	-53.32740443	Low	2	0.49	3.92	205
TCGA-VR-A8Q7-01	60	Male	Stage III	52.23	0	-54.60812908	Low	2	0.29	2.89	72
TCGA-L5-A88V-01	60	Male	Stage III	2.6	0	-55.41109354	Low	2	0.72	3.28	144
TCGA-L5-A4OP-01	67	Female	Stage I	7.16	0	-55.62208884	Low	2	0.69	1.81	100
TCGA-L5-A8NS-01	76	Male	Stage II	13.4	0	-55.69961448	Low	2	0.39	3.52	339
TCGA-L5-A4OO-01	75	Male	Stage III	3.32	0	-56.64870948	Low	2	0.33	4.28	88
TCGA-R6-A6KZ-01	42	Male		5.06	1	-56.70320347	Low	2	0.35	5.13	135
TCGA-VR-A8EZ-01	47	Male	Stage III	18.17	1	-59.50710675	Low	2	0.41	6.18	201
TCGA-R6-A6XQ-01	58	Male		6.34	1	-60.02680856	Low	2	0.8	9.95	65
TCGA-LN-A7HZ-01	49	Male	Stage II	13.17	0	-60.29923058	Low	2	0.5	10.01	60
TCGA-IG-A51D-01	63	Male	Stage II	17.02	0	-60.4165586	Low	2	0.5	4.27	134
TCGA-L5-A88S-01	84	Male	Stage I	15.47	0	-60.78792761	Low	2	0.82	3.9	75
TCGA-L5-A8NM-01	84	Female	Stage II	7.75	1	-61.38506461	Low	2	0.39	2.05	1085
TCGA-LN-A7HV-01	58	Male	Stage II	10.51	0	-63.02904193	Low	2	0.47	3.47	93
TCGA-R6-A8W8-01	72	Male		2.89	1	-64.20673312	Low	2	0.63	2.75	110
TCGA-L5-A8NN-01	81	Male	Stage III	5.49	0	-69.31018669	Low	2	0.31	5.21	98
TCGA-LN-A4A3-01	61	Male	Stage III	12.75	0	-70.93140118	Low	2	0.31	3.97	64
TCGA-LN-A4MQ-01	46	Male	Stage III	12.32	0	-74.28300264	Low	2	0.65	8.93	73
TCGA-L5-A8NI-01	79	Male	Stage III	13.47	1	-76.40098706	Low	2	0.34	5.4	167
TCGA-L5-A8NJ-01	77	Male	Stage III	16.46	0	-81.51012839	Low	2	0.75	2.83	194
TCGA-LN-A5U5-01	57	Male	Stage IV	4.47	1	-84.47230082	Low	2	0.53	4.18	45
TCGA-IG-A5S3-01	69	Female	Stage II	23.39	0	-87.4784893	Low	2	0.73	9.77	62
TCGA-VR-A8EX-01	63	Male	Stage IV	28.09	1	-87.52962306	Low	2	0.4	3.52	115
TCGA-LN-A49Y-01	77	Male	Stage II	12.45	0	-89.85395773	Low	2	0.88	3.84	199

**Table S4** (continued)



**Table S4** (continued)

	Age	Sex	Grade	OS (months)	OS status	Score	Group	TME cluster	Purity	Ploidy	TMB
TCGA-R6-A6DQ-01	74	Female		7.59	1	-114.0412025	Low	2	0.46	3.25	69
TCGA-2H-A9GQ-01	80	Male	Stage III	4.2	1	13.06857923	Low	1	0.75	2.84	231
TCGA-L5-A8NF-01	57	Male	Stage IV	2.66	1	12.69563845	Low	1	0.46	2.77	110
TCGA-LN-A49P-01	71	Male	Stage II	12.32	0	12.53733958	Low	1	0.49	4.39	63
TCGA-2H-A9GM-01	53	Male	Stage II	13.93	1	9.873298261	Low	1	0.51	3.96	91
TCGA-VR-AA4G-01	51	Female	Stage III	18.04	0	8.866454168	Low	1	0.33	3.94	62
TCGA-LN-A49O-01	47	Male	Stage II	13.4	0	5.367156069	Low	1	0.51	3.16	54
TCGA-L5-A43J-01	90	Male	Stage II	4.3	1	3.731963763	Low	1	0.57	3.52	512
TCGA-S8-A6BV-01	76	Male	Stage III	20.01	0	2.090819664	Low	1	0.45	2.99	112
TCGA-IG-A4QS-01	71	Male	Stage III	3.88	1	-1.83201075	Low	1	0.53	5.8	198
TCGA-L5-A4OW-01	56	Female	Stage II	7.13	1	-2.787619378	Low	1	0.52	4.12	240
TCGA-R6-A8WG-01	60	Male		12.68	1	-3.098706595	Low	1	0.82	3.59	93
TCGA-LN-A49M-01	62	Male	Stage II	12.65	0	-6.422834234	Low	1	0.76	1.75	192
TCGA-LN-A4A4-01	36	Male	Stage III	12.58	0	-6.813949388	Low	1	0.62	2.53	82
TCGA-L5-A88Y-01	76	Male		0.36	0	-8.955868983	Low	1	0.33	4.64	197
TCGA-Z6-A8JE-01	57	Male	Stage III	2.1	0	-10.84671593	Low	1	0.62	9.14	180
TCGA-RE-A7BO-01	72	Female	Stage II	7	1	-12.49851705	Low	1	0.5	3	185
TCGA-R6-A8WC-01	56	Male		2.3	0	-13.70848969	Low	1	0.84	2.59	109
TCGA-L5-A88W-01	67	Male	Stage II	25.1	1	-14.06053101	Low	1	0.69	2	124
TCGA-V5-A7RC-01	55	Male		3.42	1	-18.72974578	Low	1	0.57	3.74	75
TCGA-VR-A8EO-01	49	Male	Stage II	25.79	0	-23.7775511	Low	1	0.78	3.87	44
TCGA-L5-A4ON-01	65	Male	Stage II	18.33	1	-26.34589442	Low	1	0.3	5.53	135
TCGA-LN-A8I0-01	52	Male	Stage II	13.37	0	-29.53674198	Low	1	0.35	4.59	43
TCGA-R6-A6Y0-01	54	Male		53.91	0	-32.32474332	Low	1	0.2	4.78	151
TCGA-LN-A5U7-01	46	Male	Stage II	25.23	0	-35.06070703	Low	1	0.73	3.15	102
TCGA-V5-A7RE-01	45	Male	Stage I	16.43	0	-37.76349412	Low	1	0.28	3.59	139
TCGA-VR-A8ET-01	64	Male	Stage II	1.54	1	-39.55431646	Low	1	0.52	4.1	22
TCGA-IG-A3YA-01	53	Male	Stage III	20.76	0	-42.55182807	Low	1	0.27	4.11	80
TCGA-LN-A9FO-01	42	Male	Stage II	0.13	0	-44.22696249	Low	1	0.57	3.37	92
TCGA-IG-A3YC-01	62	Male	Stage III	20.11	0	-45.12874276	Low	1	0.22	3.16	48
TCGA-IG-A97H-01	36	Male	Stage II	14.49	0	-46.98362277	Low	1	0.25	6.39	87
TCGA-LN-A9FQ-01	62	Male	Stage II	12.84	0	-47.01459067	Low	1	0.53	7.97	86
TCGA-LN-A4A9-01	58	Male	Stage II	11.53	1	-47.05091624	Low	1	0.68	2.39	182
TCGA-LN-A5U6-01	54	Male	Stage II	12.32	0	-47.24856243	Low	1	0.63	8.61	92

**Table S4** (continued)

Table S4 (continued)

	Age	Sex	Grade	OS (months)	OS status	Score	Group	TME cluster	Purity	Ploidy	TMB
TCGA-XP-A8T8-01	49	Male	Stage II	14.36	0	-48.16359601	Low	1	0.8	3.87	87
TCGA-IG-A3I8-01	51	Female	Stage II	33.25	0	-48.2079175	Low	1	0.6	3.79	95
TCGA-VR-A8EU-01	51	Male	Stage IV	18.3	1	-48.50146976	Low	1	0.4	7.3	82
TCGA-R6-A6L4-01	27	Male		16.29	1	-49.71571801	Low	1	0.44	5.03	118
TCGA-VR-A8EQ-01	73	Male	Stage III	22.8	1	-51.52771905	Low	1	0.47	5.08	146
TCGA-L5-A8NR-01	81	Female	Stage III	8.71	0	-52.01169279	Low	1	0.45	5.74	270
TCGA-2H-A9GF-01	67	Male	Stage III	25.76	1	-53.23604225	Low	1	0.32	7.29	228
TCGA-LN-A49X-01	44	Male	Stage II	12.61	0	-54.12930235	Low	1	0.4	4.3	60
TCGA-L5-A4OM-01	54	Female	Stage I	47.9	1	-55.03814574	Low	1	0.48	4.35	61
TCGA-LN-A7HW-01	59	Male	Stage II	11.99	0	-57.65183778	Low	1	0.56	3.2	86
TCGA-R6-A6XG-01	64	Male		38.37	0	-58.51737922	Low	1	0.47	5.12	161
TCGA-IG-A6QS-01	54	Male	Stage II	9.95	1	-59.31469209	Low	1	0.7	1.95	60
TCGA-L5-A8NK-01	84	Female	Stage II	13.53	0	-59.54210181	Low	1	0.27	3.7	172
TCGA-LN-A9FR-01	70	Male	Stage II	12.25	0	-60.50119561	Low	1	0.65	8.88	64
TCGA-L5-A8NQ-01	71	Male	Stage II	21.35	1	-61.21314301	Low	1	0.51	4.25	216
TCGA-LN-A4A5-01	49	Male	Stage II	22.37	1	-67.35119522	Low	1	0.44	3.83	63
TCGA-IG-A50L-01	58	Male	Stage III	0.53	0	-67.3520416	Low	1	0.5	4.27	102
TCGA-R6-A6DN-01	58	Male		7.98	1	-68.73193408	Low	1	0.45	5.6	80
TCGA-LN-A4A1-01	60	Male	Stage II	12.58	0	-70.14206226	Low	1	0.64	4.15	104
TCGA-LN-A7HX-01	72	Male	Stage II	12.22	0	-72.31835444	Low	1	0.58	3.88	88
TCGA-VR-A8ER-01	54	Male	Stage III	12.42	1	-75.7553627	Low	1	0.88	3.05	52
TCGA-L5-A8NL-01	56	Male	Stage III	13.21	0	-78.04101838	Low	1	0.22	4.33	84
TCGA-2H-A9GN-01	70	Male	Stage III	8.94	1	-80.40115402	Low	1	0.23	4.63	97
TCGA-VR-A8EW-01	57	Male	Stage III	8.11	1	-81.96905515	Low	1	0.39	5.24	101

TME, tumor microenvironment; EC, esophageal carcinoma.

**Table S5** The recurrent occurring CNV regions

Group	Cytoband	q value
TMEscore high	11q13.3 (amp)	3.65E-08
	8q24.21 (amp)	1.16E-06
	6p21.1 (amp)	8.24E-05
	9p21.3 (del)	1.54E-19
	16q23.1 (del)	1.49E-11
	2q22.1 (del)	1.75E-07
	5q11.2 (del)	1.50E-06
TMEscore low	11q13.3 (amp)	9.69E-74
	17q12 (amp)	4.45E-19
	8q24.21 (amp)	1.54E-16
	7q21.2 (amp)	5.56E-13
	3q26.2 (amp)	5.17E-12
	6p21.1 (amp)	6.06E-10
	7p11.2 (amp)	3.46E-08
	12p12.1 (amp)	4.30E-08
	18q11.2 (amp)	5.82E-07
	19q12 (amp)	6.65E-07
	9p21.3 (del)	6.86E-95
	16q23.1 (del)	3.06E-54
	4q22.1 (del)	1.09E-31
	5q12.1 (del)	4.10E-18
	7q31.1 (del)	1.55E-19
	2q22.1 (del)	1.06E-15
	6p25.3 (del)	6.02E-13
	3p14.2 (del)	6.02E-13
	8p23.2 (del)	4.74E-07
	20p12.1 (del)	1.47E-05
	21q22.12 (del)	1.18E-05
	18q21.2 (del)	1.01E-05
	10p11.21 (del)	1.98E-05
	3p14.3 (del)	2.23E-05
	7q36.3 (del)	1.98E-05
7q36.3 (del)	1.98E-05	
9p23 (del)	2.80E-05	

CNV, copy number variation.

**Table S6** Purity and ploidy of patients with EC

Sample	Purity	Ploidy
TCGA-LN-A49M-01	0.76	1.75
TCGA-L5-A4OP-01	0.69	1.81
TCGA-L5-A4OJ-01	0.86	1.84
TCGA-IG-A6QS-01	0.7	1.95
TCGA-L5-A88Z-01	0.8	1.97
TCGA-KH-A6WC-01	0.61	2
TCGA-IG-A97I-01	0.65	2
TCGA-L5-A88W-01	0.69	2
TCGA-LN-A4A8-01	0.71	2.03
TCGA-L5-A8NM-01	0.39	2.05
TCGA-JY-A6FA-01	0.72	2.09
TCGA-2H-A9GJ-01	0.7	2.1
TCGA-IC-A6RF-01	0.55	2.14
TCGA-JY-A93D-01	0.25	2.25
TCGA-V5-AASV-01	0.75	2.26
TCGA-VR-A8EY-01	0.74	2.35
TCGA-LN-A4A9-01	0.68	2.39
TCGA-LN-A4A4-01	0.62	2.53
TCGA-R6-A8WC-01	0.84	2.59
TCGA-2H-A9GI-01	0.55	2.66
TCGA-L5-A4OS-01	0.19	2.7
TCGA-R6-A8W8-01	0.63	2.75
TCGA-L5-A8NF-01	0.46	2.77
TCGA-M9-A5M8-01	0.93	2.79
TCGA-L5-A8NJ-01	0.75	2.83
TCGA-2H-A9GQ-01	0.75	2.84
TCGA-VR-A8Q7-01	0.29	2.89
TCGA-S8-A6BV-01	0.45	2.99
TCGA-RE-A7BO-01	0.5	3
TCGA-VR-A8ER-01	0.88	3.05
TCGA-IG-A3QL-01	0.64	3.07
TCGA-VR-A8EP-01	0.42	3.08
TCGA-L5-A4OH-01	0.62	3.08
TCGA-L5-A8NV-01	0.38	3.14

**Table S6** (continued)

**Table S6** (continued)

Sample	Purity	Ploidy
TCGA-LN-A5U7-01	0.73	3.15
TCGA-IG-A3YC-01	0.22	3.16
TCGA-LN-A49O-01	0.51	3.16
TCGA-JY-A93C-01	0.55	3.16
TCGA-LN-A7HW-01	0.56	3.2
TCGA-IG-A8O2-01	0.61	3.2
TCGA-VR-AA7I-01	0.41	3.21
TCGA-R6-A6DQ-01	0.46	3.25
TCGA-L5-A88V-01	0.72	3.28
TCGA-S8-A6BW-01	0.56	3.29
TCGA-L5-A43E-01	0.51	3.36
TCGA-LN-A9FO-01	0.57	3.37
TCGA-L7-A56G-01	0.55	3.38
TCGA-VR-AA4D-01	0.62	3.41
TCGA-L5-A8NT-01	0.39	3.45
TCGA-LN-A8I1-01	0.63	3.46
TCGA-LN-A7HV-01	0.47	3.47
TCGA-L5-A8NS-01	0.39	3.52
TCGA-VR-A8EX-01	0.4	3.52
TCGA-L5-A43J-01	0.57	3.52
TCGA-V5-A7RE-01	0.28	3.59
TCGA-R6-A8WG-01	0.82	3.59
TCGA-L5-A43C-01	0.62	3.61
TCGA-2H-A9GK-01	0.29	3.62
TCGA-V5-A7RC-06	0.47	3.67
TCGA-L5-A8NK-01	0.27	3.7
TCGA-V5-A7RC-01	0.57	3.74
TCGA-JY-A93E-01	0.46	3.75
TCGA-L5-A8NU-01	0.38	3.76
TCGA-IG-A3I8-01	0.6	3.79
TCGA-XP-A8T6-01	0.58	3.8
TCGA-Z6-AAPN-01	0.41	3.81
TCGA-LN-A4A5-01	0.44	3.83
TCGA-V5-AASX-01	0.61	3.84
TCGA-LN-A49Y-01	0.88	3.84

**Table S6** (continued)**Table S6** (continued)

Sample	Purity	Ploidy
TCGA-L5-A4OG-01	0.5	3.85
TCGA-JY-A938-01	0.7	3.85
TCGA-2H-A9GR-01	0.2	3.87
TCGA-L5-A4OX-01	0.65	3.87
TCGA-VR-A8EO-01	0.78	3.87
TCGA-XP-A8T8-01	0.8	3.87
TCGA-LN-A49W-01	0.43	3.88
TCGA-LN-A7HX-01	0.58	3.88
TCGA-L5-A88S-01	0.82	3.9
TCGA-IG-A5B8-01	0.38	3.91
TCGA-L5-A4OT-01	0.49	3.92
TCGA-JY-A6FD-01	0.65	3.93
TCGA-VR-AA4G-01	0.33	3.94
TCGA-JY-A6FB-01	0.54	3.94
TCGA-L5-A8NH-01	0.27	3.96
TCGA-2H-A9GM-01	0.51	3.96
TCGA-LN-A4A3-01	0.31	3.97
TCGA-L5-A88T-01	0.45	4.01
TCGA-IG-A3YB-01	0.61	4.02
TCGA-LN-A9FP-01	1	4.02
TCGA-IG-A4P3-01	0.34	4.04
TCGA-JY-A939-01	0.34	4.05
TCGA-JY-A93F-01	0.55	4.09
TCGA-VR-A8ET-01	0.52	4.1
TCGA-Z6-A8JD-01	0.25	4.11
TCGA-IG-A3YA-01	0.27	4.11
TCGA-JY-A6FG-01	0.57	4.11
TCGA-L5-A4OW-01	0.52	4.12
TCGA-L5-A4OU-01	0.42	4.14
TCGA-R6-A8W5-01	0.2	4.15
TCGA-LN-A4A1-01	0.64	4.15
TCGA-IC-A6RE-01	0.2	4.17
TCGA-V5-A7RB-01	0.44	4.17
TCGA-LN-A49U-01	0.57	4.17
TCGA-LN-A5U5-01	0.53	4.18

**Table S6** (continued)

Table S6 (continued)

Sample	Purity	Ploidy
TCGA-L5-A893-01	0.37	4.2
TCGA-Q9-A6FW-01	0.5	4.21
TCGA-L5-A8NQ-01	0.51	4.25
TCGA-IG-A51D-01	0.5	4.27
TCGA-IG-A50L-01	0.5	4.27
TCGA-L5-A4OO-01	0.33	4.28
TCGA-LN-A49X-01	0.4	4.3
TCGA-L5-A8NL-01	0.22	4.33
TCGA-L5-A4OI-01	0.66	4.33
TCGA-L5-A4OM-01	0.48	4.35
TCGA-LN-A49P-01	0.49	4.39
TCGA-IG-A625-01	0.66	4.39
TCGA-L5-A8NW-01	0.4	4.4
TCGA-LN-A8I0-01	0.35	4.59
TCGA-L5-A4OE-01	0.49	4.6
TCGA-2H-A9GN-01	0.23	4.63
TCGA-L5-A88Y-01	0.33	4.64
TCGA-R6-A6Y0-01	0.2	4.78
TCGA-2H-A9GL-01	0.4	4.8
TCGA-L5-A8NE-01	0.28	4.91
TCGA-R6-A6L4-01	0.44	5.03
TCGA-VR-A8EQ-01	0.47	5.08
TCGA-R6-A6XG-01	0.47	5.12
TCGA-R6-A6KZ-01	0.35	5.13
TCGA-L5-A8NN-01	0.31	5.21
TCGA-VR-A8EW-01	0.39	5.24
TCGA-JY-A6FE-01	0.38	5.28
TCGA-L5-A8NI-01	0.34	5.4
TCGA-L5-A891-01	0.45	5.52
TCGA-JY-A6FH-01	0.22	5.53
TCGA-L5-A4ON-01	0.3	5.53
TCGA-R6-A6DN-01	0.45	5.6
TCGA-L5-A8NR-01	0.45	5.74
TCGA-IG-A4QS-01	0.53	5.8
TCGA-V5-AASW-01	0.31	6.12

Table S6 (continued)

Table S6 (continued)

Sample	Purity	Ploidy
TCGA-VR-A8EZ-01	0.41	6.18
TCGA-IG-A97H-01	0.25	6.39
TCGA-2H-A9GF-01	0.32	7.29
TCGA-VR-A8EU-01	0.4	7.3
TCGA-LN-A7HY-01	0.35	7.35
TCGA-Z6-A9VB-01	0.34	7.61
TCGA-L5-A8NG-01	0.3	7.86
TCGA-LN-A9FQ-01	0.53	7.97
TCGA-L7-A6VZ-01	0.53	8.16
TCGA-LN-A5U6-01	0.63	8.61
TCGA-2H-A9GO-01	0.43	8.63
TCGA-2H-A9GH-01	1	8.76
TCGA-LN-A9FR-01	0.65	8.88
TCGA-LN-A4MQ-01	0.65	8.93
TCGA-LN-A49S-01	0.48	8.95
TCGA-Z6-A8JE-01	0.62	9.14
TCGA-IG-A5S3-01	0.73	9.77
TCGA-R6-A6XQ-01	0.8	9.95
TCGA-LN-A7HZ-01	0.5	10.01
TCGA-LN-A8HZ-01	0.5	10.12
TCGA-IG-A7DP-01	NA	NA

EC, esophageal carcinoma.