Supplementary

Table S1 The mRNA expression of HOXC10 between cancer and normal tissues in the Oncomine database

Cancer	Cancer type	P value	Fold change	Rank (%)	Sample	Reference (PMID)
Bladder	Infiltrating bladder urothelial carcinoma	9.28E-04	–1.579	21%	27	15173019
Brain and CNS	Brain glioblastoma	2.19E-10	2.087	4%	552	TCGA
	Glioblastoma	9.90E-10	2.413	8%	104	16616334
	Glioblastoma	2.37E-07	1.505	4%	84	18565887
	Glioblastoma	6.14E-05	2.171	8%	23	16204036
Breast	Invasive ductal breast carcinoma	2.92E-30	3.28	4%	450	TCGA
	Invasive breast carcinoma	6.67E-20	3.655	3%	137	TCGA
	Invasive lobular breast carcinoma	1.87E-14	4.239	2%	97	TCGA
	Invasive ductal and lobular breast carcinoma	3.87E-05	8.303	4%	64	TCGA
	Invasive breast carcinoma stroma	2.04E-11	1.992	11%	59	18438415
	Invasive breast carcinoma	3.41E-05	1.595	3%	158	21373875
Cervical	Cervical squamous cell carcinoma epithelia	4.12E-06	2.949	3%	31	17974957
Colorectal	Rectosigmoid adenocarcinoma	1.77E-12	2.305	1%	25	TCGA
	Colon adenocarcinoma	2.16E-08	1.542	17%	123	TCGA
	Cecum adenocarcinoma	2.43E-07	1.696	11%	44	TCGA
	Colon mucinous adenocarcinoma	5.10E-05	1.538	18%	44	TCGA
	Rectal mucinous adenocarcinoma	3.77E-4	1.802	9%	28	TCGA
Esophageal	Esophageal squamous cell carcinoma	1.91E-13	1.658	4%	106	21385931
	Esophageal squamous cell carcinoma	2.51E-07	3.357	3%	34	20955586
Gastric	Gastric intestinal type adenocarcinoma	1.9E-06	3.768	13%	57	19081245
Kidney	Renal pelvis urothelial carcinoma	1.3E-05	–2.86	10%	31	16115910
Lung	Lung adenocarcinoma	1.08E-07	1.668	13%	246	22080568
	Lung adenocarcinoma	2.55E-6	1.982	13%	110	20421987
	Squamous cell lung carcinoma	6.16E-05	1.812	19%	92	20421987
	Large cell lung carcinoma	4.40E-04	3.265	17%	84	20421987
Melanoma	Benign melanocytic skin nevus	9.72E-7	–3.406	1%	25	16243793
	Cutaneous melanoma	3.62E-04	–1.74	13%	52	16243793
Ovarian	Ovarian serous adenocarcinoma	2.28E-07	–10.535	9%	48	19486012
Pancreatic	Pancreatic carcinoma	1.77E-04	1.769	10%	52	19732725
Sarcoma	Myxoid/round cell liposarcoma	1.24E-04	2.773	20%	29	20601955
	Leiomyosarcoma	7.73E-04	2.409	22%	35	20601955
	Round cell liposarcoma	1.83E-04	6.037	4%	19	15994966
Other	Vulvar intraepithelial neoplasia	2.76E-04	–1.839	3%	19	17471573

CNS, central nervous system; TCGA, The Cancer Genome Atlas; PMID, PubMed Identifier.

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Table S2 The relationships between the expression of HOXC10 and the prognoses of different cancers in the PrognoScan database

Cancer type	Subtype	Data set	End point	N	Cox P value	HR [95% CI-low CI-upp]
Bladder cancer	–	GSE5287	OS	30	0.109862	1.36 [0.93–2.00]
	–	GSE13507	OS	165	0.417422	1.37 [0.64–2.92]
	Transitional cell carcinoma	GSE13507	DSS	165	0.389573	1.58 [0.56–4.44]
Blood cancer	AML	GSE12417-GPL96	OS	163	0.560195	0.73 [0.25–2.12]
	AML	GSE12417-GPL570	OS	79	0.646702	0.69 [0.14–3.32]
	AML	GSE5122	OS	58	0.92701	0.98 [0.71–1.37]
	AML	GSE8970	OS	34	0.131566	0.63 [0.35–1.15]
	B-cell lymphoma	GSE4475	OS	158	0.151152	3.23 [0.65–16.02]
	DLBCL	E-TABM-346	OS	53	0.09165	0.69 [0.44–1.06]
	DLBCL	E-TABM-346	EFS	53	0.100929	0.72 [0.48–1.07]
	Follicular lymphoma	GSE16131-GPL96	OS	180	0.63917	0.94 [0.74–1.20]
	Multiple myeloma	GSE2658	DSS	559	0.321423	1.17 [0.85–1.61]
Brain cancer	Astrocytoma	GSE4271-GPL96	OS	77	0.028386	1.34 [1.03–1.75]
	Glioblastoma	GSE7696	OS	70	0.57152	1.14 [0.72–1.81]
	Glioma	GSE4412-GPL96	OS	74	0.059568	1.54 [0.98–2.41]
	Meningioma	GSE16581	OS	67	0.137701	0.03 [0.00–3.21]
Breast cancer	–	GSE19615	DMFS	115	0.481287	1.23 [0.69–2.22]
	–	GSE12276	PFS	204	0.405076	0.95 [0.85–1.07]
	–	GSE6532–GPL570	PFS	87	0.346351	1.10 [0.90–1.34]
	–	GSE6532-GPL570	DMFS	87	0.346351	1.10 [0.90–1.34]
	–	GSE9195	PFS	77	0.428403	1.13 [0.84–1.51]
	–	GSE9195	DMFS	77	0.573515	1.10 [0.79–1.53]
	–	GSE12093	DMFS	136	0.194555	1.32 [0.87–2.00]
	–	GSE11121	DMFS	200	0.435395	1.15 [0.81–1.63]
	–	GSE1378	PFS	60	0.024856	1.27 [1.03–1.56]
	–	GSE1379	PFS	60	0.036064	1.25 [1.01–1.54]
	–	GSE9893	OS	155	0.309388	0.89 [0.70–1.12]
	–	GSE2034	DMFS	286	0.759514	1.03 [0.85–1.24]
	–	GSE1456-GPL96	OS	159	0.480164	0.87 [0.59–1.28]
	–	GSE1456-GPL96	PFS	159	0.186285	1.30 [0.88–1.93]
	–	GSE1456-GPL96	DSS	159	0.222686	1.34 [0.84–2.14]
	–	GSE7378	DFS	54	0.273791	1.25 [0.84–1.85]
	–	E-TABM-158	DMFS	117	0.879649	1.02 [0.80–1.30]
	–	E-TABM-158	OS	117	0.751855	1.03 [0.85–1.26]
	–	E-TABM-158	PFS	117	0.751855	1.03 [0.85–1.26]
	–	E-TABM-158	DSS	117	0.971632	1.00 [0.80–1.26]

Table S2 (*continued*)

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Table S2 (*continued*)

Cancer type	Subtype	Data set	End point	N	Cox P value	HR [95% CI-low CI-upp]
	–	GSE3494-GPL96	DSS	236	0.35915	1.14 [0.86–1.51]
		GSE4922-GPL96	DFS	249	0.270416	1.13 [0.91–1.42]
	–	GSE2990	DMFS	125	0.482258	1.12 [0.82–1.52]
	-	GSE2990	PFS	125	0.773579	1.04 [0.82–1.31]
	–	GSE2990	DMFS	54	0.334923	0.86 [0.64–1.16]
	–	GSE2990	PFS	62	0.276037	0.87 [0.69–1.11]
	–	GSE7390	PFS	198	0.223364	0.91 [0.78–1.06]
	–	GSE7390	DMFS	198	0.802096	0.98 [0.82–1.16]
	–	GSE7390	OS	198	0.939142	0.99 [0.83–1.19]
Colorectal cancer	–	GSE12945	DFS	51	0.405093	4.41 [0.13–145.01]
	–	GSE12945	OS	62	0.109194	5.46 [0.68–43.58]
	–	GSE17536	OS	177	0.896046	1.06 [0.43–2.60]
	–	GSE17536	DFS	145	0.100833	2.59 [0.83–8.10]
	–	GSE17536	DSS	177	0.928002	1.05 [0.38–2.92]
	–	GSE14333	DFS	226	0.098219	1.31 [0.95–1.80]
	-	GSE17537	DFS	55	0.42966	1.69 [0.46–6.16]
	-	GSE17537	DSS	49	0.9424	0.94 [0.18–4.84]
	-	GSE17537	OS	55	0.39347	1.70 [0.50–5.73]
Eye cancer	Uveal melanoma	GSE22138	DMFS	63	0.145495	1.41 [0.89–2.25]
Head and neck cancer	Squamous cell carcinoma	GSE2837	PFS	28	0.83989	1.04 [0.73–1.47]
Lung cancer	Adenocarcinoma	jacob-00182-CANDF	OS	82	0.871072	1.03 [0.74–1.42]
	Adenocarcinoma	jacob-00182-HLM	OS	79	0.221853	0.85 [0.66–1.10]
	Adenocarcinoma	jacob-00182-MSK	OS	104	0.274592	0.81 [0.55–1.18]
	Adenocarcinoma	GSE13213	OS	117	0.820718	1.03 [0.77–1.38]
	Adenocarcinoma	GSE13213	OS	117	0.421591	1.08 [0.90–1.29]
	Adenocarcinoma	GSE31210	OS	204	0.223551	0.78 [0.53–1.16]
	Adenocarcinoma	GSE31210	PFS	204	0.85112	1.03 [0.78–1.36]
	Adenocarcinoma	jacob-00182-UM	OS	178	0.134631	0.88 [0.74–1.04]
	NSCLC	GSE3141	OS	111	0.494625	0.93 [0.74–1.16]
	NSCLC	GSE14814	OS	90	0.136038	1.35 [0.91–2.00]
	NSCLC	GSE14814	DSS	90	0.099858	1.44 [0.93–2.23]
	NSCLC	GSE8894	PFS	138	0.484781	0.95 [0.83–1.10]
	SCC	GSE4573	OS	129	0.984169	1.00 [0.70–1.44]
	SCC	GSE17710	PFS	56	0.500439	0.88 [0.60–1.28]
	SCC	GSE17710	OS	56	0.935506	0.97 [0.42–2.22]

Table S2 (*continued*)

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Table S2 (*continued*)

Cancer type	Subtype	Data set	End point	N	Cox P value	HR [95% CI-low CI-upp]
	SCC	GSE17710	OS	56	0.404159	0.85 [0.58–1.25]
	SCC	GSE17710	PFS	56	0.705531	0.94 [0.68–1.30]
	SCC	GSE17710	PFS	56	0.81684	0.91 [0.40–2.06]
	SCC	GSE17710	OS	56	0.569059	0.90 [0.64–1.28]
Ovarian cancer	–	GSE9891	OS	278	0.517708	0.94 [0.79–1.13]
	–	DUKE-OC	OS	133	0.830605	0.99 [0.86–1.13]
	–	GSE26712	OS	185	0.010987	1.43 [1.09–1.89]
	–	GSE26712	DFS	185	0.022872	1.36 [1.04–1.77]
	–	GSE17260	OS	110	0.910522	0.99 [0.76–1.27]
	–	GSE17260	OS	110	0.972928	1.00 [0.82–1.23]
	–	GSE17260	PFS	110	0.942258	0.99 [0.82–1.20]
	–	GSE17260	PFS	110	0.952676	1.00 [0.87–1.16]
	–	GSE14764	OS	80	0.609544	1.10 [0.77–1.57]
Skin cancer	Melanoma	GSE19234	OS	38	0.258189	1.35 [0.80–2.25]
Soft tissue cancer	Liposarcoma	GSE30929	DRFS	140	0.703816	0.95 [0.73–1.24]

HR, hazard ratio; CI, confidence interval; AML, acute myelocytic leukemia; DLBCL, diffuse large B cell lymphoma; NSCLC, non-small cell lung cancer; SCC, squamous cell carcinoma; OS, overall survival; DSS, disease-specific survival; EFS, event-free survival; DMFS, distant metastasis-free survival; PFS, progression-free survival; DFS, disease-free survival.

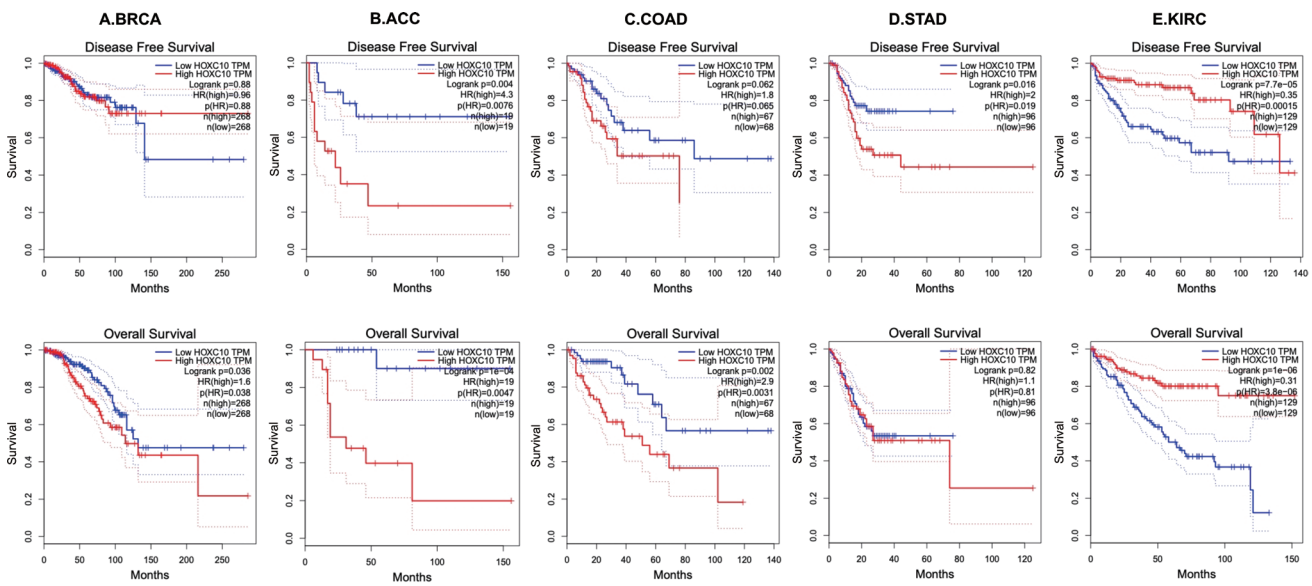

Figure S1 The predictive effect of *HOXC10* in the prognosis of different cancers in the GEPIA database (cutoff: 75–25%). (A) The Kaplan-Meier survival curves of DFS and OS in BRCA; (B) The Kaplan-Meier survival curves of DFS and OS in ACC; (C) The Kaplan-Meier survival curves of DFS and OS in COAD; (D) The Kaplan-Meier survival curves of DFS and OS in STAD; (E) The Kaplan-Meier survival curves of DFS and OS in KIRC. GEPIA, Gene Expression Profiling Interactive Analysis; DFS, disease-free survival; OS, overall survival; BRCA, breast invasive carcinoma; ACC, adrenocortical carcinoma; COAD, colon adenocarcinoma; STAD, stomach adenocarcinoma; KIRC, kidney renal clear cell carcinoma.

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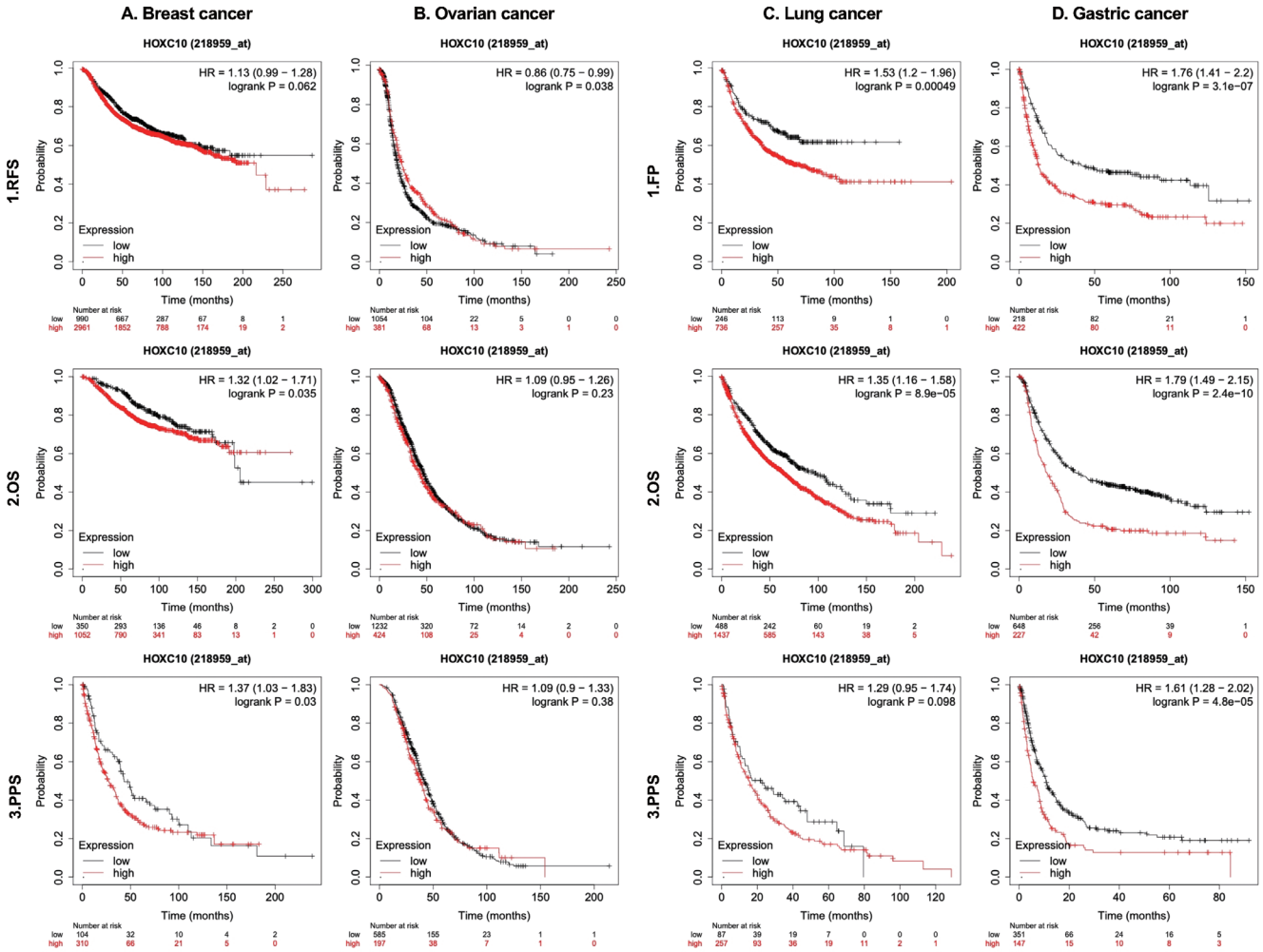

Figure S2 Kaplan-Meier survival curves comparing patients with high expression of *HOXC10* to those with low expression in breast cancer, ovarian cancer, lung cancer, and gastric cancer data sets using the Kaplan-Meier plotter database. (A,B) The Kaplan-Meier survival curves for RFS (A,B-1), OS (A,B-2), and PPS (A,B-3) in breast cancer and ovarian cancer. (C,D) The Kaplan-Meier survival curves for first progression (FP) (C,D-1), OS (C,D-2), and PPS (C,D-3) in lung cancer and gastric cancer. RFS, relapse-free survival; OS, overall survival; PPS, post-progression survival; FP, first progression.

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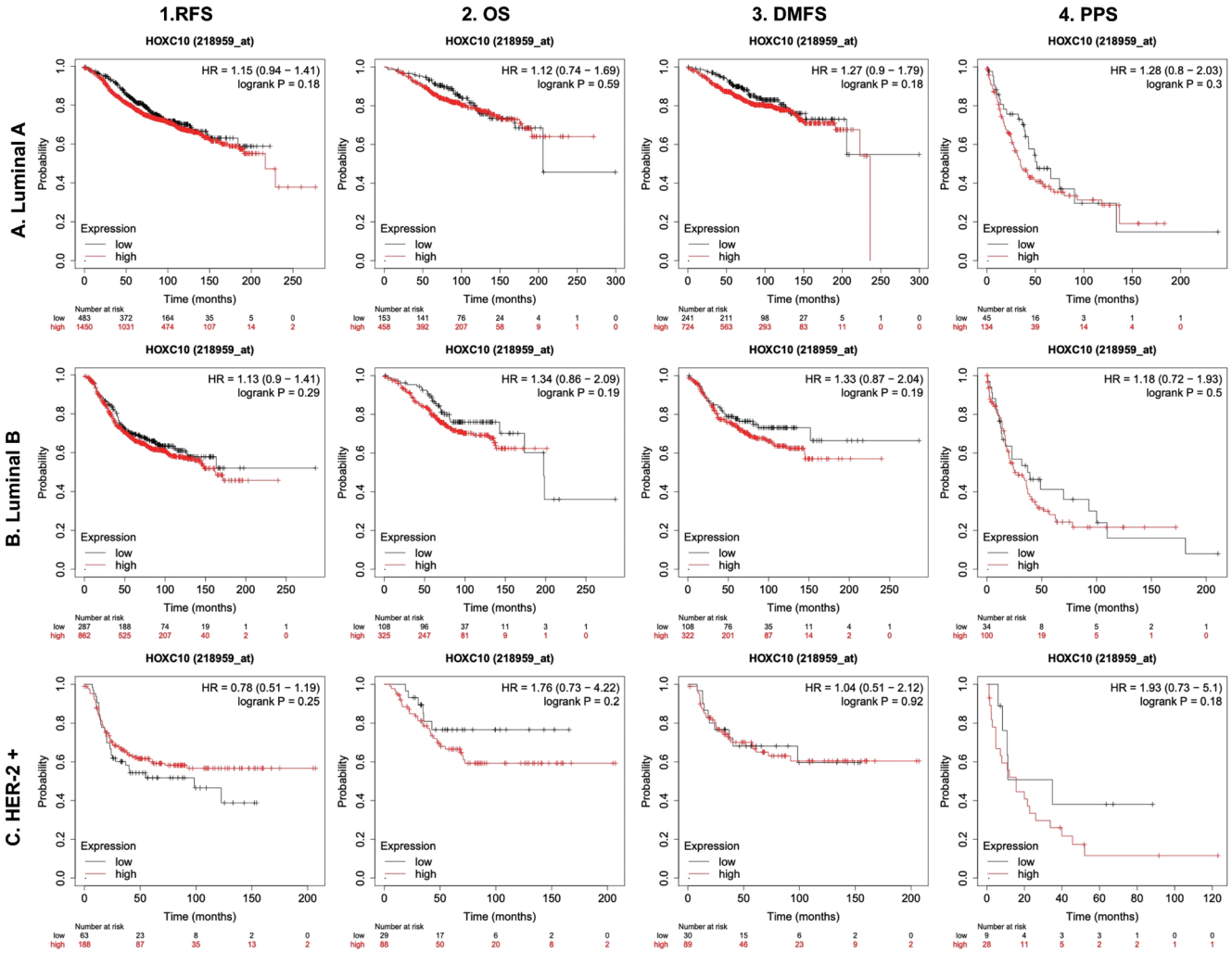

Figure S3 The relationship between the expression of *HOXC10* and the prognosis of different subtypes of breast cancer in the Kaplan-Meier plotter database. (A) The Kaplan-Meier survival curves for RFS, OS, DMFS, and PPS in luminal A breast cancer. (B) The Kaplan-Meier survival curves for RFS, OS, DMFS, and PPS in luminal B breast cancer. (C) The Kaplan-Meier survival curves for RFS, OS, DMFS, and PPS in Her-2+ breast cancer. RFS, relapse-free survival; OS, overall survival; DMFS, distant metastasis-free survival; PPS, post-progression survival; Her-2, human epidermal growth factor receptor 2.

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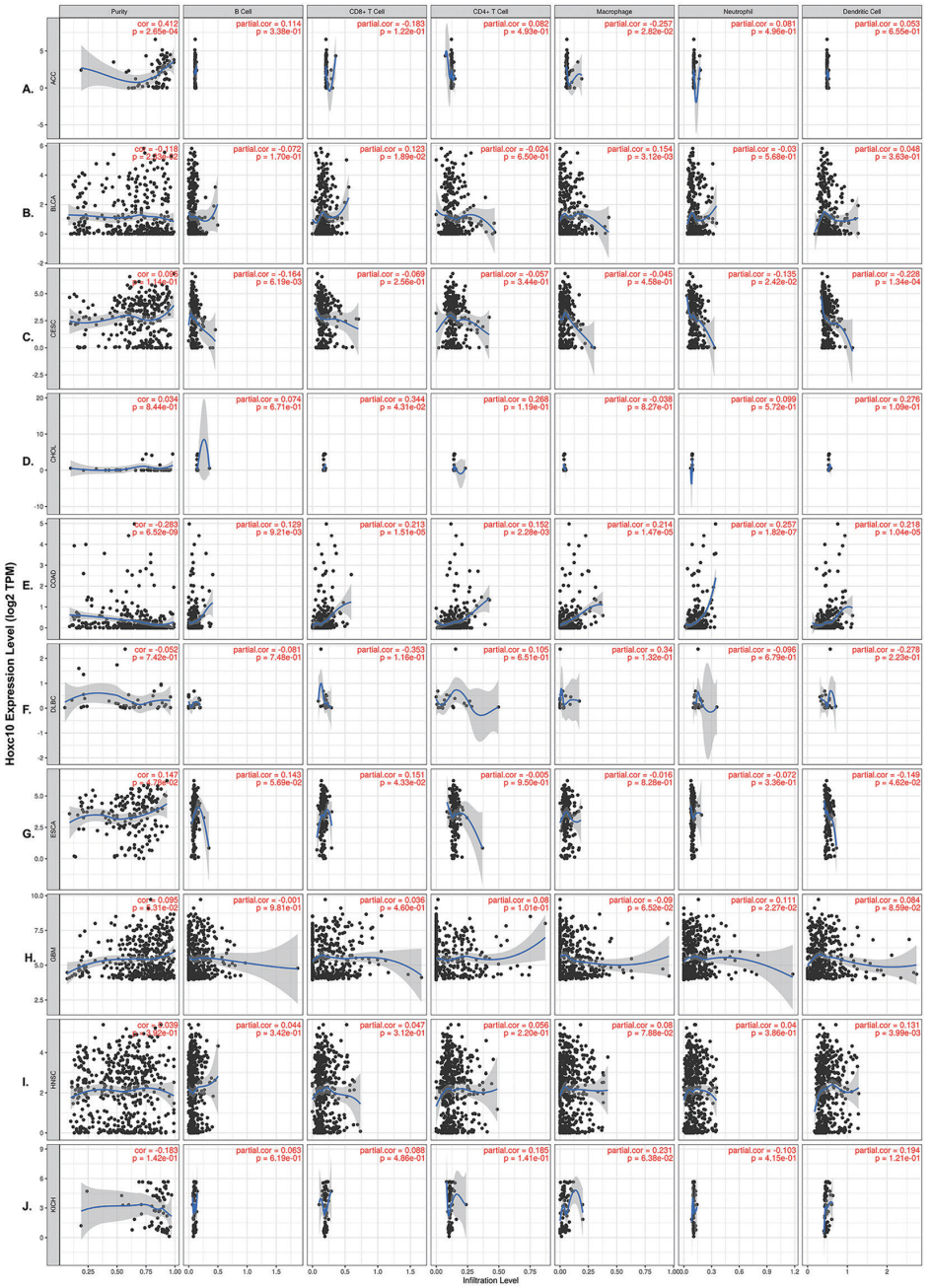

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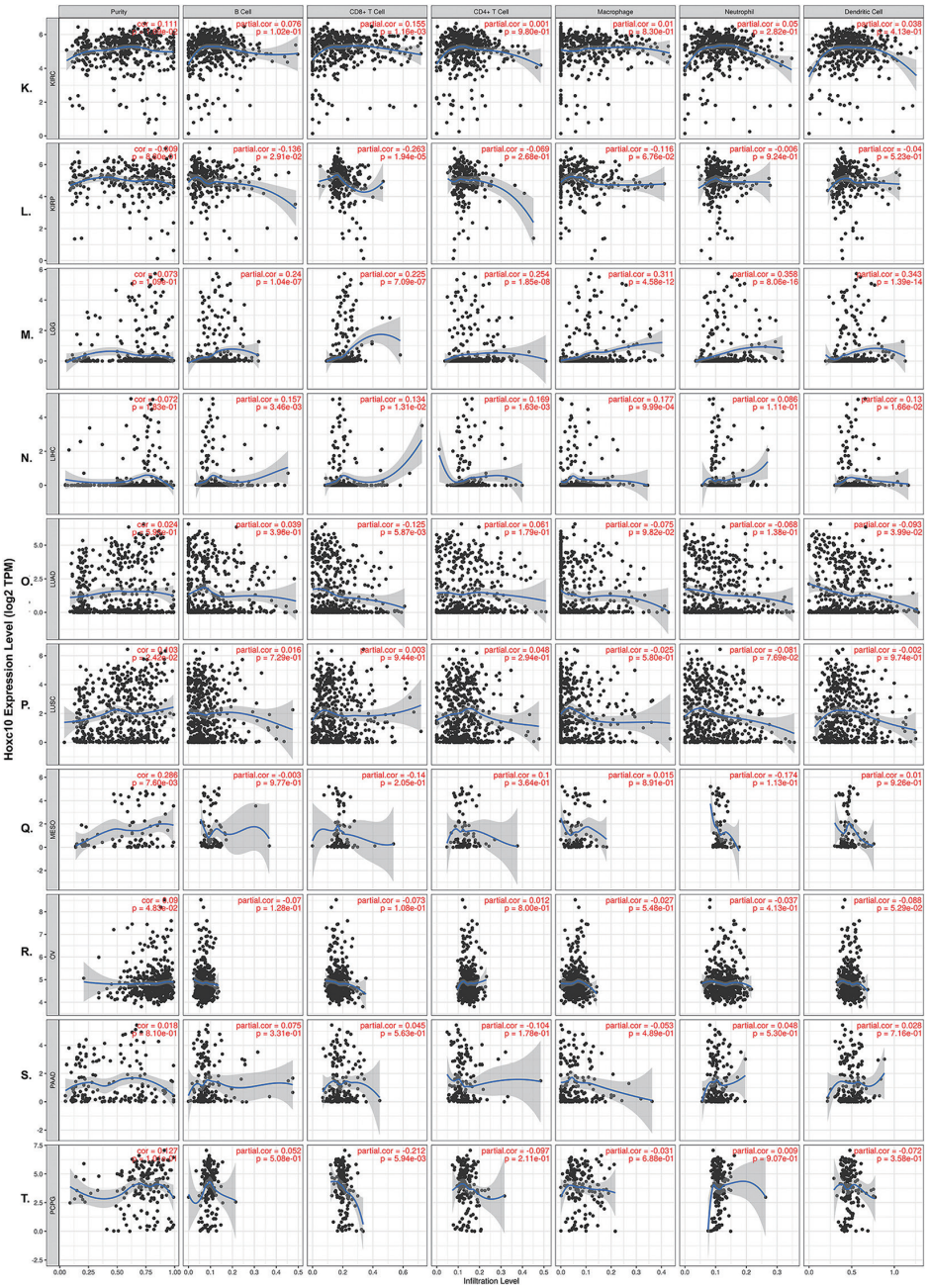

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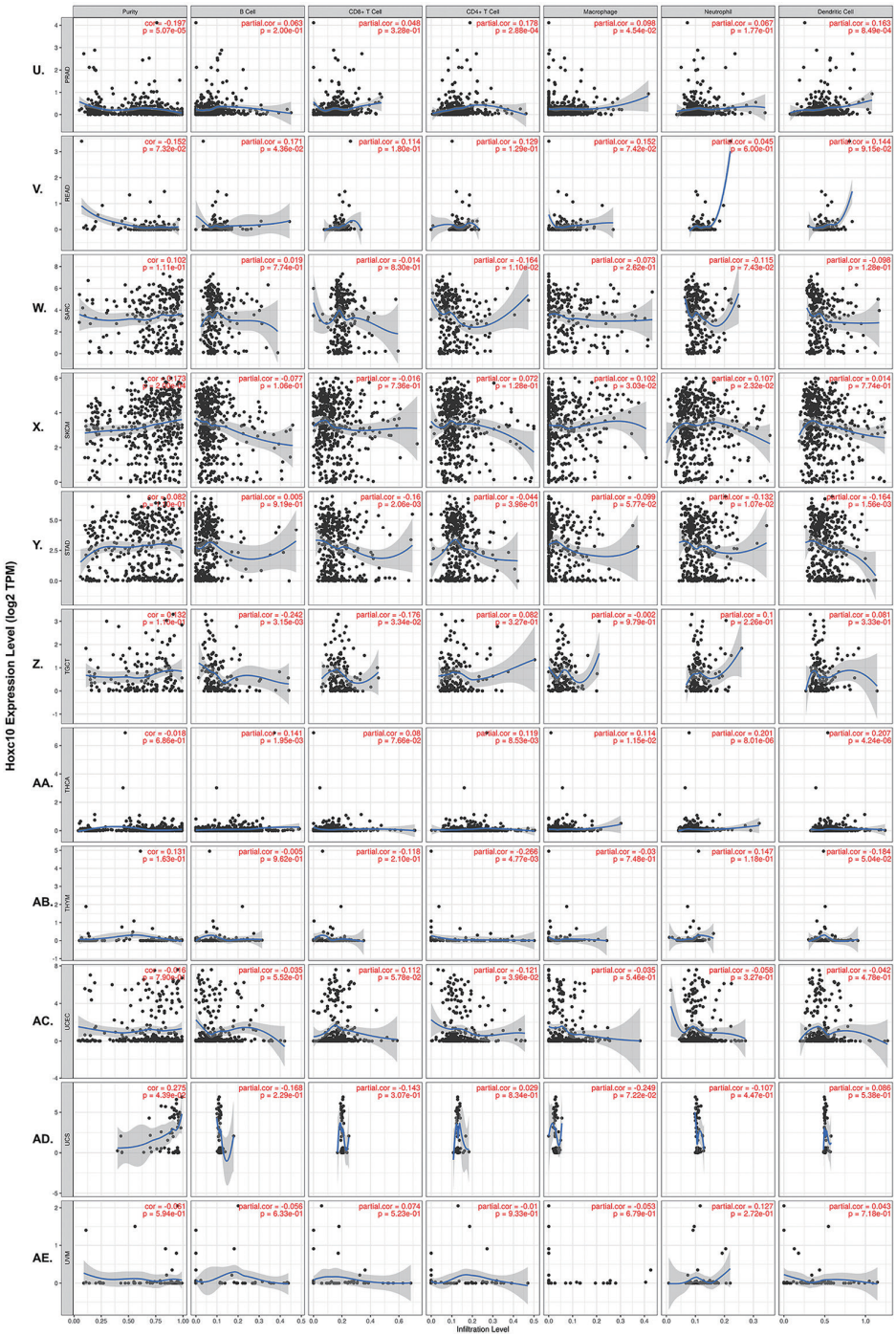

Figure S4 Correlations between *HOXC10* expression and immune infiltration in all other types of cancer, excluding breast cancer, using the Tumor Immune Estimation Resource database. (A) Adrenocortical carcinoma (ACC); (B) bladder urothelial carcinoma (BLCA); (C) cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC); (D) cholangio carcinoma (CHOL); (E) colon adenocarcinoma (COAD); (F) lymphoid neoplasm diffuse large B-cell lymphoma (DLBC); (G) esophageal carcinoma (ESCA); (H) glioblastoma multiforme (GBM); (I) head and neck squamous cell carcinoma (HNSC); (J) kidney chromophobe (KICH); (K) kidney renal clear cell carcinoma (KIRC); (L) kidney renal papillary cell carcinoma (KIRP); (M) brain lower grade glioma (LGG); (N) liver hepatocellular carcinoma (LIHC); (O) lung adenocarcinoma (LUAD); (P) lung squamous cell carcinoma (LUSC); (Q) mesothelioma (MESO); (R) ovarian serous cystadenocarcinoma (OV); (S) pancreatic adenocarcinoma (PAAD); (T) pheochromocytoma and paraganglioma (PCPG); (U) PRAD; (V) rectum adenocarcinoma (READ); (W) sarcoma (SARC); (X) skin cutaneous melanoma (SKCM); (Y) stomach adenocarcinoma (STAD); (Z) testicular germ cell tumors (TGCT); (AA) thyroid carcinoma (THCA); (AB) thymoma (THYM); (AC) uterine corpus endometrial carcinoma (UCEC); (AD) uterine carcinosarcoma (UCS); (AE) uveal melanoma (UVM).

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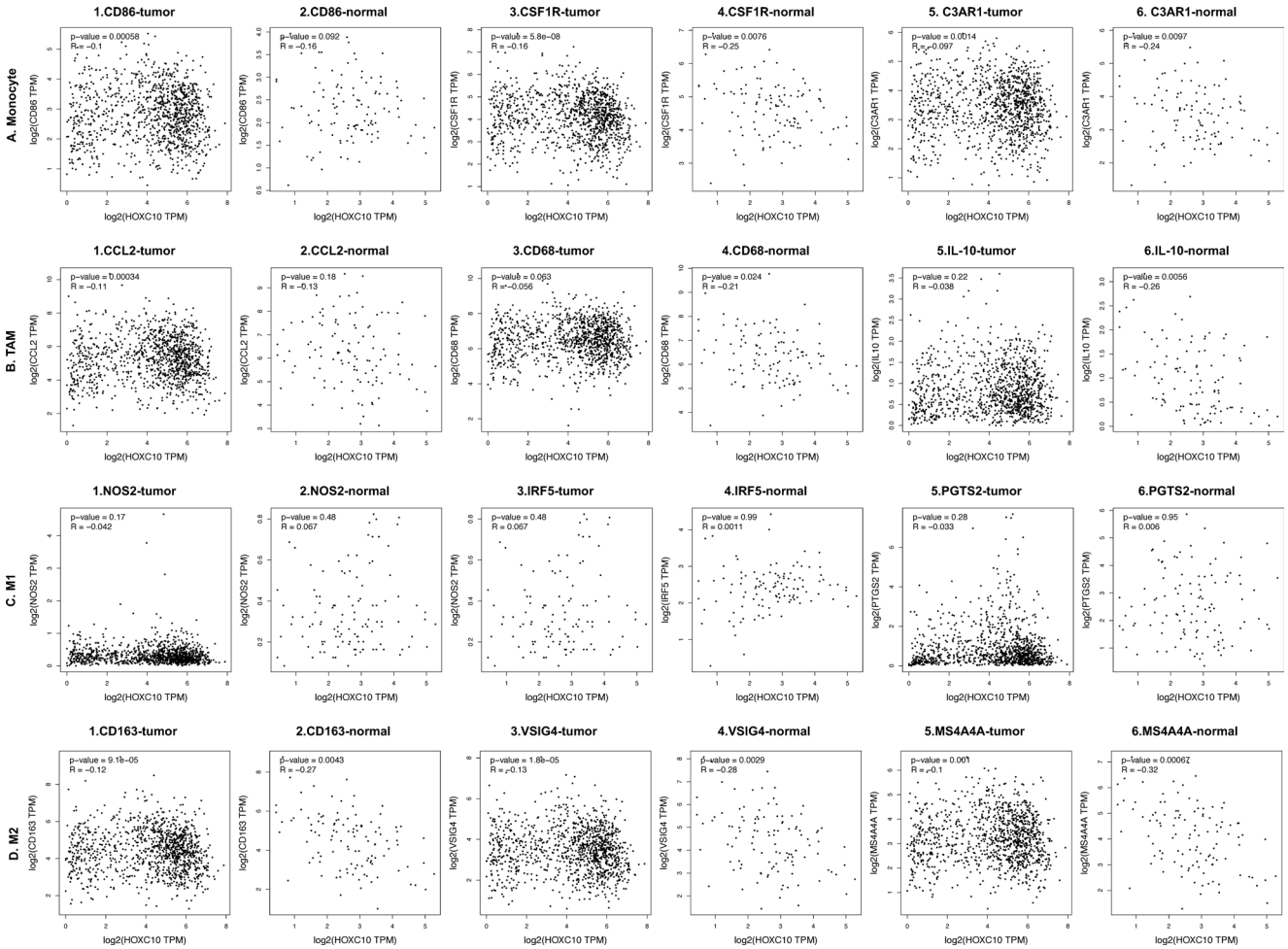

Figure S5 The correlation between *HOXC10* expression and the biomarkers of immune cells in BRCA tumors by GEPIA. (A) Monocytes; (B) TAMs; (C) M1 macrophages; and (D) M2 macrophages. BRCA, breast invasive carcinoma; GEPIA, Gene Expression Profiling Interactive Analysis; TAMs, tumor-associated macrophages.

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Table S3 The correlations between HOXC10 and genetic markers of infiltrating immune cells in luminal and Her-2+ breast cancer

Description	Gene markers	Luminal Breast Cancer				Her-2 positive Breast Cancer			
		None		Purity		None		Purity	
		COR	P	COR	P	COR	P	COR	P
B-cell	CD19	0.1352	0.00076	0.1535	0.00032	–0.085	0.49229	–0.125	0.34387
	CD79A	0.0835	0.03819	0.1074	0.012	–0.11	0.37612	–0.147	0.26448
	FCRL2	0.0902	0.02523	0.1142	0.00756	–0.033	0.79062	–0.07	0.60057
	MS4A1	0.0805	0.04589	0.1059	0.01326	–0.062	0.61686	–0.097	0.46457
CD8+ T cell	CD8A	0.1003	0.01272	0.1254	0.00332	–0.008	0.94913	–0.05	0.70405
	CD8B	0.1433	0.00037	0.1648	0.00011	–0.057	0.64432	–0.105	0.42858
T cell (general)	CD3D	0.1101	0.00623	0.1386	0.00116	–0.062	0.62004	–0.116	0.3813
	CD3E	0.1166	0.00374	0.1409	0.00096	–0.035	0.77664	–0.086	0.51492
	CD2	0.1245	0.00198	0.1472	0.00057	–0.082	0.50913	–0.125	0.34475
Neutrophils	FCGR3B	0.0136	0.73681	0.0186	0.66398	–0.211	0.08671	–0.214	0.10374
	CEACAM3	0.0762	0.05887	0.1066	0.01266	–0.014	0.91043	–0.091	0.49085
	SIGLEC5	0.0512	0.20457	0.0537	0.21035	–0.376	0.00182	–0.375	0.00361
	FPR1	0.0247	0.54126	0.0342	0.42541	–0.345	0.00447	–0.363	0.00493
	CSF3R	0.0159	0.69394	0.0068	0.87333	–0.024	0.8487	–0.031	0.81613
	S100A12	0.0306	0.44884	0.0473	0.26945	–0.082	0.51201	–0.006	0.96547
	CEACAM8	–0.008	0.83701	0.0204	0.6336	0.013	0.91553	0.0102	0.93897
	ITGAM	0.0586	0.14603	0.0497	0.24602	–0.372	0.00204	–0.383	0.00292
	CCR7	0.0922	0.02216	0.1107	0.00967	0.044	0.72202	–0.015	0.90859
Natural killer cells	KIR2DL1	0.0064	0.87377	0.0535	0.21171	–8E-04	0.99488	0.0591	0.65659
	KIR2DL3	0.0004	0.9925	0.0314	0.46361	0.002	0.98407	–0.007	0.96032
	KIR2DL4	0.0404	0.31722	0.0701	0.10166	–0.012	0.92174	–0.066	0.6196
	KIR3DL1	0.0174	0.66563	0.0373	0.38423	–0.015	0.90245	–0.045	0.73453
	KIR3DL2	0.0344	0.3947	0.0597	0.16393	0.022	0.86202	–0.001	0.99192
	KIR3DL3	–0.055	0.17198	–0.032	0.453	0.127	0.30583	0.1529	0.24768
	KIR2DS4	–0.01	0.79973	0.0274	0.52245	–0.05	0.68727	–0.006	0.96653
	NCR1	–0.004	0.9292	–3E-04	0.99453	–0.116	0.34891	–0.129	0.3295
Monocytes	C3AR1	0.0047	0.90771	0.0099	0.81748	–0.315	0.0098	–0.335	0.00972
	CD86	0.0485	0.22904	0.0628	0.14272	–0.245	0.04594	–0.27	0.03889
	CSF1R	–0.069	0.08879	–0.057	0.18521	–0.299	0.01411	–0.317	0.01492
TAM	CCL2	0.0614	0.12767	0.0854	0.046	–0.123	0.32123	–0.188	0.1538
	CD68	0.0792	0.04943	0.0818	0.05625	–0.351	0.0038	–0.354	0.00618
	IL10	0.1036	0.01009	0.1162	0.00658	–0.178	0.14987	–0.198	0.13278

Table S3 (*continued*)

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Table S3 (*continued*)

Description	Gene markers	Luminal Breast Cancer				Her-2 positive Breast Cancer			
		None		Purity		None		Purity	
		COR	P	COR	P	COR	P	COR	P
M1 macrophage	NOS2	–0.09	0.02612	–0.097	0.02338	–0.269	0.02789	–0.281	0.03143
	IRF5	–0.02	0.61896	–0.019	0.6656	–0.179	0.14611	–0.16	0.22555
	PTGS2	0.0436	0.28007	0.0469	0.27382	–0.12	0.33129	–0.111	0.39992
M2 macrophage	CD163	0.0014	0.97143	0.0188	0.66044	–0.332	0.00634	–0.336	0.0095
	VSIG4	–0.055	0.17269	–0.046	0.28762	–0.323	0.00796	–0.272	0.0376
	MS4A4A	0.0409	0.31125	0.0583	0.17351	–0.305	0.01235	–0.316	0.01518
	KIR2DS4	–0.01	0.79973	0.0274	0.52245	–0.05	0.68727	–0.006	0.96653
Dendritic cells	HLA-DPB1	0.0109	0.78641	0.0238	0.57945	–0.135	0.27646	–0.203	0.12328
	HLA-DQB1	0.0295	0.46443	0.0254	0.55354	–0.15	0.22358	–0.253	0.05332
	HLA-DRA	0.0719	0.07474	0.082	0.05558	–0.112	0.36763	–0.152	0.24968
	HLA-DPA1	0.0151	0.70767	0.0256	0.55113	–0.064	0.60512	–0.103	0.43795
	CD1C	0.0002	0.99583	0.0209	0.6258	–0.032	0.79705	–0.087	0.51437
	NRP1	0.0167	0.6784	0.0085	0.84359	–0.232	0.05912	–0.287	0.0277
	ITGAX	0.06	0.13662	0.0765	0.07423	–0.305	0.01237	–0.327	0.01168
	CD209	–0.009	0.81833	–0.007	0.86746	–0.217	0.07838	–0.232	0.07743
Th1 cells	TBX21	0.1012	0.01201	0.1262	0.00315	–0.092	0.45583	–0.126	0.34113
	STAT4	0.0819	0.04208	0.1013	0.01785	–0.065	0.59861	–0.149	0.26012
	STAT1	0.0637	0.11403	0.0693	0.10557	–0.058	0.64179	–0.083	0.53017
	IFNG	0.0753	0.06176	0.0908	0.03383	–0.158	0.20114	–0.19	0.14913
	TNF	0.068	0.09176	0.1024	0.01664	–0.136	0.27332	–0.152	0.25042
Th2 cells	GATA3	–0.184	4.72E-06	–0.177	3.32E-05	0.227	0.06506	0.2474	0.05909
	STAT6	–0.043	0.29169	–0.03	0.47886	0.14	0.25811	0.1025	0.43873
	STAT5A	–0.073	0.07053	–0.058	0.17648	–0.212	0.08473	–0.263	0.04417
	IL13	0.0896	0.02615	0.098	0.02204	0.022	0.86036	0.0119	0.92879
Tfh cells	BCL6	–0.17	2.21E-05	–0.163	0.00013	–0.063	0.60962	0.0324	0.80724
	IL21	0.0302	0.45494	0.0418	0.33013	0.144	0.24355	0.093	0.48371
Th17 cells	STAT3	–0.008	0.8475	0.009	0.83457	–0.018	0.88411	–2E-04	0.99912
	IL17A	0.0249	0.53704	0.0591	0.16767	0.143	0.24853	0.1265	0.33956
Treg	FOXP3	0.1595	7.15E-05	0.1863	1.21E-05	–0.119	0.33485	–0.153	0.24548
	CCR8	0.1429	0.00038	0.1647	0.00011	–0.276	0.02383	–0.314	0.01581
	STAT5B	–0.035	0.39027	–0.027	0.53078	–0.132	0.28632	–0.166	0.20791
	TGFB1	–0.054	0.17878	–0.075	0.08017	–0.284	0.02011	–0.305	0.01931

Table S3 (*continued*)

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Table S3 (*continued*)

Description	Gene markers	Luminal Breast Cancer				Her-2 positive Breast Cancer			
		None		Purity		None		Purity	
		COR	P	COR	P	COR	P	COR	P
T cell exhaustion	PDCD1	0.1188	0.00314	0.1478	0.00053	–0.156	0.20765	–0.23	0.08006
	CTLA4	0.1227	0.00228	0.154	0.0003	–0.078	0.52941	–0.103	0.43768
	LAG3	0.1115	0.00559	0.1277	0.0028	0.01	0.93839	–0.009	0.94676
	HAVCR2	0.0488	0.22686	0.0604	0.15884	–0.337	0.00553	–0.35	0.00691
	GZMB	0.0946	0.01881	0.1248	0.00348	–0.014	0.91285	–0.061	0.646

COR, Correlation coefficient; Her-2, human epidermal growth factor receptor 2; CD, cluster of differentiation; TAM, tumor-associated macrophage; Th, T-helper; Tfh, follicular helper T; Treg, regulatory cells; FCRL2, Fc receptor like 2; MS4A1, membrane spanning 4-domains A1; FCGR3B, Fc gamma receptor IIIb; CEACAM, CEA cell adhesion molecule; SIGLEC5, sialic acid binding Ig like lectin 5; FPR1, formyl peptide receptor 1; CSF3R, colony stimulating factor 3 receptor; S100A12, S100 calcium binding protein A12; ITGAM, integrin subunit alpha M; CCR, C-C motif chemokine receptor; KIR2DL, killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail; KIR3DL, killer cell immunoglobulin-like receptor with three domains and long cytoplasmic tail; KIR2DS4, killer cell immunoglobulin like receptor, two Ig domains and short cytoplasmic tail 4; NCR1, natural cytotoxicity triggering receptor 1; C3AR1, complement C3a receptor 1; CSF1R, colony stimulating factor 1 receptor; CCL2, C-C motif chemokine ligand 2; IL, interleukin; NOS2, nitric oxide synthase 2; IRF5, interferon regulatory factor 5; PTGS2, prostaglandin-endoperoxide synthase 2; VSIG4, V-set and immunoglobulin domain containing 4; MS4A4A, membrane spanning 4-domains A4A; HLA-DPB1, major histocompatibility complex, class II, DP beta 1; HLA-DQB1, major histocompatibility complex, class II, DQ beta 1; HLA-DRA, major histocompatibility complex, class II, DR alpha; HLA-DPA1, major histocompatibility complex, class II, DP alpha 1; CD1C, CD1c molecule; NRP1, neuropilin 1; ITGAX, integrin subunit alpha X; TBX21, T-box transcription factor 21; STAT, signal transducer and activator of transcription; IFNG, interferon gamma; TNF, tumor necrosis factor; GATA3, GATA binding protein 3; BCL6, B cell leukemia transcription repressor; FOXP3, forkhead box P3; TGFB1, transforming growth factor beta 1; PDCD1, programmed cell death 1; CTLA4, cytotoxic T-lymphocyte associated protein 4; LAG3, lymphocyte activating 3; HAVCR2, hepatitis A virus cellular receptor 2; GZMB, granzyme B.

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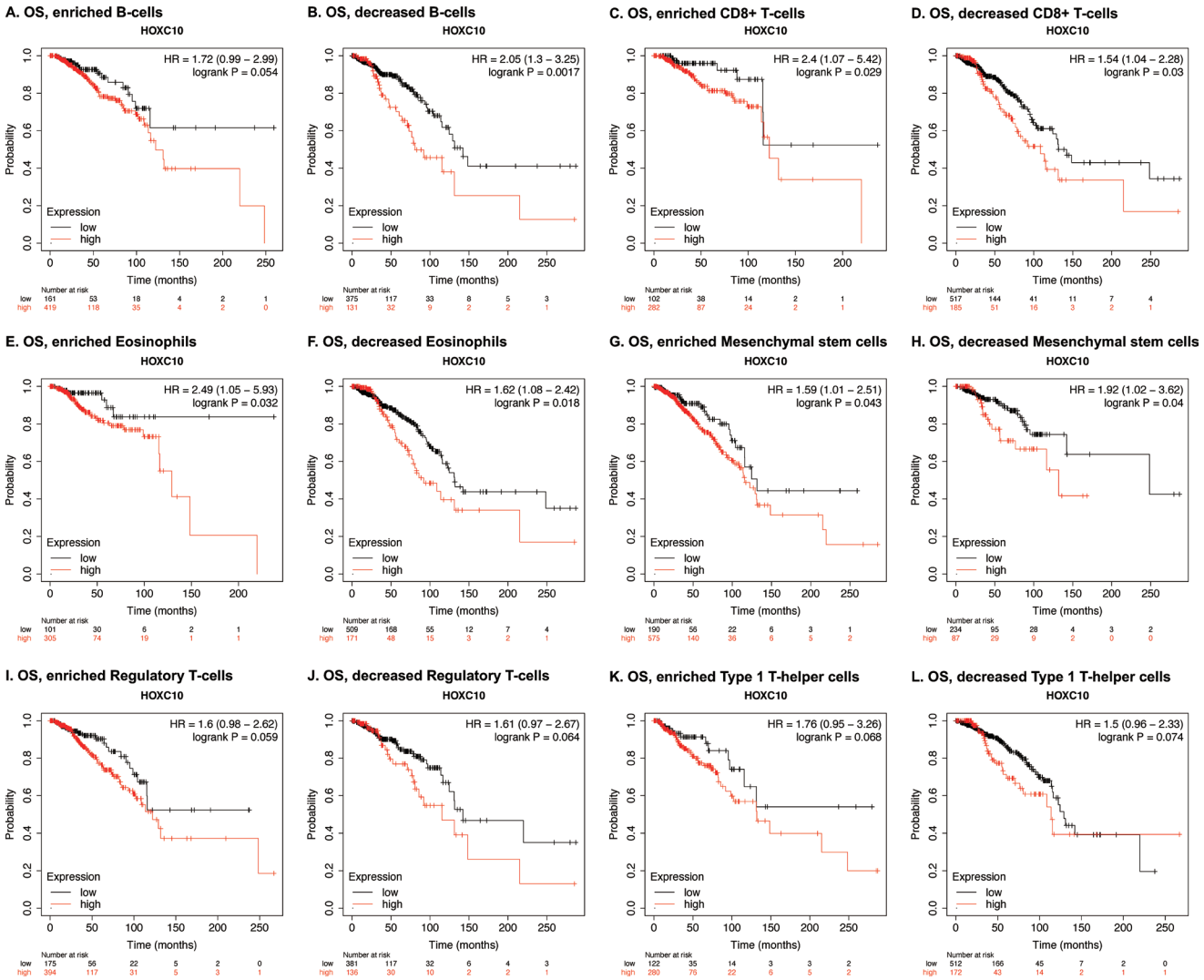

Figure S6 The correlations between *HOXC10* expression and the OS of breast cancer patients based on the different subgroups of immune cells in the Kaplan-Meier plotter database. (A) enriched B cells; (B) decreased B cells; (C) enriched $CD8^+$ T cells; (D) decreased $CD8^+$ T cells; (E) enriched eosinophils; (F) decreased eosinophils; (G) enriched mesenchymal stem cells; (H) decreased mesenchymal stem cells; (I) enriched Tregs (J) decreased Tregs; (K) enriched Type 1 T-helper cells; and (L) decreased Type 1 T-helper cells. OS, overall survival; CD, cluster of differentiation; Tregs, regulatory cells.

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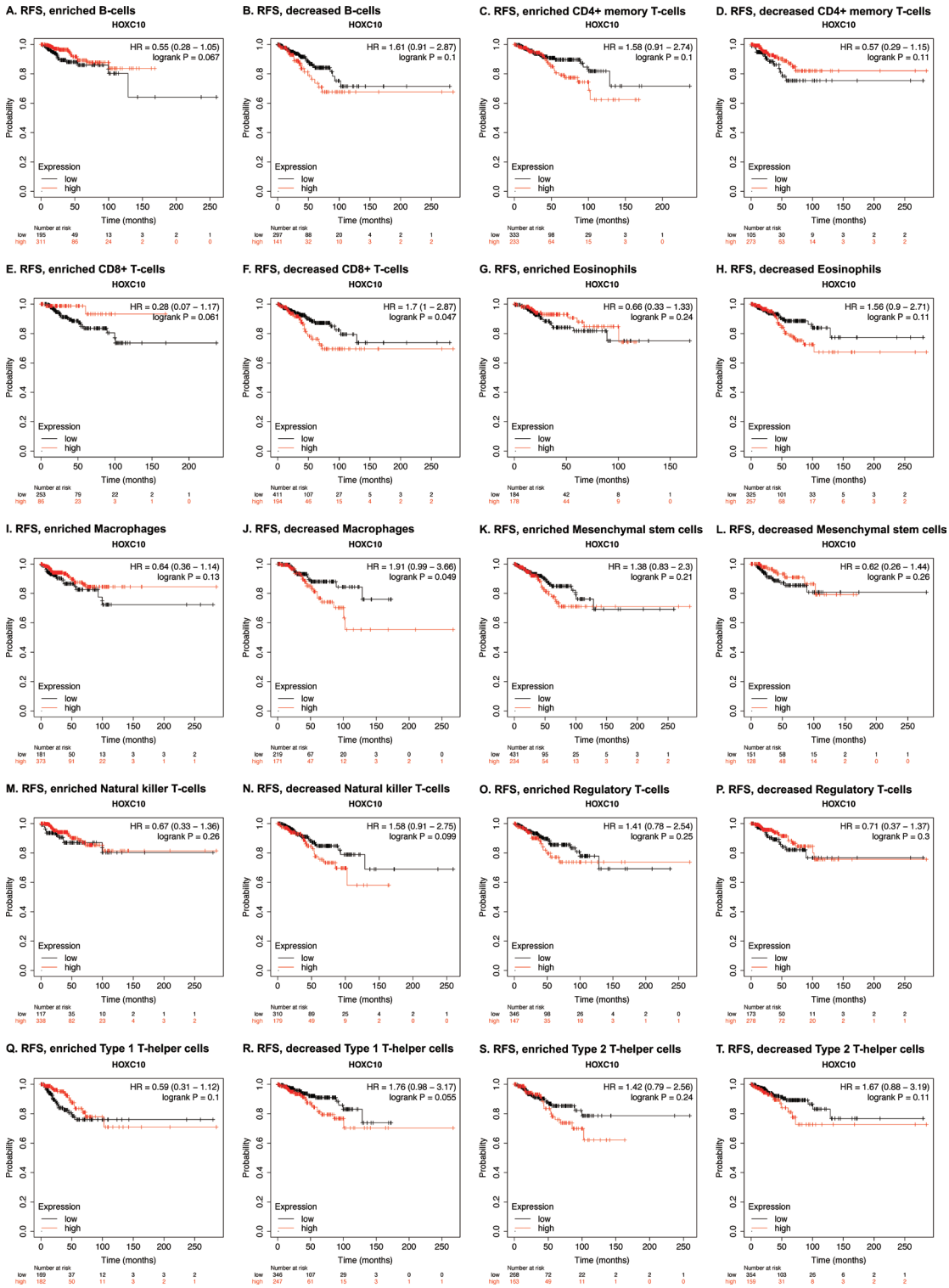

Figure S7 The interaction between *HOXC10* expression and the RFS of breast cancer patients based on the different subgroups of immune cells in the Kaplan-Meier plotter database. (A) enriched B cells; (B) decreased B cells; (C) enriched $CD4^+$ memory T cells; (D) decreased $CD4^+$ memory T cells; (E) enriched $CD8^+$ T cells; (F) decreased $CD8^+$ T cells; (G) enriched eosinophils; (H) decreased eosinophils; (I) enriched macrophages; (J) decreased macrophages; (K) enriched mesenchymal stem cells; (L) decreased mesenchymal stem cells; (M) enriched NK cells; (N) decreased NK cells; (O) enriched Tregs; (P) decreased Tregs; (Q) enriched Th1 cells; (R) decreased Th1 cells; (S) enriched Th2 cells; and (T) decreased Th2 cells. RFS, relapse-free survival; CD, cluster of differentiation; NK, natural killer; Tregs, regulatory cells; Th, T-helper.

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