

Figure S1. Immune cell infiltration analysis. Overview of levels of the 22 tumor-infiltrating immune cells in male and female patients.

Figure S2. Sex-based gene differential expression analysis. Scatter plot shows distribution of DEGs in female and male patients.

Figure S3. Sex-based functional enrichment analysis

- (A) Enriched pathways of genes exclusively downregulated in female patients.
- (B) Enriched pathways of genes exclusively upregulated in female patients.
- (C) Enriched pathways of genes exclusively downregulated in male patients.
- (D) Enriched pathways of genes exclusively upregulated in male patients.

Figure S4. Analysis of BEX4 in HCC.

- (A) Correlation between BEX4 expression and tumor grade in HCC patients.
- (B) Correlation between BEX4 expression and disease stage in HCC patients.
- (C) Correlation between immune checkpoint molecules and BEX4 expression in HCC patients.
- (D) Correlation between BEX4 expression and small molecule drug sensitivity.

Figure S5. Validation of BEX4 in GSE64041 dataset.

- (A) Comparison of BEX4 expression between paired normal and tumor samples in GSE64041.
- (B) Expression correlation between BEX4 and CD20 (B cell marker).
- (C) Expression correlation between BEX4 and CD4 (CD4 T cell marker).
- (D) Expression correlation between BEX4 and CD8A (CD8 T cell marker).
- (E) Expression correlation between BEX4 and CD68 (Macrophage marker).
- (F) Expression correlation between BEX4 and CD1C (Dendritic cell marker).
- (G) Expression correlation between BEX4 and CD16 (Neutrophil marker).
- (H) Expression correlation between BEX4 and TIM3.
- (I) Expression correlation between BEX4 and LGALS9.
- (J) Expression correlation between BEX4 and PD-L1.

Figure S1

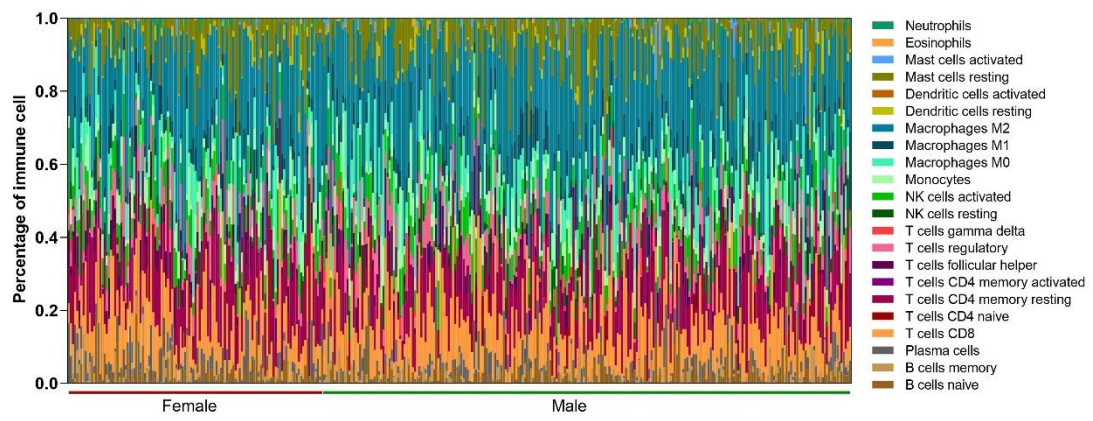


Figure S2

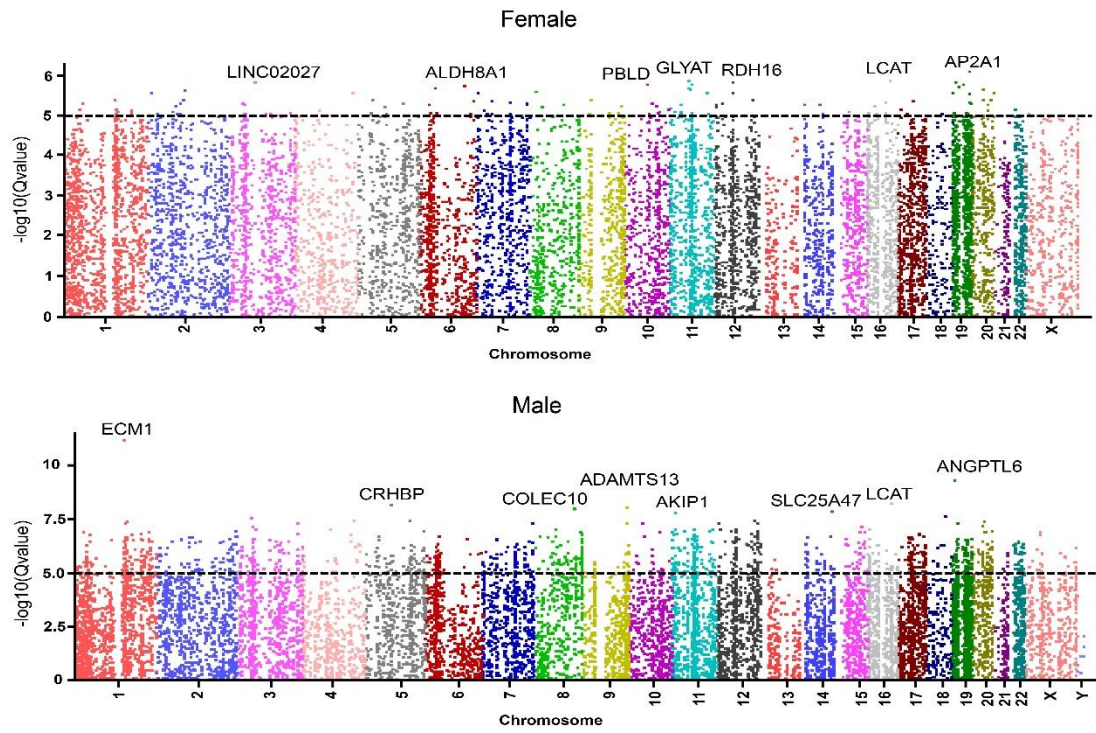


Figure S3

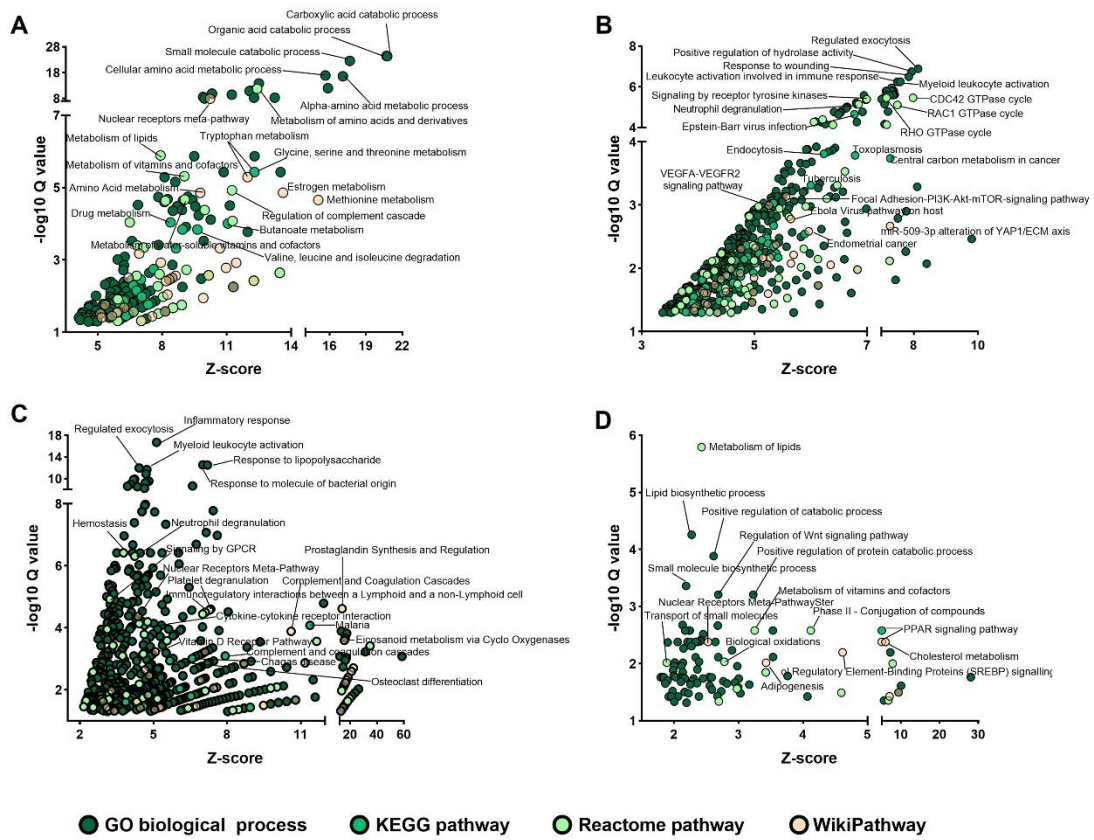
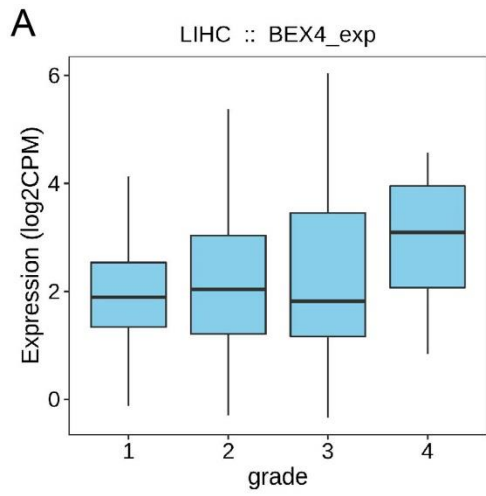
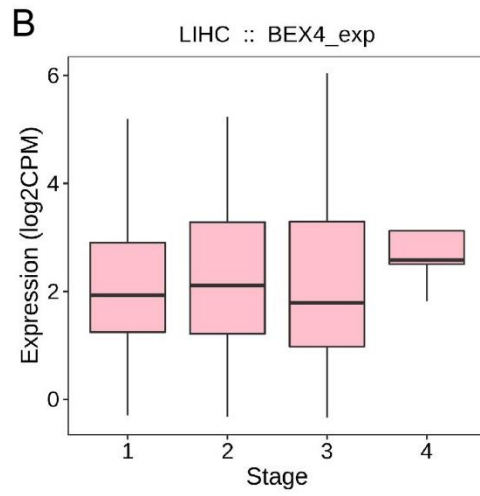


Figure S4



Spearman: rho=0.054, p=0.306



Spearman: rho=-0.02, p=0.716

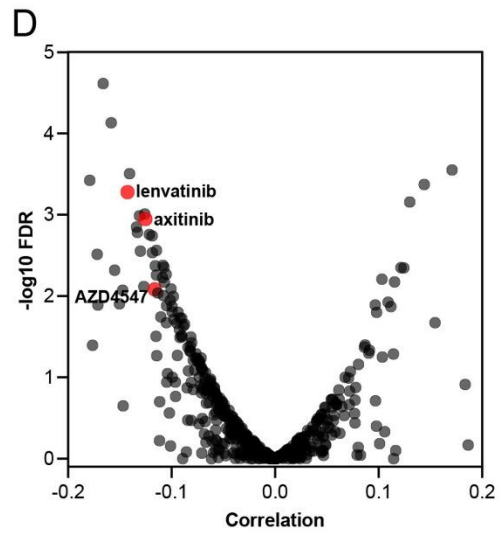
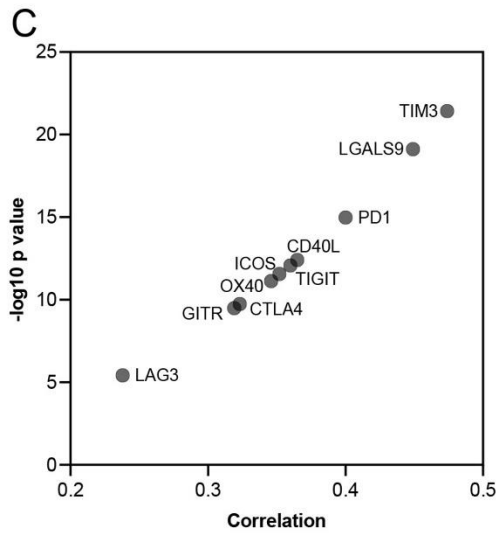


Figure S5

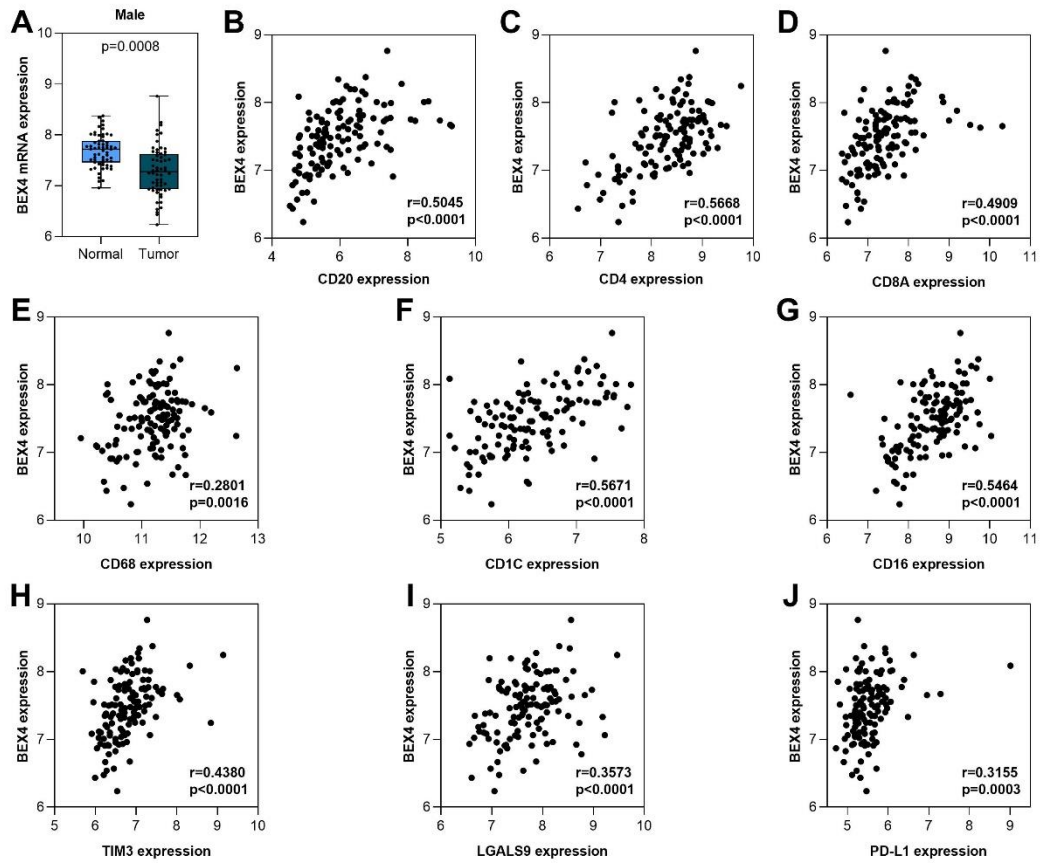


Table S1. Clinicopathologic characteristics of TCGA cohort

Characteristics	Number of cases (%)
Age (y)	
<60	171 (46.1)
≥60	200 (53.9)
Gender	
Male	250 (67.4)
Female	121 (32.6)
Race	
Caucasian	181 (48.8)
Asian	161 (43.4)
African-American	19 (5.1)
NA	10 (2.7)
Clinical stage	
I	175 (47.2)
II	82 (22.1)
III	85 (22.9)
IV	5 (1.3)
NA	24 (6.5)
Tumor grade	
G1	54 (14.6)
G2	175 (47.2)
G3	124 (33.4)
G4	13 (4.8)
NA	5 (1.3)
T classification	
T1	185 (49.9)
T2	90 (24.3)
T3	80 (21.6)
T4	13 (3.5)
Tx	1 (0.8)
N classification	
N0	255 (68.7)
N1	4 (1.1)
Nx	112 (30.2)
M classification	
M0	268 (72.2)
M1	4 (1.1)
Mx	99 (26.7)

Table S2. Correlation between BEX4 expression and clinicopathologic characteristics of TCGA cohort

Characteristics	BEX4		P value
	Low, no. cases	High, no. cases	
Age (y)			
<60	78	93	0.1299
≥60	107	93	
Gender			
Male	129	121	0.3368
Female	56	65	
Race			
Caucasian	94	87	0.521
Asian	74	87	
African-American	10	9	
Clinical stage			
I	92	83	0.4089
II	36	46	
III+IV	43	47	
Tumor grade			
G1	22	32	0.4528
G2	89	86	
G3	64	60	
G4	5	8	
T classification			
T1	95	90	0.6109
T2	39	51	
T3	41	39	
T4	7	6	
N classification			
N0	123	132	0.6234
N1	1	3	
M classification			
M0	127	141	0.3514
M1	3	1	