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SUPPLEMENTAL DATA

JAM3: A prognostic biomarker for bladder cancer via epithelial–mesenchymal transition regulation

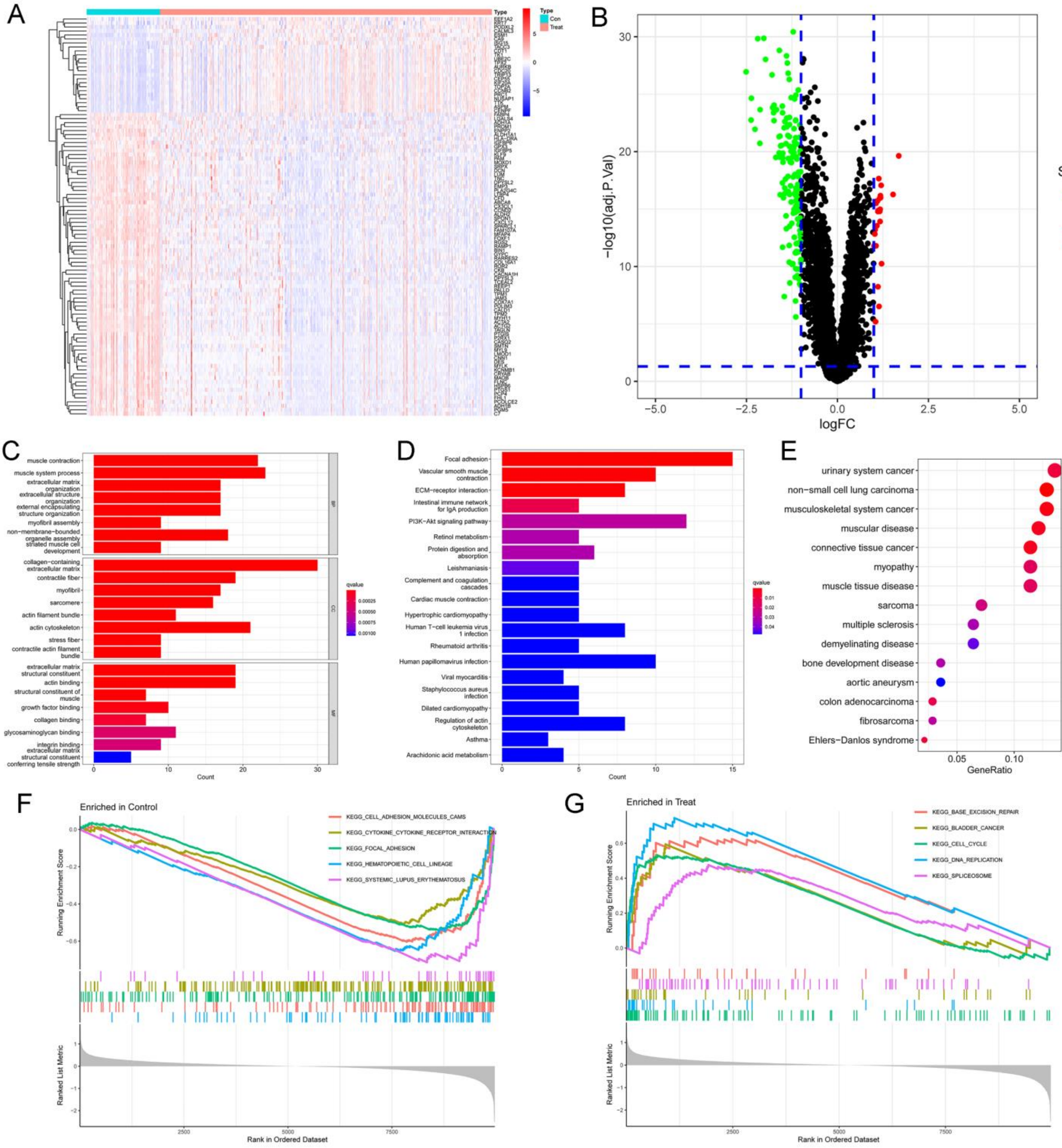

Figure S1. **DEGs and their enrichment analysis.** (A, B) The volcano plot for 172 DEGs and the heat map for most relevant 100 DEGs (24 upregulated and 148 down-regulated). (C, D) Bar plot of GO and KEGG analyses for DEGs. (E) Bubble plot of DO analysis for DEGs. (F, G) GSEA analysis in BC and normal samples. DEG: differentially expressed genes; GO: Gene ontology; KEGG: Kyoto Encyclopedia of Genes and Genomes; DO: Disease ontology; GSEA: Gene Set Enrichment Analysis.

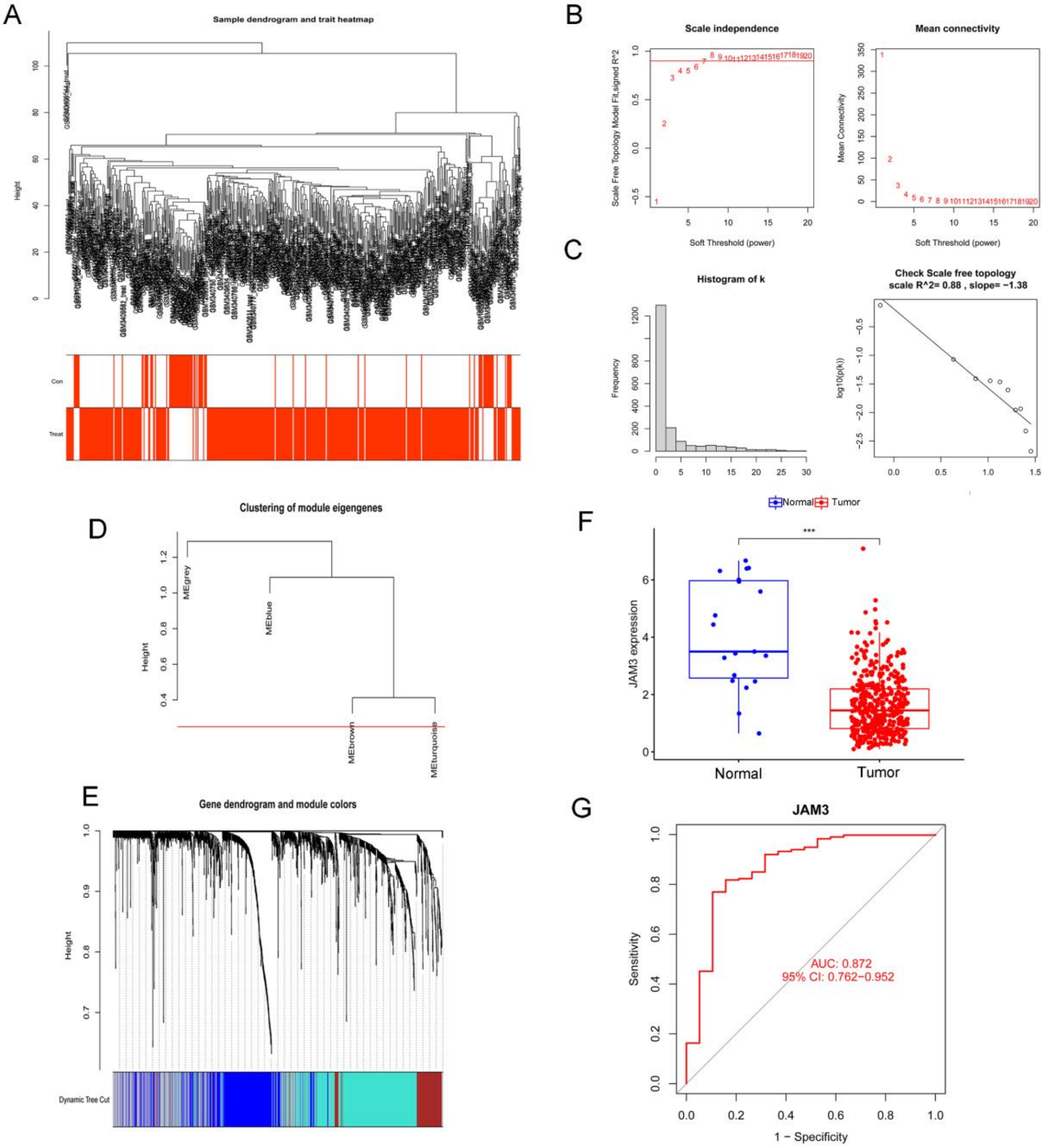

Figure S2. **Construction of BC-related gene co-expression modules.** (A) Clustering dendrogram and trait indicator of 481 samples. (B) Analysis of the scale-free fit index and the mean connectivity for various soft ‑ thresholding powers. (C) Scale free topology when the power value was seven. (D) Hierarchical clustering analysis of WGCNA modules. (E) Dendrogram of all genes clustered based on a dissimilarity measure (1 - TOM). (F) Boxplot of JAM3 expression across BC and normal samples in TCGA cohort. (G) ROC curve of JAM3 as a diagnostic gene for BC in the TCGA cohort. WGCNA: weighted correlation network analysis; JAM3: Junctional adhesion molecule 3; BC: Bladder cancer; TGCA: The Cancer Genome Atlas.

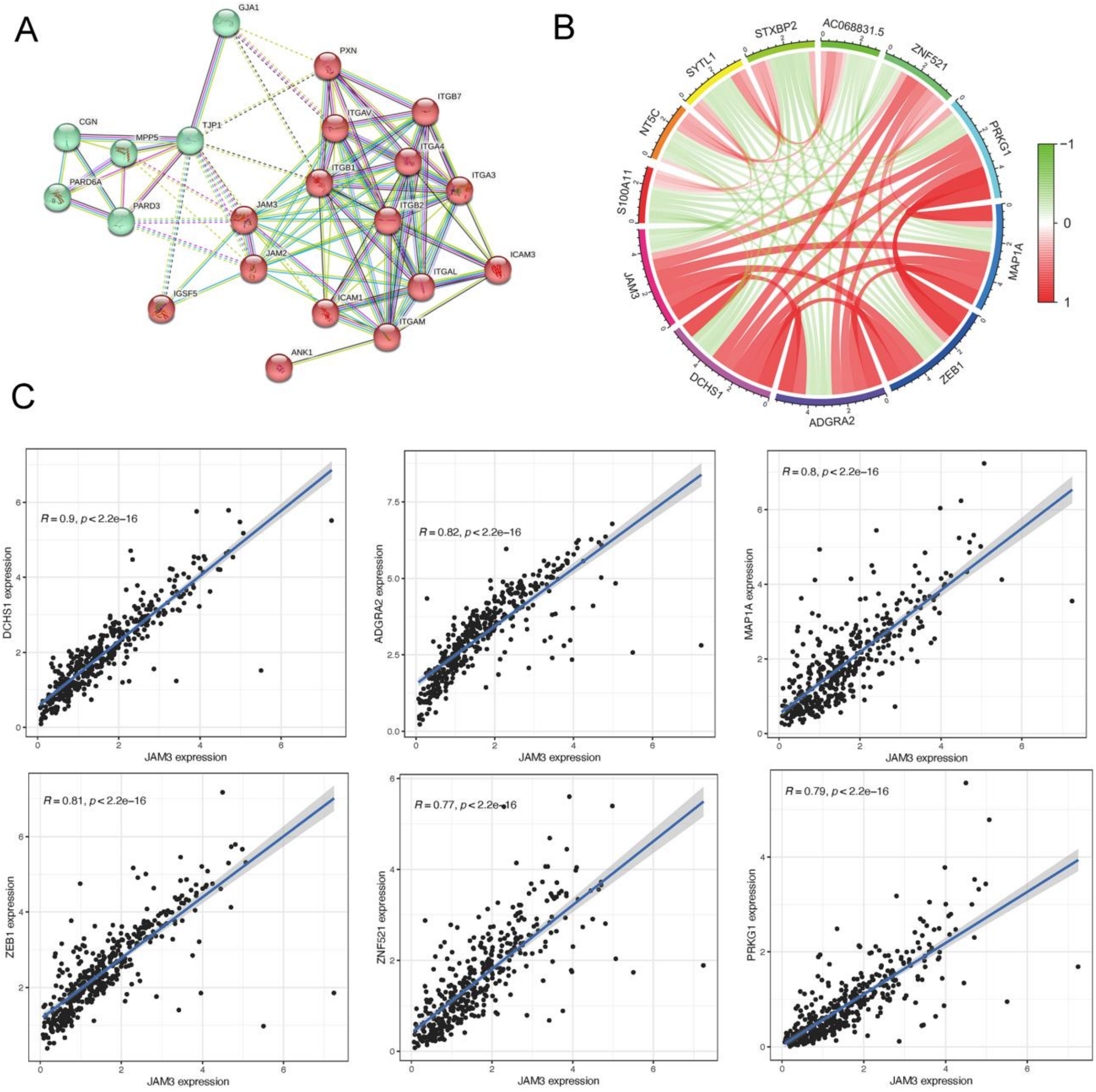

Figure S3. **Co-expression network of JAM3 in BC.** (A) Protein-protein interaction network for JAM3. (B) The top five genes negatively correlated with JAM3 and the top six genes positively correlated with JAM3. (C) The top six strongest positively co-expressed genes.

A

GEO Series	Sample source	Frequency	Percentage(%)	umulative percentage(%)
GSE3167(n=50)	Bladder timor tissue	1	2	2
	Bladder tumor tissue	40	80	82
	Normal bladder biopsy	9	18	100
GSE13507(n=265)	Bladder mucosae surrounding cancer	58	22.66	22.66
	Multipotent Progenitor Cells (MPPs)	1	0.39	23.05
	Normal bladder mucosae	9	3.52	26.56
	Primary bladder cancer	165	64.45	91.02
	Recurrent non-muscle invasive tumor	23	8.98	100
GSE52519(n=12)	Bladder cancer tissue	9	75	75
	Bladder healthy tissue	3	25	100
GSE65635(n=12)	Bladder cancer	8	66.67	66.67
	Normal bladder mucosa	2	16.67	83.33
	Pooled normal bladder mucosa samples	2	16.67	100
GSE100926(n=6)	Mucle invasive Bladder_cancer_tissue_patient1	1	16.67	16.67
	Mucle invasive Bladder_cancer_tissue_patient2	1	16.67	33.33
	Mucle invasive Bladder_cancer_tissue_patient3	1	16.67	50
	Normal_adjacent_tissue_patient1	1	16.67	66.67
	Normal_adjacent_tissue_patient2	1	16.67	83.33
	Normal_adjacent_tissue_patient3	1	16.67	100
GSE120736(n=145)	Primary bladder cancer	118	81.38	81.38
	Recurrent bladder tumor	27	18.62	100

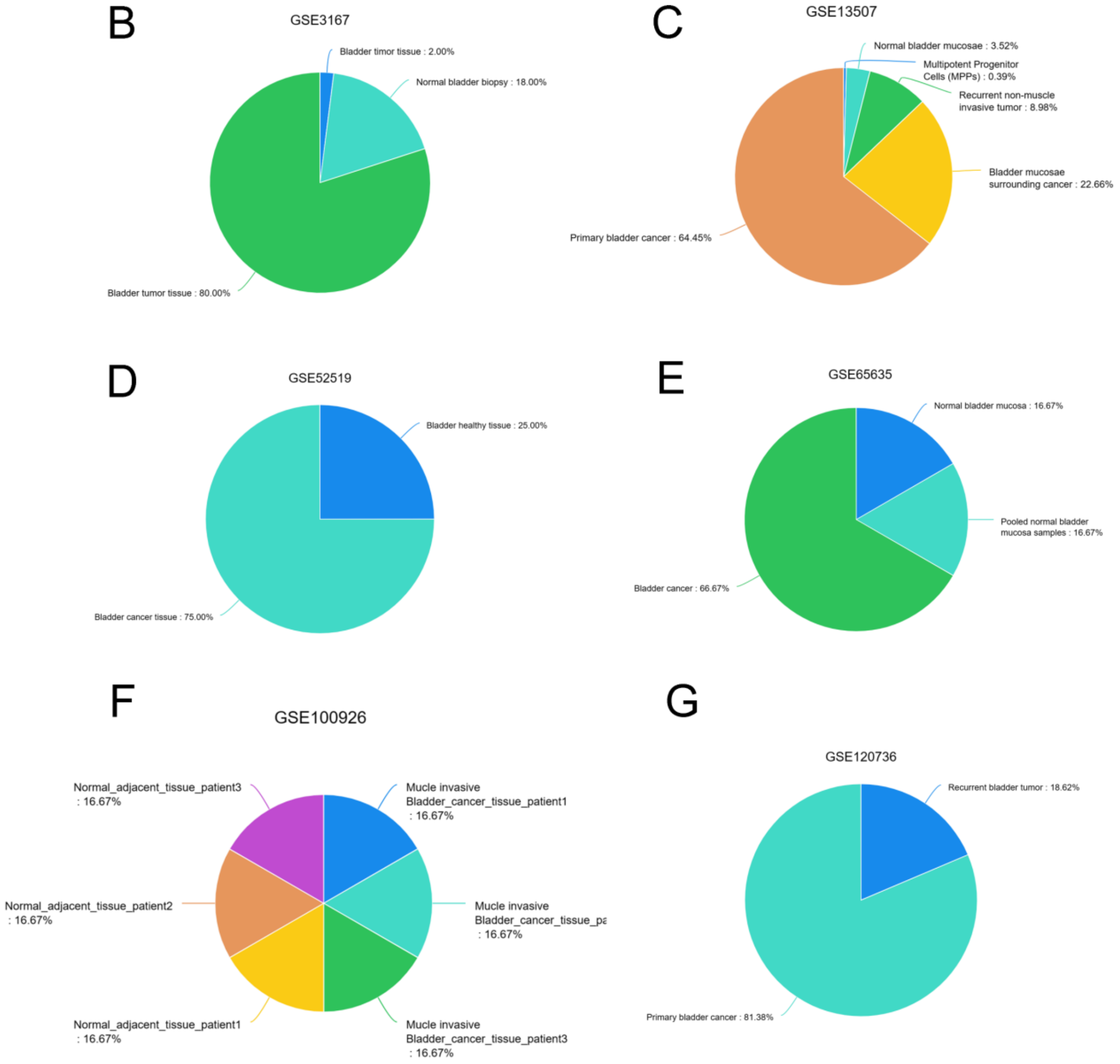

Figure S4. Demonstration of clinical traits in the GEO datasets (GSE3167, GSE13507, GSE52519, GSE65635, GSE100926, GSE120736).

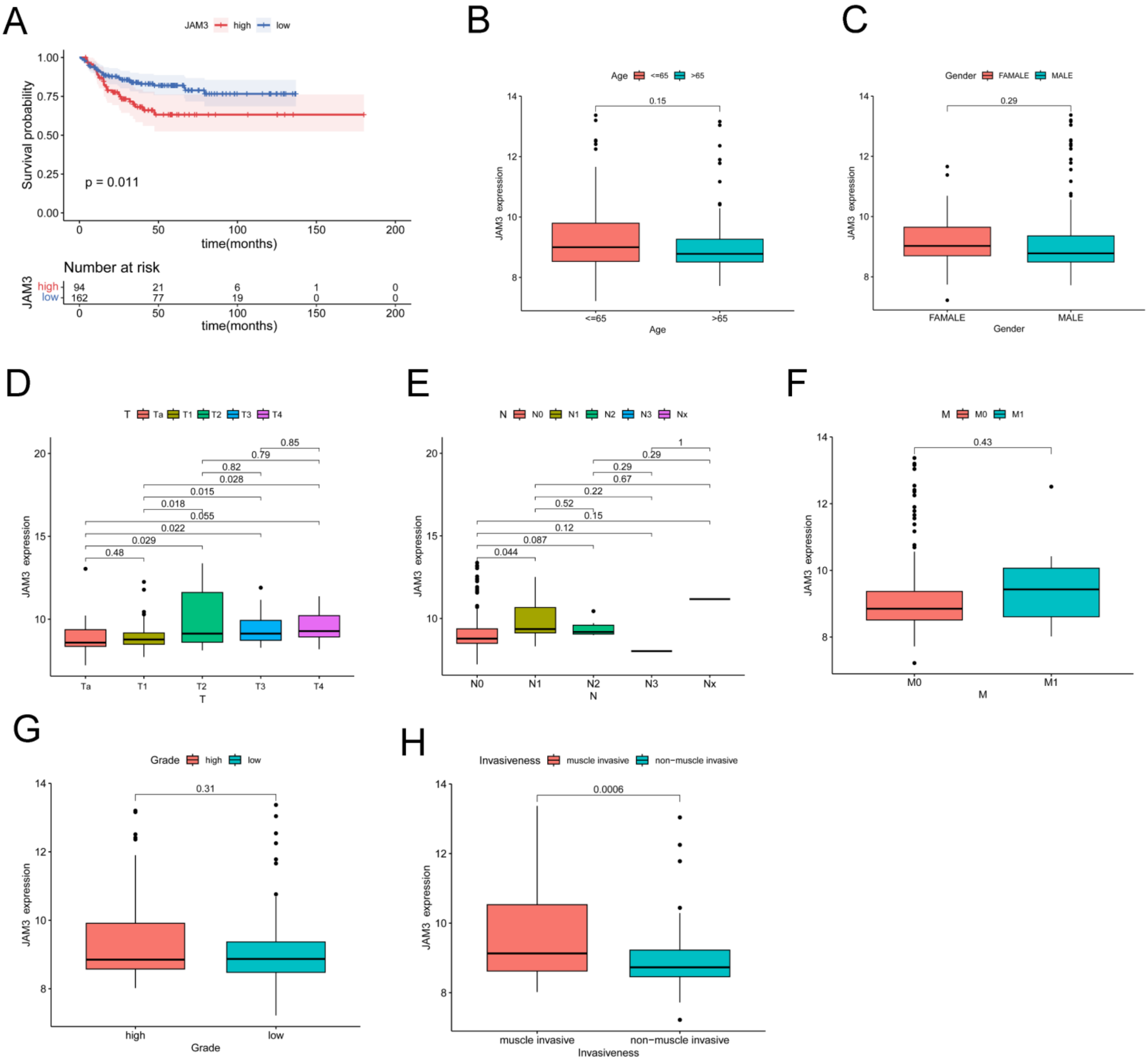

Figure S5. (A) Kaplan-Meier analysis of JAM3 in BC based on GSE13507, GSE48276, GSE37817. (B-H) Relationship between JAM3 expression level and clinical parameters based on GSE13507, GSE48276, GSE37817.

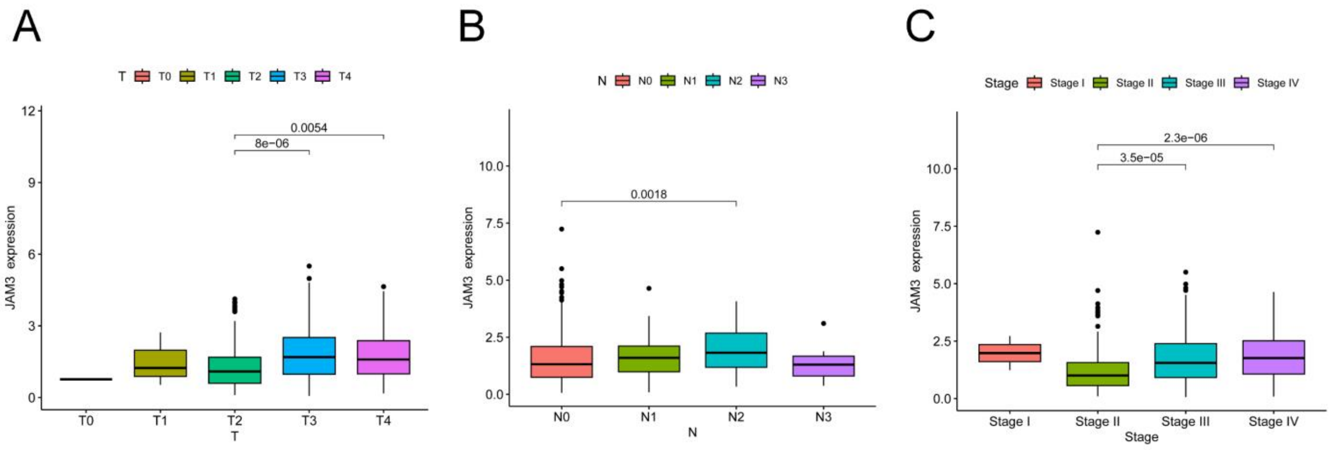

Figure S6. (A-C) Relationship between JAM3 expression level and clinical parameters based on TCGA.

Table S1. Clinical data on patients with bladder cancer from TCGA.

Type	Group	Frequency	Percentage (%)	Cumulative percentage (%)
Age	<65	151	36.65	36.65
	>=65	261	63.35	100.00
Gender	FEMALE	108	26.21	26.21
	MALE	304	73.79	100.00
Grade	High Grade	388	94.17	94.17
	Low Grade	21	5.10	99.27
	unknow	3	0.73	100.00
Stage	Stage I	2	0.49	0.49
	Stage II	131	31.80	32.28
	Stage III	141	34.22	66.50
	Stage IV	136	33.01	99.51
	unknow	2	0.49	100.00
T	T0	1	0.24	0.24
	T1	3	0.73	0.97
	T2	120	29.13	30.10
	T3	196	47.57	77.67
	T4	59	14.32	91.99
	unknow	33	8.01	100.00
M	M0	196	47.57	47.57
	M1	11	2.67	50.24
	unknow	205	49.76	100.00
N	N0	239	58.01	58.01
	N1	47	11.41	69.42
	N2	76	18.45	87.86
	N3	8	1.94	89.81
	unknow	42	10.19	100.00
	Total	412	100.0	100.00