

Figure S1. GO and KEGG analyses of the differentially expressed circRNAs in the H vs. L groups. Top ten GO terms for biological processes (A), cellular components (B), and molecular functions (C) and top ten pathways (D) for dysregulated circRNAs in the H vs. L groups. circRNA, circular RNA; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; H, high-grade bladder cancer; L, low-grade bladder cancer.

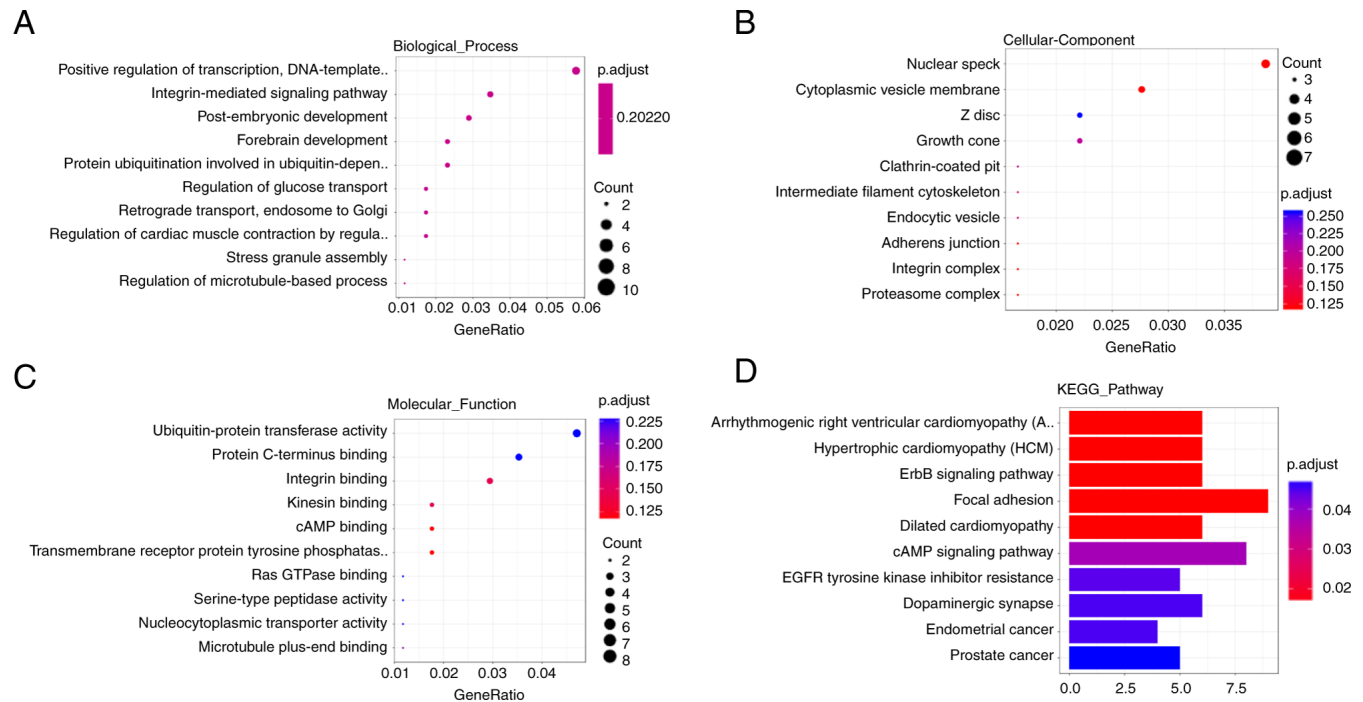


Figure S2. Enrichment network of dysregulated circular RNAs in the high-grade bladder cancer vs. low-grade bladder cancer groups. Nodes represent functions enriched for an annotated ontology term and node size indicates the number of genes that fall into that term. Nodes are clustered into subnetworks that representatively describe the annotations. $P < 0.01$ was the cutoff criteria.

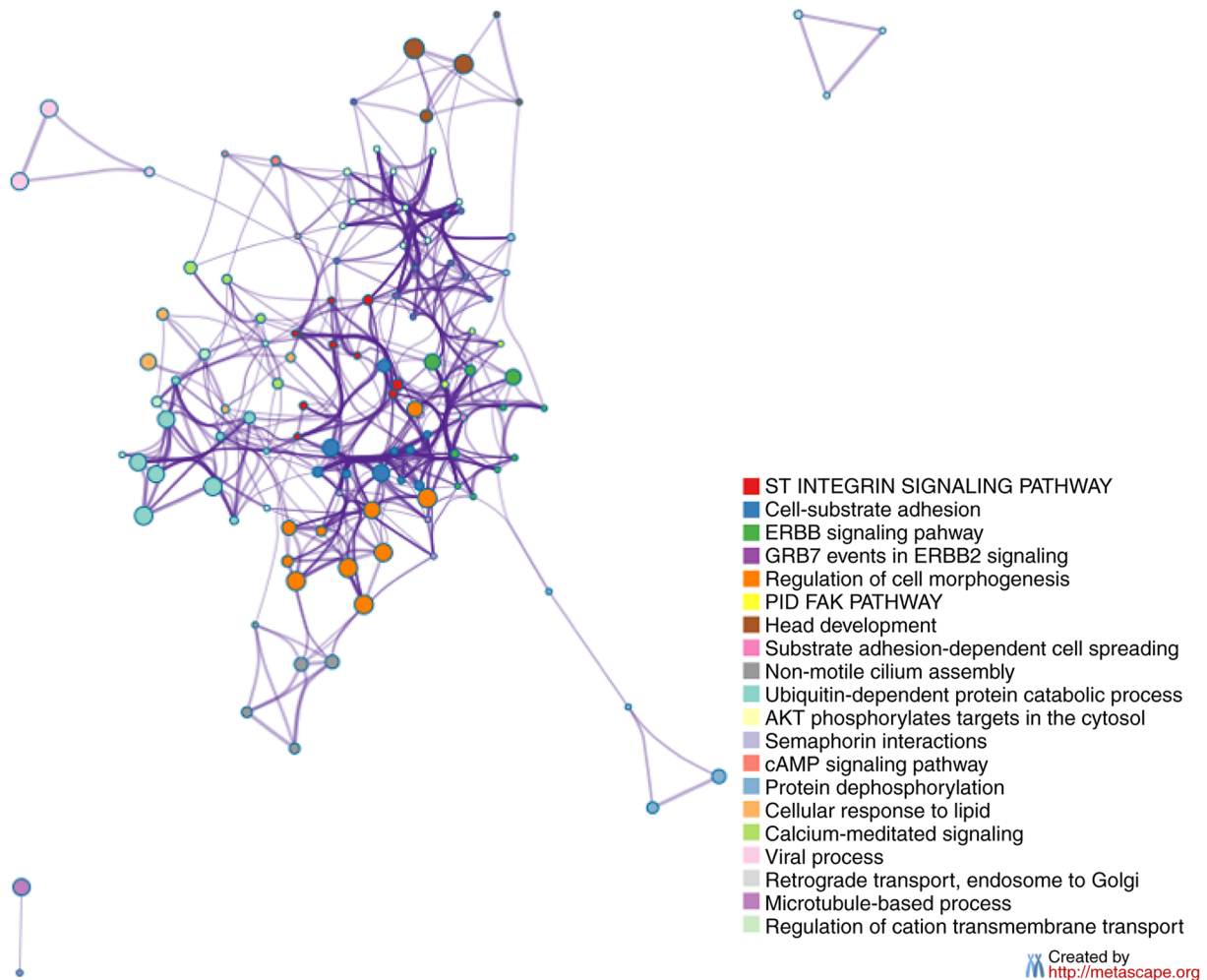


Figure S3. PPI networks of the circRNA gene symbols dysregulated in both the H vs. N and H vs. L groups. networks of the circRNA gene symbols dysregulated in the H vs. N and H vs. L groups. The network nodes are proteins and the edges represent predicted functional associations. The thickness of the line reflects the degree of confidence for the predicted interaction. circRNA, circular RNA; H, high-grade bladder cancer; L, low-grade bladder cancer; N, normal tissue; PPI, protein-protein interaction.

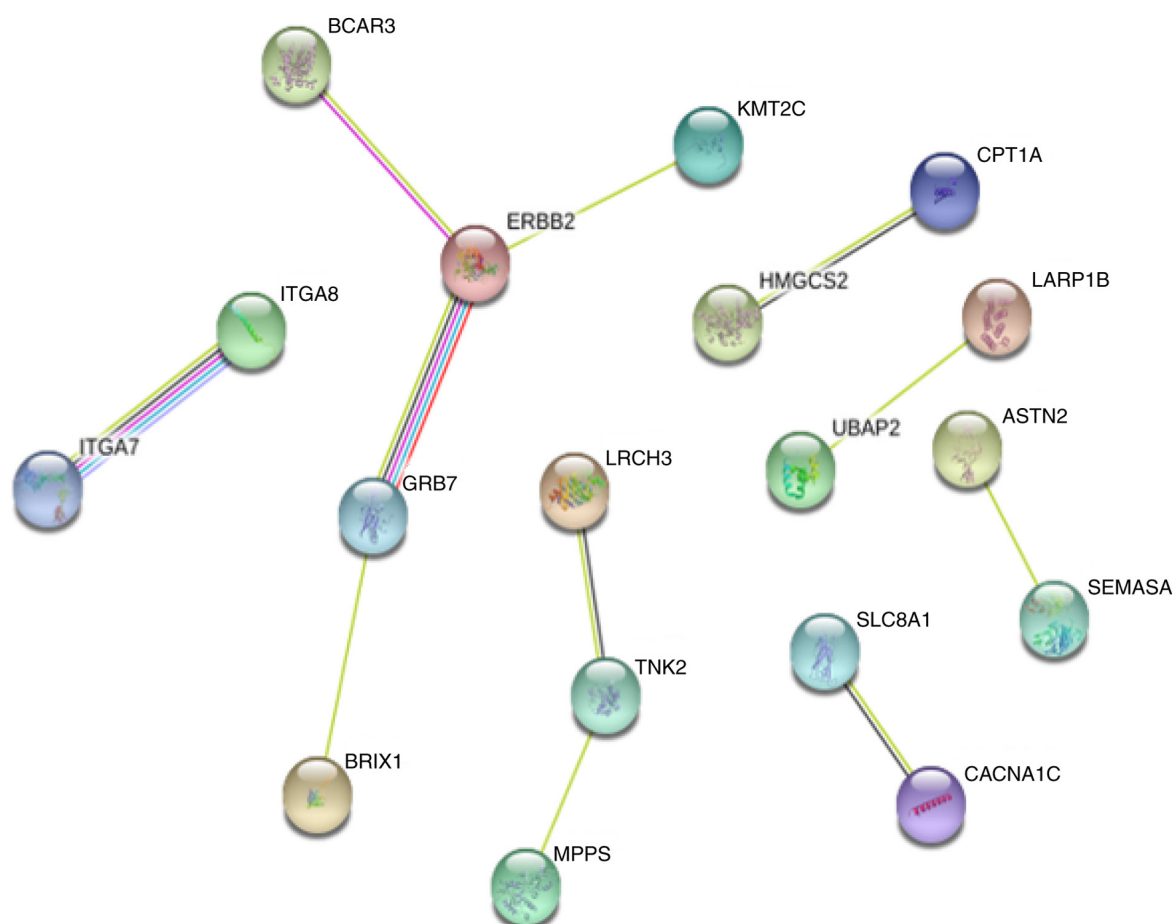


Table SI. Primers sequences of internal reference and dysregulated circular RNAs selected or reverse transcription-quantitative polymerase chain reaction.

Name	Type	Primers sequences (5'-3')
hsa_circ_0005429	F	AGGGTTTACAGACATTAGCAACG
hsa_circ_0005429	R	CCTTCACCAGAGGATGTATTGC
hsa_circ_0008510	F	AGGGTTTACAGACATTAGCAACG
hsa_circ_0008510	R	CCTTCACCAGAGGATGTATTGC
hsa_circ_0030392	F	GCAGACAGTTGTATCACGCC
hsa_circ_0030392	R	AAACAGCAAATGGAGGCCTG
hsa_circ_0072654	F	GCTGGAGAAGGAGAAGTGGA
hsa_circ_0072654	R	CTTCCTCAGCTTCCTCTCCA
hsa_circ_0096402	F	TGAAACTAGTGCAAAAGCTGGA
hsa_circ_0096402	R	GAATCAAGCTCCTGAACCGC
hsa_circ_0137606	F	TGCAGCTGGGAGACATAAGT
hsa_circ_0137606	R	TGGGTCCCGTAGCAAAAGAT
hsa_circ_0081963	F	CATTGTATCATTGGTGTATGGCA
hsa_circ_0081963	R	ACCGCCACAAAGAAGCCTT
human-GAPDH	F	GAAGGTGAAGGTCGGAGTC
human-GAPDH	R	GAAGATGGTGATGGGATTTC

F, forward; hsa, *homo sapiens*; R, reverse.