

Figure S1. Top-ranked biological functions of hsa\_circRNA\_004646 in GO analysis and Pathway analysis. (A) The top 10-fold enrichment scores in GO enrichment analysis on target genes of hsa\_circRNA\_004646. (B) The top 8 enrichment scores in the Pathway analysis on target genes of hsa\_circRNA\_004646 are presented. circRNA, circular RNA; GO, Gene Ontology; BP, biological processes; CC, cellular components; MF, molecular functions.

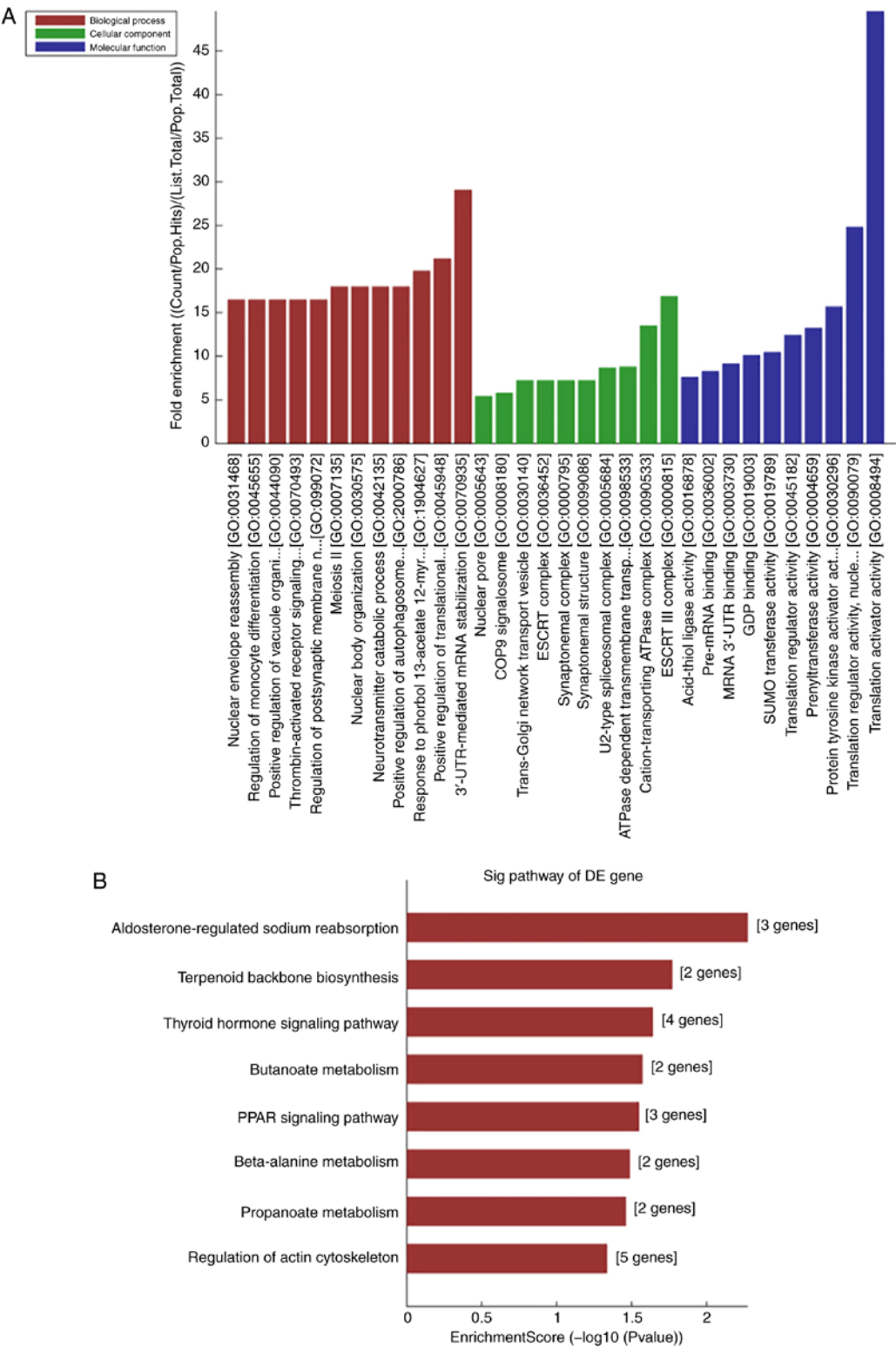


Figure S2. Top-ranked biological functions of hsa\_circRNA\_100086 in GO analysis and Pathway analysis. (A) The top 10-fold enrichment scores in GO enrichment analysis on target genes of hsa\_circRNA\_100086. (B) The top 8 enrichment scores in the Pathway analysis on target genes of hsa\_circRNA\_100086 are presented. circRNA, circular RNA; GO, Gene Ontology; BP, biological processes; CC, cellular components; MF, molecular functions.

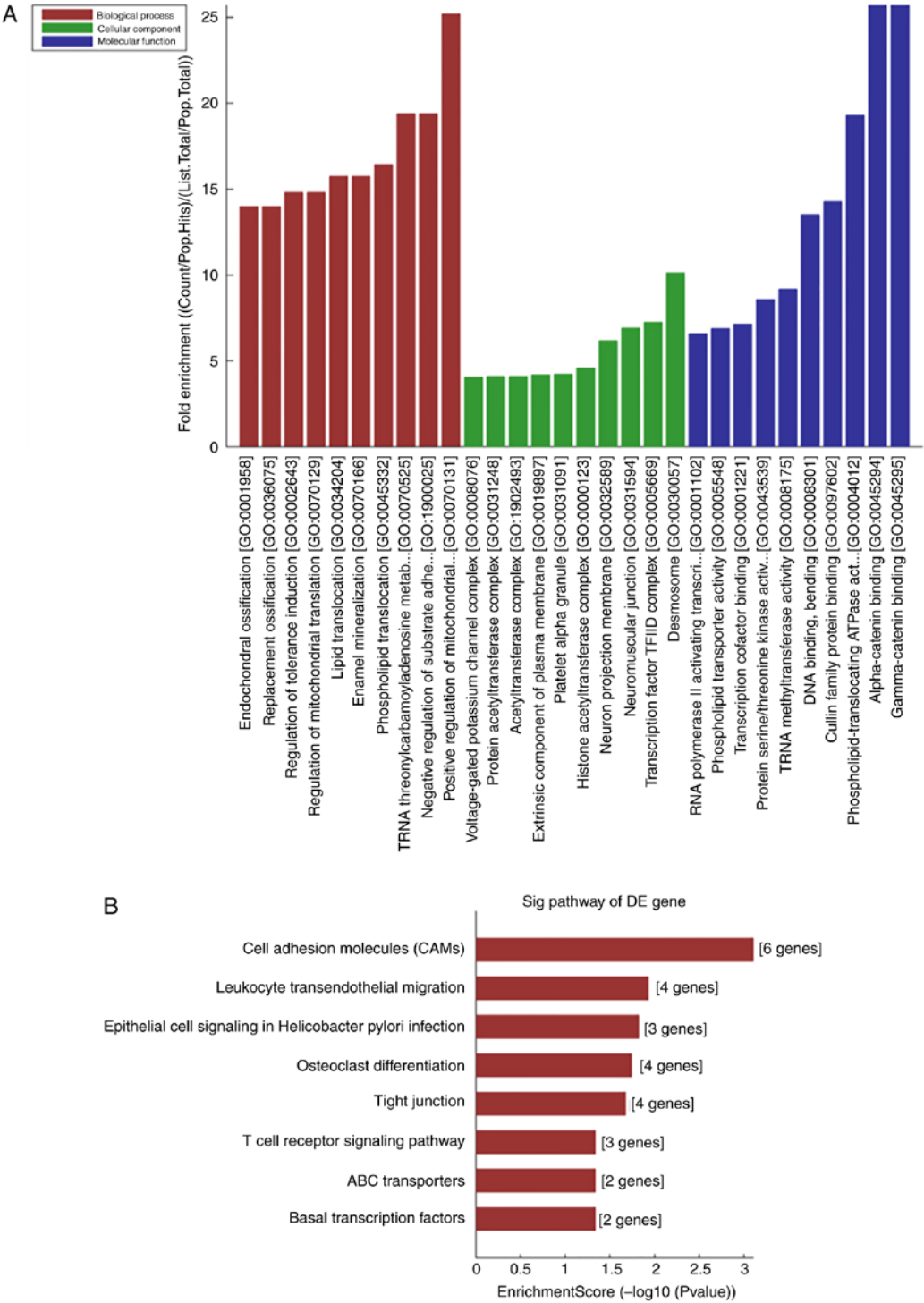


Figure S3. Top-ranked biological functions of hsa\_circRNA\_102241 in GO analysis and Pathway analysis. (A) The top 10-fold enrichment scores in GO enrichment analysis on target genes of hsa\_circRNA\_102241. (B) The top 10 enrichment scores in the Pathway analysis on target genes of hsa\_circRNA\_102241 are presented. circRNA, circular RNA; GO, Gene Ontology; BP, biological processes; CC, cellular components; MF, molecular functions.

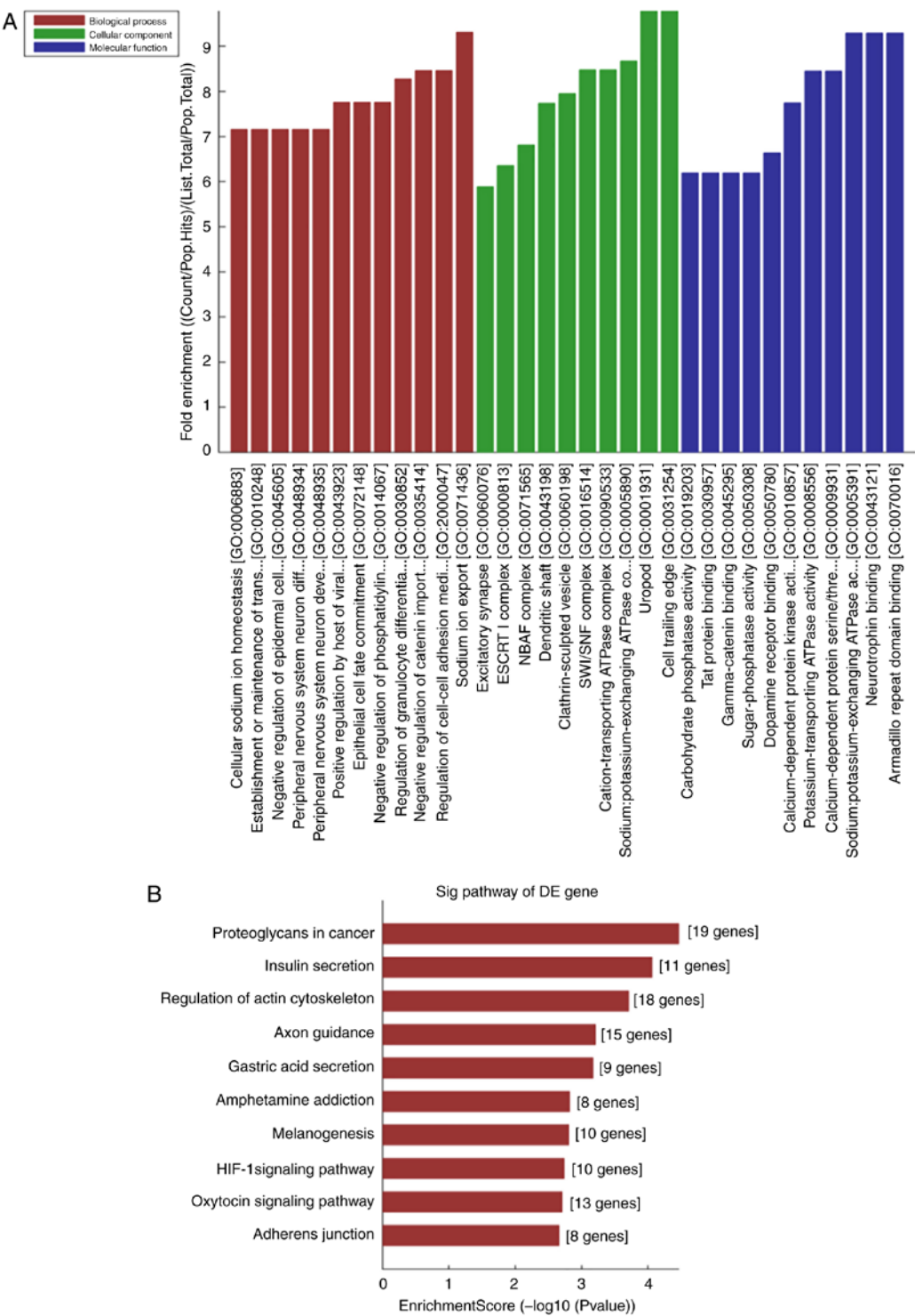


Figure S4. Top-ranked biological functions of hsa\_circRNA\_102505 in GO analysis and Pathway analysis. (A) The top 10-fold enrichment scores in GO enrichment analysis on target genes of hsa\_circRNA\_102505. (B) The top 8 enrichment scores in the Pathway analysis on target genes of hsa\_circRNA\_102505 are presented. circRNA, circular RNA; GO, Gene Ontology; BP, biological processes; CC, cellular components; MF, molecular functions.

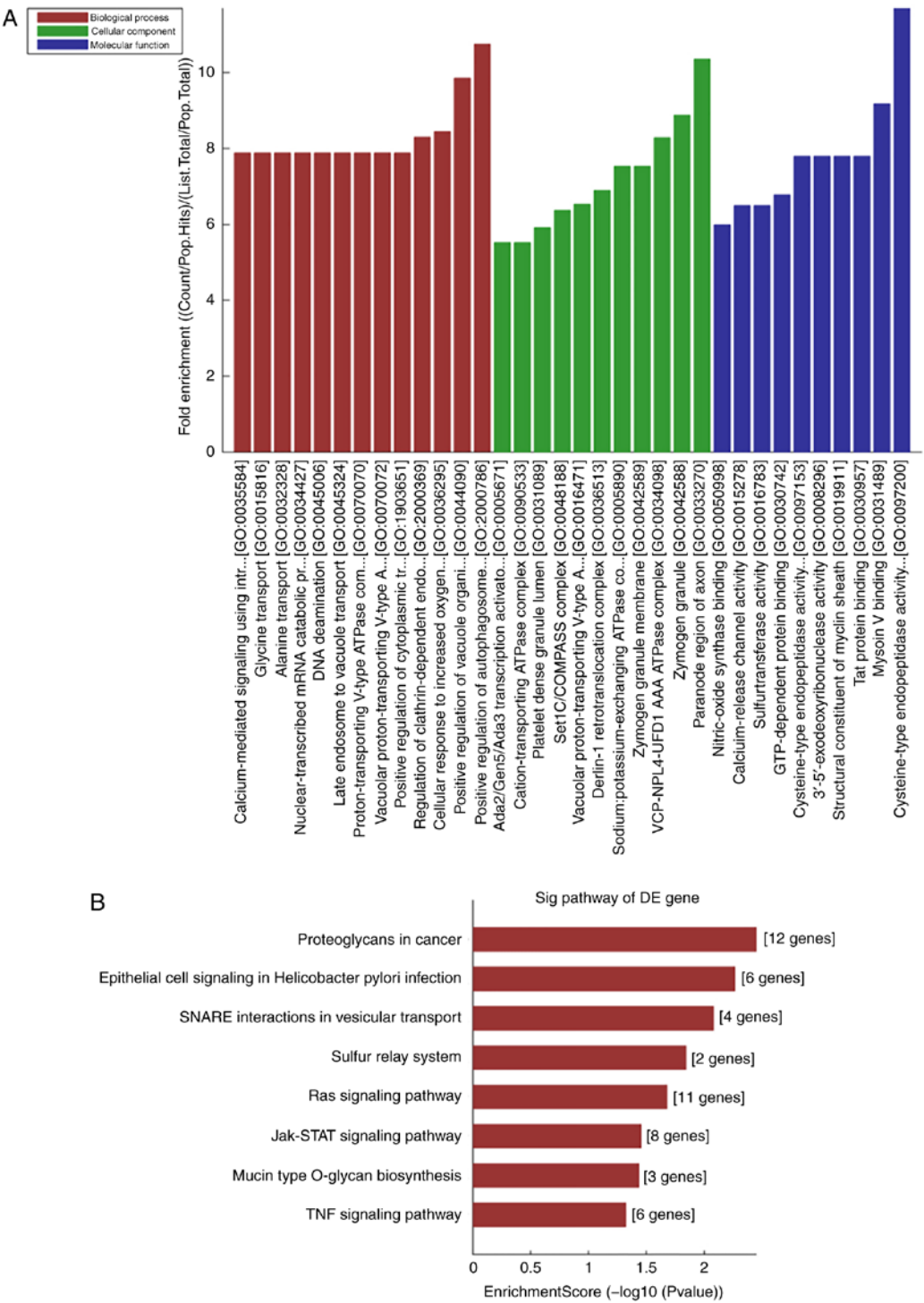


Figure S5. Top-ranked biological functions of hsa\_circRNA\_005411 in GO analysis and Pathway analysis. (A) The top 10-fold enrichment scores in GO enrichment analysis on target genes of hsa\_circRNA\_005411. (B) The top 10 enrichment scores in the Pathway analysis on target genes of hsa\_circRNA\_005411 are presented. circRNA, circular RNA; GO, Gene Ontology; BP, biological processes; CC, cellular components; MF, molecular functions.

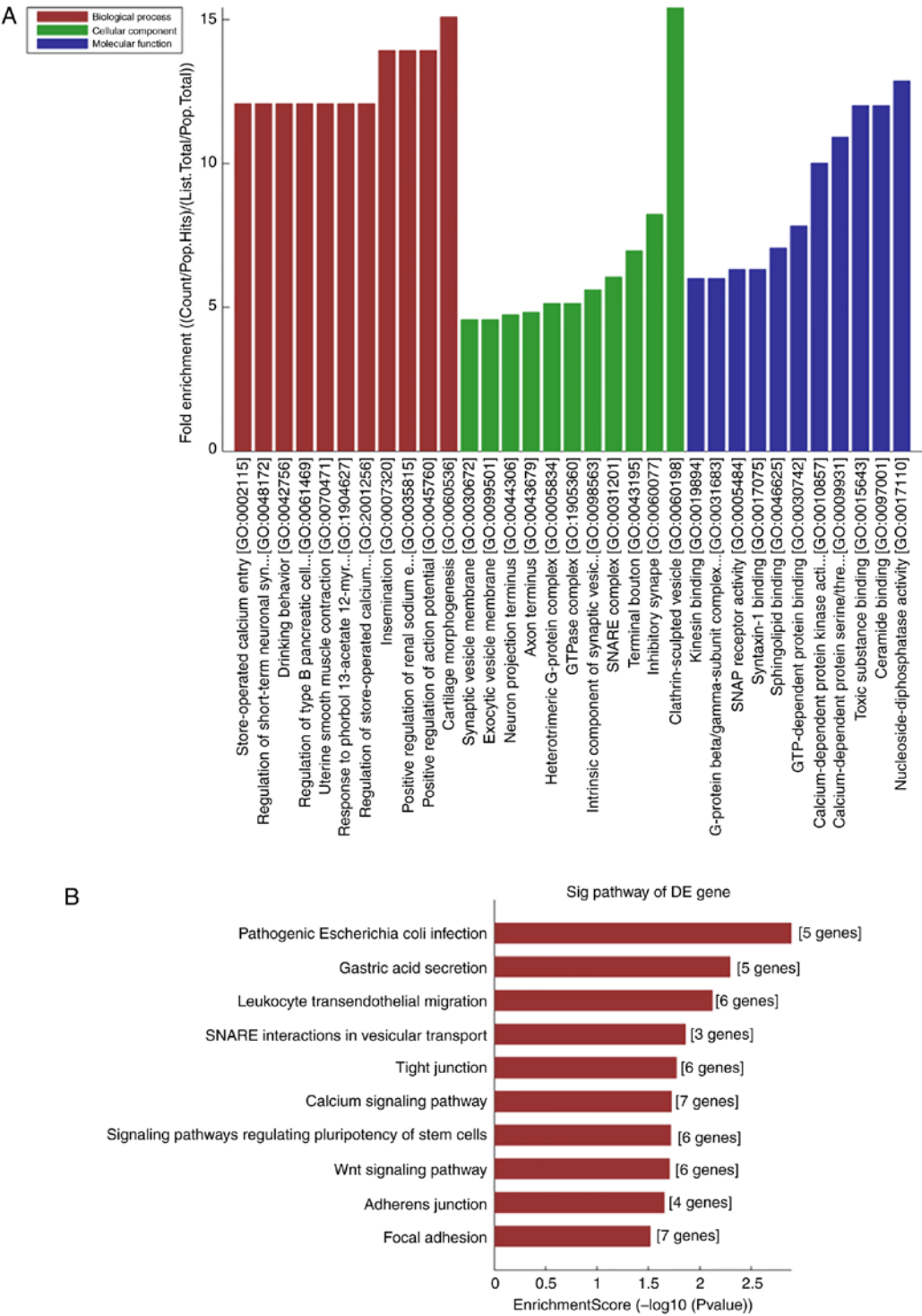


Figure S6. Top-ranked biological functions of hsa\_circRNA\_001409 in GO analysis and Pathway analysis. (A) The top 10-fold enrichment scores in GO enrichment analysis on target genes of hsa\_circRNA\_001409. (B) The top 10 enrichment scores in the Pathway analysis on target genes of hsa\_circRNA\_001409 are presented. circRNA, circular RNA; GO, Gene Ontology; BP, biological processes; CC, cellular components; MF, molecular functions.

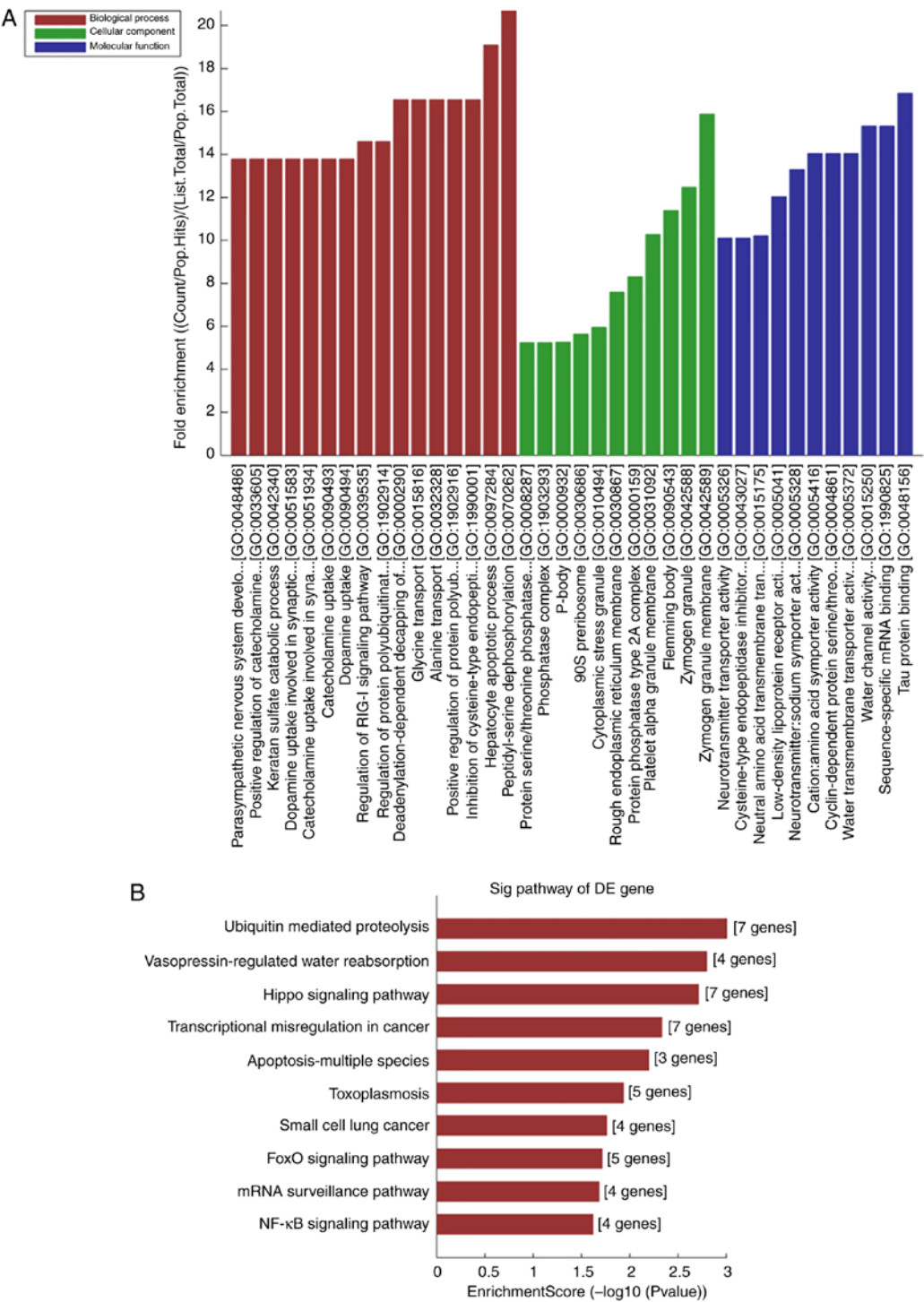


Figure S7. Top-ranked biological functions of hsa\_circRNA\_103801 in GO analysis and Pathway analysis. (A) The top 10-fold enrichment scores in GO enrichment analysis on target genes of hsa\_circRNA\_103801. (B) The top 9 enrichment scores in the Pathway analysis on target genes of hsa\_circRNA\_103801 are presented. circRNA, circular RNA; GO, Gene Ontology; BP, biological processes; CC, cellular components; MF, molecular functions.

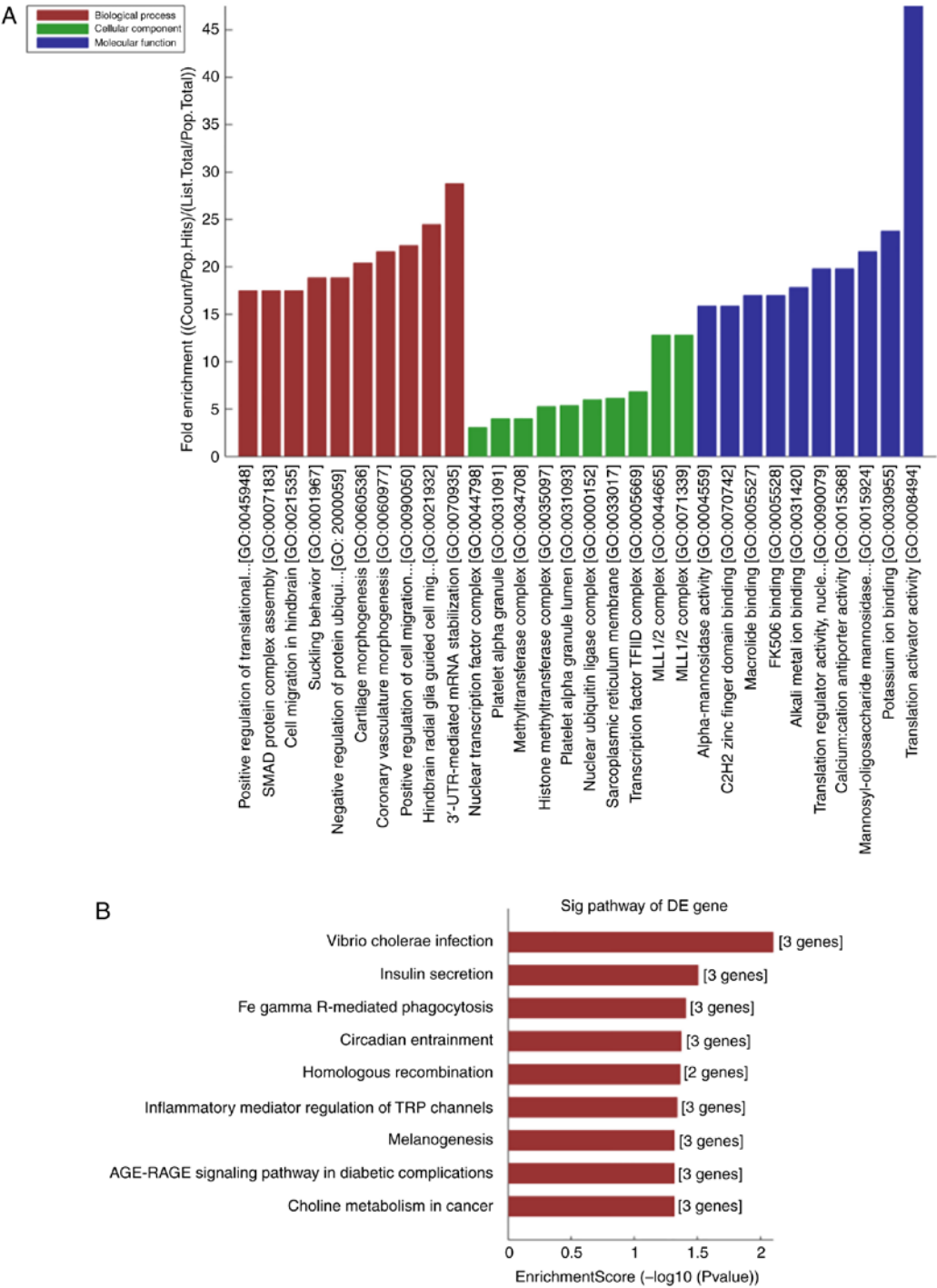


Table SI. RT-qPCR Primer sequences involved in the present study.

| Gene               | Direction | Primer sequence (5' to 3') |
|--------------------|-----------|----------------------------|
| hsa_circRNA_102241 | Forward   | ACTCACGTGGCATCAGTCC        |
|                    | Reverse   | TGGGTCTATCCTCCAGAACG       |
| hsa_circRNA_038632 | Forward   | TGAATTCGGAAGTGTCTTTCCT     |
|                    | Reverse   | CGTAGGTAGTATCGGGCCTC       |
| hsa_circRNA_102505 | Forward   | CTCTCAGATGACTTCGTCTCCC     |
|                    | Reverse   | CTGCACCACTTTTCGCAAGC       |
| hsa_circRNA_004646 | Forward   | TCAATCACAAGTTGAAGGATGCC    |
|                    | Reverse   | GATATGCAACGCCGAGTCTT       |
| hsa_circRNA_005411 | Forward   | TCTCCCACATCACTCGGAAGC      |
|                    | Reverse   | GAGTAGTTGGAGTTGTAGAGCCAG   |
| hsa_circRNA_100876 | Forward   | CTGGTGCAGTGGAAGCAGAG       |
|                    | Reverse   | CATAGCTTCATGGCCACGGT       |
| hsa_circRNA_100086 | Forward   | GGGGCATCCAAATCTTGCGG       |
|                    | Reverse   | GTTGCACAGGTCTCTAGGAAT      |
| hsa_circRNA_104600 | Forward   | TGAATTTGGAGGTTCTATCTACCAG  |
|                    | Reverse   | CCTTCAATTTCCCACTCTTCTTT    |
| hsa_circRNA_101238 | Forward   | CCAATAAAGCTGGTGCTAAAATAGGA |
|                    | Reverse   | CTTGTTTAATGACTTTGGTGCCCT   |
| hsa_circRNA_001959 | Forward   | GTCTAGTGGAGCAGGTGGAGG      |
|                    | Reverse   | AGGGCCATGACCTGGGTTA        |
| hsa_circRNA_001409 | Forward   | GCTTATAGAGGGGAGGAAGGAAC    |
|                    | Reverse   | CATCCTAGATGCTACAGACACAA    |
| hsa_circRNA_103801 | Forward   | TCTGACAGCCCTGATAGGCA       |
|                    | Reverse   | CATTGCCTTTGATCCTGCTGT      |
| hsa_circRNA_101969 | Forward   | GGCTATGCTCATGGCCTTGCTT     |
|                    | Reverse   | AATCGGTGAGCCACGCCAG        |
| hsa_circRNA_100239 | Forward   | TGCGATGCACTCCGATTGTC       |
|                    | Reverse   | ATCAAGCTCAGGCAACACGG       |
| hsa_circRNA_005525 | Forward   | GTCATTAGGCTGAGAATCCTCGTC   |
|                    | Reverse   | GTTGAACCAGAACAAAACCGAGTC   |
| miR-136-5p         | Forward   | CGGCGACTCCATTTGTTTTGA      |
|                    | Reverse   | AGTGCAGGGTCCGAGGTATT       |
| CBX4               | Forward   | CTGCTGATCGCCTTCCAGAAC      |
|                    | Reverse   | GTTGAGCTCGTACTGATGCC       |
| GAPDH              | Forward   | ACCGTCAAGGCTGAGAACG        |
|                    | Reverse   | TGGACTCCACGACGTACTCA       |

Table SII. Biological information regarding the top 10 up- and downregulated circRNAs by FC in bladder cancer.

| circRNA            | P-value     | FC (abs)   | Regulation | Chrom | Strand | circRNA_type      | GeneSymbol  |
|--------------------|-------------|------------|------------|-------|--------|-------------------|-------------|
| hsa_circRNA_405712 | 0.046366277 | 11.1919871 | Up         | chr19 | +      | Intronic          | SCAMP4      |
| hsa_circRNA_100876 | 0.022992081 | 10.0135796 | Up         | chr11 | +      | Exonic            | RNF121      |
| hsa_circRNA_405510 | 0.042050053 | 9.3199298  | Up         | chr16 | -      | Intronic          | ANKRD11     |
| hsa_circRNA_100961 | 0.035046705 | 8.2537114  | Up         | chr11 | -      | Exonic            | IFT46       |
| hsa_circRNA_038632 | 0.040370215 | 7.8333318  | Up         | chr16 | +      | Exonic            | PLK1        |
| hsa_circRNA_405011 | 0.048662457 | 7.2636926  | Up         | chr12 | +      | Intronic          | DGKA        |
| hsa_circRNA_103387 | 0.034019192 | 6.8639659  | Up         | chr3  | +      | Exonic            | RAD54L2     |
| hsa_circRNA_405498 | 0.03105109  | 6.0163836  | Up         | chr16 | -      | Exonic            | GCSH        |
| hsa_circRNA_100086 | 0.034909498 | 5.8135881  | Up         | chr1  | -      | Exonic            | EIF4G3      |
| hsa_circRNA_403293 | 0.036044855 | 5.7439099  | Up         | chr5  | +      | Exonic            | ADCY2       |
| hsa_circRNA_016346 | 0.043992725 | 33.227721  | Down       | chr1  | -      | Exonic            | KCNH1       |
| hsa_circRNA_104757 | 0.043189164 | 26.6389901 | Down       | chr9  | -      | Exonic            | UBAP2       |
| hsa_circRNA_101213 | 0.030464898 | 26.0553487 | Down       | chr12 | +      | Exonic            | RAN         |
| hsa_circRNA_001490 | 0.047442099 | 24.9018517 | Down       | chr5  | +      | Exonic            | KIF2A       |
| hsa_circRNA_401351 | 0.041172526 | 24.5109068 | Down       | chr15 | +      | Exonic            | SNURF-SNRPN |
| hsa_circRNA_005008 | 0.031761901 | 24.0059739 | Down       | chr16 | +      | Sense overlapping | HNRNPA1P48  |
| hsa_circRNA_400033 | 0.025258724 | 23.8716865 | Down       | chr17 | +      | Intronic          | RPL23A      |
| hsa_circRNA_400027 | 0.041326909 | 23.331575  | Down       | chr15 | +      | Intronic          | SNURF-SNRPN |
| hsa_circRNA_006169 | 0.032813901 | 23.0502563 | Down       | chr3  | +      | Sense overlapping | HNRNPA3P6   |
| hsa_circRNA_034642 | 0.047638973 | 22.7691016 | Down       | chr15 | +      | Exonic            | VPS18       |