



Figure S2. Probable target mRNAs of hsa\_circ\_0009910 and the Gene Ontology biological process. Pathway enrichment analysis of the 135 mRNAs regulated in the ceRNA network was performed. FDR <0.05 was considered to indicate statistically significant difference. circ, circular; ceRNA, competing endogenous RNA; FDR, false discovery rate.

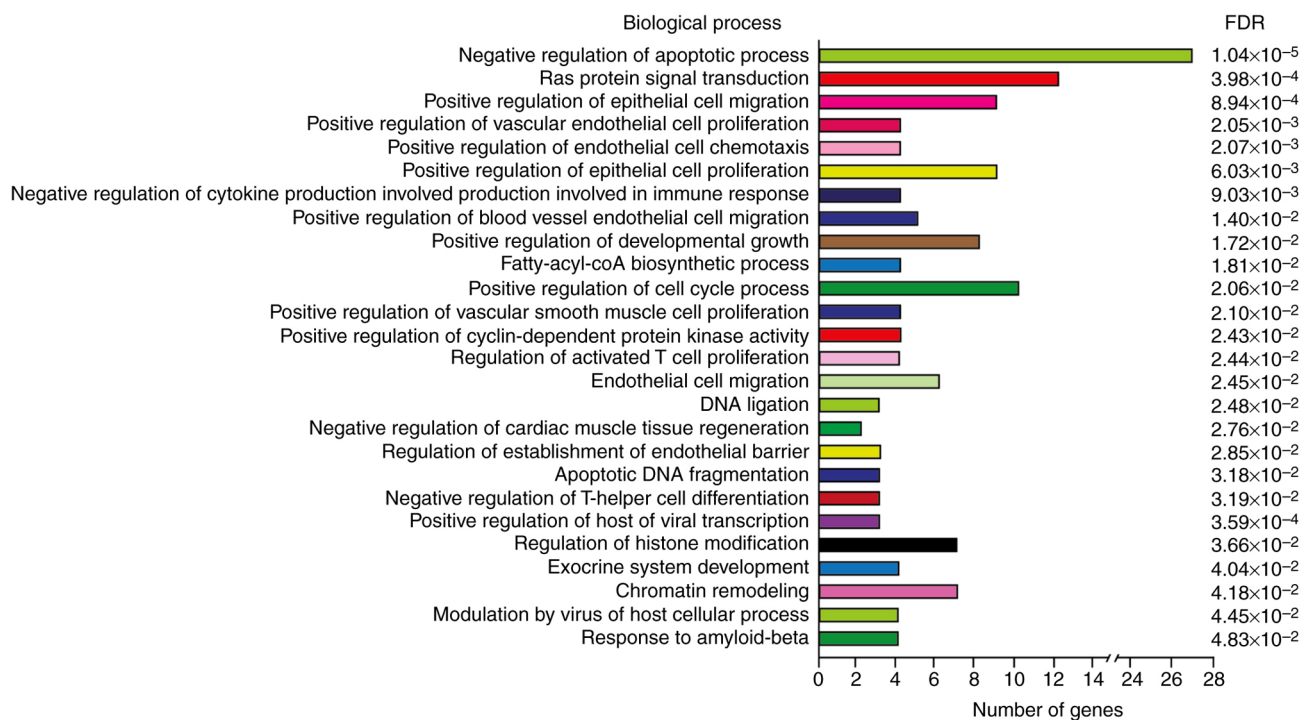


Figure S3. Expression profiles of miR-198. Expression levels of miR-198 in various non-tumor cell types. Cervical tissue had the third highest expression levels of miR-198 (indicated with a red arrow). Data were obtained from miRTarBase. miR, microRNA.

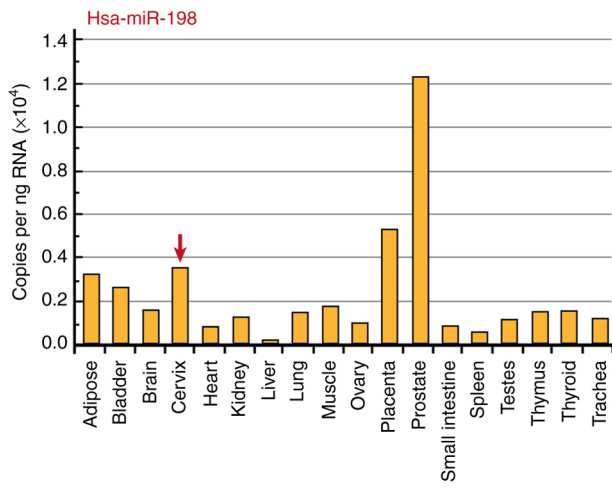


Figure S4. Expression of c-Met in cervical cancer. c-Met is encoded from the MET gene. (A) Heat map showing the expression of NTRK3, NNAT, BIRC7, CCNT1, FGFR1, JAK3, CCND2, ARHGAP1, MYB, PBX1, MET and FSTL1 in six tumor tissues and in six normal cervical epithelium tissues. (B) Comparison of MET expression in CESC tissues compared with normal tissues using data retrieved from The Cancer Genome Atlas. The data are presented as the mean  $\pm$  standard deviation. \* $P < 0.05$ . CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; TPM, transcripts per million.

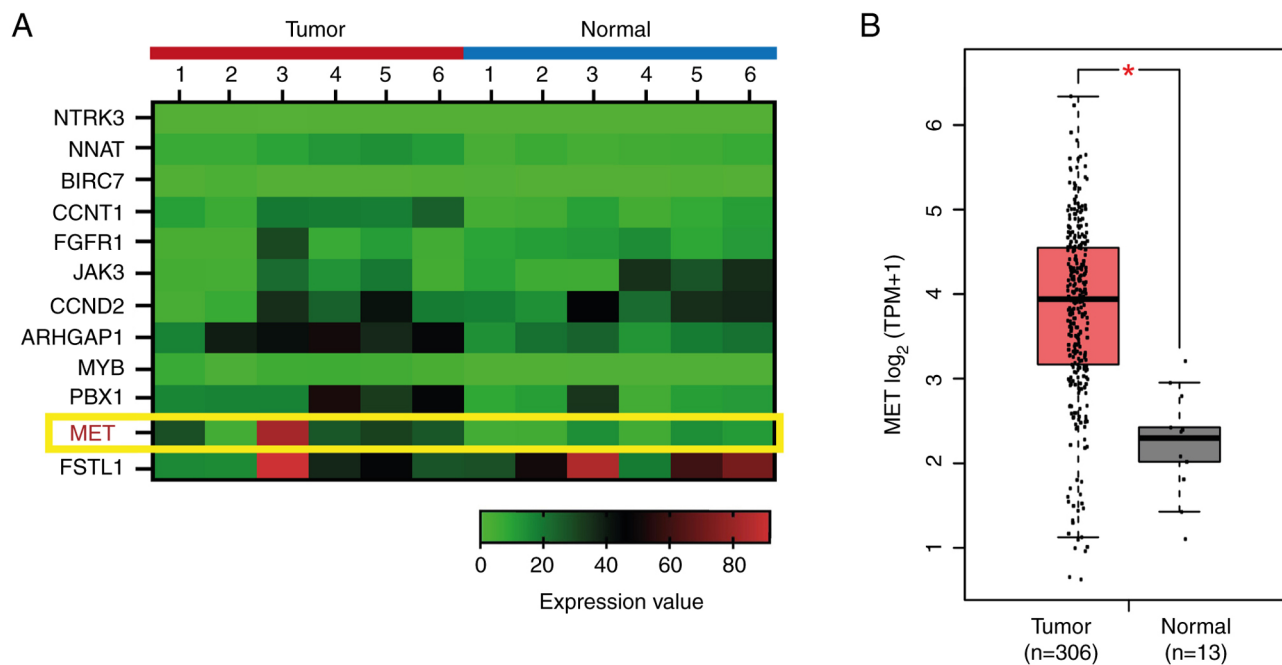


Figure S5. Knockdown of hsa\_circ\_0009910 does not affect HPV-18 E6 and E7 mRNA expression levels. Expression levels of (A) HPV-18 E6 and (B) E7 in HeLa si-circ9910 and HeLa si-NC groups. All data presented are from at least three independent experiments and are expressed as the mean  $\pm$  standard deviation. circ, circular; HPV, human papilloma virus; si-circ9910, small interfering RNA against hsa\_circ\_0009910; NC, negative control.

