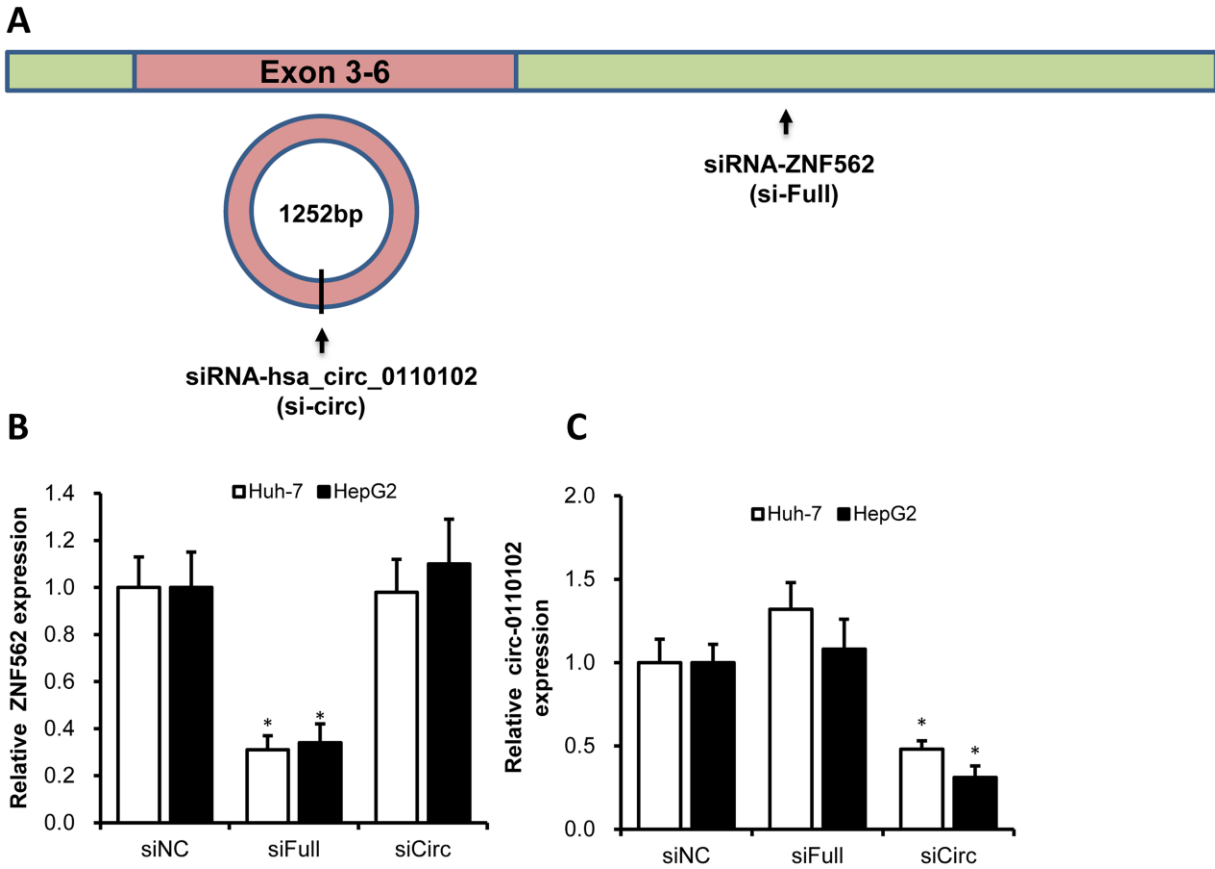


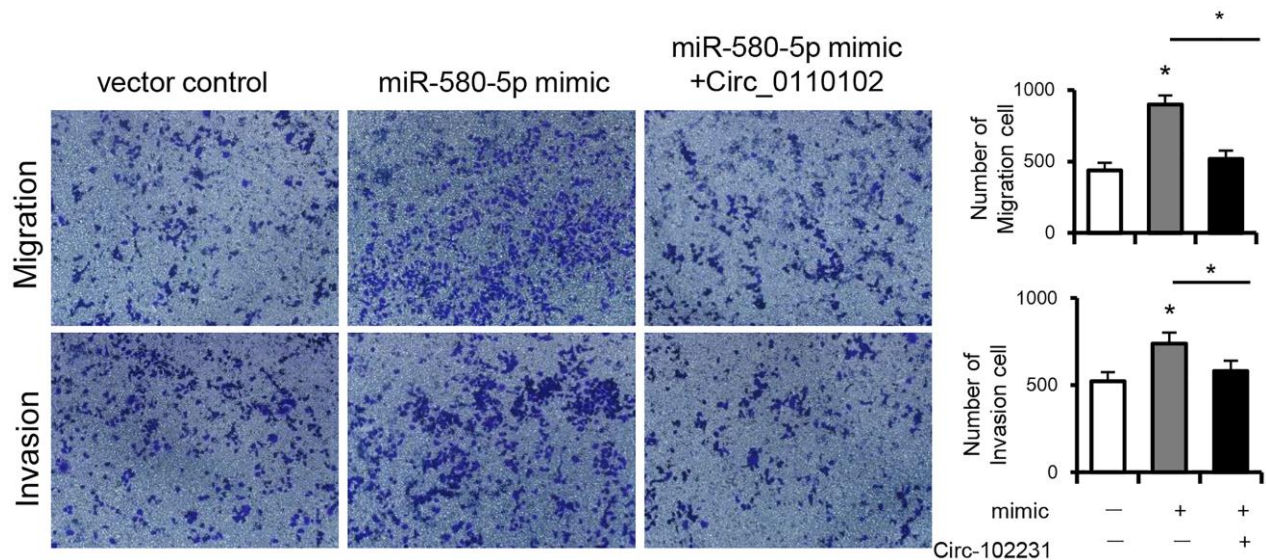
SUPPLEMENTARY FIGURES



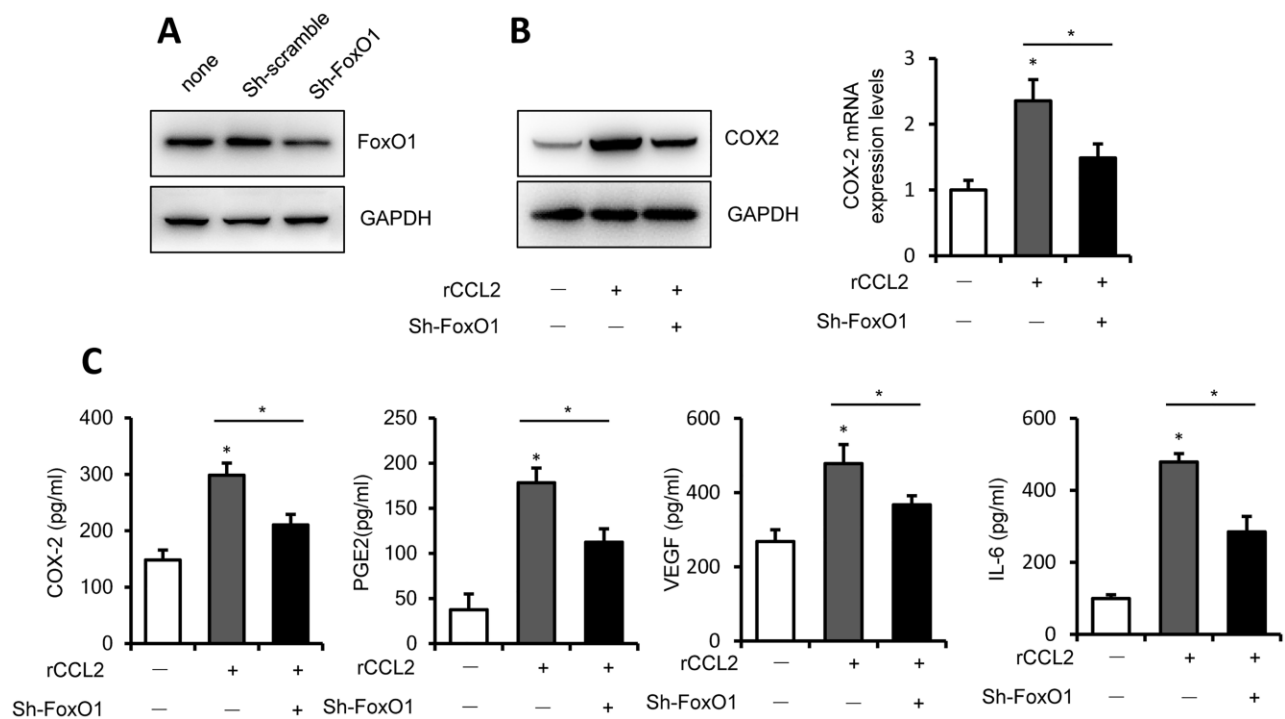
Supplementary Figure 1. hsa_circ_0110102-specific siRNA down-regulated the expression levels of hsa_circ_0110102 but not ZNF562. (A) Schematic model of the siRNAs. siFull (siRNA of ZNF562) targets the ZNF562 linear transcript, siCirc (siRNA of hsa_circ_0110102) targets the back-splice junction of hsa_circ_0110102. (B–C) Real-time PCR analysis of ZNF562 and circ-0110102 expression in HCC tumor cell lines Huh-7 and HepG2 with siFull or siCirc transfection. Data are shown as mean ± S.E., $n = 3$, * $P < 0.05$.

TargetScan miRNA predictions					
CircRNA Mirbase ID	CircRNA (Top) – miRNA (Bottom) pairing	Site Type	CircRNA Start	CircRNA End	context+ score percentile
hsa_circ_0110102 (5' ... 3') hsa-miR-338-3p (3' ... 5')	CUCUACAGAGAUGUGAUGCUGGA GUUGUUUUAGUGACUACGACCU	8mer-1a	183	190	97
hsa_circ_0110102 (5' ... 3') hsa-miR-766 (3' ... 5')	CUACAGAGAUGUGAUGCUGGAGA CGACUCCGACACCCCGACCUCA	8mer-1a	185	192	99
hsa_circ_0110102 (5' ... 3') hsa-miR-659 (3' ... 5')	GGGAAAUACAACCUAGAACCAA ACCCUGGGAGGGACUUGGUUC	8mer-1a	259	266	98
hsa_circ_0110102 (5' ... 3') hsa-miR-580-5p (3' ... 5')	GCUGUGCAUCUUGAAAUCUCAA GGAAUACUAAGUAGUAAGAGUU	8mer-1a	564	571	96
hsa_circ_0110102 (5' ... 3') hsa-miR-595 (3' ... 5')	CCAUCACAACUCCUCACACUUA UCUGUGGGUGCC-GUGUGAAG	8mer-1a	709	716	98
hsa_circ_0110102 (5' ... 3') hsa-miR-188-3p (3' ... 5')	UAUGAAUGUGUGAUGUGGGAA ACGUUUGGGACGUACACCCUC	8mer-1a	1188	1195	99
hsa_circ_0110102 (5' ... 3') hsa-miR-607 (3' ... 5')	CCCAUCGUAGUAAACAUUUGAAA CAAUAUCUAGACCUAAACUUG	8mer-1a	1228	1235	98

Supplementary Figure 2. A schematic model showing the putative binding sites for seven miRNAs and hsa_circ_0110102.



Supplementary Figure 3. The overexpression of miR-580-5p increased the migration and invasion of Huh-7 cells, and hsa_circ_0110102 significantly inhibited the effect of miR-580-5p.



Supplementary Figure 4. FoxO1 knockdown decreased the rCCL2 induced secretion of cytokines. (A) sh-scramble or sh-FoxO1 were transfected into THP-1 cells for 48 h, then cells were harvested for Western blot assay. THP-1 cells were transfected with sh-FoxO1 for 24 h, and then treated with 50 ng/ml rCCL2 for another 24 h. (B) The COX-2 protein and mRNA levels were detected with western blot and RT-qPCR. (C) The contents of COX-2, PGE2, VEGF and IL-6 in the medium were measured using ELISA. Data are shown as mean \pm S.E., n = 3, *P < 0.05.