	Orientation	Sequence (5' to 3')
ANGPT2	Forward	GTGATTGATTCGGATACTGAC
	Reverse	CTGGACCTGATATTGCTTCT
miR-145	reverse	GTCGTATCCAGTGCAGGGTCCGAGGTATT
	transcription	CGCACTGGATACGACAGGGAT
	Forward	GCGGCGGGTCCAGTTTTCCCAG
	Reverse	ATCCAGTGCAGGGTCCGAGG
LINC00184	Forward	TGAGAAGCAAGGAAGAGAC
	Reverse	GTAGATGACGGCACAGTT
U6	Forward	GCTTCGGCAGCACATATACTAA
	Reverse	AACGCTTCACGAATTTGCGT
si-ANGPT2-1	SS Sequence	GAAAGACAACAACAAGUUUCU
	AS Sequence	AAACUUGUUGUUGUCUUUCGA
si-ANGPT2-2	SS Sequence	GGAUGGAGACAACGACAAAUG
	AS Sequence	AAACUUGCACAUAACAUUCUU
si-LINC00184-1	SS Sequence	GCUUAAUGCAGUUAAGUAACA
	AS Sequence	UUACUUAACUGCAUUAAGCUG
si-LINC00184-2	SS Sequence	GACAAGUGUUGAAGGUGAAAG
	AS Sequence	UUCACCUUCAACACUUGUCUU

Supplement Table 1. The sequence information of the biomarkers

# Supplement Figure 1 Differentially expressed RNAs in GC

A-C Heatmaps of top 50 DELs, DEMis and DEMs, identified by edgeR.

D-F. Volcano plots of the expression levels of differentially expressed DELs, DEMis and DEMs, identified by edgeR.

G-I. PCA of DELs, DEMis and DEMs, by edgeR.

J. The down-regulated DELs determined by limma and edgeR.

K. The up-regulated DEMis determined by limma and edgeR.

L. The down-regulated DEMs determined by limma and edgeR.

### Supplement Figure 2 GO analysis

A-E: The top 5 biological processes (BP).

F-J: The top 5 molecular functions (MF).

K-O: The top 5 cellular components (CC).

**Supplement Figure 3** *The top 10 KEGG pathways.* 

A. cell cycle; B. DNA replication; C. homologous recombination; D. mismatch repair;

E. nucleotide excision repair; F. base excision repair; G. RNA degradation; H. one

carbon pool by folate; I. ECM receptor interaction; J. spliceosome.Supplement

# Figure 4

A. The soft-thresholding power used to construct scale-free network.

B. Visualization of hierarchical clustering dendrogram of the eigengenes (up).Heatmap of the eigengene adjacency (down).

# **Supplement Figure 5**

A, B. RT-PCR showed ANGPT2 knockdown in comparison to scrambled control in GC cells.

C, D. PCGEM1 in the cellular portions of SGC-7901s and BGC-823s.

E, F. RT-PCR showed the efficiency of LINC00184 knockdown in comparison to scrambled control in GC cells.

















В



Soft Threshold (power)

Soft Threshold (power)





С

F



BGC-823

ঙ

cytoplasm

Е



D

1.0

0.5-

0.0

LINCOO184

nucleus

Bractin

Distribution