

Supplementary Figure legends

Figure S1. The distribution of microRNAs with target genes in Chr.20

The microRNAs with target genes located at Chr.20 were mapped to the chromosomes. The ratios of microRNAs in each chromosome vs the total microRNAs in database was treated as the matrix (blue bar), and the ratios of microRNAs with target genes in Chr.20 vs the total microRNAs with target genes in Chr.20 (red bar) were compared to the matrix. It was indicated that the microRNAs with target genes in Chr.20 are enriched in chr.7, 8, 10, 12, 14, 15 and X.

Figure S2. The abundant ranks of the identified Chr.20 proteins

The identified proteins are ranked according to their iBAQ values. The green dots represent the conserved proteins and the black dots represent the left Chr.20 proteins identified.

Figure S3. The correlation analysis of gene expression abundances with the chromosomal positions in Chr.20 in gastric samples and liver samples

The normalized abundance of the identified proteins and mRNAs in gastric samples and liver samples are logarithmically treated and the log₂ values are plotted against the correspondent genes in Chr.20. The rugs of black mean the gene distribution in Chr.20, while of red and blue represent the log₂ abundances of the identified proteins and mRNAs abundances, respectively. A, gastric samples, in which Up is adjacent normal tissue of gastric cancer, Middle, gastric cancer tissue, and Bottom is gastric

cancer cell lines. B, liver samples, in which Up is normal tissues of liver and Bottom is liver cell lines.

Supplementary Tables

Table S1. The identified Chr.20 target genes of transcriptional regulators

Table S2. The identified Chr.20 target genes of microRNA

Table S3. The identified cancer-related genes in Chr.20

Table S4. The percentage of proteins or mRNAs in each Chr.20 region with expression abundances above the median