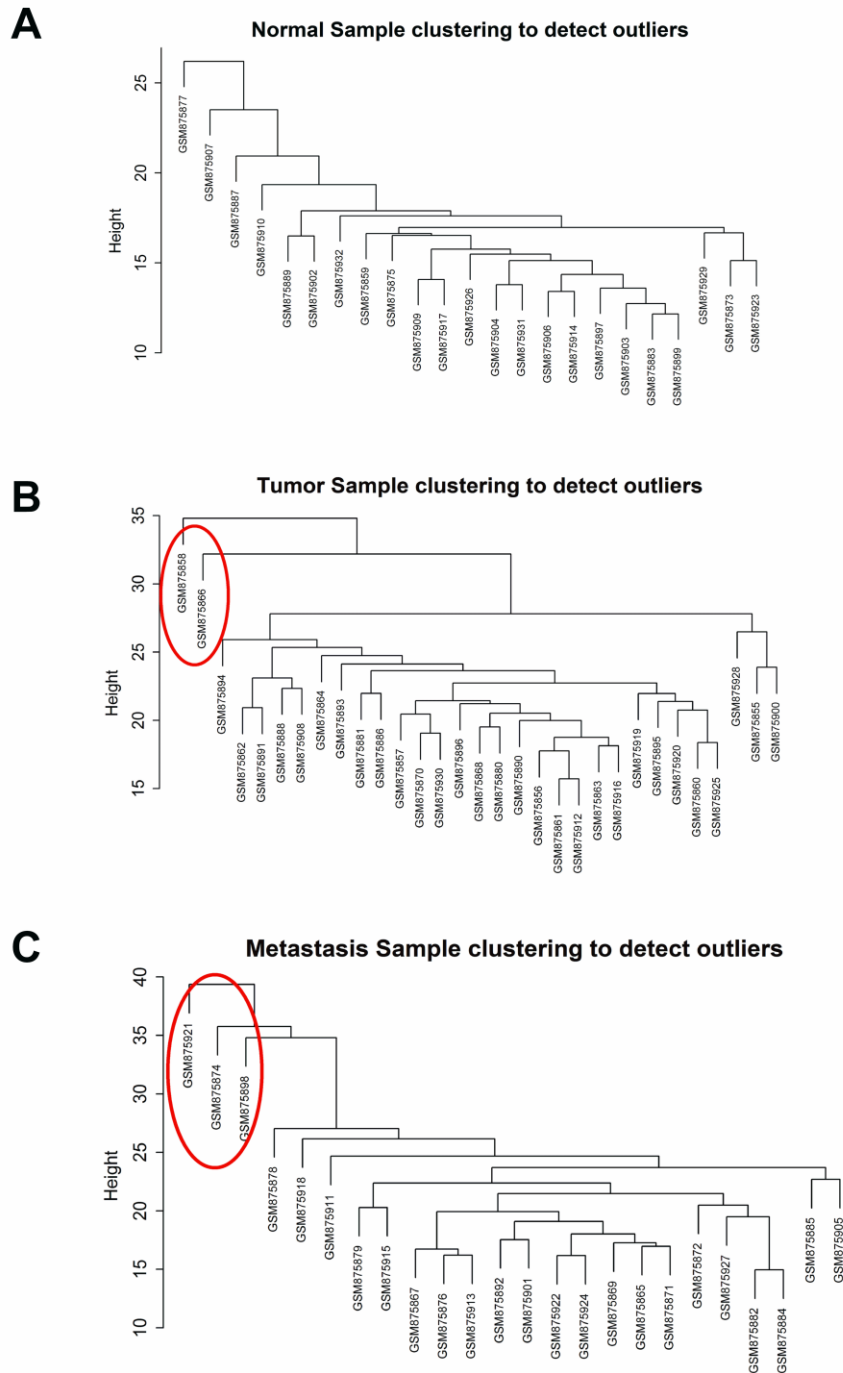


# Figure S1

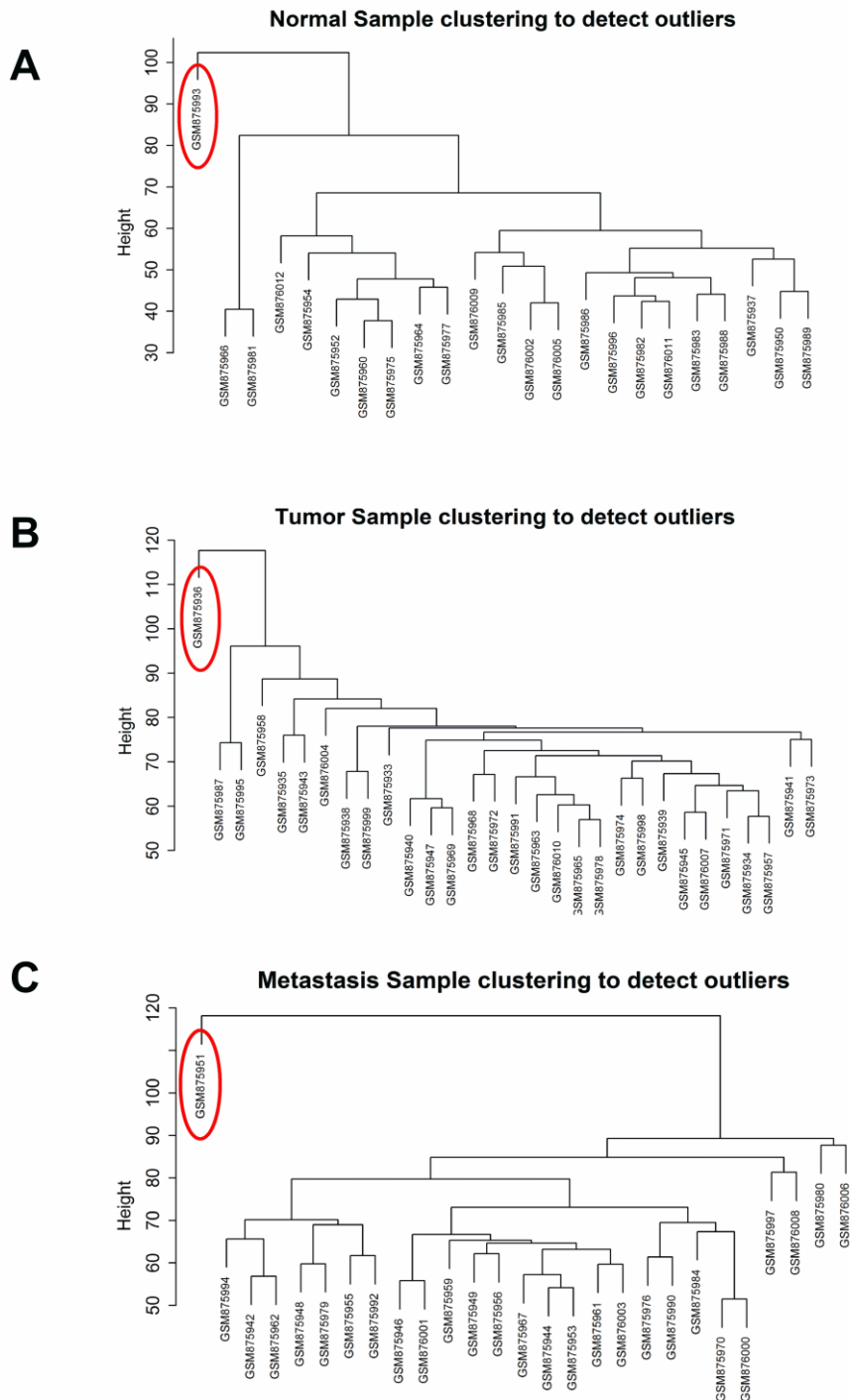


**Supplementary Figure 1: Clustering dendrogram of samples for miRNA expression**

**profiles.** A, B, C are the clustering diagrams for Normal samples, Tumor samples, and

Metastasis samples of miRNA dataset, respectively. Outliers shown in B and C were removed for the following analysis.

# Figure S2

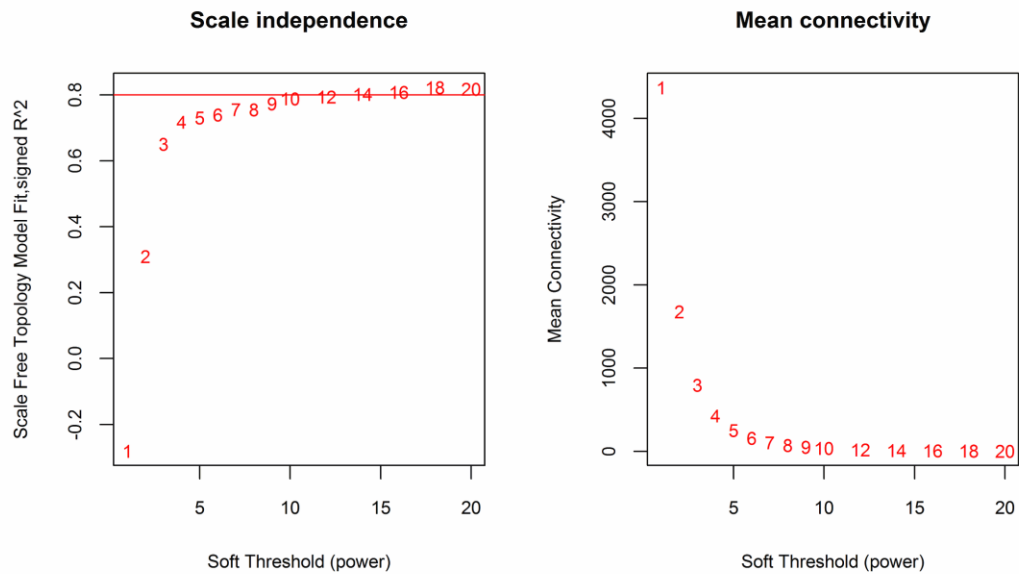


**Supplementary Figure 2: Clustering dendrogram of samples for mRNA expression**

**profiles.** A, B, C are the clustering diagrams for Normal samples, Tumor samples, and

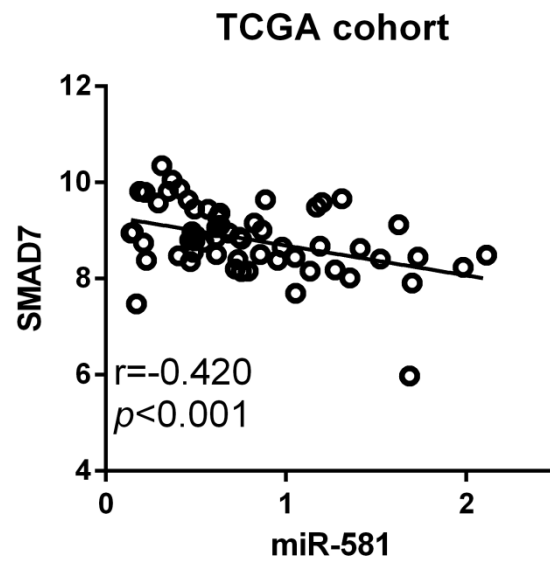
Metastasis samples of mRNA dataset, respectively. Outliers shown in A, B, and C were removed for the following analysis.

**Figure S3**



**Supplementary Figure 3: Identification of soft thresholding power for network construction.** The left panel shows the scale-free fit index for various soft-thresholding powers ( $\beta$ ) whereas the right panel displays the mean connectivity for various soft-thresholding powers.

## Figure S4



Supplementary Figure 4: miR-581 negatively correlated with SMAD7 in CRC patients with metastasis