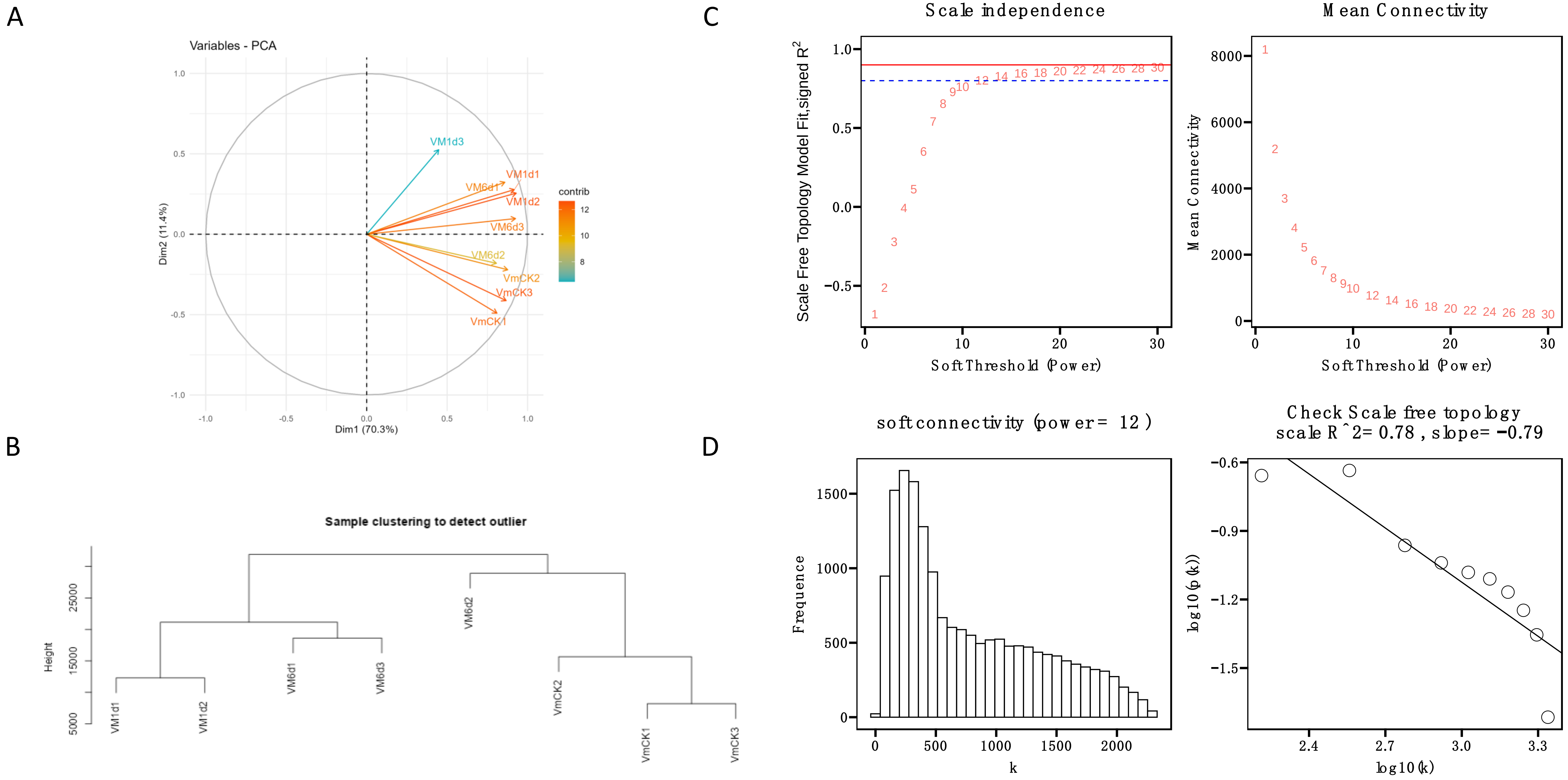

Figure S3. Detailed information on PCA and WGCNA analyses of 9 Vm RNA-seq samples.

(A) Principal Component Analysis (PCA) results of all 9 RNA-seq samples from Vm. (B) Sample clustering to detect outliers. Eight samples are within the clusters and meet the cutoff thresholds. (C) Soft-thresholding power analysis to obtain the scale-free fit index of network topology. (D) Scale-free topology when the soft-thresholding power β = 12.