

Figure S1 The annotation of the turquoise and brown module co-expression networks in the KEGG Pathway.

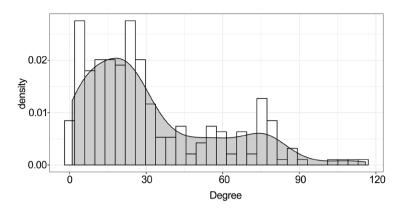


Figure S2 The degree distribution of the sub-network.

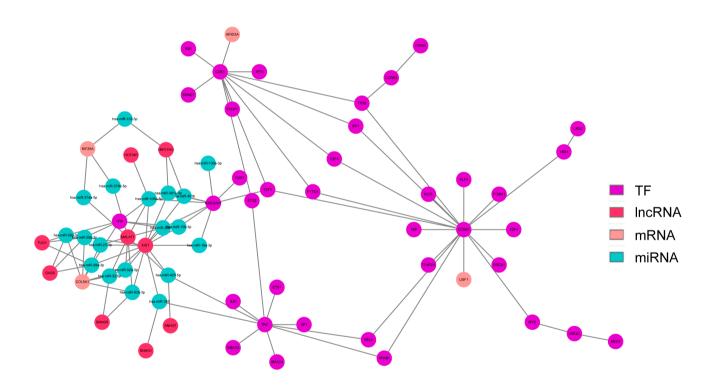


Figure S3 The multi-factor regulatory network of the miRNAs, lncRNAs, and transcription factors. The miRNAs and transcription factors that interacted with co-expressing key genes (N=10) were selected and the lncRNAs that interacted with these miRNAs were screened out.

Importance of Candidates

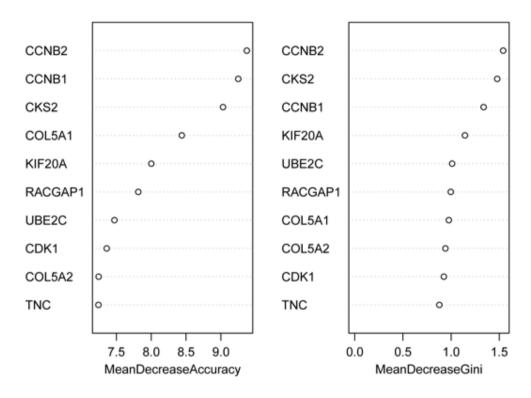


Figure S4 The significance of these 10 genes for different subtypes of SCI based on the random forest model.