Figure S1. (A) K8: Inflamed tissue sample was obtained from inflamed skin tissue following the acute stage of a keloid patient with an inflamed lesion (green arrow). The green circle is group I. The red circle is group N. The blue circle is group K. (B-I) K7, K9, K14, K36, K1, K2, K3, and K4 samples of patients.
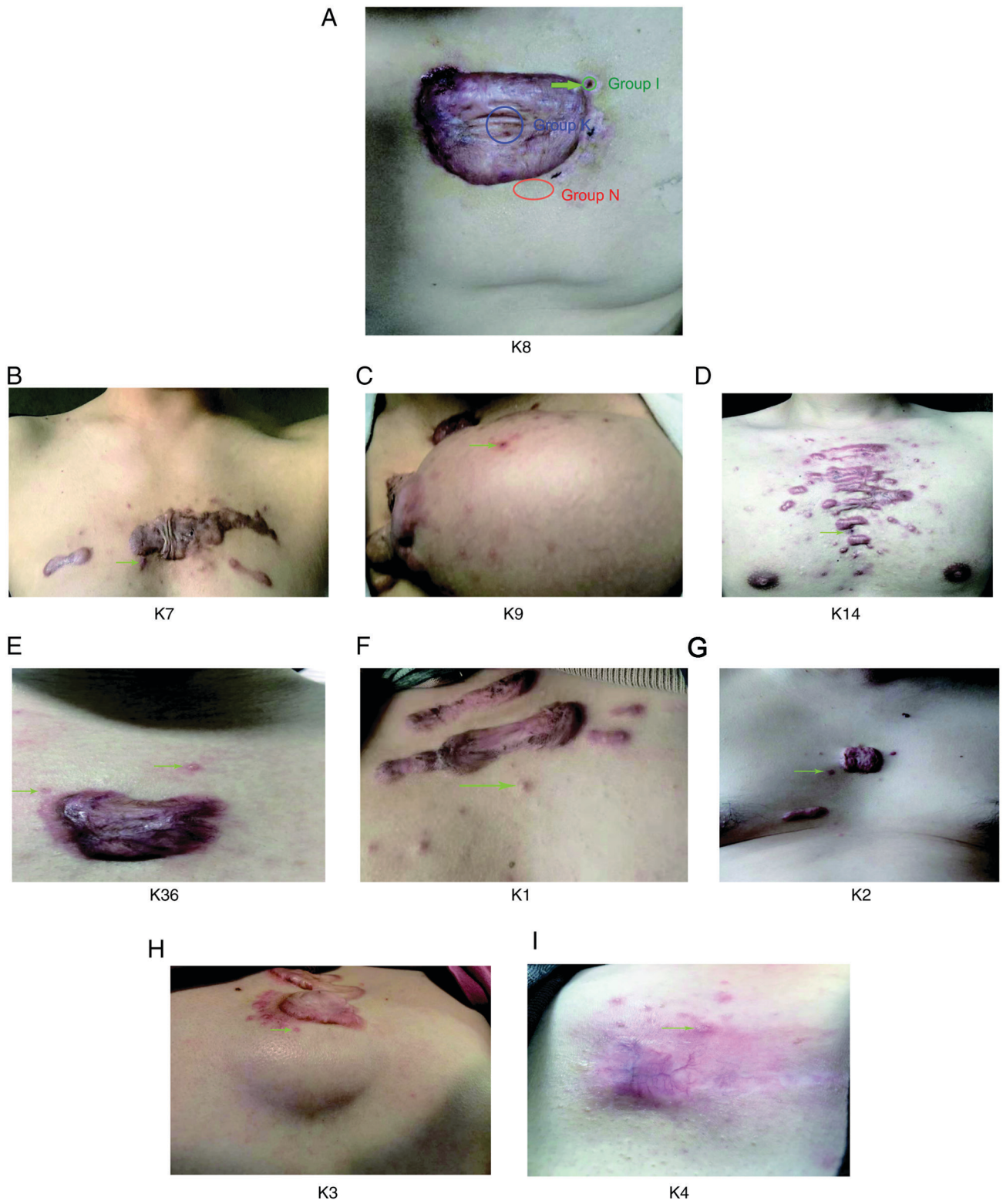
Figure S2. MCODE uses a vertex-weighting-based scheme to reveal local high-density areas in the graph. (A) MCODE was performed for groups I and N. Protein complexes are represented as graphs, using the spoke model. Vertices represent proteins and edges represent experimentally determined interactions. (B) MCODE was performed for groups I and K. (C) MCODE was performed for groups N and K.
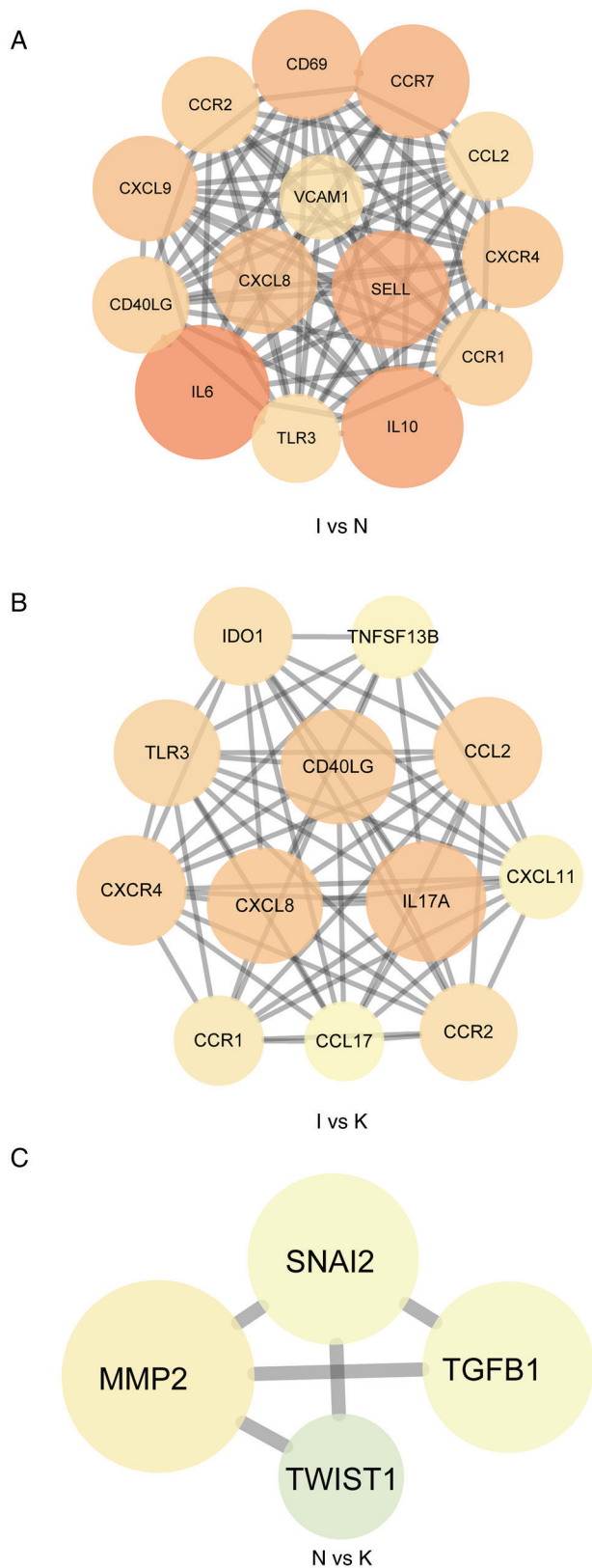

A

I vs N

B

I vs K

C

N vs K

Figure S3. (A) GO enrichment analyses of biological processes of DEGs between groups N and K. (B) GO enrichment analyses of cellular components of DEGs between groups N and K. The cutoff for log2 fold change >1.5 or <-0.5 and P<0.05 were used as screening criteria. DEGs, differentially expressed genes; GO, Gene Ontology; BP, biological processes; CC, cellular components.