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Fig. S2. Network analysis (Ingenuity Pathway Analysis) performed on robust keloid top gene signature. 456 unique genes that showed a significant (> 2-fold, $p < 0.01$) change in the keloid biopsy gene lists. Gene symbols were loaded into IPA and the build function was used to connect the genes (direct and indirect interactions). A network of 175 genes formed from the 456 genes loaded. The figure shows a pruned version of that network (genes not connected to TGFβ1, NR3C1, IFNγ or RELA have been removed). 4 central nodes appear in the network surrounding TGFβ1, NR3C1, IFNγ and RELA.