Fig. S1. Network analysis (Ingenuity Pathway Analysis) performed on robust keloid centre gene signature. 440 unique genes that showed a significant (>1.2-fold, $p < 0.05$) change in both keloid biopsy and keloid fibroblast centre 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 218 genes formed from the 440 genes loaded. The figure shows a pruned version of that network (genes not connected to TGFβ1, ITGB1 or EGFR have been removed). 3 central nodes appear in the network surrounding TGFβ1, ITGB1 and EGFR.