

Table 1: Genes that distinguish BCC- vs. normal-derived stromal cells. Global gene expression patterns of 5 BCC-stromal cultures and 5 non-tumor skin stromal cultures were characterized by DNA microarrays. Significance Analysis of Microarrays (SAM) (41) was then used to identify a set of genes whose expression levels were significantly different between tumor- and non-tumor-derived stromal cells at a false discovery rate of 5 %. The clone identifier, gene name, and SAM score are listed.

Fig. 6: *GREMLIN 1* RNA is expressed in BCC tumor stroma. Each panel shows a representative image of ISH for *GREMLIN 1* in paraffin embedded BCC tumors from a different patient. *GREMLIN 1* is represented by punctate purple dots, and nuclei are counterstained with methyl green. Tumors positive (A through J) and negative (K,L) for *GREMLIN 1*.

Fig. 7: *GREMLIN 1* RNA expression in human pancreatic tissue. ISH was performed on tissue microarrays of paraffin-embedded samples of pancreatic tissue, including normal pancreas, benign pancreatic disease, and pancreatic carcinoma. Expression was scored as negative, low, or high and then tabulated for each class of pancreatic sample.

Fig. 8: *GREMLIN 1* RNA is expressed in tumor, but not non-tumor, lung tissue from the same patient. ISH for *GREMLIN 1* RNA was performed on large sections of lung containing tumor and non-tumor tissues from the same patients. Representative images from one patient are shown. *GREMLIN 1* RNA is represented by punctate brown dots, and nuclei are counterstained with hematoxylin.

Fig. 9: Expression of other BMP antagonists in BCC tumor and non-tumor tissue. RT-PCR analysis of expression of BMP antagonists *CHORDIN* and *TSG1*. Transcript levels in whole tumor skin were compared to those in adjacent, non-tumor whole tissue from the same patient. The expression level for each gene in a sample has been normalized to averaged, duplicate measurements of *GAPDH* for that sample.