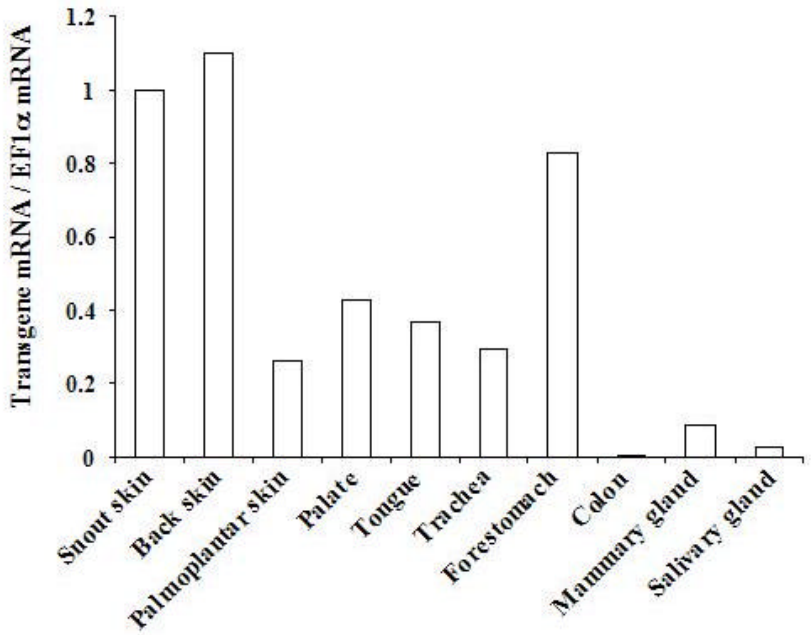
SUPPLEMENTARY MATERIALS

Supplementary Figure 1



Sup. Fig. 1. mRNA levels for the human mutant FGFR3 S249C transgene in various tissues of K5–(S249C)FGFR3 transgenic mice (line #79).

Expression of the human FGFR3 S249C transgene normalized with respect to a reference gene, EF1α, was quantified by real-time PCR analyses in snout skin, back skin, palmoplantar skin, palate, tongue, trachea, forestomach, colon, mammary gland and salivary gland in the #79 transgenic line. The expression in the snout and back skin of three other transgenic lines (#248, #392, #404) was also measured. Lines #79, #248 and #392 expressed the transgene at a similar level whereas the expression was half in line #404. It should be noted that the skin phenotypes appeared about 3-5 weeks later in lines #404 than in lines #79 and #248. No phenotype was observed in line #392. The reason for the lack of phenotype in line #392,

which expressed the transgene, is not clear. Part of the transgene may have been modified in this line, preventing the synthesis of a functional protein.

Primers for human FGFR3 and mouse EF1α were designed to ensure the specific amplification of a 152 bp (for FGFR3) and 219 bp (for EF1α) fragments of the cDNA. The sequence of these primers were as follows: FGFR3, forward 5' AGTCCTGGATCAGTGAGAG 3', reverse 5' CTGCTCGGGGCCCGTGAACG 3'; EF1α, forward 5' CTGGAGCCAAGTGCTAATATGCC 3', reverse 5' GCCAGGCTTGAGAACACCAGTC 3'. Quantitative real-time PCR was performed with the SYBR Green PCR Master Mix according to the manufacturer's instructions (Applied Biosystems).