



Fig. S2. mRNA expression was evaluated by quantitative-PCR in plucked hair samples from 6 normal control individuals and the patient. *GAPDH* was used to normalize the gene expression. The expression level of *TRPS1* was down-regulated (a). The expression levels of *STAT3*, *SOX9* and *CTNNB1* mRNA were up-regulated, but the expression level of *STAT1* mRNA was unchanged (b, c). *FGF5*, *TGF-β1* and *STAT6* mRNA were slightly up-regulated. Diagram showing how reduced TRPS1 produce the phenotype (d).