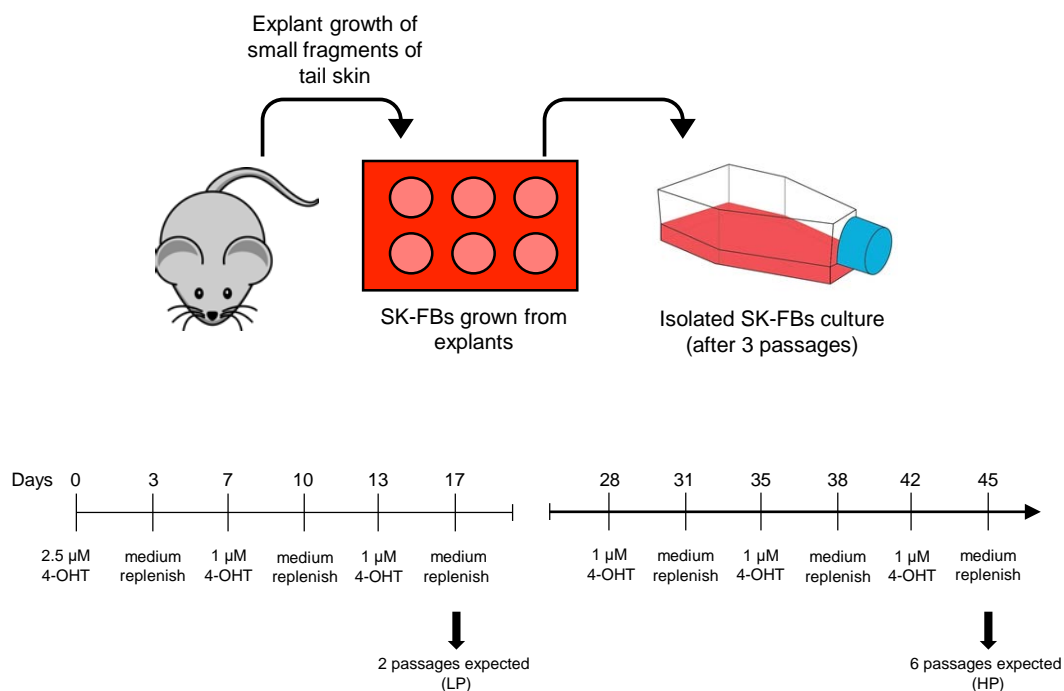
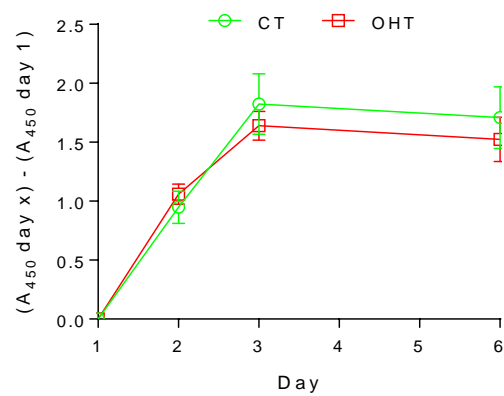


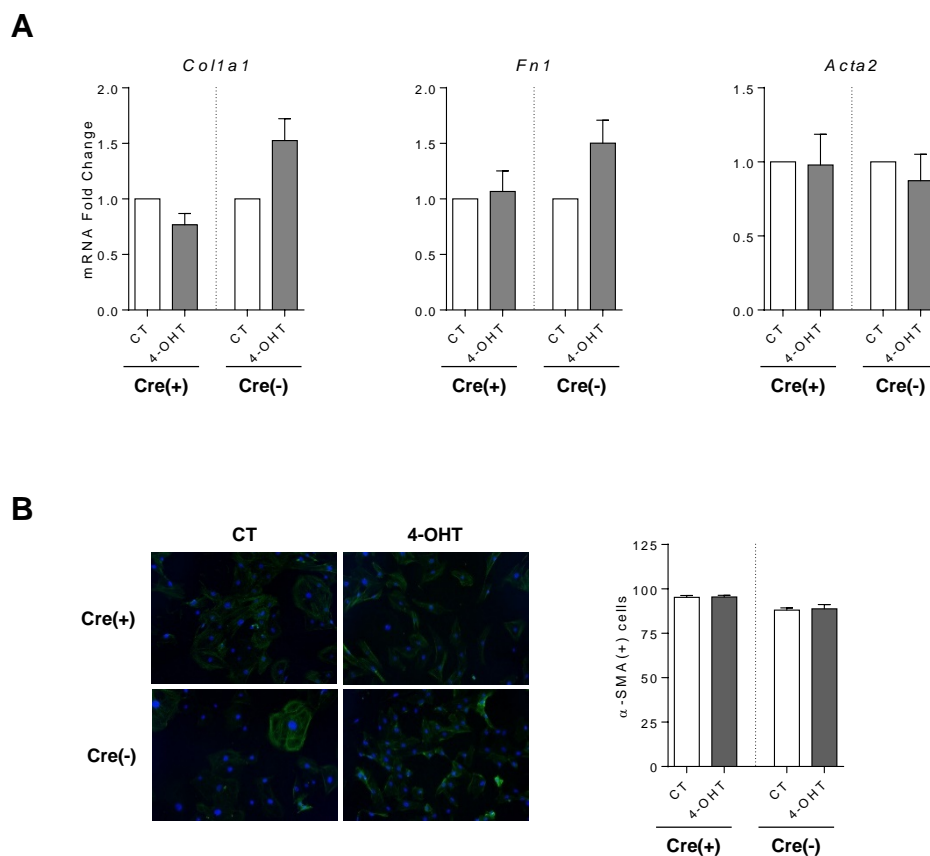
**Fig. S1. Determination of *Cre* genotype by conventional PCR.** Representative image of *Cre* amplification (630 bp) in 3 *Cre*(+) and 3 *Cre*(-) SK-FBs lines from different mice.



**Fig. S2. Schematic representation of SK-FBs culture and treatment.** The starting point (day 0) for the 4-OHT treatment should be considered after 3rd passage. Culture medium was replenished once between doses (each 3-4 days) with 4-OHT-free culture medium. Cells are predicted to be passaged with an average frequency of once per week.



**Fig. S3. Proliferation of Cre(+) SK-FBs.** Treated (4-OHT) and untreated (CT) Cre(+) SK-FBs were seeded at 2500 cells/well in 96-well plates and proliferation was addressed by colorimetric detection of WST-1 at different time-points (n=6).



**Fig. S4. Analysis of extracellular matrix components. (A)** Changes in mRNA expression of treated (4-OHT) HP Cre(+) (n=9) and Cre(-) (n=4) cells with respect to untreated cells (CT) of extracellular matrix components *Col1a1*, *Fn1*, *Acta2*. **(B)** Immunofluorescent detection of  $\alpha$ -SMA protein (green) counterstained with DAPI (blue) and quantification of  $\alpha$ -SMA(+) 4-OHT and CT Cre(-) (n=2) and Cre(+) (n=2) SK-FBs (Mean $\pm$ SEM).

**Table S1.** Primer sequences used for Genotyping *Cre* and *Tfam* (A) and qRT-PCR analysis of gene expression (B).**A**

| Gene Name   | Forward Primer Sequence      | Reverse Primer Sequence                                       |
|-------------|------------------------------|---|
| <i>Tfam</i> | 5'- CTGCCTTCCTCTAGCCCGGG -3' | 5'- GTAACAGCAGACAACCTTGTG -3'<br>5'- CTCTGAAGCACATGGTCAAT -3' |
| <i>Cre</i>  | 5'- ATCCGAAAAGAAAACGTTGA -3' | 5'- ATCCAGGTTACGGATATAGT -3'                                  |

*Tfam*: mitochondrial transcription factor A; *Cre*: cre-recombinase

**B**

| Gene Name     | Forward Primer Sequence       | Reverse Primer Sequence       |
|---------------|-------------------------------|-------------------------------|
| <i>Hprt</i>   | 5'- GTTGGGCTTACCTCACTGCT -3'  | 5'- TAATCACGACGCTGGGACTG -3'  |
| <i>Tfam</i>   | 5'- CAGGAGGCAAAGGATGATTC -3'  | 5'-CCAAGACTTCATTTTATTGTCG-3'  |
| <i>mt-Co1</i> | 5'-CTCGCCTAATTTATTCCACTTCA-3' | 5'-GGGGCTAGGGGTAGGGTTAT-3'    |
| <i>Sdhb</i>   | 5'-CTTGAATCCCTGCTCTGTGG-3'    | 5'-AAAGCTGAGAGTGCCAAGAG-3'    |
| <i>Il6</i>    | 5'-TAGTCCTTCCTACCCCAATTTCC-3' | 5'TTGGTCCTTAGCCACTCCTTC-3'    |
| <i>Ccl2</i>   | 5'-TTAAAAACCTGGATCGGAACCAA-3' | 5'-GCATTAGCTTCAGATTTACGGGT-3' |
| <i>Mmp3</i>   | 5'-ACATGGAGACTTTGTCCCTTTTG-3' | 5'-TTGGCTGAGTGGTAGAGTCCC-3'   |
| <i>Cxcl2</i>  | 5'-CCAACCACCAGGCTACAGG-3'     | 5'-GCGTCACACTCAAGCTCTG-3'     |
| <i>Ifnb1</i>  | 5'-CAGCTCCAAGAAAGGACGAAC-3'   | 5'-GGCAGTGTAACCTTCTGTCAT-3'   |
| <i>Col1a1</i> | 5'-CCTGAGTCAGCAGATTGAGAA-3'   | 5'-CCAGTACTCTCCGCTCTT-3'      |
| <i>Fn1</i>    | 5'-ACCGACAGTGGTGTGGTCTA-3'    | 5'-CACCATAAGTCTGGGTACAG-3'    |
| <i>Acta2</i>  | 5'-GTCCCAGACATCAGGGAGTAA-3'   | 5'-TCGGATACTTCAGCGTCAGGA-3'   |
| <i>Cdkn1a</i> | 5'-CCTGGTGATGTCCGACCTG-3'     | 5'-CCATGAGCGCATCGCAATC-3'     |
| <i>Cdkn2a</i> | 5'-CGCAGGTTCTTGGTCACTGT-3'    | 5'-TGTTACGAAAGCCAGAGCG-3'     |

*Hprt*: hypoxanthine-guanine phosphoribosyltransferase; *Tfam*: mitochondrial transcription factor A; *mt-Co1*: mitochondrially encoded cytochrome C oxidase I; *Sdhb*: succinate dehydrogenase cytochrome b small subunit; *Il6*: interleukin 6; *Ccl2*: chemokine (C-C motif) ligand 2; *Mmp3*: matrix Metalloproteinase 3; *Cxcl2*: chemokine (C-X-C motif) ligand 2; *Ifnb1*: interferon beta 1; *Col1a1*: collagen type I alpha 1 chain; *Fn1*: fibronectin 1; *Acta2*: actin alpha 2; *Cdkn1a*: cyclin-dependent kinase inhibitor 1a; *Cdkn2a*: cyclin-dependent kinase inhibitor 2a