Supplemental Material

Sox4 links tumor suppression to accelerated aging in mice by modulating stem cell activation

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Adenoviral Transduction

For inducing Cre-mediated recombination, we seeded target cells at a density of 0.8x10^6 cells per 10cm dish and let them attach for 2h; then we added the adenoviral particles (Provided by the University of Iowa, US) resuspended into 2ml of DMEM at a density of 100MOI (100 viral particles per cell), ensuring 100% transduction. After 1.5 at 37ºC with gentle shaking, we added 10ml of complete DMEM medium and let the cells reach confluence. Cells were then split for functional analysis.

Transfection and retroviral transduction

Transfection into 293T cells was performed using XtremeGene reagent following manufacturer’s instructions. Retroviral transduction was performed following standard procedures. Briefly, 293T cell supernatant was collected 48h after transfection with the cDNA of interest and pCL-Eco ecotropic packaging vector at a 1:1 ratio. Supernatants were filtered through 0.45µm filters and diluted 1/3 in complete DMEM medium in the presence of 8µg/ml Polybrene. Diluted supernatant was added to target cells, previously seeded at a 0.8x10^3 cells per 10cm dish. Supernatant addition was repeated three times every 12h, and target cells were selected in 2µg/ml Puromycin for 48h prior to the functional assays.

QFISH on skin sections

Skin was collected and processed as described for IHC, and after antigen retrieval samples were hybridized with a telomeric (CCCTAA)_6 probe coupled to
Cy3 as described (Samper et al., 2000). Images were captured using a confocal SP5 Leica Microscope by performing stacks of 1μm section thickness for a total of 10μm, using a 63X oil immersion objective. At least 100-300 nuclei were analyzed per skin region and mouse, and replicates arise from averaged values among mice (n). Maximum projection images were analyzed using TFL-Telo software, a kind gift of Peter Landsorp, for quantification of individual fluorescence intensity of telomeres.

**HTQFISH in PBMCs**

100μl of peripheral blood were collected from the submaxilar vein of restrained animals from the indicated ranges of age onto EDTA-containing tubes. Erythrocyte lysis was performed with QIAGEN RBC lysis buffer following manufacturer’s instructions and PBMCs were plated onto Poly-L-Lysine pre-coated Greiner 96 well plates for 2-4h at 37ºC. HTQFISH was then performed as described (Canela et al., 2007) by using the Opera-Acapella system (BD) for image acquisition and analysis. At least 5000 telomeres were analyzed per mouse and condition, and mean telomere length was used for comparison and for obtaining average values per group of mice.

**Quantitative Real-Time RTPCR (qPCR)**

Total RNA isolation and DNA digestion was done with RNA later, RNEasy and DNase I kits (QIAGEN) following manufacturer’s instructions. For cDNA synthesis, 0.5ng of total RNA were retro-transcribed with Advanced iScript and assayed using Power SYBR Green PCR Master Mix (Applied Biosystems). Samples were measured in technical triplicates and average values were used
for obtaining the biological replicates (n=number of mice in all cases). GAPDH and Actin were used as references for normalization and results were represented as relative to GAPDH levels. The primers used are listed in Supplemental Table 5.

Two-step skin carcinogenesis protocol with DMBA/TPA

TPA and DMBA treatment was performed as described (Gonzalez-Suarez et al., 2000). Briefly, 6-8 age-matched (6-10 week-old) mice were clipped and a single dose of DMBA was applied topically (20µg in 200µl). During the next 15 weeks, mice were administered topical TPA twice weekly (12.5µg in 200µl per dose). All the animals were monitored for a total of 35 weeks for tumor burden with the help of a caliper and sacrificed whenever signs of morbidity were appreciated.

Label-Retaining Cells (LRCs) assays

LRC tracing with BrdU was performed as described (Braun et al., 2003; Flores et al., 2005). In brief, P10 mice were injected with 50mg/Kg BrdU in PBS every 12h for a total of four injections. After a chase period of 70 days, mice were culled and tail skin collected and incubated during 4h at 37°C in 5mM EDTA in PBS. Epidermis was peeled-off gently with forceps and fixed in 4% paraformaldehyde for 2h at RT. After 3x5min washes in PBS, epidermal sheets were permeabilised with PB buffer (0.5% Triton-X100, 0.25% fish skin gelatin (SIGMA), 0.5% milk powder, in PBS), denatured in 2M HCl for 30min at 37°C, washed overnight at 4°C in PB buffer and then incubated in anti-BrdU antibody and DAPI and processed as described (Braun et al., 2003). Images were
captured in a SP5 Leica Confocal Microscope (15-20 follicles were quantified per mouse and values averaged for comparison among mice as number of LRC per follicle) by using a 40X objective, and performing 1µm sections projected into z-stacks spanning 30-40µm.

**Hair plucking and wound healing**

Hair plucking and wound healing were performed as described (Flores and Blasco, 2009; Flores et al., 2005). For hair plucking mice were anesthetized in 2.5% Isofluorane (kept during the whole procedure) and were intraperitoneally-administered Buprex solution as analgesic. A 1cm² dorsal patch of hair was removed by manual plucking with tweezers and tape-stripping. Hair regeneration was assessed with ImageJ; briefly, images were taken from a fixed distance including a caliper for distance calculation, and regenerated hair was calculated as percentage of Anagen skin at the indicated time point over the initial plucked area. Each mouse was quantified independently and values were used for comparison (n=number of mice). For wound healing, mice were anesthetized; 4-6cm² of dorsal hair was removed with depilatory cream (Veet) and rinsed with distilled water. Parallel, double full-thickness wounds were performed under anesthesia conditions 24h later in the upper region of the dorsal skin of the mice with a 4mm biopsy punch device (PFM, Köln, Germany). Subsequent wounds were performed following a head-to-tail progression along the back skin of the mice every 3 days and wound size assessed with a caliper and ImageJ in a similar manner to that of hair regeneration (percentage of remaining wound at the indicated times, with respect to initial wound area). At least 2 wound were
quantified per mouse, and averaged values were used for generating biological replicates (n).

**In vitro transformation and foci formation**

MEFs were isolated from E13.5 mouse embryos following standard procedures. After AdCre infection, 0.8x10⁶ low passage MEFs (P2) were seeded onto 10 cm dishes and retrovirally transduced with pLPC-\textit{E1a-IRES-HRas}^{G12V}-puro (Fernandez-Marcos et al., 2010; Palmero and Serrano, 2001) supernatant produced in 293T cells. Cells were selected in 2µg/ml puromycin for 48h. Infected cells were then seeded at a low density (2x10³ cells per 100mm dish) in triplicates and grown in DMEM 10% FBS for 2 weeks. Cells were fixed in 10% Formaldehyde 30 min at RT and stained with Giemsa. Dishes were scanned and colony size and frequency was assessed with ImageJ.
Supplemental Figure Legends

**Figure S1. Accelerated aging in Sox4 hypomorphic (Sox4<sup>lox/lox</sup>) mice, related to Figure 1**

(A) Mendelian ratios in the indicated mating settings, of Sox4<sup>lox/lox</sup>, Sox4<sup>+/lox</sup> and Sox4<sup>+/+</sup> pups at early (E13.5) and late (E18.5) developmental stages and P21 (Weaning). P values were calculated using Fisher’s exact test.

(B) Relative size of embryos (E18.5), pups (P2) and young (P90) mice of the indicated genotypes.

(C) Weight gain during the postnatal life of mice from the indicated genotypes.

(D) DEXA images of adult male Sox4<sup>+/+</sup> and Sox4<sup>lox/lox</sup> mice.

(E) Fat mass (%) in mice from the indicated genotypes

(F) Weight (grams) of lean mass in Sox4<sup>+/+</sup> and Sox4<sup>lox/lox</sup> mice.

(G) Kaplan-Meyer plots of male (left) and female (right) mice from Sox4<sup>+/+</sup>, Sox4<sup>+/lox</sup> and Sox4<sup>lox/lox</sup> cohorts. Mean life span is shown as intersection with the dashed red line. Log-rank test was used for comparison.

N=number of mice studied per genotype; Student’s t test was used unless otherwise specified.

**Figure S2. Sox4 hypomorphic mice show normal Sox11/12 expression levels and display delayed hair follicle morphogenesis, related to Figure 1**

(A) GFP IHC in tail skin sections from Sox4<sup>+/+</sup> and Sox4<sup>lox/lox</sup> mice.

(B) Variation in the Sox4 mRNA expression in adult tail skin from the indicated genotypes.
(C) Sox11 and Sox12 qPCR in the indicated tissues from Sox4<sup>+/+</sup> and Sox4<sup>lox/lox</sup> mice.

(D) (Left) CK14 and Sox9 IHC in E18.5 embryos of the indicated genotypes. Magn, magnification. (Right) Quantification of the numbers of HF in mice of the indicated genotypes at E18.5.

N=number of mice. Student’s t test was used for comparison (indicated when significant) and depicted is average and SEM.

**Figure S3.** K5-Cre transgenesis does not influence lifespan, Sox11/Sox12 expression or weight, related to Figure 2

(A) Sox11 and Sox12 qPCR from tail epidermis of Sox4<sup>WT</sup> and Sox4<sup>cKO</sup> mice.

(B) Kaplan-Meyer survival curves of the depicted cohorts, comparing the different genotypes with or without the K5Cre transgene (Top, Sox4<sup>+/+</sup>; middle, Sox4<sup>+/lox</sup>; bottom panels, Sox4<sup>lox/lox</sup>). Log-rank test was used for comparison.

(C) Weight plots (grams, g) in mice of the indicated genotypes at different time points.

(D) Tail skin hyperpigmentation in adult (6 months old) Sox4<sup>WT</sup> and Sox4<sup>cKO</sup> mice.

N=number of mice studied per genotype. Unless otherwise specified, Student’s t test was used for comparison. Depicted is average and SEM.

**Figure S4.** Reduced differentiation capabilities in vitro and normal number of LRC in Sox4<sup>cKO</sup> skin, related to Figures 3 and 4
(A) (Left) Brightfield and Giemsa-stained adult (P180) primary mouse keratinocytes undergoing differentiation. Images are representative of 2 mice per genotype. Red arrowheads mark differentiated colonies and yellow arrowheads depict small, undifferentiated clones. (Right) Total number (large, differentiated and small, undifferentiated) colonies in differentiating newborn (P1) and adult (P180) mouse keratinocyte clonogenic assays.

(B) (Left) LRCs, as assessed by BrdU staining after a 70day-chase period on tail skin whole-mounds from the indicated genotypes. (Right) Quantification of the amount of LRCs per HF.

N=number of mice per genotype, Student’s t test was used for comparison.

Figure S5. Telogen and Anagen skin microarrays show preferential downregulation in immune/metabolic pathways or HFSC pathways, respectively, in the absence of Sox4; related to Figure 5

(A) Heat map showing the top-50 DEGs during Telogen skin in the indicated genotypes.

(B) qPCR validation of some of the DEGs found in (A)

(C) GSEA of the indicated pathways, in Sox4WT and Sox4cKO mice during Telogen.

(D) Heat maps for the Sox4, Sox9 and Sox5 signatures (see Main Figure 6C). The top-twenty differentially regulated genes are shown (red=high expression levels; blue=low expression levels, referred to Sox4WT mice).

(E) Telogen skin qPCR analysis of the DEGs found in the Anagen microarray.

(F) qPCR analysis of the Wnt/Ctnnb1 signature in Telogen skin.
(D) Proposed model for Sox4 modulation of canonical Wnt pathway during HFSC activation upon plucking.

Figure S6. Early and late carcinogenesis are prevented by reduced proliferation and HFSC activation in the absence of Sox4, related to Figure 6

(A) Macroscopic aspect of mice from the indicated genotypes, at 10 and 15 weeks of treatment during the TPA/DMBA carcinogenesis protocol.

(B) Ki67 IHC in skin from Sox4<sup>WT</sup> and Sox4<sup>cKO</sup> mice, 6 weeks after initiation of DMBA/TPA treatment. Note the reduced Ki67-positive cells in Sox4-depleted mice. Magn, magnification.

(C) IFE thickness and hair follicle length after 6 weeks of TPA treatment.

(D) Loricrin, Cytokeratin 6 (CK6), p53 and phospho-Histone 3 (P-H3) IHC in benign lesions after 6 weeks of TPA treatment, in Sox4<sup>WT</sup> and Sox4<sup>cKO</sup> mice. Insets show magnification; yellow arrowheads, pan-nuclear P-H3-positive cells; red arrowheads, dotted P-H3.

N=number of mice per group, Student’s t test was used for comparison.
Supplemental References

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Supplemental Figures

**Figure S1:** Accelerated aging in Sox4 hypomorphic (Sox4\(^{lox/lox}\)) mice, related to Figure 1.

**Figure S2:** Sox4 hypomorphic mice show normal Sox11/12 expression levels and display delayed hair follicle morphogenesis, related to Figure 1.

**Figure S3:** K5-Cre transgenesis does not influence lifespan, Sox11/Sox12 expression or weight, related to Figure 2.

**Figure S4:** Reduced differentiation capabilities in vitro and normal number of LRC in Sox4\(^{cKO}\) skin, related to Figures 3 and 4.

**Figure S5:** Telogen and Anagen skin microarrays show preferential downregulation in immune/metabolic pathways or HFSC pathways, respectively, in the absence of Sox4; related to Figure 5.

**Figure S6:** Early and late carcinogenesis are prevented by reduced proliferation and HFSC activation in the absence of Sox4, related to Figure 6.
**Figure S1**

**A**

Mendelian Ratios

| Sox4^{lox/lox} x Sox4^{lox/lox} | Sox4^{lox/lox} x Sox4^{lox/lox} | Sox4^{lox/lox} x Sox4^{lox/lox} |
|----------------------------------|----------------------------------|----------------------------------|
| Expected | Observed |
| Sox4^{lox/lox} | Sox4^{lox/lox} | Sox4^{lox/lox} |
| n=12 | n=22 | n=123 |
| ns | ns | ns |

E13.5 | E18.5 | Weaning (P21)

**B**

Images showing the stages of development:

- E18.5
- P2
- P90

**C**

Weight (grams)

| Sox4^{lox/lox} | Sox4^{lox/lox} |
|----------------|----------------|
| n=8 | n=14 |
| n=182 | n=182 |

E18.5 | 2 weeks | 4 weeks

**D**

Images showing genetic outcomes:

- Sox4^{+/+}
- Sox4^{lox/lox}

**E**

Fat Mass

| Sox4^{lox/lox} | Sox4^{+/+} |
|----------------|------------|
| n=8 | n=14 |
| n=6 | n=6 |

p=0.001

**F**

Lean Mass

| Sox4^{lox/lox} | Sox4^{lox/lox} |
|----------------|----------------|
| n=6 | n=6 |

p=0.0004

**G**

Survival curves for males and females:

- Male
- Female

Survival (%) vs. Age (Weeks)

Male:

- Green circles: Sox4^{+/+} (n=34)
- Yellow circles: Sox4^{lox/lox} (n=40) p<0.001
- Blue circles: Sox4^{lox/lox} (n=139) p=0.19

Female:

- Green circles: Sox4^{+/+} (n=34)
- Yellow circles: Sox4^{lox/lox} (n=28) p<0.001
- Blue circles: Sox4^{lox/lox} (n=106) p=0.60

ns = not significant

*** p<0.001

** p=0.004

** p=0.001
Figure S2

A

| Magnification |
|---------------|
| GFP           |
| Sox4^+/+      |
| Sox4^lox/lox  |

50µm

IFE  Bulge/Pr  Bulb  SG

B

Sox4

| mRNA expression levels (Normalized to GAPDHx10^-3) |
|--------------------------------------------------|
| Sox4^+/+ (n=4) | Mean = 1.0, Var = 0.8, SD = 0.9 |
| Sox4^lox/lox (n=5) | Mean = 8.8, Var = 33.8, SD = 5.8 |

Tail skin

C

Sox11

mRNA levels (relative to GAPDH x 10^-3)

Intest. Skin Panc. Spleen Kidn. Brain Liver

Sox12

mRNA expression levels

Intest. Skin Panc. Spleen Kidn. Brain Liver

D

Sox4^+/+   Sox4^lox/lox

| CK14 | Magn | Sox9 |
|------|------|------|

E18.5

Hair Follicle morphogenesis

p=0.0086
Figure S3

A  

Sox11  

Sox12  

mRNA fold

$\text{Sox}4^{\text{WT}} (n=2)$  
$\text{Sox}4^{\text{cKO}} (n=3)$

B  

Survival (%)  

Age (Weeks)

$\text{Sox}4^{\text{lox/lo}};K5\text{Cre}^+/+ (n=79) p=0.89$

$\text{Sox}4^{\text{lox/lo}};K5\text{Cre}^+/+ (n=68)$

Male and Female

C  

Weight (g)

$\text{Sox}4^{\text{WT}} (n=5)$

$\text{Sox}4^{\text{cKO}} (n=13) p<0.001$

D  

Sox11 mRNA fold  

$\text{Sox}11 (p=0.8)$

Sox12 mRNA fold  

$\text{Sox}12 (p=0.6)$

Male and Female

$\text{Sox}4^{\text{lox/lo}};K5\text{Cre}^+/+ (n=246) p=0.93$

$\text{Sox}4^{\text{lox/lo}};K5\text{Cre}^+/+ (n=245)$

$\text{Sox}4^{\text{WT}} (n=2)$  
$\text{Sox}4^{\text{cKO}} (n=3)$

$\text{Sox}4^{\text{lox/lo}};K5\text{Cre}^+/+ (n=79) p=0.89$

$\text{Sox}4^{\text{lox/lo}};K5\text{Cre}^+/+ (n=68)$

$\text{Sox}4^{\text{lox/lo}};K5\text{Cre}^+/+ (n=79) p=0.89$

$\text{Sox}4^{\text{lox/lo}};K5\text{Cre}^+/+ (n=68)$

$\text{Sox}4^{\text{lox/lo}};K5\text{Cre}^+/+ (n=75) p=0.731$
Figure S4

A

**Sox4**

**WT**

**cKO**

**BrdU**

**cells/HF**

**LRCs**

**Magn.**

**Total colonies**

| Treatment | P1  | P180 |
|-----------|-----|------|
| Sox4**WT** | 20  | 10   |
| Sox4**cKO** | 15  | 5    |
| Sox4**lox/lox** | 10  | 5    |

**p-values:**

- P1: 0.40
- P180: 0.16

**n-values:**

- Sox4**WT**: 5
- Sox4**cKO**: 2
- Sox4**lox/lox**: 6

**B**

**Sox4**

** WT**

**cKO**

**BrdU**

**DAPI**

**SG**

**Bulge**

**BrdU**

**cells/HF**

**LRCs**

**n-values:**

- Sox4**WT**: 3
- Sox4**cKO**: 2

**p-values:**

- Sox4**WT** vs. Sox4**cKO**: 0.26
Figure S5

A: Heatmap showing DEGs in Telogen for Sox4 WT (n=3) and Sox4 cKO (n=3).

B: DEGs in Telogen with FDR values.

C: Cttnb1-sensitive and Sox9 signature.

D: Sox4 Targets:
- Sox4 WT
- Sox4 cKO

E: Anagen DEGs in Telogen skin.

F: Cttnb1-sensitive signature in Telogen skin.
Figure S6

10 weeks post-DMBA

15 weeks post-DMBA

6 weeks post-DMBA

6 weeks post-DMBA

30 weeks post-DMBA
Supplemental Tables

Table S1: Main histopathological findings in Sox4WT and Sox4lox/lox mice at humane end point, related to Figure 1 and Figure S1.

Table S2: Gene Set Enrichment Analysis (GSEA) showing the pathways differentially regulated in Sox4cKO vs Sox4WT mice in Telogen skin, related to Figure 5 and S5.

Table S3: Differentially Expressed Genes (DEGs) in Sox4cKO vs Sox4WT mice undergoing hair regeneration, 12 days after plucking, at a FDR<0.05, related to Figure 5 and S5.

Table S4: Gene Set Enrichment Analysis (GSEA) showing the pathways differentially regulated in Sox4cKO vs Sox4WT mice undergoing hair regeneration, 12 days after plucking, at a FDR<0.05, related to Figure 5 and S5.

Table S5: List of primers used for qPCR and genotyping, related to Figures 1, 5 and S5.
Table S1. Main histopathological findings in Sox4 hypomorphic (Sox4<sup>lox/lox</sup>) mice compared to their wild type counterparts (Sox4<sup>+/+</sup>) at humane end point, related to Figures 1 and S1

| Parameter                                                                 | Category | Sox4<sup>+/+</sup> n=24 | Sox4<sup>lox/lox</sup> n=22 | Fisher’s exact test |
|---------------------------------------------------------------------------|----------|------------------------|-----------------------------|--------------------|
| **Sex**                                                                   | Male     | 12 (50.0%)             | 14 (63.6%)                  | p=0.39             |
|                                                                           | (%)      |                        |                             |                    |
| **Age at H. E. P. (Weeks)**                                               | Mean     | 106.9 (72-139)         | 53.8 (17-81)                | p<0.001            |
|                                                                           | (Range)  |                        |                             |                    |
| **Diaphragmatic hernia**                                                  | Affected | 1 (4.1%)               | 16 (72.7%)                  | p<0.001            |
|                                                                           | (%)      |                        |                             |                    |
| **Dilated Cardiomyopathy and heart hypertrophy**                          | Affected | 3 (12.5%)              | 8 (36.4%)                   | p=0.086            |
|                                                                           | (%)      |                        |                             |                    |
| **Pyometra**                                                              | Affected | 0 (0%)                 | 4 (50.0%)                   | p=0.02             |
|                                                                           | (% of Female) |                    |                             |                    |
| **Intestinal failure (oedema, amiloidosis, hyperthropic caecum, etc)**    | Affected | 3 (12.5%)              | 7 (31.8%)                   | p=0.16             |
|                                                                           | (%)      |                        |                             |                    |
| **Renal failure (chronic glomerulonephritis, amiloidosis, calculus, etc)**| Affected | 7 (29.1%)              | 5 (22.7%)                   | p=0.74             |
|                                                                           | (%)      |                        |                             |                    |
| **Hepatic failure (necrosis, chronic hepatitis, amiloidosis, congestion, steatosis, etc)** | Affected | 9 (37.5%)              | 12 (54.5%)                  | p=0.38             |
|                                                                           | (%)      |                        |                             |                    |
| **Skin atrophy**                                                          | Affected | 8 (33.3%)              | 8 (36.4%)                   | p=1                |
|                                                                           | (%)      |                        |                             |                    |
| **Skin hyperpigmentation**                                                | Affected | 1 (4.2%)               | 5 (22.7%)                   | p=0.09             |
|                                                                           | (%)      |                        |                             |                    |
### Table S2

Ranked list of all gene sets significantly changed in *Sox4<sup>KO</sup> vs. Sox4<sup>WT</sup> telogen mouse skin (FDR<0.05), related to Figures 5 and S5

| Gene Set Name                                                                 | # Genes | FDR q-val | Source | Status |
|------------------------------------------------------------------------------|---------|-----------|--------|--------|
| CHOLESTEROL BIOSYNTHESIS                                                     | 19      | < 1E-05   | REACTOME | DOWN ↘ |
| GENERATION OF SECOND MESSENGER MOLECULES                                    | 20      | < 1E-05   | REACTOME | DOWN ↘ |
| GLUCOSE METABOLISM                                                          | 77      | < 1E-05   | REACTOME | UP ↗   |
| METABOLISM OF CARBOHYDRATES                                                 | 100     | < 1E-05   | REACTOME | UP ↗   |
| ELECTRON TRANSPORT CHAIN                                                     | 62      | < 1E-05   | REACTOME | UP ↗   |
| GLUCONEOGENESIS                                                             | 33      | < 1E-05   | REACTOME | UP ↗   |
| IMMUNOREGULATORY INTERACTIONS BETWEEN A LYMPHOID AND A NON-LYMPHOID CELL   | 46      | 4.42E-04  | REACTOME | DOWN ↘ |
| PARKINSON'S DISEASE                                                         | 110     | 8.54E-04  | KEGG    | UP ↗   |
| CITRIC ACID CYCLE (TCA CYCLE)                                               | 18      | 0.001     | REACTOME | UP ↗   |
| BIOSYNTHESIS OF STEROIDS                                                    | 23      | 0.001     | KEGG    | DOWN ↘ |
| GLYCOLYSIS.GLUCONEOGENESIS                                                  | 53      | 0.003     | KEGG    | UP ↗   |
| NATURAL KILLER CELL MEDIATED CYTOTOXICITY                                   | 118     | 0.004     | KEGG    | DOWN ↘ |
| ANDROGEN AND ESTROGEN METABOLISM                                            | 34      | 0.004     | KEGG    | DOWN ↘ |
| PRIMARY IMMUNODEFICIENCY                                                    | 35      | 0.005     | KEGG    | DOWN ↘ |
| GRAFT-VERSUS-HOST DISEASE                                                    | 21      | 0.005     | KEGG    | DOWN ↘ |
| TCR_PATHWAY:TCR SIGNALING IN NAIVE CD4<sup>+</sup> T CELLS                   | 61      | 0.006     | NCI     | DOWN ↘ |
| CITRATE CYCLE (TCA CYCLE)                                                   | 30      | 0.007     | KEGG    | UP ↗   |
| GLYCOLYSIS                                                                  | 22      | 0.008     | REACTOME | UP ↗   |
| PI3KCIPATHWAY:CLASS I PI3K SIGNALING EVENTS                                  | 44      | 0.008     | NCI     | DOWN ↘ |
| T CELL RECEPTOR SIGNALING PATHWAY                                           | 95      | 0.019     | KEGG    | DOWN ↘ |
| CD8TCRPATHWAY:TCR SIGNALING IN NAIVE CD8<sup>+</sup> T CELLS                | 49      | 0.02      | NCI     | DOWN ↘ |
| INSULIN SIGNALING PATHWAY                                                   | 133     | 0.021     | KEGG    | UP ↗   |
| ALZHEIMER'S DISEASE                                                        | 157     | 0.031     | KEGG    | UP ↗   |
| HEMATOPOIETIC CELL LINEAGE                                                  | 79      | 0.032     | KEGG    | DOWN ↘ |
| ARGinine AND PROline METABOLISM                                              | 33      | 0.036     | KEGG    | UP ↗   |
| FRUCTOSE AND MANNOSE METABOLISM                                             | 38      | 0.039     | KEGG    | UP ↗   |
| OXIDATIVE PHOSPHORYLATION                                                   | 110     | 0.04      | KEGG    | UP ↗   |
| STARCH AND SUCROSE METABOLISM                                               | 33      | 0.041     | KEGG    | UP ↗   |
| CALCIUM SIGNALING PATHWAY                                                   | 179     | 0.045     | KEGG    | UP ↗   |
| Symbol     | Name                                      | log₂FC | p value | Annotated Diseases                                                                 | GO ID             | Biological/Molecular GO term                                                                 |
|------------|-------------------------------------------|--------|---------|-------------------------------------------------------------------------------------|-------------------|------------------------------------------------------------------------------------------------|
| Sox4       | SRY (Sex Determining Region Y)-Box 4      | 4.90   | 2.26E-09| Neuritisis, Splenic marginal zone lymphoma, Adenoid cystic carcinoma, Endometrial   | GO:0001841        | neural tube formation                                                                           |
|            |                                           |        |         | adenocarcinoma, Ependymoma, Mantle cell lymphoma, Colorectal cancer, Melanoma,    | GO:0002328        | pro-B cell differentiation                                                                      |
|            |                                           |        |         | Hepatitis, Breast cancer, Lung cancer, Prostate cancer, Obesity, Myeloma,        | GO:0003211        | cardiac ventricle formation                                                                      |
|            |                                           |        |         | Hepatocellular carcinoma, Adenocarcinoma, Glioblastoma, Medulloblastoma, Bladder  | GO:0006355        | regulation of transcription, DNA-dependent                                                       |
|            |                                           |        |         | carcinoma                                                                           | GO:0068284        | positive regulation of cell proliferation                                                          |
|            |                                           |        |         |                                                                                   | GO:0035019        | somatic stem cell maintenance                                                                    |
|            |                                           |        |         |                                                                                   | GO:009263         | canonical Wnt signaling pathway                                                                 |
| Mex3a      | Mex-3 RNA Binding Family Member A         | 2.13   | 1.53E-05| NA                                                                                  | GO:0003723        | RNA binding                                                                                    |
|            |                                           |        |         |                                                                                   | GO:0005515        | protein binding                                                                                 |
|            |                                           |        |         |                                                                                   | GO:0008270        | zinc ion binding                                                                               |
| BC005764   | Plasticity-Related Gene 2                | 1.94   | 3.59E-07| Melanoma, Pancreatitis                                                              | GO:0003824        | catalytic activity                                                                               |
|            |                                           |        |         |                                                                                   | GO:0005515        | protein binding                                                                                 |
|            |                                           |        |         |                                                                                   | GO:0008195        | phosphatidate phosphatase activity                                                              |
| Evl        | Ena/VASP-Like Protein                    | 1.39   | 1.28E-05| Splanic abcess, Esophageal varix, Hypersplenism, Portal hypertension, Wiskott-     | GO:0007015        | actin filament organization                                                                     |
|            |                                           |        |         | aldrich syndrome, Liver cirrhosis, Hypertension, Esophagtitis, Colorectal cancer, | GO:0007166        | cell surface receptor signaling pathway                                                           |
|            |                                           |        |         | Gastric cancer, Endothelitis, Breast cancer                                        | GO:0007399        | nervous system development                                                                      |
|            |                                           |        |         |                                                                                   | GO:0007411        | axon guidance                                                                                  |
|            |                                           |        |         |                                                                                   | GO:0008154        | actin polymerization or depolymerization                                                          |
| Tead2      | TEA Domain Family Member 2               | 1.07   | 2.08E-05| Patulous eustachian tube, Alpha-mannosidosis, Plasmodium falciparum malaria, Pharyngitis, Neuronitis | GO:0001570        | vasculogenesis                                                                                  |
|            |                                           |        |         |                                                                                   | GO:0001843        | neural tube closure                                                                            |
|            |                                           |        |         |                                                                                   | GO:0003143        | embryonic heart tube morphogenesis                                                             |
|            |                                           |        |         |                                                                                   | GO:0006355        | transcription initiation from RNA pol II                                                        |
|            |                                           |        |         |                                                                                   | GO:0006367        | regulation of transcription, DNA-dependent                                                      |
| Testis Derived Transcript | Toxocariasis, Clonorchiasis, Syphilis, Pneumothorax, Gastric cancer, Glioblastoma, Ovarian cancer, Squamous cell carcinoma, Prostate cancer, Melanoma |        |         |                                                                                   | GO:0008270        | zinc ion binding                                                                               |
|            |                                           |        |         |                                                                                   | GO:0008285        | negative regulation of cell proliferation                                                        |
| Zfp184     | Zinc Finger Protein 184 (Kruppel-Like)    | 1.21   | 6.42E-05| Choriocarcinoma, Schizophrenia                                                      | GO:0006351        | transcription, DNA-dependent                                                                  |
|            |                                           |        |         |                                                                                   | GO:0006355        | regulation of transcription, DNA-dependent                                                      |
| Nme4       | NME/NM23 Nucleoside Diphosphate Kinase 4  | 1.16   | 1.37E-04| Diffuse astrocytoma, Lactic acidosis, Cystic fibrosis, Tuberculosis, Myelodysplastic syndromes, Pneumonia, Colon cancer, Pancreatitis, Prostatitis | GO:0006165        | nucleoside diphosphate phosphorylation                                                          |
|            |                                           |        |         |                                                                                   | GO:0006183        | GTP biosynthetic process                                                                         |
|            |                                           |        |         |                                                                                   | GO:0006228        | UTP biosynthetic process                                                                         |
|            |                                           |        |         |                                                                                   | GO:0006241        | CTP biosynthetic process                                                                         |
|            |                                           |        |         |                                                                                   | GO:0009116        | nucleoside metabolic process                                                                    |
|            |                                           |        |         |                                                                                   | GO:0015949        | nucleobase-containing small molecule interconverrs                                               |
|            |                                           |        |         |                                                                                   | GO:0044281        | small molecule metabolic process                                                                 |
|            |                                           |        |         |                                                                                   | GO:0055086        | nucleobase-containing small molecule metabolism                                                  |
| Dbn1       | Drebrin 1                                 | 1.11   | 1.48E-04| Mantle cell lymphoma, Down syndrome, Alzheimer's disease, Dementia, Schizophrenia, Bipolar disorder, Neuronitis, Acute lymphoblastic leukemia, Neuroblastoma, Breast cancer | GO:0007015        | actin filament organization                                                                      |
|            |                                           |        |         |                                                                                   | GO:0007399        | nervous system development                                                                       |
|            |                                           |        |         |                                                                                   | GO:0010643        | cell communication by chemical coupling                                                          |
|            |                                           |        |         |                                                                                   | GO:0010644        | cell communication by electrical coupling                                                          |
|            |                                           |        |         |                                                                                   | GO:0032507        | maintenance of protein location in cell                                                          |

Table S3. Annotated ranked list of the top-20 genes significantly downregulated in Sox4ΔKO vs. Sox4ΔWT mice undergoing hair regeneration 12 days after plucking, related to Figures 5 and S5.
| Symbol | Name | log2FC | p value | Annotated Diseases | GO ID | Biological/Molecular GO term |
|--------|------|--------|---------|--------------------|-------|-----------------------------|
| Cck    | Cholecystokinin | 0.96 | 2.40E-04 | Cholecystitis, biliary dyskinesia, dyspepsia, bile reflux, irritable bowel syndrome, gallbladder disease, alcoholic pancreatitis, cholelithiasis, neuroepithelioma, gastroparesis, bladder disease, duodenal ulcer, neuron migration | GO:0001764 | |
|        |      |        |         | release of cytochrome c from mitochondria | GO:0001836 | |
|        |      |        |         | apoptotic process | GO:0006915 | |
|        |      |        |         | activation of caspas | GO:0006919 | |
| Atp1a4 | ATPase, Na+/K+ Transporting, Alpha 4 Polypeptide | 0.89 | 4.30E-04 | diabetic neuropathy, pharyngitis, neuropathy, hypertension, pancreatitis, hepatitis | GO:0000166 | nucleotide binding |
|        |      |        |         | sodium:potassium-exchanging ATPase activity | GO:0005391 | |
|        |      |        |         | ATP binding | GO:0005524 | |
|        |      |        |         | monovalent cation transmembrane transporter | GO:015077 | |
| Zfp422 | Zinc Finger Protein 422 | 0.8 | 5.32E-04 | sipple syndrome, tooth agenesis, multiple endocrine neoplasia, retinoblastoma, leukemia | GO:0006351 | |
|        |      |        |         | transcription, DNA-dependent regulation of transcription, DNA-dependent odontogenesis | GO:0006355 | |
|        |      |        |         | anti-inflammation | GO:0042476 | |
| Samd14 | Sterile Alpha Motif Domain Containing 14 | 0.83 | 5.39E-04 | lung adenoma, adenoma, colorectal cancer, adenocarcinoma | GO:0005515 | protein binding |
| Hist3h2ba | 3, H2ba, Pseudogene | 1.01 | 5.75E-04 | | GO:0005783 | endoplasmic reticulum |
|        |      |        |         | integral to membrane | GO:0016021 | |
| Tmem98 | Transmembrane Protein 98 | 0.96 | 6.11E-04 | adenosquamous carcinoma | GO:0005783 | |
|        |      |        |         | integral to membrane | GO:0016021 | |
| Aoah   | Acyloxyacyl Hydrolase | 1.06 | 7.39E-04 | osteochondrosis, common cold, mastitis, asthma, hepatitis b, gastric cancer, hepatitis | GO:0006351 | |
|        |      |        |         | lipid metabolic process | GO:0006629 | |
|        |      |        |         | inflammatory response | GO:0006629 | |
|        |      |        |         | lipopolysaccharide metabolic process | GO:0008653 | |
|        |      |        |         | negative regulation of inflammatory response | GO:0050728 | |
| Krt8   | Keratin 8 | 1.297 | 0.00035906 | keratinizing squamous cell carcinoma, neuroendocrine carcinoma, spindle cell sarcoma, chondroblastoma, craniohypophygioma, pleomorphic carcinoma, sweat gland carcinoma, cervical intraepithelial neoplasia, cervical adenocarcinoma, cervical squamous cell carcinoma | GO:0006629 | |
|        |      |        |         | apoptotic process | GO:0006915 | |
|        |      |        |         | cytoskeleton organization | GO:0007010 | |
|        |      |        |         | modulation by virus of host physiology | GO:0019048 | |
|        |      |        |         | TNF-mediated signaling pathway | GO:0033209 | |
|        |      |        |         | sarcomere organization | GO:0045214 | |
| Dio3   | Deiodinase, Iodothyronine, Type III | 0.97 | 7.97E-04 | thyrotoxicosis, birth defects, lipodystrophy, hepatocellular carcinoma, osteoarthritis, type 1 diabetes, myocardial infarction, hepatitis, choriocarcinoma, hypothyroidism, hemangiom | GO:0006629 | |
|        |      |        |         | thyroxine 5'-deiodinase activity | GO:0004800 | |
| Marcksl1 | Macrophage Myristoylated Alanine-Rich C Kinase Substrate | 0.99 | 8.52E-04 | anencephaly, neural tube defects, achondroplasia, nephropathy, lung cancer, hepatitis b, endometriosis, breast cancer, prostate cancer, prostatitis, neuritis | GO:0007010 | |
|        |      |        |         | actin binding | GO:0003779 | |
|        |      |        |         | calmodulin binding | GO:0005516 | |
|        |      |        |         | positive regulation of cell proliferation | GO:0008284 | |
| Klk15  | Kallikrein-Related Peptidase 15 | 1.24 | 8.71E-04 | bronchogenic carcinoma, peripheral vascular disease, prostate cancer, prostatitis, meningioma, breast cancer, alzheimer's disease, ovarian cancer, thyroiditis, leukemia | GO:0003824 | catalytic activity |
|        |      |        |         | serine-type endopeptidase activity | GO:0004252 | |
|        |      |        |         | serine-type peptidase activity | GO:0008236 | |
| Gene Set Name | # Genes | FDR q-val | Source | Status |
|---------------|---------|-----------|--------|--------|
| M PHASE       | 94      | < 1E-05   | REACTOME | DOWN   |
| CELL CYCLE, MITOTIC | 317    | < 1E-05   | REACTOME | DOWN   |
| MITOTIC PROMETAPHASE | 90     | < 1E-05   | REACTOME | DOWN   |
| G2-M CHECKPOINTS | 45     | < 1E-05   | REACTOME | DOWN   |
| ACTIVATION OF THE PRE-REPLICATIVE COMPLEX | 29 | < 1E-05 | REACTOME | DOWN |
| DNA REPLICATION | 35     | < 1E-05   | REACTOME | DOWN   |
| PLK1_PATHWAY:PLK1 SIGNALING EVENTS | 40 | < 1E-05 | NCI | DOWN |
| DNA STRAND ELONGATION | 29 | 1.88E-04 | REACTOME | DOWN |
| ACTIVATION OF ATR IN RESPONSE TO REPLICATION STRESS | 35 | 2.20E-04 | REACTOME | DOWN |
| EXTENSION OF TELOMERES | 22 | 6.93E-04 | REACTOME | DOWN |
| CELL CYCLE | 108    | 0.001     | KEGG   | DOWN   |
| FANCONI_PATHWAY:FANCONI ANEMIA PATHWAY | 42 | 0.001     | NCI    | DOWN   |
| DOUBLE-STRAND BREAK REPAIR | 31 | 0.003    | REACTOME | DOWN |
| CENTROSOME MATURATION | 90 | 0.003    | REACTOME | DOWN |
| LOSS OF PROTEINS REQUIRED FOR INTERPHASE MICROTUBULE ORGANIZATION FROM THE CENTROSOME | 81 | 0.003 | REACTOME | DOWN |
| GENERATION OF SECOND MESSENGER MOLECULES | 20 | 0.003 | REACTOME | DOWN |
| HOMOLOGOUS RECOMBINATION REPAIR | 26 | 0.003 | REACTOME | DOWN |
| ELONGATION OF INTRON-CONTAINING TRANSCRIPTS AND CO-TRANSCRIPTIONAL MRNA SPlicing | 129 | 0.004 | REACTOME | DOWN |
| LOSS OF NLP FROM MITOTIC CENTROSOMES | 81 | 0.004 | REACTOME | DOWN |
| GAP-FILLING DNA REPAIR SYNTHESIS AND LIGATION IN GG-NER | 16 | 0.004 | REACTOME | DOWN |
| G2-M TRANSITION | 97     | 0.004     | REACTOME | DOWN   |
| DNA REPAIR | 98      | 0.004     | REACTOME | DOWN   |
| ELONGATION AND PROCESSING OF CAPPED TRANSCRIPTS | 129 | 0.004 | REACTOME | DOWN |
| E2F TRANSCRIPTIONAL TARGETS AT G1-S | 22 | 0.004 | REACTOME | DOWN |
| HOMOLOGOUS RECOMBINATION REPAIR OF REPLICACTION-INDEPENDENT DOUBLE-STRAND BREAKS | 26 | 0.004 | REACTOME | DOWN |
| E2F MEDIATED REGULATION OF DNA REPLICATION | 37 | 0.004 | REACTOME | DOWN |
| FORMATION AND MATURATION OF MRNA TRANSCRIPT | 146 | 0.004 | REACTOME | DOWN |
| LAGGING STRAND SYNTHESIS | 19     | 0.004     | REACTOME | DOWN   |
| CELL CYCLE CHECKPOINTS | 116    | 0.004     | REACTOME | DOWN   |
| GAP-FILLING DNA REPAIR SYNTHESIS AND LIGATION IN TC-NER | 16 | 0.004 | REACTOME | DOWN |
| HEDGEHOG_2PATHWAY:SIGNaling EVENTS MEDIATED BY THE HEDGEHOG FAMILY | 22 | 0.004 | NCI | DOWN |
| METABOLISM OF NON-CODING RNA | 17     | 0.005     | REACTOME | DOWN   |
| DNA REPLICATION | 96     | 0.005     | REACTOME | DOWN   |
| ATR_PATHWAY:ATR SIGNALING PATHWAY | 37 | 0.005 | NCI | DOWN |
| MITOTIC SPINDLE CHECKPOINT | 22     | 0.005     | REACTOME | DOWN   |
| BASE EXCISION REPAIR | 17     | 0.006     | REACTOME | DOWN   |
| INHIBITION OF THE PROTEOLYTIC ACTIVITY OF APC-C REQUIRED FOR THE ONSET OF ANAPHASE BY MITOTIC SPINDLE CHECKPOINT COMPONENTS | 21 | 0.008 | REACTOME | DOWN |
| APC-C:CDC20 MEDIATED DEGRADATION OF CYCLIN B | 30 | 0.008 | REACTOME | DOWN |
| INACTIVATION OF APC-C VIA DIRECT INHIBITION OF THE APC-C COMPLEX | 21 | 0.008 | REACTOME | DOWN |
| APC-CDC20 MEDIATED DEGRADATION OF NEK2A | 27 | 0.009 | REACTOME | DOWN |

**Table S4.** Ranked list of all gene sets significantly changed in Sox4\(^{\text{cKO}}\) vs. Sox4\(^{\text{WT}}\) mice undergoing hair regeneration 12 days after plucking (FDR<0.05), related to Figures 5 and S5.
Table S4 (Cont.). Ranked list of all gene sets significantly changed in *Sox4*KO vs. *Sox4*WT mice undergoing hair regeneration 12 days after plucking (FDR<0.05), related to Figures 5 and S5

| Gene Set Name                                                                 | # Genes | FDR q-val | Source | Status  |
|-----------------------------------------------------------------------------|---------|-----------|--------|---------|
| E2F-ENABLED INHIBITION OF PRE-REPLICATION COMPLEX FORMATION                  | 15      | 0.009     | REACTOME | DOWN ‡ |
| MRN COMPLEX RELOCALIZES TO NUCLEAR FOCI                                    | 16      | 0.009     | REACTOME | DOWN ‡ |
| BASE EXCISION REPAIR                                                        | 33      | 0.011     | KEGG    | DOWN ‡ |
| HOMOLOGOUS RECOMBINATION                                                    | 27      | 0.011     | KEGG    | DOWN ‡ |
| ATM MEDIATED RESPONSE TO DNA DOUBLE-STRAND BREAK                           | 17      | 0.012     | REACTOME | DOWN ‡ |
| CONVERSION FROM APC-C:CDC20 TO APC-C:CDH1 IN LATE ANAPHASE                  | 19      | 0.012     | REACTOME | DOWN ‡ |
| ASSEMBLY OF THE RAD50-MRE11-NBS1 COMPLEX AT DNA DOUBLE-STRAND BREAK         | 16      | 0.012     | REACTOME | DOWN ‡ |
| BARD1PATHWAY:BARD1 SIGNALING EVENTS                                         | 27      | 0.014     | NCI     | DOWN ‡ |
| BASAL CELL CARCINOMA                                                        | 55      | 0.014     | KEGG    | DOWN ‡ |
| PYRIMIDINE METABOLISM                                                       | 89      | 0.015     | KEGG    | DOWN ‡ |
| MISMATCH REPAIR                                                             | 22      | 0.016     | KEGG    | DOWN ‡ |
| DOWNSTREAM TCR SIGNALING                                                    | 51      | 0.016     | REACTOME | DOWN ‡ |
| ATM MEDIATED PHOSPHORYLATION OF REPAIR PROTEINS                             | 17      | 0.016     | REACTOME | DOWN ‡ |
| G1-S TRANSITION                                                             | 109     | 0.018     | REACTOME | DOWN ‡ |
| COLLAGEN-MEDIATED ACTIVATION CASCADE                                        | 16      | 0.019     | REACTOME | DOWN ‡ |
| FORMATION OF THE EARLY ELONGATION COMPLEX                                  | 32      | 0.019     | REACTOME | DOWN ‡ |
| SYSTEMIC LUPUS ERYTHEMATOSUS                                                | 87      | 0.019     | KEGG    | DOWN ‡ |
| DNA REPLICATION PRE-INITIATION                                              | 75      | 0.019     | REACTOME | DOWN ‡ |
| FOXM1PATHWAY:FOXM1 TRANSCRIPTION FACTOR NETWORK                             | 39      | 0.02      | NCI     | DOWN ‡ |
| GLYCOSPHINGOLIPID BIOSYNTHESIS - LACTO AND NEOACTO SERIES                   | 24      | 0.02      | KEGG    | DOWN ‡ |
| CYTOSOLIC TRNA AMINOACYLATION                                                | 27      | 0.022     | REACTOME | DOWN ‡ |
| GLOBAL GENOMIC NER (GG-NER)                                                 | 34      | 0.022     | REACTOME | DOWN ‡ |
| HEDGEHOG_GLIPATHWAY:HEDGEHOG SIGNALING EVENTS MEDIATED BY GLI PROTEINS      | 47      | 0.029     | NCI     | DOWN ‡ |
| CELL SURFACE INTERACTIONS AT THE VASCULAR WALL                             | 93      | 0.031     | REACTOME | DOWN ‡ |
| HEDGEHOG SIGNALING PATHWAY                                                  | 53      | 0.031     | KEGG    | DOWN ‡ |
| IMMUNOREGULATORY INTERACTIONS BETWEEN A LYMPHOID AND A NON-LYMPHOID CELL    | 46      | 0.033     | REACTOME | DOWN ‡ |
| NUCLEOTIDE EXCISION REPAIR                                                  | 50      | 0.035     | REACTOME | DOWN ‡ |
| RHOA_PATHWAY:RHOA SIGNALING PATHWAY                                         | 43      | 0.036     | NCI     | UP †   |
| COLLAGEN ADHESION VIA ALPHA 2 BETA 1 GLYCOPROTEIN                           | 16      | 0.041     | REACTOME | DOWN ‡ |
| APC-C-MEDIATED DEGRADATION OF CELL CYCLE PROTEINS                           | 84      | 0.043     | REACTOME | DOWN ‡ |
| NUCLEOTIDE EXCISION REPAIR                                                  | 40      | 0.044     | KEGG    | DOWN ‡ |
| MICRORNA BIOGENESIS                                                         | 17      | 0.049     | REACTOME | DOWN ‡ |
### Table S5. List of primer sequences used for qPCR and genotyping, related to figures 1, 5 and S5

| Gene      | Forward                  | Reverse                  |
|-----------|--------------------------|--------------------------|
| GenotSox4-F1 | 5’ CCA GCA TCT CTA ACC TGG TCT TC 3’ | NA                       |
| GenotSox4-F2 | 5’ TTG GAG CAC GGA AAG CAG AT 3’ | NA                       |
| GenotSox4-R  | 5’ CAG GCC AGC TCT ATG CAC TTT 3’ | NA                       |
| GAPDH     | 5’ GCA CAG TCA AGG CCG AGA AT 3’ | 5’ GCC TTC TCC ATG GTG GTG AA 3’ |
| Actin     | 5’ GGC ACC ACA CCT TCT ACA ATG 3’ | 5’ GTG GTG GTG AAG ATG TAG CC 3’ |
| Sox4      | 5’ GCC TCC ATC TTC GTA CAA CC 3’ | 5’ AGT GAA GCG GTG CTA CTC GT 3’ |
| Sox11     | 5’ ATC AAG CGG CCC ATG AAC 3’ | 5’ TGC CCA GCC TCT TGG AGA T 3’ |
| Sox12     | 5’ GAG CGG AGA AAA ATC ATG GA 3’ | 5’ CGA GGC CCG TAC TTG TAG TC 3’ |
| GATA3     | 5’ TAC CAC CTA TCC GCC CTA TG 3’ | 5’ AGG ATG TCC CTG CTC TCC TG 3’ |
| Tcf3      | 5’ GGA TTG CCA CTG GCT CCG 3’ | 5’ GCC TTC TCC ATG GTG GTG AA 3’ |
| Tcf4      | 5’ GCC ACC ACA CCT TCT ACA ATG 3’ | 5’ GTG GTG GTG AAG ATG TAG CC 3’ |
| Sox9      | 5’ GCC TCC ATC TTC GTA CAA CC 3’ | 5’ GCC TTC TCC ATG GTG GTG AA 3’ |
| c-Myc     | 5’ GCC ACC TGC GCC CGA GAA T 3’ | 5’ AAA GCC CCA GCC AAG ATG G 3’ |
| mTERT     | 5’ GGA TTG CCA CTG GCT CCG 3’ | 5’ TGCCTGACCTCCTCTTGGTAC 3’ |
| Mex3a     | 5’ TCTACAAAAAGCGCGAGCTG 3’ | 5’ CTCGCACAGGTGTCTTGATG 3’ |
| Zfp184    | 5’ GGCAATCACAATTTCCCTCCCTG 3’ | 5’ ATACCTGAGGAGCTTGTTT 3’ |
| Tes       | 5’ GGGGGTGACGTGAAATGGTTCC 3’ | 5’ GCCCTTTCAGCATAAGATGGC 3’ |
| Tead2     | 5’ TGATGCAGAGGTTGTTGGA 3’ | 5’ TCACTGAGATGTAACAAGGC 3’ |
| Evl       | 5’ AGGGATTCAAGGCGGTACACTA 3’ | 5’ ACTGATGGAAGTGAGGTTT 3’ |
| Top2A     | 5’ GCTGCTGATAACAAACAAAGGG 3’ | 5’ TAGCCATTTCGACCAACACTGT 3’ |
| Chk2      | 5’ CGGAGCTTTATGGGAAGGC 3’ | 5’ AGCCATTTTACTCCCAAC 3’ |
| Wifi      | 5’ GATTTCAGAAAGCAGCCTAC 3’ | 5’ GAGGCAGGACAGAGAACAC 3’ |
| Bach2     | 5’ GGATCATCTTCAGGAAGCA 3’ | 5’ GTTCCTGGGAAGGTCTGTA 3’ |
| Cncd1     | 5’ CCCAACAACTTCCTTCTCCTG 3’ | 5’ TCCAGAAGGGGTTCATCTG 3’ |
| Cdc20     | 5’ GCCAGCTTCTCTTTAGCAA 3’ | 5’ CCTCACTCAAAACCGGTTT 3’ |
| Tcf7      | 5’ GCCAGAAGAAGGAGGTAC 3’ | 5’ ACTGGGCACAGTCAGATGT 3’ |
| Plk1      | 5’ GGTCATTCAGAGGGACACTCA 3’ | 5’ ACTGTGCTCTTTTGTCTGCA 3’ |
| Gli1      | 5’ CCTACGGCCATCTCTCATT 3’ | 5’ GCTAGACATGTCCCTTCCA 3’ |