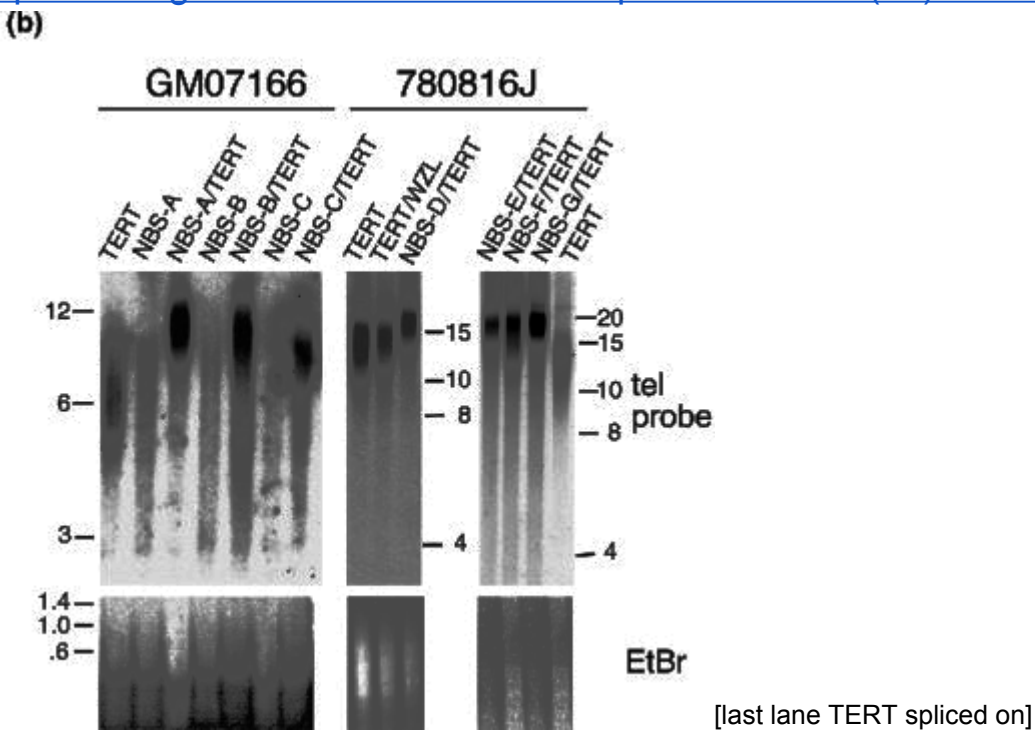
Liste der geprüften Publikationen von Karl Lenhard Rudolph Auswahl des Untersuchungsausschuss der Leibniz-Gemeinschaft

1. Ranganathan V, Heine WF, Ciccone DN, Rudolph KL, Wu X, Chang S, Hai H, Ahearn IM,Livingston DM, Resnick I, Rosen F, Seemanova E, Jarolim P, DePinho RA, Weaver DT.

Rescue of a telomere length defect of Nijmegen breakage syndrome cells requires NBS and telomerase catalytic subunit.
Curr Biol 2001; 11:962-6,
Abb. 2B.
https://linkinghub.elsevier.com/retrieve/pii/S0960-9822(01)00267-6



[last lane TERT spliced on]

2. Wirth T, Kühnel F, Fleischmann-Mundt B, Woller N, Djojosubroto M, Rudolph KL, Manns M, Zender L, Kubicka S.
Telomerase-dependent virotherapy overcomes resistance of hepatocellular carcinomas against chemotherapy and tumor necrosis factor-related apoptosis-inducing ligand by elimination of Mcl-1.

Cancer Res 2005; 65:7393-402,
Abb. 3B und 3C.
http://cancerres.aacrjournals.org/content/65/16/7393
Correction 15.10.2018
http://cancerres.aacrjournals.org/content/78/20/6026

> *"In the original version of this article (1), in Fig. 3, the images of the cell lines Hep3B and Huh7 infected with either Ad-wt or hTERT-Ad were used twice (top rows of panels B and C) because only one representative picture was taken of the infected cells. The figure legend has been edited in the latest online PDF version of the article to explain the intentional display of the same images. The authors regret this error."*

3. Jiang H, Schiffer E, Song Z, Wang J, Zürbig P, Thedieck K, Moes S, Bantel H, Saal N, Jantos J,Brecht M, Jenö P, Hall MN, Hager K, Manns MP, Hecker H, Ganser A, Döhner K, Bartke A,Meissner C, Mischak H, Ju Z, Rudolph KL.
Proteins induced by telomere dysfunction and DNA damage represent biomarkers of human aging and disease.
Proc Natl Acad Sci U S A2008; 105:11299-304,
Abb. 3G.
https://www.pnas.org/content/105/32/11299
Erratum 10.04.2018
https://www.pnas.org/content/115/15/E3600.long

> *"The authors wish to note the following: "For Figs. 1B, 3B, and 3G and Figs. S2A and S5, the figure legends should have noted that the expression control of GAPDH was run in parallel on separate gels using the same lysates and loading. We apologize for not making this explicit in the figures."*

4. Wang J, Sun Q, Morita Y, Jiang H, Gross A, Lechel A, Hildner K, Guachalla LM, Gompf A,Hartmann D, Schambach A, Wuestefeld T, Dauch D, Schrezenmeier H, Hofmann WK,Nakauchi H, Ju Z, Kestler HA, Zender L, Rudolph KL.
A differentiation checkpoint limits hematopoietic stem cell self-renewal in response to DNA damage.
Cell 2012; 148:1001-14;

https://www.cell.com/cell/fulltext/S0092-8674(12)00145-6
Abb. 3C und 4C.
Erratum zu Wang et al.: Cell 2014;158:1444,
https://www.cell.com/cell/fulltext/S0092-8674(14)01103-9 (hidden by Cell)

> *"It has come to our attention that the actin loading control for the BATF western blots depicted in Figures 3C and 4C of the article above are from different exposures of the same western blot. Although appropriate actin controls were performed for the experiments presented in Figures 3C and 4C, because the error occurred at the stage of data collection, we cannot provide an image of the correct control bands for the data presented in 4C. The magnitude and impact of this error do not affect the published conclusions. We apologize for any confusion the error may have caused."*

5. Schwitalla S, Ziegler PK, Horst D, Becker V, Kerle I, Begus-Nahrmann Y, Lechel A, Rudolph KL, Langer R, Slotta-Huspenina J, Bader FG, Prazeres da Costa O, Neurath MF, Meining A,Kirchner T, Greten FR.
Loss of p53 in enterocytes generates an inflammatory microenvironment enabling invasion and lymph node metastasis of carcinogen-induced colorectal tumors.
Cancer Cell 2013;23:93-106,
3C und 4C.
https://www.cell.com/cancer-cell/comments/S1535-6108(12)00493-X

6. Missios P, Zhou Y, Guachalla LM, von Figura G, Wegner A, Chakkarappan SR, Binz T, Gompf A, Hartleben G, Burkhalter MD, Wulff V, Günes C, Sattler RW, Song Z, Illig T, Klaus S, Böhm BO, Wenz T, Hiller K, Rudolph KL.
Glucose substitution prolongs maintenance of energy homeostasis and lifespan of telomere dysfunctional mice.
Nat Commun. 2014; 5:4924,
Abb.5E, Suppl. 5A, Suppl. 5B und Suppl. 5C.
https://www.nature.com/articles/ncomms5924

7. Wang J, Lu X, Sakk V, Klein CA, Rudolph KL.
Senescence and apoptosis block hematopoietic activation of quiescent hematopoietic stem cells with short telomeres.
Blood. 2014 Nov 20;124(22):3237-40. doi: 10.1182/blood-2014-04-568055,
Abb. 1C und 2C.
http://www.bloodjournal.org/content/124/22/3237

8. Meena JK, Cerutti A, Beichler C, Morita Y, Bruhn C, Kumar M, Kraus JM, Speicher MR, WangZQ, Kestler HA, d'Adda di Fagagna F, Günes C, Rudolph KL.
Telomerase abrogates aneuploidy-induced telomere replication stress, senescence and cell depletion.
EMBO J.2015 May 12;34(10):1371-84,
Abb. 2B und 1D.
http://emboj.embopress.org/content/34/10/1371.long
Correction 2.10.2017
http://emboj.embopress.org/content/36/19/2922

> *"The authors state that errors occurred during formatting of Fig 2B and Supplementary Fig 3C during the submission process of the original manuscript. The histogram of Fig 2B was mistakenly duplicated in Supplementary Fig S3C. The corrected histogram of Supplementary Fig S3C is shown below. In addition, Fig 2B contains two labeling errors of P values, originating from mistakes in the labeling during the graphical assembly of the figure: The P value for OSBPL3 shRNA vs. scrambled shRNA should read 0.0218 instead of 0.0216, and the P value for GJB3 shRNA vs. scrambled shRNA should read 0.0011 instead of 0.0012. The corrected Fig 2B is shown below. For the experiments shown in Fig 2B and Supplementary Fig S3C, a total number of 74–174 cells was analyzed in 3–14 vision fields per cell line.*
> *Further, γH2AX staining of IMR90 cells mentioned in the results section (page 1373, last sentence "… telomerase negative BJ and IMR90 fibroblasts exhibited a strong accumulation of DNA damage (staining positive for both γH2AX and 53BP1) at early*

passage after shRNA transduction (Fig 2A, C and D, Supplementary Fig S3A and B)…" was not depicted in the paper, and the 53BP1 staining was performed only on the BJ cells. To correct for this mistake, the text and data presentation of the result section on the description of DNA damage foci (page 1373, last sentence, and page 1374, first paragraph) is specified as follows: "The experiments on IMR90 cells were conducted only for γH2AX staining. These results are now provided in Supplementary Fig S8".

The description and presentation of Western blot results in Fig 1D (page 1372, first paragraph on the right column) is corrected as follows: The depicted analyses of p p53, p p38, and GAPDH in Fig 1D (see also the corresponding Source Data file in the original article) were all analyzed from the same blot. A repeat of the p p53 Western blot was run on a separate gel using the same protein lysates and loading buffer (see Source data for Figure 1D below).

The Western blot for p21 in Fig 1D and the corresponding beta actin control were run in parallel with the same protein lysates and the same loading on 2 separate gels; the gel probed for beta actin was not shown in the original source data file of Fig 1D. The gel was also used to repeat the analysis of p p38 expression (see Source data for Figure 1D below). Results of p21 induction were confirmed by immunofluorescence analysis (see Fig 1E and Supplementary Fig S2H–K of the original manuscript). The corrections do not affect the original conclusions presented. The authors apologize for the mistakes and any inconvenience they might have caused."

9. Tao S, Tang D, Morita Y, Sperka T, Omrani O, Lechel A, Sakk V, Kraus J, Kestler HA, Kühl M, Rudolph KL.
Wnt activity and basal niche position sensitize intestinal stem and progenitor cells to DNA damage.
EMBO J. 2015 Mar 4;34(5):624-40,
Abb. 1E und 1F.
http://emboj.embopress.org/content/34/5/624.long

Correction 2.10.2017
http://emboj.embopress.org/content/36/19/2920

> *"The authors state that it came to their attention that the figure legends of two figures were not sufficiently detailed in the original version of the manuscript.*
> *The figure legend of Fig 1E and F should read:*
> *A single representative FACS plot was chosen to illustrate (E) the gating of LGR5^{hi} and LGR5^{lo} populations within the population of LGR5^{+} (GFP positive) intestinal cells and (F) the gating of LGR5$^{hi\ high}$, LGR5$^{hi\ low}$, LGR5$^{lo\ high}$, and LGR5$^{lo\ low}$ populations. The same FACS plot is displayed in (E) and (F).*
> *The figure legend of Fig 6C should read:*
> *Representative Western blots of cell lysates for the expression of phospho p53 and cleaved caspase 3 (each n = 3; see Source Data for this figure). Samples from a single experiment were divided into identical portions and probed for phospho p53 or cleaved casp3. The expression control of beta actin was conducted on the second aliquot of the samples and was run in parallel on a separate gel.*
> *The corrections do not affect the original conclusions presented. We apologize for the lack of detail and any inconvenience it may have caused."*

10. Hartmann K, Illing A, Leithäuser F, Baisantry A, Quintanilla-Martinez L, Rudolph KL.
Gene dosage reductions of Trf1 and/or Tin2 induce telomere DNA damage and lymphoma formation in aging mice.
Leukemia. 2016 Mar;30(3):749-53,
Abb. 1F.
https://www.nature.com/articles/leu2015173
Corrigendum 10.11.2017
https://www.nature.com/articles/leu2017224

> *"Following the publication of this article the authors noted that the article was lacking the information on n-numbers for some of the panels of the figures.*

The description of the results section is specified for the following information on n-numbers of mice: The western blots in Figure 1D and Supplementary Figure 1F were conducted as biological replicates (testis and thymus) using pools of mice of the indicated genotypes (n=6 mice per genotype for thymus, n=4 mice per genotype for testis). The quantification of the expression of telomere binding proteins was conducted on RNA level (Figure 1a and b; Supplementary Figure 1A–D, n=3 mice per genotype) and on protein level (Figure 1c; Supplementary Figure 1E, wild type: n=6 mice, Trf1+/−Tin2+/−: n=7 mice, Trf1+/− mice: n=4 mice, Tin2+/−: n=4 mice). In the latter analysis, one of the total seven wild-type mice was excluded due to an oversaturated GAPDH signal by statistical outlayer analysis (Grubbs' test). The quantification of the telomeric signals of telomere binding proteins (Figure 1f and g; Supplementary Figure 1H) was carried out on a total of 37–43 nuclei per genotype from three independent cultures of mouse embryonic fibroblasts. The tumor-free survival curves (Figure 1j) and the pie chart on tumor formation (Figure 1k) were calculated from the identical number of mice as shown in Supplementary Figure 1J. For Figure 1k all mice from the three different knockout cohorts were combined.
The authors wish to apologize for any inconvenience caused."

11. Wang J, Morita Y, Han B, Niemann S, Löffler B, Rudolph KL.
Per2 induction limits lymphoid-biased haematopoietic stem cells and lymphopoiesis in the context of DNA damage and ageing.
Nat Cell Biol. 2016;18:480-90,
Abb. Suppl. 6 [Unprocessed photographs of bigger sections of the Western blots with size markers corresponding to the indicated Western blots in the main figures.]
https://www.nature.com/articles/ncb3342