

samples of never senescent cells—initiated leukaemias in recipient mice ($P=0.0275$, comparing previously senescent and never senescent groups); as expected, all Lin[−] transplants gave rise to leukaemias ($P<0.001$, comparing Lin[−] and never senescent groups; Fig. 4b, c). Notably, and further adding to SAS in oncogene-induced senescent colon mucosa cells or melanocytes (compare with Fig. 1d), TIS reprogramming is not restricted to cells of lymphoid origin, as demonstrated for an acute myeloid leukaemia (AML) mouse model²⁴, culture-established human AML cells, and primary human leukaemic blast samples obtained at diagnosis from patients with AML (Extended Data Fig. 10e–l). Thus, cellular senescence is not only associated with additional stem-cell features in tumour cells with pre-existing self-renewal capability, but also catalyses the cell-autonomous reprogramming of non-stem bulk tumour cells of lymphoid and non-lymphoid origin into *de novo* cancer stem cells.

We present here an unexpected cell-intrinsic link between the senescence program and the acquisition of self-renewing properties, which we postulate serves as a physiological rescue mechanism in development and tissue homeostasis. We and others have observed that senescence not only occurs in critically stressed cells, but also may spread to adjacent cells via SASP components in a paracrine fashion (ref. 25; J.R.D. and C.A.S., unpublished observations). We propose that nature equipped normal cells with a latent SAS capacity (compare with Extended Data Fig. 1g) to counter the imminent loss of an entire tissue compartment due to pro-apoptotic and pro-senescent stresses: in rare cells spontaneously re-entering the cell cycle when threatening stresses no longer apply, SAS may become a tissue-replenishing principle. In a neoplastic context, cellular senescence—particularly in tumour cells with apoptotic defects—appears to be primarily a beneficial response by keeping tumour growth in check. However, post-senescent cells with ‘hijacked’ SAS exert their detrimental potential at relapse by driving a much more aggressive growth phenotype. Therefore, pharmacological strategies to specifically eliminate senescent cells before a fraction of them may implement their acquired stemness capacity become, as previously reported by us regarding cancer⁹ and by others regarding ageing-related pathologies^{26,27}, a critical therapeutic need.

Online Content Methods, along with any additional Extended Data display items and Source Data, are available in the online version of the paper; references unique to these sections appear only in the online paper.

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- Muñoz-Espín, D. & Serrano, M. Cellular senescence: from physiology to pathology. *Nat. Rev. Mol. Cell Biol.* **15**, 482–496 (2014).
- Pérez-Mancera, P. A., Young, A. R. & Narita, M. Inside and out: the activities of senescence in cancer. *Nat. Rev. Cancer* **14**, 547–558 (2014).
- Zon, L. I. Intrinsic and extrinsic control of haematopoietic stem-cell self-renewal. *Nature* **453**, 306–313 (2008).
- Krizhanovsky, V. et al. Implications of cellular senescence in tissue damage response, tumor suppression, and stem cell biology. *Cold Spring Harb. Symp. Quant. Biol.* **73**, 513–522 (2008).
- Serrano, M., Lin, A. W., McCurrach, M. E., Beach, D. & Lowe, S. W. Oncogenic ras provokes premature cell senescence associated with accumulation of p53 and p16^{INK4a}. *Cell* **88**, 593–602 (1997).
- Braig, M. et al. Oncogene-induced senescence as an initial barrier in lymphoma development. *Nature* **436**, 660–665 (2005).
- Michaloglou, C. et al. BRAF^{E600}-associated senescence-like cell cycle arrest of human naevi. *Nature* **436**, 720–724 (2005).
- Schmitt, C. A. et al. A senescence program controlled by p53 and p16^{INK4a} contributes to the outcome of cancer therapy. *Cell* **109**, 335–346 (2002).
- Dörr, J. R. et al. Synthetic lethal metabolic targeting of cellular senescence in cancer therapy. *Nature* **501**, 421–425 (2013).
- Onder, T. T. et al. Chromatin-modifying enzymes as modulators of reprogramming. *Nature* **483**, 598–602 (2012).
- Krizhanovsky, V. & Lowe, S. W. Stem cells: The promises and perils of p53. *Nature* **460**, 1085–1086 (2009).
- Rea, S. et al. Regulation of chromatin structure by site-specific histone H3 methyltransferases. *Nature* **406**, 593–599 (2000).

- Narita, M. et al. Rb-mediated heterochromatin formation and silencing of E2F target genes during cellular senescence. *Cell* **113**, 703–716 (2003).
- Chen, J. et al. H3K9 methylation is a barrier during somatic cell reprogramming into iPSCs. *Nat. Genet.* **45**, 34–42 (2013).
- Mosteiro, L. et al. Tissue damage and senescence provide critical signals for cellular reprogramming *in vivo*. *Science* **354**, aaf4445 (2016).
- Ritschka, B. et al. The senescence-associated secretory phenotype induces cellular plasticity and tissue regeneration. *Genes Dev.* **31**, 172–183 (2017).
- Wong, D. J. et al. Module map of stem cell genes guides creation of epithelial cancer stem cells. *Cell Stem Cell* **2**, 333–344 (2008).
- Reya, T. et al. A role for Wnt signalling in self-renewal of haematopoietic stem cells. *Nature* **423**, 409–414 (2003).
- Wang, Y. et al. The Wnt/beta-catenin pathway is required for the development of leukemia stem cells in AML. *Science* **327**, 1650–1653 (2010).
- Lin, A. W. et al. Premature senescence involving p53 and p16 is activated in response to constitutive MEK/MAPK mitogenic signaling. *Genes Dev.* **12**, 3008–3019 (1998).
- Kelly, P. N., Dakic, A., Adams, J. M., Nutt, S. L. & Strasser, A. Tumor growth need not be driven by rare cancer stem cells. *Science* **317**, 337 (2007).
- Chaffer, C. L. et al. Normal and neoplastic nonstem cells can spontaneously convert to a stem-like state. *Proc. Natl Acad. Sci. USA* **108**, 7950–7955 (2011).
- Zhao, Z. et al. p53 loss promotes acute myeloid leukemia by enabling aberrant self-renewal. *Genes Dev.* **24**, 1389–1402 (2010).
- Zuber, J. et al. RNAi screen identifies Brd4 as a therapeutic target in acute myeloid leukaemia. *Nature* **478**, 524–528 (2011).
- Acosta, J. C. et al. A complex secretory program orchestrated by the inflammasome controls paracrine senescence. *Nat. Cell Biol.* **15**, 978–990 (2013).
- Baker, D. J. et al. Naturally occurring p16^{INK4a}-positive cells shorten healthy lifespan. *Nature* **530**, 184–189 (2016).
- Baar, M. P. et al. Targeted apoptosis of senescent cells restores tissue homeostasis in response to chemotoxicity and aging. *Cell* **169**, 132–147.e16 (2017).
- Pawlikowski, J. S. et al. Wnt signaling potentiates neovogenesis. *Proc. Natl Acad. Sci. USA* **110**, 16009–16014 (2013).
- Haugstetter, A. M. et al. Cellular senescence predicts treatment outcome in metastasised colorectal cancer. *Br. J. Cancer* **103**, 505–509 (2010).

Supplementary Information is available in the online version of the paper.

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Author Contributions M.Mi. performed mouse lymphoma and leukaemia work, stem-cell and senescence assays, and gene set enrichment analyses. J.H.M.D. and M.R. conducted analyses with human cancer cell lines and primary human material. D.N.Y.F. and D.B. carried out flow cytometric analyses. Z.Z. generated leukaemias in the p53-regulatable mouse T-ALL model, I.A.M.B. and J.Z. in the p53-regulatable mouse AML model. Y.Y. carried out biochemical analyses. J.R.D. provided transcriptome analyses and long-term outcome data from senescence-capable mouse lymphomas. L.D. and M.A.M.-P. performed chromatin immunoprecipitations and analysed related datasets. D.L. conducted Affymetrix gene expression profiling and analyses. T.K. and G.D. carried out proteome analyses. M.Me. generated β -catenin/TCF-reporter cancer cell lines and performed luciferase reporter assays. K.P. generated qPCR data. A.T., B.D., H.G. and S.L. contributed to study design, data interpretation and preparation of the manuscript. M.H. provided immunohistochemical analyses. C.A.S. designed experiments, analysed the data and wrote the manuscript.

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