

Supplementary Materials for
**A conserved long-distance telomeric silencing mechanism suppresses mTOR
signaling in aging human fibroblasts**

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The PDF file includes:

Figs. S1 to S22
Tables S1 and S3 to S7
Legend for table S2
References

Other Supplementary Material for this manuscript includes the following:

Table S2

Fig. S1

Telomeric distances of known TPE-OLD genes. For each human gene, the dendrogram presents the maximum linkage tree of its orthologues, calculated based on their telomeric distance. Only species with replicative aging are considered. The height of a connecting bar represents the maximal difference in telomeric distance. The red bar is drawn at 1 Mb and represents where the tree is cut into subtrees. The number of genes in the two largest subtrees determines the rank of that gene in the TPE-OLD candidate list. The green dots represent the distance of an orthologue to the telomere. For example, C1S has two preserved telomeric distances: ~7 Mb from the telomere (dog, bonobo, African green monkey, gorilla, human, gibbon, chimp, macaque, olive baboon) and ~16 Mb from the telomere (sheep, hybrid indicine cattle, goat, hybrid cattle, cattle).

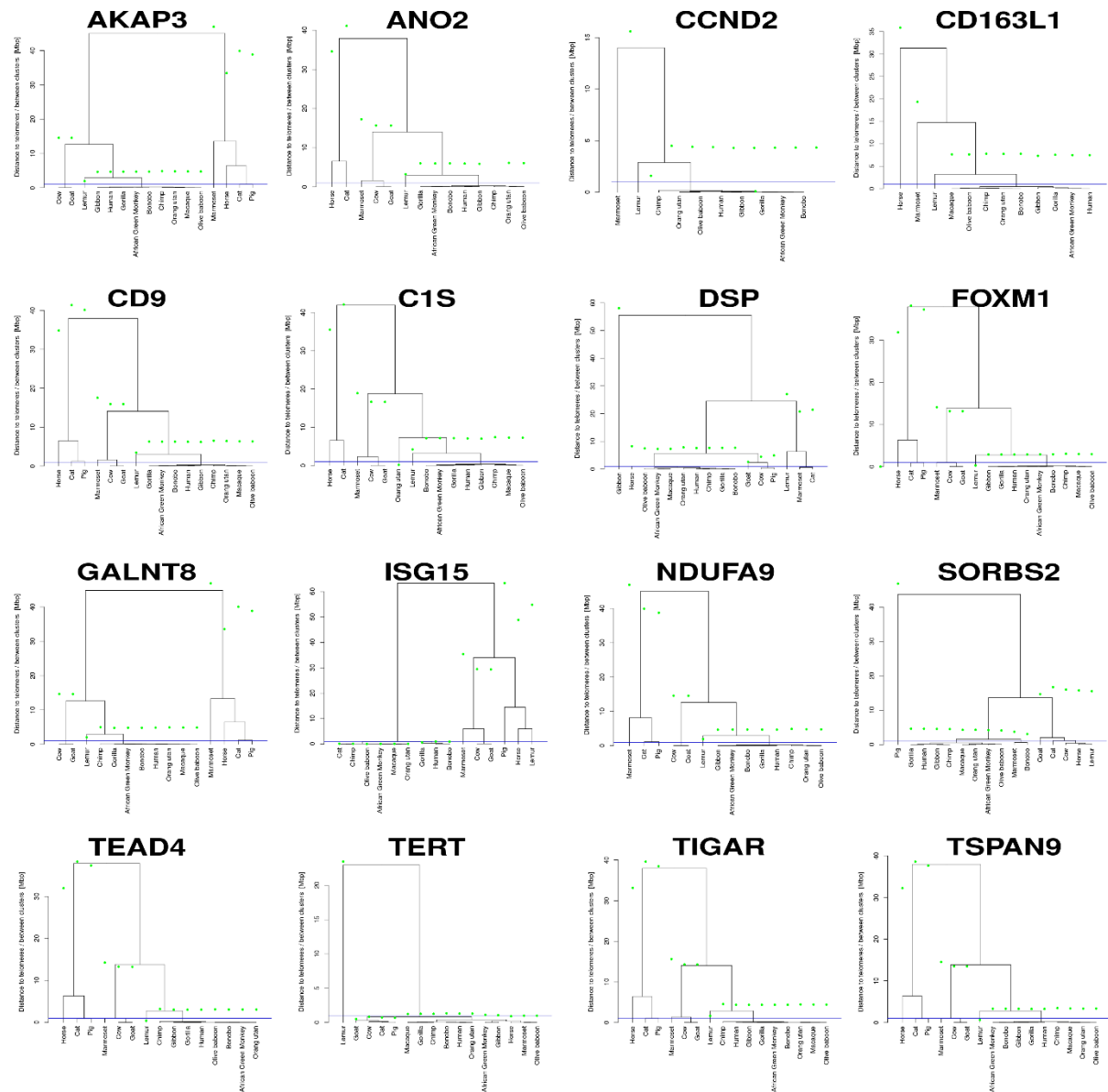


Fig. S2

Telomeric distances of selected serine/threonine specific phosphatases (PPP) that are candidates for TPE-OLD. Analogous to Figure S1, this figure presents dendrograms for the telomeric distances of selected subunits of PP2A.

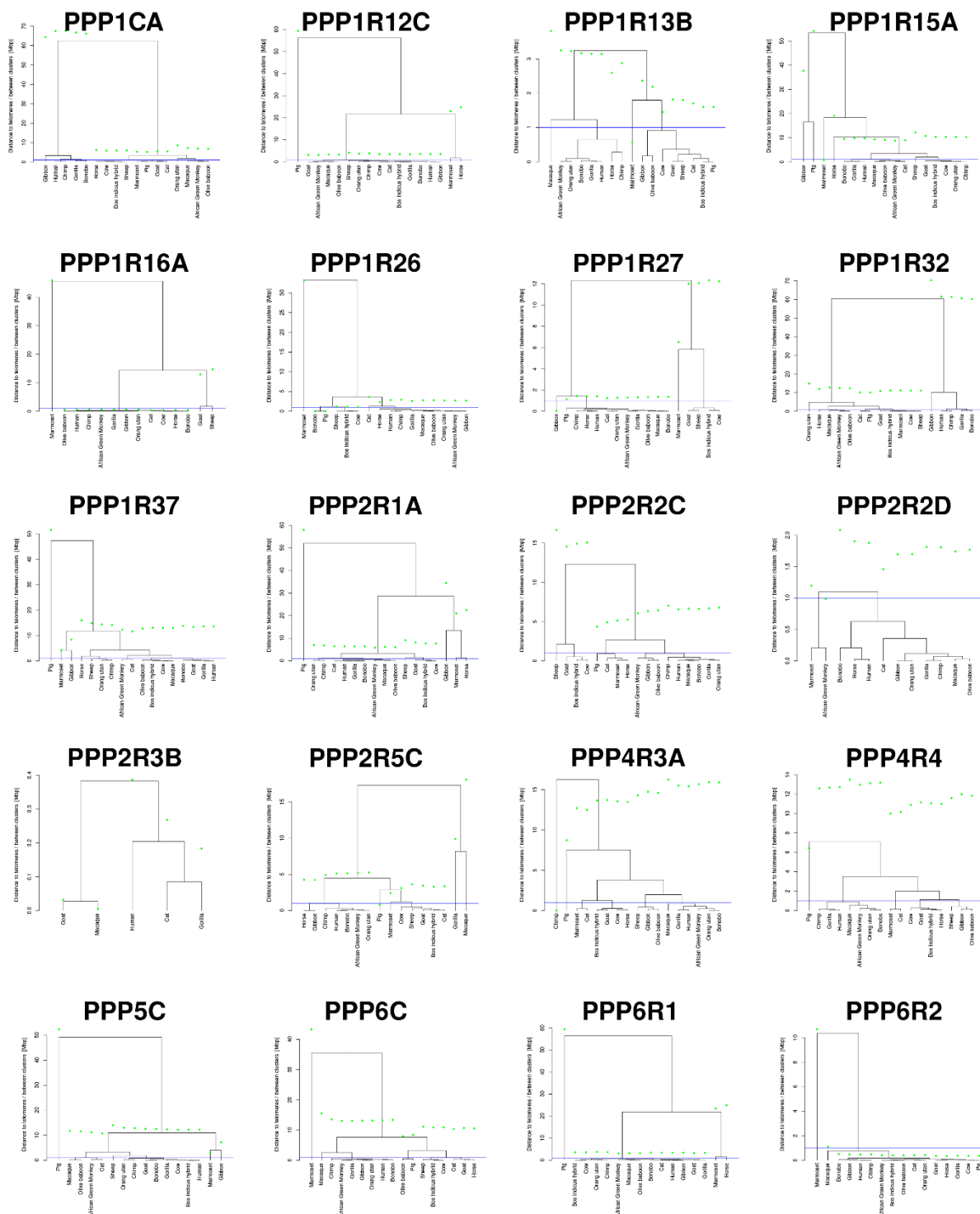


Fig. S3

TPE-OLD candidate genes are positioned by the preserved telomeric distances of their orthologues. For the selection of TPE-OLD candidates we determined for each gene the telomeric distances that appear preserved, i.e. regions that contain most of its orthologues while not exceeding 1 Mb in size. We allow two such chromosomal regions per gene. This plot positions every gene by the mean of the telomeric distances in each region. The X axis denotes the position of the “larger” region, i.e. the one that comprises more orthologues; the Y axis denotes the position of the other region. The chromosome (where the human orthologue is found) is indicated by a symbol. This helps to identify syntenic regions that appear as lines (parallel or orthogonal to the diagonal). Names of genes for which a TPE-OLD effect has previously been shown or suggested are in green. Names of protein phosphatase subunits are in blue. Known TPE-OLD genes, such as hTERT at the end of the telomere, are frequently found close to the 15 Mb (from the telomere) or close to the 5 Mb region. PPP2R2C (orange) is located close to the 15 Mb and 5 Mb regions.

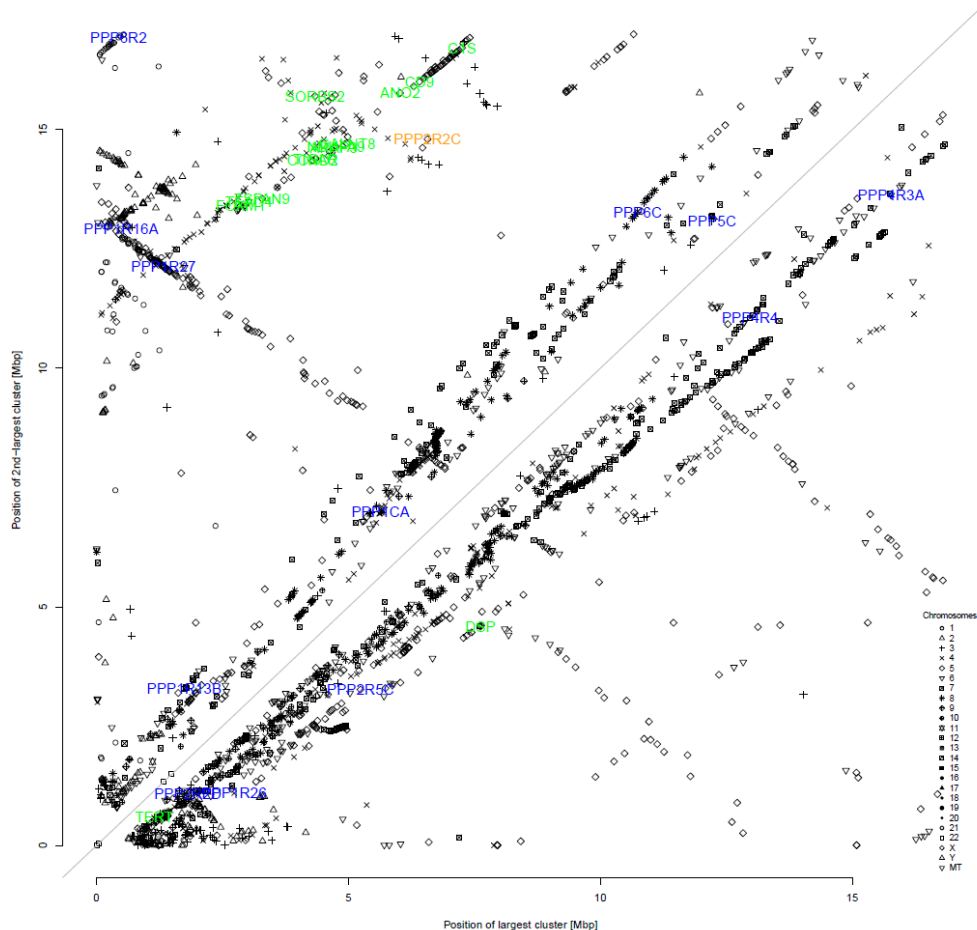


Fig. S4

TPE-OLD concept, PP2A holoenzyme structure and genomic localization of PP2A subunits.

(A), Genomic localization of regulatory PP2A subunits. **(B)**, Genomic localization of structural and catalytic PP2A subunits. Higher primates and other long-lived species with replicative aging retain the location of genes encoding some regulatory PP2A subunits at the end of their chromosomes. The location of each gene is shown in a schematic representation. Only the subtelomeric areas (up to 10 Mb) are drawn to scale, not the middle range. Each bar represents an individual chromosome; each color represents one PP2A subunit. The location of the genes relative to the telomeres is marked on the chromosome.

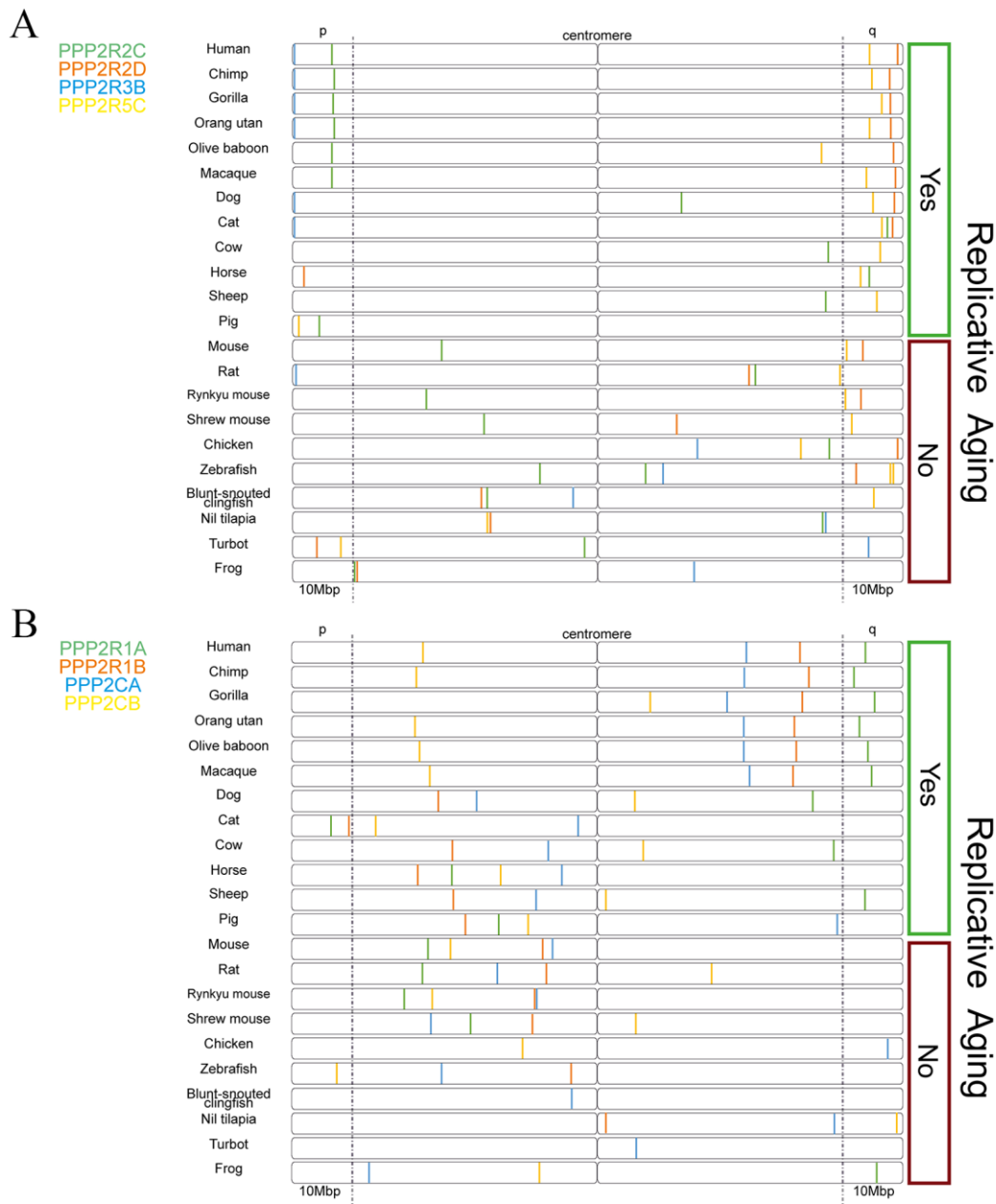


Fig. S5

Growth curves of primary (-hTERT) and immortalized (+hTERT) fibroblast cell lines.

CON, healthy controls (turquoise symbols: squares N707, triangles 731, circles 778, rhombuses 811). HGP, Hutchinson-Gilford progeria fibroblasts (magenta symbols: squares HGADFN003, triangles HGADFN164, circles HGADFN127, rhombuses HGADFN178). L, low population doubling (PD); H, high PD.

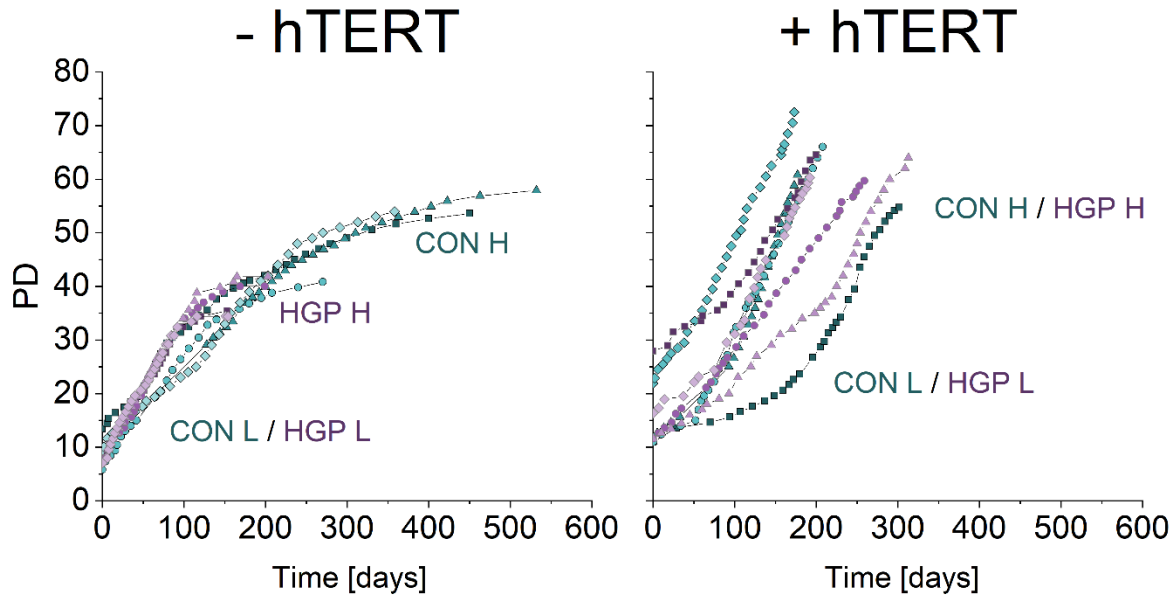
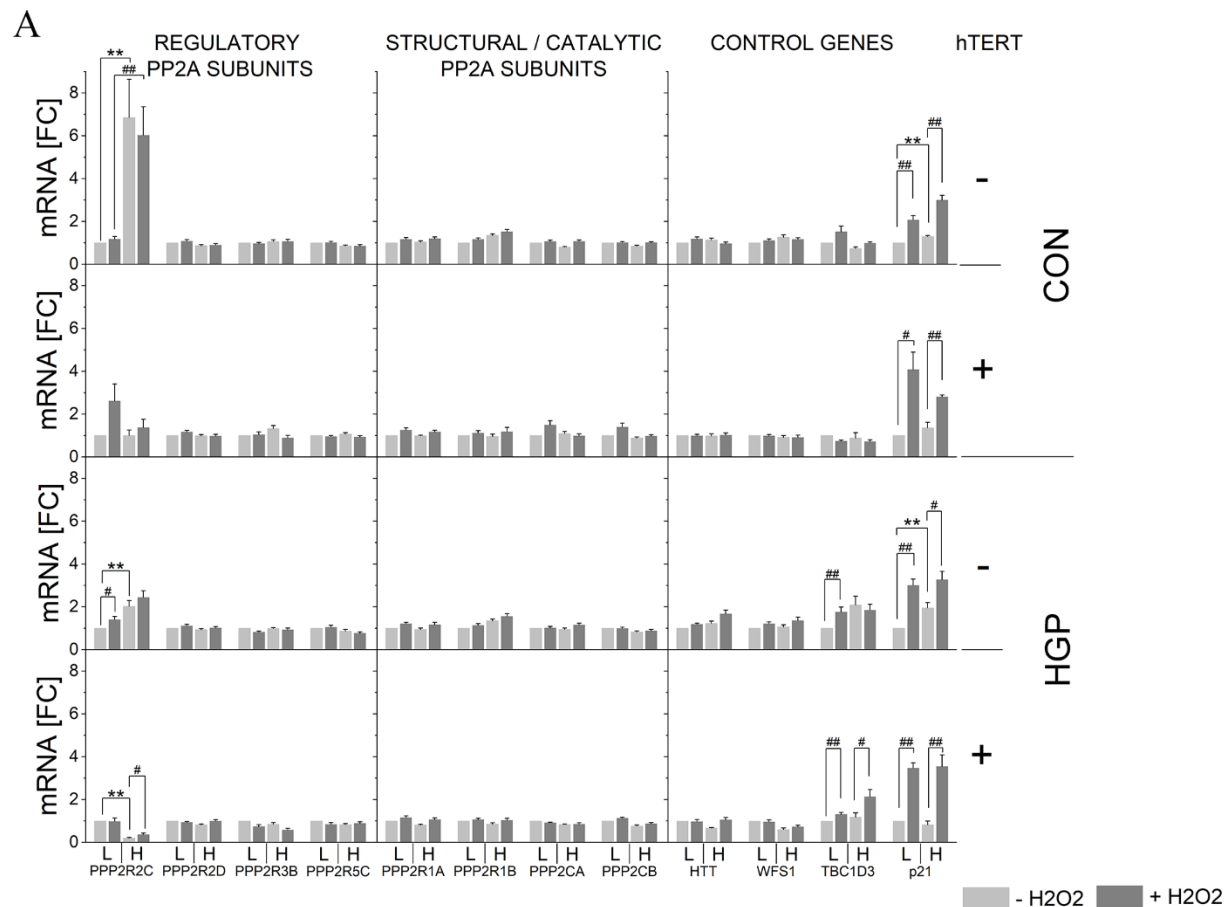
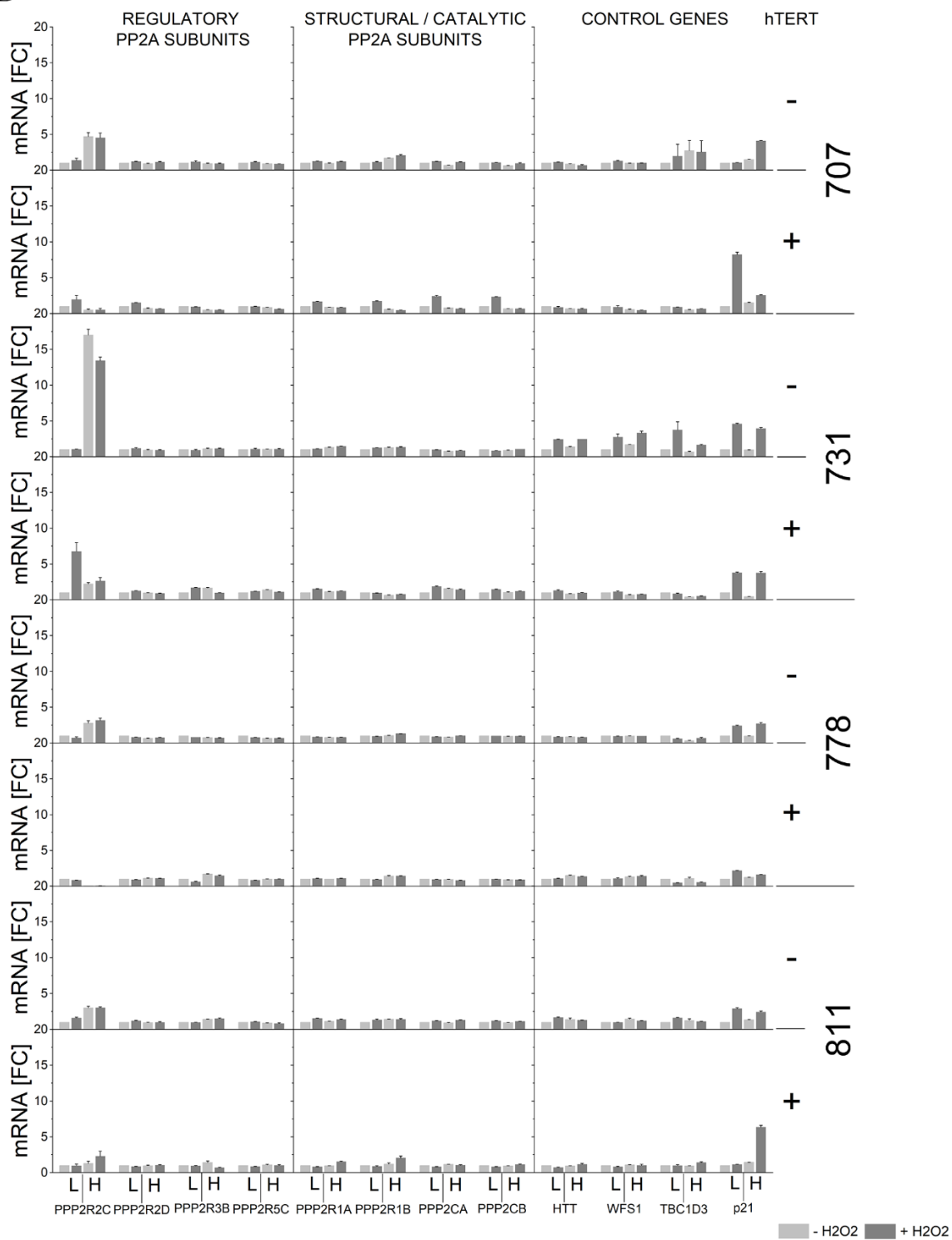


Fig. S6

Telomere length- and stress-dependent mRNA levels of regulatory, structural and catalytic PP2A subunits and control genes in healthy control (CON) and Progeria (HGP) cells. qPCR analysis of healthy CON and HGP fibroblasts at low (L) and high (H) PD was performed under basal conditions (10% FCS), in the absence of H₂O₂ (light gray columns) and in the presence of H₂O₂ (200 μ M; 2 h, gray columns). *Cyclophilin A* was used as an internal normalization control. *WFS1* and *HTT* represent internal controls, e.g., genes between *PPP2R2C* and the telomere. *P21* was used as a marker for stress-inducible activation. *TBC1D3* is a potential confounder that may influence mTOR signaling and the HGP phenotype. All values were normalized to the level (= 100%) of mRNA in young cells (PD 13–20). Each assay was performed in biological quadruplicates and technical replicates and is shown as the mean \pm SEM. The Mann-Whitney U test was employed to assess statistical significance. * indicates $p < 0.05$ and ** $p \leq 0.01$ for low PD vs high PD; # indicates $p < 0.05$ and ## $p \leq 0.01$ for $-H_2O_2$ vs. $+H_2O_2$ (A) Overall summarized data. (B) Data shown for all individual controls separately and in (C) for all individual HGP cell lines separately (with 3 technical replicates each).



B



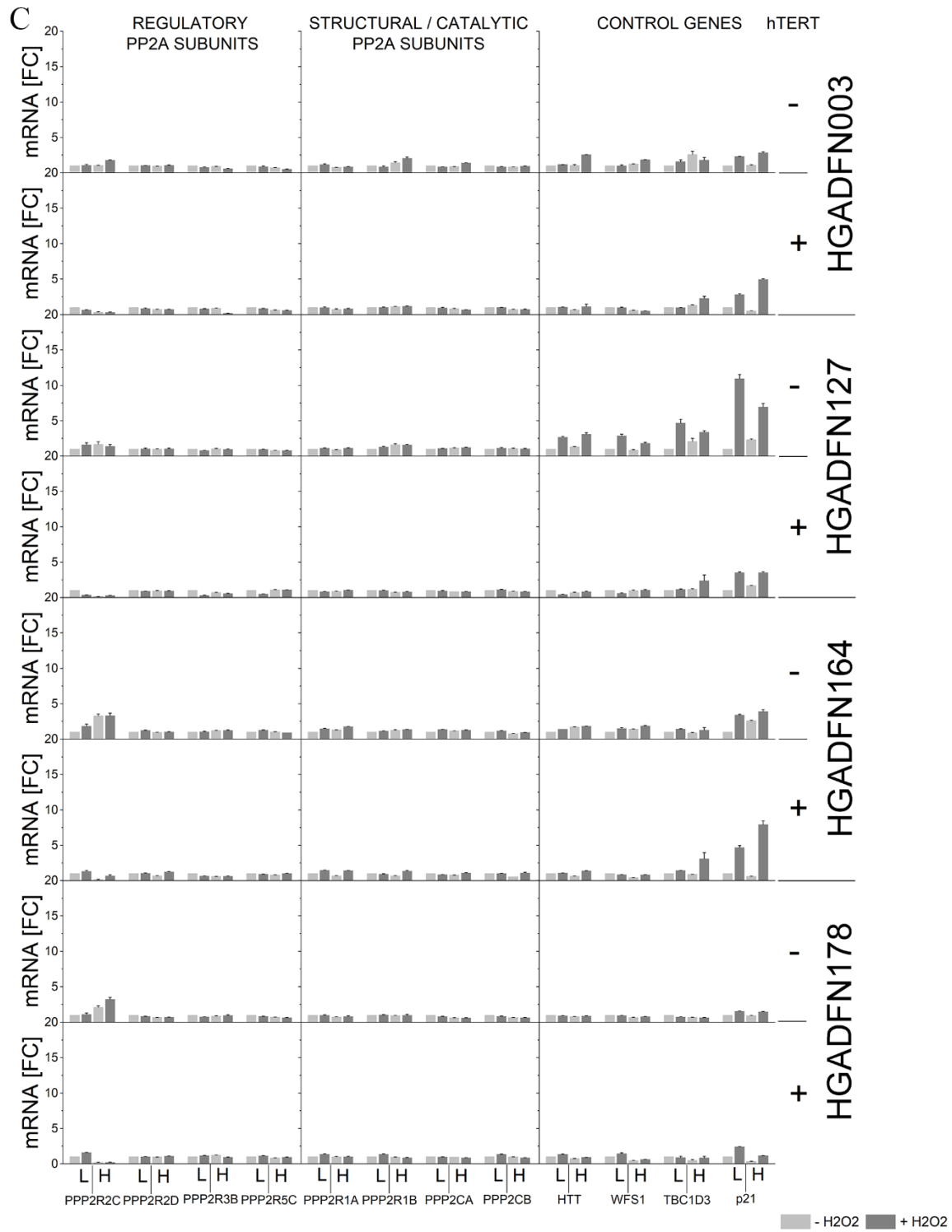


Fig. S7

Senescence associated- β -galactosidase as a marker for telomere length- and stress-dependent senescence. The number of senescence-associated β -galactosidase (SA- β -Gal)-positive cells (**A, C, E-H**) and the SA- β -Gal levels of cell extracts (measured fluorometrically as MUG) (**C, D**) were determined in primary and immortalized cells using two healthy control cell lines (light gray) and four HGP cell lines (gray) in the absence and presence of H₂O₂ (200 μ M, 2 h), as described in the Materials and Methods. (**E**), Representative SA- β -Gal staining of HGP cells (low PD) in the absence of H₂O₂. (**F**), Representative SA- β -Gal staining of HGP cells (high PD) in the absence of H₂O₂. (**G**), Representative SA- β -galactosidase staining of immortalized HGP cells (low PD) in the absence of H₂O₂. (**H**), Representative SA- β -Gal staining of immortalized HGP cells (high PD) in the absence of H₂O₂. L, low PD; H, high PD, as indicated. The percentages of SA - β -Gal-positive cells were ascertained by counting five visual fields under a light microscope at 50x magnification by two different individuals independently and blinded.

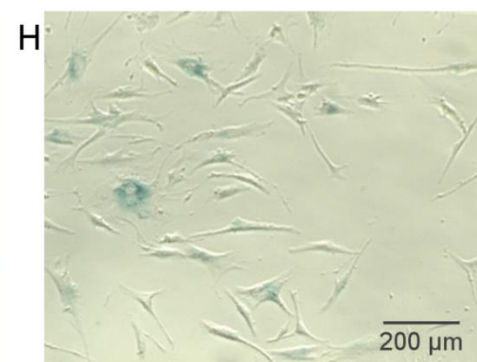
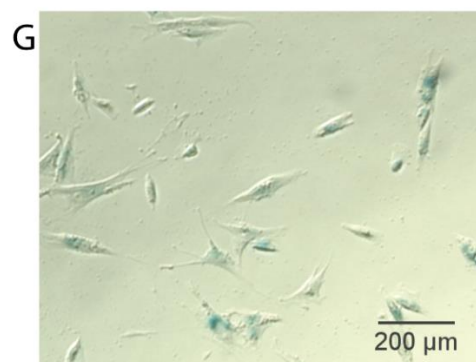
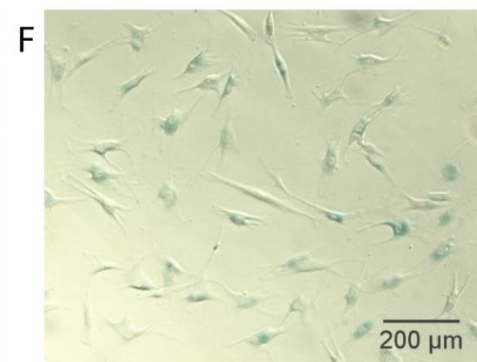
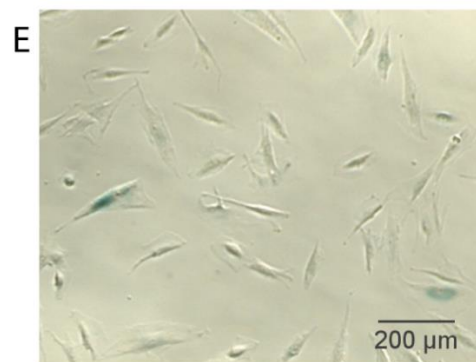
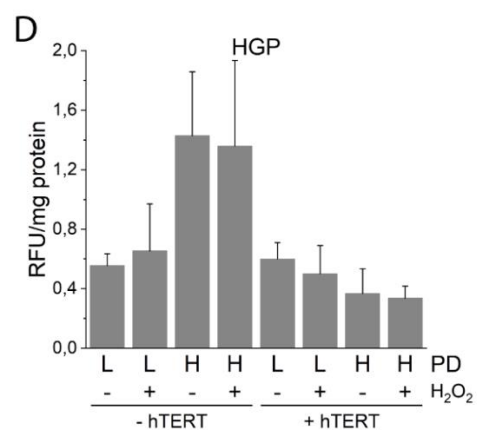
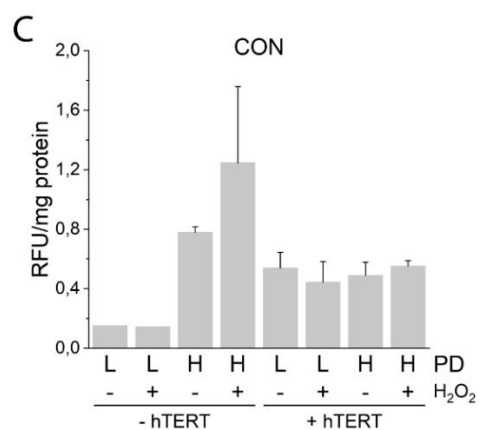
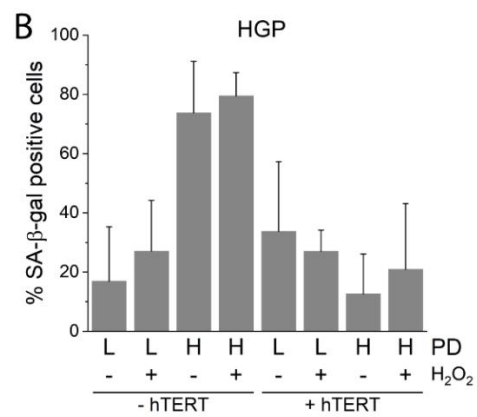
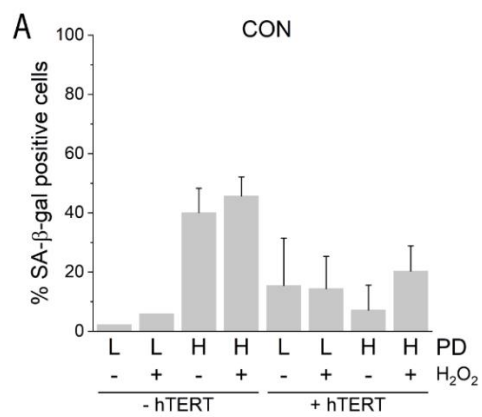
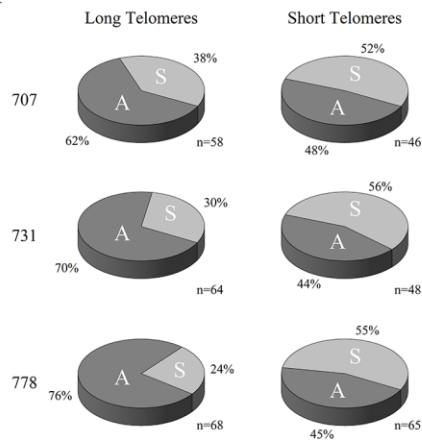


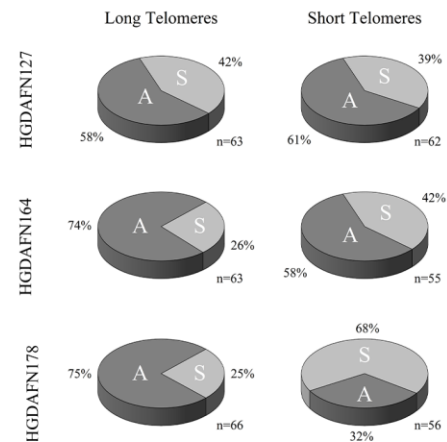
Fig. S8

Telomere length-dependent chromosomal reorganization of pre-senescent and *hTERT*-immortalized fibroblast cell lines. (A), Overall distribution of TEL-*PPP2R2C* probe distances for healthy control cells (n=208, 224, 266 for 707, 731 and 778). (B), Overall distribution of TEL-*PPP2R2C* probe distances for HGP cells (n=250, 236, 244 for HGADFN127, HGADFN164 and HGADFN176). The proportion of probe distances $\leq 2.26 \mu\text{m}$ and $> 2.26 \mu\text{m}$ are shown in circle diagrams. Adjacent (A) and separated (S) as indicated. (C), Stacked bar charts for all distances for all healthy controls (n=698) and all HGP cells (n=730), and the same data separated for the respective shortest and longest distances in each cell. The mean distances were stratified by cell lines and by immortalization status. Fibroblasts with short telomeres (-*hTERT*) show a shift to greater distances relative to cells with long telomeres (+*hTERT*); χ^2 test for trend, $p \leq 0.001$. The x-axis presents the deciles of distances from decile 1 = lowest 10% of distances to the highest decile, decile 10 = highest 10% of distances. (D), Pairwise (allele specific) TEL-*PPP2R2C* probe distances with the respective shortest and longest difference in each cell for CON (n=698) and HGP (n=730).

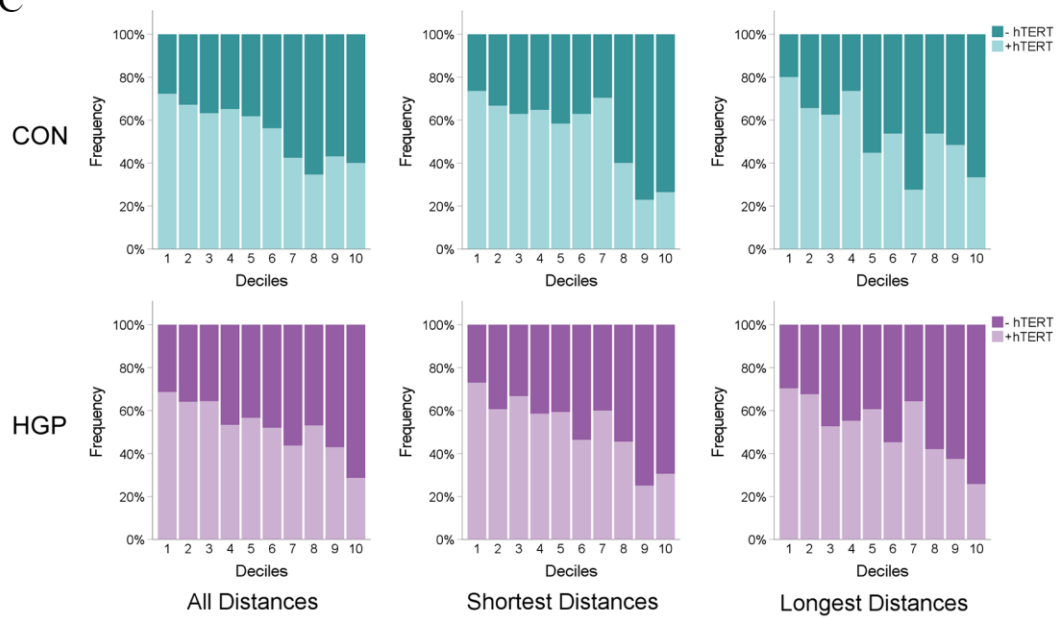
A



B



C



D

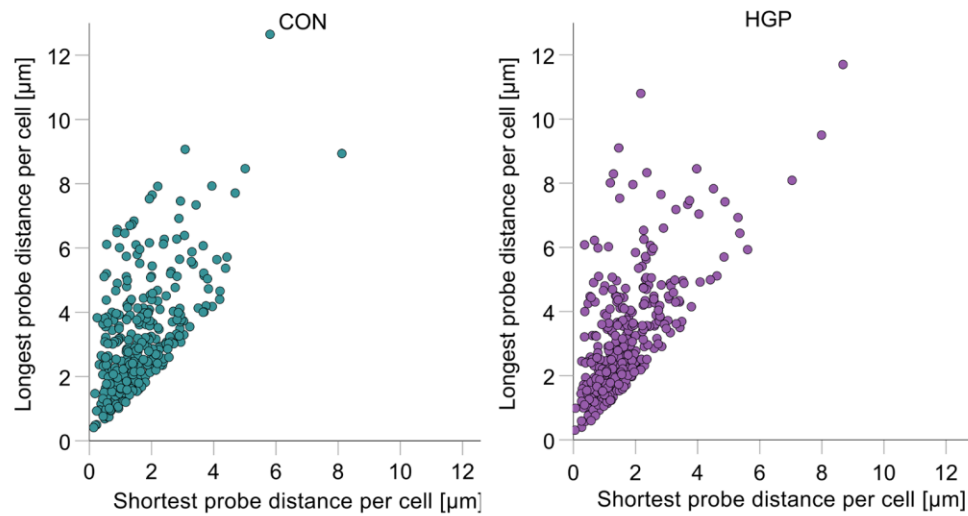


Fig. S9

Original data for all TEL-*PPP2R2C* probe distances for healthy controls and HGP cell lines. Distances were divided into deciles (0.7258 μm , 1.090 μm , 1.3442 μm , 1.606 μm , 1.93 μm , 2.28 μm , 2.773 μm , 3.49 μm , 4.451 μm) for graphical presentation. Horizontal lines indicate the bounds of deciles. The cut-off value for separation of A and S was 2.26 μm for all cell lines.

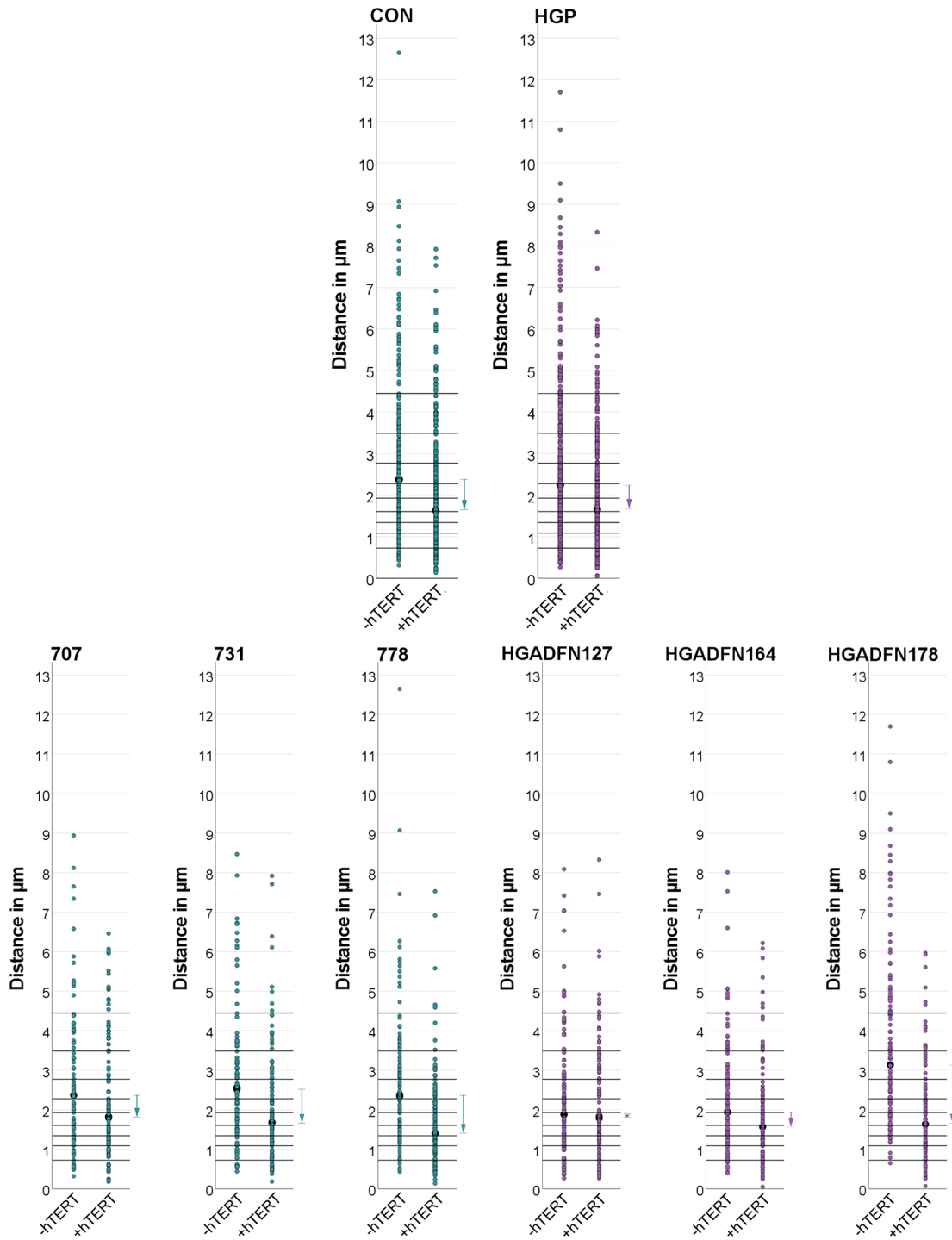


Fig. S10

Influence of chromatin modulators on *PPP2R2C* expression. Human fibroblasts were treated for the indicated time with the following: 1.) TSA at 0.2 $\mu\text{g/ml}$ (gray; n=3 cell lines, 3 technical replicates each), 5-AzaC at 1 $\mu\text{g/ml}$ (dark gray; n=3 cell lines, 3 technical replicates each), or both inhibitors (black); 2) resveratrol at a concentration of 0.25 μM (gray; n=3 cell lines, 3 technical replicates each), 1.0 μM (dark gray), or 10.0 μM (black); 3) 50 μM compound BCI-150 (dark gray) or the respective amounts of vehicle DMSO (light gray; all experiments n=3 cell lines, 3 technical replicates each). All values were normalized to the level (= 100%) of mRNA in primary cells (PD 13–17) in the absence of inhibitor. Each assay was performed in both biological and technical triplicates and is shown as the mean \pm SEM. The Mann-Whitney U test was used to assess statistical significance. * indicates $p < 0.05$ and ** $p \leq 0.01$. The experiment with compound BCI-150 was performed in technical triplicates for one cell line. *Cyclophilin A* was used as an internal normalization control. 11 of 288 measurements were excluded because of nondetectable mRNA.

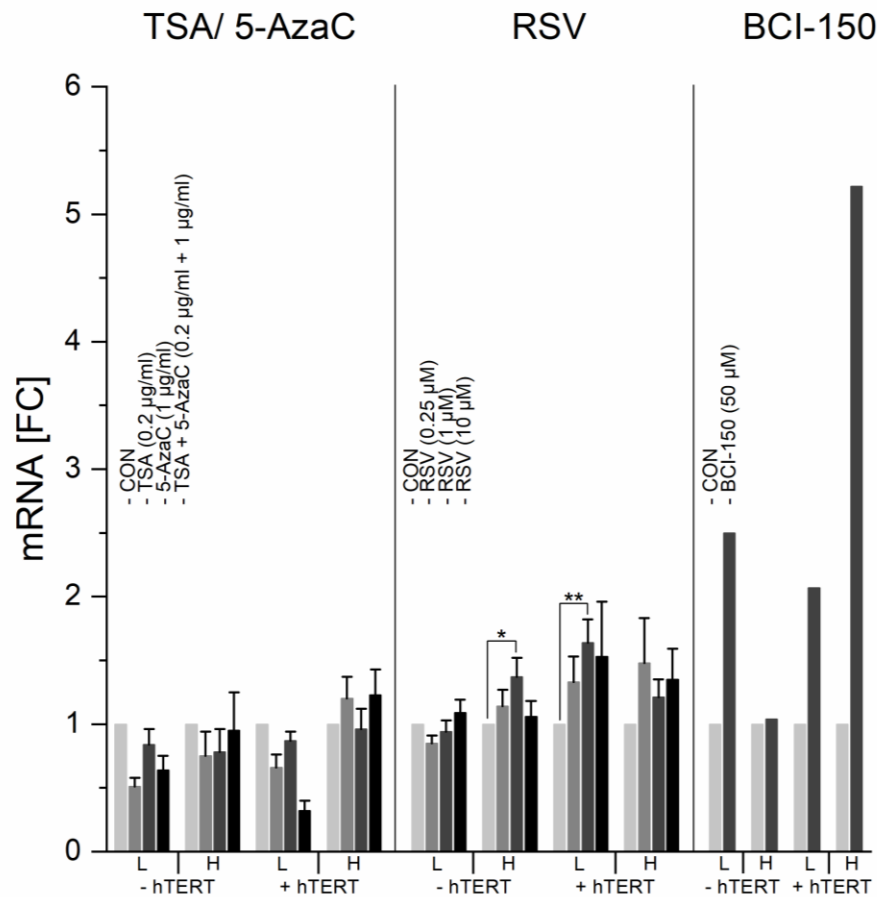
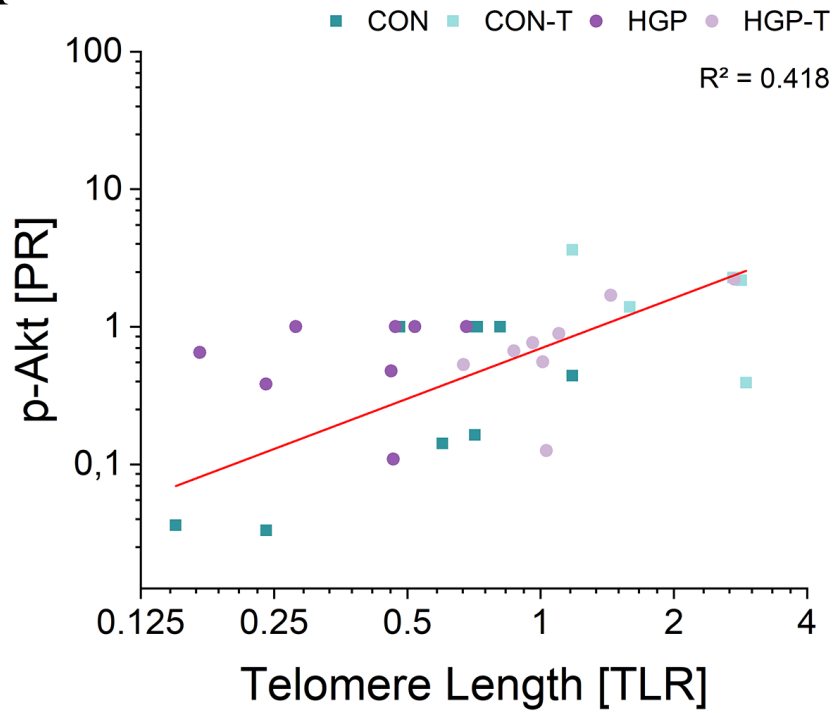


Fig. S11

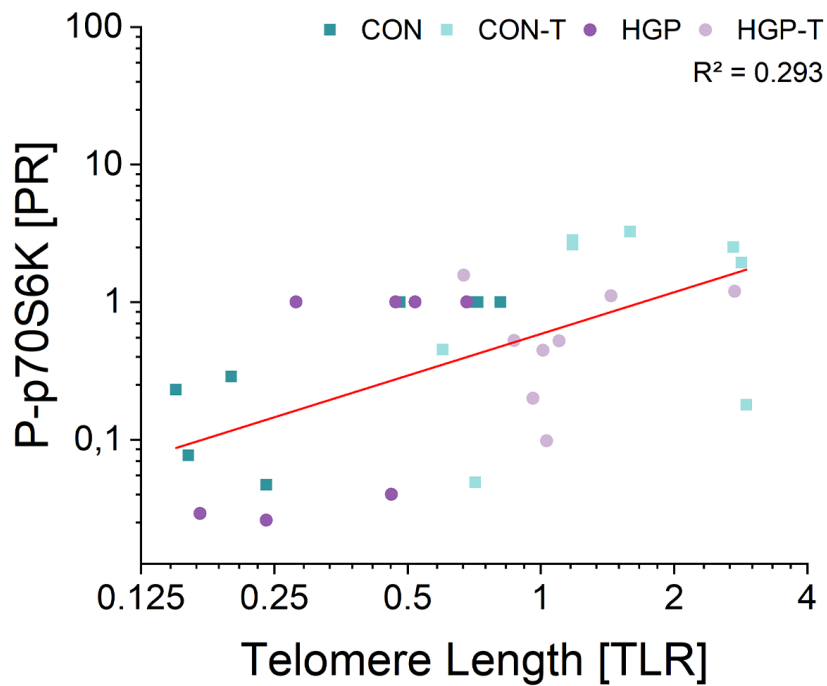
Correlation between TL and degree of phosphorylation of (A) Akt and (B) p70S6K.

All protein levels were normalized to the protein levels of β -actin. PR, protein ratio.

A



B



p70S6K dephosphorylation occurs independently of basal mTOR levels . The amount of cell protein is shown in relation to cell growth rates *in vitro*. Total protein levels of Akt, mTOR p70S6K and phosphorylated p70S6K are shown in relation to the slopes of the growth curves of control and progeria (HGP) cell lines before (-hTERT) and after *hTERT* immortalization (+hTERT) at low (L) and high (H) PDs. Data are derived from Fig 5 and Fig. S5 datasets. Relative protein levels were divided by the slope at the respective time of harvesting. To determine the growth rate, the slope between the last PD-datapoint before harvesting and the PD at time of harvesting was calculated. Despite 2-3-fold higher relative mTOR, p70S6K and AKT protein levels in pre-senescent HGP cells (HGP cells seem to have an inappropriately high mTOR tone in pre-senescence) the degree of phosphorylation of p70S6K was not enhanced but was rather further decreased (red arrow). Thus effects induced by PR55 γ in pre-senescence are not secondary due to reduced mTOR levels. By contrast, effective dephosphorylation of p70S6K may rather mitigate negative effects of inappropriately high mTOR tone in HGP cells.

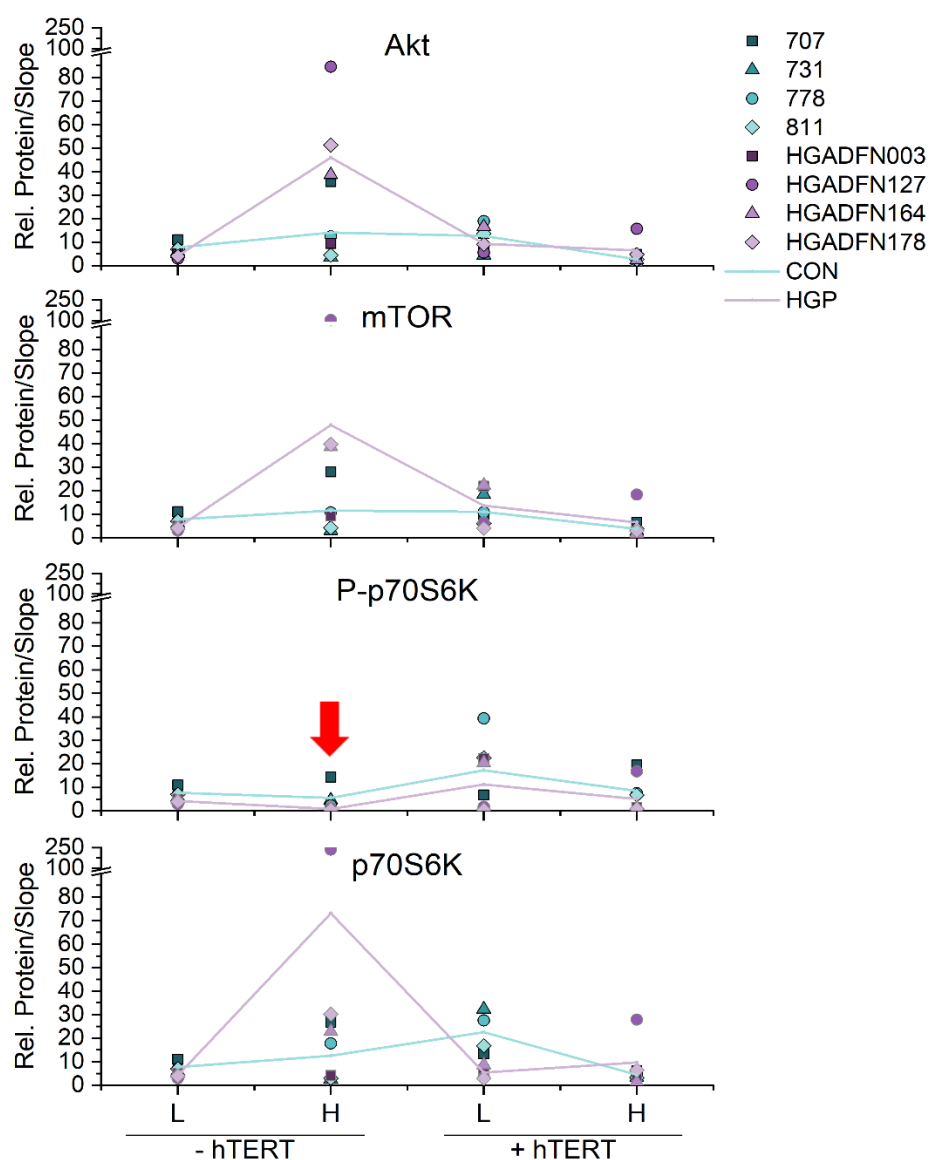


Fig. S13

Serum starvation is not a major determinant of p70S6K phosphorylation in aged fibroblasts *in vitro*. (A) Immunoblot analysis of total and phosphorylated p70S6K in immortalized control fibroblasts with long telomeres (L) and in aged control fibroblasts with short telomeres (S) without (-) or with (+) serum starvation, as described in Materials and Methods. The healthy control cell line 811 was used;. Attributable to artifacts in the Western blot densitometric analysis of protein signal was not possible, β -Actin was used as reference for input control. (B) qPCR analysis of the same healthy control cell line was performed once (with technical triplicates) for *mTOR* and *PPP2R2C* under identical conditions as in (A). *Cyclophilin A* was used as an internal normalization control.

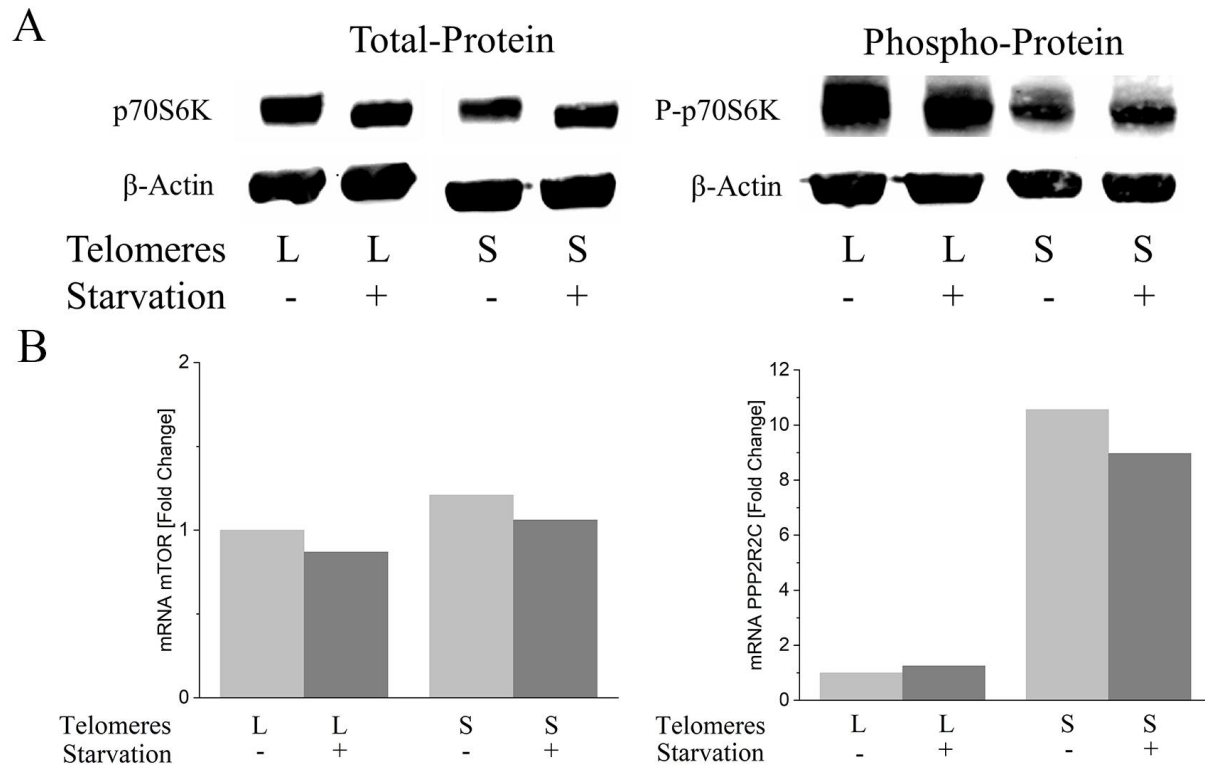


Fig. S14

Lack of metabolic suppression and cell stress in HGP fibroblasts. (A), Cellular levels of the senescence marker MUG (left panel) compared to the metabolic marker arylsulfatase A (activity in the middle panel and protein in the right panel), as shown for primary pre-senescent cells. The protein product and resulting activity of *ARSA*, which is regulated by mTOR and p70S6K and is strongly inhibited by the prototype mTOR inhibitor rapamycin, is not suppressed in pre-senescent HGP cells. Data show the mean values of three controls (707, 731, 811) and three HGP cell lines (HGADFN127, HGADFN164, HGADFN178). The Mann-Whitney *U* test was used to assess statistical significance. * indicates $p \leq 0.05$. **(B)**, Cell cycle distribution of healthy primary control cells (upper left), primary HGP cells (upper right), healthy control cells after hTERT immortalization (lower left), and HGP cells after hTERT immortalization (lower right), as described in Materials and Methods. G0/G1-phase (dark gray), S-phase (gray) and G2/M-phase (light gray). HGP cells had a higher percentage of cells in the G2/M phase and a lower percentage of cells in the S phase, which is typical for high proliferation stress. The *ARSA* activity levels were not increased in young HGP fibroblasts (low PDs) and were not increased in hTERT immortalized cells.

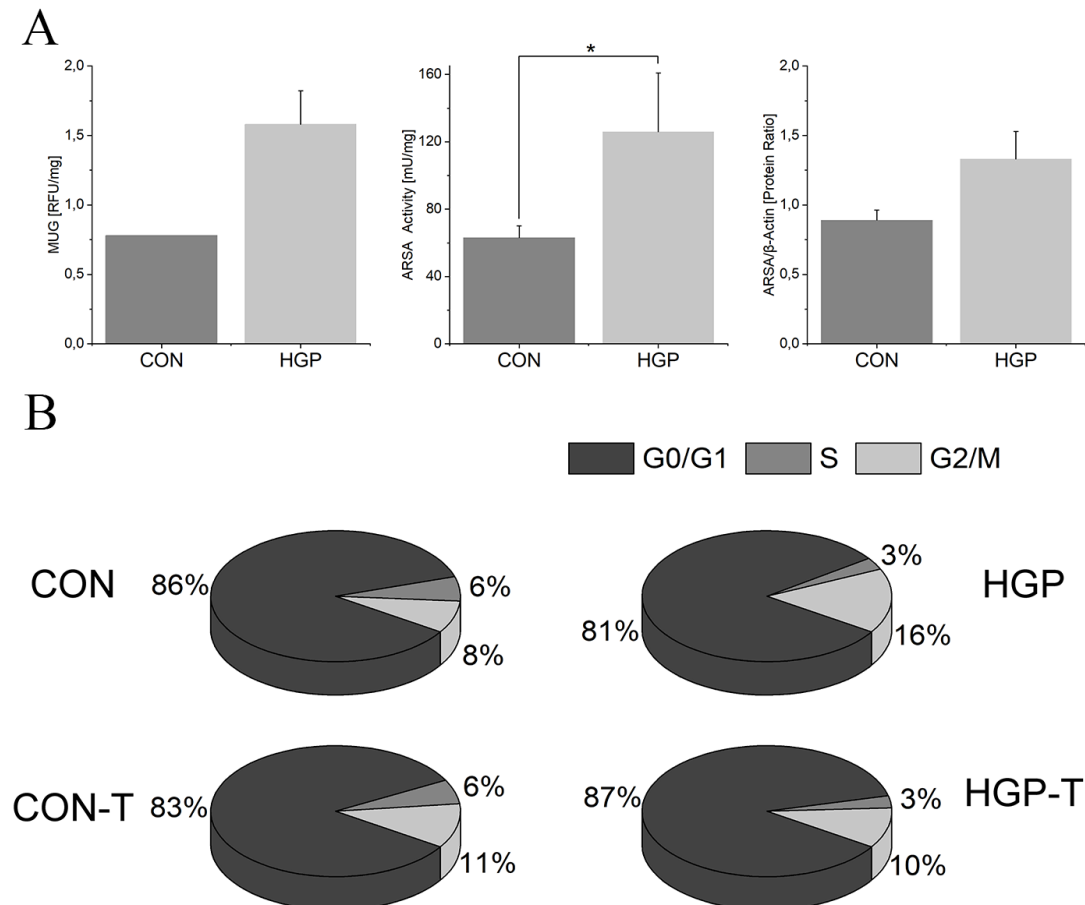
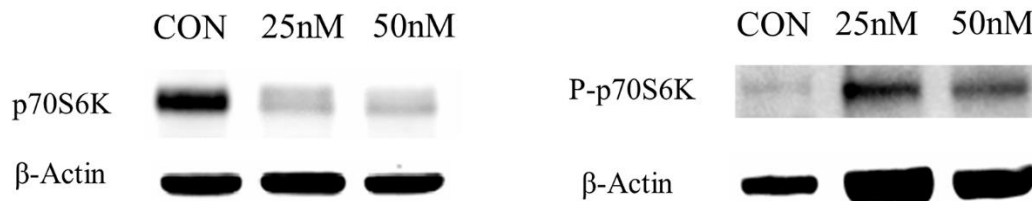


Fig. S15

***PPP2R2C* knock down by siRNA and induction of protein synthesis (A)**, Western blot analysis: effects of *PPP2R2C* knock down via siRNA in fibroblasts derived from a HGP affected individual. Depicted levels of total and phosphorylated p70S6K protein without and with siRNA treatments in two different concentrations. β -actin serves as a loading control. For densitometric illustration of blots β -actin was used as reference for input control. PR, protein ratio (B) mRNA levels of genes whose transcription is likely under control of p70S6K. *Cyclophilin A* was used as an internal normalization control. All values were normalized to the level (=100%) of mRNA in untreated cells (CON). For each gene the significance was calculated against the control (CON) of this gene. Assay was performed in duplicate using technical triplicates (total of six measurements). Data are shown as the mean \pm SD. The Mann-Whitney U test was employed to assess statistical significance. * indicates $p < 0.05$ and ** $p \leq 0.01$.

A



B

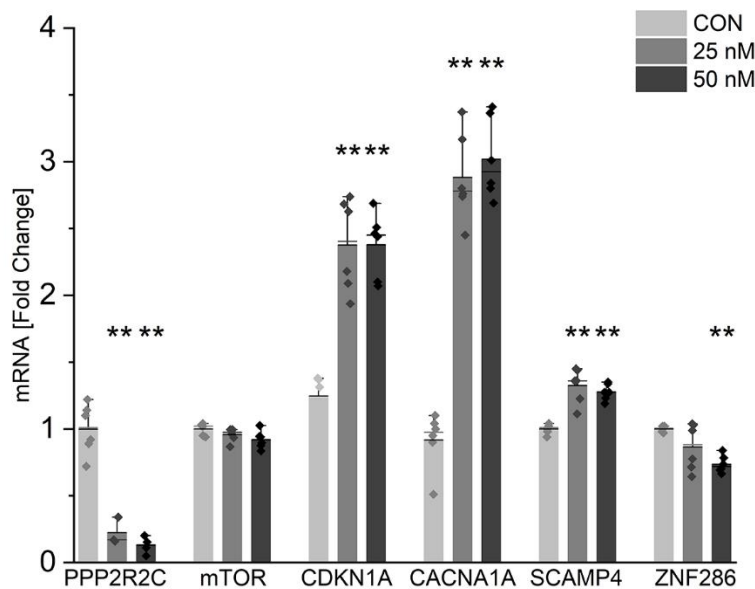


Fig. S16

Cell proliferation in control and HGP fibroblasts. First derivatives of growth curves of control and progeria cell lines before (bold line) and after *hTERT* immortalization (faint line). Progeria cell lines show a faster proliferation rate with an earlier stop of cell growth compared to healthy control cell lines. No smoothing was applied. CON, healthy controls; HGP, Hutchinson-Gilford progeria cells.

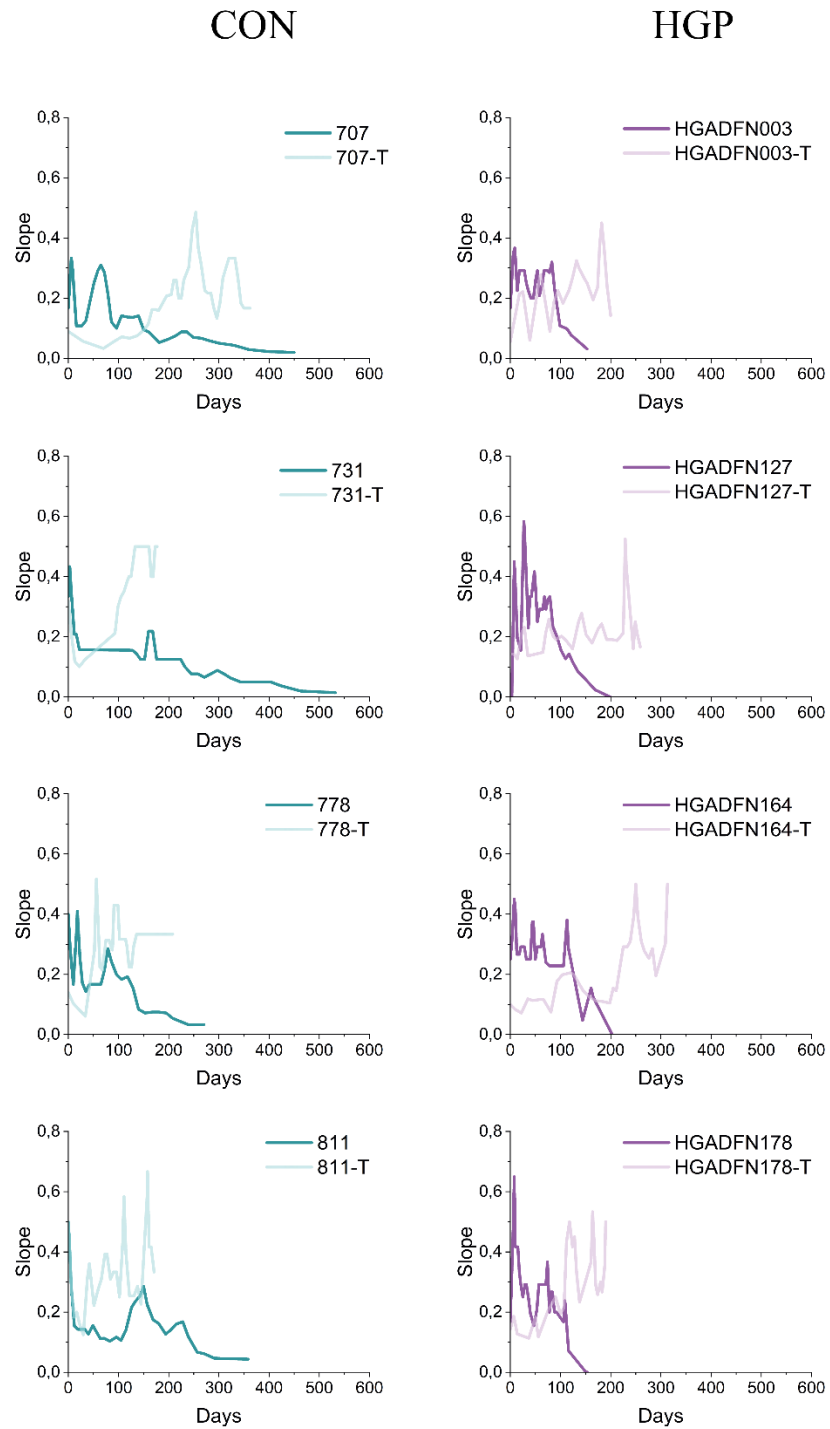


Fig. S17

Amount of *PPP2R2C* mRNA in lymphoblastoid cells (LCLs) from participants of the BASE-II correlated with telomere length, as measured by monochrome multiplex qPCR, which is described in the Materials and Methods section. All values are normalized to the level (=100%) of mRNA of the median of the TL. Data are shown for 413 LCLs (each analyzed in technical triplicates).

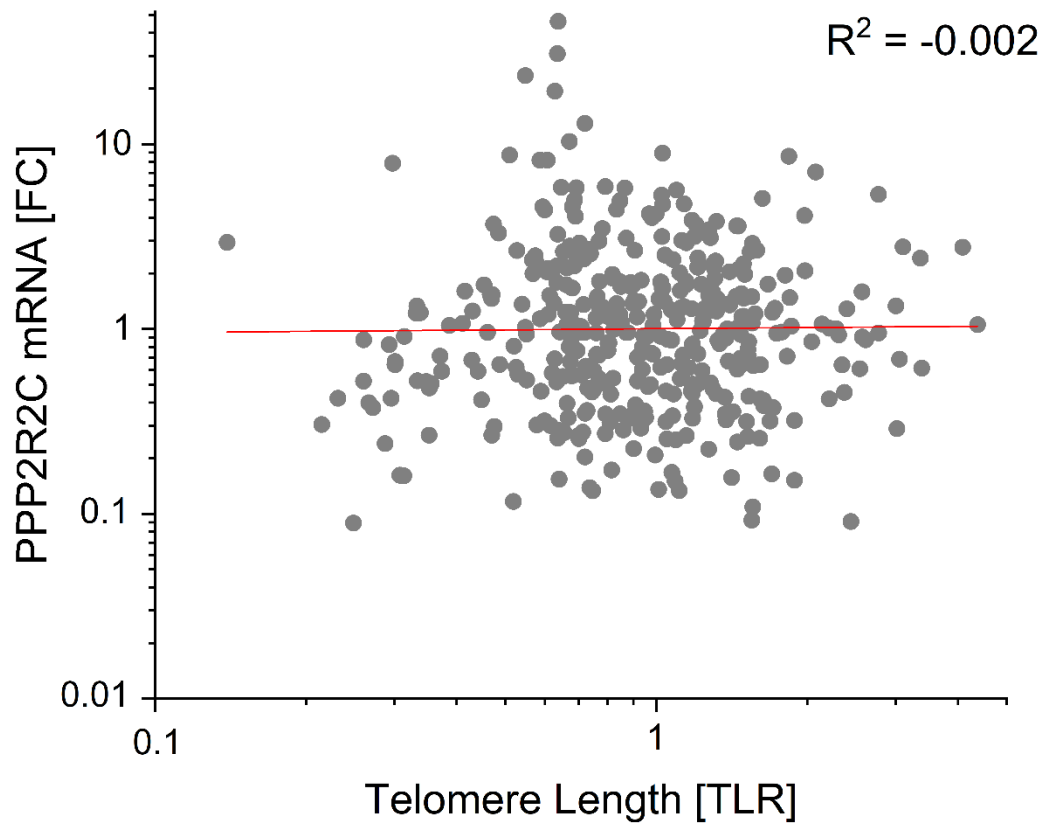


Fig. S18

mRNA levels of the four PPP TPE-OLD candidates and all confirmed TPE-OLD genes in LCLs and HUVECs with long and short telomeres. qPCR analysis was performed under basal conditions (10% FCS), in cells with long telomeres (low PDs in HUVECs) and in cells with short telomeres (high PDs in HUVECs). TL was measured by monochrome multiplex qPCR, as previously described. *Cyclophilin A* was used as an internal normalization control. All values were normalized to the level (=100%) of mRNA in cells with long telomeres. P-values indicate significance of the difference for assays done in duplicate using technical triplicates (total of six measurements). Data are shown as the mean \pm SD, the mean and median are shown. The Mann-Whitney U test was employed to assess statistical significance. * indicates $p < 0.05$ and ** $p \leq 0.01$ for an increase relative to low PD/long telomeres; # indicates $p < 0.05$ and ## $p \leq 0.01$ for a decrease relative to low PD/long telomeres (**A**) Overall summarized data shown for LCLs (**B**) Overall summarized data shown for HUVECs. For HUVECs the TL was measured in technical triplicates, the average of the three measurements (performed on different days) was used to report the mean TL.

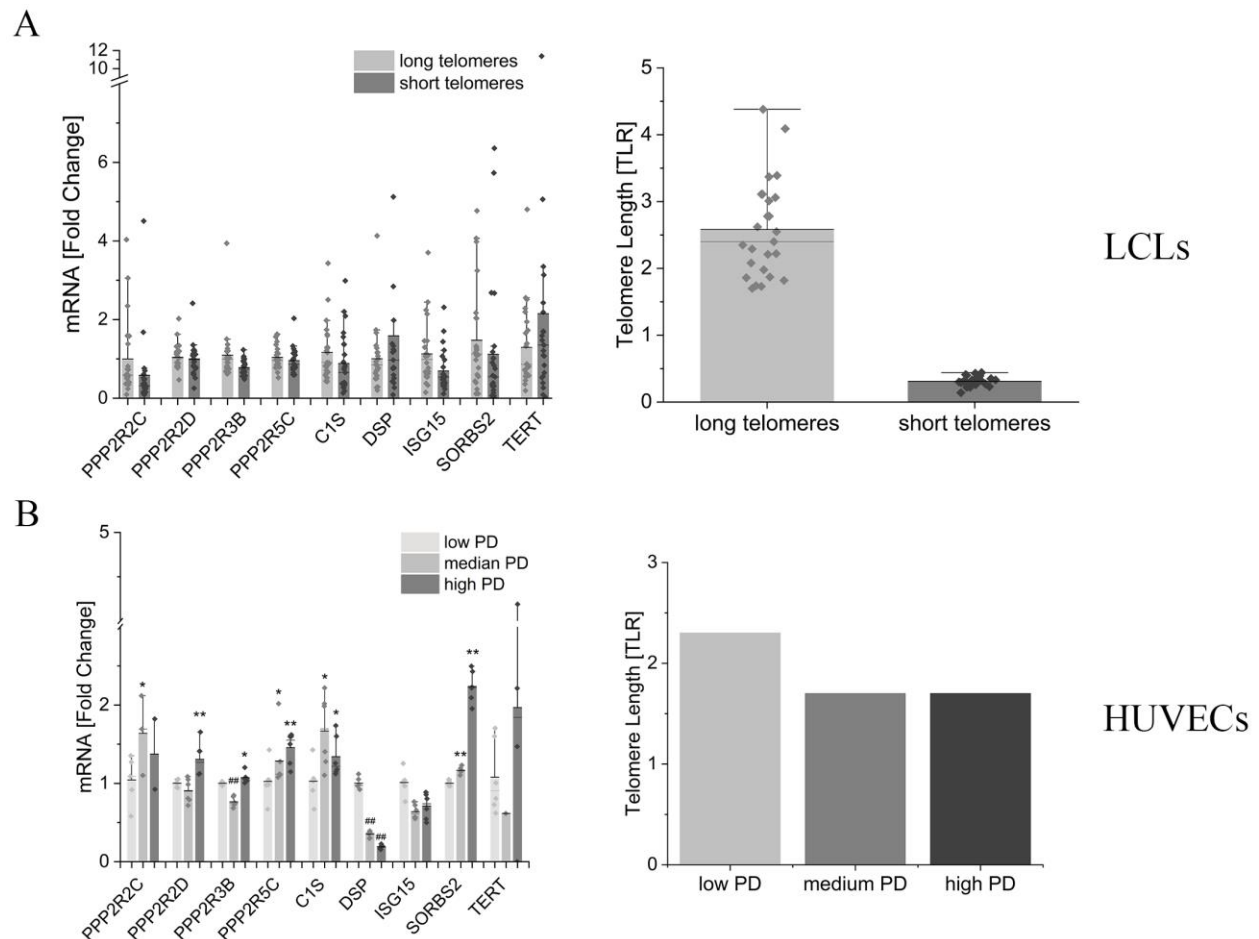
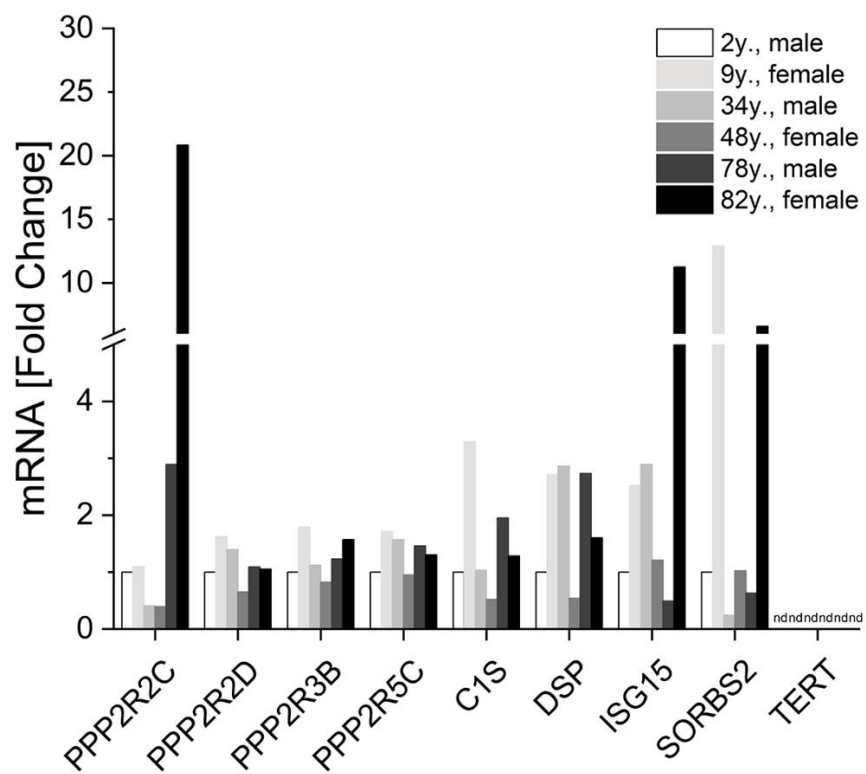


Fig. S19

mRNA levels of *PPP2R2C* in fibroblasts derived from cell donors of different ages. qPCR analysis was performed under basal conditions (10% FCS), in cells with long telomeres and in cells with short telomeres from donors of different ages. *Cyclophilin A* was used as an internal normalization control. All values were normalized to the level (=100%) of mRNA in cells with long telomeres. All assays were done twice and are shown as mean of technical triplicates **(A)**, qPCR data derived from samples of an array expression experiment (A. Herman group). Cells were harvested at high PDs >35. **(B)**, Data derived from samples of an independent experiment (M. Walter group) of different cell donors derived from children and one middle-aged woman (cell line N14 in Table S7). Cells were harvested at both low PD and high PDs. *Cyclophilin A* was used as an internal normalization control. All values were normalized to the level (=100%) of mRNA in cells with long telomeres. n.d., not detectable

A



B

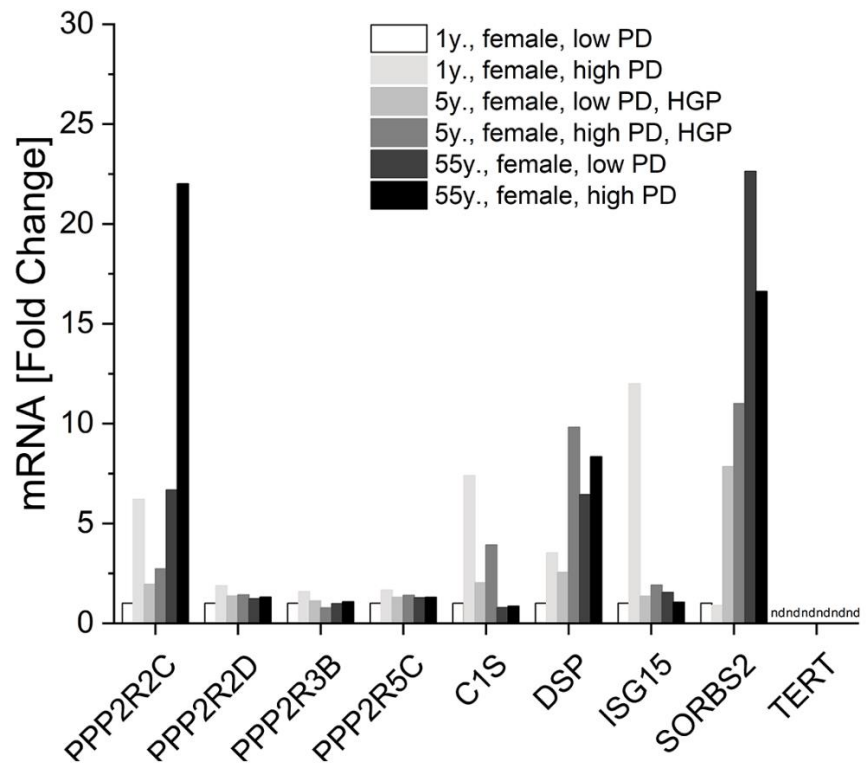


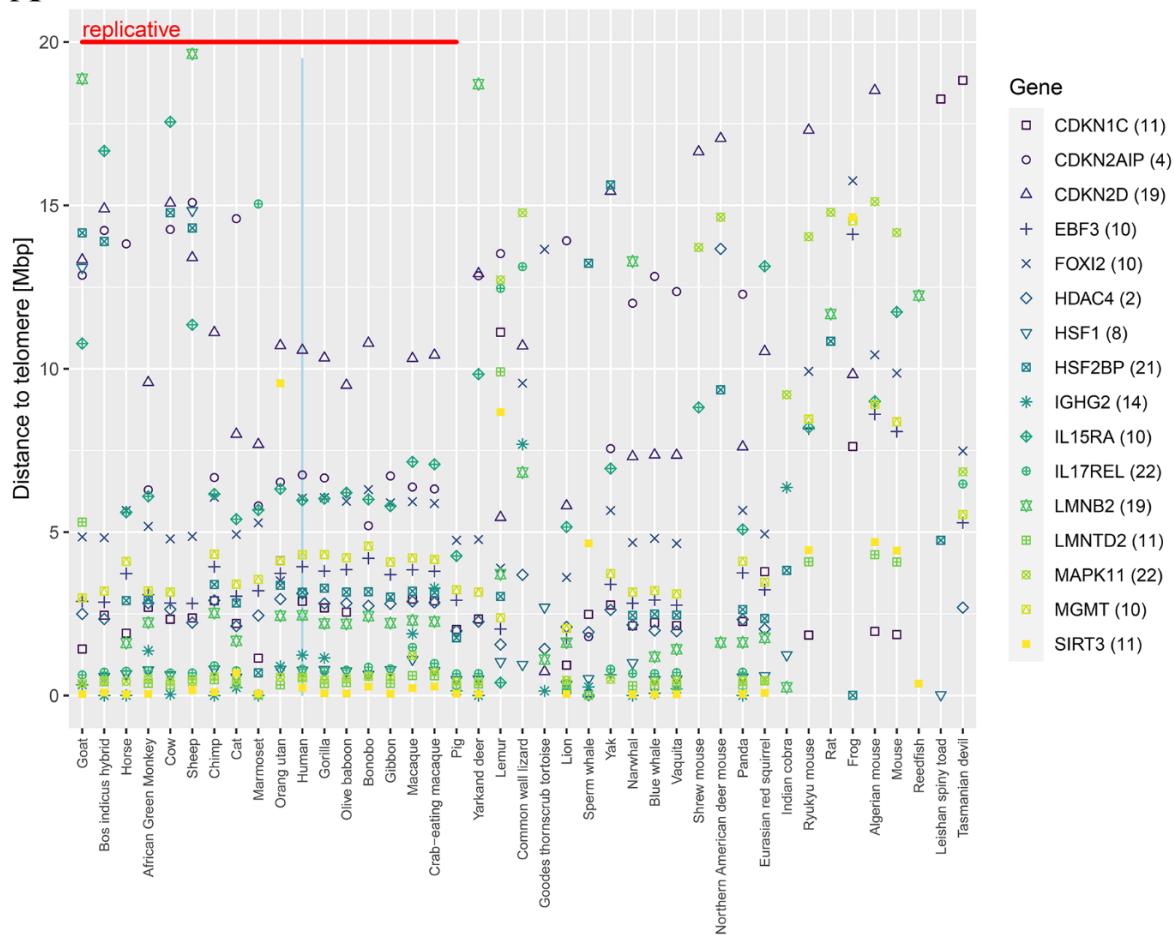
Fig. S20

Selected genes and gene families sorted by species and distance to telomeres:

Telomeric distances for TPE-OLD candidate genes. The figure shows the distance to the closest telomere in Mb for selected TPE-OLD candidate genes. Genes are distinguished by their symbol, supported by color. Species are separated horizontally, sorted by the median distance to telomeres for all genes in the genome. Species proposed to age replicatively are grouped on the left. Telomeric distances among TPE-OLD genes are preserved across species such that these appear as horizontal lines on the left. The number in parentheses behind the gene name indicates the human chromosome coding for that gene.

(A) TPE-OLD candidate genes often code for factors involved in cell cycle regulation, tumor suppression, stress response, immune defense and metabolic regulation. Examples for TPE-OLD candidates are tumor suppressor genes (*EBF*, *CDKN1C*, *CDKN2D*), stress response genes and metabolic regulators (*HSF1*, *MAPK11*, *FOXI2*), regulators of epigenetic silencing (*SIRT3*, *HDAC4*), DNA damage response genes (*HSF2BP*, *MGMT*, *CDKN2AIP*), defense response genes (*IL17REL*, *IL15RA*, *IGHG2*) but also genes coding for proteins whose expression increases or declines during aging for unknown reasons such as some coagulation factors or lamins (*LMNB2*). Within the respective gene group, only individual members are TPE-OLD candidates. Some gene families seem to have no TPE-OLD genes at all such as *HOX* (B) and *NF- κ B* (C).

A



B

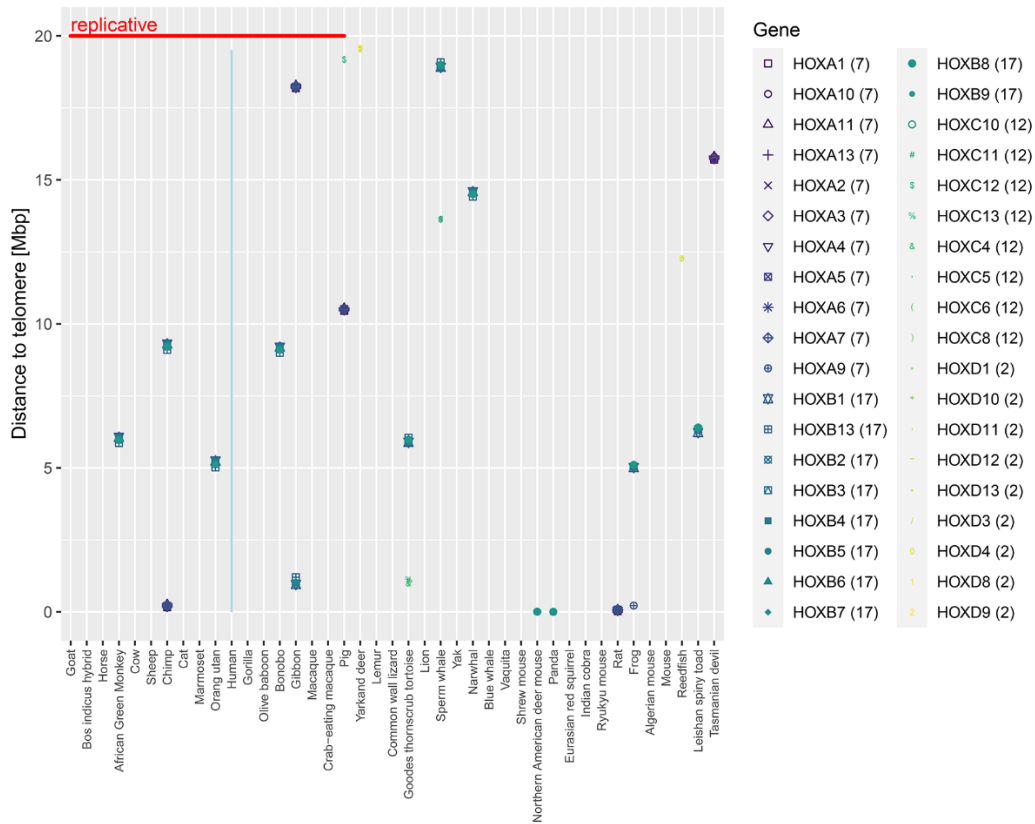
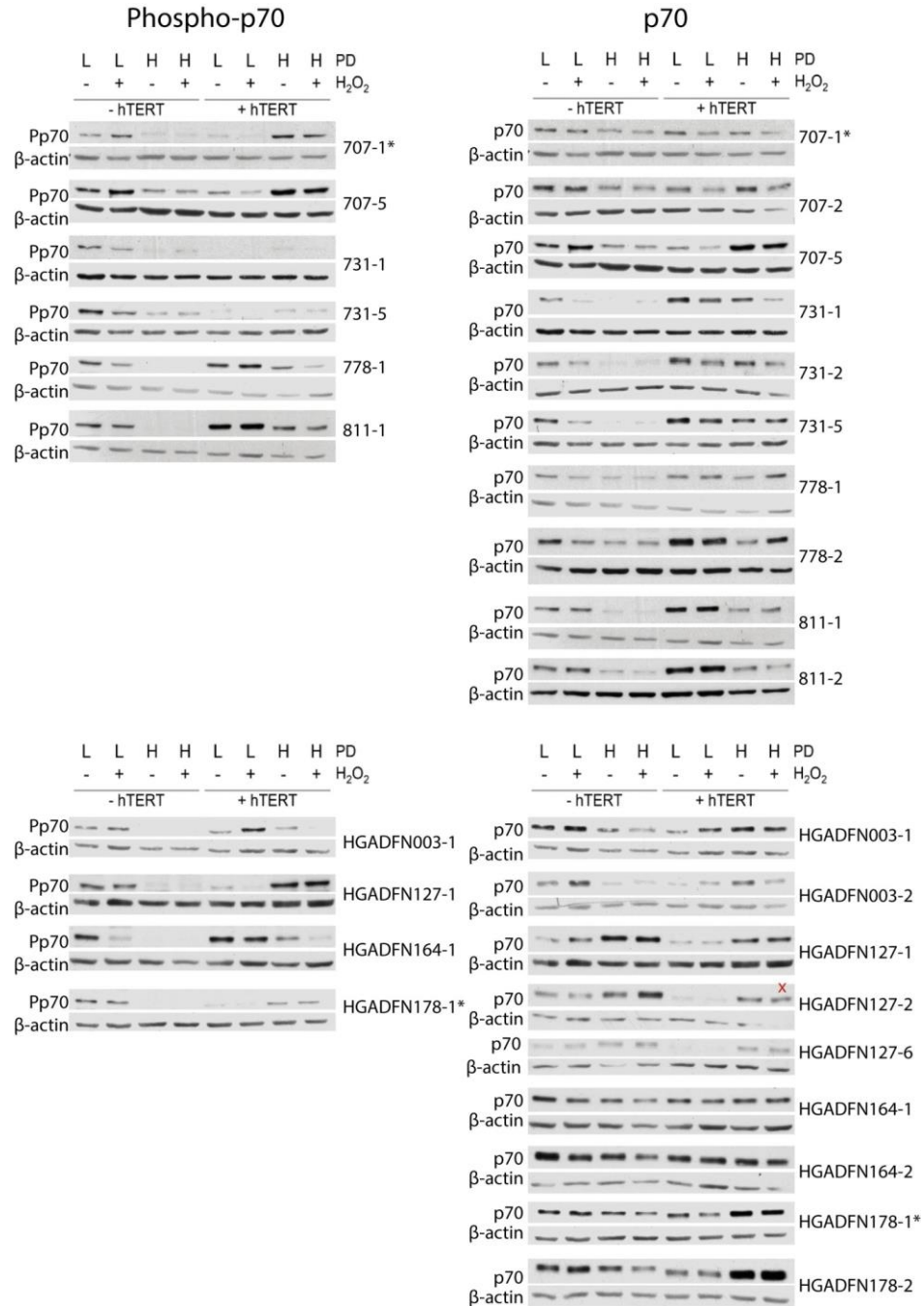
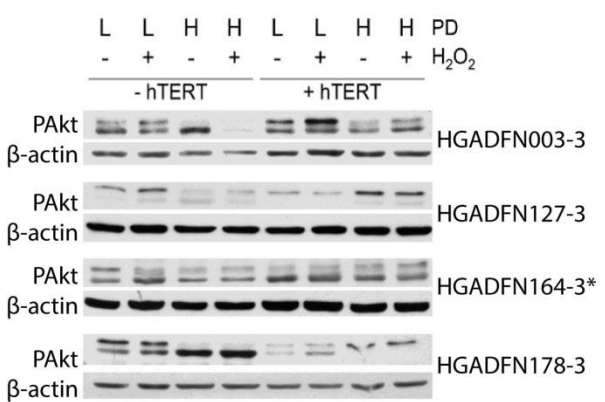
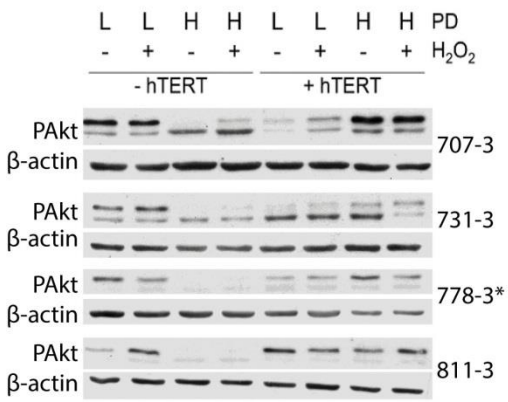


Fig. S21

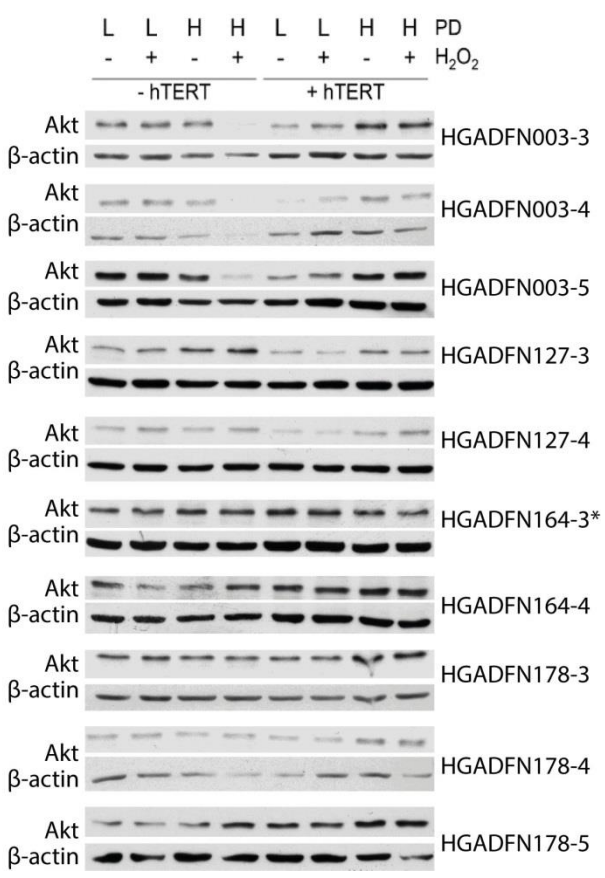
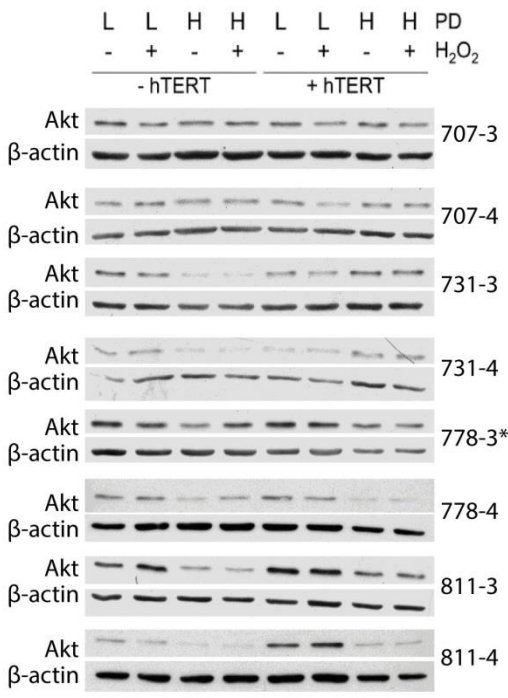
Original Western blot data. Original Western blots of Fig. 5. *Indicates the blots shown for Fig. 5a-c. The blots (per cell line) are numbered according to their order of preparation. Blots with the same cell line and number were incubated with different antibodies. Red crosses indicate single lanes that were excluded from analysis because of loss of sample due to edge effects.



Phospho-Akt



Akt



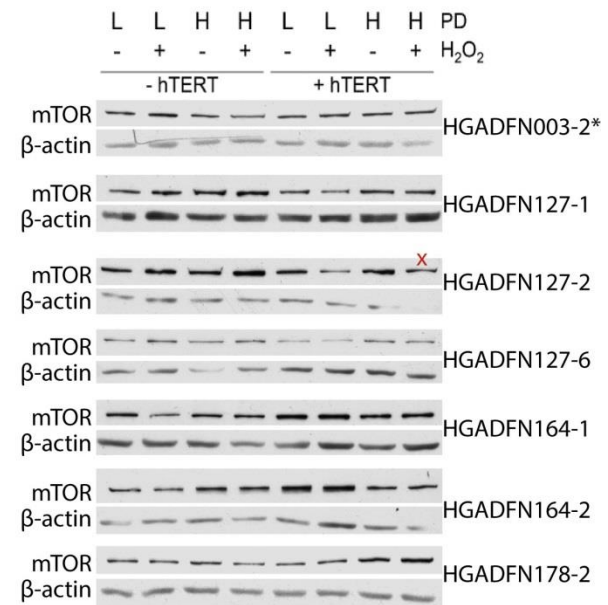
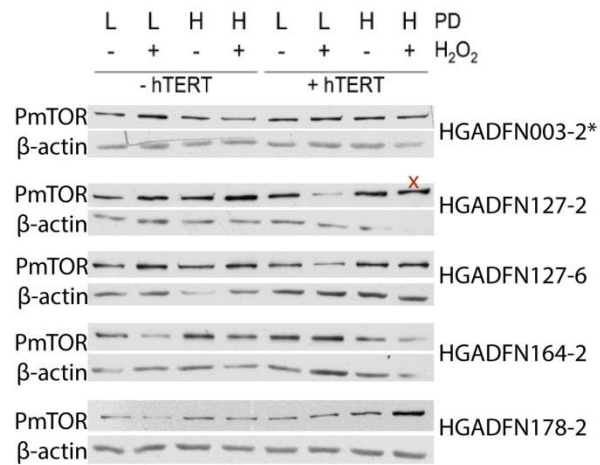
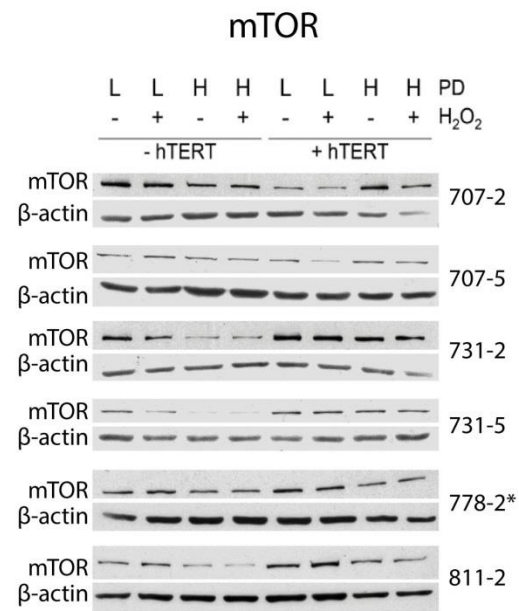
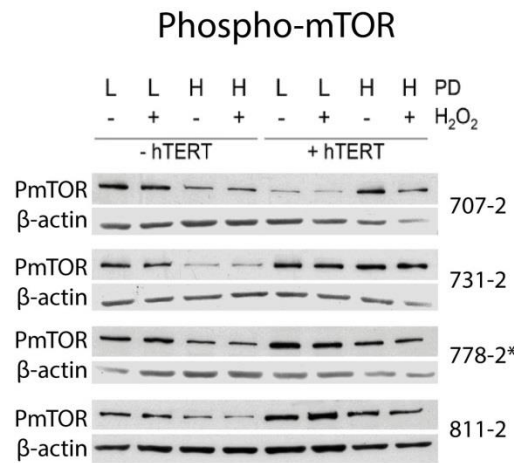


Fig. S22

Original Western blot data. Original Western blots of Figs. S13 and S15. **(A)** Serum starvation indicated with + or – sampled for cells with short telomeres (S) and long telomeres (L). **(B)** Original data for the *PPP2R2C* siRNA experiment: effect on p70S6K and P-p70S6K with different siRNA concentrations.

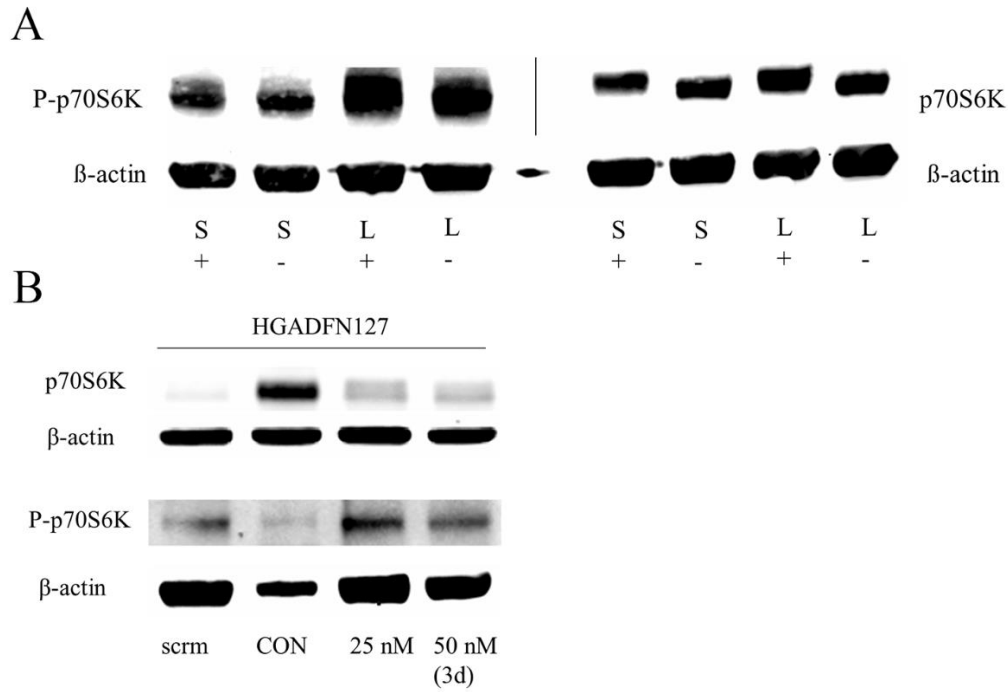


Table S1.

Regulation of gene expression with progressive telomere shortening in established and new TPE-OLD candidates. Green color, previously known or suggested TPE-OLD genes; dark green; TPE effect additionally confirmed by FISH; blue color, members of the phosphatase (PP2A) family investigated in this study

	Myoblasts¹	Fibroblasts^{1,2}	LCL	HUVEC
AKAP3	↑	n/a	n/a	n/a
ANO2	↑	n/a	n/a	n/a
C1S	↑	↑	~	↑
CCND2	↑	↑	n/a	n/a
CD163L1	↑	n/a	n/a	n/a
CD9	↓	n/a	n/a	n/a
DSP	↑	↑	~	↓
FOXM1	↓	n/a	n/a	n/a
GALNT8	↑	n/a	n/a	n/a
ISG15	↑	↑	~	~
NDUFA9	↑	n/a	n/a	n/a
SORBS2	(↑)	n/a	n/a	↑
TEAD4	↓	↓	n/a	n/a
TERT	n/a	(↑)	~	~
TIGAR	↑	n/a	n/a	n/a
TSPAN9	↑	n/a	n/a	n/a
PPP2R2C	n/a	↑	~	↑
PPP2R2D	n/a	~	~	↑
PPP2R3B	n/a	~	~	~
PPP2R5C	n/a	~	~	↑


n/a, no data available; ↑, higher expression in cells with short telomeres; ↓, lower expression in cells with short telomeres; ~, no significant change or inconclusive results; brackets, detectable in pathogenic context only (SORBS2) or for not full-length mRNA (TERT); 1, from references Robin et al. (SORBS2) (9), Robin et al. (all others) (10); 2, from references Kim et al. (TERT) (12); Lou et al (ISG15) (11).

Table S2: Ranking of TPE-OLD candidate genes. This table presents all 2322 genes that are TPE-OLD candidate genes, ranked by the number of orthologues that are at the same telomeric distance. The first two columns (x and y) provide the mean of the telomeric distances of the two 1 Mb-wide chromosomal regions that contain most of the orthologues. The columns num.x and num.y show the respective number of orthologues covered by that region and num.xy is the sum of these two, by which the gene is ranked. The next column indicates the human chromosome on which the gene is located and the last column indicates the name of the gene.


Table S2 is available as an excel file at: <https://doi.org/10.5281/zenodo.6477501>

Table S3.**Gene set enrichment analysis of all TPE-OLD candidate genes with g:Profiler**

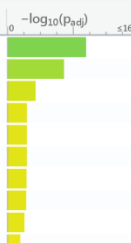
Genes from Table S1 were entered into g:Profiler (19, 20); p values are color-coded from yellow (insignificant) to blue (highly significant).

GO:MF		stats			
Term name	Term ID	P _{adj}		-log ₁₀ (P _{adj})	Show evidence codes
arylsulfatase activity	GO:0004065	2.020×10 ⁻²			
protein binding	GO:0005515	2.315×10 ⁻²			
sulfuric ester hydrolase activity	GO:0008484	4.509×10 ⁻²			


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GO:BP		stats			
Term name	Term ID	P _{adj}		-log ₁₀ (P _{adj})	Show evidence codes
cellular metabolic process	GO:0044237	8.043×10 ⁻³			
metabolic process	GO:0008152	2.237×10 ⁻²			

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GO:CC		stats			
Term name	Term ID	P _{adj}		-log ₁₀ (P _{adj})	Show evidence codes
cytoplasm	GO:0005737	2.164×10 ⁻¹⁰			
intracellular anatomical structure	GO:0005622	1.119×10 ⁻⁷			
membrane-bounded organelle	GO:0043227	3.605×10 ⁻⁴			
intracellular organelle lumen	GO:0070013	4.534×10 ⁻³			
organelle lumen	GO:0043233	4.534×10 ⁻³			
membrane-enclosed lumen	GO:0031974	4.534×10 ⁻³			
intracellular membrane-bounded organelle	GO:0043231	4.978×10 ⁻³			
organelle	GO:0043226	5.650×10 ⁻³			
cytosol	GO:0005829	9.236×10 ⁻³			
intracellular organelle	GO:0043229	3.040×10 ⁻²			

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KEGG		stats			
Term name	Term ID	P _{adj}		-log ₁₀ (P _{adj})	Show evidence codes
Metabolic pathways	KEGG:01100	2.467×10 ⁻³			
Thermogenesis	KEGG:04714	4.447×10 ⁻³			
Diabetic cardiomyopathy	KEGG:05415	1.633×10 ⁻²			

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REAC		stats			
Term name	Term ID	P _{adj}	$-\log_{10}(P_{adj})$	≤16	Show evidence codes
Gamma carboxylation, hypusine formation and arylsulfatase...	REAC:R-HSA-16...	3.379×10^{-3}			

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MIRNA		stats			
Term name	Term ID	P _{adj}	$-\log_{10}(P_{adj})$	≤16	Show evidence codes
hsa-miR-331-3p	MIRNA:hsa-miR...	2.184×10^{-3}			
hsa-miR-6791-5p	MIRNA:hsa-miR...	1.554×10^{-2}			
hsa-miR-106b-3p	MIRNA:hsa-miR...	2.118×10^{-2}			
hsa-miR-615-3p	MIRNA:hsa-miR...	2.258×10^{-2}			

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HPA		stats			
Term name	Term ID	P _{adj}	$-\log_{10}(P_{adj})$	≤16	Show evidence codes
bronchus	HPA:0060000	1.601×10^{-2}			
placenta; decidual cells[≥Low]	HPA:0380511	4.132×10^{-2}			

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CORUM		stats			
Term name	Term ID	P _{adj}	$-\log_{10}(P_{adj})$	≤16	Show evidence codes
CtBP complex	CORUM:642	1.218×10^{-2}			

1 to 1 of 1 |< < Page 1 of 1 > >|

HP		stats			
Term name	Term ID	P _{adj}	$-\log_{10}(P_{adj})$	≤16	Show evidence codes
Mitochondrial inheritance	HP:0001427	5.562×10^{-6}			
Ventricular preexcitation	HP:0004309	1.289×10^{-4}			
Centrocecal scotoma	HP:0000576	2.278×10^{-3}			
Diffuse cerebral atrophy	HP:0002506	3.105×10^{-3}			
Leber optic atrophy	HP:0001112	4.145×10^{-3}			
Wolff-Parkinson-White syndrome	HP:0001716	6.781×10^{-3}			
Ragged-red muscle fibers	HP:0003200	7.181×10^{-3}			
Central retinal vessel vascular tortuosity	HP:0007768	1.348×10^{-2}			
Retinal arterial tortuosity	HP:0000631	1.348×10^{-2}			
Postural tremor	HP:0002174	2.490×10^{-2}			
Mitochondrial respiratory chain defects	HP:0200125	3.118×10^{-2}			
Impaired visuospatial constructive cognition	HP:0010794	3.579×10^{-2}			
Stroke-like episode	HP:0002401	3.607×10^{-2}			
Slow decrease in visual acuity	HP:0007924	3.724×10^{-2}			

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TF	stats				
Term name	Term ID	Pval	$-\log_{10}(P_{adj})$	Show evidence codes	
Factor AP2 motif: GGCYGGGGN; match class: 1	TFM00867.1	3.22e-10 ⁷⁵			
Factor Churchill motif: CGGGNN; match class: 1	TFM00866.1	3.19e-10 ⁶⁸			
Factor AP-Zalpha motif: NGCCYNNGGN	TFM00857	1.407-10 ⁶⁹			
Factor AP-Zalpha motif: NSCCYNNGGN; match class: 1	TFM00857.1	7.013-10 ⁶⁷			
Factor AP-2 motif: SNNNCCNCCAGCGN; match class: 1	TFM00905.1	1.113-10 ⁶⁷			
Factor Kato motif: GCAGGGGCGGSG; match class: 1	TFM00876.1	2.773-10 ⁶⁷			
Factor AP-Jagamma motif: GCYNNNGG	TFM00430	4.407-10 ⁶⁴			
Factor AP-2 motif: GGCSCRCGGCNRNNN; match class: 1	TFM00800.1	4.154-10 ⁶⁵			
Factor SP2 motif: GGGCGGGAC	TFM00783	1.397-10 ⁶⁴			
Factor SP2 motif: NGGGGCGGGN; match class: 1	TFM00795.1	3.489-10 ⁶⁴			
Factor ER-beta motif: RGGTCASNTGACCCY; match class: 1	TFM00902.1	4.392-10 ⁶⁴			
Factor SP2 motif: GGGCGGGAC; match class: 1	TFM00783.1	5.284-10 ⁶⁴			
Factor AP2 motif: GCYCGGGGN	TFM00867	2.356-10 ⁶³			
Factor SP1 motif: NGGGGCGGGGCGGCGGGGGGG; match...	TFM00071.1	3.398-10 ⁶³			
Factor TF3C-beta motif: CCGAGAGGGTCTCTGAGGAG; ...	TFM00861.1	7.083-10 ⁶³			
Factor SP1 motif: NGGGGCGGGGCTN; match class: 1	TFM00936.1	1.602-10 ⁶²			
Factor SP1 motif: GGGGCGGGG; match class: 1	TFM00913.1	9.937-10 ⁶²			
Factor GLF1 motif: NNCCMCRCRCN; match class: 1	TFM00773.1	8.755-10 ⁶¹			
Factor AP-2 motif: MCCCSCGNGCG	TFM00089	1.888-10 ⁶⁰			
Factor ZK4 motif: NNCCNCCRYNGNGN; match class: 1	TFM00227.1	4.728-10 ⁶⁰			
Factor SP2 motif: NYSGCCCGCCCCC; match class: 1	TFM00567.1	5.329-10 ⁶⁰			
Factor TF3C-beta motif: CCGAGAGGGTCTCTGAGGAG	TFM00863	2.388-10 ⁵⁹			
Factor EIF-3 motif: GGGCGGGN; match class: 1	TFM00089.1	3.402-10 ⁵⁹			
Factor KLF15 motif: NNCCMCRCRCN	TFM00273	6.002-10 ⁵⁹			
Factor SP1 motif: GGGGCGGGGT; match class: 1	TFM00008.1	9.459-10 ⁵⁹			
Factor AP-Zbeta motif: GCNNNGSCNGGSGGN	TFM00058	5.353-10 ⁵⁸			
Factor AP-2 motif: GGCSCRCGGCNRNNN	TFM00800	7.285-10 ⁵⁸			
Factor SP1 motif: NNGGGGCGGGGNN; match class: 1	TFM00932.1	1.331-10 ⁵⁷			
Factor RXR motif: CCCCSCCCCCC	TFM00982.1	2.524-10 ⁵⁷			
Factor KLF1 motif: NNNNNNNGGGGGGCGGNGN	TFM00009	2.718-10 ⁵⁷			
Factor ZNF37A motif: CCYGGCTCCTSCCMN; match cla...	TFM00254.1	3.412-10 ⁵⁷			
Factor SP1 motif: NGGGGCGGGGNN	TFM00036	8.027-10 ⁵⁷			
Factor KLF1 motif: NNNNNNNGGGGGGCGGNGN; match c...	TFM00970.1	9.404-10 ⁵⁷			
Factor SP1 motif: GGGGCGGGG	TFM00991	9.489-10 ⁵⁷			
Factor SP1 motif: GNNGGGCGGGGNN; match class: 1	TFM00807.1	3.694-10 ⁵⁶			
Factor SP1 motif: NNWRCCAGCCCMCN; match class: 1	TFM00252.1	4.229-10 ⁵⁶			
Factor SP1 motif: NNNGGGCGGGGNN	TFM00932	4.594-10 ⁵⁶			
Factor KLF15 motif: RCRCRCRCRCN; match class: 1	TFM00260.1	6.973-10 ⁵⁶			
Factor AP-2 motif: NNCCSCGNGCG; match class: 1	TFM00039.1	5.540-10 ⁵⁶			
Factor SP1 motif: NNRCGCGGGGNN; match class: 1	TFM00905.1	1.348-10 ⁵⁵			
Factor MAZ motif: GGGAGGGGGGGGGGGGGGGGG; matc...	TFM00636.1	1.642-10 ⁵⁵			
Factor BTEB1 motif: GGGGCGGGGCGGCGGSGGSG	TFM00723	1.877-10 ⁵⁵			
Factor AP-2 motif: SNNNCCNCCAGCGN	TFM00905	2.045-10 ⁵⁵			
Factor WT1 motif: GNGSGGCGGGG; match class: 1	TFM00893.1	2.081-10 ⁵⁵			
Factor SP2 motif: GNNNGGCGGGGNN	TFM00807	4.053-10 ⁵⁵			
Factor BTEB1 motif: GGGGCGGGGCGGCGGSGGSG; match ...	TFM00723.1	5.089-10 ⁵⁵			
Factor BTEB4 motif: NCCAGCCCM; match class: 1	TFM00286.1	5.815-10 ⁵⁵			
Factor AP-Jagamma motif: GCYNNRCGN; match class: 1	TFM00811.1	2.593-10 ⁵⁵			
Factor TCF-1 motif: ACATCGAGGCTGNN; match class: 1	TFM00010.1	3.891-10 ⁵⁴			
Factor TFAP2A motif: NGCCYNNNGGCGN	TFM00448	6.457-10 ⁵⁴			
Factor TBEL1 motif: NCCCNCCCCCGCCCC; match class...	TFM00293.1	8.304-10 ⁵⁴			
Factor AP-Jagamma motif: GCYNNNGG; match class: 1	TFM00470.1	2.347-10 ⁵³			
Factor SP1 motif: NGGGGCGGGGCGGGGGGGGG	TFM00071	2.567-10 ⁵³			
Factor SP1 motif: NNWRCCAGCCCMCN; match class: 1	TFM00252.1	4.373-10 ⁵³			
Factor EIF-4 motif: SNGSGCGGGAANN; match class: 1	TFM00894.1	8.273-10 ⁵³			
Factor AP-Jagamma motif: GCYNNRCGN	TFM00811	9.000-10 ⁵³			
Factor TFAP2A motif: NGCCYNNNGGNN; match class: 1	TFM00448.1	9.248-10 ⁵³			
Factor BTEB2 motif: RGGGNGSGN; match class: 1	TFM00277.1	9.489-10 ⁵³			
Factor WT1 motif: CCCCSCCN; match class: 1	TFM00206.1	2.083-10 ⁵²			
Factor BTEB1 motif: CCGGCGGCGGCGGCGGCGGCGGCGG	TFM00806	4.627-10 ⁵²			
Factor ZNF492 motif: SYNGSGCCSCCNC; match class: 1	TFM00734.1	5.539-10 ⁵²			
Factor MOV5-B motif: GNGSGGGG; match class: 1	TFM00104.1	8.413-10 ⁵²			
Factor AP-Jag motif: NGGGGCGGGG	TFM00987	1.250-10 ⁵¹			
Factor SP1 motif: NNWRCCAGCCCMCN	TFM00252	1.459-10 ⁵¹			
Factor SP1 motif: NGGGCGGGG	TFM00795	1.460-10 ⁵¹			
Factor SP2 motif: GGGGCGGGG; match class: 1	TFM00435.1	3.400-10 ⁵¹			
Factor SP1 motif: GGGGCGGGG; match class: 1	TFM00763.1	3.460-10 ⁵¹			
Factor MOV5-B motif: GNGSGGG	TFM00104	4.004-10 ⁵¹			
Factor Churchill motif: CGGGNN	TFM00866	4.220-10 ⁵¹			
Factor AP-Zbeta motif: NSCCNNNGGNN	TFM001478	4.350-10 ⁵¹			
Factor ER-beta motif: RGGTCASNTGACCCY	TFM00902	4.495-10 ⁵¹			
Factor SP4 motif: NNWRCCAGCCCMCTYN	TFM00932	7.572-10 ⁵¹			
Factor AP-Zbeta motif: GCNNNGSCNGGSGN; match cla...	TFM00858.1	8.069-10 ⁵¹			
Factor AP-Zalpha motif: NSCCNNGGNN	TFM00748	8.962-10 ⁵¹			
Factor GLF1 motif: GCCMCRCNNN	TFM00588	1.513-10 ⁵⁰			
Factor GLF1 motif: GCCMCRCNNN; match class: 1	TFM00588.1	2.967-10 ⁵⁰			
Factor ZNF37A motif: CCYGGCTCCTSCCMN	TFM00254	4.902-10 ⁵⁰			
Factor Kato motif: GCGGGGCGGSG	TFM00826	6.579-10 ⁵⁰			
Factor EIF-3 motif: GGGCGGN	TFM00089	7.483-10 ⁵⁰			
Factor BTEB4 motif: NCCAGCCCM	TFM00286	1.049-10 ⁵⁰			
Factor SP1 motif: GGGGCGGGGNN	TFM00826.1	1.077-10 ⁵⁰			
Factor SP1 motif: GGGGCGGGGNN	TFM00915	1.302-10 ⁵⁰			
Factor HDAC1 motif: KGACATGCTC; match class: 1	TFM00941.1	2.054-10 ⁴⁹			
Factor SP4 motif: NNWRCCAGCCCMCTYN; match class: 1	TFM00932.1	2.123-10 ⁴⁹			
Factor AP-JagammaE1 motif: NGCCNNGSGRCGGAAG...	TFM00441.1	2.366-10 ⁴⁹			
Factor BTEB2 motif: GCGGCGGCGG	TFM00749	2.134-10 ⁴⁹			
Factor spk motif: NNNNNGGCGGGGRCNNNR; match cla...	TFM00872.1	2.253-10 ⁴⁹			
Factor EIF-2 motif: GCGGCGGNCN; match class: 1	TFM00529.1	4.406-10 ⁴⁹			
Factor SP1 motif: CCCCCCGCCN; match class: 1	TFM00933.1	5.740-10 ⁴⁹			
Factor BTEB2 motif: RGGGNGGNN	TFM00727	6.853-10 ⁴⁹			
Factor SP1 motif: GGGGCGGGG	TFM00008	1.049-10 ⁴⁹			
Factor RNF96 motif: BCCGCGGCCN; match class: 1	TFM00199.1	3.534-10 ⁴⁸			
Factor E7F motif: CCCCCCGCCN; match class: 1	TFM00709.1	3.777-10 ⁴⁸			
Factor SP1 motif: NNWRCCAGCCCMCN	TFM00252	5.148-10 ⁴⁸			
Factor Egr-1 motif: GCGGGGCGG; match class: 1	TFM00754.1	1.241-10 ⁴⁷			
Factor CFP motif: GNNNGGCGGGGNGGNN	TFM00897	1.384-10 ⁴⁷			
Factor TBEL1 motif: NCCCNCCCCCGCCCC	TFM00251	1.489-10 ⁴⁷			
Factor PAX5 motif: RGGGTGACNN; match class: 1	TFM00817.1	3.059-10 ⁴⁷			
Factor EIF-3FOX1 motif: NGACACCGGCGCAC; match c...	TFM0008.1	3.849-10 ⁴⁷			
Factor SP2 motif: TGGGCGGCCCA; match class: 1	TFM00848	4.261-10 ⁴⁷			

Term name	Term ID	stats	
		Pval	$-\log_{10}(P_{adj})$
Factor SP2 motif: TGGGCGGCCCA	TFM00848	7.782-10 ⁴⁷	
Factor SP2 motif: GGGNNGGGGGCGGGGCGGNNGS	TFM00658	9.843-10 ⁴⁷	
Factor SP1 motif: GGGGCGGGGNN; match class: 1	TFM00303.1	1.002-10 ⁴⁶	
Factor spk motif: NNNGCYCGGCCCCCY; match class: 1	TFM00303.1	1.386-10 ⁴⁶	
Factor CFP motif: GNNNGGCGGGGNGGNN; match class: 1	TFM00971.1	1.534-10 ⁴⁶	
Factor TCF-1 motif: ACATCGAGGCTGNN; match class: 1	TFM00010.1	2.844-10 ⁴⁶	
Factor SP1 motif: GGGGCGGGG	TFM00763	2.651-10 ⁴⁶	
Factor SP2 motif: GGGGCGGGG	TFM00435	2.651-10 ⁴⁶	
Factor Zfx motif: SNACGCGGCGGCS	TFM00593	4.609-10 ⁴⁶	
Factor ZNF43 motif: NCNCCGCGGNN	TFM00862	6.049-10 ⁴⁶	
Factor TR4 motif: ACCCGG; match class: 1	TFM00834.1	8.875-10 ⁴⁶	
Factor SP2 motif: NYSGCCCGGCCCCCY	TFM00567	2.217-10 ⁴⁵	
Factor SP1 motif: GGGGCGGGGNN; match class: 1	TFM00035.1	4.235-10 ⁴⁵	
Factor Zfx motif: SNAGGCGNR	TFM00121	4.723-10 ⁴⁵	
Factor SP2 motif: GNGGCGGCGGNN	TFM00129	8.177-10 ⁴⁵	
Factor SP1 motif: NNRCGCGGGGCGN	TFM00765	9.921-10 ⁴⁵	
Factor AP-Zbeta motif: NSCCNNNGGNN; match class: 1	TFM001478.1	1.543-10 ⁴⁵	
Factor SP4 motif: CCCCCCGGCC	TFM00273	1.624-10 ⁴⁴	
Factor KLF15 motif: NCNCCGCGGCMCN; match class: 1	TFM00258.1	2.530-10 ⁴⁴	
Factor BTEB2 motif: NGGCTGGGCGGNN; match class: 1	TFM00972.1	3.231-10 ⁴⁴	
Factor SP1 motif: RCRCRCRCRC	TFM00020	5.265-10 ⁴⁴	
Factor WT1 motif: GNGGGGCGGGG	TFM00893	2.377-10 ⁴³	
Factor SP1 motif: RCRCRCRCRC; match class: 1	TFM00020.1	2.209-10 ⁴³	
Factor RXR motif: CCCCCCGGCC	TFM00980	3.304-10 ⁴³	
Factor ELP1 motif: NGGGGCGGNGG	TFM00969	4.505-10 ⁴³	
Factor ZNF43 motif: NCNCCGCGGNNN; match class: 1	TFM00862.1	6.862-10 ⁴³	
Factor GCMaEg motif: ATGCGGGCGGAARG; match class: 1	TFM00847	6.914-10 ⁴³	
Factor ZK4 motif: NNCCNCCRYNGGN	TFM00227	1.284-10 ⁴²	
Factor WT1 motif: CCCCCCN	TFM00036	2.349-10 ⁴²	
Factor KLF4 motif: NNRCACRCRCRCN; match class: 1	TFM00243.1	2.783-10 ⁴²	
Factor SP2 motif: GNGGCGGCGGNNN; match class: 1	TFM00129.1	5.174-10 ⁴²	
Factor KLF15 motif: RCRCRCRCRCN	TFM00260	7.938-10 ⁴²	
Factor SP1 motif: CCCCCCGCCN	TFM00933	8.287-10 ⁴²	
Factor RNF96 motif: BCCGCGGCC	TFM00199	1.867-10 ⁴²	
Factor ZF5 motif: NNNGGCGGCGGN; match class: 1	TFM00333.1	1.311-10 ⁴¹	
Factor WT1 motif: NGCGGGGGGTMMCYN	TFM00527	1.382-10 ⁴¹	
Factor EIF-3HES-7 motif: NNNGSGCNCNNRCRCGN...	TFM00526.1	1.694-10 ⁴¹	
Factor EIF-3HES-7 motif: GGCRCGTGTNNNGGCGGCM...	TFM00825.1	1.713-10 ⁴¹	
Factor GNF1 motif: NNNGGCGGNNGN; match class: 1	TFM00795.1	2.094-10 ⁴¹	
Factor AP-Zalpha motif: NSCCNNGGNN; match class: 1	TFM00748.1	2.207-10 ⁴¹	
Factor SP1 motif: GGGGCGGGN	TFM00303	5.099-10 ⁴¹	
Factor Hey1 motif: NGRCRCGN	TFM00358	7.854-10 ⁴¹	
Factor ZF5 motif: NNNGGCGGCGGN	TFM00333	1.499-10 ⁴¹	
Factor ZNF492 motif: SYNGSGCGGCGGCGGCGGCGGCGG	TFM00734	3.349-10 ⁴¹	
Factor MAZ motif: GGGAGGGG	TFM00632	5.865-10 ⁴⁰	
Factor spk motif: NNNGNARGGCGGRCNNNR	TFM00072	7.036-10 ⁴⁰	
Factor EIF-4 motif: SNGGCGGGAANN	TFM00894	8.871-10 ⁴⁰	
Factor EIF-1 motif: WWGCGCGCAAA; match class: 1	TFM00515.1	1.937-10 ⁴⁰	
Factor AP-Jagamma motif: NSCCYNNNGGNN	TFM00182	1.950-10 ⁴⁰	
Factor ZF5 motif: GGGGCGG	TFM00458	1.122-10 ³⁹	
Factor E7F motif: GVGAGG	TFM00095	2.023-10 ³⁹	
Factor EIF-1E1 motif: SSCGCGCNCNNACGGAAT; match...	TFM00005.1	2.334-10 ³⁹	
Factor KLF15 motif: NCNCCGCGGCMCN	TFM00258	2.719-10 ³⁹	
Factor AP-Jagamma motif: NSCCYNNNGGNN; match class: 1	TFM00748.1	3.095-10 ³⁹	
Factor EIF-1 motif: TTTGGGCGCAAA	TFM00516	4.176-10 ³⁹	
Factor Hey1 motif: NGRCRCGN; match class: 1	TFM00358.1	6.345-10 ³⁹	
Factor Egr-1 motif: NNRCRCRCRCN	TFM00140	8.457-10 ³⁹	
Factor CTCF motif: NCCGCTGGGGGCGG	TFM00813	1.185-10 ³⁹	
Factor Egr-1 motif: CCGGCGG	TFM00797	1.245-10 ³⁹	
Factor LRF motif: GGGGKYNB	TFM00100	1.525-10 ³⁹	
Factor BTEB2 motif: WGGGTGGGCGGN	TFM00972	1.530-10 ³⁹	
Factor SP1 motif: NGCCAGCCCMCN	TFM00253	1.679-10 ³⁹	
Factor SP2 motif: NCCGCGGCC	TFM00206	1.843-10 ³⁹	
Factor KLF4 motif: NNRCACRCRCRCN	TFM00243	1.898-10 ³⁹	
Factor GCMaEg motif: ATGCGGGCGGAARG	TFM00847	2.023-10 ³⁸	
Factor HDAC1 motif: KGACATGCTC	TFM00941	4.630-10 ³⁸	
Factor RXR motif: ACNCCNNNACRYGT; match class: 1	TFM00102.1	6.712-10 ³⁸	
Factor PLAG1 motif: CCCCCGNNNGGCC	TFM00073	8.084-10 ³⁸	
Factor RXR motif: NNRCACRCRCRCN	TFM00054	9.262-10 ³⁸	
Factor EIF-1 motif: NGGGCGGARG	TFM00206	1.061-10 ³⁷	
Factor Egr-1 motif: GCGCATGCG	TFM00869	1.303-10 ³⁷	
Factor SP2 motif: GGGNNGGGGGCGGGGCGGNNGS; match...	TFM00658.1	1.002-10 ³⁷	
Factor E7F motif: GCGGCG; match class: 1	TFM00003.1	1.279-10 ³⁷	
Factor spk motif: NNNGCYCGGCCCCCY	TFM00303	1.397-10 ³⁷	
Factor p300 motif: ACNTCCG; match class: 1	TFM00406.1	1.060-10 ³⁷	
Factor E7F motif: GGGGCGGCGCS	TFM00129	3.349-10 ³⁷	
Factor AP-Zbeta motif: ANMNCCTAGGCGCT; match...	TFM00047.1	4.589-10 ³⁷	
Factor EIF-3F0E1 motif: NGACACCGGGCGGCAC	TFM00008	5.562-10 ³⁷	
Factor SP1 motif: NCCGCGGCC; match class: 1	TFM00726.1	5.970-10 ³⁷	
Factor EGR motif: CCCCCCGGCMCN; match class: 1	TFM00073.1	6.709-10 ³⁷	
Factor AP-Zbeta motif: NGGGGCGGGG; match class: 1	TFM00967.1	7.009-10 ³⁷	
Factor Pax-5 motif: NNCGGNNANBITGNTGATGCGGSH...	TFM00043	9.506-10 ³⁷	
Factor c-ets motif: CCRSAGGGGGGCGG	TFM00406	1.494-10 ³⁶	
Factor SP1 motif: GGGAGG; match class: 1	TFM00095.1	2.164-10 ³⁶	
Factor TFAP2C motif: NGCCNNGGCGCA	TFM00452	1.805-10 ³⁶	
Factor BTEB2 motif: GCGCCRCRCRC; match class: 1	TFM00409.1	2.587-10 ³⁶	
Factor SP4 motif: SCCCCCGGCC; match class: 1	TFM00273.1	1.474-10 ³⁶	
Factor TFAP2A motif: TCCGCGGCGG	TFM00046	6.005-10 ³⁶	
Factor RXR motif: ACNRYNNNACRYGT	TFM00102	7.097-10 ³⁶	
Factor MAZ motif: GGGAGGGG; match class: 1	TFM00432.1	9.643-10 ³⁶	
Factor SP1 motif: NGCCAGCGGCMCN; match class: 1	TFM00253.1	1.597-10 ³⁶	
Factor BEN motif: CAGCGGN; match class: 1	TFM00240.1	1.793-10 ³⁶	
Factor SP1 motif: NGGAGGAGGCGGGGG	TFM00209	2.893-10 ³⁶	
Factor HIC1 motif: NNNNNNTGCCSNN	TFM00072	3.260-10 ³⁶	
Factor Egr-1 motif: GCGGGGCGG	TFM00754	3.364-10 ³⁶	
Factor HNR1P1 motif: NNCACNAG; match class: 1	TFM00746.1	3.404-10 ³⁶	
Factor c-ets motif: NGGGGCGGARG; match class: 1	TFM00726.1	5.799-10 ³⁶	
Factor ZNF43 motif: TCTTCAGGAGAACCC; match class: 1	TFM00747.1	6.356-10 ³⁶	
Factor IGR1 motif: NACCGCCAGCAAN	TFM00896	1.344-10 ³⁴	

TF		stats		
Term name	Term ID	Pval	$-\log_{10}(Pval)$	Show evidence codes
Factor Sp1: motif GGNDGGGGGGGG	TFM00953	1.434e-10 ²⁴	10.84	
Factor EBF-1: motif TTTTGGCCCAAA, match class 1	TFM00516,1	1.545e-10 ²⁴	10.81	
Factor c-Myc:Max: motif GCACATGGTN	TFM00322	1.608e-10 ²⁴	10.79	
Factor EBF-3-FODK: motif NAATGACACGGCCCMC, mat...	TFM00209,1	1.709e-10 ²⁴	10.75	
Factor MAZ: motif GGGAGGGGGGGGGGGGGGGGG	TFM00806	1.907e-10 ²⁴	10.71	
Factor Hsp2: motif NNACATGGTNN, match class 1	TFM13052,1	2.288e-10 ²⁴	10.64	
Factor HES-7: motif GNACATGGTN	TFM13066	2.370e-10 ²⁴	10.62	
Factor Pax-5: motif BCNNNRNGCANGTGNRTAGCGSH...	TFM0043,1	3.479e-10 ²⁴	10.46	
Factor ZFX: motif GGSGCGCG, match class 1	TFM10038,1	3.931e-10 ²⁴	10.41	
Factor AP-Zapb: motif GCNNNRGGS	TFM00289	1.779e-10 ²³	10.75	
Factor Egr-2: motif NTGCGTGGGCG	TFM00246	4.246e-10 ²⁴	10.38	
Factor EBF-1: motif WWTGGGCGCAAA	TFM00515	5.759e-10 ²⁴	10.34	
Factor Oxc: motif CCNCCCCCN	TFM00729	8.230e-10 ²⁴	10.19	
Factor c-Myc:Max: motif GCACATGGTNN, match class 1	TFM00322,1	8.933e-10 ²⁴	10.15	
Factor GCLF: motif NNNRNGGNGGNN	TFM00789	1.779e-10 ²³	10.75	
Factor EBF-1-TBR2: motif NGGTGNANGGCGGNTNNCR...	TFM00521,1	2.523e-10 ²³	10.60	
Factor FKFI: motif BGGGNGGMM	TFM00337	2.552e-10 ²³	10.59	
Factor PATZ: motif GGGGNGGGGGGGRNGRNGRNN	TFM10026	2.813e-10 ²³	10.55	
Factor TCF-1: motif ACATCGRGGCTGG	TFM13001	2.820e-10 ²³	10.55	
Factor GCLF: motif NNNRNGRNGRNN, match class 1	TFM00789,1	3.189e-10 ²³	10.50	
Factor PATZ: motif GGGGNGGGGGGGRNGRNGRNN, mat...	TFM10026,1	3.538e-10 ²³	10.45	
Factor KLF15: motif RCACAGCCCCC	TFM12157	3.779e-10 ²³	10.42	
Factor EBF-1: motif NNNGGCGGGAARN, match class 1	TFM00892,1	5.632e-10 ²³	10.25	
Factor Hsp2: motif NNACATGGTN	TFM13052	5.989e-10 ²³	10.22	
Factor EBF-1-HES-7: motif GGCATGCTGGNNNNGGCGCGM	TFM00825	7.989e-10 ²³	10.10	
Factor EGR1: motif NACGGCCACGAGNN, match class 1	TFM00996,1	1.335e-10 ²²	10.88	
Factor PAX5: motif RNCGTGACCCN	TFM00817	1.460e-10 ²²	10.84	
Factor Zc1: motif NGGGGGGTC, match class 1	TFM00950,1	1.789e-10 ²²	10.75	
Factor Egr-1: motif GCATAGCG, match class 1	TFM10131,1	2.603e-10 ²²	10.59	
Factor KLF16: motif GACACGCCCC	TFM00914	3.095e-10 ²²	10.51	
Factor Egr-1: motif NGCGTCGCY, match class 1	TFM00950,1	3.306e-10 ²²	10.48	
Factor LRF: motif GGGGKYNH, match class 1	TFM10100,1	3.359e-10 ²²	10.47	
Factor p53: motif NRCRWCCYNGRCWWGYYY	TFM00352	3.432e-10 ²²	10.46	
Factor EBF-3-HES-7: motif NGGTGNANGGCGGNTNNCR...	TFM00521,1	3.605e-10 ²²	10.44	
Factor EBF-3-TBR2: motif ANGTGNANGGCGGNTNNCR...	TFM00521,1	4.204e-10 ²²	10.38	
Factor EGR-1: motif TCGTGGGCG	TFM00372	4.959e-10 ²²	10.31	
Factor RUNX2: motif NRACCGCAACCGCAN, match class 1	TFM00106,1	5.001e-10 ²²	10.30	
Factor EBF-2: motif NWTTTGGCCCAAMNN	TFM10130	5.800e-10 ²²	10.23	
Factor CNOT3: motif GGCGCGGG	TFM00251	6.055e-10 ²²	10.22	
Factor EBF-1: motif NNNGGCGGGAARN	TFM00892	6.594e-10 ²²	10.19	
Factor LRF: motif NRGCGKCY	TFM10115	1.007e-10 ²¹	10.99	
Factor TFAP2A: motif NGCCCNRRGCA, match class 1	TFM00432,1	1.068e-10 ²¹	10.97	
Factor Egr-1: motif GCGGGGCGCG, match class 1	TFM00975,1	1.301e-10 ²¹	10.89	
Factor Egr-1: motif NGCGTCGCY	TFM00950	1.251e-10 ²¹	10.90	
Factor EGR: motif CGCCCGCGGN	TFM00878	1.649e-10 ²¹	10.78	
Factor EBF: motif CCCCCCGCCY	TFM00709	2.854e-10 ²¹	10.54	
Factor HES-7: motif GNACATGGTN, match class 1	TFM13066,1	3.540e-10 ²¹	10.45	
Factor ZFX: motif GGSGCGCG, match class 1	TFM00735,1	3.754e-10 ²¹	10.43	
Factor EBF-1-TBR2: motif NGGTGNANGGCGGNTNNCR...	TFM00521,1	9.407e-10 ²¹	10.03	
Factor cct: motif CCRCAGGGGGCGGN, match class 1	TFM00406,1	2.001e-10 ²⁰	10.70	
Factor Egr-1: motif GCGGGGGCGG	TFM00873	2.797e-10 ²⁰	10.56	
Factor AP-Zgamma: motif NTGCGTGGGGSNN	TFM00501	2.985e-10 ²⁰	10.53	
Factor EBF-2: motif GGCGCGCGNN, match class 1	TFM10131,1	3.605e-10 ²⁰	10.44	
Factor EBF-2: motif NWTTTGGCCCAAMNN, match class 1	TFM10130,1	4.489e-10 ²⁰	10.35	
Factor TCF-1: motif ACATCGRGGCTGG	TFM13001	4.672e-10 ²⁰	10.33	
Factor ZFX: motif GGSGCGCG	TFM00735	5.816e-10 ²⁰	10.23	
Factor Spk1: motif SCCGCCCCCCCN	TFM00767	7.572e-10 ²⁰	10.12	
Factor p53: motif NRCRWCCYNGRCWWGYYY, match cl...	TFM00352,1	8.624e-10 ²⁰	10.06	
Factor Egr-3: motif NTGCGTGGGCG	TFM00435	9.503e-10 ²⁰	10.02	
Factor AP-Zgamma: motif NGCCCNRRGSGRGGGA...	TFM00441	9.700e-10 ²⁰	10.01	
Factor HES-1: motif GGRCRTGNC	TFM13063	1.009e-10 ¹⁹	10.99	
Factor ZBP1: motif CCCCXCCCCCN	TFM00797	1.344e-10 ¹⁹	10.88	
Factor NR1B1: motif NNACGCTGACCTN, match class 1	TFM13796,1	1.682e-10 ¹⁹	10.78	
Factor EBF-3-FODK: motif NAATGACACGGCCCMC	TFM00209	1.994e-10 ¹⁹	10.70	
Factor TFAP2A: motif YGCGCNNGGNN, match class 1	TFM00446,1	2.577e-10 ¹⁹	10.59	
Factor EBF-2: motif GCGGCGCGY	TFM13151	3.964e-10 ¹⁹	10.41	
Factor WFL: motif NGCGGGGGGTSAMNYN, match class 1	TFM00527,1	7.701e-10 ¹⁹	10.11	
Factor EBF-1-EB-1: motif GGCGCNAMCGAAGT	TFM00205	1.321e-10 ¹⁸	10.88	
Factor ZBTB1C: motif GCGCCGCGCG	TFM00806	1.449e-10 ¹⁸	10.84	
Factor EBF: motif NGGGYGGGCGGNNGG, match class 1	TFM00903,1	1.598e-10 ¹⁸	10.80	
Factor MAZ: motif GGGGAGGGGGGGRRRRRRNG	TFM00984	2.141e-10 ¹⁸	10.67	
Factor ZNF581: motif CAGCGCTGAGG	TFM00911	2.156e-10 ¹⁸	10.66	
Factor pax-6: motif NYACCGGTSANYANGN, match clas...	TFM13882,1	2.229e-10 ¹⁸	10.65	
Factor CTCF: motif NCCRTAGGGGGGCG, match class 1	TFM00911,1	2.456e-10 ¹⁸	10.61	
Factor HARRY: motif NNUNNANGTG	TFM00885	3.038e-10 ¹⁸	10.51	
Factor PURL: motif GGGNCAAGN	TFM00721	3.683e-10 ¹⁸	10.44	
Factor EBF-7: motif GRGGCGGGAANN	TFM00896	4.583e-10 ¹⁸	10.34	
Factor KLF17: motif NGGGCGG, match class 1	TFM00386,1	4.707e-10 ¹⁸	10.33	
Factor LKLF: motif NGGGCGG, match class 1	TFM00499,1	4.707e-10 ¹⁸	10.33	
Factor LBP-1: motif NRCCGTTNNNACCGGN	TFM10490	5.345e-10 ¹⁸	10.27	
Factor SP1: motif CCCCCCCCC	TFM00281	5.724e-10 ¹⁸	10.24	
Factor CTCF: motif NGCGCTCAGTGGGNN, match cl...	TFM00395	7.728e-10 ¹⁸	10.11	
Factor AP-Zbeta: motif NSCCYNRGGNN	TFM13477	8.635e-10 ¹⁸	10.06	
Factor HNRPUL1: motif NCCNAG	TFM00746	1.008e-10 ¹⁷	10.99	
Factor HCL1: motif NNNGGTGGCCSNNNNNN	TFM00373	1.457e-10 ¹⁷	10.84	
Factor PURL: motif GGGNCAAGN, match class 1	TFM00721,1	1.786e-10 ¹⁷	10.75	
Factor AP-Zgamma: motif NTGCGTGGGGSNN, match cl...	TFM00527,1	2.270e-10 ¹⁷	10.64	
Factor SP1: motif CCCCCCCCC	TFM00281	2.885e-10 ¹⁷	10.54	
Factor EBF-3-TBR2: motif ANGTGNANGGCGGNTNNCR...	TFM00527	3.400e-10 ¹⁷	10.47	
Factor EBF: motif GCGGCG	TFM00803	6.056e-10 ¹⁷	10.22	
Factor Pax-4: motif NNNNNNYACACCB, match class 1	TFM00178,1	6.423e-10 ¹⁷	10.20	
Factor Oxc: motif CCNCCCCCN, match class 1	TFM00729,1	7.472e-10 ¹⁷	10.13	
Factor ZNF48: motif NNNNNNCCNCCCTCCCCCACC...	TFM00634	9.509e-10 ¹⁷	10.02	
Factor EBF-4: motif NNTTCCGCCCN	TFM00423	1.026e-10 ¹⁶	10.99	
Factor Egr-1: motif NNCRCCCMCGGN, match class 1	TFM12240,1	1.174e-10 ¹⁶	10.93	
Factor LUMAN: motif CACATGTCY, match class 1	TFM00725,1	1.470e-10 ¹⁶	10.83	
Factor Sp1: motif GGGGCGGCGGGG, match class 1	TFM00553,1	1.620e-10 ¹⁶	10.79	
Factor EBF-4: motif NNTTCCGCC	TFM00780	1.689e-10 ¹⁶	10.78	
Factor AP-Zapb: motif GCNNNRGGS, match class 1	TFM00403,1	1.805e-10 ¹⁶	10.74	
Factor Egr-2: motif GNGRNGGAGGGGGG	TFM00808	2.292e-10 ¹⁶	10.64	

Term name	Term ID	stats	
		$-\log_{10}(P\text{val})$	Show evidence codes
Factor pax-2: motif NGCTGACGNSYNGNYN; match c...	TFM13877,1	3.056e-10 ²⁴	
Factor CNOT3: motif GGCGCGGSSS; match class 1	TFM00251,1	3.130e-10 ²⁴	
Factor NGFI-C: motif WTGCGTGGGCG	TFM00244	3.358e-10 ²⁴	
Factor EBF1E1A: motif CASTGNACCGGAWRNY; match cl...	TFM00568,1	4.128e-10 ²⁴	
Factor WT1: motif NGGGGCGGGNN	TFM00738	4.984e-10 ²⁴	
Factor cct: motif CCNAGAGGGGCRSTN	TFM00749	5.962e-10 ²⁴	
Factor CBP: motif NGGGCGG	TFM00444	7.774e-10 ²⁴	
Factor Spk1: motif WGGGCGG	TFM00361	7.774e-10 ²⁴	
Factor EBF-2: motif WGGGCGG	TFM00332	7.774e-10 ²⁴	
Factor Egr-1: motif NNNNGCGGGGGGNGRNN	TFM00807	8.725e-10 ²⁴	
Factor DEC1: motif NCCACRTGNC	TFM00870	1.388e-10 ²³	
Factor EBF-4: motif NGGGGGGAARN	TFM00704	1.411e-10 ²³	
Factor Sp2: motif NTAAAGYCCCGCCMCTN	TFM12156	1.441e-10 ²³	
Factor AP-Zapb: motif NNNGGCTGCGGNN	TFM00486	1.508e-10 ²³	
Factor GCLF: motif NNNRNGRNGRNNNN	TFM00780	1.761e-10 ²³	
Factor NR1B1: motif NRGCGRTGACCTN	TFM13796	1.929e-10 ²³	
Factor LRF: motif NQANAGGGTYN; match class 1	TFM00417,1	2.352e-10 ²³	
Factor TFAP2A: motif NNNGGCGYAGGGCA	TFM007231	2.688e-10 ²³	
Factor PLAG1: motif CCCCCNNNGSGGCC; match class 1	TFM00373,1	3.923e-10 ²³	
Factor HES-1: motif GNACATGNC	TFM00877	4.221e-10 ²³	
Factor HES-1: motif GNACATGNC; match class 1	TFM00877,1	4.536e-10 ²³	
Factor RUNX3: motif NRACCGCAACCGCAN	TFM00109	5.008e-10 ²³	
Factor EBF-4: motif NNTTCCGCCCN; match class 1	TFM00423,1	5.034e-10 ²³	
Factor Egr1: motif GTGGGCGGNS	TFM00807	5.146e-10 ²³	
Factor ZNF48: motif TCCCTCAGAGAACCY	TFM00477	5.657e-10 ²³	
Factor ZNF581: motif CAGGCGYAGG; match class 1	TFM10491,1	2.300e-10 ²⁴	
Factor NF-kappaB: motif GGGGATYCC	TFM00051	2.961e-10 ²⁴	
Factor EGR1: motif NGNGGGGGYGGGGS	TFM00761	3.069e-10 ²⁴	
Factor EGR1: motif NACGCGCCCGCCCN	TFM00738	3.962e-10 ²⁴	
Factor BEN: motif CAGCGRNV	TFM00240	4.430e-10 ²⁴	
Factor EGR-1: motif TCGGTGGGCGG; match class 1	TFM00372,1	4.631e-10 ²⁴	
Factor MAZ: motif NKGSGGGGGRRG	TFM00203	4.971e-10 ²⁴	
Factor cct: motif YGGCAGCAGNAGGGSRYN	TFM00800	5.132e-10 ²⁴	
Factor RUNX2: motif NRACCGCAACCGCAN; match class 1	TFM00106,1	5.980e-10 ²⁴	
Factor AP-Zapb: motif NGCCTSAGGCN	TFM13480	7.951e-10 ²⁴	
Factor p300: motif ACNTCCG	TFM00426	1.022e-10 ²³	
Factor KLF17: motif NGGGCGG	TFM00386	1.051e-10 ²³	
Factor LKLF: motif NGGGCGG	TFM00499	1.051e-10 ²³	
Factor LBP-1: motif NRCCGTTNNNACCGGN; match cl...	TFM10490,1	1.450e-10 ²³	
Factor LRF: motif NKGCGTGN	TFM00787	1.462e-10 ²³	
Factor pax-6: motif NYACGGSYANYANGN	TFM13882	2.388e-10 ²³	
Factor Zc1: motif SNACGAGGCCGCGCS; match class 1	TFM00593,1	2.909e-10 ²³	
Factor Egr-1: motif CGCGCCMGCG; match class 1	TFM00797,1	4.050e-10 ²³	
Factor FLYJ: motif GGGGAGGAG; match class 1	TFM00372,1	4.084e-10 ²³	
Factor TFAP2A: motif NGCCTSAGGCN	TFM00417	5.26e-10 ²³	
Factor AP-Zapb: motif NGCCTSAGGCN; match class 1	TFM13480,1	5.779e-10 ²³	
Factor Zc1: motif KGGGTGTC; match class 1	TFM00448,1	7.007e-10 ²³	
Factor RUNX2: motif NRACCGCAACCGCAN; match c...	TFM00106,1	7.461e-10 ²³	
Factor MAZ: motif GGGGAGG; match class 1	TFM00417	7.890e-10 ²³	
Factor FKR: motif NRGKAGCAGTGRCCNNNGG; match clas...	TFM10054,1	8.377e-10 ²³	
Factor LUMAN: motif CYCAGCYCY	TFM00729	1.099e-10 ²²	
Factor MRP4: motif CAGTCG; match class 1	TFM00383,1	1.199e-10 ²²	
Factor HTR-1: motif CAGTCG; match class 1	TFM00378,1	1.359e-10 ²²	
Factor LKLF: motif GGGGTGGSN	TFM00761	1.254e-10 ²²	
Factor MAZ: motif GGGGAGG	TFM00649	1.623e-10 ²²	
Factor BRX-1: motif NACRYNNNNNNNNYNN; match cla...	TFM13058,1	1.744e-10 ²²	
Factor CCRK: motif SCCCTCCC	TFM00175	1.927e-10 ²²	
Factor LRF: motif NGNAGGGSYNN	TFM00817	1.971e-10 ²²	
Factor Egr-1: motif WTGCGTGGGCG	TFM00243	2.331e-10 ²²	
Factor ZFX: motif SNAGGCGNCR; match class 1	TFM10121,1	2.564e-10 ²²	
Factor LRF: motif NRACCGCAACCGCAN	TFM00106	2.711e-10 ²²	
Factor LKLF: motif GNACATGNC	TFM00877	3.246e-10 ²²	
Factor ZNF48: motif NRACCGCAACCGCAN; match class 1	TFM10491,1	3.357e-10 ²²	
Factor NR1B2: motif NTGACG	TFM00111	3.962e-10 ²²	
Factor ETS2: motif GCGGAGTACTTCCGNN	TFM00978	4.993e-10 ²²	
Factor RUNX2: motif NRACCGCAACCGCAN	TFM00106	5.981e-10 ²²	
Factor CBP: motif NGGGGCGG; match class 1	TFM00444,1	6.002e-10 ²²	
Factor Sp2: motif WGGGCGG; match class 1	TFM00361,1	6.002e-10 ²²	
Factor Spk1: motif WGGGCGG; match class 1	TFM00361,1	6.002e-10 ²²	
Factor HES-1: motif GGCGRTGNC; match class 1	TFM13061,1	1.047e-10 ²¹	
Factor RUNX2: motif NRACCGCAACCGCAN	TFM00106	1.003e-10 ²¹	
Factor Egr-1: motif NTGCTGTGGGCG; match class 1	TFM00245,1	1.199e-10 ²¹	
Factor ZSCAN4: motif TTRCGCGGCMCC	TFM00412	1.228e-10 ²¹	
Factor LRF: motif RGCAACACCN	TFM12030	1.416e-10 ²¹	
Factor GLI: motif NGACCMCCCAN; match class 1	TFM00720,1	1.788e-10 ²¹	
Factor Sp1: motif ASAMTGTGGSGGGG; match class 1	TFM00665,1	1.836e-10 ²¹	
Factor SREBP-1: motif RTGCGRTGAY	TFM13181	2.115e-10 ²¹	
Factor AP-Zeta: motif NCCYNNNNNN; match class 1	TFM13477,1	2.411e-10 ²¹	
Factor SALL2: motif GGGTGGC; match class 1	TFM00595,1	2.546e-10 ²¹	
Factor EBF-4: motif NNTTCCGCCG; match class 1	TFM00380,1	2.742e-10 ²¹	
Factor ETS2: motif GCGGAGTACTTCCGNN; match clas...	TFM00978,1	3.150e-10 ²¹	
Factor KLF15: motif RCACACGCCCCC; match class 1	TFM00157,1	4.791e-10 ²¹	
Factor ZFPAT: motif GCGCGWGGGGS	TFM00739	8.051e-10 ²¹	
Factor Egr-1: motif NNNNNNGGCGGGGGNGGNN	TFM00603	1.523e-10 ²⁰	
Factor Sp1: motif RGAGGAGSGSGGGGG; match class 1	TFM10129,1	3.385e-10 ²⁰	
Factor BRX-1: motif NACRYNNNNNNNNNNYNN	TFM13058	2.614e-10 ²⁰	
Factor KLF16: motif NGACACGCCCCC; match class 1	TFM00194,1	3.386e-10 ²⁰	
Factor EBF-4: motif NGGCGGGGAARN; match class 1	TFM00704,1	3.475e-10 ²⁰	
Factor LRF: motif NGGWSGA	TFM00419	4.446e-10 ²⁰	
Factor Zc1: motif NGGGGAGTC	TFM00450	4.572e-10 ²⁰	
Factor SREBP-1: motif RTGCGRTGAY; match class 1	TFM13181,1	4.447e-10 ²⁰	
Factor AP-Zigermma-HES-1: motif NNCACGCGNNNNNNNSC...	TFM00662	6.778e-10 ²⁰	
Factor AP-Zapb: motif NNNNGCTGCGSGSG; match class 1	TFM00486,1	7.679e-10 ²⁰	
Factor DP-1: motif NNRNNGCGGGGAANN	TFM10098	7.784e-10 ²⁰	
Factor EBF-7: motif GCGGCGGGGAANN; match class 1	TFM00896,1	8.832e-10 ²⁰	
Factor MAZ: motif GGGGAGGCGGGGNNRGRNRG; mat...	TFM00993,1	1.600e-10 ¹⁹	
Factor CBP: motif SNCCCN; match class 1	TFM00822,1	1.626e-10 ¹⁹	
Factor Spk1: motif SCCCCGCCCCCN; match class 1	TFM00817,1	2.339e-10 ¹⁹	
Factor ZNF511: motif GGRRGCGGCGWG	TFM00738	2.632e-10 ¹⁹	
Factor SALL2: motif GGGTGGG	TFM00595	3.347e-10 ¹⁹	

TF	Term		stats		
Term name	Term ID	Pval	$-\log_{10}(p_{adj})$	Show evidence codes	
Factor NF-KAPPA1, motif: NKGKNTTYCCCN, match class...	TFM08952_1	3.76e+10 ⁻¹³			
Factor ZNF461, motif: NNACNCCCCCN	TFM12113_1	5.351+10 ⁻¹³			
Factor pax-6, motif: NYACGCTSRNYGCNYN	TFM11883_1	5.462+10 ⁻¹³			
Factor CP2, motif: NNNNCCAGNCN	TFM07602	5.684+10 ⁻¹³			
Factor Sp4, motif: SSNNACACCTGN	TFM07467	5.849+10 ⁻¹³			
Factor TR4, motif: ACCCCGG	TFM04934	5.948+10 ⁻¹³			
Factor SP1SP3, motif: CCSCCCCCVCC, match class: 1	TFM01219_1	6.603+10 ⁻¹³			
Factor LRF, motif: NRGGGKCC, match class: 1	TFM01135_1	8.026+10 ⁻¹³			
Factor BRB-1, motif: GGGGWCAC, match class: 1	TFM05439_1	1.067+10 ⁻¹²			
Factor E2F-1, motif: TTTTGGCCCAAWNN, match class: 1	TFM01133_1	1.401+10 ⁻¹²			
Factor E2F-1, motif: TTTTGGCCCAAWNN, match class: 1	TFM01133_1	1.402+10 ⁻¹²			
Factor c/EB, motif: NNNCCAYAGRGCCSYNN	TFM06902	1.558+10 ⁻¹²			
Factor NF-KAPPA1, motif: NKGKNTTYCCCN	TFM08952	3.825+10 ⁻¹²			
Factor HTH4, motif: CACGTG	TFM00018	4.363+10 ⁻¹²			
Factor MRF4, motif: CACGTG	TFM00031	4.563+10 ⁻¹²			
Factor ZNF511, motif: GGGGAGCCWAG, match class: 1	TFM00738_1	4.850+10 ⁻¹²			
Factor ZC4, motif: GRCCCCCGCNGN	TFM00932	5.084+10 ⁻¹²			
Factor E2F-4, motif: GCGGGAAANA	TFM02090	7.095+10 ⁻¹²			
Factor GCMA, motif: RTGGGGTGN, match class: 1	TFM11595_1	8.569+10 ⁻¹²			
Factor KLF, motif: GGGGGGG, match class: 1	TFM00901_1	1.400+10 ⁻¹⁷			
Factor CTCF, motif: WGGCCGCMCTAGTGGYN, match class...	TFM03895_1	1.576+10 ⁻¹⁷			
Factor c-EB, motif: NACCGGGAAGTCTCCGTN, match...	TFM11417_1	2.012+10 ⁻¹⁷			
Factor c-Koz, motif: NGACACCN	TFM12232	2.378+10 ⁻¹⁷			
Factor DATP1, motif: SNGGRRCCWNGGG	TFM08924	2.459+10 ⁻¹⁷			
Factor E2F1, motif: NCNCCGCCCCCN, match class: 1	TFM07208_1	3.057+10 ⁻¹⁷			
Factor E2F2, motif: NCGCTGTGGGCG, match class: 1	TFM00461_1	3.096+10 ⁻¹⁷			
Factor Sp2, motif: NTAAATGCGGCCCMCTN, match class: 1	TFM12156_1	5.983+10 ⁻¹⁷			
Factor KLF, motif: GGGGGGG	TFM07601	6.715+10 ⁻¹⁷			
Factor Bco, motif: NCAGTGN	TFM00384	6.999+10 ⁻¹⁷			
Factor E2F-4, motif: NGGCGCGAGRN	TFM00895	8.432+10 ⁻¹⁷			
Factor Sp3, motif: ASMCTGGGGGG	TFM00605	8.765+10 ⁻¹⁷			
Factor GKLf, motif: WGGGKGCCG	TFM09971	1.363+10 ⁻¹⁶			
Factor ROK, motif: GANNACSTGG	TFM00764	1.424+10 ⁻¹⁶			
Factor E2A, motif: CACCTGAY	TFM00979_1	1.440+10 ⁻¹⁶			
Factor LKLF, motif: GGGGTGGGN, match class: 1	TFM00761_1	1.486+10 ⁻¹⁶			
Factor AP-Zalpha, motif: NTNSCTGTGGGNN	TFM09690	1.721+10 ⁻¹⁶			
Factor PE3, motif: NACCGAAGTN	TFM11427	2.013+10 ⁻¹⁶			
Factor GL1, motif: NGACCMCCAN	TFM00720	2.082+10 ⁻¹⁶			
Factor c-EB-2, motif: NACCGGGAAGTCTCCGTN	TFM11417_1	2.290+10 ⁻¹⁶			
Factor BRB-1, motif: CCCCACCAAMCCCC	TFM00257	2.482+10 ⁻¹⁶			
Factor Zc1, motif: KGGGTGGT	TFM00448	2.725+10 ⁻¹⁶			
Factor GCMA, motif: RTGGCGTGN	TFM11595	2.965+10 ⁻¹⁶			
Factor c-Myc, motif: CACGTGG	TFM08967	3.715+10 ⁻¹⁶			
Factor CORD, motif: SCCTCCCCC, match class: 1	TFM01175_1	4.057+10 ⁻¹⁶			
Factor ZBP1, motif: CCCCXCCCN, match class: 1	TFM00797_1	4.206+10 ⁻¹⁶			
Factor PE3, motif: NACCGAAGTN	TFM11430	4.523+10 ⁻¹⁶			
Factor RUNX3, motif: NRACCGCANAAACRCAN, match cl...	TFM04110_1	5.429+10 ⁻¹⁶			
Factor DEC1, motif: NGACCTGAS, match class: 1	TFM00476_1	5.489+10 ⁻¹⁶			
Factor E2F-1, motif: NNNNCCGCAAN	TFM00720	6.233+10 ⁻¹⁶			
Factor c/EB, motif: YGGCCACAGRGCCSYNN, match class: 1	TFM00890_1	7.119+10 ⁻¹⁶			
Factor HARYLKE, motif: NNNNCAAGTG, match class: 1	TFM08885_1	8.033+10 ⁻¹⁶			
Factor BRB-1, motif: CCCCACCAAMCCCC, match class: 1	TFM00257_1	8.483+10 ⁻¹⁶			
Factor ARNTL, motif: NNNNACAGTGS	TFM00894	8.809+10 ⁻¹⁶			
Factor Tcfap2b, motif: TGCCCTNNNGGN	TFM11476	1.229+10 ⁻¹⁵			
Factor TFIA, motif: YRACGTGACN	TFM11090	1.399+10 ⁻¹⁵			
Factor CTCF, motif: ACCAGGKGGC	TFM04727	1.468+10 ⁻¹⁵			
Factor E2F-1, motif: NNNNCCGCAAN, match class: 1	TFM00720_1	1.476+10 ⁻¹⁵			
Factor ZNF47, motif: GGGGGGNGGNG, match class: 1	TFM00979_1	1.773+10 ⁻¹⁵			
Factor E2F-4, motif: TTTTGGCCCAAWNN	TFM11535	1.792+10 ⁻¹⁵			
Factor pax-6, motif: NYACGCTSRNYGCNYN, match class: 1	TFM11883_1	1.899+10 ⁻¹⁵			
Factor ZBTB7C, motif: GKCCCGGCGK, match class: 1	TFM03806_1	1.966+10 ⁻¹⁵			
Factor ZNF777, motif: GTCCGTCGCTCSAACAT	TFM08993	2.069+10 ⁻¹⁵			
Factor HSF4, motif: CTCGCAAN, match class: 1	TFM05732_1	3.180+10 ⁻¹⁵			
Factor LRF, motif: RCGACCAACCN, match class: 1	TFM12230_1	3.521+10 ⁻¹⁵			
Factor DEC1, motif: NGACGTGAS	TFM08976	3.635+10 ⁻¹⁵			
Factor c-Myc, motif: NGCCAGCTGN	TFM07601	3.660+10 ⁻¹⁵			
Factor AP-Zalpha, motif: ANGGCTNAGGGNNT	TFM03449	4.019+10 ⁻¹⁵			
Factor ER12, motif: ACCGAGACCGTWSANTG, m...	TFM08963_1	4.660+10 ⁻¹⁵			
Factor E2A, motif: CACCTGAY, match class: 1	TFM00973_1	5.261+10 ⁻¹⁵			
Factor WT1, motif: SMCNCCNG	TFM01118	5.497+10 ⁻¹⁵			
Factor NF-kappaB, motif: GGGGATYCCC, match class: 1	TFM00251_1	5.842+10 ⁻¹⁵			
Factor pax-6, motif: NYACGCTSRNYGCNYN, match class: 1	TFM11883_1	5.960+10 ⁻¹⁵			
Factor NF1, motif: YGCGCTGTCGCGNNGGN	TFM00941	6.113+10 ⁻¹⁵			
Factor BTEB2, motif: GNAGGGGGGGGGGNN	TFM03814	6.244+10 ⁻¹⁵			
Factor HES-1, motif: GSCACGAGAC	TFM01011	6.751+10 ⁻¹⁵			
Factor c-Myc, motif: NNNNNNACAGCTGNNNNNN...	TFM00015_1	8.275+10 ⁻¹⁵			
Factor c-Myc, motif: NNNNNNACAGCTGNNNNNN...	TFM00015	8.275+10 ⁻¹⁵			
Factor USF2, motif: CASG	TFM00726	8.794+10 ⁻¹⁵			
Factor USF2, motif: CASG, match class: 1	TFM00726_1	8.794+10 ⁻¹⁵			
Factor MAK, motif: CACGTG	TFM08950	8.794+10 ⁻¹⁵			
Factor MAK, motif: CACGTG, match class: 1	TFM08950_1	8.794+10 ⁻¹⁵			
Factor E2F-1, motif: TTGGCGGGAANNNN	TFM00938	8.967+10 ⁻¹⁵			
Factor E2F1, motif: NGNGGGGGGGG, match class: 1	TFM00761_1	1.077+10 ⁻¹⁴			
Factor Foxo2, motif: NNGCGTNNNNNAGCGNN	TFM11541	1.084+10 ⁻¹⁴			
Factor Foxo2, motif: NNGCGTNNNNNAGCGNN, match...	TFM11541_1	1.086+10 ⁻¹⁴			
Factor Sp2, motif: NTWAGTCCCGCCACTT, match class: 1	TFM12155_1	1.264+10 ⁻¹⁴			
Factor NF1, motif: NTWAGTCCCGCCACTT	TFM12155	1.266+10 ⁻¹⁴			
Factor c/EB, motif: CCNCAAGGCGGCTN, match class: 1	TFM07493_1	1.591+10 ⁻¹⁴			
Factor pax-6, motif: NYACGCTSRNYGCNYN	TFM11881	1.976+10 ⁻¹⁴			
Factor SP1, motif: CCCCXCCCC, match class: 1	TFM02813_1	2.120+10 ⁻¹⁴			
Factor E2F-1, motif: TTGGCGGGAANNNN, match class: 1	TFM00938_1	2.148+10 ⁻¹⁴			
Factor E2F, motif: NACCGAAGTN	TFM11196	2.247+10 ⁻¹⁴			
Factor CHD2, motif: TCTCGGAG, match class: 1	TFM04710_1	2.276+10 ⁻¹⁴			
Factor ER12, motif: ACCGAGACCGTWSANTG	TFM08966	2.453+10 ⁻¹⁴			
Factor Ems, motif: NNSCGAGWGN	TFM11104	2.462+10 ⁻¹⁴			
Factor SNA, motif: NCAGCTGN	TFM02255	3.048+10 ⁻¹⁴			
Factor CP2, motif: NNNNCCAGNCN, match class: 1	TFM07602_1	3.569+10 ⁻¹⁴			
Factor CTCF, motif: ACCAGGKGGC, match class: 1	TFM04727_1	4.029+10 ⁻¹⁴			
Factor ZNF501, motif: NNNCCAGCGAACAC	TFM12085	4.050+10 ⁻¹⁴			
Factor E2F-1, motif: NETSGCG	TFM00428	4.148+10 ⁻¹⁴			

Term name	Term ID	Pval	$-\log_{10}(p_{adj})$	CS	Show evidence codes
Factor pax-6, motif: NYACGCTSRNYGCNYN, match class...	TFM11883_1	5.062e-14			
Factor myogenic, motif: RCGAGSTG	TFM00712	2.297e-13			
Factor VDR10R ALPHA, motif: NRGGTCAANNNGTTCNN...	TFM08980_1	6.988e-14			
Factor M2, motif: NNRGGGGGGGGGAGGMR	TFM01012	7.170e-14			
Factor AP-4, motif: NCAGCTGNNNNNACAGTGN	TFM08952_1	7.681e-14			
Factor Pax-5, motif: RRMWGAWWTCTTAGGGRACRGRY...	TFM00144	8.366e-14			
Factor E2F-4, motif: TTTTGGCCCAAWNN, match class 1	TFM11535_1	9.656e-14			
Factor E2F-1, motif: NMRCCCMCCN	TFM12139	1.059e-13			
Factor c-Myc, motif: NACAGTGN	TFM04743	1.449e-13			
Factor Bk-1, motif: NCCGGAAGTN	TFM11415	1.670e-13			
Factor SNA, motif: NRCAGTGN	TFM12256	1.753e-13			
Factor ZNF148, motif: NNNNNNNCCNCCCTCCCCACCC...	TFM08934_1	1.781e-13			
Factor AHR, motif: NRCGTGN	TFM00976	1.835e-13			
Factor P73, motif: GNNNRNRCNTGCMNNTASN	TFM01058	2.089e-13			
Factor pax-6, motif: NYACGCTSRNYGCNYN	TFM11880	2.262e-13			
Factor NUR1R10R ALPHA, motif: NRGGTCTTGACCYN, m...	TFM08952_1	2.297e-13			
Factor ELK1, motif: NACTTCCGGGGAAGTN	TFM00971	2.807e-13			
Factor MYC, motif: NNCACGTGCMN, match class: 1	TFM09812_1	3.114e-13			
Factor RDX, motif: GANNACAGTGS, match class: 1	TFM09764_1	3.221e-13			
Factor Myc, motif: CACGTGS	TFM00979	3.296e-13			
Factor LRF, motif: NKGGGGTGN, match class: 1	TFM07387_1	3.737e-13			
Factor E2F, motif: GNGRNGWGGGGGGG, match class...	TFM08981_1	4.371e-13			
Factor GL1, motif: MCNNACACCAACCAV	TFM03871	4.386e-13			
Factor MYC, motif: NNCACGTGCMN	TFM09812	4.459e-13			
Factor Pax-2, motif: NCGTCAACCTSRNYGCNYN	TFM11377	4.602e-13			
Factor ZNF460, motif: NNACNCCCCCN, match class: 1	TFM12113_1	5.211e-13			
Factor HIF1, motif: NGTACGTGNCB	TFM00466	5.438e-13			
Factor SP3, motif: NCCACGCCCMC	TFM03921	5.484e-13			
Factor HIF1, motif: GGGCGGCGG	TFM00952	5.489e-13			
Factor TATP2, motif: RARRWGGCGGAGNGR	TFM01086	5.520e-13			
Factor DEC1, motif: NCNCACTGNSC, match class: 1	TFM08970_1	5.924e-13			
Factor ETS1, motif: ACCGGAATN	TFM03977	6.257e-13			
Factor ELK1, motif: NACTTCCGGGGAAGTN, match class: 1	TFM03971_1	8.302e-13			
Factor E2F, motif: GTGGGCGNB, match class: 1	TFM00979_1	8.658e-13			
Factor E2, motif: RRCAGTGTCV	TFM00981	1.059e-12			
Factor ZNF48, motif: NNNACCCARCC	TFM08937	1.097e-12			
Factor ATF-1, motif: GGGCGSNNGRTSACGTA, match cl...	TFM04744_1	1.109e-12			
Factor Ems, motif: ACCGGAAGTN	TFM02069	1.241e-12			
Factor E2F1, motif: NCACACCN	TFM01215	1.252e-12			
Factor Sp4, motif: KCACCTGN	TFM03565	1.717e-12			
Factor E2F-2, motif: NCACCTGN	TFM11555	1.717e-12			
Factor AHR, motif: GNGATYGGTGMVNSCC	TFM00217	1.741e-12			
Factor ATF-3, motif: GGGCGSNNGRTSACGTA	TFM04744	1.753e-12			
Factor c-Myc, motif: NACACGTGTY	TFM01154	1.767e-12			
Factor c-Myc, motif: CACGTGGC, match class: 1	TFM03867_1	1.861e-12			
Factor SNA, motif: NNRGCAAGTGCNNNN	TFM10528	1.971e-12			
Factor AP-2gamma, motif: NNNNNGCCNCRGSCN	TFM07349	1.996e-12			
Factor NF1-C, motif: WTGCTGTGGTGG, match class: 1	TFM02023_1	2.086e-12			
Factor E2F1, motif: RCGGAATN	TFM02095	2.031e-12			
Factor HIF2, motif: NGCAGTYGN	TFM11054	2.225e-12			
Factor ZD8, motif: NGGGTC, match class: 1	TFM06191_1	2.244e-12			
Factor ZD4, motif: NNGGTC, match class: 1	TFM06190_1	2.244e-12			
Factor Ems, motif: CAGGTGNNCGGAAGN	TFM00971	2.325e-12			
Factor CLOC, motif: CNNGCAGTGNMM	TFM08984	2.364e-12			
Factor E2F-1, motif: ACCGCC	TFM0918	2.415e-12			
Factor ZD8, motif: NGGGWS	TFM05775	2.573e-12			
Factor DBS, motif: GNGGNGGGG	TFM01056	2.582e-12			
Factor Bk-1, motif: NRGCGAAGN	TFM11414	2.656e-12			
Factor KLF15, motif: NGGAGGAGGNGGGGGGG, match c...	TFM09968_1	3.540e-12			
Factor ERG, motif: ACCGAWATCCGT, match class: 1	TFM03976_1	3.809e-12			
Factor HIC1, motif: NNNNNNTGCCSN, match class: 1	TFM03072_1	4.225e-12			
Factor MA2, motif: NNGGAGGGGGG, match class: 1	TFM02023_1	4.728e-12			
Factor KLF15, motif: NGGAGGAGGNGGGGGGG	TFM09968	5.156e-12			
Factor c-EB, motif: NNNRCCCGGAATNNNN	TFM01078	5.258e-12			
Factor BHF, motif: CSCGAARTN	TFM02052	6.023e-12			
Factor ER-beta, motif: NRGGTCAANTGACCTNN	TFM09620	6.608e-12			
Factor USF, motif: NACAGTGN	TFM00217	6.767e-12			
Factor AP-2gamma, motif: NNSCCYNRGGSNNNAC...	TFM08664	7.164e-12			
Factor DEC1, motif: CNCACTGASC	TFM00001	7.252e-12			
Factor BHF, motif: NNRNNSGCGAANNNNNN	TFM06066	8.018e-12			
Factor TCF1, motif: KCACGGCC	TFM11078	8.956e-12			
Factor Ant1, motif: NNNNNRNCACGTGANNNNNN	TFM00039	8.991e-12			
Factor Ant1, motif: NNNNNRNCACGTGANNNNNN, match...	TFM00039_1	8.991e-12			
Factor c-Myc, motif: NNNACACGTGTCNN, match class...	TFM00018_1	1.059e-11			
Factor c-Myc, motif: NNCACGTGTTN	TFM00018	1.059e-11			
Factor E2F-1, motif: NNNNNNGGGGGGNNR, match class...	TFM08997_1	1.097e-11			
Factor N-Myc, motif: GSSACATGS	TFM00384	1.138e-11			
Factor PL4G1, motif: GRGCGNNNNNNRRGGG	TFM00778	1.257e-11			
Factor E2F-1, motif: NNNNNNNGGGGGGGGGGG, match cl...	TFM09018_1	1.390e-11			
Factor TEL1, motif: CGCGAANNN	TFM00759	1.529e-11			
Factor ZNF515, motif: TGGGGGGGG	TFM02321	1.544e-11			
Factor AP-2gamma, motif: NTNCTTGCGGSGAN, match cl...	TFM06990_1	1.642e-11			
Factor WT1, motif: RGGGGGGGGGGGGGGGGG	TFM01018	1.690e-11			
Factor Pax-8, motif: NNNNNNNNACCCB	TFM00178	1.943e-11			
Factor AR, motif: GNNACNNNTGTGCT	TFM01201	2.050e-11			
Factor NR1B2, motif: NTGGCY	TFM01131_1	2.061e-11			
Factor VDR, motif: GGGANRRRRGGWSA, match class: 1	TFM00441_1	2.181e-11			
Factor ERG, motif: NGGAGTGG, match class: 1	TFM00012_1	2.444e-11			
Factor ZSCAN1B, motif: TTBRCRCNNCCG, match class: 1	TFM05432_1	2.995e-11			
Factor Pii-1, motif: NACCGGAAATCCG, match class: 1	TFM11199_1	3.071e-11			
Factor E2F-1, motif: NNAACCGGAAGTGN	TFM06065	3.104e-11			
Factor c-Myc, motif: NNCACGTGGK, match class: 1	TFM05453_1	3.605e-11			
Factor Sp3, motif: NNCACCCAGTGN	TFM12154	3.964e-11			
Factor PEA3, motif: NACCGGAAGTN	TFM11428	4.333e-11			
Factor Max, motif: NNAACACGTGATNN, match class: 1	TFM00139_1	4.265e-11			
Factor Max, motif: NNAACACGTGATNN	TFM00139	4.295e-11			
Factor E4f, motif: VSNACAGATGNCN	TFM00002	4.360e-11			
Factor ER-alpha, motif: AGSTCAANTGATG, match class: 1	TFM09093_1	4.571e-11			
Factor EVI1, motif: NCCGGAANNN	TFM00071	4.586e-11			
Factor VDR10R ALPHA, motif: NRGGTCAANNNGTTCNN...	TFM08980	4.726e-11			

TF		stats		p	-log ₁₀ (p _{adj})	cs	Show evidence codes
Term name	Term ID	P _{adj}					
Factor Fli-1 motif: NACCGGATATCCGGTN; match class: 1	TFM01401_1	5.05e+10					
Factor GABP: alpha motif: CTTCCK	TFM01360	5.36e+10					
Factor BTEB1 motif: NRCCACGCCCMCN	TFM01280	5.76e+10					
Factor ER-alpha motif: AGGTCAAMTGGACY	TFM0909	8.05e+10					
Factor TFAP2B motif: NGCCNNGRGGA	TFM0149	8.52e+10					
Factor GABP motif: VCGGGAAGGGR	TFM0041	8.76e+10					
Factor c-Ets-2 motif: NCCGGAAGTG	TFM0959	8.753e+10					
Factor LZF-A1 motif: GGGGTGWR; match class: 1	TFM0646_1	9.04e+10					
Factor ZNF777 motif: GTCCCTCCGCTCSAACAAT; match c...	TFM08993_1	9.77e+10					
Factor N-Myc motif: NNCACGATGNN	TFM0005	9.907e+10					
Factor myogenic motif: RCGAGTG; match class: 1	TFM0041	9.907e+10					
Factor ERK1 motif: NNCGGGAWGN	TFM1419	1.06e+10					
Factor HES-1 motif: NNCKYGTGNNN	TFM0342	1.18e+10					
Factor c-ets-2 motif: ACCGGAATN	TFM0064	1.26e+10					
Factor vef motif: NNKCGGAAGTGR	TFM0993	1.25e+10					
Factor ER-alpha motif: NAGGTCACTGACCTN	TFM1344	1.3e+10					
Factor Fli-1 motif: NACCGGATATCCGGTN	TFM1401	1.399e+10					
Factor ERG motif: ACCGGAATCCGGT	TFM0976	1.53e+10					
Factor ER7E2A motif: CASTGNACCGGAWRYN	TFM0858	1.717e+10					
Factor VDR motif: GGGGANNRRGGWFA	TFM0444	1.791e+10					
Factor Egr motif: ACCGGAAGTN	TFM0362	1.82e+10					
Factor ARNTLX motif: NNNACAGTG; match class: 1	TFM0868_1	1.921e+10					
Factor LRF motif: NGACCAACGN; match class: 1	TFM1223_1	1.990e+10					
Factor KLF4 motif: NRCCACGCCCMCN	TFM1216	2.103e+10					
Factor Fli-1 motif: NACCGGAATN	TFM0140	2.762e+10					
Factor Egr-1 motif: WTGCTGGGGCC; match class: 1	TFM0243_1	2.309e+10					
Factor NF-1C motif: NTTGGNNNNNGCCARN	TFM0002	2.317e+10					
Factor ETV6 motif: ACCGGAAGTN	TFM0382	2.365e+10					
Factor ESR2 motif: NNNNNAGGTCACTTGACCY	TFM0281	2.52e+10					
Factor HSF1 motif: CTGCMNN	TFM0322	2.86e+10					
Factor TFAP2B motif: NCCCNNGRGGA; match class: 1	TFM0149_1	2.54e+10					
Factor C-Myc motif: NGCCACGTGNN; match class: 1	TFM0903_1	2.555e+10					
Factor MYCN motif: NNCACAGTGGN	TFM0914	2.618e+10					
Factor MYCN motif: NNCACAGTGGN; match class: 1	TFM0914_1	2.618e+10					
Factor CP2LB-1a/1b motif: GCTGNTGNNYNG met...	TFM0947_1	2.704e+10					
Factor Elk-1 motif: NNNNCCGAARTN	TFM0025	2.716e+10					
Factor Egr motif: NACCGGAATCCGGTN; match class: 1	TFM1395_1	2.751e+10					
Factor NFYB motif: CTTGGGNNWCCAN	TFM0972	2.768e+10					
Factor KLF2 motif: NGCCACAGTGN	TFM1216	2.987e+10					
Factor Egr motif: NACCGGATATCCGGTN; match class: 1	TFM1397_1	3.037e+10					
Factor Zeb1/3 motif: NYACGGRNTCAACGR; match cla...	TFM1245_1	3.40e+10					
Factor HCL1 motif: NNNNGGTGCCNNNNNN; match cla...	TFM0373_1	3.437e+10					
Factor Egr motif: NACCGGAATCCGGTN	TFM1395	3.867e+10					
Factor Fli-1 motif: NACCGGAATN	TFM0140	3.945e+10					
Factor ZKD4 motif: NGGGTC	TFM0130	4.151e+10					
Factor ZKD8 motif: NGGGTC	TFM0131	4.151e+10					
Factor BTEB1 motif: BNRRGGAGGNGT	TFM0385	4.432e+10					
Factor Fli-1 motif: NNCACAGTGN; match class...	TFM0903_1	5.317e+10					
Factor KLF3 motif: CCACAGCCG	TFM0152	5.907e+10					
Factor EGR4 motif: NCCACGCCCN	TFM0389	5.539e+10					
Factor TFAP2A motif: NNNNNCCGAGGCA; match class: 1	TFM0723_1	5.672e+10					
Factor NR1B1ROR ALPHA motif: RRGTCANNNNRGTC	TFM0864	5.758e+10					
Factor LRF motif: NNCACAGTGN	TFM0005	6.535e+10					
Factor BTEB2 motif: NNCACGCCCN	TFM1254	6.774e+10					
Factor E2F-3-T motif: AGGTGTNANGGCGST; match c...	TFM0859_1	8.364e+10					
Factor RFX3 motif: NNYCCMTGGCAACM	TFM0972	8.722e+10					
Factor N-Myc motif: VNNNGACAGTGC; match class: 1	TFM0770_1	8.851e+10					
Factor Myc motif: CACGTGC; match class: 1	TFM0909_1	8.885e+10					
Factor SNA motif: NNRGCGAGTGCNNNN; match class: 1	TFM0528_1	9.298e+10					
Factor ERG motif: ACCGGAAT	TFM0172	9.305e+10					
Factor ETV7 motif: NCCGGAANNH; match class: 1	TFM0071_1	9.395e+10					
Factor N-Myc motif: NGCCACGTGNN	TFM0993	9.820e+10					
Factor Ets motif: NNCGGGAWGN; match class: 1	TFM1401_1	9.880e+10					
Factor E2F-6 motif: NGGGCGGAGARNH; match class: 1	TFM0895_1	9.950e+10					
Factor LBP1 motif: ACRYGTNNNNACYRG	TFM1342	1.067e+10					
Factor SP9 motif: RCCACGCCCMCY	TFM1249	1.108e+10					
Factor p53 motif: GGACATGCCGGCATGTCY	TFM0034	1.269e+10					
Factor C/EBD motif: TCTCCGAC	TFM0710	1.559e+10					
Factor HZF1 motif: GNNKACGTGCGGNN	TFM0197	1.486e+10					
Factor ZNF448 motif: NNNAGCCCAACC; match class: 1	TFM0837_1	1.524e+10					
Factor DP-1 motif: NNNNGCGGGAANN; match class: 1	TFM1008_1	1.715e+10					
Factor Ets motif: NNCAGGGAAGNN; match class: 1	TFM0973_1	1.917e+10					
Factor c-ets-1 motif: ACCGGAATN	TFM0041	2.25e+10					
Factor BF-1 motif: ACTTCCGGG	TFM0474	2.318e+10					
Factor AP-2gamma E2F-4 motif: NTTCCCGNNSCCCSM...	TFM0840	2.384e+10					
Factor PEA3 motif: NACCGGAATN	TFM1345	2.405e+10					
Factor SP8 motif: NRCCACGCCCMCN	TFM1248	2.659e+10					
Factor Fli-1 motif: NACCGGAATCCGGTY	TFM1399	3.067e+10					
Factor E12 motif: RRCAGGTGNCY; match class: 1	TFM0693_1	3.213e+10					
Factor LZF-A1 motif: GGGGTGWR	TFM0646	3.350e+10					
Factor XBP-1 motif: VNNNGACAGTGC	TFM0770_1	3.476e+10					
Factor E2F-4 motif: GCGGGAANNA; match class: 1	TFM0993_1	4.042e+10					
Factor BTEB2 motif: NCCACGCCCN; match class: 1	TFM1216_1	4.184e+10					
Factor F1L motif: ACCGGAATCCGGT; match class: 1	TFM0989_1	4.262e+10					
Factor c-Ets-1p56 motif: NCMGGAWGN	TFM0032	4.468e+10					
Factor sin3A motif: TGTCCNGGTGCTG; match class: 1	TFM0476_1	4.700e+10					
Factor RelA/p65 motif: ICNNGGBANK	TFM0611	4.939e+10					
Factor slug motif: RRCAGTGCN	TFM0064	5.099e+10					
Factor c/ct motif: NNNCCABYGRGGGCRSYNN; match cla...	TFM0602_1	5.194e+10					
Factor Mz-1 motif: NNRGGGCGGGGAGGMMR; match c...	TFM1012_1	5.886e+10					
Factor ERK1 motif: NNNNGCGGGAAGYRNNNNNNIS	TFM0913	5.999e+10					
Factor RST motif: GGACAGC	TFM0476	6.561e+10					
Factor ERG motif: ACCGGAATN	TFM0975	6.592e+10					
Factor CTCF motif: NNNNGCAGAGRGGRCSRN	TFM0200	7.134e+10					
Factor USF1 motif: NNNNGTCACTGGN	TFM0767	7.234e+10					
Factor ZPS motif: NACCGGAC	TFM0111	7.96e+10					
Factor Egr motif: NACCGGATATCCGGTN; match class: 1	TFM1393_1	8.04e+10					
Factor HF-1alpha motif: NCACTG	TFM0032	8.817e+10					
Factor Pax-5 motif: GTYAVCTT5RKTGVNN	TFM0474	9.121e+10					
Factor DCL1 motif: CNCACTGASC; match class: 1	TFM0372_1	1.015e+10					

		stats			
Term name	Term ID	P _{adj}	-log ₁₀ (P _{adj})	cs	Show evidence codes
Factor GABP motif: VCGGGAAGGGR; match class: 1	TFM0041_1	1.90e+10			
Factor SAP-1 motif: NNCGGGAAGTGN	TFM0905	1.30e+10			
Factor BF-1 motif: NANCGGGAAGTN	TFM1447	1.20e+10			
Factor SP9 motif: NRCCACGCCCMCN	TFM1250	1.24e+10			
Factor NR1B1ROR ALPHA motif: NRGTCRTTGACCYN	TFM0867	1.30e+10			
Factor BTEB motif: NRCCACGCCCC	TFM1246	1.37e+10			
Factor LKLF motif: CNCCACCCS	TFM0819	1.46e+10			
Factor TawCREB motif: RTGACGCATATCCCC; match class...	TFM00135_1	1.549e+10			
Factor TELL motif: CNCGGAANNH; match class: 1	TFM0020_1	1.560e+10			
Factor Elk-1 motif: RCGGGAAGTGN	TFM0904	1.69e+10			
Factor Pax-5 motif: RNNNGWANNCTNRAGCGRACSRYN...	TFM0044_1	1.71e+10			
Factor ZNF515 motif: VNCCSCCCCGWNG	TFM0805	1.717e+10			
Factor AhR/Arnt motif: GRGATYGTGCMGWNSCC; matc...	TFM00237_1	2.012e+10			
Factor DRB motif: GNNGGWGGG; match class: 1	TFM0056_1	2.057e+10			
Factor TWIST motif: CACCTGG; match class: 1	TFM0942_1	2.090e+10			
Factor SNA motif: NRCCAGTGCR	TFM1257	2.159e+10			
Factor slug motif: NRCCAGTGCR	TFM1261	2.159e+10			
Factor USF1 motif: NNCACGTGACN	TFM1094	2.171e+10			
Factor Elk-1/Pax-5 motif: ACCGGAACACGWTSAHYG	TFM0825	2.428e+10			
Factor TWIST motif: CACCTGG	TFM0942	2.467e+10			
Factor CTCF motif: NNYGCCCYCTSTGGN	TFM0944	2.50e+10			
Factor CP2LB-1a/1b motif: GCTGNTGNNNNYNG	TFM0947	3.134e+10			
Factor Egr motif: NACCGGAATN	TFM1392	3.20e+10			
Factor Egr motif: NACCGGATATCCGGTN	TFM1397	3.36e+10			
Factor BF-1 motif: NNCGGGAAGTN	TFM0905	3.467e+10			
Factor ZNF484 motif: MAAGGGGTGGACGTG	TFM0050	3.671e+10			
Factor GABPA motif: ACCGGAAGTN	TFM0990	3.738e+10			
Factor SNAID4 motif: GSRKXKAGACANCY	TFM0073	3.817e+10			
Factor AP-1alpha motif: NGCTTNAAGCN	TFM0479	3.86e+10			
Factor RXR1 motif: NACCGGAAGTN; match class: 1	TFM1430_1	4.18e+10			
Factor myogenic motif: CRCTCTBNNTTGGACGSGNC...	TFM0066_1	4.26e+10			
Factor SP3 motif: NRCCACGCCCMC; match class: 1	TFM0921_1	4.54e+10			
Factor Pax-5 motif: NTCGCAWTSAHTGMNY; match cl...	TFM0464_1	4.690e+10			
Factor NF-1B motif: CTGGAGTGN	TFM0904	5.079e+10			
Factor EGR5 motif: NCMCRCCCACTMNN	TFM0877	5.115e+10			
Factor GLIS2 motif: ACCCCCRCCGWNCG	TFM1217	5.24e+10			
Factor DAP1 motif: NNGGRRGCGWNGG; match class: 1	TFM0974_1	6.05e+10			
Factor g1b motif: GACACCCANG	TFM0104	6.26e+10			
Factor SNA motif: NRCCAGTGN; match class: 1	TFM1430_1	6.67e+10			
Factor ESR1 motif: NNNNNAGGTCACTTGACCY; match ...	TFM0281_1	6.92e+10			
Factor c-Myc motif: KACCACTGGTY; match class: 1	TFM0134_1	6.94e+10			
Factor GATAD1 motif: CCTGTG; match class: 1	TFM0976_1	7.234e+10			
Factor Egr motif: NACCGGATATCCGGTN	TFM1393	7.26e+10			
Factor NF1 motif: NNGGNGGGGNN; match class: 1	TFM0913_1	7.347e+10			
Factor ER-beta motif: NRGTCANSTGACCTNN; match cl...	TFM0930_1	7.490e+10			
Factor Egr motif: NACCGGATATCCGGTN	TFM1391	8.44e+10			
Factor SP8 motif: NRCCACGCCCMCN	TFM1247	8.470e+10			
Factor PEA3 motif: NACCGGAAGTN; match class: 1	TFM1437_1	9.25e+10			
Factor P-1 motif: CNCGGAGTG	TFM0904	1.04e+10			
Factor BTEB motif: BNRRGGAGGNGT; match class: 1	TFM0385_1	1.272e+10			
Factor ER1/5REBP-2 motif: NTSACGTGACGGAARY	TFM0857	1.278e+10			
Factor Elk-1 motif: NNCGGGAAGTN; match class: 1	TFM1435_1	1.390e+10			
Factor DBL motif: RCGGAGTGN; match class: 1	TFM1390_1	1.467e+10			
Factor NRC motif: WCCARR; match class: 1	TFM0963_1	1.49e+10			
Factor REBP-2 motif: NNYGACNNNN	TFM0117	1.512e+10			
Factor ETS1 motif: ACCGGAARYN; match class: 1	TFM0977_1	1.591e+10			
Factor BTEB motif: NRCCACGCCCMCN	TFM1242	1.637e+10			
Factor RXR1 motif: RCGGAGTGN	TFM0904	1.658e+10			
Factor GABPalpha motif: CTTCCKGY	TFM0191	1.871e+10			
Factor COUP-TF1 motif: GRGGASRAGGTCAAGN	TFM0886	1.924e+10			
Factor ESE-1 motif: NTGTGGGATGCG; match class: 1	TFM1385_1	2.002e+10			
Factor SNA motif: GCCACCTGNCNNGY	TFM0566	2.009e+10			
Factor CTCF motif: NNNCCABYGRGGGCRSYN	TFM0242	2.257e+10			
Factor DBL motif: GGGRRRRRGAGGCGGGRRR	TFM1007	2.311e+10			
Factor GLF1 motif: NNNCCARCCCN	TFM1214	2.388e+10			
Factor ZKD1 motif: NGGGGWS; match class: 1	TFM0575_1	2.629e+10			
Factor ZNF101 motif: NNNCCACGACGAC; match class: 1	TFM1396_1	2.67e+10			
Factor AP-4ERB motif: RSCGGAACAGTGNH; match cla...	TFM0844_1	3.013e+10			
Factor NR1B1ROR ALPHA motif: NRGTCANNNNNRGTT...	TFM0864_1	3.08e+10			
Factor COUP-TF1 motif: RAGGTGANCYACTY; match clas...	TFM1343_1	3.141e+10			
Factor TFRA motif: YRACGTGAGTN; match class: 1	TFM1390_1	3.222e+10			
Factor BF-1 motif: NANCGGGAAGTN	TFM0905	3.259e+10			
Factor ZC4 motif: GRCCCCCCCGNGNGN; match class: 1	TFM0992_1	3.291e+10			
Factor MR motif: NDNACNNNNNTGNT	TFM1389	3.334e+10			
Factor HIF2A motif: ACCTGATNN	TFM0756	3.493e+10			
Factor Egr-1 motif: ACCGCCCC; match class: 1	TFM0918_1	3.86e+10			
Factor slug motif: CACTCTGN; match class: 1	TFM0565_1	4.232e+10			
Factor TF-2 motif: NCACCTGN; match class: 1	TFM1155_1	4.232e+10			
Factor E2A motif: NNRCCACTGNNN	TFM0088	4.303e+10			
Factor MyoD motif: CONCAAGTCTYN	TFM1381	4.608e+10			
Factor FLE motif: ACCCGAATN	TFM0986	4.779e+10			
Factor Elk-1/Pax-5 motif: ACCGGAACACGWTSAHYN...	TFM0825	4.90e+10			
Factor Egr motif: NACCGGATATCCGGTN; match class: 1	TFM1391_1	4.92e+10			
Factor USF2 motif: NNNNACGACTGN	TFM0860	4.96e+10			
Factor ZNF593 motif: NCCGCTCTCTC	TFM0644	5.302e+10			
Factor BF-1 motif: NANCGGGAAGTN	TFM1431	5.729e+10			
Factor BF-1 motif: NANCGGGAAGTN	TFM1431	5.96e+10			
Factor GL1 motif: NTGGTGGTGN	TFM0720	6.28e+10			
Factor COUP-TF1 motif: RAGGTGANCYACTY	TFM1343	6.347e+10			
Factor TBID motif: GGGGGGAGN	TFM0895	6.776e+10			
Factor COUP-TF1 motif: RAGGTGANTCAYT	TFM1340	7.04e+10			
Factor SREBP-1 motif: CACSKCA; match class: 1	TFM0049_1	7.279e+10			
Factor NR1B1 motif: GGGGGTGTGACAYANA	TFM0014	7.96e+10			
Factor TawCREB motif: NCTGTGGCATGCGGNN	TFM0038	8.125e+10			
Factor NF-E4 motif: CTGAGG; match class: 1	TFM0808_1	8.86e+10			
Factor Bbox motif: NCACTGNCSTGN; match class: 1	TFM0014_1	8.95e+10			
Factor MZF-1 motif: GGGGGGARRR	TFM0781	9.35e+10			
Factor Tc1apc motif: TCCCCYNNRGCN	TFM13474	9.65e+10			
Factor F1-14a motif: TCCCCYNNACGCTGN	TFM0839	9.86e+10			

TF	stats				
Term name	Term ID	Pval	$-\log_{10}(P_{adj})$	131	Show evidence codes
Factor USF; motif: GYACGTGNC; match class: 1	TF-M00187.3	1.069e-10 ⁴			
Factor Bk-1;TRB2; motif: TNKACCGAAGN	TF-M00213	1.117e-10 ⁴			
Factor NF1C; motif: WGGCARR	TF-M00763	1.135e-10 ⁴			
Factor ER-beta; motif: GTCANASTGRCYNN	TF-M01875	1.308e-10 ⁴			
Factor AR; motif: NGNACNNNNYGTGNC; match class: 1	TF-M11849.3	1.352e-10 ⁴			
Factor GAP- alpha; motif: CTTCCK; match class: 1	TF-M00160.3	1.389e-10 ⁴			
Factor rfa3SRF; motif: TRGCAACNNNNNCNWTATGNGN	TF-M00823	1.329e-10 ⁴			
Factor LHM-1; motif: TCAAGTCRYGACCTTG; match class: 1	TF-M11828.3	1.344e-10 ⁴			
Factor ESE-1; motif: NTGTGCGGATG	TF-M11385	1.422e-10 ⁴			
Factor p53; motif: GCACATGCGCGGACATGTCY; match class: 1	TF-M00034.3	1.539e-10 ⁴			
Factor Bk-1; motif: NNNNCCGGAAATNN; match class: 1	TF-M0025.3	1.544e-10 ⁴			
Factor MTF-1; motif: TGGGAC	TF-M01243	1.656e-10 ⁴			
Factor E2A; motif: CAGNTGNN	TF-M07353	1.687e-10 ⁴			
Factor ZCL1; motif: NACCCTCCGTGTGCG	TF-M12129	1.719e-10 ⁴			
Factor AP-2gamma; motif: NCCYNRGGGN; match class: 1	TF-M11801.3	1.938e-10 ⁴			
Factor TFAP2A; motif: NGCYTAGGNN; match class: 1	TF-M01847.3	1.937e-10 ⁴			
Factor WT1; motif: RSGNGGGAAGGGGSGRG; match class: 1	TF-M10108.3	1.969e-10 ⁴			
Factor ZBP1; motif: GCCCTCCCCCG	TF-M12057	2.036e-10 ⁴			
Factor CP2; motif: GCHCDAMCAG	TF-M00072	2.080e-10 ⁴			
Factor CTCF; motif: NSGTGGCGG	TF-M00037	2.091e-10 ⁴			
Factor E2F-3T1; motif: AGGTGTNANGGCGCT	TF-M00829	2.138e-10 ⁴			
Factor ERB1; motif: NNNCCGGAAGY	TF-M00913	2.206e-10 ⁴			
Factor KLF15; motif: GCCACGCCCMCN	TF-M12159	2.224e-10 ⁴			
Factor ER71; motif: ACCGAATNN	TF-M00367	2.246e-10 ⁴			
Factor GCAP-PA3; motif: ATGCGCGCGGAAGTR; match class: 1	TF-M00012.3	2.277e-10 ⁴			
Factor CTCF; motif: YNRRCAASHAGRGSCRYN; match class: 1	TF-M00242.3	2.413e-10 ⁴			
Factor c-Myc; motif: NCCACGTGNN	TF-M00992	2.527e-10 ⁴			
Factor NRSE; motif: TTYAGWCCCGGASADYRCC	TF-M00325	2.577e-10 ⁴			
Factor CLOCK; motif: CYNACAGTNNNNM; match class: 1	TF-M00894.3	2.615e-10 ⁴			
Factor NF-E4; motif: GTGAGG	TF-M00826	2.679e-10 ⁴			
Factor LBP1; motif: ACYRTNNNNNACGT; match class: 1	TF-M11492.3	2.778e-10 ⁴			
Factor Hey1; motif: NGCAGTGYN	TF-M11056	2.899e-10 ⁴			
Factor BTB1; motif: NNRACCCGCCMCN	TF-M12181	2.996e-10 ⁴			
Factor LKLF; motif: CNCCACCTC; match class: 1	TF-M00893.3	3.060e-10 ⁴			
Factor AHR; motif: NTNGCTGNNN	TF-M00778	3.117e-10 ⁴			
Factor Sohlh2; motif: NNACACGTGNN; match class: 1	TF-M11075.3	3.166e-10 ⁴			
Factor E2F1; motif: NNNNNGCGSAAAN	TF-M00874	3.244e-10 ⁴			
Factor KLF8; motif: NNGGCGGGGG	TF-M00518	3.254e-10 ⁴			
Factor KLF7; motif: NNGGCGGGG	TF-M00862.3	3.254e-10 ⁴			
Factor YY1; motif: NNGCGCATTN	TF-M01024	3.273e-10 ⁴			
Factor c-Myc; motif: RACCACGTGTC	TF-M01145	3.539e-10 ⁴			
Factor Kaiso; motif: GNTCTCGAGGNNNNNGN	TF-M00632	3.526e-10 ⁴			
Factor E1K; motif: ACCGAAGTN	TF-M00509	3.652e-10 ⁴			
Factor SREBP-2; motif: NTCCACGATNN; match class: 1	TF-M00862.3	3.698e-10 ⁴			
Factor AP-2gamma; motif: NCCYNRGGGN	TF-M11801	3.702e-10 ⁴			
Factor slug; motif: CACCTGNNN	TF-M00704	3.729e-10 ⁴			
Factor GLI4; motif: RGGCTTGTAATGCCAGCYMA; match: 1	TF-M10314.3	3.775e-10 ⁴			
Factor TFAP2C; motif: NGCTTAGGNN	TF-M11847	3.867e-10 ⁴			
Factor KLF12; motif: NNKCCACNNCCCTN	TF-M00103	4.003e-10 ⁴			
Factor GR2; motif: GACCAACCCAGN	TF-M01703	4.127e-10 ⁴			
Factor FLI1; motif: ACCGGAATCCGT	TF-M00389	4.198e-10 ⁴			
Factor MZF-1; motif: TGGGAG	TF-M00733	4.312e-10 ⁴			
Factor E2F-1; motif: NTTCSCC	TF-M00896.3	4.530e-10 ⁴			
Factor MyoD; motif: NNKACCTGNN	TF-M00184	4.532e-10 ⁴			
Factor NR1B1-RXR-GAMMA; motif: RRGGTCAANNNNNRGG...	TF-M00895	4.660e-10 ⁴			
Factor NF-kappaB; motif: AGGGGAATCCCTC; match class: 1	TF-M00454.3	4.911e-10 ⁴			
Factor TR4; motif: NCCCTTGACYB	TF-M00806	5.384e-10 ⁴			
Factor COAP-TF1; motif: RGGGAGGAGTCAAGN; match class: 1	TF-M00886.3	5.360e-10 ⁴			
Factor TATF2B; motif: RABRWGCGAGNGR; match class: 1	TF-M00861.3	5.534e-10 ⁴			
Factor Pct-3; motif: GCGNGAAGY; match class: 1	TF-M00918.3	5.722e-10 ⁴			
Factor KLF3; motif: CCMCRCCCG	TF-M07460	5.778e-10 ⁴			
Factor SREBP-1; motif: CACSCCA	TF-M00149	5.786e-10 ⁴			
Factor NF-Yap; motif: NACCTGNN	TF-M07384	5.952e-10 ⁴			
Factor N-Myc; motif: NNKACGTGNN	TF-M11225	5.952e-10 ⁴			
Factor ER-alpha; motif: NAGGTCAYSYGACCTN	TF-M11842	6.085e-10 ⁴			
Factor AHR; motif: CACGNN	TF-M01855	6.413e-10 ⁴			
Factor GCAP-PA3; motif: ATNCGCGCGGAAGTR	TF-M00813	7.359e-10 ⁴			
Factor COAP-TF1; motif: RRGTCATNACGAY	TF-M11741	7.523e-10 ⁴			
Factor RelA-p65; motif: BCWGGGANNK; match class: 1	TF-M04811.3	7.675e-10 ⁴			
Factor GLI3; motif: TGGGTGTGYC	TF-M01596	8.116e-10 ⁴			
Factor BTB1; motif: NNRACCCGCCMCN	TF-M12179	8.250e-10 ⁴			
Factor USF2; motif: NNKACGTGNNN	TF-M11596	8.509e-10 ⁴			
Factor GAP- alpha; motif: NRCCGGAAGTN	TF-M11435	8.617e-10 ⁴			
Factor meis1.EF-1; motif: NTGCCGAAGTN	TF-M00877	8.730e-10 ⁴			
Factor E2F-1; motif: NKTSSCG; match class: 1	TF-M00408.3	8.929e-10 ⁴			
Factor ZNF44; motif: TCCGGCTCTN	TF-M00737	1.012e-10 ³			
Factor P1; motif: ACCGAATNN	TF-M00073	1.022e-10 ³			
Factor SNA1; motif: NCACCTGNN	TF-M01430	1.026e-10 ³			
Factor NF1B; motif: CYTGGNNCNGWCAN; match class: 1	TF-M00762.3	1.083e-10 ³			
Factor FLI-1; motif: NAYTCCGT	TF-M00813	1.088e-10 ³			
Factor nrf1; motif: NNRNSCGAAGNNNNN; match class: 1	TF-M00606.3	1.113e-10 ³			
Factor USF; motif: NNRNACGTGNNN; match class: 1	TF-M00122	1.138e-10 ³			
Factor AP-4Max; motif: NCAGTGNNNNNNCAGTGN	TF-M00874	1.138e-10 ³			
Factor Ems-HS-7; motif: NCGGAGNNNNNRCGCG	TF-M00870	1.178e-10 ³			
Factor snkA; motif: TGTCCNNGTGCTG	TF-M04756	1.223e-10 ³			
Factor NR1B1; motif: NNRGTCAANNRGTCAN	TF-M11795	1.225e-10 ³			
Factor P73; motif: GNNNRNRNTGCMNTSASN; match class: 1	TF-M01058.3	1.321e-10 ³			
Factor HES-1; motif: GSCACAGAGC; match class: 1	TF-M00211.3	1.403e-10 ³			
Factor ER71SREBP-2; motif: NTSACGTGACGGAARY; match: 1	TF-M00857.3	1.430e-10 ³			
Factor E2F-1; motif: TTTSSCG	TF-M00431	1.463e-10 ³			
Factor NTR; motif: NNSAGTGN	TF-M00638	1.502e-10 ³			
Factor c-Myc; motif: RACCACGTGCTC; match class: 1	TF-M01145.3	1.625e-10 ³			
Factor BTB2; motif: GNAGGGGNGGGGNN; match class: 1	TF-M00814.3	1.623e-10 ³			
Factor ZDXA; motif: NAGGGTG; match class: 1	TF-M00203.3	1.624e-10 ³			
Factor ZDXB; motif: NAGGGTG; match class: 1	TF-M00203.3	1.624e-10 ³			
Factor AP-2alpha; motif: NGCTNAGGTCN; match class: 1	TF-M11479.3	1.647e-10 ³			
Factor AR; motif: GGTACANNRTTCT	TF-M00981	1.783e-10 ³			
Factor CACC-binding; motif: CANNCCNNWGGGTGGG	TF-M00721	1.878e-10 ³			
Factor Sp1; motif: DNNSGGGAGNNNNN	TF-M00446	1.929e-10 ³			

Term name	Term ID	P _{adj}	$-\log_{10}(P_{adj})$	116	Show evidence codes
Factor GLI2; motif: TGGGTGGTCNS	TF-M07291	1.908e-10 ³			
Factor BAR-gamma; motif: RAGGTCRTGACTCY	TF-M11805	2.005e-10 ³			
Factor ZDXB; motif: NAGGGTG	TF-M06202	2.008e-10 ³			
Factor ZDXA; motif: NAGGGTG	TF-M06203	2.008e-10 ³			
Factor GLI3; motif: NACGCCCCACGNNNG	TF-M12215	2.123e-10 ³			
Factor AP-4; motif: NCAGCTGTNGGTCN	TF-M01060	2.174e-10 ³			
Factor CRBP; motif: NGCCACGCCCN	TF-M12166	2.249e-10 ³			
Factor NRF-1; motif: SYGCGMTGCGGNNNGN; match class: 1	TF-M0641.3	2.330e-10 ³			
Factor ZNF68A; motif: MAAGGGGTGACTGT; match class: 1	TF-M10550.1	2.353e-10 ³			
Factor GLI1; motif: RGGCTTGATGTCCAGCYMA	TF-M10554	2.563e-10 ³			
Factor MZF-1; motif: TGGGGAG; match class: 1	TF-M01733.1	3.044e-10 ³			
Factor GAPB; motif: CACTTCCGGNN	TF-M01258	3.008e-10 ³			
Factor USF2; motif: NGGTCACTGNNNNNNNN	TF-M06370	3.137e-10 ³			
Factor rfa3SRF; motif: TRGCAACNNNNNCNWTATGNGN...	TF-M08023.1	3.240e-10 ³			
Factor AP-4-EBB1; motif: RCGGAGCAAGTGN	TF-M00443	3.403e-10 ³			
Factor ER-alpha; motif: NAGGTCACTGACCTN; match class: 1	TF-M11844.1	3.515e-10 ³			
Factor Egr-1; motif: NMCRCCMCNCCN; match class: 1	TF-M12139.1	3.518e-10 ³			
Factor BMAL1; motif: NSACGTGNNN	TF-M00877	4.042e-10 ³			
Factor NRF-1; motif: GCGMTGCGCN; match class: 1	TF-M10552.1	4.138e-10 ³			
Factor Bk-1; motif: NRSCGGAAGNN; match class: 1	TF-M11434.1	4.264e-10 ³			
Factor GEMIN3; motif: NCWGGARRGNGNG	TF-M00727	4.385e-10 ³			
Factor Hey1; motif: NGCAGTGYN	TF-M11059	4.453e-10 ³			
Factor p73; motif: NNKCAWGYCARRWGYC	TF-M10025	4.804e-10 ³			
Factor ESR3; motif: NNKCCCCACTNNM; match class: 1	TF-M00877.1	4.937e-10 ³			
Factor ZNF512; motif: NNKCCAGCGGACAN	TF-M00355.3	5.485e-10 ³			
Factor YY1; motif: CAANATGGCGG; match class: 1	TF-M10436.1	5.629e-10 ³			
Factor NR1B2; motif: RAGGTCRTGACTCY	TF-M11800	5.689e-10 ³			
Factor Tal; motif: GWSNCACTGCG	TF-M07469	5.884e-10 ³			
Factor AP-2gamma; motif: NNKNNCCYACAGGGCN	TF-M07137	6.083e-10 ³			
Factor NF-1C; motif: NTGGGNNNNNGCCARRN; match class: 1	TF-M1002.3	7.384e-10 ³			
Factor Sp1; motif: AAGGGCGG	TF-M00932	7.680e-10 ³			
Factor ESE-1; motif: SATKCGGATGNN; match class: 1	TF-M11381.3	8.911e-10 ³			
Factor Bk-1-ETV7; motif: ANSCGACGAGTATCCGGNT; ma...	TF-M00214.1	9.247e-10 ³			
Factor AHR; motif: CACGNN	TF-M00894	9.274e-10 ³			
Factor ASH-2; motif: ACACGACGN	TF-M11179	9.354e-10 ³			
Factor TCF15; motif: KCACGCGCMC	TF-M10777	1.004e-10 ²			
Factor AHRant; motif: KNNNNNTTGGCTGCMG	TF-M00235	1.069e-10 ²			
Factor YY2; motif: NCCGCGATNTY	TF-M00325	1.094e-10 ²			
Factor E2F-1; motif: NTTCGCGC	TF-M00960	1.135e-10 ²			
Factor BTB1; motif: GNRGAGGAGTGGGCC	TF-M00974	1.194e-10 ²			
Factor FPM15; motif: SRGGGAGGAGGN	TF-M01587	1.204e-10 ²			
Factor GLI2; motif: TGGGTGGTGN	TF-M0455	1.228e-10 ²			
Factor P1-ETV7; motif: NNRGGGAMGATNTCCGN	TF-M00261	1.228e-10 ²			
Factor KLF15; motif: NNKCCACGCTN; match class: 1	TF-M11818.1	1.413e-10 ²			
Factor AHR; motif: CCYCNRRSTNGGCTGASA	TF-M0139	1.537e-10 ²			
Factor SAP-1; motif: NNCCGGAAGTGN; match class: 1	TF-M0095.1	1.600e-10 ²			
Factor KLF8; motif: NNGGGGTGYG	TF-M08118	1.670e-10 ²			
Factor ER-1SREBP-2; motif: RTCACGTACCGGAAGN	TF-M00829	1.700e-10 ²			
Factor FLI2; motif: CCGGABRN	TF-M00355	1.787e-10 ²			
Factor SRF; motif: RCCACGCCCMCY	TF-M00923	1.832e-10 ²			
Factor c-Myc; motif: NCCACGTGNN; match class: 1	TF-M00992.3	1.883e-10 ²			
Factor myogenin; motif: CRCTGTBTNNNTTGGCAGGNG...	TF-M00056	1.922e-10 ²			
Factor E2A; motif: NCACCTGYNNNN	TF-M00894	1.954e-10 ²			
Factor CRBP; motif: SNCCCN	TF-M01022	1.929e-10 ²			
Factor THAP1; motif: YTGCCNNNA	TF-M07407	1.977e-10 ²			
Factor NF-kappaB; motif: NNGGGANTTCCCN	TF-M00891	2.004e-10 ²			
Factor BRF1; motif: CSCGAATRN; match class: 1	TF-M00529.3	2.012e-10 ²			
Factor CP2; motif: GCHCDAMCAG; match class: 1	TF-M00072.1	2.145e-10 ²			
Factor T3R-beta; motif: NNRGTGCTGACCYNN	TF-M11815	2.164e-10 ²			
Factor NF-kappaB; motif: AGGGGAATCCCTC	TF-M0454	2.185e-10 ²			
Factor AHR1; motif: NRCCGTGNN; match class: 1	TF-M00791.1	2.190e-10 ²			
Factor ZNF782; motif: TGCTCAAGTTMCCN	TF-M12092	2.217e-10 ²			
Factor WT1; motif: SMCNCCSC; match class: 1	TF-M01137.1	2.232e-10 ²			
Factor VDR; motif: NRGTCAANNRGKCA	TF-M10106	2.335e-10 ²			
Factor Olf-1; motif: NNCDABTCCYAGRGABRNNGN	TF-M00261	2.424e-10 ²			
Factor Rli-1E2A; motif: NCCGGAWRACSTGN	TF-M00472	2.508e-10 ²			
Factor N-Myc; motif: NNCCACGTGNNN; match class: 1	TF-M0055.1	2.651e-10 ²			
Factor KLF8; motif: CCACN; match class: 1	TF-M01160.1	2.674e-10 ²			
Factor USF; motif: NNRYACGTGRYNN; match class: 1	TF-M00121.3	2.890e-10 ²			
Factor USF; motif: NNRYACGTGRYNN	TF-M00121	2.890e-10 ²			
Factor CTCFL; motif: CNKAGGGGGGCGN	TF-M00769	2.893e-10 ²			
Factor SRF; motif: NCCAGGCCCMCN; match class: 1	TF-M1248.1	2.903e-10 ²			
Factor BTB4; motif: RCCACGCCCMCY	TF-M12185.1	3.054e-10 ²			
Factor SRF; motif: NRKCCAGGCCCM	TF-M00896	3.123e-10 ²			
Factor Bk-1-1; motif: TCCACGACCGAAGNN	TF-M00261	3.265e-10 ²			
Factor DEC1; motif: GTACGTGACG; match class: 1	TF-M11074.1	3.278e-10 ²			
Factor MZF1; motif: NNKNCACGTGNN	TF-M00755	3.382e-10 ²			
Factor ER-alpha; motif: ARGGTACG	TF-M00881	3.402e-10 ²			
Factor NRF-1; motif: CNTCTGACGTGCG	TF-M00694	3.469e-10 ²			
Factor E2F; motif: NTNTTGGCGCN	TF-M00875	3.697e-10 ²			
Factor E2F-1; motif: NWTGRCGCGN	TF-M11382	3.806e-10 ²			
Factor GSK1; motif: NNKCCACRCCCN; match class: 1	TF-M12174.1	4.444e-10 ²			
Factor vMy; motif: BRACAGGTGA	TF-M12262	4.480e-10 ²			
Factor VDR; motif: BRGGTCANNRRGDTCA	TF-M00671	4.794e-10 ²			
Factor SNA; motif: NRCAAGTGTGA	TF-M1258	4.795e-10 ²			
Factor ER-alpha; motif: NAGGTCAANNNTGACYN	TF-M11845	4.904e-10 ²			
Factor Sp3; motif: SSNNKNCACCTGN; match class: 1	TF-M01787.1	5.145e-10 ²			
Factor GNF-1; motif: CCTCTCY	TF-M00961	5.445e-10 ²			
Factor NR1B2B; motif: BRGGTCANNRRRG...	TF-M00895.1	5.579e-10 ²			
Factor LKLF; motif: NRKCCARCCCN	TF-M12172	5.916e-10 ²			
Factor NF-EB; motif: CHCCTTCGCGG	TF-M10105.1	6.003e-10 ²			
Factor BAR-gamma; motif: RAGTCANNNTGCGNNNNN; m...	TF-M00105	6.091e-10 ²			
Factor c-5; motif: NCCGAGAGTCCG; match class: 1	TF-M00759.1	6.299e-10 ²			
Factor Pax-5; motif: NTGTCACGCTGSAANTGANN	TF-M00694	6.423e-10 ²			
Factor NRF-1; motif: CGCATCGCCR	TF-M00652	6.963e-10 ²			
Factor NRF-1; motif: YCGCGTGGCG; match class: 1	TF-M01032.1	6.972e-10 ²			
Factor E2F-1; motif: NANCAGCGAATN	TF-M13148	7.018e-10 ²			
Factor SREBP-3; motif: NNKNCACNNMNN	TF-M01177.1	7.229e-10 ²			
Factor KLF1; motif: CMACACCCNNS; match class: 1	TF-M00553.1	8.300e-10 ²			
Factor LKLF; motif: TACAGGTCGTGACTCTGR	TF-M13828	8.550e-10 ²			

TF	stats				
Term name	Term ID	P-val	$-\log_{10}(P\text{-val})$	100	Show evidence codes
Factor AP-2/gammaHES-1 motif: NNACGCTGNNNNNSC...	TFM00862_1	9.00E-10 ⁴			
Factor AR motif: RGGWATGTTGTTGTCNN match class 1	TFM00453_1	9.057-10 ⁴			
Factor ZNF647 motif: NVAGGCTAC	TFM12286	9.772-10 ⁴			
Factor COUNP-TFL motif: BRGGTCRTGACCTN	TFM11739	9.981-10 ⁴			
Factor BRP motif: CSAGGAARN	TFM00357	1.0E+10 ⁴			
Factor HPIA motif: NNACGTGCNN	TFM00773	1.015-10 ⁴			
Factor HTRF motif: NCACCTGN	TFM11157	1.047-10 ⁴			
Factor ZEB1 motif: NCWCACCTG	TFM07235	1.156-10 ⁴			
Factor GIL motif: TGGGTGGCTN	TFM00454	1.182-10 ⁴			
Factor SMDP motif: GGRNVCAGTACACANCY match class 1	TFM00773_1	1.320-10 ⁴			
Factor HF-1alpha motif: NCACGT match class 1	TFM0032_1	1.344-10 ⁴			
Factor GABP-alpha motif: NACCGGAAGTN	TFM11414	1.352-10 ⁴			
Factor CTCF motif: RSYGCCMYCTRSTGGN	TFM06828	1.376-10 ⁴			
Factor USF motif: NRCCACGTGASN	TFM00796	1.392-10 ⁴			
Factor GIZ motif: NACACACCACGWRG	TFM12211	1.420-10 ⁴			
Factor Elk-1 motif: NACMGGAAGTN	TFM11432	1.439-10 ⁴			
Factor Elk-1ETV7 motif: ANSCGACGATDTCCGNT	TFM00214	1.440-10 ⁴			
Factor TIR-beta motif: NRRGTGRTGACCCYN	TFM11817	1.468-10 ⁴			
Factor Erg motif: ACCGGAAGTN match class 1	TFM00362_1	1.504-10 ⁴			
Factor Net motif: NRCCGGAAGTN	TFM11439	1.504-10 ⁴			
Factor Erg motif: NACCGGAAGTN match class 1	TFM11396_1	1.515-10 ⁴			
Factor ZEB motif: NNACGAGTGN	TFM07371	1.668-10 ⁴			
Factor CSK motif: NKRAGWS	TFM10008	1.788-10 ⁴			
Factor NeunD2 motif: NNSCWCTGN	TFM00280	1.897-10 ⁴			
Factor SNA motif: NCACGAGTGN match class 1	TFM12256_1	1.820E-10 ⁴			
Factor ELFL motif: NCCGGAAGTN	TFM00253	1.830-10 ⁴			
Factor E2F motif: TTTSGCGS	TFM00026	1.902-10 ⁴			
Factor KLF1 motif: GRCCGCGCCN	TFM12163	1.985-10 ⁴			
Factor TACREB motif: RTGACGTATATACCCC	TFM00151	2.08E-10 ⁴			
Factor KLF1 motif: GAGNGGGGNGTGG	TFM00734	2.14E-10 ⁴			
Factor GLI1 motif: GACCAACAMG	TFM00702	2.171-10 ⁴			
Factor Pax5 motif: GTACAGT	TFM04065	2.207-10 ⁴			
Factor YY1 motif: CAANATGGCGG	TFM10436	2.217-10 ⁴			
Factor SNAH2 motif: NNCAGTGN	TFM11375	2.240-10 ⁴			
Factor TF-2 motif: NCACCTGC	TFM11156	2.277-10 ⁴			
Factor CTCF motif: NCCNCSAGGGGGCCYN	TFM06889	2.32E-10 ⁴			
Factor Egr-2 motif: NMCGCCACCGCN	TFM12142	2.361-10 ⁴			
Factor E2F motif: NTTSGCGS	TFM00030	2.42E-10 ⁴			
Factor DCL motif: GTACGTGAC	TFM11374	2.43E-10 ⁴			
Factor PEA3 motif: NACCGGAAGTN match class 1	TFM11425_1	2.472-10 ⁴			
Factor SAP-1 motif: NRCCGGAAGTN	TFM11437	2.507-10 ⁴			
Factor Elk-1TRB2 motif: TNRCACCGAAGN match class 1	TFM00213_1	2.507-10 ⁴			
Factor CLOCBAM motif: NNNNACCTGGTN	TFM06889	2.587-10 ⁴			
Factor KLF1 motif: GRCCGCGCCN	TFM12162	2.611-10 ⁴			
Factor ASH-2 motif: NRRCAGCTGN	TFM11176	2.759-10 ⁴			
Factor ASH-2 motif: NGCAGCTGCN	TFM11178	2.759-10 ⁴			
Factor ASH-2 motif: NRKAGCTGNN match class 1	TFM11178_1	2.759-10 ⁴			
Factor ASH-2 motif: NRKAGCTGCN match class 1	TFM11178_1	2.759-10 ⁴			
Factor slug motif: NRKAGCTGCN	TFM00229	2.803-10 ⁴			
Factor NRSE motif: TTYAGGKCCCGGASAGYRCC match ...	TFM00225_1	2.844-10 ⁴			
Factor E2F-1 motif: TTTSGCGGMNR	TFM00516	3.027-10 ⁴			
Factor Sp3 motif: NGCAGCGCCMCN match class 1	TFM12154_1	3.09E-10 ⁴			
Factor BTB8 motif: NRRCACGCCCMCN match class 1	TFM00180_1	3.12E-10 ⁴			
Factor p73 motif: NNRCANWYCCARWYTC match class...	TFM00255_1	3.28E-10 ⁴			
Factor c-Krox motif: NGCAGCACCN match class 1	TFM12212_1	3.347-10 ⁴			
Factor MTF-1 motif: TGGCGAC match class 1	TFM00243_1	3.39E-10 ⁴			
Factor E2F motif: TTTSGCGS match class 1	TFM00027_1	3.39E-10 ⁴			
Factor ATF-3 motif: GGTGACGTGN	TFM00866	3.484-10 ⁴			
Factor Elk-1 motif: ACCGGAAGTN match class 1	TFM0099_1	3.42-10 ⁴			
Factor AP-2epi motif: CAGTGGG	TFM00468	3.52E-10 ⁴			
Factor GATA-1 motif: SNNGATNNNN match class 1	TFM00075_1	3.651-10 ⁴			
Factor FTF1 motif: SCAGCTGNNNNNYCN	TFM10043	3.787-10 ⁴			
Factor AP-4 motif: NRKAGCTGC	TFM00037	3.840-10 ⁴			
Factor Uyl-1 motif: NKAICTGYTNNCN match class 1	TFM00977_1	3.927-10 ⁴			
Factor MafB motif: GNTGAC match class 1	TFM00227_1	4.117-10 ⁴			
Factor FLI1 motif: ACCGGAAGTN match class 1	TFM00881_1	4.153-10 ⁴			
Factor ER-alpha motif: GONNNNTGACCCYN	TFM00820	4.971-10 ⁴			
Factor Sall1 motif: NGTCCGGGNA	TFM05967	5.070-10 ⁴			
Factor Net motif: NACCGGAAGTN	TFM11442	5.25E-10 ⁴			
Factor ERG motif: ACCGGAAGTN match class 1	TFM00975_1	5.32E-10 ⁴			
Factor THAP1 motif: YTGCCCNNA match class 1	TFM07807_1	5.56E-10 ⁴			
Factor T14qde motif: TGCCCNNGGNCN match class 1	TFM11476_1	5.575-10 ⁴			
Factor ERG motif: AGGTCAAGTACC	TFM00720	5.687-10 ⁴			
Factor TR2 motif: NRGTCRYGACCCYN	TFM11705	5.771-10 ⁴			
Factor BF-1 motif: NAMCGGGAAGTN match class 1	TFM11447_1	5.91E-10 ⁴			
Factor MyoD motif: GNCAGTGTGN	TFM11183	5.927-10 ⁴			
Factor BF-1 motif: NAMCGGGAAGTN match class 1	TFM00815_1	5.94E-10 ⁴			
Factor NR1B2 motif: RAGGTGATGACCTN	TFM11803	5.963-10 ⁴			
Factor ER-beta motif: GTCANSTGRCCYN match class 1	TFM00875_1	6.18E-10 ⁴			
Factor GIL motif: MCNNAGCACCAACV match class 1	TFM00871_1	6.334-10 ⁴			
Factor SPH motif: RCCACGCCCMCY match class 1	TFM12149_1	6.335-10 ⁴			
Factor Pli-3 motif: NACCGGAAGTN match class 1	TFM11304_1	6.45E-10 ⁴			
Factor pax-2 motif: NSGTGACCSWTSANYGMYN	TFM11836	6.661-10 ⁴			
Factor Hey1 motif: NGCAGCTGNN match class 1	TFM11359_1	6.82E-10 ⁴			
Factor SPH motif: NCCACGCCCMCN match class 1	TFM12150_1	6.88E-10 ⁴			
Factor AP-2gamma motif: NNNNNGCCCTNGGNC match...	TFM07189_1	6.907-10 ⁴			
Factor NR1B2 motif: NRGTCANRGTCAN	TFM11792	6.950-10 ⁴			
Factor HES-1 motif: NNCKYGTGNN match class 1	TFM07042_1	7.033-10 ⁴			
Factor PPARalphaRBPalpha motif: NNRGTCATWGGGGT...	TFM00518	7.412-10 ⁴			
Factor REST motif: GGAGAGC match class 1	TFM04736_1	7.65E-10 ⁴			
Factor ERM motif: NRCMGGAAGTN match class 1	TFM12142_1	7.85E-10 ⁴			
Factor SAP-1 motif: NRRCGGAAGTN	TFM11436	7.88E-10 ⁴			
Factor ELK1 motif: ACCGGAAGTN	TFM00930	7.95E-10 ⁴			
Factor AR motif: GGNACNNRTGTCT match class 1	TFM0201_1	8.00E-10 ⁴			
Factor PLAG1 motif: GRGCNNNNNNRRGG match class 1	TFM07778_1	8.02E-10 ⁴			
Factor ZBP1 motif: GCCCTCCCCC match class 1	TFM00392_1	8.33E-10 ⁴			
Factor FLJ-1 motif: NATTCCTGGT match class 1	TFM00813_1	8.48E-10 ⁴			
Factor Elk-1Pax-9 motif: ACCGGAACACGWSANTG m...	TFM00236_1	9.294-10 ⁴			
Factor c-ets-1p54 motif: NCMGGAGWNN match class 1	TFM0032_1	9.313-10 ⁴			
Factor Pax-2 motif: CAYCCTAGT	TFM00839	9.34E-10 ⁴			

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Term name	Term ID	Pval	$-\log_{10}(P\text{-val})$	100	Show evidence codes
Factor c-ets-2 motif: ACCGGAAGTN; match class: 1	TFM00064_1	9.734E-10			
Factor HPIA motif: NNACGTGCNN; match class: 1	TFM00773_1	1.001E-10			
Factor GIL motif: TGGGTGGCTN; match class: 1	TFM00750_1	1.032E-10			
Factor CREB motif: TGACGTGTCADYN	TFM00820	1.047E-10			
Factor GATAD2A motif: CCTCTG	TFM00726	1.055E-10			
Factor ASH-2 motif: NRKACGTGNN	TFM11175	1.075E-10			
Factor ASH-2 motif: NRKACGTGNN; match class: 1	TFM11175_1	1.075E-10			
Factor MASH-1 motif: NGCAGCTGCN; match class: 1	TFM11174_1	1.075E-10			
Factor MASH-1 motif: NRKAGCTGCN	TFM11174	1.075E-10			
Factor MASH-1 motif: NRKAGCTGCN; match class: 1	TFM11173_1	1.075E-10			
Factor Fli-1 motif: NACCGGAAGTN; match class: 1	TFM11173	1.075E-10			
Factor LBP-1 motif: CAGCTG; match class: 1	TFM00644_1	1.077E-10			
Factor E2F motif: TTTSGCGS	TFM00027	1.087E-10			
Factor BTB8 motif: NRCCACGCCCMCN; match class: 1	TFM12182_1	1.099E-10			
Factor USF2 motif: NNNNGTCAGTGRNN	TFM00920	1.148E-10			
Factor NF-1 motif: NACCGGAAGTN; match class: 1	TFM11400_1	1.148E-10			
Factor Nrf-1 motif: CNSTGCGCATGCGGNN; match class: 1	TFM10018_1	1.161E-10			
Factor Hey2 motif: NGCAGCTGNN	TFM11353	1.170E-10			
Factor RAR-gamma motif: RSGTCANNTGNCNNNN	TFM10045	1.193E-10			
Factor Arnt motif: NDNNGCAGTGNNNNN	TFM00236	1.210E-10			
Factor BRB1 motif: NACCGGAAGTN; match class: 1	TFM11410_1	1.220E-10			
Factor ZNF515 motif: GTGGGGGGTN; match class: 1	TFM10121_1	1.23E-10			
Factor GABP-alpha motif: NRCCGGAAGTN; match class: 1	TFM11415_1	1.244E-10			
Factor MTF-1 motif: CCGNGTGCAV	TFM04619	1.251E-10			
Factor SPZ1 motif: CCAGGTAKWACAGN	TFM01109	1.316E-10			
Factor SREBP-2 motif: NTCACGNNNN	TFM00852	1.322E-10			
Factor TFE8 motif: RNACAGTGAC	TFM04104	1.341E-10			
Factor HF-1alpha motif: GNACGTGM; match class: 1	TFM00994_1	1.358E-10			
Factor Elk-1 motif: NACMGGAAGTN; match class: 1	TFM11412_1	1.410E-10			
Factor PPM3S motif: NDTGCTCCN	TFM12119	1.428E-10			
Factor YY1 motif: NGCCGATTNN; match class: 1	TFM00041_1	1.480E-10			
Factor E2F motif: TTTSGCGS	TFM00039	1.506E-10			
Factor HES-1 motif: ANSKCYGTGCGNG	TFM01009	1.531E-10			
Factor ERM motif: ACCGGAAGTN; match class: 1	TFM00269_1	1.609E-10			
Factor meis1EP-1 motif: NTGCGGAAGTN; match class: 1	TFM00877_1	1.620E-10			
Factor PEA3 motif: NACCGGAAGTN; match class: 1	TFM11428_1	1.623E-10			
Factor KLF4 motif: NRRCACGCCCMCN; match class: 1	TFM12184_1	1.643E-10			
Factor BTB2 motif: NMCACGCCCN; match class: 1	TFM12161_1	1.644E-10			
Factor ERG motif: ACCGGAAT; match class: 1	TFM01752_1	1.704E-10			
Factor SMDX motif: GGGGAGM	TFM04846	1.722E-10			
Factor ZFs motif: NGAGCGG; match class: 1	TFM01111_1	1.723E-10			
Factor NF-1 motif: YGCGCATGCGCN	TFM04059	1.753E-10			
Factor AP-4 motif: WGARYCAGTGYGNCNK	TFM00005	1.762E-10			
Factor TIR-beta motif: NRGTCAAAGTGRNN; match class: 1	TFM11814_1	1.833E-10			
Factor BR-alpha motif: AGGTCAANNTGACC	TFM00718	1.839E-10			
Factor TIR-beta motif: NNRGTCATGCGNN; match cla...	TFM11815_1	1.85E-10			
Factor TELG motif: GGGGGGNNNN; match class: 1	TFM00805_1	1.973E-10			
Factor meis1Mac motif: NTGACNNNNNACAGTGC	TFM00875	1.997E-10			
Factor c-Ets-1 motif: NNNRCCGGAWNNNNNN; match clas...	TFM00718_1	2.008E-10			
Factor BR-1 motif: ACTCTCGGG; match class: 1	TFM04074_1	2.025E-10			
Factor BR1 motif: NACCGGAAGTN	TFM11413	2.039E-10			
Factor BF-1 motif: NANGCGGAAGTN; match class: 1	TFM11481_1	2.18E-10			
Factor REST motif: TTCAGCACCAAGGACAGCCCN	TFM00650	2.24E-10			
Factor BRB1 motif: NACCGGAAGTN	TFM11420	2.249E-10			
Factor ZNF215 motif: RGGAGAMAM	TFM00609	2.28E-10			
Factor NR1B1 motif: NRGTCANNRGTCAN; match class: 1	TFM11796_1	2.28E-10			
Factor HF-1alpha motif: GNACGTG	TFM00994	2.325E-10			
Factor ZNF524 motif: NCTCGNACCCCN	TFM12100	2.32E-10			
Factor BRB1 motif: NNNRCCGGAAGTNNNNNNNN; mat...	TFM00611_1	2.362E-10			
Factor ERM motif: NRKAGGAAGTN	TFM11427	2.39E-10			
Factor PPARalphaRBPalpha motif: NNRGTCATWGGGGT...	TFM00518_1	2.423E-10			
Factor AP-4Rf-1 motif: RSCGAWRACAGTGN	TFM00845	2.440E-10			
Factor GABPalpha, GABPbeta motif: CTCCKG; match cla...	TFM03791_1	2.451E-10			
Factor BR-alpha motif: NAGGTCAYSYGACCTN; match cla...	TFM11842_1	2.472E-10			
Factor SpZ1 motif: DNNGGGGGGNNNNNNNN; match class: 1	TFM00446_1	2.539E-10			
Factor Hey2 motif: NGCAGCTGNN; match class: 1	TFM10754_1	2.560E-10			
Factor ZNF515 motif: WNSCCCGGCGG; match class: 1	TFM00835_1	2.579E-10			
Factor gl3 motif: NGACCCACCGGNG	TFM12213	2.64E-10			
Factor GEMN3 motif: NCWGGARRRRRRNGGNG; match clas...	TFM00727_1	2.730E-10			
Factor E2F-1 motif: TTTSGCGG; match class: 1	TFM00041_1	2.753E-10			
Factor E2F-1 motif: NTTSGCGG; match class: 1	TFM00041_1	2.783E-10			
Factor LBP-1 motif: CAGCTG	TFM00644	2.852E-10			
Factor DEAF1 motif: RNNRTTCGGGNTTCCGGRNN	TFM01002	2.861E-10			
Factor BR-alpha motif: AGGTCAANMTGACC; match class: 1	TFM04718_1	2.882E-10			
Factor E2F motif: TTTSGCGG; match class: 1	TFM00025_1	2.89E-10			
Factor PPARalphaRBPalpha motif: NNRGTCATWGGGGT...	TFM00518	2.89E-10			
Factor AP-4 motif: NAGGTCATGNCNK; match class: 1	TFM01460_1	2.953E-10			
Factor E2F motif: NRKCGCGAAAN	TFM00020	2.971E-10			
Factor AHR motif: NNNNGCTGTCNNNNNN	TFM07347	2.989E-10			
Factor GABP-alpha motif: NNNRCCGGAAGTN	TFM00935	3.116E-10			
Factor E2F motif: NACCGGAAGTN; match class: 1	TFM11192_1	3.27E-10			
Factor egr-3 motif: TGGGG; match class: 1	TFM00818_1	3.301E-10			
Factor BR-alpha motif: NAGGTCATCGTGCTTN	TFM11841	3.334E-10			
Factor Hey2 motif: NGCAGCTGNN; match class: 1	TFM11513_1	3.357E-10			
Factor GIL motif: NTRAGTAAGGTTGGCCC	TFM03311	3.453E-10			
Factor AP-2bp motif: CAGTGGG; match class: 1	TFM00968_1	3.593E-10			
Factor HEB motif: RCWGGTG	TFM00698	3.597E-10			
Factor Egr-4 motif: NMCGCGCACGAGN	TFM12145	3.598E-10			
Factor Ifg-2 motif: NGACGATGS	TFM00962	3.683E-10			
Factor GCMC-HES-7 motif: NTRNGGNNNNNACGACGAYNN	TFM00690	3.824E-10			
Factor NfYB motif: NCCNCGGCCCCC	TFM00693	4.075E-10			
Factor Luminy motif: NGCAGCATGGMN	TFM11249	4.255E-10			
Factor RREB-1 motif: GRSDDGGGTTGGGGG	TFM07062	4.36E-10			
Factor E2F motif: NCSGCSAAAN	TFM00919	4.367E-10			
Factor ZNF76 motif: NTRTGGGGACG	TFM00047	4.48E-10			
Factor ZNF363 motif: NNNNTGNNNNNCCGACGCTG	TFM01158	4.48E-10			
Factor GAPBA motif: ACCGGAAGTN; match class: 1	TFM00990_1	4.60E-10			
Factor E2F motif: RNACAGTCAV	TFM04196	4.843E-10			
Factor E2F-1LDP-1 motif: TTTTSGCGG; match class: 1	TFM00736_1	4.903E-10			

Table S4

Functional gene groups

GENE FAMILY	ALL GENES	TPE GENES	RR	FUNCTION	INVOLVED IN
ZNF	388	99	1.609	DNA binding proteins	transcriptional regulation, development, protein degradation, DNA repair
SNO	293	60	1.291	glutamine amidotransferases	pyridoxine biosynthesis, response to nutrient limitation
KCN	97	19	1.235	potassium channels	antagonism of insulin secretion
RAB	89	17	1.205	small G proteins	vesicular transport; organelle formation; cell growth and development
PPP	81	16	1.246	serine/threonine phosphatases	cell growth and energy metabolism
MRP	79	16	1.277	ATP-binding cassette transmembrane proteins	export of organic anions and drugs
WDR	62	16	1.628	WDR domain proteins	DNA damage sensing; DNA repair, protein degradation, epigenetic regulation and immunity
FBX	62	12	1.221	F-box proteins	protein degradation and hematopoiesis
ADA	58	14	1.522	adenosine deaminases	purine metabolism; immunity
SER	57	17	1.881	serine proteases	myeloid and lymphoid immunity, embryological growth and synaptic plasticity
POL	55	13	1.491	DNA polymerases	DNA repair
FOX	54	11	1.285	transcription factors	cell growth and development
MAG	48	14	1.840	cancer-associated proteins	stress adaptation
ABC	46	9	1.234	ATP binding proteins	drug resistance
UBE	43	11	1.613	ubiquitination factors	protein degradation
ZBT	43	10	1.467	DNA binding proteins	development
IL1	42	8	1.201	cytokines	regulation of immune and inflammatory responses to infections or sterile insults
TBC	40	11	1.734	GAP domain proteins	cell growth
GAL	39	11	1.779	galactose transfer proteins	metabolism; innate and adaptive immunity
CFA	38	8	1.328	poly(ADP-ribose) polymerases	ADP ribosylation; tumor suppressor mechanisms
GOL	36	21	3.680	Golgi proteins	vesicular transport and Golgi architecture
SCA	36	11	1.927	transcription factors	neuroprotection
PRK	35	7	1.261	serine/threonine kinases	regulation of meiosis and mitosis
MET	34	8	1.484	receptor tyrosine kinases	cell growth
CAC	31	9	1.831	calcium channels	cell-to-cell communication, neurotransmission and neuroprotection
FGF	31	7	1.424	growth factors	cell growth
PRS	28	11	2.478	phosphoribosylpyrophosphate synthetases	ATP dependent cellular metabolism, cell growth and DNA repair
CHR	26	7	1.698	CHR domain proteins	transcriptional regulation of the cell cycle
SH3	26	7	1.698	SH3 domain proteins	signaling pathways regulating the cytoskeleton and cell growth (Ras, Src)
ZFP	25	7	1.766	DNA binding proteins	regulation of transcriptional and translational processes
IGH	23	19	5.211	immunoglobulin heavy locus proteins	adaptive immunity
KLK	19	10	3.320	serine proteases	innate immunity and tissue specific functions (neural plasticity, amyloid hydrolysis)
LCN	9	9	6.308	transcriptional regulators	cell growth, DNA repair, ubiquitination and tumor suppression

Genes are aggregated to their first three letters that commonly indicate a gene family. The column "ALL GENES" presents the number of members in the whole genome, the "TPE-GENES" column the number among the selected TPE-OLD candidates. RR is the ratio of the relative frequency in the TPE-OLD subset to the relative frequency in the genome. The PPP genes are among the most abundant of TPE-OLD candidates.

Table S5.
Control and patient fibroblast cell lines

Cell Line	Age, Sex	Molecular Defect	Primary Cells*		Immortalized Cells*	
			PD Low	PD High	PD Low	PD High
707	5 month, female	no	17 [0.72]	54 [0.20]	18 [0.60]	70 [1.59]
731	5 month, male	no	13 [0.71]	55 [0.15]	16 [0.71]	56 [2.91]
778	8 month, male	no	15 [0.48]	41 [0.16]	14 [1.18]	66 [2.72]
811	1 month, female	no	15 [0.81]	49 [0.24]	28 [1.18]	63 [2.84]
HGADFN003	2 years 0 month, male	Exon 11 mutation C->T, clinically affected	19 [0.68]	34 [0.46]	34 [1.44]	63 [0.87]
HGADFN127	5 years 0 month, female	Exon 11 mutation C->T, clinically affected	19 [0.52]	40 [0.24]	15 [0.96]	57 [2.74]
HGADFN164	4 years 8 month, female	Exon 11 mutation C->T, clinically affected	19 [0.28]	42 [0.17]	15 [0.67]	64 [1.10]
HGADFN178	6 years 11 month, female	Exon 11 mutation C->T, clinically affected	20 [0.47]	34 [0.28]	22 [1.03]	59 [1.54]
N14	55 years, female	no	18 [1.11]	39 [0.78]		52 [2.65]
Young1[#]	2 years, male	no		42		
Young5[#]	9 years, female	no		38		
Midage1[#]	34 years, male	no		43		
Midage3[#]	48 years, female	no		40		
Old1[#]	78 years, male	no		37		
Old2[#]	82 years, female	no		40		

* Mean telomere length in brackets next to the PD (population doubling number). Telomere length was measured using a monochrome multiplex qPCR. The PD was calculated as follows: ((current cell number / previous cell number)log)/0.3, # These cell lines were only analyzed in high passage.

Table S6.**Log-transformed distance between the gravity centers after 3D-reconstruction**

Results of hierarchical linear models. The table shows the results of hierarchical linear models (HLMs) with the intracellular probe distances in gravity centers after 3D reconstruction as dependent variables. There was no significant difference between progeria cell lines and control cell lines before immortalization (mean difference -0.03, $p=0.72$), and immortalized cells showed significantly lower distances than nonimmortalized cells: mean difference = -0.34, $p < 0.0001$. The effect of immortalization did not differ between progeria cell lines and control cell lines: mean difference after immortalization: 0.03, $p = 0.76$. Similar results were found for all shortest and longest probe pair distances per cell.

Parameter	Distance AB		Distance CD		Combined distance AB and CD [#]	
	β (95%-confidence interval)	p-value	β (95%-confidence interval)	p-value	β (95%-confidence interval)	p-value
Progeria cells versus control cells	-0.03 (-0.22 to 0.16)	0.76	-0.04 (-0.25 to 0.17)	0.72	-0.03 (-0.22 to 0.15)	0.72
Immortalisation versus no immortalisation	-0.38 (-0.52 to -0.25)	< 0.0001	-0.29 (-0.41 to -0.17)	< 0.0001	-0.34 (-0.43 to -0.25)	< 0.0001
Immortalisation in Progeria cells versus immortalisation in control cells	0.04 (-0.15 to 0.23)	0.67	0.004 (-0.17 to 0.17)	0.97	0.02 (-0.11 to 0.15)	0.76

[#] Distances AB (shortest probe distance) and CD (longest probe distance) nested within cells and cells nested within cell lines.

Table S7.
List of primers used for qPCR

All TaqMan probes used for gene expression analysis with qPCR spans exons and were obtained from Applied Biosystems.

Gene name	Exon boundary	Assay location	Amplicon length	Ref. Nr.
C1S	4-5	671	85	Hs00156159_m1
CACNA1A	41-42	6195	87	Hs01579431_m1
CDKN1A (p21)	2-3	566	66	Hs00355782_m1
DSP	8-9	1385	59	Hs00950591_m1
HTT	64-65	9046	69	Hs00918174_m1
ISG15	2-2 #	482	140	Hs01921425_s1
PPP2CA	6-7	1259	77	Hs00427260_m1
PPP2CB	1-2	513	125	Hs00602137_m1
PPP2R1A	3-4	566	111	Hs01026388_m1
PPP2R1B	11-12	1505	146	Hs00988483_m1
PPP2R2C	9-10	1126	59	Hs00902099_m1
PPP2R2D	*	1904	91	Hs00908762_g1
PPP2R3B	7-8	1302	61	Hs00203045_m1
PPP2R5C	12-13	1338	65	Hs00604899_g1
SCAMP4	5-6	502	91	Hs00365263_m1
SORBS2	10-11	1598	87	Hs01125197_m1
TBC1D3	11-12	938	83	Hs04191701_gH
TERT	3-4	1826	57	Hs00972650_m1
WFS1	2-3	404	81	Hs00903605_m1
ZNF286	6-6 #	3621	142	Hs00612325_s1
Human PPI (Cyclophilin A)		435	98	4333763F

* Only amplicon spans exons, probe does not span exons; # Both primers and probe map within a single exon.

Primer telomere length measurement (73)	Primer sequence		
telg	5'-	ACACTAAGGTTTGGGTTTGGGTTTGGGTTTGGGTTAGTGT	-3'
telc	5'-	TGTTAGGTATCCCTATCCCTATCCCTATCCCTATCCCTAACA	-3'
albu	5'-	cggcggcgggcggcgcgggctgggcggAAATGCTGCACAGAATCCTTG	-3'
albd	5'-	gccccgcccgccgcgcccgctcccgccgGAAAAGCATGGTTCGCTGTT	-3'

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