**Supplementary Table 1.** List of 25 genes found with the parallel mutation strategy together with their possible role in aging based on previous studies.

Gene	Organism in GenAge	Previous association to aging or related traits	References
АКАР9	-		
ATG7	D. melanogaster and C. elegans	Pro-longevity	
BRD8	-		
C1QTNF2	-	Weight loss	Hatoum et al. 2013
C9orf96/STKLD1	-		
DSC2	-	Dilated cardiomyopathy	
EFEMP2	-		
FCGBP	-		
FGA	-	Blood fibrinogen levels	
GP5	-		
HEMK1	-		
IQCK	-	Associated to BMI	Spelliotes et al. 2010
KIAA1614	-		
KLKB1	-	Blood pressure	
MNT	D. melanogaster	Pro-longevity	
MYO16	-	Age of onset in Alzheimer Disease Red blood cell count	Herold et al. 2016 Astle WJ et al. 2016
MYOF	-	Associated to muscle repair Epigenetically modified by aging	Demontis et al. 2013 Benton et al. 2017
PLTP	-	HDL levels	Global Lipids Genetics Consortium et al. 2013
PRL	-	Ames dwarf mice lacking <i>PRL</i> , <i>GH</i> and <i>TSH</i> live much longer than their normal siblings and exhibit many symptoms of delayed aging	Brown-Borg et al. 1996
RAD51AP1	-	double-strand break repair correlated to aging important player in the cellular senescence of yeast	Lorenzini et al. 2009 Park et al. 1999
RXFP4	-		
STK31	-	Age of onset in Alzheimer Disease	Mez et al. 2017
SUPV3L1	S. cerevisae	Anti-longevity	
WDR87	-		
ZNF233	-		

**Supplementary Table 2.** Each of the 25 amino-acid changes were assessed in three mammal longlived species. The same change in the "*Increased Lifespan*" group was evaluated in these species and reported in the last column. NA: not available in the 100-way alignment. None: The long-lived species showed the reference amino-acid.

Gene	Reference	Parallel change	Long-lived not reference
AKAP9	v	I	N.A.
ATG7	A	т	N.A.
BRD8	R	Q	N.A.
C1QTNF2	А	т	N.A.
C9orf96	v	L	hetGla2, myoDav1
DSC2	v	I	hetGla2
EFEMP2	v	I	None
FCGBP	v	Α	N.A.
FGA	А	v	myoDav2, myoLuc2
GP5	н	Q	hetGla2
HEMK1	Q	R	N.A.
ΙQCK	N	D	hetGla2*
KIAA1614	м	v	N.A.
KLKB1	т	A	myoDav2, myoLuc2
мит	т	A	hetGla2*
MYO16	м	I	hetGla2, myoDav1, myoLuc2
MYOF	Р	L	hetGla2
PLTP	Р	т	None
PRL	I	м	myoDav2*, myoLuc2*
RAD51AP1	v	A	hetGla2*
RXFP4	v	A	N.A.
STK31	Y	С	myoDav2*, myoLuc2*
SUPV3L1	т	м	None
WDR87	v	1	None
ZNF233	R	Q	N.A.

\* Shares the very same aminoacid change than "Increased Lifespan" group.

**Supplementary Table 3.**Top significant genes (p=9e-05) from the 5 life-history traits assessed. The genes marginally significant after FDR (q<0.1) are highlighted in bold. Last column shows whether the gene has been previously described in relation to aging in GenAge databases and in which one.

Trait	P-value	FDR corrected p-vaue (BH)	Gene	GenAge
MLS	3.7e-06	0.06	STK17B	-
MLS	4.6e-05	0.37	ITPR1	model org., human
Female Maturity	2.6e-05	0.30	HSPB6	model org.
Female Maturity	3.8e-05	0.30	COX5B	human, model.org
Female Maturity	6.7e-05	0.38	MYL2	-
Female Maturity	8.3e-05	0.38	SLC38A5	-
Gestation Length	3e-06	0.04	IQCA1	-
Gestation Length	3e-05	0.15	TRIB2	-
Gestation Length	3.7e-05	0.15	FBXO38	-
Gestation Length	3.8e-05	0.15	MEF2D	model org.
Gestation Length	6.1e-05	0.19	SLC10A1	-
Weaning Time	1e-05	0.14	TMEM182	-
Weaning Time	2.8e-05	0.14	JARID2	-
Weaning Time	3.6e-05	0.14	AP4M1	model org.
Weaning Time	4.8e-05	0.14	PRDX1	human, model org.
Weaning Time	5.6e-05	0.14	POLR1D	-
Weaning Time	5.5e-05	0.14	S100A2	-
Weaning Time	5.6e-05	0.14	GFAP	Longevity.Map
Weaning Time	6.2e-05	0.14	CHD4	model org.
Body Mass	4.1e-06	0.06	CDC7	-
Body Mass	1.4e-05	0.09	PER3	Longevity.Map
Body Mass	1.8e-05	0.09	SPRRG2	-
Body Mass	6.2e-05	0.2	KLHL9	-
Body Mass	6.5e-05	0.2	ENO3	-
Body Mass	8.17e-05	0.2	CD79A	-
Body Mass	9.3e-05	0.2	FANCD2OS	-

**Supplementary Table 4.** FDR corrected p-values (within mitochondrial genes) of PGLS association between each mitochondrial gene and each of the assessed life-history traits. Lower table represents PGLS p-values of gene root-to-tip omegas including mitochondrial-wide omegas as covariate. Results shown in the upper part of the table did not include mitochondrial-wide omegas as covariate in the PGLS.

Without mitocondrial-wide omegas										
	MaximumLongevity	AdultWeight	FemaleMaturity	Gestation	Weaning					
ATP6	0,040	4.72e-10	0,367	1,000	0,255					
ATP8	0,905	0,242	0,389	1,000	0,939					
COX1	0,374	NA	0,572	1,000	0,939					
COX2	0,338	0,242	0,367	1,000	0,489					
COX3	0,034	0,281	1,000	1,000	0,760					
СҮТВ	0,006	0,242	0,236	1,000	0,105					
ND1	0,034	0,047	0,980	1,000	0,358					
ND2	0,338	0,242	NA	1,000	0,765					
ND3	0,338	0,505	0,572	1,000	0,340					
ND4	0,302	0,242	1,000	1,000	0,806					
ND4L	0,338	0,242	NA	1,000	0,810					
ND5	0,124	0,242	0,367	1,000	0,358					
ND6	0,726	0,599	NA	1,000	0,939					

With mitocondrial-wide omegas									
	MaximumLongevity	AdultWeight	FemaleMaturity	Gestation	Weaning				
ATP6	0,916	2,20E-06	0,800	0,477	0,893				
ATP8	0,916	0,763	0,745	0,477	0,893				
COX1	0,916	NA	0,836	0,477	0,893				
COX2	0,916	0,980	0,800	0,949	0,893				
COX3	0,916	0,980	0,800	0,611	0,893				
СҮТВ	0,916	0,980	0,745	0,638	0,893				
ND1	0,916	0,673	0,800	0,761	0,893				
ND2	0,916	0,965	0,800	0,617	0,893				
ND3	0,916	0,980	0,824	0,611	0,893				
ND4	0,916	0,980	0,800	0,611	0,893				
ND4L	0,916	0,980	0,745	0,477	0,893				
ND5	0,916	0,980	0,800	0,623	0,893				
ND6	0 932	0.980	0.800	0 477	0.893				

Species	UCSC version	Family	MLS (y)	LQ	Body weight (g)	Female maturity (d)	Gestation (d)	Weaning (d)
Homo sapiens	hg38	Hominidae	122.5	4.6	62035	4745	280	639
Pan troglodytes	panTro4	Hominidae	59.4	2.4	44983.5	3376	229	1111
Pan paniscus	panPan1	Hominidae	55	2.2	39925	3194	232	635
Gorilla gorilla	gorGor3	Hominidae	55.4	1.9	139842	2829	256	834
Pongo abelii	ponAbe2	Hominidae	58	2.2	55000	4380	227	1440
Nomascus leucogenys	nomLeu3	Hylobatidae	44.1	2.4	6000	2555	210	720
Macaca mulatta	rheMac3	Cercopithecidae	40	2.1	8235	1231	165	292
Macaca fascicularis	macFas5	Cercopithecidae	39	2.1	6362.5	1238	165	242
Papio anubis	papAnu2	Cercopithecidae	25.2	1.2	17730	2555	178.96	420
Chlorocebus sabaeus	chlSab2	Cercopithecidae	13	0.7	5620	730	165	365
Nasalis larvatus	nasLar1	Cercopithecidae	25.1	1.2	14617.5	1460	166	213
Rhinopithecus roxellana	rhiRox1	Cercopithecidae	29.5	1.4	14750	1642.5	195	365
Callithrix jacchus	calJac3	Callitrichidae	22.8	2	255.2	477	144	62
Saimiri boliviensis	saiBol1	Cebidae	30.3	2.3	615	1000.3	158	150
Tarsius syrichta	tarSyr2	Tarsiidae	16	1.6	119.2	547.5	179	83
Microcebus murinus	micMur1	Cheirogaleidae	18.2	2	64.8	243	61	37
Otolemur garnettii	otoGar3	Galagonidae	18.3	1.3	1300	600	132	140
Cercocebus atys	Caty	Cercopithecidae	26.8	1.4	8600	1650	167	300
Colobus angolensis	Cang	Cercopithecidae	35.3	1.8	8625	700	162.5	450
Macaca nemestrina	Mnem	Cercopithecidae	37.6	2	7912.5	1125	172	324
Mandrillus leucophaeus	Mleu	Cercopithecidae	39	1.8	18250	1277	179	487
Rhinopithecus bieti	Rbie	Cercopithecidae	NA	NA	9960	NA	NA	NA
Propithecus coquereli	Pcoq	Indridae	31	1.8	4190	1277	141	180.96
Aotus nancymaae	Anan	Cebidae	16	1.2	788	211	133	13
Cebus capucinus	Ссар	Cebidae	54	3.3	2655	1505	162	521

Supplementary Table 5. Life history data used. In gray, species present in the UCSC alignment.

**Supplementary Table 6.** Number of genes and species per each gene alignment after applying the pipeline for including the new 8 primate species. In gray, the number of gene alignments that include more than 17 primate species.

№ species	N <sup>o</sup> of genes
2	37
3	64
4	87
5	107
6	133
7	204
8	263
9	380
10	458
11	673
12	800
13	938
14	1055
15	1269
16	1386
17	1255
18	1170
19	1329
20	1442
21	1418
22	1371
23	986
24	646
25	192

**Supplementary Table 7.** GO terms selected for each of the molecular hallmarks of aging (López-Otín, 2013).

Hallmark of Aging	GO terms included
Genomic Instability	DNA repair (GO:0006281) Nuclear lamina (GO:00005652)
Telomere Attrition	Telomere maintenance (GO:0000723) Telomere capping (GO:0016233)
Epigenetic Alterations	Histone modification (GO:0016570) DNA methylation (GO:0006306) Chromatine remodeling (GO:0006338)
Loss of Proteostasis	Chaperone-mediated protein folding (GO:0061077) Autophagy (GO:0006914) Ubiquitin-proteasome system (GO:0043161)
Deregulated Nutrient Sensing	Insulin receptor signaling Pathway (GO:0008286) TOR signaling (GO:0031929)
Mitochondrial Dysfunction	Response to ROS (GO:0000302) Mitochondrial genome maintenance (GO:0000002)
Cellular senescence	Cellular senescence (GO:0090398)
Stem Cell Exhaustion	Stem cell proliferation (GO:0072089)
Altered Intracellular Communication	Inflammatory response (GO:0006954) Inflammasome complex (GO:0061702)

#### Supplementary Figures Legends

**Supplementary Figure 1**. Spearman correlations between all life-history traits used in the study.

**Supplementary Figure 2.** Sequential threshold selection from 0 to 2 standard deviations from the family mean. In every interval from 0.6 to 1.4 standard deviations, the same 3 species were included in the *Increased Lifespan* group, suggesting that this grouping was the more consistent across several cut-offs (*Results*). Nonetheless, we performed the analyses selecting 0.5 (less stringent) and 1.5 standard deviations (more stringent) thresholds, which modified the number of included species in the *Increased Lifespan* group to 4 (addition of *Callythrix jacchus*) and 2 (drop of *Macaca fascicularis*), respectively. Using a soft cut-off of 0.5 SD, only one gene was found: a change in Q497R residue affecting the *CNTN5* gene. Interestingly, this gene is found in the LongevityMap database. Using a threshold of 1.5 SD, only 11 genes were found to harbor parallel changes within *Homo sapiens* and *Macaca mulatta* compared to the Control group. These genes were slightly enriched in musculoskeletal abnormalities and diseases (adjP=0.0126). Among them, one gene (*COL6A3*) was also present in the LongevityMap database.

**Supplementary Figure 3.** Multiple alignment of each gene discovered in the parallel mutation approach across the 17 primate species. White: non-conserved; purple: similar; blue:>50% conserved amino-acid.

**Supplemental Figure 4.** Distribution of parallel mutations in the test groups from a random sampling in the 17 species tree. Each column represent a different sampling protocol, described in methods. Red triangles show the empirical number of parallel differences observed between hg38, macFas5 and rheMac3.

**Supplementary Figure 5.** Venn diagram showing the number of overlapping genes between the list of 25 parallel mutated genes (Common), the list of human aging genes downloaded from GenAge (Human), the list of aging genes in model animals downloaded from GenAge (Models), the set corresponding to human genetic variants associated with longevity also downloaded from AnAge genes (Longevity), and the gene set from mortality/aging GO term (GO). All lists of genes were obtained on 06/14/2016. Note that three genes (ATG7, MNT and SUPV3L1) from the discovered gene set were present in another Aging gene list (Models).

**Supplemental Figure 6**. Phylogenetic regressions of primate life-history traits and genome-wide omega. P-values for the PGLS regression are displayed inside each plot. Note that only gestation length was significantly correlated to the genome-wide omega value.

**Supplemental Figure 7.** Correlation between p-values obtained in the PGLS regression using three different species trees. UCSC tree was downloaded from the 20-way alignment data (ucsc); chronogram (chrono) and phylogram (phylo) trees were downloaded from 10KTrees webpage. Notice that all the analyses in this study were performed using the chronogram tree from 10kTrees.

**Supplemental Figure 8**. The number of overlapping occurrences between MLS, weaning time, gestation and female maturity (in red) and body mass (in blue) are plotted together with a random distribution of 4/5 bootstrapped phenotypes 1000 times. The number of overlapping significant genes is much higher than expected in the studied phenotypes.

**Supplementary Figure 9. A)** Heat map of GO, KEGG, Pathway Commons and diseases enrichment created using the enrichment analysis of overlapping significant genes between the 4 phenotypes (first column), genes showing a p-value < 0.01 in at least three life-history traits (2nd column) and genes showing a p-value < 0.01 in MLS, weaning time, female maturity and gestation length. **B)** Venn diagram of the genes with a p-value < 0.01 in the assessed life-history traits. **C)** Venn Diagram of significant genes (p-value<0.05) excluding body mass.

**Supplementary Figure 10.** Correlation plots between phenotype data from AnAge and ADW databases regarding four representative traits.

**Supplementary Figure 11. A)** Species included in the *Increased Lifespan* group are shown in red in the phylogenetic tree. Illustrations of the four levels of bootstrap to evaluate the significance in the number of parallel mutations are displayed in the figures: **B)** In the first level, shared mutations were evaluated within any possible grouping of 3 primate species (in yellow). **C)** In the second level, combinations of two Cercopithecidade (yellow) and one outgrup (green) were assessed for shared mutations. **D)** Third resampling consisted in combinations of two Cercopithecidae (yellow) and one Hominidae (green). **E)** Finally, combinations of two Cercopithecidae species (in yellow) plus Homo sapiens (in red) were evaluated. **F)** Phylogenetic tree including the new primates used. Species that were included in the *Increased Lifespan* group are shown in red.

**Supplementary Figure 12.** Violin plots showing the minimum number of species every mitochondrial gene needed to calculate  $\lambda$  correctly using the Pagel's  $\lambda$  method from *nlme* package. Distributions represent the maximum number of species used before an error appeared in calculating lambda (100 bootstraps of random subtraction of one specie without replacement). Roughly, when having less than 40 species it is not adequate to use Pagel's  $\lambda$  method and then, Brownian motion method should be prioritized.

MLS						- 0.8
0.78	Female Mat.					- 0.6
0.64	0.74	Gestation				- 0.2
0.67	0.71	0.68	Weaning			0.2
0.56	0.59	0.53	0.51	Weight		0.4
0.83	0.46	0.35	0.41	0.2	LQ	0.8



SD threshold

AKAP9	ATG7	BRD8	C1QTNF2	C9orf96	DSC2		
calJac3 saiBol1 RRLGTVQSGST hg38 RRLGTVQSGST gorGor3 RRLGTVQSGST ganTro4 RRLGTVQSGST panPan1 RRLGTVQSGST naCFas5 RRLGTVQSGST chIsa2 RRLGTVQSGST chIsa2 RRLGTVQSGST rhRox1 RRLGTVQSGST rhRox1 RRLGTVQSGST	Sixson and a six solution and a six solution and a six solution and a sol	L25   caljac3   BWREVLEGIQ     125   saiboli   BWREVLEGIQ     125   rheMac3   BWREVLEGIQ     125   rheMac3   BWREVLEGIQ     125   macFas5   BWREVLEGIQ     125   macFas5   BWREVLEGIQ     125   rhikoxi   BWREVLEGIQ     125   brakazi   BWREVLEGIQ     125   brakazi   BWREVLEGIQ     125   brakazi   BWREVLEGIQ     125   pafnad   BWREVLEGIQ     125   panTrod   BWREVLEGIQ     125   panBani   BWREVLEGIQ     125   ponAbe2   BWREVLEGIQ     125   ponAbe2   BWREVLEGIQ     125   nomL=u3   BWREVLEGIQ     125   narSuria   EWREVLEGIQ     125   narSuria   BWREVLEGIQ     125   narSuria   BWREVLEGIQ     125   narSuria   BWREVLEGIQ     125   tarSuria   BWREVLEGIQ     125   tarSuria   BWREVLEGIQ	1205 1128 1205 1205panTro4 panPan1CLCPALCPAAA CLCPALCPAAA CLCPALCPAAA CLCPALCPAAA CLCPALCPAAA 1205 	15 callac3 HITFVSGSFKS   15 saiBoll HITFVSGSFKS   15 rheMac3 HITFSGSFKS   15 rheMac3 HITFSGSFKS   15 rhAmac2 HITFSGSFKS   15 rhAmac2 HITFVSGSFKS   15 rhSan2 HITFVSGSFKS   15 rhSan2 HITFVSGSFKS   15 rhSan4 HITFVSGSFKS   15 rhSan4 HITFVSGSFKS   15 panTan4 HITFVSSSS   15 panBac4 HITFVSSSS   15 ponbac2 HITFVSSSS   15 ponLeu3 HITFVSSSSSS   16 micMur1 HITFVSNQKS   17 micMur1 HITFVSNQKS   9 otoGar3 DITFVSNQKSKS	288   CALLAC3   GUVTUDENTG   525     303   saiBol1   GUVTUDENTG   525     303   saiBol1   GUVTUDENTG   525     303   macFas5   GUVTDENTG   525     303   macFas5   GUVTDENTG   525     303   macAnu   GUVTDENTG   525     303   chalast   GUVTDENTG   525     303   naLari   GUVTUDENTG   525     303   panPaul   GUVTUDENTG   525     288   ponAbe2   GUVTUDENTG   525     303   mcMLuri   GUVTUDENTG   525     303   mcMuri   GUVTUDENTG   525     303   mcMuri   GUVTUDENTG   525		
EFEMP2	FGA	GP5	HEMK1	IQCK	KIAA1614		
nomLeu3 ch15ab2 gordor3 yrcvNEPGGF gordor3 yrcvNEPGGF gordor3 yrcvNEPGGF gordbe2 yrcvNEPGGF gallard yrcvNEPGGF gallard yrcvNEPGGF rhRox1 yrcvNEPGGF rhRox1 yrcvNEPGGF rhRox1 yrcvNEPGGF rhRox1 yrcvNEPGGF rhRox1 yrcvNEPGGF rhRox1 yrcvNEPGGF rhRox1 yrcvNEPGF rhRox1	265   callac3   ClockAPPEWA     265   saiBol1   CLE APPEWA     265   hg38   CLGKAPPEWA     264   gorGor3   CLGKAPPEWA     265   hg38   CLGKAPPEWA     265   paga   CLGKAPPEWA     265   paga   CLGKAPPEWA     265   panPani   CLGKAPPEWA     265   panPani   CLGKAPPEWA     265   panDail   CLGKAPPEWA     265   nasLari   CLGKAPPEWA     265   nasLari   CLGKAPPEWA     265   nasLari   CLGKAPPEWA     265   nasLari   CLGKAPPEWA     265   pafanu2   CLGKAPPEWA     265   pafanu2   CLGKAPPEWA     266   tafSyrz   CLGKAPPEWA     265   tafSyrz   CLGKAPPEWA     265   tafSyrz   CLGKAPPEWA     265   tafSyrz   CLGKAPPEWA     211   otoGar3   CLGKAPPEWA	250   callac3   ChHSFSGMTW     250   saiBol1   CHHSFSGMTW     250   nasLar1   CHHSFSGMTW     250   rhiRax1   CHHSFSGMTW     250   rhiRax1   CHHSFSGMTW     250   rheMac3   CHUSFSGMTW     250   rheMac3   CHUSFSGMTW     250   rheMac3   CHUSFSGMTW     250   paphnu2   CHHSFSGMTW     250   paphnu2   CHHSFSGMTW     250   paphnu2   CHHSFSGMTW     250   paphnu2   CHHSFSGMTW     250   paphanu2   CHHSFSGMTW     250   paphanu2   CHHSFSGMTW     250   paphanu2   CHHSFSGMTW     250   paphae   CHHSFSGMTW     250   momLeu3   CHHSFSGMTW     250   tar3yr2   CHHSFSGMTW     250   micMu1   CHHSFSGMTW	75 calJac3 CCODELSSRL   75 saiBol1 CCODELSSRL   75 rheMac3 OCTRELSSRL   75 macPas5 OCTRELSSRL   75 papAnu2 OCTRELSSRL   75 papAnu2 OCTRELSSRL   75 papAnu2 OCTRELSSRL   75 nasLar1 OCTQELSSRL   75 ponAbe2 OCTQELSSRL   75 ponAbe2 OCTQELSSRL   75 panTro4 OCTQELSSRL   75 panTro4 OCTQELSSRL   75 gorGor3 OCTQELSSRL   75 tsSrl NCIMEISSRL   75 pacGorGor3 OCTQELSSRL   75 tsSrl KCTQELSSRL   75 tsSrl KCTQELSSRL   75 otoGar3 KCTQELSER	105 calJac3 KPSSFANSSFT 105 saiBol1 KPSSFANSSFT 105 panTro4 KPSC5NSSFT 105 panTro4 KPSC5NSSFT 106 paPan1 KPSC5NSSFT 106 pc38 KPSC5TNSSFT 107 rheMac3 KPSC5TNSSFT 106 paPanu2 KPSC5TNSSFT 106 paPanu2 KPSC5TNSSFT 105 paPanu2 KPSC5TNSSFT 105 ponAbe2 KPSC5TNSSFT 105 nomLeu3 AFSC5TNSSFT 105 tarSyr2 ELSC5ANSSFT 105 tarSyr2 ELSC5ANSFT 105 tarSYR5ANSFT 105 tarSYR5ANSFT 105 tarSYR5ANSFT 105 t	RAPHENDER 25 caljac3 AARDMERTSAN 35 25 saiboli AARDMERTSAN 35 25 rhemac3 RASSVECTSAN 18 25 macParts RASSVECTSAN 35 25 papanu2 RASSMECTSAN 35 25 caljabi RASSMECTSAN 35 25 rhiRoxi RASSMECTSAN 35 25 parton RASSMECTSAN 35 25 porton RASSMECTSAN 35 26 porton RASSMECTSAN 35 27 porton RASSMECTSAN 35 28 porton RASSMECTSAN 35 29 porton RASSMECTSAN 35 29 porton RASSMECTSAN 35 20 porton RASSMECTSAN 35 29 porton RASSMECTSAN 35 20 porton RASSMECTSAN 35		
KLKB1	MYO16	MYOF	PLTP	PRL	RAD51AP1		
Caljac3 saiBol1 VENTFRGGD panPan1 VENTFRGGD gorGor3 VENTFRGGD gorGor3 VENTFRGGD panPan1 VENTFRGGD panPan2 VENTFRGGD panBan2 VENTFRGGD panBan2 VENTFRGGD panPan2 VENTFRGGD panPan2 VENTFRGGD panPan2 VENTFRGGD panPan2 VENTFRGGD panPan2 VENTFRGGD panPan2 VENTFRGGD masLar1 VENTFRGGD masLar1 VENTFRGGD masLar1 VENTFRGGD masLar1 VENTFRGGD midWur1 VENTFRGGD	35 caljac3 CHLUCKSIRC 35 saiBol1 CHLUCKSIRC 35 rheMac3 CHLUCKSIRC 35 rheMac3 CHLUCKSIRC 35 papAnu2 CHLUCKSIRC 35 nasLarl CHLUCKSIRC 35 nasLarl CHLUCKSIRC 35 panTro4 CHLUCKSIRC 35 panAn1 CHLUCKSIRC 35 panAn2 CHLUCKSIRC 35 momLeu3 CHLUCKSIRC 35 micMur1 CHLUCKSIC 35 micMur1 CHLUCKSIC	HITS   callac3   PHPNDP3CF30     1175   salBol1   PHPNDP3CF30     1175   panTan1   PHPNDP3CF30     1175   panTan1   PHPNDP3CF30     1175   panTan1   PHPNDP3CF30     1175   panTan1   PHPNDF3CF30     1175   panTan1   PHPNDF3CF30     1175   nomLeu3   PHPNDF3CF30     1175   nomLeu3   PHPNDF3CF30     1175   nomLeu3   PHPNDF3CF30     1175   nomLeu3   PHPNDF3CF30     1175   phasLar1   PHPNDF3CF30     1175   phasLar1   PHPNDF3CF30     1175   phasLar1   PHPNDF3CF30     1175   maCFas5   PHPNDF3CF30     1175   maCFas5   PHPNDF3CF30     1173   tarSyr2   PHPNDF3CF30     956   micMur1   PHPNDF3CF30     9126   otoGar3   PHPNDF3CF30	STAPPSTAA     140   caljac3   ASTAPPSTAA     109   saiBoli   ASTAPPSTAA     140   panFadi   ASTAPPSTAA     140   panPadi   ASTAPPSTAA     140   ponAbe2   ASTAPPSTAA     140   ponAbe2   ASTAPPSTAA     140   ponAbe2   ASTAPPSTAA     140   ponAbe2   ASTAPPSTAA     140   nomLeu3   ASTAPPSTAA     140   nbg38   ASTAPPSTAA     140   papAnu2   ASTAPPSTAA     140   papAnu2   ASTAPPSTAA     140   maCras5   ASTAPPSTAA     140   maCras5   ASTAPPSTAA     140   maLari   VSTAPPSTAA     140   rhiRoxi   VSTAPPSTAA     140   rhiRoxi   VSTAPPSTAA     140   maLari   VSTAPPSTAA     140   miCHuri   APPSTAA     140   miCHuri   APPSTAA     140   miChuri   APPSTAA     140   modearererererer	396calJac3AQQISQKDFLS440saiBol1AQQISQKDFLS440rheMac3AQQINQKDFLS440macFas5AQQINQKDFLS440paAnu2AQQINQKDFLS440paAnu2AQQINQKDFLS440naLari,QKDFLS440paTro4AQQINQKDFLS440paTro4AQQINQKDFLS440paTro4AQQINQKDFLS440gorGor3AQQINQKDFLS440gorGor3AQQINQKDFLS440mozHau3AQQINQKDFLS440mozHau3AQQINQKDFLS440hg38AQQINKDFLS440hg38AQQIHHEDLIN431otoGar3AQQIHHEDLIN438tarSyr2AQQIHHEDLIN438tarSyr2AQQIHHEDLIN	III0   tarSyr2   AASKAAVQQRK   165     110   micMur1   AASKAVQQRK   53     110   calJac3   AASKAAVQQRK   53     110   calJac3   AASKAAVQQRK   161     110   panPan1   AASKAAVQQRK   162     110   panPan1   AASKAAVQQRK   165     110   panPan1   AASKAAVQQRK   165     110   panPan1   AASKAAVQQRK   165     110   gorGor3   AASKAAVQQRK   165     110   panPan2   AASKAAVQQRK   165     110   panPan2   AASKAAVQQRK   165     110   panPan2   AASKAAVQQRK   165     110   rhemac3   AASKAAVQQRK   165     110   rhemac3   AASKAAQQRK   165     110   macFas5   AASKAAQQQRK   165     110   rhemac3   AASKAAQQQRK   165     110   rhemac3   AASKAAQQQRK   165     110   rhemac3   AASKAAQQQRK		

### Suppl. Figure 3 (contd)

RXFP4		STK3	STK31 SUPV3L1			WDF	WDR87 ZNF233			MNT						
caljac3 saiBol1 TheMac3 TATLAVWYAAA macFas5 TATLAVWAAA chlSab2 TATLAVWAAA nasLar1 TATLAVWAAA nasLar1 TATLAVWAAA nasLar1 TATLAVWYAAA nasLar1 TATLAVWYAAA nasLar1 TATLAVWYAAA gorGor3 TATLAVWYAAA MICAVWYAAA ATLAVWYAAA ATLAVWYAAA ATLAVWYAAA ATLAVWYAAA	170 168 169 169 169 169 169 170 128 170 170 170 170 170 170 170	calJac3 saiBol1 hg38 gorGor3 panTro4 panAe2 nomLeu3 nasLar1 rhiRox1 rhiRox1 rhaMac3 macFas5 chiSab2 papAnu2 micMur1 otoGar3	SLIVYRSSTA SLIVYRSSTA SLIVYRSSTA SLIVYRSSTA SLIVRSSTA SLIVRSSTA SLIVRSSTA SLIVRSSTA SLIVRSSTA SLIVRSSTA SLIVRSSTA SLIVRSSTA SLIVRSSTA	922 940 940 940 940 940 940 940 940 940 940	calJac3 saiBol1 rheMac3 macFas5 papAnu2 chlSab2 rhiRox1 panTro4 gorGor3 hg38 panPan1 ponAbe2 nomLeu3 otoGar3 tarSyr22	ADUVTELNET AIDUVTELNET AIDUVELNET AIDUVELNET AIDUVELNYT AIDUVTELNYT AIDUTELNYT AIDUTELNYT AIDUVELNYT AIDUVELNYT AIDUVELNYT AIDUVELNYT AIDUVELNYT AIDUVELNYT AIDUVELNYT AIDUVELNYT	335 335 335 335 335 335 335 335 335 335	cal.Jac3 saiBol1 panTro4 panPan1 hg38 gordor3 nomLeu3 ponAbe2 rheMac3 macFas5 papAm2 chlSab2 nasLar1 rhiRox1 tarSyr2 micKur1	DPKNS WLSD DPKNY VVLSD DPKNC VVLSD DPKNC VVLSD DPKNC VVLSD DPKNC VVLSD DPKNS VVLSD	40 40 40 40 15 40 40 40 40 40 40 40 40 40	rheMac3 macFas5 papAnu2 chISab2 nasLar1 rhiRox1 ponAbe2 panTro4 panPan1 bg38 gorGor3 micMur1 otoGar3 tarSyr2 nomLeu3 salBol1	SHLQDHQQVH SHLQDHQQVH SHLQDHQQVHT SHLQDHQQVHT SHLQDHQRVHT SHLQDHQRVHT SHLQDHQRVHT SHLQDHQRVHT SHLQDHQRVHT SHLQDHQRVHT SHLQDHQRVHT SHLDHQRVHT	558 558 559 559 559 559 559 559 559 559	panTro4 panPan1 gorGor3 ponAbe2 nomLeu3 macFas5 calJac3 saiBol1 hg38 nasLar1 rhiRox1 chlSab2 papAnu2 tarSyr2 tarSyr2	PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL PHSVALSPAHL	396 337 396 398 358 358 396 396 396 396 396 396 395 396 248
		- J	the second s											0 0 0 0 0 0 C		

FCGBP

	\$YTI/AEL(sed	
calJac3	SYTMAELCSED	505
saiBol1	SYTMAELCSED	505
rheMac3	SYTMVELC <mark>GD</mark> D	505
macFas5	SYTM <mark>V</mark> ELC <mark>GD</mark> D	505
papAnu2	SYTMAELCGDD	505
ch1Sab2	SYTMAELC <mark>GD</mark> D	505
nasLar1	SYTMAELCSED	495
rhiRox1	SYTMAELCSED	505
panTro4	SYTMAELCSED	505
panPan1	SYTMAELCSED	505
hg38	SYTMVELCSED	505
gorGor3	SYTMAELCSED	505
ponAbe2	SYTMAELCSED	505
nomLeu3	SYTMAELCSED	505
tarSyr2	SY <mark>S</mark> MAELC <mark>GT</mark> D	483
micMur1	TYTMAELCSEY	499
otoGar3	TYTMAELCSND	505











# Random merging between 4 lists



А





carbohydrate catabolic process (GO:0016052) single-organism carbohydrate catabolic process (GO:0044724) monosaccharide catabolic process (GO:0046365) single-organism carbohydrate metabolic process (GO:0044723) hexose catabolic process (GO:0019320) carbohydrate metabolic process (GO:0005975) glucose catabolic process (GO:0006007) glycolysis (GO:0006096) hexose metabolic process (GO:0019318) glucose metabolic process (GO:0006006) Neuroactive ligand-receptor interaction RNA degradation Glycosphingolipid biosynthesis - lacto and neolacto series RNA transport Glycolysis / Gluconeogenesis Insulin signaling pathway Metabolic pathways Phagosome Vibrio cholerae infection N-Glycan biosynthesis Oxidative phosphorylation p73 transcription factor network GPCR ligand binding Class A/1 (Rhodopsin-like receptors) Signaling by SCF-KIT RNA Polymerase I Chain Elongation RNA Polymerase I Transcription RNA Polymerase I Promoter Clearance Validated transcriptional targets of TAp63 isoforms Amino acid transport across the plasma membrane Asparagine N-linked glycosylation Transport to the Golgi and subsequent modification RNA Polymerase I Promoter Opening Reperfusion Injury Dyslexia Postoperative Complications Sleep Disorders Heart Failure Ischemia Li-Fraumeni syndrome Mood Disorders Bipolar Disorder Stress Mental Disorders Syndrome Post-traumatic coma Iron Overload Death Sexual Dysfunctions, Psychological Lipodystrophy Anorexia Myocardial Infarction Infarction Myocardial Ischemia Spinal Cord Diseases Heart Diseases Motor Neuron Disease Weil Disease Brain Death Gliosis





С



Maximum Lifespan









