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 |
| :---: | :---: | :---: | :---: |
| AKAP9 |  |  |  |
| 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 <br> Astle WJ et al. 2016 |
| MYOF | - | Associated to muscle repair Epigenetically modified by aging | Demontis et al. 2013 <br> Benton et al. 2017 |
| PLTP | - | HDL levels | Global Lipids Genetics Consortium et al. 2013 |
| PRL | - | Ames dwarf mice lacking PRL, GH and TSH 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 <br> 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 | T | N.A. |
| BRD8 | R | Q | N.A. |
| C1QTNF2 | A | T | N.A. |
| C9orf96 | V | L | hetGla2, myoDav1 |
| DSC2 | V | I | hetGla2 |
| EFEMP2 | V | I | None |
| FCGBP | V | A | N.A. |
| FGA | A | V | myoDav2, myoLuc2 |
| GP5 | H | Q | hetGla2 |
| HEMK1 | Q | R | N.A. |
| IQCK | N | D | hetGla2* |
| KIAA1614 | M | V | N.A. |
| KLKB1 | T | A | myoDav2, myoLuc2 |
| MNT | T | A | hetGla2* |
| MYO16 | M | I | hetGla2, myoDav1, myoLuc2 |
| MYOF | P | L | hetGla2 |
| PLTP | P | T | None |
| PRL | I | M | myoDav2*, myoLuc2* |
| RAD51AP1 | V | A | hetGla2* |
| RXFP4 | V | A | N.A. |
| STK31 | Y | C | myoDav2*, myoLuc2* |
| SUPV3L1 | T | M | None |
| WDR87 | V | I | None |
| ZNF233 | R | Q | N.A. |
|  |  |  |  |

[^0]Supplementary Table 3.Top significant genes ( $\mathrm{p}=9 \mathrm{e}-05$ ) from the 5 life-history traits assessed. The genes marginally significant after FDR ( $\mathrm{q}<0.1$ ) 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 | $3.7 \mathrm{e}-06$ | $\mathbf{0 . 0 6}$ | STK17B | - |
| MLS | $4.6 \mathrm{e}-05$ | 0.37 | ITPR1 | model org., human |
| Female Maturity | $2.6 \mathrm{e}-05$ | 0.30 | HSPB6 | model org. |
| Female Maturity | $3.8 \mathrm{e}-05$ | 0.30 | COX5B | human, model.org |
| Female Maturity | $6.7 \mathrm{e}-05$ | 0.38 | MYL2 | - |
| Female Maturity | $8.3 \mathrm{e}-05$ | 0.38 | SLC38A5 | - |
| Gestation Length | $3 \mathrm{e}-06$ | $\mathbf{0 . 0 4}$ | IQCA1 | - |
| Gestation Length | $3 \mathrm{e}-05$ | 0.15 | TRIB2 | - |
| Gestation Length | $3.7 \mathrm{e}-05$ | 0.15 | FBXO38 | - |
| Gestation Length | $3.8 \mathrm{e}-05$ | 0.15 | MEF2D | model org. |
| Gestation Length | $6.1 \mathrm{e}-05$ | 0.19 | SLC10A1 | - |
| Weaning Time | $1 \mathrm{e}-05$ | 0.14 | TMEM182 | - |
| Weaning Time | $2.8 \mathrm{e}-05$ | 0.14 | JARID2 | - |
| Weaning Time | $3.6 \mathrm{e}-05$ | 0.14 | AP4M1 | model org. |
| Weaning Time | $4.8 \mathrm{e}-05$ | 0.14 | PRDX1 | human, model org. |
| Weaning Time | $5.6 \mathrm{e}-05$ | 0.14 | POLR1D | - |
| Weaning Time | $5.5 \mathrm{e}-05$ | 0.14 | S100A2 | - |
| Weaning Time | $5.6 \mathrm{e}-05$ | 0.14 | GFAP | Longevity.Map |
| Weaning Time | $6.2 \mathrm{e}-05$ | 0.14 | CHD4 | model org. |
| Body Mass | $\mathbf{4 . 1 e - 0 6}$ | $\mathbf{0 . 0 6}$ | CDC7 | - |
| Body Mass | $\mathbf{1 . 4 e - 0 5}$ | $\mathbf{0 . 0 9}$ | PER3 | Longevity.Map |
| Body Mass | $\mathbf{1 . 8 e - 0 5 ~}$ | $\mathbf{0 . 0 9}$ | SPRRG2 | - |
| Body Mass | $6.2 \mathrm{e}-05$ | 0.2 | KLHL9 | - |
| Body Mass | $6.5 \mathrm{e}-05$ | 0.2 | ENO3 | - |
| Body Mass | $8.17 \mathrm{e}-05$ | 0.2 | FANCD2OS | - |
| Body Mass | $9.3 \mathrm{e}-05$ | 0.2 | - |  |

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 | $4.72 \mathrm{e}-10$ | 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 |
| CYTB | 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 |
| СYTB | 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 |

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

| Species | UCSC version | Family | MLS <br> (y) | LQ | Body weight ( g ) | Female maturity (d) | Gestation <br> (d) | Weaning <br> (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 | Ccap | Cebidae | 54 | 3.3 | 2655 | 1505 | 162 | 521 |

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 | № 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 (LópezOtín, 2013).

| Hallmark of Aging | GO terms included |
| :--- | :--- |
| Genomic Instability | DNA repair (GO:0006281) <br> Nuclear lamina (GO:00005652) |
| Telomere Attrition | Telomere maintenance (GO:0000723) <br> Telomere capping (GO:0016233) |
| Epigenetic Alterations | Histone modification (GO:0016570) <br> DNA methylation (GO:0006306) <br> Chromatine remodeling (GO:0006338) |
| Loss of Proteostasis | Chaperone-mediated protein folding (GO:0061077) <br> Autophagy (GO:0006914) <br> Ubiquitin-proteasome system (GO:0043161) |
| Deregulated Nutrient Sensing | Insulin receptor signaling Pathway (GO:0008286) <br> TOR signaling (GO:0031929) |
| Mitochondrial Dysfunction | Response to ROS (GO:0000302) <br> 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) <br> 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 |  | $\square$ |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| 0.78 | Female Mat. |  |  |  |  |
| 0.64 | 0.74 | Gestation |  |  |  |
| 0.67 | 0.71 | 0.68 | Weaning |  |  |
| 0.56 | 0.59 | 0.53 | 0.51 | Weight |  |
|  |  |  |  |  |  |
| 0.83 | 0.46 | 0.35 | 0.41 | 0.2 | LQ |



## Suppl. Figure 3

| AKAP9 |  | ATG7 |  |  | BRD8 |  |  | C1QTNF2 |  |  | C9orf96 |  |  | DSC2 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| cal Jac3 |  | 3880 | caljac3 |  | 25 | cal Jac3 |  | 1205 |  | $\operatorname{COA} A(G) A A A$ |  |  |  | 28 |  |  |  |
| saiBol1 | RRLGTVGSGST | 3879 | saiBol1 | Silisgatienp | 125 | saiBol1 | burrevlept | 1128 | ${ }_{\text {pantro4 }}^{\text {panPan1 }}$ | Cligpalgeat | 15 15 | ${ }_{\text {chaibold }}$ | HMTFVSGSFk | ${ }_{303}^{288}$ | calJac3 | [GEVTVDEN | 525 |
| hg38 | RRLGT LSSGST | 3890 | hg38 | KSGTALENP | 125 | rheMac3 | EMRQELLEPIC | 1205 |  | CLCPALG | 5 | rhemac | HTFLSGSF | ${ }^{303}$ | saiBol1 rheMac3 | WVTVDE | 525 502 |
| ${ }_{\text {gorchor3 }}$ | ${ }_{\text {RRLLGTVGSCST }}$ | 3814 3890 | ${ }_{\text {pon }}^{\text {ponAbe2 }}$ | STKSGAALENP | $\begin{array}{r}125 \\ 85 \\ \hline\end{array}$ | mackas | Eurievleal. | 1088 | rheMac3 | clegt | 15 | macFas | FVS | ${ }_{303}^{303}$ | ${ }_{\text {macFas5 }}$ | TGNVT DD | 525 |
| panPan1 | RRLGTVQSGST | 3833 | panPan1 | Stikscaalenp | 125 | rhiRox1 | evrreviea | 1205 | ${ }_{\text {macFass }}^{\text {mapAnu2 }}$ | CLEGP ALICPAAAA | ${ }_{15}^{15}$ | ${ }_{\text {chilsab2 }}$ | HITFVSGSFKS | ${ }_{303}$ | papanu2 | cewvivd | 525 |
| ponabe 2 | RRLGTVGSGST | 3751 | gorGor3 | STKSGAALENP | 125 125 | ${ }_{\text {papanu2 }}$ | $\frac{\text { RrevLe }}{\text { RREVLE }}$ | ${ }_{1205}^{1205}$ | cail Jac3 | palgpa | 15 | nasLar 1 | IITPVSGSE | ${ }_{3}^{263}$ | nasLar1 | IGGVTVDEN | 525 |
| nomLeu3 rheMac3 | RRLGTVGS | ${ }_{3875}^{3886}$ | ${ }_{\text {chen }}^{\text {nomLeu3 }}$ | SITKSAALENP | ${ }_{125}^{125}$ | ${ }_{\text {ch38 }}$ | EMRIQEVLEC | ${ }_{1205}^{1205}$ | saiBol1 | clegalegana | 15 | rhiRox1 | HITPVSGSFS | 303 303 | rhiRox1 | VDEN | ${ }_{5}^{525}$ |
| ${ }_{\text {macFas5 }}$ | RRLGT MSGST | 3890 | papAnu2 | STKSGAALENP | 125 | gorGor3 | Eurreviba | 1112 | ${ }_{\text {chasLar1 }}$ | clgralg ana | ${ }_{15}^{15}$ | ${ }_{\text {gorGor }}$ | Hitrvig | ${ }_{303}$ | ${ }_{\text {panTr }}$ pat | [GNVTVDEs | 525 525 |
| papAnu2 |  | 3889 | rheMac3 | STKSGTALEPP | 125 | panTro4 | Burrevieg | ${ }^{1225}$ | rhiRox1 | clepplagraa | 15 | panpan 1 | HITTVRES | 303 303 | ${ }_{\text {hg }}$ | TGWVTDE | 525 |
| ${ }_{\text {chisab }}$ |  | 3890 3809 | ${ }^{\text {mactas }}$ | SIKSGAALENP | ${ }_{125}$ | ${ }_{\text {pren }}^{\text {panAane2 }}$ | Eurrevleqia | ${ }_{1205}^{1205}$ | ${ }_{\text {hg38 }}^{\text {nomleu3 }}$ | CLGPTLCPAAA CLGPALGPAAA | 15 15 | ${ }_{\text {ngen }}^{\text {ng38 }}$ |  | 388 288 | ${ }_{\text {gorcor }}$ gonde2 | TGWVTVDE) | 525 525 |
| rhiRox 1 | RRLGTVQSGST | 3888 | rhiRox1 | STKSGAALENP | 125 | ${ }_{\text {nomLeu3 }}$ | burrevienia | 1198 | gorcor3 | clgralgpaAd | 15 | nomileu3 | HITTVRGS | ${ }^{214}$ | nomieu3 | tavvivde | 525 |
| ${ }_{\text {tarsyr }}$ | Rrictvasgsi | 3878 | ${ }_{\substack{\text { tarsyr2 } \\ \text { micMur1 }}}$ | sinscaternp | 125 111 | ${ }_{\substack{\text { tarsyr2 } \\ \text { micMur1 }}}^{\text {cel }}$ | EMOREVLEDİ | ${ }_{868}^{1203}$ | michur | CLGPA WPAAA | ${ }^{14}$ | tarsyr 2 | HSTPVSSFKS | ${ }^{303}$ | micMur1 $^{\text {cen }}$ |  | ${ }_{5}^{444}$ |
| OtoGar3 | RRLGTVGSGSI | 3824 | ${ }_{0}$ OtoGar3 | EiKschaibin | 125 | otoGar3 | [uabevlepia | 1201 | tarSyr2 | CLGPA | ${ }_{9}^{14}$ | otocar3 | DITFVKNEFSS | ${ }_{303}^{234}$ | ${ }_{\text {tarsyr2 }}^{\text {otoGar3 }}$ | KGKVIVDENS | ${ }_{473}^{525}$ |
| EFEMP2 |  | FGA |  |  | GP5 |  |  | HEMK1 |  |  | IQCK |  |  | KIAA1614 |  |  |  |
|  | NHR V/IEDODE |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| nomLeu3 | MYRCVWEPGR | 265 | calJac3 | RLQKAPPEEWRA | 250 | $1 \mathrm{Jac3}$ | Cumsec | 75 | calJac3 | QCIOELSSRRM | 105 | cal Jac3 sai Bol1 | RPSSSAANSSFT |  | caljac3 | ampmiderisay |  |
| ${ }_{\text {chlisab2 }}^{\text {char }}$ | QYRCVNEPGR | 265 265 | ${ }_{\text {sh38 }}^{\text {saibol1 }}$ |  | ${ }_{250}^{250}$ | Saibol1 nasLar1 | LQNHSFSG | $\begin{aligned} & 75 \\ & 75 \end{aligned}$ | $\underset{\substack{\text { saibol1 } \\ \text { rhellac3 }}}{ }$ | QCIQELSS | 105 105 | ${ }_{\text {chen }}^{\text {panTro4 }}$ | KPSSCTNSET | $\begin{aligned} & 25 \\ & 25 \end{aligned}$ | saibol1 rheMac3 | ${ }_{\text {a }}^{\text {ARAPMPMERISAV }}$ R | 18 18 |
| ponAbe2 | gYacvsepg | 264 | gorGor3 | QLQRAPP | 250 | rhiRox 1 | Lomisfscmi | 75 | macFas5 | QCIRELSS | $\begin{aligned} & 105 \\ & 105 \end{aligned}$ | anPan1 | KPSCSTNSSFT | ${ }_{25}^{25}$ | macFas5 | RASPVEGTSAV | 35 |
| ${ }_{\text {pantrou }}^{\text {panfen }}$ |  | 265 265 | ${ }_{\text {pantron }}^{\text {panPant }}$ | QLQKAPPEWKA | 250 250 | macFass rheMac3 | LOMGSFSCMT | $\begin{aligned} & 75 \\ & 75 \end{aligned}$ | ${ }_{\text {papan }}^{\text {paph }}$ | MCIQELSSR | $\begin{aligned} & 105 \\ & 105 \end{aligned}$ | gorgor3 | KPSCFTTS | $\begin{aligned} & 25 \\ & 25 \end{aligned}$ | ${ }_{\text {papanu2 }}$ | Raspmbersav | ${ }_{35}^{35}$ |
| hy38 | QYRC NEPGR | 265 | ponAbe2 | glikappewra | 250 | papAnu2 | LOMASFSGMT | 75 | nasLar1 | Ciciexssp | 57 | rhemac3 | KPSCSTDSS | 25 | nasLar1 | RASXMECTSAV | 18 |
| nasLar1 rhi Rox 1 |  | 154 265 | nomLeu3 nasLar1 | QLqKappew | 250 250 | ${ }_{\text {chis }}^{\text {chisab2 }}$ | HSFSGMT | $\begin{aligned} & 75 \\ & 75 \end{aligned}$ | ${ }_{\text {rhinox }}$ Poonde | MCIOELSSR | 105 105 | ${ }^{\text {macrass }}$ papanu2 | KPSCSTNSSE | $\begin{aligned} & 25 \\ & 25 \end{aligned}$ | ${ }_{\text {rhir }}^{\text {rhirax }}$ | Raspmetisay | 35 35 |
| papAnu2 | gyrcvnepg | 265 | rhiRox1 | QLQEAPPE | ${ }^{250}$ | panpan 1 | LOS Sisfscmi | 75 | nomleu3 | OCIQELSSRRI | 105 | nastar 1 | KPSCSTNS | 25 | gorGor3 | TASPMEC | 35 |
| ${ }_{\text {coile }}^{\text {caijac3 }}$ |  | 265 265 | rheMac3 macFas5 | QLQEVYPPPWEWA | ${ }_{250}^{250}$ | ${ }_{\text {gorGor3 }}$ | qsFsg | $\begin{aligned} & 75 \\ & 75 \end{aligned}$ | ${ }_{\text {pantron }}^{\text {panPan }}$ | GCiqelsshril | 76 105 | ${ }_{\text {rhincab2 }}$ | KPSCSTNSSFT | $\begin{aligned} & 25 \\ & 25 \end{aligned}$ | ${ }_{\text {hanfan }}^{\text {ha }}$ | TASPVEGTSAV | 35 18 |
| rheMac3 | QYRC NEPGR | 265 | рарAnu2 | DLQKASPEWKA | 250 | ponAbe2 | sFscmi | 75 | gorcor3 |  | 105 | ponabe2 | KPSCSTNSS | 25 | ponAbe2 | taspmegtsav | 35 |
| ${ }_{\text {mack }}^{\text {macas }}$ tarsyr2 |  | ${ }_{265}^{260}$ | ${ }_{\text {charsyr2 }}$ | QLotataplewan | 250 250 | ${ }_{\text {n }}{ }_{\text {nomileu3 }}$ | SSEVMMTV | $\begin{aligned} & 75 \\ & 75 \end{aligned}$ | ${ }_{\text {Larsyr2 }}$ | CCIRELSSR | $\begin{aligned} & 105 \\ & 105 \end{aligned}$ | ${ }_{\text {tarSyr2 }}$ | ELSCSANSS | $\begin{aligned} & 25 \\ & 24 \end{aligned}$ | ${ }_{\text {nomileu3 }}$ | RASPMEGEMNSHV | 18 |
| 3 | * |  | r1 | QLQRAPPEEKA | 250 | 101 |  |  |  |  | 105 |  |  | 21 | Mur 1 |  |  |
| micMur 1 | QYRCVNEPGRF | 211 | otoGar3 | QLQKAPPEWRA | 250 | otoGar3 |  | 75 | otocar3 | kciqelsmbri | 105 | toGar3 | EPSGSGMSSLI | 25 | otoGar3 | rampmevtisav | 35 |
| KLKB1 |  | MYO16 |  |  | mYoF |  |  | PLTP |  |  | PRL |  |  | RAD51AP1 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | ASHADOMOHSH |  |
| calJac3 | YENTfFRGGD |  | calJac3 | LLCNMSIRM | 1175 | calJac3 | PNDPSGPSV | $\begin{aligned} & 140 \\ & 100 \end{aligned}$ | calJac3 saiBol1 | ASTAPPPSTAA | $396$ | caljac3 saiBol1 | MaDISQKDFLS | 1110 | ${ }_{\text {tarSyr }}$ | MASKAAVQdRR | 165 53 |
| ${ }_{\text {sain }}^{\text {saibol1 }}$ | LYENTFFRGG | 35 35 | ${ }_{\text {shemac }}$ | PHLQRISIR | 1175 | ${ }_{\text {panTro4 }}$ | Phipndpseps | 140 | panTro4 | ASTAPP | 440 | rheMac3 | ADOM | 110 | calJac3 | AASKAAV |  |
| panPan1 | Y Yentrfag | 35 | macFas5 | Qhillokisi | 1175 | panPa | PHPNDPSGPSV | 140 140 | ${ }_{\text {panpan1 }}$ | ASTAPPPST | 440 440 | s5 | ARo | 110 | 11 | AASKAA | 162 165 165 |
| ${ }_{\text {hg38 }}^{\text {gorGor3 }}$ | LYentriged | 35 35 | ${ }_{\text {p }}$ papanu2 |  | 1175 | gorGor3 | ndPs | 140 | ponAbe2 | AStapppst | 378 | ${ }_{\text {chisab2 }}$ | ACOINQKD | 110 | panPan1 | AASKAAVQORX | 165 |
| ponabe2 | ETPFRG | 35 | nasLar1 | LQKMS | 1116 | ponAbe2 | PiPND | 140 | nomieu3 | AP | 440 | nasLar | .....aKdFL | 74 | ponAbe2 | SK | 55 |
| nomLeu3 | Yentrfrg | 35 | rhiRox1 | mllokMsirg | 1175 | nomLeu3 | PhPMDPS | 140 | ${ }^{\text {hg } 38}$ | ASTAPTPS | 440 | friRox | AMOINQUDFL | 110 |  | AASKA | 165 |
| rhemac3 | YENAFFR | 35 | panTro4 | PhlquMsira | 1175 |  | Phpmpsecrsv | 140 |  | ASTAF | 438 | ${ }_{\text {panirou }}$ | ARQINQKDFL | 1110 | gorcor3 | Aaskangin |  |
| ${ }^{\text {macFas }}$ | LYentiprch | ${ }_{35}$ | panfan1 |  | 1175 | ${ }_{\text {ch1Sab2 }}$ | NDP | 140 | macFas5 | ASTAPTPSTAA | 440 | gorGor3 | AQOINQR | 110 | papAnu2 | Aaskanv | 165 |
| chisab2 | LYENTFFR | 35 | hg38 | ahllofisira | 1175 | papAnu2 | PHPNDPS | 140 | ch1Sab2 | astapppstad | 440 | nomLeu3 | ARO | 110 | chisab2 | askany | 165 |
| nasLar1 | YENTPFRGG | 35 | ponabe2 | HLLqKMSIRO | 1168 | rheMac3 macFas5 | Pipnd | 140 | nasLar1 |  | ${ }_{40}^{421}$ |  | ADQiNQKDFLS | 110 | rheMac3 | Aaskanamark | 165 165 |
| ${ }_{\text {rex }}^{\text {ruirox }}$ tarsyr2 | LYENTFPR | 35 35 | ${ }_{\text {nomLeu3 }}$ |  | ${ }_{1173}^{1175}$ | ${ }_{\text {macFass }}$ | ND | 140 110 | ${ }_{\text {tarSyr2 }}$ | ASSAPPPSTAA | ${ }_{440}^{44}$ | ${ }_{\text {nicMur1 }}$ | ADQITHEDEL | 110 | macFass nasLar1 | AASKAAABQRK | ${ }_{165}^{165}$ |
| cMur1 | TFF | 35 | michur1 | Qhllakmsi | 956 | micMur ${ }^{\text {d }}$ |  | 140 | micMur 1 |  | 431 | otoca |  | 110 | rhiR | anskanvoqra | 165 |
| otoGar3 | QNTFPR | 35 | otoGar3 |  | 1126 | otogar3 | PHPNDP | 140 | otoGar3 | ASSASPPSMA | 438 | tarSy | aqQirhid | 110 | otoGar3 | AASKAAvQ | 59 |

Suppl. Figure 3 (contd)


Suppl. Figure 4


Suppl. Figure 5


Suppl. Figure 6

Longevity vs GW omegas


Gemome-Wide Omegas

Gestation vs GW omegas


Gemome-Wide Omegas


Gemome-Wide Omegas

Weaning vs GW omegas


Gemome-Wide Omegas

|  | Species |  |
| :---: | :---: | :---: |
| (1) hg38 | 10 chlSab2 | (9) saiBol1 |
| (2) panTro4 | 11 nasLar1 | 20 Ccap |
| (3) panPan1 | 12 rhiRox1 | 21 Anan |
| (4) gorGor3 | 13 Rbie | 22 tarSyr2 |
| $(5$ ponAbe2 | 14 Caty | 23 micMur1 |
| 6 nomLeu3 | 15 Cang | 24 otoGar3 |
| 7 rheMac3 | 16 Mnem | 25 Pcoq |
| 8 macFas5 | 17 Mleu |  |
| 9 papAnu2 | 18 calJac3 |  |

F Maturity vs GW omegas

Gemome-Wide Omegas

Body Mass vs GW omegas


Gemome-Wide Omegas

Suppl. Figure 7


## Random merging between 4 lists



## Suppl. Figure 9



B


C


## Gestation



Maximum Lifespan


Birth Mass


Adult Weight


## Suppl. Figure 11



Suppl. Figure 12



[^0]:    * Shares the very same aminoacid change than " Increased Lifespan" group.

