Positive selection and enhancer evolution shaped lifespan and body mass in great apes

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Abstract

Within primates, the great apes are outliers both in terms of body size and lifespan, since they include the largest and longest-lived species in the order. Yet, the molecular bases underlying such features are poorly understood. Here, we leveraged an integrated approach to investigate multiple sources of molecular variation across primates, focusing on ~1,550 genes previously described as tumor suppressors, oncogenes, ageing genes in addition to a novel Build of the CellAge database of cell-senescence genes (version 2), herein presented for the first time. Specifically, we analyzed dN/dS rates, positive selection, gene expression (RNA-seq) and gene regulation (ChIP-seq). By analyzing the correlation between dN/dS, maximum lifespan and body mass we identified 67 genes that in primates co-evolved with those traits. Further, we identified 6 genes, important for immunity, neurodevelopment and telomere maintenance (including *TERF2*), under positive selection in the great ape ancestor. RNA-seq data, generated from the liver of six species representing all the primate lineages, revealed that ~8% of the longevity genes are differentially expressed in apes relative to other primates. Importantly, by integrating RNA-seq with ChIP-seq for H3K27ac (which marks active enhancers), we show that the differentially expressed longevity genes are significantly more likely than expected to be located near a novel "ape-specific" enhancer. Moreover, these particular ape-specific enhancers are enriched for young transposable elements, and specifically SINE-*Vntr*-Alus (SVAs). In summary, we demonstrate that multiple evolutionary forces have contributed to the evolution of lifespan and body size in primates.

Keywords: Ageing, cancer, evolutionary genomics, cis-regulatory evolution, natural selections, apes, transposable elements, cell senescence.

Introduction

Uncovering the molecular and evolutionary bases of ageing in the tree of life is important to increase our understanding of the natural mechanisms of disease resistance (Galis and Metz 2003; Caulin and Maley 2011; Ganten and Nesse 2012; Nesse et al. 2012; Thomas et al. 2013; Petralia et al. 2014; Abegglen et al. 2015; Harris et al. 2017; Ciccarelli and DeGregori 2020). The evolution of lifespan in animals has been shaped by selective pressures arising from different environments, ecological niches, habitats, and diets (Healy et al. 2014; Tollis et al. 2017; Kacprzyk et al. 2021). Ageing and senescence are the result of gradual declines in biological functions, which lead to increased vulnerability, disease predisposition, and ultimately death (López-Otín et al. 2013). With the exception of a few species that show no signs of ageing (e.g. some jellyfishes and hydras; (Petralia et al. 2014), most animals undergo this process. Nevertheless, maximum lifespan is a highly variable trait across the tree of life, suggesting that long-lived species may have adopted several evolutionary strategies which may have favored longevity by reducing disease susceptibility (Gorbunova et al. 2014; Kacprzyk et al. 2021; Yu et al. 2021). Yet, most of these strategies remain unknown.

One of the main consequences of ageing is the increased risk of developing cancer. Cancer has been reported in almost all multicellular organisms (Aktipis et al. 2013; Albuquerque et al. 2018), and it is often associated with somatic genetic mutations that inactivate tumor suppressor genes or activate oncogenes. These mutations ultimately affect cell metabolism, promoting uncontrolled cell division (Stratton et al. 2009; Tomasetti and Vogelstein 2015). Statistically, animal species with larger body sizes and longer lifespans accumulate more cell divisions during their lives and are therefore expected to accumulate more deleterious genetic mutations. Nonetheless, large and long-lived species overall do not develop cancer at higher frequency than smaller species (Nunney 2018; Seluanov et al. 2018). This scientific paradox was first noted by Richard Peto (the "Peto's Paradox"; Peto et al. 1977; Nunney 1999).

Specific anti-cancer mechanisms have been discovered in long-lived species. These mechanisms include early contact inhibition in naked mole rats (Seluanov et al. 2009; Tian et al. 2013), positive selection in DNA repair & inflammatory genes in the giant tortoises from Galapagos (Quesada et al. 2019), and immunity pathways, telomere maintenance and cellular senescence (CS) genes in bats (Zhang et al. 2013; Foley et al. 2018; Tian et al. 2018; Wilkinson and Adams 2019). Particularly, CS - a process in which otherwise replicating cells reach the maximum number of divisions and cease proliferating - is another important mechanism of cancer suppression; previous studies indicate that genes regulating the senescent phenotype are strongly conserved amongst vertebrates compared to other

72 protein-coding genes (Avelar et al. 2020). Despite the importance of senescence processes in inhibiting
73 cancer, CS itself is detrimental for health; senescent cells produce pro-inflammatory cytokines that can
74 paradoxically promote cancer (Rao and Jackson 2016). A previous study found that senolytics - drugs
75 that specifically target and eliminate senescent cells - can enhance life- and health-span in old mice (Xu
76 et al. 2018). On another hand, in larger mammals such as elephants and whales, molecular substitutions
77 in cell senescence genes and increases in the copy number of important tumor suppressor genes have
78 contributed to significantly reduce the risk of developing cancer (Abegglen et al. 2015; Caulin et al.
79 2015; Keane et al. 2015; Tollis et al. 2019). Specific changes in the regulation and expression of specific
80 genes have also been associated with ageing (de Magalhães et al. 2009; Donlon et al. 2017; Morris et
81 al. 2019; Chatsirisupachai et al. 2021). Yet, the extent of the contribution of cis-regulatory evolution to
82 ageing is still poorly understood.

83 In primates, maximum lifespan (MLS) and body mass (BM) are correlated, despite being highly
84 variable across species, with great apes (gorillas, orangutans, humans and chimpanzees) representing
85 outliers (Finch and Austad 2012). The BM ranges from 5 kg in the grey mouse lemur (*Microcebus*
86 *murinus*) to ~140kg in the gorilla (*Gorilla gorilla*). Similarly, the MLS varies from 13 years in the
87 calabar angwantibo (*Arctocebus calabarensis*) to 55–122 years in great apes (AnAge database:
88 https://genomics.senescence.info/; Tacutu et al. 2018). Outside great apes, just a few primate species
89 can reach 50 years (e.g. the capuchin monkeys; Muntané et al. 2018; Orkin et al. 2021).

90 Consistent with Peto's Paradox, great apes develop cancer at lower rates than other primates
91 (Fowler et al. 1980; Lowenstine 1986; Cho et al. 2007; Lowenstine et al. 2016). Humans represent an
92 exception, possibly as a consequence of their life-style (Finch 2010; Hochberg and Noble 2017;
93 Albuquerque et al. 2018). In fact, in some human populations cancer rates are ~25% (Ferlay et al. 2015),
94 and some cancer types seem to be unique to our species (e.g prostate cancer and lung cancer). Several
95 studies have recently investigated the link between longevity, body mass and disease resistance in
96 several mammalian species (Tollis et al. 2017; Muntané et al. 2018; Boddy et al. 2020; Huang et al.
97 2021; Kacprzyk et al. 2021). On the other hand, the mechanisms of ageing in great apes are largely
98 uncharacterized, and several questions remain unanswered.

99 Here, we aimed at investigating the relative contribution of different sources of molecular
100 variation (molecular evolution in coding genes, positive selection, cis-regulatory and gene expression
101 evolution) to the evolution of longevity in great apes. First, we performed a literature search for genes
102 that are involved in the CS process. This led to the generation of a novel Build (version 2) of the CellAge

103 database, which includes 934 genes that induce or inhibit cellular senescence *in vitro* in human cell lines
104 following genetic manipulation (Table S2).
105 Next, we interrogated 19 mammalian genomes, focusing on ~1,550 longevity-related genes,
106 including the genes in the novel CellAge database, plus hundreds of genes previously associated with
107 tumor suppression, oncogenic activity and ageing-related genes processes. We evaluated: 1) potential
108 correlations between MLS, BM and coding gene evolution [non-synonymous/synonymous mutations];
109 2) positive selection signal in the great-ape ancestor; 3) species-specific gene expression patterns (RNA-
110 seq); 4) species-specific gene-regulation patterns (ChIP-seq for H3 lysine 27 acetylation [H3K27ac],
111 which marks active cis-regulatory elements).
112 We identified 67 longevity genes that co-evolved with lifespan and/or body mass in primates,
113 and 6 longevity genes under positive selection in the great-ape ancestor. These genes are important for
114 immunity, neurodevelopment and telomere maintenance. In addition, RNA-seq and ChIP-seq data,
115 generated from the liver of six species representing all the primate lineages (Trizzino et al. 2017),
116 revealed that ~8% of the longevity genes investigated in this study are differentially expressed in apes
117 relative to other primates, and that these lineage-specific gene expression patterns are associated with
118 the rise of novel ape-specific enhancers, most of which derived from the insertion of young transposable
119 elements.
120
121 **Results**
122 *Ape-specific patterns in the evolution of lifespan and body mass*
123 The great apes are the primates with the largest body size, and are also the most long-lived species in
124 the entire order (fig. 1a-b). Given the high diversity of phenotypes across primates, we used Phylogenetic
125 Generalized Least Squares (PGLS) models (Orme et al. 2012; Revell 2012; Pennell et al. 2014) to
126 evaluate if body mass (BM) and maximum lifespan (MLS) evolved independently in great apes. The
127 PGLS estimate the covariance among traits, MLS and BM in this case, taking into account the effect of
128 the phylogenetic signal across the tree. We found that the allometric expectations are maintained across
129 primates, with a positive correlation between BM and MLS (fig 1a). Our model revealed that the BM
130 predicts ~6% of the variation in longevity across primate species (adjusted R-squared: 0.05904, 131
131 degrees of freedom, p = 0.0028). Nonetheless, the relation between MLS and BM in great apes is
132 significantly different from the other primates (adjusted R-squared: 0.04568, degrees of freedom, p =
133 0.02888). This suggests that lineage specific molecular evolution may have shaped lifespan and body

134 mass in great apes.

135

136 *Build 2 of the CellAge Database of Cell Senescence Genes*

137 We compiled a Build 2 of the CellAge dataset by means of a scientific literature search of gene
138 manipulation experiments in primary, immortalized, or cancer human cell lines that caused cells to
139 induce or inhibit CS. The novel CellAge build comprises 934 distinct CS genes, of which 608 genes
140 affect replicative CS (our default annotation), 180 genes affect stress-induced CS, and 214 genes are
141 related to oncogene-induced CS. Of the 934 total genes, 393 genes induce CS (~ 42.1%), 518 inhibit it
142 (~ 55.5%), and 23 genes have unclear effects, both inducing and inhibiting CS depending on
143 experimental conditions (~ 2.5%). The genes in the dataset are also classified according to the
144 experimental context used to determine these associations (Table S2).

145

146 *The rate of evolution (dN/dS) in 67 genes positively correlates with the evolution of longevity and body*
147 *mass across primates*

148 The ratio between synonymous (dS) and nonsynonymous substitutions (dN) is considered a reliable
149 measure of natural selection in the evolution of the phenotypic diversity. In line with this, several studies
150 have reported a positive relationship between dN/dS and either body mass or maximum lifespan
151 (Romiguier et al. 2010; Weber et al. 2014; Figuet et al. 2016). Nonetheless, the contribution of individual
152 genes to the evolution of body size and lifespan remains largely unexplored, especially in primates. Even
153 if MLS and BM are positively correlated in most mammalian lineages, their molecular evolution is likely
154 largely independent, as has been previously reported in rodents (Seluanov et al. 2018). To investigate
155 the molecular evolution of longevity and body mass in primates, we focused on a set of 2,268 genes
156 previously implicated with lifespan, body mass and cancer (hereafter "longevity genes"). This list
157 includes genes that have been previously associated with tumor suppression, with oncogenic functions,
158 and with ageing and senescence-related processes (Table S1.2). Of these 2,268 genes, 1,553 have a six-
159 way ortholog in six species (human, chimpanzee, rhesus macaque, marmoset, bushbaby, mouse lemur),
160 representative of the main primate lineages (Catarrhini, Platyrrhini and Strepsirrhine), for which we
161 have also analyzed publicly available next generation sequencing data (see below). These 1,553 genes
162 were retained for downstream analyses. Additionally, 986/1,553 (~63.5%) of these orthologous genes
163 are also present in 11 additional primate species that we included in our molecular evolution analysis
164 (fig. 1b-c, Table S1.3). In general, the number of orthologous genes was similar across primates, with a

variation between 1,905 genes in the bushbaby to 2,183 in the chimpanzee. The species with the smallest number of orthologous genes was the tarsier (*Carlito syrichta*), likely reflecting the low sequencing coverage for the genome of this species (Table S1.1).

We correlated the rates of evolution (dN/dS) in the 986 genes with the two life history traits (body mass [BM], and maximum lifespan [MLS]) together and independently (Table S1.4-1.6). As a first step, we removed 89 genes with $\omega>2$ due to the possible overestimation of ω in the branch due to saturation or miss calculation of synonymous (dN) or non-synonymous (dN) substitutions. Next, we used the variance of the residuals from the first PGLS model (MLS ~ BM), in order to account for the expected covariance structure between the two variables and evaluate the contribution of each gene (dN/dS) in the evolution of MLS and BM simultaneously. As a result, we found 9 genes for which the dN/dS is positively correlated with both MLS and BM (figure 2a, table 1): five are tumor suppressor genes (TSGs: *PRDM2 , ADAMTS8 , NPRL2 , SGMS1 , LRIG1*), one is an TSG-oncogene (*NCOA4*), one is categorized as TSG-oncogene-senescence gene (*ATF3*) and one is an ageing gene (*TRAP1*). These genes are involved in important biological pathways. For instance, *PRDM2* is involved in cell differentiation (Fog et al. 2012) and *NCOA4* in iron signaling, which is a key autophagic cell death process (Bellelli et al. 2016). Notably, *ADAMTS8* contributes to ~30% of the variation in MLS and BM across primates. This gene encodes for a protein involved in several types of cancer (Zhao et al. 2018), it is important for the immune response (Zhang et al. 2020) and has been associated with multiple diseases such as rheumatoid arthritis (Baloğlu et al. 2020). Importantly, *ADAMTS8* has also been reported as a positively selected gene in whales, the longest-lived/most cancer-resistant group of species across mammals (Tejada-Martinez et al. 2021). Gene enrichment analysis on the nine genes ($p<0.05$, Table 1, Table S1.7; complete list of longevity genes used as background) revealed an overrepresentation in ontology process related with response to amino acid starvation (*NPRL2* and *ATF3*), which could reflect the important role that the diet plays in adaptation, longevity and species diversification (Yabu et al. 2012; Gallinetti et al. 2013; Slade and Staveley 2016).

In the second PGLS model, we only focused exclusively on lifespan. We identified 58 genes that positively coevolved with longevity across primates (fig. 2b). Most of those genes encode for transcriptional regulators (Table S1.7) and are predominantly tumor suppressor or senescence genes. The genes *SALL1*, *SALL4* and *ARID4B* contribute from 37% to 53% of the variation in longevity seen across species (table 1b) and are important developmental regulators (Hirsch et al. 2015; Buttgereit et al. 2016; Wu et al. 2019; Bon-Baret et al. 2021; GÜven and Terzİ ÇİzmecİoĞlu 2021). Among the other

196 genes, *WIPI1* is important for autophagy (Grimmel et al. 2015), *HIVEP3* for immunity and inflammation
197 processes (Hicar et al. 2001; Krovi et al. 2020), and *FXR1* for the regulation of memory and emotions
198 (Kalueff 2007; Sopova et al. 2019; Brown and Török 2021), important traits that have shaped primate
199 evolution.

200 Finally, in the third PGLS model, we focused exclusively on body mass. This analysis revealed
201 that *FAT1*, a highly conserved tumor suppressor gene involved in Wnt signaling pathway (Nusse and
202 Varmus 1992), and associated with multiple cancers (Morris et al. 2013), contributes to ~22% of the
203 variation in BM found across primates (table 1c).

204 In summary, we found that, across primates, the dN/dS ratio correlates with either longevity or
205 body mass (or both) in a total of 67 genes. These genes are involved in multiple biological functions
206 directly associated with ageing regulation, but are also related to particular features important for
207 primate diversification such as diet, metabolism and neurological development.

208

209 *Longevity genes under positive selection in the ancestor of great apes are involved in neurological*
210 *pathways, immunity and telomere length*

211 The integration of an evolutionary perspective in the study of genes related to human health could reveal
212 the discovery of novel molecular variants that underlie important biological questions, such as how to
213 live longer and healthier lives, or how to be more resistant to diseases. Here, we studied the signal of
214 positive selection in the evolution of 986 longevity genes in the ancestors of great apes, which is the
215 lineage including the species with largest body sizes and longest lifespan across primates. We found six
216 longevity genes with positive selection in the ancestors of great apes (*PAK1, ULK3, KIF1B, STAT1,*
217 *ABCC3, TERF2;* fig. 3a-g; Table S1.8-1.9). These genes are involved in important biological functions
218 that characterized the evolution of long-lived species, such as immunity, neurodevelopment, and
219 telomere maintenance (Zhang et al. 2013; Gorbunova et al. 2014; Orkin et al. 2021). For example, *PAK1*
220 is an oncogene involved in cytoskeletal reorganization and cortical development (Pan et al. 2015). The
221 codons under positive selection are located in a protein kinase domain, indicating that these changes
222 could have modified the structure or function of the gene in the ancestor of the great apes. Mutations in
223 *PAK1* have been associated with macrocephaly in humans (Harms et al. 2018), and memory deficits in
224 mice (Meng et al. 2005). In fact, this gene plays an important role in hippocampal synaptic plasticity
225 (Asrar et al. 2009). Like *PAK1*, *ULK3* is also an important component of several neurological pathways,
226 whose activity is significantly decreased in patients with Parkinson's disease (Miki et al. 2018). *KIF1B*

227 is an axonal precursor which encodes for an important motor protein that transports mitochondria. In
228 humans, *KIF1B* mutations have been associated with autoimmune and neurological diseases, including
229 multiple sclerosis (Aulchenko et al. 2008) and Charcot-Marie-Tooth (Zhao et al. 2001). *KIF1B*-
230 knockout mice do not survive after birth due to atrophies in the nervous system, resembling what is
231 observed in Charcot-Marie-Tooth patients (Zhao et al. 2001). *STAT1* regulates innate immunity and
232 protection against viral infection (Karst et al. 2003; Hossain et al. 2019). *ABCC3* has been implicated in
233 drug resistance, including chemotherapy (Balaji et al. 2016). Finally, *TERF2* is very important for
234 ageing-related processes, since it regulates telomere length (Ilyenko et al. 2011; Tian et al. 2019). For
235 this gene, the great apes show a specific substitution in the HTH myb-type Domain, a highly conserved
236 amino-terminal region (Peters et al. 1987), suggesting that the substitution could potentially have
237 affected the myb-type/DNA interaction important for TERF2 protein function.
238
239 *Longevity genes with human-specific expression patterns*
240 We reasoned that different strategies may have contributed to the evolution of longevity genes in great
241 apes. On the one hand, positive selection may lead to important changes in the amino acid composition,
242 and thus in the structure and function of the encoded protein. On the other hand, the coding sequence,
243 and hence the structure of the protein, may remain unaltered across species but the expression level of
244 the gene may change. Changes in gene expression would be reflected in the amount of translated protein,
245 which could have a significant impact on cell metabolism. Our data so far demonstrated that a number
246 of longevity genes are under positive selection in great apes. We surmised that changes in the expression
247 of longevity genes may provide an additional contribution to the differences in lifespan and size between
248 the great apes and the other primates. To test this hypothesis, we leveraged a publicly available RNA-
249 seq dataset generated from the liver of the six primate species analyzed in the present study (humans,
250 chimpanzee, rhesus macaque, marmoset, mouse lemur and bushbaby; Trizzino et al. 2017). The liver is
251 particularly relevant for this study because most genes associated with longevity and body mass are
252 highly expressed in the liver, and also because liver gene expression displays high variation across
253 species, likely reflecting adaptation to different diets and environments, in spite of a conserved core
254 function (Trizzino et al. 2017). Consistent with this premise, the liver has been employed in studies that
255 investigated biomarkers of aging (Lee et al. 2012; Bochkis et al. 2014; White et al. 2015).
256 As a first step, we examined the expression patterns of all the 1,553 six-way ortholog longevity
257 genes, and found that genes involved in both ageing & senescence are significantly more expressed in

258 humans relative to all the other primates grouped together (Wilcoxon rank-sum test, $p < 0.001$; fig. 4a).
259 Similarly, genes that are involved in both ageing and tumor suppression are more expressed in humans
260 than in other primates grouped together, although the *p*-value was only marginally significant, possibly
261 as a consequence of the small sample size (N=3; Wilcoxon rank-sum test, $p = 0.057$; fig. 4b).
262
263 *Longevity genes with ape-specific expression patterns*
264 Next, we compared the expression of the longevity genes between apes and other primates. Overall,
265 apes have a higher number of longevity genes expressed in the liver relative to other primates (fig. 4c;
266 Spearman's correlation coefficient R=0.53, *p*-value = 2.2e-16), and the expression level of the longevity
267 genes is strongly correlated between humans and chimpanzees (fig. 4d). We decomposed the longevity
268 genes across the different categories (fig. 4e), and observed that the oncogenes are significantly more
269 expressed in apes relative to other primates grouped together (Wilcoxon rank-sum test, $p = 0.027$), while
270 the senescence genes are significantly less expressed in apes (Wilcoxon rank-sum test, $p = 7.9 \times 10^{-10}$).
271 This pattern could reflect the findings from recent studies that reported that senescence genes are
272 beneficial in the younger ages, during which they increase reproductive fitness, while they might have
273 a negative impact later in life (Campisi 2003; Blagosklonny 2010; Di Micco et al. 2021). Accordingly,
274 gene expression meta-analysis across human tissues showed that cancer genes promote longevity,
275 whereas senescence genes showed anti-longevity patterns (Chatsirisupachai et al. 2019).
276
277 *Ape-specific enhancers drive the differential expression of longevity genes in apes*
278 We performed a differential gene expression analysis, comparing the expression of the longevity genes
279 in apes (human, chimpanzee) vs the other 4 primate species grouped together (rhesus macaque,
280 marmoset, bushbaby, mouse lemur). Overall, 122/1,553 (~7.9%) longevity genes were found to be
281 differentially expressed between apes and the other primates grouped together (DESeq2 FDR < 5%;
282 Supplemental Table S3). Of those, 61 genes were upregulated and 61 downregulated. We investigated
283 if cis-regulatory evolution could underlie the changes in expression of the 122 genes identified as
284 differentially expressed in apes compared to other primates. To this purpose, we leveraged H3K27ac
285 ChIP-seq data generated in the same study from the same liver samples of the same individuals (Trizzino
286 et al. 2017). Namely, this specific histone modifications marks active cis-regulatory elements (enhancers
287 and promoters). Importantly, in the original study, Trizzino and collaborators (2017) identified a set of
288 ape-specific enhancers. We thus scanned the surrounding regions of the 122 differentially expressed

genes found in the apes vs other primates comparison (fig. 5a). We focused on the 50 kilo-bases (kbs) up- down-stream of the transcription start site (TSS) of the 122 genes, and observed that 27 of the 122 differentially expressed genes (22.1%) have an ape-specific enhancer in the 50 kbs surrounding the TSS (38 total enhancers, median distance from TSS = 19.8 kb; fig. 5a; Table S3). To test if this number is higher than expected by chance, we performed a permutation test (1000 permutations), by randomly extracting (for 1000 times) 122 genes from a list including all the annotated human genes (Ensembl), and found that, on average, only 4/122 random genes (3.3%) were located within 50 kbs from an ape-specific enhancer. Together, these data indicate that the longevity genes identified as differentially expressed in apes vs other primates are ~six times more likely than expected to be found near an ape-specific enhancer (22.1% vs 3.3%; Permutation Test $p < 2.2 \times 10^{-16}$; fig. 5a).

Ape-specific enhancers associated with differentially expressed longevity genes are derived from recent Transposable Element insertions

Overall, a total of 38 ape-specific enhancers were found in the 50 kbs surrounding 27 of the 122 differentially expressed longevity genes (Table S1.10). Since multiple studies have demonstrated that Transposable Elements (TEs) are an important source of gene regulatory novelty in the primate gene regulation (Jacques et al. 2013; Chuong et al. 2016; Trizzino et al. 2017; Trizzino et al. 2018), we tested for potential association between the 38 ape-specific enhancers and TE insertions. We found that 20/38 (~52.6%) ape-specific enhancers are derived from TE insertions (fig. 5b). This was not higher than expected by chance, considering that TEs represent ~50% of the human genome. Nonetheless, TE-derived ape-specific enhancers were significantly more associated with upregulated (65%) than to downregulated (35%) longevity genes (fig. 5c, one-tailed Fisher's Exact Test $p = 0.0425$). Notably, *ADAMTS8,* a gene reported as under positive selection in other long-lived species (whales; Tejada-Martinez et al. 2021), and which in this study we identified as correlated with lifespan (fig. 2a), is upregulated in apes and is located near a TE-derived ape-specific enhancer.

Finally, we investigated if specific TE families were overrepresented in the TE-derived ape-specific enhancers associated with differentially expressed longevity genes (fig. 5d). Notably, 15% of those were derived from SINE-Vntr-Alu (SVA) insertions. SVAs are the youngest TE family, with most copies being either ape- or human-specific, and represent only 0.1% of all human (and 0.3% of chimpanzee's) annotated TEs. Overall, our data suggest that SVAs are significantly overrepresented in our set of ape-specific enhancers associated with differentially expressed longevity genes (expected:

320 0.1% - observed 15%; Fisher's Exact Test $p < 2.2 \times 10^{-16}$). These findings are consistent with recent
321 studies which demonstrated that SVA insertions contribute to human gene-regulatory networks
322 (Trizzino et al. 2017; Trizzino et al. 2018; Pontis et al. 2019). Similarly, the LTR transposons were also
323 overrepresented in our set of ape-specific enhancers (Fisher's Exact Test $p < 0.0001$). These findings
324 are also consistent with recent literature on the contribution of LTRs to human gene regulation (Wang
325 et al. 2007; Cohen et al. 2009; Sundaram et al. 2014; Chuong et al. 2016; Janoušek et al. 2016; Fuentes
326 2018).
327 In summary our analysis revealed that lineage specific enhancers may have contributed to the
328 evolution of the expression of longevity genes in great apes and that young transposon insertions may
329 have had a significant role in this process.
330
331 **Discussion**
332 Natural selection and gene regulatory evolution likely underlay the evolution of most phenotypic traits.
333 Here, we specifically focused on the evolution of lifespan and body mass in great apes. This primate
334 lineage includes species which evolved with a lifespan and body mass significantly different from the
335 rest of primates. We carried out comparative genomic analyses, examining different sources of
336 molecular variation, including both coding genes and non-coding genomic regions (i.e. cis-regulatory
337 elements: enhancers, and promoters). Cis-regulatory evolution plays an essential role in phenotypic
338 diversification (Trizzino et al. 2017; Berthelot et al. 2018; Farré et al. 2019; Feigin et al. 2019; Sundaram
339 and Wysocka 2020; Marand et al. 2021), and can lead to evolutionary innovations in disease resistance
340 across species (Gorbunova et al. 2007; MacRae et al. 2015; Tollis et al. 2020).
341 Our comparative genomic analysis revealed that 67 genes positively correlated with the
342 evolution of maximum lifespan and body mass in primates. Out of those, 85% co-evolved exclusively
343 with maximum lifespan, while the remaining 15% co-evolved with lifespan and body mass together, or
344 with body mass alone. These genes are mostly involved in tumor suppression and senescence-related
345 processes. Since the increase in longevity elicits a greater risk to develop cancer, the rise and fixation of
346 new molecular variants (non-synonymous substitutions) could have positively contributed to improve
347 the functionality of the tumor suppressor genes and thus be beneficial for the evolution of the most
348 recent primate lineage. Similar outcomes have been recently reported by a study on mammals focused
349 on copy number variation in tumor suppressor genes (Sulak et al. 2016; Tollis et al. 2020). Consistent
350 with these lines of evidence, previous studies have found that the rate of protein evolution in anti-cancer

351 and DNA damage response genes is accelerated in long-lived mammals (Li and de Magalhães 2013;
352 Tollis et al. 2019; Tejada-Martinez et al. 2021).

353 A greater lifespan correlates with a higher likelihood of being exposed to pathogens and
354 diseases. Consequently, the immune system of long-lived species is expected to be under particularly
355 strong pressure to sustain the prolonged arm-race with the pathogens (Quesada et al. 2019; Singh et al.
356 2019). Consistent with this premise, we found a significant number of immune, inflammation, and DNA
357 repair genes that coevolved with longevity in primates. Notably, several of those genes were also under
358 positive selection in the ancestors of great apes. This points towards an evolutionary strategy in which
359 disease resistance and lifespan evolved together in primates, and particularly in apes, as it has been
360 reported for other long-lived species (Harris et al. 2017; Muntané et al. 2018; Vazquez et al. 2018).

361 In the great ape ancestor, we identified genes under positive selection involved in both the
362 immune system and in the regulation of telomere length. Importantly, telomeres play a key role in
363 ageing-related processes, and the regulation of telomere length is an important mechanism to control
364 cancer in species with increases in body mass (Seluanov et al. 2008). Namely, telomeres shorten with
365 age, and this leads to increased frequency of chromosomal damage, cell senescence and apoptosis (Tian
366 et al. 2018). It has been proposed that in large-size and long-lived species the rate of telomere shortening
367 is slower than in smaller and shorter-lived species (Whittemore et al. 2019). Based on our data, we
368 speculate that genes involved in telomere function and length may have evolved to help great apes fight
369 diseases, ultimately contributing to their longer lifespan.

370 Among the genes with positive selections in apes, we identified several associated with diet,
371 metabolism, as well as with the regulation of memory and emotions, all of which are important great
372 ape features. This finding is consistent with several studies that have proposed a link between increased
373 life span and increased cognitive functions (Ghirlanda et al. 2014; Barton and Venditti 2017; Orkin et
374 al. 2021). Characterizing their molecular evolution could help us to better understand the rise of genetic
375 neurological disorders in humans, such as macrocephaly, cognitive disorders and Parkinson's disease.
376 Different molecular strategies may have contributed to the evolution of longevity genes across primates.
377 Positive selection can lead to changes in the structure and function of a protein through amino acid
378 substitutions, without affecting gene expression, and thus the amount of protein produced by a specific
379 cell-type. In parallel, the expression level of genes important for longevity and body mass could be
380 affected by evolutionary changes in the associated gene regulatory network. For example, a novel,
381 species-specific, enhancer could influence the expression of the associated gene, ultimately leading to

382 higher levels of protein production without any modification to the structure of the protein itself. Here,
383 using RNA-seq we have investigated how the expression of the longevity genes varies across primates,
384 using the liver as a proof of principle. We demonstrated that oncogenes are significantly more expressed,
385 and senescence genes less expressed, in great apes relative to other primates, suggesting a tradeoff
386 between living longer (which leads to increased likelihood to produce offspring) and disease
387 susceptibility later in life (Campisi 2003; Blagosklonny 2010; Rodríguez et al. 2017; Di Micco et al.
388 2021).

389 Overall, we report that ~8% of the longevity genes tested in this work were differentially
390 expressed in the liver of great apes relative to higher primates, and we demonstrate that lineage specific
391 (i.e. ape-specific) enhancers have significantly contributed to this process. In fact, longevity genes
392 differentially expressed between great apes and other primates are ~six times more likely than expected
393 to be located near an ape-specific enhancer. Consistent with recent studies that suggested an important
394 contribution of young transposable elements (TEs) in the evolution of primate gene regulation (Jacques
395 et al. 2013; Trizzino et al. 2017; Pontis et al. 2019), we demonstrate that SVA transposons are
396 significantly overrepresented in the DNA sequence of ape-specific enhancers located near differentially
397 expressed longevity genes. The SVAs are the youngest family of TEs, and include ape- and/or human
398 specific copies.

399 In summary, our work has shed light on the evolution of thousands of longevity genes in great
400 apes, highlighting a significant contribution to this process for both positive selection on coding genes,
401 as well as evolutionary changes in the non-coding regulatory regions.

402

403 **Materials and Methods**

404 *Relationship between body mass and longevity across primates*

405 To determine if the body mass contributes to the variation in longevity independently in primates relative
406 to other mammals, and to assess ape-specific patterns, we examined the evolution of the life history
407 traits maximum lifespan (MLS) and adult body mass (BM) across 932 mammals. We fit a linear
408 regression through the phylogenetic generalized least squares (PGLS; (Orme et al. 2012), while
409 controlling for potential phylogenetic signals. Two independent regression models were implemented:
410 the first one across primates, and in the second model, the regression was performed between great apes
411 vs other primates (log10 MLS ~ log10 BM * great_apes). The phylogenetic tree used was derived from
412 Uyeda et al. (2017) (Uyeda et al. 2017) and the MLS and BM data were gathered from AnAge database

413 (Tacutu et al. 2018).

414

415 *Genomic sampling, longevity associated genes and build 2 of CellAge Database of Cell Senescence*
416 *Genes*

417 To study the evolution of longevity in primates we carried out a phylogenetic design that included
418 genomes from 19 mammalian species. Our taxonomic sampling included 3 species from the family
419 Hominidae (*Homo sapiens* - human, *Pan troglodytes* - chimpanzee and *Pongo abelii* - sumatran
420 orangutan), one representant from Hylobatidae (*Nomascus leucogenys* - white-cheeked gibbon), three
421 Cercopithecidae (*Macaca mulatta* - Rhesus macaque, *Rhinopithecus roxellana* - Golden snub-nosed
422 monkey and *Chlorocebus sabaeus* - vervet), four Platyrrhini (*Callithrix jacchus* - white tufted ear
423 marmoset, *Aotus nancymaae* - night monkey, *Saimiri boliviensis* - bolivian squirrel monkey, and *Cebus*
424 *imitator* - white-faced capuchin), two Strepsirrhine (*Otolemur garnettii* - bushbaby and *Microcebus*
425 *murinus* - Gray mouse lemur) and finally 5 other mammalian species outside of primates (*Tupaia*
426 *chinensis* - Chinese tree shrew, *Mus musculus* - common mice, *Canis lupus familiaris* - dog, *Bos taurus*
427 - cow and *Sus scrofa* - pig).

428 The coding sequences of each species were downloaded from Ensembl v.96 and NCBI
429 databases (Table S1). To remove low quality records, sequences were clustered using CD-HIT-est
430 v.4.6(Fu et al. 2012) with a sequence identity threshold of 90% and an alignment coverage control of
431 80%. The longest open reading frame was kept using TransDecoder LongOrfs and TransDecoder-
432 predicted in TransDecoder v3.0.1 (https://github.com/TransDecoder/TransDecoder/).

433 The longevity associated coding genes, 2,268 in total, were gathered in four different categories:
434 ageing genes from GenAge Database (build 20 - 307 protein coding genes,
435 https://genomics.senescence.info/genes/index.html); TSGs from the Tumor Suppressor gene database
436 (TSGene 2.0 - 1018 protein coding genes, https://bioinfo.uth.edu/TSGene/; (Zhao et al. 2013);
437 oncogenes from the Oncogene database (698 protein coding genes, http://ongene.bioinfo-minzhao.org/;
438 (Liu et al. 2017); and finally, we compiled build 2 of the CellAge Database of Cell Senescence Genes
439 with an additional 655 genes, complementary to the 279 genes previously reported;
440 https://genomics.senescence.info/cells/, (Avelar et al. 2020).

441 Build 2 of CellAge was compiled in the same way as build 1. A robust scientific literature search
442 was performed for relevant papers before curation and annotation; genes were appended to the database
443 if they met the following criteria:

444 · Only gene manipulation experiments were used to identify the role of the genes in CS to
445 ensure objectivity in the selection process.
446 · The genetic manipulation caused cells to induce or inhibit the CS process in wet lab
447 experiments. CS was detected by growth arrest, increased SA-β-galactosidase activity, SA-
448 heterochromatin foci, a decrease in BrdU incorporation, changes in morphology, and/or
449 specific gene expression signatures such as p21 and p16.
450 · The experiments were performed in primary, immortalized, or cancer human cell lines.
451

452 The resulting list comprised 934 genes that in human cell lines can induce or inhibit the CS process
453 (Table S2). The full CellAge database, including all annotations regarding cell types and cell lines is
454 available at https://genomics.senescence.info/cells/.

455

456 *Homology inference*

457 We inferred homology relationships among the 2,268 longevity genes and the 19 mammalian species
458 included in our study using the program OMA standalone *v*.2.3.1 (Roth et al. 2008; Altenhoff et al.
459 2019). We inferred the OMA Groups (OG), containing the sets of orthologous genes, for which we
460 performed natural selection analyses. The amino acid sequences were aligned using the L-INS-i
461 algorithm from MAFFT v.7 (Katoh and Standley 2013) and the codon alignments using the function
462 pxaa2cdn in phyx (Brown et al. 2017). Finally, to reduce the chance of false positives given for low
463 quality alignment regions we used the codon.clean.msa algorithm of the rphast package (Hubisz et al.
464 2011) with the associated longevity gene from the OG as reference sequence.

465

466 *Evolution of longevity genes and life history traits*

467 To evaluate the possible co-evolution between the longevity genes and the life history traits MLS and
468 BM in primates, the rate of evolution (ω=dN/dS) was calculated. The ω ratio per gene was estimated for
469 each tip in the 14 primates species using the branch model (Yang 2007) as is implemented in ETE-
470 toolkit with the *ete-evol* function (Huerta-Cepas et al. 2016). To calculate the ω ratios the treeshrew,
471 dog, cow and pig were used as outgroups. Three independent PGLS models were performed per OG: 1)
472 between the ω and the MLS; 2) between the ω and the BM; and 3) between the ω and the PGLS residuals
473 between the MLS ~ BM. Previous to the analysis, all variables were transformed to log10. The genes
474 with a dN/dS>2 were removed from the analysis.

475

476 *Positive selection analysis*

477 To evaluate the role of natural selection in the evolution of longevity genes in the ancestor of great apes,
478 we used codon-based models through a maximum likelihood approach using the program PAML v4.9
479 (Yang 2007), as is implemented in ETE-toolkit with the *ete-evol* function (Huerta-Cepas et al. 2016).
480 We calculated the branch-site model in order to estimate changes in the ω value of individual sites. We
481 compared the null model, where the ω value in the foreground branch was set to 1, with the model in
482 which the ω value was estimated from the data (Zhang 2005). The comparisons between models were
483 made using likelihood ratio tests (LRT) and the p-values from the LRT were corrected with FDR
484 (Benjamini and Hochberg 1995). All the genes with positive selection signal but with a LRT > 1 were
485 manually checked for false positives.

486

487 *RNA-seq analysis*

488 To evaluate the contribution of the gene regulation to the evolution of longevity genes in great apes, we
489 took advantage of recently published RNAseq and Chip-seq data for histone H3 lysine 27 acetylation
490 (H3K27ac) from liver of six species representatives of the main groups of primates (human, chimpanzee,
491 rhesus macaque, marmoset, bushbaby and gray mouse lemur; (Trizzino et al. 2017). The list of the genes
492 differentially expressed between Apes and other primates was downloaded from the Supplementary
493 Materials of the same paper (Trizzino et al. 2017). To generate box-plots comparing Gene Expression
494 (GE) across species, we leveraged the transcripts per million (TPM), also available from the
495 Supplementary Materials of Trizzino et al (2017). The TPMs were quantile normalized using R version
496 3.6.3 (R Core Team 2020).

497

498 *Enhancer evolution analysis*

499 From the publicly available Chip-seq data (Trizzino et al. 2017), we downloaded the list and coordinates
500 all the enhancers previously identified as "ape-specific" by Trizzino and collaborators. We then selected
501 all the ape-specific enhancers overlapping a region encompassing +/- 50 kbs from the transcription start
502 site (TSS) of each differentially expressed longevity gene using BEDTools v2.29.2 (Quinlan and Hall
503 2010). Based on this association, we then calculated how many longevity genes were both differentially
504 expressed in the ape vs other primates comparison AND also associated with an ape-specific enhancer.
505 To evaluate if this number was higher than expected by chance, we selected 122 random genes in the
506 human genome and examined how many of them had an ape-specific enhancer within 50 kbs of the TSS

507 and assessed statistical significance by means of Fisher's exact test. Finally, using BEDTools, we looked
508 for overlap between transposable elements and ape-specific enhancers associated with genes
509 differentially expressed in ape vs primate comparison. The list and coordinates of the transposable
510 elements were downloaded from the UCSC Genome Browser (RepeatMasker; hg38 assembly).
511
512 *Enrichment analysis*
513 To gain insight into the particular functions of the longevity genes of interest, the enrichment analysis
514 was performed using WebGestaltR v0.4.4 (Liao et al. 2019). We tested for significant pathway
515 associations using the hypergeometric test for Over-Representation Analysis (ORA) (Khatri et al. 2012).
516 We selected the categories of gene ontology, biological processes, molecular pathways, diseases OMIM,
517 and human phenotype and we considered overrepresented categories to be those with a significance
518 level above that of an FDR of 0.01 after correction with the Benjamini-Hochberg multiple test. An
519 independent enrichment analysis was made using as a background the protein-coding genes and relative
520 to the 2,268 longevity genes.
521
522 *Libraries in R associated with the data treatment, statistical analysis and graphics*
523 Bioconductor, msa, ape, geiger, nlme, pythools, caper, ggpubr, gridExtra, tidyverse, grid, corrplot,
524 ggplot2, ggpubr, Hmisc, gmodels, car, DescTools, qqplotr, dplyr, RColorBrewer, calecopal.
525
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531
532 **Contributions**
533 D.T.M. and M.T. conceived the study and performed the genomic analyses. R.A., J.P.M., B.Z. and G.N.
534 compiled the Build 2 of the CellAge database. I.L. contributed to the Cellage website development.
535 D.T.M., M.T. and R.A. wrote the manuscript. M.T. and D.T.M. directed the research.
536
537

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Figures

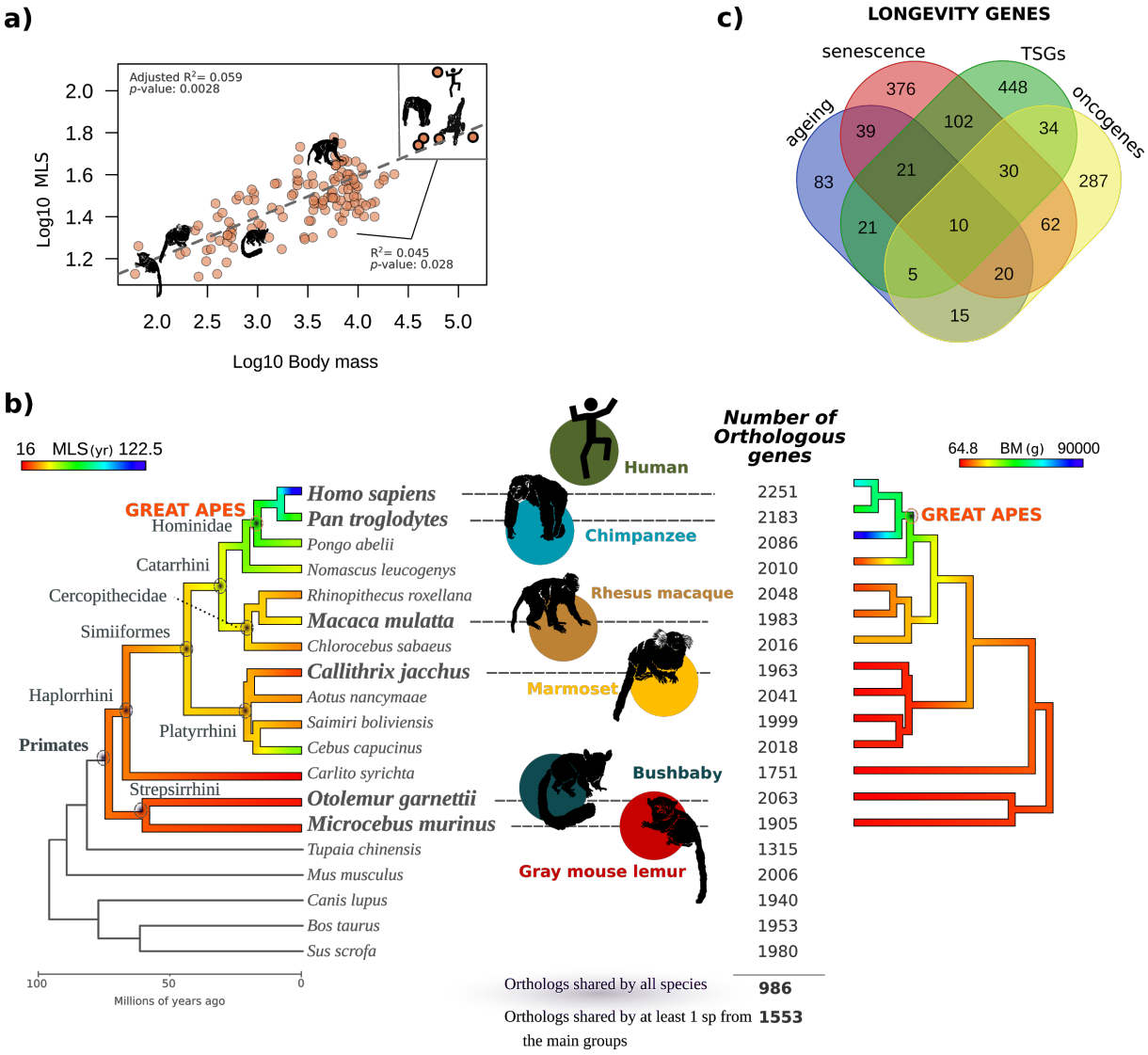

Figure 1. The evolution of body mass (BM) and maximum lifespan (MLS) across primates. a) Phylogenetic generalized least-squares models (PGLS) correlating MLS ~ BM across primates. The dashed lines represent a positive correlation between log10-transformed BM and MLS. The continuous line displays the correlation between great apes and other primates. b) Phylogenomic design. The molecular evolution analysis included 19 mammalian species. The six species highlighted are representatives from the main primates lineages (Catarrhini, Platyrrhini and Strepsirrhini). For these six species, RNA-seq and ChIP-seq data were publicly available (Trizzino et al. 2017). The colours in the phylogenetic tree reflect the values of MLS and BM in each primate branch respectively, from lowest (red) to highest (blue). c) Venn diagram representing the total number of orthologous longevity genes (1,553) shared by at least one species in each of main primates lineages, broken down based on the different categories (tumor suppressors, oncogenes, cell senescence and ageing genes).

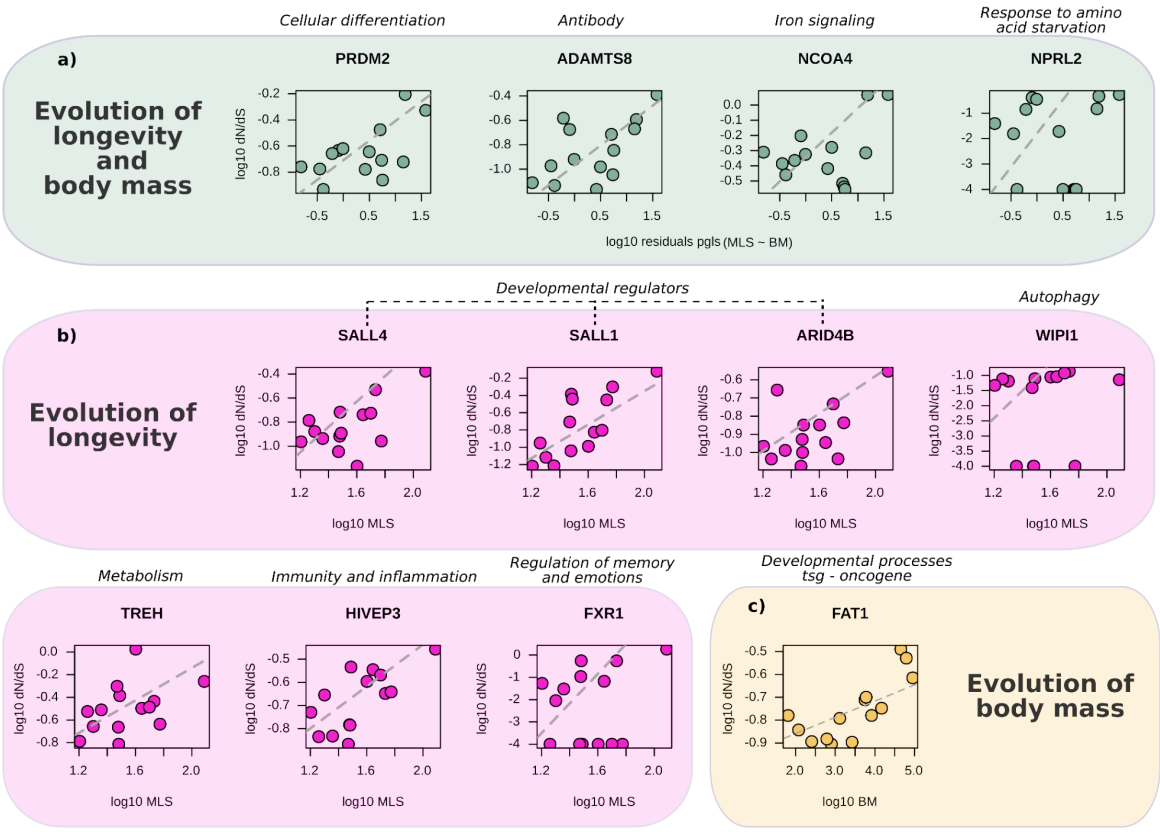

Figure 2. Examples of genes whose evolution correlated with the evolution of maximum lifespan (MLS) and/or body mass (BM). Three independent phylogenetic generalized least-squares models (PGLS) were performed in order to evaluate the independent contribution of each gene in the evolution of MLS and/or BM across primates. The dN/dS values were obtained from the branch model in PAML. a) PGLS model between dn/ds ~ residuals from the PGLS (MLS ~ BM). b) PGLS model between dn/ds ~ MLS and c) PGLS model between dn/ds ~ BM. In all the regression models the *p*-value was < 0.05 and the contribution of each gene (R^2) > 22% (Table 1).

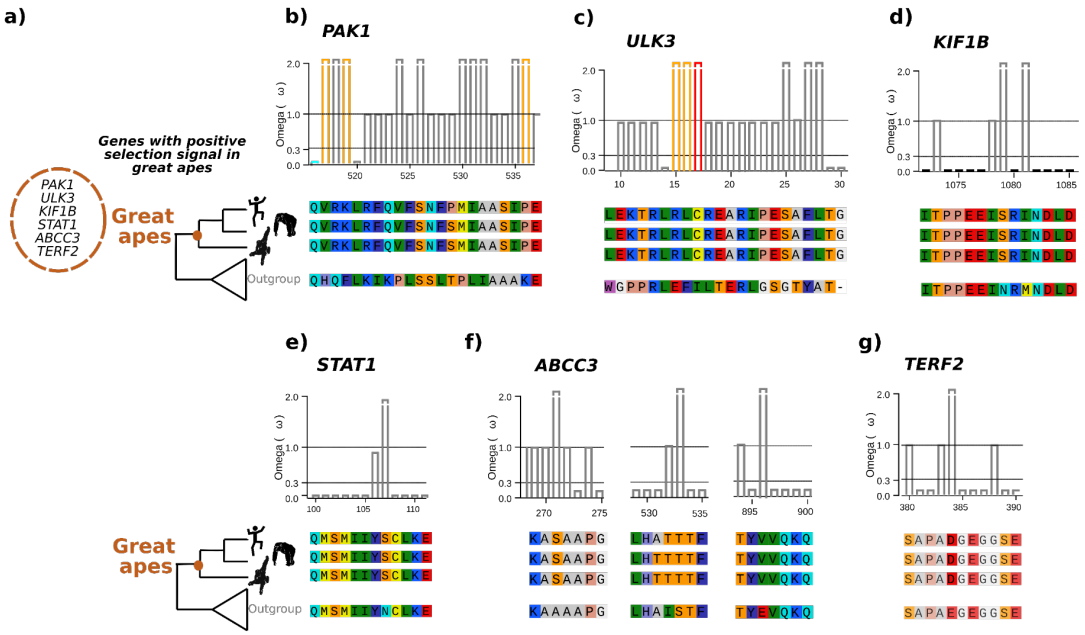

Figure 3. Genes under positive selection in the ancestor of great apes (a-g): *PAK1, ULK3, KIF1B, STAT1, ABCC3, TERF2.* The three first codon alignments on each gene represent fragments with an omega ω value >1. The colour gradients are used to display the degree and typology of amino acid change: the grey colour corresponds to the most conservative change, while red indicates the most radical. The alignments underneath display the consensus sequences across the outgroups (non-ape primates and other mammals). The amino acid colours reflect the different physicochemical properties.

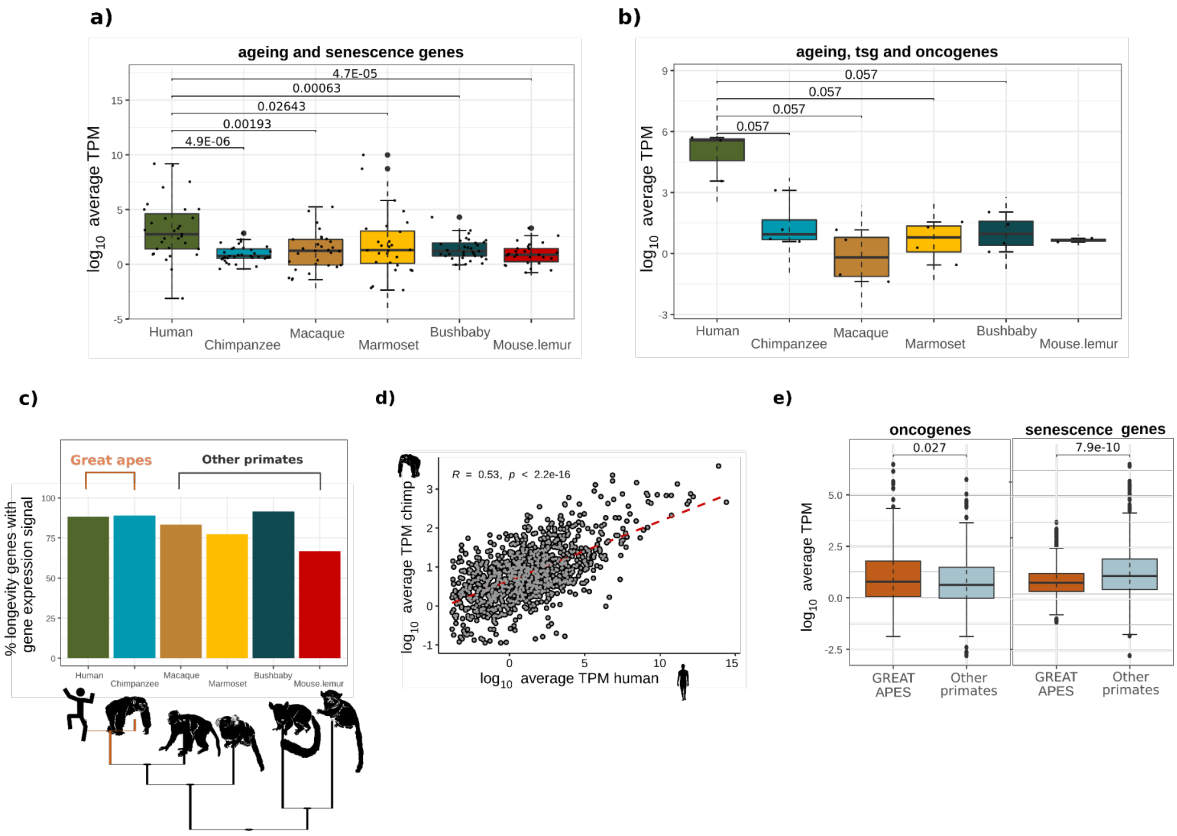

Figure 4. Evolution of longevity gene expression in the primate liver. Expression levels across species for the 1,553 longevity genes are divided into categories: ageing, senescence related genes, tumor suppressor genes (TSGs) and oncogenes; (a) ageing related genes and senescence genes (b) ageing related genes, tumor suppressors and oncogenes. In both groups, humans display higher expression compared to other primates (Wilcoxon rank-sum test, $p <$ or near 0.05). c) The percentage of longevity genes expressed in the liver is similar across the six primate species. d) The expression of the 1,553 longevity genes in the liver is positively correlated between humans and chimpanzee (Spearman's correlation coefficient, R=0.53, $p < 0.001$). e) Oncogenes are significantly more expressed in great apes compared to other primates. Senescence genes are significantly less expressed in great apes relative to the other primates (Wilcoxon rank-sum test, $p < 0.05$).

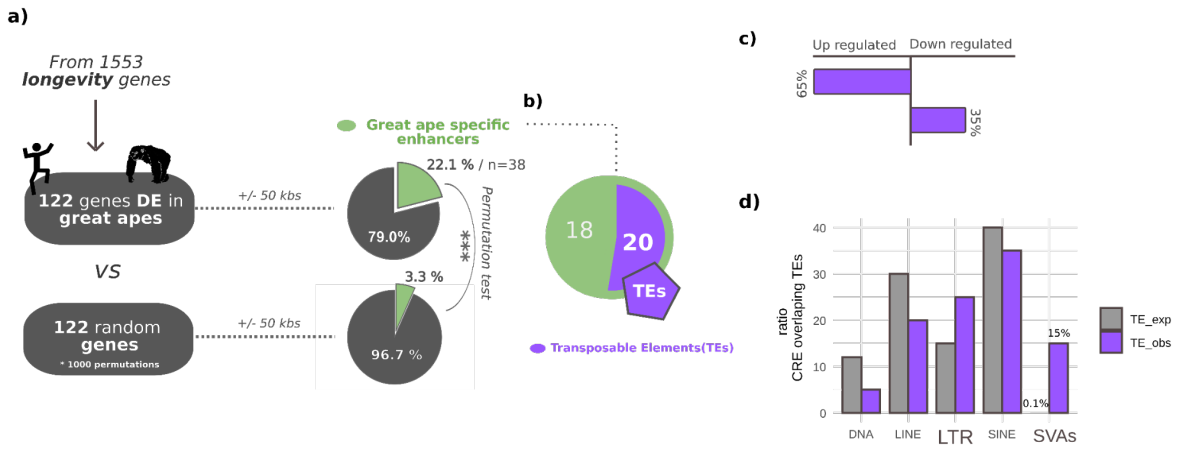

Figure 5. Ape-specific enhancers are enriched near differentially expressed longevity genes. a) 27/122 differentially expressed (DE) longevity genes (22.1%) are located within 50 kbs of an ape-specific enhancer (a total of 38 ape-specific enhancers for 27 DE genes). In comparison, only 4/122 (3.3%) randomly selected genes (1000 permutations) are located within 50 kbs of an ape-specific enhancer (Permutation Test $p < 2.2$ x 10-16).). b) 20/38 ape-specific enhancers (52%) located within 50 kbs of the DE longevity genes overlap annotated Transposable Elements (TEs). c) Of the DE longevity genes found near TE-derived ape-specific enhancers, 65% were identified as upregulated, 35% as downregulated (Fisher's Exact Test $p = 0.0425$). e) LTR and SVA transposons are overrepresented in the sequence of the ape-specific enhancers located within 50 kbs of a DE longevity gene (Fisher's Exact Test $p < 2.2 \times 10^{-16}$ for SVAs; $p < 0.0001$ for LTRs).