Diverse processes drive the origination and maturation of super-enhancers and super-silencers during a vast evolutionary timescale of the bicistronic gene *SMIM45*

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Abstract

A central question in molecular genetics concerns how transcriptional regulatory sequences and *de novo* genes originate and reach evolutionary fixation. In this study, we utilize the human bicistronic gene *SMIM45* as a model to analyze the evolutionary trajectories of gene development. This locus comprises several functional units: three enhancers (one featuring an embedded silencer), an exonic silencer that partially overlaps an ORF, a highly conserved ancestral sequence encoding a 68-aa microprotein, and a human-specific *de novo* gene encoding a 107-aa protein expressed spatiotemporally in embryonic brain tissues. We identify significant disparities in formation mechanisms; for example, the NANOG hESC enhancer originated simply via two *Alu* insertions that constitute the regulatory element. In contrast, the exonic silencer (ATAC-STARR-seq lymphoblastoid silent region 13815) originated by a combination of diverse mechanisms, including a "cultivator gene" process of base pair fixation consistent with the Cultivator Model proposed by Li Zhao and coworkers. Consequently, *SMIM45* exemplifies novel mechanisms of regulatory element development that occurred over several hundred million years, culminating in the birth of a human-specific *de novo* 107-aa cistron. The properties of these super-enhancers and super-silencers suggest a complex, intricate regulation of the 107-aa protein in fetal tissues.

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Key words: evolution of super-enhancers, super-silencers; bicistronic gene formation**;** evolutionary fixation of gene sequence; cultivator gene model; spatiotemporal gene expression; *Alu* TEs in enhancers

Author Summary

SMIM45 is one of a small number of known human bicistronic genes that encode two different proteins. It also contains a complex of super-enhancers and super-silencers, regulatory elements that likely control the expression of one of the cistrons, a human-specific, *de novo* protein cistron expressed in human embryonic brain tissues. The presence of these regulators raises questions about how these multifaceted components developed evolutionarily. We show that enhancers and silencers originated by very dissimilar processes, indicating a versatility of evolutionary mechanisms taking part in gene development. The exonic silencer stands out, having itself developed through a series of diverse processes. It appears unique; excluding the exonic splicing silencers, no other silencers are currently known to fully or partially overlap coding regions. Finally, we discuss the properties of known enhancers and silencers with respect to the spatiotemporal control of the *de novo* protein cistron, using these comparisons to gain insights into regulation of this cistron.

Introduction

Bicistronic genes are uncommon in eukaryotes, but improved detection techniques are revealing them more frequently [1–3]. These genes form a heterogeneous group with diverse mechanisms for RNA transcription and protein expression. For instance, some utilize alternative RNA transcript isoforms, such as those expressed spatiotemporally in hippocampal neurons [4], while others employ leaky scanning from an internal ribosome entry site (IRES) [5] or an upstream open reading frame (uORF) that inhibits cap-dependent translation [6]. *SMIM45* is also a bicistronic gene, encoding both an ancient 68-aa microprotein and a human-specific, de novo 107-aa protein [7]. Notably, while the 68-aa microprotein is expressed in somatic tissues, the 107-aa protein is expressed spatiotemporally in embryonic brain tissues [8, 9]. A significant feature of *SMIM45* is that it contains of an array of enhancer and silencer sequences, termed super-enhancers and super-silencers that likely regulate the transcription of the 107-aa cistron from its promoter, potentially representing a distinct transcriptional/translational mechanism for a bicistronic gene. This distinguishes the process from protein expression from a bicistronic transcript that relates to the above-mentioned processes.

Enhancers and silencers are short regulatory sequences that are found in great abundance throughout the human genome [10]. They bind transcription factors and can function by regulating cell specific transcription of genes in embryonic tissues [11-12]. Super-enhancers denote the presence of multiple enhancers in a genomic locus that ensure gene expression in specific tissues. [13-16]. Super-silencers are the presence of two of more silencers in a gene locus that act together to provide strong signals for repression of gene expression whereby repression is dependent on high CpG content of the locus [17,18].

Because of the array of regulatory elements present in *SMIM45*, the gene lends itself to an analysis of the evolutionary formation of enhancers and silencers. In this paper, we analyze the mechanisms of origination and the timeline of appearance and completion of the super-enhancer and super-silencer regulators during evolution. The study shows

regulatory elements formed through diverse mechanisms, highlighting the *SMIM45* gene's development via the continuous birth of functional elements over ~400 million years. By analyzing the evolutionary timeline of these enhancer and silencer sequences, we can assess their role in regulating the 107-aa protein cistron. A key finding is the evolutionary development of a short, ~400-million-year-old exonic silencer that overlaps an ORF and evolved through a combination of distinct molecular processes. Furthermore, comparisons made with known properties of silencers and enhancers provide insight into how the expression of the 107-aa cistron may be regulated.

Emera *et al* [19] investigated the evolution of enhancers, introducing a model of proto-enhancers as small, early developmental sequences that serve as nucleation sites for further development. We address the role of proto-enhancers/proto-silencers in *SMIM45* development but note that the Emera *et al* model aligns with the previously described evolution of the 107-aa protein cistron. Here, development proceeds by the initial formation of a proto-gene, a short amino acid (aa) sequence called an early developmental sequence [7]. In this framework, the proto-gene originates in ancient species and matures through the contiguous fixation of nearest-neighbor bases of the original as well as secondary proto-genes.

Background on *SMIM45*

Given the complex nature of the *SMIM45* gene and its regulatory landscape, a comprehensive background is provided. The *SMIM45* ultra-conserved 68-aa microprotein cistron is a pre-existing ancient gene that can be considered a cultivator gene. Lee *et al* [20] presented a model to explain origination of regulatory elements and *de novo* genes based on a proposed cultivator gene, a pre-existing gene that enables the fixation of DNA sequences. On the 3' side is a *de novo* 107-aa protein cistron found only in humans (Fig. 1). The two *SMIM45* cistrons are linked to and separated by a transcriptional silencer, *LOC130067579,* ATACSTARR-seq lymphoblastoid silent region 13815 [21] whose sequence partly overlaps with the 68-aa C-terminal end. We term this

overlapping sequence an exonic silencer. The remaining segment of the silencer, termed here silencer b resides in the intervening sequence, a promoter (Fig. 1). Given that enhancer sequences overlapping coding regions are designated exonic enhancers [22], we term the similarly situated silencer sequence an exonic silencer. About one fourth of all protein genes contain enhancers [22], however there are no reported exonic silencers that overlap or partially overlap ORFs, except for the exonic splicing silencers [23]. The enhancers are designated as enhancers 1-3 and they are approximately evenly spaced by ~4kbps (Fig.1). Thus, the *SMIM45* gene and its RNA transcripts have complex arrangements, with transcripts carrying different enhancers/silencer sequences in exons or introns (Fig. 1).

The initial study by An et al [24] that described spatiotemporal expression of the *SMIM45* 107-aa protein was partially compromised; the annotation by the *Ensembl* and GenBank data bases for the *SMIM45* locus had not yet been updated from the previous annotation as a lincRNA gene and secondly, detection of a protein was not originally reported. These have now been updated and are no longer issues. With the use of human embryonic cells, the expression of a protein from the 107 aa cistron was shown by multiple experimental techniques. Using human fetal brain cells, Chuan-Yun Li and co-workers [8] reported a protein product from the 107 aa ORF by mass spectrometry and Western blot analysis using specific polyclonal antibody. One of the peptides found, GSGLELVR represents part of the early developmental proto-gene sequence formed during evolution of the 107-aa protein [7]. The immunochemistry analyses show expression in human cerebral cortex and human cortical organoids grown from human embryonic stem cells. In addition, translation from the 107-aa ORF was detected by analysis of public Ribo-Seq datasets where ribosome footprint signals were found from cortical organoids grown from human embryonic stem cells [9]. In other independent gene expression studies, analysis of total RNA from various human tissues reveals RNA expression from *SMIM45* in fetal brain tissues (NCBI BioProject: PRJNA280600) [https://www.ncbi.nlm.nih.gov/gene/339674]. However, a 107-aa cistron transcript has not yet been isolated.

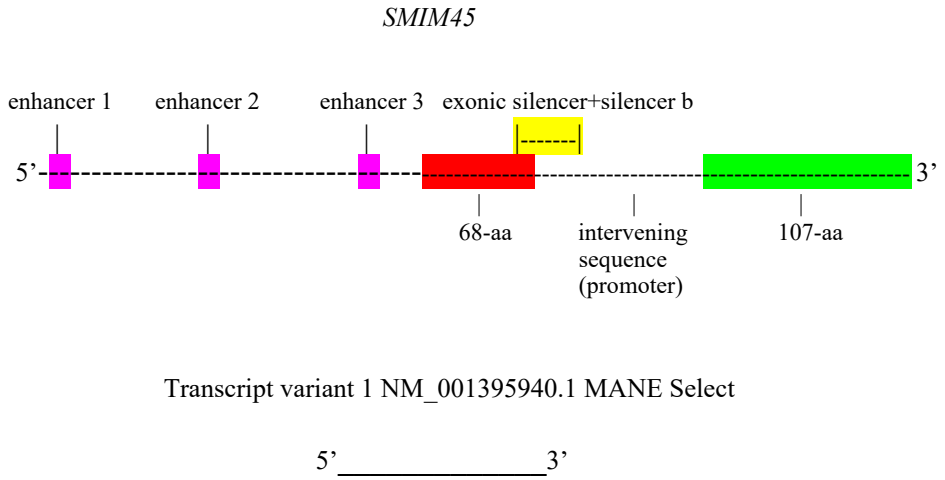

Figure 1. The*SMIM45* gene is 11,991 bps in length and contains three enhancers, the 68-aa protein ORF, the exonic silencer, the 107-aa promoter and the 107-aa protein ORF. Enhancer designations: Enhancer 1, LOC130067578 ATAC-STARR-seq lymphoblastoid active region 19151; Enhancer 2, LOC127896429 H3K4me1 hESC enhancer that also contains an embedded silencer; Enhancer 3, LOC127896430 NANOG hESC enhancer. The exonic silencer is the segment of the transcriptional silencer LOC130067579, ATACSTARR-seq lymphoblastoid silent region 13815 that overlaps the 68aa sequence by 38 bases. Silencer b is the segment of the silencer that overlaps the intervening promoter sequence by 192 bases. The yellow highlighted segment denotes the entire LOC130067579 length., The promoter in the intervening sequence is inferred. Transcript variant 1 is 1540 nt in length and encompasses the *SMIM45* sequence from the 68-aa to the end of the 107-aa sequence. It includes the exonic silencer but no enhancer sequences, however, the intron of processed transcript variant 1 contains the enhancer 3 NANOG hESC. Transcript variant 1 is termed a MANE Select transcript as it annotated in both the NCBI and *Ensembl* data bases with agreement on 5' end start sites. The 13 other transcript variants also contain the sequence from the 68-aa to the end of the 107-aa sequence and several carry enhancer 1, ATAC-STARR-seq lymphoblastoid active region 19151 in their exons.

Table 1 lists enhancers found in the *SMIM45* locus together with several known properties of related enhancers. All three show functions that can pertain to regulation of expression of the 107-aa protein. For example, Enhancer 2 related enhancers can

act as both enhancers and silencers of gene expression, which matches with the spatiotemporal expression of the 107-aa protein. Translation of the 107-aa protein was detected in human embryonic cerebral cortex and human cortical organoids [8]. Embryonic cerebral cortex tissues consist of proliferating stem/progenitor cells [25]. Enhancer 3 related enhancers bind transcription factor NANOG; NANOG is known to activate several gene promoters in embryonic stem cells [26].

Table1. Properties of enhancers related to enhancers 1-3

Enhancer	**General Properties**	**Reference**
Enhancer 1 *LOC130067578* ATAC-STARR-seq lymphoblastoid active region 19151	Binds transcription factor activators and silencers within chromatin-accessible regions	[21]
Enhancer 2 LOC127896429 H3K4me1 hESC enhancer	Active in embryonic stem cells and associated with activation of gene expression	[27]
Enhancer 2 *LOC127896429* embedded silencer, silent region_13814	Binds repressor transcription factor s and prevents transcription; essential to secure gene expression in specific tissues at specific times (spatiotemporally).	[28]
Enhancer3 *LOC127896430 NANOG* hESC enhancer	*Alus* act as enhancers and can regulate nearby promoters; NANOG is a regulator of human embryonic stem cell (hESC) identity	[29, 30]

Results

Evolution of exonic silencer: Cultivator fixes bases in silencer

The overlapping exonic silencer sequence has dual functions: it encodes the C-terminal end aa sequence of the 68-aa protein and forms a part of the silencer *LOC130067579*. Investigated were how initial bases of the exonic silencer were formed and fixed during the early evolutionary stages of development. We searched for the earliest living species that carries the sequence of *SMIM45.* The available data bank annotations in *Ensembl* show the earliest species with the annotation of *SMIM45* is that of the elephant shark (*Callorhinchus milii*) whose age of divergence is ~435 Mya. There is no

information on earlier animal species that may contain the *SMIM45* locus or its flanking genes, e.g., the sponges, members of the phylum Porifera.

A comparison of the exonic silencer sequence present the elephant shark compared with that of the human sequence shows that twenty-five out of thirty-eight bases (66%) are identical (Fig 2a). These bases were likely fixed in an ancestor to the elephant shark. Thus, much of the exonic silencer sequence is of ancient origins, over 435 Mya. Twenty-four bases are fixed because they are in either the first or second position of a codon (Fig. 2, top). A change in bases of codons can result in a change in the aa sequence of the 68-aa C-terminal end. For example, a change in the invariant G6 to C6 translates to the aa sequence RHNLAFGGPEV; the human aa sequence is RDNLAFGGPEV. Thus, twenty-four bases, which also form the sequence of the exonic silencer, are fixed by the cultivator-68 aa sequence and are fixed by natural selection. This is consistent with and supports the cultivator model of Lee et al. [20].

Located within the 38-base silencer/68-aa sequence are twelve wobble bases (Fig. 2, top, highlighted in green). Six of the twelve wobble bases, plus a seventh, T1, which is outside the ORF, are invariant between elephant shark and humans (Fig. 2a and top). Because these DNA bases do not dictate amino acid fidelity, they represent a specialized conservation within the exonic silencer, likely fixed in an ancestor to the elephant shark. This raises the important question of the mechanism of origination and fixation of these seven invariant bases. However, currently this cannot be answered. Sequence analysis of *SMIM45* or its neighbor genes (*CENPM* and *SEPTIN3)* from species ancestral to the elephant shark, such as lamprey, sea star, or sponges, is currently not possible as these genes have not yet been annotated within the available genome assemblies.

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Coding sequence:

T1 G2 CGC5 GAC8 AAC11 CTG14 GCC17 TTC20 GGC23 GGC26_CCG29 GAG32 GTC35_TGA38

Invariant wobble positions:

C11, G14, C20, C26, C35, A38.

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a.

ID	Label	5	10	15	20	25	30	35
1	eleph_shark	TCCGGGAGAACATGGGATTCCGTCCCCCCGACCTCTGA						
2	chimpanzee	TGCGCGACAACCTGGCCTTCGGCGGCCCGGAGGTCTGA						
3	human_____	TGCGCGACAACCTGGCCTTCGGCGGCCCGGAGGTCTGA						

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b.

ID	Label	5	10	15	20	25	30	35
1	elephant_shark	TCCGGGAGAACATGGGATTCCGTCCCCCCGACCTCTGA						
2	frog	TGAGGGACAATCTGGCCTACAGCCTCCCTGATGTATAG						
3	reed_fish	TGCAGGACAATTTGGGTTTCCGTGCTCCGGATGTATGA						
4	platypus	TCCGGGACAATCTGGCCTTCGGCACTCCCGAAGTCTGA						
5	koala	TCCAGGACAACCTGGCATTTGGGAGCCCCGATGTCTGA						
6	cape_elephant_shrew	TGCGTGACAACCTGGCCTTCGGAGGCCCCGAGGTCTGA						
7	elephant_	TGCGCGACAACTTGGCCTTCGGTGGCCCCGAGGTCTGA						
8	mouse	TGCGGGACAACCTGGCTTTCGGAGGCCCAGAAGTCTGA						
9	slow_loris	TGCGGGACAACCTCGCCTTTGGCGGCCCTGAGGTCTGA						
10	tarsier	TGCGTGACAACTTGGCCTTCGGCGGCGGTCCGGAGGTCTAA						
11	marmoset	TGCGCGACAACCTGGCCTTCGGCGGCCCCCGAGGTCTGA						
12	rhesus_macaque	TGCGCGACAACCTGGCCTTCGGCGGCCCCCGAGGTCTGA						
13	orangutan	TGCGCGACAACCTGGCCTTCGGCGGCCCCGGAGGTCTGA						
14	chimpanzee	TGCGCGACAACCTGGCCTTCGGCGGCCCCGGAGGTCTGA						
15	human_____	TGCGCGACAACCTGGCCTTCGGCGGCCCCGGAGGTCTGA						

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Fig. 2. Alignment of the human exonic silencer sequence with sequences from other species. Top. The C-terminal 68-aa coding sequence; highlighted are the first and second codon positions in red, the wobble positions in green. Invariant wobble positions are also shown with green highlight. Fig.2a, alignment of the human and chimp sequences with that of the elephant shark. Fig. 2b. The first codon begins with the third base, CGC. The alignment of base sequences homologous to exonic silencer from ancestral species with that of the sequence of human exonic silencer. The order of alignment of species 1-15 is by age of evolutionary appearance. The alignment is by MAFFT (https://mafft.cbrc.jp/alignment/server/index.html).

Fig. 2b shows the multiple sequence alignment of the 38-base exonic silencer in humans with that of the homologous sequences from fourteen species; it demonstrates that the exonic silencer sequence was evolutionarily completed in the marmoset (a New World primate of the Platyrrhini parvorder), approximately 40 Mya. To determine when

the amino-terminal end of the 68-aa ORF aa sequence was completed, the 38 nt sequences from different species were translated. Fig. 3 shows that the C-terminal end of the 68 aa ORF is completed in the Afrotheria. Therefore, the completion of the C-terminal end of the 68-aa ORF sequence was in the Afrotheria clade ~100 Mya, and the exonic silencer sequence was completed in the New World primates ~40 Mya.

The completion of the 68-aa C-terminal sequence within the Afrotheria clade is chronologically linked to the emergence of silencer b, the regulatory segment located in the promoter region. Silencer b was previously shown to have originated in the Afrotheria clade [7]. Because of this chronologically linkage, we propose that 35 out of 38 fixed bases of the exonic silencer may have been instrumental in the formation of silencer b. This concept implies that genetic information within these fixed bases may have dictated the initial sequence of proto-silencer b, though by an undetermined cis-acting mechanism.

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Species                     Alignment         % identity      Evolutionary age (Mya)

elephant shark              RENMGFRPPDL       36%             435
                            |:|:.|..|::
human 68-aa C-terminus      RDNLAFGGPEV



frog                        RDNLAYSLPDV       64%             352
                            |||||:..|:|
human 68-aa C-terminus      RDNLAFGGPEV



koala                       QDNLAFGSPDV       76%             160
                            :||||||.|:|
human 68-aa C-terminus      RDNLAFGGPEV



cape elephant shrew         RDNLAFGGPEV       100%            100
                            ||||||||||
human 68-aa C-terminus      RDNLAFGGPEV
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Fig.3. Translated aa sequence from the 38 nt sequence exonic silencer from different species and the percent identities. The SIB Swiss Institute of Bioinformatics, ExPASy Translational tool was used for the translation of nucleotide sequences. The aa sequences represent 5' 3' Frame 3 translations; evolutionary ages are for reference. Alignment was with EMBOSS Needle.

Evolution of exonic silencer: further development via biased mutations at nearest-neighbor invariant bases

We address the evolutionary expansion of the exonic silencer sequence. Analyzed are mutations that occur on the 5' and 3' sides of invariant bases. Thirteen bases are considered (Table 2). Excluded are invariant positions in codons where neighbor codon bases are fixed by natural selection. During evolution, nearest-neighbor mutations occurred almost entirely to produce G and C bases (Table 2). The fact that 12 out of 13 neighbors are G and C suggests that invariant bases and the sequence context steer mutational pressure toward GC accumulation within the exonic silencer. In other studies, it has been shown that biased nearest-neighbor mutations that occur during evolution depend on the identity of neighboring bases [32]. Although the small sample size precludes formal statistical analysis, the data show that mutations in nearest neighbors of invariant bases increase the GC and CpG content of the exonic silencer locus. The exonic silencer has a 70% GC content and contains five CpG dinucleotides, with three CpG sites contributed by nearest-neighbor bias. Silencers have been shown to repress gene expression in CpG -rich regions [18]. The mutations that occur at neighboring bases of invariant bases result in the total completion of the exonic silencer sequence that is present in humans.

Thus, the exonic silencer is formed through a combination of processes: codon-fixed bases (via cultivator model), GC bias at nearest-neighbor invariant bases, and invariant wobble bases that were formed by unknown means and in unknown species. The invariant wobble bases provide an estimate of over 435 Mya for origination of the exonic silencer. This timeframe estimate based on invariant wobble bases updates a previous earlier estimate of ~352 MYA to ~429 MYA]7]

Table 2. Nearest-Neighbor Bases of Invariant Bases

invariant base	5' of invariant base
C3	G2
G6	C5
A9	C8
T13	C12
T18	C17
C26	G25
T34	G33

invariant base	3' of invariant base
A10	C11
G22	T23
G15	C16
C20	G21
C28	G29
A31	G32

Silencer b (segment of silencer LOC130067579 within the promoter): detection of species-specific sequences

Silencer b originated *de novo* within the Afrotheria clade, by a pathway and at a different time than the exonic silencer [7]. Here we show that the silencer b sequence was completed in the chimpanzee ~6 Mya (Fig S1). This contrasts with completion of the exonic silencer in the New World primates ~40 Mya. Four point mutations distinguish the chimpanzee/human sequence from that of the gorilla. Thus, while the exonic silencer and silencer b greatly differ in mechanisms and timeframe of origination and completion, both constitute the sequence of silencer *LOC13006757* and function within this context. However, as proposed, the exonic silencer may have an additional function, that of participating in the formation of silencer b.

As silencer b originated *de novo*, we searched for a proto-silencer b sequence. Fig.4 shows an alignment of silencer b with orthologous sequences from the Afrotheria and

the Great Apes. The longest sequence found to be invariant is cctctgcagcc (Fig. 4). This 11-base sequence is 100% conserved across the deeply divergent mammalian lineages (Afrotheria to Primates, approximately 90 million years of separation). Furthermore, there is a synteny with the 68-aa bp sequence. Such high levels of conservation point to strong purifying selection and suggest the element is a likely a proto-silencer. For reference purposes, the Afrotheria phylogeny is shown in Fig. 5.

An alignment of silencer b sequence with homologs of the Afrotheria, the Old World monkeys and the Great Apes shows that during evolution the repeat sequence gcccgcccc was added in the Great Apes *SMIM45* locus (Fig S2). It is part of a longer repeat: gcccgccccgcccgccc. This indicates evolutionary pressure to increase the GC and CpG content of silencer b in the Great Apes.
Silencer b contains thirteen copies of CpG. Together with the five CpG dinucleotides present in the exonic silencer, there are eighteen copies of CpG in silencer *LOC130067579,* ATACSTARR-seq lymphoblastoid silent region 13815. This is consistent with the repression of gene expression that is dependent on high CpG content of a locus [17,18].

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#  Percent Identity  Matrix - created by Clustal2.1

     1: cape.golden.mole    55.15
     2: aardvark.homolog    51.70
     3: elephant            57.24
     4: gorilla             97.92
     5: chimpanzee         100.00
     6: human.silencer.b   100.00


CLUSTAL O(1.2.4) multiple sequence alignment

cape.golden.mole      ---------------------------------------------------ccctgttcc    9
aardvark.homolog      --------------------------------gctggccct---------tcccgttcc    18
elephant              ------------------------gcgggcctgtggcgccct---------ccccgttcc    27
gorilla               gccgacttgcaaaggggataggcgggcggcaccgggcgccctcccccagtccgccccgcc    60
chimpanzee            gccgacttgcaaaggggataggcgggcggcaccgggcgccctcccccagcccgccccgcc    60
human.silencer.b      gccgacttgcaaaggggataggcgggcggcaccgggcgccctcccccagcccgccccgcc    60
                                                                          *    **

cape.golden.mole      tgccttgcctgaagaccctccgaggagagggaagacgacccccctgatcctccacgctatc    69
aardvark.homolog      tgccggcctggagccctcccgga--agagggaagacgcccccctggtcctccgggcatc-    75
elephant              tgcccagcctggagaccctccga--gcagagaagactgccctctggtcctccggggatt-    84
gorilla               cgcccagcccggagacccccaaggcagagggaggcctgcctcttggccctccacgctatc    120
chimpanzee            cgcccagcccggagacccccaaggcagagggaggccggcctgttggccctccacgctatc    120
human.silencer.b      cgcccagcccggagacccccaaggcagagggaggccggcctgttggccctccacgctatc    120
                       ***   *  *    * * *       ** ** * *  **   **  *****  *

cape.golden.mole      cctctgcagccggagcccctttct--gtagaaaccaggcacttgaatcttatttgctgct    127
aardvark.homolog      cctctgcagcccaacttggggagcccggcgtgtgcagggtccaggagggccctggctgtg    135
elephant              cctctgcagcccagcttggggagcccggggtgcacc------aggagagccctggctgtg    138
gorilla               cctctgcagcctgggccctcgcgacagaggccccaggtgc----gctggcagtggaggtg    176
chimpanzee            cctctgcagcctgggccctcccgacagaggccccaggtgc----gctggcagtggaggtg    176
human.silencer.b      cctctgcagcctgggccctcccgacagaggccccaggtgc----gctggcagtggaggtg    176
                      ***********               *  *                      * *  *

cape.golden.mole      gtgggatcaaaat-------------------- 140
aardvark.homolog      gagagatggggcacctggtgcc---tt------ 159
elephant              gagagatggagcacctggtgtt---atttcttc 168
gorilla               gggcacttaggtgcctggctggcccagggcttg 209
chimpanzee            gggcacttaggtgcct----------------- 192
human.silencer.b      gggcacttaggtgcct----------------- 192
                      * *   *
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Fig.4. Alignment of silencer b with homologous sequences from representative Afrotheria and Great Apes species. Base positions 121-131 are totally conserved. Clustal Omega Multiple Sequence Alignment (MSA) was used.

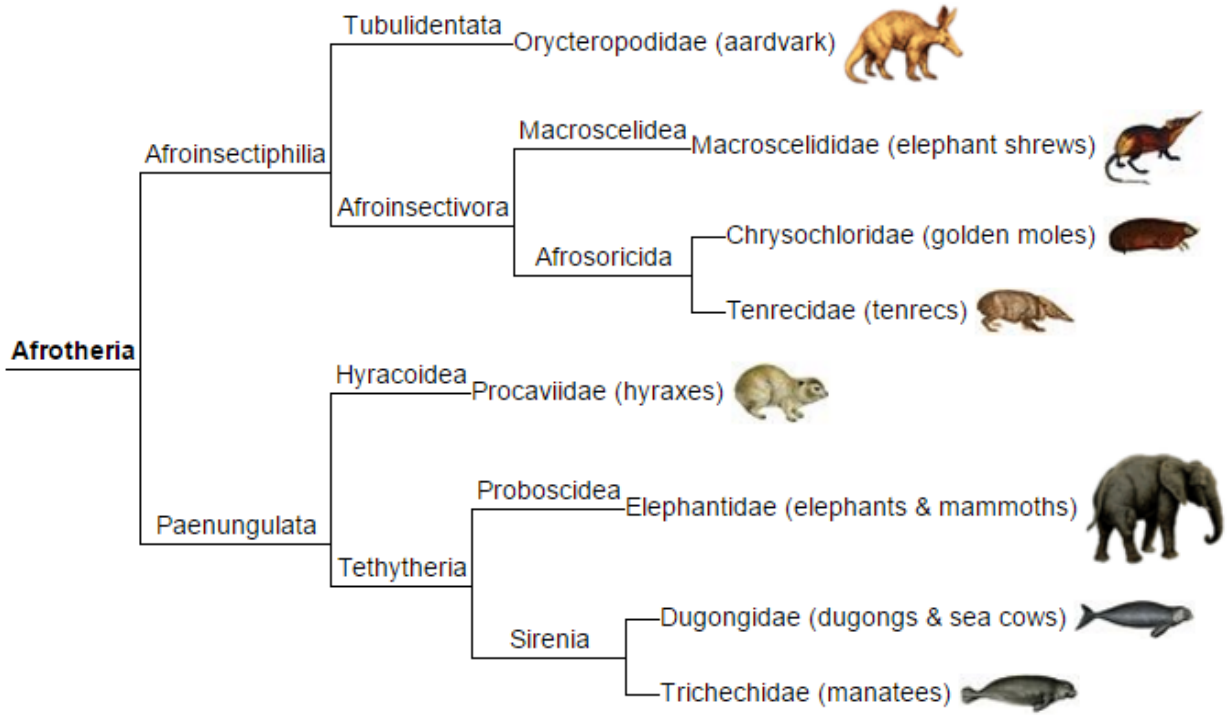

Fig. 5. Phylogeny of the Afrotheria clade. Illustration is from WikiCommons and is in the public domain.

Enhancer1: sequence origin and completion

Enhancer 1 is situated eight base pairs from the 5' start of the *SMIM45* gene and also resides within the exons of four transcript variants. Here, we investigate the evolutionary origin and sequence completion of the enhancer. Alignment with homologous regions in other primate species and in close primate relatives suggests that enhancer 1 originated *de novo*. The lemur sequence displays significant similarity with enhancer 1 (78%), the tree shrew, also a close relative to the primates, shows no significant identity (40%) (Fig. 6). The age of divergence from a common ancestor is ~63 Mya for the lemur and ~68 Mya for the tree shrew. The data suggest that enhancer 1 originated in an extinct early, stem-lineage of the lemur more than 60 Mya. It was not possible to identify a putative proto-enhancer 1 as sequence alignments with the tree shrew could not be made with accurate synteny. For reference, a phylogenetic tree of the primates is in Fig. S3.

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Percent Identity  Matrix - created by Clustal2.1


     1: tree.shrew                  39.78
     2: lemur                       71.90
     3: chimp                       98.10
     4: human                      100.00
     5: enhancer1.LOC130067578     100.00
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```
tree.shrew                  cccatctgtacctctgcctcctgttccagccagagtgtgtccacctacgagcacactggt  4705
lemur                       -------------------ccagtgcctccgagagcgcagaagccaggcctctgaggaac  2757
chimp                       ----------------------------------------ctagtggctgaagcaccgcc  20
human                       ----------------------------------------ctagtggctgaagcaccgcc  20
enhancer1.LOC130067578      ----------------------------------------ctagtggctgaagcaccgcc  20
                                                                                   *

tree.shrew                  atacgcgaggcgcaggccggccgaggtgagacgc------------------------tg  4741
lemur                       agcgggggacaggagggaggggacgatgagccgccggcacctaccaagatggtggctgtg  2817
chimp                       caggaggaaaaatcagcgggggaagcggggccgcctgcacctaccaagatggtggccgtg  80
human                       caggaggaaaaaccggcgggggaagcagggccgcctgcacctaccaagatggtggccgtg  80
enhancer1.LOC130067578      caggaggaaaaaccggcgggggaagcagggccgcctgcacctaccaagatggtggccgtg  80
                                  *        *  **    *  * * ***                       **

tree.shrew                  ctgatgtagagcaaggtggctaagaagccgtaagtgaagagaagtattgctgaagagagc  4801
lemur                       ttcaggccgggcagcttgtccagtggcctcaacaccgacatcccagtggcaagccaaacc  2877
chimp                       ttcaggccgggcagcttgtccaggggcctcaacaccgacatcacagccgcaagaccaacc  140
human                       ttcaggccgggcagcttgtccaggggcctcaacaccgacatcacagccgcaggaccaacc  140
enhancer1.LOC130067578      ttcaggccgggcagcttgtccaggggcctcaacaccgacatcacagccgcaggaccaacc  140
                             * * *  * ***   ** * *     *   *     * *        **       * *

tree.shrew                  gagaaatgatgggtggagggctggctagcaaaacgacctcagcctcttttaaaacatttg  4861
lemur                       tccgctcctgcgatgcgcgccagactttcaaaccgccctgactccggccctcagtgctca  2937
chimp                       gttgctcctgcggtgcgcgccgatctttcaaaccgccctgagtccagcccctagagcgcg  200
human                       gttgctcctgcggtgcgcgccgatctttcaaaccgccctgagtccagcccctagagcgcg  200
enhancer1.LOC130067578      gttgctcctgcggtgcgcgccgatctttcaaaccgccctgagtccagcccctagagcgcg  200
                                       * **   * *   **  **** ** *** *  *        *

tree.shrew                  aacttggaaacaaacaaaaaaaaggcctggg--------------taatggccaccatgg  4907
lemur                       gcttagggctcgtcaccctccatgggcggggcttatcgggttctcttaaaggaaccgcta  2997
chimp                       gcctgggggc-------------------------------------------------  210
human                       gcctgggggc-------------------------------------------------  210
enhancer1.LOC130067578      gcctgggggc-------------------------------------------------  210
                               * **
```

Fig.6. Alignment of enhancer 1 with genomic sequences of the tree shrew (*Tupaia chinensis*, Chinese tree shrew) and the lemur (*Lemur catta*, Ring-tailed lemur). Both species are the closest living relatives to the primates. Clustal Omega Multiple Sequence Alignment (MSA) was used for alignment.

Additionally, the species for which the enhancer 1 sequence was finalized were investigated. Fig. 7 shows there are four-point mutations that distinguish the human from the two chimpanzee sequences. Enhancer 1 was thus completed in the human genome.

```
Percent Identity  Matrix - created by Clustal2.1

     1: chimp                      98.10
     2: Bonomo                     98.10
     3: human                     100.00
     4: enhancer1.LOC130067578    100.00


CLUSTAL O(1.2.4) multiple sequence alignment


chimp                       ctagtggctgaagcaccgcccaggaggaaaaatcagcgggggaagcggggccgcctgcac  60
Bonomo                      ctagtggctgaagcaccgcccaggaggaaaaatcagcgggggaagcggggccgcctgcac  60
human                       ctagtggctgaagcaccgcccaggaggaaaaaccggcgggggaagcagggccgcctgcac  60
enhancer1.LOC130067578      ctagtggctgaagcaccgcccaggaggaaaaaccggcgggggaagcagggccgcctgcac  60
                            ******************************** * *********** *************

chimp                       ctaccaagatggtggccgtgttcaggccgggcagcttgtccaggggcctcaacaccgaca  120
Bonomo                      ctaccaagatggtggccgtgttcaggccgggcagcttgtccaggggcctcaacaccgaca  120
human                       ctaccaagatggtggccgtgttcaggccgggcagcttgtccaggggcctcaacaccgaca  120
enhancer1.LOC130067578      ctaccaagatggtggccgtgttcaggccgggcagcttgtccaggggcctcaacaccgaca  120
                            ************************************************************

chimp                       tcacagccgcaagaccaaccgttgctcctgcggtgcgcgccgatctttcaaaccgccctg  180
Bonomo                      tcacagccgcaagaccaaccgttgctcctgcggtgcgcgccgatctttcaaaccgccctg  180
human                       tcacagccgcaggaccaaccgttgctcctgcggtgcgcgccgatctttcaaaccgccctg  180
enhancer1.LOC130067578      tcacagccgcaggaccaaccgttgctcctgcggtgcgcgccgatctttcaaaccgccctg  180
                            *********** ****************************************************

chimp                       agtccagcccctagagcgcggcctgggggc  210
Bonomo                      agtccagcccctagagcgcggcctgggggc  210
human                       agtccagcccctagagcgcggcctgggggc  210
enhancer1.LOC130067578      agtccagcccctagagcgcggcctgggggc  210
                            ******************************
```

Fig.7. Completion of enhancer 1 sequence in humans. Clustal Omega Multiple Sequence Alignment (MSA) was used was used for alignment.

Enhancer2

The evolutionary origination and completion of enhancer 2, *LOC127896429* H3K4me1hesc was investigated. Similar to that of enhancer 1, enhancer 2 originated by the *de novo* process. Sequences from five members of the Afrotheria clade were

aligned with those of the chimpanzee and the human enhancer 2. The percent identities from the alignment show that the sequences from several Afrotheria species approach the “twilight zone” of significance, suggesting origination from the Afrotheria clade (Fig. 8, top). The data suggest that enhancer 2 originated within the Afroinsectivora branch of the Afrotheria clade (Fig. 5). The koala (*Phascolarctos cinereus*) lineage separated from the ancestor of Afrotheria before the Afrotheria separated from other placental mammals. Its genomic sequence does not significantly align with enhancer 2 (45% identity). This is consistent with the determination that enhancer 2 originated in the Afrotheria clade, ~100 Mya. One segment of enhancer 2 displays invariance, $_{17}$cagtcac$_{23}$ with exception of the tenrec sequence (Fig. 8, bottom); this sequence may be a candidate for a proto-enhancer 2 as the 8-base sequence is under strict purifying selection, over ~90 millions of years of separation.

```
=====================================================================
# Percent Identity  Matrix - created by Clustal2.1

     1: tenrec         48.01
     2: golden.mole    51.23
     3: elep.shrew     51.23
     4: aardvark       56.08
     5: elephant       57.74
     6: chimp          99.35
     7: enhancer2     100.00

=====================================================================
CLUSTAL O(1.2.4) multiple sequence alignment


tenrec              gctttgcattccagctcagccaccaagaagctgagtgaccgg  42
golden.mole         gttttaggttccagcccagtcactatggatctgagtggcctg  42
elephant.shrew      gttttaggttccagcccagtcactatggatctgagtggcctg  42
aardvark            gttctaaattccagctcagtcaccaaggagctgcatgacctg  42
elephant            gctttgatttctagctcagtcacagaggagctgagtgaccta  42
chimp               gctttgaattccagctcagtcactgagaagctgagggctctg  42
enhancer.2          gctttgaattccagctcagtcactgagaagctgagggctctg  42
                    * * *   *** *** *** ***   * * ***   *  *
=====================================================================
```

Fig. 8. Homologous sequences from the Afrotheria clade were aligned with sequences of the chimpanzee and enhancer 2. Top. The percent identities. Bottom, a segment of enhancer 2 aligned with homologous sequences Clustal Omega Multiple Sequence Alignment (MSA) was used.

An alignment of the chimpanzee and human *SMIM45* sequences with that of the enhancer 2 reveals two bp deletions and three point mutations that distinguish the human sequence from that of the chimpanzee (Fig. S4). Therefore, this identifies enhancer 2 as human specific. Nevertheless, similar to the mutations in enhancer 1, the functional impact of these mutations remains unknown. The completion of the embedded silencer, *LOC127896429* silent region_13814 was also determined. The sequence was completed in the chimpanzee (Fig.S5) and therefore it is not human specific. interestingly, this contrasts with enhancer 2 completion.

Enhancer 3, NANOG hESC: birth by Alu insertions

Branco and Chuong [33] provide examples of how transposable elements can drive regulatory innovation. Functioning in gene regulation, many enhancers contain *Alu* transposable elements that modulate target gene expression through promoter interactions [34-36]. Nearly half of *Alu* elements present in the human genome are in introns where they regulate gene transcription in specific tissues [37]. In accordance with this, enhancer 3 (*LOC127896430* NANOG hESC) contains two *Alu* elements (Fig. 9). In *SMIM45* RNA transcripts, enhancer 3 resides in the intron of *SMIM45* RNA transcript variant 1, NM_001395940. Given its intron location, enhancer 3 perhaps may regulate the 107-aa cistron in embryonic brain tissues.

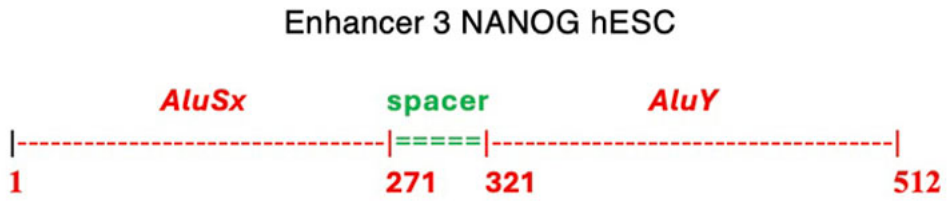

Fig.9. Schematic of components of enhancer 3. *Alu* TEs and the spacer size were determined by RepeatMasker [38].

Enhancer 3 comprises tandem transposable elements (TE) *AluSx* and *AluY* that are separated by a 50 bp spacer (Fig. 9). To investigate evolutionary origins, *SMIM45* orthologs from various primate species were aligned with the human enhancer 3. Fig.

10 demonstrates that the enhancer originated in the Old World monkey lineage, as evidenced by its presence in the rhesus monkey (*Macaca mulatta*) and olive baboon (*Papio 20nubis*) *SMIM45* loci. The enhancer sequence was not detected in Ma's night monkey (*Aotus nancymaae*), a New World primate. Both the rhesus monkey and olive baboon diverged from the human lineage approximately 25-30 million years ago. Fig. 10 shows that the rhesus and baboon sequences possess the complete *AluSx* sequence along with part of the spacer sequence. The enhancer likely originated by the insertion of the *AluSx* TE into the Old World monkey (*Catarrhini*) *SMIM45* locus. A second *Alu*, *AluY* was inserted in the Great Apes (*Hominoidae*) *SMIM45* as it is found only in the orangutan and the other Great Apes. For reference, Fig.S3 provides a diagram of primate phylogeny.

```
Ma.s.night.monkey   ------------------------------------------------------------  10577
AluSx               ------agtttcactcttgttgcccaggctggagtgcagtggcacagtcgtggctcactg  54
AluY                ------------------------------------------------------------  0
rhesus              agacagagtttcactcttgttgcccaggctggagtgcaatgacacaatcgtggctcactg  9382
olive.baboon        ggacagagtttcactcttgttgcccaggctggagtgcaatgacacaatcgtggctcactg  9782
orangutan           agacagagtttcactcttgttgcccaggctggagtgcaatggcacagtcgtggctcactg  12972
gorilla             agacagagtttcactcttgttgcccaggctggagtgcaatggcacagtcgtggctcactg  13164
chimpanzee          agacagagtttcactcttgttgcccaggctggagtgcagtggcacagtcgtggctcactg  11134
human               agacagagtttcactcttgttgcccaggctggagtgcagtggcacagtcgtggctcactg  8310
enhancer3           ------agtttcactcttgttgcccaggctggagtgcagtggcacagtcgtggctcactg  54

Ma.s.night.monkey   ------------------------------------------------------------  10577
AluSx               gaa-ctccacctcctgggttcaagcaactctcctgcctcagcctgccgagtagttgggat  113
AluY                ------------------------------------------------------------  0
rhesus              taacctctgcctcctgggttcaagcaattctcctgcctcagcctgccgagtagttgggat  9442
olive.baboon        taacctctgcctcctgggttcaagcaattctcctgcctcagcctgccaagtagttgggat  9842
orangutan           gaacctccacctcctgggttcaagcaattctcctgcctcagcctgccgagtagttcggat  13032
gorilla             gaacctccacctcctgggttcaagcaattctcctgcctcagcctgccgagtagttgggat  13224
chimpanzee          gaa-ctccacctcctgggttcaagcaattctcttgcctcagcctgccgagtagttgggat  11193
human               gaa-ctccacctcctgggttcaagcaactctcctgcctcagcctgccgagtagttgggat  8369
enhancer3           gaa-ctccacctcctgggttcaagcaactctcctgcctcagcctgccgagtagttgggat  113

Ma.s.night.monkey   ------------------------------------------------------------  10577
AluSx               tacaagcatgtgccaccacacctggctaattttgtacttttagtagagacagggtttcac  173
AluY                ------------------------------------------------------------  0
rhesus              tacaagcacgggccaccacacccggctaattttgtacttttgtagagacggggtttcac  9502
olive.baboon        tacaagcacgggccaccacacctggctaattttgtacttttgtagagacggggtttcac  9902
orangutan           tacaagcatgtgtcaccacacctggctaattttgtacttttagtagagacagggtttcac  13092
gorilla             tacaagcatgtgccactacacctggctaattttgtacttttagtagagacagggtttcac  13284
chimpanzee          cacaagcatgtgccaccacacctggctaattttgtacttttagtagagacagggtttcac  11253
human               tacaagcatgtgccaccacacctggctaattttgtacttttagtagagacagggtttcac  8429
enhancer3           tacaagcatgtgccaccacacctggctaattttgtacttttagtagagacagggtttcac  173

Ma.s.night.monkey   ------------------------------------------------------------  10577
AluSx               catgttggtcaggctggtcttgaattcctgacctcaggtgacccatcctccttggcctcc  233
AluY                ------------------------------------------------------------  0
rhesus              catgttggtcaggctggtcttgaacttctgacctcaggtgacctgcccgccttggcctcc  9562
olive.baboon        catgttggtcaggctggtcttgaactcctgacctcaggtgacctgcccgccttggcctcc  9962
orangutan           catgttggtcaggctggtcttgaactcctgacctcaggtgacccgtcctccttggcctcc  13152
gorilla             catgttggtcaggctggtcttgaactcctgacctcaggtgactcgtcctccttggcctcc  13344
chimpanzee          catgttggtcaggctggtcttgaactcctgacctcaggtgacccatcctccttggcctcc  11313
human               catgttggtcaggctggtcttgaattcctgacctcaggtgacccatcctccttggcctcc  8489
enhancer3           catgttggtcaggctggtcttgaattcctgacctcaggtgacccatcctccttggcctcc  233

Ma.s.night.monkey   ------------------------------------------------------------  10577
AluSx               caaagtgctgggatcataggcatgagcca-ttggcctgg--------------------  271
AluY                ------------------------------------------------------------  0
rhesus              caaagtgctgggattacaggcgtgagccatcatgcccagccacaaaatgctctttaggca  9622
olive.baboon        caaagtgctgggattacaggcatgagccattatgcccagccacaaaatgctctttaggca  10022
orangutan           caaagtgctgggattataggcatgagcca-tctgcccggtcgcaaaatgctctttaggca  13211
gorilla             caaagtgctgggattataggcatgagcca-tcggcccggtcgcaaaatgctctttaggca  13403
chimpanzee          caaagtgctgggattataggcatgagcca-ttggcccggtcgcaaaatgctctttaggca  11372
human               caaagtgctgggatcataggcatgagcca-ttggcctggttgcaaaatgctctttaggca  8548
enhancer3           caaagtgctgggatcataggcatgagcca-ttggcctggttgcaaaatgctctttaggca  292

Ma.s.night.monkey   ------------------------------------------------------------  10577
AluSx               ------------------------------------------------------------  271
AluY                ---------------------------ggctgcatgcggtggctcacgcctgtaatccc  32
rhesus              ttgtcttgttaaaa------------------------------------------------  9636
olive.baboon        ttgtcttgttaaaa------------------------------------------------  10036
orangutan           ttgtcttgctaaaaatgcaaagtacccaggctgggtgcggtgcctcactcctgtaatccc  13271
gorilla             ttgtcttgttaaaaatgcaaagtacccaggctgggtgcggtggctcacgcctgtaatccc  13463
chimpanzee          ttgtcttgttaaaaatgcaaagtacccaggctgcgtgcggtggctcacgcctgtaatccc  11432
human               ttgtcttgttaaaactgcaaagtacccaggctgcatgcggtggctcacgcctgtaatccc  8608
enhancer3           ttgtcttgttaaaactgcaaagtacccaggctgcatgcggtggctcacgcctgtaatccc  352
```

Fig. 10. Alignment of homologous primate species sequences with that of enhancer 3. Highlighted regions indicate *AluSx* (yellow), *AluY* (brown), and the intervening spacer (green). Note the alignment with the *AluY* shows only a segment of the total alignment.

To determine in what species the enhancer 3 sequence was completed, an alignment was made with the chimpanzee sequence with that of the human enhancer 3 (Fig. S6). Twelve point mutations differentiate the human and chimp/bonobo sequences from enhancer 3. Thus, the enhancer 3 sequence is human specific. Enhancer 3 contains the sequence TAATTTTGT, which has the transcription factor NANOG core binding motif consisting of TAAT followed by several Ts and GT [39].

Discussion

This study investigates the evolutionary origins of regulatory sequences within the *SMIM45* locus, providing insights into the mechanisms underlying the formation of silencers and enhancers. Notably, we show that over a massive time span of >400 My, *SMIM45* evolved a suite of regulatory elements believed to control the human specific 107-aa protein's activity during human fetal brain development. The complexity of these combined regulatory processes that are vital for human embryonic brain development may explain this long evolutionary time frame. The exonic silencer sequence, which overlaps the 68-aa C-terminal end, is the first of the regulatory sequences to originate evolutionarily, featuring a small number of anciently formed invariant wobble bases. This invariance reflects the silencer's functional constraints. While the mechanism of fixation of these bases is unknown, the majority of exonic silencer bases are fixed by the cultivator model described by Lee et al [20]. The data show that the cultivator-fixed bases and the wobble invariant bases carry information that guides exonic silencer maturation via nearest neighbor bias, resulting in the total completion of the 38-base-pair exonic silencer. *De novo* origination of both silencer b (segment of the ATAC-STARR-seq lymphoblastoid region 13815 in the promoter region) and the 107-aa protein cistron occurred in the Afrotheria clade [7]. Concurrently, the 68-aa C-terminal base sequence was also completed in Afrotheria, hinting at a potential role of these

bases (that also make up the exonic silencer-specific fixed bases) in the emergence of Silencer b. With the exception of a different type of exonic silencer termed exonic splicing silencers, which contribute to alternative splicing [23], little or no information exists regarding exonic silencers that overlap ORFs. The ATAC-STARR-seq lymphoblastoid silent region 13815 within the *SMIM45* gene appears to be the first of its kind to be identified and characterized.

Pu *et al* [40] provided a detailed study on the evolution of enhancers containing embedded silencers. By analyzing expression patterns across *Drosophila melanogaster* and related species, they demonstrated that the evolution of repressor sequences can precede that of the enhancer sequences. Although the embedded silencer in the enhancer 2 sequence reported here was completed before the enhancer, the significance of this timing remains uncertain.

We have shown that, during evolution, a bias in the nearest neighbors of invariant bases in the exonic silencer increases the GC content of the locus to 73%. Similarly, there is evolutionary pressure to increase in GC content within silencer b, which is in the promoter of the 107-aa cistron. High GC content facilitates chromatin accessibility, enabling the transcriptional apparatus to access DNA [41, 42] and potentially mediating suppression. We also demonstrate evolutionary pressure to add CpG motifs to the silencer *LOC130067579* sequence, consistent with the known role of high CpG content in gene repression [18]. Although Yang *et al* [43] confirmed that CpG content impacts gene expression evolution, and silencers are recognized for repressing somatic gene expression [44], the specific mechanism for silencing the 107-aa cistron has not been elucidated. But given the high GC/CpG content, it is likely that *LOC130067579* suppresses this cistron in somatic tissues. Further research is warranted. It should also be pointed out that genome-wide silencer identification is in an early stage [44].

The completion of all three enhancer sequences in the human *SMIM45* locus points to the regulation of the human 107-aa cistron, especially given that the orthologous

chimpanzee sequence encodes a truncated protein [7]. Concerning *SMIM45* regulatory element functions, a comparison with known related silencers and enhancers is instructive. Although it is not a bicistronic gene, *FGF18* (fibroblast growth factor 18) is similar to *SMIM45* in having super-silencers and super-enhancers [45]. Two silencers in the *FGF18* gene can act together through compensatory chromatin interactions. Perhaps compensatory chromatin interactions also relate to the function of the two silencers in *SMIM45, silent* region_13814 and silent_region 13815.

Both Enhancer 1 and enhancer 2 originated *de novo* from ancestral non-coding regions and appear to be part of a large class de novo of human brain specific enhancers [48]. These brain-specific enhancer sequences are completed by one or a small number of point mutations distinguishing human from chimpanzee sequences. Consistent with this, enhancer 1 and enhancer 2 show a small number of mutations that complete the human sequence. *De novo* enhancers can induce genes that are critical to cognitive function and are expressed in progenitor cells of the developing neocortex [46]. By analogy, enhancers 1 and 2 may regulate the expression of the *SMIM45* 107-aa protein shown to be produced in the embryonic cerebral cortex [8].

Enhancer 3, the NANOG gene in hESCs consists of two *Alu* elements and contains the transcription factor NANOG core binding motif. NANOG is known to bind enhancers in embryonic stem cells to regulate gene expression during developmental processes [47, 48]. This may relate to the regulation of the 107-aa cistron by enhancer 3 as the 107-aa protein is expressed in embryonic brain tissues [8]. We have considered the regulatory elements individually, however, *SMIM45* contains a complex of super-enhancer and super-silencer. These act similarly to the individual elements except function in an intense fashion; super-enhancers to strongly boost gene expression in a cooperative manner; super-silencers to act collectively and exert strong, coordinated suppression of gene expression.

Although the aforementioned analogies provide important insights as to how they may activate or suppress the 107-aa cistron, a lack of experimental data on *SMIM45* regulatory sequences hinders a more definitive characterization of their roles. These enhancers and silencers remain promising targets for future experimental studies.

Methods

Source of properties of human SMIM45

The NCBI Gene database (https://www.ncbi.nlm.nih.gov/gene) is the source for *SMIM45* properties, including enhancers, silencers and their experimental evidence, accessible chromatin regions, functions, sequences, and RNA transcript exon/intron sequences.

SMIM45 in other species

The *SMIM45* orthologous sequences from various species were also obtained from the NCBI Gene database (https://www.ncbi.nlm.nih.gov/gene) except for that of the elephant shark. The elephant shark *SMIM45* sequence is present on the website: *Ensembl:* http://may2025.archive.ensembl.org/Alignment Methods. For species where *SMIM45* has not been annotated, the total sequence between flanking genes *CENPM* and *SEPTIN 3* was used for alignments.

Nucleotide and amino acid sequence alignments

Clustal Omega, Multiple Sequence Alignment and Pairwise Sequence Alignment EMBOSS Needle Tools < EMBL-EBI) [49] were used.

Several sequences were aligned using MAFFT [50]. (https://mafft.cbrc.jp/alignment/server/index.html). This sequence program allowed for easy visualization of conserved bases.

CpG pairs in silencer b (in the promoter)

There are 13 CpG pairs in silencer b. The probability of finding 13 Cs followed by 13 Gs in a sequence of 192 bases containing 73% G+C is approximately 6.956×10^{-10}

(determined by Google statistical analysis). This supports the statement of a high CpG content present in silencer b.

Sequences of silencer LOC130067579 ATAC-STARR-seq lymphoblastoid silent region 13815 and its segments

Silencer *LOC130067579*
tgcgcgacaacctggccttcggcggcccggaggtctgagccgacttgcaaaggggatagg
cgggcggcaccgggcgccctcccccagcccgccccgcccgcccagcccggagacccccaa
ggcagagggaggccggcctgttggccctccacgctatccctctgcagcctgggccctccc
gacagaggccccaggtgcgctggcagtggaggtggggcacttaggtgcct 230 bps

exonic silencer (overlap with 68-aa)
tgcgcgacaacctggccttcggcggcccggaggtctga 38 bps

silencer b (in the promoter)
gccgacttgcaaaggggataggcgggcggcaccgggcgccctcccccagcccgccccgcc
cgcccagcccggagacccccaaggcagagggaggccggcctgttggccctccacgctatc
cctctgcagcctgggccctcccgacagaggccccaggtgcgctggcagtggaggtggggc
acttaggtgcct 192 bps

Enhancer sequences

Enhancer 1, *LOC130067578* ATAC-STARR-seq lymphoblastoid active region 19151 [*Homo sapiens* (human)] Gene ID: 130067578
ctagtggctgaagcaccgcccaggaggaaaaaccggcgggggaagcagggccgcctgcacctaccaagatggtgg
ccgtgttcaggccgggcagcttgtccaggggcctcaacaccgacatcacagccgcaggaccaaccgttgctcctgcggt
gcgcgccgatctttcaaaccgccctgagtccagcccctagagcgcggcctgggggc 210 bps

Enhancer 2 *LOC127896429* H3K4me1 hESC enhancer GRCh37_chr22:42346983-42347610 [*Homo sapiens* (human)] Gene ID: 127896429
gagactccgtctcaaaaaaaacaaaccctctgtgaactcacagtcacccccagtcccacatatgctggaaaggacctg
tcatacctgaagagcccctagatggcgcagaggtgtctgtggtgggggacctaggtcctgaagccacctcacccagagg
ctttccccctgcccatccccaggtttctgggaacggattccctagggaggtggttcctggaagccttttcccagccacgcccc
gtgggccctagggggctgctctctccctcctgagaatagccctcaacacgtggcagataccttgtctatggcatagggga
gggggaggatccatgcttgggaaggtggaccccacccccaacgtcagctcttggctttgaattccagctcagtcactgag
aagctgagggctctgggagaaggagaaggccagcagcatcacctctctgcctcatcccaaaatggggtctcaacacca
atccagctgggaggactgcaggaagtgatgttggggccagctggaagatgggagtgctcaatgcctgtgctggctgtaca
ccagccaggggtgctgtggggtagatgaggcagaatggggagggggagccatttgcaagggtcctgaa 628 bps

Embedded silencer in LOC127896429 (silent region_13814)
ctagatggcgcagaggtgtctgtggtgggggacctaggtcctgaagccacctcacccaga 60 bps

Enhancer 3 LOC127896430 NANOG hESC enhancer GRCh37_chr22:42351209-42351720 [Homo sapiens (human)] Gene ID: 127896430agtttcactcttgttgcccaggctggagtgcagtggcacagtcgtggctcactggaactccacctcctgggttcaagcaactctcctgcctcagcctgccgagtagttgggattacaagcatgtgccaccacacctggctaattttgtacttttagtagagacagggtttcaccatgttggtcaggctggtcttgaattcctgacctcaggtgacccatcctccttggcctcccaaagtgctgggatcataggcatgagccattggcctggttgcaaaatgctctttaggcattgtcttgttaaaactgcaaagtacccaggctgcatgcggtggctcacgcctgtaatcccagcactttgggaggccgaggtgggcggatcacgaggtcaggagatcaagaccatcctggctaacacggtgaaaccccgtctctactaaaaatacaaaaaattagctgggtgcagtggcggtcacctgcagtcccagctactcaggaggctgaggcaggag 512 bps

Determinations of Alus in enhancer 3

RepeatMasker [38] enabled the determination off the *Alu* transposable elements and the location in *SMIM45.*

Translation of nucleotide sequence

The ExPASy Translational tool website https://web.expasy.org/translate/ [51] was employed to translate the 68-aa C-terminal end nucleotide sequence.

Supporting Information: Supplementary File S1**.**

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Conflict of Interest: the author decares no conflict of interest

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