

Supplementary DATA for “The mutational spectrum of non-CpG DNA varies with CpG content”

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SIMILARITY BETWEEN L1Pa FAMILIES -

Table S1 shows the mono- and dinucleotide composition of the ORF2 consensus sequences of the ancestral L1 families used in this study as well as that of the currently active human-specific L1Pa1 family. An alignment of these sequences is presented in Figure S8.

Table S1 Nucleotide composition of L1 ORF2 sequences

family	A	C	G	T	N	Sum ²	%(G+C)	Ratio ³ :	AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT	%CpG ⁴	
																									consensus	orthologues
L1Pa1 ¹	1562	827	662	777	0	3828	38.9	NA	643	305	287	326	409	187	32	199	281	133	165	83	228	202	178	169	0.836	NA ¹
L1Pa3	1572	821	660	774	1	3827	38.7	1	654	283	283	327	401	188	30	202	282	131	164	83	234	196	183	161	0.789	0.668
L1Pa4	1567	821	668	771	1	3827	38.9	1	646	290	290	329	401	188	28	203	286	136	165	81	233	196	185	157	0.734	0.621
L1Pa5	1571	821	667	766	3	3825	38.9	1	642	295	295	328	406	191	23	201	290	135	164	78	232	193	182	159	0.603	0.565
L1Pa6	1581	817	662	760	8	3820	38.72	1.01	647	297	297	328	406	189	22	199	293	134	158	77	233	191	178	156	0.578	0.545
L1Pa7	1593	814	651	761	9	3819	38.36	1.01	659	295	295	329	400	188	25	198	288	133	156	74	245	189	168	159	0.658	0.521
L1Pa8	1592	806	648	767	15	3813	38.13	1.01	662	292	292	333	395	185	22	198	286	132	154	74	246	188	171	160	0.580	0.523
L1Pa10	1604	790	643	768	23	3805	37.66	1.02	675	294	294	338	395	182	10	199	291	129	150	69	239	187	180	158	0.264	0.488
L1Pa11	1609	789	642	765	23	3805	37.61	1.02	676	294	294	338	396	181	8	201	290	132	149	67	242	182	177	157	0.211	0.466
L1Pa13	1603	790	618	749	68	3760	37.45	1.03	668	281	281	339	398	183	1	194	277	126	147	60	242	174	172	147	0.027	0.456
L1Pa15	1635	795	593	745	60	3768	36.84	1.03	699	277	277	332	404	189	0	190	270	124	131	62	244	164	172	150	0.000	0.447
L1Pa16	1635	765	566	753	109	3719	35.79	1.01	714	269	269	332	383	172	0	200	254	111	125	65	243	174	160	143	0.000	0.431

¹ The L1Pa1 consensus is shown just for comparison - there are no human / chimpanzee orthologues as this family is unique to humans.

² Sum includes only A,C,G, & T. Sum + N = 3828 for each row.

³ Ratio: the %(G+C) of the ORF2 consensus relative to the mean %(G+C) of the human and chimpanzee orthologue pairs for each family (Figure 2). The fact that the %(G + C) content of the consensus sequences and that of the orthologues are essentially identical indicates that, except for CG (see note 4 below), the nucleotide compositions of the consensus sequences are valid proxies for the nucleotide composition of the orthologue pairs. There are no significant differences between the nucleotide or dinucleotide frequencies of the various L1 families that could account for their different non-CpG mutation rates. For example, chi-square generated p values for the difference between nucleotide or dinucleotide (excluding CpG) frequencies between L1Pa3 and L1Pa7 are 0.95 and 0.99 respectively. These values for other pairings are: L1Pa7 & L1Pa11 - 0.92, 1.00; L1Pa11 & L1Pa16 - 0.22, 0.88; L1Pa7 & L1Pa16 - 0.08 & 0.61.

⁴ The %CpG content of the ancestral consensus sequences will necessarily differ from that of their family members (which in this case constitute the orthologues) because a CpG is counted only if it's present in at least 60% of the orthologues. This will inflate the CpG content of the consensus sequences of the younger ancestral sequences relative to the orthologues because a CpG will be added to the CpG count of the consensus even though not all orthologues have a CpG at a given position. The opposite situation holds for the older ancestral families. In these cases the CpG content of the older consensus sequences is deflated compared to their orthologues, as a CpG won't be added to the consensus count at positions where less than 60% of the orthologues contains a CpG.

CORRELATION OF VARIOUS GENOMIC FACTORS TO THE NEUTRAL MUTATION RATE

A variety of factors have been correlated with the neutral mutation rate. These factors include recombination rate, transcription, and G + C content. As shown below none of these factors as well as several others that we examined are correlated with the non-CpG mutation rate determined from the divergence of orthologous pairs of different L1 families.

Recombination rate - We extracted the deCODE recombination rates (1 Mb intervals) (Kong et al. 2002) from the recombRate table. We mapped the average female / male recombination rates for (i.e., the decodeAvg) onto each of the human orthologues for each L1 family. Such data are not available for chimpanzee. The dots indicate the median and the +’s delimit the 95% confidence interval (CI).

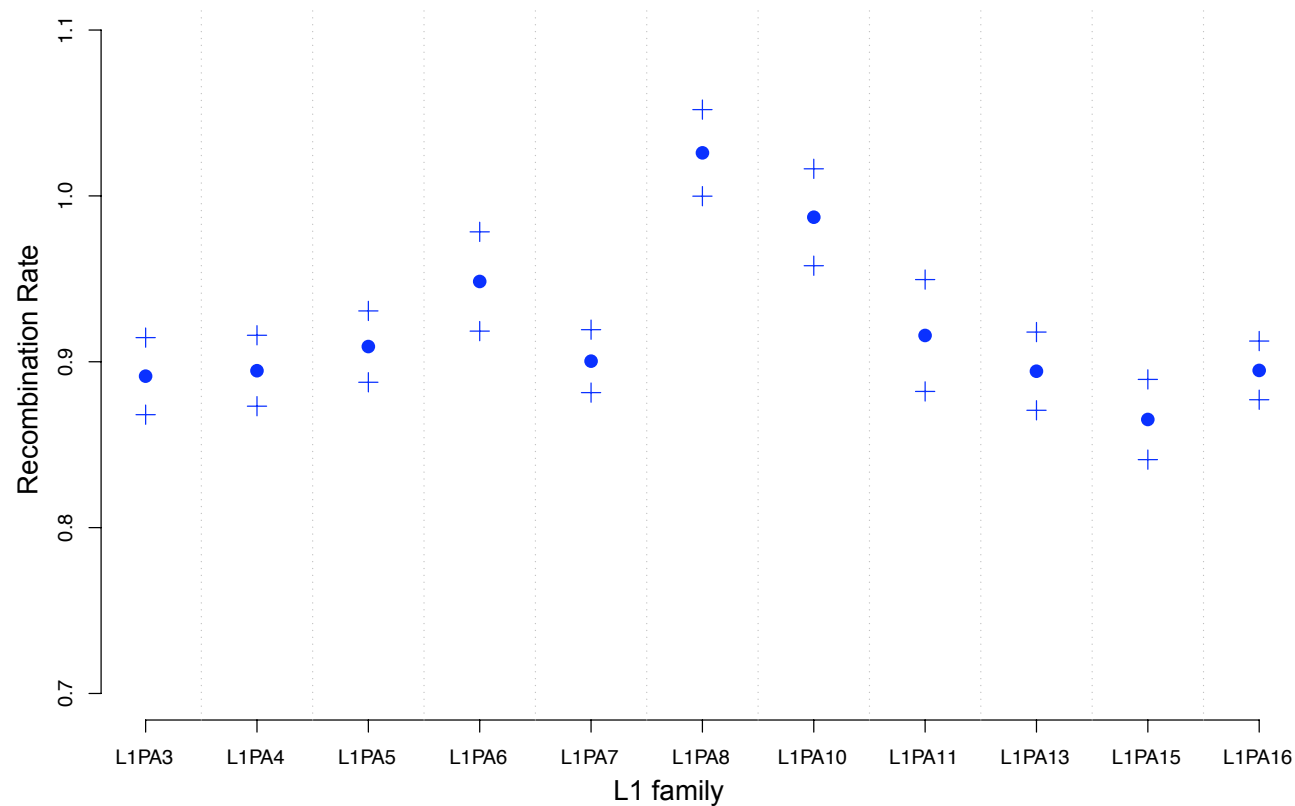


Figure S1 Recombination rate of DNA flanking L1 orthologues

SNP rate – The number of SNPs in the 0.5Mb region flanking the L1 insertion site was determined using the Affymetrix genome-wide human SNP array 6.0. Such data are not available for chimpanzee. The dots indicate the median and the +’s delimit the 95% CI.

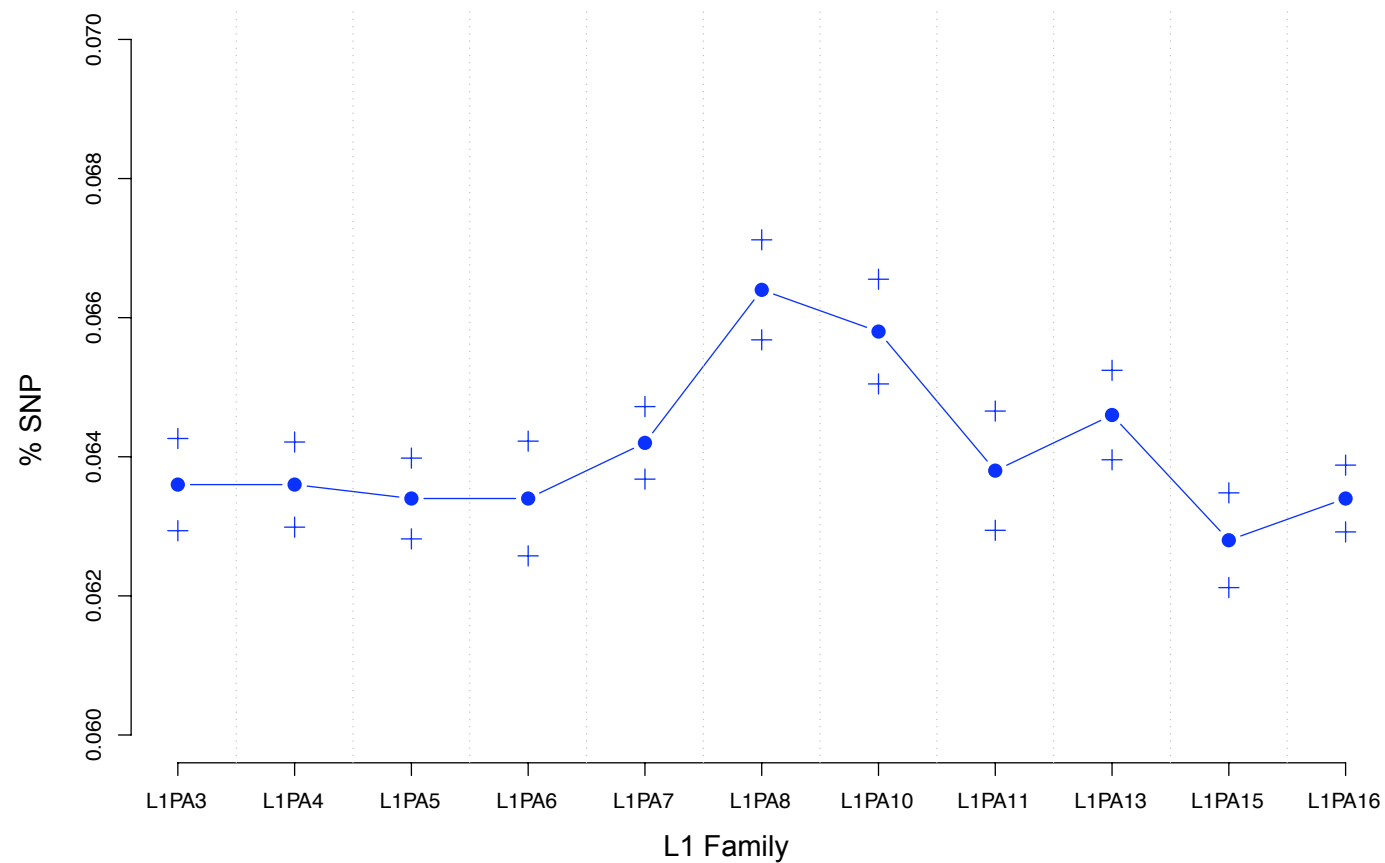


Figure S2 SNP content of DNA flanking L1 orthologues

G + C content of region flanking L1 orthologues -The symbols indicate the median and the +’s delimit the 95% CI

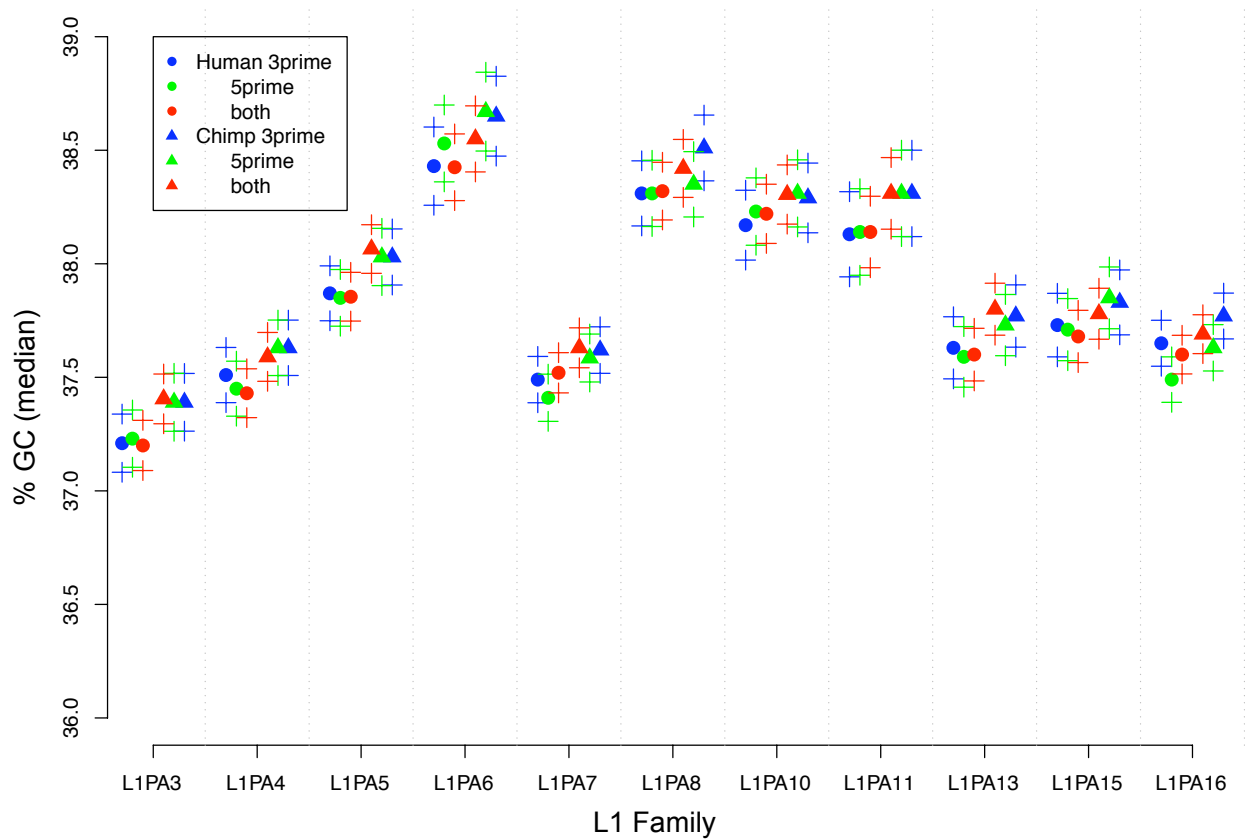


Figure S3 Median % GC of the 0.5 kb flanking sequences of L1 orthologues

Genome location – L1 insertions were localized using annotation files. Insertions were designated either as intragenic if located between a transcription-start site (TSS) and stop site, or intergenic if located otherwise. Intergenic insertions located within the 1 kb 5’ of the TSS were designated promoter insertions.

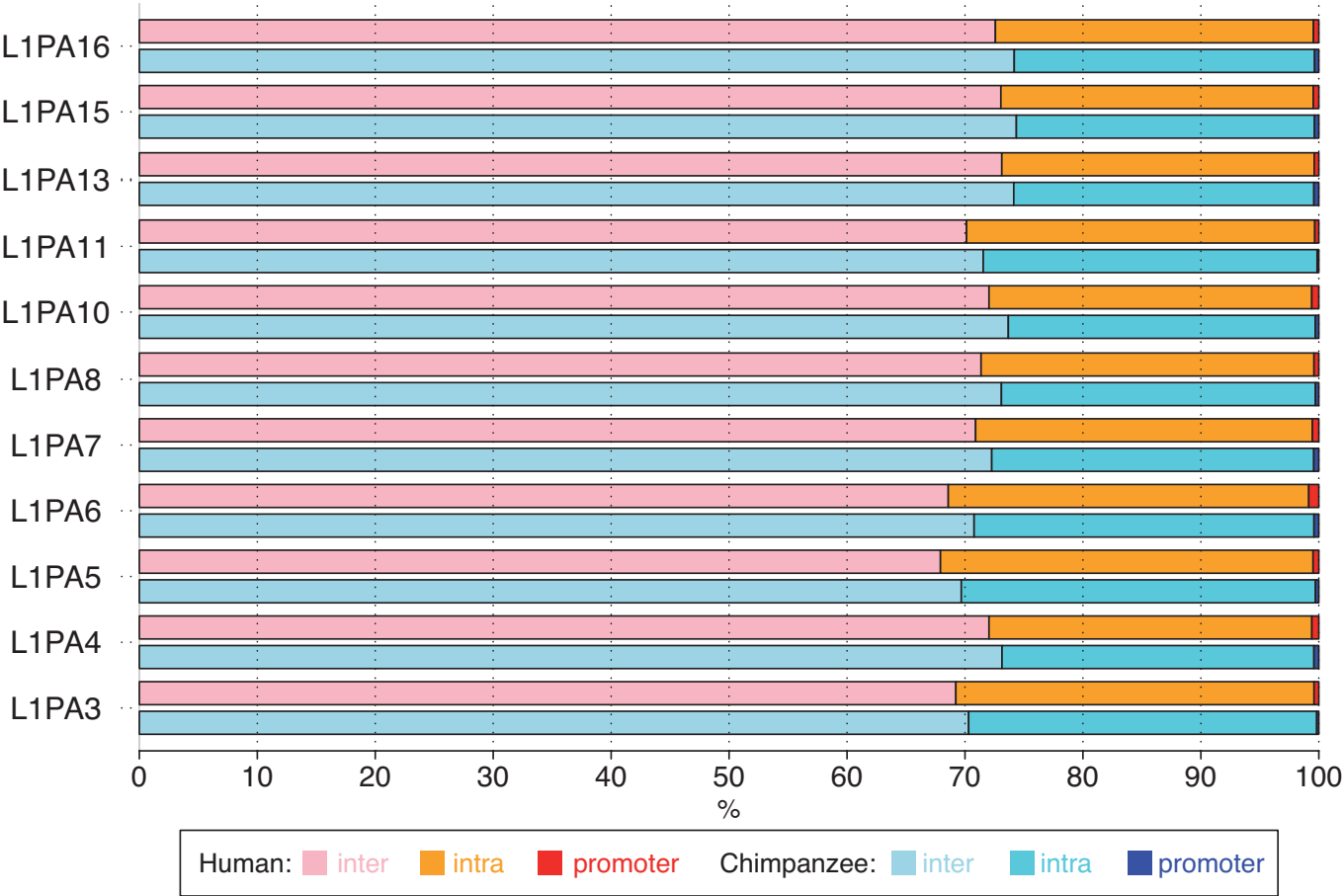


Figure S4 Genomic location of L1 orthologues

Inter, intra, and promoter indicate the percentage of orthologues located in intergenomic, intragenomic, or promoter regions of the human or chimpanzee genomes.

Transcriptional orientation

Table S2 Orientation of L1 orthologues in transcriptional units

L1 family	N _{forward}	N _{reverse}	Ratio
L1Pa3	2465	2430	1.014
L1Pa4	3409	3225	1.057
L1Pa5	3586	3436	1.044
L1Pa6	1846	1678	1.100
L1Pa7	4345	4014	1.082
L1Pa8	3113	2960	1.052
L1Pa10	2634	2568	1.026
L1Pa11	1520	1553	0.979
L1Pa13	3229	3263	0.990
L1Pa15	2825	2789	1.013
L1Pa16	5082	5220	0.974
N gives the number of orthologue pairs in the sense (forward) or antisense (reverse) orientation.			

L1 orthologues are equally represented in both the sense and antisense with respect to the transcriptional region in which they are imbedded.

Number of neighboring L1 insertions – The number of different L1 families and those belonging to the family of the L1 orthologue in the 0.5Mb flanking its insertion site. These results show that L1 families of different age are intimately intermingled in the genome.

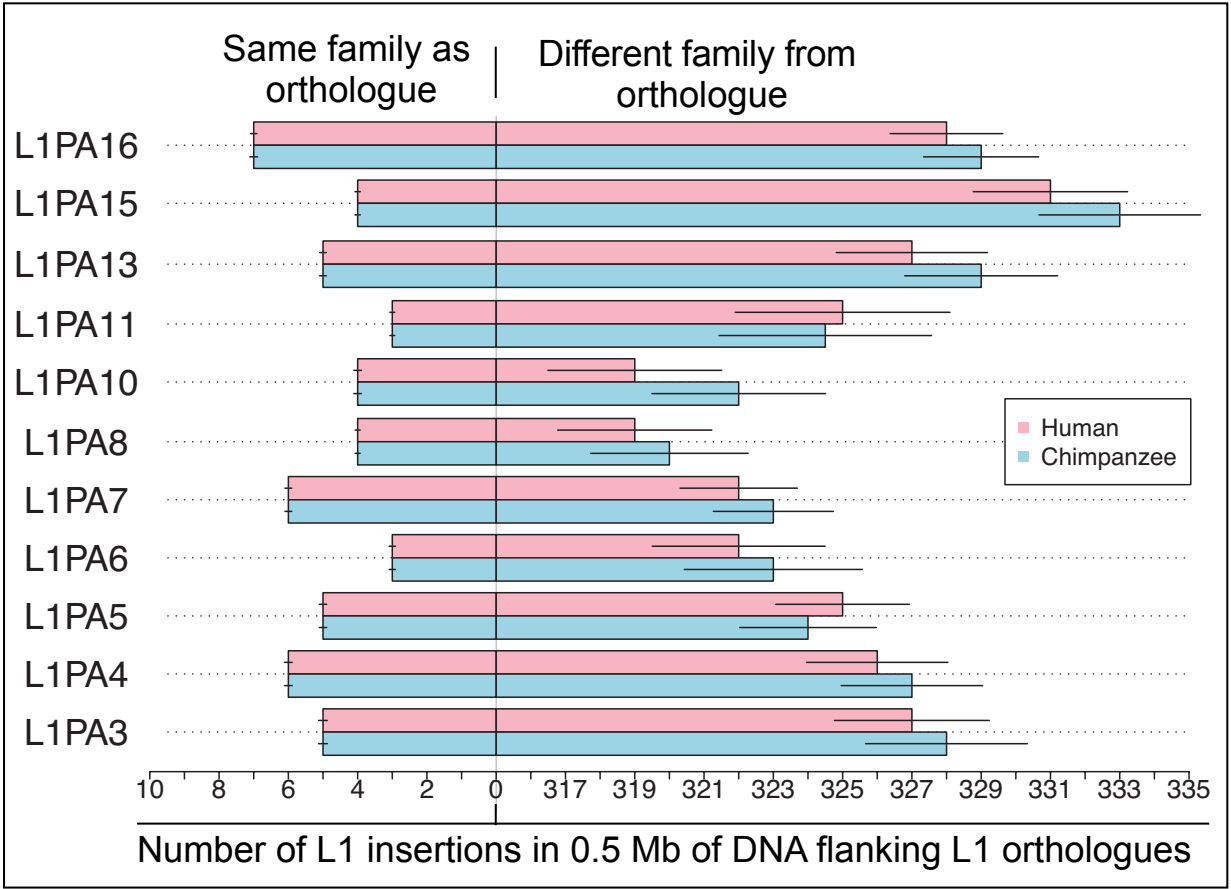


Figure S5 L1 content of L1 orthologue insertion sites

TRANSITIONS AND TRANSVERSIONS UNDERGONE BY EACH MUTATED BASE BETWEEN THE ORTHOLOGUES OF DIFFERENT L1 FAMILIES –

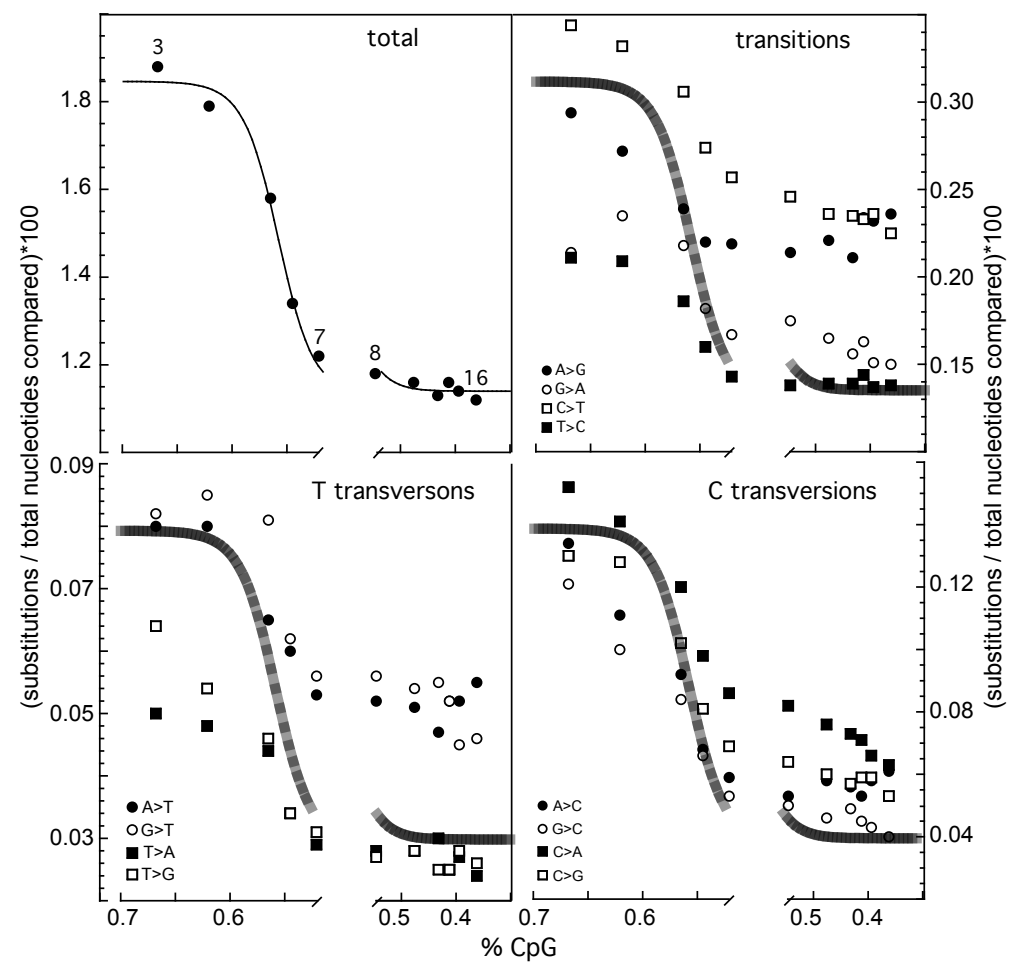


Figure S6 Transition and transversion mutations for each of the bases

Taken together all of the values for all the bases for any given family sum to that shown in the panel labeled “total”, which shows the same data presented in Figure 3B (main paper). These data are superimposed (heavy grey line) on each of the other panels. We split the X-axis (% CpG content) into two regions: >0.53% and <0.53% CpG content to facilitate comparisons between the mutational spectra at these CpG contents.

LINEAR FITS BETWEEN THE DIVERGENCE & THE CpG CONTENT OF ANCESTRAL L1 ORTHOLOGUES

Linear fit (●.....○) using all the data points.

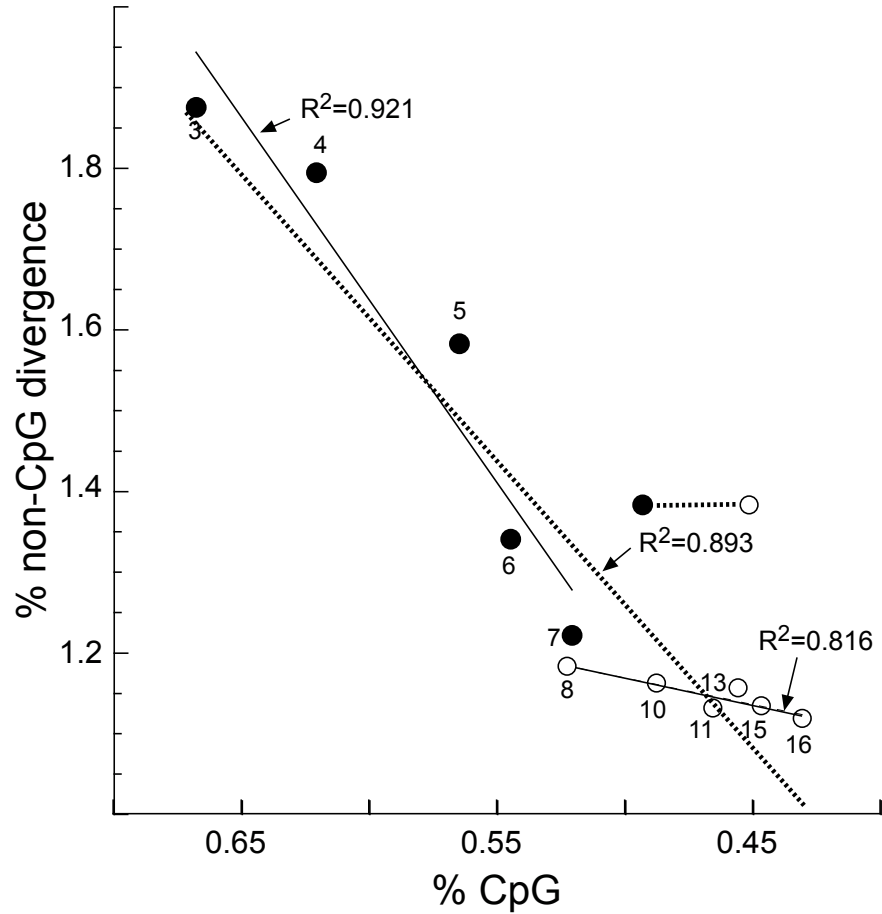


Figure S7 Linear fits of % divergence to CpG content

	810	820	830	840	850	860	870	880	890	900
L1Pa1	GGCAGAAATAAAGATGTTCTTTGAAACCAACGAGAACAAGACACCACATACCAGAATCTCTGGGACGCATTCAAAGCAGTGTGTAGAGGGAAATTTATA									
L1Pa3	GGCAGAAATAAAGATGTTCTTTGAAACCAACGAGAACAAGACACAACATACCAGAATCTCTGGGACACATTCAAAGCAGTGTGTAGAGGGAAATTTATA									
L1Pa4	GGCAGAAATAAAGATGTTCTTTGAAACCAACGAGAACAAGACACAACATACCAGAATCTCTGGGACACATTCAAAGCAGTGTGTAGAGGGAAATTTATA									
L1Pa5	GGCAGAAATAAAGATGTTCTTTGAAACCAATGAGAACAAGACACAACATACCAGAATCTCTGGGACACATTTAAAGCAGTGTGTAGAGGGAAATTTATA									
L1Pa6	GGCAGAAATAAAGATGTTCTTTGAAACCAATGAGAACAAGACACAACGTACCAGAATCTCTGGGACACATTTAAAGCAGTGTGTAGAGGGAAATTTATA									
L1Pa7	GGCAGAAATAAATAAGTTCTTTGAAACCAATGAGAACAAGACACAANGTACCAGAATCTCTGGGACACAGCTAAAGCAGTGTTTAGAGGGAAATTTATA									
L1Pa8	GGCAGAAATAAAGAAGTTCTTTGAAACCAATGAGAACAAGAGACAANGTACCAGAATCTCTGGGACACAGCTAAAGCAGTGTTAAGAGGGAAATTTATA									
L1Pa10	GGCAGAAATCAAGAAGTTCTTTGAAACCAATGAGAACAAGAGACAATGTACCAGAATCTCTGGGANGCAGCTAAAGCAGTGTTAAGAGGGAAATTTATA									
L1Pa11	GGCAGAAATCAAGAAGTTCTTTGAAACTAATGAGAACAAGAGACAATGTACCAGAATCTCTGGGATGCAGCTAAAGCAGTGTTAAGAGGGAAATTTATA									
L1Pa13	GGCAGAAATCAAGAAGTTCTTTGAAACTAATGAGAACAAGATACAACATACCAGAATCTCTGGGACACAGCTAAGGCAGTGTTAAGAGGGAAATTTATA									
L1Pa15	GGCAGAAATCAAGAAATTTCTTTGAAACTAATGAAAACAAGATACAACATACCAGAATCTCTGGGACACAGCTAAAGCAGTGTTAAGAGGAAAGTTTATA									
L1Pa16	GGCAGAAATNAAAAAATNTTTTGAATNAATGAAAACAGAGACACAACATACCCAAATCTCTGGGATGCAGCAAAAGCAGTGTTAAGAGGAAAGTTTATA									
	910	920	930	940	950	960	970	980	990	1000
L1Pa1	GCACTAAATGCCTACAAGAGAAAGCAGGAAAGATGCCAAAATTGACACCCTAACATCACAAATTAAGAAGAACTAGAAAAGCAAGAGCAAACACATTCAAAAAG									
L1Pa3	GCACTAAATGCCACAAGAGAAAGCAGGAAAGATGCCAAAATTGACACCCTAACATCACAAATTAAGAAGAACTAGAAAAGCAAGAGCAAACACATTCAAAAAG									
L1Pa4	GCACTAAATGCCACAAGAGAAAGCAGGAAAGATCTAAAATTGACACCCTAACATCACAAATTAAGAAGAACTAGAGAAGCAAGAGCAAACACATTCAAAAAG									
L1Pa5	GCACTAAATGCCACAAGAGAAAGCAGGAAAGATCTAAAATTGACACCCTAACATCACAAATTAAGAAGAACTAGAGAAGCAAGAGCAAACACATTCAAAAAG									
L1Pa6	GCACTAAATGCCACAAGAGAAAGCAGGAAAGATCTAAAATNGACACCCTAACATCACAAATTAAGAAGAACTAGAGAAGCAAGAGCAAACAAATTCAAAAAG									
L1Pa7	GCACTAAATGCCACAGGAGAAAGCAGGAAAGATCTAAAATCGACACCCTAACATCACAAATTAAGAAGAACTAGAGAAGCAAGAGCAAACAAATTCAAAAAG									
L1Pa8	GCACTAAATGCCCATCAGAAAGCNGGAAAGATCTAAAATCGACACCCTAACATCACAAATTAAGAAGAACTAGAGAAGCAAGAGCAAACAAATTCAAAAAG									
L1Pa10	GCACTAAATGCCCATCAGAAAGCTAGAAAGATCTCAATNGACACCCTAACATCACAATTAAGAAGAACTAGAGAAGCAAGAGCAAACAAACCCCAAAG									
L1Pa11	GCACTAAATGCCCATCAGAAAGCTAGAAAGATCTCAAGTTAACACCTAACATCACAATTAAGAAGAACTAGAGAAGCAAGAGCAAACAAACCCCAAAG									
L1Pa13	GCACTAAATGCCCATCAGAAAGTTAGAAAGATCTCAANTTAACACCTAACATCACAATTAAGAAGAACTAGAGAAGCAAGAGCAAACNAANCCCCAAAG									
L1Pa15	GCACTAAATGCCCATCAGAAAGTTAGAAAGATCTCAAATTAACACCTAACATCACACCTAGAGGAACTAGAAAAACAAGAGCAAACCAACCCCAAAG									
L1Pa16	GNNCTAAATNCCTACNTCAANAAGTTAGAAAGATCTCAAATTAACAACTAACATNACACCTAGAGGAACTAGAAAAACAAGAACAAACNAACCCCAAAG									
	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
L1Pa1	CTAGCAGAAGGCAAGAAATAACTAAAATCAGAGCAGAACTGAAGGAAATAGAGACACAAAAAACCCCTTCAAAAATCAATGAATCCAGGAGCTGGTTTTT									
L1Pa3	CTAGCAGAAGGCAAGAAATAACTAAAATCAGAGCAGAACTGAAGGAAATAGAGACACAAAAAACCCCTTCAAAAATTAATGAATCCAGGAGCTGGTTTTT									
L1Pa4	CTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAACTGAAGGAAATAGAGACACAAAAAACCCCTTCAAAAATCAATGAATCCAGGAGCTGGTTTTT									
L1Pa5	CTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAACTGAAGGAGATAGAGACACAAAAAACCCCTTCAAAAATCAATGAATCCAGGAGCTGGTTTTT									
L1Pa6	CTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAACTGAAGGAGATAGAGACACAAAAAACCCCTTCAAAAATCAATGAATCCAGGAGCTGGTTTTT									
L1Pa7	CTAGCAGAAGACAGAAATAACTAAGATCAGAGCAGAACTGAAGGAGATAGAGACACAAAAAACCCCTTCAAAAATCAATGAATCCAGGAGCTGGTTTTT									
L1Pa8	CTAGCAGAAGACAGAAATAACTAAGATCAGAGCAGAACTGAAGGAGATAGAGACACAAAAAACCCCTTCAAAAATCAATGAATCCAGGAGCTGGTTTTT									
L1Pa10	CTAGCAGAAGACAGAAATAACCAAGATCAGAGNAGAACTGAAGGAGATAGAGACANAAAAAACCCCTTCAAAAATCAATGAATCCAGGAGCTGGTTTTT									
L1Pa11	CTAGCAGAAGACAGAAATAACCAAGATCAGAGCTGAAGTGAAGGAGATAGAGACANAAAAAACCCCTTCAAAAATCAANNAATCCAGGAGCTGNTTTTT									
L1Pa13	CTAGCAGAAGACAGAAATAACCAAAATCAGAGCTGAAGTGAAGGAGATTGAGACANAAAAAACCATTCAAAAGATCAANNAATCCAGGAGNTGNTTTTT									
L1Pa15	CTAGCAGAAGANAAGAAATAACCAAAATCAGAGCTGAAGTGAANGAAATTGAGATGNNAAAAAACCATACAAAAGATCAANNAAACCANAAAGTTGGTTNTT									
L1Pa16	CTAGCAGAAGAAAAAGAAATAACTAAAATCAGAGNAGAACTGAATGAAATTGAGACNCAAAAAATCCATACAAANNATCAATNAAACCAAAAGTTGGTTNTT									
	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
L1Pa1	TGAAAGGATCAACAAAATTGATAGACCGCTAGCAAGACTAATAAAGAAAAAAGAGAGAAGATCAATAGACACAATAAAAAATGATAAAGGGGATATC									

	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
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L1Pa1	ACCACCGATCCACAGAAATACAAACTACCATCAGAGAATACTACAAACACCTCTACGCAAATAAACTAGAAAATCTAGAAGAAATGGATACATTCTCTG									
L1Pa3	ACCACCGATCCACAGAAATACAAACTACCATCAGAGAATACTACAAACACCTCTACGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAAATTCCTCG									
L1Pa4	ACCACCGATCCACAGAAATACAAACTACCATCAGAGAATACTATAAACACCTCTACGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAAATTCCTCG									
L1Pa5	ACCACCGATCCACAGAAATACAAACTACCATCAGAGAATACTATAAACACCTCTATGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAAATTCCTGG									
L1Pa6	ACCACCGATCCACAGAAATACAAACTACCATCAGAGAATACTATAAACACCTCTATGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAAATTCCTGG									
L1Pa7	ACCACTGATCCACAGAAATACAAACTACCATCAGAGAATACTATAAACACCTCTATGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAAATTCCTGG									
L1Pa8	ACCACTGATCCACAGAAATACAAACTACCATCAGAGAATACTATAAACACCTCTATGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAAATTCCTGG									
L1Pa10	ACCACTGACCCACAGAAATACAAACAACCATCAGAGAATACTATAAACACCTCTATGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAAATTCCTGG									
L1Pa11	ACCACTGACCCACAGAAATACAAACAACCATCAGAGAATACTATAAACACCTCTATGCACATAAACTAGAAAATCTAGAAGAAATGGATAAAATTCCTGG									
L1Pa13	ACCACTGACCCACAGAAATACAAANAACCATCAGAGAATATTATGAACACCTCTATGCACATAAACTAGAAAATCTAGAAGAAATGGATAAAATTCCTGG									
L1Pa15	ACCACTGACCCACAGAAATACAAAAAACCTCAGAGACTATTATGAACACCTCTATGCACACAAACTAGAAAACCTAGAAGAAATGGATAAAATTCCTGG									
L1Pa16	ACAACTGATCCACAGAAATACAAAAGATCCTCAGAGACTATTATGAACACCTCTATGCACACAAACTAGAAAATCTAGAGGAAATGGATAAAATTCCTGG									
	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
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L1Pa1	ACACATACACTCTCCCAAGACTAAACCAGGAAGAAGTTGAATCTCTGAATCGACCAATAACAGGCTCTGAAATTGTGGCAATAATCAATAGTTTACCAAC									
L1Pa3	ACACATACACTCTCCCAAGACTAAACCAGGAAGAAGTTGAATCTCTGAATAGACCAATAACAGGATCTGAAATTGTGGCAATAATCAATAGCTTACCAAC									
L1Pa4	ACACATACACCTCTCCCAAGACTAAACCAGGAAGAAGTTGAATCTCTGAATAGACCAATAACAGGCTCTGAAATTGAGGCAATAATTAATAGCTTACCAAC									
L1Pa5	ACACATACACCTCTCCCAAGACTAAACCAGGAAGAAGTTGAATCCCTGAATAGACCAATAACAGGCTCTGAAATTGAGGCAATAATTAATAGCTTACCAAC									
L1Pa6	ACACATACACCTCTCCCAAGACTAAACCAGGAAGAAGTTGAATCTCTGAATAGACCAATAACAGGCTCTGAAATTGAGGCAATAATTAATAGCTTACCAAC									
L1Pa7	ACACATACACCTCTCCCAAGACTAAACCAGGAAGAAGTGAATCCCTGAATAGACCAATAACAAGTTCTGAAATTGAGGCAGTAATTAATAGCTTACCAAC									
L1Pa8	ACACATACACCTCTCCCAAGACTAAACCAGGAAGAAGTGAATCCCTGAATAGACCAATAACAAGTTCTGAAATTGAGGCAGTAATTAATAGCTTACCAAC									
L1Pa10	ACACATACACCTCTCCCAAGACTGAACCAGGAAGAAGTTGAATCCCTGAATAGACCAATAACAAGTTCTGAAATTGAGGCAGTAATAAATAGCTTACCAAC									
L1Pa11	ACACATACACCTCTCCCAAGACTGAACCAGGAAGAAATTGAATCCCTGAATAGACCAATAATGAGTTCTGAAATTGAGGCAGTAATAAATAGCTTACCAAC									
L1Pa13	ACACATACACCTCTCCCAAGACTGAACCAGGAAGAAATTGAATCCCTGAACAGACCAATAATGAGCTCTGAAATTGANTCAGTAATAAATAGCTTACCAAC									
L1Pa15	AAACATACAACCTCTCCCAAGATTGAACCAGGAAGAAATTGAAACCCCTGAACAGACCAATAATGAGTTCCAAAATTGAATCAGTAATAAAAAAGCTTACCAAC									
L1Pa16	AAACACACAANCTCTCCCAAGATTGAATCAGGAAGAAATTGAAACCCCTGAACAGACCAATATNNAGTTCTNAAAATTGAATCAGTAATAAAAAACCTTACCAAC									
	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500
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L1Pa1	CAAAAAGAGTCCAGGACCAGATGGATTACAGCCGAATTCTACCAGAGGTACAAGGAGGAACTGGTACCATTCCCTTCTGAAACTATTCCAATCAATAGAA									
L1Pa3	CAAAAAGAGTCCAGGACCAGATGGATTACAGCCGAATTCTACCAGAGGTACAAGGAGGAACTGGTACCATTCCCTTCTGAAACTATTCCAATCAATAGAA									
L1Pa4	CAAAAAAAGTCCAGGACCAGATGGATTACAGCCGAATTCTACCAGAGGTACAAGGAGGAGCTGGTACCATTCCCTTCTGAAACTATTCCAATCAATAGAA									
L1Pa5	CAAAAAAAGTCCAGGACCAGANGGATTACAGCCGAATTCTACCAGAGGTACAAGGAGGAGCTGGTACCATTCCCTTCTGAAACTATTCCAATCAATAGAA									
L1Pa6	CAAAAAAAGTCCAGGACCAGANGGATTACAGCCGAATTCTACCAGAGGTACAAGAGGAGCTGGTACCATTCCCTTCTGAAACTATTCCAATCAATAGAA									
L1Pa7	CAAAAAAAGCCAGGACCAGANGGATTACAGCCGAATTCTACCAGAGGTACAAGAGGAGCTGGTACCATTCCCTTCTGAAACTATTCCAACAATAGAA									
L1Pa8	CAAAAAAAGCCAGGACCAGANGGATTACAGCCGAATTCTACCAGAGGTACAAGAGGAGCTGGTACCATTCCCTTCTGAAACTATTCCAACAATAGAA									
L1Pa10	CAAAAAAAGCCAGGACCAGATGGATTTACAGCTGAATTCTACCAGAGGTACAAGAGGAGCTGGTACCATTCTCTGAAACTATTCCAACAATTGAA									
L1Pa11	CAAAAAAAGCCAGGACCAGATGGATTACAGCTGAATTCTACCAGAGGTACAAGAAGAGCTGGTACCATTCTACTGAAACTATTCCAAAAAATTGAA									
L1Pa13	CAAAAAAAGCCAGGACCAGATGGATTACAGCTGAATTCTACCAGATGTACAAGAAGAGCTGGTACCATTCTACTGAAACTATTCCAAAAAATTGAG									
L1Pa15	CAGAAAAAGCCNGGACCAGATGGATTACAGCCAAATTCTACCAGATGTATAAGAAGAGCTGGTACCANTCTACTGAAACTATTCCAAAAAATTGAG									
L1Pa16	CAAAAAAAGCCCTGGACCAGATGGATTACAGCCAAATTCTACCAGANNTACAAGAAGAGCTGGTACCAATNCTACTGAAACTATTCCAAAAAATNNAG				</					

	1610	1620	1630	1640	1650	1660	1670	1680	1690	1700
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L1Pa1	CCTTGATGAACATTGATGCAAAAATCCTCAATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAGCTTATCCACCATGATCAAGTGGGCTTCAT									
L1Pa3	CCTTGATGAACATTGATGCAAAAATCCTCAATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAGCTTATCCACCATGATCAAGTGGGCTTCAT									
L1Pa4	CCNTGATGAACATTGATGCAAAAATCCTCAATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAGCTTATCCACCATGATCAAGTGGGCTTCAT									
L1Pa5	CCCTGATGAACATCGATGCAAAAATCCTCAATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAGCTTATCCACCATGATCAAGTGGGCTTCAT									
L1Pa6	CCCTGATGAACATCGATGCAAAAATCCTCAATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAGCTTATCCACCANGATCAAGTNGGCTTCAT									
L1Pa7	CCCTGATGAACATCGATGCGAAAATCCTCAATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAGCTTATCCACCACGATCAAGTCGGCTTCAT									
L1Pa8	CCCTGATGAACATCGATGCGAAAATCCTCAATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAGCTTATCCACCACGATCAAGTCGGCTTCAT									
L1Pa10	CCCTGATGAACATCGATGCAAAAATCCTCAATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAGCTTATCCACCANGATCAAGTNGGCTTCAT									
L1Pa11	CCTTGATGAACATCGATGCAAAAATCCTCAATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAGCTTATCCACCACGATCAAGTTGGCTTCA									
L1Pa13	CCTTGATGAACATNGATGCAAAAATCCTCAACAAAATACTGGCAAACNNAATCCAGCAGCACATCAAAAAGCTTATCCACCANNATCAAGTAGGCTTTAT									
L1Pa15	CCTTGATGAACATAGATGCAAAAATCCTCAACAAAATACTAGCAAACNAAATCCAGCAGCACATCAAAAAGCTAATCCACCATGATCAAGTAGGCTTTAT									
L1Pa16	CCCTGATGAACATAGATGCAAAAATCCTCAACAAAATACTAGCAAACNNAATCCAGCAGCACATCAAAAAGTTAATTCCACCATGATCAAGTAGGCTTTAT									
	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800
	----	----	----	----	----	----	----	----	----	----
L1Pa1	CCCTGGGATGCAAGGCTGGTTCAATATACGCAAATCAATAAATGTAATCCAGCATATAAACAGAGCCAAAGACAAAAACCACATGATTATCTCAATAGAT									
L1Pa3	CCCTGGGATGCAAGGCTGGTTCAATATACGCAAATCAATAAATGTAATCCAGCATATAAACAGAACCAAGACAAAAACCACATGATTATCTCAATAGAT									
L1Pa4	CCCTGGGATGCAAGGCTGGTTCAACATACGCAAATCAATAAACGTAATCCAGCATATAAACAGAACCAAGACAAAAACCACATGATTATCTCAATAGAT									
L1Pa5	CCCTGGGATGCAAGGCTGGTTCAACATACGCAAATCAATAAACGTAATCCAGCATATAAACAGAACCAAGACAAAAACCACATGATTATCTCAATAGAT									
L1Pa6	CCCTGGGATGCAAGGCTGGTTCAACATANGCAAATCAATAAACGTAATCCATCACATAAACAGAACCAANGACAAAAACCACATGATTATCTCAATAGAT									
L1Pa7	CCCTGGGATGCAAGGCTGGTTCAACATATGCAAATCAATAAACGTAATCCATCACATAAACAGAACCAATGACAAAAACCACATGATTATCTCAATAGAT									
L1Pa8	CCCTGGGATGCAAGGCTGGTTCAACATATGCAAATCAATAAACGTAATCCATCACATAAACAGAACCAATGACAAAAACCACATGATTATCTCAATAGAT									
L1Pa10	CCCTGGGATGCAAGGCTGGTTCAACATATGCAAATCAATAAATGTAATTCATCACATAAACAGAACTAAAGACAAAAACCACATGATTATCTCAATAGAT									
L1Pa11	CCCTGGGATGCAAGGTTGGTTCAACATATGCAAATCAATAAATGTGATTCATCACATAAACAGAACTAAAGACAAAAACCACATGATTATCTCAATAGAT									
L1Pa13	CCCTGGGATGCAAGGTTGGTTCAACATANNCAAATCAATAAATGTGATTCATCACATAAACAGAACTAAAGACAAAAACCACATGATTATCTCAATAGAT									
L1Pa15	NCCTGGGATGCAAGGTTGGTTCAACATATGCAAATCAATAAATGTGATTCATCACATAAACAGAACTAAAAACAAAAACCACATGATCATCTCAATAGAT									
L1Pa16	TCCTGGGATGCAAGGTTGGTTCAACATATGCAAATCAATAAATGTGATTCACCACATAAACAGAAATAAAAACAAAAACCATATGATCATCTCAATAGAT									
	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900
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L1Pa1	GCAGAAAAAGCCTTTGACAAAAATTCACAACCCCTTCATGCTAAAAACTCTCAATAAATTAGGTATTGATGGGACGTATTTCAAATAATAAGAGCTATCT									
L1Pa3	GCAGAAAAAGCCTTTGACAAAAATTCACAACCCCTTCATGCTAAAAACTCTCAATAAATTAGGTATTGATGGGACGTATCTCAAATAATAAGAGCTATCT									
L1Pa4	GCAGAAAAAGCCTTTGACAAAAATTCACAACCCCTTCATGCTAAAAACTCTCAATAAATTAGGTATTGATGGGACGTATCTCAAATAATAAGAGCTATCT									
L1Pa5	GCAGAAAAAGCCTTTGACAAAAATTCACACGCCCTTCATGCTAAAAACTCTCAATAAATTAGGTATTGATGGGACGTATCTCAAATAATAAGAGCTATTT									
L1Pa6	GCAGAAAAAGCCTTTGACAAAAATTCACACGCCCTTCATGCTAAAAACTCTCAATAAATTAGGTATTGATGGGACGTATCTCAAATAATAAGAGCTATTT									
L1Pa7	GCAGAAAAAGCCTTCGATAAAAAATTCACACCCCTTCATGCTAAAAACTCTCAATAAATTAGGTATTGATGGGACGTATCTCAAATAATAAGAGCTATTT									
L1Pa8	GCAGAAAAAGCCTTCGATAAAAAATTCACATCCCTTCATGCTAAAAACTCTCAATAAATTAGGTATTGATGGGACGTATCTCAAATAATAAGAGCTATTT									
L1Pa10	GCAGAAAAAGCCTTCGATAAAAAATTCACATCCCTTCATGTTAAAAACTCTCAATAAATTAGGTATTGANGGAACATACCTCAAATAATAAGAGCCATT									
L1Pa11	GCAGAAAAAGCCTTNGATAAAAAATTCACATCCCTTCATGTTAAAAACTCTCAATAAATTAGGTATTGAAGGAACATACCTCAAATAATAAGAGCCATAT									
L1Pa13	GCAGAAAAAGCCTTNGATAAAAAATTCACATCCCTTCATGTTAAAAACTCTCAATAAATTAGGTATTGAAGGAACATACCTCAAATAATAAGAGCCATCT									
L1Pa15	GCAGAAAAAGCCTTTGATAAAAAATTCACATCCCTTCATGTTAAAAACCTCAACAACTAGGCATTGAAGGAACATACCTCAAATAATAAGAGCCATCT									
L1Pa16	GCAGAAAAAGCCTTTGATAAAAAATTCACATCCCTTCATGATAAAAAACCTCAACAACTAGGCATNNAAGGAACATACCTCAAATAATAAGAGCCATCT									
	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000
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L1Pa1	ATGACAAACCCACAGCCAATATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAAAACCGGCACAAGACAGGGATGCCCTCTCTCACCCTCCT									
L1Pa3	ATGACAAACCCACAGCCAATATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAAAACCTGGCACAAGACAGGGATGCCCTCTCTCACCCTCCT									
L1Pa4	ATGACAAACCCACAGCCAATATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAAAACCTGGCACAAGACAGGGATGCCCTCTCTCACCCTCCT									
L1Pa5	ATGACAAACCCACAGCCAATATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAAAACCTGGCACAAGACAGGGATGCCCTCTCTCACCCTCCT									
L1Pa6	ATGACAAACCCACAGCCAATATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAAAACCTGGCACAAGACAGGGATGCCCTCTCTCACCCTCCT									
L1Pa7	ATGACAAACCCACAGCCAATATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAAAACCGGCACAAGACAGGGATGCCCTCTCTCACCCTCCT									
L1Pa8	ATGACAAACCCATAGCCAATATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAAAACCGGCACAAGACAGGGATGCCCTCTCTCACCCTCCT									
L1Pa10	ATGACAAACCCACAGCCAATATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAAAACCTGGCACAAGACAGGGATGCCCTCTCTCACCCTCCT									
L1Pa11	ATGACAAACCCACAGCCAATATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAAAACCTGGCACAAGACAGGGATGCCCTCTCTCACCCTCCT									
L1Pa13	ATGACAAACCCACAGCCAACATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAAAACCTGGCACAAGACAGGGATGCCCTCTCTCACCCTCCT									
L1Pa15	ATGACAAACCCACAGCCAACATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAGAACNNGACAAGACAAGGATGCCCTCTCTCACCCTCCT									
L1Pa16	ATGACAAACCCACAGCCAACATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCTTTGAGAACNNGACAAGACAAGGATGCCCTCTCTCACCCTCCT									

	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100
L1Pa1	ATTCAACATAGTGTGGAA	TTCTGGCCAGGGCAAT	CAGGCAGGAGAAGGAA	ATAAAGGGTATTCAATT	AGGAAAAGAGGAAGT	CAAATTGTCCTGTTT				
L1Pa3	ATTCAACATAGTGTGGAA	TTCTGGCCAGGGCAAT	TAGGCAGGAGAAGGAA	ATAAAGGGTATTCAATT	AGGAAAAGAGGAAGT	CAAATTGTCCTGTTT				
L1Pa4	ATTCAACATAGTGTGGAA	TTCTGGCCAGGGCAAT	CAGGCAGGAGAAGGAA	ATAAAGGGTATTCAATT	AGGAAAAGAGGAAGT	CAAATTGTCCTGTTT				
L1Pa5	ATTCAACATAGTGTGGAA	TTCTGGCCAGGGCAAT	CAGGCAGGAGAAGGAA	ATAAAGGGTATTCAATT	AGGAAAAGAGGAAGT	CAAATTGTCCTGTTT				
L1Pa6	ATTCAACATAGTGTGGAA	TTCTGGCCAGGGCAAT	CAGGCAAGAGAAAGAA	ATAAAGGGTATTCAATT	AGGAAAAGAGGAAGT	CAAATTGTCCTGTTT				
L1Pa7	ATTCAACATAGTATTGGA	AGTTCTGGCCAGGGCAAT	CAGGCAAGAGAAAGAA	ATAAAGGGTATTCAAAT	AGGAAGAGAGGAAGT	CAAATTGTCTCTGTTT				
L1Pa8	ATTCAACATAGTATTGGA	AGTTCTGGCCAGGGCAAT	CAGGCAAGAGAAAGAA	ATAAAGGGTATTCAAAT	AGGAAGAGAGGAAGT	CAAATTGTCTCTGTTT				
L1Pa10	ATTCAACATAGTATTGGA	AGTTCTGGCCAGGGCAAT	CAGGCAAGAGAAAGAA	ATAAAGGGTATTCAAAT	AGGAAGAGAGGAAGT	CAAATTGTCTCTGTTT				
L1Pa11	ATTCAACATAGTATTGGA	AGTTCTGGCCAGGGCAAT	CAGGCAAGAGAAAGAA	ATAAAGGGTATTCAAAT	AGGAAGAGAGGAAGT	CAAATTATCTTTGTTT				
L1Pa13	ATTCAACATAGTATTGGA	AGTCTTGCCAGNGCAAT	CAGGCAAGAGAAAGAA	ATAAAGGCATCCAAT	AGGAAGAGAGGAAGT	CAAACCTATCCCTGTTT				
L1Pa15	ATTCAACATAGTACTGGA	AGTCTAGCCAGAGCAAT	CAGGCAAGAGAAAGAA	ATAAAGGCATCCAAT	AGGAAGAGAGGAAGT	CAAACCTATCTCTNTTT				
L1Pa16	ATTCAACATAGTACTGGA	AGTCTAGCCAGAGCAAT	CAGGCAAGAGAAAGAA	ATAAAGGCATCCAAT	AGGAAAAGAAGTCAA	ACCTATCTCTCTTC				
	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
L1Pa1	GCAGACGACATGATTGTT	TATCTAGAAAACCCCAT	CGTCTCAGCCCAAAAT	CTCCTTAAGCTGATAAG	CAACTTCAGCAAAGTCT	CAGGATACAAAATCA				
L1Pa3	GCAGATGACATGATTGTAT	TATCTAGAAAACCCCAT	GTCTCAGCCCAAAAT	CTCCTTAAGCTGATAAG	CAACTTCAGCAAAGTCT	CAGGATACAAAATCA				
L1Pa4	GCAGATGACATGATTGTAT	TATCTAGAAAACCCCAT	GTCTCAGCCCAAAAT	CTCCTTAAGCTGATAAG	CAACTTCAGCAAAGTCT	CAGGATACAAAATCA				
L1Pa5	GCAGATGACATGATTGTAT	TTTAGAAAACCCCAT	GTCTCAGCCCAAAAT	CTCCTTAAGCTGATAAG	CAACTTCAGCAAAGTCT	CAGGATACAAAATCA				
L1Pa6	GCAGATGACATGATTGTAT	TTTAGAAAACCCCAT	GTCTCAGCCCAAAAT	CTCCTTAAGCTGATAAG	CAACTTCAGCAAAGTCT	CAGGATACAAAATCA				
L1Pa7	GCAGATGACATGATTGTAT	TTTAGAAAACCCCAT	GTCTCAGCCCAAAAT	CTCCTTAAGCTGATAAG	CAACTTCAGCAAAGTCT	CAGGATACAAAATCA				
L1Pa8	GCAGATGACATGATTGTAT	TTTAGAAAACCCCAT	GTCTCAGCCCAAAAT	CTCCTTAAGCTGATAAG	CAACTTCAGCAAAGTCT	CAGGATACAAAATCA				
L1Pa10	GCAGATGACATGATCCTAT	ATCTAGAAAACCCCAT	GTCTCAGCCCAAAAGCTT	CTTAAGCTGATAAGCA	ACTTCAGCAAAGTCT	CAGGATACAAAATCA				
L1Pa11	GCAGATGACATGATCCTAT	ATCTAGAAAACCCCAT	NGTCTCAGCCCAAAAGCTT	CTTAAGCTGATAAGCA	ACTTCAGCAAAGTCT	CAGGATACAAAATCA				
L1Pa13	GCAGATGACATGATCCTAT	ATCTAGAAAACCCCAT	AGTCTCAGCCCAAAAGCTN	CTTAAGCTGATAAACAA	CTTCAGCAAAGTCT	CAGGATACAAAATCA				
L1Pa15	GCAGATGATATGATTCTAT	ACCTAGAAAACCCCAT	AGTCTCTGCCCAAAAGCT	CCTAGATCTGATAAACAA	CTTCAGCAAAGTTT	CAGGATACAAAATCA				
L1Pa16	ACTGATGATATGATTCTAT	ACCTAGAAAACCTAAAG	ACTCTNCCAAAAGGCTC	CTAGAACTGATAANNAC	TTCAGTAAAGTTT	CAGGATACAAAATCA				
	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
L1Pa1	ATGTACAAAAATCACAAG	CATTCTTATACACCAACA	CAGACAAACAGAGAGCC	AAATCATGGTGAACTCC	CATTACAATTGCTTCAA	AGAGAATAAA				
L1Pa3	ATGTACAAAAATCACAAG	CATTCTTATACACCAATA	AACAGACAAACAGAGAG	CCAAATCATGAGTGAAC	TCCTTACAATTGCTTCAA	AGAGAATAAA				
L1Pa4	ATGTGCAAAAAATCACAAG	CATTCTTATACACCAATA	AACAGACAAACAGAGAG	CCAAATCATGAGTGAAC	TCCTTACAATTGCTTCAA	AGAGAATAAA				
L1Pa5	ATGTGCAAAAAATCACAAG	CATTCTTATACACCAATA	AACAGACAAACAGAGAG	CCAAATCATGAGTGAAC	TCCTTACAATTGCTTCAA	AGAGAATAAA				
L1Pa6	ATGTGCAAAAAATCACAAG	CATTCTATACACCAATA	AACAGACAAACAGAGAG	CCAAATCATGAGTGAAC	TCCTTACAATTGCTTCAA	AGAGAATAAA				
L1Pa7	ATGTGCAAAAAATCACAAG	CATTCTATACACCAATA	AATAGACAAACAGAGAG	CCAAATCATGAGTGAAC	TCCTTACAATTGCTTCAA	AGAGAATAAA				
L1Pa8	ATGTGCAAAAAATCACAAG	CATTCTATACACCAATA	AATAGACAAACAGAGAG	CCAAATCATGAGTGAAC	TCCTTACAATTGCTTCAA	AGAGAATAAA				
L1Pa10	ATGTGCAAAAAATCACAAG	CATTCTATACACCAACA	ANAGACAAGCAGAGAGCC	AAATCATGAATGAACTC	CCATTACAATTGCTTCAA	AGAGAATAAA				
L1Pa11	ATGTGCAAAAAATNNCTAG	CATTCTATACACCAACA	ACAGGCAAGCAGAGAGCC	AAATCATGAATGAACTC	CCATTACAATTGCTTCAA	AGAGAAATAAA				
L1Pa13	ATGTGCAAAAAATCACTAG	CATTCTATACACCAACA	ACAGTCAAGCNGAGAGCC	AAATCAGGAATGCAATC	CCATTACAATTGCCACA	AAAAAGAATAAA				
L1Pa15	ATGTACAAAAATCAGTAGC	ATTTCTATACACCAACA	ACATCCAAGCTGAGAGCC	AAATCAAGAATGCAATC	CCATTACAATAGCCACA	AAAAAGAATAAA				
L1Pa16	ATGTACAAAAATCAGTAGC	ATTTCTATACACCAATA	AANNTTCAAGCTGAGAGCC	AAATCAAGAAACAATCC	CATTACAAT					

	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500
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L1Pa1	AACATTCCATGCTCATGGGTAGGAAGAATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTACAGATTCAATGCCATCCCCATCAAGCTACCAA									
L1Pa3	AACATTCCATGCTCATGGGTAGGAAGAATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTATAGATTCAATGCCATCCCCATCAAGCTACCAA									
L1Pa4	AACATTCCATGCTCATGGGTAGGAAGAATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTATAGATTCAATGCCATCCCCATCAAGCTACCAA									
L1Pa5	AACATTCCATGCTCATGGATAGGAAGAATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTATAGATTCAATGCCATCCCCATCAAGCTACCAA									
L1Pa6	AACATTCCATGCTCATGGATAGGAAGAATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTATAGATTCAATGCCATCCCCATCAAGCTACCAA									
L1Pa7	AACATTCCATGCTCATGGATAGGAAGAATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTATAGATTCAATGCTATCCCCATCAAGCTACCAT									
L1Pa8	AACATTCCATGCTCATGGATAGGAAGAATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTATAGATTCAATGCTATTTCCATCAAGCTACCAT									
L1Pa10	AACATTCCATGCTCATGGATAGGAAGAATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTATAGATTCAATGCTATTTCCATTAAACTACCAT									
L1Pa11	AACATTCCATGCTCATGGATAGGAAGAATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTATAGATTCAATGCTATTTCCATTAAACTACCAT									
L1Pa13	AACATTCCATGCTCATGGATAGGAAGAATCAATATNNTTAAAAATGGCCATACTGCCCAAGCAATTTATAGATTCAATGCTATTTCTATTAAACTACCAN									
L1Pa15	AACATTCCATGCTCATGGATAGGAAGAATCAATATTGTTAAAAATGGCCATACTGCCCAAGCAATTTACAGATTCAATGCTATTTCTATCAAACCTACCAA									
L1Pa16	AACATTCCATGCTCATGGATTGGAAGAATCAATATNNTTAAAAATGGCCATACTGCCCAAGCAATCTACAGATTCAATGCTATTTCTATCAAACCTACCAA									
	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600
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L1Pa1	TGACTTTCTTCACAGAATTGGAaaaaactactTTAAAGTTCATATGGAACCAaaaaaAGAGCCCGCATTGCCAAGTCAATCCTAAGCCAAAAAGAACAAAGC									
L1Pa3	TGACTTTCTTCACAGAATTGGAaaaaactactTTAAAGTTCATATGGAACCAaaaaaAGAGCCCGCATTGCCAAGTCAATCCTAAGCCAAAAAGAACAAAGC									
L1Pa4	TGACTTTCTTCACAGAATTGGAaaaaactactTTAAAGTTCATATGGAACCAaaaaaAGAGCCCGCATTGCCAAGTCAATCCTAAGCCAAAAAGAACAAAGC									
L1Pa5	TGACTTTCTTCACAGAATTGGAaaaaactactTTAAAGTTCATATGGAACCAaaaaaAGAGCCCGCATTGCCAAGACAATCCTAAGCCAAAAAGAACAAAGC									
L1Pa6	TGACTTTCTTCACAGAATTGGAaaaaactactTTAAAGTTCATATGGAACCAaaaaaAGAGCCCGCATTGCCAAGACAATCCTAAGCCAAAAAGAACAAAGC									
L1Pa7	TGACTTTCTTCACAGAATTAGAAAAactactTTAAATTTTTCATATGGAACCAaaaaaAGAGCCNTATAGCCAAGACAATCCTAAGCCAAAAAGAACAAAGC									
L1Pa8	TGACTTTCTTCACAGAATTAGAAAAactactTTAAATTTTTCATATGGAACCAaaaaaAGAGCCNTATAGCCAAGACAATCCTAAGCCAAAAAGAACAAAGC									
L1Pa10	TGACATTCTTCACAGAATTAGAAAAactANTTTAAATTTTCATATGGAACCAaaaaaAGAGCCNTATAGCCAAGACAATCCTAAGCCAAAAAGAACAAAGC									
L1Pa11	TGACATTCTTCACAGAATTAGAAAAactATTTTAAATTTTCATATGGAACCAaaaaaAGAGCCNATAGCCAAGACAATCCTAAGCCAAAAAGAACAAAGC									
L1Pa13	TGACATTCTTCACAGAATTAGAAAAactATTTTAAATTTTCATATGGAACCAaaaaaAGAGCCNATAGCCAAGGCAATCCTAAGCCAAAAAGAACAAAGC									
L1Pa15	TGACATTNTTCACAGAATTAGAAAAactATTNTAAATTTTCATATGGAACCAaaaaaAGAGCCNATAGCCAAGGCAATCCTAAGCCAAAAAGAACAAAGC									
L1Pa16	TGTCATTTTTCACAGAATTAGAAAAactATTCTAAATTTTCATATGGAACCAaaaaaAGAGCCAAATAGCCAAGGCAATCCTAAGCCAAAAAGAACAAAGC									
	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700
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L1Pa1	TGGAGGCATCACACTACCTGACTTCAAACCTATACTACAAGGCTACAGTAACCAaaaacAGCATGGTACTGGTACCAaaaacAGAGATATAGATCAATGGAAC									
L1Pa3	TGGAGGCATCACGCTACCTGACTTCAAACCTATACTACAAGGCTACAGTAACCAaaaacAGCATGGTACTGGTACCAaaaacAGAGATATAGATCAATGGAAC									
L1Pa4	TGGAGGCATCACGCTACCTGACTTCAAACCTATACTACAAGGCTACAGTAACCAaaaacAGCATGGTACTGGTACCAaaaacAGAGATATAGACCAATGGAAC									
L1Pa5	TGGAGGCATCACGCTACCTGACTTCAAACCTATACTACAAGGCTACAGTAACCAaaaacAGCATGGTACTGGTACCAaaaacAGAGATATAGACCAATGGAAC									
L1Pa6	TGGAGGCATCACGCTACCTGACTTCAAACCTATACTACAAGGCTACAGTAACCAaaaacAGCATGGTACTGGTACCAaaaacAGAGATATAGACCAATGGAAC									
L1Pa7	TGGAGGCATCANGCTACCTGACTTCAAACCTATACTACAAGGCTACAGTAACCAaaaacAGCATGGTACTGGTACCAaaaacAGAGATATATAGACCAATGGAAC									
L1Pa8	TGGAGGCATCATGTACCTGACTTCAAACCTATACTACAAGGCTACAGTAACCAaaaacAGCATGGTACTGGTACCAaaaacAGAGATATATAGACCAATGGAAC									
L1Pa10	TGGAGGCATCATGTACCTGACTTCAAACCTATACTACAAGGCTACAGTAACCAaaaacAGCATGGTACTGGTACAAAAACAGACACATAGACCAATGGAAC									
L1Pa11	TGGAGGCATCATGTACCTGACTTCAAACCTATACTACAAGGCTACAGTAACCAaaaacAGCATGGTACTGGTACAAAAACAGACACATAGACCAATGGAAC									
L1Pa13	TGGAGGCATCANGCTACCNACTTCAAACCTATACTACAGGGCTACAGTAACCAaaaacAGCATGGTACTGGTACAAAAACAGACACATAGACCAATGGAAC									
L1Pa15	TGGAGGCATCACATTACCTGACTTCAAACCTATACTACAAGGCTACAGTAACCAaaaacAGCATGGTACTGGTACAAAAACAGACACATAGACCAATGGAAC									
L1Pa16	NAGAGGCATCACATTACCTGACTTCAAACCTATACTATAAGGCTACAGTAACCAaaaacAGCATGGTACTGGTACAAAAACAGACACATAGACCAATGGAAC									
	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800
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L1Pa1	AGAACAGAGCCCTCAGAAATAATGCCGCATATCTACAACCTATCTGATCTTTGACAAACCTGAGAAAAACAAGCAATGGGGAAAGGATTCCCTATTTAATA									
L1Pa3	AGAACAGAGCCCTCAGAAATAACGCCGCATATCTACAACCTATCTGATCTTTGACAAACCTGAGAAAAACAAGCAATGGGGAAAGGATTCCCTATTTAATA									
L1Pa4	AGAACAGAGCCCTCAGAAATAATGCCGCATATCTACAACCTATCTGATCTTTGACAAACCTGACAAAAACAAGAAATGGGGAAAGGATTCCCTATTTAATA									
L1Pa5	AGAACAGAGCCCTCAGAAATAATACCACACATCTACAACCTATCTGATCTTTGACAAACCTGACAAAAACAAGAAATGGGGAAAGGATTCCCTATTTAATA									
L1Pa6	AGAACAGAGCCCTCAGAAATAACACCACACATCTACAACCTATCTGATCTTTGACAAACCTGACAAAAACAAGAAATGGGGAAAGGATTCCCTATTTAATA									
L1Pa7	AGAACAGAGCCCTCAGAAATAACACCACACATCTACAACCTATCTGATCTTTGACAAACCTGACAAAAACAAGCAATGGGGAAAGGATTCCCTATTTAATA									
L1Pa8	AGAACAGAGNCCTCAGAAATAACACCACACATCTACAACCTATCTGATCTTTGACAAACCTGACAAAAACAAGCAATGGGGAAAGGATTCCCTATTTAATA									
L1Pa10	AGAATAGAGAAGCTCAGAAATAAGACCACACATCTACAACCTATCTGATCTTNGACAAACCTGACAAAAACAAGCAATGGGGAAAGGATTCCCTATTTAATA									
L1Pa11	AGAATAGAGAAGCTCAGAAATAAGACCACACCTACAACCTATCTGATCTTNGACAAACCTGACAAAAACAAGCAATGGGGAAAGGATTCCCTATTTAATA									
L1Pa13	AGAATAGAGAAGCCAGAAATAAGNCCNCACACCTACAACCTATCTGATCTTNGACAAAGTTGACAAAAACAAGCAATGGGGAAAGGACTCCCTATTCAATA									
L1Pa15	AGAATAGAGANCCAGAAATAAGGCCACACACCTACAACCTATCTGATCTTNGACAAAGTTGACAAAAACAAGCAATGGGGAAAGGACTCCCTATTCAATA									
L1Pa16	AGAATAGAGAAGCCAGAAATAAGGCCACACACCTACAACCTATCTGATCTTTGACAAAGTTGACAAAAATAAGCAATGGGGAAAGGACTCCCTATTCAATA									

	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900
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L1Pa1	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GTAGAA	GCTGAA	ACTGGAT	CCCTTC	CTTACAC
L1Pa3	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GTAGAA	GCTGAA	ACTGGAT	CCCTTC	CTTACAC
L1Pa4	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GTAGAA	GCTGAA	ACTGGAT	CCCTTC	CTTACAC
L1Pa5	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GTAGAA	GCTGAA	ACTGGAT	CCCTTC	CTTACAC
L1Pa6	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GTAGAA	GCTGAA	ACTGGAT	CCCTTC	CTTACAC
L1Pa7	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GTAGAA	GCTGAA	ACTGGAT	CCCTTC	CTTACAC
L1Pa8	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GCAGAAA	ACTGAA	ACTGGAC	CCCTTC	CTTACAC
L1Pa10	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GCAGAAA	ATTGAA	ACTGGAC	CCCTTC	CTTACAC
L1Pa11	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GCAGAAA	ATTGAA	ACTGGAC	CCCTTC	CTTACAC
L1Pa13	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GCAGAAA	ATTGAA	ACTGGAC	CCCTTC	CTTACAC
L1Pa15	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GCAGAAA	ATTGAA	ACTGGAC	CCCTTC	CTTACAC
L1Pa16	AATGGT	GCTGGG	AAAACT	GGCTAG	CCATAT	GCAGAAA	ATTGAA	ACTGGAC	CCCTTC	CTTACAC
	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000
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L1Pa1	AAACGT	TAAACCT	AAAAAC	CCATAA	AAACCT	AGAAGAA	ACCTAG	GCAATAC	CATTAG	CAGGAC
L1Pa3	AAACGT	TAGACCT	AAAAAC	CCATAA	AAACCT	AGAAGAA	ACCTAG	GCAATAC	CATTAG	CAGGAC
L1Pa4	AAATGT	TAGACCT	AAAAAC	CCATAA	AAACCT	AGAAGAA	ACCTAG	GCAATAC	CATTAG	CAGGAC
L1Pa5	AAATGT	TAGACCT	AAAAAC	CCATAA	AAACCT	AGAAGAA	ACCTAG	GCAATAC	CATTAG	CAGGAC
L1Pa6	AAATGT	TAGACCT	AAAAAC	CCATAA	AAACCT	AGAAGAA	ACCTAG	GCAATAC	CATTAG	CAGGAC
L1Pa7	AAACGT	AAGACCT	AAAAAC	CCATAA	AAACCT	AGAAGAA	ACCTAG	GCAATAC	CATTAG	CAGGAC
L1Pa8	AAATGT	AAAAAC	CNAAAA	CCATAA	AAACCT	AGAAGAA	ACCTAG	GCAATAC	CATTAG	CAGGAC
L1Pa10	AAATGT	AAAAAC	CCAAAA	CTATAA	AAACCT	AGAAGAA	ATCTAG	GCAATAC	CATTAG	CAGGAC
L1Pa11	AAATGT	AAAAAC	CCAAAA	CTATAA	AAACCT	AGAAGAA	ATCTAG	GCAATAC	CATTAG	CAGGAC
L1Pa13	AAATGT	AAAAAC	CCAAAA	CTATAA	AAACCT	AGAAGAA	ATCTAG	GCAATAC	CATTAG	CAGGAC
L1Pa15	AAATGT	AAAAAC	CTAAAA	CTNGA	AAGANA	ACCTAG	GAAATAC	CATTCT	GACATAG	GGCCTG
L1Pa16	AAATGT	AAGACCT	CAAACT	TATAAA	AATCCT	AGAAGAA	ACCTAG	GAAATAC	CATTCT	GACATAG
	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100
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L1Pa1	GCAATG	CAACAAA	AGACAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
L1Pa3	GCAATG	CAACAAA	AGGCAAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
L1Pa4	GCAATG	CAACAAA	AGGCAAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
L1Pa5	GCAATG	CAACAAA	AGGCAAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
L1Pa6	GCAATG	CAACAAA	AGGCAAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
L1Pa7	GCAATG	CAACAAA	AGGCAAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
L1Pa8	GCAATT	GCAACAAA	AGGCAAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
L1Pa10	GCAATT	GCAACAAA	AGGCAAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
L1Pa11	GCAATT	GCAACAAA	AGGCAAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
L1Pa13	GCAATT	GCAACAAA	AGGCAAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
L1Pa15	GCAATT	GCAACAAA	AGGCAAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
L1Pa16	GCAATT	GCAACAAA	AGGCAAAA	ATTGAC	AAATGG	GATCTA	ATTAACT	AAAGAG	CTTCTG	CACAGCA
	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200
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L1Pa1	CAACAT	GGGAGAA	AAATTTT	TGCAAC	TACTCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA
L1Pa3	CAAAAT	GGGAGAA	AAATTTT	TCGCAAC	TACTCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA
L1Pa4	CAGAAT	GGGAGAA	AAATTTT	TGCAAT	TACTCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA
L1Pa5	CAGAAT	GGGAGAA	AAATTTT	TGCAAT	TACTCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA
L1Pa6	CAGAAT	GGGAGAA	AAATTTT	TGCAAT	TACTCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA
L1Pa7	CAGAAT	GGGAGAA	AAATTTT	TGCAAT	TATCCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA
L1Pa8	CAGAAT	GGGAGAA	AAATTTT	TGCAAT	TATCCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA
L1Pa10	CAGAAT	GGGAGAA	AAATTTT	TGCAAT	TATCCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA
L1Pa11	CAGAAT	GGGAGAA	AAATTTT	TGCAAT	TATCCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA
L1Pa13	CAGAAT	GGGAGAA	AAATTTT	TGCAAT	TATCCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA
L1Pa15	CAGAAT	GGGAGAA	AAATTTT	TGCAAT	TATCCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA
L1Pa16	CAGAAT	GGGAGAA	AAATTTT	TGCAAT	TATCCAT	CTGACAA	AGGGCTA	ATATCC	GAGATCT	ACAATGA

	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300
L1Pa1	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----	CCCCATCAAAAAGTGGGCGAAGGACATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAAAAAACACATGAAGAAATGCTCATCATCTACTGGCC								
L1Pa3	CCCCATCAAAAAGTGGGCGAAGGACATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAAAAAACACATGAAAAAATGCTCACCATCACTACTGGCC									
L1Pa4	CCCCATCAAAAAGTGGGCGAAGGATATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAAAAAGACACATGAAAAAATGCTCATCATCACTACTGGCC									
L1Pa5	CCCCATCAAAAAGTGGGCGAAGGATATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAACAGACACATGAAAAAATGCTCATCATCACTACTGGCC									
L1Pa6	CCCCATCAAAAAGTGGGCGAAGGATATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAACAGACACATGAAAAAATGCTCATCATCACTGGTC									
L1Pa7	CCCCATCAAAAAGTGGGCGAAGGATATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAACAAACATATGAAAAAAGCTCATCATCACTGGTC									
L1Pa8	CCCCATCAAAAAGTGGGCGAAGGATATGAACAGACACTTCTCAAAAGAAGACATTTATGCGGCCAACAAACATATGAAAAAAGCTCATCATCACTGGTC									
L1Pa10	CCCCATTA AAAAGTGGGCGAAGGACATGAACAGACACTTCTCAAAAGAAGACATTTATGCGGCCAACAAACATATGAAAAAAGCTCAACATCACTGATC									
L1Pa11	CCCCATTA AAAAGTGGGCGAAGGACATGAACAGACACTTCTCAAAAGAAGACATACATGNGGCCAACAAACATATGAAAAAAGCTCAACATCACTGATC									
L1Pa13	CCCCATTA AAAAGTGGGCGAAGGACATGAACAGACACTTTTCAAAAGAAGACATACATGNGGCCAACAAATCATATGAAAAAAGCTCAACATCACTGATC									
L1Pa15	CCCCATTA AAAAGTGGGCGAAGGACATGAACAGACACTTTTCAAAAGAAGACATACATGTGGCCAACAAAGCATATGAAAAAATGCTCAACATCACTAATC									
L1Pa16	CCCCATTA AAAAANTGGGCGAANGACATGAACAGACACTTCTCAAAAGAAGACATACAAGTGGCCAACAAACATATGAAAAAATGCTCAACATCACTAATC									
	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400
L1Pa1	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----	ATCAGAGAAATGCAAATCAAACCACATATGAGATATCATCTCACACCAGTTAGAATGGCAATCATTAAAAAGTCAGGAAACAACAGGTGCTGGAGAGGAT								
L1Pa3	ATCAGAGAAATGCAAATCAAACCACAATGAGATACCATCTCACACCAGTTAGAATGGCAATCATTAAAAAGTCAGGAAACAACAGGTGCTGGAGAGGAT									
L1Pa4	ATCAGAGAAATGCAAATCAAACCACAATGAGATACCATCTCACACCAGTTAGAATGGCGATCATTAAAAAGTCAGGAAACAACAGGTGCTGGAGAGGAT									
L1Pa5	ATCAGAGAAATGCAAATCAAACCACAATGAGATACCATCTCACACCAGTTAGAATGGCGATCATTAAAAAGTCAGGAAACAACAGGTGCTGGAGAGGAT									
L1Pa6	ATCAGAGAAATGCAAATCAAACCACAATGAGATACCATCTCACACCAGTTAGAATGGCGATCATTAAAAAGTCAGGAAACAACAGATGCTGGAGAGGAT									
L1Pa7	ATTAGAGAAATGCAAATCAAACCACAATGAGATACCATCTCAGCCAGTTAGAATGGCGATCATTAAAAAGTCAGGAAACAACAGATGCTGGAGAGGAT									
L1Pa8	ATTAGAGAAATGCAAATCAAACCACAATGAGATACCATCTCANGCCAGTTAGAATGGCGATTATTA AAAAGTCAGGAAACAACAGATGCTGGNGAGGCT									
L1Pa10	ATTAGAGAAATGCAAATCAAACCACAATGAGATACCATCTCATGCCAGTCAGAATGGCGATTATTA AAAAGTCAAGAAACAACAGATGCTGGNGAGGCT									
L1Pa11	ATTAGAGAAATGCAAATCAAACCACAATGAGATACCATCTCACACCAGTCAGAATGGCTATTATTA AAAAGTCAAAAAACAACAGATGCTGGNGAGGTT									
L1Pa13	ATTAGAGAAATGCAAATCAAACCACAATGAGATACCATCTCACACCAGTCAGAATGGCTATTATTA AAAAGTCAAAAAAATACAGATGCTGGNGAGGTT									
L1Pa15	ATTAGAGAAATGCAAATCAAACCACAATGAGATACCATCTCACACCAGTCAGAATGGCTATTATTA AAAAGTCAAAAAAATACAGATGCTGGNGAGGTT									
L1Pa16	ATCAGAGAAATGCAAATCAAACCACAATGAGATACCATCTCACACCAGTCAGAATGGCTATTATTA AAAAGTCAAAAAANAACAGATGCTGGNGAGGCT									
	3410	3420	3430	3440	3450	3460	3470	3480	3490	3500
L1Pa1	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----	GCGGAGAAATAGGAACACTTTTACACTGTTGGTGGGACTGTAAACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGATTCTCAGGGATCTAGAACTAGA								
L1Pa3	GTGGAGAAATAGGAACACTTTTACACTGTTGGTGGGACTGTAAACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGATTCTCAGGGATCTAGAACTAGA									
L1Pa4	GTGGAGAAATAGGAACACTTTTACACTGTTGGTGGGACTGTAAACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGATTCTCAGGGATCTAGAACTAGA									
L1Pa5	GTGGAGAAATAGGAACACTTTTACACTGTTGGTGGGACTGTAAACTAGTTCAACCATTGTGGAAGACAGTGTGGCGATTCTCAAGGATCTAGAACTAGA									
L1Pa6	GTGGAGAAATAGGAACGCTTTTACACTGTTGGTGGGAGTGTA AATTAGTTCAACCATTGTGGAAGACAGTGTGGCGATTCTCAAGGATCTAGAACTAGA									
L1Pa7	GTGGAGAAATAGGAANGCTTTTACACTGTTGGTGGGAGTGTA AATTAGTTCAACCATTGTGGAAGACAGTGTGGCGATTCTCAAGGATCTAGAACCAGA									
L1Pa8	GTGGAGAAATAGGAANGCTTTTACACTGTTGGTGGGAGTGTA AATTAGTTCAACCATTGTGGAAGACAGTGTGGCGATTCTCAAGGATCTAGAACCAGA									
L1Pa10	GTGGAGAAATAGGAANGCTTTTACACTGTTGGTGGGAATGTAA AATTAGTTCAACCATTGTGGAAGACAGTGTGGCGATTCTCAAGATCTAGAACCAGA									
L1Pa11	GTGGAGAAAAAGGAANGCTTTTACACTGTTGGTGGGAGTGTA AATTAGTTCAACCATTGTGGAAGACAGTGTGGCGATTCTCAAGACCTAGAGGCAGA									
L1Pa13	GTGGAGAAAAAGGAANGCTTATACACTGTTGGTGGGAGTGTA AATTAGTTCAACCATTGTGGAAGACAGTGTGGCGATTCTCAAGACCTAAAGACAGA									
L1Pa15	GNAGAGAAAAGGGAATGCTTATACACTGCTGGTGGGAATGTAA AATTAGTTCAAGCCANTGTGGAAGACAGTTTGGNGATTTCTCAAGAACTTAAACAGA									
L1Pa16	GNAGAGAAAAGGGAATGCTTATACACTGTTGGTGGGAATGTAA AATTAGTTCAAGCCACTGTGGAAGACAGTTTGGAGATTTCTCAAGAACTTAAACAGA									
	3510	3520	3530	3540	3550	3560				

	3610	3620	3630	3640	3650	3660	3670	3680	3690	3700
L1Pa1	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
L1Pa3	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
L1Pa4	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
L1Pa5	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
L1Pa6	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
L1Pa7	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
L1Pa8	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
L1Pa10	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
L1Pa11	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
L1Pa13	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
L1Pa15	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
L1Pa16	CTATT	CACA	TAGC	AAAG	ACTT	GGA	ACCA	ACCC	CAA	ATGT
	3710	3720	3730	3740	3750	3760	3770	3780	3790	3800
L1Pa1	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
L1Pa3	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
L1Pa4	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
L1Pa5	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
L1Pa6	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
L1Pa7	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
L1Pa8	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
L1Pa10	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
L1Pa11	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
L1Pa13	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
L1Pa15	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
L1Pa16	CCATA	AAAA	ATG	ATG	AGTT	CAT	ATC	CTTT	G	TAGG
	3810	3820								
L1Pa1	CATAT	TCTC	ACTC	ATAG	GTGG	AATT	GA			
L1Pa3	CATAT	TCTC	ACTC	ATAG	GTGG	AATT	GA			
L1Pa4	CATGT	TCTC	ACTC	ATAG	GTGG	AATT	GA			
L1Pa5	CATGT	TCTC	ACTC	ATAG	GTGG	AATT	GA			
L1Pa6	CATGT	TCTC	ACTC	ATAG	GTGG	AATT	GA			
L1Pa7	CATGT	TCTC	ACTC	ATAG	GTGG	AATT	GA			
L1Pa8	CATGT	TCTC	ACTC	ATAG	GTGG	AATT	GA			
L1Pa10	CATGT	TCTC	ACTC	ATAG	GTGG	AATT	GA			
L1Pa11	CATGT	TCTC	ACTC	ATAG	GTGG	AATT	GA			
L1Pa13	CATGT	TCTC	ACTC	ATAG	GTGG	AATT	GA			
L1Pa15	CATGT	TCTC	ACTC	ATAG	GTGG	AATT	GA			
L1Pa16	CATGT	TCTC	ACTC	ATAG	GTGG	AATT	GA			