Supplementary Materials and Methods

Identification of human-specific mobile elements (HS-MEs): BLAT-based method (Fig. 1): In this method, DNA sequences covering the MEs and their flanking regions were retrieved from the human genome sequences based on the MEs' genomic coordinates from the input list. For each ME, three sequences were used to detect its presence or absence in the corresponding regions of the out-group genomes. Sequence 1 (S1) consists of 200 bp sequences from joining the 100 bp sequences flanking from each side of the ME as one to represent the pre-integration sequence (in most cases contains two copies of the TSD); Sequence 2 (S2) consists of 200 bp sequences with 100 bp into the 5' flanking region and 100 bp into 5' end of the ME to represent the 5' junction area of the ME; Sequence 3 (S3) is similar to sequence 2, but is for the 3' junction area of the ME. Each of these 3 sequences was aligned against each of the 9 out-group genome sequences using BLAT with a species-specific set of empirically determined blat parameters (*e.g.*, minScore and minIdentity) based on the use of a training dataset of known polymorphic MEs documented in dbRIP (see details in later section of this document). The BLAT results of the three sequences for each ME were grouped together based on their genomic positions. For a sequence with multiple mapping locations, the one that provided the best blat score and locates into the same approximate locations with the other two sequences in the out-group genomes was selected. Those with two junction sequences mapped to different locations were discarded as they likely represent random matches to non-orthologous regions. If the blat result for a sequence meet the minimal blat score and percentage of identity, coverage of the query sequences, and span length in the genome, which were determined and optimized based on the training dataset, a "+" sign was given for this sequence to indicate the presence of an orthologous sequence in the out-group genomes. Otherwise a "-" sign was assigned to indicate the absence of an orthologous

sequence in each out-group genome. A typical pattern for a HS-ME would have a pattern of "+/-/-" for the 3 sequences in the order of sequence 1, 2, and 3, representing the pre-integration, the 5'- and 3'-ME junction sequences, respectively, while the pattern for a non HS-ME (*i.e.*, shared) would be "+/+/+". A HS-ME pattern is provided only if all out-group genomes show support a HS-ME.

LiftOver-based method (Fig. 1): LiftOver is a tool originally developed by the UCSC genome team (http://genome.ucsc.edu/cgi-bin/hgLiftOver) to allow conversion of genome coordinates between different assemblies of the same genome. But its use has also been extended for finding corresponding/orthologous regions between genomes of closely related species. In this method, the genomic coordinates for the three regions of a ME, corresponding to 100 bp of the 5' flanking (R1), the ME (R2), and the 100 bp 3' flanking regions (R3), were liftOver'ed onto each of the out-group genomes using a command line version of the liftOver tool with the related chain files between hg19 and each of the out-group genomes. The best hit, which is the one with an identifiable orthologous region closest in length to the human query sequence, for each of the three sequences among the four out-group genomes was used. A query sequence is marked as "+" for having a qualified hit in any out-group genome or as "-" otherwise. The pattern for a typical HS-ME is "+/-/+" for the three regions corresponding to 5' flanking, ME, and 3' flanking, respectively, while the pattern for a typical non-HS-REs should be "+/+/+".

The final list of HS-MEs was generated by combining the results of the blat-based and liftOver-based methods. HS-MEs were then divided into four categories to reflect their types and confidence levels. Category I HS-MEs are those supported by both methods to be HS-ME with at least one of the two flanking sequences present and the ME absent in all outgroup genomes. HS-

MEs with orthologous counterpart for both flanking sequences has the highest confidence. Entries with one only one flanking sequences missing in the out-group genomes can be caused by the presence of transduced sequences or the presence of another HS-ME, and they are candidates for identifying transduction as described later. Category II HS-MEs are those with the MEs and both flanking sequences missing from all out-group genomes (*i.e.*, a pattern of "-/-/-" by both methods). These mostly represent HS-MEs in HS-MEs or with their orthologous regions in the out-group genomes falling into sequence gaps. To exclude the latter cases, we removed those with the closest identifiable chimp orthologous regions located next to a sequence gap.

Determination of optimal BLAT and liftOver criteria using dbRIP data as test datasets: We used a training dataset consisting of half of the known polymorphic retrotransposon insertions (RIPs) documented in dbRIP to identify the optimal parameters for the blat and liftOver methods described above for using with each of the outgroup genomes. RIPs are results of recent retrotransposition events and show as polymorphic for its presence or absence among the human populations. Therefore, they are considered human specific, and were used to train our algorithms to identify an optimal set of criteria that gave an error (only false negative in this case) rate no high than 5% (i.e. sensitivity >=95%). A total of four criteria were used for the BLAT based method: blat score, identity, coverage and span length. The score equals the number of matches minus numbers of mis-matches and gaps in the target sequences (Score = match – mis-match -- T gap count). A higher score means a better match. The identity is a percentage of the similarity between the query sequence and the target sequence. It is calculated as 100 *(match + repeat match (Rep. match)) / (match + mismatch + Rep.match). Span and coverage are used to provide additional constrains about the match. Span is the total length of the target

sequence (Span = Target end – Target start). Since BLAT tolerates gaps in the target sequence, it is able to report matches consisting of fragments with gaps in between. So there is possibility that an entry could have both high score and identity while having a long gap in the target sequence. Similarly, coverage is used to monitor the quality of match for the query sequence: Coverage = (Q end – Q start). The liftOver utilizes a criterion called minMatch, which represents the minimum ratio of bases that must map on to the new genome. For example, if the minMatch ratio is set to be 0.5, liftOver would report a positive hit when 50% of the region can be mapped on to the test genome.

Identification of insertion-mediated transductions and deletions: The target site duplications (TSDs), as well as transduction and RIMD for all HS-MEs were identified using in-house perl scripts incorporating the utility of the NCBI bl2seq and UCSC liftOver as described. Pre-integration site sequences retrieved from outgroup genomes were aligned against sequences consisting of the ME + both flanking sequences from human genome using blast. An in-house perl script is used to identify candidates for transduction and insertion mediated deletion. For identifying transduction, MEs were considered as candidates if they have (1) presence of TSDs and (2) extra sequences between the TSD and the ME. The extra sequence was then searched against the human reference genome using blat (with the similarity cutoff set as >=95%). The qualified candidates were then manually verified before they were included in the transduction list. For identifying insertion mediated deletion, a ME was considered as candidates if it had (1) absence of TSDs and (2) extra sequence at the pre-integration site in the outgroup genomes. The pre-integration sequence retrieved from the closest available outgroup genome was then used for BLAT searches (similarity cutoff set as >=90%) against other outgroup genomes. If the same

extra sequence was seen in at least 2 out-group genomes, then the ME was included in the insertion mediated deletion list after manually verification.

PCR verification of HS-MEs: We performed PCR analysis to verify the human-specific MEs. Genomic DNA from *Homo sapiens* (human; NA10851, Coriell Cell Repository, Camden, NJ), *Pan troglodytes* (common chimpanzee), *Gorilla gorilla* (gorilla), and *Pongo pygmaeus* (Bornean orangutan) were used as a DNA template for each PCR reaction. Genomic DNA for three apes was kindly provided by Dr. Takenaka (Primate Research Institute, Kyoto University). PCR oligonucleotide primers were designed using the software Primer3 (http://bioinfo.ut.ee/primer3-0.4.0/primer3/). Several ME loci were failed to amplify due to variable sequences in flanking sequences. Thus, we manually designed new primers for amplification of these MEs. The primers are listed in Table S3. Each PCR amplification performed in 25 µl reaction using 10 µl of a DNA polymerase kit (SolGent 2X EF-Taq, SolGent, South Korea), 2.5 µl oligonucleotide primer (4pmol/µl), 5 µl of distilled water, and 2 µl of template DNA (10-20 ng/µl). The PCR conditions were an initial denaturation at 95°C for 5 min, followed by 35 cycles of 30 sec of denaturation at 95°C, 40 sec of annealing temperature, and 1 to 5 min of extension (depending on the expected size of PCR product) at 72°C, followed by a final extension at 72°C for 10 min. Five microliters of the resulting PCR products were loaded on 1% agarose gel, stained with ethidium bromide, and visualized using UV fluorescence. In a few cases, in which the expected size of PCR product is longer than 3 kb, we alternatively used Ex TaqTM polymerase (TaKaRa Japan), KOD FX (Toyobo, Japan) in order.

Genome plots of HS-MEs: The HS-MEs were plotted onto the human chromosomes with the cyto-band ideogram (based on GRCh38/hg38) based on the cyto-band data downloaded from the UCSC genome browser with the use of an in-house perl script.

Table S1: The number of MEs in different versions of the human reference genomes

Reference Version	GRCh 35/hg17 (2,851,331,196 bp#)				GRCh 37/hg19 (2,861,327,216 bp#)				GRCh 38/hg38 (2,937,641,526 bp#)			
ME type*	raw counts	integrated counts	total size	% of genome	raw counts	integrated counts	total size	% of genome	raw counts	integrated counts	total size	% of genome
DNA	384,847	305,949	85,545,893	3.0%	450,267	368,746	97,553,533	3.4%	479,941	395,965	101,978,857	3.5%
L1	912,769	522,014	500,573,594	17.6%	938,484	535,248	513,383,945	17.9%	962,085	564,195	522,364,326	17.8%
Alu	1,173,780	1,120,316	307,699,723	10.8%	1,175,329	1,122,711	307,920,501	10.8%	1,181,072	1,132,541	308,374,836	10.5%
SVA	3,347	2,997	4,015,581	0.1%	3,608	3,028	4,015,157	0.1%	5,397	4,933	4,228,693	0.1%
LTR	654,898	453,887	249,382,220	8.7%	698,594	479,372	262,989,620	9.2%	709,475	488,208	265,865,981	9.1%
Others	1,858,138	1,625,340	243,598,757	8.5%	1,939,555	1,725,401	262,620,207	9.2%	1,949,763	1,733,490	328,324,214	11.2%
Total	4,987,779	4,030,503	1,390,815,768	48.8%	5,205,837	4,234,506	1,448,482,963	50.6%	5,287,733	4,319,332	1,531,136,907	52.1%

#All genome sizes are for non-gap sequences; *All uncerntain entries are excluded(e.g. those designated as "DNA?", "Unknown")

Table S2: Comparison of HS-MEs with results from prior studies

ME type	Mills et al 2006	Tang et al 2018	shared MEs (original*)	unique to Mills et al 2009	unique to Tang et al 2018
Alu	5530	8817	4748(4695)	782	4069
L1	1174	3912	1040(1033)	134	2872
SVA	865	1571	833(823)	32	738
LTR	170	530	117(116)	53	413
Other	47	0	0(0)	47	0
Total	7786	14830	6738(6667)	1048	8092

*number of shared MEs with Mills et al 2009 before adding the false negatives

Table S3: PCR primers and results for experimental validation of HS-MEs

Position	ID	Strand	Family	Type	ME	Category	Experiment	Forward Primer
chr5:33122370-33128395	03099614	+	L1PA2	LINE	L1	category I	HS	CATTAAGCAAAGTGTTAGGTGC
chr4:87347103-87353146	02915560	-	L1HS	LINE	L1	category II	HS	GCTGGTACTAAAGTAGACCC
chr3:58814308-58816278	02585297	+	L1PA2	LINE	L1	category II	HS(internal primer fail)	AGCCTGACTACCTGTTATGC
chr1:84052342-84058406	00151933	-	L1HS	LINE	L1	category II	Fail	AGTCTGCTTCACTATACAGCC
chr12:88708857-88714885	00907324	-	L1PA2	LINE	L1	category II	Fail	CCTGTTCAAATGCCCAATACA
chrY:22475174-22476068	04449852	+	MER11D	LTR	ERVK	category II	HS	CAACACACTGGACTAGATTCC
chr7:23039855-23040823	03595003	+	LTR5_Hs	LTR	ERVK	category II	HS	CACTTAAGACCCTGTCTCCCC
chr3:195927524-195928492	02783330	-	LTR5_Hs	LTR	ERVK	category II	HS	GAAGAAGAACAAAGCTAGAGC
chr7:23637166-23638734	03596147	+	SVA_E	Other	Other	category II	HS	CAGTGACAGAGCTTTATGGG
chr2:191397192-191399262	02184897	-	SVA_E	Other	Other	category I	HS	GGAAAGTGGTCAGAACAGGC
chr17:19627119-19628872	01579849	-	SVA_F	Other	Other	category I	HS	ACGATAAGAAACAGCCGCTG
chr11:77489410-77491145	00690834	+	SVA_D	Other	Other	category I	HS	CTAATATACCTGACAGCAGGC
chr1:112897624-112899310	00194215	-	SVA_F	Other	Other	category I	HS	GTCAAGTTTGCTTCTTTAACC
chr6:61183414-61183725	03410386	-	*Alu* Ya5	SINE	*Alu*	category II	HS	TCAATGCCTGGTTTCAAAGG
chr19:47055494-47055803	01884351	-	*Alu* Y	SINE	*Alu*	category I	No HS	GGCCTGACAATTTGAACCTG

Reverse Primer	Internal Primer	Annealing Temperature	Product sizes(+/-)
AGTAAGGCCTGCTGAATGGG	Int2R:GCGTCCGTCACCCCTTTCTT	55°C/55°C	6731bp(661bp)/438bp
TGTGCTAAGCTGGGTGTGGC	Int3F:CAAAGACTTGGAACCAACCC	55°C/59°C	6730bp(788bp)/685bp
CTATGTGTTCGTGTCAGCAG	N/A	53°C	8972bp/689bp
CTCATTTTGAAGCTACAAGGG	IntF:ATTGTGGAAGTCAGTGTGGC/IntR:GTTTACCTAAGCAAGCCTGGG	51°C	N/A
TTGGGATTTCTTTGAACCTAGC	N/A	N/A	N/A
GAGCTGGGAAATGTTTACTG	N/A	52°C	~3500bp/~1000bp
CACCAAACAAATCCACTGGC	Int2F:ATACTAAGGGAACTCAGAGGC	60°C/58°C	9753bp(2695bp)/2715bp
GAATGGGTTTGTACCTGGAC	N/A	52°C	1425bp/451bp
TTTCCATGGCAATCACCTCC	N/A	57°C	3574bp/543bp
AACCATCTTGCAGGCTACCC	N/A	56°C	2706bp/506bp
CCTCATATTGAACTATCCTG	N/A	55°C	2671bp/744bp
TCTCACTCTATCACTCAGGC	N/A	50°C	2436bp/593bp
CTTTTCATGATTGACCTGCC	N/A	55°C	2766bp/871bp
GACAAAGTCTCACTATGTTGCTC	N/A	55°C	871bp/549bp
CATCTGGTAATGTTGCTCCC	N/A	57°C	1198bp

Table S4a: Sources for novel HS-MEs (each source considered independently)

ME type	Extra in hg38 (vs. hg17)	ME integration	MEs in MEs	non-canincal MEs*	Multiple genomes
L1	54	670	1088	1598	347
Alu	86	49	2138	953	326
SVA	13	113	326	444	34
LTR	8	166	192	261	115
Total	161	998	3744	3256	822

Table S4b: Sources for novel HS-MEs (non-redundant when considered step-wise in the given order)

ME type	Extra in hg38 (vs. hg17)	ME integration	MEs in MEs	non-canincal MEs*	More primate genomes	Others	Total	% HS-MEs
L1	54	658	836	793	37	494	2872	73%
Alu	86	40	2091	479	55	1318	4069	46%
SVA	13	112	267	186	5	112	695	44%
LTR	8	162	119	82	4	38	413	78%
Total	161	972	3313	1540	101	1962	8049	54%

***Non-canonical MEs include MEs with transdutions, RMID, and no TSDs**

Table S5. Retrotransposition of different HS-ME subfamilies

Family	Subfamily*	Total copies	HS-MEs	HS%
Alu	*AluYa5*	3,861	3,007	77.9%
	AluYb8	2,828	2,108	74.5%
	AluYb9	327	240	73.4%
	AluYd8	237	154	65.0%
	AluYg6	835	363	43.5%
	AluYi6	455	164	36.0%
	AluYk12	201	68	33.8%
	AluYa8	343	103	30.0%
	AluYe5	1,318	269	20.4%
	AluYi6_4d	149	20	13.4%
	AluYh7	153	16	10.5%
	AluYc3	543	32	5.9%
	AluYk11	1,256	68	5.4%
	AluYk4	1,010	29	2.9%
	AluYh3	2,627	74	2.8%
	AluYe6	194	5	2.6%
	AluYc	4,521	107	2.4%
	AluYh9	142	3	2.1%
	AluYh3a3	313	5	1.6%
	Alu	4,280	65	1.5%
	AluYk3	1,152	17	1.5%
	AluY	102,844	1,442	1.4%
	AluYj4	3,487	38	1.1%
ERV	ERVK	7,369	217	2.9%
	ERV1	103,982	204	0.2%
L1	L1HS	1,346	991	73.6%
	L1PA2	4,096	1,739	42.5%
	L1P1	2,851	211	7.4%
	L1PA3	8,780	269	3.1%
	L1PA8	6,541	131	2.0%
	L1P2	1,231	22	1.8%
	L1P	140	2	1.4%
SVA	SVA_D	1,325	895	67.5%
	SVA_F	821	418	50.9%
	SVA_E	595	156	26.2%
	SVA_C	418	71	17.0%
	SVA_A	1,001	19	1.9%
	SVA_B	768	12	1.6%
All	**All**	**2,194,815**	**14,870**	**0.7%**

*Including subfamilies with top two activities in the family or activities at 1% or more

Table S6a: Ratio of all MEs in MEs by ME class

TE type	MEs in MEs	All MEs	MEs-in-MEs/All MEs
LINE	172773	969873	17.8%
DNA	88614	399590	22.2%
LTR	139906	496946	28.2%
SINE	526647	1689416	31.2%
SVA	1799	4933	36.5%

Table S6b. Ratios of HS-MEs in MEs by ME class

ME type	HS-MEs-in-MEs	Total HS-MEs	MEs-in-MEs%
L1	1388	3912	35.5%
LTR	187	530	35.3%
Alu	4086	8817	46.3%
SVA	640	1571	40.7%

Table S6c. The densities of HS-MEs in MEs by ME type (#HS-MEs/Mbp host MEs)

HS-ME	LINE	DNA	LTR	SINE	SVA	All MEs
L1	1.7	0.9	0.9	0.3	0.0	1.0
LTR	0.2	0.1	0.4	0.0	0.0	0.2
Alu	4.7	3.6	2.5	1.4	0.2	3.1
SVA	0.7	0.4	0.3	0.1	12.7	0.5
Total	**7.3**	**5.0**	**4.0**	**1.8**	**13.0**	**4.8**

Table S7: Chromosome distrubutions of HS-MEs by ME type

Chr	Chr length (Mb)	All MEs	MEs/ Mb	ALL HS-ME	HS-ME/ 500kb	HS/ 1K RE	Gene	Gene /Mb	*HS-Alu*	*HS-Alu/ Mb*	HS-L1	HS-L1/2 MB	HS-SVA	HS-SVA/ 10Mb	HS-LTR	HS-LTR/ 2Mb
chr1	230.5	175319	760.7	1147	5.0	6.5	5620	24.4	667	2.9	297	2.6	159	6.9	24	0.2
chr2	240.5	170039	706.9	1190	4.9	7.0	4264	17.7	735	3.1	310	2.6	128	5.3	17	0.1
chr3	198.1	138120	697.2	1036	5.2	7.5	3230	16.3	633	3.2	268	2.7	113	5.7	22	0.2
chr4	189.8	126991	669.2	1025	5.4	8.1	2699	14.2	619	3.3	321	3.4	68	3.6	17	0.2
chr5	181.3	123664	682.2	970	5.4	7.8	3086	17.0	597	3.3	256	2.8	87	4.8	30	0.3
chr6	170.1	118657	697.7	902	5.3	7.6	3160	18.6	531	3.1	257	3.0	87	5.1	27	0.3
chr7	159.0	124355	782.3	794	5.0	6.4	3084	19.4	505	3.2	188	2.4	84	5.3	17	0.2
chr8	144.8	101910	704.0	692	4.8	6.8	2507	17.3	417	2.9	196	2.7	54	3.7	25	0.3
chr9	121.8	91710	753.0	635	5.2	6.9	2443	20.1	405	3.3	144	2.4	68	5.6	18	0.3
chr10	133.3	100918	757.3	564	4.2	5.6	2433	18.3	350	2.6	137	2.1	67	5.0	10	0.2
chr11	134.5	92192	685.3	667	5.0	7.2	3434	25.5	382	2.8	184	2.7	75	5.6	26	0.4
chr12	133.1	104467	784.7	625	4.7	6.0	3104	23.3	382	2.9	155	2.3	74	5.6	14	0.2
chr13	98.0	66141	675.0	507	5.2	7.7	1464	14.9	340	3.5	113	2.3	39	4.0	15	0.3
chr14	90.6	67930	750.0	423	4.7	6.2	2341	25.8	243	2.7	120	2.6	48	5.3	12	0.3
chr15	84.6	66556	786.3	370	4.4	5.6	2310	27.3	225	2.7	92	2.2	48	5.7	5	0.1
chr16	81.8	77620	948.8	344	4.2	4.4	2639	32.3	210	2.6	78	1.9	46	5.6	10	0.2
chr17	82.9	79545	959.3	350	4.2	4.4	3153	38.0	212	2.6	49	1.2	79	9.5	10	0.2
chr18	80.1	52029	649.6	376	4.7	7.2	1227	15.3	238	3.0	110	2.7	22	2.7	6	0.1
chr19	58.4	72255	1236.4	280	4.8	3.9	3098	53.0	141	2.4	45	1.5	68	11.6	26	0.9
chr20	63.9	52602	822.6	282	4.4	5.4	1496	23.4	152	2.4	72	2.3	54	8.4	4	0.1
chr21	40.1	28896	720.8	162	4.0	5.6	903	22.5	101	2.5	35	1.7	17	4.2	9	0.4
chr22	39.2	35007	894.0	128	3.3	3.7	1417	36.2	68	1.7	29	1.5	27	6.9	4	0.2
chrX	154.9	112141	724.0	689	4.4	6.1	2550	16.5	361	2.3	257	3.3	54	3.5	17	0.2
chrY	26.4	15751	596.3	672	25.4	42.7	601	22.8	303	11.5	199	15.1	5	1.9	165	12.5
Genome	2937.6	2194815	747.1	14830	5.0	6.8	62263	21.2	8817	3.0	3912	2.7	1571	5.3	530	0.4

Table S8. HS-MEs in the Human Reference Transcriptome

ME type	protein-coding genes #			# in NR	total # in reference	protein-coding genes (bp)			NR (bp)	total bp in reference
	CDS	5'-UTR	3'-UTR			CDS	5'-UTR	3'-UTR		
Alu	1	5	41	81	128	94	639	11,298	13,133	25,164
L1	5	3	4	45	57	319	892	1,997	8,414	11,622
SVA	32	3	7	58	100	10,623	624	7,580	21,254	40,081
LTR	2	0	1	16	19	225	0	105	6,878	7,208
Total	40	11	53	200	304	11,261	2,155	20,980	49,679	84,075

Table S9. Detail list of HS-MEs in protein coding genes

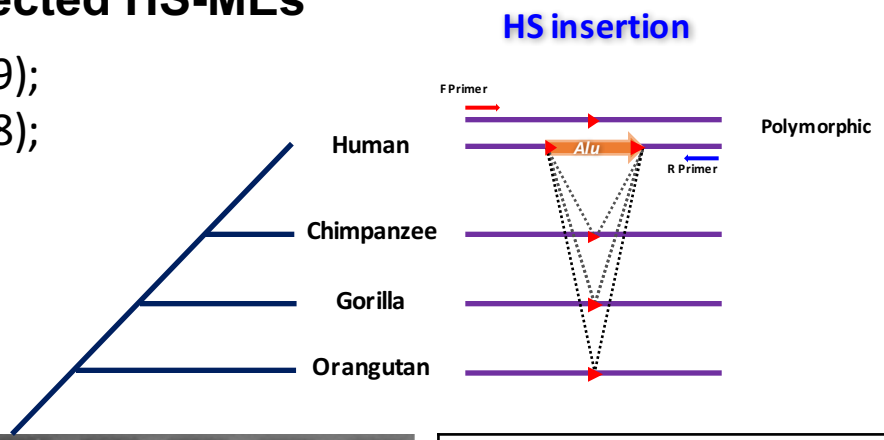
RepeatMasker ID for HS-MEs	ME position	ME strand	subfamily	Class	family	ME length (bp)	CDS position	Gene name	Transcript ID	ME-CDS size (bp)
04107359	chr9:83049539-83055571	-	L1HS	LINE	L1	6032	chr9:83055548-83055683	RASEF	ENSG00000165105.9	24
03233608	chr5:133583288-133589299	+	L1HS	LINE	L1	6011	chr5:133583265-133583396	FSTL4	ENSG00000053108.16	109
01793959_01793960	chr18:79114907-79116935	-	L1HS	LINE	L1	2029	chr18:79114994-79114999	ATP9B	ENSG00000166377.19	6
02694553	chr3:136963693-136969736	-	L1HS	LINE	L1	6043	chr3:136969273-136969378	IL20RB	ENSG00000174564.12	106
01302722	chr15:45597902-45600342	+	L1PA2	LINE	L1	2440	chr15:45597923-45597996	BLOC1S6	ENSG00000104164.10	74
03273568_03273570/03273571	chr5:156657705-156666885	-	LTR5_Hs	LTR	ERVK	9088	chr5:156660389-156660435	AC016577.1	ENSG00000279646.1	47
02431107/02431108_02431110	chr22:18938673-18947848	+	LTR5_Hs/HERVK-int	LTR	ERVK	9089	chr22:18946791-18946968	AC007326.1	ENSG00000279560.1	178
00967121	chr12:119917797-119919714	-	SVA_C	Retroposon	SVA	1917	chr12:119918001-119918372	AC004813.1	ENSG00000279777.1	372
03985473	chr8:128117822-128119386	-	SVA_D	Retroposon	SVA	1564	chr8:128118011-128118382	FKSG59	ENSG00000280151.1	372
01304702_01304703	chr15:47131719-47134222	+	SVA_D	Retroposon	SVA	2490	chr15:47133655-47134026	AC066615.1	ENSG00000259752.2	372
03132739	chr5:60430541-60432081	-	SVA_D	Retroposon	SVA	1540	chr5:60430738-60431109	FKSG52	ENSG00000280447.1	372
01508342	chr16:70224194-70225526	-	SVA_D	Retroposon	SVA	1332	chr16:70224358-70224735	FKSG63	ENSG00000280252.1	378
02207621_02207622	chr2:206355588-206357747	-	SVA_D	Retroposon	SVA	2146	chr2:206355739-206356116	AC017081.1	ENSG00000279921.1	378
01130399_01130400	chr14:20505334-20507630	+	SVA_D	Retroposon	SVA	2279	chr14:20505941-20506019	RNASE10	ENSG00000182545.6	79
03366581	chr6:31931262-31933153	-	SVA_D	Retroposon	SVA	1891	chr6:31932475-31932493	C2	ENSG00000166278.14	19
01133683_01133684	chr14:22636438-22638669	+	SVA_D	Retroposon	SVA	2213	chr14:22638102-22638473	AC243945.1	ENSG00000279510.1	372
03586447	chr7:16789065-16791103	-	SVA_D	Retroposon	SVA	2038	chr7:16789242-16789619	AC073333.1	ENSG00000280130.1	378
01870773	chr19:40647367-40649204	-	SVA_D	Retroposon	SVA	1837	chr19:40647563-40647934	FKSG66	ENSG00000279183.1	372
04269841	chrX:42285051-42286669	-	SVA_D	Retroposon	SVA	1618	chrX:42285229-42285600	FKSG70	ENSG00000279849.1	372
01216734	chr14:77416262-77416906	-	SVA_D	Retroposon	SVA	644	chr14:77416398-77416769	FKSG61	ENSG00000280308.1	372
02408498	chr21:35897707-35898625	+	SVA_D	Retroposon	SVA	918	chr21:35898058-35898429	FKSG68	ENSG00000280170.1	372
00125759	chr1:65630188-65630430	+	SVA_D	Retroposon	SVA	242	chr1:65630202-65630402	LEPR	ENSG00000116678.18	201
02792574	chr4:3537871-3539763	-	SVA_D	Retroposon	SVA	1892	chr4:3538044-3538415	FKSG51	ENSG00000280230.1	372
01293456_	chr15:40682074-40684259	+	SVA_D	Retroposon	SVA	1786	chr15:40683697-40684068	AC022405.1	ENSG00000279084.1	372
5280	chr3:130867338-130869442	+	SVA_D	Retroposon	SVA	2086	chr3:130868875-130869246	AC055733.1	ENSG00000280127.1	372
01897014	chr19:52592779-52594353	-	SVA_D	Retroposon	SVA	1574	chr19:52594212-52594304	ZNF83	ENSG00000167766.18	93
01194659	chr14:64894264-64896723	-	SVA_E	Retroposon	SVA	2459	chr14:64894339-64894710	AL135745.1	ENSG00000279654.1	372

Table S10. Contribution of HS-MEs to transcription factor binding sites (TFBS)

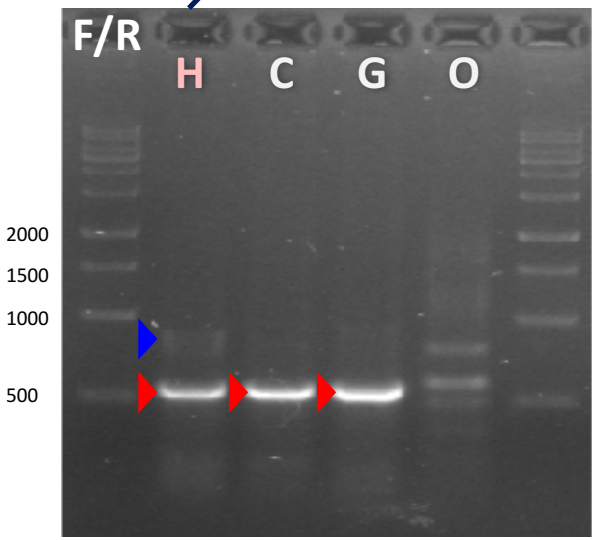
ME type	# TFBS site	#TF	# HS-ME	# total HS-ME	TFBS/ total HS-ME	% all HS-TFBS
Alu	1,621	135	581	8,817	6.6%	53.5
L1	690	114	311	3,912	7.9%	22.8
SVA	504	109	197	1,571	12.5%	16.6
LTR	217	58	78	530	14.7%	7.2
Total	3,032	142	1,167	14,830	7.9%	100.0

Fig. S1: PCR validation results 4 selected HS-MEs

A: HS_*Alu*: chr6:62053989-62054300 (hg19);
chr6:61183414-61183725 (hg38);



PCR Mixture		
1	EF taq polymerase	25 ul
2	Forward primer (4 pmol)	7.5 ul
3	Reverse primer (4 pmol)	7.5 ul
4	D.W	10 ul
5	DNA template (10 ng/ul)	2 ul
Total		52 ul

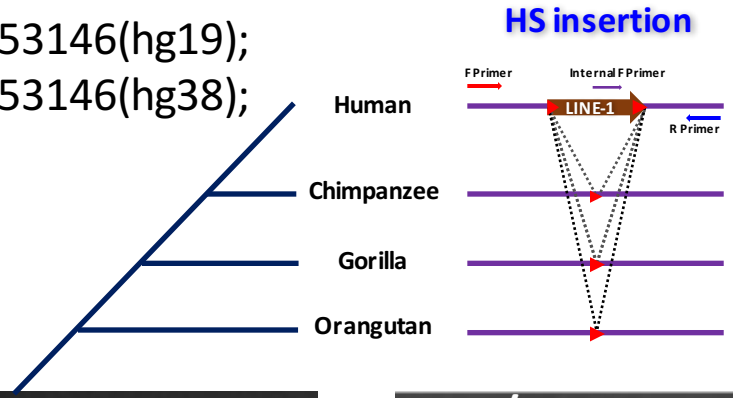


PCR Condition (35 cycles)			
1	Pre-denaturation	95℃	5 mins
2	Denaturation	95℃	30 s
3	Annealing	55℃	30 s
4	Extension	72℃	1 min
5	Termination	72℃	5 mins
6	Hold	4℃	∞

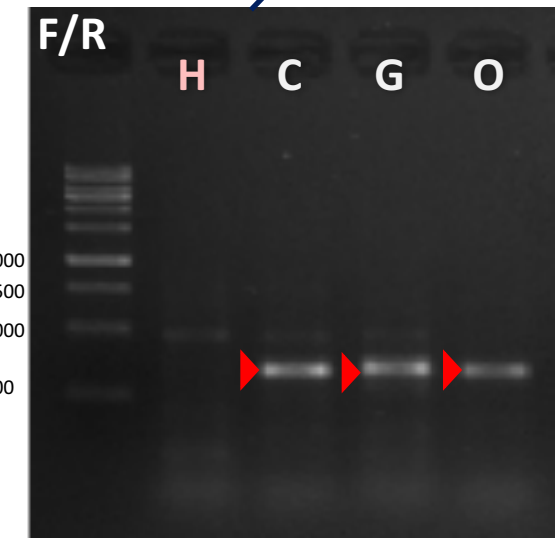
PCR primer information	
Forward Primer	Reverse primer
TCAATGCCTGGTTTCAAAGG	GACAAAGTCTCACTATGTTGCTC

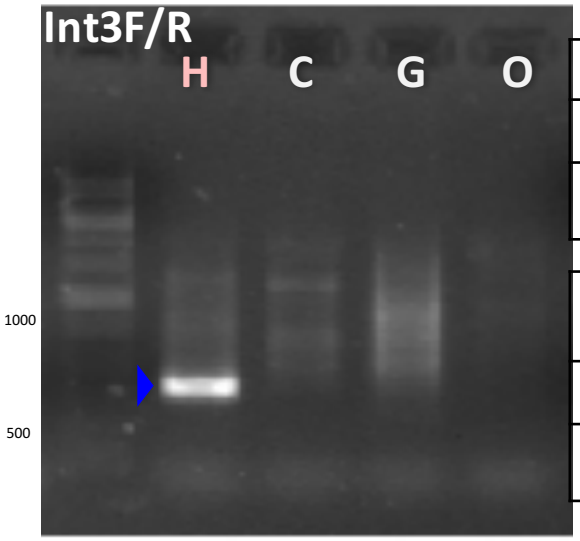
Expected PCR product size			
Human (empty size)	Chimpanzee	Gorilla	Orangutan
871 bp (550 bp)	549 bp	550 bp	?

B: HS_L1: chr4:87347103-87353146(hg19);
chr4:87347103-87353146(hg38);



PCR Mixture		
1	EF taq polymerase	25 ul
2	Forward primer (4 pmol)	7.5 ul
3	Reverse primer (4 pmol)	7.5 ul
4	D.W	10 ul
5	DNA template (10 ng/ul)	2 ul
Total		52 ul





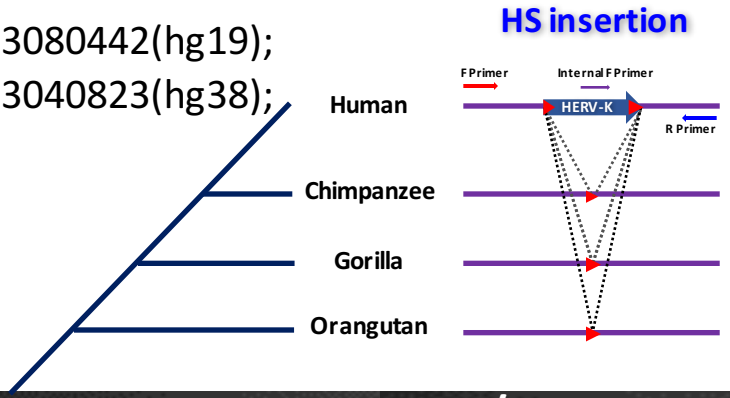
PCR Condition (35 cycles) FR			
3	Annealing	55℃	30 s
4	Extension	72℃	1 min

PCR Condition (35 cycles) Int3FR			
3	Annealing	59℃	30 s
4	Extension	72℃	1 min

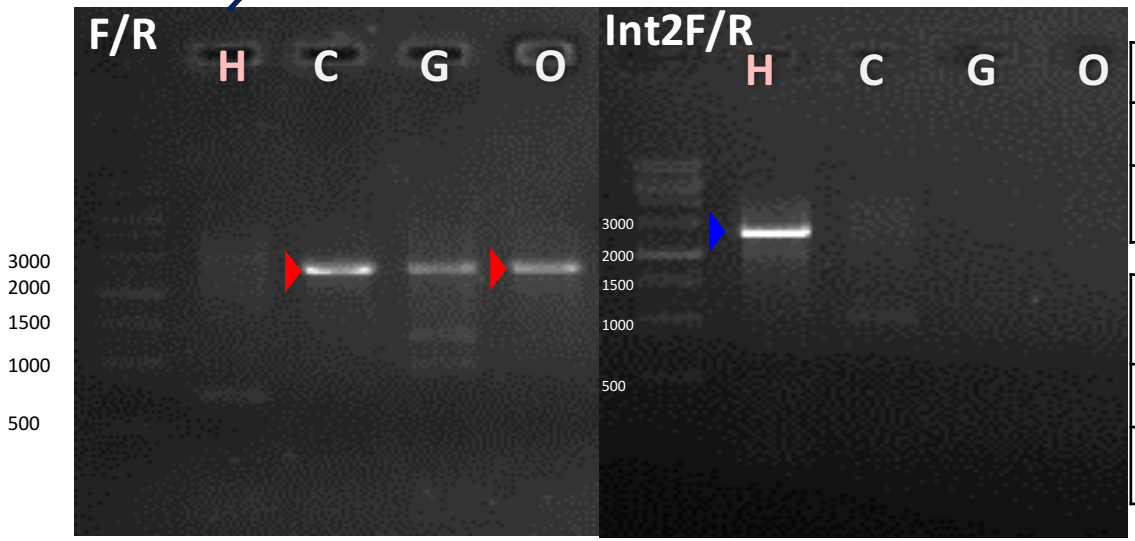
PCR primer information		
Forward Primer	Reverse primer	Internal Primer
GCTGGTACTAAAGTAGACCC	TGTGCTAAGCTGGGTGTGGC	CAAAGACTTGGAACCAACCC

Expected PCR product size				
	Human (empty size)	Chimpanzee	Gorilla	Orangutan
F/R	6730 bp (675 bp)	685 bp	687 bp	681 bp
Int3F/R	788 bp	-	-	-

C: HS_HERV-K: chr7:23079474-23080442(hg19);
chr7:23039855-23040823(hg38);



PCR Mixture		
1	EF taq polymerase	10 ul
2	Forward primer (10 pmol)	1 ul
3	Reverse primer (10 pmol)	1 ul
4	D.W	8 ul
5	DNA template (10 ng/ul)	2 ul
Total		22 ul



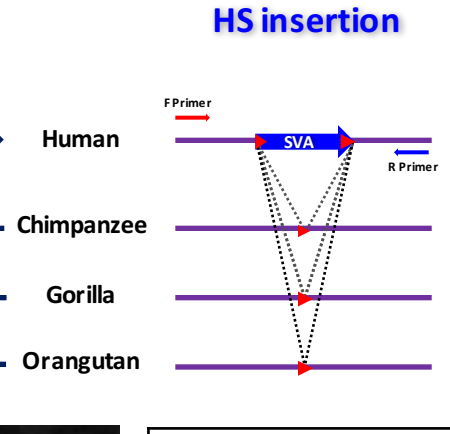
PCR Condition (35 cycles) FR			
3	Annealing	60℃	40 s
4	Extension	72℃	3 min

PCR Condition (35 cycles) Int2FR			
3	Annealing	58℃	40 s
4	Extension	72℃	3 min

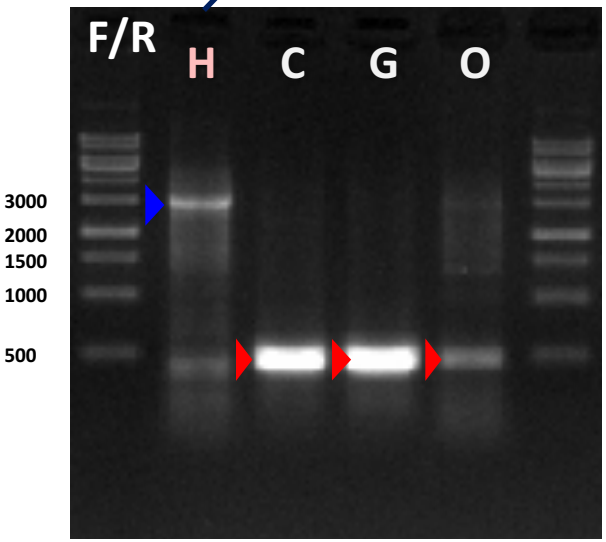
PCR primer information		
Forward Primer	Reverse primer	Internal Primer
CACTTAAGACCCTGTCTCCCC	CACCAAACAAATCCACTGGC	ATACTAAGGGAACTCAGAGGC

Expected PCR product size				
	Human (empty size)	Chimpanzee	Gorilla	Orangutan
F/R	9753 bp (1793 bp)	2715 bp	?	2698 bp
Int2F/R	2695 bp	-	-	-

D: HS_SVA: chr2:192261918-192263988(hg19);
chr2:191397192-191399262(hg38);



PCR Mixture		
1	EF taq polymerase	25 ul
2	Forward primer (4 pmol)	5 ul
3	Reverse primer (4 pmol)	5 ul
4	D.W	15 ul
5	DNA template (10 ng/ul)	2 ul
Total		52 ul



PCR Condition (35 cycles)			
1	Pre-denaturation	95℃	5 mins
2	Denaturation	95℃	30 s
3	Annealing	56℃	40 s
4	Extension	72℃	3min 10s
5	Termination	72℃	10 mins
6	Hold	4℃	∞

PCR primer information	
Forward Primer	Reverse primer
GGAAAGTGGTCAGAACAGGC	AACCATCTTGCAGGCTACCC

Expected PCR product size			
Human (empty size)	Chimpanzee	Gorilla	Orangutan
2706 bp (507 bp)	506 bp	509 bp	507 bp

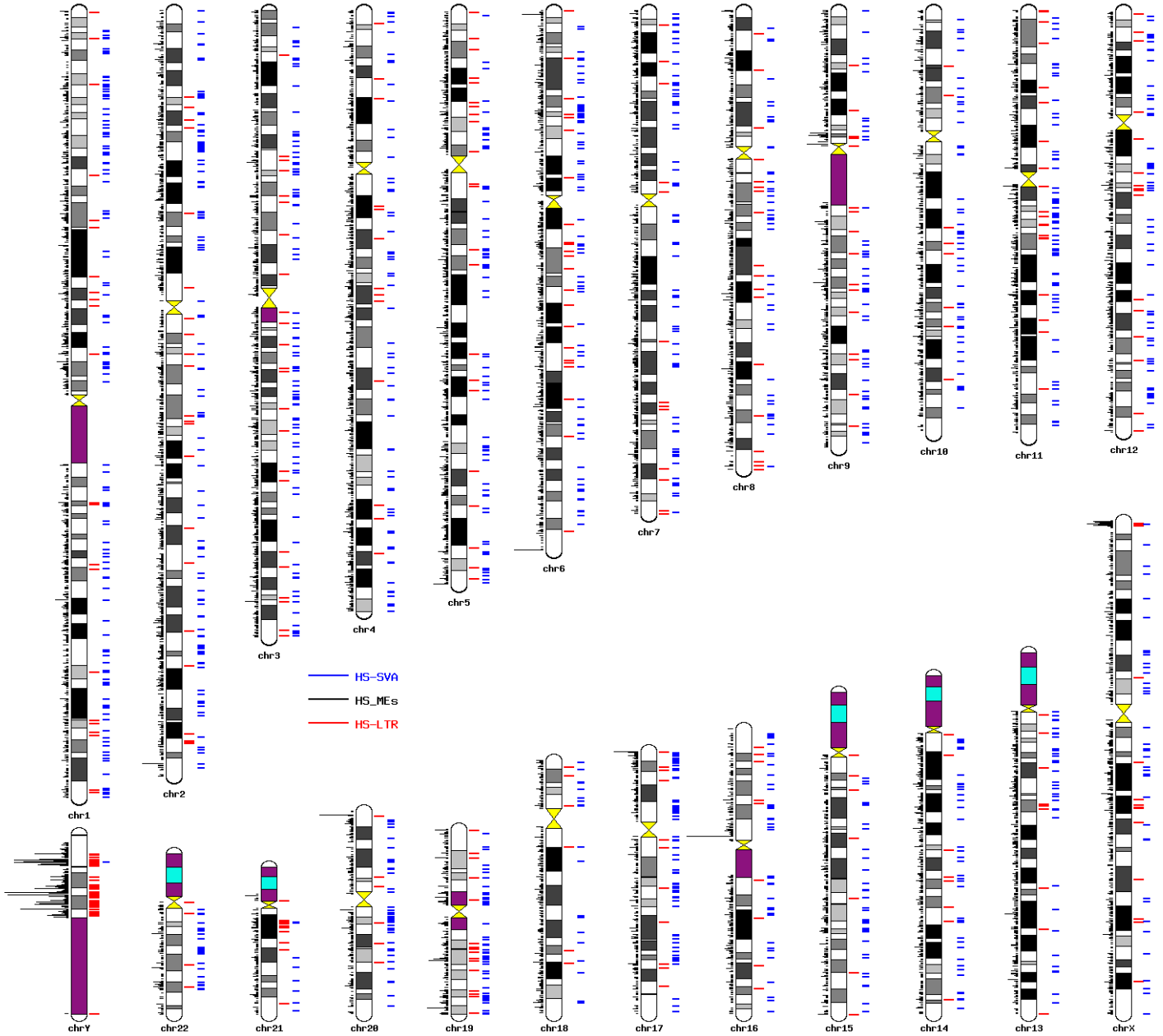


Fig. S2: Genome plots of HS-MEs. HS-MEs were plotted on the human chromosome ideograms (based on GRCh 38). The left side of the chromosome indicates the relative frequency of all HS-MEs (counts per 0.5Mb genomic region), while red track on the right represents HS-LTRs and the blue track represents HS-SVS (1 tick per entry for both tracks).