Supplementary data

Table S1. Site patterns observed across non CpG censored alignments. Patterns were observed at sites classified as one of: ERV (PV); selfish DNA (RM+); or non-repetitive or repetitive but non-selfish (RM-).

chimp:human	autosomal			X-linked		
	PV	RM+	RM-	PV	RM+	RM-
A:A	591392	1603551	1145366	26509	83350	43123
A:T	888	2496	1390	38	105	45
A:G	6651	14093	7336	242	532	225
A:C	1301	3104	1860	53	127	55
A:?	0	0	0	0	0	0
T:A	984	2572	1456	28	90	41
T:T	597941	1609580	1151417	26035	87639	43695
T:G	1396	3302	1787	58	125	68
T:C	6507	13999	7213	241	558	247
T:?	0	0	0	0	0	0
G:A	6019	13776	7188	241	585	214
G:T	1364	3528	2002	47	131	56
G:G	476441	1189167	734803	23851	59232	25988
G:C	1481	3531	1942	57	146	73
G:?	0	0	0	0	0	0
C:A	1449	3442	1914	38	117	58
C:T	6153	13605	7195	216	515	249
C:G	1420	3558	1858	54	119	72
C:C	486320	1182717	729658	19527	58921	26391
C:?	0	0	0	0	0	0
?:A	5	0	2	0	0	0
?:T	0	1	2	0	1	0
?:G	1	0	1	0	1	0
?:C	1	4	0	0	0	0
?:?	0	0	0	0	0	0
total	2187714	5666026	3804390	97235	292294	140600

Table S2. Dinucleotide pattern counts. Patterns were observed at sites classified as one of: ERV (PV); selfish DNA (RM+); or non-repetitive or repetitive but non-selfish (RM-). Pattern classification was performed on both CpG censored and non CpG censored data.

	uncensored			censored		
pattern	PV	RM+	RM-	PV	RM+	RM-
AA-GG|TT-CC|GG-AA|CC-TT	67	127	73	36	85	58
AC-AG|AG-AC|GT-CT|CT-GT	1821	4630	2649	1441	3921	2245
CG-GA|TC-CG|GA-CG|CG-TC	24	39	17	20	33	17
GC-AA|GC-TT|AA-GC|TT-GC	32	95	38	21	70	32
AA-AT|TT-AT|AT-TT|AT-AA	1020	2941	1698	1020	2941	1698
GA-AA|TC-TT|AA-GA|TT-TC	4988	11606	6371	2864	7494	4695
CA-CC|TG-GG|CC-CA|GG-TG	1678	3807	1895	1410	3172	1568
AA-CC|TT-GG|CC-AA|GG-TT	16	59	22	13	47	21
TG-TT|AA-CA|TT-TG|CA-AA	1684	4456	2627	1684	4456	2627
CT-CA|TG-AG|CA-CT|AG-TG	1098	2773	1344	1098	2773	1344
CG-AA|CG-TT|AA-CG|TT-CG	28	40	19	28	40	19
AG-TA|CT-TA|TA-CT|TA-AG	13	48	22	13	48	22
GT-CG|CG-AC|AC-CG|CG-GT	7	21	12	6	16	10
GA-CT|TC-AG|AG-TC|CT-GA	4	28	10	4	25	9
TT-TT|AA-AA	379597	1032906	788505	379597	1032906	788505
TT-GT|GT-TT|AC-AA|AA-AC	1513	3743	2321	1267	3230	1992
AC-TT|AA-GT|TT-AC|GT-AA	19	68	25	18	48	20
AA-AG|CT-TT|AG-AA|TT-CT	4967	12324	7438	4967	12324	7438
CC-TC|GA-GG|GG-GA|TC-CC	4251	9014	4818	3995	8651	4635
AG-GT|CT-AC|AC-CT|GT-AG	25	64	34	21	38	24
CG-GC|GC-CG	4	8	3	2	6	1
TT-AG|CT-AA|AG-TT|AA-CT	10	39	14	10	39	14
CT-CC|GG-AG|AG-GG|CC-CT	7385	13982	6660	3783	8107	4422
AG-AG|CT-CT	332695	832303	535497	332695	832303	535497
AG-GC|GC-CT|CT-GC|GC-AG	22	67	28	10	40	22
CA-AG|CT-TG|AG-CA|TG-CT	102	227	91	102	227	91
CT-GG|CC-AG|AG-CC|GG-CT	12	38	18	8	34	14
TA-GC|GC-TA	2	9	5	2	8	5
AG-CG|CG-CT|CT-CG|CG-AG	896	1977	1128	0	0	0
GC-GC	104712	260685	147021	93799	234971	133678
TA-CG|CG-TA	45	107	37	45	107	37
GA-GA|TC-TC	267882	700469	459056	254279	672557	444606
AT-TA|TA-AT	4	16	11	4	16	11
AT-CT|AT-AG|CT-AT|AG-AT	1462	3650	2172	1462	3650	2172
AG-CT|CT-AG	12	17	12	12	17	12
AC-GG|CC-GT|GT-CC|GG-AC	30	72	16	17	38	8
TC-GA|GA-TC	3	7	9	3	6	5

AC-AC|GT-GT	221387	594562	381313	209715	568402	364188
AT-GC|GC-AT	48	146	57	17	62	30
AT-GA|AT-TC|TC-AT|GA-AT	20	67	27	14	53	20
AC-CC|GG-GT|GT-GG|CC-AC	1381	3078	1529	1320	2967	1456
GA-GC|TC-GC|GC-GA|GC-TC	1184	2790	1404	922	2255	1111
TA-TG|TA-CA|TG-TA|CA-TA	4684	12823	7752	4684	12823	7752
CC-GG|GG-CC	8	17	3	5	13	3
AC-CA|GT-TG|TG-GT|CA-AC	11	41	20	11	36	19
GC-GG|GC-CC|CC-GC|GG-GC	1255	2883	1456	959	2339	1178
GG-TC|GA-CC|CC-GA|TC-GG	6	24	11	4	20	11
CC-CC|GG-GG	291451	631781	357328	274771	601314	340033
AT-CG|CG-AT	2	4	2	2	4	2
CG-TG|CG-CA|CA-CG|TG-CG	10365	19695	8493	0	0	0
CA-CA|TG-TG	316037	876553	540776	316037	876553	540776
CC-AT|AT-GG|GG-AT|AT-CC	30	63	33	15	44	22
AC-GT|GT-AC	61	137	56	17	53	31
TG-AT|CA-AT|AT-CA|AT-TG	7	24	12	7	24	12
GA-CA|CA-GA|TC-TG|TG-TC	1642	4399	2452	1392	3869	2199
AG-GA|CT-TC|GA-AG|TC-CT	79	156	76	43	91	56
GC-TG|GC-CA|CA-GC|TG-GC	5	20	10	4	17	8
TA-CC|CC-TA|GG-TA|TA-GG	14	45	23	12	38	22
AT-AT	143864	431368	319021	143864	431368	319021
CA-GG|TG-CC|GG-CA|CC-TG	98	219	62	82	194	60
GA-AC|GT-TC|AC-GA|TC-GT	16	59	20	11	32	12
TG-GA|GA-TG|TC-CA|CA-TC	19	62	20	18	54	19
CG-CG	20819	44375	26458	0	0	0
TT-AA|AA-TT	5	22	7	5	22	7
TG-CA|CA-TG	718	1179	377	0	0	0
TA-TA	130756	361441	280640	130756	361441	280640
GT-GC|GC-AC|AC-GC|GC-GT	5374	11537	5170	2663	6296	3356
TC-TA|GA-TA|TA-TC|TA-GA	1178	3012	1913	1024	2691	1711
AA-TC|TT-GA|GA-TT|TC-AA	13	27	23	12	25	23
TA-AA|AA-TA|TT-TA|TA-TT	887	2376	1617	887	2376	1617
TT-CA|CA-TT|TG-AA|AA-TG	21	54	17	21	54	17
GT-AT|AC-AT|AT-GT|AT-AC	7953	18962	10935	4667	12300	7413
TA-GT|TA-AC|AC-TA|GT-TA	6	17	11	6	17	11
GA-GT|GT-GA|TC-AC|AC-TC	727	1915	976	694	1838	938
CG-CC|GG-CG|CG-GG|CC-CG	1061	2105	1079	0	0	0
TG-AC|AC-TG|CA-GT|GT-CA	10	34	11	10	31	8

Table S3. Source organisms for *pol* probes used in this study grouped by ERV class of virus.

	Class I	Class II	Class III	NA
Anseriformes	1	5	0	0
Anura	9	0	1	0
Apterygiformes	0	4	0	0
Artiodactyla	10	7	0	0
Caecilia	2	0	2	0
Carnivora	30	4	0	0
Casuariformes	0	2	0	0
Caudata	4	0	0	0
Cetacea	3	1	0	0
Chiroptera	27	0	0	0
Chondricthyes	1	0	0	0
Columbiformes	0	1	0	0
Crocodilia	1	0	0	0
Cypriniformes	1	0	0	0
Didelphimorphia	2	0	1	0
Diprotodontia	0	1	0	0
Falconiformes	1	6	0	0
Galliformes	0	10	0	0
Gaviiformes	0	2	0	0
Gruiformes	0	2	0	0
Insectivora	1	1	0	0
Lagomorpha	1	2	0	0
Marsupiala	2	0	0	0
Marsupialia	2	2	0	0
Monotremata	3	2	0	0
Insecta	0	0	0	2
Fungi	0	0	0	2
Passeriformes	1	11	0	0
Perciformes	1	0	1	0
Perissodactyla	1	1	0	0
Phoenicopteriformes	0	1	0	0
Piciformes	0	3	0	0
Pinnipedia	1	0	0	0

Primates	198	51	54	0
Rheiformes	0	2	0	0
Rodentia	249	16	0	0
Scandentia	1	0	0	0
Sphenisciformes	0	1	0	0
Sphenodontia	1	0	1	0
Squamata	4	2	0	0
Strigiformes	0	2	0	0
Struthioniformes	0	1	0	0
Teleostii	1	0	0	0
Testudines	2	0	0	0
Tinamiformes	0	1	1	0
Xenarthra	1	0	0	0

Table S4. Viral diversity of *pol* probes used in this study.

	endogenous	exogenous	exogenous/endogenous
A-type	10	0	0
Alpharetrovirus	2	1	0
Avian-IIA	7	0	0
Avian-IIB	8	0	0
Betaretrovirus	14	3	2
Deltaretrovirus	0	2	0
Dev	3	0	0
Epsilonretrovirus	0	2	0
ERV-9	7	0	0
HERV-AC018462	4	0	0
HERV-AC096774	1	0	0
HERV-ADP	8	0	0
HERV-E	8	0	0
HERV-F	3	0	0
HERV-F type_b	7	0	0
HERV-F type_c	2	0	0
HERV-FRD	2	0	0
HERV-H	57	0	0
HERV-I	14	0	0
HERV-K(HML2)	14	0	0
HERV-K(HML5)	14	0	0
HERV-K(HML6)	9	0	0
HERV-K(HML9)	3	0	0
HERV-L	44	0	0
HERV-L type_b	7	0	0
HERV-P	5	0	0
HERV-R	7	0	0
HERV-R type_b	3	0	0
HERV-R type_c	3	0	0
HERV-S	5	0	0
HERV-T	13	0	0
HERV-U3	1	0	0
HERV-W	16	0	0

HERV-XA	4	0	0
HERV-Z69907	5	0	0
Lentivirus	0	4	0
LPDV-group	3	1	0
LTR-retrotransposons	4	0	0
RRHERV-I	9	0	0
SpeV	1	0	0
spumavirus	0	4	0
Unclassified	416	5	4

Table S5. The model of fitness effects of mutations into ERVs (PV) used in this study.

			male			female		
linkage	A	genotype	A_1A_1	A_1A_2	A_2A_2	A_1A_1	A_1A_2	A_2A_2
		fitness	1	$1 + h\ s_m$	$1 + s_m$	1	$1 + h\ s_f$	$1 + s_f$
	X	genotype	A_1		A_2	A_1A_1	A_1A_2	A_2A_2
		fitness	1		$1 + s_m$	1	$1 + h\ s_f$	$1 + s_f$

Figure S1. GC content of PV region by ERV kind. ERV kind was assigned using the best matching viral *pol* probe (see Detecting ERVs in Methods and Additional File 2).

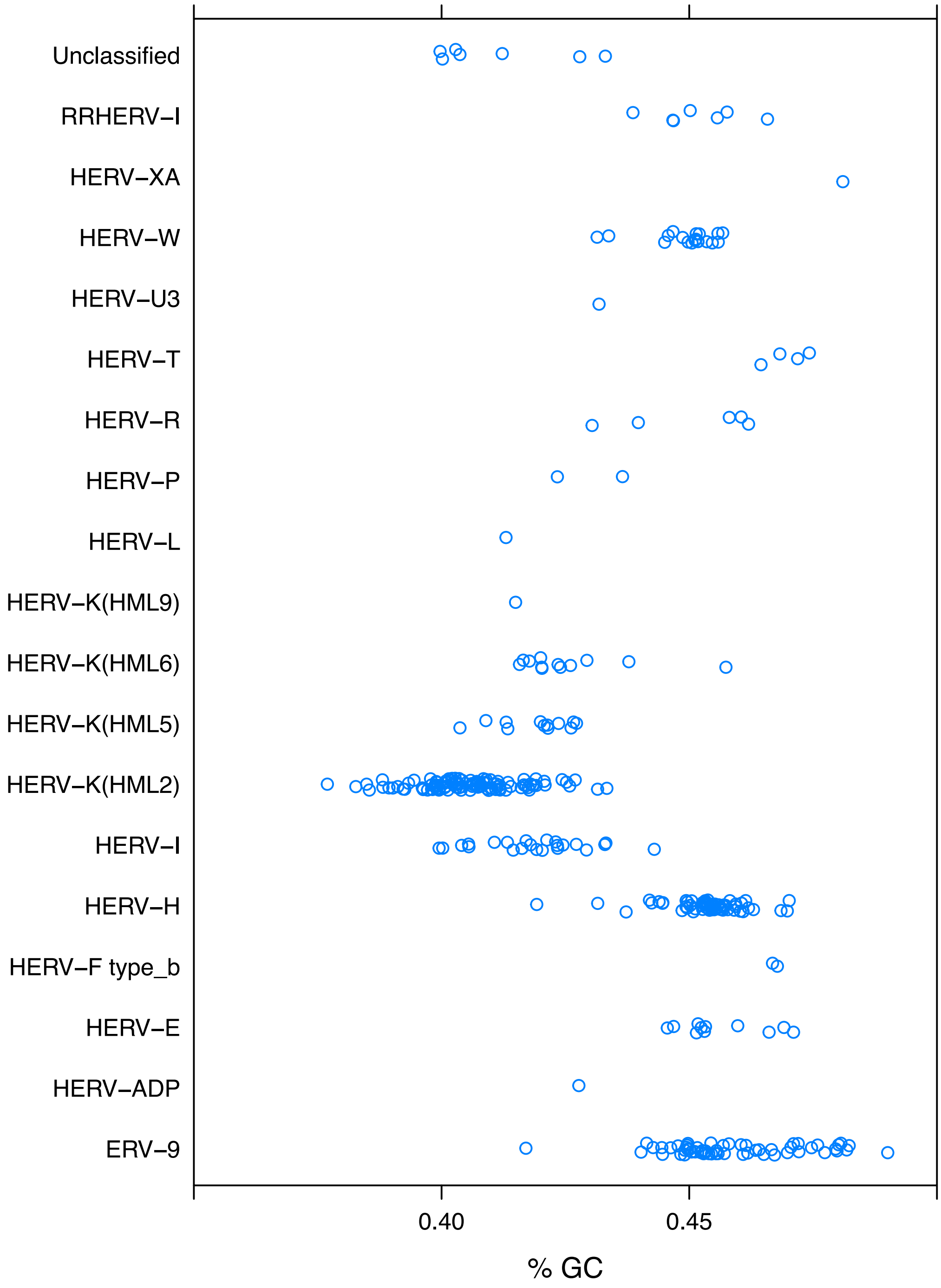


Figure S2. Dinucleotide frequencies grouped by sequence classification and transition count: no transition (0); single transition (1); double transition (2).

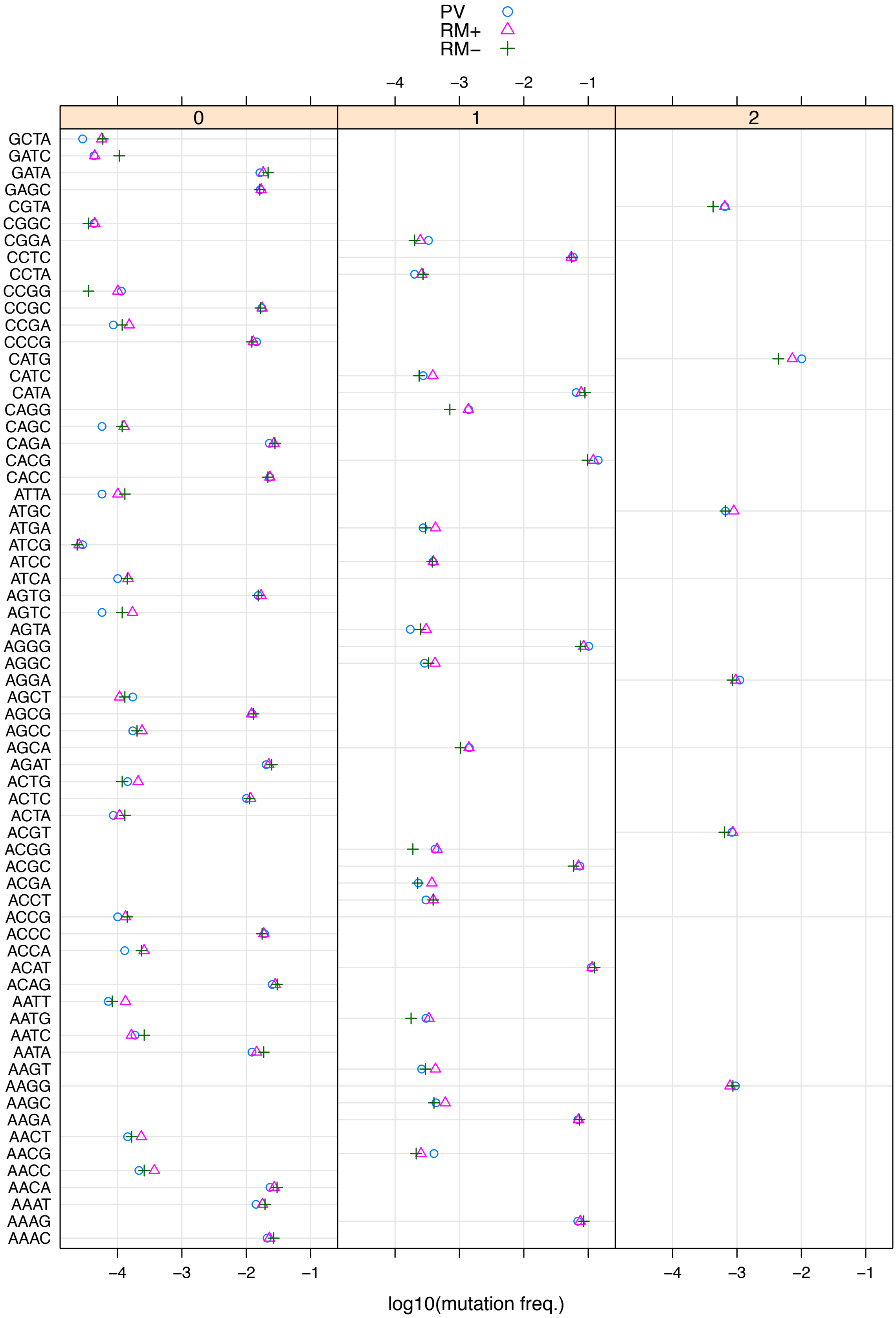
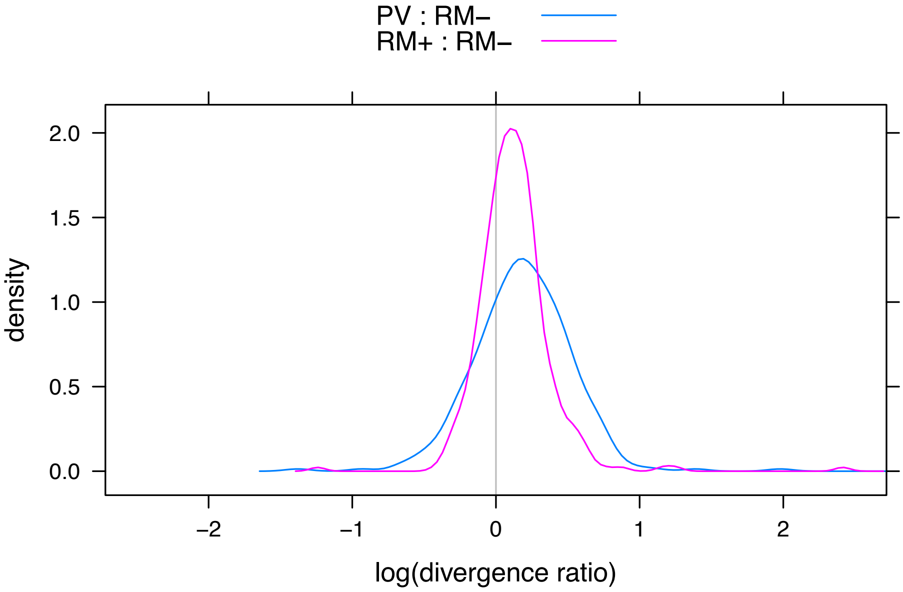


Figure S3. Distribution of divergence of ERVs (PV) and other selfish DNA (RM+) versus paired non-repetitive or non-selfish flank (RM-).


PV : RM–
RM+ : RM–
density
log(divergence ratio)