Table S3 Individual repeats and repeat families that are significantly enriched in hotspots.

	Hotspots	Coldspots	P-value*	Relative Risk
Repeat Family				
Simple_repeat	20025	18157	6.33E-20	1.103
Low_complexity	10146	9562	0.00171	1.061
L1	12842	12285	0.0235	1.045
Individual Repeats				
L1Md_F2	1739	1138	3.35E-26	1.528
MTA_Mm	616	366	1.52E-12	1.683
L1Md_T	501	290	6.55E-11	1.728
GC_rich	335	186	7.45E-08	1.801
GA-rich	1757	1399	2.23E-07	1.256
L1Md_F3	453	291	3.48E-06	1.557
L1Md_A	350	211	5.31E-06	1.659
MTA_Mm-int	122	51	7.58E-05	2.392
L1_Mus1	794	595	0.000115	1.334
L1Md_F	128	62	0.00214	2.065
B1_Mus2	2520	2202	0.00439	1.144
Simple Repeats				
(GA)n	2942	1780	1.24E-61	1.653
(TC)n	2858	1764	1.20E-55	1.62
(TA)n	2916	1829	1.98E-53	1.594
(CA)n	5986	5114	1.48E-13	1.171
(GAAA)n	715	452	1.50E-11	1.582
(TG)n	5961	5153	2.10E-11	1.157
(T)n	1283	948	1.56E-09	1.353
(TTTC)n	672	442	6.44E-09	1.52
(A)n	1302	977	1.18E-08	1.333
(GGAA)n	434	272	1.3E-06	1.596
(TCTA)n	660	467	0.000011	1.413
(GAA)n	304	189	0.00028	1.608
(TTTTC)n	234	137	0.000603	1.708

[*] P-value corrected using Bonferroni correction