

Additional file 2

Genome-wide average substitution rates and dataset sizes for four major repeat classes.

a)

	LINE		MIR		LTR		DNA	
	Sub. rate	Size	Sub. rate	Size	Sub. rate	Size	Sub. rate	Size
Primate	0.056	35.0Mbp	0.054	21.0Mbp	0.060	21.4Mbp	0.057	15.2Mbp
Rodent	0.127	5.5Mbp	0.119	2.5Mbp	0.136	2.9Mbp	0.126	1.6Mbp
Laurasiatheria	0.236	21.5Mbp	0.235	15.3Mbp	0.256	15.1Mbp	0.241	11.4Mbp

Total base pairs, the number of blocks and the average size of blocks for each class.

b)

LINE	primate rodent		laurasia-theria		laurasia-theria rodent	
	primate	rodent	primate	laurasia-theria	laurasia-theria	rodent
Correlation	0.120		0.149		0.332	
p-value	7.47e-167		0.0		0.0	
Total block	52217		197317		13638	
Total (bp)	8.43M	5.46M	26.94M	21.50M	1.49M	1.21M
Average size (bp)	175	113	145	115	153	124

c)

SINE	primate rodent		laurasia-theria		laurasia-theria rodent	
	primate	rodent	primate	laurasia-theria	laurasia-theria	rodent
Correlation	0.060		0.085		0.1388	
p-value	1.6e-28		7.8e-315		6.7e-75	
Total block	29741		198195		17225	
Total (bp)	3.08M	2.33M	18.15M	15.06M	1.62M	1.46M
Average size (bp)	103	78	91	76	94	85

d)

LTR			laurasia-		laurasia-	
	primate	rodent	primate	theria	theria	rodent
Correlation	0.078969		0.115971		0.0880	
p-value	4.64e-36		0.0		1.56e-19	
Total block	25130		137879		10504	
Total (bp)	4.18M	2.88M	18.55M	15.11M	1.49M	1.20M
Average size (bp)	178	123	142	115	153	124

DNA			laurasia-		laurasia-	
	primate	rodent	primate	theria	theria	rodent
Correlation	0.0612		0.1165		0.17002722	
p-value	2.54e-17		0.0		2.365e-72	
Total block	19069		139970		11034	
Total (bp)	2.16M	1.63M	13.45M	11.33M	1.11M	0.97M
Average size (bp)	122	92	101	85	109	95