

Additional File 6. Average (standard deviation) polymorphism estimates for lncRNA and their flanking protein coding genes in human using a distance threshold of 20,000 nt. PE: positional equivalent.

	π_T	θ_T	Tajima's D	k
coding exons	$5.48 \times 10^{-4} (5.25 \times 10^{-4})$	$6.67 \times 10^{-4} (4.73 \times 10^{-4})$	-0.38(0.84)	$8.08 \times 10^{-4} (8.94 \times 10^{-4})$
coding introns	$9.03 \times 10^{-4} (4.71 \times 10^{-4})$	$1.0 \times 10^{-3} (4.12 \times 10^{-4})$	-0.34(0.62)	$1.32 \times 10^{-3} (8.11 \times 10^{-4})$
upstream coding	$1.03 \times 10^{-3} (9.99 \times 10^{-4})$	$1.04 \times 10^{-3} (7.57 \times 10^{-4})$	-0.03(0.91)	$1.49 \times 10^{-3} (1.75 \times 10^{-3})$
lncRNA exons	$1.07 \times 10^{-3} (8.99 \times 10^{-4})$	$1.17 \times 10^{-3} (6.96 \times 10^{-4})$	-0.21(0.86)	$1.59 \times 10^{-3} (1.57 \times 10^{-3})$
lncRNA introns	$1.03 \times 10^{-3} (7.73 \times 10^{-4})$	$1.11 \times 10^{-3} (5.59 \times 10^{-4})$	-0.22(0.76)	$1.47 \times 10^{-3} (1.2 \times 10^{-3})$
upstream lncRNA	$1.13 \times 10^{-3} (1.35 \times 10^{-3})$	$1.21 \times 10^{-3} (8.76 \times 10^{-4})$	-0.13(0.93)	$1.68 \times 10^{-3} (1.98 \times 10^{-3})$
PE lncRNA exons	$9.88 \times 10^{-4} (7.84 \times 10^{-4})$	$1.13 \times 10^{-3} (6.48 \times 10^{-4})$	-0.25(0.90)	$1.48 \times 10^{-3} (1.42 \times 10^{-3})$
PE lncRNA introns	$1.04 \times 10^{-3} (7.46 \times 10^{-4})$	$1.08 \times 10^{-3} (4.57 \times 10^{-4})$	-0.19(0.77)	$1.43 \times 10^{-3} (9.1 \times 10^{-4})$
Controls lncRNA exons	$1.05 \times 10^{-3} (8.63 \times 10^{-4})$	$1.16 \times 10^{-3} (6.65 \times 10^{-4})$	-0.21(0.85)	$1.45 \times 10^{-3} (1.51 \times 10^{-3})$
Controls lncRNA introns	$1.00 \times 10^{-3} (6.65 \times 10^{-4})$	$1.08 \times 10^{-3} (5.05 \times 10^{-4})$	-0.23(0.75)	$1.45 \times 10^{-3} (1.30 \times 10^{-3})$
ancestral repeats	$1.52 \times 10^{-3} (1.82 \times 10^{-3})$	$1.69 \times 10^{-3} (1.14 \times 10^{-3})$	-0.12(0.92)	$2.36 \times 10^{-3} (3.49 \times 10^{-3})$