

Additional File 5. Average (standard deviation) polymorphism estimates for lncRNA and their flanking protein coding genes in human using a distance threshold of 5,000 nt. PE: positional equivalent.

	π_T	θ_T	Tajima's D	k
coding exons	$5.10 \times 10^{-4} (5.23 \times 10^{-4})$	$6.82 \times 10^{-4} (4.86 \times 10^{-4})$	-0.41(0.84)	$8.27 \times 10^{-4} (9.51 \times 10^{-4})$
coding introns	$8.99 \times 10^{-4} (4.84 \times 10^{-4})$	$9.97 \times 10^{-4} (4.28 \times 10^{-4})$	-0.34(0.64)	$1.32 \times 10^{-3} (8.46 \times 10^{-4})$
upstream coding	$9.89 \times 10^{-4} (9.88 \times 10^{-4})$	$9.91 \times 10^{-4} (6.93 \times 10^{-4})$	-0.03(0.93)	$1.34 \times 10^{-3} (1.52 \times 10^{-3})$
lncRNA exons	$1.05 \times 10^{-3} (8.41 \times 10^{-4})$	$1.16 \times 10^{-3} (6.60 \times 10^{-4})$	-0.21(0.86)	$1.58 \times 10^{-3} (1.52 \times 10^{-3})$
lncRNA introns	$1.03 \times 10^{-3} (7.91 \times 10^{-4})$	$1.09 \times 10^{-3} (5.49 \times 10^{-4})$	-0.22(0.89)	$1.48 \times 10^{-3} (1.21 \times 10^{-3})$
upstream lncRNA	$1.09 \times 10^{-3} (1.06 \times 10^{-3})$	$1.19 \times 10^{-3} (7.97 \times 10^{-4})$	-0.14(0.92)	$1.62 \times 10^{-3} (1.68 \times 10^{-3})$
PE lncRNA exons	$9.44 \times 10^{-4} (7.24 \times 10^{-4})$	$1.10 \times 10^{-3} (5.97 \times 10^{-4})$	-0.26(0.90)	$1.52 \times 10^{-3} (1.46 \times 10^{-3})$
PE lncRNA introns	$1.03 \times 10^{-3} (7.60 \times 10^{-4})$	$1.06 \times 10^{-3} (4.32 \times 10^{-4})$	-0.17(0.79)	$1.45 \times 10^{-3} (9.54 \times 10^{-4})$
Controls lncRNA exons	$1.02 \times 10^{-3} (8.13 \times 10^{-4})$	$1.16 \times 10^{-3} (6.55 \times 10^{-4})$	-0.23(0.85)	$1.46 \times 10^{-3} (1.51 \times 10^{-3})$
Controls lncRNA introns	$9.64 \times 10^{-4} (6.45 \times 10^{-4})$	$1.07 \times 10^{-3} (4.95 \times 10^{-4})$	-0.28(0.75)	$1.45 \times 10^{-3} (1.31 \times 10^{-3})$
ancestral repeats	$1.53 \times 10^{-3} (1.83 \times 10^{-3})$	$1.67 \times 10^{-3} (1.16 \times 10^{-3})$	-0.12(0.92)	$2.28 \times 10^{-3} (3.39 \times 10^{-3})$