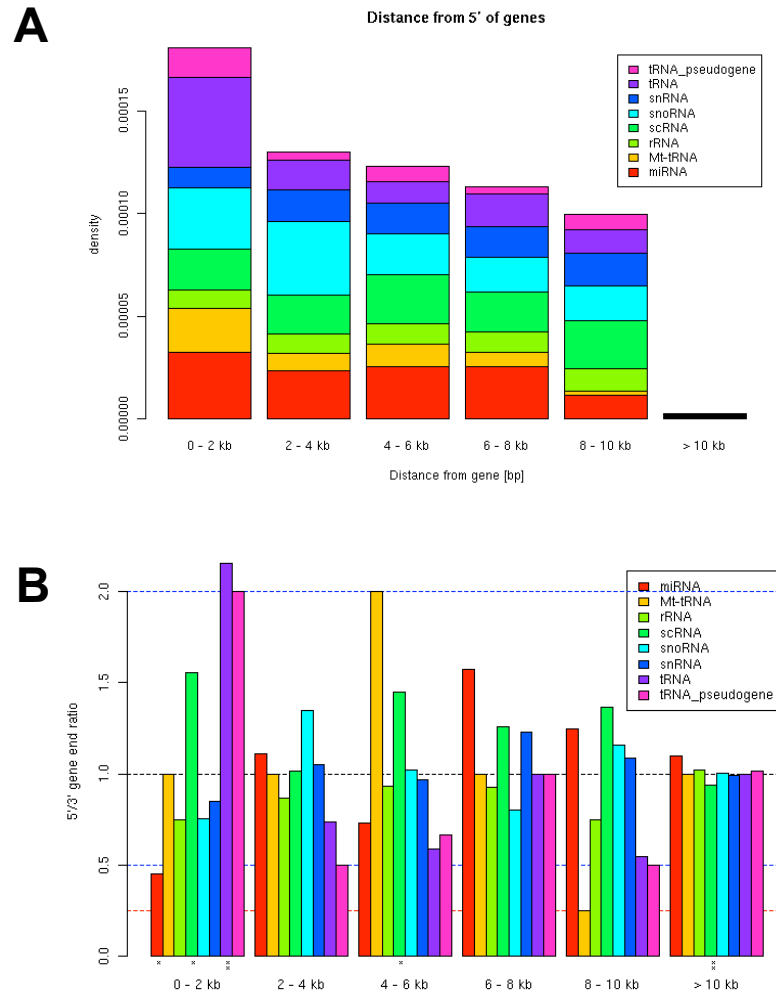


Fig. S1



**Figure S1.** (A) RNA gene distance from transcription start of Pol II genes after joining neighboring RNA loci. The density of RNA genes near transcription starts of RefSeq genes is plotted according to their absolute distance from the starts. All RNA genes of the same name that are closer than 1 kb were grouped. (B) We compared the distribution of RNA genes near 5' vs. 3' ends of protein-coding genes within six discrete intervals (0-2 kb, 2-4 kb, 4-6 kb, 6-8 kb, and >10 kb). Black dashed line indicates 5'/3' ratio of 1 (random expectation), blue and red lines indicate 2-fold and 4-fold ratios, respectively. Marks at the bottom indicate statistical significance using the Fisher exact (binomial) test (\* p-value < 0.05, \*\* < 0.01). All RNA genes of the same name that are closer than 1kb were grouped.

**Table 1. Primers used in this study**

**a. Primers used for chromatin immunoprecipitation (ChIP) assay**

Name	Forward primer	Reverse primer
C mAmylase 2	5' TTCTGCTGCTTCCCTCATT 3'	5' CGAACAGGTGGACAATAGCA 3'
C mBG 4	5' ATGGCCTGAATCACTTGGAC 3'	5' TTCTCAGGATCCACATGCAG 3'
m5s RNA	5' CTCGTCTACGGCCATACCA 3'	5' GGGGAGTCCAAAAAGCCTAC 3'
pYB/YAC cassette	5' TCACCAATGCACTCAACGAT 3'	5' CAGTAGCAGAACAGGCCACA 3'
tRNA gly	5' GTGCGCGTTGGTGGTATAGT 3'	5' TCCCCTTGAAAAACCTACAA 3'
tRNA gly ΔA box	5' TCCCGTAGAATCTGCTGGC 3'	5' TCCCCTTGAAAAACCTACAA 3'
eGFP	5' AGAACGGCATCAAGGTGAAC 3'	5' TCAGGTAGTGGTTGTCTG 3'

**b. Primers used to amplify tRNA genes from a cluster (RNC) on mouse chr1: 173 Mb**

RNC            5' GCTGGAGAGGTTGAGGATGG 3'    5' GCG CTA ATG GTC GAG TTG TG 3'

**c. Primers used to amplify Alu Yb8-1 from human chr8: 4893419-4894372 (Carter et al., 2004)**

Alu            5' CTGTCCTTGTGTGTGTGGTTT 3'    5' TCATTGAAGCGTGTCTTATCG 3'

**d. Primers used to amplify mouse 5S rDNA**

5SrDNA       5' GTCGTCGTCGTCGGGCATC 3'       5' AGCAGGGTGGTGCCGAGGT 3'

**e. Primers to amplify tDNA cassettes after their insertion into the RL5 locus**

Seq1/LCR88    5' AACGGAGTAACCTCGGTGTG 3'       5' CCAAGAGCTCGAATTGATCC 3'

Sequence of the **2 tRNA AT IVS** construct (Gly in red; Glu in blue). The number of CpG dinucleotides in intergenic and flanking sequences (GC=50%) is 18.

ACGCGTGTGATGGCTGCATTCCACACACAAGGTGGAACATTTCTCTTGATAGAGCAGTT  
TTGAAACACTCTTCCCGTAGAATCTGCTGGCGCGTGTGC**GCGTTGGTGGTATAGTGGT**  
**AGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTTCGATTCCCGGCCAACGCA**GCGTGCC  
CACGTTTTGCGCTGGCGCCGCGTGCTAGCAAAGGTCCCTTTTTCACAGAGCAGTTTTGAAA  
CACTGTTTTTGTAGTTTTTCCAAGGGGATAATTATAGCTCATTGAGCTTTGGCGCGTGC  
**TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTACCGCCGCGGCCCGGGTTCGATT**  
**CCCGGTCAGGGAA**GCCTCTCTTCTTCCCTCTCTGCTGGCGCGTGTGATGTTTGCATTGAG

GTCACAGTGTGCAACATTCCTCTTGATAGAGCAGTTGGGAAACACTCCTTTTGTAGAAT  
TTGCAATGGGATTGGCGCGT

Sequence of the 4 **tRNA AT IVS** construct (Leu in green; Asp in purple; Gly in red; Glu in blue). The number of CpG dinucleotides in intergenic and flanking sequences (GC=47%) is 28.

ACGCGTAACTACTTTGTGATGTGTACATTCAACTCACAGAGTGGAACCTCCCTCTTTAT  
AGAGCAGTGTTGAAGCACTCTTTTTGTAGAAACTGCAAGGCGATATTTGGACCCCTTTG  
AGTGGCGCGTGGCAAAGG**CGAGGCTGTCAGGAGTGGGATTCGAACCCACGCCTCCAGG**  
**GGAGACTGCGAACTTGAACGCAGCGCCTTTAGACCGCTTCGGCCATCCTGACGGCGGTT**  
TGGGCTTGGCGCGTTTTTTCATGTTACTCTAGATAGAAGAATTCTCAAACACTACTATG  
TGATGTTTGCATTCAAGTCACAGAGTGCAACATTCCTGGCGCGTTG**TCCTCGTTAGTAT**  
**AGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGTTTCGATTCCCCGACGGGGAG**  
ACGTAGCGTCCTTTTTTGGTGGCGCGTGTGATGGCTGCATTCCACACACAAGGTGGAACA  
TTTCTCTTGATAGAGCAGTTTTTGAACACTCTTCCCGTAGAATCTGCTGGCGCGTGTG**G**  
**CGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTTCGATTC**  
**CCGGCCAACGCA**GCGTGCCACGTTTTGCCTGGCGCGTAAAGGTCCCTCTTCACAGAGA  
GTTTTGAAACACTGTTTTTGTAGGTTTTCCAAGGGGATAATTATAGCTCATTGAGCTTT  
GGCGCGTGC**TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCGG**  
**TTCGATTCCCGGTCAGGGAA**GCCTCTCTTCTTCTCTCTGCTGGCGCGTGTGATGTTTC  
ATTCAGGTCACAGTGTGCAACATTCCTCTTGATAGAGCAGTTGGGAAACACTCCTTTTG  
TAGAATTTGCAATGGGATTGGCGCGT