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# Tissue-Specifically Expressed and Highly Conserved Segments in Human mlncRNA

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Since human genome and several other organisms' genomes are completely sequenced, gene regulation is realized to be more immense and more complex than expected. The functional properties are known not only on protein coding sequences but also non protein coding or untranslated regions. Recently, numerous functional non protein coding RNAs were identified. Also in our large-scale studies of human transcriptome, large numbers of putative ncRNAs have been observed. However, solid evidences for the in vivo existence of them are inadequate, and knowledge on the transcriptional mechanism of the ncRNAs remains elusive. In this study, we confirmed their cellular existence and examined fine tissue-specific patterns. From our 1.7 million full-length cDNA dataset, we selected 156 long non-coding RNA clones. The ncRNAs are from hg17 intergenic regions; all of which contained ORFs of less than 100 amino acids and showed clear trace of splicing. We surveyed the expression profiling of them in 21 human tissues and 3 human cell lines using quantitative RT-PCR. We verified the genuine expression in 76 clones (49%) of selected ncRNAs which 51% showed tissue specificity, predominantly expressed in one tissue and 17% revealed ubiquitous expression. A comparative genomic analysis using UCSC multiple alignment of 17 genomes showed that despite the generally low conservation, there were 77 highly conserved segments longer than 100 bp; of which 20 were longer than 200 bp and 2 were longer than 400 bp.