ESM Fig 2.

ESM Fig. 2. miRStart database analysis of predicted miR-153-2 regulatory sequences within 50kb from upstream region of miR-153-2 precursor. Published experimental evidences used in miRStart are described as follows:(1) CAGE (Cap Analysis of Gene Expression) tags: Recognize 5'-end of a gene. (2) TSS Seq tags: More than 300 million 5'-end sequences of human and mouse cDNAs by combining oligo-capping method and Solexa sequencing technology (3) H3K4me3 enrichment (histone H3 is trimethylated at its lysine 4 residue): Enriched surrounding TSSs. Moreover, ESTs and comparative genomics around putative miRNA TSSs are used to provide strong supports for reconfirmation. A summary is shown of the analysis of the 50kb genomic region upstream of the miR-153-2 precursor. The TSS of miR-153-2 ('TSS (To precursor)') is localised at 38909 bp from the precursor. This is indicated by the red bar in the diagram ('Putative TSS'). More detailed information can be found at http://mirstart.mbc.nctu.edu.tw/.