Supplemental Table 2. Aligning sequences for three way alignments of full OrbId prediction set. The aligning miR, mRNA, and TE sequences corresponding to each OrbId predicted target are provided in FASTA format. The TE sequence orientations have been verified for alignment, and mRNA sequences reverse complemented. All repeat annotations refer to RepBase[42, 43] identifiers except for RF numbers (e.g. “RF00026 U6” or “RF00100 7SK”) which refer to RFAM5[46,47]. ClustalW alignments can be obtained at: http://www.genome.jp/tools/clustalw/ .

3pUTR Aligning Sequences

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