

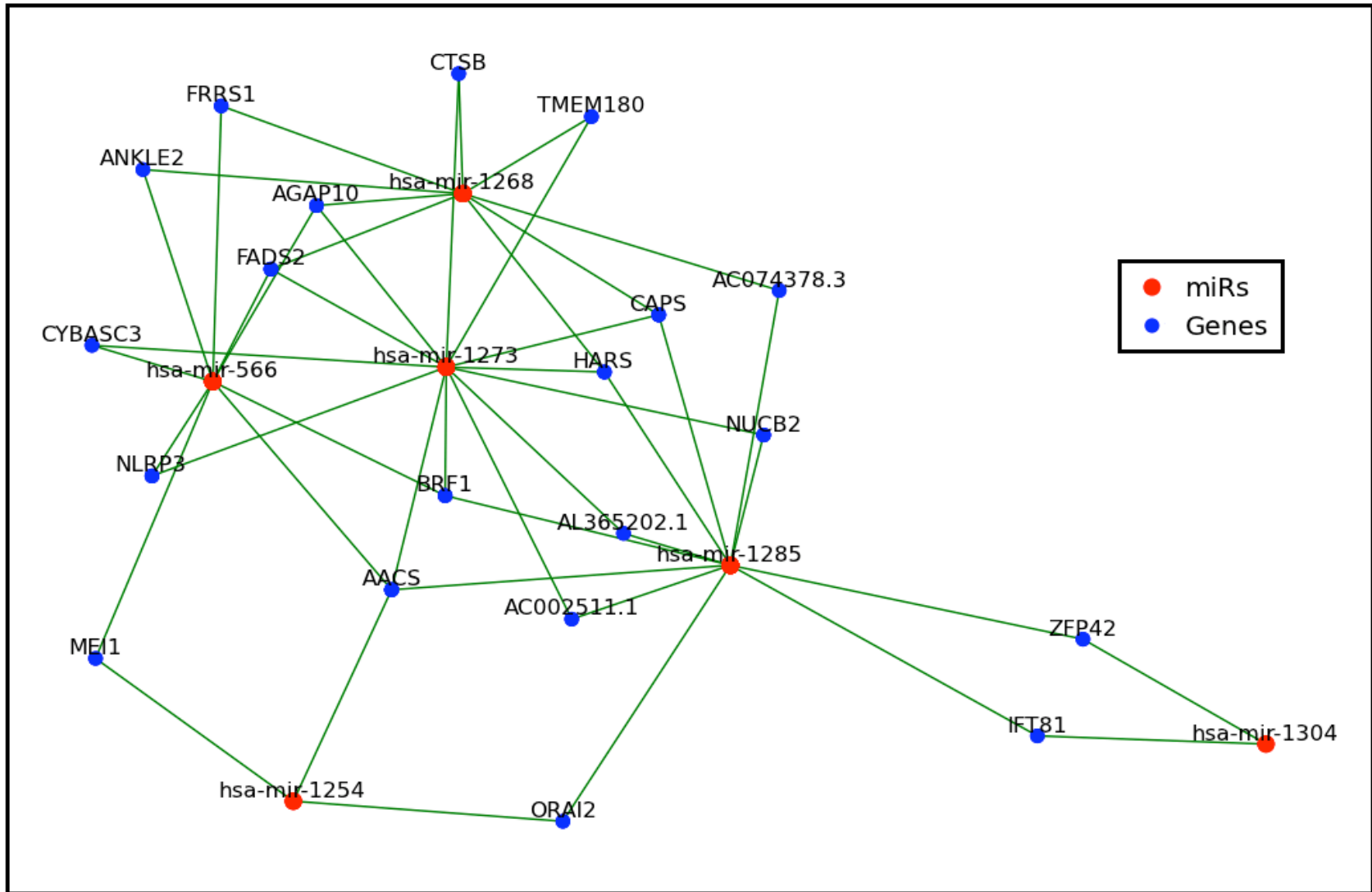
Supplemental Figure 1. MiR family mRNA targeting biases. Distributions of miRs -544 and -301a-5p, and miR-28, miR-548, and Alu-miR family target locations within mRNA transcripts as predicted by OrBld.

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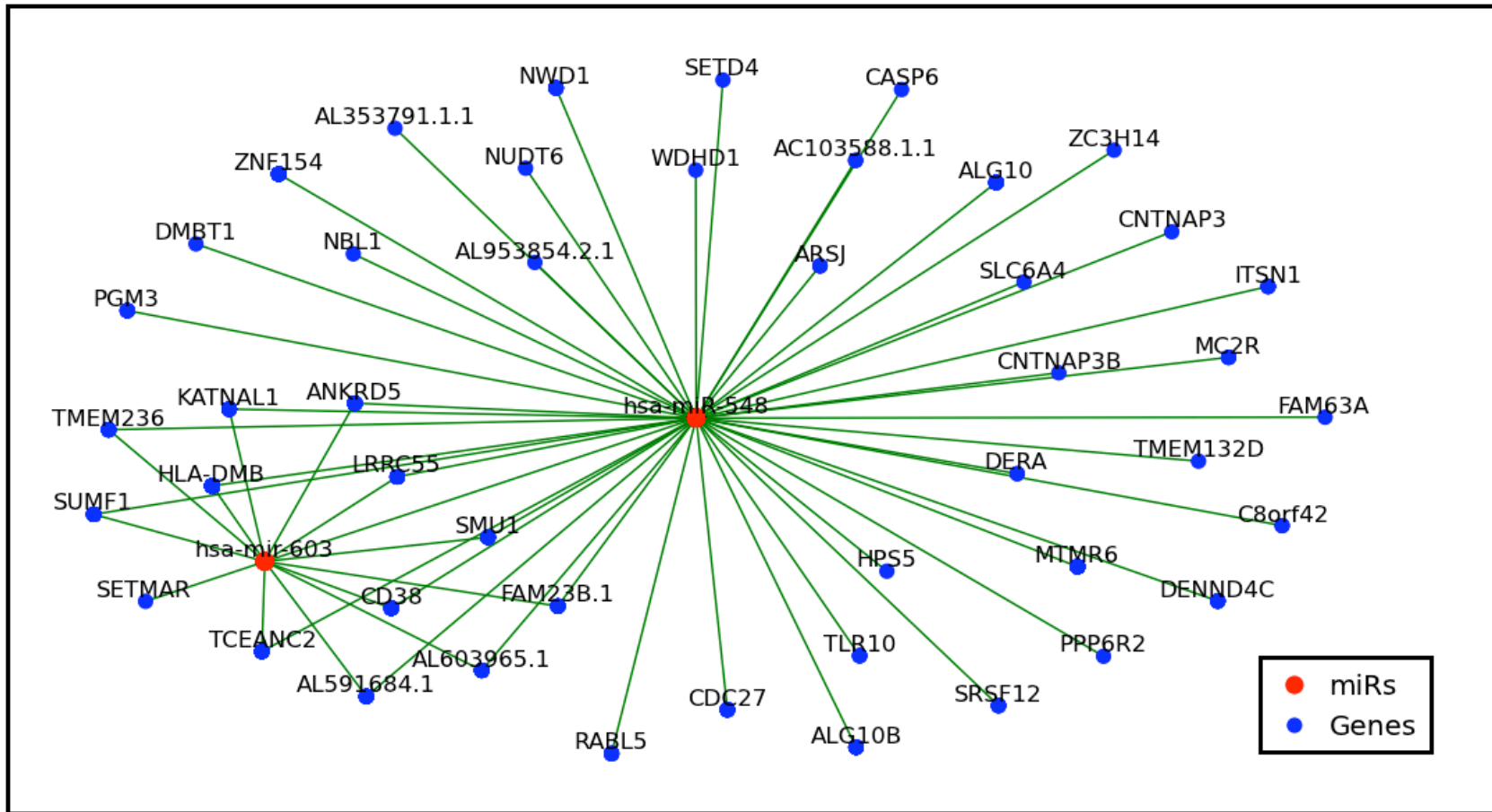
mir28      GTCCTTGCCCTCAAGGAGCTCACAGTCTAT-TGAGT-----TACCTTTCTGACTTTCC-C-ACTAGATTGTGAGCTCCTGGAAGGGCAGGCACT
mir708     GTAACCTGCCCTCAAGGAGCTTACAATCTAGCTGGGGGTAAATGACTTGCACATGAACA-CAACTAGACTGTGAGCTTCTAGAGGGCAGGGACC
mir151a    TTTCCTGCCCTCGAGGAGCTCACAGTCTAG-TATGT-----CTCATCCCCTA-CTAGACTG-AAGCTCCTTGAGGACAGGGATG
          *   * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

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Supplemental Figure 2. Pre-miRs -28, -151 and -708 alignment. ClustalW alignment of pre-miRs -28, -151 and -708. Mature miRs are highlighted in yellow. *, conserved nucleotide.



Supplemental Figure 3. Orblid Alu family target network. MiRs -1285-5p and -3p have been combined and are shown collectively as were miR-1273s. Only shared targets are depicted. Green lines indicate miR regulation.



Supplemental Figure 4. MiR-548 and miR-603 family target network. Current miR-548 family members are shown collectively. All targets of both the miR-548 family and miR-603 are depicted indicating 13 of 14 miR-603 targets are also targeted by an existing miR-548 family member. Green lines indicate miR regulation.

AAAAGGGGGTTTTCCCGCTGCTGCTGCTCAAGCTGCTCCAACGTAG	mRNA
TTTTCCCGCTGCTGCTGCTCAAGCTGC	TE
GGGTTTTCCCGC	miR

AAAAGGGGGTTTTCCCGCTGCTGCTGCTCAAGCTGCTCCAACGTAG	mRNA
TTTTCCCGCTGCTGCTGCTCAAGCTGC	TE
TTTCCCGCTGCT	miR

AAAAGGGGGTTTTCCCGCTGCTGCTGCTCAAGCTGCTCCAACGTAG	mRNA
TTTTCCCGCTGCTGCTGCTCAAGCTGC	TE
CAAGCTGCCCGC	miR

Supplemental Figure 5. Cartoon illustrating three potential scenarios for Orb1d alignment. If a miR and its corresponding TE had overlapping start and stop loci on the same mRNA, it was considered a match.