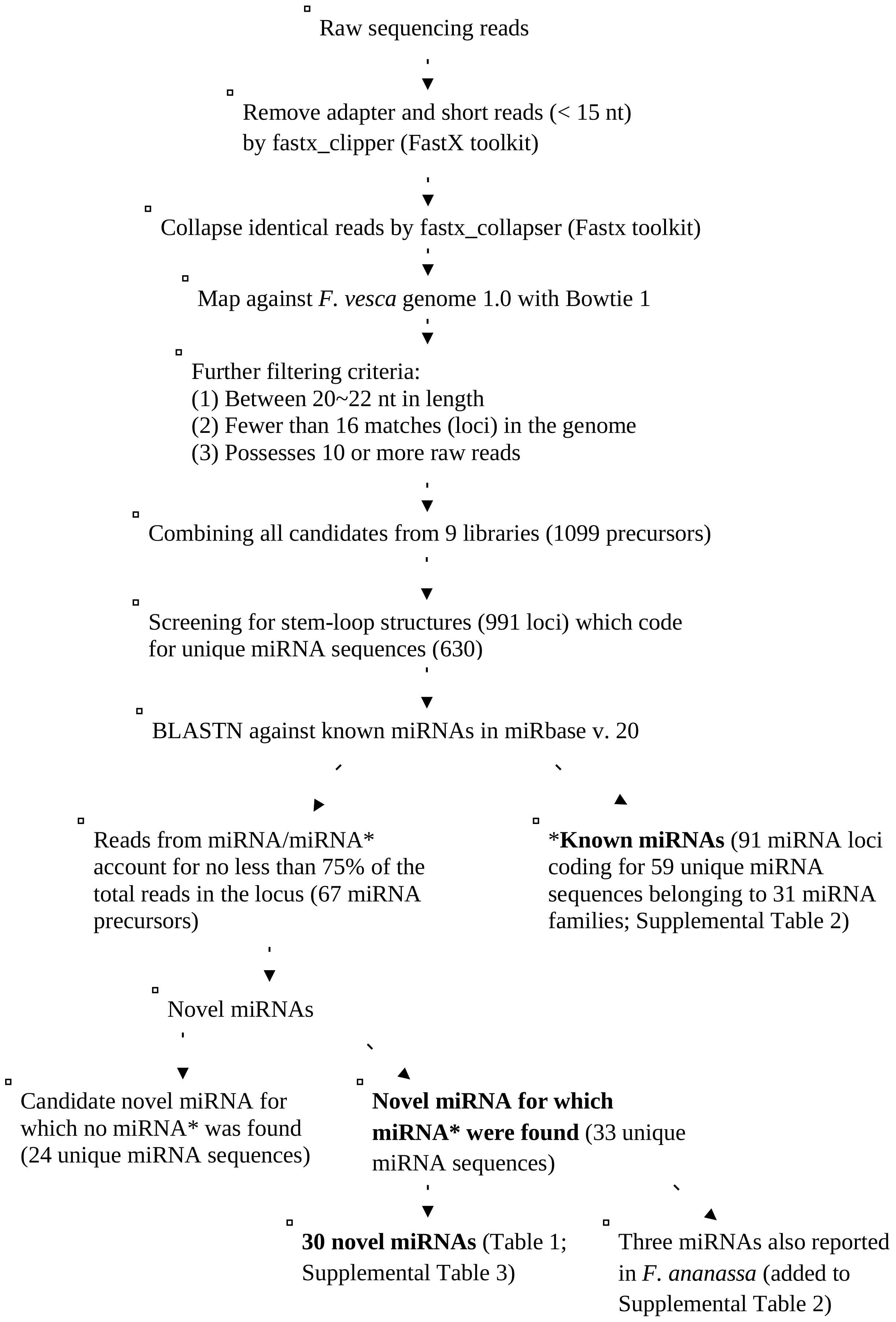
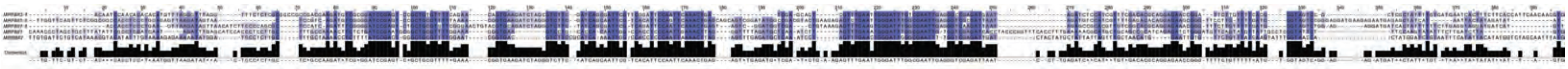


Supplemental Figure 1. Informatics pipeline for miRNA prediction.

*Known miRNAs refer to miRNAs with ≤ 2 mismatches to miRNAs deposited at the miRBase v20.

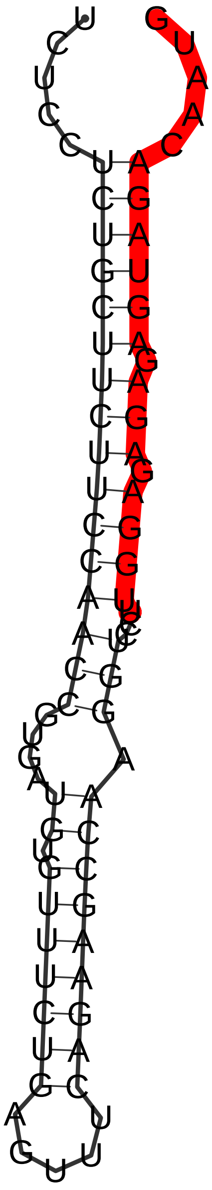


Supplemental Figure 2. Alignment of the LG3 miRFBX precursor sequences

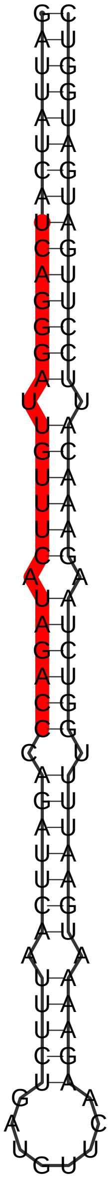
Sequences were aligned by MUSCLE (http://www.ebi.ac.uk/Tools/msa/muscle/), and the alignment was viewed in Jalview (http://www.-jalview.org/). Sequence conservation level is denoted by different color with dark color showing a high level of conservation. Consensus sequence is included in the bottom.

NAME: fve-MIR11286
SEQ:UUGGAGAGAGAGUAGACAAUG
LENGTH: 21

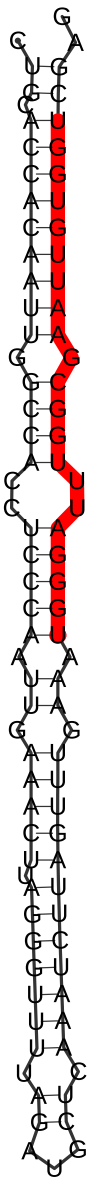
Supplemental Figure 3. Secondary structures of thirty-two novel miRNA precursors
Red signifies miRNA and green signifies miRNA*



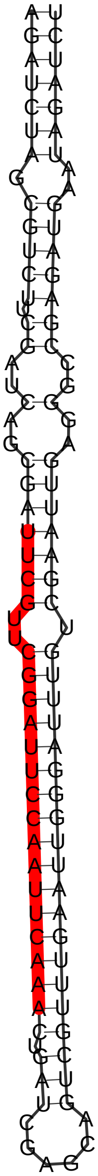
NAME: fve-MIR11287
SEQ:UCAGGGAUUGUUUCAUAGACC
LENGTH: 21



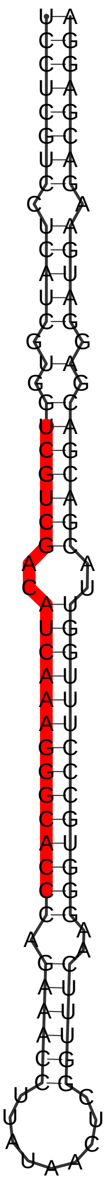
NAME: fve-MIR11288a
SEQ:UGGGAUUUGGCGAAUUGUGGU
LENGTH: 21



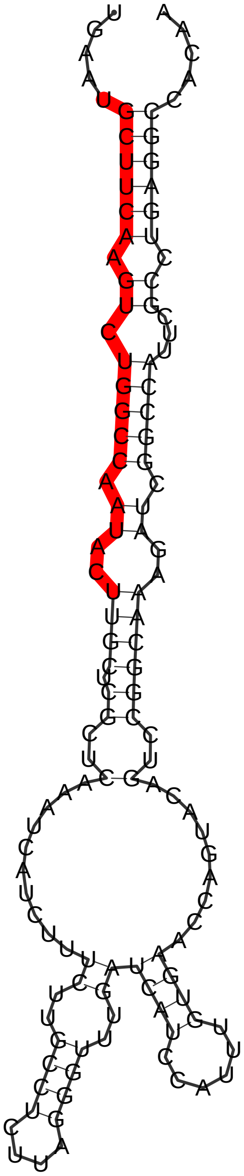
NAME: fve-MIR11288c.2*
SEQ:UUCGUUCGGAUUCCAAUUCAAA
LENGTH: 22



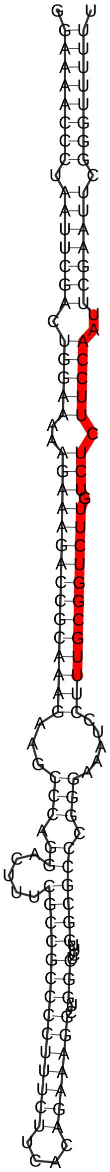
NAME: fve-MIR11289
SEQ:UCGUCGACAUCAAAGGGCACC
LENGTH: 21



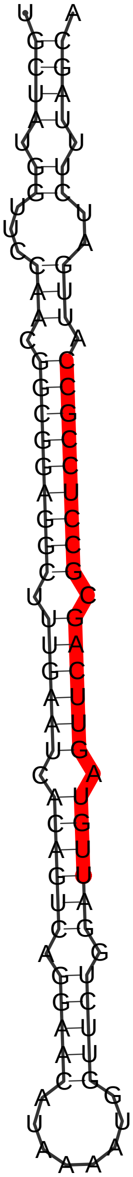
NAME: fve-MIR11290
SEQ:UGCUUCAAGUCUGGCCAAUACU
LENGTH: 22



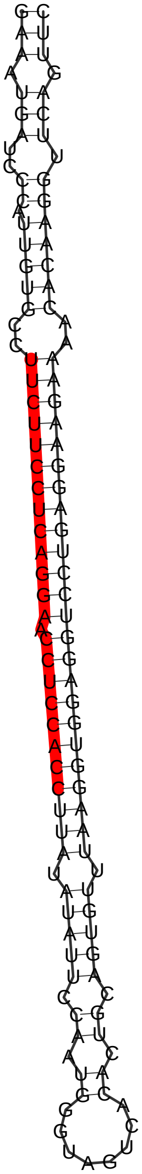
NAME: fve-MIR11291
SEQ:UUGCGGUCUUGUCUCUUCCAAU
LENGTH: 22



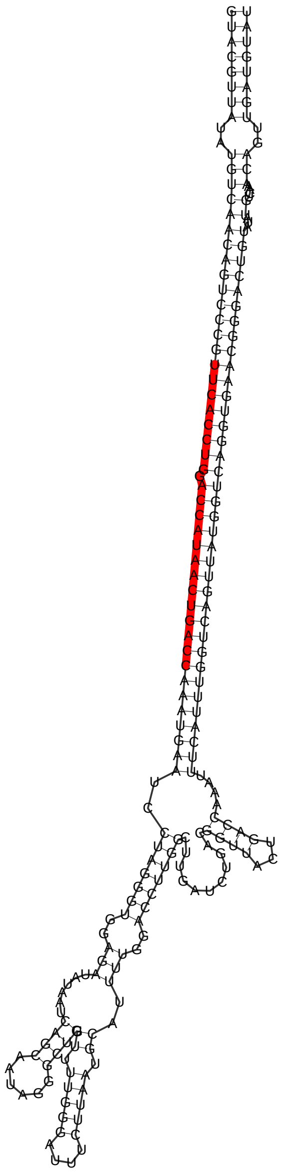
NAME: fve-MIR11292
SEQ:UUGUAGUUCAGCGCCUCCGCC
LENGTH: 21



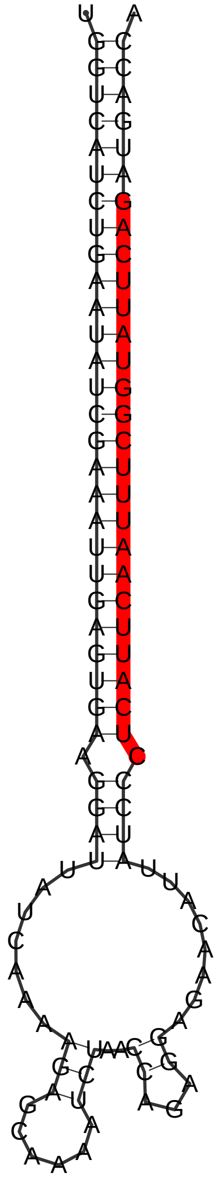
NAME: fve-MIR11293
SEQ:UUCUUCCUCAGGAACCUCCACC
LENGTH: 22



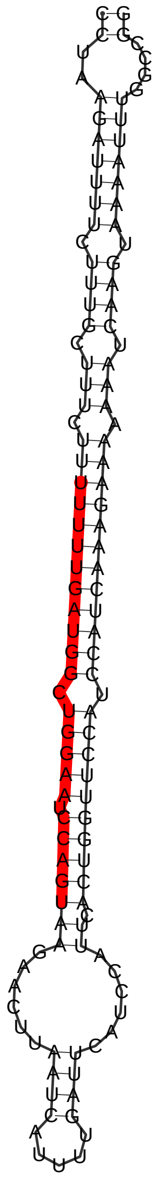
NAME: fve-MIR11294
SEQ:UUCACCUGGACCAUAACUGACC
LENGTH: 22



NAME: fve-MIR11295
SEQ:CUCAUUCAAUUUCGGUAUUCAG
LENGTH: 22

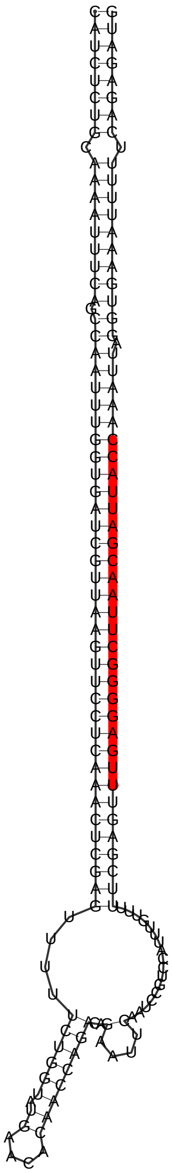


NAME: fve-MIR11296
SEQ:UUUUUGAUGGCUGGAAUCCAGU
LENGTH: 22

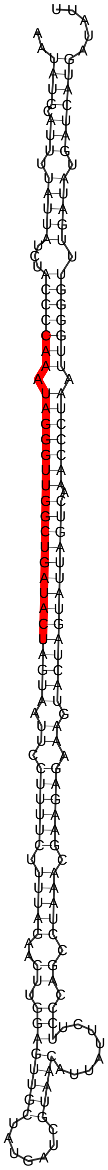


NAME: fve-MIR11297
SEQ:CAGACAAGAUCGAUCUCGCCU
LENGTH: 21

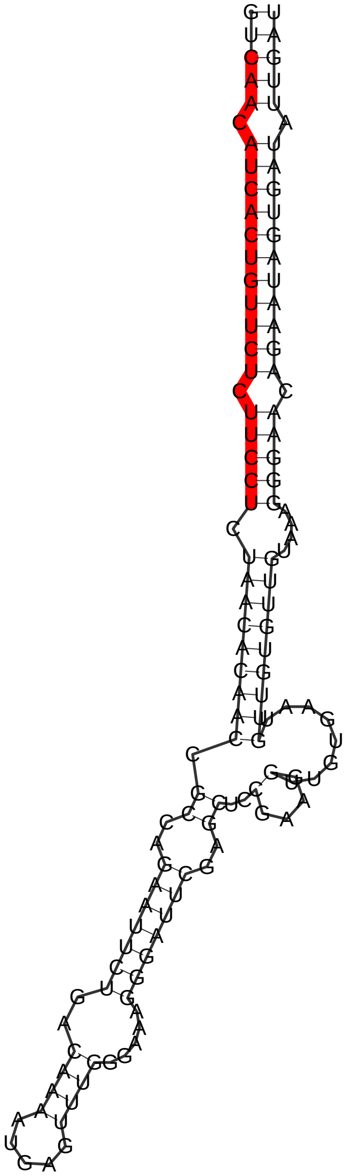
NAME: fve-MIR11298
SEQ:UUGAGGGGCUUAACGAUUACC
LENGTH: 21



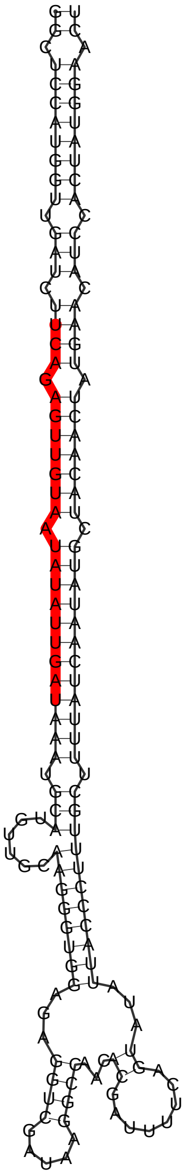
NAME: fve-MIR11299
SEQ:CAAAUAGGGUUGGCUGAUACU
LENGTH: 21



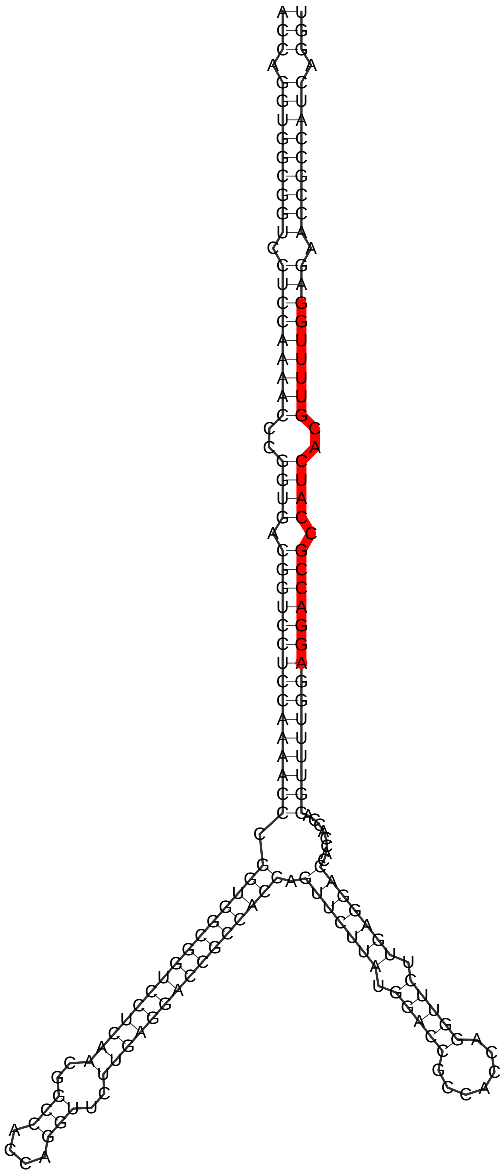
NAME: fve-MIR11300
SEQ:CAACAUCACUGUUCUCUUCCU
LENGTH: 21



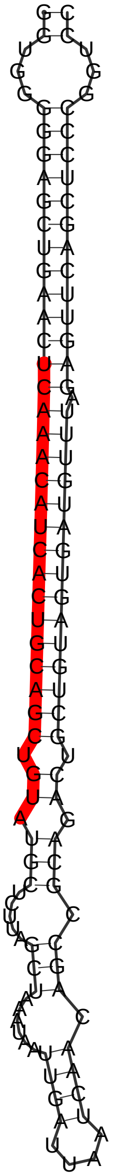
NAME: fve-MIR11301
SEQ:UCAGAGUUGUAAUAUAUUGAU
LENGTH: 21



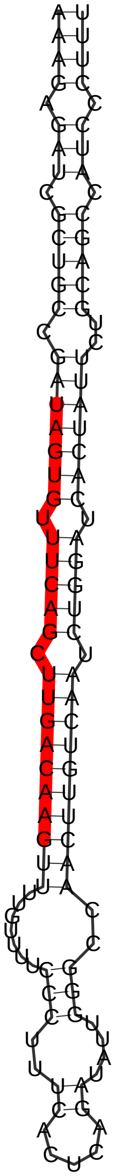
NAME: fve-MIR11302
SEQ:AGGACCGCCAUCACGUUUUGG
LENGTH: 21



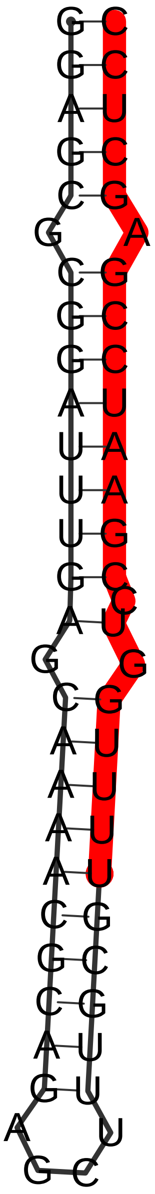
NAME: fve-MIR11303
SEQ:UCAAACAUCACUGCAGCUGUA
LENGTH: 21



NAME: fve-MIR11304
SEQ:UAGUGUUUCAGCUUGACAAG
LENGTH: 20



NAME: fve-MIR11305
SEQ:UUUUGGUCCGAAUCCGAGCUCC
LENGTH: 22



NAME: fve-MIR11306

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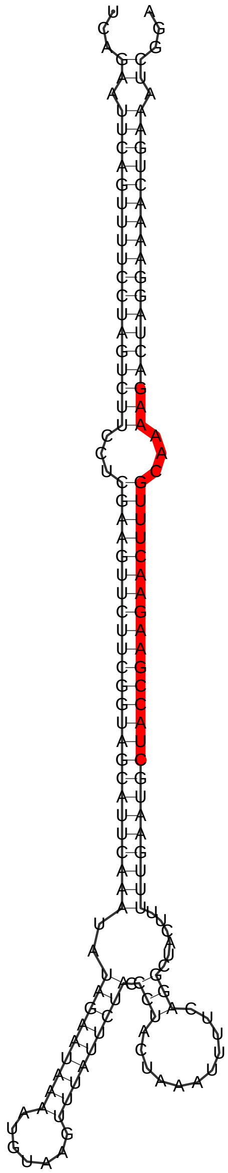
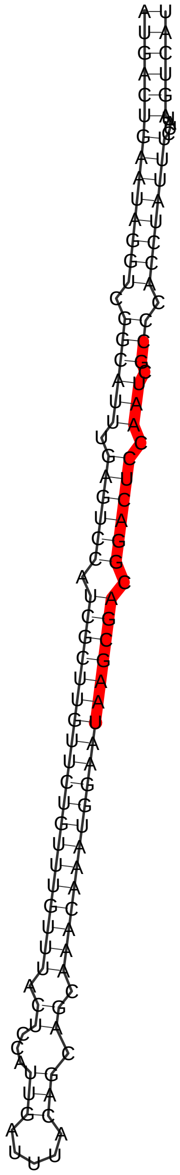
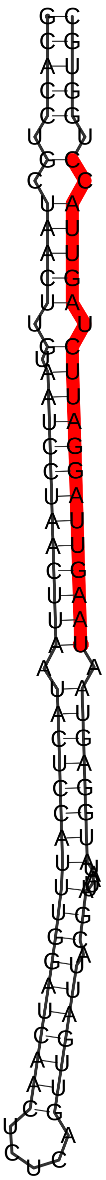
LENGTH: 22



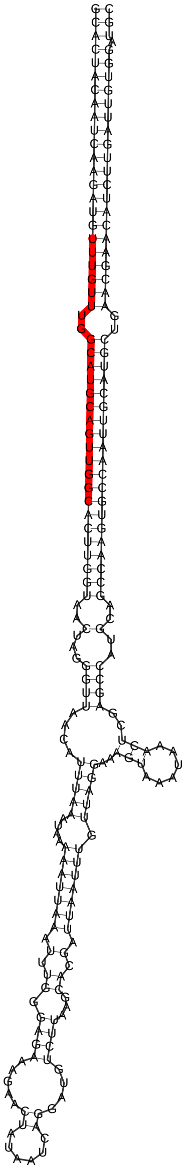
NAME: fve-MIR11307
SEQ:UAAGCGACGGACUCCAAUCGC
LENGTH: 21



NAME: fve-MIR11308
SEQ:UAAGUUAGGAUUCUAGUUACC
LENGTH: 21



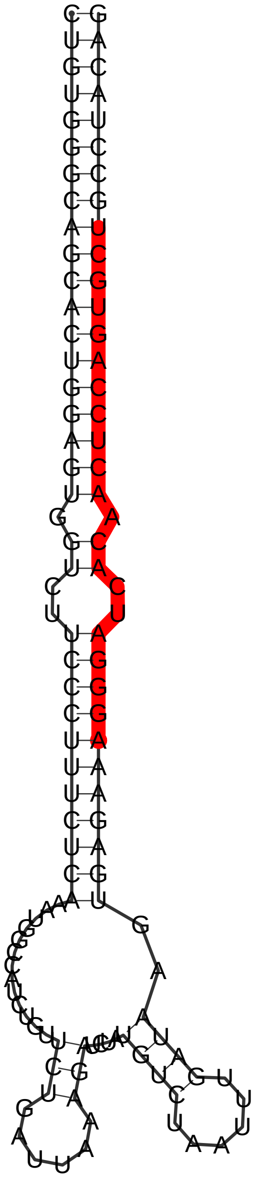
NAME: fve-MIR11309
SEQ:UUUGUUUGGCAUGCAGUUGGC
LENGTH: 21



NAME: fve-MIR11310

SEQ:AGGGAUCACAACUCCAGUGCU

LENGTH: 21



NAME: fve-MIR11311
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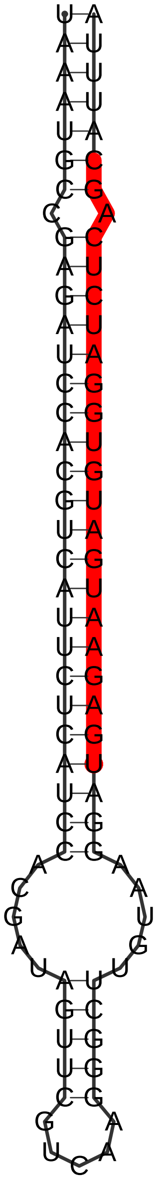
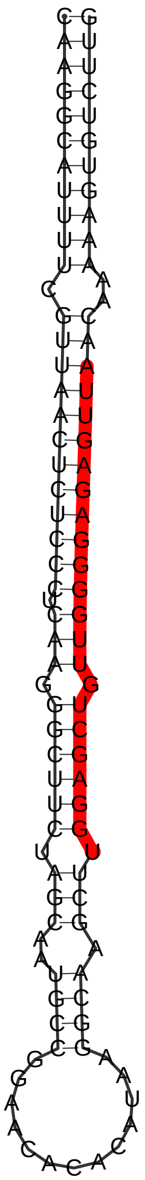
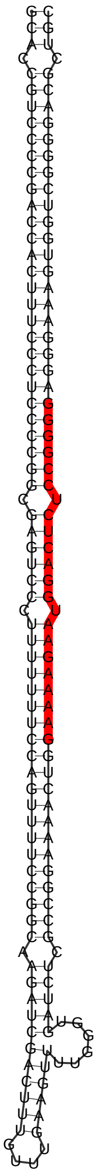
LENGTH: 22



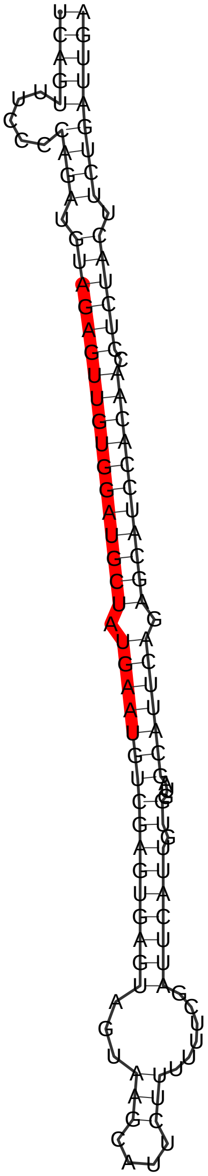
NAME: fve-MIR11312
SEQ:UGGAGCUGUUGGGGAGAGUUA
LENGTH: 21



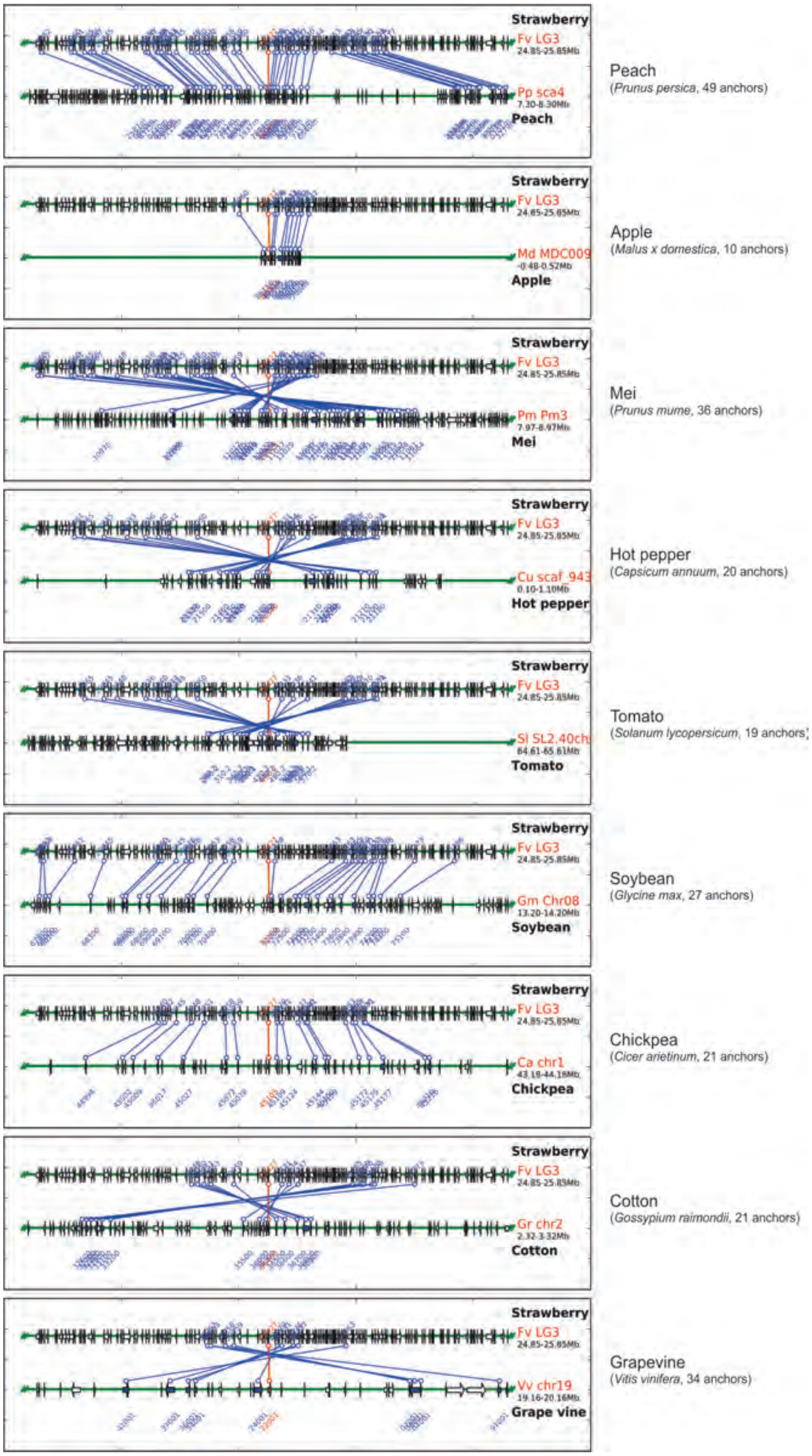
NAME: fve-MIR11313
SEQ:GAAAAGAAUGGACUCUCCGGGG
LENGTH: 22



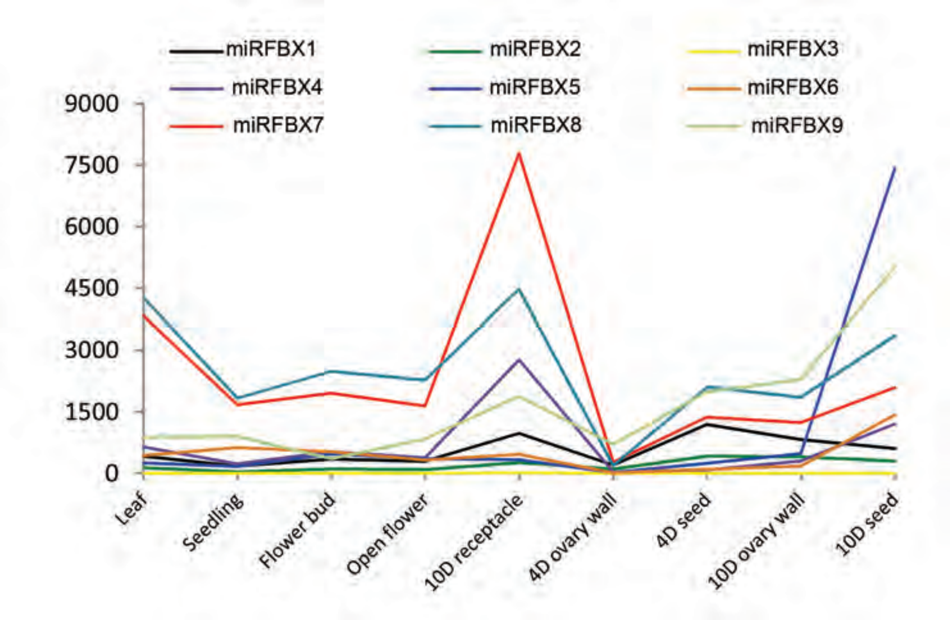
NAME: fve-MIR11314
SEQ:AGAGUUGUGGAUGCUAUGAAU
LENGTH: 21



NAME: fve-MIR11315
SEQ:CUAGUCAUUGGUCAUAGCAUC
LENGTH: 21



Supplemental Figure 4. Syntenic analysis in several plant species of the region containing the LG3 miRFBX cluster.
An alignment of syntenic regions (a window of 500 kb) was retrieved from the PGDD (http://chibba.agtec.uga.edu/duplication/index/home). A gene adjacent to the LG3 cluster in strawberry, mrna14027, was used a query to search for related syntenic regions in multiple species. Genes were denoted by small arrows, with genes of syntenic matches highlighted in blue. All syntenic genes between two species are connected by blue lines, except the one highlighted with a red line, which connects the strawberry mrna14027 to its syntenic match in the other genomes.



Supplemental Figure 5. Read abundance of all nine mature miRFBXs

Y-axis indicates read abundance in RPTM (Reads Per Ten Million). X-axis indicates nine small RNA libraries of different tissue origins.