|  |  |  |
| --- | --- | --- |
| Unaligned pairs | Emboss Water local alignment | miRNA Sequence 1  vs  miRNA Sequence 2 |
| Mir12095-Mir498 |  | GGGCCAAGAACAAAGAAAC  CAAGCCAGGGGGCGC |
| Mir218-Novel18 |  | GGCGACAACCAG  GACGGAGGACAGGGCACG |
| Mir2471-Mir27 |  | GAGGACGCAACCAGAGG  CACAGGGCAAGCGC |
| Novel5-Mir585 |  | AGGAGGACAAGGAAACCA  GGGCGACGAGCAGGG |
| Mir1911-Novel1 |  | GAGACCGCCAGCGGGG  ACGAGACGGAAC |
| Mir11995-Mir7208 |  | AAGCAGAGGAGAGGAGGACA  AAACGAGCCGCGC |
| Mir2328-Mir384 |  | GCCCCCCCCGGCGCCGGC  GAAACAACCAGGCAAG |
| Mir3090-Mir3079 |  | CCCAGGGACACCCGACCA  GACGAGAGCAAGCGGA |
| Mir4662-Mir3072 |  | AGCCAAGCCACAG  GCCCCCCCAGGAAGCCC |
| Mir1947-Mir498 |  | AGGACGAGCAGCGAGGCG  CAAGCCAGGGGGCGC |
| Mir205-Novel17 |  | CCCACCACCGGAGCG  GGCAGCAGAGCCAGGGCAG |
| Mir3075-Mir3619 |  | GCGGGAGCAGCCAAGGACAA  CAGCAGGCAGGCGGGCAGC |
| Novel15-Mir1343 |  | CACAAGCACAGACC  CCCGGGGCCCGCACCCGC |
| Mir616-Mir576 |  | ACCAAAACCCCAGGACCC  ACAACCCACGCG |
| Mir328-Mir340 |  | CGGCCCCCGCCCCCG  AAAAGCAAGAGACGA |
| Mir96-Mir5586 |  | GGCACAGCACAGC  ACCAGCGACAAG |
| Mir2382-Mir12080 |  | GCCCCCCCCGGCGCCGGC  CGCCCAGGACCGC |
| Novel6-Mir126 |  | CCACCCCACCCAGCAGC  CGACCGGAGAAAAGCG |
| Mir374-Mir433 |  | CACAGGGAGAA  ACAGAGGGCCCCGGG |
| Mir26-Mir12076 |  | CAAGAACCAGGAAGGC  CCGGCCCGGCAGGGGC |
| Mir1960-Mir1269 |  | CCAGGCGAGAAGAGGGC  CGGACGAGCCGGCACGG |
| Mir3617-Mir3146 |  | AAAGACAAGGCAAGAGGG  CAGCAGGAAGAAAGAAGGG |
| Mir204-Mir4662 |  | CCCGCACCGCCC  AGCCAAGCCACAG |
| Mir1943-Mir384 |  | AAGGGAGGACGGGCACCGGA  GAAACAACCAGGCAAG |
| Mir3173-Mir26 |  | GCCCGCCGCCCG  CAAGAACCAGGAAGGC |
| Mir1842-Mir4424 |  | GGCCGGAGGCGGCCA  GCCACAAGAACCG |
| Mir769-Novel13 |  | GAGACCCCGGGCGAGC  CAGAGCCCCCACAAGGA |
| Mir6525-Mir208 |  | CGGGGAAAGCAGGAGGAGGG  AAAGACGAACAAAAGGG |
| Mir556-Mir136 |  | GAGAGCCAGAAAGA  CACACGCCAAAGAGC |
| Mir188-Mir191 |  | CACCCGCAGGGGAGGG  CAACGGAACCCAAAAGCAGCG |

Table S2. 30 Random non-aligned miRNA pairs were aligned. Sequence alignment was performed using the EMBOSS Water tool, which employs a modified Smith-Waterman algorithm for efficient local alignment. Four continuous nucleotides were matched across various miRNA sequence pairs. For pairs Mir1911-Novel1, Mir4662-Mir3072, Mir3075-Mir3619, and Mir616-Mir576 five nucleotides were matched.