S5 Appendix. Alignment of miRNA clusters like regions.

csi – *C. sinensis*, sma – *S. mansoni*, hmi – *H. microstoma*, egr – *E. granulosus*, emu – *E. multilocularis*, sec. struc. – secondary structure

Mature miRNA sequences are in bold type and underlined.

Cluster of *C. sinensis* was obtained from scaffold 198 (gi|353342189|dbj|BADR02000773.1|) (- strand)

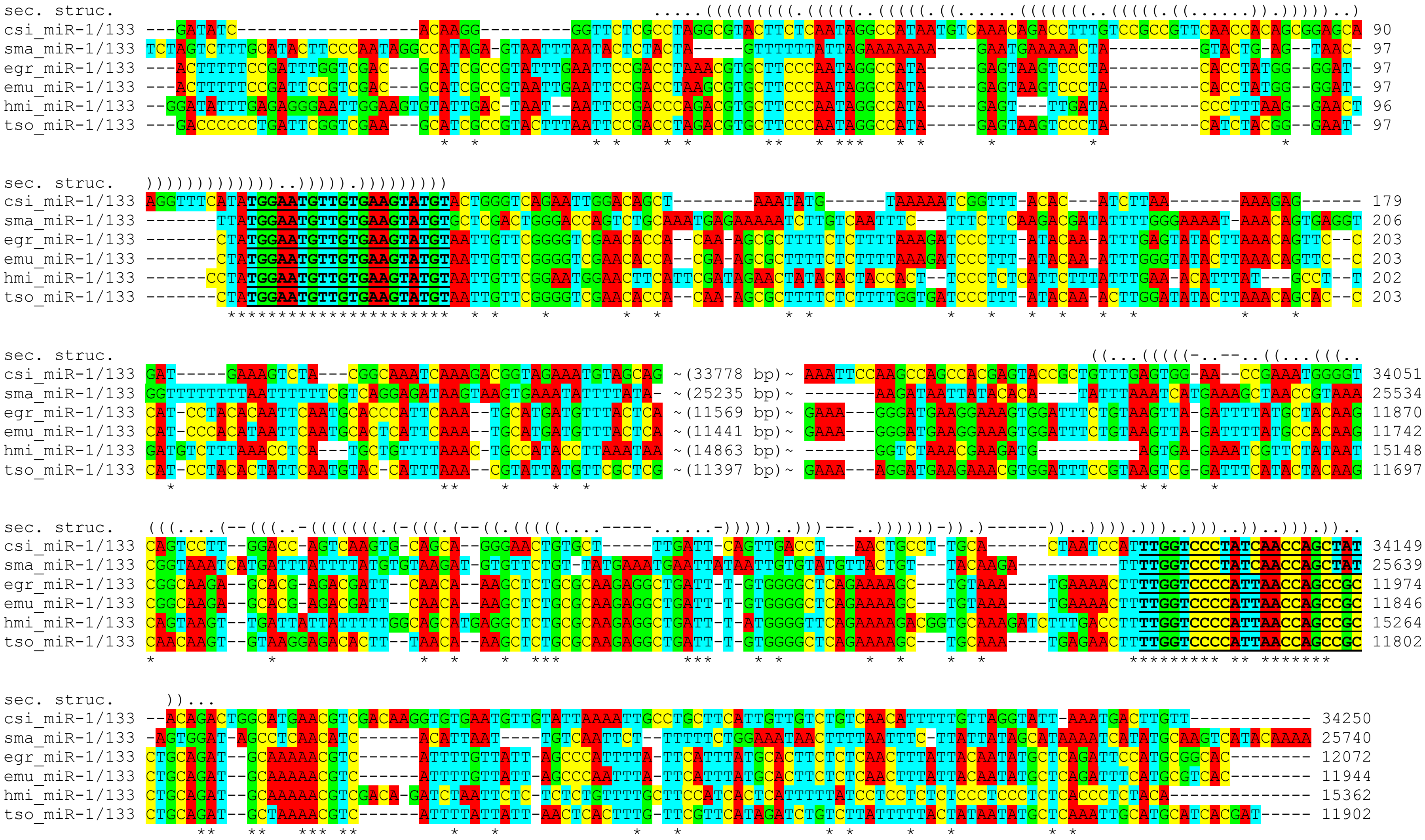
Cluster of *S. mansoni* was obtained from chromosome W (gi|360043576|emb|HE601631.1|) (- strand)

Cluster of *H. microstoma* was obtained from contig 880003 (gi|528308588|emb|CBLW010003541.1|) (- strand)

Cluster of *E. granulosus* was obtained from contig 00137 (gi|528306514|emb|CBLN010001139.1|) (+ strand)

Cluster of *E. multilocularis* was obtained from contig 007760 (gi|528775363|emb|CBLO010002096.1|) (+ strand)

Cluster of *T. solium* was obtained from contig 00015 (pathogen_TSM_contig_00015) (+ strand)



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sec. struc.                                                     .....(((((((((.(((((..(((((.((......(((((((..(((((.((......)).)))))..)
csi_miR-1/133 ---GATATC------------------ACAAGG---------GGTTCTCGCCTAGGCGTACTTCTCAATAGGCCATAATGTCAAACAGACCTTTGTCCGCCGTTCAACCACAGCGGAGCA 90
sma_miR-1/133 TCTAGTCTTTGCATACTTCCCAATAGGCCATAGA-GTAATTTAATACTCTACTA-----GTTTTTTATTAGAAAAAAA----GAATGAAAAACTA---------GTACTG-AG--TAAC- 97
egr_miR-1/133 ---ACTTTTTCCGATTTGGTCGAC---GCATCGCCGTATTTGAATTCCGACCTAAACGTGCTTCCCAATAGGCCATA-----GAGTAAGTCCCTA---------CACCTATGG--GGAT- 97
emu_miR-1/133 ---ACTTTTTCCGATTCCGTCGAC---GCATCGCCGTAATTGAATTCCGACCTAAGCGTGCTTCCCAATAGGCCATA-----GAGTAAGTCCCTA---------CACCTATGG--GGAT- 97
hmi_miR-1/133 --GGATATTTGAGAGGGAATTGGAAGTGTATTGAC-TAAT--AATTCCGACCCAGACGTGCTTCCCAATAGGCCATA-----GAGT---TTGATA---------CCCTTTAAG--GAACT 96
tso_miR-1/133 ---GACCCCCCTGATTCGGTCGAA---GCATCGCCGTACTTTAATTCCGACCTAGACGTGCTTCCCAATAGGCCATA-----GAGTAAGTCCCTA---------CATCTACGG--GAAT- 97
                                           *  *           * *    * *       **   * ***   * *      *         *                  *

sec. struc.   ))))))))))))).)))))).)))))))))
csi_miR-1/133 AGGTTTCATATGGAATGTTGTGAAGTATGTACTGGGTCAGAATTGGACAGCT--------AAATATG------TAAAAATCGGTTT-ACAC---ATCTTAA-------AAAGAG------ 179
sma_miR-1/133 -------TTATGGAATGTTGTGAAGTATGTGCTCGACTGGGACCAGTCTGCAAATGAGAAAAATCTTGTCAATTTC---TTTCTTCAAGACGATATTTTGGGAAAAT-AAACAGTGAGGT 206
egr_miR-1/133 -------CTATGGAATGTTGTGAAGTATGTAATTGTTCGGGGTCGAACACCA--CAA-AGCGCTTTTCTCTTTTAAAGATCCCTTT-ATACAA-ATTTGAGTATACTTAAACAGTTC--C 203
emu_miR-1/133 -------CTATGGAATGTTGTGAAGTATGTAATTGTTCGGGGTCGAACACCA--CGA-AGCGCTTTTCTCTTTTAAAGATCCCTTT-ATACAA-ATTTGGGTATACTTAAACAGTTC--C 203
hmi_miR-1/133 ------CCTATGGAATGTTGTGAAGTATGTAATTGTTCGGAATGGAACTTCATTCGATAGAACTATACACTACCACT--TCCCTCTCATTCTTTATTTGAA-ACATTTAT---GCCT--T 202
tso_miR-1/133 -------CTATGGAATGTTGTGAAGTATGTAATTGTTCGGGGTCGAACACCA--CAA-AGCGCTTTTCTCTTTTGGTGATCCCTTT-ATACAA-ACTTGGATATACTTAAACAGCAC--C 203
                      **********************  * *    *       *  *            * *             *   *   *  *   *  *          *    *

sec. struc.                                                                                                 ((...(((((-..--..((...(((..
csi_miR-1/133 GAT-----GAAAGTCTA---CGGCAAATCAAAGACGGTAGAAATGTAGCAG ~(33778 bp)~ AAATTCCAAGCCAGCCACGAGTACCGCTGTTTGAGTGG-AA--CCGAAATGGGGT 34051
sma_miR-1/133 GGTTTTTTTTAATTTTTTCGTCAGGAGATAAGTAAGTGAAATATTTTATA- ~(25235 bp)~ -------AAGATAATTATACACA----TATTTAAATCATGAAAGCTAACCGTAAA 25534
egr_miR-1/133 CAT-CCTACACAATTCAATGCACCCATTCAAA--TGCATGATGTTTACTCA ~(11569 bp)~ GAAA---GGGATGAAGGAAAGTGGATTTCTGTAAGTTA-GATTTTATGCTACAAG 11870
emu_miR-1/133 CAT-CCCACATAATTCAATGCACTCATTCAAA--TGCATGATGTTTACTCA ~(11441 bp)~ GAAA---GGGATGAAGGAAAGTGGATTTCTGTAAGTTA-GATTTTATGCCACAAG 11742
hmi_miR-1/133 GATGTCTTTAAACCTCA---TGCTGTTTTAAAC-TGCCATACCTTAAATAA ~(14863 bp)~ -------GGTCTAAACGAAGATG----------AGTGA-GAAATCGTTCTATAAT 15148
tso_miR-1/133 CAT-CCTACACTATTCAATGTAC-CATTTAAA--CGTATTATGTTCGCTCG ~(11397 bp)~ GAAA---AGGATGAAGAAACGTGGATTTCCGTAAGTCG-GATTTCATACTACAAG 11697
                *                          **    *    *  *                                                      * *    *

sec. struc.   (((....(--(((..-(((((((.(-(((.(--((.(((((....-----......-)))))..)))---..))))))-)).)------))..)))).)))..)))..))..))).))..
csi_miR-1/133 CAGTCCTT--GGACC-AGTCAAGTG-CAGCA--GGGAACTGTGCT-----TTGATT-CAGTTGACCT---AACTGCCT-TGCA------CTAATCCATTTGGTCCCTATCAACCAGCTAT 34149
sma_miR-1/133 CGGTAAATCATGATTTATTTTATGTGTAAGAT-GTGTTCTGT-TATGAAATGAATTATAATTGTGTATGTTACTGT---TACAAGA----------TTTTGGTCCCTATCAACCAGCTAT 25639
egr_miR-1/133 CGGCAAGA--GCACG-AGACGATT--CAACA--AAGCTCTGCGCAAGAGGCTGATT-T-GTGGGGCTCAGAAAAGC---TGTAAA----TGAAAACTTTTGGTCCCCATTAACCAGCCGC 11974
emu_miR-1/133 CGGCAAGA--GCACG-AGACGATT--CAACA--AAGCTCTGCGCAAGAGGCTGATT-T-GTGGGGCTCAGAAAAGC---TGTAAA----TGAAAACTTTTGGTCCCCATTAACCAGCCGC 11846
hmi_miR-1/133 CAGTAAGT--TGATTATTATTTTTGGCAGCATGAGGCTCTGCGCAAGAGGCTGATT-T-ATGGGGTTCAGAAAAGACGGTGCAAAGATCTTTGACCTTTTGGTCCCCATTAACCAGCCGC 15264
tso_miR-1/133 CAACAAGT--GTAAGGAGACACTT--TAACA--AAGCTCTGCGCAAGAGGCTGATT-T-GTGGGGCTCAGAAAAGC---TGCAAA----TGAGAACTTTTGGTCCCCATTAACCAGCCGC 11802
              *           *              *  *    *  ***            ***    * *        *  *    *  *              ********* ** *******

sec. struc.     ))...
csi_miR-1/133 --ACAGACTGGCATGAACGTCGACAAGGTGTGAATGTTGTATTAAAATTGCCTGCTTCATTGTTGTCTGTCAACATTTTTGTTAGGTATT-AAATGACTTGTT------------ 34250
sma_miR-1/133 -AGTGGAT-AGCCTCAACATC------ACATTAAT----TGTCAATTCT--TTTTTCTGGAAATAACTTTTAATTTC-TTATTATAGCATAAAATCATATGCAAGTCATACAAAA 25740
egr_miR-1/133 CTGCAGAT--GCAAAAACGTC------ATTTTGTTATT-AGCCCATTTTA-TTCATTTATGCACTTCTCTCAACTTTATTACAATATGCTCAGATTCCATGCGGCAC-------- 12072
emu_miR-1/133 CTGCAGAT--GCAAAAACGTC------ATTTTGTTATT-AGCCCAATTTA-TTCATTTATGCACTTCTCTCAACTTTATTACAATATGCTCAGATTTCATGCGTCAC-------- 11944
hmi_miR-1/133 CTGCAGAT--GCAAAAACGTCGACA-GATCTAATTCTC-TCTCTGTTTTGCTTCCATCACTCATTTTTATCCTCCTCTCTCCCTCCCTCTCACCCTCTACA-------------- 15362
tso_miR-1/133 CTGCAGAT--GCTAAAACGTC------ATTTTATTATT-AACTCACTTTG-TTCGTTCATAGATCTGTCTTATTTTTACTATAATATGCTCAAATTGCATGCATCACGAT----- 11902
                   **   **   *** **         *   *             *   *              * *     *   *         * *
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