Figure S1. Mammalian computational mirtron candidates with saddle-like conservation pattern and single-arm 2nd structure in at least some primate and non-primate species

Name	Location	orthologs has good 2nd structure	species #	Sequence and secondary structure of a representative primate ortholog
ENST00000273794_13 (hsa-mir-1224)	chr3:185441887-185441971	Human Chimp Rhesus Rat Mouse Hedgehog Dog Cat Horse Cow Elephant Tenrec	12	>Human chr3 185441886-185441970 GTGAGGACTCGGGAGGTGGAGGGTGGTGCCGCCGGGGCCGGGCGCGCTGTTTCAGCTCGCTTCTCCCCCCACCTCCTCTCTCCTCAG -41.90 .((((((...((((((((((.(((.((.((.(((.(((((.....))))).))..))..)).)).))).))))))))))...)))))). []
NM_032635_0	chr19:40728559-40728629	Human Chimp Rhesus Rat Mouse Rabbit Hedgehog Dog Cat Horse Shrew Opossum	12	>Human chr19 40728558-40728628 GTGAGTGCGGGAAgggcgcggggcggagagggcgcgggggccgggccgACCCTCACCTCCCGCTTCTCCAG -38.10 ..(((.(((((((.((.....((((((((...(((.....)))...))))).))))..))))))))..)))... []
NM_015847_7	chr18:46055414-46055496	Human Chimp Rhesus Rat GuineaPig Rabbit Hedgehog Dog Horse Cow Shrew Tenrec	12	>Human chr18 46055414-46055496 GTGAGGCCCCAGTGGGTGGAGGGAAGGCACAACCCTGACCTTACCCAGTACCTGCCCTGACCCCACCCCATTTGCCTCTACAG -31.80 ((((((...((((((((((.((..(((((.....(((.....))).....)))).))..)))))))).))).))))).)).. []
NM_001009944_44 (hsa-mir-1225)	chr16:2080197-2080286	Human Chimp Rhesus Rat Mouse Hedgehog Dog Horse Cow	9	>Human chr16 2080196-2080285 GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGGCTCTGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG -48.20 .((((..((((.(((.(((((..((..((....((((((((((.....))))))))))...))).)..))..))...))))))).))))..)))). []
NM_001090_11 (hsa-mir-877)	chr6:30660088-30660173	Human Rhesus Rat Mouse Dog Cow Elephant Tenrec (not Chimp)	8	>Human chr6 30660087-30660172 GTAGAGGAGATGGCGCAGGGGACACGGGCAAAGACTTGGGGGTTCCTGGGACCCTCAGACGTGTGTCCTCTTCTCCCTCCTCCCAG -35.80 ...((((((..((...(((((((((((.....(((((((((.....)))))))))...)))))))))))...)))))))).... []
NM_152345_9	chr17:24963151-24963259	Rhesus GuineaPig Hedgehog Cat Horse Cow Elephant Tenrec (not Human, Chimp)	8	>Rhesus chr16 24844746-24844854 GTGAGGCCCCTGCCCGGTGCTGGGAGAGGTGGGGGGCTGGGGCTCCAGGAGATGCTGGGAGGCCATGGCTTCCTGCAGTGTCCCTCACCCCTTGGGATCTGGTGGGGGCAG -63.53 .....(((((...(((((.(((((.(((((((((((((.....((.(((((((.....)))))))))..))))))))))))))))).))).))..))))).. []
NM_025160_1	chr1:222685907-222686006	Human Chimp Rhesus Hedgehog Dog Cow Opossum Shrew	8	>Human chr1 222685906-222686005 GTAAAGTAGGGCATATAGAGCTGTGTGACTGCTGCTAAAATTACAGATTTGATGTGCATTTTGTGACATTTCTCGTTTTCTTTTATACCAATTTTTACAG -17.10 ((((((...((.(((.(((((.(((((.((...(((.....(((((.....)))))..))))....)))))....))))).))))....))))).....))).))...)))))).. []
NM_173474_1	chr16:15049279-15049354	Human Chimp Rhesus GuineaPig Cat Horse	6	>Human chr16 15049278-15049353 GTAGGTTAGGAAGCAGTGAATTGGGCGTTATCCCAAAAGGCTATTGGATATTTTATTTTATTTCTTTTTTAAACAG -10.10 ....((((((((((.((((((.((((...((((((.....)))))).))))).)))))).))))))..)))).. []
NM_198446_0	chr1:38046699-38046789	Human Chimp Rat Mouse Hedgehog Cow (not Rhesus)	6	>Human chr1 38046698-38046788 GTGAGAGGGGGCCCGTCGGGGCGGGAGGAAGGGGCTTGGCCCCGCGCAAGCGCCGGCCCTGACCGTCTGTCTCTCGCTCTCTCCCGGGCAG -45.90 .((.((((((((.....((((((((..((..((((((.((((...((....)))))))))))))..))..)))))))).))))))))..))..... []
NM_017865_6	chr1:247116458-247116546	Human Chimp Dog Cat Horse Elephant (not Rhesus)	6	>Human chr1 247116457-247116545 GTAACCTGATGGCTGAGACAGAAAGGGCAGGGGCGTCCTGGGATGTGGCCCTCCCTCGAGGCCCTCTGCTCCCTCTTTGCTGCCCGTAG -35.70 .....(((..(((...((.(((..(((((((((((((.((..((((.....))))..))..))))).))))))..))))))...)))..)))) []
NM_015232_11	chr12:150589-150673	Human Chimp Rhesus Tenrec Opossum	5	>Human chr12 150588-150672 GTAAGTGGAGCCCTGGTTGCCCAGGTGAGTGACTACCCTGCCCCCTTGTTCTTCTTCTCACCGTCTCTGTTGTTTCTCTTCTCAG -14.20 ..(((.((((((..(((..((...((((((.(((..((.....)))...))..)))))))).))..)))))).))..... []
NM_002912_7	chr6:111815810-111815896	Chimp Rhesus Rabbit Dog Horse (not Human)	5	>Chimp chr6 113298181-113298267 GTAAGTGGTTATTTATTATAGATCTCAGAACTAATTTTATTCCTTTGTTATCTAGTCTGTTATAAAGGATATGTTTTAATTAAGCAG -9.71 .....((.(((.(((..(((.((((((((.(((((((..((.....)).))))))).....)))).))))..)))).)))..)). []
NM_001031698_9	chr12:48314506-48314587	Human Chimp Rhesus Mouse Shrew	5	>Human chr1 38046698-38046788 GTGAGAGGGGGCCCGTCGGGGCGGGAGGAAGGGGCTTGGCCCCGCGCAAGCGCCGGCCCTGACCGTCTGTCTCTCGCTCTCTCCCGGGCAG -45.90 .((.((((((((.....((((((((..((..((((((.((((...((....)))))))))))))..))..)))))))).))))))))..))..... []

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hsa-mir-1224: human, cat, chimp, cow, dog, elephant, hedgehog, horse, mouse, rat, rhesus, tenrec
>Human   chr3     185441886-185441970
         GTGAGGACTCGGGAGGTGGAGGGTGGTGCCGCCGGGGCCGGGCGCTGTTTCAGCTCGCTTCTCCCCCCACCTCCTCTCTCCTCAG
-41.90   .(((((...(((((((((.(((.((.((.((.(((((........)))))..)))..)).)).))).))))))))).....)))))).  []
>Chimp   chr3     189762312-189762396
         GTGAGGACTCGGGAGGTGGAGGGTGGTGCCGCCGGGGCCGGGCGCTGTTTCAGCTCGCTTCTCCCCCCACCTCCTCTCTCCTCAG
-41.90   .(((((...(((((((((.(((.((.((.((.(((((........)))))..)))..)).)).))).))))))))).....)))))).  []
>Rhesus  chr2     87317186-87317270
         GTGAGGACTCGGGAGGTGGAGGGTGGCGCCGCCGGGGCCAGGCGCTGTCTAAGCTCGCTTCTCCCCCCACCTCCTCTCTCCTCAG
-44.00   .(((((...(((((((((.(((.((((..((..((((........)))))..)).)))))...)))).))))))))).....)))))).  []
>Rat     chr11    5223437-5223521
         GTGAGGACTGGGGAGGTGGAGGGTAGTACCATTAGAGCCAGAGCTCTGTCTCAGCTCCCTCTCCCCCCACCTCTTCTCTCCTCAG
-41.60   .(((((..(((((((((((((((.(((.....((((((....)))))).....)))))).....))))))))))..)))))).  []
>Mouse   chr16    20517994-20518078
         GTGAGGACTGGGGAGGTGGAGGGTAGCATCATTAGAGCCAGAGCTCTGTCTCAGCTCCCTCTCCCCCCACCTCTTCTCTCCTCAG
-43.20   .(((((..(((((((((((((((.(((.....((((((....)))))).....)))))).....))))))))))..)))))).  []
>Hedgehog        scaffold_257517 500-582
         GTGAGGACTCGGGAGGTGGAGGGTGGCGCTGGCAGGCCCCGGCGCCGGCTCAGCTcgcctcccccccacctcctctctcctcaG
-53.00   .(((((...(((((((((.(((.(((((.....))).)).)))))..))).)))).))))))))))...)))))).  []
>Dog     chr34    20141853-20141938
         GTGAGGACTCGGGAGGTGGAGGGTGGCGCCGCCAAGGCCAGGGCACTGTCTCAGCTCGCTTCTCCCCCCACCTCCTCTCTCCTCAG
-45.40   .(((((...(((((((((.(((.((((..((..(((.((((....)))))).)).)))))...)))).))))))))).....)))))).  []
>Cat     scaffold_215154 298791-298876
         GTGAGGACTCGGGAGGTGGAGGGTGGTGCTGCCAGGGCCAGGGCACTGTCTCAGCTCACTTCTCCCCCCACCTCCTCTCTCCTCAG
-44.90   .(((((...(((((((((.(((.(((((.(((.((....)).)))...)))))..)))...)))).))))))))).....)))))).  []
>Horse   chr19    18636594-18636679
         GTGAGGACTCGGGAGGTGGAGGGTGGCACTGCCAGGGCCAGGGCGCCGTCTCAGCTCGCTTCTCCCCCCACCTCCTCTCTCCTCAG
-43.40   .(((((...(((((((((.(((.(((.(((...((((....)).)).....)))...)))...)))).))))))))).....)))))).  []
>Cow     chr1     80024559-80024644
         GTGAGGACTCGGGAGGTGGAGGGTGGCGCTGCCAGGGCCAGGGCACTGTCTCAGCTCGCTTCTCCCCCCACCTCCTCTCTCCTCAG
-46.60   .(((((...(((((((((.(((.(((((.(((.((....)).)))...)))))..)))...)))).))))))))).....)))))).  []
>Elephant        scaffold_73625  3876-3968
         TTGAGGACTCGAGAGGTGGAAGAGTGGCCGTCGCCCAAGGCCCAGGGCGCTGTTTCAGCTGGCCCTCTCCCCCCCCACCTCTCTCTCATCAG
-39.10   .(((((....(((((((((.((((.(((((((((((.......)))))).......)).)))))))).....)))))))))))))....  []
>Tenrec  scaffold_318235 49157-49243
         GTGAGGACTTGGGAGGTGGAgggcggcgtggccggcccggcgggcgccgTCTCAGCTCGCCGGCCCCCCACCTCCTCTCTCCTCAG
-56.80   .(((((...(((((((((.(((((((.((..((((....)))))..)).)))))))).))).))))))))).....)))))).  []
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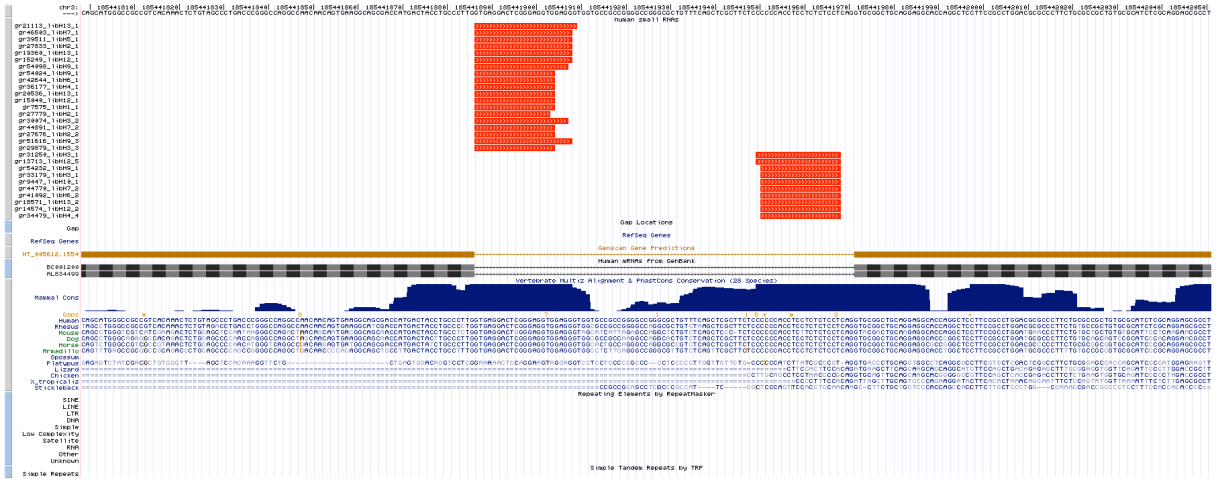

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        GTGAGTGCGGGAAgggcgcggggcggagagggcgcggggcccgggccgACCCTCACCTCCCGCTTCTCCAG
-38.10  ..(((.(((((.(((....(((((((...((((.....))))...))).)))))..)))))))))..)))...  []
>Chimp  chr19   41054125-41054195
        GTGAGTGCGGGAAgggcgcggggcggagagggcgcggggcccgggccgACCCTCACCTCCCGCTTCTCCAG
-38.10  ..(((.(((((.(((....(((((((...((((.....))))...))).)))))..)))))))))..)))...  []
>Rhesus chr19   42038790-42038860
        GTGAGTGCGGGAAgggcgcggggcggagagggcgcggggcccgggccgAGCCTCACCTCCCGCTTCTCCAG
-35.30  ..(((.(((((.(((....(((((((...((((.....))))...)))..))))).)))))))))..)))...  []
>Rat    chr1    182137567-182137638
        GTGAGTGCAGGGCGGGCGTGGGGCGGAGAGGGTGCGGGACCCGGGCCGACCCCTCACCGCCGGCTTCTCCAG
-37.50  ..(((.((..(((((....(((((((...((((.....))))...)))...))))).))))...)))))).))..)))...  []
>Mouse  chr7    114695991-114696062
        GTGAGTGCAGGGCGGGCGCGGGGTGGAGAGGGTGCGGGACCCGGGCCGACCCCTCACCGCCGGCTTCTTCAG
-34.10  .((((.((..(((((....(((((((...((((.....))))...)))...))))).))))...)))))).))...)))).  []
>Rabbit scaffold_206110 54441-54510
        GTGAGTgcggggcgggcgcggggcggagagggcgcggggcgAGCCCACCCCTCACCGCCCGCTTCTCCAG
-37.30  ........((((.((((...(((((((.(((((....(((....)))..)))))).))))))))))))..  []
>Shrew  scaffold_254988 40882-40951
        GTGAGTgcggggcggccgcggggcggggaagggggccgggcCATCGCCTCACCGCCCCGCTCCTGCAG
-41.50  .....(((((((.....(((((((((.((.(((((((....)))).)).)))))..)))))))))))))).  []
>Hedgehog       scaffold_353390 868-937
        GTGAGTGTGGGGCGGCCGTGGGGCGGGGAGGGCAGGACAGGCCCGACCCCTCAACCTCCCGCTCCCGCAG
-37.40  .....((((((((((..((.(((.(((..((((.......))))..)))))))..))...)))))..)))))).  []
>Dog    chr1    5586721-5586787
        GTGAGTgcggggcggccgcgggcgggagggcgcgggcccgggcTCGGCTCACCGCCCGCTCCTGCAG
-43.70  .....(((((((.....(((((((..((((.(((((....)))))))))..)))))))))))))))).  []
>Cat    scaffold_213929 13980-14047
        GTGAGTGCGGGGCAGCCGCGGGCGGGAGGGCGGGGGACCGGGCCAAGCCTGACCGCCCGCTCCTGCAG
-40.50  .....(((((((.....(((((((..((((..(((.......)))..)))))..)))))))))))))))).  []
>Horse  chr10   6630649-6630716
        GTGAGTGTggggcggccgcggggcgggggggcgcgggcccgggccAGCCCTCACCGCCCGCTCCTGCAG
-41.20  .....((..((((((..((((....(((((((...((((....)))).)))))))..))))))))..))..)).  []
>Opossum        chr4    373484038-373484120
        GTGAGTACTAGGGGTCCAGCATTGCAGGGAGAGACCAGTTGGGACCTTGACCCTCACCTTTGTTTAATTCCTCCCACACTCAG
-21.20  .(((((...(((((((..((((.((.((((.((((.((....)))...)))))..))))))....))))..))))))....)))))).  []
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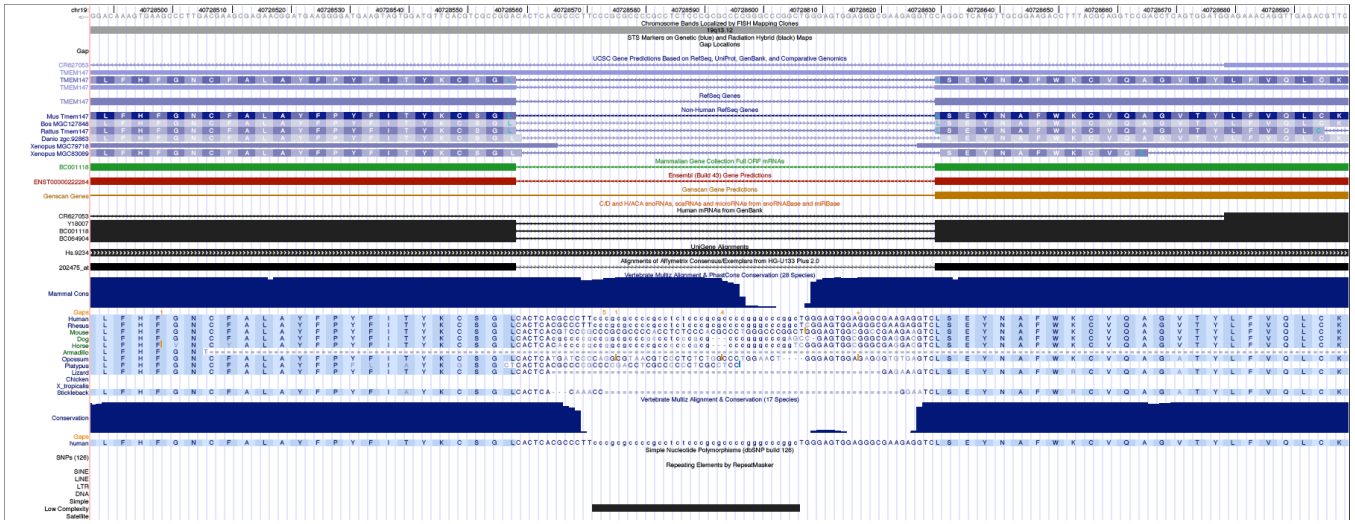

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NM_015847_7: human, chimp, cow, dog, guinea pig, hedgehog, horse, rabbit, rat, rhesus, shrew, tenrec
>Human   chr18    46055413-46055495
         GTGAGGCCCCAGTGGGTGGAGGGAAGGCACAACCCTGACCTTACCCAGTACCTGCCCTGACCCCACCCCATTTGCCTCTACAG
-31.80   (((((((...(((((((((.((..(((((.....(((........)))....))).)).)..)))))))).))).)))))..)).. []
>Chimp   chr18    46531726-46531808
         GTGAGGCCCCAGTGGGTGGAGGGAAGGCACAACCCTGACCTTACCCAGTACCTGCCCTGACCCCACCCCATTTGCCTCTACAG
-31.80   (((((((...(((((((((.((..(((((.....(((........)))....))).)).)..)))))))).))).)))))..)).. []
>Rhesus  chr18    43353111-43353193
         GTGAGGCCCCAGTGGGTGGAGGGAAGGCACAACCCTGACCTTACCCAGTACCTGCCCTGACCCCACCCCATTTGCCTCTACAG
-31.80   (((((((...(((((((((.((..(((((.....(((........)))....))).)).)..)))))))).))).)))))..)).. []
>Rat     chr18    16189781-16189861
         GTAATGCCCTGGTGGGCAGGGGGAAGGCACAATCCCGCACTCCTCAGAACCTGCCTGACCCCAGCCTGTTTGCCTCTGCAG
-28.70   ....(((...(((((((.((((..((((((...((.............))...)))))..)))))).))))....)))...))). []
>GuineaPig       scaffold_264589 25013-25095
         GTGAGGCCCTGATGGGCAGGGGGAAAGCACAGCCCTAACCTTACCCAATACCTACCCTGACCCCTCCCCGTTTGCCTCTGCAG
-26.36   (((((((...((((((.(((((.........................................)))))..)))))).)))))..)).. []
>Rabbit  scaffold_148539 10848-10929
         GTGAGGCCCCAGTGGGCGGGGGAAGGCACAACCCTACCCTTATCCGGTACCTGCCCTGACCCAACCCCGTTTGCCTCTGCAG
-27.90   (((((((......(((..(((((.....(((.......))))..)))).))..)))..)))).....)))))..)).. []
>Shrew   scaffold_211252 4116-4198
         GTGAGGCCCTGGTGGGCAGGGGAATGGCACAACCTTAATCTGACCCAGTACCTGCCCTGACCCCACCCCATTTGCCTCTGCAG
-28.43   (((((((...((((((..((((...((.(.(.................)).))..)))))...)))))).....)))))..)).. []
>Hedgehog        scaffold_338375 13357-13439
         GTAAGGATATGGTATGCAGGGGGAAGGCACAACCCTAGCCTTGGCCAATGCCTGCCCTGACCTCACCCCATTTGCCTCTACAG
-28.10   ((((((..((((..((.((((((.((((....((.......)).....)))))).)))...)))))..)))).....)))..)).. []
>Dog     chr7     2345958-2346038
         GTGAGGCCCTGGTGGGCAGGGGGAAGGCACAACCTTATCCTTACCAAGTACTTGCCCTGACCCCCCCATTTGCCTCTGCAG
-29.90   (((((((...((((((..((((..((((((....(((.........)))....))).)).)..)))))))))).))))..)).. []
>Horse   chr8     62052972-62053054
         GTGAGGCCCTAGTGGGCAGGGGGAAGGCACAACCCTAACTTCACCCAGTACCTGCCCTGACCCCACCCCATTTGCCTCTGCAG
-30.00   (((((((...((((((..((((..((((((.......................)))).)).)..)))))..)))))).))))..)).. []
>Cow     chr24    12456626-12456708
         GTGAGGCCCTGGTGGGCAGGGGGACGGCACAACCGTAACCTCACCAGCTACCTGCCCTGACCCCACCCCATTTGCCTCTGCAG
-29.43   (((((((...((((((((((((((((((.....))))..............)))..)))))..)))))))).....)))))..)).. []
>Tenrec  scaffold_307093 84313-84394
         GTGAGCCTCTGAGGGGCAGGGGAAAGACCTGACAGGAACCTTACTCAGTACAACCCTGACCCCGCCCCATTTCCCTCTGCAG
-22.82   (((((.......(((((.((((..((..((((.((....)).....)))).......)).)..)))))))))).....)))..)).. []
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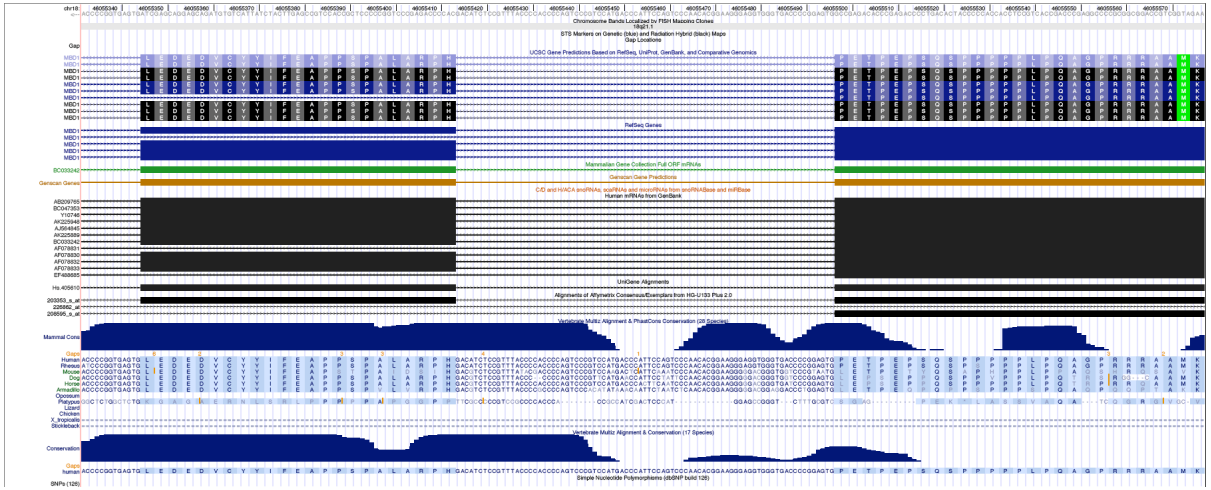

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hsa-mir-1225: human, chimp, cow, dog, hedgehog, horse, mouse, rat, rhesus
>Human   chr16    2080196-2080285
         GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGGCTCTGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
-48.20   .((((..((((.(((.(((((..((..((...((((((((((...)))))))))...))...))..))...)))))).)))).)))))..  [1]
>Chimp   chr16    2186743-2186832
         GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGGCTCTGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
-48.20   .((((..((((.(((.(((((..((..((...((((((((((...)))))))))...))...))..))...)))))).)))).)))))..  [1]
>Rhesus  chr20    2081736-2081825
         GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGGCTCTGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
-48.20   .((((..((((.(((.(((((..((..((...((((((((((...)))))))))...))...))..))...)))))).)))).)))))..  [1]
>Rat     chr10    96872038-96872131
         GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACACCCTGGGTCTCGCGAGCCCAGGGTGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
-49.90   .((((..((((.(((.(((((..((..((...((((((((.((....)))))))))))...))...))..))...)))))).)))).)))))..  [1]
>Mouse   chr17    70854749-70854842
         GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACACCCTGGGTCTCGCGAGCCCAGGGTGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
-49.90   .((((..((((.(((.(((((..((..((...((((((((.((....)))))))))))...))...))..))...)))))).)))).)))))..  [1]
>Hedgehog         scaffold_375456 27864-27955
         GTGGGTACGGCCCAGTgggggggAGAGGGACGCCCTGGGCCCACGTAGCCCGGGGCGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
-51.20   .((((..((((.(((.(((((..((..((.(((((((((.......)))))))))...))...))..))...)))))).)))).)))))..  [1]
>Dog     chr6     38736837-38736931
         GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACACCCTGGGCCCAGGTGAGCCCAGGGTGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
-51.40   .((((..((((.(((.(((((..((..((...((((((((((.......)))))))))...))...))..))...)))))).)))).)))))..  [1]
>Horse   chrUn    73886090-73886184
         GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGGCTCAGGTGAGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
-54.60   .((((..((((.(((.(((((..((..((...((((((((((....)))))))))))...))...))..))...)))))).)))).)))))..  [1]
>Cow     chr25    61293-61385
         GTGGGTACGGCCCAGGGGGGGAGAGGGACGCACCCTGGGCCCAGCAGAGCCCAGGGCGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
-53.00   .((((..((((.(((((((((.((..((..((.(((((((((.......)))))))))..))...))..))...)))))).)))).)))))..  [1]
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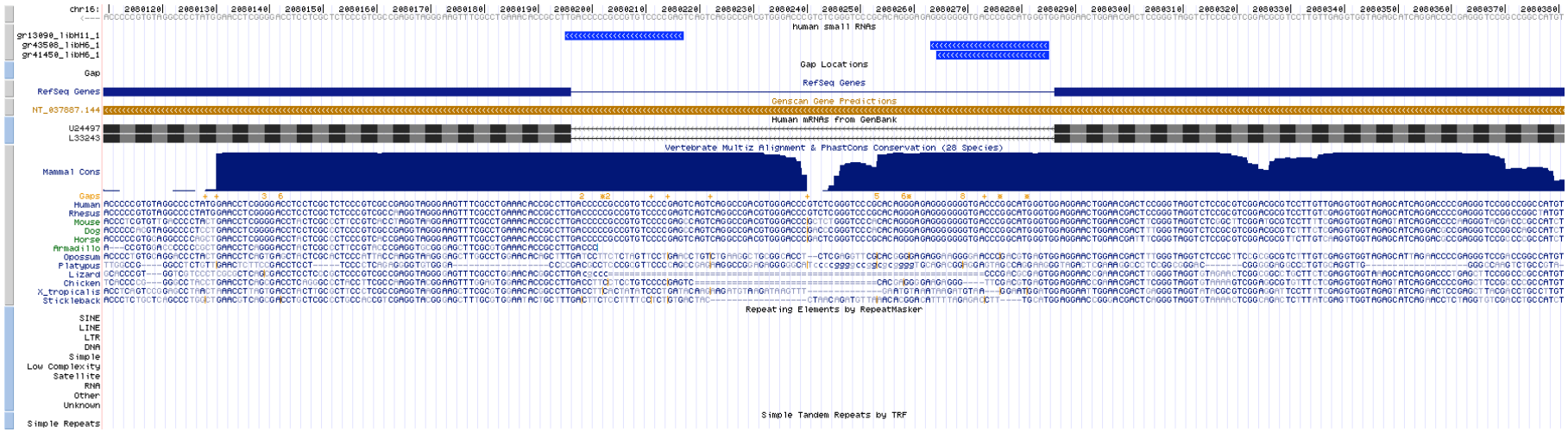

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hsa-mir-877: human, cow, dog, elephant, mouse, rat, rhesus, tenrec
>Human   chr6     30660087-30660172
         GTAGAGGAGATGGCGCAGGGGACACGGGCAAAGACTTGGGGGTTCCTGGGACCCTCAGACGTGTGTCCTCTTCTCCCTCCTCCCAG
-35.80   ...((((((..((...((((((((((.........((((((((.....)))))))))...)))))))))...))))))))....  []
>Rhesus  chr4     30166021-30166106
         GTAGAGGAGATGGCGCAGGGGACACGGGCTAAGACTCGGGGGTTCCTGGGACCCTCAGACATGTGTCCTCTTCTCCCTCCTCCCAG
-36.41   ...((((((..((...((((((((((..((.......((((((.....)))))))))...)))))))))...))))))))....  []
>Rat     chr20    2958183-2958267
         GTAGAGGAGATGGCGCAGGGGACACAAGGTAGGCCTTGCGGGTCTGTGGGCCCTTGGACATGTGTCCTCTTCTCCCTCCTCCCAG
-35.00   ...((((((..((...((((((((((..((...((....((((....)))))..)))).)))))))))...))))))))....  []
>Mouse   chr17    59608553-59608637
         GTAGAGGAGATGGCGCAGGGGACACAAGGTAGGCCTTGCGGGTCTGTGGACCCTTGGACATGTGTCCTCTTCTCCCTCCTCCCAG
-35.60   ...((((((..((...((((((((((..((...((....((((....)))))..)))).)))))))))...))))))))....  []
>Dog     chr12    3408300-3408384
         GTAGAGGAGATGGCGCAGGGGACATGGGCTGAGACTTGGGAGTTCCTAGAACCTCTAGACATGTGTCCTCTTCTCCCTCCTCCAG
-32.50   ...((((((..((...((((((((((..((((((..(((((....)))))...)))).))...)))))))))...))))))))...  []
>Cow     chr23    26513259-26513343
         GTAGAGGAGATGGCGCAGGGGACACGGGCTAAGACTGGGGGCTCCCGGGACCCCCCAACATGTGTCCTCTTCTCCCTCCTCCCAG
-38.30   ...((((((..((...((((((((((.........((((((.((....)).)))))))...)))))))))...))))))))....  []
>Elephant        scaffold_82320  103-188
         GTAGAGGAGATGGCGCAGGGGACACAGGCTATGACATGGGGGCTCCTGGGGCCCTTGAACATGTGTCCTCTTCTCCCTCCTCCCAG
-35.70   ...((((((..((...((((((((((.....((...((((((((.....)))))))..)))))))))...))))))))....  []
>Tenrec  scaffold_315780 12230-12314
         GTAGAGGAGATGGCGCAGGGGACACGGGCGGAGACTGGGGCTGGCTGGGGTCCTCCAACATGTGTCCTCTTCTCCCTCCTCCCAG
-36.20   ...((((((..((...((((((((((...((((((..((....))..)))))).)))....)))))))))...))))))))....  []
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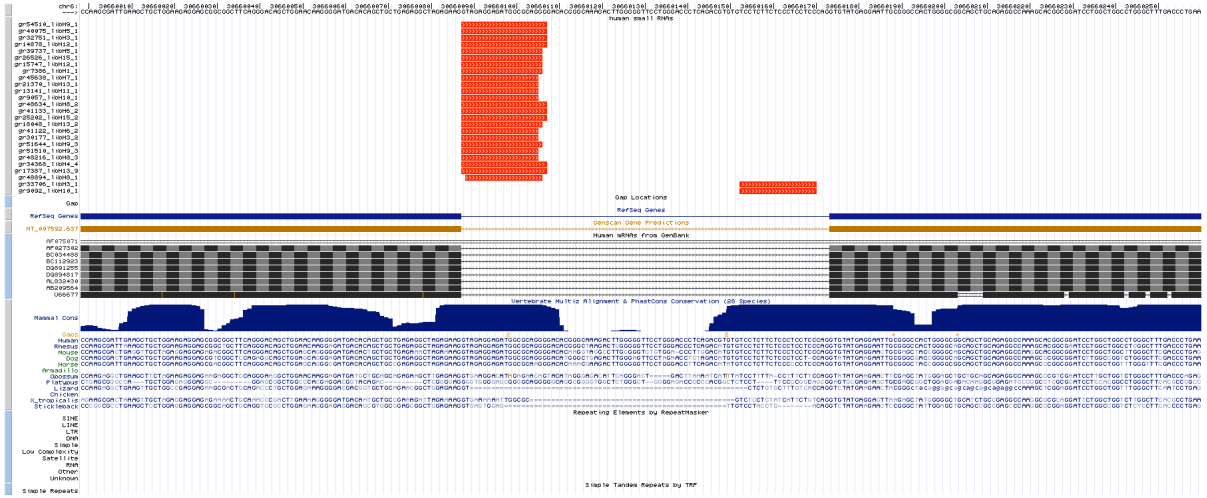

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NM_152345_9: cat, cow, elephant, guinea pig, hedgehog, horse, rhesus, shrew, tenrec
>Human  chr17   24963150-24963258
        GTGAGGCCCCTGCCGGTGCTGGGAAGGTGGGGGGCCGGGGCTCCAGGAGATGCTGGGAGGCCATGGCTTCCTGCAGTGTCCCTTACCCCTTGGGATCTGGTGGGGGCAG
-57.60  .....(((((..((((((..((((..(((((..((((((.((((.(.....)).)))).)).)))).)))))....)))).)))).....)).)))))..  []
>Rhesus chr16   24844746-24844854
        GTGAGGCCCCTGCCGGTGCTGGGAGGGTGGGGGGCTGGGGCTCCAGGAGATGCTGGGAGGCCATGGCTTCCTGCAGTGTCCCTCACCCCTTGGGATCTGGTGGGGGCAG
-63.53  .....(((((..(((((.((((.(((((((((.............(((.(((((((....)))))))))..))))))))))))))).)))..))))))..  []
>GuineaPig      scaffold_292141 27304-27414
        GTGAGGCCCCCTGCTCCTGCTGGGGAGGGGTGGGATGGGGGCTCCAGGAGGTGCCGGGAGGCCATGGCGTCCTGCAGCGTCCCTCACCCCTGGGGTCTGGGGGGCAG
-62.20  .....((((((((((((.......(((((((((..(((.((((.(((((.((((....)))).....)).)))))).)))).))))))))))))))..))))))..  []
>Hedgehog        scaffold_368176 18018-18153
        GTGAGATCCCTTGTTGGTGCTGGTGGTAGGGTGGTGGCGGGCAGGGCAGGTTTGCACAGGGGCTCCAGAAGGTGTTGGGAGGTCATGGCTTCTGCAGTGTTCCTCACACTTTGGGATCTgggggggTGGCAG
-43.80  .((..(((((((...(((.((......(((((.((((.(((((..(((((...((.((.((.((((.((.....)).)))).)).)))).)))))..)))))..))))))))))).)))..)))))))..)).  []
>Horse  chr11   42166373-42166497
        GTGAGGCCCCCTGCTGGTGCTGGGGAGGGCTGGGGCAGGGCAGGGGGTCAGGGGCTCCAGAGGTGCTGGGAGGCCATAGCTTCTACAATGTCCCTTACCCCTTGGGATCTGGTGGGGGCAG
-58.20  .....(((((.(((((.(((((.((...((((((.....((..((....(((((.....)))).)).)).)...)).)).)....)))))))...)))))))).)))..))))))..  []
>Cow    chr19   19097998-19098095
        GTGAGGGCCCCTGCTGGGGCTGGGGAGGGTTGGGGCTGGGGGAGGGGTCACGGCTTCTACAATGGCCCTCACTTTGGGATCTGCGGGGGGTCAG
-40.40  ....((.(((((((.((..((.((...(((.(((((((....((..((....)).))....)))))))).)))))).)))..)))))))).))..  []
>Elephant       scaffold_8762   27423-27536
        GTGAGGCCCCTGCTGGTGCTGGGTAGGGGTGGGGCAGGATTTCCAGGAGGTCCTGGGAGGCTATGGCTTCCTGCAATGTCCCTCACCCCTTGGGATCTTGCGGGGGGTAG
-54.60  ......(((((((.(((.((....(((((((((...((((...(((((((((.((((....)))).)))))))))....)))))))))))))).)).))))..)))))))....  []
>Tenrec scaffold_319342 84355-84464
        GTGAGGCCCTGCCGGTGCTGGGGAGGGGTGGGGCAGGGTCTCCATGAGGTGTGGGAGGTCATGGCTTCCTACAATGCCCCTCACCCCTTGGGATTTGGGGGGGCAG
-53.86  .....(((((.((((..((.(((.((((..(((((((.............((((((((((....)))))))))).)))))))...)))))))).))..)))).)))))..  []
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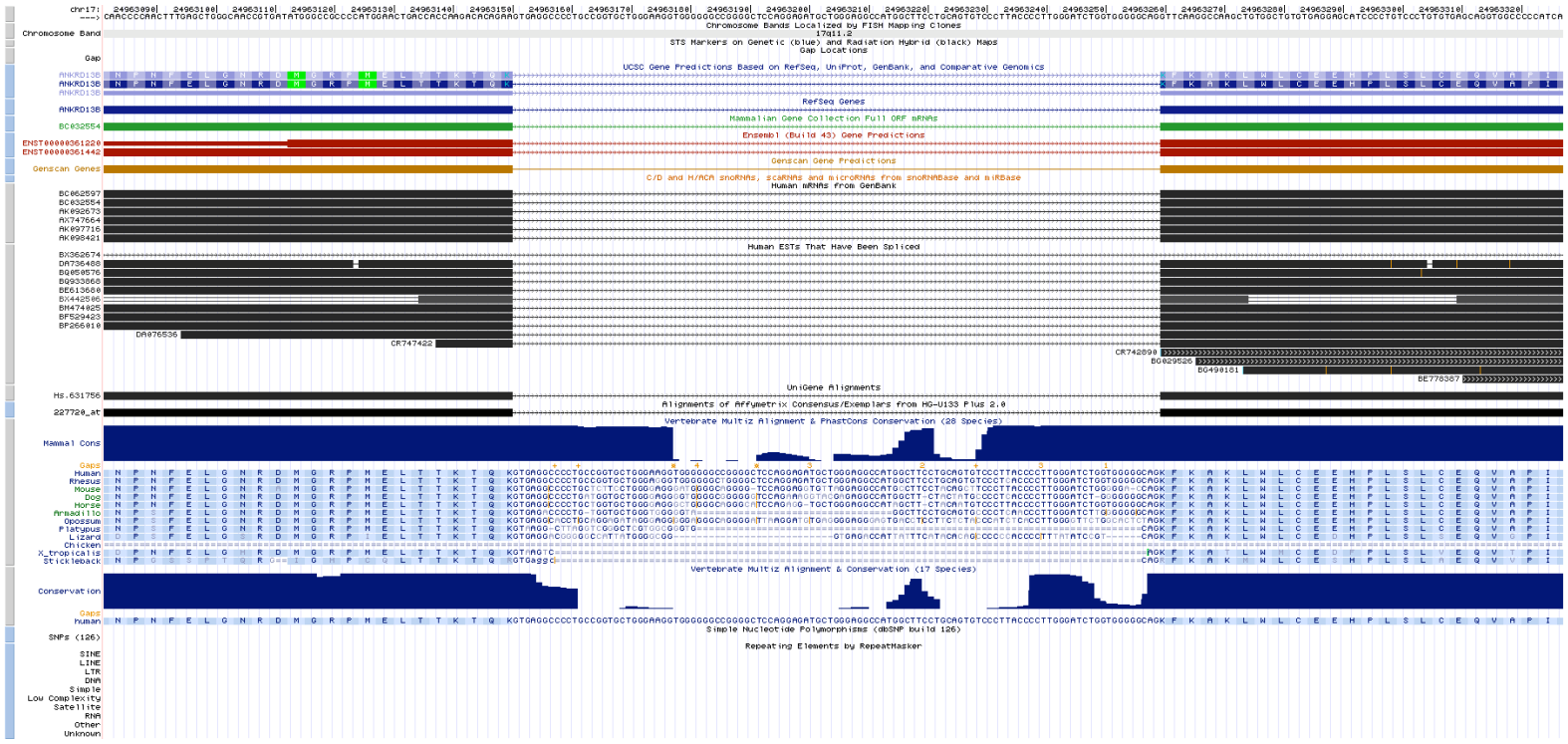
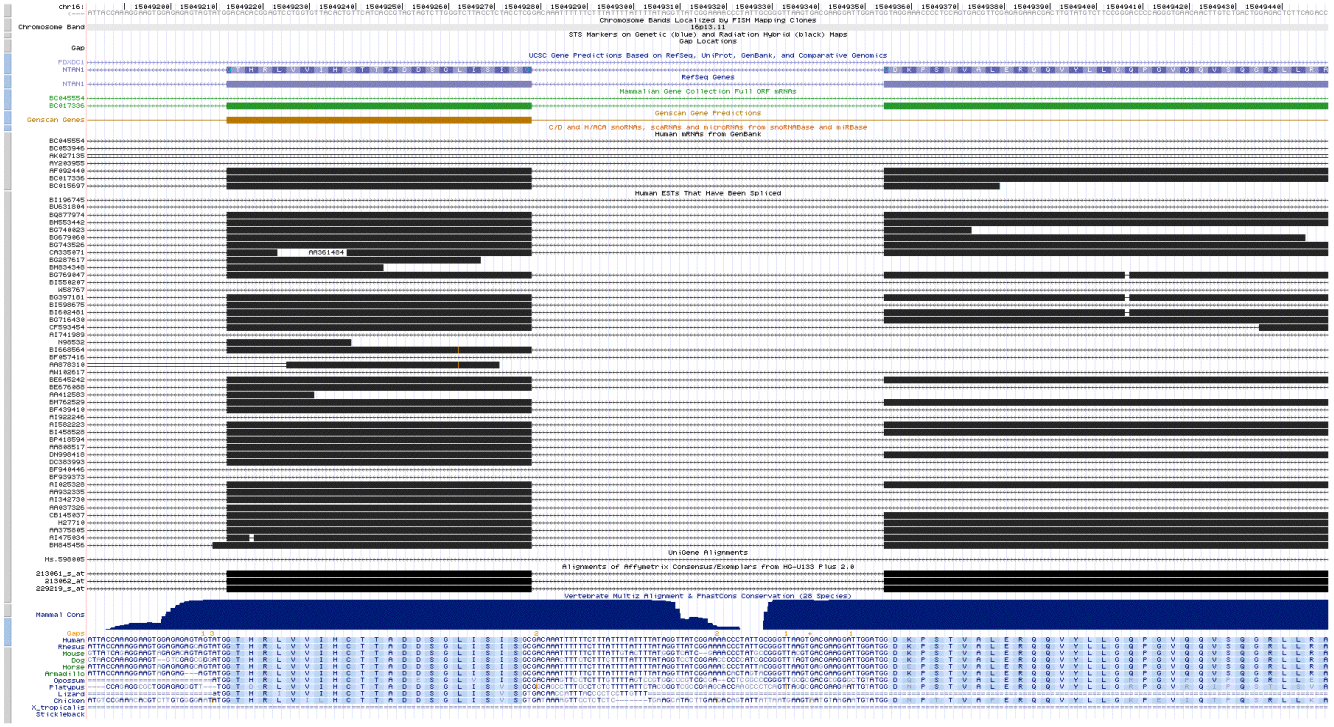
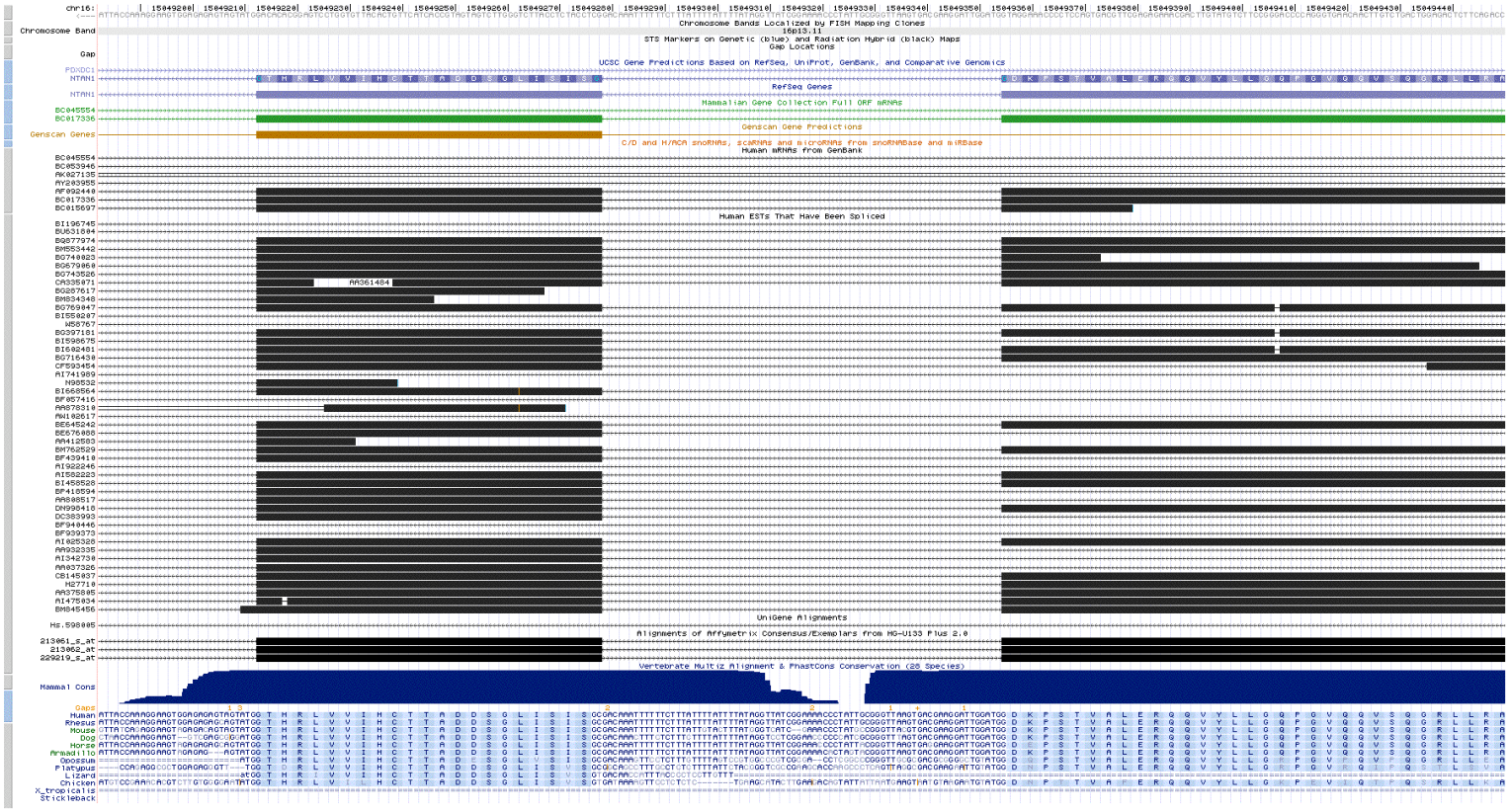


```
NM_025160_1: human, chimp, cow, dog, hedgehog, opossum, rhesus, shrew
>Human  chr1     222685906-222686005
        GTAAAGTAGGGCATATAGAGCTGTGTGACTGCTGCTAAAATTACAGATTTGATGTGCATTTTGTGACATTTCTGTTTTTCTTTTATACCAATTTTTACAG
-17.10  ((((((...((.(((.(((((.((((.((...(((....((((......))))..)))....)).))))....)))))).....)))..))...)))))).. []
>Chimp  chr1     205049905-205050004
        GTAAAGTAGGGCATATAGAGCTGTGTGACTGCTGCTAAAATTACAGATTTGATGTGCATTTTGTGACATTTCTGTTTTTCTTTTATACCAATTTTTACAG
-17.10  ((((((...((.(((.(((((.((((.((...(((....((((......))))..)))....)).))))....)))))).....)))..))...)))))).. []
>Rhesus chr1     82202846-82202945
        GTAAAGTAGGGCATATAGAGCTGTGTGACTGCTGCTAAAATTACAGATTTGATATGCATTTTGTGACATTTCTGTTTTTCTTTTATACCAATTTTTACAG
-16.20  ((((((...((.(((.(((((.((((.((...(((..(((((...)))))).....)))....)).))))....)))))).....)))..))...)))))).. []
>Shrew  scaffold_236018 46395-46494
        GTAAAGTAGGGCATATAGAGCTGTGTGACTGCTGCTAAAATTACATATTTGATGTACACtttgtgacatttctgtttttcttttataccaATTTTTACAG
-14.80  ((((((...((.(((.(((((.((((.((((..((((.....))))...)))))).....)).))))....)))))).....)))..))...)))))).. []
>Hedgehog        scaffold_315531 7725-7827
        GTAAAGTGCGGCCCGAGAGCTAGCTGTGTGACTGCTGCGGAAACGAGTCCCCGGCTGTGCATTTTGTGACATTTCTGCTTTTCTCCTATACCGATTTCTGCAG
-25.10  (((((((.(((...(((((..(((.((((.(((((.((((...((......)).)))))))....)).))))....)))).))))).....)))))))..))).. []
>Dog    chr7     41061071-41061170
        GTAAAGTAGGGCATATAGAGCTGTGTGACTGCTGCTAAAATTATATATTTGAATGTGCATGTTGTGACACTTCTGTTTTTCTTTATGCCAATTTTTGCAG
-27.10  ((((((...((((((.(((((.((((.((((.....(((.......)))....)))).)).)).)))).....)))))....)))))))...)))))).. []
>Cow    chr16    24511052-24511151
        GTAAAGTAGGGCATATAGAGCTGTGTAACTGCTGCTAAAATTATATATTTGATGTGCATTTTGTGACATTTCTGTTTTTCTCTTATACCAATTTTTGCAG
-15.90  ((((((...((.(((.(((((.((((.((...(((....((((......))))..)))....)).))))....)))))).....)))..))...)))))).. []
>Opossum         chr2     135883898-135884001
        GTAAAGTAGGGCATATGGAAATGTATAACTGGTGTTAAAATTACACATCTGATGTGCAAATCATAACACTTTTGTTTTTCTCTCTTTTATATCAATTTTTGCAG
-16.72  ((((((...((.(((.(((.......(((.(((((((..(((.(((((...)))))..)))..)))))))...)))).....)))..))).)).)...)))))).. []
```

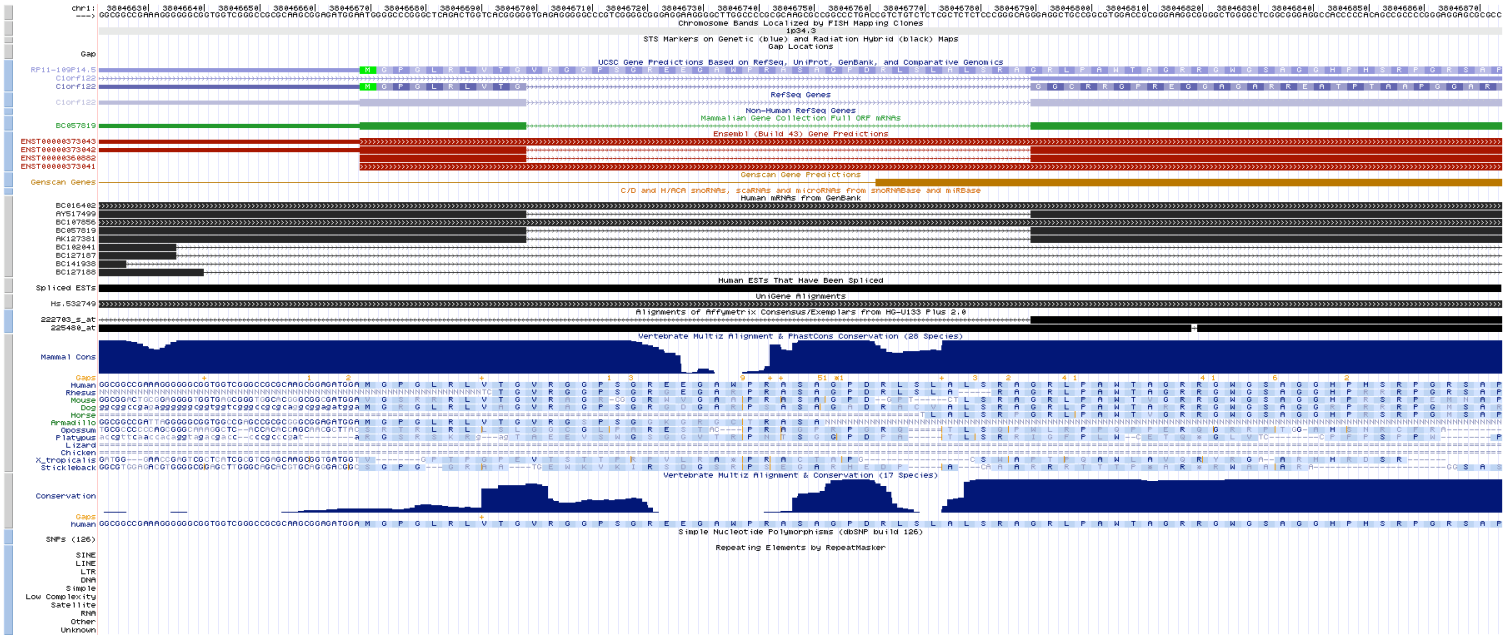


```
NM_173474_1: human, cat, chimp, guinea pig, horse, rhesus
>Human   chr16    15049278-15049353
         GTAGGTTAGGAAGCAGTGAATTGGGCGTTATCCCAAAAGGCTATTGGATATTTTATTTTATTTCTTTTTTAAACAG
-10.10   ....(((((((((.((((((.((((...(((((.............)))))).))))).)))))).)))))).))))..   []
>Chimp   chr16    15388531-15388606
         GTAGGTTAGGAAGCAGTGAATTGGGCGTTATCCCAAAAGGCTATTGGATATTTTATTTTATTTCTTTTTTAAACAG
-10.10   ....(((((((((.((((((.((((...(((((.............)))))).))))).)))))).)))))).))))..   []
>Rhesus  chr20    73259156-73259231
         GTAGGTTAGGAAGCAGTGAATTGGGCGTTATCCCAAAAGGCTATTGGATATTTTATTTTATTTCTTTTTTAAACAG
-10.10   ....(((((((((.((((((.((((...(((((.............)))))).))))).)))))).)))))).))))..   []
>GuineaPig       scaffold_156887 4308-4383
         GTAGGTTAGGAAGCAGTGAATTGGGCATTATCCCAAAAGGCTACtggatgttttattttatttctttttttaaacag
-11.90   ....(((((((((.((((((..(((((((...((....)).......)))))))...)))))).)))))).))))..   []
>Cat     scaffold_208046 252702-252777
         GTAGGTTAGGAAGCCGTGAATCGGGCATCACCCCCCGGGGCTCCTGGATGTTTCATTTTCTCTCTTTTCCAACCAG
-20.20   ...((((.(((((....((((..(((((((.((((....)))).......)))))))..)))).......)))))))))..   []
>Horse   chr13    12550994-12551069
         GTAGGTTAGGAAGGAGTGAATTGGGCATTATCCCCAAAAGGCTATTGGATATTTTATTTTATTTCTTTTTTAAACAG
-14.00   ....(((((((((((((((((.((((...(((((.............)))))).))))).)))))))))))))).))))..   []
```



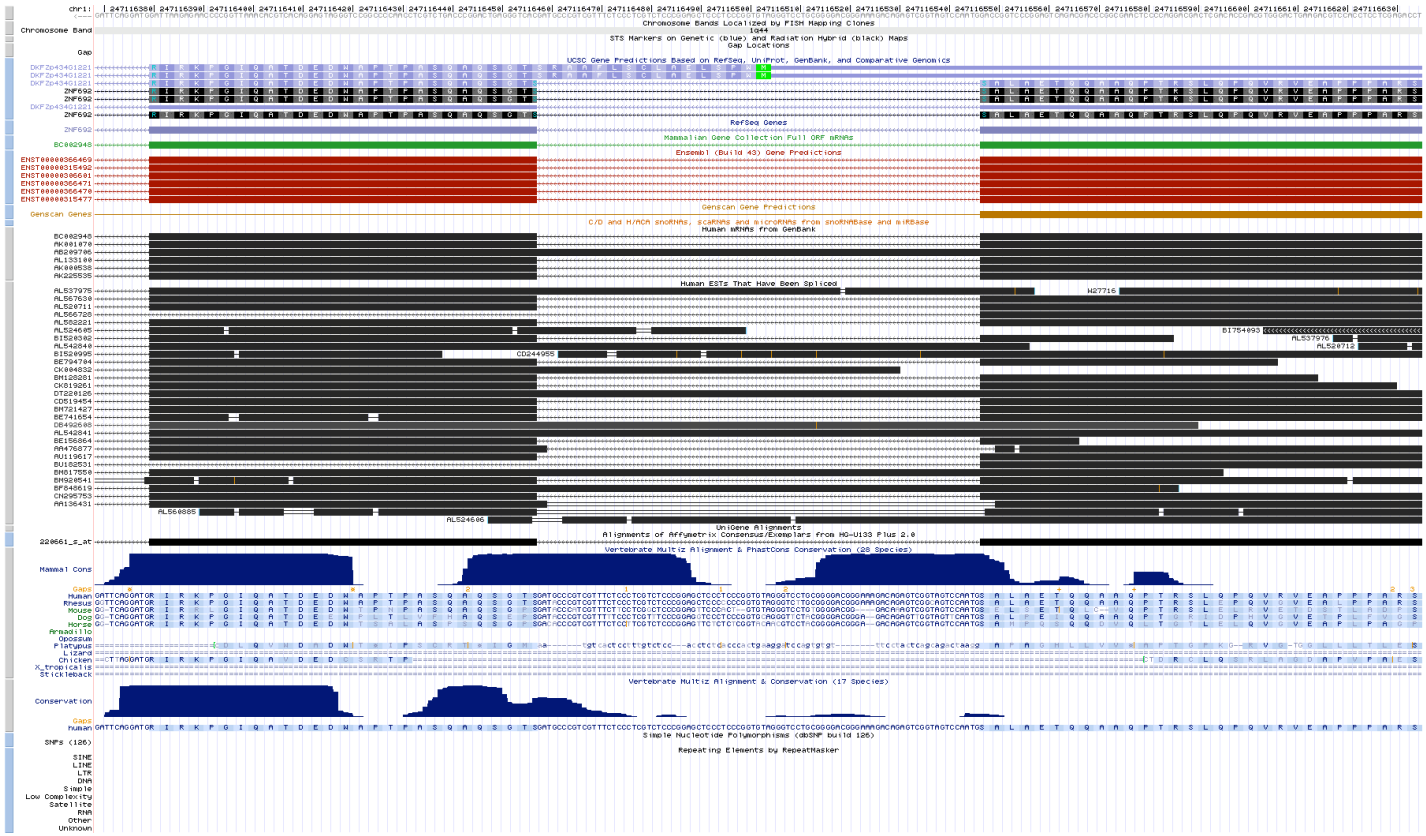
```
NM_198446_0: human, chimp, cow, hedgehog, mouse, rat
>Human   chr1     38046698-38046788
         GTGAGAGGGGGCCCGTCGGGGCGGGAGGAAGGGGCTTGGCCCCGCGCAAGCGCCGGCCCTGACCGTCTGTCTCTCGCTCTCTCCCGGGCAG
-45.90   .((.(((((((.....(((((((..((..(((((.((((...((....)))))))))))..))..))))))).))))))))..)).....  []
>Chimp   chr1     38385021-38385111
         GTGAGAGGGGGCCCGTCGGGGCGGGGGGAAGGGGCTTGGCCCCGCGCAAGCGCCGGCCCTGACCGTCTGTCTCTCGCTTTCTCCCGGGCAG
-45.50   .((.(((..(((.....(((((((((.((..(((((.((((...((....)))))))))))..))).))))))))..)))..))).)).....  []
>Rat     chr5     28912879-28912965
         GTGAGAGCGGGCCCGCGGGGCGGTGGGTTGGGGCCGCGACCTCGCGCCTCCCAGCGCCGGCCCTGACGCGGTCTCTCTCCCGGGCAG
-47.70   ..(((((.(((((((((((((((((..(((((((.((((....)))).))))))))))).)))))).)).)))))))))).......  []
>Mouse   chr4     30676876-30676963
         GTGAGAGCGGGCCGGCGGGGCGGTGGGTTGGGGCCGCGACCTCGCGCCGCCTAGCGCCGGGCCCTGACGCCGTCTCTCTCCCGGGCAG
-43.50   .......((((..((.(((((((((..((..(((((.((.....((((.....)))))))))))..))))))))))).))))))).....  []
>Hedgehog         scaffold_273501 14459-14549
         gtgagagggggcccgtcggggcgggggggagggggctcGAACTCCGCGCGAGCGCCGGCCCTGACCGCCTGTTCTCGCTCTCCCCGGGCAG
-43.80   .((...((((((...((.((..((((.((..(((((.((.....((((....)))).))))))))..)).))))..)).)).)..))))))...)).  []
>Cow     chr3     11512244-11512333
         GTGAGAGGGGGCCCGTCGGGGCGGGGGGAAGGGGTTCTGACCCGGCGCAAGCGCCGGCCCTGACCGTCTGTCTCGCTCTCTCCCGGGCAG
-44.21   .((.(((((((((.....(((((((((..((..((((.......((((((....)))))))))))..)).))))))))))))))))..))).....  []
```

intron has coding potential, but has evidence of multiple spliced ESTs

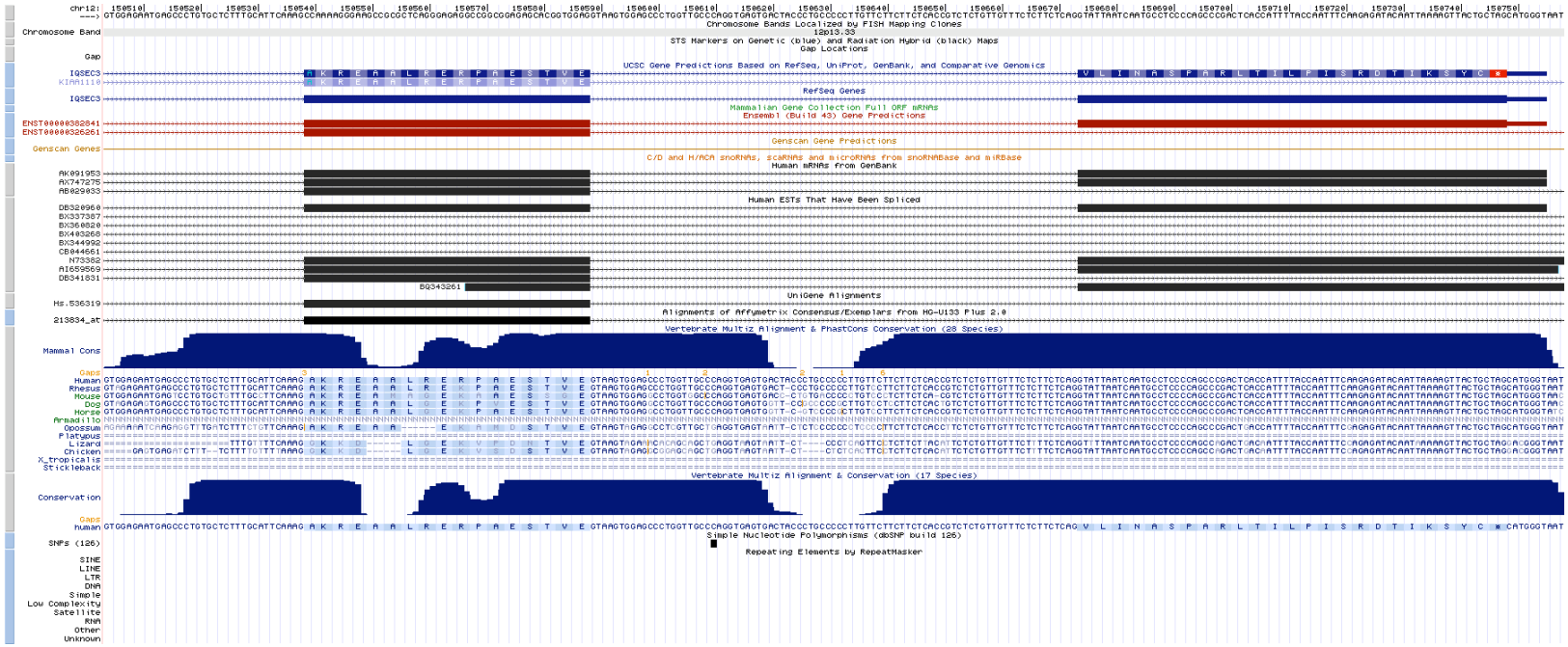


NM_017865_6: human, cat, chimp, dog, elephant, horse

```
>Human   chr1     247116457-247116545
         GTAACCTGATGGCTGAGACAGAAAGGGCAGGGGCGTCCTGGGATGTGGCCCTCCCTCGAGGCCCTCTGCTCCCTCTTTGCTGCCCGTAG
-35.70   .....(((..(((...((.((((..(((((((((((.((..((((.........))))..)).)))).)))))))..)))))...)))..)))  []
>Chimp   chr1_random      7836039-7836127
         GTAACCTGATGGCTGAGACAGAAAGGGCAGGGGCGTCCTGGGATGTGGCCCTCCCTCGAGGCCCTCTGCTCCCTCTTTGCTGCCCGTAG
-35.70   .....(((..(((...((.((((..(((((((((((.((..((((.........))))..)).)))).)))))))..)))))...)))..)))  []
>Dog     chr16    16701931-16702017
         GTAACTTGATGGTTGAGACAGAGGGCAGGGGCATCTTGGGACGTGGCCCTCCCTGGAGGCCCTTTGCTCCCTTTTTGCTGCCCATAG
-29.60   ........((((...((.(((((((((((((((.(((.((((.........)))).)))).)))))).)))).....)))))))..))))..  []
>Cat     scaffold_130241 79019-79105
         GTAACCTGATGGCTGAGACAGAGGGCAGGGGCATCCCGGAACATGGCCCTCCCTCGAGGCCCTCTGCTCCCTCTTTGCTGCCCGTAG
-30.40   ((((...((.((..((((.((((((((.((((....((((.....)))).....)))).....))))))))))))))))))).))))........  []
>Horse   chr21    341817-341904
         GTAACCTGATGGCTGAGACAGAGGGCAGGGGCATCCTGCAACATGGCTCTCTCTTGAGGCCCTCTGCTTTCCTCTTTGCTGCCCACAG
-28.03   .....(((..(((.((((..((((((((((.............(((.((((....)))))))))))))))))).))))....)))..)))  []
>Elephant        scaffold_148899 920-1008
         GTAACCGATGGCTGAGACAGAGAGGGGAGGGGAGTCTTGGGACATTGCCCCTCCTCGAGCCCCTCTGCTCCCCTCTTTGCTGCCCATAG
-39.60   .........(((..((.((((((((((((.((((.((((((.........)))).)))))...)))))).))))))))))))).....  []
```



```
NM_015232_11: human, chimp, opossum, rhesus, tenrec
>Human   chr12    150588-150672
         GTAAGTGGAGCCCTGGTTGCCCAGGTGAGTGACTACCCTGCCCCCTTGTTCTTCTTCTCACCGTCTCTGTTGTTTCTCTTCTCAG
-14.20   ..((((.(((((..(((..((...(((((((.((..((...........)).....)).))))))))..))))..)))))).))).....  []
>Chimp   chr12    175712-175796
         GTAAGTGGAGCCCTAGTTGCCCAGGTGAGTGACTACCCTGCCCCCTTGTTCTTCTTCTCACCGTCTCTGTTGTTTCTCTTCTCAG
-15.50   ..((((.(((((..(((..((...(((((((.((..((...........)).....)).))))))))..))))..)))))).))).....  []
>Rhesus  chr11    163101-163184
         GTAAGTGGAGCCCTGGTTGCCCAGGTGAGTGACTCCCTGCCCCCTTGTCCTTCTTCTCACCGTCTCTGTTGTTTCTCTTCTCAG
-15.42   ..((((.(((((..(((..((...(((((((.(((.............)))......)))))))))..))))..)))))).))).....  []
>Tenrec  scaffold_183272 1398-1484
         GTAAGTGGAGGGCTGGCTGCCCGAGGTGAGTGACTCCGAGCCCCTTTGGGCCCTTCTTCTCACCGTCTCTGTTGTTTCTCTTCTCAG
-24.39   ......((((((..(((.((..((((((((.........((((....))))).......))))))..))...)).))).))))))....  []
>Opossum         chr8     112786052-112786141
         GTAAGTAGAGGCCTCGTTGCTGAGGTGAGTAATTCTCTCCCCCCCTCCCCATCCTTTTCTTCTCACCTTCTCTGTTGTTTCTCTTCTCAG
-15.25   ..((((.(((((((..((.....((((((((.....................................)))))))))...))..))))))))).....  []
```



NM_002912_7 Chimp Rhesus Rabbit Dog Horse

```
>Chimp      chr6        113298181-113298267
         GTAAGTGGTTATTTATTATAGATCTCAGAACTAATTTTATTCCTTTGTTATCTAGTCTGTTATAAAGGATATGTTTTAATTAAGCAG
-9.71    .....((.(((.(((..(((.(((((((.((((((..((......))..)).))))))).......))))).)))..)))).))).  []

>Rhesus     chr4        15103584-15103670
         GTAAGTGGTTATTTATTATAGATCTCAGAACTAATTTTATTCCTTTGTTATCTAGTCTGTTATAAAGGATATGTTTTAATTAAGCAG
-9.71    .....((.(((.(((..(((.(((((((.((((((..((......))..)).))))))).......))))).)))..)))).))).  []

>Rabbit     scaffold 2(73828-73912
         GTAAGTGATTATTATAGATCAGAAAAAAATTTTATTGCATTTGTTATCTAATTTTTTTTATAAAAGATATGTTTTAATTAAGCAG
-10.00   ((...((((((..(((.(((.((((((((((..((.((....)).)).))..))))))))))).....)))).)))..))))))..))..  []

>Dog        chr12       70913400-70913484
         GTAAGTGGTTATTTATTATATCTCAGAACTAATTTTATTGCTTTGTAATGTAGTTTGTTATAAAGGATATGTTTTAATTAAGCAG
-13.50   .....((.(((.(((.(((((((...(((.((((.((((((...))))))).)))).))).....)))))))...)))).))).  []

>Horse      chr10       55495795-55495881
         GTAAGTGGTTATTTATTACAGATCTCAGAACTAATTTTATTGCTTTGTTGTCTAGTTTGTTATAAAGGTTATGTTTTAATTAAGCAG
-10.40   .....((.(((.(((..((((((((..((((((((..((......))..)).))))))).......)))))).)))..)))).))).  []
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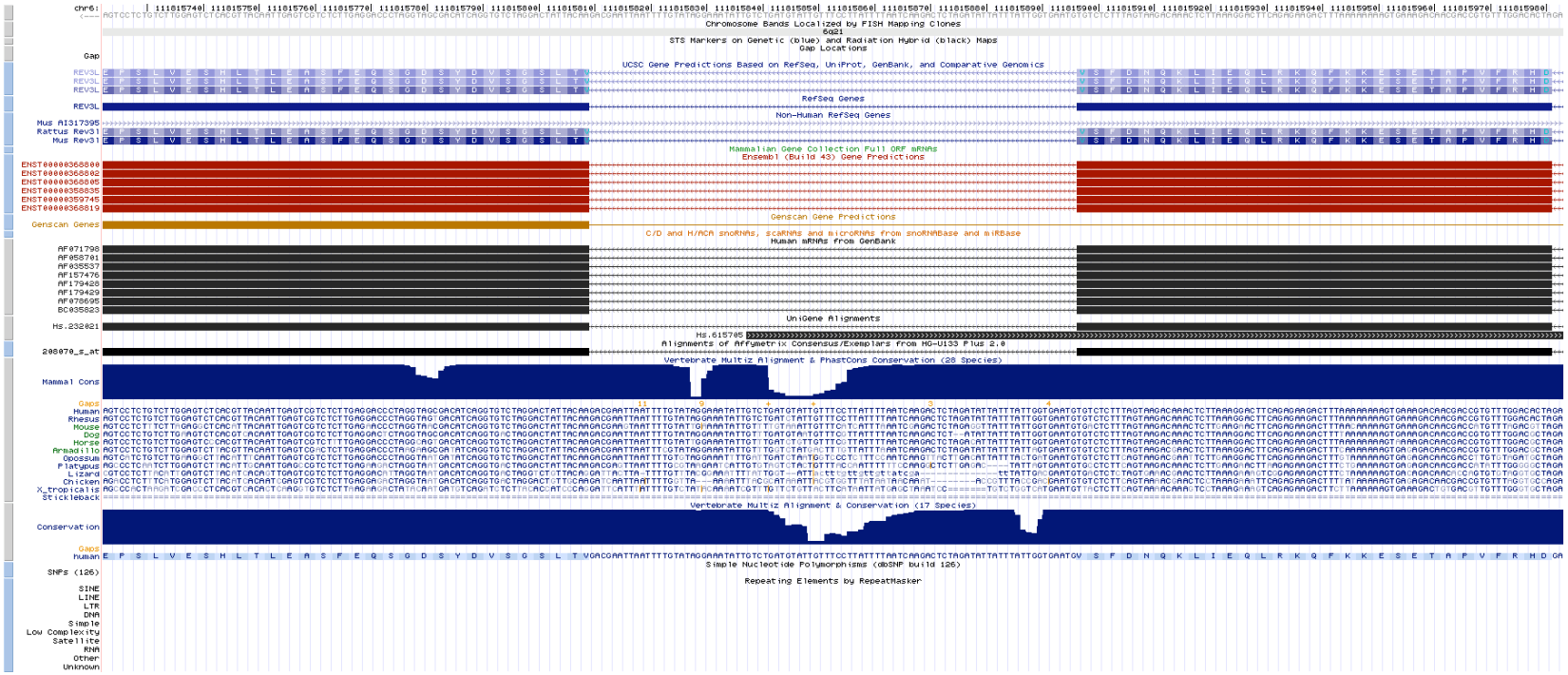

NM_001031698_9: Human Chimp Rhesus Mouse Shrew

```
>Human     chr12       48314506-48314587
        GTGCTGGAGTGGGGCTCCCAGGGAAGGTTTGGAGGGGGCTGGAGCGGGGCAGGCCCCATGACTCCCACCTGCTTCATTCCAG
-37.70  ...(((((((((..((.....((((..(((....((((.(((........)))).)))))..)))))))....))..)))))))))  []

>Chimp     chr12       95293575-95302902
        GTGCTGGAGTGGGGCTCCCAGGGAAGGTTTGGAGGGGGCTGGAGTGGGGCAGGCCCCATGACTCCCACCTGCTTCATTCCAG
-37.70  ...(((((((((..((.....((((..(((....((((.(((........)))).)))))..)))))))....))..)))))))))  []

>Rhesus    chr11       46775520-46775601
        GTGCTGGAGTGGGGCTCCCAGGGAAGGTTTGGAGGGGGCTGGAGCAGGGCAGGCCCCATGACTCCCACCTGCTTCATTCCAG
-37.70  ...(((((((((..((.....((((..(((....((((.(((........)))).)))))..)))))))....))..)))))))))  []

>Mouse     chr15       99134966-99135046
        GTGCTGGGGATGGTGCTCCCAGGGAAGGCCTGGAGGGTTTGAAAGATAACAGGCTCTGAGACCTGTGCCTCTCTGCTCCAG
-26.60  ...(((((((..((.(((...((((..(((((((....(((.....)))..)))))).))....)))))).))..))....)))))))  []

>Shrew     scaffold_2(4408-4487
        GTGCTGGAGTGGGGCTCCTGAGTAGTCCTAGAGGGGGCTAGTGGTATGCAGGCCCCATGACCCTGCCTGCTCCATTCCAG
-35.64  ...((((((((((((.....(((.......((((((.((.....)).)))))).....))))..)))))))))))  []
```

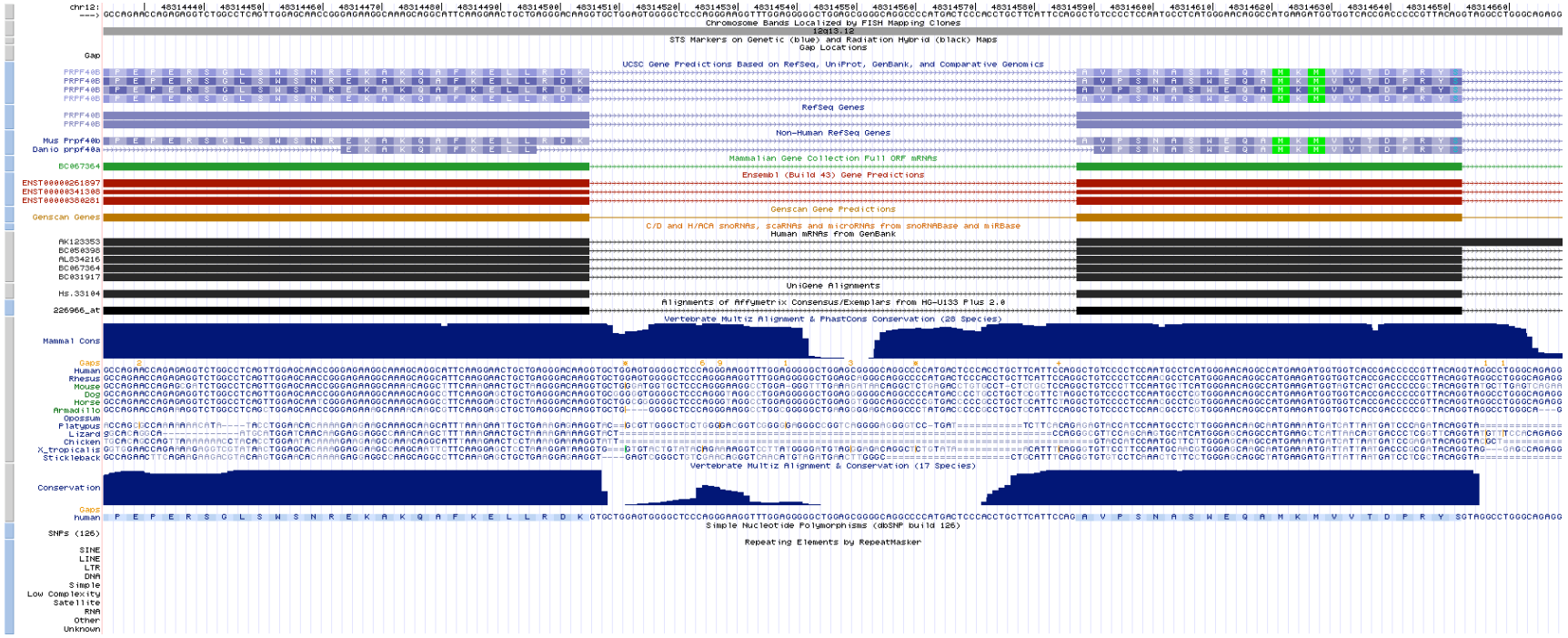

Figure S2. Conserved Hairpin Structures and Sequence of the Conserved Mammalian Mirtron, mir-1225

```
mir-1225
>Human  chr16   2080196-2080285
        GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGGCTCTGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
-48.20  .((((..((((.(((.(((((..((..((...((((((((((...))))))))))...))...))..))...))))))).))))..)))).  []

>Chimp  chr16   2186743-2186832
        GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGGCTCTGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
-48.20  .((((..((((.(((.(((((..((..((...((((((((((...))))))))))...))...))..))...))))))).))))..)))).  []

>Rhesus chr20   2081736-2081825
        GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGGCTCTGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
-48.20  .((((..((((.(((.(((((..((..((...((((((((((...))))))))))...))...))..))...))))))).))))..)))).  []

>Cow    chr25   61293-61385
        GTGGGTACGGCCCAGGGGGGGAGAGGGACGCACCCTGGGCCCAGCAGAGCCCAGGGCGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
-53.00  .((((..((((.((((((((.((..((..((.(((((((.......)))))))).))..))...))..))...))))))).))))..)))).  []

>Dog    chr6    38736837-38736931
        GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACACCCTGGGCCCAGGTGAGCCCAGGGTGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
-51.40  .((((..((((.(((.(((((..((..((...((((((((((.......)))))))))...))...))..))...))))))).))))..)))).  []

>Hedgehog       scaffold_375456         27864-27955
        GTGGGTACGGCCCAGTGGGGGGGAGAGGGACGCCCTGGGCCCACGTAGCCCGGGGCGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
-51.20  .((((..((((.(((.(((((..((..((.((((((((((.......)))))))))...))...))..))...))))))).))))..)))).  []

>Horse  chrUn   73886090-73886184
        GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGGCTCAGGTGAGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
-54.60  .((((..((((.(((.(((((..((..((...((((((((((((....)))))))))))))...))...))..))...))))))).))))..)))).  []

>Mouse  chr17   70854749-70854842
        GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACACCCTGGGTCTCGCGAGCCCAGGGTGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
-49.90  .((((..((((.(((.(((((..((..((...((((((((((.((....)))))))))))...))...))..))...))))))).))))..)))).  []

>Rat    chr10   96872038-96872131
        GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACACCCTGGGTCTCGCGAGCCCAGGGTGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
-49.90  .((((..((((.(((.(((((..((..((...((((((((((.((....)))))))))))...))...))..))...))))))).))))..)))).  []


Chimp           GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGG-CTC-----TGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
Dog             GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACACCCTGGG-CCCAGGTGAGCCCAGGGTGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
Horse           GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGG-CTCAGGTGAGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
Human           GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGG-CTC-----TGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
Mouse           GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACACCCTGGGTCTC--GCGAGCCCAGGGTGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
Rat             GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACACCCTGGGTCTC--GCGAGCCCAGGGTGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
Rhesus          GTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGG-CTC-----TGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAG
Cow             GTGGGTACGGCCCAG--GGGGGGAGAGGGACGCACCCTGGG-CCCAGCAGAGCCCAGGGCGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
Hedgehog        GTGGGTACGGCCCAGTGGGGGGGAGAGGGACG--CCCTGGG-CCCACG-TAGCCCGGGGCGCAGCCGGACTGACCGAGCCCCTGTGCCGCCCCCAG
                ***************  **************   ******* * *      **** *** ************** *********************
```

Figure S3. Small RNA Libraries Used For Mirtron Discovery.

library	mapped reads	Description	reference
mouse_lib1	23703	brain	1
human_lib1	5476	brain	1
human_lib2	3202	skin	1
human_lib3	2177	heart	1
human_lib4	3265	lung	1
human_lib7	11939	umbilical cord blood-derived endothelial progenitor cells	1
human_lib8	3490	foreskin-derived microvascular endothelial cells	1
chimp_libPT0	153316	mix of brain regions	2
human_libH0	118275	fetal brain	2
human_libH1	24167	amygdale	3
human_libH2	18613	cerebellum	3
human_libH3	44954	cingulate gyrus	3
human_libH4	48351	superior frontal gyrus	3
human_libH5	22352	superior occipital gyrus	3
human_libH6	33855	medial temporalis gyrus	3
human_libH7	44521	Hippocampus	3
human_libH8	35007	hypothalamus	3
human_libH9	44337	locus coeruleus	3
human_libH10	21306	superior parietal gyrus	3
human_libH11	38095	substantia nigra	3
human_libH12	35052	spinal-cord	3
human_libH13	43885	thalamus (pulvinar)	3
human_libH14	21648	caudate nucleus	3
human_libH15	39199	putamen	3
macaque_lib1	25856	superior frontal gyrus	3
macaque_lib2	37528	medial temporalis gyrus	3
macaque_lib3	37922	superior occipital gyrus	3
macaque_lib4	44343	superior parietal gyrus	3
macaque_lib5	28875	hippocampus	3
macaque_lib6	39652	cerebellum	3
macaque_lib7	30530	cingulate gyrus	3
macaque_lib8	38037	substantia nigra	3
macaque_lib9	34601	caudate nucleus	3
macaque_lib10	27400	putamen	3
macaque_lib11	23220	locus coeruleus	3
macaque_lib12	41084	amygdale	3
macaque_lib13	26796	thalamus (pulvinar)	3
macaque_lib14	24731	spinal-cord	3
macaque_lib15	33140	hypothalamus	3
	1,333,900		

1. Berezikov et al. Genome Research 16, 1289-1298.
2. Berezikov et al. Nat Genet *38*, 1375-1377.
3. Berezikov et al. Manuscript in preparation.

Figure S4. List of Officially Recognized Mammalian Mirtrons and the Extent of Their Cloning Evidence.

```
classI: miR/miR*cloned from multiple mammals and conserved across mammals

# mir-877
# arms: 2
# species: 4
# libraries: 32
# reads: 148
hsa       ...((((((..((.(.(((((((((((.(........(((((((((.....)))))))))).).))))))))))).).)))))))....
hsa  AGAAGGTAGAGGAGATGGCGCAGGGGACACGGGCAAAGACTTGGGGGTTCCTGGGACCCTCAGACGTGTGTCCTCTTCTCCCTCCTCCCAGGTGTA
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  1  human_libH0
hsa  .....GTAGAGGAGATGGCGCAG...........................................................  1  human_libH1
hsa  .....GTAGAGGAGATGGCGCAGGG..........................................................  1  human_libH1
hsa  ...........................................................TCCTCTTCTCCCTCCTCCCAG.....  1  human_libH10
hsa  .....GTAGAGGAGATGGCGCAGG...........................................................  1  human_libH10
hsa  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  1  human_libH12
hsa  .....GTAGAGGAGATGGCGCAGGG..........................................................  1  human_libH12
hsa  ......TAGAGGAGATGGCGCAGGG..........................................................  1  human_lib4
hsa  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  8  human_libH13
hsa  .....GTAGAGGAGATGGCGCAGGG..........................................................  2  human_libH13
hsa  .....GTAGAGGAGATGGCGCAGGGG.........................................................  1  human_libH13
hsa  .....GTAGAGGAGATGGCGCAGG...........................................................  1  human_libH13
hsa  .....GTAGAGGAGATGGCGCAGGG..........................................................  1  human_libH15
hsa  .....GTAGAGGAGATGGCGCAGGGG.........................................................  1  human_libH15
hsa  ......TAGAGGAGATGGCGCAGGGGAC.......................................................  1  human_lib7
hsa  .....GTAGAGGAGATGGCGCAGGGGA........................................................  1  human_libH15
hsa  .....GTAGAGGAGATGGCGCAGG...........................................................  2  human_libH3
hsa  .....GTAGAGGAGATGGCGCAGGGG.........................................................  1  human_libH3
hsa  ...........................................................TCCTCTTCTCCCTCCTCCCAG.....  1  human_libH3
hsa  .....GTAGAGGAGATGGCGCAGGGG.........................................................  2  human_libH4
hsa  ...........................................................TCCTCTTCTCCCTCCTCCCAG.....  2  human_libH4
hsa  .....GTAGAGGAGATGGCGCAGGGGACA......................................................  1  human_libH4
hsa  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  1  human_libH4
hsa  .....GTAGAGGAGATGGCGCAGGGG.........................................................  1  human_lib8
hsa  .....GTAGAGGAGATGGCGCAGGGG.........................................................  1  human_libH5
hsa  .....GTAGAGGAGATGGCGCAGGG..........................................................  1  human_libH5
hsa  .....GTAGAGGAGATGGCGCAGG...........................................................  2  human_libH6
hsa  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  1  human_libH6
hsa  .....GTAGAGGAGATGGCGCAGGGG.........................................................  1  human_libH6
hsa  .....GTAGAGGAGATGGCGCAGG...........................................................  1  human_libH7
hsa  .....GTAGAGGAGATGGCGCAGG...........................................................  2  human_libH8
hsa  .....GTAGAGGAGATGGCGCAGGGG.........................................................  2  human_libH8
hsa  ......TAGAGGAGATGGCGCAGGG..........................................................  1  human_libH8
hsa  .....GTAGAGGAGATGGCGCAGGGG.........................................................  3  human_libH0
hsa  .....GTAGAGGAGATGGCGCAGG...........................................................  3  human_libH9
hsa  .....GTAGAGGAGATGGCGCAGGG..........................................................  3  human_libH9
hsa  .....GTAGAGGAGATGGCGCAGGGG.........................................................  2  human_libH9
hsa  ...........................................................TCCTCTTCTCCCTCCTCCCAG.....  1  human_libH9
ptr       ...((((((..((.(.(((((((((((.(........(((((((((.....)))))))))).).))))))))))).).)))))))....
ptr  AGAAGGTAGAGGAGATGGCGCAGGGGACATGGGCAAAGACTTGGGGGTTCCTGGGACCCTCAGACGTGTGTCCTCTTCTCCCTCCTCCCAGGTGTA
ptr  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
ptr  .....GTAGAGGAGATGGCGCAGG...........................................................  1  chimp_libPT0
ptr  ...........................................................TCCTCTTCTCCCTCCTCCCAG.....  1  chimp_libPT0
mml       ...((((((..((.(.(((((((((((..((.......(((((((.....)))))))))...))))))))))).).)))))))....
mml  AGAAGGTAGAGGAGATGGCGCAGGGGACACGGGCTAAGACTCGGGGGTTCCTGGGACCCTCAGACATGTGTCCTCTTCTCCCTCCTCCCAGGTGTA
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  .....GTAGAGGAGATGGCGCAGGG..........................................................  1  macaque_lib10
mml  .....GTAGAGGAGATGGCGCAGGGG.........................................................  1  macaque_lib10
mml  .....GTAGAGGAGATGGCGCAGGGG.........................................................  3  macaque_lib11
mml  .....GTAGAGGAGATGGCGCAGGGG.........................................................  2  macaque_lib1
mml  .....GTAGAGGAGATGGCGCAGGG..........................................................  1  macaque_lib11
mml  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  1  macaque_lib11
mml  .....GTAGAGGAGATGGCGCAG............................................................  1  macaque_lib11
mml  .....GTAGAGGAGATGGCGCAGGGGA........................................................  1  macaque_lib11
mml  .....GTAGAGGAGATGGCGCAGG...........................................................  4  macaque_lib12
mml  .....GTAGAGGAGATGGCGCAGGGGACA......................................................  1  macaque_lib12
mml  .....GTAGAGGAGATGGCGCAGGGGA........................................................  1  macaque_lib12
mml  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  1  macaque_lib12
mml  .....GTAGAGGAGATGGCGCAGGGG.........................................................  1  macaque_lib12
mml  .....GTAGAGGAGATGGCGCAG............................................................  1  macaque_lib1
mml  .....GTAGAGGAGATGGCGCAGGGG.........................................................  1  macaque_lib13
mml  .....GTAGAGGAGATGGCGCAGG...........................................................  1  macaque_lib13
mml  .....GTAGAGGAGATGGCGCAG............................................................  1  macaque_lib13
mml  .....GTAGAGGAGATGGCGCAGGG..........................................................  1  macaque_lib14
mml  .....GTAGAGGAGATGGCGCAGGGGA........................................................  1  macaque_lib14
mml  .....GTAGAGGAGATGGCGCAGG...........................................................  1  macaque_lib15
mml  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  1  macaque_lib15
mml  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  1  macaque_lib2
mml  .....GTAGAGGAGATGGCGCAGGGG.........................................................  6  macaque_lib3
mml  .....GTAGAGGAGATGGCGCAGGG..........................................................  2  macaque_lib3
mml  .....GTAGAGGAGATGGCGCAGG...........................................................  2  macaque_lib3
mml  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  1  macaque_lib3
mml  .....GTAGAGGAGATGGCGCAGGG..........................................................  9  macaque_lib4
mml  .....GTAGAGGAGATGGCGCAGG...........................................................  2  macaque_lib4
mml  .....GTAGAGGAGATGGCGCAGGGG.........................................................  2  macaque_lib4
mml  .....GTAGAGGAGATGGCGCAGGGGA........................................................  1  macaque_lib4
mml  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  1  macaque_lib4
mml  .....GTAGAGGAGATGGCGCAGGGG.........................................................  5  macaque_lib5
mml  .....GTAGAGGAGATGGCGCAGGG..........................................................  1  macaque_lib5
mml  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  1  macaque_lib5
mml  .....GTAGAGGAGATGGCGCAGGGGA........................................................  1  macaque_lib5
mml  .....GTAGAGGAGATGGCGCAGG...........................................................  1  macaque_lib5
mml  .....GTAGAGGAGATGGCGCAGGG..........................................................  3  macaque_lib6
mml  .....GTAGAGGAGATGGCGCAGGGG.........................................................  3  macaque_lib6
mml  .........AGGAGATGGCGCAGGGGACA......................................................  1  macaque_lib6
mml  .....GTAGAGGAGATGGCGCAGG...........................................................  1  macaque_lib6
mml  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  4  macaque_lib10
mml  .....GTAGAGGAGATGGCGCAGGGGA........................................................  3  macaque_lib8
mml  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  2  macaque_lib8
mml  .....GTAGAGGAGATGGCGCAGGGG.........................................................  2  macaque_lib8
mml  .....GTAGAGGAGATGGCGCAGGGGAC.......................................................  2  macaque_lib9
mmu       ...((((((..((.(.(((((((((((.((....)).... (((((.....) )))).......)))))))))).).)))))))....
mmu  AAAAGGTAGAGGAGATGGCGCAGGGGACACAAGGTAGGCCTTGCGGGTCTGTGG-ACCCTTGGACATGTGTCCTCTTCTCCCTCCTCCCAGGTGTA
mmu  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++ ++++++++++++++++++++++++++++++++++++++>>>>>
mmu  .....GTAGAGGAGATGGCGCAGGG..........................................................  3  mouse_lib1
hsa  chromosome:6:30660083:30660178:1  ENST00000376575 ENSG00000204580 DDR1 Epithelial discoidin domain-containing receptor 1 precursor (EC 2.7.10.1) (Epithelial
discoidin domain receptor 1) (Tyrosine kinase DDR) (Discoidin receptor tyrosine kinase) (Tyrosine-protein kinase CAK) (Cell adhesion kinase) (TRK E) (Protein-
tyrosine ki [Source:Uniprot/SWISSPROT;Acc:Q08345]
ptr  chromosome:6:31202460:31202555:1  ENSPTRT00000033105 ENSPTRG00000017930 ABCF1 ATP-binding cassette sub-family F member 1 (ATP-binding cassette 50) (TNF-alpha-
stimulated ABC protein). [Source:Uniprot/SWISSPROT;Acc:Q8NE71]
mml  chromosome:4:30166017:30166112:1  ENSMMUT00000002661 ENSMMUG00000001886 Q5TM60_MACMU ATP-binding cassette, sub-family F (GCN20), member 1.
[Source:Uniprot/SPTREMBL;Acc:Q5TM60]
mmu  chromosome:17:35568778:35568872:-1  ENSMUST00000087205 ENSMUSG00000038762 Abcf1 ATP-binding cassette, sub-family F (GCN20), member 1
[Source:MarkerSymbol;Acc:MGI:1351658]
```

```
# mir-1224
# arms: 2
# species: 4
# libraries: 29
# reads: 232
hsa      .((((((...((((((((((.(((.((.((..(((....))) ..((((...))))..)).)).)))).)))))))))...)))))))).
hsa  CCTTGGTGAGGACTCGGGAGGTGGAGGGTGGTGCCGCCGGGGCCGG-GCGCTGTTTCAGCTCGCTTCTCCCCCCACCTCCTCTCTCCTCAGGTGCG
hsa  >>>>>+++++++++++++++++++++++++++++++++++++++++ ++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  1  human_libH0
hsa  .....GTGAGGACTCGGGAGGTGG.........................................................................  1  human_libH1
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  1  human_libH10
hsa  ......................................................................CCCCCACCTCCTCTCTCCTC.......  3  human_libH12
hsa  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  1  human_libH12
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCA......  1  human_libH12
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  1  human_libH12
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCA......  1  human_libH12
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  1  human_libH12
hsa  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  1  human_libH12
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  2  human_libH13
hsa  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  1  human_libH13
hsa  .....GTGAGGACTCGGGAGGTGG.........................................................................  1  human_libH13
hsa  .....GTGAGGACTCGGGAGGTGGAGGGT....................................................................  1  human_libH13
hsa  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  1  human_lib1
hsa  .....GTGAGGACTCGGGAGGTG..........................................................................  1  human_libH2
hsa  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  1  human_libH2
hsa  .....GTGAGGACTCGGGAGGTGG.........................................................................  1  human_libH2
hsa  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  1  human_libH2
hsa  .....GTGAGGACTCGGGAGGTGG.........................................................................  2  human_libH3
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  2  human_libH3
hsa  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  2  human_libH3
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  1  human_libH3
hsa  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  1  human_libH3
hsa  ......................................................................CCCCCACCTCCTCTCTCCTC.......  3  human_libH4
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  1  human_libH4
hsa  .....GTGAGGACTCGGGAGGTGG.........................................................................  1  human_libH4
hsa  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  1  human_libH5
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  2  human_libH6
hsa  .....GTGAGGACTCGGGAGGTGG.........................................................................  1  human_libH6
hsa  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  1  human_libH6
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  2  human_libH7
hsa  .....GTGAGGACTCGGGAGGTGG.........................................................................  2  human_libH7
hsa  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  1  human_libH7
hsa  .....GTGAGGACTCGGGAGGTGG.........................................................................  3  human_libH0
hsa  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  2  human_libH9
hsa  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  2  human_libH9
hsa  .....GTGAGGACTCGGGAGGTGGA........................................................................  1  human_libH9
hsa  .....GTGAGGACTCGGGAGGTGGAGGGT....................................................................  1  human_libH9
hsa  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  1  human_libH9
hsa  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  1  human_libH9
hsa  .....GTGAGGACTCGGGAGGTGGAGGGT....................................................................  2  human_libH0
ptr      .((((((...((((((((((.(((.((.((..(((....))) ..((((...))))..)).)).)))).)))))))))...)))))))).
ptr  CCTTGGTGAGGACTCGGGAGGTGGAGGGTGGTGCCGCCGGGGCCGG-GCGCTGTTTCAGCTCGCTTCTCCCCCCACCTCCTCTCTCCTCAGGTGCG
ptr  >>>>>+++++++++++++++++++++++++++++++++++++++++ ++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
ptr  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  12  chimp_libPT0
ptr  .....GTGAGGACTCGGGAGGTGGAGGGT....................................................................  3  chimp_libPT0
ptr  .....GTGAGGACTCGGGAGGTGG.........................................................................  1  chimp_libPT0
ptr  ......................................................................CCCCCACCTCCTCTCTCCTCA......  1  chimp_libPT0
ptr  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  1  chimp_libPT0
ptr  ......................................................................CCCACCTCCTCTCTCCTCAG.....  1  chimp_libPT0
ptr  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  1  chimp_libPT0
mml      .((((((...((((((((((.(((.(((((((((....))..) )))))....(((....)))...))))))))))))...)))))))).
mml  CCCTGGTGAGGACTCGGGAGGTGGAGGGTGGCGCCGCCGGGGCCAG-GCGCTGTCTAAGCTCGCTTCTCCCCCCACCTCCTCTCTCCTCAGGTGCG
mml  >>>>>+++++++++++++++++++++++++++++++++++++++++ ++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  1  macaque_lib9
mml  .....GTGAGGACTCGGGAGGTGGAGGGT....................................................................  1  macaque_lib10
mml  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  2  macaque_lib1
mml  .....GTGAGGACTCGGGAGGTGG.........................................................................  10  macaque_lib11
mml  .....GTGAGGACTCGGGAGGTGGAGGGT....................................................................  3  macaque_lib11
mml  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  3  macaque_lib11
mml  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  1  macaque_lib11
mml  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  1  macaque_lib11
mml  .....GTGAGGACTCGGGAGGTGG.........................................................................  5  macaque_lib12
mml  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  3  macaque_lib12
mml  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  2  macaque_lib12
mml  .....GTGAGGACTCGGGAGGTG..........................................................................  1  macaque_lib12
mml  .....GTGAGGACTCGGGAGGTGGAGGGT....................................................................  1  macaque_lib12
mml  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  1  macaque_lib13
mml  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  1  macaque_lib13
mml  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  2  macaque_lib15
mml  .....GTGAGGACTCGGGAGGTGG.........................................................................  1  macaque_lib1
mml  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  2  macaque_lib2
mml  .....GTGAGGACTCGGGAGGTGGAGGGT....................................................................  2  macaque_lib2
mml  .....GTGAGGACTCGGGAGGTGG.........................................................................  2  macaque_lib2
mml  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  1  macaque_lib2
mml  .....GTGAGGACTCGGGAGGTGG.........................................................................  12  macaque_lib3
mml  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  10  macaque_lib3
mml  .....GTGAGGACTCGGGAGGTGGAGGGT....................................................................  8  macaque_lib3
mml  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  7  macaque_lib3
mml  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  3  macaque_lib3
mml  .....GTGAGGACTCGGGAGGTGGA........................................................................  2  macaque_lib3
mml  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  2  macaque_lib4
mml  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  1  macaque_lib4
mml  .....GTGAGGACTCGGGAGGTGG.........................................................................  4  macaque_lib5
mml  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  4  macaque_lib5
mml  .....GTGAGGACTCGGGAGGTGGA........................................................................  2  macaque_lib5
mml  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  1  macaque_lib5
mml  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  1  macaque_lib5
mml  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  1  macaque_lib5
mml  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  2  macaque_lib6
mml  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  1  macaque_lib6
mml  .....GTGAGGACTCGGGAGGTGG.........................................................................  4  macaque_lib10
mml  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  4  macaque_lib10
mml  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  4  macaque_lib10
mml  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  4  macaque_lib7
mml  .....GTGAGGACTCGGGAGGTGG.........................................................................  3  macaque_lib7
mml  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  1  macaque_lib7
mml  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  2  macaque_lib10
mml  .....GTGAGGACTCGGGAGGTGGAGGGT....................................................................  4  macaque_lib8
mml  .....GTGAGGACTCGGGAGGTGGAG.......................................................................  3  macaque_lib8
mml  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  2  macaque_lib8
mml  .....GTGAGGACTCGGGAGGTGG.........................................................................  1  macaque_lib8
mml  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  1  macaque_lib8
mml  ......................................................................CCCCCACCTCCTCTCTCCTCAG.....  1  macaque_lib8
mml  .....GTGAGGACTCGGGAGGTGGAGGG.....................................................................  7  macaque_lib9
mml  .....GTGAGGACTCGGGAGGTGG.........................................................................  3  macaque_lib9
mml  .....GTGAGGACTCGGGAGGTGGAGG......................................................................  2  macaque_lib9
mmu      .((((((..(((((((((((((.(((.....((((((....))))))).....)))) )))).....)))))))))))..)))))))).
mmu  CTCTGGTGAGGACTGGGGAGGTGGAGGGTAGCATCATTAGAGCCAGAGCTCTGTCTCAGCTC-CCTCTCCCCCCACCTCTTCTCTCCTCAGGTACG
mmu  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ ++++++++++++++++++++++++++++>>>>>
mmu  .....GTGAGGACTGGGGAGGTGGAG.......................................................................  1  mouse_lib1
hsa  chromosome:3:185441882:185441976:1  ENST00000273794 ENSG00000145198 Q9BVH8_HUMAN
ptr  chromosome:3:189762308:189762402:1  ENSPTRT00000029239 ENSPTRG00000015685 Q9BVH8_HUMAN
mml  chromosome:2:102429361:102429455:-1  ENSMMUT00000026643 ENSMMUG00000018949 Q9BVH8_HUMAN
mmu  chromosome:16:20517990:20518084:1  ENSMUST00000046188 ENSMUSG00000033821 EG328644 predicted gene, EG328644 [Source:MarkerSymbol;Acc:MGI:3646631]
```

```
# mir-1225
# arms: 2
# species: 2
# libraries: 5
# reads: 7
         .((((..((((.(((.(((((..((..((...((((((((((...)))))))))))...))...))..))...)))))).))))..)))). minimum free energy = -48.2 kcal/mol
hsa  AGGAGGTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGGCTCTGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAGTTCCG
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ......................................................................TGAGCCCCTGTGCCGCCCCCAGT....  1  human_libH11
hsa  .....GTGGGTACGGCCCAGTGGGGGG.............................................................................  1  human_libH6
hsa  .....GTGGGTACGGCCCAGTGGGGGG.............................................................................  1  human_libH6
mml       .((((.....)))).(((((((((.(((...((((((((((...)))))))))))..(((((.....))).)))))).).)).)))))).
mml  AGGAGGTGGGTACGGCCCAGTGGGGGGGAGAGGGACACGCCCTGGGCTCTGCCCAGGGTGCAGCCGGACTGACTGAGCCCCTGTGCCGCCCCCAGTTCCG
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  .....GTGGGTACGGCCCAGTGG..................................................................................  1  macaque_lib9
mml  .....GTGGGTACGGCCCAGTGGG.................................................................................  1  macaque_lib9
mml  .....GTGGGTACGGCCCAGTGGGGG...............................................................................  1  macaque_lib11
mml  ......................................................................CTGAGCCCCTGTGCCGCCCCCAGT....  1  macaque_lib14
hsa  chromosome:16:2080192:2080291:-1  ENST00000382481 ENSG00000008710 PKD1 Polycystin-1 precursor (Autosomal dominant polycystic kidney disease protein 1).
[Source:Uniprot/SWISSPROT;Acc:P98161]
mml  chromosome:20:2081732:2081831:-1  ENSMMUT00000039661 ENSMMUG00000029264 PKD1 Polycystin-1 precursor (Autosomal dominant polycystic kidney disease protein 1).
[Source:Uniprot/SWISSPROT;Acc:P98161]
```

class 2: miR/miR* cloned from multiple primates and conserved in primates

```
# mir-1226
# arms: 2
# species: 3
# libraries: 32
# reads: 216
hsa       ...((((.(((((((.((((.((((((.(((.((.....)).....))).)))))))))).))))))).))))..
hsa  AACAGGTGAGGGCATGCAGGCCTGGATGGGGCAGCTGGGATGGTCCAAAAGGGTGGCCTCACCAGCCCTGTGTTCCCTAGGGAGG
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ....................................................TCACCAGCCCTGTGTTCCCT.......  1  human_libH0
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  3  human_libH1
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  4  human_libH10
hsa  ....................................................TCACCAGCCCTGTGTTCCCT.......  3  human_libH10
hsa  ....................................................TCACCAGCCCTGTGTTCCCT.......  5  human_libH11
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  5  human_libH11
hsa  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  human_libH11
hsa  ....................................................CACCAGCCCTGTGTTCCCTAG.....  1  human_libH11
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  10  human_libH12
hsa  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  human_libH12
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  5  human_libH13
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  5  human_libH14
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  11  human_libH15
hsa  ....................................................TCACCAGCCCTGTGTTCCCT.......  4  human_libH15
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAGG....  1  human_libH15
hsa  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  human_libH15
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  1  human_libH2
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  5  human_libH3
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAGG....  1  human_libH3
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  4  human_libH4
hsa  ....................................................TCACCAGCCCTGTGTTCCCT.......  1  human_libH4
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  5  human_libH5
hsa  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  human_libH5
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  8  human_libH6
hsa  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  human_libH6
hsa  ....................................................TCACCAGCCCTGTGTTCCCT.......  1  human_libH6
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  8  human_libH7
hsa  ....................................................TCACCAGCCCTGTGTTCCCTA......  6  human_libH7
hsa  .....GTGAGGGCATGCAGGCCTGGATGGGG..........................................................  8  human_libH0
hsa  ....................................................TCACCAGCCCTGTGTTCCCT.......  1  human_libH7
hsa  ....................................................TCACCAGCCCTGTGTTCCCTA......  5  human_libH0
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAGG....  1  human_libH7
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  7  human_libH8
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  12  human_libH9
hsa  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  3  human_libH0
hsa  ....................................................TCACCAGCCCTGTGTTCCCT.......  2  human_libH9
hsa  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  human_libH9
     ....................................................hsaUCACCAGCCCUGUGUUCCCUAG.....            4 landgraf
ptr       ...((((.(((((((.((((.((((((.(((.((.....)).....))).)))))))))).))))))).))))..
ptr  AACAGGTGAGGGCATGCAGGCCTGGATGGGGCAGCTGGGATGGTCCAAAAGGGTGGCCTCACCAGCCCTGTGTTCCCTAGGGAGG
ptr  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
ptr  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  4  chimp_libPT0
mml       ...((((.(((((((.((((.((((((.(((.((.....)).....))).)))))))))).))))))).))))..
mml  AACAGGTGAGGGCATGCAGGCCTGGATGGGGCAGCTGGGATGGTCCAAAAGGGTGGCCTCACCAGCCCTGTGTTCCCTAGGGAGG
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ....................................................TCACCAGCCCTGTGTTCCCT.......  1  macaque_lib10
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  3  macaque_lib11
mml  ....................................................TCACCAGCCCTGTGTTCCCT.......  2  macaque_lib11
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  3  macaque_lib12
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  2  macaque_lib1
mml  ....................................................TCACCAGCCCTGTGTTCCCT.......  1  macaque_lib12
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  8  macaque_lib13
mml  ....................................................TCACCAGCCCTGTGTTCCCT.......  1  macaque_lib1
mml  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  macaque_lib13
mml  ....................................................TCACCAGCCCTGTGTTCCCT.......  2  macaque_lib14
mml  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  macaque_lib14
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  3  macaque_lib15
mml  ....................................................TCACCAGCCCTGTGTTCCCT.......  2  macaque_lib15
mml  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  macaque_lib2
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  6  macaque_lib3
mml  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  macaque_lib3
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  1  macaque_lib4
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  3  macaque_lib5
mml  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  macaque_lib5
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  3  macaque_lib6
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  4  macaque_lib10
mml  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  macaque_lib6
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  7  macaque_lib7
mml  ....................................................TCACCAGCCCTGTGTTCCCTA......  3  macaque_lib10
mml  ....................................................TCACCAGCCCTGTGTTCCCTA......  1  macaque_lib7
mml  ....................................................TCACCAGCCCTGTGTTCCCTA......  2  macaque_lib8
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  1  macaque_lib8
mml  ....................................................CACCAGCCCTGTGTTCCCTAG.....  1  macaque_lib10
mml  ....................................................TCACCAGCCCTGTGTTCCCTAG.....  2  macaque_lib9
mml  ....................................................TCACCAGCCCTGTGTTCCCT.......  1  macaque_lib9
hsa  chromosome:3:47866044:47866128:1  ENST00000348968 ENSG00000132153 DHX30 Putative ATP-dependent RNA helicase DHX30 (EC 3.6.1.-) (DEAH box protein 30).
[Source:Uniprot/SWISSPROT;Acc:Q7L2E3]
ptr  chromosome:3:48940685:48940769:1  ENSPTRT00000027823 ENSPTRG00000014877 DHX30 Putative ATP-dependent RNA helicase DHX30 (EC 3.6.1.-) (DEAH box protein 30).
[Source:Uniprot/SWISSPROT;Acc:Q7L2E3]
mml  chromosome:2:88663196:88663280:-1  ENSMMUT00000005404 ENSMMUG00000003820 DHX30 Putative ATP-dependent RNA helicase DHX30 (EC 3.6.1.-) (DEAH box protein 30).
[Source:Uniprot/SWISSPROT;Acc:Q7L2E3]
```

```
# mir-1227
# arms: 2
# species: 2
# libraries: 5
# reads: 6
hsa       .(((((..(((.(((((((((((((((((...((((((.....)))).)))..)))))).....)).)))...)))))))))..))))).
hsa  GCCAGGTGGGGCCAGGCGGTGGTGGGCACTGCTGGGGTGGGCACAGCAGCCATGCAGAGCGGGCATTTGACCCCGTGCCACCCTTTTCCCCAGCTACG
hsa  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ......................................................................CGTGCCACCCTTTTCCCCAG.....  1  human_libH0
hsa  ......................................................................CGTGCCACCCTTTTCCCCAG.....  1  human_libH1
hsa  ......................................................................CGTGCCACCCTTTTCCCCAG.....  1  human_libH3
hsa  ......................................................................CGTGCCACCCTTTTCCCCAG.....  2  human_libH4
mml       .(((((...(((((((.....)))))))(((((..(((((((((.(((.(((...)))))))..)))).....)))))..))))..)))))).
mml  GCCAGGTGGGGCCAGGCGGTGGTGGGCACCGCTGGGGTGGGCACAGCAGCCATGCAGAGCAGGCAGCTGACCCCGTGCCATCCTCTTCCCCAGCTACG
mml  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  .....GTGGGGCCAGGCGGTGGTGG.........................................................................  1  macaque_lib8
hsa  chromosome:19:2185056:2185153:-1  ENST00000326631 ENSG00000104886 PLEKHJ1 pleckstrin homology domain containing, family J member 1
[Source:RefSeq_peptide;Acc:NP_060519]
mml  chromosome:19:2034264:2034361:-1  ENSMMUT00000014112 ENSMMUG00000010109 PLEKHJ1 pleckstrin homology domain containing, family J member 1
[Source:RefSeq_peptide;Acc:NP_060519]
```

class 3: single species loci with multiclone confidence classification

```
# mir-1228
# arms: 2
# species: 1
# libraries: 6
# reads: 6
hsa       ..(((((((((.(((((((((....((((.....(((((.....)))))))))..)))))))))))))))).....
hsa  CCCAGGTGGGCGGGGGCAGGTGTGTGGTGGGTGGTGGCCTGCGGTGAGCAGGGCCCTCACACCTGCCTCGCCCCCCAGGTGTG
hsa  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ...................................................TCACACCTGCCTCGCCCCCC.......  1  human_libH12
hsa  ...................................................CCTCACACCTGCCTCGCCCCC........  1  human_libH14
hsa  .....GTGGGCGGGGGCAGGTGTGTG.........................................................  1  human_libH15
hsa  ...................................................TCACACCTGCCTCGCCCCCC.......  1  human_libH3
hsa  ...................................................CCTCACACCTGCCTCGCCCCCCA......  1  human_libH6
hsa  ...................................................TCACACCTGCCTCGCCCCCC.......  1  human_libH9
hsa  chromosome:12:55874549:55874631:1  ENST00000338962 ENSG00000123384 LRP1 Low-density lipoprotein receptor-related protein 1 precursor (LRP) (Alpha-2-
macroglobulin receptor) (A2MR) (Apolipoprotein E receptor) (APOER) (CD91 antigen). [Source:Uniprot/SWISSPROT;Acc:Q07954]


# mir-1229
# arms: 1
# species: 1
# libraries: 10
# reads: 16
hsa       (((((.(((((.(((..(((((.(((..(((.....)))...))).)))))..)))..)))))))))..
hsa  GATCGGTGGGTAGGGTTTGGGGGAGAGCGTGGGCTGGGGTTCAGGGACACCCTCTCACCACTGCCCTCCCACAGGCTCC
hsa  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ...............................................CTCTCACCACTGCCCTCCCACAG.....  1  human_libH0
hsa  ...............................................CTCTCACCACTGCCCTCCCAC.......  3  human_libH10
hsa  ...............................................CTCTCACCACTGCCCTCCCACAG.....  1  human_libH11
hsa  ...............................................CTCTCACCACTGCCCTCCCACAG.....  1  human_libH13
hsa  ...............................................CTCTCACCACTGCCCTCCCACAG.....  2  human_libH15
hsa  ...............................................CTCTCACCACTGCCCTCCCAC.......  2  human_libH2
hsa  ...............................................CTCTCACCACTGCCCTCCCAC.......  1  human_libH4
hsa  ...............................................TCTCACCACTGCCCTCCCAC.......  1  human_libH4
hsa  ...............................................CTCTCACCACTGCCCTCCCAC.......  1  human_libH6
hsa  ...............................................CTCTCACCACTGCCCTCCCAC.......  1  human_libH7
hsa  ...............................................CTCTCACCACTGCCCTCCCAC.......  1  human_libH9
hsa  ...............................................TCTCACCACTGCCCTCCCACAG.....  1  human_libH9
hsa  chromosome:5:179157879:179157957:-1  ENST00000376937 ENSG00000161013 MGAT4B mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase,
isoenzyme B isoform 1 [Source:RefSeq_peptide;Acc:NP_055090]


# mir-1230
# arms: 1
# species: 1
# libraries: 4
# reads: 4
mml       .((((.((((((..(((((((..(.((((.(......).)))).).......)))))))..)))))).)))).
mml  GCAAGGTGGGTGGGGGCATCTCGGAGGAGGTGGGGGGTGTGGCGCCCAGCGGATGACTCCGAGCGGCTCCTTTCCCAGGTGTT
mml  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  .....GTGGGTGGGGGCATCTCGGA..........................................................  1  macaque_lib12
mml  .....GTGGGTGGGGGCATCTCGGAGGAGG.....................................................  1  macaque_lib1
mml  .....GTGGGTGGGGGCATCTCGGAG.........................................................  1  macaque_lib5
mml  .....GTGGGTGGGGGCATCTCGGA..........................................................  1  macaque_lib9
mml  scaffold:1099548049615:28157:28239:1  ENSMMUT00000000657 ENSMMUG00000000451 GRINA glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1
[Source:RefSeq_peptide;Acc:NP_000828]


# mir-1231
# arms: 1
# species: 1
# libraries: 3
# reads: 3
hsa       ........((((((((((((..(((((..((((.((((..((((.....))))).....))))....))))..))))))))))))..)))).)))
hsa  TGCAGGTCAGTGTCTGGGCGGACAGCTGCAGGAAAGGGAAGACCAAGGCTTGCTGTCTGTCCAGTCTGCCACCCTACCCTGTCTGTTCTTGCCACAGTTGGA
hsa  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  .........GTGTCTGGGCGGACAGCTGC.......................................................................  1  human_libH10
hsa  ..........TGTCTGGGCGGACAGCTGC.......................................................................  1  human_libH12
hsa  .........GTGTCTGGGCGGACAGCTGC.......................................................................  1  human_libH9
hsa  chromosome:1:200044357:200044458:1  ENST00000367302 ENSG00000134369 NAV1 neuron navigator 1 [Source:RefSeq_peptide;Acc:NP_065176]


# mir-1232
# arms: 1
# species: 1
# libraries: 3
# reads: 3
mml       (((((((((((.(.....((((((.(....).)))))..((((.....))))..).))).)))))))))..
mml  ACAAGGTGGGGTGGCGGCGACATGGCGGGGGCGGCGGGCCCTGCGGAGGCTGTGCGCCTGACCCCGACCACCCCCGCAGGACCT
mml  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  .....................................................CTGACCCCGACCACCCCCGCAG.....  1  macaque_lib11
mml  .....................................................CTGACCCCGACCACCCCCGCAG.....  1  macaque_lib1
mml  .....................................................CTGACCCCGACCACCCCGC.......  1  macaque_lib14
mml  chromosome:15:1248678:1248760:1  ENSMMUT00000030168 ENSMMUG00000021434 ABCA2 ATP-binding cassette sub-family A member 2 (ATP-binding cassette transporter 2)
(ATP-binding cassette 2). [Source:Uniprot/SWISSPROT;Acc:Q9BZC7]
```

```
# mir-1233
# arms: 1
# species: 1
# libraries: 2
# reads: 39
hsa       ....(((((((((.((((((....((((....((((..(((((.........)))))))))..)))))..)))))).))))))))..
hsa  CATCAGTGAGTGGGAGGCCAGGGCACGGCAGGGGGAGCTGCAGGGCTATGGGAGGGGCCCCAGCGTCTGAGCCCTGTCCTCCCCGCAGGAAAG
hsa  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ..............................................................TGAGCCCTGTCCTCCCGCAG.....  2  human_libH13
hsa  ..............................................................CTGAGCCCTGTCCTCCCGCA......  1  human_libH5
hsa  chromosome:15:20996204:20996295:1  ENST00000328919 ENSG00000175676 GOLGA8F golgi autoantigen, golgin subfamily a, 8E [Source:RefSeq_peptide;Acc:NP_001012423]
hsa  chromosome:15:32607778:32607869:-1  ENST00000360553 ENSG00000175265 GOLGA8A Golgin subfamily A member 8A/B (Golgi autoantigen golgin-67) (88 kDa Golgi protein)
(Gm88 autoantigen). [Source:Uniprot/SWISSPROT;Acc:Q9NZW0]
hsa  chromosome:15:28880735:28880887:1  ENST00000220188 ENSG00000103832 O60374_HUMAN
hsa  chromosome:9:130059803:130059894:-1  ENST00000357016 ENSG00000167110 GOLGA2 Golgin subfamily A member 2 (Cis-Golgi matrix protein GM130) (Gm130 autoantigen)
(Golgin-95). [Source:Uniprot/SWISSPROT;Acc:Q08379]
hsa  chromosome:15:28172299:28172390:1  ENST00000356523 ENSG00000179938
hsa  chromosome:15:32461557:32461648:-1  ENST00000360553 ENSG00000175265 GOLGA8A Golgin subfamily A member 8A/B (Golgi autoantigen golgin-67) (88 kDa Golgi protein)
(Gm88 autoantigen). [Source:Uniprot/SWISSPROT;Acc:Q9NZW0]
hsa  chromosome:15:26567368:26567459:-1  ENST00000382949 ENSG00000183629 GOLGA8G golgi autoantigen, golgin subfamily a, 8G [Source:RefSeq_peptide;Acc:NP_001012420]
hsa  chromosome:15:20257288:20257379:-1  ENST00000341390 ENSG00000185182
hsa  chromosome:15:19037379:19037470:1  ENST00000318268 ENSG00000181984
hsa  chromosome:15:26307105:26307196:1  ENST00000337838 ENSG00000153684 NP_001012455.1 golgi autoantigen, golgin subfamily a, 8G
[Source:RefSeq_peptide;Acc:NP_001012420]
hsa  chromosome:15:21161027:21161118:1  ENST00000327271 ENSG00000186399
hsa  chromosome:10:30693998:30694088:-1  ENST00000358107 ENSG00000107951 PAPD1 Poly(A) RNA polymerase, mitochondrial precursor (EC 2.7.7.19) (PAP) (mtPAP)
(Polynucleotide adenylyltransferase) (PAP-associated domain- containing protein 1). [Source:Uniprot/SWISSPROT;Acc:Q9NVV4]
hsa  chromosome:15:28483840:28483931:-1  ENST00000382922 ENSG00000196102 LOC728080


# mir-1234
# arms: 1
# species: 1
# libraries: 2
# reads: 3
hsa       .....((((((((((.(((..((((((..(((.((((.(((....))).)))))).)))..))..)))..)))..)))).))))))))))).
hsa  GCTTCGTGAGTGTGGGGTGGCTGGGGGGGGGGGGGGGGGGCCGGGGACGGCTTGGGCCTGCCTAGTCGGCCTGACCACCCACCCCACAGGCACC
hsa  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ..............................................................TCGGCCTGACCACCCACCCCAC.......  1  human_libH1
hsa  ..............................................................TCGGCCTGACCACCCACCCCAC.......  2  human_libH9
hsa  chromosome:8:145596279:145596372:-1  ENST00000349769 ENSG00000071894 CPSF1 Cleavage and polyadenylation specificity factor subunit 1 (Cleavage and
polyadenylation specificity factor 160 kDa subunit) (CPSF 160 kDa subunit). [Source:Uniprot/SWISSPROT;Acc:Q10570]


# mir-1235
# arms: 1
# species: 1
# libraries: 2
# reads: 3
mml       .((((....((.((((((.((..(((((((((.((.(((.....))).)))))))))..)).)))))..)))))).
mml  AGAAGGTGGGCCTGGGTCGGTGGGGACGGGGCGGCTGGGCGTGCCCTGCGGCCGCTGCTCTAACCGCACCGTCCCCCAGGCCCT
mml  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ....................................................TCTAACCGCACCGTCCCCCAG.....  2  macaque_lib7
mml  ....................................................TCTAACCGCACCGTCCCCCAG.....  1  macaque_lib8
mml  chromosome:8:146557001:146557084:-1  ENSMMUT00000038783 ENSMMUG00000000388 PLEC1 Plectin-1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1) (Plectin-11).
[Source:Uniprot/SWISSPROT;Acc:Q15149]


# mir-1236
# arms: 1
# species: 1
# libraries: 2
# reads: 2
hsa       (.(((.((((((((((..((((........((.(.(((((((.....)))).)))).).)).((((...)))).........)))))))))).)))).))))..
hsa  ACGCTGTGAGTGACAGGGGAAATGGGGATGGACTGGAAGTGGGCAGCATGGAGCTGACCTTCATCATGGCTTGGCCAACATAATGCCTCTTCCCCTTGTCTCTCCAGCACTA
hsa  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ..............................................................................CCTCTTCCCCTTGTCTCTCCAG.....  1  human_libH0
hsa  ..............................................................................CCTCTTCCCCTTGTCTCTCCAG.....  1  human_libH4
hsa  chromosome:6:32032590:32032701:-1  ENST00000375429 ENSG00000204356 RDBP Negative elongation factor E (NELF-E) (RNA-binding protein RD).
[Source:Uniprot/SWISSPROT;Acc:P18615]


# mir-1237
# arms: 1
# species: 1
# libraries: 2
# reads: 2
hsa       .((((.((((...((.(((((.(((((((.(.(((.((...((((((((((....)))))))...)))))).)).))).).))))))))))).))))))))).
hsa  CGCAGGTGGGAGGGCCCAGGCGCGGGCAGGGGTGGGGGTGGCAGAGCGCTGTCCCGGGGGCGGGGCCGAAGCGCGGCGACCGTAACTCCTTCTGCTCCGTCCCCCAGGCTGG
hsa  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ..............................................................................TCCTTCTGCTCCGTCCCCCAG.....  1  human_libH13
hsa  ..............................................................................TCCTTCTGCTCCGTCCCCCAG.....  1  human_libH6
hsa  chromosome:11:63892645:63892756:1  ENST00000334205 ENSG00000162302 RPS6KA4 Ribosomal protein S6 kinase alpha-4 (EC 2.7.11.1) (Nuclear mitogen- and stress-
activated protein kinase 2) (90 kDa ribosomal protein S6 kinase 4) (Ribosomal protein kinase B) (RSKB). [Source:Uniprot/SWISSPROT;Acc:O75676]


# mir-1238
# arms: 1
# species: 1
# libraries: 2
# reads: 2
hsa       .....((((.((..(((((...((...((((((.((((((.....)))).)))..)).)))).)).)).)))...)))))).
hsa  TGGAGGTGAGTGGGAGCCCCAGTGTGTGGTTGGGGCCATGGCGGGTGGGCAGCCCAGCCTCTGAGCCTTCCTCGTCTGTCTGCCCCAGTCCTT
hsa  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ..............................................................CTTCCTCGTCTGTCTGCCCC.......  1  human_libH1
hsa  ..............................................................CCTTCCTCGTCTGTCTGCCCCAGT....  1  human_libH9
hsa  chromosome:19:10523793:10523885:1  ENST00000309469 ENSG00000130734 ATG4D Cysteine protease ATG4D (EC 3.4.22.-) (Autophagy-related protein 4 homolog D)
(Autophagin-4) (Autophagy-related cysteine endopeptidase 4) (AUT-like 4 cysteine endopeptidase). [Source:Uniprot/SWISSPROT;Acc:Q86TL0]


# mir-1239
# arms: 1
# species: 1
# libraries: 2
# reads: 2
mml       .(((((((((((...(.(((((((..((((((.(.((((((.....((((((....)))))))..)))))))..))))))))))))))..)))))).
mml  AGCAGGTGGGTGGGCAGGTGGGTGGGAAGCCCTGGGACGCTGCCTCCTCTCTCCTGGGGCCTCTCTCGGGCTGGGGGCTGGTCTCAGTTTCCCCATTCTGCCTGGCCTAGGTGTG
mml  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ..................................................................................TTCCCCATTCTGCCTGGCCTAG.....  1  macaque_lib9
mml  ..................................................................................TTCCCCATTCTGCCTGGCCTAG.....  1  macaque_lib1
mml  chromosome:19:17710833:17710947:1  ENSMMUT00000004479 ENSMMUG00000003161 MAST3 Microtubule-associated serine/threonine-protein kinase 3 (EC 2.7.11.1).
[Source:Uniprot/SWISSPROT;Acc:O60307]


# mir-1240
# arms: 1
# species: 1
# libraries: 2
# reads: 2
mml       (((((.(((((.((.((..((((..((((..(((((.....)))))....))))...)))))).)).)).)))))..)))))...
mml  TGCAGGTGGGCCAGGGCCGCGGGGGGGAGCAAGCCATCTAGCATTCCTGGGAAACGCTTACATCTCACCATGACCCTGATCCCACTAGGTCCT
mml  >>>>>+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ....................................................TCACCATGACCCTGATCCCACT.......  1  macaque_lib10
mml  ....................................................TCACCATGACCCTGATCCCACT.......  1  macaque_lib13
mml  chromosome:12:83077558:83077650:-1  ENSMMUT00000044562 ENSMMUG00000019619 ATG9A Autophagy-related protein 9A (APG9-like 1).
[Source:Uniprot/SWISSPROT;Acc:Q7Z3C6]
```

```
# mir-1241
# arms: 1
# species: 1
# libraries: 2
# reads: 3
mml       .......((..(((((((.((((.(((.........)))..((((((.((.....).)))))).))))).))))))).)).
mml  ACCGGGTGAGGGGGCTGGCATGGCGAGGAGGCGCCAGAGAAGCCATAGTGTGGGGATGGGCTGCACACTCACCTCTCTGTGCCTTCCAGGCTGA
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ............................................................CTCACCTCTCTGTGCCTTCCAG.....  1  macaque_lib7
mml  ............................................................CTCACCTCTCTGTGCCTTCCAG.....  2  macaque_lib10
mml  chromosome:20:66210934:66211027:1  ENSMMUT00000016663 ENSMMUG00000011888 EDC4 Enhancer of mRNA-decapping protein 4 (Human enhancer of decapping large subunit)
(Hedls) (Autoantigen Ge-1) (Autoantigen RCD-8). [Source:Uniprot/SWISSPROT;Acc:Q6P2E9]
```

Figure S5. Sequence and Secondary Structures of Orthologous Primate Introns, Whose Cloned Small RNAs Were Found in Only One Species

mir-1226

```
>Human      chr3        47866048-47866122
        GTGAGGGCATGCAGGCCTGGATGGGGCAGCTGGGATGGTCCAAAAGGGTGGCCTCACCAGCCCTGTGTTCCCTAG
-36.90  ...((((.(((((((.((((.(((((((.(((.(((-----)).----))).))))))))))).)))))))).))))..  []
>Chimp      chr3        48940689-48940763
        GTGAGGGCATGCAGGCCTGGATGGGGCAGCTGGGATGGTCCAAAAGGGTGGCCTCACCAGCCCTGTGTTCCCTAG
-36.90  ...((((.(((((((.((((.(((((((.(((.(((-----)).----))).))))))))))).)))))))).))))..  []
>Rhesus     chr2        101083361-101083435
        GTGAGGGCATGCAGGCCTGGATGGGGCAGCTGGGATGGTCCAAAAGGGTGGCCTCACCAGCCCTGTGTTCCCTAG
-36.90  ...((((.(((((((.((((.(((((((.(((.(((-----)).----))).))))))))))).)))))))).))))..  []

**mir-1227**

>Human      chr19       2185060-2185147
        GTGGGGCCAGGCGGTGGTGGGCACTGCTGGGGTGGGCACAGCAGCCATGCAGAGCGGGCATTTGACCCCGTGCCACCCTTTTCCCCAG
-36.70  .(((((..(((.(((((((((((((((...((((((------)))).)))..)))))).----)).)))...)))))))))..))))))..  []
>Chimp      chr19       2243257-2243344
        GTGGGGCCAGGCGGTGGTGGGCACTGCTGGGGTGGGCACAGCAGCCATGCAGAGCAGGCATTTGACCCCGTGCCACCCTTTTCCCCAG
-37.40  .(((((..(((.(((((((((((((((...((((((------)))).)))..)))))).----)).)))...)))))))))..))))))..  []
>Rhesus     chr19       2034268-2034355
        GTGGGGCCAGGCGGTGGTGGGCACCGCTGGGGTGGGCACAGCAGCCATGCAGAGCAGGCAGCTGACCCCGTGCCATCCTCTTCCCCAG
-39.60  .((((((..(((.((.....((((.....((((.(((.(((.(((---)))))).))))))))))))))))))..))).))))))..  []

**mir-1228**

>Human      chr12       55874553-55874625
        GTGGGCGGGGGCAGGTGTGTGGTGGGTGGGCCTGCGGTGAGCAGGGCCCTCACACCTGCCTCGCCCCCCAG
-46.00  ..((((.((((((((((((....((((.....((((.....)))))))))).))))))))))))))))....  []
>Chimp      not found
>Rhesus     chr11       54262406-54262478
        GTGGGCAGGGGCAGGTGTGTGGTGGGCGGTGGCCTGCGGTGAGCACGGCCTTCACACCTGCCTCGCCCCCCAG
-44.10  ..((((.((((((((((((....((((.((((((---)))...))).)))).))))))))))))))))....  []

**mir-1229**

>Human      chr5        179157883-179157951
        GTGGGTAGGGTTTGGGGGAGAGCGTGGGCTGGGGTTCAGGGACACCCTCTCACCACTGCCCTCCCACAG
-36.00  (((((.(((((.(((.-((((((.((((.-)))))))-)))-----)).-)))..)))))))))..))  []
>Chimp      chr5        182271044-182271112
        GTGGGTAGGGTTTGGGGGAGAGCGTGGGCTGGGGTTCGGGGACACCCTCTCAGCGCTGCCCTCCCCCAG
-34.20  ............(((((((((.(((...((((((((---)))))))))))).))))).)))))))))..  []
>Rhesus     chr6        176480839-176480908
        GTGGGTAGGGGGCTGGGGGAGAGTGTGGGCTGGGGTTCGGGGACACCCTCTCAGCGCTGCCCTCCCCCAG
-35.60  ............(((((((((...((((((((((---)))))))))))).))))).)))))))))  []

**mir-1230**

>Human      chr8        145137960-145138032
        GTGGGTAGGGGCATCTCCAAAGGCGGTGGGGGCTGTGGCTCCCAGCGGATGACTCTGAGCGGCTCCTTCCCCAG
-35.30  .((((.((((((..(((..((.((((((((....)))))))-))-----)).-)))..)))))))))..))).  []
>Chimp      chr8        143972377-143972449
        GTGGGTAGGGGCATCTCCAAAGGCGGTGCGGGGTGTGGCTCCCAGCAGATGACTCTGAGCGGCTCCTTCCCCAG
-28.90  .((((.((((((..(((..((.((.(((.(((.......)))..)))..)))..)))..)))))))..))))).  []
>Rhesus     scaffold 10! 28162-28234
        GTGGGTGGGGGCATCTCCGGAGGAGGTGGGGGGTGTGGCGCCCAGCGGATGACTCCGAGCGGCTCCTTTCCCAG
-36.80  .((((.((((((..(((((((.....((..((((((...)))))).)).....)))))))..)))))))..))))).  []

**mir-1231**

>Human      chr1        200044361-200044452
        GTCAGTGTCTGGGCGGACAGCTGCAGGAAAGGGAAGACCAAGGCTTGCTGTCTGTCCAGTCTGCCACCCTACCCTGTCTGTTCTTGCCACAG
-33.50  ........((((((((((((..((((((..((((.((((((.((((.....)))).....)))).----)))..)))..)))..)))))))..)))))))))..))))))  []
>chimp      not found
>Rhesus     chr1        59565895-59565985
        GTCAGCATCTGGGAGGACAGCTGCAGGAAAGGGAAGACCAAGGTTTGCTACTGTCCAATCTGCCACCCTACCCTATCTGTTCTCACCACAG
-24.70  .........((((((((((((....((((..((((((.....((((.((((.....)))..)))))))....)))))..)))..)))))))))..))))...  []

**mir-1232**

>Human      chr9        139025582-139025678
        GTGGGGCGGTGACGACATGGTGGGGGTGGCGGACCCTGCGGAGGCTGTGCCCCTCACCCCGGCCACCCCTGTGCCCCTGACCCCGGCCACCCCGCAG
-46.10  ((((((.(((.....((.((((((((((((((....((.((.((((...)))))).)).)))).)))))))))..)))..)))))).....)))).))..  []
>chimp      not found
>Rhesus     chr15       108870632-108870704
        GTGGGGTGGCGGCGACATGGCGGGGGCGGGCGGGCCCTGCGGAGGCTGTGCGCCTGACCCCGACCACCCCGCAG
-40.40  ((((((((((((.....(((((((.((.((.(((((.....)))))))))).)))).)))))).))))))))..  []

**mir-1233**

>Human      chr15       20996208-20996289
        GTGAGTGGGAGGCCAGGGCGTGGCAGGGGGAGCTGCAGGGCTGTTGGAGGGGCCCCAGCGTCTGAGCCCTGTCCTCCCGCAG
-47.30  ....(((((((((.((((((.....(((((.....(((((..((((((--------)))))))))).))))).)))))))..)))))))))..  []
>chimp      not found
>Rhesus     chr7        2540002-2540083
        GTGAGTGGGAGGCCAGGGCACCGCAGGGGGAGCTACAGGGCCCTAGGAGGGGCCCCAGCGTCTGAGCCCTGTCCTCCTGCAG
-47.40  ....(((((((((.((((((.....(((((.....(((((((((--------)))))))))).))))).)))))))..)))))))))..  []

**mir-1234**

>Human      chr8        145596283-145596366
        GTGAGTGTGGGGTGGCTggggggggggggggggggccggggACGGCTTGGGCCTGCCTAGTCGGCCTGACCACCCACCCCACAG
-50.10  .....(((((((((((..((((((..((((.((((((.((((.....)))).)))))).)))..)))..)))..)))..)))).))))))))))..  []
>Chimp      chr8        144391364-144391437
        GTGAGTGTGAGGTGGCTGGGGGGGGCCGGGGACGGCTTGGGCCTGCCTAGTCGGCCTGACCACCCACCCCACAG
-38.70  .....((((.((((((...((..((((((((((..((((....)))..)))))...)))))))...)))..)))))))..)))).  []
>Rhesus     chr8        147026089-147026162
        GTGAGTGTGGGGTGGCTGGGGTGGGGCAGGGATGGCTTGGGCCTGCCCAGTCGGCCTGACCACCCACCCCACAG
-43.40  .....(((((((((.....((((((..((((..((((((((....)))))))))).))))..))))))))))))))..  []

**mir-1235**

>Human      chr8        145073491-145073564
        GTGGGCTTGGGTCGGTGGGGACGGGGCGGCTGGGCGTGCCCTGCGGCCACGGCTCTGACCACACCATCACCCAG
-36.90  .((((..((((((.(((((.((.((.((((....)))).)).)))..)))..)))..)))))))..)))..  []
>Chimp      chr8        143913846-143913919
        GTGGGCTCGGGTCGGTGGGGACGGGGCGGCTGGGCGTGCCCTGCGGCCACGGCTCTGACCACGCCATCCCCCAG
-35.60  .((((...((((.((((.((.((((((((((((....)))))...)))))).)).))))))...)))))).)).))))))))))..  []
>Rhesus     chr8        146557078-146557078
        GTGGGCCTGGGTCGGTGGGGACGGGGCGGCTGGGCGTGCCCTGCGGCCGCTGCTCTAACCGCACCGTCCCCCCAG
-42.50  .(((....(((.((((((.((..((((((((((.((((....)))).)))))))))))..)).)))))))))))))..  []

**mir-1236**

>Human      chr6        32032594-32032695
        GTGAGTGACAGGGGAAATGGGGATGGACTGGAAGTGGGCAGCATGGAGCTGACCTTCATCATGGCTTGGCCAACATAATGCCTCTTCCCCTTGTCTCTCCAG
-35.40  ..((((.((((((((((..((((------.((....((((.((((((((((.....)))))).....)).)).)))).)).)).)))).....))))))))))).))).))))...  []
>Chimp      chr6        32522315-32522416
        GTGAGTGACAGGGGAAATGGGGATGGACTGGAAGTGGGCAGCATGGAGCTGACCTTCATCATGGCTTGGCCAACATAATGCCTCTTCCCCTTGTCTCTCCAG
-35.40  ..((((.((((((((((..((((------.((....((((.((((((((((.....)))))).....)).)).)))).)).)).)))).....))))))))))).))).))))...  []
>Rhesus     chr4        31612534-31612635
        GTGAGTGACAGGGGAAATGGGGATGGACTGGAAGTGGGCAGCATGGGGCTGACCTTCATCATGGCCTGATCAACATAATGCCTCTTCCCCTTATCACTCCAG
-33.99  ..((((((.((((((((..((((..(((((((...((((((((.....)))))))...)))))).....)))..))))))))))))))))))))))...  []

**mir-1237**

>Human      chr11       63892649-63892750
        GTGGGAGGGCCCAGGCGCGGGCAGGGGTGGGGGTGGCAGAGCGCTGTCCCGGGGGCGGGGCCGAAGCGCGGCGACCGTAACTCCTTCTGCTCCGTCCCCCAG
-57.40  .((((.((((((..((((((.((((((...((((.((((((((((((.....)))))))...)))))).)).))).)).))).))...))))))))))))).))))..  []
>Chimp      chr11       62772264-62772365
        GTGGGAGGGCCCAGGCGCGGGCAGGGGTGGGGGTGGCAGAGCGCTGTCCCGGGGGCGGGGCCGAAGCGCGGCGACCGTAACTCCTTCTGCTCCGTCCCCCAG
-57.40  .((((.((((((..((((((.((((((...((((.((((((((((((.....)))))))...)))))).)).))).)).))).))...))))))))))))).))))..  []
>Rhesus     chr14       122949505-122949602
        GTGGGAGGGCCCAGGCGTGGGTAGGGGTGGGGTGGCAGAGCGCGTCCCGGGGGCGGGGCCGAAGCACGGAGACCGTAACTCCTGCTGCGTCCCCCAG
-47.00  .((((.((((....((...((((((((((((.....)))...)))))...((((..((((.....)))...)))))..))))))))))))))))))))..  [[][]]

**mir-1238**

>Human      chr19       10523797-10523879
        GTGAGTGGGAGCCCCAGTGTGTGGTTGGGGCCATGGCGGGTGGGCAGCCCAGCCTCTGAGCCTTCCTCGTCTGTCTGCCCCAG
-30.90  .....(((.((((((...((...((((((.((((((((.....)))))).)))..)).)))).)).)).)).)))...)))))))..  []
>Chimp      chr19       10815797-10815879
        GTGAGTGGGAGCCCCAGTGTGTGGTTGGGGCCGTGGCGGGTGGGCAGCCCAGCCTCTGAGCCTCCCTCGTCTGTCTGCCCCAG
-31.60  .....(((.((...((((((...((..((((((.((((((((.....)))))).)))..)).))))))).)).)).)))...)))))))..  []
>Rhesus     chr19       10356882-10356965
        GTGAGTGGGAGCCCCAGTGTGTGGTTGGGGCCCTGGCAGGTGGGCGGCAGGGGCCTCTGAGCCTCCCTCATCTGTCTGCTCCAG
-36.50  ..((((((..((((((((.......)))))))).....((((((((((.((....((((((.....)))))))))))))))))))))))))...  [[][]]

**mir-1239**

>Human      chr19       18106521-18106625
        GTGGGCGGGCAGGTGGGTGGGCAGCCCCGGGATGCCTCCTCCTCTCTCCTGGGACCTCTCTTGGGCTGGGGGCTGGCCTCAGTTTCCCCGTTCTCCCTGGCCCAG
-45.09  .((((((((.((((.((.((((((((.((.................((..((((....)))..)))))..))))))))..))).....)))...)))))))..))))).  []
>Chimp      chr19       18579075-18579179
        GTGGGCGGGCAGGTGGGTGGGCAGCCCCGGGATGCCTCCTCCTCTCTCCTGGGACCTCTCTTGGGCTGGGGGCTGGCCTCAGTTTCCCCGTTCTGCCTGGCCCAG
-51.19  .((((((((((((.((((.((.((((((((.((.................((..((((....)))..)))))..))))))))..))).....)))...)))))))))))))).  []
>Rhesus     chr19       17710837-17710941
        gtggtgggcaggtgggtgggAAGCCCTGGGAGCGCTGCCTCCTCTCTCCTGGGGCCTCTCTCGGGCTGGGGGCTGGTCTCAGTTTCCCCATTCTGCCTGGCCTAG
-52.80  .....((((((..((((((((((.(((((((...((((((((.....((((((((....)))))))))..))))))..))))))))))))))...))..)))))..))))...  []

**mir-1240**

>Human      chr2        219796988-219797070
        GTGGGCCAGGGCCACAGGCGGGAGCAAGCCGGCTAGCATTCCTGGGAAAGGCATACATCTCACCATGATCCTGATCCCACTAG
-30.50  (((((.(((((..((..((.((((....((((.....)))).....)))).....)))..)))..)))..)))..)))))...  []
>Chimp      chr2b       225159171-225159253
        GTGGGCCAGGGCCACAGTCGGGAGCAAGCCGGCTAGCATTCCTGGGAAAGGCATACATCTCACCATGATCCTGATCCCACTAG
-28.50  (((((.(((((..((..((.((((....((((.....)))).....)))).....)))..)))..)))..)))..)))))...  []
>Rhesus     chr12       83077562-83077644
        GTGGGCCAGGGCCGCGGGGGGGAGCAAGCCATCTAGCATTCCTGGGAAAGCGCTTACATCTCACCATGACCCTGATCCCACTAG
-31.40  (((((.(((((.((.((((..((((((..((((((.....)))))).....)))))..))))))..)))..)))..)))))...  []
```

Figure S6. List of Candidate Mammalian Mirtrons with Atypical Hairpin Structures or Minimal Cloning Evidence.

```
# arms: 1
# species: 1
# libraries: 2
# reads: 5
# macaque_block210826
mml       .........(((((.....(((..(((((((.((.(((((((..((..(.....)..))..)))))).......)))))))...)))).....)))))).....
mml  CGCAGGTGAGTCTGGGTGGGGTGCAGGGCCGGCGGGTGTGGGCTGTGGGCAGCAGGTAGAGGCAGACAGTCACCCTGAACCCCGTCTCTCCCATCTGCCCACCGTCAGAACGG
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ...........................................................................TCTCTCCCATCTGCCCACCGTC.......  2  macaque_lib3
mml  ...........................................................................TCCCATCTGCCCACCGTCAG.....  2  macaque_lib3
mml  ...........................................................................CTCCCATCTGCCCACCGTCAG.....  1  macaque_lib6
mml  chromosome:19:52744554:52744666:1  ENSMMUT00000038462 ENSMMUG00000000217 PPP5C Serine/threonine-protein phosphatase 5 (EC 3.1.3.16) (PP5)
(Protein phosphatase T) (PP-T) (PPT). [Source:Uniprot/SWISSPROT;Acc:P53041]


# arms: 1
# species: 1
# libraries: 2
# reads: 2
# macaque_block136403
mml       ...........(((.....(((((((((((((.....(((((...)))))).(.....)...)))))).)))))).)))).
mml  TGCACGTGAGCTTGGCGGGGCTGCTGGAGGAGTGGGTTCGCCCAGTCTGGGCACCAGACACGGAGACTCCAGCCCACCTCCTTCTCCCCAGATCCA
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ............TGGCGGGGCTGCTGGAGGAG.............................................................  1  macaque_lib11
mml  .........GCTTGGCGGGGCTGCTGG...................................................................  1  macaque_lib3
mml  chromosome:16:4686422:4686517:1  ENSMMUT00000003421 ENSMMUG00000002404 MINK1 Misshapen-like kinase 1 (EC 2.7.11.1) (Mitogen-activated
protein kinase kinase kinase kinase 6) (MAPK/ERK kinase kinase kinase 6) (MEK kinase kinase 6) (MEKKK 6) (Misshapen/NIK-related kinase) (GCK
family kinase MiNK). [Source:Uniprot/SWISSPROT;Acc:Q8N4C8]


# arms: 1
# species: 1
# libraries: 1
# reads: 3
# human_block172399
hsa       .........(((((((((((((.((((((...((((....)))).((((((((((...)))).)))))).)))))))..)).)))))..)))))
hsa  GACAAGTGGGTGGGCTGGGCGGGGGGCGGGGCAGGTGGGCGGAGGCCCTGGGGCTCTGCATAGCAGCAGCCCCATGCCCCACCTCCCTGTCCCAGGATGA
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ...........................................................................TGCCCCACCTCCCTGTCCC.......  3  human_libH12
hsa  chromosome:9:139030140:139030239:-1  ENST00000371605 ENSG00000107331 ABCA2 ATP-binding cassette sub-family A member 2 (ATP-binding
cassette transporter 2) (ATP-binding cassette 2). [Source:Uniprot/SWISSPROT;Acc:Q9BZC7]


# arms: 1
# species: 1
# libraries: 1
# reads: 2
# human_block107544
hsa       (((.(((((.((....(((((...((((((..(((.........)))...)))))))..)))))...)).)))))..)))..
hsa  GCAAGGTGAGTGGCCACCATGCGGGGACAGGGGCAGGGGCAGCCCTCACCCACAGCCTCTCACCTGCCTTTGTCCACCCACAGCGCAA
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ...........................................................CTCACCTGCCTTTGTCCACCC.........  2  human_libH9
hsa  chromosome:19:6366308:6366395:-1  ENST00000201886 ENSG00000088247 KHSRP Far upstream element-binding protein 2 (FUSE-binding protein 2)
(KH type-splicing regulatory protein) (KSRP) (p75). [Source:Uniprot/SWISSPROT;Acc:Q92945]


# arms: 1
# species: 1
# libraries: 1
# reads: 2
# chimp_block23965
ptr       (((((((.((((.(((..((((....)))).(((((((.((.....)).....)))))))))))))).)))))..)))..
ptr  CCTGGGTGAGGGCAAGGCTGGGGGGCCCCTGGGCTAAGTGGGAGCCTGGCTGGAATTCCCACTCCACCTTACTCTCCTGCAGTGTTC
ptr  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
ptr  ...........................................................CACTCCACCTTACTCTCCTG........  2  chimp_libPT0
ptr  chromosome:20:2753646:2753732:1  ENSPTRT00000024487 ENSPTRG00000013186 PTPRA Vacuolar protein sorting-associated protein 16 homolog
(hVPS16). [Source:Uniprot/SWISSPROT;Acc:Q9H269]


# arms: 1
# species: 1
# libraries: 1
# reads: 2
# human_block96092
hsa       ....(((..(((((((..((((.(..(.((((((((((.(.((.....)).).)))))))))).)..).)))))..)))).)))))..)))..
hsa  CGGCTGTGAGTGTGGGGCGCGCCGGGCTGTGGCGGGCTGGGGGCGGGCGGCCCTGGGTCCCAGCCTCCTGCTGCCCACCGCTGCCCACCGCAGGGCTG
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ....................CCGGGCTGTGGCGGGCTGG...............................................  1  human_libH9
hsa  .........GTGTGGGGCGCGCCGGGCTGTGGCGG...................................................  1  human_libH9
hsa  chromosome:17:2222294:2222391:1  ENST00000268989 ENSG00000141258 RUTBC1 RUN and TBC1 domain containing 1
[Source:RefSeq_peptide;Acc:NP_055668]


# arms: 1
# species: 1
# libraries: 1
# reads: 2
# macaque_block550558
mml       (.(((((.((.(((..(.((((((((((..((((((.............)))))))))))))..)))..)))).)))))...))).)..
mml  AACAGGTGAGCAGAGTGGGTTGGAGGGGGGTGTCCCAGGCTCTTTCTTGTCTATGGGCCTGACACCCCGACCCTGACTGGCCTGGGCCTCCCAGGACAC
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ...................................................................CCTGACTGGCCTGGGCCTCCCA......  2  macaque_lib3
mml  chromosome:X:47099255:47099353:1  ENSMMUT00000012053 ENSMMUG00000008623 CCDC22 Coiled-coil domain-containing protein 22.
[Source:Uniprot/SWISSPROT;Acc:O60826]


# arms: 1
# species: 1
# libraries: 1
# reads: 2
# macaque_block137121
mml       (..((((((((((.(..(((..((((.....)))).....(((((((.((.......)))))))))).....)))..).)))))))))..)..
mml  TCGAGGTGAGGAGGCAGGCGGGGAATGCCTGAGCCGCAGGGGGCCTGGGCCTGGATCCCAGCCGGCCCAGATTTATTTTCATCTCCTGCTTCCTGCCAGGGCTT
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ...........................................................................CATCTCCTGCTTCCTGCCAG.....  2  macaque_lib15
mml  chromosome:16:6954134:6954237:1  ENSMMUT00000014751 ENSMMUG00000010538 ACADVL Very-long-chain specific acyl-CoA dehydrogenase,
mitochondrial precursor (EC 1.3.99.-) (VLCAD). [Source:Uniprot/SWISSPROT;Acc:P49748]


# arms: 1
# species: 1
# libraries: 1
# reads: 2
# mouse_block5452
mmu       .(((((((((.(....).)).)))))))((((...))))..((((((...((((....((((((.....)))))).))))...)))))).
```

```
mmu  CTGAGGTAGTCTGGGAGCTGGCACCGCAGACTATCCCCAGGGGACACGGGGACTTGGCTGAGGCAGCTCCACTGAGAGCTGAGAGCCTTATCCCCGCAGTTCTG
mmu  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mmu  ...........................................................................TGAGAGCCTTATCCCCGCAGTT...  1  mouse_lib1
mmu  ...........................................................................CTGAGAGCCTTATCCCCGCAG.....  1  mouse_lib1
mmu  chromosome:9:56935507:56935610:1  ENSMUST00000034836 ENSMUSG00000032295 Man2c1 mannosidase, alpha, class 2C, member 1
[Source:MarkerSymbol;Acc:MGI:1920994]


# arms: 1
# species: 1
# libraries: 1
# reads: 2
# mouse_block283
mmu       .(((((((..((.(((((..((((..(((.(..(((((.....)))))..)..)))..)))))))))).))..)))))))....
mmu  CCCAGGTAAAGGCTGGGCTTAGACGTGGCCTTTGGGTGTGGAATGCACTTCCGTTTGTAACCGCCATCTAACCCTGGCCTTTGACAGGTGCG
mmu  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mmu  .....GTAAAGGCTGGGCTTAGACGTGG.............................................................  2  mouse_lib1
mmu  chromosome:1:186523190:186523281:-1  ENSMUST00000068725 ENSMUSG00000073481 Mosc2 MOCO sulphurase C-terminal domain containing 2
[Source:MarkerSymbol;Acc:MGI:1914497]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block168305
hsa       (((.((.((((..((...((.(((...(((((((((.......))).)))))))..))).))))..)))).)).)))..
hsa  CATTGGTGAGCTGGGGTGGCTGAGGCGGGATGGGGGCCACCTGAGGCTGGGGCTGGCCCTGCTCACTGCTGCTCCTGCCCACAGAGTAC
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  .....GTGAGCTGGGGTGGCTGAG..............................................................  1  human_libH13
hsa  chromosome:8:144971936:144972024:-1  ENST00000349157 ENSG00000179950 NP_055096.2 fuse-binding protein-interacting repressor isoform b
[Source:RefSeq_peptide;Acc:NP_055096]

# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block108536
hsa       (((((((.......((((((.((((.(((((((((((..(((...))).....)))))))).))))))))))))))))))..
hsa  TTGAGGTGGGCGAACGCCCGGGTGGAGCGGGTCAGGCAGGGCCAGTCACAGACACAGCTCTGTGCTGACTGCCCGCCTTGCCCACAGCTCGG
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ............................................................TGCTGACTGCCCGCCTTGCCCACA......  1  human_libH0
hsa  chromosome:19:18408053:18408144:-1  ENST00000338128 ENSG00000105655 NP_057452.1 myo-inositol 1-phosphate synthase A1
[Source:RefSeq_peptide;Acc:NP_057452]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block2497
hsa
..((((((((((((.(((((((((((((((..((((....))))...))))))...))).)))))))).))))(((((((((....)))))))).)))))((((.(((((((((..(.((((.......(((....)))...
..)))))..)))))))).))))).))))))).....
hsa
CTGGGGTGAGCAGGGCCAGTGCTGGACTCTGCTGCTGGGCCTTGGTGGGCAGGGGCAGCAAGAGAGGTTCAGCTTTGGCCCTGGCCCAGCTCTCTGGGCACAGGGGTCAGCTGGGATGGGAGTCTGGGAGAACAAGGGGTCC
CTGAAGACCAGCAACCATCTCACTCTGGCACCCCTGCTCCCCCAGGTCTG
hsa
>>>>>++++++++++++++++++++++++++++++++++++++
```

```
# reads: 1
# human_block127094
hsa       (((((..((((...(((((((((...(((((((.((...)).)).))))))))))))).)))).)))).)))))..))))))..
hsa  TCCAGGTGCGTGGTGGCTCGAGGCGGGGGTGGGGGCCTCGCCCTGCTTGGGCCCTCCCTGACCTCTCCGCTCCGCACAGAGTGC
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ......TGCGTGGTGGCTCGAGGCGGG.....................................................  1  human_libH9
hsa  chromosome:22:48742513:48742596:1  ENST00000360612 ENSG00000198355 PIM3 Serine/threonine-protein kinase Pim-3 (EC 2.7.11.1).
[Source:Uniprot/SWISSPROT;Acc:Q86V86]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block94727
hsa       ..(((((.(((.((..(((((((((.((.......)).)).)))))).....)).)))))))).............
hsa  CAAAGGTGAGGGCAGCCGGCAGGGCCCCAGGTCCTGCTTACATGTGGGCCCAGACTCCAGCTCCCCTCTCCCCACATGCAGATGTG
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  .....GTGAGGGCAGCCGGCAGGGCCCCA.....................................................  1  human_libH11
hsa  chromosome:16:66417476:66417560:1  ENST00000388833 ENSG00000102904 TSNAXIP1 translin-associated factor X interacting protein 1
[Source:RefSeq_peptide;Acc:NP_060900]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block88730
hsa       .((.((((((.((((..(((((.(((.((..((..(((((....)))...))..))..))...))).))))))..))))))))))).
hsa  GCAAGGTGAGGCGGGGCCAGGAGGGTGTGTGGCGTGGGTGCTGCGGGGCCGTCAGGGTGCCTGCGGGACGCTCACCTGGCTGGCCCGCCCAGGACCT
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ....................................................................TCACCTGGCTGGCCCGCCCAG.....  1  human_lib8
hsa  chromosome:14:104688155:104688251:-1  ENST00000347004 ENSG00000184916 JAG2 Jagged-2 precursor (Jagged2) (HJ2).
[Source:Uniprot/SWISSPROT;Acc:Q9Y219]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block713
hsa       ....(.(((((((.(((((.((((((((((...(((..((.....))..)))...))))))))))))))).)))))).)..
hsa  AGGAGGTGAGTGGGGTGGGGGTGTGGGGTGGGGGGCATGGAGCCGGCGTGGAACCAGAGCCCTCACTCCTGCCCACACCCCTCAGCAGCT
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ............................................................CTCCTGCCCACACCCCTCAG.....  1  human_libH9
hsa  chromosome:1:9703302:9703391:1  ENST00000377346 ENSG00000171608 PIK3CD Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit
delta isoform (EC 2.7.1.153) (PI3-kinase p110 subunit delta) (PtdIns-3- kinase p110) (PI3K) (p110delta). [Source:Uniprot/SWISSPROT;Acc:O00329]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block168233
hsa       ....((.(((((.....)).)))..))...((((((((((..(((((((....)))...(((.(((....))).)))....))))..)))))))))).
hsa  GACCAGTGAGCGGCCGCTGGGGGCAGGTGGCGGGTGGGAGGGAGGGAGGTGGGCTTTCCCGGTGGGCGTTCAGAAACCCCCTTTTACCTGACTCTCTCCCAGTGCTG
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ...........................................................................TTTACCTGACTCTCTCCCAG.....  1  human_lib7
hsa  chromosome:8:144715659:144715765:1  ENST00000262580 ENSG00000104518 GSDMDC1 Gasdermin domain-containing protein 1.
[Source:Uniprot/SWISSPROT;Acc:P57764]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block110912
hsa       .((.(((((((((((.((.((..((((((..((....................))..).)))))....)).)).)))))))..)))))..)).
hsa  CTGAGGTGAGCCAGTGGAATGGAGAGGCTGTGGGCAGGGGGAGATGTGAAGGAAAGAACTAGGACCCATTCATCCACTGCATTCCTGCTTGGCCCAGGACAA
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  .....GTGAGCCAGTGGAATGGAGAGG.......................................................................  1  human_libH0
hsa  chromosome:19:63753459:63753560:1  ENST00000341753 ENSG00000130726 TRIM28 Transcription intermediary factor 1-beta (TIF1-beta)
(Tripartite motif-containing protein 28) (Nuclear corepressor KAP-1) (KRAB- associated protein 1) (KAP-1) (KRAB-interacting protein 1) (KRIP-
1) (RING finger protein 96). [Source:Uniprot/SWISSPROT;Acc:Q13263]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block29395
hsa       ....(((.((((..(((((..((.(((((..((.(.....)).))...(((.(((((((((....)).)).)))))..)))).))))..)).)))))..)))))))..
hsa  CACTGGTGAGGCTGGGGCAGGGATGAGGTGGCCCAGGAGAGTGAGTCCCCGAGGGTGGGCCGCGGAAAGCCAGCAGGCTGACCAGGCCTTCGTGTCCCCTCCCTGCCAGTGTTC
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ...............................................................................CCTTCGTGTCCCCTCCCTGCC.......  1  human_libH10
hsa  chromosome:11:65148409:65148522:1  ENST00000309295 ENSG00000173442 EHBP1L1 Signal-induced proliferation-associated protein 1 (Sipa-1)
(GTPase- activating protein Spa-1) (p130 SPA-1). [Source:Uniprot/SWISSPROT;Acc:Q96FS4]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block110710
hsa       ...(((((((((..((((.((((.((((((....)))))))((....)))....))).).)))))..)))))))))..
hsa  TCCAGGTAGGGGCGGGGTGGGAGAGGTGGGGTCTGCGTGCGGGCCGGGCCGGCCCCTGACGCGCGCTCCTCCCCTGCCCCAGCACCC
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ..........................................................CGCGCTCCTCCCCTGCCCC.......  1  human_libH0
hsa  chromosome:19:60295720:60295806:-1  ENST00000376393 ENSG00000125503 PPP1R12C protein phosphatase 1, regulatory subunit 12C
[Source:RefSeq_peptide;Acc:NP_060077]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block185010
hsa       (((((.((((((((((.(((.........))).(((((..((....))..)))))).)))))))..)))))))..
hsa  CACAGGTGGGTGCGGAGGCGGGGGGACAGGGTACCCACGAGGCCTGAACTCACACCTCGGCGCCTCCTGGCCCCGCAGACCTC
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  .....GTGGGTGCGGAGGCGGGGGG.........................................................  1  human_libH8
hsa  chromosome:X:152693451:152693533:1  ENST00000361971 ENSG00000198753 PLXNB3 Plexin-B3 precursor. [Source:Uniprot/SWISSPROT;Acc:Q9ULL4]


# arms: 1
```

```
# species: 1
# libraries: 1
# reads: 1
# human_block109083
hsa       .((((...(((((((..(((((..(((((((((((.....)))).(....)..)))))))))....)))))))))))).))))).
hsa  CCACGGTGAGCCCGCAGCGGGGCAGGGTACAGGGGCGGGGGCCCCCATGGCCAGGCCCCACCCCGCTCCTATTGACCCTCCTGCTGTCCTCAGATCTC
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  .....GTGAGCCCGCAGCGGGGCAGGGTAC.............................................................  1  human_libH12
hsa  chromosome:19:40192935:40193032:1  ENST00000318014 ENSG00000089351 GRAMD1A GRAM domain containing 1A
[Source:RefSeq_peptide;Acc:NP_065946]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block91836
hsa       .....((((.....(((((..((((.(((((((((.....)))))).....)))).))))..)))))))))..
hsa  TGAAGGTGAGGGGGCTGCCAGGGGTAGGCTACAGGCCTCCATCACGGGGGACCCCTCTGAAGCCACCCCCTCCCCAGGTCTT
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  .....GTGAGGGGGCTGCCAGGGGT.......................................................  1  human_libH8
hsa  chromosome:16:2083736:2083817:-1  ENST00000382481 ENSG00000008710 PKD1 Polycystin-1 precursor (Autosomal dominant polycystic kidney
disease protein 1). [Source:Uniprot/SWISSPROT;Acc:P98161]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block152130
hsa       (((.((..((((((..........(((((.((.(((((((((....))).)))))..)).))...)))))..)))))).)))))..
hsa  GCCAGGTGAGGGGCTGGGGTTTTCGTCCCATGGCGGGCAGGGCCCAGGGAGCTGAGGCTGCTTCTAAAGCCATCTCCCCGGTACCCGCAGGCGAC
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ......................................................................CCATCTCCCCGGTACCCGCAG.....  1  human_libH13
hsa  chromosome:7:150378969:150379063:1  ENST00000377904 ENSG00000197150 ABCB8 ATP-binding cassette sub-family B member 8, mitochondrial
precursor (Mitochondrial ATP-binding cassette 1) (M-ABC1). [Source:Uniprot/SWISSPROT;Acc:Q9NUT2]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# human_block91683
hsa       ...((.(((...(((((..(((((((.(...(((.....)))).)))))))))))...))).))..
hsa  AGAAGGTAGGTCAGGCCCAGGTGTGGGTTGGGGTCCGGCTGCAGCGCCCGCTAACCCACCTGCTGCTGTCCAGTTTGA
hsa  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
hsa  ...................................................CCCACCTGCTGCTGTCCAGT....  1  human_libH1
hsa  chromosome:16:275012:275089:1  ENST00000219406 ENSG00000185615 PDIA2 Protein disulfide-isomerase A2 precursor (EC 5.3.4.1) (PDIp).
[Source:Uniprot/SWISSPROT;Acc:Q13087]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# chimp_block17609
ptr       ....(.(((((.((.((((.(((....))).....((((((.((.((.((((((....)))))))).))).)))))).))))..)).)))))..
ptr  TGAAGGTGAGTGGGCAGGGACAGGAGCCTGCGGGCTGGGGTTGGGGGGCACAGTGGGTGTGCCCGCTTGGCCTGTGACCACCTGCACTGTGCCCCAGGTGAA
ptr  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
ptr  ......................................................................TGACCACCTGCACTGTGCCCCA......  1  chimp_libPT0
ptr  chromosome:17:82136999:82137100:-1  ENSPTRT00000059474 ENSPTRG00000030738 MAFG Transcription factor MafG (V-maf musculoaponeurotic
fibrosarcoma oncogene homolog G) (hMAF). [Source:Uniprot/SWISSPROT;Acc:O15525]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# chimp_block18
ptr       .((.(((((((...........((((..((...(((((...(((.((((....)))))))).)))))..)).))..)))))))))))).
ptr  CAGCAGTGAGTGGGGGCTTCAGGCTTCAGGGCGGGGGGGAGGGGAACGCCGGAGGCCCCTCCGCGGCCCTCACCTACCCTCCCCCGCCAGATCTC
ptr  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
ptr  ......................................................................TCACCTACCCTCCCCCGCCAG.....  1  chimp_libPT0
ptr  chromosome:1:1249436:1249530:-1  ENSPTRT00000000053 ENSPTRG00000000025 DVL1 Segment polarity protein dishevelled homolog DVL-1
(Dishevelled-1) (DSH homolog 1). [Source:Uniprot/SWISSPROT;Acc:O14640]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block204975
mml       .((.((((.((.((((((((...((((((.((.((....(....)..)).)).)))))))....)))))))))).))))....
mml  TGAAGGTGAGCAGGGATGGCGGGCATTGGGGGAGCCGGGAGCGGGGGACAGCCGGGGTCCCTCTCACGCCCGCCTCGCTGCCCGGCAGACGTC
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  .....GTGAGCAGGGATGGCGGGCATT.......................................................  1  macaque_lib11
mml  chromosome:19:1825939:1826031:-1  ENSMMUT00000015758 ENSMMUG00000011265 MKNK2 MAP kinase-interacting serine/threonine-protein kinase 2
(EC 2.7.11.1) (MAP kinase signal-integrating kinase 2) (Mnk2). [Source:Uniprot/SWISSPROT;Acc:Q9HBH9]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block136233
mml       (.(((((.((((.(((((((((.(((..((((....)))).))).))).....(((...)))...)))))))))))).)).))).)....
mml  GACCGGTGAGCACGCGGGATTTCCAGGGGACGGGCAGGACGCTGCAGTCTGACTGGCGCAGGGGCCTGGGAATCCGCCTGTCTCCCACAGGATGC
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  .....GTGAGCACGCGGGATTTCCAGG........................................................  1  macaque_lib10
mml  chromosome:16:4322244:4322338:-1  ENSMMUT00000032178 ENSMMUG00000022859 MYBBP1A Myb-binding protein 1A.
[Source:Uniprot/SWISSPROT;Acc:Q9BQG0]


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block6168
mml       ....((((((..((((.(((((((((((.((((((.((((..((((((..((...(.....)..))..))))))..)))))).))))))))))))).)))))..))))))))))).....
mml  CTGAGGTACGGAAGGCCAGGGTGGTGGCGGGAATCCATTCCGGTGTGTTCTACACATTGCTTAGAGATTGGATGGGGTGCATCAGGGTGGTTTCTGATTACTTTTCTTCTTCCCTCAGCCTTT
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ....GGTACGGAAGGCCAGGGTG...........................................................................................  1
macaque_lib2
```

mml chromosome:1:46900619:46900741:1 ENSMMUT00000047311 ENSMMUG00000015154 ATP6V0B Vacuolar ATP synthase 21 kDa proteolipid subunit (EC 3.6.3.14) (HATPL). [Source:Uniprot/SWISSPROT;Acc:Q99437]

```
# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block105549
mml       ((..((.(((((....(((((((.(((((.............)))))..)))))))..)))))..))..))..
mml  AGGAGGTGAGCTGGGGGATGTGAGGGGTTGGACTGTTCCAGTTCTCTGTCTACCCTCTCTGCCTCCTGCCTGCAGGTGGA
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ...............................................CTACCCTCTCTGCCTCCTGCCTGC.......  1  macaque_lib13
mml  chromosome:14:6829722:6829801:1  ENSMMUT00000026051 ENSMMUG00000018528 NUDT8 Nucleoside diphosphate-linked moiety X motif 8, mitochondrial precursor (EC 3.6.1.-) (Nudix motif 8). [Source:Uniprot/SWISSPROT;Acc:Q8WV74]

# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block205962
mml       .((.(((((((((.((...(((((((.(((((((..(........)..)))).((....))..)))))))))))).)))).)))))))).
mml  CAAGAGTGAGGCGGGCAGACGGCATGGGAGGGCAGGCGGGCTGGGTTTCTGACTGGCCCTGGCTGACCGTGCTTCCCTCTTCCCTCTGCCCCGCCCAGCCTTG
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  .....GTGAGGCGGGCAGACGGC.............................................................................  1  macaque_lib12
mml  chromosome:19:7571608:7571710:-1  ENSMMUT00000013314 ENSMMUG00000009539 XAB2 XPA-binding protein 2 (HCNP protein). [Source:Uniprot/SWISSPROT;Acc:Q9HCS7]

# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block205753
mml       (((((((.(((((((((.(((((((.(....).)))))))).((.(((....))).)).)))).).)))).....)))))))..
mml  TCCAGGTGAGGCCGACGCGAGGCGGCTGCGAGACCCCGTGCGGCCTTGCGGGCGCGCCCTCACCCTCTGCCGTCCCTGTCTCACAGCAGCT
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ....GGTGAGGCCGACGCGAGG..................................................................  1  macaque_lib4
mml  chromosome:19:6285380:6285470:-1  ENSMMUT00000011066 ENSMMUG00000007904 GTF2F1 Transcription initiation factor IIF subunit alpha (EC 2.7.11.1) (TFIIF-alpha) (General transcription factor IIF subunit 1) (Transcription initiation factor RAP74) (General transcription factor IIF polypeptide 1 74 kDa subunit protein). [Source:Uniprot/SWISSPROT;Acc:P35269]

# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block532048
mml       .....(((((((((.....((((((..((((..(((((.(((....)))))))).)))).)))))))))))))).
mml  GCTACGTGAGTGTGGGGTGGCTGGGGTGGGGCAGGGATGGCTTGGGCCTGCCCAGTCGGCCTGACCACCCACCCCACAGGCACC
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ..............................................................CCTGACCACCCACCCCACAG.....  1  macaque_lib6
mml  chromosome:8:147026085:147026168:-1  ENSMMUT00000010324 ENSMMUG00000007380 CPSF1 Cleavage and polyadenylation specificity factor subunit 1 (Cleavage and polyadenylation specificity factor 160 kDa subunit) (CPSF 160 kDa subunit). [Source:Uniprot/SWISSPROT;Acc:Q10570]

# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block206327
mml       .((.(((((((....(((((((((((((.((((.....((((((.....)))))))))))))))....)))))))).)....)).)))))))).
mml  AAGAGGTGAGCAGGGCGATCGGGGGGGCTGGCGTGCTGGGGTGGGGCACAGGGGGTGCCTCAGCCGCCTCTGAGCTCCCACAACCCGCCCCTGCCAGGACCT
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  .....GTGAGCAGGGCGATCGGG..................................................................  1  macaque_lib10
mml  chromosome:19:9919055:9919156:-1  ENSMMUT00000024201 ENSMMUG00000017217 EIF3S4 Eukaryotic translation initiation factor 3 subunit 4 (eIF-3 delta) (eIF3 p44) (eIF-3 RNA-binding subunit) (eIF3 p42) (eIF3g). [Source:Uniprot/SWISSPROT;Acc:O75821]

# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block105550
mml
....((((((((((....((((.((((((.(((((((((..(((.....)))).......((((((..((.....(((.......)))..((((.(.....).)))))...)).)..)))))))))))))))).)).....)))
).)))).)))))).)))))......
mml
CAGCAGTGAGTAGGGGCGGGAGGAGGGGACACCCTGAGCTCAGTCCAGCCAGGAGAGGCATTGGGGTGTCCCTGCCATCTGGCCGTGGAGGGGCAAGGCAGGAGGTATGTGCCATGGGTGGGGGCAGATTGAGCTGAGGTAG
GAGGTGACCCTGCCTGCCACCTGCCTTTAGCTGCC
mml
>>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
++++++++++++++++++++++++++++++>>>>>
mml
.....GTGAGTAGGGGCGGGAGGAGG.....................................................................................................
.................................  1  macaque_lib9
mml  chromosome:14:6834207:6834383:1  ENSMMUT00000026048 ENSMMUG00000018527

# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block532079
mml       ....(((.(((((((.(((((.(((((.((((....)))).)))))..)..)))))))))..))).
mml  CCGTGGTAGGTGCGGCGGTGCGGCTGTGGGAGGGCTGCCGGTGGCGCTCCCTCTGAGCCTGCCGCCTCGCAGGCATC
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ...............................................CTCCCTCTGAGCCTGCCGCCTCGC.......  1  macaque_lib10
mml  chromosome:8:147165535:147165611:1  ENSMMUT00000021855 ENSMMUG00000015582 PPP1R16A Protein phosphatase 1 regulatory subunit 16A (Myosin phosphatase- targeting subunit 3). [Source:Uniprot/SWISSPROT;Acc:Q96I34]

# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block105910
mml       .(((((.......(((..(((.(((((((((((.((((...(((((((....))..)))))..))))))))))))))))))..)))).)))))).
mml  AGAAGGTGGGAGCAGGCAGGGCTGGGCAGGCCAGGGGTCTGGGAGGCAGGGGCCCGGGCAGCCCTGAACCCAACCCCTGGCTTCCTCTCCCATCCCAGGTCCT
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ...................................................................CTGGCTTCCTCTCCCATCCCAG.....  1  macaque_lib7
mml  chromosome:14:8179788:8179890:-1  ENSMMUT00000044557 ENSMMUG00000022520 KLC2 Kinesin light chain 2 (KLC 2). [Source:Uniprot/SWISSPROT;Acc:Q9H0B6]
```

```
# arms: 1
# species: 1
# libraries: 1
# reads: 1
# macaque_block46401
mml       (((((.((((((.....((((((..(((((((((...(((...((((.((...)).)))).....))))))))))....)))))).)))))).....))))).
mml  CCAGGGTGAGCCAGAGTGGTGGAGCAGGGAGGCGGGGGTTCAGCCAGGGCTTGCTGGGCCAGCCAGAGCGCCCCCGTGATGCCCTGCGGCTCTGTTCTCACAGCTGAG
mml  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mml  ...............................................................................CCCTGCGGCTCTGTTCTCACAG.....  1  macaque_lib11
mml  chromosome:11:7368394:7368501:-1  ENSMMUT00000012440 ENSMMUG00000006470


# arms: 1
# species: 1
# libraries: 1
# reads: 1
# mouse_block1287
mmu       .((((.((((((((((.(...((.(((.....(((((((((((((.......)))))))))))))).))).)).).))))))))))...)))).
mmu  TGGAGGTGAGAGCGGGGGGAGTGGCAAGTGAGACGGATGGGCGGGGCTGGCTCAGACTGCTAGCCCCGCCCAGCTCTCTAACTCTTCCCTTGTGCCCTCAGGAGGC
mmu  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mmu  ...............................................................................TAACTCTTCCCTTGTGCCCTCA......  1  mouse_lib1
mmu  chromosome:13:55487298:55487403:-1  ENSMUST00000054646 ENSMUSG00000034675 Dbn1 drebrin 1 [Source:MarkerSymbol;Acc:MGI:1931838]



# arms: 1
# species: 1
# libraries: 1
# reads: 1
# mouse_block5174
mmu       .((((..(((((.(((((((((((((((((((.....)))).)).)))))).).)))))))).)))))..)))).
mmu  TCTCGGTGAGGCTCAGTATGGGGTGGGGGTGTCGTCGCCTGCCCGACTGACCACCCACTCACCCTGGACTGACTCTCAGGCTGG
mmu  >>>>>++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++>>>>>
mmu  .......................................................TCACCCTGGACTGACTCTCAG.....  1  mouse_lib1
mmu  chromosome:8:75399000:75399083:-1  ENSMUST00000079510 ENSMUSG00000052488 Cherp calcium homeostasis endoplasmic reticulum protein
[Source:MarkerSymbol;Acc:MGI:106417]
```

Figure S7. Correlation between Number of Mirtron Small RNA Reads and Number of Human ESTs.

mirtron	host gene	host transcript	location	total reads	ESTs in the region	ESTs in the entire gene
hsa-mir-877	ENSG00000204580	ENST00000376575	chromosome:6:30660083:30660178:1	59	55	13804
hsa-mir-1224	ENSG00000145198	ENST00000273794	chromosome:3:185441882:185441976:1	58	9	45
hsa-mir-1225	ENSG00000008710	ENST00000382481	chromosome:16:2080192:2080291:-1	3	45	742
hsa-mir-1226	ENSG00000132153	ENST00000348968	chromosome:3:47866044:47866128:1	143	92	568
hsa-mir-1227	ENSG00000104886	ENST00000326631	chromosome:19:2185056:2185153:-1	5	111	263
hsa-mir-1228	ENSG00000123384	ENST00000338962	chromosome:12:55874549:55874631:1	6	7	951
hsa-mir-1229	ENSG00000161013	ENST00000376937	chromosome:5:179157879:179157957:-1	16	298	1287
hsa-mir-1231	ENSG00000134369	ENST00000367302	chromosome:1:200044357:200044458:1	3	15	618
hsa-mir-1233	ENSG00000175676	ENST00000328919	chromosome:15:20996204:20996295:1	3	55	128
hsa-mir-1234	ENSG00000071894	ENST00000349769	chromosome:8:145596279:145596372:-1	3	35	482
hsa-mir-1236	ENSG00000204356	ENST00000375429	chromosome:6:32032590:32032701:-1	2	165	316
hsa-mir-1237	ENSG00000162302	ENST00000334205	chromosome:11:63892645:63892756:1	2	23	206
hsa-mir-1238	ENSG00000130734	ENST00000309469	chromosome:19:10523793:10523885:1	2	38	222
human_block172399	ENSG00000107331	ENST00000371605	chromosome:9:139030140:139030239:-1	3	24	493
human_block107544	ENSG00000088247	ENST00000201886	chromosome:19:6366308:6366395:-1	2	71	602
human_block96092	ENSG00000141258	ENST00000268989	chromosome:17:2222294:2222391:1	2	11	389
human_block168305	ENSG00000179950	ENST00000349157	chromosome:8:144971936:144972024:-1	1	202	861
human_block108536	ENSG00000105655	ENST00000338128	chromosome:19:18408053:18408144:-1	1	83	595
human_block2497	ENSG00000121753	ENST00000373658	chromosome:1:31974574:31974765:-1	1	18	175
human_block145951	ENSG00000078269	ENST00000367122	chromosome:6:158405766:158405850:1	1	6	300
human_block100511	ENSG00000108840	ENST00000336057	chromosome:17:39511555:39511693:-1	1	109	366
human_block168304	ENSG00000179950	ENST00000349157	chromosome:8:144970973:144971072:-1	1	142	861
human_block127094	ENSG00000198355	ENST00000360612	chromosome:22:48742513:48742596:1	1	70	346
human_block94727	ENSG00000102904	ENST00000388833	chromosome:16:66417476:66417560:1	1	7	56
human_block88730	ENSG00000184916	ENST00000347004	chromosome:14:104688155:104688251:-1	1	5	95
human_block713	ENSG00000171608	ENST00000377346	chromosome:1:9703302:9703391:1	1	11	229
human_block168233	ENSG00000104518	ENST00000262580	chromosome:8:144715659:144715765:1	1	75	429
human_block110912	ENSG00000130726	ENST00000341753	chromosome:19:63753459:63753560:1	1	359	1532
human_block29395	ENSG00000173442	ENST00000309295	chromosome:11:65148409:65148522:1	1	25	1146
human_block110710	ENSG00000125503	ENST00000376393	chromosome:19:60295720:60295806:-1	1	33	284
human_block185010	ENSG00000198753	ENST00000361971	chromosome:X:152693451:152693533:1	1	16	117
human_block109083	ENSG00000089351	ENST00000318014	chromosome:19:40192935:40193032:1	1	64	379
human_block91836	ENSG00000008710	ENST00000382481	chromosome:16:2083736:2083817:-1	1	18	742
human_block152130	ENSG00000197150	ENST00000377904	chromosome:7:150378969:150379063:1	1	5	492
human_block91683	ENSG00000185615	ENST00000219406	chromosome:16:275012:275089:1	1	17	59

Fig. S8. Minimum Free Energies (MFEs) of 5 nt Terminal Duplexes of Mirtronic miRNAs.

```
------------------------------
>hsa-mir-877
GUAGAGGAGAUGGCGCAGGGGACACGGGCAAAGACUUGGGGGUUCCUGGGACCCUCAGACGUGUGUCCUCUUCUCCCUCCUCCCAG
...((((((..((.(.(((((((((((.(.......(((((((((.....)))))))))).).))))))))))).).))))))))).... (-39.50)
>left
GUAGA&UCCCAG
...((&)).... (  1.20)
>right
GGGAC&GUCCU
(((((&))))) ( -5.40)
```

Dominant arm: 5'
Cloning: consistent

```
------------------------------
>hsa-mir-1224
GUGAGGACUCGGGAGGUGGAGGGUGGUGCCGCCGGGGCCGGGCGCUGUUUCAGCUCGCUUCUCCCCCCACCUCCUCUCUCCUCAG
.((((((...(((((((((.(((.((.((..(((....)))..((((...)))))..)).)).))).)))))))))...)))))). (-45.00)
>left
GUGAG&CUCAG
.((((&)))). ( -3.00)
>right
GAGGG&CCCCC
(.(((&))).) ( -2.20)
```

Dominant arm: 3'
Difference between arms is small.
Cloning: 3' arm is more abundant in chimp,
in human and macaque - 5' arm is slightly more abundant.

```
------------------------------
>hsa-mir-1225
GUGGGUACGGCCCAGUGGGGGGGAGAGGGACACGCCCUGGGCUCUGCCCAGGGUGCAGCCGGACUGACUGAGCCCCUGUGCCGCCCCCAG
.((((..((((.(((.((((((..((..((...((((((((((...)))))))))))...))...)).)).))...)))))).)))).)))). (-48.20)
>left
GUGGG&CCCAG
.((((&)))). ( -5.10)
>right1
GGGGG&ACUGAGCC
((((.&.))...)) (  0.60)
>right2
GG&UGAGC
((&)...) (  8.30)
```

Dominant arm: 3'
Cloning: more 5' reads but difference in clone numbers is small

```
------------------------------

>hsa-mir-1226
GUGAGGGCAUGCAGGCCUGGAUGGGGCAGCUGGGAUGGUCCAAAAGGGUGGCCUCACCAGCCCUGUGUUCCCUAG
...((((.(((((((.((((.((((((.(((.((.....)).....))).))))))))))).)))))))).))))).. (-36.90)
>left
GUGAG&CUAG
...((&)).. (  1.40)
>right1
UGGGG&CCUCA
(((((&))))) ( -4.40)
>right2
GGAUGG&UCACC
((.(((&))))) ( -0.70)
```

Dominant arm: 5'
Cloning: inconsistent, mostly 3' reads

```
------------------------------
```

```
>hsa-mir-1227
GUGGGGCCAGGCGGUGGUGGGCACUGCUGGGGUGGGCACAGCAGCCAUGCAGAGCGGGCAUUUGACCCCGUGCCACCCUUUUCCCCAG
.(((((..(((.(((((((((((((((...((((((.....))).)))..)))))).....)).))).....))))))))))..)))))). (-36.70)
>left
GUGGG&CCCAG
.((((&)))). ( -5.10)
>right1
GGUGG&CCCGUGCC
(((((&))...))) ( -1.30)
>right2
GU&CGUGC
((&...)) (  1.90)
```

Dominant arm: 3'
Cloning: consistent

```
>hsa-mir-1228
GUGGGCGGGGGCAGGUGUGUGGUGGGUGGUGGCCUGCGGUGAGCAGGGCCCUCACACCUGCCUCGCCCCCCAG
..(((((((((.((((((((....((((.....(((((.....)))))))))).))))))))))))))))..... (-46.00)
>left
GUGGG&CCCCCCAG
..(((&))).... ( -3.30)
>right1
GUGUG&CAC
(((..&))) ( -0.80)
>right2
UGUGU&UCACA
((((.&.)))) ( -2.50)
```

Dominant arm: 3'
Cloning: consistent

```
>mml-mir-1230
GUGGGUGGGGGCAUCUCGGAGGAGGUGGGGGGUGUGGCGCCCAGCGGAUGACUCCGAGCGGCUCCUUUCCCAG
.((((.((((((..(((((((..(.((((.(.....).)))).).....)))))))..)))))))..)))). (-38.40)
>left
GUGGG&CCCAG
.((((&)))). ( -5.10)
>right
CGGAG&CUCCG
(((((&))))) ( -6.10)
```

Dominant arm: 5'
Cloning: consistent

Figure S9. MiRbase 10.0 Drosophila, human and mouse mature miRNAs annotated with a 5' G nucleotide.

dme-miR-1017	GAAAGCTCTACCCAAACTCATCC						
dme-miR-263a	GTTAATGGCACTGGAAGAATTCAC						
dme-miR-306*	GGGGGTCACTCTGTGCCTGTGC						
dme-miR-309	GCACTGGGTAAAGTTTGTCCTA						
hsa-miR-138-2*	GCTATTTCACGACACCAGGGTT	hsa-miR-138-1*	GCTACTTCACAACACCAGGGCC				
hsa-miR-139-3p	GGAGACGCGGCCCTGTTGGAGT						
hsa-miR-143*	GGTGCAGTGCTGCATCTCTGGT						
hsa-miR-144*	GGATATCATCATATACTGTAAG						
hsa-miR-145	GTCCAGTTTTCCCAGGAATCCCT	hsa-miR-145*	GGATTCCTGGAAATACTGTTCT	mmu-miR-145	GTCCAGTTTTCCCAGGAATCCCT		
hsa-miR-147b	GTGTGCGGAAATGCTTCTGCTA	hsa-miR-147	GTGTGTGGAAATGCTTCTGC	mmu-miR-147	GTGTGCGGAAATGCTTCTGCTA		
hsa-miR-183*	GTGAATTACCGAAGGGCCATAA	mmu-miR-183*	GTGAATTACCGAAGGGCCATAA				
hsa-miR-186*	GCCCAAAGGTGAATTTTTTGGG	mmu-miR-186*	GCCCTAAGGTGAATTTTTTGGG				
hsa-miR-187*	GGCTACAACACAGGACCCGGGC						
hsa-miR-191*	GCTGCGCTTGGATTTCGTCCCC	mmu-miR-191*	GCTGCACTTGGATTTCGTTCCC				
hsa-miR-198	GGTCCAGAGGGGAGATAGGTTC						
hsa-miR-203	GTGAAATGTTTAGGACCACTAG	mmu-miR-203	GTGAAATGTTTAGGACCACTAG				
hsa-miR-23a*	GGGGTTCCTGGGGATGGGATTT						
hsa-miR-296-3p	GAGGGTTGGGTGGAGGCTCTCC	mmu-miR-296-3p	GAGGGTTGGGTGGAGGCTCTCC				
hsa-miR-29b-1*	GCTGGTTTCATATGGTGGTTTAGA	mmu-miR-29b*	GCTGGTTTCATATGGTGGTTTA				
hsa-miR-330-3p	GCAAAGCACACGGCCTGCAGAGA	mmu-miR-330*	GCAAAGCACAGGGCCTGCAGAGA				
hsa-miR-331-3p	GCCCCTGGGCCTATCCTAGAA	mmu-miR-331-3p	GCCCCTGGGCCTATCCTAGAA				
hsa-miR-337-5p	GAACGGCTTCATACAGGAGTT	mmu-miR-337-5p	GAACGGCGTCATGCAGGAGTT				
hsa-miR-33b	GTGCATTGCTGTTGCATTGC	hsa-miR-33a	GTGCATTGTAGTTGCATTGCA	mmu-miR-33	GTGCATTGTAGTTGCATTGCA		
hsa-miR-345	GCTGACTCCTAGTCCAGGGCTC	mmu-miR-345-5p	GCTGACCCCTAGTCCAGTGCTT				
hsa-miR-370	GCCTGCTGGGGTGGAACCTGGT	mmu-miR-370	GCCTGCTGGGGTGGAACCTGGT				
hsa-miR-373	GAAGTGCTTCGATTTTGGGGTGT						
hsa-miR-376a*	GTAGATTCTCCTTCTATGAGTA	mmu-miR-376b*	GTGGATATTCCTTCTATGGTTA	mmu-miR-376c*	GTGGATATTCCTTCTATGTTTA	mmu-miR-376a*	GGTAGATTCTCCTTCTATGAGT
hsa-miR-382	GAAGTTGTTCGTGGTGGATTCG	mmu-miR-382	GAAGTTGTTCGTGGTGGATTCG				
hsa-miR-409-3p	GAATGTTGCTCGGTGAACCCCT	mmu-miR-409-3p	GAATGTTGCTCGGTGAACCCCT				
hsa-miR-455-3p	GCAGTCCATGGGCATATACAC	mmu-miR-455	GCAGTCCACGGGCATATACAC				
hsa-miR-485-3p	GTCATACACGGCTCTCCTCTCT						
hsa-miR-489	GTGACATCACATATACGGCAGC						
hsa-miR-505*	GGGAGCCAGGAAGTATTGATGT						
hsa-miR-511	GTGTCTTTTGCTCTGCAGTCA						
hsa-miR-515-3p	GAGTGCCTTCTTTTGGAGCGTT						
hsa-miR-518f	GAAAGCGCTTCTCTTTAGAGG	hsa-miR-518a-3p	GAAAGCGCTTCCCTTTGCTGGA				
hsa-miR-523	GAACGCGCTTCCCTATAGAGGGT						
hsa-miR-524-3p	GAAGGCGCTTCCCTTTGGAGT						
hsa-miR-525-3p	GAAGGCGCTTCCCTTTAGAGCG						
hsa-miR-526b*	GAAAGTGCTTCCTTTTAGAGGC						
hsa-miR-539	GGAGAAATTATCCTTGGTGTGT	mmu-miR-539	GGAGAAATTATCCTTGGTGTGT				
hsa-miR-551a	GCGACCCACTCTTGGTTTCCA	hsa-miR-551b	GCGACCCATACTTGGTTTCAG	hsa-miR-551b*	GAAATCAAGCGTGGGTGAGACC	mmu-miR-551b	GCGACCCATACTTGGTTTCAG
hsa-miR-554	GCTAGTCCTGACTCAGCCAGT						
hsa-miR-556-5p	GATGAGCTCATTGTAATATGAG						
hsa-miR-557	GTTTGCACGGGTGGGCCTTGTCT						
hsa-miR-560	GCGTGCGCCGGCCGGCCGCC						
hsa-miR-565	GGCTGGCTCGCGATGTCTGTTT						
hsa-miR-566	GGGCGCCTGTGATCCCAAC						
hsa-miR-572	GTCCGCTCGGCGGTGGCCCA						
hsa-miR-575	GAGCCAGTTGGACAGGAGC						
hsa-miR-590-5p	GAGCTTATTCATAAAAGTGCAG	mmu-miR-590-5p	GAGCTTATTCATAAAAGTGCAG				
hsa-miR-595	GAAGTGTGCCGTGGTGTGTCT						
hsa-miR-599	GTTGTGTCAGTTTATCAAAC						
hsa-miR-602	GACACGGGCGACAGCTGCGGCCC						
hsa-miR-607	GTTCAAATCCAGATCTATAAC						
hsa-miR-611	GCGAGGACCCCTCGGGGTCTGAC						
hsa-miR-612	GCTGGGCAGGGGCTTCTGAGCTCCTT						
hsa-miR-614	GAACGCCTGTTCTTGCCAGGTGG						
hsa-miR-615-5p	GGGGGTCCCCGGTGCTCGGATC	mmu-miR-615-5p	GGGGGTCCCCGGTGCTCGGATC				
hsa-miR-619	GACCTGGACATGTTTGTGCCCAGT						
hsa-miR-621	GGCTAGCAACAGCGCTTACCT						
hsa-miR-625*	GACTATAGAACTTTCCCCCTCA						
hsa-miR-627	GTGAGTCTCTAAGAAAAGAGGA						
hsa-miR-629*	GTTCTCCCAACGTAAGCCCAGC						
hsa-miR-632	GTGTCTGCTTCCTGTGGGA						
hsa-miR-642	GTCCCTCTCCAAATGTGTCTTG						
hsa-miR-647	GTGGCTGCACTCACTTCCTTC						
hsa-miR-653	GTGTTGAAACAATCTCTACTG	mmu-miR-653	GTGTTGAAACAATCTCTACTG				
hsa-miR-657	GGCAGGTTCTCACCCTCTCTAGG						
hsa-miR-658	GGCGGAGGGAAGTAGGTCCGTTGGT						
hsa-miR-674	GCACTGAGATGGGAGTGGTGTA	mmu-miR-674	GCACTGAGATGGGAGTGGTGTA				
hsa-miR-768-5p	GTTGGAGGATGAAAGTACGGAGTGAT						
hsa-miR-801	GATTGCTCTGCGTGCGGAATCGAC	mmu-miR-801	GATTGCTGTGCGTGCGGAATCGAC				
hsa-miR-873	GCAGGAACTTGTGAGTCTCCT	mmu-miR-873	GCAGGAACTTGTGAGTCTCCT				
hsa-miR-877	GTAGAGGAGATGGCGCAGGG	mmu-miR-877	GTAGAGGAGATGGCGCAGGG				
hsa-miR-887	GTGAACGGGCGCCATCCCGAGG						
hsa-miR-888*	GACTGACACCTCTTTGGGTGAA						
hsa-miR-920	GGGGAGCTGTGGAAGCAGTA						
hsa-miR-922	GCAGCAGAGAATAGGACTACGTC						
hsa-miR-923	GTCAGCGGAGGAAAAGAAACT						
hsa-miR-92a-2*	GGGTGGGGATTTGTTGCATTAC						
mmu-miR-133a*	GCTGGTAAAATGGAACCAAAT						
mmu-miR-146b*	GCCCTAGGGACTCAGTTCTGGT						
mmu-miR-207	GCTTCTCCTGGCTCTCCTCCCTC						
mmu-miR-24-2*	GTGCCTACTGAGCTGAAACAGT	mmu-miR-24-1*	GTGCCTACTGAGCTGATATCAGT				
mmu-miR-291b-5p	GATCAAAGTGGAGGCCCTCTCC						
mmu-miR-298	GGCAGAGGAGGGCTGTTCTTCCC						
mmu-miR-302c*	GCTTTAACATGGGGTTACCTGC						
mmu-miR-374*	GGTTGTATTATCATTGTCCGAG						
mmu-miR-434-5p	GCTCGACTCATGGTTTGAACCA						
mmu-miR-465a-3p	GATCAGGGCCTTTCTAAGTAGA						
mmu-miR-466b-5p	GATGTGTGTGTACATGTACATG	mmu-miR-466c-5p	GATGTGTGTGTGCATGTACATA	mmu-miR-466e-5p	GATGTGTGTGTACATGTACATA		
mmu-miR-467b	GTAAGTGCCTGCATGTATATG						
mmu-miR-503*	GAGTATTGTTTCCACTGCCTGG						
mmu-miR-666-3p	GGCTGCAGCGTGATCGCCTGCT						
mmu-miR-678	GTCTCGGTGCAAGGACTGGAGG						
mmu-miR-679	GGACTGTGAGGTGACTCTTGGT						
mmu-miR-680	GGGCATCTGCTGACATGGGGG						
mmu-miR-693-3p	GCAGCTTTCAGATGTGGCTGTAA						
mmu-miR-696	GCGTGTGCTTGCTGTGGG						
mmu-miR-705	GGTGGGAGGTGGGGTGGGCA						
mmu-miR-709	GGAGGCAGAGGCAGGAGGA						
mmu-miR-711	GGGACCCGGGGAGAGATGTAAG						
mmu-miR-742	GAAAGCCACCATGCTGGGTAAA						
mmu-miR-743a	GAAAGACACCAAGCTGAGTAGA	mmu-miR-743b-3p	GAAAGACATCATGCTGAATAGA				
mmu-miR-759	GCAGAGTGCAAACAATTTTGAC						
mmu-miR-761	GCAGCAGGGTGAAACTGACACA						
mmu-miR-762	GGGGCTGGGGCCGGGACAGAGC						
mmu-miR-764-5p	GGTGCTCACATGTCCTCCT						
mmu-miR-805	GAATTGATCAGGACATAGGG						
mmu-miR-878-3p	GCATGACACCACACTGGGTAGA						
mmu-miR-879*	GCTTATGGCTTCAAGCTTTCGG						

Figure S10. Cloned Human miRNA/miRNA* Duplexes that Do Not Have 2nt-3' Overhangs in Their Pre-miRNA.

```
======

>hsa-mir-9-1 hsa-miR-9 TCTTTGGTTATCTAGCTGTATGA hsa-miR-9* ATAAAGCTAGATAACCGAAAGT
cggggttggttgttaTCTTTGGTTATCTAGCTGTATGAgtggtgtggagtcttcATAAAGCTAGATAACCGAAAGTaaaaataacccca
.(((((((....(((..((((((((((((((.((((((.(((.......)))))))).))))))))))))))..)))...))))))). -42

TCTTTGGTTATCTAGCTGTATGAgtggtgtggagtcttcATAAAGCTAGATAACCGAAAGT
..((((((((((((((.((((((.(((.......)))))))).))))))))))))))...

======

>hsa-mir-9-2 hsa-miR-9 TCTTTGGTTATCTAGCTGTATGA hsa-miR-9* ATAAAGCTAGATAACCGAAAGT
ggaagcgagttgttaTCTTTGGTTATCTAGCTGTATGAgtgtattggtcttcATAAAGCTAGATAACCGAAAGTaaaaactccttca
.((((.(((((.(((..((((((((((((((.((((((..(....)..)))))).))))))))))))))..)))).)))))))))).   -40.0999984741211

TCTTTGGTTATCTAGCTGTATGAgtgtattggtcttcATAAAGCTAGATAACCGAAAGT
..((((((((((((((.((((((..(....)..)))))).))))))))))))))...

======

>hsa-mir-10b hsa-miR-10b TACCCTGTAGAACCGAATTTGTG hsa-miR-10b* ACAGATTCGATTCTAGGGGAAT
ccagaggttgtaacgttgtctatataTACCCTGTAGAACCGAATTTGTGtggtatccgtatagtcACAGATTCGATTCTAGGGGAATatatggtcgatgcaaaaacttca
...((((((....(((((.(((((((((.((((.(((((.((((((((((..(((....)))...)))))))))).)))))))))).)))))))).)))))....)))))).   -45

TACCCTGTAGAACCGAATTTGTGtggtatccgtatagtcACAGATTCGATTCTAGGGGAAT
...(((.(((((.((((((((((..(((....)))...)))))))))).)))))).)))...

======

>hsa-mir-16-1 hsa-miR-16 TAGCAGCACGTAAATATTGGCG hsa-miR-16-1* CCAGTATTAACTGTGCTGCTGA
gtcagcagtgcctTAGCAGCACGTAAATATTGGCGttaagattctaaaattatctCCAGTATTAACTGTGCTGCTGAagtaaggttgac
((((((..(((.((((((((((((.((((((((.(.(((..........))).).)))))))).)).)))))))))).)))..)))))) -37.7000007629395

TAGCAGCACGTAAATATTGGCGttaagattctaaaattatctCCAGTATTAACTGTGCTGCTGA
((((((((((.((((((((.(.(((..........))).).)))))))).)).)))))))))).

======

>hsa-mir-23a hsa-miR-23a* GGGGTTCCTGGGGATGGGATTT hsa-miR-23a ATCACATTGCCAGGGATTTCC
ggccggctGGGGTTCCTGGGGATGGGATTTgcttcctgtcacaaATCACATTGCCAGGGATTTCCaaccgacc
((.(((.((((((((((((.((((.((((((..........)))))).)))).)))))))).)))))).)))).))  -33.2000007629395

GGGGTTCCTGGGGATGGGATTTgcttcctgtcacaaATCACATTGCCAGGGATTTCC
(..(((((((((.((((.((((((..........)))))).)))).)))))))))..).

======

>hsa-mir-29c hsa-miR-29c* TGACCGATTTCTCCTGGTGTTC hsa-miR-29c TAGCACCATTTGAAATCGGTTA
atctcttacacaggcTGACCGATTTCTCCTGGTGTTCagagtctgtttttgtcTAGCACCATTTGAAATCGGTTAtgatgtaggggga
.((((((((((...((((((((((...((((((((((.....))))).))))))))))...))))))))))))))).))))))))).  -35.4000015258789

TGACCGATTTCTCCTGGTGTTCagagtctgtttttgtcTAGCACCATTTGAAATCGGTTA
((((((((((...((((((((((.....))))).))))))))))...))))))))))

======

>hsa-mir-34b hsa-miR-34b* TAGGCAGTGTCATTAGCTGATTG hsa-miR-34b CAATCACTAACTCCACTGCCAT
gtgctcggtttgTAGGCAGTGTCATTAGCTGATTGtactgtggtggttaCAATCACTAACTCCACTGCCATcaaaacaaggcac
(((((..((((...((((((((...((((.((((((((((.....)).))))))))))))...)))))))))....)))))..))))))      -33.7999992370605

TAGGCAGTGTCATTAGCTGATTGtactgtggtggttaCAATCACTAACTCCACTGCCAT
..((((((((...((((.((((((((((.....)).))))))))))))...)))))))..
```

```
======

>hsa-mir-124-1 hsa-miR-124* CGTGTTCACAGCGGACCTTGAT hsa-miR-124 TAAGGCACGCGGTGAATGCC
aggcctctctctcCGTGTTCACAGCGGACCTTGATttaaatgtccatacaatTAAGGCACGCGGTGAATGCCaagaatggggctg
.(((((((..(((..(((((((((.(((..((((((((.............)))))))).))).)))))))).))).)))))))..     -35.9199981689453

CGTGTTCACAGCGGACCTTGATttaaatgtccatacaatTAAGGCACGCGGTGAATGCC
.(((((((((.(((..(((((((((.............)))))))).))).)))))))).

======

>hsa-mir-124-3 hsa-miR-124* CGTGTTCACAGCGGACCTTGAT hsa-miR-124 TAAGGCACGCGGTGAATGCC
tgagggcccctctgCGTGTTCACAGCGGACCTTGATttaatgtctatacaatTAAGGCACGCGGTGAATGCCaagagaggcgcctcc
.(((((((.(((((.(((((((((.(((..((((((((.............)))))))).))).)))))))).)))).))).)))).   -40.2999992370605

CGTGTTCACAGCGGACCTTGATttaatgtctatacaatTAAGGCACGCGGTGAATGCC
.(((((((((.(((..(((((((((.............)))))))).))).)))))))).

======

>hsa-mir-140 hsa-miR-140-5p CAGTGGTTTTACCCTATGGTAG hsa-miR-140-3p TACCACAGGGTAGAACCACGG
tgtgtctctctctgtgtcctgcCAGTGGTTTTACCCTATGGTAGgttacgtcatgctgttcTACCACAGGGTAGAACCACGGacaggataccggggcacc
.(((((((.....((((((((((.((((((((((((.(((((((..(((.....)))))))))).))))))))))))))).))))))))).))))))).     -55

CAGTGGTTTTACCCTATGGTAGgttacgtcatgctgttcTACCACAGGGTAGAACCACGG
..((((((((((((.(((((((..(((.....)))))))))).)))))))))))..

======

>hsa-mir-141 hsa-miR-141* CATCTTCCAGTACAGTGTTGGA hsa-miR-141 TAACACTGTCTGGTAAAGATGG
cggccggccctgggtcCATCTTCCAGTACAGTGTTGGAtggtctaattgtgaagctccTAACACTGTCTGGTAAAGATGGctcccgggtgggttc
.((((.((((.(((.((((((((((((.((((((((((...((.......))...))).)))))))))))..)))))))..)))))))).))))).   -48.9000015258789

CATCTTCCAGTACAGTGTTGGAtggtctaattgtgaagctccTAACACTGTCTGGTAAAGATGG
((((((((((.((((((((((...((.......))...))).)))))))))))..)))))).

======

>hsa-mir-144 hsa-miR-144* GGATATCATCATATACTGTAAG hsa-miR-144 TACAGTATAGATGATGTACT
tggggccctggctgGGATATCATCATATACTGTAAGtttgcgatgagacacTACAGTATAGATGATGTACTagtccgggcaccccc
.(((((((.((((((.(((((((((.(((((((.....)))))..)))))))))))))))))).)))))).)))).)))..    -44.4000015258789

GGATATCATCATATACTGTAAGtttgcgatgagacacTACAGTATAGATGATGTACT
..(((((((((.(((((((((.(((.....)))))..)))))))))))))))...

======

>hsa-mir-145 hsa-miR-145 GTCCAGTTTTCCCAGGAATCCCT hsa-miR-145* GGATTCCTGGAAATACTGTTCT
caccttgtcctcacgGTCCAGTTTTCCCAGGAATCCCTtagatgctaagatggGGATTCCTGGAAATACTGTTCTtgaggtcatggtt
.(((.((.((((((.((..((((.((.((((((((((((.............)))))))))))).)).)))))..)))))))).)).)))).  -41.6199989318848

GTCCAGTTTTCCCAGGAATCCCTtagatgctaagatggGGATTCCTGGAAATACTGTTCT
(..(((((.((.((((((((((((.............)))))))))))).)).)))))..).

======

>hsa-mir-183 hsa-miR-183 TATGGCACTGGTAGAATTCACT hsa-miR-183* GTGAATTACCGAAGGGCCATAA
ccgcagagtgtgactcctgttctgtgTATGGCACTGGTAGAATTCACTgtgaacagtctcagtcaGTGAATTACCGAAGGGCCATAAacagagcagagacagatccacga
.......(((.((.((((((((((((.((((((..((((((..((((((((((((.....)))..)))))))))))))....)))))).)))))))))).))....)))))..   -
41.9000015258789

TATGGCACTGGTAGAATTCACTgtgaacagtctcagtcaGTGAATTACCGAAGGGCCATAA
((((((..((((((..((((((((((((.....)))..)))))))))))))....)))))).

======

>hsa-mir-200b hsa-miR-200b* CATCTTACTGGGCAGCATTGGA hsa-miR-200b TAATACTGCCTGGTAATGATGA
ccagctcgggcagccgtggcCATCTTACTGGGCAGCATTGGAtggagtcaggtctcTAATACTGCCTGGTAATGATGAcggcggagccctgcacg
...((..((((..((((.(.(((((((((..(((((.((((((.((.......)))))))).)))))..)))).)))).).)))).)))).))...   -44.2999992370605

CATCTTACTGGGCAGCATTGGAtggagtcaggtctcTAATACTGCCTGGTAATGATGA
((((((((..(((((.((((((.((.......)))))))).)))))..)))).)))).
```

```
======

>hsa-mir-200a hsa-miR-200a* CATCTTACCGGACAGTGCTGGA hsa-miR-200a TAACACTGTCTGGTAACGATGT
ccgggcccctgtgagCATCTTACCGGACAGTGCTGGAtttcccagcttgactcTAACACTGTCTGGTAACGATGTtcaaaggtgacccgc
.(((((.(((.((((((((((((((((((((((((.....)))))...........)))))))))))))).)))))))).))).).)))).       -47.5

CATCTTACCGGACAGTGCTGGAtttcccagcttgactcTAACACTGTCTGGTAACGATGT
((((((((((((((((((((.....)))))...........)))))))))))))).)))).

======

>hsa-mir-202 hsa-miR-202* TTCCTATGCATATACTTCTTTG hsa-miR-202 AGAGGTATAGGGCATGGGAA
cgcctcagagccgcccgccgttcctttTTCCTATGCATATACTTCTTTGaggatctggcctaaAGAGGTATAGGGCATGGGAAaacggggcggtcgggtcctccccagcg
(((....(((..((((((((((((.((((((((((.((((((.(((.....)))))))))))))))..)))))))))))).)))))))).)))))).))).....)))   -
58.7999992370605

TTCCTATGCATATACTTCTTTGaggatctggcctaaAGAGGTATAGGGCATGGGAA
.(((((((((.((((((((((((.(((.....)))))))))))))))..)))))))).

======

>hsa-mir-222 hsa-miR-222* CTCAGTAGCCAGTGTAGATCCT hsa-miR-222 AGCTACATCTGGCTACTGGGT
gctgctggaaggtgtaggtaccctcaatggCTCAGTAGCCAGTGTAGATCCTgtctttcgtaatcagcAGCTACATCTGGCTACTGGGTctctgatggcatcttctagct
...((((((((((.....((.(((..((((((((((((((((((...(((...........)))...)))))).))))))))))))))..)))).)))))))))))).   -
54.0999984741211

CTCAGTAGCCAGTGTAGATCCTgtctttcgtaatcagcAGCTACATCTGGCTACTGGGT
((((((((((((((((...(((...........)))...)))))).)))))))))))).

======

>hsa-mir-330 hsa-miR-330-5p TCTCTGGGCCTGTGTCTTAGGC hsa-miR-330-3p GCAAAGCACACGGCCTGCAGAGA
ctttggcgatcactgccTCTCTGGGCCTGTGTCTTAGGCtctgcaagatcaaccgaGCAAAGCACACGGCCTGCAGAGAggcagcgctctgccc
....(((((.(.((((((((((((((((((((.(((..((((.............)))).)))))))).)))))..)))))))))))).).)).))).   -46.5200004577637

TCTCTGGGCCTGTGTCTTAGGCtctgcaagatcaaccgaGCAAAGCACACGGCCTGCAGAGA
((((((((((((((.(((..((((.............)))).)))))))).)))))..))))))

======

>hsa-mir-338 hsa-miR-338-5p AACAATATCCTGGTGCTGAGTG hsa-miR-338-3p TCCAGCATCAGTGATTTTGTTG
tctccAACAATATCCTGGTGCTGAGTGatgactcaggcgacTCCAGCATCAGTGATTTTGTTGaaga
(((.((((((.(((((((((((((((.............))).)))))))))).))).))))))).))) -26.2199993133545

AACAATATCCTGGTGCTGAGTGatgactcaggcgacTCCAGCATCAGTGATTTTGTTG
(((((.((((((((((((((.............))).)))))))))).))).)))))).

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>hsa-mir-342 hsa-miR-342-5p AGGGGTGCTATCTGTGATTGA hsa-miR-342-3p TCTCACACAGAAATCGCACCCGT
gaaactgggctcaaggtgAGGGGTGCTATCTGTGATTGAgggacatggttaatggaattgTCTCACACAGAAATCGCACCCGTcaccttggcctactta
.....(((((.((((((((.((((((..((((((.....((((((...((....))..)))))).)))))).....))))))).))))))))))))))....      -
47.7000007629395

AGGGGTGCTATCTGTGATTGAgggacatggttaatggaattgTCTCACACAGAAATCGCACCCGT
..(((((((..((((((.....((((((...((....))..)))))).)))))).....)))))))..

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>hsa-mir-361 hsa-miR-361-5p TTATCAGAATCTCCAGGGGTAC hsa-miR-361-3p TCCCCCAGGTGTGATTCTGATTT
ggagcTTATCAGAATCTCCAGGGGTACtttataatttcaaaaagTCCCCCAGGTGTGATTCTGATTTgcttc
(((((..((((((((((.((.((((.((((((..........)))))).)))).)).)...)))))))))..)))))   -32.2999992370605

TTATCAGAATCTCCAGGGGTACtttataatttcaaaaagTCCCCCAGGTGTGATTCTGATTT
..((((((((((.((.((((.((((((..........)))))).)))).)).)...)))))))))..
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>hsa-mir-378 hsa-miR-378* CTCCTGACTCCAGGTCCTGTGT hsa-miR-378 ACTGGACTTGGAGTCAGAAGG
agggCTCCTGACTCCAGGTCCTGTGTgttacctagaaatagcACTGGACTTGGAGTCAGAAGGcct
(((.((.(((((((((((((...((((((........)))))).)))))))))))))).)).))) -39.2000007629395

CTCCTGACTCCAGGTCCTGTGTgttacctagaaatagcACTGGACTTGGAGTCAGAAGG
((.(((((((((((((...((((((........)))))).)))))))))))))).)).

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>hsa-mir-454 hsa-miR-454* ACCCTATCAATATTGTCTCTGC hsa-miR-454 TAGTGCAATATTGCTTATAGGGT
tctgtttatcaccagatcctagaACCCTATCAATATTGTCTCTGCtgtgtaaatagttctgagTAGTGCAATATTGCTTATAGGGTtttggtgtttggaaagaacaatgggcagg
.(((((((((.(((((..((((((((((((((((((((((.(((((....)))))...)))....)))))))))...)))))))))))..)))))...))....)))))))).
        -41.7000007629395

ACCCTATCAATATTGTCTCTGCtgtgtaaatagttctgagTAGTGCAATATTGCTTATAGGGT
((((((((((((((((((.(((((....)))))...)))....)))))))))...)))))))

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>hsa-mir-483 hsa-miR-483-5p AAGACGGGAGGAAAGAAGGGAG hsa-miR-483-3p TCACTCCTCTCCTCCCGTCTT
gagggggAAGACGGGAGGAAAGAAGGGAGtggttccatcacgcctccTCACTCCTCTCCTCCCGTCTTctcctctc
(((((((((((((((((.((.((.((((.(((........)))..)))).)).)).)).)))))))))))))).))))))      -44.2000007629395

AAGACGGGAGGAAAGAAGGGAGtggttccatcacgcctccTCACTCCTCTCCTCCCGTCTT
((((((((((((.((.((.((((.(((........)))..)))).)).)).)).))))))))))))

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>hsa-mir-486 hsa-miR-486-5p TCCTGTACTGAGCTGCCCCGAG hsa-miR-486-3p CGGGGCAGCTCAGTACAGGAT
gcaTCCTGTACTGAGCTGCCCCGAGgcccttcatgctgcccagctCGGGGCAGCTCAGTACAGGATac
..((((((((((((((((((((((((..........)))....)))))))))))))))))))))))..       -48.5

TCCTGTACTGAGCTGCCCCGAGgcccttcatgctgcccagctCGGGGCAGCTCAGTACAGGAT
((((((((((((((((((((((((..........)))....)))))))))))))))))))))))).

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>hsa-mir-505 hsa-miR-505* GGGAGCCAGGAAGTATTGATGT hsa-miR-505 CGTCAACACTTGCTGGTTTCCT
gatgcacccagtggGGGAGCCAGGAAGTATTGATGTttctgccagtttagCGTCAACACTTGCTGGTTTCCTctctggagcatc
(((((..((((.((((((((((((.((((.(((((((((..........)))))))).)))).)))))))))))).)))).)))))      -44.9000015258789

GGGAGCCAGGAAGTATTGATGTttctgccagtttagCGTCAACACTTGCTGGTTTCCT
(((((((((.((((.(((((((((..........)))))))).)))).)))))))))).

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>hsa-mir-512-1 hsa-miR-512-5p CACTCAGCCTTGAGGGCACTTTC hsa-miR-512-3p AAGTGCTGTCATAGCTGAGGTC
tctcagtctgtggCACTCAGCCTTGAGGGCACTTTCtggtgccagaatgaAAGTGCTGTCATAGCTGAGGTCcaatgactgagg
.(((((((..(((..((((((..(((.((((((((((((....)))).....)))))))..)))..))))))..)))..)))))))).      -46.2999992370605

CACTCAGCCTTGAGGGCACTTTCtggtgccagaatgaAAGTGCTGTCATAGCTGAGGTC
..((((((..(((.((((((((((((....)))).....)))))))..)))..))))))...

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>hsa-mir-518f hsa-miR-518f* CTCTAGAGGGAAGCACTTTCTC hsa-miR-518f GAAAGCGCTTCTCTTTAGAGG
tctcatgctgtgaccCTCTAGAGGGAAGCACTTTCTCttgtctaaaagaaaaGAAAGCGCTTCTCTTTAGAGGattactctttgaga
(((((....((((.((((((((((((((((.(((((((((.....)))).....)))))).))))))))))))))))).)))).....)))))   -42.2999992370605

CTCTAGAGGGAAGCACTTTCTCttgtctaaaagaaaaGAAAGCGCTTCTCTTTAGAGG
((((((((((((((.(((((((((.....)))).....)))))).)))))))))))))).

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>hsa-mir-518d hsa-miR-518d-5p CTCTAGAGGGAAGCACTTTCTG hsa-miR-518d-3p CAAAGCGCTTCCCTTTGGAGC
tcccatgctgtgaccCTCTAGAGGGAAGCACTTTCTGttgtctgaaagaaacCAAAGCGCTTCCCTTTGGAGCgttacggtttgaga
((.((.((((((((.((((((((((((((.((((..((((.((.....)))))..)))).)))))))))))))))))))))))).))).))   -41.2000007629395

CTCTAGAGGGAAGCACTTTCTGttgtctgaaagaaacCAAAGCGCTTCCCTTTGGAGC
((((((((((((((.((((..((((.((.....)))))..)))).)))))))))))))).
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>hsa-mir-524 hsa-miR-524-5p CTACAAAGGGAAGCACTTTCTC hsa-miR-524-3p GAAGGCGCTTCCCTTTGGAGT
tctcatgctgtgaccCTACAAAGGGAAGCACTTTCTCttgtccaaaggaaaaGAAGGCGCTTCCCTTTGGAGTgttacggtttgaga
(((((.(((((((.((.(((((((((((.((((((....(((...)))..)))))).))))))))))).)).)))))))).)))))   -46.5999984741211

CTACAAAGGGAAGCACTTTCTCttgtccaaaggaaaaGAAGGCGCTTCCCTTTGGAGT
...((((((((((.((((((....(((...)))..)))))).))))))))))....

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>hsa-mir-576 hsa-miR-576-5p ATTCTAATTTCTCCACGTCTTT hsa-miR-576-3p AAGATGTGGAAAAATTGGAATC
tacaatccaacgaggATTCTAATTTCTCCACGTCTTTggtaataaggtttggcaAAGATGTGGAAAAATTGGAATCctcattcgattggttataacca
..(((((.((.(((((((((((((.((((((((((.((((.....))).)))))))))))).))))))))))))))).)).)))))..........       -
46.5999984741211

ATTCTAATTTCTCCACGTCTTTggtaataaggtttggcaAAGATGTGGAAAAATTGGAATC
((((((((((.((((((((((((.((((.....))).)))))))))))).))))))))))).

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>hsa-mir-876 hsa-miR-876-5p TGGATTTCTTTGTGAATCACCA hsa-miR-876-3p TGGTGGTTTACAAAGTAATTCA
tgaagtgctgTGGATTTCTTTGTGAATCACCAtatctaagctaatgtggTGGTGGTTTACAAAGTAATTCAtagtgcttca
.(((((..(((((((((.((((((((((((((((.....((....)).)))))))))))))))).))))))))))..))))).  -42.7000007629395

TGGATTTCTTTGTGAATCACCAtatctaagctaatgtggTGGTGGTTTACAAAGTAATTCA
.(((((.((((((((((((((((.....((....)).)))))))))))))))).)))))).
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