Field et al. Supplemental Information

>Chrysemys-let-7a-1_pre
CCTGCACTGTGGGATGAGGTAGTAGGTTGTATAGTTTTAGGGTCATACCCACAACTGGGAGATAACTATACAATCTACTGTCTTTCCTAAAGCAGC
>Chrysemys-let-7a-1-5p
TGAGGTAGTAGGTTGTATAGTT
>Chrysemys-let-7a-1-3p
CTATACAATCTACTGTCTTT

>Chrysemys-let-7a-2_pre
GCATGCATCCAGGTTGAGGTAGTAGGTTGTATAGTTTAGAATTACACCAAGGGAGATAACTGTACAACCTCCTAGCTTTCCTTGGGTCTTGCACAA
>Chrysemys-let-7a-2-5p
TGAGGTAGTAGGTTGTATAGTT
>Chrysemys-let-7a-2-3p
CTGTACAACCTCCTAGCTTTCC

>Chrysemys-let-7a-3_pre
GTCCTTTGGGGTGAGGTAGTAGGTTGTATAGTTTTAGGGTTATACCCTGCCTGTCAGATAACTATACAATCTACTGTCTTTCCTGAAGTGGCT
>Chrysemys-let-7a-3-5p
TGAGGTAGTAGGTTGTATAGTT
>Chrysemys-let-7a-3-3p
CTATACAATCTACTGTCTTT

>Chrysemys-let-7a-4_pre
TGGAGGTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGGATTTCATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTAAAG
>Chrysemys-let-7a-4-5p
TGAGGTAGTAGGTTGTATAGTT
>Chrysemys-let-7a-4-3p
CTATACAGTCTATTGCCTTCC

>Chrysemys-let-7b_pre
GCTCTAGCAGGGTGAGGTAGTAGGTTGTGTGGTTTCAGGGTAGTGATTTTGCCCCAATCAGGAGATAACTATACAACCTACTGCCTTCCCTG
>Chrysemys-let-7b-5p (predicted)
TGAGGTAGTAGGTTGTGTGGTT

>Chrysemys-let-7c-1_pre
GTGTGCATCCGGGTTGAGGTAGTAGGTTGTATGGTTTAGAGTTACACCCTGGGAGTTAACTGTACAACCTTCTAGCTTTCCTTGGAGCACACTTGG
>Chrysemys-let-7c-1-5p
TGAGGTAGTAGGTTGTATGGTT
>Chrysemys-let-7c-1-3p
CTGTACAACCTTCTAGCTTTCC

>Chrysemys-let-7c-2_pre
TGCGTGCCCCAGGCTGAGGTAGTAGGTTGTATGGTTTAGAATAACACCCGCAGGAGATAACTGTACAGCCTCCTAGCTTTCCCTGGGGCGCTGCTT
>Chrysemys-let-7c-2-5p
TGAGGTAGTAGGTTGTATGGTT
>Chrysemys-let-7c-2-3p
CTGTACAGCCTCCTAGCTTTCC

>Chrysemys-let-7d_pre
TAGGAAGAGGTAGTAGGTTGCATAGTTTTAGGGCAGAGATTTTGCTCACAAGGAGTTAACTATACAACCTGCTGCCTTTCTTAGGGCT
>Chrysemys-let-7d-5p
AGAGGTAGTAGGTTGCATAGTT
>Chrysemys-let-7d-3p
CTATACAACCTGCTGCCTTTCT

>Chrysemys-let-7e_pre
GTCCTTGAGGCTGAGGTAGTAGATTGAATAGTTGTGGAGTCCTACCCTCCCTTTGAGCTAACTATACAATCTACTGTCTTTCCTAAGGAGA

>Chrysemys-let-7e-5p
TGAGGTAGTAGATTGAATAGTT
>Chrysemys-let-7e-3p
CTATACAATCTACTGTCTTT

>Chrysemys-let-7f-1_pre
CCGAGGCCCTGGGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCACACCCGGTCTCGGAGATAACTATACAGTCTACTGTCTTTCCCG
>Chrysemys-let-7f-1-5p
TGAGGTAGTAGATTGTATAGTT

>Chrysemys-let-7f-2_pre
GCGGAGTGAGGTAGTAGATTGTATAGTTGTAGGGTAGTTATTTTACCCTGTTCAGGAGATAACTATACAATCTATTGCCTTCCCCGAG
>Chrysemys-let-7f-2-5p
TGAGGTAGTAGATTGTATAGTT
>Chrysemys-let-7f-2-3p
CTATACAATCTATTGCCTTCC

>Chrysemys-let-7g_pre
TCCAGGCTGAGGTAGTAGTTTGTACAGTTTGAGGGTCTATGATACCACCCGGTACAGGAGATAACTGTACAGGCCACTGCCTTGCCTGGGA
>Chrysemys-let-7g-5p
TGAGGTAGTAGTTTGTACAGTT
>Chrysemys-let-7g-3p
CTGTACAGGCCACTGCCTTGC

>Chrysemys-let-7i_pre
CCCTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGATAACTGCGCAAGCTACTGCCTTGCTAGTGCTG
>Chrysemys-let-7i-5p
TGAGGTAGTAGTTTGTGCTGTT
>Chrysemys-let-7i-3p
CTGCGCAAGCTACTGCCTTGCT

>Chrysemys-mir-1a-1_pre
CTACCTGCTTGAGAGACATACTTCTTTATATGCCCATATGAACCTGGCAAGCTATGGAATGTAAAGAAGTATGTATTTCAGGTGGGGATCATT
>Chrysemys-mir-1a-1-3p
TGGAATGTAAAGAAGTATGTAT
>Chrysemys-mir-1a-1-5p
ACATACTTCTTTATATGCCCATA

>Chrysemys-mir-1a-2_pre
TCCTGCCCAGAGTACATACTTCTTTATGTACCCATATGAACATATAATGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAGGCACTG
>Chrysemys-mir-1a-2-3p
TGGAATGTAAAGAAGTATGTAT
>Chrysemys-mir-1a-2-5p
ACATACTTCTTTATGTACCCATA

>Chrysemys-mir-1b_pre
AGCCCCTCCCTCCCAACCCTACATACTTCTTCATATGCCCATAGGGAGTCAGCCGGCGTTATGGAATGTTAAGAAGTATGTATCCTTGGGCTGGGG
>Chrysemys-mir-1b-3p
TGGAATGTTAAGAAGTATGTAT
>Chrysemys-mir-1b-5p
CATACTTCTTCATATGCCCATA

>Chrysemys-mir-7a-1_pre
GGATGTTGGTCTAGTTCTGTGTGGAAGACTAGTGATTTTGTTGTTTTTTAGATAACTAAATCGACAACAAATCGCAGTCTGCCATATGGCACAGGCC
>Chrysemys-mir-7a-1-5p
TGGAAGACTAGTGATTTTGTT
>Chrysemys-mir-7a-1-3p

CAACAAATCGCAGTCTGCCATA

>Chrysemys-mir-7a-2_pre
TGGCCCCGTCCCTTATGGAAGACTAGTGATTTTGTTGTTCTATAGCTCATCTCATGACAACAAGTCACAGTCTGCCTTATGGTGCATGGCCTCCT
>Chrysemys-mir-7a-2-5p
TGGAAGACTAGTGATTTTGTT
>Chrysemys-mir-7a-2-3p
CAACAAGTCACAGTCTGCCTT

>Chrysemys-mir-7a-3_pre
ATGGTCTGGCTCTGTGTGGAAGACTAGTGATTTTGTTGTTCTGACTTATAAAAGTGACAACAAATCATAGCCTGCCATACAGCACGGACCACAGCC
>Chrysemys-mir-7a-3-5p
TGGAAGACTAGTGATTTTGTT
>Chrysemys-mir-7a-3-3p
CAACAAATCATAGCCTGCCATA

>Chrysemys-mir-7b_pre
TTCTGGGTCGGTCTGGAAGACTTGTGATTTTGTTGTTTCCAGTGTCAGGGAAGCGAACAACAAATCCCAGTCTCCTCACAGCCCCAGGACTG
>Chrysemys-mir-7b-5p
TGGAAGACTTGTGATTTTGTTGT

>Chrysemys-mir-9-1_pre
ACTTCAGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCAATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCATT
>Chrysemys-mir-9-1-5p
TCTTTGGTTATCTAGCTGTATGA
>Chrysemys-mir-9-1-3p
TAAAGCTAGATAACCGAAAGTA

>Chrysemys-mir-9-2_pre
CTGTGAGGAAGCGAGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGTGTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAAAACTCCTTCATGA
>Chrysemys-mir-9-2-5p
TCTTTGGTTATCTAGCTGTATGA
>Chrysemys-mir-9-2-3p
TAAAGCTAGATAACCGAAAGTA

>Chrysemys-mir-9-3_pre
AGAAGGAGGGCTGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTATTAAGCCATCATAAAGCTAGATAACCGAAAGTAGAAATGACTTCCAAC
>Chrysemys-mir-9-3-5p
TCTTTGGTTATCTAGCTGTATGA
>Chrysemys-mir-9-3-3p
TAAAGCTAGATAACCGAAAGTA

>Chrysemys-mir-9-4_pre
GACTGGGTTGGTTTTTGTCTTTGGTTATCTAGCTGTATGAGTGTATGTGATATCATAAAGCTAGAGAACCGAATGTAAAAACTGATTCACTATTCT
>Chrysemys-mir-9-4-5p
TCTTTGGTTATCTAGCTGTATGA
>Chrysemys-mir-9-4-3p
TAAAGCTAGAGAACCGAATGTA

>Chrysemys-mir-10a_pre
ATGCATCTGTCTTCTATATGTACCCTGTAGATCCGAATTTGTGTAAAGGAAATTGTGTCACAAATTCGTATCTAGGGGAATATGTAGTTGACACAA
>Chrysemys-mir-10a-5p
TACCCTGTAGATCCGAATTTGT
>Chrysemys-mir-10a-3p
TCACAAATTCGTATCTAGGGG

>Chrysemys-mir-10b_pre

TATTACGTTGTCTATATATACCCTGTAGAACCGAATTTGTGTGGTATTCACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATGCAAAA
>Chrysemys-mir-10b-5p
TACCCTGTAGAACCGAATTTGT
>Chrysemys-mir-10b-3p
AGATTCGATTCTAGGGGAAT

>Chrysemys-mir-10c_pre
ATACAGTCGTCTATATGTACCCTGTAGAATCGAATTTGTGTGAATATTTGAGAGTCACAAATTCGTCTCTAGGGGAGTATATGGACGATGCCAGAG
>Chrysemys-mir-10c-5p
ACCCTGTAGAATCGAATTTGTG
>Chrysemys-mir-10c-3p
CAAATTCGTCTCTAGGGGAGT

>Chrysemys-mir-15a_pre
CCTTGGGCTAACGTAGCAGCACATAATGGTTTGTGGGTTTTGAAAAGGTGCAGGCCATATTGTGCTGCCTCAAAAATACAAGG
>Chrysemys-mir-15a-5p
TAGCAGCACATAATGGTTTG

>Chrysemys-mir-15b-1_pre
ACCTTAAATTACTCTAGCAGCACATCATGGTTTGCATGATCTTGTAAAGATGCTAATCATTATTTGCTGCTTTAGGAATTTAAGGA
>Chrysemys-mir-15b-1-5p
TAGCAGCACATCATGGTTTG
>Chrysemys-mir-15b-1-3p
TAATCATTATTTGCTGCTTT

>Chrysemys-mir-15b-2_pre
GGGCTTTGAGGAGATGTAGCAGCACATCATGGTTTGTAGGGACAAGGAGATACAGACCATTCTGGGCTGCCTCATTACCTCAAGGATAA
>Chrysemys-mir-15b-2-5p
TAGCAGCACATCATGGTTTGTAG
>Chrysemys-mir-15b-2-3p
CAGACCATTCTGGGCTGCCTCATT

>Chrysemys-mir-16a_pre
CAGCAGTACATTAGCAGCACGTAAATATTGGCGTTAACTCTGTAAATATCTCCAGTATTAACTGTGCTGCTGAAGTAAAGT
>Chrysemys-mir-16a-5p
TAGCAGCACGTAAATATTGGCG
>Chrysemys-mir-16a-3p
CCAGTATTAACTGTGCTGCTGA

>Chrysemys-mir-16b_pre
TATACTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTATAAAAGTAAATCAAACCCCAATATTATTGTGCTGCTTAAGCGTGGCAGA
>Chrysemys-mir-16b-5p
TAGCAGCACGTAAATATTGGTG
>Chrysemys-mir-16b-3p
CCAATATTATTGTGCTGCTTAA

>Chrysemys-mir-16c_pre
TCAGCAGTGCTCTAGCAGCACGTAAATACTGGAGTCGAGGACTGCCTGGCTGCTCTCCAGTATTGCATTGCTGCTTGAGTGAGGCTGG
>Chrysemys-mir-16c-5p
TAGCAGCACGTAAATACTGGAGT
>Chrysemys-mir-16c-3p
TCTCCAGTATTGCATTGCTGCT

>Chrysemys-mir-17_pre
CGTCAGAGTAATGTCAAAGTGCTTACAGTGCAGGTAGTGATATATAGAACCTACTGCAGTGAAGGCACTTGTAGCATTATAGTGACAA
>Chrysemys-mir-17-5p
CAAAGTGCTTACAGTGCAGGT

>Chrysemys-mir-17-3p
CTGCAGTGAAGGCACTTGTAGC

>Chrysemys-mir-18a_pre
TGCTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCCCTAAGTGCTCCTTCTGGCATAAGAAGTTAT
>Chrysemys-mir-18a-5p
TAAGGTGCATCTAGTGCAGA
>Chrysemys-mir-18a-3p
ACTGCCCTAAGTGCTCCTTCTG

>Chrysemys-mir-18b_pre
GTTCCTTGTGTTAAGGTGCATCTAGTGCAGTTAGTGAAGTAGCTTAGAATCTACTGCCCTAAATGCTCCTTCTGGCA
>Chrysemys-mir-18b-5p
TAAGGTGCATCTAGTGCAGTTA
>Chrysemys-mir-18b-3p
ACTGCCCTAAATGCTCCTTCTGG

>Chrysemys-mir-19a_pre
TAGCTGCTCTGCAGTCCTCTGTTAGTTTTGCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCCTGTTATT
>Chrysemys-mir-19a-5p
AGTTTTGCATAGTTGCACTACA
>Chrysemys-mir-19a-3p
TGTGCAAATCTATGCAAAACTG

>Chrysemys-mir-19b-1_pre
GAACACTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTATGATACTCTGCTGTGCAAATCCATGCAAAACTGACTGTGGCAGTGACAA
>Chrysemys-mir-19b-1-3p
TGTGCAAATCCATGCAAAACTG
>Chrysemys-mir-19b-1-5p
AGTTTTGCAGGTTTGCATCC

>Chrysemys-mir-19b-2_pre
AAGATAGTGCTGACTACAGTCAGTTTTGCAGGATTGCATTCCAGCTTATTTCAAACGCTGTGCAAATCCATGCAAAACTGACTGTGGTTGCATTCA
>Chrysemys-mir-19b-2-3p
TGTGCAAATCCATGCAAAACTG
>Chrysemys-mir-19b-2-5p
AGTTTTGCAGGATTGCATTCC

>Chrysemys-mir-20a_pre
GACAGCTCCTGTAGTACTAAAGTGCTTATAGTGCAGGTAGTGTTCAGTAATCTACTGCATTATGAGCACTTAAAGTACTGCTAGCTGTAGAA
>Chrysemys-mir-20a-5p
TAAAGTGCTTATAGTGCAGGTA
>Chrysemys-mir-20a-3p
ACTGCATTATGAGCACTTAAAG

>Chrysemys-mir-20b_pre
TTTTGTCCTAGCAGTATCAAAGTGCTCATAGTGCAGGTAGTTTTTGAATTGGATCTACTGTAATGTGGGCACTTATAGTACTGCCAGATAAAATG
>Chrysemys-mir-20b-5p
CAAAGTGCTCATAGTGCAGGTA
>Chrysemys-mir-20b-3p
ACTGTAATGTGGGCACTTATAGT

>Chrysemys-mir-21_pre
CTGTACCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATCTCATGGCAACAACAGTCGGTAGGCTGTCTGACATTTTGGTATCTTT
>Chrysemys-mir-21-5p
TAGCTTATCAGACTGATGTTGA
>Chrysemys-mir-21-3p

AACAACAGTCGGTAGGCTGTCT

>Chrysemys-mir-22_pre
CCGGCTAACTAGCACCAGTTCTTCAGTGGCAAGCTTTACGTCCCTGTCTAGCAGCTAAAGCTGCCAGTTGAAGAACTGTTGAATGTAGCCACTCT
>Chrysemys-mir-22-5p
AGTTCTTCAGTGGCAAGCTTTA
>Chrysemys-mir-22-3p
AAGCTGCCAGTTGAAGAACTGT

>Chrysemys-mir-23a_pre
CCTGCCCCTGCCAGCTGGGGTTCCTGGTGATGCGATTTTTATCCTACCACCCAAAATCACATTGCCAGGGATTTCCAACGGGCGGCGGGCCA
>Chrysemys-mir-23a-3p
ATCACATTGCCAGGGATTTCC

>Chrysemys-mir-23b_pre
TAATGTTGTGGCTGTTTGGGTTCCTGGCATGCTGATTTGTGATTTAAGATTAAAATCACATTGCCAGGGATTACCACATAACCATGACTGT
>Chrysemys-mir-23b-3p
ATCACATTGCCAGGGATTACC

>Chrysemys-mir-24-1_pre
GTTGATGGACCCGTCCTCCGGTGCCTACTGAGCTGATATCAGTTCTGATTTTACATACTGGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCTAAA
>Chrysemys-mir-24-1-3p
TGGCTCAGTTCAGCAGGAACA
>Chrysemys-mir-24-1-5p
TGCCTACTGAGCTGATATCAGT

>Chrysemys-mir-24-2_pre
CTCCCGGGCTCTGCCTCCCGTGCCTACTGAGCTGATACTCAGTCGCTTTGCTTAAACTGGCTCAGTTCAGCAGGAACAGGAGTCGGGCTCCAGCC
>Chrysemys-mir-24-2-3p
TGGCTCAGTTCAGCAGGAACA
>Chrysemys-mir-24-2-5p
TGCCTACTGAGCTGATACTCAGT

>Chrysemys-mir-26-1_pre
AGGTTGTGACCTGGTTCAAGTAATCCAGGATAGGCTGTGTGCAATCTAATTGGCCTATTCTTGATTACTTGCACTGGGAGGCAACCACGA
>Chrysemys-mir-26-1-5p
TTCAAGTAATCCAGGATAGGCT
>Chrysemys-mir-26-1-3p
CCTATTCTTGATTACTTGCACT

>Chrysemys-mir-26-2_pre
TGCGGAGGCCGTAGCCCGGTTCAAGTAATCCAGGATAGGCTGTTACCAGGCAGCACGGCCTATTCTTGATTACTTGTTTCAGGAGGCGGCTGCTGG
>Chrysemys-mir-26-2-5p
TTCAAGTAATCCAGGATAGGCT
>Chrysemys-mir-26-2-3p
CCTATTCTTGATTACTTGTTTC

>Chrysemys-mir-26-3_pre
CGGAGGCCGGCGCCGGGTTCAAGTAATCCAGGATAGGCTGTGGTCTGCGCAGTCGGCCTGTTCTCGATTACTTGGCGCCGGAGCCGGCCGGCAGCT
>Chrysemys-mir-26-3-5p
TTCAAGTAATCCAGGATAGGCT
>Chrysemys-mir-26-3-3p
CCTGTTCTCGATTACTTGGCGC

>Chrysemys-mir-27a_pre
GATACCGGGGTGCAGGGCTTAGCTCACCTGTGAACAGAGTTCGCATCCGTATCGTGTTCACAGTGGCTAAGTTCCGCCCCCCGGGGTCCGTT
>Chrysemys-mir-27a-5p

AGGGCTTAGCTCACCTGTGAA
>Chrysemys-mir-27a-3p
TTCACAGTGGCTAAGTTCCGC

>Chrysemys-mir-27b_pre
ACCTCTCTAACAAGGTGCAGAGCTTAGCTGATTGGTGAACAGTGATTGATTTCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAGAAGGT
>Chrysemys-mir-27b-5p
AGAGCTTAGCTGATTGGTGAAC
>Chrysemys-mir-27b-3p
TTCACAGTGGCTAAGTTCTGC

>Chrysemys-mir-29a-1_pre
ACCCCTTTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATACTATTTTCTAGCACCATTTGAAATCGGTTATAGTGACTGGGGAATTGCAT
>Chrysemys-mir-29a-1-3p
TAGCACCATTTGAAATCGGTTA
>Chrysemys-mir-29a-1-5p
ACTGATTTCTTTTGGTGTTCAGA

>Chrysemys-mir-29a-2_pre
AATCTCTCTTACACAGGCTGACCGATCTCTCTTGGTGTTCAGAGTTTCAGTTTTTGTCTAGCACCATTTGAAATCGGTTATGATGTAGGGGGAAA
>Chrysemys-mir-29a-2-3p
TAGCACCATTTGAAATCGGTTA
>Chrysemys-mir-29a-2-5p
TGACCGATCTCTCTTGGTGTTC

>Chrysemys-mir-29b-1_pre
CTCCCTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTAACTACTCCGTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAGGAAGAATG
>Chrysemys-mir-29b-1-3p
TAGCACCATTTGAAATCAGTG
>Chrysemys-mir-29b-1-5p
CTGGTTTCATATGGTGGTTTAGA

>Chrysemys-mir-29b-2_pre
GTCTTCTTCTGGAAGCTGGTTTCACATGGTGGCTTAGATTTTCCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGAGCAAGAA
>Chrysemys-mir-29b-2-3p
TAGCACCATTTGAAATCAGTG
>Chrysemys-mir-29b-2-5p
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>Chrysemys-mir-30a_pre
GCTGTTGACAGTGAGCGACTGTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGGGCTTTCAGTCGGATGTTTGCAGCTGCCAACTGCCAC
>Chrysemys-mir-30a-5p
TGTAAACATCCTCGACTGGAC
>Chrysemys-mir-30a-3p
CTTTCAGTCGGATGTTTGCAGC

>Chrysemys-mir-30b_pre
TACTGATTTTTAGTTCATGTAAACATCCTACACTCAGCTATAAAACATAGAACGGCTGGGAGGTGGATGTTTACTTCAACTGACTTGGAAA
>Chrysemys-mir-30b-5p
TGTAAACATCCTACACTCAGCT
>Chrysemys-mir-30b-3p
CTGGGAGGTGGATGTTTACTTC

>Chrysemys-mir-30c-1_pre
GCCATGCTGTAGCATGTGTAAACATCCTACACTCTCAGCTGTGGACTCAAGGTAGCTGGGAGAGGGTTGTTTACTCCTTCTGCCATGGACTGAA
>Chrysemys-mir-30c-1-5p
TGTAAACATCCTACACTCTCAGCT

>Chrysemys-mir-30c-1-3p
CTGGGAGAGGGTTGTTTACTCC

>Chrysemys-mir-30c-2_pre
AGCTCTGAGTGGCAGGTACTGTAAACATCCTACACTCTCAGCTGTGGAAAGTAAGGAAGCTGGGAGAAGGCTGTTTACTCTCTCTGCCTTGGAAAG
>Chrysemys-mir-30c-2-5p
TGTAAACATCCTACACTCTCAGCT
>Chrysemys-mir-30c-2-3p
CTGGGAGAAGGCTGTTTACTCT

>Chrysemys-mir-30d_pre
TATTGTAGTCTGTTGTTGTAAACATCCCCGACTGGAAGCTGTAAGAGAAATTCTAGCTTTCAGTCAGATGTTTGCTGCATCCGGCTATTCATGG
>Chrysemys-mir-30d-5p
TGTAAACATCCCCGACTGGAAGC
>Chrysemys-mir-30d-3p
CTTTCAGTCAGATGTTTGCTGC

>Chrysemys-mir-30e_pre
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>Chrysemys-mir-30e-5p
TGTAAACATCCTTGACTGGAAGCT
>Chrysemys-mir-30e-3p
CTTTCAGTCGGATGTTTACAGC

>Chrysemys-mir-31_pre
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>Chrysemys-mir-31-5p
AGGCAAGATGTTGGCATAGCTG
>Chrysemys-mir-31-3p
TGCTATGCCAACATATTGTCATC

>Chrysemys-mir-32_pre
GCTTGCTCTGGTGGAGATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAGTGCAATTTAGTGTGTGCGATATTTTCACATGAGTGCATGC
>Chrysemys-mir-32-5p
TATTGCACATTACTAAGTTGCA
>Chrysemys-mir-32-3p
CAATTTAGTGTGTGCGATATT

>Chrysemys-mir-33-1_pre
GGGGGGCAGCTGTAGTGCATTGTAGTTGCATTGCATGTTCTGGCAGTACTTGTGCAATGTTTCTGCAGTGCAGTACAGAGGCACTCTC
>Chrysemys-mir-33-1-5p
GTGCATTGTAGTTGCATTGCA
>Chrysemys-mir-33-1-3p
CAATGTTTCTGCAGTGCAGT

>Chrysemys-mir-33-2_pre
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>Chrysemys-mir-33-2-5p
GTGCATTGTAGTTGCATTGCA
>Chrysemys-mir-33-2-3p
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>Chrysemys-mir-34a_pre
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>Chrysemys-mir-34a-5p
TGGCAGTGTCTTAGCTGGTTGT
>Chrysemys-mir-34a-3p

AATCAGCAAGTATACTGCCCTA

>Chrysemys-mir-34b_pre
GAAGTAGTGTTTGGTTTGTAGGCAGTGTAGTTAGCTGATTGTATCCATCTCTTTGCAATCACTAACTTTACTGCCATCAAAACAAGACACAGAATT
>Chrysemys-mir-34b-5p
AGGCAGTGTAGTTAGCTGATTG
>Chrysemys-mir-34b-3p
ATCACTAACTTTACTGCCATC

>Chrysemys-mir-34c_pre
ACATTAGCCTAGTTACCAGGCAGTGTAGTTAGCTGATTGCTAAAGGTACAATCACTAACCACACAGCCAGGTAAAAAGGTATGTAA
>Chrysemys-mir-34c-5p
AGGCAGTGTAGTTAGCTGATTGC
>Chrysemys-mir-34c-3p
AATCACTAACCACACAGCCA

>Chrysemys-mir-92a-1_pre
TGTACCCCTTTCTACACAGGTTGGGATCAGTTGCAATGCTGTGTGTGCCTGTAGTATTGCACTTGTCCCGGCCTGTTGAGGTTGGTGGGGACAG
>Chrysemys-mir-92a-1-3p
TATTGCACTTGTCCCGGCCT
>Chrysemys-mir-92a-1-5p
AGGTTGGGATCAGTTGCAATGCT

>Chrysemys-mir-92a-2_pre
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>Chrysemys-mir-92a-2-3p
TATTGCACTTGTCCCGGCCT
>Chrysemys-mir-92a-2-5p
GTGGGGATTTGTTGCATTACT

>Chrysemys-mir-92b_pre
TCCAGGGCAGCAGGAGGGACGGGATGCTGTGCAGTGTTGTTCTATCACCAACCAATATTGCACTCGTCCCGGCCTCCTGCCTCCTTGGGCT
>Chrysemys-mir-92b-5p
AGGGACGGGATGCTGTGCAGTGTT
>Chrysemys-mir-92b-3p
TATTGCACTCGTCCCGGCCTCC

>Chrysemys-mir-92c_pre
CCGGTCCCTTTCGTTCTAAGGTTGGGAGAGCTGTAATTGGCATGACTATTTTTCAGAGGCATTGCACTCGTCCCGGCCGGAGTCAGAAGGGATTTG
>Chrysemys-mir-92c-5p
AGGTTGGGAGAGCTGTAATTG
>Chrysemys-mir-92c-3p
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>Chrysemys-mir-93_pre
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>Chrysemys-mir-93-5p
CAAAGTGCTGTTCGTGCAGGT
>Chrysemys-mir-93-3p
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>Chrysemys-mir-96_pre
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>Chrysemys-mir-96-5p
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>Chrysemys-mir-98_pre

GGATGAGGTAGTACGTTGTATTGTTGTGGGGTCGGGATTCGTGCCCCAATCAGAGATAACAATACAACTTACTACTTTCCC
>Chrysemys-mir-98-5p
TGAGGTAGTACGTTGTATTGTT
>Chrysemys-mir-98-3p
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>Chrysemys-mir-99a_pre
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>Chrysemys-mir-99a-5p
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>Chrysemys-mir-99a-3p
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>Chrysemys-mir-99b_pre
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>Chrysemys-mir-99b-5p
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>Chrysemys-mir-99b-3p
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>Chrysemys-mir-100_pre
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>Chrysemys-mir-100-5p
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>Chrysemys-mir-100-3p
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>Chrysemys-mir-101-1_pre
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>Chrysemys-mir-101-1-3p
TACAGTACTGTGATAACTGAAG
>Chrysemys-mir-101-1-5p
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>Chrysemys-mir-101-2_pre
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>Chrysemys-mir-101-2-3p
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>Chrysemys-mir-101-2-5p
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>Chrysemys-mir-103-1_pre
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>Chrysemys-mir-103-2_pre
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>Chrysemys-mir-103-2-5p
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>Chrysemys-mir-106a_pre
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>Chrysemys-mir-106a-5p
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>Chrysemys-mir-106b-5p
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>Chrysemys-mir-107_pre
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>Chrysemys-mir-107-3p
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>Chrysemys-mir-122_pre
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>Chrysemys-mir-122-3p
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>Chrysemys-mir-124-1_pre
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>Chrysemys-mir-124-2_pre
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>Chrysemys-mir-124-3_pre
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>Chrysemys-mir-124-4_pre
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>Chrysemys-mir-124-3p
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>Chrysemys-mir-124-5p
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>Chrysemys-mir-125a_pre
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>Chrysemys-mir-125a-5p
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>Chrysemys-mir-125a-3p
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>Chrysemys-mir-125b-1_pre
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>Chrysemys-mir-125b-1-5p
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>Chrysemys-mir-125b-1-3p
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>Chrysemys-mir-125b-2_pre
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>Chrysemys-mir-125b-2-5p
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>Chrysemys-mir-125b-2-3p
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>Chrysemys-mir-126_pre
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>Chrysemys-mir-126-5p
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>Chrysemys-mir-128-1-5p
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>Chrysemys-mir-128-2_pre
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>Chrysemys-mir-128-2-5p
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>Chrysemys-mir-129-1_pre
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>Chrysemys-mir-129-1-3p
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>Chrysemys-mir-129-2_pre
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>Chrysemys-mir-129-2-5p
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>Chrysemys-mir-129-2-3p
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>Chrysemys-mir-130a_pre
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>Chrysemys-mir-130a-5p
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>Chrysemys-mir-130b_pre
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>Chrysemys-mir-130b-3p
CAGTGCAATAATGAAAGGGCGT
>Chrysemys-mir-130b-5p
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>Chrysemys-mir-130c_pre
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>Chrysemys-mir-130c-3p
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>Chrysemys-mir-130c-5p
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>Chrysemys-mir-130d_pre
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>Chrysemys-mir-130d-3p
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>Chrysemys-mir-132_pre

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>Chrysemys-mir-132-5p
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>Chrysemys-mir-132-3p
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>Chrysemys-mir-133a-1_pre
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>Chrysemys-mir-133a-1-3p
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>Chrysemys-mir-133a-1-5p
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>Chrysemys-mir-133a-2_pre
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>Chrysemys-mir-133a-2-3p
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>Chrysemys-mir-133a-2-5p
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>Chrysemys-mir-133b_pre
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>Chrysemys-mir-133c_pre
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>Chrysemys-mir-135-1_pre
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>Chrysemys-mir-135-2_pre
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>Chrysemys-mir-135-2-5p
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>Chrysemys-mir-135-2-3p
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>Chrysemys-mir-135-3_pre
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>Chrysemys-mir-135-3-3p
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>Chrysemys-mir-137a_pre
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>Chrysemys-mir-137b_pre

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>Chrysemys-mir137b-5p
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>Chrysemys-mir-138_pre
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>Chrysemys-mir-138-5p
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>Chrysemys-mir-138-3p
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>Chrysemys-mir-139_pre
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>Chrysemys-mir-139-3p
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>Chrysemys-mir-140-5p
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>Chrysemys-mir-142-1_pre
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>Chrysemys-mir-143_pre
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>Chrysemys-mir-143-5p
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>Chrysemys-mir-144-3p
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>Chrysemys-mir-145_pre
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>Chrysemys-mir-145-3p
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>Chrysemys-mir-146a_pre
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>Chrysemys-mir-146a-3p
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>Chrysemys-mir-146b_pre
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>Chrysemys-mir-146c_pre
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>Chrysemys-mir-147_pre
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>Chrysemys-mir-148a_pre
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>Chrysemys-mir-148b_pre
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>Chrysemys-mir-152-5p
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>Chrysemys-mir-153-1_pre
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>Chrysemys-mir-182_pre
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>Chrysemys-mir-183_pre

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>Chrysemys-mir-184_pre
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>Chrysemys-mir-192-3p
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>Chrysemys-mir-196-1_pre
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>Chrysemys-mir-196-2-3p
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>Chrysemys-mir-196-3_pre
CTGAGAACTGTTCTGTAGTTTAGGTAGTTTCATGTTGTTGGGGCTCCACCTTTCTCTCTGCAGCACGAAACTGCCTTAATTACTTCAGTTGAAATC
>Chrysemys-mir-196-3-5p
TAGGTAGTTTCATGTTGTTGGG

>Chrysemys-mir-199-1_pre
CCAGCCCAGCCTGCCCAGTGTTCAGACTACCTGTTCAGGAGGCTATCAAGGTGTACAGTAGTCTGCACATTGGTTAGATTGGGTTTGGT
>Chrysemys-mir-199-1-5p
CCCAGTGTTCAGACTACCTG
>Chrysemys-mir-199-1-3p
ACAGTAGTCTGCACATTGGTTA

>Chrysemys-mir-199-2_pre
GATCCTGCTCCGTCGCCCCAGTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGACTGGGCAAGGGAAA
>Chrysemys-mir-199-2-5p
CCCAGTGTTCAGACTACCTG
>Chrysemys-mir-199-2-3p
ACAGTAGTCTGCACATTGGTTA

>Chrysemys-mir-199-3_pre
GCTCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGACTACGAGATTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA
>Chrysemys-mir-199-3-5p
CCCAGTGTTCAGACTACCTG
>Chrysemys-mir-199-3-3p
ACAGTAGTCTGCACATTGGTTA

>Chrysemys-mir-200a_pre
TATGGTCCTCTGTGGACATCTTACTAGACAGTGCTGGATTTTTTGGATCTACTCTAACACTGTCTGGTAACGATGTTTAAAGGGTGAACCAA
>Chrysemys-mir-200a-3p
TAACACTGTCTGGTAACGATGTT
>Chrysemys-mir-200a-5p
CATCTTACTAGACAGTGCTGGA

>Chrysemys-mir-200b_pre

ACCCTGGGATGCCATTACCATCTTACTGGGCAGCATTGGATGTTTTCTGTGTTTCTAATACTGCCTGGTAATGATGATTATGGTGTCTCGCAC
>Chrysemys-mir-200b-3p
TAATACTGCCTGGTAATGATGAT
>Chrysemys-mir-200b-5p
CATCTTACTGGGCAGCATTGGA

>Chrysemys-mir-202_pre
GCTCGTTGTTCCTTTTTCCTATGCATATACTTCTTTGAGAATTGGAACTAAAGAGGCATAGGGCATGGGAAAATGGGGCGACTGAGG
>Chrysemys-mir-202-5p
TTCCTATGCATATACTTCTTTG

>Chrysemys-mir-203_pre
GCGGGCAGCCTCCTTGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTCTAGCATAATTGTGAAATGTTTAGGACCACTTGACCAGGAAGGCCCGGG
>Chrysemys-mir-203-3p
GTGAAATGTTTAGGACCACTTGA
>Chrysemys-mir-203-5p
AGTGGTTCTTAACAGTTCAACAG

>Chrysemys-mir-204-1_pre
TCATGTGACCCGTGGACTTCCCTTTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAACTGTCATCACTGGC
>Chrysemys-mir-204-1-5p
TTCCCTTTGTCATCCTATGCCT
>Chrysemys-mir-204-1-3p
GCTGGGAAGGCAAAGGGACGT

>Chrysemys-mir-204-2_pre
GACCATGTGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGTTCATAGTGAGGCAGGGACAGCAAAGGGATGCTCAGTTGTCGTCTC
>Chrysemys-mir-204-2-5p
TTCCCTTTGTCATCCTATGCCT

>Chrysemys-mir-204-3_pre
CCGGTGCGCCCTGTGAGCTTCCCTTTGTCATCCTATGCCTGAGAGATGCCTGGAGGCTGGGACGGTGAAGGGAAGCCCACGTGGCTGCCAA
>Chrysemys-mir-204-3-5p
TTCCCTTTGTCATCCTATGCCT
>Chrysemys-mir-204-3-3p
GCTGGGACGGTGAAGGGAAGC

>Chrysemys-mir-205a_pre
ATCCATGAATTCTGTTGTCCTTCATTCCACCGGAGTCTGTCTCATAACTAATCAGATTTCAGTGGAGTGAAGCACAAGAGACATGGAG
>Chrysemys-mir-205a-5p
TCCTTCATTCCACCGGAGTCTG
>Chrysemys-mir-205a-3p
GATTTCAGTGGAGTGAAGCACA

>Chrysemys-mir-205b_pre
TCCATGGCTTGCTGGTGCCCTTCATTCCACCGGAATCTGTAGAGGCAGAAACCAGATTTCAGTGTAATGAAGCCCATCAGACATGGAA
>Chrysemys-mir-205b-5p
CCCTTCATTCCACCGGAATCTGT

>Chrysemys-mir-206_pre
TTCTCTTTTGAGACAACATGCTTCTTTATATCCCCATATGAATTATGCTGCTATGGAATGTAAGGAAGTGTGTGGTTTCAGGGAGATGA
>Chrysemys-mir-206-3p
TGGAATGTAAGGAAGTGTGTGG
>Chrysemys-mir-206-5p
ACATGCTTCTTTATATCCCCAT

>Chrysemys-mir-208_pre

TTCCTCTAACAGGGAAGCTTTTGGCTCGGGTTATATTTTCACTCGCGGCGTATAAGACGAGCAAAAAGCTTGTTGGTTGGAGGAGA
>Chrysemys-mir-208-5p (predicted)
AAGCTTTTGGCTCGGGTTATAT

>Chrysemys-mir-210_pre
CAGAAGCTGGTGAGCCACTGACTAACGCACATTGTGCTGTTAAAGAATCCACTGTGCGTGTGACAGCGGCTAACCAGCTTTTCGGCC
>Chrysemys-mir-210-3p
CTGTGCGTGTGACAGCGGCTAA
>Chrysemys-mir-210-5p
AGCCACTGACTAACGCACATTG

>Chrysemys-mir-212_pre
GTCAGCGCGTCGGCACCTTGGCTCTAGACTGATTACTGCTAAGTAGCATTAAAGAAACAGTAACAGTCTACAGTCATGGCTACTGAAGCATGA
>Chrysemys-mir-212-5p
ACCTTGGCTCTAGACTGATTA

>Chrysemys-mir-214_pre
GGACGGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTCACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC
>Chrysemys-mir-214-3p
TACAGCAGGCACAGACAGGCAG
>Chrysemys-mir-214-5p
GCCTGTCTACACTTGCTGTGC

>Chrysemys-mir-215_pre
GTGTACAGGAAAATGACCTATGAATTGACAGACTGTGTCTTCTAAATTTGTCTGTCACTTCTGTAGGCCAATATTCTGCATGCCTTA
>Chrysemys-mir-215-5p
ATGACCTATGAATTGACAGAC
>Chrysemys-mir-215-3p
CTGTCACTTCTGTAGGCCAATA

>Chrysemys-mir-216a_pre
GGATGGCTGTGAATTGGCTTAATCTCAGCTGGCAACTGTGAGCAATTAATACATTCTCTCACAGTGGTATCTGGGATTATGCTAAACACAGCAATT
>Chrysemys-mir-216a-5p
TAATCTCAGCTGGCAACTGTGA

>Chrysemys-mir-216b_pre
AAGTCATAGACTGGGAAATCTCTGCAGGCAAATGTGATGTATTTATAGCAATCTCACAATTACCTGTAGAGTTTCTGCAATCTG
>Chrysemys-mir-216b-5p
AAATCTCTGCAGGCAAATGTG

>Chrysemys-mir-217_pre
AGTTTTTGATGTCGCAGATACTGCATCAGGAACTGATTGGATAATAATCAGCCACCATCAGTTCCTAATGCATTGCCTTCAGCATCTATACAAGCA
>Chrysemys-mir-217-5p
TACTGCATCAGGAACTGATTGG

>Chrysemys-mir-218-1_pre
AGCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGCAAGGTATGAGTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT
>Chrysemys-mir-218-1-5p
TTGTGCTTGATCTAACCATGTG

>Chrysemys-mir-218-2_pre
TGGGGTTTTCCTTTGTGCTTGATCTAACCATGTGGTAGAACAATACAAATTGAACATGGTTCTGTCAAGCACCATGGAAGGCTGCAT
>Chrysemys-mir-218-2-5p
TTGTGCTTGATCTAACCATGTG
>Chrysemys-mir-218-2-3p
AAACATGGTTCTGTCAAGCAC

>Chrysemys-mir-219-1_pre
CTGAACACCGGCTCCTGATTGTCCAAACGCAATTCTTGTGTCTGCGCCCAAGAATTGAGTGTGGACGTCGTGAGCCGGGGTTTCCT
>Chrysemys-mir-219-1-3p
AGAATTGTGTCTGGACATCTG
>Chrysemys-mir-219-1-5p
TGATTGTCCAAACGCAATTCTTG

>Chrysemys-mir-219-2_pre
CAGGAATCTCTGCTCCTGATTGTCCAAACGCAATTCTTGTGCAATGGAATCATACAAACCAAGAATTGTGTCTGGACATCTGTGGCAGAGATTTCA
>Chrysemys-mir-219-2-3p
AGAATTGTGTCTGGACATCTG
>Chrysemys-mir-219-2-5p
TGATTGTCCAAACGCAATTCTTG

>Chrysemys-mir-221_pre
CCAGGTTTGGGGCATGAACCTGGCATACAATGTAGAATTCTGTGTTTGTTAAGCAACAGCTACATTGTCTGCTGGGTTTCAAGCTGCCTGGA
>Chrysemys-mir-221-5p
ACCTGGCATACAATGTAGAATT
>Chrysemys-mir-221-3p
AGCTACATTGTCTGCTGGGTTT

>Chrysemys-mir-222a_pre
TGTAGTTGCCTATCAGTCGCTCAGTAGTCAGTGTAGATTCTGTCTTTACAATCAGCAGCTACATCTGGCTACTGGGTCTCTGATGACATCTT
>Chrysemys-mir-222a-3p
AGCTACATCTGGCTACTGGGTCT
>Chrysemys-mir-222a-5p
CGCTCAGTAGTCAGTGTAGATTC

>Chrysemys-mir-222b_pre
GATGCAATTGGCTGCTCAGTAGTCGGTGTAGGATCTGTCTGACATTATTACCAACAGCTACATCTGATTACTGGGTCACTGATAGCATCATCA
>Chrysemys-mir-222b-3p
AGCTACATCTGATTACTGGGTCA
>Chrysemys-mir-222b-5p
TGCTCAGTAGTCGGTGTAGGATC

>Chrysemys-mir-223_pre
TGCAGTGCTGCGCTCCGTGTATTTGACAAGCTGAGTTTGACACTCAATGTGGCAGAGTGTCAGTTTGTCAAATACCCCAAGTGAAGCATTTGCTTA
>Chrysemys-mir-223-3p
TGTCAGTTTGTCAAATACCCCA
>Chrysemys-mir-223-5p
CGTGTATTTGACAAGCTGAGTTT

>Chrysemys-mir-301a_pre
TGCTGCTAACGAATGCTCTGACTTTATTGCACTACTGTACTTTACAGCTAGCAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAGAG
>Chrysemys-mir-301a-3p
CAGTGCAATAGTATTGTCAAAGC

>Chrysemys-mir-301b_pre
CTGCTGGTATCGCTGGCTCTGACAATGTTGCACTACTGTCTGCACAAATAAAGCAGTGCAATAATATTGTCAAAGCATTTGGTTCCAGTC
>Chrysemys-mir-301b-3p
CAGTGCAATAATATTGTCAAAGC

>Chrysemys-mir-302a_pre
AGCTTAAAGGACCCCCACTACTTTAATGTGGAAGTACTTGCTTTGCTCCTGATAAAGTAAGTGCTTCCATGTTTTAGTGATGGTGAAACCTG
>Chrysemys-mir-302a-3p (predicted)
TAAGTGCTTCCATGTTTTAGTG

>Chrysemys-mir-302b_pre
CCCCTTCTACTTTAACATGGAGGTGCTTTCTGTGACTATAAAAAGTAAGTGCTTCCATGTTTTAGTAGAGGTGAATCCTGATCT
>Chrysemys-mir-302b-3p
TAAGTGCTTCCATGTTTTAGTAG

>Chrysemys-mir-302c_pre
TTAAAGGACCCCCTTTGCTTTAACATGGGGGTACCTGCTGCCTAGAAAAAGTAAGTGCTTCCATGTTTCAGTCGTGGTGG
>Chrysemys-mir-302c_3p (predicted)
TAAGTGCTTCCATGTTTCAGT

>Chrysemys-mir-302d_pre
CCCCTCTACTTTAACATGGAAGTACTTGCTGGATGCTTGAAAAAGTAAGTGCTTCCATGTTTTAGTTGTGGTGAATCCT
>Chrysemys-mir-302d-3p
TAAGTGCTTCCATGTTTTAGTT

>Chrysemys-mir-338a_pre
GCTTCTCCTCCCCAACAATATCCTGGTGCTGAGTGAGTTGCACACGGAGACTCCAGCATCAGTGATTTTGTTGAAGAGGGCGAGC
<Chrysemys-mir-338a-3p
TCCAGCATCAGTGATTTTGTTGA
>Chrysemys-mir-338a-5p
AACAATATCCTGGTGCTGAGT

>Chrysemys-mir-338b_pre
TGCAAATGTTTATTTCTGGCAACACTATCCTGATGCTGTCAGAGTATGTGGTAAAGCTCCAGCATCAGTGATTTTGTTGTTAGTGGTAAATTCAA
>Chrysemys-mir-338b-3p
TCCAGCATCAGTGATTTTGTTGT
>Chrysemys-mir-338b-5p
AACACTATCCTGATGCTGTCAGA

>Chrysemys-mir-363_pre
TGTTTTGCTGTTGTCGGGTGGATCACGATGCAATTTTGATTAGTTTAGCAGGAGAAAAATTGCACGGTATCCATCTGTAAACCGCAGGACC
>Chrysemys-mir-363-3p
AATTGCACGGTATCCATCTG
>Chrysemys-mir-363-5p
GTGGATCACGATGCAATTTTGA

>Chrysemys-mir-365-1_pre
TACCGCAGGGAAAATGAGGGACTTTTGGGGGCAGATGTGTTTCCATTACACTATCATAATGCCCCTAAAAATCCTTATTACTCTTGCAGTATT
>Chrysemys-mir-365-1-3p
TAATGCCCCTAAAAATCCTTA

>Chrysemys-mir-365-2_pre
AGAGGCAGCAAGAAAAATGAGGGACTTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTTCTTGCAATGTT
>Chrysemys-mir-365-2-3p
TAATGCCCCTAAAAATCCTTA
>Chrysemys-mir-365-2-5p
AGGGACTTTCAGGGGCAGCTGTG

>Chrysemys-mir-367_pre
TCTTAAACTGCAGGCCACTACTGTTGCTAATATGCAACTCTGTTGTGTAAAAGCTGGAATTGCACTTTAGCAATGGTGATGGACTGTAAGACATAC
>Chrysemys-mir-367-3p (predicted)
AATTGCACTTTAGCAATGGTG

>Chrysemys-mir-375_pre
AGCAACCTCTGCACTTGCCTGGCGTCGAGCCCCACGTGCAAGACCTGACGTGAACGTTTTGTTCGTTCGGCTCGCGTTAGGCAGGTCCAGCCTGTC
>Chrysemys-mir-375-3p
TTTGTTCGTTCGGCTCGCGTTA

>Chrysemys-mir-383_pre
AAGTCACCTGCTCCTCAGATCAGAAGGTGATTGTGGCTTTGAGTAGATATTAAGCAGCCACAGCACTGCCTGGTCAGAAAGAGCAAGTGTACT
>Chrysemys-mir-383-5p
AGATCAGAAGGTGATTGTGGCT

>Chrysemys-mir-425_pre
TGGCGAGAAATTGCTTTGGAATGACACGATCACTCCCGCTGAGCAAGCAGCCAGAGCCATCGGGAATATCGTGTCCGTCCAAAGCTTTTTCGGCA
>Chrysemys-mir-425-5p
AATGACACGATCACTCCCGCTGAG
>Chrysemys-mir-425-3p
CCATCGGGAATATCGTGTCCGT

>Chrysemys-mir-429_pre
TGCCTGCTGATTGATGTCTTACCAGACAAAGTTAGATCTAGCTATTTTCGTCTAATACTGTCTGGTAATGCCGTCCATCGCATTGGCTAA
>Chrysemys-mir-429-3p
TAATACTGTCTGGTAATGCCGT
>Chrysemys-mir-429-5p
NATGACACGATCACTCCCGCTGAG

>Chrysemys-mir-449a_pre
GTGTGTGCTAGGAAGGCAGTGTATTGTTAGCTGGTTGAAAATCTGACAGCAGCTAACCTACATCTGCTATCTTATTGCACATACTA
>Chrysemys-mir-449a-5p
AGGCAGTGTATTGTTAGCTGG
>Chrysemys-mir-449a-3p
CAGCTAACCTACATCTGCTATC

>Chrysemys-mir-449b_pre
TGTGTCTGGTAGGCAGTGTACTGTTAGCTGGCTGCTTTGTGTGAATCTAGCAGTCTCTACTACACTGTCACCTGCTGCAGG
>Chrysemys-mir-449b-5p (predicted)
AGGCAGTGTACTGTTAGCTGGCT

>Chrysemys-mir-449c_pre
GATGTGACAGTTTGGCAGTGCCTTGCTAGCTGGCTGTTGAGAACTTGATATATGAACAGTTGCTAGCTGCACTCCACATTGTTGCATTC
>Chrysemys-mir-449c-5p
TGGCAGTGCCTTGCTAGCTGGCT

>Chrysemys-mir-449d_pre
TGTGTATGTGCTGATTAGGCAGTGTATTGTTAGTTAGCTGTTGTTCACATACCAGCAACTAAATACGCTTCCACATTAGCACACGACCTTGCAT
>Chrysemys-mir-449d-5p
AGGCAGTGTATTGTTAGTTAGC

>Chrysemys-mir-451_pre
AGCTGAGCCCATGGGGCGTCAATGAAACCGTTACCATTACTGACTTTAGTAATGGTAACGGTTCTACTGCCGCCCCAGCATCCGGCCAGCGA
>Chrysemys-mir-451-5p
AAACCGTTACCATTACTGACTT
>Chrysemys-mir-451-3p
TTAGTAATGGTAACGGTTCT

>Chrysemys-mir-454_pre
CCTTAAGGAAGAGACCCTATCAATATTGCCTCTGCTTTTGTGATCAGGGTAGTAGTGCAATATTGCTTATAGGGTCTTTTCTTTGGAGGGT
>Chrysemys-mir-454-3p
TAGTGCAATATTGCTTATAGGGTC
>Chrysemys-mir-454-5p
ACCCTATCAATATTGCCTCTGC

>Chrysemys-mir-455_pre

TCCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGTGGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGGTTTAT
>Chrysemys-mir-455-5p
TATGTGCCCTTGGACTACATCG
>Chrysemys-mir-455-3p
ATGCAGTCCATGGGCATATAC

>Chrysemys-mir-456_pre
TGTATGTGTGAGCAGGCATCTTTTCAGCCTACATGTGGATTCCTAAATCTGCAGGCTGGTTAGATGGTTGTCATACGTTCATCTG
>Chrysemys-mir-456-3p
CAGGCTGGTTAGATGGTTGTC

>Chrysemys-mir-458_pre
TGCATGGTGCAGATGGCAGCGCCATTTTCAGAGCTATAAACAGTATCATTGTCATAGCTCTTTGAATGGTACTGCCATATGTACTGGAGAATCA
>Chrysemys-mir-458-3p
ATAGCTCTTTGAATGGTACTGC
>Chrysemys-mir-458-5p
AGCGCCATTTTCAGAGCTATAA

>Chrysemys-mir-459_pre
ACTGTTTCTTGTAATCAGTAACAAGGATTCATCCTTGTGTATAGTAAATAACAGGGAGAATCTTTGTCACTAAGTACAATTAACAGCTAT
>Chrysemys-mir-459-3p
GGGAGAATCTTTGTCACTAAG
>Chrysemys-mir-459-5p
TCAGTAACAAGGATTCATCCT

>Chrysemys-mir-460a_pre
CTGACTTTATAGAACCTGCATTGTACACACTGTGTGTATTGATTGGACATGCACAGCGCATACAATGTGGATACTGTAGACGTCAAT
>Chrysemys-mir-460a-5p
CCTGCATTGTACACACTGTGTG
>Chrysemys-mir-460a-3p
CACAGCGCATACAATGTGGAT

>Chrysemys-mir-460b_pre
TGGCTCTATGTTGTCCTCATTGTACATGCTGTGTGTATTTTTATTACATACACAGCGCATGCAATGTGGACATAATGGAGATCA
>Chrysemys-mir-460b-5p
TCCTCATTGTACATGCTGTGTG

>Chrysemys-mir-489_pre
GTGGTGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGGACTTTTAGGAGTGACATCATATGTACGGCTGCTAAACTGCTGCATGGGAC
>Chrysemys-mir-489-3p
GTGACATCATATGTACGGCTGCT
>Chrysemys-mir-489-5p
TGGTCGTATGTATGACGTCATT

>Chrysemys-mir-490_pre
TCATAAGTTCATGGTTCGACACCATGGATCTCCAGGTGGGTCAAGATTATAGAGATACACCAACCTGGAGGACTCCATGCTGTTGAGCTGTTCACA
>Chrysemys-mir-490-3p
CAACCTGGAGGACTCCATGCTGT
>Chrysemys-mir-490-5p
CCATGGATCTCCAGGTGGGT

>Chrysemys-mir-499_pre
TTGGGAGAGCGGCAGTTAAGACTTGCAGTGATGTTTAGATAATGTATTACATGAACATCACTTTAAGTCTGTGCTACCTCTCTCCTCACTCTGGAC
>Chrysemys-mir-499-5p
TTAAGACTTGCAGTGATGTTTA
>Chrysemys-mir-499-3p
AACATCACTTTAAGTCTGTGCT

>Chrysemys-miR-551-1_pre
TTTCCTGTATATGACCTTGGAAATCAAGAATGGGTGGAGCCTGTTGAATTAATTCTAGGCGACCCATACTTGGTTTCAAGGGTCAGCAGGGAA
>Chrysemys-miR-551-1-3p
GCGACCCATACTTGGTTTCAG
>Chrysemys-miR-551-1-5p
GAAATCAAGAATGGGTGGAGCCT

>Chrysemys-mir-551-2_pre
CCTCCATGGCTCCAGAAATCAAGGGTGGGTGAGACCTCGTAAGAAAACGTGAAGGCGACCCATACTTGGTTTCAGGGGCTGTGAGGA
>Chrysemys-mir-551-2-3p
GCGACCCATACTTGGTTTCAG

>Chrysemys-mir-599_pre
ATACTGTCAATAGTGTGTTTGATAACCTGATGTGGGACAGGAGTTCTTTTCACTGTTGTGTCAGTTTATCAAACCCTGGAAGCCCCTGC
>Chrysemys-mir-599-3p (predicted)
GTTGTGTCAGTTTATCAAACCC

>Chrysemys-mir-726_pre
TGGGGCGTTCACCAGGAATTCCGCTAGTTCTGAACTATTTACACTTGAAAAAAGTTCACTACTAGCAGAACTCGGGTGCGCGCCCCCC
>Chrysemys-mir-726-3p
TTCACTACTAGCAGAACTCG

>Chrysemys-mir-727_pre
TTGCCCTGTATGTCATTTTCAGTCTTCAATTCCTCCCAGCCCATTAAATGGAAAGTTGAGGCGAGTTGAAGACTAAAAATGCTGTGCAGAATCA
>Chrysemys-mir-727-3p
TTGAGGCGAGTTGAAGACTAAA

>Chrysemys-mir-737_pre
CTACTCTGCTGTTATTTTTTTAGGTTTTGATTTTTATTACATCTTCATGCGAAAATCAAAACCTAAAGAAAATGCTGCAAAGATAGAT
>Chrysemys-mir-737-5p
ATTTTTTTAGGTTTTGATTTTT

>Chrysemys-mir-875_pre
GTTTAGTGGTACAATACCTCAGTCTTATCAGGTGTTCTATAAATTCACCTGCAAAAACTGAGGTTGAGTTTCACTGAAC
>Chrysemys-mir-875-5p
AATACCTCAGTCTTATCAGGT

>Chrysemys-mir-1306_pre
TGAACAGCCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGTGGTGATGGACAGTCAGAT
>Chrysemys-mir-1306-5p
CCACCTCCCCTGCAAACGTCCA
>Chrysemys-mir-1306-3p
TGGACGTTGGCTCTGGTGGTGAT

>Chrysemys-mir-1329_pre
CAGTCTGGTTGTAGGGATACAGTGATCAGGTTACGAGGGATTTCTCAAGTAACAACCTCGTAGCTCGGTCACGATATCCCTATGACTTAGATAACA
>Chrysemys-mir-1329-5p
TACAGTGATCAGGTTACGAGG

>Chrysemys-mir-1388_pre
GTGAGGGGTGTTTCGAGGACTGTCTAACCTGAGAATGGTGAAACATGAAGGTCAATCTCAGGTTCGTCAGCCCATGAGACGCCTTCTCCAGA
>Chrysemys-mir-1388-5p
AGGACTGTCTAACCTGAGAAT
>Chrysemys-mir-1388-3p
ATCTCAGGTTCGTCAGCCCAT

>Chrysemys-mir-1397_pre
TGCGATGTGTGCATTGCATTGCGACGGGTTACATCACTGGTCGTAACATGATGTAACCCAACGCAGCATGATGTAAGCGTCGTG
>Chrysemys-mir-1397-5p
TGCATTGCGACGGGTTACATCA

>Chrysemys-mir-1416_pre
GATGGATGACACCTCCTTAACTCATGCCGCTGTGCCTTTCACCCCCACTCCCACAATTGTATGAGTTGAGTACAGAGTATCAGACT
>Chrysemys-mir-1416-5p (predicted)
TCCTTAACTCATGCCGCTGTG

>Chrysemys-mir-1641_pre
AGGGCATTTCCTGGGGATTAATGACTGTCTGGGGTCATCATCTCCTCCCAGTTAGTTATTAGTCCCCCAGGAAATACTGTGTGCCTT
>Chrysemys-mir-1641-5p (predicted)
TGGGGATTAATGACTGTCTGGG

>Chrysemys-mir-1662_pre
TGTGCTCTATGGGTTTGACATCATCATACTTGAGATGTATGACACAAAGTCCCAAGCAGGCTGATGTCAGGCCCAAGATGGCTG
>Chrysemys-mir-1662-5p
TTGACATCATCATACTTGAGAT
>Chrysemys-mir-1662-3p
CCCAAGCAGGCTGATGTCAGG

>Chrysemys-mir-1677a_pre
GTCTGGATGGGGCCTGATTCAGATCCCATTGAAGTCAATGAGAATATTTCATTTGAGCTACTGACTTCAGTGGGCTTTGGTTCAGACCCACAGTCA
>Chrysemys-mir-1677a-5p
TCAGATCCCATTGAAGTCAATGG
>Chrysemys-mir-1677a-3p
CTGACTTCAGTGGGCTTTGGTT

>Chrysemys-mir-1677b_pre
AGCAACTAAGAGCCTGGTCCAGAGCCCATTGAAGTCAGTGGGAGATGTTCTAATGACTCCAGAGGGCTTTGGATCAGGCCCTAAGTTAATCCAC
>Chrysemys-mir-1677b-5p
TCCAGAGCCCATTGAAGTCAGT
>Chrysemys-mir-1677b-3p
TGACTCCAGAGGGCTTTGGATC

>Chrysemys-mir-1677c_pre
CCTCTTCAAGGCCTAATCCAGAGCCCATTGAAGTCAGTGGGAATCTTTCTATTGACTTCAGTGGGCTTTGGATCAGGCCTTGGGAGCT
>Chrysemys-mir-1677c-5p
TCCAGAGCCCATTGAAGTCAGT
>Chrysemys-mir-1677c-3p
ATTGACTTCAGTGGGCTTTGGA

>Chrysemys-mir-1677d_pre
GTGTTTTGTGGGCCTGATCCAAAGCCCATTGAAGTCAACTGAAGTTTTTGTACTGACTTCAGGTGCTTTGAATCAAATCCCCTATTCACAGT
>Chrysemys-mir-1677d-5p
TGATCCAAAGCCCATTGAAGTCA
>Chrysemys-mir-1677d-3p
ACTTCAGGTGCTTTGAATCA

>Chrysemys-mir-1677e_pre
AATGCTCCCTCTAGGCTCTGATCCAAACCCATTGAAATCAAAGGAAAAATTCCAATGGGCTTTGAATCAGGTCCTGAGTGATGCCTCA
>Chrysemys-mir-1677e-5p
TCTGATCCAAACCCATTGAAAA
>Chrysemys-mir-1677e-3p
TTCCAATGGGCTTTGAATCAGGT

>Chrysemys-mir-1677f_pre
TACTGTGATACCAATAAATGACCATGTGAAGTTGATGGGAGTCTTTCCATTGACTTCAGTGGGCTTTGGATCAGGTCCTGTGTTGGTAAGGGGGAA
>Chrysemys-mir-1677f-3p
ATTGACTTCAGTGGGCTTTGGA

>Chrysemys-mir-1677g-1_pre
CACTTAGTCTGAAGGTGAAATCCTGGCTCTGTTGATGTCTATAGAAGTTTTACCATTGACTTCAGTAGAATCAGGATTTCTCCCTCATGAGTGTT
>Chrysemys-mir-1677g-2_pre
GTATAGCTGTTGAGCTGAATCCTGGTTCCACTGAAATAATGGTAGTTTTGTCGTTGACTTCAGTAGAATCAGGATTTGGCTCATAATTAGCTGTG
>Chrysemys-mir-1677g-3p
TGACTTCAGTAGAATCAGGATT

>Chrysemys-mir-1677h_pre
TCTGGGGCTCAACTGCTCTCCCAATTAAGTCAGTTGGACTTTTGATTTTGACTAAATTGGGAGAAGGGTTGAGTCCTCTG
>Chrysemys-mir-1677h-5p
AACTGCTCTCCCAATTAAGTCA
>Chrysemys-mir-1677h-3p
ACTAAATTGGGAGAAGGGTTGA

>Chrysemys-mir-1720_pre
TTCTGATCACCTCAGTTGTTGCTTTTGTGAGGATCTCAAGAGAAAGCAATGAGAGGGTGGGTCTGAAACCCA
>Chrysemys-mir-1720-3p (predicted)
AAGCAATGAGAGGGTGGGTCTGA

>Chrysemys-mir-1784_pre
ATTTCTTAGGGCCCAATTCTGCTCTCATTCAAATCAATGAGAGTTCTACCATTGACTTAACTGGGAGCACAATTGGGACCTAAGA
>Chrysemys-mir-1784-3p (predicted)
TGACTTAACTGGGAGCACAATT

>Chrysemys-mir-1788_pre
CCCTCTGTGTGTCGGGCTTGTTTTCAGTTGCCTGCGGTTGGTTAGAAGGACTCAGGCAGCTAAAGCAAGTCTGGGACGCGCGAGGAGAAC
>Chrysemys-mir-1788-5p
GGCTTGTTTTCAGTTGCCTGC
>Chrysemys-mir-1788-3p
CAGGCAGCTAAAGCAAGTCTG

>Chrysemys-mir-1791_pre
TGCACCATGTTGGGCTGCATCAGTCATGCCATGTTATGAAACCTAACACGATGTGACTGATGCAGGCTGACATGA
>Chrysemys-mir-1791-5p (predicted)
TGGGCTGCATCAGTCATGCCAT

>Chrysemys-mir-1805_pre
AGTGGAATATTCTGGGAGTTGTAGTCTTTCAAACAGAGCTCTGCAAGTATATACCTGTATTGGAACACTACAGCTCCCCGAACTTCCTAGTGTC
>Chrysemys-mir-1805-5p
AGTTGTAGTCTTTCAAACAGA
>Chrysemys-mir-1805-3p
TGTATTGGAACACTACAGCTC

>Chrysemys-mir-2184_pre
GCCCTTGGGTTTCCCCAAACAGTAAGAGTTTATGTGCGGTGAGAGCTAGAATCTGCATGTGGACTCCTACTGCTCCGGGAGGCTGGAAGTACCA
>Chrysemys-mir-2184-5p
AACAGTAAGAGTTTATGTGCGG
>Chrysemys-mir-2184-3p
GCATGTGGACTCCTACTGCTCC

>Chrysemys-mir-2188_pre
AATATCAAACCTGTGGGAAAGGTCCAACCTCACATGTCCTGTATGTAATAAAGGGGATGTATGTGGTCAGACCTATCCCACAGGCCCTGTATTCTT

>Chrysemys-mir-2188-5p
AAGGTCCAACCTCACATGTCCT
>Chrysemys-mir-2188-3p
GATGTATGTGGTCAGACCTAT

>Chrysemys-mir-2970_pre
GGTCTCTTCCTGTCACTGCAGACAGTCAGTAGTTGGTCTGGCGAGAGCAGGAATTCTCAGATCACCTCTTGGCTGTGAGTGGTGGTGCAGAGAACA
>Chrysemys-mir-2970-5p
GACAGTCAGTAGTTGGTCTG
>Chrysemys-mir-2970-3p
TCAGATCACCTCTTGGCTGTGAG

>Chrysemys-mir-2984_pre
CTACAGCAGATCCTGTTGAGAGTAAAACTAACAAGGATCATGCAATCCCAGGCAATTTCACTCACAGCAGGCATTGTAAGTAAAGCA
>Chrysemys-mir-2984-3p (predicted)
AATTTCACTCACAGCAGGCATT

>Chrysemys-mir-3064_pre
TTTATTTTTGATTTGGCTGTTGTGGTGTGCAAAACTTTGTACATTGCTTTTTGCCACACTGCAACACTTTACAGATGTGGAAGATGTG
>Chrysemys-3064-3p (predicted)
TGCCACACTGCAACACTTTAC

>Chrysemys-mir-3618_pre
GAATGCATTGTGATTTCCAATAATTGAGACAGTGATTCTGAAAGCTGTCTACATTAATGAAAAGAACAATGTAGTCA
>Chrysemys-mir-3618-3p (predicted)
TGTCTACATTAATGAAAAGAAC

>Chrysemys-novel-1_pre
TTGTTCTGTCCTGTTTTGGGACACAAGCAGAGCATCTGCATGACCTTCTCTACCTCATGCTCTGCCTGTGTCCCAAAATAGGCAGAACATC
>Chrysemys-novel-1-5p
TGGGACACAAGCAGAGCATCTG
>Chrysemys-novel-1-3p
CATGCTCTGCCTGTGTCCCAAA

>Chrysemys-novel-2_pre
TGTGGTAGTGATGGTGAAAGTGCTAGCGTAGAAACGGCAGATGCTTTTCATGCTCTCTTTGCTAGCGCTTCCACCAAGGTTACCACT
>Chrysemys-novel-2-5p
AAAGTGCTAGCGTAGAAACGG
>Chrysemys-novel-2-3p
CTCTCTTTGCTAGCGCTTCCA

>Chrysemys-novel-3_pre
TCTGGAGCTGATCCTGAAGCCCTTACTCACATGAGCAGTCCCACATAAGTCCTCAAGGTGAGTAAGGGCTGCGAGATTGGACCCTAAATACC
>Chrysemys-novel-3-5p
AAGCCCTTACTCACATGAGCA
>Chrysemys-novel-3-3p
CTCAAGGTGAGTAAGGGCTGCG

>Chrysemys-novel-6_pre
TCTGTGGGTATGCATACGCTATGGGGACAATACTGGCATAGCTTTAGCACCCTAGCTATGCCGGCATAGCCCCATGGTGTGTAGACTCACCAA
>Chrysemys-novel-6-5p
TATGGGGACAATACTGGCATAG
>Chrysemys-novel-6-3p
TATGCCGGCATAGCCCCATGGT

>Chrysemys-novel-7_pre
TTCGGGGCCAGCGCCTCGGCTGGCGTACGTTGGCGTTGCTCCATTGAAGCCAGCAGCTACGCCGACGTGAGCCAGCTGATGCTCTGGCCCTCGG

>Chrysemys-novel-7-5p
GGCTGGCGTACGTTGGCGTTGC
>Chrysemys-novel-7-3p
TACGCCGACGTGAGCCAGCTGA

>Chrysemys-novel-9_pre
GCATTGCCCTGCATCTTGTGTAGTTCTTTAGCATTTTCTACCCATTTTGCACAGATGTAAATAACTACACAAGGTGCAGGGCAGTGGAAGTG
>Chrysemys-novel-9-5p
TCTTGTGTAGTTCTTTAGCAT
>Chrysemys-novel-9-3p
GTAAATAACTACACAAGGTGC

>Chrysemys-novel-10_pre
GGATGGATGGGAGCCAGCAGTCGGAGAAGAAGAGACGGTGACTAACCTCCGTAACTTGTTCTTCGAGATGTTGCTCACGTCCAGTC
>Chrysemys-novel-10-5p
CAGCAGTCGGAGAAGAAGAGACG
>Chrysemys-novel-10-3p
TAACTTGTTCTTCGAGATGTTGC

>Chrysemys-novel-11_pre
AACCATCTAGAGAGCTGTGACTGTTTAGATGGTCGTGTGGGGTATGCGCACACAGCCTCAGCAGTCACTGCTTTTTAGATGTTT
>Chrysemys-novel-11-5p
CTGTGACTGTTTAGATGGTCGTG
>Chrysemys-novel-11-3p
CAGCCTCAGCAGTCACTGCT

>Chrysemys-novel-12_pre
CTCCGGAGTTGGGGCACCGATCGTTGGCGACTCAGGCTCCTCCATGGGAGCAGTACCCTGAGTCGCCAACAATCGGTGCCTCAACTCGGAGACCT
>Chrysemys-novel-12-5p
CACCGATCGTTGGCGACTCAGG
>Chrysemys-novel-12-3p
TGAGTCGCCAACAATCGGTGCC

>Chrysemys-novel-13_pre
GAGACTTGGGCCTTGATCCTGCCATGATCTCTGCAGAAACAAACCCTTGTGGAGCTCATTGCAGGACTGGGACCTTAGTTTT
>Chrysemys-novel-13-5p
TTGATCCTGCCATGATCTCTGCA
>Chrysemys-novel-13-3p
TGGAGCTCATTGCAGGACTGGG

>Chrysemys-novel-14_pre
TGCATCCGGCCATCCCTCTTCAGCAAAGCACCGAAGCACACGCATCACCTAAAGCGCATGCGTCGGTGCTGCTCAGAAGAGTGGCGGACTGCT
>Chrysemys-novel-14-5p
CAGCAAAGCACCGAAGCACACG
>Chrysemys-novel-14-3p
GCATGCGTCGGTGCTGCTCAGA

>Chrysemys-novel-16_pre
AAAGTTCAAGACTATACCCTCAGATGTGTCTACTAGTCTGGGCTCAATCACAGATTAGGGGCAACATCTGGGCTAGAGCCTGAGCTAATTC
>Chrysemys-novel-16-5p
CCTCAGATGTGTCTACTAGTCT
>Chrysemys-novel-16-3p
ATTAGGGGCAACATCTGGGCTA

>Chrysemys-novel-19_pre
CTGCAGGCCAGATTCTGCCCTCATTTATACTTGTGTCTTCAATGGGTTTACACAGGTGGAACCGAGGGCAGAATTTAGCCCTGCAA
>Chrysemys-novel-19-5p

TGCCCTCATTTATACTTGTGT
>Chrysemys-novel-19-3p
ACAGGTGGAACCGAGGGCAG

>Chrysemys-novel-20_pre
TGGGCTGATGTGCAGTGGTGCTGAGAACCTGCAGTTCCCATTAACTTTAGTGAAATCTGGAGATGCTCAGCACTTCTGAACAACAGATCAC
>Chrysemys-novel-20-5p
AGTGGTGCTGAGAACCTGCAGT
>Chrysemys-novel-20-3p
CTGGAGATGCTCAGCACTTCTGA

>Chrysemys-novel-21_pre
AGAGTGTGCGCCCTGATCTTGTAATTGGCTTCACATAGGTGTAAGGGACTGCCTAAGTGGAACCAATTATCGAATCAGTGCCTCAGTACTTA
>Chrysemys-novel-21-5p
CTTGTAATTGGCTTCACATAGGT
>Chrysemys-novel-21-3p
TAAGTGGAACCAATTATCGAAT

>Chrysemys-novel-22_pre
AGGAGTCTGATCCTGCTGACCTTATTCAGACAAAGCTCTTTTTGATTCCAGTAGGATTTTGCCTGAGTAGGGACTGCAGGGTTTGGCCCAC
>Chrysemys-novel-22-5p
GACCTTATTCAGACAAAGCTCT
>Chrysemys-novel-22-3p
ATTTTGCCTGAGTAGGGACTGC

>Chrysemys-novel-24_pre
TCTGGCCTCGGTTACGCTGGTGTAAATCTGGAGTGGATCCCCTGACTTCAGTGGCGTCACTCCGCATTTACATTGCTGTGACTGAGAGCACAAC
>Chrysemys-novel-24-5p
TGGTGTAAATCTGGAGTGGATC
>Chrysemys-novel-24-3p
CGTCACTCCGCATTTACATTGCT

>Chrysemys-novel-25_pre
TTAGGCCATATCCTCAGACAGTGTAAATCGGCATAGCGCTTTTAACTTCAGTGGATCTGTGCTAATTTACATCTGCCGAGGACCTGGCCCAT
>Chrysemys-novel-25-5p
ACAGTGTAAATCGGCATAGCGC
>Chrysemys-novel-25-3p
TCTGTGCTAATTTACATCTGCCG

>Chrysemys-novel-26_pre
CTGCTCTCCTGGCACTCTGCTACACAGCCAGAGCGTCCGTGAGCCACAAGTGGATGTCCCGGCTGTGAGTAGCGTGCAGGGAATGGAGGAAG
>Chrysemys-novel-26-5p
TCTGCTACACAGCCAGAGCGTC
>Chrysemys-novel-26-3p
TGTCCCGGCTGTGAGTAGCGT

>Chrysemys-novel-27_pre
AAGAAGTAACGCTTCCTGCTAGTTCCAGCGCAGTCCAGCATGATTAGAAGGGTACTGGACTGGGCTACAACTAGAAGGAAGTGTTGCTGCTT
>Chrysemys-novel-27-5p
TGCTAGTTCCAGCGCAGTCCAG
>Chrysemys-novel-27-3p
CTGGGCTACAACTAGAAGGAAG

>Chrysemys-novel-29_pre
CTTGGGCCCAGATCCTAAGACGTATTTAGATGCTTAACATTAGATACCTAAATATCTTTCAGGATCTGGGCCCTGA
>Chrysemys-novel-29-5p
AGATCCTAAGACGTATTTAGA

>Chrysemys-novel-29-3p
TAAATATCTTTCAGGATCTGG

>Alligator-let-7a-1_pre
GTGGGATGAGGTAGTAGGTTGTATAGTTTTAGGGTCATACCCACAACTGGGAGATAACTATACAATCTACTGTCTTTCCTAAAGCA
>Alligator-let-7a-1-5p
TGAGGTAGTAGGTTGTATAGTT
>Alligator-let-7a-1-3p
CTATACAATCTACTGTCTTT

>Alligator-let-7a-2_pre
ACTGCATGCATCCAGGTTGAGGTAGTAGGTTGTATAGTTTAGAATGACACCAAGGGAGATAACTGTACAACCTCCTAGCTTTCCTTGGGTCTTGCA
>Alligator-let-7a-2-5p
TGAGGTAGTAGGTTGTATAGTT
>Alligator-let-7a-2-3p
CTGTACAACCTCCTAGCTTTCC

>Alligator-let-7a-3_pre
TCCTTTGGGGTGAGGTAGTAGGTTGTATAGTTTTAGGGTTATACCCTGCCTGTCAGATAACTATACAATCTACTGTCTTTCCTGAAGTGGC
>Alligator-let-7a-3-5p
TGAGGTAGTAGGTTGTATAGTT
>Alligator-let-7a-3-3p
CTATACAATCTACTGTCTTT

>Alligator-let-7a-4_pre
TGGAGGTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGGATTTCATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTGAAGAG
>Alligator-let-7a-4-5p
TGAGGTAGTAGGTTGTATAGTT
>Alligator-let-7a-4-3p
CTATACAGTCTATTGCCTTC

>Alligator-let-7b_pre
GCTCTGGCAGGATGAGGTAGTAGGTTGTGTGGTTTCAGGGTAGTGATTTTGCCCCAATCAGGAGATAACTATACAACCTACTGCCTTCCCTG
>Alligator-let-7b-5p
TGAGGTAGTAGGTTGTGTGGTT
>Alligator-let-7b-3p
CTATACAACCTACTGCCTTCCC

>Alligator-let-7c-1_pre
TGTGTGCATCCGGGTTGAGGTAGTAGGTTGTATGGTTTAGAGTTACACCCTGGGAGTTAACTGTACAACCTTCTAGCTTTCCTTGGAGCACACT
>Alligator-let-7c-1-5p
TGAGGTAGTAGGTTGTATGGTT
>Alligator-let-7c-1-3p
CTGTACAACCTTCTAGCTTTCC

>Alligator-let-7c-2_pre
GGGTGGGGGCCGGGGTGAGGTAGTAGGTTGTATGGTTTAGAGTCACACCCCCGGAGATAACTGTACAGCCTCCTAGCTTTCCCCGCGCCCCCCCA
>Alligator-let-7c-2-5p
TGAGGTAGTAGGTTGTATGGTT
>Alligator-let-7c-2-3p
CTGTACAGCCTCCTAGCTTTCC

>Alligator-let-7d_pre
TAGGAAGAGGTAGTAGGTTGCATAGTTTTAGGGCAGGGATTTTGCTCACACGGAGTTAACTATACAACCTGCTGCCTTTCTTAGGGC
>Alligator-let-7d-5p
AGAGGTAGTAGGTTGCATAG
>Alligator-let-7d-3p
CTATACAACCTGCTGCCTTTC

>Alligator-let-7e_pre

GTCCTTGAGGCTGAGGTAGTAGATTGAATAGTTGTGGAGTCCTACCCTCCCTTTGAGCTAACTATACAATCTACTGTCTTTCCTAAGGAGAC
>Alligator-let-7e-5p
TGAGGTAGTAGATTGAATAGTT
>Alligator-let-7e-3p
CTATACAATCTACTGTCTTT

>Alligator-let-7f-1_pre
CCGGGCGGCGTGGGCTGAGGTAGTAGATTGTATAGTTCTGGGTCACACCCGCGCGGAGATAACTATACAGCCTACTGTCTTTCCTGCGCTGTTCCC
>Alligator-let-7f-1-5p
TGAGGTAGTAGATTGTATAGT

>Alligator-let-7f-2_pre
TATCAGAGTGAGGTAGTAGATTGTATAGTTGTGGGGTAGTTATTTTACCCTGTTCAGGAGATAACTATACAATCTATTGCCTTCCCTGAGGA
>Alligator-let-7f-2-5p
TGAGGTAGTAGATTGTATAGT
>Alligator-let-7f-2-3p
CTATACAATCTATTGCCTTCC

>Alligator-let-7g_pre
GCCTGATTCCAAGCTGAGGTAGTAGTTTGTACAGTTTGAGGGTCTATGATACCACCCGGTACAGGAGATTAACTGTACAGGCCACTGCCTTGCCTG
>Alligator-let-7g-5p
TGAGGTAGTAGTTTGTACAGTT
>Alligator-let-7g-3p
CTGTACAGGCCACTGCCTTGCT

>Alligator-let-7i_pre
CGGTCCTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACACTGCCCGCTGTGGAGATAACTGCGCAAGCTACTGCCTTGCTAGTGCG
>Alligator-let-7i-5p
TGAGGTAGTAGTTTGTGCTGTA
>Alligator-let-7i-3p
CTGCGCAAGCTACTGCCTTGCTT

>Alligator-mir-1a-1_pre
GAAACTACCTGCTTGAGAGACATACTTCTTTATATGCCCATATGAACCTGGCAAGCTATGGAATGTAAAGAAGTATGTATTTCAGGTGGGGATCAT
>Alligator-mir-1a-1-3p
TGGAATGTAAAGAAGTATGTA
>Alligator-mir-1a-1-5p
ACATACTTCTTTATATGCCCATAT

>Alligator-mir-1a-2_pre
ACCTGCCCAGAGTACATACTTCTTTATGTACCCATATGAACATACAATGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAGGCAC
>Alligator-mir-1a-2-3p
TGGAATGTAAAGAAGTATGTAT
>Alligator-mir-1a-2-5p
ACATACTTCTTTATGTACCCATA

>Alligator-mir-1b_pre
TCCCTCCCAACCCTACATACTTCTTCATATGCCCATATGGAGTCGGCTGGTATTATGGAATGTTAAGAAGTATGTATCTTTGGGCTGGGAC
>Alligator-mir-1b-3p
TGGAATGTTAAGAAGTATGTAT
>Alligator-mir-1b-5p
TACATACTTCTTCATATGCCCA

>Alligator-mir-7a-1_pre
TGGTCTAGTTCTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAATCGACAACAAATCGCAGTCTGCCATATGGCACAGACCA
>Alligator-mir-7a-1-5p
TGGAAGACTAGTGATTTTGTTGT

>Alligator-mir-7a-1-3p
AACAAATCGCAGTCTGCCATAT

>Alligator-mir-7a-2_pre
CCTGACCCTGTATGGAAGACTAGTGATTTTGTTGTTCTATGGCTCATCTCACGACAACAAGTCACAGTCTGCCTTATGGTGCATGGCCT
>Alligator-mir-7a-2-5p
TGGAAGACTAGTGATTTTGTTGT
>Alligator-mir-7a-2-3p
CAACAAGTCACAGTCTGCCTTT

>Alligator-mir-7a-3_pre
GTCGTCTGGCTCTGCGTGGAAGACTAGTGATTTTGTTGTTCTGACTTATAAAGGTGACAACAAATCATAGCCTGCCATACAGCACAGACTCGCA
>Alligator-mir-7a-3-5p
TGGAAGACTAGTGATTTTGTTGT

>Alligator-mir-7b_pre
GCCTGGGTCGGTCTGGAAGACTTGTGATTTTGTTGTTTCTGGTGTCAAGGAAGCGAACAACAAATCCCAGTCTCCTCACAGCCCCAGGGCCAGTC
>Alligator-mir-7b-5p
TGGAAGACTTGTGATTTTGTTGTT

>Alligator-mir-9-1_pre
GGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCAATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCAT
>Alligator-mir-9-1-5p
TCTTTGGTTATCTAGCTGTATG
>Alligator-mir-9-1-3p
TAAAGCTAGATAACCGAAAGT

>Alligator-mir-9-2_pre
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>Alligator-mir-9-2-5p
TCTTTGGTTATCTAGCTGTATG
>Alligator-mir-9-2-3p
TAAAGCTAGATAACCGAAAGT

>Alligator-mir-9-3_pre
AGGGCTGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTCTCGAGCCGTCATAAAGCTAGATAACCGAAAGTAGAAATGACTT
>Alligator-mir-9-3-5p
TCTTTGGTTATCTAGCTGTATG
>Alligator-mir-9-3-3p
TAAAGCTAGATAACCGAAAGT

>Alligator-mir-9-4_pre
GTGGGTTTTTGTCTTTGGTTATCTAGCTGTATGAGTGTATGTGATATCATAAAGCTAGACAACCGAATGTAAAAACCGGCTCGC
>Alligator-mir-9-4-5p
TCTTTGGTTATCTAGCTGTATG
>Alligator-mir-9-4-3p
TAAAGCTAGACAACCGAATGT

>Alligator-mir-10a_pre
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>Alligator-mir-10a-5p
TACCCTGTAGATCCGAATTTGTG
>Alligator-mir-10a-3p
ACAAATTCGTATCTAGGGGAAT

>Alligator-mir-10b_pre
CGTTGTCTATATATACCCTGTAGAACCGAATTTGTGTGGTATTCACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATGC

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>Alligator-mir-10b-5p
TACCCTGTAGAACCGAATTTGT
>Alligator-mir-10b-3p
ACAGATTCGATTCTAGGGGAAT

>Alligator-mir-10c_pre
CACAGTCGCCTATATGTACCCTGTAGAATCGAATTTGTGTGAACATTTCAGAGTCACAAATTCGTCTCTAGGGGAATATATGGACGATGC
>Alligator-mir-10c-5p
ACCCTGTAGAATCGAATTTGTG
>Alligator-mir-10c-3p
ACAAATTCGTCTCTAGGGGAA

>Alligator-mir-15a_pre
TACCTTGGCCTAACGTAGCAGCACATAATGGTTTGTGGATTTTGAAAAGGTGCAGGCCATATTGTGCTGCCTCAAAAATAC
>Alligator-mir-15a-5p
TAGCAGCACATAATGGTTTGTG
>Alligator-mir-15a-3p
CAGGCCATATTGTGCTGCCTC

>Alligator-mir-15b_pre
ACCTTAAATTACTCTAGCAGCACATCATGGTTTGCATGATCTTGTAAAGATGCTAATCATTATTTGCTGCTTTAGGAATTTAAGGA
>Alligator-mir-15b-5p
TAGCAGCACATCATGGTTTGCA
>Alligator-mir-15b-3p
CTAATCATTATTTGCTGCTTT

>Alligator-mir-15c_pre
CTTTGAGGAGATGTAGCAGCACATCATGGTTTGTAGGGACAAGGAGATACAGACCATTCTGGGCTGCCTCATTACCTCAAGG
>Alligator-mir-15c-5p
TAGCAGCACATCATGGTTTGTA
>Alligator-mir-15c-3p
CAGACCATTCTGGGCTGCCTCATT

>Alligator-mir-16a-1_pre
ATGTCAATCGTACCTTAGCAGCACGTAAATATTGGTGTTAAGATTCTGTAAATATCTCCAGTATTAACTGTGCTGCTGAAGTAAGTTTGGCCT
>Alligator-mir-16a-1-5p
TAGCAGCACGTAAATATTGGTG
>Alligator-mir-16a-1-3p
CCAGTATTAACTGTGCTGCTGA

>Alligator-mir-16a-2_pre
CTATACTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTATAAAAGTAAATCAAACCCCAATATTATTGTGCTGCTTAAGCGTGGCAGA
>Alligator-mir-16a-2-5p
TAGCAGCACGTAAATATTGGTG
>Alligator-mir-16a-2-3p
CCAATATTATTGTGCTGCTTAA

>Alligator-mir-16b_pre
TCAGCAGTGCTCTAGCAGCACGTAAATACTGGAGTCGAGGACTGCCTGGCTGCTCTCCAGTATTGCATTGCTGCTTGAGTGAGGCTGG
>Alligator-mir-16b-5p
TAGCAGCACGTAAATACTGGAG
>Alligator-mir-16b-3p
TCTCCAGTATTGCATTGCTGCT

>Alligator-mir-17_pre
GTCAGAGTAATGTCAAAGTGCTTACAGTGCAGGTAGTGATATATAGAACCTACTGCAGTGAAGGCACTTGTAGCATTATAGTGACAA
>Alligator-mir-17-5p
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CAAAGTGCTTACAGTGCAGGTAGA
>Alligator-mir-17-3p
CTGCAGTGAAGGCACTTGTAGC

>Alligator-mir-18_pre
GCTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCCCTAAGTGCTCCTTCTGGCATAAGAAGTT
>Alligator-mir-18-5p
TAAGGTGCATCTAGTGCAGATAG
>Alligator-mir-18-3p
ACTGCCCTAAGTGCTCCTTCTG

>Alligator-mir-19a_pre
TGCAGACTTCTGTTAGTTTTGCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCCTGCT
>Alligator-mir-19a-5p
TGTGCAAATCTATGCAAAACTG

>Alligator-mir-19b_pre
CACTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTATGATACTCTGCTGTGCAAATCCATGCAAAACTGACTGTGGCAGTG
>Alligator-mir-19b-3p
TGTGCAAATCCATGCAAAACTG
>Alligator-mir-19b-5p
AGTTTTGCAGGTTTGCATCCAGC

>Alligator-mir-20a_pre
GCTCCTGTAGTACTAAAGTGCTTATAGTGCAGGTAGTGTTCAGGAATCTACTGCATTATGAGCACTTAAAGTACTGCTAGC
>Alligator-mir-20a-5p
TAAAGTGCTTATAGTGCAGGTAG
>Alligator-mir-20a-3p
ACTGCATTATGAGCACTTAAAGT

>Alligator-mir-21_pre
CCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATGTCATGGCAACAACAGTCGGTAGGCTGTCTGACATTTT
>Alligator-mir-21-5p
TAGCTTATCAGACTGATGTTGAC
>Alligator-mir-21-3p
CAACAACAGTCGGTAGGCTGTC

>Alligator-mir-23a_pre
TGCCACAGCCAGCTGGGGTTCCTGGTGATGCGATTTTTTTACCCACTGCCCAAAATCACATTGCCAGGGATTTCCAACTGGCTGCGAGCCC
>Alligator-mir-23a-3p
ATCACATTGCCAGGGATTTCCA

>Alligator-mir-23b_pre
CCCAGTGTTGTGGCTGTTTGGGTTCCTGGCATGCTGATTTGTGACTTAAAATTAAAATCACATTGCCAGGGATTACCACAGAGCCATGACCATGGC
>Alligator-mir-23b-3p
ATCACATTGCCAGGGATTACCAC
>Alligator-mir-23b-5p
GGGTTCCTGGCATGCTGATTT

>Alligator-mir-24-1_pre
TGGATGGACCCGTCCTCCAGTGCCTACTGAGCTGATATCAGTTCTGATTTTACATACTGGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCCA
>Alligator-mir-24-1-3p
TGGCTCAGTTCAGCAGGAACAG
>Alligator-mir-24-1-5p
AGTGCCTACTGAGCTGATATCAGT

>Alligator-mir-24-2_pre

TCTGGGCCCTGCCTCCGGTGCCTACTGAGCTGATACTCAGTTGCTTTGGTTTAAACTGGCTCAGTTCAGCAGGAACAGGAGTCTGGCTCCAGCT
>Alligator-mir-24-2-3p
TGGCTCAGTTCAGCAGGAACAG
>Alligator-mir-24-2-5p
GTGCCTACTGAGCTGATACTCA

>Alligator-mir-26-1_pre
AAGGCTGTTACCTGGTTCAAGTAATCCAGGATAGGCTGTATGCATTGCAGTTGGCCTATTCTTGATTACTTGCACTGGGAGACAGCCACA
>Alligator-mir-26-1-5p
TTCAAGTAATCCAGGATAGGCT
>Alligator-mir-26-1-3p
CCTATTCTTGATTACTTGCACT

>Alligator-mir-26-2_pre
CATGGGGTCACGGCCCGGTTCAAGTAATCCAGGATAGGCTGGTGCCAGGCCCGTGGCCTATTCTCGATTACTTGTCTCGGGACGTGGCTGCTGGCA
>Alligator-mir-26-2-5p
TTCAAGTAATCCAGGATAGGCT
>Alligator-mir-26-2-3p
CCTATTCTCGATTACTTGTCTT

>Alligator-mir-27a_pre
GAAGCCAGGGCACAGGGCTTAGCTCACCTGTGAACAGAGTTAGCGTTGCATCATGTTCACAGTGGCTAAGTTCCGCCTCCTGGTGTCTA
>Alligator-mir-27a-3p
TTCACAGTGGCTAAGTTCCGC
>Alligator-mir-27a-5p
AGGGCTTAGCTCACCTGTGAACA

>Alligator-mir-27b_pre
CCTCTCTGACAAGGTGCAGAGCTTAGCTGATTGGTGAACAGTGATTGATTTCCCCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAGAAGGTG
>Alligator-mir-27b-3p
TTCACAGTGGCTAAGTTCTG
>Alligator-mir-27b-5p
AGAGCTTAGCTGATTGGTGAAC

>Alligator-mir-29a-1_pre
CCCTTTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCCATACTATTTTCTAGCACCATTTGAAATCGGTTATAGTGATTGGGGAA
>Alligator-mir-29a-1-3p
TAGCACCATTTGAAATCGGTTA
>Alligator-mir-29a-1-5p
ACTGATTTCTTTTGGTGTTCAGA

>Alligator-mir-29a-2_pre
TCTCTTACACAGGCTGACCGATTTCTCTTGGTGTTCAGAGTCTCAGTGTTTGTCTAGCACCATTTGAAATCGGTTATGATGTAGGGGGA
>Alligator-mir-29a-2-3p
TAGCACCATTTGAAATCGGTTA
>Alligator-mir-29a-2-5p
TGACCGATTTCTCTTGGTGTTCAG

>Alligator-mir-29b-1_pre
CTCCTTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTAACTACTTATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAGGAAGAAT
>Alligator-mir-29b-1-5p
NTGGTTTCATATGGTGGTTTAGA
>Alligator-mir-29b-1-3p
TAGCACCATTTGAAATCAGTG

>Alligator-mir-29b-2_pre
TGAGTCTTCCTCTGGAAGCTGGTTTCACATGGTGGCTTAGATTTTCCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGGGCAAGAAT

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>Alligator-mir-29b-2-5p
CTGGTTTCACATGGTGGCTTAGA
>Alligator-mir-29b-2-3p
TAGCACCATTTGAAATCAGTG

>Alligator-mir-30a_pre
CTGTTGACAGTGAGCGACTGTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGGGCTTTCAGTCGGATGTTTGCAGCTGCCAACTGCCACA
>Alligator-mir-30a-5p
TGTAAACATCCTCGACTGGAAGCT
>Alligator-mir-30a-3p
CTTTCAGTCGGATGTTTGCAGC

>Alligator-mir-30b_pre
ACTGACTTTTAGTTCATGTAAACATCCTACACTCAGCTATAACAACTGGAACGGCTGGGAGGTGGATGTTTACTTCAACTGATTTGAAAAGG
>Alligator-mir-30b-5p
TGTAAACATCCTACACTCAGCT
>Alligator-mir-30b-3p
CTGGGAGGTGGATGTTTACTTC

>Alligator-mir-30c-1_pre
ATCTACCATGCCGTAGCATGTGTAAACATCCTACACTCTCAGCTGTGAACTCAAGGTGGCTGGGAGAGGGTTGTTTACGCCTTCTGCCATGGTCTG
>Alligator-mir-30c-1-5p
TGTAAACATCCTACACTCTCAGC
>Alligator-mir-30c-1-3p
TGGGAGAGGGTTGTTTACGCC

>Alligator-mir-30c-2_pre
GCTCTGAGTGACAGGTATTGTAAACATCCTACACTCTCAGCTGTGGAAAATGAGGAAGCTGGGAGAAGGCTGTTTACTCTCCCTGNCTTAGATAGC
>Alligator-mir-30c-2-5p
TGTAAACATCCTACACTCTCAGC
>Alligator-mir-30c-2-3p
TGGGAGAAGGCTGTTTACTCT

>Alligator-mir-30d_pre
ATGGGAGTCTGTTGTTGTAAACATCCCCGACTGGAAGCTGTAAGAGAAATTCTAGCTTTCAGTCAGATGTTTGCTGCCACTGGCTACT
>Alligator-mir-30d-5p
TGTAAACATCCCCGACTGGAAGCT
>Alligator-mir-30d-3p
CTTTCAGTCAGATGTTTGCTG

>Alligator-mir-30e_pre
CCTGGGCAGTCGATGCTACTGTAAACATCCTTGACTGGAAGCTGTAAGGTGCTAGAAGGAGCTTTCAGTCGGATGTTTACAGCGGCAGGCTGCCAC
>Alligator-mir-30e-5p
TGTAAACATCCTTGACTGGAAGCT
>Alligator-mir-30e-3p
CTTTCAGTCGGATGTTTACAGC

>Alligator-mir-31_pre
CAGAGCTAGAGAGGAGGCAAGATGTTGGCATAGCTGTTGACCTAAGAACCTGCTATGCCAACATCTTGTCATCTTTCTTGTCTAC
>Alligator-mir-31-5p
AGGCAAGATGTTGGCATAGCTG
>Alligator-mir-31-3p
TGCTATGCCAACATCTTGTCAT

>Alligator-mir-32_pre
TGCTTGCTCTGGTGGATATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAGTGCAATTTAGTGTGTGCGATATTTTCACATGAGTGCAT
>Alligator-mir-32-5p
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TATTGCACATTACTAAGTTGCA
>Alligator-mir-32-3p
CAATTTAGTGTGTGCGATATT

>Alligator-mir-33-1_pre
GGGTGACCGCTGTAGTGCATTGTAGTTGCATTGCATGTTCTGGTAGTATCTGTGCAATGTTTCTGCAGTGCAGTATAGAGGCACTCT
>Alligator-mir-33-1-5p
GTGCATTGTAGTTGCATTGCA
>Alligator-mir-33-1-3p
CAATGTTTCTGCAGTGCAGTA

>Alligator-mir-33-2_pre
GCAGTGGCCTCAGCTGTGGTGCATTGTAGTTGCATTGCATGTGTCACAGAGGTGTGCAATGCCTCTGCAGTGCAGCCCAGAGGAGGCTCCTCCCAG
>Alligator-mir-33-2-5p
GTGCATTGTAGTTGCATTGCA
>Alligator-mir-33-2-3p
CAATGCCTCTGCAGTGCAGCT

>Alligator-mir-34a_pre
TGTGAGTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAACAATAGACAAGGAAGCAATCAGCAAGTATACTGCCCTAGAAGTGCTGCACA
>Alligator-mir-34a-5p
TGGCAGTGTCTTAGCTGGTTGTT
>Alligator-mir-34a-3p
GCAATCAGCAAGTATACTGCCCT

>Alligator-mir-34b_pre
AGTAGTGTTTGGTTTGTAGGCAGTGTAGTTAGCTGATTGTGTCAGTCCCTTGGCAATCACTAACTTCACTGCCATCAAAACAAGGCACAGAAT
>Alligator-mir-34b-5p
AGGCAGTGTAGTTAGCTGATTG
>Alligator-mir-34b-3p
AATCACTAACTTCACTGCCATC

>Alligator-mir-34c_pre
TACCTCAGCCTAGTTGCTAGGCAGTGTAGTTAGCTGATTGCAAAAGGCAACAATCACTAACCACACAGCCAGGTAAAAAGGTCTGTCTTGCA
>Alligator-mir-34c-5p
AGGCAGTGTAGTTAGCTGATTG
>Alligator-mir-34c-3p
AATCACTAACCACACAGCCAG

>Alligator-mir-92a_pre
ACCCCTTTCTACACAGGTTGGGATCAGTTGCAATGCTGTGTGTGTCTGTGGTATTGCACTTGTCCCGGCCTGTTGAGGTTGGTGGGGATA
>Alligator-mir-92a-3p
TATTGCACTTGTCCCGGCCTGT
>Alligator-mir-92a-5p
AGGTTGGGATCAGTTGCAATGCT

>Alligator-mir-92b_pre (incomplete)
TCCGGGGCGGCGGGAGGGCCGGGATGCGGTGCAGTGTTGTGCGTCTCCTACCAATATTGCACT
>Alligator-mir-92b-3p
AGGGCCGGGATGCGGTGCAGTGTT

>Alligator-mir-93_pre
CTTGAGCTGCGGTGGCTCCAAAGTGCTGTTCGTGCAGGTAGTGTGTGCAGCCATCTACTGCCGGGCAGCACTTCCCGAGCCCCCGCAGCCG
>Alligator-mir-93-5p
CAAAGTGCTGTTCGTGCAGGTAG
>Alligator-mir-93-3p
TACTGCCGGGCAGCACTTCCC

>Alligator-mir-96_pre
GTTCTCTGCTTGGCCCATTTTGGCACTAGCACATTTTTGCTTTTGTACGTATACTTTGAGCAATTATGTGTAGTGCCAATATGGGAGGAGATGGAC
>Alligator-mir-96-5p
TTTGGCACTAGCACATTTTTGCT
>Alligator-mir-96-3p
CAATTATGTGTAGTGCCAATAT

>Alligator-mir-98_pre
GGGTGAGGTAGTAAGTTGTATCGTTGGGGGGTCGGGATTGGAGCCCCGGTGTCGAGGTAACTATACAACTTACTACTTTCCCT
>Alligator-mir-98-5p
TGAGGTAGTAAGTTGTATCGTT
>Alligator-mir-98-3p
CTATACAACTTACTACTTTCC

>Alligator-mir-99a_pre
GTGCCAGTTGGCATAAACCCGTAGATCCGATCTTGTGGTAAAATACACCACACAAGCTCGCTTCTATGGGTCTGTGTCAGTGTGGTTATC
>Alligator-mir-99a-5p
AACCCGTAGATCCGATCTTGTG
>Alligator-mir-99a-3p
CAAGCTCGCTTCTATGGGTCTG

>Alligator-mir-99b_pre
GCCTGCCGGTCGCCATAAACCCGTAGATCCGAACTTGCGGTCGCTCCTCGTGCAAGCTCGACTCTGTGGGTCTGTGTCGGCCTCGGCCT
>Alligator-mir-99b-5p
AACCCGTAGATCCGAACTTGCG
>Alligator-mir-99b-3p
CAAGCTCGACTCTGTGGGTCTG

>Alligator-mir-100_pre
TGCCCGTTGCCACAAACCCGTAGATCCGAACTTGTGGTGATATTCCACACAAGCTTGTATCTATAGGTATGTGTCTTCATGGCAAG
>Alligator-mir-100-5p
AACCCGTAGATCCGAACTTGTG
>Alligator-mir-100-3p
CAAGCTTGTATCTATAGGTATG

>Alligator-mir-101-1_pre
ACAGGCTGCCCTGGCTCAGTTATCACAGTGCTGATGCTGTCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGCAGCCATCTTAGCTT
>Alligator-mir-101-1-3p
TACAGTACTGTGATAACTGAAG
>Alligator-mir-101-1-5p
TCAGTTATCACAGTGCTGATGCT

>Alligator-mir-101-2_pre
CATGAACTGTCCTTTTTCGGTTATCATGGTACCGGTGCTGTATACGTGAAAGGTACAGTACTGTGATAACTGAAGAATGATGGTGCCATCACA
>Alligator-mir-101-2-3p
TACAGTACTGTGATAACTGAAG
>Alligator-mir-101-2-5p
TCGGTTATCATGGTACCGGTGCT

>Alligator-mir-103_pre
TGTAATATCTCATTGTCTTTGGCTTCTTTACAGTGCTGCCTTGTTGCATATGGATCAAGCAGCATTGTACAGGGCTATGAAGACAATGAGTCTTGC
>Alligator-mir-103-3p
AGCAGCATTGTACAGGGCTATG

>Alligator-mir-106_pre
ATCCCAGGGCTAAAGTGCTTGCAGTGCAGGTAGCTGGCGCTGGCGCTACTGCAGTGTGGGGGCTTGCAGCTCTGGGGA

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>Alligator-mir-106-5p (predicted)
TAAAGTGCTTGCAGTGCAGGT

>Alligator-mir-107_pre
GTATTCTCTTTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTGCATTTATGTCAAGCAGCATTGTACAGGGCTATCAAAGCGGAGAGAGCTGCA
>Alligator-mir-107-3p
AGCAGCATTGTACAGGGCTATG
>Alligator-mir-107-5p
AGCTTCTTTACAGTGCTGCCTTG

>Alligator-mir-122_pre
TACTATCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCCAATCTATCAAACGCCATTATCACACTAAATAGCTACTGTTAGATA
>Alligator-mir-122-5p
TGGAGTGTGACAATGGTGTTTG
>Alligator-mir-122-3p
AACGCCATTATCACACTAAA

>Alligator-mir-124-1_pre
GGCCCCGCGGCCCCTCTCTGCGTGTTCACAGCGGACCTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAACGGGGCCGCCTC
>Alligator-mir-124-2_pre
TTCCCGGGGCTCTCGCCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGGCACGCGGTGAATGCCAAGAGCGGAGCCGGAAG
>Alligator-mir-124-3_pre
CCAGGCGAGCCCCTCTCTGCGTGTTCACAGCGGACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGAGCCTCACAGC
>Alligator-mir-124-4_pre
TCCGGACCGCGGCCTCGGCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCACACAATTAAGGCACGCGGTGAATGCCAAGAGAGGGGCCGCCC
>Alligator-mir-124-3p
TAAGGCACGCGGTGAATGCCA
>Alligator-mir-124-5p
CGTGTTCACAGCGGACCTTGAT

>Alligator-mir-125a_pre
CTAGGCCTCCCTCTCGGTCCCTGAGACCCTTATCCTGTGAGGGAGCCCAGAGCTCACAGGTGAGGCCTTGGGAACTGGGCGGGTGGCCCCCCCAC
>Alligator-mir-125a-5p
TCCCTGAGACCCTTATCCTGTG

>Alligator-mir-125b-1_pre
TTTGTGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTTTTAAATCCACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCTTTGG
>Alligator-mir-125b-1-5p
TCCCTGAGACCCTAACTTGTGA
>Alligator-mir-125b-1-3p
ACGGGTTAGGCTCTTGGGAGCT

>Alligator-mir-125b-2_pre
GGACTTTTCCTAGTCCCTGAGACCCTAACTTGTGAGGTTTTTTAGCAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAGGGGAACCAGC
>Alligator-mir-125b-2-5p
TCCCTGAGACCCTAACTTGTGA
>Alligator-mir-125b-2-3p
ACAAGTCAGGCTCTTGGGAC

>Alligator-mir-126_pre
CGGCCCATTATTACTTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCTGCGGCCAGCACC
>Alligator-mir-126-3p
TCGTACCGTGAGTAATAATGCG
>Alligator-mir-126-5p
CATTATTACTTTTGGTACGCG

>Alligator-mir-128-1_pre
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CATGAGCTGTTGGATTCGGGGCCGTAACACTGTCTGAGAGGGTTACATTTCTCACAGTGAACCGGTCTCTTTTTCAGCTGCTTCCTG
>Alligator-mir-128-1-3p
TCACAGTGAACCGGTCTCTTT
>Alligator-mir-128-1-5p
CGGGGCCGTAACACTGTCTGAGA

>Alligator-mir-128-2_pre
TGTGCAGTTGGAAGGGGGGCCGTTACACTGTAAGAGAGTGAGTAGCAGGTCTCACAGTGAACCGGTCTCTTTTCCTACTGTGTCGTGT
>Alligator-mir-128-2-3p
TCACAGTGAACCGGTCTCTTT
>Alligator-mir-128-2-5p
GGGGGCCGTTACACTGTAAGAGA

>Alligator-mir-129a_pre
GTCCCTCTCAGATCTTTTTGCGGTCTGGGCTTGCTGTTCCTCCAACCCACACTCAGGAAGCCCTTACCCCAAAAAGTATCCGCGGGGG
>Alligator-mir-129a-3p
AAGCCCTTACCCCAAAAAGTAT
>Alligator-mir-129a-5p
CTTTTTGCGGTCTGGGCTTGC

>Alligator-mir-129b_pre
CTTCGCGAATCTTTTTGCGGTCTGGGCTTGCTGTACATAACTACCTAGCCGGGAAGCCCTTACCCCAAAAAGCATTCGCGGAG
>Alligator-mir-129b-3p
AAGCCCTTACCCCAAAAAGCAT
>Alligator-mir-129b-5p
CTTTTTGCGGTCTGGGCTTGC

>Alligator-mir-130a_pre
CAGGCCCCTGTCCAAGGCTCTTTTCACATTGTACTACTGTATGAGCCCCTGCCAAGCAATGCAATGTAAAAAGGGCATTGGGTAGGTGGTCCC
>Alligator-mir-130a-3p (predicted)
CAATGCAATGTAAAAAGGGCAT

>Alligator-mir-130b_pre
GTATGCTGTTGTCCAGAGCCCTTTTTCTGTTGTACTACTGGCAATTATGATGAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGAAACATGACC
>Alligator-mir-130b-3p
CAGTGCAATATTAAAAGGGCAT
>Alligator-mir-130b-5p
GCCCTTTTTCTGTTGTACTAT

>Alligator-mir-130c_pre
GCATAGTGTCTGTCCAGTGCCCTTTTTATGTTGTACTACTAGTGATCGTGCACAAAAAGCAGTGCAATGTTAAAAGGGCATTGGCCAGCAATACTG
>Alligator-mir-130c-3p
AGTGCAATGTTAAAAGGGCATT

>Alligator-mir-132_pre
ACGTCGCCAGGGCAACCGTGGCTTTAGATTGTTACTGTGTGGTGCGTGGGTAACAGTCTACAGCCATGGTCGCTGGGCCGGACGC
>Alligator-mir-132-3p
TAACAGTCTACAGCCATGGTCG
>Alligator-mir-132-5p
ACCGTGGCTTTAGATTGTTAC

>Alligator-mir-133a-1_pre
CCAATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTGAT
>Alligator-mir-133a-1-3p
TTTGGTCCCCTTCAACCAGCTG
>Alligator-mir-133a-1-5p
AGCTGGTAAAATGGAACCAAAT

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>Alligator-mir-133a-2_pre
CCAAATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGTAGCTGTGCATTGATCAC
>Alligator-mir-133a-2-3p
TTTGGTCCCCTTCAACCAGCTG
>Alligator-mir-133a-2-5p
AGCTGGTAAAATGGAACCAAAT

>Alligator-mir-133a-3_pre
AGTGTGTTCCTGGGGCTGGTAAAAAGGAACCAGATCAACTTGGAACTGGATTTGGTCCCCTTCAACCAGCTGTAGTGGCACATAAA
>Alligator-mir-133a-3-3p
TTTGGTCCCCTTCAACCAGCTG

>Alligator-mir-133b_pre
AGCTGCACTCTGCTGTGGCTGGTCAAACGGAACCAAGTCCGTCTTCCTTGGAGGTTTGGTCCCCTTCAACCAGCTATAGCAGTGCTGA
>Alligator-mir-133b-3p
TTTGGTCCCCTTCAACCAGCTA

>Alligator-mir-135-1_pre
TCCCACTGTGTTATATGGCTTTTTATTCCTATGTGATTATACTACTCCTTTCATATAGGGATTGAAGCCGTGCAATACGCTGGGG
>Alligator-mir-135-1-5p
TATGGCTTTTTATTCCTATGTG
>Alligator-mir-135-1-3p
ATATAGGGATTGAAGCCGTGC

>Alligator-mir-135-2_pre
TAAATTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCTCATGTAGGGATGGAAGCCATGAAATACATTGTGAAAAA
>Alligator-mir-135-2-5p
TATGGCTTTTTATTCCTATGTG
>Alligator-mir-135-2-3p
ATGTAGGGATGGAAGCCATGAA

>Alligator-mir-135-3_pre
CCCTCTGCTGTGGTCTATGGCTTTTTATTCCTATGTGATTGCTTTTCCTAACTCATGTAGGGCTAAAAGCCATGGGCTACACAGAGGAT
>Alligator-mir-135-3-5p
TATGGCTTTTTATTCCTATGTG
>Alligator-mir-135-3-3p
ATGTAGGGCTAAAAGCCATGG

>Alligator-mir-137a_pre
TCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACGGATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCGCGGC
>Alligator-mir-137a-3p
TTATTGCTTAAGAATACGCGTA

>Alligator-mir-137b_pre
CAGCTCCCTTCGATGACGGGTATTCTTGGGTAGATAATACGGCTGGCGTTGTTATTGCTTGAGAATACGCGTAGTCGAGGGGAGA
>Alligator-mir-137b-3p
TTATTGCTTGAGAATACGCGTA

>Alligator-mir-138-1_pre
TCTGGATGGTACAGTGCTGCAGCTGGTGTTGTGAATCAGGCCGTCACCGATCAGAGAACGGCTACTTCACAACACCAGGGTTGCACCCTACCACAG
>Alligator-mir-138-1-5p
AGCTGGTGTTGTGAATCAGGC
>Alligator-mir-138-1-3p
GCTACTTCACAACACCAGGGT

>Alligator-mir-138-2_pre
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GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACAACAAGCGCATCCTACTATCCGGCTATTTCACTACACCAGGGTTGCATCATACCAC
>Alligator-mir-138-2-5p
AGCTGGTGTTGTGAATCAGGC
>Alligator-mir-138-2-3p
CTATTTCACTACACCAGGGTTA

>Alligator-mir-139_pre
AGGCCTGGCTGTATTCTACAGTGCATGTGTCTCCAGTGTTTCTAAGCGACTGGAGATACAGCCCTGTCGGAATAACAGCCAGCGCCAA
>Alligator-mir-139-5p
TCTACAGTGCATGTGTCTCCA
>Alligator-mir-139-3p
TGGAGATACAGCCCTGTCGGA

>Alligator-mir-140_pre
GCTCTCTCTCTGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACGTCATGCTGTTCTACCACAGGGTAGAACCACGGACGGGATACCGGGGCG
>Alligator-mir-140-3p
ACCACAGGGTAGAACCACGGA
>Alligator-mir-140-5p
CAGTGGTTTTACCCTATGGTAG

>Alligator-mir-142-1_pre
GACAGTGCAGTCACCCATAAAGTAGAAAGCACTACTAAACAGCACTGCAGGGTGTAGTGTTTCCTACTTTATGGATGAGTGTACTGT
>Alligator-mir-142-1-3p
TGTAGTGTTTCCTACTTTATGGA
>Alligator-mir-142-1-5p
CATAAAGTAGAAAGCACTACTA

>Alligator-mir-142-2_pre
CGGTGACAGTCTCCCCCCCCCATAAAGTAGCGAGCACGACTCCGCCCCCGCGCCCGTGTAGTGTTTCCTACTTTATGGAGGGGGTGGCTGGGAG
>Alligator-mir-142-2-3p
TGTAGTGTTTCCTACTTTATGGA
>Alligator-mir-142-5p
CATAAAGTAGCGAGCACGACT

>Alligator-mir-143_pre
ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCAGTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAAC
>Alligator-mir-143-3p
TGAGATGAAGCACTGTAGCTC
>Alligator-mir-143-5p
GGTGCAGTGCTGCATCTCTGG

>Alligator-mir-144_pre
GCGGGGGGCTCTGGGCAGGATATCATCGTATACTGTAAGTCGGCTATGAGACACTACAGTATAGATGATGTACTACCCCGGCCTTTCCCCT
>Alligator-mir-144-5p
GGATATCATCGTATACTGTAAG
>Alligator-mir-144-3p
TACAGTATAGATGATGTACTA

>Alligator-mir-145_pre
TGCTGTGTCCTCAGGGTCCAGTTTTCCCAGGAATCCCTTGGGCACTGTGTTGGGGATTCCTGGAAATACTGTTCTTGGGGCCGTGGCTCAG
>Alligator-mir-145-5p
GTCCAGTTTTCCCAGGAATCC
>Alligator-mir-145-3p
ATTCCTGGAAATACTGTTCTT

>Alligator-mir-146a_pre
ATGTATTCTTGGCTTTGAGAACTGAATTCCATGGGTTGTAATTGAATCTTGAACAGACCCATGGGGCTCAGTTCTTCAGCTTGGATATC

>Alligator-mir-146a-5p
TGAGAACTGAATTCCATGGGT

>Alligator-mir-146b_pre
CGCTCCTTGGCTTTGAGAACTGAATTCCATAGGCTTTAAAAGACAAAAAAAGCCCTATGGATTCAGTTCTGTAGCTGGGCGGCAAA
>Alligator-mir-146b-5p
TGAGAACTGAATTCCATAGGCT
>Alligator-mir-146b-3p
AGCCCTATGGATTCAGTTCTGT

>Alligator-mir-146c_pre
GGCAGTTCCCAGCTCTGAGAACTGAATTCCATGGACTGGTTCCCTCTTCATATCTTCAGTCCATAGTAGTCAGTTCTCTAGCTTGGCTGTATC
>Alligator-mir-146c-5p
TGAGAACTGAATTCCATGGACTG
>Alligator-mir-146c-3p
GTCCATAGTAGTCAGTTCTCT

>Alligator-mir-147_pre
TACTCTATGAATCTAGTGGAATCATTTCTGCACAAACTCGACTATTGAAATCAGTGTGCGGAAATGCTTCTGCTACATTTTTAGGGTCTCCC
>Alligator-mir-147-3p
GTGTGCGGAAATGCTTCTGCT
>Alligator-mir-147-5p
TGGAATCATTTCTGCACAAACT

>Alligator-mir-148b_pre
TTGAGGCGGAGTTCTGTCATACACTCGGACTGTGCTACCTGGGGTCAGTGCATCACAGAACTTTGTCTCGAGCGC
>Alligator-mir-148b-3p
TCAGTGCATCACAGAACTTTG
>Alligator-mir-148b-5p
GAGTTCTGTCATACACTCGGAC

>Alligator-mir-150_pre
CCTTCTCTGCCCCCCACTCTCTCCCAACCCTTGTACCAGTGTCATGTTACTGGAACCCTGGTACAGAGGATGGATGAGAAGGAGGCGTGGGACCCC
>Alligator-mir-150-5p
TCTCCCAACCCTTGTACCAGTG
>Alligator-mir-150-3p
CTGGTACAGAGGATGGATGAGA

>Alligator-mir-152_pre
GTCCTCTCAGCTCAGGTTCTGTGGTACACTTGGACTCGGACTCTGGAGCAGTCAGTGCATGACAGAACTTGGGTTTGGATGGAC
>Alligator-mir-152-3p
TCAGTGCATGACAGAACTTGG
>Alligator-mir-152-5p
AGGTTCTGTGGTACACTTGGAC

>Alligator-mir-153-1_pre
TCTCGCGGCTGCCGGGGGCATTTTTGTGATTTGCAGCTCGTGGTCTGGGTCCAGTTGCATAGTCACAAAAGTGATCGTCGGCGGCCGCGCCTG
>Alligator-mir-153-1-3p
TTGCATAGTCACAAAAGTGATC

>Alligator-mir-153-2_pre
AGCGGTTGCCAGTGTCATTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATTGGAAACTGTGACT
>Alligator-mir-153-2-3p
TTGCATAGTCACAAAAGTGATC
>Alligator-mir-153-3-5p
GTCATTTTTGTGATGTTGCAGCT

>Alligator-mir-155_pre
GTAGGCTGTATGTTGTTAATGCTAATCGTGATAGGGGTTTTACCTCTGACTGACTCCTACATGTTAGCATTAGCACTGTATGATGCCTGTTACC
>Alligator-mir-155-5p
TTAATGCTAATCGTGATAGGG

>Alligator-mir-181a-1_pre
GTGGTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGATTTAAAGTGAAAACCATCGACCGTTGATTGTACCCTCCAGCTAACCATC
>Alligator-mir-181a-1-5p
AACATTCAACGCTGTCGGTGAGT
>Alligator-mir-181a-1-3p
ACCATCGACCGTTGATTGTACC

>Alligator-mir-181a-2_pre
CAGATAGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGAGCATTAGAAAAAAAACCATCGACCGTTGACTGTACCTTGAGGTTTATCACA
>Alligator-mir-181a-2-5p
AACATTCAACGCTGTCGGTGA
>Alligator-mir-181a-2-3p
ACCATCGACCGTTGACTGTACC

>Alligator-mir-181a-3_pre
GATACAAAGGTTTCAGCGAACATTCAACGCTGTCGGTGAGTTTTGGCAGTCAGGTTAAACCATCGACCGTTGAGTGTACCCTGCAACCTTGGTAAC
>Alligator-mir-181a-3-5p
AACATTCAACGCTGTCGGTGAGT
>Alligator-mir-181a-3-3p
ACCATCGACCGTTGAGTGTACCC

>Alligator-mir-181b-1_pre
AAGGTCACAATCAACATTCATTGCTGTCGGTGGGTTTAACTATGCGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCACT
>Alligator-mir-181b-1-5p
AACATTCATTGCTGTCGGTGGGTT
>Alligator-mir-181b-1-3p
CTCACTGAACAATGAATGCAA

>Alligator-mir-181b-2_pre
TGCATCTAATGGCTGCAATCAACATTCATTGCTGTCGGTGGGTTTTAGTTTGTACCAACTCACTGATCAATGAATGCAAACTGCGGACCAGATAGC
>Alligator-mir-181b-2-5p
AACATTCATTGCTGTCGGTGGGTT
>Alligator-mir-181b-2-3p
ACTCACTGATCAATGAATGCA

>Alligator-mir-181b-3_pre
AAAAAGTCACAATCAACATTCATTGCTGTCGGTGGGTTGTGATGCTGAAGGGAAAACTCACGGATCAATGAATGCAACTGTGATTGGAACA
>Alligator-mir-181b-3-5p
AACATTCATTGCTGTCGGTGGGTT
>Alligator-mir-181b-3-3p
CTCACGGATCAATGAATGCAA

>Alligator-mir-182_pre
GGTCCCTCTCGCTGTCTTTGGCAATGGTAGAACTCACACTGGTGAGGTATCAGGATCCGGTGGTTCTAGACTTGCCAACTACCGCCCGAGGGCACA
>Alligator-mir-182-5p
TTTGGCAATGGTAGAACTCACACT
>Alligator-mir-182-3p
TGGTTCTAGACTTGCCAACT

>Alligator-mir-183_pre
ACTCCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACGCTATCAGTGAATTACCATAGGGCCATAAACAGAGCAGAGAA
>Alligator-mir-183-5p

TATGGCACTGGTAGAATTCACT
>Alligator-mir-183-3p
TGAATTACCATAGGGCCATA

>Alligator-mir-184_pre
ACGCCATTCCCATCTCCTTATCACTTTTCCAGCCCAGCTTTCTCATGCTCACTGTTGGACGGAGAACTGATAAGGGTATGTGACTGACACGAG
>Alligator-mir-184-3p
TGGACGGAGAACTGATAAGGGT
>Alligator-mir-184-5p
CCTTATCACTTTTCCAGCCCAGC

>Alligator-mir-187_pre
TGTGAGACCTCCGGCTACAACACAGGACATGGGAGCTTTTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC
>Alligator-mir-187-3p
TCGTGTCTTGTGTTGCAGCCAA
>Alligator-mir-187-5p
GCTACAACACAGGACATGGGAGA

>Alligator-mir-190a_pre
AGGACTCTGTGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCTACAGTGTCCTGCCCT
>Alligator-mir-190a-5p
TGATATGTTTGATATATTAGG
>Alligator-mir-190a-3p
ACTATATATCAAACATATTCCT

>Alligator-mir-190b_pre
GCCCACCTGCCTCTGTCTGATATGTTTGATATTAGGTTGTTTTATTGGAAAGCCAACTAAATATCAAACATATTCTTACAGCGCCAGGGCCCCTC
>Alligator-mir-190b-5p
TGATATGTTTGATATTAGGTTG

>Alligator-mir-191_pre
GCGACAGCGGGCAACGGAATCCCAAAAGCAGCTGTCTTCCGCTCGGCACCTCAGCTGCGCTTGGATTTCGTTCCCTGCTCTCCCGCC
>Alligator-mir-191-5p
CAACGGAATCCCAAAAGCAGCT

>Alligator-mir-192_pre
TGCGTGCATGGGGCTATGACCTATGGATTGACAGCCAGTATCGGAGCCTCGCCCTGGCTGTCTGTTCTATAGGGCATAGGACTGGGCGCAC
>Alligator-mir-192-5p
TGACCTATGGATTGACAGCCAG
>Alligator-mir-192-3p
TGGCTGTCTGTTCTATAGGGCATA

>Alligator-mir-193a_pre
CATGCGAGCTGAGGGCTGGGTCTTTGCGGGCGAGGTGAGAGGTTCGTGCGTTCAACTGGCCTACAAAGTCCCAGTTCTCGGCTCCCAGC
>Alligator-mir-193a-3p
AACTGGCCTACAAAGTCCCA
>Alligator-mir-193a-5p
TGGGTCTTTGCGGGCGAGGTG

>Alligator-mir-193b_pre
AAAGTTGTGGTTCCAGAGTCGGGGTTTTGGGGGCAAGATGAGCTTATGTTTTATCCAACTGGCCCACAAAGTCCCGCTTTTGGTGGTCACTTTGT
>Alligator-mir-193b-3p
TACTGGCCCACAAAGTCCCGCT
>Alligator-mir-193b-5p
CGGGGTTTTGGGGGCAAGATGA

>Alligator-mir-194-1_pre

ACCAGCAGTACTTTCAAATGTAACAGCAACTCCATGTGGACTACGCTGACTTCCAGTGGAGATGCTGTTACTTTTGACAGCCACTCACAGACAT
>Alligator-mir-194-1-5p
TGTAACAGCAACTCCATGTGGAC
>Alligator-mir-194-1-3p
CCAGTGGAGATGCTGTTACTTT

>Alligator-mir-194-2_pre
CGCTGGTGTCCATCCGCTGTAACAGCAACTCCATGTGGGAGGGGTCCGTGGTCCCCGTGGGGCTGCTGTTATTCTGGACGGGCACCGGGAGC
>Alligator-mir-194-2-5p
TGTAACAGCAACTCCATGTGGA
>Alligator-mir-194-2-3p
CCCGTGGGGCTGCTGTTATTCT

>Alligator-mir-196-1_pre
GAACTGCTTTGTGAATTAGGTAGTTTCATGTTGTTGGGCTTTTATTTTTAAACACAAGAACATAAAACTACCTGATTTACTCCAGTTATTCTCC
>Alligator-mir-196-2_pre
GTGCAGCTGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGGCTTTTAGCTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTAGTGTTC
>Alligator-mir-196-3_pre
CGAGAACTGCTGTGTGGTTTAGGTAGTTTCATGTTGTTGGGGCTCCACCTTTCTCTCTACAGCACGAAACTGCCTTAATTACTTCAGTTGAAATCG
>Alligator-mir-196-5p
TAGGTAGTTTCATGTTGTTGG

>Alligator-mir-199-1_pre
AGTCCAGCCCAGCCTGCCCAGTGTTCAGACTACCTGTTCAGGAGCATATGAAGTTGTACAGTAGTCTGCACATTGGTTAGATCGGGCTTGGCAT
>Alligator-mir-199-2_pre
CCTGCTCCGTCGCCCCAGTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGACTGGGCAAGGGAA
>Alligator-mir-199-3_pre
TCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGACTACGAGATTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGG
>Alligator-mir-199-3p
ACAGTAGTCTGCACATTGGTTA
>Alligator-mir-199-5p
CCCAGTGTTCAGACTACCTGTT

>Alligator-mir-200a_pre
TGGTCCTCTGTGGGCATCTTACTAGACAGTGCTGGATATTTTGGATCTACTCTAACACTGTCTGGTAACGATGTTTAAAGGGTGAACCAAA
>Alligator-mir-200a-3p
TAACACTGTCTGGTAACGATGT
>Alligator-mir-200a-5p
CATCTTACTAGACAGTGCTGG

>Alligator-mir-200b_pre
TCCTGGGATGCCGTTACCATCTTACTGGGCAGCATTGGATGTTTTCTGTGTTTCTAATACTGCCTGGTAATGATGATTATGGTGTCTCGC
>Alligator-mir-200b-3p
TAATACTGCCTGGTAATGATGAT
>Alligator-mir-200b-5p
CATCTTACTGGGCAGCATTGG

>Alligator-mir-202_pre
CTCGTTGTTCCTTTTTCCTATGCATATACTTCTTTGAGAATTGGATCTAAAGAGGCATAGGGCATGGGAAAATGGGGCGACTGAGGTA
>Alligator-mir-202-5p
TTTCCTATGCATATACTTCTTT

>Alligator-mir-203_pre
CGCTCTCCGCCTCGCGGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTTTAGGCTAATTGTGAAATGTTTAGGACCACTTGACCCGCGAGGCGCCG
>Alligator-mir-203-3p
GTGAAATGTTTAGGACCACTT
>Alligator-mir-203-5p

AGTGGTTCTTAACAGTTCAACAG

>Alligator-mir-204-1_pre
TGTGACCTGTGGACTTCCCTTTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAATTGTCATCACT
>Alligator-mir-204-1-5p
TTCCCTTTGTCATCCTATGCCT
>Alligator-mir-204-1-3p
GCTGGGAAGGCAAAGGGACGT

>Alligator-mir-204-2_pre
GACCATGTGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGATCATAGTGAGGCAGGGACAACAAAGGGATGCTCAATTGTCATCTCGTGCA
>Alligator-mir-204-2-5p
TTCCCTTTGTCATCCTATGCCT
>Alligator-mir-204-2-3p
GCAGGGACAACAAAGGGATGC

>Alligator-mir-205a_pre
TCCATGGATTCTGTTGTCCTTCATTCCACCGGAGTCTGTCTCATACCTAATCAGATTTCAGTGGAGTGAAGCACAAGAGACATGGAGTTG
>Alligator-mir-205a-5p
TCCTTCATTCCACCGGAGTCTG
>Alligator-mir-205a-3p
GATTTCAGTGGAGTGAAGCACA

>Alligator-mir-205b_pre
TCCATGGCTTTCTGGTGCCCTTCATTCCACCGGAATCTGTAGGGATCAAAACCAGATTTCAGTGAAATGAAGCCCCTCAGACGTGGAAT
>Alligator-mir-205b-5p
CCCTTCATTCCACCGGAATCTGT

>Alligator-mir-206_pre
CTTCTCTTTTGAGGCAACATGCTTCTTTATATCCCCATAGGGATAACAGTGCTATGGAATGTAAGGAAGTGTGTGGTTTCGGGGAGATG
>Alligator-mir-206-3p
TGGAATGTAAGGAAGTGTGTGG
>Alligator-mir-206-5p
ACATGCTTCTTTATATCCCCAT

>Alligator-mir-208_pre
GCTGCTTCCTCCAACAGGGAAGCTTTTGGCTTGGGTTATATTGTCACTCGCAGTGTATAAGACGAGCGAAAAGCTTCTTGGTTGGAAGAGAGAT
>Alligator-mir-208-3p
ATAAGACGAGCGAAAAGCTTCT

>Alligator-mir-210_pre
CTCCAGAAGCAGGTGAGCCACTGACTAACGCACATTGTGCTGTTAGCGATTCCACTGTGCGTGTGACAGCGGCTAACCTGNTTTTCGGACAT
>Alligator-mir-210-5p
AGCCACTGACTAACGCACATT
>Alligator-mir-210-3p
CTGTGCGTGTGACAGCGGCTA

>Alligator-mir-212_pre
CAGCGCGTCGGCACCTTGGCTCTAGACTGCTTACTGCTGAGCACGGCGACCGGAACAGTAACAGTCTACAGTCATGGCTACTGAAGCATGACA
>Alligator-mir-212-5p
ACCTTGGCTCTAGACTGCTTA
>Alligator-mir-212-3p
TAACAGTCTACAGTCATGGCTA

>Alligator-mir-214_pre
CGGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCACTCACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC
>Alligator-mir-214-3p

ACAGCAGGCACAGACAGGCAG
>Alligator-mir-214-5p
TGCCTGTCTACACTTGCTGTGC

>Alligator-mir-215_pre
AACTGTTGTGCAGGAAAATGACCTATGAATTGACAGACTGTGTATTCTAAGCTTGTCTGTCATTTCTGTAGGCCAATATTCTGCACACCTTC
>Alligator-mir-215-5p
TTGACCTATGAATTGACAGAC
>Alligator-mir-215-3p
TCTGTCATTTCTGTAGGCCAAT

>Alligator-mir-216a_pre
GATGGCTGTGAATTGGCATAATCTCAGCTGGCAACTGTGAGCAGTTCATAAATTCTCTCACAGTTGTATCTGGGATTATGCTAAACATAGCAATTT
>Alligator-mir-216a-5p
TAATCTCAGCTGGCAACTGTG

>Alligator-mir-216b_pre
CAAGTCGCAGACTGGGAAATCTCTACAGGCAAATGTGATGTCTTTATAGTAATCTCACAATTACCTATAGAGATTCTTCAATCTGGCATCTTC
>Alligator-mir-216b-5p
AAATCTCTACAGGCAAATGTGA
>Alligator-mir-216b-3p
TCACAATTACCTATAGAGATTC

>Alligator-mir-217_pre
TTTTGATGTCGCAGATACTGCATCAGGAACTGATTGGATAATAATCAGTCACCATCAGTTCCTAATGCATTGCCTTCAGCATCTAAA
>Alligator-mir-217-5p
TACTGCATCAGGAACTGATTGG
>Alligator-mir-217-3p
CATCAGTTCCTAATGCATTGCC

>Alligator-mir-218-1_pre
TAGCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGTGAGGTATGAGTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT
>Alligator-mir-218-2_pre
AATGGGGTTTTCCTTTGTGCTTGATCTAACCATGTGGTAGAACAATACAAATTGAACATGGTTCTGTCAAGCACCATGGAAGGCTGCATA
>Alligator-mir-218-5p
TTGTGCTTGATCTAACCATGT

>Alligator-mir-219a_pre
TGAGCGCCGGGTCCTGATTGTCCAAACGCAATTCTTGTGTCTGCCCCAAGAATTGAGTGTGGACGTCGGGAGCCGCCGTTCCCCA
>Alligator-mir-219a-3p
AGAATTGAGTGTGGACGTCGGG
>Alligator-mir-219a-5p
TGATTGTCCAAACGCAATTCTTG

>Alligator-mir-219b_pre
GGAGTCTCCGCTCCTGATTGTCCAAACGCAATTCTTGTGCCGTGGAAACGTACAAACCAAGAATTGTGTCTGGACATCTGTGGCGGGGAGTCC
>Alligator-mir-219b-3p
AGAATTGTGTCTGGACATCTG
>Alligator-mir-219b-5p
TGATTGTCCAAACGCAATTCTTG

>Alligator-mir-221_pre
TCCAGGTTTGGGGCATGAACCTGGCATACAATGTAGATTTCTGTATTTCTTAAGCAACAGCTACATTGTCTGCTGGGTTTCAAGCTGCCTGGAAA
>Alligator-mir-221-5p
ACCTGGCATACAATGTAGATTT
>Alligator-mir-221-3p
AGCTACATTGTCTGCTGGGTTTC

>Alligator-mir-222a_pre
TAGTTGCCCATCAATCGCTCAGTAGTCAGTGTAGATTCTGTTTTTACAATCAGCAGCTACATCTGGCTACTGGGTCTCTGATGACATCTTGTAG
>Alligator-mir-222a-3p
AGCTACATCTGGCTACTGGGTCTC
>Alligator-mir-222a-5p
CGCTCAGTAGTCAGTGTAGATTC

>Alligator-mir-222b_pre
GATGTAATTGGGTGCTCAGTAGTCGGTGTAGAATCTGTCTGACATTGATACCAACAGCTACATCTGATTACTGGGTCACTAATTGCATCATCAA
>Alligator-mir-222b-3p
AGCTACATCTGATTACTGGGTCAC
>Alligator-mir-222b-5p
TGCTCAGTAGTCGGTGTAGAATC

>Alligator-mir-223_pre
CGCAGTGCTGCACTCCGTGTATTTGACAAGCTGAGTTTGACACTCAGTGTGGCAGAGTGTCAGTTTGTCAAATACCCCAAGTGAGGC
>Alligator-mir-223-3p
TGTCAGTTTGTCAAATACCCCAA
>Alligator-mir-223-5p
CGTGTATTTGACAAGCTGAGTTT

>Alligator-mir-301a_pre
CTGCTAACGAATGCTCTGACTTTATTGCACTACTGTACTTTACAGCTAGCAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAGAG
>Alligator-mir-301a-3p
CAGTGCAATAGTATTGTCAAAGCAT
>Alligator-mir-301a-5p
GCTCTGACTTTATTGCACTACT

>Alligator-mir-301b_pre
GTGGCTGCTGGTATCGCTGGCTCTGACAATGTTGCACTACTGTCTGCACAAATAAAGCAGTGCAATAATATTGTCAAAGCATTTGGTTCCAGTCCT
>Alligator-mir-301b-3p
CAGTGCAATAATATTGTCAAAGC
>Alligator-mir-301b-5p
TCTGACAATGTTGCACTACT

>Alligator-mir-302a_pre
AGCTTAAAGGACCCCCAGAACTTTAATGTGGATGTACTTGCTTTGTTTCTGAAAAAGTAAGTGCTTCCATGTTTTGGTGCTGGTGAATCCTGCTCT
>Alligator-mir-302a-3p (predicted)
TAAGTGCTTCCATGTTTTGGTG

>Alligator-mir-302b_pre
GAAGTATGGTTTCCCTTCTACTTTAACATGGAGGTGCTTTCTGTGACTTATAAGAAGTAAGTGCTTCCATGTTTTAGTAGAGGTGAAATCCTGTTC
>Alligator-mir-302b-3p
TAAGTGCTTCCATGTTTTAGTT

>Alligator-mir-302c_pre
TTAAACAGCCTCCTTTGCTTTAACATGGAGGTACCTGCTGCCTAAAAAAAGTAAGTGCTTCCATGTTTCAGTGGTGGTGGTAGTTCCT
>Alligator-mir-302c-3p (predicted)
TAAGTGCTTCCATGTTTCAGTG

>Alligator-mir-302d_pre
CCCCTCTACTTTAACATGGGAGGTACTTGCTGGATGCTTGAAAAAGTAAGTGCTTCCATGTTTTAGTTGTGGTGAATCCT
>Alligator-mir-302d-3p
TAAGTGCTTCCATGTTTTAGTT

>Alligator-mir-338-1_pre

CCACTTGCTCCCGCCTCCCCAACAATATCCTGGTGCTGAGCGAGTTGCGCACAGAGACTCCAGCATCAGTGATTTTGTTGAGGAGGGCGAGCTCTG
>Alligator-mir-338-1-3p
TCCAGCATCAGTGATTTTGT
>Alligator-mir-338-1-5p
AACAATATCCTGGTGCTGAG

>Alligator-mir-338-2_pre
TGCAAATGTTTATTTCTGGCAACACTATCCTGATGCTGTCTGAGTATGTGGTAAAGCTCCAGCATCAGTGATTTTGTTGTTAGTGGTAAATTCAAG
>Alligator-mir-338-2-3p
TCCAGCATCAGTGATTTTGTTG
>Alligator-mir-338-2-5p
AACACTATCCTGATGCTGTCT

>Alligator-mir-365-1_pre
TTACCGCAGGGAAAATGAGGGACTTTTGGGGGCAGTTGTGTTTCCATTACACTATCATAATGCCCCTAAAAATCCTTATTGCTCTTGCAGTAT
>Alligator-mir-365-1-3p
TAATGCCCCTAAAAATCCTTA
>Alligator-mir-365-1-5p
AGGGACTTTTGGGGGCAGTTGTG

>Alligator-mir-365-2_pre
GTGGCAGCAAGAAAAATGAGGGACTTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTTCTTGCAATGTTC
>Alligator-mir-365-2-3p
TAATGCCCCTAAAAATCCTTA
>Alligator-mir-365-2-5p
AGGGACTTTCAGGGGCAGCTGT

>Alligator-mir-367_pre
TCTTCAACTACAGGCTGCTACTGTTGCTAATATGCAACTCTGTTATGTCAAAATTGGAATTGCACTTTAGCAATGGTGATGGACTGTAAGACACAC
>Alligator-mir-367-3p (predicted)
AATTGCACTTTAGCAATGGTG

>Alligator-mir-375_pre
CTGGCCGCCCTCTGCGCCTGCCTGGCGTCGAGCCCGACGTGCAAGACCTGACGTGAATGTTTTGTTCGTTCGGCTCGCGTTAGGCAGGCCCAGCCT
>Alligator-mir-375-3p
TTTGTTCGTTCGGCTCGCGTT

>Alligator-mir-383_pre
CGCCAAGTCACCTGCTCCTCAGATCAGAAGGTGATTGTGGCTTTGAGTAGATATTAAGCAGCCACAGCACTGCCTGGTCAGAAAGAGCAAGTGTAC
>Alligator-mir-383-5p
AGATCAGAAGGTGATTGTGG

>Alligator-mir-425_pre
GGAGAGAGATTGCTTTGGAATGACACGATCACTCCCGCTGAGCGAGACGCCCGACAGCCATCGGGAATATCGTGTCGGTCCAAAGCTCTTTCG
>Alligator-mir-425-5p
AATGACACGATCACTCCCGCTGA
>Alligator-mir-425-3p
CATCGGGAATATCGTGTCGGTC

>Alligator-mir-429_pre
CCTGAGTGCCTGCTGATTGACGTCTTACCAGACAAAGTTAGATCTAGCTATTTTCGTCTAATACTGTCTGGTAATGCCGTTGATCGCACTGGCA
>Alligator-mir-429-3p
TAATACTGTCTGGTAATGCC
>Alligator-mir-429-5p
TCTTACCAGACAAAGTTAGA

>Alligator-mir-449a_pre

GTGTGTGATGGGAAGGCAGTGTACTGTTAGCTGGTGTCAGTTTTTTCAACCAGCTAACATGCAGCTGCTATCCTACTGCACAAACTTTGA
>Alligator-mir-449a-5p
AGGCAGTGTACTGTTAGCTGGT

>Alligator-mir-449b_pre
TAGCGCTCCCTGTGTCTGGTAGGCAGTGTACTGTTAGCTGGCTGCTTTGTGTGAATCTAGCAGTCGCTACTGCACTGTCAACAGCTGCAGGGGCAG
>Alligator-mir-449b-5p
AGGCAGTGTACTGTTAGCTGGCT

>Alligator-mir-449c_pre
ATGTTTCAGTTTGGCAGTGCATTGCTAGCTGGCTGTTGTGTACGTGTGTTAACAGTTGCTAGCTGTACTCCATATTGTTGCATTC
>Alligator-mir-449c-5p
TTGGCAGTGCATTGCTAGCTGGC

>Alligator-mir-449d_pre
ATGTGTGTGTGATGATTAGGCAGTGTATTGTTAGTTAGCTGGCATTCACATACCAGCAACTAAACACACTTCCACATTAGCACACAAC
>Alligator-mir-449d-5p
AGGCAGTGTATTGTTAGTTAGC

>Alligator-mir-454_pre
AACCTTAAGGATAAGACCCTATCAATATTGCCTCTGCTTTTGTGATCAGGGTAGTAGTGCAATATTGCTTATAGGGTCTTTTCTTTGGAGGGT
>Alligator-mir-454-3p
TAGTGCAATATTGCTTATAGGGTCT
>Alligator-mir-454-5p
ACCCTATCAATATTGCCTCTGCT

>Alligator-mir-455_pre
TCCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGTGGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGGTTTATTT
>Alligator-mir-455-5p
TATGTGCCCTTGGACTACATCG
>Alligator-mir-455-3p
ATGCAGTCCATGGGCATATACA

>Alligator-mir-456_pre
TGTGTATGTGTGAGCAGGCATCTTCTCAGCCTACATGTGGATTCTTAAATCTGCAGGCTGGTTAGATGGTTGTCATACATTCACCTGA
>Alligator-mir-456-3p
CAGGCTGGTTAGATGGTTGT

>Alligator-mir-458_pre
TGGTGCAGATGGCAGCGCCATTTTCAGAGCTATAAACAGTATCATTGTCATAGCTCTTTGAATGGTACTGCCATATGTACTG
>Alligator-mir-458-3p
ATAGCTCTTTGAATGGTACTGC

>Alligator-mir-459_pre
TTGTTTCTTGCAATCAGTAACAAGGATTCATCTCTGTATTGTGTGAAGAACAGAGAGAGTCTTTGTAACTAAGTGCAAGTAATAGCCA
>Alligator-mir-459-5p
TCAGTAACAAGGATTCATCTCTG

>Alligator-mir-460a_pre
TGACTTTATAGGACCTGCATTGTACACACTGTGTGTATTGACTGGGCGTGCACAGCGCATACAATGTGGATACTGTAGAAGTCA
>Alligator-mir-460a-5p
CCTGCATTGTACACACTGTGTG

>Alligator-mir-460b_pre
GGACGTGGCTCTATGTTGTCCTCATTGTACATGCTGTGTGTATATTTATGACGTACACAGCGCATGCAATGTGGACAGAATGGAGACCAGCAGGCT
>Alligator-mir-460b-5p
TCCTCATTGTACATGCTGTGTG

>Alligator-mir-460b-3p
CACAGCGCATGCAATGTGGACA

>Alligator-mir-489_pre
GTGGTGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGGACTTTTAGGAGTGACATCATATGTACGGCTGCTAAACTGCTGCAT
>Alligator-mir-489-3p
TGACATCATATGTACGGCTGCT
>Alligator-mir-489-5p
TGGTCGTATGTATGACGTCATT

>Alligator-mir-490_pre
GTTCATGGTTCGACACCATGGATCTCCAGGTGGGTCAAGACTATAGAGATACACCAACCTGGAGGACTCCATGCTGTTGAGCTGTTCACA
>Alligator-mir-490-5p
CCATGGATCTCCAGGTGGGTCA
>Alligator-mir-490-3p
CAACCTGGAGGACTCCATGCTG

>Alligator-mir-497_pre
CAGGCCCAGCCCCGCCCCAGCAGCACATCATGGTTTGTGGGGTCTCGTGGCACAGACCATGGCGTGGTGCTACCGCGGGGCCGGGGAGAC
>Alligator-mir-497-5p
TAGCAGCACATCATGGTTTGT
>Alligator-mir-497-3p
CAGACCATGGCGTGGTGCTACC

>Alligator-mir-499_pre
TGAGAGAGCGGCAGTTAAGACTTGCAGTGATGTTTAGATAATGTATTACATGAACATCACTTTAAGTCTGTGCTACTTCTCTCCTC
>Alligator-mir-499-5p
TTAAGACTTGCAGTGATGTTT
>Alligator-mir-499-3p
AACATCACTTTAAGTCTGTGCT

>Alligator-mir-551-1_pre
TTCTGCTTTAACCTTGGAAATCAAGGATGGGTGAAGCCTGTTGGAATAACTCTAGGCGACCCATACTTGGTTTCAAGGGTCAGCAGGGATT
>Alligator-mir-551-1-3p
GCGACCCATACTTGGTTTCA
>Alligator-mir-551-1-5p
GAAATCAAGGATGGGTGAAGC

>Alligator-mir-551-2_pre
CATGACCCAATGGCTCCAGAAATCAAGGGTGGGTAAGACCTCGTAAGAACAGTTGAAGGCGACCCATACTTGGTTTCAGGGGCTTTGAGGGTATAG
>Alligator-mir-551-2-3p
GCGACCCATACTTGGTTTCA

>Alligator-mir-599_pre
CATATTGTCCATAGTGTGTTTGATAAGCTGACATGGGACAGGAGTTCTTTTCACTGTTGTGTCAGTTTATCAAACCCATACCTGGACATCAGTC
>Alligator-mir-599-3p
GTTGTGTCAGTTTATCAAACCC
>Alligator-mir-599-5p
GTTTGATAAGCTGACATGGGAC

>Alligator-mir-737_pre
GCTACTCTGCTGTTATTTTTTTAGGTTTTGATTTTTATTGCATCTTCATGCGAAAATCAAAACCTAAAGAAAATGCTGCAAAGATAGAT
>Alligator-mir-737-5p
ATTTTTTTAGGTTTTGATTTTT

>Alligator-mir-875_pre
GTTTAGTGGTACAATACCTCAGTCTTTTCAGGTGTTCTATAAAATCACCTGGAAATATTGAGGTTGAGTTTCACTGAACACAGGC

>Alligator-mir-875-5p
AATACCTCAGTCTTTTCAGGTG

>Alligator-mir-1306_pre
ATGAACAGCCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGTGGTGATGGACAGTCAGATAC
>Alligator-mir-1306-3p
TGGACGTTGGCTCTGGTGGTGAT
>Alligator-mir-1306-5p
CACCTCCCCTGCAAACGTCCA

>Alligator-mir-1329_pre
GGTCTGGTTGTAGAGATACAGTGATCAGGTTACGATGATTTCTCAAGTAACAACCTCGTAGCTTGATCACAATATCCCTATGACTTAGATAA
>Alligator-mir-1329-5p
TACAGTGATCAGGTTACGATGAT

>Alligator-mir-1388_pre
AGTGAGGGGCGTCCCCAGGACTGTCTAACCTGAGAATGGTGAAACACGAGGGTCAATCTCAGGTTCGTCAGCCCATGAGACGCTCTCTCCAG
>Alligator-mir-1388-5p
AGGACTGTCTAACCTGAGAATG
>Alligator-mir-1388-3p
ATCTCAGGTTCGTCAGCCCAT

>Alligator-mir-1397_pre
ACAGAGTGCGATGTGTGCATTGCATTGCGACGGGTTACATCACTGGTCGTAACATGATGTAACCCAACGCAGCATGATGTAAGCGTCGTGATACAT
>Alligator-mir-1397-5p
TGCATTGCGACGGGTTACATC
>Alligator-mir-1397-3p
ATGTAACCCAACGCAGCATGATA

>Alligator-mir-1416_pre
AGTGATGGCTGACACTCCTTCCTTAACTCATACCGCTGTGCCTGCCTTCTTTCTTTCACAATTGTGTGAGTTGAGTTCAGAGTGTCAGTCCAACCC
>Alligator-mir-1416-5p
TCCTTAACTCATACCGCTGTG

>Alligator-mir-1641_pre
AGGGCATTTCCTGGGGATTAATGACTGTCTGGGGTCATCATCTCCTCCCAGTTAGTTATTAATCCCCAGGAAATACTTTATACCTTGATC
>Alligator-mir_1641-5p (predicted)
TGGGGATTAATGACTGTCTGGG

>Alligator-mir-1662_pre
GCAGAGCTGTGCTCTATGGGTTTGACATCATCATACTTGGGATGTATGTCACAAAGTCCCAAGAAGGCTGATGTCAGGCCCAAGATTGCTGCCATC
>Alligator-mir-1662-5p
TTGACATCATCATACTTGGGA

>Alligator-mir-1677a_pre
CTCCAGGCTTGGTCCAATGCTCATTGAAGTCATGGAGAATCTTTACACTGACTTCACTGAGCTTTGGACCAGGTTTCATGAGAA
>Alligator-mir-1677a-3p
TGACTTCACTGAGCTTTGGACA

>Alligator-mir-1677b_pre
AGCAACTAGGGGCCTGATCCAGAGCCCGTTGAAGTCAGCGGGAGACATTCAAGTGACTTCAGGGGGCTTTGAATGAGGCTCTCAGTGATCACACT
>Alligator-mir-1677b-5p
TCCAGAGCCCGTTGAAGTCAG
>Alligator-mir-1677b-3p
TGACTTCAGGGGGCTTTGAATGT

>Alligator-mir-1677c_pre

GCAGCACTGTGGGCTTGACCCAGAACCCACTGAAGTTAAGGGCAGAGTCCCGTTAGCTTCTGTGGGCTGTAGGTCAGGCTCCACGTGTTAT
>Alligator-mir-1677c-5p
TGACCCAGAACCCACTGAAGTT
>Alligator-mir-1677c-3p
CTTCTGTGGGCTGTAGGTCA

>Alligator-mir-1720_pre
CTTCTGATCACCTCAGTTGTTGCTTTTGTGAGCATTTCATGGGAAAGCAACAAGAGGGCAGGTCTGAAACCC
>Alligator-mir-1720-3p (predicted)
AAGCAACAAGAGGGCAGGTCTGA

>Alligator-mir-1788_pre
GCCCGCCGCGTCCTGGGCTTGTTTTCAGTTGCCTGCGGGTTTATTTGGACGACTCAGGCAGCTAAAGCAAGTCTGGGACGGGTGAGGAGA
>Alligator-mir-1788-5p
GGCTTGTTTTCAGTTGCCTGCG
>Alligator-mir-1788-3p
CAGGCAGCTAAAGCAAGTCTG

>Alligator-mir-1791_pre
TGATGCACCATGTTGGGCTGCCTCAGTCATGCCATGTTATGAAACCTAATGCAATGTGACTGATGCAGGCTGACGTGATGTGTCA
>Alligator-mir-1791-3p
CAATGTGACTGATGCAGGCTGAC
>Alligator-mir-1791-5p
TGGGCTGCCTCAGTCATGCCATG

>Alligator-mir-1805_pre
TGGAATATTCTGGGAGTTGTAGTCTTTCAAACAGAGCTTTGCAAGTACATACCTGTATTGGAACACTACAGCTCCCTGAACTTCCTAGTGTCA
>Alligator-mir-1805-3p
TGTATTGGAACACTACAGCTCC
>Alligator-mir-1805-5p
AGTTGTAGTCTTTCAAACAGA

>Alligator-mir-2184_pre
CCCGGTCCCGGCCGCCCCCAACAGTAAGAGTTTATGTGCGGTGAGAGCTGGAATCTGCATGTGAACTCCTACTGCTCCGGGCGGCGGGGCACAGCG
>Alligator-mir-2184-5p
AACAGTAAGAGTTTATGTGCGG
>Alligator-mir-2184-3p
GCATGTGAACTCCTACTGCTCC

>Alligator-mir-2188_pre
GAATATCAGACCCGTGGGAAAGGTCCAACCTCACATGTCCTGTATGTCACGAGGAGGGATATATGTGGTCAGACCTATCCCACAGGCCCTGTATTC
>Alligator-mir-2188-5p
AAGGTCCAACCTCACATGTCC
>Alligator-mir-2188-3p
ATATATGTGGTCAGACCTATC

>Alligator-mir-2970_pre
CGGGCCTCTTCCTGCCACTGCAGACAGTCAGCAGTTGGTCTGGCGTGAGCAGCATTCTCAGATCACCTCTTGGCTGTGGGTGGTGCAGAGAGCGCC
>Alligator-mir-2970-5p
GACAGTCAGCAGTTGGTCTG
>Alligator-mir-2970-3p
AGATCACCTCTTGGCTGTGGG

>Alligator-mir-2984_pre
TGCTTTACCTGTGGCTCCTACTGTGAGTGAAATTGAGTAGGATCAGGTGATCCTAGTCAATTTCACTCGCAGCAGGTTCTGGGGATAAAGCC
>Alligator-mir-2984-3p (predicted)
AATTTCACTCGCAGCAGGTTCTG

>Alligator-mir-3064_pre
GTTTATCTTTGATTTGGCTGTTGTGGTGTGCAAAACTTTGTGCGTTGCTTTTTGCCACACTGCAACACTTTACAGATGTGGAAGATGTGA
>Alligator-mir-3064-3p
TTGCCACACTGCAACACTTTAC

>Alligator-mir-3618_pre
GAATGCATTGTGATTTCCAATAATTGAGACAGTGATTCTGAAAGCTGTCTACATTAATGAAAAGAACAATGTAGTCA
>Alligator-mir-3618-3p (predicted)
TGTCTACATTAATGAAAAGAAC

>Alligator-novel-1_pre
CTTCCCTTCTCCCCCCCCTTTCAAAATTCTAGATCTGCCTATGGGCATGGGTAGTACTAGGATTTTGGAAAGGGGGTGGGAGGGCAC
>Alligator-novel-1-5p
CTTTCAAAATTCTAGATCTGCC
>Alligator-novel-1-3p
TAGTACTAGGATTTTGGAAAGGG

>Alligator-novel-2_pre
CTTTGGCAAATACCTGGTCATTACCAAGGCTGCTAGGAAAACACTGTTTCTAGTATGCTGTGGACATGACCATAAAGAGAATCCAT
>Alligator-novel-2-5p
CTGGTCATTACCAAGGCTGCTA
>Alligator-novel-2-3p
TATGCTGTGGACATGACCATA

>Alligator-novel-8_pre
TCAGAGGAAGGCAGGGTAGCTTTGCACCTTACAGACTAACCAAAGTAGACATATTGGTTAATCTATAGGTGCAAATCGACCTTGCCTTCTATTTGA
>Alligator-novel-8-5p
GCTTTGCACCTTACAGACTAACC
>Alligator-novel-8-3p
TTAATCTATAGGTGCAAATCGA

>Alligator-novel-9_pre
GGTTGGGAGAGGTTTTAGACAAGCTGTTGAGCCCAGTGGAAGAGCACTTCATGGCCAATAGTTTGTCTAAAATCTCTCCCAACC
>Alligator-novel-9-5p
TTTAGACAAGCTGTTGAGCCCAG
>Alligator-novel-9-3p
ATGGCCAATAGTTTGTCTAAAAT

>Alligator-novel-10_pre
GGTGTCAGGAAGCAGTGGACAATGAAGAATGCAGTGCAACAACAGTAAGTGCATGTCTCATTGTCCATTGCTTCCTGATGTC
>Alligator-novel-10-5p
CAGTGGACAATGAAGAATGCA
>Alligator-novel-10-3p
CATGTCTCATTGTCCATTGCTT

>Alligator-novel-13_pre
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>Alligator-novel-13-5p
GGGCAGCCTGACTCGCAGCAGA
>Alligator-novel-13-3p
TGCTGAGGGTCAGGCTGGACTG

>Alligator-novel-14_pre
ACACATCCTTGGCAATATCTGGGGCACATCTCTAGAAGCAGGAATAGTCAGGATGCTCTGCTTCTAGTGACTTGCCTTGGAGATTGCTGGAGGT
>Alligator-novel-14-5p
TGGGGCACATCTCTAGAAGC

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>Alligator-novel-14-3p
TTCTAGTGACTTGCCTTGGAGA

>Alligator-novel-15_pre
CTGGAGGGGGAGCAGCAAGGACTAGGGACCCAAGAGACAGAGAATTAATTTCTTGGTACTCCTGCCCTTGCAGATTGTGAATGCCCTGG
>Alligator-novel-15-5p
CAGCAAGGACTAGGGACCCAAGA
>Alligator-novel-15-3p
TTGGTACTCCTGCCCTTGCAG

>Alligator-novel-16_pre
GTCCCAAATACACTGCTGGAGTCAGTGGGTACAAGTCTGTGGAGCTGATAGAGTTGTACATGTTGACACAAGCAGTGAATTTGGCCG
>Alligator-novel-16-5p
TGGAGTCAGTGGGTACAAGTCT
>Alligator-novel-16-3p
AGTTGTACATGTTGACACAAGC

>Alligator-novel-18_pre
GTGGAATGCAGAGGCAAGGATTTCTTAGGGTGATATCTTTTAATTATCTTTTCTTATCACTCTAATAAATCCTTGCCTCTTCGACACCAT
>Alligator-novel-18-5p
CAAGGATTTCTTAGGGTGAT
>Alligator-novel-18-3p
TCACTCTAATAAATCCTTGCC

>Alligator-novel-20_pre
CTCACTGTTCCCTTCTCTGTTCTTTTGCATCTTTCAGACCAGGATGAAAGAGCAGCAGAACTCAGCAGGGAGCAGAATGAG
>Alligator-novel-20-5p
CTCTGTTCTTTTGCATCTTTCA
>Alligator-novel-20-3p
AAAGAGCAGCAGAACTCAGCAG

>Alligator-novel-21_pre
CAGGTCCCTTCTGGTTCTACACTTCTATGATTCTGTAAAAGGGGAATCATAGGCTTGGAGAATGGCAAGGGGTCAG
>Alligator-novel-21-5p
GGTTCTACACTTCTATGATTCT
>Alligator-novel-21-3p
AATCATAGGCTTGGAGAATGGCA

>Alligator-novel-27_pre
CTGGGTTGCCTGTGAGTCCATGCTCAGCTCTCATGTTTCTCCAGCACAGGGGCTGCTCCATGGAAGCAAAGGCTCT
>Alligator-novel-27-5p
GAGTCCATGCTCAGCTCTCATG
>Alligator-novel-27-3p
CAGGGGCTGCTCCATGGAAGCA

>Alligator-novel-35_pre
TAACCTTGTGTGACAGTAACTCCTTCTAGGAACATGTGCATCCAGCTTTCCAGGAGGCTGTCTGTCACACCAGGAAA
>Alligator-novel-35-5p
TGTGACAGTAACTCCTTCTAGG
>Alligator-novel-35-3p
CCAGGAGGCTGTCTGTCACACCA

>Alligator-novel-36_pre
CTGTAGGAGTTTCTACCAGTACAGCTGTGCCAGTGAGGGGCCTGAAGTGGTGTGATTCCTGACTGACATTGCTGTGCTAGCAGAAGCTCCTAGTA
>Alligator-novel-36-5p
CAGTACAGCTGTGCCAGTGAGG
>Alligator-novel-36-3p
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TGACTGACATTGCTGTGCTAGCA

>Alligator-novel-39_pre
ACGAAGCAGGTATACTTAACTTCTGCTCTTCTTTCATTNCATGTCTAACATTCCATGAAAGAAGGGTAGGAGTTGAGTACACNTGCTTCATCTGT
>Alligator-novel-39-5p
TTAACTTCTGCTCTTCTTTCA
>Alligator-novel-39-3p
AAAGAAGGGTAGGAGTTGAGTAT

>Alligator-novel-41_pre
CTGCTCCTTGCTTTTTTCTGCAACAGGTGCCAGTTCACTGCTCTGTAGTTTCTGTGGAACTGGCGTCCGTTGCAGGGATGTGCGGGGAGCGTCC
>Alligator-novel-41-5p
TTCTGCAACAGGTGCCAGTTC
>Alligator-novel-41-3p
ACTGGCGTCCGTTGCAGGGAT

>Alligator-novel-42_pre
GCAGCACTGTGGGCTTGACCCAGAACCCACTGAAGTTAAGGGCAGAGTCCCGTTAGCTTCTGTGGGCTGTAGGTCAGGCTCCACGTGTTAT
>Alligator-novel-42-5p
TGACCCAGAACCCACTGAAGTT
>Alligator-novel-42-3p
CTTCTGTGGGCTGTAGGTCA

>Columba-let-7a-1_pre
CTGTGCTGTGGGATGAGGTAGTAGGTTGTATAGTTTTAGGGTCATACCCGCAACTGGGAGATAACTATACAATCTACTGTCTTTCCTAAAG
>Columba-let-7a-1-5p
TGAGGTAGTAGGTTGTATAGTT
>Columba-let-7a-1-3p
CTATACAATCTACTGTCTTTC

>Columba-let-7a-2_pre
TGCATCCAGGTTGAGGTAGTAGGTTGTATAGTTTAGAATTACACCAAGGGAGATAACTGTACAACCTCCTAGCTTTCCTT
>Columba-let-7a-2-5p
TGAGGTAGTAGGTTGTATAGTT
>Columba-let-7a-2-3p
CTGTACAACCTCCTAGCTTTCC

>Columba-let-7a-3_pre
GTCCTTTGGGGTGAGGTAGTAGGTTGTATAGTTTTAGGGCTCTGCCCTGCCTGTCACATAACTATACAATCTACTGTCTTTCCTGAAGTGG
>Columba-let-7a-3-5p
TGAGGTAGTAGGTTGTATAGTT
>Columba-let-7a-3-3p
CTATACAATCTACTGTCTTTC

>Columba-let-7a-4_pre
AGGTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGGATTTGATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTAA
>Columba-let-7a-4-5p
TGAGGTAGTAGGTTGTATAGTT
>Columba-let-7a-4-3p
CTATACAGTCTATTGCCTTCCT

>Columba-let-7b_pre
GGATGAGGTAGTAGGTTGTGTGGTTTCAGGGTAGTGATTTTGCCCCAGTCAGGAGATAACTATACAACCTACTGCCTTCCCTGATAAGCAGCATAA
>Columba-let-7b_5p
TGAGGTAGTAGGTTGTGTGGTTT
>Columba-let-7b-3p
CTATACAACCTACTGCCTTCC

>Columba-let-7c_pre
GCATCCGGGTTGAGGTAGTAGGTTGTATGGTTTAGAGTTACACCCTGGGAGTTAACTGTACAACCTTCTAGCTTTCCTTGGAGCA
>Columba-let-7c-5p
TGAGGTAGTAGGTTGTATGGTT
>Columba-let-7c-3p
CTGTACAACCTTCTAGCTTTCC

>Columba-let-7d_pre
TAGGAAGAGGTAGTAGGTTGCATAGTTTTAGGGCAGGGATTTTGCTCACAAGGAGGTAACTATACAACCTGCTGCCTTTCTTAGGGC
>Columba-let-7d-5p
AGAGGTAGTAGGTTGCATAGTT
>Columba-let-7d-3p
CTATACAACCTGCTGCCTTTCT

>Columba-let-7e_pre
CTGTCCTTGAGGCTGAGGTAGTAGATTGAATAGTTGTGGAGTCCGATCCTCCCTTTGAGCAAACTATACAATCTACTGTCTTTCCTAAGGAGA
>Columba-let-7e-5p
TGAGGTAGTAGATTGAATAGTT
>Columba-let-7e-3p
CTATACAATCTACTGTCTTTCC

>Columba-let-7f_pre

TTCTCTGTCAGAGTGAGGTAGTAGATTGTATAGTTGTAGGGTAGTTATTTTACCCTGTTCAGGAGATAACTATACAATCTATTGCCTTCCCTGCGG
>Columba-let-7f-5p
TGAGGTAGTAGATTGTATAGTT
>Columba-let-7f-3p
CTATACAATCTATTGCCTTCCC

>Columba-let-7g_pre
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>Columba-let-7g-5p
TGAGGTAGTAGTTTGTACAGTT
>Columba-let-7g-3p
CTGTACAGGCCACTGCCTTGCC

>Columba-let-7i_pre
CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGATAACTGCGCAAGCTACTGCCTTGCTA
>Columba-let-7i-5p
TGAGGTAGTAGTTTGTGCTGTTG
>Columba-let-7i-3p
CTGCGCAAGCTACTGCCTTGCT

>Columba-mir-1a-1_pre
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>Columba-mir-1a-1-3p
TGGAATGTAAAGAAGTATGTAT
>Columba-mir-1a-1-5p
ACATACTTCTTTATATGCCCATA

>Columba-mir-1a-2_pre
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>Columba-mir-1a-2-3p
TGGAATGTAAAGAAGTATGTAT
>Columba-mir-1a-2-5p
ACATACTTCTTTATGTACCCATA

>Columba-mir-1b_pre
CCTCCCAACCCTACATACTTCTTCATATACCCATATGGAGTCGGCCGGCGTTATGGAATGTTAAGAAGTATGTATTTTTGGGCTGG
>Columba-mir-1b-3p
TGGAATGTTAAGAAGTATGTATT
>Columba-mir-1b-5p
TACATACTTCTTCATATACCCAT

>Columba-mir-7a-1_pre
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>Columba-mir-7a-1-5p
TGGAAGACTAGTGATTTTGTTGTT
>Columba-mir-7a-1-3p
CAACAAATCGCAGTCTGCCATA

>Columba-mir-7a-2_pre
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>Columba-mir-7a-2-5p
TGGAAGACTAGTGATTTTGTTGTT
>Columba-mir-7a-2-3p
CAACAAGTCACAGTCTGCCCTA

>Columba-mir-7a-3_pre
GGTGGTCTGGCTCTGCGTGGAAGACTAGTGATTTTGTTGTTCTGATTTATAAAGGTGACAACAAATCATAGCCTGCCACCCAGCCCAGACCTGC

>Columba-mir-7a-3-5p
TGGAAGACTAGTGATTTTGTTGTT
>Columba-mir-7a-3-3p
CAACAAATCATAGCCTGCCACC

>Columba-mir-7b_pre
CATCCCCGGGCAGGCTGGAAGACTTGTGATTTTGTTGTTTCCAATGTCAACGGGAGCGAACAACAAATCCCAGTCTCCTCCCTGCCCCGGGCAC
>Columba-mir-7b-5p (predicted)
TGGAAGACTTGTGATTTTGTTGTT

>Columba-mir-9-1_pre
TCAGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCGATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCATT
>Columba-mir-9-1-5p
TCTTTGGTTATCTAGCTGTATGA
>Columba-mir-9-1-3p
ATAAAGCTAGATAACCGAAAGTA

>Columba-mir-9-2_pre
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>Columba-mir-9-2-3p
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>Columba-mir-9-3_pre
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>Columba-mir-9-3-5p
TCTTTGGTTATCTAGCTGTATG
>Columba-mir-9-3-3p
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>Columba-mir-10a_pre
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TACCCTGTAGATCCGAATTTGTG
>Columba-mir-10a-3p
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>Columba-mir-10b_pre
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>Columba-mir-10b-5p
TACCCTGTAGAACCGAATTTGT
>Columba-mir-10b-3p
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>Columba-mir-10c_pre
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>Columba-mir-10c-5p
TACCCTGTAGACTCGAATTTG
>Columba-mir-10c-3p
CAAATTCGTCTCTAGGGGAATA

>Columba-mir-15a_pre
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>Columba-mir-15a-5p
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>Columba-mir-15a-3p

CAGGCCATATTGTGCTGCCTC

>Columba-mir-15b_pre
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>Columba-mir-15b-5p
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>Columba-mir-15b-3p
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>Columba-mir-15c_pre
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>Columba-mir-15c-5p
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>Columba-mir-15c-3p
CAGACCATTCTGGGCTGCCTCA

>Columba-mir-16a-1_pre
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>Columba-mir-16a-1-3p
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>Columba-mir-16a-2_pre
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>Columba-mir-16a-2-5p
TAGCAGCACGTAAATATTGGTGT
>Columba-mir-16a-2-3p
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>Columba-mir-16b_pre
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>Columba-mir-16b-3p
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>Columba-mir-17_pre
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>Columba-mir-18a_pre
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>Columba-mir-18a-3p
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>Columba-mir-18b_pre
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>Columba-mir-19b-2-5p
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>Columba-mir-20a-3p
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>Columba-mir-20b-3p
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>Columba-mir-21_pre
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>Columba-mir-21-5p
TAGCTTATCAGACTGATGTTGA
>Columba-mir-21-3p
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>Columba-mir-22_pre
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>Columba-mir-22-3p
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>Columba-mir-22-5p
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>Columba-mir-23b_pre
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>Columba-mir-23b-3p
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>Columba-mir-23b-5p
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>Columba-mir-26-1_pre
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>Columba-mir-26-1-3p
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>Columba-mir-26-2_pre
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>Columba-mir-26-2-3p
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>Columba-mir-27b_pre
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>Columba-mir-27b-3p
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>Columba-mir-27b-5p
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>Columba-mir-29a-1_pre
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>Columba-mir-29a-1-3p
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>Columba-mir-29a-2-3p
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>Columba-mir-29b-1_pre
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>Columba-mir-29b-1-5p
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>Columba-mir-29b-2_pre
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>Columba-mir-30a_pre
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>Columba-mir-30a-3p
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>Columba-mir-30c-1_pre
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>Columba-mir-30c-1-3p

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>Columba-mir-30c-2_pre
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>Columba-mir-30c-2-3p
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>Columba-mir-30d_pre
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>Columba-mir-30d-3p
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>Columba-mir-30e_pre
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>Columba-mir-30e-3p
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>Columba-mir-31_pre
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>Columba-mir-31-3p
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>Columba-mir-32_pre
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>Columba-mir-32-3p
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>Columba-mir-33-1_pre
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>Columba-mir-33-1-3p
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>Columba-mir-33-2-3p
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>Columba-mir-34a-3p
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>Columba-mir-34b-3p
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>Columba-mir-34c_pre
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>Columba-mir-34c-3p
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>Columba-mir-92-1-5p
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>Columba-mir-92-2_pre
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>Columba-mir-92-2-5p
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>Columba-mir-100-1-3p
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>Columba-mir-101-1-5p
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>Columba-mir-103-2-5p
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>Columba-mir-106_pre
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>Columba-mir-106-3p
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>Columba-mir-107_pre
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>Columba-mir-107-5p
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>Columba-mir-122_pre
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>Columba-mir-122-3p
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>Columba-mir-124-1-5p
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>Columba-mir-124-2_pre
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>Columba-mir-124-2-5p
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>Columba-mir-125-1_pre
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>Columba-mir-125-1-5p

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>Columba-mir-125-1-3p
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>Columba-mir-125-2_pre
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>Columba-mir-125-2-5p
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>Columba-mir-125-2-3p
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>Columba-mir-126_pre
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>Columba-mir-126-3p
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>Columba-mir-128-1_pre
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>Columba-mir-128-2_pre
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>Columba-mir-128-2-5p
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>Columba-mir-129_pre
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>Columba-mir-129-5p
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>Columba-mir-129-3p
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>Columba-mir-130a_pre
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>Columba-mir-130a-5p
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>Columba-mir-130c_pre
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>Columba-mir-130c-3p
CAGTGCAATATTAAAAGGGCAT
>Columba-mir-130c-5p
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>Columba-mir-133a-1_pre
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>Columba-mir-133a-1-5p
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>Columba-mir-133a-2_pre
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>Columba-mir-133a-2-5p
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>Columba-mir-133b-5p
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>Columba-mir-133c_pre
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>Columba-mir-135-1_pre
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>Columba-mir-135-1-3p
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>Columba-mir-135-2-3p
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>Columba-mir-135-3_pre
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>Columba-mir-135-3-3p
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>Columba-mir-137a_pre
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>Columba-mir-137b_pre
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>Columba-mir-137b-5p
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>Columba-mir-138-1_pre
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>Columba-mir-138-1-5p
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>Columba-mir-138-1-3p
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>Columba-mir-138-2_pre
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>Columba-mir-138-2-3p
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>Columba-mir-139_pre
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>Columba-mir-139-3p
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>Columba-mir-140_pre
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ACCACAGGGTAGAACCACGGAC
>Columba-mir-140-5p
CAGTGGTTTTACCCTATGGTAG

>Columba-mir-142_pre
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CATAAAGTAGAAAGCACTACT
>Columba-mir-142-3p
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>Columba-mir-143_pre
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>Columba-mir-143-5p
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>Columba-mir-144_pre
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TACAGTATAGATGATGTACTC
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>Columba-mir-145_pre
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>Columba-mir-145-5p
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>Columba-mir-145-3p
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>Columba-mir-146a_pre
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>Columba-mir-146a-3p
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>Columba-mir-146b_pre
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>Columba-mir-146b-3p
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>Columba-mir-146c_pre
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>Columba-mir-146c-3p
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>Columba-mir-147_pre
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>Columba-mir-153b_pre
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>Columba-mir-153b-5p
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>Columba-mir-155_pre
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>Columba-mir-187-5p
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>Columba-mir-190_pre
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>Columba-mir-190-3p
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>Columba-mir-193-3p
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>Columba-mir-193-5p
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>Columba-mir-194-3p
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>Columba-mir-196-1_pre
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>Columba-mir-196-2_pre
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>Columba-mir-196-3-3p
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>Columba-mir-200b-3p

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>Columba-mir-200b-5p
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>Columba-mir-202_pre
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>Columba-mir-202-5p
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>Columba-mir-204-1_pre
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>Columba-mir-204-1-5p
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>Columba-mir-204-1-3p
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>Columba-mir-204-2_pre
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>Columba-mir-204-2-5p
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>Columba-mir-204-3p
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>Columba-mir-204-3_pre
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>Columba-mir-204-3-5p
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>Columba-mir-204-3-3p
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>Columba-mir-205a_pre
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>Columba-mir-205a-3p
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>Columba-mir-205b_pre
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>Columba-mir-205b-3p
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>Columba-mir-206_pre
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>Columba-mir-206-5p
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>Columba-mir-210_pre
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>Columba-mir-210-5p
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>Columba-mir-214_pre
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>Columba-mir-214-3p
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>Columba-mir-214-5p
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>Columba-mir-215_pre
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>Columba-mir-215-3p
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>Columba-mir-216a_pre
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>Columba-mir-216a-3p
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>Columba-mir-216b_pre
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>Columba-mir-216b-3p
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>Columba-mir-217_pre
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>Columba-mir-217-5p
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>Columba-mir-217-3p
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>Columba-mir-218-1_pre
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>Columba-mir-218-5p
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>Columba-mir-218-3p
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>Columba-mir-219_pre
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>Columba-mir-219-5p
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>Columba-mir-221_pre
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>Columba-mir-221-3p
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>Columba-mir-221-5p

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>Columba-mir-222a-5p
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>Columba-mir-222b_pre
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>Columba-mir-223_pre
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>Columba-mir-223-5p
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>Columba-mir-301a_pre
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>Columba-mir-301a-5p
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>Columba-mir-301b_pre
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>Columba-mir-301b-3p
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>Columba-mir-301b-5p
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>Columba-mir-302a_pre
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>Columba-mir-302a-3p (predicted)
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>Columba-mir-302b-1_pre
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>Columba-mir-203b_3p
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>Columba-mir-302c_pre
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>Columba-mir-302c-3p
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>Columba-mir-338a_pre
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>Columba-mir-338a-5p

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>Columba-mir-338b_pre
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>Columba-mir-338b-5p
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>Columba-mir-363_pre
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>Columba-mir-363-5p
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>Columba-mir-365-1_pre
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>Columba-mir-365-1-3p
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>Columba-mir-365-1-5p
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>Columba-mir-365-2_pre
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>Columba-mir-365-2-3p
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>Columba-mir-365-2-5p
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>Columba-mir-367_pre
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>Columba-mir-367-3p (predicted)
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>Columba-mir-375_pre
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>Columba-mir-375-3p
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>Columba-mir-375-5p
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>Columba-mir-383_pre
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>Columba-mir-383-5p
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>Columba-mir-383-3p
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>Columba-mir-425_pre
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>Columba-mir-425-5p
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>Columba-mir-425-3p
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>Columba-mir-429_pre

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>Columba-mir-429-5p
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>Columba-mir-449a_pre
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>Columba-mir-449a-5p
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>Columba-mir-449b_pre
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>Columba-mir-449b-5p
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>Columba-mir-449b-3p
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>Columba-mir-449c_pre
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>Columba-mir-449c-5p
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>Columba-mir-449c-3p
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>Columba-mir-449d_pre
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>Columba-mir-449d-5p
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>Columba-mir-449d-3p
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>Columba-mir-451_pre
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>Columba-mir-451-5p
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>Columba-mir-454_pre
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>Columba-mir-454-3p
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>Columba-mir-454-5p
ACCCTATCAATATTGCCTCTGCT

>Columba-mir-455_pre
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>Columba-mir-455-5p
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>Columba-mir-455-3p
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>Columba-mir-456_pre
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>Columba-mir-456-3p
CAGGCTGGTTAGATGGTTGTC

>Columba-mir-458_pre

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>Columba-mir-458-3p
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>Columba-mir-458-5p
AGCGCCATTTCCAGAGCTATAA

>Columba-mir-459-pre
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>Columba-mir-459-5p (predicted)
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>Columba-mir-460a_pre
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>Columba-mir-460a-5p
CCTGCATTGTACACACTGTGTG
>Columba-mir-460a-3p
CACAGCGCATACAATGTGGATT

>Columba-mir-460b_pre
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>Columba-mir-460b-5p
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>Columba-mir-460b-3p
ACAGCGCATGCAATGTGGACA

>Columba-mir-489_pre
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>Columba-mir-489-3p
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>Columba-mir-489-5p
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>Columba-mir-490_pre
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>Columba-mir-490-5p
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>Columba-mir-499_pre
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>Columba-mir-499-5p
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>Columba-mir-499-3p
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>Columba-mir-551a_pre
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>Columba-mir-551a-3p
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>Columba-mir-551a-5p
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>Columba-mir-551b_pre
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>Columba-mir-551b-3p
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>Columba-mir-551b-5p
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>Columba-mir-599_pre
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>Columba-mir-599-3p
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>Columba-mir-737_pre
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>Columba-mir-737-5p (predicted)
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>Columba-mir-875_pre
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>Columba-mir-875-5p
AATACCTCAGTCTTTTCGGATG
>Columba-mir-875-3p
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>Columba-mir-1306_pre
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>Columba-mir-1306-5p
CCACCTCCCCTGCAAACGTCC
>Columba-mir-1306-3p
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>Columba-mir-1329_pre
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>Columba-mir-1329-5p
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>Columba-mir-1329-3p
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>Columba-mir-1388_pre
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>Columba-mir-1388-5p
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>Columba-mir-1388-3p
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>Columba-mir-1416_pre
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>Columba-mir-1416-5p
TCCTTAACTCATGCCGCTGTGC
>Columba-mir-1416-3p
ACAATTGTGTGAGTTGAGTACA

>Columba-mir-1451_pre
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>Columba-mir-1451-5p
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>Columba-mir-1451-3p
AGTAACTTGCTCCTGTGAGAGG

>Columba-mir-1467_pre
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>Columba-mir-1467-3p
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>Columba-mir-1467-5p
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>Columba-mir-1550_pre
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>Columba-mir-1550-5p (predicted)
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>Columba-mir-1552_pre
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>Columba-mir-1552-5p
TTAGTGCGCGGTAAGCTAGGGTG
>Columba-mir-1552-3p
CGCTAGCTGCTCTGCACTAACT

>Columba-mir-1559_pre
ACATGAAGGTCTAGACTCCTTTCGATGCTTGTATGCTACTCCCAAGAATGCTAACAGGAGTTCCATGTATGCATCGAGCAGAGACTATACCATTTA
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>Columba-mir-1559-3p
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>Columba-mir-1641_pre
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>Columba-mir-1641-5p
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>Columba-mir-1655_pre
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>Columba-mir-1655-3p (predicted)
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>Columba-mir-1662_pre
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>Columba-mir-1662-5p
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>Columba-mir-1662-3p
CCCAAGCAGGCTGATGTCAGGC

>Columba-mir-1677_pre
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>Columba-mir-1677-3p
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>Columba-mir-1677-5p
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>Columba-mir-1720_pre
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>Columba-mir-1720-3p
GAAGCAACGAGAGGCTGGTCTGA
>Columba-mir-1720-5p
TGACCACCTCAGCCGTTGCTTTTG

>Columba-mir-1729_pre
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>Columba-mir-1729-3p
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>Columba-mir-1729-5p
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>Columba-mir-1781_pre
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>Columba-mir-1781-3p
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>Columba-mir-1782_pre
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>Columba-mir-1782-3p
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>Columba-mir-1784_pre
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>Columba-mir-1784-5p
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>Columba-mir-1788_pre
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>Columba-mir-1788-3p
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>Columba-mir-1788-5p
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>Columba-mir-1791_pre
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>Columba-mir-1791-3p
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>Columba-mir-1803-1_pre
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>Columba-mir-1803-1-3p
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>Columba-mir-1803-1-5p
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>Columba-mir-1803-2_pre
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>Columba-mir-1803-2-3p
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>Columba-mir-1805_pre
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>Columba-mir-1805-3p
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>Columba-mir-1805-5p
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>Columba-mir-2131_pre
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>Columba-mir-2131-5p
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>Columba-mir-2188-3p
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>Columba-mir-2954-5p
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>Columba-mir-2970-3p
CAGATCACCTCTTGGCTGTGGG

>Columba-mir-2984_pre
TGCTTCACCTGCGGAGCCTGCTGGGAGCGAAATTGAGAAAGGACAGCGCCAGCCCAGGCAATTTCACTCACAGCGGGCACTTGCAGGTGAAGCA
>Columba-mir-2984-5p (predicted)
AGCCTGCTGGGAGCGAAATTGA

>Columba-mir-3064_pre
TTTATCTTCGATTTGGCTGTTGTGGTGTGCAAAACTTTGTACCTTGCTTTTTGCCACACTGCAACACTTTACAGATGTGGAAGATGTG
>Columba-mir-3064-3p
TTGCCACACTGCAACACTTTAC

>Columba-mir-3618_pre
GAATGCATTGTGATTTCCAATAATTGAGACAGTGATTCTGAAAGCTGTCTACATTAATGAAAAGAACAATGTAGTCA
>Columba-mir-3618-5p
TGATTTCCAATAATTGAGACAG
>Columba-mir-3618-3p
CTACATTAATGAAAAGAACAAT

>Columba-novel-1_pre
AGTTGGTGACCATTTTTCTCCCATGGCTGTATAACCCTTTCGATATCCTTGGATTGCACAGCTTTGGTAGGAAGCTGGCCACCATCT
>Columba-novel-1-5p
TCTCCCATGGCTGTATAACCC
>Columba-novel-1-3p
TTGCACAGCTTTGGTAGGAAG

>Columba-novel-2_pre
AGTGGGGGCTGCGGCCTGGGGCAGCGCAAACCCCACTTTAGGGTGGAAAACACAAGGTTGAGCTGATCCAGGCCTGGCCTCCCCTC
>Columba-novel-2-3p
TTGAGCTGATCCAGGCCTGGC
>Columba-novel-2-5p
TGCGGCCTGGGGCAGCGCAAACC

>Columba-novel-3_pre
TGCCTGTTGTCTTATGATCATAAGGATAAATGAGCCCCATCGAGTAATTAATTTATCCGTATGATCATAAGACAGCAGACC
>Columba-novel-3-3p
ATTTATCCGTATGATCATAAGA

>Columba-novel-3-5p
TTATGATCATAAGGATAAATGA

>Columba-novel-4_pre
TCAAGCTGTGGGGTCCTGGCAGAGGGCCCACTCTTGGCCGGGGGGACAAAGCCATCAAAGATGGACCCTCTGCTGGCACCCCACAGCTGCA
>Columba-novel-4-3p
CATCAAAGATGGACCCTCTGCTGG
>Columba-novel-4-5p
TGGCAGAGGGCCCACTCTTGGC

>Columba-novel-5_pre
TGTGAGCCTGATCCAATATTCCTTAAGTAGGCAAAGTTGATTCTTTCACAGTTTTGCCTGCTCAAGGGGTAGAGGAATAG
>Columba-novel-5-3p
TTTTGCCTGCTCAAGGGGTAGA
>Columba-novel-5-5p
TATTCCTTAAGTAGGCAAAGTT

>Columba-novel-6_pre
TGCACAATTTCCCCTTTAGGAGAAAAATCTCAGTTATTGCACTTTGTGTAAATTCAATAACTAAGATATTTCTCCTGAAGGGGAAATGGTGCA
>Columba-novel-6-3p
ACTAAGATATTTCTCCTGAAGG
>Columba-novel-6-5p
TTTAGGAGAAAAATCTCAGTT

>Columba-novel-7_pre
ACCTCCCATCAGGATACATCCCGTTGGGATGCATTCTGTCAGAATGCACCTCATCAGGATACATCCCATCGGGATGCACCCCATGGGGCAG
>Columba-novel-7-5p
TCCCGTTGGGATGCATTCTGTC
>Columba-novel-7-3p
CAGGATACATCCCATCGGGATG

>Columba-novel-8_pre
GGAGGGCCAGATCCTCAGCTGATGTAAATTAGGAGAGCTCTGTCAATGTTAAACGCTTTCCTGATTTACTCCAGCTGAAGATTTGACCTGGG
>Columba-novel-8-3p
TTTCCTGATTTACTCCAGCTGA
>Columba-novel-8-5p
AGCTGATGTAAATTAGGAGAGC

>Columba-novel-9_pre
GTACCACATCCTCAGCTGGTGTAAGTCGGCTTTTACTCCATTAATACTGACTTACATTGCCTGAGGACCTGGATT
>Columba-novel-9-5p
TCCTCAGCTGGTGTAAGTCGGC
>Columba-novel-9-3p
TGACTTACATTGCCTGAGGACC

>Columba-novel-10_pre
CGTGGGGAAGATGCCGTGGGGGTTTCCCTGCCTGGGACCCGAGGTGTGAAGGGCCCGTCGGGGCTGACCCCCATGGCAGCTGGCTCCTTC
>Columba-novel-10-3p
CCCGTCGGGGCTGACCCCCATG
>Columba-novel-10-5p
TGGGGGTTTCCCTGCCTGGGAC

>Columba-novel-11_pre
TACCTAGGCCTTTTCTAGTGTGGGATTTAAAGTTGTGTGTAACTCGTGACAGCATACCTTTAAATCCTGGTCTGGACAAGGT
>Columba-novel-11-3p
ATACCTTTAAATCCTGGTCTGG
>Columba-novel-11-5p

AGTGTGGGATTTAAAGTTGTGT

>Columba-novel-12_pre
GATGGGCTCAGTTGTGTCCTGCCTTGGCTCTGCTGTGAGGAACTGTCTGGAGCCGGCCATGTCAGGCACAGTGCAGCCCCTT
>Columba-novel-12-5p
GTTGTGTCCTGCCTTGGCTCTG
>Columba-novel-12-3p
CGGCCATGTCAGGCACAGTGCT

>Columba-novel-14_pre
GAGAGCATCGGAGCTGTCGGAGCCGATGTTCTAGCTGGAATGAAAAACGGCTGACGCTGGCACCGAGAGCCCTGTGGCTTCC
>Columba-novel-14-5p
CTGTCGGAGCCGATGTTCTAGCT
>Columba-novel-14-3p
CTGACGCTGGCACCGAGAGCC

>Columba-novel-15_pre
AAGAACAGATCAGGGCTTGGAGAAATAACACGCTAAAGAGTTTCAGCTGGTGTGGTCTCTCTCTGCCCAGTTTGCCCGTCCAGT
>Columba-novel-15-5p
AGGGCTTGGAGAAATAACACGCT
>Columba-novel-15-3p
TGTGGTCTCTCTCTGCCCAGT

>Columba-novel-16_pre
GAAGGTTTTGTAGCTCAGGAGCAGTGCCAAGGCTGGGCTGGCTCTGCGCCTCAGCGTGGGCACTGCTCCAGACCTAATAAACCCTG
>Columba-novel-16-3p
CAGCGTGGGCACTGCTCCAGAC
>Columba-novel-16-5p
CAGGAGCAGTGCCAAGGCTGGG

>Columba-novel-17_pre
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>Columba-novel-17-3p
CTTGTCTCTACACCTCTGCAAC
>Columba-novel-17-5p
CAGCAGAGGAAATCCAGACGAGCT

>Columba-novel-18_pre
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>Columba-novel-18-5p
CACAGTCTGGCAGGGCTTGCAG
>Columba-novel-18-3p
GGAGGCTTTGCCAGCCTGGGC

>Columba-novel-19_pre
TCTACCATGGTCACGGCCACTCGCACGAGGAGCCGCACCACGGCCACTCGCACGAGGGGCTCTACCATGGTCAC
>Columba-novel-19-3p
CACTCGCACGAGGGGCTCTACC
>Columba-novel-19-5p
CACGGCCACTCGCACGAGGAGC

>Columba-novel-20_pre
CCACCCACACCAAGAGCCCCCAGTGTCGCCGGCCACCCCAGCTCGGCCCGCCCGGCGACACTCGGGGCTCTTGGCGTGGGCCA
>Columba-novel-20-3p
CCCGGCGACACTCGGGGCTCT
>Columba-novel-20-5p
AGCCCCCAGTGTCGCCGGCC

>Columba-novel-21_pre
GTTCAAAGGCACAGATGATAGCCAGGTGCCTCATCTCATGCCTGTGGAAAAACCTGTGTGAGAGGAGTGTCTGACTGTTTTCTGTGCCTTTGCGA
>Columba-novel-21-3p
TGTGAGAGGAGTGTCTGACTGTT
>Columba-novel-21-5p
TAGCCAGGTGCCTCATCTCATGCC

>Columba-novel-22_pre
CTACTTCTGGTCAGGCCAGAAATTTTGCAAGAGCAGCCTCTCTCATGATATTTTGGCACTTTTGCTTCTGGTCTTGCCTGAAGCCT
>Columba-novel-22-3p
CACTTTTGCTTCTGGTCTTGC
>Columba-novel-22-5p
CAGGCCAGAAATTTTGCAAGAGC

>Columba-novel-23_pre
GGGCTCCACATGCAGAGGATGGAGCTGAATGGGATTTTGCTGCCTGAAATGGTCCCATCCAGCCCCAGTCCTGCTGCACGGGGAGGCA
>Columba-novel-23-5p
AGAGGATGGAGCTGAATGGGA
>Columba-novel-23-3p
CCATCCAGCCCCAGTCCTGCTGC

>Columba-novel-24_pre
GAGGAGGGGCAGGGTCAAGGGTCAAAGGTCAGGGTGGCCAAGACCTTGACCTTGACCTTTGACCCCAGCCGGCCAAG
>Columba-novel-24-3p
TGACCTTGACCTTTGACCCCAGC
>Columba-novel-24-5p
CAGGGTCAAGGGTCAAAGGTCAG

>Columba-novel-25_pre
GTCTAAAAATCTTGTTCCCTATGTTAAGGGAGCCTGTTTGTAAATAGGGCAGGTCCCCTGCATAAGGACAGTGTTTTTATTCACA
>Columba-novel-25-3p
TCCCCTGCATAAGGACAGTGT
>Columba-novel-25-5p
CTTGTTCCCTATGTTAAGGGAGCC

>Columba-novel-26_pre
CTGAGCAACCTGAAGCATATTTATACAGATTAAGTGGTTTCTAATACTCCAAAGAGCACTTAATCTGCATGAATGTGCTTCATGTTGCTATGT
>Columba-novel-26-5p
TATTTATACAGATTAAGTGGTTTC
>Columba-novel-26-3p
AGCACTTAATCTGCATGAATGTG

>Columba-novel-27_pre
CGCTCCCCGCAAAACCAGTGGGTACCTTGTAGAAGGGACTGGTGGAGAGTGGACAAGTACCCGCTGGTTTGCTTGGGGAGGT
>Columba-novel-27-5p
CGCAAAACCAGTGGGTACCTTGTA
>Columba-novel-27-3p
CAAGTACCCGCTGGTTTGCTTG

>Columba-novel-28_pre
ATTGTCTTGGCCTGTCCTCAGGACCAGGTGCCTTCTCCTGTTCCCTGCTGAAGTCTTCCTTGTCCTGACAGGGAGCCAAGATCAT
>Columba-novel-28-3p
TGAAGTCTTCCTTGTCCTGACAG
>Columba-novel-28-5p
CTCAGGACCAGGTGCCTTCTCC

>Columba-novel-29_pre
AAATTGAGTCATCAGCAGCAAGGACCACTTAGTCCTGCTCTCCTCTCTCTCACGCCACAGGTCTAAGTGGTCCTCGCTGCCGATGACTCAATACA
>Columba-novel-29-3p
AGGTCTAAGTGGTCCTCGCTGC
>Columba-novel-29-5p
AGCAAGGACCACTTAGTCCTGC

>Columba-novel-30_pre
TCTCCGGGGCGGTGGAAGGAGCCGGTAGCTGTGCAGCCCGCTGTCCGACAGCGCTGCTGAGCTCACGGCACCGACCACCGTGCGCGGCCT
>Columba-novel-30-5p
AGGAGCCGGTAGCTGTGCAGCC
>Columba-novel-30-3p
CTGCTGAGCTCACGGCACCGAC

>Columba-novel-31_pre
CACGGGCGGCAGAGCCTCGCGCTGACTCTGAAGGTTCTGGTAACTCGACTTCAGATGGCAGAGCTGAGGCTGCGCCGCTCGCT
>Columba-novel-31-3p
TCAGATGGCAGAGCTGAGGCTGC
>Columba-novel-31-5p
GAGCCTCGCGCTGACTCTGAAG

>Columba-novel-32_pre
GTCGGCTGCTCGGGAACCGCTGGCACGTTGGAGCCCTCGCCTTTGTGCCTCTCGGCGAGCGTGATGTGCCACGGCTCTCGTCGGCCTGTC
>Columba-novel-32-3p
CGAGCGTGATGTGCCACGGCTC
>Columba-novel-32-5p
CCGCTGGCACGTTGGAGCCCTCGCC

>Columba-novel-33_pre
CGACCAGAGGTGAGAGCTCAGGTGCCTTCTCCAAATCCTTCTGAGCACGGGACGGCGCCCTGACCTCTGTCCCCTCTCGGCAG
>Columba-novel-33-3p
GACGGCGCCCTGACCTCTGTCC
>Columba-novel-33-5p
GTGAGAGCTCAGGTGCCTTCTC

>Columba-novel-34_pre
CTGTGGTACCGACCCTGCGCGGCCGGTACTGATCCTGCAGTACCAACCCTGTGCGGCCGGTACTGACCCTGCATGGCTGGTACCAATC
>Columba-novel-34-3p
TGCGGCCGGTACTGACCCTGCA
>Columba-novel-34-5p
CGCGGCCGGTACTGATCCTGCA

>Columba-novel-35_pre
TTGCCCAGAGGTGGTGTGGGGTTTGGATCTCAGTTAAAATCTCACTGGAGACCATACTGCACAGCCTTCTCTAGGTGA
>Columba-novel-35-3p
GGAGACCATACTGCACAGCCTTC
>Columba-novel-35-5p
TGGTGTGGGGTTTGGATCTCAG

>Columba-novel-36_pre
CCTGTGCAGCACTTGCCACCACAGTGGGCTGCTGCAGGACACATAGCCGGAGCACACGGTGGTGGTACCAGTGCTGGATCTG
>Columba-novel-36-5p
TGCCACCACAGTGGGCTGCTGC
>Columba-novel-36-3p
CGGAGCACACGGTGGTGGTACC

>Columba-novel-37_pre

TTAGAGTGGTATTTAGACCGATTGTTGGTAGTGTTCTTTATAAAAACGATAAAGAACACTACCAACGACCGGTCTAAATGCCACTTATC
>Columba-novel-37-3p
AAGAACACTACCAACGACCGGT
>Columba-novel-37-5p
CGATTGTTGGTAGTGTTCTTTA

>Columba-novel-38_pre
AGGTGAGGGCTGGTTCCCGCGCTGGTGTGTGGCTCCGTGGCCCCGAGCTGCCCGGGAGCCGCTCACCAGCGCTGGTGTCTCTGTCCCCAGGT
>Columba-novel-38-3p
AGCCGCTCACCAGCGCTGGTGT
>Columba-novel-38-5p
TCCCGCGCTGGTGTGTGGCTCC

>Columba-novel-39_pre
AGAGGCCATCTCATGCCATTAATTTCTAAGCAGTCAATGAGGAATTCTGCTGTAGAATTAATGGCAAAATATGGCCCAC
>Columba-novel-39-3p
CTGTAGAATTAATGGCAAAAT
>Columba-novel-39-5p
CATGCCATTAATTTCTAAGCA

>Columba-novel-40_pre
GAAGGTAAAGAAGTTACACTGGGTCTCCCACATCTCTGGTGAGATTTTTAGCTACAGAGATGCTGGGTGAAACAGTGTATCTTCATATCAGT
>Columba-novel-40-5p
CACTGGGTCTCCCACATCTCTG
>Columba-novel-40-3p
GAGATGCTGGGTGAAACAGTGT

>Python-let-7a-1_pre
CTGCTCTGTGGGATGAGGTAGTAGGTTGTATAGTTTTAGGGTCATACCCACCACTGGGAGATAACTATACAGTCTACTGTCTTTCCTAAGGAGGCA
>Python-let-7a-1-5p
TGAGGTAGTAGGTTGTATAGTT
>Python-let-7a-1-3p
CTATACAGTCTACTGTCTTTC

>Python-let-7a-2_pre
TGTCCTTTGGGGTGAGGTAGTAGGTTGTATAGTTTTAGGGTTAGACCCTGCCTGTCAGATAACTATACAATCTACTGTCTTTCCTGAAGTGGCTGT
>Python-let-7a-2-5p
TGAGGTAGTAGGTTGTATAGTT
>Python-let-7a-2-3p
CTATACAATCTACTGTCTTTCC

>Python-let-7a-3_pre
AGGTGAGGTAGTAGGTTGTATAGTTTGTGGGAGGGATTATATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTA
>Python-let-7a-3-5p
TGAGGTAGTAGGTTGTATAGTT

>Python-let-7b_pre
GGTGAGGTAGTAGGTTGTGTGGTTTCAGGGTAGTAATTTTGCCCCAATCAGGAGATAACTATACAACCTACTGCCTTCCTTGA
>Python-let-7b-5p
TGAGGTAGTAGGTTGTGTGGTT
>Python-let-7b-3p
CTATACAACCTACTGCCTTCCT

>Python-let-7c-1_pre
GTGTGCATCCGGGTTGAGGTAGTAGGTTGTATGGTTTAGAATTACACCCAGGAGTTAACTGTACAACCTTCTAGCTTTCCTTGGAGCACACTTGA
>Python-let-7c-1-5p
TGAGGTAGTAGGTTGTATGGTT
>Python-let-7c-1-3p
CTGTACAACCTTCTAGCTTTCC

>Python-let-7c-2_pre
GCGTGCCTCGTGTTGAGGTAGTAGGTTGTATGGTTGAGAATAACACCATCAGGAGATAACTATACAGCCTCCTAGCTTTCCCTGAGGCATCGCCA
>Python-let-7c-2-5p
TGAGGTAGTAGGTTGTATGGTT
>Python-let-7c-2-3p
CTATACAGCCTCCTAGCTTTCC

>Python-let-7c-3_pre
CAAGCTGAGGTAGTAGGTTGTATGGTTTAGAATTACACCAAGGGAGATAACTGTACAGCCTCCTAGCTTTACTT
>Python-let-7c-3-5p
TGAGGTAGTAGGTTGTATGGTT

>Python-let-7d_pre
GGGTTCCTAGGAAGAGGTAGTAGGTTGCATAGTTTTAGGGCAGTGGTTTTGCCTATAAGGAGTTAACTATACAACCTGCTGCCTTTCTTAGGGCT
>Python-let-7d-5p
AGAGGTAGTAGGTTGCATAGTT
>Python-let-7d-3p
CTATACAACCTGCTGCCTTTCT

>Python-let-7e_pre
ATGCTGTCCTTGAGGCTGAGGTAGTAGATTGAATAGTTGTGGAGCCATCTTCTCCCTTTGAGCTAACTATACAATCTACTGTCTTTCCTA
>Python-let-7e-5p
TGAGGTAGTAGATTGAATAGTT
>Python-let-7e-3p

CTATACAATCTACTGTCTTTCC

>Python-let-7f-1_pre
CCTGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCATACCCGGTCTTGGAGATAACTATACAATCTACTGTCTTTCCTA
>Python-let-7f-1-5p
TGAGGTAGTAGATTGTATAGTT
>Python-let-7f-1-3p
CTATACAATCTACTGTCTTTCT

>Python-let-7f-2_pre
TTATCAGGTTGAGGTAGTAGATTGTATAGTTGTAGGGCAGTTATTTTGCCCTCTTCAGGAGATAACTATACAATCTATTGCCTTCCCTGAGGA
>Python-let-7f-2-5p
TGAGGTAGTAGATTGTATAGTT
>Python-let-7f-2-3p
CTATACAATCTATTGCCTTCCT

>Python-let-7g_pre
GTTCCAGGCTGAGGTAGTAGTTTGTACAGTTTGAGGGTCTACGATACCGCCCGGTACAGGAGATAACTGTACAGGCCACTGCCTTGCCTGGGGC
>Python-let-7g-5p
TGAGGTAGTAGTTTGTACAGTT
>Python-let-7g-3p
CTGTACAGGCCACTGCCTTGC

>Python-let-7i_pre
ACCCTGGCTGAGGTAGTAGTTTGTGCTGTTCGTCGGGTTGTGACATTGCCCGCTGTGGAGATAACTGCGCAAGCTACTGCCTTGCTAGTGC
>Python-let-7i-5p
TGAGGTAGTAGTTTGTGCTGTT
>Python-let-7i-3p
CTGCGCAAGCTACTGCCTTGCT

>Python-mir-1a-1_pre
ACCTGCTTGAGTGACATACTTCTTTATATGCCCATATGAACCTGGCAAACTATGGAATGTAAAGAAGTATGTATTTCAGGCATGGA
>Python-mir-1a-1-3p
TGGAATGTAAAGAAGTATGTA
>Python-mir-1a-1-5p
CATACTTCTTTATATGCCCATA

>Python-mir-1a-2_pre
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>Python-mir-1a-2-3p
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>Python-mir-1a-2-5p
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>Python-mir-1b_pre
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>Python-mir-1b-5p
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>Python-mir-7-1_pre
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>Python-mir-7-1-5p
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>Python-mir-7-1-3p
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>Python-mir-7-2-5p
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>Python-mir-7-2-3p
CAACAAGTCACAGTCTGCCTT

>Python-mir-7-3_pre
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>Python-mir-7-3-5p
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>Python-mir-7-3-3p
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>Python-mir-9-1_pre
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>Python-mir-9-1-5p
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>Python-mir-9-1-3p
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>Python-mir-9-2_pre
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>Python-mir-9-2-3p
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>Python-mir-9-3-3p
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>Python-mir-9-4_pre
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>Python-mir-9-4-3p
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>Python-mir-10a_pre
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>Python-mir-10a-5p
TACCCTGTAGATCCGAATTTGTG
>Python-mir-10a-3p
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>Python-mir-10b-1_pre
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>Python-mir-10b-1-3p
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>Python-mir-10b-2_pre
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>Python-mir-10b-2-3p
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>Python-mir-15a_pre
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TAGCAGCACATCATGATTTGTG
>Python-mir-15a-3p
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>Python-mir-15b_pre
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>Python-mir-15b-5p
TAGCAGCACGACATGGTTTGTA
>Python-mir-15b-3p
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>Python-mir-16a_pre
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>Python-mir-16a-5p
TAGCAGCACATAAATATTGGAG (predicted)

>Python-mir-16b_pre
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>Python-mir-16b-5p
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>Python-mir-16b-3p
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>Python-mir-16c_pre
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>Python-mir-16c-5p
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>Python-mir-16c-3p
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>Python-mir-17_pre
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>Python-mir-17-3p
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>Python-mir-18a-5p
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>Python-mir-18a-3p
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>Python-mir-18b_pre
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>Python-mir-18b-5p

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>Python-mir-19a_pre
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>Python-mir-19a-3p
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>Python-mir-19a-5p
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>Python-mir-19b-1_pre
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>Python-mir-19b-1-3p
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>Python-mir-19b-2_pre
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>Python-mir-20a_pre
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>Python-mir-20a-5p
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>Python-mir-20a-3p
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>Python-mir-20b_pre
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>Python-mir-20b-5p
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>Python-mir-20b-3p
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>Python-mir-21_pre
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>Python-mir-21-3p
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>Python-mir-22-5p
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>Python-mir-23a_pre
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>Python-mir-23b-5p
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>Python-mir-24-1-5p
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>Python-mir-26-1-3p
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>Python-mir-26-3-3p
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>Python-mir-27a-3p
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>Python-mir-29b-1-5p
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>Python-mir-30c-1-3p
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>Python-mir-33-1-5p
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>Python-mir-33-2_pre
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>Python-mir-34b-3p
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>Python-mir-34c-3p
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>Python-mir-92a-1_pre
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>Python-mir-92a-2_pre
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>Python-mir-96_pre
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>Python-mir-96-3p
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>Python-mir-98-3p
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>Python-mir-99a-3p
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>Python-mir-99b-3p
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>Python-mir-101-2-5p
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>Python-mir-106-3p

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>Python-mir-107-5p
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>Python-mir-122-3p
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>Python-mir-124a-5p
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>Python-mir-124b-1_pre
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>Python-mir-124b-3p
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>Python-mir-124b-5p
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>Python-mir-125b-2_pre
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>Python-mir-128-1-5p
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>Python-mir-128-2_pre
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>Python-mir-130c-5p
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>Python-mir-138-1-3p
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>Python-mir-138-2_pre
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>Python-mir-142-3p
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>Python-mir-145-3p
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>Python-mir-146a_pre
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>Python-mir-146a-5p

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>Python-mir-153-2-5p
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>Python-mir-155b_pre
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>Python-mir-181b-1_pre
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>Python-mir-181b-2_pre
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AACATTCATTCTGTCGGTGGGT

>Python-mir-182_pre
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>Python-mir-182-5p
TTTGGCAATGGTAGAACTCACACT
>Python-mir-182-3p
TGGTTCTAGACTTGCCAACT

>Python-mir-183_pre
TCCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACTCGATCAGTGAATTACCAACGGGCCATAAACGGAGCAGAGAAAGAACC
>Python-mir-183-5p
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>Python-mir-190a-3p
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#NEXUS
[MacClade 4.08 registered to Kevin J. Peterson, Dartmouth College]


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  37  TN25,  38  TN27,  39  TN29,  40  SN1,  41  AN1,
  42  AN2,  43  AN8,  44  AN9,  45  AN10,  46  AN13,
  47  AN14,  48  AN15,  49  AN16,  50  AN20,  51  AN21,
  52  AN27,  53  AN35,  54  AN36,  55  AN39,  56  AN41,
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Supplemental File 6 – Age constraints for nodes for Bayesian analysis (Fig. 1)

Node	Age-indicative fossil	Hard Minimum (Ma)	Soft Maximum (Ma)	Reference
Gallus-Taenopygia-Columba	*Vegavis*	66	86.5	Benton et al. 2009
Chrysemys-Chelonia	*Lindholmemys*	88.6	149.6	Joyce et al. 2014
Anolis-Python	*Haasiophis*	99.6-93.5	None (point estimate)	Tchernov et al. 2000
(*Chrysemys +Chelonia*)-(*Apalone +Pelodiscus*)	*Pantrionichidae indet.*	125+-1	199.6+-0.6	Joyce et al. 2013
Birds-Crocodylians	*Arizonasaurus*	239	250.4	Benton et al. 2009
Lepidosaurs-Archosaurs	*Protorosaurus*	255.9	299.8	Benton et al. 2009
Mammals-Reptiles	*Hylonomus*	312.3	330.4	Benton et al. 2009
Xenopus-Amniotes	*Lethiscus*	330.4	350.1	Benton et al. 2009
Coelacanth-Tetrapods	*Eoactinistia*	407-409	None (point estimate)	Johanson et al. 2006
Zebrafish-Tetrapods	*Psarolepis*	416	421.75	Benton et al. 2009

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Johanson, Z., Long, J. A., Talent, J. A., Janvier, P. & Warren, J. W. Oldest coelacanth, from the Early Devonian of Australia. *Biology Letters* **2**, 443-446 (2006).

Joyce, W. G., Parham, J. F., Lyson, T. R., Warnock, R. C. M. & Donoghue, P. C. J. A divergence dating analysis of turtles using fossil calibrations: an example of best practices. *Journal of Paleontology* **87**, 612-634 (2013).

Tchernov, E., Rieppel, O., Zaher, H., Polcyn, M. J. & Jacobs, L. L. A fossil snake with legs. *Science* **287**, 2010–2012 (2000).

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Lch TTTGCCCC-ATTGGGAGATAACTATACAACCTACTGCCTTCCC----------------- [548]
Dre TTTGCCCC-ATCAGGAGTTAACTATACAACCTACTGCCTTCCC--TGGTGAGGTAGTAAG [554]

Hsa TTGTATTGTTGTGGGGTAGGGATAT-TA-GGCCCCAATT-AGAAGATAACTATACAACTT [689]
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Mmu TTGTATTGTTGTGGGGTAGGGATTT-TA-GGCCCCAGTA-AGAAGATAACTATACAACTT [689]
Mdo ------------------------------------------------------------ [477]
Meu ------------------------------------------------------------ [470]
Oan TTGTATTGTTGTGGGGTAGGGATTTCTTTTGCCCCAATT--AGCGATAACTATACAATTT [622]
Aca TTGTATTGTTGTGGGGTAGGGAT---TTGTGCCCCAAAT-CAGAGATAACTATACAACTT [693]
Pbi TTGTATTGTTGTGGGGTAGGGAT---TTGTGCCCCAAAT-CAGAGATAACTATACAACTT [692]
Cpi TTGTATTGTTGTGGGGTCGGGAT---TCGTGCCCCAA-T-CAGAGATAACAATACAACTT [692]
Cmy TTGTATTGTTGTGGGGTCAGGAT---TCATGCCCCAA-T-CAGAGATAACGATACAACTT [692]
Psi ------------------------------------------------------------ [621]
Asp ------------------------------------------------------------ [621]
Ami TTGTATCGTTGGGGGGTCGGGAT---TGGAGCCCCGGTG-TCGAGGTAACTATACAACTT [692]
Asi TTGTATCGTTGTGGGGTCGGGAT---TGGAGCCCCGGTG-TCGAGGTAACTATACAACTT [692]
Tgu ------------------------------------------------------------ [548]
Cli ------------------------------------------------------------ [548]
Gga ------------------------------------------------------------ [548]
Xtr TTGTATTGTTGTGGGGGTTTTTA-----TTTCCCCAAATTAGGAGATAACTATACAGCTT [448]
Lch ------------------------------------------------------------ [548]
Dre TTGTGTTGTTGTTGGGGATCAGTATAGTATGGCCCTTGA-AGGAGATAACTATACAATTT [613]

Hsa ACTACTTTCC--TGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCATACCCCATCTTG [747]
Mmu ACTACTTTCC--TGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCATACCCCATCTTG [747]
Mdo ------------CGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCACACCCGATCTCG [525]
Meu ------------CGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCACACCCGATCTTG [518]
Oan ACTACTTTCC--TGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCATACCCGATCTTG [680]
Aca ACTACTTTCC--TGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCATACCCGGTCTTG [751]
Pbi ACTACTTTCC--TGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCATACCCGGTCTTG [750]
Cpi ACTACTTTCC--GGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCACACCCGGTCTCG [750]
Cmy ACTACTTTCC--GGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCACACCCGGTCTCG [750]
Psi ------------------------------------------------------------ [621]
Asp ------------------------------------------------------------ [621]
Ami ACTACTTTCC--TGGGCTGAGGTAGTAGATTGTATAGTTCT-GGGTCACACCCG--CGCG [747]
Asi ACTACTTTCC--TGGGCTGAGGTAGTAGATTGTATAGTTCT-GGGTCACACCCG--CGCG [747]
Tgu ------------------------------------------------------------ [548]
Cli ------------------------------------------------------------ [548]
Gga ------------------------------------------------------------ [548]
Xtr ACTGCCTTCC--CAGGATGAGGTAGTAGATTGTATAGTTTTGGGGTCACACCCGATCTGG [506]
Lch ------------CGGGTTGAGGTAGTAGATTGTATAGTTTTAGGGTCACACCCGATCTTG [596]
Dre ACTGCCTTCC--TGGGATGAGGTAGTAGTTTGTATAGTTTTAGGATCACACCAGATCTGG [671]

Hsa GAGATAACTATACAGTCTACTGTCTTTCCCA--GGCTGAGGTAGTAGTTTGTACAGTTT- [804]
Mmu GAGATAACTATACAGTCTACTGTCTTTCCCA--GGCTGAGGTAGTAGTTTGTACAGTTT- [804]
Mdo GAGATAACTATACAGTCTACTGTCTTTCCCA--GGCTGAGGTAGTAGTTTGTACAGTTT- [582]
Meu GAGATAACTATACAGTCTACTGTCTTTCTCA---------------------------- [549]
Oan GAGATAACTATACAGTCTACTGTCTTTCCCA--GGCTGAGGTAGTAGTTTGTACAGTTT- [737]
Aca GAGATAACTATACAATCTACTGTCTTTCCTA--GGTTGAGGTAGTAGTTTGTACAGTTT- [808]
Pbi GAGATAACTATACAATCTACTGTCTTTCCTA--GGCTGAGGTAGTAGTTTGTACAGTTT- [807]
Cpi GAGATAACTATACAGTCTACTGTCTTTCCCG--GGCTGAGGTAGTAGTTTGTACAGTTT- [807]
Cmy GAGATAACTATACAGTCTACTGTCTTTCCCG--GGCTGAGGTAGTAGTTTGTACAGTTT- [807]
Psi ---------------------------------GGCTGAGGTAGTAGTTTGTACAGTTT- [647]
Asp ---------------------------------GGCTGAGGTAGTAGTTTGTACAGTTT- [647]
Ami GAGATAACTATACAGCCTACTGTCTTTCCTG--AGCTGAGGTAGTAGTTTGTACAGTTT- [804]
Asi GAGATAACTATACAGCCTACTGTCTTTCCTG--AGCTGAGGTAGTAGTTTGTACAGTTT- [804]
Tgu ---------------------------------GGCTGAGGTAGTAGTTTGTACAGTTT- [574]
Cli ---------------------------------GGCTGAGGTAGTAGTTTGTACAGTTT- [574]
Gga ---------------------------------GGCTGAGGTAGTAGTTTGTACAGTTT- [574]
Xtr GAGATAACTATACAGTTTACTGTCTTTCCTG--GGCTGAGGTAGTTGTTTGTACAGTTT- [563]
Lch GAGATAACTATACAGTCTACTGTCTTTCCTG--GGCTGAGGTAGTAGTTTGTACAGTTT- [653]
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Dre GAGATAACTATACAGTCTACTGTCTTTCCCA--GGTTGAGGTAGTTGTTTGTACAGTTTT [729]

Hsa GAGGGTCTATGATACCACCCGGTACAGGAGAT-AACTGTACAGGCCACTGCCTTGCCAG- [862]
Mmu GAGGGTCTATGATACCACCCGGTACAGGAGAT-AACTGTACAGGCCACTGCCTTGCCAG- [862]
Mdo GAGGGTCTATGATACCACCCGGTACAGGAGAT-AACTGTACAGGCCACTGCCTTGCCAG- [640]
Meu ------------------------------------------------------------ [549]
Oan CAGGGTCTACAATACCACCCGGTATAGGAGAT-AACTGTACAGGCCACTGCCTTGCCAG- [795]
Aca GAGGGTCTATGATACCACCCGGTACAGGAGAT-AACTGTACAGGCCACTGCCTTGCCTG- [866]
Pbi GAGGGTCTACGATACCGCCCGGTACAGGAGAT-AACTGTACAGGCCACTGCCTTGCCTG- [865]
Cpi GAGGGTCTATGATACCACCCGGTACAGGAGAT-AACTGTACAGGCCACTGCCTTGCCTG- [865]
Cmy GAGGGTCTATGATACCACCCGGTACAGGAGAT-AACTGTACAGGCCACTGCCTTGCCTG- [865]
Psi GAGGGTCTATGATACCACCCGGTATAGGAGAT-AACTGTACAGGCCACTGCCTTGCCTG- [705]
Asp GAGGGTCTATGATACCACCCGGTATAGGAGAT-AACTGTACAGGCCACTGCCTTGCCTG- [705]
Ami GAGGGTCTATGATACCACCCGGTACAGGAGATTAACTGTACAGGCCACTGCCTTGCCTG- [863]
Asi GAGGGTCTATGATACCACCCGGTACAGGAGATTAACTGTACAGGCCACTGCCTTGCCTG- [863]
Tgu GAGGGTCTATGATACCACCCGGTACAGGAGAT-AACTGTACAGGCCACTGCCTTGCCTG- [632]
Cli GAGGGTCTATGATACCACCCGGTACAGGAGAT-AACTGTACAGGCCACTGCCTTGCCTG- [632]
Gga GAGGGTCTATGATACCACCCGGTACAGGAGAT-AACTGTACAGGCCACTGCCTTGCCTG- [632]
Xtr AAGGGTCTGTGACACCACCCTCTGTTGGAGAT-AACTGTACAGGCCACTGCCTTGCCTA- [621]
Lch GAGGGTTTGTGATACCACCCGGTAATGGAGAT-AACTGTACAAGCCACTGCCTTGCTTA- [711]
Dre TAGGGTCTGTTATTCTGCCCTGTTAAGGAGCT-AACTGTACAGACTACTGCCTTGCCCA- [787]

Hsa -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [921]
Mmu -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [921]
Mdo -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [699]
Meu -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [608]
Oan ------------------------------------------------------------ [795]
Aca -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [925]
Pbi -CTGGCTGAGGTAGTAGTTTGTGCTGTTCGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [924]
Cpi -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [924]
Cmy -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [924]
Psi -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [764]
Asp -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [764]
Ami -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACACTGCCCGCTGTGGAGAT [922]
Asi ------------------------------------------------------------ [863]
Tgu -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [691]
Cli -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [691]
Gga -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGAT [691]
Xtr -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACACTGCCCGCTGTGGAGAT [680]
Lch -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTAGGGTTGTGACATTGCCCGCTATGGAGAT [770]
Dre -CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTTGGGATGTGACATTGCCCGTTATGGAGAT [846]

Hsa AACTGCGCAAGCTACTGCCTTGCT---------------------------------- [945]
Mmu AACTGCGCAAGCTACTGCCTTGCT---------------------------------- [945]
Mdo AACTGCGCAAGCTACTGCCTTGCT---------------------------------- [723]
Meu AACTGCGCAAGCTACTGCCTTGCT---------------------------------- [632]
Oan ------------------------------------------------------------ [795]
Aca AACTGCGCAAGCTACTGCCTTGCT--GTGAGGTAGTAGGTTGTATAGTTTG-TGGGAGGG [982]
Pbi AACTGCGCAAGCTACTGCCTTGCT--GTGAGGTAGTAGGTTGTATAGTTTG-TGGGAGGG [981]
Cpi AACTGCGCAAGCTACTGCCTTGCT--GTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGG [982]
Cmy AACTGCGCAAGCTACTGCCTTGCT--GTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGG [982]
Psi AACTGCGCAAGCTACTGCCTTGCT--GTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGG [822]
Asp AACTGCGCAAGCTACTGCCTTGCT--GTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGG [822]
Ami AACTGCGCAAGCTACTGCCTTGCT--GTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGG [980]
Asi -------------------------GTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGG [897]
Tgu AACTGCGCAAGCTACTGCCTTGCT--GTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGG [749]
Cli AACTGCGCAAGCTACTGCCTTGCT--GTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGG [749]
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Gga AACTGCGCAAGCTACTGCCTTGCT--GTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGG [749]
Xtr AACTGCGCAAGCTACTGCCTTGCT---------------------------------- [704]
Lch AACTGCGCAAGCTACTGCCTTGCT--GTGAGGTAGTAGGTTGTATAGTTTAGTGGACAGG [828]
Dre GACTGCGCAAGCTACTCCCTTGCC--GTGAGGTAGTAGGTTGTATAGTTTGGTGGGAGGG [904]

Hsa ------------------------------------------------------------ [945]
Mmu ------------------------------------------------------------ [945]
Mdo ------------------------------------------------------------ [723]
Meu ------------------------------------------------------------ [632]
Oan ----------------------------------------------GGCTGAGGTA [805]
Aca ATTACATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTA--GGCTGAGGTA [1040]
Pbi ATTATATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTA--GGCTGAGGTA [1039]
Cpi ATTTCATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTA--GGCTGAGGTA [1040]
Cmy ATTTCATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTA--GGCTGAGGTA [1040]
Psi ATTTCATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTA--GGCTGAGGTA [880]
Asp AATTCATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTA--GGCTGAGGTA [880]
Ami ATTTCATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTG--GGCTGAGGTA [1038]
Asi ATTTCATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTG--GGCTGAGGTA [955]
Tgu ATTTGATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTA--GGCTGAGGTA [807]
Cli ATTTGATCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTA--GGCTGAGGTA [807]
Gga ATTCTGTCCCATTTCAGGTGATAACTATACAGTCTATTGCCTTCCTTA--GGCTGAGGTA [807]
Xtr ------------------------------------------------------------ [704]
Lch GTTTCGTTCAGTTCCAGATGATAACTATACAGTCTATTGCCTTCCTTA--GGCTGAGGTA [886]
Dre ATCAAACCCTGTT-CAGCTGATAACTATACAGTCTATTGCCTTCCTTG--GGCTGAGGTA [961]

Hsa ------------------------------------------------------------ [945]
Mmu ------------------------------------------------------------ [945]
Mdo ------------------------------------------------------------ [723]
Meu ------------------------------------------------------------ [632]
Oan GTAGATTGAATAGTTGTGGGGTCACG--GCCTCCCTGTGTGCTAACTATACAATCTACTG [863]
Aca GTAGATTGAATAGTTGTGGAGCCTTA--TTCTCCCTCTGAGCTAACTATACAATCTACTG [1098]
Pbi GTAGATTGAATAGTTGTGGAGCCATC--TTCTCCCTTTGAGCTAACTATACAATCTACTG [1097]
Cpi GTAGATTGAATAGTTGTGGAGTCCTA--CCCTCCCTTTGAGCTAACTATACAATCTACTG [1098]
Cmy GTAGATTGAATAGTTGTGGAGTCCTA--CCCTCCCTTTGAGCTAACTATACAATCTACTG [1098]
Psi GTAGATTGAATAGTTGTGGAGTCCTA--CTCTCCCTCTGAGCTAACTATACAATCTACTG [938]
Asp GTAGATTGAATAGTTGTGGAGTCCTA--CCCTCCCTCTGAGCTAACTATACAATCTACTG [938]
Ami GTAGATTGAATAGTTGTGGAGTCCTA--CCCTCCCTTTGAGCTAACTATACAATCTACTG [1096]
Asi GTAGATTGAATAGTTGTGGAGTCCTA--CCCTCCCTTTGAGCTAACTATACAATCTACTG [1013]
Tgu GTAGATTGAATAGTTGTGGAGTCTGG--TCCTCCCTCTGAGCTAACTATACAATCTACTG [865]
Cli GTAGATTGAATAGTTGTGGAGTCCGA--TCCTCCCTTTGAGCAAACTATACAATCTACTG [865]
Gga GTAGATTGAATAGTTGTGGAGTCCTA--TCCTCCCTTTGAGCTAACTATACAATCTACTG [865]
Xtr ------------------------------------------------------------ [704]
Lch GTAGATTGAATAGTTGTGAGGCTCCT-GCTCTCCCTTTGAGATAACTATACAATCTACTG [945]
Dre GTAGATTGAATAGTTGTGGAGCCCTGCGCTCTCTCTCTGAGATAACTATACAATCTACTG [1021]

Hsa ---------CTGCTTGGGAAACATACTTCTTTATATGCCCATATGGACCTGCTAA-GCTA [995]
Mmu ---------CTGCTTTGGACACATACTTCTTTATATGCCCATATGAACCTGCTAA-GCTA [995]
Mdo ---------CTGCTTGAGAAACATACTACTTTATATGCCCATATGAACGTGCTAA-GCTA [773]
Meu ------------------------------------------------------------ [632]
Oan TCTTTCC--CTGCTTGAGGAACATACTTCTTTATATCCCCATATGAACCTGGCAA-GCTA [920]
Aca TCTTTCC--CTGCTTGAGTGACATACTTCTTTATATGCCCATATGAACCTGGCAA-ACTA [1155]
Pbi TCTTTCC--CTGCTTGAGTGACATACTTCTTTATATGCCCATATGAACCTGGCAA-ACTA [1154]
Cpi TCTTTCC--CTGCTTGAGAGACATACTTCTTTATATGCCCATATGAACCTGGCAA-GCTA [1155]
Cmy TCTTTCC--CTGCTTGAGAGACATACTTCTTTATATGCCCATATGAACCTGGCAA-GCTA [1155]
Psi TCTTTCC--CTGCTTGAGAAACATACTTCTTTATATGCCCATATGAACCTGGCAA-GCTA [995]
Asp TCTTTCC--CTGCTTGAGAAACATACTTCTTTATATGCCCATATGAACCTGGCAA-GCTA [995]
Ami TCTTTCC--CTGCTTGAGAGACATACTTCTTTATATGCCCATATGAACCTGGCAA-GCTA [1153]
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Asi TCTTTCC--CTGCTTGAGAGACATACTTCTTTATATGCCCATATGAACCTGGCAA-GCTA [1070]
Tgu TCTTTCC--CTGCTTGAGAGACATACTTCTTTATATGCCCATATGAACCTGGCAA-GCTA [922]
Cli TCTTTCC--CTGCTTGAGAGACATACTTCTTTATATGCCCATATGAACCTGGGAA-GCTA [922]
Gga TCTTTCC--CTGCTTGAGAGACATACTTCTTTATATGCCCATATGAACCTGGCAA-TCTA [922]
Xtr ---------CTATTTGGGAGACATACTTCTTTATATGTCCATATGGAAGTGCCAATGCTA [755]
Lch TCTTTCC--CTGCTTGAGGGACATACTTCTTTATATACCCATATGAACCTGTCTA-GCTA [1002]
Dre TCTTTCC--CCGCTTGGTAGACATACTTCTTTATATGCCCATATGAACAAGAGCA-GCTA [1078]

Hsa TGGAATGTAAAGAAGTATGTATCTCAGGCCG--ACCTACTCAGAGTACATACTTCTTTAT [1053]
Mmu TGGAATGTAAAGAAGTATGTATTTCAGGCTA--GCCTACTCAGAGCACATACTTCTTTAT [1053]
Mdo TGGAATGTAAAGAAGTATGTATTTCCGGTAG--ACCTACTCAGAGTACATACTTCTTTAT [831]
Meu --------------------------------ACCTGCTCAGAGTACATACTTCTTTAT [659]
Oan TGGAATGTAAAGAAGTATGTATTTCAGGTGG--ACCTGCTCAGAGTACATACTTCTTTAT [978]
Aca TGGAATGTAAAGAAGTATGTATTTCAGGTAT--ACCTGTTGAGAGCACATACTTCTTTAT [1213]
Pbi TGGAATGTAAAGAAGTATGTATTTCAGGCAT--ACCTGCCCAGAGCACATACTTCTTTAT [1212]
Cpi TGGAATGTAAAGAAGTATGTATTTCAGGTGG--TCCTGCCCAGAGTACATACTTCTTTAT [1213]
Cmy TGGAATGTAAAGAAGTATGTATTTCAGGTGG--TCCTGCCCAGAGTACATACTTCTTTAT [1213]
Psi TGGAATGTAAAGAAGTATGTATTTCAGGTGG--TCCTGCCCAGATTACATACTTCTTTAT [1053]
Asp TGGAATGTAAAGAAGTATGTATTTCAGGTGG--TCCTGCCCAGATTACATACTTCTTTAT [1053]
Ami TGGAATGTAAAGAAGTATGTATTTCAGGTGG--ACCTGCCCAGAGTACATACTTCTTTAT [1211]
Asi TGGAATGTAAAGAAGTATGTATTTCAGGTGG--ACCTGCCCAGAGTACATACTTCTTTAT [1128]
Tgu TGGAATGTAAAGAAGTATGTATTTCAGGTGG--ACCTGCTCAGAGCACATACTTCTTTAT [980]
Cli TGGAATGTAAAGAAGTATGTATTTCAGGTGG--ACCTGCCCAGAGTACATACTTCTTTAT [980]
Gga TGGAATGTAAAGAAGTATGTATTTCAGGTGG--ACCTGCTCAGAGCACATACTTCTTTAT [980]
Xtr TGGAATGTAAAGAAGTATGTATCTCCGATAG--ACCTGTTTGGAGTACATACTTCTTTAT [813]
Lch TGGAATGTAAAGAAGTATGTATTTCAGGTAG--ACCTGCCCAGAACACATACTTCTTTAT [1060]
Dre TGGAATGTAAAGAAGTATGTATCCCAGGTGA--GCCTACTTGGTGTACATACTTCTTTAT [1136]

Hsa GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGTAG--G [1110]
Mmu GTACCCATATGAACATTCAG-TGCTATGGAATGTAAAGAAGTATGTATTTTGGGTAG--G [1110]
Mdo GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGTAG--G [888]
Meu GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGTAG--- [715]
Oan GTACCCATATGAACATAAAA-AGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAG--G [1035]
Aca GTACCCATATGAAGATACAA-TGTTATGGAATGTAAAGAAGTATGTATTTTTGATAG--T [1270]
Pbi GTACCCATATGAAGATATAA-TGTTATGGAATGTAAAGAAGTATGTACTTTTGGCAG--T [1269]
Cpi GTACCCATATGAACATATAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAG--C [1270]
Cmy GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAG--C [1270]
Psi GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAG--C [1110]
Asp GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAG--C [1110]
Ami GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAG--C [1268]
Asi GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAG--C [1185]
Tgu GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAG--C [1037]
Cli GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAG--C [1037]
Gga GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGCAG--C [1037]
Xtr GTACCCATATGAACATACAA-TGCTATGGAATGTAAAGAAGTATGTATTTTTATCAG--C [870]
Lch GTACCCATATGAACATATGA-TGCTATGGAATGTAAAGAAGTATGTATTTTTGGTGG--C [1117]
Dre GTGCCCATATGAACATATAAAAGCTATGGAATGTAAAGAAGTATGTATTCTTGGTCA--G [1194]

Hsa CTTCCCGAGGCCACATGCTTCTTTATATCCCCATATGGATTACTTTGCTATGGAATGTAA [1170]
Mmu CTTCCCCAGGCCACATGCTTCTTTATATCCTCATAGATATCTCAGCACTATGGAATGTAA [1170]
Mdo CTTTCTGAGGCAACATGCTTCTTTATATCCCCATATGAATTATGCTGCTATGGAATGTAA [948]
Meu ---------------------------------------------------------- [715]
Oan CTCTCCGAGACAACATGCTTCTTTATATCCCCATATGGATTACGCTGCTATGGAATGTAA [1095]
Aca CTTTTTGAGATTACATGCTTCTTTATATCTCCATATGAATTGCCTTGCTATGGAATGTAA [1330]
Pbi CTTTTTGAGGGGACACGCTTCTTTATAATCCCATATGAATTACATTGCTATGGAATGTAA [1329]
Cpi TCTTTTGAGACAACATGCTTCTTTATATCCCCATATGAATTATGCTGCTATGGAATGTAA [1330]
Cmy TCTTTTGAGACAACATGCTTCTTTATATCCCCATATGAATTACGCTGCTATGGAATGTAA [1330]
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Psi TCTTTTGAGACAACATGCTTCTTTATATCCCCATATGAATTACGCTGCTATGGAATGTAA [1170]
Asp TCTTTTGAGACAACATGCTTCTTTATATCCCCATATGAATTACGCTGCTATGGAATGTAA [1170]
Ami TCTTTTGAGGCAACATGCTTCTTTATATCCCCATAGGGATAACAGTGCTATGGAATGTAA [1328]
Asi TCTTTTGAGGCAACATGCTTCTTTATATCCCCATAGGGATAACAGTACTATGGAATGTAA [1245]
Tgu TCTTATGAGATGACATGCTTCTTTATATCCCCATATGGATTAGGCTGCTATGGAATGTAA [1097]
Cli TCTTATGAGATTACATGCTTCTTTATATCCCCATAGGGATTAGGCTGCTATGGAATGTAA [1097]
Gga TCTTATGAGATGACATGCTTCTTTATATCCCCATATGGATTAGGCTGCTATGGAATGTAA [1097]
Xtr TCACGGGAGGTCACATGCTTCTTTATATACCCATATGAACTACATTGTTATGGAATGTAA [930]
Lch TTGCTG-AGATGACATGCTTCTTTATATCCTCATATGGGTTTCACAGCTATGGAATGTAA [1176]
Dre CCTCTTGTGAAGACATGCTTCCTTATATGCCCATATTAATGCTCAAGTTATGGAATGTAA [1254]

Hsa GGAAGTGTGTGGTTTCGGCAAGT----------------------------------- [1193]
Mmu GGAAGTGTGTGGTTTTGGCAAGT----------------------------------- [1193]
Mdo GGAAGTGTGTGGTTTCGGGAAGT----------------------------------- [971]
Meu ------------------------------------------------------------ [715]
Oan GGAAGTGTGTGGTTTCGGGCCAG--GCTCCCCGGGCCACACACTTCTTCATATGCCCATA [1153]
Aca GGAAGTGTGTGGTTTCAAGGAGA--CCTCTTGAGCCTACATACTTCTTCATATGCCCATA [1388]
Pbi GGAAGTGTGTGGTTTCAGAAAGA--CCTCCCGAGCCTACATACTTCTTCATATGCCCATA [1387]
Cpi GGAAGTGTGTGGTTTCAGGGAGA--CCTCCCAACCCTACATACTTCTTCATATGCCCATA [1388]
Cmy GGAAGTGTGTGGTTTCAGGGAGA--CCTCCCAACCCTACATACTTCTTCATATGCCCATA [1388]
Psi GGAAGTGTGTGGTTTCAGGGAGA--CCTCCCAACCCTACATACTTCTTCATATGCCCATA [1228]
Asp GGAAGTGTGTGGTTTCAGGGAGA--CCTCCCAACCCTACATACTTCTTCATATGCCCATA [1228]
Ami GGAAGTGTGTGGTTTCGGGGAGA--CCTCCCAACCCTACATACTTCTTCATATGCCCATA [1386]
Asi GGAAGTGTGTGGTTTCGGGGAGA--CCTCCCAACCCTACATACTTCTTCATATGCCCATA [1303]
Tgu GGAAGTGTGTGGTTTCAGGGAGA----------------------------------- [1120]
Cli GGAAGTGTGTGGTTTCAGGGAGA--CCTCCCAACCCTACATACTTCTTCATATACCCATA [1155]
Gga GGAAGTGTGTGGTTTCAGGGAGA--CCTCCCAACCCTACATACTTCTTCATATGCCCATA [1155]
Xtr GGAAGTGTGTGGCTTCTCTGAGT--CACCTTTAGGGCACATACTTCTTTATATGCCCATA [988]
Lch GGAAGTGTGTGGTGTCAGTGAGA--CACCTCAGGAGCACATACTTCTTCATATGCCCATA [1234]
Dre GGAAGTGTGTGGTTTCAGGGGGA----------------------------------- [1277]

Hsa ----------------------------------------------------CCTAGTT [1200]
Mmu ----------------------------------------------------CCTAGTT [1200]
Mdo ----------------------------------------------------CCTAGTT [978]
Meu ----------------------------------------------------CCTAGTT [722]
Oan GGGAGCTGCCCGAA-CTATGGAATGTTAAGAAGTGTGTGTTCTTGGGGGCT--TCTAGTT [1210]
Aca TGGAGTCGGCCAGATTTATGGAATGTTAAGAAGTATGTATCGTTGGGATGG--CCTAGTT [1446]
Pbi TGGAGTCGGCCGG--CTATGGAATGTTAAGAAGTATGTATCTTTGGGATCG--TCTAGTT [1443]
Cpi GGGAGTCAGCCGGCGTTATGGAATGTTAAGAAGTATGTATCCTTGGGCTGG--TCTAGTT [1446]
Cmy GGGAGTCAGCCGGCGTTATGGAATGTTAAGAAGTATGTATCTTTGGGCTGG--TCTAGTT [1446]
Psi GGGAGTCAGCTGGCGTTATGGAATGTTAAGAAGTATGTATCTTTGGGCTGG--TCTAGTT [1286]
Asp GGGAGTCAGCTGGCGTTATGGAATGTTAAGAAGTATGTATCTTTGGGCTGG--TCTAGTT [1286]
Ami TGGAGTCGGCTGGTATTATGGAATGTTAAGAAGTATGTATCTTTGGGCTGG--TCTAGTT [1444]
Asi TGGAGTCGGCTGGTATTATGGAATGTTAAGAAGTATGTATCTTTGGGCTGG--TCTAGTT [1361]
Tgu ----------------------------------------------------CCTAGTT [1127]
Cli TGGAGTCGGCCGGCGTTATGGAATGTTAAGAAGTATGTATTTTTGGGCTGG--TCTAGTT [1213]
Gga TGGAGTCGGCCGGCGTTATGGAATGTTAAGAAGTATGTATCCTCGGGCTGG--TCTAGTT [1213]
Xtr CTGAATGAA--AATGCTATGGAATGTTAAGAAGTATGTAACCTAAGGGGTT--TTTAGTT [1044]
Lch TGGAATAATCCCCGGTTATGGAATGTTAAGAAGTATGTATTTATGGGGTGA--TCTAGTT [1292]
Dre ----------------------------------------------------CTTGCTT [1284]

Hsa CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAATCGACAACAAATCACAG [1260]
Mmu CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAAACGACAACAAATCACAG [1260]
Mdo CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAAACGACAACAAATCACAG [1038]
Meu CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAAACGACAACAAATCACAG [782]
Oan CTGTGTGGAAGACTAGTGATTTTGTTGTTTGTAGATAACTAAATCGACAACAAATCGCAG [1270]
Aca CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAATTGACAACAAATCGCAG [1506]
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Pbi CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATTACTAAAGTGACAACAAATCGCAG [1503]
Cpi CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAATCGACAACAAATCGCAG [1506]
Cmy CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAATCGACAACAAATCGCAG [1506]
Psi CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAATCGACAACAAATCGCAG [1346]
Asp CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAAGCGACAACAAATCGCAG [1346]
Ami CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAATCGACAACAAATCGCAG [1504]
Asi CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAATCGACAACAAATCGCAG [1421]
Tgu CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTTGATAACTAAATTGACAACAAATCACAG [1187]
Cli CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACTAAATTGACAACAAATCGCAG [1273]
Gga CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAATTAAATTGACAACAAATCACAG [1273]
Xtr CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGATAACAACATTGACAACAAATCGCAG [1104]
Lch CTGTGTGGAAGACTAGTGATTTTGTTGTTTTTAGGTAACTGCATTGACAACAAATCACAG [1352]
Dre CTGTGTGGAAGACTTGTGATTTTGTTGTTGTTAGTTAGATGAAGTGACAACAAATCACGG [1344]

Hsa TCTGCCATATGGCACAGGCCA--GCTGGCCCCATCTGGAAGACTAGTGATTTTGTTGTT- [1317]
Mmu TCTGCCATATGGCACAGGCCA--GCCAGCCCCGTTTGGAAGACTAGTGATTTTGTTGTT- [1317]
Mdo TCTGCCATATGGCACAGGCCA--CCTGGCCCCATCTGGAAGACTAGTGATTTTGTTGTT- [1095]
Meu TCTGCCATATGGCACAGGCCA--CCTGGCCCCATCTGGAAGACTAGTGATTTTGTTGTT- [839]
Oan TCTGCCATATGGCACAGACCA--CCGGGCCCCGTCTGGAAGACTAGTGATTTTGTTGTT- [1327]
Aca TCTACCATATGGCACAGGCCA--CCCTGCTTCTTATGGAAGACTAGTGATTTTGTTGTT- [1563]
Pbi TCTACCATATGGCACAGTCCA--CCGGACTCCTTATGGAAGACTAGTGATTTTGTTGTTT [1561]
Cpi TCTGCCATATGGCACAGGCCA--CCCCGTCCCTTATGGAAGACTAGTGATTTTGTTGTT- [1563]
Cmy TCTGCCATATGGCACAGGCCA--CCCCGTCCCTTATGGAAGACTAGTGATTTTGTTGTT- [1563]
Psi TCTGCCATATGGCACAGGCCA--CCATGTCCCTTATGGAAGACTAGTGATTTTGTTGTT- [1403]
Asp TCTGCCATATGGCACAGGCCA--CCATGTCCCTTATGGAAGACTAGTGATTTTGTTGTT- [1403]
Ami TCTGCCATATGGCACAGACCA--CCTGACCCTGTATGGAAGACTAGTGATTTTGTTGTT- [1561]
Asi TCTGCCATATGGCACAGACCA--CCTGACCCCGTATGGAAGACTAGTGATTTTGTTGTT- [1478]
Tgu TCTGCCATATGGCACAGACCA--CCTGCTTCCCTGTGGAAGACTAGTGATTTTGTTGTT- [1244]
Cli TCTGCCATATAGCACAGACTG--CCCAGCTCCCTCTGGAAGACTAGTGATTTTGTTGTT- [1330]
Gga TCTGCCATATGGCACAGATCA--CGCGGTGCCCTCTGGAAGACTAGTGATTTTGTTGTT- [1330]
Xtr TCTGCCATATGGCACAGACCA--GCTGACTCTTTGTGGAAGACTAGTGATTTTGTTGTT- [1161]
Lch TCTACCATATAGCACAGGCCA--TCTCAGTCACGGTGGAAGACTAGTGATTTTGTTGTT- [1409]
Dre TCTGCCCTACAGCACAGGCCC--ATTTGGGCATTATGGAAGACTAGTGATTTTGTTGTT- [1401]

Hsa GTCTTAC--TGCGCTC-AACAACAAATCCCAGTCTACCTAATGGTGCCAGCCA--TCTAG [1372]
Mmu GTGTCTC--TGTATCC-AACAACAAGTCCCAGTCTGCCACATGGTGCTGGTCA--GCCAG [1372]
Mdo CTCTAACGTAAAGATT-GACAACAAATCCCAGTCTGCCTTATGGTGCTTGGCC--TCAAA [1152]
Meu CTCTAACATAAAGATT-GACAACAAATCCCAGTCTGCCTCATGGTGCCTGGCC------- [891]
Oan CTCTAGCTGACCGCAC-GACAACAAATCCCAGTCTGCCTGACGGTGCCCGGTG------- [1379]
Aca CTGTAGTTCATCTCAC-GACAACAAGTCACAGTCTGCCTTATGGGGCCTGGCC--CTGGT [1620]
Pbi CTGTAGCTCATCTCAT-GACAACAAGTCACAGTCTGCCTTCTGGAGTCTGGCC--CCTGC [1618]
Cpi CTATAGCTCATCTCAT-GACAACAAGTCACAGTCTGCCTTATGGTGCATGGCC--TCTGG [1620]
Cmy CTATAGCTCATCTCAT-GACAACAAGTCACAGTCTGCCTTATGGTGCATGGCC--TCTGG [1620]
Psi CTATAGCTCATCTCAC-GACAACAAGTCACAGTCTGCCTTATGGTGTACGGCC--TCTGG [1460]
Asp CTATAGCTCATCTCAT-GACAACAAGTCACAGTCTGCCTTATGGTGTACGGCC--TCTGG [1460]
Ami CTATGGCTCATCTCAC-GACAACAAGTCACAGTCTGCCTTATGGTGCATGGCC--TCTGG [1618]
Asi CTATGGCTCATCTCAC-GACAACAAGTCACAGTCTGCCTTATGGTGCATGGCC--TCTGG [1535]
Tgu GTATGGCTCATCCCAC-CACAACAAGTCACAGTCTGCCCTAGGGCACACGGCC--CCTGG [1301]
Cli GTATGGCTCATCCCAC-CACAACAAGTCACAGTCTGCCCTAGGGTGCGTGGCC--TCTGG [1387]
Gga GTATGGCTCATCCCAC-CACAACAAGTCACAGTCTGCCTTAGGGCGCACGGCC--TCTGG [1387]
Xtr GTAAGCCTTATTGCAT-GACAACAAGTCACAGTCTGCCTCACAGTGCCCAGCA------- [1213]
Lch ATACCACTTA-AACAG-GACAGCAAGTCACAGTCTGCCTCAGTGCTCGGGACA--TCCAG [1465]
Dre GTGACGTCATCAGTACTGACAACAAGTCACAGTCTGCCTCAGTGACCAGAATC--CCCGA [1459]

Hsa TGCTGTGTGGAAGACTAGTGATTTTGTTGTTCTGAT--GTA-CTACGA-CAACAAGTCAC [1428]
Mmu TGCTATGTGGAAGACTTGTGATTTTGTTGTTCTGAT--ATG-ATATGA-CAACAAGTCAC [1428]
Mdo TGCTGTATGGAAGACTAGTGATTTTGTTGTTGTAAT--ATA-TAAAGA-CAACAAAACAC [1208]
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Meu ---------------------------------------------------------- [891]
Oan ---------------------------------------------------------- [1379]
Aca TTCTGGGTGGAAGACTAGTGATTTTGTTGTTCTGACTTATAATTTAGA-CAACAAATCGT [1679]
Pbi TTCTGATTGGAAGACTAGTGATTTTGTTGTTCTGGTTTAGAAAGCTGA-CAACAAATCAC [1677]
Cpi CTCTGTGTGGAAGACTAGTGATTTTGTTGTTCTGACTTATAAAAGTGA-CAACAAATCAT [1679]
Cmy CTCTGTGTGGAAGACTAGTGATTTTGTTGTTCTTACTTATAAAAGTGA-CAACAAATCAT [1679]
Psi CTCTGTGTGGAAGACTAGTGATTTTGTTGTTCTGAC--ATAAAAGTGA-CAACAAATCAT [1517]
Asp CTCTGTGTGGAAGACTAGTGATTTTGTTGTTCTGAC--ATAAAAGTGA-CAACAAATCAT [1517]
Ami CTCTGCGTGGAAGACTAGTGATTTTGTTGTTCTGACTTATAAAGGTGA-CAACAAATCAT [1677]
Asi CTCTGCGTGGAAGACTAGTGATTTTGTTGTTCTGACTTATAAAGGTGA-CAACAAATCAT [1594]
Tgu CTCTGTGTGGAAGACTAGTGATTTTGTTGTTGTG-TTTGTAAAGGTGA-CAACAAATCAT [1359]
Cli CTCTGCGTGGAAGACTAGTGATTTTGTTGTTCTGATTTATAAAGGTGA-CAACAAATCAT [1446]
Gga CTCTGTGTGGAAGACTAGTGATTTTGTTGTTATGATTTATAAAGGTGA-CAACAAATCAT [1446]
Xtr ---------------------------------------------------------- [1213]
Lch CTCTGTGTGGAAGACTAGTGATTTTGTTGTTTTTGATGGTAAAGACAG-CAACAAGTCAC [1524]
Dre TTCGCTGTGGAAGACTAGTGATTTTGTTGTTGTTTCTTCTGCTTTCTGACAACAAGTCAC [1519]

Hsa AGCCGGCCTCATAGCGCAGACTC---------------------------------- [1451]
Mmu AGCCAGCCTCATAGCGTGGACTC---------------------------------- [1451]
Mdo AGCCTGCCTTACAGCGTGGACAC---------------------------------- [1231]
Meu ---------------------------------------------------------- [891]
Oan ---------------------------------------------------------- [1379]
Aca AGCCTGCCGCCCAGCGACCACAG---------------------------------- [1702]
Pbi AGCCTACCATCCAGCAGGGGCCA---------------------------------- [1700]
Cpi AGCCTGCCATACAGCACGGACCA--GGGTCGGTCTGGAAGACTTGTGATTTTGTTGTTTC [1737]
Cmy AGCCTGCCAAACAGCACAGACCA--GGGTCGGTCTGGAAGACTTGTGATTTTGTTGTTTC [1737]
Psi AGCCTGCCATACAGCACGGACCC--GGGTCGGTCTGGAAGACTTGTGATTTTGTTGTTTC [1575]
Asp AGCCTGCCATACAGCACAGACCC--GGGTCGGTCTGGAAGACTTGTGATTTTGTTGTTTC [1575]
Ami AGCCTGCCATACAGCACAGACTC--GGGTCGGTCTGGAAGACTTGTGATTTTGTTGTTTC [1735]
Asi AGCCTGCCATACAGCACAGACTC--GGGTCGGTCTGGAAGACTTGTGATTTTGTTGTTTC [1652]
Tgu AGCCTGCCATACAGCCCAGGCTG---------------------------------- [1382]
Cli AGCCTGCCACCCAGCCCAGACCT--GGG-CAGGCTGGAAGACTTGTGATTTTGTTGTTTC [1503]
Gga AGCCTGCCATACAGCACAGATCT---------------------------------- [1469]
Xtr ------------------------GGGTCGGTTTGGAAGACTAGTGATTTTGTTGTTTT [1248]
Lch AGTCTGCCATACAGCGTGGAGCC---------------------------------- [1547]
Dre AGTCTACCTCAGCGAGCGGGCCC--TCTGCGGAGTGGAAGACTAGTGATTTTGTTGTGAA [1577]

Hsa --------------------------------------------------GGGCCCC [1458]
Mmu --------------------------------------------------GGGCCTC [1458]
Mdo --------------------------------------------------GGGCCTC [1238]
Meu --------------------------------------------------GGGCCTC [898]
Oan --------------------------------------------------GGTCCTC [1386]
Aca --------------------------------------------------GGTCCTC [1709]
Pbi --------------------------------------------------GGTCCTC [1707]
Cpi CAGTGTCAG-GGAAGCGAACAACAAATCCCAGTC-TCCTCACAGCCCCAGG--GGTCCTC [1793]
Cmy CGGTGTCAG-GGAAGCGAACAACAAATCCCAGTC-TCCTCACAGCCCCAGG--GGTCCTC [1793]
Psi TGGTGTCAG-GGAAGCGAACAACAAATCCCAGTC-TCCTCACAGCCCCAGG--GGTCCTC [1631]
Asp TGGTGTCAG-GGAAGCGAACAACAAATCCCAGTC-TCCTCACAGCCCCAGG--GGTCCTC [1631]
Ami TGGTGTCAA-GGAAGCGAACAACAAATCCCAGTC-TCCTCACAGCCCCAGG--GGTCCTC [1791]
Asi TGGTGTCAA-GGAAGCGAACAACAAATCCCAGTC-TCCTCACAGCCCCAGG--GGTCCTC [1708]
Tgu --------------------------------------------------GGTCCTC [1389]
Cli CAATGTCAACGGGAGCGAACAACAAATCCCAGTC-TCCTCCCTGCCCCGGG--GGTCCTC [1560]
Gga --------------------------------------------------GGTCCTC [1476]
Xtr TATAAAAGTTTGTCACAAACAGCAAATCGTAGTC-TCCACTCTGCCCCAGG--GGTCCTC [1305]
Lch --------------------------------------------------GGTCCTC [1554]
Dre AATGAACAA---AAACCAACAACAAACCGCAGTCGTCCTCTCAGCACGGGG--GGCACTT [1632]
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Hsa TGTGAGCATCTTACCGGACAGTGCTGGATTTCCCAGCTTGACTCTAACACTGTCTGGTAA [1518]
Mmu TGTGGGCATCTTACCGGACAGTGCTGGATTTCTTGGCTTGACTCTAACACTGTCTGGTAA [1518]
Mdo TGTGGGCATCTTACTAGACAGTGCTGGATTTTT-GGATGTACTCTAACACTGTCTGGTAA [1297]
Meu TGTGGGCATCTTACTAGACAGTGCTGGATTTTT-GGATGCATTCTAACACTGTCTGGTAA [957]
Oan CGTGGGCATCTTACTAGACAGTGCTGGATTTG--GGATCTACTCTAACACTGTCTGGTAA [1444]
Aca TGTGGACATCTTACTAGACAGTGCTGGATTGTGTGCTCTGATTCTAACACTGTCTGGTAA [1769]
Pbi TGTGGACATCTTACTAGACAGTGCTGGATTTTGTCACTGTACTCTAACACTGTCTGGTAA [1767]
Cpi TGTGGACATCTTACTAGACAGTGCTGGATTTTTTGGATCTACTCTAACACTGTCTGGTAA [1853]
Cmy TGTGGACATCTTACTAGACAGTGCTGGATTTTTTGGATCTACTCTAACACTGTCTGGTAA [1853]
Psi TGTGGACATCTTACTAGACAGTGCTGGATTTTT-GGATCTACTCTAACACTGTCTGGTAA [1690]
Asp TGTGGACATCTTACTAGACAGTGCTGGATTTTT-GGATCTACTCTAACACTGTCTGGTAA [1690]
Ami TGTGGGCATCTTACTAGACAGTGCTGGATATTTTGGATCTACTCTAACACTGTCTGGTAA [1851]
Asi TGTGGGCATCTTACTAGACAGTGCTGGATATTTTGGATCTACTCTAACACTGTCTGGTAA [1768]
Tgu TGTGGGCATCTTACTAGACAGTGCTGGATTTGCTGCCTCTACTCTAACACTGTCTGGTAA [1449]
Cli TGTGGGCATCTTACTAGACAGTGCTGGATTTTTTGGATCTACTCTAACACTGTCTGGTAA [1620]
Gga TGTGGGCATCTTACTAGACAGTGCTGGATTTCTTGGATCTATTCTAACACTGTCTGGTAA [1536]
Xtr TATGGACATCTTACTAGACAGTGCTGGATTTATTTTATCTTTTCTAACACTGTCTGGTAA [1365]
Lch TATGAGCATCTTACTAGACAGTGCTGGATTTTACTAATCTTCTCTAACACTGTCTGGTAA [1614]
Dre AGCAGCCATCTTACCGGACAGTGCTGGACTGTATAACTGTTTTCTAACACTGTCTGGTAA [1692]

Hsa CGATGTTCAAAG-G-TGAC--GGGCAGCCGTGGCCATCTTACTGGGCAGCATTGGATGGA [1574]
Mmu CGATGTTCAAAG-G-TGAC--GGGCAGCCGTGGCCATCTTACTGGGCAGCATTGGATAGT [1574]
Mdo CGATGTTTAAAGAG-GGAA--GGGCTGCCATTACCATCTTACTGGGCAGCATTGGATGGT [1354]
Meu CGATGTTTAAAGAG-GGAA--GGGCTGCCATTACCATCTTACTGGGCAGCATTGGATGGT [1014]
Oan CGATGTTCAAGGAA-GGAC--GGGCCGCCACTACCATCTTACTGGGCAGCATTGGATGAG [1501]
Aca CGATGTTCAAAGGG-TGAG--GGGAGGTCATTGCCATCTTACTGGGCAGCATTGGATGTT [1826]
Pbi CGATGTTTAAAGAG-CGAG--GAGAAACCATTCTCATCTTACTGGGCAGCGTTGGACGTT [1824]
Cpi CGATGTTTAAAGGG-TGAA--GGGATGCCATTACCATCTTACTGGGCAGCATTGGATGTT [1910]
Cmy CGATGTTTAAAGGG-TGAA--GGGATGCCATTACCATCTTACTGGGCAGCATTGGATGTT [1910]
Psi CGATGTTTAAAGAG-GAAC--GGGATGCCATTACCATCTTACTGGGCAGCATTGGATGTT [1747]
Asp CGATGTTTAAAGAG-GAAC--GGGATGCCATTACCATCTTACTGGGCAGCATTGGATGTT [1747]
Ami CGATGTTTAAAGGG-TGAA--GGGATGCCGTTACCATCTTACTGGGCAGCATTGGATGTT [1908]
Asi CGATGTTTAAAGGG-TGAA--GGGATGCCGTTACCATCTTACTGGGCAGCATTGGATGTT [1825]
Tgu CGATGTTTAAAGGG-TGAT--GAGATGTCCTCAGCATCTTACTGGGCAGCATTGGATGAT [1506]
Cli CGATGTTTAAAGGG-TGAA--GAGATGCCATTACCATCTTACTGGGCAGCATTGGATGTT [1677]
Gga CGATGTTTAAAGGG-TGAA--GAGATGCCATTACCATCTTACTGGGCAGCATTGGATGTT [1593]
Xtr CGATGTTTAAAGAG-TGAG--GTGGCGCTATTGCCATCTTACTGGGCAGCATTGGATTTT [1422]
Lch CGATGTTTAAAGGGGTGAA--GGGATGTTATTGCCATCTTACTGGGCAGCATTGGATGTA [1672]
Dre CGATGTTTGTTGGG-TGAC--TGGTAGTCGTCTCCATCTTACGAGGCAGCATTGGATTTC [1749]

Hsa GTCAG-GTCTCTAATACTGCCTGGTAATGATGACGGCGGAGCCC--CCGGCCGATGGGCG [1631]
Mmu GTCTG-ATCTCTAATACTGCCTGGTAATGATGACGGCGGAGCCC--CCTGCTGATGGATG [1631]
Mdo GTCTGTGTTTCTAATACTGCCTGGTAATGATGATGATGGGGTCC--CCTGCTGATTGGTG [1412]
Meu GTCTGTGTTTCTAATACTGCCTGGTAATGATGATGATGGGGTCC--CCTGATGATTGGTG [1072]
Oan TTCTGTGTTTCTAATACTGCCTGGTAATGATGATGGCCGCGGCC--CCTGCTGATTGGTG [1559]
Aca TTCTGTCTTTCTAATACTGCCTGGTAATGATGATTGTGGCCTTC--CCTGCTGATCGCTG [1884]
Pbi TTATGAGTTTCTAATACTGCCTGGTAAAGATGTTAATGGCGTCT--CCTGCCGATCGCTG [1882]
Cpi TTCTGTGTTTCTAATACTGCCTGGTAATGATGATTATGGTGTCT--CCTGCTGATTGATG [1968]
Cmy TTCTGTGTTTCTAATACTGCCTGGTAATGATGATTATGGTGTCT--CCTGCTGATTGATG [1968]
Psi TTCTGTGTTTCTAATACTGCCTGGTAATGATGATTATGGTGTCT--CCTGCTGATTGATG [1805]
Asp TTCTGTGTTTCTAATACTGCCTGGTAATGATGATTATGGTGTCT--CCTGCTGATTGATG [1805]
Ami TTCTGTGTTTCTAATACTGCCTGGTAATGATGATTATGGTGTCT--CCTGCTGATTGACG [1966]
Asi TTCTGTGTTTCTAATACTGCCTGGTAATGATGATTATGGTGTCT--CCTGCTGATTGACG [1883]
Tgu CCATGCCGCTCTAATACTGCCTGGTAATGATGATGAAGGCTCTT---------------- [1550]
Cli TTCTGTCTTTCTAATACTGCCTGGTAATGATGATTATGGTGTTT--CCTGCTGATTGCTG [1735]
Gga CTCTGTTTTTCTAATACTGCCTGGTAATGATGATTGTGGTGTTT--CCTGCTGATTGCTG [1651]
Xtr GTCTATGTTTCTAATACTGCCTGGTAATGATGATTATGGCGCCC--CCTGTTGACCAATG [1480]
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Lch CTCTGATTTTCTAATACTGCCTGGTAATGATGATGATGGTATCC--CCTGTTGACTGACG [1730]
Dre ATTACTTTTTCTAATACTGCCTGGTAATGATGATGATTGCTGCC--CTTGTTGATGGACG [1807]

Hsa TCTTACCAGACATGGTTAGACCT----GGCCCTCTGTCTAATACTGTCTGGTAAAACCGT [1687]
Mmu TCTTACCAGACATGGTTAGATCT--GGATGCATCTGTCTAATACTGTCTGGTAATGCCGT [1689]
Mdo TCTTACCAGACAAAGTTAGATCT--CGCTATTTCTGTCTAATACTGTCTGGTAATGCCAT [1470]
Meu TCTTACCAGACAAAGTTAGATCT--CGCTATTTCCGTCTAATACTGTCTGGTAATGCCAT [1130]
Oan TCTTACCAGACAAAGTTAGATCT--GACTATTTTCGTCTAATACTGTCTGGTAATGCCGT [1617]
Aca TCTTACCAGACAAAGTTAGATCTT-AGCTATCCCCGTCTAATACTGTCTGGTAATGCCGT [1943]
Pbi TCTTACCAGACAAATTTAGATCTTAATCTATTCCTGTCTAATACTGTCTGGTAATGCCGT [1942]
Cpi TCTTACCAGACAAAGTTAGATCT--AGCTATTTTCGTCTAATACTGTCTGGTAATGCCGT [2026]
Cmy TCTTACCAGACAAAGTTAGATCT--AGCTATTT-CGTCTAATACTGTCTGGTAATGCCGT [2025]
Psi TCTTACCAGACAAAGTTAGATCT--AGCTATTTTCGTCTAATACTGTCTGGTAATGCCGT [1863]
Asp TCTTACCAGACAAAGTTAGATCT--AGCTATTTTCGTCTAATACTGTCTGGTAATGCCGT [1863]
Ami TCTTACCAGACAAAGTTAGATCT--AGCTATTTTCGTCTAATACTGTCTGGTAATGCCGT [2024]
Asi TCTTACCAGACAAAGTTAGATCT--AGCTATTTTCGTCTAATACTGTCTGGTAATGCCGT [1941]
Tgu ------------------------------------------------------------ [1550]
Cli TCTTACCAGGCAAAGTTAGATCT--AGCTATTTTTGTCTAATACTGTCTGGTAATGCCGT [1793]
Gga TCTTACCAGGCAAAGTTAGATCT--AGCTATTTCTGTCTAATACTGTCTGGTAATGCCGT [1709]
Xtr TCTTACCAGACAAGGTTAGATCT--AGTTACTCTCGTCTAATACTGTCTGGTAATGCCGT [1538]
Lch TCTTACCAGACAAGGTTAGATCT--AGCTATTTCTGTCTAATACTGTCTGGTAATGCCGT [1788]
Dre TCTTACCAGACATGGTTAGATGT--AATAACTTGTGTCTAATACTGTCTGGTAATGCCGT [1865]

Hsa CCATCCGCTGC--TGGGCGGGGGCCCTCGTCTTACCCAGCAGTGTTTGGGTGC-GGTTGG [1744]
Mmu CCATCCACGGC--TGGGTAGGGGCCCTCGTCTTACCCAGCAGTGTTTGGGTGCTGGTTGG [1747]
Mdo TGGT-CACACT--CGGGACTGGCGCCCCATCTTACCCAGCAGTGTTTGGGTGCCGCTCGG [1527]
Meu TGGT-CACACT--TGGGACTGGTGCCCCGTCTTACCCAGTAGTGTTTGGGTGCTGGTTGG [1187]
Oan CAAT-CACAGC------------------------------------------------- [1627]
Aca CGAT-CGCATT------------------------------------------------- [1953]
Pbi CGATTCGCATT------------------------------------------------- [1953]
Cpi CCAT-CGCATT------------------------------------------------- [2036]
Cmy CCAT-CGCATT------------------------------------------------- [2035]
Psi CTAT-CGCATT------------------------------------------------- [1873]
Asp CTAT-CGCATT------------------------------------------------- [1873]
Ami TGAT-CGCACT------------------------------------------------- [2034]
Asi TGAT-CGCACT------------------------------------------------- [1951]
Tgu ------------------------------------------------------------ [1550]
Cli CAAT-CGCATC------------------------------------------------- [1803]
Gga CAAT-CGCATG------------------------------------------------- [1719]
Xtr TGGT-CACATT------------------------------------------------- [1548]
Lch TGAT-TACATG--GGGAAAGTGGCCACCATCTTACCGAGCAGCATTTGA-TGT-GAGTCT [1843]
Dre CCAT-CACATG--TGGATGCCTGGCTCCATCTTACAAGGCAGT-TTTGGATGTTATATCT [1921]

Hsa GAGTCTCTAATACTGCCGGGTAATGATGGAGGCCCCTGTCC--GGCCCTGGGTCCATCTT [1802]
Mmu GAGTCTCTAATACTGCCGGGTAATGATGGAGGCCCCTGTCC--GGCTCTGGGTCCATCTT [1805]
Mdo GAGTCTCTAATACTGCCGGGTAATGATGGAGGTCCTT-TCC--AGCTCTGGGGCCATCTT [1584]
Meu GAGTCTCTAATACTGCCGGGTAACGATGGAGGTCCTT-TCC------------------- [1227]
Oan ------------------------------------------------------------ [1627]
Aca ------------------------------------------------------------ [1953]
Pbi ------------------------------------------------------------ [1953]
Cpi ------------------------------------------------------------ [2036]
Cmy ------------------------------------------------------------ [2035]
Psi ------------------------------------------------------------ [1873]
Asp ------------------------------------------------------------ [1873]
Ami ------------------------------------------------------------ [2034]
Asi ------------------------------------------------------------ [1951]
Tgu ------------------------------------------------------------ [1550]
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Cli ------------------------------------------------------------ [1803]
Gga ------------------------------------------------------------ [1719]
Xtr ------------------------------------------------------------ [1548]
Lch CAGTGTCTAATACTGCCTGGTAATGATGGAG-CCATTTTCC------------------- [1883]
Dre ---TCTCTAATACTGCCTGGTAATGATGCAGATGGTCATCT--TCTCTAGGGTACATCTT [1976]

Hsa CCAGTACAGTG-TTGGATGGTCTAATTGTGAAGCTCCTAACACTGTCTGGTAAAGATGGC [1861]
Mmu CCAGTGCAGTG-TTGGATGGTTGAAGTATGAAGCTCCTAACACTGTCTGGTAAAGATGGC [1864]
Mdo CCAGTACAGTG-GTGGATGGT--------GAAGCTTCTAACACTGTCTGGTAAAGATGCC [1635]
Meu ------------------------------------------------------------ [1227]
Oan ------------------------------------------------------------ [1627]
Aca ------------------------------------------------------------ [1953]
Pbi ------------------------------------------------------------ [1953]
Cpi ------------------------------------------------------------ [2036]
Cmy ------------------------------------------------------------ [2035]
Psi ------------------------------------------------------------ [1873]
Asp ------------------------------------------------------------ [1873]
Ami ------------------------------------------------------------ [2034]
Asi ------------------------------------------------------------ [1951]
Tgu ------------------------------------------------------------ [1550]
Cli ------------------------------------------------------------ [1803]
Gga ------------------------------------------------------------ [1719]
Xtr ------------------------------------------------------------ [1548]
Lch ------------------------------------------------------------ [1883]
Dre ACCTGACAGTGCTTGGCTGTTC-----ACTGATGTTCTAACACTGTCTGGTAACGATG-C [2030]

Hsa TCCCGGGTGGG--CGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTGG [1919]
Mmu CCCCGGGTCAG--CGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTGG [1922]
Mdo CTCCGGGTTGG--CGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCG [1693]
Meu ------------CGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCG [1274]
Oan ------------------------------------------------------------ [1627]
Aca ------------------------------------------------------------ [1953]
Pbi ------------AGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGGGTCA [2000]
Cpi ------------AGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCA [2083]
Cmy ------------AGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCA [2082]
Psi ------------AGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCA [1920]
Asp ------------AGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCA [1920]
Ami ------------AGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCA [2081]
Asi ------------AGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCA [1998]
Tgu ------------------------------------------------------------ [1550]
Cli ------------AGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCG [1850]
Gga ------------AGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGGTGTCG [1766]
Xtr ------------AGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGTTGTCA [1595]
Lch ------------AGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGAGTGTTGTCA [1930]
Dre ACTCTGGTGAC--AGGGGTTGGCTGTTATCTTTGGTTATCTAGCTGTATGAGTGTTATTC [2088]

Hsa AGTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGCGAGTTGTTATC [1977]
Mmu AGTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGCGAGTTGTTATC [1980]
Mdo AGTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGTGAGTTGTTATC [1751]
Meu AGTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGTGAGTTGTTATC [1332]
Oan ----------------------------------------GAAGCGAGTTGTTATC [1643]
Aca ----------------------------------------GAAGCGAGTTGTTGTC [1969]
Pbi AGTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGCGAGTTGTTATC [2058]
Cpi ATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGCGAGTTGTTATC [2141]
Cmy ATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGCGAGTTGTTATC [2140]
Psi ATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGCGAGTTGTTATC [1978]
Asp ATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGCGAGTTGTTATC [1978]
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Ami ATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGCGAGTTGTTATC [2139]
Asi ATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGCGAGTTGTTATC [2056]
Tgu ------------------------------------------GAAGCGAGTTGTTATC [1566]
Cli ATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGTGAGTTGTTATC [1908]
Gga ATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGCGAGTTGTTATC [1824]
Xtr ATCCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGTG-GTTGTTATC [1652]
Lch ATTCTTCATAAAGCTAGATAACCGAAAGTAAAAATAACCCCA--GAAGTGAGTTGTTATC [1988]
Dre ATTCTTCATAAAGCTAGATAACCGAAAGTAACAAGAATCCCA--GAGGCGTGTTGTTATC [2146]

Hsa TTTGGTTATCTAGCTGTATGAGTGTATTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [2037]
Mmu TTTGGTTATCTAGCTGTATGAGTGTATTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [2040]
Mdo TTTGGTTATCTAGCTGTATGAGTGTATTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [1811]
Meu TTTGGTTATCTAGCTGTATGAGTGTATTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [1392]
Oan TTTGGTTATCTAGCTGTATGAGTGTATTGGTCTTCATAAAGCTAGATAACCGAAAGTAAG [1703]
Aca TTTGGTTATCTAGCTGTATGAGTGTGTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [2029]
Pbi TTTGGTTATCTAGCTGTATGAGTGTGTTGGCCTTCATAAAGCTAGATAACCGAAAGTAAA [2118]
Cpi TTTGGTTATCTAGCTGTATGAGTGTGTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [2201]
Cmy TTTGGTTATCTAGCTGTATGAGTGTGTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [2200]
Psi TTTGGTTATCTAGCTGTATGAGTGTGTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [2038]
Asp TTTGGTTATCTAGCTGTATGAGTGTGTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [2038]
Ami TTTGGTTATCTAGCTGTATGAGTGTTTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [2199]
Asi TTTGGTTATCTAGCTGTATGAGTGTTTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [2116]
Tgu TTTGGTTATCTAGCTGTATGAGTGTTTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [1626]
Cli TTTGGTTATCTAGCTGTATGAGTGTTTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [1968]
Gga TTTGGTTATCTAGCTGTATGAGTGTTTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [1884]
Xtr TTTGGTTATCTAGCTGTATGAGTGTATTGGTTTTCATAAAGCTAGATAACCGAAAGTAAA [1712]
Lch TTTGGTTATCTAGCTGTATGAGTGTGTTGGTCTTCATAAAGCTAGATAACCGAAAGTAAA [2048]
Dre TTTGGTTATCTAGCTGTATGAGTGTGCTGGCCGTCATAAAGCTAGATAACCGAAAGTAAG [2206]

Hsa AACTCCTTC--AGGCCCGTTTCTCTCTTTGGTTATCTAGCTGTATGAGTGCCACAGAGCC [2095]
Mmu AACTCCTTC--AGGCCCGTTTCTCTCTTTGGTTATCTAGCTGTATGAGTGCCACAGAGCC [2098]
Mdo AACTCCTTC--AGGCCCGTTTCTCTCTTTGGTTATCTAGCTGTATGAGTGTTATTGAGCT [1869]
Meu AACTCCTTC----------------------------------------------------- [1401]
Oan AACTCCTTC----------------------------------------------------- [1712]
Aca AACTCCTTC--AGGGCCGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTAATCGACCC [2087]
Pbi AACTCCTTC--AGGGCCGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTATCAAGCC [2176]
Cpi AACTCCTTC--AGGGCTGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTATTAAGCC [2259]
Cmy AACTCCTTC--AGGGCTGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTATTAAGCC [2258]
Psi AACTCCTTC--AGGGCTGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTATTAAGCC [2096]
Asp AACTCCTTC--AGGGCTGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTATTAAGCC [2096]
Ami AACTCCTTC--AGGGCTGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTCTCGAGCC [2257]
Asi AACTCCTTC--AGGGCTGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTCTCGAGCC [2174]
Tgu AACTCCTTC--AGGGATGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTGTGGAGCC [1684]
Cli AACTCCTTC--AGGGATGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTGTGGAGCC [2026]
Gga AACTCCTTC--AGGGATGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTGTGGAGCC [1942]
Xtr AACTCCTTC--GAGTTTGTTTCTATCTTTGGTTATCTAGCTGTATGAGTGTAAATAAGCC [1770]
Lch AACTGCTTC--GAGTCCGTTTCTGTCTTTGGTTATCTAGCTGTATGAGTGTTATTAAGCC [2106]
Dre AGCCGCTTC--GAGGTAGTTGCTATCTTTGGTTATCTAGCTGTATGAGTGTTTATCTGCC [2264]

Hsa GTCATAAAGCTAGATAACCGAAAGTAGAAATGATTCT---------------------- [2132]
Mmu GTCATAAAGCTAGATAACCGAAAGTAGAAATGACTCT---------------------- [2135]
Mdo ATCATAAAGCTAGATAACCGAAAGTAGAAATGACTTT--CTGAGCTGG-TTTTGATCTTT [1926]
Meu ------------------------------------CTGAGCTGGGTTTTGATCTTT [1422]
Oan ------------------------------------CTGAGCTGG-CTTTGGTCTTT [1732]
Aca ATCATAAAGCTAGATAACCGAAAGTAGAAATGACTCC--CAGGGCCGG-CTCTTCTCTTT [2144]
Pbi ATCATAAAGCTAGATAACCGAAAGTAGAAATGACTTC--CAGGGTCGG-TTTCTCTCTTT [2233]
Cpi ATCATAAAGCTAGATAACCGAAAGTAGAAATGACTTC--CTGGGTTGG-TTTTTGTCTTT [2316]
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Cmy ATCATAAAGCTAGATAACCGAAAGTAGAAATGACTTC--CTGGGTTGG-TTTTTGTCTTT [2315]
Psi ATCATAAAGCTAGATAACCGAAAGTAGAAATGACTTC--CTGGGTTGG-TTTTTGTCTTT [2153]
Asp ATCATAAAGCTAGATAACCGAAAGTAGAAATGACTTC--CTGGGTTGG-TTTTTGTCTTT [2153]
Ami GTCATAAAGCTAGATAACCGAAAGTAGAAATGACTTC--CTGGGTGGG-TTTTTGTCTTT [2314]
Asi GTCATAAAGCTAGATAACCGAAAGTAGAAATGACTTC--CTGGGTGGG-TTTTTGTCTTT [2231]
Tgu ATCATAAAGCTAGATAACCGAAAGTAGAAATGACTTC---------------------- [1721]
Cli ATCATAAAGCTAGATAACCGAAAGTAGAAATGACTTC--CTGGGTTGG-TTTTTCTCTTT [2083]
Gga ATCATAAAGCTAGATAACCGAAAGTAGAAATGACTTC--TTGGGTTGG-TTTTTCTCTTT [1999]
Xtr GTCATAAAGCTAGATAACCGAAAGTAGGAATCACTTC--TTGAATTGG-TTTCTGTCTTT [1827]
Lch ATCATAAAGCTAGATAACCGAAAGTAGAAATGACTTC--ATAGGTTAG-TTTTTTTCTTT [2163]
Dre TTCATAAAGCTAGATAACCGAAAGTAGAAATGTCCTC--ATGGGTTAG-TTTTTCTCTTT [2321]

Hsa ------------------------------------------------------------ [2132]
Mmu ------------------------------------------------------------ [2135]
Mdo GGTTTCCTAGCTGTGTGAGTGTCTCTGA-ATCATAAAGCTGGAGAACCGAATGTGGAAAC [1985]
Meu GGTTTCCTAGCTGTGTGAGTATTTCTGA-ATCATAAAGCTGGAGAACCGAATGTGGAAAC [1481]
Oan GGTTATCTAGCTGTATGAGTGTATGTGATGTCATAAAGCTAGAGAACCGAATGTAAAAAC [1792]
Aca GGTTATCTAGCTGTATGAGTGCGCCTGGTTTCATAAAGCTAGAGAACCGAACGTACGAAC [2204]
Pbi GGTTATCTAGCTGTATGAGTGTATCTGATGTCATAAAGCTAGAGAACCGAATGTACAAAC [2293]
Cpi GGTTATCTAGCTGTATGAGTGTATGTGATATCATAAAGCTAGAGAACCGAATGTAAAAAC [2376]
Cmy GGTTATCTAGCTGTATGAGTGTATGTGATATCATAAAGCTAGAGAACCGAATGTAAAAAC [2375]
Psi GGTTATCTAGCTGTATGAGTGTATGTGATATCATAAAGCTAGAGAACCGAATGTAAAAAC [2213]
Asp GGTTATCTAGCTGTATGAGTGTATGTGATATCATAAAGCTAGAGAACCGAATGTAAAAAC [2213]
Ami GGTTATCTAGCTGTATGAGTGTATGTGATATCATAAAGCTAGACAACCGAATGTAAAAAC [2374]
Asi GGTTATCTAGCTGTATGAGTGTATGTGATATCATAAAGCTAGACAACCGAATGTAAAAAC [2291]
Tgu ------------------------------------------------------------ [1721]
Cli GGTTATCTAGCTGTATGAGTGTATGTGATATCATAAAGCTAGAGAACCGAATGTAAAAAC [2143]
Gga GGTTATCTAGCTGTATGAGTGTATGTGATATCATAAAGCTAGAGAACCGAATGTAAAAAC [2059]
Xtr GGTTACCTAGCTGTATGAGTATAACTAATGTCATAAAGCTAGACAACCGAACGTATAAAC [1887]
Lch GGTTATCTAGCTGTATGAGTGTATCTGATATCATAAAGCTAGAGAACCGAATGTAAAAAC [2223]
Dre GGTTATCTAGCTGTATGAGTTTATGTGATATCATAAAGCTAGAGAACCGAATGTATAAAC [2381]

Hsa ---------CTTCTGTATATACCCTGTAGATCCGAATTTGTGTAAGGAATTTTGTGGTCA [2183]
Mmu ---------CTTCTGTATATACCCTGTAGATCCGAATTTGTGTAAGGAATTTTGTGGTCA [2186]
Mdo CAGCTGC--CTTCTGTATATACCCTGTAGATCCGAATTTGTGTAAGGAATTTTGTGGTCA [2043]
Meu CAGCTGC--CTTCTGTATATACCCTGTAGATCCGAATTTGTGTAAGGAATTTTGTGGTCA [1539]
Oan CAGCTTC--CTTCTGTATATACCCTGTAGATCCGAATTTGTGTAAGGAGTTTCGTGGTCA [1850]
Aca CGGCCCG--CTTCTGTATGTACCCTGTAGATCCGAATTTGTGTAAAAGAAACTGCG-TCA [2261]
Pbi CGCCCCG--CTTCTGTATGTACCCTGTAGATCCGAATTTGTGTAAAAGAAGCTGCC-TCA [2350]
Cpi TGATTCA--CTTCTATATGTACCCTGTAGATCCGAATTTGTGTAAAGGAAATTGTG-TCA [2433]
Cmy TGATTCA--CTTCTATATGTACCCTGTAGATCCGAATTTGTGTAAAGGAAGTTGTG-TCA [2432]
Psi TGATTCA--CTTCTATATGTACCCTGTAGATCCGAATTTGTGTAAAGGAAGTTGTG-TCA [2270]
Asp TGATTCA--CTTCTATATGTACCCTGTAGATCCGAATTTGTGTAAAGGAAGTTGTG-TCA [2270]
Ami CGGCTCG--CTTCTATATGTACCCTGTAGATCCGAATTTGTGTAAAGGAAGTTGCG-TCA [2431]
Asi CGGCTCG--CTTCTATATGTACCCTGTAGATCCGAATTTGTGTAAAGGAAGTTGCG-TCA [2348]
Tgu ------------------------------------------------------------ [1721]
Cli CCGCTCG--CTTCTATATGTACCCTGTAGATCCGAATTTGTGTAAAGGAAGTTGGG-TCA [2200]
Gga CCGCTCG--CTTCTATATGTACCCTGTAGATCCGAATTTGTGTAAAGGAAGTTGGG-TCA [2116]
Xtr CAGTTCC--CCTCTGTATGTACCCTGTAGATCCGAATTTGTGTGAGCGCAATCATA-TCA [1944]
Lch TAATTCT--CTTCTATATATACCCTGTAGATCCGAATTTGTGTGAACAGATTTGTGGTCA [2281]
Dre TAATTCC--CATCTATATATACCCTGTAGATCCGAATTTGTGTGAATA----TACAGTCG [2435]

Hsa CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2241]
Mmu CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2244]
Mdo CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2101]
Meu CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [1597]
Oan CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [1908]
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Aca CAAATTCGCGTCTAGGGGAATATGTAGTAG--GTTGTCTATATATACCCTGTAGAACCGA [2319]
Pbi CAAATTCGCATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2408]
Cpi CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2491]
Cmy CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2490]
Psi CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2328]
Asp CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2328]
Ami CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2489]
Asi CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2406]
Tgu ------------------------------GTTGTCTATATATACCCTGTAGAACCGA [1749]
Cli CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2258]
Gga CAAATTCGTATCTAGGGGAATATGTAGTTG--GTTGTCTATATATACCCTGTAGAACCGA [2174]
Xtr CAAATTCGTGTCTGGGGGGATATGCAGTTG--GTTGTCTATATGTACCCTGTAGAACCGA [2002]
Lch CAAATTCGTGTCTAGGGGAGTATGTAGTTG--GTCGTCTATATATACCCTGTAGAACCGA [2339]
Dre CAAATTCGTGTCTTGGGGAATATGTAGTTG--GTCGTCTATATATACCCTGTAGAACCGA [2493]

Hsa ATTTGTGTGGTATCCGTATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--- [2298]
Mmu ATTTGTGTGGTACCCACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--- [2301]
Mdo ATTTGTGTGGTATTTACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--- [2158]
Meu ATTTGTGTGGTATTCACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--- [1654]
Oan ATTTGTGTGGTATTCACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--- [1965]
Aca ATTTGTGTGGTATTTACACAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--G [2377]
Pbi ATTTGTGTGGTATTTACGTAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--A [2466]
Cpi ATTTGTGTGGTATTCACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--G [2549]
Cmy ATTTGTGTGGTATTCACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--G [2548]
Psi ATTTGTGTGGTATTCACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--G [2386]
Asp ATTTGTGTGGTATTCACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--G [2386]
Ami ATTTGTGTGGTATTCACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--G [2547]
Asi ATTTGTGTGGTATTCACATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--G [2464]
Tgu ATTTGTGTGATATTCATATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--- [1806]
Cli ATTTGTGTGATATTCATATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--G [2316]
Gga ATTTGTGTGATATTCATATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG--- [2231]
Xtr ATTTGTGTGGT--TCGTACAGTCACAGATTCGATTCTAGGGGGATATATGGTCGATG--G [2058]
Lch ATTTGTGTGATGTTATCAGAATCACAGATTCAATTCTAGGGGAGTATATGGTCGATG--G [2397]
Dre ATTTGTGTGAAAAAATAACATTCACAGATTCGATTCTAGGGGAGTATATGGTCGATG--G [2551]

Hsa ------------------------------------------------------------ [2298]
Mmu ------------------------------------------------------------ [2301]
Mdo ------------------------------------------------------------ [2158]
Meu ------------------------------------------------------------ [1654]
Oan ------------------------------------------------------------ [1965]
Aca TCGTTTATATGTACCCTGTAGAATCGAATTTGTGTGAGCACCTCAA---TCACAAATTCG [2434]
Pbi TCGTTTATATATACCCTGTAGAACCGAATTTGTGTGAGCACCTCTA---TTGCAAATTCG [2523]
Cpi TCGTCTATATGTACCCTGTAGAATCGAATTTGTGTGAATATTTGAGAG-TCACAAATTCG [2608]
Cmy TCGTCTATATGTACCCTGTAGAATCGAATTTGTGTGAATATTTGAGAG-TCACAAATTCG [2607]
Psi TCGTCTATATGGACCCTGTAGAATCGAATTTGTGTGAATATCT--GAG-TCACAAATTCG [2443]
Asp TCGTCTATATGGACCCTGTAGAATCGAATTTGTGTGAATATCT--GAG-TCACAAATTCG [2443]
Ami TCGCCTATATGTACCCTGTAGAATCGAATTTGTGTGAACATTTCAGAG-TCACAAATTCG [2606]
Asi TCGCCTATATGTACCCTGTAGAATCGAATTTGTGTGAACATTTCAGAG-TCACAAATTCG [2523]
Tgu ------------------------------------------------------------ [1806]
Cli TCTCCTATATGTACCCTGTAGACTCGAATTTGTGTGAGCGTCTCCCAG-TCACAAATTCG [2375]
Gga ------------------------------------------------------------ [2231]
Xtr GCGCTTATATGCACCCTGTAGAATCGAATTTGTGTGAG---TTCTGAA-CCACAGATTCG [2114]
Lch TCGTCTATATATACCCTGTAGAACCGAATTTGTGTGAGCTCTCGATAA-TCACAAATTCG [2456]
Dre TCGTCTATATGTACCCTGTAGAACCGAATTTGTGTCCAAAACATCAAAATCGCAAATACG [2611]

Hsa --------------------------CCTGTTGCCACAAACCCGTAGATCCGAACTTGTG [2332]
Mmu --------------------------CCTGTTGCCACAAACCCGTAGATCCGAACTTGTG [2335]
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Mdo --------------------------CCTGTTGCCACAAACCCGTAGATCCGAACTTGTG [2192]
Meu --------------------------CCTGTTGCCACAAACCCGTAGATCCGAACTTGTG [1688]
Oan --------------------------CCTGTTGCCACAAACCCGTAGATCCGAACTTGTG [1999]
Aca TCTCTAGGGGAGTATATGGACGAT--CTAGTTGCCACAAACCCGTAGATCCGAACTTGTG [2492]
Pbi TCTCTAGGGGGATATGTGGATGAT--CCAGTTGCCACAAACCCGTAGATCCGAACTTGTG [2581]
Cpi TCTCTAGGGGAGTATATGGACGAT--CCCGTTGCCACAAACCCGTAGATCCGAACTTGTG [2666]
Cmy TCTCTAGGGGAGTATATGGACGAT--CCCGTTGCCACAAACCCGTAGATCCGAACTTGTG [2665]
Psi TCTCTAGGGGAGTATATGGACGAT--CCCGCTGCCACAAACCCGTAGATCCGAACTTGTG [2501]
Asp TCTCTAGGGGAGTATATGGACGAT--CCCGCTGCCACAAACCCGTAGATCCGAACTTGTG [2501]
Ami TCTCTAGGGGAATATATGGACGAT--CCCGTTGCCACAAACCCGTAGATCCGAACTTGTG [2664]
Asi TCTCTAGGGGAATATATGGACGAT--CCCGTTGCCACAAACCCGTAGATCCGAACTTGTG [2581]
Tgu --------------------------CCTGCTGCCACAAACCCGTAGATCCGAACTTGTG [1840]
Cli TCTCTAGGGGAATATATGGGCGAT--CCTGTTGCCACAAACCCGTAGATCCGAACTTGTG [2433]
Gga --------------------------CCTGTTGCCACAAACCCGTAGATCCGAACTTGTG [2265]
Xtr TCTCTAGGGGGGTATATGGGTGAT---------------------------------- [2138]
Lch TCTCTAGGGGAGTATATGGTCGAT--CCTGTTGCCACAAACCCGTAGATCCGAACTTGTG [2514]
Dre TCTCTACAGGAATACATGGGCGAC--CCTGCTGACACAAACCCGTAGATCCGAACTTGTG [2669]

Hsa GTATTAGTCCGCACAAGCTTGTATCTATAGGTATGTGTCTGTTAGG--CCCATTGGCATA [2390]
Mmu CTGATTCTGCACACAAGCTTGTGTCTATAGGTATGTGTCTGTTAGG--CCCATTGACATA [2393]
Mdo GTGATATTCCACACAAGCTTGTGTCTATAGGTATGTGTCTGTCAGG-------------- [2238]
Meu GTGATATTCCACACAAGCTTGTGTCTATAGGTATGTGTCTGTCAGG--CTAACTGGTACA [1746]
Oan GTGATATTCCACACAAGCTTGTGTCTATAGGTATGTGTCTGTGGGC--CCAGTTGGCATA [2057]
Aca CTTCTATGTTACACAAGCTTGTGTCTATAGGTATGTGTCTGCTTGG--CCAATTGGCATA [2550]
Pbi CTCCTATCCTACACAAGCTTGTATCTATAGGTATGTGTCTGCTTGG--CCAATTGGCATA [2639]
Cpi GTCATATTCCACACAAGCTTGTATCTATAGGTATGTGTCTGCATGG--CCAATTGGCATA [2724]
Cmy GTCATATTCCACACAAGCTTGTATCTATAGGTATGTGTCTGCATGG--CCAACTGGCATA [2723]
Psi GTCATATTCCACACAAGCTTGTATCTATAGGTATGTGTCTGCATGG--CCAATTGGCATA [2559]
Asp GTCATATTCCACACAAGCTTGTATCTATAGGTATGTGTCTGCATGG--CCAATTGGCATA [2559]
Ami GTGATATTCCACACAAGCTTGTATCTATAGGTATGTGTCTTCATGG--CCAGTTGGCATA [2722]
Asi GTGATATTCCACACAAGCTTGTATCTATAGGTATGTGTCTTCATGG--CCAGTTGGCATA [2639]
Tgu CTCATATTCCACACAAGCTTGTATCTATAGGTCTGTGGCTGGCTGG--CCAATTGGCATA [1898]
Cli GTCATATTCCACACAAGCTTGTATCTATAGGTATGTGTCTGTCTGG--CCAATTGGCATA [2491]
Gga GTCATATTCCACACAAGCTTGTATCTATAGGTATGTGTCTGTCTGG--CCAATTGGCATA [2323]
Xtr ------------------------------------------------CCTACTAACATA [2150]
Lch ATCAGATCCCACACAAGCTCGTATCTATAGGTATGTGTCTACATGG--CCAATTGCCATA [2572]
Dre GTGACTGTCCACACAAGCTTGTATCTATAGGTATCTGTCTGTGTGG--CCACTTGTCATT [2727]

Hsa AACCCGTAGATCCGATCTTGTGGTGAAGTGGACCGCACAAGCTCGCTTCTATGGGTCTGT [2450]
Mmu AACCCGTAGATCCGATCTTGTGGTGAAGTGGACCGCGCAAGCTCGTTTCTATGGGTCTGT [2453]
Mdo ------------------------------------------------------------ [2238]
Meu AACCCGTAGATCCGATCTTGTGGTGAAATTGACTTCACAAGCTCGCCTCTTTGGGTCTGT [1806]
Oan AACCCGTAGATCCGATCTTGTGGTGAAGTGAAATACACAAGCTCGCCTCTCTGGGTCTGT [2117]
Aca AACCCGTAGATCCGATCTTGTGGTGAAGTATAATGCACAAGCTCGCTTCTATGGGTCTGT [2610]
Pbi AACCCGTAGATCCGATCTTGTGGTGAAATATAGTGCACAAGCTCGTTTCTATGGGTCAGT [2699]
Cpi AACCCGTAGATCCGATCTTGTGGTAAAGTATACTGCACAAGCTCGCTTCTATGGGTCTGT [2784]
Cmy AACCCGTAGATCCGATCTTGTGGTAAAGTATACTGCACAAGCTCGCTTCTATGGGTCTGT [2783]
Psi AACCCGTAGATCCGATCTTGTGGTAAAGTACATTGCACAAGCTCGCTTCTATGGGTCTGT [2619]
Asp AACCCGTAGATCCGATCTTGTGGTAAAGTACATTGCACAAGCTCGCTTCTATGGGTCTGT [2619]
Ami AACCCGTAGATCCGATCTTGTGGTAAAATACACCACACAAGCTCGCTTCTATGGGTCTGT [2782]
Asi AACCCGTAGATCCGATCTTGTGGTAAAATACACCGCACAAGCTCGCTTCTATGGGTCTGT [2699]
Tgu AACCCGTAGATCCGATCTTGTGTTGAAACGCACTGCACAAGCTCGCTTCTATGGGTCTGT [1958]
Cli AACCCGTAGATCCGATCTTGTGTTGAAACGCACTGCACAAGCTCGCTTCTATGGGTCTGT [2551]
Gga AACCCGTAGATCCGATCTTGTGTTGAAATGCACTGCACAAGCTCGCTTCTATGGGTCTGT [2383]
Xtr AACCCGTAGATCCGATCTTGTGGTGAATTCCTTTGCTCAAGCTCGTTTCTATGGGTCTGT [2210]
Lch AACCCGTAGATCCGATCTTGTGATAAA-TGTACTGCACAAGCTCGCTTCTATGGGTCTGT [2631]
Dre AACCCGTAGATCCGATCTTGTGATAAGTTTGATGGCACAAGCTCGATTCTATGGGTCTCT [2787]
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Hsa GTCAGTGTG--GGTCCTGGCACCCACCCGTAGAACCGACCTTGCGGGGCCTTCGCCGCAC [2508]
Mmu GGCAGTGTG--GGTCCTGGCACCCACCCGTAGAACCGACCTTGCGGGGCCTTCGCCGCAC [2511]
Mdo ------------------------------------------------------------ [2238]
Meu GTCAGTGTA--CAGCCTGGCACCCACCCGTAGATCCGACCTTGCGGGGCGCCGGCCACAC [1864]
Oan GTCAGTGTG------------------------------------------------- [2126]
Aca GTCCCTATG--CCAGTTGCCATAAACCCGTAGATCCGAACTTGCGGTACAACTGATTCAC [2668]
Pbi GTCAGTCTG--CCGGTTGCCATAAACCCGTAGATCCGAACTTGCGGTACGACTGCCTCAC [2757]
Cpi GTCACTCTG--CCGGTTGCCATAAACCCGTAGATCCGAACTTGCGGTACGACTGCCTCAC [2842]
Cmy GTCATTCTG--CCGGTTGCCATAAACCCGTAGATCCGAACTTGCGGTACGACTGCCTCAC [2841]
Psi GTCACTCTG--CCGGTTGCCATAAACCCGTAGATCCGAACTTGCGGTACGACTGCCTCAC [2677]
Asp GTCACTCTG--CCGGTTGCCATAAACCCGTAGATCCGAACTTGCGGTACGACTGCCTCAC [2677]
Ami GTCAGTGTG--CCGGTCGCCATAAACCCGTAGATCCGAACTTGCGGT-CG-CT-CCTCGT [2837]
Asi GTCAGTGTG--CCGGTCGCCATAAACCCGTAGATCCGAACTTGCGGT-CG-CT-CCTCGT [2754]
Tgu GTCAGTGTG------------------------------------------------- [1967]
Cli GTCAGTATG------------------------------------------------- [2560]
Gga GTCAGTATG------------------------------------------------- [2392]
Xtr GTCATTATG--CTGGTTGCCATAAACCCGTAGATCCGAACTTGTGCTGTGCC--CCTCTC [2266]
Lch GCCAGTGTG--CCGGTTGCCACAAACCCGTAGAGCCGAACTTGTGGTGAAGC--TCGTTC [2687]
Dre GTCTCTGTG------------------------------------------------- [2796]

Hsa ACAAGCTCGTGTCTGTGGGTCCGTGTCGGGGGCT--TGCCAGTCTCTAGGTCCCTGAGAC [2566]
Mmu ACAAGCTCGTGTCTGTGGGTCCGTGTCGGGGGCT--TGCCGGCCTCTGGGTCCCTGAGAC [2569]
Mdo ------------------------------------------------------------ [2238]
Meu ACAAGCTCGAGTCTGTGGGTCTGTGTCGGGATTG------------------------- [1898]
Oan ------------------------------------------------------------ [2126]
Aca ACAAGCTCGAGTCTGTGGGTATGTGTCGACCTCG--GGGCATCTTCTCTGTCCCTGAGAC [2726]
Pbi ACAAGCTCGAGTCTGTGGGTATGTGTCGACCTTG--TGGCATCTTCTCTGTCCCTGAGAC [2815]
Cpi ACAAGCTCGAGTCTGTGGGTATGTGTCGATCCTG--GGCAGCCGTCTCTGTCCCTGAGAC [2900]
Cmy ACAAGCTCGAGTCTGTGGGTATGTGTCGATCCTG--GGCAGCCGTCTCTGTCCCTGAGAC [2899]
Psi ACAAGCTCGAGTCTGTGGGTATGTGTCGATCCTG--GGCAGCCGGCTCTGTCCCTGAGAC [2735]
Asp ACAAGCTCGAGTCTGTGGGTATGTGTCGATCCTG------------------------- [2711]
Ami GCAAGCTCGACTCTGTGGGTCTGTGTCGGCCTCG--GGCCTCCCTCTCGGTCCCTGAGAC [2895]
Asi GCAAGCTCGACTCTGTGGGTCTGTGTCGGCCTCG--GGCCTCCCTCTCGGTCCCTGAGAC [2812]
Tgu ------------------------------------------------------------ [1967]
Cli ------------------------------------------------------------ [2560]
Gga ------------------------------------------------------------ [2392]
Xtr ACAAGCTCGAGTGTGCGGGTCTGTGTCGGCTTGG--GGTGTGATGTTCTGTCCCTGAGAC [2324]
Lch ACAAGCTCGTGTCTAGGGGTCTGTGTCGGCTTGG--AGCATGCTTCGCTGTCCCTGAGAC [2745]
Dre ----------------------------------AGTATGTCTCTTTGTCCCTGAGAC [2820]

Hsa CCTTTAACCTGTGAGGA-CATCCAGGG-TCACAGGTGAGGTTCTTGGGAGCCTGGCGTCT [2624]
Mmu CCTTTAACCTGTGAGGA-CGTCCAGGG-TCACAGGTGAGGTTCTTGGGAGCCTGGCGCCT [2627]
Mdo ------------------------------------------------------------ [2238]
Meu ------------------------------------------------------------ [1898]
Oan ------------------------------------------------------------ [2126]
Aca CCTT-AACCTGTGAGGA-AGCCCAGAGGTCACAGGTGAGGTTCTTGGGAACTGAGCGGAG [2784]
Pbi CCTT-AACCTGTGAGGA-AGCCCAGAGGTCACAGGTGAGGGCCTTGGGAACTGAGTGGGT [2873]
Cpi CCTT-AACCTGTGAGGGCAGCGCAGAATTCACAGGTGAGGTTCTTGGGAACCGAGCGACT [2959]
Cmy CCTT-AACCTGTGAGGGCAGCGCAGAATTCACAGGTGAGGTTCTTGGGAACTGAGCGACT [2958]
Psi CCTT-AACCTGTGAGGGCAGCGCAGAGTTCACAGGTGAGGTTCTTGGGAGCTGAGCGACT [2794]
Asp ------------------------------------------------------------ [2711]
Ami CCTT-ATCCTGTGAGGG-AGCCCAGAGCTCACAGGTGAGG-CCTTGGGAACTGGGCGGGT [2952]
Asi CCTT-ATCCTGTGAGGG-AGCCCAGAGCTCACAGGTGAGG-CCTTGGGAACTGGGCGGGC [2869]
Tgu ------------------------------------------------------------ [1967]
Cli ------------------------------------------------------------ [2560]
Gga ------------------------------------------------------------ [2392]
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Xtr CCTT-AACCTGTGAGGA--AGACATATGTCACAGGTGAGGTTCTGAGGAGCTGGACGCCA [2381]
Lch CCTT-AACCTGTGAGGA---CATCAAGGTCACAGGTGAGGTTCTTGGGAACTGTGTGGCA [2801]
Dre CCTT-AACCTGTGAGGT--CAAACTAGGTCACAGGTGAGGTCCTCAGGAACAGGGCTGCA [2877]

Hsa GGCC--TGCGCTCCTCTCAGTCCCTGAGACCCTAACTTGTGATGTTTACCGTTTAAA-TC [2681]
Mmu GGCC--TGCGCTCCCCTCAGTCCCTGAGACCCTAACTTGTGATGTTTACCGTTTAAA-TC [2684]
Mdo ------TGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTACCGTTTAAA-TC [2291]
Meu ---------------------------------------------------------- [1898]
Oan ------TGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTCCCGTTTAAA-TC [2179]
Aca AGCC--TGCGCCCCTCTCTGTCCCTGAGACCCTAACTTGTGACGTTTAGTTTTTAAG-TC [2841]
Pbi TGCC--TGCGCCCCTCTCTGTCCCTGAGACCCTAACTTGTGACGTTTTGGTTTCAAG-TC [2930]
Cpi GGCC--TGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTTTTAAA-TC [3016]
Cmy GGCC--TGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTTTTAAA-TC [3015]
Psi GACC--TGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTTTCAAA-TC [2851]
Asp ------TGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTTTCAAA-TC [2764]
Ami GGCC--TGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTTTTAAA-TC [3009]
Asi GGCC--TGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTTTTAAA-TC [2926]
Tgu ------TGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTTTTAAA-TC [2020]
Cli ------TGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTTTTAAA-TC [2613]
Gga ------TGCGCCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTTTTAAA-TC [2445]
Xtr TGCA--TGCACCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTTTAAAAATC [2439]
Lch TGCA--TGCACCCCTCTCAATCCCTGAGACCCTAACTTGTGATGTTTAGCTGTTAAA-TC [2858]
Dre TGCG--TGTGCCTCTCACAATCCCTGAGACCCTAACTTGTGACGTTTTCCTGTTATG-TG [2934]

Hsa CACGGGTTAGGCTCTTGGGAGCTGCGAGTCGTGCT--GACTTTTCCTAGTCCCTGAGACC [2739]
Mmu CACGGGTTAGGCTCTTGGGAGCTGCGGGTCGTGCC--GACTTTGCCTAGTCCCTGAGACC [2742]
Mdo CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCC--GACTTTTCCTAGTCCCTGAGACC [2349]
Meu ------------------------------------GACTTTTCCTAGTCCCTGAGACC [1921]
Oan CACGGGTTAGGTTCTTGGGAGCTGTGAGTTGTGCC--GACTTTTCCTAGTCCCTGAGACC [2237]
Aca CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCC--GACTTTTCCTAGTCCCTGAGACC [2899]
Pbi CACGGGTTAGGCTCTCGGGAGCTGTGAGTTGTGCC--GACTTTTCCTAGTCCCTGAGACC [2988]
Cpi CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCT--GACTTTTCCTAGTCCCTGAGACC [3074]
Cmy CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCT--GACTTTTCCTAGTCCCTGAGACC [3073]
Psi CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCT--GACTTTTCCTAGTCCCTGAGACC [2909]
Asp CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCT--GACTTTTCCTAGTCCCTGAGACC [2822]
Ami CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCT--GACTTTTCCTAGTCCCTGAGACC [3067]
Asi CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCT--GACTTTTCCTAGTCCCTGAGACC [2984]
Tgu CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCT--TACTTTTCCTAGTCCCTGAGACC [2078]
Cli CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCT--GACTTTTCCTAGTCCCTGAGACC [2671]
Gga CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCT--GACTTTTCCTAGTCCCTGAGACC [2503]
Xtr CACGGGTTAGGCTCTTGGGAGCTGTGAGTTGTGCT--GACTTTTCCTAGTCCCTGAGACC [2497]
Lch CACGGGTTAGGCTCTTGGGAGCTGTGAGTGGTGCC--AACTTCTCCTAGTCCCTGAGACC [2916]
Dre CACGGGTTAGGTTCTTGGGAGCTGAGAGGGGTGCT--CACTCCTCCTGGTCCCTGAGACC [2992]

Hsa CTAACTTGTGAGG-TATTTTAGTAACA-TCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [2797]
Mmu CTAACTTGTGAGG-TATTTTAGTAACA-TCACAAGTCAGGTTCTTGGGACCTAGGCGGAG [2800]
Mdo CTAACTTGTGAGG-CTTTTCAGCGACAACCACAGGTCAGGCTCTTGGGACCTAGGCGGAG [2408]
Meu CTAACTTGTGAGG-TTTTTTAGCAACAATCACAGGTCAGGTTCTTGGGACCTAGGCGGAG [1980]
Oan CTAACTTGTGAGG-TTTTTGAGCAACGATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [2296]
Aca CTAACTTGTGAGG-TTTT-TAGTAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [2957]
Pbi CTAACTTGTGAGG-TTTTTTAGTAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [3047]
Cpi CTAACTTGTGAGG-TTTTTTAGCAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [3133]
Cmy CTAACTTGTGAGG-TTTTTTAGCAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [3132]
Psi CTAACTTGTGAGG-TTTTTTAGCAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [2968]
Asp CTAACTTGTGAGG-TTTTTTAGCAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [2881]
Ami CTAACTTGTGAGG-TTTTTTAGCAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [3126]
Asi CTAACTTGTGAGG-TTTTTTAGCAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [3043]
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Tgu CTAACTTGTGAGG-TTTTTTAGCAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [2137]
Cli CTAACTTGTGAGG-TTTTTTAGCAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [2730]
Gga CTAACTTGTGAGG-TTTTGTAGCAACAATCACAAGTCAGGCTCTTGGGACCTAGGCGGAG [2562]
Xtr CTAACTTGTGAGGATTTTTTAGCAACAATCACAAGTTAGGCTCTTGGGACCTAGGCGGAG [2557]
Lch CTAACTTGTGAGC-TCTTTGCATTAATGTCACGGGTTAGGCTCTTGGGACCTAGGCGGAG [2975]
Dre CTAACTTGTGAGCTTTGTGTGCTAAAAATCACAGGTTAAGCTCTTGGGACCTGGGCAGAG [3052]

Hsa GG--TGGAGTAAAGTAGCAGCACATAATGGTTTGTGGATTTT-GAAAAGG--TGCAGGCC [2852]
Mmu GG--TGGAGTAAAGTAGCAGCACATAATGGTTTGTGGATGTT-GAAAAGG--TGCAGGCC [2855]
Mdo GG--TGGGGTAAAGTAGCAGCACATAATGGTTTGTTGGTTTT-GAAAAGG--TGCAGGCC [2463]
Meu GG--TGGGGTAAAGTAGCAGCACATAATGGTTTGTTGGTTTT-GAAAAGG--TGCAGGCC [2035]
Oan TG--TGGGGTAAAGTAGCAGCACATAATGGTTTGTGAGTTTT-GAAA-----TACAGGCC [2348]
Aca GG---------------------------------------------------------- [2959]
Pbi GG---------------------------------------------------------- [3049]
Cpi GG--TGGGCTAACGTAGCAGCACATAATGGTTTGTGGGTTTT-GAAAAGG--TGCAGGCC [3188]
Cmy GG--TGGGCTAACGTAGCAGCACATAATGGTTTGTGGGTTTT-GAAAAGG--TGCAGGCC [3187]
Psi GG--TGGGCTAACGTAGCAGCACATAATGGTTTGTGGGTTTT-GAAAAGG--TGCAGGCC [3023]
Asp GG--TGGGCTAACGTAGCAGCACATAATGGTTTGTGGGTTTT-GAAAAGG--TGCAGGCC [2936]
Ami GG--TGGCCTAACGTAGCAGCACATAATGGTTTGTGGATTTT-GAAAAGG--TGCAGGCC [3181]
Asi GG--TGGCCTAACGTAGCAGCACATAATGGTTTGTGGATTTT-GAAAAGG--TGCAGGCC [3098]
Tgu GG--TGGCATAACGTAGCAGCACATAATGGTTTGTGGGTTTT-GAAAAGG--TGCAGGCC [2192]
Cli GG--TGGCATAACGTAGCAGCACATAATGGTTTGTGGGTTTT-GAAAAGG--TGCAGGCC [2785]
Gga GG--TGGCATAACGTAGCAGCACATAATGGTTTGTGGGTTTT-GAAAAGG--TGCAGGCC [2617]
Xtr GG--TGACGTAAAGTAGCAGCACATAATGGTTTGTGGGTTAC-ACAGAGG--TGCAGGCC [2612]
Lch GA--TGGAGCACTGTAGCAGCACATAATGGTTTGTGAGTTAT-ATAGAATTATGCAGGCC [3032]
Dre GG--GTCGGTACTGTAGCAGCACAGAATGGTTTGTGAGTTATAACGGGGG--TGCAGGCC [3108]

Hsa ATATTGTGCTGCCTCAAAAATAC--CCTTAAAGTACTGTAG-CAGCACATCATGGTTTAC [2909]
Mmu ATACTGTGCTGCCTCAAAA-TAC--CCTTAAAGTACTGTAG-CAGCACATCATGGTTTAC [2911]
Mdo ATATTGTGCTGCCTCAAAAATAC--CCTTAAAGTGCTATAGGCAGCACATCATGGGTTAC [2521]
Meu ATATTGTGCTGCCTCAAAAATAC----------------------------------- [2058]
Oan ATATTGTGCTGCCTCAAAAATAC--CCTTGGACTGCTATAG-CAGCACATCATGGTTTGC [2405]
Aca -------------------------CTTTAAAGTACTCTAG-CAGCACATCATGATTTGT [2993]
Pbi -------------------------CCTCAAAGTACTATAG-CAGCACATCATGATTTGT [3083]
Cpi ATATTGTGCTGCCTCAAAAATAC--CCTTAAATTACTCTAG-CAGCACATCATGGTTTGC [3245]
Cmy ATATTGTGCTGCCTCAAAAATGC--CCTTAAAGTACTCTAG-CAGCACATCATGGTTTGC [3244]
Psi ATATTGTGCTGCCTCAAAAATAC--CCTTAAAGTACTCTAG-CAGCACATCATGGTTTGC [3080]
Asp ATATTGTGCTGCCTCAAAAATAC--CCTTAAAGTACTCTAG-CAGCACATCATGGTTTGC [2993]
Ami ATATTGTGCTGCCTCAAAAATAC--CCTTAAATTACTCTAG-CAGCACATCATGGTTTGC [3238]
Asi ATATTGTGCTGCCTCAAAAATAC--CCTTAAATTACTCTAG-CAGCACATCATGGTTTGC [3155]
Tgu ATATTGTGCTGCCTCAAAAATAC--CCTCGAAGTGCTGTAG-CAGCACATCATGGTTTGC [2249]
Cli ATATTGTGCTGCCTCAAAAATAC--CCTTAAAGTACTCTAG-CAGCACATCATGGTTTGC [2842]
Gga ATATTGTGCTGCCTCAAAAATAC--CCTTAAAGTACTCTAG-CAGCACATCATGGTTTGC [2674]
Xtr ATACTGTGCTGCCGCCAAAACAC--TCCTAAAGAAGTGTAG-CAGCACATCATGATTTGC [2669]
Lch ATGTTGTGCTGCTGCAAAAATAC--CCTTAAAGTGCTGTAG-CAGCACATCATGGTTTGC [3089]
Dre GTACTGTGCTGCGGCAACAACGA--CCTTAGACCGCTAAAG-CAGCGCGTCATGGTTTTC [3165]

Hsa ATGCTACAGTCAAGATGCGAATCATTATTTGCTGCTCTAGAAATTTAAG----------- [2958]
Mmu ATACTACAGTCAAGATGCGAATCATTATTTGCTGCTCTAGAAATTTAAG----------- [2960]
Mdo ATGGTGGGAGCGCGCTGCGAATCATTATTTGCTGCTTTAGAAATTTAAG--CTTTAGGAG [2579]
Meu ------------------------------------------------CTTTAGGAG [2067]
Oan ATGGTATAGCCAAGATGCGAATCATTATTTGCTGCTTTAGAAATTTAAG--CTTGAGGGG [2463]
Aca ATGTCATAGTAAATATGCAAGTCATTATTTGCTGCTTTAGAATTTTAAA--CCGGAGGTG [3051]
Pbi GTTTCATAATAAATATGCAAGTCATTATTTGCTGCTTTAGAATTTTAAG--CTTGAGGTG [3141]
Cpi ATGATCTTGTAAAGATGCTAATCATTATTTGCTGCTTTAGGAATTTAAG--TTTGAGGAG [3303]
Cmy ATGCTCTAGCAAAAATGCGAATCATTATTTGCTGCTTTGGAAATTTAAG--TTTGAGGAG [3302]
Psi ATGCTTTAGCAAAAATGCGAATCATTATTTGCTGCTTTGGAAATTTAAG--TTTGAGGAG [3138]
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Asp ATGCTCTAGCAAAAATGCGAATCATTATTTGCTGCTTTGGAAATTTAAG--TTTGAGGAG [3051]
Ami ATGATCTTGTAAAGATGCTAATCATTATTTGCTGCTTTAGGAATTTAAG--TTTGAGGAG [3296]
Asi ATGATCTTGTAAAGATGCTAATCATTATTTGCTGCTTTAGGAATTTAAG--TTTGAGGAG [3213]
Tgu ATGCTCTGCTCAGGGTGCAAATCATGATTTGCTGCTGTAGGAATTGAAG--TTTGAGGAG [2307]
Cli ATGCTCTAATAAAGATGCGAATCATTATTTGCTGCTTTAGAAATTTAAG--TTTGAGGAG [2900]
Gga ATGCTGTAGTGAAGATGCGAATCATTATTTGCTGCTTTAGAAATTTAAG--TTTGAGGAG [2732]
Xtr ATGCTGTATTATAGATTCTAATCATTTTTTGCTGCTTCATGATATTGGG--TTTGAGGTG [2727]
Lch AACA-CTAGTTAAGATGCAAATCATTATTTGCTGCTTTAGAATTTTAGG--TTTGAGGAA [3146]
Dre AACA-TTAGAGAAGGTGCAAGCCATCATTTGCTGCTCTAGAGTTTTAAG---------- [3213]

Hsa ---------------------------------------------------------- [2958]
Mmu ---------------------------------------------------------- [2960]
Mdo AA-ATAGCAGCACGCCATGGTTTGTAGAGATA-CGGTGATACAAACCATCGTGGGCTGTT [2637]
Meu AA-ATAGCAGCACGCCATGGTTTGTAGAGATA-AGGTGATGCAAACCATCGTGGGCTGTT [2125]
Oan GTTGTAGCAGCACATCATGGTTTGTAGGGACA-AGGAGATACAGACCATTCTGGGCTGCC [2522]
Aca AT-GTAGCAGCACAACATGGTTTGTAGGGACACAGAAGATACAGACCGTTCTGGGCTGCC [3110]
Pbi GC-GTAGCAGCACGACATGGTTTGTAGAGAAA-AGAAGATACAGACCGTTCTGGGCTGCC [3199]
Cpi AT-GTAGCAGCACATCATGGTTTGTAGGGACA-AGGAGATACAGACCATTCTGGGCTGCC [3361]
Cmy AT-GTAGCAGCACATCATGGTTTGTAGGGACA-AGGAGATACAGACCATTCTGGGCTGCC [3360]
Psi AT-GTAGCAGCACATCATGGTTTGTAGGGACA-AGGAGATACAGACCATGCTGGGCTGCC [3196]
Asp AT-GTAGCAGCACATCATGGTTTGTAGGGACA-AGGAGATACAGACCATGCTGGGCTGCC [3109]
Ami AT-GTAGCAGCACATCATGGTTTGTAGGGACA-AGGAGATACAGACCATTCTGGGCTGCC [3354]
Asi AT-GTAGCAGCACATCATGGTTTGTAGGGACA-AGGAGATACAGACCATTCTGGGCTGCC [3271]
Tgu AT-GTAGCAGCACATCATGGTTTGTAGGGACA-AGGAGATACAGACCATTCTGGGCTGCC [2365]
Cli AT-GTAGCAGCACATCATGGTTTGTAGGGACA-AGGAGATACAGACCATTCTGGGCTGCC [2958]
Gga AT-GTAGCAGCACATCATGGTTTGTAGGGACA-AGGAGATACAGACCATTCTGGGCTGCC [2790]
Xtr AT-CTAGCAGCACATCATGGTTTGTAGAAACA-AGGAGATACAGACCATTCTGAGCTGCC [2785]
Lch AT-GTAGCAGCACATCATGGTTTGTAGGGATA-AGGAGATACAGACCATTCTGAGCTGCC [3204]
Dre ---------------------------------------------------------- [3213]

Hsa ---------------CCTGCTCCCGCCCCAGCAGCACACTGTGGTTTGTACGGCACTGTG [3003]
Mmu ---------------CCTGCCCCCGCCCCAGCAGCACACTGTGGTTTGTACGGCACTGTG [3005]
Mdo ACATTTTCCTAAA--CCTGCCTCCGCCCCAGCAGCACACTGTGGTTTGTTCAGTGTTATG [2695]
Meu ACATTTTCCTAAA--CCTGCCTCCGCCCCAGCAGCACACTGTGGTTTGTTCAGTGTTGTG [2183]
Oan TCAATCCCCCAAG---------------------------------------------- [2535]
Aca TCATTACCTTTTG---------------------------------------------- [3123]
Pbi TCATGACCTCAAG---------------------------------------------- [3212]
Cpi TCATTACCTCAAG---------------------------------------------- [3374]
Cmy TCATTACCTCAAG---------------------------------------------- [3373]
Psi TCATTACCTCAAG--CCAGCCTTCGCCCCAGCAGCACATCATGGTTTGTCTGGAGCTCTG [3254]
Asp TCATTACCTCAAG---------------------------------------------- [3122]
Ami TCATTACCTCAAG--CCAGCCC-CGCCCCAGCAGCACATCATGGTTTGT-GGGGTCTCGT [3410]
Asi TCATTACCTCAAG--CCAGCCC-CGCCCCAGCAGCACATCATGGTTTGT-GGGGTCTCGT [3327]
Tgu TCATTACCTCAAG---------------------------------------------- [2378]
Cli TCATTACCTCAAG---------------------------------------------- [2971]
Gga TCATTACCTCAAG---------------------------------------------- [2803]
Xtr TCTTGACCTCAGA---------------------------------------------- [2798]
Lch TCAGTTCCCCAAG---------------------------------------------- [3217]
Dre ---------------CCTGAGTGCCCTGTAGCAGCACATCATGGTTTGTAAGTTATAAGG [3258]

Hsa GCCACGTCCAAACCACACTGTGGTGTTAGAGCGAGGGTG--CAGCAGTGCCTTAGCAGCA [3061]
Mmu GCCACGTCCAAACCACACTGTGGTGTTAGAGCGAGGGTA--CAGCGGTGCCTTAGCAGCA [3063]
Mdo GCCAAGTCCAAACCACACTGTGGTGTTAGAGCGAGGGTA--CAACAGTGCCTTAGCAGCA [2753]
Meu GCCAAGTCCAAACCACACTGTGGTGTTAGAGTGAGGGTA--CAACAGTGCCTTAGCAGCA [2241]
Oan ----------------------------------------CAGCAGTACCTTAGCAGCA [2554]
Aca ---------------------------------------------------------- [3123]
Pbi ----------------------------------------CAGTTGTGCCTTAGCAGCA [3231]
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Cpi ----------------------------------------CAGCAGTACATTAGCAGCA [3393]
Cmy ----------------------------------------CAGCAGTACATTAGCAGCA [3392]
Psi AATGCA--CAAACCATTTTGTGATGTTACCGCGCGGGCC--CAACAGTACATTAGCAGCA [3310]
Asp ----------------------------------------CAACAGTACATTAGCAGCA [3141]
Ami GGCACA----GACCATGGCGTGGTGCTACCGCG-GGGCC--CAATCGTACCTTAGCAGCA [3463]
Asi GGCACA----GACCATGGCGTGGTGCTACCGCG-GGGCC--CAATCGTACCTTAGCAGCA [3380]
Tgu ----------------------------------------CTGTCATACTTTAGCAGCA [2397]
Cli ----------------------------------------CTGTCATACTTTAGCAGCA [2990]
Gga ----------------------------------------CTGTCATACTCTAGCAGCA [2822]
Xtr ----------------------------------------CAGCAGTCCTTTAGCAGCA [2817]
Lch ----------------------------------------CAGTGGTACCTTAGCAGCA [3236]
Dre GCAAATTCCGAATCATGATGTGCTGTCACTGGGAGCCTG--CTGCCTGGCTGTAGCAGCA [3316]

Hsa CGTAAA-TATTGGCGTTAAGATTCTAAAATTATCTCCAGTATTAACTGTGCTGCTGAAGT [3120]
Mmu CGTAAA-TATTGGCGTTAAGATTCTGAAATTACCTCCAGTATTGACTGTGCTGCTGAAGT [3122]
Mdo CGTAAA-TATTGGCGTTAAGATTTTAAAAGTATCTCCAGTATTAACTGTGCTGCTGAAGT [2812]
Meu CGTAAA-TATTGGCGTTAAGATTTTAAAAGTATCTCCAGTATTAACTGTGCTGCTGAAGT [2300]
Oan CGTAAA-TATTGGCGTTAAGACTCTAAAAGTATCTCCAGTATTGACTGTGCTGCTGAAGT [2613]
Aca ------------------------------------------------------------ [3123]
Pbi CATAAA-TATTGGAGTTATTATTAGTAAAGTATCTCCAGTATCAATTGTGCTGCTGAAGT [3290]
Cpi CGTAAA-TATTGGCGTTAACT--CTGTAAATATCTCCAGTATTAACTGTGCTGCTGAAGT [3450]
Cmy CGTAAA-TATTGGCGTTAACT--CTGTAAATATCTCCAGTATTAACTGTGCTGCTGAAGT [3449]
Psi CGTAAA-TATTGGTGTTAACT--CTATAAATATCTCCAGTATTAACTGTGCTGCTGAAGT [3367]
Asp CGTAAA-TATTGGTGTTAACT--CTATAAATATCTCCAGTATTAACTGTGCTGCTGAAGT [3198]
Ami CGTAAA-TATTGGTGTTAAGATTCTGTAAATATCTCCAGTATTAACTGTGCTGCTGAAGT [3522]
Asi CGTAAA-TATTGGTGTTAAGATTCTGTAAATATCTCCAGTATTAACTGTGCTGCTGAAGT [3439]
Tgu CGTAAA-TATTGGTGTT-AAGA-CTGTAAATATCTCCAGTATTAACTGTGCTGCTGAAGT [2454]
Cli CGTAAA-TATTGGTGTTAAGA--CTGTAAATATCTCCAGTATTAACTGTGCTGCTGAAGT [3047]
Gga CGTAAA-TATTGGTGTTAAAA--CTGTAAATATCTCCAGTATTAACTGTGCTGCTGAAGT [2879]
Xtr CGTAAA-TATTGGTGTTAAAA--TGGTC-------CCAATATTAACTGTGCTGCTAGAGT [2867]
Lch CGTAAAATACTAGAGTTTAGTGTTTATGAATGCCTCCAGTATTGGTCGTGCTGCTGAAGT [3296]
Dre CGTAAA-TATTGGAGTCAAAGCACTTGCGAATCCTCCAGTATTGACCGTGCTGCTGGAGT [3375]

Hsa AAGG--CTTGTTCCACTCTAGCAGCACGTAAATATTGGCGTAGTGAAATATATATTAAAC [3178]
Mmu AAGG--CTTGTTCCACTCTAGCAGCACGTAAATATTGGCGTAGTGAAATAAATATTAAAC [3180]
Mdo AAGG--CTTGTTCCACTCTAGCAGCACGTAAATATTGGCGTAGTGAAATCAGTCTGAAAC [2870]
Meu AAGG--CCTGCCCCGCTCTAGCAGCACGTAAATATTGGCGTCGTGAGATA-CTGGTGAAC [2357]
Oan AAGG--CTTATTACGCTCTAGCAGCACGTAAATATTGGTGTAGTGAAG----TCTTAAAC [2667]
Aca ------CTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTAGTAAAGATAATCTT-AAC [3176]
Pbi AAGG--CTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTAGTAAAGATAATCTT-AAC [3347]
Cpi AAAG--CTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTATAAAAGTAAATCA--AAC [3506]
Cmy AAAG--CTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTAGTAAAGTAAATATTAAAC [3507]
Psi AAAG--CTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTAGTAATGTAAATCTT-AAC [3424]
Asp AAAG--CTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTAGTAATGTAAATCTT-AAC [3255]
Ami AAGT--CTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTATAAAAGTAAATCA--AAC [3578]
Asi AAGT--CTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTATTAAAGTAAATCA--AAC [3495]
Tgu AAGG--CTCGTTCCGCCCTAGCAGCACGTAAATATTGGAGTGTCAAAG-AAACCTTCAAC [2511]
Cli AAGG--CTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTAGTAAAATAAACCTTAAAC [3105]
Gga AAGG--CTTGTTCCGCCCTAGCAGCACGTAAATATTGGTGTAGTAAAATAAACCTTAAAC [2937]
Xtr AAGG--ATTGCTCCGCATTAGCAGCACGTAAATATTGG-GTGATATGATATGGA----GC [2920]
Lch AAGG--CCAGCTCCACTCTAGCAGCATGTAAATATTGGTGTATAAAGATAGACTA-AAAC [3353]
Dre TAGG--CCTTCCTCGCTTTAGCAGCACGTAAATATTGGTGTGTTATAGTCAAGGC-CAAC [3432]

Hsa ACCAATATTAC-TGTGCTGCTTTAGTGTGACAGG-------------------------- [3211]
Mmu ACCAATATTAT-TGTGCTGCTTTAGTGTGACAGG-------------------------- [3213]
Mdo CCCAATATTAC-TGTGCTGCTTTAGTGTGGCAGG--TCGGCTGTGCCCTAGCAGCACGTC [2927]
Meu CCCAATATTAT-TGTGCTGCTTCAGCGTGGCAGG--TCGGCTGTGCCCTAGCAGCACGTC [2414]
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Oan CCCAATATTAT-TGTGCTGCTTTAGCGTGATAGG--TCGGCCGTGCCCTAGCAGCACGTA [2724]
Aca CCCAATATTGT-TGTGCTGCTTAAGCGTGGCAGG--TCCGCCCGGCTCTAGCAGCACGTA [3233]
Pbi GCCAATATTAT-TGTGCTGCTTAAGCGTGACAGG--TCTGCTCTGCTTTAGCAGCACGTA [3404]
Cpi CCCAATATTAT-TGTGCTGCTTAAGCGTGGCAGA--TCAGCAGTGCTCTAGCAGCACGTA [3563]
Cmy CCCAATATTAT-TGTGCTGCTTAAGCGTGGCAGA--TCAGCAGTGCTCTAGCAGCACGTA [3564]
Psi CCCAATATTAT-TGTGCTGCTTAAGCGTGGCAGA--TCAGCAGTGCTCTAGCAGCACGTA [3481]
Asp CCCAATATTAT-TGTGCTGCTTAAGCGTGGCAGA--TCAGCAGTGCTCTAGCAGCACGTA [3312]
Ami CCCAATATTAT-TGTGCTGCTTAAGCGTGGCAGA--TCAGCAGTGCTCTAGCAGCACGTA [3635]
Asi CCCAATATTAT-TGTGCTGCTTAAGCGTGGCAGA--TCAGCAGTGCTCTAGCAGCACGTA [3552]
Tgu CCCAATATTAT-TGTGCTGCTTCAGCGTGGCAGA--TCAGCAGTGCTCTAGCAGCACGTA [2568]
Cli CCCAATATTAT-TGTGCTGCTTAAGCGTGGCAGA--TCAGCAGTGCTCTAGCAGCACGTA [3162]
Gga CCCAATATTAT-TGTGCTGCTTAAGCGTGGCAGA--TCAGCAGTGCTCTAGCAGCACGTA [2994]
Xtr CCCAGTATTAT-TGTACTGCTTAAGTGTGGCAAG--GCAATCTTGCTTTAGCAGCACGTA [2977]
Lch CCCAATGTTGT-TGTGCTGCTTCAGTGTGGCAGG--TCAGCAGTACTTTAGCAGCACGTA [3410]
Dre CCCAATATTATGTGTGCTGCTTCAGTAAGGCAGG------------------------- [3466]

Hsa ------------------------------------------------------------ [3211]
Mmu ------------------------------------------------------------ [3213]
Mdo AAAACTGGAGTCACAAA-----GTTCAATCCTCCAGTATTGCCTTGCTGCTTGAGTGAGG [2982]
Meu AAAACTGGAGTTAACTG-----GTTAAATCCTCCAGTATTGCCTTGCTGCTTGAGCGAGG [2469]
Oan AATACTGGAGTTTGGGGATGCCTCGTTGCTCTCCAGTATTGCATTGCTGCTTGAGCGAGG [2784]
Aca AATACTGGAGTCTAGGATGATACATTTGCCCTCCAGTATTGCTTTGCTGCTTTAATCGGG [3293]
Pbi AATACTGGAGTTTA-GATGCT----CTGCCCTCCAGTATTGCTTTGCTGCTTTAGTCAAG [3459]
Cpi AATACTGGAGTCGAGGACTGCCTGGCTGCTCTCCAGTATTGCATTGCTGCTTGAGTGAGG [3623]
Cmy AATACTGGAGTTTAGGATTGCCTAGCTGCTCTCCAGTATTGCATTGCTGCTTTAGTGAGG [3624]
Psi AATACTGGAGTTTAGGATTGCCTAGCTGCTCTCCAGTATTGCGTTGCTGCTTTAGTGAGG [3541]
Asp AATACTGGAGTTTAGGATTGCCTAGCTGCTCTCCAGTATTGCGTTGCTGCTTTAGTGAGG [3372]
Ami AATACTGGAGTCGAGGACTGCCTGGCTGCTCTCCAGTATTGCATTGCTGCTTGAGTGAGG [3695]
Asi AATACTGGAGTCGAGGACTGCCTGGCTGCTCTCCAGTATTGCATTGCTGCTTGAGTGAGG [3612]
Tgu AATACTGGAGTTTGGGATTGCCT-GTTGCTCTCCAGTATTGCATTGCTGCTTTAGTGAGG [2627]
Cli AATACTGGAGTTTAGGATTGCCTG-TTGCTCTCCAGTATTGCATTGCTGCTTTAGTGAGG [3221]
Gga AATACTGGAGTGGGGGATCGCCTG-TTGCTCTCCAGTATTGCATTGCTGCTTTAGTGAGG [3053]
Xtr AATACTGGAGTTCATGACCATATCTGCACTCTCCAGTATTACTTTGCTGCTATATTAAGA [3037]
Lch AATATTGGAGTTCAGA---ATTGCTGCTATCTCCAGTATTGCAATGCTGCTATTGTGAGG [3467]
Dre ------------------------------------------------------------ [3466]

Hsa ------GCTTCCCTGGCTCTAGCAGCACAGAAATATTGGCACAG------GGAAGCGAGT [3259]
Mmu ------ACTCTCCTGGCTCTAGCAGCACAGAAATATTGGCATGG------GGAAGTGAGT [3261]
Mdo CAGG--GCTTCCCTGGCTTTAGCAGCACAAAAATATTGGCACCTG-----AGGGAAAGCC [3035]
Meu TAGG--GCCCCCCTGGCTTTAGCAGCACAGAAATATTGGCACCTG-----AGGGAAAACC [2522]
Oan CCGG------------------------------------------------------- [2788]
Aca TTTG--GCCGGTCCCGCTCCAGCAGCACTTCAATATTGGCAGTGTCC--ACCCCCTCCGG [3349]
Pbi CTGG------------------------------------------------------- [3463]
Cpi CTGG------------------------------------------------------- [3627]
Cmy CTGG------------------------------------------------------- [3628]
Psi CTGG--GCCTGTCCCGCTCCAGCAGCACATAAATATTGGCAGCGTCCTGGGCATGCCTGC [3599]
Asp CTGG--GCCTGTCCCGCTCCAGCAGCACATAAATATTGGCAGCGTCCTGGGCATGCCTGC [3430]
Ami CTGG------------------------------------------------------- [3699]
Asi CTGG------------------------------------------------------- [3616]
Tgu CTGG------------------------------------------------------- [2631]
Cli CTGG------------------------------------------------------- [3225]
Gga CTGG------------------------------------------------------- [3057]
Xtr TTGC------------------------------------------------------- [3041]
Lch CTGT------------------------------------------------------- [3471]
Dre ------GTGTGCCTGACAGAAGCAGCACATCAATATTGGCAGCTGCC--CTCTCTCTGGG [3518]

Hsa CTGCCAATATTGGCT-GTGCTGCTCCAGGCAGGGTGGT--GAATAATGTCAAAGTGCTTA [3316]
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Mmu CTGCCAATATTGGCT-GTGCTGCTCCAGGCAGGGTGGT--GAATAATGTCAAAGTGCTTA [3318]
Mdo ATGCCAGTATTGAGA-GTGCTGCTCTAGACAGGGTAGC--GAATAATGTCAAAGTGCTTA [3092]
Meu ATGCCAGTATTGA---GTGCTGCTCCAGACAGGGTGGC--GAATAATGTCAAAGTGCTTA [2577]
Oan ----------------------------------------GAATAATGTCAAAGTGCTTA [2808]
Aca CCGCCAGTATTGCCT-GTGCTGCTCCAGGGGGGCTCGG--GAGTAATGTCAAAGTGCTTA [3406]
Pbi ----------------------------------------GAATAATGTCAAAGTGCTTA [3483]
Cpi ----------------------------------------GAGTAATGTCAAAGTGCTTA [3647]
Cmy ----------------------------------------GGGTAATGTCAAAGTGCTTA [3648]
Psi CTGCCAGTATTTCCTTGTGCTGCTCCAGCGGGGCCGGG--GAGTAATGTCAAAGTGCTTA [3657]
Asp CTGCCAGTATTTCCTTGTGCTGCTCCAGCGGGGCCGGG--GAGTAATGTCAAAGTGCTTA [3488]
Ami ----------------------------------------GAGTAATGTCAAAGTGCTTA [3719]
Asi ----------------------------------------GAGTAATGTCAAAGTGCTTA [3636]
Tgu ----------------------------------------GAGTAATGTCAAAGTGCTTA [2651]
Cli ----------------------------------------GAGTAATGTCAAAGTGCTTA [3245]
Gga ----------------------------------------GAGTAATGTCAAAGTGCTTA [3077]
Xtr ----------------------------------------GAGTAATGTCAAAGTGCTTA [3061]
Lch ----------------------------------------AAGTAATGACAAAGTGCTTA [3491]
Dre TTGCCAGTATGGTTT-GTGCTGCTCCCGTCAGACAGAC--ATGTATTGTCAAAGTGCTTA [3575]

Hsa CAGTGCAGGTAGTGATATG-T-GC--ATCTACTGCAGTGAAGGCACTTGTAGCATTATGG [3372]
Mmu CAGTGCAGGTAGTGATGTG-T-GC--ATCTACTGCAGTGAGGGCACTTGTAGCATTATGC [3374]
Mdo CAGTGCAGGTAGTGATATG-TAGA--ATCTACTGCAGTGAAGGCACTTGTAGCATTATAG [3149]
Meu CAGTGCAGGTAGTGATATG-TAGA--ATCTACTGCAGTGAAGGCACTTGTAGCATTATAG [2634]
Oan CAGTGCAGGTAGTGGTATG-TAGA--ATCTACTGCAGTGAAGGCACTTGTAGCATTATGT [2865]
Aca CAGTGCAGGTAGTGATAAG-TAGA--ACCTACTGCAGTGAAGGCACTTGTAGCATTATGC [3463]
Pbi CAGTGCAGGTAGTGATTTA-TAGA--ACCTACTGCAGTGAAGGCACTTGTAGCATTATGC [3540]
Cpi CAGTGCAGGTAGTGATATA--AGA--ACCTACTGCAGTGAAGGCACTTGTAGCATTATAG [3703]
Cmy CAGTGCAGGTAGTGATATA--AGA--ACCTACTGCAGTGAAGGCACTTGTAGCATTATAT [3704]
Psi CAGTGCAGGTAGTGATATA--AGA--ATCTACTGCAGTGAAGGCACTTGTAGCATTATAT [3713]
Asp CAGTGCAGGTAGTGATATA--AGA--ATCTACTGCAGTGAAGGCACTTGTAGCATTATAT [3544]
Ami CAGTGCAGGTAGTGATATA-TAGA--ACCTACTGCAGTGAAGGCACTTGTAGCATTATAG [3776]
Asi CAGTGCAGGTAGTGATATA-TACA--ACCTACTGCAGTGAAGGCACTTGTAGCATTATAG [3693]
Tgu CAGTGCAGGTAGTGATATA-TAGA--ACCTACTGCAGTGAAGGCACTTGTAGCATTATGT [2708]
Cli CAGTGCAGGTAGTGATATA-TAGA--ACCTACTGCAGTGAAGGCACTTGTAGCATTATGT [3302]
Gga CAGTGCAGGTAGTGATATA-TAGA--ACCTACTGCAGTGAAGGCACTTGTAGCATTATGT [3134]
Xtr CAGTGCAGGTAGTGATTTAACAGA--ACCTACTGCAGTGAAGGCACTTGTAGCATTATAT [3119]
Lch CAGTGCAGGTAGTAATATG-TAGA--ACCTACTGCAGTGAAGGCACTTGTAGCATTATAT [3548]
Dre CAGTGCAGGTAGTATTATG-GAAT--ATCTACTGCAGTGGAGGCACTTCTAGCAATACAC [3632]

Hsa T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3430]
Mmu T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3432]
Mdo T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3207]
Meu T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [2692]
Oan T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [2923]
Aca T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGACTAGCATCTACTGCC [3521]
Pbi T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3598]
Cpi T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3761]
Cmy T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3762]
Psi T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3771]
Asp T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3602]
Ami T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3834]
Asi T--CTTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3751]
Tgu T--CTTTTTGTACTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [2766]
Cli T--CTTTTTGTACTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3360]
Gga T--CTTTTTGTACTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3192]
Xtr T--CTTTTTGTCCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3177]
Lch T--CTTTTTGTGCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCC [3606]
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Dre T--GGCTTTGTGCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGACTAGCACCTACTGCC [3690]

Hsa CTAAGTGCTCCTTCTGGCATAAGAAG--TCTGTAGCACTAAAGTGCTTATAGTGCAGGTA [3488]
Mmu CTAAGTGCTCCTTCTGGCATAAGAAG--TCTGTAGCACTAAAGTGCTTATAGTGCAGGTA [3490]
Mdo CTAAGTGCTCCTTCTGGCATAAGAAG--TTTGTAGCACTAAAGTGCTTATAGTGCAGGTA [3265]
Meu CTAAGTGCTCCTTCTGGCATAAGAAG--TTTGTAGCACTAAAGTGCTTATAGTGCAGGTA [2750]
Oan CTAAGTGCTCCTTCTGGCATAAGAAG--CTTGTAGCACTAAAGTGCTTATAGTGCAGGCA [2981]
Aca CTAAGTGCTCCTTCTGGCATAAGAAG--CCTGTAGCACTAAAGTGCTTATAGTGCAGGTA [3579]
Pbi CTAAGTGCTCCTTCTGGCATAAGAAG--CCTGTAGCACTAAAGTGCTTATAGTGCAGGTA [3656]
Cpi CTAAGTGCTCCTTCTGGCATAAGAAG--CCTGTAGTACTAAAGTGCTTATAGTGCAGGTA [3819]
Cmy CTAAGTGCTCCTTCTGGCATAAGAAG--TCTGTAGTACTAAAGTGCTTATAGTGCAGGTA [3820]
Psi CTAAGTGCTCCTTCTGGCATAAGAAG--TCAGTAGTACTAAAGTGCTTATAGTGCAGGTA [3829]
Asp CTAAGTGCTCCTTCTGGCATAAGAAG--CCAGTAGTACTAAAGTGCTTATAGTGCAGGTA [3660]
Ami CTAAGTGCTCCTTCTGGCATAAGAAG--CCTGTAGTACTAAAGTGCTTATAGTGCAGGTA [3892]
Asi CTAAGTGCTCCTTCTGGCATAAGAAG--CCTGTAGTACTAAAGTGCTTATAGTGCAGGTA [3809]
Tgu CTAAGTGCTCCTTCTGGCATAAGAAG--CTTGTAGCACTAAAGTGCTTATAGTGCAGGTA [2824]
Cli CTAAGTGCTCCTTCTGGCATAAGAAG--CTTGTAGCACTAAAGTGCTTATAGTGCAGGTA [3418]
Gga CTAAGTGCTCCTTCTGGCATAAGAAG--CTTGTAGCACTAAAGTGCTTATAGTGCAGGTA [3250]
Xtr CTAAGTGCTCCTTCTGGCATAAAAAG--AAAGTGGTGCTAAAGTGCTTATAGTGCAGGTA [3235]
Lch CTAAGTGCTCCTTCTGGCATAAGAAG--TTAGCAGCGCTAAAGTGCTTATAGTGCAGGTA [3664]
Dre CTAAGTGCTCCTTCTGGCACGAGGGT--TCAGCAGTGCTAAAGTGCTTATAGTGCAGGTA [3748]

Hsa GTGTTTA-GTTATCTACTGCATTATGAGCACTTAAAGTACTGCTAG--TTGGCCATGTAA [3545]
Mmu GTGTGTA-GCCATCTACTGCATTACGAGCACTTAAAGTACTGCCAG--TTGGCCATGTCA [3547]
Mdo GTGTTTA-GTTATCTACTGCATTATGAGCACTTGAAGTACTGCTAG--TCGGTTGTGTAA [3322]
Meu GTGTTTA-GTTATCTACTGCATTATGAGCACTTGAAGTACTGCTAG--TCGGTTGTGTAA [2807]
Oan ATGTTTA-GTCGTCTACTGCATTATGAGCACTTCAAGTCCTGCAAG--TTGGTTGTGCAA [3038]
Aca GTGATTA-ATAATCTACTGCATTACGAGCACTTAAAGTACTGCTAG--TCGG-GGTGCAA [3635]
Pbi GTGTTTC-ATAATCTACTGCATTAGGAGCACTTAAAGTACTACTAG--TCGGTGGTGCAA [3713]
Cpi GTGTTCA-GTAATCTACTGCATTATGAGCACTTAAAGTACTGCTAG--TGAGTTGTGCAA [3876]
Cmy GTGTTCA-GTAATCTACTGCATTATGAGCACTTAAAGTACTGCTAG--TGAGTTGTGCAA [3877]
Psi GTGTTCA-GTAATCTACTGCATTATGAGCACTTAAAGTACTGCTAG--TCAGTTGTGCAA [3886]
Asp GTGTTCA-GTAATCTACTGCATTATGAGCACTTAAAGTACTGCTAG--TGAGTTGTGCAA [3717]
Ami GTGTTCA-GGAATCTACTGCATTATGAGCACTTAAAGTACTGCTAG-------------- [3937]
Asi GTGTTCA-GGAATCTACTGCATTATGAGCACTTAAAGTACTGCTAG--TGTGTTGTGTAA [3866]
Tgu GTGTTCA-CTAATCTACTGCATTATAAGCACTTAAAGTACTGCTAG--CAAGTTGTGCAA [2881]
Cli GTGTTCA-CTAATCTACTGCATTATAAGCACTTAAAGTACTGCTAG--TGAGTTGTGCAA [3475]
Gga GTGTTCA-CTAATCTACTGCATTATAAGCACTTAAAGTACTGCTAG--TGAGTTGTGCAA [3307]
Xtr GTTTTTCTGTATTCTACTGCATAATGAGCACTTAAAGTACTCCTAG--TGTAAACTGCAA [3293]
Lch GTGTTTA-GTAATCTACTGCATTGTGAGCACTTAAAGTTCTGCTAG--GGAGTTATGCAA [3721]
Dre GTATTTCTGTCATCTACTGCAGTGTGAGCACTTGAAGTACTTCTAG-------------- [3794]

Hsa AAGTGCTTACAGTGCAGGTAGCTTTTTGAGATCTACTGCAATGTAAGCACTTCTTACATT [3605]
Mmu AAGTGCTAACAGTGCAGGTAGCTTTTTGAGTTCTACTGCAGTGCCAGCACTTCTTACATT [3607]
Mdo AAGTGCTTATAGTGCAGGTAGGTC-GT-GTAACTACTGCCCTGTGAGCACTTCCAACATG [3380]
Meu AAGTGCTTATAGTGCAGGTAGGTCGGT-GTAACTACTGCCCTGTGAGCACTTCCAACATG [2866]
Oan AAGTGCTTACAGTGCAGGTAG-CTTTTAGTACCTACTGCAATGTAAGCACTTCTAGCATT [3097]
Aca AAGTGCTTATAGTGCAGGTAGTGTGTTGGCATCTACTGCAGTGTTGGCACTTCCGTGCC- [3694]
Pbi AAGTGCTTATAGTGCAGGTAGTCCAGTGATCTCTACTGCAGTGTTAGCACTTCAGTGGC- [3772]
Cpi AAGTGCTTACAGTGCAGGTAGTGTGTTGGTATCTACTGCAGTGGAAGCACTTCTAGCATT [3936]
Cmy AAGTGCTTACAGTGCAGGTAGCATTTTGGTATCTACTGCAGTGGAAGCACTTCTAGCATT [3937]
Psi AAGTGCTTACAGTGCAGGTAGCATTTTGGGATCTACTGCAGTGGTAGCACTTCTAGCATT [3946]
Asp AAGTGCTTACAGTGCAGGTAGCATTTTGGGATCTACTGCAGTGGTAGCACTTCTAGCATT [3777]
Ami ---------------------------------------------------------- [3937]
Asi AAGTGCTTACAGTGCAGGTAGTGTTTTGGTATCTACTGCAGTATAAGCACTTCTAGCATT [3926]
Tgu AAGTGCTTACAGTGCAGGTAGAGTT-CAGGATCTACTGCAGTTTAAGCACTTCTGGCATT [2940]
Cli AAGTGCTTACAGTGCAGGTAGAGTT-TAGGATCTACTGCAGTATAAGCACTTCTGGCATT [3534]
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Gga AAGTGCTTACAGTGCAGGTAGAGCT-CAGCACCTACTGCAGTATAAGCACTTCTGGCATG [3366]
Xtr AAGTGCTTATAGTGCAGGTAGAAT--TTAAACCTACTGCACCATAAGCACTTCCTGCATC [3351]
Lch AAGTGCTTACAGTGCAGGTAGTAAG-CAGTCTCTACTGCAGTGCAAGCACTTCTAGCATT [3780]
Dre ------------------------------------------------------------ [3794]

Hsa ACCAT--TCTCTTGTGTTAAGGTGCATCTAGTGCAGTTAGTGAAGCAGCTTAGAATCTAC [3663]
Mmu ACCAT--TCTCTTGTGTTAAGGTGCATCTAGTGCTGTTAGTGAAGCAGCTTACAATCTAC [3665]
Mdo ACCAC--TCCCTTGTGCTAAGGTGCATCTAGTGCAGTTAGTGATGTAGTTTAGTATCTAC [3438]
Meu ACCAC--TCCCTTGTGCTAAGGTGCATCTAGTGCAGTTAGTGATGTAGCTTAGTATCTAC [2924]
Oan ACCAT--TCCCTTGTGTTAAGGTGCATCTAGTGCAGTTAGTGAAGTAGCTTAGAATCTAC [3155]
Aca ACGAT--CTTCCTGTGCTAAGGTGCATCTAGTGCAGTTAGTGAAGTAGCTTAGAATCTAC [3752]
Pbi ACAAT--TTTCTTGTGCTAAGGTGCATCTAGTGCAGTTAGTGAACTAGCTTAGACTCTAC [3830]
Cpi ACAAT--TTCCTTGTGTTAAGGTGCATCTAGTGCAGTTAGTGAAGTAGCTTAGAATCTAC [3994]
Cmy ACAAT--TTCCTTGTGTTAAGGTGCATCTAGTGCAGTTAGTGAAGTAGCTTAGAATCTAC [3995]
Psi ACAAT--TTCCTTGTGCTAAGGTGCATCTAGTGCAGTTAGTGAAGTAGCTTAGAATCTAC [4004]
Asp ACAAT--TTCCTTGTGCTAAGGTGCATCTAGTGCAGTTAGTGAAGTAGCTTAGAATCTAC [3835]
Ami ------------------------------------------------------------ [3937]
Asi ACCAT--TTCCTTGTGTTAAGGTGCATCTAGTGCAGTTAGTGAAGTAGCTTAGAATCTAC [3984]
Tgu ACTGT--GTCCTTGTGTTAAGGTGCATCTAGTGCAGTTAGTGATGTAGCGTAGAATCTAC [2998]
Cli ACTGT--GTTCTTGTGTTAAGGTGCATCTAGTGCAGTTAGTGAAGTAGCGTAGAATCTAC [3592]
Gga ACCGT--GTCCTTGTGTTAAGGTGCATCTAGTGCAGTTAGTGACGTAGCGTAGAATCTAC [3424]
Xtr ACTAA--CTCCTTGTGTTAAGGTGCATCTAGTGCAGTTAGTGACATAGTGTAGCATCTAC [3409]
Lch GCTTT--TATCTTGTGGTAAGGTGCATCTAGCGCAGTTAGTGAGGTAGCTTAGAATCTAC [3838]
Dre -------GCCTTCCTGCTAAGGTGCATCTTGTGTAGTTAGTGAAGTAGTCTAGTATCTAC [3847]

Hsa TGCCCTAAATGCCCCTTCTGGCACAGGCTG--CTAGTA-GTACCAAAGTGCTCATAGTGC [3720]
Mmu TGCCCTAAATGCCCCTTCTCGCACAGGCTA--CTAGTA-GTGCCAAAGTGCTCATAGTGC [3722]
Mdo TGCCCTAAATGCTCCTTCCGGCACAAGCCG--CTGGTA-GTGCCAAAGTGCTCATAGTGC [3495]
Meu TGCCCTAAATGCTCCTTCTGGCACAAGCCG--CTGGTA-GTGCCAAAGTGCTCATAGTGC [2981]
Oan TGCCCTAAATGCTCCTTCTGGCACAAGCTG--CTGACA-GTACCAAAGTGCTCATAGTGC [3212]
Aca TGCCCTGAATGCTCCTTCTGGCATAGGAGG--CTCGCA-GTGTCAAAGTGCTCATAGTGC [3809]
Pbi TGCCCTGAGTGCTCCTTCTGGCACACGGAG--CTGGCA-GTGCCAAAGTGCTCATAGTGC [3887]
Cpi TGCCCTAAATGCTCCTTCTGGCACAAGCTG--CTAGCA-GTATCAAAGTGCTCATAGTGC [4051]
Cmy TGCCCTAAATGCTCCTTCTGGCACAAGCTG--CTAGCA-GTATCAAAGTGCTCATAGTGC [4052]
Psi TGCCCTAAATGCTCCTTCTGGCACAAGCTG--CTAGCA-GTGTCAAAGTGCTCATAGTGC [4061]
Asp TGCCCTAAATGCTCCTTCTGGCACAAGCTG--CTAGCA-GTGTCAAAGTGCTCATAGTGC [3892]
Ami ------------------------------------------------------------ [3937]
Asi TGCCCTAAATGCTCCTTCTGGCACGAGGTG--CTAGCA-GTATCAAAGTGCTCATAGTGC [4041]
Tgu TGCCCTAAATGCTCCTTCTGGCACAAGCTG--CTAGCA-GTATCAAAGTGCTCATAGTGC [3055]
Cli TGCCCTAAATGCTCCTTCTGGCACAAGCTG--CTAGCA-GTATCAAAGTGCTCATAGTGC [3649]
Gga TGCCCTAAATGCTCCTTCTGGCACAAGCTG--CTAGCA-GTATCAAAGTGCTCATAGTGC [3481]
Xtr TGCCCTAAATGCTCCTTTTGGCACAGGTTG--AAAGCA-GTTCCAAAGTGCTCATAGTGC [3466]
Lch TGCCCTAAATGCTCCTTCTGGCACAAGAAA--CATGCA-GTTCCAAAGTGCTCATTGTGC [3895]
Dre TGCGCTAGATGTTCCTTTTGGCAGGAGTAG--CTGGCA-GTTCCAAAGTGCTCACAGTGC [3904]

Hsa AGGTAGTTTTGGCATGACT---CTACTGTAGTATGGGCACTTCCAGTA-CTCTTG--CTG [3774]
Mmu AGGTAGTTTTTATACCACT---CTACTGCAGTGTGAGCACTTCTAGTA-CTCCTG--CTG [3776]
Mdo AGGTAGTTTTTTGCAAATGA--CTACTGTACTATGGGCACTT-CAGCG-CTCCTG----- [3546]
Meu AGGTAGTTTTTTGCAAATAA--CTACTGTACTATGGGCACTT-CAGCG-CTCCTG----- [3032]
Oan AGGTAGTTTTTTTCAATTGATTCTACTGTAATGTGGGCACTTACAGTA-CTCCAG----- [3266]
Aca AGGTAGTTAATGCACCCAAA-TCTACTGTAATGTGGGCACTTACAGTA-CTGCCG----- [3862]
Pbi AGGTAGTTG-TGGACCCAAATTCTACTGTAATGTGGGCACTTCCAGTC-CTGCTG----- [3940]
Cpi AGGTAGTTTTTGAATTGGA--TCTACTGTAATGTGGGCACTTATAGTA-CTGCCA--TCC [4106]
Cmy AGGTAGTTTTTGAATTGGA--TCTACTGTAATGTGGGCACTTATAGTA-CTGCCA--TCC [4107]
Psi AGGTAGTCTTTGAATTGGA--TCTACTGTAATGTGGGCACTTATAGTA-CTGCCA----- [4113]
Asp AGGTAGTTTTTGAATTGGA--TCTACTGTAATGTGGGCACTTATAGTA-CTGCCA----- [3944]
Ami ------------------------------------------------------ATC [3940]
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Asi AGGTAGCTTTTGTATTGGA--TCTACTGTAATGTGGGCACTTACAGTA-CTGCCA--ATC [4096]
Tgu AGGTAGCTTG-GAAATGGA--CCTACTGTAATGTGGGCACTTACAGTA-CTGCTA----- [3106]
Cli AGGTAGCTTT-GAATTGAA--CCTACTGTAATGTGGGCACTTATAGTA-CTGCTA----- [3700]
Gga AGGTAGCTTG-GCATTGGA--CCTACTGTAATGTGGGCACTTACAGTA-CTGTTA----- [3532]
Xtr AGGTAGTTGTATTGATGT---TCTACTGTAATATGGGCACTTACAGTA-CTGCTA----- [3517]
Lch AGGTAGTATTA-AATAAAA--CCTACTGTAATATGAGCACTTATAGTA-CTGCTG--CTC [3949]
Dre AGGTAGTGCC---AGTGGA--TCTACTGCAATGTCTGCACTTCAAGTA-TTGCCG----- [3953]

Hsa CCGGGGCTAAAGTGCTGACAGTGCAGATAGTGGTCCTCTCCGTG-CTACCGCACTGTGGG [3833]
Mmu CTGGGACTAAAGTGCTGACAGTGCAGATAGTGGTCCTCTCTGTG-CTACCGCACTGTGGG [3835]
Mdo ---------------------------------------------------------- [3546]
Meu ---------------------------------------------------------- [3032]
Oan ---------------------------------------------------------- [3266]
Aca ---------------------------------------------------------- [3862]
Pbi ---------------------------------------------------------- [3940]
Cpi GCAGGGCTAAAGTGCTGACAGTGCAGGTAGCTAGCGTCTGGTTG-CTACTGCAGTGTGGG [4165]
Cmy ACAGGGCTAAAGTGCTGACAGTGCAGGTAGCTGGCGTCTGTGTG-CTACTGCAGTGTGGG [4166]
Psi ---------------------------------------------------------- [4113]
Asp ---------------------------------------------------------- [3944]
Ami CCAGGGCTAAAGTGCTTGCAGTGCAGGTAGCTGGCG-CTGGC-G-CTACTGCAGTGTGGG [3997]
Asi CCAGGGCTAAAGTGCTTGCAGTGCAGGTAGCTGGCG-CTGGC-G-CTACTGCAGTGTGGG [4153]
Tgu ---------------------------------------------------------- [3106]
Cli ---------------------------------------------------------- [3700]
Gga ---------------------------------------------------------- [3532]
Xtr ---------------------------------------------------------- [3517]
Lch CTAGTGCTAAAGTGCTTACAGTGCAGGTAGAAACTGTCACACCACCTACTGCATTGTGGG [4009]
Dre ---------------------------------------------------------- [3953]

Hsa TACTTGCTGCTCCAGCA--CTGGGGGCTCCAAAGTGCTGTTCGTGCAGGTAGTGTGATTA [3891]
Mmu TACTTGCTGCTCCAGCA--ATGGGGGCTCCAAAGTGCTGTTCGTGCAGGTAGTGTAATTA [3893]
Mdo ------------------TGGGGGGCTCCAAAGTGCTGTTCGTGCAGGTAGTGTGATAA [3587]
Meu ---------------------------------------------------------- [3032]
Oan ---------------------------------------------------------- [3266]
Aca ---------------------------------------------------------- [3862]
Pbi ---------------------------------------------------------- [3940]
Cpi GGCTTGCAGCTCTGGGG--CCAGAGGCTCCAAAGTGCTGTTCGTGCAGGTAGCGTGTGCA [4223]
Cmy GGCTTGCAGCTCTGGGG---------------------------------------- [4183]
Psi ---------------------------------------------------------- [4113]
Asp ---------------------------------------------------------- [3944]
Ami GGCTTGCAGCTCTGGGG--GCGGTGGCTCCAAAGTGCTGTTCGTGCAGGTAGTGTGTGCA [4055]
Asi GGCTTGCAGCTCTGGGG--GCGGTGGCTCCAAAGTGCTGTTCGTGCAGGTAGTGTGTGCA [4211]
Tgu ---------------------------------------------------------- [3106]
Cli ---------------------------------------------------------- [3700]
Gga ---------------------------------------------------------- [3532]
Xtr ------------------CTATGGGCTTCAAAGTGCTGTTCGTGCAGGTAGCTTAATAA [3558]
Lch CACTTTCTGCACTGGCT---------------------------------------- [4026]
Dre ------------------TGTGTGTGTTAAAAGTGCTGTTTGTGCAGGTAGTGTG-TTT [3993]

Hsa CCCAACCTACTGCTGAGCTAGCACTTCCCGAGCCCCCGG--GCAGTCCTCTGTTAGTTTT [3949]
Mmu CCTGACCTACTGCTGAGCTAGCACTTCCCGAGCCCCCAG--GCAGCCCTCTGTTAGTTTT [3951]
Mdo CCTGACCTACTGCTGAGCTAGCACTTCCAGAGCCCCTGG--GCAGTCCTCTGTTAGTTTT [3645]
Meu ----------------------------------------GCAGTCCTCTGTTAGTTTT [3051]
Oan ----------------------------------------GCAGCTCTCTGTTAGTTTT [3285]
Aca ----------------------------------------GCAGTCCTCTGTTAGTTTT [3881]
Pbi ----------------------------------------GCAGTCCTCTGTTAGTTTT [3959]
Cpi GCCGA-CTACTGCCGAGTCAGCGCTTCGCGAGCCCCCCG--GCAGTCCTCTGTTAGTTTT [4280]
Cmy ----------------------------------------GCAGTCCTCTGTTAGTTTT [4202]
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Psi ----------------------------------------GCAGTTCTCTGTTAGTTTT [4132]
Asp ----------------------------------------GCAGTTCTCTGTTAGTTTT [3963]
Ami GCCAT-CTACTGCCGGG-CAGCACTTCCCGAGCCCCCGC--GCAGACTTCTGTTAGTTTT [4111]
Asi GCCAT-CTACTGCCGGG-CAGCACTTCCCGAGCCCCCGC--GCAGTCTTCTGTTAGTTTT [4267]
Tgu ----------------------------------------GCAGACTTCTGTTAGTTTT [3125]
Cli ----------------------------------------GCAGTCTTCTGTTAGTTTT [3719]
Gga ----------------------------------------GCAGTCTTCTGTTAGTTTT [3551]
Xtr -CAGACCTACTGCATGGGCGGCACTTCCCAAGCCCATTG--GCAGTCTTCTGTTAGTTTT [3615]
Lch ----------------------------------------GCAGTCCTCTGTTAGTTTT [4045]
Dre CCT---CTACTGTAGGAGCAGCACTTCACAACACACACA--GCAGTTCTCTGCTAGTTTT [4048]

Hsa GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [4009]
Mmu GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [4011]
Mdo GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [3705]
Meu GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [3111]
Oan GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGACGGTGGCC [3345]
Aca GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATTGTGGCC [3941]
Pbi GCATAGTTGCACTACAGGAAGAGTGTAGTTGTGCAAATCTATGCAAAACTGATTGTGGCC [4019]
Cpi GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [4340]
Cmy GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [4262]
Psi GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [4192]
Asp GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [4023]
Ami GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [4171]
Asi GCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [4327]
Tgu GCATAGTTGCACTACAAGAAGAGAGTGGTTGTGCAAATCTATGCAAAGCTGATGGTGGCC [3185]
Cli GCATAGTTGCACTACAAGAAGAGTGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [3779]
Gga GCATAGTTGCACTACAGGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [3611]
Xtr GCATAGTTGCACTACAAGAAAAATGTAGTTGTGCAAATCTATGCAAAACTGATGGCAGCC [3675]
Lch GCATAGTTGCACTACAAGAAGAATTGAGTTGTGCAAATCTATGCAAAACTGATGGTGACC [4105]
Dre GCATAGTTGCACTACAAGAAAACGGGAGTTGTGCAAATCTATGCAAAACTGATGGTGGCC [4108]

Hsa TG--CTGTTCTATGGTTAGTTTTGCAGGTTTGCATCCAGCTGTG---TGATATTCTGCTG [4064]
Mmu TG--CTGGTCTATGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TAATATTCTGCTG [4066]
Mdo TG--CTGTTCTATGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGATATTCTGCTG [3760]
Meu TG---------------------------------------------------------- [3113]
Oan TG--CTGTTCTATGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGGTACTCTGCTG [3400]
Aca TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TAATGTGTTGCTG [3996]
Pbi TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGATACTCTGCTG [4074]
Cpi TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGATACTCTGCTG [4395]
Cmy TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGATACTCTGCTG [4317]
Psi TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGATACTCTGCTG [4247]
Asp TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGATACTCTGCTG [4078]
Ami TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGATACTCTGCTG [4226]
Asi TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGATACTCTGCTG [4382]
Tgu TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGATACTCTGCTG [3240]
Cli TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGATACTCTGCTG [3834]
Gga TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTGTA---TGATACTCTGCTG [3666]
Xtr TG--GTGCTTCATGGTTAGTTTTGCAGGTTTGCATCCAGTTGTTC--TTCTGGCTCACTG [3731]
Lch TG--CTGTTCTCTGGTTAGTTTTGCAGGTTTGCATCCAGCTTTTCACTATACACTTGCTG [4163]
Dre TG--TGGACCCCCGGTCAGTTTTGCTGGTTTGCATTCAGCTTTTA--AGACTGTGCGCTG [4164]

Hsa TGCAAATCCATGCAAAACTGACTGTGGTA--CTACTTACAATTAGTTTTGCA--GGTTTG [4120]
Mmu TGCAAATCCATGCAAAACTGACTGTGGTG--CTACTTACGATTAGTTTTGCA--GATTTG [4122]
Mdo TGCAAATCCATGCAAAACTGACTGTGGTG--CTGCTCACAGTCAGTTTTGCA-GGTCTTG [3817]
Meu ------------------------------CTACTCACAGTCAGTTTTGCA-GGTCTTG [3141]
Oan TGCAAATCCATGCAAAACTGACTGTGGCA--CTGCTTACAGTCAGTTTTGCA--GGTTTG [3456]
Aca TGCAAATCCATGCAAAACTGACTGTGGCA--ACCACCACAGTCAGTTTTGCATGGATTTG [4054]
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Pbi TGCAAATCCATGCAAAACTGACTGTGGCA--TCCACCACAGTCAGTTTTGCATGGATTTG [4132]
Cpi TGCAAATCCATGCAAAACTGACTGTGGCA--CTGACTACAGTCAGTTTTGCA--GGATTG [4451]
Cmy TGCAAATCCATGCAAAACTGACTGTGGCA--CTGACTACAGTCAGTTTTGCA--GGATTG [4373]
Psi TGCAAATCCATGCAAAACTGACTGTGGCA--CTGACTACAGCCAGTTTTGCA--GGATTG [4303]
Asp TGCAAATCCATGCAAAACTGACTGTGGCA--CTGACTACAGCCAGTTTTGCA--GGATTG [4134]
Ami TGCAAATCCATGCAAAACTGACTGTGGCA------------------------------ [4255]
Asi TGCAAATCCATGCAAAACTGACTGTGGCA--CTGCTTACAGTCAGTTTTGCA--GGTTTG [4438]
Tgu TGCAAATCCATGCAAAACTGACTGTGGCA--CTGATTACAGTCAGTTTTGCA--GGTTTG [3296]
Cli TGCAAATCCATGCAAAACTGACTGTGGCA--CTAATTACAGTCAGTTTTGCA--GGTTTG [3890]
Gga TGCAAATCCATGCAAAACTGACTGTGGCA--CTGCTCACAGTCAGTTTTGCA--GGTTTG [3722]
Xtr TGCAAATCCATGCAAAACTGATTATGGCA--CCTGCTCCTGTCAGTTTAGCT--GGTTTG [3787]
Lch TGCAAATCCATGCAAAACTGACTGTAGCA------------------------------ [4192]
Dre TGCAAATCCATGCAAAACTGATTGTGGCA--TTATCTGGGGTGAGTTTTGCA--GGATTG [4220]

Hsa CATTTCAGCGTATA--TATGTATATGTGGCTGTGCAAATCCATGCAAAACTGATTGTGAT [4178]
Mmu CAGTTCAGCGTATA--TGTGAATATATGGCTGTGCAAATCCATGCAAAACTGATTGTGGG [4180]
Mdo CAT--CGGCCTA--------TGTCAATTGCTGTGCAAATCCATGCAAAACTGATTAGGAG [3867]
Meu CAT--CGGCCTA--------TGTCGATTGCTGTGCAAATCCATGCAAAACTGATTATGAG [3191]
Oan CATCCCAGCGTA--------TACAAATTGCTGTGCAAATCCATGCAAAACTGATTGTGAT [3508]
Aca CACAGCGACGGA-------CAGCAAGCTGGGATGCAAA-CC-TGCAAAACGGACTGTAGA [4105]
Pbi CACAGCAACAGA-------CGCCAAGCTGAGATGCAAA-CC-AGCAAAACCCACCGTAGG [4183]
Cpi CATTCCAGCTTA-------TTTCAAA-CGCTGTGCAAATCCATGCAAAACTGACTGTGGT [4503]
Cmy CATTCCAGCTTA-------TTCCAAA-CGCTGTGCAAATCCATGCAAAACTGACTGTGGT [4425]
Psi CATTCCAGCTTA-------TTTCAAA-TGCTGTGCAAATCCATGCAAAACTGACTGTGGT [4355]
Asp CATTCCAGCTTA-------TTTCAAA-TGCTGTGCAAATCCATGCAAAACTGACTGTGGT [4186]
Ami ------------------------------------------------------------ [4255]
Asi CATCCCAGCTTA--------TATCCGTTGCTGTGCAAATCCATGCAAAACTGACTGTGGT [4490]
Tgu CATCCCAGCTTA--------CTAAAATTGCTGTGCAAATCCATGCAAAACTGACTGTGGT [3348]
Cli CATCCCAGCTTA--------CTAAAATTGCTGTGCAAATCCATGCAAAACTGACTGTGGT [3942]
Gga CATCCCAGCTTG--------CTAAAATTGCTGTGCAAATCCATGCAAAACTGACTGTGGT [3774]
Xtr CATC--AGCTGA--------CTATTG-TGCTGTGCAAATCCATGCAAAACTGACTGTGGC [3836]
Lch ------------------------------------------------------------ [4192]
Dre CATCC-GGCTTT------ATTACAACATGCTGTGCAAATCCATGCAAAACTCGCTGCGCC [4273]

Hsa AAT--CCACCTTGTCGGGTAGCTTATCAGACTGATGTTGACTGTTGAATCT-CATGGCAA [4235]
Mmu AAT--CCACCTTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGAATCT-CATGGCAA [4237]
Mdo GGC--CCGTCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATCT-CATGGCAA [3924]
Meu GGC--CCGTCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATCT-CATGGCAA [3248]
Oan GGT--CCATCCTATCGGATAGCTTATCAGACTGATGTTGACTGTTAGATCT-CCTGGCAA [3565]
Aca TCA--CCTTTCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATGT-CATGGCAA [4162]
Pbi TCA--CCTTTCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATGT-CATGGCAA [4240]
Cpi TGC--CCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATCT-CATGGCAA [4560]
Cmy TGC--CCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATCT-CATGGCAA [4482]
Psi TGC--CCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATCT-CATGGCAA [4412]
Asp TGC--CCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATCT-CATGGCAA [4243]
Ami -----CCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATGT-CATGGCAA [4309]
Asi GGT--CCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATGT-CATGGCAA [4547]
Tgu GGT--CCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATCT-CATGGCAA [3405]
Cli GGT--CCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATCT-CATGGCAA [3999]
Gga GGT--CCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATCT-CATGGCAA [3831]
Xtr TGG--CCATCCTGTCGGATAGCTTATCAGACTGATGTTGACTGTTGGATGT-CATGGCAA [3893]
Lch -----CCATCCTGTCGGATAGCTTATCAGACTGGTGTTGGCTGTTAGATCA-CATGGCGA [4246]
Dre AGG--CCAGTGTGTCAGATAGCTTATCAGACTGGTGTTGGCTGTTACATTCGCCCGGCGA [4331]

Hsa CACCAGTCGATGGGCTGTCTGACATTTTGG-TAT--GGCTGAGCCGCAGTAGTTCTTCAG [4292]
Mmu CAGCAGTCGATGGGCTGTCTGACATTTTGG-TAT--GGCTGAGCCGCAGTAGTTCTTCAG [4294]
Mdo CAGCAGTCGATGAGCTGTCTGACATTTTGG-TAT--GGCCGAGCCACAGCAGTTCTTCAG [3981]
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Meu CAGCAGTCGATGGGCTGTCTGACATTTTGG-TAT--GGCCGAGCCACAGCAGTTCTTCAG [3305]
Oan CAGCAGTCGATGGGCTGTCTGACATTTTGG-TAT--GGCTGAGTCACAGCAGTTCTTCAG [3622]
Aca CAACAGTCGGTAGGCTGTCTGACATTTTGG-TGT-----------CAGCAGTTCTTCAG [4209]
Pbi CAACAGTCGGTAGGCTGTCTGACATTTTGG-TAT--GGCTACCCAGCAGCAGTTCTTCAG [4297]
Cpi CAACAGTCGGTAGGCTGTCTGACATTTTGG-TAT--GGCTAACTAGCACCAGTTCTTCAG [4617]
Cmy CAACAGTCGGTAGGCTGTCTGACATTTTGG-TAT--GGCTAACTTGCACCAGTTCTTCAG [4539]
Psi CAACAGTCGGTAGGCTGTCTGACATTTTGG-TAT--GGC-AACGTGCACCAGTTCTTCAG [4468]
Asp CAACAGTCGGTAGGCTGTCTGACATTTTGG-TAT--GGCTAACGCGCACCAGTTCTTCAG [4300]
Ami CAACAGTCGGTAGGCTGTCTGACATTTTGG-TAT-------------------------- [4342]
Asi CAACAGTCGGTAGGCTGTCTGACATTTTGG-TAT-------------------------- [4580]
Tgu CAACAGTCGGTAGGCTGTCTGACATTTTGG-TAT-------------------------- [3438]
Cli CAACAGTCGGTAGGCTGTCTGACATTTTGG-TAT--GGCTAACCAGCACCAGTTCTTCAG [4056]
Gga CAACAGTCGGTAGGCTGTCTGACATTTTGG-TAT--GGCTGCCCGGCAGCAGTTCTTCAG [3888]
Xtr CAACAGTCGGTAGGCTGTCTGACATTTTGG-TGT--GGCCCGCTAGAAGCAGTTCTTCAG [3950]
Lch CAACAGTCGGTAGGCTGTCTGACATTTTGG-TGT--GGCAAACCTGCACCAGTTCTTCCC [4303]
Dre CAACAGTCTGTAGGCTGTCTGACATTTTGGGCAT--GGCTGACCTGCAGCAGTTCTTCAC [4389]

Hsa TGGCA-AGCTTTATGTCCTGACCC---AGCTAAAGCTGCCAGTTGAAGAACTGTTGCCCT [4348]
Mmu TGGCA-AGCTTTATGTCCTGACCC---AGCTAAAGCTGCCAGTTGAAGAACTGTTGCCCT [4350]
Mdo TGGCG-AGCTTTATGTCTTGTCCC---AGCTAAAGCTGCCAGTTGAAGAACTGCTGAGCT [4037]
Meu TGGCG-AGCTTTATGTCTTGTCCC---AGCTAAAGCTGCCAGTTGAAGAACTGCTGAGCT [3361]
Oan TGGCA-AGCTTTACGTCCTGTCCC---AGCTAAAGCTGCCAGTTGAAGAACTGTTGAACT [3678]
Aca CGGCATCGCTTTACGTCCCCTTTAAGAAGCTAAAGCTGCCAGTTGAAGAACTGTTGGCCC [4269]
Pbi TGGCA-CGCTTTACGTCCCCTCCA-GCAGCTAAAGCTGCCAGTTGAAGAACTGTTGACCG [4355]
Cpi TGGCA-AGCTTTACGTCCCTGTCTAGCAGCTAAAGCTGCCAGTTGAAGAACTGTTGAATG [4676]
Cmy TGGCA-AGCTTTAAGTCCCTGTCTAGCAGCTAAAGCTGCCAGTTGAAGAACTGTTGAATG [4598]
Psi TGGCA-AGCTTTACGTCCCTGTCTCGTAGCTAAAGCTGCCAGTTGAAGAACTGTTGAACG [4527]
Asp TGGCA-AGCTTTACGTCCCTGTCTCGTAGCTAAAGCTGCCAGTTGAAGAACTGTTGAACG [4359]
Ami ---------------------------------------------------------- [4342]
Asi ---------------------------------------------------------- [4580]
Tgu ---------------------------------------------------------- [3438]
Cli TGGCA-AGCTTTATGTCCTTCTCTAGTAGCTAAAGCTGCCAGTTGAAGAACTGTTGAATG [4115]
Gga TGGCA-AGCTTTATGTCCTTCTCTAGTAGCTAAAGCTGCCAGTTGAAGAACTGTTGAATG [3947]
Xtr TGGCA-AGCTTTATGTTGTTCCTCTGT-GCTAAAGCTGCCAGTTGAAGAACTGTTGAAAG [4008]
Lch TGGCT-AGCCTTATGTCCATCCTTGCTAGCTAAAGCTGCCAGTTGAAGAACTGTTGTGGT [4362]
Dre TGGCA-AGCTTTATGTCCTTGTGTACCAGCTAAAGCTGCCAGCTGAAGAACTGTTGTGGT [4448]

Hsa CTGCCCC--CCACGGCCGGCTGGGG-TTCCTGGGGATGGGATTT-----GCTTCCT-GTC [4399]
Mmu CTGCCCC--CCTCGGACGGCTGGGG-TTCCTGGGGATGGGATTT-----GATGCCA-GTC [4401]
Mdo CTGCTCC--CCTTGGCCGGCTGGGG-TTCCTGGGGATGGGATTT-----GATTACT-GCC [4088]
Meu CTGCTCC--CCTTGGCCGGCTGGGG-TTCCTGGGGATGGGATTT-----GATTACT-GCC [3412]
Oan CAGCCCC--CCGCCGGCGGCTGGGG-TTCCTGGTGATGCGATTTTCT--TGTGCTC-GCC [3732]
Aca GGGCCCA--CCGCTGCCAGCTGGGG-TTCCTGGTGATGTGATTTT---ATTTTGGT-GTT [4322]
Pbi TAGCTGC--CTGCTGCCTGCTGGGG-TTCCTGGTGATGTGATTTT---ACCCTGAT-GTT [4408]
Cpi TAGCCAC--CCCCTGCCAGCTGGGG-TTCCTGGTGATGCGATTTTT--ATCCTACC-ACC [4730]
Cmy TAGCCAC--CCCCTGCCAGCTGGGG-TTGCTGGTGATGCGATTTTT--ATCCTACC-ACC [4652]
Psi TAGCCCC---------------------------------------------------- [4534]
Asp TAGCCCC---------------------------------------------------- [4366]
Ami ---------CCACAGCCAGCTGGGG-TTCCTGGTGATGCGATTTTTTTACCCACT--GCC [4390]
Asi ---------CCACAGCCAGCTGGGG-TTCCTGGTGATGCGATTTTTTTACCCACT--GCC [4628]
Tgu ---------------------------------------------------------- [3438]
Cli TAGCCAC--CTGCCGCCCGCCGGGG-TTCCTGGCGATGGGATTTTTT-ACCGTTTTTGCC [4171]
Gga TAGCCAC---------------------------------------------------- [3954]
Xtr TGGCTAC--CTGCTGACAGCGGGGGATTCCTGGAGATGGGATTTTATT--TTGGCAGCCA [4064]
Lch TTGCTGG--CTGTTGTCAATGGGGG-TTCCTGGTAACGTGATTTTA-----TAACACAAG [4414]
Dre TGGCTCT--CTGCCGGCCAGGGGAA-TTCCTGGCAGAGTGATTTTTAAACCTAA---TGA [4502]
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Hsa ACAAATCACATTGCCAGGGATTTCCAACCGACCCTG--CTCTGGCTGCTTGGGTTCCTGG [4457]
Mmu ACAAATCACATTGCCAGGGATTTCCAACTGACCCTG--CTCTGGCTGCTTGGGTTCCTGG [4459]
Mdo ACAAATCACATTGCCAGGGATTTCCAACTGACCACT--CTCTGGCTGCTTGGGTTCCTGG [4146]
Meu ACAAATCACATTGCCAGGGATTTCCAACTGACCACT--CTCTGGCTGCTTGGGTTCCTGG [3470]
Oan A-AAATCACATTGCCAGGGATTTCCAACTGGCGGCG--GCCCGGCTGCCTGGGTTCCTGG [3789]
Aca CAGAATCACATTGCCAGGGATTTCCAACCATCAGTG--TTTTGGTTGTTTGGGTTCCTGG [4380]
Pbi CAGAATCACATTGCCAGGGATTTCCAACTGTTGGCA--TTTTGGTTGTTTGGGTTCCTGG [4466]
Cpi CAAAATCACATTGCCAGGGATTTCCAACGGGCGGCG--TTGTGGCTGTTTGGGTTCCTGG [4788]
Cmy CAAAATCAAATTGCCAGGGATTTCCAACGGGCAGCG--TTGTGGCTGTTTGGGTTCCTGG [4710]
Psi ------------------------------------TTGTGGCTGTTTGGGTTCCTGG [4556]
Asp ------------------------------------TTGTGGCTGTTTGGGTTCCTGG [4388]
Ami CAAAATCACATTGCCAGGGATTTCCAACTGGCTGCG--TTGTGGCTGTTTGGGTTCCTGG [4448]
Asi CAAAATCACATTGCCAGGGATTTCCAACCGGCTGCG--TTGTGGCTGTTTGGGTTCCTGG [4686]
Tgu ------------------------------------TTATGGCTGTTTGGGTTCCTGG [3460]
Cli CAAAATCACATTGCCAGGGATTTCCAACGGGCCCCA--TTGTGGCTGTTTGGGTTCCTGG [4229]
Gga ------------------------------------TTGTGGCTGTTTGGGTTCCTGG [3976]
Xtr ATAAATCACATTGCCAGGGATTTCCAACTGTCGGCC--GTGTGGCTGTTTGGGTTCCTGG [4122]
Lch TAGAATCACATTGCCAGGGATTTCCAACTGATAACA--TTGTGGCTGTTTGGGTTCCTGG [4472]
Dre CTGAATCACATTGCCAGGGATTTCCAATGGCTCGTG--TTGTGGCTGTGTGGGTTCTTGG [4560]

Hsa CATGCTGATTTGTGACTTAA---GATTAAAATCACATTGCCAGGGATTACCACGCAACC- [4513]
Mmu CATGCTGATTTGTGACTTGA---GATTAAAATCACATTGCCAGGGATTACCACGCAACC- [4515]
Mdo CATGCTGATTTGTGACTTAA---GATGAAAATCACATTGCCAGGGATTACCACGCAGCC- [4202]
Meu CATGCTGATTTGTGACTTAA---GATTAAAATCACATTGCCAGGGATTACCACGCAACC- [3526]
Oan CATGCTGATTTGTGACTTAA---GAGAAAAATCACATTGCCAGGGATAACCACGCATCC- [3845]
Aca CATGCTGATTTGTGACTTAA---GATGAAAATCACATTGCCAGGGATTACCACATAACC- [4436]
Pbi CATGCTGATTTGTGATTTAA---GATTAAAATCACATTGCCAGGGATTACCACATAACC- [4522]
Cpi CATGCTGATTTGTGATTTAA---GATTAAAATCACATTGCCAGGGATTACCACATAACC- [4844]
Cmy CATGCTGATTTGTGATTTAA---GATTAAAATCACATTGCCAGGGATTACCACATAACC- [4766]
Psi CATGCTGATTTGTGATTTAA---GATTAAAATCACATTGCCAGGGATTACCACATAACC- [4612]
Asp CATGCTGATTTGTGATTTAA---GATTAAAATCACATTGCCAGGGATTACCACATAACC- [4444]
Ami CATGCTGATTTGTGACTTAA---AATTAAAATCACATTGCCAGGGATTACCACAGAGCC- [4504]
Asi CATGCTGATTTGTGACTTAA---AATTAAAATCACATTGCCAGGGATTACCACAGAGCC- [4742]
Tgu CATGATGATTTGTGACTTAA---GATTAAAATCACATTGCCAGGGATTACCACGCAGCC- [3516]
Cli CATGATGATTTGTGACTTAA---GATTAAAATCACATTGCCAGGGATTACCACACAGCC- [4285]
Gga CATGATGATTTGTGAGTTAA---GATTAAAATCACATTGCCAGGGATTACCACATAGCC- [4032]
Xtr CATGCTGATTTGTGAGTTAA---GATTAAAATCACATTGCCAGGGATTACCACACAACC- [4178]
Lch CATGCTGATTTGTGACTAAA---GATAAAAATCACATTGCCAGGGATTACCACACAGCC- [4528]
Dre CATGCTGATTTGTGACTGTAGTAAAAAAAAATCACATTGCCAGGGATTACCACACTACC- [4619]

Hsa ------------------------------------------------------------ [4513]
Mmu ------------------------------------------------------------ [4515]
Mdo ------------------------------------------------------------ [4202]
Meu ------------------------------------------------------------ [3526]
Oan ------------------------------------------------------------ [3845]
Aca ------------------------------------------------------------ [4436]
Pbi ------------------------------------------------------------ [4522]
Cpi ------------------------------------------------------------ [4844]
Cmy ------------------------------------------------------------ [4766]
Psi ------------------------------------------------------------ [4612]
Asp ------------------------------------------------------------ [4444]
Ami ------------------------------------------------------------ [4504]
Asi ------------------------------------------------------------ [4742]
Tgu ------------------------------------------------------------ [3516]
Cli ------------------------------------------------------------ [4285]
Gga ------------------------------------------------------------ [4032]
Xtr -CTGTGGCTGGTAGGATTCCTGGCAGAGTGATTTGGAAATGTATGGTACAAAA----TCA [4233]
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Lch -CTGTGATTGGTGGGATTCCTGGCAGAGTGATTTGGGTTTCTCTGCTACAAAAAAAATCA [4587]
Dre -CTGTGGCGGGGAGGGTTCCTGGCACCGTGATTTGGTGGATAAACAGAAATGAAAA-TCA [4677]

Hsa ----------------------------GGGCTCT-GCCTCCCGTGCCTACTGAGCTGA [4543]
Mmu ----------------------------GGGCTCC-GCCTCCCGTGCCTACTGAGCTGA [4545]
Mdo ----------------------------GGGCTCT-GCCTCCTGTGCCTACTGAGCTGA [4232]
Meu ----------------------------GGGCTCT-GCCTCCTGTGCCTACTGAGCTGA [3556]
Oan ----------------------------GGGCTCT-GCCTCCTGTGCCTACTGAGCTGA [3875]
Aca ----------------------------GGGCTTG-GCCTTCCGTGCCTACTGAGCTGA [4466]
Pbi ----------------------------GGGCCCAAGCCTCCCGTGCCTACTGAGCTGA [4553]
Cpi ----------------------------GGGCTCT-GCCTCCCGTGCCTACTGAGCTGA [4874]
Cmy ----------------------------GGGCTCT-GCCTCCCGTGCCTACTGAGCTGA [4796]
Psi ------------------------------------------------------------ [4612]
Asp ------------------------------------------------------------ [4444]
Ami ----------------------------GGGCCCT-GCCTCCGGTGCCTACTGAGCTGA [4534]
Asi ------------------------------------------------------------ [4742]
Tgu ------------------------------------------------------------ [3516]
Cli ----------------------------GGGCGCT-GCCTCCTGTGCCTACTGAGCTGA [4315]
Gga ------------------------------------------------------------ [4032]
Xtr CATTGCCAGGGATTTCCAATCAGTCCC--TGGCTCC-GCCTCCCGTACCTACTGGGCTGA [4290]
Lch CATTGCCAGGGATTTCCAACCAGGCAC--GGGCTTT-GCCTCCTGTGCCTACTGAGCTGA [4644]
Dre CATTGCCAGGGATTTCCACTCCTGCAC--GGGCT-G-GTCTCCTGTGCCTGCTGTGCTGA [4733]

Hsa AACACAGTTGGTTT-GTGTACACTGGCTCAGTT---CAGCAGGAACAGGGGTCAAGCCCC [4599]
Mmu AACA--GTTGATTC-CAGTGCACTGGCTCAGTT---CAGCAGGAACAGGAGTCCAGCCCC [4599]
Mdo AACACAGTTGCTTT-GGATAAACTGGCTCAGTT---CAGCAGGAACAGGAGTCTGGCCCT [4288]
Meu AACACAGTTGCTTT-GTATAAACTGGCTCAGTT---CAGCAGGAACAGGAGTCTGGCCCT [3612]
Oan AACGCAGTTGCTTT-GCTTAAACTGGCTCAGTT---CAGCAGGAACAGGAGTCTAGCCCA [3931]
Aca TACTCAGTTGCTTT-AGATAAACTGGCTCAGTT---CAGCAGGAACAGGAGTCCAGCCCA [4522]
Pbi TACTCAGTTGCTTT-GGAAAAACTGGCTCAGTT---CAGCAGGAACAGGAG--------- [4600]
Cpi TACTCAGTCGCTTT-GCTTAAACTGGCTCAGTT---CAGCAGGAACAGGAGTCGGGCTCC [4930]
Cmy TACTCCGTTGCTTT-GGTTAAACTGGCTCAGTTCTCCAGCAGGAACAGGAGTCCGGCCCC [4855]
Psi ------------------------------------------------------------ [4612]
Asp ------------------------------------------------------------ [4444]
Ami TACTCAGTTGCTTTGGTTTAAACTGGCTCAGTT---CAGCAGGAACAGGAGTCTGGCTCC [4591]
Asi ------------------------------------------------------------ [4742]
Tgu ------------------------------------------------------------ [3516]
Cli TTTGCAGTTGCTTT-GGTTAAACTGGCTCAGTT---CAGCAGGAACAGGAGTCTGCGC-- [4369]
Gga ------------------------------------------------------------ [4032]
Xtr TAATCAGTGGTTATATCTTCCCCTGGCTCAGTT---CAGCAGGA-CAGGAGTTGCAGCCG [4346]
Lch CATTCAGTTTTAT--GAATATACTGGCTCAGTT---CAGCAGGAACAGGAGTTGAGCTCC [4699]
Dre TAATCAGTGGACG--GCTGTGACTGGCTCAGTT---CAGCAGGAACAGGGGCCTGGTCTT [4788]

Hsa CT--ATTGGACCCGCCCTCCGGTGCCTACTGAGCTGATATCAGTTCTCATTTTACACACT [4657]
Mmu CT--ATTGGACCCGCCCTCCGGTGCCTACTGAGCTGATATCAGTTCTCATTTCACACACT [4657]
Mdo CT--GTTGGACCCGCCCTCCGGTGCCTACTGAGCTGATAACAGTTCTGATTTTACACACT [4346]
Meu CT--ATTGGACCCGCCCTCCGGTGCCTACTGAGCTGATAACAGTTCTGATTTTACACACT [3670]
Oan GC--ATCGGACTGACCCTCCAGTGCCTACTGAGCTGATATCAGTTCTCGTTG-ACCCACT [3988]
Aca GT--GATGGACCCGTCCTCCGGTGCCTACTGAGCTGATATCAGTTCTGATTTTACACACT [4580]
Pbi ----GATGGACCCGTCCTCCGGTGCCTACTGAGCTGATATCAGTTCTGATTTTACATACT [4656]
Cpi AG--GATGGACCCGTCCTCCGGTGCCTACTGAGCTGATATCAGTTCTGATTTTACATACT [4988]
Cmy AG------------------------------------------------------------ [4857]
Psi ------------------------------------------------------------ [4612]
Asp ----GATGGACCCGTCCTCCGGTGCCTACTGAGCTGATATCAGTTCTGATTTTACATACT [4500]
Ami AG--GATGGACCCGTCCTCCAGTGCCTACTGAGCTGATATCAGTTCTGATTTTACATACT [4649]
Asi ------------------------------------------------------------ [4742]
Tgu ----GATGGACCCGTCCTCCGGTGCCTACTGAGCTGATATCAGTTCTGATTTTACACACT [3572]
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Cli ----GATGGACCCGTCCTCCGGTGCCTACTGAGCTGATATCAGTTCTGATTTTACACACT [4425]
Gga ----GATGGACCCGTCCTCCGGTGCCTACTGAGCTGATATCAGTTCTGATTTTACATACT [4088]
Xtr AG--GATGGACCTGTCCTCTTGTGCCTACTGAACTGATATCAGTTCT-ATTTCACACACT [4403]
Lch AT--GGTGGACTCGACCTCCTGTGCCTACTGAGCTGATATCAGTTCTTATTTAACATACT [4757]
Dre CT--TCAGGACCTGAGCTCCGGTGCCTTCTGAGCTGATATCAGTTGT-AGTAAA-TCACT [4844]

Hsa GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCTTGA--GCCGTGGCCTCGTTCAAGTAAT [4715]
Mmu GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCTTGA--GCCGTGGCCTCGTTCAAGTAAT [4715]
Mdo GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCGAGA--GCTGTGACCTGGTTCAAGTAAT [4404]
Meu GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCGAGA--GCTGTGACCTGGTTCAAGTAAT [3728]
Oan GGCTCAGTTCAGCAGGAACAGGAGTGCGGCCCACGT--GCTGCGACCTGGTTCAAGTAAT [4046]
Aca GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCTAAA--GCTGTGACCTGCTTCAAGTAAT [4638]
Pbi GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCCAAA--GCTGTGGCTAGGTTCAAGTAAT [4714]
Cpi GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCTAAA--GTTGTGACCTGGTTCAAGTAAT [5046]
Cmy ------------------------------------GCTGTGACCTGGTTCAAGTAAT [4879]
Psi ------------------------------------GCTGTGACCTGGTTCAAGTAAT [4634]
Asp GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCTAAA--GCTGTGACCCGGTTCAAGTAAT [4558]
Ami GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCCAAA--GCTGTTACCTGGTTCAAGTAAT [4707]
Asi ------------------------------------GCTGTTACCTGGTTCAAGTAAT [4764]
Tgu GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCTAGA--GCTGTGGCCTGGTTCAAGTAAT [3630]
Cli GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCTAGA--GCTGCGGCCTGGTTCAAGTAAT [4483]
Gga GGCTCAGTTCAGCAGGAACAGGAGTCGAGCCCTAGA--GCTGTCACCTGGTTCAAGTAAT [4146]
Xtr GGCTCAGTTCAGCAGGAACAGGAGTCGGGCCCTTGA--GCAGTGGCCCGGTTCAAGTAAT [4461]
Lch GGCTCAGTTCAGCAGGAACAGGAGTTGAGCCCTAAA--GCTGAGACCTGGTTCAAGTAGT [4815]
Dre GGCTCAGTTCAGCAGGAACAGGAGTGTGGCCCCTCC--GTTGTTCCCTTGTTCAAGTAAT [4902]

Hsa CCAGGATAGGCTGTGCAGGTCCCAATGGGCCTATTCTTGGTTACTTGCACGGGGACGCGG [4775]
Mmu CCAGGATAGGCTGTGCAGGTCCCAAGGGGCCTATTCTTGGTTACTTGCACGGGGACGCGG [4775]
Mdo CCAGGATAGGCTGGACCCATTCTCATCGGCCTATTCTCGACTACTTGCACTCGGGCGCGG [4464]
Meu CCAGGATAGGCTGGACCCATTCTCATTGGCCTATTCTCGGTTACTTGCACTCGGGCACGG [3788]
Oan CCAGGATAGGCTGTGTGCGCTCAGATTGGCCTGTTCTCGGTTACTTGCCCCAGGGGGCGG [4106]
Aca CCAGGATAGGCTGTGTGCATTCTTAATGGCCTATCCTTGATTACTTGCACTGGGAAATAG [4698]
Pbi CCAGGATAGGCTGTAGGTACAGCAGTCAGCCTGTTCTCGATTACTTGGCCTTGGAGGCAG [4774]
Cpi CCAGGATAGGCTGTGTGCAATCTAATTGGCCTATTCTTGATTACTTGCACTGGGAGGCAA [5106]
Cmy CCAGGATAGGCTGTGTGCAATCTAATTGGCCTATTCTTGATTACTTGCACTGGGAGGCAA [4939]
Psi CCAGGATAGGCTGTGTGCAATCTAATTGGCCTATTCTTGGTTACTTGCACTGGGAGGCAA [4694]
Asp CCAGGATAGGCTGTGTGCAATCTAATTGGCCTATTCTTGATTACTTGCACTGGGAGGCAA [4618]
Ami CCAGGATAGGCTGTATGCATTGCAGTTGGCCTATTCTTGATTACTTGCACTGGGAGACAG [4767]
Asi CCAGGATAGGCTGTATGCATTGCAGTTGGCCTATTCTCGATTACTTGCACTGGGAGACAG [4824]
Tgu CCAGGATAGGCTGTATCCATTCTAACTCGCCTATTCTTGGTTACTTGCACTGGGACAGGG [3690]
Cli CCAGGATAGGCTGTATCCATCCGAGCTGGCCTATTCTTGGTTACTTGCACTAGGAGGCAA [4543]
Gga CCAGGATAGGCTGTATCCATTCCTGCTGGCCTATTCTTGGTTACTTGCACTGGGAGGCAG [4206]
Xtr CCAGGATAGGCTGTTCACATTCTGCGTGGCCTATTCTTGATTACTTGCATTGGGAGGCAG [4521]
Lch CCAGGATAGGCTGTGAGTTTTAGAATTAGCCTGTTCTTGATTACTTGCACTAGGGGGCAG [4875]
Dre CCAGGATAGGCTGTCTG---TCCTGGAGGCCTATTCATGATTACTTGCACTAGGTGGCAG [4959]

Hsa GC--GCTGTGGCTGGATTCAAGTAATCCAGGATAGGCTGTTTCCAT-CTGTGAGGCCTAT [4832]
Mmu GC--GCTGCGGCTGGATTCAAGTAATCCAGGATAGGCTGTGTCCGT-CCATGAGGCCTGT [4832]
Mdo CC--GCTGCGGCCAGGTTCAAGTAATCCAGGATAGGCTGTGTCCAG-CTGCG-GGCCTAT [4520]
Meu CC--GCTGCGGCCAGGTTCAAGTAATCCAGGATAGGCTGTGTCCAG-CTGCT-GGCCTAT [3844]
Oan CC--GCTCCCGCCCGGTTCAAGTAATCCAGGATAGGCTGTCGGCA--CCAC--GGCCTGT [4160]
Aca CC--GCTTCAGCCTGGTTCAAGTAATCCAGGATAGGCTGTTACCAGGCAGTACGGCCTAT [4756]
Pbi CC--GTCTCAGCCTGGTTCAAGTAATCCAGGATAGGCTGTTACCAGGCAACACGGCCTAT [4832]
Cpi CC--GCCGTAGCCCGGTTCAAGTAATCCAGGATAGGCTGTTACCAGGCAGCACGGCCTAT [5164]
Cmy CC--GCCGCAGCCCGGTTCAAGTAATCCAGGATAGGCTGTTACCAGGCAGCACGGCCTAT [4997]
Psi CC--GCCACAGCCCGGTTCAAGTAATCCAGGATAGGCTGTTACCAGGCAGCACGGCCTAT [4752]
Asp CC---------------------------------------------------------- [4620]
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Ami CC--GTCACGGCCCGGTTCAAGTAATCCAGGATAGGCTGGTGCCAGGCC-CGTGGCCTAT [4824]
Asi CC--GTCACGGCCCGGTTCAAGTAATCCAGGATAGGCTGGTGCCAGGCC-CGTGGCCTAT [4881]
Tgu CC---------------------------------------------------------- [3692]
Cli CC--GCCGCAGCCCGGTTCAAGTAATCCAGGATAGGCT-GTTCCAGCC----CGGCCTGT [4596]
Gga CC---------------------------------------------------------- [4208]
Xtr CT--GCTGCTGCCTGGTTCAAGTAATCCAGGATAGGCTGTTTCCTCAAAGCACGGCCTAC [4579]
Lch CA--GCTCCGGCCTGGTTCAAGTAATCCAGGATAGGCTGTTTCCACCCAGTGAGGCCTAT [4933]
Dre CC--GCCTTTGCCTGGTTCAAGTAATCCAGGATAGGTTAGTTCCCACTAGTACGGCCTAT [5017]

Hsa TCTTGATTACTTGTTTCTGGAGGCAGC--CCCGGGACCCAGTTCAAGTAATTCAGGATAG [4890]
Mmu TCTTGATTACTTGTTTCTGGAGGCAGC--CCCGGGACCCAGTTCAAGTAATTCAGGATAG [4890]
Mdo CCTTGATTGCTTGTTTCTGGAGGTGGC--GCCGGGACCCGTTTCAAGTAATCCAGGATAG [4578]
Meu TCTTGATTACTTGTTTCTGGAGGCAGC--GCCAGGACCCGTTTCAAGTAATCCAGGATAG [3902]
Oan CCTCGGTTACTTGTCTCGGGAGGTGGC---------------------------------- [4187]
Aca TCTTGATTACTTGTTTCAGGAGGCGGC--ACTGTGGCCAGTTTCAAGTAATCCAGGATAG [4814]
Pbi TCTTGATTACTTGTTTCAGGAGGCGGC--GCTGTGGCTAGGTTCAAGTAATCCAGGATAG [4890]
Cpi TCTTGATTACTTGTTTCAGGAGGCGGC--GCCGGCGCCGGGTTCAAGTAATCCAGGATAG [5222]
Cmy TCTTGATTACTTGTTTCAGGAGGCGGC---------------------------------- [5024]
Psi TCTTGGTTACTTGTTTCGGGAGGCGGC---------------------------------- [4779]
Asp ---------------------------------------------------------- [4620]
Ami TCTCGATTACTTGTCTCGGGACGTGGC---------------------------------- [4851]
Asi TCTCGATTACTTGTCTCGGGACGTGGC---------------------------------- [4908]
Tgu ----------------------------GCCAGACCCAGTTTCAAGTAATCCACTATTG [3723]
Cli TCCCGGTTACTTGTCCCGGGAGGTGGC--GCCGGCCCCAGGTTCAAGTAATCCAGGATAG [4654]
Gga ----------------------------GCTGGCGCTGGGTTCAAGTAATCCAGGATAG [4239]
Xtr TCTTGATTACTTGTTTCAGGAAGTAGC--TTGGGCGCTCGCTTCAAGTAATCCAGGATAG [4637]
Lch TCTCGATTACTTGTTTCAGGAGGAAGC--GCCGGGACCAGCTTCAAGTAATCCAGGATAG [4991]
Dre TCTTGGTTACTTGTTTCAGGAGGAGGC--GCTTTGGCCTGGTTCAAGTAATCCAGGATAG [5075]

Hsa GTTGTG----TGCTGTCCAGCCTGTTCTCCATTACTTGGCTCGGGGACCGGTG--TGGCC [4944]
Mmu GTTGTGG---TGCTGACCAGCCTGTTCTCCATTACTTGGCTCGGGGGCCGGTG--TGGCC [4945]
Mdo GCTGTT----TTCTCTTCAGCCTGTTCTCCATTACTTGGTTCGGGGGCCGGTA--TGGCT [4632]
Meu GCTGTT----TTCTCTTCAGCCTGTTCTCCATTACTTGGTTCGGGGGCTGGTA--TGGCC [3956]
Oan ----------------------------------------------------GGTCC [4192]
Aca GCTGTGGGTACTGATGTCAGCCTGTTCTTGATTACTTGGCCTTGGAGGCAGCC--GATGA [4872]
Pbi GCTGTAGGTACAGCAGTCAGCCTGTTCTCGATTACTTGGCCTTGGAGGCAGCC--GACTG [4948]
Cpi GCTGTGGTCTGCGCAGTCGGCCTGTTCTCGATTACTTGGCGCCGGAGCCGGCC--GATAC [5280]
Cmy ----------------------------------------------------GACAC [5029]
Psi ---------------------------------------------------------- [4779]
Asp ---------------------------------------------------------- [4620]
Ami ----------------------------------------------------GAAGC [4856]
Asi ----------------------------------------------------GAAGC [4913]
Tgu GCTGTGGTCTGGGCAGTCTTACTGTTCTCGGTTACTTGGATCTGGATCCGGCC------- [3776]
Cli GCTGTGATCTGGGCAGTCAGCCTGTTCTTGGTTACTTGGCTCTGGAGCTGGCC--GGGGC [4712]
Gga GCTGTGGTCTG-GCAGTCAGCCTGTTCTAGGTTACTTGGCTCCGGAGCCCGCC------- [4291]
Xtr GCTGTAATGTCTCCTGTCAGCCTTTTCTCGATTACTTGGGACCAGAGCCAATC--CAGCC [4695]
Lch GCTGTTAGTCACTAGCCCAGCCTATTCTTGATTACTTGGGTCTGGAGACGGCT--TTTGA [5049]
Dre GCT-TGTGATGTCCGGAAAGCCTATTCGGGATGACTTGGTTCAGGAATGAGAC--GTTGT [5132]

Hsa TGAGGAGCAGGGCTTAGCT-GC-TTGTGAGCAGGGTCCACACCAA-GTCGTGTTCACAGT [5001]
Mmu TGAGGAGCAGGGCTTAGCT-GC-TTGTGAGCAAGGTCCACAGCAAAGTCGTGTTCACAGT [5003]
Mdo TGAGGAGCAGGACTTAGCT-GCCTTGTGAACAGAGTCAGCATCAT-ATTGTGTTCACAGT [4690]
Meu TGAGGAGCAGGACTTAGCT-GCCTTGTGAACAGAGTTAGCATCAT-ATTGTGTTCACAGT [4014]
Oan GGCGGAGCAGGGCTTAGCTGGC-CTGTGAACAG--TTAGTTCCC--TGCGTGTTCACAGT [4247]
Aca CAAGCCGTAGGGCTTAGCCCAC-CTGTGAACAGCATTGGATTCA--GCCATGTTCACAGT [4929]
Pbi CCTAGGGTAGGGCTTAGCTCAC-TTGTGAACAGCGTTTGGTTCA--GCCGTGTTCACAGT [5005]
Cpi CGGGGTGCAGGGCTTAGCTCAC-CTGTGAACAGAGTTCGCATCCGTATCGTGTTCACAGT [5339]
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Cmy CGGGGTGCAGGGCTTAGCTCAC-TTGTGAACAGAGTTCGCATCCGCATCGTGTTCACAGT [5088]
Psi ------------------------------------------------------------ [4779]
Asp ------------------------------------------------------------ [4620]
Ami CAGGGCACAGGGCTTAGCTCAC-CTGTGAACAGAGTTAGCGTTG-CATCATGTTCACAGT [4914]
Asi CAGGGCACAGGGCTTAGCTCAC-CTGTGAACAGAGTTAGCGTTG-CATCATGTTCACAGT [4971]
Tgu ------------------------------------------------------------ [3776]
Cli CGGGGGGCAGGGCTTAGCCCAC-CTGTGAACAGAGTCCAGCCGT--GCCGTGTTCACAGT [4769]
Gga ------------------------------------------------------------ [4291]
Xtr GGCGGCCCAGGGCTTAGCTGTA-TTGTGAGCACTGTCACTCTCG--CACCTGTTCACAGT [4752]
Lch AATGGCACAGAGCTTAGCTATA-TGGAGAGCAGTGTATCTGTCAGTATCTTGTTCACAGT [5108]
Dre GTGGTGTCAGGACTTAACCCAC-TTGTGAACAATGCATCGAACT--TCAATGTTCACAGT [5189]

Hsa GGCTAAGTTCCGCCCCCC-AGGCC--TCTAACAAGGTGCAGAGCTTAGCTGATTGGTGAA [5058]
Mmu GGCTAAGTTCCGCCCCCT-GGACC--TCTAACAAGGTGCAGAGCTTAGCTGATTGGTGAA [5060]
Mdo GGCTAAGTTCCGCTCCCC-TTGCC--TCTGACAAGGTGCAGAGCTTAGCCGATTGGTGAA [4747]
Meu GGCTAAGTTCCGCCCCCC--------TCTAACAAGGTGCAGAGCTTAGCTGATTGGGGAA [4066]
Oan GGCTAAGTTCCGCCCCTCCAGGGC--TCTGTCGCGGCGCAGAGCTTAGCTGATTGGTGAA [4305]
Aca GGCTAAGTTCCGCTGCTT-GGAGT--TCTGGTGAGGTGCAGAGCTTAGCTGATTGGTGAA [4986]
Pbi GGCTAAGTTCCGCCACTT-GGAGT--TCTAGTGAGGTGCAGAGCTTAGCTGATTGGTGAA [5062]
Cpi GGCTAAGTTCCGCCCCCC-GGGGT--TCTAACAAGGTGCAGAGCTTAGCTGATTGGTGAA [5396]
Cmy GGCTAAGTTCCGCCCCCT-GGGGT--TCTAATGAGGTGCAGAGCTTAGCTGATTGGTGAA [5145]
Psi -------------------------TCTAACAAGGTGCAGAGCTTAGCTGATTGGTGAA [4813]
Asp -------------------------TCTAACAAGGTGCAGAGCTTAGCTGATTGGTGAA [4654]
Ami GGCTAAGTTCCGCCTCCT-GGTGT--TCTGACAAGGTGCAGAGCTTAGCTGATTGGTGAA [4971]
Asi GGCTAAGTTCCGCCTCCT-GGTGT--TCTGACAAGGTGCAGAGCTTAGCTGATTGGTGAA [5028]
Tgu -------------------------TCTGGCGAGGTGCAGAGCTTAGCTGATTGGTGAA [3810]
Cli GGCTAAGTTCCGCCTCCC-GCCCC--TCTGGCGAGGTGCAGAGCTTAGCTGATTGGTGAA [4826]
Gga -------------------------TCTGGTGAGGTGCAGAGCTTAGCTGATTGGTGAA [4325]
Xtr GGCTAAGTTCCGCGCCTC-TCTGG--TCTACCAAGGTGCAGAGCTTAGCTGATTGGTGAA [4809]
Lch GGCTAAGTTTAGTGCCCA-AAGAG--TCTGACAAGGTGCAGAGCTTAGCTGACTGGTGAA [5165]
Dre GGTTAAGTTCTGCCGCCCCTAGAC--TCTGAGCGGGTGCAGAGCTTGGCTGATTGGTGAA [5247]

Hsa CAGTGATTGGTTTCCGCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [5110]
Mmu CAGTGATTGGTTTCCGCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [5112]
Mdo CAGTCACTGATTTCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [4799]
Meu CAGTAATTGATTTCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [4118]
Oan CAGTGATTGCTGGACTCTTTGTTCACAGTGGCTAAGTTCTGCGCCCGCAGAG-------- [4357]
Aca CAGTGATTGATTTCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTAAAGAG-------- [5038]
Pbi CAGTGATTGATTTCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [5114]
Cpi CAGTGATTGATTTCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [5448]
Cmy CAGTGATTGATTTCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGCAGAG-------- [5197]
Psi CAGTGATTGATCTCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [4865]
Asp CAGTGATTGATCTCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [4706]
Ami CAGTGATTGATTTCCCCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [5023]
Asi CAGTGATTGATTTCCCCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [5080]
Tgu CAGTGATTGTTTTCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [3862]
Cli CAGTGATTGTTTCCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAGGAG-------- [4878]
Gga CAGTGATTGTTTCCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG-------- [4377]
Xtr CAGTGATTGATTCCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAG--CTAGAG [4867]
Lch CAGTAATTGATTTCCTCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAGGAG--TTATCG [5223]
Dre CGTGCATGGCTTGTGTTTTTGTTCACAGTGGCTAAGTTCTTCACCCGAAAAG--CTCACG [5305]

Hsa ------------------------------------------------------------ [5110]
Mmu ------------------------------------------------------------ [5112]
Mdo ------------------------------------------------------------ [4799]
Meu ------------------------------------------------------------ [4118]
Oan ------------------------------------------------------------ [4357]
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Aca ------------------------------------------------------------ [5038]
Pbi ------------------------------------------------------------ [5114]
Cpi ------------------------------------------------------------ [5448]
Cmy ------------------------------------------------------------ [5197]
Psi ------------------------------------------------------------ [4865]
Asp ------------------------------------------------------------ [4706]
Ami ------------------------------------------------------------ [5023]
Asi ------------------------------------------------------------ [5080]
Tgu ------------------------------------------------------------ [3862]
Cli ------------------------------------------------------------ [4878]
Gga ------------------------------------------------------------ [4377]
Xtr AGGCAGGACTTAGCTGGCTCTGTGAACAGGTCTT--GTGTG-TCAATGTTCACAGTGGCT [4924]
Lch GTGCAGGGCTTAGCTTAC-CTGTGAACAGTTAAA--TAGACCTTGTTGTTCACAGTGGCT [5280]
Dre GCGCAGAGCTTAGCTAAT-CGGTGAGCATTGATCCCTTAAGAAAACTGTTCACAGTGGCT [5364]

Hsa --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATATAATT [5155]
Mmu --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATAGAATT [5157]
Mdo --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATATCATT [4844]
Meu --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATATCATT [4163]
Oan --------------CTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATATCATT [4402]
Aca --------------TTAAAGGATGACTGATTTCTTCTGGTGTTCGGAGTCTAGTTCTCT [5083]
Pbi --------------TTAAAGGATAACTGATTTCTTCTGGTGTTCGGAGTCTATTCCTCT [5159]
Cpi --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATACTATT [5493]
Cmy --------------TCAAAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATACTATT [5242]
Psi --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATACTATT [4910]
Asp --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATACTATT [4751]
Ami --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCCATACTATT [5068]
Asi --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCCATACTATT [5125]
Tgu --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATAATAAT [3907]
Cli --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATAATATT [4923]
Gga --------------TTAGAGGATGACTGATTTCTTTTGGTGTTCAGAGTCAATAATATT [4422]
Xtr AAGTTCCACCCCA--TTAAAGGATGACTGATTTCTTCTGGTGTTCAGAGTC--TTTTGTT [4980]
Lch AAGTTCCGCATCT--TTAAAGGATGACTGATTTCTTTCGGTGTTCAGAGTCTGTTAT-TT [5337]
Dre AAGTTCAGTGTCT--CCAAACGATGACTGATTTCCTTTGGTGCTTAGAGTCCCATCTGTC [5422]

Hsa TTCTAGCACCATCTGAAATCGGTTATAATGATTGGGGA--CTTCAGGAAGCTGGTTTCAT [5213]
Mmu TTCTAGCACCATCTGAAATCGGTTATAATGATTGGGGA--CTTCAGGAAGCTGGTTTCAT [5215]
Mdo TTCTAGCACCATTTGAAATCGGTTATAATGATTGGGGA--CTTCAGGAAGCTGGTTTCAT [4902]
Meu TTCTAGCACCATTTGAAATCGGTTATAATGATTGGGGA--CTTCAGGAAGCTGGTTTCAT [4221]
Oan TTCTAGCACCATTTGAAATCGGTTATAATGATTGGGGA--CTTCAGGAAGCTGGTTTCAT [4460]
Aca TTCTAGCACCATTTGAAATCGGTTATAGTGATTGGGGA--CCTCAGGAAGCTGGTTTCAT [5141]
Pbi TTCTAGCACCATTTGAAATCGGTTATAGTGATTGGGGA--CTTCAGGAATCTGGTTTCAT [5217]
Cpi TTCTAGCACCATTTGAAATCGGTTATAGTGACTGGGGA--CCTCAGGAAGCTGGTTTCAT [5551]
Cmy TTCTAGCACCATTTGAAATCGGTTATAGTGACTGGGGA--CCTCAGGAAGCTGGTTTCAT [5300]
Psi TTCTAGCACCATTTGAAATCGGTTATAGTGACAGGGGA--CCTCAGGAAGCTGGTTTCAT [4968]
Asp TTCTAGCACCATTTGAAATCGGTTATAATGACAGGGGA--CCTCAGGAAGCTGGTTTCAT [4809]
Ami TTCTAGCACCATTTGAAATCGGTTATAGTGATTGGGGA--CTTCAGGAAGCTGGTTTCAT [5126]
Asi TTCTAGCACCATTTGAAATCGGTTATAGTGATTGGGGA--CTTCAGGAAGCTGGTTTCAT [5183]
Tgu TTCTAGCACCATTTGAAATCGGTTATAGTGATTGGGGA--CCTCAGGAAGCTGGTTTCAT [3965]
Cli TTCTAGCACCATTTGAAATCGGTTATAGTGATTGGGGA--CCTCAGGAAGCTGGTTTCAT [4981]
Gga TTCTAGCACCATTTGAAATCGGTTATAGTGATTGGGGA--CCTCAGGAAGCTGGTTTCAT [4480]
Xtr TTCTAGCACCATTTGAAATCGGTTATAATGATGGGGTA--TTTCAGGAGGCTGGTTTCAT [5038]
Lch GTCTAGCACCATTTGAAATCGGTTATAGTGATTGGGGA--CTCCAGGAAGCTGGTTTCAT [5395]
Dre ATCTAGCACCATTTGAAATCGGTTATAATGACTGGGGA--CCTCCAGATGCTGGTTTCAC [5480]

Hsa ATGGTGGTTTAGATTTAAATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGGG [5273]
Mmu ATGGTGGTTTAGATTTAAATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGTG [5275]
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Mdo ATGGTGGTTTAGATTTAACTACTGAGTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAG [4962]
Meu ATGGTGGTTTAGATTTAACTGCTGAGTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAG [4281]
Oan ATGGTGGTTTAGATTTAACTACTGAGTGTCTAGCACCATTTGAAATCAGTGTTCTTGGTG [4520]
Aca ATGGTGGTTTAGATTTAAGTACACAATGTCTAGCACCATTTGAAATCAGTGCTCTTGGAG [5201]
Pbi ATGGTGGTTTAGATTTAAGTACACAATGTCTAGCACCATTTGAAATCAGTGTTTTTGGGG [5277]
Cpi ATGGTGGTTTAGATTTAACTACTCCGTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAG [5611]
Cmy ATGGTGGTTTAGATTTAACTACTCAGTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAG [5360]
Psi ATGGTGGTTTAGATTTAACTACTCGGTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAG [5028]
Asp ATGGTGGTTTAGATTTAACTACTCGGTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAG [4869]
Ami ATGGTGGTTTAGATTTAACTACTTATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAG [5186]
Asi ATGGTGGTTTAGATTTAACTACTTATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAG [5243]
Tgu ATGGTGGTTTAGATTTAACTATTCATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAG [4025]
Cli ATGGTGGTTTAGATTTAACTATTCATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAG [5041]
Gga ATGGTGGTTTAGATTTAACTATTCATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGAG [4540]
Xtr GTGGTGGTTTAGATTTAACTGCACAATGTCTAGCACCATATGAAATCAGTGTCCTTAGAA [5098]
Lch ATGGTGGTTTAGATTTAACTTGACAGCATCTAGCACCATTTGAAATCAGTGTTCTTGGAG [5455]
Dre ATGGTGGTTTAGATGTGTTCTACCAAAGTCTAGCACCATTTGAAATCAGTGTTCTTGGGG [5540]

Hsa GAGA--ACACAGGCTGACCGATTTCTCCTGGTGTTCAGAGTCT---GTTTTTGTCTAGCA [5328]
Mmu GAGA--ACACAGGCTGACCGATTTCTCCTGGTGTTCAGAGTCT---GTTTTTGTCTAGCA [5330]
Mdo GAGA--ACACAGGCTGACCGATTTCTCTTGGTGTTCAGAGTCT---GTTTTTGTCTAGCA [5017]
Meu GAGA--ACACAGGCTGACCGATTTCTCTTGGTGTTCAGAGTCT---GTTTTTGTCTAGCA [4336]
Oan GAGA--ACACAGGCTGACCGATTTCTCTTGGTGTTCAGAGTCTCA-GTTCTTGTCTAGCA [4577]
Aca GAAG--ACACAGGCTGACCGATTTCTCTTGGTGTTCAGAGTCTTA-GTTTTTGTCTAGCA [5258]
Pbi GAAG--ACACAGGCTGACCGATTTCTCTTGGTGTTCAGAGTCTTA-GTTTTTGTCTAGCA [5334]
Cpi GAAG--ACACAGGCTGACCGATCTCTCTTGGTGTTCAGAGTTTCA-GTTTTTGTCTAGCA [5668]
Cmy GAAG--ACACAGGCTGACCGATCTCTCTTGGTGTTCAGAGTTT---GTTTTTGTCTAGCA [5415]
Psi GAAG--ACACAGGATGACCGGTCTCTCTTGGTGTTCAGAGTCAG--ATTTTTGTCTAGCA [5084]
Asp GAAG--ACACAGGCTGACCGGTCTCTCTTGGTGTTCAGAGTCAG--ATTTTTGTCTAGCA [4925]
Ami GAAG--ACACAGGCTGACCGATTTCTCTTGGTGTTCAGAGTCTCA-GTGTTTGTCTAGCA [5243]
Asi GAAG--ACACAGGCTGACCGATTTCTCTTGGTGTTCAGAGTCTCA-GTGTTTGTCTAGCA [5300]
Tgu GAAG--ACACAGGCTGACCGATTTCTCTTGGTGTTCAGAGTCTCA-GTTTTTGTCTAGCA [4082]
Cli GAAG--ACACAGGCTGACCGATTTCTCTTGGTGTTCAGAGTCTCA-GTTTTTGTCTAGCA [5098]
Gga GAAG--ACACAGGCTGACCGATTTCTCTTGGTGTTCAGAGTCTCA-GTTTCTGTCTAGCA [4597]
Xtr GGAG--ACACAGGATGACCGATCTCTCTTGGTGTTCAGAGGCTCAGGTCTTCATCTAGCA [5156]
Lch GAAG--ACCCAGGTTGACTGATTTCTTCTGGTGTTCAGAGTCAG---TTCATTTCTAGCA [5510]
Dre AGGG---------------------------------------------------------- [5544]

Hsa CCATTTGAAATCGGTTATGATGTAGGGGGA--TTCTGGAAGCTGGTTTCACATGGTGGCT [5386]
Mmu CCATTTGAAATCGGTTATGATGTAGGGGGA--TTCTGGAAGCTGGTTTCACATGGTGGCT [5388]
Mdo CCATTTGAAATCGGTTATGATGTAGGGGGA--TTCTGGAAGCTGGTTTCACATGGTGGCT [5075]
Meu CCATTTGAAATCGGTTATGATGTAGGGGGA------------------------------ [4366]
Oan CCATTTGAAATCGGTTATGATGTAGGGGGA--TTCTGGAAGCTGGTTTCACATGGTGGCT [4635]
Aca CCATTTGAAATCGGTTATGATGTAGGGGGA--CTCTGGAAGCTGGTTTCACATGGTGGCT [5316]
Pbi CCATTTGAAATCGGTTATGATGTAGGGGGA--CTCTGGAAGCTGGTTTCACATGGTGGCT [5392]
Cpi CCATTTGAAATCGGTTATGATGTAGGGGGA--TTCTGGAAGCTGGTTTCACATGGTGGCT [5726]
Cmy CCATTTGAAATCGGTTATGATGTAGGGGGA--TTCTGGAAGCTGGTTTCACATGGTGGCT [5473]
Psi CCATTTGAAATCGGTTATGATGTAGGGGGA--TTCTGGAAGCTGGTTTCACATGGTGGCT [5142]
Asp CCATTTGAAATCGGTTATGATGTAGGGGGA--TTCTGGAAGCTGGTTTCACATGGTGGCT [4983]
Ami CCATTTGAAATCGGTTATGATGTAGGGGGA--CTCTGGAAGCTGGTTTCACATGGTGGCT [5301]
Asi CCATTTGAAATCGGTTATGATGTAGGGGGA--CTCTGGAAGCTGGTTTCACATGGTGGCT [5358]
Tgu CCATTTGAAATCGGTTATGATGTAGGGGGA--CTCTGGAAGCTGGTTTCACATGGTGGCT [4140]
Cli CCATTTGAAATCGGTTATGATGTAGGGGGA--CTCTGGAAGCTGGTTTCACATGGTGGCT [5156]
Gga CCATTTGAAATCGGTTATGATGTAGGGGGA--CTCTGGAAGCTGGTTTCACATGGTGGCT [4655]
Xtr CCATTTGAAATCGGTTATAATGTAAGGTGA--TCCCGGAAGCTGGTTTCTTGTGGTGACT [5214]
Lch CCATTTGAAATCGGTTACAATGTAGAGGAA--CCCTGGAAGCTGGTTTCACATGGTGGCT [5568]
Dre ------------------------------TCCTGGAAGCTGAATTCAGATGGTGCCA [5572]
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Hsa TAGATTTTTCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTTTAGGAG--GCGACT [5444]
Mmu TAGATTTTTCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTTTAGGAG--GCGACT [5446]
Mdo TAGATTTTTCCATCTCTGTATCTAGCACCATTTGAAATCAGTGTTTTAGGAG--GCGGCT [5133]
Meu ---------------------------------------------------------- [4366]
Oan TAGATTTTTCCATCTCTGTATCTAGCACCATTTGAAATCAGTGTTTTAGGAG--GCGACT [4693]
Aca TAGATTTTTCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGAG--GCGACT [5374]
Pbi TAGATTTTTCCATCTCTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGAG--GCGATT [5450]
Cpi TAGATTTTCCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGAG--GCGACT [5784]
Cmy TAGATTTTCCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGAG--GCGACT [5531]
Psi TAGATTTTCCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGAG--GCGACT [5200]
Asp TAGATTTTCCCATCTCTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGAG--GCGACT [5041]
Ami TAGATTTTCCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGGG--GCGACT [5359]
Asi TAGATTTTCCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGGG--GCGACT [5416]
Tgu TAGATTTTCCCA-CTTTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGAG--GCGACT [4197]
Cli TAGATTTTCCCA-CTTTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGAG--GCGACT [5213]
Gga TAGATTTTCCCA-CTTTGTATCTAGCACCATTTGAAATCAGTGTTCTAGGAG--GCGACT [4712]
Xtr TAGATTTATCCATCGCTGCATCTAGCACCATTTGAAATCAGTGTTCTAGGAG--GCGACT [5272]
Lch TAGATAGTTCCATCCCTGCATCTAGCACCATTTGAAATCAGTGTTCTAGGAG--GTGACT [5626]
Dre TAGAGTATTTTA---TGGCATCTAGCACCATTTGAAATCAGTGTTCCTGGGC--GCAGTT [5627]

Hsa GTAAACATCCTCGACTGGAAGCTGTGAAGCCACAGATGG--GCTTTCAGTCGGATGTTTG [5502]
Mmu GTAAACATCCTCGACTGGAAGCTGTGAAGCCACAAATGG--GCTTTCAGTCGGATGTTTG [5504]
Mdo GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [5192]
Meu ---------------------------------------------------------- [4366]
Oan GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [4752]
Aca GTAAACATCCTCGACTGGAAGCTGTGAAGCAGTAGATGAA-GCTTTCAGTCGGATGTTTG [5433]
Pbi GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [5509]
Cpi GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [5843]
Cmy GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [5590]
Psi GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [5259]
Asp GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [5100]
Ami GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [5418]
Asi GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [5475]
Tgu GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [4256]
Cli GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [5272]
Gga GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGGG-GCTTTCAGTCGGATGTTTG [4771]
Xtr GTAAACATCCTCGACTGGAAGCTGTGAAGCAGTTGAAGG--GCTTTCAGTCAGATGTTTG [5330]
Lch GTAAACATCCTCGACTGGAAGCTGTGAAGCAGCAGATGTG-GCTTTCAGTCGGATGTTTG [5685]
Dre GTAAACATTCCCGACTGGAAGTTGTAATGCAGAAAATCTCAGCTTTCAGTCTGATGTTTG [5687]

Hsa CAGCTGC--AGATACTGTAAACATCCTACACTCTCAGCTGTG--GAAAGTAAGAAAGCTG [5558]
Mmu CAGCTGC--AGATATTGTAAACATCCTACACTCTCAGCTGTG--AAAAGTAAGAAAGCTG [5560]
Mdo CAGCTGC--AGATATTGTAAACATCCTACACTCTCAGCTGTG--GAAAGTCAGAAAGCTG [5248]
Meu ---------AGATATTGTAAACATCCTACACTCTCAGCTGTG--GAAAGTCAGAAAGCTG [4415]
Oan CAGCTGC--AGGTACTGTAAACATCCTACACTCTCAGCTGTA--GATG-TGAGAAAGCTG [4807]
Aca CAGCTGC--AGGTAATGTAAACATCCTACACTCTCAGCTGTGTAGATAAGAAGAAAGCTG [5491]
Pbi CAGCTGC--------TGTAAACATCCTACACTCTCAGCTGTGTGGAAAAGAAGAAAGCTG [5561]
Cpi CAGCTGC--AGGTACTGTAAACATCCTACACTCTCAGCTGTG--GAAAGTAAGGAAGCTG [5899]
Cmy CAGCTGC--AGGTACTGTAAACATCCTACACTCTCAGCTGTG--GAAAGTAAGGAAGCTG [5646]
Psi CAACTGC--AGGTACTGTAAACATCCTACACTCTCAGCTGTG--GAAAGTAAGGAAGCTG [5315]
Asp CAACTGC--AGGTACTGTAAACATCCTACACTCTCAGCTGTG--GAAAATAAGGAAGCTG [5156]
Ami CAGCTGC--AGGTATTGTAAACATCCTACACTCTCAGCTGTG--GAAAATGAGGAAGCTG [5474]
Asi CAGCTGC--AGGTATTGTAAACATCCTACACTCTCAGCTGTG--GAAAATGAGGAAGCTG [5531]
Tgu CAGCTGC--AGGTATTGTAAACATCCTACACTCTCAGCTGTG--GAAACTAAGAAAGCTG [4312]
Cli CAGCTGC--AGGTACTGTAAACATCCTACACTCTCAGCTGTG--GAAACTAAGAAAGCTG [5328]
Gga CAGCTGC--AGGTACTGTAAACATCCTACACTCTCAGCTGTG--GAAACTAAGAAAGCTG [4827]
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Xtr CAGCTGC--AGATACTGTAAACATCCTACACTCTCAGCTGTG--GAAAT--ACAAAGCTG [5384]
Lch CTGCTGC--AGTGCGTGTAAACATCCTACACTCTCAGCTGTG--TATGTGAGCA-AGCTG [5740]
Dre CTGCTAC---------------------------------------------------- [5694]

Hsa GGAGAAGGCTGTTTACTCTTTCT--TTTGCTACTGTAAACATCCTTGACTGGAAGCTGTA [5616]
Mmu GGAGAAGGCTGTTTACTCTCTCT--TTTGCTACTGTAAACATCCTTGACTGGAAGCTGTA [5618]
Mdo GGAGAAGGCTGTT-ACTCTGTCT--TTTGCCGCTGTAAACATCCTTGACTGGAAGCTGTA [5305]
Meu GGAGAAGGCTGTTTACTCTGTCT--TGTGCCGCTGTAAACATCCTTGACTGGAAGCTGTA [4473]
Oan GGAGAAGGCTGTTTACTCTCTCT--TTTGCTACTGTAAACATCCTTGACTGGAAGCTGGA [4865]
Aca GGAGAAGGCTGTTTACTCTCTCT--GT-GCTCCTGTAAACATCCTTGACTGGAAGCTGTG [5548]
Pbi GGAGAAGGCTGTTTACTCTCTCT--GTTGCTCCTGTAAACATCCTTGACTGGAAGCTGTA [5619]
Cpi GGAGAAGGCTGTTTACTCTCTCT--GTTGCTACTGTAAACATCCTTGACTGGAAGCTGTA [5957]
Cmy GGAGAAGGCTGTTTACTCTCTCT--GTTGCTACTGTAAACATCCTTGACTGGAAGCTGTA [5704]
Psi GGAGAAGGCTGTTTACTCTCTCT--ATTGCTACTGTAAACATCCTTGACTGGAAGCTGTA [5373]
Asp GGAGAAGGCTGTTTACTCTTTCT--GTTGCTACTGTAAACATCCTTGACTGGAAGCTGTA [5214]
Ami GGAGAAGGCTGTTTACTCTCCCT--GATGCTACTGTAAACATCCTTGACTGGAAGCTGTA [5532]
Asi GGAGAAGGCTGTTTACTCTTCCT--GATGCTACTGTAAACATCCTTGACTGGAAGCTGTA [5589]
Tgu GGAGAAGGCTGTTTACTCTCTCT--AGTGCCTCTGTAAACATCCTTGACTGGAAGCTGGA [4370]
Cli GGAGAAGGCTGTTTACTCTCCCT--CTTGCTGCTGTAAACATCCTTGACTGGAAGCTGTG [5386]
Gga GGAGAAGGCTGTTTACTCTCCCT--ATCGCTGCTGTAAACATCCTTGACTGGAAGCTGTG [4885]
Xtr GGGGAAGGCTGTTTACTCTCTCT--ACAGCCTCTGTAAACATCCTTGACTGGAAGCTGTG [5442]
Lch GGAGAGGGGTGTTTACTCTCATT------------------------------------ [5763]
Dre ------------------------CGGGCTACTGTAAACATCCTTGACTGGAAGCTGGT [5729]

Hsa AGGTGTTCAGAGG-AGCTTTCAGTCGGATGTTTACAGCGGCA--GTAGTGTGTGTAAACA [5673]
Mmu AGGTGTTGAGAGG-AGCTTTCAGTCGGATGTTTACAGCGGCA--GTAGTGTGTGTAAACA [5675]
Mdo AGGTGCTTGGAGG-AGCTTTCAGTCGGATGTTTACAGCGGCA--GTAGTGTGTGTAAACA [5362]
Meu AGGTGCTTGGAGG-AGCTTTCAGTCGGATGTTTACAGCGGCA--GTAGTGTGTGTAAACA [4530]
Oan AGGTGCC-GAAGG-AGCTTTCAGTCGGATGTTTACAGCGGCA--GTGGGGGGTGTAAACA [4921]
Aca CAAGGCTCAAAGG-GGCTTTCAGTCGGATGTTTACAGCGGCA--GCAGCGCATGTAAACA [5605]
Pbi CA-GGCTCAAAGA-GGCTTTCAGTCGGATGTTTACAGCGGCA----------TGTAAACA [5667]
Cpi AGGTGCTAGAAGGGAGCTTTCAGTCGGATGTTTACAGCGGCA--GTAGCATGTGTAAACA [6015]
Cmy AGGTGCTAGAAGGGAGCTTTCAGTCGGATGTTTACAGCGGCA--GTAGCATGTGTAAACA [5762]
Psi AGGTGTTAGAAGGGAGCTTTCAGTCGGATGTTTACAGCGGCA--GTAGCATGTGTAAACA [5431]
Asp AGGTGTTAGAAGGGAGCTTTCAGTCGGATGTTTACAGCGGCA--GTAGCATGTGTAAACA [5272]
Ami AGGTGCTAGAAGG-AGCTTTCAGTCGGATGTTTACAGCGGCA--GTAGCATGTGTAAACA [5589]
Asi AGGTGCTAGAAGG-AGCTTTCAGTCGGATGTTTACAGCGGCA--GTAGCATGTGTAAACA [5646]
Tgu AGG-GCTGGAAGG-AGCTTTCAGTCGGATGTTTACAGCAGCA--GTAGCACGTGTAAACA [4426]
Cli AGGTGCGAGCAGG-AGCTTTCAGTCGGATGTTTGCAGCAGCA--GTAGCACGTGTAAACA [5443]
Gga AGGTGTCAGCGGG-GGCTTTCAGTCGGATGTTTACAGCTGCA--GTAGCACGTGTAAACA [4942]
Xtr AAATAATGATAGT-AGCTTTCAGTCGGATGTTTACAGCTGCT--GCAGTGATTGTAAACA [5499]
Lch ---------------------------------------------ACAGACAATGTAAACA [5779]
Dre GCACA-TGATGG--AGCTTTCAGTCGGATGTTTGCAGCAGCC--TCAGGGAGTGTAAACA [5784]

Hsa TCCTACACTCTCAGCTGTGAGCTCAAGGTG-GCTGGGAGAGGGTTGTTTACTCCTTC--T [5730]
Mmu TCCTACACTCTCAGCTGTGAGCTCAAGGTG-GCTGGGAGAGGGTTGTTTACTCCTTC--T [5732]
Mdo TCCTACACTCTCAGCTGTGAGCTCAAGGTG-GCTGGGAGAGGGCTGTTTACTCCTTC--T [5419]
Meu TCCTACACTCTCAGCTGTGAGCTCAAGGTG-GCTGGGAGAGGGCTGTTTACTCCTTC--T [4587]
Oan TCCTACACTCTCAGCTGTCAAGTCAAGGAG-GCTGGGAGAGGGTTGTTTACTCCCTC--T [4978]
Aca TCCTACACTCTCAGCTGTGAATTTGTGGTG-GCTGGGAGAAGGTTGTTTACACCTTC--T [5662]
Pbi TCCTACACTCTCAGCTGTGACTTTGTGGTG-GCTGGGAGAAGGTTGTTTACGCCTCC--T [5724]
Cpi TCCTACACTCTCAGCTGTGGACTCAAGGTA-GCTGGGAGAGGGTTGTTTACTCCTTC--T [6072]
Cmy TCCTACACTCTCAGCTGTGGACTTAAGGTG-GCTGGGAGAGGGTTGTTTACTCCTTC--T [5819]
Psi TCCTACACTCTCAGCTGTGGACTCAAGGTG-GCTGGGAGAGGGTTGTTTACTCCTTC--T [5488]
Asp TCCTACACTCTCAGCTGTGGACTCAAGGTG-GCTGGGAGAGGGTTGTTTACTCCTTC--T [5329]
Ami TCCTACACTCTCAGCTGTGAACTCAAGGTG-GCTGGGAGAGGGTTGTTTACGCCTTC--T [5646]
Asi TCCTACACTCTCAGCTGTGAACTCAAGGTG-GCTGGGAGAGGGTTGTTTACGCCTTC--T [5703]
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Tgu TCCTACACTCTCAGCTGTGAACTCGAGGTG-GCTGGGAGAGGATTGTTTACGCCTTC--T [4483]
Cli TCCTACACTCTCAGCTGTGAACT-GAGGTG-GCTGGGAGAGGATTGTTTACTCCTTC--C [5499]
Gga TCCTACACTCTCAGCTGTGAACTCGAGGTG-GCTGGGAGAGGATTGTTTACGCCTTC--T [4999]
Xtr TCCTACACTCTCAGCTGTGAACATAAGGTG-GCTGGGAGAAGGGTGTTTACTCCCCC--T [5556]
Lch TCCTACACTCTCAGCTGTGGCAAGTAAAGGAGCTGGGAGAAGGATGTTTACGCTTTC--T [5837]
Dre TCCTACACTCTCAGCTGGAGCGCAGCCGAG-GCCGGGAGTGGGATGTTTGCGCTCTC--C [5841]

Hsa GTTGTTGTAAACATCCCCGACTGGAAGCTGTAA---GACACAGCTAAGCTTTCAGTCAGA [5787]
Mmu GTGTCTGTAAACATCCCCGACTGGAAGCTGTAA---GCCACAGCCAAGCTTTCAGTCAGA [5789]
Mdo GTTGTTGTAAACATCCCCGACTGGAAGCTGTAA---GACACAGCCAAGCTTTCAGTCAGA [5476]
Meu GTCGTTGTAAACATCCCCGACTGGAAGCTGTAA---GACACAGCCAAGCTTTCAGTCAGA [4644]
Oan GTGGCTGTAAACATCCCCGACTGGAAGCTGTAA---AATACCTTCAAGCTTTCAGTCAGA [5035]
Aca GTTGTTGTAAACATCCCCGACTGGAAGCTGTAA--------ATTTCAGCTTTCAGTCAGA [5714]
Pbi GTTGTTGTAAACATCCCCGACTGGAAGCTGGAA--------AATGTAGCTTTCAGTCCGA [5776]
Cpi GTTGTTGTAAACATCCCCGACTGGAAGCTGTAA---GAGAAATTCTAGCTTTCAGTCAGA [6129]
Cmy GTTGTTGTAAACATCCCCGACTGGAAGCTGTAA---GAGAAATTCTAGCTTTCAGTCAGA [5876]
Psi GTTGTTGTAAACATCCCCGACTGGAAGCTGTAA---GACACATTCTAGCTTTCAGTCAGA [5545]
Asp GTTGTTGTAAACATCCCCGACTGGAAGCTGTAA---GACAAATTCTAGCTTTCAGTCAGA [5386]
Ami GTTGTTGTAAACATCCCCGACTGGAAGCTGTAA---GAGAAATTCTAGCTTTCAGTCAGA [5703]
Asi GTTGTTGTAAACATCCCCGACTGGAAGCTGTAA---GAGAAATTCTAGCTTTCAGTCAGA [5760]
Tgu GTTGCTGTAAACATCCCCGACTGGAAGCTGTAC------CTGCTCCAGCTTTCAGTCAGA [4537]
Cli GGTGCTGTAAACATCCCCGACTGGAAGCTGTTC-------CCGTCCAGCTTTCAGTCAGA [5552]
Gga GTTGCTGTAAACATCCCCGACTGGAAGCTGTAG------CAGCTTGAGCTTTCAGTCAGA [5053]
Xtr GTCGCTGTAAACATCCCCGACTGGAAGCTGTGAG--GCTGCATTTGAGCTTTCAGTCTGG [5614]
Lch GTTGCTGTAAACATCCCCGACTGGAAGCTGTAAA--TCATGACGACAGCTTTCAGTCAGA [5895]
Dre ATGCCTGTAAACATCCCCGACTGGAAGCTGTGCTACGCGGAAAACGAGCTTTCAGTTGGA [5901]

Hsa TGTTTGCTGCTACC--TCAGTTCATGTAAACATCCTACACTCAGCTGTAATACA-TGGAT [5844]
Mmu TGTTTGCTGCTACT--TCAGTTCATGTAAACATCCTACACTCAGCTGTCATACA-TGCGT [5846]
Mdo TGTTTGCTGCTACC--CCAGTTCATGTAAACATCCTACACTCAGCTGTAACACA-TGGAT [5533]
Meu TGTTTGCTGCTACC--CCAGTTCATGTAAACATCCTACACTCAGCTGTAACACA-TGA-T [4700]
Oan TGTTTGCTACCACT--CGAGTTCATGTAAACATCCTACACTCAGCTGTGACCCA-CCCAG [5092]
Aca TGTTTGCTGCCACC--TTAGTTCATGTAAACATCCTACACTCAGCTGTATCACA-TGAAA [5771]
Pbi TGTTTGCTGCCGCC--TTAGTTTATGTAAACATCCTACACTCAGCTTTATCACA-TGAAA [5833]
Cpi TGTTTGCTGCATCC--TTAGTTCATGTAAACATCCTACACTCAGCTATAAAACA-TAGAA [6186]
Cmy TGTTTGCTGCATCC--TTAGTTCATGTAAACATCCTACACTCAGCTGTAAAACA-TGGAA [5933]
Psi TGTTTGCTGCATCC--TTAGTTCATGTAAACATCCTACACTCAGCTATAACACA-TGAAA [5602]
Asp TGTTTGCTGCATCC--TTAGTTCATGTAAACATCCTACACTCAGCTATAACACA-TGAAA [5443]
Ami TGTTTGCTGCCACT--TTAGTTCATGTAAACATCCTACACTCAGCTATAACAAC-TGGAA [5760]
Asi TGTTTGCTGCCACT--TTAGTTCATGTAAACATCCTACACTCAGCTATAACAAC-TGGAA [5817]
Tgu TGTTTGCTGCACCT--TTAGTTCCTGTAAACATCCTACACTCAGCTATTATAAG-TGGTG [4594]
Cli TGTTTGCTGCACCT--TTAGTTCCTGTAAACATCCTACACTCAGCTATAACAAG-TGGTG [5609]
Gga TGTTTGCTGCACCT--TTAGTTCCTGTAAACATCCTACACTCAGCTATAACAAG-TGGTA [5110]
Xtr TGTTTGCTGCTACC--TTAGTCTATGTAAACATCCTACACTCAGCTCGTATGTA-TAACC [5671]
Lch TGTTTGCTGAGTCT--CCAGTCCATGTAAACATCCTACACTCAGCTGTAACACA-GGGAA [5952]
Dre TGTTTGCTGTCATC--GTAGTCGCTGTAAACATCCTACACTCAGCTGTGAGCTGCAGACG [5959]

Hsa TGGCTGGGAGGTGGATGTTTACTTCAGC--CTTGGAACTGGAGAGGAGGCAAGATGCTGG [5902]
Mmu TGGCTGGGATGTGGATGTTTACGTCAGC--CTCGGAACTGGAGAGGAGGCAAGATGCTGG [5904]
Mdo CGGCTGGGAGGTGGATGTTTACTTCAGC--TTCAGAGCTGGAGAGGAGGCAAGATGTTGG [5591]
Meu TGGCTGGGAGGTGGATGTTTACTTCAGC--TTCAGAGCTGGAGAGGAGGCAAGATGTTGG [4758]
Oan CGGCTGGGAGGGGGATGTTTGCTTCAAC--CTCAGAGCTGGAGAGAAGGCAAGATGTTGG [5150]
Aca TGGCTGGGAGATGAATGTTTACTTCAAC--TTCAGAGCTGGAGCGGAGGCAAGATGTTGG [5829]
Pbi TGGCTGGGAGATGGAAGTTTACTTCAAC--TTGAGAGCTGGAGAGGAGGCAAGATGTTGG [5891]
Cpi CGGCTGGGAGGTGGATGTTTACTTCAAC--ATCAGACTTTGAGGGGAGGCAAGATGTTGG [6244]
Cmy CGGCTGGGAGGTGGATGTTTACTTCAAC--ATCAGACCTTGAGGGGAGGCAAGATGTTGG [5991]
Psi CGGCTGGGAGGTGGATGTTTACTTCAAC--CTCAGACTTGGAGGGGAGGCAAGATGTTGG [5660]
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Asp CGGCTGGGAGATGGATGTTTACTTCAAC--CTCAGACGTGGAGGGGAGGCAAGATGTTGG [5501]
Ami CGGCTGGGAGGTGGATGTTTACTTCAAC--TTCAGAGCTAGAGAGGAGGCAAGATGTTGG [5818]
Asi CGGCTGGGAGGTGGATGTTTACTTCAAC--TTCAGAGCTAGAGAGGAGGCAAGATGTTGG [5875]
Tgu GGGCTGGGGGTTGGGTGTTTACTTCAAC--TGCAGAGCTGGAGAGGAGGCAAGATGTTGG [4652]
Cli GGGCTGGGGGGTAGATGTTTACATCAAC--TGCAGAGCTGGAGGGGAGGCAAGATGTTGG [5667]
Gga GGGCTGGGGGGTGGATGTTTACTTCAAC--TGCAGAGCTGGAGGGGAGGCAAGATGTTGG [5168]
Xtr TGACTGGGTGGGGGGTGTTTGCCTCGAC--CCTAGTTCTAGAGAGGAGGCAAGATGTTGG [5729]
Lch AGACTGGGAGAAGGGTGTTTACTTCGGC--CTCAGAGCTGGAGAGGAGGCAAGATGTTGG [6010]
Dre AGGCTGGGCGGAGGGTGTTTGCTGTGAC--TCTGGAAGAGAAGAGATGGCAAGATGTTGG [6017]

Hsa CATAGCTGTTGAA--CTGGGAACCTGCTATGCCAACATATTGCCATCTTTCCTGTCTG-- [5958]
Mmu CATAGCTGTTGAA--CTGAGAACCTGCTATGCCAACATATTGCCATCTTTCCTGTCTG-- [5960]
Mdo CATAGCTGTTGAA--CTGAGAACCTGCTATGCCAACATATTGCCATCTTTCTTGTCTA-- [5647]
Meu CATAGCTGTTGAA--CTAAGAACCTGCTATGCCAACATATTGCCATCTTTCTTGTCTA-- [4814]
Oan CATAGCTGTTGAG--TTAAGAACCTGCTATGCCGACATGTTGTCATCTTTCTTGTCTA-- [5206]
Aca CATAGCTGATGAG--TTAAGAACCTGCTATGCCAACATATTGCCCTCTTTCCTGTCTG-- [5885]
Pbi CATAGCTGATGAA--CTGAGAACCTGCTATGCCAACATATTGCCCTCTTTCACCTCTG-- [5947]
Cpi CATAGCTGTTGAC--CTAATAACCTGCTATGCCAACATATTGTCATCTTTCTCGTCTA-- [6300]
Cmy CATAGCTGTTGAC--CTAATAACCTGCTATGCCAACATATTGTCATCTTTCTTGTCTA-- [6047]
Psi CATAGCTGTTGAT--CTAAAAACCTGCTATGCCAACGTATTGCCATCTTTCTCGTCTA-- [5716]
Asp CATAGCTGTTGAT--CTAAAAACCTGCTATGCCAACGTATTGCCATCTTTCTCGTCTA-- [5557]
Ami CATAGCTGTTGAC--CTAAGAACCTGCTATGCCAACATCTTGTCATCTTTCTTGTCTA-- [5874]
Asi CATAGCTGTTGAC--CTAAGAACCTGCTATGCCAACATCTTGTCATCTTTCTTGTCTA-- [5931]
Tgu CATAGCTGTTGAT--CTAAAAACCTGCTATGCCAACATATTGTCATCTTTCCTGTCTG-- [4708]
Cli CATAGCTGTAGAC--CTAAAAACCTGCTATGCCAACATATTGTCATCTTTCCTCTCTG-- [5723]
Gga CATAGCTGTTAAC--CTAAAAACCTGCTATGCCAACATATTGTCATCTTTCCTGTCTG-- [5224]
Xtr CATAGCTGTTGCA--TCTGAAACCAGTTGTGCCAACCTATTGCCATCTTTCTTGTCTA-- [5785]
Lch CATAGCTGTTGTG--TCAAGAACCTGCTATGCCAATATATTGTCATCTTTCCTGTCTA-- [6066]
Dre CATAGCTGTTAATGTTTATGGGCCTGCTATGCCTCCATATTGCCATTTCTGCACTTCC-- [6075]

Hsa AGATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAATGCAATTTAGTGTGTGTG [6018]
Mmu AGATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAATGCAATTTAGTGTGTGTG [6020]
Mdo AGATATTGCACATTACTAAGTTGCATGTTGTCACGGCTTTAGTGCAATTTAGTATGTGTG [5707]
Meu AGATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTTGGTGCAATTTAGTATGTGTG [4874]
Oan AGATATTGCACATTACTAAGTTGCATGTTGTCAAGGCCTCTGTGCAATTTAGTGTGTGCG [5266]
Aca GGATATTGCACATTACTAAGTTGCATGTTGTCACGGGCTCAGTGCAATTTAGTGTGTGCG [5945]
Pbi TGATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAGTGCAATTTAGTGTGTGTG [6007]
Cpi AGATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAGTGCAATTTAGTGTGTGCG [6360]
Cmy AGATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAGTGCAATTTAGTGTGTGCG [6107]
Psi AGATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAGTGCAATTTAGTGTGTGCG [5776]
Asp AGATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAGTGCAATTTAGTGTGTGCG [5617]
Ami ATATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAGTGCAATTTAGTGTGTGCG [5934]
Asi ATATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAGTGCAATTTAGTGTGTGCG [5991]
Tgu AGATATTGCACATTACTAAGTTGCACGTTCTCACGGCCTCAGTGCAATTTAGTGTGTGCG [4768]
Cli AGATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAGTGCAATTTAGTGTGTGCG [5783]
Gga AGATATTGCACATTACTAAGTTGCATGTTGTCACGGCCTCAGTGCAATTTAGTGTGTGCG [5284]
Xtr ---------------------------------------------------------- [5785]
Lch AGATATTGCACATTACCAAGTTGCATGTCATCAGGGCCTCAGTGCAACTTAGTATGTGCG [6126]
Dre ---------------------------------------------------------- [6075]

Hsa ATATTT--GGCGGGCAGCTGTGGTGCATTGTAGTTGCATTGCATGTTCTGGTGGTACCCA [6076]
Mmu ATATTT--GGCGGGCAGCTGTGGTGCATTGTAGTTGCATTGCATGTTCTGGCAATACCTG [6078]
Mdo ATATTT--AGCGAGCGGCTGGGGTGCATTGTAGTTGCATTGCACGTCGTGTC-CGGGCCG [5764]
Meu ATATTT--TGCGGGCGGCTGGGGTGCATTGTAGTTGCATTGCACGTCGTGTC--GGGCCG [4930]
Oan ATATTT--GGTTGGCCACTGTCGTGCATTGTAGTTGCATTGCACGTTCCGGCAGTACTGG [5324]
Aca ATATTT--GGGTGGCAGCTGTAGTGCATTGTAGTTGCATTGCATGTTCTAGCAGTATTTG [6003]
Pbi ATATTT--GGGTGGCAACTGTAGTGCATTGTAGTTGCATTGCATGTTCTGGCAATACTCA [6065]
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Cpi ATATTT--GGGGGGCAGCTGTAGTGCATTGTAGTTGCATTGCATGTTCTGGCAGTACTTG [6418]
Cmy ATATTT--GGGGGGCAGCTGTCGTGCATTGTAGTTGCATTGCACGTTCTGGCCATACTTG [6165]
Psi ATATTT--GGGGGGCAGCTGTAGTGCATTGTAGTTGCATTGCATGTTCTGGCAGTATTTG [5834]
Asp ATATTT--GGGGGGCAGCTGTAGTGCATTGTAGTTGCATTGCATGTTCTGGCAGTATTTG [5675]
Ami ATATTT--GGGTGACCGCTGTAGTGCATTGTAGTTGCATTGCATGTTCTGGTAGTATCTG [5992]
Asi ATATTT--GGGTGACCGCTGTAGTGCATTGTAGTTGCATTGCATGTTCTGGTAGTATCTG [6049]
Tgu ATACTT--GGGTGGCAGCTGTAGTGCATTGTAGTTGCATTGCATGTTGTGGCAGTGACTG [4826]
Cli ATACTT--GGGTGGCAGCTGTAGTGCATTGTAGTTGCATTGCATGTTGTGGCAGTAACTG [5841]
Gga ATACTT--GGGTGGCAGCTGTAGTGCATTGTAGTTGCATTGCATGTGCTGGCAGTAACTG [5342]
Xtr --------TTGGGGTCACCCTGGTGCATTGTTGTTGCATTGCATGTCACCTTGGACGTTG [5837]
Lch ATATTT--TGGAGACAGCTGTGGTGCATTGTAGTTGCATTGCATGTTGGAGCTGCAAGTG [6184]
Dre ---------------------------------------------------------- [6075]

Hsa TGCAATGTTTCCACAGTGCATCACAGAGGCCTGCC--CGGGCGGCCCCGCGGTGCATTGC [6134]
Mmu TGCAATGTTTCCACAGTGCATCACGGAGGCCTGCC------------------------ [6113]
Mdo TGCAATGTTTCCACAGTGCATCCCAGAGGCCCGCG------------------------ [5799]
Meu TGCAATGTTCCCGCAGTGCATCCCGGAGGCCCGCA------------------------ [4965]
Oan TGCAATGTTCCCACAGTGCATTACAGAGACCCGCT--CGGCTGCCGCTGTAGTGCATTGT [5382]
Aca TGCAATGTTTCCGCAGTGCAATACAGAGGCATACC--TGGCAGTTTCGGGGGTGCATTGT [6061]
Pbi TGCAATGTTTCTGCAGTGCAGTTCAGAGGCATGCC--TGGCTGTGTCGGTGGTGCATTGT [6123]
Cpi TGCAATGTTTCTGCAGTGCAGTACAGAGGCACTCT--TGGCCGCAGCTGTGGTGCATTGT [6476]
Cmy TGCAATGTTTCTGCAGCGCAGCACAGAGGCACTCT--TGGCCGCAGCTGTGGTGCATTGT [6223]
Psi TGCAATGTTTCTGCAGTGCAGTACAGAGGCACTCT------------------------ [5869]
Asp TGCAATGTTTCTGCAGTGCAGTACAGAGGCACTCT------------------------ [5710]
Ami TGCAATGTTTCTGCAGTGCAGTATAGAGGCACTCT--TGGCCTCAGCTGTGGTGCATTGT [6050]
Asi TGCAATGTTTCTGCAGTGCAGTACAGAGGCACTCT--TGGCCTCAGCTGTGGTGCATTGT [6107]
Tgu TGCAATGTTTCTGCAGTGCAGTACAGAGGCACTCT------------------------ [4861]
Cli TGCAATGTTCCTGCAGTGCAGTACAGAGGCACTCT--CGGCCCTCGCGGGGGTGCATTGT [5899]
Gga TGCAATGTTCCTGCAGTGCAGTACAGAGGCGCTTT--CGGCCCTCGCGGGGGTGCATTGT [5400]
Xtr TGCAATGTTTCTTCAGTGCAGTATGGTGGTTCCAG--TGACTGCCGCTGTGGTGCATTGT [5895]
Lch TGCAATGTGTCTGCAGTGCAGTACAGAGAATCTCC--TAGCTGCAGCTGTGGTGCATTGT [6242]
Dre ---------------------------------------------------------- [6075]

Hsa TGTTGCATTGCACGTGTGTGAG-GCGGGTGCAGTGCCTCGGCAGTGCAGCCCGGAGCCGG [6193]
Mmu ---------------------------------------------------------- [6113]
Mdo ---------------------------------------------------------- [5799]
Meu ---------------------------------------------------------- [4965]
Oan AGTTGCATTGCATGTGTCTGAC-CAGGGTGCAATGCCCCTGCAGTGCAATACAGAGCCAG [5441]
Aca AGTTGCATTGCATGTGT-GGCCAAGCTGTGCAATGCCCCTCCAGTGCAGCCCTGAGGCCG [6120]
Pbi AGTTGCATTGCACGTGCAGGTGAAGATGTGCAATGCCCCTCCAGTGCAGCCCTGGGGCAG [6183]
Cpi AGTTGCATTGCATGTGTGAGAACAGGTGTGCAATGCCCCTGCAGTGCAGCCCAGATGGGG [6536]
Cmy AGTTGCATTGCATGTGTGAGAACAGGTGTGCAATGCCCCTGCAGTGCAGCCCAGATGGGG [6283]
Psi ---------------------------------------------------------- [5869]
Asp ---------------------------------------------------------- [5710]
Ami AGTTGCATTGCATGTGTCACAG-AGGTGTGCAATGCCTCTGCAGTGCAGCCCAGAGGAGG [6109]
Asi AGTTGCATTGCATGTGTCACAG-AGGTGTGCAATGCCTCTGCAGTGCAGCCCAGAGGAGG [6166]
Tgu ---------------------------------------------------------- [4861]
Cli AGTTGCATTGCATGTGTCAGACTGGGAGTGCAATGCCCCTGCCATGCAGCCCGGCGGGGG [5959]
Gga AGTTGCATTGCATGTGTCAGACTGGGAGTGCAATGCCCCTGCCATGCAGCCCGGCGGGGG [5460]
Xtr AGTTGCATTGCATGTGATATCAGCGGTGTGCAATGTGCCTGCAGTGCAACACAGAGGTAG [5955]
Lch AGTTGCATTGCATGTGTCTGTCAGGTTGTGCAATGCACCTGCAATGCAATACGGAGTCTG [6302]
Dre ---------------------------------------------------------- [6075]

Hsa CCCC--GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAGCAATAGT-AAGGAAGCA [6250]
Mmu ------GTAATTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAGTATTAGCTAAGGAAGCA [6167]
Mdo ------GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAGTAATAGATAAGGAAGCA [5853]
Meu ------GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAGTAATACATGAGGAAGCA [5019]
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Oan CCCC---------------------------------------------------------- [5445]
Aca TCCT--GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGCGCAGTGATTGAGGAAGCA [6178]
Pbi CATC--GTGCTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGTGCGATGATTGAAGCAGCA [6241]
Cpi CTTC--GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAGCAATAATCAAGGAAGCA [6594]
Cmy CTTC--GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAGCAATAATCAAGGAAGCA [6341]
Psi ------GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAGCAATAATCAAGGAAGCA [5923]
Asp ------GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAGCAATAATCAAGGAAGCA [5764]
Ami CTCC--GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAACAATAGACAAGGAAGCA [6167]
Asi CTCC--GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAACAATAGACAAGGAAGCA [6224]
Tgu ------GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAGCAATAGTCAAGGAAGCA [4915]
Cli CCCC--GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAGCAATAGTCAAGGAAGCA [6017]
Gga TCCC--GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGAGCAATAGTTAAGGAAGCA [5518]
Xtr TGCC--GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGGCACGTTATAGAAGTAGCA [6013]
Lch GCTA--GTGTTTCTTTGGCAGTGTCTTAGCTGGTTGTTGTGACAAGTAATAGAAAAAGCA [6360]
Dre ------GTGGTTCTCTGGCAGTGTCTTAGCTGGTTGTTGTGTGGAGTGAG-AACGAAGCA [6128]

Hsa ATCAGCAAGTATACTGCCCTAGAAGTG--GCTCGGTTTGTAGGCAGTGTCATTAGCTGAT [6308]
Mmu ATCAGCAAGTATACTGCCCTAGAAGTG--GCTCGGTTTGTAGGCAGTGTAATTAGCTGAT [6225]
Mdo ATCAGCAAGTATACTGCCCTAGAAGTG--GCTCGGTTTGTAGGCAGTGTAGTTAGCTGAT [5911]
Meu ATCAGCAAGTATACTGCCCTAGAAGTG--GCTCGGTTTGTAGGCAGTGTAGTTAGCTGAT [5077]
Oan ----------------------------GCTCGGTTTGTAGGCAGTGTAGTTAGCTGAT [5476]
Aca ATCAGCAAGAATACTGCCCCAGAAGTG--GCTTGGTTTGTAGGCAGTGTAGTTAGCTGAT [6236]
Pbi ATCAGCAAGCATACTGCTGCAGAAGTA--GTTTGGTTTGTAGGCAGTGTAGTTAGCTGAT [6299]
Cpi ATCAGCAAGTATACTGCCCTAGAAGTG--GTTTGGTTTGTAGGCAGTGTAGTTAGCTGAT [6652]
Cmy ATCAGCAAGTATACTGCCCTAGAAGTG--GTTTGGTTTGTAGGCAGTGTAGTTAGCTGAT [6399]
Psi ATCAGCAAGTATACTGCCCTAGAAGTG--GTTTGGTTTGTAGGCAGTGTAGTTAGCTGAT [5981]
Asp ATCAGCAAGTATACTGCCCTAGAAGTG--GTTTGGTTTGTAGGCAGTGTAGTTAGCTGAT [5822]
Ami ATCAGCAAGTATACTGCCCTAGAAGTG--GTTTGGTTTGTAGGCAGTGTAGTTAGCTGAT [6225]
Asi ATCAGCAAGTATACTGCCCTAGAAGTG--GTTTGGTTTGTAGGCAGTGTAGTTAGCTGAT [6282]
Tgu ATCAGCAAGTATACTGCCCTAGAAGTG--GCTTGGTTTGCAGGCAGTGTAGTTAGCTGAT [4973]
Cli ATCAGCAAGTATACTGCCCTAGAAGTG--GCTTGGTTTGTAGGCAGTGTAGTTAGCTGAT [6075]
Gga ATCAGCAAGTATACTGCCCTAGAAGTG--GCTTGGTTTGCAGGCAGTGTAGTTAGCTGAT [5576]
Xtr ATCAGCAAATATACTGCCCTAGAAGTT--GTTGGGTTTTCAGGCAGTGTAGTTAGCTGAT [6071]
Lch ATCAGCAAGTATACTGCTGCAGAAATG--GCTTAGTTTGTAGGCAGTGTAGTTAGCTGAT [6418]
Dre ATCAGCAAGTATACTGCCGCAGAAACT--GGTTGGTCTGTAGGCAGTGTTGTTAGCTGAT [6186]

Hsa TGTACTG---TGGTGGTTACAATCACTAACTCCACTGCCATCAAAACA--GTCTAGTTAC [6363]
Mmu TGTAGTG---CGGTGCTGACAATCACTAACTCCACTGCCATCAAAACA--GTCTAGTTAC [6280]
Mdo TGTATTC---TACTGCCTACAATCACTAACTCCACTGCCATCAAAACA--GTCTAGTTAC [5966]
Meu TGTATTC---TACTGCCTGCAATCACTAACTCCACTGCCATCAAAACA------------ [5122]
Oan TGGACCA---TCCCGCCCGCAATCACTAACTCCACTGCCATCAAAACA--GTCTAGTTAC [5531]
Aca TGTGAGG---TTTCCTTGGCAATCACTAGCTTTACTGTCATCAAAACA--GCCTGGTTGC [6291]
Pbi TGTGTG----TCTCCCCAGCAATCACTAGCTTCACTGTCATCAAAACA--GCCTTGTCAC [6353]
Cpi TGTATCC---ATCTCTTTGCAATCACTAACTTTACTGCCATCAAAACA--GCCTAGTTAC [6707]
Cmy TGTATCC---ATCTCTTTGCAATCACTAACTTTACTGCCATCAAAACA--GCCTAGTTAC [6454]
Psi TGTATCC---ATCTATTTGCAATCACTAACTTTACTGCCATCAAAACA--GCCTAGTTAC [6036]
Asp TGTATCC---ATCTATTTGCAATCACTAACTTTACTGCCATCAAAACA--GCCTAGTTAC [5877]
Ami TGTGTCA---GTCCCTTGGCAATCACTAACTTCACTGCCATCAAAACA--GCCTAGTTGC [6280]
Asi TGTGTCA---GTCCCTTGGCAATCACTAACTTCACTGCCATCAAAACA--GCCTAGTTGC [6337]
Tgu TGTCTGC---AGAATTCCACAATCACTAACTTCACTGCCACCAAAACA--GCCTGGTTGC [5028]
Cli TGTAACC---ACTGCTCCGCAATCACTACACTCACTGCCATCAAAACA--GCCTAGTTAC [6130]
Gga TGTACCC---AGCGCCCCACAATCACTAAATTCACTGCCATCAAAACA--GCCTGGTTAC [5631]
Xtr TGTGTTAACATAAGACTTGCAATCACTAGCTAAACTACCAGCAAAACT------------ [6119]
Lch TGTGTCC--CTGCAGTCTGCAATCACTAACCACACTACCATCAAAACA--GCCTAGTTAC [6474]
Dre TGTTTCA---TATGAACTATAATCACTAACCATACTGCCAACACAACA--GTGTGGTCAC [6241]

Hsa TAGGCAGTGTAGTTAGCTGATTGCTAAT---AGTACCAATCACTAACCACACGGCCAGGT [6420]
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Mmu TAGGCAGTGTAGTTAGCTGATTGCTAAT---AGTACCAATCACTAACCACACAGCCAGGT [6337]
Mdo TAGGCAGTGTAGTTAGCTGATTGCTAGCAGTAGTACCAATCACTAACCACACAGCCAAGT [6026]
Meu ------------------------------------------------------------ [5122]
Oan TAGGCAGTGTAGTTAGCTGATTGCTATT---AACACCAATCACTAGCCACACAGCCAGGT [5588]
Aca CAGGCAGTGTAGTTAGCTGATTGACGA----GGCAACAGTCACTAACAACACGGCCAGGT [6347]
Pbi CAGGCAGTGTAGTTAGCTGATTGACAAA---GGCAACAGTCGCTAACAACACAGCCAAGT [6410]
Cpi CAGGCAGTGTAGTTAGCTGATTGCTAAA---GGTA-CAATCACTAACCACACAGCCAGGT [6763]
Cmy CAGGCAGTGTAGTTAGCTGATTGCTAAA---GGTAACAATCACTAACCACACAGCCAGGT [6511]
Psi CAGGCAGTGTAGTTAGCTGATTGCCAAA---GGTAACAATCACTAACCACACAGCCAGGT [6093]
Asp CAGGCAGTGTAGTTAGCTGATTGCCAAA---GGTAACAATCACTAACCACACAGCCAGGT [5934]
Ami TAGGCAGTGTAGTTAGCTGATTGCAAAA---GGCAACAATCACTAACCACACAGCCAGGT [6337]
Asi TAGGCAGTGTAGTTAGCTGATTGCAAAA---GGCAACAATCACTAACCACACAGCCAGGT [6394]
Tgu CAGGCAGTGTAGTTAGCTGATTGCCCAA---AGCAACAATCACTAGCCACACGGCCAGGT [5085]
Cli TAGGCAGTGTAGTTAGCTGATTGCCAAA---AGTACCAATCACTAGCCACACAGCCAGGT [6187]
Gga CAGGCAGTGTAGTTAGCTGATTGCCACC---AGGACCAATCACTAACCACACAGCCAGGT [5688]
Xtr ------------------------------------------------------------ [6119]
Lch TAGGCAGTGTCGTTAGCTGATTGGTAAC---AGCAGCAATCACTAACCACACAGCCAGGT [6531]
Dre CAGGCAGTGCAGTTAGTTGATTACAATCCA-TAAAGTAATCACTAACCTCACTACCAGGT [6300]

Hsa AAAA--TGTGATGAGCTGGCAGTGTATTGTTAGCTGGTTGAATATGTGAATGGCATCGGC [6478]
Mmu AAAA--TGTGATGGCTTGGCAGTGTATTGTTAGCTGGTTGAGTATGTGAGCGGCACCAGC [6395]
Mdo AAAC--TGTGATGGGATGGCAGTGTATTGTTAGCTGGTTGACTATCTGAACG-TGCCAGC [6083]
Meu ------TGTGATGGGATGGCAGTGTATTGTTAGCTGGTTGAATATCTGAAT-GTACCAGC [5175]
Oan AAAA--TGCGATAGTTTGGCAGTGT-TTGTTAGCTGGTTGAATATTTAAATGGCACCAGC [5645]
Aca GAAA--TGTGGTGGAATGGCAGTGTATTGTTAGCTGGATGAGTATCTCAATGCCCCCAGC [6405]
Pbi GAAA--TGTAGTGGAATGGCAGTGTATTGTTAGCTGGATGGATATCCAAATGGCACCAGC [6468]
Cpi AAAA--TGTGCTAGGAAGGCAGTGTATTGTTAGCTGGT----TGAAAATCTGACAGCAGC [6817]
Cmy AAAA--TGTGCTAAGAAGGCAGTGTATTGTTAGCTGGT----TGAAAATCCGACACCAGC [6565]
Psi AAAA--TGTGCTGGGAAGGCAGTGTATTGTTAGCTGGT----TGAACATCTGACACCAGC [6147]
Asp AAAA--TGTGCTGGGAAGGCAGTGTATTGTTAGCTGGT----TGAACATCTGACACCAGC [5988]
Ami AAAA--TGTGATGGGAAGGCAGTGTACTGTTAGCTGGTG---TCAGTTTTTTCAACCAGC [6392]
Asi AAAA--TGTGGTGGGAAGGCAGTGTACTGTTAGCTGGTT---GAAAAAACTGACACCAGC [6449]
Tgu AAAA--TGTGATGGGATGGCAGTGTA-TGTTGGCTGCTTG----AAGTTCTGACAGCAGC [5138]
Cli AAAA--TGGGATGGGATGGCAGTGTG-TGTTAGCTGGTTG---AAATTCT-GACATCAGC [6240]
Gga AAAA--TGCGGTGGGGTGGCAGTGTA-TGTTAGCTGGTTG---AAACTCTTGACATCAGC [5742]
Xtr ------TTTAGAAGGAAGGCAGTGTAATGTTAGCTGGTTG-GAAAATAGCAGACACTGGT [6172]
Lch AAAC------------------------------------------------------- [6535]
Dre GAAG------------------------------------------------------- [6304]

Hsa TAACATGCAACTGCTGTCTTATT--GAATCAGGTAGGCAGTGTATTGTTAGCTGGCTGC- [6535]
Mmu TAACATGCGACTGCTCTCCTATT--GAATCAGGTAGGCAGTGTATTGTTAGCTGGCTGC- [6452]
Mdo TAACATGCAACTGCTATCCCATT------------------------------------- [6106]
Meu TACTATGCAACTGCTGTCCTATT--GGGTCAGGTAGGCAGTGTGCTGTAAGCTGGCTGCT [5233]
Oan TGACAGACAGCTGCTTTCCTATT--GGGTCAAGTAGGCAGTGTGATGTTTGCTGGCTGCT [5703]
Aca TGACATTCAGCTGCCAATCTACG------------------------------------ [6428]
Pbi TGACATTCAGCTGCCAGCCTACG--GTGACTGATAGGCAGTGTAGAATTAGCTGGCTGCT [6526]
Cpi TAACCTACATCTGCTATCTTATT--GTGTCTGGTAGGCAGTGTACTGTTAGCTGGCTGCT [6875]
Cmy TAACTTACACCTGCTATCTTATT--GTGTCTGGTAGGCAGTGTACTGTTAGCTGGCTGCT [6623]
Psi TAACTTACAGCTGCTATCTTATT--GTGTCTGGTAGGCAGTGTACTGTTAGCTGGCTGCT [6205]
Asp TAACTTACAGCTGCTATCTTATT--GTGTCTGGTAGGCAGTGTACTGTTAGCTGGCTGCT [6046]
Ami TAACATGCAGCTGCTATCCTACT--GTGTCTGGTAGGCAGTGTACTGTTAGCTGGCTGCT [6450]
Asi TAACATGCAGCTGCTATCCTACT--GTGTCTGGTAGGCAGTGTACTGTTAGCTGGCTGCT [6507]
Tgu TAACATGCTGCTGCTCTCTCTTC------------------------------------ [5161]
Cli TAACATGCAGTTGCTATCCTTTT--GTGTCTGGTAGGCAGTGTACTGCTAGCTGGCTGCC [6298]
Gga TAACACGCAGTTGCTAACCTGCT--GTGGCTGGAAGGCAGTGTGCTGTTAGC-GGCTGCT [5799]
Xtr TAACTTACACCTGCCCCCCTTCT--GCTTTGGGTAGGCAGTGTAGTTTTAGCTGGCTGCT [6230]
Lch ------------------------GCATCAAGTAGGCAGTGTACTGTTAGCTGGCTGCT [6570]
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Dre ------------------------------------------------------------ [6304]

Hsa TTGGGTCAAG--TCAGCAGCCACAACTACCCTGCCACTTGCTT--ATGTGTCAGGTAGGC [6591]
Mmu TTGGGTCAAG--TCAGCAGCCACAACTACCCTGCCACTTGCTT--GTGTGTCAGGCAGGC [6508]
Mdo ------------------------------------------------------------ [6106]
Meu TGGGTTCAGT--TCAGCAGTCACAACCACCCTGCCACTTGCTC----------------- [5274]
Oan TTGAATCGAT--TCAGCAGCCACCGTTACTCTGCCACTTGCTA--ATGTGCCGGTTTGGC [5759]
Aca ----------------------------------------CTGTGTCGCTTTGGC [6443]
Pbi TTGT-TTAATT-CTAGCAGTCGCTACCACACTGCTATCTGCTG--GTGTGTCACTTTGGC [6582]
Cpi TTGTGTGAAT--CTAGCAGTCTCTACTACACTGTCACCTGCTG--ATGTGACAGTTTGGC [6931]
Cmy TTGTGTGAAT--CTAGCAGTCTCTACTACACTGTCACCTGCTG--ATGTGACAGTTTGGC [6679]
Psi TTGTGTGGAT--CTAGCAGTCTCTACTACACTGTCACCAGCTG--ATGTGACAGTTTGGC [6261]
Asp TTGTGTGAAT--CTAGCAGTCTCTACTACACTGTCACCAGCTG--ATGTGACAGTTTGGC [6102]
Ami TTGTGTGAAT--CTAGCAGTCGCTACTGCACTGTCAACAGCTG--ATGTTTCAGTTTGGC [6506]
Asi TTGTGTGAAT--CTAGCAGTCGCTACTGCACTGTCAACAGCTG--ATGTTTCAGTTTGGC [6563]
Tgu ------------------------------------------------------------ [5161]
Cli GTATCTGGAT--GGAGCAGTCACTCCTGCACTGCCACCTGCTG--ATGTAACAGTCTGGC [6354]
Gga GTGC-TGAAT--GGAGCAGTCACTACCACACTGCCACCTGCTG--ATGTAACAGTCTGGC [5854]
Xtr TGCTATTAACT-CCAGCAGTCGCTAATACTCTGCCACCGGCAG--TTGGACCAATGAGGC [6287]
Lch GGGTTTCTGCGGATAGCAGTCGCTACTACTCTGCCACCTGTTG--ATGCTTCAGTTAGGC [6628]
Dre ------------------------------------------------------------ [6304]

Hsa AGTGTA-TTGCTAGC-GGCTGTTAA-------TGATTTTAACAGTTGCTAGTTGCACTCC [6642]
Mmu AGTGCA-TTGCTAGCTGGCTGTTAGA---ACTTTATCCCAACAGTTGCTAGCTGCACTAC [6564]
Mdo ------------------------------------------------------------ [6106]
Meu ------------------------------------------------------------ [5274]
Oan AGTGCT-TTGCTAGCTGGCTGTTCAA-----TAAATGATTCCAGCAGCTGGTTGCACGCC [5813]
Aca AGTGCA-CTACTAGCTGGCTGTTGAGATATATTCATTTTTACAGTGGTTAGTTGCACTCC [6502]
Pbi AGTGCA-GTACTAGCTGGCTGTTTGGATACCTTCTGTGTTACAGCAGCTGGTTGCACTCC [6641]
Cpi AGTGCC-TTGCTAGCTGGCTGTTGAGAACTTGATATATGAACAGTTGCTAGCTGCACTCC [6990]
Cmy AGTGCA-TTGCTAGCTGGCTGTTGAGAACTTGATATATGAACAGTTGCTAGCTGCACTCC [6738]
Psi AGTGCA-CTGCTAGCTGGCTGTTGAAAACTTTGTATATGAACAGTTGCTAAGTGCACTCC [6320]
Asp AGTGCA-CTGCTAGCTGGCTGTTGAAAACTTTGTATATGAACAGTTGCTAACTGCACTCC [6161]
Ami AGTGCA-TTGCTAGCTGGCTGTTGTG---TACGTGTGTTAACAGTTGCTAGCTGTACTCC [6562]
Asi AGTGCA-TTGCTAGCTGGCTGTTGTG---TACGTGTGTTAACAGTTGCTAGCTGTACTCC [6619]
Tgu ------------------------------------------------------------ [5161]
Cli AGTGCA--TGTTAGCTGGCTGTTGTG--TCTGATGTGTCAACAGCTGCTAGCTGTGCTCC [6410]
Gga AGTGCA--TGTTAGCTGGCTGTTGTG--TCTGATGTGTCAACAGCTGCTAGCTGTGCTCC [5910]
Xtr AGTGCACTTGCTAGCTGGCTGTTGTG--TTCTGGAAGCTTACAGCTGCTAGCTGCACTCC [6345]
Lch AGTGTA-TTGCTAGCTGGCTGTTGTGTATTTGACAGGTCAACAGCTGCTGGGTACACTCC [6687]
Dre ------------------------------------------------------------ [6304]

Hsa TCTCTGTTGC---------------------------------------------------- [6652]
Mmu CCTCTGCTGC---------------------------------------------------- [6574]
Mdo ------------ATGTGGTGATTGGGCAGTGTATT-GTTAGTTAGCTGTTTTTCATAAGT [6153]
Meu ------------GTGTGGTGATTGGGCAGTGTATT-GTTAGTTAGCTGTTTTTCATAATT [5321]
Oan CCACTGTCAC---------------------------------------------------- [5823]
Aca ACACTGATGC--ATGTGATGGTTTGGCAGTGTACT-CTTAGTTAGCTGTTGTATATATTA [6559]
Pbi AGAGTGCTGC--GTGTGATGGTTTGGCAGTGTACTTCTTAGTTAGCTGTTGTACATATTC [6699]
Cpi ACATTGTTGC--ATGTGCTGATTAGGCAGTGTATT-GTTAGTTAGCTGTTGTTCACATAC [7047]
Cmy ACATTGTTGC--ATGTGCTGATTAGGCAGTGTATT-GTTAGTTAGCTGTTGTTCACATAC [6795]
Psi ACATTGTTGC--GTGTACTGATTAGGCAGTGTATT-GTTAGTTAGCTGTTGCTTACATAC [6377]
Asp ACATTGTTGC--GTGTACTGATTAGGCAGTGTATT-GTTAGTTAGCTGTTGCTTACATAC [6218]
Ami ATATTGTTGC--GTGTGATGATTAGGCAGTGTATT-GTTAGTTAGCTGGCATTCACATAC [6619]
Asi ATATTGTTGC--GTGTGATGATTAGGCAGTGTATT-GTTAGTTAGCTGGCATTCACATAC [6676]
Tgu ------------GTGTGGTGATTAGGCAGTGTATT-GTTAGTTAGCTGTTCCTCACACAC [5208]
Cli ACATTGTTTC--GTGTGGTGATGAGGCAGTGTATT-GTTAGTTAGCTGTTCTTCATACAC [6467]
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Gga ACATTGTTTC--GTGTGGTGATTAGGCAGTGTATT-GTTAGTTAGCTGCGCTTCATACAC [5967]
Xtr ACATTGTTTC---------------------------------------------------- [6355]
Lch ACATTGCTGC--GTGCGGTGATTAGGCAGTGTAAT-GTTAGCTGACTGTGATTTACATAT [6744]
Dre ------------------------------------------------------------ [6304]

Hsa --------------------------------TTCTACACAGGTTGGGATCGGTTGCAAT [6680]
Mmu --------------------------------TTCTACACAGGTTGGGATTTGTCGCAAT [6602]
Mdo GCAGCAACTGCATACACTTCCATATTTCCA--TTCTACACAGGTTGGGATCAGTTGCAAT [6211]
Meu ACAGCAACTGCATACACTTCCATATTTCCA---------------------------- [5351]
Oan --------------------------------TTCTACGCAGGTTGGGATCAGTTGCAAT [5851]
Aca -CAGCAACTAAATACACTTCCATATTATTG--TTCTACACAGGTTGGGATTGGTTGCAAT [6616]
Pbi -CAGCAACTAAATACACTTCCATATTATTG--TTCTACACAGGTTGGGATCGGTTGCAAT [6756]
Cpi -CAGCAACTAAATACGCTTCCACATTAGCA--TTCTACACAGGTTGGGATCAGTTGCAAT [7104]
Cmy -CAGCAACTAAATACACTTCCACATTAGCA--TTCTACACAGGTTGGGATCAGTTGCAAT [6852]
Psi -CAGCAACTAAATACACTTCCACATTAGCA--TTCTACACAGGTTGGGATTAGTTGCAAT [6434]
Asp -CAGCAACTAAATACACTTCCACATTAGCA--TTCTACACAGGTTGGGATTAGTTGCAAT [6275]
Ami -CAGCAACTAAACACACTTCCACATTAGCA--TTCTACACAGGTTGGGATCAGTTGCAAT [6676]
Asi -CAGCAACTAAACACACTTCCACATTAGCA--TTCTACACAGGTTGGGATCAGTTGCAAT [6733]
Tgu -CAGCAACTGACTACACTGTCAGATTAGCA--TTCTACACAGGTTGGGATCAGTTGCAAT [5265]
Cli -CAGCAACTGACTACACTGCCACATCAACA--TTCTACACAGGTTGGGATCAGTTGCAAT [6524]
Gga -CAGCAACTAACTACACTGCCACATTAGCA--TTCTACACAGGTTGGGATCAGTTGCAAT [6024]
Xtr --------------------------------TTCTGTATAGGTTGGGATTGGTTGCAAT [6383]
Lch -GAGCAACTACATGCACTATCATATTTGCG--TTCTACGCAGGTTGGGATTAGTTGCAAT [6801]
Dre --------------------------------TTCTGCGCAGGTTGGGATTGGTAGCAAT [6332]

Hsa GCTGTGTTT--CTGTATGGTATTGCACTTGTCCCGGCCTGTTGAGTTT--TCATCCCTGG [6736]
Mmu GCTGTGTTTCTCTGTATGGTATTGCACTTGTCCCGGCCTGTTGAGTTT--TCATCCACAG [6660]
Mdo GCTGTGTCT--GTCTGTAGTATTGCACTTGTCCCGGCCTGTTGAGTTT--TTCTCTGCGG [6267]
Meu ------------------------------------------------TTCTCTGCGG [5361]
Oan GCTTTGTTT--GTCTATGGTATTGCACTTGTCCCGGCCTGTTGAGGTT--TCCTCCATGG [5907]
Aca GCTGTCTATGTGTATGTGGTATTGCACTTGTCCCGGCCTGTTGAGGTT--TTCTCCCTGG [6674]
Pbi GCTGTGTTG-AGTCTGTGGTATTGCACTTGTCCCGGCCTGT-GAGGTT--TCCTCCGTGG [6812]
Cpi GCTGTGTGT--GCCTGTAGTATTGCACTTGTCCCGGCCTGTTGAGGTT--TTCTCCATGG [7160]
Cmy GCTGTGTGT--GTCTGTAGTATTGCACTTGTCCCGGCCTGTTGAGGTT--TTCTCCATGG [6908]
Psi GCTGTGTGT--GCCTGTAGTATTGCACTTGTCCCGGCCTGTTGAGGTT--TTCTCCATGG [6490]
Asp GCTGTGTGT--GCTTGTAGTATTGCACTTGTCCCGGCCTGTTGAGGTT--TTCTCCATGG [6331]
Ami GCTGTGTGT--GTCTGTGGTATTGCACTTGTCCCGGCCTGTTGAGGTT------------ [6722]
Asi GCTGTGTGT--GTCTGTGGTATTGCACTTGTCCCGGCCTGTTGAGGTT--TTCTCCATGG [6789]
Tgu GCTGTGTGT--GTCTGTGGTATTGCACTTGTCCCGGCCTGTTGAGGTT--TTCTCCATGG [5321]
Cli GCTGTGTGT--GTCTCTGGTATTGCACTTGTCCCGGCCTGTTGAGGTT--TTCTCCATGG [6580]
Gga GCTGTGCGT--TTCTGTGGTATTGCACTTGTCCCGGCCTGTTGAGGTT--TCCTCCGTGG [6080]
Xtr GCTGTACTA-TTTATGTAGTATTGCACTTGTCCCGGCCTGTTTAGGAT--TCCTCTGTGG [6440]
Lch GCTGTATGT--TGCTGAAGTATTGCACTTGTCCCGGCCTGTTGAGGAC--TTCTGTATGG [6857]
Dre GCTGTGTGT--TTTGAAGGTATTGCACTTGTCCCGGCCTGTAAAGGAT------------ [6378]

Hsa GTGGGGATTTGTTGCATTACTTGTGT---TCTATA-TA-AAGTATTGCACTTGTCCCGGC [6791]
Mmu GTGGGGATTGGTGGCATTACTTGTGT---TAGATA-TA-AAGTATTGCACTTGTCCCGGC [6715]
Mdo GTGGGGATTTGTTGCATTACTTGATCATGTGACTA-TAAGAGTATTGCACTTGTCCCGGC [6326]
Meu GTGGGGATTTGTTGCATTACTTGATCTTGTGTCTA-TAAGAGTATTGCACTTGTCCCGGC [5420]
Oan GTGGGGATTTGTTGCATTACTTGTAGC--TATGTT-TA-GAGTATTGCACTTGTCCCGGC [5963]
Aca GTTGGGATTTGTTGCATTACTTGTGGGT-TCCCTG-AA-CAGTATTGCACTTGTCCCGGC [6731]
Pbi GTTGGGATTTGTTGTATTACTCGGAGA--TCTCTG-AA-CAGTATTGCACTTGTCCCGGC [6868]
Cpi GTGGGGATTTGTTGCATTACTTGTAGC--TATGTG-TA-GAGTATTGCACTTGTCCCGGC [7216]
Cmy GTGGGGATTTGTTGCATTACTTGTAGC--TATGTG-TA-GAGTATTGCACTTGTCCCGGC [6964]
Psi GTGGGGATTTGTTGCATTACTTGTAGC--TATGTG-CA-GAGTATTGCACTTGTCCCGGC [6546]
Asp GTGGGGATTTGTTGCATTACTTGTAGC--TATGTG-CA-GAGTATTGCACTTGTCCCGGC [6387]
Ami ------------------------------------------------------------ [6722]
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Asi GTGGGGATTTGTTGCATTACTTGTAGC--TATGTT-TA-GAGTATTGCACTTGTCCCGGC [6845]
Tgu GTGGGGATTTGTTGCATTACTTGTAGC--TGTATG-TA-GAGTATTGCACTTGTCCCGGC [5377]
Cli GTGGGGATTTGTTGCATTACTTGTAGC--TGTATG-TA-GAGTATTGCACTTGTCCCGGC [6636]
Gga GTGGGGATTTGTTGCATTACTTGTAGC--TGTGTG-TA-GAGTATTGCACTTGTCCCGGC [6136]
Xtr GTGGGGATTTGTTGCACTACT-GTA----TGTATG-AA-AAGTATTGCACTTGTCCCGGC [6493]
Lch GTGGGGACTTGTTGCATTACTTCA-----TATATT-AA-AAGTATTGCACTTGTCCCGGC [6910]
Dre ------------------------------------------------------------ [6378]

Hsa CTGTGGAAG--CAGTGTTGAGAGGCGGAGACTTGGGCAATTGCTGGACGCTGCCC-TGGG [6848]
Mmu CTGAGGAAG--CAGTGTTGAGAGGCGGAGACTTGGGCAATTGCTGGACGCTGCCC-TGGG [6772]
Mdo CTGTGGAGG--CAGTGTTGAGAGGCGGAGACTTGGGCAATTGCTGAACTCTGCCC-TGGG [6383]
Meu CTGTGGAGG---------------------------------------------------- [5429]
Oan CTGTGGAGG---------------------------------------------------- [5972]
Aca CTGTGGAGG---------------------------------------------------- [6740]
Pbi CTGTGGAGG---------------------------------------------------- [6877]
Cpi CTGTGGAGG---------------------------------------------------- [7225]
Cmy CTGTGGAGG---------------------------------------------------- [6973]
Psi CTGTGGAGG---------------------------------------------------- [6555]
Asp CTGTGGAGG---------------------------------------------------- [6396]
Ami ------------------------------------------------------------ [6722]
Asi CTGTGGAGG---------------------------------------------------- [6854]
Tgu CTGTGGAGG---------------------------------------------------- [5386]
Cli CTGTGGAGG---------------------------------------------------- [6645]
Gga CTGTGGAGG---------------------------------------------------- [6145]
Xtr CTGTGGGTG--TGGTGTTGACAGGCAGAGACAGGAGCAACTGCTGGTGTGCCTTG-GTAG [6550]
Lch CTGTGGAGG--TAGTGTTGAGAGGCGGAGACTTGGGCAATTGCTGGCAATCCCAG-AGGG [6967]
Dre -----------CGGCGCTGAGAGGCGGAGACTTGGGCAGCTGCCGTCATTCCCAG-AAGG [6426]

Hsa CATTGCACTTGTCTCGGTCTGACAGTGCCG--GCGGGCGGGAGGGACGGGACGCGGTGCA [6906]
Mmu CATTGCACTTGTCTCGGTCTGACAGTGCCG--GTGGGCGGGAGGGACGGGACGTGGTGCA [6830]
Mdo CATTGCACTTGTCTCGGTCTGACAGTGCTG--GCGGGCGGGAGGGACGGGACGTGGTGCA [6441]
Meu ------------------------------------------------------------ [5429]
Oan ------------------------------------------------------------ [5972]
Aca ------------------------------------------------------------ [6740]
Pbi --------------------------------GTTGGGGGCAGGGTTGGGGCTGAGTGCA [6905]
Cpi --------------------------------GGCAGCAGGAGGGACGGGATGCTGTGCA [7253]
Cmy --------------------------------GGCAGCAGGAGGGACGGGATGCTGTGCA [7001]
Psi --------------------------------GGTAGCAGGAGGGACGGGATGTTGTGCA [6583]
Asp ----------------------------------------AGGGACGGGATGTTGTGCA [6415]
Ami --------------------------------GGCGGCGGGAGGGCCGGGATGCGGTGCA [6750]
Asi ------------------------------------------------------------ [6854]
Tgu ------------------------------------------------------------ [5386]
Cli --------------------------------GGCGGCGGGAGGGCCGGGATGCGGTGCA [6673]
Gga ------------------------------------------------------------ [6145]
Xtr CATTGCACTTGTCTCGGTCTGACAGTGTCG--------AGAAGGATCGGGATGTTGTGCA [6602]
Lch CATTGCACTTGTCTCGGTCTGACAGTGCTG--CTGACCTGAAGGAACGGGATGTGGTGCA [7025]
Dre CATTGCACTTGTCTCGGTCTGACAGTGGCG--CGGGCAGGGAGGTGTGGGATGTTGTGCA [6484]

Hsa GTGTTGTTTTTTCCCCCGCCAATATTGCACTCGTCCCGGCCTCCGGCCCCCCC--CTGCT [6964]
Mmu GTGTTGTTCTTTCCCCTGCCAATATTGCACTCGTCCCGGCCTCCGGCCCCCTC--CTGCT [6888]
Mdo GTGTTGTTCTTTCCCC-GCCAATATTGCACTCGTCCCGGCCTCCGGCCCCCCC--CTGCT [6498]
Meu ----------------------------------------------------CTGCT [5434]
Oan ----------------------------------------------------CTGCT [5977]
Aca ------------------------------------------------------------ [6740]
Pbi ATGTTGTGATTTTTCCCACGAATATTGCACTCGTCCTGGCCTCCCGCTGTTCT--CTGCT [6963]
Cpi GTGTTGTTCTATCACCAACCAATATTGCACTCGTCCCGGCCTCCTGCCTCCTT--CTGCT [7311]
Cmy GTGTTGTTCTATCACCAACCAATATTGCACTCGTCCCGGCCTCCTGCCTCCCT--CTGCT [7059]
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Psi GTGTTGTTCTATCCCCTGCCAATATTGCACTCGTCCCGGCCTCCTGCCTCCTT--CTGCT [6641]
Asp GTGTTGTTCTATCCCCTGCCAATATTGCACTCGTCCCGGCCTCCTGCCTCCTT--CTGCT [6473]
Ami GTGTTGTGC-GTCTCCTACCAATATTGCACT----------------------CTGCT [6785]
Asi ----------------------------------------------------CTGCT [6859]
Tgu ---------------------------------------------------------- [5386]
Cli GTGTTGTGCTCTCGCCCACCAATATTGCACTCGTCCCGGCCTCCCGCCGCCGC--CCGCC [6731]
Gga ----------------------------------------------------CCGCC [6150]
Xtr CTGTTGTCCTTTCTCCTGCCAATATTGCACTCGTCCCGGCCTCCTGCGTCTCT--CTGTC [6660]
Lch TTGTTGTCGTATCTCCTGCCAATATTGCACTCGTCCCGGCCTCCTGG-TCTCC--CTTCT [7082]
Dre GTGTTGTTCAATCTCCCGCCAATATTGCACTCGTCCCGGCCTCCCTGACCACG--CTTCT [6542]

Hsa TGGCCGATTTTGGCACTAGCACATTTTTGCTTGTGTCT--CTCCGCTCTGAGCAATCATG [7022]
Mmu TGGCCGATTTTGGCACTAGCACATTTTTGCTTGTGTCT--CTCCGCTGTGAGCAATCATG [6946]
Mdo TGGCCCGTTTTGGCACTAGCACATTTTTGCTTCTGTCT--CTCTGCTCTGAGCAATCATG [6556]
Meu TGGCCCGTTTTGGCACTAGCACATTTTTGCTTCTGTCT--GTCTGCTCTGAGCAATCATG [5492]
Oan TGGCCTCTTTTGGCACTAGCACATTTTTGCTTTTGTCT--CTCTGCTCTGAGCAATCATG [6035]
Aca ---------------------------------------------------------- [6740]
Pbi TGGCCCTTTTTGGCACTAGCACATTTTTGCTGTTCTCT--ATAAACATTGAGCAATTATG [7021]
Cpi TCGCCCGGTTTGGCACTAGCACATTTTTGCTTTTGTAT--AACTACTTTGAGCAATTATG [7369]
Cmy TCGCCCAGTTTGGCACTAGCACATTTTTGCTTTTGTGTCTATATACTTTGAGCAATTATG [7119]
Psi TTGCCCGTTTTGGCACTAGCACATTTTTGCTTTTGTAT--ATCTACTTTGAGCAATTATG [6699]
Asp TTGCCCGTTTTGGCACTAGCACATTTTTGCTTTTGTAT--ATATACTTTGAGCAATTATG [6531]
Ami TGGCCCATTTTGGCACTAGCACATTTTTGCTTTTGTAC--GTATACTTTGAGCAATTATG [6843]
Asi TGGCCCATTTTGGCACTAGCACATTTTTGCTTTTGTAC--GTATACTTTGAGCAATTATG [6917]
Tgu ---------------------------------------------------------- [5386]
Cli CGGCCCGTTTTGGCACTAGCACATTTTTGCTTTGATTT--GTAGCTTTTGAGCAATTATG [6789]
Gga CGGCCCGCTTTGGCACTAGCACATTTTTGCTTTGCTTT--ATGTGTTTTGAGCAATTATG [6208]
Xtr TGGCCTGCTTTGGCACTAGCACATTTTTGCTTTTGTAC--ATATACTTTGAGCAATTATG [6718]
Lch TTGCCCGTTTTGGCACTAGCACATTTTTGCTTCTGTCT--ATACATATTGAGCAATTATG [7140]
Dre TTGCCTGTTTTGGCACTAGCACATTTTTGCTTTTTTAT--ATATACCTTGAGCAATTATG [6600]

Hsa TGCAGTGCCAATATGGGAAAAGCAGG--CTCCCCCCGTTTTTGGCAATGGTAGAACTCAC [7080]
Mmu TGTAGTGCCAATATGGGAAAAGCGGG--CCACCACCATTTTTGGCAATGGTAGAACTCAC [7004]
Mdo TGTAGTGCCAATATGGGAAAAGCAAG--CTCCTGCTGTGTTTGGCAATGGTAGAACTCAC [6614]
Meu TGCAGTGCCAATATGGGAGAAGC-----CTCCTGCTGTGTTTGGCAATGGTAGAACTCAC [5547]
Oan TGTAGTGCCAATATGGGAAAAGCTGG--CTCCTGCTGTGTTTGGCAATGGTAGAACTCAC [6093]
Aca ---------------------------CTCCGGCTGTTTTTGGCAATGGTAGAACTCAC [6772]
Pbi TGTAGTGCCAATATGGGAGAAGTCAG--CTCTTGCTGTCTTTGGCAATGGTAGAACTCAC [7079]
Cpi TGTAGTGCCAATCTGGGAGAAGACGG--CTCTCGCTGTCTTTGGCAATGGTAGAACTCAC [7427]
Cmy TGTAGTGCCAATATGGGAGGAGACGG--CTCTGGCTGTCTTTGGCAATGGTAGAACTCAC [7177]
Psi TGTAGTGCCAATATGGGAGAAGATGG--CTCCCGCTGTCTTTGGCAATGGTAGAACTCAC [6757]
Asp TGTAGTGCCAATATGGGAGAAGATGG--CTCCCGCTGTCTTTGGCAATGGTAGAACTCAC [6589]
Ami TGTAGTGCCAATATGGGAGGAGATGG--CTCTCGCTGTCTTTGGCAATGGTAGAACTCAC [6901]
Asi TGTAGTGCCAATATGGGAGGAGATGG--CTCTCGCTGTCTTTGGCAATGGTAGAACTCAC [6975]
Tgu ---------------------------------------------------------- [5386]
Cli TGTAGTGCCAATATGGGAGAAGGCGG--CCGGGGCTGCTTTTGGCAATGGTAGAACTCAC [6847]
Gga TGTAGTGCCAATATGGGAGAAGGCGG--TCCTGGCTGCTTTTGGCAATGGTAGAACTCAC [6266]
Xtr TGTAGTGCCAATATAGGACTATACAG--CTCTGGCAGTGTTTGGCAATGGTAGAACTCAC [6776]
Lch TGTAGTGCCAATATGGGAAAAGTTGG--CTCTTGTGGTGTTTGGCAATGGTAGAACTCAC [7198]
Dre TGTAGTGCCAATATGGGACAAGACAG--CTCTGATGGTATTTGGCAATGGTAGAACTCAC [6658]

Hsa ACTGGTGAGGTAACAGGATCCGGTGGTTCTAGACTTGCCAACTATGGGGC-GAGG--ACT [7137]
Mmu ACCGGTAAGGTAATGGGACCCGGTGGTTCTAGACTTGCCAACTATGGTGT-AAGT--ACT [7061]
Mdo ACTGGTGAGATAATGGAATCCGGTGGTTCTAGACTTGCCAACTACGGCTT-GAGA--ACT [6671]
Meu ACTGGTGAGATAACAGAATCCGGTGGTTCTAGACTTGCCAACTACGGCTT-GAGA--ACT [5604]
Oan ACTGGTGAGGTAATGGGATCCGGTGGTTCTAGACTTGCCAACTATGGCCC-GAGG--ACT [6150]
Aca ACTGGTGAGGTATCAGGATCCGGTGGTTCTAGACTTGCCAACTACGGCCC-GAGG----- [6826]
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Pbi ACTGGTGAGATATCTGGATCCGGTGGTTCTAGACTTGCCAACTACCGCCT-GGGG--CGT [7136]
Cpi ACTGGTGAGGTATCAGGATCCGGTGGTTCTAGACTTGCCAACTACCGCCC-GAGG--ACT [7484]
Cmy ACTGGTGAGGTATCAGGATCCGGTGGTTCTAGACTTGCCAACTACCGCCC-GAGG--ACT [7234]
Psi ACTGGTGAGGTATCAGGATCCGGTGGTTCTAGACTTGCCAACTACCGCCC-GAGG--ACT [6814]
Asp ACTGGTGAGGTATCAGGATCCGGTGGTTCTAGACTTGCCAACTACCGCCC-GAGG----- [6643]
Ami ACTGGTGAGGTATCAGGATCCGGTGGTTCTAGACTTGCCAACTACCGCCC-GAGG--ACT [6958]
Asi ACTGGTGAGGTATCAGGATCCGGTGGTTCTAGACTTGCCAACTACCGCCC-GAGG--ACT [7032]
Tgu ---------------------------------------------------------- [5386]
Cli ACTGGTGCGGTAGCAGGATCCGGTGGTTCTAGACTTGCCAACTACAGCCCCGGGG--ACT [6905]
Gga ACTGGTGCGCTCGCAGGATCCGGTGGTTCTAGACTTGCCAACTACAGCCCCGGGA--ACT [6324]
Xtr ACTGGTGAGCTATGAAGATCCGGTGGTTCTAGACTTGCCAACTATGGCCT-GGGA--CCT [6833]
Lch ACTGGTGAGGTAACTGGATCCGGTGGTTCTAGACTTGCCAACTACTGCCT-GAAA--ACT [7255]
Dre ACTGGTGAGGTAGTCAGATCCGGTGGTTCTAGACTTGCCAACTACTACCT-GAGA--ACT [6715]

Hsa CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAACAGTCTCAGTCAGTGAATTACC [7197]
Mmu CCTGTCCTGTGTATGGCACTGGTAGAATTCACTGTGAACAGTCTCAGTCAGTGAATTACC [7121]
Mdo CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACACTATCAGTGAATTACC [6731]
Meu CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACACTATCAGTGAATTACC [5664]
Oan CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACACTATCAGTGAATTACC [6210]
Aca ---------------------------------------------------------- [6826]
Pbi CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACTCGATCAGTGAATTACC [7196]
Cpi CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACACTATCAGTGAATTACC [7544]
Cmy CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACACTATCAGTGAATTACC [7294]
Psi CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACACTATCAGTGAATTACC [6874]
Asp ---------------------------------------------------------- [6643]
Ami CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACGCTATCAGTGAATTACC [7018]
Asi CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACGCTATCAGTGAATTACC [7092]
Tgu ---------------------------------------------------------- [5386]
Cli CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGCAACCCCGCGGTCAGTGAATTACC [6965]
Gga CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGCAACCCCGCGGTCAGTGAATTACC [6384]
Xtr CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACACAAAATCAGTGAATTACC [6893]
Lch CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAACATACTATCAGTGAATTACC [7315]
Dre CCTGTTCTGTGTATGGCACTGGTAGAATTCACTGTGAAAGCACACTATCAGTGAATTACC [6775]

Hsa GAAGGGCCATAAACAGAGCAGAGAC--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [7255]
Mmu GAAGGGCCATAAACAGAGCAGAGAC--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [7179]
Mdo AAAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [6789]
Meu AAAGGGCCATAAACAGAGCAGAGAA---------------------------------- [5689]
Oan AAAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [6268]
Aca --------------------------TGCCCTGGCTCAGTTATCACTGTGCTGATGCTG [6859]
Pbi AACGGGCCATAAACGGAGCAGAGAA--TGCCCTGGCTCAGTTATCACTGTGCTGATGCTG [7254]
Cpi ATAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [7602]
Cmy ATAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [7352]
Psi ATAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [6932]
Asp --------------------------TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [6676]
Ami ATAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [7076]
Asi ATAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [7150]
Tgu --------------------------TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [5419]
Cli ATAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [7023]
Gga ATAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [6442]
Xtr ATAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [6951]
Lch ATAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGCTCAGTTATCACAGTGCTGATGCTG [7373]
Dre AAAGGGCCATAAACAGAGCAGAGAA--TGCCCTGGTTCAGTTATCACAGTGCTGATGCTG [6833]

Hsa TCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [7313]
Mmu TCCATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGCCCTTTTTCGGTT [7237]
Mdo TCCGTTCTCAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [6847]
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Meu ----------------------------------------ACTGTCCTTTTTCGGTT [5706]
Oan TCCATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [6326]
Aca TCTATACTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [6917]
Pbi TCTATACTAAAGGTACAGTACTGTGATAACTGAAGGATGGT--ACTGTCCTTTTTCGGTT [7312]
Cpi TCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [7660]
Cmy TCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [7410]
Psi TCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [6990]
Asp TCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [6734]
Ami TCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [7134]
Asi TCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [7208]
Tgu TCTCTTGTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [5477]
Cli TCTCTTGTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTGTCCTTTTTCGGTT [7081]
Gga TCTCTTGTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ACTATCCTTTTTCGGTT [6500]
Xtr TCTACTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGT--ACTGTCCTTTTTCGGTT [7009]
Lch TCCATTCTAAAGGTACAGTACTGTGATAACTGAATGATGGC--ACTGTCCTTTTTCGGTT [7431]
Dre TCCATCTTAAAGGTACAGTACTGTGATAACTGAAGGATGGC--ATTGTCCATTTTCAGTT [6891]

Hsa ATCATGGTACCGATGCTGTATATCTGAAAGGTACAGTACTGTGATAACTGAAGAATGGTG [7373]
Mmu ATCATGGTACCGATGCTGTAGCTCTGAAAGGTACAGTACTGTGATAGCTGAAGAATGGCG [7297]
Mdo ATCATGGTACCGATGCTGTATATGTGAAAGGTACAGTACTGTGATAACTGAAGAATGGTG [6907]
Meu ATCATGGTACCGATGCTGTATATGTGAAAGGTACAGTACTGTGATAACTGAAGAATGGTG [5766]
Oan ATCACGGTACCGATGCTGTATATGTGAAAGGTACAGTACTGTGATAACTGAAGAATGGTG [6386]
Aca ATCATGGTACCGGTGCTGTATATCTGAAAGGTACAGTACTGTGATAACTGAAGAATGATG [6977]
Pbi ATCATGGTACCGGTGCTGTATGTACGAAAGGTACAGTACTGTGATAACTGAAGAATGATA [7372]
Cpi ATCATGGTACCGGTGCTGTATACGTGAAAGGTACAGTACTGTGATAACTGAAGAATGATG [7720]
Cmy ATCATGGTACCGGTGCTGTATATGTGAAAGGTACAGTACTGTGATAACTGAAGAATGATG [7470]
Psi ATCATGGTACCGGTGCTGTATACGTGAAAGGTACAGTACTGTGATAACTGAAGAATGATG [7050]
Asp ATCATGGTACCGGTGCTGTATACGTGAAAGGTACAGTACTGTGATAACTGAAGAATGATG [6794]
Ami ATCATGGTACCGGTGCTGTATACGTGAAAGGTACAGTACTGTGATAACTGAAGAATGATG [7194]
Asi ATCATGGTACCGGTGCTGTATACGTGAAAGGTACAGTACTGTGATAACTGAAGAATGATG [7268]
Tgu ATCATGGTACCGGTGCTGTATACGTGAAAGGTACAGTACTGTGATAACTGAAGAATGGTG [5537]
Cli ATCATGGTACCGGTGCTGTATACGTGAAAGGTACAGTACTGTGATAACTGAAGAATGGTG [7141]
Gga ATCATGGTACCGGTGCTGTATACGTGAAAGGTACAGTACTGTGATAACTGAAGAATGGTG [6560]
Xtr ATCATGGTACCGGTGCTGTGTATATGAAAGGTACAGTACTGTGATAACTGAAGAATGGTG [7069]
Lch ATCATGGTACCGATGCCGTGTTCCTCAAAGGTACAGTACTGTGATAACTGAAGAATGGCA [7491]
Dre ATCATGGTACCGGTGCTGTGTGCCTGTCAAGTACAGTACTATGATAACTGAAGATTGACG [6951]

Hsa GT--TACTGCCCTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [7430]
Mmu GT--TACTGCCCTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [7354]
Mdo GT--TATTGTCTTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [6964]
Meu GT--TATTGTCTTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [5823]
Oan GT--CCTTGCCCTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [6443]
Aca GT--CGCTGCCTTCAGCTTCTTTACAGTGCTGCCTTGTTGCTT-ATGGATCAAGCAGCAT [7034]
Pbi GT--TGCTGTCTTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [7429]
Cpi GT--CATTGTCTTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [7777]
Cmy GT--CATTGTCTTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [7527]
Psi GT--CACTGTCTTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [7107]
Asp GT--CACTGTCTTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [6851]
Ami GT--CATTGTCTTTGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [7251]
Asi GT--CATTGTCTTTGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [7325]
Tgu GT--TACTGCCTTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [5594]
Cli GT--TACTGTCTTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [7198]
Gga GT--TGCTGCCTTCGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [6617]
Xtr GT--CATTTCCTTTGGCTTCTTTACAGTGCTGCCTTGTTGCAT-ATGGATCAAGCAGCAT [7126]
Lch GT--CCTTGCTTTTGGCTTCTCTACAGTGCTGCCTTGTTGCATTAAGGTTCAAGCAGCAT [7549]
Dre GT---------------------------------------------------------- [6953]
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Hsa TGTACAGGGCTATGAAGGCATTG--TGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTAG [7488]
Mmu TGTACAGGGCTATGAAGGCATTG--CGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTAG [7412]
Mdo TGTACAGGGCTATGAAGACATTG--GGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [7022]
Meu TGTACAGGGCTATGAAGGCACTG--AGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [5881]
Oan TGTACAGGGCTATGAGGGCATTG--GGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [6501]
Aca TGTACAGGGCTATGAAGGCATTG--GGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [7092]
Pbi TGTACAGGGCTATGAGGACACCG--GGCGCTTCCAGCTTCTTTACAGTGCTGCCTTGTTG [7487]
Cpi TGTACAGGGCTATGAAGGCATTA--TGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [7835]
Cmy TGTACAGGGCTATGAAGGCATTA--TGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [7585]
Psi TGTACAGGGCTATGAAGGCATTA--TTTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [7165]
Asp TGTACAGGGCTATGAAGGCATTA--TTTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [6909]
Ami TGTACAGGGCTATGAAGACAATG---------------------------------- [7274]
Asi TGTACAGGGCTATGAAGACAATG--TGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [7383]
Tgu TGTACAGGGCTATGAAGGCATTG--TGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [5652]
Cli TGTACAGGGCTATGAAGGCATTG--TGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [7256]
Gga TGTACAGGGCTATGAAGGCACTG--TGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTTG [6675]
Xtr TGTACAGGGCTATGAAGGATCTG--TGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTAG [7184]
Lch TGTACAGGGCTATGAAGGCACTG--TGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTAG [7607]
Dre ------------------------TGGTCTGTCAGCCTCTTTACGGTGCTGCCTTGTGG [6988]

Hsa CATTCAGGTCAAGCAGCATTGTACAGGGCTATGAAAGAACCA--CTCTCTGCTTTCAGCT [7546]
Mmu CATTCAGGTCAAGCAGCATTGTACAGGGCTATGAAAGAACCA--CTCTGTGCTTTCAGCT [7470]
Mdo CATTGATGTCAAGCAGCATTGTACAGGGCTATGAAAGAACCA--CTTTCTGCTTTCGGCT [7080]
Meu CATTGATGTCAAGCAGCATTGTACAGGGCTATGAAAGAGCCG------------------ [5923]
Oan CATTCATGTCAAGCAGCATTGTACAGGGCTATGAAAGAACCA--CTCTTTGCTTTCAGCT [6559]
Aca CAACCATGTCAAGCAGCATTGTACAGGGCTATGAAAGAACCA--CTCTTTGCTTTCAGCT [7150]
Pbi CAACCATGTCAAGCAGCATTGTACAGGGCTATGAAAGAACCC--CTCTTTGCTTTCAGCT [7545]
Cpi CATTCATGTCAAGCAGCATTGTACAGGGCTATGAAAGAACTG--CTTTTTGCTTTCAGCT [7893]
Cmy CATTCATGTCAAGCAGCATTGTACAGGGCTATGAAAGAACTG--CTTTTTGCTTTCAGCT [7643]
Psi CATTCAGATCAAGCAGCATTGTACAGGGCTATGAAAGAATTG--CTTTTTGCTTTCAGCT [7223]
Asp CATTCAGATCAAGCAGCATTGTACAGGGCTATGAAAGAATTG--CTTTTTGCTTTCAGCT [6967]
Ami ------------------------------------------CTCTTTGCTTTCAGCT [7290]
Asi CATTTATGTCAAGCAGCATTGTACAGGGCTATGAAAGAACAG--CTCTTTGCTTTCAGCT [7441]
Tgu CATTCATGTCAAGCAGCATTGTACAGGGCTATGAAAGAGCAG--CTCTTTGCTTTCAGCT [5710]
Cli CGTTCATGTCAAGCAGCATTGTACAGGGCTATGAAAGAGCAG--CTCTTTGCTTTCAGCT [7314]
Gga CGTTCATGTCAAGCAGCATTGTACAGGGCTATGAAAGAACAG--CTCTTTGCTTTCAGCT [6733]
Xtr CATCTATGTCAAGCAGCATTGTACAGGGCTATGAAGGAGCAG--CTTACTGCTTTCAGCT [7242]
Lch CATCAATGTCAAGCAGCATTGTACAGGGCTATGAAAGAGCTG--CTCTGTGCTTTCAGCT [7665]
Dre AATCTGGATCAAGCAGCATTGTACAGGGCTATGAGAGACCCG--TGTGTTGCTCTGAGCT [7046]

Hsa TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7606]
Mmu TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7530]
Mdo TCTCTACAGTGTTGCCTTGTGGCGTGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7140]
Meu ---------------------------------------------------------- [5923]
Oan TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [6619]
Aca TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7210]
Pbi TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7605]
Cpi TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7953]
Cmy TCTTTACAGTGTTGCCTTGTGGCACGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7703]
Psi TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7283]
Asp TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7027]
Ami TCTTTACAGTGCTGCCTTGTTGCATTTATGTCAAGCAGCATTGTACAGGGCTATCAAAGC [7350]
Asi TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7501]
Tgu TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [5770]
Cli TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7374]
Gga TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [6793]
Xtr TCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGC [7302]
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Lch TCTTTACAGTGTTGCCTTGTGGCATGAGGATCAAGCAGCATTGTACAGGGCTATCAAAGC [7725]
Dre TCTTTACAGTGTTGTCTTGTGGCATGGAGATCAAGCAGCATTGTACAGGGCTATCACAGC [7106]

Hsa ACA--CCTTAGCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCTAAAC-TATCAAACG [7663]
Mmu ACA--CCTTAGCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCCAAAC-CATCAAACG [7587]
Mdo ATA--CCCTACCAGAGCTATGGAGTGTGACAATGGTGTTTGTGTCCAGTC-TATCAAACG [7197]
Meu -----CCCTGCCAGAGCTATGGAGTGTGACAATGGTGTTTGTGTCCAGTC-TATCAAACG [5977]
Oan CTA--TGCTACCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCCAGTC-TATCAAACG [6676]
Aca GCA--TCCTGCTGGAGCTGTGGAGTGTGACAATGGTGTTTGTATCCAATC-CGTCAAACG [7267]
Pbi ATA--TTCTGCTGGAGCTTTGGAGTGTGACAATGGTGTTTGTATCCAATC-TCTCAAACG [7662]
Cpi ATC--TACTGCCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCCAATC-TATCAAACG [8010]
Cmy ATC--TACTGCCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCCAATC-TATCAAACG [7760]
Psi ATC--TACTGCCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCCAATA-TATCAAACG [7340]
Asp ATC--TACTGCCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCCAATA-TATCAAACG [7084]
Ami GGA--TACTATCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCCAATC-TATCAAACG [7407]
Asi GGA--TACTATCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCCAATC-TATCAAACG [7558]
Tgu ATG--TGCTCCCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCC-ATC-TATCAAACG [5826]
Cli ATG--TGCTGCCCGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCCTGGC-TATCAAACG [7431]
Gga ATG--TACGGCCAGAGCTATGGAGTGTGACAATGGTGTTTGTGTCCAATC-TATCAAACG [6850]
Xtr ATT--GACTGCTGGAGCTATGGAGTGTGACAATGGTGTTTGTGTCAGAGC-TATCAAACG [7359]
Lch ACT--ATCTGTCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCTGATCATATCAAACG [7783]
Dre ACA--GTCCTCCAGAGCTGTGGAGTGTGACAATGGTGTTTGTATCATCTGTCGTCAAACG [7164]

Hsa CCATTATCACACTAAATAGCTACTGCTAGG--GGCCTCTCTCTCCGTGTTCACAGCGGAC [7721]
Mmu CCATTATCACACTAAATAGCTACTGCTAGG--GGCCTCTCTCTCCGTGTTCACAGCGGAC [7645]
Mdo CCATTATCACACTAAATAGCTACTGTTGGG--GGCCTCTCTCTCCGTGTTCACAGCGGAC [7255]
Meu CCATTATCACACTAAATAGCTACTGTTGGG--GGCCTCTCTCTCCGTGTTCACAGCGGAC [6035]
Oan CCATTATCACACTAAATAGCTACTGTAGGG------------------------------ [6706]
Aca CCATTATCACACTAAATAGCTACTGCTAGA--GGCCCCTCTCTGCGTGTTCACAGCGGAC [7325]
Pbi CCATTATCACACTAAATAGCTACTGTTAGA--GGCCCCTCTCTGCGTGTTCACAGCGGAC [7720]
Cpi CCATTATCACACTAAATAGCTACTGTTAGA--GGCCCCTCTCTCCGTGTTCACAGCGGAC [8068]
Cmy CCATTATCACACTAAATAGCTACTGTTAGA--GGCCCCTCTCTCCGTGTTCACAGCGGAC [7818]
Psi CCATTATCACACTAAATAGCTACTGTTAGA--GGCCCCTCTCTCCGTGTTCACAGCGGAC [7398]
Asp CCATTATCACACTAAATAGCTACTGTTAGA--GGCCCCTCTCTCCGTGTTCACAGCGGAC [7142]
Ami CCATTATCACACTAAATAGCTACTGTTAGA--GGCCCCTCTCTGCGTGTTCACAGCGGAC [7465]
Asi CCATTATCACACTAAATAGCTACTGTTAGA------------------------------ [7588]
Tgu CCATTATCACACTAAATAGTTCCTGTTAAA---------CTCTCCGTGTTCACAGCGGAC [5877]
Cli CCATTATCACACTAAATAGCTACTGGTAGA--GGCCCCTCTCTCCGTGTTCACAGCGGAC [7489]
Gga CCATTATCACACTAAATAGCTACTGGTAGA------------------------------ [6880]
Xtr CCATTATCACACTAATGAGCTACTGCAGGC--GCCCCTTCTCTCCGTGTTCACAGCGGAC [7417]
Lch CCATTATCACACTAAATAGCTATAGCAAGA--TTTTTCTCTCTTCGTGTTCACAGCGGAC [7841]
Dre CCATTATCACACTAAATAGCCACGGTGTGA--CCTGCTTTTCTTCGTGTTCACAGCGGAC [7222]

Hsa CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAATGGGGCT--AGA [7779]
Mmu CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAATGGGGCT--AGA [7703]
Mdo CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAATGGGGCT--AGA [7313]
Meu CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAATGGGGCT--AGA [6093]
Oan ------------------------------------------------------GGA [6709]
Aca CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCTAAGAACGAGGCT--GGA [7383]
Pbi CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCTAAGAACGAGGCT--CGA [7778]
Cpi CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAACGAGGCT--CGA [8126]
Cmy CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAACGAGGCT--CGA [7876]
Psi CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAACGGGGCT--CGG [7456]
Asp CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAACGGGGCT--CGG [7200]
Ami CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAACGGGGCC--CGG [7523]
Asi ------------------------------------------------------------ [7588]
Tgu CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAACGAGGCT--TAA [5935]
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Cli CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAACGAGGCT--CAA [7547]
Gga ----------------------------------------------------------CCA [6883]
Xtr CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGGGCT--TAA [7475]
Lch CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGAGGCC--TGA [7899]
Dre CTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGATGGC--TCA [7280]

Hsa GGCTCT-G-CTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7836]
Mmu GACTCT-G-CTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7760]
Mdo GACTCT-GTCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7371]
Meu GACTCT-GTCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [6151]
Oan GACTCT-GCCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGGGCAC [6768]
Aca GGCGCT-GCCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7441]
Pbi GGCTCT-GTCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7836]
Cpi GGCTCT-GACTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [8184]
Cmy GGCTCT-GACTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7934]
Psi GGCTCT-GCCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7514]
Asp GGCTCT-GCCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7258]
Ami GGCTCTCGCCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7582]
Asi ---------------------------------------------------------- [7588]
Tgu GGCTCT-GACTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [5993]
Cli GGCTCT-GACTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7605]
Gga GGCTCT-GCCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [6941]
Xtr GTCTCT-GACTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7533]
Lch GACTCT-GACTCTGCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGG-CAC [7957]
Dre GACTCT-GGCTTTCCGTGTTCACAGCGGACCTTGATTTAATGTCTTACAATTAAGG-CAC [7338]

Hsa GCGGTGAATGCCAAGAGCGGAGCCTACGG--CCTGAGGGCCCCTCTGCGTGTTCACAGCG [7894]
Mmu GCGGTGAATGCCAAGAGCGGAGCCTACGG--CCTGAGGGCCCCTCTGCGTGTTCACAGCG [7818]
Mdo GCGGTGAATGCCAAGAGCGGAGCCTGAAA--CCAGAGTACCCCTCTGCGTGTTCACAGCG [7429]
Meu GCGGTGAATGCCAAGAGCGGAGCCTGAAA--CCAGAGTGCCCCTCTGCGTGTTCACAGCG [6209]
Oan TCGGTGAATGCCAAGAGCGGAGCCCCGGA------------------------------ [6797]
Aca GCGGTGAATGCCAAGAGCGGGGCTGGAAG--CCCGGGCCCTTCTCTGCGTGTTCACAGCG [7499]
Pbi GCGGTGAATGCCAAGAGCAGGGCTTGAAG--CCTGGGCCCTTCTCTCCGTGTTCACAGCG [7894]
Cpi GCGGTGAATGCCAAGAGCGGAGCCTGAAG--GACGAGCCCCTCTCTGCGTGTTCACAGCG [8242]
Cmy GCGGTGAATGCCAAGAGCGGAGCCTGAAG--GCCGAGCCCCTCTCTGCGTGTTCACAGCG [7992]
Psi GCGGTGAATGCCAAGAGCGGAGCCTGAAG--GCCGAGCCCCTCTCTGCGTGTTCACAGCG [7572]
Asp GCGGTGAATGCCAAGAGCGGAGCCTGAAG--GCCGAGCCCCTCTCTGCGTGTTCACAGCG [7316]
Ami GCGGTGAATGCCAAGAGCGGAGCCGGAAG--GGCGAGCCCCTCTCTGCGTGTTCACAGCG [7640]
Asi ------------------------------GCCGATCCCCTCTCTGCGTGTTCACAGCG [7617]
Tgu GCGGTGAATGCCAAGAGCGGATCCTCAAA--CCCGAGCCCCTCTCTGCGTGTTCACAGCG [6051]
Cli GCGGTGAATGCCAAGAGCGGATCCTCAAG--CCCGAGCCCCTCTCTGCGTGTTCACAGCG [7663]
Gga GCGGTGAATGCCAAGAGCGGATCCTCCAG--CCCGAGCCTCTCTCTGCGTGTTCACAGCG [6999]
Xtr GCGGTGAATGCCAAGAGTGGAGCCTACAT--ACGGAGCCCCCCTCTGCGTGTTCACAGCG [7591]
Lch GCGGTGAATGCCAAGAGTGGAGCCTTCAC--ATAGACTCCCTCTCTACGTGTTCACAGCG [8015]
Dre GCGGTGAATGCCAAGAGCGGAGCCTTTTA--CAGGCCCGCCACTCTGCGTGTTCACGGCG [7396]

Hsa GACCTTGATTTAATGTCTATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGCGCCTCC [7954]
Mmu GACCTTGATTTAATGTCTATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGCGCCTCC [7878]
Mdo GACCTTGATTTAATGTCTATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGTGTCTCC [7489]
Meu GACCTTGATTTAATGTCTATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGTGTCTCC [6269]
Oan ---------------------------------------------------------- [6797]
Aca GACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAG-CGGCTCT [7558]
Pbi GACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGACCGGTTCCC [7954]
Cpi GACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGAGCCTCA [8302]
Cmy GACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGAGCCTCA [8052]
Psi GACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGAGCCTCA [7632]
Asp GACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGAGCCTCA [7376]
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Ami GACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGAGCCTCA [7700]
Asi GACCTTGATTTAATGTCTATAAAATTAAGGCACGCGGTGAATGCCAAGAGAGGAGCCTCA [7677]
Tgu GACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGAGCCTCA [6111]
Cli GACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGAGCCTCA [7723]
Gga GACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGAGCCTCA [7059]
Xtr GACCTTGATTTAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGGGCTTTA [7651]
Lch GACCTTGATTTAATGTTCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGAGCCTCA [8075]
Dre GACCTTGATTTAATATCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGGGTCTTA [7456]

Hsa GC---------------------------------------------------------- [7956]
Mmu GC---------------------------------------------------------- [7880]
Mdo GC---------------------------------------------------------- [7491]
Meu GC---------------------------------------------------------- [6271]
Oan ------------------------------------------------------------ [6797]
Aca CA--CCAGGGCTTGGCCCTTCGTGTTCACAGTGGACCTTGATTTCATGTGGACACAATTA [7616]
Pbi CT--CTTGGCTTAAGCCCTTCGTGTTCACAGCGGACCTTGATTTAATTTCGATACAATTA [8012]
Cpi CA--CTCGGCTTCCGCTTTTCGTGTTCACAGCGGACCTTGATTTAATTTC-ATACAATTA [8359]
Cmy CA--CTCGGCTTCCGCTTTTCGTGTTCACAGCGGACCTTGATTTAATTTC-ATACAATTA [8109]
Psi CA---------------------------------------------------------- [7634]
Asp CA---------------------------------------------------------- [7378]
Ami CA--CGCGGCCTCGGCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTC-ACACAATTA [7757]
Asi CA---------------------------------------------------------- [7679]
Tgu CA---------------------------------------------------------- [6113]
Cli CA---------------------------------------------------------- [7725]
Gga CA--ATCAGCCCCAGCGTTTTGTGTTCACTGCAGACCTTGATTTAATGTC-ACACGATTA [7116]
Xtr TC---------------------------------------------------------- [7653]
Lch AA--TGTGGTTGAAGCTCTGCGTGTTCACCGTGGACCTTGATTTAATTTT-ATACAATTA [8132]
Dre AA--TTGGGTTTTTGCTCTTTGTGTTCACAGTGGACCTTGATTTAATTTCAATACAATTA [7514]

Hsa ------------------------------------GCTGGCGACGGGA-CATTATTAC [7978]
Mmu ------------------------------------GCCGGTGACAGCA-CATTATTAC [7902]
Mdo ------------------------------------GCTGACAATGGGT-CATTATTAC [7513]
Meu ------------------------------------GCTGACAATGGGT-CATTATTAC [6293]
Oan ------------------------------------GCTGGCAACTGCC-CATTATTAC [6819]
Aca AGGCACGCGGTGAATGCCAAGAGCCCAGCCCCTGC--GCTCCCCGCGGTC-CATTATTAC [7673]
Pbi AGGCACGCGGTGAATGCCAAGAGAGAAGCCACGTC--GCTGACTGCGGCT-CATTATTAC [8069]
Cpi AGGCACGCGGTGAATGCCAAGAGAGAAGCCGGACT--GCTGGTGCCGGCC-CATTATTAC [8416]
Cmy AGGCACGCGGTGAATGCCAAGAGAGAAGCCGGACT--GCTGGTGCCGGCC-CATTATTAC [8166]
Psi ------------------------------------GCTGGTGCCGGCT-CATTATTAC [7656]
Asp ------------------------------------------------------------ [7378]
Ami AGGCACGCGGTGAATGCCAAGAGA-GGGGCCGCCC--GCTGGTGACGGCC-CATTATTAC [7813]
Asi ------------------------------------GCTGGTGACGGCC-CATTATTAC [7701]
Tgu ------------------------------------GCTGGTGACGGCC-CATTATTAC [6135]
Cli ------------------------------------GCTGGTGACGGCC-CATTATTAC [7747]
Gga AGGCACGCAGTGAATGCCAAAGTTTGGGGCAGCCT--GCTGGTGACGGCC-CATTATTAC [7173]
Xtr ------------------------------------GTTGGTGGCTGTG-CATTATTAC [7675]
Lch AGGCACGCGGTGAATGCCAAGAGAGAAACCAACAT--GTTGGTGACGGTC-CATTATTAC [8189]
Dre AGGCACGCGGTGAATGCCAAGAGAGAAGCCAACAG--CGGCCTCACGGTT-CATTATTAC [7571]

Hsa TTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCCGTCCA-CG [8037]
Mmu TTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCGGTCAG-CA [7961]
Mdo TTTTGGTACGCGCTGTGACACATCAAACTCGTACCGTGAGTAATAATGCGCCATTGG-CA [7572]
Meu TTTTGGTACGCGCTGTGACACATCAAACTCGTACCGTGAGTAATAATGCGCCATTGG-CA [6352]
Oan TTTTGGTACGCGCTGTGACGCTTCAAACTCGTACCGTGAGTAATAATGCGTGGCTGG-CA [6878]
Aca TTTTGGTACGCGCTGTGCCACTTCAAACTCGTACCGTGAGTAATAATGCGCTGAGGGACA [7733]
Pbi TTTTGGTACGCGCTGTGCCACTTCAAACTCGTACCGTGAGTAATAATGCGCGGAGGGCCA [8129]
Cpi TTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCTGCGGC-CA [8475]
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Cmy TTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCTGCGGC-CA [8225]
Psi TTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCTGCGGC-CA [7715]
Asp ---------------------------------------------------------- [7378]
Ami TTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCTGCGGC-CA [7872]
Asi TTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCTGCGGC-CA [7760]
Tgu TTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCTGTGGC-CA [6194]
Cli TTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCTGTGGC-CA [7806]
Gga TTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCTGTGGT-CA [7232]
Xtr TTTTGGTACGCGCTGTGTCACATCAAACTCGTACCGTGAGTAATAATGCGCAGCTGC-CA [7734]
Lch TTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCAGTGGC-CA [8248]
Dre TTTTGGTACGCGCTATGCCACTCTCAACTCGTACCGTGAGTAATAGTGCACTGTGAC-TG [7630]

Hsa GC--GAGCTGTTGGATTCGGGGCCGTAGCACTGTCTGAGAGG-TTTACATTTCTCACAGT [8094]
Mmu GC--GAGCTGTTGGATTCGGGGCCGTAGCACTGTCTGAGAGG-TTTACATTTCTCACAGT [8018]
Mdo GC--GAGCTGTTGGATTCGGGGCCGTAGCACTGTCTGAGAGG-TTTACATTTCTCACAGT [7629]
Meu GC--GAGCTGTTGGATTCGGGGCCGTAGCACTGTCTGAGAGG-TTTACATTTCTCACAGT [6409]
Oan GC--GAGCCGCTGGATTCGGGGCCGATACACGGTCTGAGGGG-TTTACGAGTCTCACAGT [6935]
Aca GC--GAGCTGTTGGATTCGGGGCCGTAACACTGTCTGAGAGG-GTTACATTTCTCACAGT [7790]
Pbi GC--GAGCTGTTGGATTCGGGGCCGTAACACTGTCTGAGAGG-GTTACATTTCTCACAGT [8186]
Cpi GC--GAGCTGTTGGATTCGGGGCCGTAACACTGTCTGAGAGG-GTTACATTTCTCACAGT [8532]
Cmy GC--GAGCTGTTGGATTCGGGGCCGTAACACTGTCTGAGAGG-GTTACATTTCTCACAGT [8282]
Psi GC--GAGCTGTTGGATTCGGGGCCGTAACACTGTCTGAGAGA-GTTACATTTCTCACAGT [7772]
Asp ----GAGCTGTTGGATTCGGGGCCGTAACACTGTCTGAGAGA-GTTACATTTCTCACAGT [7433]
Ami GC--GAGCTGTTGGATTCGGGGCCGTAACACTGTCTGAGAGG-GTTACATTTCTCACAGT [7929]
Asi GC--GAGCTGTTGGATTCGGGGCCGTAACACTGTCTGAGAGG-GTTACATTTCTCACAGT [7817]
Tgu GC--GAGCTGTTGGATTCGGGGCCGTAACACTGTCTGAGAGG-TTTACATTTCTCACAGT [6251]
Cli GC--GAGCTGTTGGATTCGGGGCCGTAACACTGTCTGAGAGG-TTTACATTTCTCACAGT [7863]
Gga GC--GAGCTGTTGAATTCGGGGCCGTAACACTGTCTGAGAGG-TTTATATTTCTCACAGT [7289]
Xtr AT--GAGCGGCTGGAACCGGGCCCGGAGCGCTGTCTGAGAGGGTTTAAGTTTCTCACAGT [7792]
Lch GC--GAGCTGTTGGATACGGGGCCGGAGCACTGTCTGAGAGG-GCTGTATTTCTCACAGT [8305]
Dre GT--GAGCGGCTGAATGCGGGGCCGTGGCGCTGTCTGAGACGCTCTACTATTCTCACAGT [7688]

Hsa GAACCGGTCTCTTTTTCAGCTGCTTC--GTGCAGTGGGAAGGGGGGCCGATACACTGTAC [8152]
Mmu GAACCGGTCTCTTTTTCAGCTGCTTC--GTGCAGTGGGAAGGGGGGCCGATGCACTGTAA [8076]
Mdo GAACCGGTCTCTTTTTCAGCTGCTTC--GTGCAGCAGGAAGGGGGGCCGTTACACTGTCA [7687]
Meu GAACCGGTCTCTTTTTCAGCTGCTTC--GTGCAGCGGGAAGGGGGGCCGTTACACTGTTA [6467]
Oan GAACCGGTCTCTTTTTCAGTTGCTCC--GGACAGCCGGAAGGGGGGCCGTTACACTGTAA [6993]
Aca GAACCGGTCTCTTTTTCAGCTGCTTC--GTACAGTTGGAAGGGGGGCCGTTACACTGTAA [7848]
Pbi GAACCGGTCTCTTTTTCAGCTGCTTT--GTGCAGTTGGAAGGGGGGCCGTTACACTGTAA [8244]
Cpi GAACCGGTCTCTTTTTCAGCTGCTTC--GGGCAGTTGGAAGGGGGGCCGTTACACTGTAA [8590]
Cmy GAACCGGTCTCTTTTTCAGCTGCTTC--GGGCAGTTGGAAGGGGGGCCGTTACACTGTAA [8340]
Psi GAACCGGTCTCTTTTTCAGCTGCTTC--GGGCAGTTGGAAGGGGGGCCGTTACACTGTAA [7830]
Asp GAACCGGTCTCTTTTTCAGCTGCTTC--GGGCAGTTGGAAGGGGGGCCGTTACACTGTAA [7491]
Ami GAACCGGTCTCTTTTTCAGCTGCTTC--GTGCAGTTGGAAGGGGGGCCGTTACACTGTAA [7987]
Asi GAACCGGTCTCTTTTTCAGCTGCTTC--GTGCAGTTGGAAGGGGGGCCGTTACACTGTAA [7875]
Tgu GAACCGGTCTCTTTTTCAGCTGCTTC--GTGCGGCTGGAAGGGGGGCCGTTACACTGTAA [6309]
Cli GAACCGGTCTCTTTTTCAGCTGCTTC--GTGCAGCTGGAAGGGGGGCCGTTACACTGTAA [7921]
Gga GAACCGGTCTCTTTTTCAGCTGCTTC--GTCCAGCTGGAAGGGGGGCCGTTACACTGTAA [7347]
Xtr GAACCGGTCTCTTTTTCAGTCTCTTC--GTGCAGCTGGAACGGGGGCCGTTACACTGTAA [7850]
Lch GAACCGGTCTCTTTTTCAGCTGTCTC--TTACAGTTGGAGAGGGGGCCGTTACACTGTAA [8363]
Dre GAACCGGTCTCTTTTCCAGCCGCTAC--GAGTGCTGGGAGACGGGGCCGTGGCACTGTAT [7746]

Hsa GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-CCCTACTGT--CTCCTTTG [8208]
Mmu GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-CCCTACTGT--CTCCTTTG [8132]
Mdo GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-CCCTGCTGT--CTCCTTTG [7743]
Meu GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-CCCTGCTGT--CTCCTTTG [6523]
Oan GAGAGTGAGTACCAGG-TCTCACAGTGAACCGGTCTCTTT-CCCGACTGG--CTCCCTTG [7049]
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Aca GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCCTACTGT--CTCTCTCG [7904]
Pbi GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCTTACTGT--CTCTCTCG [8300]
Cpi GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCCTACTGT--CTCTCTTG [8646]
Cmy GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCCTACTGT--CTCTCTTG [8396]
Psi GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCCTACTGT---------- [7878]
Asp GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCCTACTGT---------- [7539]
Ami GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCCTACTGT--CCCTCTCA [8043]
Asi GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCCTACTGT--CCCTCTCA [7931]
Tgu GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCCTGCTGT---------- [6357]
Cli GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCCTACTGT--CCCTCTCG [7977]
Gga GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCCTGCTGT---------- [7395]
Xtr GAGAGTGAGTAGTAGG-TCTCACAGTGAACCGGTCTCTTT-TCTTACTGT--CTCTCTCA [7906]
Lch GAGAGTGAGTAGCAGG-TCTCACAGTGAACCGGTCTCTTT-TCCTGCTGT--CTCTCTCG [8419]
Dre GAGATTCATGTAGGCTTTCTCACAGTGAACCGGTCTCTTTTTCCAGCCCT--CCTTTTCA [7804]

Hsa GATCTTTTTGCGGTCTGGGCTTGCTGTTCCTCTCAACAGTAGTCAGGAAGCCCTTACCCC [8268]
Mmu GATCTTTTTGCGGTCTGGGCTTGCTGTT-CTCTCGACAGTAGTCAGGAAGCCCTTACCCC [8191]
Mdo GATCTTTTTGCGGTCTGGGCTTGCTGTTCCTTAAATCAGTAGTCAGGAAGCCCTTACCCC [7803]
Meu GATCTTTTTGCGGTCTGGGCTTGCTGTTTGTCTAATCAGTAGTCAGGAAGCCCTTACCCC [6583]
Oan GATCTTTTTGCGGTCTGGGCTTGCTGTTCCTCTAATCAGTAGTCAGGAAGCCCTTACCCC [7109]
Aca GATCTTTTTGCGGTCTGGGCTTGCTGTTCCTCCAGTCAGCAGTCAGGAAGCCCTTACCCC [7964]
Pbi GATCTTTTTGCGGTCTGGGCTTGCTGTTCCTCCAATAAGTAGCCAGGAAGCCCTTACCCC [8360]
Cpi GATCTTTTTGCGGTCTGGGCTTGCTGTTCCTCCAATCAGTAGTCAGGAAGCCCTTACCCC [8706]
Cmy GATCTTTTTGCGGTCTGGGCTTGCTGTTCCTCCAATCAGTAGTCAGGAAGCCCTTACCCC [8456]
Psi ---------------------------------------------------------- [7878]
Asp ---------------------------------------------------------- [7539]
Ami GATCTTTTTGCGGTCTGGGCTTGCTGTTCCTCCAACCCACACTCAGGAAGCCCTTACCCC [8103]
Asi GATCTTTTTGCGGTCTGGGCTTGCTGTTCCTCCAACCCACACTCAGGAAGCCCTTACCCC [7991]
Tgu ---------------------------------------------------------- [6357]
Cli GGTCTTTTTGCGGTCTGGGCTTGCTGTTCCTCCCGCA-GCACTCAGGAAGCCCTTACCCC [8036]
Gga ---------------------------------------------------------- [7395]
Xtr AAGCTTTTTGCGGTCTGGGCTTGCTGTTCTCAATCAAAGTATCCAGGAAGCCCTTATCCC [7966]
Lch GATCTTTTTGCGGTCTGGGCTTGCTGTTCCTTGAACCAGTAGTCAGGAAGCCCTTACCCC [8479]
Dre GGTCTTTTTGCGGTCTGGGCTTGCTGTTCCTTGAACCAGTAGCCAGGAAGCCCTTACCCC [7864]

Hsa AAAAAGTATCTGCGGGAGGCC--TTCGC-GAATCTTTTTGCGGTCTGGGCTTGCTGTACA [8325]
Mmu AAAAAGTATCTACGGGAGGCT--TTCGC-GAATCTTTTTGCGGTCTGGGCTTGCTGTACA [8248]
Mdo AAAAAGTATCTACAGGGGGAC---------------------------------------- [7824]
Meu AAAAAGTATTTACAGGGGGCC--TTCGC-GAATCTTTTTGCGGTCTGGGCTTGCTGTATA [6640]
Oan AAAAAGTATCTGCGAGAGACC---------------------------------------- [7130]
Aca AAAAAGTATTTGCGAGGGATC--TTCCCTGGGTCTTTTTGCGGTCTGGGCTTTCTGGGTC [8022]
Pbi AAAAAGTATTTGCGAGGGATC--TTCTCTGGGTCTTTTTGCGGTCTGGGCTTTCTGGGTC [8418]
Cpi AAAAAGTATTTGCGAGGGATA--TTCGC-GAATCTTTTTGCGGTCTGGGCTTGCTGTATA [8763]
Cmy AAAAAGTATTTGCGAGGGATA--TTCGC-GAATCTTTTTGCGGTCTGGGCTTGCTGTATA [8513]
Psi ----------------------TTCGC-GAATCTTTTTGCGGTCTGGGCTTGCTGTATA [7914]
Asp ---------------------------------------------------------- [7539]
Ami AAAAAGTATCCGCGGGGGAGC--TTCGC-GAATCTTTTTGCGGTCTGGGCTTGCTGTACA [8160]
Asi AAAAAGTATCCGCGGGGGAGC---------------------------------------- [8012]
Tgu ----------------------TTCGC-GAATCTTTTTGCGGTCTGGGCTTGCTGTACA [6393]
Cli AAAAAGTATCTGCGGGGGGTC--TTCGC-GAATCTTTTTGCGGTCTGGGCTTGCTGTACA [8093]
Gga ---------------------------------------------------------- [7395]
Xtr AAAAAGAATTTGCGAGGGAGG--TTCTC-AAATCTTTTTGCGGTCTGGGCTTGCTGTATG [8023]
Lch AAAAAGTATCTGCGAGGGATA--TCCTC-GAATCTTTTTGCGGTCTGGGCTTGCTGTAAA [8536]
Dre AAAAAGTATCTGCAGAGGACC--TTCAC-GAATCTTTTTGCGGTCTGGGCTTGCTGTTCT [7921]

Hsa TAACTCAA----TAGCCGG-AAGCCCTTACCCCAAAAAGCATTTGCGGAGGGCG--GCTG [8378]
Mmu TAACTCAA----TAGCCGG-AAGCCCTTACCCCAAAAAGCATTCGCGGAGGGCG--GCTG [8301]
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Mdo ----------------------------------------------------ACTC [7828]
Meu TAACTATG----TAGCCGGGAAGCCCTTACCCCAAAAAGCATTCGAGGAGGACA--ACTC [6694]
Oan ----------------------------------------------------GCTC [7134]
Aca TGTCCAACCCCCGTATCAGAAAGCCCTTACCCCAAAAAGCATCCGGGGCTGGAC--GCCC [8080]
Pbi TGTCCAACCCC-GTATCAGAAAGCCCTTACCCCAAAAAGCATCCGGGGTTGTAC--GCCC [8475]
Cpi TAACTACC----TAGCCGGGAAGCCCTTACCCCAAAAAGCATTCGCGGAGGGCG--GCCG [8817]
Cmy TAACTACC----TAGCCGGGAAGCCCTTACCCCAAAAAGCATTCGCGGAGGGCG--GCCG [8567]
Psi TAACTACC----TAGCCGGGAAGCCCTTACCCCAAAAAGCATTCGCGGAGGGCG--GCCG [7968]
Asp ----------------------------------------------------GCCG [7543]
Ami TAACTACC----TAGCCGGGAAGCCCTTACCCCAAAAAGCATTCGCGGAGGGCG--GCCC [8214]
Asi ----------------------------------------------------GCCC [8016]
Tgu TAACTACC----TACCCGGGAAGCCCTTACCCCAAAAAGCATTCGCGGAGGGCG------ [6443]
Cli TAACTACC----TACCCGGGAAGCCCTTACCCCAAAAAGCATTCGCGGAGGGCG------ [8143]
Gga ---------------------------------------------------------- [7395]
Xtr TAAATACC----TAGCCGGGAAGCCCTTACCCCAAAAAGCATTTGCGGAGGGCG------ [8073]
Lch TGAATACC----TATCCGGGAAGCCCTTACCCCAAAAAGCATTTGCGGAGGGCG--TTGT [8590]
Dre CAACTA------TCAATGGGAAGCCCTTACCCCAAAAAGCATTTGCGGAGGGCG------ [7969]

Hsa CTGGCCAGAGCTCTTTTCACATTGTGCTACTGTCTGCACCTGTCACTAGCAGTGCAATGT [8438]
Mmu CTGGCCGGAGCTCTTTTCACATTGTGCTACTGTCTA-ACGTGTACCGAGCAGTGCAATGT [8360]
Mdo CTGGCCAGAGCTCTTTTCACATTGTGCTACTGTCTGCACCTATCACTAGCAGTGCAATGT [7888]
Meu CTGGCCGGGGCTCTTTTCACATTGTGCTACTGTCTGCGCTTGTCACTAGCAGTGCAATGT [6754]
Oan CCGGCCGGAGCTCTTTTCACATTGTGCTACTGTCTGCGCCCGTCACTAGCAGTGCAATGT [7194]
Aca CTGTCCAAGGCTCTTTTCACATTGTGCTTCTGTCTGTGCCCGACCCAAGCAGTGCAATGT [8140]
Pbi CTGCCCGAGGCTCTTTTCACATTGTGCTACTG----AGCCCAACCCAAGCAGTGCAATGT [8531]
Cpi CCGTCCTGGGCTCTTTTCACATTGTGCTACTGTCTGAGCCCCTGCCAAGCAGTGCAATGT [8877]
Cmy CCATCCTGGGCTCTTTTCACATTGTGCTACTGTCTGAGCCCCTGCCAAGCAGTGCAATGT [8627]
Psi CCGTCCTGGGCTCTTTTCACATTGTGCTACTGTCTGAGCCCCTGCCAAGCAGTGCAATGT [8028]
Asp CCGTCCTGGGCTCTTTTCACATTGTGCTACTGTCTGAGCCCCTGCCAAGCAGTGCAATGT [7603]
Ami CTGTCCAAGGCTCTTTTCACATTGTACTACTGTATGAGCCCCTGCCAAGCAATGCAATGT [8274]
Asi CTGTCCAAGGCTCTTTTCACATTGTACTACTATATGAGCCCCTGCCAAGCAATGCAATGT [8076]
Tgu ---------------------------------------------------------- [6443]
Cli ---------------------------------------------------------- [8143]
Gga ---------------------------------------------------------- [7395]
Xtr ---------------------------------------------------------- [8073]
Lch GTTGTCTGAACCCTTTTCACATTGTACTACTGTATG--CTATCCAAAGGCAGTGCAATAT [8648]
Dre ---------------------------------------------------------- [7969]

Hsa TAAAAGGGCATT-GGCCGTGTAG--GGCCTGCCCGACACTCTTTCCC-TGTTGCACTACT [8494]
Mmu TAAAAGGGCATC-GGCCTTGTAG--GGCTTGTTGGACACTCTTTCCC-TGTTGCACTACT [8416]
Mdo AAAAAGGGCATT-GGCTGGGCAG--GGCCTGCCCGAAGCTCTTTCCC-TGTTGCCCTGCT [7944]
Meu AAAAAGGGCATT-GGCTGGGCAG--GGGCTGCCCAAAGCTCTTTCCC-TGTTGCCCTGCT [6810]
Oan AATAAGGGGCTTCGGCGGGGCAG------------------------------------ [7217]
Aca TAAAAGGGCATT-GGGTGGGTGG--GGGCGTCTGCCCACTCTTTCCCCTGTTGCACTACT [8197]
Pbi AAAAAGGGCATT-GGGTTGGTGG--GAGCAGTCTGCTACTCTTTCCT-TGTTGCGCTACT [8587]
Cpi CAAAAGGGCATC-GGGCAGGCGG--AGGCAGGCTGCCACTCTTTCCC-TGTTGCACTACT [8933]
Cmy CAAAAGGGCATC-GGGCGGGCGG------------------------------------ [8649]
Psi CAAAAGGGCATC-GGGCAGGTGG------------------------------------ [8050]
Asp CAAAAGGGCATC-GGGCAGGCGG--AGGCAGGCTGCCACTCTTTCCCTGTTGCACTACTG [7660]
Ami AAAAAGGGCATT-GGGTAGGTGG------------------------------------ [8296]
Asi AAAAAGGGCATT-GGGTAGGTGG------------------------------------ [8098]
Tgu ------------------------GCCGGGCTGCCC-CTCTTTCCC-TGTTGCACTACT [6476]
Cli ------------------------GCCGGGCTGCCC-CTCTTTCCC-TGTTGCACTACT [8176]
Gga ------------------------GGCGGGCTGCCC-CTCTTTCCC-TGTTGCACTACT [7428]
Xtr ------------------------AGGCCGCCTGACACTCTTTCCC-TGTTGCACTACT [8107]
Lch CAAAAGGGCATT-AGCCATCCTC--GGACTGCCTGTCACTCTTTCCC-TGTTGCACTACT [8704]
Dre ------------------------CTGTTGCCTGACACTCTTTCCC-TGTTGCACTACT [8003]
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Hsa AT--AGGCCGCTGGGAAGCAGTGCAATGATGAAAGGGCATCGGTCAGGT--GCTGGCCGC [8550]
Mmu GT--GGGCCTCTGGGAAGCAGTGCAATGATGAAAGGGCATCTGTCGGGC--GCTGGCTGC [8472]
Mdo GT----CCGGTCACCTAGCAGTGCAATTGTGAAAGGGCATTGGTGAGGC----------- [7989]
Meu GT----CCAGTCACTGAGCAGTGCAATTGTGAAAGGGCATTGGTCAGGC----------- [6855]
Oan ----------------------------------------------------GCTGCCGCC [7226]
Aca GTCCAACGTCACAGCTAGCAGTGCAATAATGAAAGGGCGTCAGCCGCTC--GCTGGGATT [8255]
Pbi GTTCAGCTTCGCCTCTAGCAGTGCAATAATGAAAGGGCATCAGCCCCTC--GCTGGAACC [8645]
Cpi GTT-AAACTTGTAGCTAGCAGTGCAATAATGAAAGGGCGTCGGTCTGCC--GCTGGTATC [8990]
Cmy ----------------------------------------------------GCTGGTATC [8658]
Psi ----------------------------------------------------GCTGGTATC [8059]
Asp TC--AAACTTGTAGCTAGCAGTGCAATAATGAAAGGGCGTCGGTCTGCC--GCTGGTATC [7716]
Ami ----------------------------------------------------GCTGGTATC [8305]
Asi ----------------------------------------------------GCTGGTATC [8107]
Tgu GTC-ACGGTCGCAGCGAGCAGTGCAATAATGAAAGGGCGTCAGTGCGCC--GCTGGTATC [6533]
Cli GTC-ACGGTCGCAGCGAGCAGTGCAATAATGAAAGGGCGTCAGTGCGCC--GCTGGTATC [8233]
Gga GTC-ACGGTCGCAGCGAGCAGTGCAATAATGAAAGGGCGTCAGTGCGCC--GCTGGTATC [7485]
Xtr GTG-GCAGTGAATAA-AGCAGTGCAATGATGAAAGGGCATCAGTCTGCA--GCTTGTGTG [8163]
Lch GTG--GAACCTCT---AGCAGTGCAATAATGAAAGGGCGTCAGTCTGCC--GCTGGTGTC [8757]
Dre GTGGGAGCTGCAGCAAAGCAGTGCAATAATGAAAGGGCATCAGTCCACT--GCTAAGGTC [8061]

Hsa AGGTGCTCTGACGAGGTTGCACTACTGTGCTCTGAGA----AGCAGTGCAATGATATTGT [8606]
Mmu GGGTGCTCTGACTAGGTTGCACTACTGTGCTGTGAGA----AGCAGTGCAATGGTATTGT [8528]
Mdo ---------------------------------------------------------- [7989]
Meu ---------------------------------------------------------- [6855]
Oan GGCGGCTCTGACGATATTGCAC-ATAGTGTGCGCTCAGGGAAGCAGTGCAATAGTATTGT [7285]
Aca GATGGCTCTGACAGTGTTGCACTACTGTCTACACAAATTA-AGCAGTGCAATAATATTGT [8314]
Pbi GCTGGCTCTGACAATGTTGCACTACTGTTTTCACAAATTT-AGCAGTGCAATAATATTGT [8704]
Cpi GCTGGCTCTGACAATGTTGCACTACTGTCTGCACAAATAA-AGCAGTGCAATAATATTGT [9049]
Cmy GCTGGCTCTGACAATGTTGCACTACTGTCTGCACAAATAA-AGCAGTGCAATAATATTGT [8717]
Psi GCTGGCTCTGACAATGTTGCACTACTGTCTGCACAAATAA-AGCAGTGCAATAATATTGT [8118]
Asp GCTGGCTCTGACAATGTTGCACTACTGTCTGCACAAATAA-AGCAGTGCAATAATATTGT [7775]
Ami GCTGGCTCTGACAATGTTGCACTACTGTCTGCACAAATAA-AGCAGTGCAATAATATTGT [8364]
Asi GCTGGCTCTGACAATGTTGCACTACTGTCTGCACAAATAA-AGCAGTGCAATAATATTGT [8166]
Tgu GCTGGCTCTGACAATGTTGCACTACTGTCTGCACAAATAA-AGCAGTGCAATAATATTGT [6592]
Cli GCTGGCTCTGACAATGTTGCACTACTGTCTGCACAAATAA-AGCAGTGCAATAATATTGT [8292]
Gga GCTGGCTCTGACAATGTTGCACTACTGTCTGCACAAATAA-AGCAGTGCAATAATATTGT [7544]
Xtr AATTGCTCTGACAGTGTTGCACTACTGTGATCTCAAATGA-AGCAGTGCAATAGTATTGT [8222]
Lch AGCTGCTCTGACAGTGTTGCACTACTGTATACACAAGTTA-AGCAGTGCAATAGTATTGT [8816]
Dre TGTTGCTTTGACGATGTTGCACTACTGAACCATCTAATCA-AGCAGTGCAATAGTATTGT [8120]

Hsa CAAAGCATCTGGGACCAGC----------------------------------------- [8625]
Mmu CAAAGCATCTGGGACCAGC----------------------------------------- [8547]
Mdo ---------------------------------------------------------- [7989]
Meu ---------------------------------------------------------- [6855]
Oan CAAAGCATC-GAATCCACC----------------------------------------- [7303]
Aca CAAAGCATTTGGTTCCAGT--GTTGCTGTCCGGAGCCCTTTTTCTGTTGTACTACTGGCA [8372]
Pbi CAAAGCATTTGGTTCTAGT--CTTGTCGTCCTGTGCCCTTTTTCTGTTGTACTACTGGGA [8762]
Cpi CAAAGCATTTGGTTCCAGT--ACTGTTGTCCAGAGCCCTTTTTCTGTTGTACTACTGGCA [9107]
Cmy CAAAGCATTTGGTTCCAGT--ACTGTTGTCCAGAGCCCTTTTTCTGTTGTACTACTGGCA [8775]
Psi CAAAGCATTTGGTTCCAGT--ACTGTTGTCCAGAGCCCTTTTTCTGTTGTACTACTGGCA [8176]
Asp CAAAGCATTTGGTTCCAGT--ACTGTTGTCCAGAGCCCTTTTTCTGTTGTACTACTGGCA [7833]
Ami CAAAGCATTTGGTTCCAGT--GCTGTTGTCCAGAGCCCTTTTTCTGTTGTACTACTGGCA [8422]
Asi CAAAGCATTTGGTTCCAGT--GCTGTTGTCCAGAGCCCTTTTTCTGTTGTACTACTGGCA [8224]
Tgu CAAAGCATTTGGTTCCAGT--GCTGTTGTCCAGAGCCCTTTTTCTGTTGTACTACTGGCA [6650]
Cli CAAAGCATTTGGTTCCAGT--GCTGTTGTCCAGAGCCCTTTTTCTGTTGTACTACTGGCA [8350]
Gga CAAAGCATTTGGTTCCAGT--GCTGTTGTCCAGAGCCCTTTTTCTGTTGTACTACTGGCA [7602]
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Xtr CAAAGCATTTCATTCCAGC--CCTGTTATCCGTGGCCCTTTTTCTGTTGTACTACTGGAA [8280]
Lch CAAAGCATCTGGGCCCAGT--ACTGTTGGCCAGGGCCCTTTTTCTGTTGTACTACTGGAA [8874]
Dre CATTGCATTCGGCTTTCGC--TGTTTTGTCCATTGCCCTTTTTCTGTTGTACTACTGGCC [8178]

Hsa ------------------------------------------------------------ [8625]
Mmu ------------------------------------------------------------ [8547]
Mdo ----------------------------------------------TTGTCTAGTGCCCT [8003]
Meu ------------------------------------------------------------ [6855]
Oan ----------------------------------------------CTGTCTAGTGCCCT [7317]
Aca AGTATGAGTAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGG--CTGTCCACTGCCCT [8430]
Pbi GCTCTCATTAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGA--CTGTCCACTGCCCT [8820]
Cpi ATTATGATGAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGA--CTGTCCAGTGCCCT [9165]
Cmy ATTATGATGAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGA--CTGTCCAGTGCCCT [8833]
Psi ATTATGATGAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGA--CTGTCGAGTGCCCT [8234]
Asp ATTATGATGAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGA--CTGTCGAGTGCCCT [7891]
Ami ATTATGATGAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGA--CTGTCCAGTGCCCT [8480]
Asi ATTATGATGAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGA--CTGTCCAGTGCCCT [8282]
Tgu ATTATGATGAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGA--CTGTCCAGTGCCCT [6708]
Cli ATTATGATGAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGA--CTGTCCAGTGCCCT [8408]
Gga ATTATGATGAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGA--CTGTCCAGCGCCCT [7660]
Xtr TTTGTAATTAGCAGTGCAATATTAAAAGGGCATTGGCTGACAGA--CTGTCCAGTGCCCT [8338]
Lch ATTAAGATGAGCAGTGCAATATTAAAAGGGCATTGGCTGGCAGA--CTGTCCAGCGCCCT [8932]
Dre AATCAGAAGAGCAGTGCAATATTAAAAGGGCATTGGCTGATAGA--CTGTCCAGTGCCCC [8236]

Hsa ------------------------------------------------------------ [8625]
Mmu ------------------------------------------------------------ [8547]
Mdo TTTTATGTTGTACTACTAGTGATCCTGCACAAGAA--GCAGTGCAATGTTAAAAGGGCAT [8061]
Meu ------------------------------------------------------------ [6855]
Oan TTTTATGTTGTACTACTAGTGATCTTGCACAAAAA--GCAGTGCAATGTTAAAAGGGCAT [7375]
Aca TTTTATGTTGTACTACTAGTGAACATGCGCAAAAA--GCAGTGCAATGTTAAAAGGGCAT [8488]
Pbi TTTTATGTTGTACTACTAGTGAACACACACAAAAA--GCAGTGCAATGTTAAAAGGGCAT [8878]
Cpi TTTTATGTTGTACTACTAGTGATCATACACAAAAA--GCAGTGCAATGTTAAAAGGGCAT [9223]
Cmy TTTTATGTTGTACTACTAGTGATCATGCACAAAAA--GCAGTGCAATGTTAAAAGGGCAT [8891]
Psi TTTTATGTTGTACTACTAGTGATCATGCACAAAAA--GCAGTGCAATGTTAAAAGGGCAT [8292]
Asp TTTTATGTTGTACTACTAGTGATCATGCACAAAAA--GCAGTGCAATGTTAAAAGGGCAT [7949]
Ami TTTTATGTTGTACTACTAGTGATCGTGCACAAAAA--GCAGTGCAATGTTAAAAGGGCAT [8538]
Asi TTTTATGTTGTACTACTAGTGATCGTGCACAAAAA--GCAGTGCAATGTTAAAAGGGCAT [8340]
Tgu TTTTATGTTGTACTACTGGTGATGATGCACAAAAA--GCAGTGCAATGTTAAAAGGGCAT [6766]
Cli TTTTATGTTGTACTACTGGTGATCATGCACAAAAA--GCAGTGCAATGTTAAAAGGGCAT [8466]
Gga TTTTATGTTGTACTACTAGTGATCATACACAAA----GCAGTGCAATGTTAAAAGGGCAT [7716]
Xtr TTTTATGTTGTACTACTAGTGGTCACACACAAAAAAAGCAGTGCAATGTTAAAAGGGCAT [8398]
Lch TTTTATGTTGTACTACTGGTGACAATATAATAAAA--GCAGTGCAATGTTAAAAGGGCAT [8990]
Dre TTTTATATTGTACTACTGATAACCCAGTTATTAAA--GCAGTGCAATGTTAAAAGGGCAT [8294]

Hsa -----------CTGCTAACGAATGCTCTGACTTTATTGCACTACTGTACTTTACAGCTAG [8674]
Mmu -----------CTGCTAACGGCTGCTCTGACTTTATTGCACTACTGTACTTTACAGCGAG [8596]
Mdo TGGCCAGTG--CTGCTAACGAATGCTCTGACTTTATTGCACTACTGTACTTTACAGCTAG [8119]
Meu ------------------------------------------------------------ [6855]
Oan TGGCCAGTG--CTGCTAACGAATGCTCTGACTTTATTGCACTACTGTTCTTTACAGCTAG [7433]
Aca TGGCCAGCA--CTGCGGACAAGGGCTCTGACTTCATTGCACTACTGTACTTCCCAACTAG [8546]
Pbi TGGCCAGCA--CTGCTGACAAGTGCTCTGACTTCATTGCACTACTGTACTTCCCAGCTAG [8936]
Cpi TGGCCAGTG--CTGCTAACGAATGCTCTGACTTTATTGCACTACTGTACTTTACAGCTAG [9281]
Cmy TGGCCAGTG--CTGCTAACGAATGCTCTGACTTTATTGCACTACTGTACTTTACAGCTAG [8949]
Psi TGGCCAGTG--CTGCTAACGAATGCTCTGACTTTATTGCACTACTGTACTTTACAGCTAG [8350]
Asp TGGCCAGTG--CTGCTAACGAATGCTCTGACTTTATTGCACTACTGTACTTTACAGCTAG [8007]
Ami TGGCCAGCA--CTGCTAACGAATGCTCTGACTTTATTGCACTACTGTACTTTACAGCTAG [8596]
Asi TGGCCAGCA--CTGCTAACGAATGCTCTGACTTTATTGCACTACTGTACTTTACAGCTAG [8398]
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Tgu TGGCCAGCA--CTGCTAACGAGTGCTCTGACTTTATTGCACTACTGTACTATACAGAGAG [6824]
Cli TGGCCAGCA--CTGCTAACGAACGCTCTGACTTTATTGCACTACTGTACTTCCCAGCTAG [8524]
Gga TGGCCAGCA--CTGCTAACGAATGCTCTGACTTTATTGCACTACTGTACTTCACAGCTAG [7774]
Xtr TGGCCAGGG--CTGCTAATGTGTGCTCTGACTTTATTGCACTACTGTACTATACAGCTAG [8456]
Lch TGGCCAGTT--CTGCTGATGGGTGCTCTGACTTTATTGCACTACTGTGGTTTACATCAAG [9048]
Dre TGGCCAGGG--CTGTTAACAGGTGCTCTGACTTCATTGCACTACTGTATTGGACAGCTAG [8352]

Hsa CAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAG--CGTCTCCAGGGCAACCGTGGCTT [8732]
Mmu CAGTGCAATAGTATTGTCAAAGCATCCGCGAGCAG--CGTCTCCAGGGCAACCGTGGCTT [8654]
Mdo CAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAG--CGTCTCCAGGGCAACCGTGGCTT [8177]
Meu ------------------------------------CGTCTCCAGGGCAACCGTGGCTT [6878]
Oan CAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAG---------------------------- [7468]
Aca CAGTGCAATAGTATTGTCAAAGCACTTGCAAGCAG--CGTCTCCAGGGCAACCGTGGCTT [8604]
Pbi CAGTGCAATAGTATTGTCAAAGCACTTGCGAGCAG--CGTCTCCAGGGCAACCGTGGCTT [8994]
Cpi CAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAG--TGTCTCCAGGGCAACCGTGGCTT [9339]
Cmy CAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAG--TGTCTCCAGGGCAACCGTGGCTT [9007]
Psi CAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAG--TGTCTCCAGGGCAACCGTGGCTT [8408]
Asp CAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAG--TGTCTCCAGGGCAACCGTGGCTT [8065]
Ami CAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAG--CGTCGCCAGGGCAACCGTGGCTT [8654]
Asi CAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAG---------------------------- [8433]
Tgu CAGTGCAATAGTATTGTCAAAGCATCTGAGAGCAG---------------------------- [6859]
Cli CAGTGCAATAGTATTGTCAAAGCATCCGAAAGCAG--CGCCGCCCGGGCGACCGTGGCTT [8582]
Gga CAGTGCAATAGTATTGTCAAAGCATCTGAAAGCAG---------------------------- [7809]
Xtr CAGTGCAATAGTATTGTCAAAGCATCTGCAAGCAG--TGTCTCCAGGGCAACCGTGGCTT [8514]
Lch CAGTGCAATAGTATTGTCAAAGCATCTAAAAGCAG--GGTCTCCGAGGCAACCGTGGCTT [9106]
Dre CAGTGCAATAGTATTGTCAAAGCGTCTGAGAGCAG--TGTCTCCATGGCGACCGTGGCAT [8410]

Hsa TCGATTGTTACTGTG--GGAACTGGA---GGTAACAGTCTACAGCCATGGTCGCC---CC [8784]
Mmu TCGATTGTTACTGTG--GGAACCGGA---GGTAACAGTCTACAGCCATGGTCGCC---CC [8706]
Mdo TCGATTGTTACTGTG--GGAACCAGG---GGTAACAGTCTACAGCCATGGTCGCC---CC [8229]
Meu TCGATTGTTACTGTG--GGAACCGGG---GGTAACAGTCTACAGCCATGGTCGCC---CC [6930]
Oan ---------------------------------------------------------- [7468]
Aca TAGATTGTTACTGTGCGGACGTGGGTTT-GGTAACAGTCTACAGCCATGGTTGGT---CC [8660]
Pbi TAGATTGTTACTGTGTGGATGTGGGCT--GGTAACAGTCTACAGCCATGGTTGCCT--GG [9050]
Cpi TAGATTGTTACTGTG--GTTGTGTGTT--GGTAACAGTCTACAGCCATGGTCGCTT--GG [9393]
Cmy TAGATTGTTACTGTG--GTTGTGTGTC--GGTAACAGTCTACAGCCATGGTCGCTT--GG [9061]
Psi TAGATTGTTACTGTG---TCTTGTGTT--GGTAACAGTCTACAGCCATGGTCGCTT--GG [8461]
Asp TAGATTGTTACTGTG---GCTTGTGTT--GGTAACAGTCTACAGCCATGGTCGCTT--GG [8118]
Ami TAGATTGTTACTGTG---TGGTGCGTG--GGTAACAGTCTACAGCCATGGTCGCT---GG [8706]
Asi ---------------------------------------------------------- [8433]
Tgu ---------------------------------------------------------- [6859]
Cli TAGATTGTTACTGTG--CCGCTGGGGG--GGTAACAGTCTACAGCCATGGTCGCC---GG [8635]
Gga ---------------------------------------------------------- [7809]
Xtr TAGATTGTTACTGTA--GTTCTGCATT--GGTAACAGTCTACAGCCATGGTCGCTC--GG [8568]
Lch TAGATTGTTACTGTA--TGTATGCAGT--GGTAACAGTCTACAGCCATGGTCGTTC--GG [9160]
Dre TAGATTGTTACTGTAGGAACAGAATTTTTGGTAACAGTCTACAGCCATGGTCGCTAGTGG [8470]

Hsa GCAGCACG--ACAGCGCGCCGGCACCTTGGCTCTAGACTGCTTACTGC-----CCGGGCC [8837]
Mmu GCAGCACG--GCAGCGCGCCGGCACCTTGGCTCTAGACTGCTTACTGC-----CCGGGCC [8759]
Mdo GCAGCACG--GCAGCGCGCCGGCACCTTGGCTCTAGACTGCTTACTGC-----CCGGGCC [8282]
Meu GCAGCACG--GCAGCGCGCCGGCACCTTGGCTCTAGACTGCTTACTGC-----CCGGGCC [6983]
Oan ---------------------------------------------------------- [7468]
Aca GGCGGACG--CCAGCGTGCCGGGACCTTGGCTCTAGACTGCTTACTGCGAAATCCAAGGG [8718]
Pbi AGTGGACG--TCAGTTCGTCGGGACCTTGGCTCTAGACTGCTTACTGCTACAGGCAATGA [9108]
Cpi GCTAGACA--TCAGCGCGTCGGCACCTTGGCTCTAGACTGATTACTGCTAAGTAGCATTA [9451]
Cmy GCCAGACG--TCAGCGCGTCGGCACCTTGGCTCTAGACTGATTACTGCTAAATAGCGTTC [9119]
Psi GCCAGACG--TCAGCGCGTCGGCACCTTGGCTCTAGACTGCTTACTGCTACGTAGCGTGA [8519]
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Asp GCCAGACG---------------------------------------------------- [8126]
Ami GCCGGACG--TCAGCGCGTCGGCACCTTGGCTCTAGACTGCTTACTGCTGAGCACGGCGA [8764]
Asi ------------------------------------------------------------ [8433]
Tgu ------------------------------------------------------------ [6859]
Cli GACAGGCG--TCAGAGCGTCGGCACCTTGGCTCTAGACTGCTTACTGCTGCGTAGGG--A [8691]
Gga ------------------------------------------------------------ [7809]
Xtr GCAAGATG--TCATTGCATCGGCACCTTGGCTCTAGACTGCTTACTGTGAAACTGTGCTA [8626]
Lch GTAAGACG--TCAGAGCGTCAACACCTTGGCTCTAGACTGCTTACTGCTAAATGTTGTGA [9218]
Dre GCAGAAAC--TCAGAACTTCATGACCTTGGCTCTAGACTGCTTACTGCTTATGGAGTCCG [8528]

Hsa GCCCT-CAGTAACAGTCTCCAGTCACGGCCACCGACGCCTGGCCC--AATGCTTTGCTAG [8894]
Mmu GCCTT-CAGTAACAGTCTCCAGTCACGGCCACCGACGCCTGGCCC--AATGCTTTGCTGA [8816]
Mdo ACCCT-CAGTAACAGTCTCCAGTCACGGCCACCGACGCCTGGCCC--AATGCTTTGCTAA [8339]
Meu ACCCT-CAGTAACAGTCTCCAGTCACGGCCACCGACGCCTGGCCC--AATGCTTTGCTAA [7040]
Oan ----------------------------------------------AATGCTTTGCTAA [7481]
Aca GCGAAACAGTAACAGTCCACAGTCATGGCTACTGACGGCTGGCGG--AATGCTTTGCTAA [8776]
Pbi GAGACACAGTAACAGTCTACAGTCATGGCTACTGAAGTCTGGCAG--AATGCTTTGCTAA [9166]
Cpi AAGAAACAGTAACAGTCTACAGTCATGGCTACTGAAGCATGACAG--AATGCTTTGCTAA [9509]
Cmy AGGAAACAGTAACAGTCTACAGTCATGGCTACTGAAGCATGACAG--AATGCTTTGCTAA [9177]
Psi GAGACACAGTAACAGTCTACAGTCATGGCTACTGAAGCATGACAG--AATGCTTTGCTAA [8577]
Asp ----------------------------------------------AATGCTTTGCTAA [8139]
Ami CCGGAACAGTAACAGTCTACAGTCATGGCTACTGAAGCATGACAG--AATGCTTTGCTAA [8822]
Asi ----------------------------------------------AATGCTTTGCTAA [8446]
Tgu ----------------------------------------------AATGCTTTGCTAA [6872]
Cli CAGGA-CAGTAACAGTCTACAGTCATGGCTACTGAAGCATGACCC--AATGCTTTGCTAA [8748]
Gga ----------------------------------------------AATGCTTTGCTAA [7822]
Xtr TAGGAACAGTAACAGTCTACAGTCATGGCTACTGACGTATGACTG--AATGCTTTGCTAA [8684]
Lch AAGATACAGTAACAGTCTACAGTCATGGCTACTGAAGCATGACAA--AATGCTTTGCTAA [9276]
Dre ACAGTACAGTAACAGTCTACAGTCATGGCTACTGAAGTCTGGCTC--AATGCTTTGCTAA [8586]

Hsa AGCTGGTAAAATGGAACCAAATCGACTGTCCAATGGATTTGGTCCCCTTCAACCAGCTGT [8954]
Mmu AGCTGGTAAAATGGAACCAAATCAGCTGTTGGATGGATTTGGTCCCCTTCAACCAGCTGT [8876]
Mdo AGCTGGTAAAAAGGAACCAAATCACCTGTGCGATGGATTTGGTCCCCTTCAACCAGCTGT [8399]
Meu AGCTGGTAAAAAGGAACCAAATCACCTGTGCGATGGATTTGGTCCCCTTCAACCAGCTGT [7100]
Oan AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [7541]
Aca AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [8836]
Pbi AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [9226]
Cpi AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [9569]
Cmy AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [9237]
Psi AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [8637]
Asp AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [8199]
Ami AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [8882]
Asi AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [8506]
Tgu AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [6932]
Cli AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [8808]
Gga AGCTGGTAAAATGGAACCAAATCAACTGTTCAATGGATTTGGTCCCCTTCAACCAGCTGT [7882]
Xtr AGCTGGTAAAATGGAACCAAATCAACTGTTGAATGGATTTGGTCCCCTTCAACCAGCTGC [8744]
Lch AGCTGGTAAAATGGAACCAAATCAACTGTTCTATGGATTTGGTCCCCTTCAACCAGCTGT [9336]
Dre AGCTGGTAAAATGGAACCAAATCAACTGTTTTATGGATTTGGTCCCCTTCAACCAGCTGT [8646]

Hsa AGCTGTGCATTG--AATGCTTTGCTAGAGCTGGTAAAATGGAACCAAATCGCCTCTTCAA [9012]
Mmu AGCTGCGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCGCCTCTTCAA [8934]
Mdo AGCTGTGCATTA--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTATTCAA [8457]
Meu AGCTGTGCATTA--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTATTCAA [7158]
Oan AGCTGCGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTCTTCAA [7599]
Aca AGCTGTGCATTG--GATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTGTTAAA [8894]
Pbi AGCTGTGCATTG--AATGCTTTGCTTAAGCTGGTAAAATGGAATCAAATCACATGTTTAA [9284]
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Cpi AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTCTTCAA [9627]
Cmy AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTCTTCAA [9295]
Psi AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTCTTCAA [8695]
Asp AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTCTTCAA [8257]
Ami AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTGTTCAA [8940]
Asi AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTGTTCAA [8564]
Tgu AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTCTTCAA [6990]
Cli AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTCTTCAA [8866]
Gga AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTCTTCAA [7940]
Xtr AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTCTTCAA [8802]
Lch AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTCTTCAA [9394]
Dre AGCTGTGCATTG--AATGCTTTGCTAAAGCTGGTAAAATGGAACCAAATCACCTCTTCAA [8704]

Hsa TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TGCCCCCTGCTCTGGCTGG [9070]
Mmu TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--GGCCCCCTGCTCTGGCTGG [8992]
Mdo TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TGCACCTTGCTCTGGCTGG [8515]
Meu TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG---------------------- [7197]
Oan TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TGAACCCTGCTCTGGCTGG [7657]
Aca TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGTATTG--TGAGTCCTGCTCTGGCTGG [8952]
Pbi TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGTATTG--AGAGCATTGCTCTGGCTGG [9342]
Cpi TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TGCACCCTGCTCTGGCTGG [9685]
Cmy TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TGCACCCTGCTCTGGCTGG [9353]
Psi TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TGCACCCTGCTCTGGCTGG [8753]
Asp TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TGCACCCTGCTCTGGCTGG [8315]
Ami TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TGCACTCTGCTGTGGCTGG [8998]
Asi TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TGCACTCTGCTGTGGCTGG [8622]
Tgu TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TATGCTCTGCTCTGGCTGG [7048]
Cli TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TATGCTCTGCTCTGGCTGG [8924]
Gga TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG--TATGCTCTGCTCTGGCTGG [7998]
Xtr TGGATTTGGTCCCCTTCAACCAGCTGTAGGATTGCATTG--TACAGGCTGCTATGGCTGG [8860]
Lch TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCATTG---------------------- [9433]
Dre TGGATTTGGTCCCCTTCAACCAGCTGTAGCTATGCTTTG--CACGCCTTGCTGTGGCTGG [8762]

Hsa TCAAACGGAACCAAGTCCG-TCTTCCTGAGAGGTTTGGTCCCCTTCAACCAGCTACAGCA [9129]
Mmu TCAAACGGAACCAAGTCCG-TCTTCCTGAGAGGTTTGGTCCCCTTCAACCAGCTACAGCA [9051]
Mdo TCAAACGGAACCAAGTCCG-TCTGACTGAGAGGTTTGGTCCCCTTCAACCAGCTACAGCA [8574]
Meu ------------------------------------------------------------ [7197]
Oan TCAAACGGAACCAAGTCCG-TCTGCCTGAGAGGTTTGGTCCCCTTCAACCAGCTACAGCG [7716]
Aca TCAAAGGGAACCACGGCTG-TCTTCCTTGAAGGTTTGGTCCCCTTTAACCAGCTACAGCA [9011]
Pbi TCAAAAGGAACCAAGGCCG-TCTTTCCTGGAGGTTTGGTCCCCTTCAACCAGCTATAGCA [9401]
Cpi TCAAACGGAACCAAGTCCG-TCTTCCTTGGAGGTTTGGTCCCCTTCAACCAGCTACAGCA [9744]
Cmy TCAAACGGAACCAAGTCCG-TCTTCCTTGGAGGTTTGGTCCCCTTCAACCAGCTACAGCA [9412]
Psi TCAAACGGAACCAAGTCCG-TCTTCCTTGAAGGTTTGGTCCCCTTCAACCAGCTACAGCA [8812]
Asp TCAAACGGAACCAAGTCCG-TCTTCCTTGGAGGTTTGGTCCCCTTCAACCAGCTACAGCA [8374]
Ami TCAAACGGAACCAAGTCCG-TCTTCCTTGGAGGTTTGGTCCCCTTCAACCAGCTATAGCA [9057]
Asi TCAAACGGAACCAAGTCCG-TCTTCCTTGGAGGTTTGGTCCCCTTCAACCAGCTATAGCA [8681]
Tgu TCAAACGGAACCAAGCCCG-TCTTCCTCGGAGGTTTGGTCCCCTTCAACCAGCTATAGCA [7107]
Cli TCAAACGGAACCAAGCCCA-TCTTCCTCGGAGGTTTGGTCCCCTTCAACCAGCTATAGCA [8983]
Gga TCAAACGGAACCAAGCCCG-TCTTCTTCGGAGGTTTGGTCCCCTTCAACCAGCTATAGCA [8057]
Xtr TCAAACGGAACCAAGTCCG-TCTTCCTTAGAGGTTTGGTCCCCTTCAACCAGCTATTGCA [8919]
Lch ------------------------------------------------------------ [9433]
Dre TCAAATGGAACCAAGTCAGGTGTTTCTGCGAGGTTTGGTCCCCTTCAACCAGCTACTGCG [8822]

Hsa GGGCTGG------------------------------------------------------ [9136]
Mmu GGGCTGG------------------------------------------------------ [9058]
Mdo GGGCTGA------------------------------------------------------ [8581]
Meu ------------------------------------------------------------ [7197]
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Oan GGGCCGA--GGCCAGCTGCTGGGGCTGGTCAAAAGGAACCAGATCGCCTC-TCCACCTGA [7773]
Aca GTCCTGA--TATGTGTCCCTAGGGCTGGTAAAAAGGAACCAGATCGACTG-GCAACTGGA [9068]
Pbi GTGCTGA--CTTGTGCTCCTGGGGCTGGTAAAAAGGAACCAGATCGACTG-GCAACTG-A [9457]
Cpi GTGCTGA--AGTGTGTCCCTGGGGCTGGTAAAAAGGAACCAGATCAACTT-GGAACTGGA [9801]
Cmy GTGCTGA--AGTGTGTCCCTGGGGCTGGTAAAAAGGAACCAGATCAACTT-GGAACTGGA [9469]
Psi GTGCTGA--AGTGCGTCCCTGGGGCTGGTAAAAAGGAACCAGATCAACCT-GGAAATGGA [8869]
Asp GTGCTGA--AGTGCGTTCCTGGGGCTGGTAAAAAGGAACCAGATCAACCT-GGAAATGGA [8431]
Ami GTGCTGA--AGTGTGTTCCTGGGGCTGGTAAAAAGGAACCAGATCAACTT-GGAACTGGA [9114]
Asi GTGCTGA---------------------------------------------------- [8688]
Tgu GTGTGGA---------------------------------------------------- [7114]
Cli GTGTTGA--GGTGCGTCCCTGGGGCTGGTAAAAAGGAACCAGATCAACTT-GCAACTGGA [9040]
Gga GTGTTGA--GGTGCCTTCCTGGGGCTGGTAAAAAGGAACCAGATCAACT--ACAACTGGA [8113]
Xtr GTACTGA--GCTGTCTGGTTGCGGCTGGTGAAAAGGAACCACATCAACCCAGAAAAAGGA [8977]
Lch ---------AATGCTTTGCTGAAGCTGGTAAAATGGAACCAGATCAACTT-TCTATTGGA [9483]
Dre TCGTGAA---------------------------------------------------- [8829]

Hsa ------------------------------------GGCCTCGCTGTTCTCTATGGCTT [9159]
Mmu ------------------------------------GGCCTCACTGTTCTCTATGGCTT [9081]
Mdo ---------------------------------------------------------- [8581]
Meu ---------------------------------------------------------- [7197]
Oan TTTGGTCCCCTTCAACCGGCTGCAGCGGGTTGCCG--GGCCCCGCTGTGCTCTATGGCTT [7831]
Aca TTTGGTCCCCTTCAACCAGCTGTGGTGGCACGTGA--TGCCCCATTGTCTTCTATGGCTT [9126]
Pbi TTTGGTCCCCTTCAACCAGCTGGGGGGGCACAAAC--TATCCCATTGTCTTCTATGGCTT [9515]
Cpi TTTGGTCCCCTTCAACCAGCTGCAGTGGCGCATAC--TGTCCCACTGTCTTCTATGGCTT [9859]
Cmy TTTGGTCCCCTTCAACCAGCTGCGGTGGCGCATAT--TGTCCCACTGTCTTTTATGGCTT [9527]
Psi TTTGGTCCCCTTCAACCAGCTGCGGTGGCGCATGC--GGTCCCATTGTCTTCTATGGCTT [8927]
Asp TTTGGTCCCCTTCAACCAGCTGCAGTGGCGCATGC--GGTCCCATTGTCTTCTATGGCTT [8489]
Ami TTTGGTCCCCTTCAACCAGCTGTAGTGGCACATAA--GGTCCCACTGTGTTATATGGCTT [9172]
Asi ------------------------------------GGTCCCACTGTGTTATATGGCTT [8711]
Tgu ------------------------------------CAGCCTGCCGTCTTGTATGGCTT [7137]
Cli TTTGGTCCCCTTCAACCAGCTGCAGCGGCGCATGT--TGGCCTGCTGTCTTGTATGGCTT [9098]
Gga TTTGGTCCCCTTCAACCAGCTGCAGTGGGGCACGA--CGCCTCACTGTCCTGTATGGCTT [8171]
Xtr TTTGGTCCCCTTCAACCAGCCGCAACTGGTCAGGA------------------------ [9012]
Lch TTTGGTCCCCTTCAACCAGCTGTAGCTGTGCATTT--CTATCCATCATGCTGTATGGCTT [9541]
Dre ------------------------------------TTGCTCTTTGCCCCGTATGGCTT [8852]

Hsa TTTATTCCTATGTGATTCTACTGCTCA--CTCATATAGGGATTGGAGCCGTGGCGCACGG [9217]
Mmu TTTATTCCTATGTGATTCTATTGCTCG--CTCATATAGGGATTGGAGCCGTGGCGTACGG [9139]
Mdo ---------------------------------------------------------- [8581]
Meu ---------------------------------------------------------- [7197]
Oan TTTATTCCTATGTGATCCTGCTGCTCA--CTCATATAGGGATTGGAGCCGTGCAACACGG [7889]
Aca TTTATTCCTATGTGATTATATCACTAA-TTTCATATAGGGATTGAAGCCATGTAATACGC [9185]
Pbi TTTATTCCTATGTGATTATATTGCTAA-TTTCATATAGGGATTGAAGCCATGCAATACAC [9574]
Cpi TTTATTCCTATGTGATTATACTGCTAA-TTTCATATAGGGATTGAAGCCGTGCAATACGC [9918]
Cmy TTTATTCCTATGTGATTATACTGCTCA-TTTCATATAGGGATTGAAGCCGTGCAATACGC [9586]
Psi TTTATTCCTATGTGATTATACTGCTCA-TTTCATATAGGGATTGAAGCCGTGCAATACGG [8986]
Asp TTTATTCCTATGTGATTATACTGCTCA-TTTCATATAGGGATTGAAGCCGTGCAATACGG [8548]
Ami TTTATTCCTATGTGATTATACTACTCC-TTTCATATAGGGATTGAAGCCGTGCAATACGC [9231]
Asi TTTATTCCTATGTGATTATACTACTCC-TTTCATATAGGGATTGAAGCCGTGCAATACGC [8770]
Tgu TTTATTCCTATGTGATTATACATCCCA-CTTCATATAGGGATTGAAGCCGTGCAGTACGC [7196]
Cli TTTATTCCTATGTGATTATACATCCCA-CTTCATATAGGGATTGAAGCCGTGCAATACAC [9157]
Gga TTTATTCCTATGTGATTATACATCCCG-CTTCATATAGGGATTGAAGCCGTGCAAGGCGC [8230]
Xtr ---------------------------------------------------------- [9012]
Lch TTTATTCCTATGTGATTGTGCTTGTGTATTTCATATAGGGATGGAAGCCATGAAGTATGG [9601]
Dre TTTATTCCTATCTGAGAATTGCTCAGG-ACTCATATAGGGATGGAAGCCATGCAGGGCTG [8911]

Hsa CGGGGA--TTCACTCTAGTGCTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [9275]
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Mmu TGAGGA--TTCACTCTAGTGCTTTATGGCTTTTTATTCCTATGTGATCGTAATAAAGTCT [9197]
Mdo --------TTCACTCTAGTGTCTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [8633]
Meu --------TTCACTCTAGTGTCTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [7249]
Oan AGGGGG--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [7947]
Aca TGGGGA--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [9243]
Pbi TGGGGA--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [9632]
Cpi TGGGGC--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [9976]
Cmy TGGGGC--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [9644]
Psi TGGGGC--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [9044]
Asp TGGGGC--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [8606]
Ami TGGGGA--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [9289]
Asi TGGGGA--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [8828]
Tgu CGGGGT--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [7254]
Cli TGGGGT--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [9215]
Gga TGGGGT--TTCACTCTAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [8288]
Xtr --------TTCACTGTGGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAATGTCT [9064]
Lch TGGGAG--TTCACTCCAGTGTTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCT [9659]
Dre GGGGAC--ACAGCTGTCGTGTCTTATGGCTTTTTATTCCTATGTGAAGGTGAACAAGGCT [8969]

Hsa CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CACTCTGCTGTGGCCTATGGC [9333]
Mmu CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CGCTCTGCTGTGGCCTATGGC [9255]
Mdo CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAT--CTCTCTGCTGTGGCCTATGGC [8691]
Meu CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAT--AACTCTGCTGTGGCTTATGGC [7307]
Oan CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CTCTCTGCTGTGGCCTATGGC [8005]
Aca CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CCCTCTGCTGTGGTCTATGGC [9301]
Pbi CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--TCCTCTGTTGTGGTCTATGGC [9690]
Cpi CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CCCTCTGCTGTGGTCTATGGC [10034]
Cmy CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CCCTCTGCTGTGGTCTATGGC [9702]
Psi CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CCCTCTGCTGTGGTCTATGGC [9102]
Asp CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CCCTCTGCTGTGGTCTATGGC [8664]
Ami CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CCCTCTGCTGTGGTCTATGGC [9347]
Asi CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CCCTCTGCTGTGGTCTATGGC [8886]
Tgu CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CCCTCTGCTGTGGTTTATGGC [7312]
Cli CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CCCTCTGCTGTGGTTTATGGC [9273]
Gga CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CCCTCTGCTGTGGTCTATGGC [8346]
Xtr CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--CCCCCTGCTGAGGTATATGGC [9122]
Lch CATGTAGGGATGGAAGCCATGAAATACATTGTGAAAA--ATCCCTGTTGTGTTCTATGGC [9717]
Dre CATGTAGGGATACAAGCCACTAAACACGCAGTCAGAA--GTCACTGCTGTGTTTTATGGC [9027]

Hsa TTTTCATTCCTATGTGATTGCTGTCCCAA-ACTCATGTAGGGCTAAAAGCCATGGG-CTA [9391]
Mmu TTTTCATTCCTATGTGATTGCTGCTCCGA-ACTCATGTAGGGCTAAAAGCCATGGG-CTA [9313]
Mdo TTTTCATTCCTATGTGATTGCTGTTCCCA-ACTCATGTAGGGCTAAAAGCCATGGG-CTA [8749]
Meu TTTTCATTCCTATGTGATTACTGTTCCCA-ACTCATGTAGGGCTAAAAGCCATGGG-CTA [7365]
Oan TTTTTATTCCTATGTGATTGCTGCTTTGA-ACTCATGTAGGGCTGAAAGCCATGGG-CTA [8063]
Aca TTTTTATTCCTATGTGATTGCTTTTCATA-ACTCATGTAGGGCTAAAAGCCATGGG-CTA [9359]
Pbi TTTTTATTCCTATGTGATTGCTTTTCATA-ATTCATGTAGGGCTAAAAGCCATGGG-TTA [9748]
Cpi TTTTTATTCCTATGTGATTGCGTTTCCTA-ACTCATGTAGGGCTAAAAGCCATGGG-CTA [10092]
Cmy TTTTTATTCCTATGTGATTGCGTTTCCTA-ACTCATGTAGGGCTAAAAGCCATGGG-CTA [9760]
Psi TTTTTATTCCTATGTGATTGCTTTTCCTA-CCTCATGTAGGGCTAAAAGCCATGGG-CTA [9160]
Asp TTTTTATTCCTATGTGATTGCTTTTCCTA-CCTCATGTAGGGCTAAAAGCCATGGG-CTA [8722]
Ami TTTTTATTCCTATGTGATTGCTTTTCCTA-ACTCATGTAGGGCTAAAAGCCATGGG-CTA [9405]
Asi TTTTTATTCCTATGTGATTGCTTTTCCTA-ACTCATGTAGGGCTAAAAGCCATGGG-CTA [8944]
Tgu TTTTTATTCCTATGTGATTGCTTTCCCGA-ACTCATGTAGGGCGAAAAGCCATGGG-CTA [7370]
Cli TTTTTATTCCTATGTGATTGCTTTTCCTA-ACTCATGTAGGGCGAAAAGCCATGGG-CTA [9331]
Gga TTTTTATTCCTATGTGATTGCTTTTCCTA-ACTCATGTAGGGCGAAAAGCCATGGG-CTA [8404]
Xtr TTTTTATTCCTATGTGATTGC-TTTCCTA-ATTCACATAGGGCAGAAAGCCATGTG-CTG [9179]
Lch TTTTTATTCCTATGTGATTACTGTTTCTA-ACTCATGTAGGGTTGAAAGCCATGGG-CTA [9775]
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Dre TTTCTATTCCTATGTGATTTTCTTCTGCCGTGTCACATAGGGTTCAAAGCCATTGG-GTA [9086]

Hsa CAGTGAGGGG--GGTCCTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9449]
Mmu CAGTGAGGGG--GGCCCTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9371]
Mdo CAGGGAGGGG--ATCTTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [8807]
Meu CAGGGAGGGG--ATCTTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [7423]
Oan CAGAGAGGGG--GTCTTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [8121]
Aca CACAGAGGAA--AGCTTCCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9417]
Pbi CACAAAGGAA--AGCTTTCCGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9806]
Cpi CACAGAGGAC--AGCTTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [10150]
Cmy CATAGAGGAC--AGATTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9818]
Psi CACAGAGGAC--AGATTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9218]
Asp CACAGAGGAC--AGATTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [8780]
Ami CACAGAGGAT--AGCTTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9463]
Asi CACAGAGGAT--AGCTTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9002]
Tgu CACAGAGGAG--AGCTTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [7428]
Cli CACAGAGGAG--AGCTTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9389]
Gga CTCAGGGGAG--AGCTTTCTGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [8462]
Xtr CACAGGGGAC--TGCTCTGTGGCTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9237]
Lch CTCAGTGGGA--CTTTATAAGACTCTTTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9833]
Dre CAGAGTGGAA--CTATAAAGGACTCTCTTCGGTGACGGGTATTCTTGGGTGGATAATACG [9144]

Hsa GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCAGCGGC------- [9502]
Mmu GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCAGCGGC------- [9424]
Mdo GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCTGCAGC--ATTGC [8865]
Meu GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCTGCGGC--AATGG [7481]
Oan GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTATCTGCGGC--AGCCC [8179]
Aca GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACTCGCGGC--ACTGA [9475]
Pbi GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACTCGCGGC--ATGAC [9864]
Cpi GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCGGCGGC--GCCCA [10208]
Cmy GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCCGCGGC--GCCCG [9876]
Psi GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCCGCGGC--GCTCA [9276]
Asp GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCCGCGGC--GCTCA [8838]
Ami GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACC-GCGGC--GGAGC [9520]
Asi GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACC-GCGGC------- [9054]
Tgu GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCGGCGGC------- [7481]
Cli GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCGGCGGC--GGCCC [9447]
Gga GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCGGCGGC------- [8515]
Xtr GATTACGTTGTTATTGCTTAAGAATACGCGTAGTTGAGGAGAGTATCTTCAGC------- [9290]
Lch GATTACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTACCTTCTCC--TCAAT [9891]
Dre GCTCTCGTTGTTATTGCTTAAGAATACGCGTAGTCGAGGAGAGTCATGTCGGC------- [9197]

Hsa ---------------------------------------------------------- [9502]
Mmu ---------------------------------------------------------- [9424]
Mdo CTAGCCCCCCGCGATGACGGGTATTCTTGGGTAGATAATACCAATGGCGCTGTTATTGCT [8925]
Meu CTGGCCCCCCGCGATGACGGGTATTCTTGGGTAGATAATACCGATGGCGCTGTTATTGCT [7541]
Oan CCAGCCCCTTTCGATGACGGGTATTCTTGGGTACATAATACGGATGGCGCTGTTATTGCT [8239]
Aca CTAGCTCCCTTCAATAACGGGTATTCTTGGGTATATAATACAGATGGCGTTGTTATTGCT [9535]
Pbi TATGCTCCCTTCGATGACGGGTATTCTTGGGTATATAATACAGATGGCGTTGTTATTGCT [9924]
Cpi CTAGCTCCCTTCGATGACGGGTATTCTTGGGTAGATAATACGGATTGCGTTGTTATTGCT [10268]
Cmy CTAGCTCCCTTCGGCGACGGGTATTCTTGGGTAGATAATACGGATTGCGTTGTTATTGCT [9936]
Psi CGAGCTCTCTTCGGCGACGGGTATTCTTGGGTAGATAATACGGATTGCGTTGTTATTGCT [9336]
Asp CGAGCTCTCTTCGGCGACGGGTATTCTTGGGTAGATAATACGGATTGCGTTGTTATTGCT [8898]
Ami CCAGCTCCCTTCGATGACGGGTATTCTTGGGTAGATAATACGGCTGGCGTTGTTATTGCT [9580]
Asi ---------------------------------------------------------- [9054]
Tgu ---------------------------------------------------------- [7481]
Cli CCCGCTCCCTTCGGCAACGGGTATTCTCGGGCGGATAATACGGAC-GCGCTGTTATTGCT [9506]
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Gga ------------------------------------------------------------ [8515]
Xtr ------------------------------------------------------------ [9290]
Lch GCTATTCCCTTCGGCAACGGGTATTCTTGGGTAGATAATACGGATTGCGTTGTTATTGCT [9951]
Dre ------------------------------------------------------------ [9197]

Hsa ---------------------------------------TGGTGTGGTGGGGCAGCTGGTG [9524]
Mmu ---------------------------------------TGGTGTTGTGGGACAGCTGGTG [9446]
Mdo TGAGAATACACGTAGTCGAGGG-GAGGCCTCTTCGA--CGGCCTGGTGTGGCAGCTGGTG [8982]
Meu TGAGAATACACGTAGTCGAGGG-GAGGCGCCTTCGA--TGGCAAGGTGTGGCAGCTGGTG [7598]
Oan TGAGAATACGCGTAGTCGAGGGAGAGGCACCGACGT--AGGTATGGTGAAGCAGCTGGTG [8297]
Aca TGAGAATACGCGTAGTTGAGGG-GATGCTGATTCAT--TGGCTTGGTGTAGCAGCTGGTG [9592]
Pbi TGAGAATACGCGTAGTTGAGGG-GAAGTTGCTTCAG--TGGCTCAGTGTAGCAGCTGGTG [9981]
Cpi TGAGAATACGCGTAGCCGAGGG-GAGAGTCGCTCAT---------------------- [10303]
Cmy TGAGAATACGCGTAGCCGAGGG-GAGAGTCTCTCAT--TGGTATGGTGCAGCAGCTGGTG [9993]
Psi TGAGAATACGCGTAGCCGAGGG-GAGCGCTGCTCAT--TGGTATGGTATAGCAGCTGGTG [9393]
Asp TGAGAATACGCGTAGCCGAGGG-GAGAGCTGCTCAT--TGGTATGGTATAGCAGCTGGTG [8955]
Ami TGAGAATACGCGTAGTCGAGGG-GAGAGACACTCGC--TGGTACAGTGCTGCAGCTGGTG [9637]
Asi ---------------------------------------TGGTACAGTGCTGCAGCTGGTG [9076]
Tgu ---------------------------------------AGGTGCTGTGCAACAGCTGGTG [7503]
Cli TGAGAATACGCGTAGCCGAGGG-GACGCCCCGCCCC--AGGTGCCGTGCAGCAGCTGGTG [9563]
Gga ---------------------------------------GGGTGCCGTGCAGCAGCTGGTG [8537]
Xtr ---------------------------------------CGGTGCGGAGCAGCAGCTGGTG [9312]
Lch TGAGAATACGCGTAGTCGAGGG-GAGTCGTGCTCAG--TGGTTTGGTGCAGCAGCTGGTG [10008]
Dre ---------------------------------------TGATGGAGCAGGACAGCTGGTG [9219]

Hsa TTGTGAATCAGGCCGTTGCCAATCAGAGA-ACGGCTACTTCACAACACCAGGGCCACACC [9583]
Mmu TTGTGAATCAGGCCGTTGCCAATCAGAGA-ACGGCTACTTCACAACACCAGGGCCACACT [9505]
Mdo TTGTGAATCAGGCCGTCGCCAGTCTGAGA-ACGGCTACTTCACAACACCAGGGTCACCCC [9041]
Meu TTGTGAATCAGGCCGGCGCCAGTCTCAGA-ACGGCTCCTTCACAACACCAGGGTCACCCC [7657]
Oan TTGTGAATCAGGCCGTCGCCAATCTGAGA-ACGGCTACTTCACAACACCAGGGTTGCACC [8356]
Aca TTGTGAATCAGGCCGTTGCCAAAGAGAGA-ACGGCTACTTCACAACACCAGGGTTGCCCC [9651]
Pbi TTGTGAATCAGGCCGTCACCTATTAGAGA-ACGGCTACTTCACAACACCAGGGTTGCCCT [10040]
Cpi ------------------------------------------------------------ [10303]
Cmy TTGTGAATCAGGCCGTCACCAATCAGAGA-ACGGCTACTTCACAACACCAGGGTTGTACC [10052]
Psi TTGTGAATCAGGCCGTTGCCAATCAGAGA-ACGGCTACTTCACAACACCAGGGTTGTATC [9452]
Asp TTGTGAATCAGGCCGTTGCCAATCACAGA-ACGGCTACTTCACAACACCAGGGTTGTATC [9014]
Ami TTGTGAATCAGGCCGTCACCGATCAGAGA-ACGGCTACTTCACAACACCAGGGTTGCACC [9696]
Asi TTGTGAATCAGGCCGTCACCGATCAGAGA-ACGGCTACTTCACAACACCAGGGTTGCACC [9135]
Tgu TTGTGAATCAGGCCGTCACCAGTCGGAGA-ACGGCTACTTCACAACACCAGGGTCGCACC [7562]
Cli TTGTGAATCAGGCCGTCACCAGTCGGAGA-ACGGCTACTTCACAACACCAGGGTCGCACC [9622]
Gga TTGTGAATCAGGCCGTCACCAGTCGGAGA-ACGGCTACTTCACAACACCAGGGTGGCACT [8596]
Xtr TTGTGAATCAGGCCGTGACCACTCAGAAA-ACGGCTACTTCACAACACCAGGGTTGCTTC [9371]
Lch TTGTGAATCAGGCCGCCACCAATCACAGA-ACGGCTACTTCACAACACCAGGGTTGCACC [10067]
Dre TTGTGAATCAGGCCGCCGTGGTGAAAGGGTACGGCTTCTTCACAACACCAGGGTCTCACT [9279]

Hsa ACACT--GTATCGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACGAGCAGCGCATCCTC [9641]
Mmu GCACT--GTATGGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACGAGCAGCGCATCCTC [9563]
Mdo CTGCC--GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACAAGCAGCTCATCCTA [9099]
Meu CCGCC--GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACAAGCAGCTCATCCTA [7715]
Oan CTGCC--GTATCGGTGCTGCAGCTGGTGTTGTGAATCAGGCCGACGAGCAGCGAGTCCTA [8414]
Aca CTGCC--GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACAAAAAGCGCATCTTA [9709]
Pbi GTACC--GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACATAAAGTGCATCTTA [10098]
Cpi -------GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACAACAAGCTCATCCTA [10356]
Cmy CTACC--GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACAACAAGCTCATCCTA [10110]
Psi CTGCC--GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACAACAAGCTCATCCTA [9510]
Asp TTGCC--GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACAACAAGCTCATCCTA [9072]
Ami CTACC--GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACAACAAGCGCATCCTA [9754]
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Asi CTACC--GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACAACAAGCGCATCCTA [9193]
Tgu GCACC--GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACGACAAGCGCTTCCTA [7620]
Cli GCACC--GTATTGGTGCTGCAGCTGGTGTTGTGAATCAGGCCGACGACAAGCGCATCCTA [9680]
Gga GCACC--GTATTGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACGGCAAGCGCTTCCTA [8654]
Xtr TCACC---------------------------------------------------- [9376]
Lch TTGCT--GTATTGGTGCTGCAGCTGGTGTTGTGAATCAGGCCGGCAAAAAGTACCTGCTA [10125]
Dre TCATC--GTGTGTGTGCTGCAGCTGGTGTTGTGAATCAGGCCGATGTCACACGTCAGCGA [9337]

Hsa TTACCCGGCTATTTCACGACACCAGGGTTGCATCATACC--GGCTCAGGTGTATTCTACA [9699]
Mmu TTACCCGGCTATTTCACGACACCAGGGTTGCACCCTACC--GGCGCAGGTGTATTCTACA [9621]
Mdo TTACCCGGCTATTTCACTACACCAGGGTTGCATCATACC--GGCCCGGGTGTATTCTACA [9157]
Meu TTACCCGGCTATTTCACCACACCAGGGTTGCATCATACC--GGCCCGGGTGTATTCTACA [7773]
Oan ATACCCGGCTATTTCACTACACCAGGGTTGCATCATACC--GGCCCGGGTGTAGTCTACA [8472]
Aca CTATCCGGCTATTTCACTACACCAGGGTTGCATCATACC--GGCCTGGCTGTATTCTACA [9767]
Pbi CTATCCGGCTATTTCACTACACCAGGGTCGCATCGTACC--GGCCTGGCTGTATTCTACA [10156]
Cpi CTATCCGGCTATTTCACTACACCAGGGTTGCATCATACC--GGCCTGGCTGTATTCTACA [10414]
Cmy CTATCCGGCTATTTCACTACACCAGGGTTGCATCATACC--GGCCTGGCTGTATTCTACA [10168]
Psi CTATCCGGCTATTTCACTACACCAGGGTTGCATCATACC--GGCCTGGCTGTATTCTACA [9568]
Asp CTATCCGGCTATTTCACTACACCAGGGTTGCATCATACC---------------------- [9111]
Ami CTATCCGGCTATTTCACTACACCAGGGTTGCATCATACC--GGCCTGGCTGTATTCTACA [9812]
Asi CTATCCGGCTATTTCACTACACCAGGGTTGCATCATACC--GGCCTGGCTGTATTCTACA [9251]
Tgu CAATCCGGCTATTTCACTACACCAGGGTTGCATCATACC--GGCCTGGCTGTATTCTACA [7678]
Cli CTATCCGGCTATTTCACTACACCAGGGTTGCATCATACC--GGCCTGGCTGTATTCTACA [9738]
Gga CTATCCGGCTATTTCACTACACCAGGGTTGCATCATACC--GGCCAGGCTGTATTCTACA [8712]
Xtr ----------------------------------------GGCCTGGGTGTATTCTACA [9395]
Lch CGATCCGGCTATTTCACAACACCAGGGTTGCATCATACC--GGCTTGGCTGTATTCTACA [10183]
Dre TAACCCGGCTATTTCACAACACCAGGGTGGCACCACACC--GGTCTGGCTGTATTCTACA [9395]

Hsa GTGCACGTGTCTCCAGTGTGGCTC-GGAGGCTGGAGACGCGGCCCTGTTGGAGTAACAAC [9758]
Mmu GTGCACGTGTCTCCAGTGTGGCTC-GGAGGCTGGAGACGCGGCCCTGTTGGAGTAACAAC [9680]
Mdo GTGCATGTGTCTCCAGTGTGACTA-AGGGACTGGAGATACAGCCCTGTTGGAATAACAAC [9216]
Meu GTGCATGTGTCTCCAGTGTGACTA-AGGGACTGGAGATACAGCCCTGTTGGAATAACAAC [7832]
Oan GTGCATGTGTCTCCAGGGACACTA-GACAGCTGGAGACACAGCTCTGTTGGA-TA-CAAC [8529]
Aca GTGCATGTGTCTCCAGTGTTTTCC-AGCGACTGGAGATACGGCCCTGTTGGAATAACAGC [9826]
Pbi GTGCATGTGTCTCCAGCGTCTGTA-AGCAGCTGGAGATACGGCCCTGTTGGAATAACAGC [10215]
Cpi GTGCATGTGTCTCCAGTGTTACTA-AGCAACTGGAGATGCAGCCCTGTTGGAATAACAGC [10473]
Cmy GTGCATGTGTCTCCAGTGTTACTA-AGCAACTGGAGATGCAGCCCTGTTGGAATAACAGC [10227]
Psi GTGCATGTGTCTCCAGTGTTACTA-AGCAACTGGAGAGACAGCCCTGTGGGAAT------ [9621]
Asp ---------------------------------------------------------- [9111]
Ami GTGCATGTGTCTCCAGTGTTTCTA-AGCGACTGGAGATACAGCCCTGTCGGAATAACAGC [9871]
Asi GTGCATGTGTCTCCAGTGTTTCTA-AGCGACTGGAGATACAGCCCTGTCGGAATAACAGC [9310]
Tgu GTGCATGTGTCTCCAGTGTGAGTA-AGTGACTGGAGATGCGGCCCTGTTGGAATAACATC [7737]
Cli GTGCATGTGTCTCCAGTGTGAGTA-AGTGACTGGAGATGCAGCCCTGTTGGAATAACAAC [9797]
Gga GTGCATGTGTCTCCAGTGTCACTC-AGCAACTGGGGACACAGCCCTGTTGGAATCACAGC [8771]
Xtr GTGCATGTGTCTCCAGTCATATAG-AGGCACTGGGGATACAGCTCTGTTGGAATAACAAT [9454]
Lch GTGCATGTGTCTCCAGTGGTTCTA-GGCAGCTGGAGATACAGCCCTGTTGGAATAACAAC [10242]
Dre GTGCATGTGTCTCCAGTGTTTCTATGGCGACTGGGGAGGCAGCGCTGTTGGAATAACAAC [9455]

Hsa TGAAGCC--GTGTCT--CTCTCTGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [9814]
Mmu TGAAGCC--GTGTCT--CTCTCTGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [9736]
Mdo CGAAGCC--GTGTCT--CTCTCTGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [9272]
Meu CGAAGCC--GTGTCT--CTCTCTGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [7888]
Oan CGAAGCC--GTGTCT--CTCTCTGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [8585]
Aca CAGAGCC--CTTCCT--CTCTCTGTGTCCTTCCAGTGGTTTTACCCTATGGTAGGTTACG [9882]
Pbi CAGAGCT---------------------------------------------------- [10222]
Cpi CAGAGCC--CTGTCT--CTCTCTGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [10529]
Cmy CAGAGCC--GTGTCT--CTCTCTGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [10283]
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Psi ------------------------------------------------------------ [9621]
Asp ------------------------------------------------------------ [9111]
Ami CAGCGCC--TGCTCT--CTCTCTGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [9927]
Asi CAGCGCC--TGCTCT--CTCTCTGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [9366]
Tgu CAGTGCC--CCACCT--CTCTCCGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [7793]
Cli CGGGACC--CCGCCT--CTCTCCGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [9853]
Gga CTGTGCC--CTGCGT--CTCTCCGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACG [8827]
Xtr CAGTGCC--CTCTCC--CTCTCTGTGTCCTCCCAGTGGTTTTACCCTATGGTAGGTTACG [9510]
Lch TAAGACC--GTGTGT--TTCCCTGTGTCTAGCCAGTGGTTTTACCCTATGGTAGGTTACG [10298]
Dre CAGAACC--GTGTTTG-TCTCCTGTGTCCCGTCAGTGGTTTTACCCTATGGTAGGTTACG [9512]

Hsa TCATGCTGTTCTACCACAGGGTAGAACCACGGACAGGATACCGGGGCACC--CAGTGCAG [9872]
Mmu TCATGCTGTTCTACCACAGGGTAGAACCACGGACAGGATACTGGAGCACC--CAGTGCAG [9794]
Mdo TCATGCTGTTCTACCACAGGGTAGAACCACGGACAGGATACTGGGGCGCT--CAGTGCAG [9330]
Meu TCATGCTGTTCTACCACAGGGTAGAACCACGGACAGGATACTGGGGCGCT--CAGTGCAG [7946]
Oan TCATGCTGTTCTACCACAGGGTAGAACCACGGACAGGATACCGGGACGCT--CAGTGCAG [8643]
Aca TCATGCTGTTCTACCACAGGGTAGAACCACGGACGGGATGCCGGGGCTCT--CAGTGGAC [9940]
Pbi ----------------------------------------------------CAGTGGAC [10230]
Cpi TCATGCTGTTCTACCACAGGGTAGAACCACGGACAGGATACCGGG-CGCT--CAGTGCAG [10586]
Cmy TCATGCTGTTCTACCACAGGGTAGAACCACGGACAGGATACCGGG-CGCT--CAGTGCAG [10340]
Psi ------------------------------------------------------------ [9621]
Asp ------------------------------------------------------------ [9111]
Ami TCATGCTGTTCTACCACAGGGTAGAACCACGGACGGGATACCGGGGCGCG--CAGTGCAG [9985]
Asi TCATGCTGTTCTACCACAGGGTAGAACCACGGACGGGATACCGGGGCGCG--CAGTGCAG [9424]
Tgu TCATGCTGTTCTACCACAGGGTAGAACCACGGACAGGATGCCGGGGCTGC--CAGTGCAG [7851]
Cli TCATGCTGTTCTACCACAGGGTAGAACCACGGACGGGATGCTGGGGCTGC--CAGTGCAG [9911]
Gga TCATGCTGTTCTACCACAGGGTAGAACCACGGACGGGATGCCGGGGCTGC--CAGTGCAG [8885]
Xtr TCAGGCTGTTCTACCACAGGGTAGAACCACGGACAGGATACGGGGAGCTC--CAGTGCAG [9568]
Lch TCATGCTGTTCTACCACAGGGTAGAACCACGGACCGGATACCAGGGGTTC--CAGTGGAG [10356]
Dre TCATGCTGTTCTACCACAGGGTAGAACCACGGACGGGATGTCTGGAGGTG--CAGTGCAG [9570]

Hsa TCACCCATAAAGTAGAAAGCACTACTAA-CAGCACTG-GAGGGTGTAGTGTTTCCTACTT [9930]
Mmu TCACCCATAAAGTAGAAAGCACTACTAA-CAGCACTG-GAGGGTGTAGTGTTTCCTACTT [9852]
Mdo TCACCCATAAAGTAGAAAGCACTACTAA-CAGCAATG-TAGGGTGTAGTGTTTCCTACTT [9388]
Meu TCACCCATAAAGTAGAAAGCACTACTAA-CAGCAATG-TAGGGTGTAGTGTTTCCTACTT [8004]
Oan TCATCCATAAAGTAGAAAGCACTACTAA-CAGCGCTG-TAGGGTGTAGTGTTTCCTACTT [8701]
Aca TCATCCATAAAGTAGAAAGCACTACTAAACGCCTGTGCCCAAGTGTAGTGTTTCCTACTT [10000]
Pbi TCATCCATAAAGTAGAAAGCACTACTAAACGCTTGTGTCCAAGTGTAGTGTTTCCTACTT [10290]
Cpi TCACCCATAAAGTAGAAAGCACTACTAAACAGCACTG-CAGGGTGTAGTGTTTCCTACTT [10645]
Cmy TCACCCATAAAGTAGAAAGCACTACTAAACAGCACTG-CAGGGTGTAGTGTTTCCTACTT [10399]
Psi ------------------------------------------------------------ [9621]
Asp ------------------------------------------------------------ [9111]
Ami TCACCCATAAAGTAGAAAGCACTACTAAACAGCACTG-CAGGGTGTAGTGTTTCCTACTT [10044]
Asi TCACCCATAAAGTAGAAAGCACTACTAAACAGCACTG-CAGGGTGTAGTGTTTCCTACTT [9483]
Tgu TCACCCATAAAGTAGAAAGCACTACTAAACAGCACTG-CAGGGTGTAGTGTTTCCTACTT [7910]
Cli TCACCCATAAAGTAGAAAGCACTACTAAACAGCACTG-CAGGGTGTAGTGTTTCCTACTT [9970]
Gga TCACCCATAAAGTAGAAAGCACTACTAAACAGCACTG-CAGGGTGTAGTGTTTCCTACTT [8944]
Xtr CCACCCATAAAGTAGAAAGCACTACTAGACAGGACTG-AACGCTGTAGTGTTTCCTACTT [9627]
Lch TCATCCATAAAGTAGAAAGCACTACTAAACCTTTCAA-TTCAGTGTAGTGTTTCCTACTT [10415]
Dre TCATCCATAAAGTAGAAAGCACTACTAAACCCCTCGC-CACAGTGTAGTGTTTCCTACTT [9629]

Hsa TATGGATGAGTGTACTGT--CTGTCTCCCAGCCTGAGGTGCAGTGCTGCATCTCTGGTCA [9988]
Mmu TATGGATGAGTGCACTGT--CTGTCTCCCAGCCTGAGGTGCAGTGCTGCATCTCTGGTCA [9910]
Mdo TATGGATGAGTGTACTGT--CTGTCTCCCAGCCCGAGGTGCAGTGCTGCATCTCTGGTCA [9446]
Meu TATGGATGAGTGTACTGT--TTGTCTCCCAGCCCGAGGTGCAGTGCTGCATCTCTGGTCA [8062]
Oan TATGGATGAGTGTACTGT--ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [8759]
Aca TATGGATGAGTGTACTGT--ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [10058]
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Pbi TATGGATGAGTGTACTGT--ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [10348]
Cpi TATGGATGAGTGTACTGT--ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [10703]
Cmy TATGGATGAGTGTACTGT--ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [10457]
Psi --------------------ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [9661]
Asp --------------------ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [9151]
Ami TATGGATGAGTGTACTGT--ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [10102]
Asi TATGGATGAGTGTACTGT--ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [9541]
Tgu TATGGATGAGTGTACTGT---------------------------------------- [7928]
Cli TATGGATGAGTGTACTGT--ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [10028]
Gga TATGGATGAGTGTACTGT--ATGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [9002]
Xtr TATGGATGAGTGTACTGG--CTGTCTCCCAGCCCAAGGTGCAGTGCTGCATCTCTGGTCA [9685]
Lch TATGGATGAGTGTACTGT--ATGTCTCCCAGCCCGAGGTGCAGTGCTGCATCTCTGGTCA [10473]
Dre TATGGATGAGTGTACTGT--CAGTCGTCTGGCCCGCGGTGCAGTGCTGCATCTCTGGTCA [9687]

Hsa GTTGGGAGTCTGAGATGAAGCACTGTAGCTCAGGAAGAGAGAAGT--GGGGCCCTGGCTG [10046]
Mmu GTTGGGAGTCTGAGATGAAGCACTGTAGCTCAGGAAGGGAGAAGA--AGGACCTTGGCTG [9968]
Mdo GTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAAC--GGGGCCCAGGCCG [9504]
Meu GTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAAC--GGTGCCCTGGCCA [8120]
Oan GTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAGC--GGGGCCCTGGCGG [8817]
Aca GTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAAC--AAGTCTCTGGGCC [10116]
Pbi GTTGTGAGTCTGAGATGAAGCACTGTAGCTCAGGAAGGGAGGAAC--GGGGCTCCAGCTC [10406]
Cpi GTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAAC--GGGGCTCTGGGCA [10761]
Cmy GTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAAC--GGGGCTCTGGGCA [10515]
Psi GTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAGC--------------- [9706]
Asp GTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAGC--GGGGCTCTGGGCA [9209]
Ami GTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAAC--GGGGCTCTGGGCA [10160]
Asi GTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAAC--GGGGCTCTGGGCA [9599]
Tgu ----------------------------------------------GCTGTCCCGGGCA [7941]
Cli ATTGGGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAAC--GCTCCCCTGGGCA [10086]
Gga ATTGGGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGAGGAAC--GCCGCCCTGGGCT [9060]
Xtr GTTGTGAGTCTGAGATGAAGCACTGTAGCTCGGGAAGGGGGAATA--GGGACTGTGTTTG [9743]
Lch GTTGTGAGTCTGAGATGAAGCACTGTAGCTCAGGAAGGGGGAAAC--AACAGTCAGAGTA [10531]
Dre ACTGGGAGTCTGAGATGAAGCACTGTAGCTCGGGA-GGACAACAC--TGCTCTCTAGACA [9744]

Hsa GGATATCATCATATACTGTAAGTTTGCGAT-GAGACACTACAGTATAGATGATGTACTAG [10105]
Mmu GGATATCATCATATACTGTAAGTTTGTGAT-GAGACACTACAGTATAGATGATGTACTAG [10027]
Mdo GGATATCATCGTATACTGTAAGTTTGCAAT-GAGACACTACAGTATAGATGATGTACTGG [9563]
Meu GGATATCATCGTATACTGTAAGTTTGCAAT-GAGACACTACAGTATAGATGATGTACTGG [8179]
Oan GGATATCATCGTATACTGTAAGTTTGCTAT-GAGACACTACAGTATAGATGATGTACTAG [8876]
Aca GGATATCATCATATACTGTAAGTTGG-AAT-GAGACACTACAGTATAGATGATGTACTAC [10174]
Pbi GGATATCATCATATACTGTAAGTTGG-AAT-CAGACACTACAGTATAGATGATGTACTAT [10464]
Cpi GGATATCATCGTATACTGTAAGTTTGCTAT-GAGACACTACAGTATAGATGATGTACTAT [10820]
Cmy GGATATCATCGTATACTGTAAGTTTGCTAT-GAGACACTACAGTATAGATGATGTACTAT [10574]
Psi ---------------------------------------------------------- [9706]
Asp GGATATCATCATATACTGTAAGTTTGCTAT-GAGACACTACAGTATAGATGATGTACTAT [9268]
Ami GGATATCATCGTATACTGTAAGTCGGCTAT-GAGACACTACAGTATAGATGATGTACTAC [10219]
Asi GGATATCATCGTATACTGTAAGTCGGATAT-GAGACACTACAGTATAGATGATGTACTAC [9658]
Tgu GGATATCATCGTATACTGTAAGTTGGCTAT-GAGACACTACAGTATAGATGATGTACTCC [8000]
Cli GGATATCATCGTATACTGTAAGTCGGCTAT-GAGACACTACAGTATAGATGATGTACTC- [10144]
Gga GGATATCATCATATACTGTAAGTTCACTAT-GAGACACTACAGTATAGATGATGTACTCC [9119]
Xtr GGATATCATCATATACTGTAAGTTTGTTTT-AAGACACTACAGTATAGATGATGTACTAC [9802]
Lch GGATATCATCATATACTGTAAGTTTGCTATAGAGACACTACAGTATAGATGATGTACTAC [10591]
Dre GGATATCATCGTATACTGTAAGTTCATTATTGAGACACTACAGTATAGATGATGTACTAT [9804]

Hsa TCCGGGCACC--CTTGTCCTCACGGTCCAGTTTTCCCAGGAATCCCTTAGATGCTAAGAT [10163]
Mmu TCTGGGTACC--CTTGTCCTCACGGTCCAGTTTTCCCAGGAATCCCTTGGATGCTAAGAT [10085]
Mdo CGAGGGCCGC--CTTGTCCTCAGGGTCCAGTTTTCCCAGGAATCCCTTAGATGCTAAGAT [9621]
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Meu TATGGGTCAC--CTTGTCCTCAGGGTCCAGTTTTCCCAGGAATCCCTTAGGTGCTAAGAT [8237]
Oan CCCGGGTGCC--CGTGTC-TCA-GGTCCAGTTTTCCCAGGAATACAT-AGGTGCTGAGAT [8931]
Aca CTTCACCTAA--TGTGTCCTCGGGGTCCAGTTTTCCCAGGAATCCCTTAGATGATAAGAG [10232]
Pbi CTGGAGCTCC--TATGTCCTCGGGGTCCAGTTTTCCCAGGAATCCCTTAGATGCTAAGAA [10522]
Cpi CCTGAGCTTC--CGTGTCCTCAGGGTCCAGTTTTCCCAGGAATCCCTTAGGCACTATGAC [10878]
Cmy CCTGAGCTTC--CGTGTCCTCAGGGTCCAGTTTTCCCAGGAATCCCTTAGGCACTATGAC [10632]
Psi ------------CGTGTCCTCAGGGTCCAGTTTTCCCAGGAATCCCTTAGGCACTCTGAG [9754]
Asp CCTGAGCCTC----------------------------------------------------- [9278]
Ami CCCGGCCTTT--TGTGTCCTCAGGGTCCAGTTTTCCCAGGAATCCCTTGGGCACTGTGTT [10277]
Asi CCCGGCCTCT--CGTGTCCTCAGGGTCCAGTTTTCCCAGGAATCCCTTGGGCACTGTGTT [9716]
Tgu CCGGGCTGCA----------------------------------------------------- [8010]
Cli ------------CGTGCCCTCAGGGTCCAGTTTTCCCAGGAATCCCTTAGGCGCTACGTT [10192]
Gga CCTGGGCTGC--CGTGCTCTCAGGGTCCAGTTTTCCCAGGAATCCCTTAGGCGCTACGTT [9177]
Xtr ACCAAGTCTC--CTATTCCTCAAGGTCCAGTTTTCCCAGGAATCCCTTGGGTGCTGTGGT [9860]
Lch CCCAGACTGT--CTTGTCCTCGGGGTCCAGTTTTCCCAGGAATCCCTTGGGTGCTAAAAA [10649]
Dre CCAGGGGGTC--CTCATCCCCGGGGGTCCAGTTTTCCCAGGAATCCCTTGGGCAATCGAAA [9862]

Hsa GGG-GATTCCTGGAAATACTGTTCTTGAGGTCATGG--ATCCTCAGCTTTGAGAACTGAA [10220]
Mmu GGG-GATTCCTGGAAATACTGTTCTTGAGGTCATGG--ATCCCCAGCTCTGAGAACTGAA [10142]
Mdo GGG-GATTCCTGGAAATACTGTTCTTGAGGTCATGG--ATCTTCAGCTTTGAGAACTGAA [9678]
Meu GGG-GATTCCTGGAAATACTGTTCTTGAGGTCATGG--ATCTTCAGCTTTGAGAACTGAA [8294]
Oan GGG-GATTCCTGGAAATACTGTTCTTGAGGTCATGG--ACGCTCAGCTTTGAGAACTGAA [8988]
Aca GGG-GATTCCTGGAAATACTGTTCTTGGGGTCATGG----------------------- [10267]
Pbi GGG-GATTCCTGGAAATACTGTTCTTGGGGTCATGG----------------------- [10557]
Cpi GGG-GATTCCTGGAAATACTGTTCTTGAGGCCATGG--ATTCTCAGCTTTGAGAACTGAA [10935]
Cmy GGG-GATTCCTGGAAATACTGTTCTTGAGGCCATGG--ATTCTCAGCTTTGAGAACTGAA [10689]
Psi GGG-GATTCCTGGAAATACTGTTCTTGAGGCCATGG--ATTCTCAGCTTTGAGAACTGAA [9811]
Asp ------------------------------------ATTCTCAGCTTTGAGAACTGAA [9300]
Ami GGG-GATTCCTGGAAATACTGTTCTTGGGGCCGTGG--ATTCTTGGCTTTGAGAACTGAA [10334]
Asi GGG-GATTCCTGGAAATACTGTTCTTGGGGCCGTGG--ATTCTTGGCTTTGAGAACTGAA [9773]
Tgu ------------------------------------ATTCTCAGCTTTGAGAACTGAA [8032]
Cli GGG-GATTCCTGGAAATACTGTTCTTGAGGCCACGG--ATTCTCAGCTTTGAGAACTGAA [10249]
Gga GGG-GATTCCTGGAAATACTGTTCTTGGGGCCACGG--ATCCTCAGCTTTGAGAACTGAA [9234]
Xtr GGG-GATTCCTGGAAATACTGTTCTTGGGGTGTAGG--GTTCTTAGCTTTGAGAACTGAA [9917]
Lch GGG-GATTCCTGGAAATACTGTTCTTGGGGGCAAGG--ACTCCCAGCTTTGAGAACTGAG [10706]
Dre GGGGGATTCCTGGAAATACTGTTCTTGGGGTTGGGG--GCTCTTGGCTTTGAGAACTGAA [9920]

Hsa TTCCATGGGTTGTG-TCAGT------GTCAGACCTCTGAAATTCAGTTCTTCAGCTGGGA [10273]
Mmu TTCCATGGGTTATA-TCAAT------GTCAGACCTGTGAAATTCAGTTCTTCAGCTGGGA [10195]
Mdo TTCCATGGGTTGTC-TTTGT------ATCAGACCTATGAAACTCAGTTCTTCAGCTGGAA [9731]
Meu TTCCATGGGTTGTC-TTTGT------ATCAGACCTATGAAACTCAGTTCTTCAGCTGGGA [8347]
Oan TTCCACGGGTTGTG-ATTGCAACTCTGACAGACCCGTGGGGCTCAGTTCTTGAGCTGGGG [9047]
Aca ---------------------------------------------------------- [10267]
Pbi ---------------------------------------------------------- [10557]
Cpi TTCCATGTGTTGTAATTGAATC-TCTGTCAGACCCATGGGGCTCAGTTCTTCAGCTTGGA [10994]
Cmy TTCCATGGGTTGTAATTGAATC-TCTGTCAGACCCATGGGGCTCAGTTCTTCAGCTTGGA [10748]
Psi TTCCACAGGTTGTAATTGAG-C-TGTGTCAGACCTATGGGGCTCAGTTCTGCAGCTTGGA [9869]
Asp TTCCATAGGTTGTAATTGAG-C-TCTGTCAGACCTATGGGGCTCAGTTCTTCAGCTTGGA [9358]
Ami TTCCATGGGTTGTAATTGAATC-TTGAACAGACCCATGGGGCTCAGTTCTTCAGCTTGGA [10393]
Asi TTCCATGGGTTGTAATTGAATC-TTGAACAGACCCATGGGGCTCAGTTCTTCAGCTTGGA [9832]
Tgu TTCCATGGGTTGTAATTGAATCTGCTGTCAGACCCATGGGGCTCAGTTCTTCAGCTTGGA [8092]
Cli TTCCATGGGTTGTAATTGAATTCGCTGTCAGACCCATGGGGCTCAGTTCTTCAGCTTGGA [10309]
Gga TTCCATGGGTTGTAATTGAATCCTTTGTCAGACCCATGGGGCTCAGTTCTTCAGCTTGGA [9294]
Xtr TTCCATAGGTTGTTAGAG--------GTTAGACCTATGGTGCTTAGTTCCATAGCTTGGA [9969]
Lch TTCCATGAACTGTAATCAGTA-----CCCAG-CTCATGGGGTTCAGTTCTGTAGCTTGGA [10760]
Dre TTCCAAGGGTGTCTGCTTTAT----ATTCAG-CCCACGGAGTTCAGTTCTTAAGTTTGGA [9975]
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Hsa TATCT--CACCTGGCACTGAGAACTGAATTCCATAGGCTGTGAGCTC----TAGCAA-TG [10326]
Mmu TAGCT--CACCTGGCTCTGAGAACTGAATTCCATAGGCTGTGAGCTC----TAGCAGACG [10249]
Mdo TATCT--CATCTGGCTCTGAGAACTGAATTCCATAGGCTGTGAGCTC----ATGCAAATG [9785]
Meu TATCT---------------------------------------------------- [8352]
Oan TACCT--TGCTTGGCTCTGAGAACTGAATTCCATAGGCTGTGAGTTGA---TGAGGA-TG [9101]
Aca -------TGCCTAGCTCTGAGAACTGAATTCCATAGGCTTTAGAATAA---TTGAAA-CG [10316]
Pbi -------TGCTTAGCTCTGAGAACTGAATTCCATAGGCTTTAGAAGAA---ATGAAA-CG [10606]
Cpi TATCT--TGCTTGGCTTTGAGAACTGAATTCCATAGGCTTTAAAATA----ATGAAAACG [11048]
Cmy TATCT--TGCTTGGCTTTGAGAACTGAATTCCATAGGCTTTAAAATA----ATGAAAACG [10802]
Psi TATCT--TGCTTGGCTTTGAGAACTGAATTCCATAGGCTTTAAAATA----AGAAAAATG [9923]
Asp TATCT--TGCTTGGCTTTGAGAACTGAATTCCATAGGCTTTAAAATA----AGAAAAATG [9412]
Ami TATCT--TCCTTGGCTTTGAGAACTGAATTCCATAGGCTTTAAAAGA----CAAAAAAAG [10447]
Asi TATCT--TCCTTGGCTTTGAGAACTGAATTCCATAGGCTTTAAAAGA----CAAAAAAAG [9886]
Tgu TATTT--TGCTTGGCTCTGAGAACTGAATTCCATAGGCGTTGAAGCCT---CCAAAA-TG [8146]
Cli TATTT--TACTTGGCTCTGAGAACTGAATTCCATAGGCATTAAAGCCT---CTAAAAATG [10364]
Gga TATTT--TGCTTGGCTTTGAGAACTGAATTCCATAGGCGTTAAAGCAT---CCAAAAATG [9349]
Xtr TCCCA---------------------------------------------------- [9974]
Lch TGTTG--TGCTTGGCTGTGAGAACTGAATTCCATAGATGGTTGGAGTAGAATGGAAAACG [10818]
Dre TGCAG--CACTTTTCCCTGAGAACTGAATTCCATAGATGGTGTTCAT----GAAAAGTTC [10029]

Hsa CCCTGTGGACTCAGTTCTG-GTG-CCCGGCAGTG-------------------------- [10358]
Mmu CCCTAGGGACTCAGTTCTG-GTG-CCCGGCTGTG-------------------------- [10281]
Mdo CCCTAGGAAGTCAGTTCTG-GAG-TCCGGTGACC------------------------- [9817]
Meu ---------------------------------------------------------- [8352]
Oan CCCTAGGGATTCAGTTCCA-CAG-CCCAGCAACC------------------------- [9133]
Aca CCCCGTGGATTCAGTTCTA-CAG-CTAGGCAGCA--GTTCCAAGCTTTGAGAACTGGTTT [10372]
Pbi CCCCGTGGATTCAGTTCTA-CAG-CTAGACAGCT--GTCCCAGGCTCTGAGAACTGGTTT [10662]
Cpi CCCTGTGGCTTCAGTTCTG-TAG-CTGGGTAGCA--GTTCCCAGCTCTGAGAACTGAATT [11104]
Cmy CCCTGTGGATTCAGTTCTG-TAG-CTGGGTAGCA--GTTCCCAGCTCTGAGAACTGAATT [10858]
Psi CCCTGTGGATTCAGTTCTG-TAG-CTAGGCAGCA--GTTCCCAGCTCTGAGAACTGAATT [9979]
Asp CCCTGTGGATTCAGTTCTG-TAG-CTAGGTAGCA--GTTCCCAGCTCTGAGAACTGAATT [9468]
Ami CCCTATGGATTCAGTTCTG-TAG-CTGGGCGGCA--GTTCCCAGCTCTGAGAACTGAATT [10503]
Asi CCCTATGGATTCAGTTCTG-TAG-CTGGGCGGCA--GTTCCCAGCTCTGAGAACTGAATT [9942]
Tgu CCCTATGGATTCAGTTCTG-CAG-CTGGGCAGCA--GTTCCCAGCTCTGAGAACTGAATT [8202]
Cli CCCTATGGATTCAGTTCTG-CAG-CTGGGCAGCA--GTTCCCAGCTCTGAGAACTGAATT [10420]
Gga CCCTATGGATTCAGTTCTG-CAG-TTGGGCAGCA--GTTCCCAGCTCTGAGAACTGAATT [9405]
Xtr ----------------------------------GGGCCCGGCTCTGAGAACTGAATT [9998]
Lch GTCTGTGGATTCAGTTCTTTCAG-TCTGGTGACC--GGTCCCGGCTCTGAGAACTGAATT [10875]
Dre ATCTATGGGCTCAGTTCTTCTGG-CAATCTGTTT------------------------- [10062]

Hsa ---------------------------------------------------------- [10358]
Mmu ---------------------------------------------------------- [10281]
Mdo ---------------------------------------------------------- [9817]
Meu ---------------------------------------------------------- [8352]
Oan ---------------------------------------------------------- [9133]
Aca TCGTGGACTGGTTTCCATTTAGTCTTCTCAGTCCATAATGCTCAGTTTTCCAGCTTGGCT [10432]
Pbi TGATGGACTAGTTTCCTTTCAGTTTTTTCAGTCCATAATATCCAGTTCTCTAGCTTGGCT [10722]
Cpi CCATGGACTGGTTTCAGTTCTGTATCTTCAGTCCATGGTAGTCAGTTCTCTAGCTTGGCT [11164]
Cmy CCATGGACTGGTTTCAGTTCTGTATCTTCAGTCCATGGTAGTCAGTTCTCTAGCTTGGCT [10918]
Psi CCATGGACTGGTTTCAGTGCTGTATCTTCAGTTCATGGTAGTCAGTTCTCTAGCTTGGCT [10039]
Asp CCATGGACTGGTTTCAGTGCTGTATCTTCAGTTCATGGTAGTCAGTTCTCTAGCTTGGCT [9528]
Ami CCATGGACTGGTTCCCTCTTCATATCTTCAGTCCATAGTAGTCAGTTCTCTAGCTTGGCT [10563]
Asi CCATGGACTGGTTCCCTCTTCATATCTTCAGTCCATAGTAGTCAGTTCTCTAGCTTGGCT [10002]
Tgu CCATGGACTGGTTCCAGTTCCATGTGTTCAGTCCATGGTATTCAGTTCTCTAGCTTGGCT [8262]
Cli CCATGGACTGGTTCCAGTTCCATGTGTTCAGTCCATGGTATTCAGTTCTCTAGCTTGGCT [10480]
Gga CCATGGACTGGTTTCAATTCCATGCGTTCAGTCCATGGTATTCAGTTCTCTAGCTTGGCT [9465]
Xtr CCATGGACTGTTCCACTCACAGCACCCTCAGTCCACAGTGTTCAGTGCTCCAGTCTGGCT [10058]
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Lch CCATGGGCTGGTCCAA-TCAGAACTCTTCAGTCCATAGTAGTCAGTTCTCCAGCTTGGCT [10934]
Dre ------------------------------------------------------------ [10062]

Hsa -----TATAAATCTAGTGGAAACATTTCTGCACAAACTAGATTCTG--GACACCAGTGTG [10411]
Mmu -----TATGAATCTAGTGGAAACATTTCTGCACAAACTAGATG-TT--GATGCCAGTGTG [10333]
Mdo -----TATGAATCTAGTGGAAACATCTCCGCACAAACTAGACTACT--GAAACCAGTGTG [9870]
Meu -----TATGAATCTAGTGGAAACATTTCTGCACAAACTATACTACT--GAAACCAGTGTG [8405]
Oan -----TGGGAATCCAGCGGAATCACCTCTGCACAAACTCGTCTTCT--GAA-CCAGTGTG [9185]
Aca GCA--TATGAATCTAGTGGAATCACTTCCGCACAAACTAGATGAAT--GAAACCAGTGTG [10488]
Pbi GCA--TATGAATCTAGTGGAATCACTTCTGCACAAACTAGAGGATT--GAAACCAGTGTG [10778]
Cpi GTA--TATGAATCTAGTGGAATCATTTCTGCACAAACTCGACTACT--GAAATCAGTGTG [11220]
Cmy GTA--TATGAATCTAGTGGAATCATTTCTGCACAAACTCGACTACT--GAAATCAGTGTG [10974]
Psi GTA--TATGAATCTAGTGGAATCATTTCTGCACAAACTCGACTTTT--GAAATCAGTGTG [10095]
Asp GTA--TATGAGTCTAGTGGAATCATTTCTGCACAAACTCGACTATT--GAAATCAGTGTG [9584]
Ami GTA--TATGAATCTAGTGGAATCATTTCTGCACAAACTCGACTATT--GAAATCAGTGTG [10619]
Asi GTA--TATGAATCTAGTGGAATCATTTCTGCACAAACTCGACTATT--GAAATCAGTGTG [10058]
Tgu GCA--TATGAATCTAGTGGAATCATTTCTGCACAAACTTGACTACT--GAAATCAGTGTG [8318]
Cli GCA--TATGAATCTAGTGGAATCACTTCTGCACAAACTTGACTACT--GAAATCAGTGTG [10536]
Gga GCA--TATGAATCTAGTGGAATCACTTCTGCACAAACTTGACTACT--GAAATCAGTGTG [9521]
Xtr GCC------------------------------------------------------- [10061]
Lch GCA--TATGAATCTAGCGGAATCATTTCTGCACAAACTCGACTATTTGCAAAACAGTGTG [10992]
Dre ------------------------------------------------------------ [10062]

Hsa CGGAAATGCTTCTGCTACATTTTT--GTCTTTTGAGGCAAAGTTCTGAGACACTCCGACT [10469]
Mmu CGGAAATGCTTCTGCTACATTTGT--GTCTTTTGAGACAAAGTTCTGAGACACTCCGACT [10391]
Mdo CGGAAGTGCTTCTGCTACATTTTT--GCCGTCGGAGGCAAAGTTCTGGGACACTCAGACT [9928]
Meu CGGAAGTGCTTCTGCTACATTTTT--GCCGTCGGAGGCAAAGTTCTGTGACGCTCAGACT [8463]
Oan CGGAGATGCTTCCGCCGCATTCTC--GTCTTTTGAGGCAAAGTTCTGTGACACTCAGACT [9243]
Aca CGGAAATGCTTCTGCTACATTTTT--GTCTCTGGAAGCAAAGTTCTGTGACACTCGGACT [10546]
Pbi CGGAAATGCTTCTGCTACATTTTT--GTTTCTGGAAGCAAAGTTCTGTGACACTCGGACT [10836]
Cpi CGGAAATGCTTCTGCTACATTTTT--GTCTCTTGAAGCAAAGTTCTGTGACACTCAGACT [11278]
Cmy CGGAATTGCTTCTGCTACATTTTT--GTCTCTTGAAGCAAAGTTCTGTGACACTCAGACT [11032]
Psi CGGAAATGCTTCTGCTACATTTTT--GTCTCTTGAAGCAAAGTTCTGTGACACTCAGACT [10153]
Asp CGGAAATGCTTCTGCTACATTTTT--GTCTCTTGAAGCAAAGTTCTGTGACACTCAGACT [9642]
Ami CGGAAATGCTTCTGCTACATTTTT---------------------------------- [10643]
Asi CGGAAATGCTTCTGCTACATTTTT--GTCCCTTGAAGCAAAGTTCTGTGACACTCCGACT [10116]
Tgu CGGAAATGCTTCTGCTACATTTTT--GCCTCCGGAAGCAAAGTTCTGTGACACTCCGACT [8376]
Cli CGGAAATGCTTCTGCTACATTTTT--GCCTCCGGAAGCAAAGTTCTGTGACACTCCGACT [10594]
Gga CGGAAATGCTTCTGCTACATTTTT--GTCTCCTGAAGCAAAGTTCTGTGACACTCAGACT [9579]
Xtr --------------------------GTCTTTTAAATCAAAGTTCTGTGACACTTAGACT [10095]
Lch CGGAAGTGCTTCTGCTACATTTTT--GTCTCTTAAGGCAAAGTTCTGTATCACTTAGACT [11050]
Dre --------------------------GGCTTTCCAAGTAAAGTTCTGTGATACACTCCGA [10096]

Hsa CTGAGTATGATAGAAGTCAGTGCACTACAGAACTTTGTCTCTAGAGG--AGCATTTGAGG [10527]
Mmu CTGAGTATGATAGAAGTCAGTGCACTACAGAACTTTGTCTCTAGAGG--AGCATTTGAGG [10449]
Mdo CTGATTAGGATAGAAGTCAGTGCACTACAGAACTTTGTCTCCGGAGG------------- [9975]
Meu CTG-TTAGCCAAGAAGTCAGTGCACTACAGAACTTTGTCTCCGGGGG--AGCATTTGAGG [8520]
Oan CTGATTATGATAGAAGTCAGTGCACTACAGAACTTTGTCTCCAGAGG------------- [9290]
Aca CTGATTATGATAGAAGTCAGTGCACTACAGAACTTTGTCGCCGGGGG--AGCGCTTGAGG [10604]
Pbi CTGATTATAATAGAAGTCAGTGCACTACAGAACTTTGTCTCCAGGGG--AGCGCTTGAGG [10894]
Cpi CTGATTATGATAGAAGTCAGTGCACTACAGAACTTTGTCTTTGGGGG--AGCATTTGAGG [11336]
Cmy CTGATTATGATAGAAGTCAGTGCACTACAGAACTTTGTCTTTGGGGT--AGCGTTTGAGG [11090]
Psi CTGATTATGATAGAAGTCAGTGCACTACAGAACTTTGTCTCTGGGGG--AGCGTTTGAGG [10211]
Asp CTGATTACGATAGAAGTCAGTGCACTACAGAACTTTGTCTCTGGGGG------------- [9689]
Ami ------------------------------------------------GGCCTTTGAGG [10654]
Asi CTGAGTAC-ATAGCAGTCAGTGCACTACAGAACTTTGTCTCTGGGGG------------- [10162]
Tgu CTGGGTACGATAGCAGTCAGTGCACTACAGAACTTTGTCTCCGGCGG------------- [8423]
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Cli CTGGGTACGATAGCAGTCAGTGCACTACAGAACTTTGTCTCCGGCGG--AGCGCCCGGGG [10652]
Gga CTGGTTACGATAGCAGTCAGTGCACTACAGAACTTTGTCTCCGGGGG------------ [9626]
Xtr CTGAATATGATAGCAGTCAGTGCACTACAGAACTTTGTTTTGGGAGT--AGCGTTTGAGG [10153]
Lch CTGAGTACTATAGAAGTCAGTGCACTACAGAACTTTGTTTTGGGAGT--AGCACTTGAGG [11108]
Dre CTCTGAATGTTTGCAGTCAGTGCATTACAGAACTTTGTTTTGGGAGT------------ [10143]

Hsa TGAAGTTCTGTTATACACTCAGGCTGTGGCTCTCTGAAAGTCAGTGCATCACAGAACTTT [10587]
Mmu TGAAGTTCTGTTATACACTCAGGCTGTGGCTCT--GAAAGTCAGTGCATCACAGAACTTT [10507]
Mdo ------------------------------------------------------------ [9975]
Meu TGAAGTTCTGTTATACACTCAGACTGTGGCTCTCTGAAAGTCAGTGCATCACAGAACTTT [8580]
Oan ------------------------------------------------------------ [9290]
Aca TGAAGTTCTGTTATACACTCTGACTGTGGCTATGTGGAAGTCAGTGCATCACAGAACTTT [10664]
Pbi TGAAGTTCTGTTATACACTTTGACTGTGGCTACATGGAAGTCAGTGCATCACAGAACTTT [10954]
Cpi TGAAGTTCTGTTATACACTCTGACTGTGGCTACGTGGAGGTCAGTGCATCACAGAACTTT [11396]
Cmy TGAAGTTCTGTTATACACTCCGACTGTGGCTATGTGGAGGTCAGTGCATCACAGAACTTT [11150]
Psi TGAAGTTCTGTGTTACACTCCGGCCGTGGCTACGAGG-GGTCAGTGCATCACAGAACTTT [10270]
Asp ------------------------------------------------------------ [9689]
Ami CGGAGTTCTGTCATACACTCGGACTGTG-CTACCTGG-GGTCAGTGCATCACAGAACTTT [10712]
Asi ------------------------------------------------------------ [10162]
Tgu ------------------------------------------------------------ [8423]
Cli CGAGGTTCTGTCCTACACTCCGGCTGTAGCTACA-GACAGTCAGTGCATCACAGAACTTG [10711]
Gga ------------------------------------------------------------ [9626]
Xtr TGAAGTTCTGTTATACACTCCGGCTGTGAGTAAGTGGAAGTCAGTGCATCACAGAACTTT [10213]
Lch TGAAGTTCTGTTATACACTCCGGCTGTGAGTAACGAGAAGTCAGTGCATCACAGAACTTT [11168]
Dre ------------------------------------------------------------ [10143]

Hsa GTCTCGAAAGCTT--CCCCCGGCCCAGGTTCTGTGATACACTCCGACTCGGGCTCTGGAG [10645]
Mmu GTCTCGAAAGCTT--CCCCGGGCCTAGGTTCTGTGATACACTCCGACTCGGGCTCTGGAG [10565]
Mdo ---------------TCCCCGGCCCAGGTTCTGTGATACACTCCGACTTAGACTCTGGAG [10020]
Meu GTCTCGAAAGCTT--TCCCCAGCCCAGGTTCTGTGATACACTCCGACTTAGACTCTGGAG [8638]
Oan ------------------------------------------------------------ [9290]
Aca GTCTCGAGAGCTT---------------------------------------------- [10677]
Pbi GTCTCGAGAGCTT---------------------------------------------- [10967]
Cpi GTCTCGAGAGCTT--CTCTCGGCCCAGGTTCTGTGGTACACTTGGACTTGGACTCTGGAG [11454]
Cmy GTCTCGAGAGCTT--CTCTCGGCCCAGGTTCTGTGGTACACTTGGACTTGGACTCTGGAG [11208]
Psi GTCTCGAGAGCTT--CTCTCGGCTCAGGTTCTGTGGTACACTTGGACTCGGACTCTGGAG [10328]
Asp ---------------CTCTCGGCCCAGGTTCTGTGGTACACTTGGACTCGGACTCTGGAG [9734]
Ami GTCTCGAGCGCCC--CTCTCAGCTCAGGTTCTGTGGTACACTTGGACTCGGACTCTGGAG [10770]
Asi ---------------CTCTCAGCCCAGGTTCTGTGGTACACTTGGACTCGGACTCTGGAG [10207]
Tgu ------------------------------------------------------------ [8423]
Cli GTCCCGGGAGCTC----------------------------------------------- [10724]
Gga ------------------------------------------------------------ [9626]
Xtr GTCTCGAGGGCTT---------------------------------------------- [10226]
Lch GTCTCGAGAGCTT---------------------------------------------- [11181]
Dre ---------------CACCTGGCTCAAGTTCTGTGATACACTCAGACTTTGAATCAGTGG [10188]

Hsa CAGTCAGTGCATGACAGAACTTGGGCCCGGAAGGAC--TCCCCATGGCCCTGTCTCCCAA [10703]
Mmu CAGTCAGTGCATGACAGAACTTGGGCCCGGTAGGAC--TTCTCAATGCCCTGTCTCCCAA [10623]
Mdo CAGTCAGTGCATGACAGAACTTGGGCTTGGGTGGAC--CCTCCGGGGCCCCTTCTCCCAA [10078]
Meu CAGTCAGTGCATGACAGAACTTGGGTTTGGGTGGAC--GGCCTGGAGCCCCCTCTCCCAA [8696]
Oan -------------------------------------CCCTCGGCGCCCCCTCTCCCAA [9312]
Aca ------------------------------------ACTCTCTTTCCCTCTCTCCCAA [10699]
Pbi ------------------------------------ACTCTTCTCCTTTCTCTCCCAA [10989]
Cpi CAGTCAGTGCATGACAGAACTTGGGTTTGGATGGAC----------------------- [11490]
Cmy CAGTCAGTGCATGACAGAACTTGGGTTTGGATGGAC--TCTGCTCCCCACTCTCTCCCAA [11266]
Psi CAGTCAGTGCATGACAGAACTTGGGCTTGGACGGAC----------------------- [10364]
Asp CAGTCAGTGCATGACAGAACTTGGGCTTGGACGGAC----------------------- [9770]
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Ami CAGTCAGTGCATGACAGAACTTGGGTTTGGATGGAC--TCTGCCCCCCACTCTCTCCCAA [10828]
Asi CAGTCAGTGCATGACAGAACTTGGGTTTGGATGGAC--TCTGCCCCCCACTCTCTCCCAA [10265]
Tgu ------------------------------------------------------------ [8423]
Cli ------------------------------------------------------------ [10724]
Gga ------------------------------------------------------------ [9626]
Xtr ------------------------------------GTCTACTCTTTCTCTCTCCCAA [10248]
Lch ------------------------------------GACGGAGTTCTCTGTCTCCCAA [11203]
Dre TAGTCAGTGCATGACAGAACTTTGGCCCGGACGGAC--AGTCCATCTCCGTCTCTCCCAA [10246]

Hsa CCCTTGTACCAGTGCTG---GGC-TCAGACCCTGGTACAG-GCC-TGGGGG-ACAGGGAC [10756]
Mmu CCCTTGTACCAGTGCTG---TGCCTCAGACCCTGGTACAG-GCC-TGGGGG-ATAGGGAC [10677]
Mdo CCCTTGTACCAGAGTCC----ATCAGAGACCC-GGTACGGGCTG-TGGGGG-ACGGGGAG [10131]
Meu CCCTCGTACCAGAGTCC----ATCAGAGACCC-GGTACGGGCTG-TGGGGG-ATGGGGAG [8749]
Oan CCCTTGTACCAGAGCAT---AAACTGAACCCCTGGTACGGGGCCGTGGGAG-AGGGGGAG [9368]
Aca CCCTTGTACCAGTGCCA-ACTGTAGTCCTCACTGGTACAGAGGA-TGGAAG-GGTGGG-C [10755]
Pbi CCCTTGTACCAGTGTCA-GCTGTTGCACCTACTGGTACAGAGGA-TGGAAG-GGAGAGTG [11046]
Cpi ------------------------------------------------------------ [11490]
Cmy CCCTTGTACCAGTGTCATGCTGCAGCGAACCCTGGTGCAGAGGA-TGGATG-AGAAGGGG [11324]
Psi ------------------------------------------------------------ [10364]
Asp ------------------------------------------------------------ [9770]
Ami CCCTTGTACCAGTGTCATGTTACTG-GAACCCTGGTACAGAGGA-TGGATG-AGAAGGAG [10885]
Asi CCCTTGTACCAGTGTCATGTTACTG-GAACCCTGGTACAGAGGA-TGGATG-AGAAGGAG [10322]
Tgu ------------------------------------------------------------ [8423]
Cli ------------------------------------------------------------ [10724]
Gga ------------------------------------------------------------ [9626]
Xtr CCCTTGTACCAGAGTGA---TAATGGGAACTCTGGTACAGAGGA-TGGCTG-AAAGGAAG [10303]
Lch CCCTTGTACCAGTGTGA--GATTAGAGAACACTGGTACGGAGGA-GGGGGG-AGAGAGAG [11259]
Dre TCCTTGTACCAGTGTCT--GATTTACAGATGACGCTGGACGGGG-TTTGGG-GGGGGCTG [10302]

Hsa CTGGGGA--CTCACAGCTGCCAGTGTCATTTTTGTGATCTGCAGCT-AGTATTCTCACTC [10813]
Mmu TTGGGAA------------------------------------------------------ [10684]
Mdo TCGGGGC--CTCACAGCTGCCAGTGTCATTTTTGTGATCTGCAGCT-AGTATTCTGGCTT [10188]
Meu CCAGGTG--CTCACAGCTGCCTGTGTCATTTTTGTGATCTGCAGCT-AGTATTCTGACTT [8806]
Oan CCGGGGC--CTCACAGCTGCCAGTGTCATTTTTGTGATCTGCAGCTTAGTACTCTGGCTC [9426]
Aca CTGCAGA--TTCACAGCCGTCAGTGTCATTTTTGTGATTTGCAGCT-AGTAATCCTGGCC [10812]
Pbi GTTCAGA--CTCACAGCTGCCAGTGTCATTTTTGTGATTTGCAGCT-AGTAATCCTGGCC [11103]
Cpi ---------CGTGCAGCTGCCAGTGCCATTTTTGTGATTTGCAGCT-AGTAATCTGGGTC [11540]
Cmy GGGTGGG------------------------------------------------------ [11331]
Psi ------------------------------------------------------------ [10364]
Asp ------------------------------------------------------------ [9770]
Ami GCGTGGG--CTCGCGGCTGCCGGGGGCATTTTTGTGATTTGCAGCT-CGTGGTCTGGGTC [10942]
Asi GCGTGGG------------------------------------------------------ [10329]
Tgu ---------CTCGCAGCTGCCGGCGTCATTTTTGTGATTTGCAGCT-AGTAATCTGGCTC [8473]
Cli ---------CTCGCAGCTGCCGGCGTCATTTTTGTGATTTGCAGCT-AGTAATCTGGCTC [10774]
Gga ------------------------------------------------------------ [9626]
Xtr CAGTGGA--ATCACGGCTGCCCTTGTCATTTTTGTGATTTGCAGCT-TGTAATTTTGGTC [10360]
Lch CGCTCTC--TTCATGGCTGCCAGTGTCATTTTTGTGATTTGCAGCT-AGTAATCTTCAGT [11316]
Dre AGGGAGG--AGCACACCTCCCAGTGTCATTTTTGTGATTTGCAGCT-AGTAGTCTGGGTC [10359]

Hsa -CAGTTGCATAGTCACAAAAGTGATCATTGGCAGGTGTGGC--AGCGGTGGCCAGTGTCA [10870]
Mmu ------------------------------------------AGCGGTGGCCGGTGTCA [10701]
Mdo -CAGTTGCATAGTCACAAAAGTGATCATTGGCAGGTGTGGC--AGCGGTTGCCGGTGTCA [10245]
Meu -CAGTTGCATAGTCACAAAAGTGATCATTGGCAGGTGTGGC------------------- [8846]
Oan -CAGTTGCATAGTCACAAAAGTGATCATTGGCAGGTGTGGC--AGCGGTTGCCAGTGTCA [9483]
Aca -CAGTTGCATAGTCACAAAAGTGATCATTGGCCGCTGTGCC--AGCGGTTGCCAGTGTCA [10869]
Pbi -CAGTTGCATAGTCACAAAAGTGATCATTGGCCACTGTGCC--AGCAGTTGCCAGTGTCA [11160]
Cpi -CAGTTGCATAGTCACAAAAGTGAGCATTGGCAGCCGTGCC--AGCGGTTGCCAGTGTCA [11597]
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Cmy ----------------------------------------AGCGGTTGCCAGTGTCA [11348]
Psi ----------------------------------------AGCGGTTGCCAGTGTCA [10381]
Asp ----------------------------------------AGCGGTTGCCAGTGTCA [9787]
Ami -CAGTTGCATAGTCACAAAAGTGATCGTCGGCGGCCGCGCC--AGCGGTTGCCAGTGTCA [10999]
Asi ----------------------------------------AGCGGTTGCCAGTGTCA [10346]
Tgu -CAGTTGCATAGTCACAAAAGTGATCGTTGGCAGCCGTGCC--AGCGGTTGCCAGTGTCA [8530]
Cli -CAGTTGCATAGTCACAAAAGTGATCGTTGGCAGCCGTGCC--AGCGGTTGCCAGTGTCA [10831]
Gga ----------------------------------------AGCGGTTGCCAGTGTCA [9643]
Xtr TCAGTTGCATAGTCACAAAAGTGATCATGGGCAGGTGGGGC--AGCGGTTGCCAGTGTCA [10418]
Lch CCAGTTGCATAGTCACAAAAGTGATCATTGGCAGCTGTGTC--AGCGGTTGCCAGTGTCA [11374]
Dre -CAGTTGCATAGTCACAAAAATGATCATTGGTAGGTGTGAG--AGCGGTTGCCAGTGTCA [10416]

Hsa TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [10930]
Mmu TTTTTGTGACGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [10761]
Mdo TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [10305]
Meu ------------------------------------------------------------ [8846]
Oan TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [9543]
Aca TTTTTGTGATGTTGCAGCTAGTAATATAAGCCAAGTTGCATAGTCACAAAAGTGATCATT [10929]
Pbi TTTTTGTGATGTTGCAGCTAGTAATATAAGCCCAGTTGCATAGTCACAAAAGTGATCATT [11220]
Cpi TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [11657]
Cmy TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [11408]
Psi TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [10441]
Asp TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [9847]
Ami TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [11059]
Asi TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [10406]
Tgu TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [8590]
Cli TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [10891]
Gga TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [9703]
Xtr TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [10478]
Lch TTTTTGTGATGTTGCAGCTAGTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [11434]
Dre TTTTTGTGATGTTGCAGCTAGTTATATGAGCCCAGTTGCATAGTCACAAAAGTGATCATT [10476]

Hsa GGAAACTGTGAC--TGTATGCTGTTAATGCTAATCGTGATAGGGGTTTTT-------GCC [10981]
Mmu GGAAACTGTGAC--TGTATGCTGTTAATGCTAATTGTGATAGGGGTTTTG-------GCC [10812]
Mdo GGAAACTGTGAC--TATATGTTGTTAATGCTAATCGTGATAGGGGTTTTTCTTTTTGACT [10363]
Meu --------------TATATGTTGTTAATGCTAATCGTGATAGGGGTTTGTCTTTTTCACT [8892]
Oan GGAAACTGTGAC--CGCAGGTCGTTAATGCTAATCGTGATAGGGGTTTTCT------CTG [9595]
Aca GGAAACTGTGAC--CACACGTTGTTAATGCTAATCGTGATAGGGGTTTTT-------ATC [10980]
Pbi GGAAACTGTGAC--CATACACTGTTAATGCTAATTGTGATAGGTGTTTT--------ATC [11270]
Cpi GGAAACTGTGAC--TGTATGTTGTTAATGCTAATCGTGATAGGGGTTTTT-------ACC [11708]
Cmy GGAAACTGTGAC--TGTATGTTGTTAATGCTAATCGTGATAGGGGTTTTT-------ACC [11459]
Psi GGAAACTGTGAC--TGTATGTTGTTAATGCTAATCGTGATAGGGGTTTTT-------ACC [10492]
Asp GGAAACTGTGAC--TGTATGTTGTTAATGCTAATCGTGATAGGGGTTTTT-------ACC [9898]
Ami GGAAACTGTGAC--TGTATGTTGTTAATGCTAATCGTGATAGGGGTTTT--------ACC [11109]
Asi GGAAACTGTGAC--TGTATGTTGTTAATGCTAATCGTGATAGGGGTTTT--------ACC [10456]
Tgu GGAAACTGTGAC--TGTATGTTGTTAATGCTAATCGTGATAGGGGTTTTT-------ACC [8641]
Cli GGAAACTGTGAC--TGTATGTTGTTAATGCTAATCGTGATAGGGGTTTTT-------ACC [10942]
Gga GGAAACTGTGAC--TGTATGTTGTTAATGCTAATCGTGATAGGGGTTTTT-------ACC [9754]
Xtr GGAAACTGTGAC--TGCACAGTATTAATGCTAATCGTGATAGGGGTTTTTT------AAT [10530]
Lch GGAAACTGTGAC--TGTACGTTGCTAATGCTAATTGTGATAGGGGTTTTT-------GAC [11485]
Dre GGAAACTGTATC--GGTGCAGGTTTAATGCTAATCGTGATAGGGGTTT---------AGT [10525]

Hsa TCCAACTGACTCCTACA-TATTAGCATTAACAGTGTATGATG------------------ [11022]
Mmu TCTGACTGACTCCTACC-TGTTAGCATTAACAGGACACAAGG------------------ [10853]
Mdo TCGAACTGACTCCTACA-TGTTAGCATTAACAGTATATGGCC------------------ [10404]
Meu TCTAACTGACTCCTACA-TGTTAGCATTAACACTATATGGCC------------------ [8933]
Oan TCTGACTGACCCCTGCC-CGTTAGCATTAGCAACGTGCGGCC------------------ [9636]
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Aca TCTGACTGACTCCTACA-TGTTAGCATTAAGAATGTGTAGTG--CAGAAGGTGTTTATGC [11037]
Pbi TCTGATCAACTCCTACA-TGTTAGCATTAATAGGGTGTGGTG--CAGACAGTGTTAATGC [11327]
Cpi TATGACTGACTCCTACA-TGTTAGCATTAACACTGTATGATG--CAGAAAGTGTTAATGC [11765]
Cmy TATGACTGACTCCTACA-TGTTAGCATTAACACTGTATGATG--CAGAAAGTGTTAATGC [11516]
Psi TATGACTGACTCCTACA-TGTTAGCATTAACACTGTATGATG--CAGGAAGTGTTAATGC [10549]
Asp TATGACTGACTCCTACA-TGTTAGCATTAACACTGTATGATG--CAGGAAGTGTTAATGC [9955]
Ami TCTGACTGACTCCTACA-TGTTAGCATTAGCACTGTATGATG------------------ [11150]
Asi TCTGACTGACTCCTACA-TGTTAGCATTAGCACTGTATGATG------------------ [10497]
Tgu TATGACTGACTCCTACA-CGTTAGCATTAACACTGTATCTCT------------------ [8682]
Cli TCTGACTGACTCCTACA-TATTAGCATTAACACTGTATCATG------------------ [10983]
Gga TCTGAATGACTCCTACA-TGTTAGCATTAACACTGTACCATG------------------ [9795]
Xtr ACATATTGACTCCTACA-TGTTAGCATTATTATCATGTGGTT------------------ [10571]
Lch TTTAGCTAACTCCTACA-TATTAGCATTAATACTGTATATGA------------------ [11526]
Dre GCTGATGAACACCTATGCTGTTAGCATTAATCTTGCGCTAGT------------------ [10567]

Hsa ------------------------------------------------------------ [11022]
Mmu ------------------------------------------------------------ [10853]
Mdo ------------------------------------------------------------ [10404]
Meu ------------------------------------------------------------ [8933]
Oan ------------------------------------------------------------ [9636]
Aca TCCTTACGTCGGGAGTTTGAGATCTGATGCAACTCCTCTCCTGGTAGCATTGACTCTTAC [11097]
Pbi TACTCATGTTGGGAGTTTGA-AATAACACTCACTCCTCTTCCAGTAGCATTTACTCTTAC [11386]
Cpi TACTCATGTTAGGGGTGTGA--AATGAAGTAGCCCCTTGCCTGGTAGCATTGGCCCTTAC [11823]
Cmy TACTCATGTTAGGGGTGTGA--AGTGAAGTAGCTCCTTGCCTGGTAGCATTGGCCCTTAC [11574]
Psi TACTCATGTTAGGGGTGTGG--AATGAAGTCGCTCCTAGCGGGGTAGCATTGACCCTTAC [10607]
Asp TACTCATGTTAGGGGCGTGG--AATGAAGTCGCTCCTGGCAGGGTAGCATTGGCCCTTAC [10013]
Ami ------------------------------------------------------------ [11150]
Asi ------------------------------------------------------------ [10497]
Tgu ------------------------------------------------------------ [8682]
Cli ------------------------------------------------------------ [10983]
Gga ------------------------------------------------------------ [9795]
Xtr ------------------------------------------------------------ [10571]
Lch ------------------------------------------------------------ [11526]
Dre ------------------------------------------------------------ [10567]

Hsa -----GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTAAAA-TCAAAA- [11075]
Mmu -----GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTCAAA-TAAAAA- [10906]
Mdo -----GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTAAAA-TGAAAA- [10457]
Meu -----GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTAAAA-TGAAAA- [8986]
Oan -----GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTAAAG-TAGAAA- [9689]
Aca TGA--GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGGATTAAAG-TGAAAA- [11153]
Pbi TGA--GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGGATTAAAG-TGAAAA- [11442]
Cpi TGA--GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTAAAG-TGAAAA- [11879]
Cmy TGA--GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTAAAG-GGAAAA- [11630]
Psi TGA--GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTAAAG-TGAAAA- [10663]
Asp TGA--GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTAAAG-TGAAAA- [10069]
Ami -----GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGATTTAAAG-TGAAAA- [11203]
Asi -----GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTAAAG-TGAAAA- [10550]
Tgu -----GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTAAAG-TGAAAA- [8735]
Cli -----GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTAAAG-TGAAAA- [11036]
Gga -----GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTGGAATTTAAG-TGAAAA- [9848]
Xtr -----GCTACTTTAGTGAACATTCAACGCTGTCGGTGAGTTTGGTATCTAAA-GGCAAA- [10624]
Lch -----GTTGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTTAGAA-TACAT-TGAAAA- [11578]
Dre -----TTTGCCTCAGTGAACATTCAACGCTGTCGGTGAGTTTGAGCTAAATG-GAAAAAA [10621]

Hsa -CCATCGACCGTTGATTGTACCCTATGGCTAAC--GGTCACAATCAACATTCATTGCTGT [11132]
Mmu -CCATCGACCGTTGATTGTACCCTATAGCTAAC--GGTCACAATCAACATTCATTGCTGT [10963]
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Mdo -CCATCGACCGTTGATTGTACCCTACAGCTAAC--GGTCACAATCAACATTCATTGCTGT [10514]
Meu -CCATCGACCGTTGATTGTACCCTACAGCTAAC--GGTCACAATCAACATTCATTGCTGT [9043]
Oan -CCATCGACCGTTGATTGTACCCTGCGGC-AAC--GGTCCCAATGAACATTCATTGCTGT [9745]
Aca -CCATCGACCGTTGATTGTACCCTCCAGCTAAC--GGTCACAATCAACATTCATTGCTGT [11210]
Pbi -CCATCGACCGTTGATTGTACCCTCCAGCTAAC--GGTCACAATCAACATTCATTGCTGT [11499]
Cpi -CCATCGACCGTTGATTGTACCCTCCAGCTAAC--GGTCACAATCAACATTCATTGCTGT [11936]
Cmy -CCATCGACCGTTGATTGTACCCTCCAGCTAAC--GGTCACAATCAACATTCATTGCTGT [11687]
Psi -CCATCGACCGTTGATTGTACCCTCCAGCTAAC--GGTCACAATCAACATTCATTGCTGT [10720]
Asp -CCATCGACCGTTGATTGTACCCTCCAGCTAAC--GGTCACAATCAACATTCATTGCTGT [10126]
Ami -CCATCGACCGTTGATTGTACCCTCCAGCTAAC--GGTCACAATCAACATTCATTGCTGT [11260]
Asi -CCATCGACCGTTGATTGTACCCTCCAGCTAAC--GGTCACAATCAACATTCATTGCTGT [10607]
Tgu -CCATCGACCGTTGATTGTACCCTCCAGCTAAC--GGTCACAATGAACATTCATTGCTGT [8792]
Cli -CCATCGACCGTTGATTGTACCCTCCAGCTAAC--GGTCACAATCAACATTCATTGCTGT [11093]
Gga -CCATCGACCGTTGATTGTACCCTCCAGCTAAC--GGTCACAATCAACATTCATTGCTGT [9905]
Xtr -CCATCGATCGTTGACTGTACATTACGGCAATG--GGTCACAATCAACATTCATTGCTGT [10681]
Lch -CCACTGACCGTTGATTGTACCCTGTAGCTAAC--GGTCACAATCAACATTCATTGCTGT [11635]
Dre ACCATCGACCGTTGATTGTACCCTGCGGCCGAG--GGTCACAATCAACATTCATTGCTGT [10679]

Hsa CGGTGGGTTGAACTGTGTGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCG--A [11190]
Mmu CGGTGGGTTGAACTGTGTAGAAAAGCTCACTGAACAATGAATGCAACTGTGGCCCCG--A [11021]
Mdo CGGTGGGTTTAACTGTATGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [10572]
Meu CGGTGGGTTTAACTGTGTGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [9101]
Oan CGGTGGGTTTAACTCTGAGGACAAGCTCACTGAACAATGAATGGAACTGTGGCTC-A--A [9802]
Aca CGGTGGGTTTAACTATGTGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [11268]
Pbi CGGTGGGTTTAACTTTGTGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [11557]
Cpi CGGTGGGTTTAACTATGTGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [11994]
Cmy CGGTGGGTTTAACTATGTGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [11745]
Psi CGGTGGGTTTAACTCTGTGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [10778]
Asp CGGTGGGTTTAACTATGTGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [10184]
Ami CGGTGGGTTTAACTATGCGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [11318]
Asi CGGTGGGTTTAACTATGCGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [10665]
Tgu CGGTGGGTTTAACTATGTGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [8850]
Cli CGGTGGGTTTAACTATGTGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [11151]
Gga CGGTGGGTTTAACTATGTGGACAAGCTCACTGAACAATGAATGCAACTGTGGCCCCA--A [9963]
Xtr CGGTGGGTTGAGTTAAGAACACAAGCTCGCTGAACGATGAATGCAACTGTGTCCCCA--A [10739]
Lch CGGTGGGTTTAACTATGTGGAAAAGCTCACTGAACAATGAATGCAACTGTGGCCCGG--G [11693]
Dre CGGTGGGTTGGATTGTAAAAGAAAGCTCACTGAACAATGAATGCAACTGTGTCCCAG--G [10737]

Hsa GGACTCCAAGGAACATTCAACGCTGTCGGTGAGTTT-GGGA---TTTGAAA-------AA [11239]
Mmu GGACTCCATGGAACATTCAACGCTGTCGGTGAGTTT-GGGA---TTCAAAAACAAAA-AA [11076]
Mdo TAACTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-TTAGA--TTTAAAAG------AA [10623]
Meu TAACTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GGAGA--TTTAAAAG------AA [9152]
Oan GAACCGCAGGGAACATTCAACGCTGTCGGTGAGTTT-GAGA---TAGAGAAG------AA [9852]
Aca TAGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GGAA---TCGAGAGC------AA [11318]
Pbi TAGCTTCAGCGAACATTCAACGCTGTCGGTGAGTTT-GACA---TGTCAGGAT-----AA [11608]
Cpi TAGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GAGA---ATTAGAAA------AA [12044]
Cmy TAGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GAGA---ATTAGAAA------AA [11795]
Psi TAGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GAGA---ATTAGAAAAAA---AA [10831]
Asp TAGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GAGA---ATTAGAAAAAA---AA [10237]
Ami TAGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GAGC---ATTAGAAAAA----AA [11370]
Asi TAGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GAGC---ATTAGAAAAAA---AA [10718]
Tgu TAGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GAGA---ACTAGAAA------AA [8900]
Cli TAGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GAGA---ACTACAA-------AA [11200]
Gga TAGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GAGA---ACTAAGAA------AA [10013]
Xtr GGGCTTCAGAGAACATTCAACGCTGTCGGTGAGTTT-GAGAAAGTGTAAAAATAT---AA [10795]
Lch TGGCTTCAGTGAACATTCAACGCTGTCGGTGAGTTT-GAGC---TTTATAAG------AA [11743]
Dre TCCCTTG-GTGAACATTCAACGCTGTCGGTGAGTTTTGCGC---TTCTGTAAC-----AA [10788]
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Hsa ACCACTGACCGTTGACTGTACCTTGGGGTCCTT--ATGGCTGCACTCAACATTCATTGCT [11297]
Mmu ACCACCGACCGTTGACTGTACCTTGGGATTCTT--ATGGCTGCACTCAACATTCATTGCT [11134]
Mdo ACCATCGACCGTTGACTGTGCCTTGAGGTTTAT--ATGTCTGCAATCAACATTCATTGCT [10681]
Meu ACCATCGACCGTTGACTGTACCTTGAGGTTTAT--ATGTCTGCAATAAACATTCATTGCT [9210]
Oan ACCATCGACCGTTGACTGTACCTTGAGGTTTAT--ATGGCTGCAATCAACATTCATTGCT [9910]
Aca ACCATCGACCGTTGACTGTACCTTGAGGTTTAT--ACGGCTGCAATCAACATTCATTGCT [11376]
Pbi ACCATCGACCGTTGACTGTACCTTGAGGTTTAT--ATGGCTGCACTCAACATTCATTGCT [11666]
Cpi ACCATCGACCGTTGACTGTACCTTGAGGTATAT--ATGGCTGCAATCAACATTCATTGCT [12102]
Cmy ACCATCGACCGTTGACTGTACCTTGAGGTTTAT--ATGGCTGCAATCAACATTCATTGCT [11853]
Psi ACCATCGACCGTTGATTGTACCTTGAGGTTTAT--ATGGCTGCAATCAACATTCATTGCT [10889]
Asp ACCATCGACCGTTGATTGTACCTTGAGGTTTAT--ATGGCTGCAATCAACATTCATTGCT [10295]
Ami ACCATCGACCGTTGACTGTACCTTGAGGTTTAT--ATGGCTGCAATCAACATTCATTGCT [11428]
Asi ACCATCGACCGTTGACTGTACCTTGAGGTTTAT--ATGGCTGCAATCAACATTCATTGCT [10776]
Tgu ACCATCGACCGTTGACTGTACCTTGAGGTTTAT--ATGGCTGCAATCAACATTCATTGCT [8958]
Cli ACCATCGACCGTTGACTGTACCTTGAGGTTTAT--ATGGCTGCAATCAACATTCATTGCT [11258]
Gga ACCATCGACCGTTGACTGTACCTTGAGGTTTAT--ATGGCTGCAATCAACATTCATTGCT [10071]
Xtr ACCATCGGCCGTTGACTGTACCCTGAGGCTTTT--ATGGCTGCAATAAACATTCATTGCT [10853]
Lch ACCATCGACCGTTGACTGTACCTTGAGGTCTAT--ATGGCTGCAATCAACATTCATTGCT [11801]
Dre ACCATCGACCGTTGACTGTACCCTGAGGGTGGC--ATGACTGCAATAAACATTCATTGCT [10846]

Hsa GTCGGTGGGTTTGAGTCTGAATCAACTCACTGATCAATGAATGCAAACTGCGGACCA--A [11355]
Mmu GTCGGTGGGTTTGAATGTCAACCAACTCACTGATCAATGAATGCAAACTGCGGGCCA--A [11192]
Mdo GTCGGTGGGTTTTTGATTCAATCAACTCACTGATCAATGAATGCAAACTGCGGATCA--A [10739]
Meu GTCGGTGGGTTTTTATCTCAATCAACTCACTGATCAATGAATGCAAACTGCGGATCA--A [9268]
Oan GTCGGTGGGTTTTTGTCTGAATCAACTCACTGATCAATGAATGCAAACTGCGGACCA--A [9968]
Aca GTCGGTGGGTTTTAGGTTCAGTCAGCTCTCTGACCAATGAATGCAAACTGCAGACCA--A [11434]
Pbi GTCGGTGGGTTTCGGGTTCAGTCAGCCCTCTGGCCAATGAATGCAAACTGCGGATCA--A [11724]
Cpi GTCGGTGGGTTTTAGTTTGTATCAACTCACTGATCAATGAATGCAAACTGCGGACCA--A [12160]
Cmy GTCGGTGGGTTTTAGTTTGTATCAACTCACTGATCAATGAATGCAAACTGCGGACCA--A [11911]
Psi GTCGGTGGGTTTTAGTTTGTATCAACTCACTGATCAATGAATGCAAACTGCGGACCA--A [10947]
Asp GTCGGTGGGTTTTAGTTTGTATCAACTCACTGATCAATGAATGCAAACTGCGGACCA--A [10353]
Ami GTCGGTGGGTTTTAGTTTGTACCAACTCACTGATCAATGAATGCAAACTGCGGACCA--A [11486]
Asi GTCGGTGGGTTTTAGTTTGTACCAACTCACTGATCAATGAATGCAAACTGCGGACCA--A [10834]
Tgu GTCGGTGGGTTTTCATTTCTATCAACTCACTGACCAATGAATGCAAACTGCGGACCA--- [9015]
Cli GTCGGTGGGTTTTCTTTTCTGTCAACTCACTGATCAATGAATGCAAACTGCGGACCA--- [11315]
Gga GTCGGTGGGTTTTCATTGCTATCAACTCACTGATCAATGAATGCAAACTGCGGACCA--- [10128]
Xtr GTCGGTGGGTTGTAGTTTAGAAAAGCTCATTGATCAATGAATGCAAACTGCAGACCA--- [10910]
Lch GTCGGTGGG-TTTACTTTAGATCAACTCACTGATCAATGAATGCAAACTGCAGTCCA--A [11858]
Dre GTCGGTGGGTTTCTAATAGACACAACTCACTGATCAATGAATGCAAACTGCGGTGCA--C [10904]

Hsa GGGTTTGGGGGAACATTCAAC-CTGTCGGTGAGTTTGGGCAGCTCA-GGCAAACCATCGA [11413]
Mmu GGGTTTGGGGGAACATTCAAC-CTGTCGGTGAGTTTGGGCAGCTCA-GACAAACCATCGA [11250]
Mdo AGGTTTGGGGGAACATTCAACGCTGTCGGTGAGTTTGAGCAGCTGAAGGCAAACCATCGA [10799]
Meu AGGTTTGGGGGAACATTCAACGCTGTCGGTGAGTTTGAGCAGCTGAAGGCAAACCATCGA [9328]
Oan AGGTTTGGGGGAACATTCAACGCTGTCGGTGAGTTTGGGCAGTAGAGGTTAAACCACCGA [10028]
Aca AGGTCTTGGGAAACATTCAACGCTGTCGGTGAGTTTTGTCAATGAA-GTCAAACCATCGA [11493]
Pbi AGTTCTCAGGGAACATTCAACGCTGTCGGTGAGTTTTGTCAGTGGG-ATTAAACCATCGA [11783]
Cpi AGGTTTCAGTGAACATTCAACGCTGTCGGTGAGTTTTCTCAATAAG-GTTAAACCATCGA [12219]
Cmy AGGTTTCAGTGAACATTCAACGCTGTCGGTGAGTTTTCTTAGTAAG-GCTAAACCATCGA [11970]
Psi AGGTTTCAGTGAACATTCAACGCTGTCGGTGAGTTTTCTCAGTAAG-GTTAAACCATCGA [11006]
Asp AGGTTTCAGTGAACATTCAACGCTGTCGGTGAGTTTTCTCAGTAAG-GTTAAACCATCGA [10412]
Ami AGGTTTCAGCGAACATTCAACGCTGTCGGTGAGTTTTGGCAGTCAG-GTTAAACCATCGA [11545]
Asi AGGTTTCAGCGAACATTCAACGCTGTCGGTGAGTTTTGGCAGTCAG-GTTAAACCATCGA [10893]
Tgu ------------------------------------------------------------ [9015]
Cli ------------------------------------------------------------ [11315]
Gga ------------------------------------------------------------ [10128]
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Xtr ------------------------------------------------------------ [10910]
Lch AGGTTTCAGTGAACATTCAGCGCTGTCGGTGAGTTTGGGCAGTAAG-ATTAAACCATCGA [11917]
Dre GAGTCTCAGAGAACATTCAACGCTGTCGGTGAGTTT--GCAAGTGA-GAAAAACCATCGA [10961]

Hsa CCGTTGAGTGGACCCTGAGGCCTGG--GAGGTCACAATCAACATTCATTGTTGTCGGTGG [11471]
Mmu CCGTTGAGTGGACCCCGAGGCCTGG--AAGGTCACAATTAACATTCATTGTTGTCGGTGG [11308]
Mdo CCGTTGAGTGGACCCCGCAGCCTTA--AAGGTCACAATCAACATTCATTGCTGTCGGTGG [10857]
Meu CCGTTGAGTGGACCCTGCAACCTTA--AAGGTCACAATCAACATTCATTGCTGTCGGTGG [9386]
Oan CCGTTGAGTGTACCCCTCAGCCTAG--AAAGTCACAATCAACATTCATTACTGTCGGTGG [10086]
Aca CTGTTGAGTGTACCCTGCGGCTTTT--AAAGTCACAATCAACATTCATT-CTGTCGGTGG [11550]
Pbi CTGTTGAGTGTACCCTGCGGCCTTT--AAAGTCACAATCAACATTCATT-CTGTCGGTGG [11840]
Cpi CCGTTGAGTGTACCCTGCGGCCGGA--AAAGTCACAATCAACATTCATTGCTGTCGGTGG [12277]
Cmy CCGTTGAGTGTACCCTGCGGCCTGA--AAAGTCACAATCAACATTCATTGCTGTCGGTGG [12028]
Psi CCGTTGAGTGTGCCCTGCGGCCTGA--AAAGTCACAATCAACATTCATTGCTGTCGGTGG [11064]
Asp CCGTTGAGTGTGCCCTGCGGCCCGA--AAAGTCACAATCAACATTCATTGCTGTCGGTGG [10470]
Ami CCGTTGAGTGTACCCTGCAACCTTG--AAAGTCACAATCAACATTCATTGCTGTCGGTGG [11603]
Asi CCGTTGAGTGTACCCTGCAACCTTG--AAAGTCACAATCAACATTCATTGCTGTCGGTGG [10951]
Tgu ------------------------------------------------------------ [9015]
Cli ------------------------------------------------------------ [11315]
Gga ------------------------------------------------------------ [10128]
Xtr ------------------------------------------------------------ [10910]
Lch CCGCTGACTGTACCCTGCAACTGCA--AAAGTCACAATTAACATTCATTGCTGTCGGTGG [11975]
Dre GTGTTGAGTGTACCCTGCCTCTCGA--AAGGTCATAATCAACATTCATTGCTGTCGGTGG [11019]

Hsa GTTGTGAGGACTGAGGCCAGACCCACCGGGGGATGAATGTCACTGT-GGCTGGG--CCAG [11528]
Mmu GTTGTGAGGAG-GCAGCCAGACCCACCGGGGGATGAATGTCACTGT-GGCTGGG--CAGA [11364]
Mdo GTTGTGAGATCTGAGGAAAAACTCACCGATGGATGAATGTCACTGT-GGCTGGG--CCAG [10914]
Meu GTTGTGAGATGTGAGGCAAAACTCACCGATGGATGAATGTCACTGT-GGCTGGG--CCAG [9443]
Oan GTTGTGATAAATGA-AAAAAACTCACCGCCAGATGAATGCCACTGT-GGCTAGG--CCCA [10142]
Aca GTTGTGATGCTGGAGGAGAACCTCACTGATCAGTGAATGCAACTGT-GGCTGGA--CCGC [11607]
Pbi GTTGTTATGCTGGAGGAGAAGCTCACTGATCAGTGAATGCAACTGT-GGCTGGA--TTCC [11897]
Cpi GTTGTGTTGTTGAAGGAAAAACTCACTGATCAATGAATGCAACTGT-GATTGGA--CCAT [12334]
Cmy GTTGTGTTGTTGAAGGAAAAACTCACTGATCAATGAATGCAACTGT-GATTGGA--CCAT [12085]
Psi GTTGTGTTATTGAAGGAAAAACTCACTGATCAATGAATGCAACTGT-GATTGGA--CCAT [11121]
Asp GTTGTGTTGTTGAAGGAAAAACTCACTGATCAATGAATGCAACTGT-GATTGGA--CCAT [10527]
Ami GTTGTGATGCTGAAGGGAAAACTCACGGATCAATGAATGCAACTGT-GATTGGA--CCAT [11660]
Asi GTTGTGATGCTGAAGGGAAAACTCACGGATCAATGAATGCAACTGT-GATTGGA--CCAT [11008]
Tgu ------------------------------------------------------CCGC [9019]
Cli ------------------------------------------------------CCAT [11319]
Gga ------------------------------------------------------CCGC [10132]
Xtr ------------------------------------------------------CCAG [10914]
Lch GTTGTGATGTTTAAAAAGAAACTCACTGCACAATGAATGCCACTGT-GGCTGTC--TCGT [12032]
Dre GTTTAGTCTTGTAA----CAGCTCTCTGAACAATGAATGTAACTGT-GGCCCAG--TCGA [11072]

Hsa TCACGTCCCCTTATCACTTTTCCAGCCCAGCTTTGTGACTGTA-AGTGTTGGACGGAGAA [11587]
Mmu TCCCCTTTCCTTATCACTTTTCCAGCC-AGCTTTGTGACTCTA-AGTGTTGGACGGAGAA [11422]
Mdo TCACATCCCCTTATCACTTTTCCAGCCCAGCTTTCTAATGCTA-ATTGTTGGACGGAGAA [10973]
Meu TCACGTCCCCTTATCACTTT-CCAGCCCAGCTTTCTAATTCTA-ATTGTTGGACGGAGAA [9501]
Oan TCACGTCTCTTTATCACTTTTCCAGCCCAGCTTTCTGGTTCTA-GCCGTTGGACGGAGAA [10201]
Aca TCACGTCCCCTTATCACTTTTCCAGCC-AGCTTTCTTGTCATA-ACCGTTGGACGGAGAA [11665]
Pbi CCACGTCTCCTTATCACTCTTCCAGCC-AGCTTTCTTCTTGCA-AGTGTTGGACGGAGAA [11955]
Cpi TCTCGTGTCCTTATCACTTTTCCAGCCCAGCTTTTTCATTGTA-ACTGTTGGACGGAGAA [12393]
Cmy TCTCATGTCCTTATCACTTTTCCAGCCCAGCTTTTTCATTGTA-TCTGTTGGACGGAGAA [12144]
Psi TCTCGTCTCCTTATCACTTTTCCAGCCCAGCTGTCTCACTGCA-GGTGTTGGACGGAGAA [11180]
Asp TCTCGTCTCCTTATCACTTTTCCAGCCCAGCTGTCTCACTGCA-GGTGTTGGACGGAGAA [10586]
Ami TCCCATCTCCTTATCACTTTTCCAGCCCAGCTTTCTCATGCTC-ACTGTTGGACGGAGAA [11719]
Asi TCCCATCTCCTTATCACTTTTCCAGCCCAGCTTTCTCATGCTC-ACTGTTGGACGGAGAA [11067]
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Tgu TCTCGTGCCCTTATCACTTTTCCAGCCCAGCTTCTGCACTCTG-ACTGTTGGACGGAGAA [9078]
Cli TCTCATCTCCTTATCACTTTTCCAGCCCAGCTTCTTCACTGTA-ACTGTTGGACGGAGAA [11378]
Gga TCTCACCCCCTTATCACTTTTCCAGCCCAGCTTCTTCGCTCTG-ACTGTTGGACGGAGAA [10191]
Xtr TATCACTTCCTTATCACTTTTCCAGCCCAGCTTTTCATGACAA-ACTGTTGGACGGAGAA [10973]
Lch TCACATGTCCTTATCATTTTTCCTGCCCAGCTTTCAAATGATC-TTTGTTGGACGGAGAA [12091]
Dre ACACGTCTCCTTATCACTTTTCCAGCCCAGCTATCCATTTAGTATTCGTTGGACGGAGAA [11132]

Hsa CTGATAAGGGTAGGTGATTG--TGTGAGACCTCGGGCTACAACACAGGACCCGGGCGCTG [11645]
Mmu CTGATAAGGGTAGGTGACTG--TGCGGGTCCTCAGGCTACAACACAGGACCCGGGCGCTG [11480]
Mdo CTGATAAGGGTAGGTGATTG--TGTGAGACCTCTGGCTACAACACAGGACACGGGAGCTT [11031]
Meu CTGATAAGGGTAGGTGACTG--TGTGAGACCTCTGGCTACAACACAGGACATGGGAGCTT [9559]
Oan TTGATAAGGGTACGGGGTCG--TGTGAGACCTCCGGCTACAACAGAGGACACAGGAGCTT [10259]
Aca CTGATAAGGGTTTGTGGGTG--TGTGAGACCTTTGGCTACAACACAGAACATGGGCGCTT [11723]
Pbi CTGATAAGGGTATGTGGGTG---------------------------------------- [11975]
Cpi CTGATAAGGGTATGTGACTG--TGTGAGACCTCGGGCTACAACACAGGACATGGGAGCTT [12451]
Cmy CTGATAAGGGTATGTGACTG--TGTGAGACCTCGGGCTACAACACAGGACATGGGAGCTT [12202]
Psi CTGATAAGGGAACGGGACTG--TGTGAGACCTCGGGCTACAACACAGGACATGGGAGCTT [11238]
Asp CTGATAAGGGAATGGGACTG--TGTGAGACCTCGGGCTACAACACAGGACATGGGAGCTT [10644]
Ami CTGATAAGGGTATGTGACTG--TGTGAGACCTCCGGCTACAACACAGGACATGGGAGCTT [11777]
Asi CTGATAAGGGTATGTGACTG--TGTGAGACCTCCGGCTACAACACAGGACATGGGAGCTT [11125]
Tgu CTGATAAGGGTGCGCGAGTG--TGTGAGACCTCCGGCTACAACACAGGACATGGGAGCTT [9136]
Cli CTGATAAGGGTATGCGAGTG--TGTGAGACCTCCGGCTACAACACAGGACATGGGAGCTT [11436]
Gga CTGATAAGGGTGTGCGGGTG--TGTGAGACCTCCGGCTACAACACAGGACATGGGAGCTT [10249]
Xtr CTGATAAGGCTGTGTGACTG--TGGTATACCTTTGGTTACAACACAGGACATGGGAGCTT [11031]
Lch TTGATAAGGGTGTGAGATTG--TGCGATGCCTCGGGCTGCAACACAGGACATGGGAGCTT [12149]
Dre CTGATAAGGGCATGTGCCCG--GGCTGGGCCAGGGGCTGCAACACAGGACATGGGAGCTG [11190]

Hsa ----CTCTGACCCCTCGTGTCTTGTGTTGCAGCCGGAGGGACGCAGG--GCAGGCCTCTG [11699]
Mmu ----CTCTGACCCCTCGTGTCTTGTGTTGCAGCCGGAGGGACGCAGG--GCAGGCCTCTG [11534]
Mdo ----TTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAGGCCTCTG [11085]
Meu ----TTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAGGCCTCTG [9613]
Oan ----TTCAGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGAGCACATC--GCAGGCCTCTG [10313]
Aca ----TCTTGGACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAGGGCTCTG [11777]
Pbi ------------------------------------------------GTGAGACTCTG [11986]
Cpi ----TTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAGGGCTCTG [12505]
Cmy ----TTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAGGGCTCTG [12256]
Psi ----TTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAGGGCTCTG [11292]
Asp ----TTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAGGGCTCTG [10698]
Ami ----TTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAGGACTCTG [11831]
Asi ----TTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAGGACTCTG [11179]
Tgu ----TTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAAGACTCTG [9190]
Cli ----TTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAGGACTCTG [11490]
Gga ----TTCTGAACCCTCGTGTCTTGTGTTGCAGCCAGAGGGGCACATC--GCAGGACTCTG [10303]
Xtr A---CTTGGAACCCTCGTGTCTTGTGTTGCAGCCAGTGGTGGCCAAA------------- [11075]
Lch ----ATTGTAACCCTCGTGTCTTGTGTTGCAGCCAGTGGGGTTGCAT--GCAGGACTCTG [12203]
Dre TCTCTCACTCCCGCTCGTGTCTTGTGTTGCAGCCAGTGGAACGGCTA--GCAGGCCTCTG [11248]

Hsa TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [11759]
Mmu TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAGCATATTCCT [11594]
Mdo TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [11145]
Meu TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [9673]
Oan TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [10373]
Aca TGTGATATGTTTGATATATTAGGTTGTAATTGAGCCCAACTATATATCAAACAT--TCCT [11835]
Pbi TGTGATATGTTTGATATATTAGGTTGTAATTTGGCCCAACTATATATCAAACAT--TCCT [12044]
Cpi TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [12565]
Cmy TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [12316]
Psi TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [11352]
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Asp TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [10758]
Ami TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [11891]
Asi TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [11239]
Tgu TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [9250]
Cli TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [11550]
Gga TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [10363]
Xtr ---------------------------------------------------------- [11075]
Lch TGTGATATGTTTGATATATTAGGTTGTTATTTAATCCAACTATATATCAAACATATTCCT [12263]
Dre TTTGATATGTTTGATATATTAGGTTGTTATTCTGTCCAACTATATATCAAACATATTCCT [11308]

Hsa ACAGTGTCTTGCC--GCCTGCTTCTGTGTGATATGTTTGATATTGGGTTGTTTAATTAGG [11817]
Mmu ACAGTGTCTTGCC--GCCTGCTTCTGTGTGATATGTTTGATATTGGGTTGTTAAATTATG [11652]
Mdo ACAGTGTCCTGCC--CCCTACTTCTGTGTGATATGTTTGATATTGGGTTGTTTGATTGGG [11203]
Meu ACAGTGTCCTGCC-------------------ATGTTTGATATTAGGTTGTTTGATTGAG [9714]
Oan ACAGTGTCTTGCC--------CTCTGTGTGATATGTTTGATATTAGGTTGTTACGCTAGA [10425]
Aca ACAGGGCCCCGCT--CCCTGCTTCTG-CTGATATGTTTGATATTAGGTTGTTCTACTGGG [11892]
Pbi ACGGTGTCTCGCT--CCCAGCCTCTGTCTGATATGTTTGATATTAAGTTGTTCTCCTGGG [12102]
Cpi ATAGTGTCCTGCC--CCCTGCCGCTGGCTGATATGTTTGATATTAGGTTGTTTTATTGGA [12623]
Cmy ATAGTGTCCTGCC--CCCTGCCGCTGGCTGATATGTTTGATATTAGGTTGTTTTATTGGA [12374]
Psi ATAGTGTCCTGCC---------------------------------------------- [11365]
Asp ATAGTGTCCTGCC---------------------------------------------- [10771]
Ami ACAGTGTCCTGCC--ACCTGCCTCTGTCTGATATGTTTGATATTAGGTTGTTTTATTGGA [11949]
Asi ACAGTGTCCTGCC--ACCTGCCTCTGTCTGATATGTTTGATATTAGGTTGTTTTATTGGA [11297]
Tgu ACAGTGTCCTGCC--CCCTGTCTCTGTCTGATATGTTTGATATTAGGTTGTTTTATTGGA [9308]
Cli ACAGTGTCCTGCC--CCCTGTCTCTGTCTGATATGTTTGATATTAGGTTGTTTTATTGGA [11608]
Gga ACAGTGTCCTGCC--CCCTGCCTCTGTCTGATATGTTTGATATTAGGTTGTTTGATTGGA [10421]
Xtr ---------------CCGTGGTTCTGTCTGATATGTTTGATATTAGGTTGTTTTACTAA- [11119]
Lch ACAGTGTCCTGCC--GTTTGGTTCTGTGTGATATGTTTGATATTAGGTTGTTTTATTAA- [12320]
Dre ACAGTGTCCTGCT--GTTACAGACTATGTGATATGTTTGATATTCGGTTGCTTTCTTTAT [11366]

Hsa AA-CC---AACTAAATGTCAAACATATTCTTACAGCAGCAGGT--TGGACAGCGGGCAAC [11871]
Mmu AA-CC---AACTGAATGTCAAGCATACTCTCACAGCAGTAAGG--TGGACAGCGGGCAAC [11706]
Mdo AA-TC---AACTAAATGTCAAACATATTCTTACAGCGGTTGGG--TTGACAGCGGGCAAC [11257]
Meu AA-TC---AACTAAATGTCAAACATATTCTTACAGCGGTTGGG--TTGACAGCGGGCAAC [9768]
Oan CC-TC---ACCTGAATATCAGACATATTCCTACAGCGGCTGGG--TTGACAGCAGGCAAC [10479]
Aca AAACC---AACTAAATATCAAACATATTCTTACAGCGCCAGGG--TTGATAGTGGGCAAC [11947]
Pbi AAACCC--AACTAAATATCAGACATATTCCGACAGCGACTGGG--ATAAGAATGGGCAAC [12158]
Cpi AAACC---AACTAAATATCAAACATATTCTTCCGGCGCCAGGG--ACGACAGCGGGCAAC [12678]
Cmy AAACC---AACTAAATATCAAACATATTCTTCCCGCGCCAGGG--GTGACAGCAGGCAAC [12429]
Psi ---------------------------------------------------------- [11365]
Asp ---------------------------------------------------------- [10771]
Ami AAGCC---AACTAAATATCAAACATATTCTTACAGCGCCAGGG--GCGACAGCGGGCAAC [12004]
Asi AAGCC---AACTAAATATCAAACATATTCTTACAGCGCCAGGG--GCGACAGCGGGCAAC [11352]
Tgu AAACC---AACTAAATATCAAACATATTCTTACAGCGCCAGGG----------------- [9348]
Cli AAACC---AACTAAATATCAAACATATTCTTACAGCGCCAGGG--GCCACCGCGGGCAAC [11663]
Gga AA-CC---AACTAAATATCAAACATATTCTTACAGCGGCAGGG----------------- [10460]
Xtr AA-CTC--GACTAAATATCATACATATTGCTACAGCGCCCTGG--GGTAGCTCTGACAAC [11174]
Lch AAACC---AACTAAATATCAGACATATTCCTACAGCGCCAGAT----------------- [12360]
Dre ATCATGTCAACTAAATATCAGACATATTCCTATAGACTGTGAC----------------- [11409]

Hsa GGAATCCCAAAAGCAGCTGTTGTCTCCAGAGCATTCCAGCTGCGCTTGGATTTCGTCCCC [11931]
Mmu GGAATCCCAAAAGCAGCTGTTGTCTCCAGAGCATTCCAGCTGCACTTGGATTTCGTTCCC [11766]
Mdo GGAATCCCAAAAGCAGCTGTTGTCTCCAGAGCATTCCAGCTGCAATTGGATTTCGTTCCC [11317]
Meu GGAATCCCAAAAGCAGCTGTTGTCTCCAGAGCATTCCAGCTGCGATTGGATTTCGTTCCC [9828]
Oan GGAATCCCAAAAGCAGCTGTTGTCTCCAGAGCATTCCAGCTGCAGTTGGATTTCGTTCCC [10539]
Aca GGAATCCCAAAAGCAGCTGTTTTCCTCTTAAAGTTCCAGCTGCACTTGGATTTCGTTCCT [12007]
Pbi GGAATCCCAAAAGCAGCTGTTTTCCTCTGAGTCTTCCAGCTGCACTTGGATTCCGTTCCT [12218]
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Cpi GGAATCCCAAAAGCAGCTGTCTTCCTCTGAGCATTCCAGCTGCGGTTGGATTTCGTTACC [12738]
Cmy GGAATCCCAAAAGCAGCTGTCTTCCTCTGAGCATCCCAGCTGCGGTTGGATTTCGTTACC [12489]
Psi ------------------------------------------------------------ [11365]
Asp ------------------------------------------------------------ [10771]
Ami GGAATCCCAAAAGCAGCTGTCTTCCGCTCGGCACCTCAGCTGCGCTTGGATTTCGTTCCC [12064]
Asi GGAATCCCAAAAGCAGCTGTCTTCCGCTCGGCACCTCAGCTGCGCTTGGATTTCGTTCCC [11412]
Tgu ------------------------------------------------------------ [9348]
Cli GGAATCCCAAAAGCAGCTGTCCCCGCTG----TGCCCAGCTGCCCTGGGGTTTCGTTACC [11719]
Gga ------------------------------------------------------------ [10460]
Xtr GGAATCCCAAAAGCAGCTGTTGTGAAAA----TGTTCAGCTGCAGTTGGGACCCGTTCAC [11230]
Lch ------------------------------------------------------------ [12360]
Dre ------------------------------------------------------------ [11409]

Hsa TGCTCTCCTGCC--GTGCACAGGG-CTCTGACCT-ATGAATTGACAGCCAGTGCTCTCGT [11987]
Mmu TGCTCTCCTGCC--GTGCACAGGG-CTCTGACCT-ATGAATTGACAGCCAGTACTCTTTT [11822]
Mdo TGCTCTCCTGCC------------------------------------------------- [11329]
Meu TGCTCTCCTGCC--GTGCGCAGGGGCTCTGACCTTATGAATTGACAGCCAGTACTCATTC [9886]
Oan TGCTATCCTGCA--GCGCACAGGG-CTCTGACCT-ATGAATTGACAGCCAGTTCTCTC-T [10594]
Aca TGCTTTCCTACC------------------------------------------------- [12019]
Pbi TGCTCTTTTGCT------------------------------------------------- [12230]
Cpi TGCTCTCCTGCC--GTGCACAGGA-CTATGACCT-ATGAATTGACAGCCAGTCCTTCTGC [12794]
Cmy TGCTCTCCTGCC--GTGCACAGGC-CTATGACCT-ATGAATTGACAGCCAGTCCTGCTGC [12545]
Psi --------------GTGCACAGGA-CTATGACCT-ATGAATTGACAGCCAGTCCTGCCAT [11409]
Asp --------------GTGCACAGGA-CTATGACCT-ATGAATTGACAGCCAGTCCTGCCAT [10815]
Ami TGCTCTCCCGCC--GTGCATGGGG-CTATGACCT-ATGGATTGACAGCCAGTATCGGAGC [12120]
Asi TGCTCTCCCGCC--GTGCATGGGG-CTATGACCT-ATGGATTGACAGCCAGTATCCGAGC [11468]
Tgu ------------------------------------------------------------ [9348]
Cli CGCGCTCCCGCC------------------------------------------------ [11731]
Gga ------------------------------------------------------------ [10460]
Xtr GGATCTATTGCC--GTGTACGGGC-CTATGACCT-ATGAATTGACAGCCAGTGGATGTGA [11286]
Lch --------------CTGGACAGGC-CTATGACCT-ATGTATTGACAGTCAGTTGGCCATC [12404]
Dre --------------GGACACAGGG-TGATGACCT-ATGAATTGACAGCCAGTGTTTGCAG [11453]

Hsa CTCCCCTCTGGCTGCCAATTCCATAGGTCACAGGTATGTTCGCC--GTATACAGGAAAAT [12045]
Mmu CTCTCCTCTGGCTGCCAATTCCATAGGTCACAGGTATGTTCACC--GTGTACAGGAGAAT [11880]
Mdo ----------------------------------------------GTGTGTAGGAAAAT [11343]
Meu TCCCTTTCTGGCTGCCAATTCCATAGGTCACAGGTATGTTCGCC---------------- [9930]
Oan GACCCCTCTGGCTGCCAATTCCATAGGTCACAGGTATGTTCGCC--GTGTACAGGAAAAT [10652]
Aca ----------------------------------------------AGGCTTAGGGTAAT [12033]
Pbi ----------------------------------------------AGGTCCAGGGTAAT [12244]
Cpi CGCGCC-CTGGCTGTCAGTTCTGTAGGGCACAGGTATGTTCACC--GTGTACAGGAAAAT [12851]
Cmy ---GCC-CTGGCTGTCAGTTCTGTAGGGCACAGGTATGTTCACC--GTGTACAGGAAAAT [12599]
Psi ---GCC-TTGGCTGTCAGTTCTGTAGGGCACAGGTATGTTCACC--GTATATAGGAAAAT [11463]
Asp ---GCC-TTGGCTGTCAGTTCTGTAGGGCACAGGTATGTTCACC--GTGTATAGGAAAAT [10869]
Ami CTCGCC-CTGGCTGTCTGTTCTATAGGGCATAGGACTGGGCGCA--TTGTGCAGGAAAAT [12177]
Asi TTCGCC-CTGGCTGTCTGTTCTATAGGGCATAGGACTGGGCGCA--TTGTGCAGGAAAAT [11525]
Tgu ----------------------------------------------GTGTCCAGGAAAAT [9362]
Cli ----------------------------------------------GTGTCCAGGAAAAT [11745]
Gga ----------------------------------------------GTGTCCAGGAAAAT [10474]
Xtr AGT----CTGCCTGTCAATTCTGTAGGCCACAGGTTCGTCCACC--GTAACCAGGAGGAT [11340]
Lch TAGAAT-CTGGCTGTCAATTCTGTAGGTCACAGGTATGTTAGCC--GCTAACAGGACAAT [12461]
Dre TCCAG--CTGCCTGTCAGTTCTGTAGGCCACTGCCCTGTTTATC---------------- [11495]

Hsa GACCTATGAATTGACAGACAATATAGCT---GAGTTTGTCTGTCATTTCTTTAGGCCAAT [12102]
Mmu GACCTATGATTTGACAGACCGTGCAGCT---GTGTATGTCTGTCATT-CTGTAGGCCAAT [11936]
Mdo GACCTATGAATTGACAGACATTATATTTA--AAGTTTGTCTGTCATTTCTGTAGGCCAAT [11401]
Meu ------------------------------------------------------------ [9930]
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Oan GACCTATGAATTGACAGACAGTATATTTA----GATTGTCTGTCATTTCTGTAGGCCAAA [10708]
Aca GACCTATGATTTGACAGACTGTGCTTTCT--ATGTCTGCCTGTCATTTCTGTAGGCCAAT [12091]
Pbi GACCTATGATTTGACAGACTGTGCTATGT--AAGTCTGCCTGTCATTTCTGTAGGCCAAT [12302]
Cpi GACCTATGAATTGACAGACTGTGTCTTCT--AAATTTGTCTGTCACTTCTGTAGGCCAAT [12909]
Cmy GACCTATGAATTGACAGACTGTGTCTTCT--AAATTTGTCTGTCACTTCTGTAGGCCAAT [12657]
Psi GACCTATGAATTGATAGACTGTGACTTTT--AAATTTGTCTGTCAGTTCTGTAGGCCAAT [11521]
Asp GACCTATGAATTGATAGACTGTGACTTTT--AAATTTGTCTGTCAGTTCTGTAGGCCAAT [10927]
Ami GACCTATGAATTGACAGACTGTGTATTCT--AAGCTTGTCTGTCATTTCTGTAGGCCAAT [12235]
Asi GACCTATGAATTGACAGACTGTGTATTCT--AAGCTTGTCTGTCATTTCTGTAGGCCAAT [11583]
Tgu GACCTATGAATTGACAGACTGTCTTTT----GCATTTGCCTGTCACTTCTATAGGCCAAT [9418]
Cli GACCTATGAATTGACAGACTGCTTTCT----AAACTTGCCTGTCATTTCTATAGGCCAAT [11801]
Gga GACCTATGAATTGACAGACTGCTTTCA----AAATGTGCCTGTCATTTCTATAGGCCAAT [10530]
Xtr GACCTATGAAATGACAGCCA-CTTCCATACCAAACATGTCTGTCATTTCTGTAGGCCAAT [11399]
Lch GACCTATGAATTGACAGCCAGTGAAGTTGATGAATTTGTCTGTCAGTTCTATAGGCCACT [12521]
Dre ------------------------------------------------------------ [11495]

Hsa ATTCTGTATGAC--ATGGGAGCTGAGGGCTGGGTCTTTGCGGGCGAGATGAGGG------ [12154]
Mmu ATTCTGTATGTC--ACGGGAGCTGAGAGCTGGGTCTTTGCGGGCAAGATGAGAG------ [11988]
Mdo GCCTTGTATGTC--ACGGGAGTTGAGGATTGGGTCTTTGTGGGCGAGATGAGGG------ [11453]
Meu --------------ACGGGAGTTGAGGACTGGGTCTTTGCGGGCGAGATGAGGG------ [9970]
Oan GTTCTGCATGCC---------------------------------------------- [10720]
Aca ACTCTGTACGCC--TTGGGGGTCTGGGCCTGGGTCTTTGCGGGCGAGATGAGAAGTTT-- [12147]
Pbi ACTCTGCATATC--CTGGGAGTTTGGGGCTGGGTCTTTGCGGGCGAGATGAGAAGTT--- [12357]
Cpi ATTCTGCATGCC--GGGCGAGTCTAGGGCTGGGTCTTTGCGGGCGAGATGAGAGGTT--- [12964]
Cmy ATTCTGCATGCC--GGGCGAGTCTAGGGCTGGGTCTTTGCGGGCGAGATGAGAGGTT--- [12712]
Psi TTTCTGTATGCC--GGGTGAGTCTAGGGCTGGGTCTTTGCGGGCGAGATGAGAGGTT--- [11576]
Asp TTTCTGAATGCC--GGGTGAGTCTAGGGCTGGGTCTTTGCGGGCGAGATGAGAGGTT--- [10982]
Ami ATTCTGCACACC--ATGCGAGCTGAGGGCTGGGTCTTTGCGGGCGAGGTGAGAGGTT--- [12290]
Asi ATTCTGCACACC--ATGCGAGCTGAGGGCTGGGTCTTTGCGGGCGAGGTGAGAGGTT--- [11638]
Tgu ATTCTGTGCACT--------------GCTGGGTCTTTGCGGGCGAGATGAGAGGTT--- [9460]
Cli ATTCTGCACACT--GGGCGAGCTGAGGGCTGGGTCTTTGCGGGCGAGATGAGAGGTT--- [11856]
Gga ATTCTGTGCACT--GGGCGAGCTGAGGGCTGGGTCTTTGCGGGCGAGATGAGAGGTT--- [10585]
Xtr ATTCTGATTGCT---------------------------------------------- [11411]
Lch ATTCTGTATCCA--ATGTGGGTTTGGGGCTGGGTCTTTGCGGGCGAGATGAGGTCAGT-- [12577]
Dre --------------TAATGTGTTAGAGGTTGGGTCTTTGCGGGCAAGGTGAGTAGTTAAA [11541]

Hsa TGTCGGATCAACTGGCCTACAAAGTCCCAGTTCTCGGCCCCC--AAGAAAAATGAGGGAC [12212]
Mmu TGTCAGTTCAACTGGCCTACAAAGTCCCAGTCCTCGGTCCCC--AAGAAAAATGAGGGAC [12046]
Mdo TGTCAGTTCAACTGGCCTACAAAGTCCCAGTTCTCGGTTCCC------------------ [11495]
Meu TGTCAATTCAACTGGCCTACAAAGTCCCAGTTCTCGGTTCCC--AAGAAAAAGGAGGGAC [10028]
Oan ---------------------------------------------AAGAAAAATGAGGGAC [10736]
Aca CCTGCCTTCAACTGGCCTACAAAGTCCCAGTCCTCGGCCCCT--AAGAAAAATGAGGGAC [12205]
Pbi TCTGCCTTCAACTGGCCTACAAAGTCCCAGTTCTCGGCTCTT--AAGAAAAATGAGGGAC [12415]
Cpi TGTGGATTCAACTGGCCTACAAAGTCCCAGTTCTCGGCTCCC--AAGAAAAATGAGGGAC [13022]
Cmy TGTGCATTCAACTGGCCTACAAAGTCCCAGTTCTCGGCTCCC--AAGAAAAATGAGGGAC [12770]
Psi TGTGGATTCAACTGGCCTACAAAGTCCCAGTTCTCGGCTCCC--AAGAAAAATGAGGGAC [11634]
Asp TGTGGATTCAACTGGCCTACAAAGTCCCAGTTCTCGGCTCCC--AAGAAAAATGAGGGAC [11040]
Ami CGTGCGTTCAACTGGCCTACAAAGTCCCAGTTCTCGGCTCCC--AAGAAAAATGAGGGAC [12348]
Asi CGTGCGTTCAACTGGCCTACAAAGTCCCAGTTCTCGGCTCCC--AAGAAAAATGAGGGAC [11696]
Tgu CCTGTCTTCAACTGGCCTACAAAGTCCCAGTTCTCGGCTCCC--AAGAAAAATGAGGGAC [9518]
Cli CATGTCTTCAACTGGCCTACAAAGTCCCAGTTCTCGGCTCCC--AAGAAAAATGAGGGAC [11914]
Gga CGTGTCTTCAACTGGCCTACAAAGTCCCAGTTCTCGGCTCCC--AAGAAAAATGAGGGAC [10643]
Xtr ------------------------------------------------------------ [11411]
Lch TCTTCAATCAACTGGCCTACAAAGTCCCAGTTCTCAGCTCAT--AAGAAAAATGAGGGAC [12635]
Dre TTTACTCTCAACTGGCCTACAAAGTCCCAGTTTCTGGCTCAT--AAGAAAAATGAGGGAC [11599]

Hsa TTTCAGGGGCAGCTGTGTTTT-CTGACTCAGTCATAATGCCCCTAAAAATCCTTATTGTT [12271]
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Mmu TTTCAGGGGCAGCTGTGTTTC-CTGACTCAGTCATAATGCCCCTAAAAATCCTTATTGTT [12105]
Mdo ------------------------------------------------------------ [11495]
Meu TTTCAGGGGCAGCTGTGTTTTATTAACTCAGTCATAATGCCCCTAAAAATCCTTATTGTT [10088]
Oan TTTCAGGGGCAGCTGTGTTTTACTGACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [10796]
Aca TTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [12265]
Pbi TTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [12475]
Cpi TTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [13082]
Cmy TTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [12830]
Psi TTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [11694]
Asp TTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [11100]
Ami TTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [12408]
Asi TTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [11756]
Tgu TTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [9578]
Cli TTTCAGGGGCAGCTGTGTTTTGCTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [11974]
Gga TTTCAGGGGCAGCTGTGTTTTACTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [10703]
Xtr ------------------------------------------------------------ [11411]
Lch TTTTAGGGGCAGCTGTGTTTTGCTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGTT [12695]
Dre TTTTAGGGGCAGCTGTGTTTTATTAACCCAGTCATAATGCCCCTAAAAATCCTTATTGCT [11659]

Hsa C--GTGGTCTCAGAATCGGGGTTTTGAGGGCGAGATGAGTTT-ATGTTTTATCCAACTGG [12328]
Mmu C--GTGGGCCCAGAATCGGGGTTTTGAGGGCGAGATGAGTTT-GTGTTTTATCCAACTGG [12162]
Mdo ---GTGATTCCAGAGTCGGGGTTTTGAGGGCGAGATGAGTTT-ATGTTTTATCCAACTGG [11551]
Meu C------------------------------------------------------------ [10089]
Oan C--GTGATTCCAGAGTCGGGGTTTTGAGGGCGAGATGAGTTT-GTGTTTTATCCAACTGG [10853]
Aca C------------------------------------------------------------ [12266]
Pbi C--GTGAATCCGGGGCCGGGGCTTTGGGGGCGAGATGAGCTT-GCCCGGTATCCAACTGG [12532]
Cpi C--GTGGTTCCAGAGTCGGGGTTTTGGGGGCGAGATGAGCTT-ATGTTTTATCCAACTGG [13139]
Cmy C--GTGGTTCCAGAGTCGGGGTTTTGGGGGCGAGATGAGCTT-ATGTTTTATCCAACTGG [12887]
Psi C--GTGGTTCCAGAGTCGGGGTTTTGGGGGCGAGATGAGCTT-ATGTTTTATCCAACTGG [11751]
Asp C--GTGGTTCCAGAGTCGGGGTTTTGGGGGCGAGATGAGCTT-ATGTTTTATCCAACTGG [11157]
Ami C--GTGGTTCCAGAGTCGGGGTTTTGGGGGCAAGATGAGCTT-ATGTTTTATCCAACTGG [12465]
Asi C--GTGGTTCCAGAGTCGGGGTTTTGGGGGCAAGATGAGCTT-ATGTTTTATCCAACTGG [11813]
Tgu C--GTGGTTCCAGAGTCGGGGTTTTGGGGGCGAGATGAGCTT-ATGTTTTATCCAACTGG [9635]
Cli C--GTGGTTCCAGAGTCGGGGTTTTGGGGGCGAGATGAGCTT-ATGTTTTATCCAACTGG [12031]
Gga C--GTGGTTCCAGAGTCGGGGTTTTGGGGGCGAGATGAGCTT-ATGTTTTATCCAACTGG [10760]
Xtr ---GTGGTTTCGGAGTCGGGATTTTGGGGGCGAGATGAGCTA-ATGATTTATCCAACTGG [11467]
Lch C--GTGGTTCCAAACTCGGGGGTTTGGGGGCCGGATGAGCTG-ATTTTTAATCCAACTGG [12752]
Dre C--GTGATTTCAGTGACGGGACTTTGGGGGCGAGATGAGTATTGATCTCTATCCAACTGG [11717]

Hsa CCCTCAAAGTCCCGCTTTTGG-GGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [12385]
Mmu CCCACAAAGTCCCGCTTTTGG-GGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [12219]
Mdo CCCACAAAGTCCCGCTTTTGGTGGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [11609]
Meu ----------------------------AGGGAAAATGAGGGACTTTTGGGGGCAGATG [10120]
Oan CCCACAAAGTCCCGCTTTTGGTGGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [10911]
Aca ------------------------------------------------------------ [12266]
Pbi CCCACAAAGTCCCGCTTCTGG-GGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGCTG [12589]
Cpi CCCACAAAGTCCCGCTTTTGGTGGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [13197]
Cmy CCCACAAAGTCCCGCTTTTGGTGGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [12945]
Psi CCCACAAAGTCCCGCTTTTGGTGGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [11809]
Asp CCCACAAAGTCCCGCTTTTGGTGGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [11215]
Ami CCCACAAAGTCCCGCTTTTGGTGGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGTTG [12523]
Asi CCCACAAAGTCCCGCTTTTGGTGGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGTTG [11871]
Tgu CCCACAAAGTCCCGCTTTTGGTGGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [9693]
Cli CCCACAAAGTCCCGCTTTTGGTGGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [12089]
Gga CCCACAAAGTCCCGCTTTTGGTGGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [10818]
Xtr CCCGCAAAGTCCCGCTTCTGGAAGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [11525]
Lch CCCGCAAAGTCCCGCTTTTGGAAGTCA--AGGGAAAATGAGGGACTTTTGGGGGCAGATG [12810]
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Dre CCCGCAAAGTCCCGCTTCTGGGACTCA--AGGGAGAATGAGGGGCTTTTGGGGGCACTTG [11775]

Hsa TGTTTCCAT-TCCACTATCATAATGCCCCTAAAAATCCTTATTGCT--GGTTCCCGCCCC [12442]
Mmu TGTTTCCAT-TCCGCTATCATAATGCCCCTAAAAATCCTTATTGCT--GGCTCCCACCCT [12276]
Mdo TGTTTCCAT-TACACTATCATAATGCCCCTAAAAATCCTTATTGCT-------------- [11654]
Meu TGTTTCCAT-TACACTATCATAATGCCCCTAAAAAGCGTTATTGCT--GGCGCTCACTCC [10177]
Oan TGTTTCCAT-TGCACTATCATAATGCCCCTAAAAATCCTTATTGCT--GGAGCCCACCCC [10968]
Aca ----------------------------------------------GGTTCCCATCGG [12278]
Pbi TGTT-CTTC-CATGCTACCATAATGCCCCTAAAAATCCTTATTGCT--GGTGTCTATCGG [12645]
Cpi TGTTTCCAT-TACACTATCATAATGCCCCTAAAAATCCTTATTACT--GATGCCTATTGG [13254]
Cmy TGTTTCCAT-TACACTATCATAATGCCCCTAAAAATCCTTATTACT--GATGCCTAATGG [13002]
Psi TGTTTCCAT-TACACTATCATAATGCCCCTAAAAATCCTTATTACT--GATGCCTATTGG [11866]
Asp TGTTTCCAT-TACACTATCATAATGCCCCTAAAAATCCTTATTACT--GATGCCTATTGG [11272]
Ami TGTTTCCAT-TACACTATCATAATGCCCCTAAAAATCCTTATTGCT--GGTGTCCATCCG [12580]
Asi TGTTTCCAT-TACACTATCATAATGCCCCTAAAAATCCTTATTGCT--GGTGTCCATCCG [11928]
Tgu TGTTTCCAT-TACACTATCATAATGCCCCTAAAAATCCTTATTGCT-------------- [9738]
Cli TGTTTCCAT-TACACTATCATAATGCCCCTAAAAATCCTTATTGCT-------------- [12134]
Gga TGTTTCCAT-TACACTATCATAATGCCCCTAAAAATCCTTATTGCT-------------- [10863]
Xtr TGTTTCACT-TACACTACCATAATGCCCCTAAAAATCCTTATTGTT--GATGCTCATAAC [11582]
Lch TGTTTCAGTGTACACTATCATAATGCCCCTAAAAATCCTTATTGCT--AGTGTGCTTCAG [12868]
Dre TGTTTCAGT-TTCACCATCATAATGCCCCTAAAAATCCTTATTGCT--GGTGCTGACTGC [11832]

Hsa CTGTAACAGCAACTCCATGTGGAAGT--GCCCACTGGTTCCAGTGGGGCTGCTGTTATCT [12500]
Mmu CTGTAACAGCAACTCCATGTGGAAGT--GCCCACTGGTTCCAGTGGGGCTGCTGTTATCT [12334]
Mdo ------------------------------------------------------------ [11654]
Meu CTGTAACAGCAACTCCATGTGGGACA--GCTTCCTGCTTCCAGTGGGGGTGCTGTTACCT [10235]
Oan TTGTAACAGCAACTCCATGTGGAAGG--GTCTCCTGGTTCCAGTGGAGCTGCTGTTATCT [11026]
Aca CTGTAACAGCAACTCCATGTGGAAGC-AGTCCGGCCGTTCCAGTGGAGCGGCTGTTATAG [12337]
Pbi CTGTAACAGCAACTCCATGTGGAAGC--ATGAGGCAGTTCCCGTGGGGGGGCTGTTATTT [12703]
Cpi ATGTAACAGCAACTCCATGTGGAAGGTTTCATCCCTTTTCCAGTGGGGCTGCTGTTATTT [13314]
Cmy ATGTAACAGCAACTCCATGTGGAAGGTTTCATCCTGTTTCCAGTGGGGCTGCTGTTATTT [13062]
Psi ATGTAACAGCAACTCCATGTGGAAGGTTTCATTCTGTTTCCAGTGGGGCTGCTGTTATTT [11926]
Asp ATGTAACAGCAACTCCATGTGGAAGGTTTCATCCTGTTTCCAGTGGGGCTGCTGTTATTT [11332]
Ami CTGTAACAGCAACTCCATGTGGGAGG--GGTCCGTGGTCCCCGTGGGGCTGCTGTTATTC [12638]
Asi CTGTAACAGCAACTCCATGTGGGAGG--GGTCCGTGGTCCCCGTGGGGCTGCTGTTATTC [11986]
Tgu ------------------------------------------------------------ [9738]
Cli ------------------------------------------------------------ [12134]
Gga ------------------------------------------------------------ [10863]
Xtr CTGTAACAGCAACTCCATGTGGAAGT-AGATATAATATTCCGGTGGAGATGCTGTTATCT [11641]
Lch GTGTAACAGCAACTCCATGTGGATGG----CAATGGCTTCCAGTGGAGCTGCTGTTACTT [12924]
Dre TTGTAACAGCAACTCCATGTGGAAGG---TTTGTGTCTTCCAGTGGAGCTGCTGTTGCGT [11889]

Hsa GG-GGCGAGGGCC--TGGTGT-TATCAAGTGTAACAGCAACTCCATGTGGACTGTGTACC [12556]
Mmu GG-GGTGGCGGCT--TGGAGT-CATCGGGTGTAACAGCAACTCCATGTGGACTGTGCTC- [12389]
Mdo ------------------------------------------------------------ [11654]
Meu TG-GGTGGGCAGC---------------------------------------------- [10247]
Oan TG-GGTGGGTCAT--CAGTGT-TATCATATGTAACAGCAACTCCATGTGGATTAT--GCT [11080]
Aca TC-GGTGGGGGCT--CAGTGT-CGTCAAGTGTAACAGCAACTCCATGTGGAATAA--GTA [12391]
Pbi TG-GATGGGCACT--CGGTGT-TATCAAGTGTAACAGCAACTCCATGTGGAATAA--GCC [12757]
Cpi TT-GATAGGCTGT--CAGTGT-TATCAGATGTAACAGCAACTCCATGTGGACTAC--ACT [13368]
Cmy TT-GATAGGCTGT--CAGTAT-TATCAGATGTAACAGCAACTCCATGTGGACTAC--ACT [13116]
Psi TT-GATAGGCTAT--CAGTGT-TATCAGATGTAACAGCAACTCCATGTGGACTAC--ACC [11980]
Asp TT-GATAGGCCAT--CAGTGT-TATCAGATGTAACAGCAACTCCATGTGGACTAC--ACC [11386]
Ami TG-GACGGGCACC--CAGTAC-TTTCAAATGTAACAGCAACTCCATGTGGACTAC--GCT [12692]
Asi TG-GACGGGCACC--CAGTAC-TTTCAAATGTAACAGCAACTCCATGTGGACTAC--GCT [12040]
Tgu ---------------TGGTGC-TCTCATATGTAACAGCAACTCCATGTGGACTAC--ACT [9780]
Cli ---------------GGGCGC-TCTCAGATGTAACAGCAACTCCATGTGGACTAC--ACT [12176]
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Gga ---------------TGGTGC-TCTCATATGTAACAGCAACTCCATGTGGACTAC--ACT [10905]
Xtr GT-AATGTGTATC--TAGTGTGTATCAGGTGTAACAGCAACTCCATGTGGACTTG--TCC [11696]
Lch TT-GATGGGCACT--CAGTGTGCTTCAGGTGTAACAGCAACTCCATGTGGATGGC--AAT [12979]
Dre GCAGATAGTCACC-------------------------------------------------- [11902]

Hsa AATTTCCAGTGGAGATGCTGTTACTTTTGATGGTTACCAA--GCTGAGTGAATTAGGTAG [12614]
Mmu GGATTCCAGTGGAGCTGCTGTTACTTCTGATGGCCTCCAA--GTTGAGTGAAGTAGGTAG [12447]
Mdo ----------------------------------------GCTCAGTGGGTTAGGTAG [11672]
Meu ----------------------------------------GCTCAGTGGGTTAGGTAG [10265]
Oan GATTTCCAGTGGAGAGGCTGTTACTTTTGATGGAAACTGG------------------- [11120]
Aca GATTTCCAGTGGAGGTGCTGTTACTTTTGAA-GCTACTGA--GTTCTGTGGATTAGGTAG [12448]
Pbi TCTTTCCAGTGGAGGTGGTGTTACTTTTGAAAGCCACTGA--GTTCTGTGAATTAGGTAG [12815]
Cpi GACTTCCAGTGGAGATGCTGTTACTTTTGATATCTACTGA--GCTTTGTGAATTAGGTAG [13426]
Cmy GACTTCCAGTGGAGATGCTGTTACTTTTGATATCTACTGA--GCTCTGTGAATTAGGTAG [13174]
Psi AACTTCCAGTGGAGATGCTGTTACTTTTGATATCTACTGA--GCTTTGTGAATTAGGTAG [12038]
Asp AACTTCCAGTGGAGATGCTGTTACTTTTGATATCTACTGA--GCTTTGTGAATTAGGTAG [11444]
Ami GACTTCCAGTGGAGATGCTGTTACTTTTGACAGCCACTCA--GCTTTGTGAATTAGGTAG [12750]
Asi GACTTCCAGTGGAGATGCTGTTACTTTTGACAGCCACTCA--GCTTTGTGAATTAGGTAG [12098]
Tgu GACTTCCAGTGGAGATGCTGTTACTTTTGATGGTCACTCA------------------- [9820]
Cli GACTTCCAGTGGAGATGCTGTTACTTTTGATAGCCTCTCA--GCTCTGTGAATTAGGTAG [12234]
Gga GACTTCCAGTGGAGATGCTGTTACTTTTGATAGCGGCTCA--GCTCTGTGAATTAGGTAG [10963]
Xtr GTATTCCAGTGGAGATGCTGTTACTTTTGATGGGCACTTA------------------- [11736]
Lch GGCTTCCAGTGGAGCTGCTGTTACTTTTGATGGGCACTAA--GCGGTGTGTTTTAGGTAG [13037]
Dre ----------------------------------------GGTCTGTGATTTAGGTAG [11920]

Hsa TTTCATGTTGTTGGGCCTGGGTTTCTGA--ACACAACAACATTAAACCACCCGATTCACG [12672]
Mmu TTTCATGTTGTTGGGCCTGGCTTTCTGA--ACACAACGACATCAAACCACCTGATTCATG [12505]
Mdo TTTCCTGTTGTTGGGCCTAGATTTCTAA--ACACAAGAACATCAAACCACCTGATTCACT [11730]
Meu TTTCCTGTTGTTGGGCCTAGATTTCTAA--ACACAAGAACATCAAACCACCTGATTCACT [10323]
Oan ---------------------------------------------------------- [11120]
Aca TTTCACGTTGTTGGGAATTCATTTTTAAC-ACACAAGAACATAAAACTACCTGATTTACT [12507]
Pbi TTTCACGTTGTTGGGAATTCATTTTTAAT-ACACAAGAACATAAAACTACCTGATTTACT [12874]
Cpi TTTCATGTTGTTGGGGTTTTATTTTTAA--ACACAAGAACATAAAACTACCTGATTTACT [13484]
Cmy TTTCATGTTGTTGGGGTTTTATTTTTAA--ACACAAGAACATAAAACTACCTGATTTACT [13232]
Psi TTTCATGTTGTTGGGCTTCTAGTTTTTTAAACACAAGAACATAAAACTACCTGATTTACG [12098]
Asp TTTCATGTTGTTGGGCTTCTAGTTTTTTAAACACAAGAACATAAAACTACCTGATTTACG [11504]
Ami TTTCATGTTGTTGGGCTTTTATTTTTAA--ACACAAGAACATAAAACTACCTGATTTACT [12808]
Asi TTTCATGTTGTTGGGCTTTTATTTTTAA--ACACAAGAACATAAAACTACCTGATTTACT [12156]
Tgu ---------------------------------------------------------- [9820]
Cli TTTCATGTTGTTGGGCTTTTAATTTTAA--ACACAAGAACATCAAACTACCTGATTTACT [12292]
Gga TTTCATGTTGTTGGGCTTTAAATTTTAA--ACACAAGAACATCAAACTACCTGATTTACT [11021]
Xtr ---------------------------------------------------------- [11736]
Lch TTTCATGTTGTTGGGCTTTT-TTTTTAA--TCACAGGAACATCAAACTGCCTGAATTACT [13094]
Dre TTTCAAGTTGTTGGGCTGGACGTTTAAT-TTCACAGGAACCTGAAACTGCCTGAATTGCT [11979]

Hsa GCAGTT-ACT--TGATCTGTGGCTTAGGTAGTTTCATGTTGTTGGGATTGAGTTTTG--A [12727]
Mmu GCAGTT-ACT--TGATCTGTGGCTTAGGTAGTTTCATGTTGTTGGGATTGAGTTTTG--A [12560]
Mdo GCAGTT-ACT---------------------------------------------------- [11739]
Meu GCAGTT-ACT---------------------------------------------------- [10332]
Oan ------------TGGTCTGTGGCTTAGGTAGTTTCATGTTGTTGGGATTGAATTTTG--A [11166]
Aca CCAGTTTATT--TGATCCGTGGTTTAGGTAGTTTCATGTTGTTGGGGTTGGCTTTT---A [12562]
Pbi CCAGTTTATT--TGTTCCGTGGTTTAGGTAGTTTCATGTTGTTGGGGTTGGCTTTT---A [12929]
Cpi CCAGTT-ATT--TGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGGCTTTT---A [13538]
Cmy CCAGTT-ATT--TGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGGCTTTT---A [13286]
Psi CCAGTT-ATT--TGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGGCTTTT---A [12152]
Asp CCAGTT-ATT--TGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGGCTTTT---A [11558]
Ami CCAGTT-ATT--TGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGGCTTTT---A [12862]
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Asi CCAGTT-ATT--TGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGGCTTTT---A [12210]
Tgu ------------TGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATGGGCTTTA---G [9865]
Cli CCAGTT-ATC--TGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGGCTTTT---A [12346]
Gga CCAGTT-ATC--TGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGGCTTTT---A [11075]
Xtr ------------TGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGCTTTTTCTTA [11784]
Lch CCAGTT-ACC--TGATCTGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGGCTTTT---A [13148]
Dre CCAGTT-AAA--TGGTGCGTGGTTTAGGTAGTTTCATGTTGTTGGGATTGGCTTCC--TG [12034]

Hsa ACTCGGCAACAAGAAACTGCCTGAGTTACATCAGTCGGT--TGGTCGGTGATTTAGGTAG [12785]
Mmu ACTCGGCAACAAGAAACTGCCTGAGTTACATCAGTCGGT--TGGTCGGTGATTTAGGTAG [12618]
Mdo ----------------------------------------TGGTCTGTGATTTAGGTAG [11758]
Meu ------------------------------------------------------------ [10332]
Oan ACTCGGCAACAAGAAACTGTCTGAGTTACATCAGTCGGT--TGGTCTGTGATTTAGGTAG [11224]
Aca ACTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTAGT--TGGTCGGTGATTTAGGTAG [12620]
Pbi ACTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTAGT--TGGTCGGTGATTTAGGTAG [12987]
Cpi GCTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTAGT--TGTTCTGTAGTTTAGGTAG [13596]
Cmy GCTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTAGT--TGTTCTGTGGTTTAGGTAG [13344]
Psi GCTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTAGT--TGGTCAGTGGTTTAGGTAG [12210]
Asp GCTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTAGT--TGGTCAGTGGTTTAGGTAG [11616]
Ami GCTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTAGT--TGCTGTGTGGTTTAGGTAG [12920]
Asi GCTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTAGT--TGCTGTGTGGTTTAGGTAG [12268]
Tgu GCTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTCGT--TGCTCTGTGGTTTAGGTAG [9923]
Cli GCTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTAGT--TGCTCTGTGGTTTAGGTAG [12404]
Gga GCTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTAGT--TGCTCTGTGGTTTAGGTAG [11133]
Xtr ACGCGGCAACAAGAAACTGCCTTAATTACGTCAGTTCGT--CGCTGTGTGGTTTAGGTAG [11842]
Lch ACTCGGCAACAAGAAACTGCCTTAATTACGTCAGTTCGT--TGAAGTGTGATTTAGGTAG [13206]
Dre GCTCGACAACAAGAAACTGCCTTGATTACGTCAGTTCGT--TGTCGAGTGGTTTAGGTAG [12092]

Hsa TTTCCTGTTGTTGGGAT-----CCACCTTTCTCTC--GACAGCACGACACTGCCTTCATT [12838]
Mmu TTTCCTGTTGTTGGGAT-----CCACCTTTCTCTC--GACAGCACGACACTGCCTTCATT [12671]
Mdo TTTCCTGTTGTTGGGGC----TCCACCTTTCTCTC--GACAGCACGATACTGCCTTCATT [11812]
Meu ------------------------------------------------------------ [10332]
Oan TTTCCTGTTGTTGGGGCT----CCACCTTTCTCTC--GACAGCACGACACTGCCTTCATT [11278]
Aca TTTCATGTTGTTGGGGCTATGGCTCTCTCTTTCTC--GACAGCACGAAACTGCCTTCATT [12678]
Pbi TTTCTCGTTGTTGAGGCT--GAACATTTCTCTCTC--TGCAGCACGAAACTGCCTTCATC [13043]
Cpi TTTCATGTTGTTGGGGCT----CCACCTTTCTCTC--TGCAGCACGAAACTGCCTTAATT [13650]
Cmy TTTCATGTTGTTGGGGCT----CCACCTTTCTCTC--TGCAGCACGAAACTGCCTTAATT [13398]
Psi TTTCATGTTGTTGGGGCT----CCACCTTTCTCTC--TGCAGCACGAAACTGCCTTGATT [12264]
Asp TTTCATGTTGTTGGGGCT----CCACCTTTCTCTC--TGCAGCACGAAACTGCCTTGATT [11670]
Ami TTTCATGTTGTTGGGGCT----CCACCTTTCTCTC--TACAGCACGAAACTGCCTTAATT [12974]
Asi TTTCATGTTGTTGGGGCT----CCACCTTTCTCTC--TACAGCACGAAACTGCCTTAATT [12322]
Tgu TTTCATGTTGTTGGGGCT----CCACCTTTCTCTC--TACAGCACGAAACTGCCTTAATT [9977]
Cli TTTCATGTTGTTGGGGCT----CCACCTTTCTCTC--TACAGCACGAAACTGCCTTAATT [12458]
Gga TTTCATGTTGTTGGGGCT----CCACCTTTCTCTC--TACAGCACGAAACTGCCTTAATT [11187]
Xtr TTTTATGTTGTTGGGCAT----TCACCTTTCTCTC--TACAACAAGAAACTGCCTTAATT [11896]
Lch TTTCATGTTGTTGGGGCT----CCAAATTTATCTC--TATAACAAGAAACTGCCTGAATT [13260]
Dre TTTCATGTTGTTGGGAT-----TACATTCAAACTC--TGCAACGTGAAACTGTCTTAATT [12145]

Hsa ACTTCAGTTG--CCGGCCCCGCCAACCCAGTGTTCAGACTACCTGTTCAGGAGGCTCTCA [12896]
Mmu ACTTCAGTTG--CCATCCCCGCCATCCCAGTGTTCAGACTACCTGTTCAGGAGGCTGG-G [12728]
Mdo ACTTCAGTTG--CCAGCCCCACCAGCCCAGTGTTCAGACTACCTGTCCAGGAGATTGCAA [11870]
Meu ------------CCAGCCCCACCAGCCCAGTGTTCAGACTACCTGTCCAGGAGATTGCAA [10380]
Oan ACTTCAGTTG---------------------------------------------------- [11288]
Aca ACTTCAGTTT--CCAGCCCCGCCTTCCCAGTGTTCAGACTACCTGTTCAGGAAGCTACAA [12736]
Pbi ACTTCAGTTT--CTGGCCCCACCTGCCCAGTGTTCAGACTACCTGTTCAGGAAACTACAA [13101]
Cpi ACTTCAGTTG--CCAGCCCAGCCTGCCCAGTGTTCAGACTACCTGTTCAGGAGGCTATCA [13708]
Cmy ACTTCAGTTG--CCAGCCCAGCCTGCCCAGTGTTCAGACTACCTGTTCAGGAGGCTATAA [13456]
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Psi ACTTCAGTTA--CCAGCCCAGCCTGCCCAGTGTTCAGACTACCTGTTCAGGAGGCTATAA [12322]
Asp ACTTCAGTTG--CCAGCCCAGCCTGCCCAGTGTTCAGACTACCTGTTCAGGAGGCTATAA [11728]
Ami ACTTCAGTTG--CCAGCCCAGCCTGCCCAGTGTTCAGACTACCTGTTCAGGAGCATATGA [13032]
Asi ACTTCAGTTG--CCAGCCCAGCCTGCCCAGTGTTCAGACTACCTGTTCAGGAGCATATGA [12380]
Tgu ACTTCAGTTG-------------------------------------------------- [9987]
Cli ACTTCAGTTG--CCGGCCCGGCCTGCCCAGTGTTCAGACTACCTGTTCAGGATGCTTCCC [12516]
Gga ACTTCAGTTG-------------------------------------------------- [11197]
Xtr ACATCAGTGG--GTGGTCCCGTTCCCCCAGTGTTCAGACTACGTGTTCGTTGGACAG--A [11952]
Lch ACTCCAGTTA--CTGACCCCGCCTGCCCAGTGTTCAGACTACCTGTTCAGGAAGCCA--A [13316]
Dre GCCCCAGTTT--CCCGTCCCGCCTGCCCAGTGTTCAGACTACCTGTTCAGGAATTAGT-- [12201]

Hsa ATGTGTACAGTAGTCTGCACATTGGTTAGGCTGGGCTTGGG--CCTGCTCCGTCGCCCCA [12954]
Mmu ACATGTACAGTAGTCTGCACATTGGTTAGGCTGGGCTTGGG--CCTGCTCCGTCGCCCCA [12786]
Mdo AGGTGTACAGTAGTCTGCACATTGGTTAGGCTGGGCTTGGA--CCTGCTCCGTCGCCCCA [11928]
Meu ATGTGTACAGTAGTCTGCACATTGGTTAGGCTGGGCTTGGA--CCTGCTCCGTCGCCCCA [10438]
Oan ------------------------------------------CCTGCTCCGTCGCCCCA [11305]
Aca AGGTGTACAGTAGTCTGCACATTGGTTAGACTGGGCTTGGG--CCTGCTCCGTCGCCCCA [12794]
Pbi AGGTGTACAGTAGTCTGCACATTGGTTAGATTGGGTTTGGA--CCTGCTCCGTCGCCCCA [13159]
Cpi AGGTGTACAGTAGTCTGCACATTGGTTAGATTGGGTTTGGT--CCTGCTCCGTCGCCCCA [13766]
Cmy AGGTGTACAGTAGTCTGCACATTGGTTAGATTGGGTTTGGT--CCTGCTCCGTCGCCCCA [13514]
Psi AGGTGTACAGTAGTCTGCACATTGGTTAGATTGGGTTTGGC--CCTGCTCCGTCGCCCCA [12380]
Asp AGGTGTACAGTAGTCTGCACATTGGTTAGATTGGGTTTGGC--CCTGCTCCGTCGCCCCA [11786]
Ami AGTTGTACAGTAGTCTGCACATTGGTTAGATCGGGCTTGGC--CCTGCTCCGTCGCCCCA [13090]
Asi AGTTGTACAGTAGTCTGCACATTGGTTAGATCGGGCTTGGC--CCTGCTCCGTCGCCCCA [12438]
Tgu ------------------------------------------CCTGCTCCGTCGCCCCA [10004]
Cli GGTTGTACAGTAGTCTGCACATTGGTTAGATCGGATCCGGC--CCTGCTCCGTCGCCCCA [12574]
Gga ------------------------------------------CCTGCTCCGTCGCCCCA [11214]
Xtr ACCTGAACAGTAGTCTACACACTGGTTAAACTGGGCCATGC--CCTGCTCCGTCGCCCCA [12010]
Lch AGGTGGACAGTAGTCTGCACATTGGTTAGGCTGGGCAAGAG--CCTGCTCCGTCGGCCCA [13374]
Dre GTTTGTACAGTAGTCTGCACATTGGTTAGGCTGGATGGGGA--CCTGCTCCGTCATCCCA [12259]

Hsa GTGTTCAGACTACCTGTTCAGGACAATGCCGTTGTACAGTAGTCTGCACATTGGTTAGAC [13014]
Mmu GTGTTCAGACTACCTGTTCAGGACAATGCCGTTGTACAGTAGTCTGCACATTGGTTAGAC [12846]
Mdo GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [11988]
Meu GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [10498]
Oan GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [11365]
Aca GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [12854]
Pbi GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [13219]
Cpi GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [13826]
Cmy GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [13574]
Psi GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [12440]
Asp GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [11846]
Ami GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [13150]
Asi GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [12498]
Tgu GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [10064]
Cli GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [12634]
Gga GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [11274]
Xtr GTGTTCAGACTACCTGTTCAGGACAATGCTGTTGTACAGTAGTCTGCACATTGGTTAGAC [12070]
Lch GTGTTCAGACTACCTGTTCAGGACAATACTGTTGTACAGTAGTCTGCACATTGGTTAGAC [13434]
Dre GTGTTCAGACTACCTGTTCAGGATCATACTGGTGTACAGTAGTCTGCACATTGGTTAGAC [12319]

Hsa TGGGCAAGGG--TCCACTCCGTCTACCCAGTGTTTAGACTATCTGTTCAGGACTCCCAAA [13072]
Mmu TGGGCAAGGG--TCCACTCCGTCTACCCAGTGTTTAGACTACCTGTTCAGGACTCCCAAA [12904]
Mdo TGGGCAAGGG--TCCACTCCGTCTACCCAGTGTTTAGACTATCTGTTCAGGACTCCAATA [12046]
Meu TGGGCAAGGG-------------------------------------------------- [10508]
Oan TGGGCAAGGG-------------------------------------------------- [11375]
Aca TGGGCAAGGA--TCCACTCCGTCTGCCCAGTGTTCGGACTACCTGTTCAGGACTACGAGA [12912]
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Pbi TGGGCAAGGG--TCCACTCCGTCTTCCCAGTGTTCGGACTACCTGTTCAGGACTACAAGA [13277]
Cpi TGGGCAAGGG--TCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGACTACGAGA [13884]
Cmy TGGGCAAGGG--TCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGACTACGAGA [13632]
Psi TGGGCAAGGG--TCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGACTACGAGA [12498]
Asp TGGGCAAGGG--TCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGACTACGATA [11904]
Ami TGGGCAAGGG--TCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGACTACGAGA [13208]
Asi TGGGCAAGGG--TCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGACTACGAGA [12556]
Tgu TGGGCAAGGG--TCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGACTACGAGA [10122]
Cli TGGGCAAGGG--TCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGACTACGAGA [12692]
Gga TGGGCAAGGG--TCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGACTACGAGA [11332]
Xtr TGGGCATGGG---------------------------------------------------- [12080]
Lch TGGGCATGGG--TCCACTCCGTCTGCCCAGTGTTCAGACTACCTGTTCAGGGGGAAAAGA [13492]
Dre TGTGCATGGA--TCCCCCTCGCCTGCCCAGTGTTCAGACTACCTGTTCATCATGCTGCAG [12377]

Hsa TTGTACAGTAGTCTGCACATTGGTTAGGCTGGGCTGGGT--CCCGCCGTTCCTTTTTCCT [13130]
Mmu TTGTACAGTAGTCTGCACATTGGTTAGGCTGGGCTGGGT--CTGGCTGTTCCTTTTTCCT [12962]
Mdo TTGTACAGTAGTCTGCACATTGGTTAGGCTGGGCTGGGC---------------------- [12085]
Meu ----------------------------------------CTCGTGGTTCCTTTTTCCT [10527]
Oan ---------------------------------------------------------- [11375]
Aca TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA--CTCATTGTTCCTTTTTCCT [12970]
Pbi TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA----------------TCCT [13320]
Cpi TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA--CTCGTTGTTCCTTTTTCCT [13942]
Cmy TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA--CTCGTTGTTCCTTTTTCCT [13690]
Psi TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA--CTCGTTGTTCCTTTTTCCT [12556]
Asp TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA--CTCGTTGTTCCTTTTTCCT [11962]
Ami TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA--CTCGTTGTTCCTTTTTCCT [13266]
Asi TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA--CTCGTTGTTCCTTTTTCCT [12614]
Tgu TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA--CTCGTTGTTCCTTTTTCCT [10180]
Cli TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA--CTCGTTGTTCCTTTTTCCT [12750]
Gga TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCTGGGA--CTCGTTGTTCCTTTTTCCT [11390]
Xtr ----------------------------------------CTCGCTGTTCCTTTTTCCT [12099]
Lch TTGTACAGTAGTCTGCACATTGGTTAGGCTGTGCCTGGA--CTCGTTGTTCCTTTTTCCT [13550]
Dre CTGAACAGTAGTCCGCACATTGGTTAGGCTGGGCTGGGA--CTCGCTGTTCCTTTTTCCT [12435]

Hsa ATGCATATACTTCTTTGAGGATCTGGCCTAAAGAGGTATAGGGCATGGGAAAACGGGGCG [13190]
Mmu ATGCATATACTTCTTTGTGGATCTGGTCTAAAGAGGTATAGCGCATGGGAAGATGGAGCA [13022]
Mdo ---------------------------------------------------------- [12085]
Meu ATGCATATACTTCTTTGAGAATAAAATCTAAAGAGGCGTAGGGCATGGGAAAATGGGGCC [10587]
Oan ---------------------------------------------------------- [11375]
Aca ATGCATATACTTCTTTGAGAATCTGATCTAAAGAGGCATACGGCATGGGAAAATGGGGCA [13030]
Pbi ATGCATATACTTCTTTGAGAATTGAATCTAAAGAGGCATACGGCATGGGAAAATGGGGCG [13380]
Cpi ATGCATATACTTCTTTGAGAATTGGAACTAAAGAGGCATAGGGCATGGGAAAATGGGGCG [14002]
Cmy ATGCATATACTTCTTTGAGAATTGGAACTAAAGAGGCATAGGGCATGGGAAAATGGGGCG [13750]
Psi ATGCATATACTTCTTTGAGAATTGGAACTAAAGAGGCATAGGGCATGGGAAAATGGGGCG [12616]
Asp ATGCATATACTTCTTTGAGAATTGGAACTAAAGAGGCATAGGGCATGGGAAAATGGGGCG [12022]
Ami ATGCATATACTTCTTTGAGAATTGGATCTAAAGAGGCATAGGGCATGGGAAAATGGGGCG [13326]
Asi ATGCATATACTTCTTTGAGAATTGGATCTAAAGAGGCATAGGGCATGGGAAAATGGGGCG [12674]
Tgu ATGCATATACTTCTTTGAGAATTGCTTCTAAAGAGGTATAGGGCATGGGAAAATGGGGCA [10240]
Cli ATGCATATACTTCTTTGAGAATTTGATCTAAAGAGGCATAGGGCATGGGAAAATGGGGCG [12810]
Gga ATGCATATACTTCTTTGAGAGTTTGATCTAAAGAGGCATAGAGCATGGGAAAATGGGGCG [11450]
Xtr ATGCATATACCTCTTTGAAAAATGAATGTAAAGGGGCATAGGGCATGGGAAAATGGCGCA [12159]
Lch ATGCATATACCTCTTTGAGAATCAGATATGAAGAGGCATAGGGCATGGGAAAATGGGGCG [13610]
Dre ATGCATATACCTCTTTGACATGCTGCTTTAAAGAGGCATAGGGCATGGGAAAATGGGGCG [12495]

Hsa GTCGGGTC--CGCGCGCTGGGTCCAGTGGTTCTTAACAGTTCAACAGTTCTGTAGCGCAA [13248]
Mmu GTGAGATC--GGCGCGCCTGGTCCAGTGGTTCTTGACAGTTCAACAGTTCTGTAGCACAA [13080]
Mdo ----------AGCTGCCCTGGTCCAGTGGTTCTTAACAGTTCAACAGTTCTGTGTAGAGA [12135]
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Meu ACGGAGCT--AGCTTCTCTGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTATTAAAAAA [10645]
Oan ----------AGTCTCCCTGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTCTGGCCTAA [11425]
Aca ATTGAGGT--AGCCTGCTGGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTCTATTATAA [13088]
Pbi ATTGAGGG--AGCCTGCTGGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTGTAGCATAA [13438]
Cpi ACTGAGGT--AGCCTCCTTGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTCTAGCATAA [14060]
Cmy ACTGAGGT--GGCCTCCTTGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTCTAGCATAA [13808]
Psi ACTGAGGT--AGCCTCTTTGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTCTAGCATAA [12674]
Asp ACTGAGGT--AGCCTCTTTGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTCTAGCATAA [12080]
Ami ACTGAGGT--CGCCTCGCGGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTTTAGGCTAA [13384]
Asi ACTGAGGT---------------------------------------------------- [12682]
Tgu ACTGAGGT--AGCCTCCTTGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTCTAGCATAA [10298]
Cli ACTGAGGT--AGCCTCCTTGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTCTAGCATAA [12868]
Gga ACTGAGGT--AGCCTCCTTGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTCTATCATAA [11508]
Xtr GCTGAGCC--TGTCTCCCTGGCCGAGTGGTTCTTAACAGTTCAACAGTTCTCTATCGAAA [12217]
Lch ACTGAGGT--TGTCTTTTTGGTGCAGTGGTTCTAAATAGTTCAACAGTTCTCTACCAAAA [13668]
Dre GCAGAGGT--GGTCCCTCTGGTGCAGTGGTTCTTAACAGTTCAACAGTTCTATCTCAAAA [12553]

Hsa TTGTGAAATGTTTAGGACCACTAGACCCGGCGGGCGCG--TGTGACTCGTGGACTTCCCT [13306]
Mmu TTGTGAAATGTTTAGGACCACTAGACCCGGCGCGCACG--TGTGACTCGTGGACTTCCCT [13138]
Mdo TTGTGAAATGTTTAGGACCACTTGATCTGGGTAGGCAT--TGTGACTCGTGGACTTCCCT [12193]
Meu TTGTGAAATGTTTAGGACCACTCGATCAGGGCAGGCCT--TGTGACTCGTGGACTTCCCT [10703]
Oan TTGTGAAATGTTTAGGACCACTTGACCCGGGCAGGCCT--TGTGACCCGTGGGCTTCCCT [11483]
Aca TTGTGAAATGTTTAGGACCACTTGATCCGGCGGGCCCA--TGTGACCCGTGGACTTCCCT [13146]
Pbi TTGTGAAATGTTTAGGACCACTTGATCCGGACGGCTTG--TGTGACCTGTGGACTTCCCT [13496]
Cpi TTGTGAAATGTTTAGGACCACTTGACCAGGAAGGCCCG--TGTGACCCGTGGACTTCCCT [14118]
Cmy TTGTGAAATGTTTAGGACCACTTGACCCGGGAGGCCCG--TGTGACCCGTGGACTTCCCT [13866]
Psi TTGTGAAATGTTTAGGACCACTTGACCAGGGAGGCCCG--TGTGACCCGTGGACTTCCCT [12732]
Asp TTGTGAAATGTTTAGGACCACTTGACCAGGGAGGCCCG--TGTGACCCGTGGACTTCCCT [12138]
Ami TTGTGAAATGTTTAGGACCACTTGACCCGCGAGGCGCC--TGTGACCTGTGGACTTCCCT [13442]
Asi ----------------------------------------TGTGACCCGTGGACTTCCCT [12702]
Tgu TTGTGAAATGTTTAGGACCACTTGACCAGCGAGGCCCG--TGTGACCCGTGGACTTCCCT [10356]
Cli TTGTGAAATGTTTAGGACCACTTGACCAGCGAGGCCCG--TGTGACCCGTGGACTTCCCT [12926]
Gga TTGTGAAATGTTTAGGACCACTTGACCAGCGAGGCCCG--TGTGACCCGTGGACTTCCCT [11566]
Xtr TTGTGAAATGTTTAGGACCACTTGATCCGGGTGACTCT--TGTGACCTGTGGGCTTCCCT [12275]
Lch TTGTGAAATGTTTAGGACCACTTGATCAAGAAGGCCTT--TGTGGCCCGTGGGCTTCCCT [13726]
Dre TTGTGAAATGTTTAGGACCACTTGACCAGAGTGACACT--TGTGACCTGTGGACTTCCCT [12611]

Hsa TTGTCATCCTATGCCTGAGAATATATGAAGGAGGCTGGGAAGGCAAAGGGACGTTCAATT [13366]
Mmu TTGTCATCCTATGCCTGAGAATATATGAAGGAGGCTGGGAAGGCAAAGGGACGTTCAATT [13198]
Mdo TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAATC [12253]
Meu TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAATT [10763]
Oan TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAACT [11543]
Aca TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAATT [13206]
Pbi TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAGTT [13556]
Cpi TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAACT [14178]
Cmy TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAACT [13926]
Psi TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAATT [12792]
Asp TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAATT [12198]
Ami TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAATT [13502]
Asi TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAATT [12762]
Tgu TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGGAGGCAAAGGGACGTTCAACT [10416]
Cli TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAACT [12986]
Gga TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAACT [11626]
Xtr TTGTCATCCTATGCCTGAGAATATATGAAGGGGGCTGGGAAGGCAAAGGGACGTTCAGTT [12335]
Lch TTGTCATCCTATGCCTGAGAATAAATGAAGGGGGCTGGGAAGGCAAAGGGATGTTCAACT [13786]
Dre TTGTCATCCTATGCCTG-GAGTA-ATAGAGGGGGCTGGGAAGTCAAAGGGACGCTCAGGC [12669]
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Hsa GTCATC--ATGTGACTTGTGGGCTTCCCTTTGTCATCCTTCGCCTAGGGCTCTGAGCAGG [13424]
Mmu GTCATC--CTGTGACCTGTGGGCTTCCCTTTGTCATCCTTTGCCTAGGCCTCTGAGTGAG [13256]
Mdo GTCATC--ATGTGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAAATCAGAGTGGG [12311]
Meu GTCATC--ATGTGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAAATCAGAGTGGG [10821]
Oan GTCATC--TTGTGACTGCTGAGCTTCCCTTTGTCATCCTATGCCTGGAAGTCAAAATGGG [11601]
Aca GTCATC--ACATGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGATCGCAGAGAG [13264]
Pbi GTCATC--ACATGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGCTCACAGTGAG [13614]
Cpi GTCATC--ATGTGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGTTCATAGTGAG [14236]
Cmy GTCATC--ATGTGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGATCATAGTGAG [13984]
Psi GTCATC--ATGTGAC-TGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGATCATAGTGAG [12849]
Asp GTCATC---------------------------------------------------- [12204]
Ami GTCATC--ATGTGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGATCATAGTGAG [13560]
Asi GTCATC--ATGTGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGATCATAGTGAG [12820]
Tgu GTCATC--ATGTGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGATCACAGTGAG [10474]
Cli GTCATC--ATGTGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGATCACAGTGAG [13044]
Gga GTCATC--GTGTGACCTGTGGGCTTCCCTTTGTCATCCTATGCCTGGAGATCACAGTGAG [11684]
Xtr GTCATC--TTGTGACCCATGGGCTTCCCTTTGTCATCCTATGCCTGAGAATGCTGGAGAG [12393]
Lch GTCATC--ATGTGACCTGTGGGTTTCCCTTTGTCATCCTATGCCTGGAGTTAGTAGCAAG [13844]
Dre GTCATC--CGTGACCTCCTGGGTTTCCCTTTGTCATCCTATGCCTGCAGTTCCTGATGAG [12727]

Hsa GCAGGGACAGCAAAGGGGTGCTCAGTTGTCACT---------------------------- [13457]
Mmu GCAAGGACAGCAAAGGGGGGCTCAGTGGTCACC---------------------------- [13289]
Mdo GCAGGGACAGCAAAGGGATGCTCAGCTGTCGTC---------------------------- [12344]
Meu GCAGGGACAGCAAAGGGAGGCTCAGCTGTCGTC---------------------------- [10854]
Oan GCAGGGACAGCAAAGGGATGATCAACCGTCACC---------------------------- [11634]
Aca GCAGGGACAGCAAAGGGGTGCTCAGCTGTTGTC---------------------------- [13297]
Pbi GCAGGGCCAGCAAAGGGTTGCTCAGCTGTTGTC--CTTGGCTCTGTAGCTTTCCCTTTGT [13672]
Cpi GCAGGGACAGCAAAGGGATGCTCAGTTGTCGTC--GTGCGCCCTGTGAGCTTCCCTTTGT [14294]
Cmy GCAGGGACAGCAAAGGGATGCTCAGCTGTCGTC--GTGCGCCCTGTGAGCTTCCCTTTGT [14042]
Psi GCAGGGACAGCAAAGGGTTGCTCAGCTGTCATC--ATGCGCCCTGTGGGCTTCCCTTTGT [12907]
Asp ----------------------------------ATGCGCCCTGTGGGCTTCCCTTTGT [12229]
Ami GCAGGGACAACAAAGGGATGCTCAATTGTCATC--CTGCGCTCTGTGAGCTTCCCTTTGT [13618]
Asi GCAGGGACAACAAAGGGATGCTCAATTGTCATC--CTGCGCTCTGTGAGCTTCCCTTTGT [12878]
Tgu GCAGGGACAGCAAAGGGATGCTCAGCTGTCGTC--CTGCCCCCTGTGAGCTTCCCTTTGT [10532]
Cli GCAGGGACAGCAAAGGGATGCTCAGCTGTCGTC--CTGCCCCCTGTGAGCTTCCCTTTGT [13102]
Gga GCAGGGACAGCAAAGGGATGCTCAGCTGTCGTC--CTCGCTCCTGTGAGCTTCCCTTTGT [11742]
Xtr GCAGGGACAGCAAAGGGATGCTCAGATGTTACC---------------------------- [12426]
Lch GCAGGGACAGCAAAGGGATGCTCAGCTGTCATC--CAGTGAAATGGGGGCTTCCCTTTCT [13902]
Dre GCTGGGACAGCAAAGGGAGGTTCAGATGTCGAC---------------------------- [12760]

Hsa ------------------------------------------------------------ [13457]
Mmu ------------------------------------------------------------ [13289]
Mdo ------------------------------------------------------------ [12344]
Meu ------------------------------------------------------------ [10854]
Oan ------------------------------------------------------------ [11634]
Aca ------------------------------------------------------------ [13297]
Pbi CATCCTATGCCTGAGAAATTCAGGGAGGCTGGGACGGTGAAGGGAAGCCCACAGCGTTAT [13732]
Cpi CATCCTATGCCTGAGAGATGCCTGGAGGCTGGGACGGTGAAGGGAAGCCCACGTGGCTGC [14354]
Cmy CATCCTATGCCTGAGAGATGCCTGGAGGCTGGGACGGTGAAGGGAAGCCCACGTGGCTGC [14102]
Psi CATCCTATGCCTGAGAGATGCCTGGAGGCTGGGACGGTGAAGGGAAGCCGACGGGGCTGC [12967]
Asp CATCCTATGCCTGAGAGATGCCTGGAGGCTGGGACGGTGAAGGGAAGCCGACGTGGCTGC [12289]
Ami CATCCTATGCCTGAGAGATGCCTGGAGGCTGGGACGGTGAAGGGAAGCCCACGGGGCTGC [13678]
Asi CATCCTATGCCTGAGAGATGCCTGGAGGCTGGGACGGTGAAGGGAAGCCCACGGGGCTGC [12938]
Tgu CATCCTATGCCTGAGCGATGCCTGGAGGCTGGGACGGCCAAGGGAGGCCCACGGG-CTGC [10591]
Cli CATCCTATGCCTGAGCCATGGCCG-AGGCTGGGACGGTGAAGGGAGGCCCACGGG-CTGG [13160]
Gga CATCCTATGCCTGAGCGATGCCTGGAGGCTGGGACGGTGAAGGGAGGCCCACGGG-CTGC [11801]
Xtr ------------------------------------------------------------ [12426]
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Lch CATCCTATGCCTGAGAATTCACTGAAGGCTGGGAAGGTAAAGGGAGGCTCACATCTCACC [13962]
Dre ------------------------------------------------------------ [12760]

Hsa ---TTCTCTTGTCCTTCATTCCACCGGAGTCTGTCTCATACCCAA-CCAGATTTCAGTGG [13513]
Mmu ---TCCTCTTGTCCTTCATTCCACCGGAGTCTGTCTTATGCC-AA-CCAGATTTCAGTGG [13344]
Mdo ---TTCTCTTGTCCTTCATTCCACCGGAGTCTGTCTCATATCTAA-TCAGATTTCAGTGG [12400]
Meu ---TTCTCTTGTCCTTCATTCCACCGGAGTCTGTCTCATATGTAA-TCAGATTTCAGTGG [10910]
Oan ---TTCTGTTGTCCTTCATTCCACCGGAGTCTGTTTCGTACCTAA-TCAGATTTCAGTGG [11690]
Aca ---TTCTATTGTCCTTCATTCCACCGGAGTCTGTCTCATATCTAA-TCAGATTTCAGTGG [13353]
Pbi A--TTCTGTTGTCCTTCATTCCACCGGAGTCTGTCGAATACCTAA-TCAGATTTCAGTGG [13789]
Cpi C--TTCTGTTGTCCTTCATTCCACCGGAGTCTGTCTCATAACTAA-TCAGATTTCAGTGG [14411]
Cmy C--TTCTGTTGTCCTTCATTCCACCGGAGTCTGTCTCATACCTAA-TCAGATTTCAGTGG [14159]
Psi C--TTCTATTGTCCTTCATTCCACCGGAGTCTGTCTCATACCTAA-TCAGATTTCAGTGG [13024]
Asp C--TTCTATTGTCCTTCATTCCACCGGAGTCTGTCTCATACCTAA-TCAGATTTCAGTGG [12346]
Ami C--TTCTGTTGTCCTTCATTCCACCGGAGTCTGTCTCATACCTAA-TCAGATTTCAGTGG [13735]
Asi C--TTCTGTTGTCCTTCATTCCACCGGAGTCTGTCTCATACCTAA-TCAGATTTCAGTGG [12995]
Tgu C--TTCTGTTGTCCTTCATTCCACCGGAGTCTGTCTC-TAGCTAA-CCAGATTTCAGTGG [10647]
Cli C--TTCTGTTGTCCTTCATTCCACCGGAGTCTGTCTCATACCTAAACCAGATTTCAGTGG [13218]
Gga C--TTCTGTTGTCCTTCATTCCACCGGAGTCTGTCTCGTACCTAA-CCAGATTTCAGTGG [11858]
Xtr ---TCCTGCTGTCCTTCATTCCACCGGAGTCTGTCTCATACATAA-TCAGATTTCAGTGG [12482]
Lch C--TTCTGTTGTCCTTCATTCCACCGGAGTCTGTTTCATAACCAA-TCAGATTTCAGTGG [14019]
Dre ---GCATTCTATCCTTCATTCCACCGGAGTCTGTGTAGTTGTTCAATCAGATTTCAGTGG [12817]

Hsa AGTGAAGTTCAGGAGGCATGGAG------------------------------------- [13536]
Mmu AGTGAAGCTCAGGAGGCATGGAG------------------------------------- [13367]
Mdo AGTGAAGCATAAGAGGCATGGAG------------------------------------- [12423]
Meu GGTGAAGCATAAGAGGCGTGGAG------------------------------------- [10933]
Oan AGTGAAGCACAAGAGGCATGGAG------------------------------------- [11713]
Aca AGTGAAGCACAAGAGACATGGAG--CTTGGGTGCCCTTCATTCCACCGGAATCTGTCACC [13411]
Pbi CGTGAAGTACATGAGACATGGAG--CTTGGGTGCCCTTCATTCCACCGGAATCTGTAAAA [13847]
Cpi AGTGAAGCACAAGAGACATGGAG--TGCTGGTGCCCTTCATTCCACCGGAATCTGTAGAG [14469]
Cmy AGTGAAGCACAAGAGACATGGAG--TGCTGGTGCCCTTCATTCCACCGGAATCTGTAGAG [14217]
Psi CGTGAAGCACAAGAGACATGGAG--TGCTGGTGCCCTTCATTCCACCGGAATCTGTAGAG [13082]
Asp CGTGAAGCACAAGAGACATGGAG--TGCTGGTGCCCTTCATTCCACCGGAATCTGTAGAG [12404]
Ami AGTGAAGCACAAGAGACATGGAG--TTCTGGTGCCCTTCATTCCACCGGAATCTGTAGGG [13793]
Asi AGTGAAGCACAAGAGACATGGAG--TTCTGGTGCCCTTCATTCCACCGGAATCTGTAGGG [13053]
Tgu AGTGAAGCACAAGAGGCATGGAG--TCCTGGTGCCCTTCATTCCACCGGAATCTGTCGAT [10705]
Cli AGTGAAGTACGAGAGACATGGAG--TCTTGGCACCCTTCATTCCACCGGAATCTGTCTAT [13276]
Gga AGTGAAGCACAAGAGACATGGAG--TCCTGATGCCCTTCATTCCACCGGAATCTGTCAGT [11916]
Xtr AGTGAAGCACAAGAGGCATGTAG--TGCTGCTGTCCTTCATTCCACCGGATCCTGTGTAA [12540]
Lch AGTGAAGTACAGGAGACATGGAG--TCCTGCTGTCCTTCATCCCTCCGGATCCC-TGTGC [14076]
Dre TGTGAAGTGTAGGAAACACGGAA------------------------------------- [12840]

Hsa ----------------------------------------------TTCCTGTGACGGG [13549]
Mmu ----------------------------------------------TTCCTTTGACGGG [13380]
Mdo ----------------------------------------------TTCCTGTGACAGG [12436]
Meu ------------------------------------------------------------ [10933]
Oan ----------------------------------------------TTCCTGTGACAGA [11726]
Aca GCAAAAACCGGATTTC-TGTGAAATGAAGCCCACCAGGCATGGAA--TTCCTCTAACAAG [13468]
Pbi GCAGACACCAGATTTC-TGTGAAATGAAGCCCACCTGGCATGGAA--TTCCTCTAATGGA [13904]
Cpi GCAGAAACCAGATTTC-AGTGTAATGAAGCCCATCAGACATGGAA--TTCCTCTAACAGG [14526]
Cmy GCAGAAACCAGATTTC-AGTGTAATGAAGCCCATCAGACATGGAA--TTCCTCTAACAGG [14274]
Psi GCAGAAACCAGATTTC-AGTGTAATGAAGCCCATCAGACATGGAA--GTCCTCCAACGGG [13139]
Asp GCAGAAACCAGATTTC-AGTGTAATGAAGCCCATCAGACATGGAA--------------- [12448]
Ami ATCAAAACCAGATTTC-AGTGAAATGAAGCCCCTCAGACGTGGAA--TTCCTCCAACAGG [13850]
Asi ATCAAAACCAGATTTC-AGTGAAATGAAGCCCCTCAGACGTGGAA--TTCCTCCAACAGG [13110]
Tgu GCAGAACCCGGATTTC-AGTGAAATGAAGCCCCTCAGAAAGGCAG--------------- [10749]
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Cli ACAGAAACCAGATTTC-AGTGAAATGAAGCCTGTCAGAGAGGCAG--------------- [13320]
Gga GCAGAAACCAGATTTC-AGTGAAATGAAGCCCATCAGAGAGGCAG--------------- [11960]
Xtr ATATAATCCAGATTCCCAGTGGCATGAAGTGCATTAGCTGAGCCT--TCCTTTCAACAGG [12598]
Lch ACTGAATCCAGATTCCCAGTGGGATGAAGTG---TAGCTGGTTGG--CTCTTGTAACATA [14131]
Dre ------------------------------------------------------------ [12840]

Hsa CGAGCTTTTGGCCCGGGTTATACCTGATGCTCAC---GTATAAGACGAGCAAAAAGCTTG [13606]
Mmu TGAGCTTTTGGCCCGGGTTATACCTGACACTCAC---GTATAAGACGAGCAAAAAGCTTG [13437]
Mdo TGAGCTTTTGGTCCGGGTTATACCTGATGCATGT---GTATAAGACGAGCAAAAAGCTCG [12493]
Meu ------------------------------------------------------------ [10933]
Oan CAAGCTTTTGGCCCAGATTATACCTGACATTCCC---GTATAAGACGAGCAAAAAGCTTG [11783]
Aca GAAGCTTTTGGCTCGGGTTATATTTTAGAATGGCAGTGTATAAGACGAGCAAAAAGCTTG [13528]
Pbi GAAGCTTTTGGCTCGGGTTATATTTGAAAATGGCAGTGTATAAGACGAGCAAAAAGCTTG [13964]
Cpi GAAGCTTTTGGCTCGGGTTATATTTTC-ACTCGCGGCGTATAAGACGAGCAAAAAGCTTG [14585]
Cmy GAAGCTTTTGGCTTGGGTTATATTTTC-ATTCTCAGCATATAAGACGAGCAAAAAGCTTG [14333]
Psi GAAGCTTTTGGCTCTGGTTATATTTCC-ACTCGCAGCGTATAAGACGAGCGAAAAGCTTG [13198]
Asp ------------------------------------------------------------ [12448]
Ami GAAGCTTTTGGCTTGGGTTATATTGTC-ACTCGCAGTGTATAAGACGAGCGAAAAGCTTC [13909]
Asi GAAGCTTTTGGCTTGGGTTATATTGTC-ACTCGCAGTGTATAAGACGAGCGAAAAGCTTC [13169]
Tgu ------------------------------------------------------------ [10749]
Cli ------------------------------------------------------------ [13320]
Gga ------------------------------------------------------------ [11960]
Xtr CAAGCTTTTTGCTTGGATTATGTTTTC-TGTTGTT--GTATAAGACGAGCATAAAGCTTG [12655]
Lch TAAGCTTTTTGCTTGGATTATGTTT-C-ATTTTAT-CATATAAGACGAGCAAAATGCTTG [14188]
Dre ------------------------------------------------------------ [12840]

Hsa TTGGTCAGAGG--TTCTCCTCTCAGGGAAGCTTTTTGCTCGAATTATGTTTCTGATCCGA [13664]
Mmu TTGGTCAGAGG--TGCTCCTCTCAGGGAAGCTTTTTGCTCGCGTTATGTTTCTCATCCGA [13495]
Mdo TTGGTCGGAGG--TTCTCCTCTCAGGGAAGCTTTTTGCTCGGGTTATGTTTTGGATCTGA [12551]
Meu ------------TTCTCCTCTCAGGGAAGCTTTTTGCTCGCGTTATGTTTTGGATTTGA [10980]
Oan TTGGTCAGAGG--------------------------------------------------- [11794]
Aca TTGGTTGGAGG--------------------------------------------------- [13539]
Pbi TTGGTTGGAGG--------------------------------------------------- [13975]
Cpi TTGGTTGGAGG--------------------------------------------------- [14596]
Cmy TTGGTTGGAGG--------------------------------------------------- [14344]
Psi TCGGTTGGCGG--------------------------------------------------- [13209]
Asp ------------------------------------------------------------ [12448]
Ami TTGGTTGGAAG--------------------------------------------------- [13920]
Asi TTGGTTGGAAG--------------------------------------------------- [13180]
Tgu ------------------------------------------------------------ [10749]
Cli ------------------------------------------------------------ [13320]
Gga ------------------------------------------------------------ [11960]
Xtr TTTGTTAGAAG--------------------------------------------------- [12666]
Lch TTCGCTACAAG--TTCTCCTCACAGGGAGGCTTTTTGTTCGCGTTATGTTCGGTGTGA-A [14245]
Dre ------------CTCTACTGACAGAGAAGCTTTTTGTTTGTGTTATGTTTATTTTCA-A [12886]

Hsa ATATAAGACGAACAAAAGGTTTGTCTGAGGGCAGAG--CAGGCGCAGGGCAGCCCCTGCC [13722]
Mmu ATATAAGACGAACAAAAGGTTTGTCTGAGGGCTGAG--CAGGCTCAGGACAGCCACTGCC [13553]
Mdo ATATAAGACGAACAAAAGGTTTGTCTGTGTGCAGAG--CGGCCGCAGGGGAGCCACTGAC [12609]
Meu ATATAAGACGAACAAAAGGTTTGTCTGTGTGCAGAG--CGGCAGCAGGGGAGCCACTGAC [11038]
Oan ------------------------------------------------------------ [11794]
Aca ----------------------------------------CAGGAGCAGATGAGCCACTGAC [13561]
Pbi ----------------------------------------CAGAAGCAGGTGAGCCACTGAC [13997]
Cpi ----------------------------------------CAGAAGCTGGTGAGCCACTGAC [14618]
Cmy ----------------------------------------CAGAAGCTGGTGAGCCACTGAC [14366]
Psi ----------------------------------------CAGAAGCAGGTGAGCCACTGAC [13231]
Asp ----------------------------------------CAGAAGCAGGTGAGCCACTGAC [12470]
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Ami ------------------------------------CAGAAGCAGGTGAGCCACTGAC [13942]
Asi ------------------------------------CAGAAGCAGGTGAGCCACTGAC [13202]
Tgu ------------------------------------------------------------ [10749]
Cli ------------------------------------CAGGAGCAGGTGAGCCACTGAC [13342]
Gga ------------------------------------CAGGAGCAGGTGAGCCACTGAC [11982]
Xtr ------------------------------------CAGATGCAGGTCAGCCACTGAC [12688]
Lch ATATAAGACGAACAAAAAGTTTGTCTGTTTGTAGAT--CAGAAGCAGGTGAGCCACTGAC [14303]
Dre ATGTAAGACGAACAAAAAGTTTTTCTGTTAGTAGGT--TGAAAGCAGGTAAGCCACTGAC [12944]

Hsa CACCGCACACTGCGCTGCCC---CAGACCCACTGTGCGTGTGACAGCGGCTGATCTGTGC [13779]
Mmu CACCGCACACTGCGTTGCTC---CGGACCCACTGTGCGTGTGACAGCGGCTGATCTGTCC [13610]
Mdo TAACGCACATTGCGCTC------AGGACCCACTGTGCGTGTGACAGCGGCTA-CCGTGCA [12662]
Meu CAACGCACATTGCGCTG------AGGACCCACTGTGCGTGTGACAGCGGCTA-CCGTGCA [11091]
Oan ------------------------------------------------------------ [11794]
Aca TAACGCACATTGTGCTTCTC--GTGTCCCCACTGTGCGTGTGACAGCGGCTAACCTGCTT [13619]
Pbi TAACGCACATTGTGCTGCTA--ATGTCCCCACTGTGCGTGTGACAGCGGCTAACCTGCTT [14055]
Cpi TAACGCACATTGTGCTGTTA--AAGAATCCACTGTGCGTGTGACAGCGGCTAACCAGCTT [14676]
Cmy TAACGCACATTGTGCTGTTA--AAGACTCCACTGTGCGTGTGACAGCGGCTAACCTGCTT [14424]
Psi TAACGCACATTGTGCTGTTA--AAGACTCCACTGTGCGTGTGACAGCGGCTAACCTGCTT [13289]
Asp TAACGCACATTGTGCTGTTA--AAGACTCCACTGTGCGTGTGACAGCGGCTAACCTGCTT [12528]
Ami TAACGCACATTGTGCTGTTA--GCGATTCCACTGTGCGTGTGACAGCGGCTAACCTGNTT [14000]
Asi TAACGCACATTGTGCTGTTA--GCGATTCCACTGTGCGTGTGACAGCGGCTAACCTGCTT [13260]
Tgu ------------------------------------------------------------ [10749]
Cli TAACGCACATTGTGCTCTCG--GCGACTCCACTGTGCGTGTGACAGCGGCTAACCTGCTC [13400]
Gga TAACGCACATTGTGCTCTCG--GCGACTCCACTGTGCGTGTGACAGCGGCTAACCTGCTC [12040]
Xtr TAACGCACATTGCGCTGCTCCTAAAATGCCACTGTGCGTGTGACAGCGGCTAACCAGCAT [12748]
Lch TAACGCACATTGTGCTGTCA--GTGATTCCACTGTGCGTGTGACAGCGGCTAACCTGCTT [14361]
Dre TAACGCACATTGCGCCTATT-CTCCACTCCACTGTGCGTGTGACAGCGGCTAACCAGCTT [13003]

Hsa CTGGGCA--AGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCGCTC [13837]
Mmu CTGGGCA--AGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCGCTC [13668]
Mdo ACCGGCC--GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [12720]
Meu GCCGGCC------------------------------------------------------ [11098]
Oan ---------GGAGTTGTCACGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [11845]
Aca TTCGGAC--AGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [13677]
Pbi CTAGGAC--AGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [14113]
Cpi TTCGGCC--GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [14734]
Cmy TTCGGAC--GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [14482]
Psi TTCGGAC--GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [13347]
Asp TTCGGAC--GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [12586]
Ami TTCGGAC--GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCACTC [14058]
Asi TTCGGAC--GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCACTC [13318]
Tgu ---------GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [10800]
Cli CTCGGAC--GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [13458]
Gga CTCGGAC--GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [12098]
Xtr CTAGGAA--GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [12806]
Lch TTAGGAC--GGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCTCTC [14419]
Dre TTGGATC--AGCGTTGTC---TGTCTGCCTGTCTACACTTGCTGTGCAGAACTTCC-TGC [13057]

Hsa ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAGTTGGCTTA [13895]
Mmu ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTATGAGTTGGTTTA [13726]
Mdo ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAATTGGCTTA [12778]
Meu ----------------------------------------GGCTGTGAATTGGCTTA [11115]
Oan ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAATCGGCTTA [11903]
Aca ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAATTGGTTTA [13735]
Pbi ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAATCC--GGCTGTGAATTGGTTTA [14171]
Cpi ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAATTGGCTTA [14792]
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Cmy ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAATTGACTTA [14540]
Psi ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAATTGGCTTA [13405]
Asp ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAATTGGCTTA [12644]
Ami ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAATTGGCATA [14116]
Asi ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAACTGGCATA [13376]
Tgu ACCTGTACAGCAGGCACAGACAGGCAGTCGCATGACAACCC--GGCTGTGAGTTGGCTTA [10858]
Cli ACCTGTACAGCAGGCACAGACAGGCAGTCGCATGACAACCC--GGCTGTGAATTGGCTTA [13516]
Gga ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAATTGGCTTA [12156]
Xtr ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGAATTGGCTTA [12864]
Lch ACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCC--GGCTGTGACTTGGCTTA [14477]
Dre ACCTGTACAGCAGGCACAGACAGGCAGACAGATGGCAGCCC--AGCTGATTTTTGGCATA [13115]

Hsa ATCTCAGCTGGCAACTGTGAGATGTTCATACAATC-CCTCACAGTGGTCTCTGGGATTAT [13954]
Mmu ATCTCAGCTGGCAACTGTGAGATGTCCCTATCATT-CCTCACAGTGGTCTCTGGGATTAT [13785]
Mdo ATCTCAGCTGGCAACTGTGAGATGTTAATAAATTC-CCTCACAGTGGTCTCTGGGATTAT [12837]
Meu ATCTCAGCTGGCAACTGTGAGATATTAATAAATTC-CCTCACAGTGGTCTCTGGGATTAT [11174]
Oan ATCTCAGCTGGCAACTGTGAGATGCTAACCAATTC-TCCCACAGTGGCATCTGGGATTAT [11962]
Aca ATCTCAGCTGGCAACTGTGAGCAGTTTCCAAATCC-TCTCACAGTGGTTTCTGGGATTAT [13794]
Pbi ATCTCAGCTGGCAACTGTGAGCAGTTAATAAATTC-TCTCACAGTGGTATCTGGGATTAT [14230]
Cpi ATCTCAGCTGGCAACTGTGAGCAATTAATACATTC-TCTCACAGTGGTATCTGGGATTAT [14851]
Cmy ATCTCAGCTGGCAACTGTGAGCAATTTATAAATTC-TCTCACAGTGGTATCTGGGATTAT [14599]
Psi ATCTCAGCTGGCAACTGTGAGCAATTAATAAATTC-TCTCACAGTGGTATCTGGGATTAT [13464]
Asp ATCTCAGCTGGCAACTGTGAGCAATTAATAAATTC-TCTCACAGTGGTATCTGGGATTAT [12703]
Ami ATCTCAGCTGGCAACTGTGAGCAGTTCATAAATTC-TCTCACAGTTGTATCTGGGATTAT [14175]
Asi ATCTCAGCTGGCAACTGTGAGCAGTTCATAAATTC-TCTCACAGTTGTATCTGGGATTAT [13435]
Tgu ATCTCAGCTGGCAACTGTGAGCAGTTAATAA-CTC-TCTCACAGTTGTAGCTGGGATTAT [10916]
Cli ATCTCAGCTGGCAACTGTGAGCCGCTAATAA-CTC-TCTCACAGTGGTATCTGGGATTAT [13574]
Gga ATCTCAGCTGGCAACTGTGAGCAGTTAATAA--T--TCTCACAGTGGTATCTGGGATTAT [12212]
Xtr ATCTCAGCTGGCAACTGTGAGCAGTTAATAAATTA-TCTCACAGTGGTCTCTGGGATTAT [12923]
Lch ATCTCAGCTGGCAACTGTGAGCAGCTAATAACTTC-TCCCACAGTGGTCTCTGGGATTAT [14536]
Dre ATCTCAGCTGGCAACTGTGAGTAGTGTTTTCATCCCTCTCACAGGCGCTGCTGGGGTTCT [13175]

Hsa GCTAAACAGAGCAA--TGGCAGACTGGAAAATCTCTGCAGGCAAATGTGATGTCACTGAG [14012]
Mmu GCTAAACAGAGCAA--TGGCAGACTGGGAAATCTCTGCAGGCAAATGTGATGTCACTGAA [13843]
Mdo GCTAAACAGAGCAA--TTGCAGACTGGGAAATCTCTGCAGGCAAATGTGGTGTCGCTATA [12895]
Meu GCTAAACAGAGCAA--TTACAGACTGGGAAATCTCTGCAGGCATATGTGGTGTTGCTACA [11232]
Oan GCTAAACACAGCAA--TCGCAGACTGGGAAATCTCTGCTGGCAAATGTGGTGTCACGGTA [12020]
Aca GCTAAACACAGCAA--TCACAGACTGAGAAATCTCTGCAGGCAAATGTGATGTCTTGACC [13852]
Pbi GCTAAACGCAGCAA--TCACAGATTGAGAAATCTCTGCAGGCAAATGTGATGTCATGATT [14288]
Cpi GCTAAACACAGCAA--TCATAGACTGGGAAATCTCTGCAGGCAAATGTGATGTATTTATA [14909]
Cmy GCTAAACACAGCAA--TCATAGACTGGGAAATCTCTGCAGGCAAATGTGATGTACTAATA [14657]
Psi GCTAAACACAGCAA--TCATAGACTGGGAAATCTCTGCAGGCAAATGTGATGTATTTATA [13522]
Asp GCTAAACACAGCAA--TCATAGACTGGGAAATCTCTGCAGGCAAATGTGATGTATTTATA [12761]
Ami GCTAAACATAGCAA--TCGCAGACTGGGAAATCTCTACAGGCAAATGTGATGTCTTTATA [14233]
Asi GCTAAACATAGCAA--TCGCAGACTGGGAAATCTCTACAGGCAAATGTGATGTCTTTATA [13493]
Tgu GCTAAACACAGCAA--TCACAGACTGGGAAATCTCTGCAGGCAAGTGTGATGTCTTTATA [10974]
Cli GCTAAACACAGCGA--TCGCAGACTGGGAAATCTCTGCAGGCAAATGTGATGTCTTTATA [13632]
Gga GCTAAACACAGCAA--TCACAGACTGGGAAATCTCTGCAGGCAAATGTGATGTCTTTATA [12270]
Xtr ACTAAACACAGCAA---------------------------------------------- [12937]
Lch GCTAAACACTGCAA--CAGCAGACTGTCTAATCTCTGCAGGCAATTGTGACGTTCTTTTT [14594]
Dre GTCACACACAGCAC--AAACTGACTGGGTAATCTCTGCAGGCAACTGTGATGTGATTA-- [13231]

Hsa --GAAATCACACACTTACCCGTAGAGATTCTACAGTCTGACATC--TTGATGTCGCAGAT [14068]
Mmu --GAAACCACACACTTACCTGTAGAGATTCTTCAGTCTGACAAC--TTGATGTTGCAGAT [13899]
Mdo --GTTATCACACAATTACCCGTAGAGATTCTGCAATCTGACATC--TTGATGTCGTAGAT [12951]
Meu --GTTATCACACAATTACCTGTAGAGATTCTGCAATCTGACATC--TTGATGTCGTAGAT [11288]
Oan --GCAATCGCACAATTACCTGTAGAGATTCTGCAATCTGGCTTT---------------- [12062]
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Aca -AGCAATCTCACAGTTACCAGCAGAGGTTCTGCAATCTGGACTG--TTGATGTCGCAGAT [13909]
Pbi --GCAATCTCACAGTTACCAGTAGAGGTTCTGCAATCTGGAGGG--TTGATGTCGCAGAT [14344]
Cpi --GCAATCTCACAATTACCTGTAGAGTTTCTGCAATCTGATCTC--TTGATGTCGCAGAT [14965]
Cmy --GCAATCTCACAATTACCTGTAGAGTTTCTGCAATCTGGCATC--TTGATGTTGCAGAT [14713]
Psi --GCAATCTCACAATTACCTGTAGAGTTTCTGCAATCTGGCATC--TTGATGTCGCAGAT [13578]
Asp --GCAATCTCACAATTACCTGTAGAGTTTCTGCAATCTGGCATC--TTGATGTCGCAGAT [12817]
Ami --GTAATCTCACAATTACCTATAGAGATTCTTCAATCTGGCATC--TTGATGTCGCAGAT [14289]
Asi --GTAATCTCACAATTACCTATAGAGATTCTTCAATCTGGCATC--TTGATGTCGCAGAT [13549]
Tgu --GCAATCTCACAATTACCTGTAGAGATTCTACAATCTGGCATC--TTGATGTCGCAGAT [11030]
Cli --GCAATCTCACAATTACCTGTAGAGATTCTACAATCTGGCACC--TTGATGTCGCAGAT [13688]
Gga --GCAATCTCACAATTACCTGTAGAGATTCTACAATCTGGCATC--TTGATGTCGCAGAT [12326]
Xtr ----------------------------------------------TTGATGTTGTAGAT [12951]
Lch CAATAATCTCCCAGTCACCTGTAGAGGTTCTGTAGTCTGTCTTC--GTGATGTCGCAGAT [14652]
Dre ---CAGTCTCACATTGACCTGAAGAGGTTGAGCAGTCTGTTTAC--CTGATGTTGGTGAT [13286]

Hsa ACTGCATCAGGAACTGATTGGATAAGAATCAGTCACCATCAGTTCCTAATGCATTGCCTT [14128]
Mmu ACTGCATCAGGAACTGACTGGATAAGACTTAATCCCCATCAGTTCCTAATGCATTGCCTT [13959]
Mdo ACTGCATCAGGAACTGATTGGATAATATTCAGGCACCATCAGTTCCTAATGCATTGCCTT [13011]
Meu ACTGCATCAGGAACTGATTGGATAATATTCAGGCACCATCAGTTCCTAATGCATTGCCTT [11348]
Oan ------------------------------------------------------------ [12062]
Aca ACTGCATCAGGAACTGATTGGGGAATAATCATGTACCATCAGTTCCTAATGCATTGCCTT [13969]
Pbi ACTGCATCAGGAACTGATTGGATAATAATCAGGCACCATCAGTTCTTAATGCATTGCCTT [14404]
Cpi ACTGCATCAGGAACTGATTGGATAATAATCAGCCACCATCAGTTCCTAATGCATTGCCTT [15025]
Cmy ACTGCATCAGGAACTGATTGGATAATAATCAGCCACCATCAGTTCCTAATGCATTGCCTT [14773]
Psi ACTGCATCAGGAACTGATTGGATAATAATCAGCCACCATCAGTTCCTAATGCATTGCCTT [13638]
Asp ACTGCATCAGGAACTGATTGGATAATAATCAGCCACCATCAGTTCCTAATGCATTGCCTT [12877]
Ami ACTGCATCAGGAACTGATTGGATAATAATCAGTCACCATCAGTTCCTAATGCATTGCCTT [14349]
Asi ACTGCATCAGGAACTGATTGGATAATAATCAGTCACCATCAGTTCCTAATGCATTGCCTT [13609]
Tgu ACTGCATCAGGAACTGATTGGATAATAATCACTCACCATCAGTTCCTAATGCATTGCCTT [11090]
Cli ACTGCATCAGGAACTGATTGGATAATAATCAGTCACCATCAGTTCCTAATGCATTGCCTT [13748]
Gga ACTGCATCAGGAACTGATTGGATAATAATCAGTCACCATCAGTTCCTAATGCATTGCCTT [12386]
Xtr ACTGCATCAGGAACTGATTGGATCCCAGGGAGCAGCCATCAGTTCCTAATGCACTGCCTT [13011]
Lch ACTGCATCAGGAACTGATTGGATACAACTTAACTACCATCAGTTCCTAATGCATTGCCTT [14712]
Dre ACTGCATCAGGAACTGATTGGATGATATTCAGGAGCCATCAGTTCCTGATGCACTCCCAT [13346]

Hsa CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGCGAGGTATGA [14186]
Mmu CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGCTTGCGAGGTATGA [14017]
Mdo CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGTGAGGTATGA [13069]
Meu CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGTGAGGTATGA [11406]
Oan -----------GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGCAAGGTATGA [12111]
Aca CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGCGAGGTATGA [14027]
Pbi CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGTGAGGTATGC [14462]
Cpi CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGCAAGGTATGA [15083]
Cmy CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGCAAGGTATGA [14831]
Psi CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGCAAGGTATGA [13696]
Asp CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGCAAGGTATGA [12935]
Ami CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGTGAGGTATGA [14407]
Asi CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGTGAGGTATGA [13667]
Tgu CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGTGAGGTATGA [11148]
Cli CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGTGAGGTATGA [13806]
Gga CAGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGTGAGGTATGA [12444]
Xtr CGGCATCTA--GCGAGATTTTCTGTTGTGCTTGATCTAACCATGTGGTTGTGAGGTATGA [13069]
Lch CAGCATCTA--GCGGGATTTTCCTTTGTGCTTGATCTAACCATGTGGTTGCGAGGTATGA [14770]
Dre CAGCATCGA--GCGGGGTTTTCCTTTGTGCTTGATCTAACCATGTGGTTGCAGACTCAGA [13404]

Hsa GTAAAACATGGTTCCGTCAAGCACCATGGAACGTCACGCAGCT--GCGGGGCTTTCCTTT [14244]
Mmu GAAAAACATGGTTCCGTCAAGCACCATGGAACGTCACGCAGCT--GCGGGGCTTTCCTTT [14075]
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Mdo GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ACGGGGCTTTCCTTT [13127]
Meu GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT----------------- [11449]
Oan GTAAAACATGGTTCTGTCAAGCACCATGGAAAGTCACGCAGCT--ATGGGGCTTTCCTTT [12169]
Aca GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ATGGGATTTTCCTTT [14085]
Pbi GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ATGGGATTTTCCTTT [14520]
Cpi GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ATGGGGTTTTCCTTT [15141]
Cmy GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ATGGGGTTTTCCTTT [14889]
Psi GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ATGAGGTTTTCCTTT [13754]
Asp GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ATGAGGTTTTCCTTT [12993]
Ami GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ATGGGGTTTTCCTTT [14465]
Asi GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ATGGGGTTTTCCTTT [13725]
Tgu GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ATGGGGTTTTCCTTT [11206]
Cli GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--GTGGGGTTTTCCTTT [13864]
Gga GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ATGGGGTTTTCCTTT [12502]
Xtr GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--ATGGGGTTTTCCTTT [13127]
Lch GTAAAACATGGTTCTGTCAAGCACCATGGAACGTCACGCAGCT--CTGGGGTTTTCCTTT [14828]
Dre CTAATACATGGTTCTGTCAAGCACCATGGAAGGTCTTGCAGCA--GCGGGGTTTTCCTTT [13462]

Hsa GTGCTTGATCTAACCATGTGGTGGAACGATGGAAACGGAACATGGTTCTGTCAAGCACCG [14304]
Mmu GTGCTTGATCTAACCATGTGGTGGAACGATGGAAACGGAACATGGTTCTGTCAAGCACCG [14135]
Mdo GTGCTTGATCTAACCATGTGGTGGAACGATAGAAACAGAACATGGTTCTGTCAAGCACCG [13187]
Meu ---------------------------------------------------------- [11449]
Oan GTGCTTGATCTAACCATGTGGTGGAACAATATAAACAGAACATGGTTCTGTCAAGCACCA [12229]
Aca GTGCTTGATCTAACCATGTGGTAGAACAATACAAATTGAACATGGTTCTGTCAAGCACCA [14145]
Pbi GTGCTTGATCTAACCATGTGGTAGAACAATACAAATTGAACATGGTTCTGTCAAGCACCA [14580]
Cpi GTGCTTGATCTAACCATGTGGTAGAACAATACAAATTGAACATGGTTCTGTCAAGCACCA [15201]
Cmy GTGCTTGATCTAACCATGTGGTAGAACAATACAAATTGAACATGGTTCTGTCAAGCACCA [14949]
Psi GTGCTTGATCTAACCATGTGGTAGAACAATACAAATTGAACATGGTTCTGTCAAGCACCA [13814]
Asp GTGCTTGATCTAACCATGTGGTAGAACAATACAAATTGAACATGGTTCTGTCAAGCACCA [13053]
Ami GTGCTTGATCTAACCATGTGGTAGAACAATACAAATTGAACATGGTTCTGTCAAGCACCA [14525]
Asi GTGCTTGATCTAACCATGTGGTAGAACAATACAAATTGAACATGGTTCTGTCAAGCACCA [13785]
Tgu GTGCTTGATCTAACCATGTGGTAGAACAATACAAATGGAACATGGTTCTGTCAAGCACCA [11266]
Cli GTGCTTGATCTAACCATGTGGTAGAACAATACAAATGGAACATGGTTCTGTCAAGCACCA [13924]
Gga GTGCTTGATCTAACCATGTGGTAGAACAATACAAATTGAACATGGTTCTGTCAAGCACCA [12562]
Xtr GTGCTTGATCTAACCATGTGGTAGAACAATACATATTGAACATGGTTCTGTCAAGCACCA [13187]
Lch GTGCTTGATCTAACCATGTGGTAGAGAAATACAAGTAAAACATGGTTCTGTCAAGCACCA [14888]
Dre GTGCTTGATCTAACCATGTGGTTGCAGACTCAGACTAATACATGGTTCTGTCAAGCACCA [13522]

Hsa CGGAAAGCACCGTGCTC--CGGGCCGCGGCTCCTGATTGTCCAAACGCAATTCTCGAGTC [14362]
Mmu CGGAAAGCATCGCTCTC--CGGGCCGCGGCTCCTGATTGTCCAAACGCAATTCTCGAGTC [14193]
Mdo CGGAAAGCTCCGTGCTT--CGGGCCGCGGCTCCTGATTGTCCAAACGCAATTCTCGTGGC [13245]
Meu ------------------CGGGCCGTGGCTCTTGATTGTCCAAACGCAATTCTCGTGGC [11490]
Oan CGGAAGGCTCCGTGTTT---------------------------------------------- [12246]
Aca TGGAAGGCTCCATGCTT--TGACCGCTGGGTCCTGATTGTCCAAACGCAATTCTTGTCTC [14203]
Pbi TGGAAGGCTCCATGCTT--GGAGCCCTGGCCTGTGATTGTCCAAACGCAATTCTTGTCTC [14638]
Cpi TGGAAGGCTGCATACTT--TGAACACCGGCTCCTGATTGTCCAAACGCAATTCTTGTGTC [15259]
Cmy TGGAAGGCTGCATACTT--TGAATGCCGGCTCCTGATTGTCCAAACGCAATTCTTGTGTC [15007]
Psi TGGAAGGCTGCATACTT---------------------------------------------- [13831]
Asp TGGAAGGCTGCATACTT---------------------------------------------- [13070]
Ami TGGAAGGCTGCATACTT--TGAGCGCCGGGTCCTGATTGTCCAAACGCAATTCTTGTGTC [14583]
Asi TGGAAGGCTGCATACTT--TGAGCGCTGGGTCCTGATTGTCCAAACGCAATTCTTGTGTC [13843]
Tgu TGGAAGGCTGCATACTC---------------------------------------------- [11283]
Cli TGGAAGGCTGCATACTC---------------------------------------------- [13941]
Gga TGGAAGGCTGCATACTC---------------------------------------------- [12579]
Xtr TGGAAGGCCACATACTT---------------------------------------------- [13204]
Lch TGGAAGGCCACGCACTT--GGAATTTTAGCTCCTGATTGTCCAAACGCAATTCTTGTGTC [14946]
Dre TGGAAGGTCTTGCAGCA--TGACGGTCAGGTGCTGATTGTCCAAACGCAATTCTTGTGCT [13580]
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Hsa T---ATGGCTCCGGCC---GAGAGTTGAGTCTGGACGTCCCGAGCCGCCGC--AGGGGCT [14414]
Mmu T---CTGGCTCCGGCC---GAGAGTTGCGTCTGGACGTCCCGAGCCGCCGC--AGGGGCT [14245]
Mdo T---------CCGGCCCTCGAGAGTTGGGTCTGGACATCCCGAGCCGCGGC--AGGGGTT [13294]
Meu T---------CCGGCCCTCGAGAGTTGGGTCTGGACATCCCGAGCCGCGGC--AGGGGTT [11539]
Oan ----------------------------------------------------CGGGGCC [12253]
Aca C------GCTCCA-CC---GAGAGTTGAGTCTGGACATCAGGAGCCGGAGG--GGAACCT [14251]
Pbi T---------CCA-CC---GAGAGTTGAGTCTGGACATCATGAGCCGGGGT--GGAACCT [14683]
Cpi T---------GCGCCC---AAGAATTGAGTGTGGACGTCGTGAGCCGGGGT--GGAATCT [15305]
Cmy T---------GCGCCC---AAGAATTGAGTGTGGACGTCGTGAGCCGGGGT--GGAATCT [15053]
Psi ----------------------------------------------------GGAATCT [13838]
Asp ----------------------------------------------------GGAATCT [13077]
Ami T---------GC-CCC---AAGAATTGAGTGTGGACGTCGGGAGCCGCCGT--GGAGTCT [14628]
Asi T---------GC-CCC---AAGAATTGAGTGTGGACGTCGGGAGCCGCCGT--GGAGTCT [13888]
Tgu ----------------------------------------------------GGAATCT [11290]
Cli ----------------------------------------------------GGAATCT [13948]
Gga ----------------------------------------------------GGAATCT [12586]
Xtr ----------------------------------------------------GGAGCTC [13211]
Lch TTCTCAGATCCAAACC---AAGAATTGTGTCTGGACATCCTGAGCTGGAAT--GAAATTT [15001]
Dre TGTGTGAAAC---------AGGAGTTGTGGATGGACATCACGCTCCTGTCT--AGGGTCC [13629]

Hsa TCGCCACTGATTGTCCAAACGCAATTCTTGTACGA--GTCTGCGGCCAACCGAGAATTGT [14472]
Mmu TCGCCACTGATTGTCCAAACGCAATTCTTGTACGA--GTCTGCGGCCAACCGAGAATTGT [14303]
Mdo CCGCCGCTGATTGTCCAAACGCAATTCTTGTGCGA--GTCTGCAGCCAACCGAGAATTGT [13352]
Meu CCGCCGCTGATTGTCCAAACGCAATTCTTGTGCGA--GTCTGCAGCCAACCGAGAATTGT [11597]
Oan CCGCCGCTGATTGTCCAAACGCAATTCTTGTGCGA--GTTTGCGGCCAACCGAGAATTGT [12311]
Aca TTGCTCCTGATTGTCCAAACGCAATTCTTGTCCAG--AAAACATGCAAACCAAGAATTGT [14309]
Pbi TTGCTCCTGATTGTCCAAACGCAATTCTTGTGCAG-AAAAACATGCCAACCAAGAATTGT [14742]
Cpi CTGCTCCTGATTGTCCAAACGCAATTCTTGTGCAATGGAATCATACAAACCAAGAATTGT [15365]
Cmy CTGCTCCTGATTGTCCAAACGCAATTCTTGTGCAATGGAAACATACAAACCAAGAATTGT [15113]
Psi CTGCTCCTGATTGTCCAAACGCAATTCTTGTGCAATGGAAACATACAAACCAAGAATTGT [13898]
Asp CTGCTCCTGATTGTCCAAACGCAATTCTTGTGCAATGGAAACATACAAACCAAGAATTGT [13137]
Ami CCGCTCCTGATTGTCCAAACGCAATTCTTGTGCCGTGGAAACGTACAAACCAAGAATTGT [14688]
Asi CCGCTCCTGATTGTCCAAACGCAATTCTTGTGCCGTGGAAACGTACAAACCAAGAATTGT [13948]
Tgu CCGCTCCTGATTGTCCAAACGCAATTCTTGTGCGATGGAGCCGTACGAACCAAGAATTGT [11350]
Cli CCGCTCCTGATTGTCCAAACGCAATTCTTGTGCGATGGAGCCGTACGAACCAAGAATTGT [14008]
Gga CTGCTCCTGATTGTCCAAACGCAATTCTTGTGCGCTGGAGCCGTACGAACCAAGAATTGT [12646]
Xtr TCGCCCTTGATTGTCCAAACGCAATTCTTGTTCCAATAGAAATATCAAGCCAAGAATTGT [13271]
Lch TAGCTTCTGATTGTCCAAACGCAATTCTTGTGAAATCAAAAATAAATA-TCAAGAATTGT [15060]
Dre CAGAGATTGATTGTCCAAACGCAATTCTTGTAACATATAATATAAAT--CCAAGAATTGT [13687]

Hsa GGCTGGACATCTGTGGCTGAGCT--TCTGGGGCATGAACCTGGCATACAATGTAGATTTC [14530]
Mmu GGCTGGACATCTGTGGTTGAGCT--TCTGGGGCATGAACCTGGCATACAATGTAGATTTC [14361]
Mdo GGCTGGACATCTGTGGCTGAGCT--TTTGGGGCATGAACCTGGCATACAATGTAGAATTC [13410]
Meu GGCTGGACATCTGTGGCTGAGCT--TTTGGGGCATGAACCTGGCATACAATGTAGAATTC [11655]
Oan GACTGGACATCTGTGGCTGGGCT--TTTGAGGCATGAACCTGGCATACAATGTAGAATTC [12369]
Aca GTCTGGACATCTGTGGCCAAGTC--CTTGGGGCCTGAACCTGGCATACAATGTAGAATTC [14367]
Pbi GTCTGGACATCGGTGGCTAAGCC--CTTTGGGCCTTGACCTGGCATACAATGTAGAATAC [14800]
Cpi GTCTGGACATCTGTGGCAGAGAT--TTTGGGGCATGAACCTGGCATACAATGTAGAATTC [15423]
Cmy GTCTGGACATCTGTGGCAGAGAT--TTTGGGGCATGAACCTGGCATACAATGTAGAATTC [15171]
Psi GTCTGGACATCTGTGGCAGAGAT--TTTGGGGCATGAACCTGGCATACAATGTAGAATTC [13956]
Asp GTCTGGACATCTGTGGCAGAGAT--TTTGGGGCATGAACCTGGCATACAATGTAGAATTC [13195]
Ami GTCTGGACATCTGTGGCGGGGAG--TTTGGGGCATGAACCTGGCATACAATGTAGATTTC [14746]
Asi GTCTGGACATCTGTGGCGGGGAG--TTTGGGGCATGAACCTGGCATACAATGTAGATTTC [14006]
Tgu GTCTGGACATCTGTAGCAGAGGT--TTTGGGGCATGAACCTGGCATACAATGTAGATTTC [11408]
Cli GTCTGGACATCTGTAGCAGAGAT--TTTGGGGCATGAACCTGGCATACAATGTAGATTTC [14066]
Gga GTCTGGACATCTGTAGCAGAGAT--TTTGGGGCATGAACCTGGCATACAATGTAGATTTC [12704]
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Xtr GCCTGGACATCTGTGGCTGGTGA--ACTTTGGCGTGCACCTGGCATACAATGTAGAAAAC [13329]
Lch GGCTGGACATCTGTAGCTGGAGT--TCTTGGGCATGAACCTGGCATACAATGTAGAATCC [15118]
Dre GCCTGGACATCTGTTGCTGGAGA--GTTTTGTCGTGAACCTGGCATACAATGTAGATTTC [13745]

Hsa TGTGTTCGTTAGGCAACAGCTACATTGTCTGCTGGGTTTCAGGCTACCT--AGGTACCC- [14587]
Mmu TGTGTTTGTTAGGCAACAGCTACATTGTCTGCTGGGTTTCAGGCTACCT--GGGTGCCC- [14418]
Mdo TGTGTTTATTAAGTAACAGCTACATTGTCTGCTGGGTTTCAGGCTACCT--TTTTGTCCC [13468]
Meu TGTGTTTATTAAGTAACAGCTACATTGTCTGCTGGGTTTCAGGCTACCT---TTTGTCCC [11712]
Oan TGTATTTGTTAAGCAACAGCTACATTGTCTGCTGGGTTTCAAGCTACCT--AGTTGCCCC [12427]
Aca TG--TTTGTTAAGCAACAGCTACATTGTCTGCTGGGTTTCAGGCTGTCT--AGCTGTTCC [14423]
Pbi TGTGTTTGTTAAGCAACAGCTACATTGTCTGCTGGGTTTCAGGCTGTCT--AGCTGCTCA [14858]
Cpi TGTGTTTGTTAAGCAACAGCTACATTGTCTGCTGGGTTTCAAGCTGCCT--AGTTGCCTA [15481]
Cmy TGTGTTTGTTAAGCAACAGCTACATTGTCTGCTGGGTTTCAAGCTGCCT--AGTTGCCTA [15229]
Psi TGTGTTTGTTAAGTAACAGCTACATTGTCTGCTGGGTTTCAAGCTGCCT--AGTTGTCCT [14014]
Asp TGTGTTTGTTAAGCAACAGCTACATTGTCTGCTGGGTTTCAAGCTGCCT--AGTTGTCCT [13253]
Ami TGTATTTCTTAAGCAACAGCTACATTGTCTGCTGGGTTTCAAGCTGCCT--AGTTGCCCA [14804]
Asi TGTATTTCTTAAGCAACAGCTACATTGTCTGCTGGGTTTCAAGCTGCCT--AGTTGCCCA [14064]
Tgu TGTGTTTGTTAAGCAACAGCTACATTGTCTGCTGGGTTTCCAGCTGCCT--AGCTGCCCA [11466]
Cli TGTGTTTGTTAAGCAACAGCTACATTGTCTGCTGGGTTTCCAGCTGCCT--AGTTGCTCA [14124]
Gga TGTGTTTGTTAAGCAACAGCTACATTGTCTGCTGGGTTTCCAGCTGCCT--AGTTGCCCA [12762]
Xtr TGTGTTTGCAAAGCAACAGCTACATTGTCTGCTGGGTTTCATGCTGAAT--CCACTGGAG [13387]
Lch TGTGTTAGAATAGCAACAGCTACATTGTCTGCTGGGTTTCAGGCTACCT--AGTTGTCCA [15176]
Dre TGTGTGGTACTATCTACAGCTACATTGTCTGCTGGGTTTCAGGCCAGCA--GGGTGCTCA [13803]

Hsa TCAATGGCTCAGTAGCCAGTGTAGATCCTGTCTTTCGTAATCAGCAGCTACATCTGGCTA [14647]
Mmu TCAGTGGCTCAGTAGCCAGTGTAGATCCTGTCTTTGGTAATCAGCAGCTACATCTGGCTA [14478]
Mdo TCATTCGCTCAGTAGTCAGTGTAGATACTGTCTCTTTCCATCAGCAGCTACATCTGGCTA [13528]
Meu TCATTCGCTCAGTAGTCAGTGTAGATCCTGTCTCTG--AATCAGCAGCTACATCTGGCTA [11770]
Oan TCAATCGCTCAGTAGTCAGTGTAGATCCTGTATTC--TAATCAGCAGCTACATCTGGCTA [12485]
Aca TCAGTCGCTCAGTAGTCAGTGTAGATTCTGTCTTCT-CAATCAGCAGCTACATCTGGCTA [14482]
Pbi TCAGTCGCTCAGTAGTCAGTGTAGATTCTGTTTCTT-CGGTCAGCAGCTACATCTGGCTA [14917]
Cpi TCAGTCGCTCAGTAGTCAGTGTAGATTCTGTCTTTA-CAATCAGCAGCTACATCTGGCTA [15540]
Cmy TCAGTCGCTCAGTAGTCAGTGTAGATTCTGTCTTTA-CAATCAGCAGCTACATCTGGCTA [15288]
Psi TCAGTCGCTCAGTAGTCAGTGTAGATTCTGTCTTTA-CAATCAGCAGCTACATCTGGCTA [14073]
Asp TCAGTCGCTCAGTAGTCAGTGTAGATTCTGTCTTTA-CAATCAGCAGCTACATCTGGCTA [13312]
Ami TCAATCGCTCAGTAGTCAGTGTAGATTCTGTTTTTA-CAATCAGCAGCTACATCTGGCTA [14863]
Asi TCAATCGCTCAGTAGTCAGTGTAGATTCTGTTTTTA-CAATCAGCAGCTACATCTGGCTA [14123]
Tgu TCAGTCGCTCAGTAGTCAGTGTAGATTCTGTCTTTA-CAATCAGCAGCTACATCTGGCTA [11525]
Cli TCAATCGCTCAGTAGTCAGTGTAGATCCTGTCTTTA-CAATCAGCAGCTACATCTGGCTA [14183]
Gga TCAATCGCTCAGTAGTCAGTGTAGATTCTGTCTTTA-CAATCAGCAGCTACATCTGGCTA [12821]
Xtr TTGTTCGCTCAGTAATCAGTGTAGATCCTGTATAT--CTGTCAGCAGCTACATCTGGCTA [13445]
Lch TGAGTTGCTCAGTAGTCAGTGTAGATTCTGTGTCT--CAATCAGCAGCTACATCTGGCTA [15234]
Dre TGAGATGCTCAGTAGTCAGTGTAGATCCTGTGTCA--CAATCAGCAGCTACATCTGGCTA [13861]

Hsa CTGGGTCTCTGATGGCATCTT---------------------------------------- [14668]
Mmu CTGGGTCTCTGGTGGCATCAT---------------------------------------- [14499]
Mdo CTGGGTCTCTGATGGCATCTT---------------------------------------- [13549]
Meu CTGGGTCTCTGATGGCATTTT---------------------------------------- [11791]
Oan CTGGGTCTCTGAGGGTACCTT--GGATGCTAATTGGCTGCTCAGTAGTTGGTGTAGGATC [12543]
Aca CTGGGTCTCTGAGGACATCTT--GGATGCCAATGGGCTGCTCAGTAGTCGGTGTAGAATC [14540]
Pbi CTGGGTCTCTGAAGACGTCTT--TGATGTGAACAGGCTGCTCAGTAGTTGGTGTAGGATC [14975]
Cpi CTGGGTCTCTGATGACATCTT--TAGATGCAATTGGCTGCTCAGTAGTCGGTGTAGGATC [15598]
Cmy CTGGGTCTCTGATGACATCTT--TAGATGCAATTGGCTGCTCAGTAGTCGGTGTAGGATC [15346]
Psi CTGGGTCTCTGATGACATCTC--AAGATGCAATTGGCTGCTCAGTAGTCGGTGTAGGATC [14131]
Asp CTGGGTCTCTGATGACATCTC--AAGATGCAATTGGCTGCTCAGTAGTCGGTGTAGGATC [13370]
Ami CTGGGTCTCTGATGACATCTT--TGGATGTAATTGGGTGCTCAGTAGTCGGTGTAGAATC [14921]
Asi CTGGGTCTCTGATGACATCTT--TGGATGTAATTGGCTGCTCAGTAGTCGGTGTAGAATC [14181]
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Tgu CTGGGTCTCTGATGACATCT---------------------------------------- [11545]
Cli CTGGGTCTCTGATGACAACTC--ATGGTGCTCTTGGCTGCTCAGTAGTCGGTGTAGGATC [14241]
Gga CTGGGTCTCTGATGACATCTC--ACGGTGCCCTTGGCTGCTCAGTAGTCAGTGTAGGATC [12879]
Xtr CTGGGTCTCTAACTCCATTGC---------------------------------------- [13466]
Lch CTGGGTCTCTAATGGCAACAC--GGATGCTTGTTGGCCGCTCAGTACTCAGTGTAGAGTC [15292]
Dre CTGGGTCTCTGATGGCATTTT--TGACGTGATCTGCAGACTCAGTACTCGGTGTAGAGTC [13919]

Hsa ----------------------------------------------------------GCA [14671]
Mmu ----------------------------------------------------------GCA [14502]
Mdo ----------------------------------------------------------TCA [13552]
Meu ----------------------------------------------------------GCA [11794]
Oan TGTCTGACATGATTAAGAACAGCTACATCTGATTACTGGGTCACCGATAGCATCA--GCA [12601]
Aca TGTCTGA---TGATACCCACAGCTACATCTGATTACTGGGTTTCCTGTGGCATCA--GCA [14595]
Pbi TGTCCGA---TAAAACCAACAGCTACATCTGATTACTGGGTCTCCTGTGGCATCA--TCA [15030]
Cpi TGTCTGACATTATTACCAACAGCTACATCTGATTACTGGGTCACTGATAGCATCA--GCA [15656]
Cmy TGTCTGACATTATTACCAACAGCTACATCTGATTACTGGGTCACCGATAGCATCA--GCA [15404]
Psi TGTCTAACATTGCTACCAACAGCTACATCTGATTACTGGGTCGCTGATGGCATCG--GCA [14189]
Asp TGTCTAACATTGCTACCAACAGCTACATCTGATTACTGGGTCACTGATCGCATCA--GCA [13428]
Ami TGTCTGACATTGATACCAACAGCTACATCTGATTACTGGGTCACTAATTGCATCA--GCA [14979]
Asi TGTCTGACATTGATACCAACAGCTACATCTGATTACTGGGTCACTAATTGCATCA--GCA [14239]
Tgu ----------------------------------------------------------GCA [11548]
Cli TGTCTGACAGTCTCGCTAACAGCTACATCTGATTACTGGGTCACCAAAGGGTGAC--GCG [14299]
Gga TGTCCGACAGTCTCACTAACAGCTACATCTGATTACTGGGTCACCAAAGGACCAC--GCA [12937]
Xtr ----------------------------------------------------------TAA [13469]
Lch TGTCTGACATTAATA--AACAGCTACATCTGATTACTGGGTCACTAGCAGCATCC--CCA [15348]
Dre TGTGTGATTCAGAAG--AGCAGCTACATCTGAATACTGGGTCAGTGGAGACGTCA--TAG [13975]

Hsa GTGCCACGCTCCGTGTATTTGACAAGCTGAGTTGGACACTCCAT--GTGGTAGAGTGTCA [14729]
Mmu GTGTCACGCTCCGTGTATTTGACAAGCTGAGTTGGACACTCTGT--GTGGTAGAGTGTCA [14560]
Mdo GTGCCACACTCCGTGTATTTGACAAGCTGAGTTGGACACTCCGT--GTCGTAGAGTGTCA [13610]
Meu GTGCCACACTCCGTGTATTTGACAAGCTGAGTCAGACACTCCGT--GTGGTAGAGTGTCA [11852]
Oan GTGCCGCGCTCCGTGTATTTGACAAGCTGAGTTGGACACTCCGT--GTGGTTGAGTGTCA [12659]
Aca GGGCTTCCCTCCGTGTATTTGACGATCTGA-TCGCACACTCCGTCTGCACCAGAGTGTCA [14654]
Pbi GTGTTGCCCTCTGTGTATTTGACAAGCTGGGTTCAACACTCAGT--GTAGCA--GTGTCA [15086]
Cpi GTGCTGCGCTCCGTGTATTTGACAAGCTGAGTTTGACACTCAAT--GTGGCAGAGTGTCA [15714]
Cmy GTGCTGCGCTCCGTGTATTTGACAAGCTGAGTTTGACACTCAGT--GTGGCAGAGTGTCA [15462]
Psi GTGCTGCACTCCGTGTATTTGACAAGCTGAGTTTGACACTCAGT--GTGGCAGAGTGTCA [14247]
Asp GTGCTGCACTCCGTGTATTTGACAAGCTGAGTTTGACACTCAGT--GTGGCAGAGTGTCA [13486]
Ami GTGCTGCACTCCGTGTATTTGACAAGCTGAGTTTGACACTCAGT--GTGGCAGAGTGTCA [15037]
Asi GTGCTGCACTCCGTGTATTTGACAAGCTGAGTTTGACACTCAGT--GTGGCAGAGTGTCA [14297]
Tgu GTGTGGCACTGCGTGTATTTGACAAGCTGAGTCCGACACTCAGT--GTG-CAGAGTGTCA [11605]
Cli GTGCCGCGCTGCGTGTATTTGACAAGCTGAGTCCGACACTCAGT--GCG--AGAGTGTCA [14355]
Gga GTGCAGCACTGCGTGTATTTGACAAGCTGAGTTTGACACTCAGT--CTGGCAGAGTGTCA [12995]
Xtr GTGTGGCACTGAGTGTATTTGACAAGCTGAGTCCGACACTCAAT--GAGACAGAGTGTCA [13527]
Lch GCACAGCGCTCAGTGTATTTGACAAGCTGAATTCGACACTCAGT--TCTGTAGAGTGTCA [15406]
Dre ACTCTTCTCTTAGAGTATTTGACAGACTGTGGTTGACACTCGAT--CTAAAGGGGTGTCA [14033]

Hsa GTTTGTCAAATACCCCAAGTGCGGCACA--GACATGCTGTCCACAGTGTGTTTGATAAGC [14787]
Mmu GTTTGTCAAATACCCCAAGTGTGGCTCA--GATGTGCTGTCCACAGTGTATTTGATAAGA [14618]
Mdo GTTTGTCAAATACCCCAAGTGAGGCATT--GACAAACTGTCCAGAGTGTGTTTGATAATC [13668]
Meu GTTTGTCAAATACCCCAAGTGAGACATT--GATAAACTGTCCAGAGTGTGTTTGATAAGC [11910]
Oan GTTTGTCAAATACCCTAAGTGAGGCATT--AACACACTGTCCTCAGTGCGTTTGATAAGC [12717]
Aca GTTTGTCAAATATACAAAGGGCGGCCTC---------------------------------- [14682]
Pbi GTTTGTCAAATATACAAAGTGCGGCATT--AACAGAACATCCACAGTGTGTTTGATAAGC [15144]
Cpi GTTTGTCAAATACCCCAAGTGAAGCATT--GATATACTGTCAATAGTGTGTTTGATAACC [15772]
Cmy GTTTGTCAAATACCCCAAGTGAGGCATT--GATATACTGTCCACAGTGTGTTTGATAACC [15520]
Psi GTTTGTCAAATACCCCAAGTGAGGCATT--AACACACTGTCCCCAGTGTGTTTGATAAGC [14305]
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Asp GTTTGTCAAATACCCCAAGTGAGGCATT--AATACATTGTCCCCAGTGTGTTTGATGAGC [13544]
Ami GTTTGTCAAATACCCCAAGTGAGGCATT--GACATATTGTCCATAGTGTGTTTGATAAGC [15095]
Asi GTTTGTCAAATACCCCAAGTGAGGCATT--GACATATCGTCCATAGTGTGTTTGATAAGC [14355]
Tgu GTTTGTCAAATACCCCAAGTGAGGCACT--GGCAAACTGTCCTCAGTGTGTTTCATAAGC [11663]
Cli GTTTGTCAAATACCCCAAGCGAGGCACT--GACAGACTGTCCACAGTGTGTTTGATAAGC [14413]
Gga GTTTGTCAAATACCCCAAGTGAGGCACT------------------------------- [13023]
Xtr GTTTGTCAAATACCCCAAGTGAGGCACC------------------------------- [13555]
Lch GTTTGTCAAATACCCCAAGTGAGGTGTT--CATTCACAGTCCATAGTGTGTTTGATAAGC [15464]
Dre GTTTGTCAAATACCCCAAGAGAGGGGGC------------------------------- [14061]

Hsa TGACATGGGACAGGGATTCTT--------TTCACTGTTGTGTCAGTTTATCAAACCCATA [14839]
Mmu TGACATAGGAGAGGAACTTCT--------TTCACCTTTGTGTCAGTTTATCAAACCCATA [14670]
Mdo TGACATGGGACAGAGGTTCTT--------TTCACTGTTGTGTCAGTTTATCAAACCCATA [13720]
Meu TGACATGGGACAGGCTTACTT--------TTCACTGTTGTGTCAGTTTATCAAACCCATA [11962]
Oan TAACATGAGACAGGAGCTTTTT-------TTCACGGTTGTGTCAGTGTATCAGACACAAG [12770]
Aca ------------------------------------------------------------ [14682]
Pbi TGACATGGGACAGGAATTCTTT-------TTCACTGTTGTGTCAATTTATCAAACCCATA [15197]
Cpi TGATGTGGGACAGGAGTTCTT--------TTCACTGTTGTGTCAGTTTATCAAACCCTGG [15824]
Cmy TGATGTGGGACCGGAGTTCTT--------TTCGCTGTTGTGTCAGTTTCTCAAACCTATA [15572]
Psi TGATATTATATGGGAGGTTTCGCCCCG--CCCTCCGTTGTATCAGTTTATCAAACCCATA [14363]
Asp TGATATGATATGGGAGGTTTCGCCCCCCACCCCCTGCTGTGTCAGTTTATCAAACCCATA [13604]
Ami TGACATGGGACAGGAGTTCTT--------TTCACTGTTGTGTCAGTTTATCAAACCCATA [15147]
Asi TGACATGGGACAGGAGTTCTT--------TTCACTGTTGTGTCAGTTTATCAAACCCATA [14407]
Tgu TGACGTGGGACAGGATTTCTT--------TTTGCTGCTGTGTCAGTATATCAAAATCATA [11715]
Cli TGACATGGGACAGGATTTCTT--------TTCACTGTTGTGTCAGTATATCAAACTCATA [14465]
Gga ------------------------------------------------------------ [13023]
Xtr ------------------------------------------------------------ [13555]
Lch AGACATGAGACAGGCATCTTT--------CTCACTGTTGTGTCAGTTCATCAAACCCATA [15516]
Dre ------------------------------------------------------------ [14061]

Hsa CTTGGATGA--GGCTGTCCTCTCCAACAATATCCTGGTGCTG---AGTG-ATGACTCAG- [14892]
Mmu CCTGGATGA--GGCCGTCCTCCCCAACAATATCCTGGTGCTG---AGTGGGTG-CACAG- [14723]
Mdo CCTGGATAC--GGCCTTCCTCCCCAACAATATCCTGATGCTG---AGTGAGCGGCACAT- [13774]
Meu CCTGGACAC--GGCCTTCCTCCCCAACAATATCCTGATGCTG---AGTGAGCGGCACAC- [12016]
Oan CCTGAGCAC---------------------------------------------------- [12779]
Aca -----------GCTCCTTGTCCTCAACAATATCCTGGTGCTG---AGTGAGTGGCACTC- [14727]
Pbi CGTGGATAG--GTTCCTCCCCGTCAACAATATCCTGGTGCTG---AGTGAGTGGCACTC- [15251]
Cpi AAGCCCCTG--GCTTCTCCTCCCCAACAATATCCTGGTGCTG---AGTGAGTTGCACAC- [15878]
Cmy CATGGACAT--GCTTCCCCTCCCCAACAATATCCTGGTGCTC---AGTGAGTTGCACAC- [15626]
Psi CCTGGACAT---------------------------------------------------- [14372]
Asp CCTGGACAT---------------------------------------------------- [13613]
Ami CCTGGACAT--CTCCCGCCTCCCCAACAATATCCTGGTGCTG---AGCGAGTTGCGCAC- [15201]
Asi CCTGGACAT--CTCCCGCCTCCCCAACAATATCCTGGTGCTG---AGCGAGTTGCGCAC- [14461]
Tgu CCTGCACAT---------------------------------------------------- [11724]
Cli CCTGGTCAT--GCTCCTCCTGCCCAACAATATCCTGGTGCTG---AGTGAGTTGCAGAC- [14519]
Gga -----------GCTCCTCCTGCCCAACAATATCCTGGTGCTG---AGTGAGTTGCACAC- [13068]
Xtr -----------GTTTGTCCCCTGGAACAATATCCTGATGCTG---AATGAGTGGGACAT- [13600]
Lch CCTGGACAT--GTTCACCTGCTACAACAATATCCTGGTGCTG---AATGAGTGGGACTTG [15571]
Dre -----------GGTGTCTCCTGGCAACAATATCCTGGTGCTG---CCTGAGTACATCTC- [14106]

Hsa -GCGACTCCAGCATCAGTGATTTTGTTGAAGAGGGCAGCT-------------------- [14931]
Mmu --TGACTCCAGCATCAGTGATTTTGTTGAAGAGGGCAGCT-------------------- [14761]
Mdo GGAGACTCCAGCATCAGTGATTTTGTTGAAGAGGGTGGCT-------------------- [13814]
Meu AGAGACTCCAGCATCAGTGATTTTGTTGAAGAGGGTGGCT-------------------- [12056]
Oan ------------------------------------------------------------ [12779]
Aca AAAGACTCCAGCATCAGTGATTTTGTTGAAGAGGGTGAGC-------------------- [14767]
Pbi AGAGACTCCAGCATCAGTGATTTTGTTGAAGAGGGGGTGC-------------------- [15291]
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Cpi GGAGACTCCAGCATCAGTGATTTTGTTGAAGAGGGCGAGC--TTATTTCTGGCAACACTA [15936]
Cmy GGAGACTCCAGCATCAGTGATTTTGTTGAAGAGGGCGAGC--TTATTTCTGGCAACACTA [15684]
Psi ----------------------------------------TTATTTCTGGCAACACTA [14390]
Asp ----------------------------------------TTATTTCTGGCAACACTA [13631]
Ami AGAGACTCCAGCATCAGTGATTTTGTTGAGGAGGGCGAGC--TTATTTCTGGCAACACTA [15259]
Asi AGAGACTCCAGCATCAGTGATTTTGTTGAGGAGGGCGAGC--TTATTTCTGGCAACACTA [14519]
Tgu ----------------------------------------TTACTTCTAGCAACACTA [11742]
Cli AGAGACTCCAGCATCAGTGATTTTGTTGAGGAGGGGGTGC--TTACTTCTAGCAACACTA [14577]
Gga AGAGACTCCAGCATCAGTGATTTTGTTGAGGAAGGGGAGC--TTACTTCTAGCAGCACTA [13126]
Xtr ACATGCTCCAGCATCAGTGATTTTGTTGCAGGCGGCACAC--TTACTTCTGGCAACAATA [13658]
Lch GGAGACTCCAGCATCAGTGATTTTGTTGCGGAGGGTGATC--TTGCCTCTGACAACAATA [15629]
Dre ACAGACTCCAGCATCAGTGATTTTGTTGCCGGGGGAAAAC--TGCCTGCTGAGAACAATA [14164]

Hsa ---------------------------------------------------------- [14931]
Mmu ---------------------------------------------------------- [14761]
Mdo ---------------------------------------------------------- [13814]
Meu ---------------------------------------------------------- [12056]
Oan ---------------------------------------------------------- [12779]
Aca ---------------------------------------------------------- [14767]
Pbi ---------------------------------------------------------- [15291]
Cpi TCCTGATGCTGTCAGAGTATGTGGTA--AAGCTCCAGCATCAGTGATTTTGTTGTTAGTG [15994]
Cmy TCCTGATGCTGTCAGAGTATGTGGTA--AAGCTCCAGCATCAGTGATTTTGTTGTTAGTG [15742]
Psi TCCTGATGCTGTCAGAGTATGTGGTA--AAGCTCCAGCATCAGTGATTTTGTTGTTGGTG [14448]
Asp TCCTGATGCTGTCAGAGTGTGTGGTA--AAGCTCCAGCATCAGTGATTTTGTTGTTGGTG [13689]
Ami TCCTGATGCTGTCTGAGTATGTGGTA--AAGCTCCAGCATCAGTGATTTTGTTGTTAGTG [15317]
Asi TCCTGATGCTGTCTGAGTATGTGGTA--AAGCTCCAGCATCAGTGATTTTGTTGTTAGTG [14577]
Tgu TCCTGATGCTGTCAGAGTAAGTGGTA--AAGCTCCAGCATCAGTGATTTTGTTGTTAGTG [11800]
Cli TCCTGATGCTGTCAGAGTAAGTGGTA--AAGCTCCAGCATCAGTGATTTTGTTGTTAGTG [14635]
Gga TCCTGATGCTGTCAGAGTAAGTGGTA--AAGCTCCAGCATCAGTGATTTTGTTGTTAGTG [13184]
Xtr TCCTGATGCCGTCTGAGTGTGCGGGA--AAGCTCCAGCATCAGTGATTTTGTTGGTGGTG [13716]
Lch TCCTGGTGCTGTCCGAGTATGTGGAA--AAGCTCCAGCATCAGTGATTTTGTTGTTAGAG [15687]
Dre TCCTGATGCTGAATGAGTGTGTTGAAGGAAACTCCAGCATCAGTGATTTTGTTGCCAGAG [14224]

Hsa -------TTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATGAGTATCATAGG-- [14981]
Mmu -------TTTTGCTGTTATCAGGTGGAACACGATGCAA-TTTTGGTTGGTGTAATAGG-- [14811]
Mdo -------TTTTGCTGT-GTCGGGTGGATCACGATGCAAATTTTGATAAGTTTAATAGG-- [13864]
Meu -------GTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATAAGTTTAGTAGG-- [12106]
Oan -------TTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATTAGTTTAGTAGG-- [12829]
Aca -------TTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATTAGATTAGCAGG-- [14817]
Pbi -------TGTTGCTGTTGTCGGGTGGATCACGGTGCAA-TTTTGATTAGATTAGCAGG-- [15341]
Cpi GTAAA--TTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATTAGTTTAGCAGG-- [16049]
Cmy GTAAA--TTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATTAGTTTAGCAGG-- [15797]
Psi GTAAA--TTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATTAGTTTAGCAGG-- [14503]
Asp GTAAA--TTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATTAGTTTAGCAGG-- [13744]
Ami GTAAA---------------------------------------------------------- [15322]
Asi GTAAA--TTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATTAGTTTAGAAGG-- [14632]
Tgu GTAAA--TTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATTAGTTTAGTAGG-- [11855]
Cli GTAAA--TTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATTAGTTTAGTAGG-- [14690]
Gga GTAAA--TTTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTTGATTAGTTTAGTAGG-- [13239]
Xtr GTAAA--TTTTGTTGTTCGCGGGTGGATCACGATGCAA-TTTTATTTAGTTTGGTAGG-- [13771]
Lch GTGAA--TCTTGCTGTTGTCGGGTGGATCACGATGCAA-TTTT-TTT-GTTTTTGCGA-- [15740]
Dre GAGCAC---TTGCTGTTTTCGGGTGGATGACTCTGCAA-TTTTATTAGTGATGGAAAAAC [14280]

Hsa ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAGG--CCATTACTGTTGCTAATA [15035]
Mmu ---AGGAAAA-TTGCACGGTATCCATCTGTAAACCGCAGG--CCGTCACTGTTGCTAACA [14865]
Mdo ---AGAAAAAATTGCACGGTATCCATCTGTAAACCGCAAG--CCACTACTGTTGCTAACA [13919]
Meu ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAAG--CCACTACTGTTGCTAACA [12160]
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Oan ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAGG--CCATTACTGTTGCTAACA [12883]
Aca ---ACGAAAA-TTGCACGGTATCCATCTGTAAACCGCAGG--CCTTTACTGTTGCTAATG [14871]
Pbi ---ACGGAAA-TTGCACGGTATCCATCTGTAAACCGCAGG------------------- [15377]
Cpi ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAGG--CCACTACTGTTGCTAATA [16103]
Cmy ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAGG--CCACTACTGTTGCTAATA [15851]
Psi ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAGG--CCACTACTGTTGCTAACA [14557]
Asp ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAGG--CCACTACTGTTGCTAACA [13798]
Ami ----------------------------------------CTGCTACTGTTGCTAATA [15340]
Asi ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAGG--CTGCTACTGTTGCTAATA [14686]
Tgu ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAAG--CTAATACTGTTGCTAATA [11909]
Cli ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAAG--CTAATACTGTTGCTAATA [14744]
Gga ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAAG--CTAATACTGTTGCTAACA [13293]
Xtr ---AGAAAAA-TTGCACGGTATCCATCTGTAAACCGCAGA--CAGTTACTGTTGCCTATG [13825]
Lch ---TTTAAAA-TTGCACGGTATCCATCTGTAATCCGCTAG------------------- [15776]
Dre TTCAATAAAAATTGCACGGTATCCATCTGTAATCCGCTGG------------------- [14320]

Hsa TGCAA-CTCTGTTGAATATAAATTGGAATTGCACTTTAGCAATGGTGATGG--GGCCCTC [15092]
Mmu TGCAA-CTCTGTTGAATAGAAATTGGAATTGCACTTTAGCAATGGTGATGG--GGTCTTC [14922]
Mdo TGCAA-CTCTGTTCTATGTAAACGGGAATTGCACTTTAGCAATGGTGATGG--GACTCTC [13976]
Meu TGCAA-CTCTGTTATATGTAAACGGGAATTGCACTTTAGCAATGGTGATGG--CCCCTCC [12217]
Oan TGCAA-CTCTGTTATGTATAAACTGGAATTGCACTTTAGCAATGGTGATGG--------- [12933]
Aca TGCAA-CTCTGTTATGTATAATCTGGAATTGCACTTTAGCAATGGTGATGG--CTACTGC [14928]
Pbi ----------------------------------------------------CACTAGC [15384]
Cpi TGCAA-CTCTGTTGTGTAAAAGCTGGAATTGCACTTTAGCAATGGTGATGG--CAACCTC [16160]
Cmy TGCAA-CTCTGTTGTGTAAAAGCTGGAATTGCACTTTAGCAATGGTGATGG--CAACCTC [15908]
Psi TGCAA-CTCTGTTGTGTAAAAGCTGGAATTGCACTTTAGCAATGGTGATGG--CAACCTC [14614]
Asp TGCAA-CTCTGTTGTGTAAAAGCTGGAATTGCACTTTAGCAATGGTGATGG--------- [13848]
Ami TGCAA-CTCTGTTATGTCAAAATTGGAATTGCACTTTAGCAATGGTGATGG--CGCCCTC [15397]
Asi TGCAA-CTCTGTTACGTCAAAATTGGAATTGCACTTTAGCAATGGTGATGG--CGCCCTC [14743]
Tgu TGCAA-CTCTGTTGTATAAAAATTGGAATTGCACTTTAGCAATGGTGATGG--GCATCTC [11966]
Cli TGCAA-CTCTGTTGTATAAAAATTGGAATTGCACTTTAGCAATGGTGATGG--GCAACTC [14801]
Gga TGCAA-CTCTGTTGTATAAAAATTGGAATTGCACTTTAGCAATGGTGATGG--GCGACTC [13350]
Xtr TGCAAACTCTGTGCTATATTGTCTAGAATTGCACTGTAGCAATGGTGACTG--CCGGCTC [13883]
Lch ----------------------------------------------------GACTTTC [15783]
Dre ----------------------------------------------------ATAAAAC [14327]

Hsa CGCTCCC-GCCCCGCGACGAGCCCC-TCGCACAA-ACCGGACCTGAGCGTTTTGTTCGTT [15149]
Mmu CGCTCCG-GCCCCGCGACGAGCCCC-TCGCACAA-ACCGGACCTGAGCGTTTTGTTCGTT [14979]
Mdo CGCTCCC-GACCCGCGCCGAGCCCC-TCGCACAA-ACCGGACCTGAGCGTTTTGTTCGTT [14033]
Meu CGCTCCCCGGCCCGCGCCGAGCCCCCTCGCACAAAACCGGAC-TGAACGTATTGTTCGTT [12276]
Oan ------------------------------------------------------------ [12933]
Aca TGTGCTT-GCCTCGCGTCGAGCCCCACGCACAAG-ACCTGACGTGAATGTTTTGTTCGTT [14986]
Pbi TGGGCTT-GCCTCGCGTCGAGCCCCACGCACAAG-ACCTGACGTGAATGTTTTGTTCGTT [15442]
Cpi TGCACTT-GCCTGGCGTCGAGCCCCACGTGCAAG-ACCTGACGTGAACGTTTTGTTCGTT [16218]
Cmy TGCACTT-GCCTGGCGTCGAGCCCCACGTGCAAG-ACCTGACGTGAACGTTTTGTTCGTT [15966]
Psi TGCACTT-GCCTGGCGTCGAGCCCCACGTGCAAG-ACCTGACGTGAACGTTTTGTTCGTT [14672]
Asp ------------------------------------------------------------ [13848]
Ami TGCGCCT-GCCTGGCGTCGAGCCCGACGTGCAAG-ACCTGACGTGAATGTTTTGTTCGTT [15455]
Asi TGCGCCT-GCCTGGCGTCGAGCCCGACGTGCAAG-ACCTGACGTGAATGTTTTGTTCGTT [14801]
Tgu TGCACTT-GCCTGGCGTCGAGCCCCACGTGCAAT-ACCTGACCTGAACGTTTTGTTCGTT [12024]
Cli TGCACTT-GCCTGGCGTCGAGCCCCACGTGCAAG-ACCTGACCTGAACGTTTTGTTCGTT [14859]
Gga TGCACTT-GCCTGGCGTCGAGCCCCACGTGCAAG-ACCTGACCTGAACGTTTTGTTCGTT [13408]
Xtr CGCACTT-GCCTGACGCCGAGCCTGACGTGCAAT-GCTTTGTGTCAACGTTTTGTTCGTT [13941]
Lch TGCACTT-GCCTCACGTTGAGCCAGACTAACAAT-ACCTGAAGTCAAAGTTTTGTTCGTT [15841]
Dre TGCACTT-GCTTTACGTTGAGCCACACGCACAAT-ACATGTGGATTCAGTTTTGTTCGTT [14385]

Hsa CGGCTCGCGTGAGGCAGGGGCGGCCTC--CTCAGATCAGAAGGTGATTGTGGCTTTGGGT [15207]
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Mmu CGGCTCGCGTGAGGCAGGGGCGGCTTC--CTCAGATCAGAAGGTGACTGTGGCTTTGGGT [15037]
Mdo CGGCTCGCGTGAGGCGGAGGCGACCAG--CTCAGATCAGAAGGTGATTGTGGCTTTCGGT [14091]
Meu CGGCTCGCGTGAGGCGGAGGCGGTCTA-------------------------------- [12303]
Oan ----------------------------CTCAGATCAGAAGGTGATTGTGGCTTTGGGT [12964]
Aca CGGCTCGCGTTAGGCAGGTCCAGCCTA--CTCAGATCAGAAGGTGATTGTGGCTTTGCTT [15044]
Pbi CGGCTCGCGTTAGGCAGGTCCAGCCTG--CTCAGATCAGAAGGTGATTGTGGCTTTGGTT [15500]
Cpi CGGCTCGCGTTAGGCAGGTCCAGCCTG--CTCAGATCAGAAGGTGATTGTGGCTTTGAGT [16276]
Cmy CGGCTCGCGTTAGGCAGGTCCAGCCTG--CTCAGATCAGAAGGTGATTGTGGCTTTGAGT [16024]
Psi CGGCTCGCGTTAGGCAGGTCCAGCCTG--CTCAGATCAGAAGGTGATTGTGGCTTTGACT [14730]
Asp ----------------------------CTCAGATCAGAAGGTGATTGTGGCTTTGAGT [13879]
Ami CGGCTCGCGTTAGGCAGGCCCAGCCTG--CTCAGATCAGAAGGTGATTGTGGCTTTGAGT [15513]
Asi CGGCTCGCGTTAGGCAGGCCCAGCCTG--CTCAGATCAGAAGGTGATTGTGGCTTTGAGT [14859]
Tgu CGGCTCGCGTTAGGCAGGTCCAGCCCA--CTCAGATCAGAAGGTGATTGTGGCTTTGAGT [12082]
Cli CGGCTCGCGTTAGGCAGGTCCAGCCCA--CTCAGATCAGAAGGTGATTGTGGCTTTGAAT [14917]
Gga CGGCTCGCGTTAGGCAGGTCCAGCCTG--CTCAGATCAGAAGGTGATTGTGGCTTTGGGT [13466]
Xtr CGGCTCGCGTTAAGCAGGTGCGGCTTG--CTCAGATCAGAAGGTGATTGTGGCTTTTAGT [13999]
Lch CGGCTCGCGTTACGCAGGTACAGTTTC-------------------------------- [15868]
Dre CGGCTCGCGTTAAGCAAGTGCAGAACT-------------------------------- [14412]

Hsa GGATATTAATCAGCCACAGCACTGCCTGGTCAGAAAGAG--AAAGCGCTTTGGAATGACA [15265]
Mmu GGATATTAATCAGCCACAGCACTGCCTGGTCAGAAAGAG--AAAGTGCTTTGGAATGACA [15095]
Mdo AGACATGGAACAGCCACATCACTGGCTGGTCAGAAAGAG--AAAGTGCTTTGGAATGACA [14149]
Meu ----------------------------------------AAAGCGCTTTGGAATGACA [12322]
Oan AGCTACTAAGCAGCCACAACACTGCCTGGTCAGAAAGAG--AAATCGCTTTGGAATGACA [13022]
Aca TTATATGAAACAGCCACAGCACTGCCTGGTCAGAAAGAG--GAATGGTTTTGGAATGACA [15102]
Pbi TGATATGAAACAGCCACAGCACTGCCTGGTCAGAAAGAG--AAATTGCCGAGGAATGACA [15558]
Cpi AGATATTAAGCAGCCACAGCACTGCCTGGTCAGAAAGAG--AAATTGCTTTGGAATGACA [16334]
Cmy AGATATTAAGCAGCCACAGCACTGCCTGGTCAGAAAGAG--AAATTGCTTTGGAATGACA [16082]
Psi AGATACTAAGCAGCCACAGCACTGCCTGGTCAGAAAGAG---------------------- [14769]
Asp AGATACTAAGCAGCCACAGCACTGCCTGGTCAGAAAGAG---------------------- [13918]
Ami AGATATTAAGCAGCCACAGCACTGCCTGGTCAGAAAGAG--AGATTGCTTTGGAATGACA [15571]
Asi AGATATTAAGCAGCCACAGCACTGCCTGGTCAGAAAGAG--AGATTGCTTTGGAATGACA [14917]
Tgu AAATATTAAGCAGCCACAGCACTGCCTGGTCAGAAAGAG--AGATGGCTTTGGAATGACA [12140]
Cli AGCTATTAAGCAGCCACAGCACTACCTGGTCAGAAAGAG--AGACGGCTTTGGAATGACA [14975]
Gga AAATATTGAGCAGCCACAGCACTGCCTGGTCAGAAAGAG--AGACAGCTTTGGAATGACA [13524]
Xtr AGATATTAAGCAGCCACAGCACTGCCTGGTCAGAAAGAG--ACTTAGCCTTGGAATGACA [14057]
Lch ---------------------------------------------------------- [15868]
Dre ---------------------------------------------------------- [14412]

Hsa CGATCACTCCCGTTGAGTGGGCACCCGAGAAGCCATCGGGAATGTCGTGTCCGCCCAGTG [15325]
Mmu CGATCACTCCCGTTGAGTGGGCACCCAAGAAGCCATCGGGAATGTCGTGTCCGCCCAGTG [15155]
Mdo CGATCACTCCCGTTGAGCGGACAGCCAAGAAGCCATCGGGAATATCGTGTCCGTCCAATG [14209]
Meu CGATCACTCCCGTTGAGCGGACAGCCAAGAAGCCATCGGGCATATCGTGTCTGTCCAATG [12382]
Oan CGATCACTCCCGTTGAGCGGACAGCCAAGAAGCCATCGGGAATATCGTGTCCGTCCAAAG [13082]
Aca CGATCACTCCCGCTGAGCGAGCAGAGCCACGGCCA-CGGGGATGTCGTGTCTGTCCAAAA [15161]
Pbi CGATCACTCCCGCTGAGCGAGTGGACGCAGAGCCA-CGGGGCTGTCGTGTCTGTCCTGAG [15617]
Cpi CGATCACTCCCGCTGAGCAAGCAGCCAGA--GCCATCGGGAATATCGTGTCCGTCCAAAG [16392]
Cmy CGATCACTCCCGCTGAGCGAGCAGCCAGAGAGCCATCGGGAATGTCGTGTCCGTCCAAAG [16142]
Psi ---------------------------------------------------------- [14769]
Asp ---------------------------------------------------------- [13918]
Ami CGATCACTCCCGCTGAGCGAGACGCCCGACAGCCATCGGGAATATCGTGTCGGTCCAAAG [15631]
Asi CGATCACTCCCGCTGAGCGAGACGCCCGACAGCCATCGGGAATATCGTGTCCGTCCAAAG [14977]
Tgu CGATCACTCCCGCTGAGCCAGCAGCCAGAGAGCCATCGGGGATGTCGTGTCTTTCCAAAG [12200]
Cli CGATCACTCCCGCTGAGC-GGGCAGCCTGAGGCCATCGGGGATGTCGTGTCTGTCCAAAG [15034]
Gga CGATCACTCCCGCTGAGCACGCAGCCAGAGAGCCATCGGGGATGTCGTGTCTGTCCTAAG [13584]
Xtr CGATCACTCCCGTTGAGCCGAAACTCACAGCGCCATCGGGAATATCGTGTCGCTCCAAAG [14117]
Lch ---------------------------------------------------------- [15868]
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Dre ------------------------------------------------------------ [14412]

Hsa CTCTTTCGGC--CCACCACTTAAACGTGGATGTACTTGCTTTGAAACTAAAGA-AGTAAG [15382]
Mmu CTCTTTCGGC--CCACCACTTAAACGTGGTTGTACTTGCTTTAGACCTAAGAA-AGTAAG [15212]
Mdo CTCTTTCAGC--CCACTACTTAAACGTGGATTTACTTGCTTTGTTTCTAAAAA-AGTAAG [14266]
Meu CCCTTTCGGC--CCACCACTTAAACGTGGATTTACTTGCTTTGTTTCTAAAAA-AGTAAG [12439]
Oan CTCTTTCGGG--CTGTCACTTAAACGTGGATAAACTTGCTTTACTTTTAA----AGTAAG [13136]
Aca CTATTTCAAA--CCACTACTTTAATATGAAAGTACTTGTTTTTGTTCCTTTT--AAAAAG [15217]
Pbi CTTTTTCCAA---------------------------------------------------- [15627]
Cpi CTTTTTCGGC--CCACTACTTTAATGTGGAAGTACTTGCTTTGCTCCTGATAA-AGTAAG [16449]
Cmy CTCTTTCGGC--CCACTACTTTAATGTGGAAGTACTTGCTTTGCTCCTGAAAA-AGTAAG [16199]
Psi ------------CCACTACTTTAATGTGGAAGTACTTGCTTTGCTCCTGAAAA-AGTAAG [14816]
Asp ------------CCACTACTTTAATGTGGAAGTACTTGCTTTGCTCCTGAAAA-AGTAAG [13965]
Ami CTCTTTCGGC--CCAGAACTTTAATGTGGATGTACTTGCTTTGTTTCTGAAAA-AGTAAG [15688]
Asi CTCTTTCGGC--CCAGAACTTTAATGTGGATGTACTTGCTTTGTTTCTGAAAA-AGTAAG [15034]
Tgu CTCTTTCGGC--CCACAACTTAAATGTGGACGTGCTTGCTTTGGCTCACAACA--GTAAG [12256]
Cli CTCTTTCGGT--CCATAACTTAAATGTGGATGTACTTGCTTTGTTCCTGAAAA--GTAAG [15090]
Gga CTCTTTCTGC--CCACAACTTAAATGTGGATGTGCTTGCTTTGTT-CTGAAAA--GAAAG [13639]
Xtr CTCTCTCTTC--CCACTACTTTAACATTGGTGTACTTTCTATGTCTTTAAAAAGGGTAAG [14175]
Lch ------------------------------------------------------------ [15868]
Dre ------------------------------------------------------------ [14412]

Hsa TGCTTCCATGTTTTGGTGATGG--CTTCAACTTTAACATGGAAGTGCTTTCTGTGACT-T [15439]
Mmu TGCTTCCATGTTTTGGTGATGG--CTTCAACTTTAACATGGGAATGCTTTCTGTCTCA-T [15269]
Mdo TGCTTCCATGTTTTAGTGATGG--CTTCTACTTTAACATGGAGGTACTTTCTGTG--T-T [14321]
Meu TGCTTCCATGTTTTAGTGATGG---------------------------------------- [12461]
Oan TGCTTCCATGTTTTAGTGATGG--CTTCTACTTTAACATGGAGGTGCTTTCTGTG-AT-T [13192]
Aca TGCTTTCATATTTTAGTGATGG--CTTCTACTTTAACATGGAGGTGCTTTCTGTGCAT-A [15274]
Pbi ------------------------------------------------------------ [15627]
Cpi TGCTTCCATGTTTTAGTGATGG--CTTCTACTTTAACATGGAGGTGCTTTCTGTGACT-A [16506]
Cmy TGCTTCCATGTTTTAGTGATGG--CTTCTACTTTAACATGGAGGTGCTTTCTGTGACT-A [16256]
Psi TGCTTCCATGTTTTAGTGATGG--CTTCTACTTTAACATGGAGGTGCTTTCTGTGACT-A [14873]
Asp TGCTTCCATGTTTTAGTGATGG--CTTCTACTTTAACATGGAGGTGCTTTCTGTGACT-A [14022]
Ami TGCTTCCATGTTTTGGTGCTGG--CTTCTACTTTAACATGGAGGTGCTTTCTGTGACTTA [15746]
Asi TGCTTCCATGTTTTAGTGCTGG--CTTCTACTTTAACATGGAGGTGCTTTCTGTGACTTA [15092]
Tgu TGCTTCCATGTTTTAGTGGTGG--CTTTTACTTTACCATGGAGGTGCTTTCTGTGACATA [12314]
Cli TGCTTCCATGTTTTGGTGATGG--CTTTTACTTTAACATGGAGGTGCTTTCTGTGACTTA [15148]
Gga TGCTTCCATGTTTTAGTGATGG--CTTTTACTTTAACATGGAGGTGCTTTCTGTGATTTT [13697]
Xtr TGCTCCAATGTTTTAGTGGTGG---------------------------------------- [14197]
Lch ------------------------------------------------------------ [15868]
Dre ------------------------------------------------------------ [14412]

Hsa T-AAA------AGTAAGTGCTTCCATGTTTTAGTAGGAG--CCTTTGCTTTAACATGGGG [15490]
Mmu CGAAG------AGTAAGTGCTTCCATGTTTTAGTAGAAG--CCTCTGCTTTAACATGGGG [15321]
Mdo TAAAAA-----GGTAAGTGCTTCCATGTTTTGGTAGGAG--TCTCTGCTTTAACATGGGG [14374]
Meu ----------------------------------------TCTCTGCTTTAACATGGGG [12480]
Oan TAAAA------AGTAAGTGCTTCCATGTTTTAGTAGAGG--CCTTTGCTTTAACATGGGG [13244]
Aca TAAAA------AGTAAGTGCTTCCATGTTTTAGTAGAGG---------------------- [15307]
Pbi ------------------------------------------------------------ [15627]
Cpi TAAAA------AGTAAGTGCTTCCATGTTTTAGTAGAGG--CCTTTGCTTTAACATGGGG [16558]
Cmy TAAAA------AGTAAGTGCTTCCATGTTTTAGTAGAGG--TCTTTGCTTTAACATGGGG [16308]
Psi TAAAA------AGTAAGTGCTTCCATGTTTTAGTAGAGG--CCTTTGCTTTAACATGGAG [14925]
Asp TAAAA------AGTAAGTGCTTCCATGTTTTAGTAGAGG--CCTTTGCTTTAACATGGAG [14074]
Ami TAAGA------AGTAAGTGCTTCCATGTTTTAGTAGAGG--CCTTTGCTTTAACATGGAG [15798]
Asi TAAGA------AGTAAGTGCTTCCATGTTTTAGTAGAGG--CCTTTGCTTTAACATGGAG [15144]
Tgu GAAAA------AGTAAGTGCTTCCATGTTTTAGTAGAGG--CCTTTGCTTTAACATGGAG [12366]
Cli AAAGA------AGTAAGTGCTTCCATGTTTTAGTAGAGG--CCTTTGCTTTAACATGGAG [15200]
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Gga ACAAA------AGTAAGTGCTTCCATGTTTTAGTAGAGG--CCTCCGCTTTAACATGGAG [13749]
Xtr ---------------------------------------------------------- [14197]
Lch ----------------------------------------TTGTTGCTCTAACA--GGA [15885]
Dre ---------------------------------------------------------- [14412]

Hsa GTACCTGCTGTGTGAAACAAAAGTAAGTGCTTCCATGTTTCAGTGGAGG--CCTCTACTT [15548]
Mmu TTACCTGCTGTGTTAAACAAAAGCAAGTGCTTCCATGTTTCAGTGGGGG--CCTTTACTT [15379]
Mdo GTACCTGCTACGTAATA-AAAAGTAAGTGCTTCCATGTTTCAGTGGAGA--CCTCTGCTT [14431]
Meu GTACCTGCTACGTAATAAAAAAGTAAGTGCTTCCATGTTTCAGTGGAGG--CTTCTACTT [12538]
Oan GTACCTGCTACGTAAG--AAAAGTAAGTGCTTCCATGTTTCAGTGGAGG--CTTCTCCTT [13300]
Aca ---------------------------------------------------------- [15307]
Pbi ---------------------------------------------------------- [15627]
Cpi GTACCTGCTGCCTAGAAA--AAGTAAGTGCTTCCATGTTTCAGTCGTGG--CCTCTACTT [16614]
Cmy GTACCTGCTGCCTAGAA------AAAGTGCGTCTATGTTTCAGTGGTGG--CCTCTACTT [16360]
Psi GTACCTGCTGCCTAGAAA--AAGTAAGTGCTTCCATGTTTCAGTGGTGG--CCTCTACTT [14981]
Asp GTACCTGCTGCCTAGAAA--AAGTAAGTGCTTCCATGTTTCAGTGGTGG--CCTCTACTT [14130]
Ami GTACCTGCTGCCTAAAAA--AAGTAAGTGCTTCCATGTTTCAGTGGTGG--CCTCTACTT [15854]
Asi GTACCTGCTGCCTAAAAA--AAGTAAGTGCTTCCATGTTTCAGTGGTGG--CCTCTACTT [15200]
Tgu GTACCTGCTGCCTAAAAA---AGTAAGTGCTTCCATGTTTCAGTGGCGG--CCTCTACTT [12421]
Cli GTACCTGCTGCTTAGAA---AAGTAAGTGCTTCCATGTTTCAGTGGCGG--CCTCTACTT [15255]
Gga GTACCTGCTGCCTACAA---AAGTAAGTGCTTCCATGTTTCAGTGGTGG--CCTCAACTT [13804]
Xtr ---------------------------------------------------------- [14197]
Lch GTACATACTGTTGTGAACTTAAGTAAGTGCTTCCTTGTTAGGGTAATGG---------- [15934]
Dre ---------------------------------------------------------- [14412]

Hsa TAACATGG-AGGCACTTGCTGTGACATGACAAAAA--TAAGTGCTTCCATGTTTGAGT-G [15604]
Mmu TAACATGG-AGGCACTTGCTGTGCATTTAAAAA----TAAGTGCTTCCATGTTTGAGT-G [15433]
Mdo TAACATGG-AAGTGCTTGCTGTGATTTTAAAAAAT--TAAGTGCTTCCATGTTTGAGTTG [14488]
Meu TAACATGG-AGGTACTTTCTGTGATTAAAAAAAAG--TAAGTGCTTCCATGTTTTGGTAG [12595]
Oan TAACATGG-AGGTGCTTGCTGTGAGTTTGAAAAAT--TAAGTGCTTCCATGTTTTAGTTG [13357]
Aca ---------------------------------------------------------- [15307]
Pbi ---------------------------------------------------------- [15627]
Cpi TAACATGG-AAGTACTTGCTGGATGCTTGAAAAAG--TAAGTGCTTCCATGTTTTAGTTG [16671]
Cmy TAACATGG-AAGTACTTGCTGGATGCTTGAAAAAG--TAAGTGCTTCCATGTTTTAGTTG [16417]
Psi TAACATGG-AAGTACTTGCTGGATGCTTGAAAAAG--TAAGTGCTTCCATGTTTTAGTTG [15038]
Asp TAACATGG-AAGTACTTGCTGGATGCTTGAAAAAG--TAAGTGCTTTCATGTTTTAGTTG [14187]
Ami TAACATGGGAGGTACTTGCTGGATGCTTGAAAAAG--TAAGTGCTTCCATGTTTTAGTTG [15912]
Asi TAACATGGGAGGTACTTGCTGGATGCTTGAAAAAG--TAAGTGCTTCCATGTTTTAGTTG [15258]
Tgu TAACATGG-AGGTACTTGCTGGATGCCT-AAAAAG--TAAGTGCTTCCATGTTTTAGTTG [12477]
Cli TAACATGGGAGGTACTTGCTGGATGCCTAAAAAAG--TAAGTGCTTCCATGTTTTAGTTG [15313]
Gga TAACATGG-AGGTACTTGCTGGACACCTGAAAAAG--TAAGTGCTTCCATGTTTTAGTTG [13861]
Xtr ---------------------------------------------------------- [14197]
Lch ---------------------------------------------------------- [15934]
Dre ---------------------------------------------------------- [14412]

Hsa TGG--CTTGGGAATGGCAAGGAAACCGTTACCATTACTGAGTTTAGTAATGGTAATGGTT [15662]
Mmu TGG--CTTGGGAATGGCGAGGAAACCGTTACCATTACTGAGTTTAGTAATGGTAACGGTT [15491]
Mdo TGG--GGGCAGCCTGGCGGGGAAACCGTTACCATTACTGTGTTTAGTAATGGTAAGGGTT [14546]
Meu GAG--ATGGAGCGTGGGGAGGAAACCGTTACCATTACTGTGTTTAGTAATGGTAACGGTT [12653]
Oan AAG--CGAGGGTCTGGCGAGGAAACCGTTACCATTACTGAGTTTAGTAATGGTAACGGTT [13415]
Aca -----GACCGGTGTGTTGGCGAAACCGTTACCATTACTGAGTTTAGTAATGGTAAGGGTT [15362]
Pbi ---------------------------------------------------------- [15627]
Cpi TGG--CCATGGGGCGTCAATGAAACCGTTACCATTACTGACTTTAGTAATGGTAACGGTT [16729]
Cmy TGG--CCATGGAGTGTCAATGAAACCGTTACCATTACTGACTTTAGTAATGGTAACGGTT [16475]
Psi TGG---------------------------------------------------------- [15041]
Asp TGG---------------------------------------------------------- [14190]
Ami TGG---------------------------------------------------------- [15915]
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Asi TGG--CCCCGGGGCGTCGGGGAAACCGTTACCATTACTGAGTTTAGTAATGGTGACGGTT [15316]
Tgu TGG--CCCGCGGCCGGCGGGGAAACCGTTACCATTACTGAGTTTAGTAATGGTAACGGTT [12535]
Cli TGG--CCCGCGGCCGGCGGGGAAACCGTTACCATTACTGTGTTTAGTAATGGTAATGGTT [15371]
Gga TGG--CACATGGCTGGCAGGGAAACCGTTACCATTACTGAGTTTAGTAATGGTAACGGTT [13919]
Xtr -----CTGTAGAGTGGCAATGAAACCGTTACCATTACTGAGTTTAGTAATGGTAAGGGTT [14252]
Lch -----TGGGGAAGTGCCAATCAAACCGTTACCATTACTGAATTTAGTAATGGTAAGGGTT [15989]
Dre -----ACAGAGAGAGGCGGCGAAACCGTTACCATTACTGAGTTTAGTAATGGTAAGGGTT [14467]

Hsa CTCTTGCTATACCCAGA--CCAGATCCTAGAACCCTATCAATATTGTCTCTGCTGTGTAA [15720]
Mmu CTCTTGCTGCTCCCACA---------------------------------------------- [15508]
Mdo CTCCCGCTGCGCTGAGT--ATAGATCCATGAACCCTATCAATGTGGTCTCTGCTGTGTAC [14604]
Meu CTCTTGCTGCGCTTGGT--CCAGATCCTAGAACCCTATCGATATTGTCTCTGCTGTGTAC [12711]
Oan CTCTGGCTGGGCCCACC--CCAGATCCTGGAACCCTATCGATATTGTCTCTGCTGTGTAA [13473]
Aca CTTCTATCACGCCGACT---------------------------------------------- [15379]
Pbi ------------------------------------------------------------ [15627]
Cpi CTACTGCCGCCCCAGCA---------------------------------------------- [16746]
Cmy CTACTGCCACGCCAGCA---------------------------------------------- [16492]
Psi ------------------------------------------------------------ [15041]
Asp ------------------------------------------------------------ [14190]
Ami ------------------------------------------------------------ [15915]
Asi CTACCGCCGCCTCGCCT---------------------------------------------- [15333]
Tgu CTGCCGACGGCCGGCAA---------------------------------------------- [12552]
Cli CTGCCGACGGCTGGGCG---------------------------------------------- [15388]
Gga CTGCTGACAGCCAGGCA---------------------------------------------- [13936]
Xtr CTGTTGCTGCTCTTCCA---------------------------------------------- [14269]
Lch CTGTTGCTATTCCCACT--CCAGATCCTGGAACCCTATCAATGTTGCCTCTGCTGTGTAG [16047]
Dre CTGCTGCCTTTTCTCAA--CTAATTCTTGGGACCCTATCAGTATTGCCTCTGCTGTCCAC [14525]

Hsa ATAGTTCTGAGTAGTGCAATATTGCTTATAGGGTTTTGGTGTTTGG-------------- [15766]
Mmu ------------------------------------------------------------ [15508]
Mdo ATAGCTGTAAGTAGTGCAATATTGCTTATAGGGTTTTAGTTTTTGG-------------- [14650]
Meu ATAGCTGTGAGTAGTGCAATATTGCTTATAGGGTTTTAGTGTTTGG-------------- [12757]
Oan ATAGCTGTGAGTAGTGCAATATTGCTTATAGGGTTTTAGTGTTTGG-------------- [13519]
Aca ----------------------------------------------AACTCTGAGGAT [15391]
Pbi ----------------------------------------------AACTCTGAGGAT [15639]
Cpi ----------------------------------------------AACCTTAAGGAA [16758]
Cmy ----------------------------------------------AACCTTAAGGAA [16504]
Psi ----------------------------------------------ACCCTTAAGGAA [15053]
Asp ----------------------------------------------ACCCTTAAGGAA [14202]
Ami ----------------------------------------------AACCTTAAGGAT [15927]
Asi ----------------------------------------------AACCTTAAGGAT [15345]
Tgu ----------------------------------------------AACCTTAAGGAT [12564]
Cli ----------------------------------------------AACCTTAAGGAT [15400]
Gga ----------------------------------------------AACCTTAAGGAT [13948]
Xtr ----------------------------------------------AGCCTTAAGGAA [14281]
Lch ATGGCTGAGAGTAGTGCAATATTGCTTATAGGGTTTTAGTGTTTGG--ATCCTCAAAGAA [16105]
Dre TGTGTTCAGAGTAGTGCAATATTGCTAATAGGGTTTTAGGTTTTAG--CATCTTGCAGGC [14583]

Hsa ------------------------------------------------------------ [15766]
Mmu ------------------------------------------------------------ [15508]
Mdo ------------------------------------------------------------ [14650]
Meu ------------------------------------------------------------ [12757]
Oan ------------------------------------------------------------ [13519]
Aca AAGACCCTATCAATATTGCCTCTGCTTCTGTGCTGGATT--CAAGTAGTGCAATATTGCT [15449]
Pbi AAAACCCTATCAATATTGCCTCTGCTTCTTCACTCGGTC--TTAGTAGTGCAATATTGCT [15697]
Cpi GAGACCCTATCAATATTGCCTCTGCTTTTGTGATCAGG---GTAGTAGTGCAATATTGCT [16815]
Cmy GAGACCCTATCAATATTGCCTCTGCTTTTGTGATCAGG---GTAGTAGTGCAATATTGCT [16561]
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Psi GAGACCCTATCAATATTGCCTCTGCTTTTGTGATCAGG---GTAGTAGTGCAATATTGCT [15110]
Asp GAGACCCTATCAATATTGCCTCTGCTTTTGTGATCAGG---GTAGTAGTGCAATATTGCT [14259]
Ami AAGACCCTATCAATATTGCCTCTGCTTTTGTGATCAGG---GTAGTAGTGCAATATTGCT [15984]
Asi AAGACCCTATCAATATTGCCTCTGCTTTTGTCATCAGG---GTAGTAGTGCAATATTGCT [15402]
Tgu GAGACCCTATCAATATTGCCTCTGCTTTTGTGATCAGG---GTAGTAGTGCAATATTGCT [12621]
Cli GAGACCCTATCAATATTGCCTCTGCTTTTGTGATCAGG---GTAGTAGTGCAATATTGCT [15457]
Gga GAGACCCTATCAATATTGCCTCTGCTTTTGTGCTCAGG---GTAGTAGTGCAATATTGCT [14005]
Xtr GTGACCCTATCAATATTGCCTCTGCTTTTGTGCTCGGA---GTAGTAGTGCAATATTGCT [14338]
Lch AAGACCCTATCAATACTGCCTCTGCTTTTAGAAATAGT---GGAGTAGTGCAATATTGCT [16162]
Dre GAGACCCTATCAATATTGCCTCTGCTTTTCTCACTGTTTATGGAGTAGTGCAATATTGCT [14643]

Hsa ----------------------CCCTGGCGTGAGGGTATGTGCCTTTGGACTACATCGT [15803]
Mmu ----------------------CCCTGGTGTGAGCGTATGTGCCTTTGGACTACATCGT [15545]
Mdo ----------------------CCCTGGCGTGAGGGTATGTGCCCTTGGACTACATCGT [14687]
Meu ------------------------------------------------------------ [12757]
Oan ------------------------------------------------------------ [13519]
Aca TATAGGGTCTTTTCTTTGGGG--CCCTGGCGTGGGGGTATGTGCCCTTGGACTACATCGT [15507]
Pbi AATAGGGTCTTTTCTTTGGGG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [15755]
Cpi TATAGGGTCTTTTCTTTGGAG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [16873]
Cmy TATAGGGTCTTTTCTTTGGAG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [16619]
Psi TATAGGGTCTTTTCTTTGGAG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [15168]
Asp TATAGGGTCTTTTCTTTGGAG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [14317]
Ami TATAGGGTCTTTTCTTTGGAG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [16042]
Asi TATAGGGTCTTTTCTTTGGAG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [15460]
Tgu TATAGGGTCTTTTCTTTTGAG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [12679]
Cli TATAGGGTCTTTTCTTTTGAG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [15515]
Gga TATAGGGTCTTTTCTTTTGAG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [14063]
Xtr TATAGGGTCTTTTCCTTGAGA--CCCTGGCGTGAGGGTATGTGCCCTTGGACTACATCGT [14396]
Lch TATAGGGTCTTGAATTTGAGG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [16220]
Dre TATAGGGTCTTGACTTTAAGG--CCCTGGTGTGAGGGTATGTGCCCTTGGACTACATCGT [14701]

Hsa GGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG------------- [15850]
Mmu GAACGC-AGCACCATGCAGTCCACGGGCATATACACTTGCCTCAAGG------------- [15591]
Mdo GGAAGCCAACACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG------------- [14734]
Meu ------------------------------------------------------------ [12757]
Oan ------------------------------------------------------------ [13519]
Aca GGGAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGTATGTGTGA [15565]
Pbi GGAAAATATCACCATGCAGTCCATGGGCATATACACTTGCCCCAAGG--TGTATGTGTGC [15813]
Cpi GGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGTATGTGTGA [16931]
Cmy GGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGTATGTGTGA [16677]
Psi GGAAACCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGCATGTGTGA [15226]
Asp GGAAACCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGCATGTGTGA [14375]
Ami GGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGTATGTGTGA [16100]
Asi GGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGTATGTGTGA [15518]
Tgu GGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGTGTGTGTGA [12737]
Cli GGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGCGTGTGTGA [15573]
Gga GGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGCGTGTGTGA [14121]
Xtr GGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGTGTGTGTGA [14454]
Lch GGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGTGTGTGTGT [16278]
Dre GGAAGCCAGCACCATGCAGTCCATGGGCATATACACTTGCCTCAAGG--TGGTTGTGTGT [14759]

Hsa ------------------------------------------------------------ [15850]
Mmu ------------------------------------------------------------ [15591]
Mdo ------------------------------------------------------------ [14734]
Meu ------------------------------------------------------------ [12757]
Oan ------------------------------------------------------------ [13519]
Aca GCAGGCATCTTCTCAGCCTACATGTGGATTCCTAAATCTGCAGGCTGGTTAGATGGTTGT [15625]
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Pbi GCAGGCATCTTCTCAGCCTACATGTGGATTCTTAAATCTGCAGGCTGGTTAGATGGTTGT [15873]
Cpi GCAGGCATCTTTTCAGCCTACATGTGGATTCCTAAATCTGCAGGCTGGTTAGATGGTTGT [16991]
Cmy GCAGGCATCTTCTCAGCCTACATGTGGATTCCTAAATCTGCAGGCTGGTTAGATGGTTGT [16737]
Psi GCAGGCATCTTCTCAGCCTACATGTGGATTCCTAAATCTGCAGGCTGGTTAGATGGTTGT [15286]
Asp GCAGGCATCTTCTCAGCCTACATGTGGATTCCTAAATCTGCAGGCTGGTTAGATGGTTGT [14435]
Ami GCAGGCATCTTCTCAGCCTACATGTGGATTCTTAAATCTGCAGGCTGGTTAGATGGTTGT [16160]
Asi GCAGGCATCTTCTCAGCCTACATGTGGATTCTTAAATCTGCAGGCTGGTTAGATGGTTGT [15578]
Tgu GCAGGCATCTTCTCAGCCTACATGTGGATTCCTAAATCTGCAGGCTGGTTAGATGGTTGT [12797]
Cli GCAGGCATCTTCTCAGCCTACACGTGGATTCCTAAATCTGCAGGCTGGTTAGATGGTTGT [15633]
Gga GCAGGCATCTTCTCAGCCTACATGTGGATTCCTAAATCTGCAGGCTGGTTAGATGGTTGT [14181]
Xtr GCAGGCATCTTCTCAGCCTACATGTAGATTGTCAAATCTGCAGGCTGGTTAGATGGTTGT [14514]
Lch GCAGGCATCTTCCCAGCCTACATGTGGATTCCTAAATCTGCAGGCTGGTTAGATGGTTGT [16338]
Dre GCAGGCATCTTTCCAGTCTACATGTGGATCCAGGAGTCTGCAGGCTGGTTAGATGGTTGT [14819]

Hsa ---------------------------------------------------------- [15850]
Mmu ---------------------------------------------------------- [15591]
Mdo ---------------------------------------------------------- [14734]
Meu ---------------------------------------------------------- [12757]
Oan -----------CTCGGTGCAGATGGCAGCGCCATTTTCAGAGCTATAAACAGTATCATTG [13568]
Aca CATACATTC--CATGGTGCAGATGGCAGCGCCATTTTTGGAGCTATAAACACTCTCACTG [15683]
Pbi CATACATTC--CATGGTGCAGATGGCAGCGCCATTTTCAGAGCTATAAACAGTATCATTG [15931]
Cpi CATACGTTC--CATGGTGCAGATGGCAGCGCCATTTTCAGAGCTATAAACAGTATCATTG [17049]
Cmy CATACGTTC--CATGGTGCAGATGGCAGCGCCATTTTCAGAGCTATAAACAGTATCATTG [16795]
Psi CATACGTTC--CATGGTGCAGATGGCAGCGCCATTTTCAGAGCTATAAACAGTATCGTTG [15344]
Asp CATACGTTC--CATGGTGCAGATGGCAGCGCCATTTTCAGAGCTATAAACAGTATAGTTG [14493]
Ami CATACATTC--CATGGTGCAGATGGCAGCGCCATTTTCAGAGCTATAAACAGTATCATTG [16218]
Asi CATACATTC--CATGGTGCAGATGGCAGCGCCATTTTCAGAGCTATAAACAGTATCATTG [15636]
Tgu CATGCATTC--CGTGGTGCCGATGACAGCGCCATTTCCAGAGCTATCAACAGTGTCATTG [12855]
Cli CATGCATTC--CGTGGTGCAGATGGCAGCGCCATTTCCAGAGCTATAAACAGTCTCATTG [15691]
Gga CATGCATTC--CGTGGTGCAGATGGCAGCGCCATTTTCAGAGCTATAAACAGCGTCATTG [14239]
Xtr CATACATTC---------------------------------------------------- [14523]
Lch CGTACATTC--CGAGGTGCAGATGGCAGTGCCATTTGCAAAGCTATAAACAGTATCATTG [16396]
Dre CACGTACCC--TGTGGTGCAGATAGCAGCGCCATTTACAGAGCTATAAGCATCATAGTTG [14877]

Hsa ----------------------------------TTATTTGCAGTCAGTAACAAAGA [15873]
Mmu ----------------------------------TTATTTGCAATCAGTAACAAAGA [15614]
Mdo ---------------------------------------------------------- [14734]
Meu ---------------------------------------------------------- [12757]
Oan CCATAGCTCTTTGAATGGTACTGCCATATGTACTG--TTTCTTGCAGTCAGTAACAAAGA [13626]
Aca TCATAGCTCTTTGAATGGTACTGCCATATGTACCG------------------------ [15718]
Pbi TCATAGCTCTTTGAATGGTACTGCCGTATGTACCG------------------------ [15966]
Cpi TCATAGCTCTTTGAATGGTACTGCCATATGTACTG--TTTCTTGTAATCAGTAACAAGGA [17107]
Cmy TCATAGCTCTTTGAATGGTACTGCCATATGTACTG--TTTCTTGTCATCAGTAACAAGGA [16853]
Psi TCATAGCTCTTTGAATGGTACTGCCATATGTACTG--TTTCTTGTAATCAGTAACCAGGA [15402]
Asp TCATAGCTCTTTGAATGGTACTGCCATATGTACTG--TTTCTTGCAATCAGTAACCAGGA [14551]
Ami TCATAGCTCTTTGAATGGTACTGCCATATGTACTG--TTTCTTGCAATCAGTAACAAGGA [16276]
Asi TCATAGCTCTTTGAATGGTACTGCCATATGTACTG--TTTCTTGCAATCAGTAACAAGGA [15694]
Tgu TCATAGCTCTTGGAATGGTTCTGCCATAAGCACTG------------------------ [12890]
Cli TCATAGCTCTTTGAATGGTACTGCCATATGTACCG--GGTTTTGCACTCAGTAACAAGGA [15749]
Gga TCATAGCTCTTTGAATGGTACTGCCATATGTACTG--GGCTTTGCAGTCAGTAACGAGGA [14297]
Xtr ----------------------------------TTTTTTGCTCTCAGTAACAACGA [14546]
Lch TCATAGCTCTTTGAATGGTACTGCCATATGTACTA------------------------ [16431]
Dre TCATAGCTCTTTGAATGGTACTGCCATATGCACTG--CCTCTTGCTCTCAGTAACAAGGA [14935]

Hsa TTCATCCTTGTGTCCATCATGCAACA--AGGAGAATCTTTGTCACTTAGTGTAATTAATA [15931]
Mmu TTCATCCTTGTGTCAATCATACAACA--CGGAGAGTCTTTGTCACTCAGTGTAATTAATA [15672]
Mdo ---------------------------------------------------------- [14734]
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Meu ------------------------------------------------------------ [12757]
Oan TTCATCCTTGTGTCCTGTAAGCAACA--GGGAGGGTCTTTGTCACTGAGTGCAATTAATG [13684]
Aca ------------------------------------------------------------ [15718]
Pbi ------------------------------------------------------------ [15966]
Cpi TTCATCCTTGTGTATAGTAAATAACA--GGGAGAATCTTTGTCACTAAGTACAATTAACA [17165]
Cmy TTCATCCTTGTGTATAGTAAATAACA--GGGAGAATCTTTGTCACTAAGTGCAATTAACA [16911]
Psi TTCAGCCTTGTGTATAATAAATAACA--AGGAGAACCTTTGTCACTAAATGCAAATAAAA [15460]
Asp TTCATACTCATGTATAATAAATAACA--GGGAGAACCTTTGTCACTAAATGCAAATAAAA [14609]
Ami TTCATCTCTGTATTGTGTGAAGAACA--GAGAGAGTCTTTGTAACTAAGTGCAAGTAATA [16334]
Asi TTCATCTCTGTATTGTGTGAAGAACA--GAGAGAGTCTTTGTAACTAAGTGCAAGTAATA [15752]
Tgu ------------------------------------------------------------ [12890]
Cli TTCATCCTCGTTTCTGGCAAATAACG--GGGAGAATCTTTGTCACTAAGTGCAATTAATA [15807]
Gga TTCATCCTTGTGTCCAGCAAATAACA--GGGAGAATCTTTGTTACTATGTGCAATTAACA [14355]
Xtr TTCAGCCTTGTCATTA-TATATAACC--AAGGGGATCTTTGTCACTAAGTGCAATTAATA [14603]
Lch ------------------------------------------------------------ [16431]
Dre TTCATCCTGTTGTGGTACTCAAATCCAACAGGGAATCTCTGTTACTGGGGTTAAGGTTCA [14995]

Hsa GC-------------------------------------------------------- [15933]
Mmu GC-------------------------------------------------------- [15674]
Mdo ----TG-ACTTTATAGAACCTGCATTGTACACACTGTGTGTTTTCA-TTCCCATGCACAG [14788]
Meu ----TG-ACTTTATAGAACCTGCATTGTACACACTGTGTGTTTTCA-CTACTATGCACAG [12811]
Oan GT--TG-ACTGTATAGAACCTGCATTGTACACACTGTGTGTCTCGCTCTCTGCA-CACAG [13740]
Aca ----TG-ACCTTATAGGACCTGCATTGTACACACTGTGTGTATGGACTGGAGGTGCACAG [15773]
Pbi ------------------------------------------------------------ [15966]
Cpi GC--TG-ACTTTATAGAACCTGCATTGTACACACTGTGTGTATTGATTGGACATGCACAG [17222]
Cmy GC--TG-ACTTTATAGAACCTGCATTGTACACACTGTGTGTATTGATTGGACATGCACAG [16968]
Psi GC--TG-ACTTTATAGAACCTGCATTGTACACACTGTGTGTATTGATGGCACATGCACAG [15517]
Asp GC--TG-ACTTTATAGAACCTGCATTGTACACACTGTGTGTATTGATGGCACATGCACAG [14666]
Ami GC--TG-ACTTTATAGGACCTGCATTGTACACACTGTGTGTATTGACTGGGCGTGCACAG [16391]
Asi GC--TG-ACTTTATAGGACCTGCATTGTACACACTGTGTGTATTGACTGGGCGTGCACAG [15809]
Tgu ----TG-ACTTTATAGCACCTGCATTGTACACACTGTGTGTGTGG-CTGGAAATGCACAG [12944]
Cli GC--TG-ACTTTATAGCACCTGCATTGTACACACTGTGTGTATTGACTGGAAATGCACAG [15864]
Gga GC--TG-ACTATATAGCACCTGCATTGTACACACTGTGTGTGTTAACTGGAAATGCACAG [14412]
Xtr GC--TG-GCTTTATAGAGCCTGCATTGTACACACTGTGTGTGCACCTCAGACTTGCACAG [14660]
Lch ----TG-GCTTTATAGCGCCTGCATTGTACACACTGTGTGTATTGATTTGGTGTACACAG [16486]
Dre GA--TGGACTCCTCGGCTCCTGCATTGTACACACTGTGCGGAACACATGGACATGCACAG [15053]

Hsa ------------------------------------------------------------ [15933]
Mmu ------------------------------------------------------------ [15674]
Mdo CGCATACAATGTGGATACTATAAGAGTC-------------------------------- [14816]
Meu CGCATACAATGTGGATACTATAAGAGTC-------------------------------- [12839]
Oan CGCGTACAATGTGGATACTATAGAAGTC-------------------------------- [13768]
Aca CGCATACAATGTGGATGCTATAGAAGTC--GGACTCCATCTTGCCCTCATTGTACATGCT [15831]
Pbi ------------------------------------------------------------ [15966]
Cpi CGCATACAATGTGGATACTGTAGACGTC--TGGCTCTATGTTGTCCTCATTGTACATGCT [17280]
Cmy CGCATACAATGTGGATACTGTAGAAGTC--TGGCTCTATGTTGTCCTCATTGTACATGCT [17026]
Psi CGCATACAATGTGGATACTGTATAAGTC--TGTCTCTATGCGGTCCTCATTGTACATGCT [15575]
Asp CGCATACAATGTGGATACTGTAGAAGTC--TGGCTCTATGCGGTCCTCATTGTACATGCT [14724]
Ami CGCATACAATGTGGATACTGTAGAAGTC--TGGCTCTATGTTGTCCTCATTGTACATGCT [16449]
Asi CGCATACAATGTGGATACTGTAGAAGTC--TGGCTCTATGTTGTCCTCATTGTACATGCT [15867]
Tgu CGCATACAATGTGGATTCTGTACAAGTC--TGGCTCTATCGTGCCCTCATTGTACATGCT [13002]
Cli CGCATACAATGTGGATTCTGTAGAAGTC--TGGCTCTATAGTGTCCTCATTGTACATGCT [15922]
Gga CGCATACAATGTGGATTCTGTAGAAGTC--TGGCTCTACGTTGTCCTCATTGTACATGCT [14470]
Xtr CGCATACAATGTGGATGCTATATGAGTC--TGACTCTACATTGTCCTCATTGTACATGCT [14718]
Lch CGCATACAATGTGGATACTGTAAAAGGC--TGGCTCTACATTGTCCTCATTGTACATGCT [16544]
Dre CGCATACAATGTGGATGCTGTGGAGCCC--GGGTTCTCCGGTCTCCTCATTGTGCATGCT [15111]
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Hsa ----------------------------------------------------GTGG [15937]
Mmu ----------------------------------------------------GTGG [15678]
Mdo ------------------------------------------------------- [14816]
Meu ------------------------------------------------------- [12839]
Oan ------------------------------------------------------- [13768]
Aca GTGTGTATTCCTTTGGCGT-ACACAGCGCATGCAATGTGGACAGGAGGGAGGCC--GTGA [15888]
Pbi ----------------------------------------------------GTGA [15970]
Cpi GTGTGTATTTTTATTACAT-ACACAGCGCATGCAATGTGGACATAATGGAGATC--GTGG [17337]
Cmy GTGTGTATTTTTATTACAT-ACACAGCGCATGCAATGTGGACATAATGGAGATC--GTGG [17083]
Psi GTGTGTATCTTTATTACAT-ACACAGCGCATGCAATGTGGACATCATGGAGATC--GTGG [15632]
Asp GTGTGTATCTTTATTACAT-ACACAGCGCATGCAATGTGGACATCATGGAGATC--GTGG [14781]
Ami GTGTGTATATTTATGACGT-ACACAGCGCATGCAATGTGGACAGAATGGAGACC--GTGG [16506]
Asi GTGTGTATATTTATGACGT-ACACAGCGCATGCAATGTGGACGTAATGGAGACC--GTGG [15924]
Tgu GTGTGAAT--TTGTCACAT-ACACAGCGCATGCAATGTGGACATAATGGAGCTC--GTGG [13057]
Cli GTGTGTAT--TTGTCACGT-ACACAGCGCATGCAATGTGGACATAATGGAGCTC--GTGG [15977]
Gga GTGTGTAT--TTGCCACGT-ACACAGCGCATGCAATGTGGACATAATGGAGCTC--GTGG [14525]
Xtr GTGTGTATCTATTTCTCTT-ACACAGCGCATGCAATGTGGATATATTGGATGTC--GTGG [14775]
Lch GTGTGTAT-TCCATTACAT-ACACAGCGCATACAATGTGGATATCGTCGAGACC--GTGG [16600]
Dre GTGTGTCTTCAGTCTGGTCCTCACAGCGCCTGCAATGTGGAGGCTAGGGGACTC--GTGG [15169]

Hsa CAGCTTGGTGGTCGTATGTGTGACGCCATTTACTTGAACC-TTTAGGAGTGACATCACAT [15996]
Mmu CAGCTTGGTTGTCATATGTGTGATGACACTTTCTAAAGTC-TTCCAGAATGACACCACAT [15737]
Mdo ------------------------------------------------------------ [14816]
Meu ------------------------------------------------------------ [12839]
Oan ------------------------------------------------------------ [13768]
Aca TGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGTTCT-TTTAGGAGTGACATCATAT [15947]
Pbi TGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGTACT-TTTAGGAGTGACATCTTAT [16029]
Cpi TGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGGACT-TTTAGGAGTGACATCATAT [17396]
Cmy TGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGGACT-TATAGGAGTGACATCATAT [17142]
Psi TGGCTTGGTGGTCGTATGCATGACGTCATTTACTTGGACT-TTTAGGAGTGACATCATAT [15691]
Asp TGGCTTGGTGGTCGTATGCATGACGTCATTTACTTGGACT-TTTAGGAGTGACATCATAT [14840]
Ami TGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGGACT-TTTAGGAGTGACATCATAT [16565]
Asi TGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGGACT-TTTAGGAGTGACATCATAT [15983]
Tgu TGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGGACT-TTTAGGAGTGACATCATAT [13116]
Cli TGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGGACT-TTTAGGAGTGACATCATAT [16036]
Gga TGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGGACT-TTTAGGAGTGACATCATAT [14584]
Xtr TGGCTTAGTGGTCGTATGTATGACGTCATTTACTGGATTT-TTTAGGAGTGACATCATAT [14834]
Lch TGGCTTGGTGGTCGTATGTATGACGTCATTTACTTGGACT-TTTAGGAGTGACATCATAT [16659]
Dre TGGCCTGGTGGTCGTATGTATGACGTCATTTACTTCAAAG-TTT-GGAGTGACATCATAT [15227]

Hsa ATACGGCAGCT-AAACTGCTAC--GCGGGCGGCTGTTAAGACTTGCAGTGATGTTTAACT [16053]
Mmu ATATGGCAGCT-AAACTGTTAC--GTGGGCAGCTGTTAAGACTTGCAGTGATGTTTAGCT [15794]
Mdo ------------------------------------------------------------ [14816]
Meu ------------------------------------------------------------ [12839]
Oan ----------------------GGGGGCAGCGGTTAAGACTTGTAGTGATGTTTAGCT [13804]
Aca GTACGGCTGCT-AAACTGCCAC--GGGGGAGGCAGTTAAGACTTGCAGTGATGTTTAGAA [16004]
Pbi GTACGGCTGCT-AAACTGCCAC--GGGAGAGGCAGTTAAGACTTGCAGTGATGTTTAGAT [16086]
Cpi GTACGGCTGCT-AAACTGCTGC--GAGAGCGGCAGTTAAGACTTGCAGTGATGTTTAGAT [17453]
Cmy GTACGGCTGCT-AAACTGCTGC--GAGAGCGGCAGTTAAGACTTGCAGTGATGTTTAGAT [17199]
Psi GTACGGCTGCT-AAACTGCTGC--GAGAGCGGCGGTTAAGACTTGCAGTGATGTTTAGCT [15748]
Asp GTACGGCTGCT-AAACTGCTGC--GAGAGCGGCAGTTAAGACTTGCAGTGATGTTTAGAT [14897]
Ami GTACGGCTGCT-AAACTGCTGC--GAGAGCGGCAGTTAAGACTTGCAGTGATGTTTAGAT [16622]
Asi GTACGGCTGCT-AAACTGCTGC--GAGAGCGGCAGTTAAGACTTGCAGTGATGTTTAGAT [16040]
Tgu GTACGGCTGCT-AAACTGCTGC--GAGAGCGGCAGTTAAGACTTGTAGTGATGTTTAGAT [13173]
Cli GTACGGCTGCT-AAACTGCTGC--GAGAGCGGCAGTTAAGACTTGTAGTGATGTTTAGAT [16093]
Gga GTACGGCTGCT-AAACTGCTGC--GGGAGCGGCAGTTAAGACTTGTAGTGATGTTTAGAT [14641]
Xtr GTACGGCTGCT-AAACTGCTGC--GAGCGAGGCAGTTAAGACTTGCAGTGATGTTTAGTT [14891]
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Lch GTACGGCTGCT-AAACTGCTAC--GAGAGAGGCAGTTAAGACTTGCAGTGATGTTTAGAA [16716]
Dre GTACGGCTGCT-AAACTGCTAC--GAGGGAGGCAGTTAAGACTTGCAGTGATGTTTAGAG [15284]

Hsa CCTCTCC--ACGTGAACATCACAGCAAGTCTGTGCTG-CTTCCCGTCC--TGACCCTGGA [16108]
Mmu CCTCTGC--ATGTGAACATCACAGCAAGTCTGTGCTG-CTGCCTGCCC------------ [15839]
Mdo ----------------------------------------------------TGACCCTGGA [14826]
Meu ----------------------------------------------------TGACCCTGGA [12849]
Oan CATCTCC--ACGTGAACATCACTGCAAGTCTGTGCTG-CTTCTCCCCT------------ [13849]
Aca AATTTACT-ACATGAACATCACTTTAAGTCTGTGCTA-CTTCTTTCCT------------ [16050]
Pbi AATTTATT-ACATAAACATCACTTTAAGTCTGTGCTA-TTTCTCTCCT--TCACCTGGGA [16142]
Cpi AATGTATT-ACATGAACATCACTTTAAGTCTGTGCTA-CCTCTCTCCT--TGACCTTGGA [17509]
Cmy AATGTATT-ACATGAACATCACTTTAAGTCTGTGCTA-CCTCTCTCCT--TGACCTTGGA [17255]
Psi AATGTATT-ACATGAACATCACGGTGAGTCTGTGCTA-CCTCTCTCCT--TAATCTTAGA [15804]
Asp AATGTATT-ACATGAACATCACTTTAAGTCTGTGCTA-CTTCTCTCCT--TAATCTTAGA [14953]
Ami AATGTATT-ACATGAACATCACTTTAAGTCTGTGCTA-CTTCTCTCCT--TAACCTTGGA [16678]
Asi AATGTATT-ACATGAACATCACTTTAAGTCTGTGCTA-CTTCTCTCCT--TAACCTTGGA [16096]
Tgu AATTAATT-ACATGAACATCACTTTAAGTCTGTGCTA-CTTCTCTCCT------------ [13219]
Cli AATGTATT-ACATGAACATCACTTTAAGTCTGTGCTA-CTTCTCTCCT--TGACCTTGGA [16149]
Gga AATGTATT-ACATGAACATCACTTTAAGTCTGTGCTA-CTTCTCTCCT------------ [14687]
Xtr AAAATCTTTTCATGAACATCACTTTAAGTCTGTACTG-CTTCTCCCTC--TGACCTTGGA [14948]
Lch AATTCAAA-TCATGAACATCACTTTAAGTCTGTGCTA-CTTCTTTTCT--AGGCCTAGGA [16772]
Dre AAATGTC--ACATGAACATCACTTTAAGTCTGTGCTGGCTCCTGTTCT------------ [15330]

Hsa AATCCAGAGTGGGTGGGGCCAGTCTGACCGTTT-CTAGGCGACCCACTCTTGGTTTCCAG [16167]
Mmu ---------------------------------------------------------- [15839]
Mdo AATCCAGAAGGGGTGGAGCCTGTTGGACAGTTT-CTAGGCGACCCATTCTTGGTTTCAAG [14885]
Meu AATCCAGAAGGGGTGGAGCCTGTTGGACAGTTT-CTAGGCGACCCATTCTTGGTTTCAAG [12908]
Oan ---------------------------------------------------------- [13849]
Aca ---------------------------------------------------------- [16050]
Pbi AATCAAGAATGGGTGGGGCCTGTGAATATGAGA-GGAGGCGACCCACTCTTGGTTTCCAA [16201]
Cpi AATCAAGAATGGGTGGAGCCTGTTGAATTAATT-CTAGGCGACCCATACTTGGTTTCAAG [17568]
Cmy AATCAAGAATGGGTGGAGCCTGTTGAATTAATT-CTAGGCGACCCATACTTGGTTTCAAG [17314]
Psi AATCAAGAATGGGTGGAGCCTGTTAAATTATT--TTAGGCGACCCATACTTGGTTTCAAG [15862]
Asp AATCAAGAATGGGTGTAGCCTGTTAAATTATT--TTAGGCGACCCATACTTGGTTTCAAG [15011]
Ami AATCAAGGATGGGTGAAGCCTGTTGGAATAACT-CTAGGCGACCCATACTTGGTTTCAAG [16737]
Asi AATCAAGGATGGGTGAAGCCTGTTGGAATAACT-CTAGGCGACCCATACTTGGTTTCAAG [16155]
Tgu ---------------------------------------------------------- [13219]
Cli AATCAAGTGTAGGTGGAGCCTGTGGCAGCGAT--CAAGGCGACCCACACTTGGTTTCAAG [16207]
Gga ---------------------------------------------------------- [14687]
Xtr AACCAAGAGTGGGTTGGGCCTGTTAGATCAC---ATAGGCGACCCATACTTGGTTTCAAG [15005]
Lch GATCAAGTGTGGGTGAAGCCTGTAGAGATTGTTGCTAGGCGACCCATATTTGGTTTCAGA [16832]
Dre ---------------------------------------------------------- [15330]

Hsa GGTTGCCCTG--TGGCCCATGAAATCAAGCGTGGGTGAGACCTGGTGCAGA-ACGGGAAG [16224]
Mmu ------------TGGCCCATGAAATCAAGCTTGGGTGAGACCTGGTGCAGA-ACAGGAAG [15886]
Mdo GGTTGCCATG--TGGCCCCAGAAATCAAGGATGGGTGAGACCTCGTGTGCAAACTGAAAG [14943]
Meu GGTTGCCATG--TGGCCCCAGAAATCAAGGATGGGTGAGACCTCGTGTGCAAACTGAAAG [12966]
Oan ------------TGGCCCCAGAAATCAAGGATGGGTGAGACCTCTTGCACA-AGTGGAAG [13896]
Aca ------------TGGCTCCAGAAATCAAGGTTGGGTGAGACCTCGTGAACAGACTGGAAG [16098]
Pbi GGTCAGCAGG--TGGCTCCAGAAATCAAGGCTGGGTGAGACCTCGTGAAGAAACTAGAAG [16259]
Cpi GGTCAGCAGG--TGGCTCCAGAAATCAAGGGTGGGTGAGACCTCGTAAGAAAACGTGAAG [17626]
Cmy GGTCAGGAGG--TGGCTCCAGAAATCAAGGGTGGGTGAGACCTCGTAAGAAAACGTGAAG [17372]
Psi GGTTAACAGG--TGGCTCCAGAAATCAAGAATGGGTGAGACCTCGTAAGAAAACATGAAG [15920]
Asp GGTTAACAGG--TGGCTCCAGAAATCAAGAGTGGGTGAGACCTCGTAAGAAAACATGAAG [15069]
Ami GGTCAGCAGG--TGGCTCCAGAAATCAAGGGTGGGTAAGACCTCGTAAGAACAGTTGAAG [16795]
Asi GGTCAGCAGG--TGGCTCCAGAAATCAAGGGTGGGTAAGACCTCGTAAGAACAGTTGAAG [16213]
Tgu ------------TGGCTCCAGAAATCAAGGGTGGGTAAGACCTGGTGAGCAAACTCTAAG [13267]
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Cli GGTCCGCAGG--TGGCTCCAGAAATCAAGGGTGGGTAAGACCTCGTCAGCAAAGTTTAAG [16265]
Gga ----------TGGCTCCAGAAATCAAGGGTGGGTAAGACCTTGTAGGATAACTGGCAG [14735]
Xtr GGTTAGCAGG--TGACCTTAGAAATCAAGCTTGGGTTAGACCTGGTTCTTATACACTGAG [15063]
Lch GGCCGGTGGG--TTGCCCCAGAAATCAAGGATGGGTGAGACCTCGTAATGAACGATGAAG [16890]
Dre ------------------------------------------------------------ [15330]

Hsa GCGACCCATACTTGGTTTCAGAGGCTGTGAGA---------------------------- [16256]
Mmu GCGACCCATACTTGGTTTCAGTGGCTGCAAGA---------------------------- [15918]
Mdo GCGACCCATACTTGGTTTCAGGGGCTTCGAGA---------------------------- [14975]
Meu GCGACCCATACTTGGTTTCAGGGGCTTCGAGA---------------------------- [12998]
Oan GCGACCCATACTTGGTTTCAGGGGCTTCCGGA---------------------------- [13928]
Aca GCGACCCATACTTGGTTTCAGGAGCTTCGAGG--GGGCGCTCGTCAGGAATTCCGCTAGT [16156]
Pbi GCGACCCATACTTGGTTTCAGGAGCTGTGAGG---------------------------- [16291]
Cpi GCGACCCATACTTGGTTTCAGGGGCTGTGAGG--GGGCGTTCACCAGGAATTCCGCTAGT [17684]
Cmy GCGACCCATACTTGGTTTCAGGGGCTGTGAGG---------------------------- [17404]
Psi GCGACCCATACTTGGTTTCAGGGGCTGTGAGG---------------------------- [15952]
Asp GCGACCCATACTTGGTTTCAGGGGCTGTGAGG---------------------------- [15101]
Ami GCGACCCATACTTGGTTTCAGGGGCTTTGAGG---------------------------- [16827]
Asi GCGACCCATACTTGGTTTCAGGGGCTTTGAGG---------------------------- [16245]
Tgu GCGACCCATACTTGGTTTCAGGGGCTGTGGGC--------------------------- [13299]
Cli GCGACCCATACTTGGTTTCAGGGGCTGTGTGG--GGCCGTGCGGCCGGAATTCCGCTAGT [16323]
Gga GCGACCCATACTTGGTTTCAGGGGCTGTGTGG---------------------------- [14767]
Xtr GCGACCCATACTTGGTTTCTGAGGCTGAAGTG--GGGTGCTTGTCAGGAATTCCGCTAGT [15121]
Lch GCGACCCATTCTTGGTTTCAGGGACCTTGGTG---------------------------- [16922]
Dre ---------------------------------CTACTAGCAGAAGGAATTCCGCTAGT [15356]

Hsa ------------------------------------------------------------ [16256]
Mmu ------------------------------------------------------------ [15918]
Mdo ------------------------------------------------------------ [14975]
Meu ------------------------------------------------------------ [12998]
Oan ------------------------------------------------------------ [13928]
Aca TCTGAACTATTTACAGTTAGAAAAA-----GTTCACTACTAGCAGAACTCGGCCGCGCGC [16211]
Pbi ------------------------------------------------------------ [16291]
Cpi TCTGAACTATTTACACTTGAAAAAA-----GTTCACTACTAGCAGAACTCGGGTGCGCGC [17739]
Cmy ------------------------------------------------------------ [17404]
Psi ------------------------------------------------------------ [15952]
Asp ------------------------------------------------------------ [15101]
Ami ------------------------------------------------------------ [16827]
Asi ------------------------------------------------------------ [16245]
Tgu ------------------------------------------------------------ [13299]
Cli TCTGAACTTTTTCCTGGAAAAAAAAAAA--GCTCACTACTGGCAGAACTCGGCCGCGCGC [16381]
Gga ------------------------------------------------------------ [14767]
Xtr TCTGAACTATT-CCATGTTAGTAAGTAAAAGTTCACTACTAGCAGAACTCGGCCACGTAC [15180]
Lch ------------------------------------------------------------ [16922]
Dre TCTGAACTATT-CGTGATTGGCAAAA----GTTCACTACTAGCAGAACTCGGATATACAA [15411]

Hsa ------------------------------------------------------------ [16256]
Mmu ------------------------------------------------------------ [15918]
Mdo ------------------------------------------------------------ [14975]
Meu ------------------------------------------------------------ [12998]
Oan ------------------------------------------------------------ [13928]
Aca --CTACTCTGCTGTTGTTTTTTTAGGTTTTGATTTTTATGCCATCCTCATGCGAAAATCA [16269]
Pbi --CTACTCTGCTGTTGTTTTCTTAGGTTTTGATTTTTATGCCATGCTCATGTGAAAATCA [16349]
Cpi --CTACTCTGCTGTTATTTTTTTTAGGTTTTGATTTTTATTACATCTTCATGCGAAAATCA [17797]
Cmy --CTACTCTGCTGTTATTTTTTTTAGGTTTTGATTTTTATTACATCTTCATGCGAAAATCA [17462]
Psi --CTACTCTGCTGTTATTTTTTTTAGGTTTTGATTTTTATTACATCTTCATGAGAAAATCA [16010]
Asp --CTACTCTGCTGTTATTTTTTTTAGGTTTTGATTTTTATTACATCTTCATGCGAAAATCA [15159]
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Ami --CTACTCTGCTGTTATTTTTTTAGGTTTTGATTTTTATTGCATCTTCATGCGAAAATCA [16885]
Asi --CTACTCTGCTGTTATTTTTTTAGGTTTTGATTTTTATTACATCTTCATGCGAAAATCA [16303]
Tgu ------------------------------------------------------------ [13299]
Cli --TGGTTTGGGTTGAGTTTTTTTAGGTTTTGATTTTTATTACATCTTTGTACAAAAATCA [16439]
Gga ------------------------------------------------------------ [14767]
Xtr ------------------------------------------------------------ [15180]
Lch --CTGCTCTGCTGTAGTTTTTTTAGGTTTTGATTTTTATTATGTCTGTGCAGGAAAATCA [16980]
Dre --CTGCTGTGCTGTTGTTTTTTTAGGTTTTGATTTTTGTGAAATGTCGATGAGAAAATCA [15469]

Hsa -------------------------------TTAGTGGTACTATACCTCAGTTTTATCA [16284]
Mmu -------------------------------TCTGTGGTACTATACCTCAGTTTTATCA [15946]
Mdo -------------------------------TCTGTGGTACAATACCTCAGTCTTATCA [15003]
Meu ------------------------------------------------------------ [12998]
Oan -------------------------------TTAGTGGTACAATACCTCAGTCTTATCA [13956]
Aca AAACCTAAAGAAAATGCTGCAAAGATAGAT--TTAGTGGTACAATACCTCAGCCTTATCA [16327]
Pbi AAACCTAAAGAAAATGCTGCAAAGATAGAT--TTAGTGGTACAATACCTCAGCCTTATCA [16407]
Cpi AAACCTAAAGAAAATGCTGCAAAGATAGAT--TTAGTGGTACAATACCTCAGTCTTATCA [17855]
Cmy AAACCTAAAGAAAATGCTGCAAAGATAGAT--TTAGTGGTACAATACCTCAGGCTTATCA [17520]
Psi AAACCTAAAGAAAATGCTGCAAAGATAGAT--TCAATGGTACAATACCTCAGTCTTATCA [16068]
Asp AAACCTAAAGAAAATGCTGCAAAGATAGAT--TAAATGGTACAATACCTCAATCTTATCA [15217]
Ami AAACCTAAAGAAAATGCTGCAAAGATAGAT--TTAGTGGTACAATACCTCAGTCTTTTCA [16943]
Asi AAACCTAAAGAAAATGCTGCAAAGATAGAT--TTAGTGGTACAATACCTCAGTCTTTTCA [16361]
Tgu -------------------------------TAAGTGGTACAATATCTCAATTTTTCCA [13327]
Cli AAACGTAAAGAAAATGCTGCAAAGATAGAT--TTAGTGGTACAATACCTCAGTCTTTTCG [16497]
Gga -------------------------------CTAGTGATACAATAACTCAGTATTTTCT [14795]
Xtr ------------------------------------------------------------ [15180]
Lch AAACCTAAAGAAAGTATTGCAAAGATAGAC--TTAGCGGTACAATACCTCAGTCTTTTCA [17038]
Dre AAACCTAAAGAAAATACTGCGCAGATAGAT------------------------------ [15499]

Hsa GGTGTTC-TTAAAA--TCACCTGGAAACACTGAGGTTGTGTCTCACTGAAC--TGAGCAG [16339]
Mmu GGTGTTCATTAAAA--TCACCTGAAAATACTGAGGCTATGTTTCACTGAGC--TGAACAG [16002]
Mdo GGTGTTAATTAAAA--TCACCTGGAAATGCTGAGGTTGCGTTTCACTGAAC--CGAAGAG [15059]
Meu ----------------------------------------------------CAAAGAG [13005]
Oan GGTGTTCTTTCAAT--TCACCTGGCAATACTGAGGTTGTGTCTCACTGAAC--------- [14005]
Aca GGTGTTGTATATAT--TCACCTGGAAGTACTGAGGTTGAGTTTCACTGAAC--TGAACAG [16383]
Pbi GGTGCTATATATATATTCACCTGGAAGTTCTGAGGTTGAGTTTCACTGAAC--TGAACAG [16465]
Cpi GGTGTTCTATAAAT--TCACCTGCAAAAACTGAGGTTGAGTTTCACTGAAC--TGAACAG [17911]
Cmy GGTGTTCTGTAAAT--TCACCTGGAAAAACTGAGGTTGAGTTTCACTGAAC--TGAACAG [17576]
Psi GGTGTTCTATAAAT--TCACCTTGAAAAACTGAGGTTGAGTTTCACTGAAC--TGAACAG [16124]
Asp GGTGTTCTATAAAT--TCACCTTGAAAAACGGAGGTTGAGTTTCACTGAAC--TGAACAG [15273]
Ami GGTGTTCTATAAAA--TCACCTGGAAATATTGAGGTTGAGTTTCACTGAAC--TGAACAG [16999]
Asi GGTGTTCTATAAAA--TCACCTGGAAATATTGAGGTTGAGTTTCACTGAAC--TGAACAG [16417]
Tgu GATGTTCTATAAAT--TTGCCTGGAAATACCTAGGTGAAGTTTCACTGAAC--------- [13376]
Cli GATGTTCTATAAAT--TCACCTGGAAATACTGAGGTTGCGTTTCACTGAAC--CGAACAG [16553]
Gga GTTGGACTAGAAAT--TCACCTGGAAATACCAAGGTTGAGTTGCACTGAAC--TGAACAG [14851]
Xtr ----------------------------------------------------AGAAGAG [15187]
Lch GGTGCTGTTCACAT--TCACCTGTAAGTACTGAGGTTATGTTCCACTGAAC--TCAACAG [17094]
Dre ----------------------------------------------------TAAAGCA [15506]

Hsa TCTCCACCACCTCCCCTGCAAACGTCCAGTGGTGCAGAGGTAATGGACGTTGGCTCTGGT [16399]
Mmu TCTCCACCACCTCCCCTGCAAACGTCCAGTGATGCAGAGGTAATGGACGTTGGCTCTGGT [16062]
Mdo CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGACGTAATGGACGTTGGCTCTGGT [15119]
Meu CCTCCACCAGCTCCCCTGCAAAAGTCCAGTGATGCAGACGTAATGGATGTTGGCTCTGGT [13065]
Oan ------------------------------------------------------------ [14005]
Aca CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGT [16443]
Pbi CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGT [16525]
Cpi CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGT [17971]
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Cmy CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGT [17636]
Psi CCTCCACCACCTCCCCTGCAAACGTCCAGTGATGCAGAGGTAATGGACGTTGGCTCTGGT [16184]
Asp CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGT [15333]
Ami CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGT [17059]
Asi CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGT [16477]
Tgu ------------------------------------------------------------ [13376]
Cli CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGT [16613]
Gga CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGT [14911]
Xtr CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGTAATGGACGTTGGCTCTGGT [15247]
Lch CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGCTAATGGACGTTGGCTCCGGT [17154]
Dre CCTCCACCACCTCCCCTGCAAACGTCCAGTGACGCAGAGGAAATGGACGTTAGCTCTGGT [15566]

Hsa GGTGATGGACAGTCCG---------------------------------------------- [16415]
Mmu GGTGATGGACAGTCCG---------------------------------------------- [16078]
Mdo GGTGCTGGACAGTCAG--GGTCTGGTTGTAGGGGTACAGTGATCAGGTTATGATGGATTT [15177]
Meu GGTGTTGGACAGTCAG---------------------------------------------- [13081]
Oan ------------------AATCTGGTTGTAGGGGTACAGTGATCAGGTTACGATGGATTT [14047]
Aca GGTGATGGACAGTCAG--CATCGGACTGTAGGGGTACAGTGATCAGGTTACGATGGATTT [16501]
Pbi GGTGATGGACAGTCAG--CATCTGGTTGTAGGGGTACAGTGATCAGGTTACGACGGATTT [16583]
Cpi GGTGATGGACAGTCAG--AGTCTGGTTGTAGGGATACAGTGATCAGGTTACGAGGGATTT [18029]
Cmy GGTGATGGACAGTCAG--AGTCTGGTTGTAGGGATACAGTGATCAGGTTACGAGGGATTT [17694]
Psi GGTGATGGACAGTCAG--AGTCTGGTTGTAGGGATACAGTGATCAGGTTACGAGGGATTT [16242]
Asp GGTGATGGACAGTCAG--AGTCTGGTTGTAGGGATACAGTGATCAGGTTACGAGGGATTT [15391]
Ami GGTGATGGACAGTCAG--GGTCTGGTTGTAGAGATACAGTGATCAGGTTACGATG-ATTT [17116]
Asi GGTGATGGACAGTCAG--GGTCTGGTTGTAGAGATACAGTGATCAGGTTACGATG-ATTT [16534]
Tgu ------------------GGTCTGGTTGTAGAGATACAGTGATCAGGTTACGATGGATTT [13418]
Cli GGTGATGGACAGTCAG--GGTCTGGTTGTAGAGATACAGTGATCAGGTTACGATGGATTT [16671]
Gga GGTGATGGACAGTCAG--GGTCTGGTTGTAGAGATACAGTGATCACGTTACGATGGATTT [14969]
Xtr GGTGATGGACAGTCAC--AATCTAGTTGTAGGGGTACAGTGATCAGGTTACGATGGATTT [15305]
Lch GGTGATGGACAATTTG--AATCTAGTTGTAGGGGTACAGTGACCAGGTTACGATGGATTT [17212]
Dre GGTGATGGACACCAAC---------------------------------------------- [15582]

Hsa ------------------------------------------------------------ [16415]
Mmu ------------------------------------------------------------ [16078]
Mdo CTCAAGTAAGCACCTCGTAGCTTGGTCACGATATCCATATGACTCAGAT--AATGGAAGG [15235]
Meu ------------------------------------------------------------ [13081]
Oan CTCAAGTAACAACCTCGTAGCTCGGTCACGATATCCATATGACTCGAAG--AGTGGGGGG [14105]
Aca CTCTAGTAACAGCCTCGTAGCTTGATCACCATCTCCCTATGATTCAGAT--GGTGAGGAG [16559]
Pbi CTCTAGTAACAACCCCGTAGCTTGATCACCATCTCCCTATGACTCAGAT--GCTGAGGAG [16641]
Cpi CTCAAGTAACAACCTCGTAGCTCGGTCACGATATCCCTATGACTTAGAT--AGTGAGGGG [18087]
Cmy CTCAAGTAACAACCTCATAGCTCGATCACGATATCCCTATGACTTAGAT--AGTGAGGGG [17752]
Psi CTCAAGTAACAACCTCGAAGCTCGATCACGATATCCCTATGACTTAGGT--AATGAGGGG [16300]
Asp CTCAAGTAACAACCTCGTAGCTCGATCACGATATCCCTATGACTTAGAT--AATGAGGGG [15449]
Ami CTCAAGTAACAACCTCGTAGCTTGATCACAATATCCCTATGACTTAGAT--AGTGAGGGG [17174]
Asi CTCAAGTAACAACCTCGTAGCTTGATCACGATATCCCTATGACTTAGAT--AGTGAGGGG [16592]
Tgu CTCAAGTAACAACCTCGTAGCTTGATCACGATATCCCTATGACTTGAGA--AGTGAGGGG [13476]
Cli CTCAAGTAACAACCTCGTAGCTTGATCACGATATCCCTATGACTTGAGA--AGCGAGAGG [16729]
Gga CTCAAGTAACAACCTCGTAGCTTGATCACGATATCCCTATGACTTGAGA--AGCGAGGGG [15027]
Xtr CTGAAGTAACGGCCTCGTAACTTGGTCACCATATCCATATGACTCAGAT----------- [15354]
Lch TACAAGAAAC---CTCGTAGCTTGGTCACGATATCCATATGACTTGGAT--ACTGAGTGG [17267]
Dre ----------------------------------------------------ATGAGCAGT [15591]

Hsa ------------------------------------------------------------ [16415]
Mmu ------------------------------------------------------------ [16078]
Mdo TGCATCTAGGACTGTCTAACCTGAGAATGGTGAA-TCTCAGGGTCAATCTCAGGTTTGTC [15294]
Meu ------------------------------------------------------------ [13081]
Oan CGTGTCTAGGACTGTCTAACCTGAGAATGGTGATGTGTGAGGGTCAATCTCAGGTTCGTC [14165]
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Aca TTTTTTGAGGACTGTCTAACCTGAGAATGGTGAATCATGAAGGTCAATCTCAGGTCCGTC [16619]
Pbi TGTTTCAAGGACTGTCTAACCTGAGAATGGTGAAACAAAATGCTCAATCTCAGGTCCGTC [16701]
Cpi TGTTTCGAGGACTGTCTAACCTGAGAATGGTGAAACATGAAGGTCAATCTCAGGTTCGTC [18147]
Cmy TGTTTCGAGGACTGTCTAACCTGAGAATGGTGAAACATGAAGGTCAATCTCAGGTTCGTC [17812]
Psi TGTTTCGAGGACTGTCTAACCTGAGAATGGTGAAACATGAAGGTCAATCTCAGGTTCGTC [16360]
Asp TGTTTCGAGGACTGTCTAACCTGAGAATGGTGAAACATGAAGGTCAATCTCAGGTTCGTC [15509]
Ami CGTCCCCAGGACTGTCTAACCTGAGAATGGTGAAACACGAGGGTCAATCTCAGGTTCGTC [17234]
Asi CGTCCCCAGGACTGTCTAACCTGAGAATGGTGAAACACGAGGGTCAATCTCAGGTTCGTC [16652]
Tgu CACCTCGAGGACTGTCTAACCTGAGAATGGTGAAACATCAAGGTCAATCTCAGGTTCGTC [13536]
Cli CACCTCGAGGACTGTCTAACCTGAGAATGGTGAAATGTAAGGGTCAATCTCAGGTTCGTC [16789]
Gga CACCTCGAGGACTGTCTAACCTGAGAATGGTGAAACATGAGGGTCAATCTCAGGTTCGTC [15087]
Xtr ------------------------------------------------------------ [15354]
Lch TGTTTGGAGGACTGTCTAACCTGAGAATGGTGAA-CTCGAAGGTCAATCTCAGGTTCGTC [17326]
Dre GCTTTCCAGGACTGTCCAACCTGAGAATGCTTGA--GTTTTGGTCAATCTCAGGTTCGTC [15649]

Hsa ------------------------------------------------------------ [16415]
Mmu ------------------------------------------------------------ [16078]
Mdo AGCCCATGAGGTGCCTTCC------------------------------------------ [15313]
Meu ------------------------------------------------------------ [13081]
Oan AGCCCATGAAACGCCTTCT------------------------------------------ [14184]
Aca AGCCCACGAGAAGCTGCCT--CTGTGGGCTTGACATCATCCTACTTGAGATGTAATGTAA [16677]
Pbi AGCCCATGAGACGTTCCTT--CTGTGGGTTTGACATCATCATACTTGGGATGTGCTAACA [16759]
Cpi AGCCCATGAGACGCCTTCT--CTATGGGTTTGACATCATCATACTTGAGATGTA-TGACA [18204]
Cmy AGCCCATGAGACGCCTTCT--CTATGGGTTTGACATCATCATACTTGAGATGTA-TGACA [17869]
Psi AGCCCATGAGACACTTTCT--CTATGGGCTTGACATCATCATACTTGAGATGTA-TGACA [16417]
Asp AGCCCATGAGACACTTTCT--CTATGGGCTTGACATCATCATACTTGAGATGTA-TGACA [15566]
Ami AGCCCATGAGACGCTCTCT--CTATGGGTTTGACATCATCATACTTGGGATGTA-TGTCA [17291]
Asi AGCCCATGAGACGCTCTCT--CTATGGGTTTGACATCATCATACTTGGGATGTA-TGTCA [16709]
Tgu AGCCCATGAGATGCCTTCT--CGATGGGCTTGACATCATCATACTTGGGATGTA-TGACA [13593]
Cli AGCCCATGAGACGCCTTCT--CTATGGGTTTGACATCATCATACTTGGGATGTA-TGACA [16846]
Gga AGCCCATGAGATGCCTTCT--CTATGGGTTTGACATCATCATACTTGGGATGTA-TGACA [15144]
Xtr --------------------CTCTGGGTTTGACATCATCATACTTGGGATGTA-TGACA [15392]
Lch AGCCCATAAAACGCTTCTT------------------------------------------ [17345]
Dre AGCCCATGAAAAACTGTCT------------------------------------------ [15668]

Hsa ------------------------------------------------------------ [16415]
Mmu ------------------------------------------------------------ [16078]
Mdo ------------------------------------------------------------ [15313]
Meu ------------------------------------------------------------ [13081]
Oan ------------------------------------------------------------ [14184]
Aca TGCAAAGTCCCAAGTAGGTTGATGTCTGGCCCAAGATGG--ACCTCCCTGTGCTGGGCTT [16735]
Pbi TT-AAAACCCCAAGCAGGTTGATGTCTGGCCCAAGATGG--ACCTACTTGTGCTGGGCTT [16816]
Cpi C--AAAGTCCCAAGCAGGCTGATGTCAGGCCCAAGATGG--CCCTCTGTGTGTCGGGCTT [18260]
Cmy C--AAAGTCCCAAGCAGGCTGATGTCAGGCCCAAGATGG--CCCTCTGTGTGTCAGGCTT [17925]
Psi C--AAAGTCCCAAGCAGGCTGATGTCAGGTCCAAAATGG---------------------- [16454]
Asp C--AAAGTCCCAAGCAGGCTGATGTCAGGCCCAAGATGG---------------------- [15603]
Ami C--AAAGTCCCAAGAAGGCTGATGTCAGGCCCAAGATTG--CCCGCCGCGTCCTGGGCTT [17347]
Asi C--AAAGTCCCAAGAAGGCTGATGTCAGGCCCAAGATTG--CCCGCCGCGTCCTGGGCTT [16765]
Tgu C--GAAGTCCCAAGCAGGCTGATGTCAGGCCCAAGATGC--CCCGCTGTCTCCAGGGCTT [13649]
Cli C--AAAGTCCCAAGCAGGCTGATGTCAGGCCCAAGATGG--CACACTGTCTCCGGGGCTT [16902]
Gga C--AAAGTCCCAAGCAGGCTGATGTCAGGCCCAAGATGG--CCTGCTGTGTCCCGGGCTT [15200]
Xtr C--AAAGTCCCAAGCAAGCTGATGTTAGGCCCAAGATGG--CCTCCTGGGTCCTGGGCTT [15448]
Lch ----------------------------------------TCTCTTGGGTTCTGGGCTT [17364]
Dre ----------------------------------------TGTCTTGTATCCGAGGCTT [15687]

Hsa ------------------------------------------------------------ [16415]
Mmu ------------------------------------------------------------ [16078]
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Mdo ---------------------------------------------------------- [15313]
Meu ---------------------------------------------------------- [13081]
Oan ---------------------------------------------------------- [14184]
Aca GTTTTCAGTTGCCTGCGG-CTGATTAATAGGGACTCAGGCAGCTAAAGCAAGTCTGATAC [16794]
Pbi GTTTTCAGTTGCCTGCGG-CTGGCTAATATG-ACTCAGGCAGCTAAAGCAAGTCTGGGGC [16874]
Cpi GTTTTCAGTTGCCTGCGG-TTGGTTAGAAGG-ACTCAGGCAGCTAAAGCAAGTCTGGGAC [18318]
Cmy GTTTTCAGTTGCCTGTGG-TTGGTTAGAAGG-ACTCAGGCAGCTAAAGCAAGTCTGGGAC [17983]
Psi ---------------------------------------------------------- [16454]
Asp ---------------------------------------------------------- [15603]
Ami GTTTTCAGTTGCCTGCGGGTTTATTTGGACG-ACTCAGGCAGCTAAAGCAAGTCTGGGAC [17406]
Asi GTTTTCAGTTGCCTGCGGGTTTATTCAGACA-ACTCAGGCAGCTAAAGCAAGTCTGGGAC [16824]
Tgu GTTTTCCGTTGCCTGAGGTTTGTTTCAGTG--ACTCAGGCAGCGAAAGCAAGTCTGGGAG [13707]
Cli GTTTTCCGTTGCCTGCGG-TTTGTTCCAGTG-ACTCAGGCAGCGAAAGCAAGTCTGGGAG [16960]
Gga GTTTTCCGTTGCCTGCGG-TGTGTTGCAGTG-ACTCAGGCAGCGAAAGCAAGTCTGGGAG [15258]
Xtr GTTTTAAGTTGCCTGTGA-TTGTTGGATAGA-GCACAGGCAGCTAAAGCAAGTCTGGGAA [15506]
Lch GTTTTAAGTTGCCTGTGA-TTACATAGCAGA-ACTCAGGCAGCTAAAGCAAGTCTGGAAA [17422]
Dre GTTTTAAGTTGCCTGCGA-TCTCTTAATG---ACTCAGGCAGCTAAAGCAAGTCTGGGAG [15743]

Hsa ---------------------------------------------------------- [16415]
Mmu ---------------------------------------------------------- [16078]
Mdo -----------GATGGATTCTGGGAGTTGTAGCCTTTCAAACAGAGCTCT-GCATGTACA [15361]
Meu -----------GATGGATTCTGGGAGTTGTAGCCTTTCAAACAGAGCTCT-GAATGTACA [13129]
Oan ---------------------------------------------------------- [14184]
Aca ATGAAAGGA--GGAACATTCTAGGAGTTGTAGTCTTTCAAACAGAGCTTT-GCAAGTACA [16851]
Pbi ATGAAAGGT--GGAATATTCTAGGAGTTGTAGTGTTTCAAACAGAGCTTT-GCAAGAACA [16931]
Cpi GCGCGAGGA--GGAATATTCTGGGAGTTGTAGTCTTTCAAACAGAGCTCT-GCAAGTATA [18375]
Cmy GCGTGAGGA--GGAATATTCTGGGAGTTGTAGTCTTTCAAACAGAGCTCT-GCAAGTATA [18040]
Psi -----------GGAATATTCTGGGAGTTGTAGTCTTTCAAACAGAGCTCT-GCAAGTATA [16502]
Asp -----------GGAATATTCTGGGAGTTGTAGTCTTTCAAACAGAGCTCT-GCAAGTATA [15651]
Ami GGGTGAGGA--GGAATATTCTGGGAGTTGTAGTCTTTCAAACAGAGCTTT-GCAAGTACA [17463]
Asi GGGTGAGGA--GGAATATTCTGGGAGTTGTAGTCTTTCAAACAGAGCTTT-GCAAGTACA [16881]
Tgu GCTGCGGAG--GGAATATTCTGGGAGTTGTAGTCTTTCAAACAGAGCTTC-ACAAGGACA [13764]
Cli GCTGTGGAG--GGAATATTCTGGGAGTTGTAGTCTTTCAAACAGAGCTTC-GCAAGGACA [17017]
Gga GCTGTGGAG--GGAATATTCTGGGAGTTGTAGTCTTTCAAACAGAGCTTT-GCAAGGACA [15315]
Xtr GCTGGAGAC--GGAATGCTCTGGGAGTTGTAGTCTTTCAAACAG--CTGT-GAATTTCTA [15561]
Lch GCAGGAGTC------------------------------------------------------ [17431]
Dre GCCAGAGAC------------------------------------------------------ [15752]

Hsa ---------------------------------------------------------- [16415]
Mmu ---------------------------------------------------------- [16078]
Mdo CACCTGTATTGGAACACTACA----GCTCCCCGAACTTCC------------------- [15397]
Meu CACCTGTATTGGAACACTACA----GCTCCCCGAACTTCC------------------- [13165]
Oan ---------------------------------------------------------- [14184]
Aca TACCTGTATTGGAACACTACA----GCTCCAGGAACTTTC------------------- [16887]
Pbi TACCTGTATTGGAACACTACA----GCTCCAGGAACTTCC------------------- [16967]
Cpi TACCTGTATTGGAACACTACA----GCTCCCCGAACTTCC--GTTTCCCCAAACAGTAAG [18429]
Cmy TACCTGTATTGGAACACTACA----GCTCCCCGAACTTCC--GTTTCCCCAAACAGTAAG [18094]
Psi TACCTGTATTGGAATACTACA----GCTCCCTGAACTTCC--GTCTCCCCAAACAGTAAG [16556]
Asp TACCTGTATTGGAATACTACA----GCTCCCTGAACTTCC--GTCTCCCCAAACAGTAAG [15705]
Ami TACCTGTATTGGAACACTACA----GCTCCCTGAACTTCC--GCCGCCCCCAACAGTAAG [17517]
Asi TACCTGTATTGGAACACTACA----GCTCCCTGAACTTCC------------------- [16917]
Tgu TACCTGTATTGGAACACTACA----GCTCCCTGAACTTCC------------------- [13800]
Cli TACCTGTATTGGAACACTACA----GCTCCCTGAACTTCC--GCCCCCCCGAACAGTAAG [17071]
Gga TACCTGTATTGGAACACTACA----GCTCCCTGAACTTCC------------------- [15351]
Xtr TACCTGTATTGGAACACTACA----GCTCCTAGAAATTCC--GCGTCTCGGAACAGTAAG [15615]
Lch ------------------------------------------GGTTCTCAGAACAGTAAG [17449]
Dre ---------------------------------------------------------- [15752]
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Hsa ------------------------------------------------------------ [16415]
Mmu ------------------------------------------------------------ [16078]
Mdo ------------------------------------------------------------ [15397]
Meu ------------------------------------------------------------ [13165]
Oan ------------------------------------------------------------ [14184]
Aca ------------------------------------------------------------ [16887]
Pbi ------------------------------------------------------------ [16967]
Cpi AGTTTATGTGCGGTGAGAGCTAG-AATCTGCATGTGGACTCCTACTGCTCCGGGAGGCTG [18488]
Cmy AGTTTATGTGCGGTGAGAGCTAG-AATCTGCATGTGAACTCCTACTGCTCTGGGAGGCTG [18153]
Psi AGTTTACGTGCGGTGAGAGCTGG-AATCTGCAGGTGAACTCCTACTGCTCTGGGAGGCTG [16615]
Asp AGTTTATGTGCGGTGACAGCTGC-AATCTGCATGTGAACTCCTACTGCTCTGGGAGGCTG [15764]
Ami AGTTTATGTGCGGTGAGAGCTGG-AATCTGCATGTGAACTCCTACTGCTCCGGGCGGCGG [17576]
Asi ------------------------------------------------------------ [16917]
Tgu ------------------------------------------------------------ [13800]
Cli AGTTGATGTGCGGT--GAGCTGC-ATCCTGCATGTGAGCTCCTACTGCCCCGGGAGGCGG [17128]
Gga ------------------------------------------------------------ [15351]
Xtr AGATTATGTGCTGTGTTATCAGGCAGCCGGCACATGGCCTTTTACTGCTCAGAGAGGCAG [15675]
Lch AGTTTATGTGCTGTGAGTGTCTTCAACCAGCACATCAACTTTTACAGTTCAGGGCGGCGG [17509]
Dre ------------------------------------------------------------ [15752]

Hsa ------------------------------------------------------------ [16415]
Mmu ------------------------------------------------------------ [16078]
Mdo ---AGCCCTATGGGAAAGGTCCAATTTTACATGCCCTGTATGAAATAAAAA-GGGCTATG [15453]
Meu ------------------------------------------------------------ [13165]
Oan ---AGACCTGTGGGACAGGTCCAATCTCACATGTCCTGTATAGAATAAAGG-GGGATATA [14240]
Aca ---ACACTTGTGGTCAAGGTCCAACCTCACGTGTCCTGTATGCGATAAAAGAGGGATGCG [16944]
Pbi ---ACACTTGTGGTCAAGGTCCAACCTCATGTGTCCTGTATGCAATGAAAGTGGGATGCA [17024]
Cpi G--AAACCTGTGGGAAAGGTCCAACCTCACATGTCCTGTATGTAATAAAG--GGGATGTA [18544]
Cmy G--AGACCTGTGGGAAAGGTCCAACCTCACATGTCCTGTATATAATAAAG--GGGATATA [18209]
Psi G--AGACCTGTGGGAAAGGTCCAACCTCACATGTCCTGTATGTACGGAAG--GGGATATA [16671]
Asp G--AGACCTGTGGGAAAGGTCCAACCTCACATGTCCTGTGTGCAAGGAGG--GGGATATA [15820]
Ami G--AGACCCGTGGGAAAGGTCCAACCTCACATGTCCTGTATGTCACGAGGA-GGGATATA [17633]
Asi ---AGACCCGTGGGAAAGGTCCAACCTCACATGTCCTGTATGTCACGAGGA-GGGATATA [16973]
Tgu ---AGACCTGTGGGAAAGGTCCAACCTCACATGTCCTGTATAGAATAAAGA-GGGATATA [13856]
Cli G--AGACCTGTGGGAAAGGTCCAACCTCACATGTCCTGTATAGAATAAAGA-GGGATATA [17185]
Gga ---AGACCTGTGGGAAAGGTCCAACCTCACATGTCCTGTATAGAATAAGGA-GGGATATA [15407]
Xtr G--GGGCGTGTGGGAAAGGTCCAGCCTCATATGTCCTGTG-ATCCTGAGG--GGGAGATA [15730]
Lch G--AGACCTGTGGGAAAGGTCCAACCTCACATGTCCTGTATTAAATAAGGA-GGGATATA [17566]
Dre ---AGCAATGTGAGAAAGGTCCAACCTCACATGTCCTGTGAGGCTGAAGGA-AGGCTGTG [15808]

Hsa ------------------------------------------------------------ [16415]
Mmu ------------------------------------------------------------ [16078]
Mdo TGTGGTTGGACCTGTCCCACA-GGCCC--CTTCCTGTCACTGCAGACAGTCAGTAGTTGG [15510]
Meu ----------------------------CTTCCTGTCACTGCAGACAGTCAGTAGTTGG [13196]
Oan TGTGGTCAGACCTATCCCACA-GGCCC--CTTCCTGTCACTGCAGACGGTCAGTAGTTGG [14297]
Aca TGTGGTCAGACCTAGCCCACA-AGCCC--AGATCTGTCACTGCAGACAGTCAGTAGTTGG [17001]
Pbi TGTGGTCAGACCTAGACCACA-AGGCC--TCTTCTGCCACTGCTGACAGTCAGTAGTTGG [17081]
Cpi TGTGGTCAGACCTATCCCACA-GGCCC--CTTCCTGTCACTGCAGACAGTCAGTAGTTGG [18601]
Cmy TGTGGTCAGACCTATCCCACA-GGCCC--CTTCCTGTCACTGCAGACAGTCAGTAGTTGG [18266]
Psi TGTGGTCAGACCTGTCCCACA-GGCCC---------------------------------- [16697]
Asp TGTGGTCAGACCTATCCCACA-GGCCC---------------------------------- [15846]
Ami TGTGGTCAGACCTATCCCACA-GGCCC--CTTCCTGCCACTGCAGACAGTCAGCAGTTGG [17690]
Asi TGTGGTCAGACCTATCCCACA-GGCCC--CTCCCTGCCACTGCAGACAGTCAGCAGTTGG [17030]
Tgu TGTGGTCAGACCTATCCCACA-AGTCC--GCTCCTGCC-CTGCGGACAGTCAGCAGTTGG [13912]
Cli TGTGGTCAGACCTATCCCACA-GGCCC--GCTCCTGCC-CTGCGGACAGTCAGCAGTTGG [17241]
Gga TGTGGTCAGACCTATCCCACA-GGCCC---------------------------------- [15433]
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Xtr TGTGGTCAGACCTGTCCCACA-GGCCG--TCTCCTGTTGCTGCAGACAGTCAGAAGTTGG [15787]
Lch TGTGGTCAGACCTATCCCACA-GGCTC--TCTC-TGTCCCCACGGACAGTCAGCAGTTGG [17622]
Dre TGAGGTTAGACCTATCCCACACGGCCC-------------------------------- [15835]

Hsa ------------------------------------------------GGTCTGGCTGT [16426]
Mmu ------------------------------------------------GGTCTGGCTGT [16089]
Mdo TCTGGTGTGAGCAGGAATTCTCAGATCACCTCTTGGCTGTGAGTGGT--GGTCTGGCTGT [15568]
Meu TCTGGCGTGAGCAGGAATTCTCAGATCACCTCTTGGCTGTGAGTGGT------------- [13243]
Oan TCTGGTGTGAGCAGCAATTCTCAGATCATCTCTTGGCTATGGATGGT--GGTCTGGCTGT [14355]
Aca TCTGGCATAAGCAGAAAGTTTCAGATCACCTCTTGGCTGTGAGTAGT--CATCTGGCTGT [17059]
Pbi TCTGGGGTAAGCAGGAAATCTCAGATCATCTCTTGACTGTGGATGGT--CATCTGGCTGT [17139]
Cpi TCTGGCGAGAGCAGGAATTCTCAGATCACCTCTTGGCTGTGAGTGGT--GATTTGGCTGT [18659]
Cmy TCTGGCGTGAGCAGGAATTCTCAGATCACCTCTTGGCTGTGAGTGGT--GATTTGG--GT [18322]
Psi ------------------------------------------------GATTTGGCTGT [16708]
Asp ------------------------------------------------GATTTGGCTGT [15857]
Ami TCTGGCGTGAGCAGC-ATTCTCAGATCACCTCTTGGCTGTGGGTGGT--GATTTGGCTGT [17747]
Asi TCTGGCGTGAGCAGC-ATTCTCAGATCACCTCTTGGCTGTGGGTGGT--GATTTGGCTGT [17087]
Tgu TCTGGTGTGAGCAGCAATTCTCAGATCACCTCTTGGCTGTGGGTGGT--GATTTGGCTGT [13970]
Cli TCTGGTGTGAGCAGCGATTCTCAGATCACCTCTTGGCTGTGGGTGGT--GATTTGGCTGT [17299]
Gga ------------------------------------------------GATTTGGCTGT [15444]
Xtr TCTGGCGTGAGAATAGATTCTCAGATCATCTCTTGGCTGATGCCAGC--GGTCTGACCCT [15845]
Lch TCTGGTGTGAGGGGA---TCTCAGATCAGCTCTTGACTGTGGGTGGT--GGTCTGGCTGT [17677]
Dre -------------------------------------------------------------- [15835]

Hsa TGTGGTGTGCAAAACTCCGTA---CATTGCTATTTTGCCACACTGCAACACCTTACAG-- [16481]
Mmu TGTGGTGTGCAAAACTCCGTA---CATTGCTATTTTGCCACACTGCAACACCTTACAG-- [16144]
Mdo TGTGGTGTGCAAAACTTCCTA---TGTTGCTTTTTTGCCACACTGCAACACTTTACAG-- [15623]
Meu -------------------------------------------------------------- [13243]
Oan TGTGGTGTGCAAAACTTCGTA---CATTGCTTTTTTGCCACACTGCAACACTTTACAG-- [14410]
Aca TGTGGTGTGCAAATTTTTGTG---CATTGCC-TTTTGCTGCACTGCAACACTTTACAG-- [17113]
Pbi TGTGGTGTGCAAAATTTTGTA---CATTGC--TTTTGCTGCACTGCAACACTTTACAG-- [17192]
Cpi TGTGGTGTGCAAAACTTTGTA---CATTGCT-TTTTGCCACACTGCAACACTTTACAG-- [18713]
Cmy TGTGGTGTGCAAAACTTTGTA---CATTGCT-TTTTGCCACACTGCAACACTTTACAG-- [18376]
Psi TGTGGTGTGCAAAATCTTGTA---CATTGCC-TTTTGCTGCACTGCAACACTTTACAG-- [16762]
Asp TGTGGTGTGCAAAACCTTGTA---CATTGCC-TTTTGCTGCACTGCAACACTTTACAG-- [15911]
Ami TGTGGTGTGCAAAACTTTGTG---CGTTGCT-TTTTGCCACACTGCAACACTTTACAG-- [17801]
Asi TGTGGTGTGCAAAACTTTGTG---CGTTGCT-TTTTGCCACACTGCAACACTTTACAG-- [17141]
Tgu TGTGGTGTGCAAAACTTTGTA---CCTCGCT-TTTTGCCACACTGCAACACTTTACAG-- [14024]
Cli TGTGGTGTGCAAAACTTTGTA---CCTTGCT-TTTTGCCACACTGCAACACTTTACAG-- [17353]
Gga TGTGGTGTGCAAAACTTTGTA---CCTTGCT-TTTTGCCACACTGCAACACTTTACAG-- [15498]
Xtr TGTGGTGTGCAAAACCTTATTTGCCCTCCCTGTTTTGCCACACTGCGACACTCTACAG-- [15903]
Lch TGTGGTGTGCAAAATTCTGTA---CATTTTC-TTTTGCCACACTGCAACACTTTACAG-- [17731]
Dre -------------------------------------------------------------- [15835]

Hsa GAGTGCATTGTGATTTCCAATAATTGAGGCAGTGGT-TCT-AAAAGCTGTCTACATTAAT [16539]
Mmu GAGTGCATTGTGATTTCCAATAATTGAGGCAGTGGT-TCT-AAAAGCTGTCTACATTAAT [16202]
Mdo GAATGCATTGTGATTTCCAATAATTGAGACAGTGAT-TCT-AAAAGCTGTCTACATTAAT [15681]
Meu GAATGTATTGTGATTTCCAATAATTGAGGCAGTGAT-TTT-AAAAGCTGTCTACATTAAT [13301]
Oan -------------------------------------------------------------- [14410]
Aca GAATGCATTGTGATTTCCAGTAATTGAGACAGTGAT-TCT-GAAAGCTGTCTACATTAAT [17171]
Pbi GAATGCATTGTGATTTCCAGTAATTGAGACAGTGAT-TCT-GAAAGCTGTCCACATTAAT [17250]
Cpi GAATGCATTGTGATTTCCAATAATTGAGACAGTGAT-TCT-GAAAGCTGTCTACATTAAT [18771]
Cmy GAATGCATTGTGATTTCCAATAATTGAGACAGTGAT-TCT-GAAAGCTGTCTACATTAAT [18434]
Psi GAATGCATTGTGATTTCCAATAATTGAGACAGTGAT-TCT-GAAAGCTGTCTACATTAAT [16820]
Asp GAATGCATTGTGATTTCCAATAATTGAGACAGTGAT-TTT-GAAAGCTGTCTACATTAAT [15969]
Ami GAATGCATTGTGATTTCCAATAATTGAGACAGTGAT-TCT-GAAAGCTGTCTACATTAAT [17859]
Asi GAATGCATTGTGATTTCCAATAATTGAGACAGTGAT-TCT-GAAAGCTGTCTACATTAAT [17199]
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Tgu ------------------------------------------------------------ [14024]
Cli GAATGCATTGTGATTTCCAATAATTGAGACAGTGAT-TCT-GAAAGCTGTCTACATTAAT [17411]
Gga GAATGCATTGTGATTTCCAATAATTGAGACAGTGAT-TCT-GAAAGCTGTCTACATTAAT [15556]
Xtr GAATACATTGTGATTTCCAGTAATAGAGACAGTATT-TCT-GAAGGCTGTCTACATTAAT [15961]
Lch GAATGCATTGTGATTTCCAATAATTGAGACAGTAAT-TCT-GACAGCTGTCTACATTAAT [17789]
Dre GAATGCATTGTGATTTCCAATAATTGAGACAGTAATTTCTAAAAAGCTGTCTACATTAAT [15895]

Hsa GAAAAGAGCAATGTGGCCA [16558]
Mmu GAAAAGAGCAATGTGGCCA [16221]
Mdo GAAAAGAACAATGTAGTCA [15700]
Meu CAAAAGAACAATGCAGTCA [13320]
Oan ------------------- [14410]
Aca GAAAAGAACAATGTAGTCA [17190]
Pbi GAAAAGAACAATGTAGTCA [17269]
Cpi GAAAAGAACAATGTAGTCA [18790]
Cmy GAAAAGAACAATGTAGTCA [18453]
Psi GAAAAGAACAATGTAGTCA [16839]
Asp GAAAAGAACAATGTAGTCA [15988]
Ami GAAAAGAACAATGTAGTCA [17878]
Asi GAAAAGAACAATGTAGTCA [17218]
Tgu ------------------- [14024]
Cli GAAAAGAACAATGTAGTCA [17430]
Gga GAAAAGAACAATGTAGTCA [15575]
Xtr GAAAAGAGCAATGTAGTCA [15980]
Lch GAAAAGAACAATGTAGTCA [17808]
Dre GAAAAGAACAATGTAGTCA [15914]

;
END;
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New Name	Gentic Anchor(s)	Hsa	Mmu	Gga	Aca	Xtr	Dre
Let-7							
let-7-P1	miR-100, miR-125b-1	let-7a-2	let-7a-2	let-7a-2	let-7a-2 (new, I	X	
let-7-P1a							let-7a-2
let-7-P1b							let-7a-4
let-7-P2	miR-99b, miR-125a	let-7e	let-7e	X	let-7c-2	let-7a	
let-7-P2a							let-7d-1
let-7-P2b							let-7d-2
let-7-P3	miR-99a, miR-125b-2	let-7c	let-7c-1	let-7c	let-7c-1	let-7c	
let-7-P3a							let-7c-1
let-7-P3b							let-7c-2
let-7-P4	let-7a-1, let-7f-1	let-7d	let-7d	let-7d	let-7d	X	X
let-7-P5	let-7a-1, let-7d	let-7f-1	let-7f-1	let-7f	let-7f-2	X	let-7f
let-7-P6	PDPDC1, let-7d, let-7f-1	let-7a-1	let-7a-1	let-7a-1	let-7a	let-7e-1	let-7a-1
let-7-P7	let-7b	let-7a-3	let-7c-2	let-7a-3	let-7a-3 (new)	let-7e-2	let-7a-3
let-7-P8	let-7a-3	let-7b	let-7b	let-7b	let-7b	let-7b (?)	let-7b
let-7-P9	let-7f-2	miR-98	miR-98	X	miR-98	miR-98	let-7h
let-7-P10	miR-98	let-7f-2	let-7f-2	X	let-7f-1	let-7f	
let-7-P10a							let-7g-2
let-7-P10b							let-7g-1
let-7-P11	WRD82, miR-135a-1	let-7g	let-7g	let-7g	let-7g	let-7g	let-7j
let-7-P12	MON2, PPM1H	let-7i	let-7i	let-7i	let-7i	let-7i	let-7i
let-7-P13	Pl16, MTCH1	X	X	let-7j	let-7a-4 (new -	X	
let-7-P13a							let-7a-5
let-7-P13b							let-7a-6
let-7-P14	Pl16, MTCH1	X	X	let-7k	let-7e	X	
miR-1							
miR-1-P1	GATA5, NTSR1	miR-1-1	miR-1a-1	miR-1a-1	miR-1a-2	miR-1a-2 (phylog	miR-1-1
miR-1-P2	MIB1	miR-1-2	miR-1a-2/miR-1	miR-1a-2	miR-1a-1	miR-1a-1	miR-1-2

miR-1-P3	IL17A, PKHD1	miR-206	miR-206	miR-206	miR-206 (phylo	miR-206	
miR-1-P3a							miR-206-1
miR-1-P3b							miR-206-2
miR-1-P4	miR-133c	X	X	miR-1b	miR-1b	miR-1b	X
miR-7							
miR-7-P1	HNRNPK	miR-7-1	miR-7a-1	miR-7a-1	miR-7-2	miR-7-1	miR-7b
miR-7-P2	AEN, ISG20	miR-7-2	miR-7a-2	miR-7a-2	miR-7-3	miR-7-2	miR-7a-2 ?
miR-7-P3	FEM1A, TICAM1	miR-7-3	miR-7b	miR-7a-3	miR-7-1 (phylo	X	miR-7a-1 ?
miR-7-P4	ubqln4, apoa1bp	X	X	X	X	miR-7-3	miR-7a-3
miR-8							
miR-8-P1	miR-200b, miR-429	miR-200a	miR-200a	miR-200a	miR-200a	miR-200a	miR-200a
miR-8-P2	miR-200a, miR-429	miR-200b	miR-200b	miR-200b	miR-200b	miR-200b	miR-200b
miR-8-P3	miR-200a, miR-200b	miR-429	miR-429	miR-429	miR-429	miR-429	
miR-8-P3a							miR-429a
miR-8-P3b							miR-429b
miR-8-P4	miR-141	miR-200c	miR-200c	X	X	X	miR-200c
miR-8-P5	miR-200c	miR-141	miR-141	X	X	X	miR-141
miR-9-P1	MEF2D, RHBG	miR-9-1	miR-9-1	X	X	miR-9a-1	miR-9-1
miR-9-P2	MEF2C	miR-9-2	miR-9-2	miR-9-2	miR-9-1	miR-9a-2	
miR-9-P2a							miR-9-2
miR-9-P2b							miR-9-5
miR-9-P3	POLG, KIF7	miR-9-3	miR-9-3	miR-9-3 (new, I	miR-9-2	miR-9-3	miR-9-6
miR-9-P4	gatad2a, tmem161a	X	X	miR9-1	miR-9-3	miR-9b	miR-9-4
miR-9-P5							
miR-9-P6							
miR-9-P7							
miR-9-P8							
miR-9-o1							miR-9-3

miR-9-o2							miR-9-7
miR-10							
miR-10-P1a	HOXB3	miR-10a	miR-10a	miR-10a	miR-10a	miR-10a	
miR-10-P1a1							miR-10a
miR-10-P1a2							miR-10c
miR-10-P1b	HOXD3	miR-10b	miR-10b	miR-10b	miR-10b	miR-10b	miR-10b-1
miR-10-P1c	HoxC4, HoxC5	X	X	X	miR-10c	miR-10c	
miR-10-P1c1							miR-10b-2
miR-10-P1c2							miR-10d
miR-10-P1d							
miR-10-P1e							
miR-10-P2							
miR-10-P2a	LET-7a-2, miR-125b-1	miR-100	miR-100	miR-100	miR-100	X	
miR-10-P2a1							miR-100-1
miR-10-P2a2							miR-100-2
miR-10-P2b	LET-7c, miR-125b-2	miR-99a	miR-99a	miR-99	miR-99a	miR-99	
miR-10-P2b1							miR-99-1
miR-10-P2b2							miR-99-2
miR-10-P2c	LET-7e, miR-125a	miR-99b	miR-99b	X	miR-99b	miR-100	X
miR-10-P3							
miR-10-P3a	LET-7e, miR-99b	miR-125a	miR-125a	X	miR-125a	miR-125a	
miR-10-P3a1							miR-125a-1
miR-10-P3a2							miR-125a-2
miR-10-P3b	LET-7a-2, miR-100	miR-125-b1	miR-125b-1	miR-125b-1 (ne	miR-125b-1	miR-125b-1 (phy	
miR-10-P3b1							miR-125b-1
miR-10-P3b2							miR-125b-2
miR-10-P3c	LET-7c. miR-99a	miR-125b-2	miR-125b-2	miR-125b	miR-125b-2	miR-125b-2	
miR-10-P3c1							miR-125c
miR-10-P3c2							miR-125b-3

miR-15-P1	KPNA3, TRIM13	miR-15a	miR-15a	miR-15a	X	miR-15a	
miR-15-P1a							miR-15a-1
miR-15-P1b							miR-15a-2
miR-15-P2	SMC4, miR-16-2	miR-15b	miR-15b	miR-15b	miR-15a	miR-15b	miR-15c
miR-15-P3	hprt1, fam122	X	X	miR-15c	miR-15b	miR-15c	X
miR-15-P4	RNaseK, miR-195	miR-497	miR-497	X	X	X	miR-15b
miR-15-P5	KPNA3, TRIM13	miR-16-1	miR-16-1	miR-16-1	X	miR-16a	
miR-15-P5a							miR-16b
miR-15-P5b							miR-16c
miR-15-P6	SMC4, miR-15b	miR-16-2	miR-16-2	miR-16-2	miR-16a	miR-16b	miR-16a
miR-15-P7	hprt1, fam122	X	X	miR-16c	miR-16b	miR-16c	X
miR-15-P8	RNAseK, miR-497	miR-195	miR-195	X	miR-457 (phylo	X	
miR-15-P8a							miR-457a
miR-15-P8b							miR-457b
miR-17-P1	miR-18a, miR-20a	miR-17	miR-17	miR-17	miR-17	miR-17	
miR-17-P1a							miR-17a-1
miR-17-P1b							miR-17a-2
miR-17-P2	miR-17, miR-20a	miR18a	miR-18a	miR-18a	miR-18a	miR-18a	
miR-17-P2a							miR-18a
miR-17-P2b							miR-18b
miR-17-P3	miR-17, miR-18a	miR-20a	miR-20a	miR-20a	miR-20a	miR-20a	miR-20a
miR-17-P4	miR-18b, miR-20b	miR-106a	miR-106a	miR-106	miR-106 (new,	miR-106	X
miR-17-P5	miR-106a, miR-20b	miR-18b	miR-18b	miR-18b	miR-18b	miR-18b	miR-18c
miR-17-P6	miR-106a, miR-18b	miR-20b	miR-20b	miR-20b	miR-20b	miR-20b	miR-20b
miR-17-P7	miR-25, miR-93	miR-106b	miR-106b	X	X	X	X
miR-17-P8	miR-25, miR-106b	miR-93	miR-93	X	X		miR-93
miR-17-P8a						miR-93a	
miR-17-P8b						miR-93b	
miR-19-P1	miR-17 cluster	miR-19a	miR-19a	miR-19a	miR-19a	miR-19a	miR-19a

miR-19-P2	miR-17 cluster	miR-19b-1	miR-19b-1	miR-19b-1 (old	miR-19b-1 (old	miR-19b-2	
miR-19-P3	miR-106/18b cluster	miR-19b-2	miR-19b-2	miR-19b-2 (nev	miR-19b-2 (nev	miR-19b-1	
miR-23-P1	miR-23a/24-2/27a cluster	miR-23a	miR-23a	X	miR-23a	miR-23a-1	
miR-23-P1a							miR-23a-2
miR-23-P1b							miR-23a-4
miR-23-P2	miR-23b/24-1/27b cluster	miR-23b	miR-23b	miR-23b	miR-23b	miR-23b	
miR-23-P2a							miR-23b
miR-23-P2b							miR-23c (new, (
miR-23-P3		X	X	X	X	miR-23a-2	
miR-23-P3a							miR-23a-1
miR-23-P3b							miR-23a-3
miR-24-P1	miR-23a/24-2/27a cluster	miR-24-2	miR-24-2	X	miR-24-1	miR-24b	
miR-24-P1a							miR-24-2
miR-24-P1b							miR-24-5
miR-24-P2	miR-23b/24-1/27b cluster	miR-24-1	miR-24-1	miR-24	miR-24-2	miR-24a	
miR-24-P2a							miR-24-1
miR-24-P2b							miR-24-3
miR-24-P3		X	X	X	X	X	miR-24-4
miR-26-P1	CTDSPL	miR-26a-1	miR-26a-1	miR-26a	miR-26-2	miR-26-3 (new)	
miR-26-P1a							miR-26a-2
miR-26-P1b							miR-26a-3
miR-26-P2	CTDSP2	miR-26a-2	miR-26a-2	X	miR-26-3 (new,	miR-26-1	miR-26b
miR-26-P3	CTDSP1	miR-26b	miR-26b	miR-26a-2 (nev	miR-26-1	miR-26-2	miR-26a-1
miR-27-P1	miR-23a/24-2/27a cluster	miR-27a	miR-27a	X	miR-27a	miR-27a	
miR-27-P1a							miR-27c-1
miR-27-P1b							miR-27c-2
miR-27-P2	miR-23b/24-1/27b cluster	miR-27b	miR-27b	miR-27b	miR-27b	miR-27b	

miR-27-P2a							miR-27d
miR-27-P2b							miR-27b
miR-27-P3a		X	X	X	X		miR-27e
miR-27-P3b							miR-27a
miR-27-P3c						miR-27c-1	
miR-27-P3d						miR-27c-2	
miR-29							
miR-29-P1	miR-29a cluster	miR-29a	miR-29a	miR-29a	miR-29a-1	miR-29a	miR-29a
miR-29-P2	miR-29a cluster	miR-29b-1	miR-29b-1	miR-29b-1	miR-29b-2	miR-29d	miR-29b-2
miR-29-P3	miR-29c cluster	miR-29c	miR-29c	miR-29c	miR-29a-2	miR-29c	X
miR-29-P4	miR-29c cluster	miR-29b-2	miR-29b-2	miR-29b-2	miR-29b-1	miR-29b	miR-29b-1
miR-30-P1	miR-30c-2	miR-30a	miR-30a	miR-30a	miR-30a	miR-30a	miR-30a
miR-30-P2	miR-30a	miR-30c-2	miR-30c-2	miR-30c-2	miR-30c	miR-30c-2	X
miR-30-P3	miR-30c-1	miR-30e	miR-30e	miR-30e	miR-30e	miR-30e	miR-30e-2
miR-30-P4	miR-30e	miR-30c-1	miR-30c-1	miR-30c-1	miR-30c-2 (nev	miR-30c-1	miR-30c
miR-30-P5	miR-30b	miR-30d	miR-30d	miR-30d	miR-30d	miR-30d	miR-30d
miR-30-P6	miR-30d	miR-30b	miR-30b	miR-30b	miR-30b	miR-30b	miR-30b
miR-33							
miR-33-P1	SREBF2	miR-33a	miR-33	miR-33	miR-33-1	miR-33b	X
miR-33-P2	SREBF1	miR-33b	X	miR-33-2 (new,	miR-33-2	miR-33a	X
miR-34							
miR-34-P1	GPR157, H6PD	miR-34a	miR-34a	miR-34a	miR-34b	miR-34a	
miR-34-P2a	BTG4	miR-34b	miR-34b	miR-34b	miR-34c	miR-34b-1-4	
miR-34-P2b	BTG4	miR-34c	miR-34c	miR-34c	miR-34a	X	
miR-34-P3a	CDC20B	miR-449a	miR-449a	miR-449a	miR-449a	miR-449a	
miR-34-P3b	CDC20B	miR-449b	miR-449b	miR-449b	X	miR-449b	
miR-34-P3c	CDC20B	miR-449c	miR-449c	X	miR-449b	miR-449c	

miR-34-P3d	cdc20b	X	X	X	miR-449c	X	
miR-92							
miR-92-P1	miR-17 cluster	miR-92a-1	miR-92a-1	miR-92	miR-92a-1	miR-92a-1	
miR-92-P1a							miR-92a-1
miR-92-P1b							miR-92a-2
miR-92-P2	miR-106/18b cluster	miR-92a-2	miR-92a-2	miR-92a-2 (nev	miR-92a-2	miR-92a-2	X
miR-92-P3	miR-93 cluster	miR-25	miR-25	X	X	miR-25	miR-25
miR-92-P4	MTX1	miR-92b	miR-92b	X	X	miR-92b (phylog	miR-92b
miR-96-P1	miR-96 cluster	miR-96	miR-96	miR-96 (new, E	Reads detectec	miR-96	
miR-96-P2	miR-96 cluster	miR-182	miR-182	miR-182 (new,	miR-182 (locus	miR-182	
miR-96-P3	miR-96 cluster	miR-183	miR-183	miR-183	Reads detectec	miR-183	
miR-101-P1	JAK1, AK4	miR-101-1	miR-101a	miR-101-2	miR-101-1	miR-101a-2	miR-101a
miR-101-P2	JAK2, RCL1	miR-101-2	miR-101b	miR-101-1	miR-101-2	miR-101a-1	miR-101b
miR-103-P1	PANK3	miR-103a-1/miR	miR-103-1	miR-103-1	miR-103	miR-103-1	X
miR-103-P2	PANK2	miR-103a-2/miR	miR-103-2	miR-103-2	miR-103-2 (nev	miR-103-2	miR-103
miR-103-P3	PANK1	miR-107	miR-107	miR-107	miR-107	miR-107	
miR-103-P3a							miR-107a
miR-103-P3b							miR-107b
miR-124							
miR-124-P1	MSRA	miR-124-1	miR-124a-1	X	miR-124b	miR-124-2 (new)	miR-124-2
miR-124-P2	CYP7B1, GGH	miR-124-2	miR-124-2	miR-124a/miR-	miR-124a-1	miR-124	
miR-124-P2a							miR-124-1 (phy
miR-124-P2b							miR-124-3 (phy
miR-124-P3	YTHDF1	miR-124-3	miR-124-3	miR-124a-2	miR-124a-2	miR-124-3 (new)	miR-124-6
miR-124-P4	ythdf2	X	X	miR-124b	miR-124a-3	X	miR-124-4
miR-124-Po1							miR-124-5 (mig

miR-128-P1	R3HDM1	miR-128-1	miR-128-1	miR-128-1	miR-128-2	miR-128-1	miR-128-2 (new
miR-128-P2	ARPP21	miR-128-2	miR-128-2	miR-128-2	miR-128-1	miR-128-2 (phylo	miR-128-1
miR-129-P1	LRRC4	miR-129-1	miR-129-1	X	miR-129a (phyl	miR-129-2?	
miR-129-P1a							miR-129-1
miR-129-P1b							miR-129-3 (new
miR-129-P2	HSD17B12	miR-129-2	miR-129-2	X	miR-129b (phy	miR-129-1	
miR-129-P2a							miR-129-2
miR-129-P2b							miR-129-4 (new
miR-130-P1	UBE2L6	miR-130a	miR-130a	X	miR-130a-1	X	X
miR-130-P2	PPIL2, miR-301b	miR-130b	miR-130b	miR-130b	miR-130b	miR-130b	miR-130b
miR-130-P3	PPIL2, miR-130b	miR-301b	miR-301b	miR-301a	miR-301b	miR-301-2	
miR-130-P3a							miR-301b
miR-130-P3b							miR-301c
miR-130-P4	ppil2, miR-130b	X	X	miR-130a	miR-130c	miR-130c	
miR-130-P4a							miR-130c-2
miR-130-P4b							miR-130c-1
miR-130-P5	ska2, smg8	X	X	miR-130c	miR-130a-2	miR-130a	miR-130a
miR-130-P6	SKA2, SMG8	miR-301a	miR-301a	miR-301b	miR-301a	miR-301-1	miR-301a
miR-132-P1	miR-132/miR-212	miR-132	miR-132	X	miR-132 (phylo	miR-132	
miR-132-P1a							miR-132-1
miR-132-P1b							miR-132-2/132-
miR-132-P2	miR-132/miR-212	miR-212	miR-212	X	miR-212 (phylo	miR-212	miR-212
miR-133							
miR-133-P1	GATA5, NTSR1	miR-133a-2	miR-133a-2	miR-133a-2	miR-133a-1	miR-133c	miR-133a-2
miR-133-P2	MIB1	miR-133a-1	miR-133a-1	miR-133a-1	miR-133a-2	miR-133a	miR-133a-1
miR-133-P3	IL17A, PKHD1	miR-133b	miR-133b	miR-133b	miR-133b (new	miR-133b	

miR-133-P3a							miR-133b
miR-133-P3b							miR-133c
miR-133-P4	miR-1b	X	X	miR-133c	miR-133a-3 (ne	miR-133d	X
miR-135-P1	WRD82, let-7g	miR-135a-1	miR-135a-1	miR-135a-1	miR-135-1	X	miR-135b
miR-135-P2	NEDD1	miR-135a-2	miR-135a-2	miR-135a-2	miR-135-2	miR-135-1	miR-135a
miR-135-P3	LEMD1, CDK18	miR-135b	miR-135b	miR-135a-3	miR-135-3	miR-135-2	
miR-135-P3a							miR-135c-1
miR-135-P3b							miR-135c-2
miR-137							
miR-137-P1	DPYD	miR-137	miR-137	miR-137	miR-137a	miR-137-1/2/3	
miR-137-P1a							mir-137-1
miR-137-P1b							miR-137-2/3
miR-137-P2		X	X	X	miR-137b	X	
miR-138-P1	TOPAZ1 (C3ORF77), c3orf2	miR-138-1	miR-138-1	miR-138-1	miR-138-2	miR-138	miR-138-2 (new
miR-138-P2	SLC12A3	miR-138-2	miR-138-2	miR-138-2	miR-138-1	X	miR-138
miR-146-P1	ATP10B, PTTG1	miR-146a	miR-146a	miR-146a	X	miR-146a (phylo	miR-146b
miR-146-P2	ACTR1A, FBXL15	miR-146b	miR-146b	miR-146b	miR-146a (phyl	X	miR-146a
miR-146-P3	ddrgk1	X	X	miR-146c	miR-146b	miR-146b	X
miR-148-P1	SNX10, CBX3	miR-148a	miR-148a	miR-148a	miR-148a	miR-148a	miR-148
miR-148-P2	COPZ1	miR-148b	miR-148b	X	miR-148b	miR-148b	X
miR-148-P3	COPZ2	miR-152	miR-152	X	X	X	miR-152
miR-153							
miR-153-P1	PTPRN	miR-153-1	X	X	miR-153-2	miR-153-1	
miR-153-P1a							miR-153b
miR-153-P1b							miR-153c

miR-153-P2	PTPRN2	miR-153-2	miR-153	miR-153	miR-153-1	miR-153-2 (phylo	miR-153a
miR-155-P1	JAM2, APP	miR-155	miR-155	miR-155	miR-155	miR-155	miR-155
miR-155-P2	?	X	X	X	miR-155b (new	X	X
miR-181-P1	miR-181b-1	miR-181a-1	miR-181a-1	miR-181a-1	miR-181a-1	miR-181a-1	miR-181a-1
miR-181-P2	miR-181a-1	miR-181-b1	miR-181b-1	miR-181b-1	miR-181b-2	miR-181-b1	new (CABZ0103
miR-181-P3	miR-181b-2	miR-181a-2	miR-181a-2	miR-181a-2	miR-181a-2	miR-181a-2	miR-181a-2
miR-181-P4	miR-181a-2	miR-181b-2	miR-181b-2	miR-181b-2	miR-181b-1	miR-181b-2	miR-181b-2
miR-181-P5	miR-181d	miR-181c	miR-181c	X	miR-181a-3	X	
miR-181-P5a							new (BX649502
miR-181-P5b							new (CU571393
miR-181-P6	miR-181c	miR-181d	miR-181d	X	miR-181c (new	X	
miR-181-P6a							miR-181b-1
miR-181-P6b							miR-181c
miR-190							
miR-190-P1	TLN2	miR-190a	miR-190a	miR-190	miR-190a	X	miR-190a
miR-190-P2	TPM3	miR-190b	miR-190b	miR-190b (new	miR-190b (phyl	miR-190	miR-190b
miR-192-P1	EHD1, miR-194-2	miR-192	miR-192	X	X	miR-192	miR-192
miR-192-P2	IARS2, miR-194-1	miR-215	miR-215	miR-215	miR-215	miR-215	X
miR-193							
miR-193-P1	miR-365b	miR-193a	miR-193a	miR-193a (phyl	miR-193	X	
miR-193-P1a							miR-193a-1
miR-193-P1b							miR-193a-2
miR-193-P2	miR-193a	miR-365b	miR-365-2	miR-365-2 (phy	miR-365	X	
miR-193-P2a							miR-365-2
miR-193-P2b							miR-365-3
miR-193-P3	miR-365a	miR-193b	miR-193b	miR-193b	X	miR-193	miR-193b

miR-193-P4	miR-193b	miR-365a	miR-365-1	miR-365-1	X	miR-365	miR-365-1
miR-194-P1	EHD1, miR-192	miR-194-2	miR-194-2	X	miR-194-2	miR-194-2	
miR-194-P1a							miR-194a
miR-194-P1b							miR-194b
miR-194-P2	IARS2, miR-215	miR-194-1	miR-194-1	miR-194	miR-194-1	miR-194-1	X
miR-196-P1	HOXB	miR-196a-1	miR-196a-1	miR-196-1	miR-196c	X	miR-196b
miR-196-P2	HOXC	miR-196a-2	miR-196a-2	miR-196-3	miR-196a-2	miR-196a	
miR-196-P2a							miR-196a-1
mir-196-P2b							miR-196c
miR-196-P3	HOXA	miR-196b	miR-196b	miR-196-2	miR-196a-1	miR-196b	
miR-196-P3a							miR-196a-2
miR-196-P3b							miR-196d
miR-199-P1	DNM2	miR-199a-1	miR-199a-1	X	miR-199a-1	miR-199b	miR-199-2
miR-199-P2	DNM3, miR-214 (?)	miR-199a-2	miR-199a-2	miR-199-2	miR-199a-2 (pl	miR-199a	miR-199-1
miR-199-P3	DNM1	miR-199b	miR-199b	miR-199-1	miR-199b	X	miR-199-3
miR-204-P1	TRPM3	miR-204	miR-204	miR-204-1	miR-204a-2	miR-204-2	miR-204-1
miR-204-P2	TRPM1	miR-211	miR-211	miR-204-2	miR-204a-1	miR-204-1	
miR-204-P2a							miR-204-2
miR-204-P2b							new (ENSDARG
miR-204-P3	?	X	X	miR-211	X	X	X
miR-205-P1	LAMB3, CAMK1G	miR-205	miR-205	miR-205a	miR-205a	miR-205a	
miR-205-P2	ENSGALG00000008449	X	X	miR-205b	miR-205b	miR-205b (phylogeny)	
miR-208-P1	MYH6	miR-208a	miR-208a	X	miR-208 (phylo	miR-208	X
miR-208-P2	MYH7	miR-208b	miR-208b	X	X	X	miR-736

miR-216							
miR-216-P1	miR-216b, miR-217	miR-216a	miR-216a	miR-216a	miR-216a	miR-216	miR-216a
miR-216-P2	miR-216a, miR-217	miR-216b	miR-216b	miR-216b	miR-216b	X	miR-216b
miR-218-P1	SLIT2	miR-218-1	miR-218-1	miR-218-1	miR-218-1	miR-218-1	miR-218a-2
miR-218-P2	SLIT3	miR-218-2	miR-218-2	miR-218-2	miR-218-2	miR-218-2	miR-218a-1
miR-218-P3		X	X	X	X	X	miR-218b
miR-219							
miR-219-P1	RING1	miR-219a-1	miR-219a-1/mil	X	miR-219-2 (phy	X	miR-219-3
miR-219-P2	URM1	miR-219a-2/miR	miR-219a-2/mil	miR-219a/miR-	miR-219-1	miR-219 (phylogeny)	
miR-219-P2a							miR-219-1
miR-219-P2b							miR-219-2
miR-221-P1	miR-222	miR-221	miR-221	miR-221	miR-221	miR-221	miR-221
miR-221-P2	miR-221	miR-222	miR-222	miR-222a	miR-222	miR-222	miR-222a
miR-221-P3	fundc2	X	X	miR-222b	miR-222b (new	X	miR-222b
miR-223-P1	MSN, HEPH	miR-223	miR-223	miR-223	miR-223	miR-223	miR-223
miR-223-P2	VPS13B	miR-599	miR-599	X	X	X	X
miR-338-P1	AATK	miR-338	miR-338	miR-338 (new,	miR-338	miR-338-1	
miR-338-P1a							miR-338-1
miR-338-P1b							new (ENSDARG
miR-338-P2	lmtk2	X	X	X	X	miR-338-2	miR-338-2
miR-430-P1	miR-302/367 cluster	miR-302a	miR-302a	miR-302a	miR-302a (new	miR-302	
miR-430-P2	miR-302/367 cluster	miR-302b	miR-302b	miR-302b	miR-302	X	
miR-430-P3	miR-302/367 cluster	miR-302c	miR-302c	miR-302c	X	X	
miR-430-P4	miR-302/367 cluster	miR-302d	miR-302d	miR-302d	X	X	

miR-454-P1	SKA2, miR-301a	miR-454	X	X	X	X	miR-454a
miR-454-P2	ppil2, miR-130b	X	X	miR-454	miR-454	miR-454 (new EN	miR-454b
miR-460-P1	pth1r	X	X	miR-460a	miR-460a	miR-460a (new,	miR-460
miR-460-P2	htr2c	X	X	miR-460b	miR-460b	miR-460b (new,	miR-730
miR-551-P1	MEGF6	miR-551a	X	X	X	miR-551a (new)	X
miR-551-P2	MECOM	miR-551b	miR-551b	miR-551	miR-551	miR-551b (new,	X

```
#NEXUS

[MacClade 4.08 registered to Kevin J. Peterson, Dartmouth
College]

BEGIN DATA;    DIMENSIONS  NTAX=19 NCHAR=238;     FORMAT
SYMBOLS= " 0 1 2" MISSING=? GAP=- ;

CHARSTATELABELS          1  'let-7-P1 (1-72)',  2  'let-7-
P2 (75-150)',  3  'let-7-P3 (153-225)',  4  'let-7-P4 (228-
310)',  5  'let-7-P5 (313-397)',  6  'let-7-P6 (400-479)',
7  'let-7-P7 (482-558)',  8  'let-7-P8 (561-643)',  9
'let-7-P9 (646-730)',  10  'let-7-P10 (733-811)',  11
'let-7-P11 (814-899)',   12  'let-7-P12 (902-984)',  13
'let-7-P13 (987-1068)',  14  'let-7-P14 (1071-1147)',  15
'miR-1-P1 (1150-1231)',  16  'miR-1-P2 (1234-1317)',   17
'miR-1-P3 (1320-1403)',  18  'miR-1-P4 (1406-1491)',  19
'miR-7-P1 (1494-1581)',  20  'miR-7-P2 (1584-1673)',  21
'miR-7-P3 (1676-1763)',   22  'miR-7-P4 (1766-1851)',  23
'miR-8-P1 (1854-1939)',  24  'miR-8-P2 (1942-2024)',  25
'miR-8-P3 (2027-2111)',  26  'miR-8-P4 (2114-2201)',   27
'miR-8-P5 (2204-2291)',  28  'miR-9-P1 (2294-2382)',  29
'miR-9-P2 (2385-2469)',  30  'miR-9-P3 (2472-2557)',  31
'miR-9-P4 (2560-2647)',   32  'miR-10-P1a (2650-2730)',  33
'miR-10-P1b (2733-2817)',  34  'miR-10-P1c (2820-2904)',
35  'miR-10-P2a (2907-2986)',  36  'miR-10-P2b (2989-3069)',
37  'miR-10-P2c (3072-3154)',  38  'miR-10-P3a (3157-3244)',
39  'miR-10-P3b (3247-3335)',  40  'miR-10-P3c (3338-3422)',
41  'miR-15-P1 (3425-3503)',   42  'miR-15-P2 (3506-3589)',
43  'miR-15-P3 (3592-3673)',  44  'miR-15-P4 (3676-3759)',
45  'miR-15-P5 (3762-3844)',  46  'miR-15-P6 (3847-3934)',
47  'miR-15-P7 (3937-4024)',  48  'miR-15-P8 (4027-4118)',
49  'miR-17-P1 (4121-4201)',  50  'miR-17-P2 (4204-4286)',
51  'miR-17-P3 (4289-4366)',   52  'miR-17-P4 (4369-4445)',
53  'miR-17-P5 (4448-4530)',  54  'miR-17-P6 (4533-4615)',
55  'miR-17-P7 (4618-4697)',  56  'miR-17-P8 (4700-4779)',
57  'miR-19-P1 (4782-4862)',  58  'miR-19-P2 (4865-4949)',
59  'miR-19-P3 (4952-5043)',  60  'miR-21 (5046-5134)',  61
'miR-22 (5137-5227)',   62  'miR-23-P1 (5230-5316)',  63
'miR-23-P2 (5319-5499)',  64  'miR-23-P3 (5402-5487)',  65
'miR-24-P1 (5490-5582)',  66  'miR-24-P2 (5585-5676)',   67
'miR-26-P1 (5679-5762)',  68  'miR-26-P2 (5765-5847)',  69
'miR-26-P3 (5850-5933)',  70  'miR-27-P1 (5936-6024)',  71
'miR-27-P2 (6027-6112)',   72  'miR-27-P3 (6115-6198)',  73
'miR-29-P1 (6196-6278)',  74  'miR-29-P2 (6281-6364)',  75
'miR-29-P3 (6367-6450)',  76  'miR-29-P4 (6453-6532)',   77
'miR-30-P1 (6535-6607)',  78  'miR-30-P2 (6610-6683)',  79
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>Gallus-mir-145_pre
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>Anolis-let-7a-4-3p
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>Anolis-mir-222b_pre
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>Anolis-mir-737-5p
GTTTTTTTAGGTTTTGATTTTT

>Anolis-mir-1641_pre
CAGGGCTTTTCCTG-GGATTAATGACAGTCTGGGGGTCATCATCTCCTCCCAGTTAGTTATTAATCCTCAGGAAACACTCAGTGCCTT
>Anolis-mir-1641-5p (predicted)
TGGGATTAATGACAGTCTGGGG

>Aca-novel-1_pre
TCTCTGGGTTACTGTGGGTTTTCCAGTCTGTATGGCCATGTTCCAGAAGCATACAGCCTGGAAAACTTGCAGCAACCCAGTGG
>Aca-novel-1-3p
TACAGCCTGGAAAACTTGCAGC
>Aca-novel-1-5p
TGTGGGTTTTCCAGTCTGTATG

>Aca-novel-2_pre
TGAAATAAAGTGACATGGACAATTTTGGTTTTGATGTTTAATGAGTATCAAAACTAGGATTGTCTATGCCATTGTGTTTC
>Aca-novel-2-3p
TCAAAACTAGGATTGTCTATGC
>Aca-novel-2-5p
ATGGACAATTTTGGTTTTGATG

>Aca-novel-3_pre
GCCCAGAATGGGGCATCCACACAACCAGCAAGAAGGAAATAAGATTAATCCCTTTCTTCTTGCTGTTTGTGCAGGTGCCTCATCCTGACA

>Aca-novel-3-5p
CCACACAACCAGCAAGAAGGAA
>Aca-novel-3-3p
TCTTCTTGCTGTTTGTGCAGGT

>Aca-novel-4_pre
TGTTTCCCCAGCCTTCTTTCATCTCTGAAATGCATATGTTTTAGCACCATTTGTATTTCAGAGATGGAGGGCCGAAGAAACGCAT
>Aca-novel-4-5p
TTTCATCTCTGAAATGCATATG
>Aca-novel-4-3p
TTTGTATTTCAGAGATGGAGGG

>Aca-novel-5_pre
CTCTACAGTCCTTCTCAAAATGGAAACAGGAAATAGAGTCAGATCACTTCTTGTTGTCATTTTGAGATGAACTTTATAGAA
>Aca-novel-5-3p
TCTTGTTGTCATTTTGAGATGA
>Aca-novel-5-5p
TTCTCAAAATGGAAACAGGAA

>Aca-novel-6_pre
TCCCAGGTTCCTTCTACACTGCCATATAATCCAGATTATCTGTTTTGATTTTATATGGCAATGTAGAGGAAGGTTTCTTTT
>Aca-novel-6-3p
ATTTTATATGGCAATGTAGAGG
>Aca-novel-6-5p
TTCTACACTGCCATATAATCCA

>Aca-novel-7_pre
CCCTTCTACACTGGCCCAAACTCTTATGAAATCAGTATTTAAAGCCCCAATTTCATGAGAATTTGGTGCTCGTGCAGGCGGC
>Aca-novel-7-3p
TTTCATGAGAATTTGGTGCTCG
>Aca-novel-7-5p
TGGCCCAAACTCTTATGAAATC

READ ADJUSTMENTS:
>Aca-miR-5407-5p
TTTCGGATTTTCAGTCACAGTTT
>Aca-miR-5407-3p
TCTGTGTGGGATAATCCGAAAGA

>Aca-miR-5417-3p
TCATCCCAGCCCCTTTTCTCCC
>Aca-miR-5417-5p
GAGAGAAGGCGTGGGAAGGAGC

>Aca-miR-5426-5p
CACTCTAAGTCTACTTCCACAG
>Aca-mir-5426-3p
GAGGAAGTAAACTTGGACTACT

>Xenopus-mir-26-3_pre
GTGGCCCGGTTCAAGTAATCCAGGATAGGCTGTTCACATTCTGCGTGGCCTATTCTTGATTACTTGCATTGGGAGGC
>Xenopus-mir-26-3-5p
TTCAAGTAATCCAGGATAGGC

>Xenopus-mir-124-2_pre
GGCCCCTTCTCTCCGTGTTCACAGCGGACCTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGGGCT
>Xenopus-mir-124-3_pre
ACGGAGCCCCCCTCTGCGTGTTCACAGCGGACCTTGATTTAA-TGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGGGCTTTATC
>Xenopus-mir-124-3p
TTAAGGCACGCGGTGAATGCCA

>Xenopus-mir-454_pre
AGTGCCCTCAGCCTTAAGGAAGTGACCCTATCAATATTGCCTCTGCTTTTGTGCTCGGAGTAGTAGTGCAATATTGCTTATAGGGTCTTTTCCTTG
>Xenopus-mir-454-3p (predicted)
TAGTGCAATATTGCTTATAGGGT

>Xenopus-mir-460a_pre
TGGCTTTATAGAGCCTGCATTGTACACACTGTGTGTGCACCTCAGACTTGCACAGCGCATACAATGTGGATGCTATATGAGTC
>Xenopus-mir-460a-3p (predicted)
CACAGCGCATACAATGTGGATGC

>Xenopus-mir-460b_pre
TGACTCTACATTGTCCTCATTGTACATGCTGTGTGTATCTATTTCTCTTACACAGCGCATGCAATGTGGATATATTGGATGTC
>Xenopus-mir-460b-3p (predicted)
CACAGCGCATGCAATGTGGATA

>Xenopus-mir-551a_pre
TGACCTTGGAAACCAAGAGTGGGTTGGGCCTGTTAGATCACATAGGCGACCCATACTTGGTTTCAAGGGTTAGCAGG
>Xenopus-mir-551a-3p (predicted)
GGCGACCCATACTTGGTTTCA

>Xenopus-mir-551b_pre
TGACCTTAGAAATCAAGCTTGGGTTAGACCTGGTTCTTATACACTGAGGCGACCCATACTTGGTTTCTGAGGCTGAAGTG
>Xenopus-mir-551b-3p (predicted)
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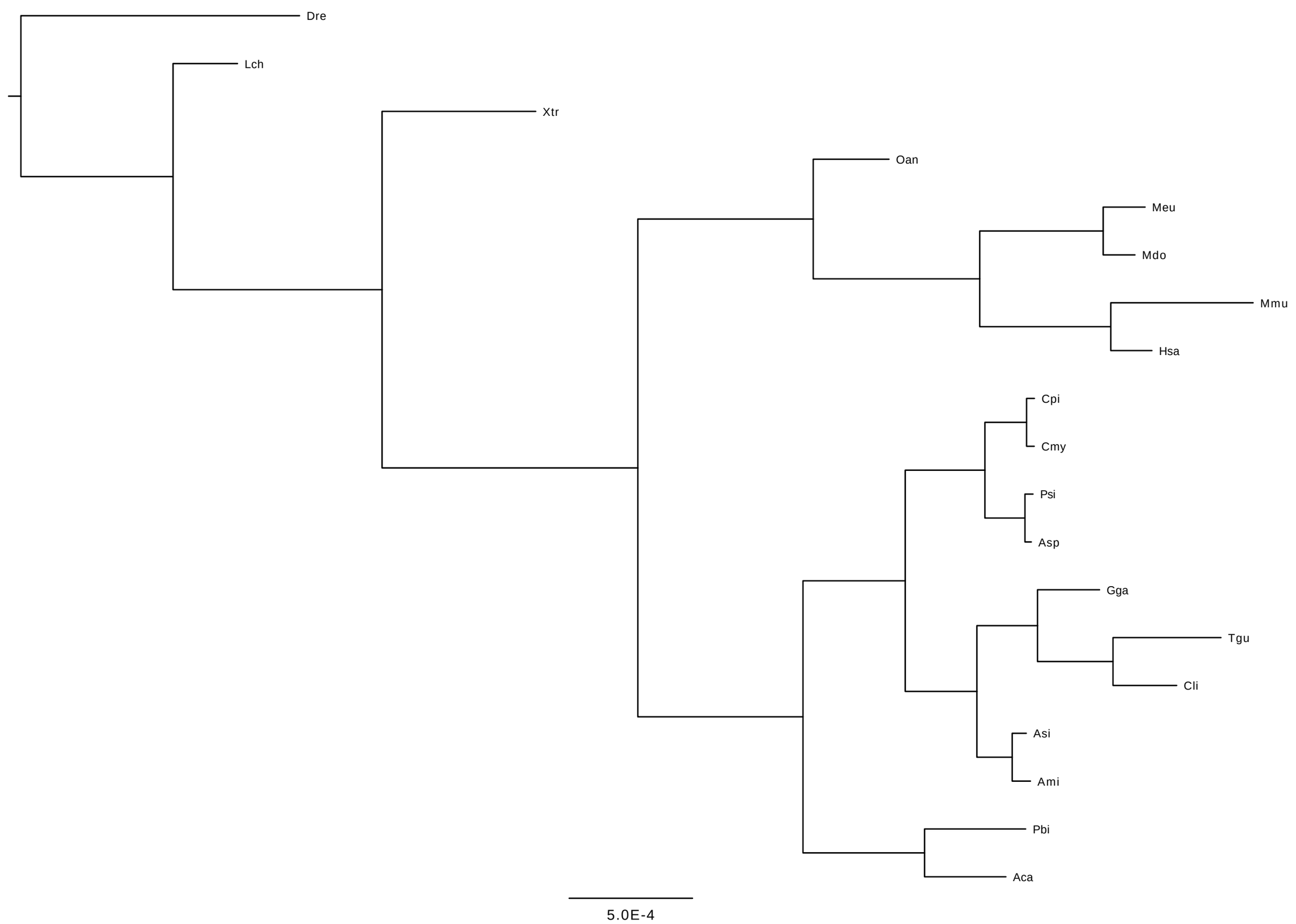
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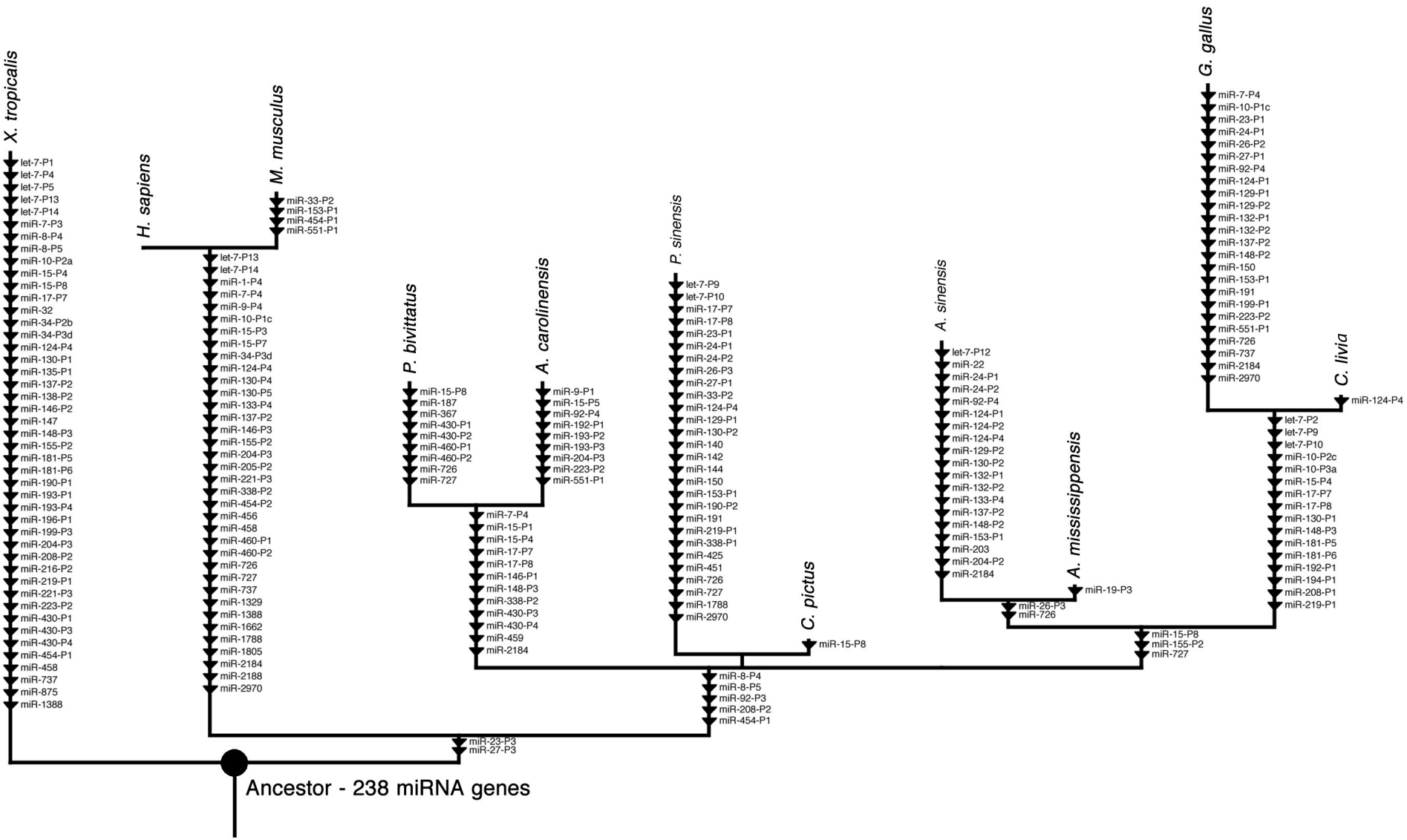
X. tropicalis
let-7-P1
let-7-P4
let-7-P5
let-7-P13
let-7-P14
miR-7-P3
miR-8-P4
miR-8-P5
miR-10-P2a
miR-15-P4
miR-15-P8
miR-17-P7
miR-32
miR-34-P2b
miR-34-P3d
miR-124-P4
miR-130-P1
miR-135-P1
miR-137-P2
miR-138-P2
miR-146-P2
miR-147
miR-148-P3
miR-155-P2
miR-181-P5
miR-181-P6
miR-190-P1
miR-193-P1
miR-193-P4
miR-196-P1
miR-199-P3
miR-204-P3
miR-208-P2
miR-216-P2
miR-219-P1
miR-221-P3
miR-223-P2
miR-430-P1
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miR-430-P4
miR-454-P1
miR-458
miR-737
miR-875
miR-1388
H. sapiens
M. musculus
miR-33-P2
miR-153-P1
miR-454-P1
miR-551-P1
let-7-P13
let-7-P14
miR-1-P4
miR-7-P4
miR-9-P4
miR-10-P1c
miR-15-P3
miR-15-P7
miR-34-P3d
miR-124-P4
miR-130-P4
miR-130-P5
miR-133-P4
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A. carolinensis
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C. pictus
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A. sinensis
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A. mississippensis
miR-19-P3
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C. livia
miR-124-P4
let-7-P2
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miR-23-P3
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