A. human AmnSINE1

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AmnSINE1(human) cons            1:------------------------------------GYCT-RCAGCCAYASCACCTCGGGCTRTGATCTCGTCAGATCTCACAAGCTAAGCAGGGTCGGGCCTG-GTCAATDCTTGGATGGAAG-MC-CTCCAAG 95
chr3:71,253,317-71,253,593      1:TTCACTTCTGTTTTACTTCACTGCAATGCTAATGTG.C..-A...T..T.G..T.CTA....G......T.....C....GTG......A....C..A...T..-.G..C.G....A......T-C.-......A 131
chr2:162,091,545-162,091,796    1:---------TCAGATGCAAGACACTAAGCTGTCTTT.CT.-T......TCCT...ATAT...C.....C.A...C.............T.T...T.T.....A.-.A.C..T.........G.A-AT-...T... 122
chr7:83,949,737-83,950,057      1:-----------AACCACTTGCTTTCATATACTCATG.C.C-A.T....CCGT...C.A....A.A....TA....CC..TG...A.AG.T..-....A.ATA..-A.AT.CAT..........A-CA-T...... 119
chr8:82,268,732-82,269,055      1:GCAGAATAACCTAGTTAATGAACATGCAGCCTGTCCCA..GG..-.GTA.G.....TT...CA.AG..C.AA..C....T.GTGA...TT..A....AA.TT.T-.....CA.....G.....A-T.-A...-.. 130
chr12:64,746,242-64,746,744     1:-----------AGAAAAATGACAAGCACATAATTTA.T..GG......T.C...TCT.T...G...G.CT.....T...TT.T.......T.A.TG.T......CT.TGG.G.AA.....AG..-A.-....C.. 122
chr13:72,893,777-72,894,129     1:---------------CTTACACCAGCACTGTAGTGAAT..CA.TA...C.CT.....T..T.G...C..TA....G.T...T.....G.AT...C.TT...-..G.A....TTG..AG...C.--A.-AA..C.A 116
chr3:89,846,279-89,846,546      1:---------------------------------------------.T.C.C.....T.....A...G...A.....G...T......C..TG.....AAAT...-..T...GT....GA..GT.-A.-....... 87
chr2:164,247,265-164,247,831    1:-------------------------------------------------------------.T.T.AAC.T.G.A......T..AT......TCA.T.A.....-...CCAT...TC..AAC..-CT-....-.. 70
chr5:90,643,402-90,643,596      1:-----------------------------------------------------------------------------------...C.GT.......A..G.A-G.G..GCA.....CCT..T.-CTC....-.. 49
chr2:144,395,188-144,395,593    1:-----------------------------------------------------------------------------------------------------...-..A..AG-....TAA.T..-TG-...A..C 30
chr7:26,673,363-26,673,571      1:--------------------------------------------------------------------------------------------------------------------------------.....TA 7
chr12:20,405,780-20,406,105     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr12:24,237,357-24,237,651     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr18:51,915,906-51,916,501     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chrX:153,856,966-153,857,385    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:213,896,131-213,896,553    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chrX:38,767,448-38,767,836      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr2:212,507,037-212,507,352    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr7:103,526,240-103,526,739    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr4:13,193,150-13,193,490      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr11:41,155,815-41,156,232     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr2:164,809,136-164,809,576    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr2:144,311,459-144,311,756    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr13:29,877,923-29,878,304     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr13:43,252,940-43,253,297     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr3:70,515,281-70,515,679      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr7:102,922,249-102,922,677    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr3:29,283,688-29,284,100      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chrX:109,369,727-109,370,017    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr12:23,715,537-23,715,833     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr5:30,707,921-30,708,306      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr10:21,398,890-21,399,190     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr2:103,864,004-103,864,242    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr14:79,103,505-79,103,870     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:118,588,292-118,588,615    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr2:144,716,638-144,717,013    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr13:93,717,771-93,718,116     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr14:97,162,255-97,162,487     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chrX:132,495,699-132,495,932    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr10:100,747,350-100,747,685   0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr15:93,091,456-93,091,703     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr7:31,429,753-31,430,106      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr6:156,380,618-156,380,943    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr9:13,609,412-13,609,640      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr4:166,963,237-166,963,460    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr10:107,041,227-107,041,551   0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:24,436,699-24,437,003      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr3:189,029,144-189,029,348    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chrX:124,284,055-124,284,268    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr18:52,109,735-52,109,898     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr13:21,581,137-21,581,402     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr18:60,149,311-60,149,468     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr14:72,089,689-72,089,952     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr11:39,445,366-39,445,585     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr15:51,569,626-51,569,873     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr3:117,375,737-117,375,940    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
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A. human AmnSINE1 (continued)

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AmnSINE1(human) cons               96:GAAAA-------CCCAGG-TGCTRCAGGAA----------GT-GGTG-YTGGTGATT---CAGTAGGTGGCACTCTTCCCTCTGAG--TCAGT------ACTG---AACCAATGYCCCAGC-ATGGTG-TTAGGG 194
chr3:71,253,317-71,253,593        132:..C..-------.T....-...CGG..-.C----------T.-....--.A......---...CGTC.......---GG...CA..-AGGG.C------.ACC---.G...G..C.T....-.A....G...TA. 227
chr2:162,091,545-162,091,796      123:A.TC.-------.....C-...CA..A...----------..-AA..-TA.A.A.C.---G..--..AA..-G.G..A..---A.T--...C.------.TAA--A.TGA.T.ACT...A.-.GA.CA-G..... 216
chr7:83,949,737-83,950,057        120:A....-------......-..T.A......----------..-.A.A-TG......A---..........TGA....T........--...T.------T...---G......TA....A.-...AG.-C-.A.. 217
chr8:82,268,732-82,269,055        131:AG...A-----C..T...-..TGG..A..G----------A.-A-..-T..A.....---..T...T.....T...C.TT......--..GA.------GA.T---....------.....-...C.A-...TT. 224
chr12:64,746,242-64,746,744       123:...C.-------AGT...-.A..T.....G----------A.-....-T.TCGC...---...........-....C.T...C.G.--..CA.------G-..---..T.G...C...-..-G.....-...... 218
chr13:72,893,777-72,894,129       117:AG...-------A.....-....A......----------..-..AA-CG.......---....CA.GTT..T....T.T.A...T--....-------G...---.C...C.AA.TA.T.-..--..-.G..T. 212
chr3:89,846,279-89,846,546         88:.....-------T.....-...AAG....T----------A.-AA..-C.A..A...---..A...A..A..TGA..T...T.A..--...C.------.A.A---.G.A.T.CT...TTA-.G.CCA-...TCA 186
chr2:164,247,265-164,247,831       71:AG...-------.T.TAAAA..--.....CACTCTGAGAT.A-.C..-TG.A.....---.............AA..TT.A.....--.....------....---...TG...C......-.....A-.G.A.. 178
chr5:90,643,402-90,643,596         50:A.T..A------..A.AC-A..CA......----------..-...T-TCT......---.............A.....T.T....--....A------....---..T..------------------------ 127
chr2:144,395,188-144,395,593       31:AC...TCTCCAA.T...A--...ATTA...----------A.-TA..-T.TA.....---..A..AA...G-T.G..GTT.TCTTTTT.A.C.------.T..CCC..A.TG..C......-...A---CCC..C 137
chr7:26,673,363-26,673,571          8:.G...A------......-....A-....G----------..A....AC.AT..G.GACT.....................T.A-----..-.------...C---.G......T.....A-.G.AA.-...T.. 107
chr12:20,405,780-20,406,105         1:---------------...A....G.....T----------..-....-GC.......---...........C.......A..CC..G-GTG..------G...---.G....C--TT....-C...G--...T.. 90
chr12:24,237,357-24,237,651         1:-------------------------..C..----------A.-.T.T-C..TCA...T--.T.........C..T.AGT.......--....G------.T..---.-.TTCA.T...T.G-G.A...-GC.... 82
chr18:51,915,906-51,916,501         1:----------------------------..----------..TAC..-C..C.T.AG--GAGT....GTT...CT..T..AGA.CTCT.....GCCAACC.A.---C......AT......-G.C.CT-GG.... 89
chrX:153,856,966-153,857,385        1:----------------------------..----------A.A.A..-T..A..C.GC--T..G..C..CT-......T....A.A--.....------..CA---.GT.----------.-T.....-A.CA.. 70
chr1:213,896,131-213,896,553        1:---------------------------------------------..-C..A..C..---T....A.CAAGG..G...T-..-A..--.....------TTG.---...T....TTT....-.--------.... 64
chrX:38,767,448-38,767,836          1:------------------------------------------------T...A.GG.---...A.AA-...-..GC....C-G..C--AGCC.------G.AC--------T..C..-G.A-GCTT..-...... 62
chr2:212,507,037-212,507,352        1:------------------------------------------------T.T......---.....CT.A...T..ACTT.C...TTT-GT..A------.A..--TC.GT.G.TAG.A...A....A.-C.-..A 73
chr7:103,526,240-103,526,739        1:---------------------------------------------------------------------------------------------------------------------------.A..A-..T..A 11
chr4:13,193,150-13,193,490          1:---------------------------------------------------------------------------------------------------------------------------------..G.T. 6
chr11:41,155,815-41,156,232         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr2:164,809,136-164,809,576        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr2:144,311,459-144,311,756        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr13:29,877,923-29,878,304         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr13:43,252,940-43,253,297         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr3:70,515,281-70,515,679          0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr7:102,922,249-102,922,677        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr3:29,283,688-29,284,100          0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chrX:109,369,727-109,370,017        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr12:23,715,537-23,715,833         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr5:30,707,921-30,708,306          0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr10:21,398,890-21,399,190         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr2:103,864,004-103,864,242        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr14:79,103,505-79,103,870         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:118,588,292-118,588,615        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr2:144,716,638-144,717,013        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr13:93,717,771-93,718,116         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr14:97,162,255-97,162,487         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chrX:132,495,699-132,495,932        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr10:100,747,350-100,747,685       0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr15:93,091,456-93,091,703         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr7:31,429,753-31,430,106          0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr6:156,380,618-156,380,943        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr9:13,609,412-13,609,640          0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr4:166,963,237-166,963,460        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr10:107,041,227-107,041,551       0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:24,436,699-24,437,003          0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr3:189,029,144-189,029,348        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chrX:124,284,055-124,284,268        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr18:52,109,735-52,109,898         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr13:21,581,137-21,581,402         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr18:60,149,311-60,149,468         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr14:72,089,689-72,089,952         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr11:39,445,366-39,445,585         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr15:51,569,626-51,569,873         0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr3:117,375,737-117,375,940        0:--------------------------------------------------------------------------------------------------------------------------------------- 0
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A. human AmnSINE1 (continued)

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AmnSINE1(human) cons           195:GGCACTGTGYT-GCYGGAGGT-GCCGTC-TTT-CGGATGAGACGT-AAAACCGAGGTCCTGACCACTTGCGGTCATTAAAGAT-CCCATGG-CA-CTTTTC-------GTAA-GAGTAG--------------GG 299
chr3:71,253,317-71,253,593     228:...C..A..T.-AAT..GA..------------------------------------------------------------------------------------------------------------------ 247
chr2:162,091,545-162,091,796   217:.-..AA.GTC.--------------.A.-...-ATC..AT.T.A.-...TGA..--------------------------------------------------------------------------------- 252
chr7:83,949,737-83,950,057     218:.A-..A...G.-.TGT..-------------.-G.CC..TC..---......A..T..T---------------------------------------------------------------------------- 257
chr8:82,268,732-82,269,055     225:.-..T.-------.T.A...C-T.T..A-C..-..T...-.CTT.-.....TA.AC..AGTCTA.AG.A.T.GTCA.......---------------------------------------------------- 294
chr12:64,746,242-64,746,744    219:........CTG-CACT...C.-.TTTA.C...-T.T....A..T.-......ACA.A...A....T...T.....CC.G....-.TT....-..GAC....-------TA.--...C..--------------TT 324
chr13:72,893,777-72,894,129    213:......C..C.-TTCA.G.A.-.----.-..G-T.A..A......-.T.GTAA.T...T.A.T.....TT.C.G.C.G..A.G-.TTTCA--..----------------------------------------- 294
chr3:89,846,279-89,846,546     187:.A...CA..C.-A.T......----T..-...-GTA.A..--TT.-..T.TA----------------..T..A...T.....-.T....A-ATT.....--------A..------------------------ 262
chr2:164,247,265-164,247,831   179:.......CAC.-..T......-.T....-.AA-T.......G-..-......A......T.......CA..A..T.....A..-.......-..-......-------AA..-.....AAGA-----------T. 285
chr5:90,643,402-90,643,596     128:--------------------------------------------------------------------------------------------------------------------------------------- 128
chr2:144,395,188-144,395,593   138:T.G...AATCCA.ATA.....-A.TA.--...-G....--.C.A.-C..TATA..C.T...G.T.T..CTA.........C..-.......-A.-......-------A...-C.C.GA--------------.. 240
chr7:26,673,363-26,673,571     108:.A....AGATA-CACCATAAA-TAAT..TCA.-A...---A.AA.-......A.AA.GT......---------A...T.A..------..-A.-....GG-------AA.G-.T.G.A---------------- 195
chr12:20,405,780-20,406,105     91:A......A.C.-A.A....A--A..A..-.A.-T...........-.TG..T.....T..........CT.C........A..-T...A..-..--....T-------A...-.GT..A--------------.. 193
chr12:24,237,357-24,237,651     83:A.G...-.AC.-..T..TT..CAT.A..-...-.A......GT..-GG.CAT.....T..AG...T...TA........G...-T..TCA.-A.-.C...-------------T..C.A------------GA.. 185
chr18:51,915,906-51,916,501     90:AATGA..G--C-..C--------.T.CA-...-.A..GA...TT.-.........A....A..TG..CATCA........A..-.T.CA..-..-G.....-------A...-...C.A------------GG.. 187
chrX:153,856,966-153,857,385    71:.CAT....TC.-.TA.A....-..T.A.-...-T.TGG..TT.A.C.G.T..C......A.-..GA.GAT.TC......G.G.-T.T....-..-A...C.-------AA.G-....CA-----------ATTTC 178
chr1:213,896,131-213,896,553    65:.C.......T.-C.CA.G.A.-.GAAGA-AA.-.AA....A.T..-..C..TC....C.........C.CT...CCA..G.C.-TG.T...-A.-...C..-------AC.G-..-...AAGCCTTCCTGTTTCT 182
chrX:38,767,448-38,767,836      63:...G.....GG-..T.C.A..-..T.-.-..C-ACC.CCCT..AG-..CTG.TG.C.T.CC.AGG.C.AT..CGG.....ACC-.....A.-.T-.....G-------.C..A......--------------.T 167
chr2:212,507,037-212,507,352    74:A........T.-C.CAT....-A.T..T-..C-TA.....C.T..-.....TCTATG.T......TAAA.A.C.T.....A.AAT..CA..G..C....-.-------AGGG-A.A...--------------CA 180
chr7:103,526,240-103,526,739    12:.--....G.-.-..CT....GG..T...-CA.-.A.CA.....A.-...G.A..AT..T..G.TG.A..T.A...A....T..-.T.G...-.--....CT-------..G.AT..CG.--------------A. 114
chr4:13,193,150-13,193,490       7:AAT.....--.-..TAT.AA.-.A..---...-.T........T.-.TG.GAA..CATT..G....C...A..TG.....T..C...C...-..-.....T-------C...-....T.--------------AA 108
chr11:41,155,815-41,156,232      1:TC...AT.TA.-..TTT..-.-.AT..AA.GGG.TTGG.....ACTGG.GATTTTA.A....G.C..GT.ATG..C....T.G-GAGG..A-..-TG..AT-------A..G-A.A.GC--------------A. 107
chr2:164,809,136-164,809,576     1:-----...AT--C.CT..AA.-..TC..-.AG-T..C..GC.T.G-G.GTT.ACA.........TG...A.T..TC....T.A-..TCA..-G.-A..C.T-------..TT-.TT.GC---------------T 98
chr2:144,311,459-144,311,756     1:--------.T.-..GA.....-.AG.C.-...-..CTG.GCTGCA-GG.TAGCG.CC.T.-........T...........T.-...G...-TG-.....T-------.----....GAAG-----------G.A 97
chr13:29,877,923-29,878,304      1:----------------...AA-A..C.GAG..--A..G....T.A-...G...T...-....TA----.A.A...CAG...T.-G..TG..-TG-......-------AC..-A..A.A--------------.. 85
chr13:43,252,940-43,253,297      1:-----------------....-A.TC..-..G-.AA.......-C-.G.G.AA...CTT..G.T...GAA.-......C...C-.T..CCTGTGG......TCCCACT..T.-...A------------------ 92
chr3:70,515,281-70,515,679       1:-----------------.TAA-TTA...A...------..AGAC.-.....TAT..C.A.....G..CAT.T..T..G.G.T.-T...C.CC..-....C.-------...T-..A.T.--------------.. 86
chr7:102,922,249-102,922,677     1:-------------------..-.GT.G.-...-.TA.....G-A.-...C.T...C..AGTTAG.....T..CT.GCCC.TG.T......T-.T-T.....-------AT..-..A.CA--------------.A 88
chr3:29,283,688-29,284,100       1:-----------------------.T.C.-...-GAA....TT.C.-....G.TA...A.T...........CC...G...T..-.TGG..A-TC-......-------CCC.AC..AT.-----GGAAGGGCCTC 94
chrX:109,369,727-109,370,017     1:------------------------TT..-...-TA.....A.T.C-.G...TA...A.A...T...G.T.C.T..........-T..T..C-T.-T.....-------AC..-......--------------.. 84
chr12:23,715,537-23,715,833      1:-------------------------.A.-...-.---.TTT.TA.-G...TGA.AAAT.A...T.T.A..........G....-......T-.T-.....T-------.C---T.A.G.------------TG.A 79
chr5:30,707,921-30,708,306       1:--------------------------..-.C.-T.T...A....GAA.A...TT.T.ACA...G...T.ATAA.GT.....A.G-TT....-..A.....G------AAA..C..AG.A--------------T. 85
chr10:21,398,890-21,399,190      1:-----------------------------...-.AT.GC....AC-......T...........G...CAA..G.....CA..-..T.GA.-..-....C.-------A...-C...CC--------------.. 79
chr2:103,864,004-103,864,242     1:-----------------------------...-G.CT....TT..-.....AC..........C....TC.............-.......-GC-TC...T-------.A..G..C..A-------------G.. 81
chr14:79,103,505-79,103,870      1:------------------------------------------------------.C....A.TT....AA.T.T.....GA..-....G.A-T.-.C.C.T-------AG..-TG....-----------AGGT. 59
chr1:118,588,292-118,588,615     1:-------------------------------------------------------------------.G.T.....C-..G.--......A-T---..C.G-------.GG.-...G.A--------------.. 40
chr2:144,716,638-144,717,013     1:-------------------------------------------------------------------CAT...T........A-T.-.GA.-.TT..C...--------...-..C.G.--------------A. 42
chr13:93,717,771-93,718,116      1:-------------------------------------------------------------------------..C..GCCT.T.T..GA---.-TAG.CT-------AGTGTC....T--------------A. 37
chr14:97,162,255-97,162,487      1:-----------------------------------------------------------------------------.G...G-...-..A-TGC....G.-------AAC.-.TC-----------------.. 30
chrX:132,495,699-132,495,932     1:------------------------------------------------------------------------------------..TG...-..-...C.T--------------AA..--------------.A 21
chr10:100,747,350-100,747,685    1:------------------------------------------------------------------------------------------.-TG-......-------A.T.-CGAC..--------------AT 21
chr15:93,091,456-93,091,703      1:--------------------------------------------------------------------------------------------.T-...AAT-------....-.....A--------------T. 20
chr7:31,429,753-31,430,106       1:-----------------------------------------------------------------------------------------------GCC...-------T.GGT.GT.T.--------------T. 19
chr6:156,380,618-156,380,943     1:-----------------------------------------------------------------------------------------------G...C.T------AC..-......--------------T. 19
chr9:13,609,412-13,609,640       1:------------------------------------------------------------------------------------------------.....-------TCCT-......--------------A. 17
chr4:166,963,237-166,963,460     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr10:107,041,227-107,041,551    0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:24,436,699-24,437,003       0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr3:189,029,144-189,029,348     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chrX:124,284,055-124,284,268     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr18:52,109,735-52,109,898      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr13:21,581,137-21,581,402      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr18:60,149,311-60,149,468      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr14:72,089,689-72,089,952      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr11:39,445,366-39,445,585      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr15:51,569,626-51,569,873      0:--------------------------------------------------------------------------------------------------------------------------------------- 0
chr3:117,375,737-117,375,940     0:--------------------------------------------------------------------------------------------------------------------------------------- 0
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A. human AmnSINE1 (continued)

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AmnSINE1(human) cons          300:GTGTTAA-CCCCGGTGTCCT-GGCCAAATTCC--AATTCGGG-TAATTACA-------TTCT--GCC-----TACCTAAA--TT--CCCYCTGCAGTTT---CAATTGGATACGGTATTC----------TTCAC 398
chr3:71,253,317-71,253,593    248:--------------------------------------------------------------------------------------------------------------------------------------- 248
chr2:162,091,545-162,091,796  253:--------------------------------------------------------------------------------------------------------------------------------------- 253
chr7:83,949,737-83,950,057    258:--------------------------------------------------------------------------------------------------------------------------------------- 258
chr8:82,268,732-82,269,055    295:--------------------------------------------------------------------------------------------------------------------------------------- 295
chr12:64,746,242-64,746,744   325:.......-.T..A.AA....-....GG.G...--..C.AAA.-........-------....--...-----.C......A-.A--...C.........---......A....AA..G..----------..AG. 424
chr13:72,893,777-72,894,129   295:--------------------------------------------------------------------------------------------------------------------------------------- 295
chr3:89,846,279-89,846,546    263:--------------------------------------------------------------------------------------------------------------------------------------- 263
chr2:164,247,265-164,247,831  286:A......-A...T.......-...T..T....--..A.T...-C.....T.-------....--...-----...T....A-..---T.T...T.A...---T.G.......ATA.....----------....T 384
chr5:90,643,402-90,643,596    128:--------------------------------------------------------------------------------------------------------------------------------------- 128
chr2:144,395,188-144,395,593  241:T.T....T.TT.A.CT..-.-..........--..C.G.AA-AC.....G-------...--..TTACTG.......------...T..-..-.A.----GGAA.C..GA..G.GCTCTTTTATTGTA...T 349
chr7:26,673,363-26,673,571    196:--------------------------------------------------------------------------------------------------------------------------------------- 196
chr12:20,405,780-20,406,105   194:A..--C.-T..TT....T..-A-.A.TC..GATCC.G.T...-..GGA.T.-------.---------------------------------------------------------------------------- 240
chr12:24,237,357-24,237,651   186:A.T....-.TGTA....T..-..T..GT....--..A...A.-........-------...A--...-----.-.T...TA-.C---TTC.....G...---.TG..---------------------------- 265
chr18:51,915,906-51,916,501   188:...G.TG--..T.AG..TT.-...TG.CAGT.--..CC.AAC-........-------...--.T.-----...TGT----G.--..TC.C.......---..........T.T.T..T--------TT..T.T 285
chrX:153,856,966-153,857,385  179:AA....-----...-A....-.A.T..G.G.T----..T.TT-G.C..G.T-------...--...-----...G...-C-C.--.T.T.........---..C...C.----......----------....T 266
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chr15:51,569,626-51,569,873   23:...-TCCC.AAG.ATACCA--.GAA--------...-----------------..G.C-....A.AACC.T--G.A.G--G..GG.T....A.-C..GA..T.....G--.C..------T.AT.C..T-T.A.. 114
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AmnSINE1(human) cons            486:GG----GTGAARTGA--TC-YCTATA-----TGT--AGCTTGTAAAGC--GCTTTGGGA-TCCTT---CGGGATGAAAGG-CG-CTATA-TAAA--CGT--AAGGTATTATTATTATT                  576
chr3:71,253,317-71,253,593      248:--------------------------------------------------------------------------------------------------------------------------------------- 248
chr2:162,091,545-162,091,796    253:--------------------------------------------------------------------------------------------------------------------------------------- 253
chr7:83,949,737-83,950,057      258:--------------------------------------------------------------------------------------------------------------------------------------- 258
chr8:82,268,732-82,269,055      295:--------------------------------------------------------------------------------------------------------------------------------------- 295
chr12:64,746,242-64,746,744     442:--------------------------------------------------------------------------------------------------------------------------------------- 442
chr13:72,893,777-72,894,129     295:--------------------------------------------------------------------------------------------------------------------------------------- 295
chr3:89,846,279-89,846,546      263:--------------------------------------------------------------------------------------------------------------------------------------- 263
chr2:164,247,265-164,247,831    440:.A----.G...G...--.G-CT.C.T-----..A--.AAA...CTT..AA.G.C.....-..--A---G..........-TA--------...--.A.------------------------------------- 507
chr5:90,643,402-90,643,596      128:--------------------------------------------------------------------------------------------------------------------------------------- 128
chr2:144,395,188-144,395,593    407:--------------------------------------------------------------------------------------------------------------------------------------- 407
chr7:26,673,363-26,673,571      196:--------------------------------------------------------------------------------------------------------------------------------------- 196
chr12:20,405,780-20,406,105     241:--------------------------------------------------------------------------------------------------------------------------------------- 241
chr12:24,237,357-24,237,651     266:--------------------------------------------------------------------------------------------------------------------------------------- 266
chr18:51,915,906-51,916,501     368:--------------------------------------------------------------------------------------------------------------------------------------- 368
chrX:153,856,966-153,857,385    351:..----A....G...--.TGC.A.ATAC---..--A.CAGAAC....G-A..A.A------T...---..----------------------------------------------------------------- 399
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chrX:38,767,448-38,767,836      356:.A----C.AC.AA..--.TTC------------------------------------------------------------------------------------------------------------------ 370
chr2:212,507,037-212,507,352    317:--------------------------------------------------------------------------------------------------------------------------------------- 317
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chr4:13,193,150-13,193,490      211:--------------------------------------------------------------------------------------------------------------------------------------- 211
chr11:41,155,815-41,156,232     298:..----.C..TG...--.TGC.....-----.A.--.AT.GT...G..--A......A.-.A...---.T...-....AA-T.A.....-....--T.G--...TC....C.G..G.GCTTAAATTAGAATTTCT 406
chr2:164,809,136-164,809,576    274:..GTAA.....A...--.TGCTCCA------.A.--.A...TAT..AG--TG-.AAA..--...C---T.A.........-A.-.....-....--T..--....CTG.CG.T...AATTGCCATTACCGTTTGA 383
chr2:144,311,459-144,311,756    276:--------------------------------------------------------------------------------------------------------------------------------------- 276
chr13:29,877,923-29,878,304     269:-------....ACA.--.-------------..G----TC..C...-G--TGA..T.A.-G....-CGG...C.A...A.-.A-...A.-AT..GAAACCTGG.AC.....C..C...ATTAATTATTAGTGATA 369
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chr3:70,515,281-70,515,679      272:..----T....GCAG--.A-T...A.-----.A.--...A......AA--..C..A..C-.AAC.---GTA.......A.-.A-T.C..-G.T.--T..--...........GC..C.AACGCATTATTATTTTA 379
chr7:102,922,249-102,922,677    235:A.---AA...GCCAG--AA-TA..ATT----...TA....AA...GAG-GA.......G---..G---AA..G.T...T.-TA---------------------------------------------------- 299
chr3:29,283,688-29,284,100      277:A.----...C.AA.G--.T-TTCT.C-----..C--..AA.AC...TTGT..CC.A...A.-------------------------------------------------------------------------- 323
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chr10:21,398,890-21,399,190     280:A.----.G.C-GCAG--..-C...AGCCGC--------------------------------------------------------------------------------------------------------- 301
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chr1:118,588,292-118,588,615    239:..----A....GCA.------------------------------------------------------------------------------------------------------------------------ 249
chr2:144,716,638-144,717,013    234:AT----AATTTG.A.--C.----..------.C.-C..--...-------.......A.-..T..---.A.........TGTTA.CC..--...--T.C--...A...C..C..C...TTAAAGACATACAGTAC 332
chr13:93,717,771-93,718,116     218:.A----....GGCA.--.-------------.T.--GTTA...T...T--........G-AAAAA---A.CAC.T.T..TG.TC.CG..-G...--..C--...C..A.....C.CAATGAGCCTTCCTTTCAGC 320
chr14:97,162,255-97,162,487     209:..----T.C..AC..--GGCTTG.G.GAACA-------------------------------------------------------------------------------------------------------- 233
chrX:132,495,699-132,495,932    205:--------------------------------------------------------------------------------------------------------------------------------------- 205
chr10:100,747,350-100,747,685   208:.C----A....A..T--..-TTCC..-----.------------------------------------------------------------------------------------------------------- 227
chr15:93,091,456-93,091,703     200:.A----.....A.T.--.TTCTCT.T-----CA.--GA.-...TTT..--------------------------------------------------------------------------------------- 233
chr7:31,429,753-31,430,106      205:..----....GC.CG--..-C.GG..TAATT.A.-C.A....TC..----T...T.A.----------------------------------------------------------------------------- 251
chr6:156,380,618-156,380,943    205:.A----....TGCT.AT..-TA.G..-----C..--GTTC..CTG..T--....G....-.....---.T..GG.G..C--T.-..GC.G...G--.A.--G..C........G.C.ACTCTCAAAAAAAGAACT 314
chr9:13,609,412-13,609,640      192:--------------------------------------------------------------------------------------------------------------------------------------- 192
chr4:166,963,237-166,963,460    178:CA----C....G.A.--..-T..---------------------------------------------------------------------------------------------------------------- 193
chr10:107,041,227-107,041,551   189:..----..A..A...--.T-C..TGT-----.A.----------------------------------------------------------------------------------------------------- 210
chr1:24,436,699-24,437,003      169:.A----.AA..A.TG--C.-C..T..-----.CC----..CCC..------.CC.....A...C.---------------------------------------------------------------------- 211
chr3:189,029,144-189,029,348    169:A.----..A..AAT.--.TTC------------------------------------------------------------------------------------------------------------------ 183
chrX:124,284,055-124,284,268    153:CA----....CA...--.T-------------------------------------------------------------------------------------------------------------------- 165
chr18:52,109,735-52,109,898     131:.T----.---------------------------------------------------------------------------------------------------------------------------------- 133
chr13:21,581,137-21,581,402     131:.-----.....G.A.--.G-C..G.T-TATA...-GC.....C....G--.T.....A.-CA...---T.AC......A.-.AT..TAC-A.T.--.A.--C.TTAG.G...TC..ACAATCACTAATTGAGAAG 243
chr18:60,149,311-60,149,468     122:A.----T.A..A..T--.--------------------------------------------------------------------------------------------------------------------- 133
chr14:72,089,689-72,089,952     128:..----....-G...--..-C.GG-------C..-TC..ACACTCTCTAAT..G...A.-.....---.T.C.CAG....-T.-T.CC.--...--T-------------------------------------- 198
chr11:39,445,366-39,445,585     112:.A----T.A.GA...--..-C..G.TTA---...--GA.......-T.--AA....TA.-.TT.G---.TT..GC.C.A--T.-AG.C.-.TTG--.A.-G..A.CCCC.GATAGGACACTACAGTGCCTGGAGG 220
chr15:51,569,626-51,569,873     115:..----A-...G...--..-C.AGG.----------G...GCAC.T.G-T.........-.T...---A.A.......A.-TA-.....-..C.--T..--C..A........CACAGCACTTATAAAAAATGTT 219
chr3:117,375,737-117,375,940     82:..----.....G...--.ACC.A.G.A----.A.--G.....C.G.AT--AT.......-..AGC---TCAC..A.....-.A-.C...-A...--A.C--.....G.C.....C.A.AGTCATAACAGTGTTGG 191
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B. chicken AmnSINE1

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AmnSINE1(chicken) cons        1:----------------------AGCCTGYAGCC--ATACCA-CCTC-GGGCTGTGATCTCGTCAGATCTCACAAGCTAA-GCAGGGTCGGGCCTGG-TCARTACTTGG-ATGGAAGACCTCCAAGGAAAACC----CAGG-TGCT 111
chr2:118,843,690-118,844,129  1:TCTCCTTCATCATTTTATATAC....CTA....--......-...T-.T.........C.T...........G.....A......G.A.-----------.......-.G..G...T.............A----.CA.-CA.. 124
chr2:86,373,833-86,374,350    1:GCCAAGTACACAAGACAGTATA..T...T...T--......-...T-.....T......T........C..T..A....-...A.A.T.......T-.GTG..A....G.......................----...C-..T. 134
chr8:27,424,135-27,424,435    1:GACTCTACACTAAACATATCCT.CTGG.T....--...GT.-TG..-A.T.....GA..TC.....C.....T.AG...-A..A...TAC.G....-...G...A..T-C...GGC.T...........T.----....G.... 134
chr5:35,360,218-35,360,495    1:ATTTTCTTTGCAAACTACCTATT.....G...T-A.CT...-T-..-A.TA.........A..T..CTG..G......G-.......TA...T...-...GCC....A-CG..G.T.......G.......AAAGAA.A.G.... 138
chr4:2,135,009-2,135,345      1:AGCGTGGCTTGGCATGATAATCCA....C....CC.C....-....C.A.......C..TC..........T.......-T....A.T.....A..-...G.G.....-....G.AG.A.T..........A----....G.... 137
chr1:182,768,840-182,769,245  1:CTCTCTGGATATTAATACTGATGT....C....--...TT.-...T-.T.T.A.....--T.AGA......T.G.AG..-...A....A.A-..T.G...A....CAA-..A...C....A...A.T...T.----....-...C 131
chr5:22,251,128-22,251,514    1:GTAACTGTTTCTCACAGTTAATTCT...T....--......-T...-A..T...-...C...TGC..............-A..AA.CT..A-...CT...G.GTG...-...T..T.........C..C.T.AA--T.T.-CAA. 134
chr4:53,214,621-53,214,914    1:TGATGGCTGCAGATGGTAATGT.TGT..C....--..GGTG-T...-A....A......T.C..C..A.T.-...TA.TG.AGCAT..A.......-..TG..T...A----...ACT-.....A.......----T.A.-..T. 129
chr2:32,524,517-32,524,738    1:AAACATCCCCAATGAGTAATATG..TA.C....--...A..G....-A..........G...T.C.....T.......-A......TA.T.T...CCA.A.G.A.T---...G..CT...........T..----....G.... 134
chr2:16,367,040-16,367,209    1:------------------------------------------------------------------..A.-..CTT...A.T...A..A......C-.G.AC...GAA-...TT.AGT......A.G...AA---G...A-.... 72
chr1:99,961,657-99,961,966    1:-------------------------------------------------------------------------------------------------...A...A...-G...TTC.TTG....T.......----....-.... 42
chr2:143,078,494-143,078,851  1:---------------------------------------------------------------------------------------------------------------------.TCAA.G.A.T.C..C---..-.--A.. 22
chr4:88,091,993-88,092,407    1:-----------------------------------------------------------------------------------------------------------------------.....---....A----..A.-CA.. 18
chr2:107,246,547-107,246,900  1:-----------------------------------------------------------------------------------------------------------------------------....GA.----.G..C...A 16
chr1:153,559,699-153,560,039  1:-----------------------------------------------------------------------------------------------------------------------------....G..----...A-...A 15
chr20:13,249,097-13,249,471   1:------------------------------------------------------------------------------------------------------------------------------...TT.----....-.... 14
chr2:31,974,977-31,975,183    1:----------------------------------------------------------------------------------------------------------------------------------------.C..-C... 8
chr1:182,563,004-182,563,356  0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr2:105,966,005-105,966,354  0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr2:144,872,567-144,872,759  0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr5:17,303,737-17,304,206    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr5:44,206,127-44,206,327    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr5:38,838,574-38,838,873    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chrZ:29,464,952-29,465,275    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:149,690,682-149,690,989  0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:166,227,721-166,228,104  0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr4:76,706,356-76,706,828    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:40,679,313-40,679,604    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:31,190,942-31,191,311    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr7:21,147,037-21,147,325    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chrUn:56,584,430-56,584,748   0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:92,362,519-92,362,846    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr8:5,961,389-5,961,692      0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr19:5,230,102-5,230,344     0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr7:9,125,064-9,125,466      0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr24:914,218-914,454         0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr5:48,440,921-48,441,289    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:95,263,137-95,263,489    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr6:29,821,890-29,822,266    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr12:13,944,536-13,945,003   0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr18:5,356,496-5,356,930     0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:124,675,247-124,675,690  0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr20:7,155,282-7,155,630     0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr5:44,208,732-44,208,929    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr11:5,130,826-5,131,233     0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr7:34,704,354-34,704,742    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chrUn:53,327,606-53,327,809   0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
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B. chicken AmnSINE1 (continued)

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AmnSINE1(chicken) cons        112:GY-AGRAAGYGGTGYTGGTGAT-TCAG-TAGGTGGCACTC----TTCCCTCT--GAGTCAGTAC-T--GAACCAATGCCCC-AGCATGGTGTTARR----GGGCACTGTG-TTGYTGGAG-GTGCCG----TCT-TTCG------ 226
chr2:118,843,690-118,844,129  125:ACA.AA...A.-.TT....A..-...--.T.A...AG...-----..TG...--A.A.T...TA-.--..GT..G....TT-...TC......TAA----CA....C..CC.ATTA...A-A..TTT----...-..T.------ 238
chr2:86,373,833-86,374,350    135:.T-..G...T....G....C.C-..T.-.........T..----...AT...--.GC..C....-.--...T.......AT-.CT.A.A...--------------...------.....-..ATTA----...-G.-.------ 233
chr8:27,424,135-27,424,435    135:AT-CAA...CA...CA.C.A.A-....-.T.C.....T..----........--........T.-.--...GTGC.AT...---G..ACGC..TGG----..A....A.TT...G.A...-....T.----G..-.GT.------ 248
chr5:35,360,218-35,360,495    139:.T-.AG...CA.CAG...CAG.-.T..-......AT...G----C.T.....--......A..G-A--..GGT..G.A...AG.GCAAA.....AA---CCAA..AG.GA-.A.TGA...-.C---------GG-A.-.------ 249
chr4:2,135,009-2,135,345      138:.C-..G...T....C.......-G.T.-.......-G...----.----C..--C..C...AG.-C--.....T.-.A..G-.T.T..-----.GG----.A..G.A.A.-CC.C.....-.CA.TC-----.G--..T------ 239
chr1:182,768,840-182,769,245  132:CT-.AGTCATA...T...CA..-.T..-...CAA.A....----...TGC..-----.G..C.T-.--T..T..C.A....AG.......CA..AA----..T..T.C.A-C.CT....A-A...T.----C..-C.-.------ 243
chr5:22,251,128-22,251,514    135:.G-.AA--.CATCAC..A.T..-..CA-G..A.......T----...T..TG--.......A.A-A--.G....G..T..T-.CA...C.A..TTT----.ACA.ACAA.-CCAC.A.CA-.AA.T.----...-..T.------ 247
chr4:53,214,621-53,214,914    130:AT-.AT...T.AC.T.T.....-.T.A-G.....A....T----.C.T....--.TA.T.A.-.-.TA.GG....C.T.T.-......A..C..AA---G.AAAT..T.T-..A---..-....TTA----.GC-..T.------ 242
chr2:32,524,517-32,524,738    135:TC-..G...CA.AAC.......-....-.........TA.----.....CTG--....G..C..-C--...G...C-TG.G-..GGAA.....GGT----A..TG.--------------------------------------- 222
chr2:16,367,040-16,367,209     73:TG-..AC.CTT...T..A....-.T..-....ATA..-..---TG....C..--.......-C.-.--...AT....T.A.-..A........GGG--A.C...G..C.-C.CCC------------------------------ 170
chr1:99,961,657-99,961,966     43:.T-T.A.TTC-T..TGA.....-...----A.CA...G..----........--......AG.G-A--A.......A....C..A.....T...AT----A..GG..C..-...-GAAGT-TGC------------..A------ 146
chr2:143,078,494-143,078,851   23:.A-G.G...TCAA.C-A.....-...T-.GA.......C.----..T.....--........C.-.--....A..G.T.T.-...C....C...AA--GAT..G.AA...-C..T....T-......----..C-.CT.------ 138
chr4:88,091,993-88,092,407     19:.TT.AA..AT...AC.AA....-...C-C.T.G..AG...----..T.....--C.ACTGT..T----....T...---------.AA...GG.AGTTGG..T..A....-..TC....T-.CCATT----...-.AAA------ 129
chr2:107,246,547-107,246,900   17:----.G...C....C......G-....-G.TA.....GC.----.......C--......TCCT-.--.....GC......-GATG..C.CA..GT----...A.T..GAT.A.GA.AGA-TGCT.T----..C-...A------ 129
chr1:153,559,699-153,560,039   16:.AA..A..AT..AAG.......-....-G..ACACT....G---C.T.....--.....CA...-.--..GGA.C..TTT.-C..C.....C..AG---...A..TCA..-C..G...T.-....T.----...-...A------ 132
chr20:13,249,097-13,249,471    15:.T--.G...A-.CCT...A...-.A.--..A-.ATAGTGA----..TT....--......AC.T-.--..G.T--G...A.-CT.C.CACAGC.GG----A..T..CAG.A.GCT....--A....A----C.C-A.A.------ 123
chr2:31,974,977-31,975,183      9:.C-T.A.CAA..C.TCCA....-.T..-.......G.A..-----..T..T.-G.......A.T-.--...TGC...A...-...C...AT..TAA----.A.-......-C..A.A...-C.A...----.G.-..GA------ 122
chr1:182,563,004-182,563,356    1:-C-..A..ACA-GCAA....C.A.G..-.-...-A.TG..AACA..TT.AT.AAT..A.T..GTC.--C..TTTG.....--......-...G.TG-----ACTG....A-...C.....-..CGT.----...-...A------ 116
chr2:105,966,005-105,966,354    1:-----A..AC--..TAT....--..C-ATAC.TA.T...G----....T.-.--.TT.T...G.-A--AC.G..C...A.A-..A.A....C.GAG----..-...A..A-..CC..T..-.A.TTT----...-..T.------ 106
chr2:144,872,567-144,872,759    1:------...T....C......G-...C-..AA.....T..----.....T..--..C.....G.-A--..GT..G.....G-......T..C..TG----....T.....-...T.....-....TC----.T.-.G.A------ 110
chr5:17,303,737-17,304,206      1:-----------..TC.T..C..-....-...T....TA..----.C.TA-..---.A...TGC.-.TCC..AT.C..G.TA-TCTC....A..GTA----CTAA..GC..-..TG..CT.-A...T.AAAG.T.-GA.A------ 109
chr5:44,206,127-44,206,327      1:-----------...C......G-....C...A...G.A.G----C.......--........G.-G--..G....GCCT..-.........C.TGG----..A....C..-G..C.T...-C...AA----..A-..TA------ 106
chr5:38,838,574-38,838,873      1:-----------..CA..T.A..-.TC--...T.AT.T..G---C.A......--...---A..A-.---C....TATATT.A..TT....T.C.GG----.A..TTCA..-C..TA.A..TA...TA----.-.-..T.------ 102
chrZ:29,464,952-29,465,275      1:-------------.T..-C..GTG.T.-...A........----..TGA..C------..C.CA----.TCAA....TT..-.C..-ATCAC.GCA----.....----.-...GA..T.-C.....----.----..A------ 90
chr1:149,690,682-149,690,989    1:-------------.G.......-....-.........AG.----....T...--.--...A..T-.--...TTT......T-GCT..CAGAG.GCA----CA.......T-.A-----.A-..A.T.----...-...C------ 96
chr1:166,227,721-166,228,104    1:-----------------....A-A...G.G...A.TGT..----.GT.....--..A..T.C..-A--..G.....A.T.A-T.GG..C...C.AA----A....---A.-AAAAG.A.T-A.AAAT----...-ACT.AGGAGG 103
chr4:76,706,356-76,706,828      1:------------------....-.TG.-..T..T.T..C.----.GT...G.--C.....A..G-.--A..TG...A..T.-....-...CG..GA----T.A.--------.TTA.-T.-C..TAC----..A-..T.------ 90
chr1:40,679,313-40,679,604      1:------------------....-...C-...A..T.....----..AT..T.--AT.AA.C.GG-.--...AG.C.ATT..-.T.....CAGG.GA----CAA..-.TCC-...T....A-A....A----...-C.TA------ 97
chr1:31,190,942-31,191,311      1:------------------------...-....AT.....T----...TT..A--..T...C.-T-.--...TG......TT-TA......AC.-CA----A.AA.A.CACA.CAT.A...-....TT.----.T-...A------ 92
chr7:21,147,037-21,147,325      1:------------------------------.TCA.CCTG..---T.ATT...--.C-..TCAG.-C--.GG.AGGCAT.AG-G.AG..CAT.C.AG----A....G.AGAGGATCACC..-CAT..A----...-...A------ 91
chrUn:56,584,430-56,584,748     1:----------------------------...T...A....----A.T.....--......CA.A-.--..G.G.TA.T..T--C..-..CAACGCTC---TCAG..AA.T-A.TT..-..-....T.----.T.G...A------ 89
chr1:92,362,519-92,362,846      1:---------------------------------------------..TT..----.TC..T.TG-.--C.G..C...A.T...........AA.GG----AT..G.A.A.--..ACTC.A-....-A----...-..-.------ 73
chr8:5,961,389-5,961,692        1:---------------------------------------------------------------------.....G.C..TT-CCTGCA...C.GGA----T...TGCT.--C..C..TGA-AGA.T.----C..-..T.------ 57
chr19:5,230,102-5,230,344       1:---------------------------------------------------------------------------....G--...--.A..G..GG----AA..G.CTGC-C..CA..-.-T..T.A----G..-..G.------ 48
chr7:9,125,064-9,125,466        1:--------------------------------------------------------------------------------------------..AA----..C.....A-AG.GGA...-.....T.----A.-....A------ 36
chr24:914,218-914,454           1:--------------------------------------------------------------------------------------------------------------------------.ATT.----.T.-GC.T------ 12
chr5:48,440,921-48,441,289      0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:95,263,137-95,263,489      0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr6:29,821,890-29,822,266      0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr12:13,944,536-13,945,003     0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr18:5,356,496-5,356,930       0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr1:124,675,247-124,675,690    0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr20:7,155,282-7,155,630       0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr5:44,208,732-44,208,929      0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr11:5,130,826-5,131,233       0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chr7:34,704,354-34,704,742      0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
chrUn:53,327,606-53,327,809     0:------------------------------------------------------------------------------------------------------------------------------------------------- 0
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B. chicken AmnSINE1 (continued)

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AmnSINE1(chicken) cons          227:------GATGAGACGTAAAACCGAG-GTCCT-GACCACTTGCGGTCATTAAAGAT------CCCATGGCACTT-----TTC--GT-AAGAGTARGGGTGTTAA--CYCCGGTGTCCTGGCCAAATTCCARYTCGGG-TAATT-AC 345
chr2:118,843,690-118,844,129    239:------.T...A..AA.G...A..T-T..A.-A..TG....TAC.T.A.....T.ATTAAGTA.G......A.--TTT...--AA-.C...G.A.A......--GA.AAA....T.........T..AC.T.---.....-.T 364
chr2:86,373,833-86,374,350      234:------C.C..T..A....T.TA..-C.G..-.....AG..G.C.A....G.T..------...C......G.-----...--A.A.GAGC..AAAT......--.TG.A.CA.T....A....A....AACT.A.-...A.-.. 353
chr8:27,424,135-27,424,435      249:------..CAG.GTA.....TG...-...T.-....T..CAG.A.T...G....G------......------------------------------------------------------------------------------ 301
chr5:35,360,218-35,360,495      250:------.......T.......A..C-A...-...-.A------------------------------------------------------------------------------------------------------------ 278
chr4:2,135,009-2,135,345        240:--------..T..A..T.G.TT.GA-.....--....------------------------------------------------------------------------------------------------------------ 265
chr1:182,768,840-182,769,245    244:------..AT..CT.....TTGC..--C..-......C..AA...C....GA..------G.....T.C...------C.--T.-.....C.G.A.CA....--.C.TTC.AGGTCCT...T..AT..GCCA..A--.G.G-.T 359
chr5:22,251,128-22,251,514      248:------TGGA...T..TT...A..A-.CA.--....TT....T......GG....------..A.C.T.....----T..G--CAA..CT...A..A....G.--GC..T.........T..TT..------------....-TT 356
chr4:53,214,621-53,214,914      243:------..A......C....----------------------------------------------------------------------------------------------------------------------------- 256
chr2:32,524,517-32,524,738      223:------------------------------------------------------------------------------------------------------------------------------------------------- 223
chr2:16,367,040-16,367,209      171:------------------------------------------------------------------------------------------------------------------------------------------------- 171
chr1:99,961,657-99,961,966      147:------..CA....AA....TA...-.....-.....TG.CTA...........------.....A.TG..G-----..T--..-.GAG...A.A.CA.G.G--.C.----------------------------------- 230
chr2:143,078,494-143,078,851    139:------..G....T.G.....AA.C-A....-.C.TGTGACT.CCAC...-..G.------.T..--...GC.-----C..--TC-.GA.T.CA.TT.-...G-C.TTA.TGT.T.........A....GC.GCT.-.....-T. 254
chr4:88,091,993-88,092,407      130:------A.G...GTA.....---G.-CA...T...A.G...T---..........------TT.......A.A-----.CT--..-...T.C.G..A...GT.--.T...T..C.G....A......ACAT..A.A-.G...-.. 243
chr2:107,246,547-107,246,900    130:------.......TT.C....TTG.-...G.-.........AT........GAG.------TA.G..C..T..----C...--T.-G...AC.T..A.C.A..---------------------------------------- 211
chr1:153,559,699-153,560,039    133:------.......T.......T..--..T..-...A......A.........T..------..........-----...--AC-.G.....CAT.......--.C.ATA.........T.T......AA.-.CA-.....-G. 249
chr20:13,249,097-13,249,471     124:------..GA...G..C..G.T..A-C.T..-.....G.GTGATCAT.G...A..------.TGTG.CTG...-----..G--CAAG..TTA.CACCA.....--.--------TGAA.T..G......GC.T...-.....-C. 235
chr2:31,974,977-31,975,183      123:------.G...A..T..........-.....-.T.TG....T............-------.TTC.....TACATCCTC..--C.A..CC.C-TAT......C---------------------------------------- 207
chr1:182,563,004-182,563,356    117:------.......T.G....TGAG.-T..A--A.TG.TA..T.....C...CA..------......C..GCC-----.CT--..-..A..C.GAA.--A...--.C.A....CT..AAAAG.GAC.TGAT.ATAA-.....-.. 232
chr2:105,966,005-105,966,354    107:------.......TA....TGGA..-.....-AC...AA.-T.......GCA..------....G..A...C-----...--A.-.......G.T.......--.TT.A..C........G.......GC..A..-.....-.. 224
chr2:144,872,567-144,872,759    111:------.......A.C......C.AT.....-....-------------------------------------------------------------------------------------------------------------- 139
chr5:17,303,737-17,304,206      110:------CTGC..GT.....G..A.A-.-...-T.T.....TT.TCT.........------.TT...A..-..---GACCT--.C-....A..A-AT.....C--TAT.T..T..T.CTAT...C.G..G-.TC.CGA....-.. 227
chr5:44,206,127-44,206,327      107:------...C...--G......A.A-.C...-..A..G.........C.TG....------.AG....A.-----------------.A.AC.GA.AGA...T---G..A..A....CAG....C..A.A-------------- 201
chr5:38,838,574-38,838,873      103:------T....A.TA.G....--.T-..T.C-A..TG.....AT.TT.GC.....------.A.T.AATGT..-----...--AGA..AGT.GAAA.......--TTT.A...................CT..AT.-..G..-.T 220
chrZ:29,464,952-29,465,275       91:------.C......A......A...-..T.A-.G.A.A....CA........A..------G...C.......----C.G.--AGC..C....G.A..AC..G--.T..A...AT.AA.....CG.TT.ATCT.A.-.....T.. 212
chr1:149,690,682-149,690,989     97:------A...G..TAC..G.GTA.C-A.GGG-....GG..A.TA.TG..C.....------.........G..-AATT..T--TGC.T.G..GGAAA.A.....--.T.TT.A.CATCA....GG..T..GT.T..A-G..G.-.. 220
chr1:166,227,721-166,228,104    104:GGGGAG....T..A.--GG.AT..AAC..T.-A.T...A.CT..C.....GCA..------AT..GA.T.T..-----...--C.A.GAC.A.A...A.GAG.--GC.T........T.T..GC.C...ATATATA-..-..-.T 227
chr4:76,706,356-76,706,828       91:------..GC...TC....G.T..T-..TT.-.........GTAGT.......G.------.TG..........-----.A.--AG-G....-.T..A-..GC.GGTTTT..............G.....GTA....-.....-.A 209
chr1:40,679,313-40,679,604       98:------.C..GA.TA....G..ATA-.CA..-.G.T.T.C..A........GAGG------....CAC.CT..-----...AAA.G.CC..G.ACAT......--.CATA.AAAT...C---------.GG.T..CG..TG.-.. 211
chr1:31,190,942-31,191,311       93:------......CT........A..-.C...-.....-.....A......G..T.------........T...-----...--AA-......TGA...T..G.--.C.....................AT.T.T.-.....-.. 210
chr7:21,147,037-21,147,325       92:------..A.....AC.C...T...-.-------.....CAG.AC......G...------.......T....-----.------GT.C.AGCAAAAA-C..--TG..A.A.A.T............GCCTCTT-.....-.. 200
chrUn:56,584,430-56,584,748      90:------.G....T.A......A...-...T.-A...-----TT..A.........------G.A......GA.----T.AG--.AA....CATT...C...C.CC.TA.AA.......C..-----------.ATT-A.T..-G. 196
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chr8:5,961,389-5,961,692         58:------..CA....AAG....T..A-.-...-..T..TC.C.A.........A..------.T.C.C..G..A-----..T--.C-.G.....T..A.--------TT.AA-...T...G.C.......TT.T...-.....-.. 168
chr19:5,230,102-5,230,344        49:------..G..A..A......TA.A-.ATG.-.......CCG..A..G....TC.----CTTT....AAG.C.-----...--CC-.CA.T..A.A......G--TC..A.C.CT.......C.G....GT.GAA.-A....-.. 169
chr7:9,125,064-9,125,466         37:------..-----.AC..C.-------..A.-T.--.....T........G.AGA----AT......AT....-----..T--.A-..A....GT.TA.....--.CTT....G.T......GCC....AC.TTT.-.....-G. 144
chr24:914,218-914,454            13:------..CA.AG.A.C.......A-.C...-....G..C..A.........A..------.......T.G..-----.----------------------------------G..GA.GGC....AT.T..C-.....-.. 100
chr5:48,440,921-48,441,289        1:-------------TA.....GT..A-.GTTG-...TG....T....T..G.....------..T.G...TT..-----CA.--A.-GCA.A..-CTT...---------A.CAA.TG.C.A....C.AGGT.G..C--....A.. 104
chr1:95,263,137-95,263,489        1:--------------------------A.G..GC..AT..AATAT.T.....GA.A------GT..A.AA.GC------...--C.-.......A.CT.-....--TT.T.A.........T.....T..GC..A..-.....-.. 99
chr6:29,821,890-29,822,266        1:-----------------------------------------------........------.TT..TC....-----...--AC-.....C.A..T......--GCTGA..T.TG.............GG.A.CT-AC...--. 80
chr12:13,944,536-13,945,003       1:------------------------------------------------------.------T.......TC.-----..T--A.-..T..ATG....C....--.C..A.........AT...C....GT..T..-.....-G. 74
chr18:5,356,496-5,356,930         1:----------------------------------------------------------------------...------..--A.--T..C.TTCT.-A...---.TT.TAGC..-.A..T.G.AA...GTAT...-.....-G. 58
chr1:124,675,247-124,675,690      1:------------------------------------------------------------------------.-----..T--..-.....A.GAAA......--.C.TA..AG........GC.....GCA.AA.-C....-.. 61
chr20:7,155,282-7,155,630         1:---------------------------------------------------------------------------------------.C.C.GAAAACA..TG--TT.AT.CC.A.......G......AC.G.T.-.....-.A 54
chr5:44,208,732-44,208,929        1:----------------------------------------------------------------------------------------------A......----.C.T.A-A.......TG.CA....GC.T...-.....-.T 45
chr11:5,130,826-5,131,233         1:--------------------------------------------------------------------------------------------------------------..T........C..A....ACC.T..-.....-.T 33
chr7:34,704,354-34,704,742        1:-----------------------------------------------------------------------------------------------------------------............A...AC.T..A-.....-.- 29
chrUn:53,327,606-53,327,809       1:--------------------------------------------------------------------------------------------------------------------...AA.CT.....GT.T..A-.....-G. 27
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B. chicken AmnSINE1 (continued)

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AmnSINE1(chicken) cons          346:ATTCTGCCTACCTA------AATTCCCTCT-GCAGTTTCAATTGGATACGGTATTCTTC---AYTTCC----TGTCCTAAA-CTGTTGTGTAGTGTTGCTGTG-CGCTGTTAAACAGCTGCCGCGTTTCACCCCAGAGRTGGCTG 474
chr2:118,843,690-118,844,129    365:G..T..........-CAGGC........GC-.........C...A....A.-G..------------------------------------------------------------------------------------------ 416
chr2:86,373,833-86,374,350      354:...A....A..T..------...ATT....-CT...........A...AA.....--.AAAT.C..TTGATTC.CAA..T.-..A.CT...GTAA..TA...A-.A...C......A.....A.A...T..T.T....GG.ATGA 487
chr8:27,424,135-27,424,435      302:------------------------------------------------------------------------------------------------------------------------------------------------- 302
chr5:35,360,218-35,360,495      279:------------------------------------------------------------------------------------------------------------------------------------------------- 279
chr4:2,135,009-2,135,345        266:------------------------------------------------------------------------------------------------------------------------------------------------- 266
chr1:182,768,840-182,769,245    360:T..TG..-A.....------..A.------------------------------------------------------------------------------------------------------------------------- 376
chr5:22,251,128-22,251,514      357:GAC..A..------------.....-A..G-.T.T......C.A.---------------------------------------------------------------------------------------------------- 387
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chr2:32,524,517-32,524,738      223:------------------------------------------------------------------------------------------------------------------------------------------------- 223
chr2:16,367,040-16,367,209      171:------------------------------------------------------------------------------------------------------------------------------------------------- 171
chr1:99,961,657-99,961,966      231:------------------------------------------------------------------------------------------------------------------------------------------------- 231
chr2:143,078,494-143,078,851    255:.------------------------------------------------------------------------------------------------------------------------------------------------ 255
chr4:88,091,993-88,092,407      244:...T.......T..------C.C..AGC..-...T......C.CCG..T.TC.......CC-.TC.T.---T.C..T....-T..C...A.G...C.......-.AT.A........T....A.A.....A..TT.T.AATC... 375
chr2:107,246,547-107,246,900    212:------------------------------------------------------------------------------------------------------------------------------------------------- 212
chr1:153,559,699-153,560,039    250:..............------........A.-....C....G.A.C..G.A...C.A..T---.T.CT.----.T..--------------------------------------------------------------------- 311
chr20:13,249,097-13,249,471     236:.........CT...-----A.......CA.-TT.-......ACA...G.AA....T...---.C....----.T.AT...--TGAC..CCA...AG.TT...A-T.T.T.----------------------------------- 328
chr2:31,974,977-31,975,183      208:------------------------------------------------------------------------------------------------------------------------------------------------- 208
chr1:182,563,004-182,563,356    233:...T.A.TG.T...-----A.T......-.-.GG.....C...AA.A.TTA.....C.A---GCC.AT----..AA.A..C-..........----------------------------------------------------- 309
chr2:105,966,005-105,966,354    225:....A.........------.T.....A..-...A..A...A..C.G.GA.-..C...A---.T....----A....C..G-...C...AC.......----------------------------------------------- 306
chr2:144,872,567-144,872,759    140:------------------------------------------------------------------------------------------------------------------------------------------------- 140
chr5:17,303,737-17,304,206      228:....A....T....------.......T..-.TT..GC..T..T....-----..T...---.C..T.----.C.......A.........A.A......T.A-T............T...T.TA..C........T.G..T... 352
chr5:44,206,127-44,206,327      202:------------------------------------------------------------------------------------------------------------------------------------------------- 202
chr5:38,838,574-38,838,873      221:GAA..CT.C.T..G-----AC...TA..T.-.A.A..C..CA...C.CT...TGG..G.-AC.G..T.----..C....C.-.A....G.C.----------------------------------------------------- 300
chrZ:29,464,952-29,465,275      213:..G..AGT....C.-----G.....T.C.G-ATGA......GCA....A..C.-------------------------------------------------------------------------------------------- 259
chr1:149,690,682-149,690,989    221:G......T..--AG------CT...-------------------------------------T.....----......T.--.GC.G.--------------------------------------------------------- 257
chr1:166,227,721-166,228,104    228:TGGAATTT..T...GCTCAT..A....A..A.T.......GC......AA........----GT...T----....A.T..-...C..CA--.CA..C..T.------------------------------------------- 318
chr4:76,706,356-76,706,828      210:......T.C.T...-----A.C.....C..-.TG.C..TCC...C.CA..........A---.T....----....T....-A....CCA.........A...GT.........T..T..T.AG........T.G.CAA..TG.. 340
chr1:40,679,313-40,679,604      212:......TG..GAT.T----AA.TA.TTG..-.A.T..AA...CAA...T--.....----------------------------------------------------------------------------------------- 260
chr1:31,190,942-31,191,311      211:..C..T...T..----------------..-..GC..A-..C..........G.....T---.CC..G----........--...-.A..C.ACA...TCT..-T........------.A.AGA.C...TT....AA....... 320
chr7:21,147,037-21,147,325      201:......T.C.T..T------T........C-TT.......GC....A.AA...GA.AC.---.T..T.----.------------------------------------------------------------------------ 259
chrUn:56,584,430-56,584,748     197:CA...T....TT..------.CACTGTC..-A...CAC.G..G...TT....C...AAA---.CAGT-----...G.C.G.-GCC..T..ACAA.......CA-TC..------------------------------------- 287
chr1:92,362,519-92,362,846      192:.....T...T..A.------C.....GA..-.T-.......A.......AAC.G..C..---.T...G----.C...A...-.A.C.A...-----......A-GA.CAC....TT-..A.A...C.G..--------------- 298
chr8:5,961,389-5,961,692        169:.C.....T......----TAT...TT....-...A..CT..A.......AA....T.C.---.A..AG----..C.T....-TG...C..C.T...AATC...-.A..A.....A.....A.A....C.....A...AA...... 299
chr19:5,230,102-5,230,344       170:.G..GT.T.CA.C.--TGCTCCC...TC.CGT..C.C.-GG..C...G.T.G.C..C..---.C....----CA.....C.-.A.------------------------------------------------------------ 243
chr7:9,125,064-9,125,466        145:..C......GG...-----A....G.AGTGCA..CGC...G...C..GG...........---.---.----.T.TACCCT-GA.C..--CT.A..A...C..-.T-----C..T.TT.T.TATA.....A......AA..T..T 265
chr24:914,218-914,454           101:........AT--A.------.TA....C..-.......T......T..T...G......---.T....----....TAT..-.A.C..G..G....G...C..-..T.C...CGT......T.T...-.......A..C...... 226
chr5:48,440,921-48,441,289      105:.....CT.......-----A....T..C.AGTAGC...-GG.......T.....CTC.T---.G...A----......G.G-.A....AAC.....GA...C.-T..C.........T...TA.A.C...ATTA..CAGAA...C 234
chr1:95,263,137-95,263,489      100:..G......G.T.C------.T..T..CT.-...T...TT...A...T...C.......---TGC.TT----...T....G-.A...T.AC.....G......-.T.......C..CTGCAGCAT.C.ACA..ACA.ATGC.... 228
chr6:29,821,890-29,822,266       81:.GC..A....AA..-----CTC.AAAAGT.-AT.T..GA.TA.A-CCGTAT.......A---.C....----.AC.T.CCT-...G.A.....C...T..ACA-T..A.CCG....A.A..TT.A..GT...TTT...----.A. 205
chr12:13,944,536-13,945,003      75:.......A..GT..------..A....C..-..........A..A..C.AT........---.C....----.T.......-T..C....C..CC.....T..-T....C.G..G..T...TTT........TG..G.A..ATG. 203
chr18:5,356,496-5,356,930        59:.....T.....A..-------......C..-....C....G...C...T..C......T---GGC..T----.ACTG.TTT-TGC......TTGT......A.-AA..AG.G.....T.-.TATA..G....TG...AT...... 185
chr1:124,675,247-124,675,690     62:..C..C..C..AGTAGTTAA..A.....-.-.TT.C.......A...GT.A........---.G..G.----.C..TG...G.....CA..T.....A...-.-T..AA...T..G....TT.T...C..GA.A....GACC.A. 195
chr20:7,155,282-7,155,630        55:..CTC..-AG...GTTACCT..A.A.T..CCA.......TGC.CAG.G.T..C.C....---GT...-----..G...C..-..A..-.T.GC...A...T..-.A...C.GC.........A.A..CT.T.A...G.A...... 187
chr5:44,208,732-44,208,929       46:.....A.T...AC.-----A.......CT.-...............C...------------.C..TG----CA...C..C-A.T..C..C.....G.T.A..-T.-----------------T.C.....AG.....A...... 149
chr11:5,130,826-5,131,233        34:TG.TA.GT.TTG..------.T...T..T.-C..C.....TC.CA...G..........---CT...TG-CC.......G.-...C...........AA....-G................T.T.....T.A.TGC.AG...... 165
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chrUn:53,327,606-53,327,809      28:......T.....A.-----C.....T.-..-............A.....A..G.....T----T..A.----......G.G-..C.....C...A...G..CT-.A.A...T..........A.A......TATG..AGC.CTCA 155
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B. chicken AmnSINE1 (continued)

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AmnSINE1(chicken) cons          475:CATTTCAGTGGTGG-RTGAAATGATCYBTA-------TATG--TAGYTTGTAAAGCGC----TTTGRGA---TCCTTCGGGATGAAAGGCGCTATATAAACGT-AARG-TATYATTATA                           574
chr2:118,843,690-118,844,129    417:------------------------------------------------------------------------------------------------------------------------------------------------- 417
chr2:86,373,833-86,374,350      488:T......C..T.T.-T....C.A..TCT.TCA----------------------------------------------------------------------------------------------------------------- 518
chr8:27,424,135-27,424,435      302:------------------------------------------------------------------------------------------------------------------------------------------------- 302
chr5:35,360,218-35,360,495      279:------------------------------------------------------------------------------------------------------------------------------------------------- 279
chr4:2,135,009-2,135,345        266:------------------------------------------------------------------------------------------------------------------------------------------------- 266
chr1:182,768,840-182,769,245    377:------------------------------------------------------------------------------------------------------------------------------------------------- 377
chr5:22,251,128-22,251,514      388:------------------------------------------------------------------------------------------------------------------------------------------------- 388
chr4:53,214,621-53,214,914      257:------------------------------------------------------------------------------------------------------------------------------------------------- 257
chr2:32,524,517-32,524,738      223:------------------------------------------------------------------------------------------------------------------------------------------------- 223
chr2:16,367,040-16,367,209      171:------------------------------------------------------------------------------------------------------------------------------------------------- 171
chr1:99,961,657-99,961,966      231:------------------------------------------------------------------------------------------------------------------------------------------------- 231
chr2:143,078,494-143,078,851    256:------------------------------------------------------------------------------------------------------------------------------------------------- 256
chr4:88,091,993-88,092,407      376:.....A.A.AA...-A.-------------------------------------------------------------------------------------------------------------------------------- 391
chr2:107,246,547-107,246,900    212:------------------------------------------------------------------------------------------------------------------------------------------------- 212
chr1:153,559,699-153,560,039    312:------------------------------------------------------------------------------------------------------------------------------------------------- 312
chr20:13,249,097-13,249,471     329:------------------------------------------------------------------------------------------------------------------------------------------------- 329
chr2:31,974,977-31,975,183      208:------------------------------------------------------------------------------------------------------------------------------------------------- 208
chr1:182,563,004-182,563,356    310:------------------------------------------------------------------------------------------------------------------------------------------------- 310
chr2:105,966,005-105,966,354    307:------------------------------------------------------------------------------------------------------------------------------------------------- 307
chr2:144,872,567-144,872,759    140:------------------------------------------------------------------------------------------------------------------------------------------------- 140
chr5:17,303,737-17,304,206      353:--A....C....A.-G..T.----------------------------------------------------------------------------------------------------------------------------- 369
chr5:44,206,127-44,206,327      202:------------------------------------------------------------------------------------------------------------------------------------------------- 202
chr5:38,838,574-38,838,873      301:------------------------------------------------------------------------------------------------------------------------------------------------- 301
chrZ:29,464,952-29,465,275      260:------------------------------------------------------------------------------------------------------------------------------------------------- 260
chr1:149,690,682-149,690,989    258:------------------------------------------------------------------------------------------------------------------------------------------------- 258
chr1:166,227,721-166,228,104    319:------------------------------------------------------------------------------------------------------------------------------------------------- 319
chr4:76,706,356-76,706,828      341:-.GA.G.T.CA.AC-C.T.C.-...TTGC.GATA---.C..--C.CG.CA-CTGCA..---C.A..A..----...---...G......TAGAG..G...T.AC..GA-.G.C..A..GACTATTTCCTCAATTAATTTTCTAAT 465
chr1:40,679,313-40,679,604      261:------------------------------------------------------------------------------------------------------------------------------------------------- 261
chr1:31,190,942-31,191,311      321:..........CAAAGTGAC.CA....CT.-------------------------------------------------------------------------------------------------------------------- 349
chr7:21,147,037-21,147,325      260:------------------------------------------------------------------------------------------------------------------------------------------------- 260
chrUn:56,584,430-56,584,748     288:------------------------------------------------------------------------------------------------------------------------------------------------- 288
chr1:92,362,519-92,362,846      299:------------------------------------------------------------------------------------------------------------------------------------------------- 299
chr8:5,961,389-5,961,692        300:...CC-------------------------------------------------------------------------------------------------------------------------------------------- 304
chr19:5,230,102-5,230,344       244:------------------------------------------------------------------------------------------------------------------------------------------------- 244
chr7:9,125,064-9,125,466        266:....-...CTT.---T.TTTT.TT.TTT.TTTTTG--A...-A...T........T..----....AA.---....C.T..C......TT...G.C..-C.A.-..AT-GTAA...T.CTTTGTTGCCAGCTGTAAAATCATACA 393
chr24:914,218-914,454           227:.G...TG.G..-------------------------------------------------------------------------------------------------------------------------------------- 237
chr5:48,440,921-48,441,289      235:A....TG..A..---T.T..-....TTG.GTATGTATA.AT--C..C.G......T..----.C..GAG---......T.....GC...T.-...G...G.A.-..A.CC..C.....CAGGAGCAGGTGTTTTGGCCTGGCAGA 364
chr1:95,263,137-95,263,489      229:..GAA.T.AC-..A-AGC..T.TC.TTC.GTATTGCT...A----.CA.-A...CA.T----....A.G---CAT.C.A...A...CA.TC..C.......A.-.TG.-..ACT..G..TGAAATCAATGTAGCACACAAA---- 353
chr6:29,821,890-29,822,266      206:..C.GTG--AC..C-A...GC...AGAG.T-------.T..--.CCTA.T...G.T..----.C..A..---.T...GAA.G......A.--.GC...C.TA.-.GA.-.G.T-....TCTTAATTTCAAAACCTAGCTAAAATT 326
chr12:13,944,536-13,945,003     204:.......TG.C..C-A.....C.GG.C-.G-------AG..CAC..T.....C.A.AG----ACA.G..-AACA...T.....T.------------------------------------------------------------ 274
chr18:5,356,496-5,356,930       186:.........A.CT.-A......AT.TTG..TTT----.G..-G.G.T.-A......C.----.CA.-..---CTA..T.....T.....TC.C..C.G..TTGA..A.-...C-....TTCTATCCTTGACATCCTTCATAATGT 313
chr1:124,675,247-124,675,690    196:T....T...TA.AA-A....G..T..CC.G----------------CA......AG..----..---------.TG...A.GA.------...C.--G.G.A.---C.-...A.A.CA.TAAACACCAGACAAACTTGTATTGTA 298
chr20:7,155,282-7,155,630       188:......---TT...-GAA......CTTTC.TATA---..AA--..AT..TG....T..----....GA.ACC...C.G...-....GA..A.C..-.G..AA.-T.AT-A.GTC...C.GATACATTATTAATATCGATCCCATT 315
chr5:44,208,732-44,208,929      150:.........A.G.A-GCA..G.T...TTCC-------...A--...C.CA..T.---.----.A..------------------------------------------------------------------------------- 198
chr11:5,130,826-5,131,233       166:............A.-G.A..TGA----C..-------C..--------C...C..T..----C...A..---ATTCA......A..G.A.A..---------------------------------------------------- 231
chr7:34,704,354-34,704,742      150:.......C.T....-G...TGC....CAA.GAG----.T..AA..TCAGT.T..T.A.----....GC.---......A...AC....T.A....T....T..-..GA-.TATTG..G.GAATAAAATTGTCAATAAATGTAGTA 280
chrUn:53,327,606-53,327,809     156:......G..AT.A--A...GT...G.TT..-------..A.-AGG.T..TC..-TTA.----.C--------------------------------------------------------------------------------- 204
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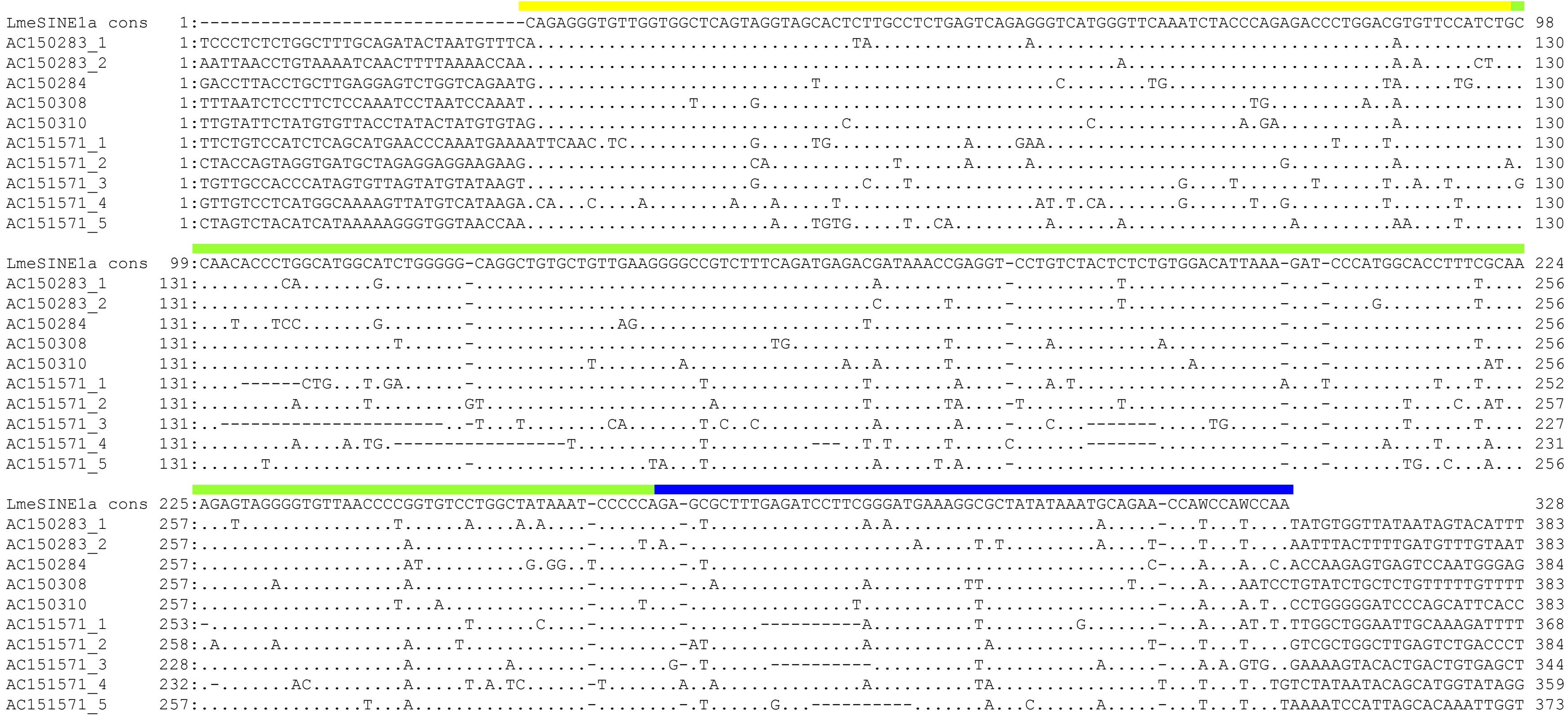
C. LmeSINE1a



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LmeSINE1a cons    1:--------------------------------CAGAGGGTGTTGGTGGCTCAGTAGGTAGCACTCTTGCCTCTGAGTCAGAGGGTCATGGGTTCAAATCTACCCAGAGACCCTGGACGTGTTCCATCTGC 98
AC150283_1        1:TCCCTCTCTGGCTTTGCAGATACTAATGTTTCA...............................TA...............A...................................A............ 130
AC150283_2        1:AATTAACCTGTAAAATCAACTTTTAAAACCAA..........................................................A..........................A.A.....CT... 130
AC150284          1:GACCTTACCTGCTTGAGGAGTCTGGTCAGAATG...........................T.......................C........TG.....................TA.....TG..... 130
AC150308          1:TTTAATCTCCTTCTCCAAATCCTAATCCAAAT................T.....G................................................TG.........A..A............ 130
AC150310          1:TTGTATTCTATGTGTTACCTATACTATGTGTAG..............................C.......................C..............A.GA...........A............ 130
AC151571_1        1:TTCTGTCCATCTCAGCATGAACCCAAATGAAAATTCAAC.TC............G.....TG.............A....GAA............................T....T............. 130
AC151571_2        1:CTACCAGTAGGTGATGCTAGAGGAGGAAGAAG......................CA............T......A.....A........................G..........A..........A. 130
AC151571_3        1:TGTTGCCACCCATAGTGTTAGTATGTATAAGT......................G..........C...T..........................G....T.......T......T..A..T......G 130
AC151571_4        1:GTTGTCCTCATGGCAAAAGTTATGTCATAAGA.CA...C....A........A...A.....T...................AT.T.CA.......G......T..G.........T......T...... 130
AC151571_5        1:CTAGTCTACATCATAAAAAGGGTGGTAACCAA........................A...TGTG.....T..CA.........A......A................A.........AA....T...... 130

LmeSINE1a cons   99:CAACACCCTGGCATGGCATCTGGGGG-CAGGCTGTGCTGTTGAAGGGGCCGTCTTTCAGATGAGACGATAAACCGAGGT-CCTGTCTACTCTCTGTGGACATTAAA-GAT-CCCATGGCACCTTTCGCAA 224
AC150283_1      131:........CA.......G........-.......................................A............-..........T...............-...-..............T.... 256
AC150283_2      131:..........................-.......................................C......T.....-..........T...............-...-....G.........T.... 256
AC150284        131:...T...TCC.......G........-..............AG......................T.............-..........................-...-................... 256
AC150308        131:...................T......-.............................TG...............T.....-...A..........A...........-...-..............T.... 256
AC150310        131:..........................-...........T........A...............A..A......T.....-.................A........-...-...............AT.. 256
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AC151571_3      131:..----------------------..-T...T........CA.......T.C..C...........A.......A....-...C...-------.....TG.....-...-.......T......T.... 227
AC151571_4      131:.........A....A.TG.-----------------T............T..........---..T.T.....T.....C.......-------............-...-.....A....T....A... 231
AC151571_5      131:......T...................-.................TA...T................A.....T.A....-..........................-...-.......TG..C...A... 256

LmeSINE1a cons  225:AGAGTAGGGGTGTTAACCCCGGTGTCCTGGCTATAAAT-CCCCCAGA-GCGCTTTGAGATCCTTCGGGATGAAAGGCGCTATATAAATGCAGAA-CCAWCCAWCCAA                        328
AC150283_1      257:...T...............T......A....A.A....-........-.T...............A.A....................A.....-...T...T....TATGTGGTTATAATAGTACATTT 383
AC150283_2      257:....................A.................-....T.A.-......................A.....T.T.........A....T-...T...T....AATTTACTTTTGATGTTTGTAAT 383
AC150284        257:....................AT..........G.GG..T........-.T...........................................C-...A...A..C.ACCAAGAGTGAGTCCAATGGGAG 384
AC150308        257:.......A............A.................-........-..A..............A.........TT..............T..-...A...AATCCTGTATCTGCTCTGTTTTTGTTTT 383
AC150310        257:...................T...A..............-....T...-................T...........T.................-...A...A.T..CCTGGGGGATCCCAGCATTCACC 383
AC151571_1      253:-.........................T......C....-........-.......----------A..........T.........G.......-...A...AT.T.TTGGCTGGAATTGCAAAGATTTT 368
AC151571_2      258:.A.....A............A....T............-........-AT...............A...........A...............T-...T...T....GTCGCTGGCTTGAGTCTGACCCT 384
AC151571_3      228:....................A.........A.......-.......G-.T......----------..........T...........A.....-...A.A.GTG..GAAAAGTACACTGACTGTGAGCT 344
AC151571_4      232:.-.......AC.........A.....T.A.TC......-T.......A..A..............A..........TA................T...T...T..TGTCTATAATACAGCATGGTATAGG 359
AC151571_5      257:................T...A.................-........-.T......G...----------.......A...C......A.....-...T...T...TAAAATCCATTAGCACAAATTGGT 373
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D. LmeSINE1b

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LmeSINE1b cons   1:-------------------GGTGGCTCAGTAGGTAKCACTGTT-GCCTCTGAGTCAGAA-AGTCG-AAGGTTCGAATCCCACCTGAGGAA---CCTGGACATATTCCATCTRCCAACGCCCCAGC 100
AC147788_2       1:ATCTGACACCAATGGTGTTT....T......A...G....C..-...............-..CTA-C.....T...CT...AT.......---........G...T.....G.....A...AGCA 119
AC150283_2       1:TTCTTCATAGGTTATTTAT....A...........G-.T....A.T.............-T..T.-..CT.CT.T........A..CA..---TA....T...CATTG.-.A....T..A..... 118
AC150310_2       1:ATTACATTTCCTCTTTATA.......T.....T..T-...T..-.............GG-G..T.C.....C.A.-..T..........TCTT..........G..T....A...GTATA.T... 121
AC151571_5       1:TACTTTTTTGTTTTGTTAGTTAA........T...T.....C.-...............A.A..A-T......AG.......T.......---..........G.......A.....A....... 120
AC150308_2       1:-------------------------------------------------------------...A-C.....G..-.G-...ACCT....AAC..CT..G...........GT...AT....... 61
AC151571_4       1:------------------------------------------------------------------.......A..CT............---.....G............G....T.......T 56
AC150308_1       1:-------------------------------------------------------------------------------------.....AA-.T.CC..C..........G.T..AT....... 39
AC151571_6       1:------------------------------------------------------------------------------------------------------------------..GA....... 11
AC147788_3       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC151571_1       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC151571_7       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC150283_1       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC150310_1       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC147788_1       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC151571_2       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC151571_3       0:----------------------------------------------------------------------------------------------------------------------------- 0

LmeSINE1b cons 101:ATGGTGTTTGG-GGGCGC-------TG-TGCTGCTGAAGGTGCCTTCTTTT-GGATGAGACGTTAAACCG--AGGTCCTGTCTACTTTGTGGACATTAAA--GATCCCATGGCACTTTT----CG 207
AC147788_2     120:TGATGC..GA.--A.T.T-------..-..T.............A.....C-.........A......T.--...G-.....---------------------...T.....TT.....----.. 205
AC150283_2     119:.A.....C...-..-.A.-------..-C......C...A.T.A.....G.-ATC.A...T.C......A--CAT.........T.....T..T.G...G--....T............----T. 224
AC150310_2     122:..AA.....T.-..TACT-------.T-......C...........T..C.-A.......T.A....TT.--....T...C..---.CA.AA...G.C..--..........T......----.A 225
AC151571_5     121:G..ACA.A...A...A..AGAGTTA..-.....A......A..TG......-......A..A......T.--....A..T..C............A....--C..T......T.T....----.A 235
AC150308_2      62:..A........-...T.G-------..G..G..G..GC..C.G..-G.GC.-.-C...AG-..G...-----.......A..A............A....--....T..G.....AA.A----T. 163
AC151571_4      57:........A..-......-------..-....A.....A.....A......-.........A.......A--....T.......................--.G.T......T......T---T. 164
AC150308_1      40:......G....-...A..-------..-..T.A......-------G.GG.-ATT.AG.CT......TT.--..A..T...G........A.........--.T.T....A........----.A 139
AC151571_6      12:...........-......-------..-...............TG.GC...-...C....AAC.....G.--....G.......................--.................TTTT.. 122
AC147788_3       1:---...CCA..-......-------..-.AT.....CT...T..C..C.C.A................T.--...------------------....T.G--...T..G.AA.....------.C 85
AC151571_1       1:----------------------------------------------.....-.-------.T.......T--................A....A...G.C--......GCA.TG.....----T. 63
AC151571_7       1:----------------------------------------------.....-....A...T.....C.T.AG....T......G..........C.....--.........A.G..C..----T. 72
AC150283_1       1:-------------------------------------------------------------------.T.--.T..T.............A..T..A...AT........AA..TC...----.A 52
AC150310_1       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC147788_1       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC151571_2       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC151571_3       0:----------------------------------------------------------------------------------------------------------------------------- 0

LmeSINE1b cons 208:AAAGAGTA------------------GGGGTGTTAACCCCAGTGTCCTGGCCACAATTCCCCCA-------------------------------------DTAATGACTGGAAGCTG------T 271
AC147788_2     206:........------------------T...CA.......AGC..C....A...A.....TAT..-------------------------------------T..G..G..........AAGCTG. 275
AC150283_2     225:........------------------A....A.........T.C...A..TT.A....T...T.------------------ATACAGTCTTCATCAGGTCA..G.A.......A...------. 307
AC150310_2     226:.....T..------------------T....A...........T..T..A.............CCCCCCACACACACACACACAACAATTGTCATCAGGTCC...A.G..........------. 326
AC151571_5     236:...T.C.C------------------AA.............C......T.T.G...C..T....-------------------------------------T...C..T.A.......AAGCTTC 305
AC150308_2     164:..T..-..------------------........T...A.................C.T..TT.-------------------------------------G...............A------. 226
AC151571_4     165:.......GTGTGTGTGTGTGGGGGGG..........T..................G....T...-------------------------------------G.G....T.........AGGCTG. 252
AC150308_1     140:...A.TG-------------------------------------.AAG.......T......---------------------------------------A..G.....A...A...------. 182
AC151571_6     123:.G......-------------------.............G......A..........T...-.-------------------------------------A.............T..AAGCTG. 190
AC147788_3      86:........------------------.A....G..G............A..T..GG..TT..TC------------------ATACAATC--CATCATGTTAA...A.......AT..------. 166
AC151571_1      64:...T....------------------.............TG....T..CA..............-------------------------------------GG...............AAGCTG. 133
AC151571_7      73:.......T------------------...A.....G.TG.....G........A.G..A.T...-------------------------------------T........T....T..------. 136
AC150283_1      53:.....T..------------------......C....T.AG......CA.T....G..T.T...-------------------------------------A............A...------. 116
AC150310_1       1:-------.------------------.....A.....................A....G.....-------------------------------------T................AAGGTG. 63
AC147788_1       1:----------------------------------------------------....A.......-------------------------------------GC.....T..C.G....------. 30
AC151571_2       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC151571_3       0:----------------------------------------------------------------------------------------------------------------------------- 0
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D. LmeSINE1b (continued)

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LmeSINE1b cons 272:TGTGTGGTGT-G----------------------------------------------------------------------------------------------------------------- 282
AC147788_2     276:..........-.----------------------------------------------------------------------------------------------------------------- 286
AC150283_2     308:AA.ACTAA..-.----------------------------------------------------------------------------------------------------------------- 318
AC150310_2     327:CC...A....-.----------------------------------------------------------------------------------------------------------------- 337
AC151571_5     306:.C........T.----------------------------------------------------------------------------------------------------------------- 317
AC150308_2     227:....CCC...-.----------------------------------------------------------------------------------------------------------------- 237
AC151571_4     253:..........T.----------------------------------------------------------------------------------------------------------------- 264
AC150308_1     183:..........-.----------------------------------------------------------------------------------------------------------------- 193
AC151571_6     191:..........-.----------------------------------------------------------------------------------------------------------------- 201
AC147788_3     167:CT..CA-G..------------------------------------------------------------------------------------------------------------------- 175
AC151571_1     134:..G.......T.CTGGAACAGGCCCATAGCTGGGGGGGGGCATGAGGGGGCACGAGGGGGCACTGCCCCCCTTTAAACTTCTTTGCCCCCCCCCGTCGGAACTAAGATGTGTTCCAGCAACAACG 258
AC151571_7     137:......A...-.----------------------------------------------------------------------------------------------------------------- 147
AC150283_1     117:...T....A.-.----------------------------------------------------------------------------------------------------------------- 127
AC150310_1      64:...TC...A.-.----------------------------------------------------------------------------------------------------------------- 74
AC147788_1      31:....GCA...-.----------------------------------------------------------------------------------------------------------------- 41
AC151571_2       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC151571_3       0:----------------------------------------------------------------------------------------------------------------------------- 0

LmeSINE1b cons 283:---------------------------------------------------------------------------------------CTGGCACTAAAA-TGGTTGCCT---------------- 303
AC147788_2     287:---------------------------------------------------------------------------------------.......C....-.........TCAGAGCTGGACTGGC 323
AC150283_2     319:---------------------------------------------------------------------------------------......TG...--.......TG---------------- 338
AC150310_2     338:---------------------------------------------------------------------------------------..A.T..AG..--.AT....TA---------------- 357
AC151571_5     318:---------------------------------------------------------------------------------------.......C...GA.......T.---------------- 339
AC150308_2     238:---------------------------------------------------------------------------------------..A.....G...-..A.G....---------------- 258
AC151571_4     265:---------------------------------------------------------------------------------------.......C....A.........---------------- 286
AC150308_1     194:---------------------------------------------------------------------------------------...A.CA...C.CA.A.A..TC---------------- 215
AC151571_6     202:---------------------------------------------------------------------------------------A...........A.........---------------- 223
AC147788_3     176:---------------------------------------------------------------------------------------ACA.T...TG.--..C.....G---------------- 195
AC151571_1     259:GGGCCCATTACTTTCTCTTCGCAACTGCCTCCCTTTTCATGCAGTCTGCCCCCCCCCCATGTTGATGTCCTAGCTACGGGCTTGTGCTG.AACTA...--.........---------------- 365
AC151571_7     148:-------------------------------------------------------------------------------------TG......T.....-....CA...---------------- 170
AC150283_1     128:---------------------------------------------------------------------------------------......TA.-------...T..---------------- 142
AC150310_1      75:---------------------------------------------------------------------------------------...CA..A....A....CA..A---------------- 96
AC147788_1      42:---------------------------------------------------------------------------------------....T.......A-A.......---------------- 62
AC151571_2       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC151571_3       0:----------------------------------------------------------------------------------------------------------------------------- 0

LmeSINE1b cons 303:----------------------------------------------------------------------------------------------------------------------------- 303
AC147788_2     324:AGTAAAAGGGCATACCTGGAAGTGTTAGGCAGGGGGGCATTACGCATGTATAATGTGGATGAAAACCGTCTCCCAGCCCACCAGGGGTCTGCGGCCCCCAGTTTGAGAACCCATGCCGTATGGCA 448
AC150283_2     338:----------------------------------------------------------------------------------------------------------------------------- 338
AC150310_2     357:----------------------------------------------------------------------------------------------------------------------------- 357
AC151571_5     339:----------------------------------------------------------------------------------------------------------------------------- 339
AC150308_2     258:----------------------------------------------------------------------------------------------------------------------------- 258
AC151571_4     286:----------------------------------------------------------------------------------------------------------------------------- 286
AC150308_1     215:----------------------------------------------------------------------------------------------------------------------------- 215
AC151571_6     223:----------------------------------------------------------------------------------------------------------------------------- 223
AC147788_3     195:----------------------------------------------------------------------------------------------------------------------------- 195
AC151571_1     365:----------------------------------------------------------------------------------------------------------------------------- 365
AC151571_7     170:----------------------------------------------------------------------------------------------------------------------------- 170
AC150283_1     142:----------------------------------------------------------------------------------------------------------------------------- 142
AC150310_1      96:----------------------------------------------------------------------------------------------------------------------------- 96
AC147788_1      62:----------------------------------------------------------------------------------------------------------------------------- 62
AC151571_2       0:----------------------------------------------------------------------------------------------------------------------------- 0
AC151571_3       0:----------------------------------------------------------------------------------------------------------------------------- 0
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D. LmeSINE1b (continued)

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LmeSINE1b cons 304:--------------------------------------------------------------------------CGTTCCACCCCAGAGGTGGCTGCACTTCAGTGGATTGCACAA-------TA 347
AC147788_2     449:TAGGGCATTCAAGTAGAGGGGCATACCTGGAAAATTCCAGGTTTCCGGGCTGGCCAGTCCGGCTCTGGTTGCCTT...G..........A...T....T..G.............G-------.. 566
AC150283_2     339:--------------------------------------------------------------------------.A...A..........CA.....TGG...A..A.G....T.TAGTT---GC 386
AC150310_2     358:--------------------------------------------------------------------------.-.......A..AT...........A...A......T....TGGTTCTAGT 407
AC151571_5     340:--------------------------------------------------------------------------T...T............A....TG............A.....-------C. 383
AC150308_2     259:--------------------------------------------------------------------------.C..........A.T....T....T.A..A....C...G.T.-------.. 302
AC151571_4     287:--------------------------------------------------------------------------.A..G........G............................-------.G 330
AC150308_1     216:--------------------------------------------------------------------------.T...-...A....A...A...T......A.......TG...-------.. 258
AC151571_6     224:--------------------------------------------------------------------------.T.......AT......................GA..T.T..-------.T 267
AC147788_3     196:--------------------------------------------------------------------------.A...TT..............A.......A..A..CA..A.C-------CG 239
AC151571_1     366:--------------------------------------------------------------------------TA......T.........................CA......-------CC 409
AC151571_7     171:--------------------------------------------------------------------------..........TG..............................---GGACGG 218
AC150283_1     143:--------------------------------------------------------------------------T...GA.A......AC...T......GT.............G--------- 184
AC150310_1      97:--------------------------------------------------------------------------.A.....T..............T..G.............A..-------.. 140
AC147788_1      63:--------------------------------------------------------------------------.A..T.T........A...........T....AGCG.A....-------C. 106
AC151571_2       1:----------------------------------------------------------------------------------------------....T..A......A..T....-------CG 24
AC151571_3       1:---------------------------------------------------------------------------------------------------..AT.......ATG...-------.. 19

LmeSINE1b cons 348:TCT--------CTGTAAAG-CGCTTTGA-GATCCTT-CGGGATGAAAGGCGCTATATAAATCCAAA-ATTCA-TTCATTCA                                             415
AC147788_2     567:G..--------.......T-T.......-...A...-.A...........A.C.......C..C..-.....-..T.....TAATATCTGTCTTGCTTCCTGATACAAGACTACTTATTGACCAC 678
AC150283_2     387:.GCATGGCCTCT.......-.AT.....-...T...---.A.CA.T...TAT.........GT..--G...TA...CA.ATAAATCA-GTTTGTAAAATCATTTATCATTTGGGAAATATTTTAA 503
AC150310_2     408:.GCAATGTTTA-.......T.T..C...-.......-T....A..G.A.T...G.......GTC..-...A.-...TG.ACTACACAAAGTCTAACATAACTATTTTTGATCATGTTTAGATATG 527
AC151571_5     384:...--------......G.-.A....C.-.......-TA...........T....G...G......-.....-........GTGTGAAAGCACAACAGCTGTATCCCTAGCTGGATTTTTCCTCT 495
AC150308_2     303:...----------.....T-T.....C.-.......-...A..A.....TA..G.G.C...G....GG....-...C....CTCAAGTTTCCTTTTCAGAAGTATATCAGTATAACTGTTGTGGA 413
AC151571_4     331:C..--------..A.....-T..A....-.......-.A...........A.......G...T...-...TG-........ATTCAAAAGAAAGTACTAGGGATTAAATACCACAGAACGTTGTT 442
AC150308_1     259:..C--------.CA.....-.A.A..A.-..C....-.AA........ATA.A.A..--T.GGTC.-G.-..T....A.T.CACTCCAGCCTTTTGACTGGTTCCACTGAGATGAAAGATCTCTC 368
AC151571_6     268:...------CTT.......-G.......-....T..-.A...........................-..C..-........GTCAGTCATACTTCCTATTGTTTATTGTCATATGTCTTACATTG 381
AC147788_3     240:...-----TAG.A...TT.T.T..GCA.T.C..T..-GA.-.CA.......A....A....AT...-T.CTT-...TA.ACTGAATTGTCATTTGGGGTTACAAAACCAAACATACCATTACAAA 355
AC151571_1     410:.A.--------........-T....G..-......GAG.......G...TT...C.......T...-.....-...CAG.TTTCAAAACTGTGGATGTACTTCTTTTTTCCCCAATGAATGGTGC 522
AC151571_7     219:...--------........-T...C..G-A......-T............A...C.......TG..-G....-..GTCCTGGTTTAAAAACGTAAGCTGTTGTTGGCATTCAGGTGCAAACTGCA 330
AC150283_1     185:-----------T.TG....-.TA.AAC.-..ATGCA---------------AAT.T...CATA.T.-C..A.-A.GTAAG.AATGCAT-TTAAAATAGTAATCTTAAAATAATTACTACTTTATA 278
AC150310_1     141:...--------T.A.....-.A......-.T.....-.A..........T..C.............A...A.-....C..GTTCATTCATTCCATCCTTTGGTATAGAAAAGGTGTTCAGGCCAA 253
AC147788_1     107:...--------........-T.......-.......-.A..........TT........T.G....-C.CAC-..A...TCATTTAAATTGGTTGTACTTTATGCTTCTAAATTGTTGTCCATTA 218
AC151571_2      25:...--------........-A...C...-.......-...........-T.G...T.C........-....C-........TAGCAGGCCAACGTGTGAAGATTTGAAACTTTTTAAGCTAGAAG 135
AC151571_3      20:...--------........-AA..--..-.......-T................C...........-.....-..A.....TTACAGTTCTGAATTAACCTTTCTTGCATTTATTCTTCTTGCTC 129
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E. SINE3_IP

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SINE3_IP cons     1:-------------------------------------GCCAGAGCCATATCTCCCTGCAGTTCTCGCCTGGTTTCCCACTGAAGCTAAGCAGGGTTGAGCCTGGCCAGTACCTGGATGGGAGACCTCCTGGGG-AAAA 100
CK417334          1:CTTCCTGTGTGTTTAATAAAACCTGTACACTTTATAC..T....A..-------..AG.......A..................A.........C........................T..........C..-...G 130
CK417958          1:TGCAAATAAACATCGCATCACATATGTGCTTACACAC.TTC-..AA.----...-.......G.-.T.....-.......T............-.....A....G............................G.... 129
CF262350          1:ATTGCCCAGCCGTATTATAAGAACAACAAAACAAATT........A...................A...T............T............---A........................T.......------- 128
CK419868          1:ACAATGGGGAAAAGAAAGCGGCTTTTTATTTTACCTTA..T.....T....A........C........A................G....C............-............................-.... 136
CK421507          1:ATTATATTTATTCAGTAAATATGCCATATGTGATAATAT.T.......................T.A..........................C....A................T...T.............-.... 137
CK405811          1:AATGTGTAAGTAGAAAAGATGATAGATAGATTTATAT..............A........C.............AT.......T...............G....T......................T.....-.... 137
CK416663          1:GTTGGTTTGGAAGGTCATGAGTTTAAATCCCAGCAAC..T.....AC......A..........T..T....G...T............................TT......C....A.....T........-...G 137
AC148720          1:--------------------------------------------------..G.......C..................G......G.....T....................A.............-.....G.... 87
AC148615          1:-------------------------------------------------------------...T.....C...........T.T..............T..................A..............-.... 76
CK415416          0:------------------------------------------------------------------------------------------------------------------------------------------ 0
CK413847          0:------------------------------------------------------------------------------------------------------------------------------------------ 0
CK416055          0:------------------------------------------------------------------------------------------------------------------------------------------ 0
CK417608          0:------------------------------------------------------------------------------------------------------------------------------------------ 0
CK417407          0:------------------------------------------------------------------------------------------------------------------------------------------ 0
AC148615_2        0:------------------------------------------------------------------------------------------------------------------------------------------ 0

SINE3_IP cons   101:CTAAGGTTGCTGCTGGAAGTGGTATT----AGTGAGGCCAGCAGGGGGCGCTCACCCTGTGGTCTGTGTGGGKCCTAATGCCCCAGTATAGTGACGGGGACACTATACTGTAAAAACAGCACYGTCTTTCGGATGAGA 234
CK417334        131:.......CA.................----.......--------...........................GT.....................A..........................T.A............. 256
CK417958        130:...........A.......-----------------.........................-----------------------------------T........C................A............G.. 215
CF262350        129:--...C..-...---........----------...............T.......................G......A..T............A..A..-------..............T.......A....... 243
CK419868        137:........................A.----....------------------------------------------------GT.T....A...T.T....G....G...............C.G...---------- 212
CK421507        138:..............A...........----...................A.....T................AAA...............................................C.......A.....A. 271
CK405811        138:..........................----.......--------...T.........C.............T......................T.....G................C...A.........C..... 263
CK416663        138:.....T............A.......TATT.................AT.....................A.GGG.....G.T.......C...T.T....T...A..............GAC......T.T.---.. 272
AC148720         88:.............G.........G..----..G.....................T.................T............T....................................T...........A... 221
AC148615         77:....................T..T..----...A................G..............C......T........A.................................-......T......T.A...... 209
CK415416          1:--------------------------------------------------------------------------------------------------...T..G---.AC...........T..T...T........ 37
CK413847          1:---------------------------------------------------------------------------------------------------------------.....A.ATC.C..G....A.G..... 27
CK416055          0:------------------------------------------------------------------------------------------------------------------------------------------ 0
CK417608          0:------------------------------------------------------------------------------------------------------------------------------------------ 0
CK417407          0:------------------------------------------------------------------------------------------------------------------------------------------ 0
AC148615_2        0:------------------------------------------------------------------------------------------------------------------------------------------ 0

SINE3_IP cons   235:CGTTAAACCGAGGTCCTG-ACTCTCTGTGGTCATTAAAAATCCCAGG-ACACTTATCGTAAAA-GAGTAGGGG-TATAACCCCGGTGT-CCTGGCGAAATTCCCCCAT-TGGCCCTT-CTCT----ATCAT-GGCCCC 360
CK417334        257:........T.........-............................-........G.....--.........-..G..A...A....-....C.C...........C-........-....----.....-...... 381
CK417958        216:......C...........-...........C...............A-.....C..G......-......A..-..............-....C.C.......T...C-..A.....-...C----.G...----... 338
CF262350        244:.A......T...A...---------------------------..A.-....A...G......-.........-...GT..----------...T.............-..----------------------T.... 318
CK419868        213:----.....A........-............................-.A....C..A....--......C..-......AGT.....-...................-........-AA..----.....-..G... 333
CK421507        272:........T.........-....................T....------------------------------------------------------------....-.A......-A...----.....-...... 341
CK405811        264:.........A.......C-.....G..--..................-.........A.....-....T....-........T.....-...TA.A.........GT.-........-....----.....-.T.... 387
CK416663        273:T.................-.................C.......GC.-........G......-.........-........T.....-.....T............C-........-....----....C-...... 398
AC148720        222:........T.........-.......-....................-....A..........-A........-....C......CA.-.....T............C-........-....----.....-..A... 346
AC148615        210:........T..A......-.T..........................-............C..-....TA...-......---T...A-T...CT.............-........-A...TATA..A..T..T... 337
CK415416         38:.............A....-......C..........CG........A-....G.T..A.G..--.........-.......A......-.....T..G.G........-.T......-T..C----.....-.....A 162
CK413847         28:........A.........-...................C........-...T..G..A.....-......AT.-........T.T...-....A.A.......T....-........-...C----.....-...... 153
CK416055          1:-------...........-............................AC-.............-A.....-..-...........CA.-....A.T............-........-....----.----------- 108
CK417608          1:-------...........G...............A.C.......G..G...A....T......A.........G........T.....N....TN.....C......AN........N....----....C-...... 126
CK417407          1:-----------------.-...T..G.....................A.A..C.....C....-.C..G....-........GT.GTC-....TGA....C.......-A..T.T..-....----.....-...T.. 110
AC148615_2        0:------------------------------------------------------------------------------------------------------------------------------------------ 0
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E. SINE3_IP (continued)

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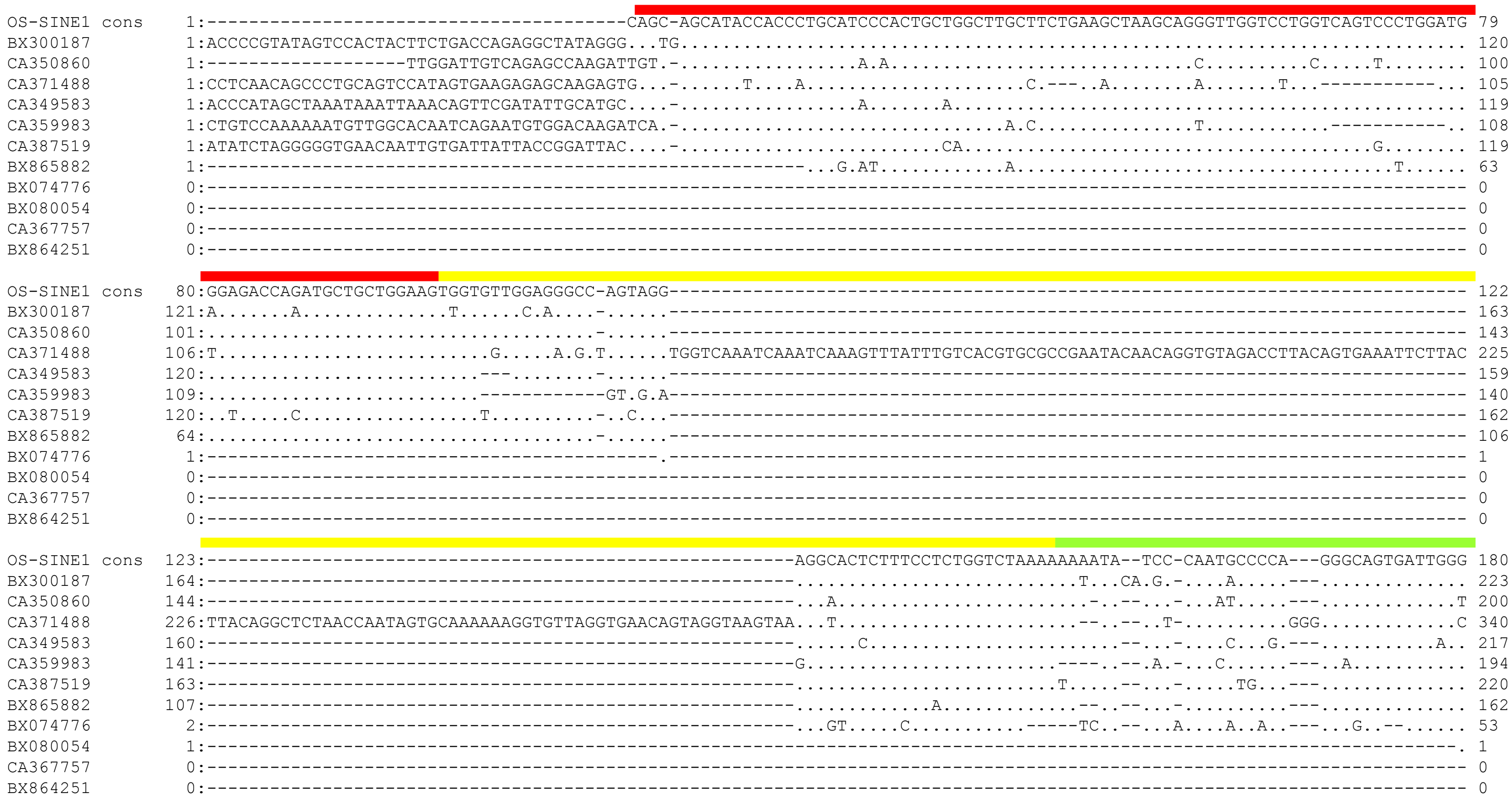
SINE3_IP cons  361:C-TAATAATCCC-CATCTC-TGAATTGGCTACATCACTCTCTCCTCT-----CCACTAATAGCTGGTGTGTGGTGGGCGTTCTGGCGCACTATGGCTGCCGTCGCATCATCCAGGTGGATGCTACAC-ACTAG-TGGT 488
CK417334       382:.-........NT-......-................--.........-----A........................A.......G.GT.C..C......-..T...............A....-..-....AN..T. 506
CK417958       339:.-.....C..T.-......-....G.....T................-----.......C......A....---------.....A........T....G-..T........------------------...-..C. 439
CF262350       319:.-..........-......-....C.........T............-----.G.......................T.......T...G..........C.T.......G...A..A.........-.....-.... 446
CK419868       334:.-........T.-....C.C..........T....C--.........-----T...C.T------------------------------------------.................G........-...G.G..TG 419
CK421507       342:.-........T.-T...C.-.............C..--.........-----..T..------------------------------------------------------------------C...C.G.C.C.CA. 403
CK405811       388:.-..........-......-.....................CT....--TCT...................T...........................T...A..C.....CT..T..........-...G.-.A.. 518
CK416663       399:.-..........-......-................TG.........-----.........A...............A.A.....A............................T....C.......-.....-.... 526
AC148720       347:.-....C.....-....C.-....C....................G.-----..T....C............C................A.......AGT...........................-.....-.... 474
AC148615       338:.-..........-......-...........................CCTCT.......G.........................TA..T.C...........C......T................-.A...-.... 470
CK415416       163:.-..........-T.A.C.-....C...G......G....T......-----......G..TT..................T..............C...T.T........................-.....-.... 290
CK413847       154:.-..........-......-...........................-----........................AG...........A..........A.........................A-..-------- 274
CK416055       108:------------------------------------------------------------------------------------------------------------------------------------------ 108
CK417608       127:.C.......T..C......-.....G..........TG.........-----.........A..........-....A.A.....A............................T....C.......-.....-.... 255
CK417407       111:-C.....----------------------------------------------------------------------------------------------------------------------------------- 116
AC148615_2       1:--------------------------------------------------------................C................T.............A.......................-.....-.... 80

SINE3_IP cons  489:GGTTGAGGAGATCCCTCCCCCCCCCCC-----ACCATACTATGTAAAAGCGCTTTGAGTGTCTAGAAAAGCGCTA-----TGTAACTGTAACTGTAACTAACTAA                                  583
CK417334       507:......A....A..AC....T..T...-------A........GTG.GTG..A-...........G......G..-----.T...TAT..CTG...C..--------------------------------------- 592
CK417958       440:.......A---------------------------....G.............---------------------.-----.A...A.A.CTT.C.....GCA...TATTACAATCGTTACTCTGCTTAACCTGGATAT 524
CF262350       447:...........C...C-------------------...A........----------------------.T....-----...G...........C.........CCAAAAAGTGGTTATAGGAAATTGTGTGTATAT 538
CK419868       420:............TT.C.....---------------.G..G.A....G------------------------------------------------------------------------------------------ 452
CK421507       404:...G..-------------------------------------------------------------.T..AA.G-----.............AAGCA.GTAAG.GATGAAATCTGCAAACTTAATTTTTTTTAAATT 475
CK405811       519:...........------------------------------------------------------------------------------------------------------------------------------- 529
CK416663       527:.T...................--------------------------------------------------------------------------------------------------------------------- 547
AC148720       475:......A.....T.TG...........C----...--..........-.......................A...-----.............--........G.GAAAAAATAGTGTAGATCTGGTTTGATAAAATC 598
AC148615       471:...........CAG.C.........A.CCCCCC.-.....G......---------------------------G-----............AT.C.G.CTGGG.AGGGTTAAAAAACTATTTCAAAGGCTCTGGGAC 575
CK415416       291:...............AAATG.......CCCCCC..........-------------...................GGCTA.A.C.A......C............CTCAGACCTGTGATGACCACAGTAGCATTATCT 415
CK413847       275:------------------...T..G.ACACAC..A.........G..-..A........................-----.A...A..C.............A..CATTTAATCCTGAAATGTTTTGATTCAATTTTA 388
CK416055       108:------------------------------------------------------------------------------------------------------------------------------------------ 108
CK417608       256:.T.........A...............-----.....-.....A...-............CA........T....-----..........T............GCCAAGCAATCACTGCTGGGCCCTTCAGCAAGGCC 381
CK417407       116:------------------------------------------------------------------------------------------------------------------------------------------ 116
AC148615_2      81:.....C.............TA.----------...............-.T.........A........G......-----.....AC...TGCAC.TTG...CTCATTGGGGTCCCCCCAATAATACCAGTGACAATA 202
```

F. OS-SINE1



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OS-SINE1 cons    1:----------------------------------------CAGC-AGCATACCACCCTGCATCCCACTGCTGGCTTGCTTCTGAAGCTAAGCAGGGTTGGTCCTGGTCAGTCCCTGGATG 79
BX300187         1:ACCCCGTATAGTCCACTACTTCTGACCAGAGGCTATAGGG...TG........................................................................... 120
CA350860         1:-------------------TTGGATTGTCAGAGCCAAGATTGT.-.................A.A.............................C..........C.....T........ 100
CA371488         1:CCTCAACAGCCCTGCAGTCCATAGTGAAGAGAGCAAGAGTG...-......T....A.....................C.---..A........A.......T..-----------.... 105
CA349583         1:ACCCATAGCTAAATAAATTAAACAGTTCGATATTGCATGC....-.................A.......A................................................. 119
CA359983         1:CTGTCCAAAAAATGTTGGCACAATCAGAATGTGGACAAGATCA.-...............................A.C...............T............-----------.. 108
CA387519         1:ATATCTAGGGGGTGAACAATTGTGATTATTACCGGATTAC....-.........................CA.......................................G........ 119
BX865882         1:---------------------------------------------------------...G.AT............A....................................T...... 63
BX074776         0:------------------------------------------------------------------------------------------------------------------------ 0
BX080054         0:------------------------------------------------------------------------------------------------------------------------ 0
CA367757         0:------------------------------------------------------------------------------------------------------------------------ 0
BX864251         0:------------------------------------------------------------------------------------------------------------------------ 0

OS-SINE1 cons   80:GGAGACCAGATGCTGCTGGAAGTGGTGTTGGAGGGCC-AGTAGG---------------------------------------------------------------------------- 122
BX300187       121:A.......A..............T......C.A....-......---------------------------------------------------------------------------- 163
CA350860       101:.....................................-......---------------------------------------------------------------------------- 143
CA371488       106:T..........................G.....A.G.T......TGGTCAAATCAAATCAAAGTTTATTTGTCACGTGCGCCGAATACAACAGGTGTAGACCTTACAGTGAAATTCTTAC 225
CA349583       120:..........................---........-......---------------------------------------------------------------------------- 159
CA359983       109:..........................------------GT.G.A---------------------------------------------------------------------------- 140
CA387519       120:..T.....C.................T..........-..C...---------------------------------------------------------------------------- 162
BX865882        64:.....................................-......---------------------------------------------------------------------------- 106
BX074776         1:-------------------------------------------.---------------------------------------------------------------------------- 1
BX080054         0:------------------------------------------------------------------------------------------------------------------------ 0
CA367757         0:------------------------------------------------------------------------------------------------------------------------ 0
BX864251         0:------------------------------------------------------------------------------------------------------------------------ 0

OS-SINE1 cons  123:--------------------------------------------------------AGGCACTCTTTCCTCTGGTCTAAAAAAAATA--TCC-CAATGCCCCA---GGGCAGTGATTGGG 180
BX300187       164:--------------------------------------------------------...........................T...CA.G.-....A.....---.............. 223
CA350860       144:--------------------------------------------------------...A........................-..--...-...AT.....---.............T 200
CA371488       226:TTACAGGCTCTAACCAATAGTGCAAAAAAGGTGTTAGGTGAACAGTAGGTAAGTAA...T.......................--..--..T-..........GGG.............C 340
CA349583       160:--------------------------------------------------------......C........................--...-....C...G.---...........A.. 217
CA359983       141:--------------------------------------------------------G........................----..--.A.-...C......---..A........... 194
CA387519       163:--------------------------------------------------------.........................T.....--...-.....TG...---.............. 220
BX865882       107:--------------------------------------------------------.............A.............--..--...-..........---.............. 162
BX074776         2:--------------------------------------------------------...GT.....C...........-----TC..--...A....A..A..---...G..--...... 53
BX080054         1:-----------------------------------------------------------------------------------------------------------------------. 1
CA367757         0:------------------------------------------------------------------------------------------------------------------------ 0
BX864251         0:------------------------------------------------------------------------------------------------------------------------ 0
```

F. OS-SINE1 (continued)

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OS-SINE1 cons  181:GACATTGCCCTGTGTAGGGTGCCGTCTTTCGGATGGGACGTT-AAACGGGTGTCCTGACTCTCTGAGGTCATTAAAGATCCCATGGCACTTATCGTAAGAGTAGGGGTGTTAACCCYGGT 299
BX300187       224:..............------------------..........T....A..........----...T.....C................T.........T.................T... 321
CA350860       201:....C.................T.......A.......T...-.......................................................A.................C... 319
CA371488       341:......T...........T...................T...-...T.A................T.A.T.C..............G.................A........T..T... 459
CA349583       218:....A...............A.........A...........-.CC.C.................C.A...............................C.....C..........T... 336
CA359983       195:..............A.......A...................-..............----....T.....C.G...........C............A...........C.....T... 309
CA387519       221:......T...............T.......AC......T...-............C..........T..............A.............C..........C.........CA-- 337
BX865882       163:....C......................C...A..........-.........................................................................C... 281
BX074776        54:......................T................T..-...T...............T..T..........A.......-................C..............T.T. 171
BX080054         2:....C........................T.T....A.....-...................--....................................................C... 118
CA367757         1:--------------------------------------------------...T.A............................................................C... 70
BX864251         1:------------------------------------------------------------------.....C..........CAA.T...........................G.T... 54

OS-SINE1 cons  300:GTCCTGGCTAAA-TTCCCAATCTGGCCCTCAAACCATCACGG------------------------TCACCT---AATAATCCCC--AGYTTACAATTGGCTCAT-TCATCCCCCTCCTC 388
BX300187       322:..T....T....-..................T.......TT.------------------------C.....---...C......CC..T..C............-.......TG.---- 408
CA350860       320:............-......G.............T........------------------------......---..........--..T...........C...-.T............ 408
CA371488       460:............-G...........T.....T.......-----------------------------------------.....--..C..N............-..C..T....---- 530
CA349583       337:............-...........A.................------------------------......---........T.----------------------------------- 393
CA359983       310:............-.........A.A...A..T.......T..------------------------C.....---...C.C....--..C..C.C..A.......-.TG......----- 393
CA387519       337:------------------------------------------------------------------------------------------------------------------------ 337
BX865882       282:............-...........A.................------------------------......---..........--..T...............-.............. 370
BX074776       172:..T...A.....-.......C.......---------------------------------------.....---...C......CTCAT.CCT.......AG..A...CT..T.A.... 248
BX080054       119:............A....T.......A................------------------------......---..........--..T...............-....---------- 198
CA367757        71:............-..........................T..------------------------C.....---...C......--..C.....G.........-...........T.. 159
BX864251        55:............-....................T....C.CAGCTTCCAATTGGCTCATCCCCCTC......GTA.C..T.....--..C.----------------------------- 142

OS-SINE1 cons  389:TCCCCTGTAACTATTCCCCAGGTCGTTGCTGTAAATGAGAACGTGTTCTCAGTCAACTTACCTGGTAAAATAACGGTAAAATAAATAAA                               477
BX300187       409:--------.............A.T...........C.........G............C.AAA...----CCCT...C....GTTGTGCACTAGATAAGGAAACCTGTGCCATTGGAGAT 516
CA350860       409:.......................T.......C....A............T..................GT......AT------------------------------------------ 486
CA371488       531:-----......C..................C..........T........................................T..AG.G------------------------------- 614
CA349583       393:------------------------------------------------------------------------------------------------------------------------ 393
CA359983       393:------------------------------------------------------------------------------------------------------------------------ 393
CA387519       337:------------------------------------------------------------------------------------------------------------------------ 337
BX865882       371:...............................C............................................AT...........TACAAATAAAAATTTCTGCTCTGCTGATCTC 490
BX074776       249:...--------------------------------------------------------------------------------------------------------------------- 251
BX080054       198:------------------------------------------------------------------------------------------------------------------------ 198
CA367757       160:.........................................T................................A..............AAGAGGACGCTGCGTGAATCAGGCCTTCATG 279
BX864251       143:-----------------------.............T....AT...........T..................AAA.CT.CA.GCGGCTCCTGGCATTATACCTAAAGTGAACATTGCCA 239
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G. SacSINE1

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SacSINE1 cons   1:-----------------------TCAGCTGTGGCTCAGTTGRTAGCACTCTAGCCTCTG-AGTCAGAAGGTTGTGGGTTCA-AGTCCCACTCCAGGGACTTGAGCACAAAAATCTARGCTGACACTY-CAGTGC-AGTAC 113
CV798249        1:AACATTTTTTCCTNTTAGCTGTG................A.A......A.CC.......-..........C..C...C...-...............G.CC...............G.........C-......-..CG. 136
CV652579        1:CAAATTTATTTATTTTACTTCAA......-...T......AA...T...T.TA......-.T.......A...C.......-.AC.....A....-.....A.T.......-....A.G.......T-......-..C.. 133
CX196462        1:GAGCCATCCACTGCCATTACATTC.................G...A.....T....G..-GC.........C.........T....T......G.AA...................G.........CCG.....-T.C.. 138
CV547929        1:CTCAAAACAGTTACTATCTCTAG..T.T.........A.-.G.....T...........G.A........C..........-.............A.....T..T.........A.A....G..A.T-...C..-..... 136
CV652594        1:----------------------------------------------..A..CTTG....-...T...............A.-..CTTT...G....-.........G.T..-CT..N..GA.T.TGT-....T.-....T 88
CV720313        1:-----------------------------------------------------......-............----------------....................T...G...G...-------------------- 50
CV889426        1:------------------------------------------------------.....-...........C....C....-.................C................G....G....C-......-...G. 82
CV798150        1:------------------------------------------------------------G....AG....CC......TG-.A---------..A..--G..A.CG.T..-..C.A......G..T-......-..... 65
CV888980        1:----------------------------------------------------------------------------------------------------------------------------..C-.G....C...G. 15
CX197412        1:--------------------------------------------------------------------------------------------------------------------------------....A.-..... 11
CV720481        0:-------------------------------------------------------------------------------------------------------------------------------------------- 0
CV889296        0:-------------------------------------------------------------------------------------------------------------------------------------------- 0
CV798390        0:-------------------------------------------------------------------------------------------------------------------------------------------- 0
CV547727        0:-------------------------------------------------------------------------------------------------------------------------------------------- 0
CV798466        0:-------------------------------------------------------------------------------------------------------------------------------------------- 0
CV652222        0:-------------------------------------------------------------------------------------------------------------------------------------------- 0

SacSINE1 cons 114:TGAGGGAGTGCTGCACTGTCGGAGGTGCCGTCTTTCGG-ATGAGACGTTAAAC-CGAGG----------CCCCGTCTGCTCTCTCAGGTGGATGTAA-AAGATCCC-ATGG-CACTATTTCGAAGAAGAGCA----GGGG 234
CV798249      137:C...................A........C..C.....-.C.....A.C....-.....----------T...AC........C........C....-........-....-.....C..............----.... 257
CV652579      134:........A.-....T.............A......T.-.......A.....T-.A--------------T.T.C...T.----.......G.....-........-C..T-.G..G....-....-.....----...C 243
CX196462      139:..TC....----------------.....T........-.....G....G...-..G..----------................G.T....C..G.AG.......-.C..-....................----.... 244
CV547929      137:...................G.....C......C.....-...G..........-...-A----------T...A..CC...---.G.NCAAG.--.C-C..--------CC-TG..T..GAC..AC-------------- 234
CV652594       89:.......-----A..T.T.-A..T....T......TC.-......T..C....-.C...----------A..GA.....C.GT......CC..AC.C-T.T--------------------------------------- 170
CV720313       51:-............T......................A.-..............-.A...----------.........G..................-........-....-..-------------------------- 148
CV889426       83:.............T........G......A........-.......A.....A-.....----------T......................CT...C........-....-....GC.-....---------------- 191
CV798150       66:A.............C.....A.......T.-A...T..-......T.......-G....----------.AT.A.G.......--G..........G-........-....C.......-G...T.......----.... 183
CV888980       16:........C..C................T.........G...G.........GC.....GTCCCCCCCC...G......C.C.........GACGT.A........C....C.......-G...........GAGC.... 154
CX197412       12:..GA.....A....G..-..AA.A-----------------..A..A......-.A...----------....A...A---------..........-......T.-.A.C-.......-..CT........----.... 105
CV720481        1:---------------------------...........-G.............-.....----------...T....ATC...G...A....C..G.A....C...-...T-..............T.....----.... 95
CV889296        1:---------------------------------..T..-......T.......-.A...----------..TT..T...C..--..A.......C.G-......T.-....-..G....-.A.....---.T----..T. 82
CV798390        1:------------------------------------------------------------------------------------------------.-.G......-G.ATG..-...A.............----..A. 37
CV547727        1:--------------------------------------------------------------------------------------------------------------.-....................----.... 25
CV798466        1:-----------------------------------------------------------------------------------------------------------------------ATC.....A....----.... 17
CV652222        0:-------------------------------------------------------------------------------------------------------------------------------------------- 0
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G. SacSINE1 (continued)

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SacSINE1 cons 235:AGTTCTCCCC-------GGTGTCCT--GGCCAAYA------TTTATCCCTCAACCAACATCACTAAAA--CAGATTATCTGGTCATT-ATCTCATT-GCTGTTTGTGGGAGCTTGCTGTGCGCAAATTGGCTGCCGCGTT 355
CV798249      258:..G.A.....-------.......C--......C.------.CC.........T.....CA..A....--.......C.......CC-.C.A..CC-....CCC........CC..C.C........A.........A.. 378
CV652579      244:G-.......T-------A-......--.A.A..C.CCCCCACCCCCA......T..CAC.-..C...TA-.....G.A.........C........T...A....AT...ATC..------------------------- 345
CX196462      245:..........CACCCGCC...C...--.A....C.------.................CG..T.....--..-T........CG..CC.A..A...-T.----------------------------------------- 331
CV547929      234:-------------------------------------------------------------------------------------------------------------------------------------------- 234
CV652594      170:-------------------------------------------------------------------------------------------------------------------------------------------- 170
CV720313      148:-------------------------------------------------------------------------------------------------------------------------------------------- 148
CV889426      191:-------------------------------------------------------------------------------------------------------------------------------------------- 191
CV798150      184:..A....-TT-------.C......------------------------------------------------------------------------------------------------------------------- 200
CV888980      155:..GGGGAT.T-----TGTAC.....GG......T.------.......................TT.T------------------------------------------------------------------------ 211
CX197412      106:TA..A..T-T-------.A.A....--......C.------.A.............T..CT..C....--.......A.....T...T.......G-.............T...T......A.....A.T......T... 226
CV720481       96:.T..A.....-------........--..T.C.T.------......G.....T.........A....AG....AC.C....C....-...A....-..................................GA....... 218
CV889296       83:G.......-T-------A..A....--......C.------.C........G..A.......T.....--....C.....T..T...TT.GCTG..-.A...........C...T..A.ATA......AC.....AT... 203
CV798390       38:..........------CA.......--......T.------......A..........G.........--.................-...A.G..----....................T................... 156
CV547727       26:.....-....-------........--......T.------................T..........A-A.A..G.....A.....-CC......-........................CA...........T..A.. 146
CV798466       18:TA........-------........--......T.------...........G...............A-.................T........-........................................C.. 140
CV652222        1:-------------------------------------------------------------------T--..CTAA.....C.....-..G.....-..................................A...A.... 69

SacSINE1 cons 356:T-C-CTACATTACAACAGTGACTACACTTCAAAA-GTACTTCATTGGCTGTRAAGCGCTTTGGGACGTCCTGAGGTCGTGAAAGGCGCWATATAAATSCAAGTTCTTTTTT                             463
CV798249      379:.-.-.C...CC...........C....CC.....-.C..C..........CA......---------------------------------------------------------------------------------- 433
CV652579      345:-------------------------------------------------------------------------------------------------------------------------------------------- 345
CX196462      331:-------------------------------------------------------------------------------------------------------------------------------------------- 331
CV547929      234:-------------------------------------------------------------------------------------------------------------------------------------------- 234
CV652594      170:-------------------------------------------------------------------------------------------------------------------------------------------- 170
CV720313      148:-------------------------------------------------------------------------------------------------------------------------------------------- 148
CV889426      191:-------------------------------------------------------------------------------------------------------------------------------------------- 191
CV798150      200:-------------------------------------------------------------------------------------------------------------------------------------------- 200
CV888980      211:-------------------------------------------------------------------------------------------------------------------------------------------- 211
CX197412      227:.T.-.....AA......A---------..GCG.C-TCTT..........T.G...TA...G..ATAT...A...TATA.....A.T..TG.......C.............CTTTCAGTTTGATTTTCTATAGTGTTCAT 355
CV720481      219:.-.-....T.........................-A...GG.....T....G........................T...........A..T....GG...C.CT.CC...TTAAATATATTTAGGTGGGTCTGTGTTAG 355
CV889296      204:.-.AT.......TG.----------------------------------------------------------------------------------------------------------------------------- 217
CV798390      157:.-.-....GC.....--T................A................A..............A.AT.......A..........T...G....C.....AT.....ATTTATTCTTTCCAGCAAGGCCAGCATTTA 292
CV547727      147:.-.-..............................-.C..............G....A.........A.....T....A......A.T.A.......GTTCTTGC...C...TCTCTAGCAGAAAATTCAATGCTTTAAGG 283
CV798466      141:.T.-..G.G..G....................T.-A......TA...AA..G....C........T..........T.......C...AG..A....G.....CT......AAAAGGGGCTTAGGCCATCGGGAATGCAG 278
CV652222       70:.-.-...T............G..CTT........-................A....AT...T.......................T..T.A......A.G........C..TATGGGAATAAACGATAATAAATGGGAAT 206
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H. EbuSINE1

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EbuSINE1 cons    1:-------------------------GGGCTGACAGGATGGCCTAGA-GGTACGCACAC------TCACCTCTAAGCTGTCTAGCCTGGGTTTGAATCCCGACCCAGC--TATA 79
BJ645639         1:TCTTTTACGGAGAGTAGGGTGGGAA..AA..GTCT-.GACT.A...-....T...T..------A.GT...A...T.......A.......................--.... 103
BJ649721         1:ATAATTACAATATGTGTAATTTGGG......G.C..G....A....-T..G.AT....------..C...TA.GCT..---------------....T.A.......--.... 89
BJ650190         1:TATTGCTATGTAATGGAAAGTAGGA................T.C..-..........G------.....A..C.......C..........................--.... 104
BJ650899         1:GCAGTGGTTTGTTCATGATCATATC.......AT........A...-.A.......G.------..G.T...........G..........A......T....T...--.... 104
BJ665682         1:------AATGGACAGCAGAATACCA...A.....A...T.TTG...-....T......------ATG...N.G.......G..T...T...................--.... 98
BJ666394         1:ATTCACATCAAATGAGATTCATTATC..T..G.......A..A...-T.........A------...A..-----------------................A..A--.T.T 87
BJ666655         1:GATTGAGAGCATTCAGTAATATCATT........A...A...C...-...........------.......G..............CA...C..T............--.... 104
BJ649573         1:TTTGGGGTTTTATAAATAAATCTCA..A...G........T..C.C-T...T......------........G...C.....C........................--.... 104
BJ656982         1:TACGTTTTGACTACTTATTTTGATT..T...G.....AA...G...-.........CA-----C..GG..T.G..A....................TT.C.....A.--.G.C 105
BJ657082         1:ATTTTATATTTGCACTTATTTACACAA.T...T.TT......AC.TA.A...A...C.------..G....C....CA......A........C.A...........--.--- 102
BJ654403         1:GGCACGAGGGTAAGAGAGGTGTTTA...G.............G...-T.C..T.GT.T------......T..........C.........C..T...T.....G..--.... 104
BJ662848         1:------------------------------------------....-....T...T..AGCAAC........G.......G.......A..CT....T.AG.....TGC.C.. 70
BJ653004         1:------------------------------------------------..........------..G........A.........C.A.................A.--.... 57
BJ650142         1:------------------------------------------------------------------------------------------------------...A.--.... 9
BJ658735         0:----------------------------------------------------------------------------------------------------------------- 0
BJ659800         0:----------------------------------------------------------------------------------------------------------------- 0
BJ656117         0:----------------------------------------------------------------------------------------------------------------- 0

EbuSINE1 cons   80:AACTGTCATCCCGGTGTTTCA-CAGGCAGGGTG----ATTCATCAATGTGTGTG--CCGTCCC-TCGGATGGACGTTAAACTGGGCGTCCCGTCT-GCCGGCATTAGTTGGTG 183
BJ645639       104:...C....C..T.......TG-......T.A..----..GTGC......A....--..A....-..................T............-..T.A............ 207
BJ649721        90:.....................-....T......----......TG.........--....T..-......A...A.......A...A.T.T....-..GA............. 193
BJ650190       105:............A........-......AT.CA----.................--...C...C..T...A..........-.......A.A...-...A.....C....... 208
BJ650899       105:............-------..-...........----.........A.......--.......-........G........A..-T....T.GT.-...AT...CCA.A.... 200
BJ665682        99:....C.....GT.T.......-........A..----.GG...G..........--..A...T-.......A..C..........T.....A...-.T.A...A......... 202
BJ666394        88:..--.......-..C......-TCA--....CA----...T.....G......C--.......-.......A.T.....................-.........C......T 186
BJ666655       105:.....................-...A.......----.................--.T..A..-.........T.......-..TT....T....-.........CA...... 207
BJ649573       105:.......G...T.........-.GA...A..G.----...G.....C.......CGT.....T-..CA.............A...T.....T...-...A......T...... 210
BJ656982       106:.T.-------.....A.....-...A.GA....----........G........--.......-..................A...C.G......-..G...G.....-.... 201
BJ657082       103:---------------......-.........C.----.................--..A.T..-......A...............A........-...A...........-- 189
BJ654403       105:.........T..A........-A..A.......----.....G...........--.......-GT...............G.AT.T.T...GT.-.........C....... 208
BJ662848        71:...........T.A.A.....-..T.....A..----..A....GG.A.A....--.T..TGA-..AA.A...T.A.....A...T...T.A...-..TA......A...... 174
BJ653004        58:...............A..G..-...A.......----...TG..........----..A.GTT-G.AC.....T..........A.A...TA..A-..ACT.G..----.... 155
BJ650142        10:....TC.....T.....GC..-...........GGTG........T.T......--.......-......................A...T....-.TTA.....CA...... 117
BJ658735         1:---------------T....G-...........----...T.....A.......--..A.G.N-..A....A.T.....T.CN............T...A............. 90
BJ659800         1:------------------...G......T..CC----.GG....G.........TG.......-.N....T...................T..N.-..........-...... 88
BJ656117         1:----------------------.....G.....----..........C...C..--......T-....................AG.A.......-................. 83
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H. EbuSINE1 (continued)

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EbuSINE1 cons 184:GACGTTAAAGATCCCAC------------------GGTGTCCTTCGCGAAGAGTAGGCGAGCTATCGCCGGCACCCTGAACAAATTCCAAA-TTCCTGCCCTAACCTACAGAG 277
BJ645639      208:.GG....GG...A.A..------------------.A..........A.....C...........TC.T.....T....T......T.T..A.G.....T.G..G......G. 302
BJ649721      194:..T.G...........T------------------...........T.C........T...T......AA.T...................-..TG..T........-T..-T 285
BJ650190      209:...A............G------------------......GC.T.......................G..GT.A................-.C...........TAG..... 302
BJ650899      201:..T.........AT..T------------------........C.A........TC.....T......A......AA.GC...........-........TG...TG...A.. 294
BJ665682      203:.................------------------..A.......A.A.............A...T....................A....-...A...T.A..T......TT 296
BJ666394      187:................T------------------....C.......CG.....T...........A.A......................-.........G....AG..... 280
BJ666655      208:................A------------------T...........A......C..TA.................A.GC...........-.......T..C.....G.A.. 301
BJ649573      211:.................TTTAAAGATTTAAAGATAAAG...T...A........C...A.........A......A..GC...........T.A.-.T.TT....T.....G. 322
BJ656982      202:CGT...G....C....T------------------.....A....A........C......T.....T................C.A....-........AGG..T------- 288
BJ657082      190:-..A.............------------------A.........AT...........A.......T........A..TC....----------------------------- 254
BJ654403      209:.................------------------C........-----........T..............----------------------------------------- 257
BJ662848      175:.............A..T------------------......T..T.T......G.......TC...A...........G.......A...T-.......T.A..T.C.G..-. 267
BJ653004      156:................T------------------...A.....T.T.......----------------------------------------------------------- 191
BJ650142      118:.................------------------..........A...................T.........A......G....T...-.C..........--------- 202
BJ658735       91:..T..............------------------..C........T..........T...T......A.................A....-......T..G....AG..... 184
BJ659800       89:.................------------------.....A....A......................A.....TN..GC..C........-.C.A...............-. 181
BJ656117       84:.................------------------....C................--------------------------------------------------------- 121

EbuSINE1 cons 278:GGCATTGCATCAG-CGGCACAGCCGCG---CCCTCAGCCAATRATGCTACCCCGCAGCGTTGTGCTGCATACGAA-CGAAGAA                               355
BJ645639      303:.T..C..T.....-.A.A..T....T.---...A.CAG..G.A....A.A..A.....CA....T....C..A..AT...TG.ATGAAGGAGGAAAAGTACCTTCTGTTTGAA 411
BJ649721      286:CAA..GT...------------------------------------------------------------------------------------------------------- 295
BJ650190      303:.............-.A.........TT---............G.........T...A...............A..-.......AGGAAAAGCAGTAGAAACACAAAATGTATT 410
BJ650899      295:.......T.....-...........T.---............A..A.......A..A.C................-------------------------------------- 365
BJ665682      297:....G......G.-T......T..T..C--....TC....T.GT.T....T.-A..C.CAG.A.AG.A...T...T.TTT.TCAAGGCCTGTGAGAGTCTGCATTAGTGGACA 405
BJ666394      281:.........G...-.A........CA.---......A.....G..............TC.......A.....A..-.T....TTCATTTTCATTTAATCCTCGGACATCCCTT 388
BJ666655      302:.............C.AATGA...TC-C---...G.....--------------------...........CT...-.......NAAGAAAGTAAAATCATAAAGCAATAATAA 389
BJ649573      323:..--------------------------------------------------------------------------------------------------------------- 324
BJ656982      288:----------------------------------------------------------------------------------------------------------------- 288
BJ657082      254:----------------------------------------------------------------------------------------------------------------- 254
BJ654403      257:----------------------------------------------------------------------------------------------------------------- 257
BJ662848      268:.......T.....-T.........AT.---..-....T-...G.CA.A..G-A...-.....-----A..T.----------------------------------------- 326
BJ653004      191:----------------------------------------------------------------------------------------------------------------- 191
BJ650142      202:----------------------------------------------------------------------------------------------------------------- 202
BJ658735      185:............C-.A......TGA.A---..........G.A.........T.....C............T...-A....C.GAATACCTGGACAATAATGAGGGCAGCTCA 292
BJ659800      182:.......T..T..-.A.A...A....ACCT..........GCA.....---TTT..CT.ACA..-G.....T...-.......TGGAGGTAGAACATATTACGTGTAGGATAT 288
BJ656117      121:----------------------------------------------------------------------------------------------------------------- 121
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I. EbuSINE2

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EbuSINE2 cons    1:------------------------------------------GGCAGGATGGCCTAAAC-------CCTAGAGGCACGCACACTCRCCTCTAAGCTGTCTAGCCTGGGTTTGAATCCTGA 71
BJ657443         1:TAACAAAAGAATATTCAAGACCATCTAATACTGATCAAGACT.................------T.T......T..........A..C.........T.......A...........T. 114
BJ667239         1:GAAGAGCAAGTTCATCGCATGATTTATACATCATGATGGGTT..............GG.-------...............TT..--.......GA...C...............T.AA. 111
BJ657740         1:GAGCAGTTACAGAAGAGATGTGCCATTTTTACTTGTCCGGTA.AT..T..A.G..G...AGCACGG...G...............G..............C.T..T....C......... 120
BJ664529         1:---------------------------------------------------------------------------------------..GA.........T................... 33
BJ666536         1:--------------------------------------------------------------------------------------------------------------.......CA. 10
BJ653688         1:-----------------------------------------------------------------------------------------------------------------------. 1
BJ664267         0:------------------------------------------------------------------------------------------------------------------------ 0

EbuSINE2 cons   72:CCCAGC---TATAAACTGTCATCCCGGTGTT-TCACAGGCAGGGTGATTCATCAATGTGTGTGCCGTCCCTCAGATGGACGTTAAACT-GGCGTCCCGTCTGCCGGCATTAGTTGGTGGA 186
BJ657443       115:...T..---................A....G-C..........TC.............A.............................-........-------.......A........ 222
BJ667239       112:..G...TCA.......GAC......C.....TC....T................T.............A...................T.A.A....C.....T.C.....C........ 231
BJ657740       121:......---.......CA.......A.....-............C......-A..A............T...G.........C....G-..A...TT...C.T...............A. 234
BJ664529        34:......---....--.........T......-..GT.............G......................................-..T.......T....T............... 146
BJ666536        11:....T.---...G..........TT......-...........T..G..................C....A.G..............CG...A....A.T...TT..........A.... 126
BJ653688         2:.....T---................A..A..-.T.......A.............A.......................T........G.......T...CA..TA.............. 117
BJ664267         0:------------------------------------------------------------------------------------------------------------------------ 0

EbuSINE2 cons  187:CGTTAAAGATCCC-ACGGTGTCCTTCGCGAAGAGWAGGCGAGCTATCGCCGGCACCTTGAACAAATTACAAA-TTCYTGCCCTGACTA-CTGCTGGGAAGGCAATGGCAAACCA-CCCAG 302
BJ657443       223:...G.........-..........G...A.....TCA.T....C...A.T......C.............C.C...TG....AA....-.................A.......-..... 339
BJ667239       232:.............-.G...........T..T..AT...T.......T...A.....AC.........C..--------...A....A---...GA.................A.-..T.. 338
BJ657740       235:.A.......C...-...........T........T.N..A.T.....A.......TG..........CA...-...C....T.....---.C.CTTTGTT.G.G......-.-------- 340
BJ664529       147:....G........C.T......T....TA....CA...T...................CGC..G........-...T.........G.-.CA............CA........-T.... 263
BJ666536       127:T....G.......-..A.....G..TT.A....AA.T.T.......T.........N...............-C..C....G.....TC...TGTCAG..TG.--------...-..... 235
BJ653688       118:T............-.T........-.AT......AC.........C.......................T..-C..C.A.TG.A....-.........................-..A.. 232
BJ664267         1:--------------------------------------------------------------..........-..TTA.TG.C...A.AA..........A.TC.........GGT...- 56

EbuSINE2 cons  303:-------TATAACCCTTGCCAAGAAACTGCTTCGGCAGCACTGACGCTCTGTCACAGAGTATGGTACATCAGAAT                                             370
BJ657443       340:-------.T.....A...................A....T.CAG.T..A.C..TATCTC...CTCTG..T.CTG.GTGGTACATCGGTATCAGAAATACGGACTCTTCCAATTAATCTTC 452
BJ667239       339:-------C...........A..........................................T............ACAGTACGAGAGTCTATAAAAAATATCTGAACGCGAGTTGAAATT 451
BJ657740       340:------------------------------------------------------------------------------------------------------------------------ 340
BJ664529       264:-------.....................A....A....T....--.ACT..C.GTCCGCC.--.A...C..C..CAAAAAGATTTCTTTCCATTGAAGGCATGATCACTGGTTGAGTTTA 372
BJ666536       236:CCAGGAT.C.......CA.A..A------------------------------------------------------------------------------------------------- 258
BJ653688       233:-------.........C..T............T....ATG.C........CCA.....C.T...A.....G....CACAATAACTTTGGCAGATTTCTAATGCTTTTTGTTGCAGAGTGC 345
BJ664267        57:-------C.C....T..T..C..G..A.....T...........T.........-..........T...NT..TAGATTGGCATTTGCATCACATTGACCTTGAGGTAGGCACACTCACC 168
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J. BflSINE1

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BflSINE1 cons    1:----------------------------TGTGAGACCGCATGGCGCAG-CGGCAGCGTGTTCGGCTCGGGACCGAG-AGGTCCCGAGTCC 60
AC150431         1:AAACAGTGTACTAACTACTGTGTACATC....G..............C-.......A........C..T.......-....TGT.G.... 88
AC150429         1:CCTGTCAGCATTGTTGGGTTGCCTGACGC.........TG........-.AA...T.....T..........T...-..A..T....... 88
AC150429-2       1:TATTCAGTGACCTGATAAAACTATTGCA.......T...........AT......A.....A....AA..C..A.A-......T....T. 89
AC150387         1:-------------------------------------------------------------------.......T.TTT.G....T.A.. 23
AC150415         1:-----------------------------------------------------------------------------------.A...TT 7
AC150421         0:------------------------------------------------------------------------------------------ 0

BflSINE1 cons   61:GAATC---CTGCCGTGTCACCGATCTTGTGCCCTTGGGAAAGGCACTTTACACGACTTTCCTCACTTTACTCAGGTGAAAATGAGTACCT 147
AC150431        89:.....CGG...........................................................................T...... 178
AC150429        89:.....---............................................T.G................................... 175
AC150429-2      90:...C.---.....AC......A.......................A..G..................C.....A..............-- 174
AC150387        24:...AG--G........C..................................G.....................................C 111
AC150415         8:.....---......C....A.................................AG.............C...................A. 94
AC150421         1:---------------------------------------------------------------...CA....................T. 27

BflSINE1 cons  148:AGCTTCGGCTAGGGCCGTCCCTCGGATAGGACGTTAAATGGAGGTCCCGTGTCTGGGGAGAGCCATACCCCAGGCACGTTAAAGAACCCA 237
AC150431       179:.......A............................................A...................A..............T.- 267
AC150429       176:.....T.................A............................G............C......T..........A...... 265
AC150429-2     175:------------------------------------------------------------------------------------------ 175
AC150387       112:......................T...........A..........................................A...........- 200
AC150415        95:............T..T.......T.....................T......G.T.......A..C.T....C...T............. 184
AC150421        28:......A...........................A......................................................- 116

BflSINE1 cons  238:CCACACGTGCGATGGTGCGGTGTGAGATGGTGCAAA-TCCTTCCGTCTAGAATTGGTGATTCTCTACAAATCACCCGGACTCCAGGAAGA 326
AC150431       268:......A......A......................-.........G.................C..........T.............. 356
AC150429       266:.....T...A.............AT....A......-...........G..C.....................A..A.G..TTG...... 354
AC150429-2     175:-------------------------------------------------------------------G.T.....T...........C.. 197
AC150387       201:..........A.......A.....C.T.........A..A....A.................A........................... 290
AC150415       185:G................------------------------------------------------------------------------- 201
AC150421       117:......-----------------------------------------........................................... 165

BflSINE1 cons  327:ATAGTGACATATCAGTCACTAATGGAGATCTGTATAA--CCAAACCAAACCAAACCTAA                                383
AC150431       357:...................A.................--.........G.....A...CTTCCTGTAGGGAAATCAAATTAGTAATGGGG 444
AC150429       355:..CA-AC....----------------------------......T.............CTTTGTGTAGATAGGAGAGGTCTGTAGCACA 415
AC150429-2     198:........T...T.................CTA..T.----..................ACTATTCACCGACCTGCAGAATGTTCTGCTG 283
AC150387       291:.....................................--...............TAAT.CCTAGCCCTAAGTTTGTCCTGTTGTACATTT 378
AC150415       202:----------TC...................A...C.AAT................A..TACTTAACATTTTTTGTCCGCATCTGAACTG 281
AC150421       166:.....A...............................--........TTTA.CTAT.CCATGTCCCTTAGTACACACTTTTTAGCTTAAA 253
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