

8 Appendix

A. Multiple Sequence Alignments of Experimentally-Mapped Nucleosome Datasets

The sequence datasets were aligned using *Clustal W* (Aiyar, 2000; Higgins *et al.*, 1996; Thompson *et al.*, 1994) and coloured using the *MView* multiple sequence alignment viewer application (Brown *et al.*, 1998). The results are also sorted by pairwise sequence identity.


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175 CC126_146/1-183 -----TTTTCCCCTAAATCAAAGTGACA-TTCCCTAAGGATGA--AATTATACAACCTA-----AATTACTTGAATCATGATGGCTCCTAGTTTCACCACCTGCTTGC-CAAAATTTGTACAATGCGTCATTTAACTTCTCAGCCCTTCTTAAGGA
176 CC158_144/1-183 -----TGCCAGTTGGTCTCTAAAAACCGTGGGTACGTAG-GCA-----GGCAGCTTCTCTACCC-----TCAGCTTTGGCGCTGGCACTCCCAAAACCTGCCAAGCTCCGC---TTCTCTCAGAGTATCTCAGAG-AGCTTTAGAAAGCTGAGGCTCTCA-----
177 CC60_145/1-183 -----TCCCCACCCACGATGCTAGCCCC--CATGTGACGGAGTGCATGGGTGGGGCATATTCTCGCCGACACCACA-----CTCTCAACTGAGAGAAGCTGGAGAACCTCCCTACTGCCATCCCGTGCAAAAGCCGGCCCCATCAG-----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

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LEVITSKY NUCLEOSOME DATASET

Identities computed with respect to: (1) NM0014/1-331
Colored by: consensus/65.0% and property

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1 NM0014/1-331 -----TGAAGGACCTGGAA-TATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
2 NM0006/1-331 -----AGGACATGGAA-TATGGAGA--GAAACTGAAAATCACCAGAAATG--AAA-AATACACACTTTAGGACG----TGAAAATAGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
3 NM0004/1-331 -----TGAAGGACCTGGAA-TATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGT--
4 NM0034/1-331 -----TAGGACCTGGAG-TATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGATG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG-
5 NM0016/1-331 -----GAGGACCTGGAA-TATGGTGA--GAAGACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
6 NM0033/1-331 -----AGAGGACCTGGAA-TATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACA----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
7 NM0010/1-331 -----TGACCTGGAA-TATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACA----TGAAAATGGTG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
8 NM0019/1-331 -----AGGACCTGGAA-CATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGCGG----TGAAAATGACG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
9 NM0038/1-331 -----AGGACCTGGAA-TATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AACACCGCTTAAGGACA----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTGTA--
10 NM0054/1-331 -----GACCTGGAA-AATGGCGA--GAAACTGAAAATCACCAGAAATG--TGA-AATACACACTTTAGGACA----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
11 NM0009/1-331 -----CCGGAA-TATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACG----TGAGATATCGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
12 NM0042/1-331 -----AAGGACCTGGAA-TATGACGA--GAAACTGAAAATCACCAGAAATG--AGA-GATACACACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
13 NM0049/1-331 -----AGGACCTGGAA-CATGGTGA--GAAACTGAAAATCACCAGAAATG--AGA-AATAGACACTTTAGGACG----TGAAAATGACG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
14 NM0041/1-331 -----ATGCACACTGTAGGACCTGGAA-TATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
15 NM0022/1-331 -----GGAA-TATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACG----TGAAAATAGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
16 NM0015/1-331 -----AA-TGTGGCGA--GAAAGTGAATAATCACCAGAAATG--AGA-AATAAACACTTTAGGAAAG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
17 NM0017/1-331 -----AGA--GAAACCAGAAAATCACCAGAAATG--AGA-AATACGCACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
18 NM0013/1-331 -----TAGGACCTGGAA-TATGGCAA--GAAACTGAAAATCACCAGAAATG--AGA-AACATCCACTTTGATGACT--TGAAAATGACG--AAATCACTAAAAACGTTGAAAAATTTAGAAATGCCACTGTAGG/
19 NM0039/1-331 -----ATGGCGA--GAAACTGAAAATCACCAGAAATG--AAA-AATACACACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
20 NM0070/1-331 -----AGGACCTGGAA-TACGGCAA--GAAACTGAAAATCACCAGAAATG--AGA-AACATCCACTTTAGGACG----TGAAAATGACG--AAATCACTAAAAACGTTGAAAAATTTAGAAATGCCACTGTAGG/
21 NM0046/1-331 -----A--GAGAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
22 NM0012/1-331 -----TAGGACCTGGAA-TATGGCAA--GAAACTGAAAATCACCAGAAATG--ATA-AGCATCCACTTTAGGACG----TGAAAATGACG--AAATCACTAAAAACGTTGAAAAATTTAGAAATGCCACTGTAGG/
23 NM0053/1-331 -----ATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACG----TGAAGTATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
24 NM0069/1-331 -----TAGGACCTGGAA-TATGGCAA--GAAACTGAAAATCACCAGAAATG--AGA-AGCATCCACTTTGATGACT--TGAAAA-TGACG--AAATCACTAAAAACGTTGAAAAATTTAGAAATGCCACTGTAGG/
25 NM0037/1-331 -----AGGACCTGGAGTATGGCAA--GAAACTGAAAATCACCAGAAATG--AGA-AACATCCACTTTAGGACG----TGAAAATGACG--AAATCACTAAAAACGTTGAAAAATTTAGAAATGCCACTGTAGG/
26 NM0011/1-331 -----ATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGATGACG--TGAAAATTTGAGCGAAGGAAAACGTTGAAAAATTTAGAAATGCCACTGTAGG/
27 NM0031/1-331 -----A--GAACACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
28 NM0024/1-331 -----TGACGACTTGAATAATGACGA--GATCACTAAAAAATTTGAAAATG--AGA-AATGCACACTGAAAGGACT--TGAAAATGGTG--GGAAAACGAAAAATTTAGAAATGCCACTTTAGG/
29 NM0002/1-331 -----AGAACCTGGAA-TAAGGCAA--GGAACCGAAAATCACCAGAAATG--AGG-AACATCCAATTTAGGACG----GGAAAATGACG--AAATCACTAAAAACGTTGAAAAATTTAGAAATGCCACTGTAGG/
30 NM0005/1-331 -----AGGACCTGAAA--TTGGCGA--GAAACTGAAAAG-GTGGAAATTT--AGA-GATGTGCACCTTTAGGACG----TGAAAATGGCGA--AGAAAAGTGAAGAAGCTGAAAAATTTAGAAATGCCACTGTAGG/
31 NM0048/1-331 -----A--GAAACTGAAAATCACCAGAAATTT--AGA-AATACACACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
32 NM0021/1-331 -----A--GAAACTGAAAATCACCAGAAATG--AGG-AATACACACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
33 NM0072/1-331 -----AGGACCTGCAA-TAAGGCAA--GAAACTGAAAATCACCAGAAATG--AGA-AACATCCACTTTAGGACG----TGAAAATGACA--AAATCACTAAAAACGTTGAAAAATTTAGAAATGCCACTGTAGG/
34 NM0050/1-331 -----AGGACCTGCAA-TAAGGCAA--GAAACTGAAAATCACCAGAAATG--AGA-AACATCCACTTTAGGACG----TGAAAATGACA--AAATCACTAAAAACGTTGAAAAATTTAGAAATGCCACTGTAGG/
35 NM0086/1-331 -----ATGGCAA--GAAACTGAAAATCACCAGAAATG--AGA-AACATCCACTTTAGGACG----TGAAAATGACG--AAATCACTAAAAACGTTGAAAAATTTAGAAATGCCACTGTAGG/
36 NM0023/1-331 -----ACGTGAAAAATGAGAAATGCACACTGAAAGGACCTGAAA-TATGGCGA--GAAACTGAAAATCACCAGAAATG--AGA-AATACACACTTTAGGACG----TGAAAATGGCG--AGGAAAACGAAAAAGGTGAAAAATTTAGAAATGCCACTGTAGG/
37 NM0003/1-331 -----ATGGCTA--GAAACTGAAAATCACCAGAAATG--AGA-AACATCCACTTTAGGACG----TGAAAATGTCC--AAATCACTAAAAACGTTGAAAAATTTAGAAATGCCACTGTAGG/
38 NM0080/1-331 -----TGGAAAATTTAGAAATCCACTTTGATGACTTGAAT-AATGACGA--AATCACTAAAAACGTTGAAAAGT--AGA-AATGCACACTGAAAGGACT--TGAAAATGGCG--AGAAAACGAAAATCACCAGAA
39 NM0047/1-331 -----ATTGTGAGACAGTGTATATCAATGAGTTACATGAAAATCACCAGAAATGATAAA--TACCACACTGTAGAACATA--TTAG---ATGAGT--GAGTTACGCTGAAAAAACCATACGTTGAAAACCGGCTTGG---
40 NM0043/1-331 -----ATGTAGGACAGTGTATATCAACGAGTTACATGAGAAA-CATGGAATGATAAA--AACACACTGTAGAACAGA--TTAG---ATGAGT--GAGTTACACTGAAAAACCATCTGTTGAAAACCGGCTTGG---
41 NM0008/1-331 -----ATTGTGAGACAGTGTATATCAATGAGTTACATGAAAATCACCAGAAATGATAAA--AACACACTGTAGAACATA--TTAG---ATGAGT--GAGTTACACTGAAAAACCATCTGTTGAAAACCGGCTTGG---
42 NM0020/1-331 -----AACAGGATTTGTGAGACAGTGTATATCAATGAGTTACATGAGAAA-CGTGGAATGATAGA--AACACACTGTAGAACATA--TTAT---CTGAGT--GAGTTACACGAAAAACCATCTGTTGAAAACCGGCTTGG---
43 NM0079/1-331 -----TTACACAGGAAACAGCTCGGGATCCGCCGGCTAGAGCGG---CCGCCCGCGTGGAGCTCCAGCTT-TGTTCCTTTAGTGGAGGTTAATGGCGCT-TGCATAATCGTGTACAGTGTTCCTATGTAAGTTGTTATCCGC---
44 NM0078/1-331 -----AAGACAAAATATGCACAGTGTCCATGTCCAGCGGCGGATTTGATATCCATTACGTTTGTGGCTGGAAGCTCGGCTGT---AGTCTTAAGCGCACCCCG---ACGAGTCTGTG--GTACGAAAC--CTACAGTCTTTCGAC---
45 NM0030/1-331 -----CAAACGACCAATACGCCCGTTATCTTAG--ACTTATCGAGTATTC---GCTGGTA-AACTATCACATGCA-ACC---AATGTTTGTGGCTGTGCTCAATGCCCTCAACCAATATATGGGCTCCGACCCACTGT

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166 NS0005/1-331 -----AAAGAACGTCGCTCTG-CTCTCGAATCGGCACGGGTATC-TCTTGGAGCTCACTGGTGGACTCA-AGGAGTCAAGCCCTCTGAGCGG--TTTGGAGAGAGTCCGGAGATGGTCTC--TAGGCCACGCAGGAGACGAAGGCCCTCATCTCTCGATGACGGG--GAATCTCGGGTGTCTC
167 NS0004/1-331 -----TGGCCACAGCAAGTCCAATCTCCATTCCGATTCGGAAGGAAAGC-TGGGATTTGCTCTCGAGTGACTGCA-GGGCCATAGAACCTCATCTAGCC--TTGTGTCGACAGCCAGTG-TTCCTCTC--CAGGGGACAGGGGATCTCGGGTTCGATTCAGACGCCACCCGG--GGAGACAGGCATTCTC
168 NS0004/1-331 -----AAAGAACCCTGTTTAGCTGCCAATCCACTCAATTCAGAGATCCAAAGG-TGTTCGTGTGAACCTCTCAAAAATGGA-TTATGACGGCTCCAA--TTGCAAGACTACAAA--ATTGAATTTACTCCCTCATGACTGACTGAAAGCTGAAATCTGCATTTGCCAACGAAK
169 NR0007/1-331 -----CCGAATCCGAAGTAAAGCGTTTAAAGGCTTAAAGTACTGA--GGTGGGGACCACTCGGGAATTCAGGTGCTGATAGCTTTTGGCTCGCA-GCTACTTT--TTGACTCTTCTT-TTATCTATCCACCTTCAGTAC-TTCTCACACTCCAGGTGGCCGATTTTGTCTCGTCTC
170 NG0002/1-331 -----ATGAAAAGATGCCAATGGCATCTGTACTTTCAATACAACCAACTATGGGATACGCCATTTGGGGCCATGCTACTTCCGAT-ATTT-GACTAATTGGGA--AGATCAACCCATTGGCTATCGCTCCCAAGCGTAAAGTCTC--AGTGCCTTCTCTGGCTCCA
171 NG0032/1-331 -----AGGCCAAGCAAGGAGTGGCATTTCTGAGCACTTCTTCAAGTCTCTTCTCATCACTGAGCGAGTAAGGATTTAAGTGTGTTAAGTGTACTTTGACAGCACTCTTG-ATAAATGTAATTGACGGAATCACTCTCTTAAAGAAGATATAAAACTT-----TGAAGTACAGCATGAGTACTAA-ATGTTA
172 NR0020/1-331 -----CTCTTCAATAATAACACATCTTCAGTTA-ACACATGGAAAAATATAAATAGCTA-GTTTTATTTTATTA--TTTCTGTATTATATAAATAATGCC-GTCATC--AATGTAATTCATTAAATTCAAACTGTCTTACACAGAAATCAGATTTTTTTTTTAGATGTTTAAAGTTCAGAGTCC
173 NS0009/1-331 -----GAGGCCACGTCTGGA-ATGCTCTCGTG-AGACCGGCTC-ATCCTGAGGTGGACCGGAAGGATCGGGAACCCCTCCAGACAAGCA-GGGGAGTCGACCCCTCTCTGTCAG--ATCAGGAGGGGAGAAAGGCTCAGAGGA--GGGGTCCCGAAAACCTCAGTGTCTCTCTCGAG-GGAGACCGG--GATTTCCGGGAACCTTGT
174 NG0014/1-331 -----AGTGCCTTCAAGGCTTCTGGTGGCCATAGAGAACGACCTCGCCCAATGTTACCAAGATGTTCCCTCCACAAGGTGTCTTATGTAGTACACCGATATTT-AAAAGTCCAGCATACGATATATATACATGTGTATATATGATACCTATGAATCTCAGTAACTATGATATACGAAAGTATGATAK
175 NS0006/1-331 -----GTGTGCGGTTT-CTCACAGGTTACGACGGCGAGG-TCAGTGAAGCTCTCGTGGGGGCCA-GGAAGTGGGTCCTCCATGCGAG--TGGCGAGGGGAGCGCGTCAATGCTCCC--GAGCCATGGTAGGGAAATGTGGCC-TCGAGACGTGTTGAAGAAG--GTCTCTCGAGGCTTTCTC
176 NG0040/1-331 -----ATGTGGATTGCGCATACT-TTGTGAACAGAAAGTATAGCGTTGATGATT--CTTCATTGGTCAGA-AAATTAGAACGGTTT-CTT--CTATTTTGTCT-TCTATATACTACGTATAGGAAA--TGTTTACATTTTCGTATGTTTTGATTCACTCTA-TGAATAGTCTTACTACAATTTT
177 NG0029/1-331 -----GTACGTAATTTAAATTAACAACTAACAACTCATCTGCATGCAATGTCTGTATTAATCTAATAAATAAATAGCTTTTAAAGTATGATAAATACAT-TTTGAAGAATATCTTGTCAAAGT--TCCATAGGCCCTTCTCGGGG--ACAACATCCG--CTAACA--AACCCCTCGATTATCT
178 NP0023/1-331 -----CTCAGACCTGAGGCGCCGGCCATGGCCCACTGAGACACAGGAAGGGCCGCGCCAGAGCACTGAAGACGCTTGGGGAAGGAAACCCACTG--GGACCCAGCCCTGGTGGCTCGGGTGCATCCAGG-TGGGCCCTCCCGAGGCTCTCAAGGCTCAAGAGAAAGC---CAGTGTGAAAAGCAAK
179 NG0022/1-331 -----TCGATGTTGCCCTTCTATGAGCCCTACTACTCCAGCGCCAGA-GGAATCCCTACTTGGCCCTGTT--GG--ACCGATGGAGCAGCAGCTGCGCCAGCT-GGAGAAACAGTGG-GCGCTCTCGGGATCGTCGG-GAGCGTGT-CGAAAATCGGAA-AGGATGGCTCCAGGCTCTGCATG
180 NG0006/1-331 -----ACTGCACTGGTACCCTAGAGTTTGGATTGGTTACGCTGTTAAACACCACACAACCATATCCAAATCCGCTTTGCGGACTT-ATCACTTT--GGTTC-AGGGTTGAGAAGTCTCGAAGA-ATATTTGAAATGGGTTTGAAGTCAGTGTTC---TCTCTCTTTTGGACCGTGGTA
181 NP0019/1-331 -----ACCAAGCTGAGAGTCAGCTTGTGTGCCAGGAGGGAGGCTTGGGTCA----GAGCCTCGGAGGACCCCTGAAGTCTCTCTCAGTGTCTCTATCACAGGAGAGCTGTACGCCCTTGAAGTGTGGTCT--ATGCTAGAAAATATC--CCATAAATAACAGGAAGCCCAAGTTTACCA
182 NG0008/1-331 -----CCTACTTCATGACCACGGTAAAGCTCTAGGATCTGTGAACATGACCACCTGGTGTGATA-ATTTGTTCTCATTTGACA--AGTTC-CAAGTAGGGAAG-T-AAAATAGAGTTTATAAACTTATGTCTTTTTTATTTTTT---CAAAGCCATCTAAG-GGCTTTAGCAACGAGTG
183 NP0013/1-331 -----GCGCACTAGCTCTGCTTTTGGCGGTACGACAACACTACATTTAAATTTCTGA-AACTCATGGCATTATTTGGGAAAGGTTAGTTA--GTTTTATT-TTTG-----TTTTAGAGCAGCATCAATTTAGACTTTTATAAAGAAATTTCTAATT-TGATCCCTCGTTTATCAACAGTA
184 NP0011/1-331 -----ATTTGTTTCTCAGTGCACTTCTCGGTGTTCCATTTTCTATT-GGGCTCTTACCCTGGATTTGTTGAGATCACTCTGTTGGCATTTTTA--TTGC-ATT-TTACATATACACATTTTGAACCGCCCTGTGCTGCATCCGTCG--ACGTGCACTGCACCTGCCCCACGA-GAGAACAGT
185 NP0022/1-331 -----TAACCGATGGGAACACGCTCCCAACAGACAGCGCTCAGGACTGTTCTCTCTGCTGGCTCCCAATTCAGTCCAGGAGAAGCAGAGATTTTGTCCCATGGTGGTCACTGGAAGAAGCCCTGGTCAAGG-CAGGCTTCTCAGACC-----CTGAGCGCCGCCCATGGC---CCCATGAGACACAGGA
186 NP0026/1-331 -----CGGATCACCGGCTTTTGGTCTCTCACCAAATCAGCTGCAAGAAGATTAGAGCTCAAAAAGATTACA-SAAAGAGAGCC-----TTTTCTTTCTTCTCTGTGGG-GTTCCTTCTATT--CGTGTCTCTCTCTGCCCAGCCAGTCCGTCGCTCTTGGC--TCCACTGCACCTGCAC
187 NG0034/1-331 -----TACCTGGGCGGGACCGCCAGGCCACTCCCGGCGAGAGATGGGGCCAGACTTGGGCTCTGCGCTGGCAGG-AAGGTGGGCCCGACTGGATTTCCCTTTTCTGCTGCGCGGGAGGCCAGTGTCTG-ATTTCTGCCCGGATCTGCTGCCCGGTGAG--GTCTTTGC--CTGCGGCGCCCTCGCC
188 NG0038/1-331 -----GCAGCTCACAGAAACTCATTCGTTTATTCCTTGT--TGATTCAGAAGAGTGGGACAGGTGAACCTTTGGA--TTGGACTCGATTCTGAC--TGGGT-TGGAAGGCAAGAGAGCCCGGAAA--GCTTACATTTATGTTAGCTGTGGACTGACGCCAGAAAATGTTGGTGTGCGCTTAG
189 NR0017/1-331 -----GTTTACTAAAATCCGTAAGAAGTCTCAATTTG-ACGCCAAT--TAAG-----ACCATGTAATTTGATC-CGACTCTCTTTTAGAC-TTAT--CT-CCAATACGCCACAATTTGTAAGGTAAGTACTGACTTGTGTTGTGTCAGAAATAGTGGGAGTATTTACTTTG-TAAGAGAA
190 NG0019/1-331 -----CGCCGTTTGGAGTGTGGCGTACCAGGAAGTGGCAGCATATTTCCCGCTGGCAGGAGCAGGAGTTGGCTCCGCGCCACCCTCAACAAGGATGGCTACAACCTCACCCCTGGA--CGTCAAGGACTACAGCGAGTGAAGGT--CAAGGTGCTGGACGAGAGCGTGGTCTGTTGGAGGCAAAATCGG--AGCAGCAGGAGGCC----
191 NG0024/1-331 -----GATCCAGAGGTGGACCCGCCATCTCAATGTGAA--GGAAATCCCAAGGAGCGGTGGAGCAGGACAATGGCAAGGATAAGTAGAGGACTCGTCCGGGAGATGCCCTGATTTTAAACCA
192 NG0026/1-331 -----GCTTTCATTTGCTTAAAGT-TGAGGTGAGCGGGTCCCACTTGCTGAATTTGAATGATGCGCTCC-TTGGACTTG--TCTCGACGCGCTCGGGT-TGGGAATACTGACGGTG-AGC--ACGCCATCCGACGACAGCTCGAGACCCTTGTCTCCGCTTG-TAGCCATCGG-----GAACCTGTGAGCGCGCAC
193 NG0023/1-331 TGAGGCTGATAAGGTGGCTCCACTTGTCTCCGATGCTCTGACCATCAAGGTGCCCAAGCCACCGCAATCGAGGATAAGGGCAACGAGCGCATGTTGATGCTCAGTCCAGCAGTGGGACCCGCCATCTCAATGTGAA--GGAAATCCCAAGGAGCGCTGGAGCAGGACAATGGCAAGGATAAGTAGAGGACTCGTT-----
consensus/100% .....x.....y..x.....
consensus/90% .....x.....y..x.....
consensus/80% .....x.....y..x.....
consensus/70% .....x.....y..x.....

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1-CGTG-----
1-CG-----
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1-CG-----
1-CGTGG-----
1-CGTG-----
1-CGTGG-----
1-CGTGGA-----
1-CGTG-----
1-GTGA-----
1-CGTGG-----
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1-CGTGGAATATGGC-----
1C-----
1-CGTGGT-----
1CCTGG-----
1-CGTGGAATATGGC-----
1CTGG-----
1CATGGA-----
1-CGAGGAATATGG-----
1-CGTGGAATATGGC-----
1CCTG-----
1CCTGG-----
1TT-----
1-GGTGGAATATGGCA-----
1CCTGGAATATAGCAGGC-----
1CCTGGAATATGGCGAG-----
1CCTGGAATATGGCGAG-----
1CCTG-AATATGG-----
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1CCTGGAATATGGCGAG-----
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1CGATGT-----
1CACCGCTTCGCC-----

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FAAGTTTACCATGACATGATCAGA-----

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ZGCT-----
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FATTGGAAAAGCTGAAAA-----
ATATATCTTACTTTTTTTTCTC-----
FGCTCATGGGACAGGGC-----

ZCCA-----
VACTACAATA-----
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FTGATTGTACTGAGTTCAATTCTAGCGC-----

ZCAATTACACTCG--TCAATC-----
FTTACCGAGGARGAAGCTCA-----
FGGTAGATGGATCGATGGCAAACA-----
ZCATGTTTAGAGCAAGCGCCTTGTGAG-----
FTAAATTAACCGGGAAGCTT-----

ZCATTTCAGCAATATATATATATATTC-----
FTACGGCATGGATATC-----
ZGTCATAGAGGGCTATGGTAAAA-----
VTTGTAC-----
FGGGTTGAG-----
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ZAGAGTGGTTCAAGGCT-----
FATA-TAAATGCAAAAAGCTGATAAACCATT-----
FGTTGATTGAG-----
FTTTAATCCGGACAAGCTCATTGGCT-----

ZTGGAGAGG-----
ZGAAGAGAA-----
FTTTCGCAACAGCTATG-AGCATTGTGCAAAACATATT-----
VTTTTAAAACAA-----
FTCTCTTGAACCGTAAATATC-----
ZCGCTCTAG--GATCTGTGAA-----
ZCCGTACGCAGTTGTCGAACCTGGT-----
ZAACTCGCCAAATTTAAG-----
FTAGAGCAATCATTGAAAGTACTAGATA-----
ZCCTTACTATAATTTACGCTATCGGC-----
FGGT-ACGGCACCCA-----
F--GCCTTAAGCTTGAGGTGAGC-----
ZATATTTGTAAAATCATATATAATCAAAT-----
ZAGTTT--GCATTTCTCTTAATCT-----
ZACTCCACTCAATTCAGA-----
ZATTGTCC-CGTACGACCTCTCAATAATAACACAT-----
ZCTAATTTATTACTTATACATAAA-----
ZATGTGG-----
ZATCAATCTAGAG-----
ZGTGCAGGAGACACTCAAG-----
ZATCTCGGCGC-----
ZAGTTCATCC-----
ZATTCTTCAGTTTCCACCCGGGA-----
FTCTATTACT-----
ZGACATGAAGCACTGGCCT-----
ZAACTGTAATGTAGTTGCCTTACA-----
ZCAGTCCACTTATTACTACTGCGGCC-----

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:GAGTGGAAAGCAAGAAC-----
:GTTTCTTAGGCTACCAATACGAAT-----
:GCATAATGGAAATC-----
:GGTGGTGTATTACAACAACACAGTGGG-----
:TTTGCACCGCTT-----
:CTTGCCC--CGCACGACACTTTCA-----
:GG-----
:TGAAGATG-----
:GGGTTGAGGCAGGAAACCCCTGGGTTCCCT-----
:TTGCTAAAGAGTAATACTAGAGATAA-----
:TAAC--ATAATTAAGCAGCC-----
:AGGTCAGGCCCG-----
:ATGTGTGCGCACTTCAAGCCAGCGA-----
:CTCTAAGGTCAGTTTGTCAAGGAG-----
:TCTCTGCTGTACAGGATGTTCTA-----
:CGAAT--GTAARACTTTATGATTTCAAG-----
:CAAAGCTATATCATAATTTTTCTCT-----
:TTAAGGAGCTGCGAAGTCC-----
:GGCCCGCCAGAGC-----
:AGGTCA--CCCCGACCCGCACTGTTCTA-----
:AGGGCAAAGTCCCAGCC-----
:TTAAATGGCGTTATTGGTGT-----
:GGAAGACGATGGTGTGGTGTGCGCTGGGAT-----

:TTATCAAAGTCATACATCTGTTTTATAAGCTGTAGTTATCCAAGGACACTTCACTCATAACAATAGCCATTAAGG-----
:AAGTGGCGCATGATGT-----

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