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                                 *      * * * * *   ********
Bt1-196 -GTGAACTGGAACTGCTGAGTGAA-TTAGGTAGTTTCATGTTGTTGGGCC-TGGATTTCTGAAC--ACAACGACATTAAACCACCCGACTCACGGC--AGTTACTGCTCCTCGCTTAG---   111
Cf2-196 -GTGAACTGGAACTGCTGAGTGAA-TTAGGTAGTTTCATGTTGTTGGGCC-TGGATTTCTGAAC--ACAACAACATTAAACCACCCGACTCACGGC--AGTTACTGCTCCTCGCTTAG---   111
Ss2-196 -GTGAACTGGAACTGCTGAGTGAA-TTAGGTAGTTTCATGTTGTTGGGCC-TGGATTTCTGAAC--ACAACGACATTAAACCACCCGACTCACGGC--AGTTACTGCTCCTCGCTTAG---   111
HsB-196 -TTGAATTGGAACTGCTGAGTGAA-TTAGGTAGTTTCATGTTGTTGGGCC-TGGGTTTCTGAAC--ACAACAACATTAAACCACCCGATTCACGGC--AGTTACTGCTCCTCGCTTAG---   111
Pt2-196 -TTGAATTGGAACTGCTGAGTGAA-TTAGGTAGTTTCATGTTGTTGGGCC-TGGGTTTCTGAAC--ACAACAACATTAAACCACCCGATTCACGGC--AGTTACTGCTCCTCGCTTAG---   111
Ph2-196 -TTGAACTGGAACTGCTGAGTGAA-TTAGGTAGTTTCATGTTGTTGGGCC-TGGGTTTCTGAAC--ACAACAACATTAAACCACCCGATTCACGGC--AGTTACTGCTCCTCGCTTAG---   111
 Fc-196 -TTGACCTGGAGCTGCTGAGTGAA-TTAGGTAGTTTCATGTTGTTGGGCC-TGGATTTCTGAAC--ACAACGACATTAAACCACCCGACTCACGGC--AGCTACTGCTCCTCGCTTAG---   111
MmB-196 -TTGAGCCGGGACTGTTGAGTGAA-GTAGGTAGTTTCATGTTGTTGGGCC-TGGCTTTCTGAAC--ACAACGACATCAAACCACCTGATTCATGGC--AGTTACTGCTTCTTGCTTAG---   111
RnB-196 -TTGAACTGGGACTGCTGAGTGAA-GTAGGTAGTTTCGTGTTGTTGGGCC-TGGCTTTCTGAAC--ACAACAACACCAAACCACCTGATTCACTGC--AGTTACTGCTTCTTGCTTAG---   111
HfB-196 -GTGAAATGGAACTGCTGTGTGAC-TTAGGTAGTTTCATGTTGTTGGGCT-T--CTGTTTGATC--GCAGTGACAAGAAACTGCCTGAATTACTCC--AGTTATTG-TCATCGCAAAC---   108
Gg3-196 -ATGAACTAGAACTGCTCTGTGAA-TTAGGTAGTTTCATGTTGTTGGGCT-TTAAATTTTAAAC--ACAAGAACATCAAACTACCTGATTTACTCC--AGTTATCC-CCCTCGGTGTGC--   111
LmB-196 -ACGGACAAAAACTGCGGTGTGTT-TTAGGTAGTTTCATGTTGTTGGGCT-TTTT-TTTTAATC--ACAGGAACATCAAACTGCCTGAATTACTCC--AGTTACCCGCCTTCAGTTCT---   110
HsA-196 -CAGCACCAGAACTGGTCGGTGAT-TTAGGTAGTTTCCTGTTGTTGGGA--TCC-ACCTTTCTC--TCGACAGCACGACACTGCCTTCATTACTTC--AGTTGAAA-TCGTCTCCAGGT--   109
Og1-196 -CAGCACCAGAACTGGTCGGTGAT-TTAGGTAGTTTCCTGTTGTTGGGA--TCC-ACCTTTCTC--TCGACAGCACGACACTGCCTTCATTACTTC--AGTTGAAA-TCGTCTCCAGGT--   109
Ph1-196 -CAGCACCAGAACTGGTCGGTGAT-TTAGGTAGTTTCCTGTTGTTGGGA--TCC-ACCTTTCTC--TCGACAGCACGACACTGCCTTCATTACTTC--AGTTGAAA-TCGTCTCCAGGT--   109
 Pt-196 -CAGCACCAGAACTGGTCGGTGAT-TTAGGTAGTTTCCTGTTGTTGGGA--TCC-ACCTTTCTC--TCGACAGCACGACACTGCCTTCATTACTTC--AGTTGAAA-TCGTCTCCAGGT--   109
Cp2-196 -CAGCACCAGAACTGGTCGGTGAT-TTAGGTAGTTTCCTGTTGTTGGGA--TCC-ACCTTTCTC--TCGACAGCACGATACTGCCTTCATTACTTC--AGTTGAAA-TCGTCTCCAGGT--   109
MmA-196 -CAGCATCAGAACTGGTCGGTGAT-TTAGGTAGTTTCCTGTTGTTGGGA--TCC-ACCTTTCTC--TCGACAGCACGACACTGCCTTCATTACTTC--AGTTGAAA-GCATCTCCAGGT--   109
RnA-196 -CAGCATCTGAACTGGTCGGTGAT-TTAGGTAGTTTCCTGTTGTTGGGA--TCC-ACCTTTCTC--TCGACAGCACGACACTGCCTTCATTACTTC--AGTTGAAA-GCGTCTCCAGGT--   109
Ss1-196 -CAGCATCAGAACTGGTCGGTGAT-TTAGGTAGTTTCCTGTTGTTGGGA--TCC-ACCTTTCTC--TCGACAGCACGACACTGCCTTCATTACTTC--AGTTGAAA-TCGTCTCCNAGG--   109
Gg1-196 -GCGCCTGAGAACTGCTCTGTGGT-TTAGGTAGTTTCATGTTGTTGGGGC-TCC-ACCTTTCTC--TCTACAGCACGAAACTGCCTTAATTACTTC--AGTTGATA-TCATCACCAGGT--   110
XtA-196 -TTAGAACAGAGCCGCTGTGTGGT-TTAGGTAGTTTTATGTTGTTGGGCA-TTC-ACCTTTCTC--TCTACAACAAGAAACTGCCTTAATTACATC--AGTGGGAA-TCATCACCCAGG--   110
TrAa-196 GCCCGGACC-GACTGTCGAGTGGT-TTAGGTAGTTTCATGTTGTTGGGGT-CCA--TTTCAAAC--TCTGCAACATGAAACTGTCTTAATTGCCCC--AGTTACAT-ACAACGAAGCCA--   109
TnAa-196 GCCCGGATC-GACTGTCGAGTGGT-TTAGGTAGTTTCATGTTGTTGGGGT-CCA--TTTCAAAC--TCTGCAACATGAAACTGTCTTAATTGCCCC--AGTTACAC-ACGACGAATCCA--   109
OnAa-196 GCCCGGATC-GACTGTCGAGTGGT-TTAGGTAGTTTCATGTTGTTGGGGT-CCA--TTTCTAAC--TCTGCAACATGAAACTGTCTTAATTGCCCC--AGTTACAT-ACATCGAAACCG--   109
MsA-196 GCCCGGATC-GACTGTCGTGTGGT-TTAGGTAGTTTCATGTTGTTGGGGT-CCA--TTTCTAAC--TCTGCAACATGAAACTGTCTTAATTGCCCC--AGTTACAC-ACATCGACACCA--   109
Ga1-196 GCCCGGATT-GACTGCCGGGTGGT-TTAGGTAGTTTCATGTTGTTGGGGT-CCA--TTTCTAAC--TCTGCAACACGAAACTGTCTTAACTGCCCC--AGTTCCAC-ACATCAAAACCA--   109
DrAa-196 -TTTGAACCAGACTGTCGAGTGGT-TTAGGTAGTTTCATGTTGTTGGGAT-TAC--ATTCAAAC--TCTGCAACGTGAAACTGTCTTAATTGCCCC--AGTTTCAT-TCCTCTGTATAA--   109
PsA-196 AAGTGTTTAAGACTG-CATGTGAT-TTAGGTAGTTTCATGTTGTTGGGGC-TCCATTTTCAATC--CCTACAACACGAAAGTGCCTTAATTGCTCC--AGTTAAAG-TCGTCTTCGCAG--   111
HfM-196 -CTGTGATAGAACTGGCGTGTGAT-TTAGGTAGTTTCATGTTGTTGGGGC-TC--AAGTCTATC--TCTACAACACGAAACTGCCTGAATTACTGC--AGTTATAG-TCTTCGCCAGTGAG   111
LmA-196 -CGTGGACTAAACTGAAGTGTGAT-TTAGGTAGTTTCATGTTGTTGGGGC-TCC-AAATTTATC--TCTATAACAAGAAACTGCCTGAATTACTCC--AGTTAAAA-TCTTCACACGTC--   110
DrAb-196 -AACAAAGACAACTGCTAAGTGAT-TAAGGTAGTTTTATGTTGTTGGGCT-CTA-TTTTATATC--CCCGCAACACGAAACTGTCTTAATTGCCTCGCAGTGAGAT-TCAGCACAAC----   110
TnAb-196 -AGGAGAGTGAGCTGTTGTGTGGT-TTAGGTAGTCTCATGTTGTTGGGTT-CTA-ATATTTCTC--CC-ACAACAGGAAACTGCCTTGATTACCTC--AGTAAAAA-TCATCGCAACAT--   109
Ph3-196 -TGCTCGCTCAGCTGATCTGTGGC-TTAGGTAGTTTCATGTTGTTGGGAT-TGA-GTTTTGAAC--TCGGCAACAAGAAACTGCCTGAGTTACATC--AGTCGGTTTTCGTCGAGGGC---   110
Pt3-196 -TGCTCGCTCAGCTGATCTGTGGC-TTAGGTAGTTTCATGTTGTTGGGAT-TGA-GTTTTGAAC--TCGGCAACAAGAAACTGCCTGAGTTACATC--AGTCGGTTTTCGTCGAGGGC---   110
HsC-196 -TGCTCGCTCAGCTGATCTGTGGC-TTAGGTAGTTTCATGTTGTTGGGAT-TGA-GTTTTGAAC--TCGGCAACAAGAAACTGCCTGAGTTACATC--AGTCGGTTTTCGTCGAGGGC---   110
Cf1-196 -TGCTCGCTCAGCTGATCTGTGGC-TTAGGTAGTTTCATGTTGTTGGGAT-TGA-GTTTTGAAC--TCGGCAACAAGAAACTGCCTGAGTTACATC--AGTCGGTTTTCGTCGAGGGC---   110
Bt2-196 -TGCTCGCTCAGCTGATCTGTGGC-TTAGGTAGTTTCATGTTGTTGGGAT-TGA-GTTTTGAAC--TCGGCAACAAGAAACTGCCTGAGTTACATC--AGTCGGTTATCGTCGAGGGC---   110
Ss3-196 -TGCTTGCTCAGCTGATCTGTGGC-TTAGGTAGTTTCATGTTGTTGGGAT-TGA-GTTTTGAAC--TCGGCAACAAGAAACTGCCTGAGTTACATC--AGTCGGTTATCGTCGAGGGC---   110
Cp1-196 -TGCTTGCTCAGCTGATCTGTGGC-TTAGGTAGTTTCATGTTGTTGGGAT-TGA-GTTTTGAAC--TCGGCAACAAGAAACTGCCTGAGTTACATC--AGTCGGTTTTCGTCGAGGGC---   110
MmC-196 -TGCTTGCTCAGCTGATCTGTGGC-TTAGGTAGTTTCATGTTGTTGGGAT-TGA-GTTTTGAAC--TCGGCAACAAGAAACTGCCTGAGTTACATC--AGTCGGTTTTCGTCGAGGGC---   110
RnC-196 -TGTTTGCTCAGCTGATCTGTGGC-TTAGGTAGTTTCATGTTGTTGGGAT-TGA-GTTTTGAAC--TCGGCAACAAGAAACTGCCTGAGTTACATC--AGTCGGTTTTCGTCGAGGGC---   110
TrCa-196 -TTTGCGCGAAGCTGGAGCGTGGT-TTAGGTAGTTTCATGTTGTTGGGGA-TGG-CTTCCTGGC--TCGGCAACAAGAAACTGCCTTGATTACGTC--AGTTCGTCTTCATCAAGGGC---   110
TnCa-196 -TTTGCGGGAAGCTGGAGCGTGGTCTTACGTACTTTCATGTTGTTGGGGA-TGG-CTTCCTGGC--TCGGCAACAAGAAACTGCCTTGATTACGTC--AGTTCGTCTTCATCAAGGGC---   111
Ga2-196 -TTTGCGTGAAGCTGAAGCGTGGT-TTAGGTAGTTTCATGTTGTTGGGGT-TGG-CTTCCTGGC--TCGGCAACAAGAAACTGCCTTGATTACGTC--AGTTCGTCTTCATCAAGGGC---   110
DrCa-196 -GTTACGCGCGGCTGGTGCGTGGT-TTAGGTAGTTTCATGTTGTTGGGAT-TGG-CTTCCTGGC--TCGACAACAAGAAACTGCCTTGATTACGTC--AGTTCGTCTTCATCAAGGGC---   110
DrCb-196 -AGCCCGTCCAGCTGATGCGTGGT-TTAGGTAGTTTGATGTTGTTGGGGT-TGA-CTTCCTGGC--TCGACAACAAGAAACTGCCTTGATTACGTC--AGTTTGCCTTCATCAAGGCC---   110
Gg2-196 -CTTTCATGCAGCTGATCTGTGGT-TTAGGTAGTTTCATGTTGTTGGGAT-TGG-CTTT-TAGC--TCGGCAACAAGAAACTGCCTTAATTACGTC--AGTTAGTCTTCATCAAGGGC---   109
LmC-196 -CTTTCGTGCAGCTGATCTGTGGT-TTAGGTAGTTTCATGTTGTTGGGAT-TGG-CTTT-TAAC--TCGGCAACAAGAAACTGCCTTAATTACGTC--AGTTCGTCTTCATCAAGGGC---   109
 Pm-196 -CCTGCAGCTGGCTGGTCCGTGGT-CTAGGTAGTTTCATGTTGTTGGGGT-TTACGCTCCAGATGTCCGACAGCAGAAAACTGCCCGGACCGCGCC--AGCCAATA-ACGGCGTAGGCG--   113
TrBa-196 -GGTTCACACCGGAGCGGTGTGAT-ATAGGTAGTTTCAAGTTGTTGGGCT-GAACTCTTGTGAT-CACAGGAACCTGAAACTGCCTGAGTCACGCT--GACCTCCGCTGCACATCTAC---   112
XtB-196 -TCCAGGGAAGGTCTACATCTCAA-TTAGGCAGTTTCATGTTGTTGGTTTGTCTTTTGTTTTGCGGCTTTTCATAAAGGGATACAGGAATCACACATAGTGCACACGAAAAC---------   110
  ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.
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