```
          G- - - GCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC
                 10        20        30        40        50        60        70        80        90

Yb8AD687      G- - - GCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
Yb8AD688      - - GG- CCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
Yb8AD689      G- - - GCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
Yb8AD693      G- - - GCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
Yb8AD721      G- - - GCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
AluYb8NCB108  - CGG- CCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  85
AluYb8NCB109  G- - - GCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
AluYb8NCB111  G- - - GCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
Yb8-110       - - GGGCTGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  85
AluYb8NCB112  G- - - - - - - - - - - - - - - GCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  71
Yb8-114       G- - - GCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
AluYb8NCB160  GCGGGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCAAGTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  87
AluYb8NCB268  G- - - GCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
Yb8-496       G- - - GCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGAGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
AluYb8NCB507  G- - - GCCAGGCGCGGTGGCTCTTGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
AluYb8NCB535  G- - - GCCGGGTGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
Yb8AD690      - - GG- CCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA- - TGAGGTCAGGAGATCGAG- ACC  84
Yb8AD720      G- - - - - - - GCATGGTGGCTCATGCCTGTAATCCCAGAACGTTCTGAGGCCGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCTAGCACT  82
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          ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT
                 100       110       120       130       140       150       160       170       180

Yb8AD687      ATCCTGGCTAACATGGTGAAACCCCGTC- TCTACTAAAAATACA- - - AAAAATTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  170
Yb8AD688      ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  170
Yb8AD689      ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAAATACA- - - AAAAATTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  170
Yb8AD693      ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTAGCCGGGCGCGGTGGCGGGAGCCTGTAGTCCCAGCT  170
Yb8AD721      ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAAATACAAAAAA- TTAGCCGGGCACGGTGGCGGGTGCCTGTAGTCCCAGCT  172
AluYb8NCB108  ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  171
AluYb8NCB109  ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  170
AluYb8NCB111  ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAAAATACAAAAA- TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  172
Yb8-110       ATCCTGGCTAACAAGGTGAAACCCCGTC- TCCACTAAAA- - TACAAAAA- TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  171
AluYb8NCB112  ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  157
Yb8-114       ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAAATACAAAAAAATTGGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  173
AluYb8NCB160  ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  173
AluYb8NCB268  ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  170
Yb8-496       ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  170
AluYb8NCB507  ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTAGCCGGGCGCGGTGGCGGGTGCCTGTAGTCCCAGCT  170
AluYb8NCB535  ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  170
Yb8AD690      ATCCTGGCTAACAAGGTGAAACCCCGTC- TCTACTAAAA- - TACAAAAA- TTAGCCAGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCT  170
Yb8AD720      CTCCTGGCCAACATGGTGAAACCCCACCCTCTACCAAAAATACA- - - AAAAATTAGCCGGGCGCGGTGGCGGGCACCTGTAGTCCCAGCT  169
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            ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCG
                   190         200         210         220          230         240         250         260         270

Yb8AD687      ACT CGGGAGGCT GAGGCA GAA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CC-  259
Yb8AD688      ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCG  259
Yb8AD689      ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGGGAA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CT G  260
Yb8AD693      ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AGGCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CT G  259
Yb8AD721      ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCC  261
AluYb8NCB108   ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCG  260
AluYb8NCB109   ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCG  259
AluYb8NCB111   ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC AGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCAC AGT CCG  261
Yb8-110       ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CT G  260
AluYb8NCB112   ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCG  246
Yb8-114       ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCC  262
AluYb8NCB160   ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCG  262
AluYb8NCB268   ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AGGCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCG  259
Yb8-496       ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCG  259
AluYb8NCB507   ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GT GGAGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCG  259
AluYb8NCB535   ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAGCT T GCA GT GAGC T GA GAT T GCGCC ACT GCA GT CCGC AGT CCG  259
Yb8AD690      ACGCGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGGGCT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CCG  259
Yb8AD720      ACT CGGGAGGCT GAGGCA GGA GAA T GGCGT GAA CCC GGG-  AA GCGGAA CT T GCA GT GAGC CGA GAT T GCGCC ACT GCA GT CCGC AGT CT G  258
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            GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AAA AAA AAA AXX XXX XX XX XX XX XX XXX XX XXX
                   280         290         300         310         320         330         340         350

Yb8AD687      - - - - - - - - - - - - - AGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA A                                              294
Yb8AD688      GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA T AAAAT AAA AT A AAA CAA ACA AAC AAA CAA AAA AAC ACA AA- - - A      337
Yb8AD689      GCCT GGGT GACA GAGCGA GACT CCGT T T AA AAA AAA AAA AAA AAA A- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - A  307
Yb8AD693      GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA         340
Yb8AD721      ACCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AAA AAA AAA- - - - - - - - - - - - - - - - - - - A  321
AluYb8NCB108   GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA T AAAAT AAA AT A AAA CAA ACA AAC AAA CAA AAA AAC ACA AA- - - A      338
AluYb8NCB109   GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AAA                                             313
AluYb8NCB111   GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA- - - - - - - - A          333
Yb8-110       GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AA                                             313
AluYb8NCB112   ACCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAAA- - - - - - - - - - - - - - - - - - - AAA AAA AAA AAA AAA AAGAAA  308
Yb8-114       GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AAA A                                           314
AluYb8NCB160   GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AAA GAA A                                       320
AluYb8NCB268   GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA ACA- - - - - - - - - - - - - AA CAA ACA AAC AAA CAA ACA AAA ACT GGT AGA  327
Yb8-496       GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AAA AAA AAA AAA A                               326
AluYb8NCB507   GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AAA AAA AGA A                                   317
AluYb8NCB535   GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AAA AAA GAA A                                   317
Yb8AD690      ACCT GGGCGACA GAGCGA GACT CCGCCT CAAAA AAA- - - - - - - - - - - - - - - - - - - - - - - - - - AAA AAA- - - AAA- - - A  305
Yb8AD720      GCCT GGGCGACA GAGCGA GACT CCGT CT CAAAA AAA AAA AAA AAA AAA AAA AAA AAA                                     313
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