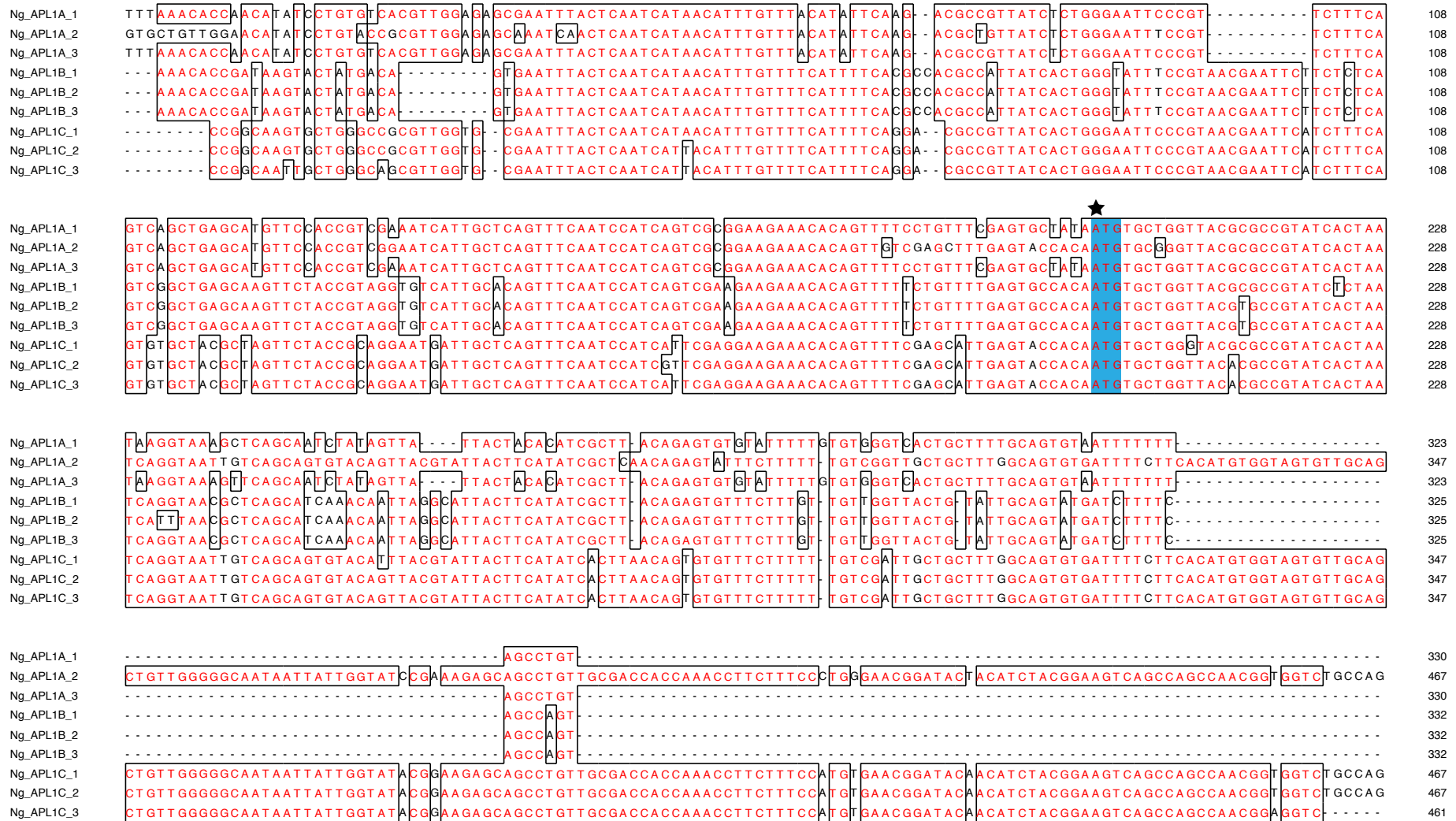


Figure S1: Alignment of genomic regions coding for *APL1A*, *APL1B* and *APL1C* alleles in Ngousso mosquitoes



Ng_APL1A_1 ACCA 334
 Ng_APL1A_2 CCACAACCTACACACAAAGTCACA CAACCTACA CAAGA GAC CAAAACCTTCGGAGGT CAGT CAGCCAACGGAGGT T GCCG GCCAACGGAGGT CT TCC AGCCAACGGA GGA CT CCA GCCA 587
 Ng_APL1A_3 ACCA 334
 Ng_APL1B_1 ACCT 336
 Ng_APL1B_2 ACCT 336
 Ng_APL1B_3 ACCT 336
 Ng_APL1C_1 CCACAACCTACACACAAAGTCACA CAACCTACA CAAGA GAC CAAAACCTTCGGAGGT CAGT CAGCCAACGGAGGT T GCCG GCCAACGGAGGT CT GCT AGCCAACGGA GGT CT CCA GCCA 587
 Ng_APL1C_2 CCACAACCTACACACAAAGTCACA CAACCTACA CAAGA GAC CAAAACCTTCGGAGGT CAGT CAGCCAACGGAGGT T GCCG GCCAACGGAGGT CT TCC AGCCAACGGA GGA CT CCA GCCA 587
 Ng_APL1C_3 CAACCTACA GAAGT GAG CAAAACCTTCGGAGGT CAGT CAGCCAACGGAGGT T GCCG GCCAACGGAGGT CT TAC AGCCAACGGT GGT CT CCA GCCA 557

Ng_APL1A_1 ACGGAGGACTGCCATCCTACAGS AGT CAGC CAAAT TACGGAA AT A A A D A C A C T A C T A C G A A G G T C A G C A A T C T A C A G A A G T C A G C C A A A T T A C G G A G G T C A G C A A C G C T A C A A C G C A A G A C C A C 424
 Ng_APL1A_2 ACGGAGGTCTGCCAGCCAACAGAGGGCAGCTGCCGTATGGAACCTCCAACCCATATAGGTCA ACAATCTACAGAAGTCAGCCAAAT TACGGAGGT CAGCAACGCTACAACGC AAGACCAC 707
 Ng_APL1A_3 ACGGAGGACTGCCATCCTACAGS AGT CAGC CAAAT TACGGAA AT A A A C A A C G C T A C T A C G G A A A T C A G C A A T A C T A C A C G T A C A A C C A C 424
 Ng_APL1B_1 ACGGAGGACAGCTATCCTACAAAAGTATGCAC A A A C A A C G C T A C T A C G G A A A T C A G C A A T A C T A C A C G T A C A A C C A C 368
 Ng_APL1B_2 ACGGAGGACAGCTATCCTACAAAAGTATGCAC A A A C A A C G C T A C T A C G G A A A T C A G C A A T A C T A C A C G T A C A A C C A C 368
 Ng_APL1B_3 ACGGAGGA T A C T A T C C T A C A A A G T A T G C A C A A A C A A C G C T A C T A C G G A A A T C A G C A A T A C T A C A C G T A C A A C C A C 368
 Ng_APL1C_1 ACGGAGGTCTGCCAGCCAACAGAGGGCAGCTGCCGTACGGAACTCCAACCCATATAGGTCA GACAATCTACAGAAGTCAGCCAAAT TACGGAGGT CAGCAACGCTACAACGC AAGACCAC 707
 Ng_APL1C_2 ACGGAGGTCTGCCAGCCAACAGAGGGCAGCTGCCGTACGGAACTCCAACCCATATAGGTCA ACAATCTACAGAAGTCAGCCAAAT TACGGAGGT CAGCAACGCTA T A A C G T A A G A C C A C 707
 Ng_APL1C_3 ACGGAGGTCT T C C A G C C A A C G S A G G G C A G C T G C C G T A C G G A A C T C C A A C C C A T A T A G G T C A G A C A A T C T A C A G A A G T C A G C C A A T T A C G G A G G T C A G C A A C G C T A C A A C C G T A A G A C C A C 677

Ng_APL1A_1 GACAGC C G A A T A C A A A T G C A T T G A G A S A A A T C T G C A G T A C G A C T G T G T G T T C T A C G A T G T G C A C A T T G A C A T G C A A A C G C A A G A C G T A T A C T T T G G C T T T G A G G A T A T A A C A C T A A A C A 544
 Ng_APL1A_2 GACAGC T A S A A T A C A A A T G C A T T G A G G C T A A T C T G C A G T A C G A C T G T G T G T T C T A C A A T G T G C A C A T T G A C A T G C A A A C G C A A G A C G C A T A C T T T G G C T T T G A G A T T T A A C S C T A A A C A 827
 Ng_APL1A_3 T A C A A C C G A A T A C A A A T G C A T T G A G A S A A A T C T G C A G T A C G A C T G T G T G T T C T A C A A T G T G C A C A T T G A C A T G C A A A C G C A A G A C G T A T A C T T T G G C T T T G A G G A T A T A A C A C T A A A C A 544
 Ng_APL1B_1 T T S A C T C C T T T C A C T T T G A G 388
 Ng_APL1B_2 T T S A C T C C T T T C A C T T T G A G 388
 Ng_APL1B_3 T T S A C T C C T T T C A C T T T G A G 388
 Ng_APL1C_1 GACAGC T A S A A T A C A A A T G C A T T G A G S S T A A T C T G C A G T A C G A C T G T G T G T T C T A C G A T G T G C A C A T T G A C A T G C A A A C G C A A G A C G T A T A C T T T G G C T T T G A G G A T A T A A C A C T A A A C A 827
 Ng_APL1C_2 GACAGC C G A A T A C A A A T G C A T T G A G G S T A A T C T G C A G T A C G A C T G T G T G T T C T A C G A T G T G C A C A T T G A C A T G C A A A C G C A A G A C G T A T A C T T T G G C T T T G A G G A T A T A C A C T A A A C A 827
 Ng_APL1C_3 GACAGC A C G A A T A C A A A T G C A T T G A G A S A A A T C T G C A G T A C G A C T G T G T G T T C T A C G A T G T G C A C A T T G A T A T G C A A T T C G C A A G A C G T A T A C T T T G G C T T T G A G G A T A T A A C A C T A A A C A 797

Ng_APL1A_1 ACCAGAAGAT T G T T A C C T T C A A A A A C T A C C A T G C G T A A A C T G C C G C T G C T T T A C T C G C C T C C T T C G C C A G G T T G A G S T G C T C A A T C T G A A C G A C C T G C A G A T A G A G C A G A T C G A T A 664
 Ng_APL1A_2 ACCAGAAGAT T G T T A C C T T C A A A A A C T A C C A T G C G C A A A C T G C C G C T G C T T T A C T C G C C T C C T T C G C C A G G T T G A G S T G C T C A A T C T G A A T S G C C T G C A G A T A G A G G A G A T C G A T A 947
 Ng_APL1A_3 ACCAGAAGAT T G T T A C C T T C A A A A A C T A C C A T G C G T A A A C T G C C G C T G C T T T A C T C G C C T C C T T C G C C A G G T T G A G C T G C T C A T C T G A A C G A C C T G C A G A T A G A G C A G A T C G A T A 664
 Ng_APL1B_1 T G C T T T A C T C G C C T C C T T C C A C A A G G T T G A G S T G C T C A A T C T G A A C G G C C T G C A G A T A G A G G A G A T C G A T A 459
 Ng_APL1B_2 T G C T T T A C T C G C C T C C T T C C A C A A G G T T G A A C T G C T C A A T C T G A A C G C C C T G C A G A T A G T S G A G A T C G A T A 459
 Ng_APL1B_3 T G C T T T A C T C G C C T C C T T C C A C A A G G T T G A A C T G C T C A A T C T G A A C G G C C T G C A G A T A G A G G A G A T C G A T A 459
 Ng_APL1C_1 ACCAGAAGAT T G T T A C C T T C A A A A A C T A C C A T G C G C A A A C T G C C G C T G C T T T A C T C G C C T C C T T C G C C A G G T T G A G C T G C T C A A T C T G A A T S A C C T G C A G A T A G A G G A G A T C G A T A 947
 Ng_APL1C_2 ACCAGAAGAT T G T T A C C T T C A A A A A C T A C C A T G C G C A A A C T G C C G C T G C T T T A C T C G C C T C C T T C G C C A G G T T G A G C T G C T C A A T C T G A A T S A C C T G C A G A T A G A G G A G A T C G A T A 947
 Ng_APL1C_3 ACCAGAAGAT T G T T A C C T T C A A A A A C T A C C A T G C G C A A A C T G C C G C T G C T T T A C T C G C C T C C T A C G C C A G G T T G A G C T G C T C A T C T G A A C T G A A C T G A A C G A C C T G C A G A T A G A G C A G A T C G A T A 917

Ng_APL1A_1 CGAACGCGTTTCGCTTACGCGCACACAATT CAGAAGCTGTACATGGGATTCAATGCGATTGATATTTGCCACCGTACGTGTTTCAGAACGTCCCATCGCTCACGGTGCTTGTGCTGGAAC 784
Ng_APL1A_2 CGAACGCGTTTCGCTTACGCGCACACAATACAGAAGCTGT ----- 986
Ng_APL1A_3 CGAACGCGTTTCGCTTACGCGCACACAATT CAGAAGCTGTACATGGGATTCAATGCGATTGATATTTGCCACCGTACGTGTTTCAGAACGTCCCATCGCTCACGGTGCTTGTGCTGGAAC 784
Ng_APL1B_1 CGAACGCGTTTCGCTTACGCGCACACAATACAGAAGCTGTACATGAGATTCAATGAGATTAGATATTTGCCACCGTACGTGTTTCAGAACGTCCCATCGCTCACGGTGCTTGTGCTGGAAC 579
Ng_APL1B_2 CGAACGCGTTTCGCTTACGCGCACACAATACAGAAGCTGTACATGAGATTCAATGAGATTAGATATTTGCCACCGTACGTGTTTCAGAACGTCCCATCGCTCACGGTGCTTGTGCTGGAAC 579
Ng_APL1B_3 CGAACGCGTTTCGCTTACGCGCACACAATACAGAAGCTGTACATGAGATTCAATGAGATTAGATATTTGCCACCGTACGTGTTTCAGAACGTCCCATCGCTCACGGTGCTTGTGCTGGAAC 579
Ng_APL1C_1 CGAACGCGTTTCGCTTACGCGCACACAATT CAGAAGCTGTACATGGGATTCAATGCGATTGATATTTGCCACCGTACGTGTTTCAGAACGTCCCATCGCTCACGGTGCTTGTGCTGGAAC 1067
Ng_APL1C_2 CGAACGCGTTTCGCTTACGCGCACACAATT CAGAAGCTGTACATGGGATTCAATGCGATTGATATTTGCCACCGTACGTGTTTCAGAACGTCCCATCGCTCACGGTGCTTGTGCTGGAAC 1067
Ng_APL1C_3 CGAACGCGTTTCGCTTACGCGCACACAATACAGAAGCTGTACATGGGATTCAATGCGATTGATATTTGCCACCGTACGTGTTTCAGAACGTCCCATCGCTCACGGTGCTTGTGCTGGAAC 1037

Ng_APL1A_1 GGAACGATTTAACCGAGCCTGCCACGCGGAATCTTCCACAACACACCCAAAGCTCAGCATGCTGTCGATGTCAAACAACAACCTGGAGCGCATCGAAGACGAACTTTCCAAGCACTACA 904
Ng_APL1A_2 GGAACGATTTAACCGAGCCTGCCACGCGGAATCTTCCACAACACACCCAAAGCTCAGCATGCTGTCGATGTCAAACAACAACCTGGAGCGCATCGAAGACGAACTTTCCAAGCACTACA 1043
Ng_APL1A_3 GGAACGATTTAACCGAGCCTGCCACGCGGAATCTTCCACAACACACCCAAAGCTCAGCATGCTGTCGATGTCAAACAACAACCTGGAGCGCATCGAAGACGAACTTTCCAAGCACTACA 904
Ng_APL1B_1 GGAACGATTTAACCGAGCCTGCCACGCGGAATCTTCCACAACACACCCAAAGCTCAGCATGCTGTCGATGTCAAACAACAACCTGGAGCGCATCGAAGACGAACTTTCCAAGCACTACA 699
Ng_APL1B_2 GGAACGATTTAACCGAGCCTGCCACGCGGAATCTTCCACAACACACCCAAAGCTCAGCATGCTGTCGATGTCAAACAACAACCTGGAGCGCATCGAAGACGAACTTTCCAAGCACTACA 699
Ng_APL1B_3 GGAACGATTTAACCGAGCCTGCCACGCGGAATCTTCCACAACACACCCAAAGCTCAGCATGCTGTCGATGTCAAACAACAACCTGGAGCGCATCGAAGACGAACTTTCCAAGCACTACA 699
Ng_APL1C_1 GGAACGATTTAACCGAGCCTGCCACGCGGAATCTTCCACAACACACCCAAAGCTCAGCATGCTGTCGATGTCAAACAACAACCTGGAGCGCATCGAAGACGAACTTTCCAAGCACTACA 1187
Ng_APL1C_2 GGAACGATTTAACCGAGCCTGCCACGCGGAATCTTCCACAACACACCCAAAGCTCAGCATGCTGTCGATGTCAAACAACAACCTGGAGCGCATCGAAGACGAACTTTCCAAGCACTACA 1187
Ng_APL1C_3 GGAACGATTTAACCGAGCCTGCCACGCGGAATCTTCCACAACACACCCAAAGCTCAGCATGCTGTCGATGTCAAACAACAACCTGGAGCGCATCGAAGACGAACTTTCCAAGCACTACA 1157

Ng_APL1A_1 CGCTTCAAATCTTCAACTGTCCAGCAACAGGCTTACGCATGTTGACCTTCTCTCATTCCAGTCTCTTCCAGTCAACGTGCTTCAAACCTGCTCTCAACGCTTGCCATACCGATCG 1024
Ng_APL1A_2 CGCTTCAAATCTTCAACTGTCCAGCAACAGGCTTACGCATGTTGACCTTCTCTCATTCCAGTCTCTTCCAGTCAACGTGCTTCAAACCTGCTCTCAACGCTTGCCATACCGATCG 1163
Ng_APL1A_3 CGCTTCAAATCTTCAACTGTCCAGCAACAGGCTTACGCATGTTGACCTTCTCTCATTCCAGTCTCTTCCAGTCAACGTGCTTCAAACCTGCTCTCAACGCTTGCCATACCGATCG 1024
Ng_APL1B_1 CGCTTCAAATCTTCAACTGTCCAGCAACAGGCTTACGCATGTTGACCTTCTCTCATTCCAGTCTCTTCCAGTCAACGTGCTTCAAACCTGCTCTCAACGCTTGCCATACCGATCG 819
Ng_APL1B_2 CGCTTCAAATCTTCAACTGTCCAGCAACAGGCTTACGCATGTTGACCTTCTCTCATTCCAGTCTCTTCCAGTCAACGTGCTTCAAACCTGCTCTCAACGCTTGCCATACCGATCG 819
Ng_APL1B_3 CGCTTCAAATCTTCAACTGTCCAGCAACAGGCTTACGCATGTTGACCTTCTCTCATTCCAGTCTCTTCCAGTCAACGTGCTTCAAACCTGCTCTCAACGCTTGCCATACCGATCG 819
Ng_APL1C_1 CGCTTCAAATCTTCAACTGTCCAGCAACAGGCTTACGCATGTTGACCTTCTCTCATTCCAGTCTCTTCCAGTCAACGTGCTTCAAACCTGCTCTCAACGCTTGCCATACCGATCG 1307
Ng_APL1C_2 ACGCTTCAAATCTTCAACTGTCCAGCAACAGGCTTACGCATGTTGACCTTCTCTCATTCCAGTCTCTTCCAGTCAACGTGCTTCAAACCTGCTCTCAACGCTTGCCATACCGATCG 1307
Ng_APL1C_3 CGCTTCAAATCTTCAACTGTCCAGCAACAGGCTTACGCATGTTGACCTTCTCTCATTCCAGTCTCTTCCAGTCAACGTGCTTCAAACCTGCTCTCAACGCTTGCCATACCGATCG 1277

Ng_APL1A_1 CGGTGGAAGAGCTAGAGCGCATCGCACAAATAGCATCAACGCCGTACGCGGGCCCGTCAACATGGAGTTGACCATTCTGAAGCTGCAACACAACTTACTGACTGACTGCCTGGCTGCTGA 1144
Ng_APL1A_2 CGGTGGAAGAGCTAGAGCGCATCGCACAAATAGCATCAACGCCGTACGCGGGCCCGTCAACATGGAGTTGACCATTCTGAAGCTGCAACACAACTTACTGACTGACTGCCTGGCTGCTGA 1283
Ng_APL1A_3 CGGTGGAAGAGCTAGAGCGCATCGCACAAATAGCATCAACGCCGTACGCGGGCCCGTCAACATGGAGTTGACCATTCTGAAGCTGCAACACAACTTACTGACTGACTGCCTGGCTGCTGA 1144
Ng_APL1B_1 CAGTTCGAAGAAGCTAGAGCGCATCGCACAAATAGCATCAACGCCGTACGCGGGCCCGTCAACATGGAGTTGACCATTCTGAAGCTGCAACACAACTTACTGACTGACTGCCTGGCTGCTGA 939
Ng_APL1B_2 CAGTTCGAAGAAGCTAGAGCGCATCGCACAAATAGCATCAACGCCGTACGCGGGCCCGTCAACATGGAGTTGACCATTCTGAAGCTGCAACACAACTTACTGACTGACTGCCTGGCTGCTGA 939
Ng_APL1B_3 CAGTTCGAAGAAGCTAGAGCGCATCGCACAAATAGCATCAACGCCGTACGCGGGCCCGTCAACATGGAGTTGACCATTCTGAAGCTGCAACACAACTTACTGACTGACTGCCTGGCTGCTGA 939
Ng_APL1C_1 CGGTGGAAGAGCTAGAGCGCATCGCACAAATAGCATCAACGCCGTACGCGGGCCCGTCAACATGGAGTTGACCATTCTGAAGCTGCAACACAACTTACTGACTGACTGCCTGGCTGCTGA 1427
Ng_APL1C_2 CGGTGGAAGAAGCTAGAGCGCATCGCACAAATAGCATCAACGCCGTACGCGGGCCCGTCAACATGGAGTTGACCATTCTGAAGCTGCAACACAACTTACTGACTGACTGCCTGGCTGCTGA 1427
Ng_APL1C_3 CGGTGGAAGAGCTAGAGCGCATCGCACAAATAGCATCAACGCCGTACGCGGGCCCGTCAACATGGAGTTGACCATTCTGAAGCTGCAACACAACTTACTGACTGACTGCCTGGCTGCTGA 1397

Ng_APL1A_1	ATTATCCCGGACTGGTTGAGGTGGATCTTTCTACAACGAGTTGGAGAAGATAA	1264
Ng_APL1A_2	ACTATCCCA	1403
Ng_APL1A_3	ATTATCCCGGACTGGTTGAGGTGGATCTTTCTACAACGAGTTGGAGAAGATAA	1264
Ng_APL1B_1	ACTATCC	1059
Ng_APL1B_2	ATTATCC	1059
Ng_APL1B_3	ACTATCC	1059
Ng_APL1C_1	ACTATCCCGGACTGGTTGACGTGGATCTTTCTACAACGAGTTGGAGAAGATAA	1547
Ng_APL1C_2	ACTATCCCGGACTGGTTGACGTGGATCTTTCTACAACGAGTTGGAGAAGATAA	1547
Ng_APL1C_3	ATTATCCCGGACTGGTTGAGGTGGATCT	1517

Ng_APL1A_1	CGCTCAATCTTTACGGTCA	1384
Ng_APL1A_2	CGCTCGA	1523
Ng_APL1A_3	CGCTCGA	1384
Ng_APL1B_1	CGCTCGA	1179
Ng_APL1B_2	CGCTCGA	1179
Ng_APL1B_3	CGCTCGA	1179
Ng_APL1C_1	CGCTCAATCTTTACGGTCA	1667
Ng_APL1C_2	CGCTCAATCTTTACGGTCA	1667
Ng_APL1C_3	CGCTCAATCTTTACGGTCA	1637

Ng_APL1A_1	ACCACAACCTCCATCGTGACGCTTAAGCTTAGCACCAGT	1504
Ng_APL1A_2	ACCACAACCT	1643
Ng_APL1A_3	ACCACAACCT	1504
Ng_APL1B_1	ACCACAACCT	1299
Ng_APL1B_2	ACCACAACCT	1299
Ng_APL1B_3	ACCACAACCT	1299
Ng_APL1C_1	ACCACAACCT	1787
Ng_APL1C_2	ACCACAACCT	1787
Ng_APL1C_3	ACCACAACCT	1757

Ng_APL1A_1	CTGTG	1624
Ng_APL1A_2	CTGCAGT	1763
Ng_APL1A_3	CTGTG	1616
Ng_APL1B_1	CTGTG	1419
Ng_APL1B_2	CTGCAGT	1419
Ng_APL1B_3	CTGCAGT	1419
Ng_APL1C_1	CTGCAGT	1907
Ng_APL1C_2	CTGCAGT	1907
Ng_APL1C_3	CTGCAGT	1877

Ng_APL1A_1	GCGTGGCGGA	AAGTTGCAGCGTGCACAA	GGACGCTGCAGTGCCACAGATGCCATCAACAGCGTGCA	AAGTCTGTCCCACTACATCACACAGCAGGGTGATGTGCCACTGCAGGGTAACG	1744
Ng_APL1A_2	GCGTGGTGGAGAA	TTGTCGTCACAGGGACGCTGCAGT	GAACACAGATGCCATCAACAGCGTGCA	TAGTCTGTCCCACTACATCACACAGCA	1883
Ng_APL1A_3	GCGTGGCGGAGAAGTTGCAGCGT	AACAGGGACGCTGCAGT	ACCGCAGATGCCATCAACAGCGT	GCAAGTCTGTACCACTCATCACACAGCAGGGTGTGTGGA	1736
Ng_APL1B_1	GCGTGGT	TGAGAA	ACAGCGTA	AAATGAAACCGTGCAGTGCCACAGATGCCATCAACAGCGT	1536
Ng_APL1B_2	GCGTGGCGGA	AAGTTGCAGCGT	AACAGGAAACGCTGCAGT	ACCGCAGATGCCATCAACAGCGT	1539
Ng_APL1B_3	GCGTGGCGGAGAAGTTGCAGCGT	AACAGGAAACGCTGCAGT	ACCGCAGATGCCATCAACAGCGT	GCAAGTCTGTACCACTCATCA	1539
Ng_APL1C_1	GCGTGGTGGAGAA	TTGCAGCGTGCACAA	GGACGCTGCAGTGCCACAGAT	CCATCAACAGCGTGCA	2027
Ng_APL1C_2	GCGTGGCGGA	AAGTTGCAGCGTGCACAA	GGACGCTGCAGTGCCACAGAT	GCCATCAACAGCGTGCA	2027
Ng_APL1C_3	GCGTGGTGGAGAA	TTGCAGCGTGCACAA	GGACGCTGCAGTGCCACAGAT	CCATCAACAGCGTGCA	1997

Ng_APL1A_1	AAACAGCTCGAGGCCGAAGTCAACGAGCTGAGGGCT	GCGTGCAGCAGTAACCA	TGAGCAGAT	CAACAGC	AGCAGCTCCT	AGCAA	GA	CT	GCA	AGCCGAGATCGATACCAATCT	1864
Ng_APL1A_2	AAACAGCTCGAGGCCGAAGT	AAACGAGCTGAGGGCTGAGGTGCAGCAGCT	TACCAACGAGCA	TATAC	ACAGGAGCAGCTCCT	GGAA	GA	CT	GCA	AGCCGAGATCGATACCAATCT	2003
Ng_APL1A_3	TACAGCTCGAGGCC	TGAAGT	AAACGAGCTGAGGGCT	GCGTGCAGCAGCTAACCA	TGAGCAGAT	CAACAGC	AGCAGCTCCT	AGCAA	GA	CT	1856
Ng_APL1B_1	AAACAGCTCGAGGCCGAAGTCAACGAGCTGAGGGCT	GAGGTGCAGCAGCTAACCA	ACGAGCAGATACAACAGGAGCAGCT	CCTGCAGGGGCT	ACAGCCGAGATCGATACCAATCT	1656					
Ng_APL1B_2	AAACAGCTCGAGGCCGAAGTCAACGAGCTGAGGGCT	GAGGTGCAGCAGCTAACCA	ACGAGCAGATACAACAGGAGCAGCT	GCTGCAGGGGCT	ACAGCCGAGATCGATACCAATCT	1659					
Ng_APL1B_3	AAACAGCTCGAGGCCGAAGTCAACGAGCTGAGGGCT	GAGGTGCAGCAGCTAACCA	ACGAGCAGATACAACAGGAGCAGCT	GCTGCAGGGGCT	ACAGCCGAGATCGATACCAATCT	1659					
Ng_APL1C_1	AAACAGCTCGAGGCCGAAGTCAACGAGCTGAGGGCT	GAGGTGCAGCAGCTAACCA	ACGAGCAGATACAACAGGAGCAGCT	GCTGCAGGGGCT	ACAGCCGAGATCGATACCAATCT	2147					
Ng_APL1C_2	AAACAGCTCGAGGCCGAAGTCAACGAGCTGAGGGCT	GAGGTGCAGCAGCT	TACCAACGAGCAGATACAACAGGAGCAGCT	GCTGCAGGGGCT	ACAGCCGAGAT	2147					
Ng_APL1C_3	AAACAGCTCGAGGCCGAAGT	AAACGAGCTGAGGGCTGAGGTGCAGCAGCT	TACCAACGAGCAGATACAACAGGAGCAGCT	GCTGCAGGGGCT	TACAGCCGAGATCGATACCAATCT	2117					



Ng_APL1A_1	GCTACCA	CCTGCCGAA	AGATGAGT	FAGCACGCCCGAGT	GATAGTCT	TAA	CAAA	CT	ATTACCCCA	CTGAAGGA	ACGC	CA	TTT	GCAT	GAGTTG	GT	AAAT	CA	CT	AGT	ACT	CAT	GAAA	AGG	1984
Ng_APL1A_2	GCTACCA	CCTGCCGAA	AGATGAGT	FAGCACGCCCGAGT	GATAGTCT	TAA	CAAA	CA	TTT	GCAT	GAGTTG	GT	AAAT	CA	CT	AGT	ACT	CAT	GAAA	AGG	2123				
Ng_APL1A_3	GCTACCA	CCTGCCGAA	AGATGAGT	FAGCACGCCCGAGT	GATAGTCT	TAA	CAAA	CT	ATTACCCCA	CTGAAGGA	ACGC	CA	TTT	GCAT	GAGTTG	GT	AAAT	CA	CT	AGT	ACT	CAT	GAAA	AGG	1976
Ng_APL1B_1	GGT	CCGCCT	GC	CAAGGAT	GAACTAGCGCGCCGAGCGA	AAATCTAAATAAAGTGTT	TACCCATCT	CA	AGGAGCGGCACGCGTTT	AAAGTTGCGT	GAAACT	CA	GGCACGCGT	ACGGAGG	1776										
Ng_APL1B_2	GGT	ACCGCCT	GC	CAAGGAT	GAACTAGCGCGCCGAGCGA	AAATCTAAATAAAGTGTT	TACCCATCT	CA	AGGAGCGGCACGCGTTT	AAAGTTGCGCGAAACGCAGGCACGCGCACGGAA	AG	1779													
Ng_APL1B_3	GGT	ACCGCCT	GC	CAAGGAT	GAACTAGCGCGCCGAGCGA	AAATCTAAATAAAGTGTT	TACCCATCT	CA	AGGAGCGGCACGCGTTT	AAAGTTGCGCGAAACGCAGGCACGCGCACGGAA	AG	1779													
Ng_APL1C_1	GGT	ACCGCCT	GCCGAAGGAT	GAACTAGCGCGCT	CGAGCGATAATCTAAATAAAGTGTT	CACCCATCT	GAA	AGCGGCACGCGTTT	AAAGTTGCGCGAAACGCAGGCACGCGCACGGAGG	2267															
Ng_APL1C_2	GGT	CCGCCT	GCC	CAAGGAT	GAACTAGCACGCC	AGCGATAATCTAAATAAAGTGTT	CACCCATCT	GAA	AGCGGCACGCGTTT	AAAGTTGCGCGAAACGCAGGCACGCGCACGGAGG	2267														
Ng_APL1C_3	GGT	ACCGCCT	GCCGAAGGAT	GAACTAGCGCGCT	CGAGCGATAATCTAAATAAAGTGTT	CACCCATCT	GAA	AGCGGCACGCGTTT	AAAGTTGCGCGAAACGCAGGCACGCGCACGGAGG	2237															

Ng_APL1A_1	CT	GATGAT	AAGCT	CAAGG	ACCAGAT	GGAT	GT	TAT	TGGAACA	AAAT	TAT	TAGAT	CTC	CGT	TT	GGAA	CGGAT	AGCT	AACTT	AGG	-	-	AAGCA	AT	TGCA	TT	GAG	G	CAGGA	-	-	-	-	-	GAAGC	2092
Ng_APL1A_2	CT	TATGAT	AAGCT	CAAGG	ACCAGAT	GGAT	GT	TAT	TGGAACA	AAAT	TAT	TAGAT	CTC	CGT	TT	GGAA	CGGAT	AGCT	AACTT	AGG	-	-	AAGCA	AT	TGCA	TT	GAG	G	CAGGA	T	ACGAT	GCT	GAAGC	2240		
Ng_APL1A_3	CT	GATGAT	AAGCT	CAAGG	ACCAGAT	GGAT	GT	TAT	TGGAACA	AAAT	TAT	TAGAT	CTC	CGT	TT	GGAA	CGGAT	AGCT	AACTT	AGG	-	-	AAGCA	AT	TGCA	TT	GAG	G	CAGGAG	ACGCT	GAAGC	2093				
Ng_APL1B_1	CGGAT	GCT	AAGCAGA	AGG	-	-	AAACGGAG	CACCT	GGAACAGGAAAA	CATT	GC	ACT	T	GAG	CG	CAGTT	GGATA	AATA	AAGAA	T	CAAT	GC	GAT	CT	GTT	GAG	CAG	CT	GAC	GT	GCT	GAAGC	1893			
Ng_APL1B_2	CGGAT	GCT	AAGCAGA	AGG	-	-	AAACGGAGG	ACCT	GGAACAGGAAAA	CATT	GC	ACT	T	GAG	CG	CAGTT	GGATA	AATA	AAGAA	T	CAAT	GC	GAT	CT	GTT	GAG	CAG	CT	GAC	GT	GCT	GAAGC	1896			
Ng_APL1B_3	CGGAT	GCT	AAGCAGA	AGG	-	-	AAACGGAGG	ACCT	GGAACAGGAAAA	CATT	GC	ACT	T	GAG	CG	CAGTT	GGATA	AATA	AAGAA	T	CAAT	GC	GAT	CT	GTT	GAG	CAG	CT	GAC	GT	GCT	GAAGC	1896			
Ng_APL1C_1	CGGAT	GCT	AAGCAGA	AGG	-	-	AAACGGAGG	ACCT	GGAACAGGAAAA	CATT	GC	GCT	T	GAG	CG	CAGTT	GGATA	AATA	AAGAA	T	CAAT	GC	GAT	CT	GTT	GAG	CAG	CT	GAC	GT	GCT	GAAGC	2384			
Ng_APL1C_2	CGGAT	GCT	AAGCAGA	AGG	-	-	AAACGGAGG	ACCT	GGAACAGGAAAA	CATT	GC	GCT	T	GAG	CG	CAGTT	GGATA	AATA	AAGAA	T	CAAT	GC	GAT	CT	GTT	GAG	CAG	CT	GAC	GT	GCT	GAAGC	2384			
Ng_APL1C_3	CGGAT	GCT	AAGCAGA	AGG	-	-	AAACGGAGG	ACCT	GGAACAGGAAAA	CATT	GC	GCT	T	GAG	CG	CAGTT	GGATA	AATA	AAGAA	T	CAAT	GC	GAT	CT	GTT	GAG	CAG	CT	GAC	GT	GCT	GAAGC	2354			

