```
SLap_dup          1 GCTATCC---AGCGCCGCTCCGTCTCGCAGGCGGTAAACCAGATGTTGCAGCTCCAGCAGATGGATATGTGTGCGGATCCTCCATCGCGCGGGCTTG---------- 94
SLap              1 ACCGTGCTGAGGCGTTCGTACGCCTCGCAGGCCATCAACCAGATGCTGCAGCTGCAACAGATGGACATCTGTGCGGATCAGCCCTCACGCGGCTTGGTGATCGGTGT 107
SLap_Y_consensus  1 GCTATTC---AGCGCCGCTCCGCCTCGCAGGCGGTAAACCAGATGTTGCAGCTCCAGCAGATGGACATGTGTGCGGATCCTCCATCCCGCGGACTTGTGGTCGGCGT 104

SLap_dup         95 -------------CGGACCGCAATGATGCTGGCATCCTCACCGCGGCCGGTTGGCGGTACAATGTCCAGAAGACTGCAGGCCTATTGTTAGAGGTTCTCCGCATGT 187
SLap            108 CTTCGCGGATGAGGAGGACAAGAACGATGCCGGCATCCTGACACCGGCCGGTTGGCGGTACAACGTGACCAAGACCAACGGCCGCCTCATCCAGGTCCTGCGTATGT 214
SLap_Y_consensus 105 GTTCGCCGACGAAACGGACCGCAATGATGCTGGCGTCCTCACCGCGGCCGGTTGGCGGTACAATGTCCAGAAGACTGCCGGCCGATTGCTAGAGGTCCTCCGCATGT 211

SLap_dup         188 CCGGACCCATGCGCAAGCGGGGCGAGGCTCGCCTTTTCTTTGCGATCGAGCCAGAGCGCATCCCCTGTTACTCTGTGGTGGCTGTGGTCGGCCTCGGCAAGGAGTGC 294
SLap             215 CCGGACCCATGCCCAAGCGGGGCGAGGCCCGTCTGCTCTTCGCGATCGAGCCAGAGCGCATCCCCTACTACTCTGTGGTGGCTGTGGTCGGCCTCGGCAAGGAGTGC 321
SLap_Y_consensus 212 CCGGACCCATGCCCAAGCGGGGCGAGGCTCGCCTTTTCTTCGCGATCGAGCCAGAGCGCATCCCCTATTACTCTGTGGTGGCTGTGGTCGGCCTCGGCAAGGAGTGC 318

SLap_dup         295 CTCGGCTACAATCCCTACGAGGTGCTCGACGAACAGAAGGAGGCGATCCGTCGCTCCGTGGCCGCCGCCTGCCGCATCCTGGCCGAGCTGGACACCGACAGAATCGA 401
SLap             322 CTCGGCTACAATCCCTACGAGGTGCTCGACGAACAGAAGGAGGCGATCCGTCGCTCCGTGGCCGCCGCCTGCCGCATCCTGGCCGAGCTGGACACCGACAGAATCGA 428
SLap_Y_consensus 319 CTCGGCTACAATCCCTACGAGGTGCTCGACGAACAGAAGGAGGCGATCCGTCGTTCCGTGGCCGCCGCCTGCCGTATCCTGGCCGAGCTGGACACCGACAGAATCGA 425

SLap_dup         402 AGTTGAAAACTGCGGCCACGCCGAGTCCGCCGCCGAGGGGGCCGCGTTGGGGATCTGGCTCTACCAGGAGCTGCGCAACCCACAGAACAGGATTCCAGTGCCGTCGC 508
SLap             429 AGTTGAAAACTGCGGCCACGCCGAGTCCGCCGCCGAGGGGGCCGCGTTGGGCATCTGGGCCTATCAAGAGCTGCGAGACCCCAAGCAACGCGTCTCCGTACCGTCCA 535
SLap_Y_consensus 426 AGTTAAAAACTGCGGCCACGCCGAGTCCGCCGCCGAGGGGGCCGTATTGGGCATCTGGCTCTACCAGGAGCTGCGCAACCCACAGAACAGGATTCCAGTGCCGTCGC 532

SLap_dup         509 TGGACTTATACGCAAGAAAAGACGAGTTCTGCGACCTCGAAGGACGGCGCATTGGTCTGCAGAAGGCAGCCACCCAGAACCTGACGAGACAGCTGCAGGAGATGCCC 615
SLap             536 TTGATTTGTTTGCCACCCCAGATGATATTTGCGACATCGAAGGATGGCGCATTGGTCTGCAGAAGGCAGCCGCCCAGAACCTGACGCGGCAGCTGCAGGAGATGCCC 642
SLap_Y_consensus 533 TGGACTTATACGCAAGAAAAGACGAGGTCTGCGACCTCGAAGGATGGCGTATTGGTCTGCAGAAGGCAGCCGCCCAGAACCTGACGAGACAGCTGCAGGAGATGCCC 639

SLap_dup         616 TCCAACCTCCTCCAACCTTTA-----------------------------------------------TGTCAATAG-----------------------------------------------
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3APsec             1 AGGCAAAAACAATCAAAATCAAGTATTTAAAACAAGACAGTTAAGTAGAAAATTGATTCATTAATCGGATAAAACTATGTGGGCAGGACTGAGAGATCTAGATAT 105
3APsec_dup           ----------------------------------------------------------------------------------------------------
3APsec_Y_consensus   ----------------------------------------------------------------------------------------------------

3APsec           106 CTAAAAATATTCGACGGAATATCAAAATTGTTTCTGCTTCGAACTGTATTGGAAAAAGCAATAATGCAGCTGGCTGGATGACAACAAAGCAATAATATACGTCCA 210
3APsec_dup           ----------------------------------------------------------------------------------------------------
3APsec_Y_consensus   ----------------------------------------------------------------------------------------------------

3APsec           211 GTCCACATCATTGCAACGCGACTGTCCCTGCATGGAGCAGACCAAGATCCACGCCCGCATACAGCCAAAGCATGTCTATTTTCAAGGCGCGGTATGGACGACACA 315
3APsec_dup           ----------------------------------------------------------------------------------------------------
3APsec_Y_consensus   1 ------------------------------------------------------------------------CATGTCTATTTTCAAGGCGCGGTATGGACGACACA 35

3APsec           316 AAAATGTGATGTGTTTTCGGGAATTAAGAACAAAAGATTGTTATCCCCCCTGTATCTTTCAGTGTAAAAGAGTTTGAGTTTGATGATGCGCTGGCCCAGGATGTG 420
3APsec_dup         1 ----------------------------------------------------------TGTATCTTTCAGAGTAAAA------GAGTTCGATGATGCGCTGGCCCAGGATGTG 49
3APsec_Y_consensus 36 AAAATGTGATGTGTTTTCGGGAATTAAGAACAAAAGATTGTTATCCCCCCTGTATCTTTCAGTGTAAAA------GAGTTCGATGATGCGCTGGCCCAGGATGTG 134

3APsec           421 GTTGACCTAAAGGAGCTGCGCAGACTTACGTTTAATGGTGGGATATCACACTTCTGATAGGCTTAGCAATTCATGGACATGAATCCAATCCAATCCAATCCACAG 525
3APsec_dup        50 GTTGACCTAAAGGAGCTGCGCAGACTGACGTTTAATGGTGGGATATCACACTTCTGATAGGCGTAGCAGTTCATGGACATG-----AATCCAATCCAATCCACAG 149
3APsec_Y_consensus 135 GTTGACCTAAAGGAGCTGCGCAGACTGACGTTTAATGGTGGGATATCACACTTCTGATAGGCGTAGTAATTCATGGACATG----------------AATCCACAG 224

3APsec           526 GTGTGCCCGATGTACAAAGCTTCCGTGCACTCAGCTGGAAACTGCTGTTGGGCTACTTGGGACCAAGACGCAGCAGTTGGACGACCACGCTGGCCCAGAAGCGAG 630
3APsec_dup       150 GTGTGCCCGACGTACAAAGCTTCCGTGCACTCAGCTGGAAACTGCTGTTGGGCTACTTGGGACCAAGGCGCAGCAGTTGGACGACAACGCTGGCGAAGAAGCGAG 254
3APsec_Y_consensus 225 GTGTGCCCGATGTACAAAGCTTCCGTGCACTCAGCTGGAAACTGCTGTTGGGCTACTTGGGACCAAGGCGCAGCAGTTGGACGACCACGCTGGCCCAGAAGCGAG 329

3APsec           631 CCCTGTACAAGCAGTTCATTGAGGAATTGGTACTCCCCCCGGGACACAGCTGCAATGGAGCTGGAGAAGGCGACGGGGACGGGGACGTCGCTGTTGATTCAAGGG 735
3APsec_dup       255 CCCTGTACAAGCAGTTCATTGAGGAATTGGTACTTCCCCCGGGACACAGCTGCAATGGAGCTGGA-------------------------------GTTTCAAGGG 329
3APsec_Y_consensus 330 CCCTGTACAAGCAGTTCA------------------------------------------------------------------------------------ 347

3APsec           736 GCGTTGGCCTACAAGATCATCCGCTTAGCGAGGGGCCAGAAAGCGCCTGGAACACATTCTTCAATGACAACGAATTTCTGCTGCAGATCGACAAAGATGTGAGGC 840
3APsec_dup       330 GCGTTGGC------------CCGCTTAGCGAGGGGCCAGAAAGCGCCTGGAACACATTAT------------------------------------------- 377
3APsec_Y_consensus 348 ----------------------------CGAGGGGCCAGAAAGCGCCTGGAACACATTCTTCAATGACAACGAATTTCTGCTGCAGAT----------------- 407

3APsec           841 GCCTGTGTCCCGACATCTCGTTCTTTCAACAGCCCACAGAGTATCCCTGTGACATTGTGGTGCACAGTAAAGGCGAGCACGGGCGGCGGCTTCACGAACGGGTAG 945
3APsec_dup           ----------------------------------------------------------------------------------------------------
3APsec_Y_consensus 408 ---------------------------------CCACAGAGTATCCCTGTGACATTGTGGTGCACAGTAAAGGCGAGCACGGGCGGCGGCTTCACGAACGGGTAG 479

3APsec           946 TGCCCACGGTGCTCAGCTCGGCGAACGTCGAGCGCAAGGGCTTGGGCATGACCAAGGTGAGTTTCGGTCGGAAATTGTGCTAGAAAATAAGCTCAAAGTTTGTTC 1050
3APsec_dup           ----------------------------------------------------------------------------------------------------
3APsec_Y_consensus 480 TGCCCACGGTGCTCAGCTCGGCGAACGTCGAGCGCAAGGGCTTGGGCATGACCAAGGTGAGTTTCGGTCGGAAATTGTGCTAGAAAATAAGCTCAAAGTTTGTTC 584

3APsec          1051 CATTATGCATACCATTGTGGACGTTTAGCAGCAAGTAAGTGACCCCCACTCAAGCGACACTCGATTTAATGAGCCTCTTTGCTCCCAATCAGATCAATTTAATCA 1155
3APsec_dup           ----------------------------------------------------------------------------------------------------
3APsec_Y_consensus 585 CATTATGCATACCATTGTGGACGTTTAGCAGCAAGTAAGTGACCCCCACTCAAGCGACACTCGATTTAATGAGCCTCTTTGCTCCCAATCAGATCAATTTAATCA 689

3APsec          1156 CAAAGCGTTCGGTGGAGACCTATGCCGCCATGGAGGACGGCCAGGAGGCCCACTGGGAGGTTGTGCAGCGCATCCTATTCATCTACGCCAAGCTGAATCCTGGCC 1260
3APsec_dup           ----------------------------------------------------------------------------------------------------
3APsec_Y_consensus 690 CAAAGCGTTCGGTGGAGACCTATGCCGCCATCGAGGACGGCCAGGAGGCCCACTGGGAAGTTGTGCAGCGCATCCTATTCATCTACGCCAAGCTGAATCCTGGCC 794

3APsec          1261 AGGGTTACGTACAGGGCATGAATGAGATTGTCGGACCCATCTACTATGTGATGGCCTCGGATCCGGATCTCTCGTACCGCGCCCACGCGGAGGCAGACTGTTTCT 1365
3APsec_dup           ----------------------------------------------------------------------------------------------------
3APsec_Y_consensus 795 AGGGTTACGTACAGGGCATGAATGAGATTGTCGGACCCATCTACTATGTGATGGCCTCGGATCCGGATCTCTCGTACCGCGCCCACGCGGAGGCAGACTGTTTCT 899

3APsec          1366 TCTGCTTCACGGCTCTAATGAGCGAGATACGCGACTTCTTCATCAAGACTCTGGACGATGCGGAGGGTGGCATAAAGTTCATGATGGGCCTGCTATCTAACATGC 1470
3APsec_dup           ----------------------------------------------------------------------------------------------------
3APsec_Y_consensus 900 TCTGCTTCACTGCTCTAATGAGCGAGATACGCGACTTCTTCATCAAGACTCTGGACGATGCGGAGGGTGGCATAAAGTTCATGATGGGCCTGCTATCTAACATGC 1004

3APsec          1471 TGAAGACTAAAGATATAGACATATACGAGCATCTGAAGAGCCAGGAGCTGCATCCGCAGTACTACAGCTTCAGGTGGCTCACCCTCCTGCTCTCGCAGGAGTTTC 1575
3APsec_dup        378 ----------------------------------------------------------TACACAGTACTACAGCTTCAGGTGGCTAACCCTCCTGCTCTCGCGGGAGTTCC 430
3APsec_Y_consensus 1005 TGAAGACTAAAGATATAGACATCTACGAGCATCTGAAGAGCCAAGAGCTGCATCCGCAGTACTACAGCTTCAGGTGGCTCACCCTCCTGCTCTCGCAGGAGTTTC 1109

3APsec          1576 CACTGCCCGATGTGCTGCGAA-TTTGGGATTCGGTATTCTCGGACGAGCAGCGCTTTAATTTTCTCATCAAAATCTGCTGTTCCATGATATTGTAAGCATGCGCT 1679
3APsec_dup        431 CACTGCCCGATGTGCTGCGAATTTTGGGATTCGATATTCTCGGACGAGCAGCGCTTTAATTTTCTCATAAAAATCTGCTGTTACATGATATTGTAAGCATGCGCT 535
3APsec_Y_consensus 1110 CACTGCCCGATGTGCTGCGAA-TTTGGGATTCGGTATTCTCGGACGAGCAGCGCTTTAATTTTCTCATCAAAATCTGCTGTTCCATGATATTGTAAGCATGCGCT 1213

3APsec          1680 GACTTTCTACTGATTCATTTGCATTTACTGATGTATTTACTGACTTATAGAATCCAAAGGGAAGCAATTTTGGAGAACGACTTTGCCTCGAATGTGAAGCTGCTG 1784
3APsec_dup        536 GACTTTCAACTGATTCATTTACATTTACTGATGTATTTACTGATTTATAAAATCCAAAGGGAAGAAATTTTGGAGAACGACTTTGCCTCGAATGTGAAGCTGCTG 640
3APsec_Y_consensus 1214 GACTTTCAACTGATTCATTTGCATTTACTGATGTATTTACTGATTTATAGAATCCAACGGGATGCAATTTTGGAGAACGACTTTGCCTCGAATGTGAAGCTGCTG 1318

3APsec          1785 CAAAACTATCCACCCATTGACATAAACGTTGTGATTACTCATGCAGTCTCCCTGGCGTAGCACTCACTTTTAGTGATACCACAGATATTACACACATATAATACC 1889
3APsec_dup        641 CAAAACTATCCACCTATTGACATAAAGGTTG------------------------------------------------------------------------ 671
3APsec_Y_consensus 1319 CAAAACTATCCACCCATTGACATAAACGTTGTGATTACTCATGCAGTCTCCCTGGCG------------------------------------------------ 1375

3APsec          1890 CGATTCCGGGTAGAGTCTGACAAAGCAATAATCCACAGTATCTGGTTATCATGTTCAATAGTTCGAAGCCCAGGACCCAACAAAAGATCGAACACTAGCGCTGTT 1994
3APsec_dup           ----------------------------------------------------------------------------------------------------
3APsec_Y_consensus   ----------------------------------------------------------------------------------------------------

3APsec          1995 TCTCTGTTTTATACGTTAAAATTTCATAATAAACGAATGTGCCGCATGTGTTTGTGTGGAGATTAAAAATGCGAAAACATATTTAACATAGAGTGATCATAGCTC 2099
3APsec_dup           ----------------------------------------------------------------------------------------------------
3APsec_Y_consensus   ----------------------------------------------------------------------------------------------------

3APsec          2100 AAGTGTAA                                                                                              2107
3APsec_dup           --------
3APsec_Y_consensus   --------
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Figure S6