

File S7. Comparison of *Ac* insertion sites from standard transposition in *p1* (Athma *et al.* 1992) and alternative transposition in *p2* (this study)

Intergenic sequences and introns are shown in plain type; Exons are shown in bold type; *Ac* insertion sites in *p2* are shown in blue type; *Ac* insertion sites in *p1* are shown in red type.

```

p2      TCCCCCAGTCCCACGTAACGGACAGGTCGGTCCGTAACGTGCACTCTACTAAACGCTAG 480
p1      CTGTTTAAGGGCTAAAATACAACG-----TGCACCTCTGCACTCTACTAAGCGCTAG 295
      .** * *..:*.**. * * .*****.*****

p2      TGCACGTACG---TACTCCGTCCGCTGCTATATTATGGCCGGCCGTGGCGTGCCTCTC 536
p1      TGTACGTACGTACGTACTCCGTCCGCTGCTATATTATGGCCGGCCGTGGCGTGCCTCTC 355
      ** *****

p2      TAGCCAGCACAGCACACACACTGGAAAGTGAAGCTGTAGTGAGACCTGTGCGACTGCCA 596
p1      TAGCCAGCACAGCACACACTGGAAAGTGAAGCTGTAGTGAGACCTGTGCGACTGCCA 415
      *****

p2      GCGTGTGTCCGCGG-----GTCGTCCGCCCGCACGGCCACCAACT 637
p1      GCGTGTATCCGCGCGCAAGGAGCGTAGCGCGGTCGTCCGCCCGCACGGCCACCAACT 475
      *****

p2      CCCTTGGACGCACGCGCGCACGCGACCAGCTGCTAGCCGTGCGCAAGTAG---TGCGAGC 694
p1      CCCTTGGACGCACGCGCGCGCACGCGACCAGCTGCTAACC GTGCGCAAGTAGTAGTGCGACT 535
      *****

p2      TCGCCGCCGCGCCAGGGTCGCTAGCTCGATTGG-AGGGACCAGCTGATACGACTCCGGTGT 753
p1      TCGCCGCCGCGCGGGATCGCTAGCTCGATCGATCGGGGGACCACATACGACTCCGGTGT 595
      *****

p2      G----- 754
p1      GGGCAGGGCGGCGGGCCGGGAACGCACGTGCTGCGAGCGAGGGCAGACGCTAG 655
      *

p2      -----GCGCGCATGGGGAGGGCGCCGTGCTGCGAGAAGGTGGGG 794
p1      CTGTTGCCGGGAGCTAGCCGGCGCGATGGGGAGGACGCCGTGCTGCGAGAAGGTGGGG 715
      *****

p2      CTCAAGCGAGGGAGGTGGACGGCGGAGGAGGACCAGTTACTTGCCAACTACATTGCGGGAG 854
p1      CTCAAGCGAGGGAGGTGGACGGCGGAAAGAGGACCAGTTACTTGCCAACTACATTGCGGGAG 775
      *****

p2      CACGGCGAGGGGTCCTGGAGGTCGCTGCCAAGAATGCAGG-TAACCAAAGCCGGCCGCG 913
p1      CACGGCGAGGGGTCCTGGAGGTCGCTGCCAAGAATGCAGGTAACCAAAGCCGGCCGCG 835
      *****

p2      CGCCATGCATCGCCACGTAGCATCAATCTCCGATCCATGCATATATGAGCTAGCTTCTTC 973
p1      CGCCATGCATCGCCACGTAGCATCAATCTCCGATCCATGCATATATGAG---CTTCTTC 891
      *****

p2      TTCGTCGCCGTGCTCGTCTTCTTAGCTAGTTAGGACGCGCATGCAGGCCTGCTCCGGTGC GG 1033
p1      TTCGTCGCCGTGCTCGTCTTCTTAGCTAGTTAGGACGCGCATGCAGGCCTGCTCCGGTGC GG 951
      *****

p2      CAAGAGTGC CGGCTCCGGTGGATCAACTACCTCCGGCGGACGTCAAGAGGGGGAACAT 1093
p1      CAAGAGTGC CGGCTCCGGTGGATCAACTACCTCCGGCGGACGTCAAGAGGGGGAACAT 1011
      *****

p2      CTCCAAGGAGGAAGAAGACATCATCATCAAGCTCCACGCCACCTCGGGAACAGGTAACA 1153
p1      CTCCAAGGAGGAAGAAGACATCATCATCAAGCTCCACGCCACCTCGGGAACAGGTAACA 1071
      *****

p2      ATAAGCGCGCCCTAATCTCAACGCTGATCGACTGTGCATCCGACTAGAGAGTAGTACTAC 1213
p1      ATAAGCGCGCCCTAATCTCAACGCTGATC-ACTGTGCATCCGACTAGAGAGTAGTACTAC 1130
      *****

p2      TACTACTTCCTTCTTTATGCATGG----GAGTCAATGCACGCAGTCCCGAAAACTTG 1268
p1      TACTACTTCCTTCTTTATGCATGGGATGGGAGTCAATGCACGCAGTCCCGAAAACTTG 1190

```

```

*****
p2 GTATACGTACTTCCTCCTTCACACGAAGAACGGAAATCTAGTCCAACAATATCAACTTTG 1328
p1 GTATACGTACTTCCTCCTTCACACGAAGAACGGAAATCTAGTCCAACAATATCAACTTTG 1250
*****

p2 ATCAAGACATTCATATAAAAATACAACACTACTTTCGCATATATATATGAAATATATT 1388
p1 ATCAAGCATTCATAT-----ATATATGAAATATATT 1283
*****

p2 TTATAAGAACTTCCATAAATATATAAATGTTGATAGTACTATAAATATAGTTGATT--G 1446
p1 TTATAAGAACTTCCATAAATATATAAATGTTGATAGTACTATAAATATAGTTGATTGAG 1343
*****

p2 AGAGTTTCTTAAATTGTGAGGTACCATGTATACTT--ATATATACTACTCAAACGCTTC 1504
p1 AGAGTTTCTTAAATTGTGAGGTACCATGTATACTTTTATATATACTACTTAAACGCTTC 1403
*****

p2 TCGACGTACAAATTTGGAGAAAAGGATTTCTGGCAGAAGACTAGAACAGTCAGCACAGAC 1564
p1 TCGACGTACAAATTTGGGAAAAGGATCTCTGGCACAAGACTAGAACAGTCAGCACAGAC 1463
*****

p2 AATAAAGGGCTACTCCGATGGAAATCTCGTTTTCATTCATAGGAG----AGCAGTGTAG 1619
p1 AATAAAGGGCTACTCCGATGAAATCTCGTTTTCATTCATAGGAGTATAGAGTAGTGTAG 1523
*****

p2 TAACAATTGCCCTGCTCTATATGCTCTCTCAATTACTGAAATCTTAGAGCAAGTATAATA 1679
p1 TAACAATTGCCCTGCTCTATATGCTCTCTCAATTACTGAAATCTTAGAGCAA----- 1574
*****

p2 ATGGATATAAGCCGGCTCAATATTGAGATTGATGAGAGAGAGAGCAGAATCGGACTGCAA 1739
p1 -----ATATTGAGATTGATGAGAGAGAGAGCAGAATCGGACTGCAA 1615
*****

p2 ACTTAAAGCCGGGCTTAGACACAGAACTAAAACTTTTTTG-TGAGAAAGACATGCAAA 1798
p1 ACTTAAAGTCGGGCTTAGACACAGAACTAAAACTTTTTTGTGAGAAAGACATGCAAA 1675
*****

p2 TCATAAATTAACAGTGAAGAGCTAACTACTATACGGATAG----- 1838
p1 TTATAAATTAATAGTGAAGAGCTAACCCTACACGGATAGGCTAATGTAAATCATAAATT 1735
* *****

p2 -----GCTAAGAAGTAGACTATAATGTTCCCTTAC 1867
p1 AATAGTAAAGAGCTAACTACTACAGATAGACTAAGAAGTAGACTATAAGGTTCCCTTAC 1795
*****

p2 TTACAACCAGCGGTTAGCTATATTATTAACCTGATCTTATAATTTTCGATGGCTGGCCCG 1927
p1 TTATAACCAGCGGTTGACTATATTATTAACCTGATCTTATAATTTTCGATAGCTGCCCG 1855
*** *****

p2 ATCGGTTGAGAGTTAAGACACCGTATACCATACACGTACACAGTACTAAATAAAGAATTA 1987
p1 ATCGGTTGAGAGTTAAGACACCGTATACCATACACGTACACAGTACTAAATAAAGAATTA 1915
*****

p2 AATGATGTAGGGGCACACGCTGCTGGAATTGAGGCGCGCAGCAGCAATAGTAGGCTAA 2047
p1 AATGATGTAGGGGCACACGCTGCTGGAATTGAGGCGCGCAGCAGCAATAGTAGGCTAA 1972
*****

p2 TGTCCTTTTTT-CTATGCTTGGTATGGGTTCCAATCGGCTTTATTATCACTGTTTAGCTA 2106
p1 TGTCCTTTTTTCTATGCATGGTATGGGTTCCCGATCGGCTT--TATCACTGTTTAGCTA 2029
*****

p2 CTGTAGTGATAATGTCCAAAAGATGGTTTCATCAGCGAAAAGACAAAAGAGAGAGAAGAG 2166
p1 CTGTAGTGATAATGTCCAAAAGATGGTTTCATCAGCGAAAAGACAAAAGAGAGAGAAGAG 2089
*****

p2 AGAAGAGAGAAGAGAGAAGAGAGAG--AGAAAGAAAGACTCCTATAAAGAGTAGTGTG 2223
p1 AGAAGAGAGAAGAGAGAAGAGAGAAGAGAGAGAGAGACTCCTATAAAGAGTAGTGTG 2149
*****

p2 CTATAGTGCTAGAATGGTGCATATTACTACAGTGCATATATGTGAGAAAGAACCGGAGCT 2283

```

p1 CTATAGTGCTAGAATGGTGCATATTACTACAGTGCATATATGTGAGAAAGAGCCGGAGCT 2209

p2 ATTGAGCTAATACAATCTATAGGGCCTAAAT---AGAGACATGGCTG-----AGG 2330
p1 ATTGAGCTAATACAATCTATAGGGCCTAAATTAATAGAGACATGGCTGAAAACAATATGG 2269
***** :**

p2 CCATCTGGTCCCTCCGATCGATGTGCTGTAGTATGTTTATGTACACGCGGGCTCTACGCA 2390
p1 CCATCTGGTCCCTCCGATCGATGTGCTGTAGTATGTTTATGTACACGCGGGCTCTACGCA 2329

p2 CGCTTGCTCTAGCATTGAGCAGTGTACTTTACTACACT---ATCAGTCCGGTCCTTGTC 2447
p1 CGCTTGCTCTAGCATTGAGCAGTGTACTTTACTACACTACTATCAGTCCGGTCCTTGTC 2389

p2 AGTCACTGGCTCAGCATGTGTCTCTGAAGTTGCCCGTACGTGTGGCAGCAGCCAAAAGGG 2507
p1 AGTCACTGGCTCAGCATGTGTCTCTGAAGTTGCCCGTACGTGTGGCAGCAGCCAAAAGGG 2449

p2 CGTGCTGCGTGTGAAGTTTACTGTCCAGTCAGATGCCTGTGATTTCCGAGGCCACGTGC 2567
p1 CGTGCTGCGTGTGAAGTTTACTGTCCAGTCAGATGCCTGTGATTTCCGAGGCCACGTGC 2509

p2 ACGAGCATGCATGACGCCAACATGGTATGATAGCCCTCTTTGTTTAGGCTTTTTTTTCGG 2627
p1 ACGAGCATGCATGACGCCAACATGGCATGATG-TGATGTTTGTTCGGCCTTTTTTTTAG 2568
***** .***** * . * ***** .*** ***** .*

p2 TTTATGGCCATCAAAATCTGTACAACTGTCAAACACTCAGCTTTTCAGCTCGCTTCTA 2687
p1 ATTTTGGCTACCAAAATCTGGTACAGACAGTCAAATATTCA-ATTTTATGCTCACTTCT- 2626
: ** : **** * ***** * ** : ***** * *** . **** ** * . *****

p2 AAAAAATCGATTTGGTAAAAATCAACAACAAAAGTCG-CATGAACACAAAATTGGTCGG 2746
p1 AAAAAATCGATTTGGTAAAAATCATCCAACAAAATCAACATAAACACAAAATCGGTCCG 2686
* . ***** : . ***** . * . * . ***** *****

p2 GTCGTTGCAATATAGTAGGATTCGGTCACTTCTAGATCATGAACCATATGTACACATTC 2806
p1 -ACGTTGCAATA--GTAGGAATCTATCACTTCTAGATTGTTAACCCATATAGACACATTA 2743
: ***** ***** : ** . ***** * ***** . * ***** . ***** .

p2 ATCTTTCTCCGCACATAATCC-CACAATGCTCAGATTATCTCCACAGCCAAATCTCT-G 2864
p1 ATCTTCTCCGCACATAATCTCACAATACTCATATTCTCTCTGCAGCCAAATCTTTTA 2803
***** ***** ***** . ***** * . ***** . ***** * .

p2 AAAAGCTGGTTAGAAAAAGTTC AACCAAACAGTCCCGATGATGCCCGCACTTCTTATG 2924
p1 AAAAATCGTAAAGAAAAAGATGAACCAAACAGGCTCGATGATGCTCGCACTTCTTATG 2863
**** . ***** . ***** : * ***** * ***** *****

p2 GCTTCGCATATGTGGCAACGGGGCGAACTAGGTTGCTTGATGTGGATGCAAATGCACC 2984
p1 ACTTCGCATATGTGGCAAGAGGGGCG-AAATAGGTTGCTAACTGTGGATGCAAATGCACC 2922
. ***** . ***** * . ***** : . *****

p2 CTATAAAATACAATTTCTATAAATTCAGTTAAATGTCACATATATGCACTCCTACAAA 3044
p1 CTGTAATAATACAATTTCTATAAATTCAGTCAAAATTCACATATATGCACTCCTAGAAA 2982
** . ***** * . ***** ***** *

p2 AAAGTTCTTATGTACCCACAAGGCTAAATACACCCTCTCAATCTTACTCTAGCTTCGC 3104
p1 AAG-TTCTTATGTACCCACAAGACTAAATACACCCTCTCAAT--TATAATCTGGCTTCGC 3039
** . ***** ***** . ***** * . ***** . *****

p2 CACTGTGGTAATGATGAGGTATAAGCTAGTGGGGTGTGGTATATATGACTAATTT 3164
p1 TATTATG--TGGTAATGAGGTCTAAAAGTAG-GGGGTGTTTGGTTTATATGACTAATTT 3096
* * . * . : . * . ***** . ***** . ***** ***** . *****

p2 TTAGTCCTTCATTTTATCTATTTTAGTTTCTAAATGTCAAATACGAAAATAAAATAG 3224
p1 T-----AGTTTCTGTATT----- 3109
* ***** . : **

p2 AGTTTTAACTTTCCGATTTTCCCAATTTAAAGACTAACATAAAAATAAAATAGGTGGGAT 3284
p1 -----TGACAATTTAAGGACTAAAATAAAAATAAAATAGATAGGCT 3149
** . ***** . ***** . ***** . * . * . *

p2 AAAAATTAATCCTCAGAAACCAAACTCTCTAAGTTGATCCGTCATATATATAGTCGTT 3344
p1 AAAAATTAATCTTTAGAAACCAAACTCTCTAAGCTGATCCGTCATATAT----TCGTT 3205
***** * *****

p2 ACATTACATCTCTAAGACGAGAAGCAGCAGCAGGAGAAATGCTCGATCTAGGCACCTTC 3404
p1 ACATTTTCATCTCTAAGACGAAAAGCAGCAGCAGGAGAAAT----GATCTAGGCACCTTC 3261
***** *****

p2 TCGTGCTCAAAGATATGTGCAACTGAAGGAAGATTAGAAAGTACTACTGAGCAGTACTG 3464
p1 TCGTGCTCAAAGATTTGTGCAACTAAGGAAGATTAGAAAGTACTACTGAGCAGTACTG 3321
***** *****

p2 TGATAGCGTCATGCATGCATATATATACACACAAACACCTTCCACTCCATAAAATGCAGT 3524
p1 TGATAGCGTCATGCGTGCATATA-----CACACACACCTTCCACTCCATAAAATGCAGG 3375
***** *****

p2 TTTTTTTTTGTTACATCAGTTTTGTTTAACT-TTTTTTCCAAGCAACTTATGTGATTT 3583
p1 GTTTTTTTTGCTCCATCAGTTTTGTTTAACTATTTTTTCCAAGCAACTTCTTTGATTT 3435
***** * *****

p2 TGA CTG----- 3589
p1 TGACCAGTGGCGGGACGAAAGTCCAGGTGAGGCCAATCCGTAATAAAGAAATCACAAAGAA 3495

p2 -----A 3590
p1 AAAATGCTAAACTATAAGTGGTTTTTTGGTAATAGCATGAAATTAAGTTGTAATATCATG 3555

p2 ACTTGGATAAAAATAT----- 3606
p1 ACTATTATAAAAATAATGTGGATATCGAAAATCTTTTTAGCGACGCCAAATCATCGATAGA 3615
: **: **

p2 ----- 3675
p1 AAATTC AATCTACAATTAGAAGAAAAAGTATTAGGTAAGCATCAATGTAAGTAAAAGACA

p2 ----- 3735
p1 AAACTATATAGAAAAACATCGAAAACACCATTAAACCATCAATCTTGTGGTTGTGGCAG

p2 ----- 3795
p1 CTGCACTCTAGTGC GGGCCGTGGCCGAGTGGAGGCAGGAAGACGAGCAGCAAGCTAGC

p2 -----ACTGGCCAT----- 3615
p1 GACAGTGCCTGACAGCTGGCGATGACGGTTGGGTGGCGGCCAACGATGATGAACTGAC 3855
.***** **

p2 ----- 3915
p1 GGTGGACGCTCAATTGGACAGCGGGCACAACGCTAGGACGAGCGCTAAGCGGGGGTTGGA

p2 ----- 3975
p1 TGCTACAACGTCGGTTGATGCC TTTCTCATCTGTGTTTTATTTCGATATAGGTCGTGA

p2 ----- 4035
p1 CCTAAGATGATGGCTAGATCTGTGGTTAGTCGATGGTATGATGTGGTGGACCCGGTG

p2 -----AGTATTTATAATA---- 3628
p1 TTTATCTAATTTAGTCGCATATACCTTATATTTTTTATTTTATAGTATATATAAAAGGTA 4095
*****:*****:*

p2 ----- 4155
p1 GGTATAAACAGTTC AAAAATTAAGGTGGCGCCATGGCCTACTTTGCCACATTGTGGAT

p2 -----TAATACCC 3636
p1 CCGCCCTGATTTTGACTGAACTTGGATAAAATATACTGGTCATAGTATTTATAATACCC 4215

p2 -----
p1 GTTAATACACAAAAATAAGTCAGTTTTGGATAAAATAAATACATATAGAAGACATGAATT 5322

p2 -----
p1 GATATGCAGGGAGTATAAATAAATACATATAGGAGAACATGAATCTGTGAACTAACACGG 5382

p2 -----
p1 CTGGGAGCTAGGCAGCTAGCAGCTAGCGCCTAACAGCTGGGAGCCTAACAGCTAGCAGCT 5442

p2 -----
p1 AGCAGCCAATCAAAACAAGGCGACAAGGCGCATGCAGTGAGATCAAAAATCTGTTAATGC 5502

p2 -----
p1 CAGCCATGCAGGGAGTATAACACGGCTGGGCAGCAAGGCGCATGCATCAAAACAAGGCGA 5562

p2 -----
p1 CAGCAACAGCCCATGCATCAAAACAGTAGTGAATAATAGCAAATTAATAGCCCATGCAC 5622

p2 -----
p1 GAAGTAAATAAATAATCTTTAAATACCTCATCCATATGATTTCATGATTTGTTGCAGCAG 5682

p2 -----
p1 CAATAACAGAGTCTAGCACCTCGAGATCACCAATCATGTGGAAAATATGTAGCACCTT 5742

p2 -----
p1 GAATGACACAAATATGCATCAATATAAGTAAAATAAATGTTGAATAACTATAAATTGGAA 5802

p2 -----
p1 CTTCAATTATAACATATATGCATTCACCTTTTCTAGATGCTGCTACCCAATCTTTTGTGCA 5862

p2 -----
p1 TATCAAAGCTTCAACAATCTCCGAACCAAGACGATTGCGGTAAGGATCAACAACACGACC 5922

p2 -----
p1 ACCAGCACTGAACGCAGACTCAGAAGCAACAGTTGACACTTGATTGCTAGCACATCCCT 5982

p2 -----
p1 TGCAATTTGGGTGAGAATAGGATATCTGCAACCCTTCCCCTCCACCATGATAAAATATC 6042

p2 -----
p1 AAACTGACCACTATGCTTCAAAGGGGTTCAGACATATATTTATCCAATTCATTTGACTC 6102

p2 -----
p1 TACTTGATCATAATCCTTCAACTCATGCAAATAGTTTTGAAATTCATCATCTTCATTTTC 6162

p2 -----
p1 CATCAAGGTATCATCCATACTATCATTAGTAGTTGTCTTTGTCTTTGGAGCTGAAGGACT 6222

p2 -----
p1 ACAACTAGAATAGAATTGATACAATTTCTAATGACCCTAACAAAGTCATCTACATGAAC 6282

p2 -----

p1 TTTGTATGAATCACCATGAAATTTTTTCATATAGAACTCAATCAATATTTCTTGTACCT 6342

p2 -----
p1 AGGGTCAAGGAAGCATGCTACAGCTAGTGCAATATTAGACACTTTCCAATATTTCTCAA 6402

p2 -----
p1 CTTTTCACTCATTGCAACGGCCATTCTCCTAATGACAAATTTTCATGAACACACCATTG 6462

p2 -----
p1 GTCAATCAAATCCTTTATCTCACAGAAACCTTGTAAATAAATTTGCAGTGAATATTG 6522

p2 -----
p1 AGTACCAGATAGGAGTTCAGTGAGATCAAAAACTTCTTCAAACACTTAAAAAGAGTTAA 6582

p2 -----
p1 TGCCATCTTCCACTCCTCGGCTTTAGGACAAATTGCATCGTACCTACAATAATTGACATT 6642

p2 -----
p1 TGATTAATTGAGAATTTATAATGATGACATGTACAACAATTGAGACAAACATACCTGCGA 6702

p2 -----
p1 GGATCACTTGTTTTAAGCCTTATTAGTGCAGGCTAGTAATTAGTTAGTAATTAGTTAAGC 6762

p2 -----
p1 TAGTAATTAGTTAAGCTGCTTTCACAAACCATGTTTCCATGACTGTGTGGCACCGCTAGC 6822

p2 -----CCACATGGTGTGCGAGAGCTAGCGGTGCCACA 4173
p1 TCTCGCAACACCATGTGGTGTAGTCCCACATGGTGTGCGAGAGCTAGCGGTGCCACA 6882

p2 CACTCATGGAACATGGTTTGTGAAAGCAGCTTAATTAATTACTAGCTGACAGTGAGAG- 4232
p1 CAGTCATGGAACATGGTTTGTGAAAGCAGCTTAATAATTACTAGCTAGCTGTGAGAGA 6942
** ***** . * : *****

p2 -----TGAGAGGACCACGCGAAATAAACGACAATCT-- 4263
p1 GTCGTCAGCGGCTAGCGGAGA GTGAGTGAGAGGACCACGCGAAAGAAACGACAATAATCT 7002
***** . :

p2 -----GGTCCAACACTCCCTCTTCATTCAAGCTAGCTA 4296
p1 CCGCTTCGTTTTTCGTTACCGATCTCGAGGTCCAACACTCGCTCTTCATTCAAGCTAGCTA 7062

p2 GCGCTGGGAGCGAACTCGCGTCGCATGGCAGAGCCTGCCTGCTGCCGAGCGGACAGGTCA 4356
p1 GCGCTGGGAGCGAACTCGCGTCGCATGGCAGAG-CTGCCTGCTGCCGAGCGGACAGGTCA 7121

p2 CGGTCCAT-----GTCCGTGGCGTTG---GCGTCAGGTCCATTTTCGCTTT 4398
p1 CGGTCTTCTTGACGCACGCACAGTCCATGGCGTTGGTTGGCGTCTGTCATTTTCGCTTT 7181
***** :

p2 GCTGCCTCGCCATCACCGCCGCGGCTACTGTGCAAAGCGCGCATTTGGCTAGCTTCCCTG 4458
p1 GCTGCCTCGCCATCACCGCCGCGGCTACTGTGCAAAGCGCGCATTTGGCTAGCTTCCCTG 7241

p2 TTGCCTTGATCTGATCATAGAGGGTCCATGTCCGTGGCACACAGTGGGATTAATGACGG 4518
p1 TTGCCTTGATCTGATCATAGAGGGTCCCTGTCCGTGGCAAACAGTGGGATTAATGACGG 7301
***** . ***** . *****

p2 GCCCACGCCGCGCCTCCCTAATGATTTCCCCCGCCTTAACGTTGACACTGCGGACGGTGA 4578
p1 -CCACGCCGCGCCTCCCTAATGATTTCCCCCGCCTTAACGTTGACACTGCGGACGGTGA 7360

p2 GAGGCGGGCTGTGGACGTACGGCGAGATCTATCGGGGGCCCATCGTCCTTCGCGAACGA 4638
p1 GAGGCGGGCTGTGGACGTACGGCGAGATCTATCGGGGGCCCATCGTCCTTCGCGAACGA 7420

p2 TCGGTACATTTAGCGCCATATATAAACACACGCCGGCACATGATTACTACGGCCTATA-- 4696
p1 TCGGTACATTTAGCGCCATATATAAACACACGCCGGCACATGATTACTACGGCCTATATA 7480

p2 ---CGTCGTGAGCGGGCGGATCAATGAGTGAGCTAGTTTGTGACCAAATGTGCGATC 4752
p1 CGCGCGTCGTGAGCGGGCGGATCAATGAGTGAGCTAGTTTGTGACCAAATGTGCGATC 7540

p2 AAGTTGCATCAGA-----CAGTAGAGTACTGTATACTCTCTCTATATATATAT----- 4800
p1 AAGTTGCATCAGAGATCAGACAGTAGAGTACTGTATACTCTCTCTATATATATACTCCCT 7600

p2 -----
p1 CCGTTTCTTTTTATTTGTCGCTGGATAGTGTAAATTTTACACTATCCTGCGACAAATAAAA 7660

p2 -----GTTATATGTAAGTACTAGGCAGGCTAAGAAACACGATAGATACCACGCATTCCG 4850
p1 AGAAACGGAGGAGTATGTACTAGGCAGGCTAAGAAACACGATAGATACCACGCATTCCG 7720
* : *****

p2 TTCTCATTACGAAGCTGCAGCT-----GCCCAACCAGCAGCGATGATCACGTACGCT 4902
p1 TTCTCATTACGAAGCTGCAGCTGCCCAAGTGCCCAACCAGCAGCGATGATCACGTACGCT 7780

p2 CACCATCCTGCGTCCTTGCGGTTTAAATTAATTACGTATGTATCCGCATCCGCATGCAGG 4962
p1 CACCATCCTGCGTCCTTGCGGTTTAAATTAATTACGTATGTATCCGCATCCGCATGCAGG 7840

p2 TGGTCCCTGATCGCCAGCCACCTCCCCGGCCGAACAGACAACGAGATTAAGAACTACTGG 5022
p1 TGGTCCCTGATCGCCAGCCACCTCCCCGGCCGAACAGACAACGAGATCAAGAACTACTGG 7900

p2 AACTCGCACCTCAGCCGGCAGATCCACACGTACCGCCGGAATACACCGCCGGGCCGGAC 5082
p1 AACTCGCACCTCAGCCGGCAGATCCACACGTACCGCCGGAATACACCGCCGGGCCGGAC 7960

p2 GATACCGCCATCGCCATCGACATGAGCAAGCTGCAGAGCGCCGACAGGCGGGCGGGCGGC 5142
p1 GACACCGCCATCGCCATCGACATGAGCAAGCTGCAGAGCGCCGACAGGCGGGCGGGCGGC 8020
** *****

p2 AGGACCCCGGGCGGGCCGCGGAAGACTAGCGCCAGCAGGACCAAGCATTCCGACGCCGAT 5202
p1 AGGACCCCGGGCGGGCCGCGGAAGACTAGCGCCAGCAGGACCAAGCAGGCGGACGCCGAT 8080

p2 CAGCCCGGGCGGGCGAGGCGAAAGG-----CGCGGCGGCGTCGAGCCCGGGCACAGCGAC 5256
p1 CAGCCCGGGCGGGCGAGGCGAAAGGCGGGCCGCGGCGGCGTCGAGCCCGGGCACAGCGAC 8140

p2 GCGGTGAACCCGGGCCCGAACCAGCCCAACAGCAGCAGCGGCAGCACGGGCACGGCCGAG 5316
p1 GTGGTGAACCCGGGCCCGAACCAGCCCAACAGCAGCAGCGGCAGCACGGGCACGGCCGAG 8200
* *****

p2 GAGGAAGGGCCAGCAGCGAGGACCGGAGCGGGCCGTGGGTGCTGGAGCCGATAGAGCTC 5376
p1 GAGGAGGGCCAGCAGCGAGGACCGGAGCGGGCCGTGGGTGCTGGAGCCGATAGAGCTC 8260

p2 GGGGACCT---CTGGGGGAGGCCAGCAGGATGGACGCCCTGATGCCTATCGGGCCC 5433
p1 GGGGACCTAGTCTGGGGAGGCCAGCAGGATGGACGCCCTGATGCCTATCGGGCCC 8320

p2 GGCGGCCACGACTCGGCTGCCCTCCAAGGGCTTGGCGGGTTCGGCGGCGAGGCCAGGTG 5493
p1 GGCGGCCACGACTCGGCTGCCCTCCAAGGGCTTGGCGGGTTCGGCGGCGAGGCCAGGTG 8380

p2 GACGACCTGTTTCGACATGGACTGGGATGGCTTCGCGGCCATCTGTGGGGCGGGCCGGAG 5553
p1 GACGACCTGTTTCGACATGGACTGGGATGGCTTCGCGGCCATCTGTGGGGCGGGCCGGAG 8440

```

p2          CAGGACGACCACAGCGCGCAGCTGCGGCAGGCCGCCGAGCCGATGGAAGCGGCTGCTGTT 5613
p1          CAGGACGAGCACAGCGCGCAGCTGCGGCAGGCCGCCGAGCCGATGGAAG-----TT 8491
           *****
           *****

p2          GCCGCTGCCGCTGCCGCTGCGACGGCGGCCTGCACCCCGGACGATCGCGAGCTGGAGGCG 5673
p1          GTCGCTGCTGCTGCTGCTGCGACGGCGCCGCCGACCCCGGACGATCGCGAGCTGGAGGCG 8551
           ** **
           *****

p2          TTCGAGACTTGGCTCCTGTCCGACTCGTTCTGACGGCTCCGGTCATCGGACCGATCAGAC 5733
p1          TTCGAGACTTGGCTCCTGTCCGACTCGTTCTGACGGCTCCGGTCACCGGACCGATCAGAC 8511
           *****

p2          AGACAGACAGACCAACCAAGGTG-GCCCGGCCATATGGTCGACGCCG-CTAGTAGGCGTT 5791
p1          AGACCAATAATGGGTCACGTGCTCGCTCGCTCGCTCGCTCGCTCGGTCGCGTGGGTTCTT 8671
           ****.*.:.* .. .* ** ** * .: * * . * * . * * . * . * . * . *

p2          G-CTCGTGTGTACAGTTTTT-----TTCTTT----- 5818
p1          GTCAGATGGCCAAATAATGGGAAAAAATCTACGGCGCAGGCCGTAAGCCACCA 8731
           * ** . ** . * . : * : * : * * : * * * :

p2          -----TTTATTGTAGAT-----GTTGTTCTTAG----- 5842
p1          CCGTGCCTCCTGATGTCGATGCCTGCCGCGTGGAGCTCTTGCATCTAACGCTCCAC 8791
           * * . : * * . * * * * * * : * * * * .

p2          -----CTCGTGCTGACG-----TGCTGTTTCG-----TGATGAC 5872
p1          GACAATCACCCCTCCAGACGGCTCGAATTACATACGACAGGATCGGCTCCGCTCTACTCC 8851
           * * * * * : * * * * * . : * * : * * * * * * . * * . *

p2          GTACTG---GCATGTAGAATAG-----AGAGCAGAGATCGTATGGATGGCGGTG-- 5919
p1          GTTCTGTTTCGCTTCTGCTTTAGGTGCGTGCCTAGCAGATGGTGAGGCGGCGTCGCGCGGC 8911
           ** : * * * * * * * * * * . * * * * * * * * * * * * * * * *

p2          -----TAAAGGTAGTCT-----CCCGCC 5938
p1          CCTCCCAGCGGCTCGCCGGCCGCGCTACGGGGCCTGCTGCAGCAGCCCCTCCTCCACGCC 8971
           * * . * * * . * * * * * * * * * * * . * * * *

p2          GGTGAAG-----TGAAGACAAGTGTCCGATT-----TTGTG----- 5969
p1          TGTAAGAGACTTTGTATTTACCTGTTTGTGTTGTTGTGCTTTTGTGCAATGGAATAACAATG 9031
           ** . * * * * * : * * * * * * : * * * * * * * * * * *

```