

Additional file 3: Polymorphisms detected in 73 BAC end sequences.

>001-1A_T7 vs. chr2: 114,458,029-114,458,998 (+), 549 bp overlap

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1 TTAACCATCAGGGAAATGCAAATCAAAACAACCCCTGAGAGTCCATCTCACACCAATCAGAATGGCTAAGA 001-1A_T7
  TTAACCATCAGGGAAATGCAAATCAAAACAACCCCTGAGAGTCCATCTCACACCAATCAGAATGGCTAAGA chr2

71 TCAAAAAATTCAGGTGACAGCAGATGCTGGCGAGGATGTAGAGAAAAGATGAACACTCCTCCACTGTTGGTG 001-1A_T7
  TCAAAAAATTCAGGTGACAGCAGATGCTGGCGAGGATGTAGAGAAAAGATGAACACTCCTCCACTGTTGGTG chr2

141 GGATTGCAAGCTTGTACAACCACGCTGGAATCAGTCTGGGGATTCTCAGAAAAATTGGACATGATACTA 001-1A_T7
  GGATTGCAAGCTTGTACAACCACGCTGGAATCAGTCTGGGGATTCTCAGAAAAATTGGACATGATACTA chr2

211 CCGGAGGATCCCGCAATACCTCTCCTGGGCATATATCCAGAAGATGTTCCAAC TAGTAAGAAGACACAT 001-1A_T7
  CCGGAGGATCCCGCAATACCTCTCCTGGGCATATATCCAGAAGATGTTCCAAC TAGTAAGAAGACACAT chr2

281 GCTCCACTATGTTTCATAGCAGCCTTATTTATAATAGCCAGAAGCTGAAAAGAACCCAGATGCCTCTCAAC 001-1A_T7
  GCTCCACTATGTTTCATAGCAGCCTTATTTATAATAGCCAGAAGCTGAAAAGAACCCAGATGCCTCTCAAC chr2

351 AGANNNNNGGATACGAAAC-TGTGGTACATTTACACAATGGAGTACTACTCAGCTATTAAGAAATGAA 001-1A_T7
  AGAGGAATGGATACGAAACAAATGTGGTACATTTACACAATGGAGTACTACTCAGCTATTAAGAAATGAA chr2

420 TTTATGAAATTCCTAGGCAAAATGTTGGACCTGGAGGGCATTATCCTGAGTGAGGTAACCCAATCACAA 001-1A_T7
  TTTATGAAATTCCTAGGCAAAATGTTGGACCTGGAGGGCATTATCCTGAGTGAGGTAACCCAATCACAA chr2

489 GAACTCAAATGATATGTACTCACTGATAAGTGGATATTAGCCAGAAACTTAGAATAACCA 001-1A_T7
  GAACTCAAATGATATGTACTCACTGATAAGTGGATATTAGCCAGAAACTTAGAATAACCA chr2
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>001-1A_SP6 vs. chr2: 114,474,592-114,474,817 (-), 227 bp overlap

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1 GTCTCTCAAAACACACAGGCAGGTAGACAGACAGGCAGACAAATGAAAGTTGAGTGAATGGGTTCAAGTG 001-1A_SP6
  GTCTCTCAAAACACACAGGCAGGTAGACAGACAGGCAGACAAATGAAAGTTGAGTGAATGGGTTCAAGTG chr2

71 TTGTATCTCCAAATATTCTTAGTTTTAAGCAGATGTTGCTATTACCTATCACTTACCCTCCTTATACT 001-1A_SP6
  TTGTATCTCCAAATATTCTTAGTTTTAAGCAGATGTTGCTATTACCTATCACTTACCCTCCTTATACT chr2

141 TATCATATCTTAAAGCTAATTGTCTATGCAGCTCAACCTCTCTGATAAGGACCATGCAGTTGAAGTTAGG 001-1A_SP6
  TATCATATCTTAAAGCTAATTGTCTATGCAGCTCAACCTCTCTGATAAGGACCATGCAGTTGAAGTTAGG chr2

211 TCACTGCAGGTGAATTC 001-1A_SP6
  TCACTGCAGGTGAATTC chr2
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>008-2A_SP6 vs. chr1: 14,956,384-14,956,470 (+), 87 bp overlap

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1 GAATTCTAATAAGAATAGGAGAGAATCATCAGTCACTGAAAAACCTTTGAAGGTCCTGCCCGTGTGTGAC 008-2A_SP6
  GAATTCTAATAAGAATAGGAGAGAATCATCAGTCACTGAAAAACCTTTGAAGGTCCTGCCCGTGTGTGAC chr1

71 AGGGACCACAGAAGTTG 008-2A_SP6
  AGGGACCACAGAAGTTG chr1
```

>016-3A_SP6 vs. chr19: 49,663,546-49,663,715 (-), 171 bp overlap

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1 TCCTCTATTGCTCACCTCAATGACTCCTTCTCTGTAAGCCTTCTCCTGCATACCTAGCTTCTCTCTGG 016-3A_SP6
  TCCTCTATTGCTCACCTCAATGACTCCTTCTCTGTAAGCCTTCTCCTGCATACCTAGCTTCTCTCTGG chr19

71 CCTTATTCTCCAAAGGCTTGTGGTCCAACAGTGCAGTCCTTCCAACACTACTGATACATGTATATATATAG 016-3A_SP6
  CCTTATTCTCCAAAGGCTTGTGGTCCAACAGTGCAGTCCTTCCAACACTACTGATACATGTATATATATAG chr19

141 TTGTAGTCTCCATAAATGCTTGATATCAAAG 016-3A_SP6
  TTGTAGTCTCCATAAATGCTTGATATCAAAG chr19
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>016-3A_T7 vs. chr19: 49,530,675-49,530,901 (+), 227 bp overlap

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1 TTTTTGTCCATTGTCAGAACATCAGAATAAAGAAAATGTCCAGGTGTCATTGTGGGTACAATGAATTG 016-3A_T7
TTTTTGTCCATTGTCAGAACATCAGAATAAAGAAAATGTCCAGGTGTCATTGTGGGTACAATGAATTG chr19

71 CAATCGTTACTGAACTGTTTGGCCAAGCTCAGTAGTTTTGAGTGCTGCCAGCCACCAGGAATGATCCTAG 016-3A_T7
CAATCGTTACTGAACTGTTTGGCCAAGCTCAGTAGTTTTGAGTGCTGCCAGCCACCAGGAATGATCCTAG chr19

141 GTGCTCAGAACACCTGACACAGGGTGGAGCTTCTAGTTTTGAAGAGGGAAGGCAGTTTTGAAGAGGGAAG 016-3A_T7
GTGCTCAGAACACCTGACACAGGGTGGAGCTTCTAGTTTTGAAGAGGGAAGGCAGTTTTGAAGAGGGAAG chr19

211 GCAGTGAAGTACGAAGC 016-3A_T7
GCAGTGAAGTACGAAGC chr19
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>032-11C_SP6 vs. chr9: 5,307,663-5,307,872 (-), 210 bp overlap

```
1 CAAAATTCCAACTCAATTCCTCATAGAGCTACAAAGAGCAATTTGCAAATTCATTTGGTATAACAAAAA 032-11C_SP6
CAAAATTCCAACTCAATTCCTCATAGAGCTACAAAGAGCAATTTGCAAATTCATTTGGTATAACAAAAA chr9

71 TAAAAGATAGCAAAAGCTATTCTCAAAAATACAACAACCTTCTCTCTGATTTTCTTGTGTTTTGCAA 032-11C_SP6
TAAAAGATAGCAAAAGCTATTCTCAAAAATACAACAACCTTCTCTCTGATTTTCTTGTGTTTTGCAA chr9

141 ATGTGATTTGGGTGTTCTATGTTCTGGGCTAATACCCACTTATCAGTGAGTGCACATCTAATGAATTC 032-11C_SP6
ATGTGATTTGGGTGTTCTATGTTCTGGGCTAATACCCACTTATCAGTGAGTGCACATCTAATGAATTC chr9
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>032-11C_T7 vs. chr9: 5,196,339-5,196,861 (+), 527 bp overlap

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1 TCTCAAATACTTAAAAAAATGTCCCATGAAATATGACTGTGTGGATCTGGGGGTGTAGGGGAAGGTGGG 032-11C_T7
TCTCAAATACTTAAAAAAATGTCCCATGAAATATGACTGTGTGGATCTGGGGGTGTAGGGGAAGGTGGG chr9

71 GGTAGAGCCCACATCTCTCAGAAATTCCTGTGCTCTGGGCAGGCAGAAATCAGAAGGACTGCCAGATGCTT 032-11C_T7
GGTAGAGCCCACATCTCTCAGAAATTCCTGTGCTCTGGGCAGGCAGAAATCAGAAGGACTGCCAGATGCTT chr9

141 TCCACTTGCCCCAGGTGGGAATCTGGCTGTGTGAAGCCACTGACCTCACTCAGTGGGCGTGGACAAGG 032-11C_T7
TCCACTTGCCCCAGGTGGGAATCTGGCTGTGTGAAGCCACTGACCTCACTCAGTGGGCGTGGACAAGG chr9

211 GGTAGCCCCTGTACCAGTTCTCAGTCTCCGGCATCCCATGCTGGATACGGCAGAGATCTGAGAACAGA 032-11C_T7
GGTAGCCCCTGTACCAGTTCTCAGTCTCCGGCATCCCATGCTGGATACGGCAGAGATCTGAGAACAGA chr9

281 ATAGGGGATACAGGAAGAGGGAAGAGGGAGAGATGTTTCCACACAGGTGAGAGTCTTGGTCCGGGCCTT 032-11C_T7
ATAGGGGATACAGGAAGAGGGAAGAGGGAGAGATGTTTCCACACAGGTGAGAGTCTTGGTCCGGGCCTT chr9

351 GACTGGAGCACAGGAAGGCCTTCTGATGAGAGATTAGGCACAGCTCTTAGGAATAAGTCTATCCATTG 032-11C_T7
GACTGGAGCACAGGAAGGCCTTCTGATGAGAGATTAGGCACAGCTCTTAGGAATAAGTCTATCCATTG chr9

421 TCCAAGTACAGCAGGCCTTGTATGAACAGAGACAGTCTAGAGTTTTAGAGCTTTATTGTAGAAAGGCAGGA 032-11C_T7
TCCAAGTACAGCAGGCCTTGTATGAACAGAGACAGTCTAGAGTTTTAGAGCTTTATTGTAGAAAGGCAGGA chr9

491 TAAAAGAGAAAAGGTAGAAAAGAGAGAAAACCTGCATG 032-11C_T7
TAAAAGAGAAAAGGTAGAAAAGAGAGAAAACCTGCATG chr9
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>048-7A_SP6 vs. chr9: 32,904,919-32,905,421 (+), 504 bp overlap

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1 GAATTCCTAAAAGATAAGGCTCAGTATACAATCTTCTTGAGATCACACTGATGGGTTATGTGTAATACCT 048-7A_SP6
GAATTCCTAAAAGATAAGGCTCAGTATACAATCTTCTTGAGATCACACTGATGGGTTATGTGTAATACCT chr9

71 CCAGACTAAATTTATGGGTGTCACTAGGCTGTGGATAAATTTGTTTCAGATGGAATCTTTGATTAGATCC 048-7A_SP6
CCAGACTAAATTTATGGGTGTCACTAGGCTGTGGATAAATTTGTTTCAGATGGAATCTTTGATTAGATCC chr9
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141 ATTTTTAAAAATGATAAAACCCGTCAGAAAAATGTATTCACTCTCAGACTGTAAAGTGAAATTGCC 048-7A_SP6
 ACTTTTTAAAAATGATAAAACCCATCAGAAAAATGATAATTCACTCTCAGACTGTAAAGTGAAATTGCC chr9

211 CTCTAAAGAAGCCACATGGTAGCCAGACCTGATATCACAGGCTCCCTTTCCAACCAATCTGGACGCTGG 048-7A_SP6
 CTCTAAAGAAGCCACATGGTAGCCAGACCTGATATCACAGGCTCCCTTTCCAACCAATCTGGACGCTGG chr9

281 AGCAGGAGGATAGCAAGTTTAAAGCCTGCCTAGGTTACAAAGTGAATTCAGGAACAGCCTCAGCAATATA 048-7A_SP6
 AGCAGGAGGATAGCAAGTTCAAAGCCTGCCTAGGTTACAAAGTGAATTCAGGAACAGCCTCAGCAATATA chr9

351 ATGCGACATCATCTTGAAACAAAACGTTAAGAGATGGCTGGGAGTGTGCCTCAATGATAAAAAATGTACCT 048-7A_SP6
 ATGCGACATCATCTTGAAACAAAACGTTAAGAGATGGCTGGGAGTGTGCCTCAATGATAAAAAATGTACCT chr9

421 TACATTCACAGAGCCCTAGGCTCCATCTCTAATACAGTGAGAAAAATAAAAGAGGCAAAAAATGTTATA 048-7A_SP6
 AACATTCACAGAGCCCTAGGCTCCATCTCTAATACAGTGAGAAAAATAAAAGAGGCAAAAAATGTTATA chr9

491 TGTGCTATTTTCAGG 048-7A_SP6
 TGTGCTATTTTCAGG chr9

>048-7A_T7 vs. chr9: 33,012,575-33,012,986 (-), 412 bp overlap

1 TTGCTGATACGGCGGTTTGTATGATTGTTTTCTGAATGCTGAATTAGTCCTGCATGTGTGAAAGAAAGCCC 048-7A_T7
 TTGCTGATACGGCGGTTTGTATGATTGTTTTCTGAATGCTGAATTAGTCCTGCATGTGTGAAAGAAAGCCC chr9

71 AGTTAGTCATGGGTGGAATTCATTTGTACATTGCTGACTCAATTTGCTAATTTTATTGTAGGCATT 048-7A_T7
 AGTTAGTCATGGGTGGAATTCATTTGTACATTGCTGACTCAATTTGCTAATTTTATTGTAGGCATT chr9

141 TACATCTAAATTAGTGAGGGATATTCATCTATTATTTTTCTGGTACTTTCTTTTCTTTCTTTCTGGCTTT 048-7A_T7
 TACATCTAAATTAGTGAGGGATATTCATCTATTATTTTTCTGGTACTTTCTTTTCTTTCTTTCTGGCTTT chr9

211 GGTATCAGGACAATTTTAACTCATGAAAAATCACACAGAGAGAGGCTATATAAGATTGATTTGAATTTTT 048-7A_T7
 GGTATCAGGACAATTTTAACTCATGAAAAATCACACAGAGAGAGGCTATATAAGATTGATTTGAATTTTT chr9

281 TTTTAAATGCTTAATAGAATTCCTGAGTGAAACTACATGGGCCAATATNNATCCTTTTTGTAAGATTTTCA 048-7A_T7
 TTTTAAATGCTTAATAGAATTCCTGAGTGAAACTACATGGGCCAATATACATCCTTTTTGTAAGATTTTCA chr9

351 TTACAAATTTGATTTCTTGATAGGCACAGTACTATTTCAGGTGAATGGTTTCGTGTTAAGGAG 048-7A_T7
 TTACAAATTTGATTTCTTGATAGGCACAGTACTATTTCAGGTGAATGGTTTCGTGTTAAGGAG chr9

>072-10A_SP6 vs. chr6: 93,249,869-93,250,399 (-), 533 bp overlap

1 TTCTAAAATTTAACTATTTTTTAAATTTAAAGCAAATAGAAAGTACCCAGAAAGAATAATTGCTGTCT 072-10A_SP6
 TTCTAAAATTTAACTATTTTTTAAATTTAAAGCAAATAGAAAGTACCCAGAAAGAATAATTGCTGTCT chr6

71 TTCAAAACTGGGTTTTTGTCTGATTTGTTTCTCTTTCCTATTTCCCTATTTCCCTATTTGTTTTCTTTT 072-10A_SP6
 TTCAAAACTGGGTTTTTGTCTGATTTGTTTCTCTTTCCTATTTCCCTATTTCCCTATTTGTTTTCTTTT chr6

141 TCTATTTCCCTATTTTCCCTGTTTCCCTATCAACCGGTTCTGGATAGGTTCTTTTTCCCTGCCATCAGGAATCC 072-10A_SP6
 TCTATTTCCCTATTTTCCCTGTTTCCCTATCAACCGGTTCTGGATAGGTTCTTTTTCCCTGCCATCAGGAATCC chr6

211 CTGAGCCAAATTTGGGAAGAAAACAACAAGATAAGGACCCTCAAGTCTGGTGGTGCCCTTCTTGCCCTA 072-10A_SP6
 CTGAGCCAAATTTGGGAAGAAAACAACAAGATAAGGACCCTCAAGTCTGGTGGTGCCCTTCTTGCCCTA chr6

281 GTTAGTGCTGGATGCGCCAACCTTTAATCTCTCTGTTTACTCTGTGCATGCTATCCCAAATCTAGGGTG 072-10A_SP6
 GTTAGTGCTGGATGCGCCAACCTTTAATCTCTCTGTTTACTCTGTGCATGCTATCCCAAATCTAGGGTG chr6

351 CAATGACATAGCCTGATCATTAAAGAGCAGCCAACGCAAAGCATCAATTGTCAGACAAAATTAAGAATA 072-10A_SP6
 CAATGACATAGCCTGATCATTAAAGAGCAGCCAACGCAAAGCATCAATTGTCAGACAAAATTAAGAATA chr6

421 ACAGCAAATCTGGAATGGAAAAGAATTCATGGAATTAAGTGCCTTGGGTACCTTGGGTCTCCAGGCC 072-10A_SP6
 ACAGCAAATCTGGAATGGAAAAGAATTCATGGAATTAAGTGCCTTGGGTACCTTGGGTATCCAGGCC chr6

491 TGAAGTCCACCAGCTCTCTCCACAGCCCCAGCTGAAGAATTC 072-10A_SP6
 TGAAGTCCACCAGCTCTCTCCACAGCCCTCCAGCTGAAGAATTC chr6

>072-10A_T7 vs. chr6: 93,125,121-93,125,326 (+), 207 bp overlap

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1 AGTTTTAAAGTCAAGTAGAGGAGCATTCCGGGGGGTAGGTGATCTATATCTTGATTGATGGGTTCTATCT 072-10A_T7
  AGTTTTAAAGTCAAGTAGAGGAGCATTCCGGGGGGTAGGTGATCTATATCTTGATTGATGGGTTCTATCT chr6

71 CTGGGAGTCTGGATGATGCTATGATTACAGACTAATTATTCTTGTTTCATGCCAAGGAAGGGTAGTTCTTG 072-10A_T7
  CTGGGAGTCTGGATGATGCTATGATTACAGACTAATTATTCTTGTTTCATGCCAAGGAAGGGTAGTTCTTG chr6

141 ACCTCTTGGCCACAACCTTGGCTAACTGTCCTTCGTAAGCCTGAGGTTTGGTGCAGTAACTGACTTA 072-10A_T7
  ACCTCTTGGCCACAACCTTGGCTAACTGTCCTTCGTAAGCCTGAGGTTTGGTGCAGTAACTGACTTA chr6
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>088-12A_SP6 vs. chrX: 141,997,504-141,997,948 (-), 460 bp overlap

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1 TTTTCCAGCCTTCTGGGCTATCACAATAAGACTGCTATGAACACAGTGGAAACACGTGCCCTGTGACA 088-12A_SP6
  TTTTCCAGCCTTCTGGGCTATCACAATAAGACTGCTATGAACACAGTGGAAACACGTGCCCTGTGACA chrX

71 TGGTGGGGTGGGGCATCTTTGGATATATATATATATATATATATATATATATATATATATATATA 088-12A_SP6
  TGGTGGGGTGGGGCATCTTTGGATATATATATATATATATATATATATATATATATATATATATA chrX

141 ATATATAATCTTTCTCCATTAATAATTACCTTTGCTCCCTTGTTCAGATCATTGATTAGATCTGTGCTTA 088-12A_SP6
  TATAATCTTTCTCCATTAATAATTACCTTTGCTCCCTTGTTCAGATCATTGATTAGATCTGTGCTTA chrX

211 CTCCATCTTCTCTGATTTTTTTGTTATGGAAAAAGGGTTATTTTGAATAATTTTAAATTTAGAAATAG 088-12A_SP6
  CTCCATCTTCTCTGATTTTTTTGTTATGGAAAAAGGGTTATTTTGAATAATTTTAAATTTAGAAATAG chrX

281 AAAACCTCATAGGAAGGAGGAAAGAAACAAAATACATAAAGCATCCAGGCAACGTTTTACTTCATGAGCT 088-12A_SP6
  AAAACCTCATAGGAAGGAGGAAAGAAACAAAATACATAAAGCATCCAGGCAACGTTTTACTTCATGAGCT chrX

351 CATCACTATCTCATTGGTTCACCTTGTCCCATGATGAGAAAGGACTCAGCCACCCATAGTAATGTTATTA 088-12A_SP6
  CATCACTATCTCATTGGTTCACCTTGTCCCATGATGAGAAAGGACTCAGCCACCCATAGTAATGTTATTA chrX

421 TAGGGATATGGATCAGTTTCACAAAGAAGCCAATGAATTC 088-12A_SP6
  TAGGGATATGGATCAGTTTCACAAAGAAGCCAATGAATTC chrX
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>096-1B_T7 vs. chr4: 29,734,830-29,735,232 (+), 415 bp overlap

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1 CTGTACTTCAGTTTGCTTTTAAATTGTATGTGACTAATATTAATAAATAAAAAATACAATTTGTGGTTA 096-1B_T7
  CTGTACTTCAGTTTGCTTTTAAATTGTATGTGACTAATATTAATAAATAAAAAATACAATTTGTGGTTA chr4

71 TTCAATGTTTTTTGTTTCTATATATATTTTAAAGGCTGACCACTTGGTATCAGATAAAGTGTTAGGGGCTC 096-1B_T7
  TTCAATGTTTTTTGTTTCTATATATATTTTAAAGGCTGACCACTTGGTATCAGATAAAGTGTTAGGGGCTC chr4

141 ATCCCTGGGGAAGTCTGATTCTCCCTCTCTAGGTATTAATTGTATGTAATTCTTAATCTGGGGATGGGGT 096-1B_T7
  ATCCCTGGGGAAGTCTGATTCTCCCTCTCTAGGTATTAATTGTATGTAATTCTTAATCTGGGGATGGGGT chr4

211 CAAGNGAGATTTTCTTTACCTCTTTGAGACGTCAGTTTATGGTGTCAATTATCCAGGCCTTGTTTAGCCG 096-1B_T7
  CTTGTGAGATTTTCTTTACCTCTTTGAGACGTCAGTTTATGGTGTCAATTATCCAGGCCTTGTTTAGCCA chr4

281 ACAGTATTGTTTAGAGTTTACA-GTGAGATAGCCTATCAAATATAAAACATACAATCTTGTAACAGACTT 096-1B_T7
  ACTATTATTGTTTAGAGTTTACAAGTGAGATAGCCTATCAAATATAAAACATACAATCTTGTAACAGACTT chr4

350 CATGAATCTTCTGGCTGTTAACAAATTATTCTATCCCTGTTCCCTGCGTGCCCTTGTCTTATGTG 096-1B_T7
  CATGATCTTCTGGCTGTTAACAAATTATTCTATCCCTGTTCCCTGCGTGCCCTTGTCTTATGTG chr4
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>120-4B_SP6 vs. chr15: 40,526,985-40,527,497 (-), 513 bp overlap

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1 TTTACAGTTGAGTAAGAATTTTCTTTACACATGAAAGACATATTGTAGAGTCTTTGTAGCGAAAAGATT 120-4B_SP6
  TTTACAGTTGAGTAAGAATTTTCTTTACACATGAAAGACATATTGTAGAGTCTTTGTAGCGAAAAGATT chr15
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141 GCAAGGGCTACCTTCAAACCACAGAAAAAACTTTAGACAAGTCAGTCTACCAAATAAGTAATGAAAT 136-6B_SP6
GCAAGGGCTACCTTCAAACCACAGAAAAAACTTTAGACAAGTCAGTCTACCAAATAAGTAATGAAAT chr13

211 TCACTAGTAATTAGAGAAACACAAATTTAAAAA-GATTGTACCTTACAAACATAAAAAACAA---GCCCC 136-6B_SP6
TCACTAGTAATTAGAGAAACACAAATTTAAAAAAGATTGTACCTTACAAACATAAAAAACAAAAAAGCCCC chr13

277 TTCTGTGTTCTACTCCTAAAGACAATTCTATGAAAGGGGAAAGTGTGAAGTTCTAAGCTTTGTCCAACA 136-6B_SP6
TTCTGTGTTCTACTCCTAAAGACAATTCTATGAAAGGGGAAAGTGTGAAGTTCTAAGCTTTGTCCAACA chr13

347 ACAAATAGCCCTCCCCTATCACCACCCAAAAAAATACACATGGCACAGTAAATCATGAGTGGCCTTTTCTA 136-6B_SP6
ACAAATAGCCCTCCCCTATCACCACCCAAAAAAATTAACACATGGCACAGTAAATCATGAGTGGCCTTTTCTA chr13

417 AAGAGTCTGCTTTGAATATACACAAAAAGAAA-TACAACCTTTAAAGATGCCCTGGGATTCTTACAGAAGT 136-6B_SP6
AAGAGTCTGCTTTGAATATACACAAAAAGAAAATACAACCTTTAAAGATGCCCTGGGATTCTTACAGAAGT chr13

486 TTATTTATTGACTATCAA-TACAACCTTTCTTTTCCCTCTTAAAAACAAATGGTCTTTACATTAA-CTG 136-6B_SP6
TTATTTATTGACTATCAAATACAACCTTTCTTTTCCCTCTTAAAAACAAATGGTCTTTACATTAAACTG chr13

554 A-GTATAATAACATTTTAAAAATTCTTGCAAAAGAATACCTTGGG-CTGGTGAGATGGCTTA-CGGGTAAG 136-6B_SP6
AAGTATAATAACATTTTAAAAATTCTTGCAAAAGAATACCTTGGGCTGGTGAGATGGCTTACGGGTAAG chr13

621 AACACTA-CTGCTCTTCGGA-GGTCCTGA 136-6B_SP6
AACACTA-CTGCTCTTCGGAAGGTCCTGA chr13

>144-7B_SP6 vs. chr19: 3,257,612-3,257,787 (-), 176 bp overlap

1 ATCTCCTACCCAGATCTCCTACTCCCTTGGGCGGGTGGGGGGTGAGGTGGGGGCATAAGCAAGAGGGCA 144-7B_SP6
ATCTCCTACCCAGATCTCCTACTCCCTTGGGCTGGTGGGGGGTGAGGTGGGGGCATAAGCAAGAGGGCA chr19

71 CAAATGTGGACCAGCTGAACAAGCCTAAGGTTTGGAGTTTACAAGTAGACTGTAAAGAAATGTTTTAAAA 144-7B_SP6
CAAATGTGGACCAGCTGAACAAGCCTAAGGTTTGGAGTTTACAAGTAGACTGTAAAGAAATGTTTTAAAA chr19

141 TTGCCTGAGCCTAATTTGATTCTCCTAGTGAATTCC 144-7B_SP6
TTGCCTGAGCCTAATTTGATTCTCCTAGTGAATTCC chr19

>144-7B_T7 vs. chr19: 3,132,629-3,132,986 (+), 359 bp overlap

1 TATTCACAGAGCACGTCGCACTGTGTAGCATTGTAACCAAGTGGGAACATTTTTATCAACCCCTCCAAA 144-7B_T7
TATTCACAGCA-ACGTCGCACTGTGTAGCATTGTAACCAAGTGGGAACATTTTTATCAACCCCTCCAAA chr19

71 TACTCCTTCTTAGCCTCATCCAGCCTCCCCTGGTGTGTCCCTGGCTGCTCTGGTCTTTCCCTTCTGTAG 144-7B_T7
TACTCCTTCTTAGCCTCATCCAGCCTCCCCTGGTGTGTCCCTGGCTGCTCTGGTCTTTCCCTTCTGTAG chr19

141 GTTTGTCTGTTCTGGACACGTCATGTAATGGAGTGAGACATTGGCTTCCCTGGCTTCCCTGCCATGCTG 144-7B_T7
GTTTGTCTGTTCTGGACACGTCATGTAATGGAGTGAGACATTGGCTTCCCTGGCTTCCCTGCCATGCTG chr19

211 GTTTGGTTTGTCTTGGTTTTGTGAGACAGGGTCTCCTGTAGCTCAGGCTAACTTCTAGCTAAANNNGATT 144-7B_T7
GTTTGGTTTGTCTTGGTTTTGTGAGACAGGGTCTCCTGTAGCTCAGGCTAACTTCTAGCTAAAGGATGATT chr19

281 TGAACATCTGATCCTCCACCTCCTCTCTCAAGTGTCTGACCTCAGGAGAGTGCCACCATGCTGTGTT 144-7B_T7
TGAACATCTGATCCTCCACCTCCTCTCTCAAGTGTCTGACCTCAGGAGAGTGCCACCATGCTGTGTT chr19

351 ATGTGTCGC 144-7B_T7
ATGTGTCGC chr19

>152-7B_T7 vs. chr2: 180,150,561-180,150,943 (-), 392 bp overlap

1 CCGGAAATCCAACTTTAGAAAAACAAAATCAACAACAAGAAAGCCATGTGTTCCAGGGCACAGAATTCA 152-7B_T7
CCGTGAAATCCAACTTTAGAAAAACAAAATCAACAACAAGAAAGCCATGTGTTCCAGGGCACAGAATTCA chr2

71 GGCATTACTCCTTGCAAGGCAAACACTTTTTACCAGCTGAGCTCCGGTGTGCGCTCTCAAACATTTATGTTT 152-7B_T7
 GGCATTACTCCTTGCAAGGCAAACACTTTTTACCAGCTGAGCTCCGGTGTGCGCTCTCAAACATTTATGTTT chr2

141 TATTTATGTG**N**CTGAGTGGAGTTTATGCCTTCTATGTGTGGGTGCCACAGAGGACAGAAAAGGGCATT 152-7B_T7
 TATTTATGTG**G**CTGAGTGGAGTTTATGCCTTCTATGTGTGGGTGCCACAGAGGACAGAAAAGGGCATT chr2

211 GATCTCCTGGAGCTGAAGTTATAGGTAGTTGTAAGACACCTTC**A**GGTGTGG**C**AACAGAACTCG**G**GTCCT 152-7B_T7
 GATCTCCTGGAGCTGAAGTTATAGGTAGTTGTAAGACACCTTC**G**GGTGTGG**C**AACAGAACTCG**A**GTCCT chr2

281 CTGGGAGATACCGCCTTAACTGCTGAGTCATCACTACAGCCTTAC**A**GGCCCC**CCCC**TTTTTTTT**T**TTTTGA 152-7B_T7
 CTGGGAGATACCGCCTTAACTGCTGAGTCATCACTACAGCCTTAC**C**GGCCCC**TTT**-TTTTTTTT**C**TTTTGA chr2

351 GTCAGAATCTCCAGCTTAGATTGGTCTTGAACCTTGTAATCCT 152-7B_T7
 GTCAGAATCTCCAGCTTAGATTGGTCTTGAACCTTGTAATCCT chr2

>160-9B_SP6 vs. chr14: 79,957,422-79,957,995 (+), 573 bp overlap

1 TCTTTATAAAAATAGCAATTCACATGTCACAAAACTATA**T**TCCCCTATTGTATGAGAAGGAACTTTTTA 160-9B_SP6
 TCTTTATAAAAATAGCAATTCACATGTCACAAAACTATA**C**TCCCCTATTGTATGAGAAGGAACTTTTTA chr14

71 TTTTGTCTGTTTACTATAATTTTACAGAGGAGATTTGCTAGACCAAAGGAAATCTTCTAAATTATGCTAAG 160-9B_SP6
 TTTTGTCTGTTTACTATAATTTTACAGAGGAGATTTGCTAGACCAAAGGAAATCTTCTAAATTATGCTAAG chr14

141 TAGACAGCCTTGAATAACAATCAAATGGGTAGTGAGTACTCTGCAAGAGGAAAAATTTGAGGACTAACTA 160-9B_SP6
 TAGACAGCCTTGAATAACAATCAAATGGGTAGTGAGTACTCTGCAAGAGGAAAAATTTGAGGACTAACTA chr14

211 CCATGAATCCCATATAAGCAAAAAGGAAATATTAAGTGTGAGAAAAAGGAAAGAACAGGCCAATAGGATT 160-9B_SP6
 CCATGAATCCCATATAAGCAAAAAGGAAATATTAAGTGTGAGAAAAAGGAAAGAACAGGCCAATAGGATT chr14

281 CTGCATGAAGTGGGTGAGTGTAAACATTGAAGGCAAGTACTCAGGGATGTAAAAATGACAAGCTTTAGT 160-9B_SP6
 CTGCATGAAGTGGGTGAGTGTAAACATTGAAGGCAAGTACTCAGGGATGTAAAAATGACAAGCTTTAGT chr14

351 GGATTCCACTGAGAATTCAGAAGGAAGAGGG**T**TGG**N**AAGCACCCAATATCCTAGCAAGGAATATCAGTT 160-9B_SP6
 GGATTCCACTGAGAATTCAGAAGGAAGAGGG**C**TGG**G**AAGCACCCAATATCCTAGCAAGGAATATCAGTT chr14

421 AGTATAATGGATAAGAGTTGTAGTAGATTAATAAGTACTTTAGGGCAGTTTAAAGACAA**G**GCTAGAAGAC 160-9B_SP6
 AGTATAATGGATAAGAGTTGTAGTAGATTAATAAGTACTTTAGGGCAGTTTAAAGACAA**A**GCTAGAAGAC chr14

490 ACGAAAATAGAGAGTAGACAAAACAGACTAATTATTGGCAGAATAATAGAGGAAGGCGAGATTTTTTCATAT 160-9B_SP6
 ACGAAAATAGAGAGTAGACAAAACAGACTAATTATTGGCAGAATAATAGAGGAAGGCGAGATTTTTTCATAT chr14

560 GCATATTTATGAAT 160-9B_SP6
 GCATATTTATGAAT chr14

>160-9B_T7 vs. chr14: 80,075,786-80,076,150 (-), 365 bp overlap

1 CCCTACAGTGGGACATCAAGCCTTCAGAAGACCAAGGGCCTTTCCTCCCATTGATGTCCTACAAGGCCAT 160-9B_T7
 CCCTACAGTGGGACATCAAGCCTTCAGAAGACCAAGGGCCTTTCCTCCCATTGATGTCCTACAAGGCCAT chr14

71 CCTCTGCTACATATGTAGTTGGAGTCCATGGGTCCCTCAATGTGTACTCTTTGGTTGGCTGTTTAAATCTC 160-9B_T7
 CCTCTGCTACATATGTAGTTGGAGTCCATGGGTCCCTCAATGTGTACTCTTTGGTTGGCTGTTTAAATCTC chr14

141 TGAGAGCTCTGGCGAATCTGGATGATTGATATTATTGTTCTTCCCTATGGGGTTGCAAACCCCTTCAACTC 160-9B_T7
 TGAGAGCTCTGGCGAATCTGGATGATTGATATTATTGTTCTTCCCTATGGGGTTGCAAACCCCTTCAACTC chr14

211 CTTCACTCTTTTCACTTACTCCATTGGGGACCCCAAGCTCAGTCCAATGGTTGGCTGTGAGCATCTGCCT 160-9B_T7
 CTTCACTCTTTTCACTTACTCCATTGGGGACCCCAAGCTCAGTCCAATGGTTGGCTGTGAGCATCTGCCT chr14

281 CTGTATATGTCAGGCTCTATCAGAGCTTCTCAGGAGACAGTTATA**C**CAGGCTCCTGTGAGCATGCACTT**C** 160-9B_T7
 CTGTATATGTCAGGCTCTATCAGAGCTTCTCAGGAGACAGTTATA**T**CAGGCTCCTGTGAGCATGCACTT**T** chr14

351 **T****C**ACATCAGCAATA 160-9B_T7
T**A**ACATCAGCAATA chr14

>182-12B_SP6 vs. chr17: 15,428,227-15,428,613 (-), 387 bp overlap

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1 CAAGCTAGACCCATCAGAGAGGAGAGTCTCTCAATTGAGAAAATGTTGTGTAGTTTTATGCCCTACCC 182-12B_SP6
  CAAGCTAGACCCATCAGAGAGGAGAGTCTCTCAATTGAGAAAATGTTGTGTAGTTTTATGCCCTACCC chr17

71 ACTGATATTCTGGGAGTTGACTTGGCTACCAGCCCCACTGGGTATCCCTTGAATCCTCAGACAAAGGTC 182-12B_SP6
  ACTGATATTCTGGGAGTTGACTTGGCTACCAGCCCCACTGGGTATCCCTTGAATCCTCAGACAAAGGTC chr17

141 ACACACACACACACACACACACACACACACACACACACACACACACACACACAGAGTTTATTCCTTTTCAACTTGC 182-12B_SP6
  ACACACACACACACACACACACACACACACACACACACACACACACACACACAGAGTTTATTCCTTTTCAACTTGC chr17

211 CTTAGGACTCAATTGTTGTTTGGCAAACCTCCCTAACCCACCTGTAGTAGTGGCCACAGGCCCCAGTT 182-12B_SP6
  CTTAGGACTCAATTGTTGTTTGGCAAACCTCCCTAACCCACCTGTAGTAGTGGCCACAGGCCCCAGTT chr17

281 CCTCCCAAGACCTCACATGGCTGCTGGCTTTTTCTGCCTCCACAGCATGGCCAATGTACCTTATCTCTTC 182-12B_SP6
  CCTCCCAAGACCTCACATGGCTGCTGGCTTTTTCTGCCTCCACAGCATGGCCAATGTACCTTATCTCTTC chr17

351 CCTGTCATCTGCTTTTTCTTCTGGGACCTGGAATTC 182-12B_SP6
  CCTGTCATCTGCTTTTTCTTCTGGGACCTGGAATTC chr17
```

>192-6C_T7 vs. chr17: 33,999,368-33,999,883 (-), 515 bp overlap

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1 CCTGTCTCTGTGTTGGGCTTTTGGGGCTCTCCATGTCCTGTGTCCCCACTCCCTCTGACTTCTTTGTCC 192-6C_T7
  CCTGTCTCTGTGTTGGGCTTTTGGGGGCTCTCCATGTCCTGTGTCCCCACTCCCTCTGACTTCTTTGTCC chr17

70 TGGGAAGCTGTCCTTTGTGCTGGGGTCCCGAAGGTTTATGCCAGGTACAGGAGAGAAGATGCACTAGGT 192-6C_T7
  TGGGAAGCTGTCCTTTGTGCTGGGGTCCCGAAGGTTTATGCCAGGTACAGGAGAGAAGATGCACTAGGT chr17

140 GCCCAGCATTCAAGTTGACTCGATCTTGGCAGAAGTAAAGCCAGGGGCTGCTGAAACACCACGTGAGTATA 192-6C_T7
  GCCCAGCATTCAAGTTGACTCGATCTTGGCAGAAGTAAAGCCAGGGGCTGCTGAAACACCACGTGAGTATA chr17

210 GTGTCCACTGTCTCTACTTGCAGTTCTGCTGAGTCCCAACCCAGGCTGCACCAGACCCAGCTTACAGGA 192-6C_T7
  GTGTCCACTGTCTCTACTTGCAGTTCTGCTGAGTCCCAACCCAGGCTGCACCAGACCCAGCTTACAGGA chr17

280 CAGGCTGTGTGCACCACAGCTGCTACCATTTGGTCCCCATTACAAAAGCGCTAATGACTTAAGGGCTCAAA 192-6C_T7
  CAGGCTGTGTGCACCACAGCTGCTACCATTTGGTCCCCATTACAAAAGCGCTAATGACTTAAGGGCTCAAA chr17

350 TGTGCTCCATTGTGTAGAAAAGCTTGCCTTCTGGAGAACAATAACCTTCCCTATTCTGCAGCCTTTATAC 192-6C_T7
  TGTGCTCCATTGTGTAGAAAAGCTTGCCTTCTGGAGAACAATAACCTTCCCTATTCTGCAGCCTTTATAC chr17

420 AGCCCTGTGAGCCTTCCAGGAGCCCAGGTAAGACAGGGTCCCCAGAGCTGGTTGCCTCTCAGAGGCAG 192-6C_T7
  AGCCCTGTGAGCCTTCCAGGAGCCCAGGTAAGACAGGGTCCCCAGAGCTGGTTGCCTCTCAGAGGCAG chr17

490 ATTGATGGTACATCTACAATGAATTC 192-6C_T7
  ATTGATGGTACATCTACAATGAATTC chr17
```

>200-9C_T7 vs. chr6: 99,758,420-99,758,598 (+), 180 bp overlap

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1 GAATTCAAACCTCTTATCCATTCCCTTGGTCCATATTCCTTTCCCTTAGTGGTTTTACTCTGAAATGTTGC 200-9C_T7
  GAATTCAAACCTCTTATCCATTCCCTTGGTCCATATTCCTTTCCCTTAGTGGTTTTACTCTGAAATGTTGC chr6

71 ATGACCCAACAAAGTCCTGCCANNGCATAGTGGTGCAGATGCGAACTTCAGAACTCTATAGTGGCTGAAG 200-9C_T7
  ATGACCCAACAAAGTCCTGCCAGGCATAGTGGTGCAGATGCGAACTTCAGAACTCTATAGTGGCTGAAG chr6

141 AAGGAGGTAGATCCTAAGTTTGTATGTCAGACTAAGTTACA 200-9C_T7
  AAGGAGGTAGATCCTAAGTTTGTATGTCAGACTAAGTTACA chr6
```

>245-11P_SP6 vs. chr17: 12,000,500-12,000,962 (+), 465 bp overlap

1 GAATTCTATCCCAAACACATGCTTAAAAAGCAGTGTGCGGAGAAGTGGAGAAGTGAATCAGCAGTTAAG 245-11P_SP6
 GAATTCTATCCCAAACACATGCTTAAAAAGCAGTGTGCGGAGAAGTGGAGAAGTGAATCAGCAGTTAAG chr17

71 AGCAATTTTGGCTTTGGAAGACGACCTGAGTTCAATATCCAGCACCAACATGGTGGCTAACCCACAGCCA 245-11P_SP6
 AGCAATTTTGGCTTTGGAAGACGACCTGAGTTCAATATCCAGCACCAACATGGTGGCTAACCCACAGCCA chr17

141 TAACTCCAGTTCTAGGGGATCCTATGCCTTCTTTGGGCTTCTGCGGGCATCCGGCATATATATGGTTTAC 245-11P_SP6
 TAACTCCAGTTCTAGGGGATCCTATGCCTTCTTTGGGCTTCTGCGGGCATCCGGCATATATATGGTTTAC chr17

211 AGACACACATGCAGGAAAAACACTCATACACATAAAAATATGTAATCATAAAATACATAAAATAAAAAAAA 245-11P_SP6
 AGACACACATGCAGGAAAAACACTCATACACATAAAAATATGTAATCATAAAATACATAAAATAAAAAAAA chr17

281 TTAACCAAGCATGCTTATGGATTCTTGGATTTCAACACTAAGGAGGCAGAACCCCTGGGATTTCAGTAT 245-11P_SP6
 TTAACCAAGCATGCTTATGGATTCTTGGATTTCAACACTAAGGAGGCAGAACCCCTGGGATTTCAGTAT chr17

351 CAGGGCAGCCAGCCTGGCCTACTTAATGAGTCTCAGGCCAGGTAAGAGACCATATCTCAAGAAGGAAGAA 245-11P_SP6
 CAGGGCAGCCAGCCTGGCCTACTTAATGAGTCTCAGGCCAGGTAAGAGACCATATCTCAAGAAGGAAGAA chr17

421 CATCATCTGAGGAAAGGTGCCTGAGGTTGGCCTCTGTTTTCCATA 245-11P_SP6
 CATCATCTGAGGAAAGGTGCCTGAGGTTGGCCTCTGTTTTCCATA chr17

>245-11P_T7 vs. chr17: 12,186,842-12,187,321 (-), 480 bp overlap

1 TATGTTAGCTATTTTGGCTAGATTGCTGGTTGAGATATCCTGATGATGGAGATTGGTCTTACCCCAAGAA 245-11P_T7
 TATGTTAGCTATTTTGGCTAGATTGCTGGTTGAGATATCCTGATGATGGAGATTGGTCTTACCCCAAGAA chr17

71 ACCCAAGGCTGCTAGTCAGCAAGAAAGTAGTCTAAGGAGGCCTACACCAGGAGATCTACACCTTCTCTGG 245-11P_T7
 ACCCAAGGCTGCTAGTCAGCAAGAAAGTAGTCTAAGGAGGCCTACACCAGGAGATCTACACCTTCTCTGG chr17

141 TCTTCTTTCTCCCCTACCTAGTGTGGGTAGTTGGACGGGATTGGGGTAGAATAAGGGTTGGAAGGATGG 245-11P_T7
 TCTTCTTTCTCCCCTACCTAGTGTGGGTAGTTGGACGGGATTGGGGTAGAATAAGGGTTGGAAGGATGG chr17

211 TAGATACTAGAACCCAATAAAGTAGCCCAAGAAGCAAGTCAACAAGAATTAATATGACGACATGTACT 245-11P_T7
 TAGATACTAGAACCCAATAAAGTAGCCCAAGAAGCAAGTCAACAAGAATTAATATGACGACATGTACT chr17

281 GGATAGTTTTCTGACAACCTGACACAAGCTAGAATATCTGAAAGAAGGAACCTCAACTGAAGGAAAAAAC 245-11P_T7
 GGATAGTTTTCTGACAACCTGACACAAGCTAGAATATCTGAAAGAAGGAACCTCAACTGAAGGAAAAAAC chr17

351 TCAATAAAATCCATCTATAAGGCATTGTCTTAATGAGTATTGATGGGTGAGGGCCAGCTCATTGGGG 245-11P_T7
 TCAATAAAATCCATCTATAAGGCATTGTCTTAATGAGTATTGATGGGTGAGGGCCAGCTCATTGGGG chr17

421 TGGTGCTTGTAGTCCTAGGTTCTATAAGAAAGCAGGCTGAACAATTCATGTGAGCAAGC 245-11P_T7
 TGGTGCTTGTAGTCCTAGGTTCTATAAGAAAGCAGGCTGAACAATTCATGTGAGCAAGC chr17

>245-9D_SP6 vs. chr4: 92,886,305-92,886,528 (+), 223 bp overlap

1 AGGAACTACGAACTTCTTGGCACTGTGACTGTGGGTGACATTCTGAACTTGGGTNNCAGGTGTTTGTG 245-9D_SP6
 AGGAACTACGAACTTCTTGGCACTGTGACTGTGGGTGAAATTCTGAACTTGGGTCTCAGGTGTTTGTG chr4

71 NTGTGGGTTTTTTTTTAATGCTGTGTGTAATGTGAAAATAATCAGAATCTATTAATAGNGGT--CAGTG 245-9D_SP6
 TTGTGGGTTTTTTTTTAATGCTGTGTGTAATGTGAAAATAATCAGAATCTATTAATAGTGGTGGT CAGTG chr4

138 CTTACACGGCATTGTGAACTACTTCCCAGCCACAGATCCTCTACGGAGATCGGGGAAACCACCAAGT 245-9D_SP6
 CTTACACGGCATTGTGAACTACTTCCCAGCCACAGATCCTCTACGGAGATCGGGGAAACCACCAAGT chr4

208 AAAAGAAACCGCGAAA 245-9D_SP6
 AAAAGAAACCGCGAAA chr4

>245-9D_T7 vs. chr4: 93,023,688-93,024,308 (-), 621 bp overlap

1 AAACAGTCATATACCTAAGAATAAACAAATTGATTAATAAAAAATTACTTATGTGCCCCACCCGGCAAA 245-9D_T7
 AAACAGTCATATACCTAAGAATAAACAAATTGATTAATAAAAAATTACTTATGTGCCCCACCCGGCAAA chr4

71 AAAGAAAACCTTGCTAACACTCTTGAGACCAGGAGCTGACCCACACTGCCTCTCCGATGGATTAACATTC 245-9D_T7
AAAGAAAACCTTGCTAACACTCTTGAGACCAGGAGCTGACCCACACTGCCTCTCCGATGGATTAACATTC chr4

141 CTCTGCTAATTGCCCTTGAAAAATCTTTTTACCTTTATCTTTACCTAAAATTCTAATGAAAAACTGCACA 245-9D_T7
CTCTGCTAATTGCCCTTGAAAAATCTTTTTACCTTTATCTTTACCTAAAATTCTAATGAAAAACTGCACA chr4

211 TAAACGATTAAGATATTAACCTGCTAGAGTTGGCCACCTAGTTAACAGAGTGCTCAGTAGCATTAGGAACA 245-9D_T7
TAAACGATTAAGATATTAACCTGCTAGAGTTGGCCACCTAGTTAACAGAGTGCTCAGTAGCATTAGGAACA chr4

281 GTTACAGGAGCTTGCTGTTCTGAGAACTGGCTTTCTGACACCTGTGTTTCTGGGCTGTCTTCATGAG 245-9D_T7
GTTACAGGAGCTTGCTGTTCTGAGAACTGGCTTTCTGACACCTGTGTTTCTGGGCTGTCTTCATGAG chr4

351 CACTGGAGTTGGAATTGTGTACCTGTACCCTATCAGAGTCTATTTGGAATAATAGTATATGATATTGTT 245-9D_T7
CACTGGAGTTGGAATTGTGTACCTGTACCCTATCAGAGTCTATTTGGAATAATAGTATATGATATTGTT chr4

421 GGGATCAGGAAAAGAGTGTCTTGAATGAGTCCCGGAGACAACACTGGTTGAAATTTAATTCACACCATC 245-9D_T7
GGGATCAGGAAAAGAGTGTCTTGAATGAGTCCCGGAGACAACACTGGTTGAAATTTAATTCACACCATC chr4

491 CAAGGCAGGCTGCATGTAGAAATTCCTAGAAAACAGCTTTGGTAGAAGAGAGCAGAAAGGAGACATTCTAAA 245-9D_T7
CAAGGCAGGCTGCATGTAGAAATTCCTAGAAAACAGCTTTGGTAGAAGAGAGCAGAAAGGAGACATTCTAAA chr4

561 GAGATACTTAGCCAGGGTAGGATTTGGAGAAGGATTGTGAGTGGGGAAGACAGGGAGGGCC 245-9D_T7
GAGATACTTAGCCAGGGTAGGATTTGGAGAAGGATTGTGAGTGGGGAAGACAGGGAGGGCC chr4

>255-3L_SP6 vs. chrX: 94,890,859-94,891,345 (-), 475 bp overlap

1 AAAGGGCCGAGATGGGGCCCGCAAGCTAACACCTCAGGGTCAGGAAACACATCTGGACAGGATCGCTGAA 255-3L_SP6
AAAGGGCCGAGATGGGGCCCGCAAGCTAACACCTCAGGGTCAGGAAACACATCTGGACAGGATCGCTGAA chrX

71 CAGGTGGCAGCTGCCAACAAAGAAGCATTAGAACAAATAACTGTTAATAAATGCCTCATTCAATAA 255-3L_SP6
CAGGTGGCAGCTGCCAACAAAGAAGCATTAGAACAAATAACTGTTAATAAATGCCTCATTCAATAA chrX

141 AAAGAAAAGAAATAAAGAAAGAGAAGCCTATAAACATACAAGAAGCTTATAGAGTACCAATTATAACCAA 255-3L_SP6
AAAGAAAAGAAATAAAGAAAGAGAAGCCTATAAACATACAAGAAGCTTATAGAGTACCAATTATAACCAA chrX

211 AAAAAAAAAAAAAAAAAA-----CAAACAACAAAAACAAACCCTCTGGCATGTAATAATCAA 255-3L_SP6
AAAAAAAAAAAAAAAAAAACCAAAACAAACAACAAAAACAAACCCTCTGGCATGTAATAATCAA chrX

268 ATGTAATAACAAATAATAATGTTTTGGGAAGATGTAATGATCCATTCCATTAATACGAGCACTTGGGA 255-3L_SP6
ATGTAATAACAAATAATAATGTTTTGGGAAGATGTAATGATCCATTCCATTAATACGAGCACTTGGGA chrX

338 AGCAGAGCCATGGTGGATGCTCTCAGAGGAGTGTGAACCTAATGTGGCCTCTGCTGTAGTAGCAAGTG 255-3L_SP6
AGCAGAGCCATGGTGGATGCTCTCAGAGGAGTGTGAACCTAATGTGGCCTCTGCTGTAGTAGCAAGTG chrX

408 TTCTTAGCTGCTAAGCCATCTCTGTGGCTTCTTTTATTCCAAGGACTGTTAAGCTGACCTGGAATTC 255-3L_SP6
TTCTTAGCTGCTAAGCCATCTCTGTGGCTTCTTTTATTCCAAGGACTGTTAAGCTGACCTGGAATTC chrX

>255-3L_T7 vs. chrX: 94,756,622-94,757,143 (+), 524 bp overlap

1 GTTTTACAGAGACATATGAATGTCCACAACAGTATTTACATAATATATAAATGATGAAAGGAATCCAAAT 255-3L_T7
GTTTTACAGAGACATATGAATGTCCACAACAGTATTTACATAATATATAAATGATGAAAGGAATCCAAAT chrX

71 GTCATTACCAGGTGAGTGGATAAGAAAAATATGATCTACTGCAACAATAAAATACTATTTATCCATTA 255-3L_T7
GTCATTACCAGGTGAGTGGATAAGAAAAATATGATCTACTGCAACAATAAAATACTATTTATCCATTA chrX

141 AGGAATGAAGCTCTAATAAATGACACAATATGAAGAACCTAGAGGACACACTAAGCAAAAGGTGTCAGAA 255-3L_T7
AGGAATGAAGCTCTAATAAATGACACAATATGAAGAACCTAGAGGACACACTAAGCAAAAGGTGTCAGAA chrX

211 GCAATGTATTTTATAATATAGTTTTTTGAAAAGCCCTGCTAAAGAAATACTAACTCATAACACAGACTA 255-3L_T7
GCAATGTATTTTATAATATAGTTTTTTGAAAAGCCCTGCTAAAGAAATACTAACTCATAACACAGACTA chrX

281 ATTGTTGCNTAGGATCGGGGATGAGAATTGGGGCAGGGGCTATTGAAAAACGAGGCAATGGAAATATTC 255-3L_T7
ATTGTTGCNTAGGATCGGGGATGAGAATTGGGGCAGGGGCTATTGAAAAACGAGGCAATGGAAATATTC chrX

351 TAAAATTAGTTTCTGATGATGACTGCACCATTCTGTAAATTGACTAATATCACTAACATGCATACTTTAA 255-3L_T7
TAAAATTAGTTTCTGATGATGACTGCACCATTCTGTAAATTGACTAATATCACTAACATGCATACTTTAA chrX

421 CAAACAACACTATCTTTTAAAAACACTCTCAGACCATTAAACCTGAGACTTTGTGCCTCAGTCAGCCATCT 255-3L_T7
CAAACAACACTATCTTTTAAAAACCTCTCAGACCATTAAACCTGAGACTTTGTGCCTCAGTCAGCCATCT chrX

491 ATTAGCCGAGAGAATGACCCTCATGACCTTCTT 255-3L_T7
ATTAGCCGAGAGAATGACCCTCATGACCTTCTT chrX

>257-22B_SP6 vs. chrX: 130,761,904-130,762,049 (+), 174 bp overlap

1 TCCGCTGNCCTCTGTCAATCCGAGNGCCTGGGATTAAGAAGGTGCGCCACCACGNCNGGCTCAATTTA 257-22B_SP6
TCCGCTGNCCTCTGTCAATCCGAGNGCCTGGGATTAAGAAGGTGCGCCACCACGNCNGGCTCAATTTA chrX

71 TCTTTTGNAANGCANNTTGNCTCCATCATANAGACTCTTCCTGTCTCTTACATTANCCANATTTTGA 257-22B_SP6
TCTTTTCAGTAAATACATTTGCTCCATCACACACATCTATCTGTCTCTTACATTTCATATTTTGA chrX

140 TTTTTCGTTGACTATGAAGTGATTTNTTTACAT 257-22B_SP6
TTTTTGTGACTATGAAGTGATTTNTTTACAT chrX

>257-22B_T7 vs. chrX: 130,885,586-130,886,114 (-), 539 bp overlap

1 TTGGAATTCACCTGTAATAAGGCTGTACTTGAATGTCCTCACCATCACCAAAGGATTTTACCTCCATAGT 257-22B_T7
TTGGAATTCACCTGTAATAAGGCT-----GTCCTCACCATCACCAAAGGATTTTACCTCCATAGT chrX

71 AGATAAGTTAAGAGTTGACAGTTCTGCTGCACCAAGGAAAGAATTGTAGGCACCATTTTGGATACAGAT 257-22B_T7
AGATAAGTTAAGAGTTGACAGTTCTGCTGCACCAAGGAAAGAATTGTAGGCACCATTTTGGATACAGAT chrX

141 TTCCTGCTACGGTCAAAGCTTTTTGACTGGAGTGATTGTCGTCATTCTCAGCCCACAGGGAACAGGTTAC 257-22B_T7
TTCCTGCTACGGTCAAAGCTTTTTGACTGGAGTGATTGTCGTCATTCTCAGCCCACAGGGAACAGGTTAC chrX

211 ATTCATTTAAGAAATGCTGTGTGATTAAGATGGTCTATGATGAAGTCATTACCAACTGTTTCAATGT 257-22B_T7
ATTCATTTAAGAAATGATGTGTGATTAAGATGGTCTATCCCATGAAGTCATTACCAACTGTTTCAATGA chrX

281 ACAATGTTCTGCTTGGAGGTGGCAGCAACATTAGGTGAGGTAAGATTCTGGTTCATTGGCTGTGATGA 257-22B_T7
ACAATGTTCTGCTTGGAGGTGGCAGCAACATTAGGTGAGGTAAGATTCTGGTTCATTGGCTGTGATGA chrX

351 TTTTGAAGCACTCATCTCAGAATAAGAGTAACCTTATAAAGTCTCTTCTTCAATGTTTCTATGGTAT 257-22B_T7
TTTTGAAGCACTCATCTCAGAATAAGAGTAACCTTATAAAGTCTCTTCTTCAATGTTTCTATGGTAT chrX

421 CTTCTGCACTTGAGATTCTCTCTTCTATCTCTTGTATTCTGTTGGTGATGCTTGCATCTATGACTCCTAG 257-22B_T7
CTTCTGCACTTGAGATTCTCTCTTCTATCTCTTGTATTCTGTTGGTGATGCTTGCATCTATGACTCCTAG chrX

491 GTTTTCTAACTCCAGGGTTGTCTCCTTTTGTGATTTCTTTATTGTTTCT 257-22B_T7
TTTTTCTAACTCCAGGGTTGTCTCCTTTTGTGATTTCTTTATTGTTTCT chrX

>262-11G_T7 vs. chr12: 35,192,049-35,192,443 (-), 397 bp overlap

1 CTCAGCTCGACTGGAGGCCAGGCTATATGTGCATAGCCATTGCCCCACATTCTCCACCTAAGAAGATG 262-11G_T7
CTCAGCTCGACTGGAGGCCAGGCTATATGTGCATAGCCATTGCCCCACATTCTCCACCTAAGAAGATG chr12

71 CCAAATACTTAGAGAGACGACTTACAGGTATCCTGTGATGCAGCTGCTCTCTACCCTTATTTACCTTC 262-11G_T7
CCAAATACTTAGAGAGACGACTTACAGGTATCCTGTGATGCAGCTGCTCTCTACCCTTATTTACCTTC chr12

141 ATCTCTTATTTATATGTATGGCCAAAAAGGCAAAATGTCTACAGAAAAAACAACAAAAACCTTAG 262-11G_T7
ATCTCTTATTTATATGTATGGCCAAAAAGGCAAAATGTCTACAGAAAAAACAACAAAAACCTTAG chr12

211 GCACCTCTTTAAAGAATTGTTTTAGAAAAAGTAACAAGAGCTGAGAAGCTGTCTCAGTCAGAAAAAGCACT 262-11G_T7
GCACCTCTTTAAAGAATTGTTTTAGAAAAAGTAACAAGAGCTGAGAAGCTGTCTCAGTCAGAAAAAGCACT chr12

281 TGTCACAAACATCAGGGCCTGAGTTCAAAACCAAGAACCTATGCAAACACCCTGGGCTGTAGCATACCT 262-11G_T7
 TGTCACAAACATCAGGGCCTGAGTTCAAAACCAAGAACCTATGCAAACACCCTGGGCTGTAGCATACCT chr12

351 GTAATCCTAGCATTGTGGAAGTGAAGACAGGAAGACCCTAGAATTC 262-11G_T7
 GTAATCCTAGCATTGTAGAAGTGAAGACAGGAAGACCCTAGAATTC chr12

>266-2E_SP6 vs. chr12: 35,090,782-35,091,223 (+), 442 bp overlap

1 GAATTCAACTGATGACACCCCTAAAGAAATGTCAACTATGGGCGAGGTCAGGAATTCAACAGTGGAGCCT 266-2E_SP6
 GAATTCAACTGATGACACCCCTAAAGAAATGTCAACTATGGGCGAGGTCAGGAATTCAACAGTGGAGCCT chr12

71 TGTGATTGACTCTTCCATATGAACTCAAATGAGTGTCCACAGGTAAGACTCCACTGTTGATTTAATGGA 266-2E_SP6
 TGTGATTGACTCTTCCATATGAACTCAAATGAGTGTCCACAGGTAAGACTCCACTGTTGATTTAATGGA chr12

141 TTAATAAATTAGTTACAATTAACACATGAGAATCTGTGCCTAGAATGTTATAAGATCAATATGGAGAC 266-2E_SP6
 TTAATAAATTAGTTACAATTAACACATGAGAATCTGTGCCTAGAATGTTATAAGATCAATATGGAGAC chr12

211 CAGATTTAAATGATAAGACCACATGAGATCACCTTGGCCTGGAATACTCCAGTGCTTAGAGGCCAAGCAG 266-2E_SP6
 CAGATTTAAATGATAAGACCACATGAGATCACCTTGGCCTGGAATACTCCAGTGCTTAGAGGCCAAGCAG chr12

281 AGTAAAGCCC AACCTCGCTGGGAATGTGGAGACATCTAGCTCATCAGAAAAATATGCTCAACAAACAGT 266-2E_SP6
 AGTAAAGCCCTAACCTCTCTGGGAATGTGGAGACATCTAGCTCATCAGAAAAATATGCTCAACAAACAGT chr12

351 ACAAGTTGACTGTGGTAAATGCCTGCCTGTGGCTGGTTAAGAAAAACAAGATCAGAGAAGTGATCTTTGA 266-2E_SP6
 ACAAGTTGACTGTGGTAAATGCCTGCCTGTGGCTGGTTAAGAAAAACAAGATCAGAGAAGTGATCTTTGA chr12

421 AAGCACTGTGCTCATTACCCCC 266-2E_SP6
 AAGCACTGTGCTCATTACCCCC chr12

>266-2E_T7 vs. chr12: 35,199,619-35,200,180 (-), 561 bp overlap

1 AAATGCGTGTATATCTAAATGTGATGAAGATATTTATGTGTGAATAAAGAAAATAAAATTAATAGGA 266-2E_T7
 AAATGCGTGTATATCTAAATGTGATGAAGATATTTATGTGTGAATAAAGAAAATAAAATTAATAGGA chr12

71 CGTGTTCATACAATTTGGCAGTAGAGGCTCCGGGTGACAAATTAAGCTTATATAAAAAATTAACATA 266-2E_T7
 CGTGTTCATACAATTTGGCAGTAGAGGCTCCGGGTGACAAATTAAGCTTATATAAAAAATTAACATA chr12

141 AATGTAACCTGACGATGTGGAACATGCCTGGATTGTATCCAGGAGCAACAAAGTGTCTTAAGACACT 266-2E_T7
 AATGTAACCTGACGATGTGGAACATGCCTGGATTGTATCCAGGAGCAACAAAGTGTCTTAAGACACT chr12

211 GGGTCTCCCACTGGCTTCTGGAAATTTCTGATAGCTAGGATGCGCTAACTCCAGAAGCAACAGTTATTTAA 266-2E_T7
 GGGTCTCCCACTGGCTTCTGGAAATTTCTGATAGCTAGGATGCGCTAACTCCAGAAGCAACAGTTATTTAA chr12

281 GACGCACACACAAAGTAGAGACAGACCAGCCTGAAGTACTTACTTATTAGAAAGATGGCGAAGAAGACCA 266-2E_T7
 GACGCACACACAAAGTAGAGACAGACCAGCCTGAAGTACTTACTTATTAGAAAGATGGCGAAGAAGACCA chr12

351 GAGCCAGGCTGACCGTCAACACCAGGAGCAGCCCCACAAAAACAGCCCCCGCCTTCCATTTCTGGGGC 266-2E_T7
 GAGCCAGGCTGACCGTCAACACCAGGAGCAGCCCCACAAAAACAGCCCCCGCCTTCCATTTCTGGGGC chr12

421 TGTGCCAGCATTGGGGATTTGTCTCTAAAGCTGATGGGAAACAAAGTGACAATCTCCGCATCTCAC 266-2E_T7
 TGTGCCAGCATTGGGGATTTGTCTCTAAAGCTGATGGGAAACAAAGTGACAATCTCCGCATCTCAC chr12

491 AGAGATGTGATGCACACACTCATTTCCTAGACAGCCCTGAAAAGTGACTTCTGCATTGCGAAATGCCT 266-2E_T7
 AGAGATGTGATGCACACACTCATTTCCTAGACAGCCCTGAAAAGTGACTTCTGCATTGCGAAATGCCT chr12

560 TT 266-2E_T7
 TT chr12

>269-9H_SP6 vs. chrX: 94,817,775-94,818,021 (+), 247 bp overlap

1 AAAAAGAAGTACACAGGACCTACTCCTTCATGCCAATACTCACTAGATCACAGAGATTTCTTAATACTT 269-9H_SP6
 AAAAAGAAGTACACAGGACCTACTCCTTCATGCCAATACTCACTAGATCACAGAGATTTCTTAATACTT chrX

71 CTACCCTAGCTGAAGGAAAATGTAGAGGTCAATGTTTTCTAAGACCTCCATGGAAGATAGGCATTTAGGA 269-9H_SP6
 TTACCCTAGCTGAAGGAAAATGTAGAGGTCAATGTTTTCTAAGACCTCCATGGAAGATAGGCATTTAGGA chrX

141 TACTACAGAGGTGTGTCTTCTCTGGCTTCTACCCATTCCCAATACCCTGAGGCTCTCCAGACTCCGCCCC 269-9H_SP6
 TACTACAGAGGTGTGTCTTCTCTGGCTTCTACCCATTCCCAATACCCTGAGGCTCTCCAGACTCCGCCCC chrX

211 TCAAATTGACCCACCCACGACGAGCTGTGATAAAA 269-9H_SP6
 TCAAATTGACCCACCCACGACGAGCTGTGATAAAA chrX

>269-9H_T7 vs. chrX: 94,967,482-94,968,088 (-), 613 bp overlap

1 GGCAACTGTCTTAGCGGCATGGTTTCAGGCAGCAGGAGGCCACACAATGATTCTGACACTGTGCCATCTGGA 269-9H_T7
 GGCAACTGTCTTAGCGGCATGGTTTCAGGCAGCAGGAGGCCACACAATGATTCTGACACTGTGCCATCTGGA chrX

71 GGAAGAGAATGAGAGAAAATGCGTCATCATCTTTTCATCGCAGTGCAGCGACCTGGCACAAAACACCTA 269-9H_T7
 GGAAGAGAATGAGAGAAAATGCGTCATCATCTTTTCATCGCAGTGCAGCGACCTGGCACAAAACACCTA chrX

141 GAAAGGGAATGTGCATTGGCAAATGACAAGATTACATTTTCCACAGTGGAAAGGCGTGAAGGACATGG 269-9H_T7
 GAAAGGGAATGTGCATTGGCAAATGACAAGATTACATTTTCCACAGTGGAAAGGCGTGAAGGACATGG chrX

211 ACAGGCAAAGCTTGACACATTT 269-9H_T7
 ACAGGCAAAGCTTGACACATTT chrX

281 ATTTTCTGTTTTCTGTGTTTGCATATGTTAGTGAATATGCATGTGCACCACATTTGTATAGGTGAATGT 269-9H_T7
 ATTTTCTGTTTTCTGTGTTTGCATATGTTAGTGAATATGCATGTGCACCACATTTGTATAGGTGAATGT chrX

351 AAAAGTCAAAGCTGCATCAAGTTACTTGACTGTGGAGTTACAGATGGTTGGGAGCCATCTTGTGGGTCC 269-9H_T7
 AAAAGTCAAAGCTGCATCAAGTTACTTGACTGTGGAGTTACAGATGGTTGGGAGCCATCTTGTGGGTCC chrX

421 ATTACAGCTCCTATTCCTAGAAATCGTTTTTTAAGGCTTTTAATTCTTTTTCTGCGCCAAAAAATATC 269-9H_T7
 ATTACAGCTCCTATTCCTAGAAATCGTTTTTTAAGGCTTTTAATTCTTTTTCTGCGCCAAAAAATATC chrX

491 TGTAAGATTGCAAGAGGAGGCTCCTTCTCCAAATGGACAGTTGCCCAAGCAGGGCTACAAGAACAAAGT 269-9H_T7
 TGTAAGATTGCAAGAGGAGGCTCCTTCTCCAAATGGACAGTTGCCCAAGCAGGGCTACAAGAACAAAGT chrX

561 CAGGAAAAACATGAAACTATCAGTCACAAAATAAACTCCCAGAACCCTTAGAA 269-9H_T7
 CAGGAAAAACATGAAACTATCAGTCACAAAATAAACTCCCAGAACCCTTAGAA chrX

>271-12L_SP6 vs. chrX: 94,854,496-94,854,839 (+), 344 bp overlap

1 GAATTCTCTAAAACCTTCAGAAAGGAATAATTTCAATTTAATTTCAAATAATAATTTCAATTTCAACTAGG 271-12L_SP6
 GAATTCTCTAAAACCTTCAGAAAGGAATAATTTCAATTTAATTTCAAATAATAATTTCAATTTCAACTAGG chrX

71 TGTCTCACACTGAACTTCTGACTTCTAAAATTATAAGGTTATAGATCTGTGTTGCTTTAAGCCACCAAGT 271-12L_SP6
 TGTCTCACACTGAACTTCTGACTTCTAAAATTATAAGGTTATAGATCTGTGTTGCTTTAAGCCACCAAGT chrX

141 TTGTTGGGGGCTTAAACAAAATACAGCACTGTAGTGCTACCTGTGTCTCTGTATCTTCGTAGAGGTTAAGG 271-12L_SP6
 TTGTTGGGGGCTTAAACAAAATACAGCACTGTAGTGCTACCTGTGTCTCTGTATCTTCGTAGAGGTTAAGG chrX

211 TGTTATGAAGACATCCAGAAAAGGAATCATGAGATAGGCTAAGGCACAGAGTATGTCTTTTATTACAG 271-12L_SP6
 TGTTATGAAGACATCCAGAAAAGGAATCATGAGATAGGCTAAGGCACAGAGTATGTCTTTTATTACAG chrX

281 TTTCTTTGTAGAACACCTTTACCTAATGTCTTAATCAGCTAATTAGCATAGTAAAATACAACCTT 271-12L_SP6
 TTTCTTTGTAGAACACCTTTACCTAATGTCTTAATCAGCTAATTAGCATAGTAAAATACAACCTT chrX

>271-12L_T7 vs. chrX: 94,985,811-94,986,461 (-), 616 bp overlap

1 TAACCATTCCAAAGACCTTCTATTATTTCCAGCTTTACTATGACTAACTAAATGACCTGGACTCATTTC 271-12L_T7
 TAACCATTCCAAAGACCTTCTATTATTTCCAGCTTTACTATGACTAACTAAATGACCTGGACTCATTTC chrX

71 CACATAGTAGTTCCACCGCTTCTCATCTGTACAGGTACCTGAACATGTTTAAATAACTAAATTTAGGGATA 271-12L_T7
CACATAGTAGTTCCACCGCTTCTCATCTGTACAGGTACCTGAACATGTTTAAATAACTAAATTTAGGGATA chrX

141 AAATTAGACTTCTTTATATGCCTTTAATAACTATCCTAAAGTTGGGCTGACATACTGGCATAACACCTTTA 271-12L_T7
AAATTAGACTTCTTTATATGCCTTTAATAACTATCCTAAAGTTGGGCTGACATACTGGCATAACACCTTTA chrX

211 GTCTGAGCACTTCAGAGGCAGAAGCAGGTTGTATCTCTATGAGTTGGAGGCCAGCTTGCTACACAGTGAG 271-12L_T7
GTCTGAGCACTTCAGAGGCAGAAGCAGGCTGTATCTCTATGAGTTGGAGGCCAGCTTGCTACACAGTGAG chrX

281 TTCTAGGGCACCAGAACTACATAATGAGACCCTTTCCCCACCCCTAATGTTCTAAAACCTTCTGTCAAATT 271-12L_T7
TTCTAGGGCACCAGAACTACATAATGAGACCCTTTCCCCACCCCTAATGTTCTAAAACCTTCTGTCAAATT chrX

351 TACAGAAATCAGCATATATACTTTATAACTTTATAATTTCTGCGTGCTAAAATTGAAATGATTTTATATAA 271-12L_T7
TACAGAAATCAGCATATATACTTTATAACTTTATAATTTCTGCGTGCTAAAATTGAAATGATTTTATATAA chrX

421 TCCTCAATAGCAAATTTTTTCAAAAAGCAAATACAGAGGCTCAGCTGAATTTTACAGAAGAGGAAAGAG 271-12L_T7
TCCTCAATAGCAAATTTTTTCAAAAAGCAAATACAGAGGCTCAGCTGAATTTTACAGAAGAGGAAAGAG chrX

490 -----AAAAAGGAAAAGCATATTTGTGAAGTGAGGACCAAC 271-12L_T7
ATATTTGTGCATAAAAATAAAGCATATTTACAGAAAAAGGAAAAGCATATTTGTGAAGTGAGGACCAAC chrX

527 TGCATACGTAGCCCAATCCCGTATCTTCATATTTAAGTGAATTTGAAGGATTTTATTGTAAGATGTAAAG 271-12L_T7
TGCATACGTAGCCCAATCCCGTATCTTCATATTTAAGTGAATTTGAAGGATTTTATTGTAAGATGTAAAG chrX

597 AATCCTGTCTGTAGAAATTC 271-12L_T7
AATCCTGTCTGTAGAAATTC chrX

>272-12L_SP6 vs. chr3: 147,530,230-147,530,623 (+), 394 bp overlap

1 GAATTTCTTCTTTGTAGAATGTACAGAGATGAGATATAAATGTGACCTCTTGACTTACCATGTTGGCCTGT 272-12L_SP6
GAATTTCTTCTTTGTAGAATGTACAGAGATGAGATATAAATGTGACCTCTTGACTTACCATGTTGGCCTGT chr3

71 GCCCAACTTTCTGTTATTTCCCTAGAAAGCTTGAAAATATATCAAAGACAAGAAGCAATGAAGAAATGTA 272-12L_SP6
GCCCAACTTTCTGTTATTTCCCTAGAAAGCTTGAAAATATATCAAAGACAAGAAGCAATGAAGAAATGTA chr3

141 CGTCAGCCATGGAATGCAGAGTTAGATCTTATAAAATGTCACCCATTTAGAAAACCAAAGATTTAACTAA 272-12L_SP6
CGTCAGCCATGGAATGCAGAGTTAGATCTTATAAAATGTCACCCGTTTAGAAAACCAAAGATTTAACTAA chr3

211 CGTTATTAGATGTGGATTAATCGGATGCATCATTCTTTAGCTCTGCTCCTGTGGGATGCAGTTGCTAAG 272-12L_SP6
CGTTATTAGATGTGGATTAATCGGATGCATCATTCTTTAGCTCTGCTCCTGTGGGATGCAGTTGCTAAG chr3

281 TGAGGATAATTAGAAGTGAAGGAGGCTTCTATGGGGAGCACCAAGGGGAGAGATCTGAAGGAGGCAGGA 272-12L_SP6
TGAGGATAATTAGAAGTGAAGGAGGCTTCTATGGGGAGCACCAAGGGGAGAGATCTGAAGGAGGCAGGA chr3

351 AGAGCATTTCAGCTACAGCACAGGTCAGACTTGTGAGCTGAGGG 272-12L_SP6
AGAGCATTTCAGCTACAGCACAGGTCAGACTTGTGAGCTGAGGG chr3

>272-12L_T7 vs. chr3: 147,663,827-147,664,390 (-), 565 bp overlap

1 ACTGGTCTAGCCAAGCAGGATCAACTGGCTGGAGAGGCATGACAGTCCCAAGACAAGGTCACCTTATAGT 272-12L_T7
ACTGGTCTAGCCAAGCAGGATCAACTGGCTGGAGAGGCATGACAGTCCCAAGACAAGGTCACCTTATAGT chr3

71 AGAGGCCAAGATGTGGTATTGCTTCTTTTGTAGATACCTCTTTATAAAAATAAGGCTCCAGTCAGGATG 272-12L_T7
AGAGGCCAAGATGTGGTATTGCTTCTTTTGTAGATACCTCTTTATAAAAATAAGGCTCCAGTCAGGATG chr3

141 CTGTTACCCTCCACTGGGCAGTGAATGACATCCAGGGAAACCTTTGAAAGGCTTACTCTCCAATGTG 272-12L_T7
CTGTTACCCTCCACTGGGCAGTGAATGACATCCAGGGAAACCTTTGAAAGGCTTACTCTCCAATGTG chr3

211 TGGACATGAGGAAAATGGCAGGAACTCCGATTGATGAAAACCTGTTAGCACATCCTGCTAGAAAATCAT 272-12L_T7
TGGACATGAGGAAAATGGCAGGAACTCCGATTGATGAAAACCTGTTAGCACATCCTGCTAGAAAATCAT chr3

281 GCTGCTCTGCCTCGGTTTTGAAATGTGAAGAAAAGAAGAGTCTCCCTTTTATCACTTTGGTAGCCAGGAGCT 272-12L_T7
GCTGCTCTGCCTCGGTTTTGAAATGTGAAGAAAAGAAGAGTCTCCCTTTTATCACTTTGGTAGCCAGGAGCT chr3

211 TTAATAATGAAAAATCAACACCTTGCTTGTCTGATTCTTGAGACGGGGTCTTGTAAATACAGCCCTTGC 279-5I_SP6
TTAATAATGAAAAATCAACACCTTGCTTGTCTGATTCTTGAGACGGGGTCTTGTAAATACAGCCCTTGC chr17

281 CAGGCTGGGTGGCAGTGTGGCACAACCTTTAATCCCAGCACTTGGGAGGCAGAGGCAGGTGGATTCTGA 279-5I_SP6
CAGGCTGGGTGGCAGTGTGGCACAACCTTTAATCCCAGCACTTGGGAGGCAGAGGCAGGTGGATTCTGA chr17

351 GTTCAAGGCCAGCCT 279-5I_SP6
GTTCAAGGCCAGCCT chr17

>279-5I_T7 vs. chr17: 12,182,179-12,182,701 (-), 523 bp overlap

1 CCTAGAGCACTGGATCATGCTATAGCCCATGGGTGCAATCAGGTACACAGCTATTTTGTAAATATTTTT 279-5I_T7
CCTAGAGCACTGGATCATGCTATAGCCCATGGGTGCAATCAGGTACACAGCTATTTTGTAAATATTTTT chr17

71 ACTGGGATACAGCCATCCCATTGCTTATGTGTGGACTGGCTGATTTGCCACAAGAGCAGAGATAAT 279-5I_T7
ACTGGGATACAGCCATCCCATTGCTTATGTGTGGACTGGCTGATTTGCCACAAGAGCAGAGATAAT chr17

141 AGAAACCATGGCCTGAAGAGCCTAAAGTATCTACATTTAACCATGACCCTCACCAAGAAAACCTACCCAA 279-5I_T7
AGAAACCATGGCCTGAAGAGCCTAAAGTATCTACATTTAACCATGACCCTCACCAAGAAAACCTACCCAA chr17

211 CACCTCTTTTAGGTTCCAGTCCAGGAGTGCCTTTAAACCAGCAGTTTGGGTCTCATCTGCCAGC 279-5I_T7
CACCTCTTTTAGGTTCCAGTCCAGGAGTGCCTTTAAACCAGCAGTTTGGGTCTCATCTGCCAGC chr17

281 CTATTAGAACTCTCAGTTCTAATACAAGCTATAACAGTTTAAATTTGTTGGGCATAGTAATCCAGCTCTG 279-5I_T7
CTATTAGAACTCTCAGTTCTAATACAAGCTATAACAGTTTAAATTTGTTGGGCATAGTAATCCAGCTCTG chr17

351 GAACAAGTAGGAGGATCAGACATTCAAAATCATCTTTAGCTACGAGTATTTTCCAGGCCAGCCTGCAC 279-5I_T7
GAACAAGTAGGAGGATCAGACATTCAAAATCATCTTTAGCTACGAGTATTTTCCAGGCCAGCCTGCAC chr17

421 TATGAGACCTGATATTTAAAGTTAAATGTTTTAAATATATATCAGAAACATCACACATGGTGGTGCATC 279-5I_T7
TATGAGACCTGATATTTAAAGTTAAATGTTTTAAATATATATCAGAAACATCACACATGGTGGTGCATC chr17

491 ACTATAATCACAACACCTGGGAGGCACAGGCTG 279-5I_T7
ACTATAATCACAACACCTGGGAGGCACAGGCTG chr17

>282-5D_SP6 vs. chr17: 12,172,619-12,172,970 (-), 352 bp overlap

1 CAAAAACACAGAAGATAAAAAATAAATTTAAAAACAACAACAACAACAACAACCACCTCAGCATCCAGGA 282-5D_SP6
CAAAAACACAGAAGATAAAAAATAAATTTAAAAACAACAACAACAACAACAACCACCTCAGCATCCAGGA chr17

71 TGGTGAATACAATGACAGTTAGGGGAAATGAACCTTCCCCGTCCCCTCACAGATCCTAGAGTTAAACAA 282-5D_SP6
TGGTGAATACAATGACAGTTAGGGGAAATGAACCTTCCCCGTCCCCTCACAGATCCTAGAGTTAAACAA chr17

141 TAAGGAAATCTGTGTCCTTGGGGTGCCAGTGATCCCAAAGAGGAGAGATTTTGTCTGGTTGGAGTTTC 282-5D_SP6
TAAGGAAATCTGTGTCCTTGGGGTGCCAGTGATCCCAAAGAGGAGAGATTTTGTCTGGTTGGAGTTTC chr17

211 ATCCGAAATGTCTAGGGACATTTTCCTTTGTGTACCAAGGTAAGGGCATATGGTGAAGAGCCCTGGACC 282-5D_SP6
ATCCGAAATGTCTAGGGACATTTTCCTTTGTGTACCAAGGTAAGGGCATATGGTGAAGAGCCCTGGACC chr17

281 TACTGGGTATGGGCAGGAACATTGCCTAACACCCAACAATGCACAGGAAGGCTCCTCCAGGGATGGAAT 282-5D_SP6
TACTGGGTATGGGCAGGAACATTGCCTAACACCCAACAATGCACAGGAAGGCTCCTCCAGGGATGGAAT chr17

351 TC 282-5D_SP6
TC chr17

>282-5D_T7 vs. chr17: 12,028,446-12,028,807 (+), 349 bp overlap

1 GAATTCACATCTCATAGCAAGGAATCAAAGCAAACACTACATCAAAGCATTAGACATCAAAACAGAGACAAG 282-5D_T7
GAATTCACATCTCATAGCAAGGAATCAAAGCAAACACTACATCAAAGCATTAGACATCAAAACAGAGACAAG chr17

71 AAATTAGTGAAAATGCCATAGGAGGATTGGTTATAATTCACAGCTTCATAATGGGCAAGGTCAGTCTAAA 282-5D_T7
AAATTAGTGAAAATGCCATAGGAGGATTGGTTATAATTCACAGCTTCATAATGGGCAAGGTCAGTCTAAA chr17

141 TGTGACAAAAA-----CAGAAACAACAACAAAAACAACAACAACAAAAATGGT 282-5D_T7
TGTGACAAAAA-----CAGAAACAACAACAAAAACAACAACAACAAAAATGGT chr17

198 CCAGGGCCTATGGGAGAGGGATTAGTCTGTATGCATTACCCACAGAAATACAGAGTTGAATTGAAACGCT 282-5D_T7
CCAGGGCCTATGGGAGAGGGATTAGTCTGTATGCATTACCCACAGAAATACAGAGTTGAATTGAAACGCT chr17

268 GTCACCACTGGTAAACCTGGATAAAGTGTGTTAGTGTATACAAAGGGCTGGCTTTCTGAATGTATGTGGA 282-5D_T7
GTCACCACTGGTAAACCTGGATAAAGTGTGTTAGTGTATACAAAGGGCTGGCTTTCTGAATGTATGTGGA chr17

338 AAGCTCTAACAA 282-5D_T7
AAGCTCTAACAA chr17

>293-21P_SP6 vs. chrX: 44,270,572-44,271,061 (-), 491 bp overlap

1 CAACCAGCCACCTTCTGGCGAGAGCCACAGAGCTTCTGAGGCGGCGACATCTTCGACTCCAGACAACCG 293-21P_SP6
CAACCAGCCACCTTCTGGCGAGAGCCACAGAGCTTCTGAGGCGGCGACATCTTCGACTCCAGACAACCG chrX

71 GCCNCTTCTGGCCAAAGCAACACAGCTTCTGGGAAAGATCCTGTTTTGGGCCTTCACCTTCAGCCAG 293-21P_SP6
GCCA-CCTTCTGGCCAAAGCAACACAGCTTCTGGGAAAGATCCTGTTTTGGGCCTTCACCTTCAGCCAG chrX

141 GAGGAGGTCCAAACACCAGATAACTGTACACCTTCCCCGAAAGAGGAGAGCTTGCTGCAGAGACTGCTC 293-21P_SP6
GAGGAGGTCCAAACACCAGATAACTGTACACCTTCCCCGAAAGAGGAGAGCTTGCTGCAGAGACTGCTC chrX

211 TGACCACTGAAACTCAGAGGAGAGCTTGTCTCCACGCCTGCTGATTGAGGGTAACAAAATCAACAGA 293-21P_SP6
TGACCACTGAAACTCAGAGGAGAGCTTGTCTCCACGCCTGCTGATTGAGGGTAACAAAATCAACAGA chrX

281 GGAACAATCTCTTAAACAAAGACAACATAACAACAACTCCAGAGATTGCCAGATGGCGAAAGGTAAACG 293-21P_SP6
GGAACAATCTCTTAAACAAAGACAACATAACAACAACTCCAGAGATTGCCAGATGGCGAAAGGTAAACG chrX

351 TAAGAATCTACTAACAGAAACCAGGACCACTCACCATCATCAGAACCCAGAACGCCCACTTCGCCCCAGT 293-21P_SP6
TAAGAATCTACTAACAGAAACCAGGACCACTCACCATCATCAGAACCCAGAACGCCCACTTCGCCCCAGT chrX

421 CCAGGACACCTAACACACCTGAAAAGGTAGACCTGGATTTAAAGCATATCTCATGATGATGGTAGAGG 293-21P_SP6
CCAGGACACCTAACACACCTGAAAAGGTAGACCTGGATTTAAAGCATATCTCATGATGATGGTAGAGG chrX

491 A 293-21P_SP6
A chrX

>293-21P_T7 vs. chrX: 44,086,068-44,086,651 (+), 586 bp overlap

1 AATGCAGTAAACTGCAATGCCTGATTACTTTCACTATCTCTGTCAACACTGGAGGCTTTTTGTCTGAA 293-21P_T7
AATGCAGTAAACTGCAATGCCTGATTACTTTCACTATCTCTGTGTCAACACTGGAGGCTTTTTGTCTGAA chrX

71 TGAATAGCATTCTTACTAAATTCAACGATTTCTTAAATATTTGGAACACTGGTGGAGGCCAATCTAACTT 293-21P_T7
TGAATAGCATTCTTACTAAATTCAACGATTTCTTAAATATTTGGAACACTGGTGGAGGCCAATCTAACTT chrX

141 ATCTATTTGTCAAATCATTCTTTGAAGCACTTATAATAAAACAATACTGAAAGAAAACCTTCACTAGA 293-21P_T7
ATCTATTTGTCAAATCATTCTTTGAAGCACTTATAATAAAACAATACTGAAAGAAAACCTTCACTAGA chrX

211 CTATCGCAAGGACATATCTGGGCCACATTGTGTTATGGAATGCCAAAAAGCACCAGGAGACCAGTTTCTG 293-21P_T7
CTATCGCAAGGACATATCTGGGCCACATTGTGTTATGGAATGCCAAAAAGCACCAGGAGACCAGTTTCTG chrX

281 TGAAACTTTTTGCCTCAGGGCTGCGGCCAAGCTTTTGGACTTGTACGCATACTGACTGGAGTGGTGTGTG 293-21P_T7
TGAAACTTTTTGCCTCAGGGCTGCGGCCAAGCTTTTGGACTTGTACGCATACTGACTGGAGTGGTGTGTG chrX

351 GCACATACTACACACACAACACACACACACACACACACACACACACACACACACACAGTCT 293-21P_T7
GCACATACTACACACACAACACACACACACACACACACACACACACACACACACACAG--TCT chrX

421 AGGGAGAAGGTGGATTATACAATAGACTAGGATTGTAACATATGGCAAGGGCATAAAGCCCTTGCCCCTGG 293-21P_T7
AGGGAGAAGGTGGATTATACAATAGACTAGGATTGTAACATATGGCAAGGGCATAAAGCCCTTGCCCCTGG chrX

281 GTGGTAGTACAGGCTCAGGTCAGATTCATCCCACACTTACCACTGTTCTTAGCAGATATCCCAGGTCCGA 297-2I_T7
 GTGGTAGTACAGGCTCAGGTCAGATTCATCCCACACTTACCACTGTTCTTAGCAGATATCCCAGGTCCGA chr17

351 GCTGCTCCAATATCTGCTACAACCTCATGTTCTGCCTTACCAATAGCTTCTTGGGCCTCTCTGCAGGTAC 297-2I_T7
 GCTGCTCCAATATCTGCTACAACCTCATGTTCTGCCTTACCAATAGCTTCTTGGGCCTCTCTGCAGGTAC chr17

421 CCCAACCCCTGCAACAGGGTGCCAGTCCTCAGCTTCTCTTTATGACCCCTTCAATCAAGAGCTTTCCTGCC 297-2I_T7
 CCCAACCCCTGCAACAGGGTGCCAGTCCTCAGCTTCTCTTTATGACCCCTTCAATCAAGAGCTTTCCTGCC chr17

491 TTTAAAACCCAGTAACAGGTGGGT 297-2I_T7
 TTTAAAACCCAGTAACAGGTGGGT chr17

>300-19K_T7 vs. chr1: 31,429,439-31,430,003 (+), 562 bp overlap

1 GAATTTAGAAAGCA--GGAGAGCTATGGTTGGAGAGATTGAGCGGTTTCCGATTGTGAAAGATCAGGA 300-19K_T7
 GAATTTAGAAAGCAAGAAGGAGAGCTATGGTTGGAGAGATTGAGCGGTTTCCGATTGTGAAAGATCAGGA chr1

68 AGGTGAACATGTAATTTGACTTACACTTTTTAAACCGGGGGCCTCTAATATCTGATTAGAGTTAGAAGAGGC 300-19K_T7
 AGGTGAACATGTAATTTGACTTACACTTTTTAAACCGGGGGCCTCTAATATCTGATTAGAGTTAGAAGAGGC chr1

138 CATCCAGGGGCAGCAGGCTTTGTGACAGTGAAGTGGGGGAGGCTGTGAAGCACACTGCCAAATCTGACGC 300-19K_T7
 CATCCAGGGGCAGCAGGCTTTGTGACAGTGAAGTGGGGGAGGCTGTGAAGCACACTGCCAAATCTGACGC chr1

208 TGCACAAGCTAACGCTGCCTCAAGGGCACTGTGACAGAACTTCACTGTCAGGTAAGTATTTGGGTGGAG 300-19K_T7
 TGCACAAGCTAACGCTGCCTCAAGGGCACTGTGACAGAACTTCACTGTCAGGTAAGTATTTGGGTGGAG chr1

278 AACTCTTTACAAGTTCCCTCACTACAGGCCATGGCTCTCTGTTGTCATGTCTACTCTTACCAAAGTATCT 300-19K_T7
 AACTCTTTACAAGTTCCCTCACTACAGGCCATGGCTCTCTGTTGTCATGTCTACTCTTACCAAAGTATCT chr1

348 TCAATTTCTAAAACAGTGGGCAAGGAAAAGGAGTGCTTGGCCGTCCTCCCATCATTGGGAGGTGGAGGA 300-19K_T7
 TCAATTTCTAAAACAGTGGGCAAGGAAAAGGAGTGCTTGGCCGTCCTCCCATCATTGGGAGGTGGAGGA chr1

418 AGGAGGATCACAAATTCAGGTCACCCCTTGGCCTTGTAAATGAGTTTGAAGGCTGTCTAGGCTACATGAAA 300-19K_T7
 AGGAGGATCACAAATTCAGGTCACCCCTTGGCCTTGTAAATGAGTTTGAAGGCTGTCTAGGCTACATGAAA chr1

488 CCATGTCTTTAAAAGAAAACCAGACTTTGTTCTTCTGTTGATTCTCACAGTTAAAGTGATTTGGTGT 300-19K_T7
 CCATGTCTTTAAAAGAAAACCAGACTTTGTTCTTCTGTTGATTCTCACAGTTAAAGTGATTTGGTGT chr1

558 TAGCA 300-19K_T7
 TAGCA chr1

>301-19K_SP6 vs. chr8: 35,545,676-35,546,221 (+), 545 bp overlap

1 GAATTCACCTTTGTAGACCAGGCTGGCCTCGAACTCAGAAATCTGCCTGCTTTTGCCTCCCAAGTGCTCGG 301-19K_SP6
 GAATTCACCTTTGTAGACCAGGCTGGCCTCGAACTCAGAAATCTGCCTGCTTTTGCCTCCCAAGTGCTCGG chr8

71 ATTAAGGTGTGAGCCACCACCGCCGGCTCTTTTTTTTTTTTTTTAATTAACAAAAACAAAAACAAAA 301-19K_SP6
 ATTAAGGTGTGAGCCACCACCGCCGGCTCTTTTTTTTTTTTTTTAATTAACAAAAACAAAAACAAAA chr8

140 CAAAAAACCCACTTTTACATTTTCAATGATGTCTCAGGTCATGGACATCAAACAAGCAGTGAACAGTTCT 301-19K_SP6
 CAAAAAACCCACTTTTACATTTTCAATGATGTCTCAGGTCATGGACATCAAACAAGCAGTGAACAGTTCT chr8

210 GGAAGAGTTATGTGACATTTCTCAAAGCTTCTGAAACTGCTCCTTCAATAGCCTTCAGACTATCGAAT 301-19K_SP6
 GGAAGAGTTATGTGACATTTCTCAAAGCTTCTGAAACTGCTCCTTCAATAGCCTTCAGACTATCGAAT chr8

280 TCAGACTTGGGAGTGACGTAACAAATAAATCAGCCTTAATCACAGATCACTTGGCACTCAATGCTATTTT 301-19K_SP6
 TCAGACTTGGGAGTGACGTAACAAATAAATCAGCCTTAATCACAGATCACTTGGCACTCAATGCTATTTT chr8

350 CCTATCCACTTGTAGCTGTTTCTAGCCAGAATATCTATATTCGATGTGGCAGAAATCTAGCACCATGGT 301-19K_SP6
 CCTATCCACTTGTAGCTGTTTCTAGCCAGAATATCTATATTCGATGTGGCAGAAATCTAGCACCATGGT chr8

420 GGTGCACAGTCACTTGAAGGCGTTCCTTTCTGAGCTCAGTCACTACCCAGTGAAGCACCCCTGTTGGG 301-19K_SP6
 GGTGCACAGTCACTTGAAGGCGTTCCTTTCTGAGCTCAGTCACTACCCAGTGAAGCACCCCTGTTGGG chr8

1 CCCAACATAAATGGTGAGGTAATGATGGCAGTGTGGCAGTGTAGTGTCTGTCTTAGAGGGGAGCCTGGT 304-90_T7
 CCCAACATAAATGGTGAGGTAATGATGGCAGTGTGGCAGTGTAGTGTCTGTCTTAGAGGGGAGCCTGGT chrX

71 GGACCTATATGAAACTTTTCCAGTCTCAGCTCTGTAACCTCCGCTTGATGACAACTAGGAGTGATT 304-90_T7
 GGACCTATATGAAACTTTTCCAGTCTCAGCTCTGTAACCTCCGCTTGATGACAACTAGGAGTGATT chrX

141 GTCAACAACCTGTCCACAGCCATGGTAATTCTCTGAAATGCCTCAAATTCATATTAGCCATAAACGTTCC 304-90_T7
 GTCAACAACCTGTCCACAGCCATGGTAATTCTCTGAAATGCCTCAAATTCATATTAGCCATAAACGTTCC chrX

211 ATGTTGGTTATAGAATTAATAAATAAGGTAGGCATCTGGCATAGCTGGCAAGAATGGGATATCGATGCA 304-90_T7
 ATGTTGGTTATAGAATTAATAAATAAGGTAGGCATCTGGCATAGCTGGCAAGAATGGGATATCGATGCA chrX

281 ATCTATCGTATTTACCAGAGCAAGTGAAGTCACTGTTAGATCTAAGAATAGTAGTATCAATTTCAAGA 304-90_T7
 ATCTATCGTATTTACCAGAGCAAGTGAAGTCACTGTTAGATCTAAGAATAGTAGTATCAATTTCAAGA chrX

351 TCATTTTTTATGAACCTTCAGCCCTATAGACAAACCGTTCAAGTAGAAGGAATTGAGAATTGAGTATATAG 304-90_T7
 TCATTTTTTATGAACCTTCAGCCCTATAGACAAACCGTTCAAGTAGAAGGAATTGAGAATTGAGTATATAG chrX

421 AATCTACTACCAGTAAAGATTTAGGGCAAAGCACCCCCAGTACCCAGAAAGAAAACCATTAGTTCTATGT 304-90_T7
 AATCTACTACCAGTAAAGATTTAGGGCAAAGCACCCCCAGTACCCAGAAAGAAAACCATTAGTTCTATGT chrX

491 TTTCTAGGGTGATAGGGCAAAGTAGATAATATGTAGGATTCACAATTTTTTCTCCCCTAGCCTGAGAAA 304-90_T7
 TTTCTAGGGTGATAGGGCAAAGTAGATAATATGTAGGATTCACAATTTTTTCTCCCCTAGCCTGAGAAA chrX

561 GAGCATGGCAATTTTGGATGAAATTTGGGAAGTTTCATTC 304-90_T7
 GAGCATGGCAATTTTGGATGAAATTTGTACAAGTTTCATTC chrX

>307-90_SP6 vs. chr5: 134,432,514-134,433,030 (-), 517 bp overlap

1 CCAGAATTTCAACTCTGGAAGGAGAAAACGAACTCCTGTAAGTAAATTTCTGATCTCCACAGGCAAGCGT 307-90_SP6
 CCAGAATTTCAACTCTGGAAGGAGAAAACGAACTCCTGTAAGTAAATTTCTGATCTCCACAGGCAAGCGT chr5

71 GTGCAGGAATGAACAGACACACATATGCATGCACACAAAATGAGGAAATTAACAAACAATAAAGATGCA 307-90_SP6
 GTGCAGGAATGAACAGACACACATATGCATGCACACAAAATGAGGAAATTAACAAACAATAAAGATGCA chr5

141 ATTCCCATCTGCGCTCATTGGCATCATCTGCAGTTACGGGTGACAAGGAGCTTCACGGCACTGTCTCGCT 307-90_SP6
 ATTCCCATCTGCGCTCATTGGCATCATCTGCAGTTACGGGTGACAAGGAGCTTCACGGCACTGTCTCGCT chr5

211 CCTCCTCCCTAACCCCATCTCACCTGTGTCTGCATCATCAAACTGAGGTAGCCTCTTGCCAGCTG 307-90_SP6
 CCTCCTCCCTAACCCCATCTCACCTGTGTCTGCATCATCAAACTGAGGTAGCCTCTTGCCAGCTG chr5

281 GGGGAGGCCGGCATGGGGTTCATCTGGAAGTTGTCTTCTCCAATGCCTCCAGCTGTGCGTTGATCCGC 307-90_SP6
 GGGGAGGCCGGCATGGGGTTCATCTGGAAGTTGTCTTCTCCAATGCCTCCAGCTGTGCGTTGATCCGC chr5

351 CGCTGCCTGGCTGCCCTGTCCAGCACCCGCCGTGTCCAGGGTCTGGGAGCGAACTAGATGGGGCAAAG 307-90_SP6
 CGCTGCCTGGCTGCCCTGTCCAGCACCCGCCGTGTCCAGGGTCTGGGAGCGAACTAGATGGGGCAAAG chr5

421 AGAGTTACCGGGTCAAGACAGAGGAAAGTTGCACTGCTGTTGCCTAGAGCCCCAGTCTCCTCGCCTCG 307-90_SP6
 AGAGTTACCGGGTCAAGACAGAGGAAAGTTGCACTGCTGTTGCCTAGAGCCCCAGTCTCCTCGCCTCG chr5

491 GCCCCTTATTATGCTGTGAGGAATTC 307-90_SP6
 GCCCCTTATTATGCTGTGAGGAATTC chr5

>307-90_T7 vs. chr15: 78,792,690-78,792,809 (+), 120 bp overlap

1 TTTCTGCCTCCTGTCCCCTCCTCTATCCCATCCTCCACATTGTACCCCAAAGATCTCCTGACTCCTGCC 307-90_T7
 TTTCTGCCTCCTGTCCCCTCCTCTATCCCATCCTCCACATTGTACCCCAAAGATCTCCTGACTCCTGCC chr15

71 CTCATCCACTGGGTCTGAATCCTTCCATGCTCTCCAAACAACCACACCATG 307-90_T7
 CTCATCCACTGGGTCTGAATCCTTCCATGCTCTCCAAACAACCACACCATG chr15

>316-22B_T7 vs. chr7: 82,268,557-82,269,022 (-), 480 bp overlap

351 AAAGTGGGTCACCTGAAAGGCATTAATGCAGTGACATTTACTAAACTGACTGGTTAACCTTTAGATCCA 317-22A_T7
AAAGTGGGTCACCTGAAAGGCATTAATGCAGTGACATTTACTAAACTGACTGGTTAACCTTTAGATCCA chr19

421 AAAGAAGGTAATGAAATAAAACAAACAAATTAGAAAAGAAAATAAACATATCCACAGTCTTTAACAAATGG 317-22A_T7
AAAGAAGGTAATGAAATAAAACAAACAAATTAGAAAAGAAAATAAACATATCCACAGTCTTTAACAAATGG chr19

491 ATCTATTTGGCAGGTGCCATAATTGAACGATTTTGCAGATATTTTGACAACCTGGATAGAATTC 317-22A_T7
ATCTATTTGGCAGGTGCCATAATTGAACGATTTTGCAGATATTTTGACAACCTGGATAGAATTC chr19

>319-20E_T7 vs. chr6: 143,502,805-143,503,360 (+), 556 bp overlap

1 GAATTCACAAAGGTCTAGGGATATGTTGTTGTTAGGGACTGGAAGAAGCCTTAGTGAAAGTCTAAAGGAAGT 319-20E_T7
GAATTCACAAAGGTCTAGGGATATGTTGTTGTTAGGGACTGGAAGAAGCCTTAGTGAAAGTCTAAAGGAAGT chr6

71 TTGGAATCTTGAGTGAGTGTGTATTGTTGACAGGGGCCAGTGCCTCAGACAGACGCTTCAGGGTATGCC 319-20E_T7
TTGGAATCTTGAGTGAGTGTGTATTGTTGACAGGGGCCAGTGCCTCAGACAGACGCTTCAGGGTATGCC chr6

141 CCTTTCCCATATGGCTTAGGCATGGAATTCACAAAGCCTTCCTTGGACTGAGAGAAAATGTTGGTGGT 319-20E_T7
CCTTTCCCATATGGCTTAGGCATGGAATTCACAAAGCCTTCCTTGGACTGAGAGAAAATGTTGGTGGT chr6

211 ATGTAAATTCAAAGTGTCTTCTGGATGACTACTTGTGCAAAAACAAGGAATTCAGCCTCCTCTCCTGGA 319-20E_T7
ATGTAAATTCAAAGTGTCTTCTGGATGACTACTTGTGCAAAAACAAGGAATTCAGCCTCCTCTCCTGGA chr6

281 TATTGACATTCTGAAACTGTCACCTGCAGACATGGCTGTGACTATAAATTCCTGTTGTGTGCTTTA 319-20E_T7
TATTGACATTCTGAAACTGTCACCTGCAGACATGGCTGTGACTATAAATTCCTGTTGTGTGCTTTA chr6

351 AGTAAGTAGGCTGAGATTCTGGGTCAATTATGGTAATTTGGTGCAGCTCCATCAGAGTGCACACAGTCAACC 319-20E_T7
AGTAAGTAGGCTGAGATTCTGGGTCAATTATGGTAATTTGGTGCAGCTCCATCAGAGTGCACACAGTCAACC chr6

421 TGAGCAGGTTTTCTGACACATATGTCTATGTGTCTGTCTTTCCTTCATTCTTGGCTGTCCCAGTCAGGT 319-20E_T7
TGAGCAGGTTTTCTGACACATATGTCTATGTGTCTGTCTTTCCTTCATTCTTGGCTGTCCCAGTCAGGT chr6

491 CTCTAGGACCAAGCCATGTCAGGTGGTGGTGCATAGTGAAAGTGGGTGTATCTAACCCCTTGAACATT 319-20E_T7
CTCTAGGACCAAGCCATGTCAGGTGGTGGTGCATAGTGAAAGTGGGTGTATCTAACCCCTTGAACATT chr6

>320-4J_SP6 vs. chr13: 101,596,209-101,596,723 (+), 516 bp overlap

1 GAATTCACCTTTTGGCCATATCTGTTCTGATGTTTCTAGTTTGGGGTATAGTCCTAATATTTAGATTGC 320-4J_SP6
GAATTCACCTTTTGGCCATATCTGTTCTGATGTTTCTAGTTTGGGGTATAGTCCTAATATTTAGATTGC chr13

71 TGAGCTAACTTTTTAAAGATTTTTAAATTAAGACATAAGTCTTAGTTAGGGTTTCGTTGCTGTGAACAGA 320-4J_SP6
TGAGCTAACTTTTTAAAGATTTTTAAATTAAGACATAAGTCTTAGTTAGGGTTTCGTTGCTGTGAACAGA chr13

141 CTCCATGACCAAAGCAACTCTTACTAAGGACAGCATTTAATTTGGCCCTGGCTTAACAGGTTTCAGAGTTCA 320-4J_SP6
CTCCATGACCAAAGCAACTCTTACTAAGGACAGCATTTAATTTGGCCCTGGCTTAACAGGTTTCAGAGTTCA chr13

211 GTCCATTATCATCAAGGCAGGAACATGGCAGCATCCAGGCAGGCATGGTGCAGGAGAGCTGCGAGTTCC 320-4J_SP6
GTCCATTATCATCAAGGCAGGAACATGGCAGCATCCAGGCAGGCATGGTGCAGGAGAGCTGCGAGTTCC chr13

281 ACCTCTTGTTCCAAAGGCAGGTAGGAGAAGATTGGCTTCCAGGCAGCTAGGACAAGGGTCTTAAAGTCCA 320-4J_SP6
ACCTCTTGTTCCAAAGGCAGGTAGGAGAAGATTGGCTTCCAGGCAGCTAGGACAAGGGTCTTAAAGTCCA chr13

351 TACTCACGTGTGACACACTTCTCCAAACAAGATCACACCTACTCCAACAAGACCACATCTCCAAATAGTGC 320-4J_SP6
TACTCACGTGTGACACACTTCTCCAAACAAGATCACACCTACTCCAACAAGACCACATCTCCAAATAGTGC chr13

421 TATTCCTGAGCCAAGCATATTCAAACCACACAACATAATTGCAATAATTTCTCTCTTCCCTTTTCCCT 320-4J_SP6
TATTCCTGAGCCAAGCATATTCAAACCACACAACATAATTGCAATAATTTCTCTCTTCCCTTTTCCCT chr13

491 CCAAGGCTCCCATATACCCTCCACTC 320-4J_SP6
CCAAGGCTCCCATATACCCTCCACTC chr13

>320-4J_T7 vs. chr13: 101,703,433-101,704,061 (-), 636 bp overlap

491 TCTACAGAGGCCTTCCTCAGGTTGTAATTAGGGCCTAAGGCCTTCTCAGCATCTCACTGGGACCTAAGAC 327-5I_T7
TCTACAGAGGCCTTCCTCAGGTTGTAATTAGGGCCTAAGGCCTTCTCAGTGTCTCACTGGGACCTAAGAC chr7

561 CTTCCCCTGCATCTCACTTGTGTCTAAGGACATTCTAAAGTTCTAATTGGCACCTA 327-5I_T7
CTTCCCCTGCATCTCACTTGTGTCTAAGGACATTCTAAAGTTCTAATTGGCACCTA chr7