





## Segment Hd16

Sequences used for alignment:

- (i) DRJs from genome: Hd16\_DRJ1R, Hd16\_DRJ1L
- (ii) DRJs from BAC clone # BG-42L09+BL-56G14: left\_jct\_BGBL2, right\_jct\_BGBL2
- (iii) HdIV segments: Contig\_BGBL2-12, Contig\_BGBL2-16, Contig\_BGBL2-19, SH\_BGBL2

## Alignment

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left_jct_BGBL2 -----
Hd16_DRJ1L -----
Contig_BGBL2-19 ATAGAGTTGTCATGAGCGTAACTACATTTAAACTTGAAGCACTGTAAGAAGGAACGGTCT
Contig_BGBL2-12 ATAGAGTTGTCATGAGCGTAACTACATTTAAACTTGAAGCACTGTAAGAAGGAACGGTCT
Contig_BGBL2-16 ATAGAGTTGTCATGAGCGTAACTACATTTAAACTTGAAGCACTGTAAGAAGGAACGGTCT
SH_BGBL2 ATAGAGTTGTCATGAGCGTAACTACATTTAAACTTGAAGCACTGTAAGAAGGAACGGTCT
right_jct_BGBL2 ATAGAGTTGTCATGAGCGTAACTACATTTAAACTTGAAGCACTGTAAGAAGGAACGGTCT
Hd16_DRJ1R -----TTGTCATGAGCGTAACTACATTTAAACTTGAAGCACTGTAAGAAGGAACGGTCT
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left_jct_BGBL2 -----ATAAAATTGTCATGAGAG-----GAACTAA
Hd16_DRJ1L -----TTGTCATGAGAG-----GAACTAA
Contig_BGBL2-19 CACAGTACCTTACCTACACAAGTCTCCATCATCTTACACTAATAAGGATAAGAAAAATAA
Contig_BGBL2-12 CACAGTACCTTACCTACACAAGTCTCCATCATCTTACACTAATAAGGATAAGAAAAATAA
Contig_BGBL2-16 CACAGTACCTTACCTACACAAGTCTCCATCATCTTACACTAATAAGGATAAGAAAAATAA
SH_BGBL2 CACAGTACCTTACCTACACAAGTCTCCATCATCTTACACTAATAAGGATAAGAAAAATAA
right_jct_BGBL2 CACAGTACCTTACCTACACAAGTCTCCATCATCTTACACTAATAAGGATAAGAAAAATAA
Hd16_DRJ1R CACAGTACCTTACCTACACAAGTCTCCATCATCTTACACTAATAAGGATAAGAAAAATAA
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left_jct_BGBL2 ATTTAAACTTGTACCAACGTAAGAGG-----AAACGCTCTCACAGTACC-TTTAGCTGC
Hd16_DRJ1L ATTTAAACTTGTACCAACGTAAGAGG-----AAACGCTCTCACAGTACC-TTTAGCTGC
Contig_BGBL2-19 AAGTAAACACATTC AACACAAAACCTTTTATTTCAATCTAAGGAACAGTATATGCTGCACTA
Contig_BGBL2-12 AAGTAAACACATTC AACACAAAACCTTTTATTTCAATCTAAGGAACAGTATATGCTGCACTA
Contig_BGBL2-16 AAGTAAACACATTC AACACAAAACCTTTTATTTCAATCTAAGGAACAGTATATGCTGCACTA
SH_BGBL2 AAGTAAACACATTC AACACAAAACCTTTTATTTCAATCTAAGGAACAGTATATGCTGCACTA
right_jct_BGBL2 AAGTAAACACATTC AACACAAAACCTTTTATTTCAATCTAAGGAACAGTATATGCTGCACTA
Hd16_DRJ1R AAGTAAACACATTC AACACAAAACCTTTTATTTCAATCTAAGGAACAGTATATGCTGCACTA
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left_jct_BGBL2 AAGCTTTAGATTAGATTCAACTGCACCATGGCCGGAACCTGTTGCGAGCCGAGTCAAGCAA
Hd16_DRJ1L AAGCTTTAGATTAGATTCAACTGCACCATGGCCGGAACCTGTTGCGAGCCGAGTCAAGCAA
Contig_BGBL2-19 TTAACACTACTCAGATTAAGCTGCACCATGGCCGGAACCTGTTGCGAGCCGAGTCAAGCAA
Contig_BGBL2-12 TTAACACTACTCAGATTAAGCTGCACCATGGCCGGAACCTGTTGCGAGCCGAGTCAAGCAA
Contig_BGBL2-16 TTAACACTACTCAGATTAAGCTGCACCATGGCCGGAACCTGTTGCGAGCCGAGTCAAGCAA
SH_BGBL2 TTAACACTACTCAGATTAAGCTGCACCATGGCCGGAACCTGTTGCGAGCCGAGTCAAGCAA
right_jct_BGBL2 TTAACACTACTCAGATTAAGCTGCACCATGGCCGGAACCTGTTGCGAGCCGAGTCAAGCAA
Hd16_DRJ1R TTAACACTACTCAGATTAAGCTGCACCATGGCCGGAACCTGTTGCGAGCCGAGTCAAGCAA
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left_jct_BGBL2 CACTTCTGTGTCCGTACGTTTCAGCCATAGAATAATATTCCAAGACGCTCTGGATTGTTTTG
Hd16_DRJ1L CACTTCTGTGTCCGTACGTTTCAGCCATAGAATAATATTCCAAGACGCTCTGGATTGTTTTG
Contig_BGBL2-19 CACTTCTGTGTCCGTACGTTTCAGCCATAGAATAATATTCCAAGACGCTCTGGATTGTTTTG
Contig_BGBL2-12 CACTTCTGTGTCCGTACGTTTCAGCCATAGAATAATATTCCAAGACGCTCTGGATTGTTTTG
Contig_BGBL2-16 CACTTCTGTGTCCGTACGTTTCAGCCATAGAATAATATTCCAAGACGCTCTGGATTGTTTTG
SH_BGBL2 CACTTCTGTGTCCGTACGTTTCAGCCATAGAATAATATTCCAAGACGCTCTGGATTGTTTTG
right_jct_BGBL2 CACTTCTGTGTCCGTACGTTTCAGCCATAGAATAATATTCCAAGACGCTCTGGATTGTTTTG
Hd16_DRJ1R CACTTCTGTGTCCGTACGTTTCAGCCATAGAATAATATTCCAAGACGCTCTGGATTGTTTTG
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left_jct_BGBL2 ATGCACATTTGCAATGATCTCAGTGAACATCTCTTTAGATTCTTTAAGAAGAATCGCGGG
Hd16_DRJ1L ATGCACATTTGCAATGATCTCAGTGAACATCTCTTTAGATTCTTTAAGAAGAATCGCGGG
Contig_BGBL2-19 ATGCACATTTGCAATGATCTCAGTGAACATCTCTTTAGATTCTTTAAGAAGAATCGCGGG
Contig_BGBL2-12 ATGCACATTTGCAATGATCTCAGTGAACATCTCTTTAGATTCTTTAAGAAGAATCGCGGG
Contig_BGBL2-16 ATGCACATTTGCAATGATCTCAGTGAACATCTCTTTAGATTCTTTAAGAAGAATCGCGGG
SH_BGBL2 ATGCACATTTGCAATGATCTCAGTGAACATCTCTTTAGATTCTTTAAGAAGAATCGCGGG
right_jct_BGBL2 ATGCACATTTGCAATGATCTCAGTGAACATCTCTTTAGATTCTTTAAGAAGAATCGCGGG
Hd16_DRJ1R ATGCACATTTGCAATGATCTCAGTGAACATCTCTTTAGATTCTTTAAGAAGAATCGCGGG
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left\_jct\_BGBL2 GATCATATATTTAGTCAACCATGCGGAGACGTGCGCCGTACAGAAATGATGCCAGTGGAG  
Hd16\_DRJ1L GATCATATATTTAGTCAACCATGCGGAGACGTGCGCCGTACAGAAATGATGCCAGTGGAG  
Contig\_BGBL2-19 GATCATATATTTAGTCAACCATGCGGAGACGTGCGCCGTACAGAAATGATGCCAGTGGAG  
Contig\_BGBL2-12 GATCATATATTTAGTCAACCATGCGGAGACGTGCGCCGTACAGAAATGATGCCAGTGGAG  
Contig\_BGBL2-16 GATCATATATTTAGTCAACCATGCGGAGACGTGCGCCGTACAGAAATGATGCCAGTGGAG  
SH\_BGBL2 GATCATATATTTAGTCAACCATGCGGAGACGTGCGCCGTACAGAAATGATGCCAGTGGAG  
right\_jct\_BGBL2 GATCATATATTTAGTCAACCATGCGGAGACGTGCGCCGTACAGAAATGATGCCAGTGGAG  
Hd16\_DRJ1R GATCATATATTTAGTCAACCATGCGGAGACGTGCGCCGTACAGAAATGATGCCAGTGGAG  
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left\_jct\_BGBL2 TTCGTTCTTACACTCACGTCCAGGTGAAACCACTTTATTTGGGTTTTTCTCGCAGGAGCA  
Hd16\_DRJ1L TTCGTTCTTACACTCACGTCCAGGTGAAACCACTTTATTTGGGTTTTTCTCGCAGGAGCA  
Contig\_BGBL2-19 TTCGTTCTTACACTCACGTCCAGGTGAAACCACTTTATTTGGGTTTTTCTCGCAGGAGCA  
Contig\_BGBL2-12 TTCGTTCTTGCACACTCACGTCCAGGTGAAACCACTTTATTTGGGTTTTTCTCGCAGGAGCA  
Contig\_BGBL2-16 TTCGTTCTTGCACACTCACGTCCAGGTGAAACCACTTTATTTGGGTTTTTCTCGCAGGAGCA  
SH\_BGBL2 TTCGTTCTTGCACACTCACGTCCAGGTGAAACCACTTTATTTGGGTTTTTCTCGCAGGAGCA  
right\_jct\_BGBL2 TTCGTTCTTGCACACTCACGTCCAGGTGAAACCACTTTATTTGGGTTTTTCTCGCAGGAGCA  
Hd16\_DRJ1R TTCGTTCTTGCACACTCACGTCCAGGTGAAACCACTTTATTTGGGTTTTTCTCGCAGGAGCA  
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left\_jct\_BGBL2 GGTGTCGCTGGCGACCGCCTTGCACTTCTGGAAGCGAATCTTCTTCACGAACGTGTAGTAT  
Hd16\_DRJ1L GGTGTCGCTGGCGACCGCCTTGCACTTCTGGAAGCGAATCTTCTTCACGAACGTGTAGTAT  
Contig\_BGBL2-19 GGTGTCGCTGGCGACCGCCTTGCACTTCTGGAAGCGAATCTTCTTCACGAACGTGTAGTAT  
Contig\_BGBL2-12 GGTGTCGCTGGCGACCGCCTTGCACTTCTGGAAGCGAATCTTCTTCACGAACGTGTAGTAT  
Contig\_BGBL2-16 GGTGTCGCTGGCGACCGCCTTGCACTTCTGGAAGCGAATCTTCTTCACGAACGTGTAGTAT  
SH\_BGBL2 GGTGTCGCTGGCGACCGCCTTGCACTTCTGGAAGCGAATCTTCTTCACGAACGTGTAGTAT  
right\_jct\_BGBL2 GGTGTCGCTGGCGACCGCCTTGCACTTCTGGAAGCGAATCTTCTTCACGAACGTGTAGTAT  
Hd16\_DRJ1R GGTGTCGCTGGCGACCGCCTTGCACTTCTGGAAGCGAATCTTCTTCACGAACGTGTAGTAT  
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left\_jct\_BGBL2 TACGGGCAGCCTCACAAAATCTCTCTCACCCGGCGCCGCTCCAAAATAGAGGCATGAG  
Hd16\_DRJ1L TACGGGCAGCCTCACAAAATCTCTCTCACCCGGCGCCGCTCCAAAATAGAGGCATGAG  
Contig\_BGBL2-19 TACGGGCAGCCTCACAAAATCTCTCTCACCCGGCGCCGCTCCAAAATAGAGGCATGAG  
Contig\_BGBL2-12 TACGGGCAGCCTCACAAAATCTCTCTCACCCGGCGCCGCTCCAAAATAGAGGCATGAG  
Contig\_BGBL2-16 TATGGGCAGCCTCACAAAATCTCTCTCACCCGGCGCCGCTCCAAAATAGAGGCATGAG  
SH\_BGBL2 TACGGGCAGCCTCACAAAATCTCTCTCACCCGGCGCCGCTCCAAAATAGAGGCATGAG  
right\_jct\_BGBL2 TACGGGCAGCCTCACAAAATCTCTCTCACCCGGCGCCGCTCCAAAATAGAGGCATGAG  
Hd16\_DRJ1R TACGGGCAGCCTCACAAAATCTCTCTCACCCGGCGCCGCTCCAAAATAGAGGCATGAG  
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left\_jct\_BGBL2 CCAGTCCCAATTTATCAGCAGGCGATCTTCTTCTGGCCTTGTTGCATCGAAGCTGTAGCG  
Hd16\_DRJ1L CCAGTCCCAATTTATCAGCAGGCGATCTTCTTCTGGCCTTGTTGCATCGAAGCTGTAGCG  
Contig\_BGBL2-19 CCAGTCCCAATTTATCAGCAGGCGATCTTCTTCTGGCCTTGTTGCATCGAAGCTGTAGCG  
Contig\_BGBL2-12 CCAGTCCCAATTTATCAGCAGGCGATCTTCTTCTGGCCTTGTTGCATCGAAGCTGTAGCG  
Contig\_BGBL2-16 CCAGTCCCAATTTATCAGCAGGCGATCTTCTTCTGGCCTTGTTGCATCGAAGCTGTAGCG  
SH\_BGBL2 CCAGTCCCAATTTATCAGCAGGCGATCTTCTTCTGGCCTTGTTGCATCGAAGCTGTAGCG  
right\_jct\_BGBL2 CCAGTCCCAATTTATCAGCAGGCGATCTTCTTCTGGCCTTGTTGCATCGAAGCTGTAGCG  
Hd16\_DRJ1R CCAGTCCCAATTTATCAGCAGGCGATCTTCTTCTGGCCTTGTTGCATCGAAGCTGTAGCG  
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left\_jct\_BGBL2 GACGGGGCATGCCTTCCCGTTCAGGAAAGTCAAGTCCAGGTTTCGGATCGATGTAAGAAA  
Hd16\_DRJ1L GACGGGGCATGCCTTCCCGTTCAGGAAAGTCAAGTCCAGGTTTCGGATCGATGTAAGAAA  
Contig\_BGBL2-19 GACGGGGCATGCCTTCCCGTTCAGGAAAGTCAAGTCCAGGTTTCGGATCGATGTAAGAAA  
Contig\_BGBL2-12 GACGGGGCATGCCTTCCCGTTCAGGAAAGTCAAGTCCAGGTTTCGGATCGATGTAAGAAA  
Contig\_BGBL2-16 GACGGGGCATGCCTTCCCGTTCAGGAAAGTCAAGTCCAGGTTTCGGATCGATGTAAGAAA  
SH\_BGBL2 GACGGGGCATGCCTTCCCGTTCAGGAAAGTCAAGTCCAGGTTTCGGATCGATGTAAGAAA  
right\_jct\_BGBL2 GACGGGGCATGCCTTCCCGTTCAGGAAAGTCAAGTCCAGGTTTCGGATCGATGTAAGAAA  
Hd16\_DRJ1R GACGGGGCATGCCTTCCCGTTCAGGAAAGTCAAGTCCAGGTTTCGGATCGATGTAAGAAA  
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left\_jct\_BGBL2 CTGTTGATATGCTACGTTGAAACGTATAAATTCGATGAAGCTGAAAGGGGCGCCATTCCG  
Hd16\_DRJ1L CTGTTGATATGCTACGTTGAAACGTATAAATTCGATGAAGCTGAAAGGGGCGCCATTCCG  
Contig\_BGBL2-19 CTGTTGATATGCTACGTTGAAACGTATAAATTCGATGAAGCTGAAAGGGGCGCCATTCCG  
Contig\_BGBL2-12 CTGTTGATATGCTACGTTGAAACGTATAAATTCGATGAAGCTGAAAGGGGCGCCATTCCG  
Contig\_BGBL2-16 CTGTTGATATGCTACGTTGAAACGTATAAATTCGATGAAGCTGAAAGGGGCGCCATTCCG  
SH\_BGBL2 CTGTTGATATGCTACGTTGAAACGTATAAATTCGATGAAGCTGAAAGGGGCGCCATTCCG  
right\_jct\_BGBL2 CTGTTGATATGCTACGTTGAAACGTATAAATTCGATGAAGCTGAAAGGGGCGCCATTCCG  
Hd16\_DRJ1R CTGTTGATATGCTACGTTGAAACGTATAAATTCGATGAAGCTGAAAGGGGCGCCATTCCG  
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left_jct_BGBL2      CATGGCAGGCCCGCGGAACGTGAAGGTGTCCACCGGGTAAGTATGTGTTCTGTGCGTGATC
Hd16_DRJ1L         CATGGCAGGCCCGCGGAACGTGAAGGTGTCCACCGGGTAAGTATGTGTTCTGTGCGTGATC
Contig_BGBL2-19    CATGGCAGGCCCGCGGAACGTGAAGGTGTCCACCGGGTAAGTATGTGTTCTGTGCGTGATC
Contig_BGBL2-12    CATGGCAGGCCCGCGGAACGTGAAGGTGTCCACCGGGTAAGTATGTGTTCTGTGCGTGATC
Contig_BGBL2-16    CATGGCAGGCCCGCGGAACGTGAAGGTGTCCACCGGGTAAGTATGTGTTCTGTGCGTGATC
SH_BGBL2           CATGGCAGGCCCGCGGAACGTGAAGGTGTCCACCGGGTAAGTATGTGTTCTGTGCGTGATC
right_jct_BGBL2    CATGGCAGGCCCGCGGGACGTGAAGGTGTCCACCGGGTAAGTAAGTGTTCTGTGCGTGATC
Hd16_DRJ1R         CATGGCAGGCCCGCGGGACGTGAAGGTGTCCACCGGGTAAGTAAGTGTTCTGTGCGTGATC
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left_jct_BGBL2      TTCGTTGAACGGCATGTTGAGTTCTGGATATCACCTGCGTCTGGACGATGTTCCCTTTGTG
Hd16_DRJ1L         TTCGTTGAACGGCATGTTGAGTTCTGGATATCACCTGCGTCTGGACGATGTTCCCTTTGTG
Contig_BGBL2-19    TTCGTTGAACGGCATGTTGAGTTCTGGATATCACCTGCGTCTGGACGATGTTCCCTTTGTG
Contig_BGBL2-12    TTCGTTGAACGGCATGTTGAGTTCTGGATATCACCTGCGTCTGGACGATGTTCCCTTTGTG
Contig_BGBL2-16    TTCGTTGAACGGCATGTTGAGTTCTGGATATCACCTGCGTCTGGACGATGTTCCCTTTGTG
SH_BGBL2           TTCGTTGAACGGCATGTTGAGTTCTGGATATCACCTGCGTCTGGACGATGTTCCCTTTGTG
right_jct_BGBL2    TTCGTGAACGGCATGTTGAGTTCTGGATATCACCTGCGTCTGGATGATGTTCCCTCGTG
Hd16_DRJ1R         TTCGTGAACGGCATGTTGAGTTCTGGATATCACCTGCGTCTGGATGATGTTCCCTCGTG
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left_jct_BGBL2      AATGTTCACGGTTGAGTGTCTAGCCGTCGACTGCGCGCAAATCCATTTATACCACTCCA
Hd16_DRJ1L         AATGTTCACGGTTGAGTGTCTAGCCGTCGACTGCGCGCAAATCCATTTATACCACTCCA
Contig_BGBL2-19    AATGTTCACGGTTGAGTGTCTAGCCGTCGACTGCGCGCAAATCCATTTATACCACTCCA
Contig_BGBL2-12    AATGTTCACGGTTGAGTGTCTAGCCGTCGACTGCGCGCAAATCCATTTATACCACTCCA
Contig_BGBL2-16    AATGTTCACGGTTGAGTGTCTAGCCGTCGACTGCGCGCAAATCCATTTATACCACTCCA
SH_BGBL2           AATGTTCACGGTTGAGTGTCTAGCCGTCGACTGCGCGCAAATCCATTTATACCACTCCA
right_jct_BGBL2    AATGTTCACGGTTGAGTGTCTAGCCGTCGACTGCGCGCAAATCCATTTATACCACTCCA
Hd16_DRJ1R         AATGTTCACGGTTGAGTGTCTAGCCGTCGACTGCGCGCAAATCCATTTATACCACTCCA
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left_jct_BGBL2      TAGCTTATCAT
Hd16_DRJ1L         TAGCTTATCAT
Contig_BGBL2-19    TAGCTTATCAT
Contig_BGBL2-12    TAGCTTATCAT
Contig_BGBL2-16    TAGCTTATCAT
SH_BGBL2           TAGCTTATCAT
right_jct_BGBL2    TAATTTATCAT
Hd16_DRJ1R         TAATTTATCAT
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## Segment Hd29 (present in BAC clone # BR-08001)

Sequences used for alignment:

- (i) DRJs from genome: Hd29\_DRJ1R, Hd29\_DRJ1L
- (ii) DRJs from BAC clone # BR-08001: left\_jct\_BR, right\_jct\_BR
- (iii) HdIV segments: Contig\_BR-1, Contig\_BR-4, Contig\_BR-7, Contig\_BR-10, SH\_BR

## Alignment

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left_jct_BR      -----TAGCGATCGCAGTGCCTCGCTGCAT
Hd29_DRJ1L      ATTTTCGTGGCAGGCTTAGTT-TTGATGGAGGGACGTAGCGATCGCAGTGCCTCGCTGCAT
Contig_BR-10    -----TGGCCACCGCTGTGCGTTGTTGAAC
Contig_BR-1     -----TGGCCACCGCTGTGCGTTGTTGAAC
Contig_BR-7     -----TGGCCACCGCTGTGCGTTGTTGAAC
SH_BR          -----TGGCCACCGCTGTGCGTTGTTGAAC
Contig_BR-4     -----TGGCCACCGCTGTGCGTTGTTGAAC
right_jct_BR    -----TGGCCACCGCTGTGCGTTGTTGAAC
Hd29_DRJ1R      ATTTTCGTGGCAAGCGACTTTTCATCGTAGAACGGATGGCCACCGCTGTGCGTTGTTGAAC
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left_jct_BR      CAATGATGCAGCTTTGTGTTCTTCTCGAACGGTGAACATTCGTGCAACCACTGACACG
Hd29_DRJ1L      CAATGATGCAGCTTTGTGTTCCTTCTCGAACGGTGAACATTCGTGCAACCACTGACACG
Contig_BR-10    CAATGATCCAACTTTGTGTTCTTCAGGAACGGTGAACATTCGTGCAACTACTTGACACG
Contig_BR-1     CAATGATCCAACTTTGTGTTCTTCAGGAACGGTGAACATTCGTGCAACTACTTGACACG
Contig_BR-7     CAATGATCCAACTTTGTGTTCTTCAGGAACGGTGAACATTCGTGCAACTACTTGACACG
SH_BR          CAATGATCCAACTTTGTGTTCTTCAGGAACGGTGAACATTCGTGCAACTACTTGACACG
Contig_BR-4     CAATGATCCAACTTTGTGTTCTTCAGGAACGGTGAACATTCGTGCAACTACTTGACACG
right_jct_BR    CAATGATCCAACTTTGTGTTCTTCAGGAACGGTGAACATTCGTGCAATCAACTTGACACG
Hd29_DRJ1R      CAATGATCCAACTTTGTGTTCTTCAGGAACGGTGAACATTCGTGCAATCAACTTGACACG
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## Segment Hd22

Sequences used for alignment:

- (i) DRJs from genome: Hd22\_DRJ1R, Hd22\_DRJ1L
- (ii) DRJs from BAC clone # CN-29M18: left\_junction, right\_junction
- (iii) HdIV segments: Contig\_CN-31, Contig\_CN-33, Contig\_CN-36, Contig\_CN-39

## Alignment

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left_junction      CAATAGGGTGAATTCAAACGCTGGTCCAATGGCAGGAGCTTGGCAGGACAGATGACATC
Hd22_DRJ1L        -----AATTCAAACGCTGGTCCCAATGGCAGGAGCTTGGCAGGACAGATGACATC
Contig_CN-31      CAATAGGGTGAATTCAAACGCTGGTCCAATGGCAGGAGCTTGGCAGGACAGATGACATC
Contig_CN-33      CAATAGGGTGAATTCAAACGCTGGTCCAATGGCAGGAGCTTGGCAGGACAGATGACATC
Contig_CN-39      CAATAGGGTGAATTCAAACGCTGGTCCAATGGCAGGAGCTTGGCAGGACAGATGACATC
Contig_CN-36      CAATAGGGTGAATTCAAACGCTGGTCCAATGGCAGGAGCTTGAACAAGGCAGATGATATC
right_junction    CATTGAGAAAACTCAAGCGCCGATAGCAATGGCAGGAGCTTGACAAGGCAGATGATATC
Hd22_DRJ1R        -----AACTCAAGCGCCGATAGCAATGGCAGGAGCTTGACAAGGCAGATGATATC
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left_junction      GAGTGAAATGCGTAGGAGTCTGAAACAGCGCGTCGTGAACAATATCGTGACCATTGATCGC
Hd22_DRJ1L        GAGTGAAATGCGTAGGAGTCTGAAACAGCGCGTCGTGAACAATATCGTGACCATTGATCGC
Contig_CN-31      GAGTGAAATGCGTAGGAGTCTGAAACAGCGCGTCGTGAACAATATCGTGACCATTGATCGC
Contig_CN-33      GAGTGAAATGCGTAGGAGTCTGAAACAGCGCGTCGTGAACAATATCGTGACCATTGATCGC
Contig_CN-39      GAGTGAAATGCGTAGGAGTCTGAAACAGCGCGTCGTGAACAATATCGTGACCATTGATCGC
Contig_CN-36      GAGTGAGTGCCTAGGTCCTGGAACCGCGGGTCGTGAACAATATCGTGACCATTGATCGC
right_junction    GAGTGAGTGCCTAGGTCCTGGAACCGCGGGTCGTGAACAATATCGTGACCATTGATCGC
Hd22_DRJ1R        GAGTGAGTGCCTAGGTCCTGGAACCGCGGGTCGTGAACAATATCGTGACCATTGATCGC
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left_junction      CATAGCGACTTGCCGCACTCTCAGGATCGTGATCTAAAA-----CGTTTCACGTGA
Hd22_DRJ1L        CATAGCGACTTGCCGCACTCTCAGGATCGTGATCTAAAA-----CGTTTCACGTGA
Contig_CN-31      CACAGCGACTTGGCGACTTGGCACACGTCAGCGTCAAGTTCACAAAAATCTGACGCGA
Contig_CN-33      CACAGCGACTTGGCGACTTGGCACACGTCAGCGTCAAGTTCACAAAAATCTGACGCGA
Contig_CN-39      CATAGCGACTTGCGCACTTGGCACACGTCAGCGTCAAGTTCACAAAAATCTGACGCGA
Contig_CN-36      CACAGCGACTTGGCGACTTGGCACACGTCAGCGTCAAGTTCACAAAAATCTGACGCGA
right_junction    CACAGCGACTTGCCGCACTTGGCACACGTCAGCGTCAAGTTCACAAAAATCTGACGCGA
Hd22_DRJ1R        CACAGCGACTTGCCGCACTTGGCACACGTCAGCGTCAAGTTCACAAAAATCTGACGCGA
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## Segment Hd19

Sequences used for alignment:

- (i) DRJs from genome: Hd19\_DRJ1R, Hd19\_DRJ1L
- (ii) DRJs from BAC clone # CP-38F08+CQ-40J21: CPCQ\_right, CPCQ\_left
- (iii) HdIV segments: jct\_CPCQ-28, jct\_CPCQ-27, jct\_CPCQ-23, jct\_CPCQ-22

## Alignment

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CPCQ_left         TTTTTGCTGGTTCATGTTTCAGAGCAGCCGGTCTATGTGATACACGCTGCTTAGCCTGGT
Hd19_DRJ1L        TTTTTGCTGGTTCATGTTTCAGAGCAGCCGGTCTATGTGATACACGCTGCTTAGCCTGGT
jct_CPCQ-28      TTTTTGCTGCTTCATGTTCTCAGAGCAGCTTGTCTACATGATACACGCTGATTTGTC-TGT
jct_CPCQ-27      TTTTTGCTGCTTCATGTTCTCAGAGCAGCTTGTCTACATGATACACGCTGATTTGTC-TGT
jct_CPCQ-23      TTTTTGCTGCTTCATGTTCTCAGAGCAGCTTGTCTACATGATACACGCTGATTTGTC-TGT
jct_CPCQ-22      TTTTTGCTGCTTCATGTTCTCAGAGCAGCTTGTCTACATGATACACGCTGATTTGTC-TGT
CPCQ_right       TTTTTGCTGCTTCATGTTCTCAGAGCAGCTTGTCTACATGATACACGCTGATTTGTC-TGT
Hd19_DRJ1R        TTTTTGCTGCTTCATGTTCTCAGAGCAGCTTGTCTACATGATACACGCTGATTTGTC-TGT
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CPCQ_left	GACGGCACGATGGTTCCCTCATGCTGCACGAGCTCTGTGAGCTTT
Hd19_DRJ1L	GACGGCACGATGGTTCCCTCATGCTGCACGAGCTCTGTGAGCTTT
jct_CPCQ-28	GACGGCACGATGGTTCCCTCATGCTGCACGAGCTCTGTGAGCTTT
jct_CPCQ-27	GACGGCACGATGGTTCCCTCATGCTGCACGAGCTCTGTGAGCTTT
jct_CPCQ-23	GACGGCACGATGGTTCCCTCATGCTGCACGAGCTCTGTGAGCTTT
jct_CPCQ-22	GACGGCACGATAATTCCCTCATGCTGCACGAGCTCTGTGAGCTTT
CPCQ_right	GACGGCACGATAATTCCCTCATGCTGCACGAGCTTTGTGAGCTTT
Hd19_DRJ1R	GACGGCACGATAATTCCCTCATGCTGCACGAGCTTTGTGAGCTTT

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## Segments Hd28

Sequences used for alignment:

- (i) DRJs from genome: Hd28\_DRJ1R, Hd28\_DRJ1L, Hd24\_DRJ1R (reverse), Hd24\_DRJ1L (reverse)
- (ii) DRJs from BAC clone # CR-47M17: CR\_left, CR\_right
- (iii) HdIV segments: Contig\_CR-05, Contig\_CR-06, Contig\_CR-09, Contig\_CR-10

## Alignment

CR_left	GCCTTTGAGCTGAGCT-GCATGAGGTTTTCATGTCCGATAACTGGATTCATTTGTCA
Hd28_DRJ1L	GCCTTTGAGCTGAGCT-GCATGAGGTTTTCATGTCCGATAACTGGATTCATTTGTCA
Contig_CR-05	GCCTTTGGAGCTAAACTTGCACGAGATTTCCGGTGTCCGTGATAACTGAATGGCATTGTCA
Contig_CR-06	GCCTTTGGAGCTAAACTTGCACGAGATTTCCGGTGTCCGTGATAACTGAATGGCATTGTCA
CR_right	GCCTTTGAGCTAAACTTGCACGAGATTTCCGGTGTCCGTGATAACTGAATGGCATTGTCA
Hd28_DRJ1R	GCCTTTGAGCTAAACTTGCACGAGATTTCCGGTGTCCGTGATAACTGAATGGCATTGTCA

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CR_left	GGCGTAAGCATTATGACGGCGGTGGTGTAGGCGTTGCTTGGGAAGGTTGGTGAACCG
Hd28_DRJ1L	GGCGTAAGCATTATGACGGCGGTGGTGTAGGCGTTGCTTGGGAAGGTTGGTGAACCG
Contig_CR-05	GGCGTAATATTTATGACGGC-----GGTGATG
Contig_CR-06	GGCGTAATATTTATGACGGC-----GGTGATG
CR_right	GGCGTAAATTTATGACGGC-----GGTGATG
Hd28_DRJ1R	GGCGTAAATTTATGACGGC-----GGTGATG

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CR_left	TCCACGTAGATTTCAGGCGTGAACGGAGAGCTGAAGGTATAGTAGTCGTTTCGACCAACT
Hd28_DRJ1L	TCCACGTAGATTTCAGGCGTGAACGGAGAGCTGAAGGTATAGTAGTCGTTTCGACCAACT
Contig_CR-05	TTAACGTAGGTTTCAGGCGTTAGACTGAGAGCCGGAAGGTATGGTAGTCGTTTCGACCGTCT
Contig_CR-06	TTAACGTAGGTTTCAGGCGTTAGACTGAGAGCCGGAAGGTATGGTAGTCGTTTCGACCGTCT
CR_right	TTAACGTAGGTTTCAGGCGTTAGACTGAGAGCCGGAAGGTATGGTAGTCGTTTCGACCGTCT
Hd28_DRJ1R	TTAACGTAGGTTTCAGGCGTTAGACTGAGAGCCGGAAGGTATGGTAGTCGTTTCGACCGTCT

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CR_left	CGGAATCACACCGACGAAACTATTGTCCATTGCTCAGGCTATGAGGACTTGAGGCAAT
Hd28_DRJ1L	CGGAATCACACCGACGAAACTATTGTCCATTGCTCAGGCTATGAGGACTTGAGGCAAT
Contig_CR-05	CCGAATCACGCTGACGAGAACTTTCGTTTCATCGCTTAAGCTCTGAGGACTTGACGCAAT
Contig_CR-06	CCGAATCACGCTGACGAGAACTTTCGTTTCATCGCTTAAGCTCTGAGGACTTGACGCAAT
CR_right	CCGAATCACGCTGACGAGAACTTTCGTTTCATCGCTTAAGCTCTGAGGACTTGACGCAAT
Hd28_DRJ1R	CCGAATCACGCTGACGAGAACTTTCGTTTCATCGCTTAAGCTCTGAGGACTTGACGCAAT

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CR_left	CAAGTTCGGACGCAAAAGT-----TTTGTTCGGCCATAGATCACAAGTAAGAA
Hd28_DRJ1L	CAAGTTCGGACGCAAAAGT-----TTTGTTCGGCCATAGATCACAAGTAAGAA
Contig_CR-05	CAAGTTCGGATGATAAACGCCAGACGCAAAAGTTTGTTCATAGATCACAAGTAAGAA
Contig_CR-06	CAAGTTCGGATGATAAACGCCAGACGCAAAAGTTTGTTCATAGATCACAAGTAAGAA
CR_right	CAAGTTCGGATGATAAACGCCAGACGCAAAAGTTTGTTCATAGATCACAAGTAAGAA
Hd28_DRJ1R	CAAGTTCGGATGATAAACGCCAGACGCAAAAGTTTGTTCATAGATCACAAGTAAGAA

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CR_left	CAGTTCTGGACAGCTGGACAGTCCACCGATACCTCACAAGACTGTAAA-ACCTCTGGAC
Hd28_DRJ1L	CAGTTCTGGACAGCTGGACAGTCCACCGATACCTCACAAGACTGTAAA-ACCTCTGGAC
Contig_CR-05	CAGTTCTTACGGACCTGACAGTCCAACATTACTCTCAGACACTGTAAA-ACCTATGGAC
Contig_CR-06	CAGTTCTTACGGACCTGACAGTCCAACATTACTCTCAGACACTGTAAA-ACCTATGGAC
CR_right	CAGTTCTTACGGACCTGACAGTCCAACATTACTCTCAGACACTGTAAA-ACCTATGGAC
Hd28_DRJ1R	CAGTTCTTACGGACCTGACAGTCCAACATTACTCTCAGACACTGTAAA-ACCTATGGAC

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CR\_left GTACTGCGCACGTACCCAGTCCACGAAACACTCGTGCCACATCCATTTGATGTTGGCTT  
Hd28\_DRJ1L GTACTGCGCACGTACCCAGTCCACGAAACACTCGTGCCACATCCATTTGATGTTGGCTT  
Contig\_CR-05 GTACTTCGCACGTACCCGAGTCCACGAAACACTCGTGCTACATCCATTTGACGTTGGCCT  
Contig\_CR-06 GTACTTCGCACGTACCCGAGTCCACGAAACACTCGTGCTACATCCATTTGACGTTGGCCT  
CR\_right GTACTTCGCACGTACCCGAGTCCACGAAACACTCGTGCTACATCCATTTGACGTTGGCCT  
Hd28\_DRJ1R GTACTTCGCACGTACCCGAGTCCACGAAACACTCGTGCTACATCCATTTGACGTTGGCCT  
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CR\_left CTGCCAGGCATGTCGTAT--AGATTCCACGCGTGTGCCGTGTCCAGAAAAGCTTT  
Hd28\_DRJ1L CTGCCAGGCATGTCGTAT--AGATTCCACGCGTGTGCCGTGTCCAGAAAAGCTTT  
Contig\_CR-05 TCT---GACAAGGCCACTATAGAGTCCAGCGTGTGCCGTGTCCCGAAGGAGCTTT  
Contig\_CR-06 TCT---GACAAGGCCACTATAGAGTCCAGCGTGTGCCGTGTCCCGAAGGAGCTTT  
CR\_right TCT---GACAAGGCCACTATAGAGTCCAGCGTGTGCCGTGTCCCGAAGGAGCTTT  
Hd28\_DRJ1R TCT---GACAAGGCCACTATAGAGTCCAGCGTGTGCCGTGTCCCGAAGGAGCTTT  
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CR\_left GTTCACAACCGCGACTTTTGACTGTACCTTTGTGTTACAGTTGCGTTACGTAACACTACT  
Hd28\_DRJ1L GTTCACAACCGCGACTTTTGACTGTACCTTTGTGTTACAGTTGCGTTACGTAACACTACT  
Contig\_CR-05 T-ACTCCAACCGACTTTTTAGTGTGACCTTTGTCGTTACAGTTGCGTTACGTAACACTACT  
Contig\_CR-06 T-ACTCCAACCGACTTTTTAGTGTGACCTTTGTCGTTACAGTTGCGTTACGTAACACTACT  
CR\_right T-ACTCCAACCGACTTTTTAGTGTGACCTTTGTCGTTACAGTTGCGTTACGTAACACTACT  
Hd28\_DRJ1R T-ACTCCAACCGACTTTTTAGTGTGACCTTTGTCGTTACAGTTGCGTTACGTAACACTACT  
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CR\_left ACTGTGGAACCTTCTCACTGCCACAGTCAACAACAGCTATCGACAACGTGTTCTTTCAGTAT  
Hd28\_DRJ1L ACTGTGGAACCTTCTCACTGCCACAGTCAACAACAGCTATCGACAACGTGTTCTTTCAGTAT  
Contig\_CR-05 ACTGTGGAACCTTCTCACTACCACAGTTACAACAGCTTATCGGCAACAGTCCCTTCAGTAT  
Contig\_CR-06 ACTGTGGAACCTTCTCACTACCACAGTTACAACAGCTTATCGGCAACAGTCCCTTCAGTAT  
CR\_right ACTGTGGAACCTTCTCACTACCACAGTTACAACAGCTTATCGGCAACAGTCCCTTCAGTAT  
Hd28\_DRJ1R ACTGTGGAACCTTCTCACTACCACAGTTACAACAGCTTATCGGCAACAGTCCCTTCAGTAT  
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CR\_left CAAGAAGTCATTATGCAAGTAGAGAATGGCCGGGGTTTAAGTTGCATGAAA-GCACTCAA  
Hd28\_DRJ1L CAAGAAGTCATTATGCAAGTAGAGAATGGCCGGGGTTTAAGTTGCATGAAA-GCACTCAA  
Contig\_CR-05 CAAGAAGTAATTATCAAGTGGAGAATGGCCGGGGTTTAAGTTGCATGAAA-GCACTCAA  
Contig\_CR-06 CAAGAAGTAATTATCAAGTGGAGAATGGCCGGGGTCGG-AGTTGCATGAAA-GCACTCAA  
CR\_right CAAGAAGTAATTATCAAGTGGAGAATGGCCGGGGTCGG-AGTTGCATGAAAAGCACGGAA  
Hd28\_DRJ1R CAAGAAGTAATTATCAAGTGGAGAATGGCCGGGGTCGG-AGTTGCATGAAAAGCACGGAA  
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CR\_left TTGTCTACAATGCAGACGAG  
Hd28\_DRJ1L TTGTCTACAATGCAGACGAG  
Contig\_CR-05 TTGTCTACAATGCAGACGAG  
Contig\_CR-06 TTGTCTACAATGCAGACGAG  
CR\_right GTGTGTACAATACAGACGGG  
Hd28\_DRJ1R GTGTGTACAATACAGACGGG  
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