

1 **Supplementary Figures and Tables for**

2 **Chromosomal inversion polymorphisms in two sympatric ascidian lineages**

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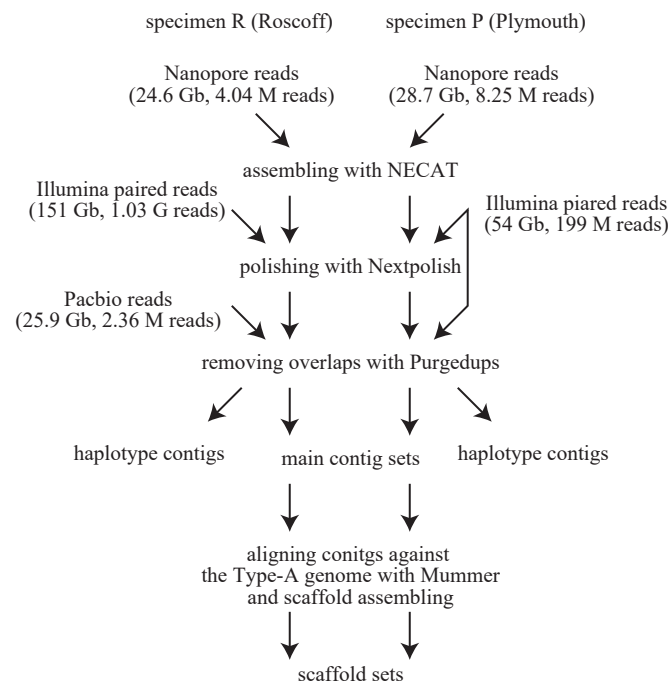
23 **This PDF document contains:**

24 **supplementary figures S1 to S10**

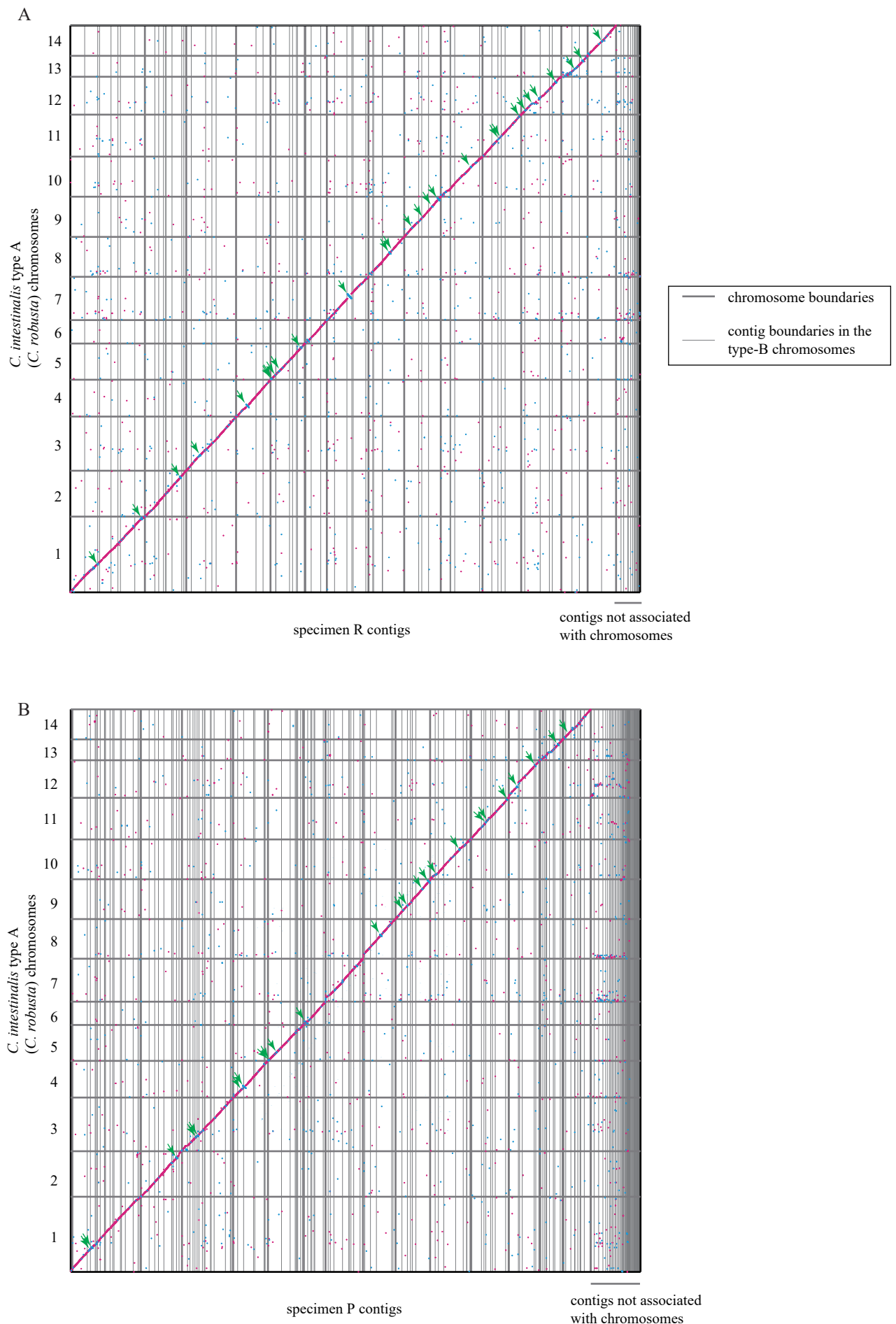
25 **supplementary tables S1 to S7**

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Figure S1

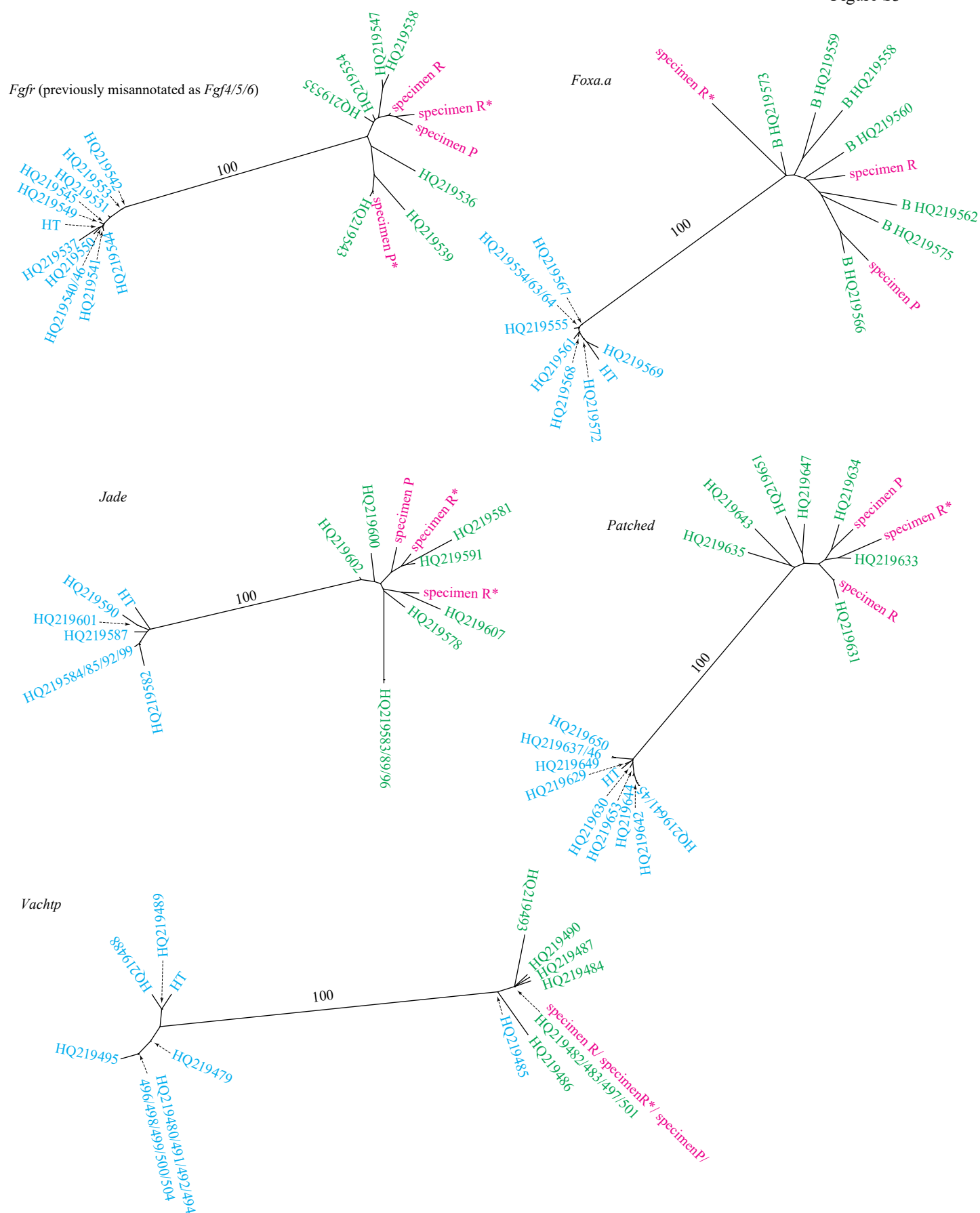


Supplementary Figure S1. Chromosomal assembly of two *Ciona intestinalis* type-B individuals. The assembling strategy adopted in the present study.



Supplementary Figure S2. Alignments of all contigs against the inbred type-A genome. Contigs for (A) specimen R and (B) specimen P are sorted on the basis of the alignments. Forward-to-forward alignments are shown by magenta, and Forward-to-reverse alignments are shown by cyan. Green arrows indicate inversions identified from gene orders and genomic alignments.

Figure S3



Supplementary Figure S3. Molecular phylogenetic analyses to confirm that the animals we used were type B. The sequences retrieved from chromosomes and haplotype contigs of specimens R and P are shown by magenta. Sequences retrieved from haplotype contigs are marked by asterisks. Note that *Jade* was not found in the specimen-R chromosomes, but two *Jade* loci were found in the specimen-R haplotype contig set. The sequences from the inbred type-A animals (HT-line) are shown by 'HT'. Labels for other sequences indicate their accession numbers for the DDBJ/EMBL/Genbank database. Sequences for type-A and type-B animals are shown in cyan and green, respectively. These classifications are based on a previous study (Nydam and Harrison 2011), although HQ219485 is likely to be mis-annotated. Separation between type-A and type-B animals is supported by 100 bootstrap pseudoreplications. The alignments before removing gaps are shown in figure S4.

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HQ219546 (A) -----CTTGTTAGCTATTTTCGTTACGGTAGCGAAG---ATTAATAATGGACA
HQ219545 (A) -----CTTGTTAGCTATTTTCGTTACGGTAGCGAAG---ATTAATAATGGACA
HQ219544 (A) -----CTTGTTAGCTATTTTCGTTACGGTAGCGAAG---ATTAATAATGGACA
HQ219542 (A) -----CTTGTTAGCTATTTTCGTTACGGTAGCGAAG---ATTAATAATGGACA
HQ219541 (A) -----CTTGTTAGCTATTTTCGTTACGGTAGCGAAG---ATTAATAATGGACA
HQ219540 (A) -----CTTGTTAGCTATTTTCGTTACGGTAGCGAAG---ATTAATAATGGACA
HQ219537 (A) -----CTTGTTAGCTATTTTCGTTACGGTAGCGAAG---ATTAATAATGGACA
HQ219531 (A) -----CTTGTTAGCTATTTTCGTTACGGTAGCGAAG---ATTAATAATGGACA
HQ219547 (B) -----AACATAACTTGTATTCTCTTCGATTACGTTAGCGAAGATTAATAATGATGGACA
HQ219543 (B) -----CATAACTTGTATTCTCTTCGATTACGTTAGCGAAGATTAATAATAATGGACA
HQ219539 (B) -----CATAACTTGTATTCTCTTCGATTACGTTAGCGAAGATTAATAATAATGGACA
HQ219538 (B) -----AACATAACTTGTATTCTCTTCGATTACGTTAGCGAAGATTAATAATGATGGACA
HQ219536 (B) -----ATAACTTATTATCTCTTCGATTACGTTAGCGAAG---ATTAATAATGGACA
HQ219535 (B) -----TAACTTGTATTCTCTTCGATTACGTTAGCGAAG---ATTAATAATGGACA
HQ219534 (B) -----TATATAACATAACTTGTATTCTCTTCGATTACGTTAGCGAAG---ATTAATAATGGACA
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specimen P* -----CATAACTTGTATTCTCTTCGATTACGTTAGCGAAGATTAATAATAATGGACA
specimen R -----TATATAACATAACTTGTATTCTCTTCGATTACGTTAGCGAAGATTAATAATGATGGACA
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HQ219546 (A) CGAGCGAAACGACGGGATATAGCGACAAAAACAACAGTCGTTAAAAACCGCTCACGGTTAAAAACG-----AACATTA
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HQ219547 (B) CAAACGAAACGACGATGATATAGCGACAAAAACAACAGTCATTAAAAACCGCTCATGCT-AATA-CGTACATTGGTACATAA
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 specimen P ATTTTT-TTCAAATATCACGATCAGTTTTTAACAAGTTTTATTTTCCAGCTTCTATTGAAATATCCCATACAAC
 specimen R ATTTTTTTCAAATATCACGACCAGTTTTTAACAAGTTTTATTTTCCAGCTTCTATTGAAATATCCCATACAAC
 specimen R* ATTTTTTTCAAATATCACGACCAGTTTTTAACAAGTTTTATTTTCCAGCTTCTATTGAAATATCCCATACAAC

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 HT (TYPE A) AAGTACCAACCCCTCCAACAGTCTTATGCTACTGGTATGAACA
 specimen P AAGTATCAACCATTCCAACAGTCTTATGCTACTGGTATGAACA
 specimen R AAGTACCAACCCCTCCAACAGTCTTATGCTACTGGTATGAACA
 specimen R* AAGTACCAACCCCTCCAACAGTCTTATGCTACTGGTATGAACA

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 HQ219602 (B) TGACGTATTTCTCAATTTAATGTATTTTAA-----CCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT
 HQ219600 (B) TGACGTATTTCTAATTTAAGGTATTT-AA-----CCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT
 HQ219596 (B) TGACGTTTTTCTAATTTGAATGTATTT-AA-----CCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT
 HQ219591 (B) TGTCGTATTTCTCAATTTGAATGTATTTTAA-----CCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT
 HQ219589 (B) TGACGTTTTTCTAATTTGAATGTATTT-AA-----CCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT
 HQ219583 (B) TGACGTTTTTCTAATTTGAATGTATTT-AA-----CCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT
 HQ219581 (B) TGATGTATTTCTCAATTTGAATGTATTTTAA-----CCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT
 HQ219578 (B) TGACGTATTTCTCAATTTGAATGTATTTTAA-----CCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT
 HT (TYPE A) TGACGTATTTCTCAG-----TGTGTTTTAA-----CCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT
 Specimen P TGTCGTATTTCTCAATTTGAATGTATTTTAA-----CCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT
 Specimen R* TGTCGTATTTCTCAATTTGAATGTATTTTAA-----CCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT
 Specimen R* TGATGTATTTCTCAATTTGAATGTATTTAAGTTTTTAACCATCTCATTTTCAATGCAGCCAGATTGTGAGGAAGGGAAT

HQ219601 (A) GAAATGGTTTTCTGTGATGGGTGTAACCTATGTGTTCCACCAAGCTTGTATGGGATTTTGAAGGTCAGTGTATCAGTTA
 HQ219599 (A) GAAATGGTTTTCTGTGATGGGTGTAACCTATGTGTTCCACCAAGCTTGTATGGGATTTTGAAGGTCAGTGTATCAGTTA
 HQ219592 (A) GAAATGGTTTTCTGTGATGGGTGTAACCTATGTGTTCCACCAAGCTTGTATGGGATTTTGAAGGTCAGTGTATCAGTTA
 HQ219590 (A) GAAATGGTTTTCTGTGATGGGTGTAACCTATGTGTTCCACCAAGCTTGTATGGGATTTTGAAGGTCAGTGTATCAGTTA
 HQ219587 (A) GAAATGGTTTTCTGTGATGGGTGTAACCTATGTGTTCCACCAAGCTTGTATGGGATTTTGAAGGTCAGTGTATCAGTTA
 HQ219585 (A) GAAATGGTTTTCTGTGATGGGTGTAACCTATGTGTTCCACCAAGCTTGTATGGGATTTTGAAGGTCAGTGTATCAGTTA
 HQ219584 (A) GAAATGGTTTTCTGTGATGGGTGTAACCTATGTGTTCCACCAAGCTTGTATGGGATTTTGAAGGTCAGTGTATCAGTTA
 HQ219582 (A) GAAATGGTTTTCTGTGATGGGTGTAACCTATGTGTTCCACCAAGCTTGTATGGGATTTTGAAGGTCAGTGTATCAGTTA
 HQ219607 (B) GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTGAAGGTCAGTGTATCTCTTA
 HQ219602 (B) GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTGAAGGTCAGTGTATCAGTTA
 HQ219600 (B) GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTGAAGGTCAGTGTATCAGTTA
 HQ219596 (B) GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTAAAGGTCAGTGTATCTGTTA
 HQ219591 (B) GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTAAAGGTCAGTGTATCTCTTA
 HQ219589 (B) GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTAAAGGTCAGTGTATCTCTTA
 HQ219583 (B) GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTAAAGGTCAGTGTATCTGTTA
 HQ219581 (B) GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTAAAGGTCAGTGTATCTCTTA
 HQ219578 (B) GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTAAAGGTCAGTGTATCTCTTA
 HT (TYPE A) GAAATGGTTTTCTGTGATGGGTGTAACCTATGTGTTCCACCAAGCTTGTATGGGATTTTGAAGGTCAGTGTATCAGTTA
 Specimen P GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTAAAGGTCAGTGTATCTCTTA
 Specimen R* GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTAAAGGTCAGTGTATCTCTTA
 Specimen R* GAAATGGTTTTCTGTGATGGATGTAACCTATGTGTGCACCAAGCTTGTATGGAATTTTAAAGGTCAGTGTATCTCTTA

HQ219601 (A) TGCT-----ATAACAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCGTTACACACATT
 HQ219599 (A) TACT-----ATAACAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCAGTACACACATT
 HQ219592 (A) TACT-----ATAACAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCAGTACACACATT
 HQ219590 (A) TGCT-----ACAACAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCCTTACACACATT
 HQ219587 (A) TACT-----ATAACAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCGGTACACACATT
 HQ219585 (A) TACT-----ATAACAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCAGTACACACATT
 HQ219584 (A) TACT-----ATAACAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCAGTACACACATT
 HQ219582 (A) TACT-----ATAACAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCAGTACACACATT
 HQ219607 (B) TGCTTCTTGTATGCT--ATATCAAACATAATCAAAAAAGTGTATGCAGCTTTTTATAATGAATTCGATACACACA--
 HQ219602 (B) TGCTTCTTGTATGCT--ATATCAAACATAATCAAAAAAGTGTATGCAGCTTTTTATAATGAATTCGATACACACA--
 HQ219600 (B) TGCTTCTTGTATGCT--ATATCAAACATAATCAGAAAATGTTTTATGCAGCTTTTTATAATGAATTCGATACACACACA
 HQ219596 (B) TGCT-----TATTTCTAATATCAAAACAAAATCAAAAAAGTGTATGCAGCTTTTTATAATGAATTCGATACACACA--
 HQ219591 (B) TGCTTCTTGTATGCT--ATATCAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCGATACACACA--
 HQ219589 (B) TGCT-----TATTTCTAATATCAAAACAAAATCAAAAAAGTGTATGCAGCTTTTTATAATGAATTCGATACACACA--
 HQ219583 (B) TGCT-----TATTTCTAATATCAAAACAAAATCAAAAAAGTGTATGCAGCTTTTTATAATGAATTCGATACACACA--
 HQ219581 (B) TGCTTCTTGTATGCT--ATATCAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCGATACACACA--
 HQ219578 (B) TGCTTATTTATA-----ATATCAAACAAAATCAAAAAAGTGTATGCAGCTTTTTATAATGAATTCGATACACACATT
 HT (TYPE A) TGCT-----ACAACAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCGGTACACGCATT
 Specimen P TGCTTCTTGTATGCT--ATATCAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCGATACACACA--
 Specimen R* TGCTTCTTGTATGCT--ATATCAAACATAATCAAAAAATGTTTTATGCAGCTTTTTATAATGAATTCGATACACACA--
 Specimen R* TGCT-----TATTTATAATATCAAAACAAAATCAAAAAAGTGTATGCAGCTTTTTATAATGAATTCGATACACACATT

HQ219601 (A) ATTTCTTTTAAATATTT----TAGTATAACGCACCT----GGGACGAAAACTTTTCGCAGATCTGCTGATTTTCAGAA
 HQ219599 (A) ATTTCTTTTAAATATTT----TAGTATAACGCACCT----GGGACGAAAACTTCCCGGGATCA-----
 HQ219592 (A) ATTTCTTTTAAATATTT----TAGTATAACGCACCT----GGGACGAAAACTTCCCGGGATCA-----
 HQ219590 (A) ATTTCTTTTAAAGTATTT----TAGTATAACCCACCTGGCATGGGACAAAAATCTTTTCGCAGATCTGCTGATTTTCAGAA
 HQ219587 (A) ATTTTAAAAAATATTT----TAGTATAACGCACCT----GGGACGAAAACTTCCCGGGATCTGCTGATTTTCAGAA
 HQ219585 (A) ATTTCTTTTAAATATTT----TAGTATAACGCACCT----GGGACGAAAACTTCCCGGGATCA-----
 HQ219584 (A) ATTTCTTTTAAATATTT----TAGTATAACGCACCT----GGGACGAAAACTTCCCGGGATCA-----
 HQ219582 (A) ATTTCTTTTAAATATTT----TAGTATAACGCACCT----GGGACGAAAACTTCCCGGGATCA-----
 HQ219607 (B) --ATTTTCT-TTTTGGTTTTCTTAGTATTACACACCTTAGATTGTGCAAAAGTACTATTTTGCAA-AAAAATTGCTAG
 HQ219602 (B) ----TTTTCTTTTTGGTTATCTTAGTATTACACACCTTAGATTGTGCAAAAGTACTATTTTGCAA-AAAAATTGCTAG
 HQ219600 (B) TT--TTTTCTTTTTGGGTTATCGTAGTATTACACACCTTAGATTGTGCAAAAGTACTATTTTGCAA-AAAAATTGCTAG
 HQ219596 (B) --TTTTTCTTTTTGGGTTATCTTAGTATTACACACCTTAGATTGTGCAAAAGTACTATTTTGCAA--AAAAATTGCTAG
 HQ219591 (B) --AATTCCTTTTTGGTTTTCTTAGTATTACACACCTTAGATTGTGCAAAAGTACTATTTTGCAA-AAAAATTGCTAG
 HQ219589 (B) --TTTTTCTTTTTGGGTTATCTTAGTATTACACACCTTAGATTGTGCAAAAGTACTATTTTGCAA--AAAAATTGCTAG
 HQ219583 (B) --TTTTTCTTTTTGGGTTATCTTAGTATTACACACCTTAGATTGTGCAAAAGTACTATTTTGCAA--AAAAATTGCTAG
 HQ219581 (B) --AATTCCTTTTTGGTTTTCTTAGTATTACACACCTTAGATTGTGCAAAAGTACTATTTTGCAA-AAAAATTGCTAG
 HQ219578 (A) GATTTTCTCTTTTTGGGTTATCTTAGTATTACACACCTTAGATTGTGCAAAAGTACTATTTTGCAA-AAAAATTGCTAG
 HT (TYPE A) AAAAATAT-----TT----TAGTATAAC----GCACCTGGGACAAAAATCTTCCCGGGATCTGCTGATTTTCAGAA
 specimen P ----TTTTTCTCTTTTTGGTTATCTTAGTATTACACTCTTAGATTGTGCATAAGTACTATTTTGCAA-AAAAATTGCTAG
 Specimen R* --AATTCCTTTTTGGTTTTCTTAGTATTACACACCTTAGATTGTGCAAAAGTACTATTTTGCAA-AAAAATTGCTAG
 Specimen R* ----TTTTTCTTTTTGGTTATCTTAGTATTACACACCTTAGATTGTGCAAAAGTACTATTTTGCAA-AAAAATTGCTAG

HQ219601 (A) CCTTTTTTGTGTTAAAAAGGTCA-----TCGTATAGACTTGT-----
 HQ219599 (A) -----GGTCA-----TCGTATAGACTTAT-----
 HQ219592 (A) -----GGTCA-----TCGTATAGACTTAT-----
 HQ219590 (A) CCTTTTTTGTGTTAAAAAGGTCA-----TCGTATAGACTTGT-----
 HQ219587 (A) CCTTTTTTGTGTTAAAAAGGTCA-----TCGTATAGACTTGT-----
 HQ219585 (A) -----GGTCA-----TCGTATAGACTTAT-----
 HQ219584 (A) -----GGTCA-----TCGTATAGACTTAT-----
 HQ219582 (A) -----GGTCA-----TCGTATAGACTTAT-----
 HQ219607 (B) CTCGTATTGTGTGCACAATTAACAATAATGTGCCAGCCTGTTTATTAATTCGCATACAGTTACATGGCAACGTTACCAAAAAG
 HQ219602 (B) CTCGTATTGTGTGCACAAA--TACAATAATGTGCCAGCCTGTTTATTAATTCGCATATAGTTACATGGCAACGTTACCAAAAAG
 HQ219600 (B) CCGGTATTGTGTGCACAATTAACAATAATGTGCCAGCCTGTTTATTAATTCGCATATAGTTACATGGCAACGTTACCAAAAAG
 HQ219596 (B) CTCGTATTGTGTGCACAATTAACAATAATGTGCCATCCTGTTTATTAATTCGCATATAGTTACATGGCAACGTTACCAAAAAG
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 HQ219589 (B) CTCGTATTGTGTGCACAATTAACAATAATGTGCCATCCTGTTTATTAATTCGCATATAGTTACATGGCAACGTTACCAAAAAG
 HQ219583 (B) CTCGTATTGTGTGCACAATTAACAATAATGTGCCATCCTGTTTATTAATTCGCATATAGTTACATGGCAACGTTACCAAAAAG
 HQ219581 (B) CTCGTATTGTGTGCACAATTAACAATAATGTGCCATCCTGTTTATTAATTCGCATATAGTTACATGGCAACGTTACCAAAAAG
 HQ219578 (B) CTCGTATTGTGTGCACAATTAACAATAATGTGCCAGCCTGTTTATTAATTCGCATATAGTTACATGGCAACGTTACCAAAAAG
 HT (TYPE A) CCTTTTTTGTGTTAAAAAGGTCA-----TCGTATAGACTTGT-----
 specimen P CTCGTATTGTGTGCACAATTAACAATAATGTGCCAGCCTGTTTATTAATTCGCATATAGTTACATAGCACTGTTACCAAAAAG
 Specimen R* CTCGTATTGTGTGCACAATTAACAATAATGTGCCATCCTGTTTATTAATTCGCATATAGTTACATGGCAACGTTACCAAAAAG
 Specimen R* CTCGTATTGTGTGCACAATTAACAATAATGTGCCATCCTGTTTATTAATTCGCATATAGTTATATGGCAACGTTACCAAAAAG

HQ219601 (A) -----
 HQ219599 (A) -----
 HQ219592 (A) -----
 HQ219590 (A) -----
 HQ219587 (A) -----
 HQ219585 (A) -----
 HQ219584 (A) -----
 HQ219582 (A) -----
 HQ219607 (B) TAATGCTTACAATAGGTATGA-AATCTTCCGTTGGATGCTCTGATTTCCGAACCTTTTTT-----
 HQ219602 (B) TAATGCTTACAGTAGGTATGA-GATCTTCCGCGGATGCTCTGATTTCCGAACCTTCTTCTGTTAAAAAGGCTCTCGTCGT
 HQ219600 (B) TAATCTTACAGCAGGGATGAGAATCGTATCGCGGATGCGCTAATTTCCGAACCTTCTTCTGTTAAAAAGGCTCTCGTCGT
 HQ219596 (B) TAATCTTACAGCAGGGATGAGAATCGTCCCGGATGCGCTAATTTCCGAATCTTCTTCTGTTAAAAAGGCTCTCGTCGT
 HQ219591 (B) TAATGCTTACAACAGGCATGAGAATCTTCCGTGAATGCTCTGATTTCTGAACCTTCTTCTGTTAAAAAGGCTCTCGTCGT
 HQ219589 (B) TAATCTTACAGCAGGGATGAGAATCGTCCCGGATGCGCTAATTTCCGAATCTTCTTCTGTTAAAAAGGCTCTCGTCGT
 HQ219583 (B) TAATCTTACAGCAGGGATGAGAATCGTCCCGGATGCGCTAATTTCCGAATCTTCTTCTGTTAAAAAGGCTCTCGTCGT
 HQ219581 (B) TAATGCTTACAACAGGCATGAGAATCTTCCGTGAATGCTCTGATTTCTGAACCTTCTTCTGTTAAAAAGGCTCTCGTCGT
 HQ219578 (B) TAATCTTACAATAGGTATGAGAATCGTCCCGGATGCGCTAATTTCCGAACCTTCTTCTGTTAAAAAGGCTCTCGTCGT
 HT (TYPE A) -----
 specimen P TAATCTTACAGCAGGAATGAGAATCGTCCCGGATGCGCTAATTTCCGAACCTTCTTCTGTTAAAAAGGCTCTCGTCGT
 Specimen R* TAATCTTACAGCAGGGATGAGAATCGTCCCGGATGCGCTAATTTCCGAACCTTCTTCTGTTAAAAAGGCTCTCGTCGT
 Specimen R* TAATCTTACAGCAGGGATGAGAATCGTCCCGGATGCGCTAATTTCCGAATCTTCTTCTGTTAAAAAGGCTCTCGTCGT

HQ219601 (A) ATTTTAGCCTTTACACATGTTGTAGTTTAACTTTTACATGCATCGTACTTAACGCCCC-AAGACCCCGAGGACAAACATT
HQ219599 (A) ATTTTAGCCTTTACACATGTTGTGTTTAGCCTTTACATGCATCGTACTTAACGCCCC-AAGACCCCGAGGACAAACATT
HQ219592 (A) ATTTTAGCCTTTACACATGTTGTGTTTAGCCTTTACATGCATCGTACTTAACGCCCC-AGACCCCGAGGACAAACATT
HQ219590 (A) ATTTTAGCCTTTACACATGTTGTGTTTAACTTTTACATGCATCGTACTTAACGCCCC-AAGACCCCGAGGACAAACATT
HQ219587 (A) ATTTTAGCCT-----TTACATGCATCGTACTTAACGCCCC-AAGACCCCGAGGACAAACATT
HQ219585 (A) ATTTTAGCCTTTACACATGTTGTGTTTAGCCTTTACATGCATCGTACTTAACGCCCC-AAGACCCCGAGGACAAACATT
HQ219584 (A) ATTTTAGCCTTTACACATGTTGTGTTTAGCCTTTACATGCATCGTACTTAACGCCCC-AAGACCCCGAGGACAAACATT
HQ219582 (A) ATTTTAGCCTTTACACATGTTGTGTTTAGCCTTTACATGCATCGTACTTAACGCCCC-AAGACCCCGAGGACAAACATT
HQ219607 (B) -----TACGCGCACCGTATTTAACGCCCCCAGACCCC-GCTACAAACATT
HQ219602 (B) ATTTTAGCCTATAGAGCCTACG-----TGATCGTATTTAACGCCCCCAGACCCC-GCTACAAACATT
HQ219600 (B) ATTTTA-----GCCTTTCATGCGTCGTATTTAACACCCCCAAGATTCCTCGCTACAAACATT
HQ219596 (B) ATTTTAGCCTTCACATAAGTTGTAGTTTAGCCTTTATGTGCGTCGTATTTAACGCCCC-AGACCCCGCTACAAACATT
HQ219591 (B) ATTTTAGCCTTCACATACGTTGAAGTTTAGCCTTTACGTGGGTCGTATTTAACACCCCCAAGATTCCTCGCTACAAACATT
HQ219589 (B) ATTTTAGCCTTCACATAAGTTGTAGTTTAGCCTTTATGTGCGTCGTATTTAACGCCCC-AGACCCCGCTACAAACATT
HQ219583 (B) ATTTTAGCCTTCACATAAGTTGTAGTTTAGCCTTTATGTGCGTCGTATTTAACGCCCC-AGACCCCGCTACAAACATT
HQ219581 (B) ATTTTAGCCTTCACATACGTTGAAGTTTAGCCTTTACGTGGGTCGTATTTAACGCCCC-----CCCTACAAACATT
HQ219578 (B) ATTTTAGCCTTCACATACGTTGTAGTTTAGCCT--TTCATGCGTCGTATTTAACACCCCCAAGATTCCTCGCTACAAACATT
HT (TYPE A) ATTTTAGCCTTTACATATGTTGTAGTTTAACTTTTACATGCATCGTACTTAACGCCCC-AAGACCCCGAGGACAAACATT
specimen P ATTTTAGT-----TAGCCTTTTCATGCGTCGTATTTAACACCCCCAAGATTCCTCGCTACAAACATT
Specimen R* ATTTTAGCCTTCACATACGTTGTAGTTTAGCCTTT-CATGCGTCGTATTTAACACCCCCAAGATTCCTCGCTACAAACATT
Specimen R* ATTTTAGCCTTCACATACTGTAGTT--TAGCCTTTTCATGCGTCGTATTTAACACCCCCAAGATTCCTCGCTACAAACATT

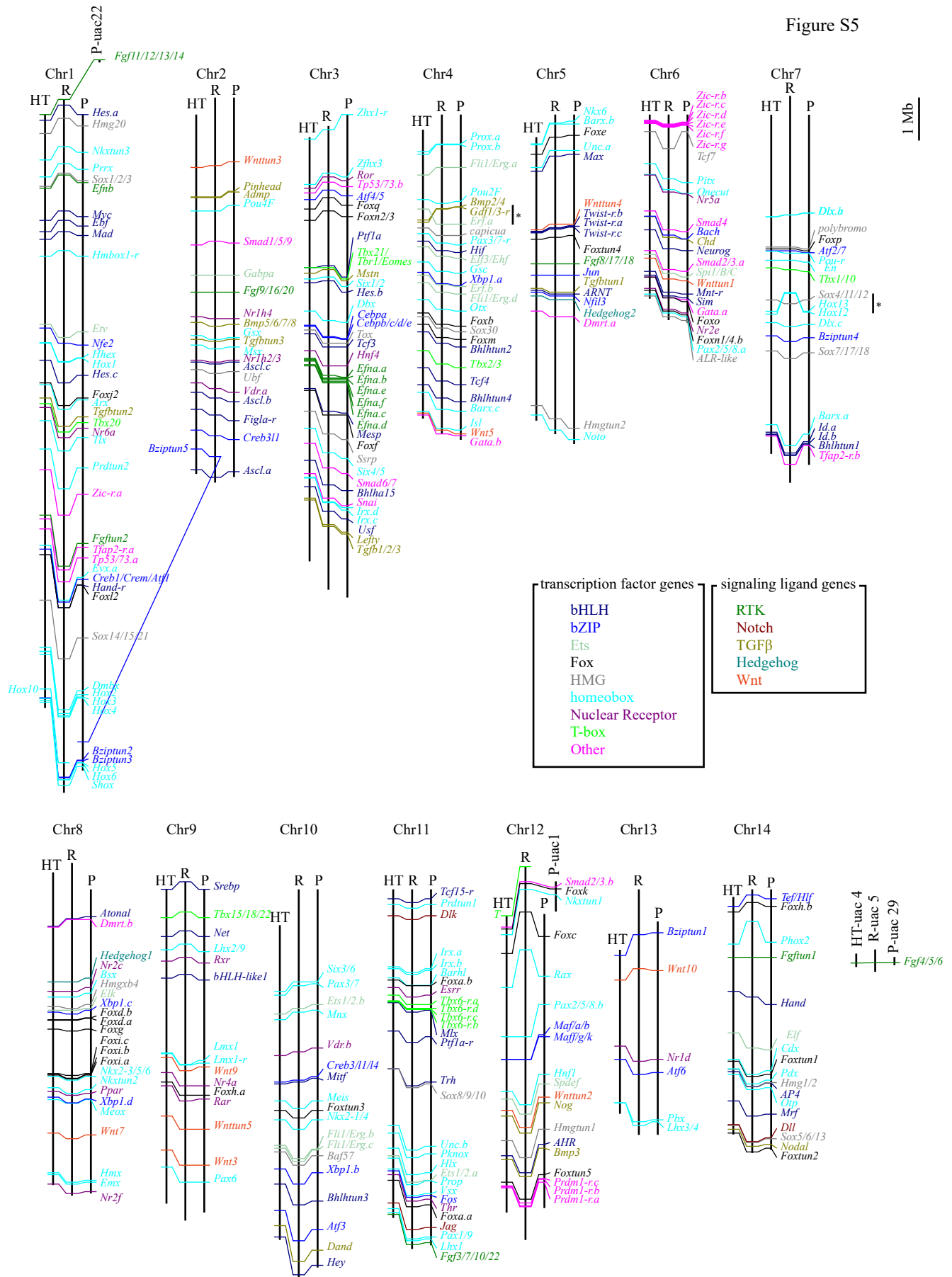
HQ219601 (A) TTGAGGAATTTTGATCAAACCTCTGTTCTCATCCTTGTACAAAATATCAGCATGCTCACTGATGACA
HQ219599 (A) TTGAGGAATTTTGATC----TCTATTCTCATCCTTGTAAACAAAATATCAGCATGCTCACTGATGACA
HQ219592 (A) TTGAGGAATTTTGATC----TCTATTCTCATCCTTGTAAACAAAATATCAGCATGCTCACCAGATGACA
HQ219590 (A) TTGAGGAATTTTGATCAC--TCTGTTCTCATCCTTGTACAAAATATCAGCATGCTCACTGATGACA
HQ219587 (A) TTGAGGAATTTTGATC----TCTATTCTCATCCTTGTACAAAATATCAGCATGCTCACTGATGACA
HQ219585 (A) TTGAGGAATTTTGATC----TCTATTCTCATCCTTGTAAACAAAATATCAGCATGCTCACCAGATGACA
HQ219584 (A) TTGAGGAATTTTGATC----TCTATTCTCATCCTTGTAAACAAAATATCAGCATGCACACAGATATCA
HQ219582 (A) TTGAGGAATTTTGATC----TCTATTCTCATCCTTGTAAACAAAATATCAGCATGCTCACCAGATGACA
HQ219607 (B) TTCAGAAATTTTGAACAAACTCAATTCCTCATCTCTGTTACAAAATCATTAGCATTACACAGATATCA
HQ219602 (B) TTCAGAAATTTTGAATAAACTCAATTCCTCATCTCTGTTACAAAATCATTAGCATTACACAGATRTCA
HQ219600 (B) TTCAGAAATTTTAAATAAACTCAATTCCTCATCCCTGTTACAAAATCATTAGCATTACACAGATATCA
HQ219596 (B) TTCAGAAATTTTGAACAAACTCAATTCCTTATCTCTGTTACAAAATCATTAGCATTACACAGATATCA
HQ219591 (B) TTCAGAAATTTTGAATAAACTCAATTCCTATCCCTGTTACAAAATCATTAGCATTACACAGATATCA
HQ219589 (B) TTCAGAAATTTTGAACAAACTCAATTCCTATCTCTGTTATAAAAATCATTAGCATTACACAGATATCA
HQ219583 (B) TTCAGAAATTTTGAACAAACTCAATTCCTTATCTCTGTTACAAAATCATTAGCATTACACAGATATCA
HQ219581 (B) TTCAGAAATTTTGAATAAACTCAATTCCTATCCCTGTTACAAAATCATGAGCATCCACACAGATATCA
HQ219578 (B) TTCAGAAATTTTGAACAAACTCAATTCCTATCCCTGTT-CAAAATCATTAGCAATCACACAGATATCA
HT (TYPE A) TTGAGGAATTTTGATC----TCTATTCTCATCCTTGTACAAAATATCAGCATGCTCACTGATGACA
specimen P TTCAGAAATTTTGAATAAACTCAATTCCTATCCCTGTTACAAAATCATTAGCATTACACAGATATCA
Specimen R* TTCAGAAATTTTGAACAAACTCCATTTATCATCCCTGTTACAAAATCATTAGCATTACACAGATATCA
Specimen R* TTCAGAAATTTTGAACAAACTCAATTCCTATCCCTGTTACAAAATATCATTAGCATTACACAGATATTA

HQ219504 (A) CGCTTGGCCTCGCTCTAGCATTTA
HQ219500 (A) CGCTTGGCCTCGCTCTAGCATTTA
HQ219499 (A) CGCTTGGCCTCGCTCTAGCATTTA
HQ219498 (A) CGCTTGGCCTCGCTCTAGCATTTA
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HQ219485 (A) CGCTTGGCCTCGCTCTCGCATTTA
HQ219480 (A) CGCTTGGCCTCGCTCTAGCATTTA
HQ219479 (A) CGCTTGGCCTCGCTCTAGCATTTA
HQ219501 (B) CGCTTGGCCTCGCTCTCGCATTTA
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HQ219490 (B) CGCTTGGCCTCGCTCTCGCATTTA
HQ219487 (B) CGCTTGGCCTCGCTCTCGCATTTA
HQ219486 (B) CGCTTGGCCTCGCTCTCGCATTTA
HQ219484 (B) CGCTTGGCCTCGCTCTCGCATTTA
HQ219483 (B) CGCTTGGCCTCGCTCTCGCATTTA
HQ219482 (B) CGCTTGGCCTCGCTCTCGCATTTA
HT (TYPE A) CGCTTGGCCTCGCTCTAGCATTTA
specimen P CGCTTGGCCTCGCTCTCGCATTTA
specimen R CGCTTGGCCTCGCTCTCGCATTTA
specimen R* CGCTTGGCCTCGCTCTCGCATTTA

HQ219653 (A) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCGTTTATAGTTTTGAAATC
 HQ219650 (A) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC
 HQ219649 (A) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC
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 HQ219644 (A) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCGTTTATAGTTTTGAAATC
 HQ219642 (A) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCGTTTATAGTTTTGAAATC
 HQ219641 (A) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCGTTTATAGTTTTGAAATC
 HQ219637 (A) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC
 HQ219630 (A) CTGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC
 HQ219629 (A) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC
 HQ219651 (B) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGTAAGGGGTATTGGGTCATTTATAGTTTTGAAATC
 HQ219647 (B) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGGGTCATTTATAGTTTTGAAATC
 HQ219643 (B) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC
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 HQ219634 (B) CCGACGCCGGGTTGAAATTATATATATAAAGGTCCTACTGGGTGGTAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC
 HQ219633 (B) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGCGAGGTCATTTATAGTTTTGAAATC
 HQ219631 (B) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC
 HT (TYPE A) CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC
 specimen P CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC
 specimen R CCGACGCCGGGTTGAAATTATAATATATAAAGGTCCTACTGGGTGGCAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC
 specimen R* CCGACGCCGGGTTGAAATTAT--AATATAAAGGTCCTACTGGGTGGTAAGGGGTGTGAGGTCATTTATAGTTTTGAAATC

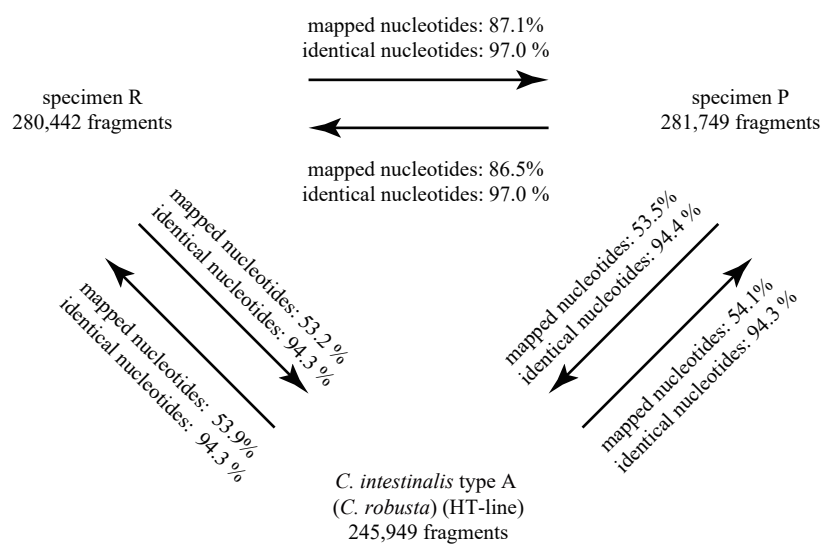
HQ219653 (A) ATGATATCCTGAGCCCTGAAAGAAGTTTACAAAATAATTTGATCACTTGACTTGGA
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 HQ219649 (A) ATGATATCCTGAGCCCTGAAAGAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219646 (A) ATGATATCCTGAGCCCTGAAAGAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219645 (A) ATGATATCCTGAGCCCTGAAAGAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219644 (A) ATGATATCCTGAGCCCTGAAAGAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219642 (A) ATGATATCCTGAGCCCTGAAAGAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219641 (A) ATGATATCCTGAGCCCTGAAAGAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219637 (A) ATGATATCCTGAGCCCTGAAAGAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219630 (A) ATGATATCCTGAGCCCTGAAAGAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219629 (A) ATGATATCCTGAGCCCTGAAAGAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219651 (B) ATGATATCTCGGGCCCTGAAACAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219647 (B) ACGATATCTAGCCCTGAAACAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219643 (B) ATGATATCCCGGCCCTGAAACAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219635 (B) ATGATATCTCGGGCCCTGAAACAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219634 (B) ATGATATCCCGGCCCTGAAACAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219633 (B) ATGATATCTCGGGCCCTGAAACAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HQ219631 (B) ATGATATCTAGCCCTGAAACAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 HT (TYPE A) ATGATATCCTGAGCCCTGAAAGAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 specimen P ATGATATCCCGGCCCTGAAACAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 specimen R ATGATATCTAGCCCTGAAACAAGTTTACAAAATAATTTGATCACTTGACTTGGA
 specimen R* ATGATATCTCGGGCCCTGAAACAAGTTTACAAAATAATTTGATCACTTGACTTGGA

Figure S5



Supplementary Figure S5. Chromosomal positions of several transcription factor family genes and several signaling molecule family genes. Vertical lines represent chromosomes of the type-A HT line (HT), specimen R, and specimen P. Several genes were found in contigs that were not assigned to chromosomes (HT-uac, R-uac, and P-uac). *Hox10* and *T(Brachyury)* were not found in the current genomic assembly of specimen P. While *Bziptun5* was found in chromosome 2 of the type A and specimen R, it was found in chromosome 1 of specimen P. Two possible inversions are shown by asterisks. Gene families shown here (except the class 'Other') have been comprehensively annotated previously, and are indicated by different colors. The color code is in the middle of the figure. Identifiers of these genes are shown in supplementary table S6. The scale bar on the right represents 1 Mb.

Figure S6



Supplementary Figure S6. Nucleotide-level comparisons among genomic sequences for two type-B animals and an inbred type-A animal. Each genomic sequence was divided into 500-bp long fragments and these fragments were aligned to other genomes. Proportions of successfully mapped nucleotides and nucleotide identities in mapped nucleotide regions are shown.

Figure S7

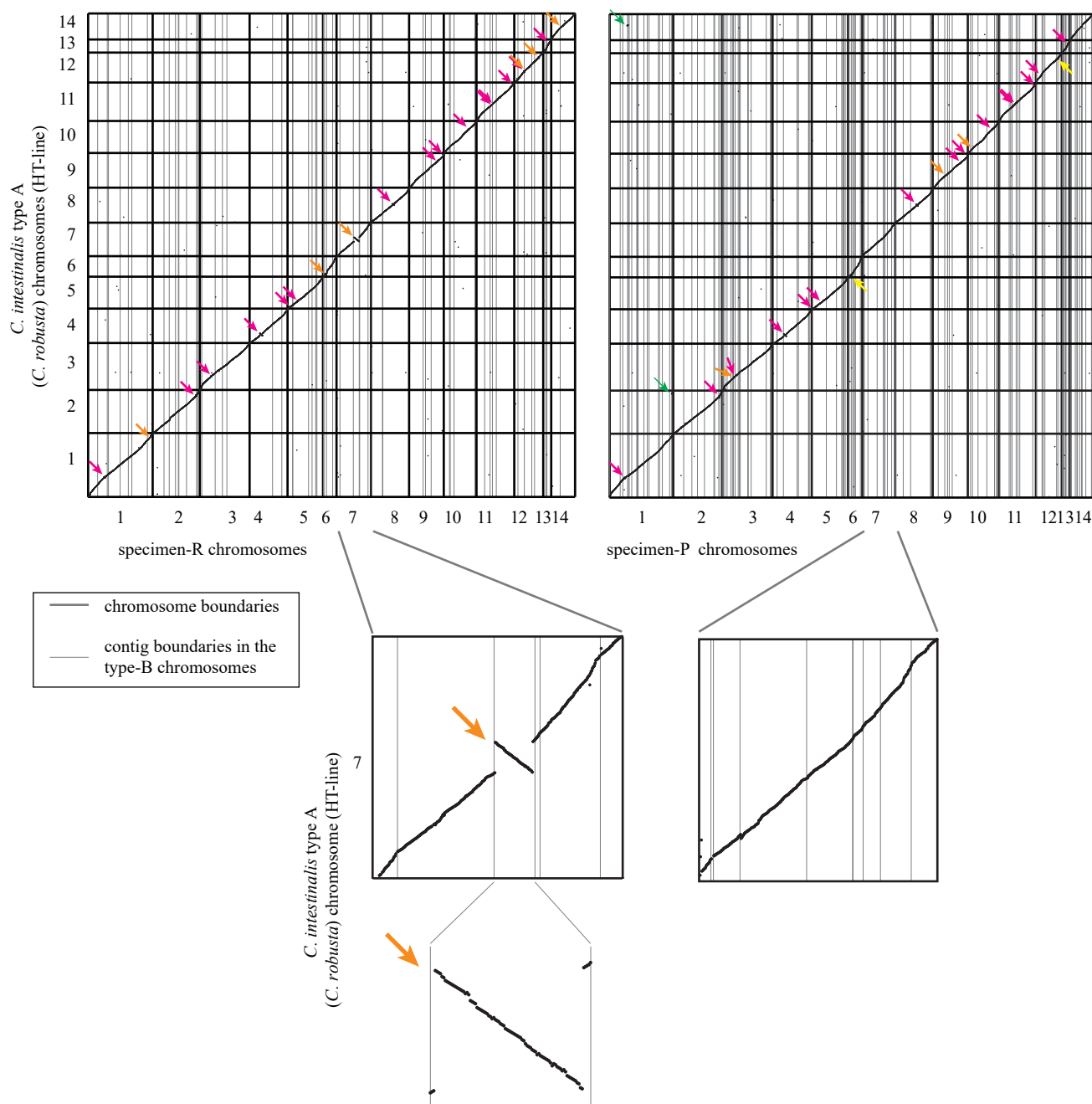
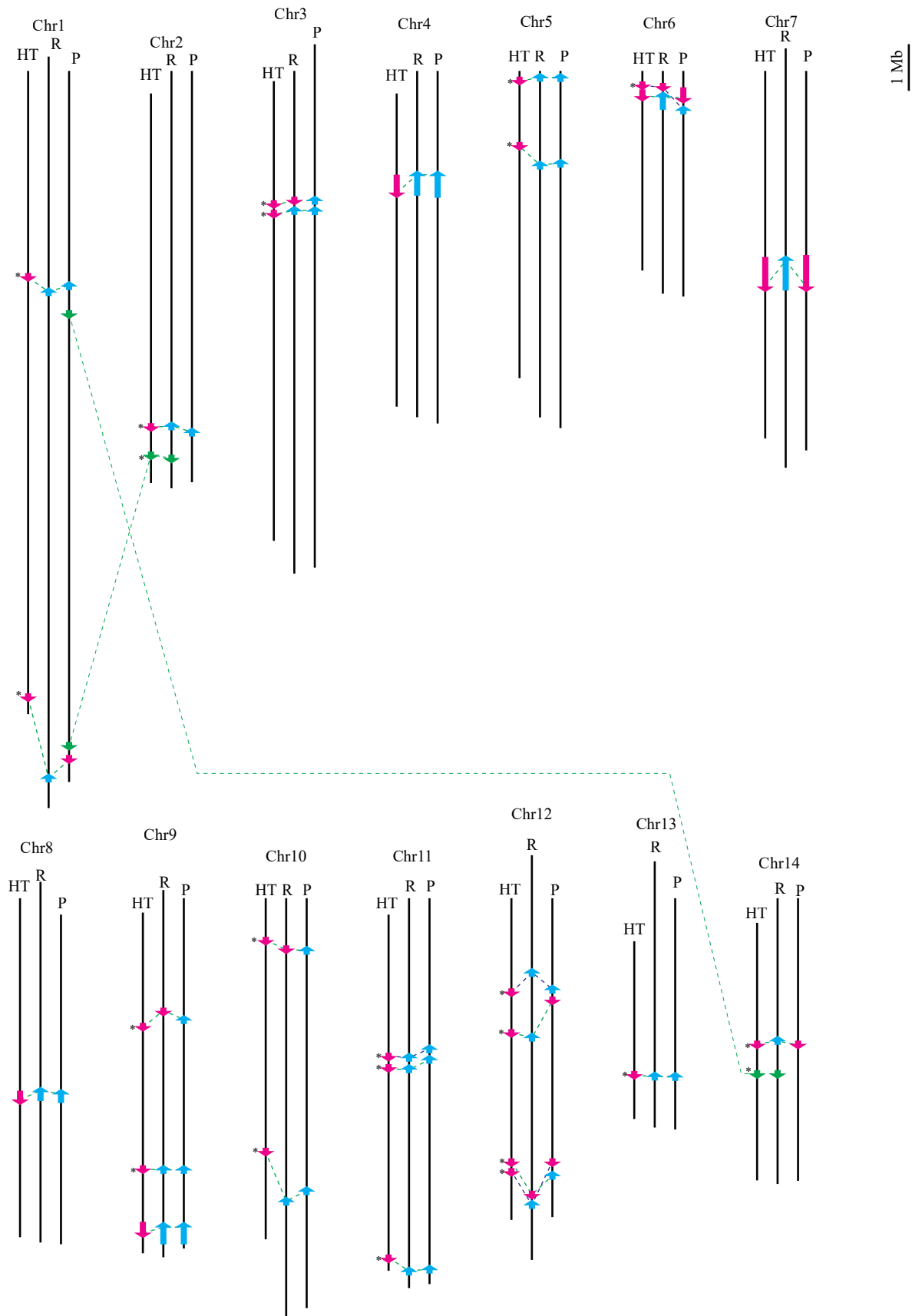


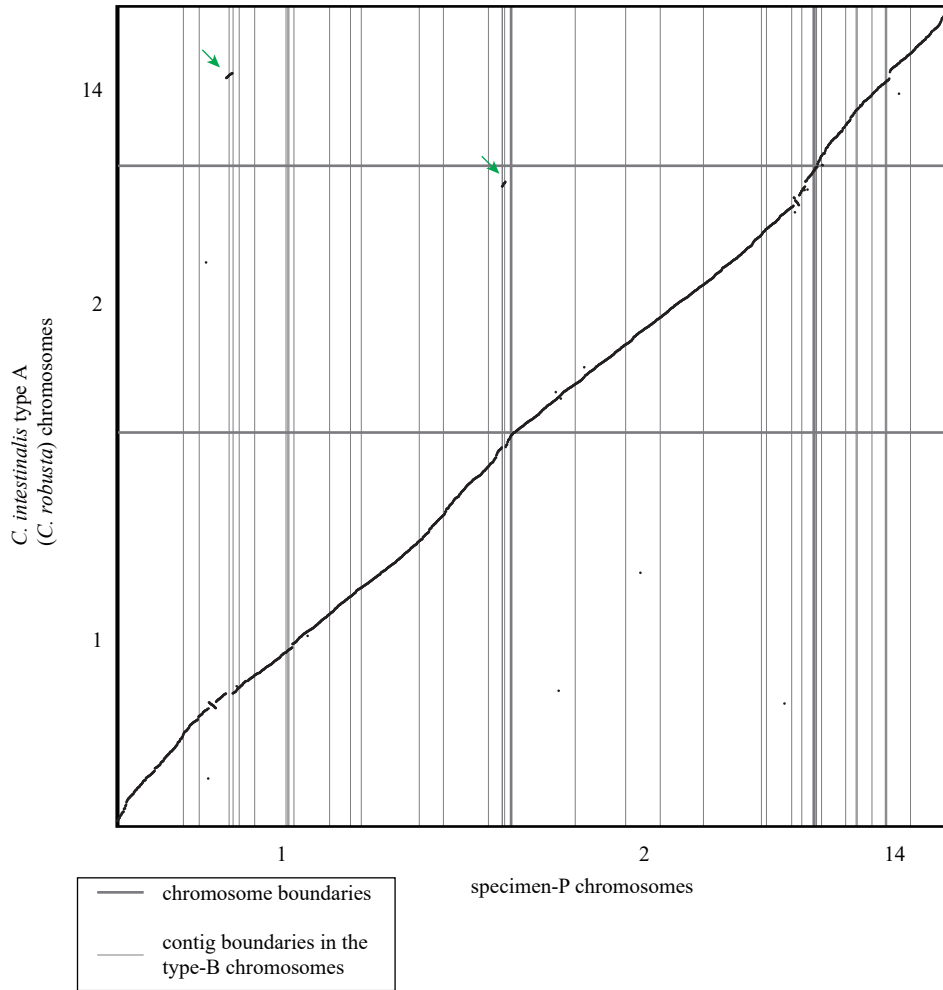
Figure S7. Comparisons of gene orders between type-A and type-B animals. Dot plots showing the rank-order position of genes in chromosomes of specimen R (left) and specimen P (right) against chromosomes of the inbred type-A animal (y-axes). High-magnification views of chromosome 7 are shown beneath the main dot plots. High-magnification views for other inversions are provided in supplementary figure S7. Magenta arrows indicate inversions common to specimens R and P. Orange arrows indicate inversions specific to specimen R or P. Yellow arrows indicate sites where two successive inversions likely occurred. Green arrows indicate inter-chromosomal translocations.

Figure S8

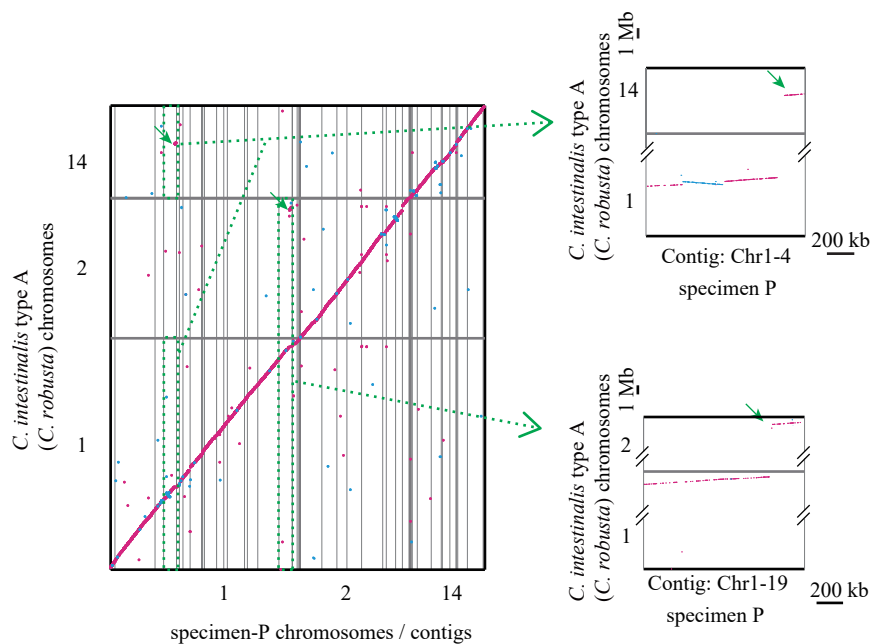


Supplementary Figure S8. An overview of chromosomes of the inbred type-A animal and two type-B animals. Vertical lines represent chromosomes of the type-A HT line (HT), specimen R, and specimen P. Magenta and cyan arrows indicate approximate positions of inversions. Cyan arrows indicate inversions against the type-A HT chromosomes. Green arrows indicate approximate positions of inter-chromosomal translocations. Sizes of small arrows marked with asterisks are not proportional to actual sizes. These structural changes were identified by dot plots of the rank-order position of genes in chromosomes of specimens R and P against chromosomes of the inbred type-A animal shown in supplementary figure S6.

A

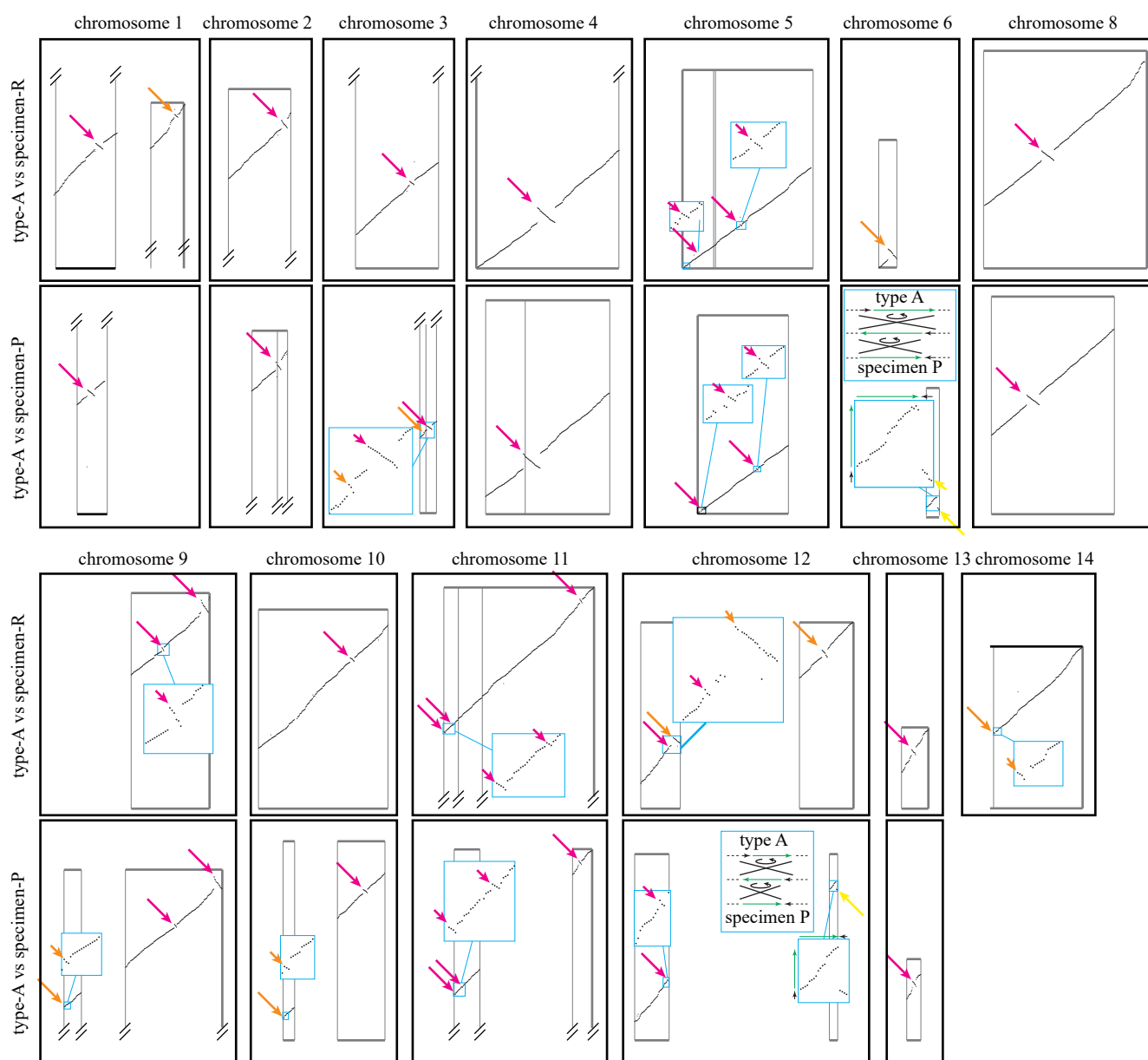


B



Supplementary Figure S9. Possible translocations observed in specimen P. (A) Dot plots showing the rank-order position of genes in chromosomes 1, 2, and 14 of specimen P (x-axis) against corresponding chromosomes of the inbred type-A animal (y-axis). Possible translocations are shown by green arrows. This is a high magnification view of Figure 5. (B) Genomic alignments of the same chromosomes. These alignments also indicate translocations. High magnification views are shown on right.

Figure S10



Supplementary Figure S10. High magnification views of dot plot showing the rank order position of genes shown in supplementary figure S5. Magenta arrows indicate inversions common to specimens R and P. Orange arrows indicate inversions specific to specimen R or P. Yellow arrows indicates sites where two successive inversions likely occurred as illustrated in panels.

Supplementary Table S1. Estimation of genome sizes and repeat lengths by Genomescope and Illumina sequencing reads

	specimen R	specimen P
Estimated genome size	124 Mb	137 Mb
Repeat length	29 Mb	46 Mb
Unique length	95 Mb	91 Mb
Heterozygosity	3.0 %	3.6 %

Supplementary Table S2. Genes found in possible translocated regions.

Gene model	protein model	Blast E-values	Accession number in the human proteome (UniProtKB)	human protein annotation
KY.Chr2.2226	KY.Chr2.2226.v7.ND6-5	1.52E-14	Q02817	MUC2 (mucin 2, oligomeric mucus/gel-forming)
KY.Chr2.2227	KY.Chr2.2227.v3.SL4-3	5.91E-108	P61266	STX1B (syntaxin 1B)
KY.Chr2.2230	KY.Chr2.2230.v1.SL1-1	9.68E-109	Q8WUY9	DEPDC1B (DEP domain containing 1B)
KY.Chr2.2238	KY.Chr2.2238.v1.SL1-1	0	O75691	UTP20 (UTP20 small subunit processome component)
KY.Chr2.2242	KY.Chr2.2242.v2.SL3-2	1.47E-40	Q2TB18	ASTE1 (asteroid homolog 1)
KY.Chr2.2243	KY.Chr2.2243.v1.nonSL6-1	3.62E-83	Q5T8I3	FAM102B (family with sequence similarity 102 member B)
KY.Chr2.2244	KY.Chr2.2244.v1.SL1-1	0	P17980	PSMC3 (proteasome 26S subunit, ATPase 3)
KY.Chr2.2245	KY.Chr2.2245.v2.ND2-2	2.59E-88	P48651	PTDSS1 (phosphatidylserine synthase 1)
KY.Chr2.2247 (<i>Bzipun5</i>)	KY.Chr2.2247.v1.nonSL3-1	0.13	P12270	TPR (translocated promoter region, nuclear basket protein)
KY.Chr2.2251	KY.Chr2.2251.v1.SL1-1	0	Q5THR3	EFCAB6 (EF-hand calcium binding domain 6)
KY.Chr14.540	KY.Chr14.540.v1.SL2-1	2.25E-12	Q06520	SULT2A1 (sulfotransferase family 2A member 1)
KY.Chr14.541	KY.Chr14.541.v1.SL2-1	8.18E-54	Q96RY5	CRAMP1 (cramped chromatin regulator homolog 1)
KY.Chr14.542	KY.Chr14.542.v1.nonSL3-5	1.66E-141	Q9BXP5	SRRT (serrate, RNA effector molecule)
KY.Chr14.544	KY.Chr14.544.v1.SL3-1	5.06E-58	Q5T8P6	RBM26 (RNA binding motif protein 26)
KY.Chr14.545	KY.Chr14.545.v2.SL1-2	7.37E-119	Q8NBS9	TXNDC5 (thioredoxin domain containing 5)
KY.Chr14.548	KY.Chr14.548.v2.nonSL8-2	4.98E-26	P24539	ATP5PB (ATP synthase peripheral stalk-membrane subunit b)
KY.Chr14.549	KY.Chr14.549.v1.nonSL7-1	6.98E-54	P83881	RPL36A (ribosomal protein L36a)
KY.Chr14.550	KY.Chr14.550.v1.nonSL7-1	1.71E-141	Q9U110	EIF2B4 (eukaryotic translation initiation factor 2B subunit delta)
KY.Chr14.552	KY.Chr14.552.v1.SL1-1	1.09E-04	Q14554	PDIA5 (protein disulfide isomerase family A member 5)
KY.Chr14.554	KY.Chr14.554.v1.SL1-1	1.50E-85	Q9NUQ2	AGPAT5 (1-acylglycerol-3-phosphate O-acyltransferase 5)
KY.Chr14.555	KY.Chr14.555.v1.ND1-1	3.68E-89	Q9BW85	YJU2 (YJU2 splicing factor homolog)
KY.Chr14.556	KY.Chr14.556.v2.nonSL5-2	1.28E-37	Q16629	SRSF7 (serine and arginine rich splicing factor 7)
KY.Chr14.557	KY.Chr14.557.v1.SL2-1	9.50E-177	Q8N584	TTC39C (tetratricopeptide repeat domain 39C)
KY.Chr14.558	KY.Chr14.558.v1.SL3-1	1.02E-135	O00625	PIR (pirin)
KY.Chr14.559	KY.Chr14.559.v1.SL3-1	6.06E-20	A6H8Y1	BDP1 (B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB)
KY.Chr14.560	KY.Chr14.560.v1.SL1-1	3.3	Q6PL18	ATAD2 (ATPase family AAA domain containing 2)
KY.Chr14.561	KY.Chr14.561.v1.nonSL9-1	4.41E-53	Q9BY84	DUSP16 (dual specificity phosphatase 16)
KY.Chr14.562	KY.Chr14.562.v1.SL1-1	1.81E-28	O43529	CHST10 (carbohydrate sulfotransferase 10)

Supplementary Table S3. Inversions identified from gene orders

inversions found commonly in specimens R and P^{*1}

KY.Chr1.1018-1053 (235k, 33), KY.Chr2.2124-2164 (249k, 39), KY.Chr3.483-499 (154k, 17), KY.Chr4.377-454 (560k, 78)^{*2}, KY.Chr5.25-28 (28k, 4), KY.Chr5.265-272 (76k, 8)^{*3}, KY.Chr8.779-842 (336k, 59), KY.Chr9.843-864 (123k, 21), KY.Chr9.1061-1127 (554k, 65), KY.Chr10.1133-1149 (100k, 17), KY.Chr11.532-537 (46k, 6), KY.Chr11.572-574 (14k, 3), KY.Chr11.1268-1295 (116k, 20), KY.Chr12.338-342 (78k, 5), KY.Chr13.346-371 (322k, 26)

inversions found only in specimen R

KY.Chr1.2558-2567 (57k, 10), KY.Chr6.59-102 (327k, 43), KY.Chr7.593-722 (873k, 127), KY.Chr12.439-466 (213k, 25), KY.Chr12.905-938 (233k 34), KY.Chr14.437-442 (67k, 6)

inversions found only in specimen P

KY.Chr3.461-467 (45k, 7), KY.Chr6.38-45 (67k, 8)^{*3}, KY.Chr9.407-409 (34k, 3), KY.Chr10.148-150 (24k, 3), KY.Chr12.898-901 (27k, 4)^{*3}

^{*1} Numbers in parentheses indicate inversion sizes estimated from gene model positions, and numbers of genes included in each gene block.

^{*2} This inversion is shown to occur specifically in the HT inbred line of type-A animals, and therefore there is not an inversion between wild type-A animals and the sequenced type-B animals.

^{*3} KY.Chr5.269 to KY.Chr5.272 were not mapped to the genome of specimen R.

^{*4} In these inversion sites (KY.Chr6.38–KY.Chr6.102 and KY.Chr12.898–KY.Chr12.938), two successive inversions probably occurred in the specimen P lineage, and one in the specimen R lineage.

Supplementary Table S4. Genes found in inverted regions.

Gene model	Specimens with inversions*1	protein model	Blast E-values	Accession number in the human proteome (UniProtKB)	human protein annotation
KY.Chr1.1018	R/P	KY.Chr1.1018.v1.nonSL1-1	4.30E-46	Q9Y2B2	PIGL (phosphatidylinositol glycan anchor biosynthesis class L)
KY.Chr1.1019	R/P	KY.Chr1.1019.v1.SL1-1	5.17E-57	Q92574	TSC1 (TSC complex subunit 1)
KY.Chr1.1021	R/P	KY.Chr1.1021.v3.nonSL2-1	2.36E-58	Q14766	LTBP1 (latent transforming growth factor beta binding protein 1)
KY.Chr1.1022	R/P	KY.Chr1.1022.v2.nonSL2-1	0	Q5HYA8	TMEM67 (transmembrane protein 67)
KY.Chr1.1023	R/P	KY.Chr1.1023.v1.SL1-1	1.7	Q81YG6	LRRC56 (leucine rich repeat containing 56)
KY.Chr1.1024	R/P	KY.Chr1.1024.v5.nonSL6-2	0	Q12955	ANK3 (ankyrin 3)
KY.Chr1.1027	R/P	KY.Chr1.1027.v1.ND1-1	1.6	Q8NE35	CPEB3 (cytoplasmic polyadenylation element binding protein 3)
KY.Chr1.1028	R/P	KY.Chr1.1028.v1.nonSL5-1	8.49E-13	Q8TDP1	RNASEH2C (ribonuclease H2 subunit C)
KY.Chr1.1029	R/P	KY.Chr1.1029.v1.SL1-1	4.05E-24	Q8TB45	DEPTOR (DEP domain containing MTOR interacting protein)
KY.Chr1.1030	R/P	KY.Chr1.1030.v1.ND1-1	1.56E-09	Q8WW35	TCTEX1D2 (Tctex1 domain containing 2)
KY.Chr1.1031	R/P	KY.Chr1.1031.v1.SL7-1	4.76E-53	P62330	ARF6 (ADP ribosylation factor 6)
KY.Chr1.1032	R/P	KY.Chr1.1032.v1.ND1-2	0	Q00341	HDLBP (high density lipoprotein binding protein)
KY.Chr1.1033	R/P	KY.Chr1.1033.v1.SL2-1	2.12E-104	Q96G2	PASK (PAS domain containing serine/threonine kinase)
KY.Chr1.1034	R/P	KY.Chr1.1034.v4.ND4-1	5.88E-23	Q8N6F1	CLDN19 (claudin 19)
KY.Chr1.1035	R/P	KY.Chr1.1035.v1.ND1-1	2.48E-21	Q99715	COL12A1 (collagen type XII alpha 1 chain)
KY.Chr1.1036	R/P	KY.Chr1.1036.v1.SL3-1	1.82E-75	P46736	BRCC3 (BRCA1/BRCA2-containing complex subunit 3)
KY.Chr1.1037	R/P	KY.Chr1.1037.v1.ND1-1	0.86	Q9H5L6	THAP9 (THAP domain containing 9)
KY.Chr1.1038	R/P	KY.Chr1.1038.v1.ND1-1	0.16	POCJ78	ZNF865 (zinc finger protein 865)
KY.Chr1.1039	R/P	KY.Chr1.1039.v1.ND1-1	1.34E-14	B2RNN3	C1QTNF9B (C1q and TNF related 9B)
KY.Chr1.1040	R/P				no significant match found
KY.Chr1.1041	R/P	KY.Chr1.1041.v2.nonSL2-2	0	Q60832	DKC1 (dyskerin pseudouridine synthase 1)
KY.Chr1.1042	R/P	KY.Chr1.1042.v1.nonSL2-1	2.55E-161	Q9Y376	CAB39 (calcium binding protein 39)
KY.Chr1.1043	R/P	KY.Chr1.1043.v1.SL4-1	2.18E-63	Q01804	OTUD4 (OTU deubiquitinase 4)
KY.Chr1.1044	R/P	KY.Chr1.1044.v1.ND1-1	3.4	Q8TEU8	WFIKKN2 (WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2)
KY.Chr1.1045	R/P	KY.Chr1.1045.v1.ND1-3	1.24E-41	Q96MD2	C12orf66 (chromosome 12 open reading frame 66)
KY.Chr1.1046	R/P	KY.Chr1.1046.v1.nonSL5-1	4.54E-79	P08621	SNRNP70 (small nuclear ribonucleoprotein U1 subunit 70)
KY.Chr1.1047	R/P	KY.Chr1.1047.v1.ND1-2	1.5	B1AJZ9	FHADI (forkhead associated phosphopeptide binding domain 1)
KY.Chr1.1048	R/P	KY.Chr1.1048.v1.ND1-1	1.6	B1AJZ9	FHADI (forkhead associated phosphopeptide binding domain 1)
KY.Chr1.1049	R/P	KY.Chr1.1049.v1.nonSL9-1	0	Q9UN76	SLC6A14 (solute carrier family 6 member 14)
KY.Chr1.1050	R/P	KY.Chr1.1050.v1.ND1-1	0.3	Q75151	PHE2 (PHD finger protein 2)
KY.Chr1.1051	R/P	KY.Chr1.1051.v1.ND1-1	0	Q9UN76	SLC6A14 (solute carrier family 6 member 14)
KY.Chr1.1052	R/P	KY.Chr1.1052.v1.nonSL3-1	0	Q9UN76	SLC6A14 (solute carrier family 6 member 14)
KY.Chr1.1053	R/P	KY.Chr1.1053.v1.SL1-1	7.40E-153	Q15021	NCAPD2 (non-SMC condensin I complex subunit D2)
KY.Chr1.2558	R	KY.Chr1.2558.v1.ND1-1	3.85E-32	P28358	HOXD10 (homeobox D10)
KY.Chr1.2559	R				no significant match found
KY.Chr1.2560	R	KY.Chr1.2560.v1.nonSL3-1	0.098	A8MT70	ZBBX (zinc finger B-box domain containing)
KY.Chr1.2561	R	KY.Chr1.2561.v1.SL1-1	4.03E-83	Q9U140	SLC24A2 (solute carrier family 24 member 2)
KY.Chr1.2562	R	KY.Chr1.2562.v1.nonSL4-2	1.01E-116	Q676U5	ATG16L1 (autophagy related 16 like 1)
KY.Chr1.2563	R	KY.Chr1.2563.v1.nonSL5-1	9.61E-89	P48052	CPA2 (carboxypeptidase A2)
KY.Chr1.2564	R	KY.Chr1.2564.v1.nonSL3-1	3.30E-31	Q96EA4	SPDL1 (spindle apparatus coiled-coil protein 1)
KY.Chr1.2565	R	KY.Chr1.2565.v1.nonSL9-1	6.81E-98	Q6UB28	METAP1D (methionyl aminopeptidase type 1D mitochondrial)
KY.Chr1.2566	R	KY.Chr1.2566.v1.ND1-1	0.4	Q6P9A2	GALNT18 (polypeptide N-acetylgalactosaminyltransferase 18)
KY.Chr1.2567	R	KY.Chr1.2567.v2.nonSL2-1	0	Q504Q3	PAN2 (poly(A) specific ribonuclease subunit PAN2)
KY.Chr2.2124	R/P	KY.Chr2.2124.v1.SL1-1	0.15	Q9UPT6	MAPK8IP3 (mitogen-activated protein kinase 8 interacting protein 3)
KY.Chr2.2125	R/P	KY.Chr2.2125.v1.ND1-1	0.74	A6NJY1	SLC9B1P1 (solute carrier family 9 member B1 pseudogene 1)
KY.Chr2.2126	R/P	KY.Chr2.2126.v1.SL1-1	0	Q96G46	DUS3L (dihydrouridine synthase 3 like)
KY.Chr2.2127	R/P	KY.Chr2.2127.v1.nonSL2-1	3.83E-51	Q8TCD6	PHOSPHO2 (phosphatase, orphan 2)
KY.Chr2.2128	R/P	KY.Chr2.2128.v1.ND1-1	1.45E-14	Q9H628	RERGL (RERGL like)
KY.Chr2.2129	R/P	KY.Chr2.2129.v1.SL2-1	4.14E-26	Q9UM22	SYNRG (synergin gamma)
KY.Chr2.2130	R/P	KY.Chr2.2130.v1.SL1-1	3.14E-10	Q9BUT9	MCRIP2 (MAPK regulated corepressor interacting protein 2)
KY.Chr2.2131	R/P	KY.Chr2.2131.v1.SL1-1	1.65E-57	Q95825	CRYZL1 (crystallin zeta like 1)
KY.Chr2.2132	R/P	KY.Chr2.2132.v2.nonSL2-2	2.58E-70	Q9H841	NIPAL2 (NIPA like domain containing 2)
KY.Chr2.2133	R/P	KY.Chr2.2133.v1.nonSL9-1	5.96E-92	Q9UBK7	RABL2A (RAB, member of RAS oncogene family like 2A)
KY.Chr2.2134	R/P	KY.Chr2.2134.v1.SL1-1	0.005	Q12918	KLRB1 (killer cell lectin like receptor B1)
KY.Chr2.2135	R/P	KY.Chr2.2135.v2.nonSL3-1	1.01E-81	Q9Y6C9	MTCH2 (mitochondrial carrier 2)
KY.Chr2.2136	R/P	KY.Chr2.2136.v1.nonSL2-1	1.00E-115	Q96017	CHEK2 (checkpoint kinase 2)
KY.Chr2.2137	R/P	KY.Chr2.2137.v1.nonSL8-4	1.05E-142	Q9HBI1	PARVB (parvin beta)
KY.Chr2.2138	R/P	KY.Chr2.2138.v2.SL2-1	0	Q9H1V8	SLC6A17 (solute carrier family 6 member 17)
KY.Chr2.2139	R/P	KY.Chr2.2139.v1.SL1-1	0.74	P52948	NUP98 (nucleoporin 98)
KY.Chr2.2140	R/P	KY.Chr2.2140.v1.SL1-1	0	Q60337	MARCH6 (membrane associated ring-CH-type finger 6)
KY.Chr2.2141	R/P	KY.Chr2.2141.v2.SL2-1	0	Q9Y5L0	TNPO3 (transportin 3)
KY.Chr2.2142	R/P	KY.Chr2.2142.v1.SL1-1	0.59	Q9H6D7	HAUSA (HAUS augmin like complex subunit 4)
KY.Chr2.2143	R/P	KY.Chr2.2143.v1.SL2-1	2.24E-56	Q60239	SH3BP5 (SH3 domain binding protein 5)
KY.Chr2.2144	R/P	KY.Chr2.2144.v1.ND1-2	1.7	P67775	PPP2CA (protein phosphatase 2 catalytic subunit alpha)
KY.Chr2.2145	R/P	KY.Chr2.2145.v1.ND1-1	2.58E-11	P47972	NPTX2 (neuronal pentraxin 2)
KY.Chr2.2146	R/P	KY.Chr2.2146.v1.nonSL2-1	1.08E-08	Q86X45	LRRC6 (leucine rich repeat containing 6)
KY.Chr2.2147	R/P	KY.Chr2.2147.v5.ND4-3	2.87E-37	Q6UXH9	PAMR1 (peptidase domain containing associated with muscle regeneration 1)
KY.Chr2.2149	R/P	KY.Chr2.2149.v1.nonSL9-2	2.90E-25	P07305	H1FO (H1 histone family member 0)
KY.Chr2.2151	R/P	KY.Chr2.2151.v1.SL6-1	0.64	O15015	ZNF646 (zinc finger protein 646)
KY.Chr2.2152	R/P	KY.Chr2.2152.v2.nonSL9-5	7.77E-08	Q8NHG7	SVIP (small VCP interacting protein)
KY.Chr2.2153	R/P	KY.Chr2.2153.v1.nonSL7-1	1.03E-83	P15531	NME1 (NME/NM23 nucleoside diphosphate kinase 1)
KY.Chr2.2154	R/P	KY.Chr2.2154.v1.ND1-1	0.12	Q9BQ88	FYCO1 (FYVE and coiled-coil domain containing 1)
KY.Chr2.2155	R/P	KY.Chr2.2155.v1.SL2-1	1.32E-24	Q96B77	TMEM186 (transmembrane protein 186)
KY.Chr2.2156	R/P	KY.Chr2.2156.v2.SL1-1	5.44E-77	Q8WUB8	PHF10 (PHD finger protein 10)
KY.Chr2.2157	R/P	KY.Chr2.2157.v1.nonSL3-1	8.39E-39	Q9H218	LRMDA (leucine rich melanocyte differentiation associated)
KY.Chr2.2158	R/P	KY.Chr2.2158.v3.SL1-3	1.07E-42	P12110	COL6A2 (collagen type VI alpha 2 chain)
KY.Chr2.2159	R/P	KY.Chr2.2159.v1.ND1-1	0.65	Q9P2P5	HECW2 (HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2)
KY.Chr2.2160	R/P	KY.Chr2.2160.v1.nonSL9-1	1.07E-20	Q86VR8	FJX1 (four-jointed box kinase 1)
KY.Chr2.2161	R/P	KY.Chr2.2161.v2.ND2-2	2	P49821	NDUFV1 (NADH:ubiquinone oxidoreductase core subunit V1)
KY.Chr2.2162	R/P	KY.Chr2.2162.v1.ND1-1	1	A6NHS7	MANSC4 (MANSC domain containing 4)
KY.Chr2.2163	R/P	KY.Chr2.2163.v1.nonSL3-1	1	A6NGR9	MROH6 (maestro heat like repeat family member 6)
KY.Chr2.2164	R/P	KY.Chr2.2164.v2.nonSL5-2	1.70E-50	Q13148	TARDBP (TAR DNA binding protein)
KY.Chr3.461	P	KY.Chr3.461.v2.SL2-2	1.72E-30	Q96K78	ADGRG7 (Adhesion G protein-coupled receptor G7)
KY.Chr3.462	P	KY.Chr3.462.v2.SL1-2	1	Q06609	RAD51 (RAD51 recombinase)
KY.Chr3.463	P	KY.Chr3.463.v1.ND1-1	2.9	P21266	GSTM3 (glutathione S-transferase mu 3)
KY.Chr3.464	P	KY.Chr3.464.v1.SL1-1	1.90E-67	Q96NT5	SLC46A1 (solute carrier family 46 member 1)
KY.Chr3.465	P	KY.Chr3.465.v1.SL1-1	8.59E-28	Q96NT5	SLC46A1 (solute carrier family 46 member 1)
KY.Chr3.466	P	KY.Chr3.466.v1.ND1-1	1.03E-10	Q96NT5	SLC46A1 (solute carrier family 46 member 1)
KY.Chr3.467	P	KY.Chr3.467.v2.SL6-1	3.17E-24	Q8WU39	MZB1 (marginal zone B and B1 cell specific protein)
KY.Chr3.483	R/P	KY.Chr3.483.v1.nonSL5-1	0	Q9BTY2	FUCA2 (alpha-L-fucosidase 2)
KY.Chr3.484	R/P	KY.Chr3.484.v1.nonSL8-2	1.10E-07	P02511	CRYAB (crystallin alpha B)
KY.Chr3.485	R/P	KY.Chr3.485.v1.nonSL9-1	1.90E-09	P02511	CRYAB (crystallin alpha B)
KY.Chr3.486	R/P	KY.Chr3.486.v1.SL3-1	2.6	Q8WVT3	TRAPP12 (trafficking protein particle complex 12)
KY.Chr3.487	R/P	KY.Chr3.487.v1.ND1-1	4.10E-95	Q15326	ZMYND11 (zinc finger MYND-type containing 11)
KY.Chr3.488	R/P	KY.Chr3.488.v1.nonSL6-1	0	Q96KA5	CLPTM1L (CLPTM1 like)
KY.Chr3.489	R/P	KY.Chr3.489.v4.nonSL9-1	3.56E-178	P07237	P4HB (prolyl 4-hydroxylase subunit beta)
KY.Chr3.490	R/P	KY.Chr3.490.v1.SL1-2	0	Q9Y5B9	SUPT16H (SPT16 homolog facilitates chromatin remodeling subunit)
KY.Chr3.491	R/P	KY.Chr3.491.v1.ND1-2	0.88	Q68CQ4	UTP25 (UTP25 small subunit processor component)
KY.Chr3.492	R/P	KY.Chr3.492.v1.SL5-1	5.97E-97	Q8NCC3	PLA2G15 (phospholipase A2 group XV)
KY.Chr3.493	R/P	KY.Chr3.493.v1.ND1-1	2.4	Q9UPX0	IGSF9B (immunoglobulin superfamily member 9B)
KY.Chr3.494	R/P	KY.Chr3.494.v1.SL2-4	1.05E-98	Q6P6C2	ALKBH5 (alkB homolog 5 RNA demethylase)
KY.Chr3.495	R/P	KY.Chr3.495.v1.nonSL1-1	0	Q9Y2A7	NCKAP1 (NCK associated protein 1)
KY.Chr3.496	R/P	KY.Chr3.496.v1.ND1-1	2.10E-04	Q15149	PLEC (plectin)
KY.Chr3.497	R/P	KY.Chr3.497.v1.ND1-1	2.30E-154	Q14028	CNGB1 (cyclic nucleotide gated channel beta 1)
KY.Chr3.498	R/P	KY.Chr3.498.v1.ND1-1	2.76E-92	Q8TB37	NUBPL (nucleotide binding protein like)
KY.Chr3.499	R/P	KY.Chr3.499.v1.ND1-2	0	Q15393	SF3B3 (splicing factor 3b subunit 3)
KY.Chr4.377	R/P	KY.Chr4.377.v1.ND1-1	1.76E-33	Q13546	RIPK1 (receptor interacting serine/threonine kinase 1)
KY.Chr4.378	R/P	KY.Chr4.378.v1.ND1-1	1.7	Q7Z7A3	CTU1 (cytosolic thouridylase subunit 1)
KY.Chr4.379	R/P	KY.Chr4.379.v1.ND1-1	1.13E-132	P38117	ETFB (electron transfer flavoprotein subunit beta)
KY.Chr4.380	R/P	KY.Chr4.380.v1.SL2-1	2.30E-81	Q96JD6	AKR1E2 (aldo-keto reductase family 1 member E2)
KY.Chr4.381	R/P	KY.Chr4.381.v1.nonSL9-1	7.74E-34	P25963	NFKBIA (NFKB inhibitor alpha)
KY.Chr4.382	R/P	KY.Chr4.382.v1.ND1-1	0.23	Q4W4Y0	C14orf28 (chromosome 14 open reading frame 28)
KY.Chr4.383	R/P	KY.Chr4.383.v1.SL1-1	7.93E-46	Q96011	PEX11B (peroxisomal biogenesis factor 11 beta)
KY.Chr4.384	R/P	KY.Chr4.384.v1.nonSL2-1	3.38E-79	Q53G59	KLHL12 (kelch like family member 12)

KY.Chr4.385	R/P	KY.Chr4.385.v1.ND1-1	1.4	P18074	ERCC2 (ERCC excision repair 2 TFIIH core complex helicase subunit)
KY.Chr4.386	R/P	KY.Chr4.386.v2.nonSL3-2	0	O15523	DDX3Y (DEAD-box helicase 3 Y-linked)
KY.Chr4.387	R/P	KY.Chr4.387.v1.nonSL3-1	0	Q96CW5	TUBGP3 (tubulin gamma complex associated protein 3)
KY.Chr4.388	R/P	KY.Chr4.388.v1.nonSL3-1	2.4	Q96SM3	CPXM1 (carboxypeptidase X M14 family member 1)
KY.Chr4.389	R/P	KY.Chr4.389.v1.nonSL4-2	2.4	Q6NSJ2	PHLDB3 (pleckstrin homology like domain family B member 3)
KY.Chr4.390	R/P	KY.Chr4.390.v1.ND1-1	1	A5PLN7	FAM149A (family with sequence similarity 149 member A)
KY.Chr4.391	R/P	KY.Chr4.391.v1.nonSL9-1	3.00E-23	Q5VYJ5	MALRD1 (MAM and LDL receptor class A domain containing 1)
KY.Chr4.392	R/P	KY.Chr4.392.v1.ND1-1	4.84E-10	Q8NFP4	MDGA1 (MAM domain containing glycosylphosphatidylinositol anchor 1)
KY.Chr4.393	R/P	KY.Chr4.393.v1.ND1-1	1.2	Q9C037	TRIM4 (tripartite motif containing 4)
KY.Chr4.394	R/P	KY.Chr4.394.v1.SL3-1	8.02E-101	Q76082	SLC22A5 (solute carrier family 22 member 5)
KY.Chr4.395	R/P	KY.Chr4.395.v1.ND1-1	5.4	P47890	OR1G1 (olfactory receptor family 1 subfamily G member 1)
KY.Chr4.396	R/P	KY.Chr4.396.v1.ND1-1	1.9	Q9BZE4	GTPBP4 (GTP binding protein 4)
KY.Chr4.397	R/P	KY.Chr4.397.v1.SL4-1	0	Q9H7Z6	KAT8 (lysine acetyltransferase 8)
KY.Chr4.398	R/P	KY.Chr4.398.v1.SL1-1	0.6	Q86YH2	ZNF280B (zinc finger protein 280B)
KY.Chr4.399	R/P	KY.Chr4.399.v1.SL1-1	7.24E-97	Q9NUM3	SLC39A9 (solute carrier family 39 member 9)
KY.Chr4.400	R/P	KY.Chr4.400.v1.ND1-1	2.7	Q7RTX7	CATSPER4 (cation channel sperm associated 4)
KY.Chr4.401	R/P	KY.Chr4.401.v1.SL1-1	4.69E-69	Q96NE9	FRMD6 (FERM domain containing 6)
KY.Chr4.402	R/P	KY.Chr4.402.v1.nonSL4-1	2.96E-92	O43462	MBTPS2 (membrane bound transcription factor peptidase site 2)
KY.Chr4.403	R/P	KY.Chr4.403.v1.ND1-1	0.008	O60637	TSPAN3 (tetraspanin 3)
KY.Chr4.404	R/P	KY.Chr4.404.v1.nonSL9-1	2.59E-87	O96008	TOMM40 (translocase of outer mitochondrial membrane 40)
KY.Chr4.405	R/P	KY.Chr4.405.v1.ND1-1	0.42	Q99996	AKAP9 (A-kinase anchoring protein 9)
KY.Chr4.406	R/P	KY.Chr4.406.v1.SL1-1	1.30E-10	A6NLC5	C3orf70 (chromosome 3 open reading frame 70)
KY.Chr4.407	R/P	KY.Chr4.407.v1.ND1-1	2.97E-63	P41182	BCL6 (BCL6 transcription repressor)
KY.Chr4.408	R/P	KY.Chr4.408.v2.SL11-3	6.42E-169	Q8WUM0	NUP133 (nucleoporin 133)
KY.Chr4.409	R/P	KY.Chr4.409.v1.ND1-2	3.5	P24592	IGFBP6 (insulin like growth factor binding protein 6)
KY.Chr4.410	R/P	KY.Chr4.410.v1.ND1-1	1.1	Q8N8R1	TRPV1 (transient receptor potential cation channel subfamily V member 1)
KY.Chr4.411	R/P	KY.Chr4.411.v1.nonSL9-1	3.33E-107	P51159	RAB27A (RAB27A member RAS oncogene family)
KY.Chr4.412	R/P	KY.Chr4.412.v1.nonSL6-1	4.07E-155	P23229	ITGA6 (integrin subunit alpha 6)
KY.Chr4.413	R/P	KY.Chr4.413.v1.ND1-1	1.6	Q9UGJ1	TUBGPC4 (tubulin gamma complex associated protein 4)
KY.Chr4.414	R/P	KY.Chr4.414.v1.ND1-2	4.8	O43909	EXTL3 (exostosin like glycosyltransferase 3)
KY.Chr4.415 (<i>ErfA</i>)	R/P	KY.Chr4.415.v1.ND1-1	6.09E-25	P50548	ERF (ETS2 repressor factor)
KY.Chr4.416	R/P	KY.Chr4.416.v1.ND1-1	0.4	Q14517	FAT1 (FAT atypical cadherin 1)
KY.Chr4.417	R/P				no significant match found
KY.Chr4.418	R/P	KY.Chr4.418.v2.SL1-2	0.016	P25940	COL5A3 (collagen type V alpha 3 chain)
KY.Chr4.419	R/P	KY.Chr4.419.v1.ND1-1	7.96E-28	Q9UL12	SARDH (sarcosine dehydrogenase)
KY.Chr4.420	R/P	KY.Chr4.420.v1.SL3-1	7.00E-82	Q08623	PUDP (pseudouridine 5'-phosphatase)
KY.Chr4.421	R/P	KY.Chr4.421.v1.SL1-1	0	Q9UL12	SARDH (sarcosine dehydrogenase)
KY.Chr4.422	R/P	KY.Chr4.422.v1.ND1-1	1.5	Q9UL12	SARDH (sarcosine dehydrogenase)
KY.Chr4.423	R/P	KY.Chr4.423.v1.nonSL5-1	1.62E-55	Q96CG8	CTHRC1 (cthr1 triple helix repeat containing 1)
KY.Chr4.424	R/P	KY.Chr4.424.v2.ND3-1	6.46E-100	O95571	ETHE1 (ETHE1 persulfide dioxygenase)
KY.Chr4.425	R/P	KY.Chr4.425.v2.SL18-3	4.95E-158	Q8NBT3	TMEM145 (transmembrane protein 145)
KY.Chr4.426	R/P	KY.Chr4.426.v1.SL2-1	0	Q7ZGZ7	HUWE1 (HECT UBA and WWE domain containing 1 E3 ubiquitin protein ligase)
KY.Chr4.427	R/P	KY.Chr4.427.v1.ND1-1	0.54	Q709F0	ACAD11 (acyl-CoA dehydrogenase family member 11)
KY.Chr4.428	R/P	KY.Chr4.428.v1.SL2-1	6.03E-180	Q9BRS2	RIOK1 (RIO kinase 1)
KY.Chr4.429	R/P	KY.Chr4.429.v1.ND1-1	4.51E-26	Q6PJT7	ZC3H14 (zinc finger CCCH-type containing 14)
KY.Chr4.430	R/P	KY.Chr4.430.v1.SL3-1	5.06E-45	Q9BSG0	PRADC1 (protease associated domain containing 1)
KY.Chr4.431	R/P	KY.Chr4.431.v1.ND1-1	0	Q13936	CACNA1C (calcium voltage-gated channel subunit alpha 1 C)
KY.Chr4.432	R/P	KY.Chr4.432.v1.ND1-1	1.5	O20283	NAAA (N-acyl ethanolamine acid amidase)
KY.Chr4.433	R/P	KY.Chr4.433.v7.ND2-5	0.088	Q9H1D0	TRPV6 (transient receptor potential cation channel subfamily V member 6)
KY.Chr4.434	R/P	KY.Chr4.434.v1.ND1-1	1.92E-13	Q7Z4M0	REC114 (REC114 meiotic recombination protein)
KY.Chr4.435	R/P	KY.Chr4.435.v1.SL1-1	4.89E-29	O43603	GALR2 (galanin receptor 2)
KY.Chr4.436	R/P	KY.Chr4.436.v1.ND1-1	0.19	Q9NYF0	DACT1 (dishevelled binding antagonist of beta catenin 1)
KY.Chr4.437	R/P	KY.Chr4.437.v2.SL3-1	0	P20807	CAPN3 (calpain 3)
KY.Chr4.438	R/P	KY.Chr4.438.v1.SL1-1	0.15	P43359	MAGEA5 (MAGE family member A5)
KY.Chr4.439	R/P	KY.Chr4.439.v1.nonSL9-1	0.18	Q5TYX0	PRAMEF5 (PRAME family member 5)
KY.Chr4.440	R/P	KY.Chr4.440.v1.nonSL1-1	1.18E-54	Q8N309	LRRC43 (leucine rich repeat containing 43)
KY.Chr4.441	R/P	KY.Chr4.441.v1.SL2-1	0.85	Q7Z7G8	VPS13B (vacuolar protein sorting 13 homolog B)
KY.Chr4.442	R/P	KY.Chr4.442.v1.nonSL2-1	1.76E-39	Q4LDE5	SVEP1 (sushi von Willebrand factor type A EGF and pentraxin domain containing 1)
KY.Chr4.443	R/P	KY.Chr4.443.v1.ND1-1	2.9	O60469	DSCAM (DS cell adhesion molecule)
KY.Chr4.444	R/P	KY.Chr4.444.v1.nonSL3-1	3.93E-74	Q4LDE5	SVEP1 (sushi von Willebrand factor type A EGF and pentraxin domain containing 1)
KY.Chr4.445	R/P	KY.Chr4.445.v1.SL1-1	0	O15439	ABCC4 (ATP binding cassette subfamily C member 4)
KY.Chr4.446	R/P	KY.Chr4.446.v1.SL2-1	1.13E-149	Q9UJM8	HAO1 (hydroxyacid oxidase 1)
KY.Chr4.447	R/P	KY.Chr4.447.v1.nonSL1-1	2.7	Q9HCH5	SYTL2 (synaptotagmin like 2)
KY.Chr4.448	R/P	KY.Chr4.448.v1.nonSL1-1	0.3	Q9UL01	DSE (dermatan sulfate epimerase)
KY.Chr4.449 (<i>Bmp2/4</i>)	R/P	KY.Chr4.449.v4.ND4-1	9.67E-122	P12643	BMP2 (bone morphogenetic protein 2)
KY.Chr4.450 (<i>Gdf1/3-r</i>)	R/P	KY.Chr4.450.v1.ND1-1	4.58E-41	P12644	BMP4 (bone morphogenetic protein 4)
KY.Chr4.451	R/P	KY.Chr4.451.v1.ND1-1	0.81	A6PVS8	LRR1Q3 (leucine rich repeats and IQ motif containing 3)
KY.Chr4.452	R/P	KY.Chr4.452.v1.ND1-1	1.57E-31	Q969H0	FBXW7 (F-box and WD repeat domain containing 7)
KY.Chr4.453	R/P	KY.Chr4.453.v2.ND2-2	2.49E-24	Q9P2E3	ZNFX1 (zinc finger NFX1-type containing 1)
KY.Chr4.454	R/P	KY.Chr4.454.v1.ND1-1	0	Q9P2E3	ZNFX1 (zinc finger NFX1-type containing 1)
KY.Chr5.25	R/P	KY.Chr5.25.v1.SL1-1	7.74E-23	Q6P2S7	TTC41P (tetrapeptide repeat domain 41, pseudogene)
KY.Chr5.26	R/P	KY.Chr5.26.v1.ND1-1	5.42E-14	A6NKG5	RTL1 (retrotransposon Gag like 1)
KY.Chr5.27	R/P	KY.Chr5.27.v2.ND1-1	0.14	Q9NY10	PSD3 (pleckstrin and Sec7 domain containing 3)
KY.Chr5.28	R/P	KY.Chr5.28.v1.SL1-1	3.85E-42	Q8TC57	M1AP (meiosis 1 associated protein)
KY.Chr5.265	R/P	KY.Chr5.265.v1.SL1-1	1.36E-09	Q86X45	LRRC6 (leucine rich repeat containing 6)
KY.Chr5.266	R/P	KY.Chr5.266.v1.SL1-1	5.7	Q14643	ITPR1 (inositol 1 4 5-trisphosphate receptor type 1)
KY.Chr5.267	R/P	KY.Chr5.267.v1.SL3-1	0	O15042	U2SURP (U2 snRNP associated SURP domain containing)
KY.Chr5.268	R/P	KY.Chr5.268.v2.nonSL1-1	1.25E-63	Q8NCA5	FAM98A (family with sequence similarity 98 member A)
KY.Chr5.269	(R/P) (this model was not mapped to the specimen R genome)	KY.Chr5.269.v1.ND1-1	4.48E-75	Q9Y226	SLC22A13 (solute carrier family 22 member 13)
KY.Chr5.270	(R/P) (this model was not mapped to the specimen R genome)	KY.Chr5.270.v1.ND1-1	8.70E-01	Q8IXQ6	PARP9 (poly(ADP-ribose) polymerase family member 9)
KY.Chr5.271	(R/P) (this model was not mapped to the specimen R genome)	KY.Chr5.271.v2.ND2-1	5.00E+00	Q13698	CACNAIS (calcium voltage-gated channel subunit alpha 1 S)
KY.Chr5.272	(R/P) (this model was not mapped to the specimen R genome)	KY.Chr5.272.v1.ND1-1	5.60E-01	P62191	PSMC1 (proteasome 26S subunit, ATPase 1)
KY.Chr6.38	P	KY.Chr6.38.v3.ND1-3	8.06E-130	Q00534	CDK6 (cyclin dependent kinase 6)
KY.Chr6.39	P	KY.Chr6.39.v1.nonSL1-1	1.20E-151	P55157	MTPP (microsomal triglyceride transfer protein)
KY.Chr6.40	P	KY.Chr6.40.v2.nonSL9-1	1.79E-106	Q13126	MTAP (methylthioadenosine phosphorylase)
KY.Chr6.41	P	KY.Chr6.41.v2.SL1-2	3.85E-18	P56470	LGALS4 (galectin 4)
KY.Chr6.42	P				no significant match found
KY.Chr6.43	P	KY.Chr6.43.v3.nonSL2-2	1.72E-31	P56470	LGALS4 (galectin 4)
KY.Chr6.44	P	KY.Chr6.44.v1.SL1-1	0.4	Q81Y21	DDX60 (DEAD/H-box helicase 60)
KY.Chr6.45	P	KY.Chr6.45.v1.SL1-2	5.47E-43	Q641Q2	WASHC2A (WASH complex subunit 2A)
KY.Chr6.59	R	KY.Chr6.59.v2.SL2-1	2.82E-162	Q5SZQ8	CELF3 (CUGBP Elav-like family member 3)
KY.Chr6.60	R	KY.Chr6.60.v1.ND1-1	1.76E-66	Q9NQB0	TCF7L2 (transcription factor 7 like 2)
KY.Chr6.61	R	KY.Chr6.61.v1.ND1-1	6.2	P51170	SCNN1G (sodium channel epithelial 1 gamma subunit)
KY.Chr6.62	R	KY.Chr6.62.v1.ND1-1	5.9	Q8TDV2	GPR148 (G protein-coupled receptor 148)
KY.Chr6.63	R	KY.Chr6.63.v1.nonSL2-1	1.07E-53	Q16514	TAF12 (TATA-box binding protein associated factor 12)
KY.Chr6.64	R	KY.Chr6.64.v1.ND1-1	0.08	Q9NYF8	BCLAF1 (BCL2 associated transcription factor 1)
KY.Chr6.65	R	KY.Chr6.65.v1.ND1-1	4.6	P13797	PLS3 (plastin 3)
KY.Chr6.66	R	KY.Chr6.66.v2.ND2-1	0.73	O60271	SPAG9 (sperm associated antigen 9)
KY.Chr6.67	R	KY.Chr6.67.v1.ND1-1	5.1	Q9C0F0	ASXL3 (ASXL transcriptional regulator 3)
KY.Chr6.68	R	KY.Chr6.68.v5.nonSL9-1	3.27E-75	O75899	GABBR2 (gamma-aminobutyric acid type B receptor subunit 2)
KY.Chr6.69	R	KY.Chr6.69.v1.ND1-1	0.002	P18583	SON (SON DNA binding protein)
KY.Chr6.70	R	KY.Chr6.70.v1.SL1-1	0.001	P62079	TSPAN5 (tetraspanin 5)
KY.Chr6.71	R	KY.Chr6.71.v1.SL1-1	2.06E-49	Q9H3S4	TPK1 (thiamin pyrophosphokinase 1)
KY.Chr6.72	R	KY.Chr6.72.v1.nonSL4-1	2.21E-27	Q9H3S4	TPK1 (thiamin pyrophosphokinase 1)
KY.Chr6.73	R	KY.Chr6.73.v4.SL1-3	7.92E-16	Q5JXM2	METTL24 (methyltransferase like 24)
KY.Chr6.75	R	KY.Chr6.75.v1.ND1-2	0.93	Q8WXI7	MUC16 (mucin 16 cell surface associated)

KY.Chr6.76	R	KY.Chr6.76.v2.nonSL3-2	2.94E-19	Q96RW7	HMCN1 (hemicentin 1)
KY.Chr6.77	R	KY.Chr6.77.v1.ND1-3	2.05E-19	Q96RW7	HMCN1 (hemicentin 1)
KY.Chr6.78	R	KY.Chr6.78.v1.ND1-1	0.43	O75943	RAD17 (RAD17 checkpoint clamp loader component)
KY.Chr6.79	R	KY.Chr6.79.v1.ND1-1	1.8	Q99623	PHB2 (prohibitin 2)
KY.Chr6.80	R	KY.Chr6.80.v1.ND1-1	1.58E-18	Q96RW7	HMCN1 (hemicentin 1)
KY.Chr6.81	R	KY.Chr6.81.v1.ND1-1	6.79E-20	O60241	ADGRB2 (adhesion G protein-coupled receptor B2)
KY.Chr6.82	R	KY.Chr6.82.v2.SL3-2	0.12	Q86Y13	DZIP3 (DAZ interacting zinc finger protein 3)
KY.Chr6.83	R	KY.Chr6.83.v1.SL2-1	1.49E-49	Q9NXU5	ARL15 (ADP ribosylation factor like GTPase 15)
KY.Chr6.84	R	KY.Chr6.84.v1.SL1-1	1.75E-92	Q7L210	MEPCE (methylphosphate capping enzyme)
KY.Chr6.85	R	KY.Chr6.85.v1.ND1-1	0.07	Q14896	MYBPC3 (myosin binding protein C cardiac)
KY.Chr6.86	R	KY.Chr6.86.v1.ND1-1	1.11E-13	Q6ZRI0	OTOG (stogelin)
KY.Chr6.87	R	KY.Chr6.87.v1.ND1-1	0	P04275	VWF (von Willebrand factor)
KY.Chr6.88	R	KY.Chr6.88.v1.ND1-1	0.58	A0ZSE6	TMEM30CP (transmembrane protein 30C pseudogene)
KY.Chr6.89	R	KY.Chr6.89.v1.nonSL5-1	2.20E-108	P50416	CPT1A (carnitine palmitoyltransferase 1A)
KY.Chr6.90	R	KY.Chr6.90.v1.SL5-1	0.28	P33151	CDH5 (cadherin 5)
KY.Chr6.91	R	KY.Chr6.91.v3.nonSL12-2	9.20E-44	O43617	TRAPP3 (trafficking protein particle complex 3)
KY.Chr6.92	R	KY.Chr6.92.v1.nonSL1-1	0	Q7Z6B7	SRGAP1 (SLIT-ROBO Rho GTPase activating protein 1)
KY.Chr6.93	R	KY.Chr6.93.v1.ND1-1	1.7	O75800	ZMYND10 (zinc finger MYND-type containing 10)
KY.Chr6.94	R	KY.Chr6.94.v1.nonSL3-1	2.70E-163	O60733	PLA2G6 (phospholipase A2 group VI)
KY.Chr6.95	R	KY.Chr6.95.v1.nonSL6-1	1.58E-06	P82914	MRPS15 (mitochondrial ribosomal protein S15)
KY.Chr6.96	R	KY.Chr6.96.v2.SL1-2	2.78E-37	P49406	MRPL19 (mitochondrial ribosomal protein L19)
KY.Chr6.97	R	KY.Chr6.97.v1.SL1-1	0	Q9NUB1	ACSS1 (acyl-CoA synthetase short chain family member 1)
KY.Chr6.98	R	KY.Chr6.98.v1.SL2-1	1.53E-112	O95905	ECD (ecdysoneless cell cycle regulator)
KY.Chr6.99	R	KY.Chr6.99.v1.SL1-1	2.02E-71	Q53G59	KLHL12 (kelch like family member 12)
KY.Chr6.100	R	KY.Chr6.100.v1.ND1-1	2.16E-68	Q53G59	KLHL12 (kelch like family member 12)
KY.Chr6.101	R	KY.Chr6.101.v1.ND1-1	0.51	Q9UBU6	FAM8A1 (family with sequence similarity 8 member A1)
KY.Chr6.102	R	KY.Chr6.102.v2.ND1-2	2.22E-33	Q53G59	KLHL12 (kelch like family member 12)
KY.Chr7.593	R	KY.Chr7.593.v1.nonSL1-1	0.044	P13611	VCAN (versican)
KY.Chr7.594	R	KY.Chr7.594.v1.SL5-1	1.58E-116	Q8WYN0	ATG4A (autophagy related 4A cysteine peptidase)
KY.Chr7.595	R	KY.Chr7.595.v1.ND1-1	0.16	Q9BS86	ZBPB (zona pellucida binding protein)
KY.Chr7.596	R	KY.Chr7.596.v1.SL9-4	5.1	Q15034	HERC3 (HECT and RLD domain containing E3 ubiquitin protein ligase 3)
KY.Chr7.597	R	KY.Chr7.597.v1.SL4-1	1.2	O00634	NTN3 (netrin 3)
KY.Chr7.598	R	KY.Chr7.598.v1.ND1-1	0.15	Q92576	PHF3 (PHD finger protein 3)
KY.Chr7.599	R	KY.Chr7.599.v2.SL2-1	8.12E-131	Q9Y305	ACOT9 (acyl-CoA thioesterase 9)
KY.Chr7.600	R	KY.Chr7.600.v2.SL3-3	2.67E-73	P23919	DTYMK (deoxythymidylate kinase)
KY.Chr7.601	R	KY.Chr7.601.v3.SL2-2	4.70E-05	Q8NGP4	OR5M3 (olfactory receptor family 5 subfamily M member 3)
KY.Chr7.602	R	KY.Chr7.602.v1.ND1-1	0.34	Q8NAV2	Csorf58 (chromosome 8 open reading frame 58)
KY.Chr7.603	R	KY.Chr7.603.v1.SL3-1	2.17E-18	Q8NG65	CSGALNACT2 (chondroitin sulfate N-acetylgalactosaminyltransferase 2)
KY.Chr7.604	R	KY.Chr7.604.v1.ND1-1	0.3	Q155Q3	DIXDC1 (DIX domain containing 1)
KY.Chr7.605	R	KY.Chr7.605.v1.ND1-2	4.6	Q7Z3K3	POGZ (pogo transposable element derived with ZNF domain)
KY.Chr7.606	R	KY.Chr7.606.v1.ND1-1	2.16E-18	Q9NR99	MXRA5 (matrix remodeling associated 5)
KY.Chr7.607	R	KY.Chr7.607.v1.SL3-1	1.04E-22	O94933	SLITRK3 (SLIT and NTRK like family member 3)
KY.Chr7.608	R	KY.Chr7.608.v1.ND1-1	4.92E-30	Q8N137	CNTR0B (centrobin centriole duplication and spindle assembly protein)
KY.Chr7.609	R	KY.Chr7.609.v2.SL6-4	1.43E-148	O60678	PRMT3 (protein arginine methyltransferase 3)
KY.Chr7.610	R	KY.Chr7.610.v1.nonSL4-1	0.028	Q96Q27	ASB2 (ankyrin repeat and SOCS box containing 2)
KY.Chr7.611	R	KY.Chr7.611.v1.SL1-1	5.36E-136	P57076	CFAP298 (cilia and flagella associated protein 298)
KY.Chr7.612	R	KY.Chr7.612.v1.ND1-1	9.42E-19	Q496A3	SPATS1 (spermatogenesis associated serine rich 1)
KY.Chr7.613	R	KY.Chr7.613.v1.ND1-1	0	Q8N136	DAWI (dynein assembly factor with WD repeats 1)
KY.Chr7.614	R	KY.Chr7.614.v1.SL1-1	0	O94788	ALDH1A2 (aldehyde dehydrogenase 1 family member A2)
KY.Chr7.615	R	KY.Chr7.615.v1.ND1-1	1.2	P57071	PRDM15 (PR-SET domain 15)
KY.Chr7.616	R	KY.Chr7.616.v1.SL1-1	0	O94788	ALDH1A2 (aldehyde dehydrogenase 1 family member A2)
KY.Chr7.617	R	KY.Chr7.617.v1.ND1-1	1.52E-151	O94788	ALDH1A2 (aldehyde dehydrogenase 1 family member A2)
KY.Chr7.618	R	KY.Chr7.618.v1.SL1-1	0	O43451	MGAM (maltase-glucoamylase)
KY.Chr7.619	R	KY.Chr7.619.v1.ND1-1	0	Q96RP9	GFM1 (G elongation factor mitochondrial 1)
KY.Chr7.620	R	KY.Chr7.620.v1.nonSL1-1	1.1	Q14957	GRIN2C (glutamate ionotropic receptor NMDA type subunit 2C)
KY.Chr7.621	R				no significant match found
KY.Chr7.622	R	KY.Chr7.622.v1.nonSL9-1	0.17	Q9P2K8	EIF2AK4 (eukaryotic translation initiation factor 2 alpha kinase 4)
KY.Chr7.623	R	KY.Chr7.623.v1.ND1-1	0.96	O14782	KIF3C (kinesin family member 3C)
KY.Chr7.624	R	KY.Chr7.624.v2.ND2-1	6.4	Q8NBJ9	SIDT2 (SID1 transmembrane family member 2)
KY.Chr7.625	R	KY.Chr7.625.v2.SL4-4	0	P05166	PCCB (propionyl-CoA carboxylase subunit beta)
KY.Chr7.626	R	KY.Chr7.626.v1.nonSL6-1	8.30E-39	Q9NZ42	PSENE1 (presenilin enhancer gamma-secretase subunit)
KY.Chr7.627	R	KY.Chr7.627.v1.SL1-1	3.73E-17	Q9Y5U9	IERSIP1 (immediate early response 3 interacting protein 1)
KY.Chr7.628	R	KY.Chr7.628.v1.nonSL1-1	1.49E-104	Q9H3K2	GHTIM (growth hormone inducible transmembrane protein)
KY.Chr7.629	R	KY.Chr7.629.v1.nonSL4-1	1.53E-177	Q5JVF3	PCID2 (PCI domain containing 2)
KY.Chr7.630	R	KY.Chr7.630.v1.nonSL4-1	1.19E-56	Q8WV35	TCTEXID2 (Tetex1 domain containing 2)
KY.Chr7.631	R	KY.Chr7.631.v2.SL2-2	0.45	A0PJX4	SHISA3 (shiisa family member 3)
KY.Chr7.632	R	KY.Chr7.632.v1.SL2-1	1.32E-108	P17706	PTPN2 (protein tyrosine phosphatase non-receptor type 2)
KY.Chr7.633	R	KY.Chr7.633.v1.ND1-1	5.2	Q5VWK5	IL23R (interleukin 23 receptor)
KY.Chr7.634	R	KY.Chr7.634.v1.SL1-1	1.80E-10	Q9NQ78	KIF13B (kinesin family member 13B)
KY.Chr7.635	R	KY.Chr7.635.v1.SL1-1	1.61E-72	Q9BUL8	PDCD10 (programmed cell death 10)
KY.Chr7.636	R	KY.Chr7.636.v2.SL2-1	6.38E-13	Q9UMX3	BOK (BCL2 family apoptosis regulator BOK)
KY.Chr7.637	R	KY.Chr7.637.v1.SL4-1	2.91E-111	Q9NVU0	POLR3E (RNA polymerase III subunit E)
KY.Chr7.638	R	KY.Chr7.638.v2.ND3-1	8.52E-13	P54368	OAZ1 (ornithine decarboxylase antizyme 1)
KY.Chr7.639	R	KY.Chr7.639.v1.nonSL1-1	5.11E-48	Q7Z407	CSMD3 (CUB and Sushi multiple domains 3)
KY.Chr7.640	R	KY.Chr7.640.v1.nonSL3-1	3.46E-06	P54852	EMP3 (epithelial membrane protein 3)
KY.Chr7.641	R	KY.Chr7.641.v1.SL1-1	0	Q9P210	CPSP2 (cleavage and polyadenylation specific factor 2)
KY.Chr7.642	R	KY.Chr7.642.v2.SL1-3	1.16E-18	P08174	CD55 (CD55 molecule (Cromer blood group))
KY.Chr7.643	R	KY.Chr7.643.v1.SL4-1	2.87E-178	Q9UH17	SLC23A1 (solute carrier family 23 member 1)
KY.Chr7.644	R	KY.Chr7.644.v1.SL1-1	2.10E-53	Q9H418	SERHL2 (serine hydrolase like 2)
KY.Chr7.645	R	KY.Chr7.645.v1.SL1-1	5.01E-46	Q9H418	SERHL2 (serine hydrolase like 2)
KY.Chr7.646	R	KY.Chr7.646.v1.nonSL4-1	4.28E-28	Q8WZA0	LZIC (leucine zipper and CTNNBIP1 domain containing)
KY.Chr7.647	R	KY.Chr7.647.v1.ND1-1	0.53	P05129	PRKCG (protein kinase C gamma)
KY.Chr7.648	R	KY.Chr7.648.v1.ND1-2	3.56E-118	Q8WVP7	LMBR1 (limb development membrane protein 1)
KY.Chr7.649	R	KY.Chr7.649.v1.nonSL8-1	0.74	Q9C0B5	ZDHHC5 (zinc finger DHHC-type containing 5)
KY.Chr7.650	R	KY.Chr7.650.v1.ND1-1	0.29	Q9UMX0	UBQLN1 (ubiquilin 1)
KY.Chr7.651	R	KY.Chr7.651.v1.nonSL1-3	0	P24928	POLR2A (RNA polymerase II subunit A)
KY.Chr7.652	R	KY.Chr7.652.v1.nonSL1-1	1.2	Q03111	MLLT1 (MLLT1 super elongation complex subunit)
KY.Chr7.653	R	KY.Chr7.653.v1.SL2-1	1.01E-103	A0INW5	UHRF1BP1 (UHRF1 binding protein 1 like)
KY.Chr7.654	R	KY.Chr7.654.v1.ND1-1	8.15E-45	Q9H9Y4	GNP2 (GNP-loop GTPase 2)
KY.Chr7.655	R	KY.Chr7.655.v3.ND3-3	1.16E-129	Q9H9Y4	GNP2 (GNP-loop GTPase 2)
KY.Chr7.658	R	KY.Chr7.658.v6.SL5-5	2.82E-67	Q9UBS9	SUCO (SUN domain containing ossification factor)
KY.Chr7.659	R	KY.Chr7.659.v1.SL2-1	6.53E-33	Q06945	SOX4 (SRY-box 4)
KY.Chr7.660	R	KY.Chr7.660.v1.nonSL1-1	0	Q92626	PXDN (peroxidase)
KY.Chr7.661	R	KY.Chr7.661.v2.SL4-4	0.56	Q9Y3D2	MSRB2 (methionine sulfoxide reductase B2)
KY.Chr7.662	R	KY.Chr7.662.v2.SL3-3	0	Q9HCS7	XAB2 (XPA binding protein 2)
KY.Chr7.663	R	KY.Chr7.663.v2.SL26-1	4.82E-29	O15212	PFND6 (prefoldin subunit 6)
KY.Chr7.665	R	KY.Chr7.665.v1.SL1-1	1.97E-41	P0DP23	CALM1 (calmodulin 1)
KY.Chr7.666	R	KY.Chr7.666.v1.ND1-1	2.55E-05	Q8N7Z5	ANKRD31 (ankyrin repeat domain 31)
KY.Chr7.667	R	KY.Chr7.667.v1.SL1-1	2.29E-17	P22674	CCNO (cyclin O)
KY.Chr7.668	R				no significant match found
KY.Chr7.669	R	KY.Chr7.669.v1.nonSL5-1	0	O75191	XYLB (xylulokinase)
KY.Chr7.670	R	KY.Chr7.670.v2.ND1-2	2.5	Q7Z317	ZNF572 (zinc finger protein 572)
KY.Chr7.671	R	KY.Chr7.671.v1.ND1-1	5.24E-18	Q01484	ANK2 (ankyrin 2)
KY.Chr7.672	R	KY.Chr7.672.v1.ND1-1	6.15E-37	Q96ER3	SAAL1 (serum amyloid A like 1)
KY.Chr7.673	R	KY.Chr7.673.v2.nonSL8-2	6.83E-05	Q96MW1	CCDC43 (coiled-coil domain containing 43)
KY.Chr7.674	R	KY.Chr7.674.v1.ND1-1	1.26E-38	A2RUB1	MEIOC (meiosis specific with coiled-coil domain)
KY.Chr7.675	R	KY.Chr7.675.v1.SL2-1	1.8	Q9NXG6	P4HTM (poly(4-hydroxy)lase transmembrane)
KY.Chr7.676	R	KY.Chr7.676.v4.SL3-2	3.85E-65	O60583	CCNT2 (cyclin T2)
KY.Chr7.677	R	KY.Chr7.677.v1.SL4-1	1.45E-84	Q7Z429	GRINA (glutamate ionotropic receptor NMDA type subunit associated protein 1)
KY.Chr7.678	R	KY.Chr7.678.v1.nonSL4-1	6.34E-06	Q86Y26	MIB1 (mindbomb E3 ubiquitin protein ligase 1)
KY.Chr7.679	R	KY.Chr7.679.v1.ND1-1	8.04E-39	Q14554	PDIA5 (protein disulfide isomerase family A member 5)
KY.Chr7.680	R	KY.Chr7.680.v2.SL3-1	0.002	Q14554	PDIA5 (protein disulfide isomerase family A member 5)
KY.Chr7.681	R	KY.Chr7.681.v1.ND1-1	2.32E-141	Q14554	PDIA5 (protein disulfide isomerase family A member 5)
KY.Chr7.682	R	KY.Chr7.682.v1.SL1-1	9.91E-91	Q6UWV6	ENPP7 (ectonucleotide pyrophosphatase/phosphodiesterase 7)
KY.Chr7.683	R	KY.Chr7.683.v1.nonSL8-1	1.38E-64	Q96E52	OMA1 (OMA1 zinc metallopeptidase)
KY.Chr7.684	R	KY.Chr7.684.v1.SL1-1	1.20E-71	O75391	SPAG7 (sperm associated antigen 7)

KY.Chr7.685	R	KY.Chr7.685.v1.ND1-1	0	P51797	CLCN6 (chloride voltage-gated channel 6)
KY.Chr7.686	R	KY.Chr7.686.v1.SL2-1	0.6	Q8NI32	LYPD6B (LY6/PLAUR domain containing 6B)
KY.Chr7.687	R	KY.Chr7.687.v1.ND1-1	0.23	Q86W11	PKHD1L1 (PKHD1 like 1)
KY.Chr7.688	R	KY.Chr7.688.v2.ND2-1	3.98E-34	Q9BQR3	PRSS27 (serine protease 27)
KY.Chr7.689	R	KY.Chr7.689.v1.nonSL6-1	2.5	A6NM11	LRRC37A2 (leucine rich repeat containing 37 member A2)
KY.Chr7.690	R	KY.Chr7.690.v1.SL2-1	2.2	Q16853	AOC3 (amine oxidase copper containing 3)
KY.Chr7.691	R	KY.Chr7.691.v1.SL1-1	1.68E-103	Q9BU14	POLR3C (RNA polymerase III subunit C)
KY.Chr7.692	R	KY.Chr7.692.v1.SL1-1	3.57E-17	Q9NUP1	BLOC1S4 (biogenesis of lysosomal organelles complex 1 subunit 4)
KY.Chr7.693	R	KY.Chr7.693.v1.SL1-1	4.55E-64	Q8N9V3	WDSUB1 (WD repeat sterile alpha motif and U-box domain containing 1)
KY.Chr7.694	R	KY.Chr7.694.v1.SL2-1	4.46E-114	Q9NRA2	SLC17A5 (solute carrier family 17 member 5)
KY.Chr7.695	R	KY.Chr7.695.v2.ND2-2	2.32E-18	P16109	SELP (selectin P)
KY.Chr7.696	R	KY.Chr7.696.v1.nonSL1-1	4.40E-116	Q9HCS2	CYP4F12 (cytochrome P450 family 4 subfamily F member 12)
KY.Chr7.697	R	KY.Chr7.697.v1.nonSL3-1	0.01	Q4LDE5	SVEP1 (sushi von Willebrand factor type A EGF and pentraxin domain containing 1)
KY.Chr7.698	R	KY.Chr7.698.v1.SL1-1	0	Q9CZS0	DNAI2 (dynein axonemal intermediate chain 2)
KY.Chr7.699	R	KY.Chr7.699.v2.SL2-2	4.25E-30	O60232	SSSCA1 (Sjogren syndrome/scleroderma autoantigen 1)
KY.Chr7.700	R	KY.Chr7.700.v1.SL1-1	0	Q96NH3	TBC1D32 (TBC1 domain family member 32)
KY.Chr7.701	R	KY.Chr7.701.v1.SL2-2	1.18E-58	P31947	SFN (stratifin)
KY.Chr7.702	R	KY.Chr7.702.v1.SL1-1	4.49E-15	Q2M3R5	SLC35G1 (solute carrier family 35 member G1)
KY.Chr7.703 (Hox13)	R	KY.Chr7.703.v2.SL2-1	3.63E-21	P35452	HOXD12 (homeobox D12)
KY.Chr7.704 (Hox12)	R	KY.Chr7.704.v1.ND1-1	3.26E-20	P35452	HOXD12 (homeobox D12)
KY.Chr7.705	R	KY.Chr7.705.v2.SL1-2	3.20E-66	O15484	CAPN5 (calpain 5)
KY.Chr7.706	R	KY.Chr7.706.v2.nonSL3-4	0	Q13153	PAK1 (p21 (RAC1) activated kinase 1)
KY.Chr7.707	R	KY.Chr7.707.v2.ND2-1	0	Q9UPN4	CEP131 (centrosomal protein 131)
KY.Chr7.708	R	KY.Chr7.708.v1.ND1-1	1.47E-08	P32245	MC4R (melanocortin 4 receptor)
KY.Chr7.709	R	KY.Chr7.709.v2.nonSL9-3	0	Q96KG9	SCYL1 (SCY1 like pseudokinase 1)
KY.Chr7.710	R	KY.Chr7.710.v1.SL4-1	2.75E-132	P02708	CHRNA1 (cholinergic receptor nicotinic alpha 1 subunit)
KY.Chr7.711	R	KY.Chr7.711.v1.SL1-3	2.61E-22	Q7Z410	TMPPRS9 (transmembrane serine protease 9)
KY.Chr7.712	R	KY.Chr7.712.v2.ND1-2	2.46E-21	Q6HA08	ASTL (astacin like metalloendopeptidase)
KY.Chr7.713	R	KY.Chr7.713.v2.ND1-1	6.67E-15	P07996	THBS1 (thrombospondin 1)
KY.Chr7.714	R	KY.Chr7.714.v1.nonSL2-2	9.02E-16	Q92847	GHSR (growth hormone secretagogue receptor)
KY.Chr7.715	R	KY.Chr7.715.v1.SL1-1	8.43E-20	Q92847	GHSR (growth hormone secretagogue receptor)
KY.Chr7.716	R	KY.Chr7.716.v1.nonSL9-1	0	Q8IY16	EXOC8 (exocyst complex component 8)
KY.Chr7.717	R	KY.Chr7.717.v1.ND1-1	0.68	P12110	COL6A2 (collagen type VI alpha 2 chain)
KY.Chr7.718	R	KY.Chr7.718.v3.SL6-1	3.77E-31	Q53S33	BOLA3 (bola family member 3)
KY.Chr7.719	R	KY.Chr7.719.v1.SL1-1	0	Q9NV17	ATAD3A (ATPase family AAA domain containing 3A)
KY.Chr7.720	R	KY.Chr7.720.v1.nonSL3-1	2.45E-97	Q96G74	OTUD5 (OTU deubiquitinase 5)
KY.Chr7.721	R	KY.Chr7.721.v1.SL5-5	9.07E-115	Q96Q11	TRNT1 (tRNA nucleotidyl transferase 1)
KY.Chr7.722	R	KY.Chr7.722.v1.SL1-1	1.34E-37	Q9H0R6	QRSL1 (glutaminylnRNA amidotransferase subunit QRSL1)
KY.Chr8.779	R/P	KY.Chr8.779.v2.SL1-2	3.85E-95	Q96S53	TESK2 (testis associated actin remodeling kinase 2)
KY.Chr8.780	R/P	KY.Chr8.780.v2.nonSL2-2	0	Q0JRZ9	FCHO2 (FCH domain only 2)
KY.Chr8.781	R/P	KY.Chr8.781.v1.ND1-1	0.46	Q9H400	RAD21L1 (RAD21 cohesin complex component like 1)
KY.Chr8.782	R/P	KY.Chr8.782.v2.SL1-1	6.7	P56937	HSD17B7 (hydroxysteroid 17-beta dehydrogenase 7)
KY.Chr8.783	R/P	KY.Chr8.783.v1.SL1-1	1.42E-136	Q16543	CDC37 (cell division cycle 37)
KY.Chr8.784	R/P	KY.Chr8.784.v1.SL1-1	0.12	O43488	AKR7A2 (aldo-keto reductase family 7 member A2)
KY.Chr8.785	R/P	KY.Chr8.785.v3.SL2-3	2.3	Q7Z569	BRAP (BRCA1 associated protein)
KY.Chr8.786	R/P	KY.Chr8.786.v1.ND1-1	3.3	Q13618	CUL3 (cullin 3)
KY.Chr8.787	R/P	KY.Chr8.787.v4.ND4-6	1.06E-93	Q4G0N4	NADK2 (NAD kinase 2 mitochondrial)
KY.Chr8.788	R/P	KY.Chr8.788.v1.ND1-1	4	Q96KN3	PKNOX2 (PBX/knotted 1 homeobox 2)
KY.Chr8.789	R/P	KY.Chr8.789.v1.ND1-1	1.8	Q96F81	DISP1 (dispatched RND transporter family member 1)
KY.Chr8.790	R/P	KY.Chr8.790.v1.SL2-1	3.45E-69	P16233	PNLIP (pancreatic lipase)
KY.Chr8.791	R/P	KY.Chr8.791.v1.ND1-1	3.35E-07	Q8N0U7	C1orf87 (chromosome 1 open reading frame 87)
KY.Chr8.792	R/P	KY.Chr8.792.v1.SL2-1	0	Q94889	KLHL18 (kelch like family member 18)
KY.Chr8.793	R/P	KY.Chr8.793.v1.nonSL5-1	1.14E-16	P14927	UQCRB (ubiquinol-cytochrome c reductase binding protein)
KY.Chr8.794	R/P	KY.Chr8.794.v1.nonSL1-1	0	Q92947	GCDH (glutaryl-CoA dehydrogenase)
KY.Chr8.795	R/P	KY.Chr8.795.v1.SL2-1	4.70E-11	Q9NNZ3	DNAJC4 (Dnal heat shock protein family (Hsp40) member C4)
KY.Chr8.796	R/P	KY.Chr8.796.v1.nonSL1-1	0.72	Q9Y4H2	IRS2 (insulin receptor substrate 2)
KY.Chr8.797	R/P	KY.Chr8.797.v6.nonSL9-1	0	P48729	CSNK1A1 (casein kinase 1 alpha 1)
KY.Chr8.798	R/P	KY.Chr8.798.v3.nonSL2-3	4.77E-80	Q9NYB5	SLCO1C1 (solute carrier organic anion transporter family member 1C1)
KY.Chr8.801	R/P	KY.Chr8.801.v2.nonSL9-5	2.72E-157	Q96D17	SNRNP40 (small nuclear ribonucleoprotein U5 subunit 40)
KY.Chr8.804	R/P	KY.Chr8.804.v3.nonSL6-3	4.67E-16	Q9BXS4	TMEM59 (transmembrane protein 59)
KY.Chr8.805	R/P	KY.Chr8.805.v1.ND1-1	0.1	Q7L9B9	EPPD1 (endonuclease/exonuclease/phosphatase family domain containing 1)
KY.Chr8.806	R/P	KY.Chr8.806.v1.nonSL2-1	1.04E-41	Q9BTX1	NDC1 (NDC1 transmembrane nucleoporin)
KY.Chr8.807	R/P	KY.Chr8.807.v1.ND1-1	2.4	P37231	PPARG (peroxisome proliferator activated receptor gamma)
KY.Chr8.808	R/P	KY.Chr8.808.v1.ND1-1	0.7	Q3KQZ1	SLC25A35 (solute carrier family 25 member 35)
KY.Chr8.809	R/P	KY.Chr8.809.v1.ND1-1	2.4	Q5TH14	VPS13D (vacuolar protein sorting 13 homolog D)
KY.Chr8.810	R/P	KY.Chr8.810.v1.ND1-1	2.25E-25	Q6QNK2	ADGRD1 (adhesion G protein-coupled receptor D1)
KY.Chr8.811	R/P	KY.Chr8.811.v1.ND1-1	0.35	Q8NEG5	ZSWIM2 (zinc finger SWIM-type containing 2)
KY.Chr8.812	R/P	KY.Chr8.812.v1.SL2-5	2.43E-155	Q01973	ROR1 (receptor tyrosine kinase like orphan receptor 1)
KY.Chr8.813	R/P	KY.Chr8.813.v1.ND1-1	1.4	Q5TAA0	TTC22 (tetratricopeptide repeat domain 22)
KY.Chr8.815	R/P	KY.Chr8.815.v6.SL6-2	1.78E-22	P17612	PRKACA (protein kinase cAMP-activated catalytic subunit alpha)
KY.Chr8.816	R/P	KY.Chr8.816.v4.ND4-3	1.37E-07	Q92673	SORL1 (sortilin related receptor 1)
KY.Chr8.817	R/P	KY.Chr8.817.v1.SL1-1	1.15E-48	Q8N7M0	TCTEX1D1 (Tctex1 domain containing 1)
KY.Chr8.818	R/P	KY.Chr8.818.v1.SL1-1	0.42	Q8ND82	BANK1 (B cell scaffold protein with ankyrin repeats 1)
KY.Chr8.819	R/P	KY.Chr8.819.v2.SL2-2	2.14E-14	O95402	MED26 (mediator complex subunit 26)
KY.Chr8.820	R/P				no significant match found
KY.Chr8.821	R/P	KY.Chr8.821.v1.ND1-1	0.11	Q9HDC5	JPH1 (junctophilin 1)
KY.Chr8.822	R/P	KY.Chr8.822.v1.ND1-1	1.3	Q0VDD8	DNAH14 (dynein axonemal heavy chain 14)
KY.Chr8.823	R/P	KY.Chr8.823.v1.ND1-1	1	P48643	CCT5 (chaperonin containing TCP1 subunit 5)
KY.Chr8.824	R/P				no significant match found
KY.Chr8.825	R/P	KY.Chr8.825.v1.ND1-1	0.19	Q4KMP7	TBC1D10B (TBC1 domain family member 10B)
KY.Chr8.826	R/P	KY.Chr8.826.v1.nonSL7-1	0.31	Q8IZD9	DOCK3 (dedicator of cytokinesis 3)
KY.Chr8.827	R/P	KY.Chr8.827.v3.SL1-3	0.004	Q5VTH9	WDR78 (WD repeat domain 78)
KY.Chr8.828	R/P	KY.Chr8.828.v2.SL2-2	6.20E-80	O60502	OGA (O-GlcNAcase)
KY.Chr8.829	R/P	KY.Chr8.829.v1.SL1-1	8.48E-27	Q96N64	PWWP2A (PWWP domain containing 2A)
KY.Chr8.830	R/P	KY.Chr8.830.v3.ND4-1	0	P49902	NT5C2 (5'-nucleotidase cytosolic II)
KY.Chr8.831	R/P	KY.Chr8.831.v1.ND1-1	0.42	Q9HBJ7	USP29 (ubiquitin specific peptidase 29)
KY.Chr8.832	R/P	KY.Chr8.832.v1.ND1-1	0.02	O14776	TCERG1 (transcription elongation regulator 1)
KY.Chr8.833	R/P	KY.Chr8.833.v2.ND4-8	9.42E-74	Q96CD2	PPCDC (phosphopantothenoylcysteine decarboxylase)
KY.Chr8.834	R/P	KY.Chr8.834.v1.SL1-1	2.74E-119	O95395	GCNT3 (glucosaminyl (N-acetyl) transferase 3 mucin type)
KY.Chr8.835	R/P	KY.Chr8.835.v1.SL1-1	0.15	Q3T8J9	GON4L (gon-4 like)
KY.Chr8.836	R/P	KY.Chr8.836.v2.SL3-1	0.48	P07911	UMOD (uromodulin)
KY.Chr8.837	R/P	KY.Chr8.837.v1.ND1-1	2.9	Q01484	ANK2 (ankyrin 2)
KY.Chr8.838	R/P	KY.Chr8.838.v2.SL1-2	2.25E-92	Q9UIL4	KIF25 (kinesin family member 25)
KY.Chr8.839	R/P	KY.Chr8.839.v3.SL3-1	1.96E-57	O60513	B4GALT4 (beta-1,4-galactosyltransferase 4)
KY.Chr8.840	R/P	KY.Chr8.840.v2.SL3-1	2.17E-103	Q96HU8	DIRAS2 (DIRAS family GTPase 2)
KY.Chr8.841	R/P	KY.Chr8.841.v1.ND1-1	0.2	P53814	SMTN (smoothelin)
KY.Chr8.842	R/P	KY.Chr8.842.v1.SL1-1	5.63E-13	O75443	TECTA (tectorin alpha)
KY.Chr9.407	P	KY.Chr9.407.v2.SL7-2	1.11E-64	Q9Y6D9	MAD1L1 (mitotic arrest deficient 1 like 1)
KY.Chr9.408	P	KY.Chr9.408.v1.nonSL9-1	5.33E-13	Q8IYW8	SPNS2 (sphingolipid transporter 2)
KY.Chr9.409	P	KY.Chr9.409.v1.nonSL4-2	3.02E-64	Q08379	GOLGA2 (golgin A2)
KY.Chr9.843	R/P	KY.Chr9.843.v3.nonSL8-8	1.00E-56	Q14684	RRP1B (ribosomal RNA processing 1B)
KY.Chr9.844	R/P	KY.Chr9.844.v1.ND1-1	1.85E-20	Q86WB7	UNC93A (unc-93 homolog A)
KY.Chr9.845	R/P	KY.Chr9.845.v1.SL1-1	0.84	Q6ZNG2	DBX2 (developing brain homeobox 2)
KY.Chr9.846	R/P	KY.Chr9.846.v1.nonSL1-1	0.23	Q96QU1	PCDH15 (protocadherin related 15)
KY.Chr9.847	R/P	KY.Chr9.847.v1.SL1-1	2	A4UGR9	XIRP2 (xin actin binding repeat containing 2)
KY.Chr9.848	R/P	KY.Chr9.848.v1.ND1-1	0.1	O00116	AGPS (alkylglycerone phosphate synthase)
KY.Chr9.849	R/P	KY.Chr9.849.v1.SL2-1	0.3	Q4KWH8	PLCH1 (phospholipase C eta 1)
KY.Chr9.850	R/P	KY.Chr9.850.v1.ND1-1	0.93	O96005	CLPTM1 (CLPTM1 regulator of GABA type A receptor forward trafficking)
KY.Chr9.851	R/P	KY.Chr9.851.v2.SL16-2	3.83E-17	Q13501	SQSTM1 (sequestosome 1)
KY.Chr9.852	R/P	KY.Chr9.852.v1.nonSL9-2	3.00E-22	Q13501	SQSTM1 (sequestosome 1)
KY.Chr9.853	R/P	KY.Chr9.853.v1.nonSL6-1	0.059	Q9UBG0	MRC2 (mannose receptor C type 2)
KY.Chr9.854	R/P	KY.Chr9.854.v2.ND2-2	0.006	Q9UBG0	MRC2 (mannose receptor C type 2)
KY.Chr9.855	R/P	KY.Chr9.855.v1.ND1-1	0.35	Q9UBG0	MRC2 (mannose receptor C type 2)
KY.Chr9.856	R/P	KY.Chr9.856.v2.ND2-2	6.95E-147	Q13233	MAP3K1 (mitogen-activated protein kinase kinase kinase 1)
KY.Chr9.858	R/P	KY.Chr9.858.v1.ND1-1	2.42E-19	Q8XWDX0	RFXP2 (relaxin family peptide receptor 2)

KY.Chr9.859	R/P	KY.Chr9.859.v1.ND1-1	2.25E-12	Q07954	LRP1 (LDL receptor related protein 1)
KY.Chr9.860	R/P	KY.Chr9.860.v1.nonSL9-1	3.48E-75	Q5JTD7	LRRC73 (leucine rich repeat containing 73)
KY.Chr9.861	R/P	KY.Chr9.861.v1.SL1-1	1.73E-163	P24821	TNC (tenascin C)
KY.Chr9.862	R/P	KY.Chr9.862.v1.ND1-1	6.03E-04	Q9NR30	DDX21 (DEXD-box helicase 21)
KY.Chr9.863	R/P	KY.Chr9.863.v1.ND1-1	0.009	P02751	FN1 (fibronectin 1)
KY.Chr9.864	R/P	KY.Chr9.864.v1.SL3-1	0	Q9NR30	DDX21 (DEXD-box helicase 21)
KY.Chr9.1061	R/P	KY.Chr9.1061.v2.SL3-1	5.63E-36	O00622	CCN1 (cellular communication network factor 1)
KY.Chr9.1062	R/P	KY.Chr9.1062.v1.ND1-1	0.45	Q9NS00	C1GALT1 (core 1 synthase glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1)
KY.Chr9.1063	R/P	KY.Chr9.1063.v1.ND1-1	1.2	Q81ZU2	WDR17 (WD repeat domain 17)
KY.Chr9.1064	R/P	KY.Chr9.1064.v2.nonSL3-2	1.39E-28	P29279	CCN2 (cellular communication network factor 2)
KY.Chr9.1065	R/P	KY.Chr9.1065.v1.ND1-1	2.1	Q14139	UBE4A (ubiquitination factor E4A)
KY.Chr9.1066	R/P	KY.Chr9.1066.v2.nonSL7-2	1.24E-36	Q9NWK9	ZNHIT6 (zinc finger HIT-type containing 6)
KY.Chr9.1067	R/P	KY.Chr9.1067.v2.SL4-1	9.68E-35	P48745	CCN3 (cellular communication network factor 3)
KY.Chr9.1068	R/P	KY.Chr9.1068.v1.ND1-1	1	Q81WK6	ADGRA3 (adhesion G protein-coupled receptor A3)
KY.Chr9.1069	R/P	KY.Chr9.1069.v1.ND1-1	0.25	Q9Y3A2	UTP11 (UTP11 small subunit processome component)
KY.Chr9.1070	R/P	KY.Chr9.1070.v1.ND1-2	0.046	Q8TEB1	DCAF11 (DDB1 and CUL4 associated factor 11)
KY.Chr9.1071	R/P	KY.Chr9.1071.v1.nonSL5-1	2.47E-43	P28845	HSD11B1 (hydroxysteroid 11-beta dehydrogenase 1)
KY.Chr9.1072	R/P	KY.Chr9.1072.v1.ND1-1	0.56	Q9NZP5	OR5AC2 (olfactory receptor family 5 subfamily AC member 2)
KY.Chr9.1073	R/P	KY.Chr9.1073.v1.nonSL7-1	7.03E-172	Q81UR7	ARMC8 (armadillo repeat containing 8)
KY.Chr9.1074	R/P	KY.Chr9.1074.v1.nonSL3-1	0	O60341	KDM1A (lysine demethylase 1A)
KY.Chr9.1075	R/P	KY.Chr9.1075.v1.ND1-1	1.3	Q99884	SLC6A7 (solute carrier family 6 member 7)
KY.Chr9.1076	R/P	KY.Chr9.1076.v2.nonSL4-4	2.91E-36	Q16819	MEP1A (meprin A subunit alpha)
KY.Chr9.1077	R/P	KY.Chr9.1077.v1.ND1-3	0.003	Q9XB69	CARD6 (caspase recruitment domain family member 6)
KY.Chr9.1078	R/P	KY.Chr9.1078.v3.nonSL7-1	0.003	Q9NVA4	TMEM184C (transmembrane protein 184C)
KY.Chr9.1079	R/P	KY.Chr9.1079.v1.ND1-1	4.92E-12	Q86UW1	SLC51A (solute carrier family 51 alpha subunit)
KY.Chr9.1080	R/P	KY.Chr9.1080.v1.SL1-1	2.73E-92	Q8NSZ0	AADAT (aminoadipate aminotransferase)
KY.Chr9.1081	R/P	KY.Chr9.1081.v1.ND1-1	1.92E-78	Q8NSZ0	AADAT (aminoadipate aminotransferase)
KY.Chr9.1082	R/P	KY.Chr9.1082.v1.ND1-1	2.89E-40	Q7L985	LINGO2 (leucine rich repeat and Ig domain containing 2)
KY.Chr9.1083	R/P	KY.Chr9.1083.v1.SL1-1	2.81E-87	Q76083	PDE9A (phosphodiesterase 9A)
KY.Chr9.1084	R/P	KY.Chr9.1084.v2.nonSL3-2	3.69E-27	Q5TZF3	ANKRD45 (ankyrin repeat domain 45)
KY.Chr9.1085	R/P	KY.Chr9.1085.v1.ND1-1	8.95E-28	Q6HA08	ASTL (astacin like metalloendopeptidase)
KY.Chr9.1086	R/P	KY.Chr9.1086.v1.nonSL6-1	5.4	Q13360	ZNF177 (zinc finger protein 177)
KY.Chr9.1087	R/P	KY.Chr9.1087.v1.SL2-1	3.98E-08	Q75445	USH2A (usherin)
KY.Chr9.1089	R/P	KY.Chr9.1089.v5.ND3-4	1.51E-04	Q75445	USH2A (usherin)
KY.Chr9.1090	R/P	KY.Chr9.1090.v1.nonSL1-1	6.07E-04	Q75445	USH2A (usherin)
KY.Chr9.1091	R/P	KY.Chr9.1091.v1.ND1-1	0.006	Q96NN9	AIFM3 (apoptosis inducing factor mitochondria associated 3)
KY.Chr9.1092	R/P	KY.Chr9.1092.v1.ND1-1	0	Q9Y2E4	DIP2C (disco interacting protein 2 homolog C)
KY.Chr9.1093	R/P	KY.Chr9.1093.v1.nonSL2-1	3.66E-107	Q9Y221	NIP7 (nuclear pre-rRNA processing protein NIP7)
KY.Chr9.1094	R/P	KY.Chr9.1094.v1.SL2-1	3.48E-29	A6NGC4	TLCD2 (TLC domain containing 2)
KY.Chr9.1095	R/P	KY.Chr9.1095.v2.nonSL3-1	4.65E-114	N8E827	NME8 (NME/NM23 family member 8)
KY.Chr9.1096	R/P	KY.Chr9.1096.v2.SL2-1	4.69E-25	Q15398	DLGAP5 (DLG associated protein 5)
KY.Chr9.1097	R/P	KY.Chr9.1097.v1.SL1-1	3.12E-66	P37288	AVPR1A (arginine vasopressin receptor 1A)
KY.Chr9.1098	R/P	KY.Chr9.1098.v1.SL1-1	7.04E-10	Q8N8K9	KIAA1958 (KIAA1958)
KY.Chr9.1099	R/P	KY.Chr9.1099.v3.ND3-1	0.96	P35580	MYH10 (myosin heavy chain 10)
KY.Chr9.1100	R/P	KY.Chr9.1100.v1.SL1-1	1.35E-37	Q6ZWJ1	STXBP4 (syntaxin binding protein 4)
KY.Chr9.1101	R/P	KY.Chr9.1101.v1.nonSL7-1	0	Q5T2E6	ARMH3 (armadillo like helical domain containing 3)
KY.Chr9.1102	R/P	KY.Chr9.1102.v2.nonSL4-3	1.64E-92	A43824	GTPBP6 (GTP binding protein 6 (putative))
KY.Chr9.1103	R/P	KY.Chr9.1103.v2.SL2-1	0.84	Q8N6M8	IQCF1 (IQ motif containing F1)
KY.Chr9.1104	R/P	KY.Chr9.1104.v1.nonSL7-1	1.5	Q8WZ42	TTN (titin)
KY.Chr9.1105	R/P	KY.Chr9.1105.v2.ND1-2	0.86	Q96PZ7	CSMD1 (CUB and Sushi multiple domains 1)
KY.Chr9.1106	R/P	KY.Chr9.1106.v1.SL1-1	1.82E-50	P35408	PTGER4 (prostaglandin E receptor 4)
KY.Chr9.1107	R/P	KY.Chr9.1107.v1.nonSL3-1	2.70E-36	Q9BTV7	CABLES2 (Cdk5 and Abl enzyme substrate 2)
KY.Chr9.1108	R/P	KY.Chr9.1108.v1.SL2-1	6.58E-135	O95208	EPN2 (epsin 2)
KY.Chr9.1109	R/P	KY.Chr9.1109.v1.ND1-1	1.8	Q8NCG7	DAGLB (diacylglycerol lipase beta)
KY.Chr9.1110	R/P	KY.Chr9.1110.v1.nonSL1-1	3.09E-176	P53611	RABGGTB (Rab geranylgeranyltransferase subunit beta)
KY.Chr9.1111	R/P	KY.Chr9.1111.v1.nonSL8-1	4.85E-71	Q5VZ52	MORN5 (MORN repeat containing 5)
KY.Chr9.1112	R/P	KY.Chr9.1112.v1.nonSL1-1	5.48E-15	P51970	NDUFA8 (NADH:ubiquinone oxidoreductase subunit A8)
KY.Chr9.1113	R/P	KY.Chr9.1113.v1.nonSL1-1	4.75E-32	P51970	NDUFA8 (NADH:ubiquinone oxidoreductase subunit A8)
KY.Chr9.1114	R/P	KY.Chr9.1114.v1.ND1-1	0.006	Q9Y493	ZAN (zonadhesin (gene/pseudogene))
KY.Chr9.1115	R/P	KY.Chr9.1115.v1.ND1-1	2.83E-147	P05186	ALPL (alkaline phosphatase biomineralization associated)
KY.Chr9.1116	R/P	KY.Chr9.1116.v1.nonSL1-1	5.70E-72	Q96FB5	RRNAD1 (ribosomal RNA adenine dimethylase domain containing 1)
KY.Chr9.1117	R/P	KY.Chr9.1117.v1.ND1-2	1.27E-16	Q96FB5	RRNAD1 (ribosomal RNA adenine dimethylase domain containing 1)
KY.Chr9.1118	R/P	KY.Chr9.1118.v2.ND1-2	1.5	P51610	HCFC1 (host cell factor C1)
KY.Chr9.1119	R/P	KY.Chr9.1119.v1.nonSL1-1	0.047	Q81ZF4	ADGRG5 (adhesion G protein-coupled receptor G5)
KY.Chr9.1120	R/P	KY.Chr9.1120.v1.SL1-1	4.43E-107	O60318	MCM3AP (minichromosome maintenance complex component 3 associated protein)
KY.Chr9.1121	R/P	KY.Chr9.1121.v1.ND1-1	6.97E-98	Q9UG56	PISD (phosphatidylserine decarboxylase)
KY.Chr9.1122	R/P	KY.Chr9.1122.v1.nonSL3-1	9.24E-10	Q96Q35	FLACC1 (flagellum associated containing coiled-coil domains 1)
KY.Chr9.1123	R/P	KY.Chr9.1123.v1.SL1-1	0	Q8WWZ7	ABCA5 (ATP binding cassette subfamily A member 5)
KY.Chr9.1124	R/P	KY.Chr9.1124.v2.SL3-3	5.87E-137	Q02040	AKAP17A (A-kinase anchoring protein 17A)
KY.Chr9.1126	R/P	KY.Chr9.1126.v1.SL1-1	3.93E-145	Q96J16	GMPPA (GDP-mannose pyrophosphorylase A)
KY.Chr9.1127	R/P	KY.Chr9.1127.v5.ND6-1	0	Q8WZ42	TTN (titin)
KY.Chr10.148	P	KY.Chr10.148.v1.SL1-1	2.44E-06	Q8N6G6	ADAMTSL1 (ADAMTS like 1)
KY.Chr10.149	P	KY.Chr10.149.v2.ND2-2	2.50E-14	Q9NYQ7	CELSR3 (cadherin EGF LAG seven-pass G-type receptor 3)
KY.Chr10.150	P	KY.Chr10.150.v2.SL1-1	1.48E-101	P23469	PTPRE (protein tyrosine phosphatase receptor type E)
KY.Chr10.1133	R/P	KY.Chr10.1133.v1.SL2-1	0	Q08211	DHX9 (DEXH-box helicase 9)
KY.Chr10.1134	R/P	KY.Chr10.1134.v1.SL2-1	4.80E-121	Q96RS6	NUDCD1 (NudC domain containing 1)
KY.Chr10.1135	R/P	KY.Chr10.1135.v2.SL2-2	0	P54198	HIRA (histone cell cycle regulator)
KY.Chr10.1136	R/P	KY.Chr10.1136.v1.ND1-1	3.18E-78	Q9HAE3	EFCAB1 (EF-hand calcium binding domain 1)
KY.Chr10.1137	R/P	KY.Chr10.1137.v1.nonSL5-1	0	Q9P2E3	ZNFX1 (zinc finger NFX1-type containing 1)
KY.Chr10.1138	R/P	KY.Chr10.1138.v1.SL1-1	4.55E-87	Q9H0C1	ZMYND12 (zinc finger MYND-type containing 12)
KY.Chr10.1139	R/P	KY.Chr10.1139.v1.nonSL7-9	2.81E-53	Q8TBF2	PRXL2B (peroxiredoxin like 2B)
KY.Chr10.1140	R/P	KY.Chr10.1140.v1.nonSL8-1	6.80E-79	Q81YD2	KLHDC8A (kelch domain containing 8A)
KY.Chr10.1141	R/P	KY.Chr10.1141.v1.ND1-1	1.7	Q7Z429	GRINA (glutamate ionotropic receptor NMDA type subunit associated protein 1)
KY.Chr10.1142	R/P	KY.Chr10.1142.v1.ND1-1	6.69E-26	Q86WB7	UNC93A (unc-93 homolog A)
KY.Chr10.1143	R/P	KY.Chr10.1143.v2.nonSL2-2	1.68E-43	Q9Y617	PSAT1 (phosphoserine aminotransferase 1)
KY.Chr10.1144	R/P	KY.Chr10.1144.v1.ND1-2	0.77	Q8WZ92	OR5P2 (olfactory receptor family 5 subfamily P member 2)
KY.Chr10.1145	R/P	KY.Chr10.1145.v1.nonSL3-1	1.11E-58	Q9U114	RABAC1 (Rab acceptor 1)
KY.Chr10.1146	R/P	KY.Chr10.1146.v1.nonSL9-1	1.29E-74	Q8TF42	UBASH3B (ubiquitin associated and SH3 domain containing B)
KY.Chr10.1147	R/P	KY.Chr10.1147.v1.nonSL2-1	0	P38919	EIF4A3 (eukaryotic translation initiation factor 4A3)
KY.Chr10.1148	R/P	KY.Chr10.1148.v2.SL6-1	0	Q5TD94	RSPH4A (radial spoke head component 4A)
KY.Chr10.1149	R/P	KY.Chr10.1149.v1.nonSL9-1	4.97E-91	Q9Y5A7	NUB1 (negative regulator of ubiquitin like proteins 1)
KY.Chr11.532	R/P	KY.Chr11.532.v3.ND1-1	3.30E-103	Q16659	MAPK6 (mitogen-activated protein kinase 6)
KY.Chr11.533	R/P	KY.Chr11.533.v1.ND1-1	4.5	Q5TC58	AK9 (adenylate kinase 9)
KY.Chr11.534	R/P	KY.Chr11.534.v1.ND1-1	0.004	Q9BQ14	CCDC3 (coiled-coil domain containing 3)
KY.Chr11.535	R/P	KY.Chr11.535.v1.SL1-1	7.53E-06	Q9NPC4	A4GALT (alpha 1,4-galactosyltransferase (P blood group))
KY.Chr11.536	R/P	KY.Chr11.536.v1.ND1-1	1.9	P20929	NEB (nebulin)
KY.Chr11.537	R/P	KY.Chr11.537.v1.SL2-1	6.80E-12	Q5JXM2	METTL24 (methyltransferase like 24)
KY.Chr11.572	R/P	KY.Chr11.572.v3.ND1-4	0	O14983	ATP2A1 (ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 1)
KY.Chr11.573	R/P	KY.Chr11.573.v1.ND1-1	8.01E-17	Q9C300	GSTT2B (glutathione S-transferase theta 2B (gene/pseudogene))
KY.Chr11.574	R/P	KY.Chr11.574.v1.ND1-1	7.31E-17	P0CG30	GSTT2B (glutathione S-transferase theta 2B (gene/pseudogene))
KY.Chr11.1268	R/P	KY.Chr11.1268.v1.SL1-2	3.98E-77	Q95406	CNIH1 (cornichon family AMPA receptor auxiliary protein 1)
KY.Chr11.1269	R/P	KY.Chr11.1269.v1.SL1-1	8.39E-14	Q6QNK2	ADGRD1 (adhesion G protein-coupled receptor D1)
KY.Chr11.1270	R/P	KY.Chr11.1270.v1.SL1-1	1.74E-47	P36639	NUDT1 (nudix hydrolase 1)
KY.Chr11.1271	R/P	KY.Chr11.1271.v4.nonSL3-2	4.09E-07	Q9Y2E6	DTX4 (deltex E3 ubiquitin ligase 4)
KY.Chr11.1272	R/P	KY.Chr11.1272.v2.SL2-2	0	P56192	MARS (methionyl-tRNA synthetase)
KY.Chr11.1273	R/P	KY.Chr11.1273.v7.ND1-2	1.99E-153	P05388	RPLP0 (ribosomal protein lateral stalk subunit P0)
KY.Chr11.1274	R/P	KY.Chr11.1274.v2.ND1-3	0.76	Q8NSZ0	AADAT (aminoadipate aminotransferase)
KY.Chr11.1275	R/P	KY.Chr11.1275.v3.ND6-1	1.20E-04	Q15700	DLG2 (discs large MAGUK scaffold protein 2)
KY.Chr11.1276	R/P	KY.Chr11.1276.v1.SL1-1	2.99E-31	P0C024	NUDT7 (nudix hydrolase 7)
KY.Chr11.1277	R/P	KY.Chr11.1277.v1.nonSL9-1	3.89E-119	P15259	PGAM2 (phosphoglycerate mutase 2)
KY.Chr11.1278	R/P	KY.Chr11.1278.v2.nonSL2-1	0.92	P51449	RORC (RAR related orphan receptor C)
KY.Chr11.1279	R/P	KY.Chr11.1279.v1.nonSL9-1	1.49E-32	P20674	COX5A (cytochrome c oxidase subunit 5A)
KY.Chr11.1280	R/P	KY.Chr11.1280.v1.SL1-1	0.71	Q86X12	NCAPG2 (non-SMC condensin II complex subunit G2)
KY.Chr11.1281	R/P	KY.Chr11.1281.v1.SL1-1	1.45E-41	Q9Y2Y6	TMEM98 (transmembrane protein 98)
KY.Chr11.1282	R/P	KY.Chr11.1282.v1.nonSL2-1	8.94E-12	Q8WWQ8	STAB2 (stabilin 2)
KY.Chr11.1283	R/P	KY.Chr11.1283.v1.SL4-1	3.86E-40	P17026	ZNF22 (zinc finger protein 22)
KY.Chr11.1284	R/P	KY.Chr11.1284.v1.ND1-1	3.46E-68	Q96PF2	TSSK2 (testis specific serine kinase 2)

KY.Chr11.1285	R/P	KY.Chr11.1285.v1.ND1-1	3.2	Q9P0L9	PKD2L1 (polycystin 2 like 1, transient receptor potential cation channel)
KY.Chr11.1291	R/P	KY.Chr11.1291.v2.SL4-2	0	P78504	JAG1 (jagged canonical Notch ligand 1)
KY.Chr11.1295	R/P	KY.Chr11.1295.v1.ND1-1	0.39	Q9NQ90	ANO2 (anoctamin 2)
KY.Chr12.338	R/P	KY.Chr12.338.v1.ND1-1	1.6	Q9NXL6	SIDT1 (SID1 transmembrane family member 1)
KY.Chr12.339	R/P	KY.Chr12.339.v4.ND3-3	1.79E-124	A6NHR9	SMCHD1 (structural maintenance of chromosomes flexible hinge domain containing 1)
KY.Chr12.340	R/P	KY.Chr12.340.v1.nonSL1-1	0.56	Q7Z698	SPRED2 (sprouty related EVH1 domain containing 2)
KY.Chr12.341	R/P	KY.Chr12.341.v1.nonSL5-1	3.04E-83	Q9NRA2	SLC17A5 (solute carrier family 17 member 5)
KY.Chr12.342	R/P	KY.Chr12.342.v1.nonSL9-1	3.28E-11	P50895	BCAM (basal cell adhesion molecule (Lutheran blood group))
KY.Chr12.439	R	KY.Chr12.439.v1.ND1-1	2.28E-05	Q9BYE9	CDHR2 (cadherin related family member 2)
KY.Chr12.440	R	KY.Chr12.440.v1.ND1-1	1.06E-14	Q9C040	TRIM2 (tripartite motif containing 2)
KY.Chr12.441	R	KY.Chr12.441.v2.ND1-2	2.29E-09	Q9C040	TRIM2 (tripartite motif containing 2)
KY.Chr12.442	R	KY.Chr12.442.v1.ND1-2	7.25E-71	Q9BYE9	CDHR2 (cadherin related family member 2)
KY.Chr12.443	R	KY.Chr12.443.v2.SL2-1	1.56E-68	Q02548	PAX5 (paired box 5)
KY.Chr12.444	R	KY.Chr12.444.v1.SL1-1	8.2	Q8N110	DOCK4 (dedicator of cytokinesis 4)
KY.Chr12.445	R	KY.Chr12.445.v1.ND1-2	0.26	Q9BX66	SORBS1 (sorbin and SH3 domain containing 1)
KY.Chr12.446	R	KY.Chr12.446.v2.ND4-1	3.47E-178	P06493	CDK1 (cyclin dependent kinase 1)
KY.Chr12.447	R	KY.Chr12.447.v1.SL2-1	3.3	Q6P5W5	SLC39A4 (solute carrier family 39 member 4)
KY.Chr12.448	R	KY.Chr12.448.v1.SL2-1	9.10E-99	P62079	TSPAN5 (tetraspanin 5)
KY.Chr12.449	R	KY.Chr12.449.v2.nonSL9-1	1.42E-95	Q8IU8	RIOX2 (ribosomal oxygenase 2)
KY.Chr12.450	R	KY.Chr12.450.v2.nonSL9-7	2.76E-159	P08559	PDHA1 (pyruvate dehydrogenase E1 alpha 1 subunit)
KY.Chr12.451	R	KY.Chr12.451.v2.nonSL5-4	0	P17812	CTPS1 (CTP synthase 1)
KY.Chr12.452	R	KY.Chr12.452.v1.ND1-1	2.57E-14	P46109	CRKL (CRK like proto-oncogene adaptor protein)
KY.Chr12.453	R	KY.Chr12.453.v1.SL2-1	2.76E-37	P46109	CRKL (CRK like proto-oncogene adaptor protein)
KY.Chr12.454	R	KY.Chr12.454.v1.SL1-1	9.70E-103	P46109	CRKL (CRK like proto-oncogene adaptor protein)
KY.Chr12.455	R	KY.Chr12.455.v1.nonSL7-1	7.39E-143	Q6NUT3	MFSD12 (major facilitator superfamily domain containing 12)
KY.Chr12.456	R				no significant match found
KY.Chr12.457	R	KY.Chr12.457.v1.ND1-1	2.8	Q03721	KCNK4 (potassium voltage-gated channel subfamily C member 4)
KY.Chr12.458	R	KY.Chr12.458.v1.nonSL5-1	2.13E-160	P43353	ALDH3B1 (aldehyde dehydrogenase 3 family member B1)
KY.Chr12.459	R	KY.Chr12.459.v1.SL1-1	7.92E-85	Q9BXD5	NPL (N-acetylneuraminic pyruvate lyase)
KY.Chr12.460	R	KY.Chr12.460.v1.ND1-1	0.002	O75882	ATRN (atractin)
KY.Chr12.461	R	KY.Chr12.461.v1.ND1-1	1	P78329	CYP4F2 (cytochrome P450 family 4 subfamily F member 2)
KY.Chr12.465	R	KY.Chr12.465.v2.SL6-6	0	Q00610	CLTC (clathrin heavy chain)
KY.Chr12.466	R	KY.Chr12.466.v1.SL1-1	0	Q96QK1	VPS35 (VPS35 retromer complex component)
KY.Chr12.898	P	KY.Chr12.898.v1.ND1-1	1.8	P22897	MRC1 (mannose receptor C-type 1)
KY.Chr12.899	P	KY.Chr12.899.v1.nonSL9-1	0	O75439	PMPCB (peptidase mitochondrial processing beta subunit)
KY.Chr12.900	P	KY.Chr12.900.v2.ND2-1	2.05E-06	Q96PP4	TSGA13 (tissue specific 13)
KY.Chr12.901	P	KY.Chr12.901.v1.SL1-1	4.42E-17	P16112	ACAN (aggregran)
KY.Chr12.905	R	KY.Chr12.905.v1.nonSL4-1	1.10E-123	Q9H7B2	RPF2 (ribosome production factor 2 homolog)
KY.Chr12.906	R	KY.Chr12.906.v1.nonSL4-1	1.53E-72	Q3SXY8	ARL13B (ADP ribosylation factor like GTPase 13B)
KY.Chr12.907	R	KY.Chr12.907.v1.nonSL9-1	1.17E-25	P0C875	FAM228B (family with sequence similarity 228 member B)
KY.Chr12.908	R	KY.Chr12.908.v1.nonSL9-1	1.41E-28	Q8NHR9	PFN4 (profilin family member 4)
KY.Chr12.909	R	KY.Chr12.909.v1.SL1-1	5.39E-18	Q8N2Z9	CENPS (centromere protein S)
KY.Chr12.910	R	KY.Chr12.910.v1.nonSL8-1	2.1	Q15849	SLC14A2 (solute carrier family 14 member 2)
KY.Chr12.911	R	KY.Chr12.911.v2.nonSL2-1	2.26E-60	Q9UFN0	NIPSNAP3A (nipsnap homolog 3A)
KY.Chr12.912	R	KY.Chr12.912.v1.SL1-1	2.01E-115	Q12767	TMEM94 (transmembrane protein 94)
KY.Chr12.913	R	KY.Chr12.913.v1.SL1-1	4.25E-74	Q9NZJ6	COQ3 (coenzyme Q3 methyltransferase)
KY.Chr12.914	R	KY.Chr12.914.v1.nonSL1-1	4.46E-76	Q86YH6	PDSS2 (decaprenyl diphosphate synthase subunit 2)
KY.Chr12.915	R	KY.Chr12.915.v1.SL2-2	6.10E-42	Q9HBL7	PLGRKT (plasminogen receptor with a C-terminal lysine)
KY.Chr12.916	R	KY.Chr12.916.v1.SL1-1	3.00E-17	Q9BS16	CENPK (centromere protein K)
KY.Chr12.917	R	KY.Chr12.917.v1.ND1-3	4.82E-134	Q02094	RHAG (Rh associated glycoprotein)
KY.Chr12.918	R	KY.Chr12.918.v2.ND1-1	2.33E-08	Q9P2H0	CEP126 (centrosomal protein 126)
KY.Chr12.919	R	KY.Chr12.919.v2.SL2-2	1.70E-25	Q5TID7	CCDC181 (coiled-coil domain containing 181)
KY.Chr12.920	R	KY.Chr12.920.v2.SL3-2	6.16E-31	Q96EK9	KTI12 (KTI12 chromatin associated homolog)
KY.Chr12.921	R	KY.Chr12.921.v1.nonSL2-1	0.26	Q9BQG0	MYBBP1A (MYB binding protein 1a)
KY.Chr12.922	R	KY.Chr12.922.v1.SL1-1	0	P40692	MLH1 (mutL homolog 1)
KY.Chr12.923	R	KY.Chr12.923.v1.nonSL6-1	4.25E-101	Q96BW1	UPRT (uracil phosphoribosyltransferase homolog)
KY.Chr12.924	R	KY.Chr12.924.v2.nonSL6-2	8.21E-66	Q7Z7C8	TAF8 (TATA-box binding protein associated factor 8)
KY.Chr12.925	R	KY.Chr12.925.v1.nonSL2-1	0.088	O15047	SETD1A (SET domain containing 1A histone lysine methyltransferase)
KY.Chr12.926	R	KY.Chr12.926.v1.SL3-1	3.59E-16	Q6P197	C11orf88 (chromosome 11 open reading frame 88)
KY.Chr12.927	R	KY.Chr12.927.v1.SL1-1	4.41E-142	Q8IZN3	ZDHHC14 (zinc finger DHHC-type containing 14)
KY.Chr12.928	R	KY.Chr12.928.v1.ND1-1	0.4	Q9NUQ2	AGPAT5 (1-acylglycerol-3-phosphate O-acyltransferase 5)
KY.Chr12.929	R	KY.Chr12.929.v2.SL2-2	2.03E-100	Q96PU8	QKI (QKI KH domain containing RNA binding)
KY.Chr12.930	R	KY.Chr12.930.v1.SL1-1	4.2	Q92796	DLG3 (discs large MAGUK scaffold protein 3)
KY.Chr12.931	R	KY.Chr12.931.v1.SL2-1	2.72E-73	P98170	XIAP (X-linked inhibitor of apoptosis)
KY.Chr12.932	R	KY.Chr12.932.v1.ND1-1	1.48E-122	Q14832	GRM3 (glutamate metabotropic receptor 3)
KY.Chr12.933	R	KY.Chr12.933.v1.ND1-1	8.57E-13	Q9Y6W5	WASF2 (WASP family member 2)
KY.Chr12.934	R	KY.Chr12.934.v1.nonSL2-1	0.26	Q9H0B3	IQCN (IQ motif containing N)
KY.Chr12.935	R	KY.Chr12.935.v1.ND1-1	1.7	Q86YW0	PLCZ1 (phospholipase C zeta 1)
KY.Chr12.936	R	KY.Chr12.936.v1.ND1-1	7.18E-04	Q5S5E7	NHSL1 (NHS like 1)
KY.Chr12.937	R	KY.Chr12.937.v2.nonSL7-1	1.44E-25	P58658	EVA1C (eva-1 homolog C)
KY.Chr12.938	R	KY.Chr12.938.v1.SL1-1	2.06E-05	Q13591	SEMA5A (semaphorin 5A)
KY.Chr13.346	R/P	KY.Chr13.346.v3.ND6-4	0.57	A6H8M9	CDHR4 (cadherin related family member 4)
KY.Chr13.347	R/P	KY.Chr13.347.v1.SL2-1	2.54E-16	P43166	CA7 (carbonic anhydrase 7)
KY.Chr13.348	R/P	KY.Chr13.348.v1.ND1-1	6.07E-62	Q460N5	PARP14 (poly(ADP-ribose) polymerase family member 14)
KY.Chr13.349	R/P	KY.Chr13.349.v1.ND1-1	2.71E-40	Q460N5	PARP14 (poly(ADP-ribose) polymerase family member 14)
KY.Chr13.350	R/P	KY.Chr13.350.v1.ND1-1	7.18E-37	Q86SG7	LYG2 (lysozyme g2)
KY.Chr13.351	R/P	KY.Chr13.351.v1.nonSL1-1	5.57E-17	Q8N1E2	LYG1 (lysozyme g1)
KY.Chr13.352	R/P	KY.Chr13.352.v1.SL2-1	6.03E-04	P07996	THBS1 (thrombospondin 1)
KY.Chr13.353	R/P	KY.Chr13.353.v1.SL1-1	3.4	Q6UY14	ADAMTSL4 (ADAMTS like 4)
KY.Chr13.354	R/P	KY.Chr13.354.v1.ND1-1	6.5	Q96AY4	TTC28 (tetratricopeptide repeat domain 28)
KY.Chr13.355	R/P	KY.Chr13.355.v1.ND1-1	6.11E-04	P07996	THBS1 (thrombospondin 1)
KY.Chr13.356	R/P	KY.Chr13.356.v1.ND1-1	0.001	A2VEC9	SSPO (SCO-spondin)
KY.Chr13.357	R/P	KY.Chr13.357.v2.SL5-5	0	P49189	ALDH9A1 (aldehyde dehydrogenase 9 family member A1)
KY.Chr13.358	R/P	KY.Chr13.358.v2.SL6-4	0	Q92759	GTF2H4 (general transcription factor IIH subunit 4)
KY.Chr13.359	R/P	KY.Chr13.359.v1.SL1-1	5.80E-125	Q9Y483	MTF2 (metal response element binding transcription factor 2)
KY.Chr13.360	R/P	KY.Chr13.360.v1.SL1-1	1.43E-20	Q9GZU5	NYX (nyctalopin)
KY.Chr13.361	R/P	KY.Chr13.361.v1.ND1-1	1.44E-42	Q94811	TPPP (tubulin polymerization promoting protein)
KY.Chr13.362	R/P	KY.Chr13.362.v1.nonSL4-1	5.06E-161	Q92643	PIGK (phosphatidylinositol glycan anchor biosynthesis class K)
KY.Chr13.363	R/P	KY.Chr13.363.v1.ND1-1	1.81E-09	P07550	ADRB2 (adrenoreceptor beta 2)
KY.Chr13.364	R/P	KY.Chr13.364.v3.SL1-1	1.79E-128	Q6P1R4	DUS1L (dihydrouridine synthase 1 like)
KY.Chr13.365	R/P	KY.Chr13.365.v1.ND1-1	0.85	P48065	SLC6A12 (solute carrier family 6 member 12)
KY.Chr13.366	R/P	KY.Chr13.366.v1.nonSL6-1	2.7	Q7Z5P9	MUC19 (mucin 19, oligomeric)
KY.Chr13.367	R/P	KY.Chr13.367.v1.ND1-1	6.45E-09	Q7Z5P9	MUC19 (mucin 19, oligomeric)
KY.Chr13.368	R/P	KY.Chr13.368.v1.SL1-1	0	P16066	NPR1 (natriuretic peptide receptor 1)
KY.Chr13.369	R/P	KY.Chr13.369.v2.SL2-1	4.23E-86	P37198	NUP62 (nucleoporin 62)
KY.Chr13.370	R/P	KY.Chr13.370.v2.SL2-1	2.16E-171	P46059	SLC15A1 (solute carrier family 15 member 1)
KY.Chr13.371	R/P	KY.Chr13.371.v1.SL1-1	5.09E-172	P46059	SLC15A1 (solute carrier family 15 member 1)
KY.Chr14.437	R	KY.Chr14.437.v1.SL2-1	0	P00558	PGK1 (phosphoglycerate kinase 1)
KY.Chr14.438	R	KY.Chr14.438.v1.SL1-1	3.23E-68	Q86S22	TRAPP6B (trafficking protein particle complex 6B)
KY.Chr14.439	R	KY.Chr14.439.v1.ND1-1	8.31E-14	Q05707	COL14A1 (collagen type XIV alpha 1 chain)
KY.Chr14.440	R	KY.Chr14.440.v1.nonSL1-1	0	Q14191	WRN (Werner syndrome RecQ like helicase)
KY.Chr14.441	R	KY.Chr14.441.v1.SL1-1	2.29E-62	A0AVK6	E2F8 (E2F transcription factor 8)
KY.Chr14.442	R	KY.Chr14.442.v1.SL1-1	0	P53618	COPB1 (coatomer protein complex subunit beta 1)

*1 The HT inbred line (type A) has an inversion in chromosome 4, and therefore there are no inversions between chromosome 4 of wild type-A animals and those of specimen R or P.

Supplementary Table S5. Chromosomal inversions identified from genomic alignments

Chromo -somes	approx. genomic positions ^{*1}			approx. size of inversion s	Genes contained in inverted regions ^{*2}
	HT (type-A)	R	P		
1	4.66M	-	4.70M	99k	KY.Chr1.974 (hemicentin 1) KY.Chr1.975 (tubulin gamma complex associated protein 6) KY.Chr1.976 (transmembrane protein 68)
4	1.82M	-	2.27M	7k	KY.Chr4.352 (pannexin 2)
5	286k	390k	285k	5k	KY.Chr5.37 (Tetex1 domain containing 1) KY.Chr5.38 (RAN binding protein 3)
5	952k	1.11M	-	6k	KY.Chr5.123 (collagen type XIV alpha 1 chain)
9	1.88M	1.95M	1.90M	28k	KY.Chr9.269 (phosphofructokinase, muscle) KY.Chr9.269 (tectonic family member 3) KY.Chr9.270 (karyopherin subunit beta 1)
9	4.00M	4.33M	-	4k	KY.Chr9.544 (C-type lectin domain family 1 member B)
12	835k	1.02M	-	38k	KY.Chr12.130 (methyltransferase like 14)
13	1.15M	2.92M	-	3k	KY.Chr13.149 (tolloid like 2)

^{*1} Hyphens indicate that no inversion was observed in specimen R or P against the type-A genome.

^{*2} The best hit proteins in human proteome are shown in parentheses.

Supplementary Table S6. KY model identifiers for regulatory genes

Gene name	KY model identifier
<i>Admp</i>	KY.Chr2.773
<i>AHR</i>	KY.Chr12.869
<i>ALR-like</i>	KY.Chr6.695
<i>AP4</i>	KY.Chr14.930
<i>ARNT</i>	KY.Chr5.617
<i>Arx</i>	KY.Chr1.1318
<i>Ascl.a</i>	KY.Chr2.2314
<i>Ascl.b</i>	KY.Chr2.2022
<i>Ascl.c</i>	KY.Chr2.1484
<i>Atf2/7</i>	KY.Chr7.484
<i>Atf3</i>	KY.Chr10.1341
<i>Atf4/5</i>	KY.Chr3.264
<i>Atf6</i>	KY.Chr13.318
<i>Atonal</i>	KY.Chr8.248
<i>Bach</i>	KY.Chr6.369
<i>Baf57</i>	KY.Chr10.1118
<i>Barhl</i>	KY.Chr11.403
<i>Barx.a</i>	KY.Chr7.1127
<i>Barx.b</i>	KY.Chr5.30
<i>Barx.c</i>	KY.Chr4.1242
<i>Bhlha15</i>	KY.Chr3.1309
<i>bHLH-like1</i>	KY.Chr9.350
<i>Bhlhtun1</i>	KY.Chr7.1158
<i>Bhlhtun2</i>	KY.Chr4.1008
<i>Bhlhtun3</i>	KY.Chr10.1238
<i>Bhlhtun4</i>	KY.Chr4.1211
<i>Bmp2/4</i>	KY.Chr4.449
<i>Bmp3</i>	KY.Chr12.885
<i>Bmp5/6/7/8</i>	KY.Chr2.1328
<i>Bsx</i>	KY.Chr8.559
<i>Bziptun1</i>	KY.Chr13.44
<i>Bziptun2</i>	KY.Chr1.2593
<i>Bziptun3</i>	KY.Chr1.2594
<i>Bziptun4</i>	KY.Chr7.780
<i>Bziptun5</i>	KY.Chr2.2247
<i>capicua</i>	KY.Chr4.472

<i>Cdx</i>	KY.Chr14.625
<i>Cebpa</i>	KY.Chr3.744
<i>Cebpb/c/d/e</i>	KY.Chr3.743
<i>Chd</i>	KY.Chr6.371
<i>Creb1/Creml/Atf1</i>	KY.Chr1.2051
<i>Creb3/11/14</i>	KY.Chr10.829
<i>Creb3l1</i>	KY.Chr2.2188
<i>Dand</i>	KY.Chr10.1375
<i>Dbx</i>	KY.Chr3.681
<i>Dlk</i>	KY.Chr11.146
<i>Dll</i>	KY.Chr14.1158
<i>Dlx.a</i>	KY.Chr7.358
<i>Dlx.b</i>	KY.Chr7.359
<i>Dlx.c</i>	KY.Chr7.738
<i>Dmbx</i>	KY.Chr1.2439
<i>Dmrt.a</i>	KY.Chr5.698
<i>Dmrt.b</i>	KY.Chr8.251
<i>Ebf</i>	KY.Chr1.724
<i>Efna.a</i>	KY.Chr3.887
<i>Efna.b</i>	KY.Chr3.888
<i>Efna.c</i>	KY.Chr3.891
<i>Efna.d</i>	KY.Chr3.893
<i>Efna.e</i>	KY.Chr3.889
<i>Efna.f</i>	KY.Chr3.890
<i>Efnb</i>	KY.Chr1.563
<i>Elf</i>	KY.Chr14.539
<i>Elf3/Ehf</i>	KY.Chr4.609
<i>Elk</i>	KY.Chr8.613
<i>Emx</i>	KY.Chr8.1337
<i>En</i>	KY.Chr7.532
<i>Erf.a</i>	KY.Chr4.415
<i>Erf.b</i>	KY.Chr4.757
<i>Esrr</i>	KY.Chr11.439
<i>Ets1/2.a</i>	KY.Chr11.1070
<i>Ets1/2.b</i>	KY.Chr10.606
<i>Etv</i>	KY.Chr1.1124
<i>Evx.a</i>	KY.Chr1.2037
<i>Fgf11/12/13/14</i>	KY.Chr1.1
<i>Fgf3/7/10/22</i>	KY.Chr11.1355

<i>Fgf4/5/6</i>	KY.UAContig4.60
<i>Fgf8/17/18</i>	KY.Chr5.496
<i>Fgf9/16/20</i>	KY.Chr2.1217
<i>Fgftun1</i>	KY.Chr14.235
<i>Fgftun2</i>	KY.Chr1.1891
<i>Figla-r</i>	KY.Chr2.2108
<i>Fli1/Erg.a</i>	KY.Chr4.259
<i>Fli1/Erg.b</i>	KY.Chr10.1095
<i>Fli1/Erg.c</i>	KY.Chr10.1096
<i>Fli1/Erg.d</i>	KY.Chr4.801
<i>Fos</i>	KY.Chr11.1133
<i>Foxa.a</i>	KY.Chr11.1167
<i>Foxa.b</i>	KY.Chr11.406
<i>Foxb</i>	KY.Chr4.915
<i>Foxc</i>	KY.Chr12.156
<i>Foxd.a</i>	KY.Chr8.661
<i>Foxd.b</i>	KY.Chr8.660
<i>Foxe</i>	KY.Chr5.63
<i>Foxf</i>	KY.Chr3.1005
<i>Foxg</i>	KY.Chr8.702
<i>Foxh.a</i>	KY.Chr9.672
<i>Foxh.b</i>	KY.Chr14.65
<i>Foxi.a</i>	KY.Chr8.901
<i>Foxi.b</i>	KY.Chr8.900
<i>Foxi.c</i>	KY.Chr8.896
<i>Foxj2</i>	KY.Chr1.1301
<i>Foxk</i>	KY.Chr12.74
<i>Foxl2</i>	KY.Chr1.2069
<i>Foxm</i>	KY.Chr4.979
<i>Foxn1/4.b</i>	KY.Chr6.670
<i>Foxn2/3</i>	KY.Chr3.371
<i>Foxo</i>	KY.Chr6.627
<i>Foxp</i>	KY.Chr7.474
<i>Foxq</i>	KY.Chr3.324
<i>Foxtun1</i>	KY.Chr14.637
<i>Foxtun2</i>	KY.Chr14.1201
<i>Foxtun3</i>	KY.Chr10.939
<i>Foxtun4</i>	KY.Chr5.382
<i>Foxtun5</i>	KY.Chr12.963

<i>Gabpa</i>	KY.Chr2.1145
<i>Gata.a</i>	KY.Chr6.625
<i>Gata.b</i>	KY.Chr4.1344
<i>Gdf1/3-r</i>	KY.Chr4.450
<i>Gsc</i>	KY.Chr4.686
<i>Gsx</i>	KY.Chr2.1386
<i>Hand</i>	KY.Chr14.359
<i>Hand-r</i>	KY.Chr1.2070
<i>Hedgehog1</i>	KY.Chr8.497
<i>Hedgehog2</i>	KY.Chr5.635
<i>Hes.a</i>	KY.Chr1.28
<i>Hes.b</i>	KY.Chr3.580
<i>Hes.c</i>	KY.Chr1.1234
<i>Hey</i>	KY.Chr10.1431
<i>Hhex</i>	KY.Chr1.1187
<i>Hif</i>	KY.Chr4.583
<i>Hlx</i>	KY.Chr11.1030
<i>Hmbox1-r</i>	KY.Chr1.858
<i>Hmg1/2</i>	KY.Chr14.924
<i>Hmg20</i>	KY.Chr1.127
<i>Hmgtun1</i>	KY.Chr12.809
<i>Hmgtun2</i>	KY.Chr5.1054
<i>Hmgxb4</i>	KY.Chr8.597
<i>Hmx</i>	KY.Chr8.1335
<i>Hnf1</i>	KY.Chr12.632
<i>Hnf4</i>	KY.Chr3.849
<i>Hox1</i>	KY.Chr1.1189
<i>Hox10</i>	KY.Chr1.2558
<i>Hox12</i>	KY.Chr7.704
<i>Hox13</i>	KY.Chr7.703
<i>Hox2</i>	KY.Chr1.2455
<i>Hox3</i>	KY.Chr1.2456
<i>Hox4</i>	KY.Chr1.2458
<i>Hox5</i>	KY.Chr1.2598
<i>Hox6</i>	KY.Chr1.2599
<i>Id.a</i>	KY.Chr7.1153
<i>Id.b</i>	KY.Chr7.1157
<i>Irx.a</i>	KY.Chr11.343
<i>Irx.b</i>	KY.Chr11.347

<i>Irx.c</i>	KY.Chr3.1404
<i>Irx.d</i>	KY.Chr3.1399
<i>Isl</i>	KY.Chr4.1318
<i>Jag</i>	KY.Chr11.1291
<i>Jun</i>	KY.Chr5.536
<i>Lefty</i>	KY.Chr3.1493
<i>Lhx1</i>	KY.Chr11.1327
<i>Lhx2/9</i>	KY.Chr9.235
<i>Lhx3/4</i>	KY.Chr13.449
<i>Lmx1</i>	KY.Chr9.589
<i>Lmx1-r</i>	KY.Chr9.594
<i>Mad</i>	KY.Chr1.761
<i>Maf/a/b</i>	KY.Chr12.532
<i>Maff/g/k</i>	KY.Chr12.534
<i>Max</i>	KY.Chr5.121
<i>Meis</i>	KY.Chr10.902
<i>Meox</i>	KY.Chr8.1018
<i>Mesp</i>	KY.Chr3.993
<i>Mitf</i>	KY.Chr10.837
<i>Mlx</i>	KY.Chr11.477
<i>Mnt-r</i>	KY.Chr6.608
<i>Mnx</i>	KY.Chr10.622
<i>Mrf</i>	KY.Chr14.1058
<i>Mstn</i>	KY.Chr3.534
<i>Msx</i>	KY.Chr2.1417
<i>Myc</i>	KY.Chr1.686
<i>Net</i>	KY.Chr9.174
<i>Neurog</i>	KY.Chr6.427
<i>Nfe2</i>	KY.Chr1.1136
<i>Nfil3</i>	KY.Chr5.623
<i>Nkx2-1/4</i>	KY.Chr10.964
<i>Nkx2-3/5/6</i>	KY.Chr8.909
<i>Nkx6</i>	KY.Chr5.29
<i>Nkxtun1</i>	KY.Chr12.93
<i>Nkxtun2</i>	KY.Chr8.969
<i>Nkxtun3</i>	KY.Chr1.212
<i>Nodal</i>	KY.Chr14.1181
<i>Nog</i>	KY.Chr12.723
<i>Noto</i>	KY.Chr5.1093

<i>Nr1d</i>	KY.Chr13.291
<i>Nr1h2/3</i>	KY.Chr2.1479
<i>Nr1h4</i>	KY.Chr2.1300
<i>Nr2c</i>	KY.Chr8.539
<i>Nr2e</i>	KY.Chr6.665
<i>Nr2f</i>	KY.Chr8.1390
<i>Nr4a</i>	KY.Chr9.646
<i>Nr5a</i>	KY.Chr6.223
<i>Nr6a</i>	KY.Chr1.1411
<i>Onecut</i>	KY.Chr6.222
<i>Otp</i>	KY.Chr14.946
<i>Otx</i>	KY.Chr4.867
<i>Pax1/9</i>	KY.Chr11.1306
<i>Pax2/5/8.a</i>	KY.Chr6.685
<i>Pax2/5/8.b</i>	KY.Chr12.443
<i>Pax3/7</i>	KY.Chr10.303
<i>Pax3/7-r</i>	KY.Chr4.548
<i>Pax6</i>	KY.Chr9.1034
<i>Pbx</i>	KY.Chr13.445
<i>Pdx</i>	KY.Chr14.916
<i>Phox2</i>	KY.Chr14.181
<i>Pinhead</i>	KY.Chr2.772
<i>Pitx</i>	KY.Chr6.170
<i>Pknox</i>	KY.Chr11.941
<i>polybromo</i>	KY.Chr7.473
<i>Pou2F</i>	KY.Chr4.359
<i>Pou4F</i>	KY.Chr2.851
<i>Pou-r</i>	KY.Chr7.486
<i>Ppar</i>	KY.Chr8.993
<i>Prdm1-r.a</i>	KY.Chr12.980
<i>Prdm1-r.b</i>	KY.Chr12.977
<i>Prdm1-r.c</i>	KY.Chr12.975
<i>Prdtun1</i>	KY.Chr11.115
<i>Prdtun2</i>	KY.Chr1.1582
<i>Prop</i>	KY.Chr11.1073
<i>Prox.a</i>	KY.Chr4.62
<i>Prox.b</i>	KY.Chr4.64
<i>Prrx</i>	KY.Chr1.525
<i>Ptfla</i>	KY.Chr3.526

<i>Ptfla-r</i>	KY.Chr11.543
<i>Rar</i>	KY.Chr9.692
<i>Rax</i>	KY.Chr12.292
<i>Ror</i>	KY.Chr3.206
<i>Rxr</i>	KY.Chr9.286
<i>Shox</i>	KY.Chr1.2618
<i>Sim</i>	KY.Chr6.618
<i>Six1/2</i>	KY.Chr3.556
<i>Six3/6</i>	KY.Chr10.279
<i>Six4/5</i>	KY.Chr3.1139
<i>Smad1/5/9</i>	KY.Chr2.1018
<i>Smad2/3.a</i>	KY.Chr6.515
<i>Smad2/3.b</i>	KY.Chr12.69
<i>Smad4</i>	KY.Chr6.342
<i>Smad6/7</i>	KY.Chr3.1211
<i>Snai</i>	KY.Chr3.1382
<i>Sox1/2/3</i>	KY.Chr1.559
<i>Sox14/15/21</i>	KY.Chr1.2243
<i>Sox30</i>	KY.Chr4.941
<i>Sox4/11/12</i>	KY.Chr7.659
<i>Sox5/6/13</i>	KY.Chr14.1160
<i>Sox7/17/18</i>	KY.Chr7.829
<i>Sox8/9/10</i>	KY.Chr11.676
<i>Spdef</i>	KY.Chr12.665
<i>Spi1/B/C</i>	KY.Chr6.534
<i>Srebp</i>	KY.Chr9.7
<i>Ssrp</i>	KY.Chr3.1078
<i>T</i>	KY.Chr12.6
<i>Tbx1/10</i>	KY.Chr7.563
<i>Tbx15/18/22</i>	KY.Chr9.115
<i>Tbx2/3</i>	KY.Chr4.1104
<i>Tbx20</i>	KY.Chr1.1392
<i>Tbx21/Tbr1/Eomes</i>	KY.Chr3.529
<i>Tbx6-r.a</i>	KY.Chr11.460
<i>Tbx6-r.b</i>	KY.Chr11.470
<i>Tbx6-r.c</i>	KY.Chr11.469
<i>Tbx6-r.d</i>	KY.Chr11.468
<i>Tcf15-r</i>	KY.Chr11.73
<i>Tcf3</i>	KY.Chr3.781

<i>Tcf4</i>	KY.Chr4.1160
<i>Tcf7</i>	KY.Chr6.60
<i>Tef/Hlf</i>	KY.Chr14.42
<i>Tfap2-r.a</i>	KY.Chr1.1901
<i>Tfap2-r.b</i>	KY.Chr7.1173
<i>Tgfb1/2/3</i>	KY.Chr3.1499
<i>Tgfbtun1</i>	KY.Chr5.606
<i>Tgfbtun2</i>	KY.Chr1.1371
<i>Tgfbtun3</i>	KY.Chr2.1400
<i>Thr</i>	KY.Chr11.1143
<i>Tlx</i>	KY.Chr1.1455
<i>Tox</i>	KY.Chr3.766
<i>Tp53/73.a</i>	KY.Chr1.1942
<i>Tp53/73.b</i>	KY.Chr3.226
<i>Trh</i>	KY.Chr11.674
<i>Twist-r.a</i>	KY.Chr5.356
<i>Twist-r.b</i>	KY.Chr5.355
<i>Twist-r.c</i>	KY.Chr5.357
<i>Ubf</i>	KY.Chr2.1521
<i>Unc.a</i>	KY.Chr5.106
<i>Unc.b</i>	KY.Chr11.892
<i>Usf</i>	KY.Chr3.1438
<i>Vdr.a</i>	KY.Chr2.1584
<i>Vdr.b</i>	KY.Chr10.739
<i>Vsx</i>	KY.Chr11.1126
<i>Wnt10</i>	KY.Chr13.110
<i>Wnt3</i>	KY.Chr9.955
<i>Wnt5</i>	KY.Chr4.1328
<i>Wnt7</i>	KY.Chr8.1185
<i>Wnt9</i>	KY.Chr9.610
<i>Wnttun1</i>	KY.Chr6.556
<i>Wnttun2</i>	KY.Chr12.713
<i>Wnttun3</i>	KY.Chr2.458
<i>Wnttun4</i>	KY.Chr5.350
<i>Wnttun5</i>	KY.Chr9.807
<i>Xbp1.a</i>	KY.Chr4.754
<i>Xbp1.b</i>	KY.Chr10.1174
<i>Xbp1.c</i>	KY.Chr8.629
<i>Xbp1.d</i>	KY.Chr8.1015

<i>Zfhx3</i>	KY.Chr3.191
<i>Zhx1-r</i>	KY.Chr3.15
<i>Zic-r.a</i>	KY.Chr1.1698
<i>Zic-r.b</i>	KY.Chr6.26
<i>Zic-r.c</i>	KY.Chr6.27
<i>Zic-r.d</i>	KY.Chr6.28
<i>Zic-r.e</i>	KY.Chr6.29
<i>Zic-r.f</i>	KY.Chr6.30
<i>Zic-r.g</i>	KY.Chr6.31

Supplementary Table S7. Primers used for experimental evaluation of inversions

Primer	Nucleotide sequence
primer1	5'-GGCTATGTGGAAGTTCAGTTGGACAT-3'
primer2	5'-TTCCTTTGTTGACCGAAACTGGTCAC-3'
primer3	5'-GGTCGATCATGGTGATACATTGGAAGT-3'
primer4	5'-GTTCCGTGTTATGCTTTCGGAATGCT-3'
primer5	5'-TTTGGCAAACAACGTACGATTCCAGAA-3'
primer6	5'-CCTTGTAATGTTTCATTGTGTTCTCCTA-3'
primer7	5'-TTGACCTGCCCGATCAAACATCTGAT-3'
primer8	5'-TTTACCGACAGTATATTTAGGCACAAGT-3'
primer9	5'-ATCATAGACCAGTACCTAGAAGGCTTT-3'
primer10	5'-AGTCATGGTACAAGGTGTATATGTGCT-3'
primer11	5'-TACTGCCATCTGACGGACGTTACCA-3'
primer12	5'-CACGCGACTTATTTAATACGAGGGAAA-3'