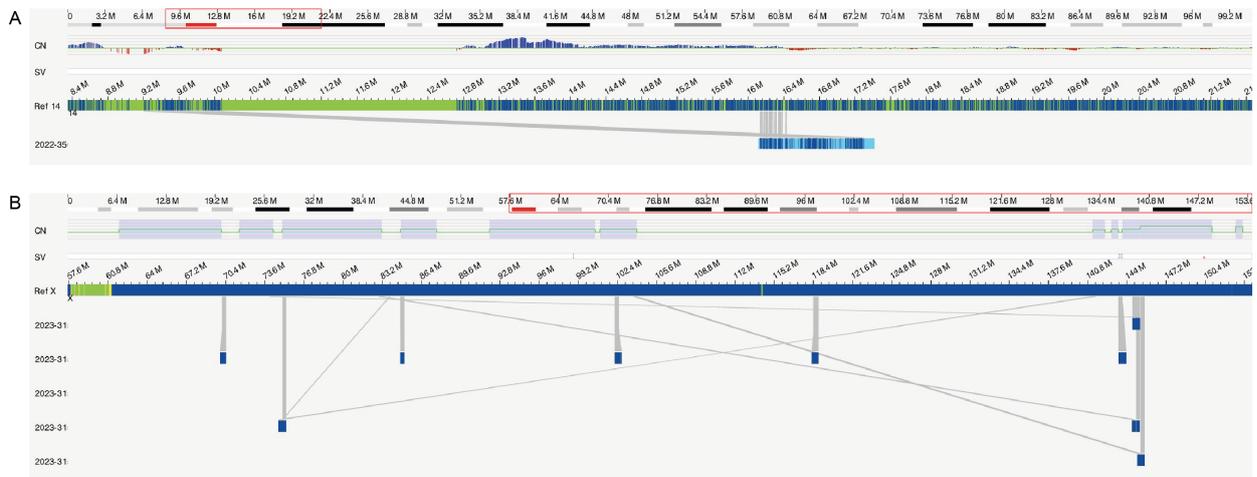
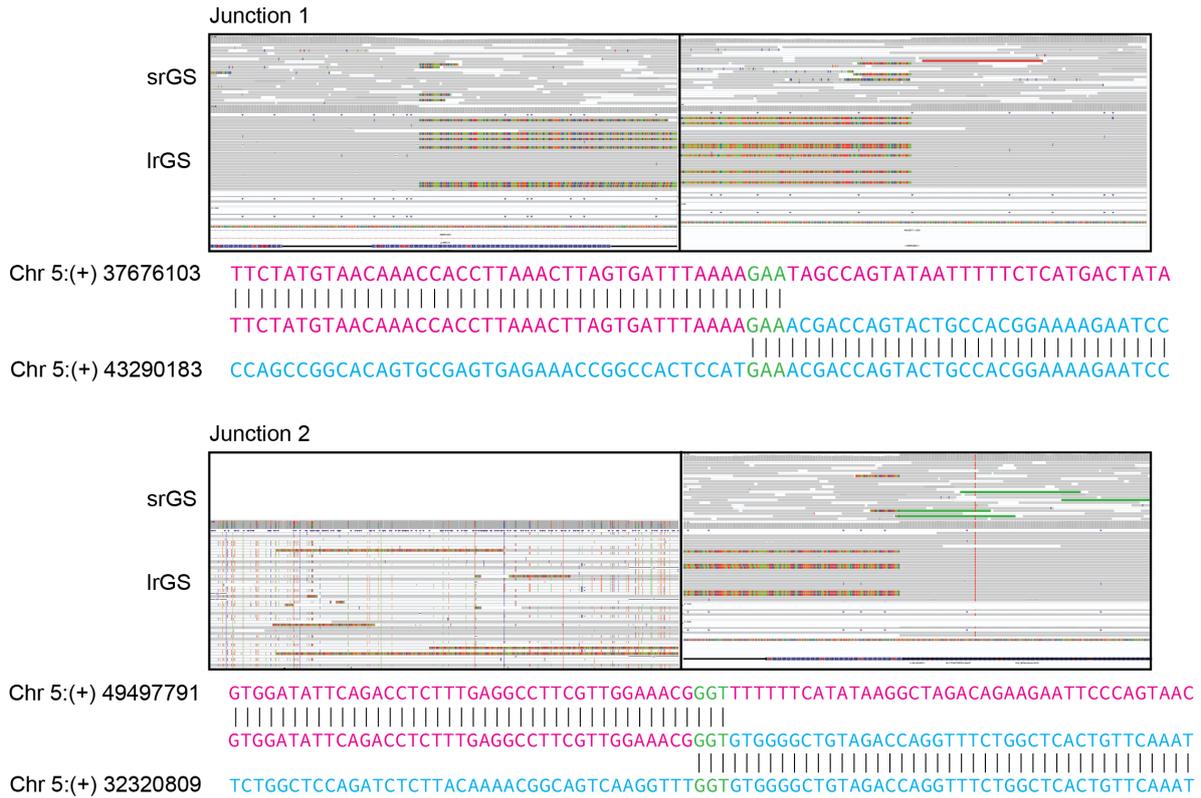


## Supplemental Material



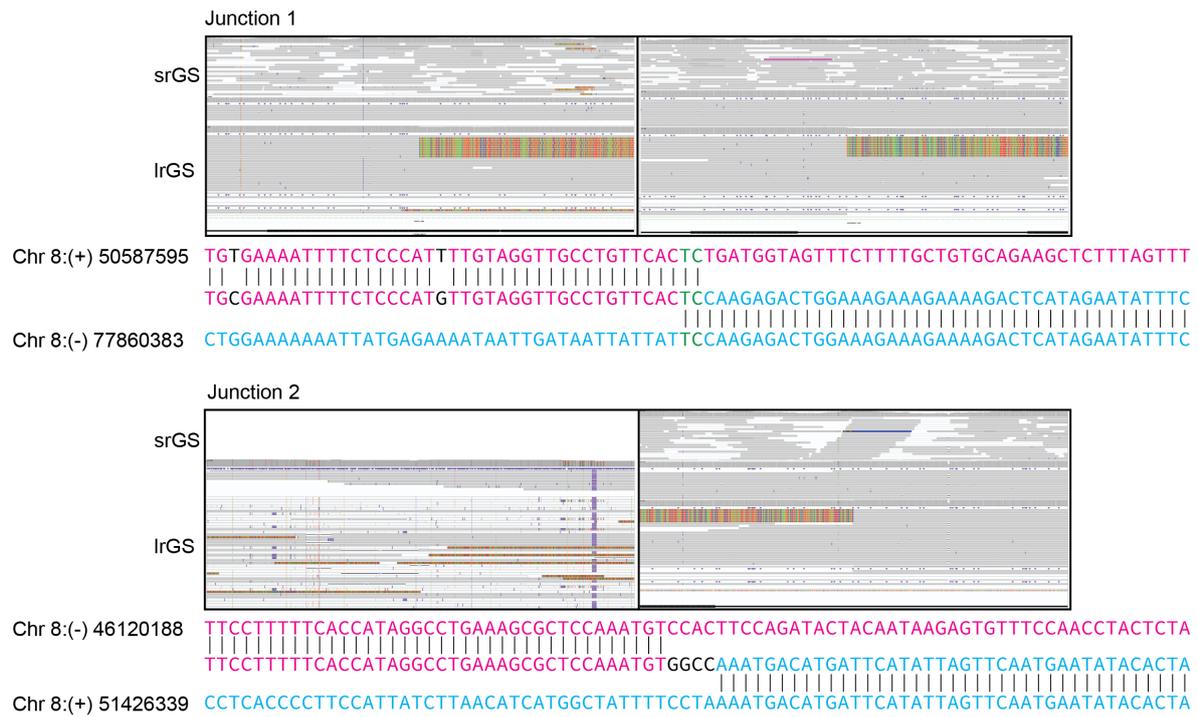
**Figure S1: Optical genome mapping of two small supernumerary marker chromosomes (sSMCs) A) r(14) carried by RD\_P550 and B) der(X) carried by RD\_P586.** On top, a schematic of the respective chromosomes are shown with a red frame around the zoomed in region. Below, a copy number track (CN) illustrates the gains across the chromosomes. At the bottom, a zoom in of the region from 8.4 Mbp to 21.6 Mbp for Chromosome 14 and 58 Mbp to 154 Mbp for chromosome X, respectively. Maps are shown in blue and grey lines indicate alignments to different parts of the chromosome according to genome build T2T-CHM13v2.0.



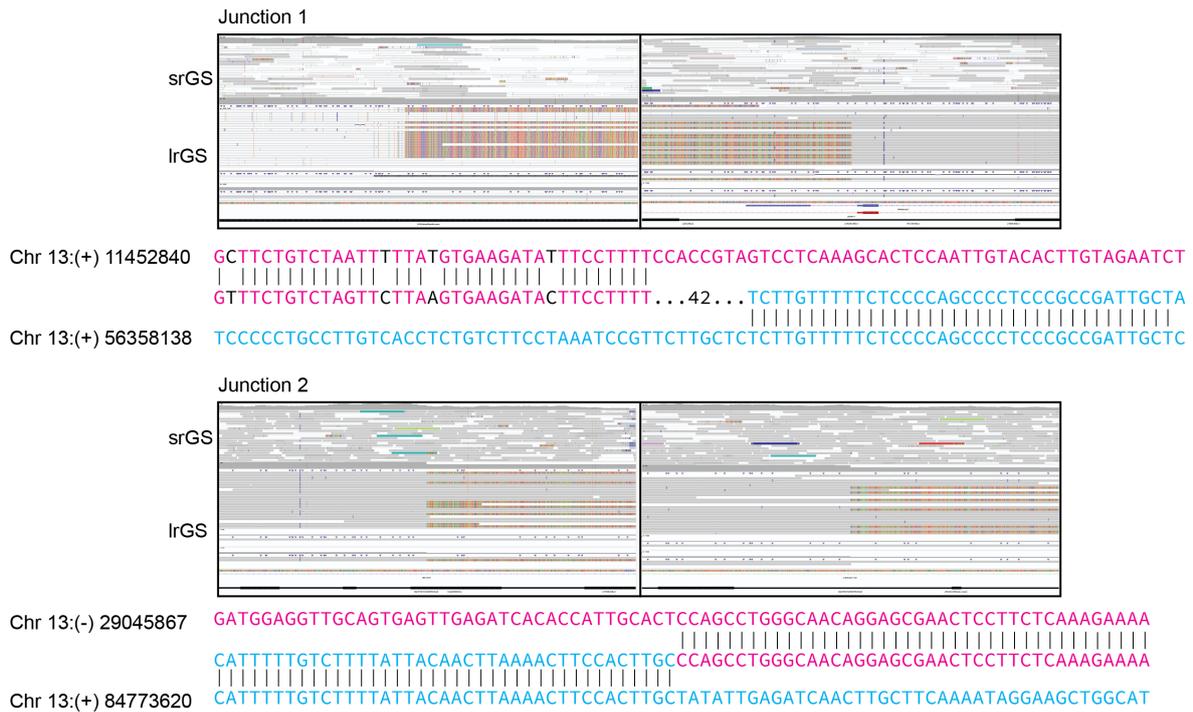
**Figure S2: Breakpoint junction sequences of r(5) (RD\_P276):** Integrative Genomics Viewer images of short read genome sequencing (srGS) and long read genome sequencing (lrGS) data for the two breakpoint junctions. Breakpoint sequences with the chimeric sequence in the center aligned to the reference sequences shown in pink and blue. Microhomology is indicated in green. Coordinates according to genome build T2T-CHM13v2.0.



**Figure S3: Breakpoint junction sequences of r(7) (RD\_P278):** Integrative Genomics Viewer images of short read genome sequencing (srGS) and long read genome sequencing (lrGS) data for the two breakpoint junctions. Breakpoint sequences with the chimeric sequence in the center aligned to the reference sequences shown in pink and blue. Microhomology is indicated in green. Coordinates according to genome build T2T-CHM13v2.0.

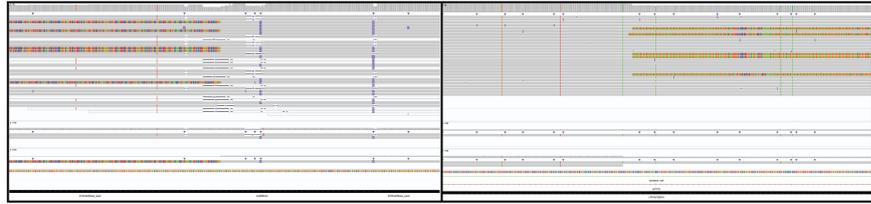


**Figure S4: Breakpoint junction sequences of r(8) (RD\_P273):** Integrative Genomics Viewer images of short read genome sequencing (srGS) and long read genome sequencing (lrGS) data for the two breakpoint junctions. Breakpoint sequences with the chimeric sequence in the center aligned to the reference sequences shown in pink and blue. Microhomology is indicated in green. Coordinates according to genome build T2T-CHM13v2.0.



**Figure S5: Breakpoint junction sequences of r(13) (RD\_P166):** Integrative Genomics Viewer images of short read genome sequencing (srGS) and long read genome sequencing (lrGS) data for the two breakpoint junctions. Breakpoint sequences with the chimeric sequence in the center aligned to the reference sequences shown in pink and blue. Microhomology is indicated in green. Coordinates according to genome build T2T-CHM13v2.0.

Junction 1

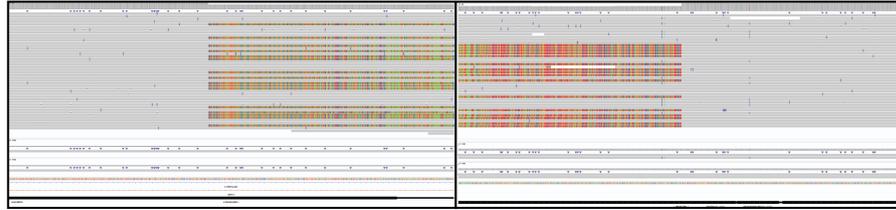


Chr 14:(+) 9208604 AATGGAATGGAATGGAATGGAATGGAATGGAAGGAAATG AATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG  
GCCACCATCTTGAAGTGGCCTGCCACCACTTTG . AAGTG AATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG  
Chr 14:(+) 16434843 GCCACCATCTTGAAGTGGCCTGCCGCACTTTGG AAGTG GCCCACCACCATCTTGGGAGCTCTAGAAGCAAGGACCCC

**Figure S6: Breakpoint junction sequences of r(14) (RD\_P550):** Integrative Genomics Viewer images of short read genome sequencing (srGS) and long read genome sequencing (lrGS) data for the two breakpoint junctions. Breakpoint sequences with the chimeric sequence in the center aligned to the reference sequences shown in pink and blue. Microhomology is indicated in green. Coordinates according to genome build T2T-CHM13v2.0.



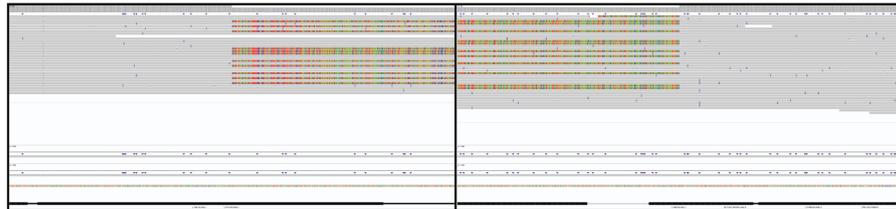
Junction 1



Chr X:(+) 103977823 TCTAGTTAGTAAAGCTGTTAGATTTTCTTACTCACCTTGTGTCCTCAAGATGATCACTTCCACTGACAACACGGTTGGGCATG  
 TCTAGTTAGTAAAGCTGTTAGATTTTCTTACTCACCTTGTGACTTCATCAGTACCAGACCTGTTGCACAGGTATTTATATA

Chr X:(+) 145148123 GACGGAGAAATAAAGACTTTCCAGAAAAACAAAAGCTGAGACTTCATCAGTACCAGACCTGTTGCACAGGTATTTATATA

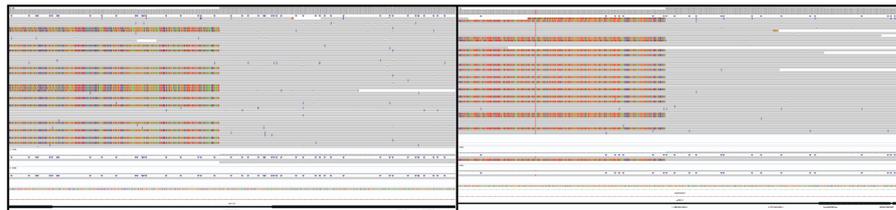
Junction 2



Chr X:(+) 89566572 CAATCAGAGAATAGGAAAGAAATATGTGATATATCAATACCATATATTACTATGCAGAAAAATGAAAATGTAGATACATA  
 CAATCAGAGAATAGGAAAGAAATATGTGATATATCAATACCTCACAGTTCTGGGGCTGGAAGTCCAAGATCAAGATGTCAG

Chr X:(+) 89651697 AAGACACGCTGTGTGGCTTCAACAATGGACATTTATTTTCTCACAGTTCTGGGGCTGGAAGTCCAAGATCAAGATGTCAG

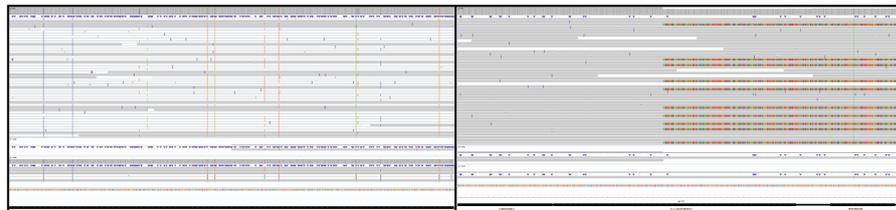
Junction 3



Chr X:(+) 66181028 TACCTTTTCCATATGCAGTGAAGCAGTACAAGTTAGTGCACTGGCTTTGACAGAGGTGGCATCAGCAGGGCCAGTGACAAT  
 TAGGACCTATTAACAAATAAAACCCCTTAAAGAATAATTTCCGCTTTGACAGAGGTGGCATCAGCAGGGCCAGTGACAAT

Chr X:(-) 84675390 TAGGACCTATTAACAAATAAAACCCCTTAAAGAATAATTTCCACATCTTAATGCAAAATAGTCAGTTATTAATAATGTATTA

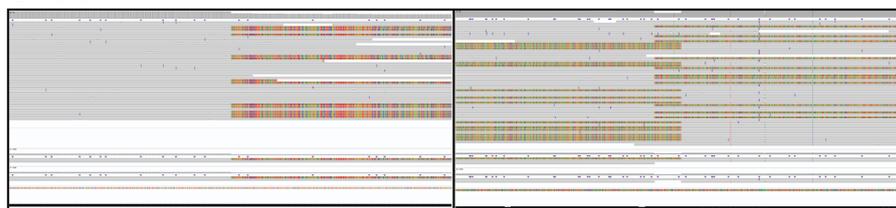
Junction 4



Chr X:(+) 58080098 AAGGCTTTTCAGGCCTTTTCCACCACAGGCCTGAAAGCGCTCCAAATGTCCACTTGCGATTCTGCCAAAAGAATATTTCAA  
 TCAACCCAGAATGTCTGATTACTCTCTACCTCTTTCACTCAAAATGTCCACTTGCGATTCTGCCAAAAGAATATTTCAA

Chr X:(+) 66184481 TCAACCCAGAATGTCTGATTACTCTCTACCTCTTTCACTTAGATTTCAACTAAAATCTCCAGGAGTTATCAAATC

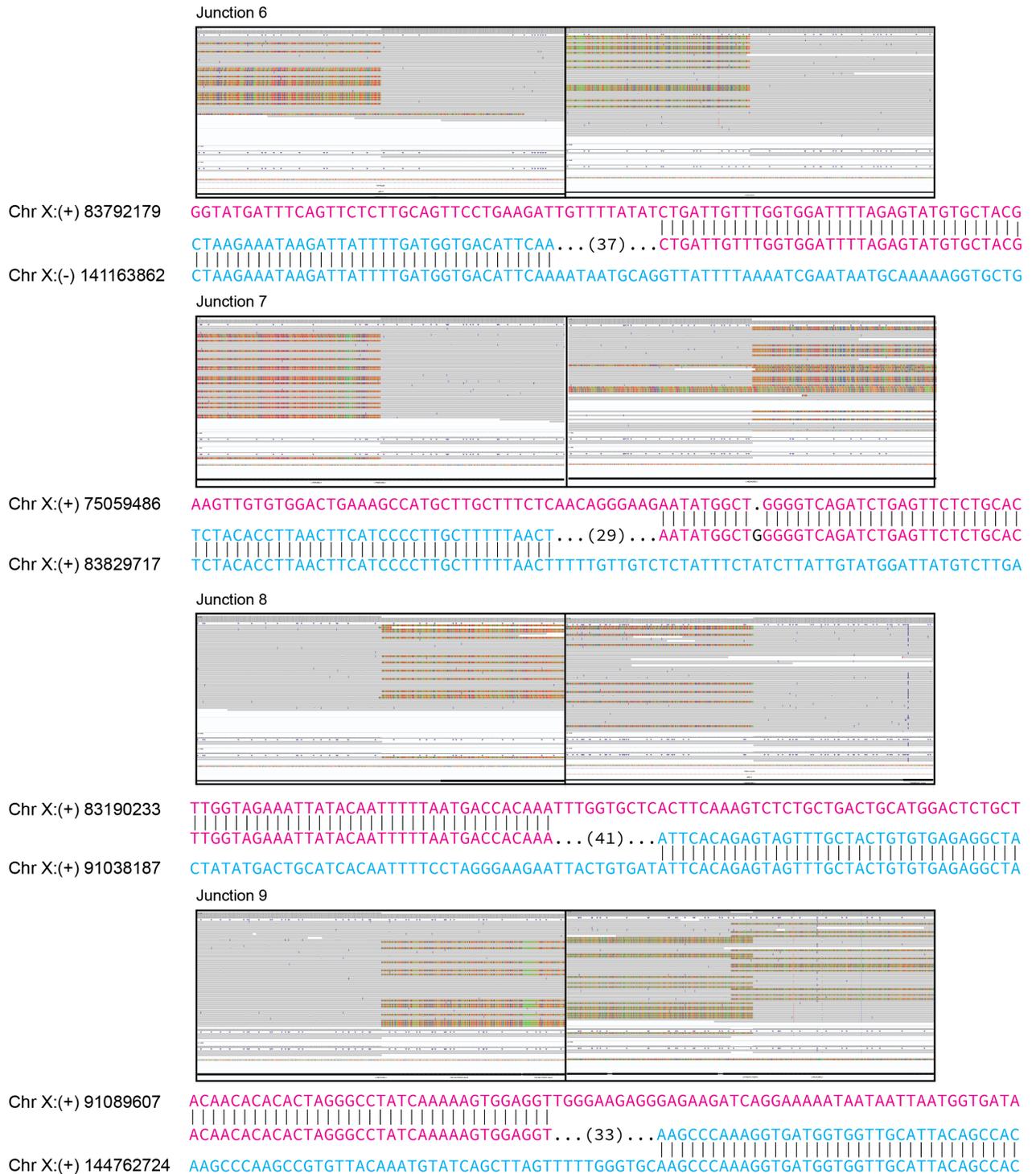
Junction 5



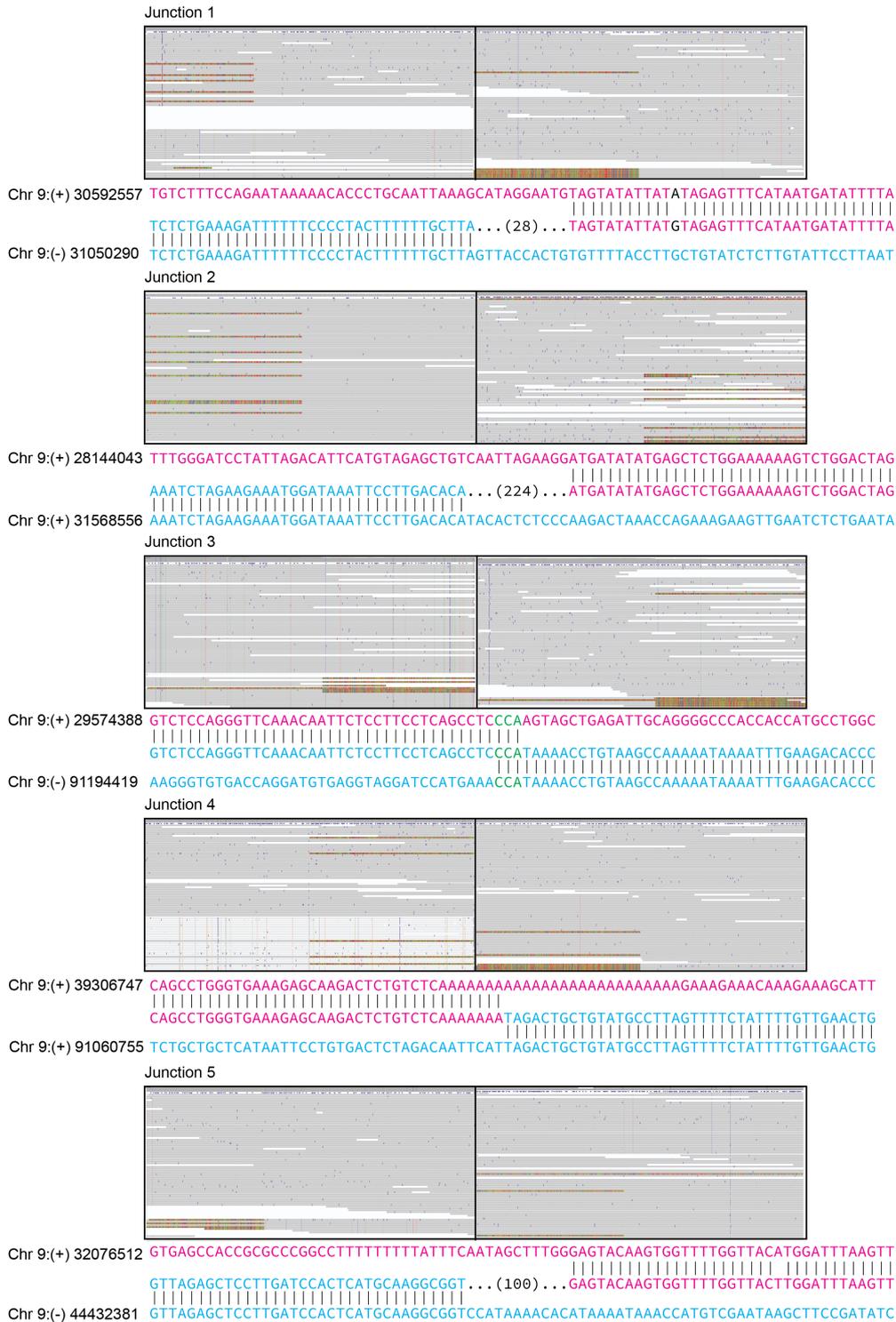
Chr X:(+) 74310915 CTGTGAAGAAAGTCAATGGTAGCTCAATGGGAATAGCATTGGATCTATAAATGCTTTGGGCAGTATGGCCATTTTCACAA  
 CTGTGAAGAAAGTCAATGGTAGCTCAATGGGAATAGCATTAACTATGACAGGTGGTGTGAGGGGCTGAGCTATCTGCTGA

Chr X:(-) 144762602 CATATGGCCATAGGTGTGCAATAAATGTGGAACCTGAAACAACATGACAGGTGGTGTGAGGGGCTGAGCTATCTGCTGA

Image continues on next page.

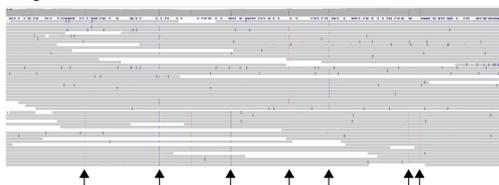


**Figure S8: Breakpoint junction sequences of der(X) (RD\_P586):** Integrative Genomics Viewer images of short read genome sequencing (srGS) and long read genome sequencing (lrGS) data for the two breakpoint junctions. Breakpoint sequences with the chimeric sequence in the center aligned to the reference sequences shown in pink and blue. Microhomology is indicated in green. Coordinates according to genome build T2T-CHM13v2.0.

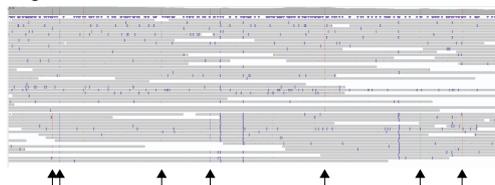


**Figure S9: Breakpoint junction sequences of r(9) (RD\_P272):** Integrative Genomics Viewer images of short read genome sequencing (srGS) and long read genome sequencing (lrGS) data for the two breakpoint junctions. Breakpoint sequences with the chimeric sequence in the center aligned to the reference sequences shown in pink and blue. Microhomology is indicated in green. Coordinates according to genome build T2T-CHM13v2.0.

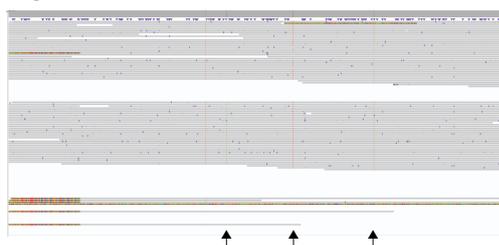
RD\_P166  
Chr 13  
Segment B



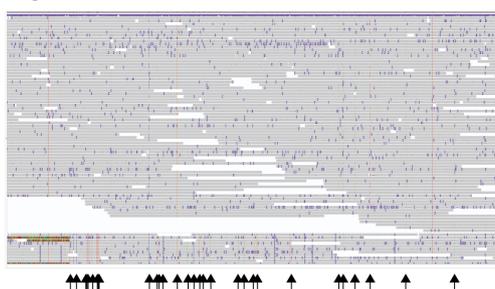
Segment C



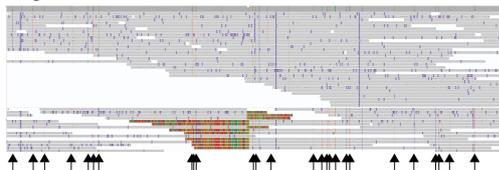
RD\_P272  
Chr 9  
Segment C



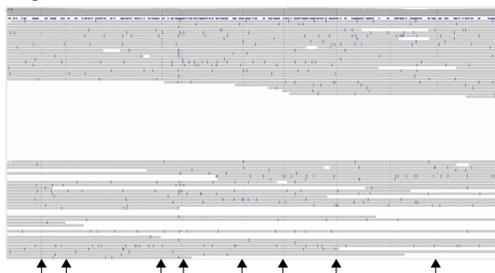
Segment D



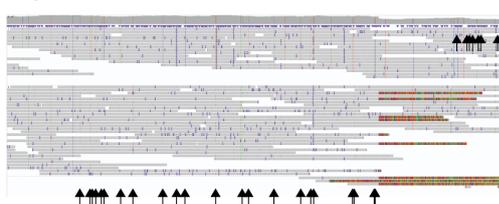
RD\_P586  
Chr X  
Segment H-I



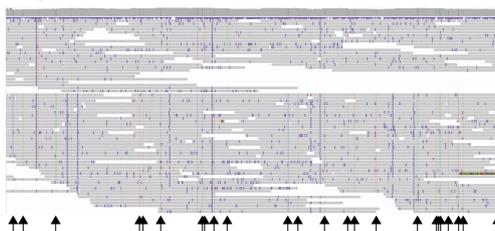
Segment J



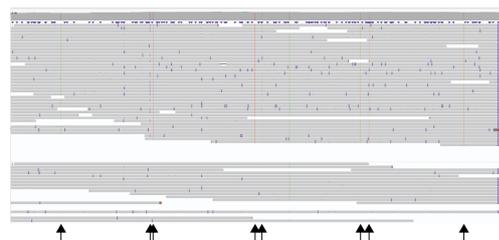
RD\_P328  
Chr 7  
Segment B



Chr 5  
Segment A



Chr X  
Segment C



Chr X  
Segment C Chr X

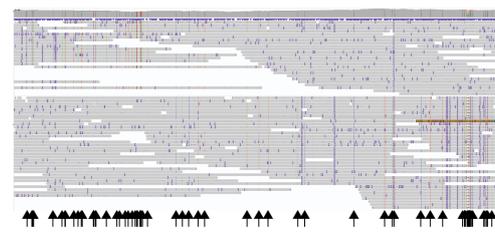


Figure S10: Triallelic sites discovered through haplotype analysis. The phased

long read genome sequencing data is shown in the Integrative Genomics Viewer with informative single nucleotide variants indicated by arrows.