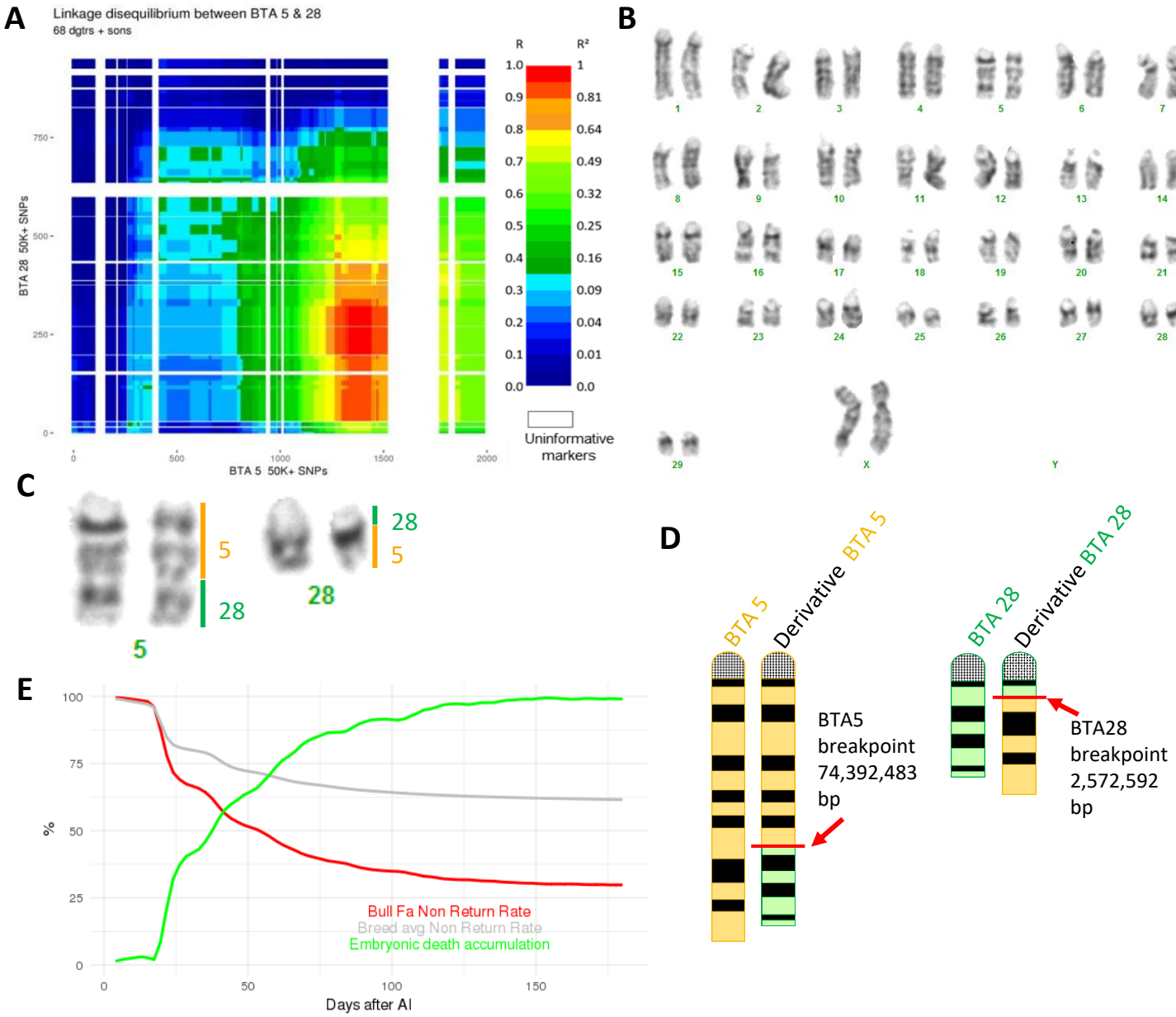


F

Paternal grand sire	haplo. BTA5	haplo. BTA28
1	AAAGAGAGAA	GAAGCGAAAA
2	**AAAGAGAGAG**	AAAGCGAAAA

Paternal grand dam	haplo. BTA5	haplo. BTA28
1	*CCTAGACAAA*	***GCCAAGAAAG***
2	*AAAGGACGAA*	*GCCAAGAAAA*

Mat. grand sire: Healthy (884 tests)	haplo. BTA5	haplo. BTA28
1	CCTAGACAAA	AAAGCGAAAG
2	CCTAGACAAG	AACACGAGAG

Maternal grand dam	haplo. BTA5	haplo. BTA28
1	*CCTAGACAAA*	*AAAAAGGAAA*
2	*CCAGAGCGAG*	*AACACGAAAA*

Sire: Healthy (>1000 tests)	haplo. BTA5	haplo. BTA28
1	**AAAGAGAGAG**	AAAGCGAAAA
2	CCTAGACAAA	**GCCAAGAAAG**

Presumed translocation apparition

Dam	haplo. BTA5	haplo. BTA28
1	CCAGGACAAA	AAAGCGAAAG
2	CCAGAGCGAG	AACACGAAAA

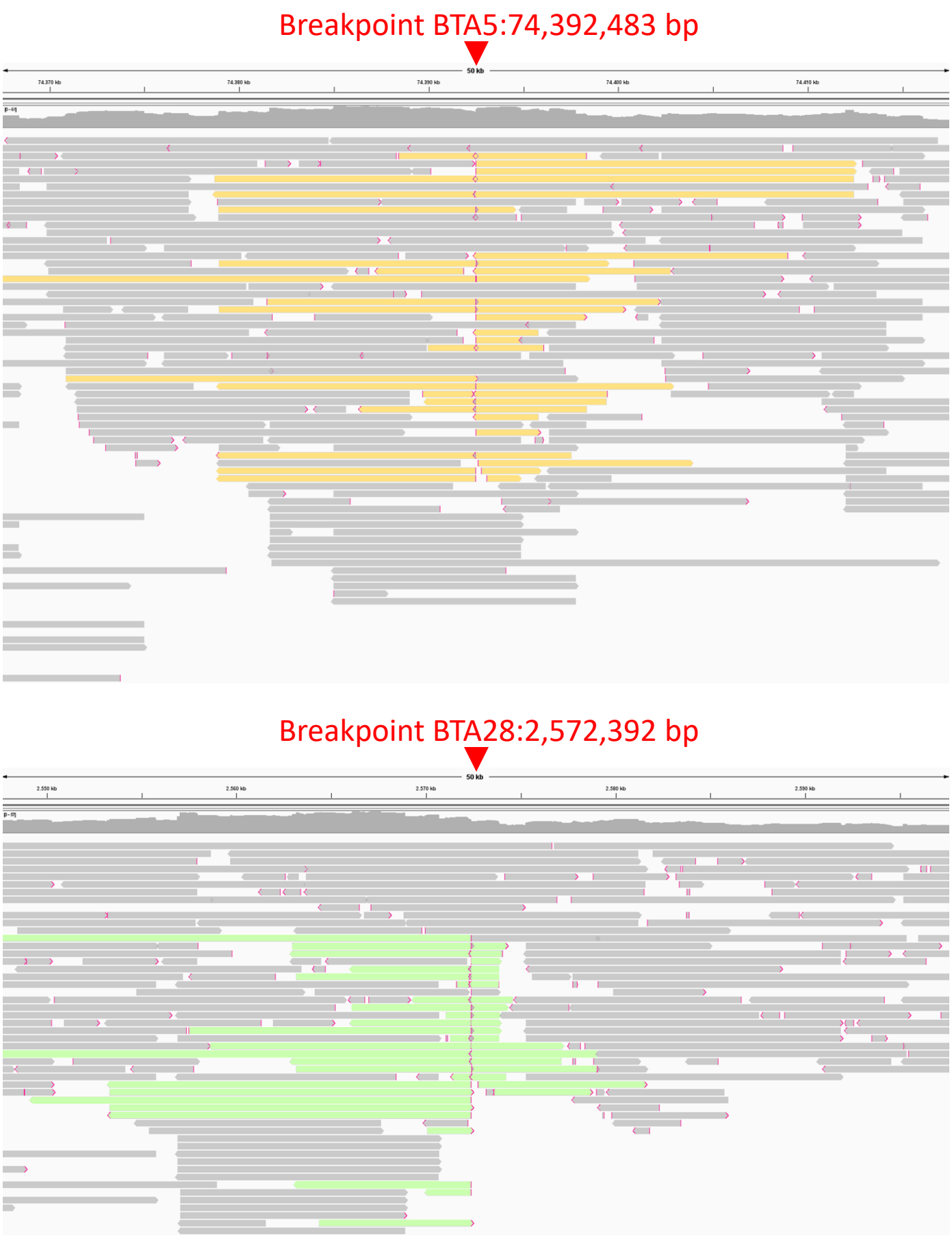
Bull Fa	haplo. BTA5	haplo. BTA28
1	**AAAGAGAGAG**	**GCCAAGAAAG**
2	CCAGGACAAA	AAAGCGAAAG

Fa's daughter	haplo. BTA5	haplo. BTA28
1	***AAAGAGAGAG***	***GCCAAGAAAG***
2	*CCTAGACAAA*	*AAAGCGAAAA*

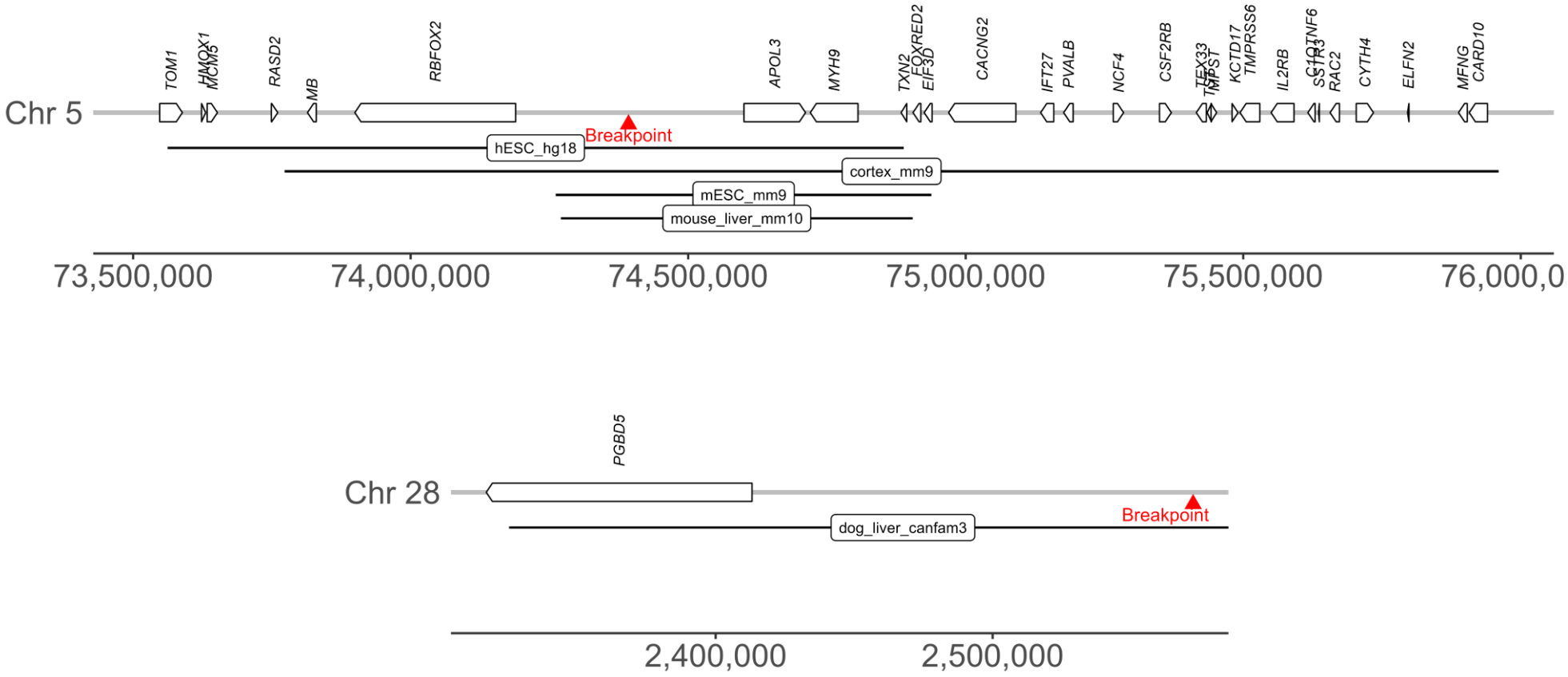
Karyotyped **Grand-Daughter**	haplo. BTA5	haplo. BTA28
1	AAAGGACGAA	AACACGAAAA
2	**AAAGAGAGAG**	**GCCAAGAAAG**

Supplemental Figure S1. Information on t(5;28) and bull Fa. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of an affected granddaughter of Fa and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome combining information from cytogenetic analyses and long-read sequencing. *(E)* Daily non-return rate of inseminations performed with the semen of Fa semen compared to the average non-return rate of the breed. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of Fa based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives. Note that the karyotyped animal is a descendant of a daughter of Fa, which explains why it carries the IR on its maternal phases.

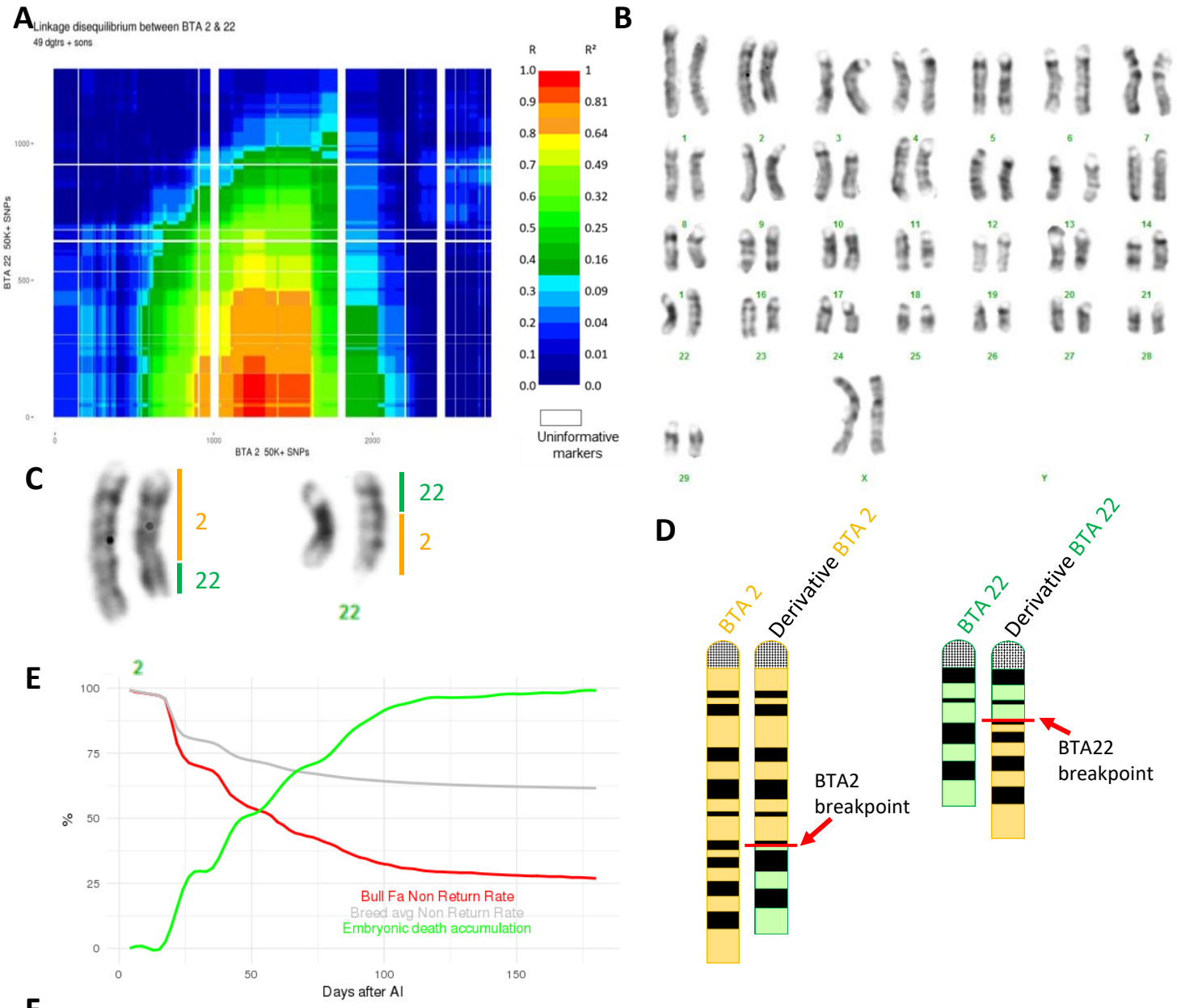
Note that bull Fa inherited the two haplotypes in LD with the translocation from its sire, which showed normal LD pattern in our initial screen. We concluded that the bull Fa was the first mutant and that the rearrangement was the result of an abnormal male meiosis.



Supplemental Figure S1 (continued). *(G)* IGV screenshot of long read sequence alignments around the breakpoints +/-50kb on BTA5 and BTA28. Reads with partial alignment on the reciprocally translocated chromosome are highlighted in yellow and green.



Supplemental Figure 1 (continued). *(H)* Annotated map of the chromosomal regions flanking the breakpoints for t(5;28) in bull Fa. Gene annotation has been obtained using Ensembl Biomart Tool. Information on TAD locations has been determined by orthology comparison with human, mouse and dogs (Wang et al.,2018). The tool liftOver was used to convert the positions of bovine UMD3.1 to ARS-UCD1.2 assembly.



F

Paternal grand sire		
	haplo. BTA2	haplo. BTA22
1	GAGACAAAGC	ATAAACAGAA
2	GGGACAAGAC	CTGAACAAGC

Paternal grand dam		
	haplo. BTA2	haplo. BTA22
1	***GAGACAGGGC***	*CTAAACAGAA*
2	*GAGACAAAGC*	***CTGAACAAGC***

Mat. grand sire: Healthy (645 tests)		
	haplo. BTA2	haplo. BTA22
1	AAGACAAGAC	CTAGCCAAGC
2	GGGACAAAGC	ATAGCCAAGC

Maternal grand dam		
	haplo. BTA2	haplo. BTA22
1	*GGGGCAAGGC*	*ATAAACAGAA*
2	NA	NA

Sire: Healthy (>1000 tests)		
	haplo. BTA2	haplo. BTA22
1	GAGACAAAGC	CTAAACAGAA
2	***GAGACAGGGC***	***CTGAACAAGC***

Presumed translocation apparition

Dam		
	haplo. BTA2	haplo. BTA22
1	*GGGACAAAGC*	*ATAGCCAAGC*
2	*GGGGCAAGGC*	*ATAAACAGAA*

Bull Fe		
	haplo. BTA2	haplo. BTA22
1	***GAGACAGGGC***	***CTGAACAAGC***
2	GGGACAAAGC	ATAGCCAAGC

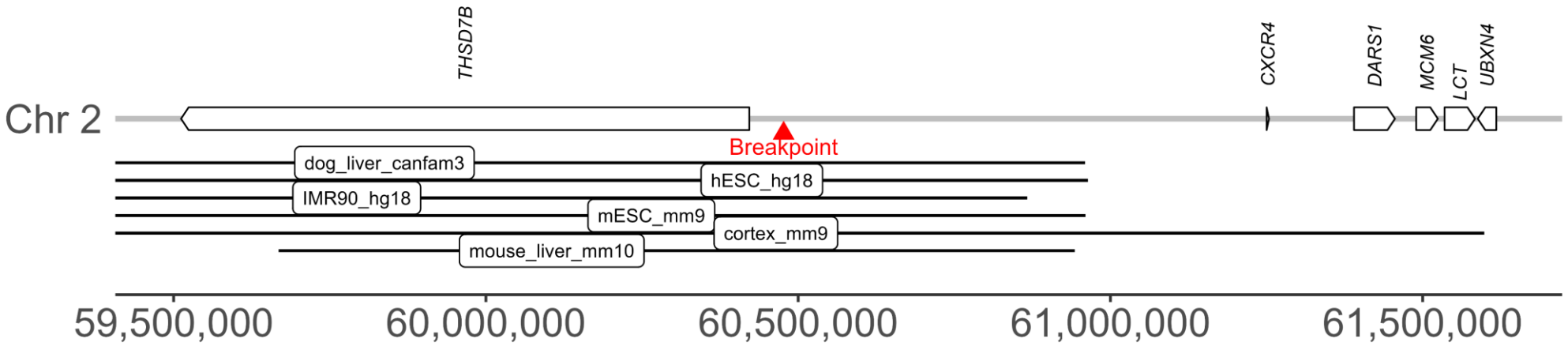
Fe's daughter		
	haplo. BTA2	haplo. BTA22
1	***GAGACAGGGC***	***CTGAACAAGC***
2	*GAGACAAGAA*	*CTGGACAGAC*

Karyotyped **Grand-Daughter**		
	haplo. BTA2	haplo. BTA22
1	GAGACAAAGC	CTAGCCAAGC
2	***GAGACAGGGC***	***CTGAACAAGC***

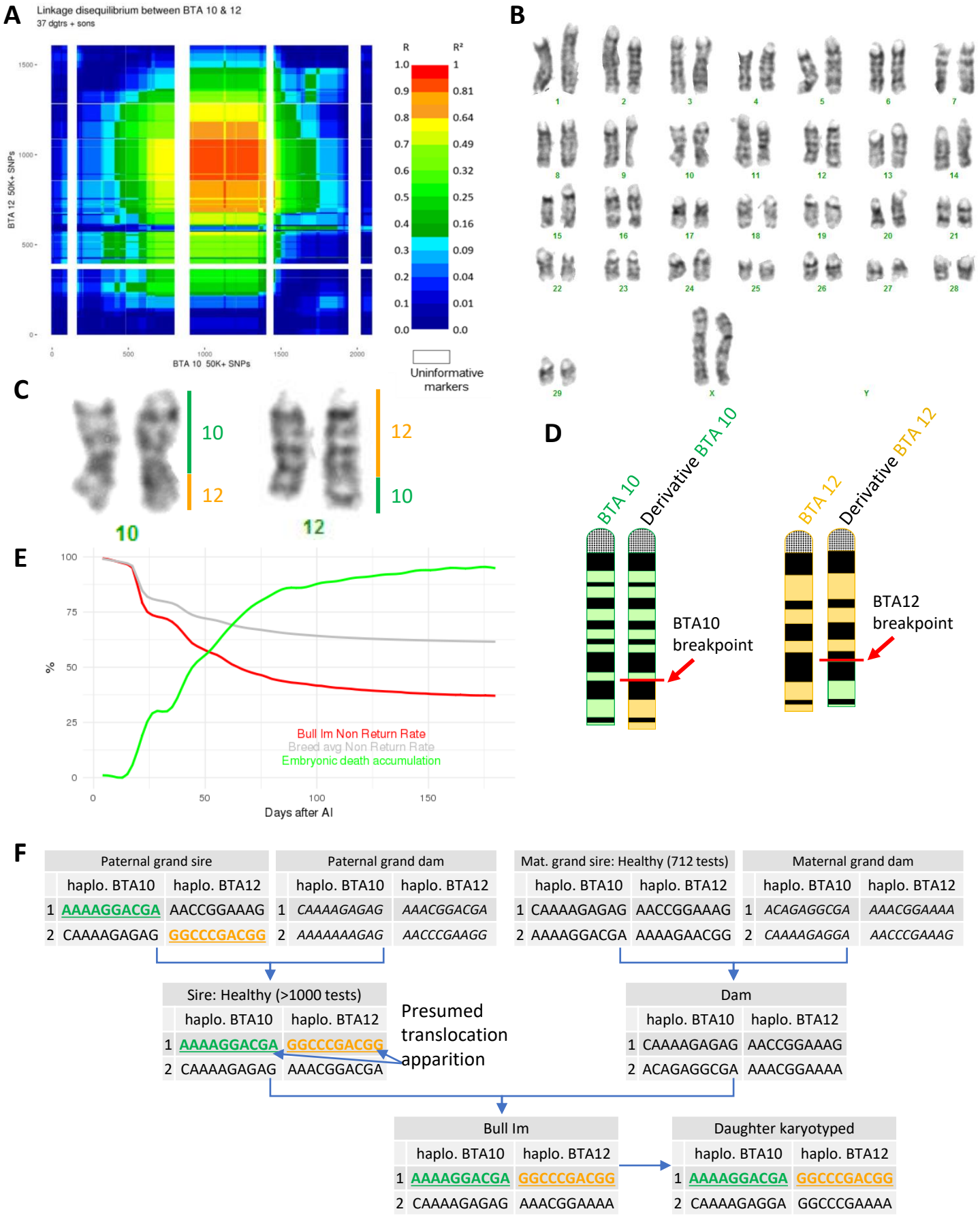
Supplemental Figure S2. Information on t(2;22) and bull Fe. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of an affected granddaughter of Fe and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome combining information from cytogenetic analyses and long-read sequencing. *(E)* Daily non-return rate of inseminations performed with the semen of Fe semen compared to the average non-return rate of the breed. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of Fe based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives. Note that the karyotyped animal is a descendant of a daughter of Fe, which explains why it carries the IR on its maternal phases.

Note that bull Fe inherited the two haplotypes in LDwith the translocation from its sire, which showed normal LD pattern in our initial screen. We concluded that the bull Fe was the first mutant and that the rearrangement was the result of an abnormal male meiosis.

Supplemental Figure S2 (continued). *(G)* IGV screenshot of long read sequence alignments around the breakpoint +/- 50kb on BTA2. Reads with partial alignment on BTSAT2 material are highlighted in yellow and green.



Supplemental Figure 2 (continued). *(H)* Annotated map of the chromosomal regions flanking the breakpoints for t(2;22) in bull Fe. Gene annotation has been obtained using Ensembl Biomart Tool. Information on TAD locations has been determined by orthology comparison with human, mouse and dogs (Wang et al.,2018). The tool liftOver was used to convert the positions of bovine UMD3.1 to ARS-UCD1.2 assembly.



F

Paternal grand sire		Paternal grand dam	
	haplo. BTA10	haplo. BTA12	haplo. BTA10	haplo. BTA12
1	**AAAAGGACGA**	AACCGGAAAG	1	*CAAAAGAGAG*	*AAACGGACGA*
2	CAAAAGAGAG	**GGCCCGACGG**	2	*AAAAAAAGAG*	*AACCCGAAGG*

Mat. grand sire: Healthy (712 tests)		Maternal grand dam	
	haplo. BTA10	haplo. BTA12	haplo. BTA10	haplo. BTA12
1	CAAAAGAGAG	AACCGGAAAG	1	*ACAGAGGCGA*	*AAACGGAAAA*
2	AAAAGGACGA	AAAAGAACGG	2	*CAAAAGAGGA*	*AACCCGAAAG*

Sire: Healthy (>1000 tests)		
	haplo. BTA10	haplo. BTA12
1	**AAAAGGACGA**	**GGCCCGACGG**
2	CAAAAGAGAG	AAACGGACGA

Presumed translocation apparition

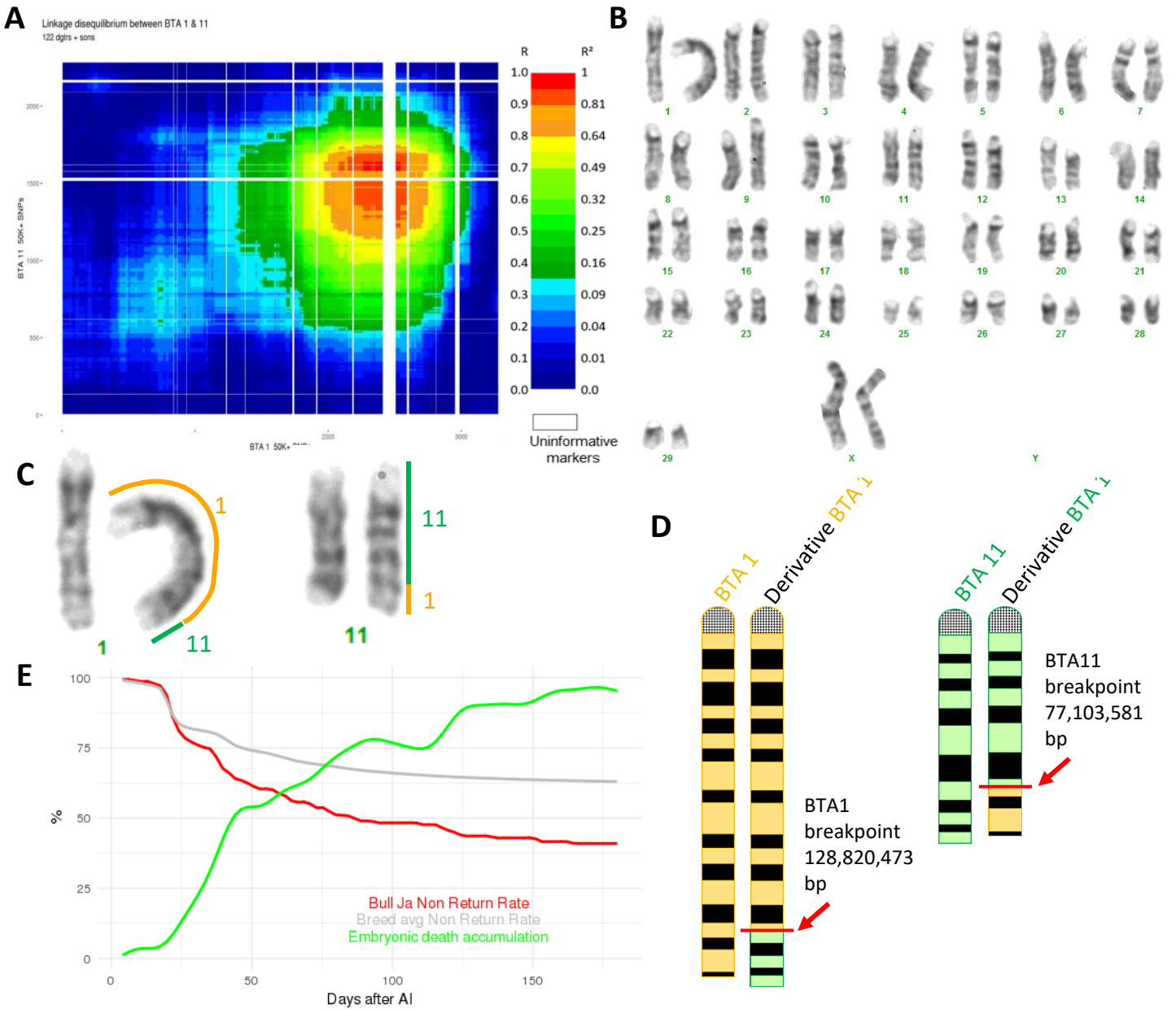
Dam		
	haplo. BTA10	haplo. BTA12
1	CAAAAGAGAG	AACCGGAAAG
2	ACAGAGGCGA	AAACGGAAAA

Bull Im		
	haplo. BTA10	haplo. BTA12
1	**AAAAGGACGA**	**GGCCCGACGG**
2	CAAAAGAGAG	AAACGGAAAA

Daughter karyotyped		
	haplo. BTA10	haplo. BTA12
1	**AAAAGGACGA**	**GGCCCGACGG**
2	CAAAAGAGGA	GGCCCGAAAA

Supplemental Figure S3. Information on t(10;12) and bull Im. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of an affected daughter of Im and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome using information from cytogenetic analyses. *(E)* Daily non-return rate of inseminations performed with the semen of Im semen compared to the average non-return rate of the breed. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of Im based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives.

Note that bull Im inherited the two haplotypes in LD with the translocation from its sire, which showed normal LD pattern in our initial screen. We concluded that the bull Im was the first mutant and that the rearrangement was the result of an abnormal male meiosis.



F

Paternal grand sire	haplo. BTA1	haplo. BTA11
1	AGAAGAAGAG	GAAGGGGGAG
2	CGAAAGAGGG	GGGGGGGAAA

Paternal grand dam	haplo. BTA1	haplo. BTA11
1	CGAAAAAGAG	GAGGGGGACG
2	CGGAGAGGAA	GGGAGGGAAG

Mat. grand sire: Healthy (384 tests)	haplo. BTA1	haplo. BTA11
1	CGGAGAGGAA	**AAGGAGGACG**
2	**AGGAGAAGAA**	AGGGGGGGAG

Maternal grand dam	haplo. BTA1	haplo. BTA11
1	*CGAGAAAGAA*	*GAAAGAGAAG*
2	*CGAAGAAGAG*	*GAAAGAGAAG*

Sire: Healthy (265 tests)	haplo. BTA1	haplo. BTA11
1	AGAAGAAGAG	GAAGGGGGAG
2	CGGAGAGGAA	GGGAGGGAAG

Presumed translocation apparition

Dam	haplo. BTA1	haplo. BTA11
1	**CGGAGAAGAA**	**AAGGAGGACG**
2	CGAGAAAGAA	GAAAGAGAAG

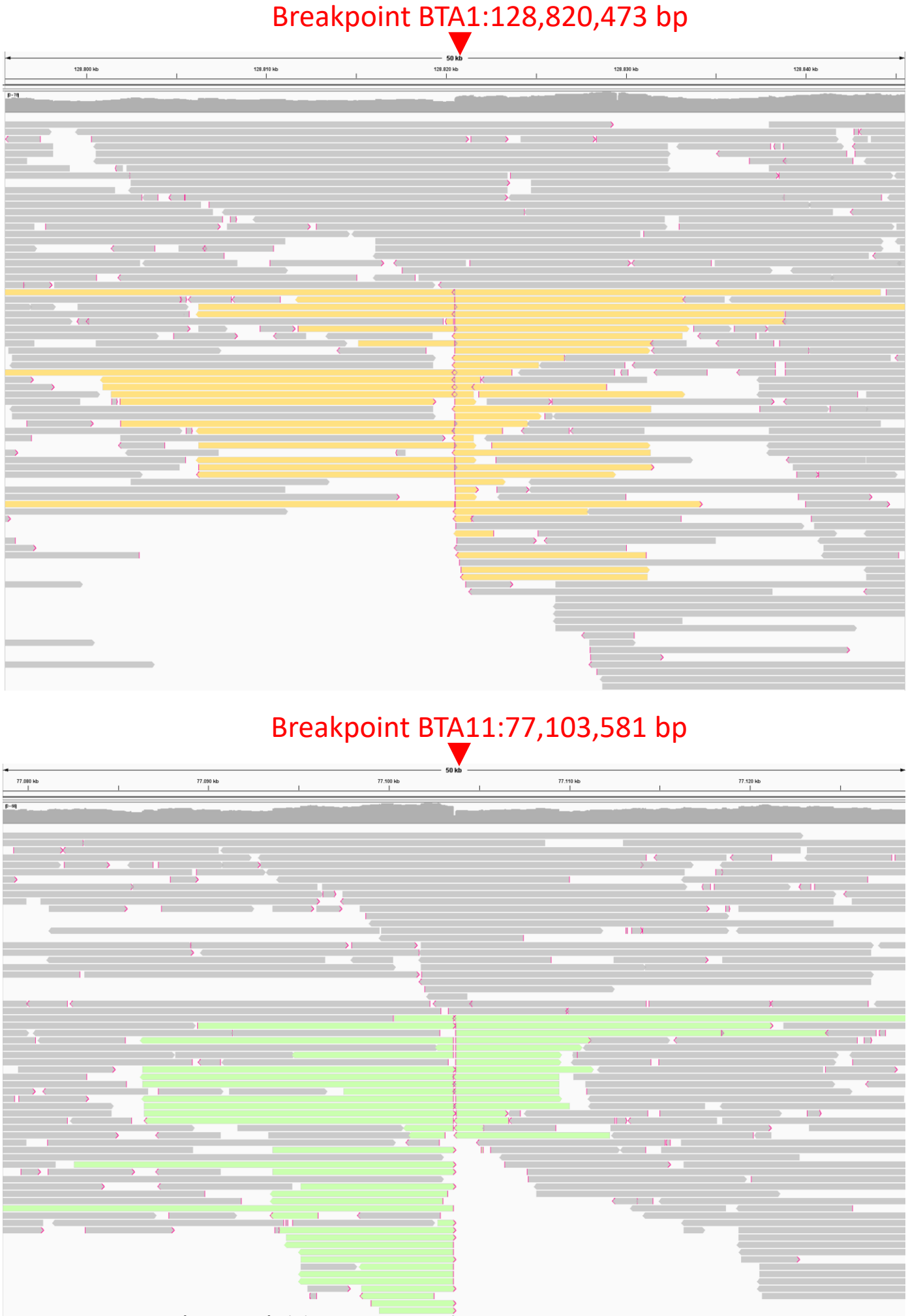
Probably affected (low fertility: 7 AI for 1st calving; 5 for the 2nd + involved haplotypes)

Bull Ja	haplo. BTA1	haplo. BTA11
1	CGGAGAGGAA	GAAGGGGGAG
2	**CGGAGAAGAA**	**AAGGAGGACG**

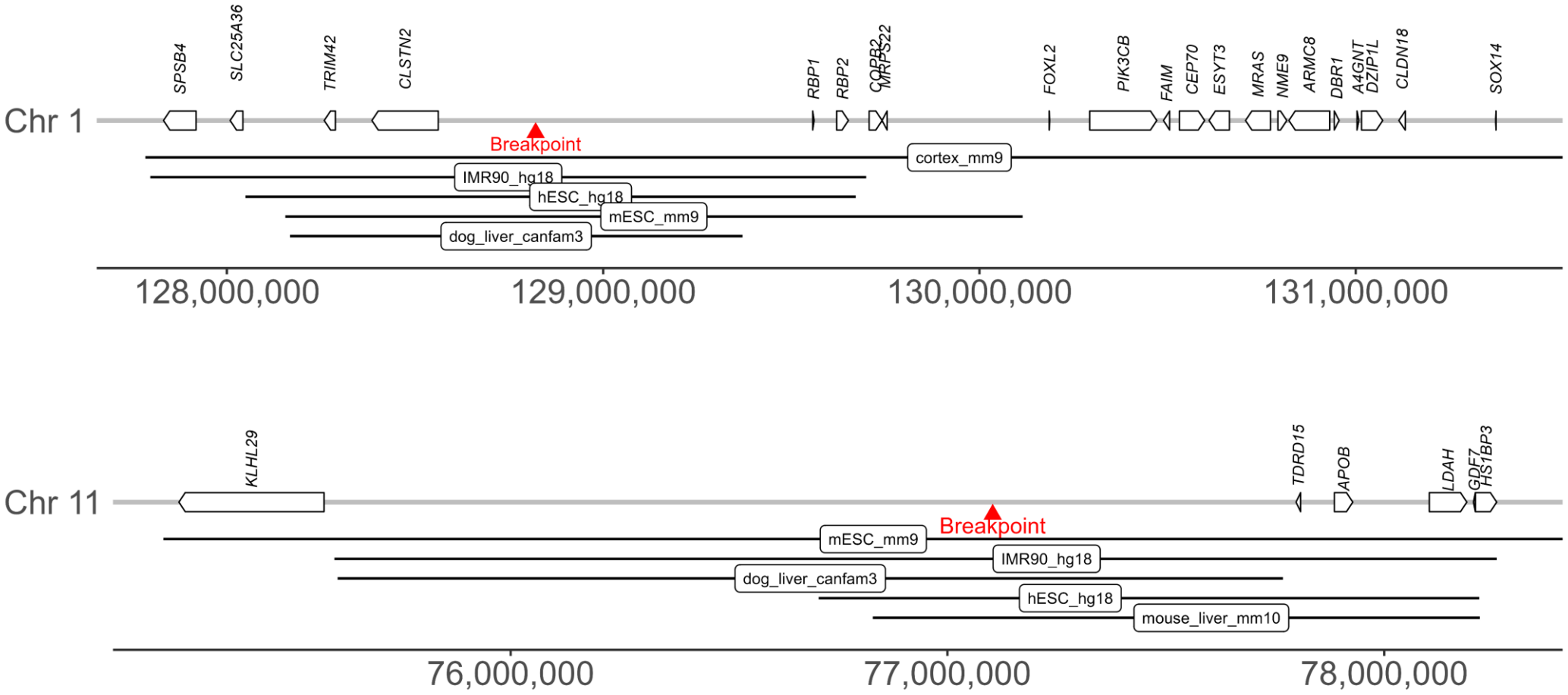
Karyotyped daughter	haplo. BTA1	haplo. BTA11
1	**CGGAGAAGAA**	**AAGGAGGACG**
2	CGAAAGAGAA	GAGGGGGACG

Supplemental Figure S4. Information on t(1;11) and bull Ja. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of an affected daughter of Ja and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome combining information from cytogenetic analyses and long-read sequencing. *(E)* Daily non-return rate of inseminations performed with the semen of Ja semen compared to the average non-return rate of the breed. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of Ja based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives.

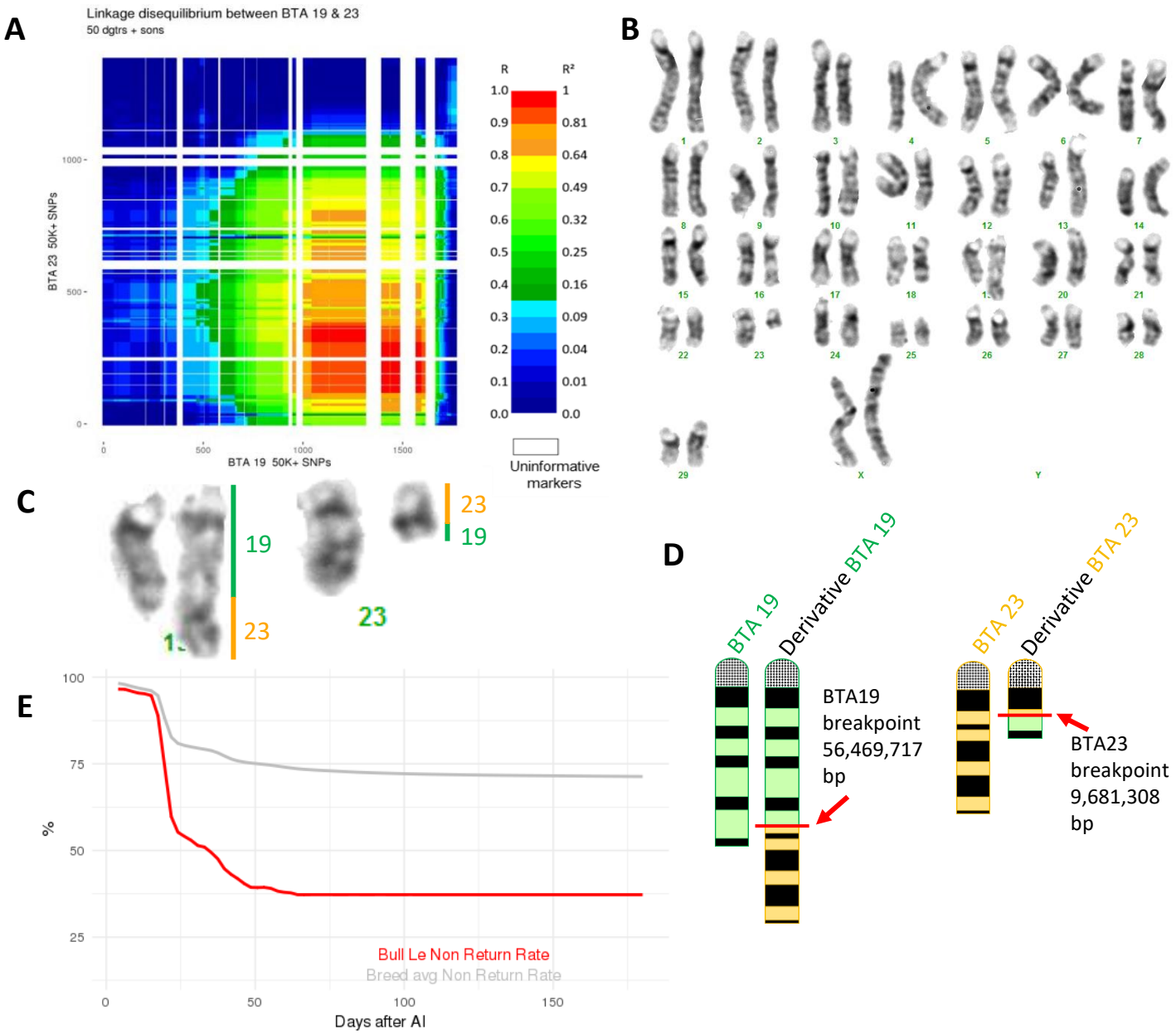
Note that bull Ja inherited the two haplotypes in LD with the translocation from its maternal grand sire, which showed normal LD pattern in our initial screen. The dam of Ja, which was genotyped, also had these haplotypes and was extremely subfertile with 7 AI to conceive its first calf and 5 for its second, supporting the evidence that it carried the IR. We concluded that the dam of Ja was the first mutant and that the rearrangement was the result of an abnormal male meiosis.



Supplemental Figure S4 (continued). *(G)* IGV screenshot of long read sequence alignments around the breakpoints +/-50kb on BTA1 and BTA11. Reads with partial alignment on the reciprocally translocated chromosome are highlighted in yellow and green.



Supplemental Figure 4 (continued). *(H)* Annotated map of the chromosomal regions flanking the breakpoints for t(1;11) in bull Ja. Gene annotation has been obtained using Ensembl Biomart Tool. Information on TAD locations has been determined by orthology comparison with human, mouse and dogs (Wang et al.,2018). The tool liftOver was used to convert the positions of bovine UMD3.1 to ARS-UCD1.2 assembly.



F

Paternal grand sire			Paternal grand dam		
	haplo. BTA19	haplo. BTA23		haplo. BTA19	haplo. BTA23
1	GGAAGGAAGA	CTAGAGATGC	1	GACAGGAAAG	ATAAAGGAGA
2	GAACGGGGGG	CTAGAGATGC	2	**GAACGGGGGA**	**CTAGAGAAGA**

Mat. grand sire: Healthy (308 tests)			Maternal grand dam		
	haplo. BTA19	haplo. BTA23		haplo. BTA19	haplo. BTA23
1	GACAGGAAAG	ATAGAGGTGC	1	*GACAGGAAAG*	*ATAGGGGAGA*
2	GAACGGGGGA	CTAGAGGTGC	2	*AACAAGGAAG*	*ATGGGGGAGA*

Sire: Healthy (459 tests)		
	haplo. BTA19	haplo. BTA23
1	GGAAGGAAGA	CTAGAGATGC
2	**GAACGGGGGA**	**CTAGAGAAGA**

Presumed translocation apparition

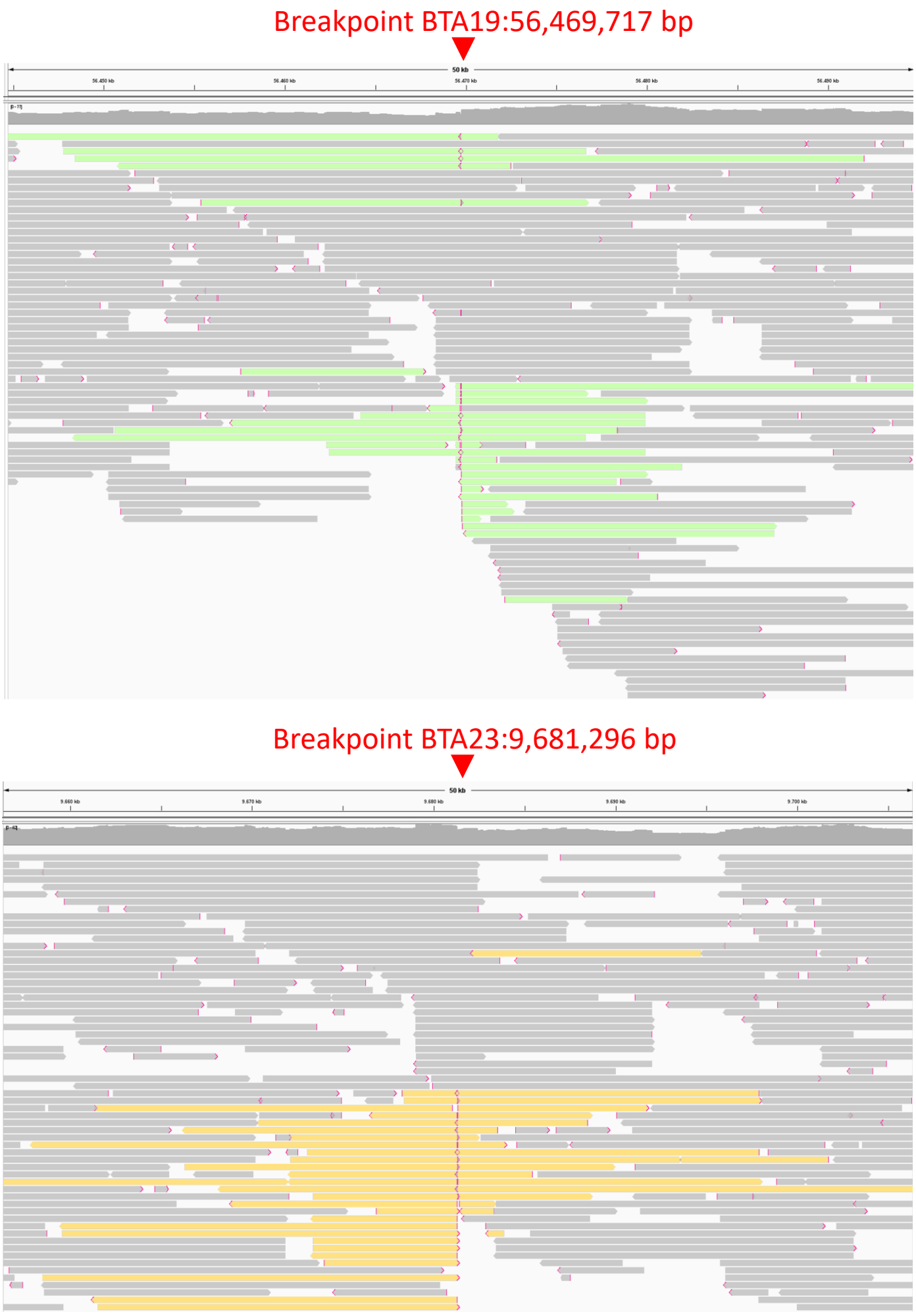
Dam		
	haplo. BTA19	haplo. BTA23
1	GACAGGAAAG	CTAGAGGTGC
2	GACAGGAAAG	ATGGGGGAGA

Bull Le		
	haplo. BTA19	haplo. BTA23
1	**GAACGGGGGA**	**CTAGAGAAGA**
2	GACAGGAAAG	ATGAGAGAGA

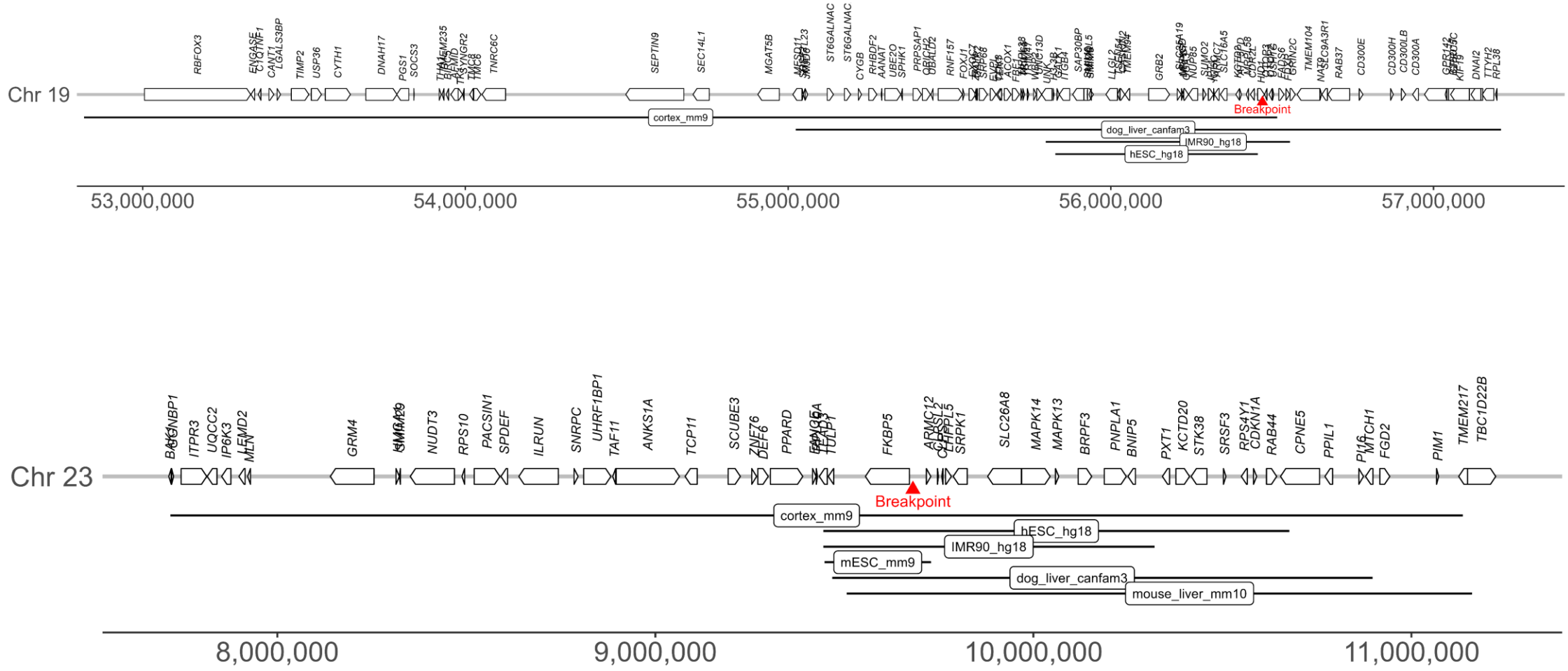
Daughter karyotyped		
	haplo. BTA19	haplo. BTA23
1	**GAACGGGGGA**	**CTAGAGAAGA**
2	GAAAGAAAGG	CTGGAAAAGA

Supplemental Figure S5. Information on t(19;23) and bull Le. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of an affected daughter of Le and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome combining information from cytogenetic analyses and long-read sequencing. *(E)* Daily non-return rate of inseminations performed with the semen of Le semen compared to the average non-return rate of the breed. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of Le based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives.

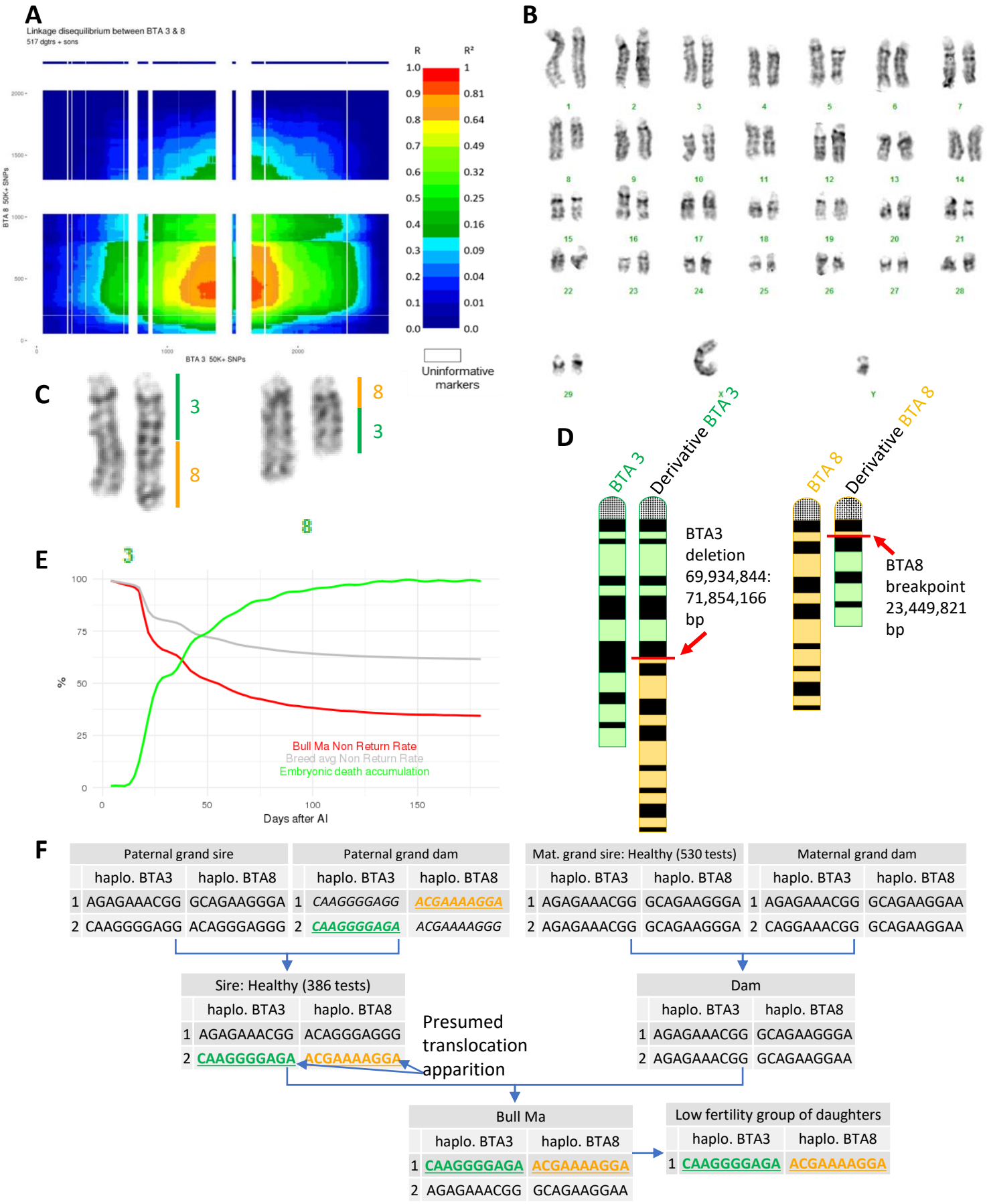
Note that bull Le inherited the two haplotypes in LD with the translocation from its sire, which showed normal LD pattern in our initial screen. We concluded that the bull Le was the first mutant and that the rearrangement was the result of an abnormal male meiosis.



Supplemental Figure S5 (continued). *(G)* IGV screenshot of long read sequence alignments around the breakpoints +/-50kb on BTA19 and BTA23. Reads with partial alignment on the reciprocally translocated chromosome are highlighted in yellow and green.

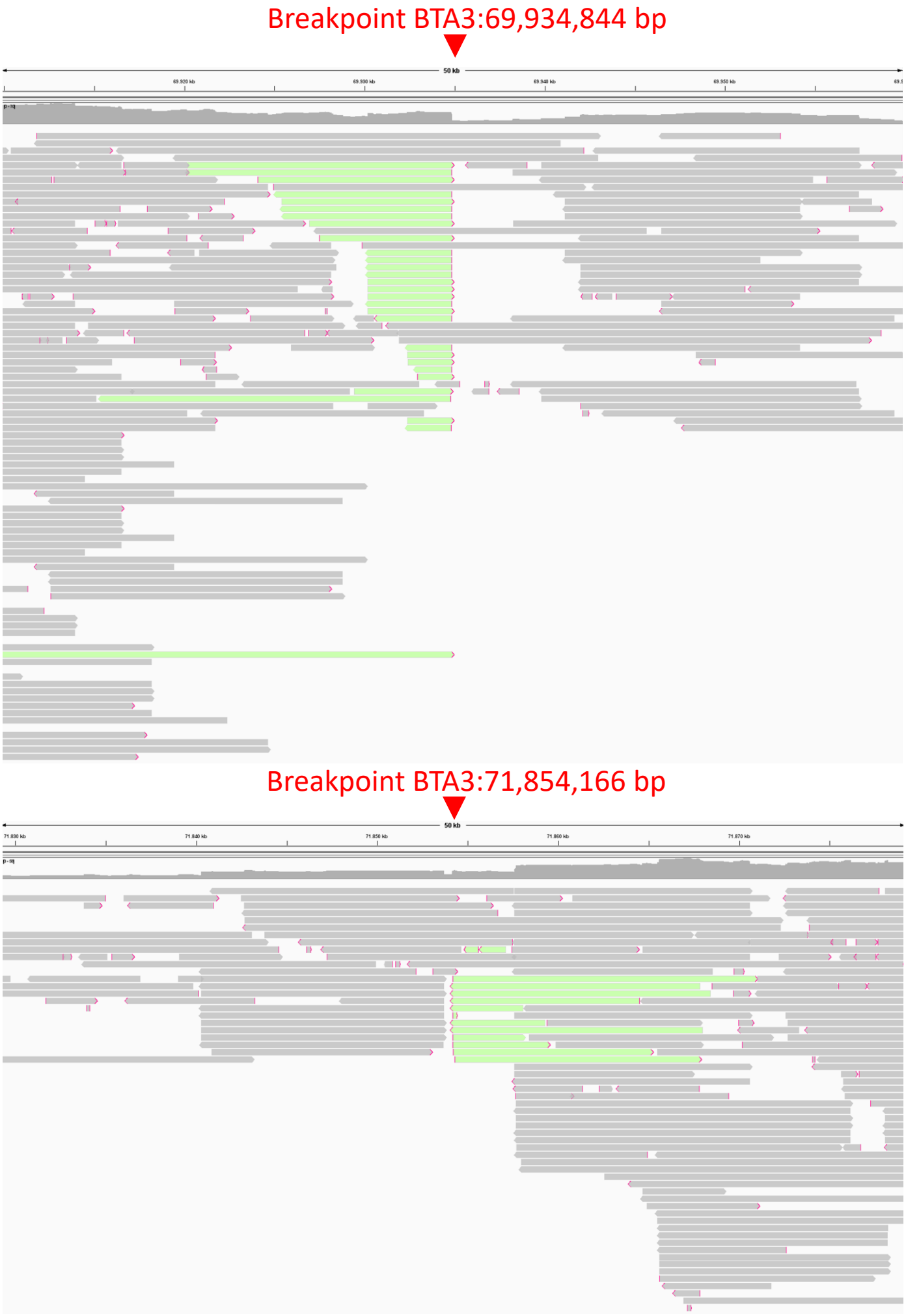


Supplemental Figure 5 (continued). *(H)* Annotated map of the chromosomal regions flanking the breakpoints for t(19;23) in bull Ja. Gene annotation has been obtained using Ensembl Biomart Tool. Information on TAD locations has been determined by orthology comparison with human, mouse and dogs (Wang et al.,2018). The tool liftOver was used to convert the positions of bovine UMD3.1 to ARS-UCD1.2 assembly.



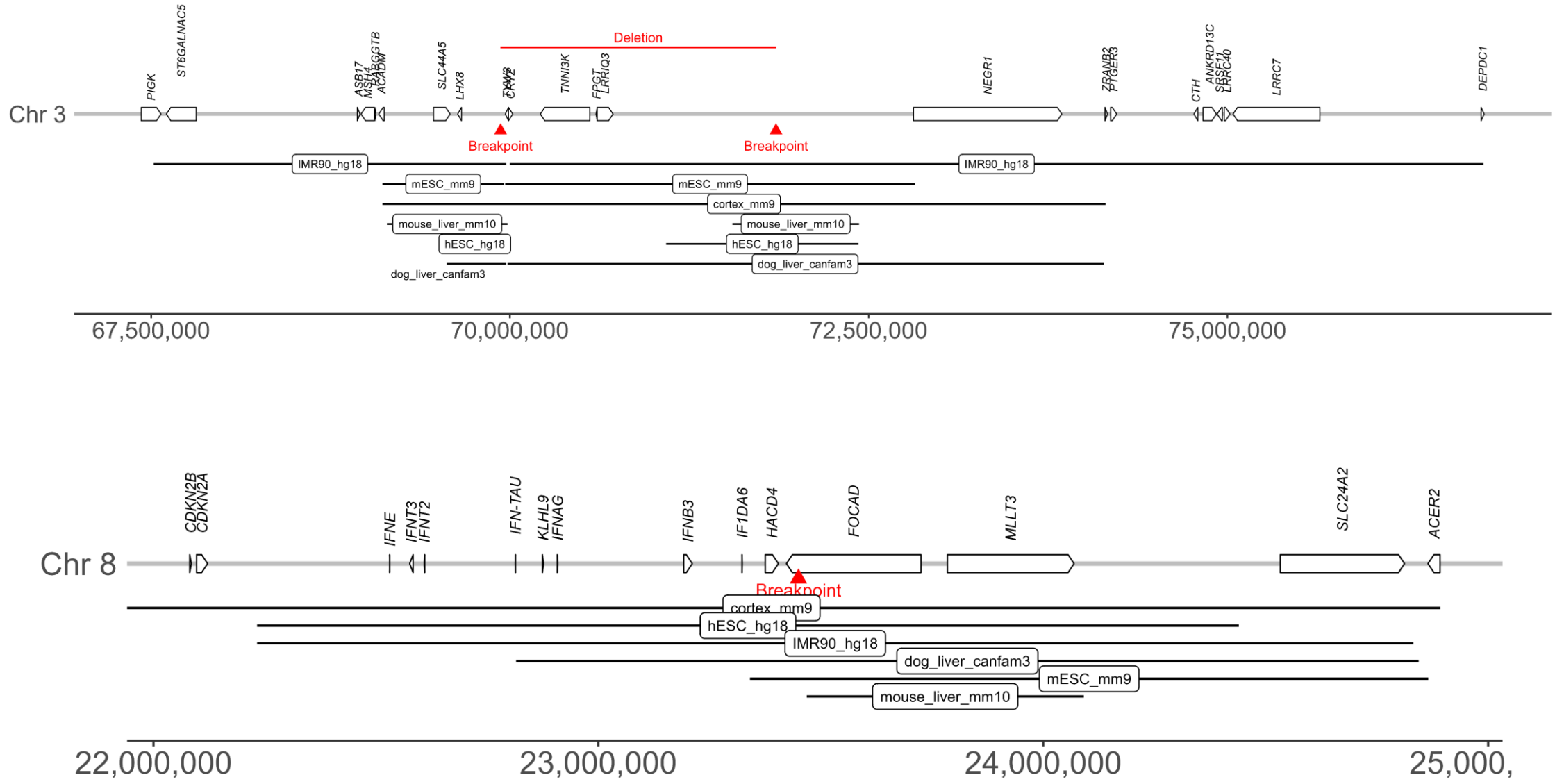
Supplemental Figure S6. Information on t(3;8) and bull Ma. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of Ma and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome combining information from cytogenetic analyses and long-read sequencing. *(E)* Daily non-return rate of inseminations performed with the semen of Ma semen compared to the average non-return rate of the breed. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of Ma based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives. Note that the karyotyped animal is a Ma itself.

Note that bull Ma inherited the two haplotypes in LD with the translocation from its sire, which showed normal LD pattern in our initial screen. We concluded that the bull Ma was the first mutant and that the rearrangement was the result of an abnormal male meiosis.

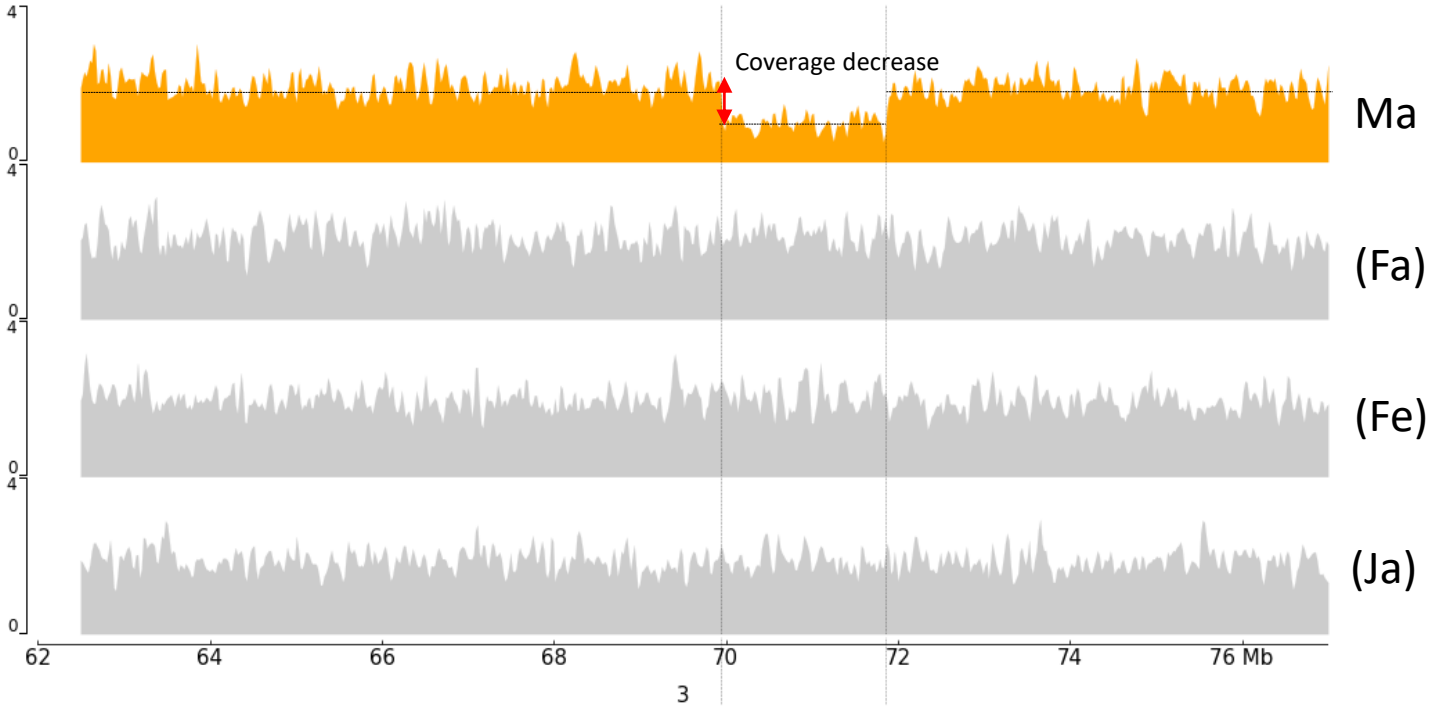


Supplemental Figure S6 (continued). *(G)* IGV screenshot of long read sequence alignments around the breakpoints +/-50kb on BTA3 and BTA8. Reads with partial alignment on the reciprocally translocated chromosome are highlighted in yellow and green.

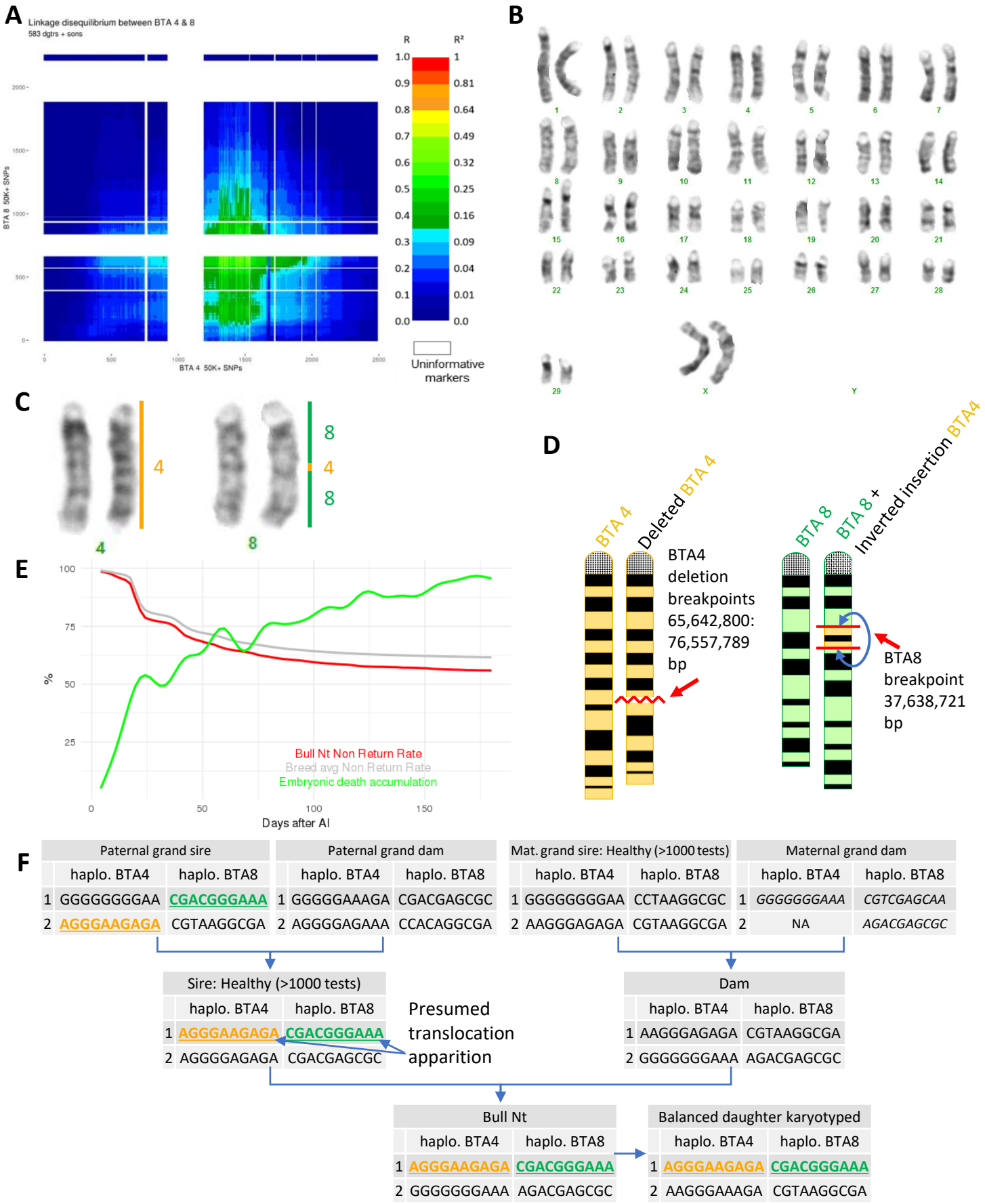
Supplemental Figure S6 (continued). *(G)* IGV screenshot of long read sequence alignments around the breakpoints +/-50kb on BTA3 and BTA8. Reads with partial alignment on the reciprocally translocated chromosome are highlighted in yellow and green.



Supplemental Figure 6 (continued). *(H)* Annotated map of the chromosomal regions flanking the breakpoints for t(3;8) in bull Ma. Gene annotation has been obtained using Ensembl Biomart Tool. Information on TAD locations has been determined by orthology comparison with human, mouse and dogs (Wang et al.,2018). The tool liftOver was used to convert the positions of bovine UMD3.1 to ARS-UCD1.2 assembly.

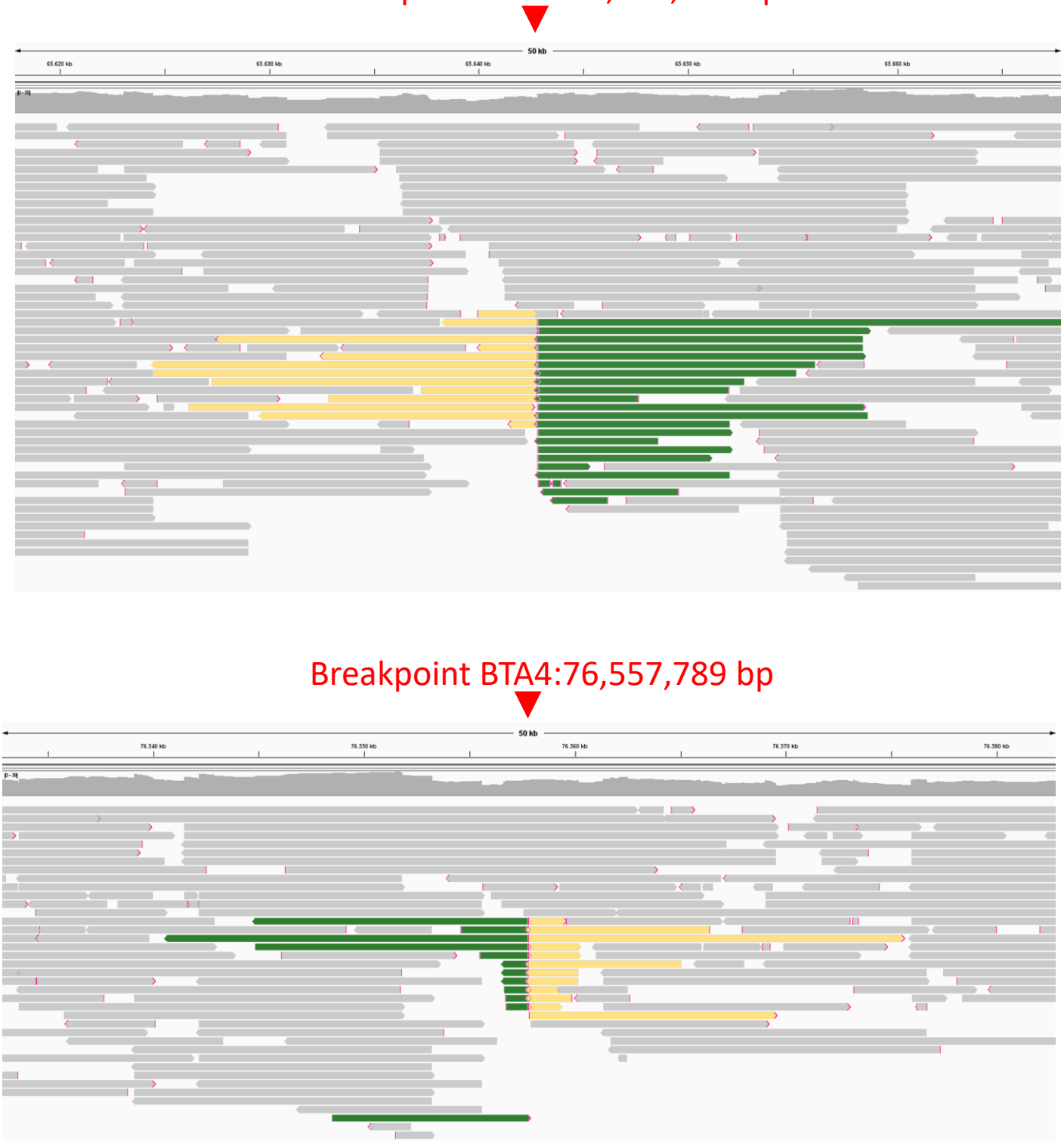


Supplemental Figure S6 (continued). *(l)* Coverage rate analysis around chimeric reads in the sequence of Ma compared to three control sequences. Note the coverage decrease between 79.9 and 81.9 Mb.

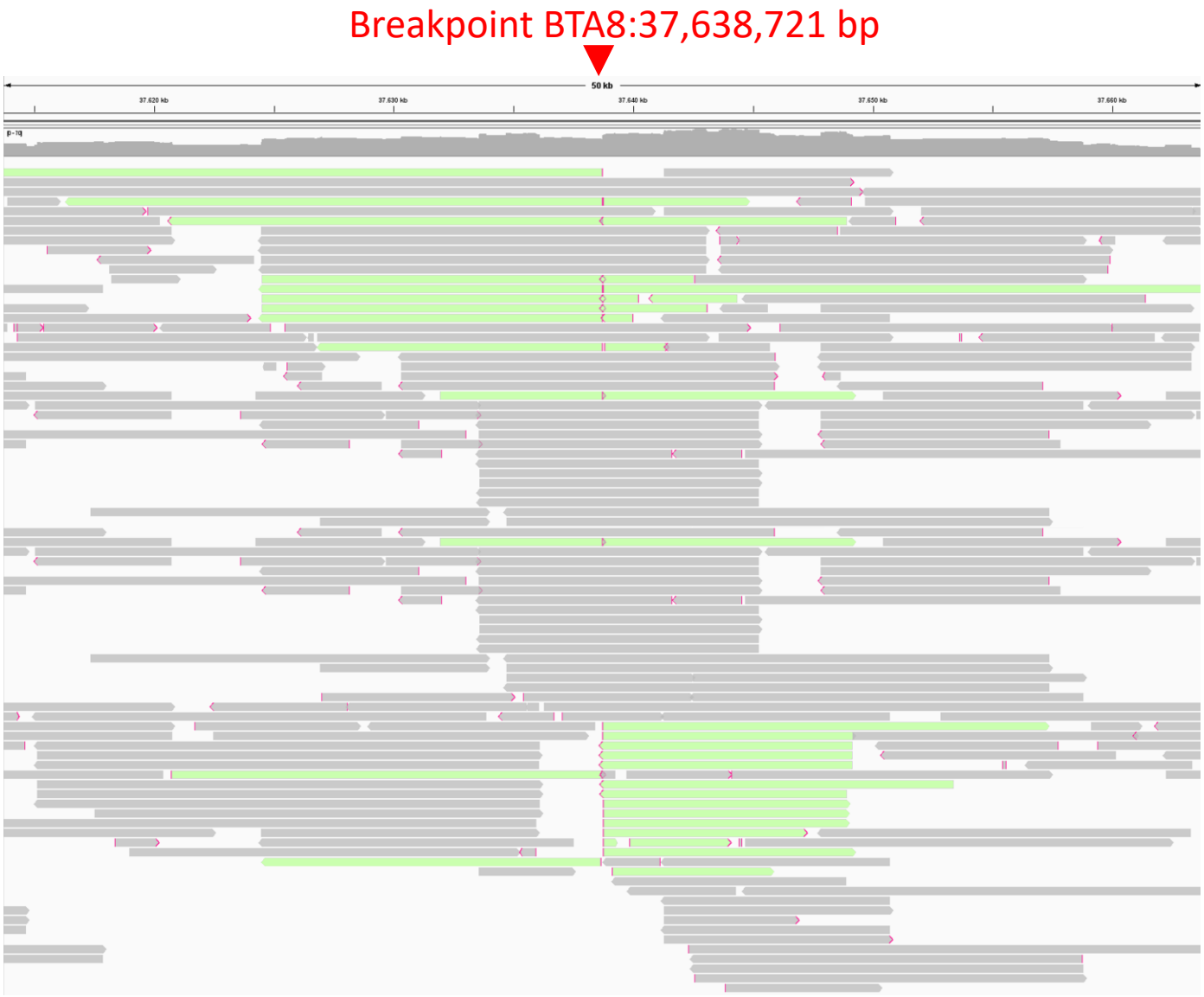


Supplemental Figure S7. Information on inv ins (8;4) and bull Nt. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of an affected daughter of Nt and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome combining information from cytogenetic analyses and long-read sequencing. *(E)* Daily non-return rate of inseminations performed with the semen of Nt semen compared to the average non-return rate of the breed. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of Nt based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives.

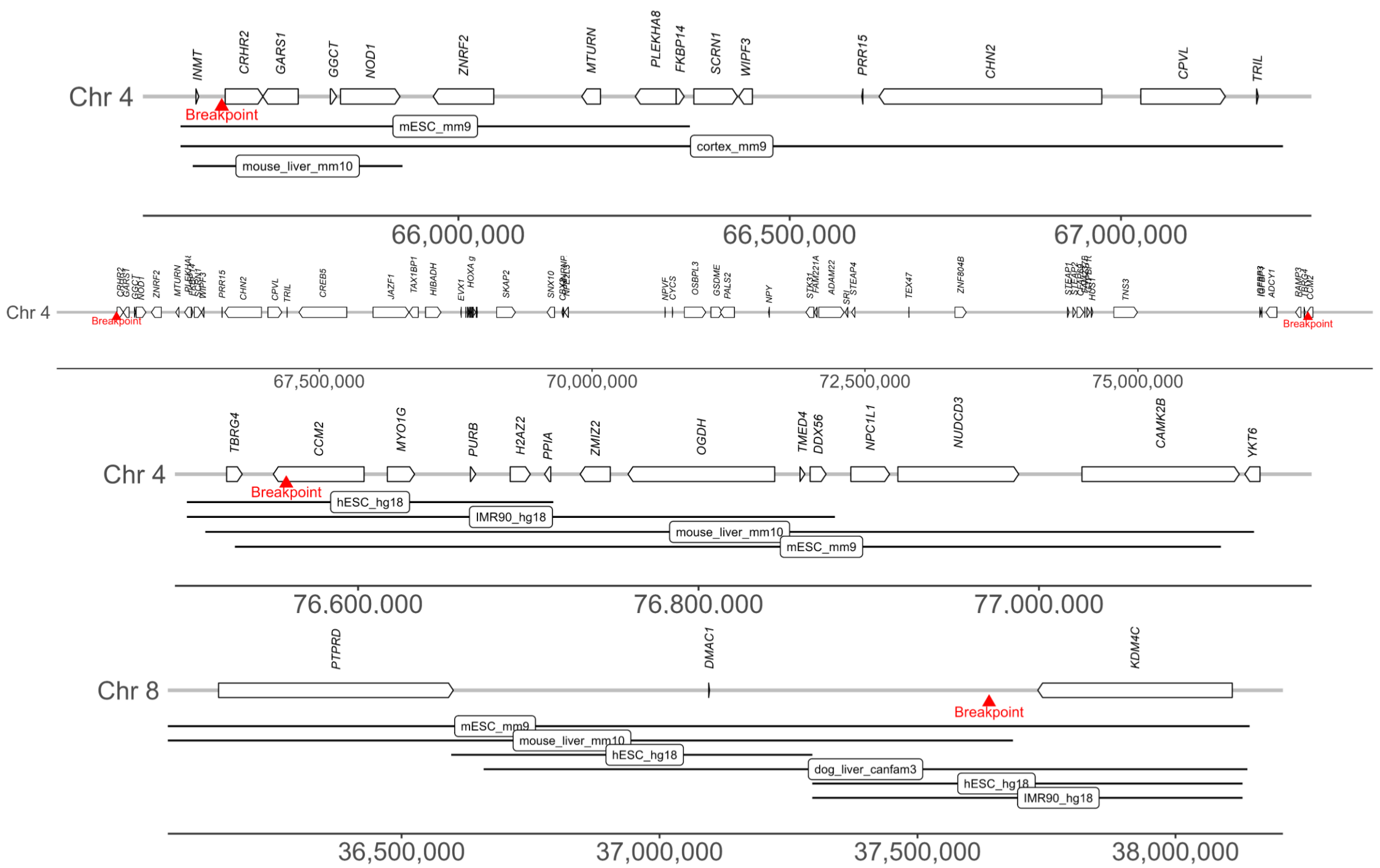
Note that bull Nt inherited the two haplotypes in LD with the translocation from its sire, which showed normal LD pattern in our initial screen. We concluded that the bull Nt was the first mutant and that the rearrangement was the result of an abnormal male meiosis.



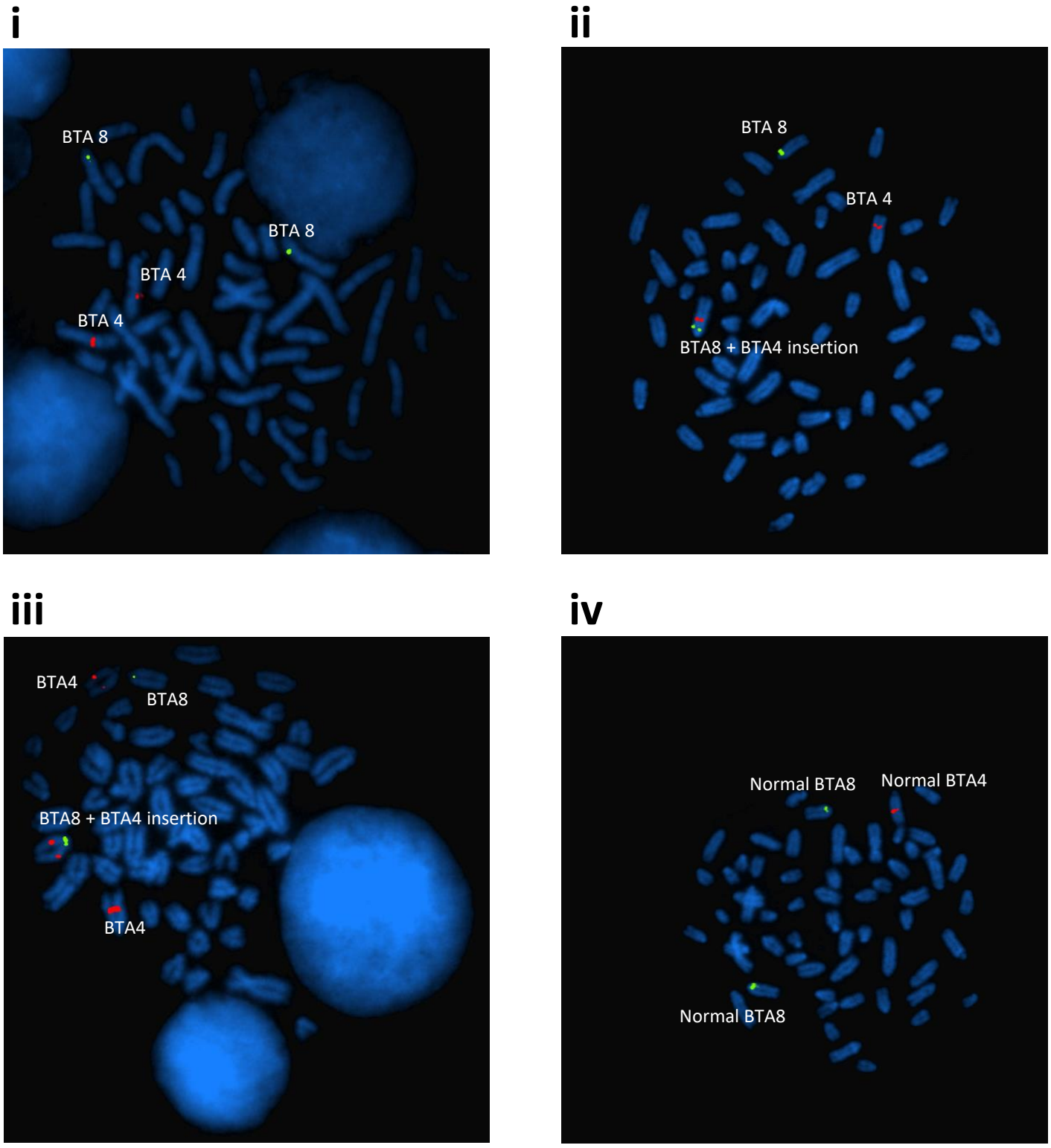
Supplemental Figure S7 (continued). *(G)* IGV screenshot of long read sequence alignments around the breakpoints +/-50kb on BTA4 and BTA8. Reads with partial alignment on the reciprocally translocated chromosome are highlighted in yellow and green.



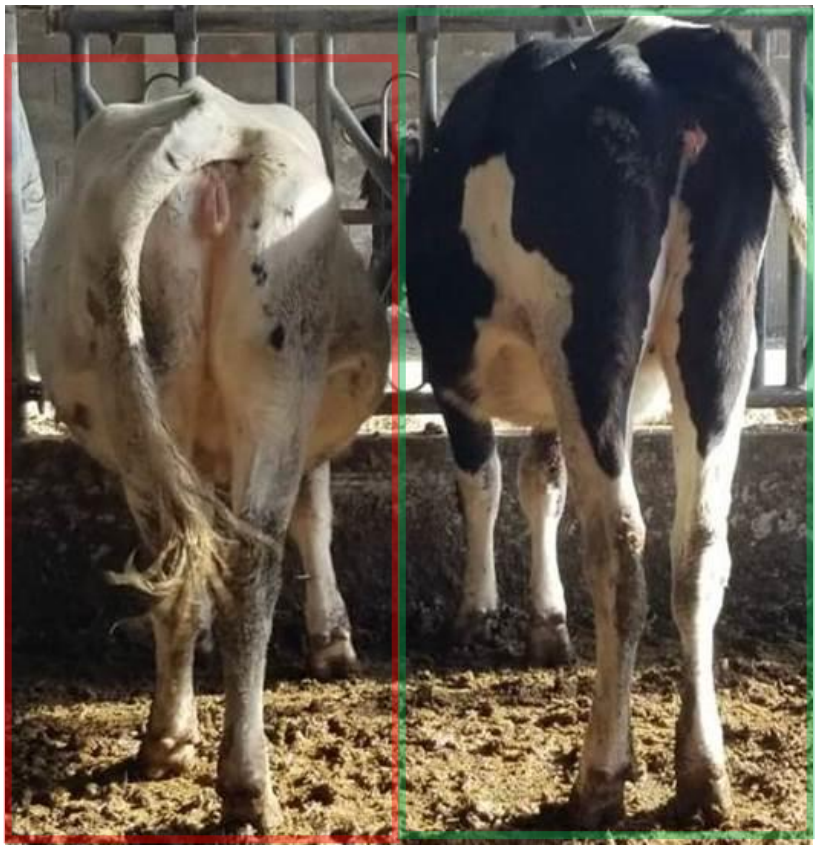
Supplemental Figure S7 (continued). *(G)* IGV screenshot of long read sequence alignments around the breakpoints +/-50kb on BTA4 and BTA8. Reads with partial alignment on the reciprocally translocated chromosome are highlighted in yellow and green.



Supplemental Figure 7 (continued). *(H)* Annotated map of the chromosomal regions flanking the breakpoints for inv ins (8;4) in bull Nt. Gene annotation has been obtained using Ensembl Biomart Tool. Information on TAD locations has been determined by orthology comparison with human, mouse and dogs (Wang et al.,2018). The tool liftOver was used to convert the positions of bovine UMD3.1 to ARS-UCD1.2 assembly.



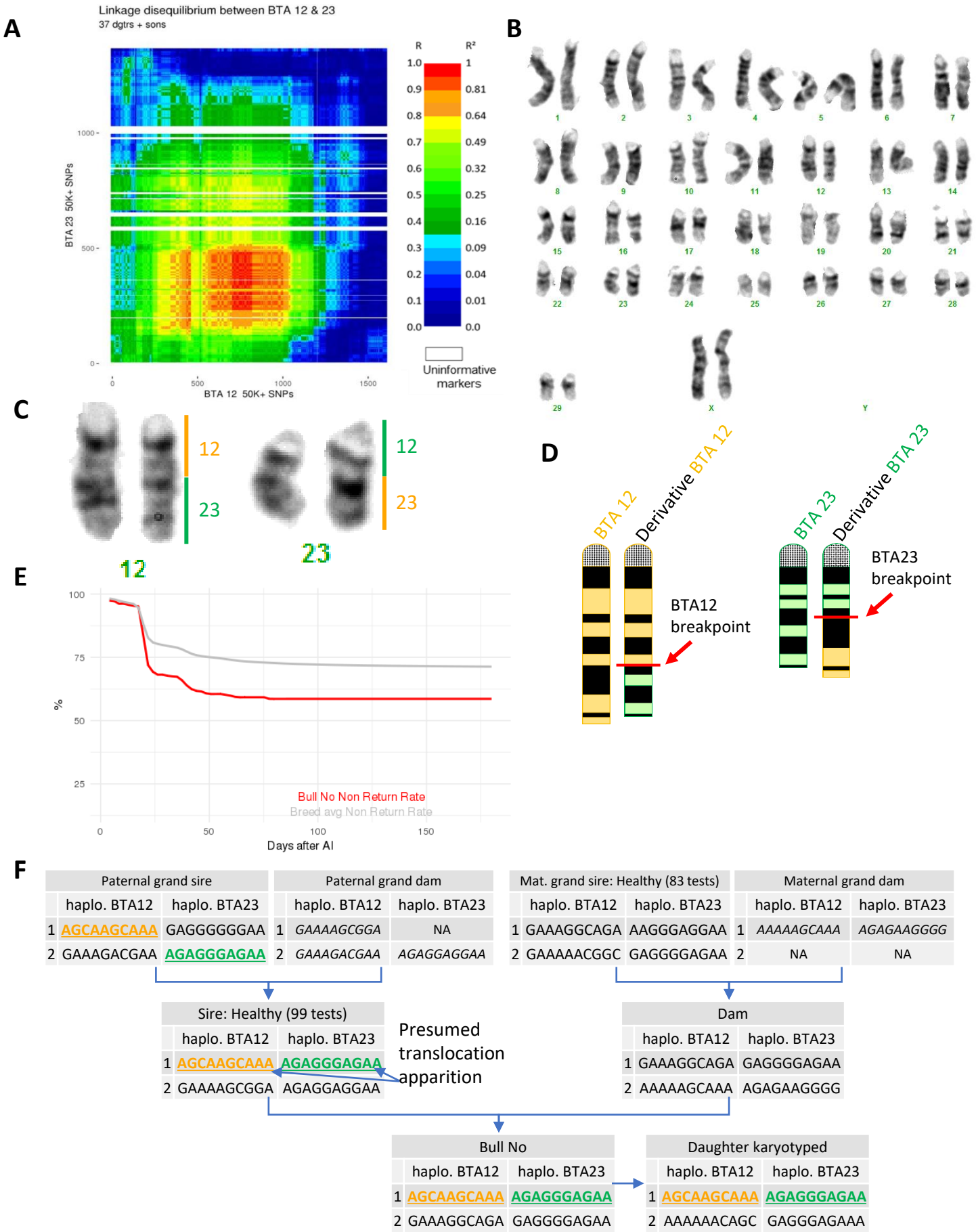
Supplemental Figure S7 (continued). *(J)* Full view of FISH (Fluorescence *In Situ* Hybridization) performed on Nt's daughters.
i: non-affected daughter (wild type).
ii: balanced daughter.
iii: partially trisomic daughter.
iv: partially monosomic daughter.
Green spots are hybridized in BTA8 centromere.
Red spots are hybridized in the specific translocated and inverted region of BTA4.



Left heifer (red frame): Nt's balanced daughter, 15.0 months
Right heifer (green frame): control heifer, 15.1 months

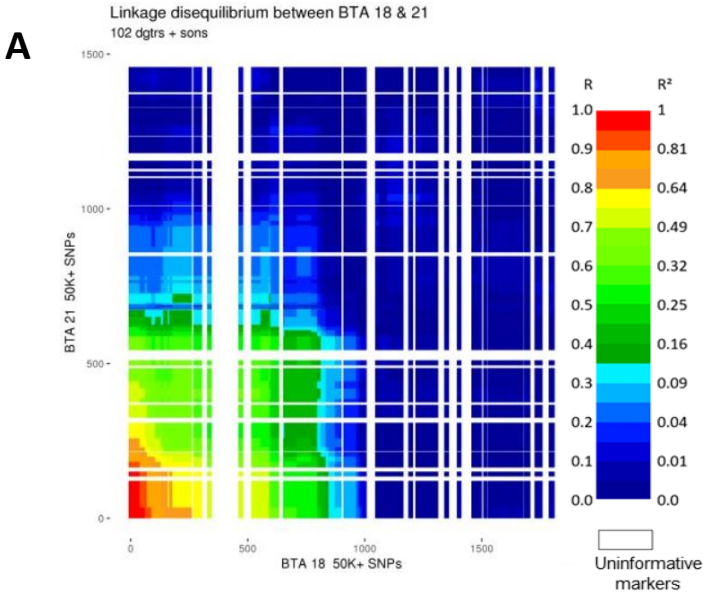
Left heifer (red frame): Nt's partially monosomic daughter, 18.7 months
Right heifer (green frame): control heifer, 16.3 months

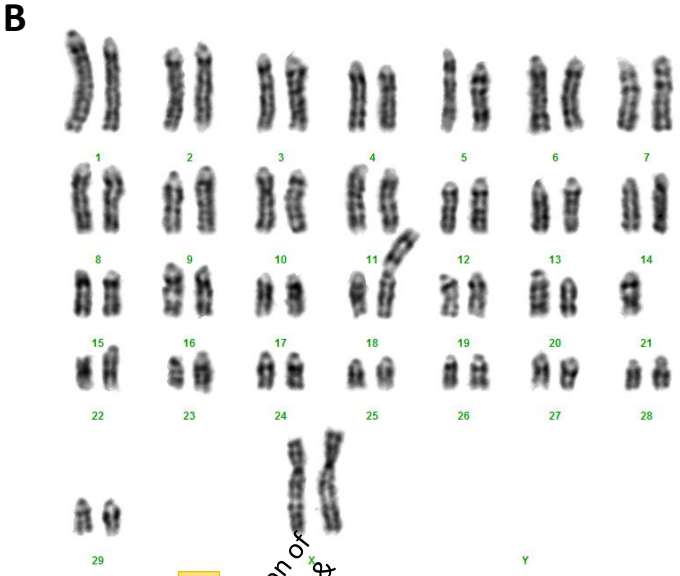
Supplemental Figure S7 (continued). *(K)* Pictures of affected Nt's daughters

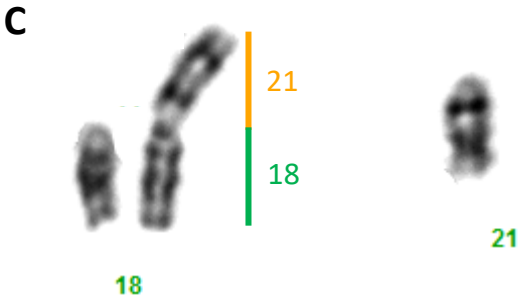


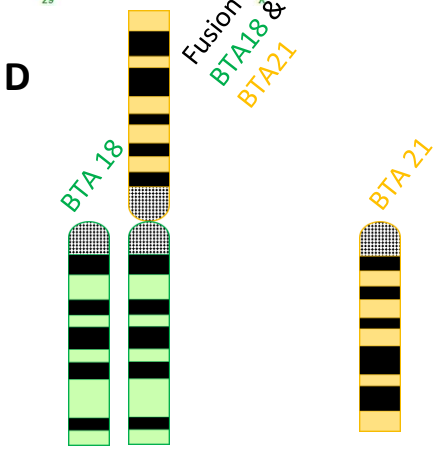
Supplemental Figure S8. Information on t(12;23) and bull No. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of an affected daughter of No and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome combining information from cytogenetic analyses and long-read sequencing. *(E)* Daily non-return rate of inseminations performed with the semen of No semen compared to the average non-return rate of the breed. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of No based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives.

Note that bull No inherited the two haplotypes in LD with the translocation from its sire, which showed normal LD pattern in our initial screen. We concluded that the bull No was the first mutant and that the rearrangement was the result of an abnormal male meiosis.









F

MGGS: Healthy (155 tests)			MGGD		
	haplo. BTA18	haplo. BTA21		haplo. BTA18	haplo. BTA21
1	GGATAGGAAG	GGGCAGAGAG	1	NA	*GGGCAGAGAG*
2	GGATAGGAAA	**CAGCAGAGAG**	2	***GAGTGAGGGA***	NA

Paternal grand sire			Paternal grand dam		
	haplo. BTA18	haplo. BTA21		haplo. BTA18	haplo. BTA21
1	GAGTGGGAAA	GGGCAGAGAG	1	GGATAGGGGG	CAGCAGCAAG
2	GGATAGGGAG	GGGCAGAGAG	2	GGATAGGGGG	GAGCAGAGAG

Mat. grand sire: Healthy (200 tests)			Maternal grand dam		
	haplo. BTA18	haplo. BTA21		haplo. BTA18	haplo. BTA21
1	GGATAGGAAA	CAGCAGCAAG	1	*GGATAGGAAG*	***CAGCAGAGAG***
2	AAAAAGAAAA	GGGCAGAGAG	2	***GAGTGAGGGA***	*GGGCAGAGAG*

Sire: Healthy (166 tests)		
	haplo. BTA18	haplo. BTA21
1	GGATAGGGAG	GGGCAGAGAG
2	GGATAGGGGG	CAGCAGCAAG

Dam		
	haplo. BTA18	haplo. BTA21
1	GGATAGGAAA	CAGCAGCAAG
2	**GAGTGAGGGA**	**CAGCAGAGAG**

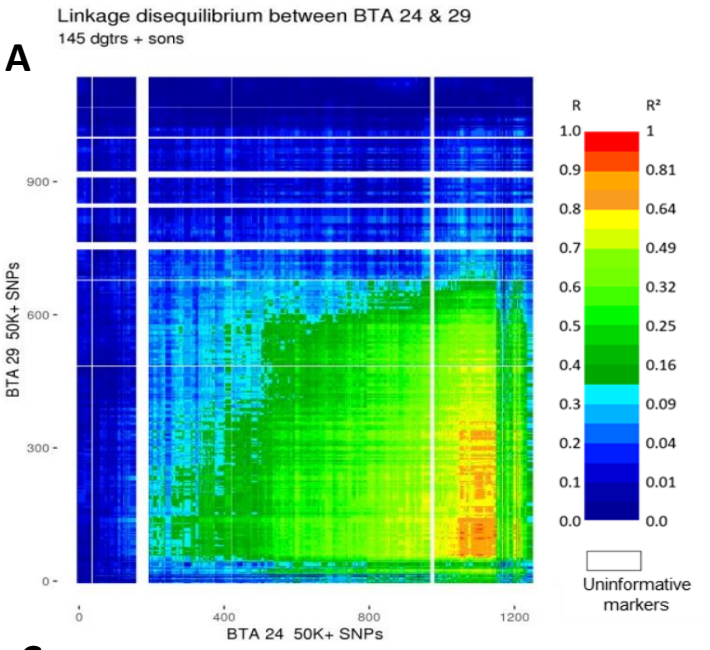
Presumed translocation apparition (at zygote stage)

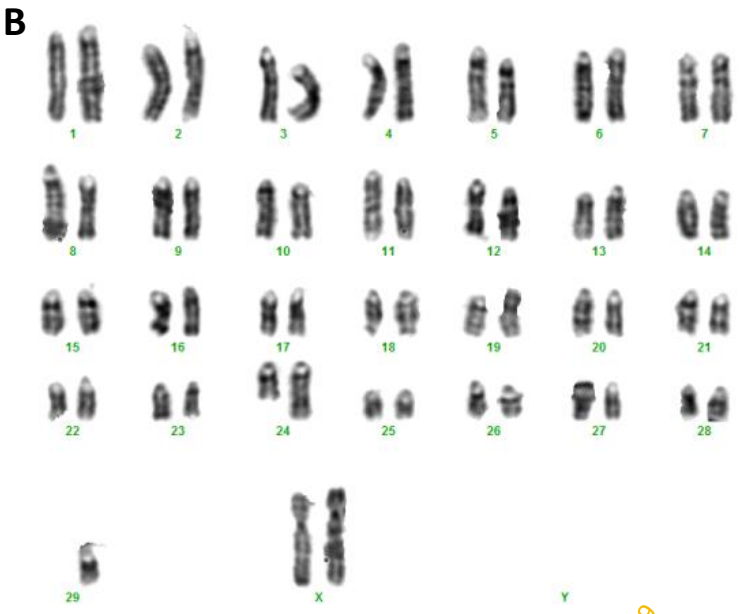
Bull Ob		
	haplo. BTA18	haplo. BTA21
1	GGATAGGGGG	CAGCAGCAAG
2	**GAGTGAGGGA**	**GAGCAGAGAG**

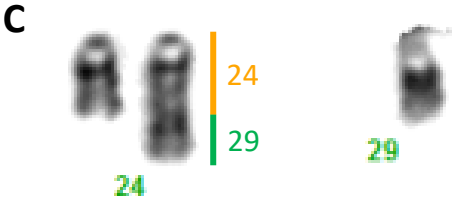
Daughter karyotyped		
	haplo. BTA18	haplo. BTA21
1	**GAGTGAGGGA**	**GAGCAGAGAG**
2	AAAAAAGAAA	GGGCAGAGAG

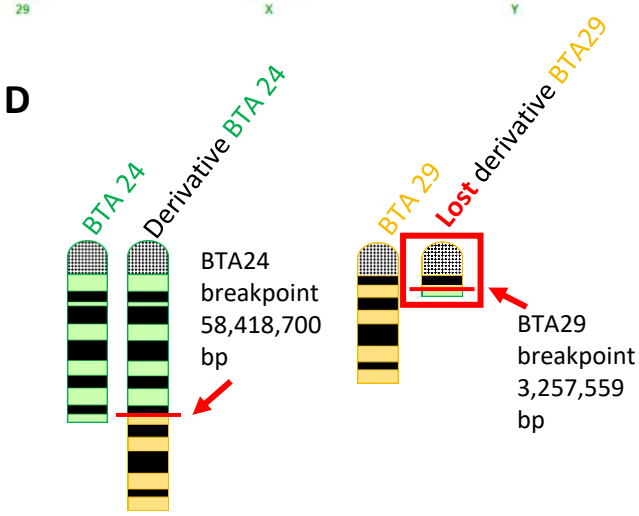
Supplemental Figure S9. Information on Rob(18;21) and bull Ob. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of an affected daughter of Ob and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome using information from cytogenetic analyses. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of Ob based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives.

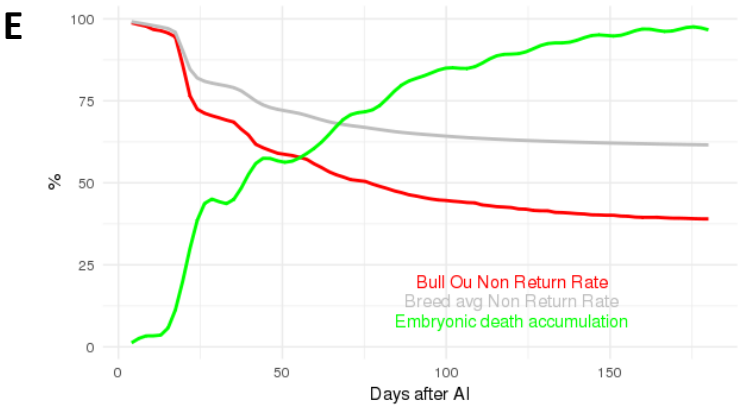
Note that the maternal grandmother of bull Ob was the first animal in which the haplotypes in linkage disequilibrium with the translocation co-occurred. The BTA18 haplotype was inherited from its own sire (which was genotyped) and the BTA21 haplotype from its dam (which was not genotyped). Furthermore, among seven genotyped offspring of this animal, we found only two combinations of BTA18-BTA21 haplotypes, instead of the four expected in the case of normal segregation. We concluded that the fusion probably occurred at the zygote stage in this female ancestor of Ob. Note also that panel E is missing due to insufficient number of AI to calculate the non-return rate.











F

Paternal grand sire			Paternal grand dam		
	haplo. BTA24	haplo. BTA29		haplo. BTA24	haplo. BTA29
1	GAGGGCGAGG	AAGACAGCAC	1	AGGGACGAGA	AAAACAGAGA
2	GAGAGCGAGG	ACACAAAAAA	2	AGGGACGAGA	ACACAAAAAA

Mat. grand sire: Healthy (598 tests)			Maternal grand dam		
	haplo. BTA24	haplo. BTA29		haplo. BTA24	haplo. BTA29
1	GAGGGCGAGG	AAAACAGAGA	1	GAGGGCGGGG	AAAACAGAGA
2	GAGAGCGAGG	AAGACAGCAC	2	GGGAGGGAAA	ACACAAAAAA

Sire: Healthy (760 tests)		
	haplo. BTA24	haplo. BTA29
1	GAGAGCGAGG	AAAACAGAGA
2	AGGGACGAGA	ACACAAAAAA

Dam		
	haplo. BTA24	haplo. BTA29
1	GAGAGCGAGG	AAGACAGCAC
2	GGGAGGGAAA	ACACAAAAAA

Presumed translocation apparition

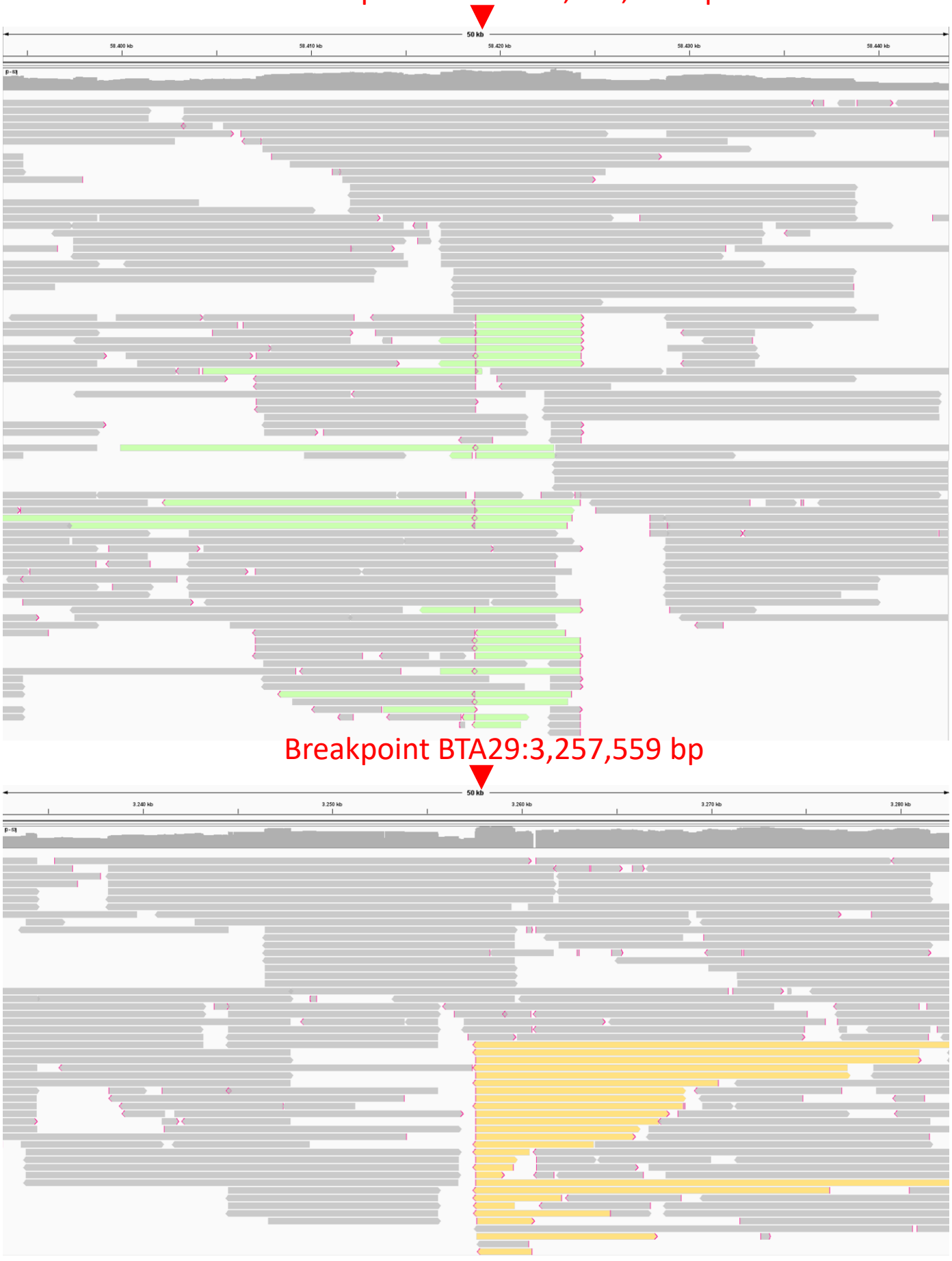
Daughter karyotyped		
	haplo. BTA24	haplo. BTA29
1	GGGAGGGAAA	AAGACAGCAC
2	GAGAGCAGGG	AAGACAAAAA

Bull Ou		
	haplo. BTA24	haplo. BTA29
1	GAGAGCGAGC	ACACAAAAAA
2	GGGAGGGAAA	AAGACAGCAC

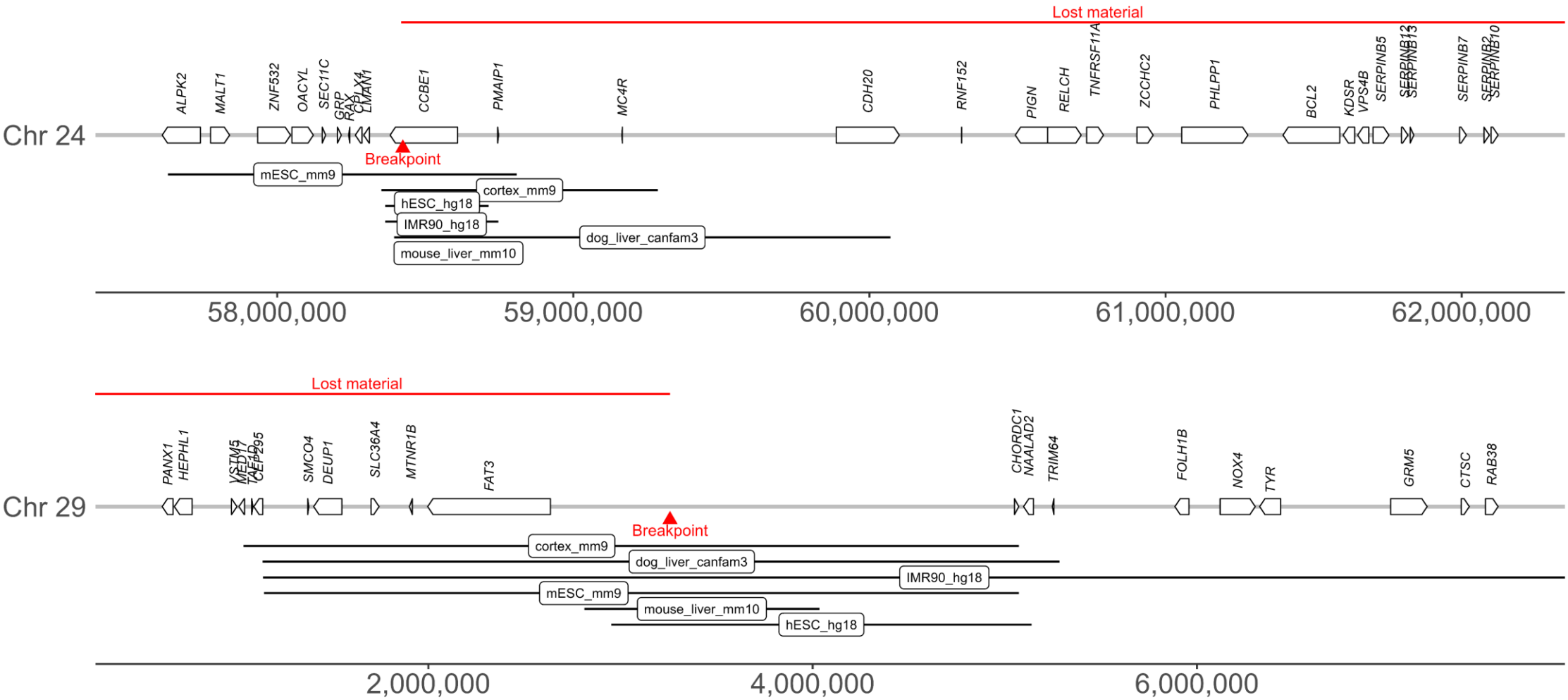
OU's half sister		
	haplo. BTA24	haplo. BTA29
1	GAGAGCAGAA	AAGACAGCAA
2	GGGAGGGAAA	ACACAAAAAA

Supplemental Figure S10. Information on t(24;29),-der29 and bull Ou. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of an affected daughter of Ou and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome combining information from cytogenetic analyses and long-read sequencing. *(E)* Daily non-return rate of inseminations performed with the semen of Ou semen compared to the average non-return rate of the breed. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of Ou based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives.

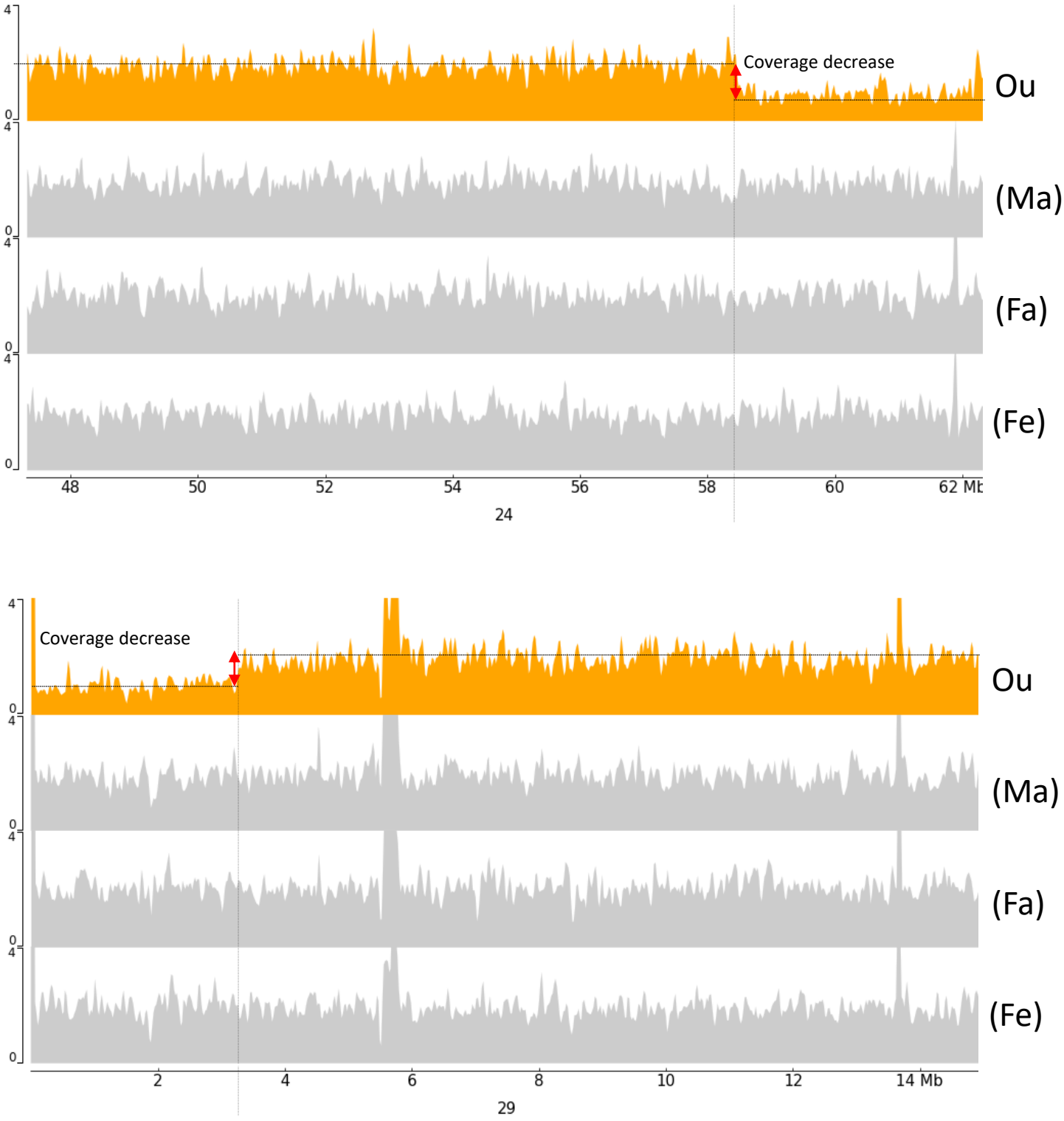
Note that bull Ou inherited the two haplotypes in LD with the translocation from its dam, which had other progeny carrying four different combinations of haplotypes, such as the half-sister shown which received only one of the haplotypes in LD with the IR (namely on BTA24). We concluded that the bull Ou was the first mutant and that the rearrangement was the result of an abnormal female meiosis.



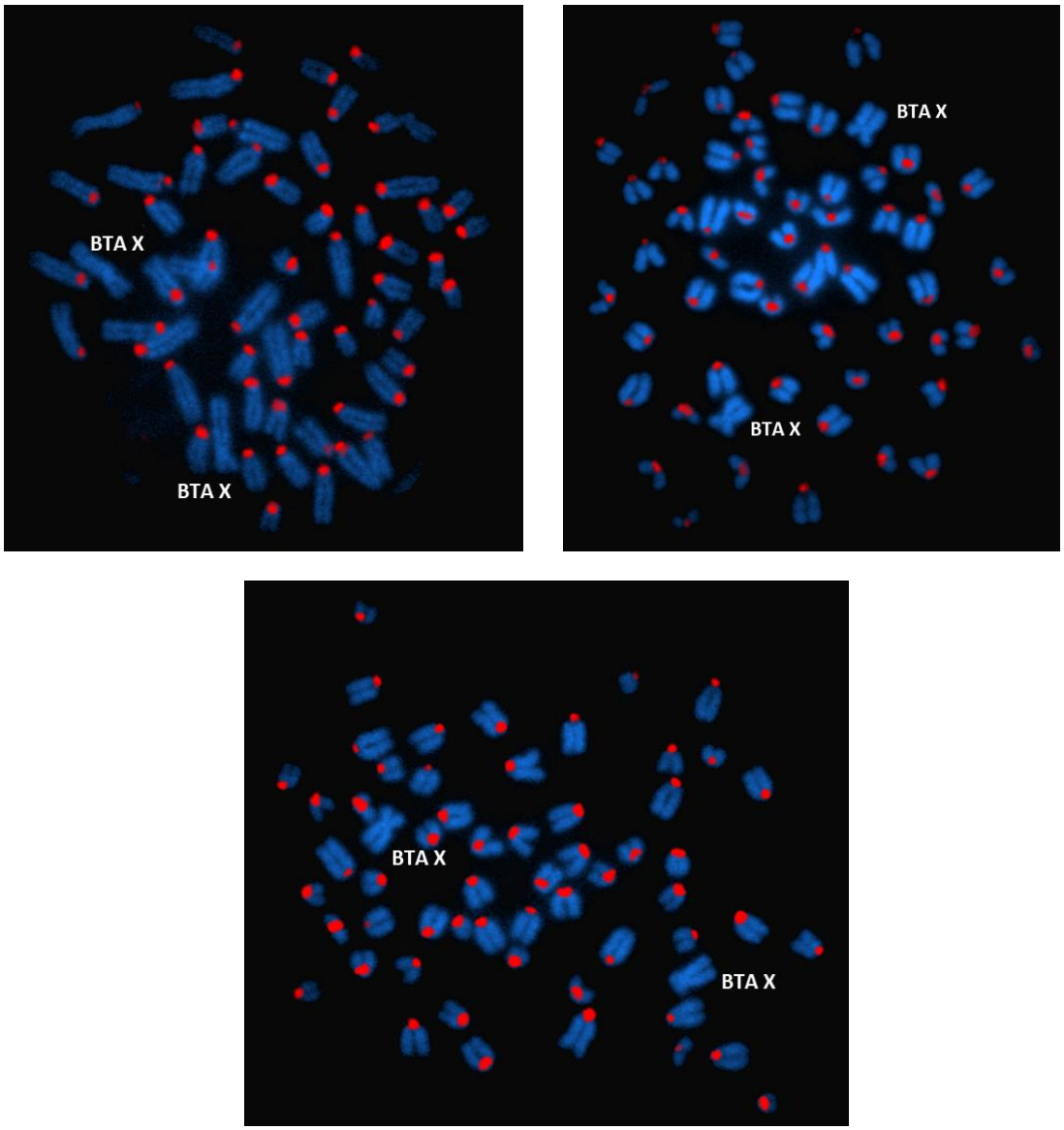
Supplemental Figure S10 (continued). *(G)* IGV screenshot of long read sequence alignments around the breakpoints +/-50kb on BTA24 and BTA29. Reads with partial alignment on the reciprocally translocated chromosome are highlighted in yellow and green.



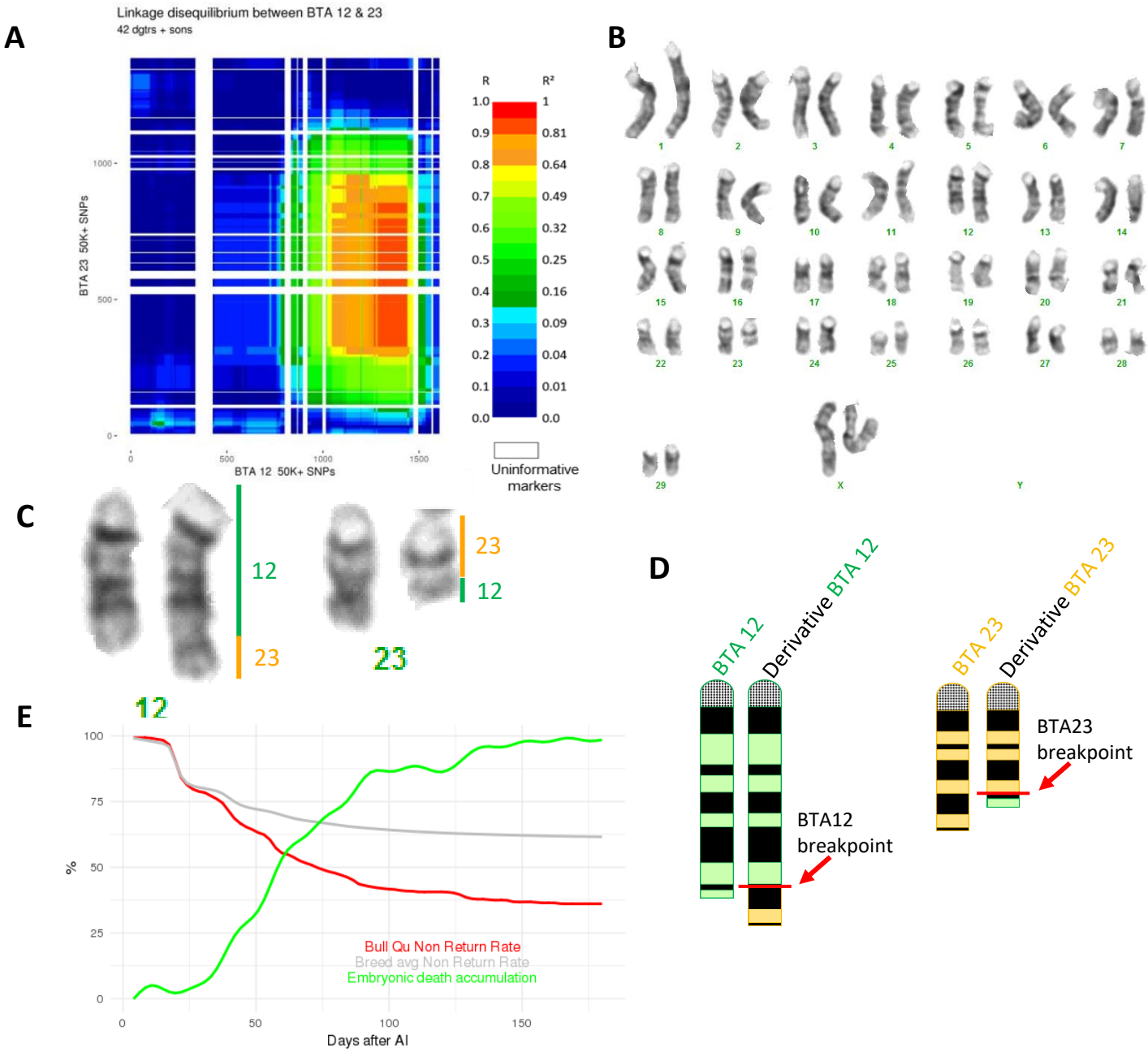
Supplemental Figure 10 (continued). *(H)* Annotated map of the chromosomal regions flanking the breakpoints for t(24;29) -der29 in bull Ou. Gene annotation has been obtained using Ensembl Biomart Tool. Information on TAD locations has been determined by orthology comparison with human, mouse and dogs (Wang et al.,2018). The tool liftOver was used to convert the positions of bovine UMD3.1 to ARS-UCD1.2 assembly.



Supplemental Figure S10 (continued). *(I)* Coverage rate analysis around chimeric reads in the sequence of Ou compared to three control sequences. Note the coverage decrease after 58.4 Mb in BTA24 and before 3.3 Mb in BTA29.



Supplemental Figure S10 (continued). *(J)* Full view of FISH (Fluorescence *In Situ* Hybridization) performed on three affected daughters of Ou. Counting of the red spots revealed the presence of only 57 autosomal centromeres, whereas 58 are expected in wild-type individuals.



F

Paternal grand sire		Paternal grand dam	
	haplo. BTA12	haplo. BTA23	haplo. BTA12	haplo. BTA23
1	AACGAGGAAA	GAGGAGGACG	1	GGCAGGGAAA	GAAAAAGACG
2	GACAGGGGAA	GAGGGGGAAG	2	**GGCAAGGGCA**	**GAGAAGGACG**

Mat. grand sire: Healthy (>1000 tests)			Maternal grand dam	
	haplo. BTA12	haplo. BTA23		haplo. BTA12	haplo. BTA23
1	GACAGGGAAA	GAAAAAGACG	1	NA	
2	AACAGCAGAA	GAGGAGGGCA	2		

Sire: Healthy (268 tests)		
	haplo. BTA12	haplo. BTA23
1	AACAGGGAAA	GAGGGGGACG
2	**GGCAGGGAAA**	**GAAAAAGACG**

Presumed translocation apparition

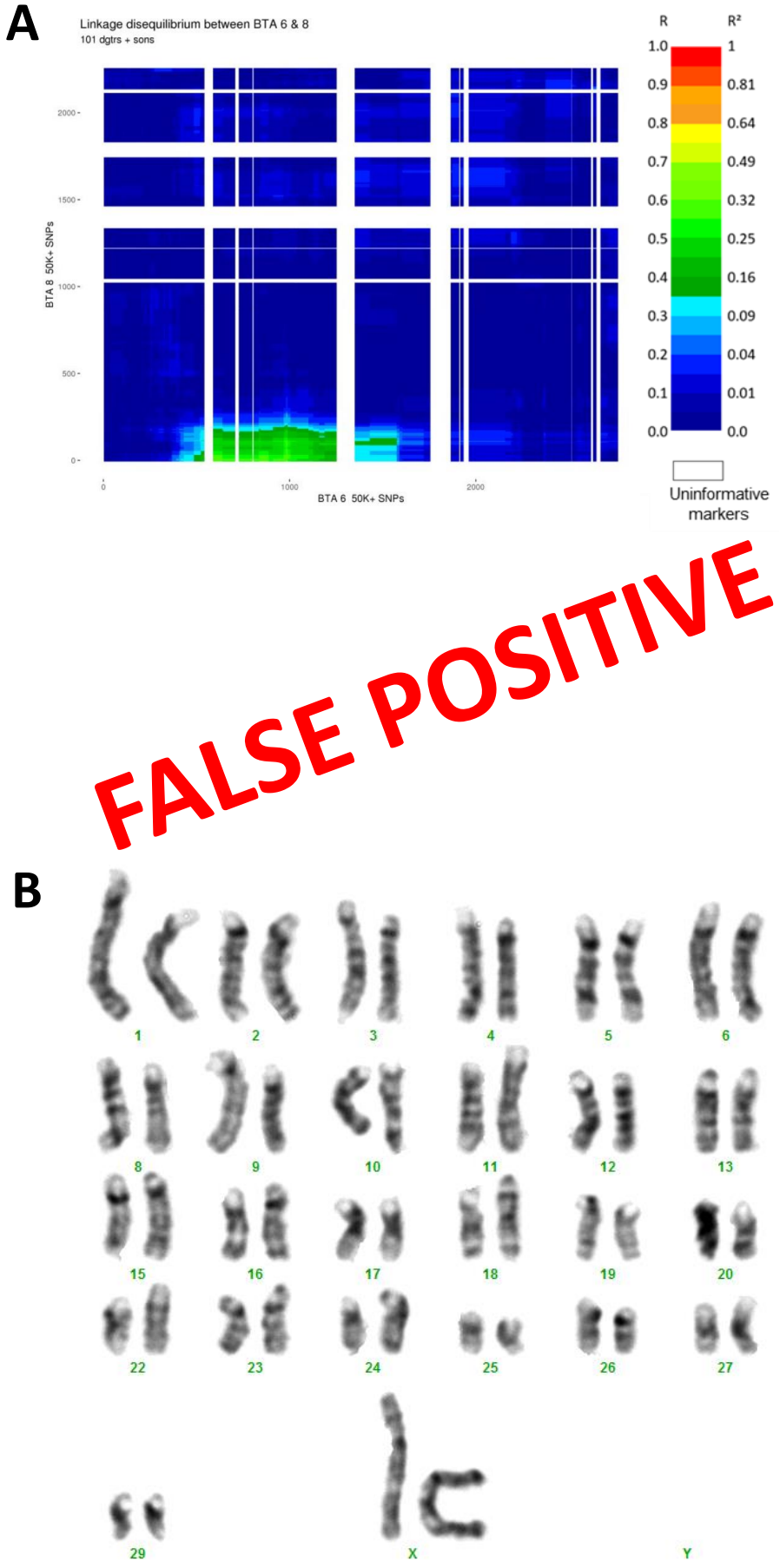
Dam		
	haplo. BTA12	haplo. BTA23
1	*AACAGCAGAA*	*GAGGAGGACG*
2	NA	NA

Bull Qu		
	haplo. BTA12	haplo. BTA23
1	**GGCAGGGAAA**	**GAAAAAGACG**
2	AACAGCAGAA	GAGGAGGACG

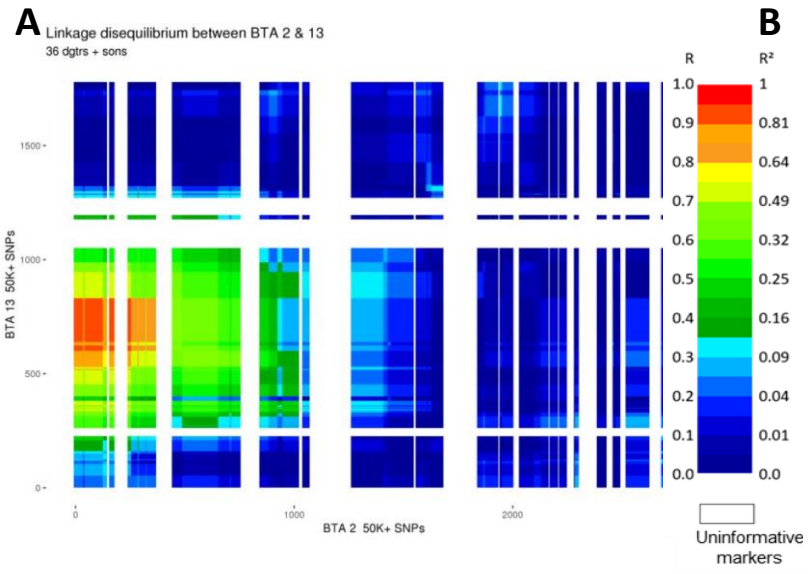
Daughter karyotyped		
	haplo. BTA12	haplo. BTA23
1	**GGCAGGGAAA**	**GAAAAAGACG**
2	GACAGGGAAA	GAGGAGGAAG

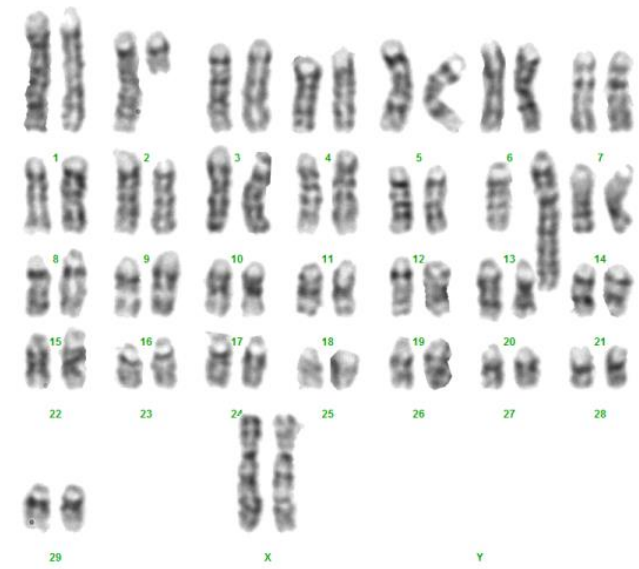
Supplemental Figure S11. Information on t(12;23) and bull Qu. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of an affected daughter of Qu and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome using information from cytogenetic analyses. *(E)* Daily non-return rate of inseminations performed with the semen of Qu semen compared to the average non-return rate of the breed. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of Qu based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives.

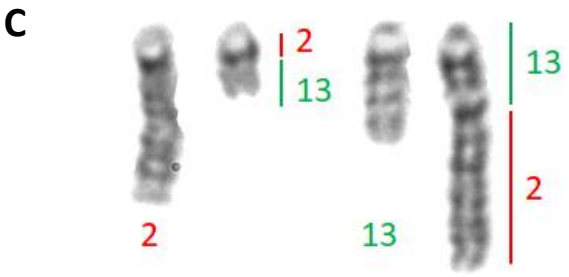
Note that bull Qu inherited the two haplotypes in LD with the translocation from its sire, which showed normal LD pattern in our initial screen. We concluded that the bull Qu was the first mutant and that the rearrangement was the result of an abnormal male meiosis.

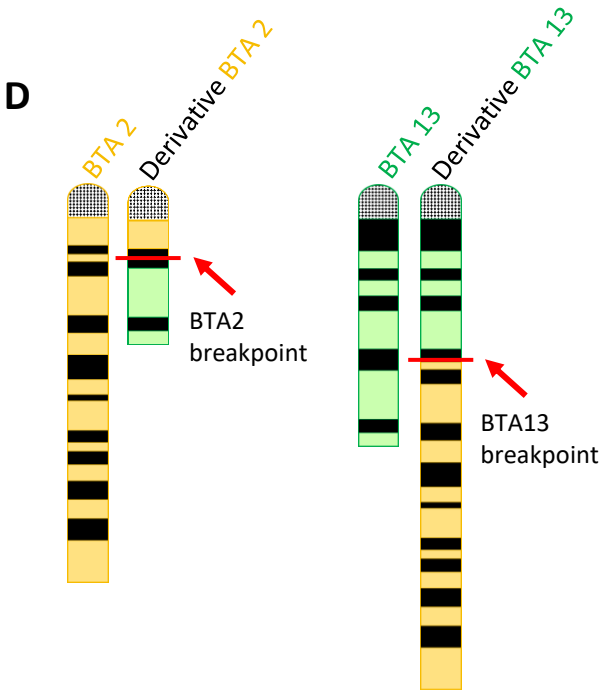


Supplemental Figure S12. Information on bull Ra. *(A)* Linkage disequilibrium heat map. *(B)* Complete GTG banding karyotype of an affected daughter of Ra.









F

Paternal grand sire			Paternal grand dam		
	haplo. BTA2	haplo. BTA13		haplo. BTA2	haplo. BTA13
1	AAGTAGAGGG	**AGAAAACGGA**	1	*TGAAAAAAGG*	*GAAGAACGGG*
2	AGAAAAGAAG	**AGAAAACGGA**	2	***TGATAGGAGG***	*AGAAAACGGG*

Mat. grand sire: Healthy (233 tests)			Maternal grand dam		
	haplo. BTA2	haplo. BTA13		haplo. BTA2	haplo. BTA13
1	TGAAAAAAGG	AGAAAACGGA	1	NA	*GAAGAACGGG*
2	AGAAAAGGAG	GAAGAAAAGA	2	*TGATAGGAAG*	NA

Sire: Healthy (353 tests)		
	haplo. BTA2	haplo. BTA13
1	AGAAAAGAAG	**AGAAAACGGA**
2	**TGATAGGAGG**	GAAGAACGGG

Presumed translocation apparition

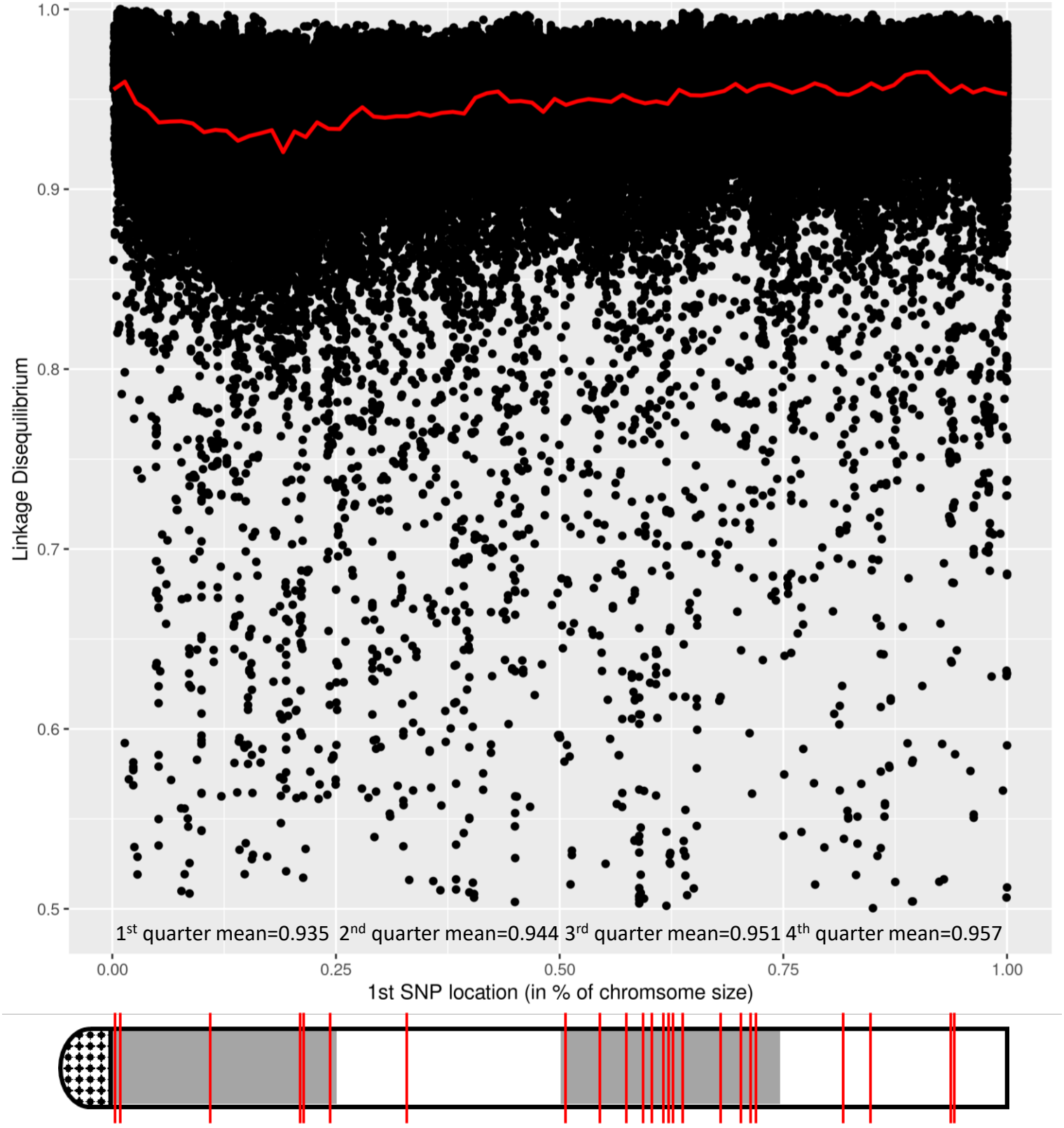
Dam		
	haplo. BTA2	haplo. BTA13
1	*TGAAAAAAGG*	*AGAAAACGGA*
2	*TGATAGGAAG*	*GAAGAACGGG*

Bull Sa		
	haplo. BTA2	haplo. BTA13
1	**TGATAGGAGG**	**AGAAAACGGA**
2	TGAAAAAAGG	GAAGAACGGG

Daughter karyotyped		
	haplo. BTA2	haplo. BTA13
1	**TGATAGGAGG**	**AGAAAACGGA**
2	AAGTAGAGGG	GAAGAAAAGA

Supplemental Figure S13. Information on t(5;28) and bull Sa. *(A)* Linkage disequilibrium heat map. *(B), (C)* Complete GTG banding karyotype of an affected granddaughter of Sa and annotated close-up of the rearranged chromosomes. *(D)* Schematic representation of the rearranged chromosome using information from cytogenetic. *(F)* Analysis of the transmission of the segments involved in IR in the pedigree of Sa based on haplotype information. 1) and 2) refer to the paternal and maternal phases, respectively. Haplotypes involved in the rearrangement are shown in bold and underlined. They are colored to match those of the original chromosomes. Italic haplotypes are inferred from the genotypes of relatives.

Note that bull Sa inherited the two haplotypes in LD with the translocation from its sire, which showed normal LD pattern in our initial screen. We concluded that the bull Sa was the first mutant and the rearrangement was that the result of an abnormal male meiosis. Note also that panel E is missing due to insufficient number of AI to calculate the non-return rate.



Supplemental Figure S14. Distribution of linkage disequilibrium in chromosome. The top graph was generated using LD calculations from the simulations performed with 100 bull progeny (same cohorts as in simulations, see 2nd paragraph in *Methods*). The LD between SNPs separated by 1.975 to 2.025 Mb was then drawn and a fitting curve traced with *ggplot2*. Note that the lowest LD level (*i.e.*, the highest level of recombination in meiosis) is reached in the first quarter of chromosomes. The third quarter, where we found more than half of the breakpoints, is a low region for meiotic recombination.