Supplementary Information

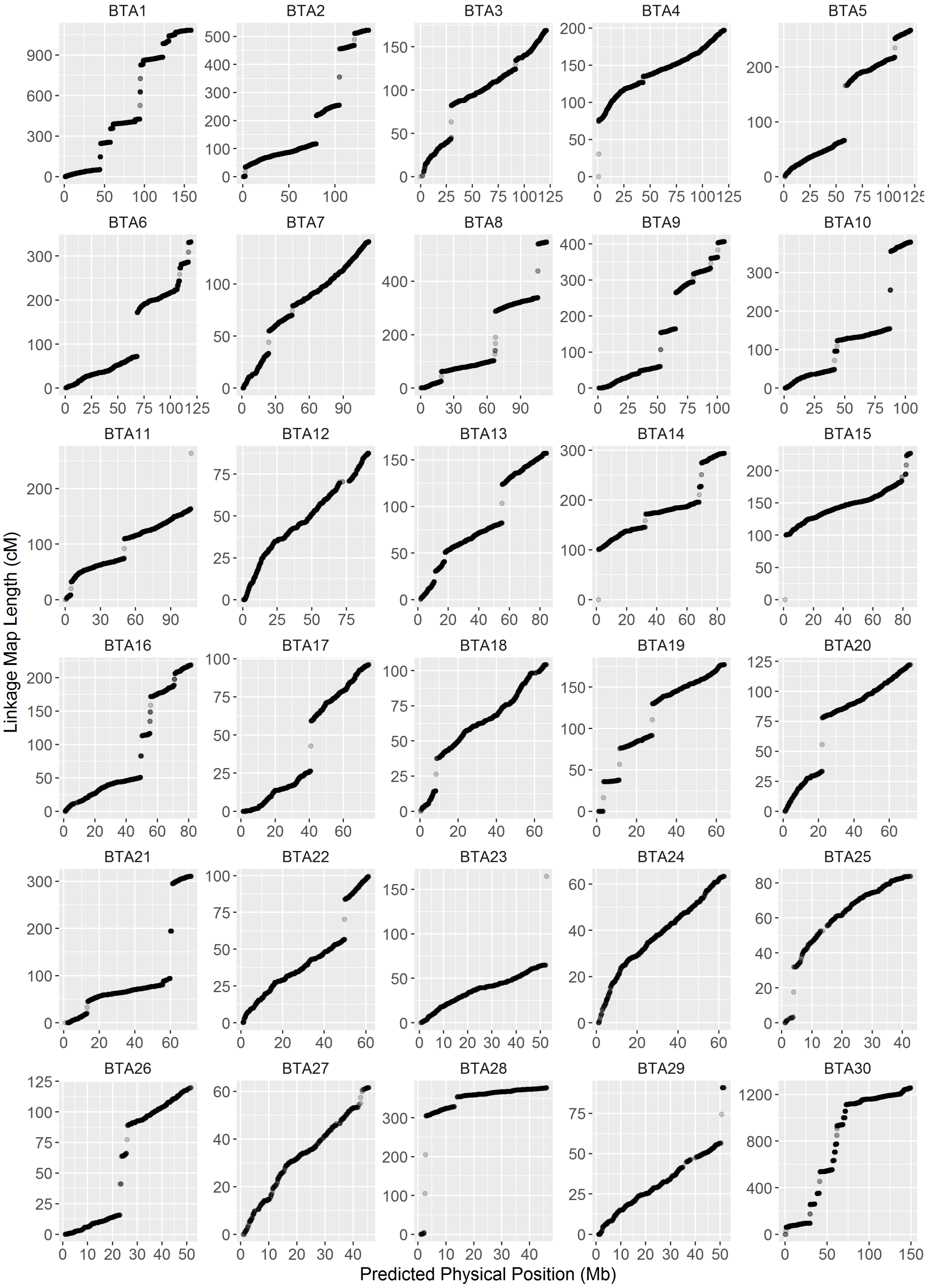

Figure S1: Build 1: Sex-averaged linkage maps assuming complete synteny of chromosomes and locus positions with the cattle genome. The x-axis gives the predicted cattle positions, and the y-axis gives the linkage map positions.

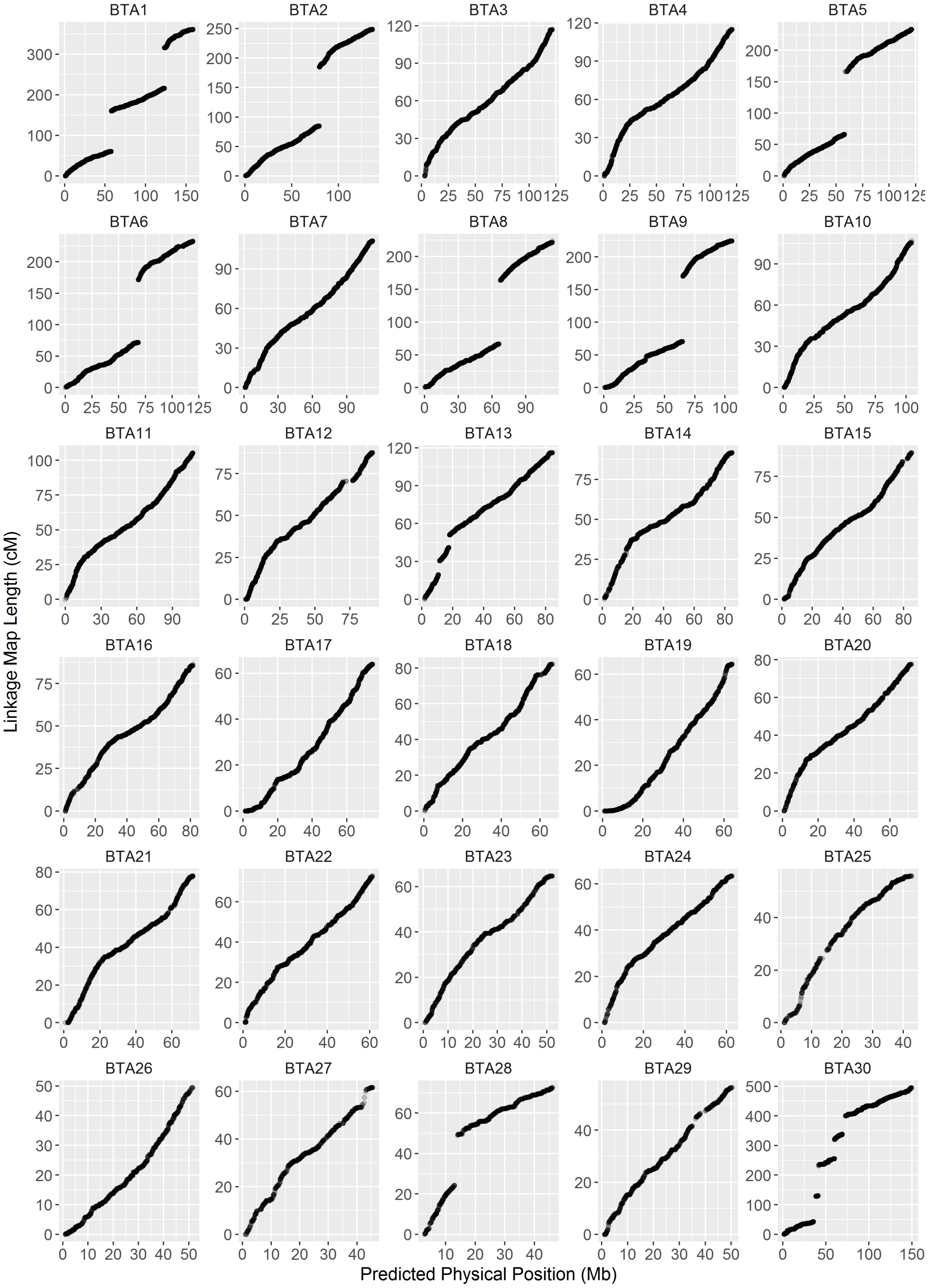

Figure S2: Build 2: Sex-averaged linkage maps after removing SNPs that were predicted to be wrongly mapped. Chromosome numbers are based on synteny with the cattle genome. The x-axis gives the predicted cattle positions, and the y-axis gives the linkage map positions.

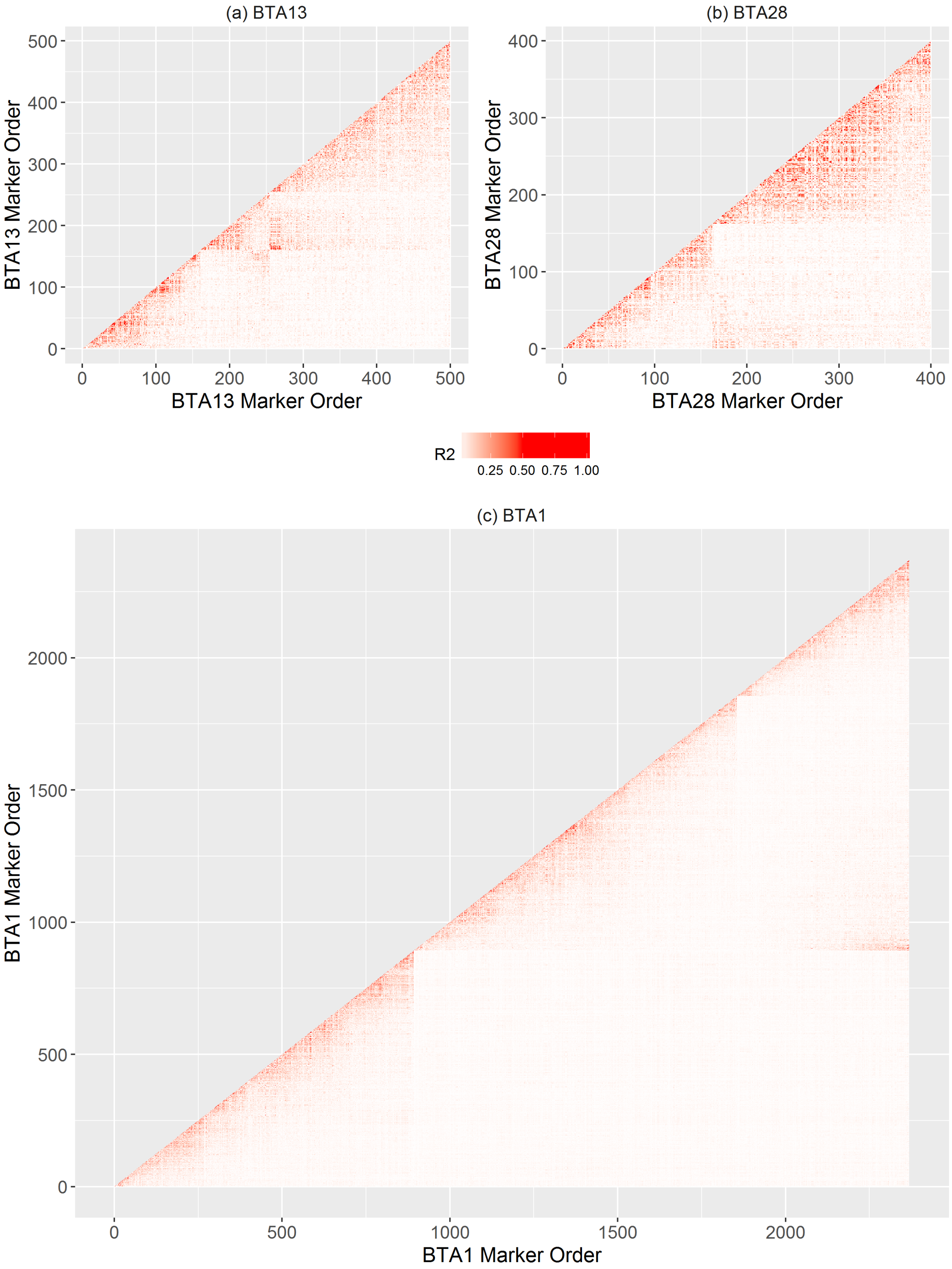

Figure S3: Patterns of LD (R^2) on (a) BTA13, (b) BTA28 and (c) all SNPs on BTA1.

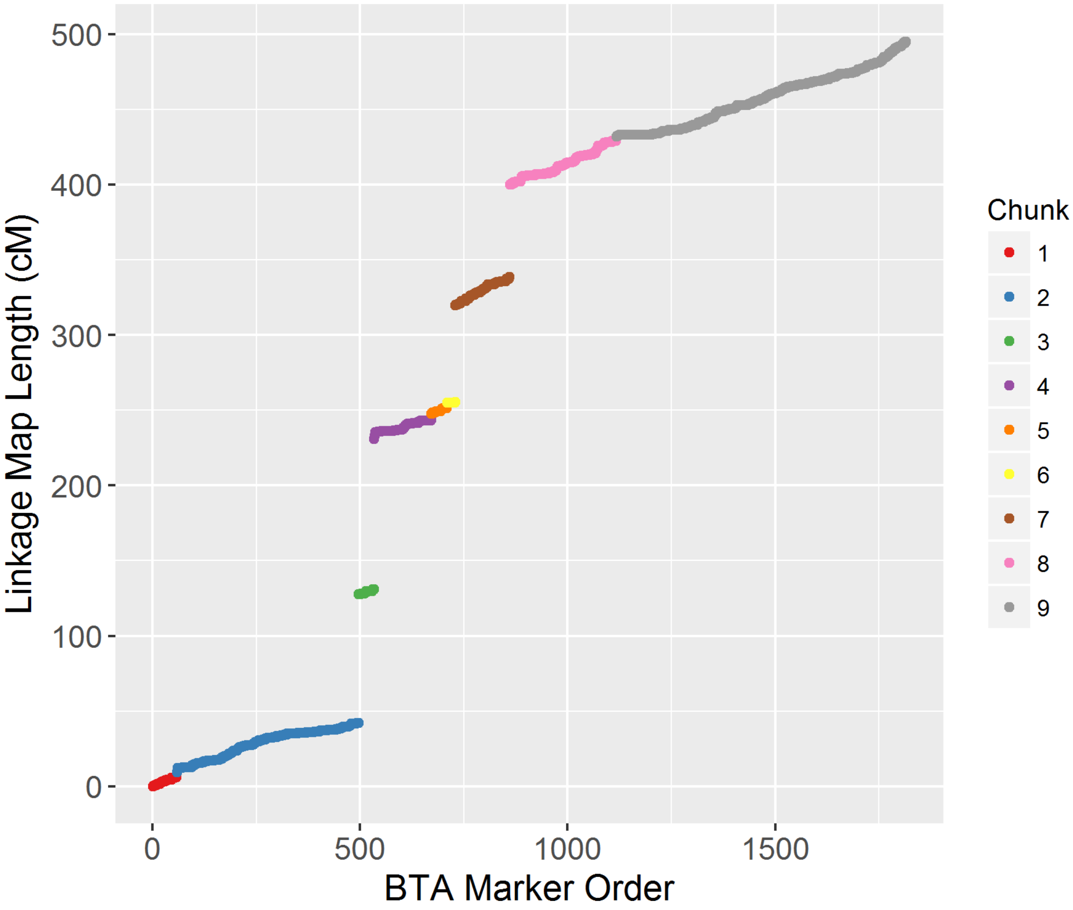

Figure S4: Marker order and linkage map distance on BTA30 (CEL34) after Build 2. Colours indicate chunks flanked by recombination fractions of $\geq$ 3cM.

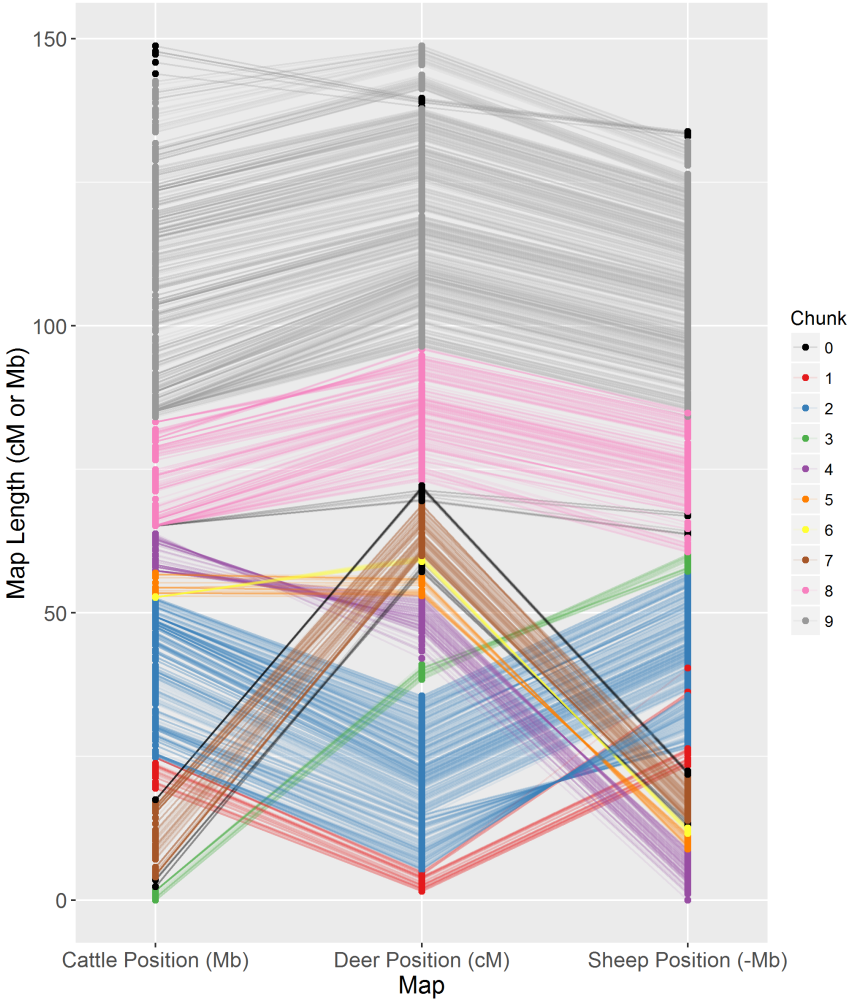

Figure S5: Comparison of map positions on the X chromosome between cattle (BTA30, distance in Mb from genome build BTA vUMD 3.0), deer (CEL34, distance in cM from Build 5) and sheep (OAR27, distance in Mb and reversed from genome build Oar_v3.1). Colours indicate chunks flanked by recombination fractions of $\geq$ 3cM in Build 2. Chunk 0 indicates markers unmapped in Build 2 that were retrospectively added to Build 5. Full data for this figure is provided in Table S2.

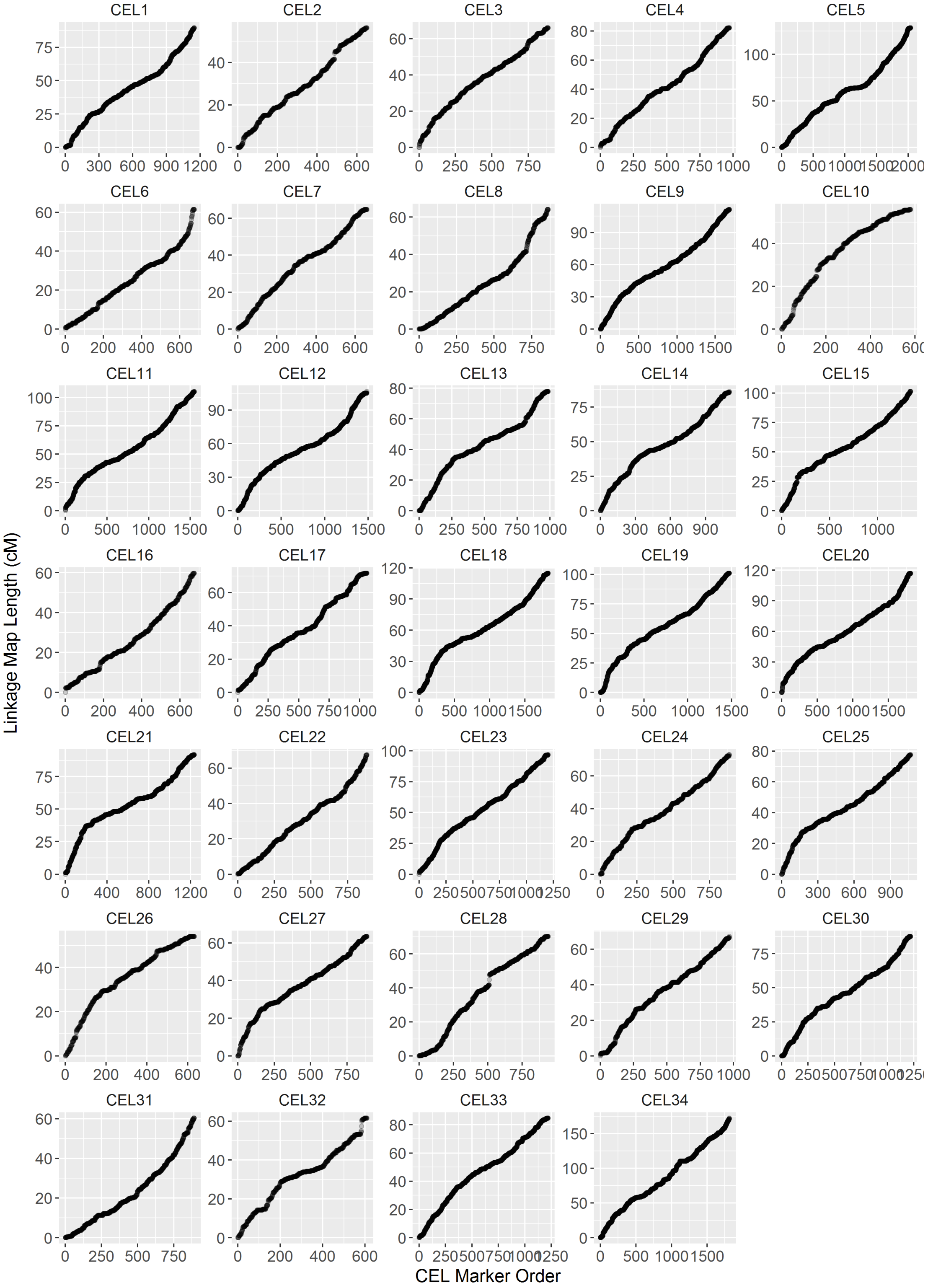

Figure S6: Build 3: Sex-averaged linkage maps after carrying out chromosomal re-arrangements outlined in the main text. Chromosome numbers are *Cervus elaphus* (CEL) linkage groups assuming grouping as in Slate et al (Slate *et al.*, 2002) (Table **??**). The x-axis gives the predicted order of the deer loci on the linkage groups after Build 3.

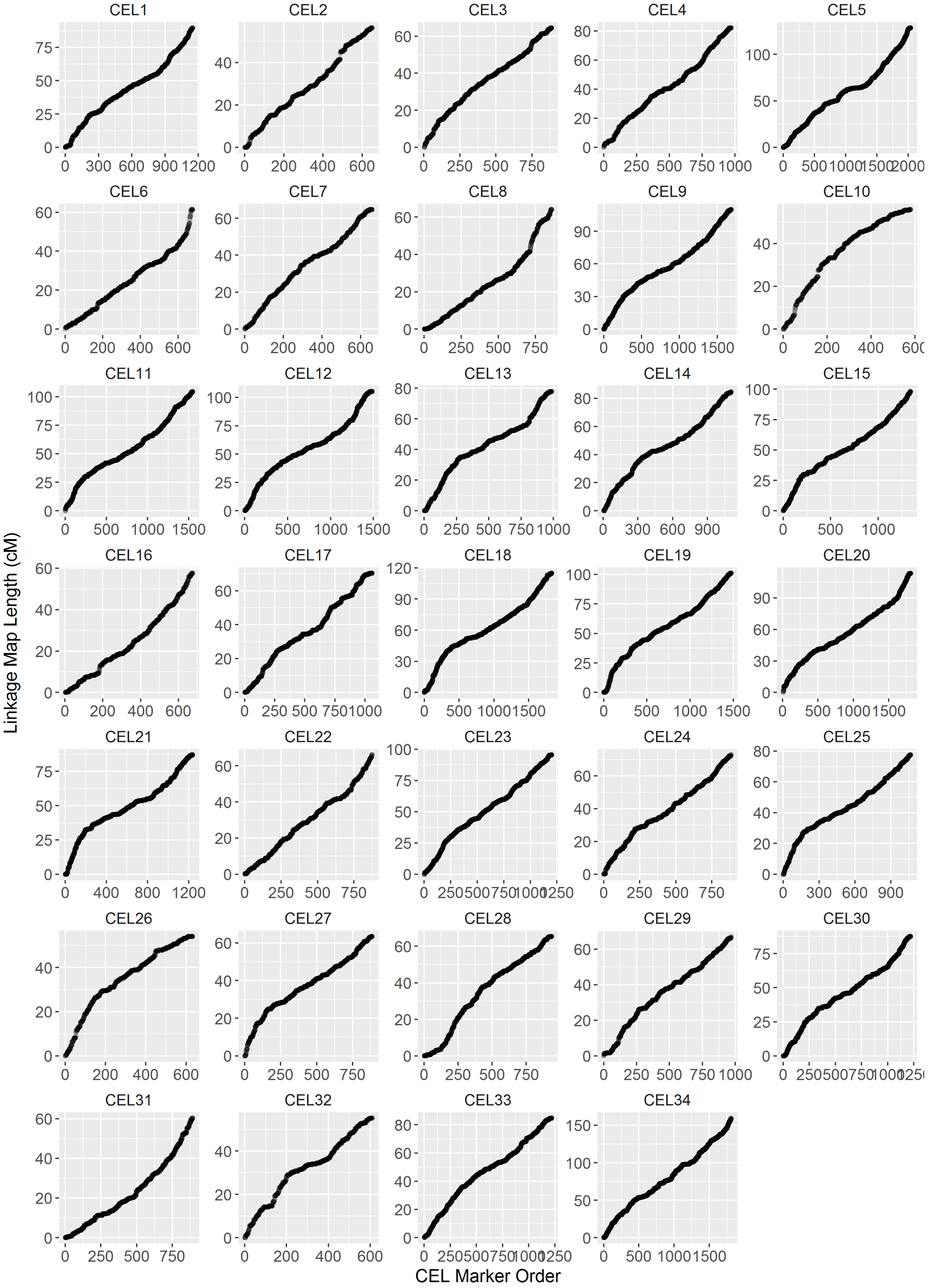

Figure S7: Build 4: Sex-averaged linkage maps after testing inversion and deletion of short chunks as outlined in the main text. Chromosome numbers are *Cervus elaphus* (CEL) linkage groups. The x-axis gives the predicted order of the deer loci on the linkage groups after Build 4.

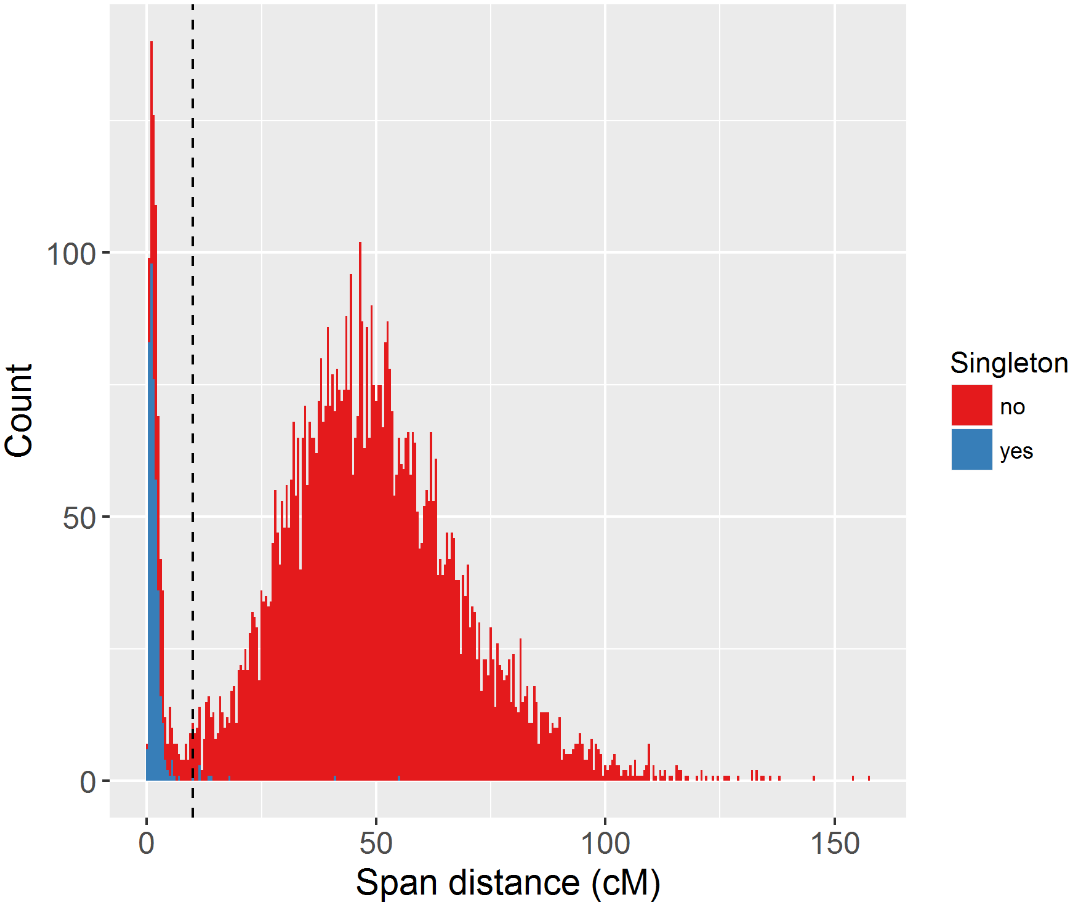

Figure S8: Histogram of the span distances (in Mb) between double crossovers on autosomal chromatids. Bar segments are colour coded as double crossovers spanning a single SNP locus (blue) and those spanning more than one SNP (red). All double crossovers across a single SNP were discarded from the dataset, as they are likely to be the result of a genotyping error at that SNP. Short crossovers below a span distance of 10cM were also discarded (see text for rationale)

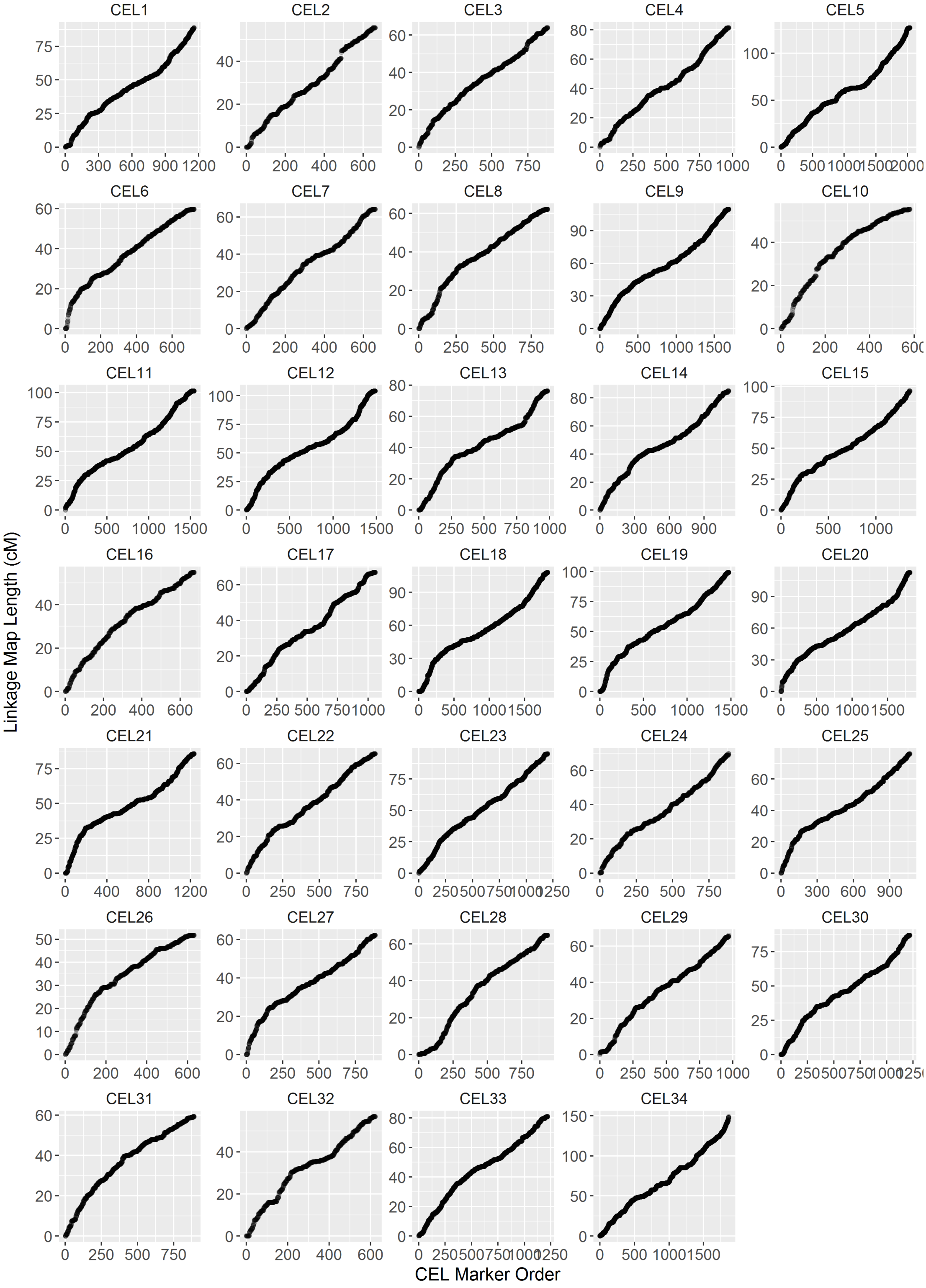

Figure S9: Build 5: Sex-averaged linkage maps after removing incorrectly-called double crossovers. Chromosome numbers are *Cervus elaphus* (CEL) linkage groups. The x-axis gives the predicted order of the deer loci on the linkage groups after Build 4, and the y-axis gives the linkage map positions.

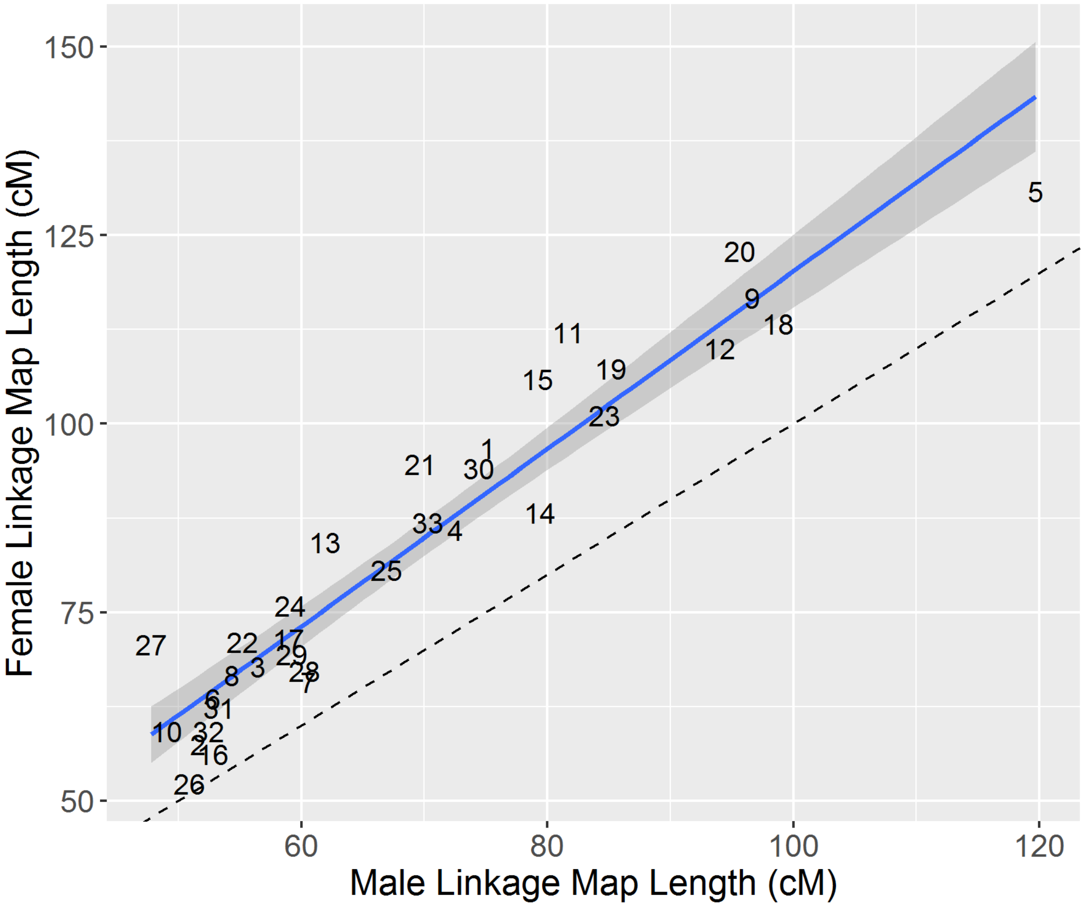

Figure S10: Correlation between male and female linkage map lengths (cM). The line and the gray-shaded area indicates the regression slope and standard error, respectively. The dashed line in C indicates where male and female linkage maps would be of equal length.

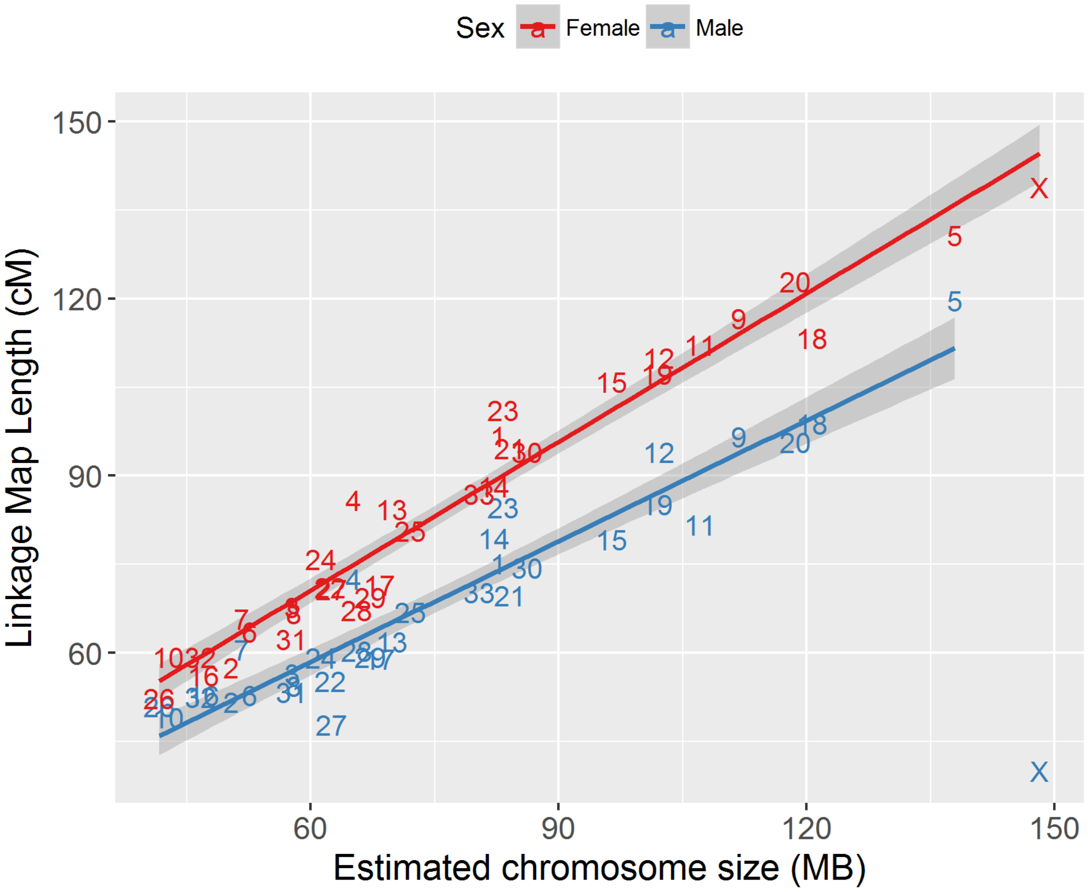

Figure S11: Sex-specific correlations between male and female linkage map lengths (cM). The line and the gray-shaded area indicates the regression slope and standard error, respectively.

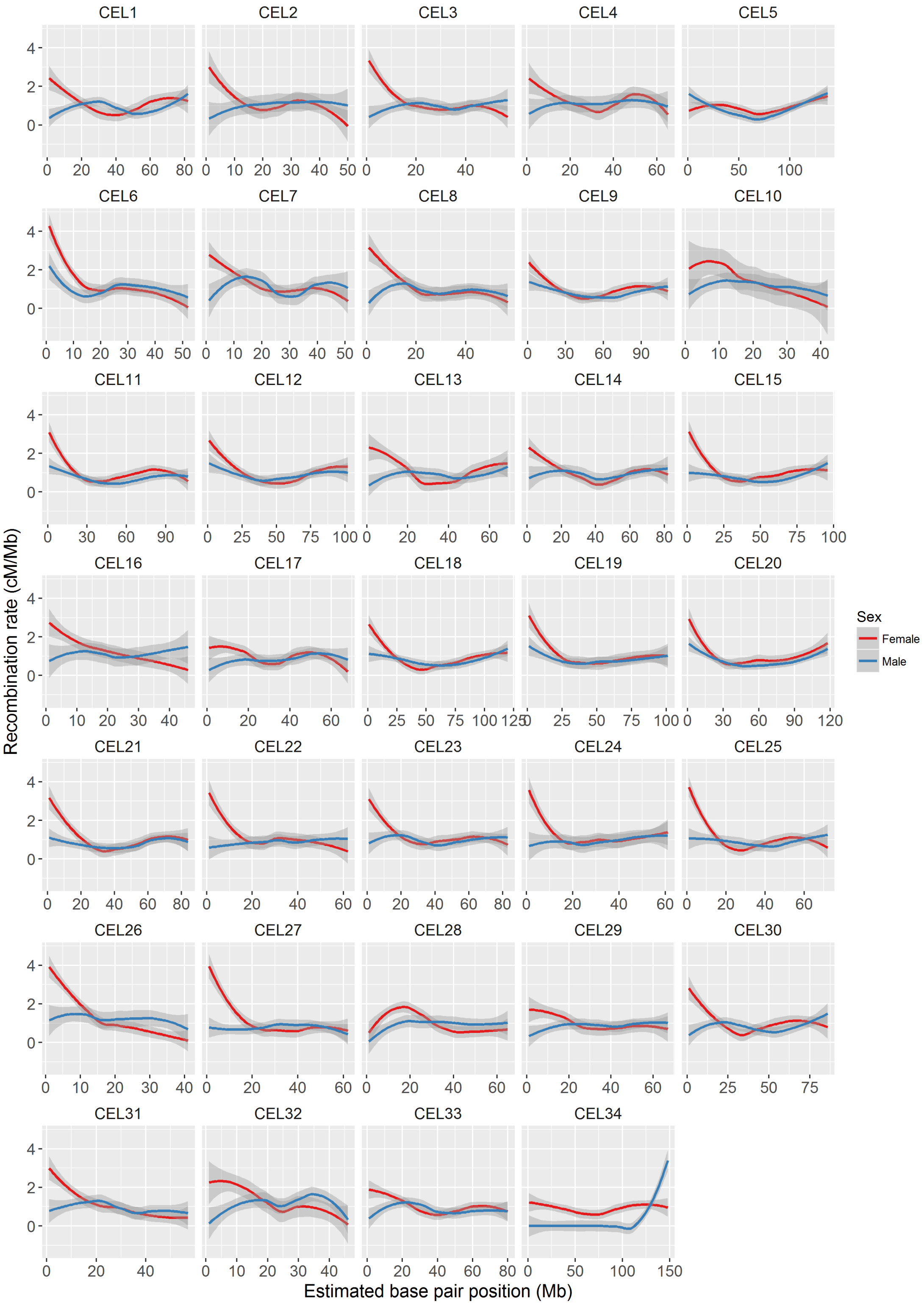

Figure S12: Loess smoothed splines of recombination rates in 1Mb windows across 33 autosomes for males and females. With the exception of one unknown linkage group, all chromosomes are acrocentric with the centromere at the beginning of the chromosome (Gustavsson & Sundt, 1968).

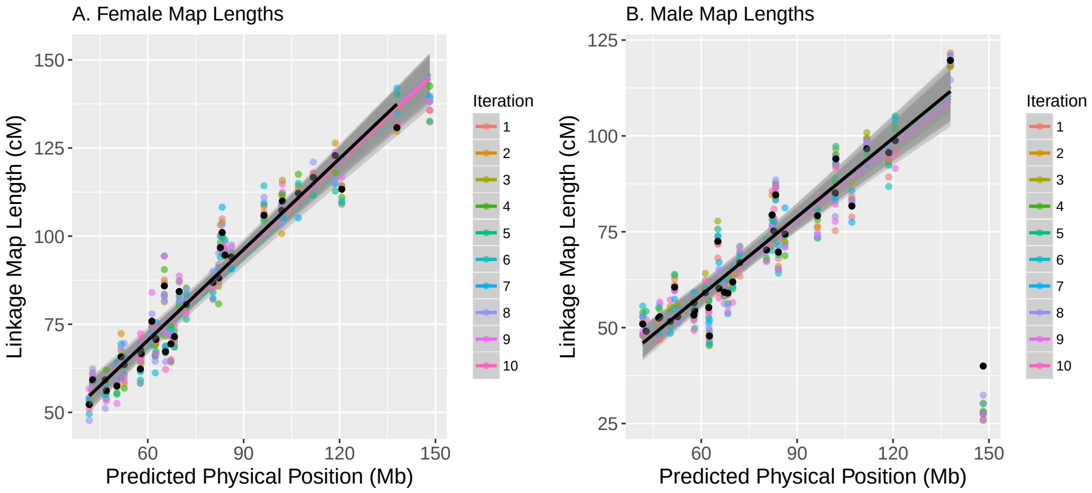

Figure S13: Correlations between the predicted physical position (Mb) and linkage map lengths (cM) for ten subsets of 483 females (A) and males (B) randomly sampled with replacement (coloured lines) and as observed in the data (black line).

Table S1: Rum red deer (*Cervus elaphus*) linkage map after Build 5. Table is provided in file TableS1_CervusElaphus_Final_Linkage_Map.txt Column header are as follows:

SNP.Name	SNP Name
BTA.Chr	cattle chromosome
BTA.Position	cattle base pair position (BTA UMD v3.0)
CEL.LG	Deer linkage group
CEL.Order	Marker order on deer linkage group
cMPosition.SexAveraged	sex-averaged linkage map position (cM)
cMPosition.Female	female linkage map position (cM)
cMPosition.Male	male linkage map position (cM)
Skeleton.SNP	indicates if SNP is included in the skeleton map (see main text)
PAR	indicates if SNP is in the pseudoautosomal region
Estimated.Mb.Position	the estimated genomic position on the deer genome (see methods)
inf.mei	number of informative meioses
inf.mei.PK	number of informative meioses where grandparental phase was known
tot_f	number of informative meioses in females
tot_m	number of informative meioses in males
pk_f	number of informative meioses in females with phase known
pk_f	number of informative meioses in males with phase known
A1	major reference allele
A2	minor reference allele
CallRate	SNP call rate in original dataset (N_{IDS} = 2361)
Q.2	minor allele frequency
PseudoAutosomalSNP	indicates if sex-linked SNPs (CEL34) are in the pseudoautosomal region.

Table S2: Data for Figure S5, comparison of map positions between Cattle (bp, build vUMD 3.0), Deer (cM, Build 5) and Sheep (bp, build Oar_v3.1) for the X chromosome. Table is provided in file TableS2_X_Cattle_Cervus_Ovis.txt.

Table S3: Predicted approximate positions of unmapped SNP loci from Build 5. Table is provided in file TableS3_Predicted_Positions_of_Unmapped_Loci.txt. Column headers are as follows:

Window.Start	cM position of the start of the window of most likely position
Window.Stop	cM position of the end of the window
CEL.LG	Deer linkage group identifier
SNP.Start	First mapped SNP at the start cM position
SNP.Stop	Last mapped SNP at the end cM position
chunk	chunk identifier
SNP.Start.Of.Chromosome	Indicates if the most likely position is at the beginning of the chromosome
SNP.End.Of.Chromosome	Indicates if the most likely position is at the end of the chromosome
Unmap.SNP.vec	Vector of SNPs within the unmapped chunk