602 Supplementary Information

Table S1: Fixed effect solutions for animal models outlined in Table 1.

Analysis	Effect	Estimate	S.E.	Z	P (Wald Test)
Both	Intercept	26.32	0.246	107.00	<2e-16
Both	Fhat3	-7.729	7.557	-1.02	0.306
Both	Male	-4.321	0.409	-10.57	<2e-16
Female	Intercept	26.309	0.272	96.70	<2e-16
Female	Fhat3	-7.103	9.58	-0.74	0.458
Male	Intercept	22.169	0.325	68.19	<2e-16
Male	Fhat3	0.097	11.392	0.009	0.993

Table S2: Genome-wide association study results for autosomal chromosome count (ACC) in both sexes and in males and females only. SNP.Name is the SNP identifier. BTA.Chromosome and BTA.Position are the chromosome and base pair position relative to the cattle genome vBTA_vUMD_3.1, respectively. CEL.LG and cMPosition.SexAveraged are the deer linkage group and centi-Morgan map position for each marker, respectively (JOHNSTON *et al.*, 2017). Sex indicates whether the analysis was carried out in both sexes ("all"), females ("f") or males ("m") only. CisTrans indicates whether the ACC value was used (cistrans) or whether total ACC minus the crossovers on that linkage group were used (trans). A1 and A2 are the SNP alleles, with effB the slope of the effect of allele A2, with standard error se_effB. P1df and Pc1df indicate the raw and genomic control corrected P-values at that SNP. ExpP is the corresponding P value for that locus assuming a null distribution of P-values (Figure 2 in main text). chi2.1df.adj is the genomic control-corrected $\chi^{[}2]$ value. Q.2 is the minor allele frequency at that locus.

File: TableS2_Cervus_ACC_GWAS_Results.txt

Table S3: Regional heritability results for autosomal chromosome count (ACC) in both sexes and in males and females only. Analysis.ID is the unique identifier for the model. RRID.Sex indicates association for both sexes, males or females. model1.Li and model2.Li are the log Likelihood values for models excluding and including the 20 SNP window, respectively. CEL.LG is the deer linkage group. Start.Order and Stop.Order are the order position of the first and last SNP in the window relative to the chromosomes linkage map in Johnston et al 2017. Cumu.Start.Position and Cumu.Stop.Position are the same as before, but the cumulative order across the genome (from CEL1 to CEL33). Start.Position, Stop.Position, Start.Cumu.Position, Stop.Cumu.Position are as before, with the estimated base pair positions from Johnston et al 2017. Start.BTA.Position and Stop.BTA.Position are the positions relative to the cattle genome vBTA_vUMD_3.1. The prefix Mid indicates the position halfway between the start and stop positions as before. Window.bp is the estimated base pair size of the window. Start.SNP.Name and Stop.SNP.Name are the SNP identifiers for the first and last SNP of the window. Chi2 is the χ^2 statistic of a likelihood ratio test with 1 d.f. and P is the associated P-value.

File: TableS3_Cervus_ACC_Regional_Heritability_Results.txt

Table S4: Regional heritability results for autosomal chromosome count (ACC) in both sexes and in males and females only for the most highly associated region on deer linkage group 12. This analysis was run for sliding windows of 6, 10 and 20 SNPs overlapping by n-1 SNPs, where n the number of SNPs in the window. Headers are for Table S3.

File: TableS4_Cervus_ACC_Regional_Heritability_Results_sig_region.txt

Table S5: Effect sizes from animal models of female autosomal crossover count for alleles of 10 SNP haplotypes spanning *cela1_red_10_20476277* to *cela1_red_10_20939342* relative to all other haplotypes. Genotype indicates whether the haplotype was heterozygous (A/B) or homozygous (B/B) relative to all other haplotypes in the model. Count indicates the number of ACC measures for that genotype, and Count A/A indicates the number of genotypes that did not contain that haplotype.

Haplotype	Genotype	Solution	S.E.	Z.ratio	Count	Count A/A	P <0.05
AAAAAGGAAA	A/B	-0.702	1.704	-0.412	14	849	
AAAAGGGGAG	A/B	0.961	0.542	1.774	240	597	
	B/B	0.58	1.369	0.424	26	597	
AAAGAGGAAG	A/B	1.616	1.423	1.135	33	830	
AAGGAAGAAA	A/B	-1.381	0.892	-1.548	84	779	
AGAAAGAAGG	A/B	0.086	2.182	0.04	11	852	
AGAAAGGGGG	A/B	-0.75	1.189	-0.631	36	827	
AGAGAAGAAA	A/B	-1.79	1.78	-1.006	19	844	
AGAGAAGAGA	A/B	-2.244	1.005	-2.233	68	795	*
AGGAAGAAGG	A/B	-1.515	1.05	-1.443	57	806	
AGGAGAGAAG	A/B	2.387	0.573	4.166	160	690	*
	B/B	8.701	1.73	5.029	13	690	*
AGGAGAGAGA	A/B	-0.75	0.512	-1.465	335	455	
	B/B	-1.354	0.966	-1.402	73	455	
AGGAGGGGGG	A/B	0.071	1.077	0.066	56	807	
AGGGAGAAGG	A/B	-0.984	2.049	-0.48	10	853	
GGAGAAGAAA	A/B	0.421	0.723	0.582	126	737	
GGAGAAGAGA	A/B	0.949	1.533	0.619	25	838	
GGGAAGAAGG	A/B	-0.408	1.094	-0.373	50	813	
GGGGAGGGGG	A/B	-0.507	0.626	-0.81	158	702	

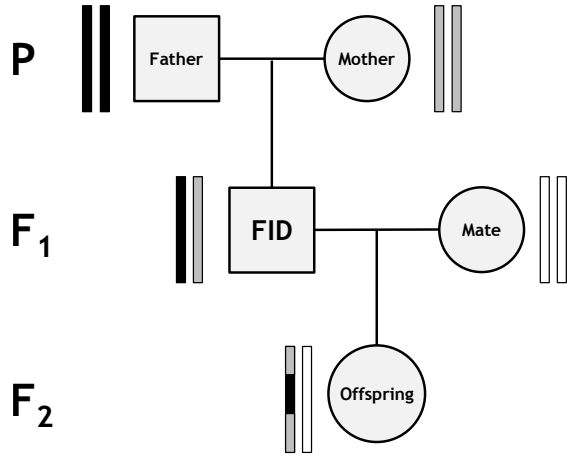

Figure S1: Sub-pedigree structure used to phase chromatids transferred from the focal individual (FID) to its offspring (indicated by the grey arrow). Rectangle pairs next to each individual represent chromatids, with black and grey shading indicating chromosome or chromosome sections of FID paternal and FID maternal origin, respectively. White shading indicates chromatids for which the origin of SNPs cannot be determined.

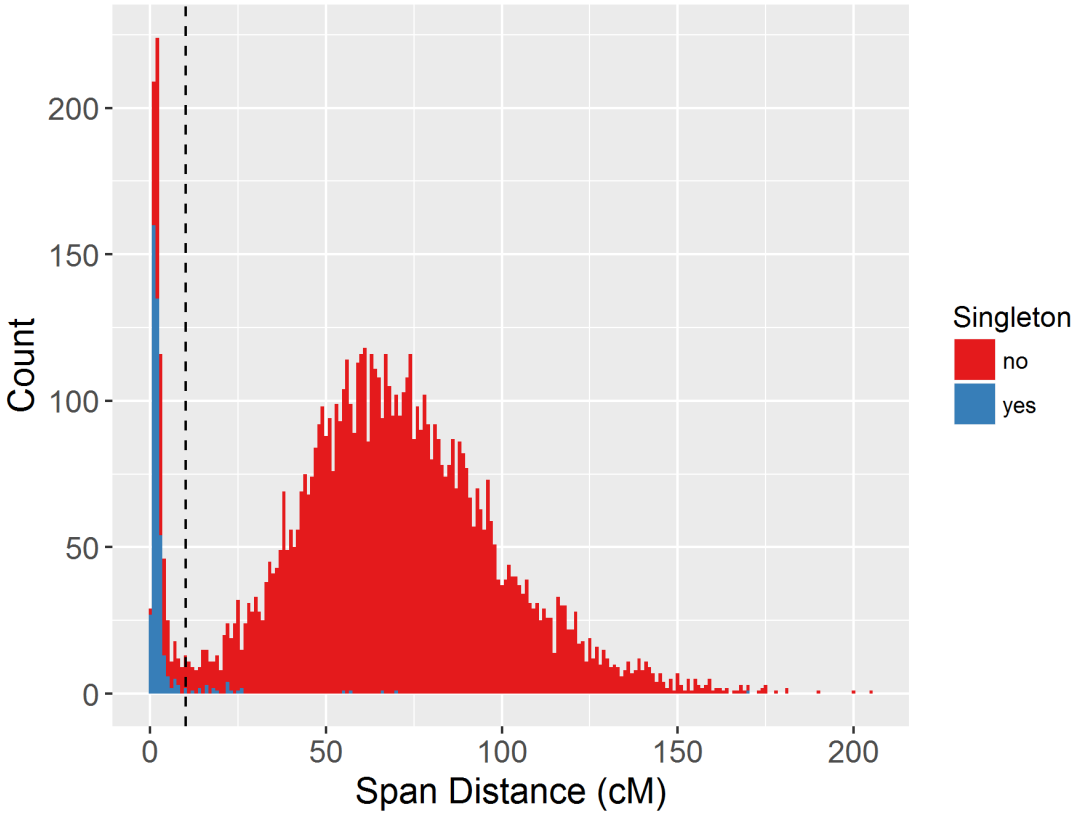

Figure S2: Histogram of the span distances (in cM) between double crossovers on autosomal chromatids. Bar segments are colour coded as double crossovers spanning a single SNP locus (blue) and those spanning more than one SNP (red). All double crossovers across a single SNP and below a span distance of 10cM were discarded (as indicated by the vertical dashed line).

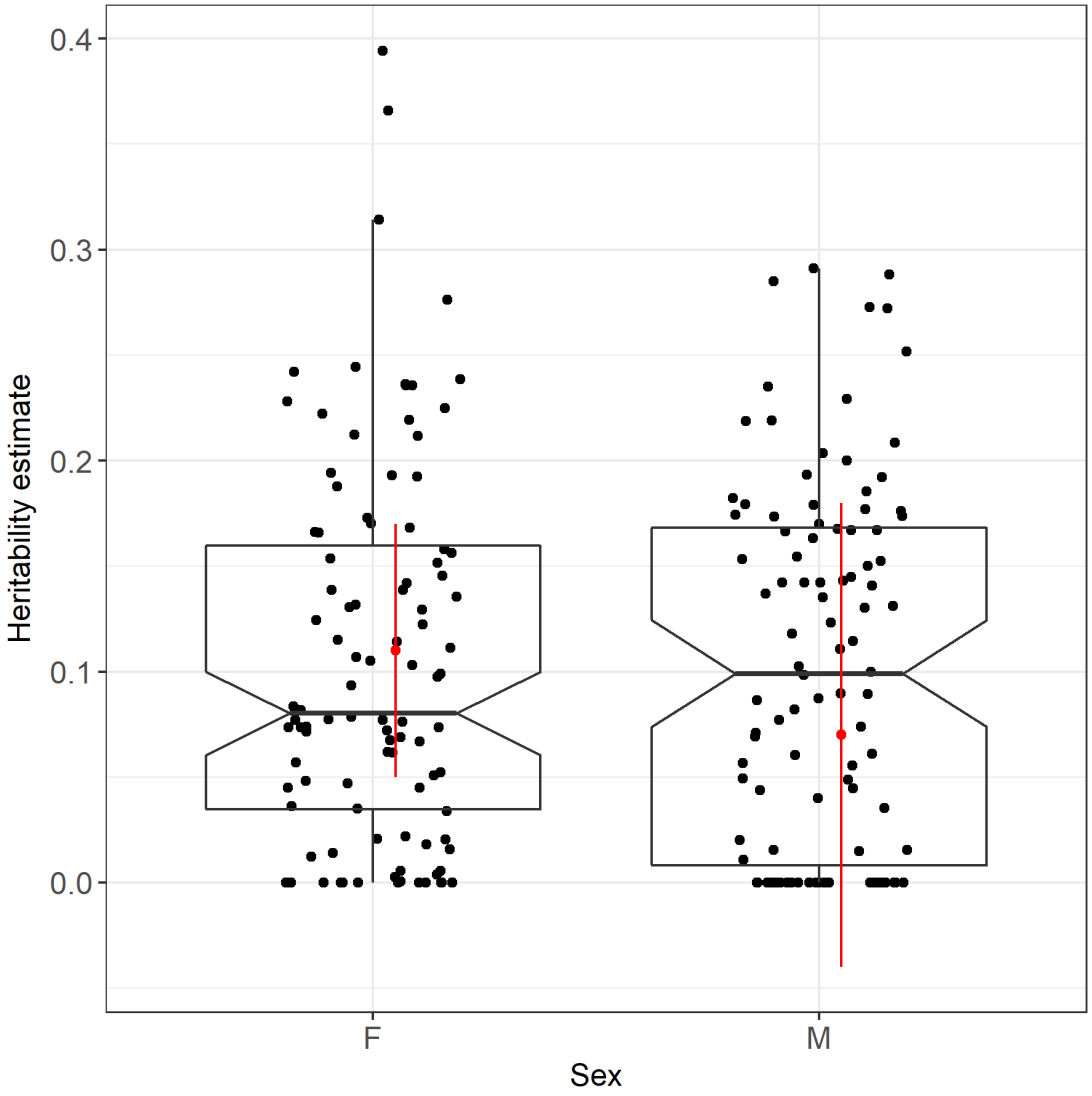

Figure S3: Barplot of male and female heritability point estimates from sampling with replacement of 482 measures within each sex. The red point with error bars represents the estimate from the full dataset as outlined in Table 1.

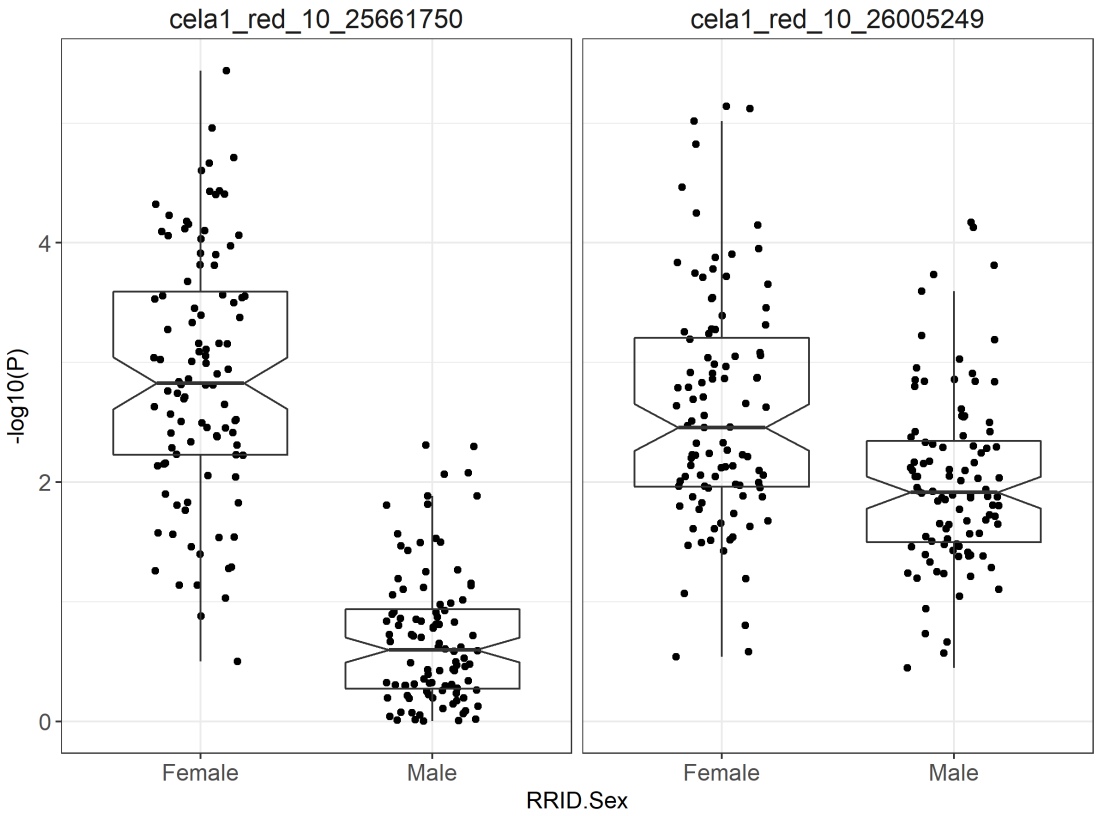

Figure S4: Barplot of association statistics between male and female ACC and genotypes at the two most highly associated GWAS loci. Each point represents association from sampling with replacement of 482 measures within each sex.

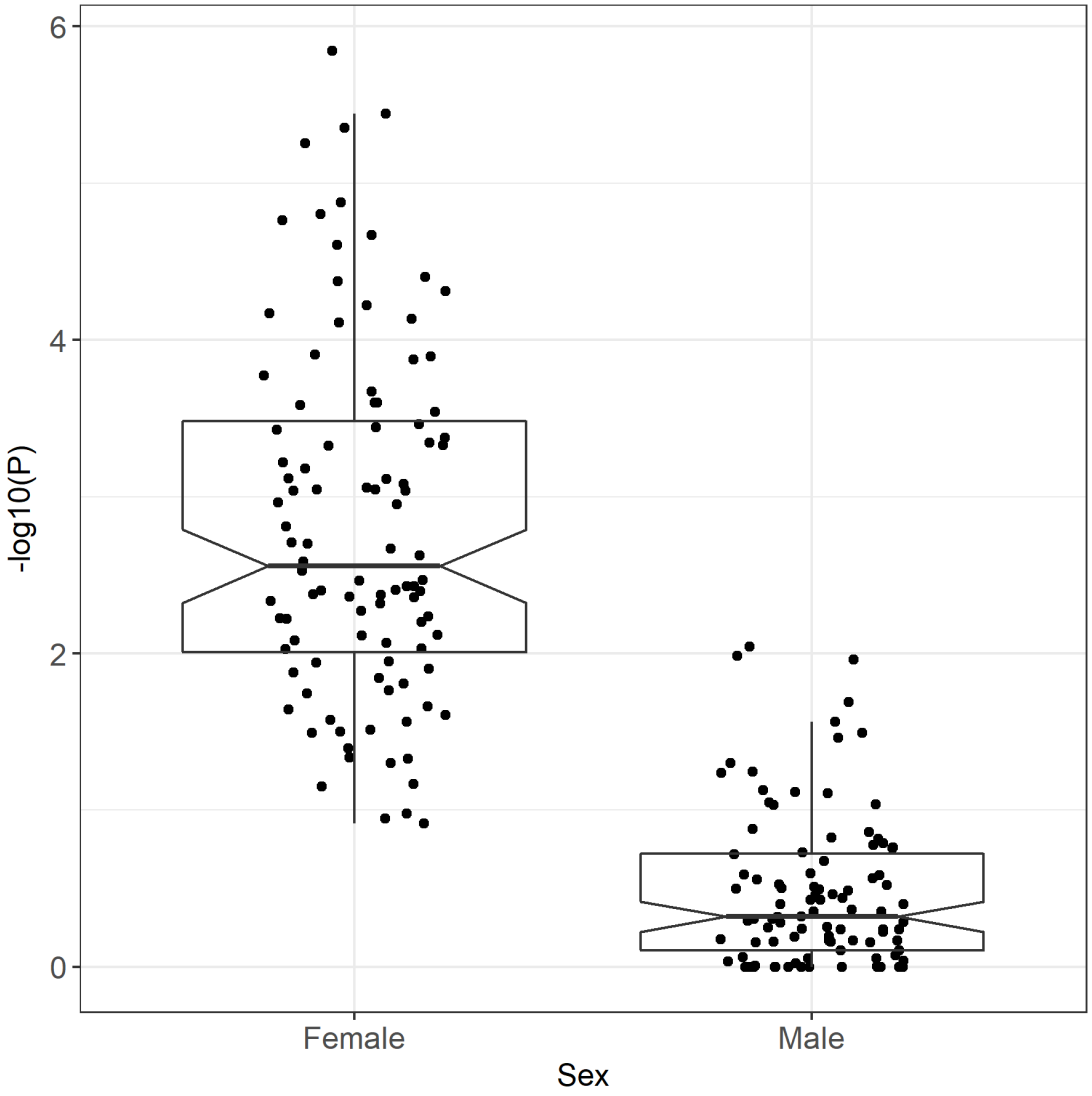

Figure S5: Barplot of association statistics between male and female ACC and the most highly associated region from the regional heritability analysis (Table 3). Each point represents association from sampling with replacement of 482 measures within each sex.

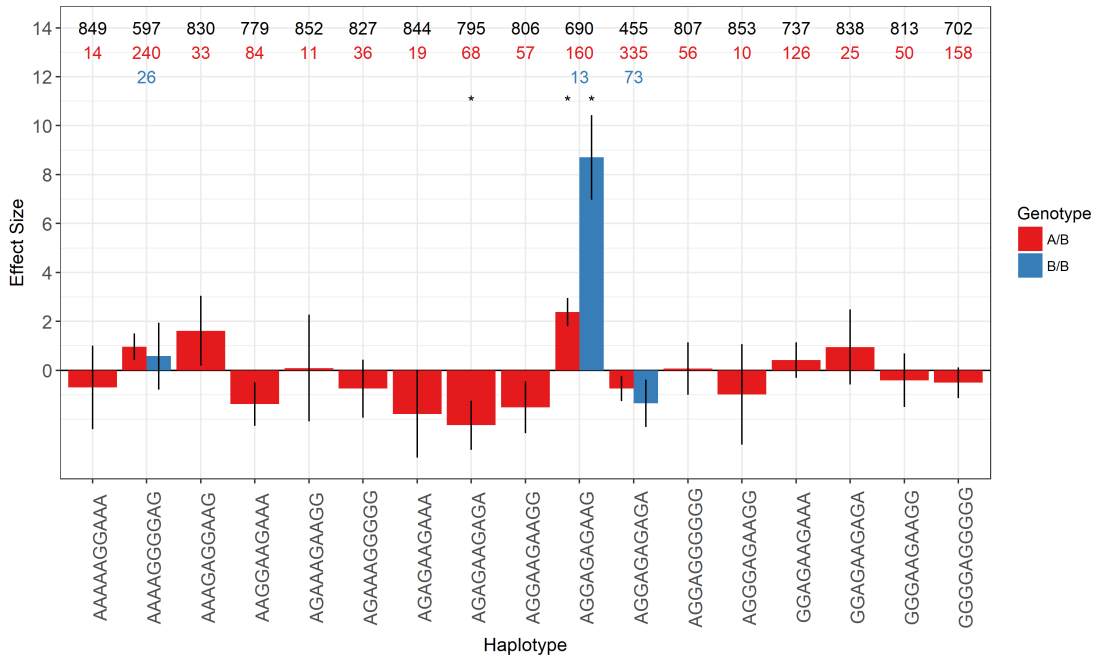

Figure S6: Barplot of association statistics between female ACC and haplotypes at the most highly associated region from the regional heritability analysis. A full description and the data underlying this figure is provided in Table S4. Sample sizes are provided above and are colour-coded by the bar. Numbers in black text indicate the sample size for genotype for all other haplotypes.