Additional_file_1: Manhattan plots of GWAS results. Shown is the significance of association [-log10(p)] between SNPs across the bovine genome and the target traits from the two groups feed efficiency (A-C) and metabolites (D-N). The red line marks the significance level of p=0.05 before correction for multiple testing. SNPs above this line theoretically had the chance to be represented via a gene in the AWM.

(A) residual feed intake (RFI), **(B)** feed conversion rate (FCR), **(C)** daily energy intake (dEI), **(D)** arginine, **(E)** lysine, **(F)** free carnitine (C0), **(G)** acetylcarnitine (C2), **(H)** valerylcarnitine (C5), **(I)** suberylcarnitine (C8:1), **(J)** myristylcarnitine (C14), **(K)** stearoylcarnitine (C18); **(L)** diacylphosphatidylcholine C32:0 (PC_aa_C32:0), **(M)** acylethylphoshatidylcholine C36:1 (PC_ae_C36:1), **(N)** sphingomyelin C20:2 (SM_C20:2).

### (A) Residual feed intake (RFI)
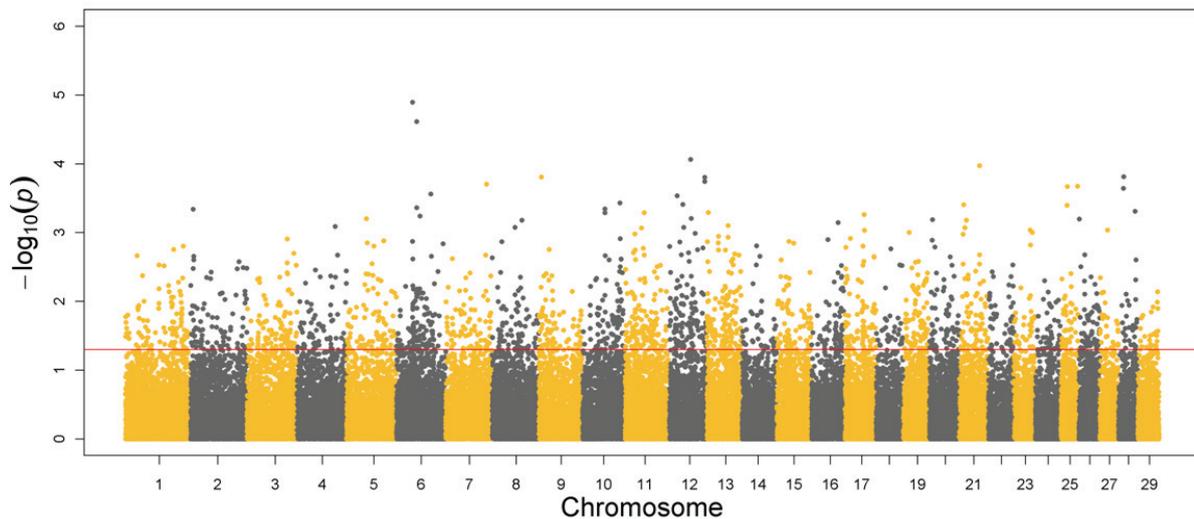

(B) Feed conversion rate (FCR)
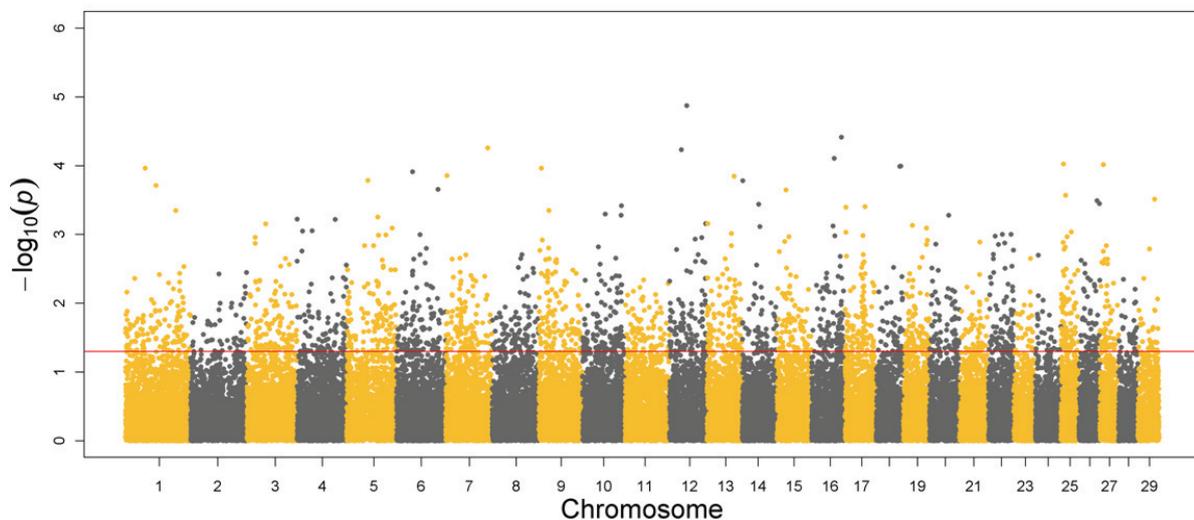
**(C) Daily energy intake (dEI)**
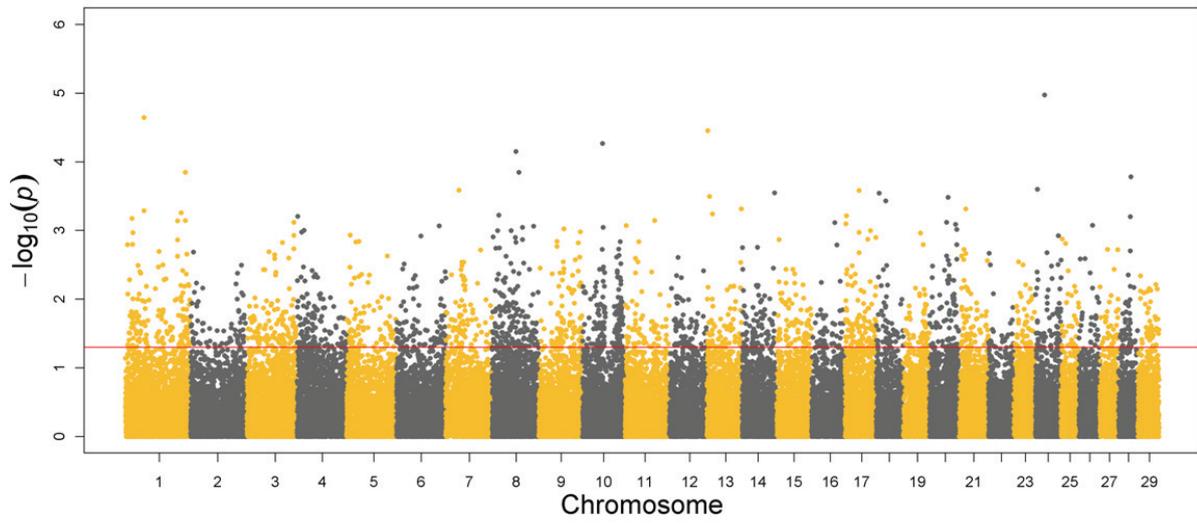
(D) Arginine
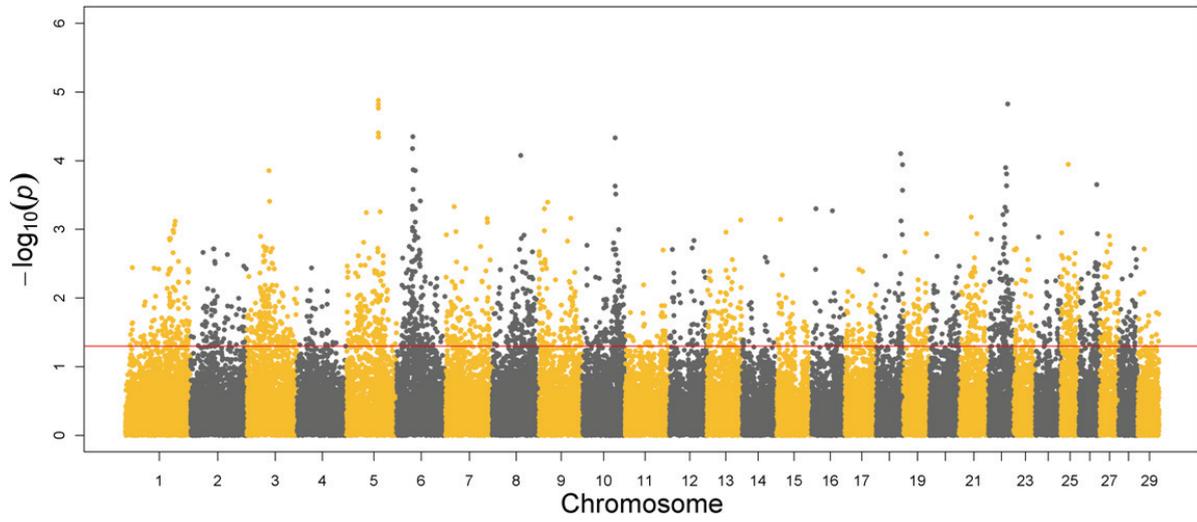
(E) Lysine
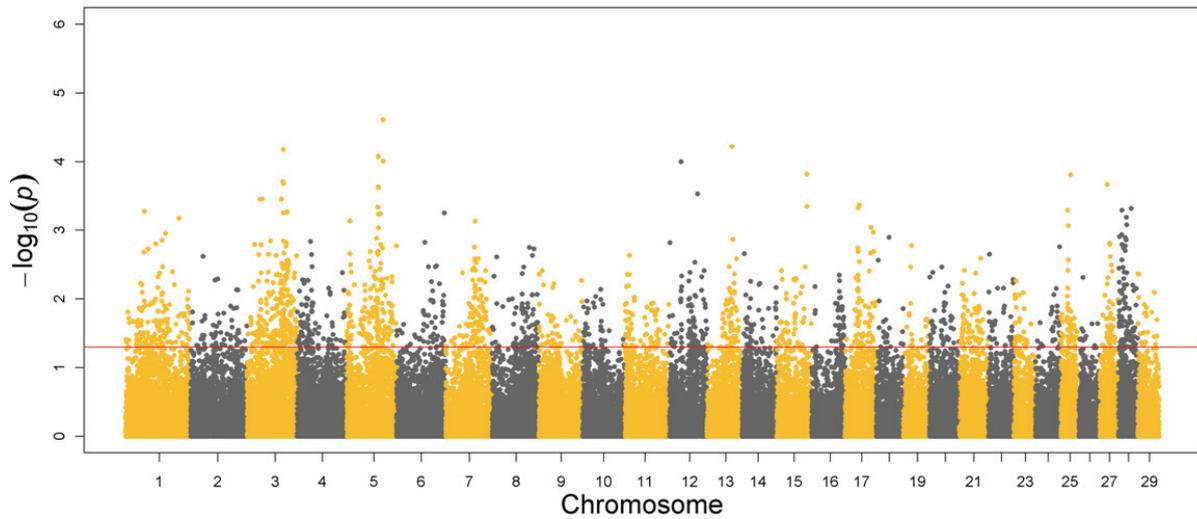
(F) C0
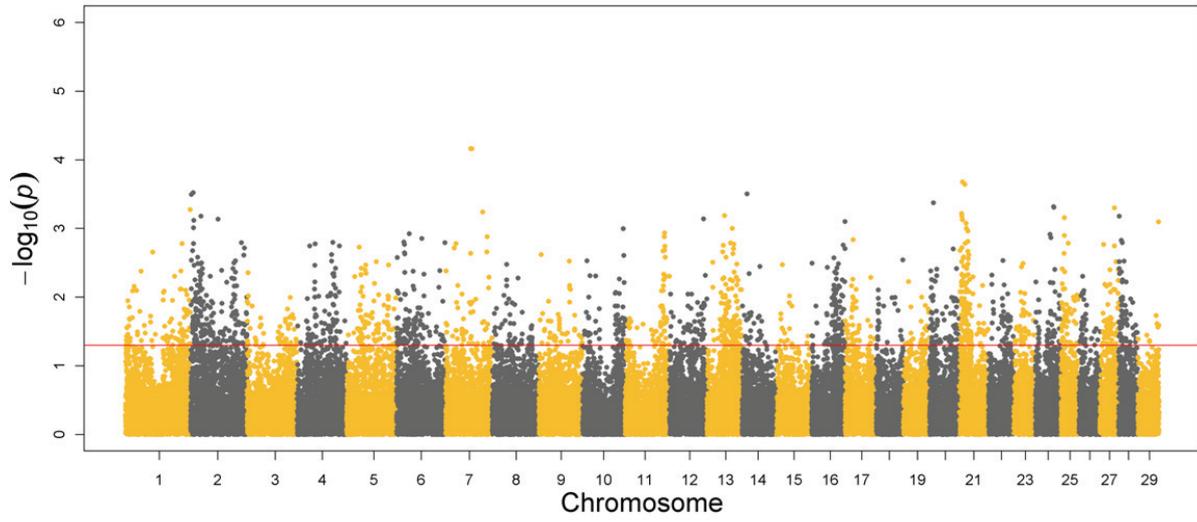
(G) C2
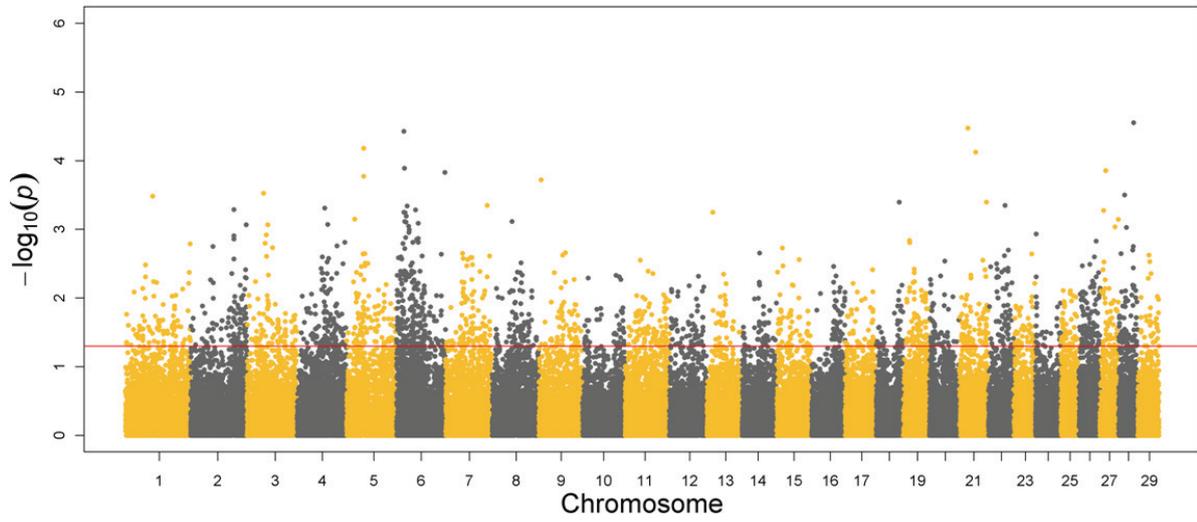
(H) C5
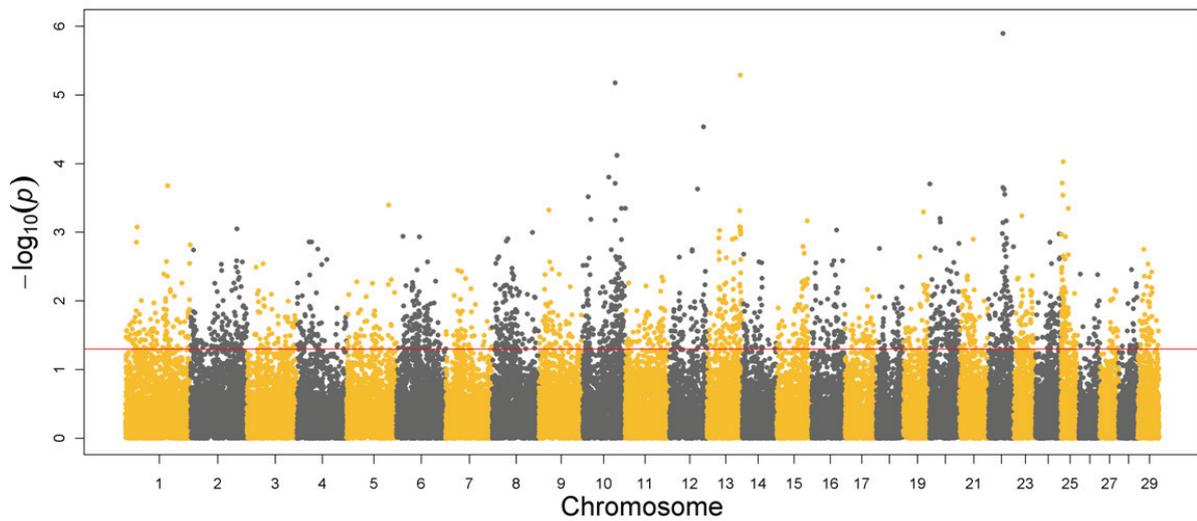
(I) C8:1
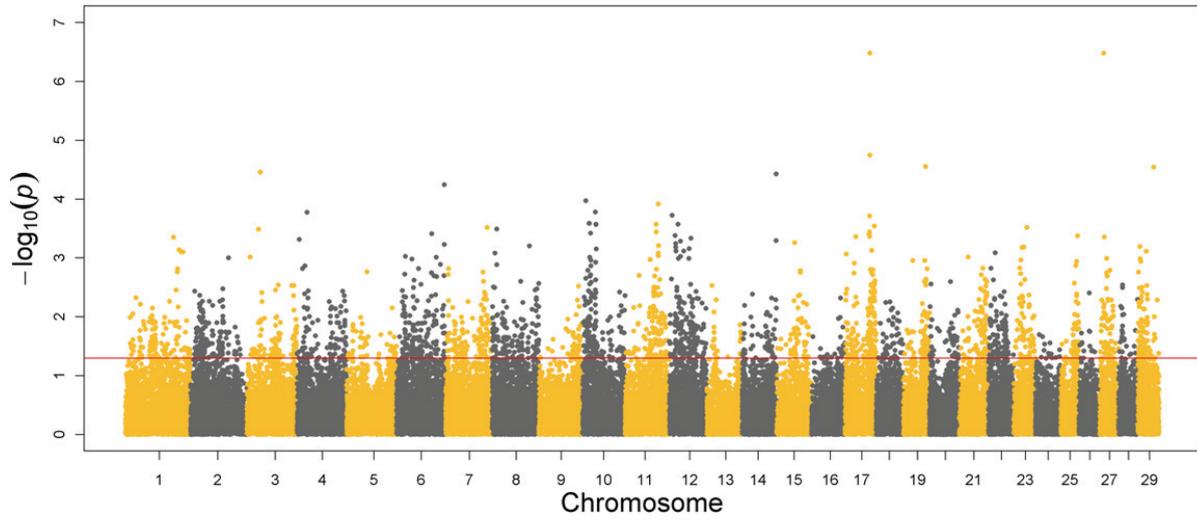
(J) C14
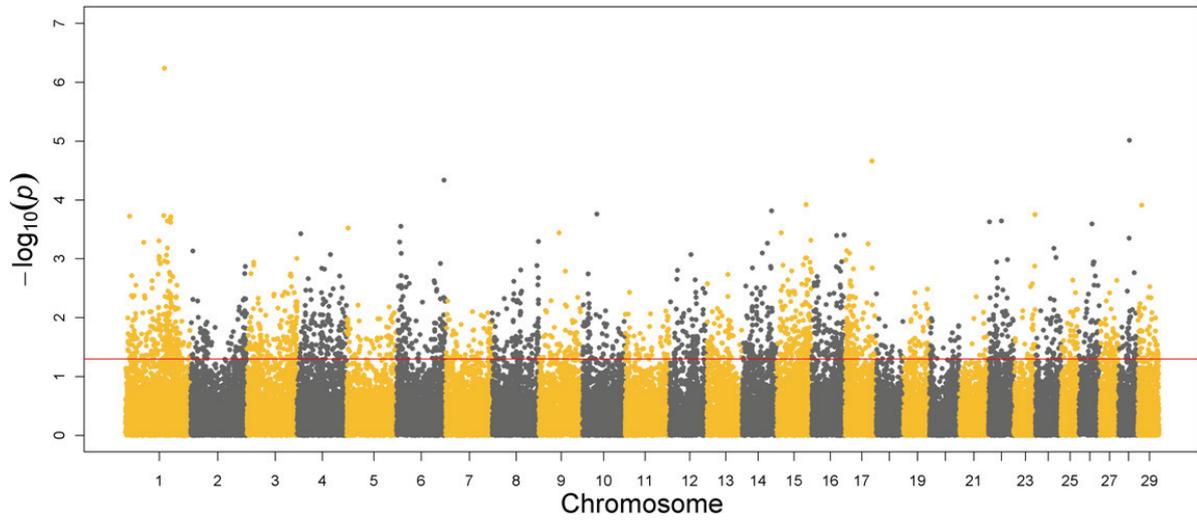
(K) C18
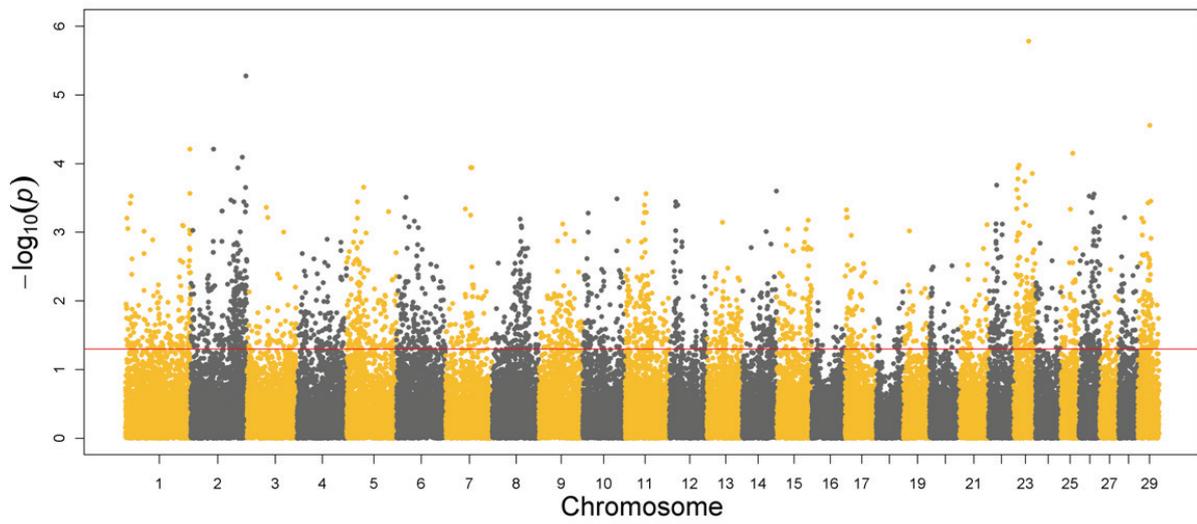
(L) PC_aa_C32:0

(M) PC_ae_C36:1

(N) SM_C20:2