

SUPPLEMENTARY INFORMATION FROM:

Unravelling genetic variation underlying *de novo*-synthesis of bovine milk fatty acids.

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Supplementary Table S1. Table showing GWAS results. All significant ($p < 1e-5$) marker – trait combinations from the GWA analysis.

Supplementary Table S2. Results for single-marker association analyses ($p < 1e-5$) of C4:0 on imputed sequence data in the region between 100 and 107 Mb on BTA11.

Supplementary Table S3. Results for single-marker association analyses ($p < 1e-5$) of C6:0 to C14:0 on imputed sequence data in the region between 60 and 70 Mb on BTA13.

Supplementary Table S4. Results table for single-marker association analyses ($p < 1e-5$) of C4:0 and C6:0 on imputed sequence data in the region between 20 and 60 Mb on BTA17.

Supplementary Table S5. Results for single-marker association analyses ($p < 1e-5$) of C6:0 to C14:0 on imputed sequence data in the region between 45 and 55 Mb on BTA19.

Supplementary Figure S6. Results for single-marker association analyses of C4:0 using imputed sequence variant data in the region between 100 and 107 Mb on BTA11. The ordinate provides $-\log_{10}(p\text{-value})$ for each marker – trait association, while the abscissa denotes marker position.

Supplementary Figure S7. Results for single-marker association analyses of C6:0 to C14:0 using imputed sequence variant data in the region between 60 and 70 Mb on BTA13. The ordinate provides $-\log_{10}(p\text{-value})$ for each marker – trait association, while the abscissa denotes marker position.

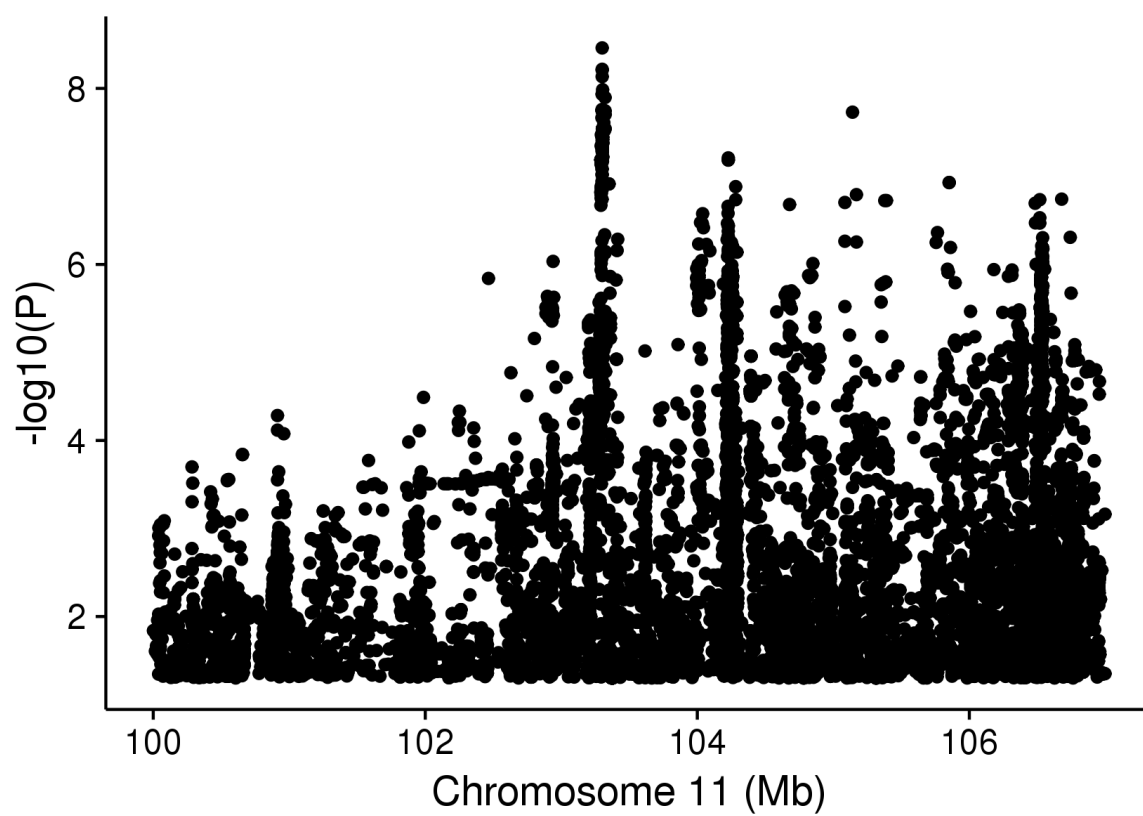
Supplementary Figure S8. Results for single-marker association analyses of C4:0 to C14:0 using imputed sequence variant data in the region between 45 and 55 Mb on BTA17. The ordinate provides $-\log_{10}(p\text{-value})$ for each marker – trait association, while the abscissa denotes marker position.

Supplementary Figure S9. Results for single-marker association analyses of C4:0 to C14:0 using imputed sequence variant data in the region between 45 and 55 Mb on BTA19. The ordinate provides $-\log_{10}(\text{p-value})$ for each marker – trait association, while the abscissa denotes marker position.

Supplementary Table S10.

Mean normalized read count with standard deviation (SD) for the genes in the QTL regions on BTA11, 13, 17 and 19.

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72 Figure S6.

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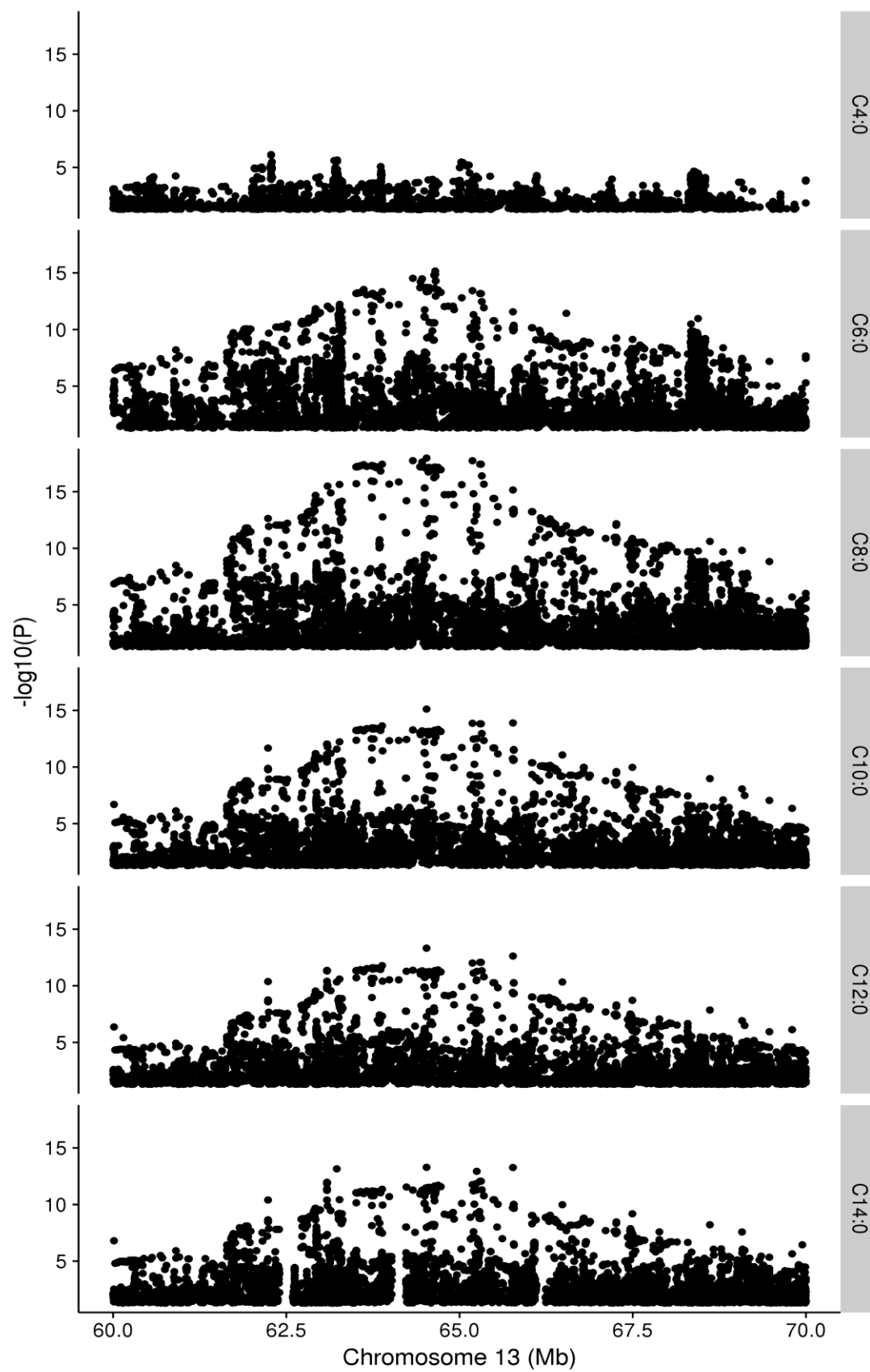
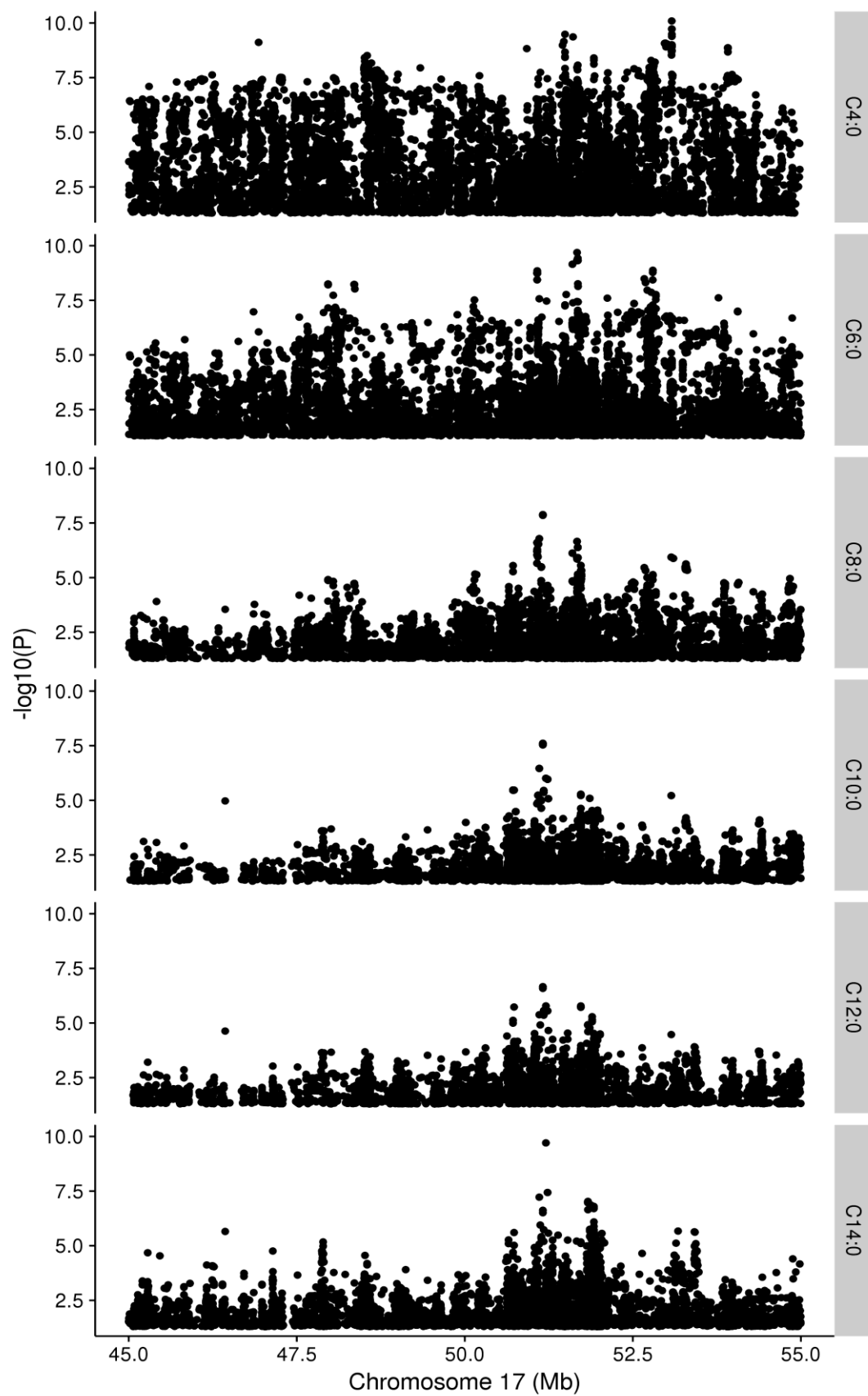


Figure S7



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78 Figure S8

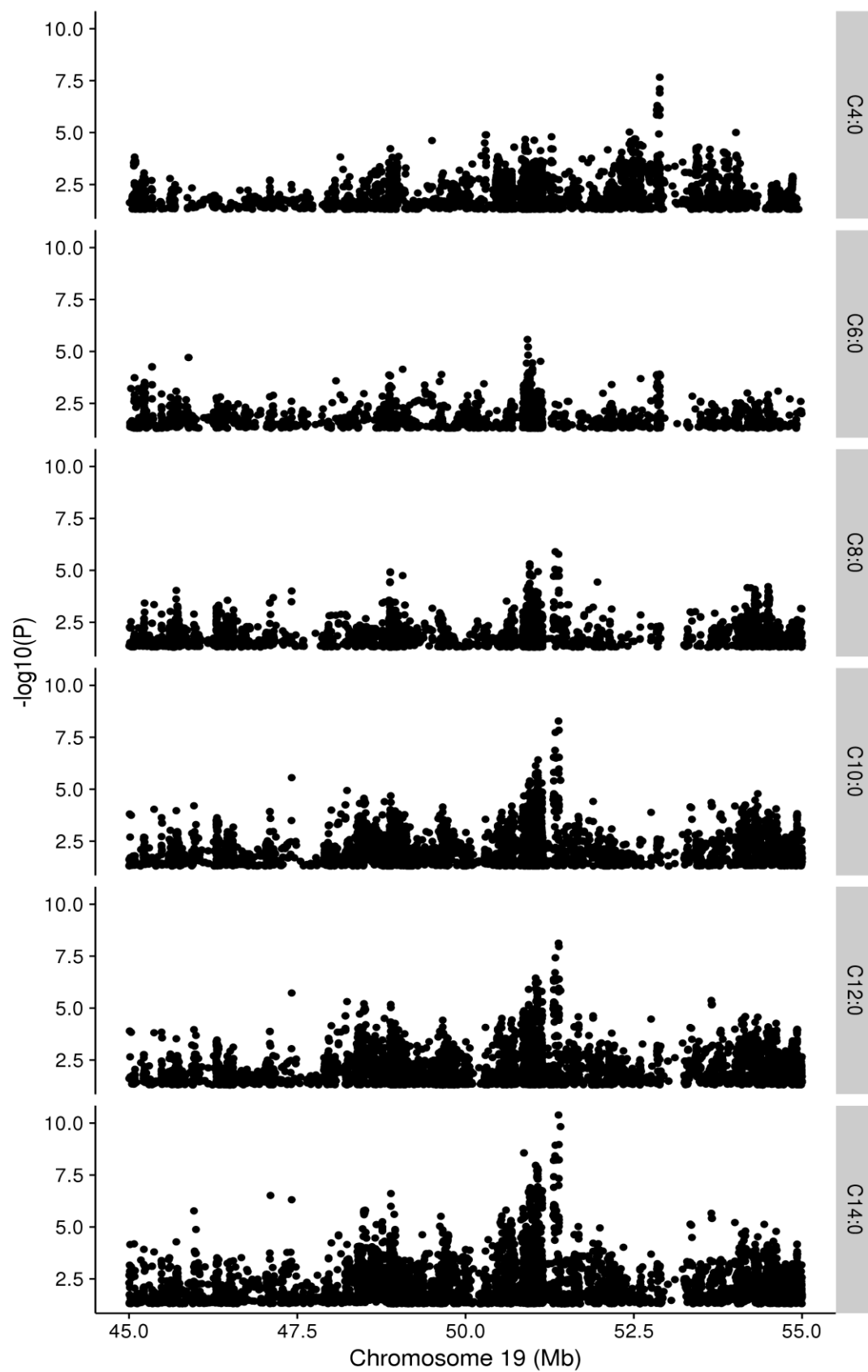


Figure S9