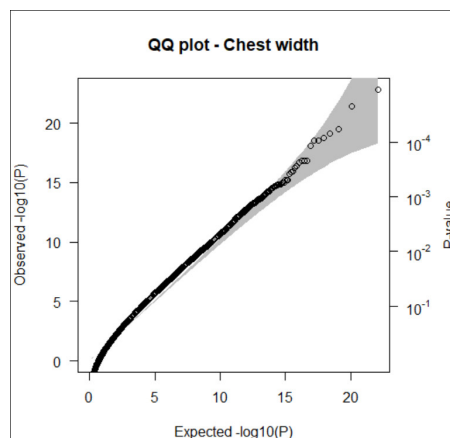
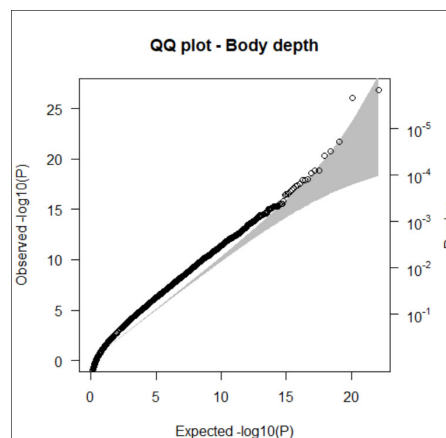


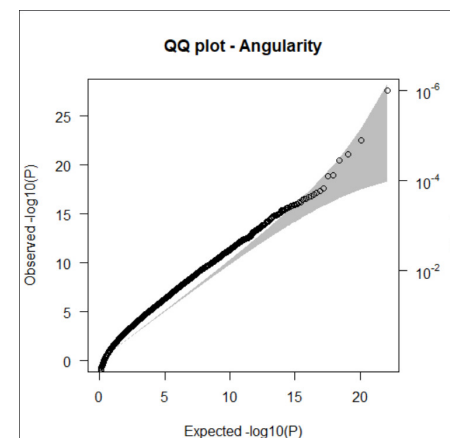
$\lambda = 1.81$



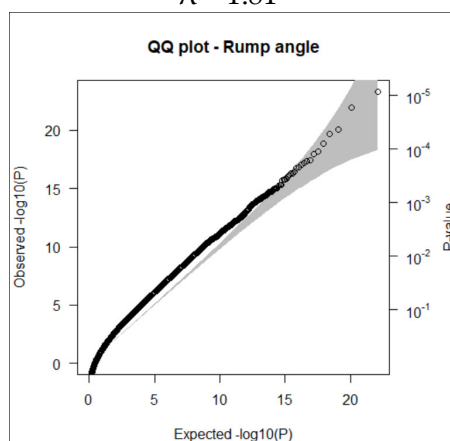
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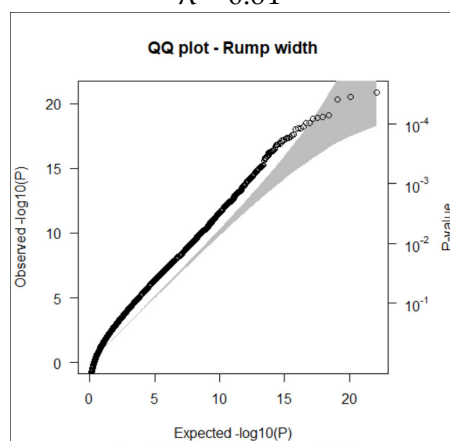
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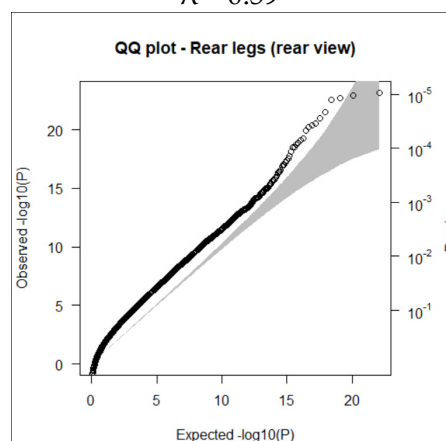
$\lambda = 0.82$



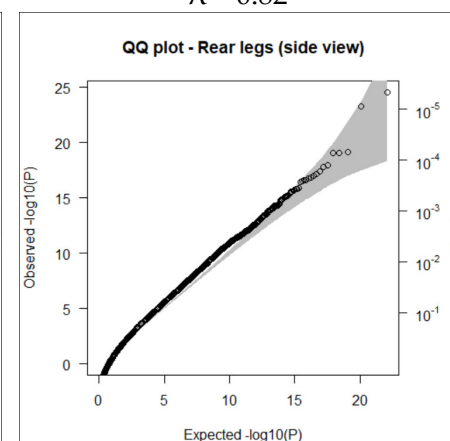
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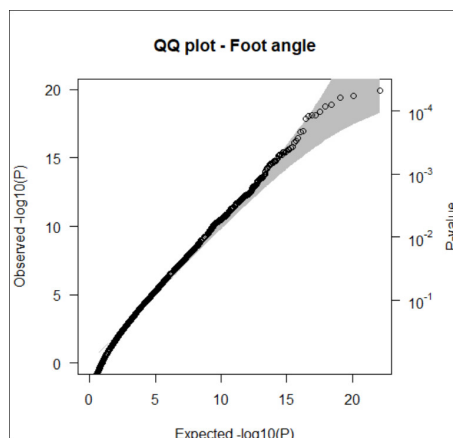
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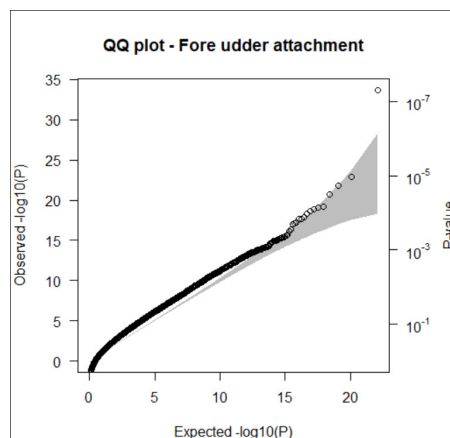
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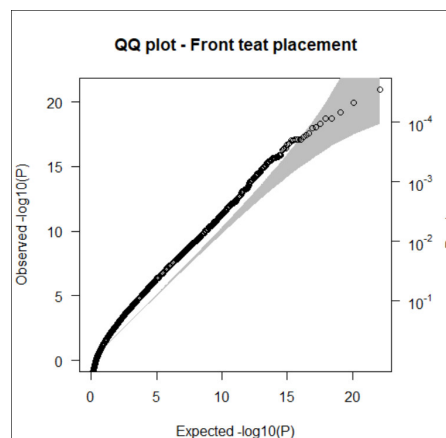
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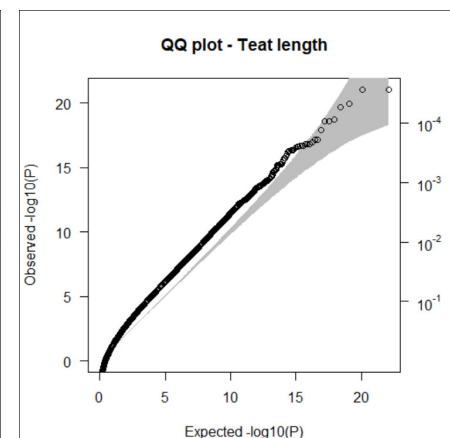
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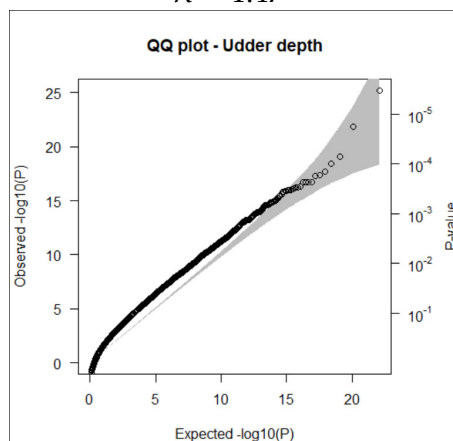
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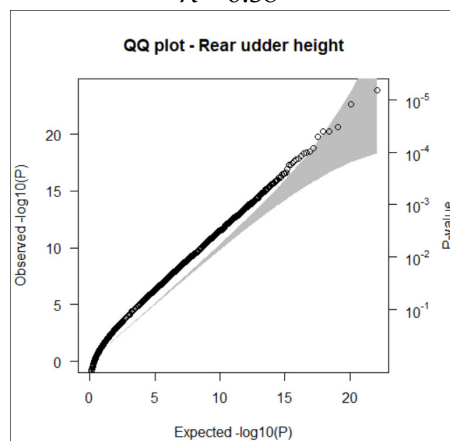
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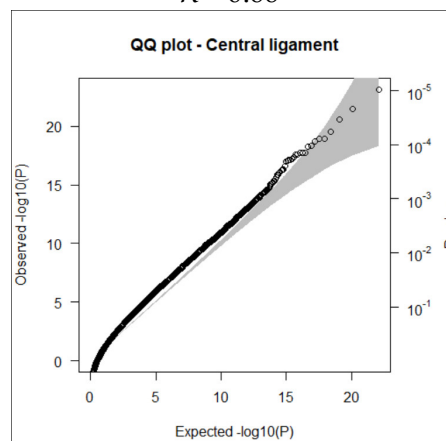
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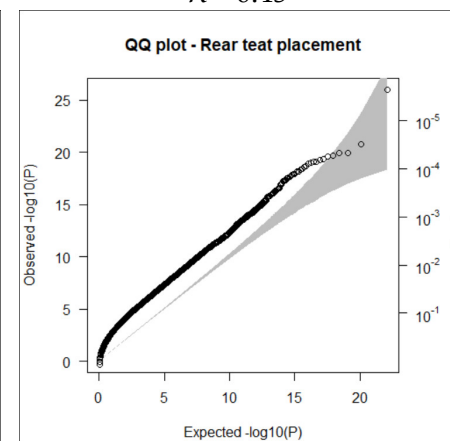
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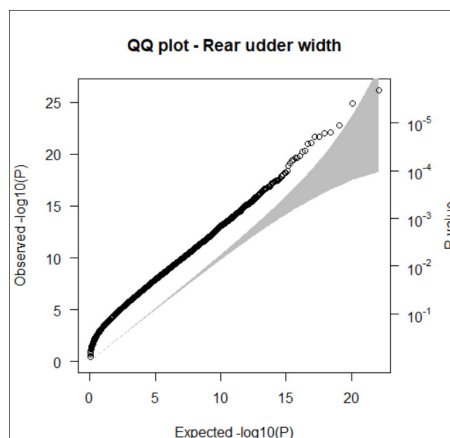
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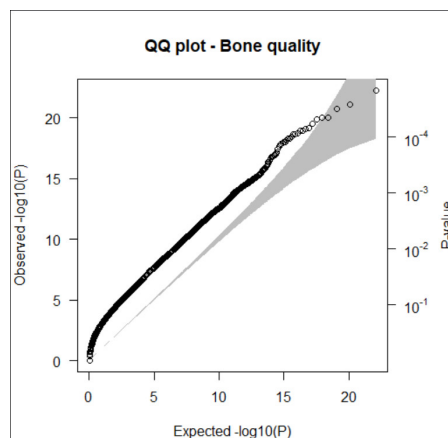
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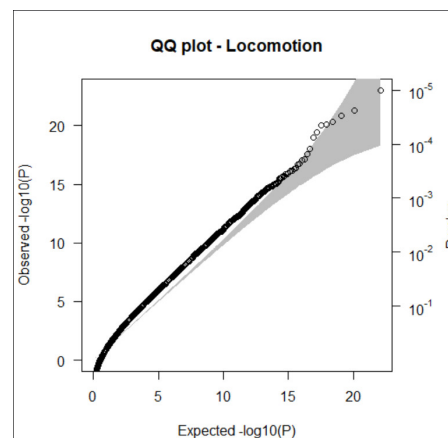
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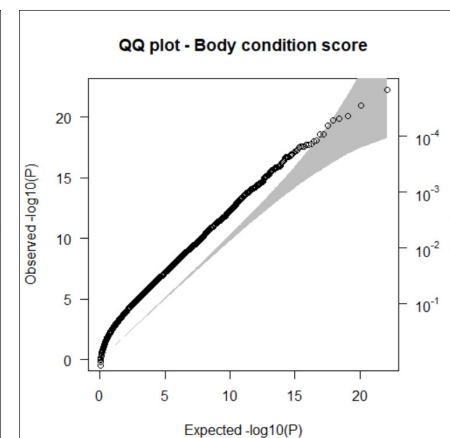
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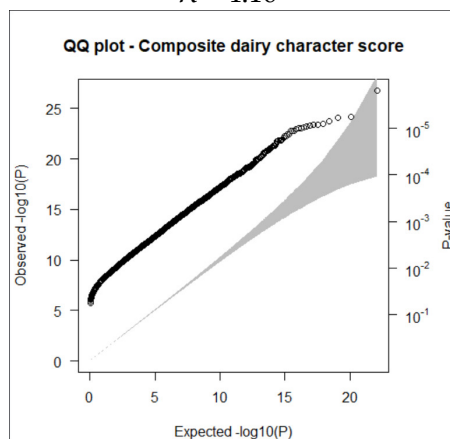
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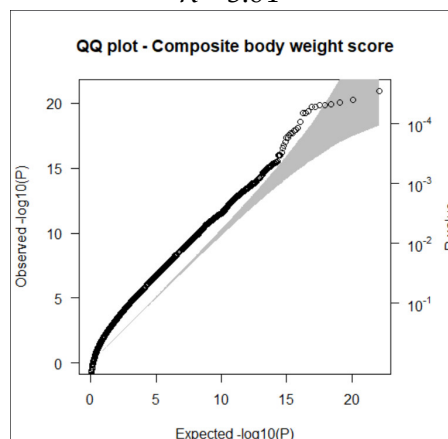
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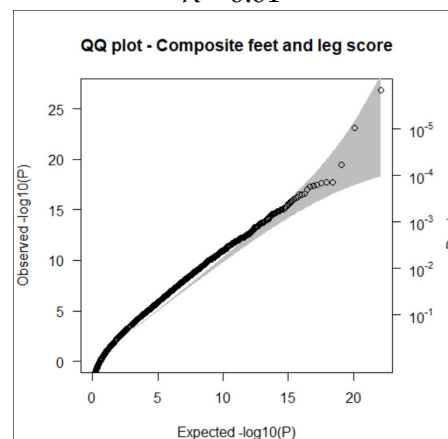
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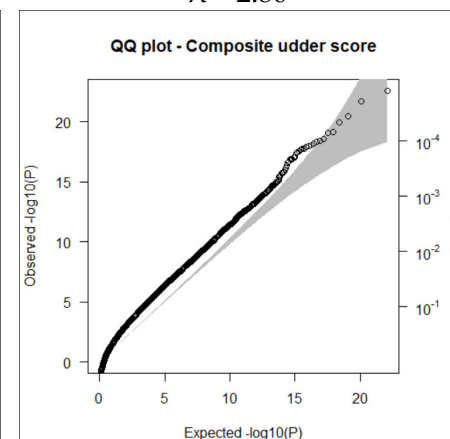
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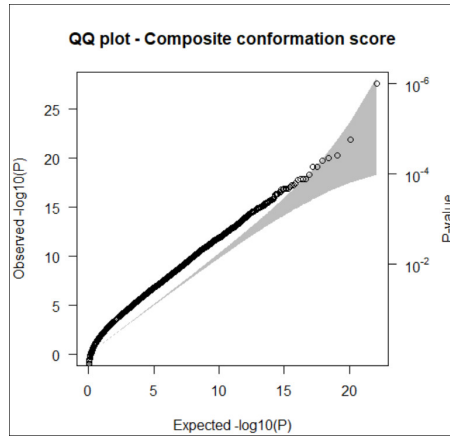
$\lambda = 1.75$



$\lambda = -0.18$

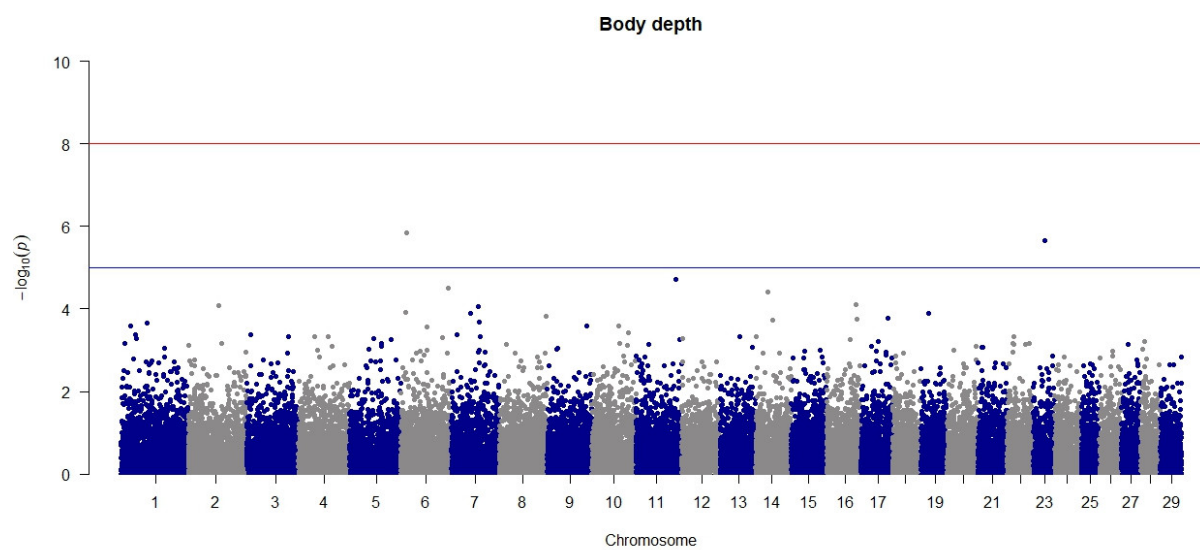
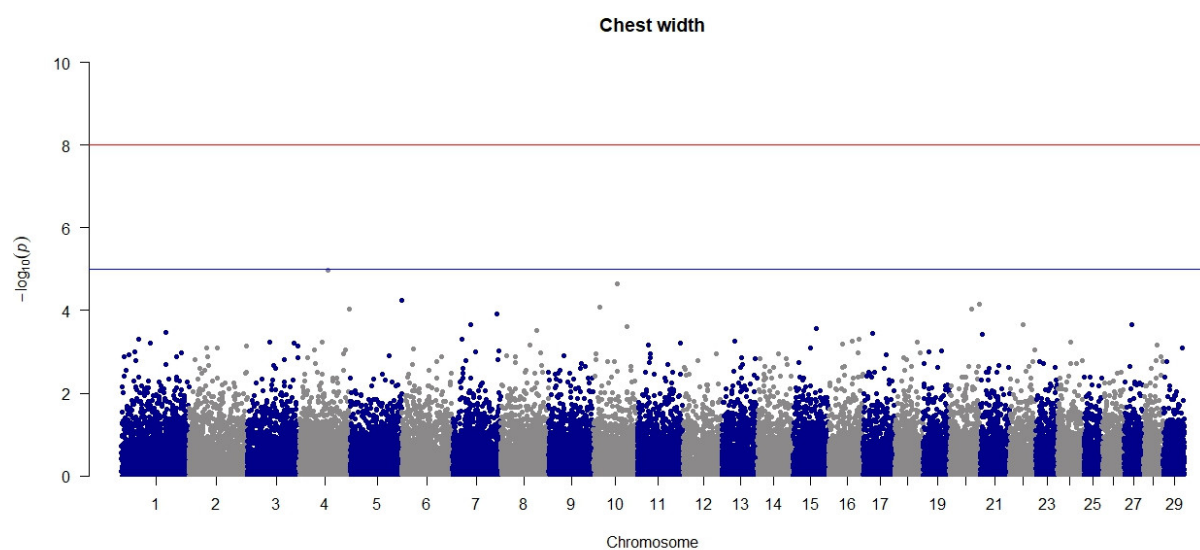
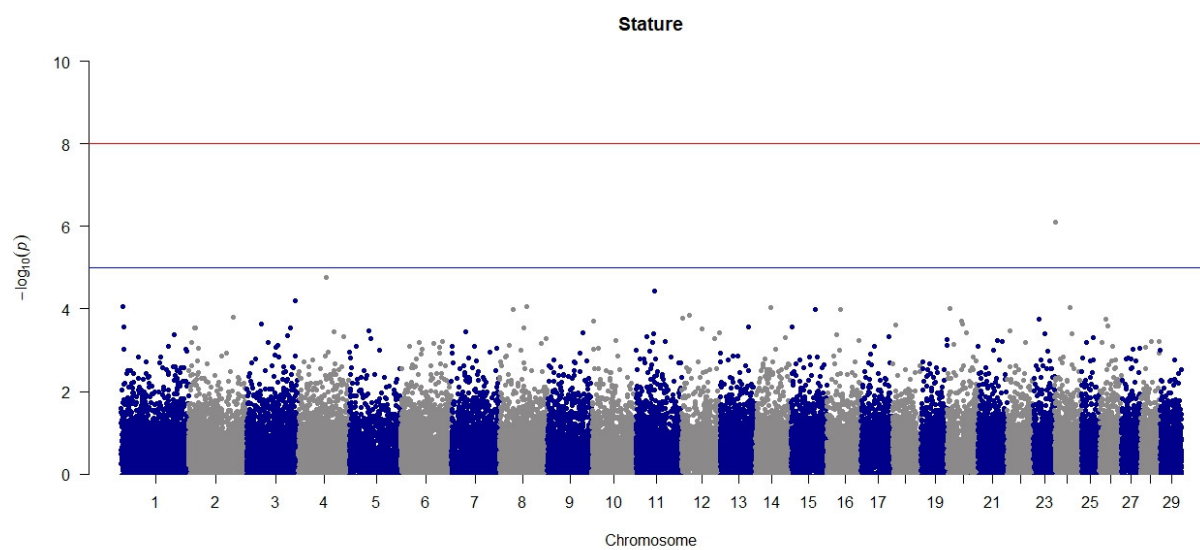


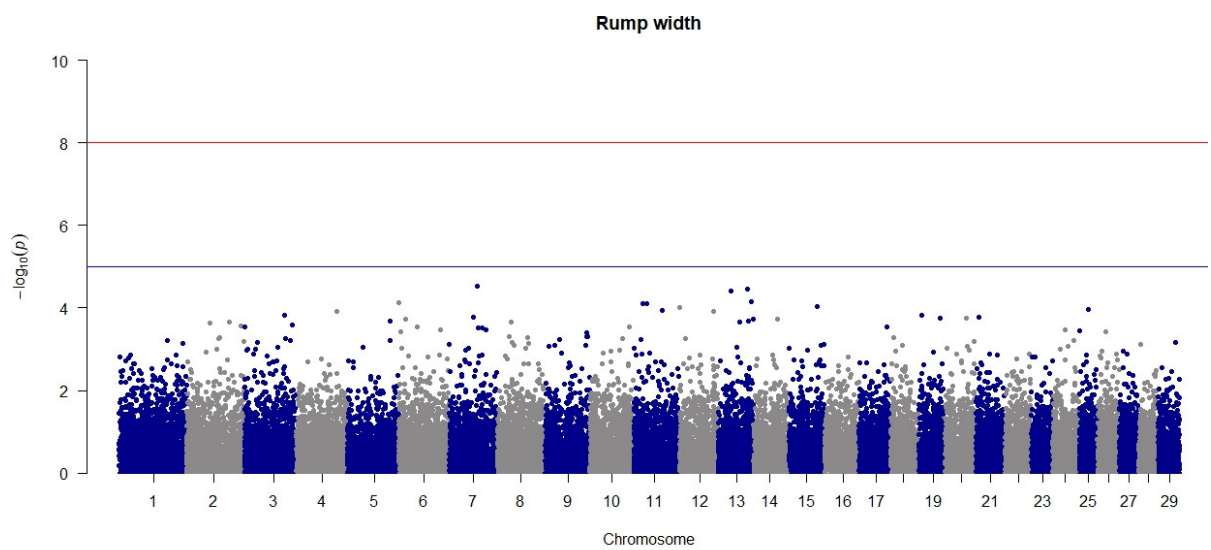
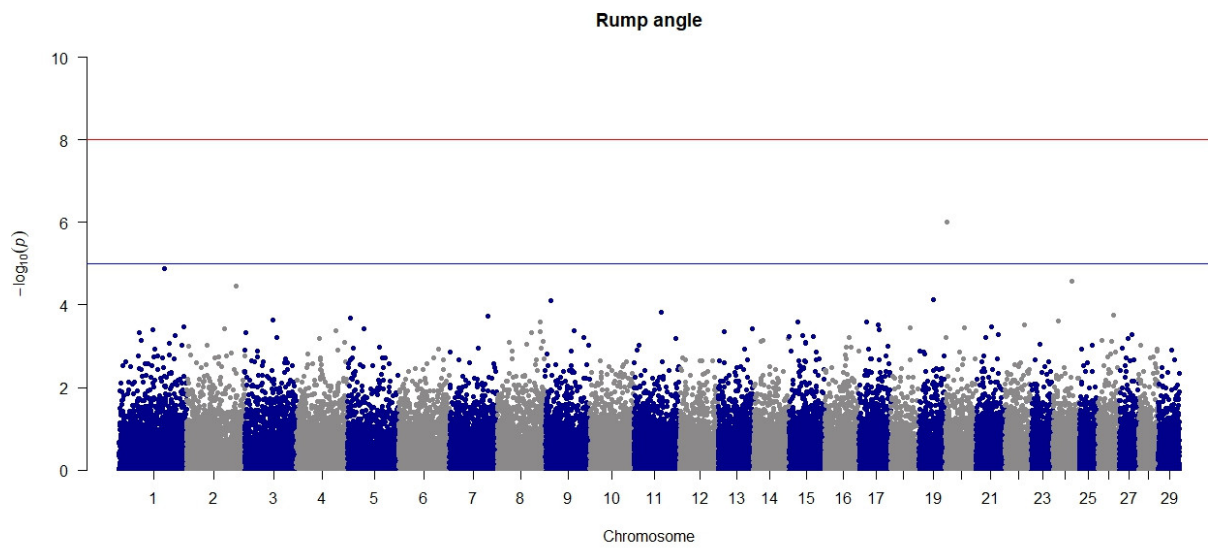
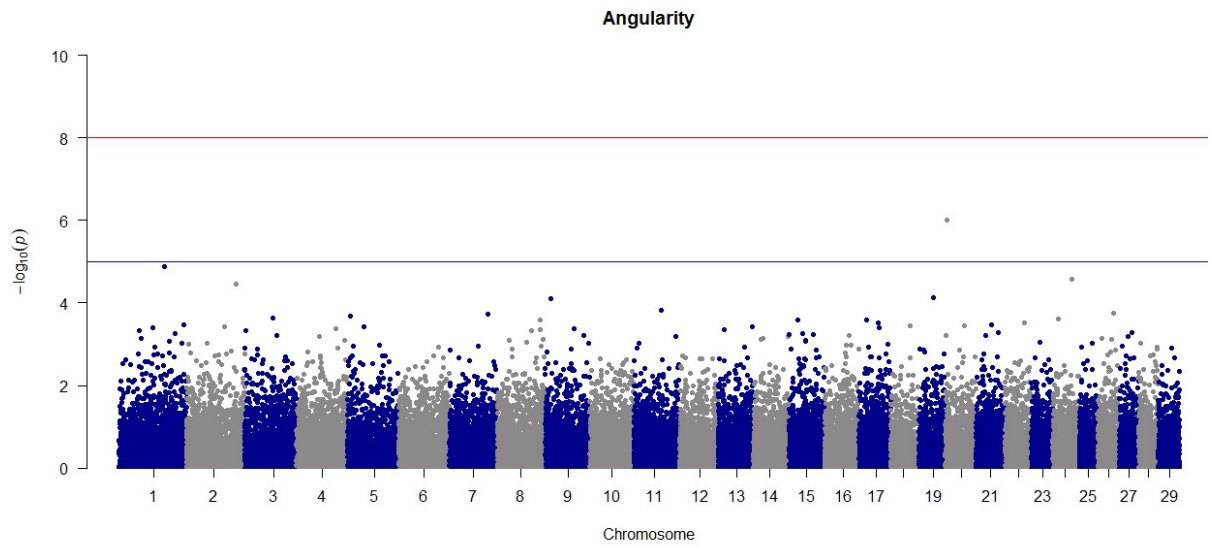
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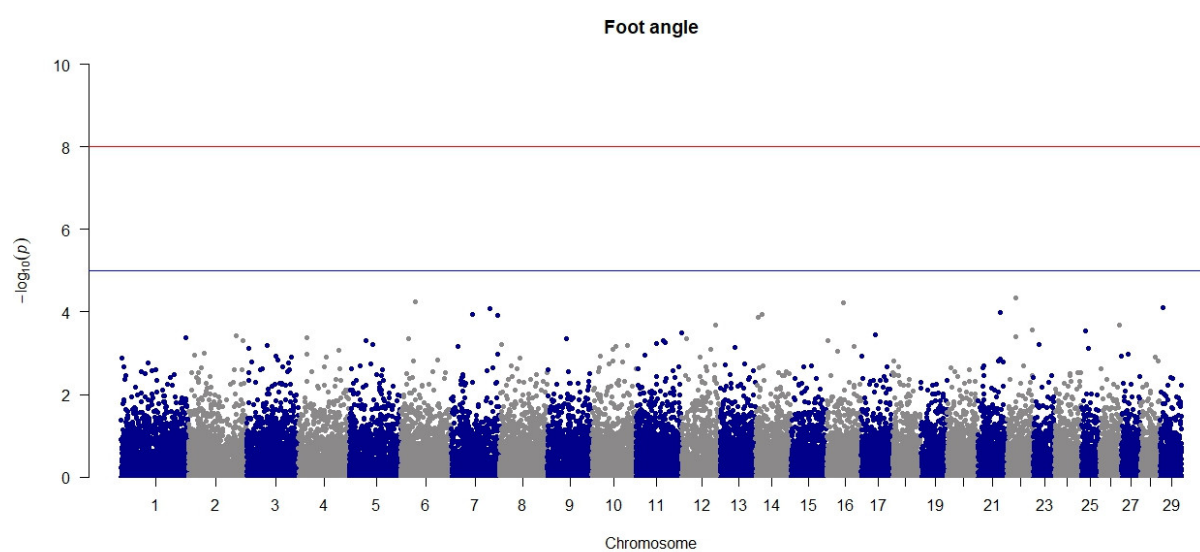
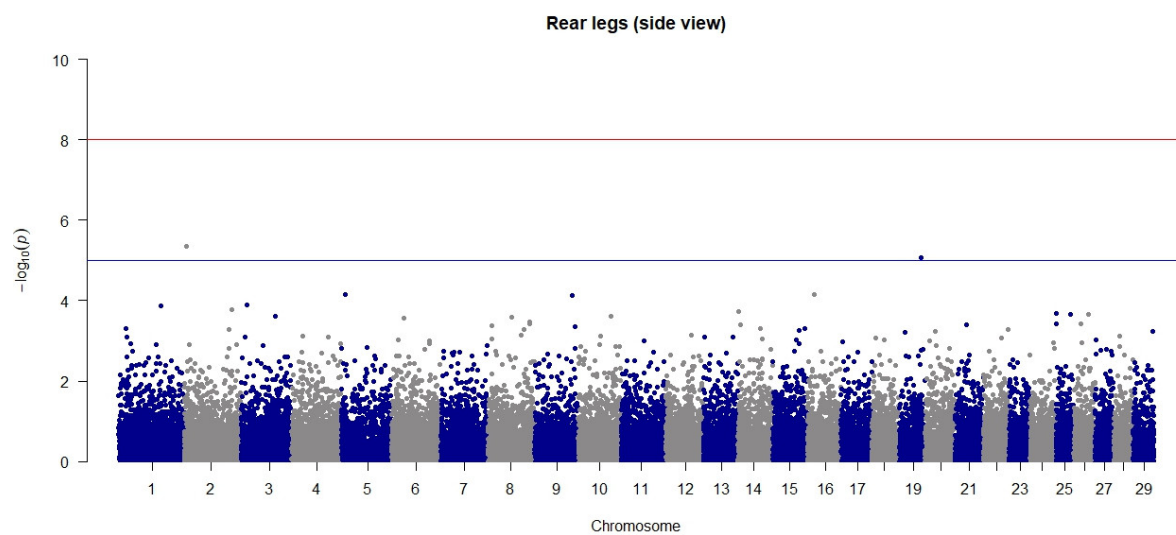
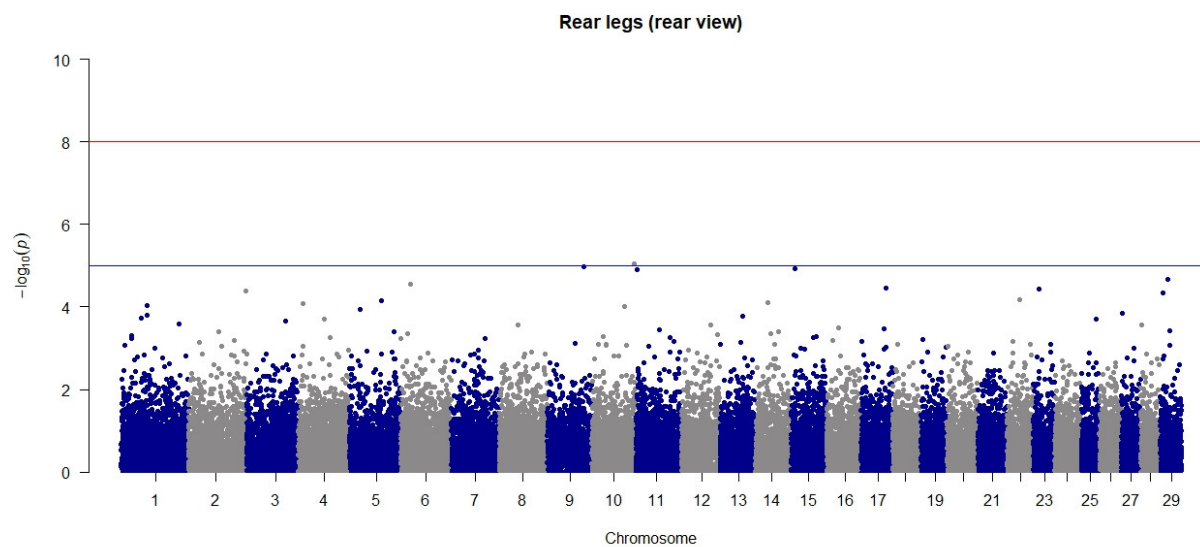


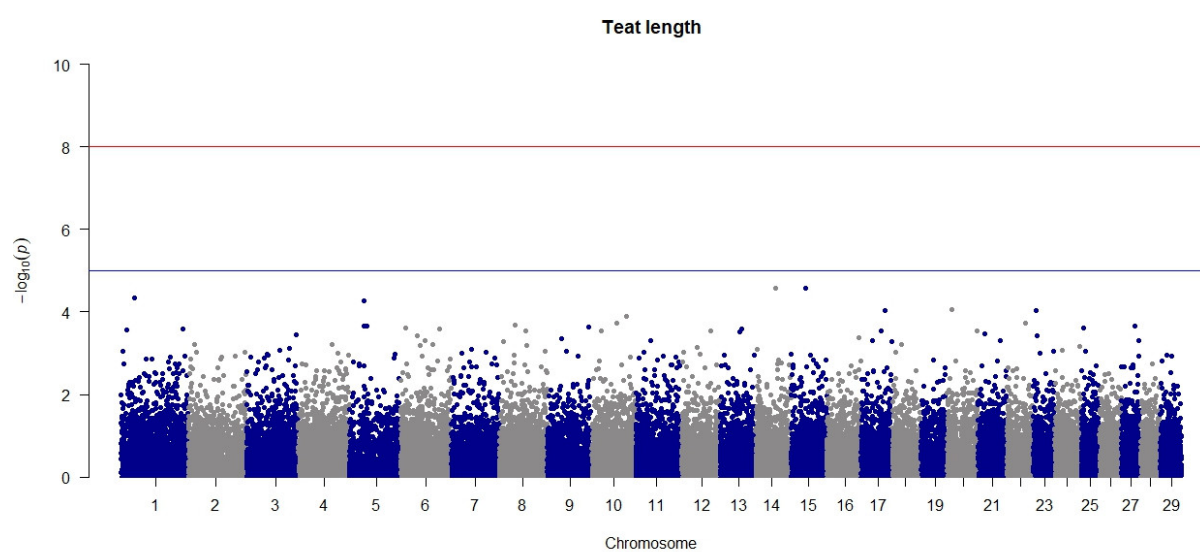
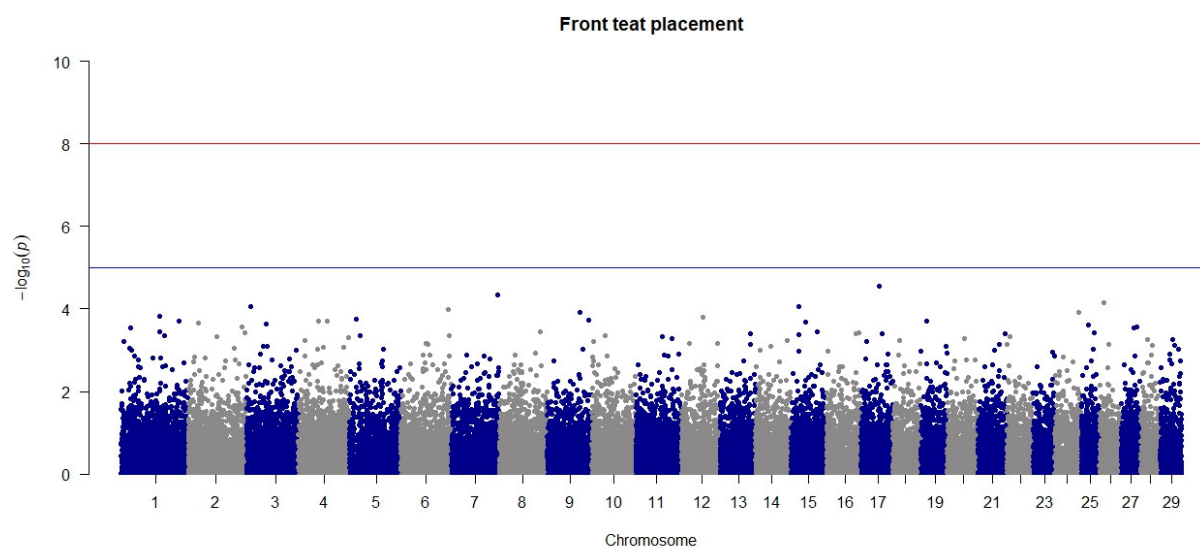
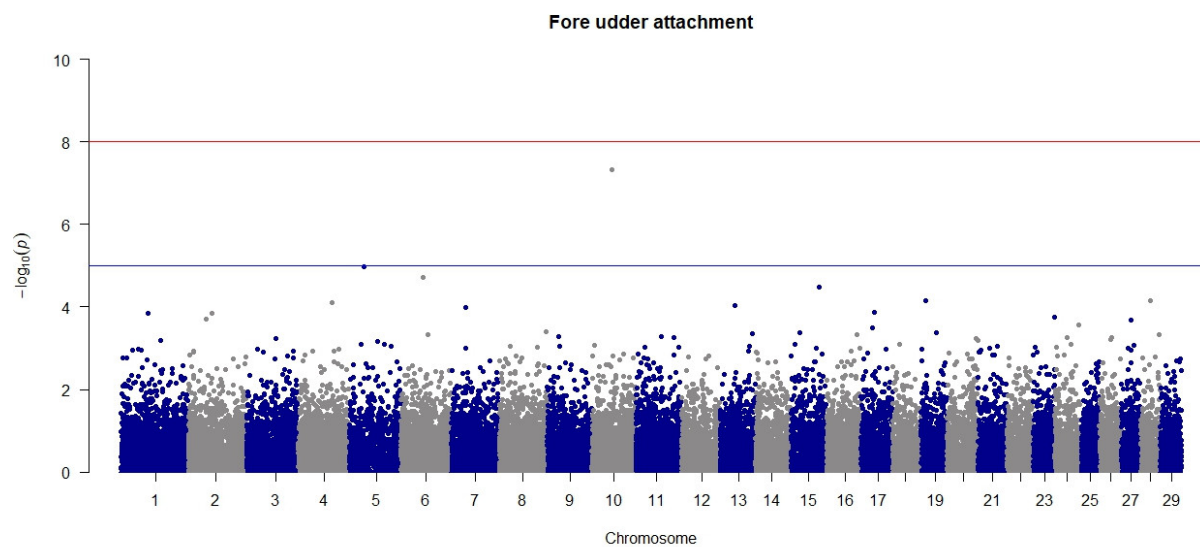
$$\lambda = 1.80$$

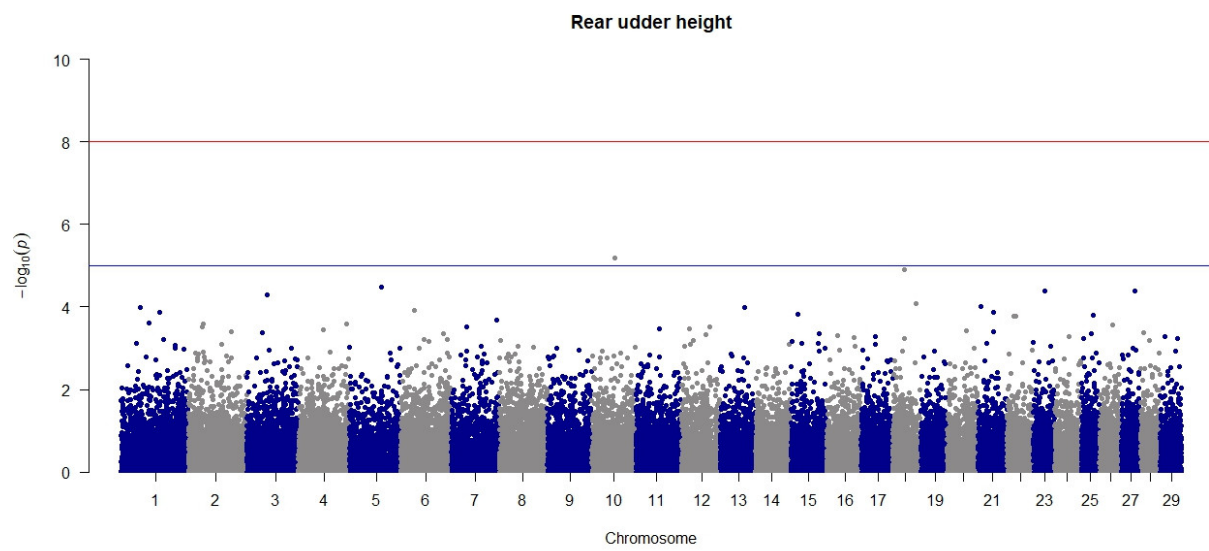
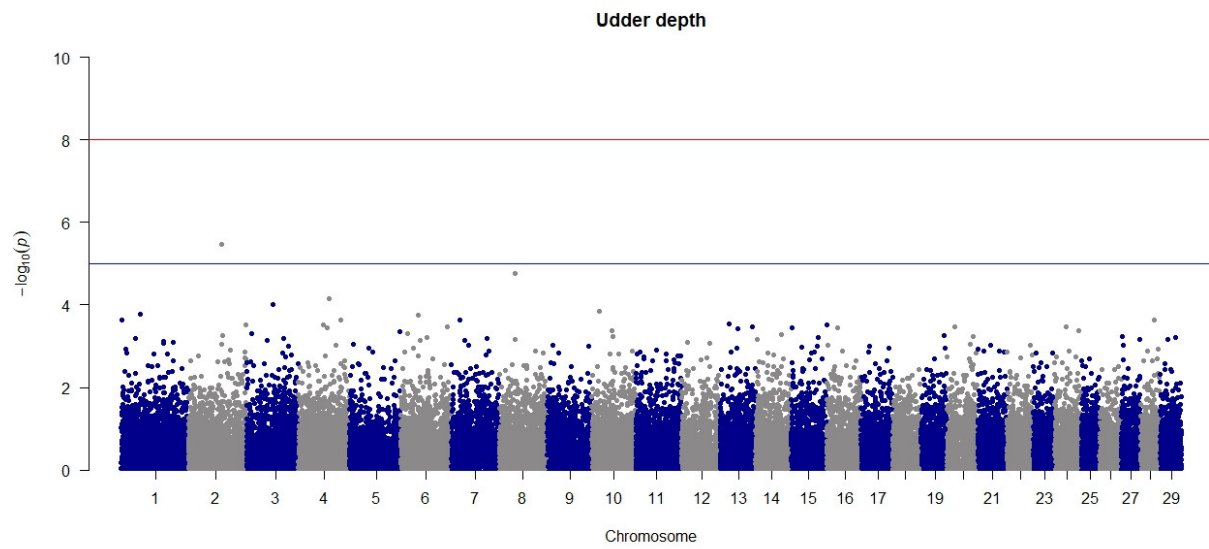
Figure S1. Quantile-quantile (Q-Q) plots with the 95% confidence interval (grey colored area) and genomic inflation factor (below the QQ plots) of the GWAS analysis for 25 linear type traits in Czech Holstein.

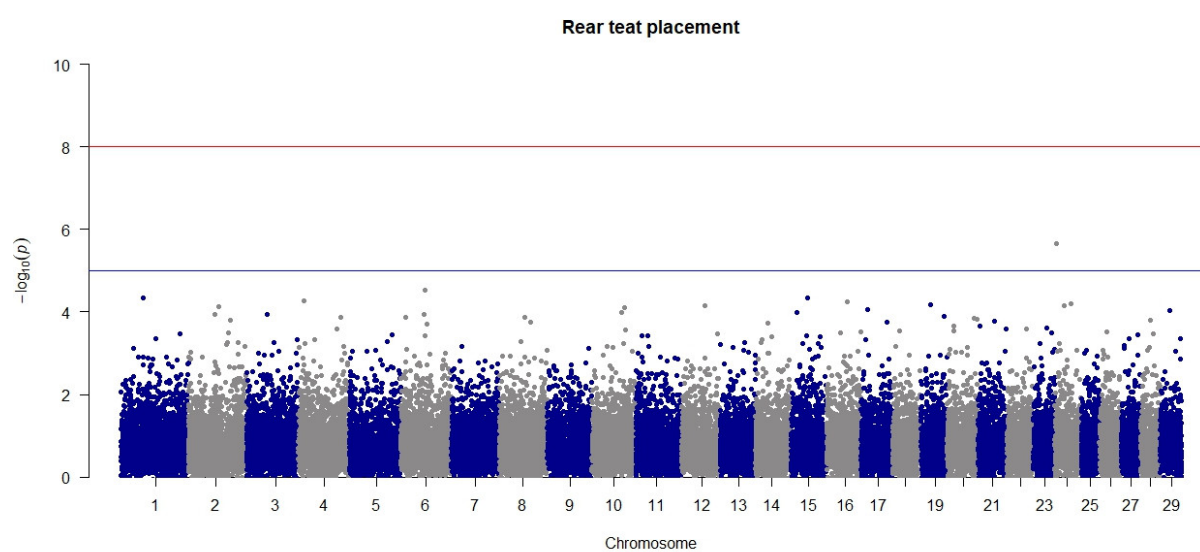
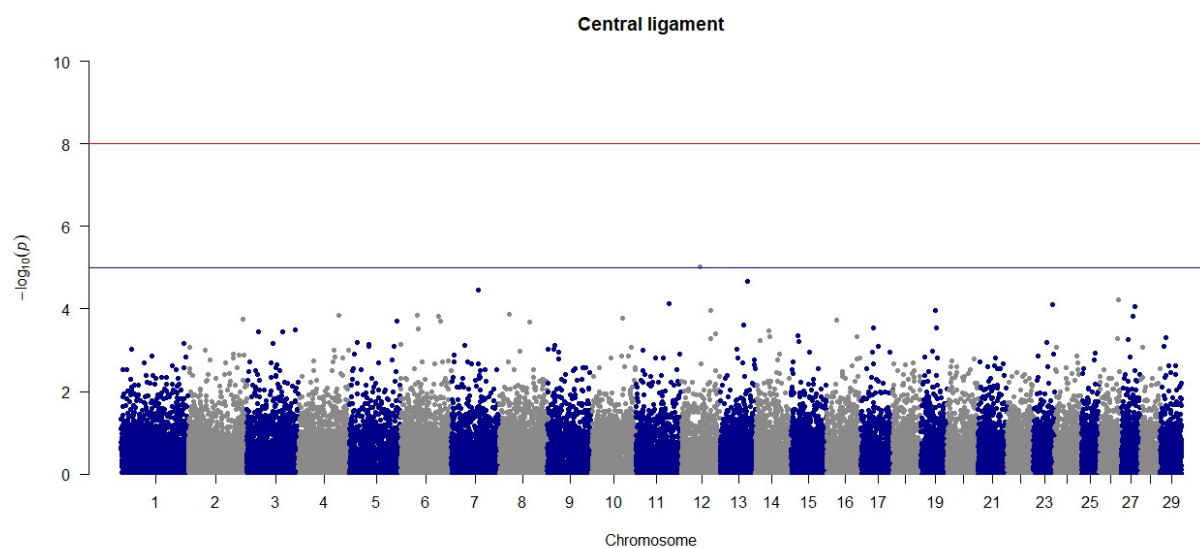
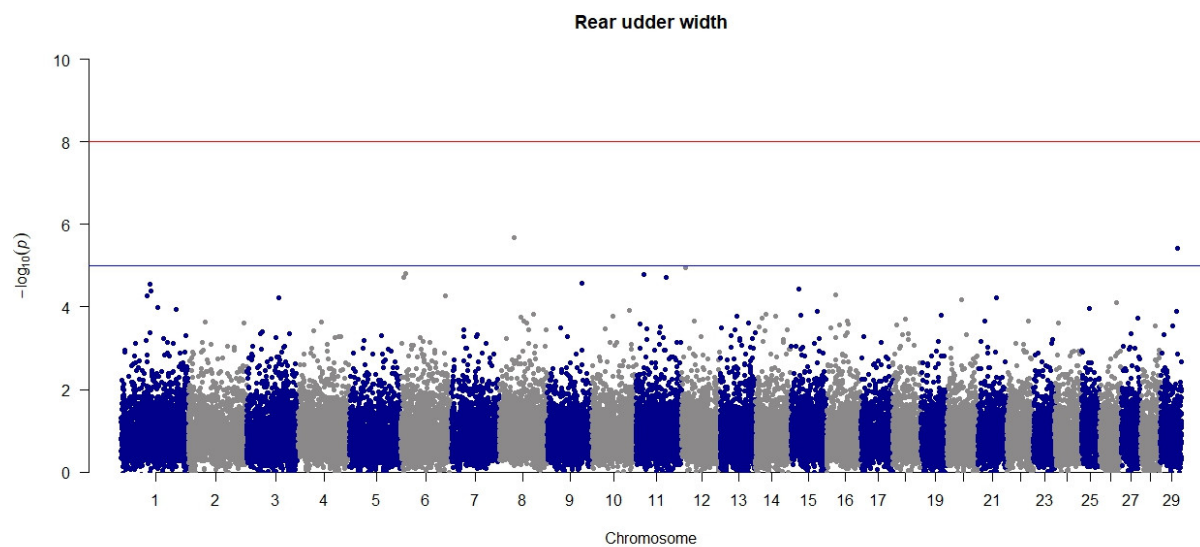


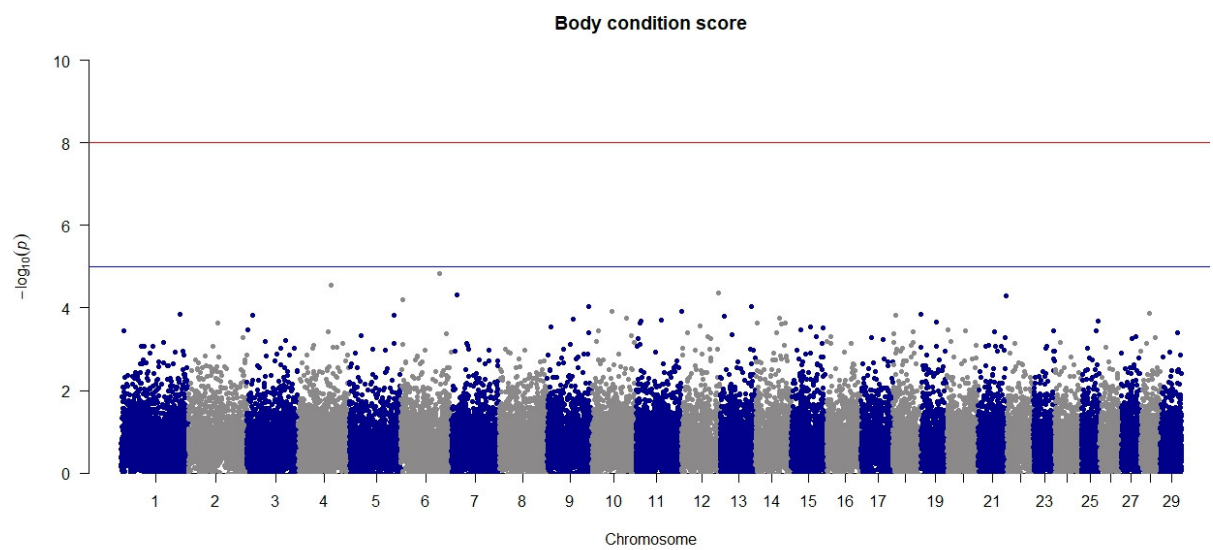
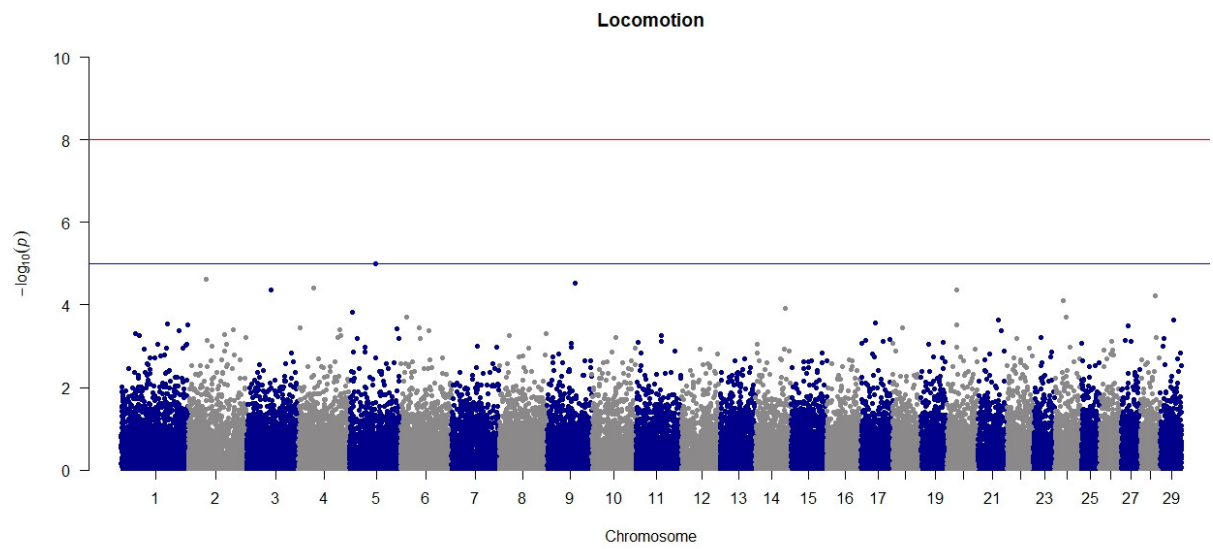
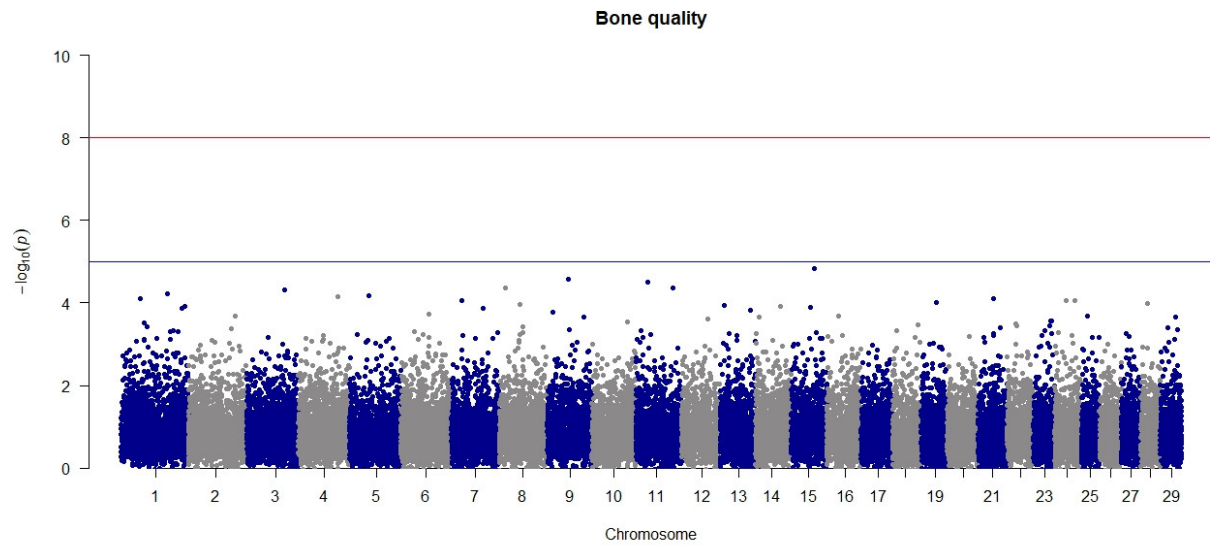


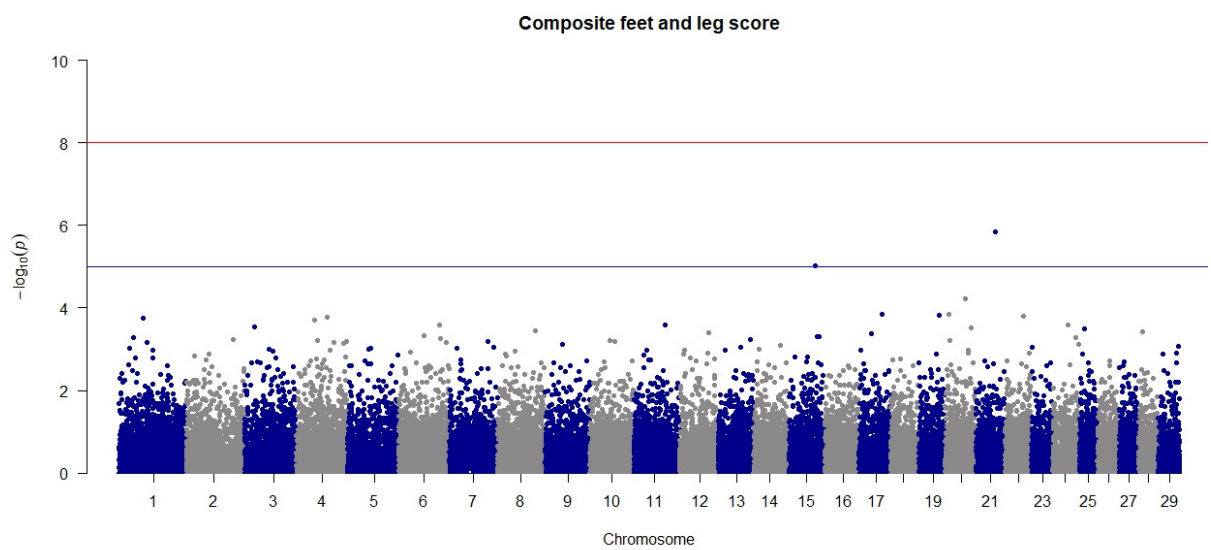
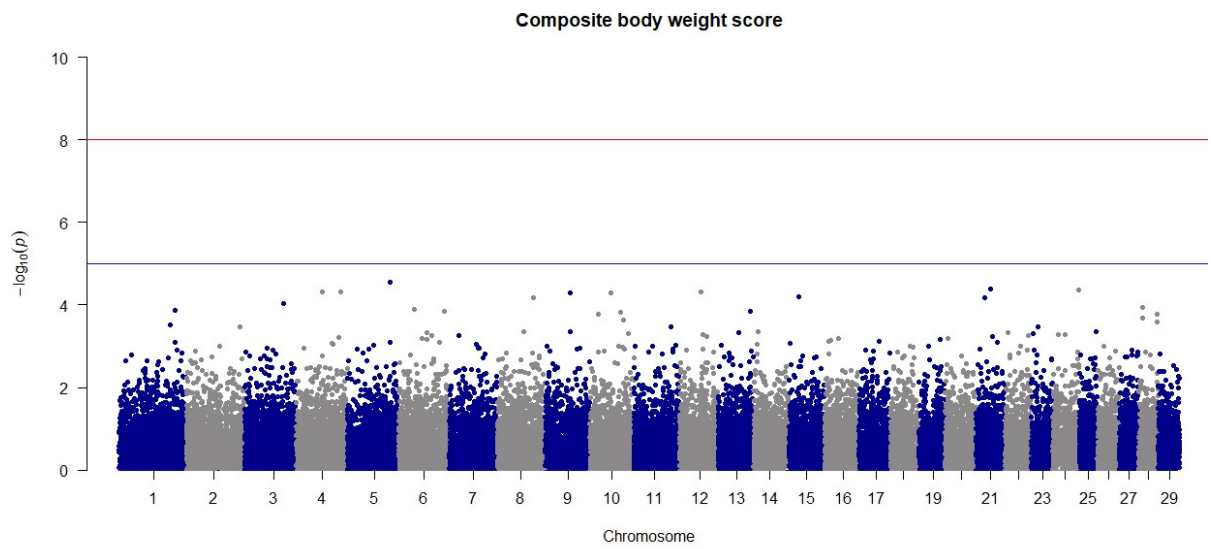
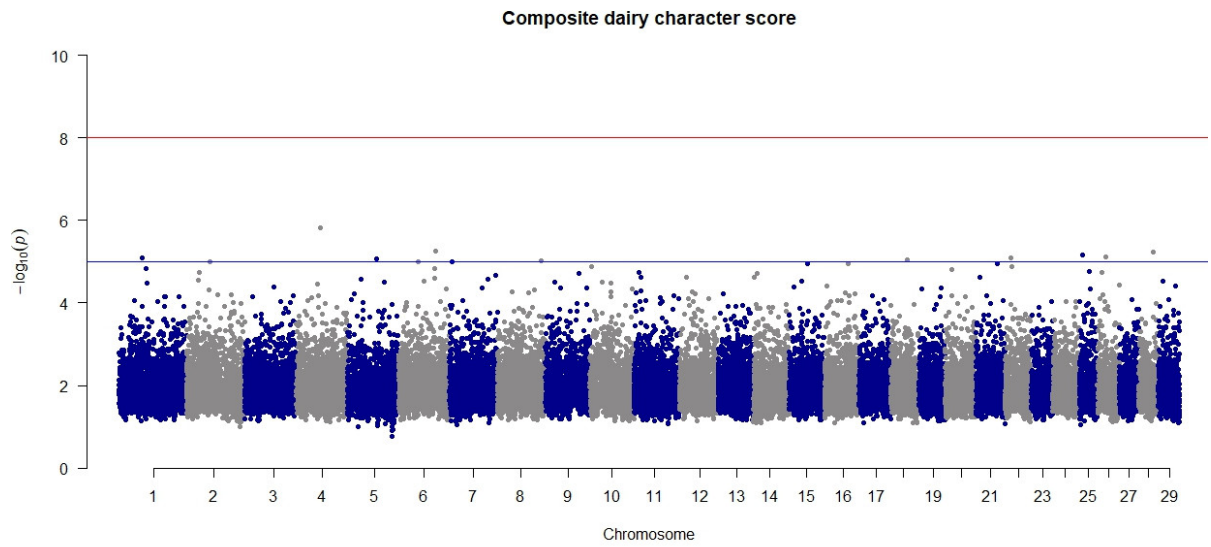












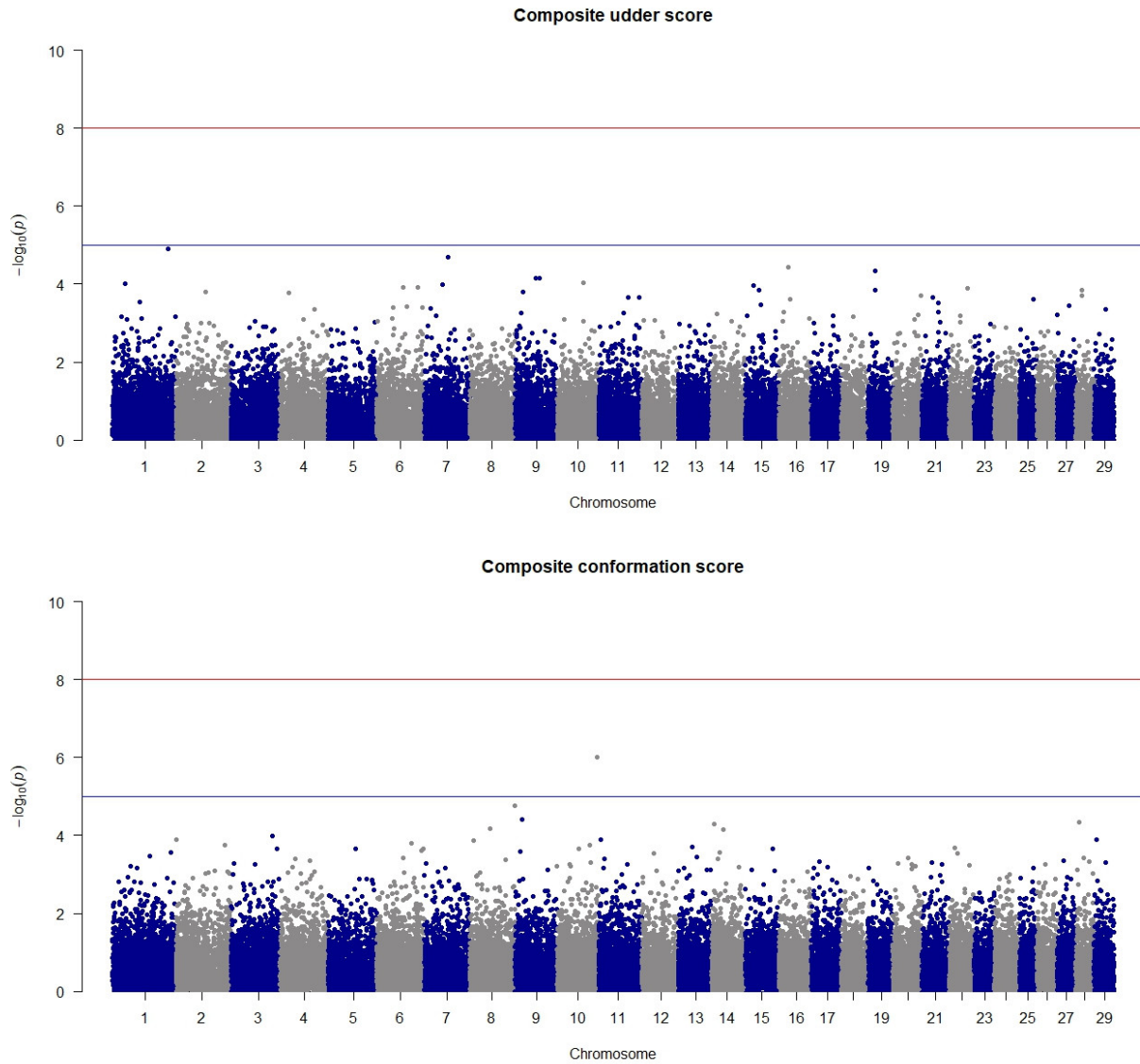


Figure S2. Manhattan plots of the GWAS analysis for 25 linear type traits in Czech Holstein. The level of significance was expressed by a p-value of 1.00×10^{-8} (genome-wide significance threshold, red line) and 1.00×10^{-5} (suggestive significance threshold, blue line).