

Supplementary file: A. LOD plot for rank transformed relative abundance values for significant genera. The dotted lines (Green – 85%, Blue – 90%, Red – 95%) represent significant thresholds.
B. Founder effect plot for the significant chromosomes. C. Genotype X Phenotype plot for the highest SNP on the significant chromosome.

Fig Q1: Micabf1 - g_Enterorhabdus

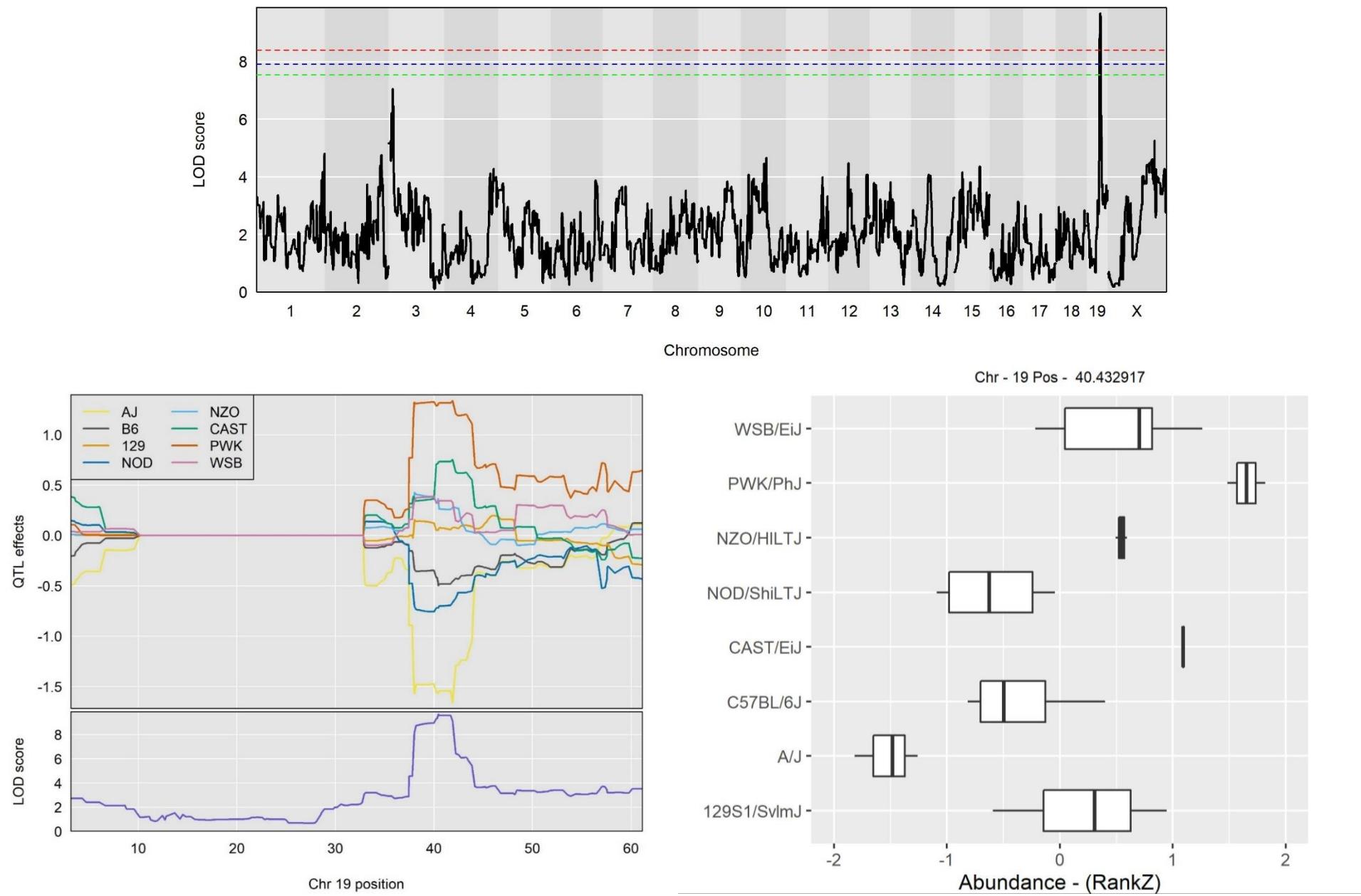


Fig Q2: Micabf2 - g_Bacteroides

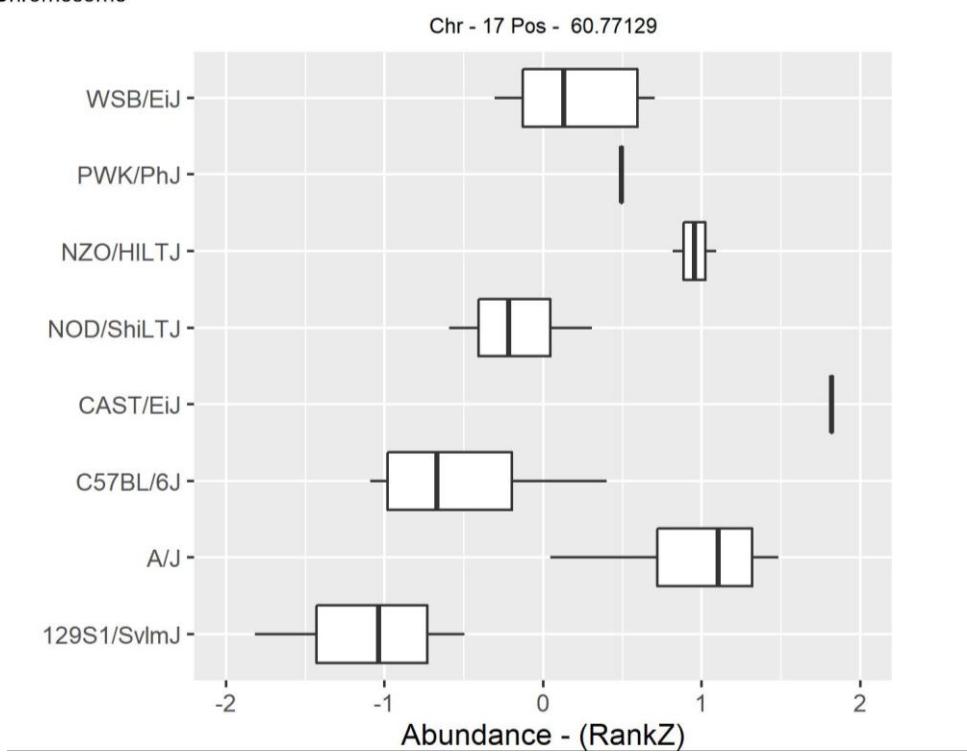
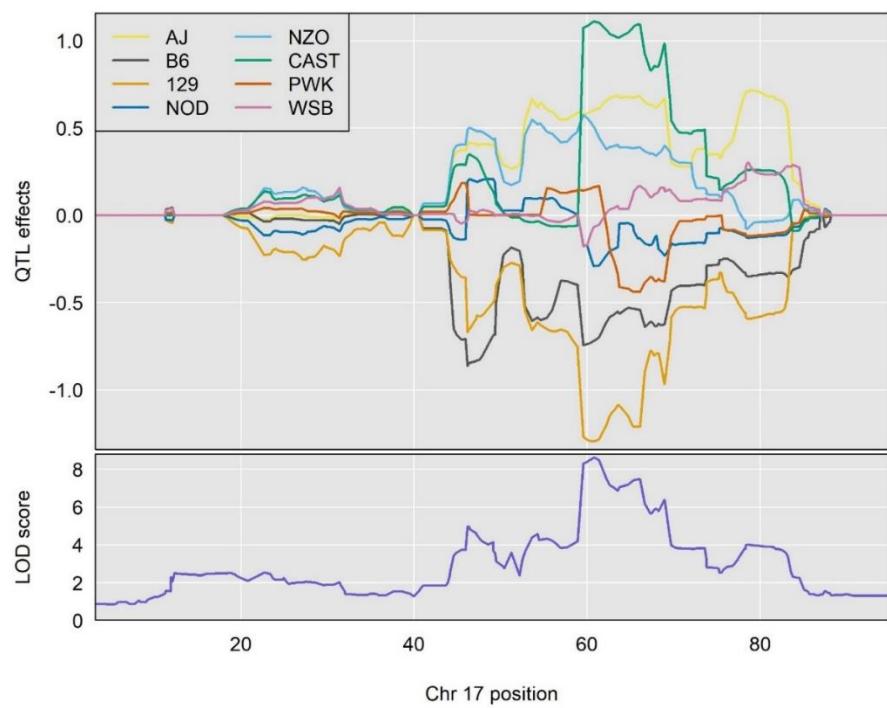
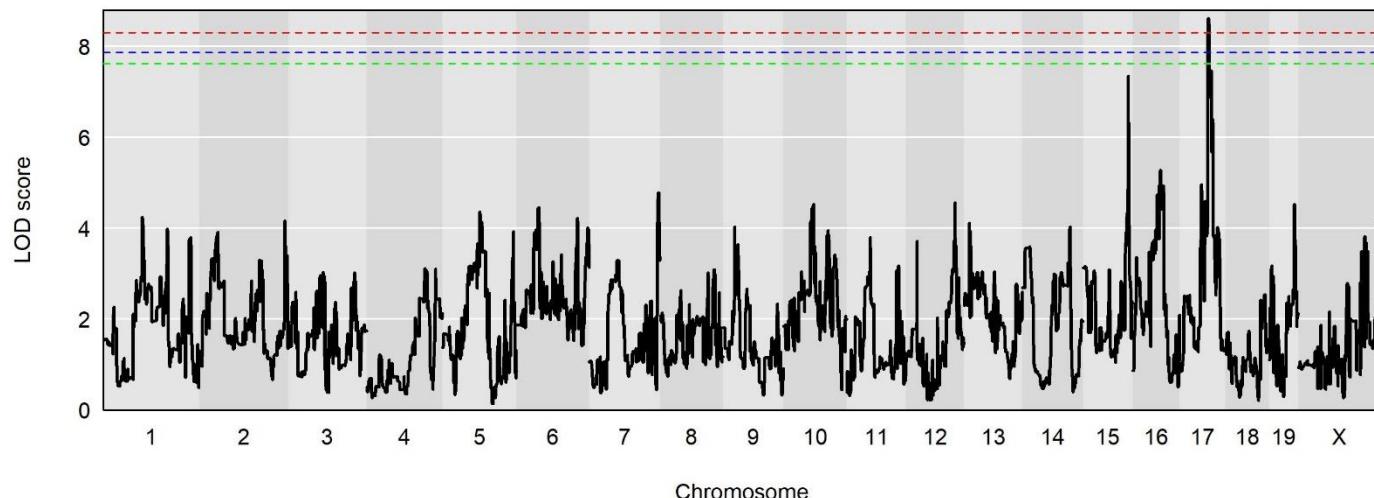


Fig Q3: Micabf3 - g_Muribaculaceae

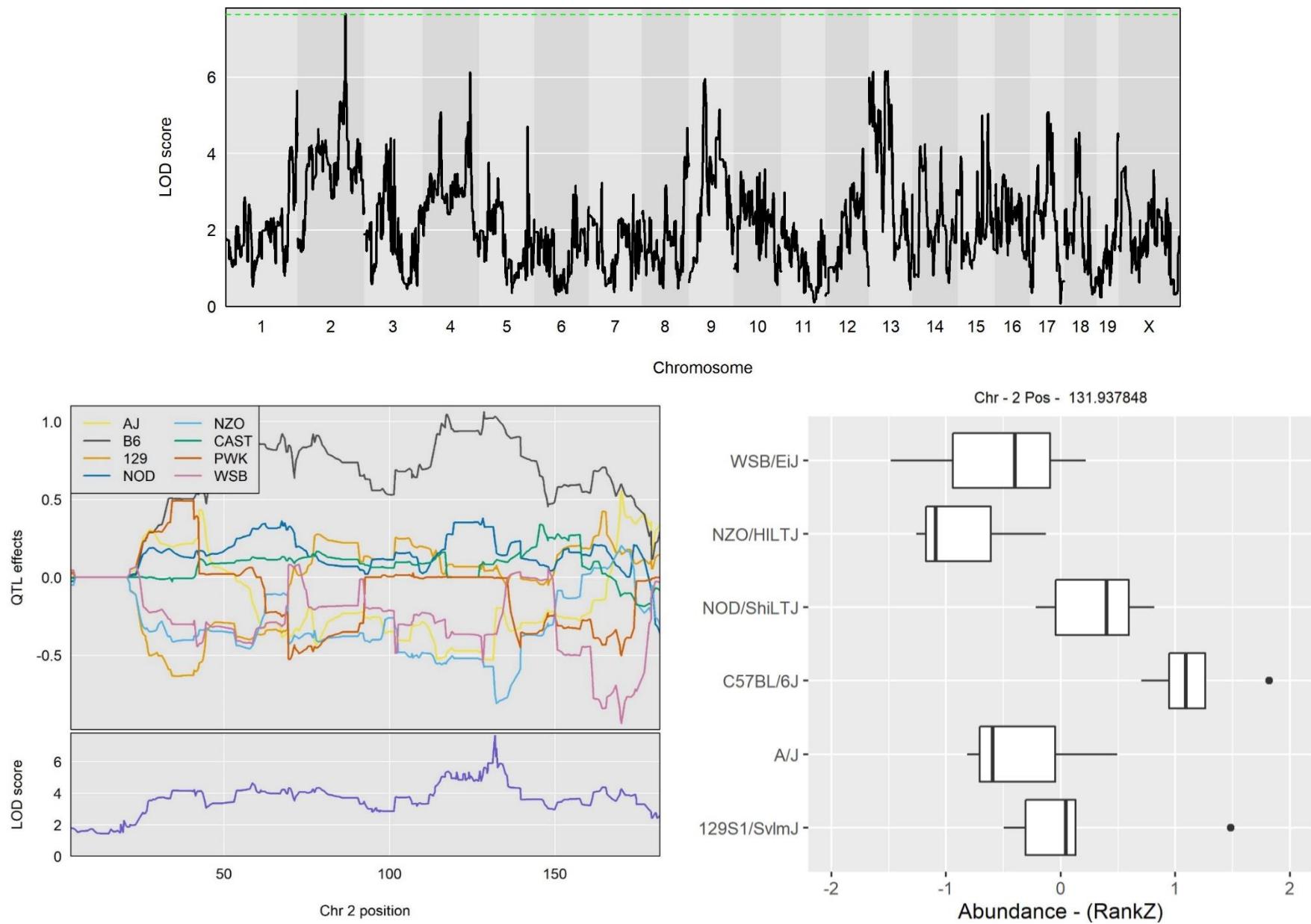


Fig Q4: Micabf4 - g_Alloprevotella

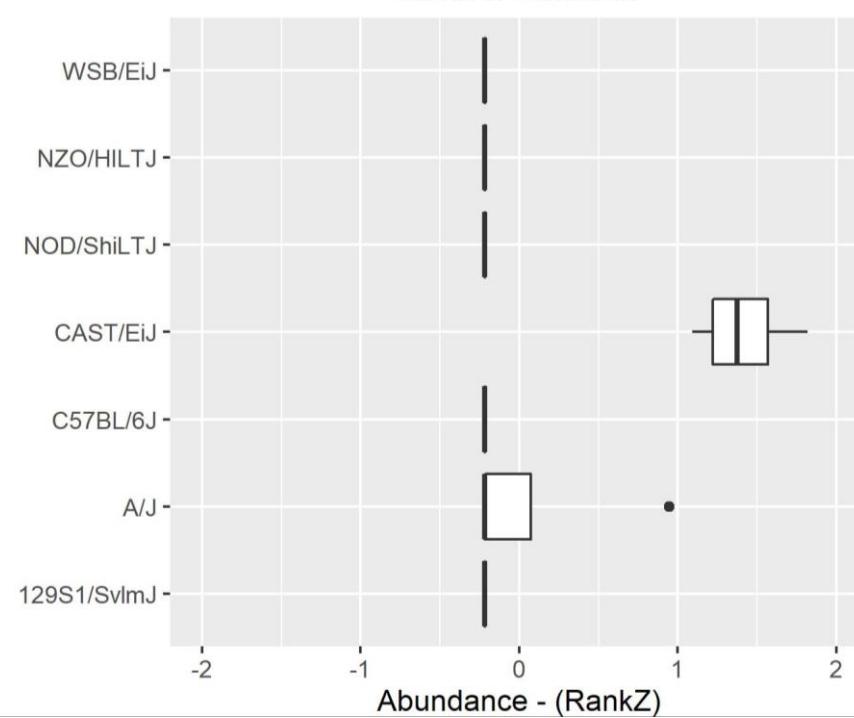
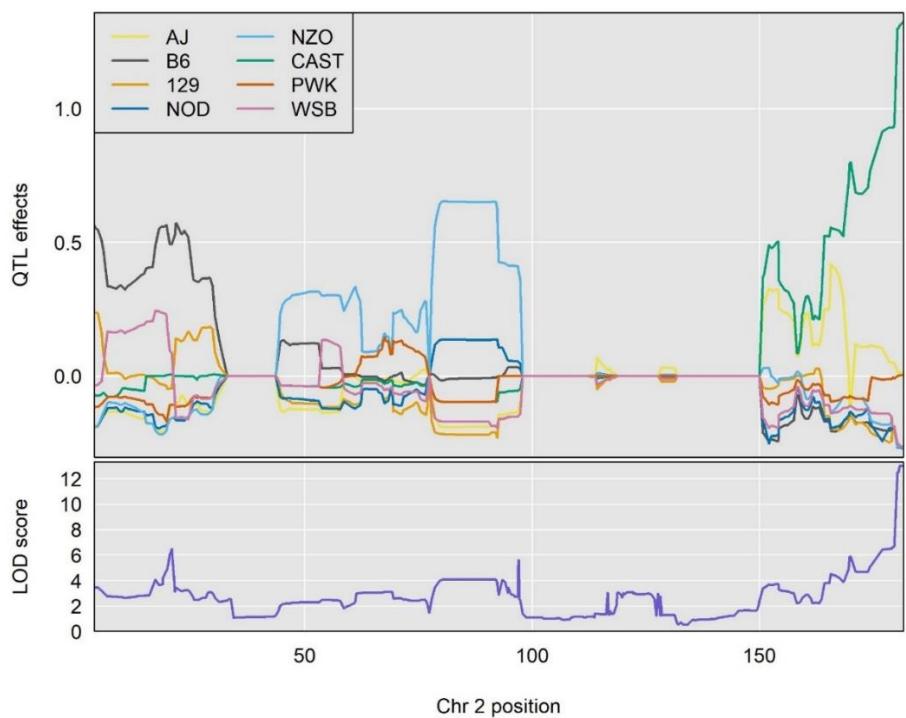
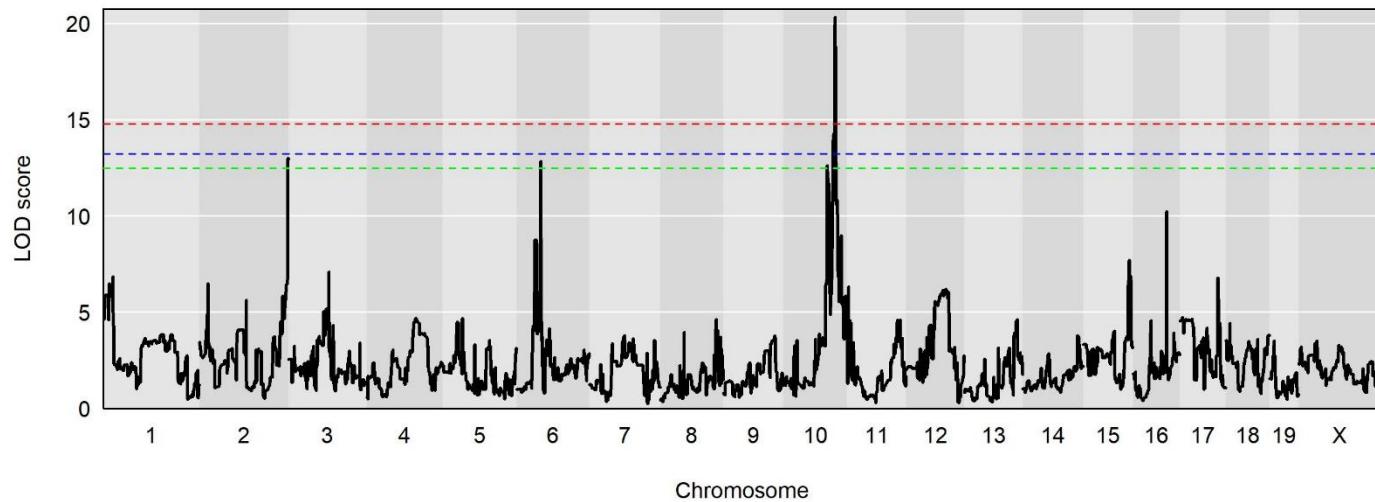


Fig Q5: Micabf5 - g_Alloprevotella

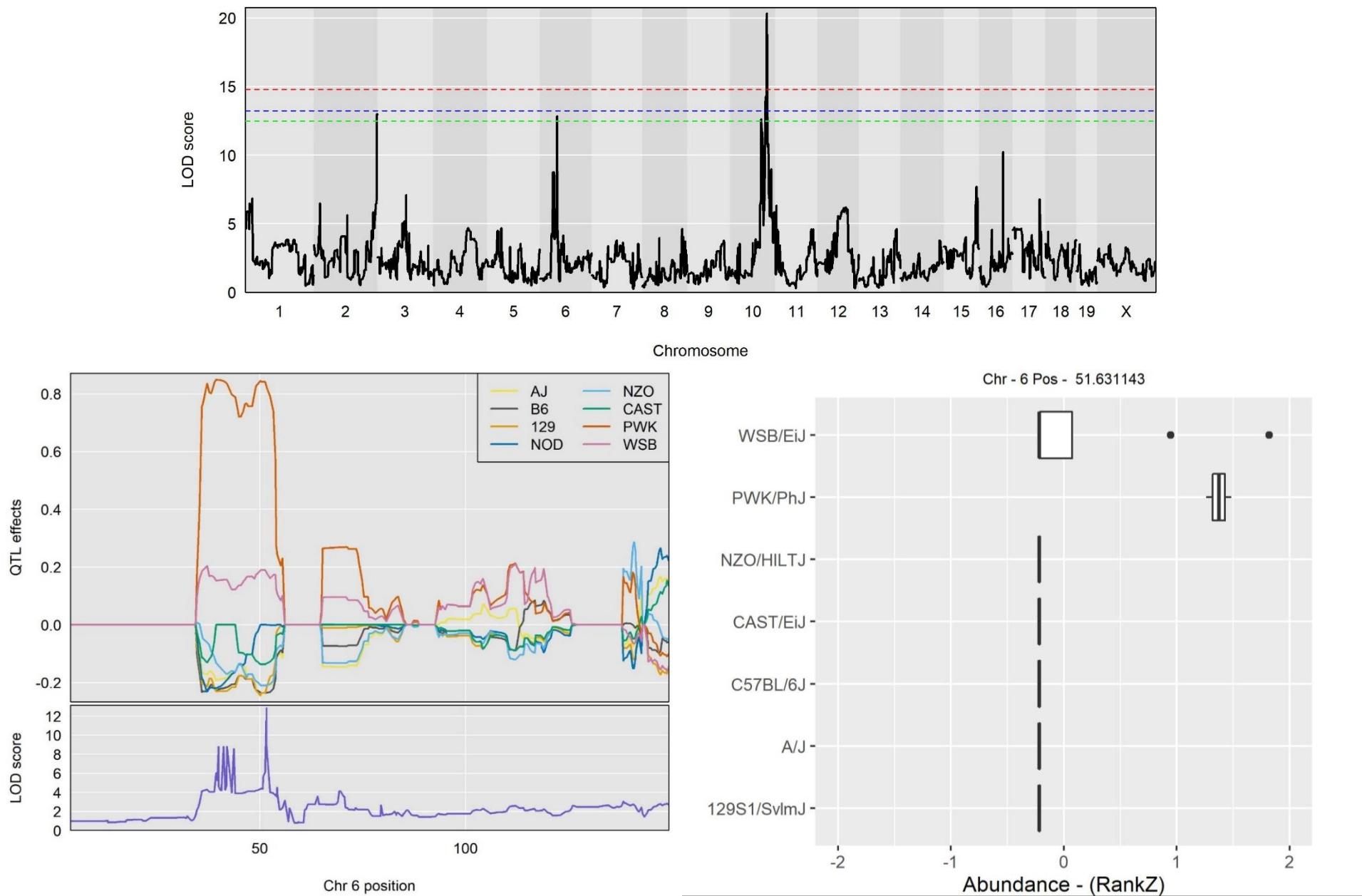


Fig Q6: Micabf6 - g_Alloprevotella

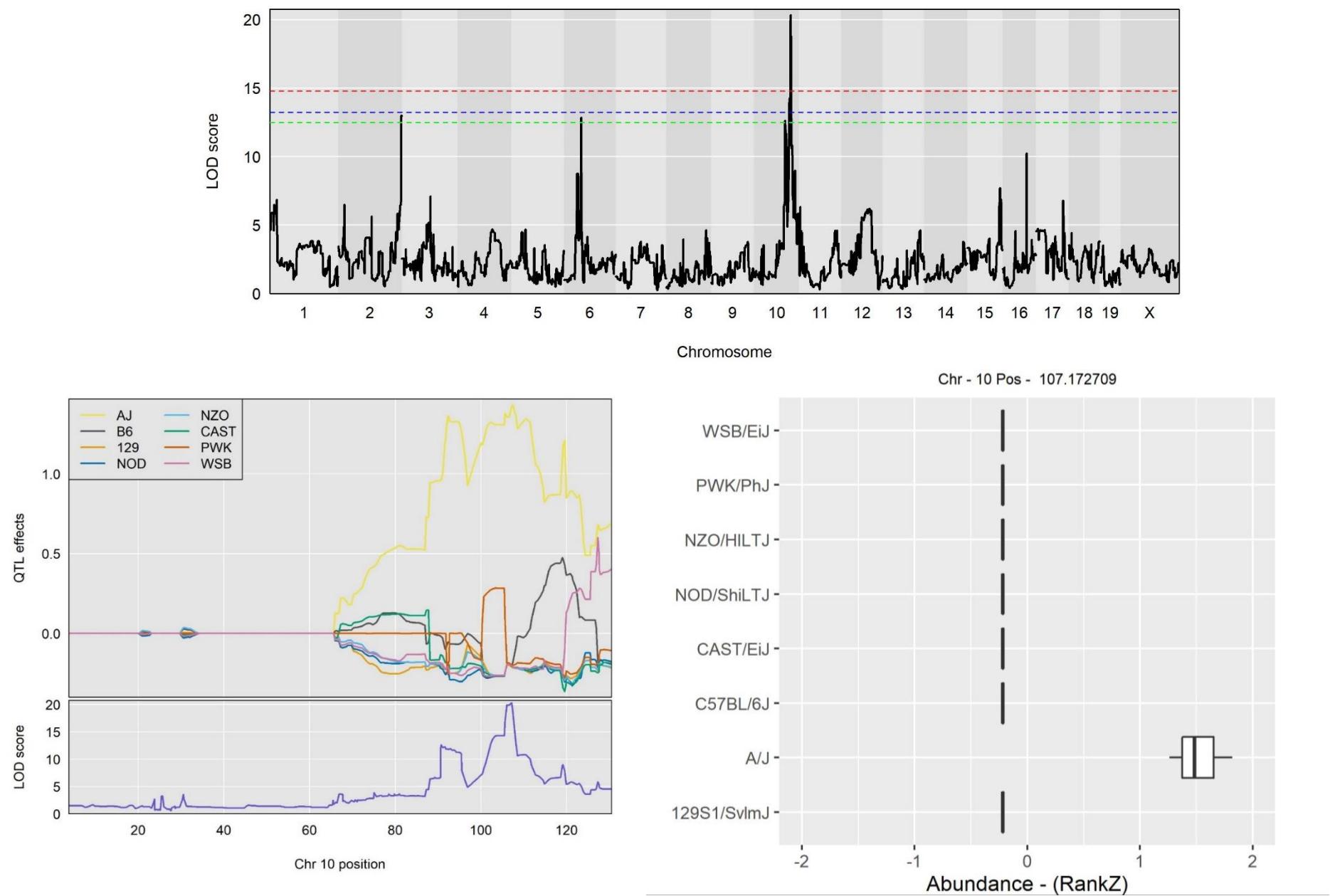


Fig Q7: Micabf7 - g_Mucispirillum

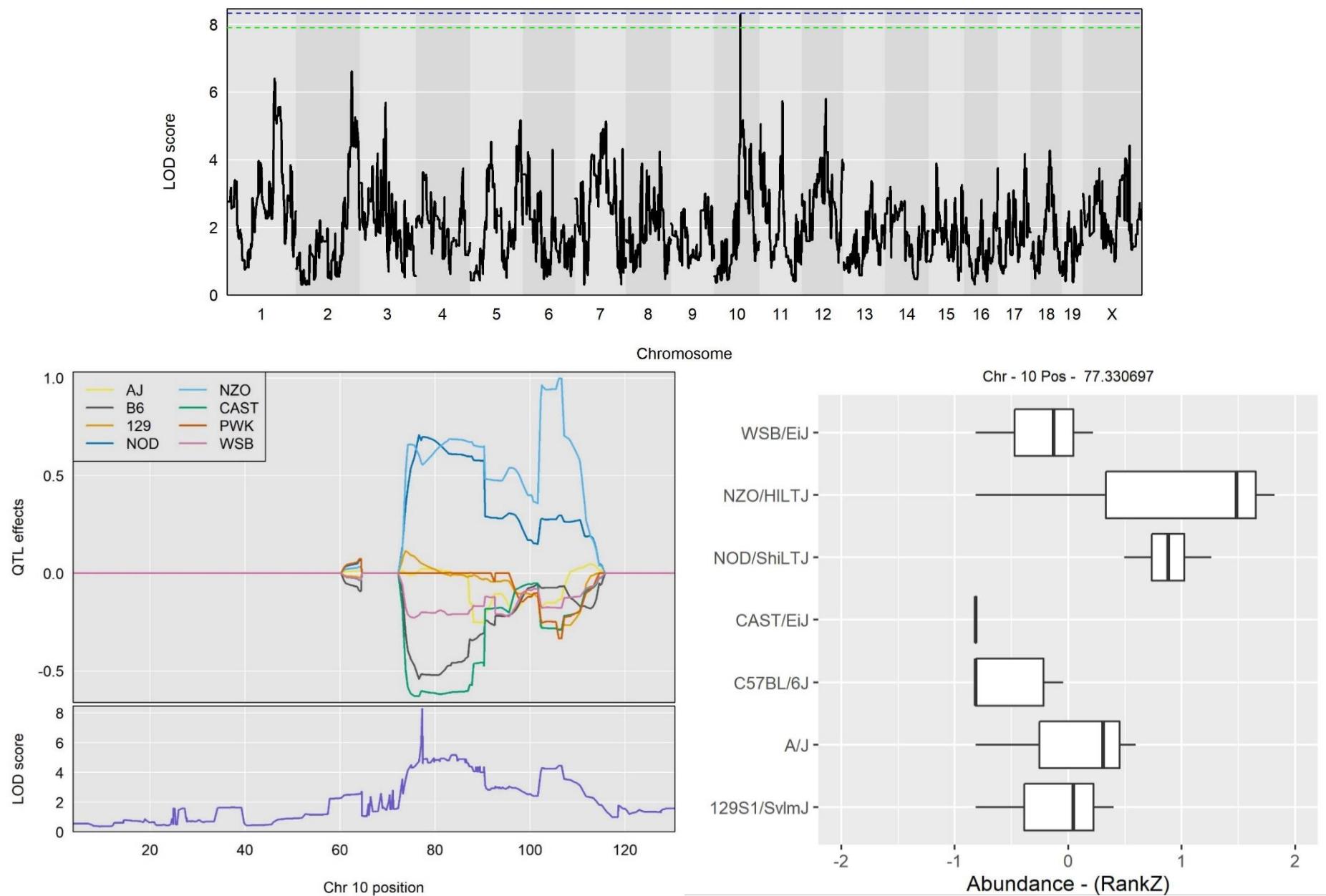


Fig Q8: *Micabf8 - f_Erysipelotrichaceae / g_A1*

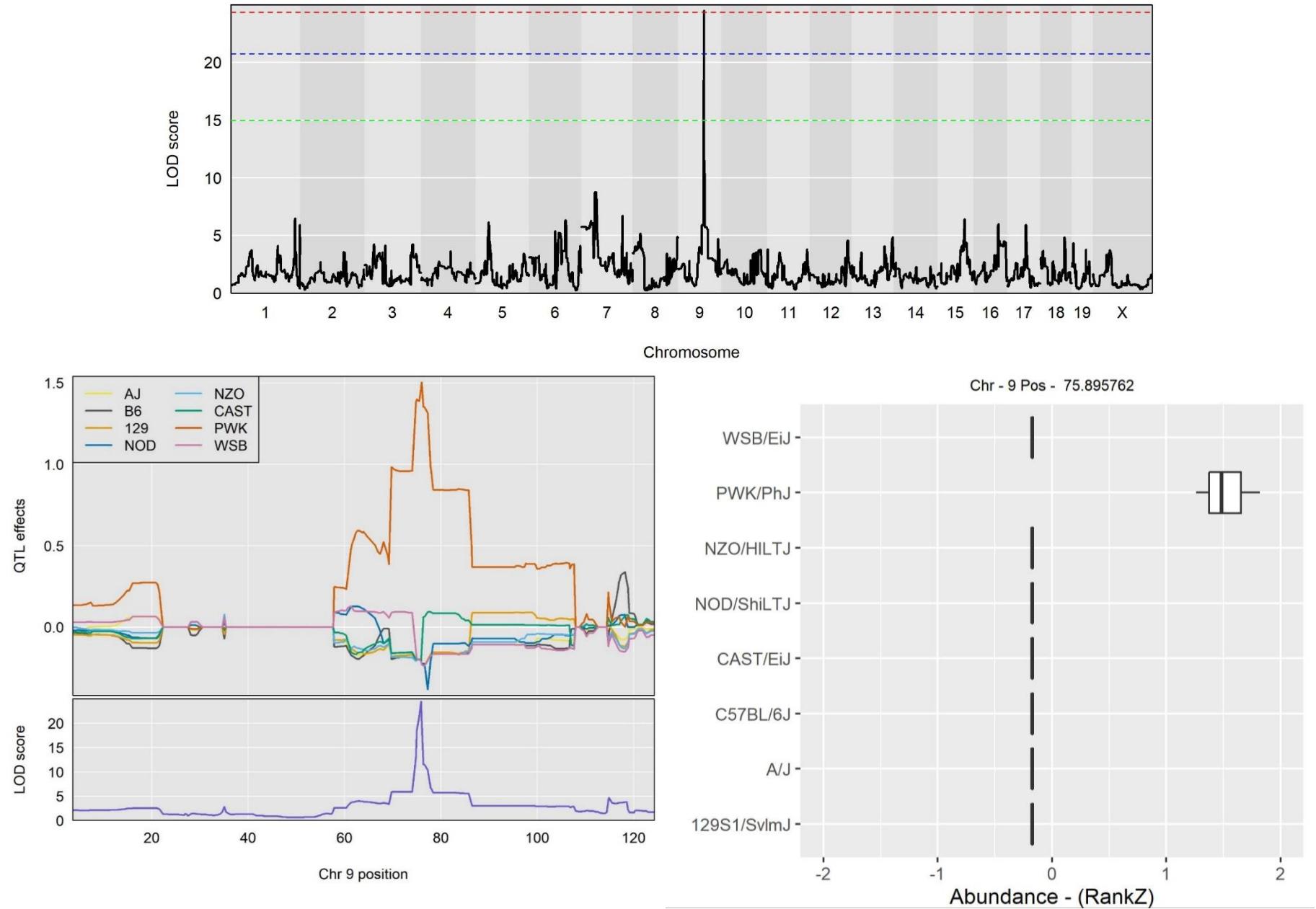


Fig Q9: Micabf9 - g_Erysipelotrichaceae

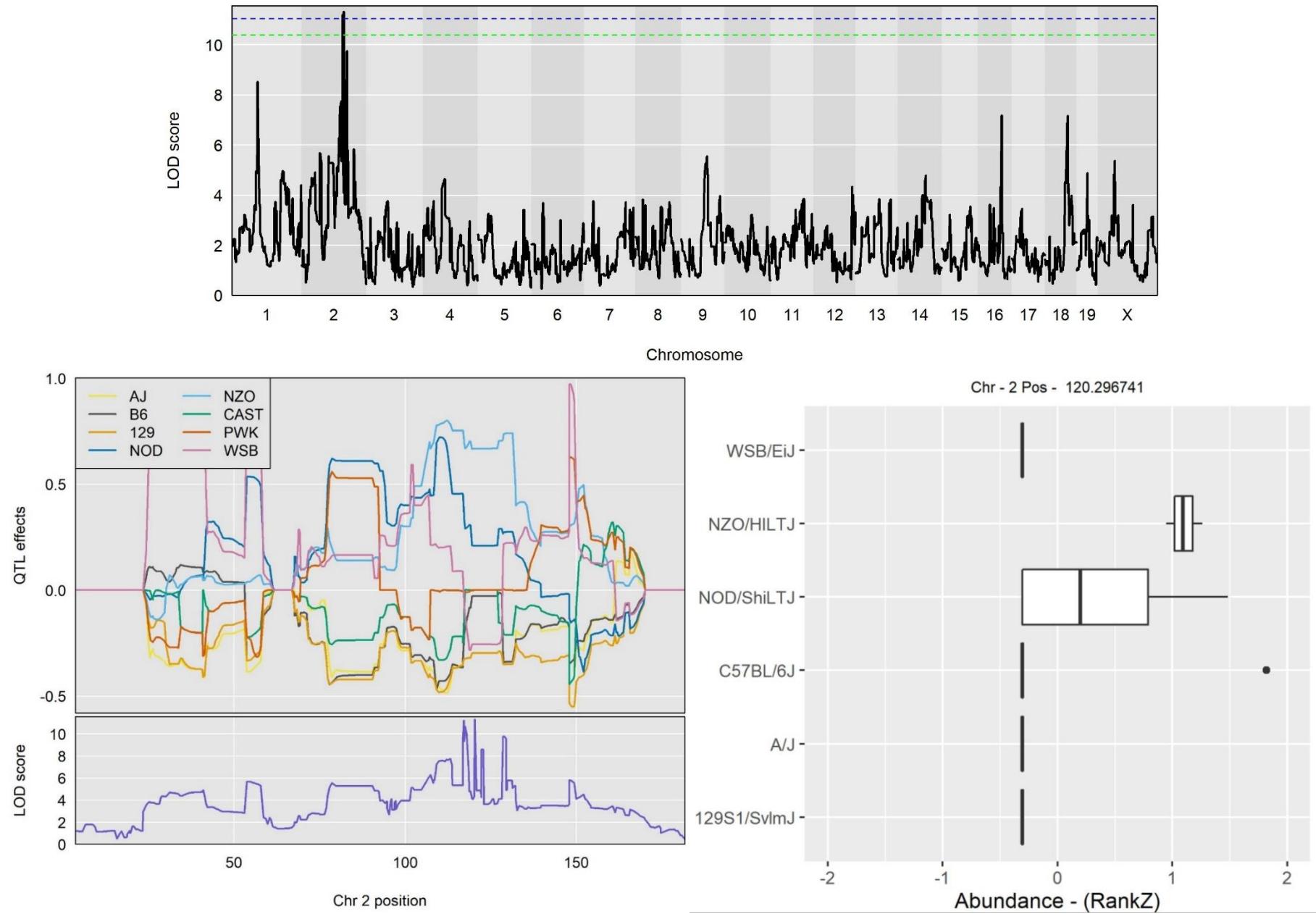


Fig Q10: Micabf10 - g_Candidatus_Arthromitus

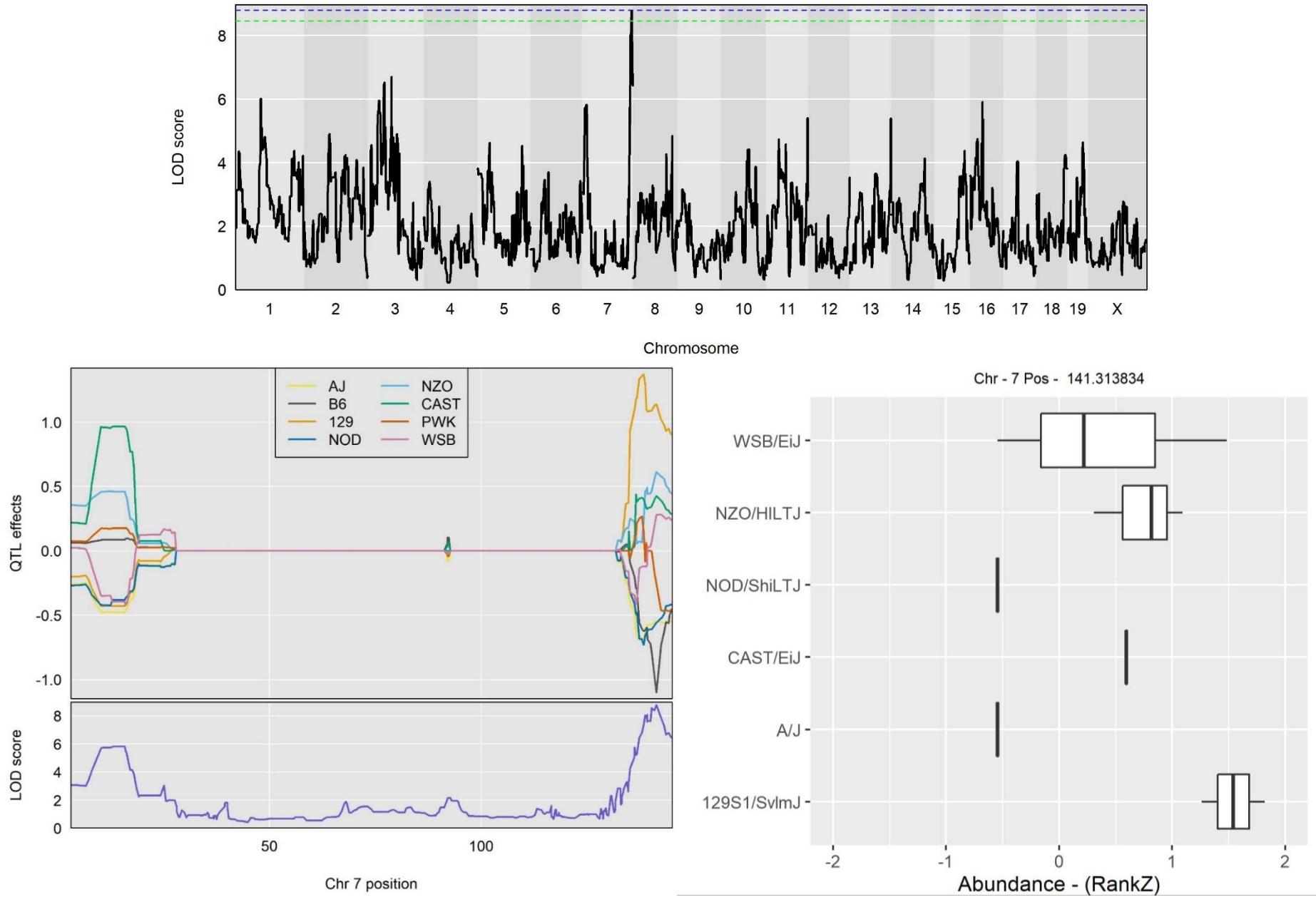


Fig Q11: Micabf11 - f_Lachnospiraceae / g_A2

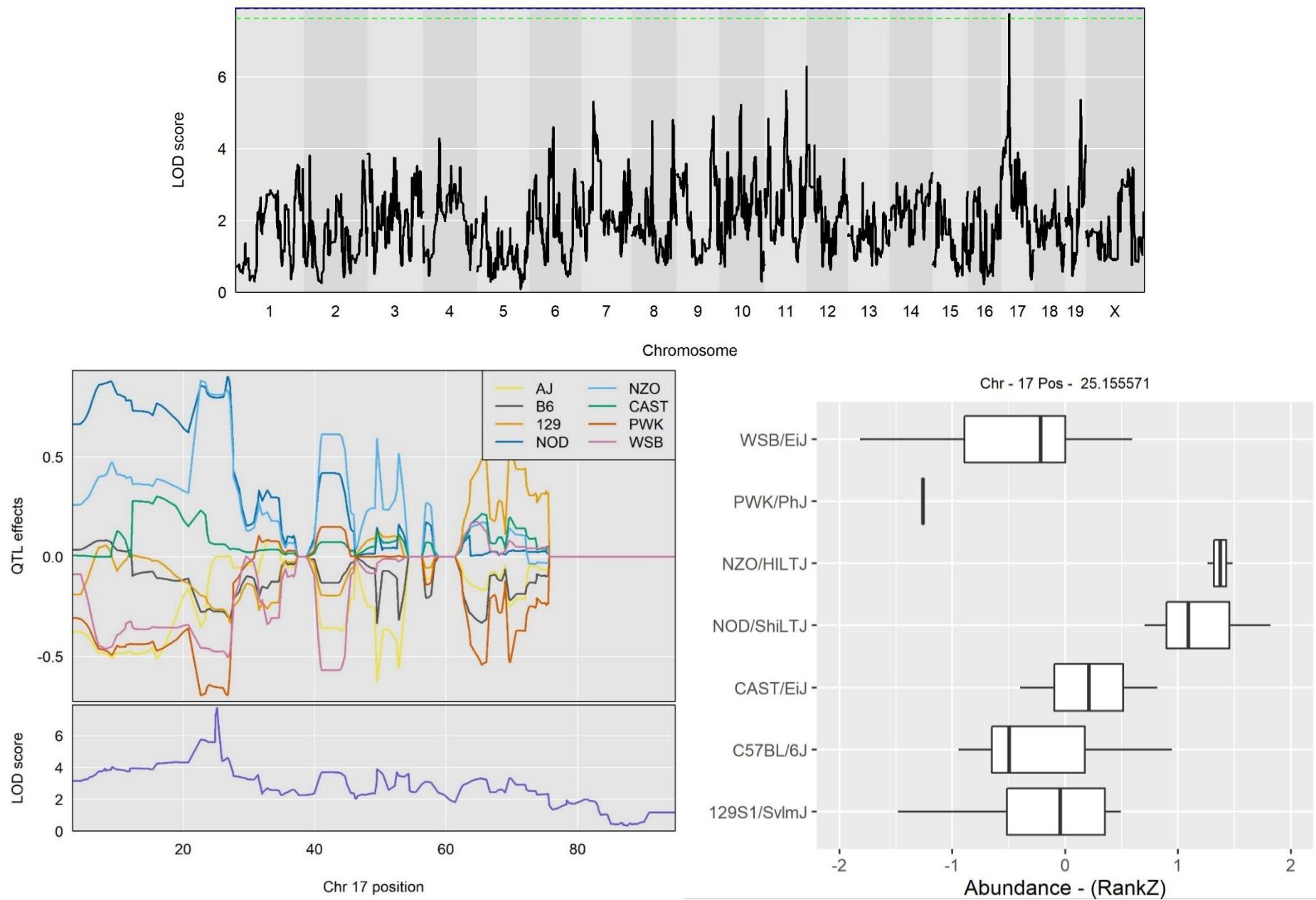


Fig Q12: Micabf12 - g_Lachnoclostridium

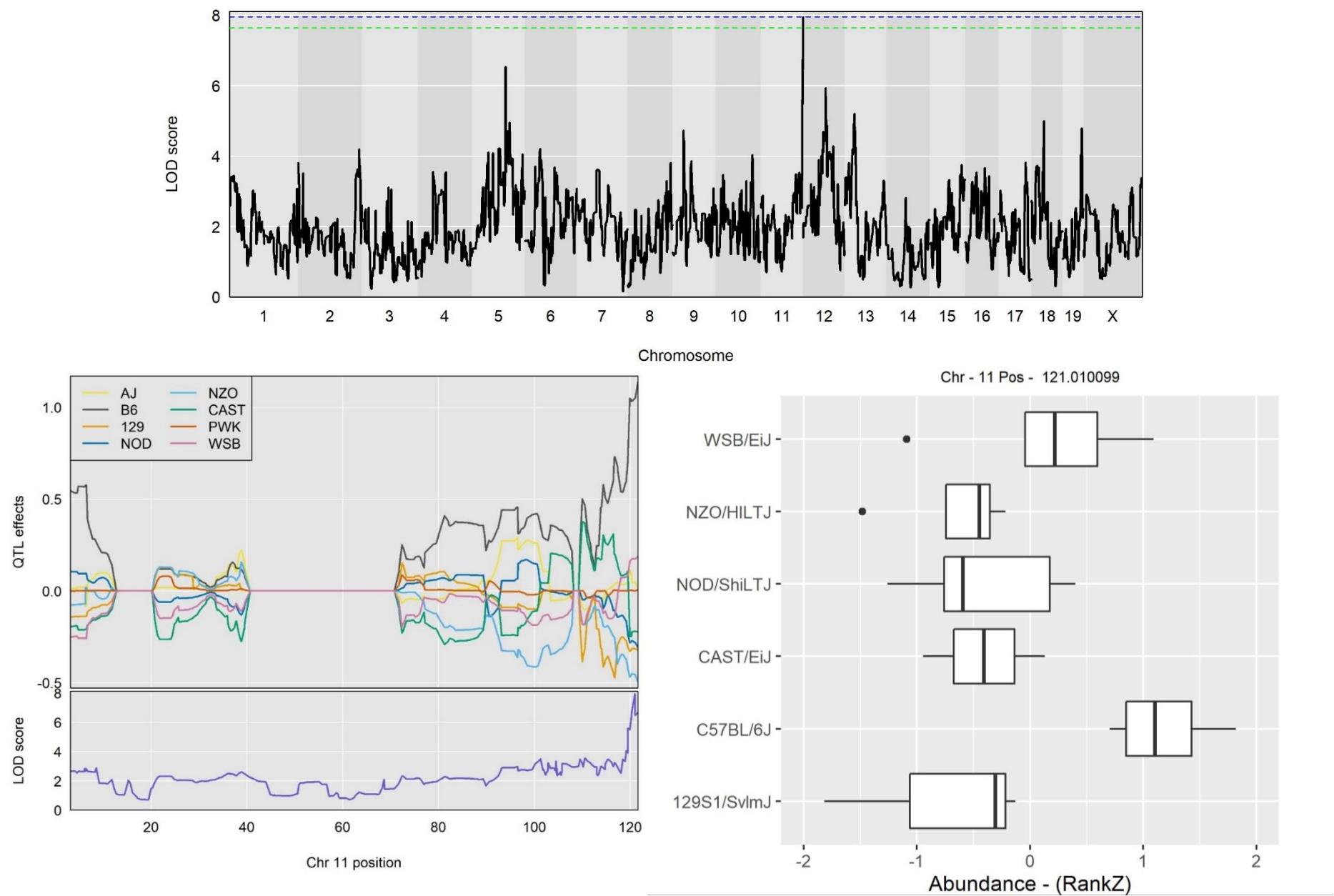


Fig Q13: *Micabf13 - g_Lachnospiraceae_UCG006*

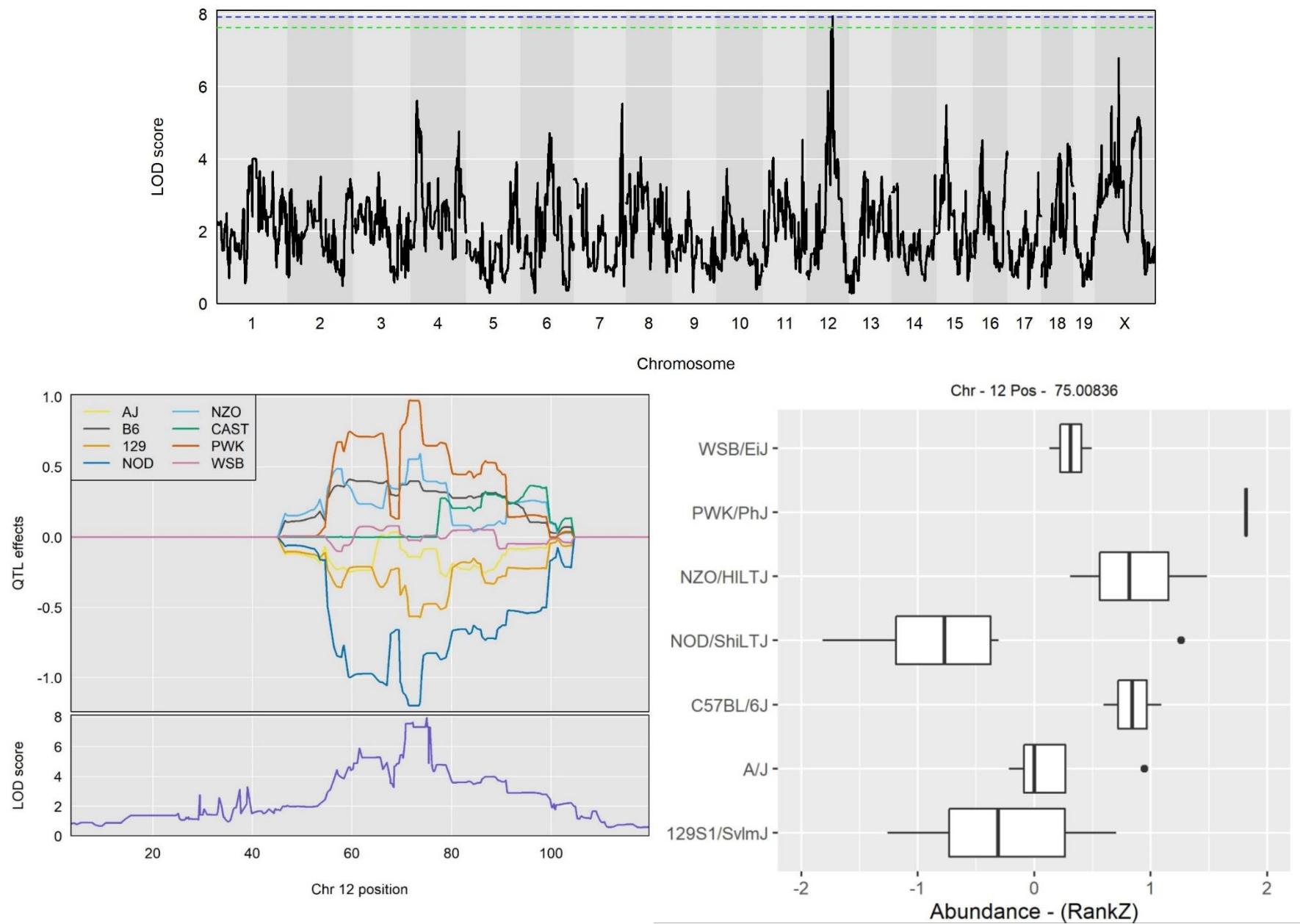


Fig Q14: Micabf14 - g_Ruminococcaceae

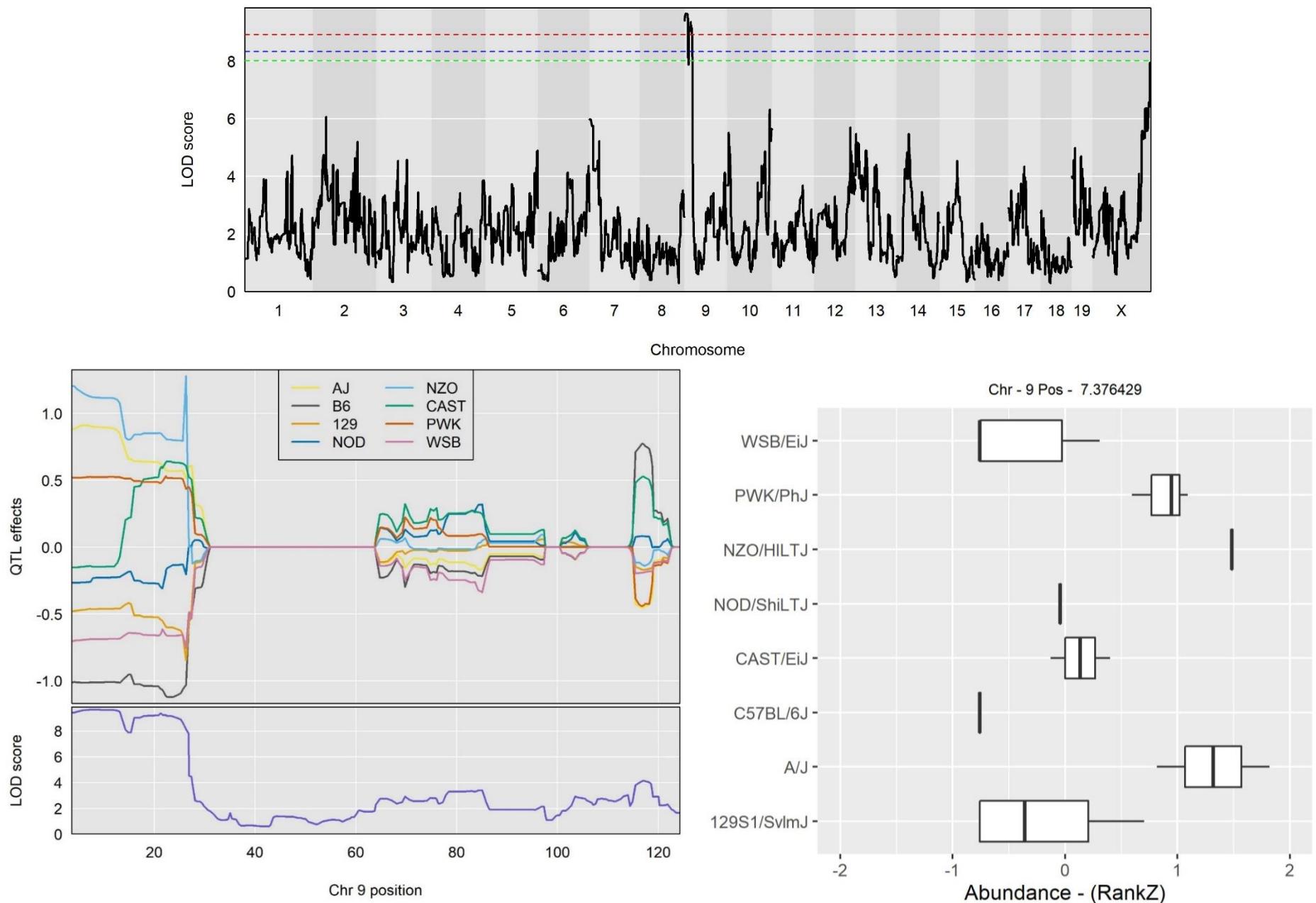


Fig Q15: *Micabf15* - o_Oscillospirales / g_UCG10

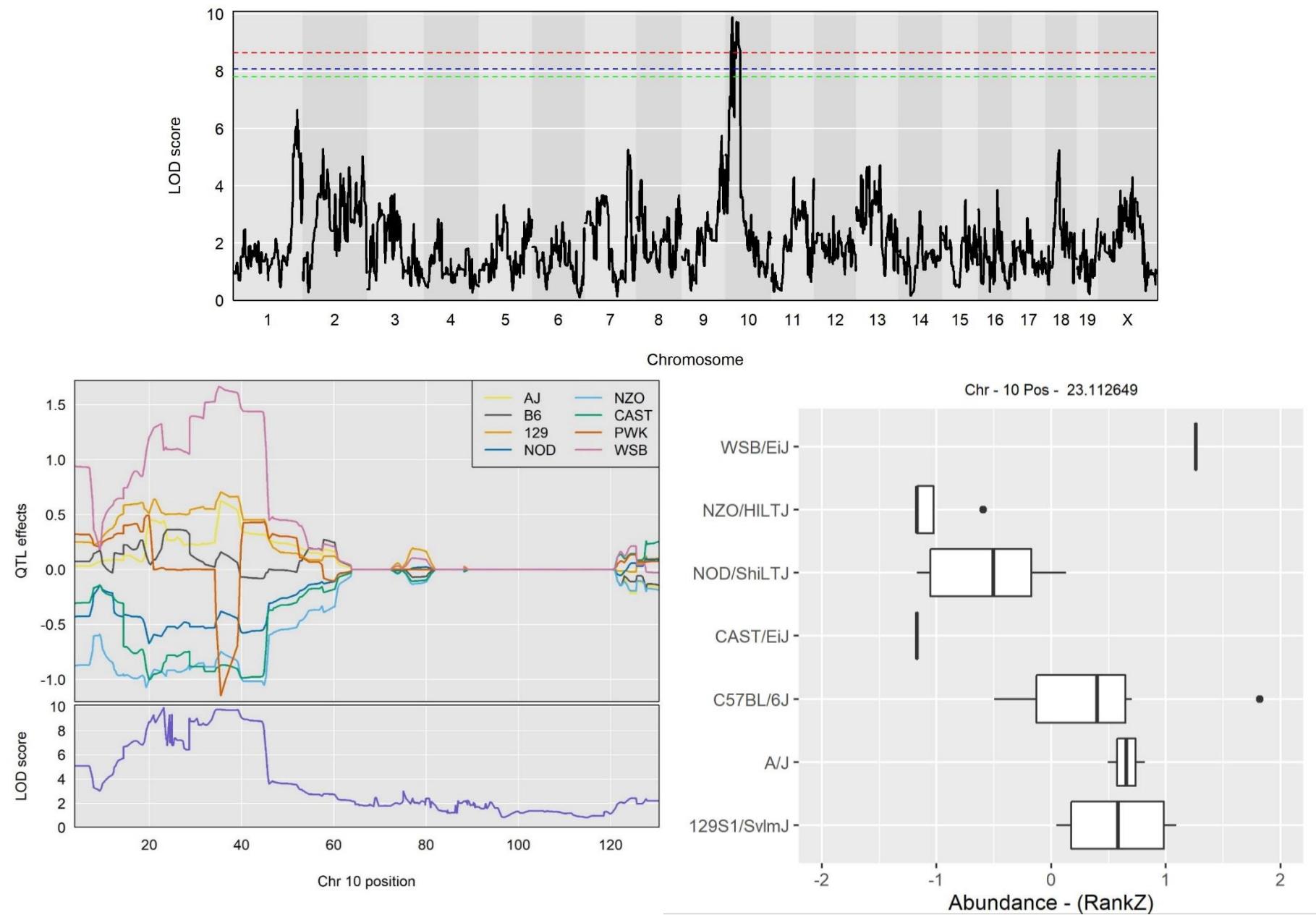


Fig Q16: Micabf16 - g_Peptococcus

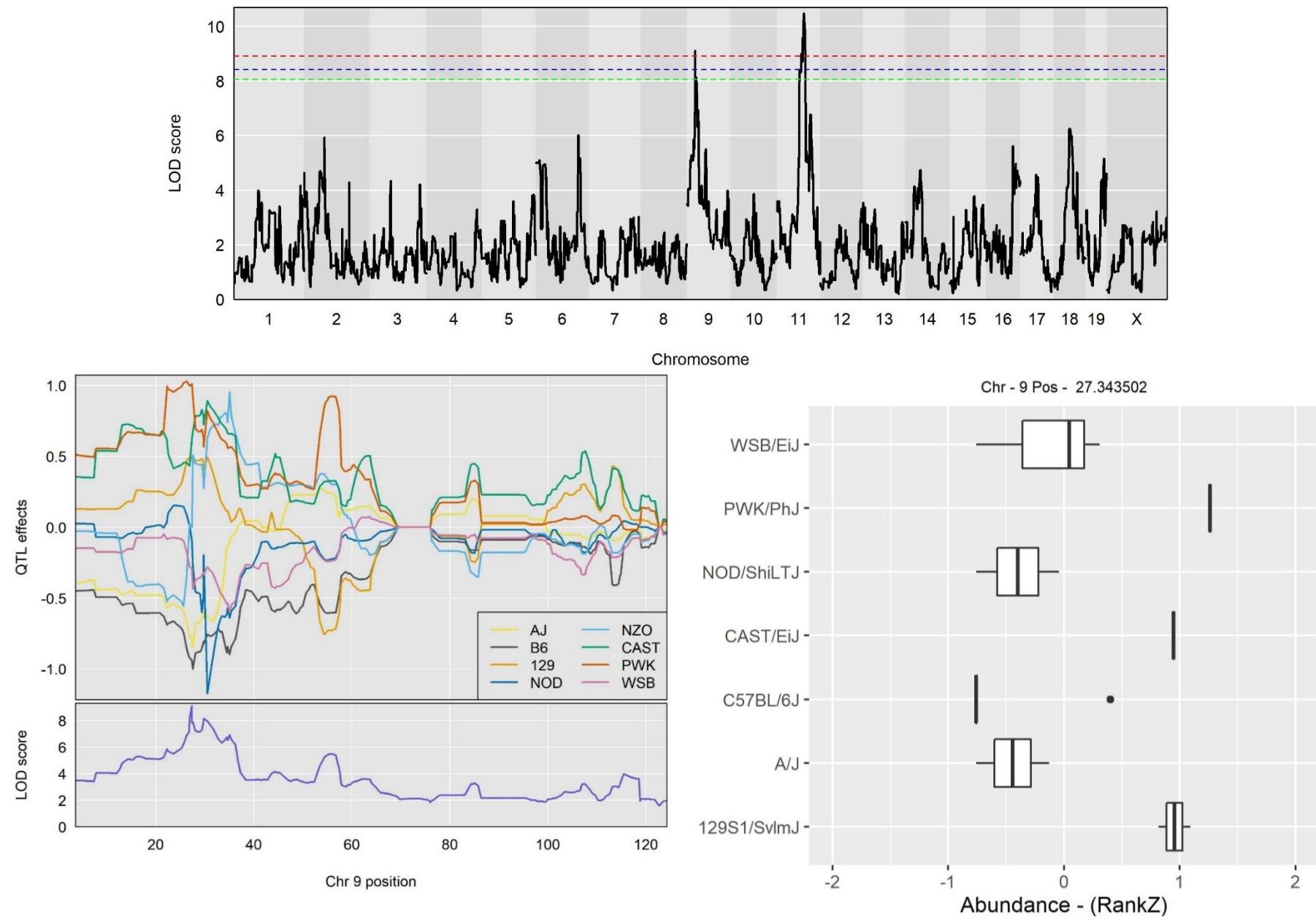


Fig Q17: Micabf17 - g_Peptococcus

