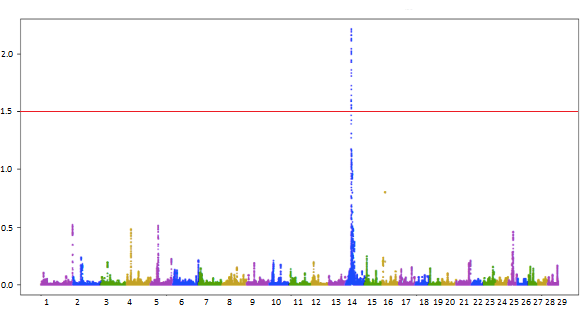
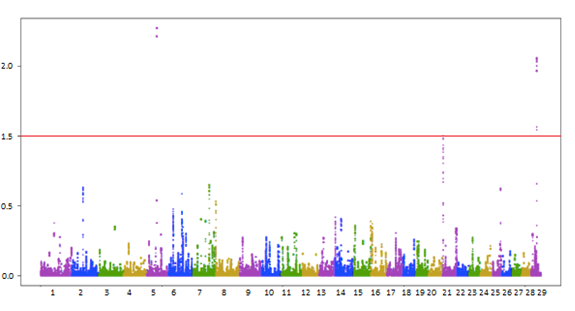
# Genome-wide association study for growth traits in Nelore cattle

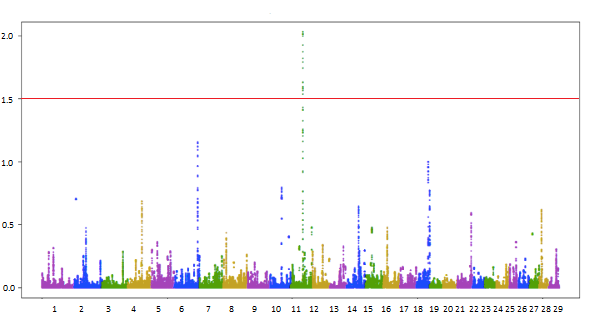
Ana Paula Nascimento Terakado1, Raphael Bermal Costa2\*, Gregório Miguel Ferreira de Camargo2, Natália Irano1, Tiago Bresolin1, Luciana Takada1, Caio Victor Damasceno Carvalho2, Henrique Nunes Oliveira1, Roberto Carvalheiro1, Fernando Baldi1, Lucia Galvão de Albuquerque1



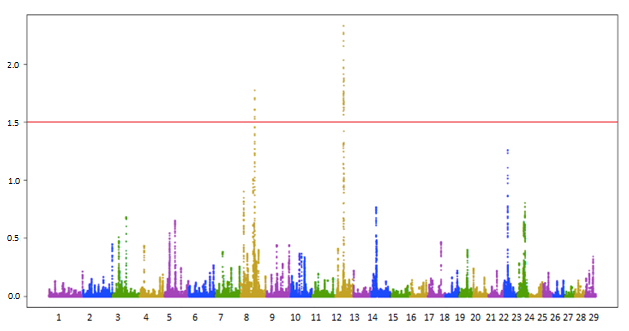
Supplementary Figure S1. Manhattan plot for birth weight. Proportion of genetic variance explained by windows of 50 adjacent SNPs (y-axis) per chromosome (x-axis).



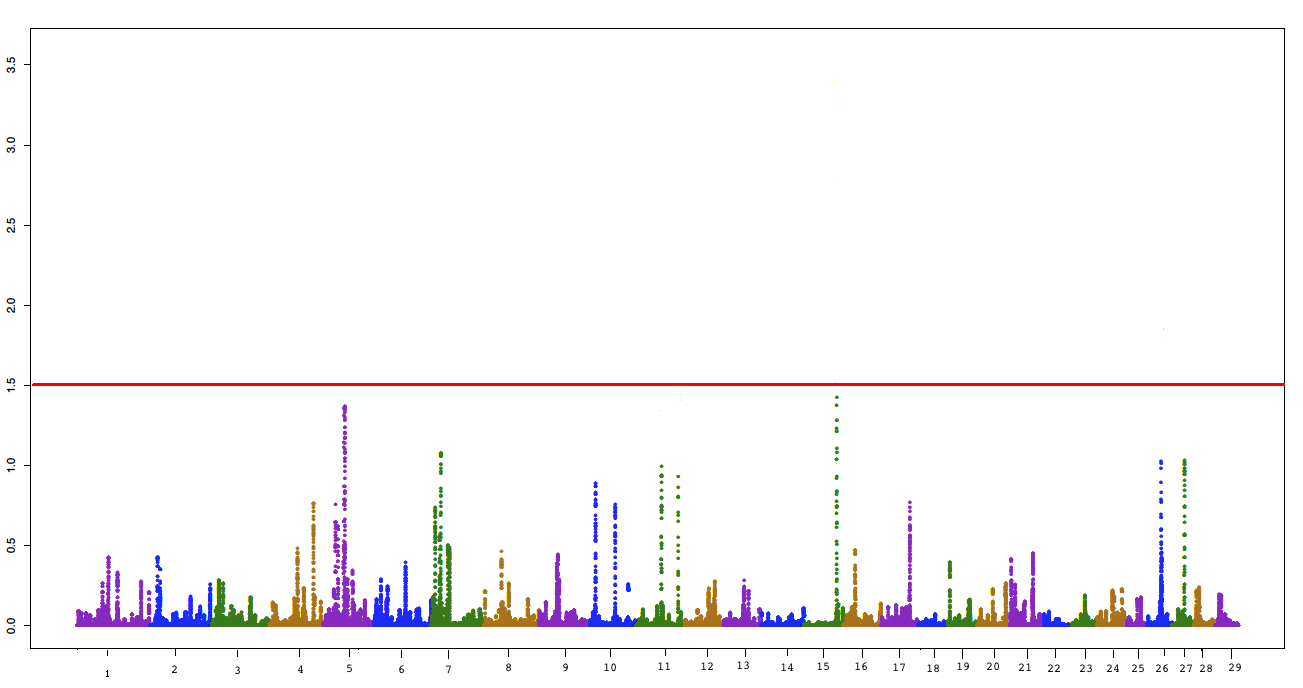
Supplementary Figure S2. Manhattan plot for weight gain from birth to weaning. Proportion of genetic variance explained by windows of 50 adjacent SNPs (y-axis) per chromosome (x-axis).



Supplementary Figure S3. Manhattan plot for weight gain from weaning to yearling. Proportion of genetic variance explained by windows of 50 adjacent SNPs (y-axis) per chromosome (x-axis).



Supplementary Figure S4. Manhattan plot for yearling height. Proportion of genetic variance explained by windows of 50 adjacent SNPs (y-axis) per chromosome (x-axis).



Supplementary Figure S5. Manhattan plot for cow weight. Proportion of genetic variance explained by windows of 50 adjacent SNPs (y-axis) per chromosome (x-axis).