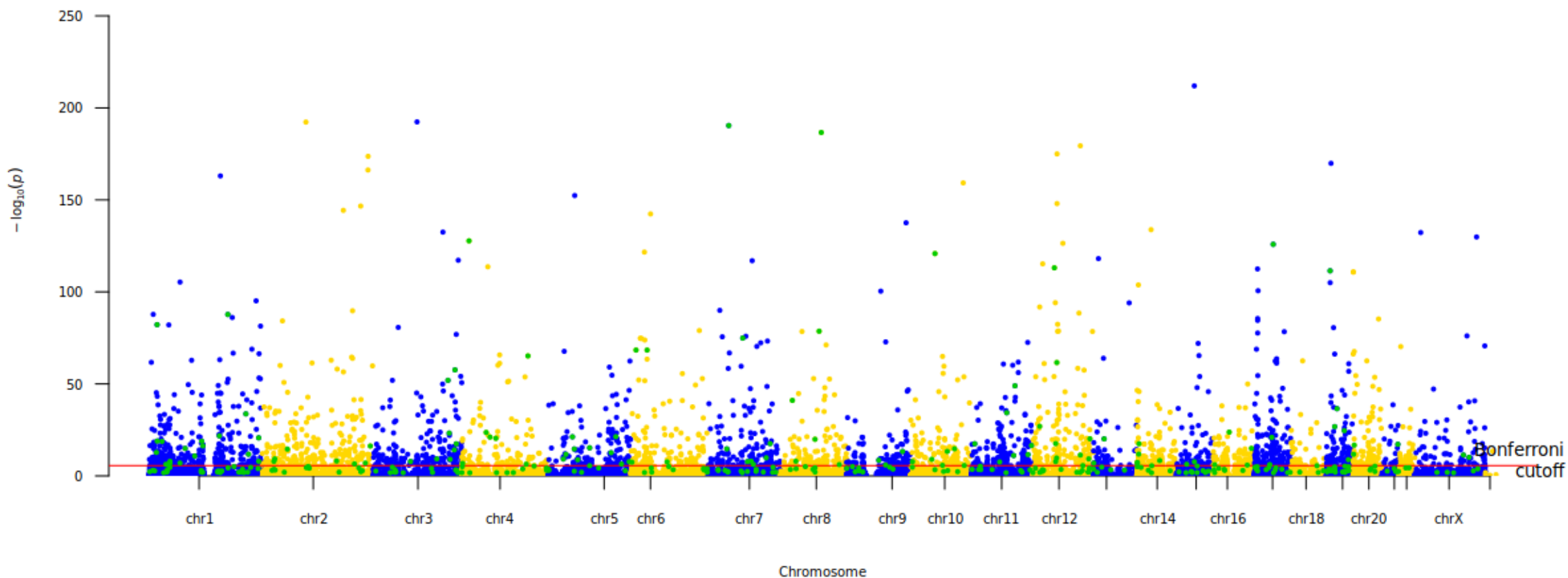


# pvalue - group\_full\_UWB1.289\_ctr vs\_UWB1.289\_CT913

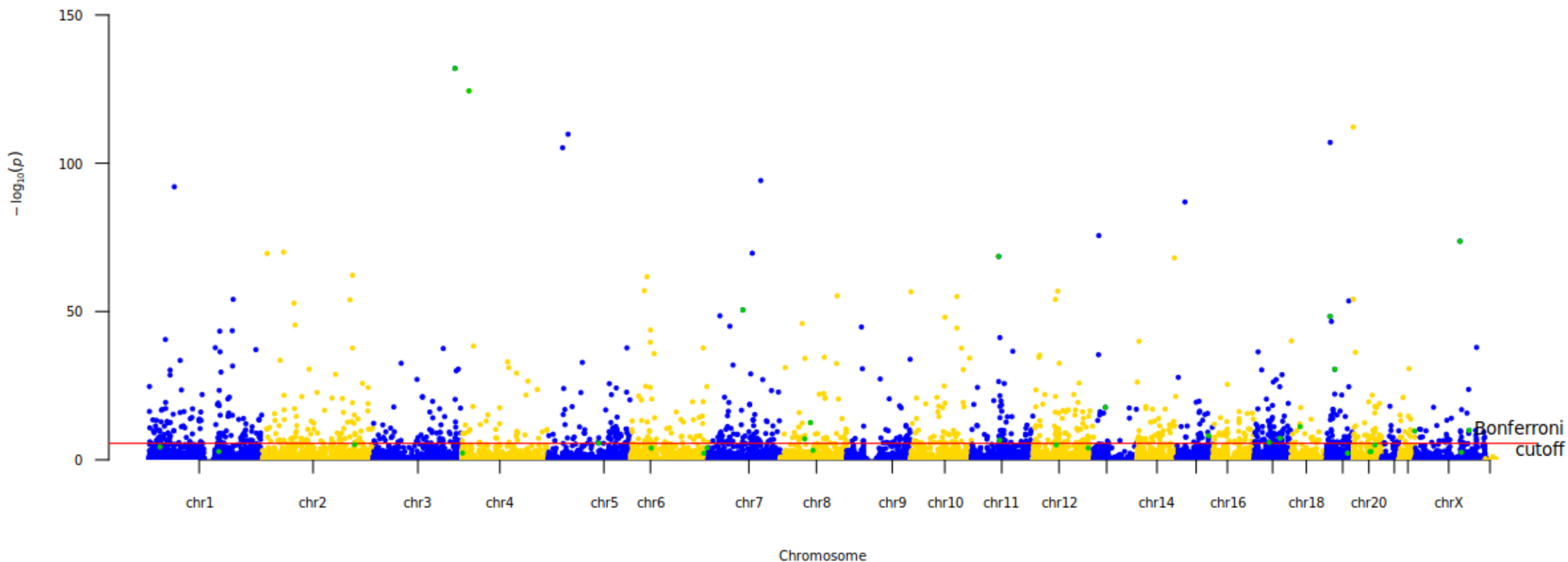
6572 genes with p-adjusted  $< 0.05$

green: padj $<0.05$  & abs(log2FC)  $>2$  -> 331 genes



# pvalue - group\_full UWB1.289 ctr vs UWB1.289\_CT\_M1

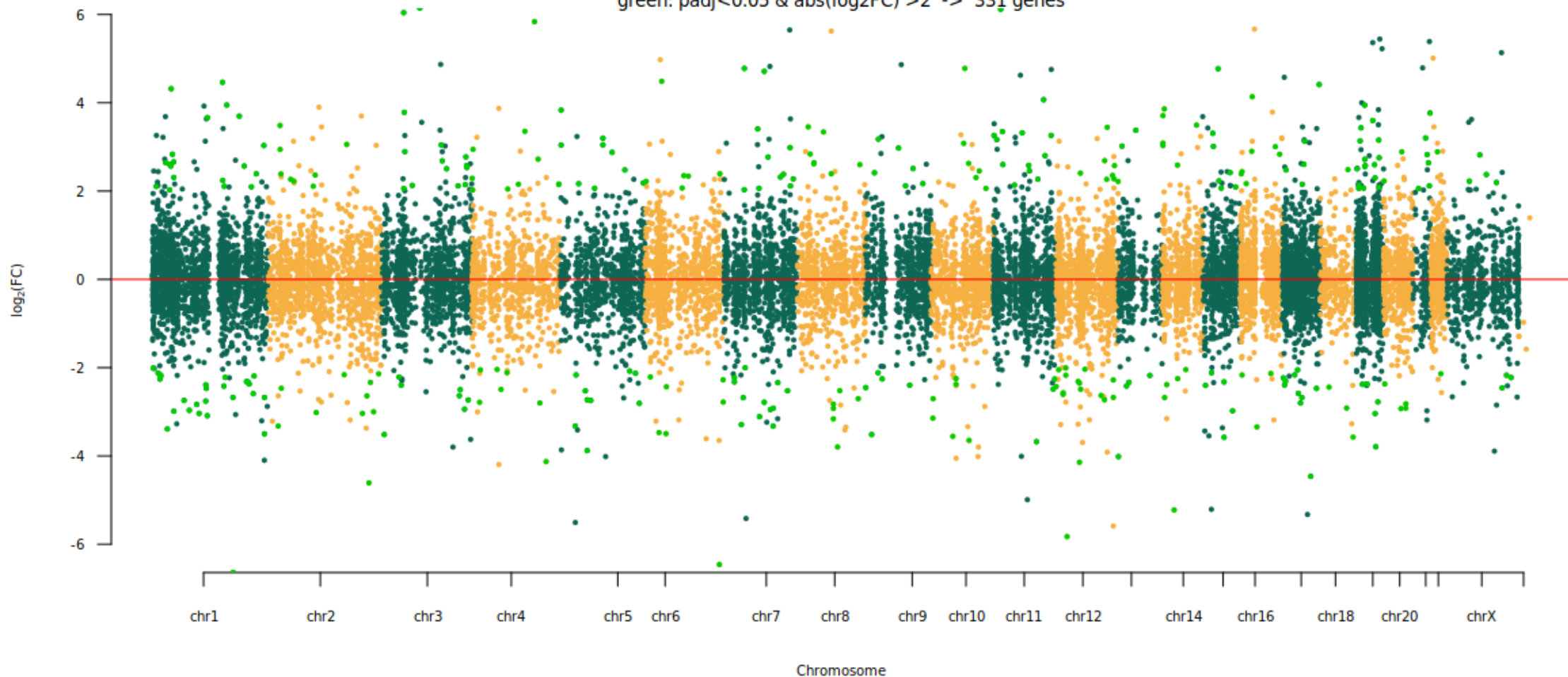
3440 genes with p-adjusted  $< 0.05$   
green: padj $<0.05$  & abs(log2FC)  $>2$  -> 34 genes



# log2FoldChange - group\_full\_UWB1.289\_ctr\_vs\_UWB1.289\_CT913

6572 genes with p-adjusted < 0.05

green: padj<0.05 & abs(log2FC) >2 -> 331 genes



# log2FoldChange - group\_full\_UWB1.289\_ctr\_vs\_UWB1.289\_CT\_M1

3440 genes with p-adjusted < 0.05

green: padj<0.05 & abs(log2FC) >2 -> 34 genes

