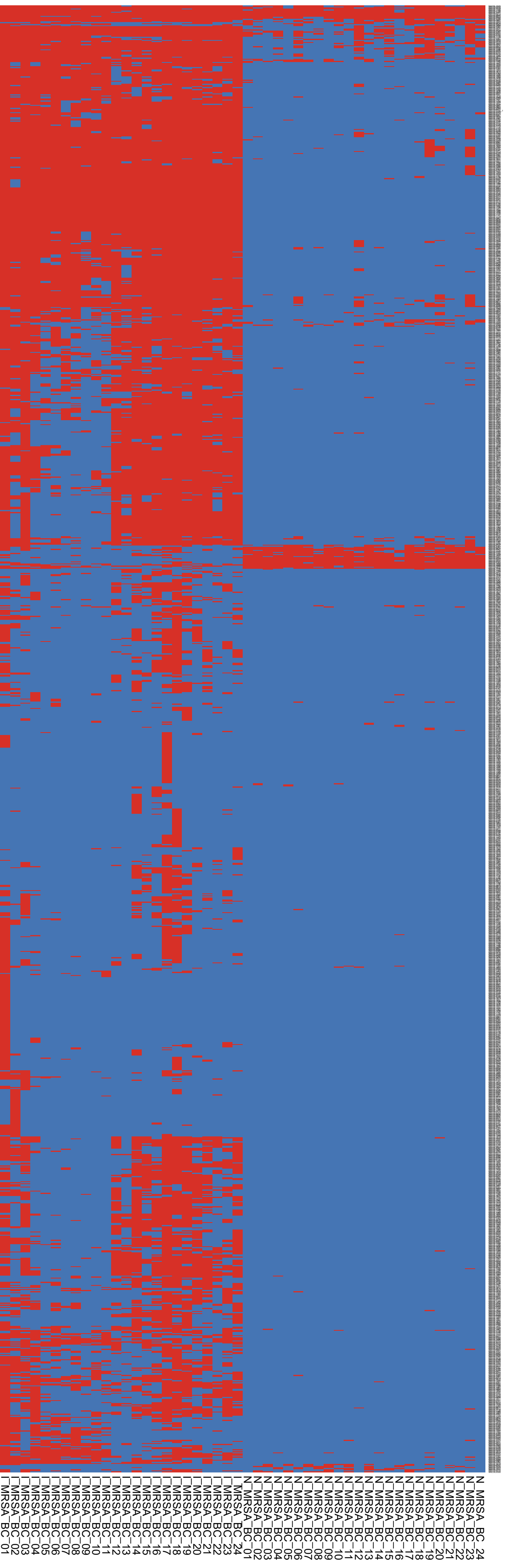
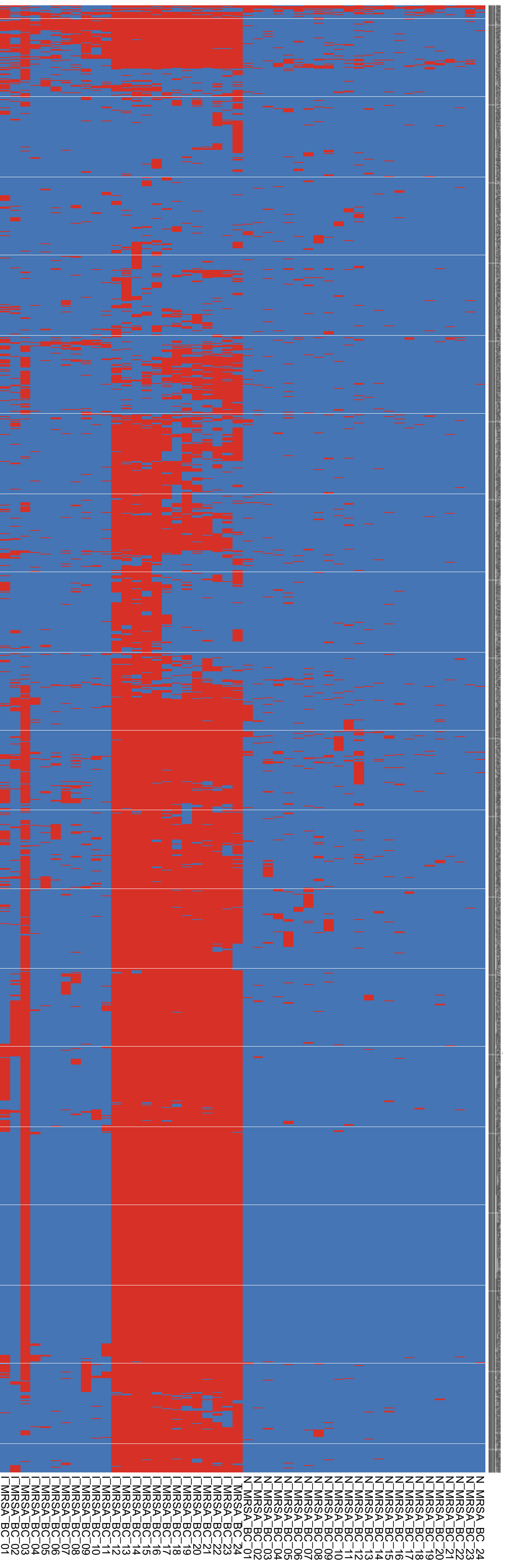


Genes with mapQ <55 (MRSA, Hybrid)



Genes with coverage that differs $\pm 25\%$ from the mean (MRSA, Hybrid)



Supplementary Figure 5: Heatmaps of eye-catching and potentially due to different filters excluded genes in the hybrid validation experiment 3 part 1 on MRSA data. Shown are genes with more than 50% of heterozygous variant-calls, genes with below 55 mapping quality and genes with a coverage that differs more than 25% from the mean.