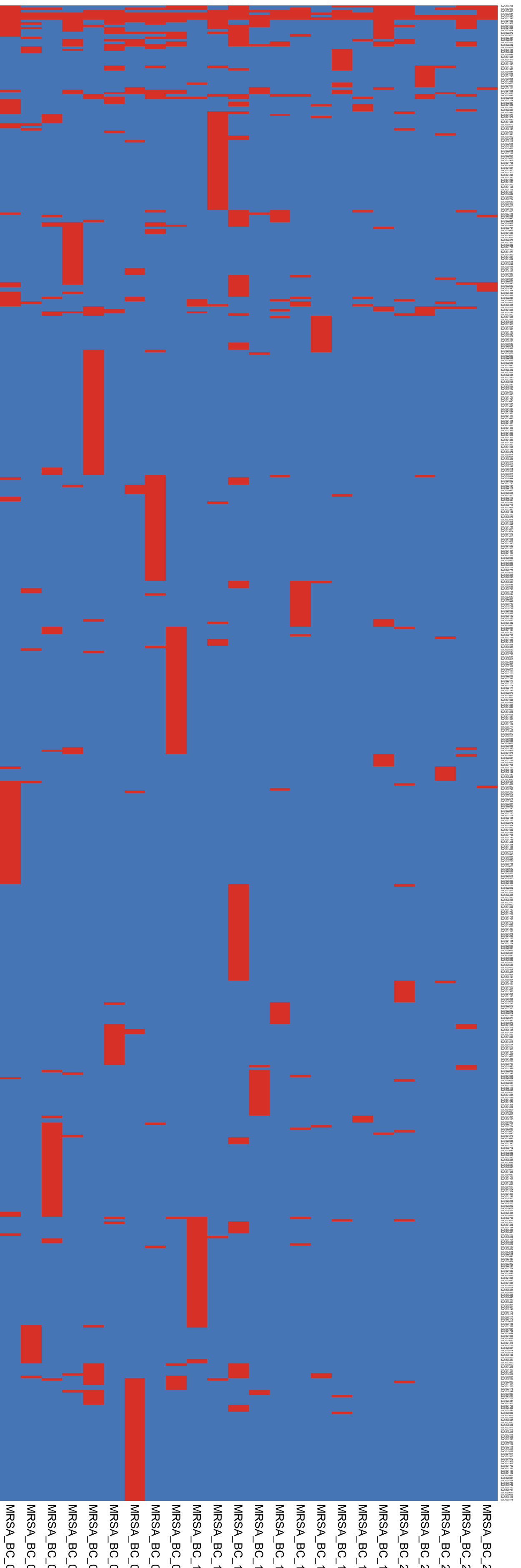






Genes with coverage that differs  $\pm 25\%$  from the mean (MRSA, Nanopore-only)



**Supplementary Figure 2:** Heatmaps of eye-catching and potentially due to different filters excluded genes in the Nanopore-only validation experiment 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.