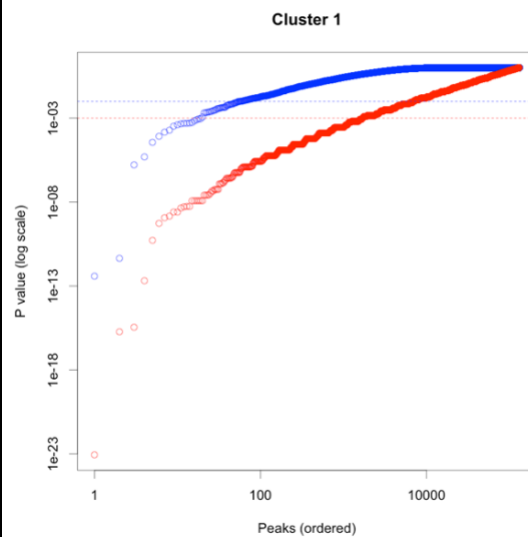
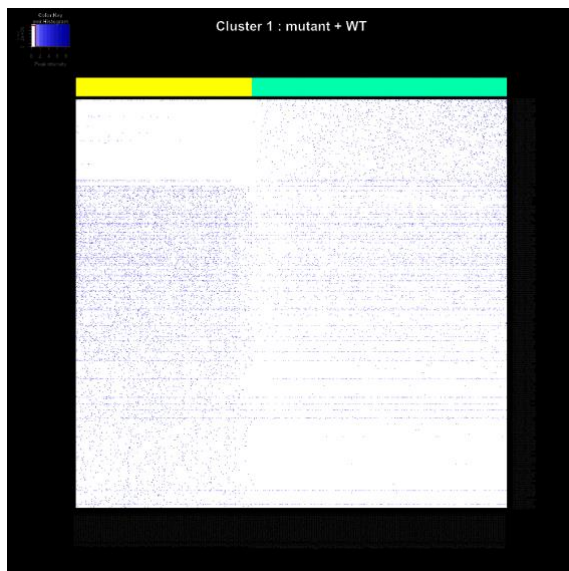
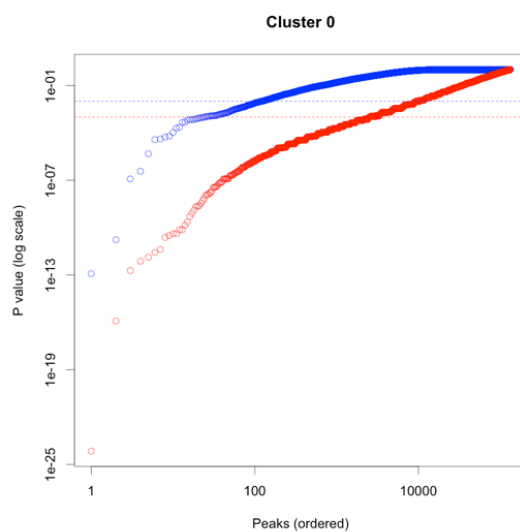
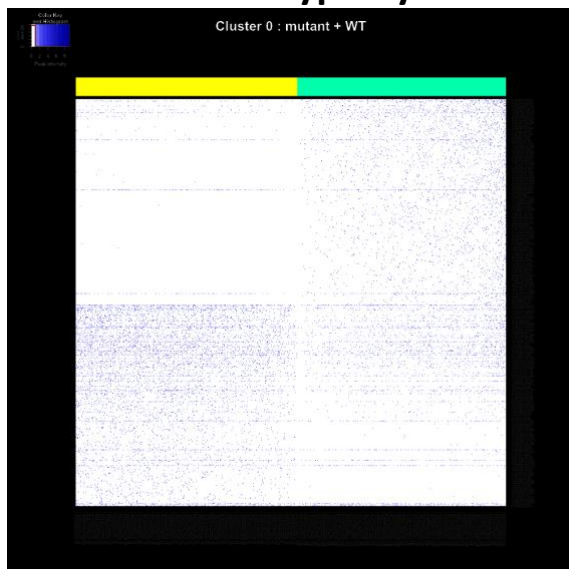
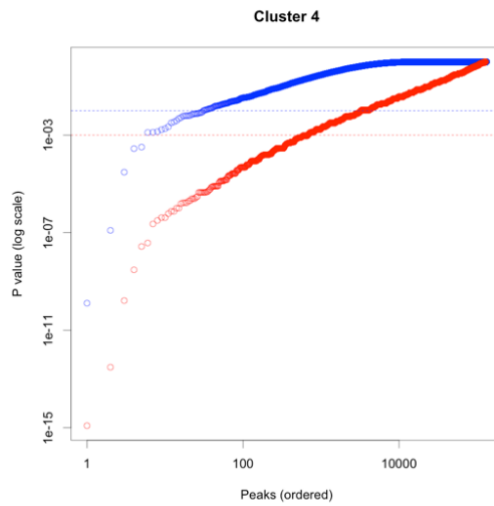
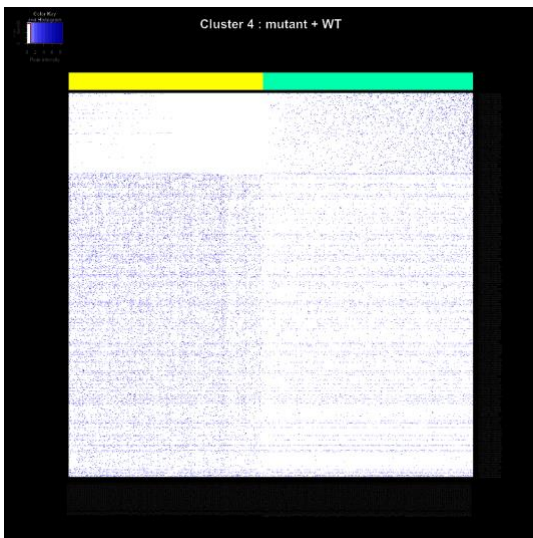
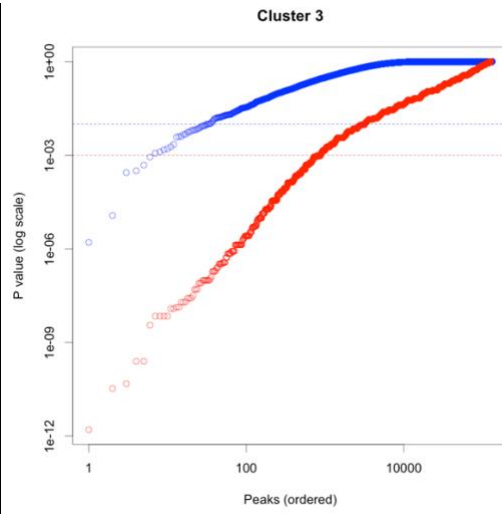
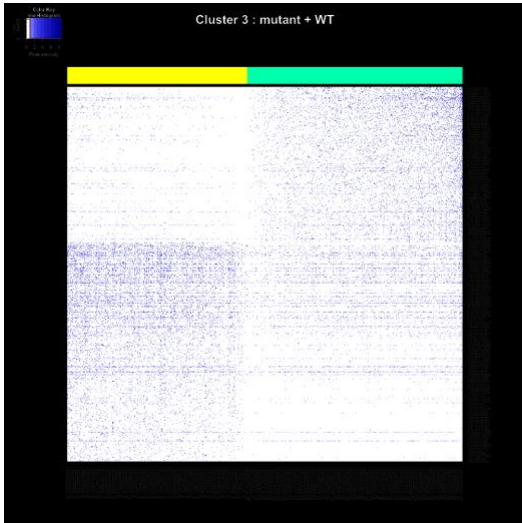
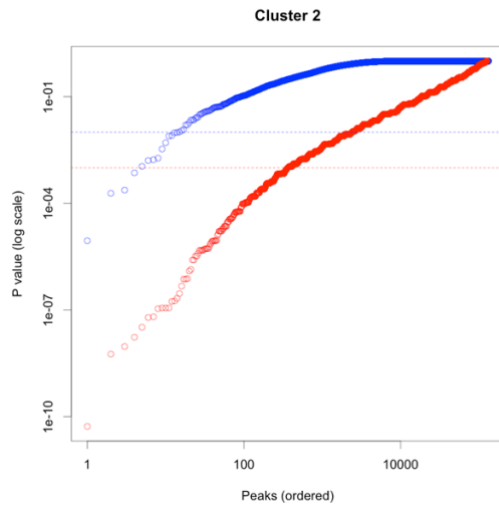
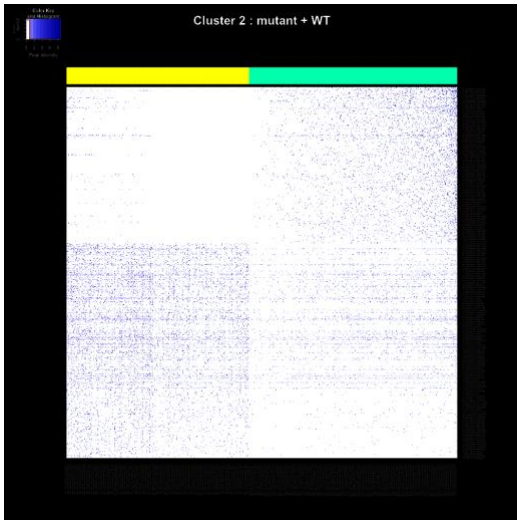


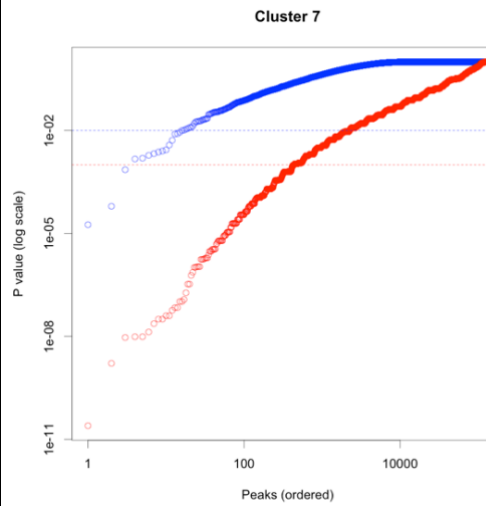
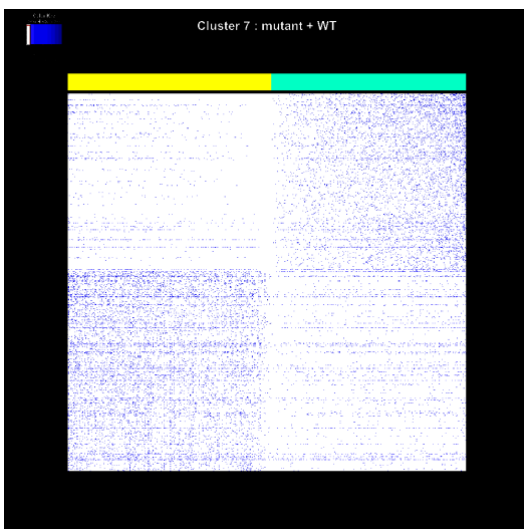
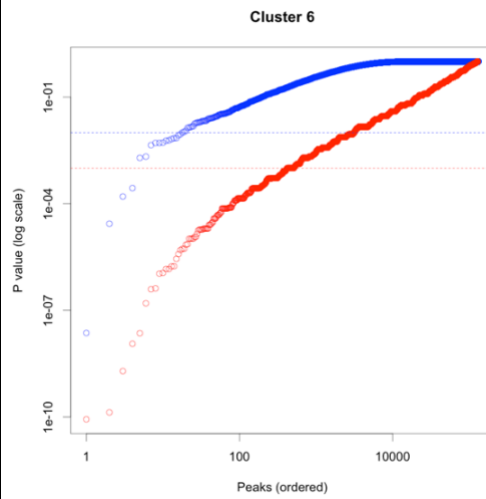
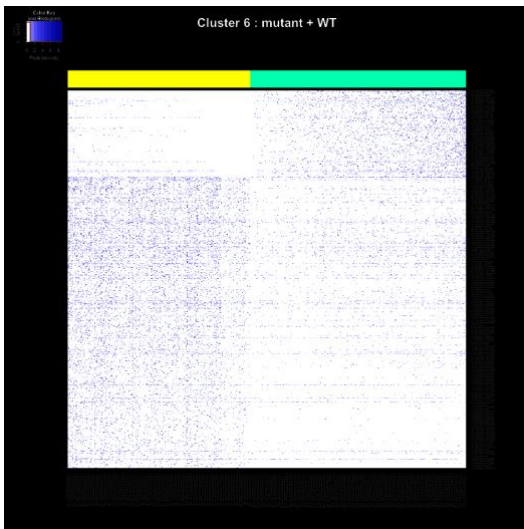
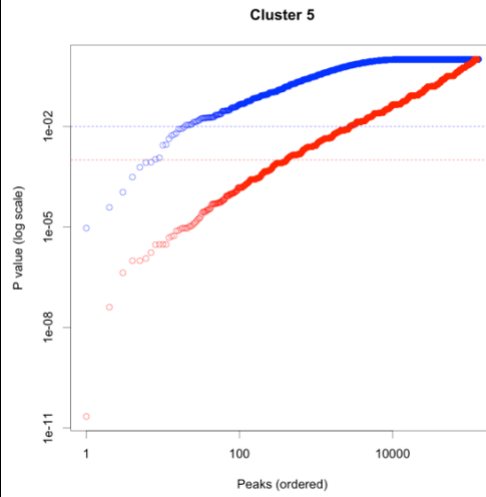
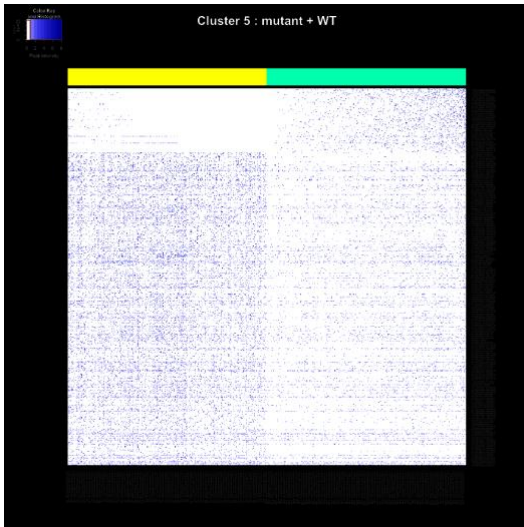
Supplementary Figure 1. ATAC peak intensity plots for statistically different peaks between wild type and *linc-mipep1* cells. Per cluster: top, heat-map of chromatin accessibility by peak (blue scale increasing in accessibility); bottom, P value of statistically different chromatin accessibility peaks between wild type and mutant cells, using Wilcoxon rank sum (red) and the Kolmogorov-Smirnov (blue) methods using one-tailed tests for each condition. Raw p-value thresholds of 0.001 and 0.01 for the Wilcoxon and the KS tests, respectively, were deemed to be significant peaks for further analysis.

Wild type - yellow

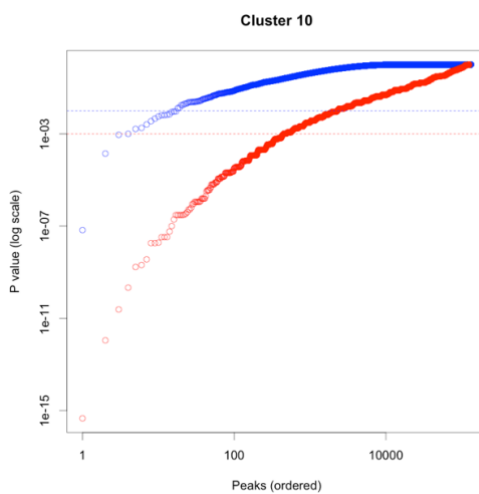
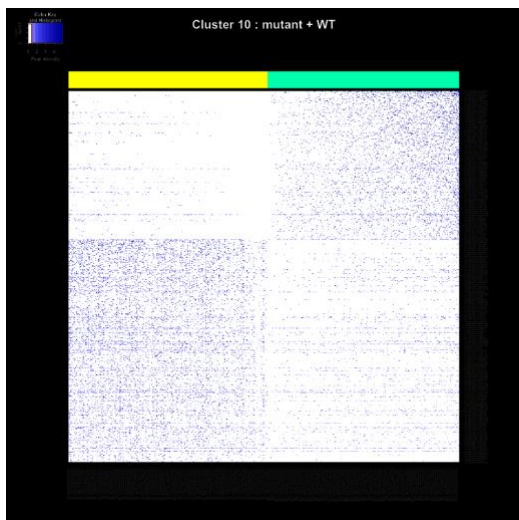
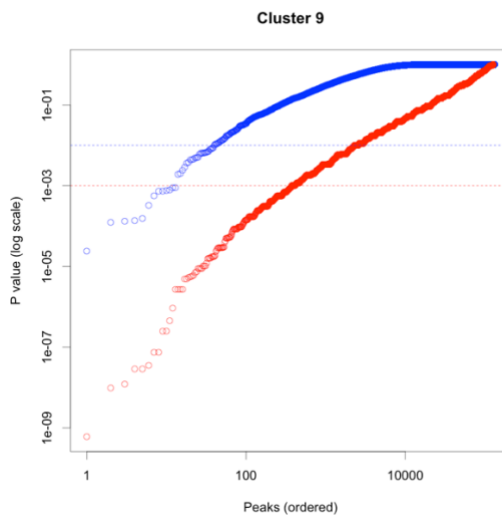
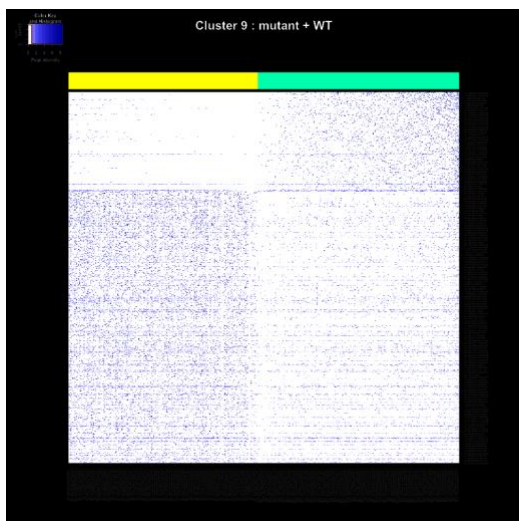
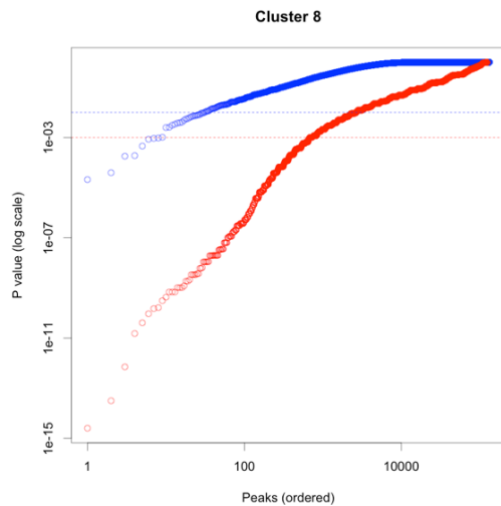
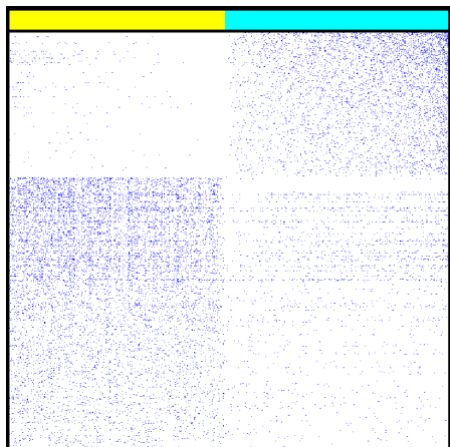
linc-mipep1 mutant - green

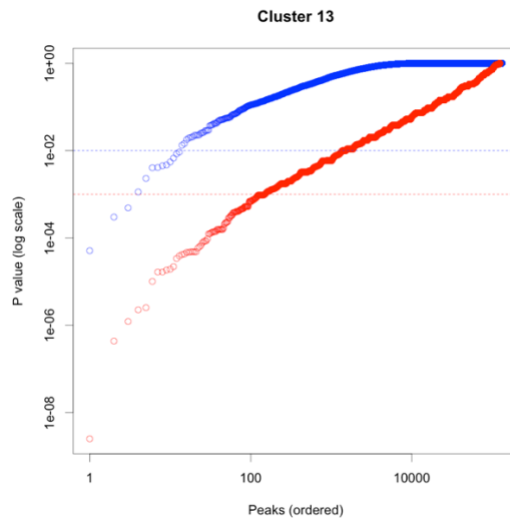
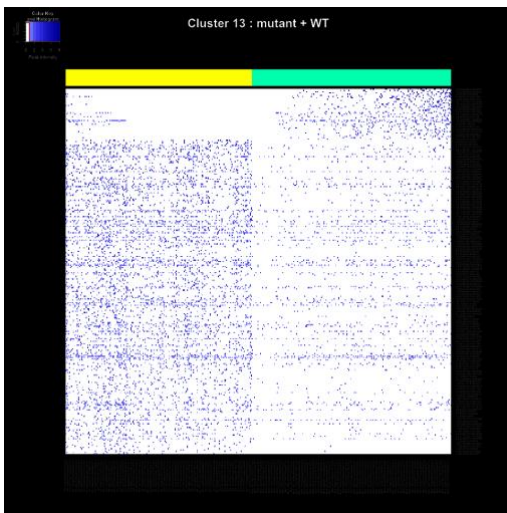
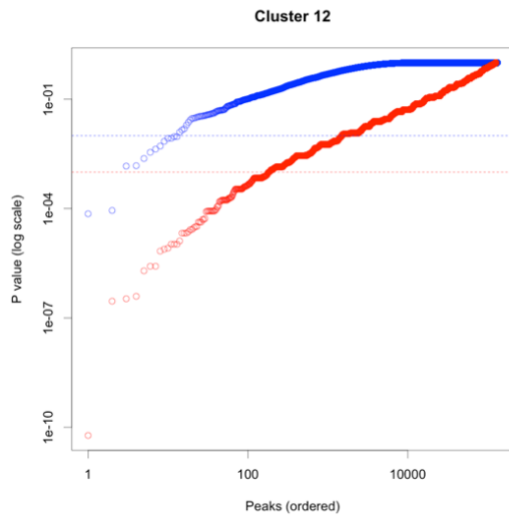
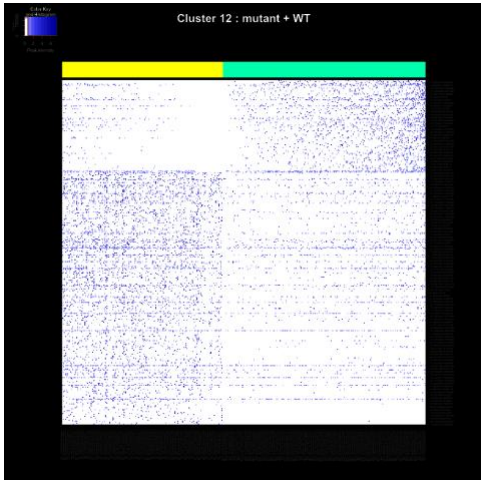
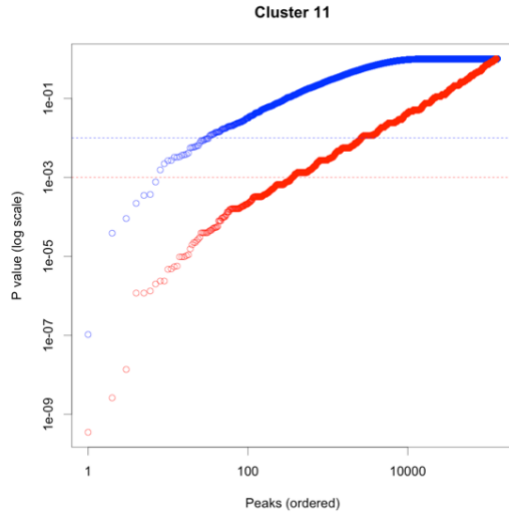
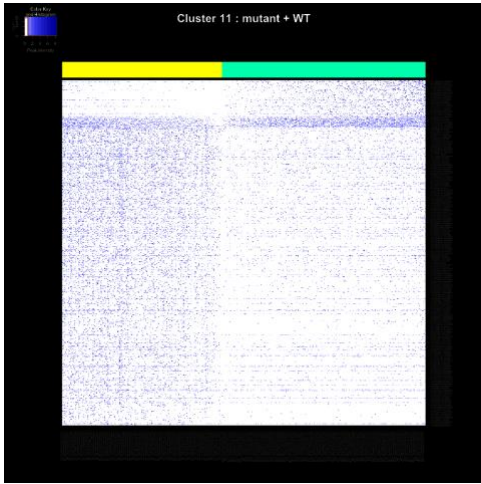


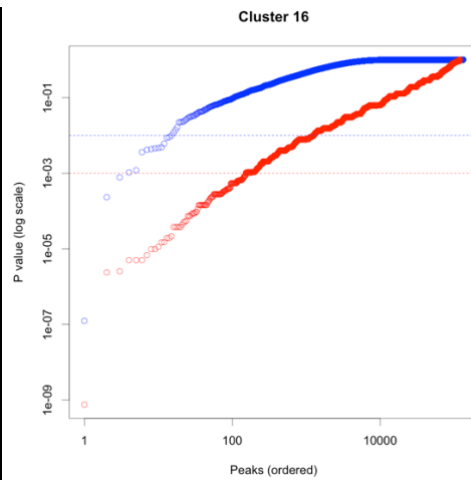
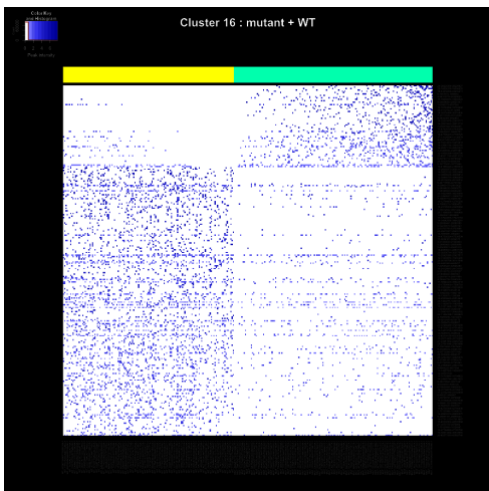
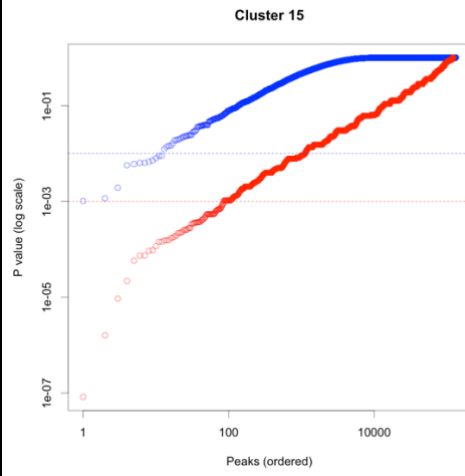
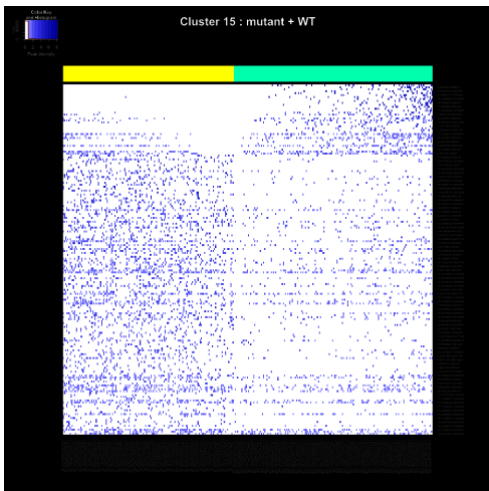
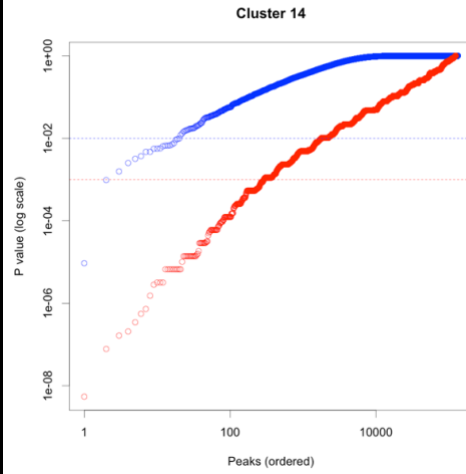
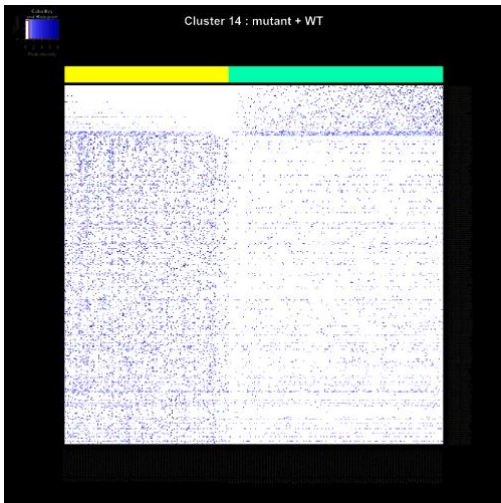


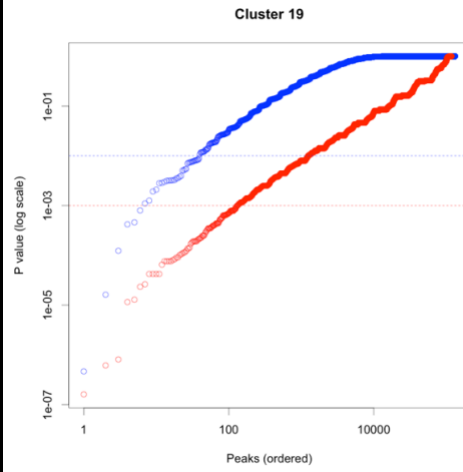
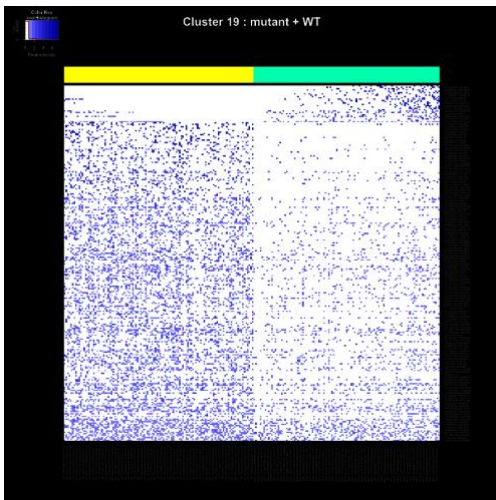
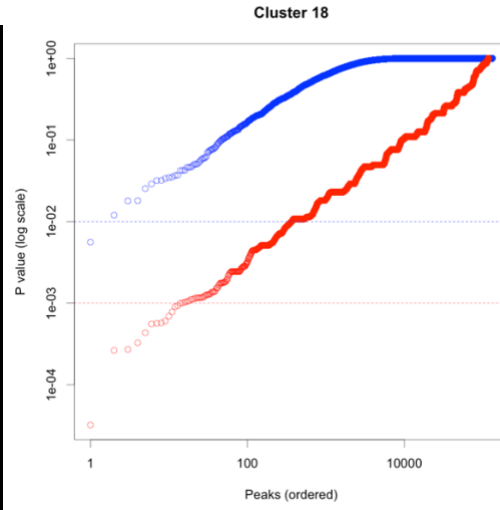
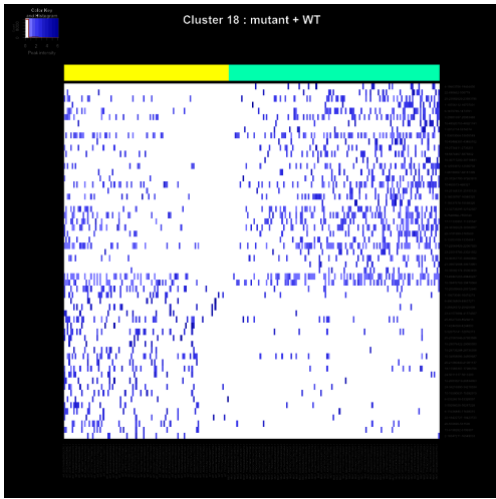
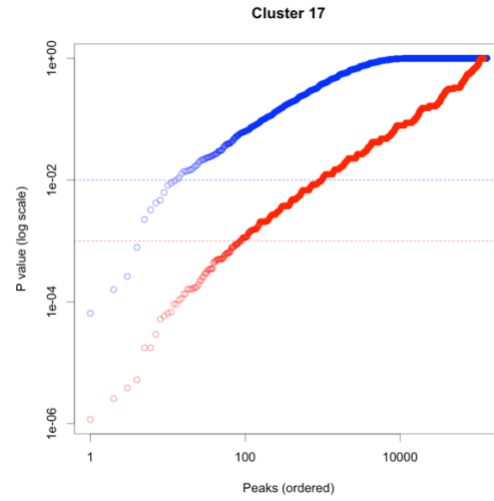
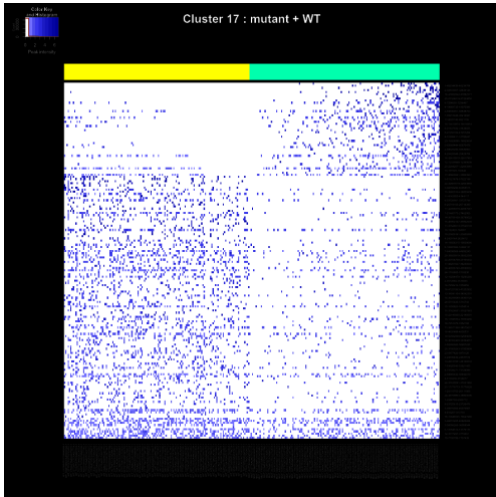


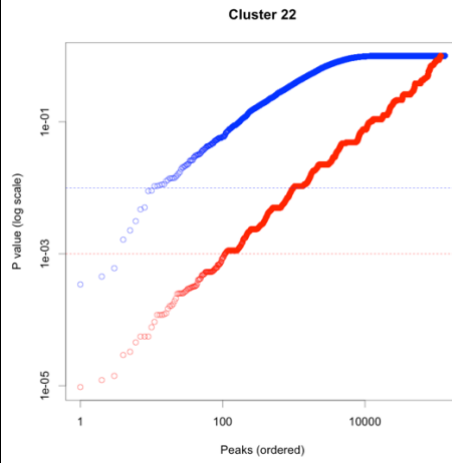
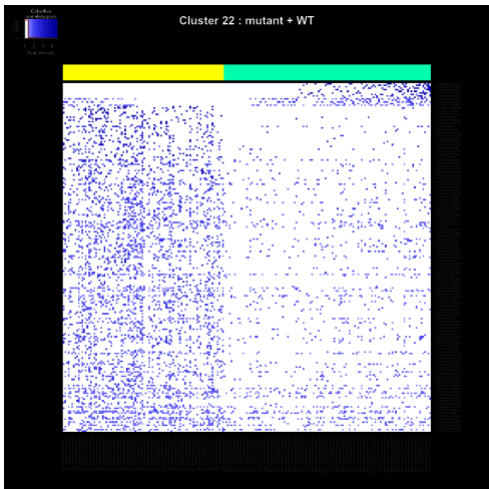
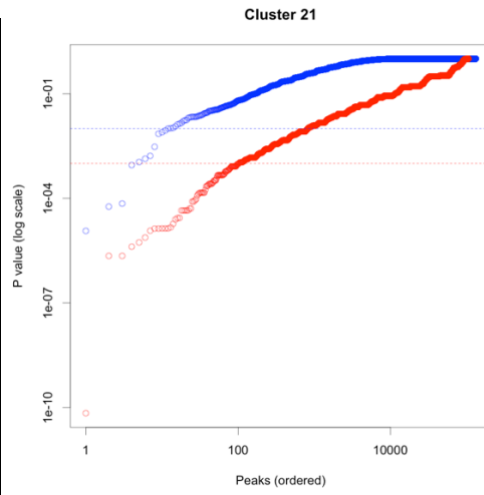
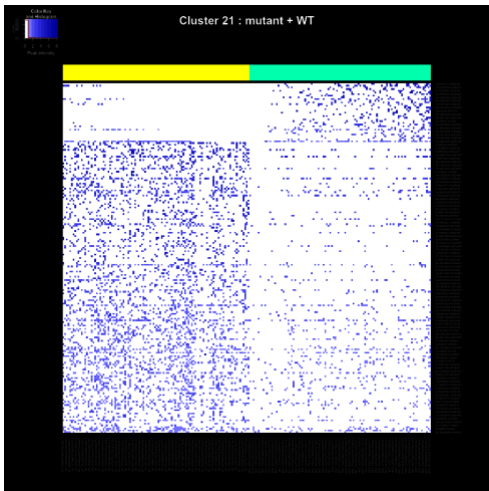
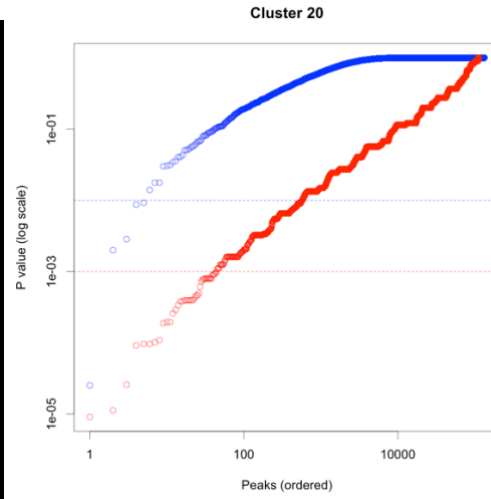
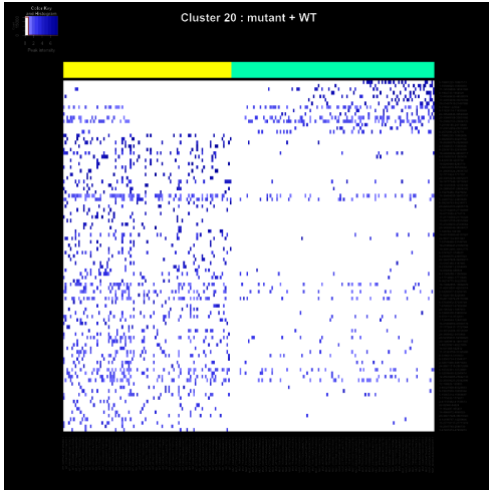
Cluster 8

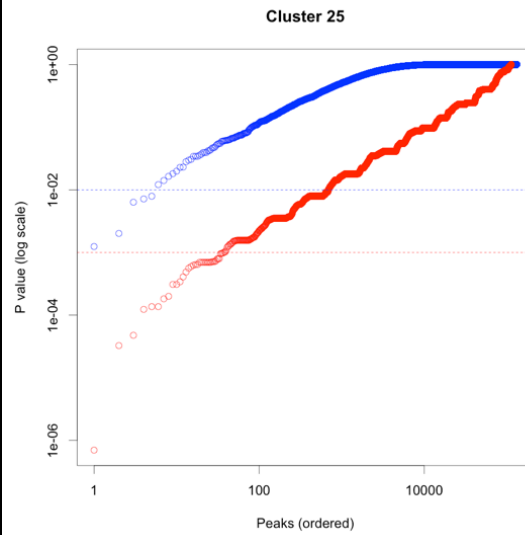
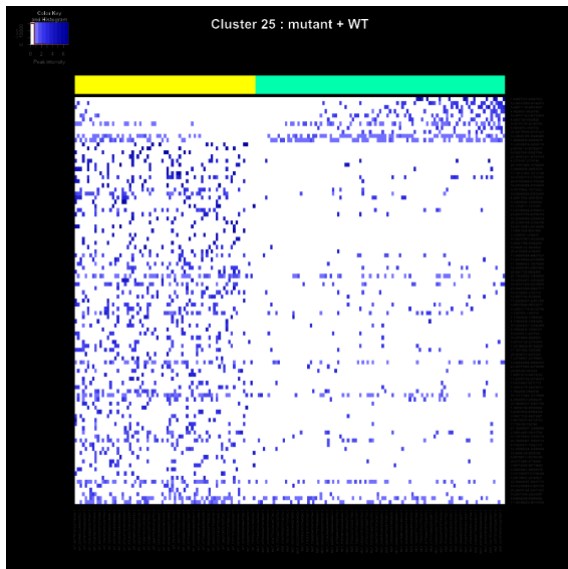
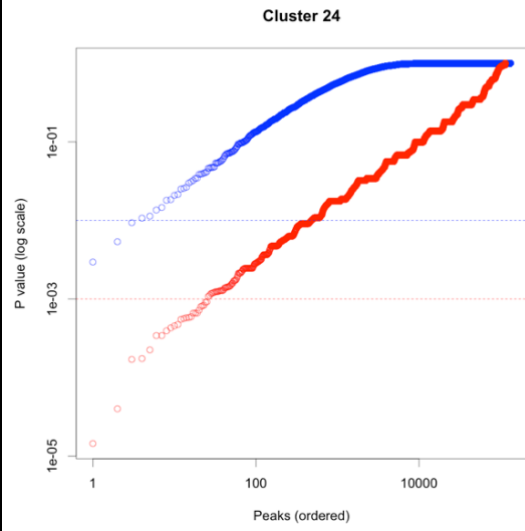
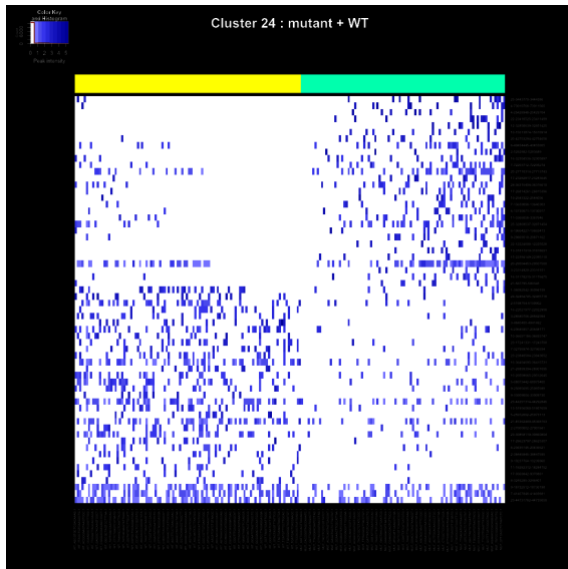
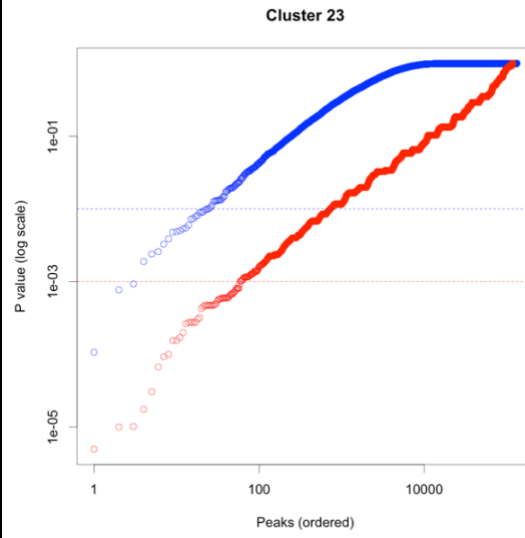
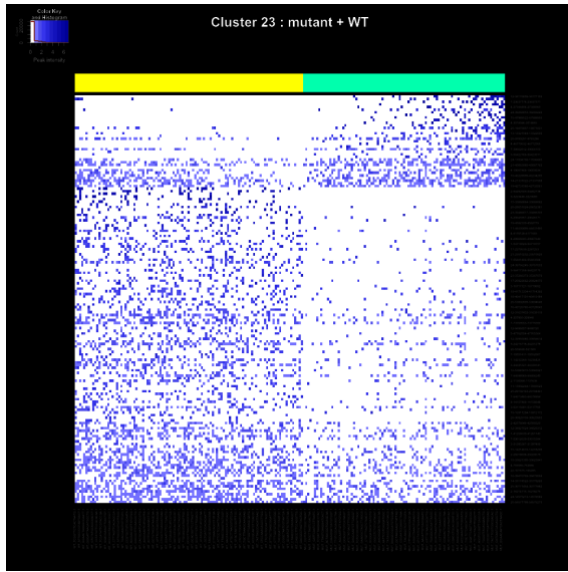


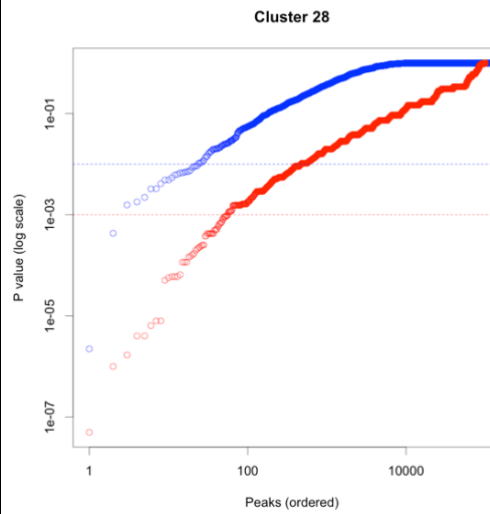
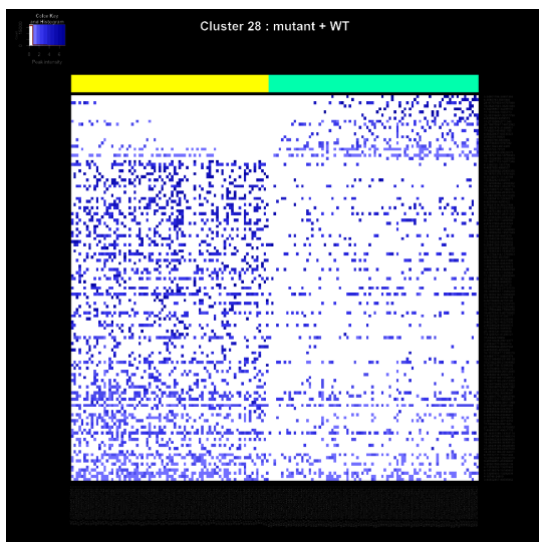
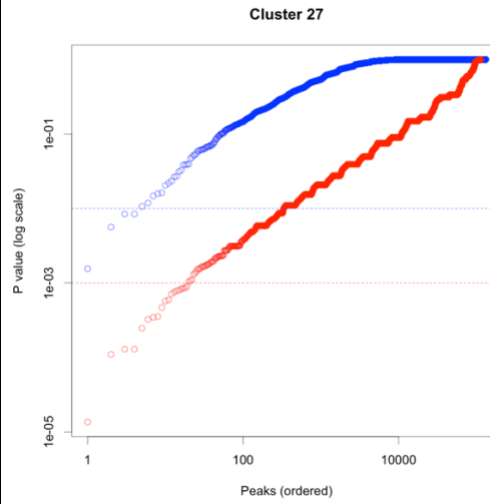
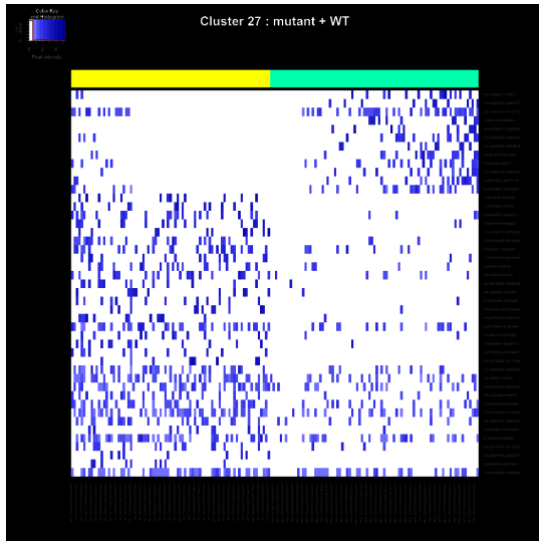
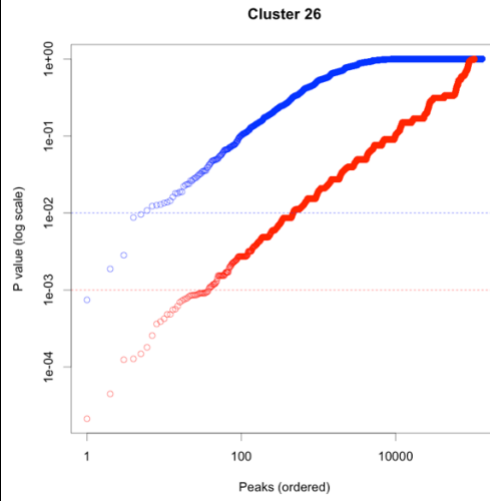
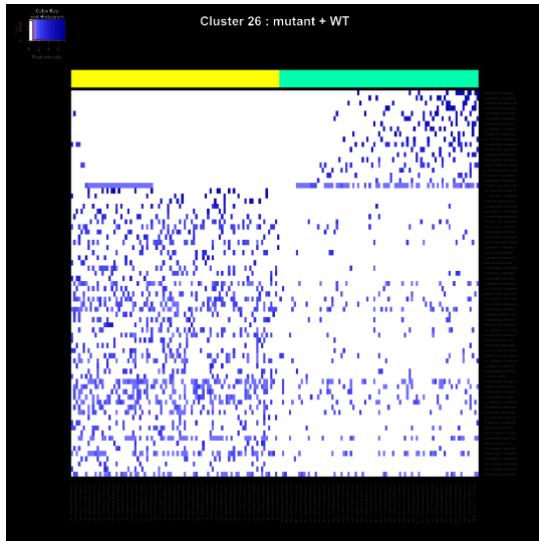


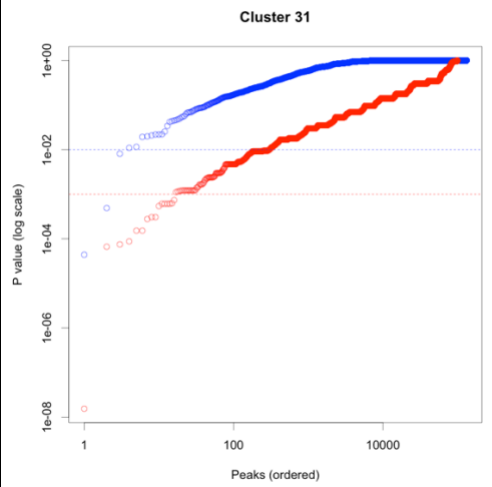
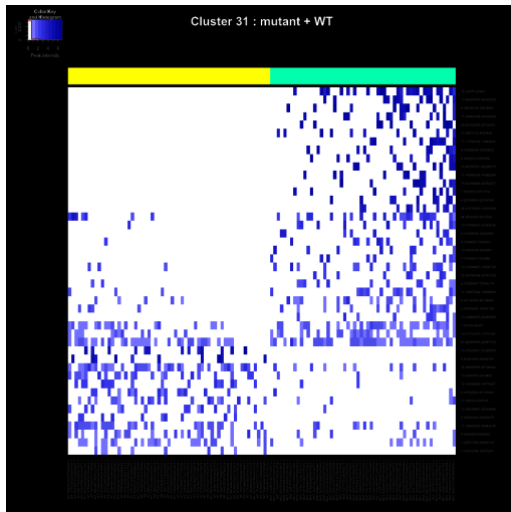
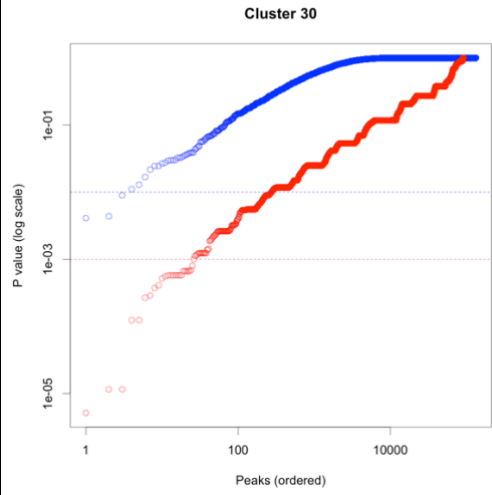
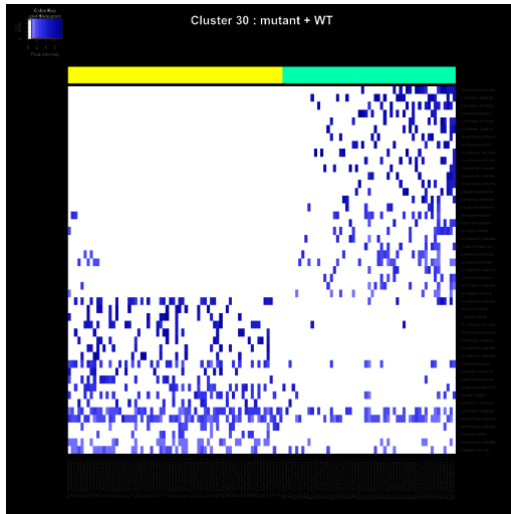
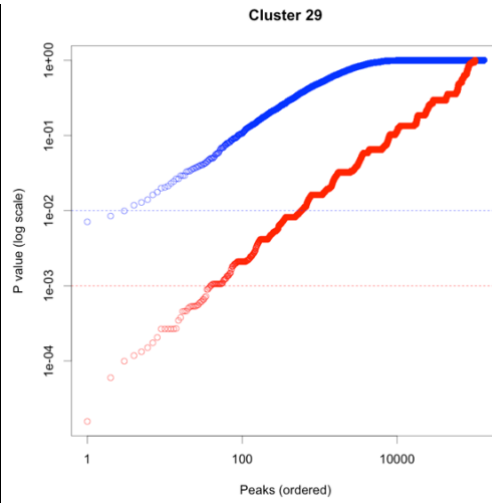
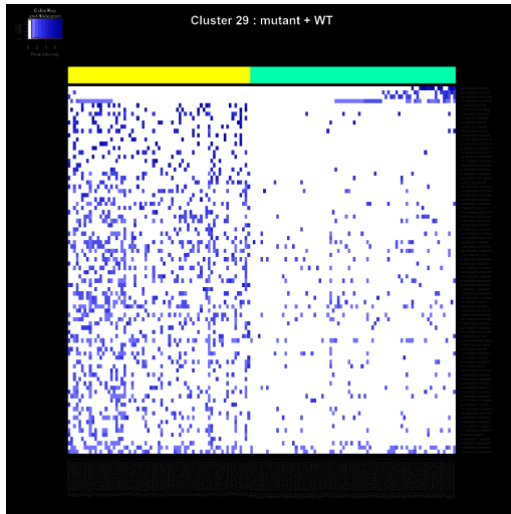


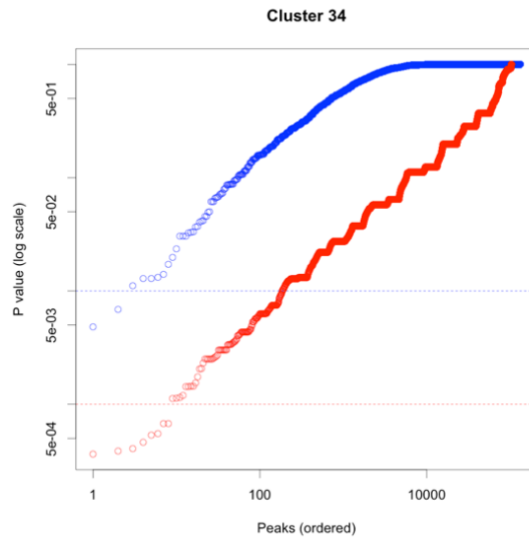
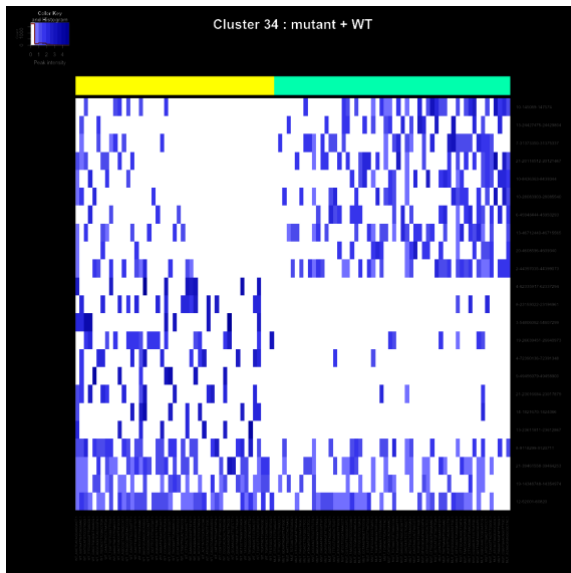
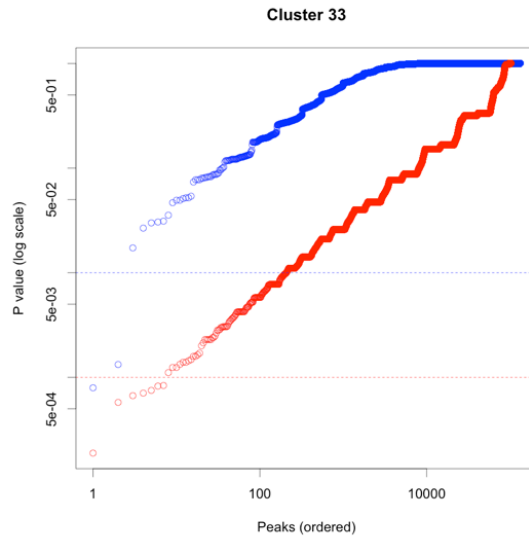
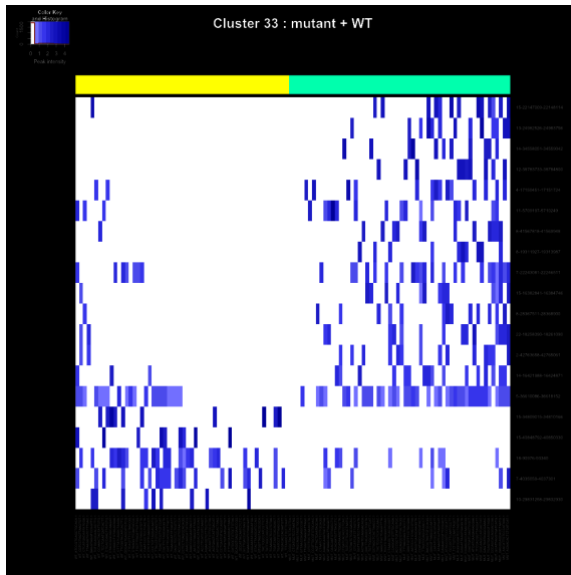
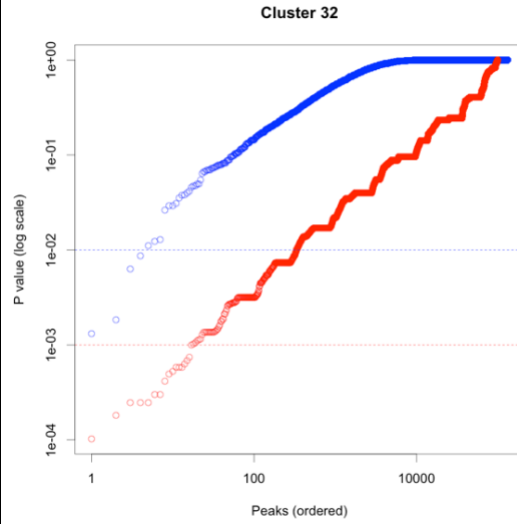
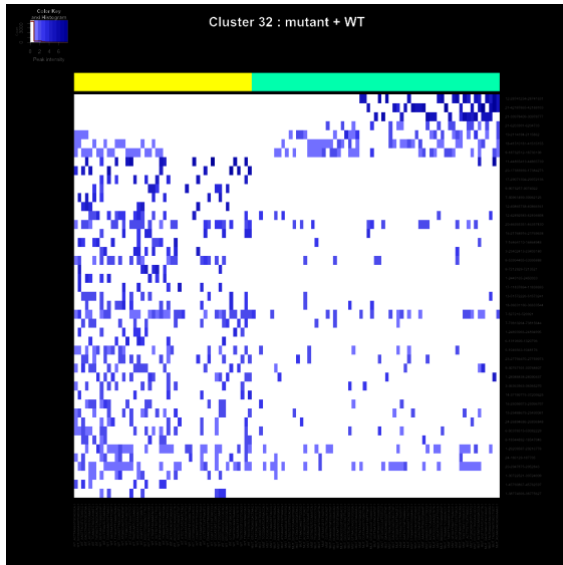












Cluster 35

