Residuals vs Fitted

Residuals

Predicted values
glm(log2FoldChange ~ gene_length + GC_prop + exon_number + SSR + HPF

Normal Q–Q

Std. deviance resid.

Theoretical Quantiles

glm(log2FoldChange ~ gene_length + GC_prop + exon_number + SSR + HPF

Scale−Location

glm(log2FoldChange ~ gene_length + GC_prop + exon_number + SSR + HPF

Residuals vs Leverage

Std. Pearson resid.

10005

9621
8017

Cook's distance

Leverage

glm(log2FoldChange ~ gene_length + GC_prop + exon_number + SSR + HPF