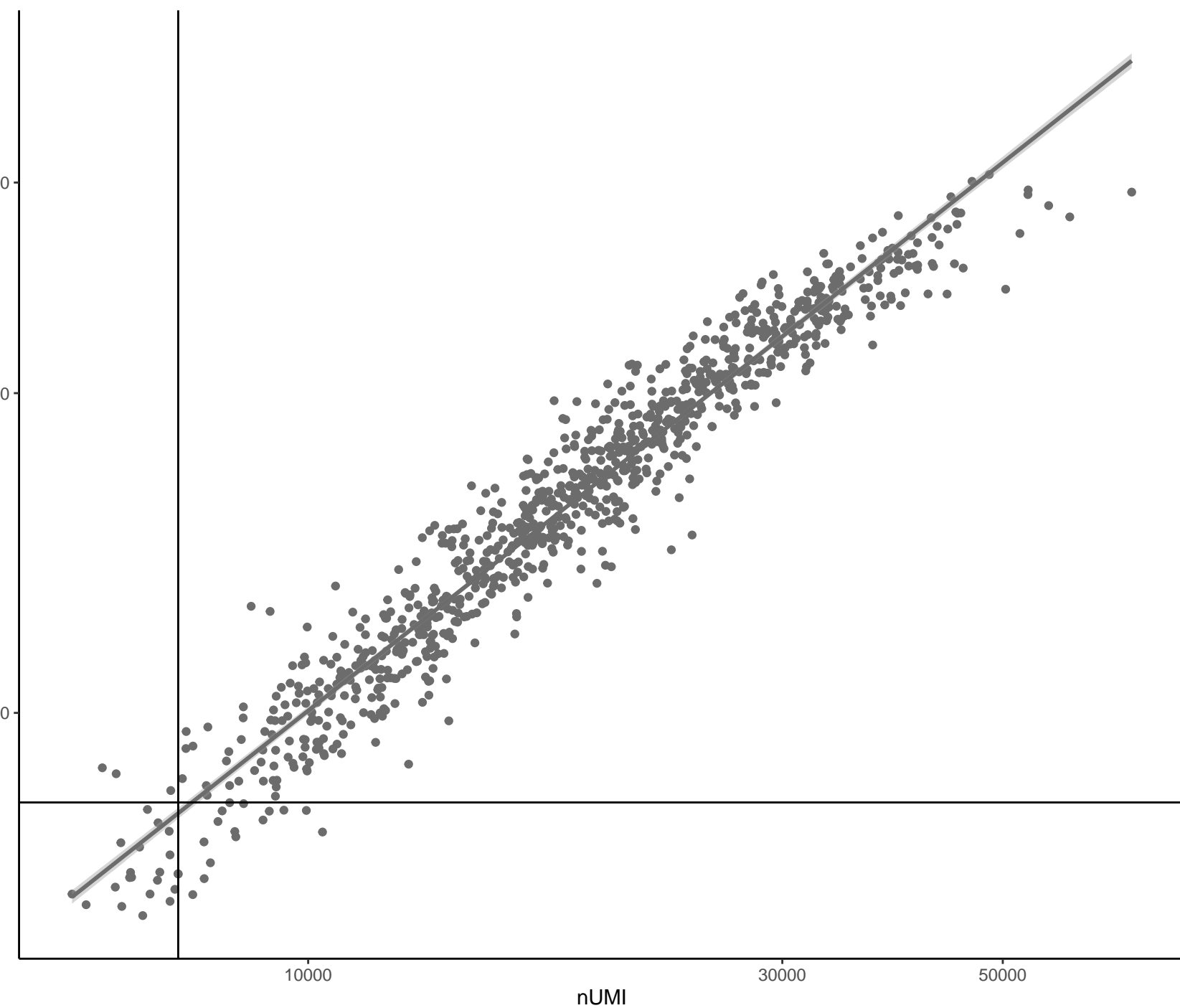


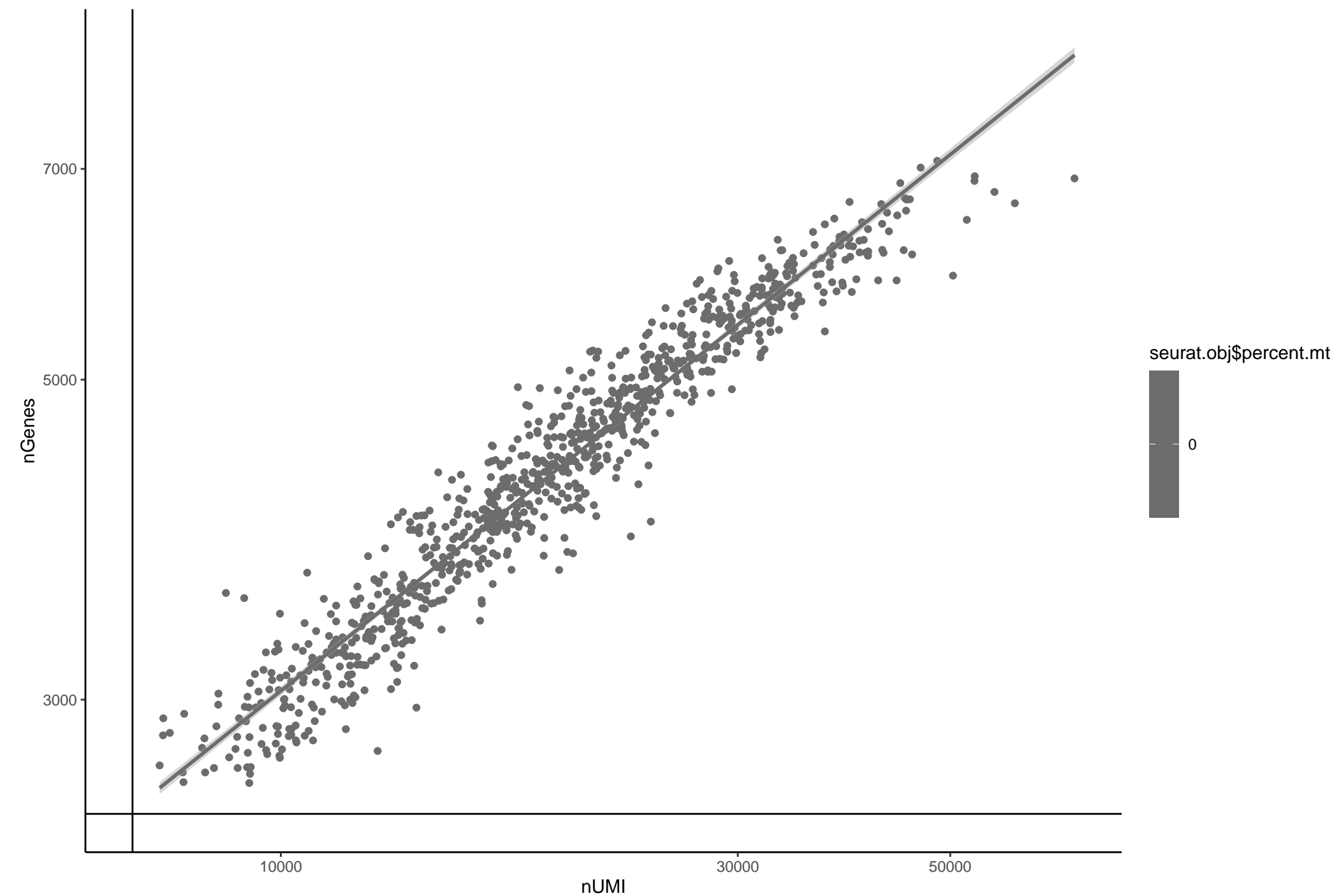
UMI counts and Genes per Cell Correlation
(Integrated Long Reads)



seurat.obj\$percent.mt



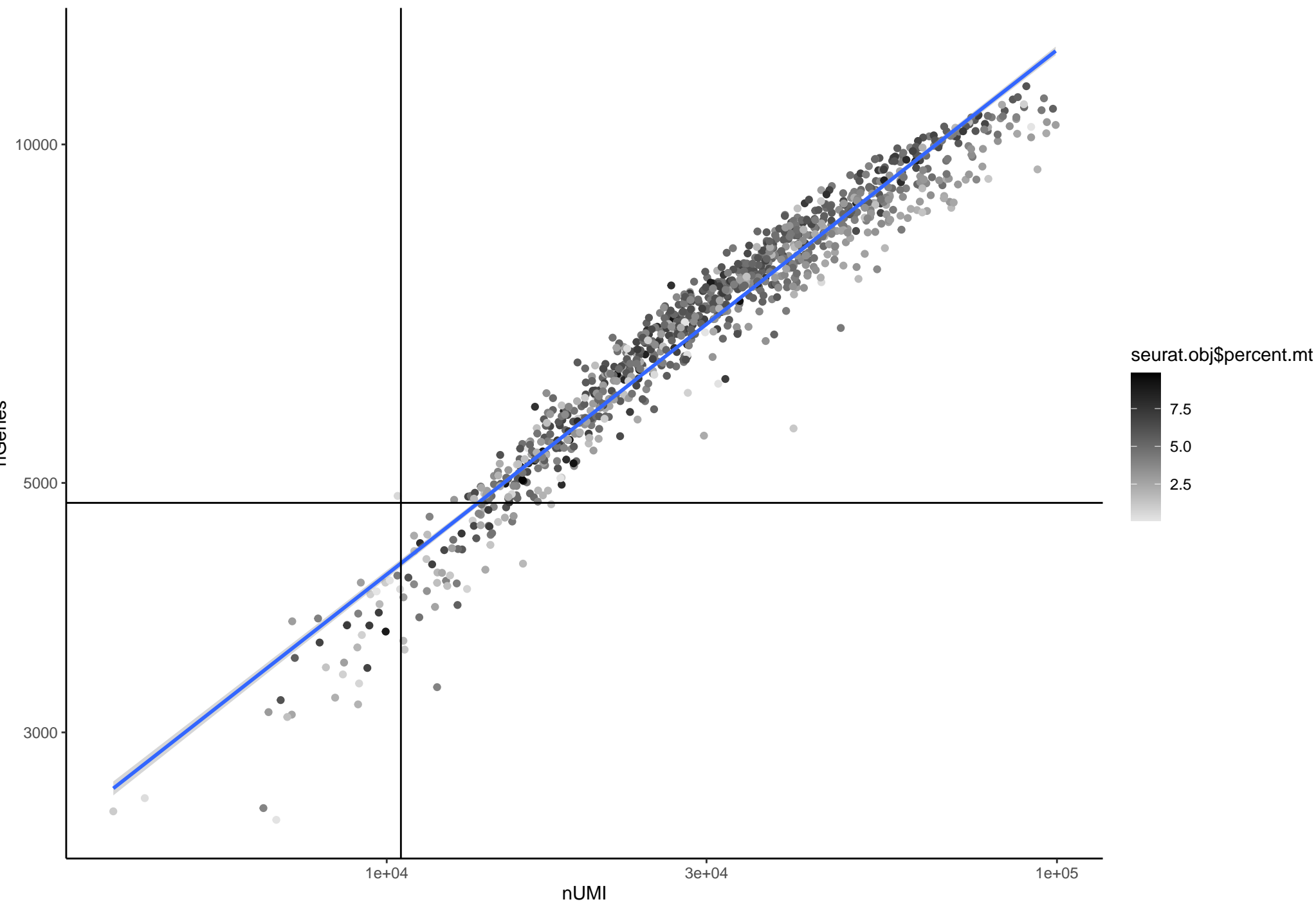
UMI counts and Genes per Cell Correlation
(Filtered Integrated Long Reads)



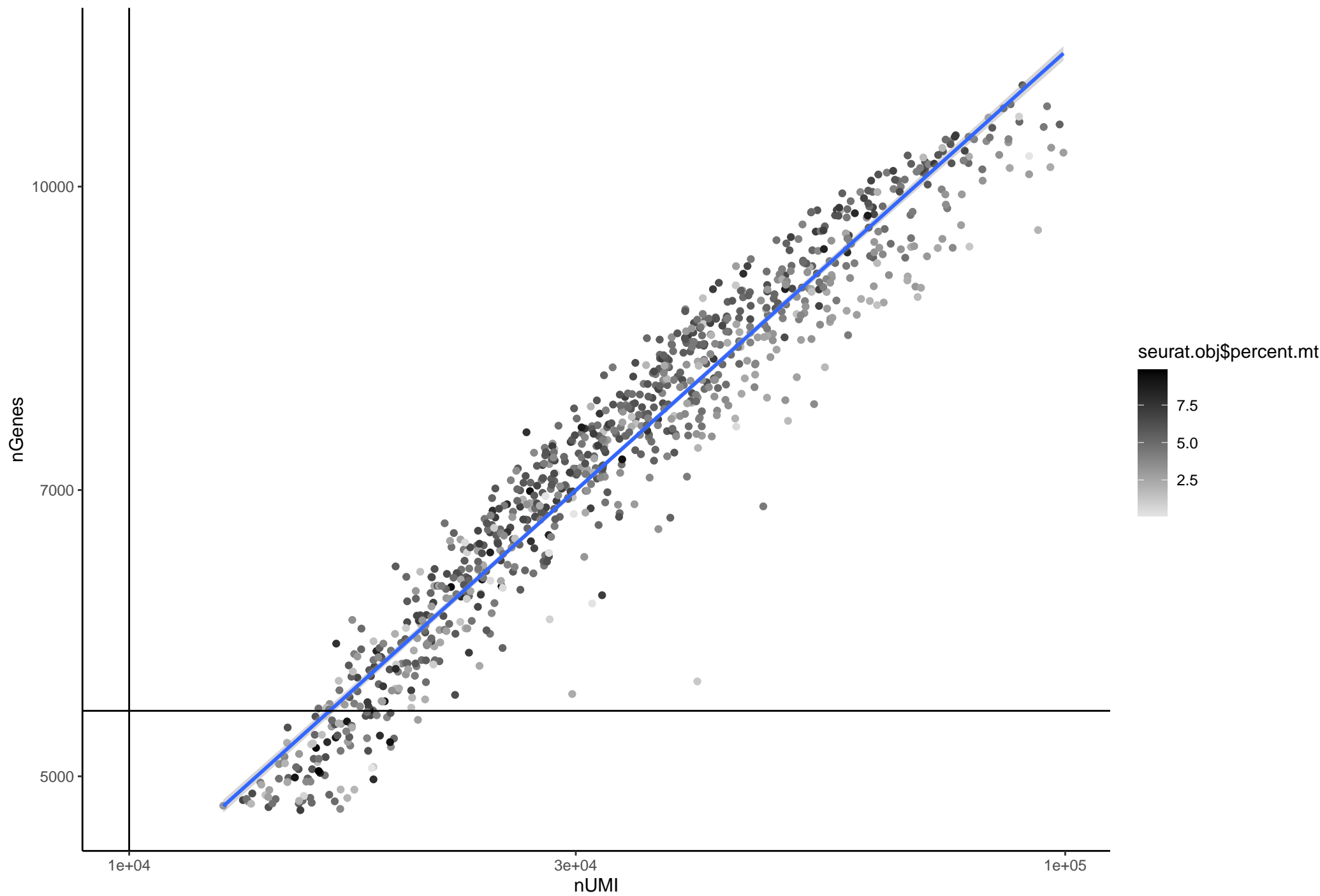
seurat.obj\$percent.mt



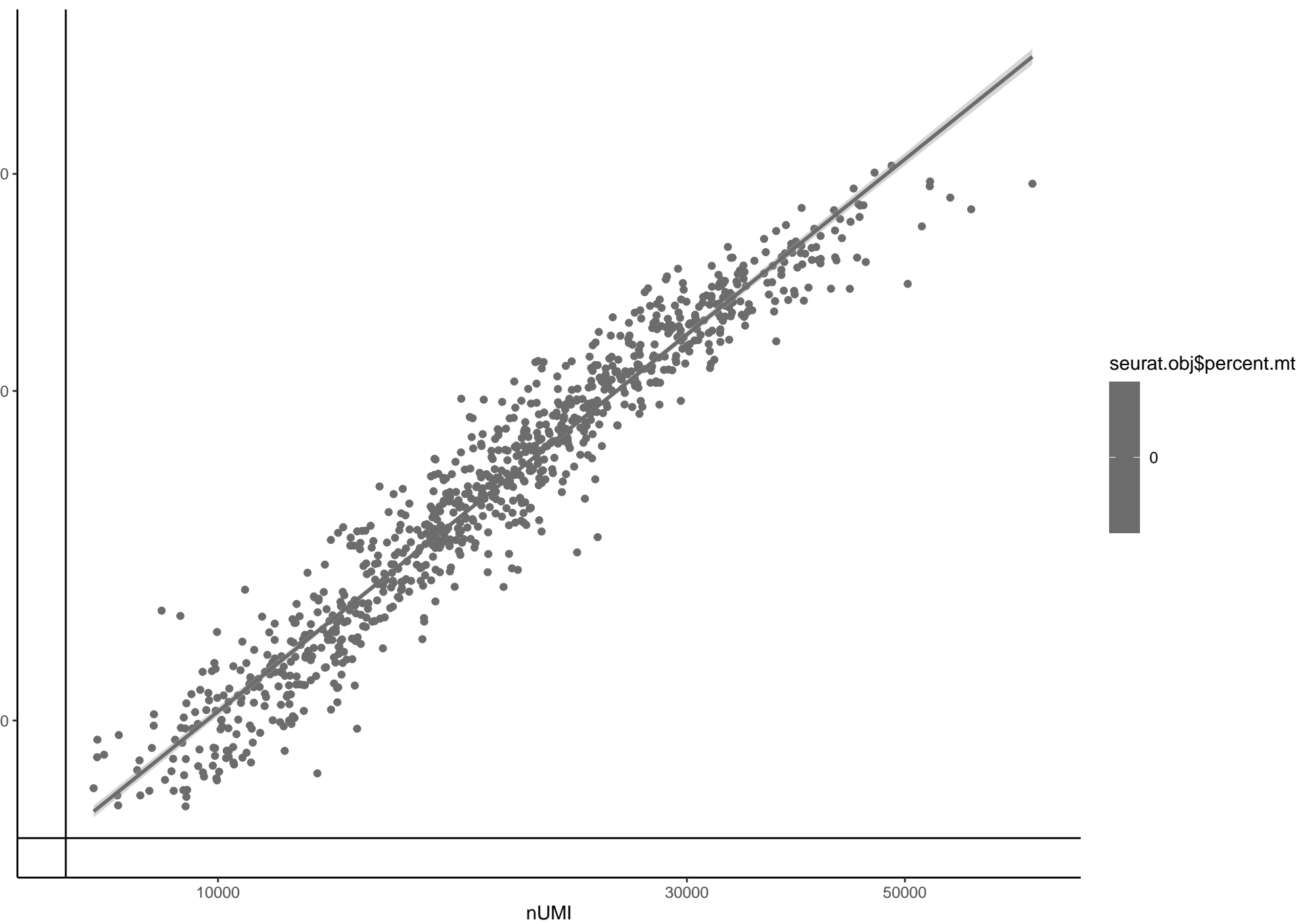
UMI counts and Genes per Cell Correlation
(Integrated Short Reads)



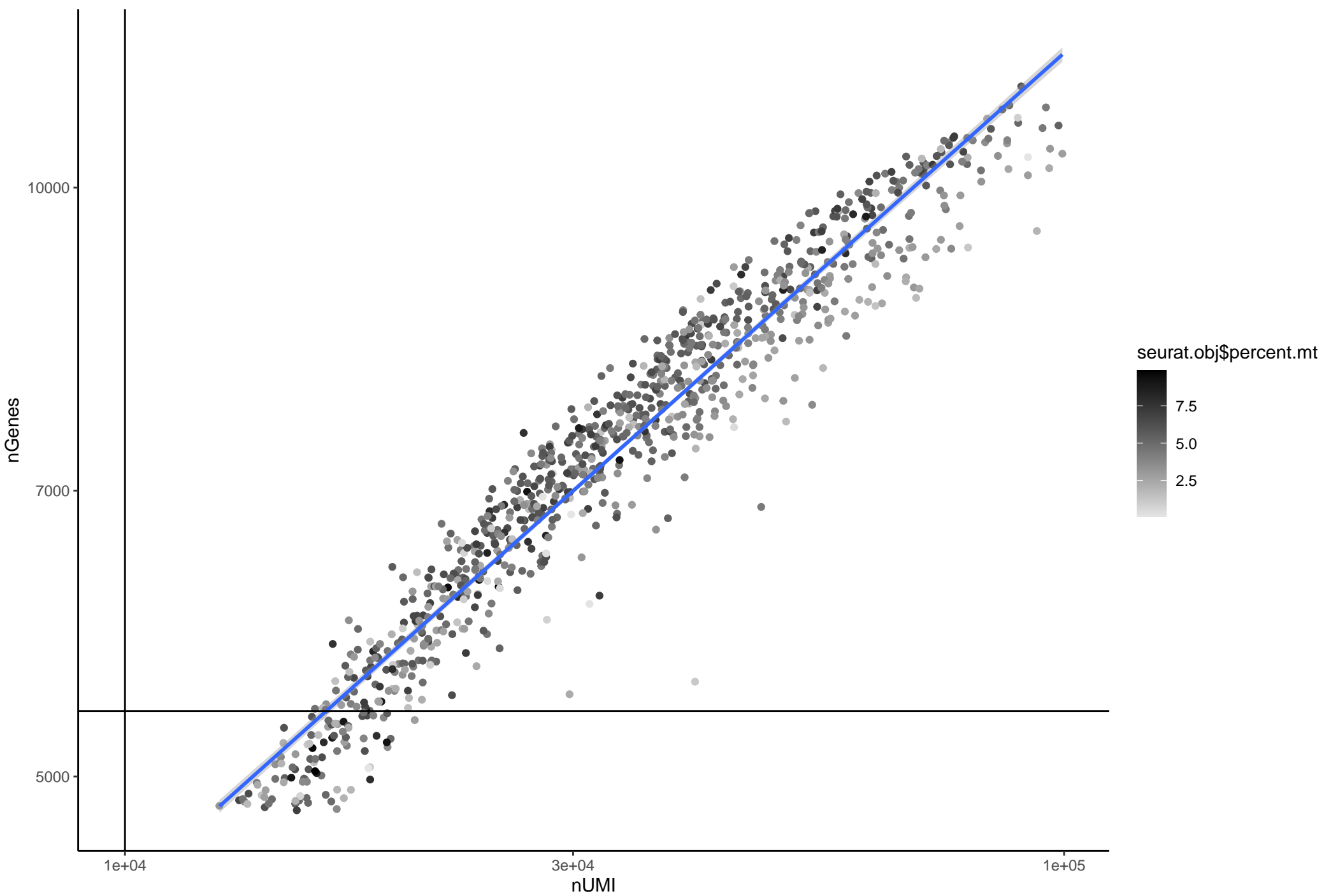
UMI counts and Genes per Cell Correlation
(Filtered Integrated Short Reads)



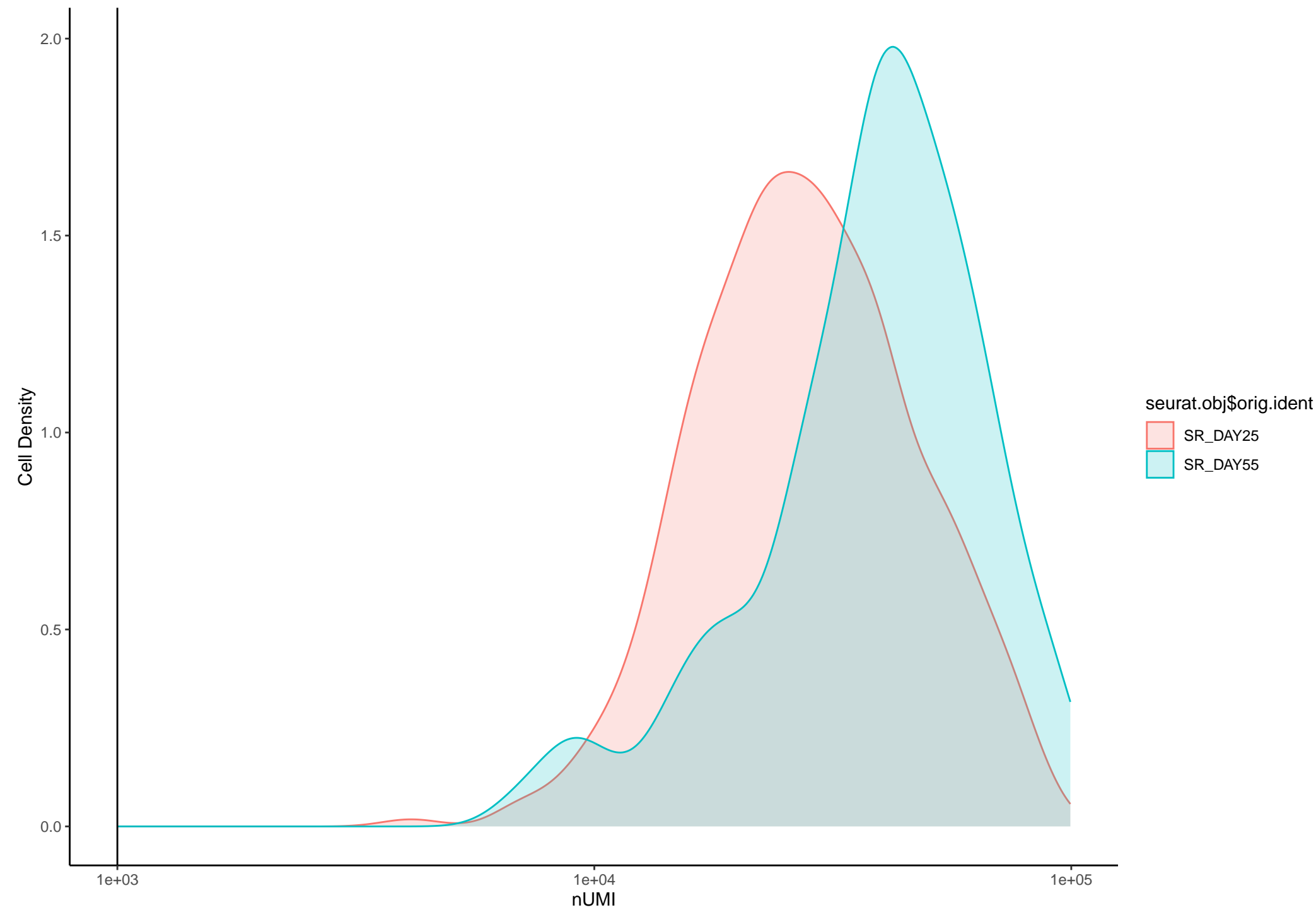
UMI counts and Genes per Cell Correlation
(Filtered Integrated Long Reads)



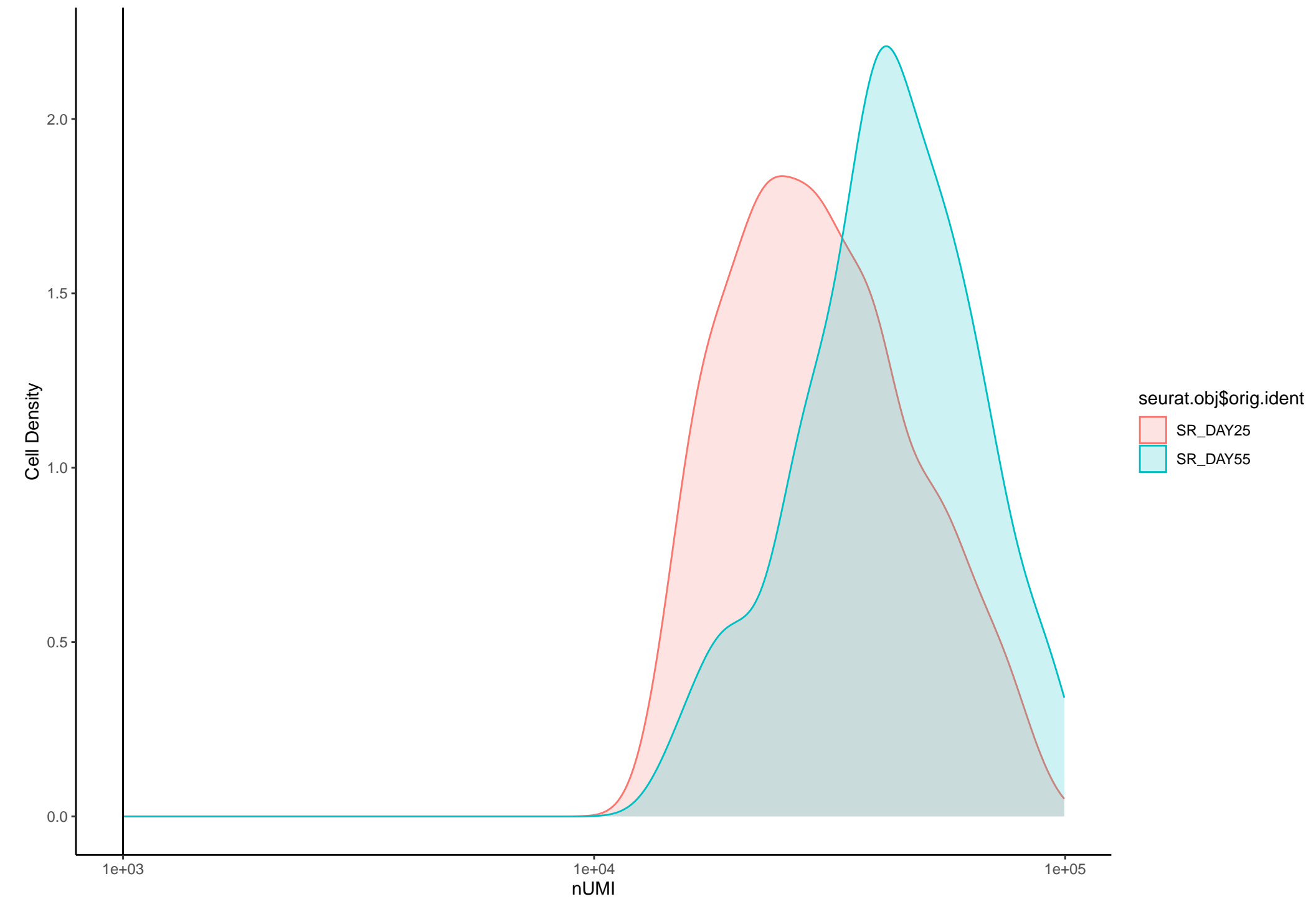
UMI counts and Genes per Cell Correlation
(Filtered Integrated Short Reads)



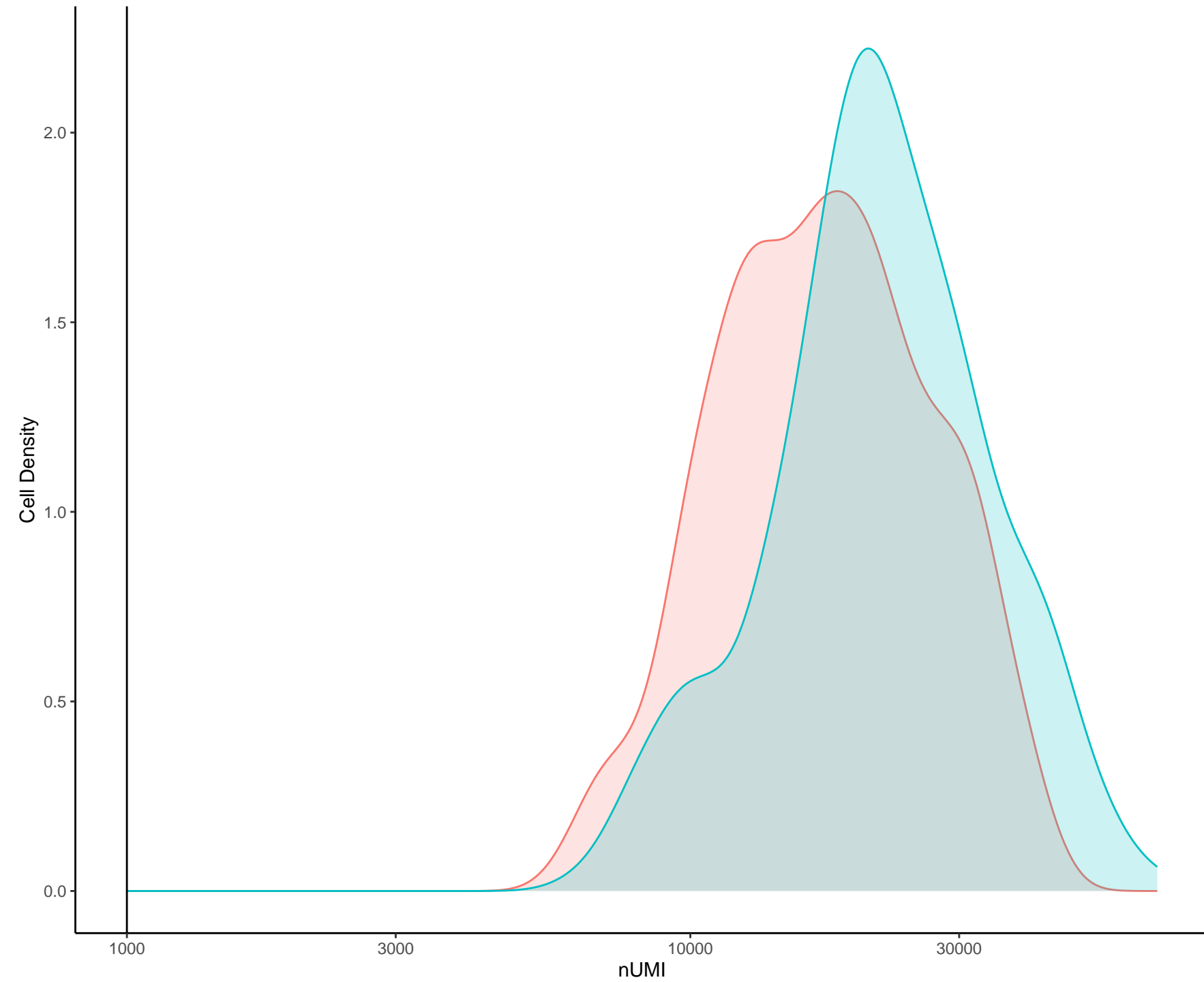
UMI counts per cell (Short Reads)



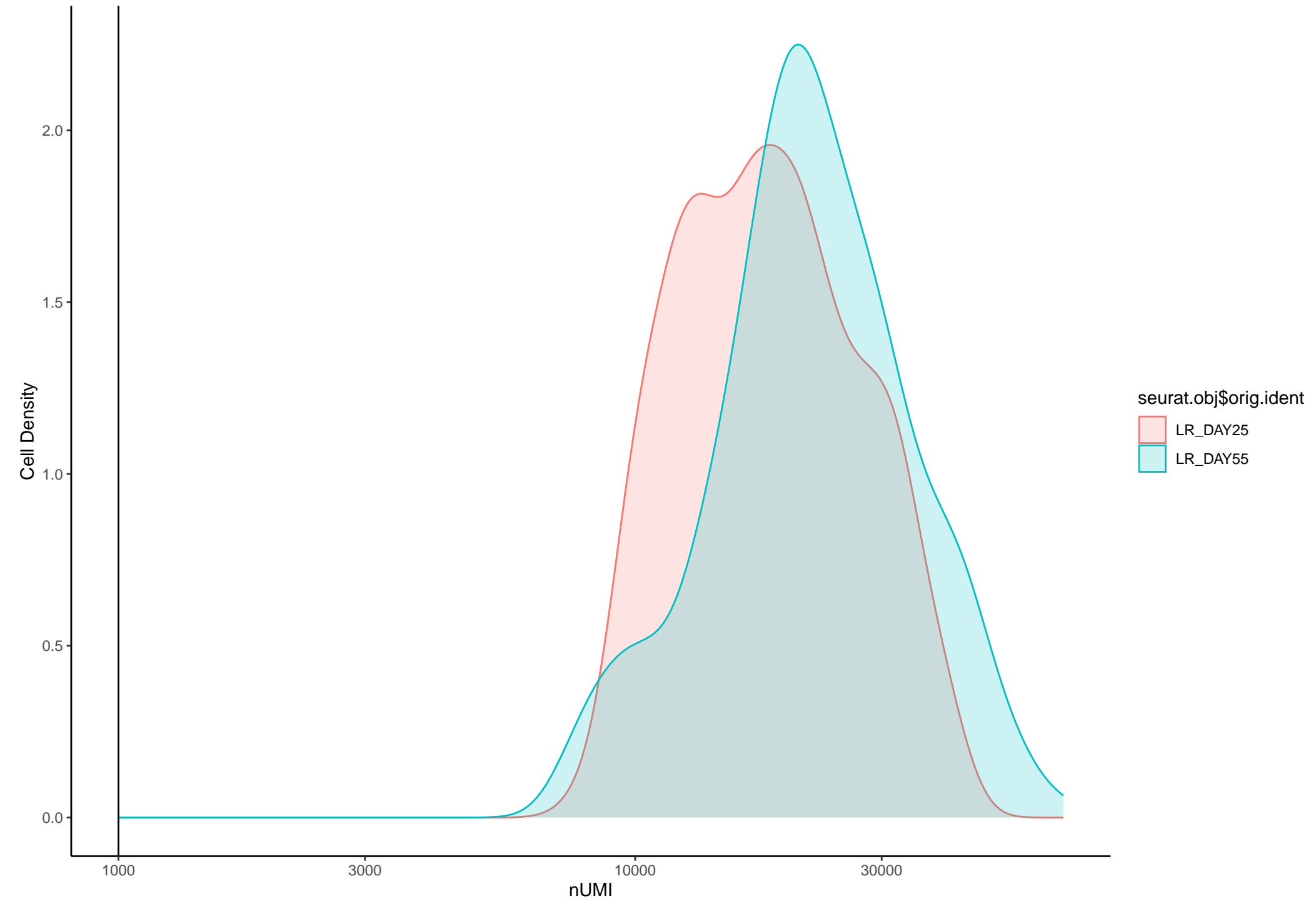
UMI counts per cell (Filtered Short Reads)



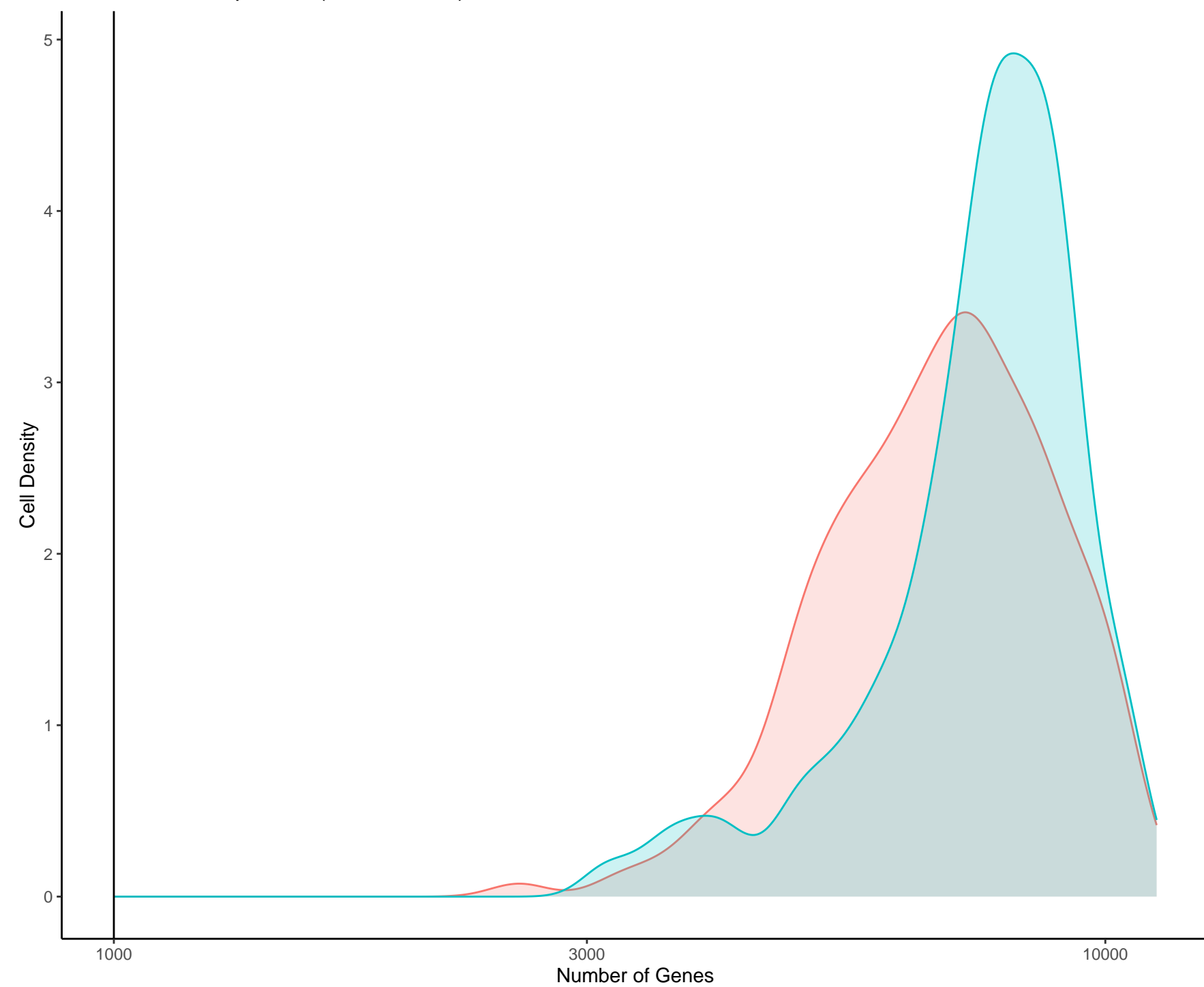
UMI counts per cell (Long Reads)



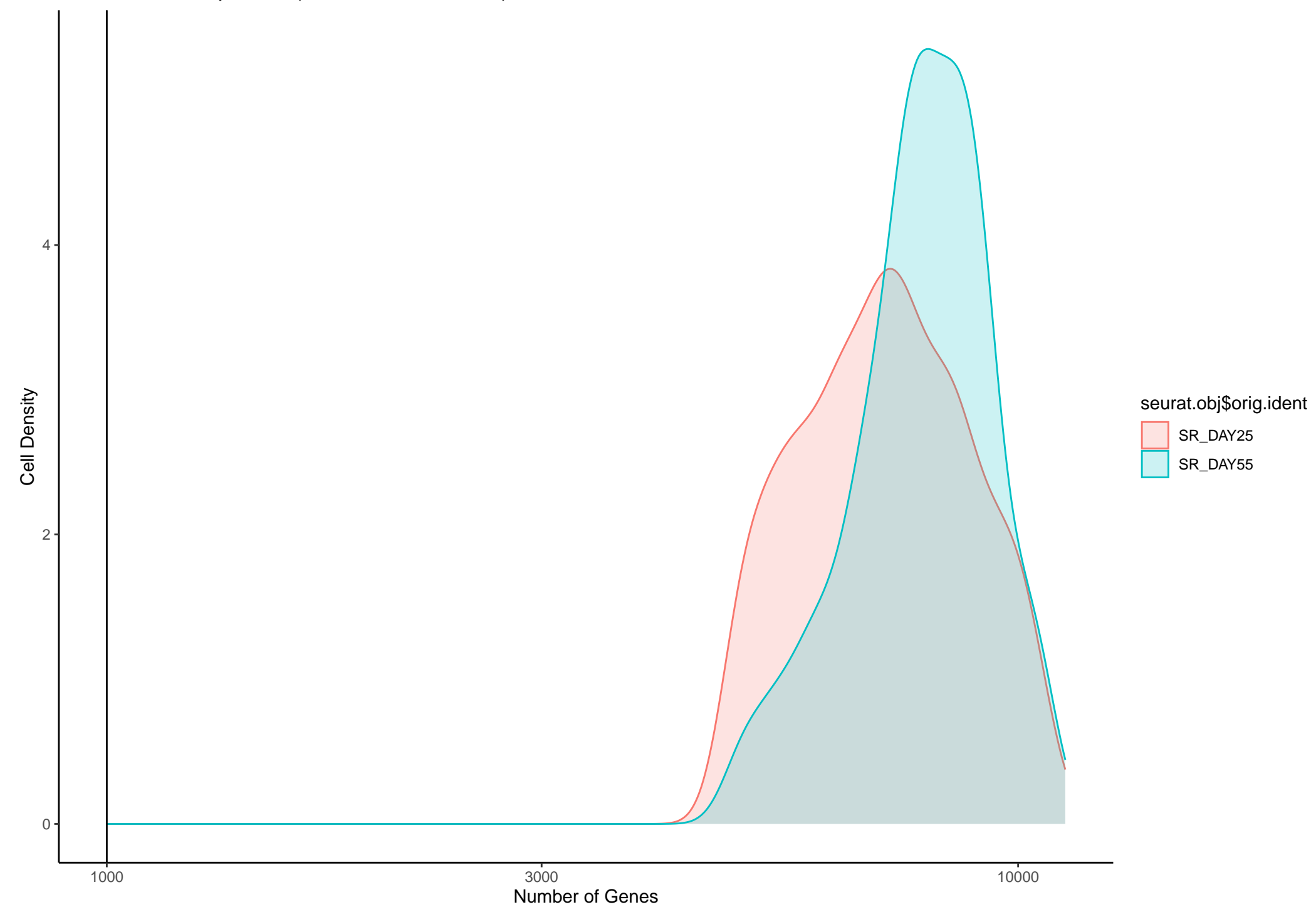
UMI counts per cell (Filtered Long Reads)



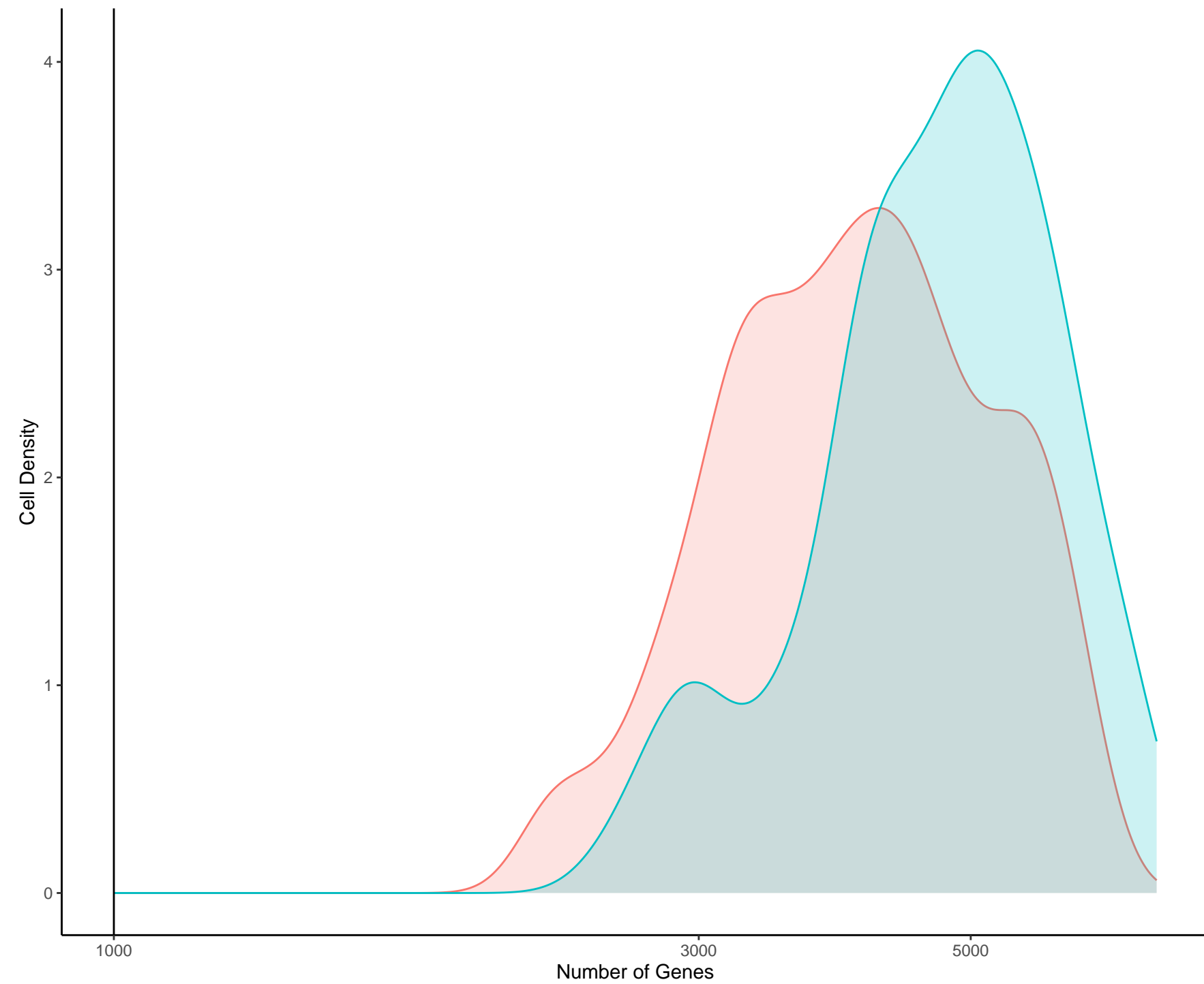
Genes detected per cell (Short Reads)



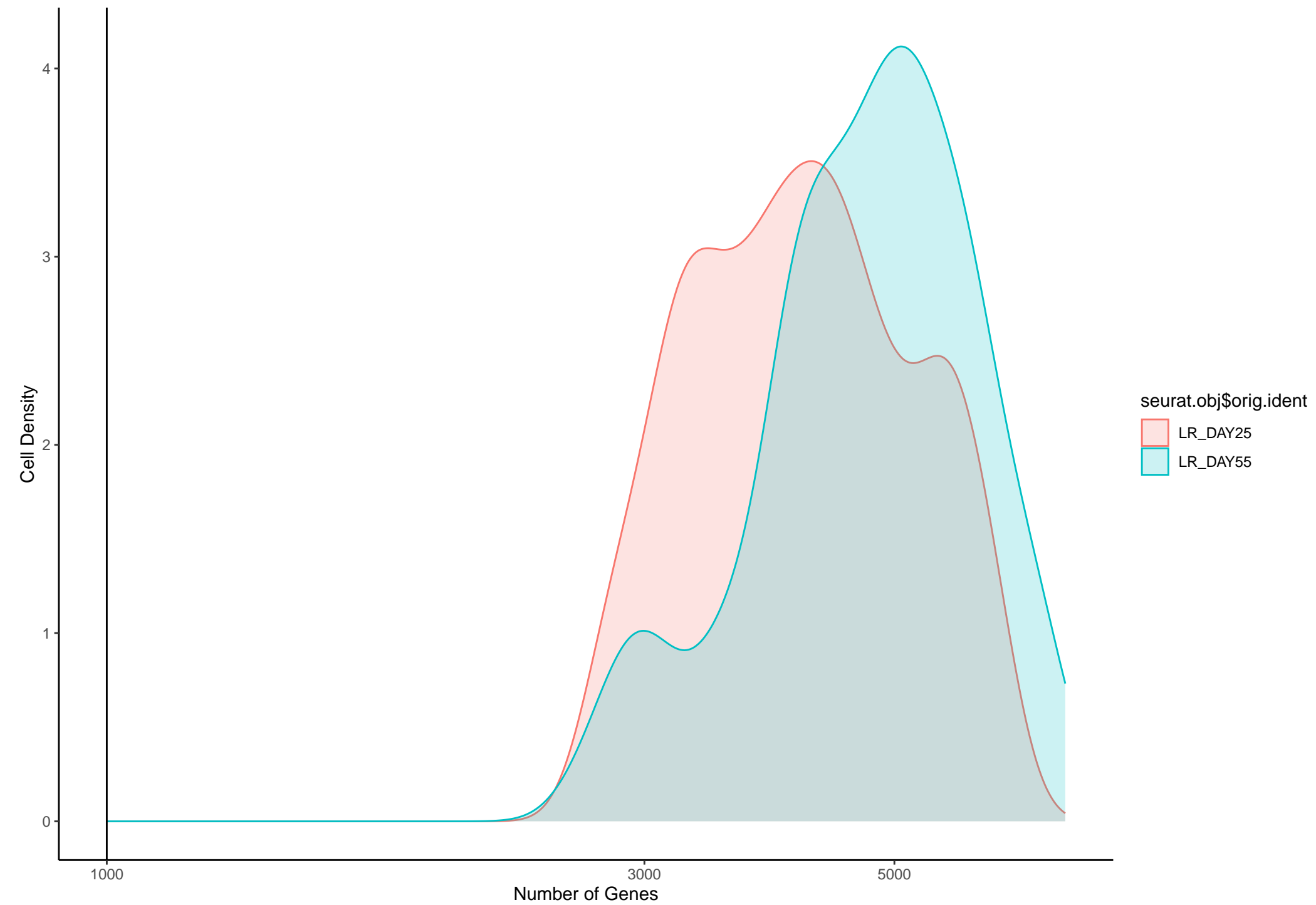
Genes detected per cell (Filtered Short Reads)



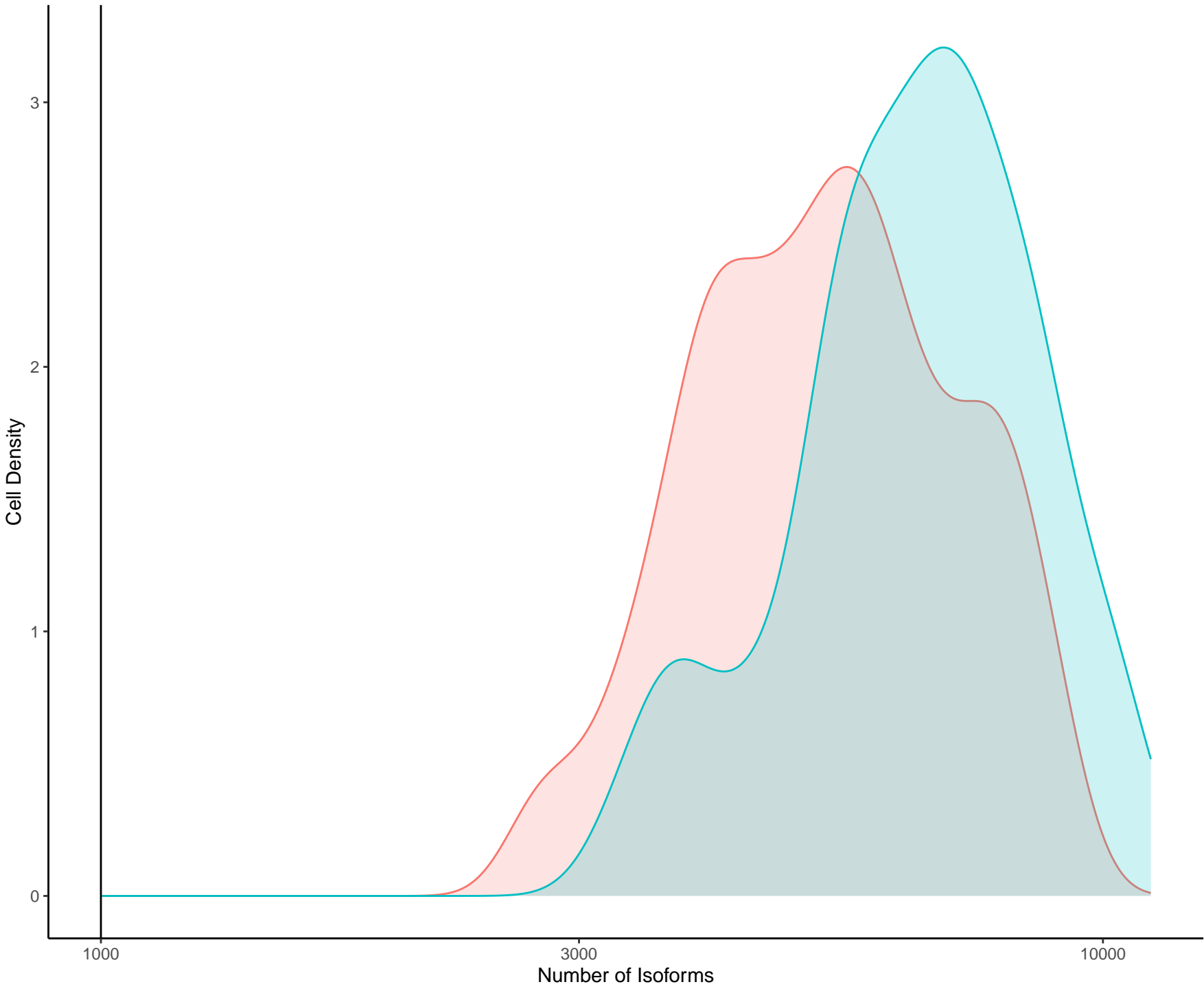
Genes detected per cell (Long Reads)



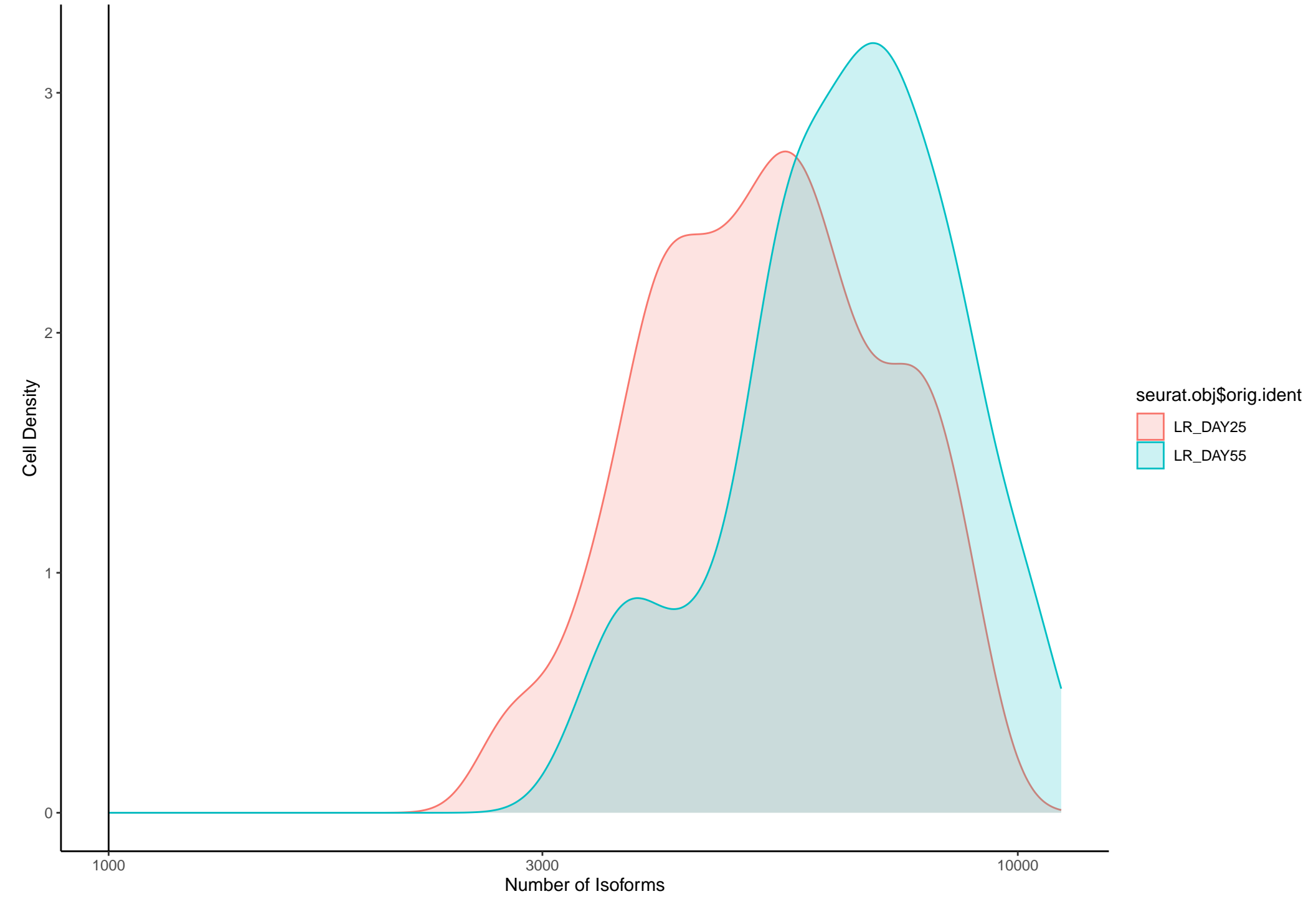
Genes detected per cell (Filtered Long Reads)



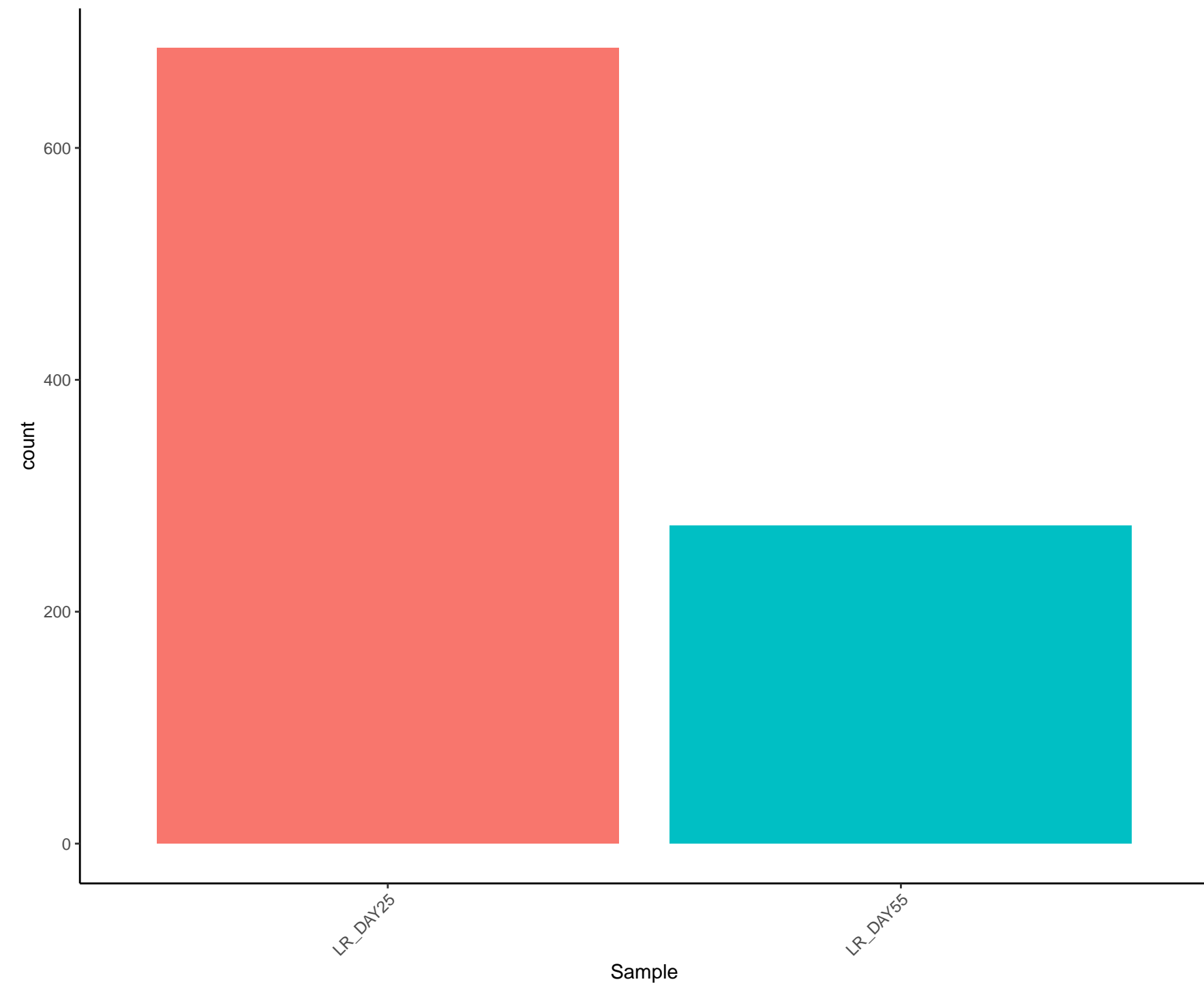
Isoforms detected per cell (Long Reads)



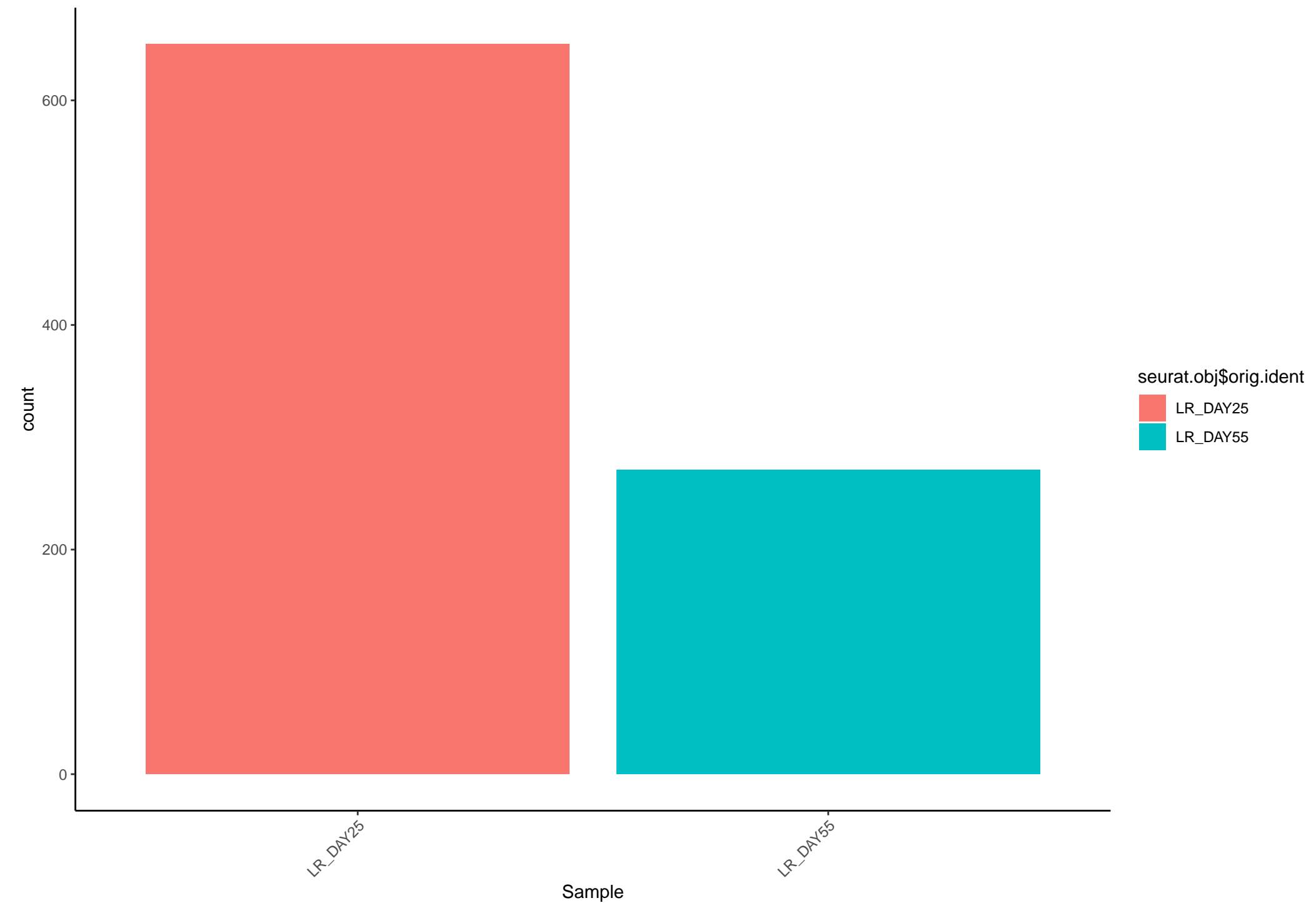
Isoforms detected per cell (Long Reads) After Filtering



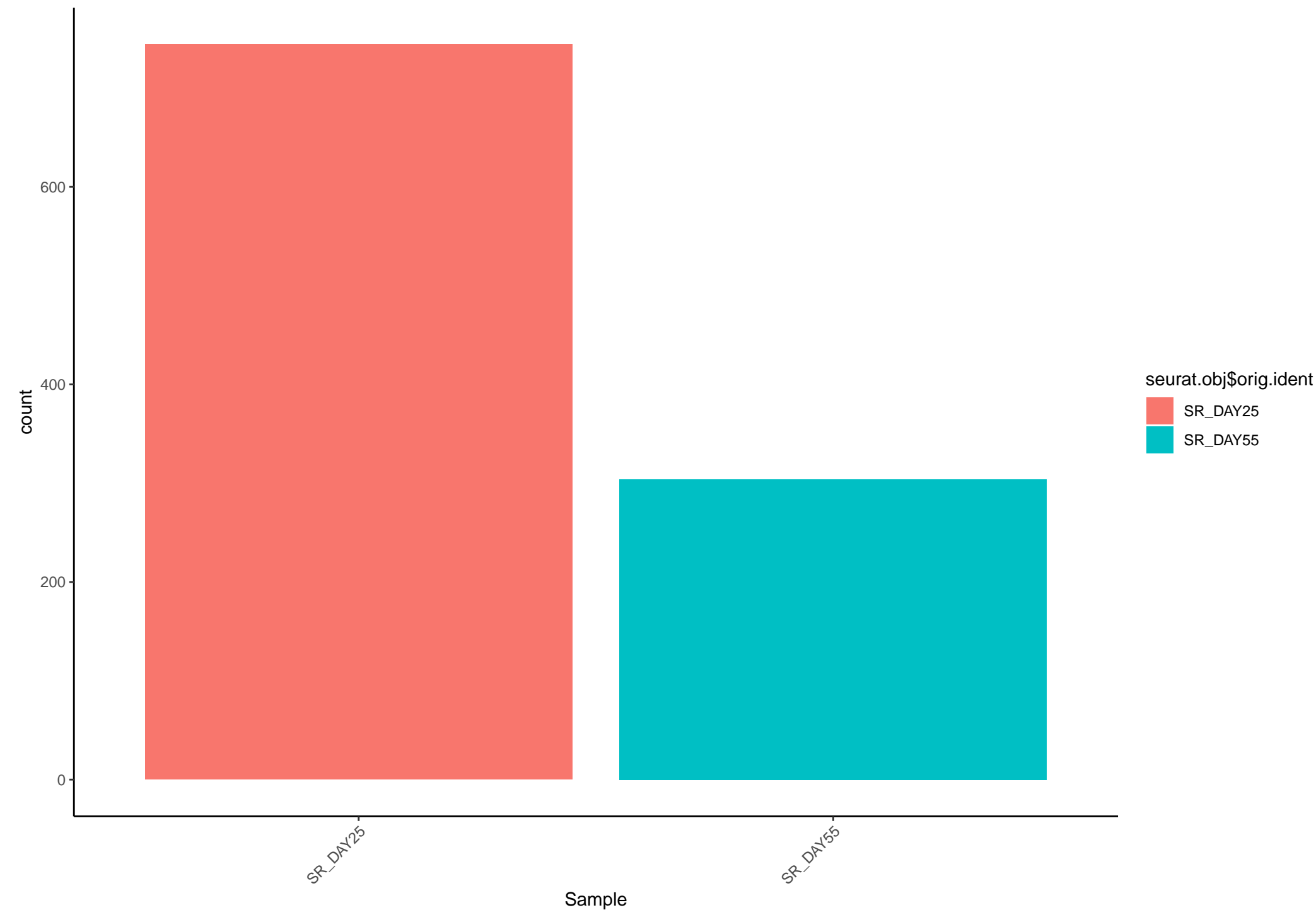
Number of Cells (Integrated Long Reads)



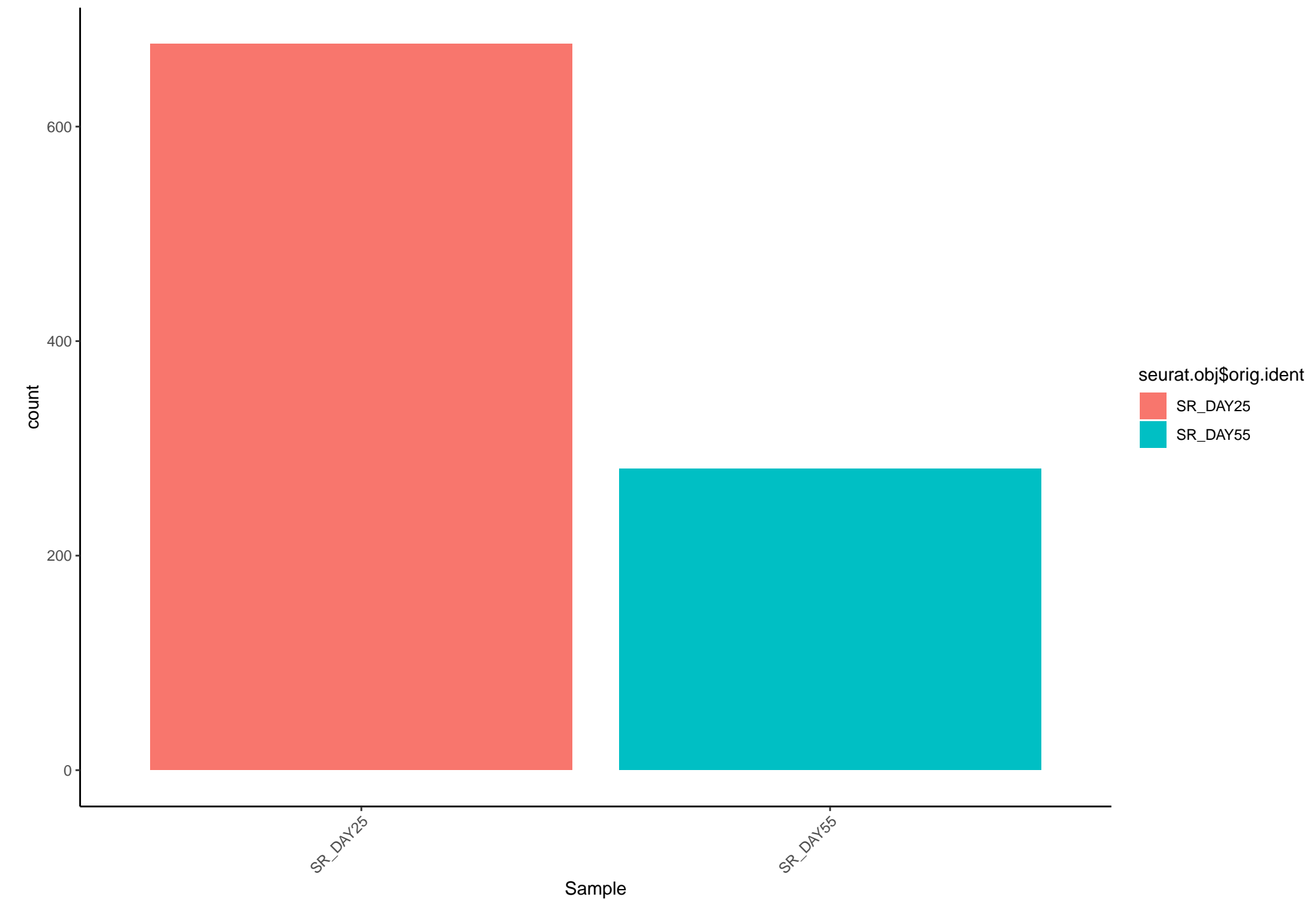
Number of Cells (Filtered Long Reads)



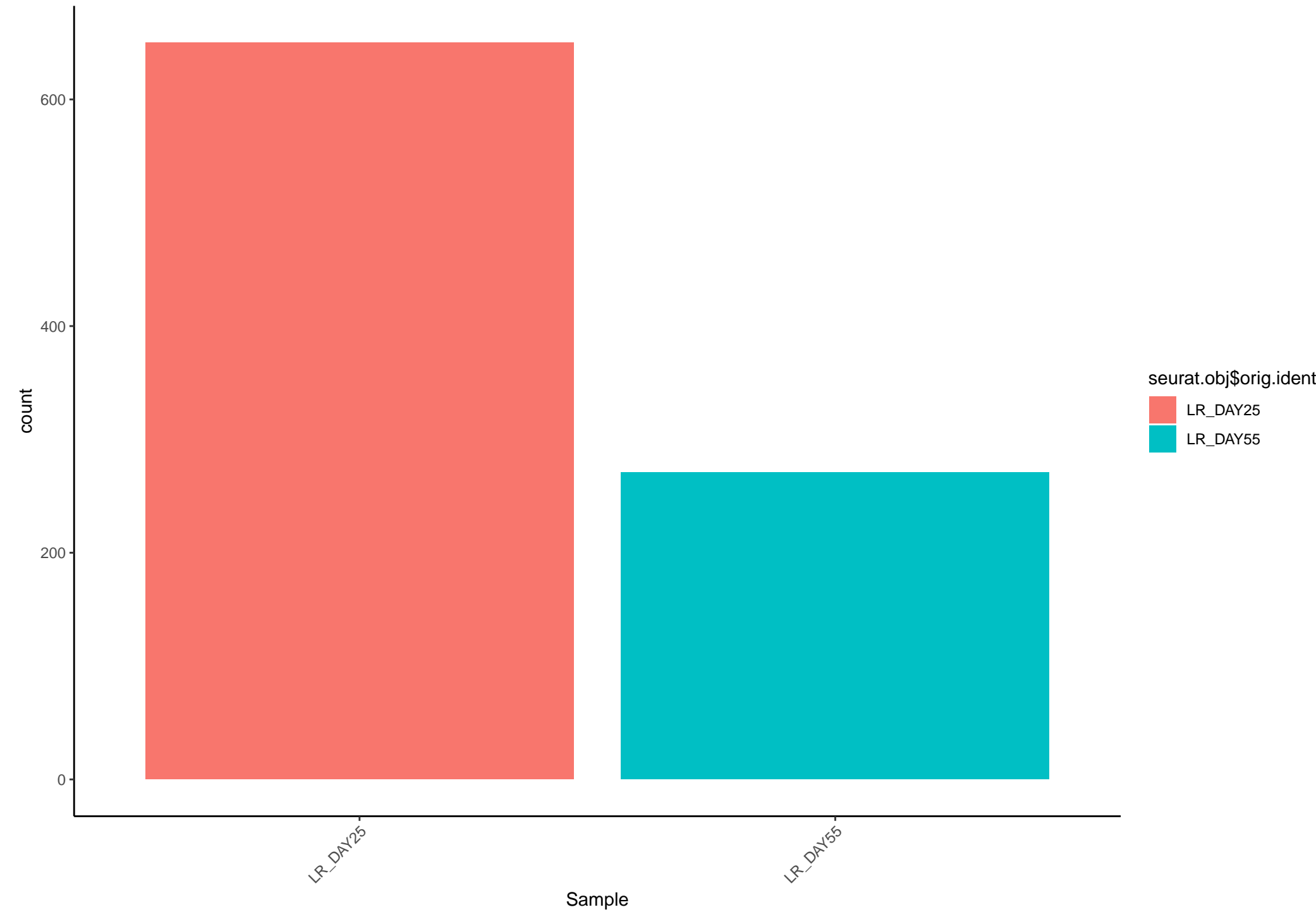
Number of Cells (Integrated Short Reads)



Number of Cells (Filtered Short Reads)



Number of Cells (Filtered Long Reads)



Number of Cells (Filtered Short Reads)

