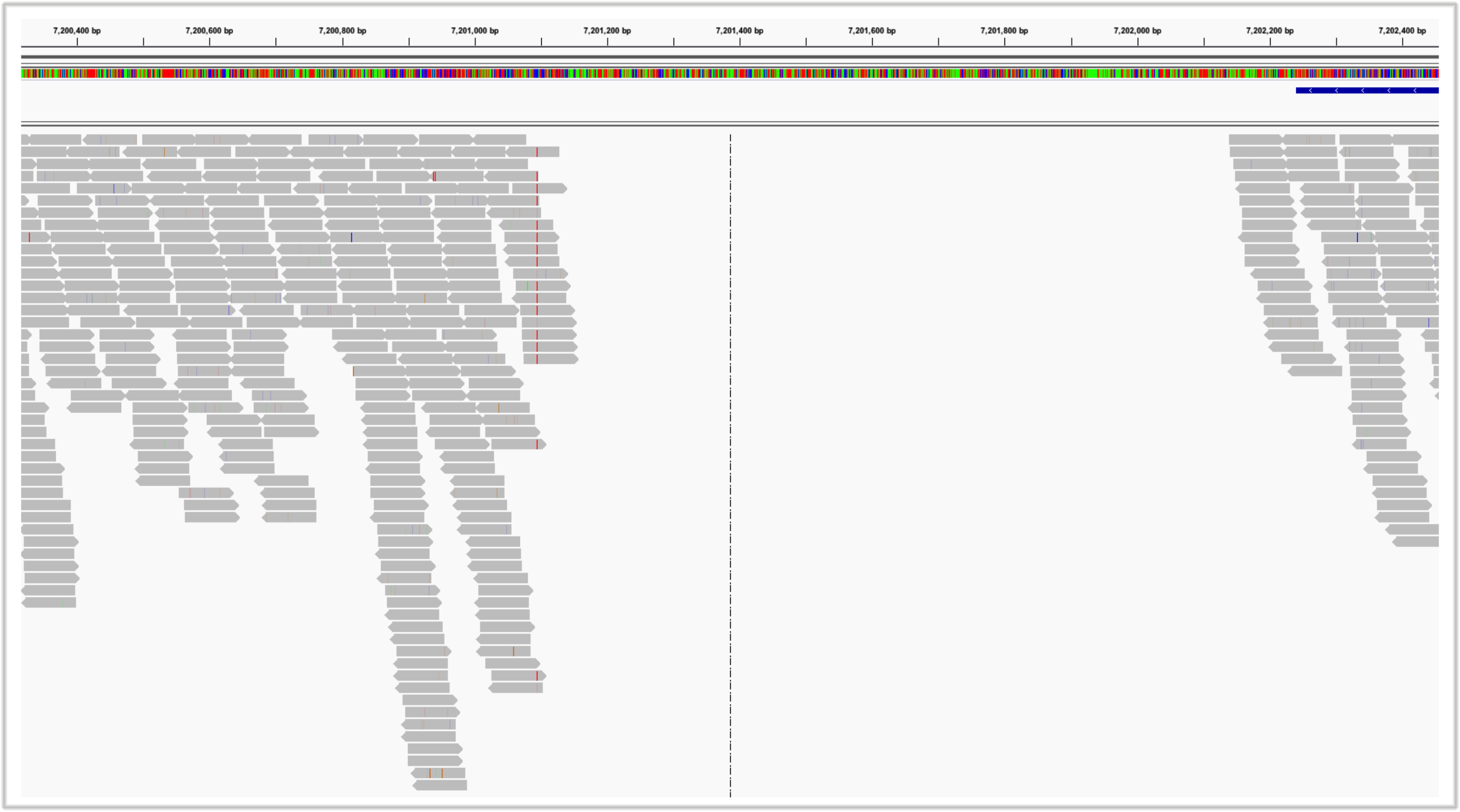

Figure S2 Uncovered region confirmed to be a genomic deletion. CloudMap contains a workflow for annotating uncovered regions that may be genomic deletions. Users are encouraged to check if uncovered regions repeatedly appear in other strains and also to view these putative deletions in an alignment viewer. We find that true deletions tend to exhibit a cliff of high coverage followed by zero coverage on both uncovered boundary regions. Regions of high coverage flanking the putative deletion also often have SNPs or insertions present in many of the reads — indicating that distant genomic regions are now adjacent to one another. The deletion shown was confirmed to be a deletion via PCR and Sanger sequencing. The IGV viewer is used to display the alignment (Robinson et al., 2011, *Nature Biotechnology* 29, 24–26).