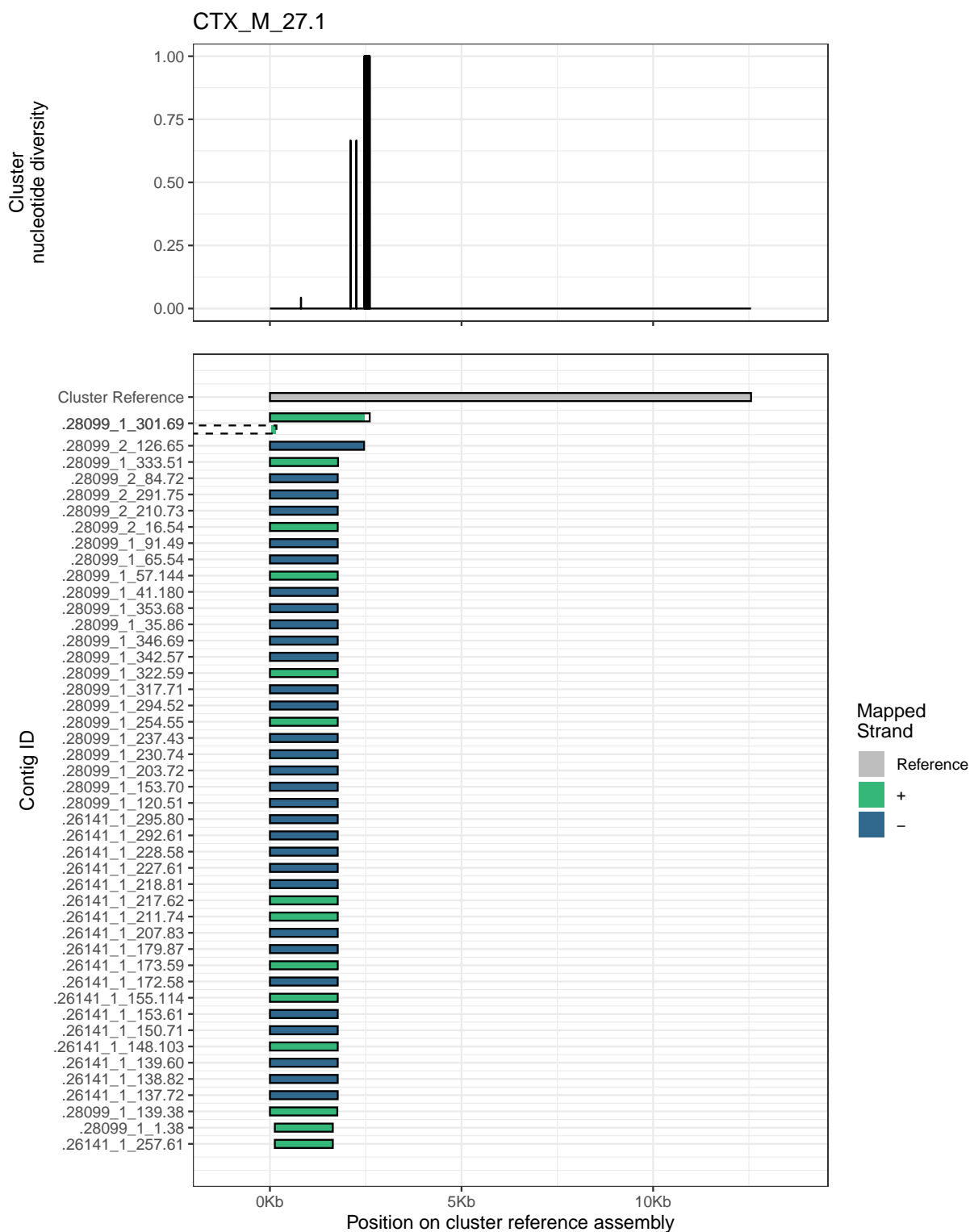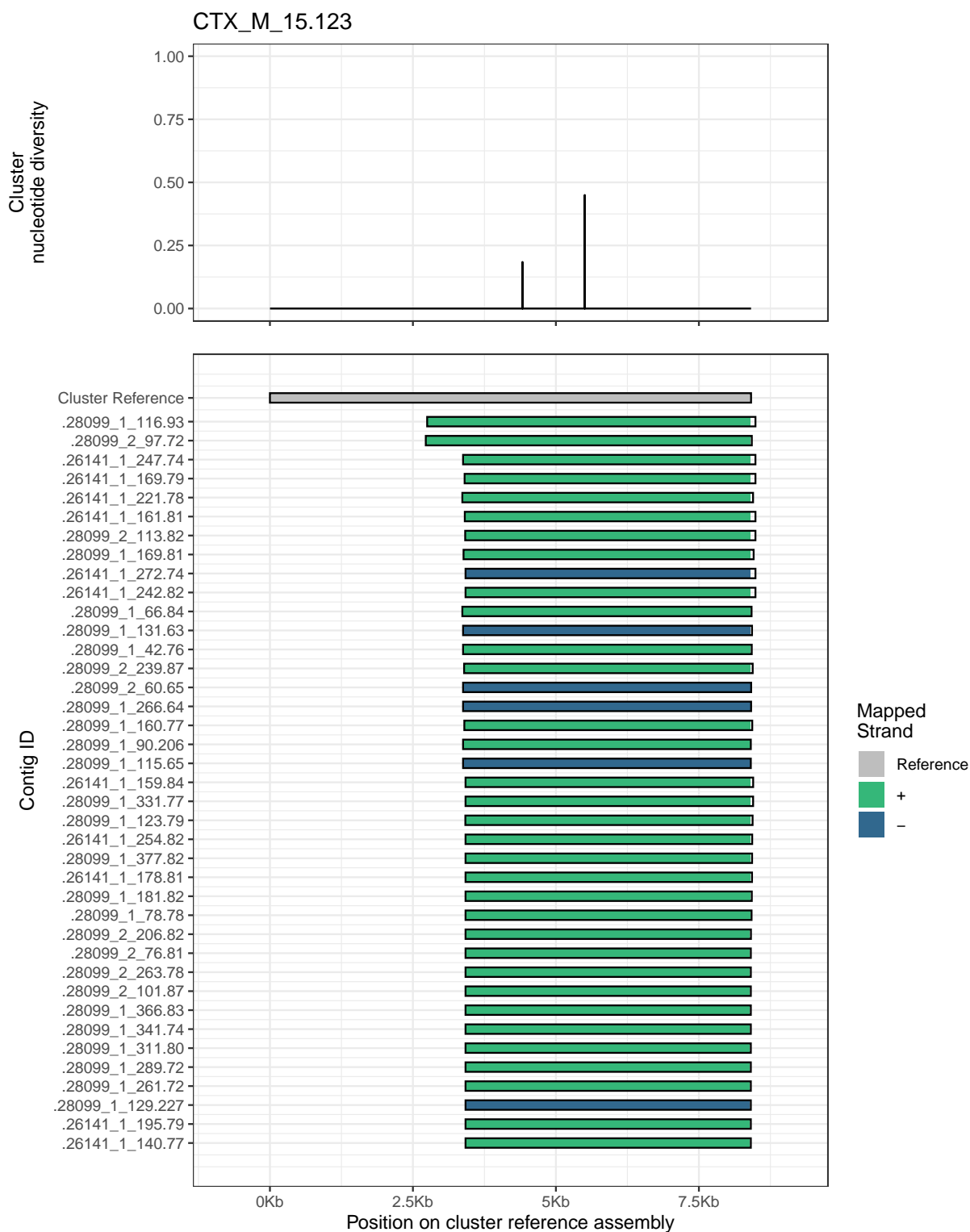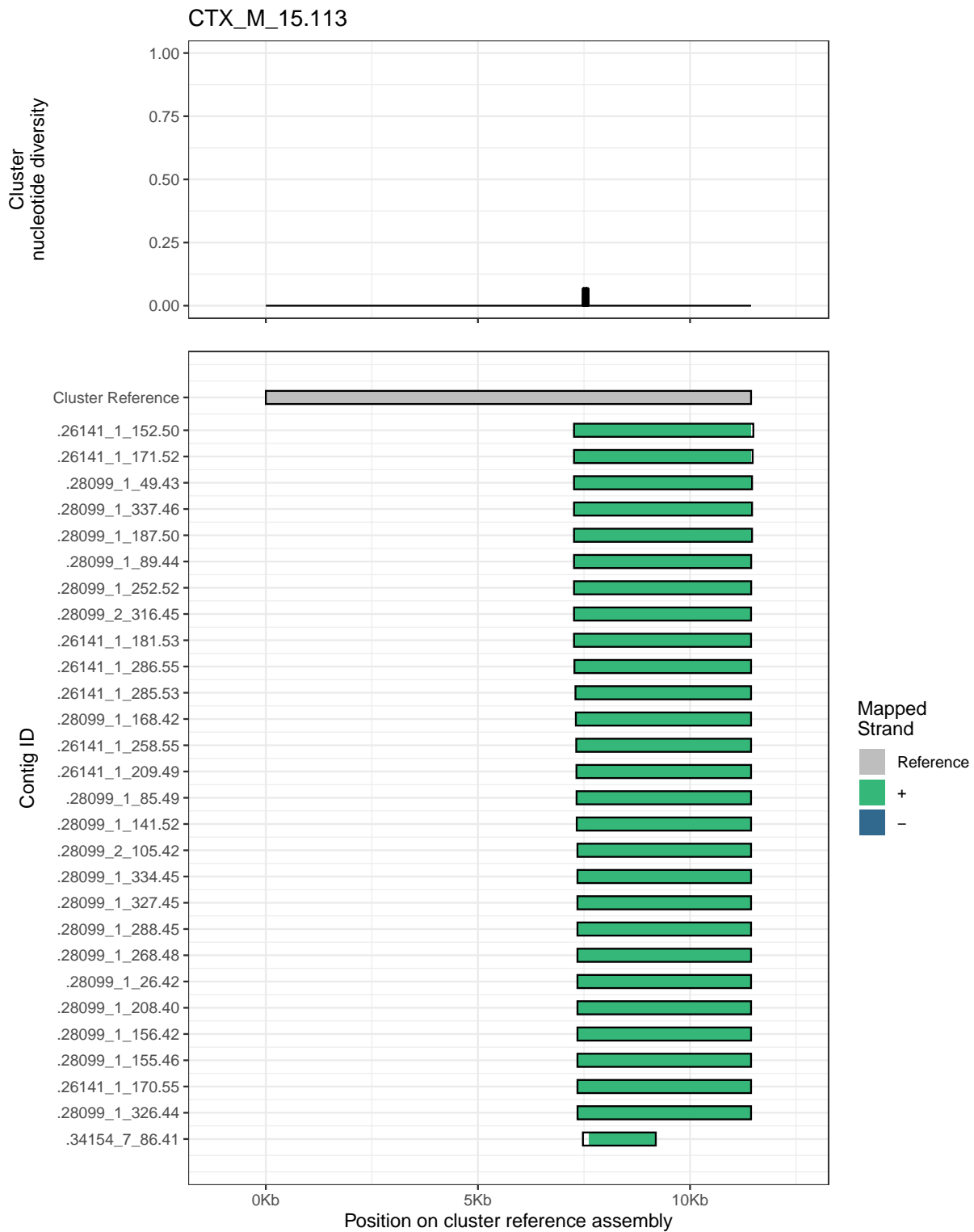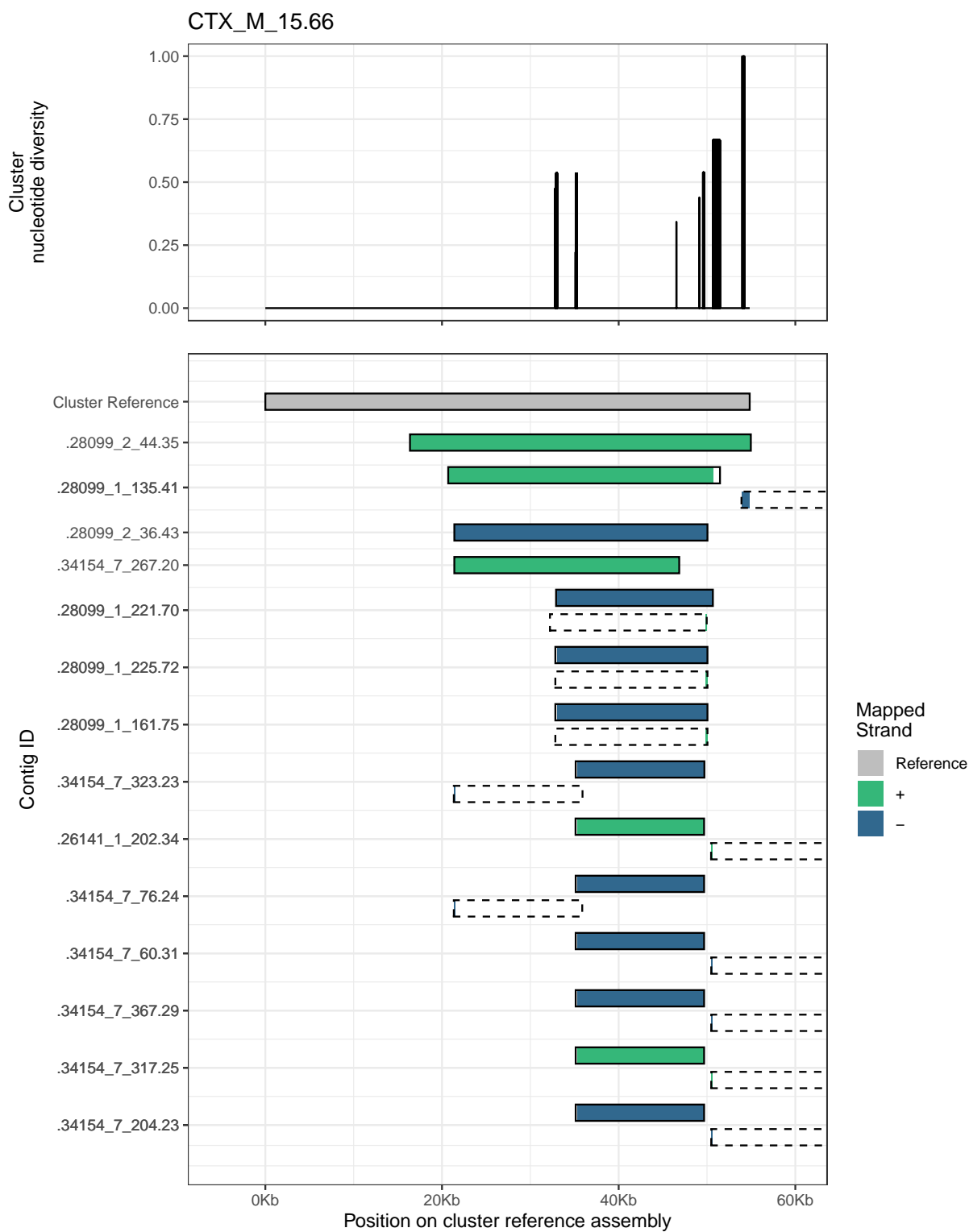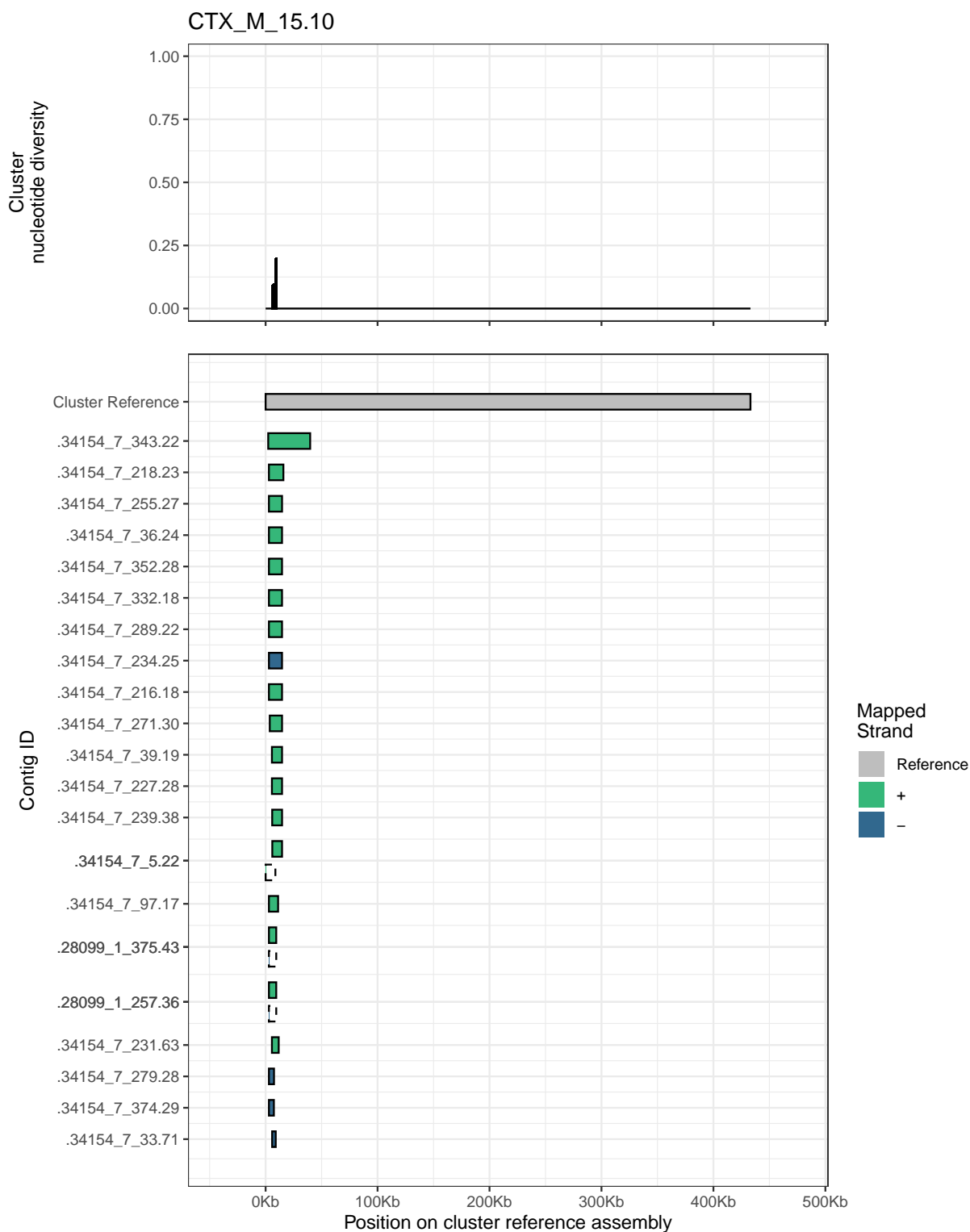# Plot ESBL cluster MSAs

Introduction

This document provides details of the top 10 largest ESBL contig clusters. Clusters were mapped to the cluster reference with minimap2 v2.16 and the -asm5 option. SAM files were used to generate a multiple sequence alignemnt then nucleotide diversity at each position calculated using PopGenome v2.7.5 in R. Alignments were plotted from the generated PAF files with coverage of the reference sequence indicated by colour and whether the sequence is mapped on the forward (+) or reverse (-) strand. Secondary alignments are shown with dashed outlines. Plots are in order of cluster size from largest to smallest.
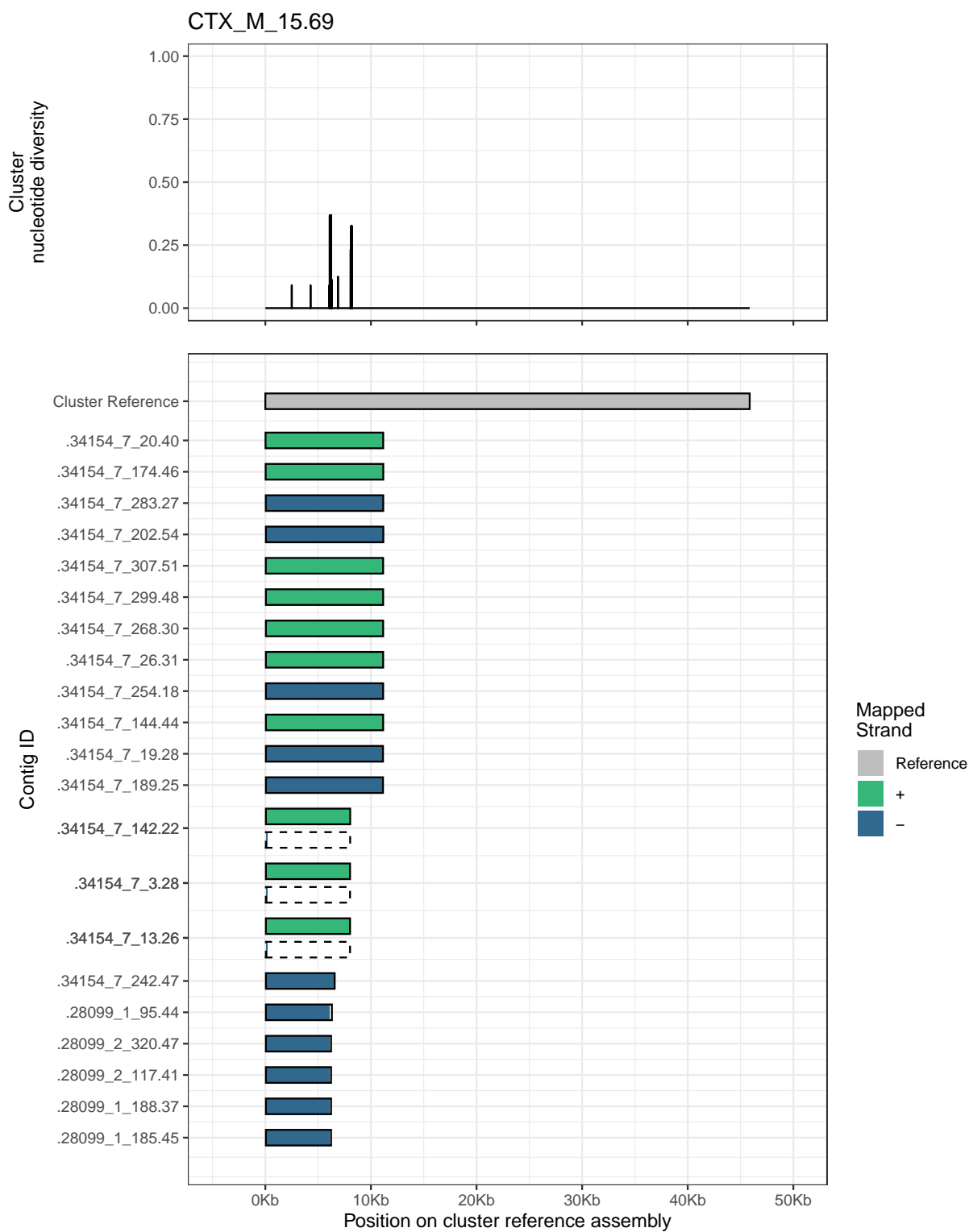
CTX_M_27.1

CTX_M_15.123

CTX_M_15.113

CTX_M_15.66

CTX_M_15.10
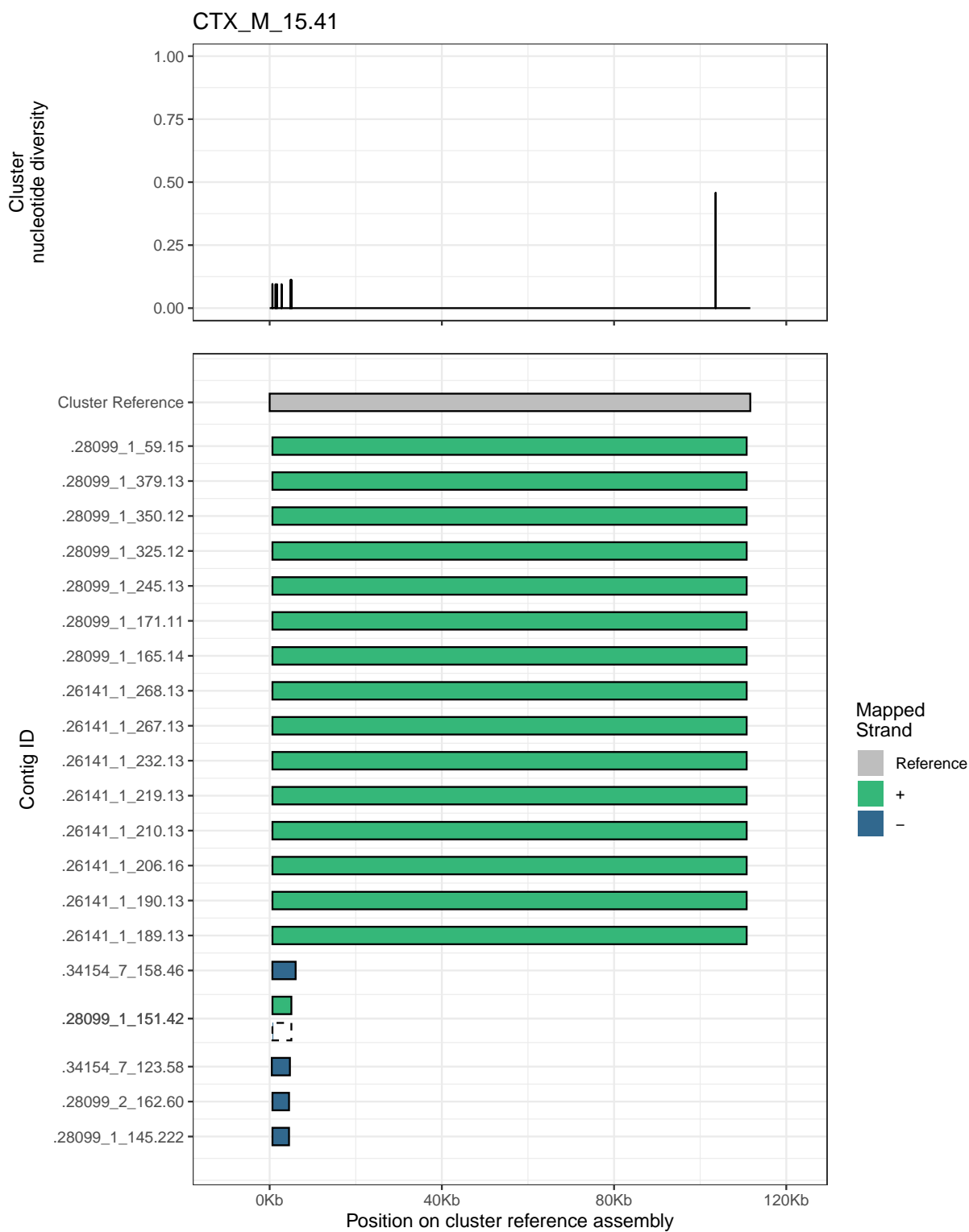
CTX_M_15.69

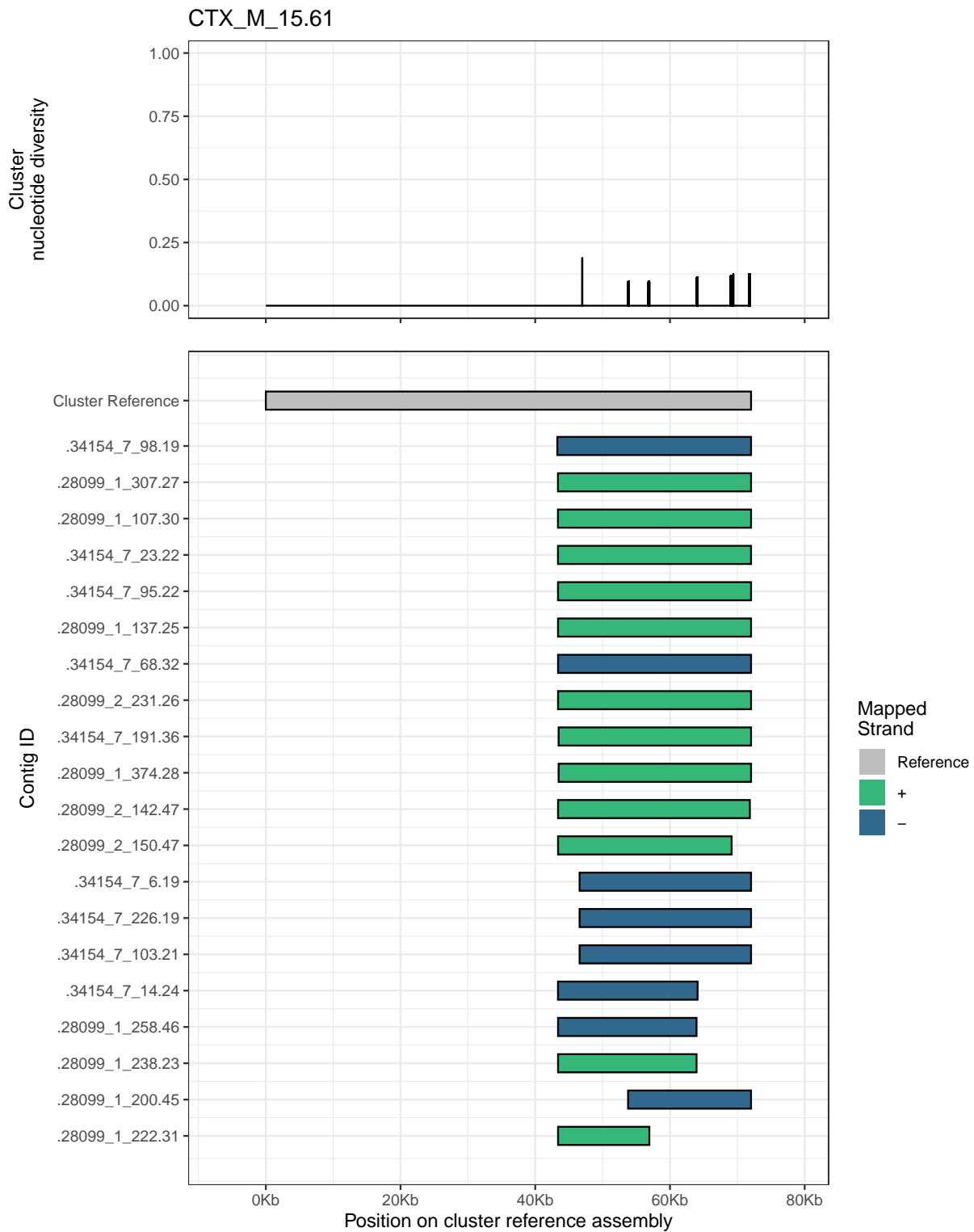CTX_M_15.41
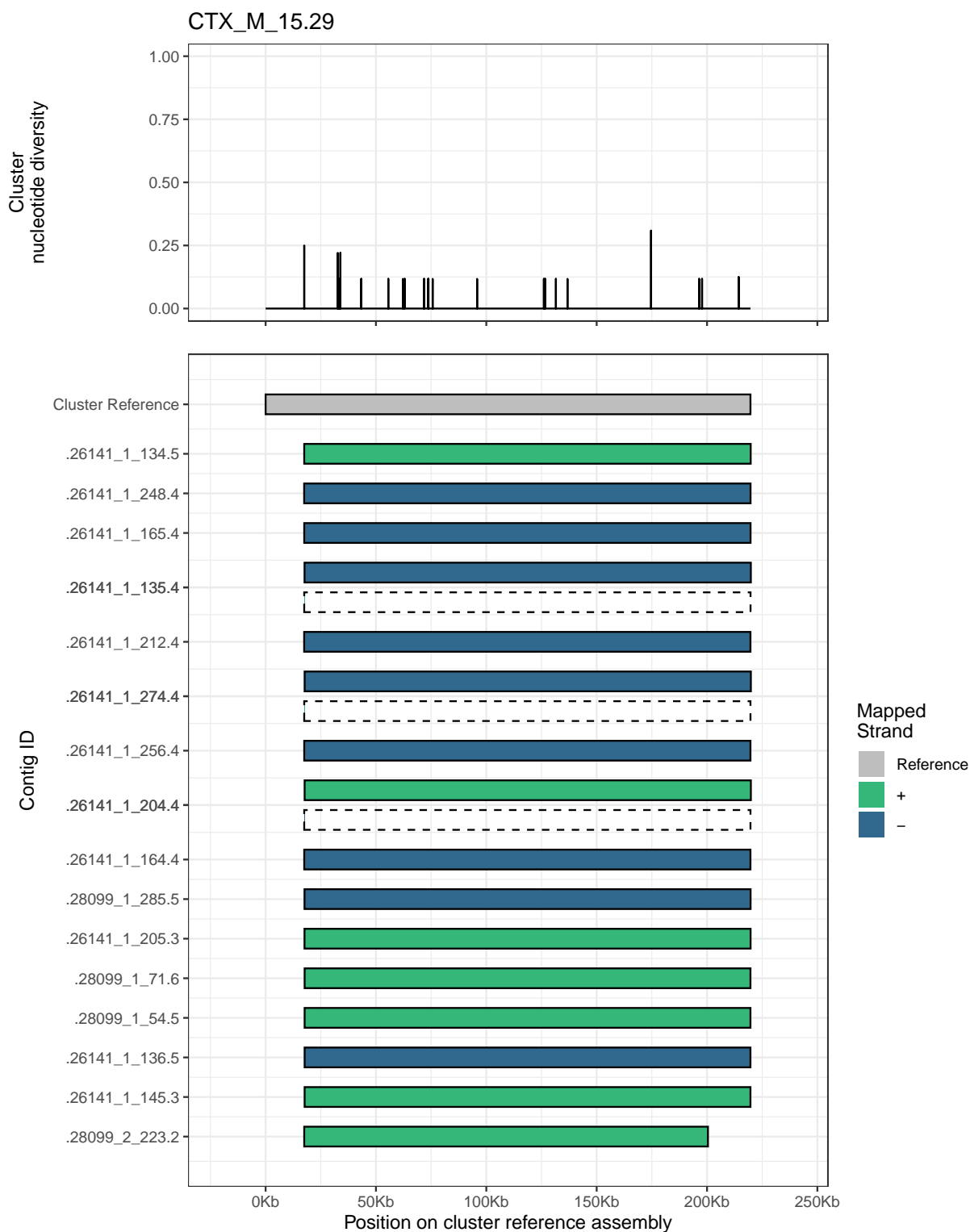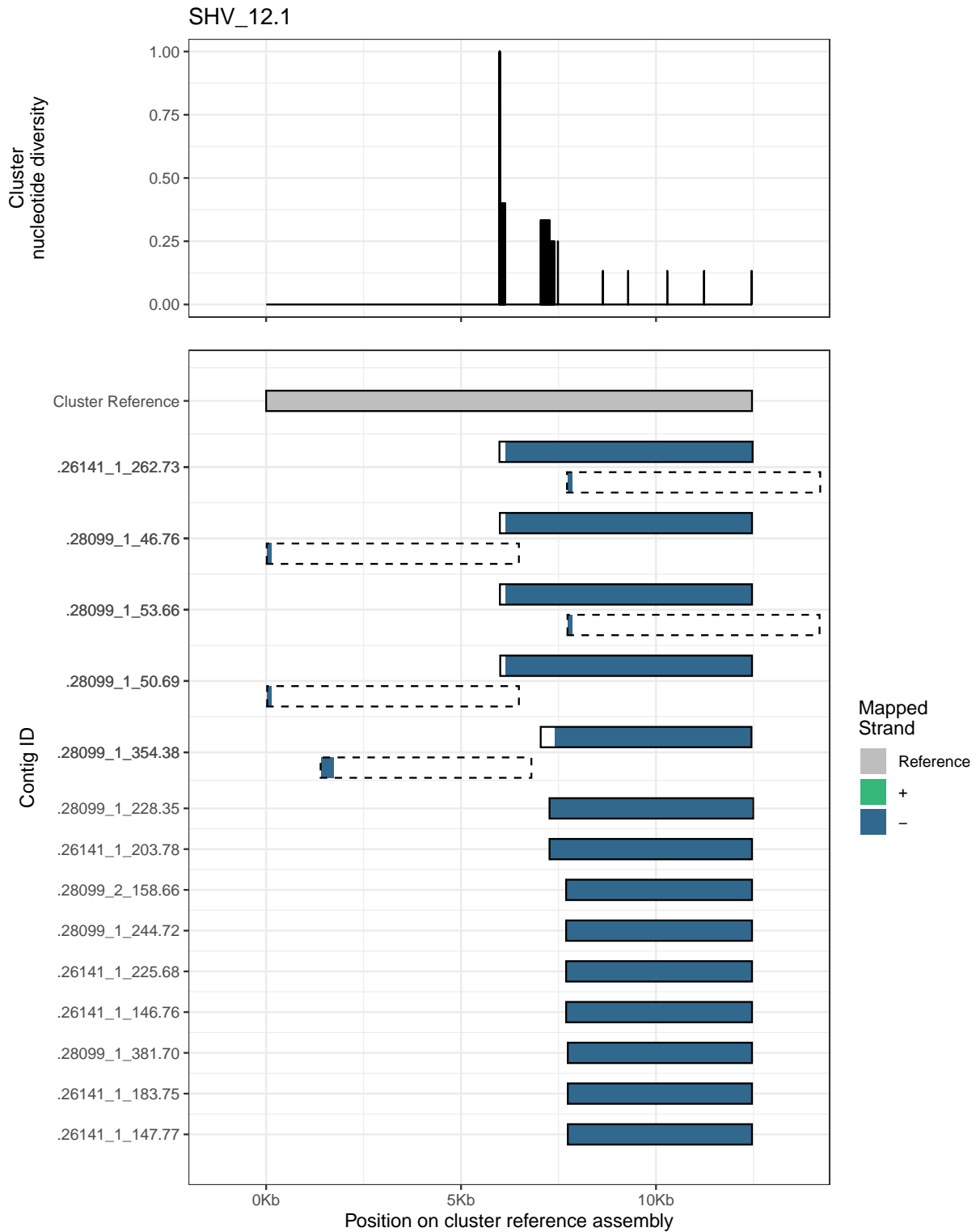
CTX_M_15.61

CTX_M_15.29

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.