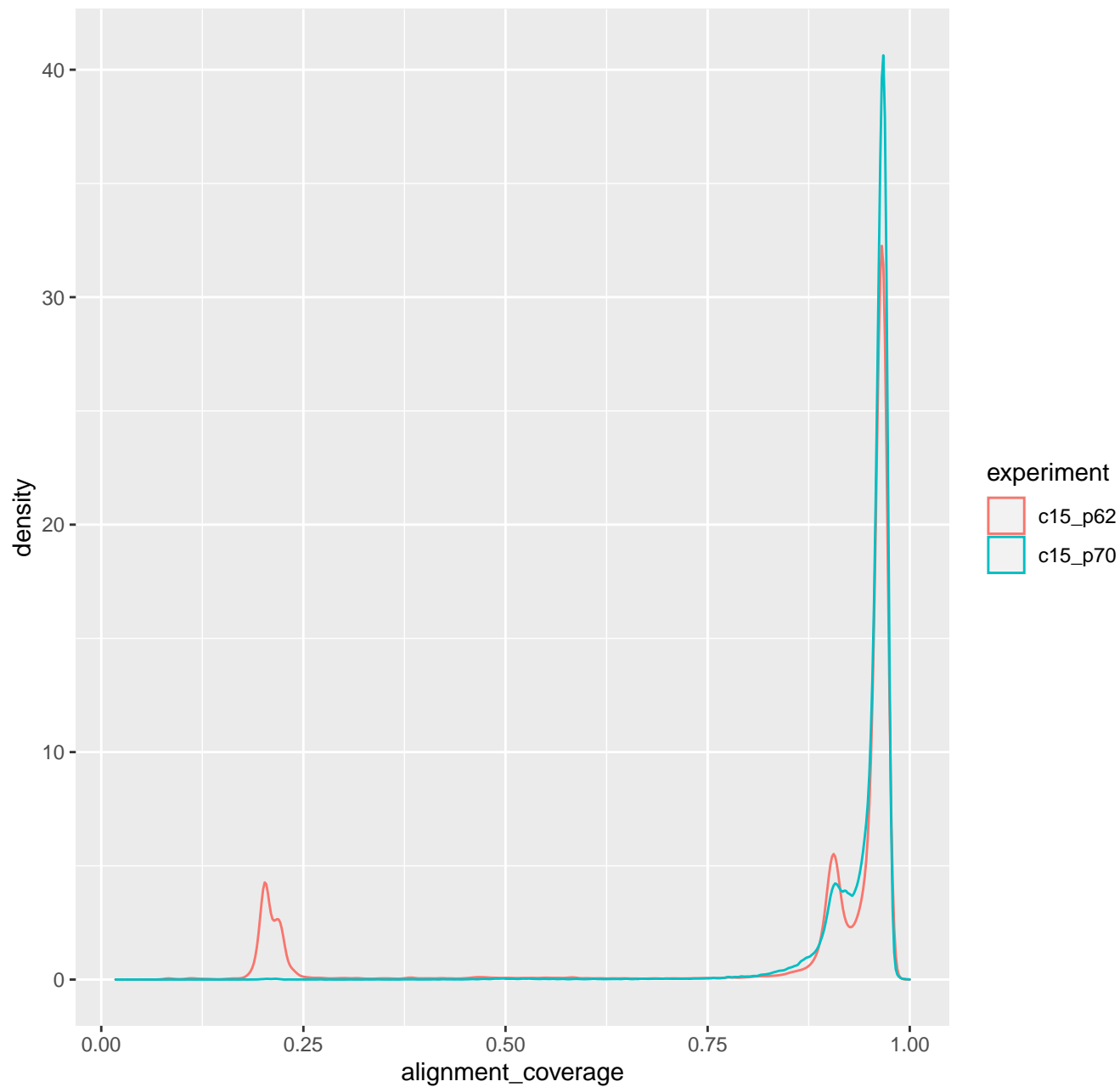
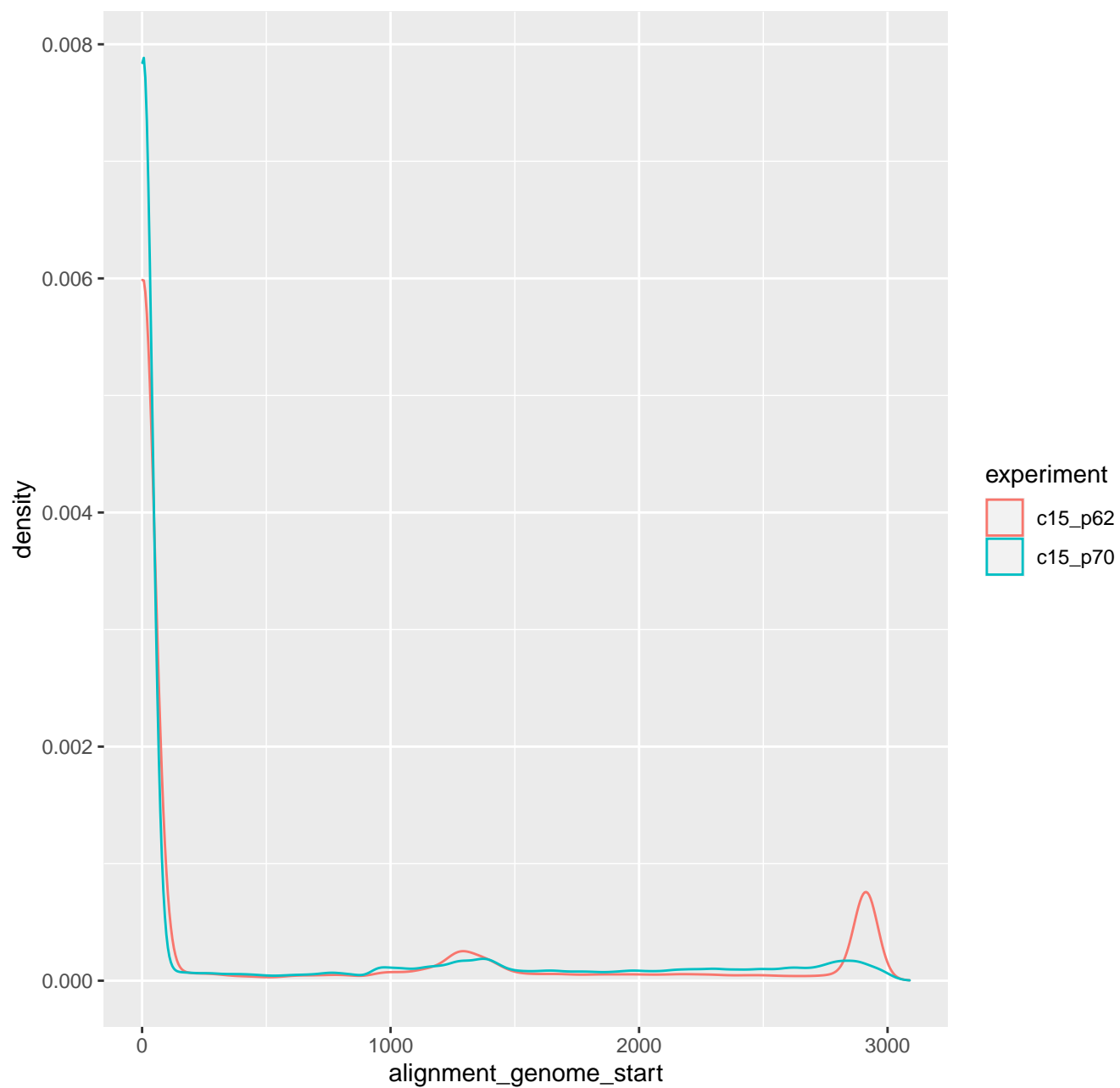


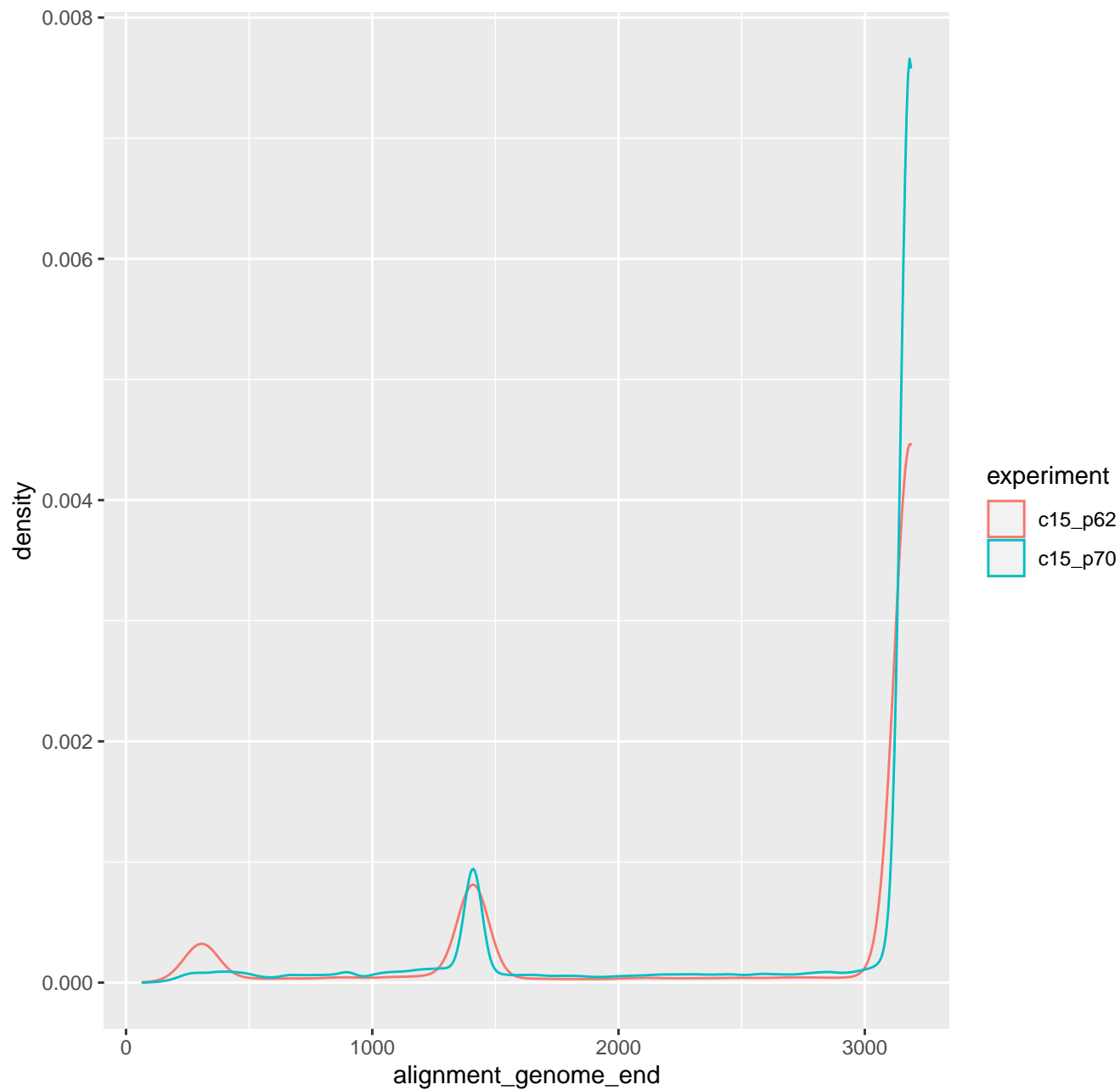
Alignment Coverage



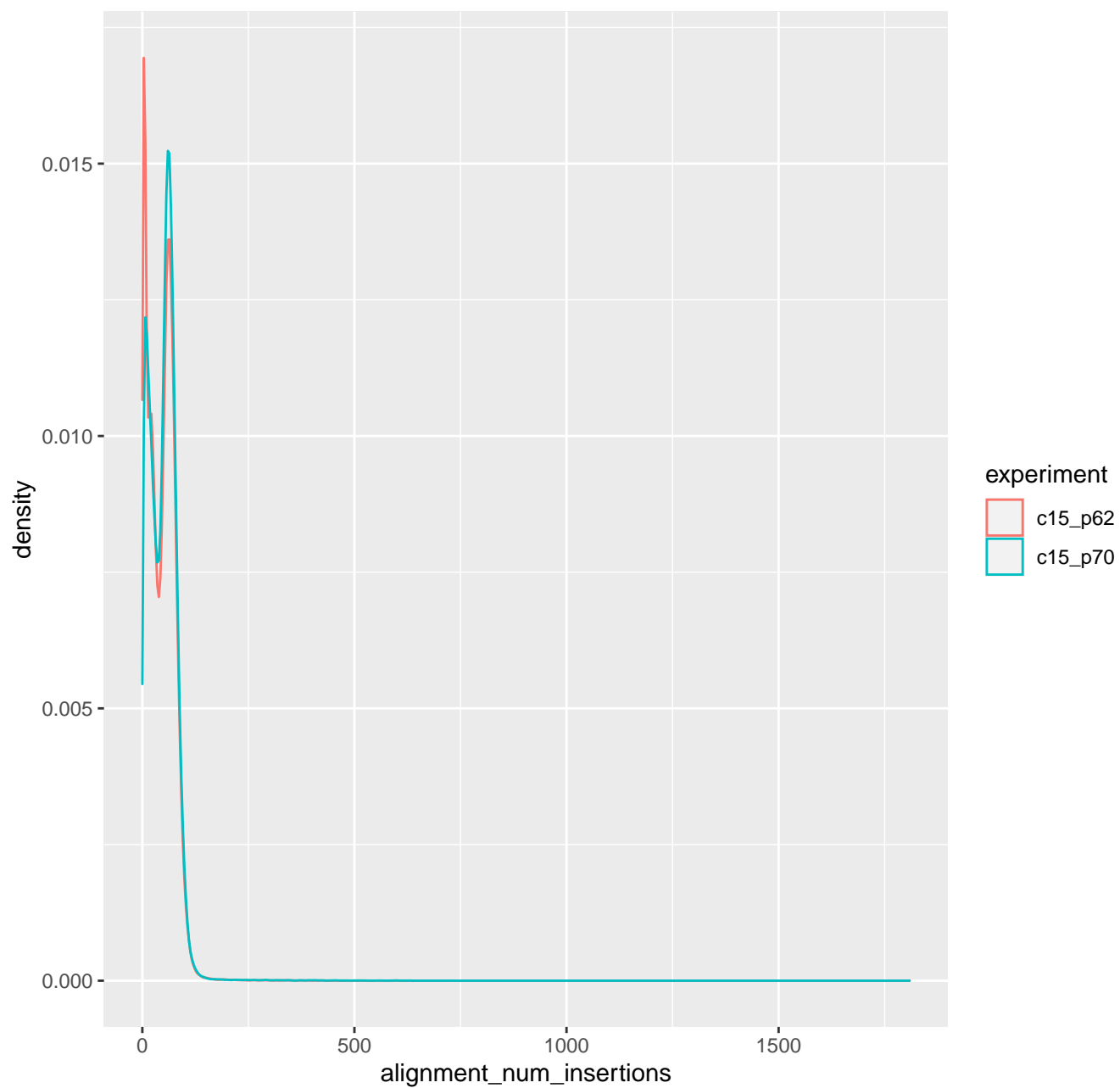
Alignment genome_start



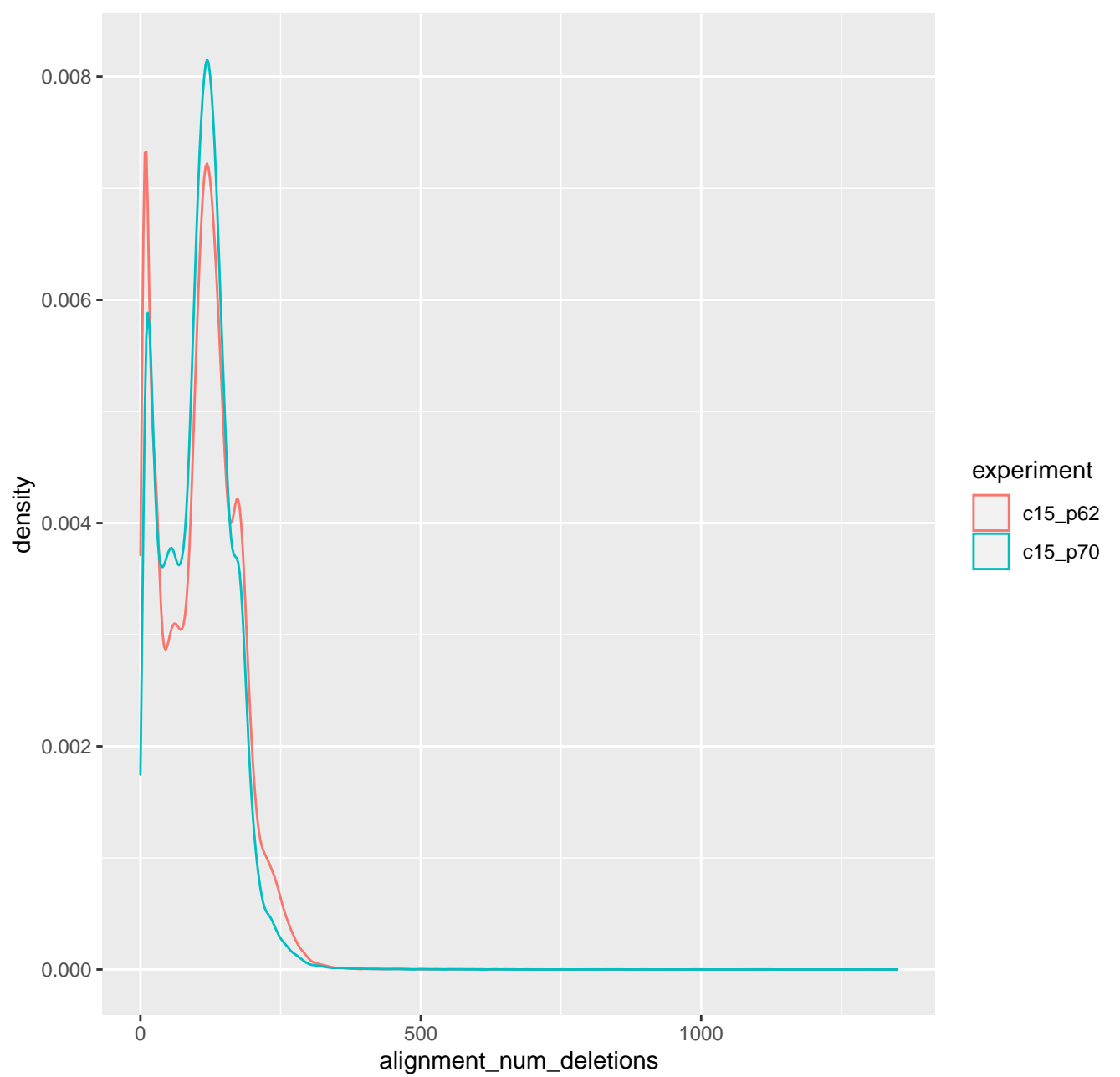
Alignment genome_end



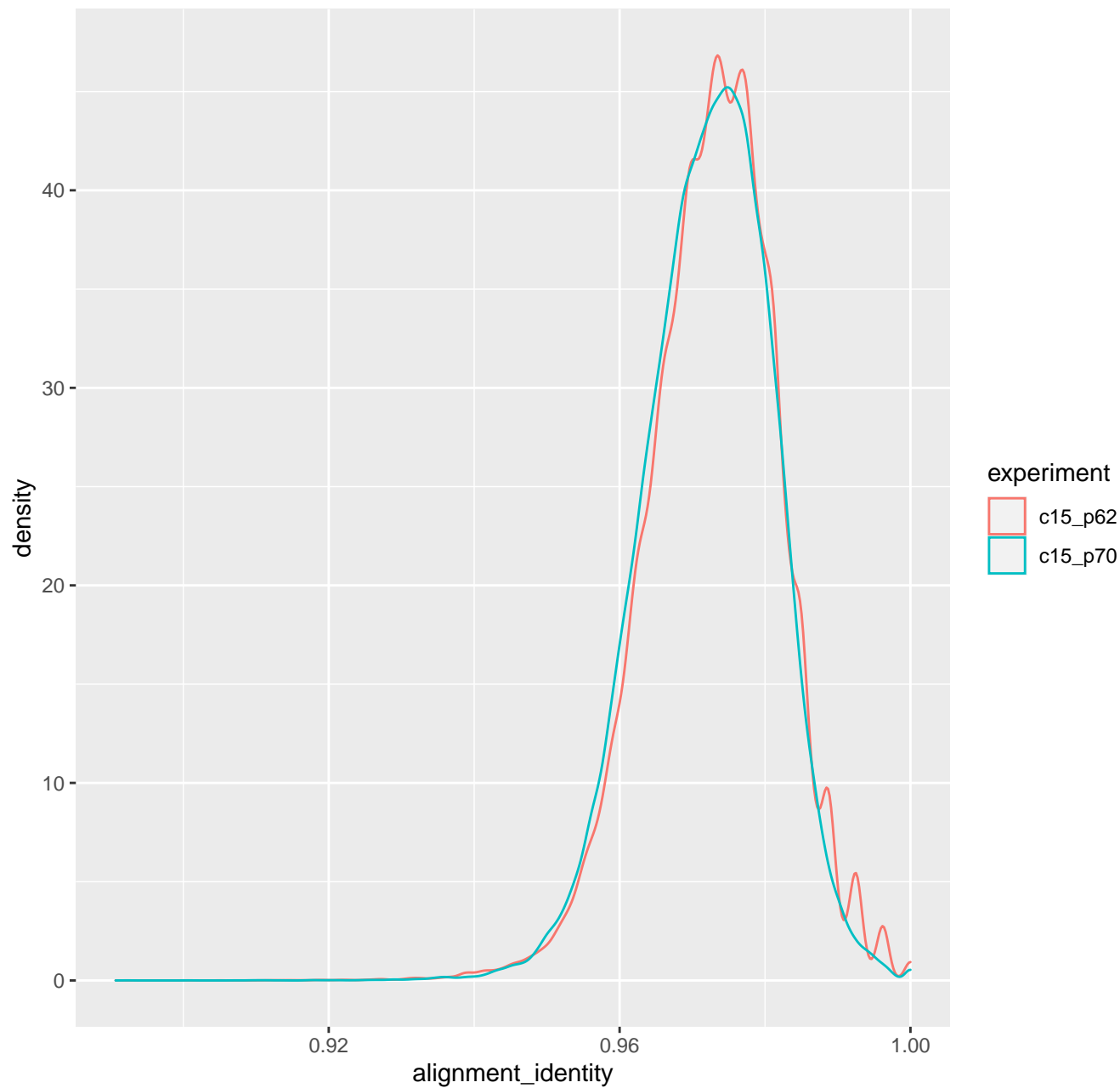
Number of insertions



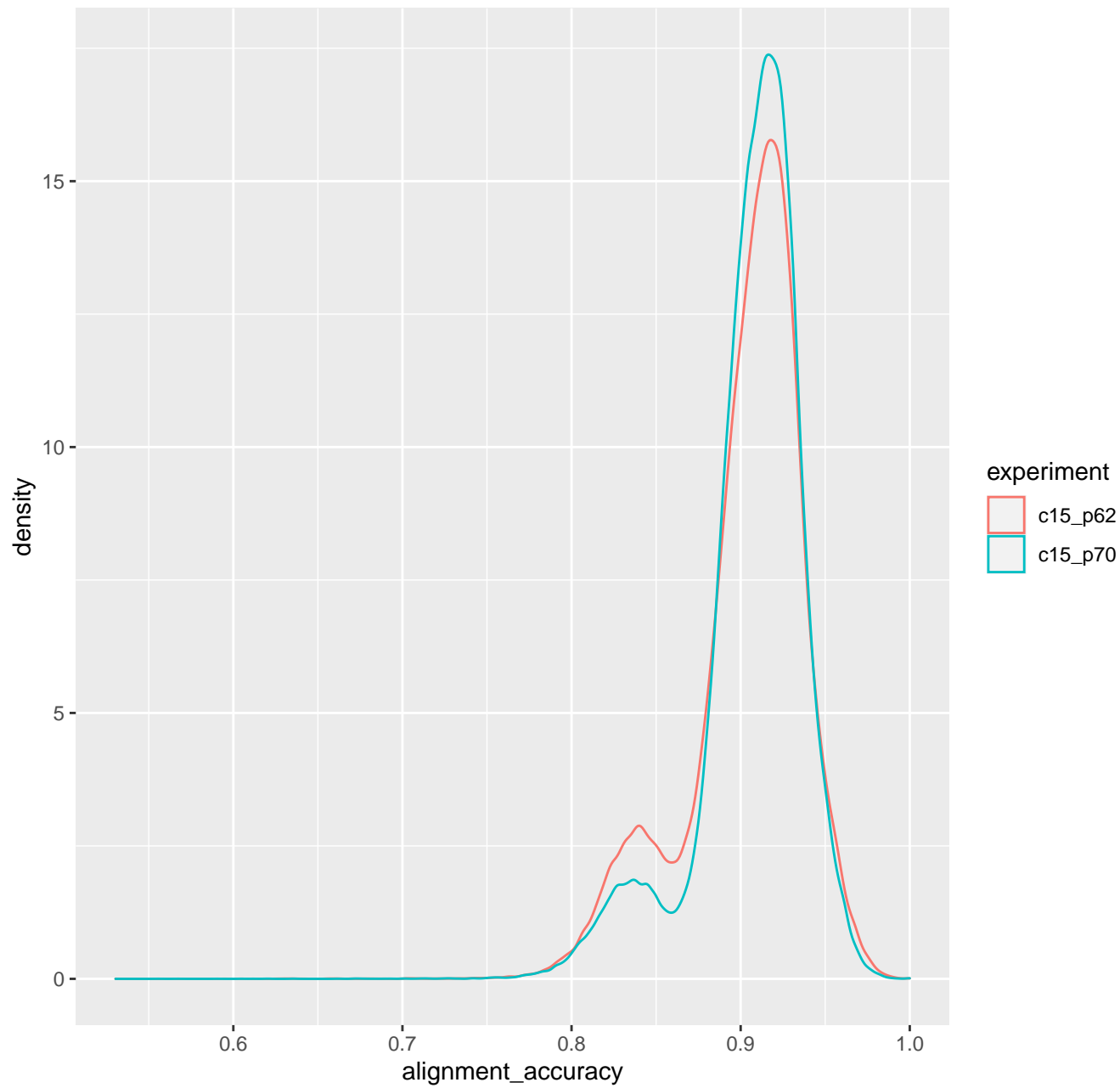
Number of deletions



Alignment_identity



Alignment_accuracy



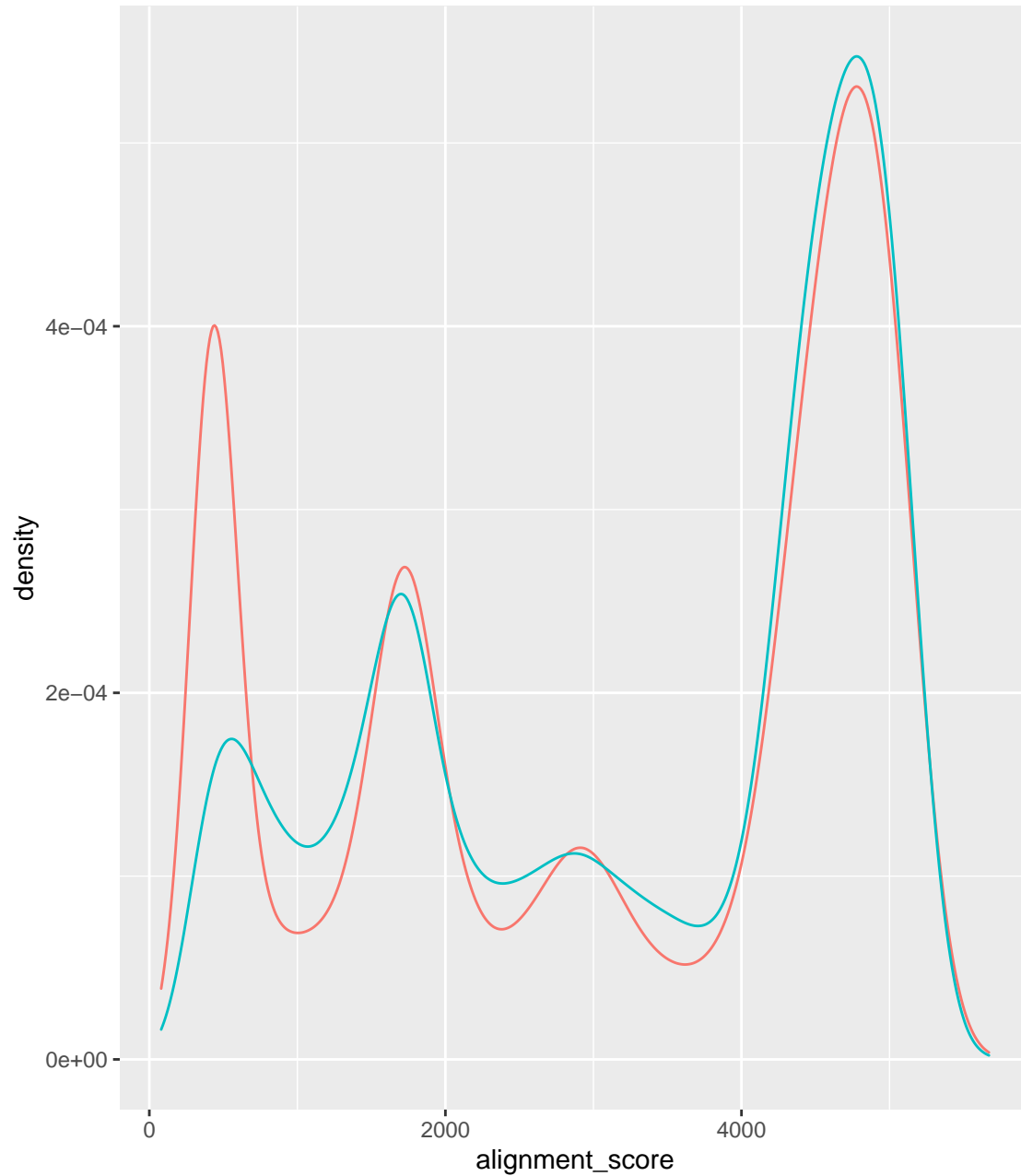
Alignment_score

density

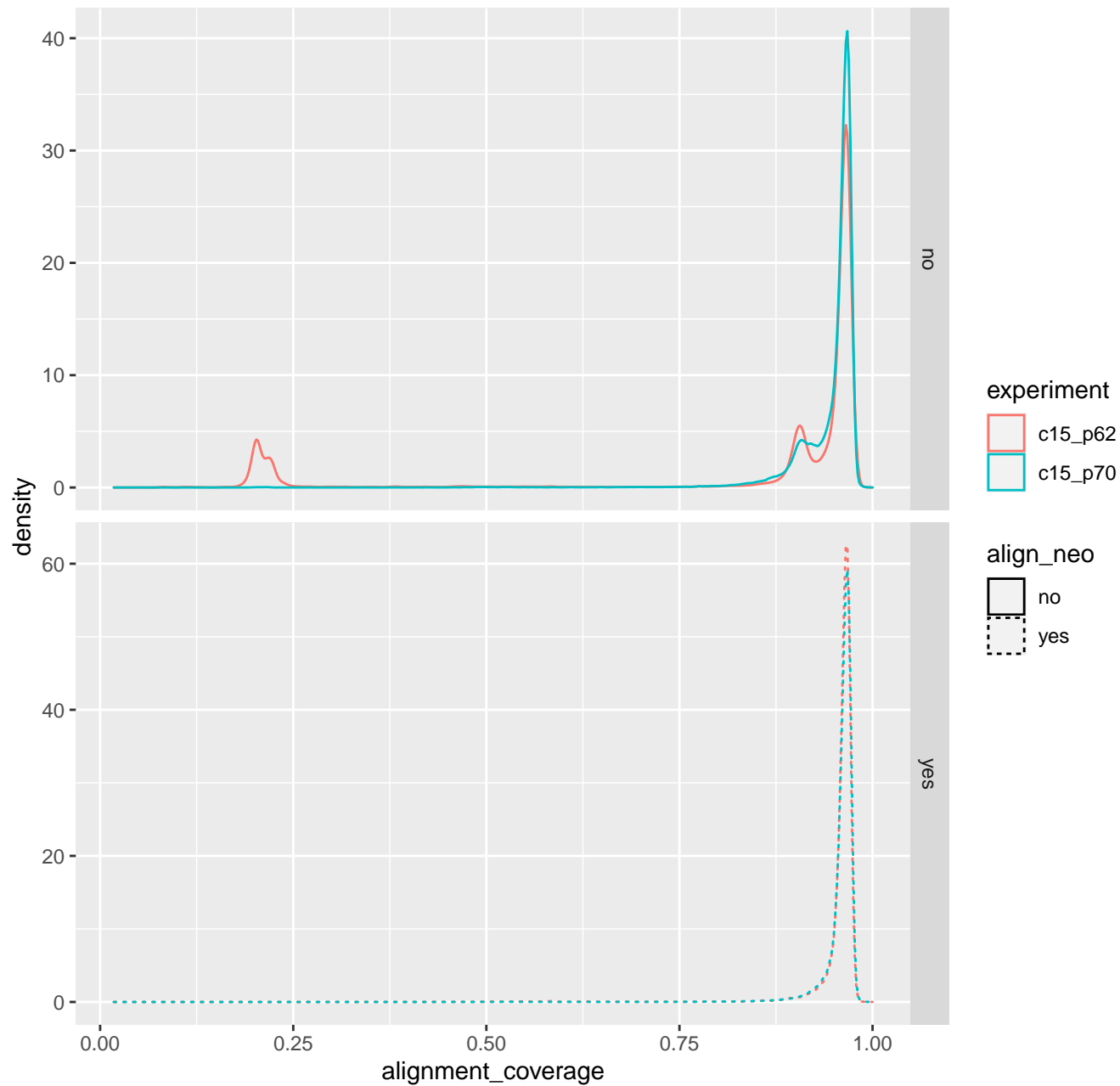
experiment

c15_p62

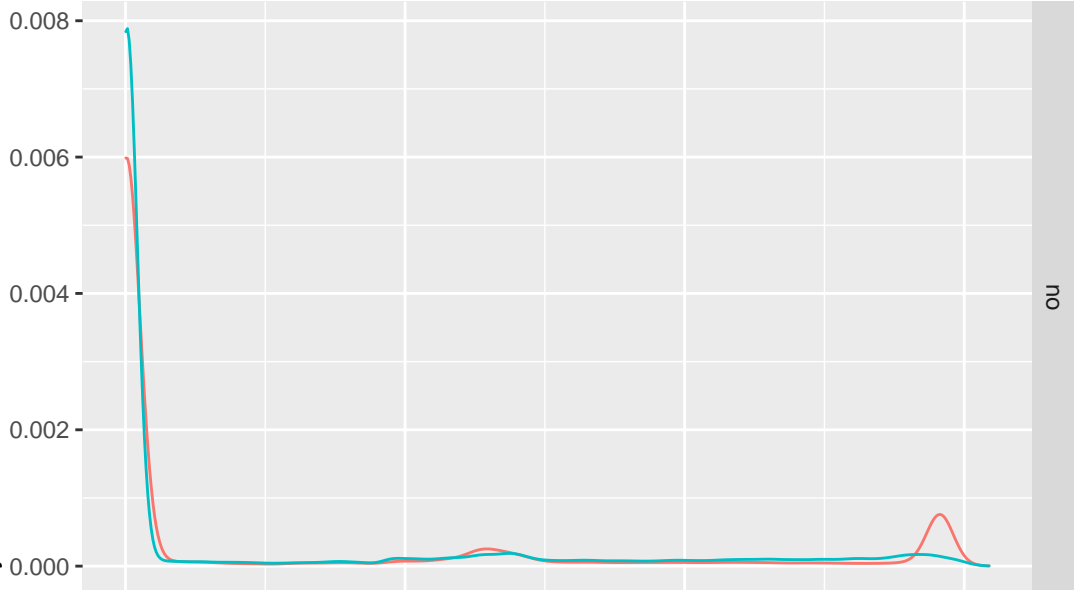
c15_p70



Alignment Coverage



Alignment genome_start



experiment

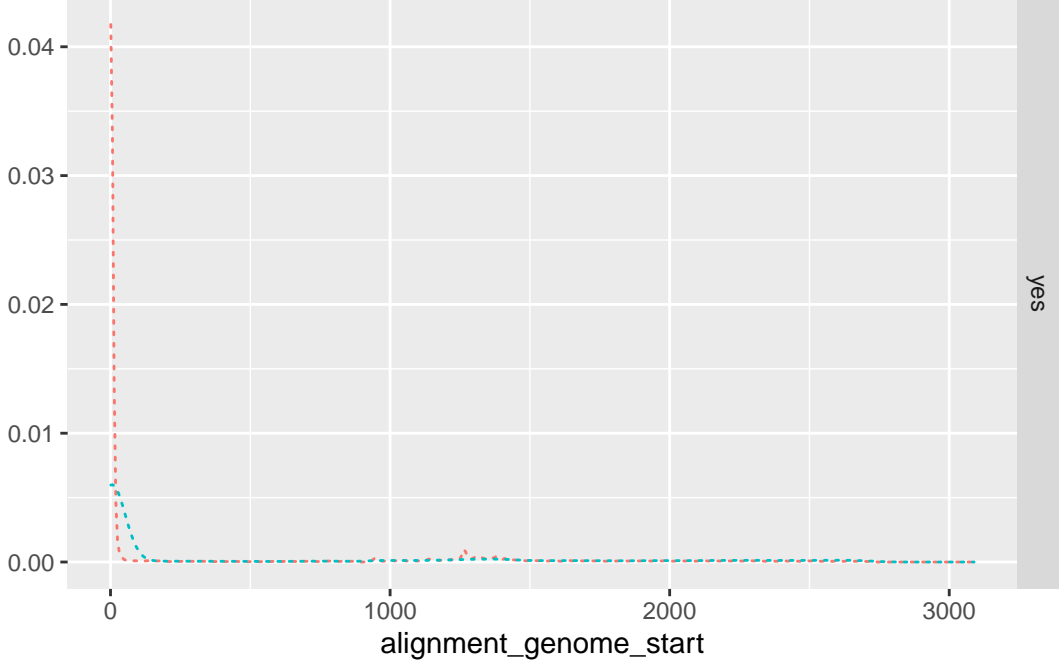
c15_p62

c15_p70

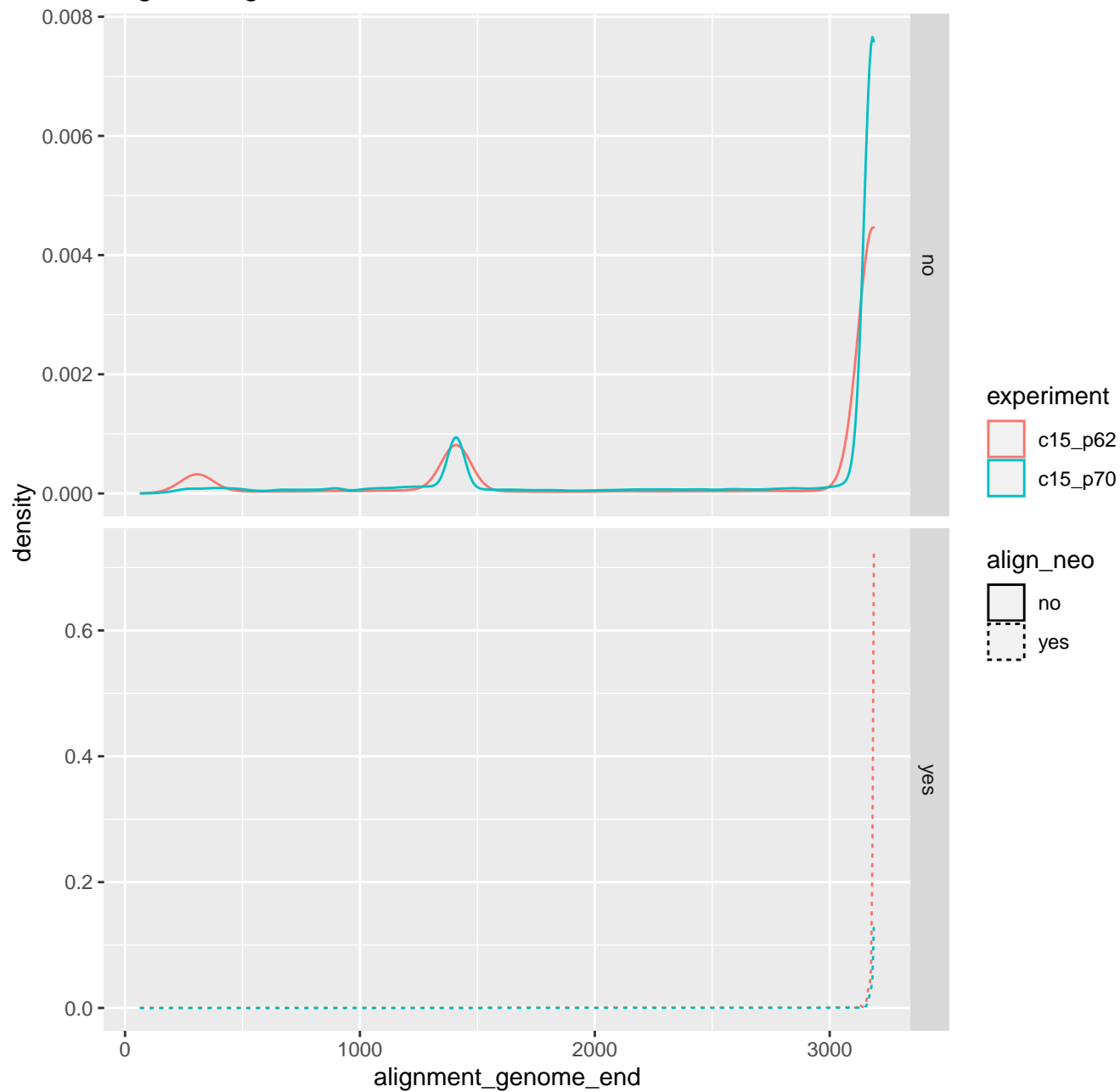
align_neo

no

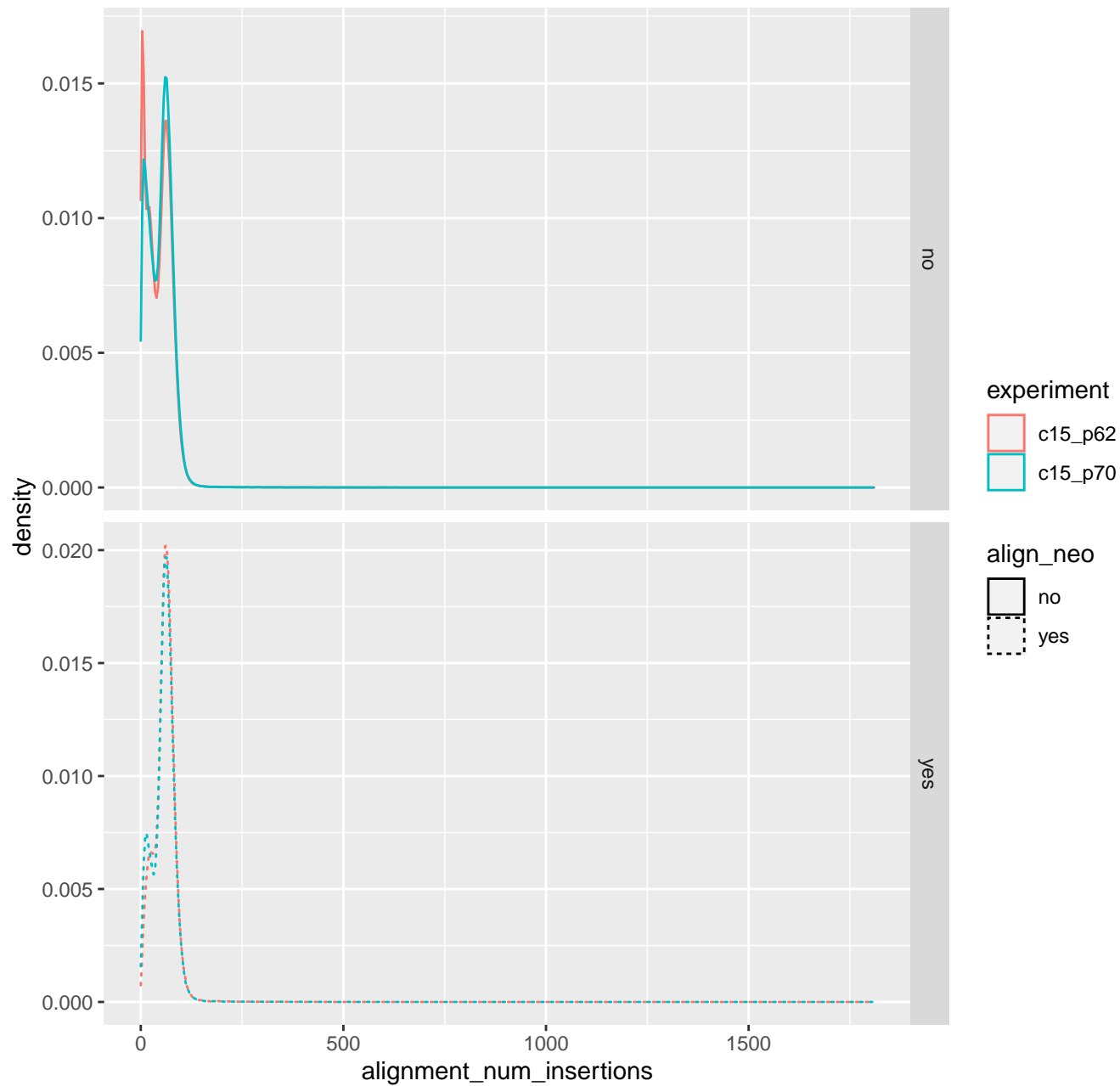
yes



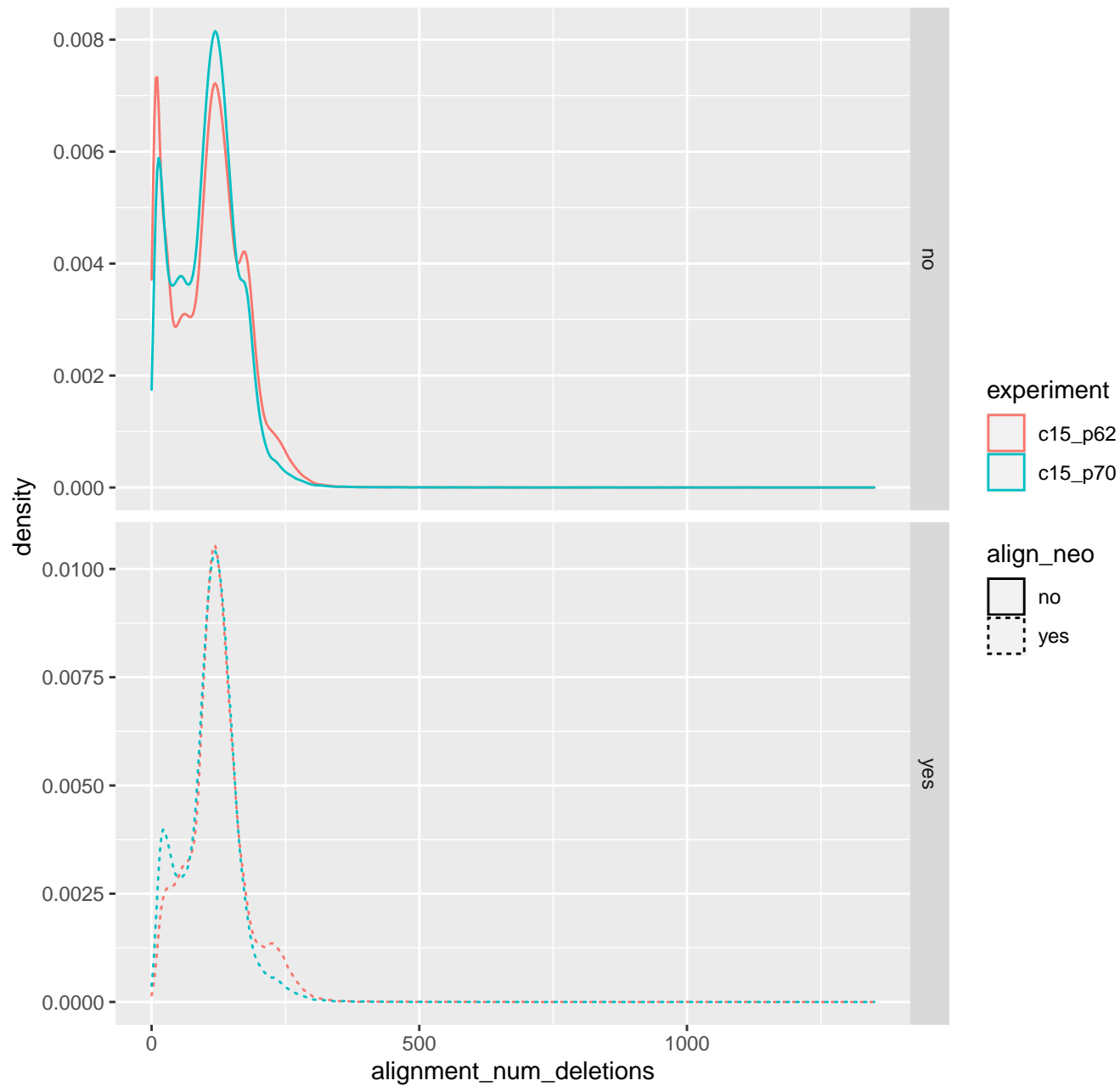
Alignment genome_end



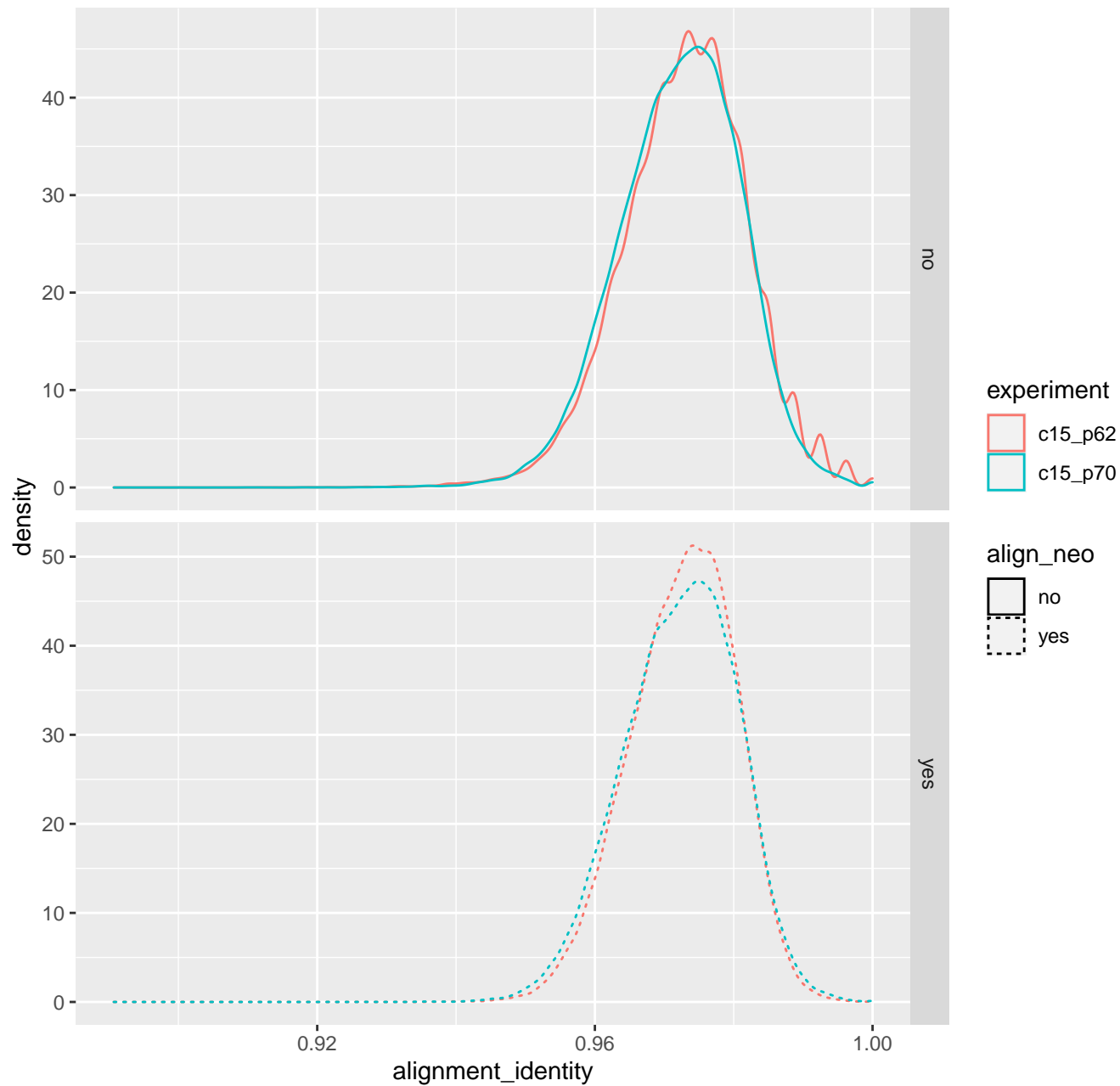
Number of insertions



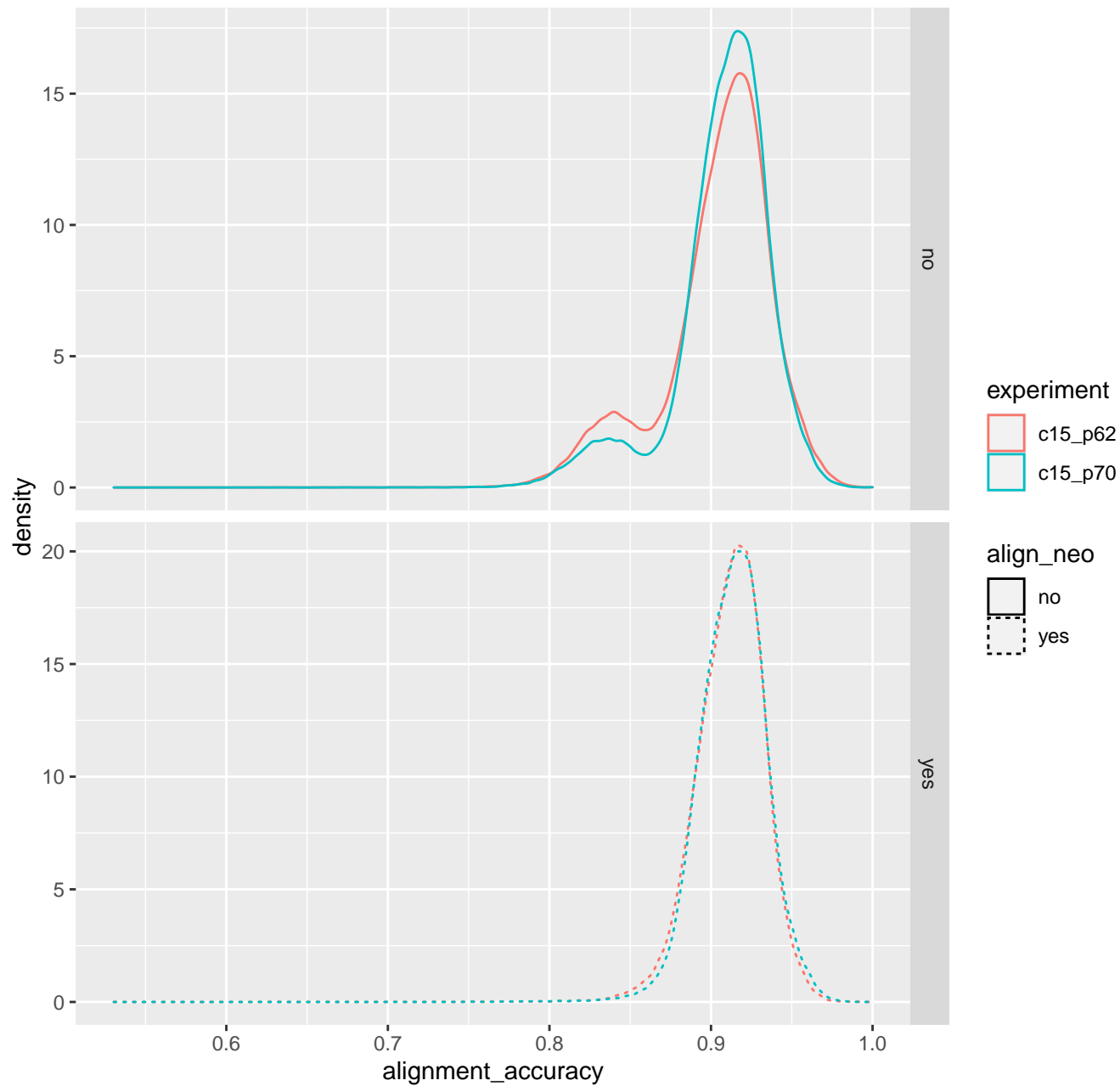
Number of deletions



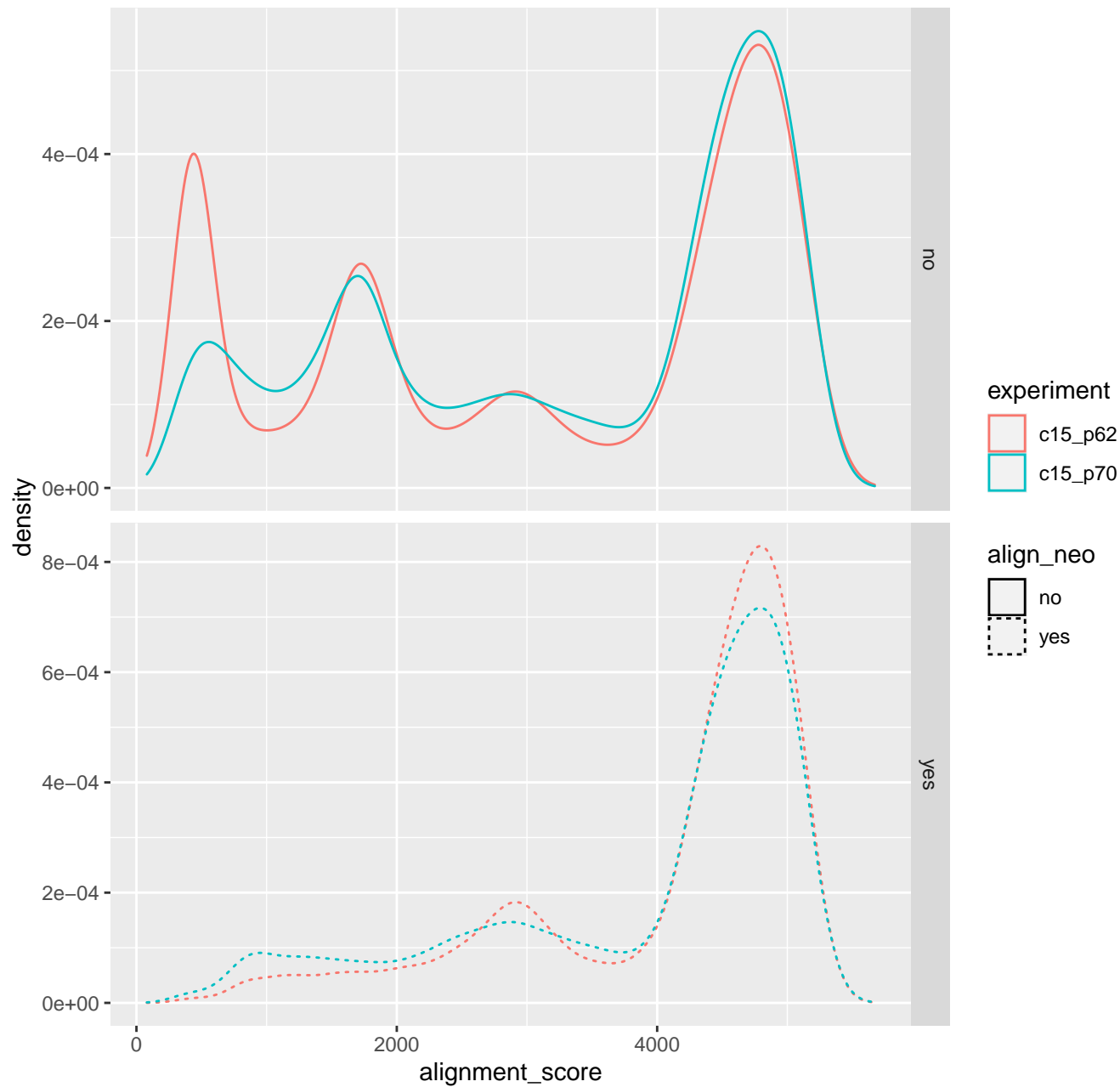
Alignment_identity



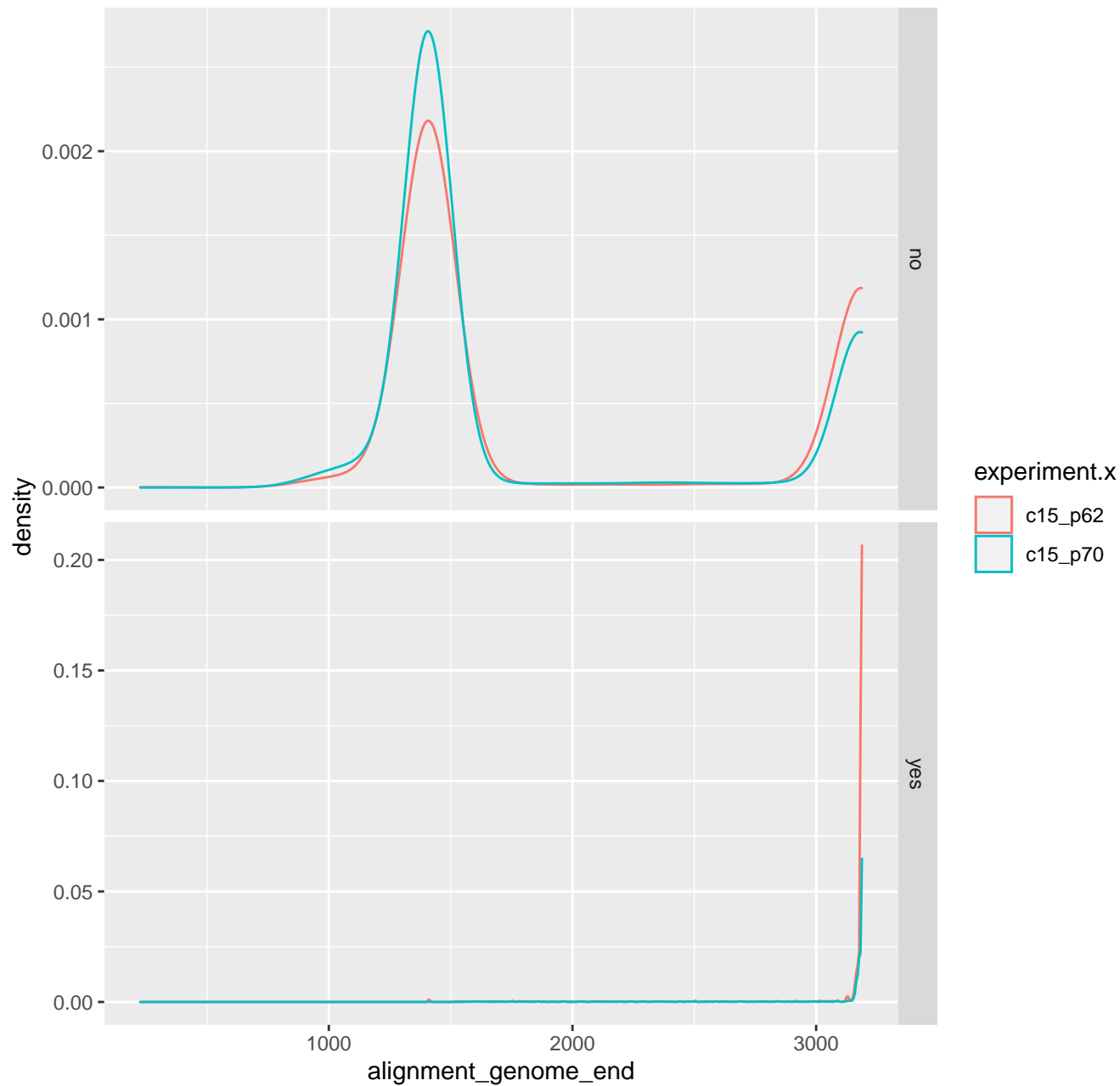
Alignment_accuracy



Alignment_score



Genome End for reads with count > 0 & count < 37.5



Genome End for reads with count > 37.5

