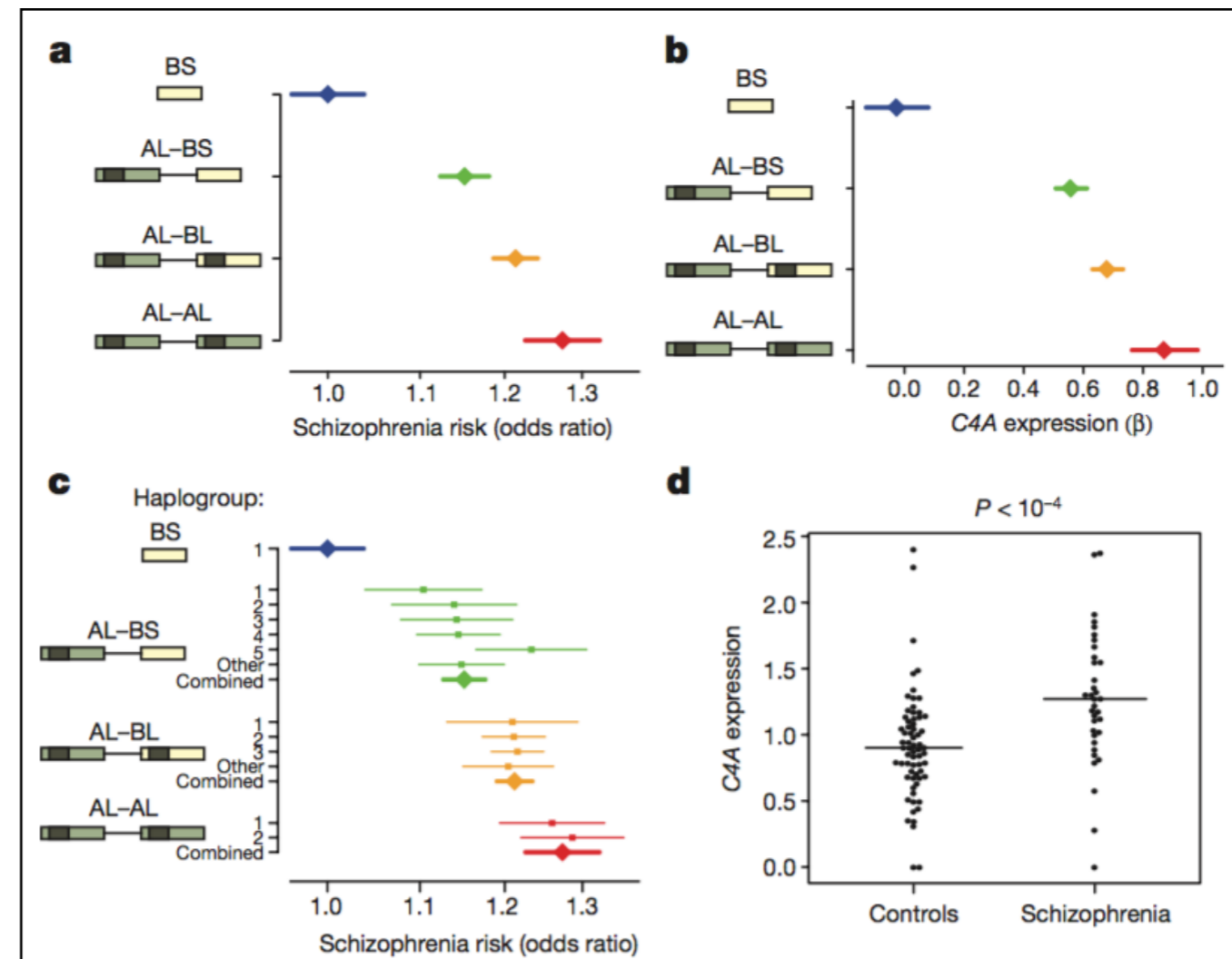
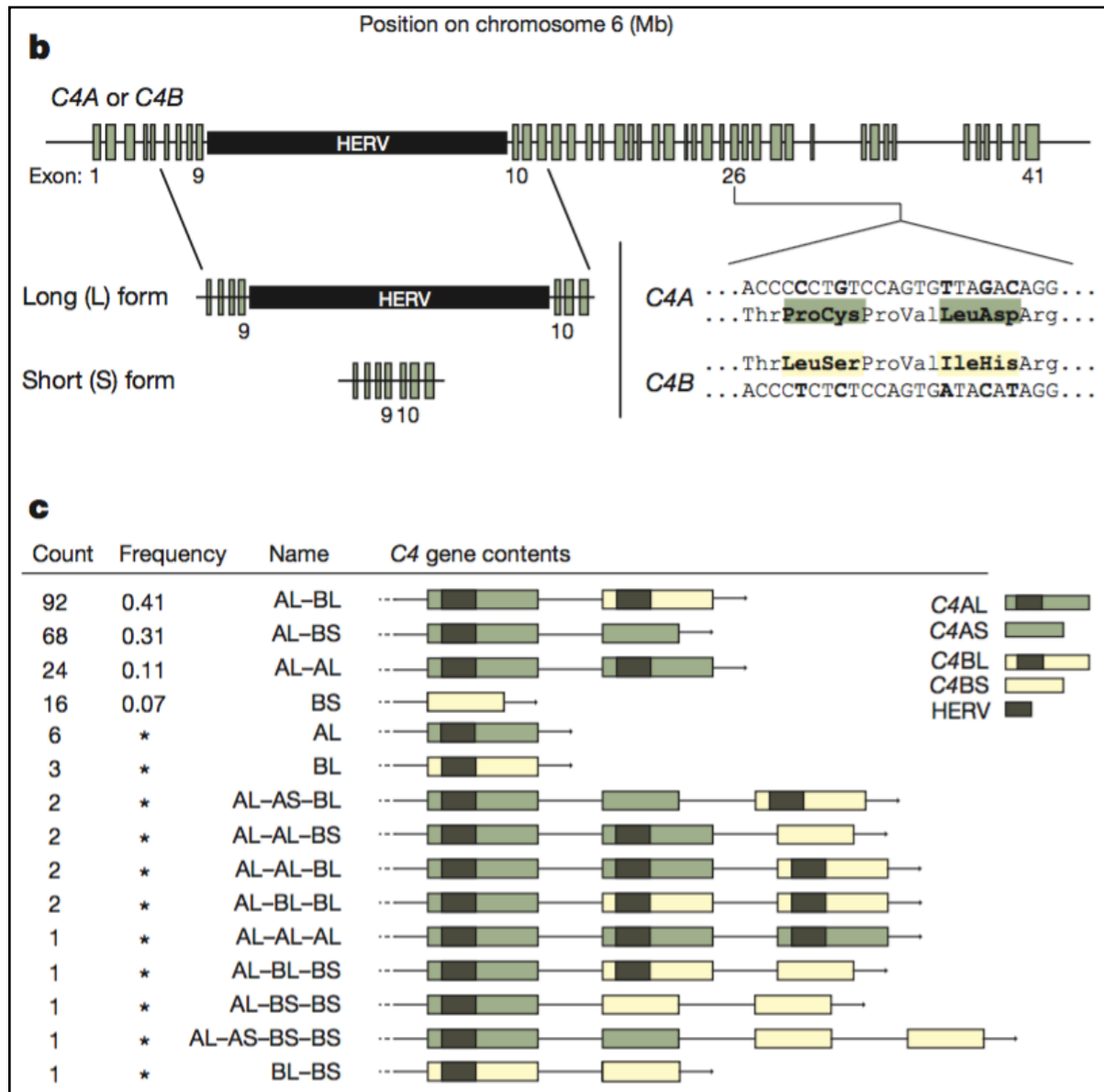


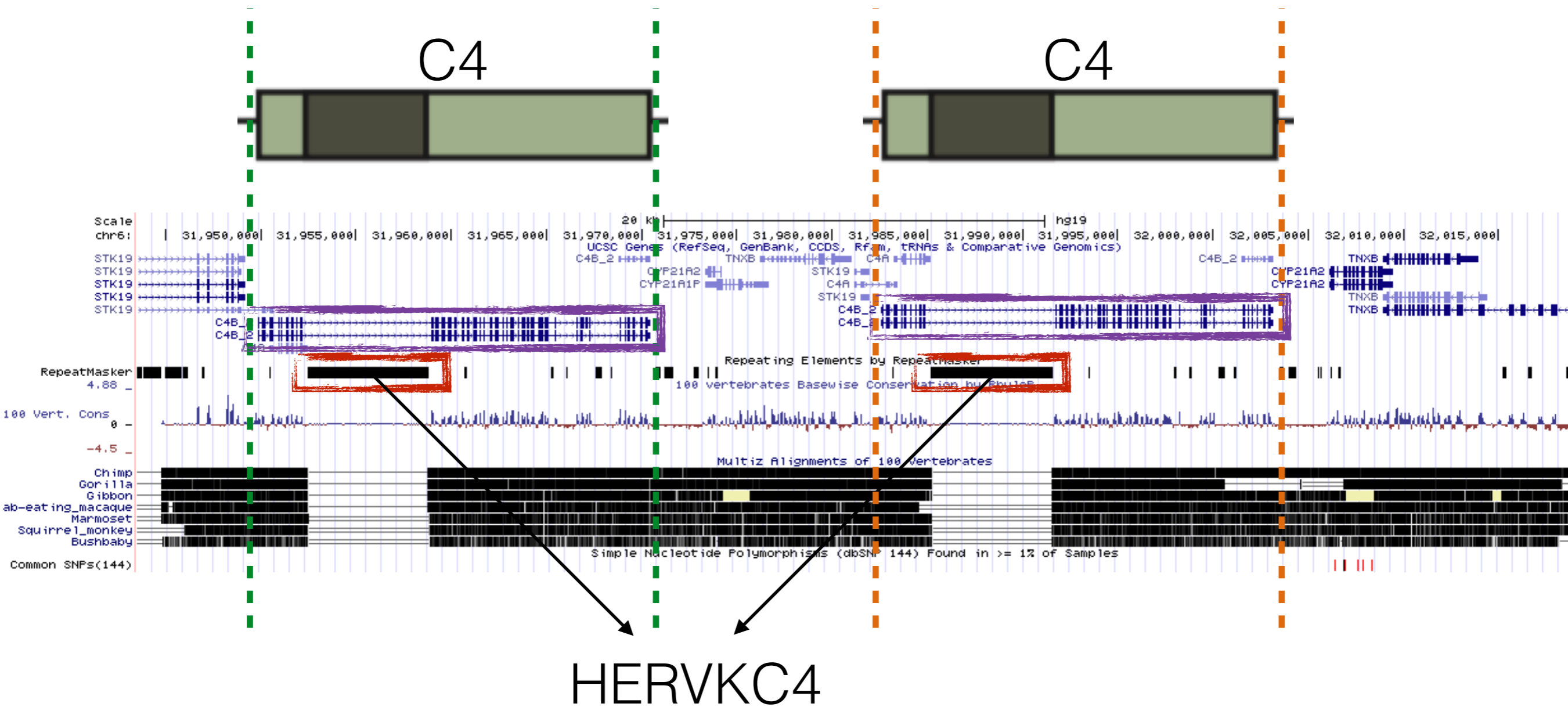
# Z and the schizophrenia HERVs

# Schizophrenia risk from complex variation of complement component 4

Aswin Sekar<sup>1,2,3</sup>, Allison R. Bialas<sup>4,5</sup>, Heather de Rivera<sup>1,2</sup>, Avery Davis<sup>1,2</sup>, Timothy R. Hammond<sup>4</sup>, Nolan Kamitaki<sup>1,2</sup>, Katherine Tooley<sup>1,2</sup>, Jessy Presumey<sup>5</sup>, Matthew Baum<sup>1,2,3,4</sup>, Vanessa Van Doren<sup>1</sup>, Giulio Genovese<sup>1,2</sup>, Samuel A. Rose<sup>2</sup>, Robert E. Handsaker<sup>1,2</sup>, Schizophrenia Working Group of the Psychiatric Genomics Consortium\*, Mark J. Daly<sup>2,6</sup>, Michael C. Carroll<sup>5</sup>, Beth Stevens<sup>2,4</sup> & Steven A. McCarroll<sup>1,2</sup>



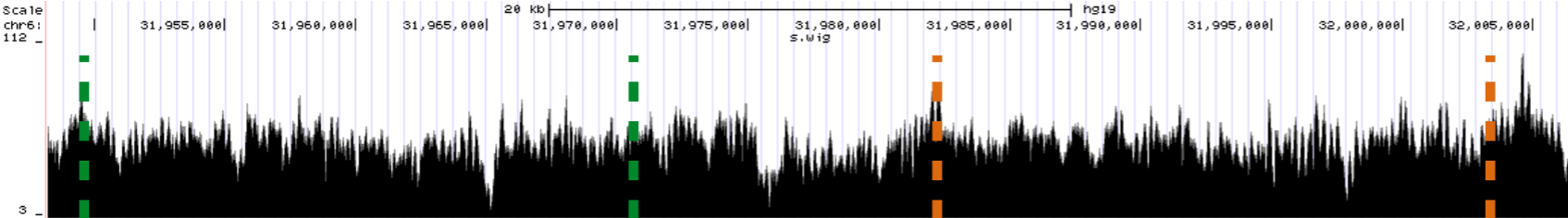
# The C4 locus in hg19



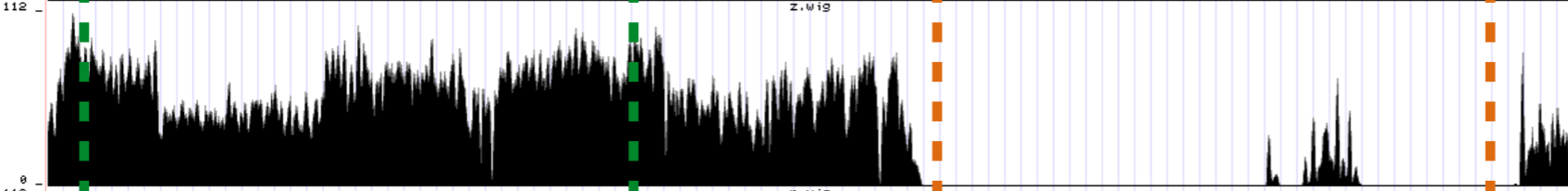
# Most frequent genotypes:

92	0.41	AL-BL	
68	0.31	AL-BS	
24	0.11	AL-AL	
16	0.07	BS	
6	*	AL	

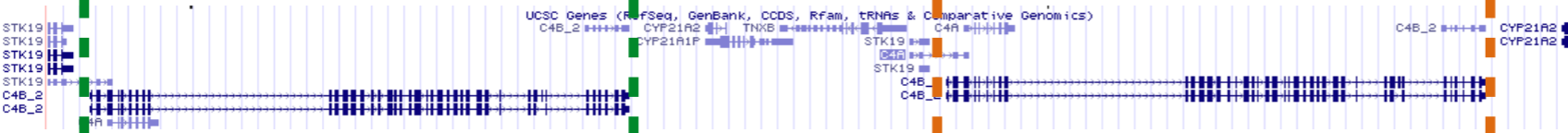
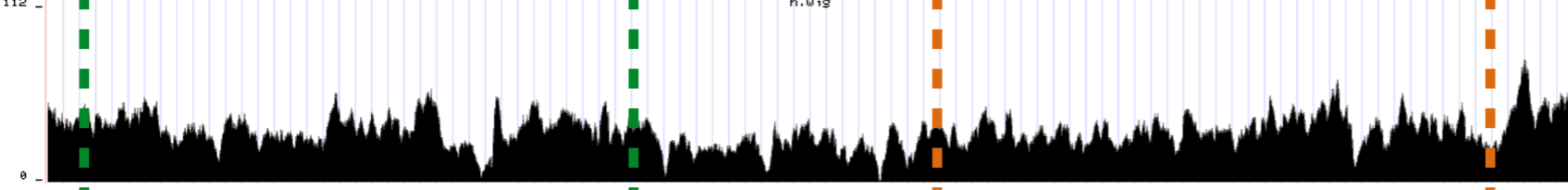
S



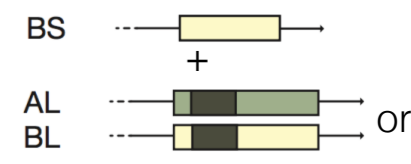
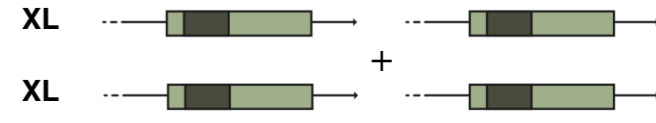
Z



N



CNVnator

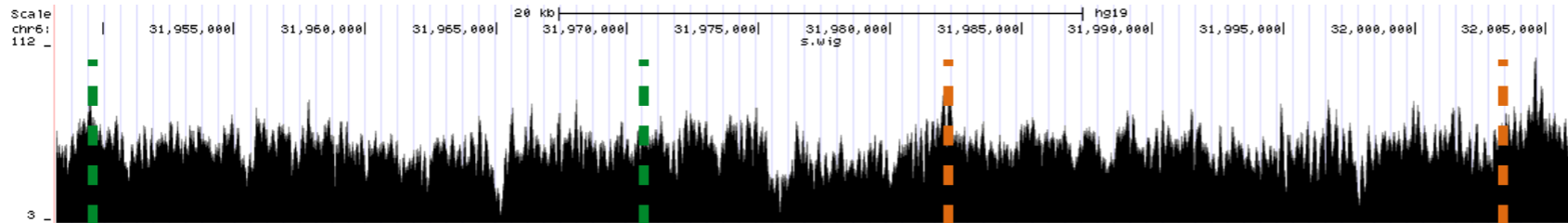


# Most frequent genotypes:

92	0.41	AL-BL	
68	0.31	AL-BS	
24	0.11	AL-AL	
16	0.07	BS	
6	*	AL	

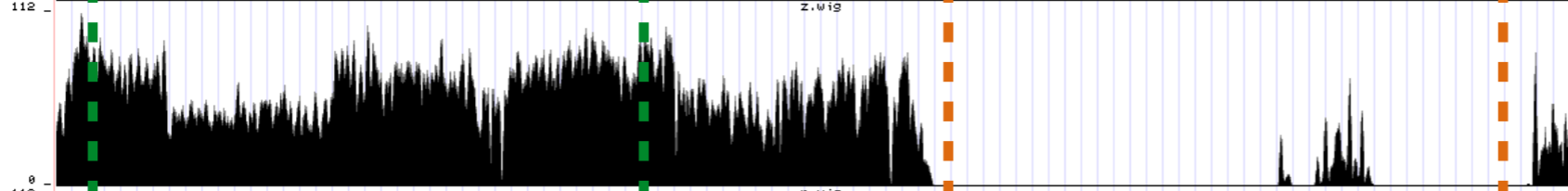
S

s.wig



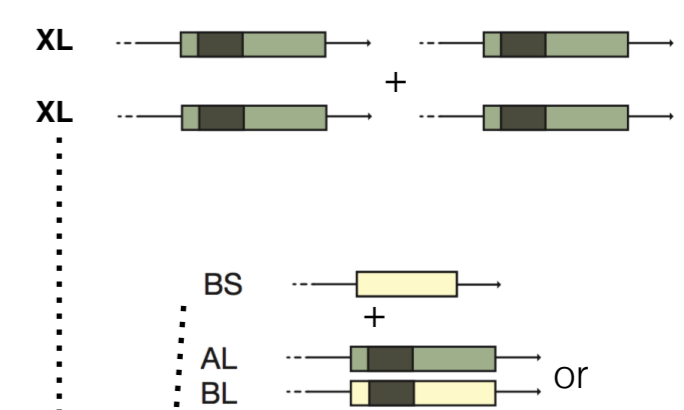
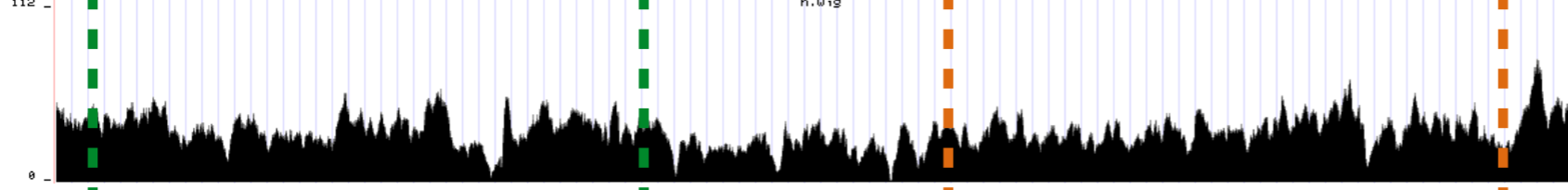
Z

z.wig



N

n.wig



CNVnator

