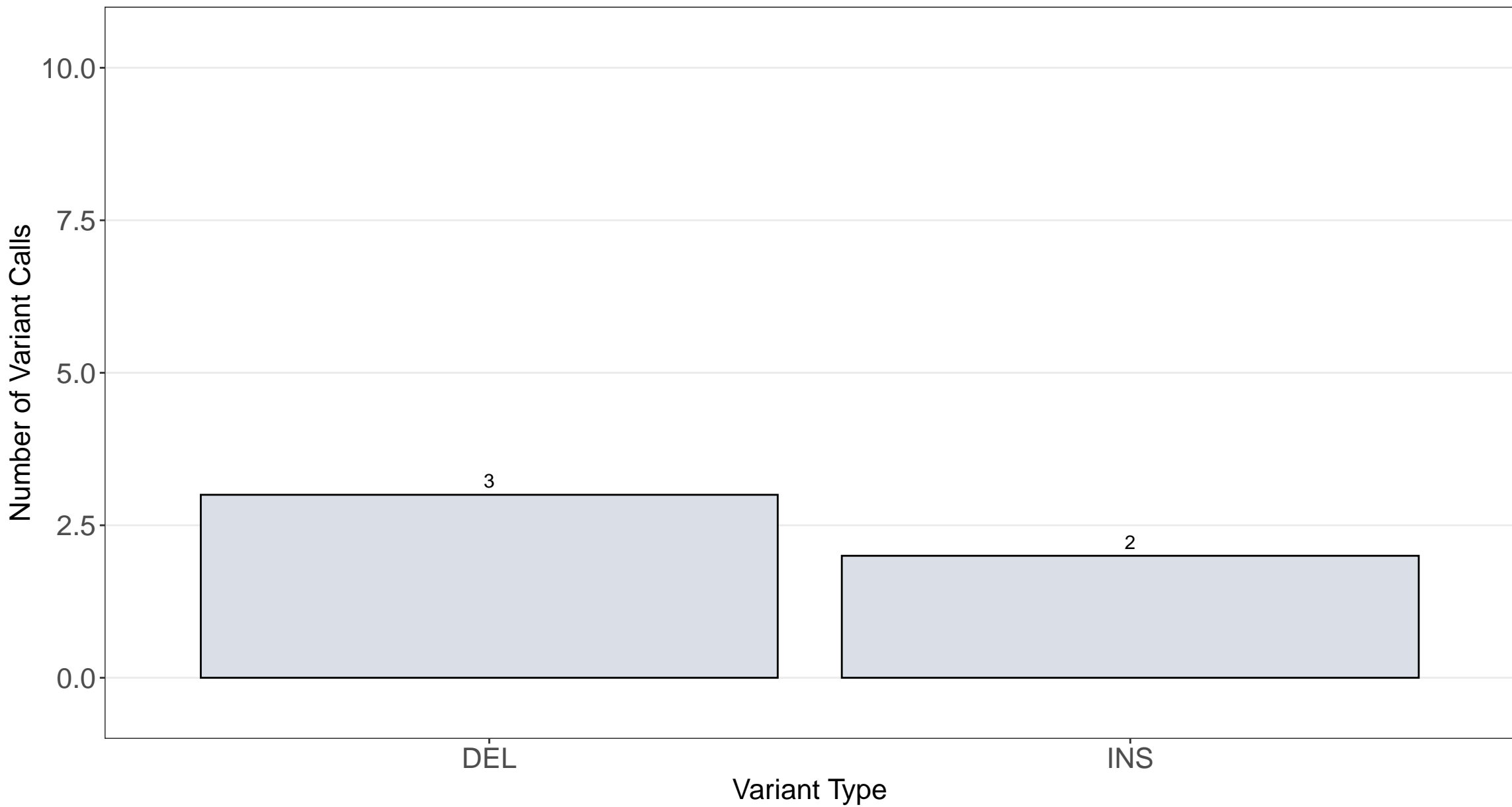
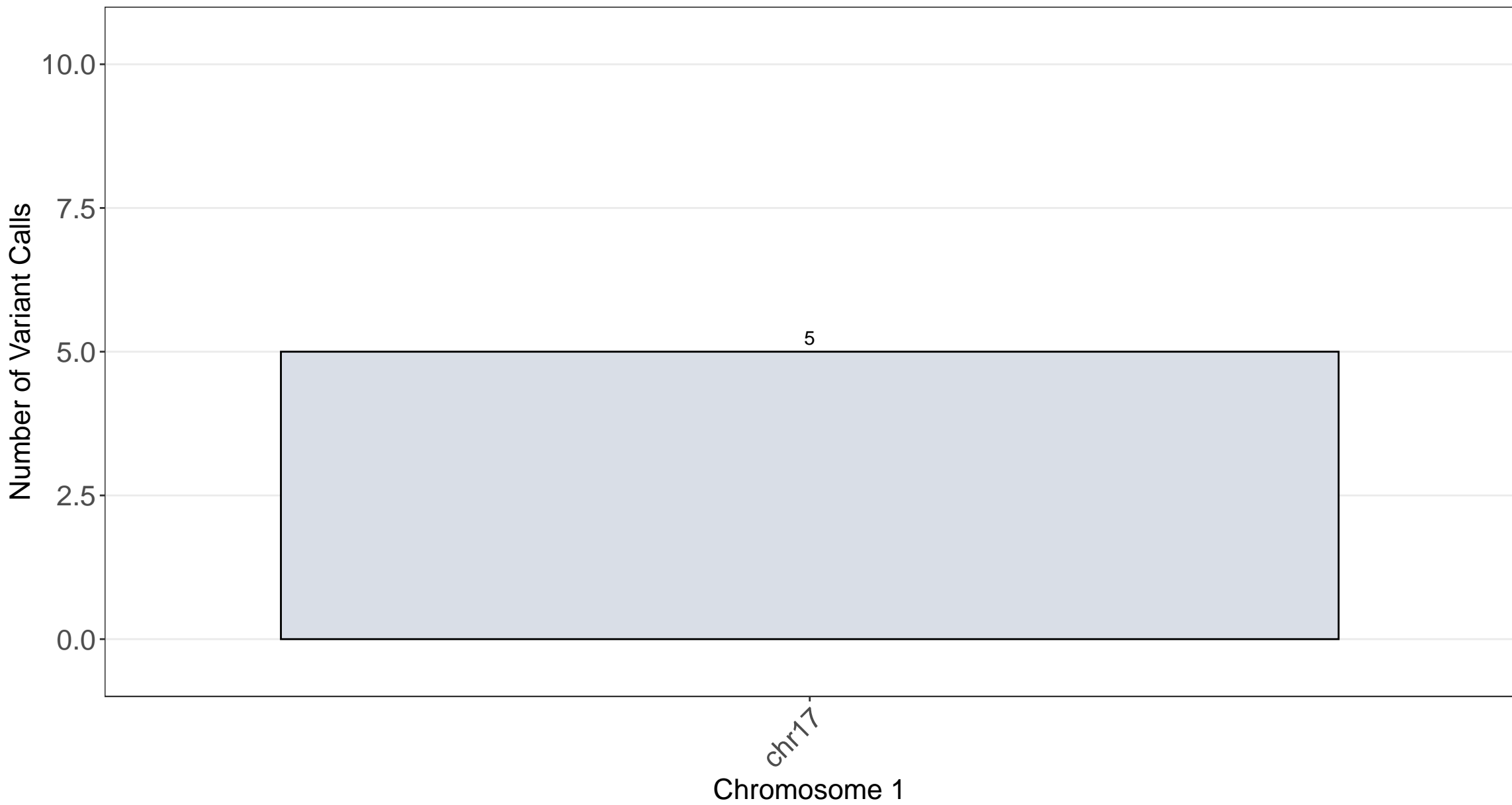


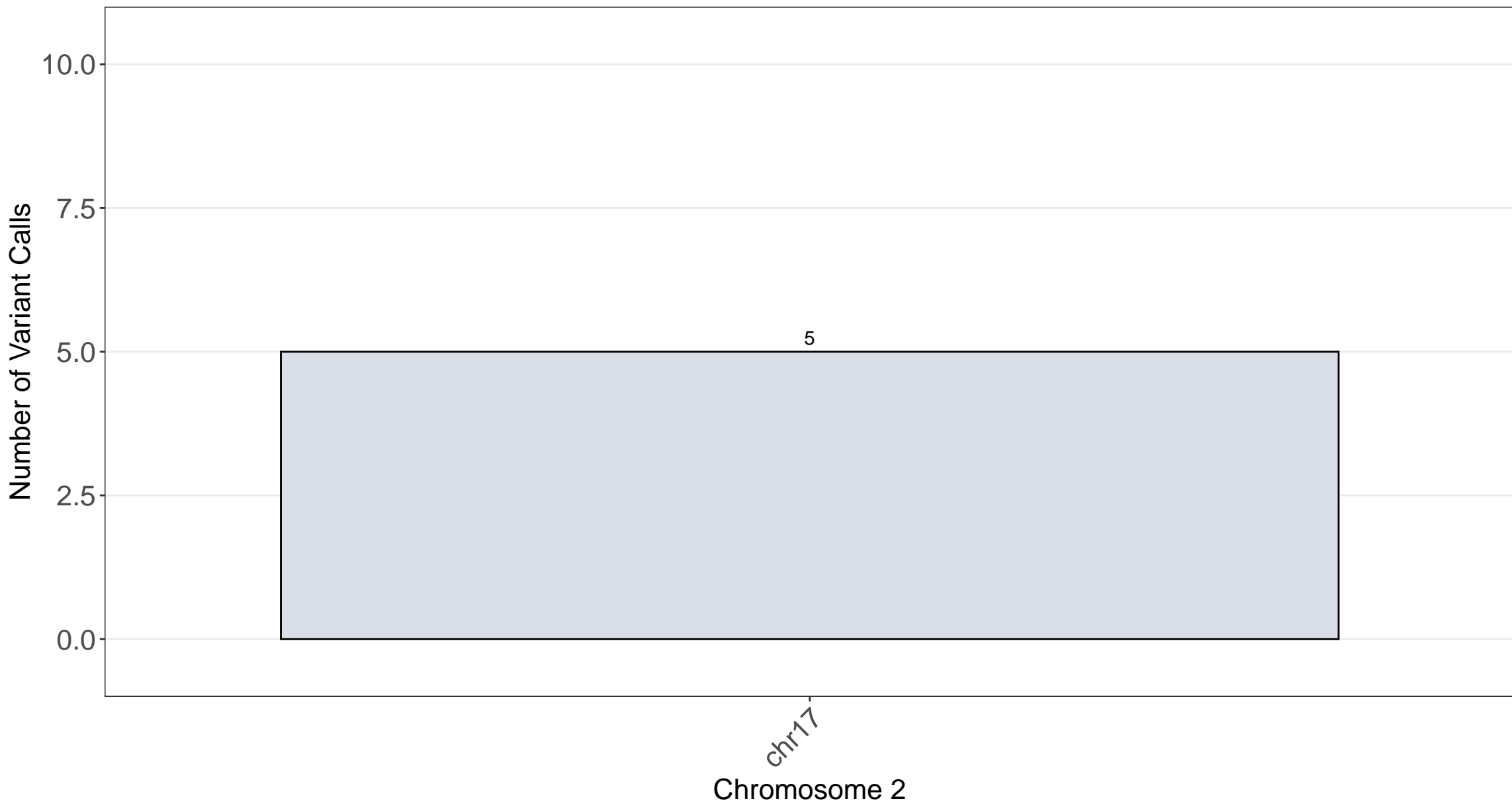
Number of Variant Calls by variant\_type



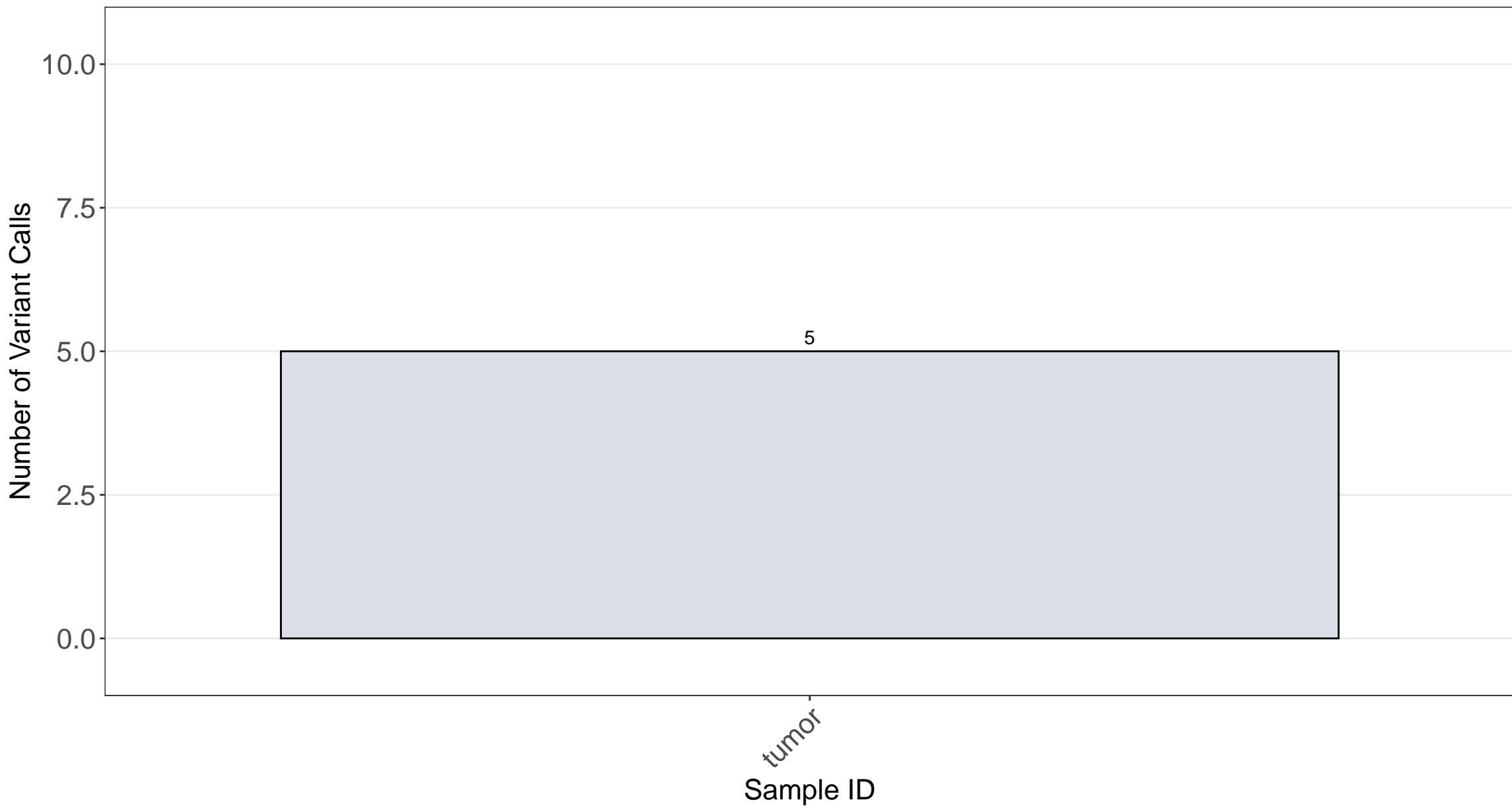
Number of Variant Calls by chromosome\_1



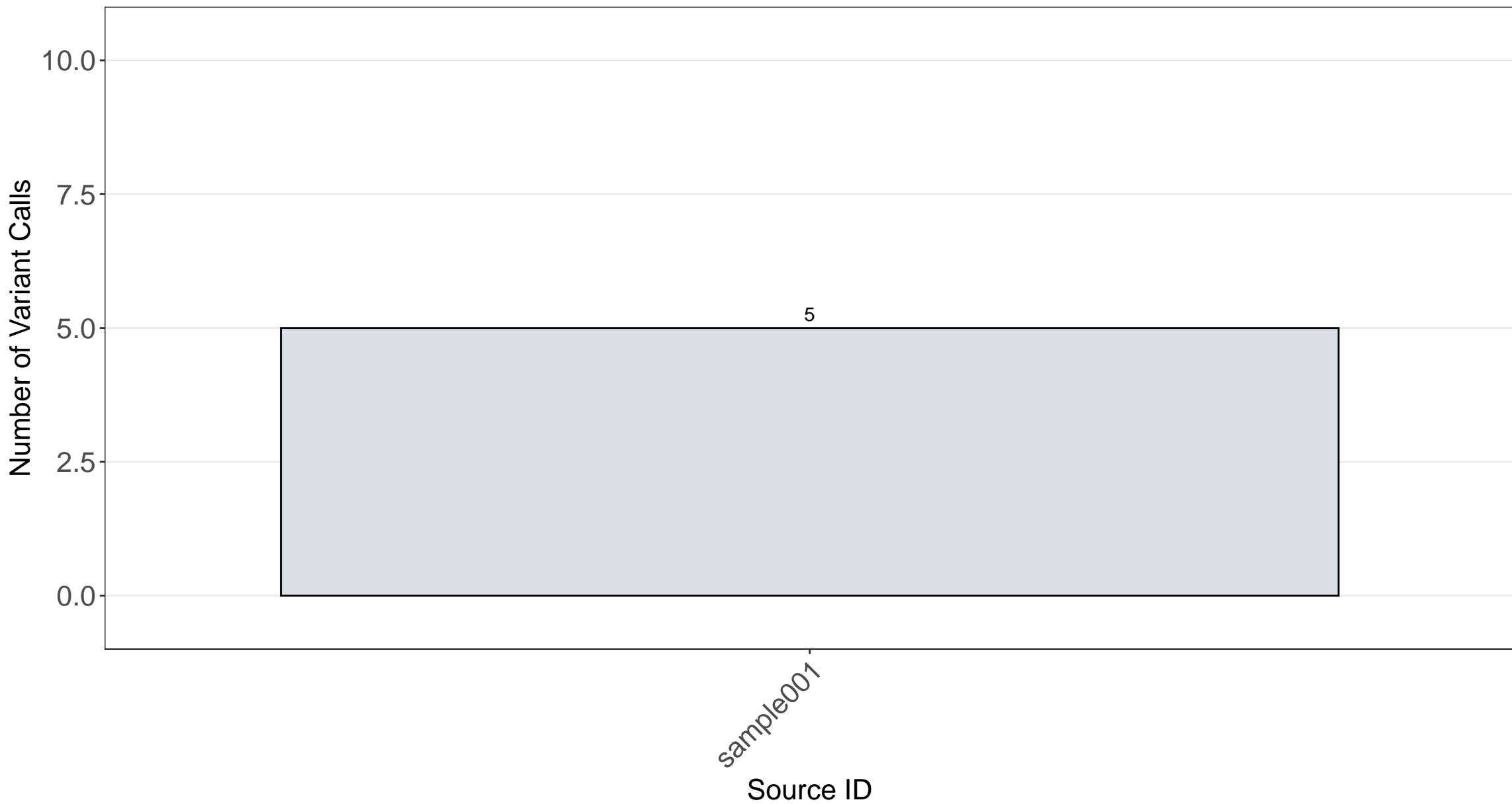
Number of Variant Calls by chromosome\_2



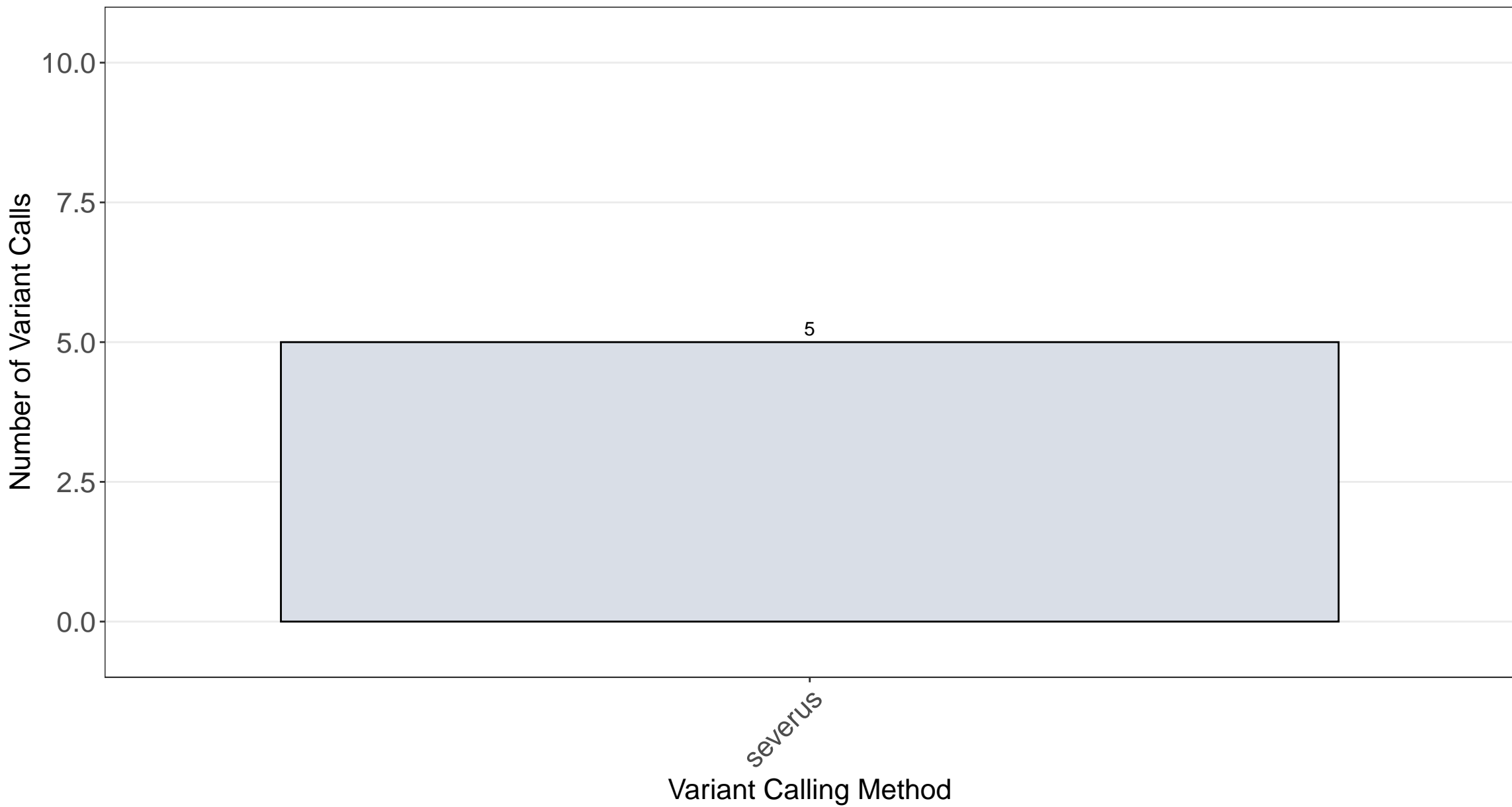
Number of Variant Calls by sample\_id



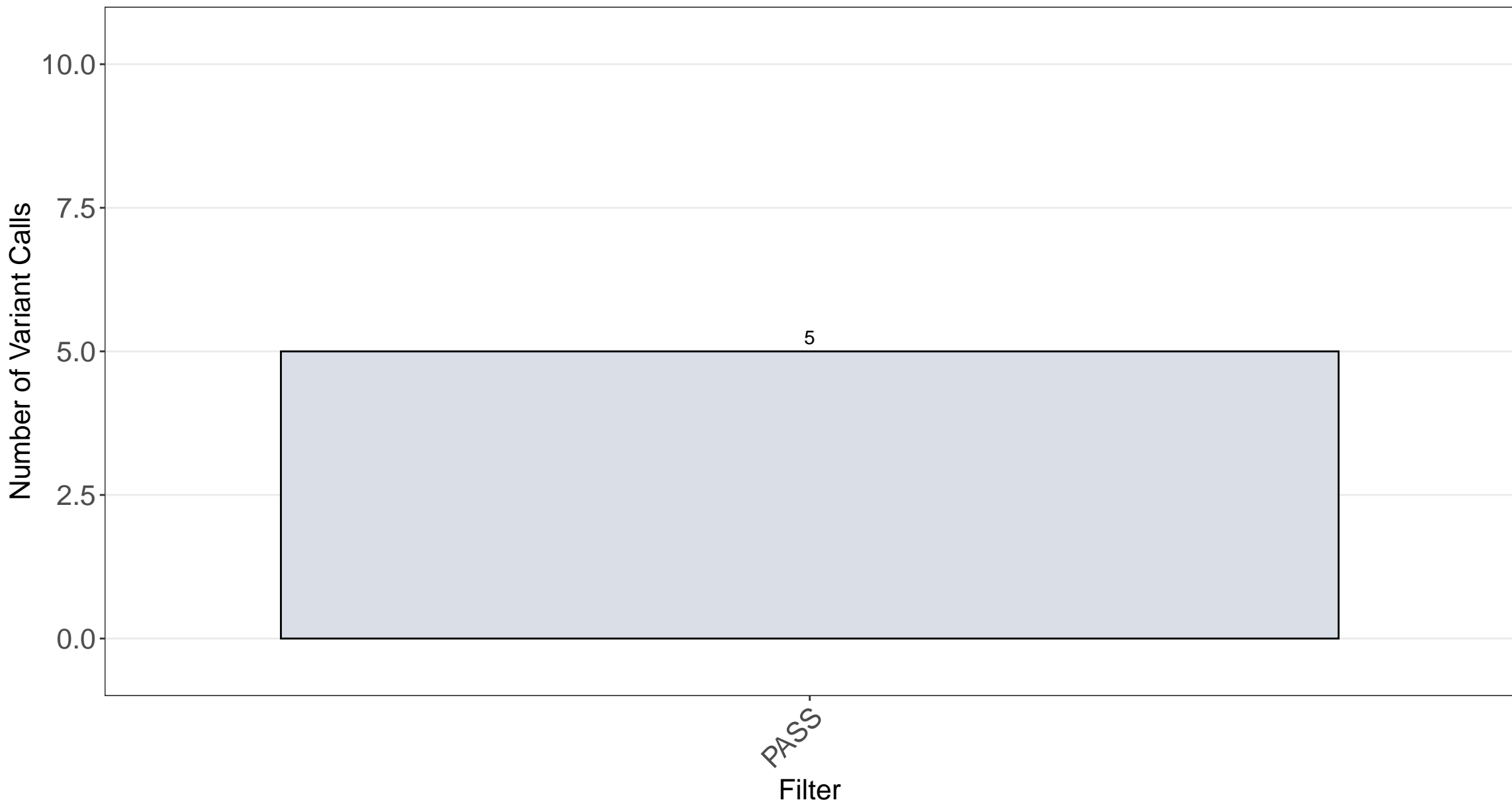
Number of Variant Calls by source\_id



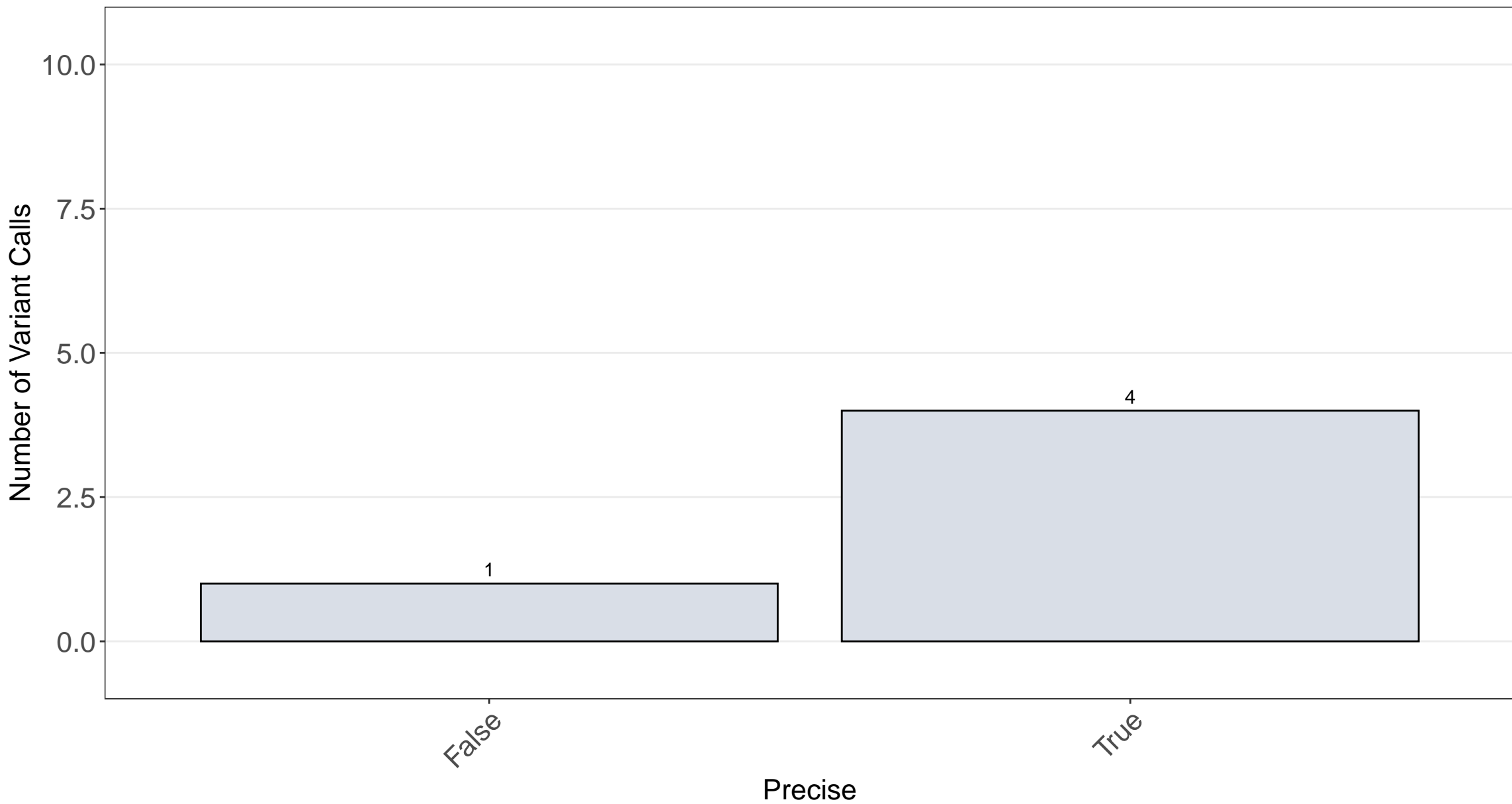
Number of Variant Calls by variant\_calling\_method



Number of Variant Calls by filter

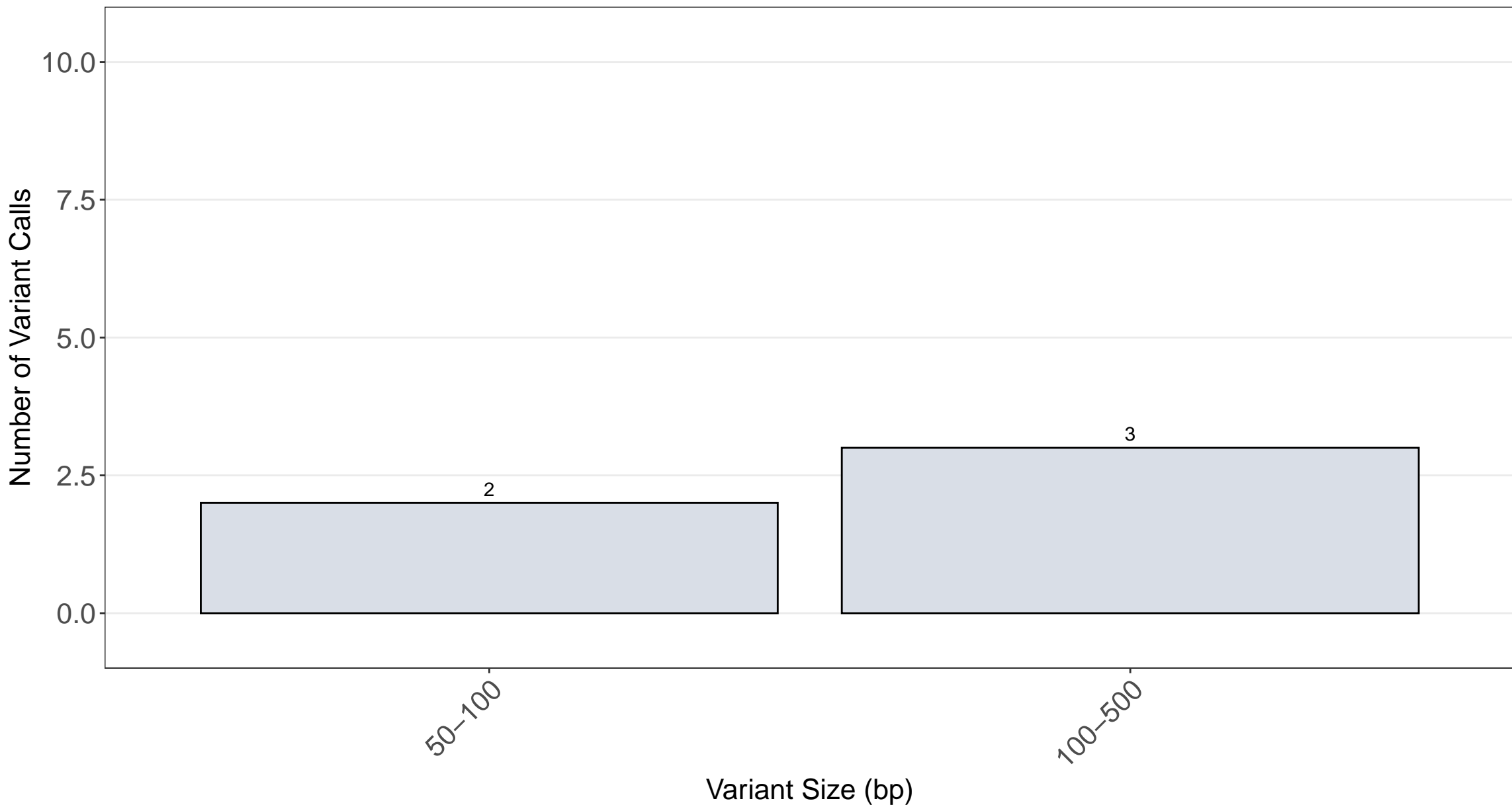


Number of Variant Calls by precise

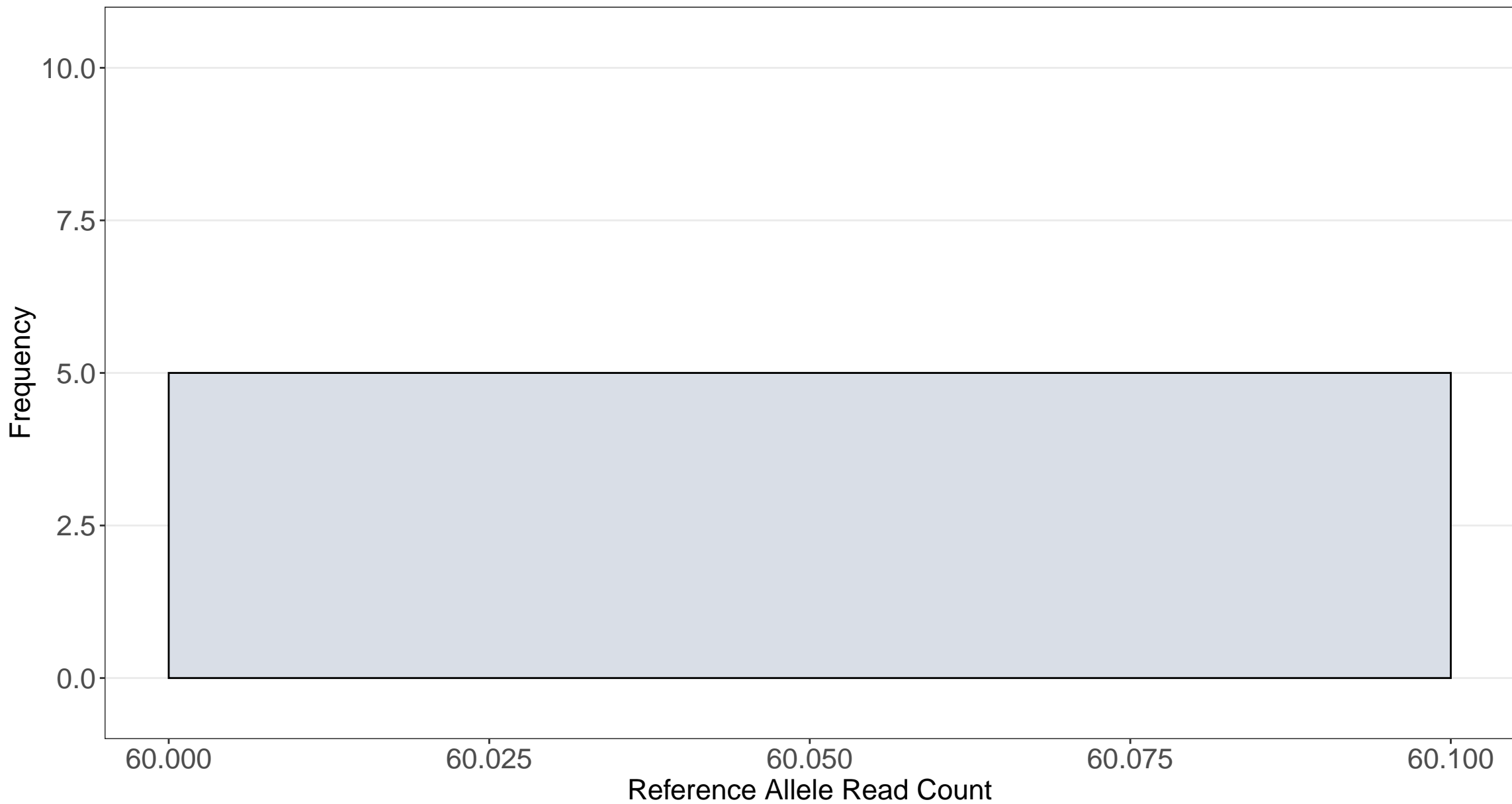




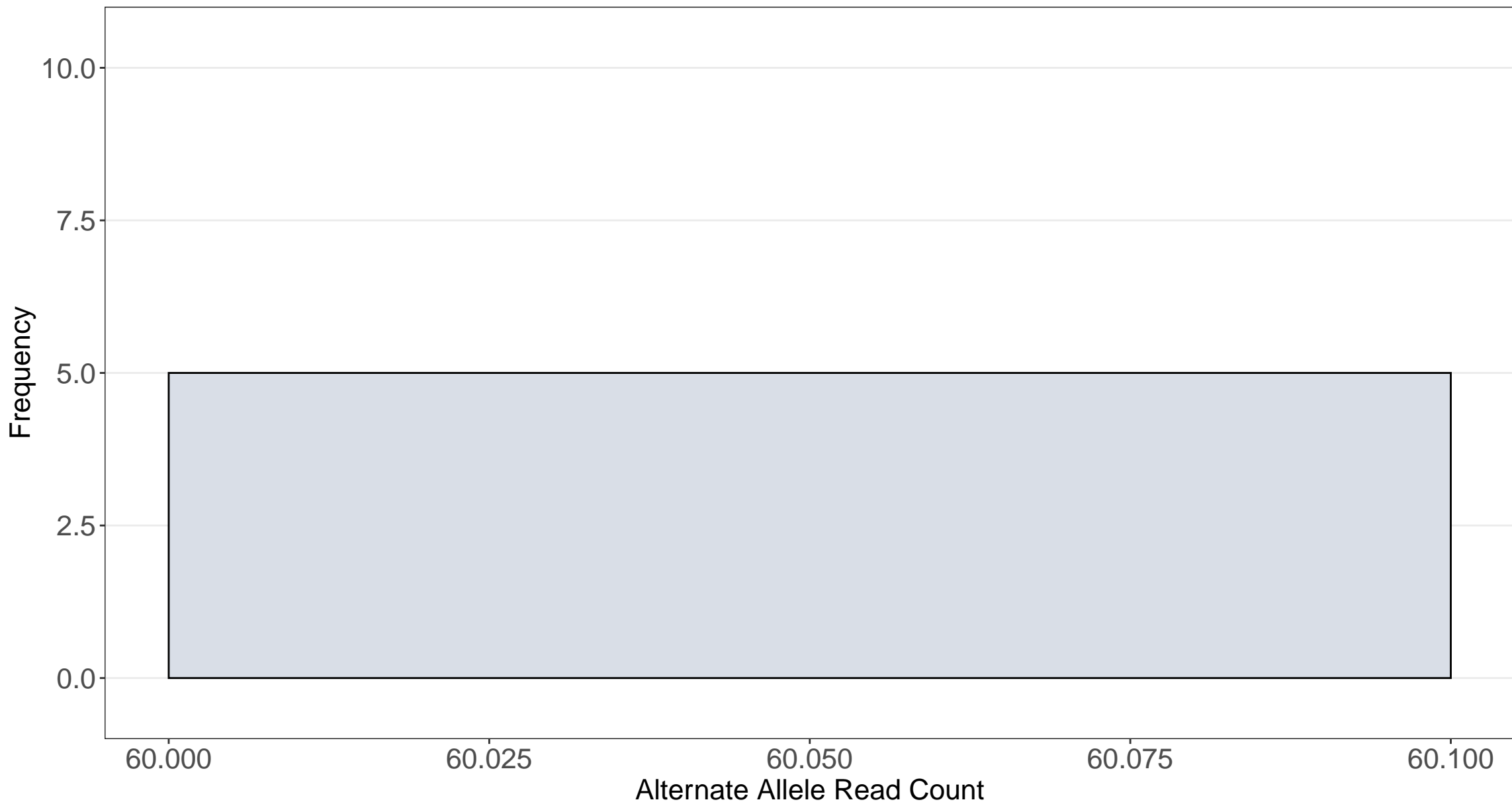
Number of Variant Calls by variant\_size



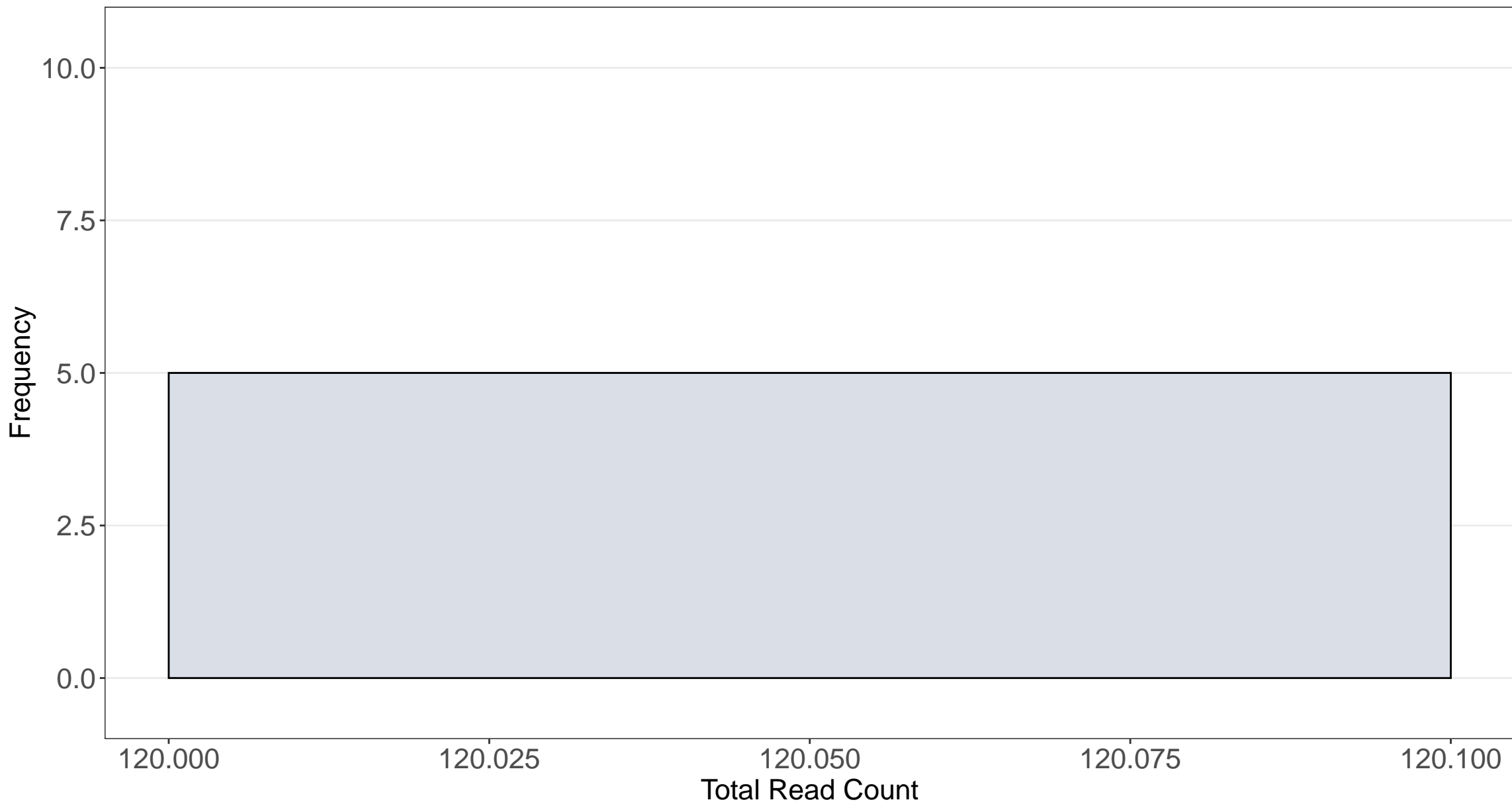
Histogram of reference\_allele\_read\_count



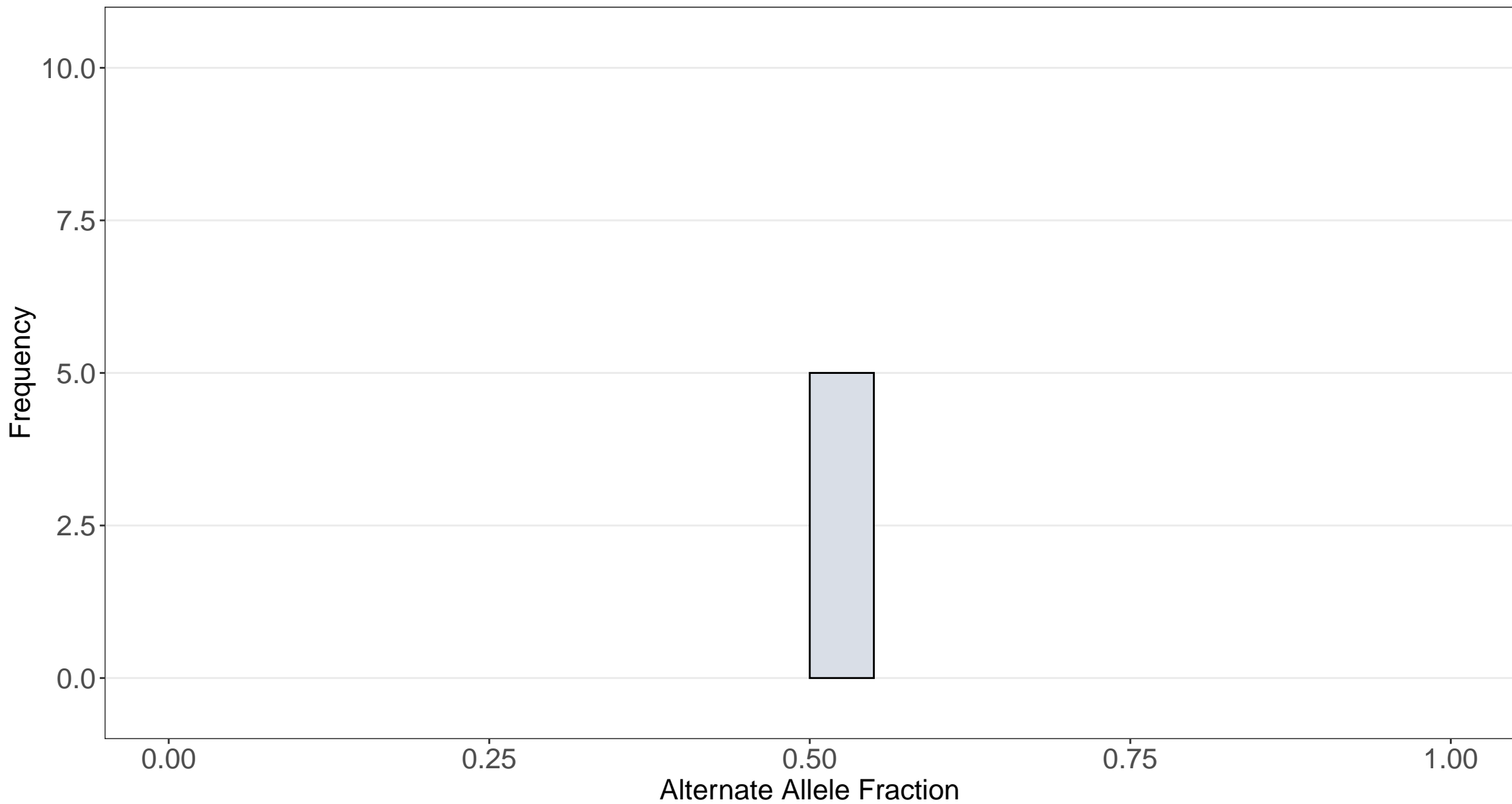
Histogram of alternate\_allele\_read\_count



Histogram of total\_read\_count



Histogram of alternate\_allele\_fraction



Histogram of quality\_score

