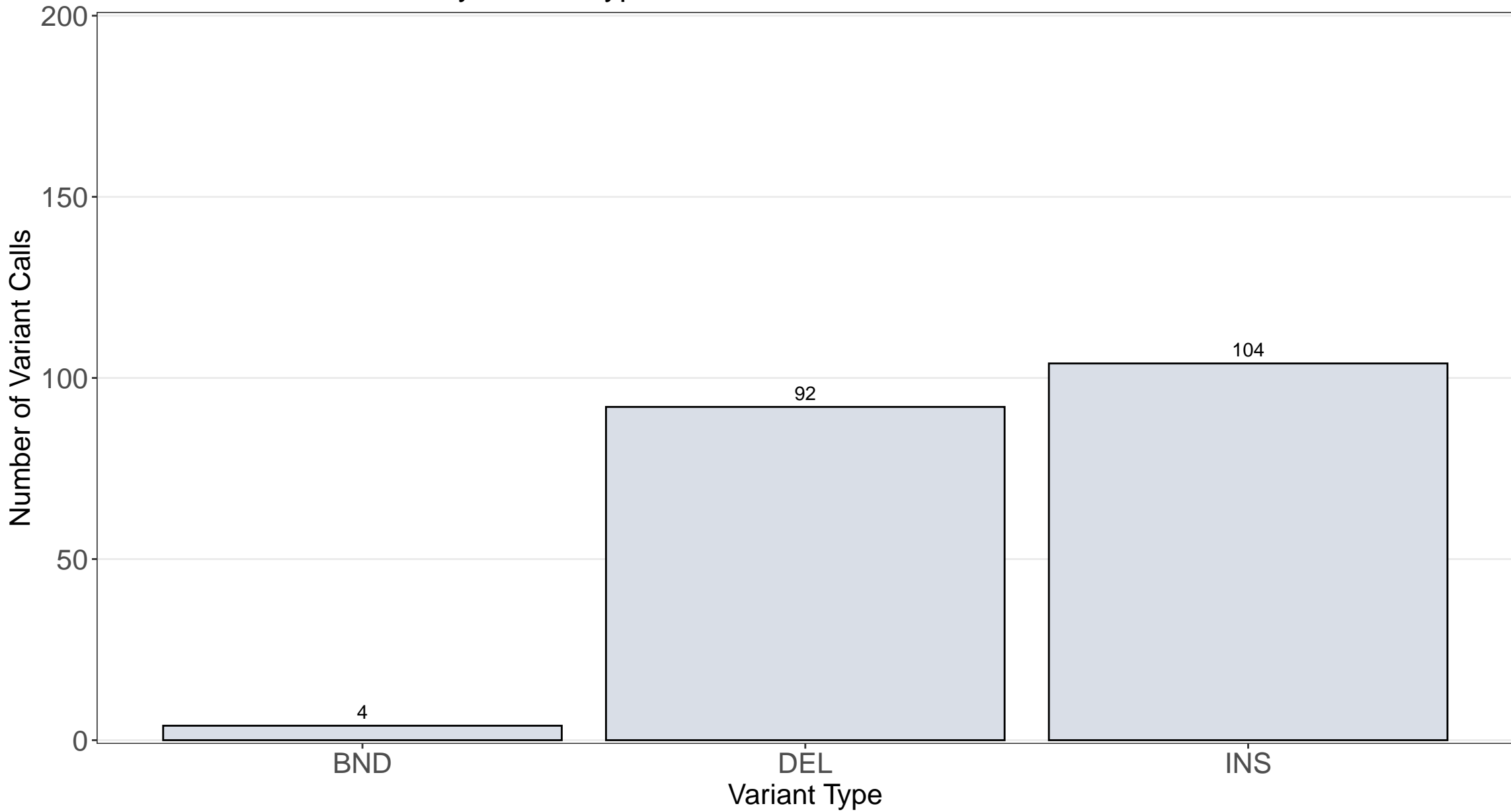
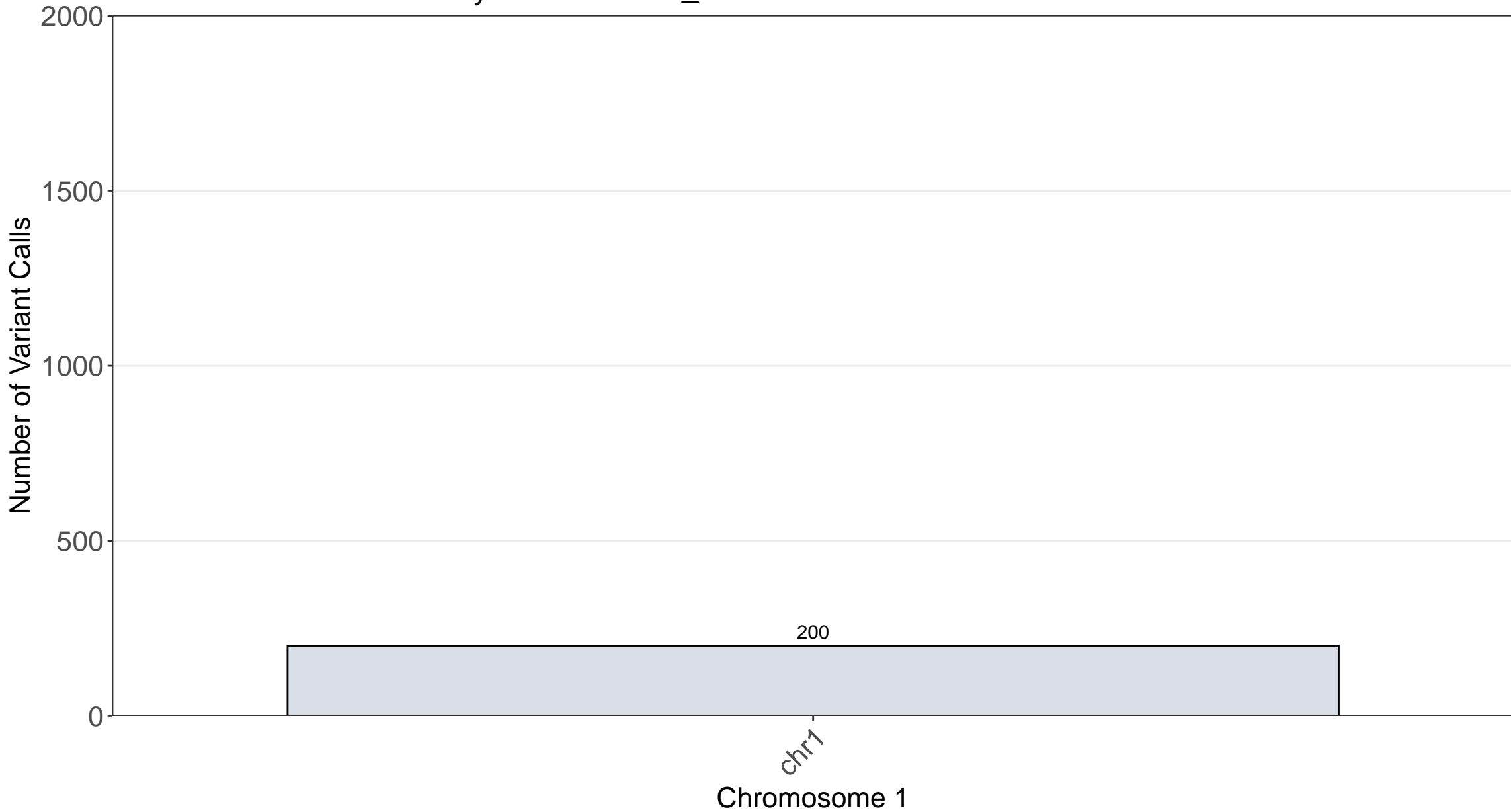


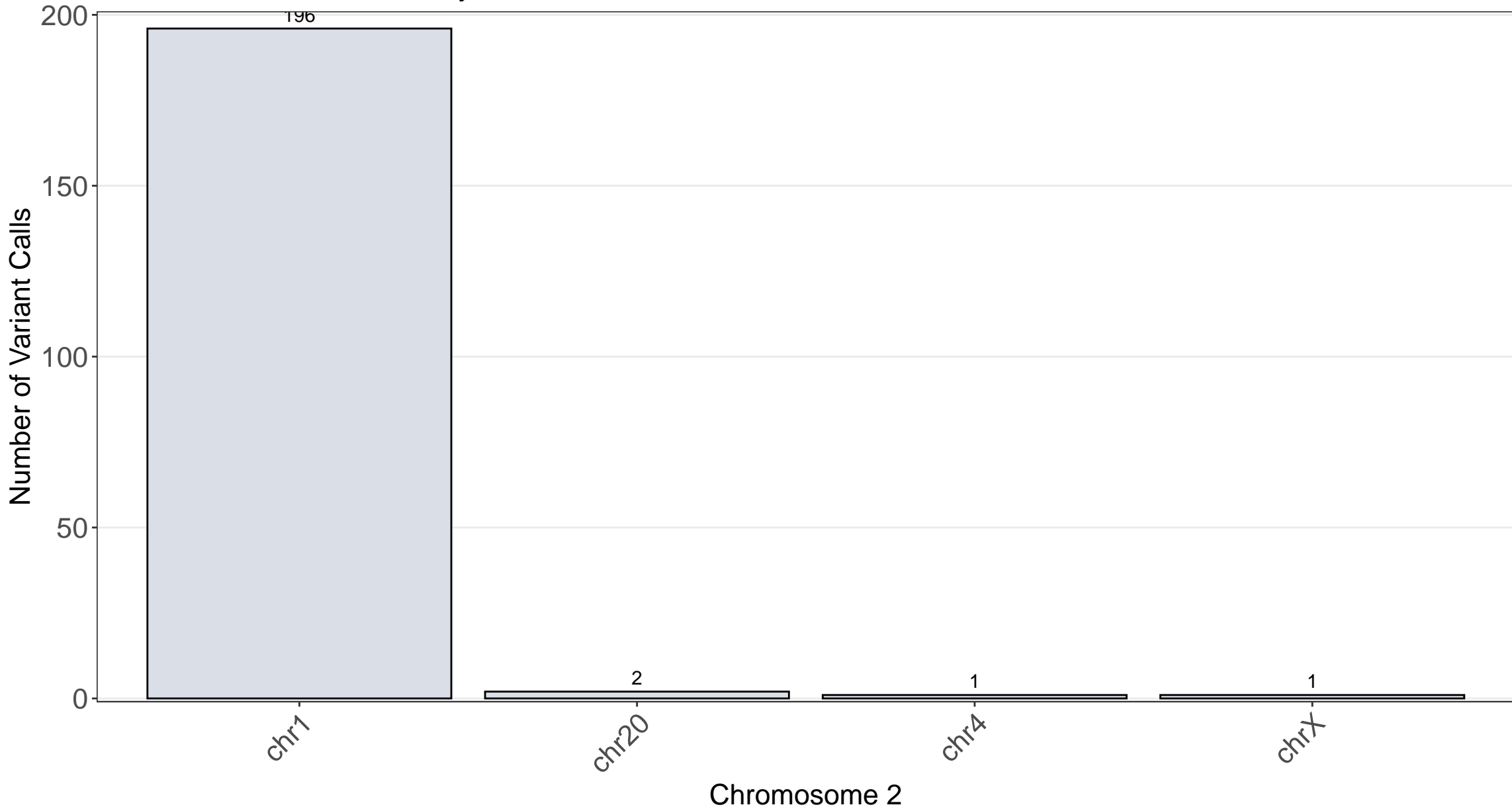
Number of Variant Calls by variant_type



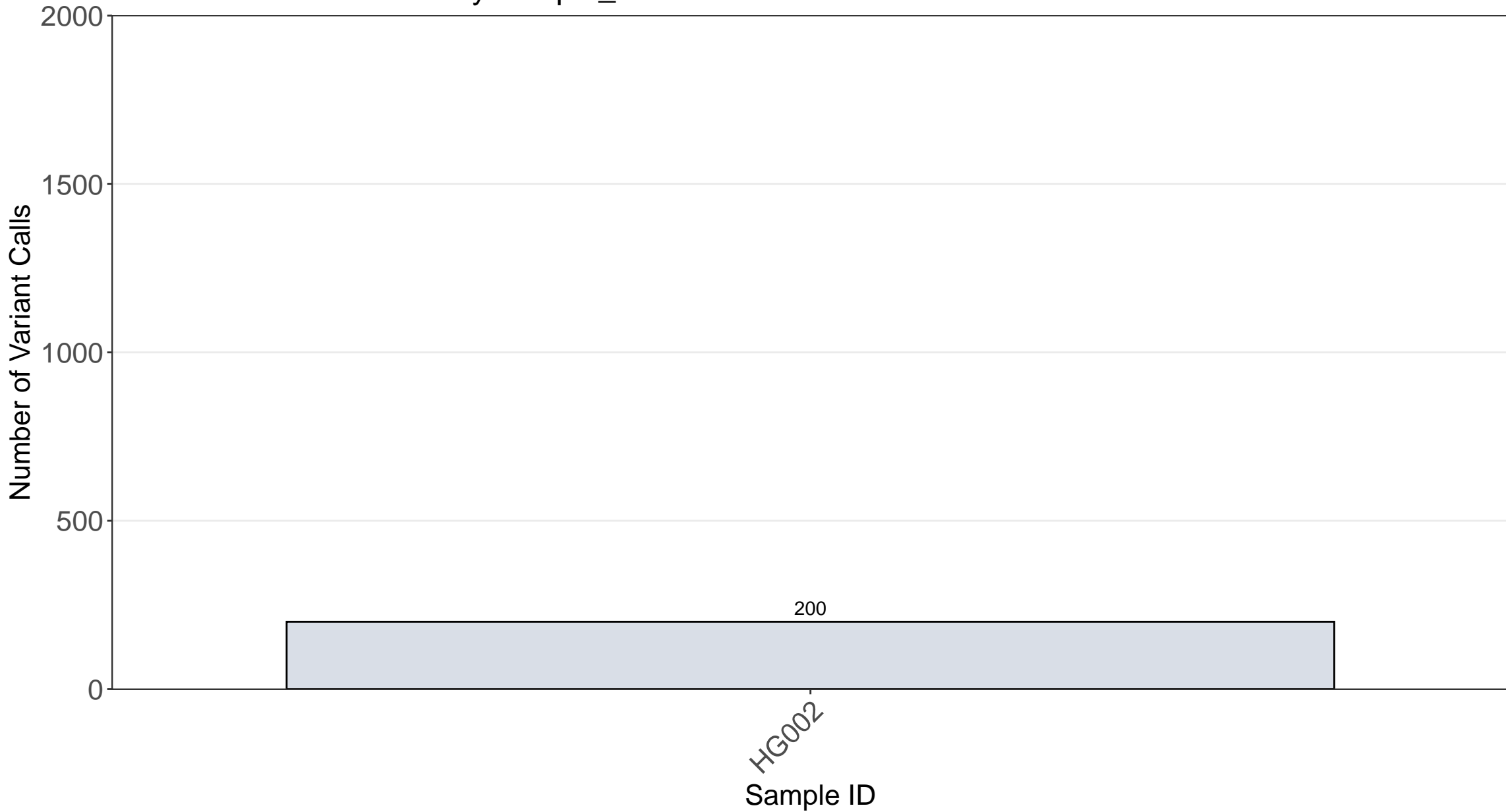
Number of Variant Calls by chromosome_1



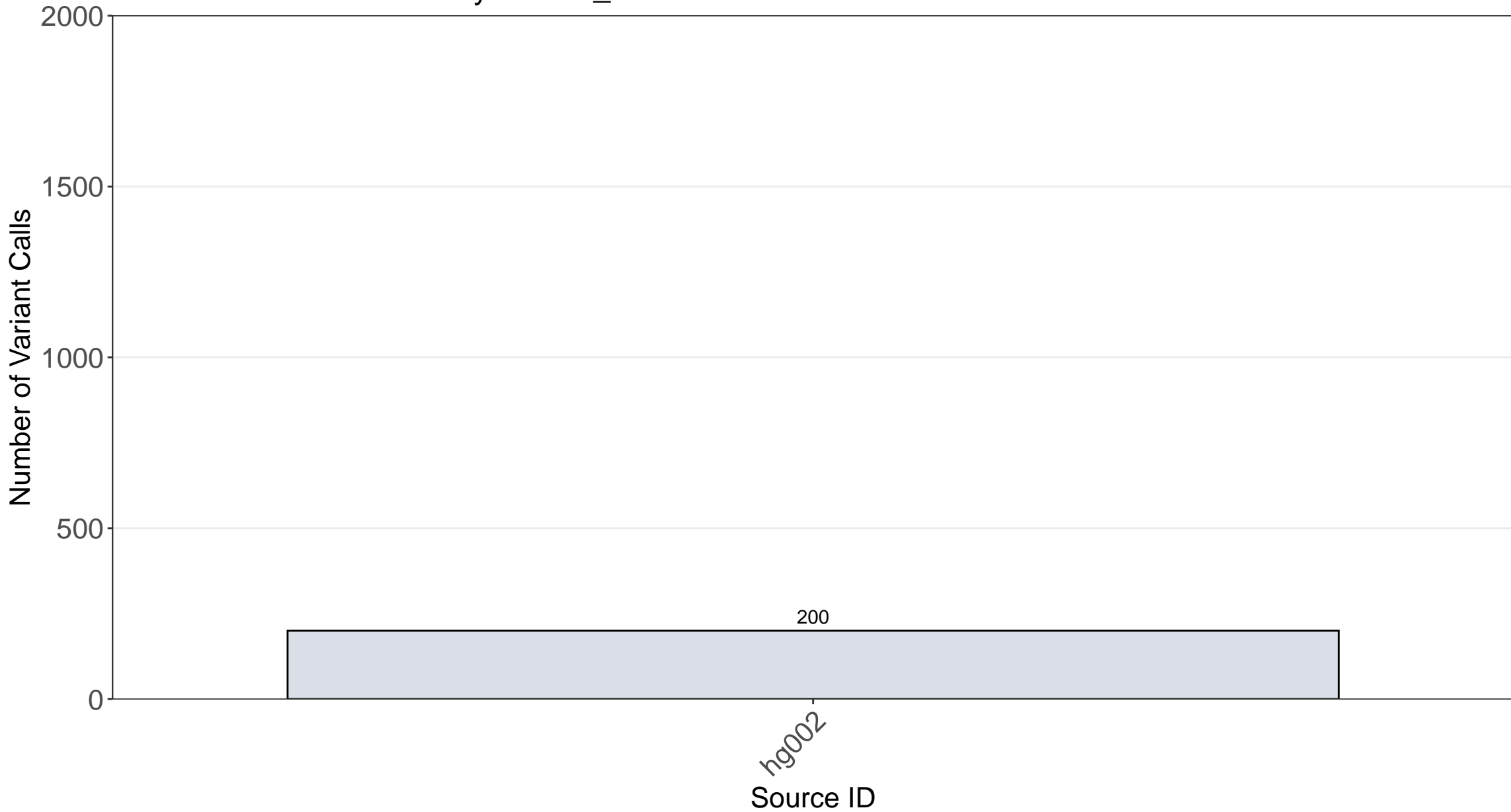
Number of Variant Calls by chromosome_2



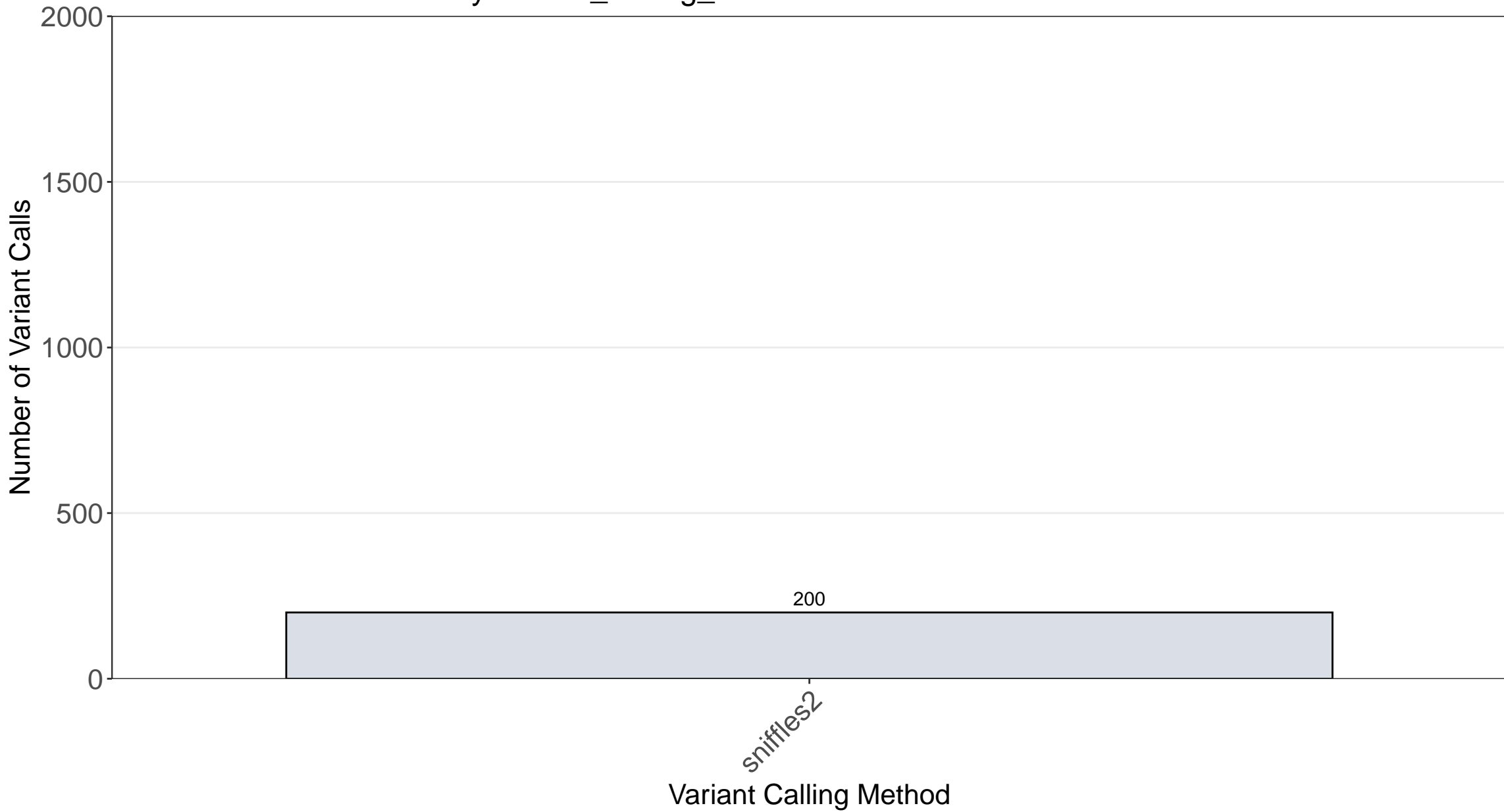
Number of Variant Calls by sample_id



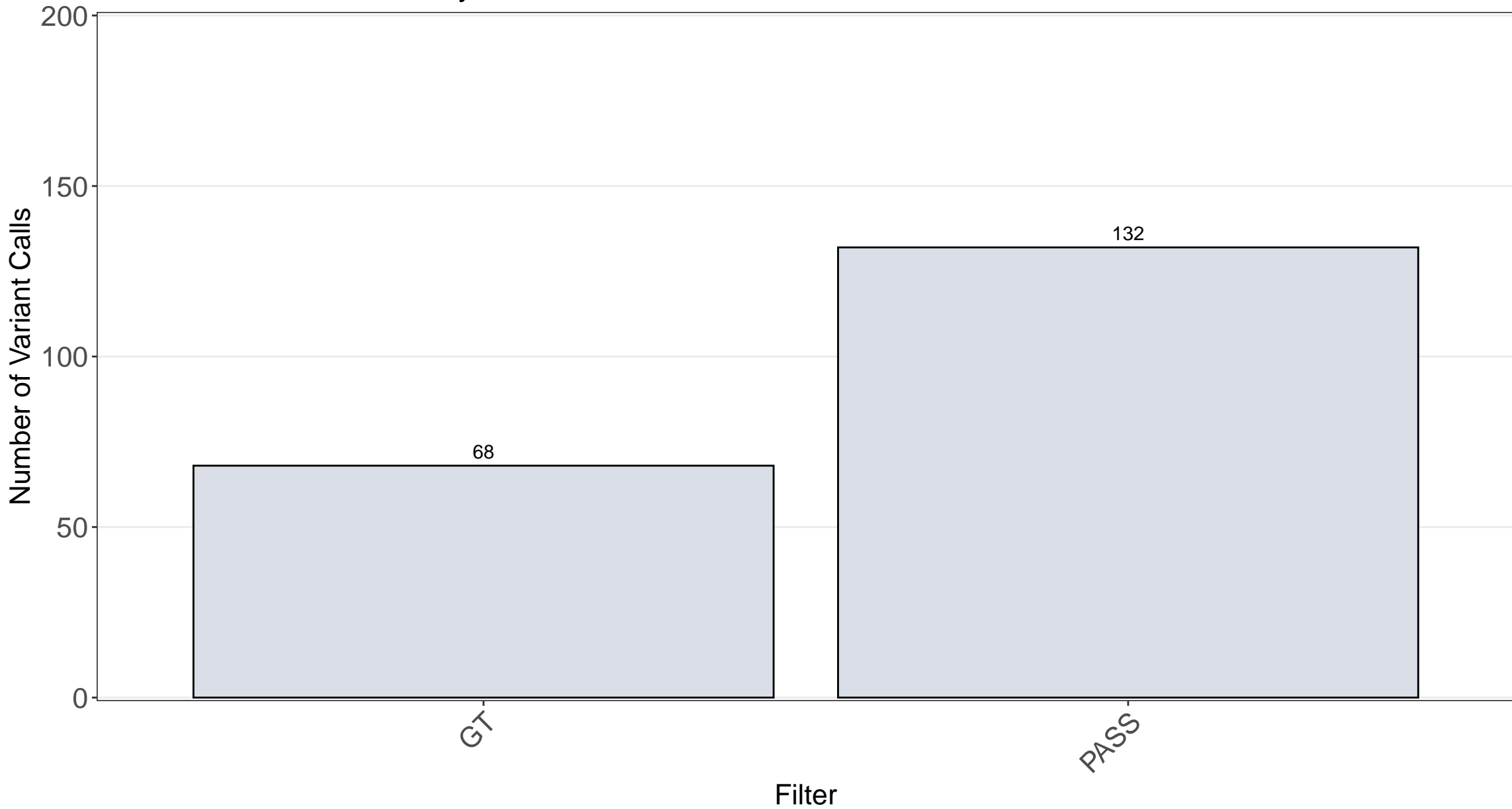
Number of Variant Calls by source_id



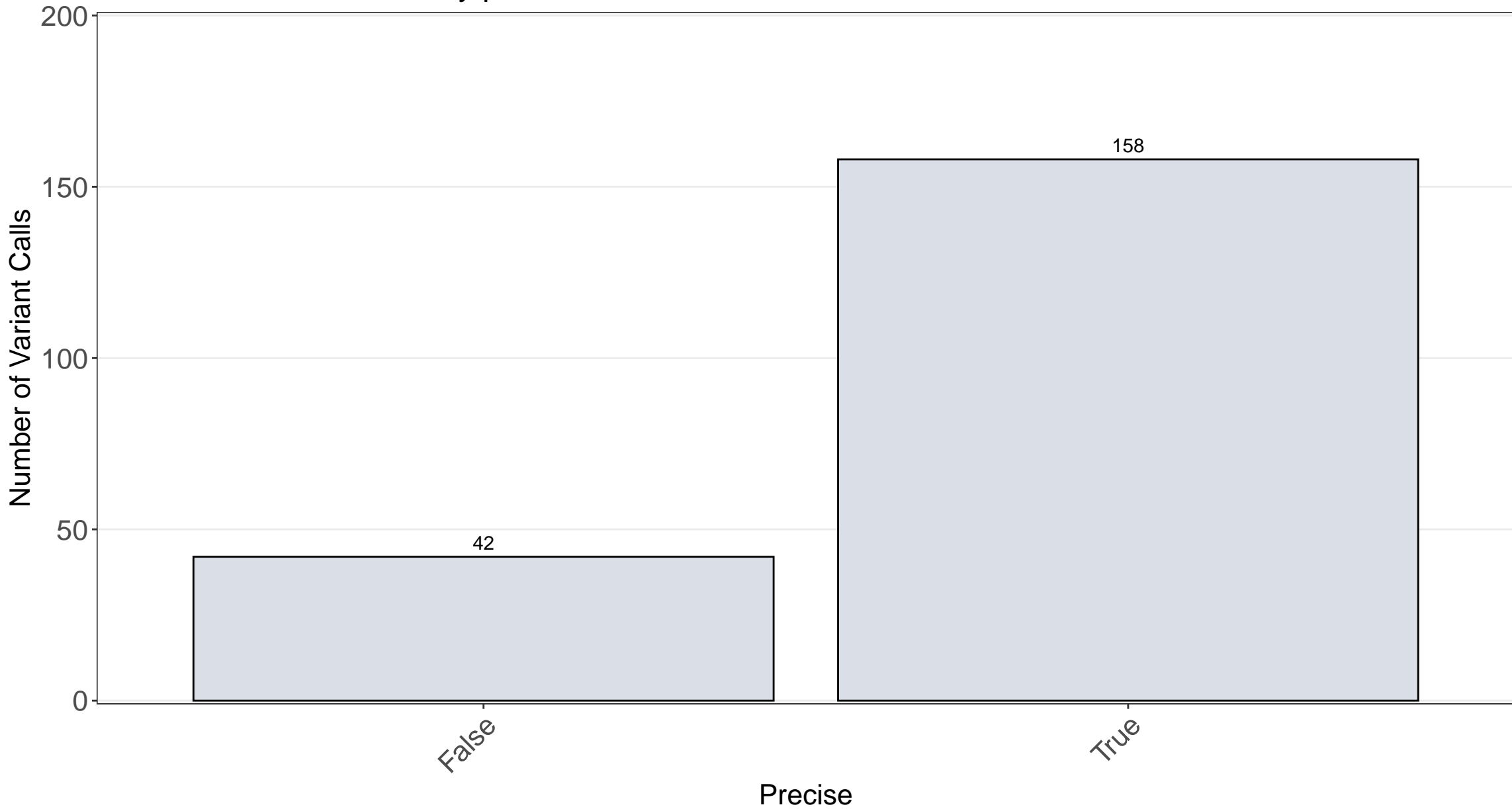
Number of Variant Calls by variant_calling_method



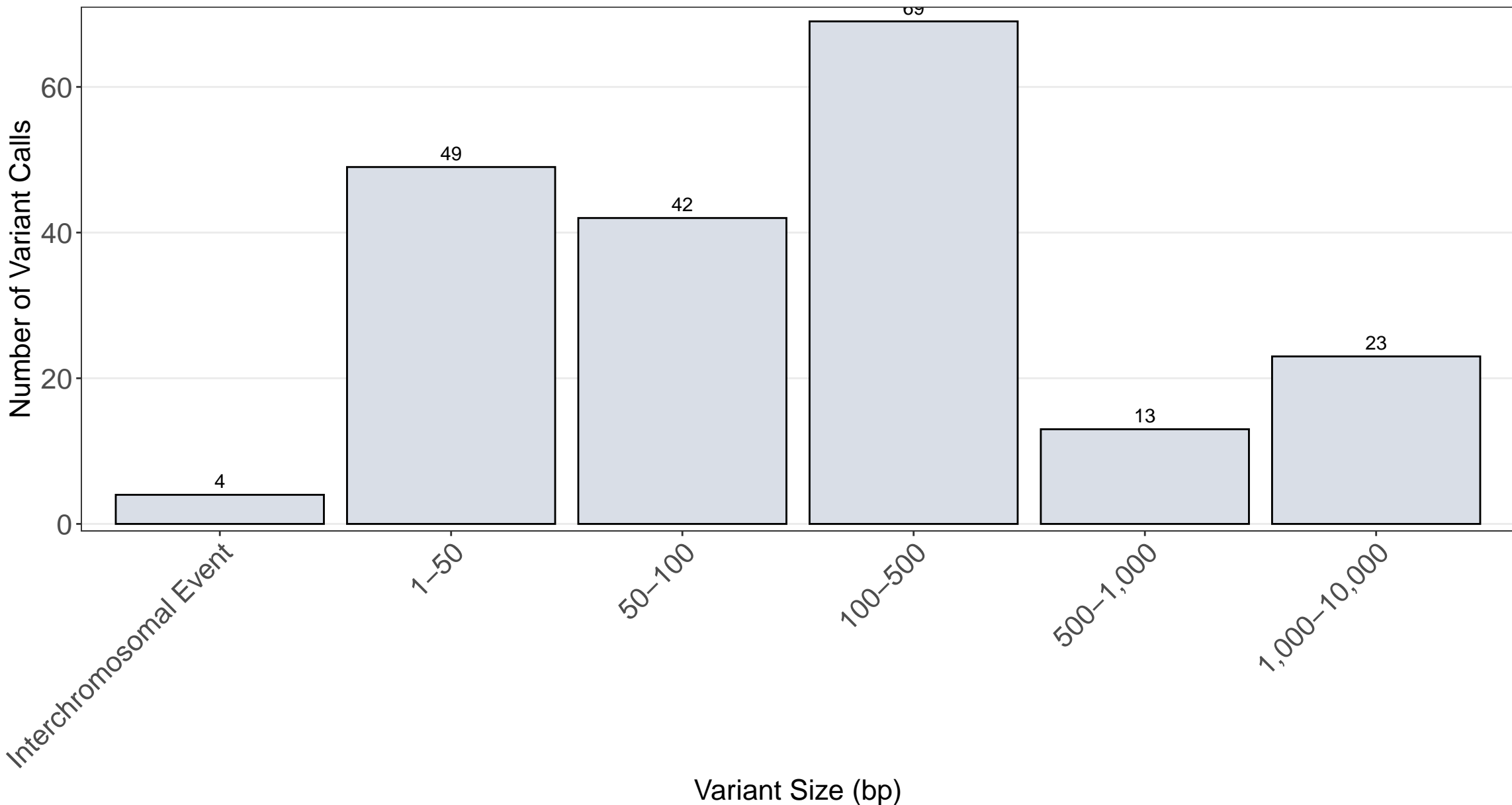
Number of Variant Calls by filter



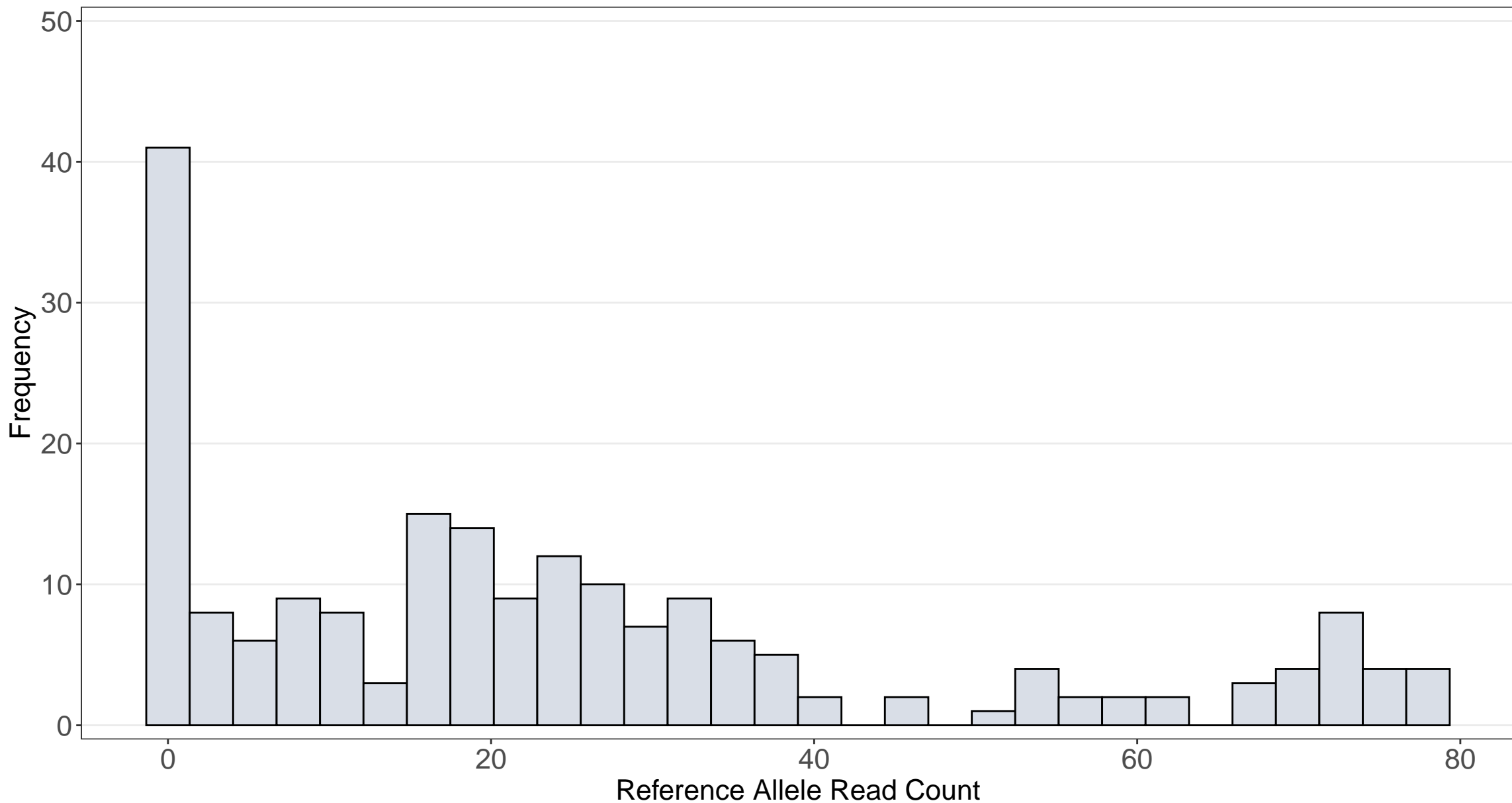
Number of Variant Calls by precise



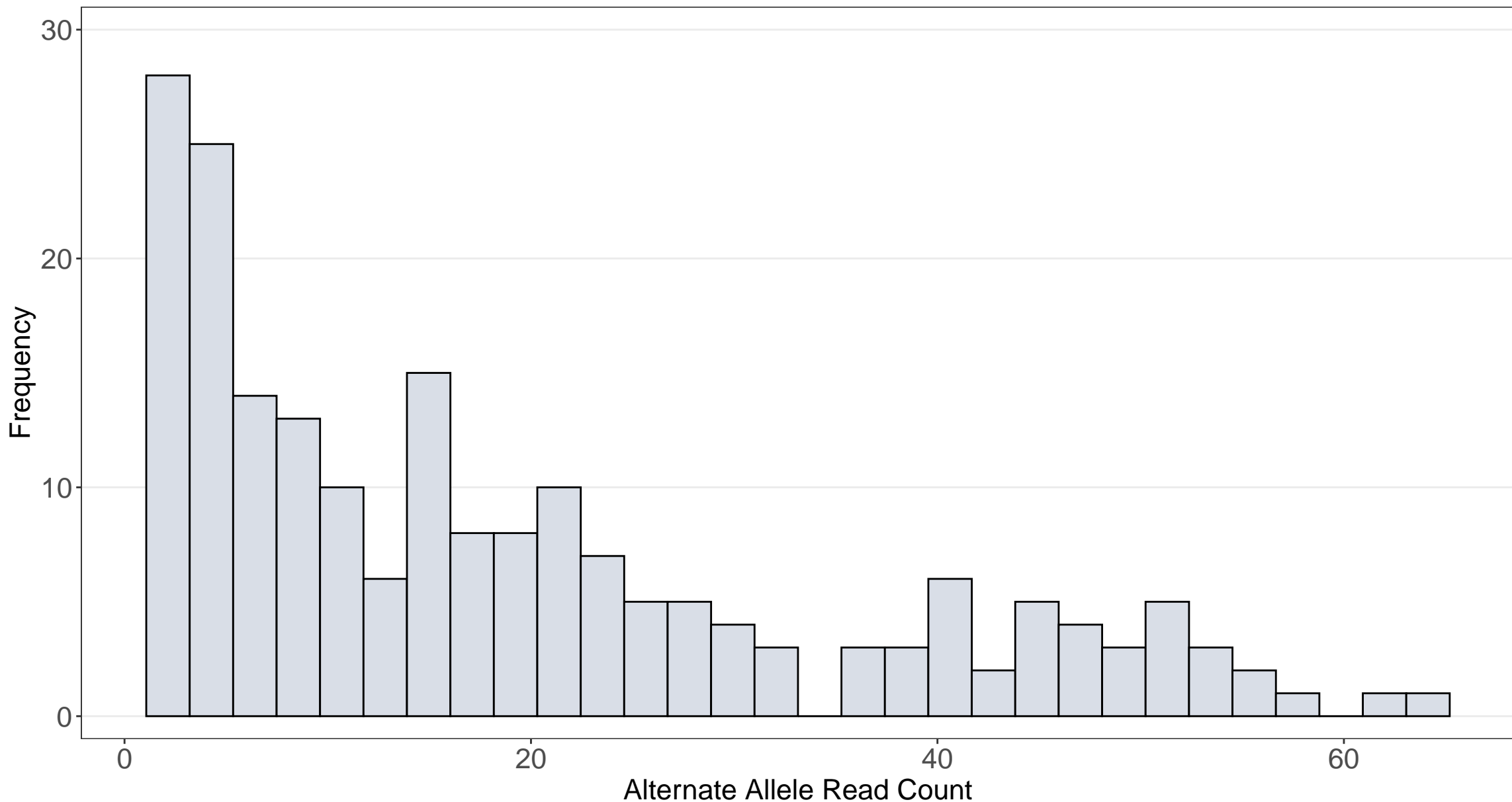
Number of Variant Calls by variant_size



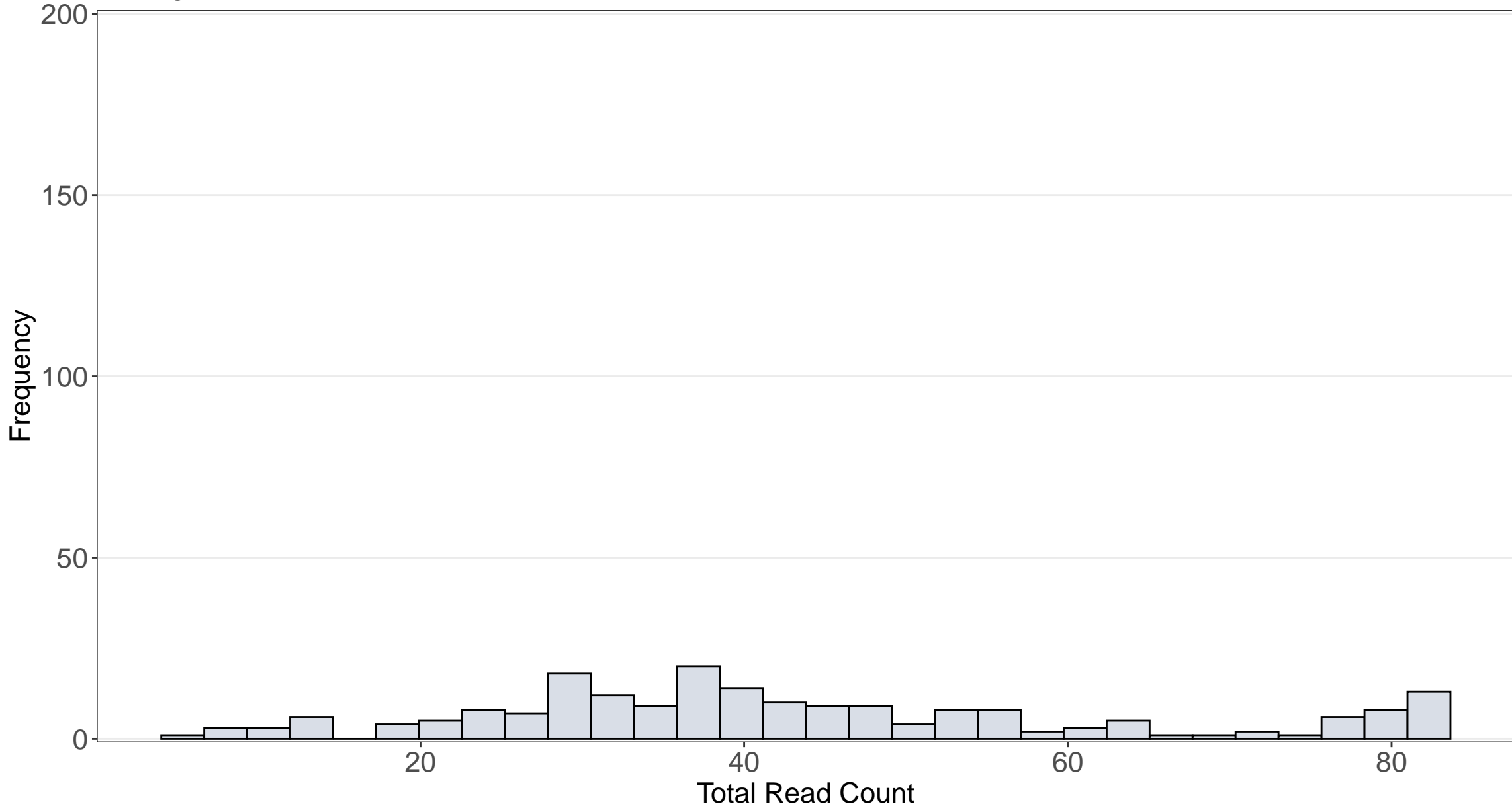
Histogram of reference_allele_read_count



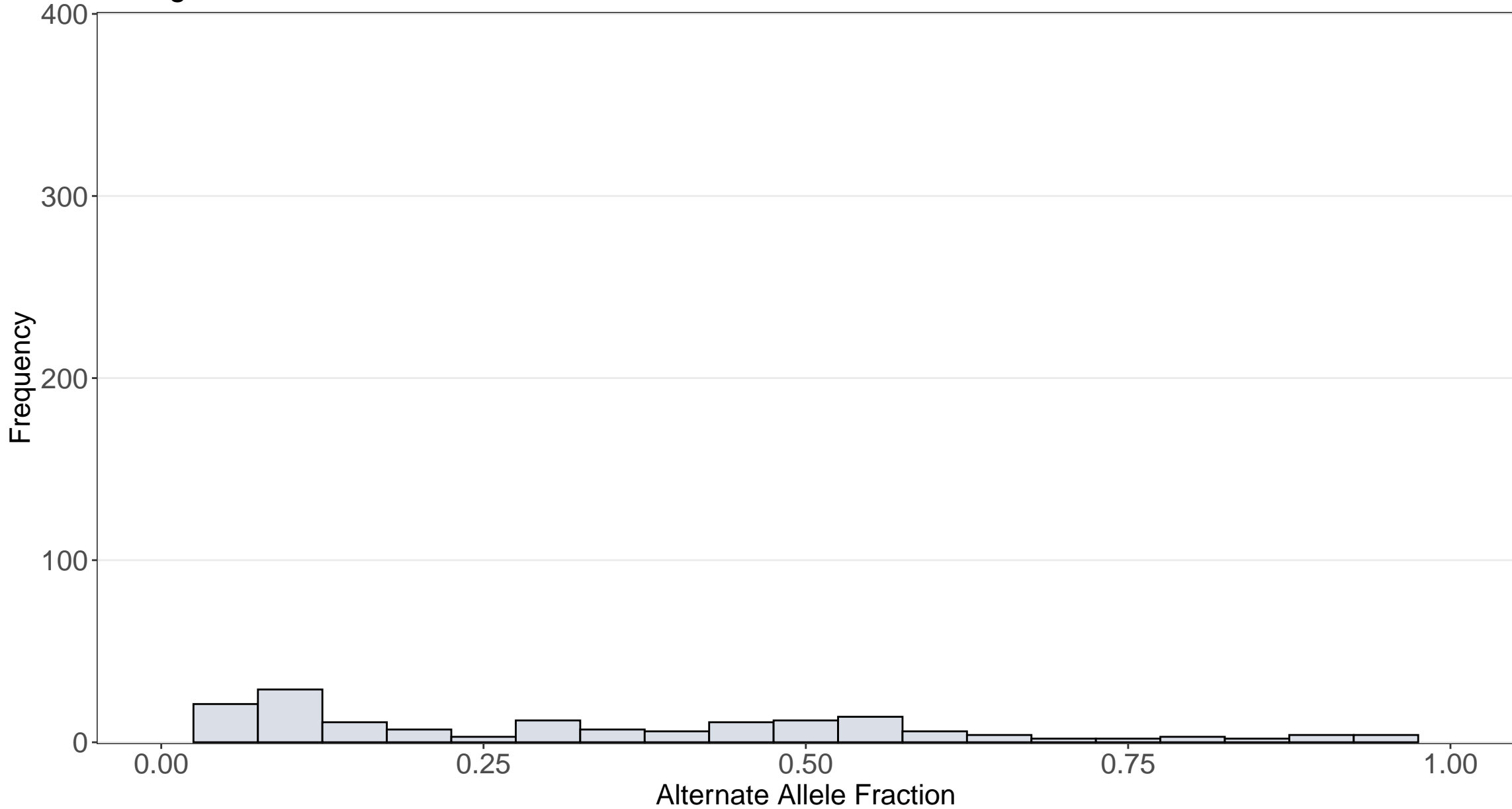
Histogram of alternate_allele_read_count



Histogram of total_read_count



Histogram of alternate_allele_fraction



Histogram of quality_score

