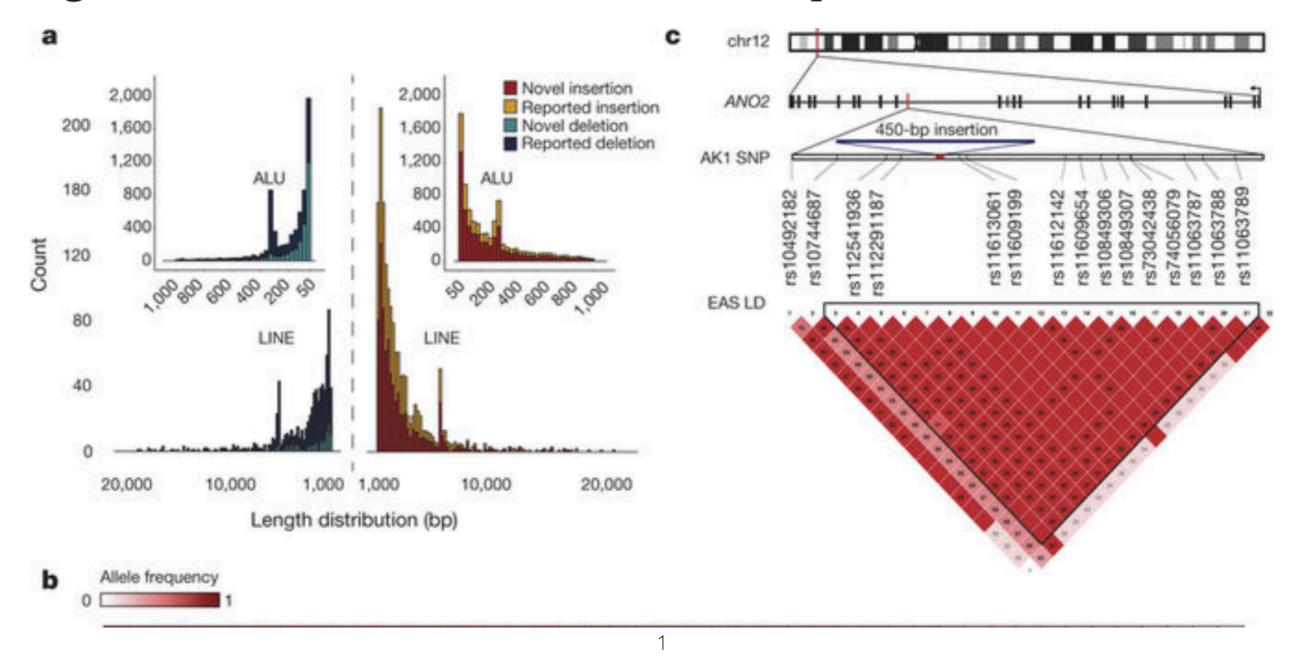
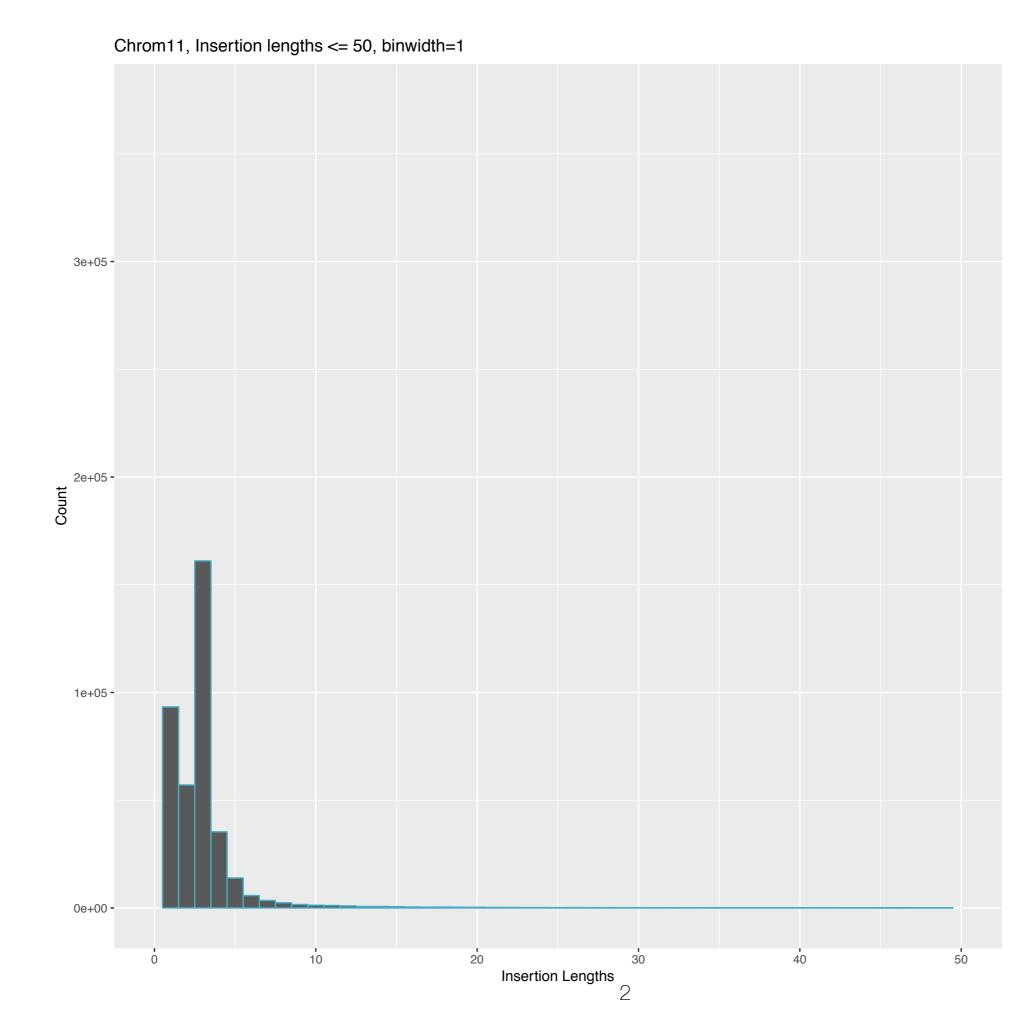
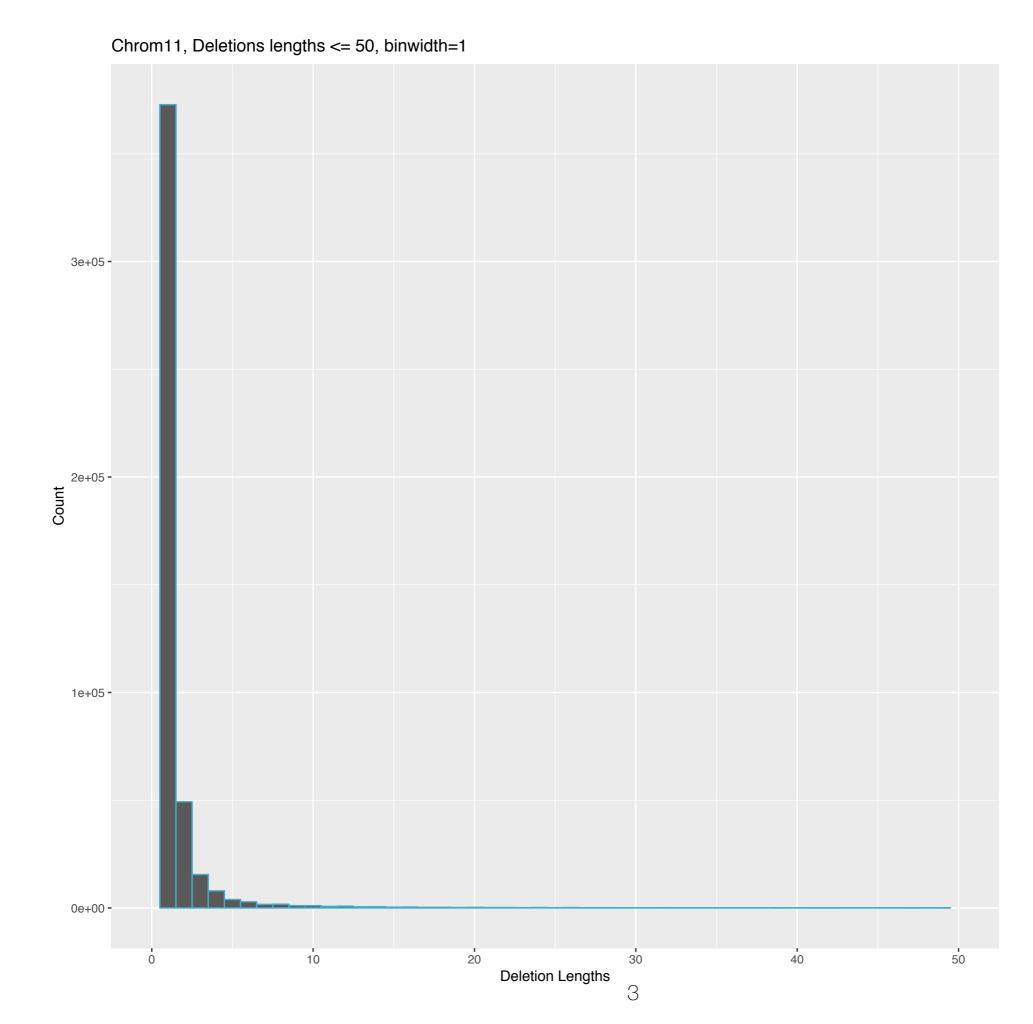
## Nancy Hansen, May 2017:

""The paper you found is great, although much more recent stats are available, e.g., in the Korean genome paper <a href="http://www.nature.com/nature/journal/v538/n7624/full/nature20098.html">http://www.nature.com/nature/journal/v538/n7624/full/nature20098.html</a>, which presumably are more accurate (see the histograms in Figure 2). The "symmetry" I referred to is simply the observation that if detection were perfect, we'd expect to see equal numbers of insertions and deletions of each size (notice how the left histogram mirrors the right histogram in Fig. 2a), since the reference sequence is an arbitrarily chosen human, so shouldn't have longer or shorter alleles in general."

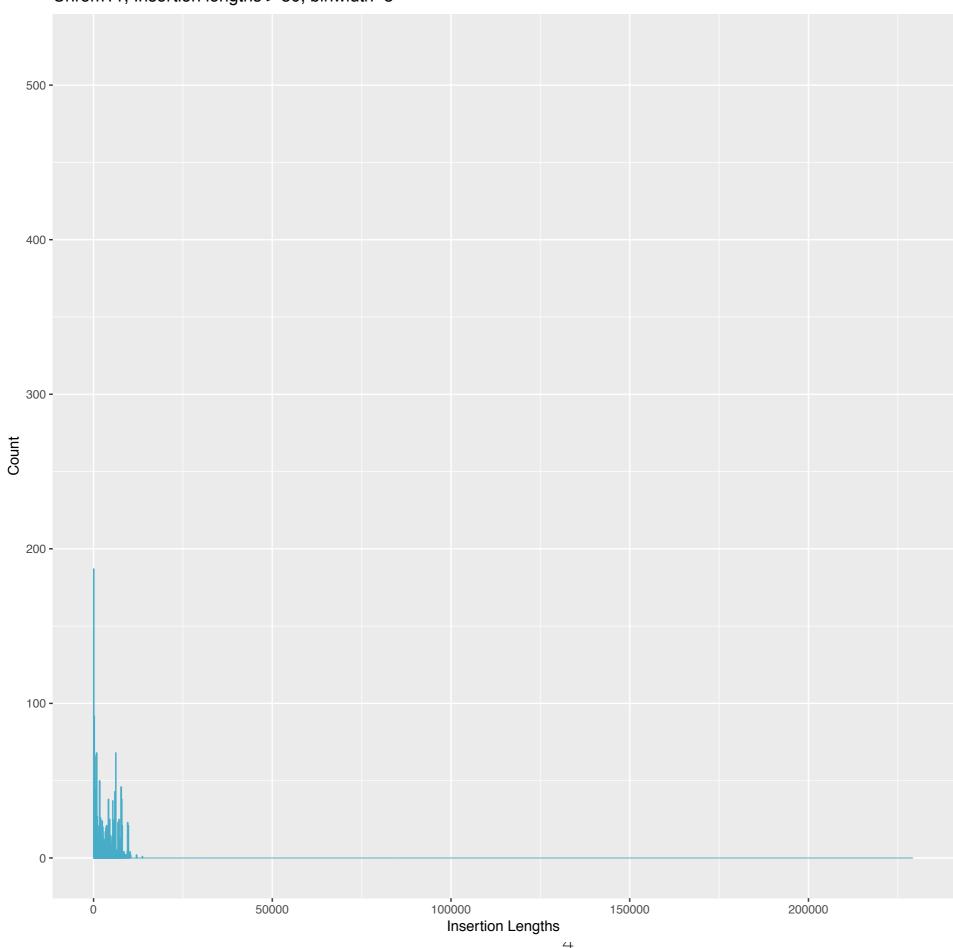
## Figure 2: AK1 SV distribution and Asian-specific variants.



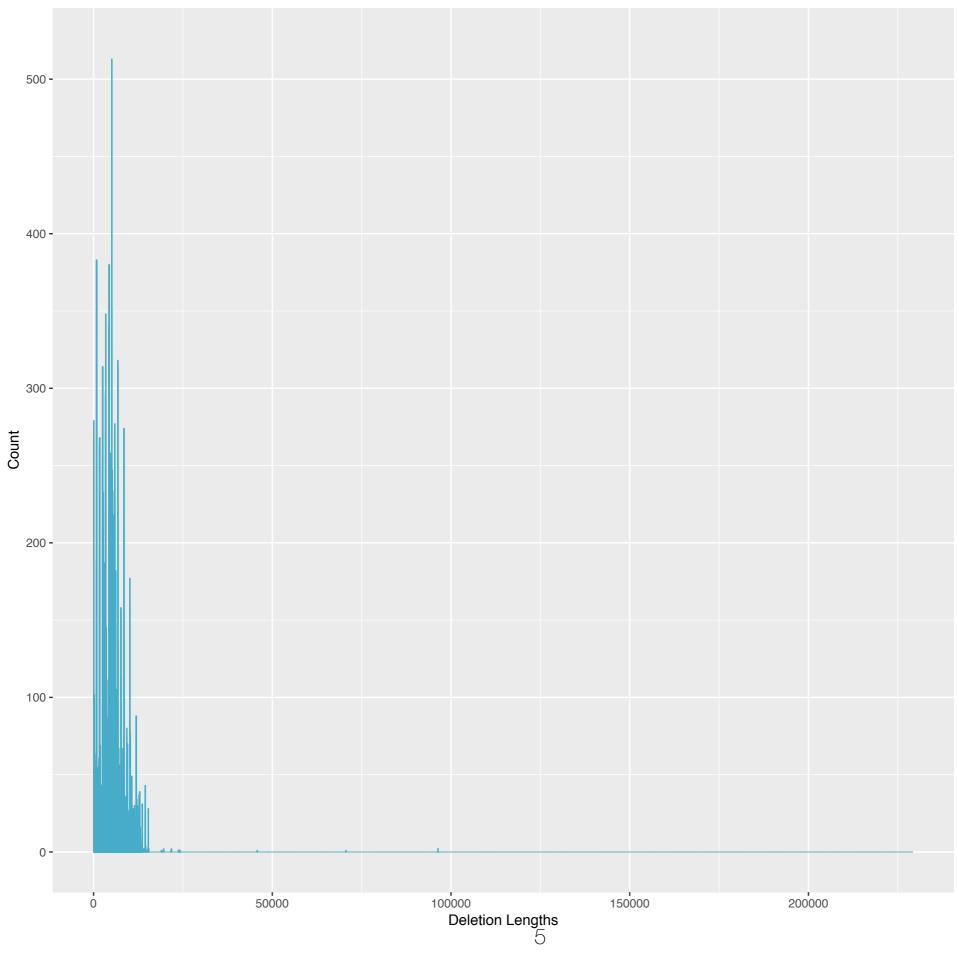




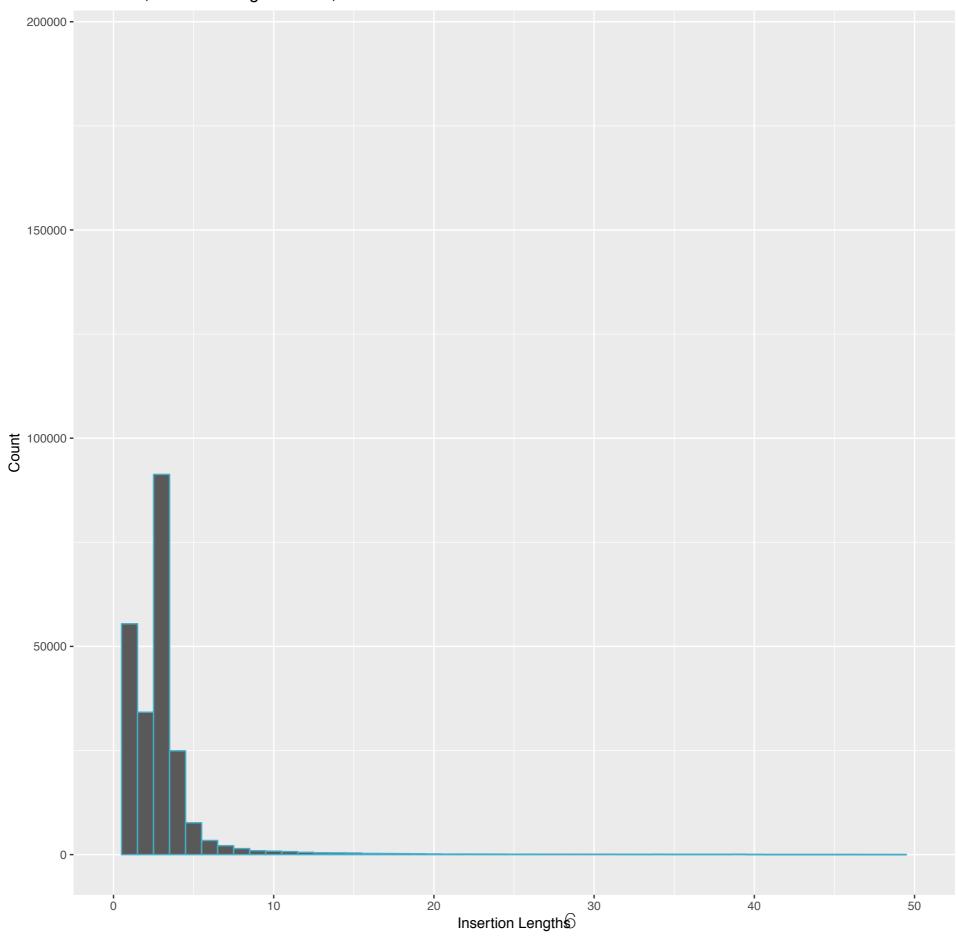
Chrom11, Insertion lengths > 50, binwidth=5



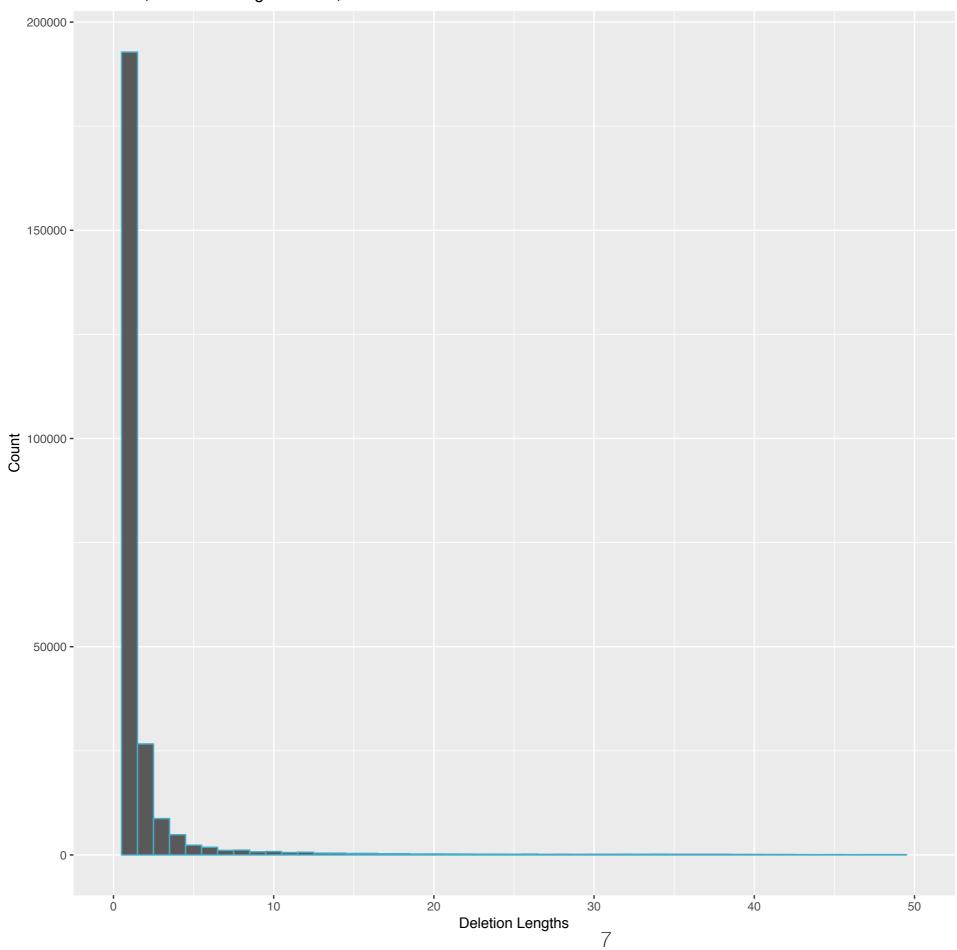
Chrom11, Deletion lengths > 50, binwidth=5

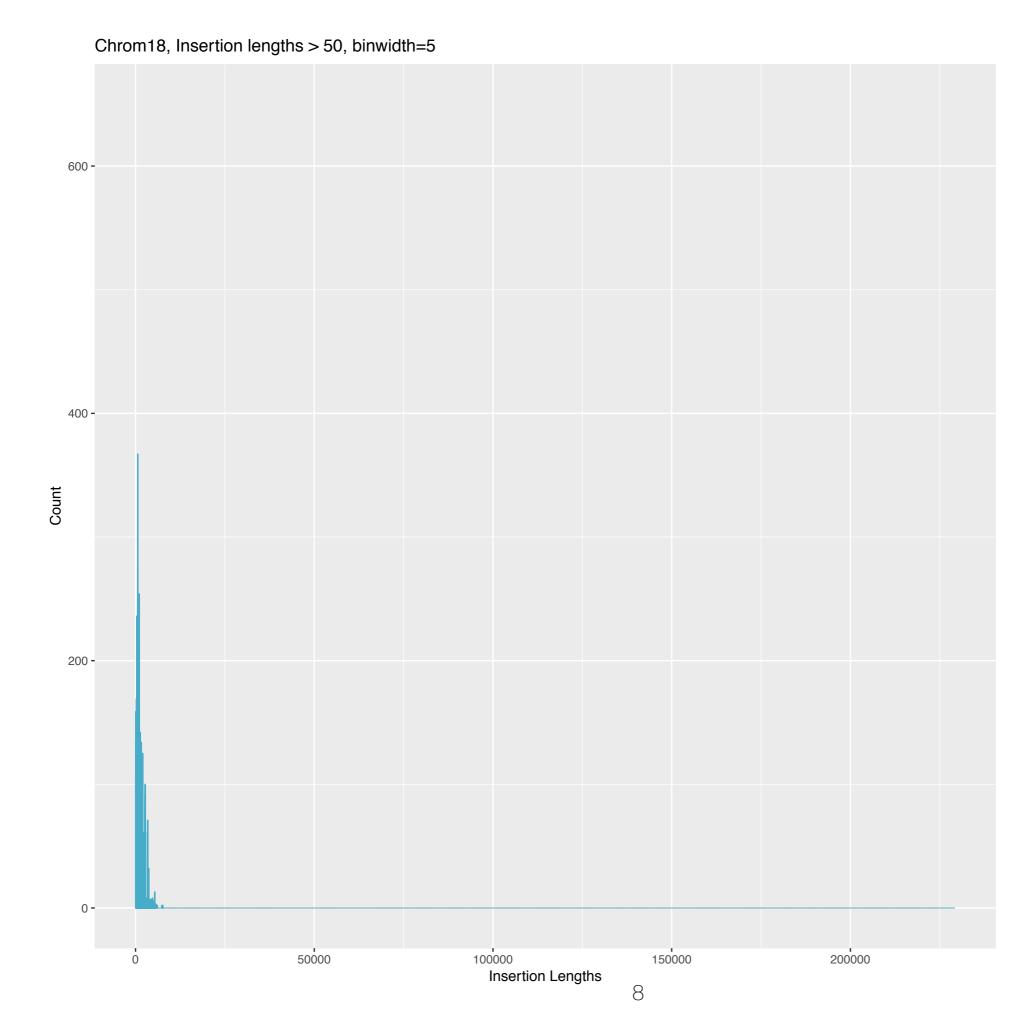


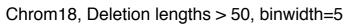
Chrom18, Insertion lengths <= 50, binwidth=1

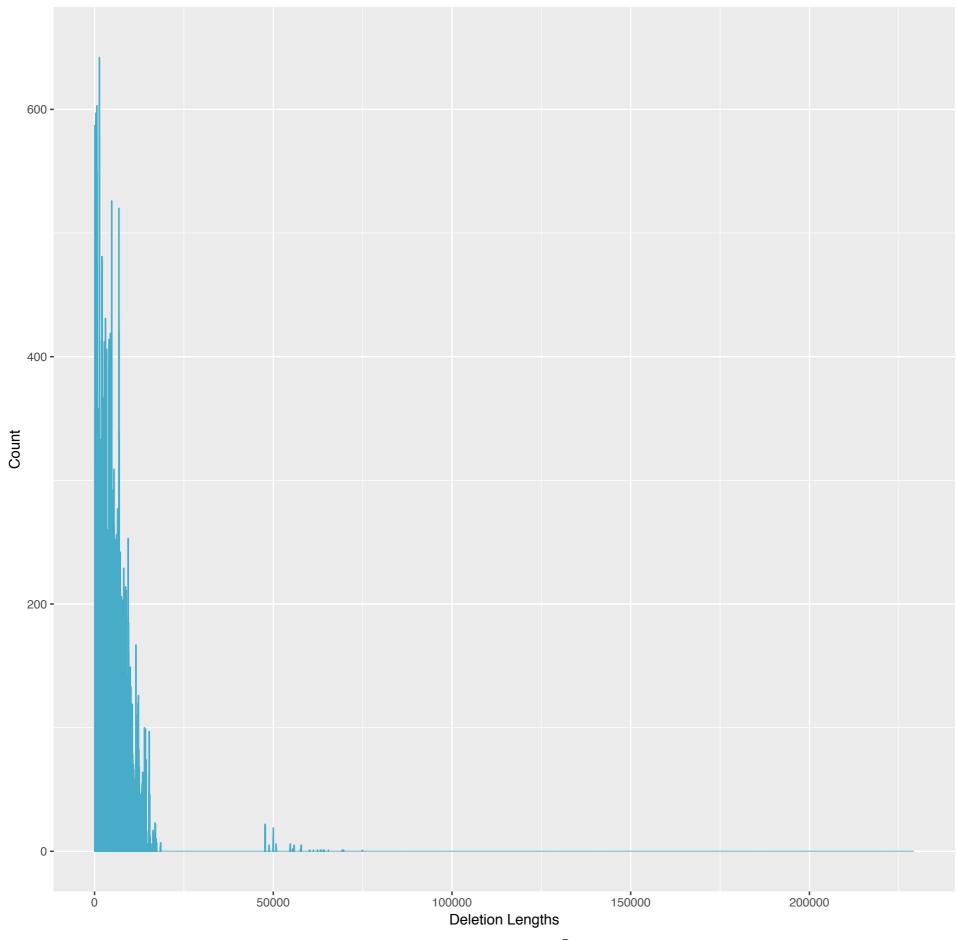


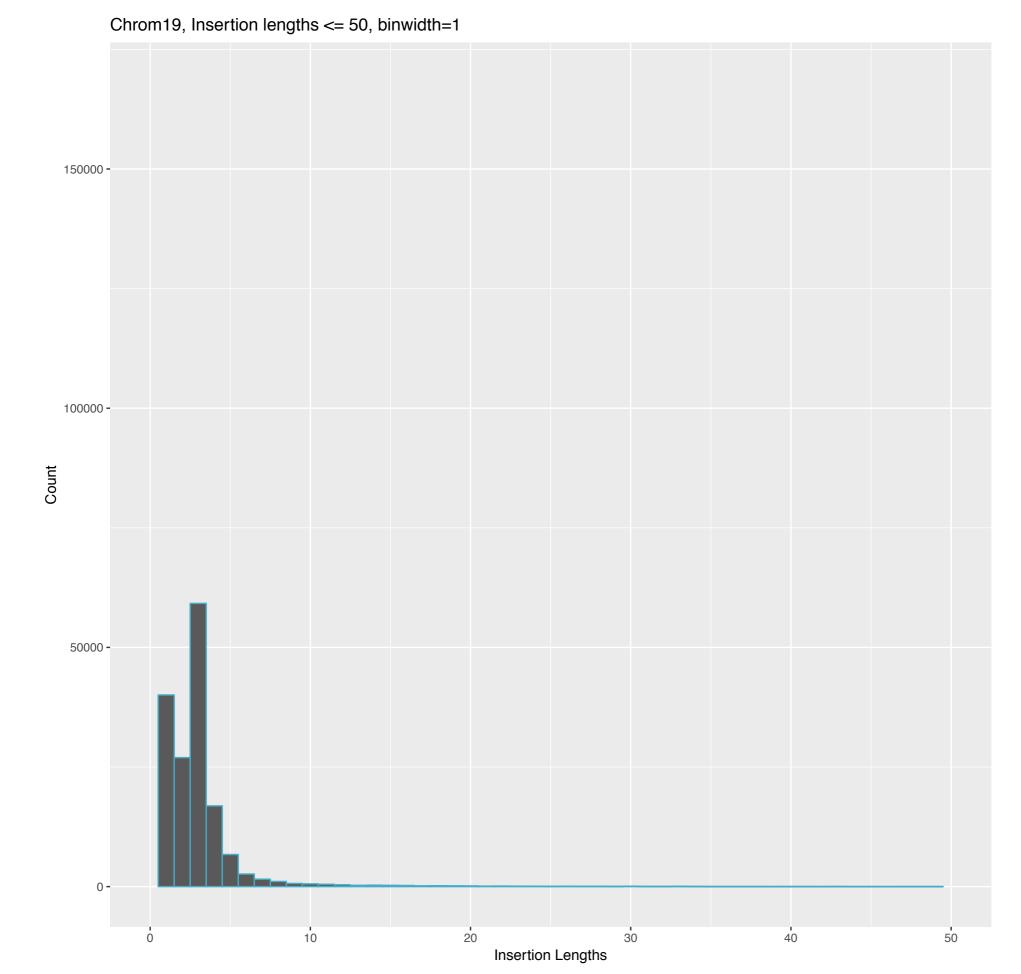
Chrom18, Deletions lengths <= 50, binwidth=1











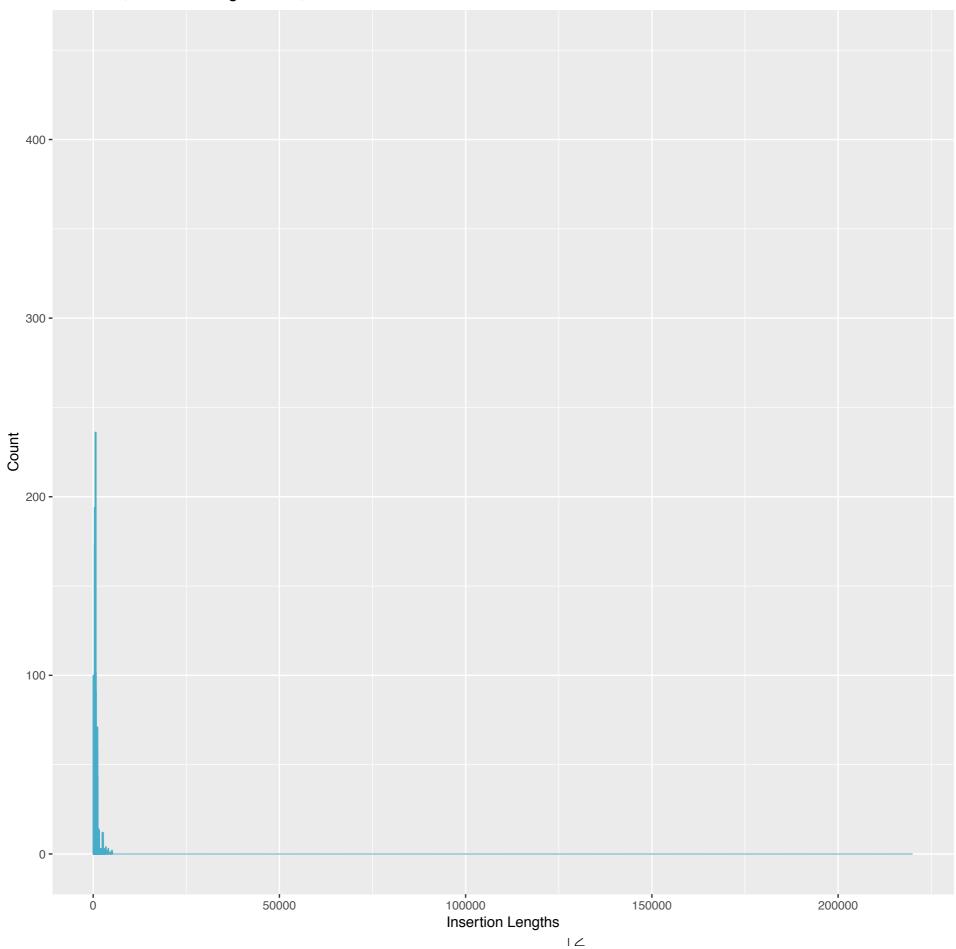
Chrom19, Deletions lengths <= 50, binwidth=1 150000 -100000 -50000 -

Count

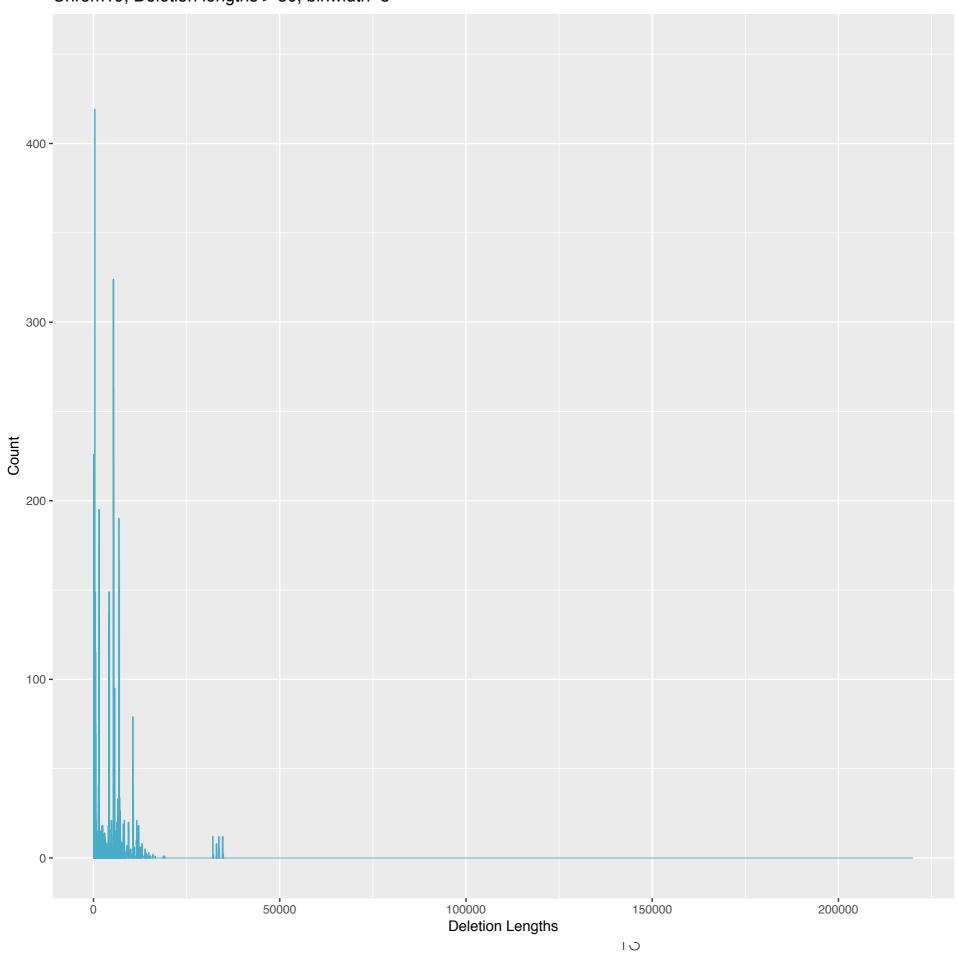
Deletion Lengths

10

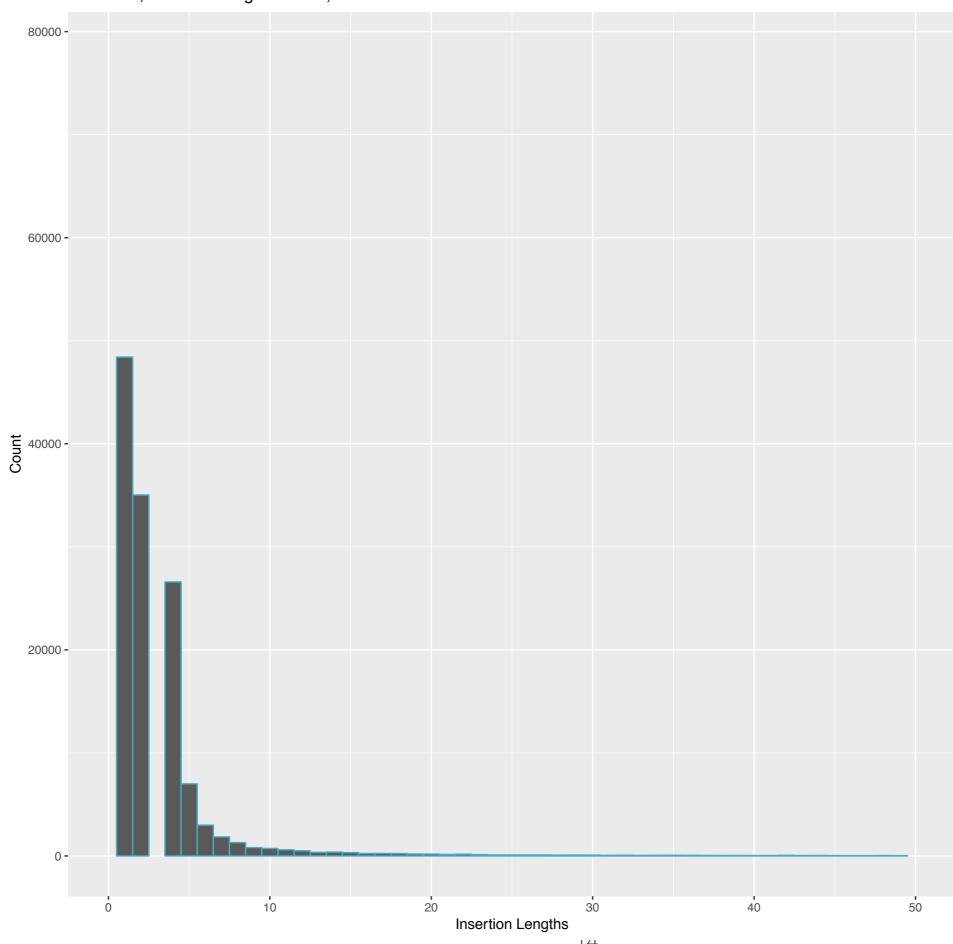
Chrom19, Insertion lengths > 50, binwidth=5



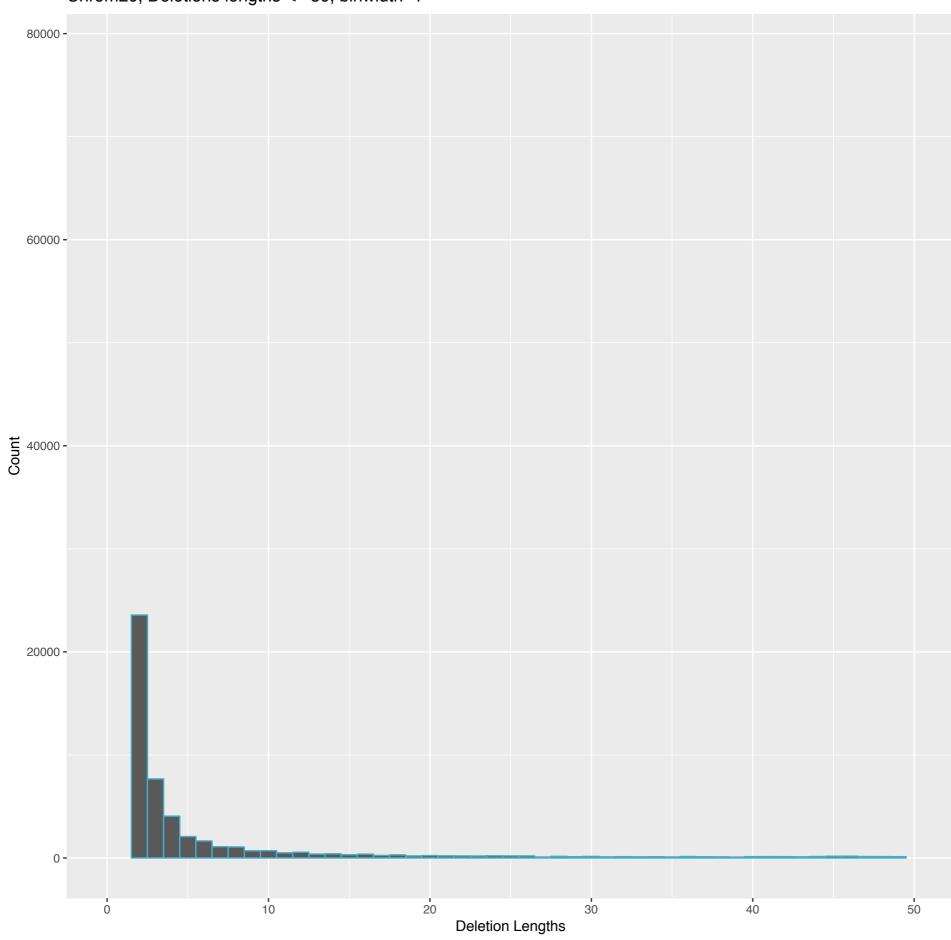
Chrom19, Deletion lengths > 50, binwidth=5

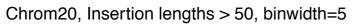


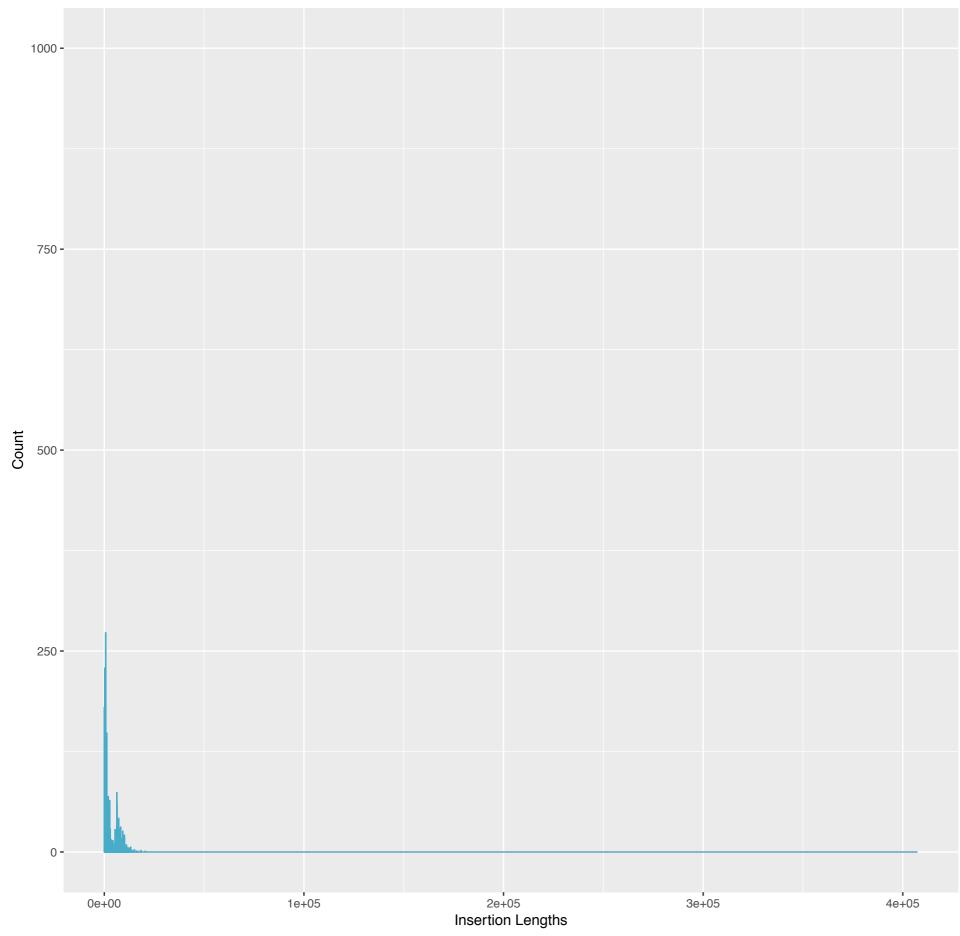




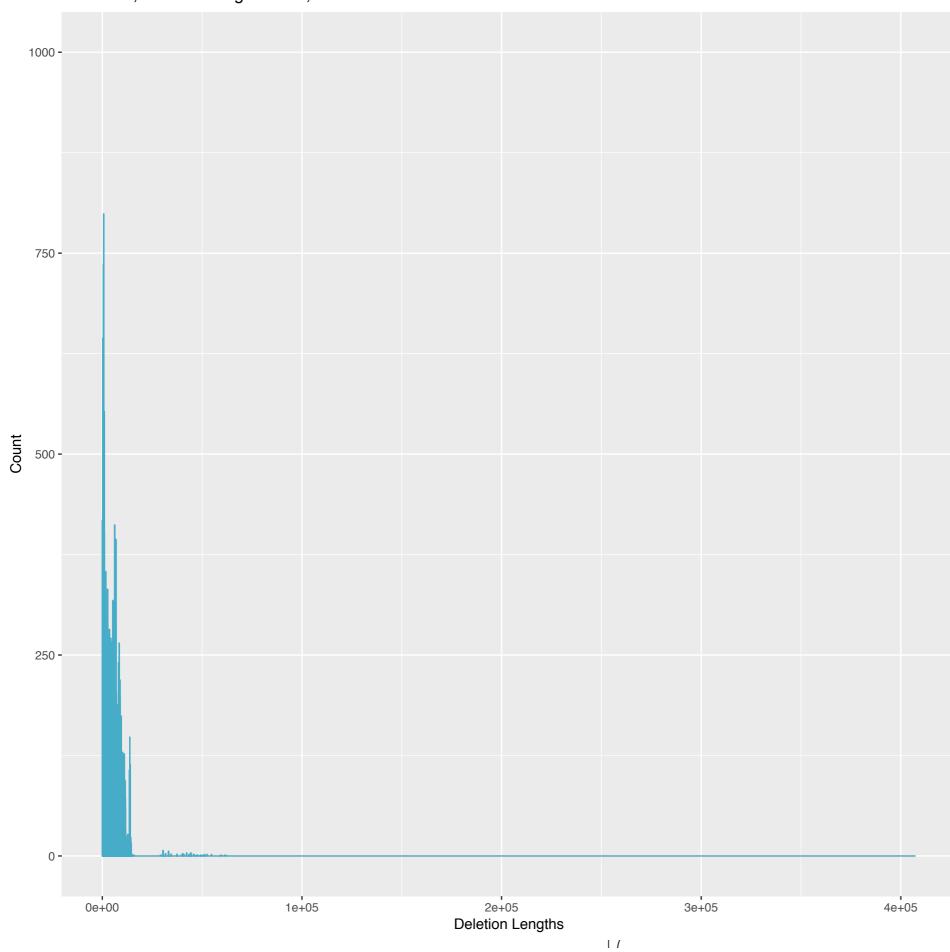


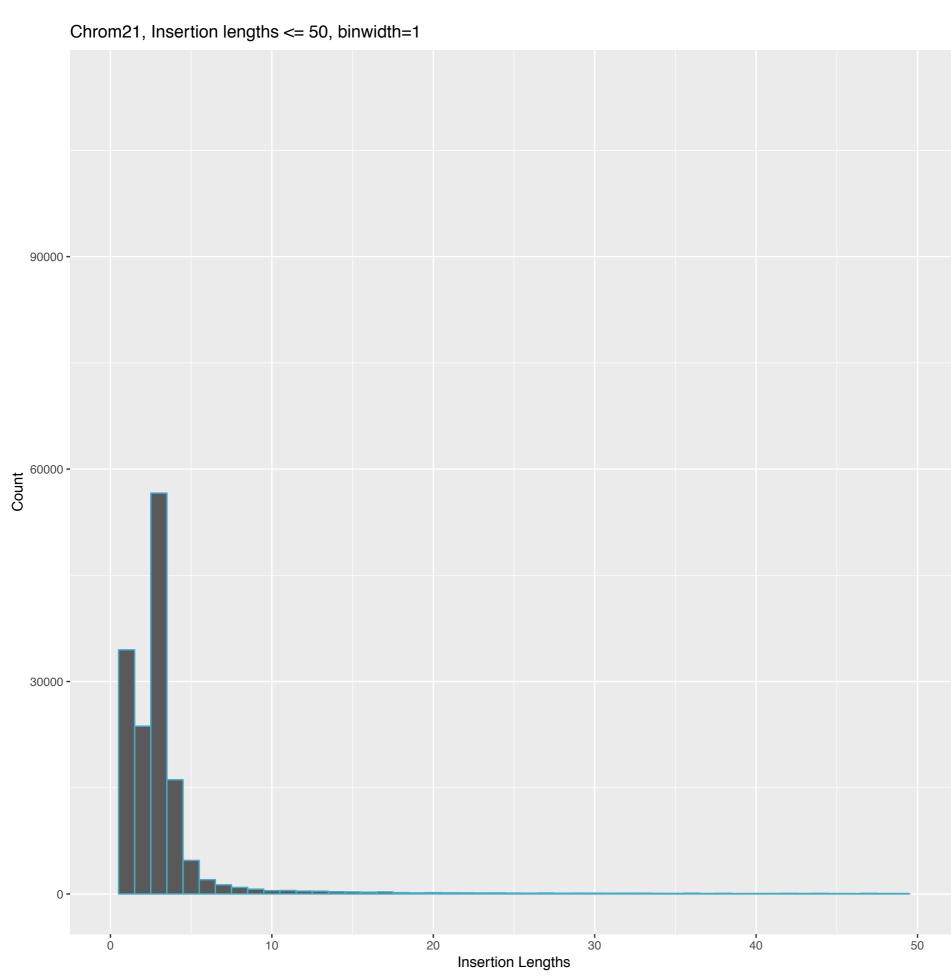


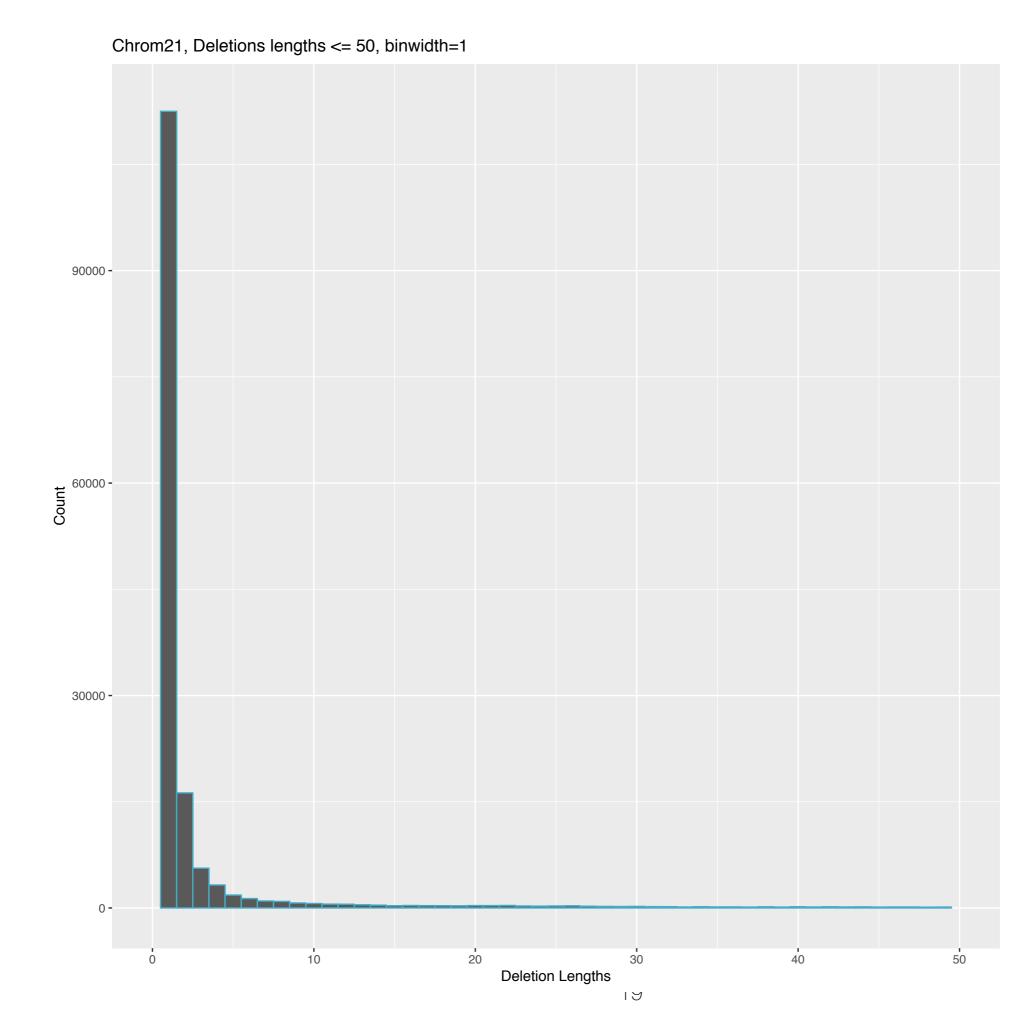




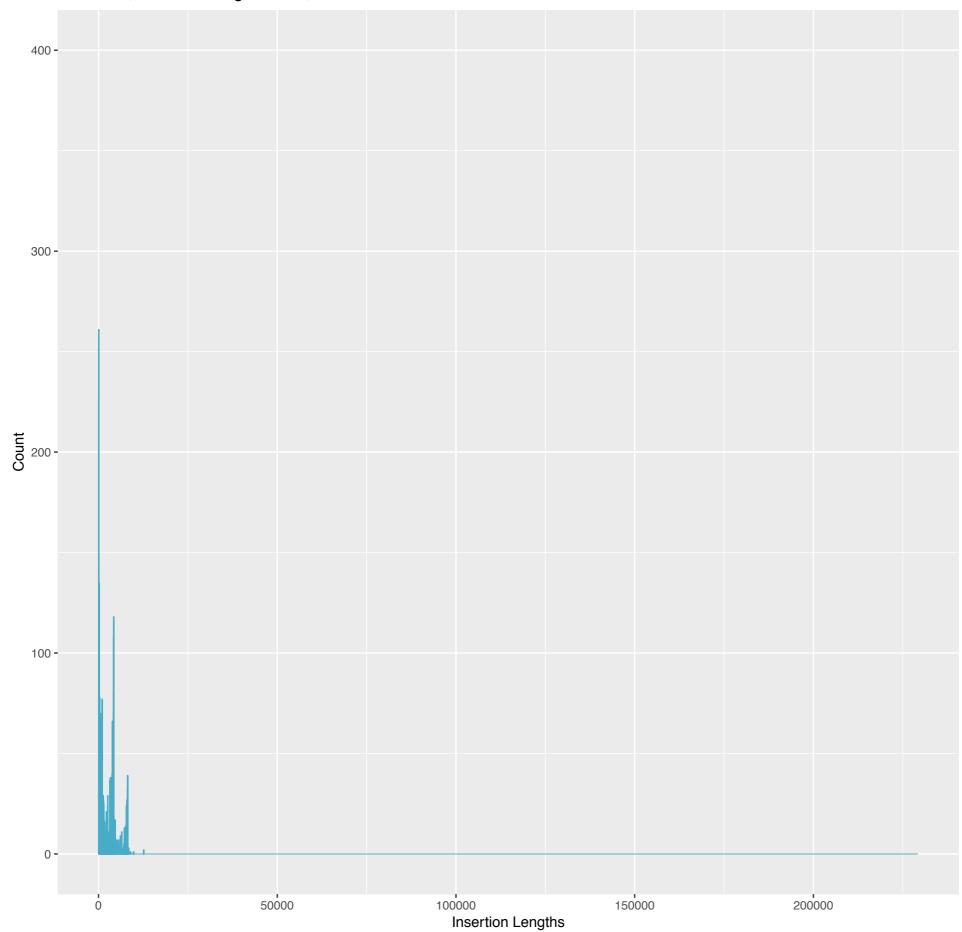
Chrom20, Deletion lengths > 50, binwidth=5

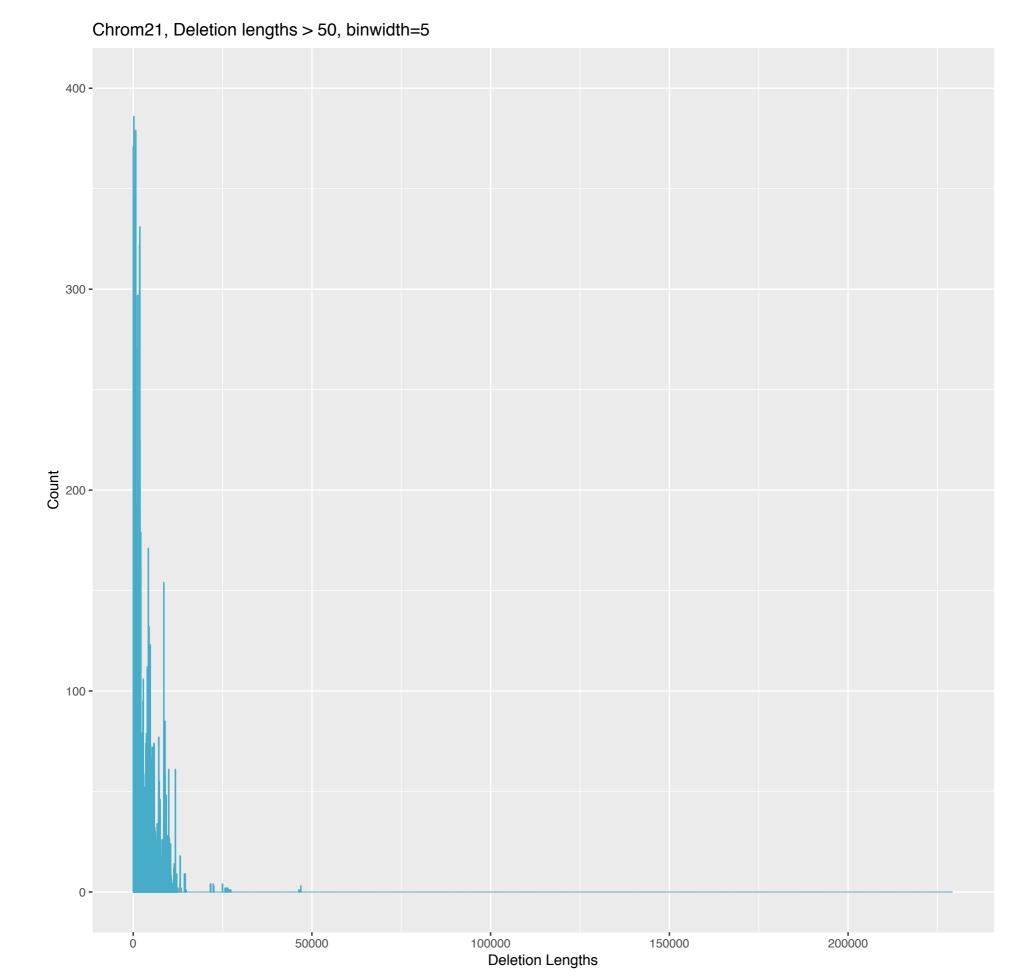


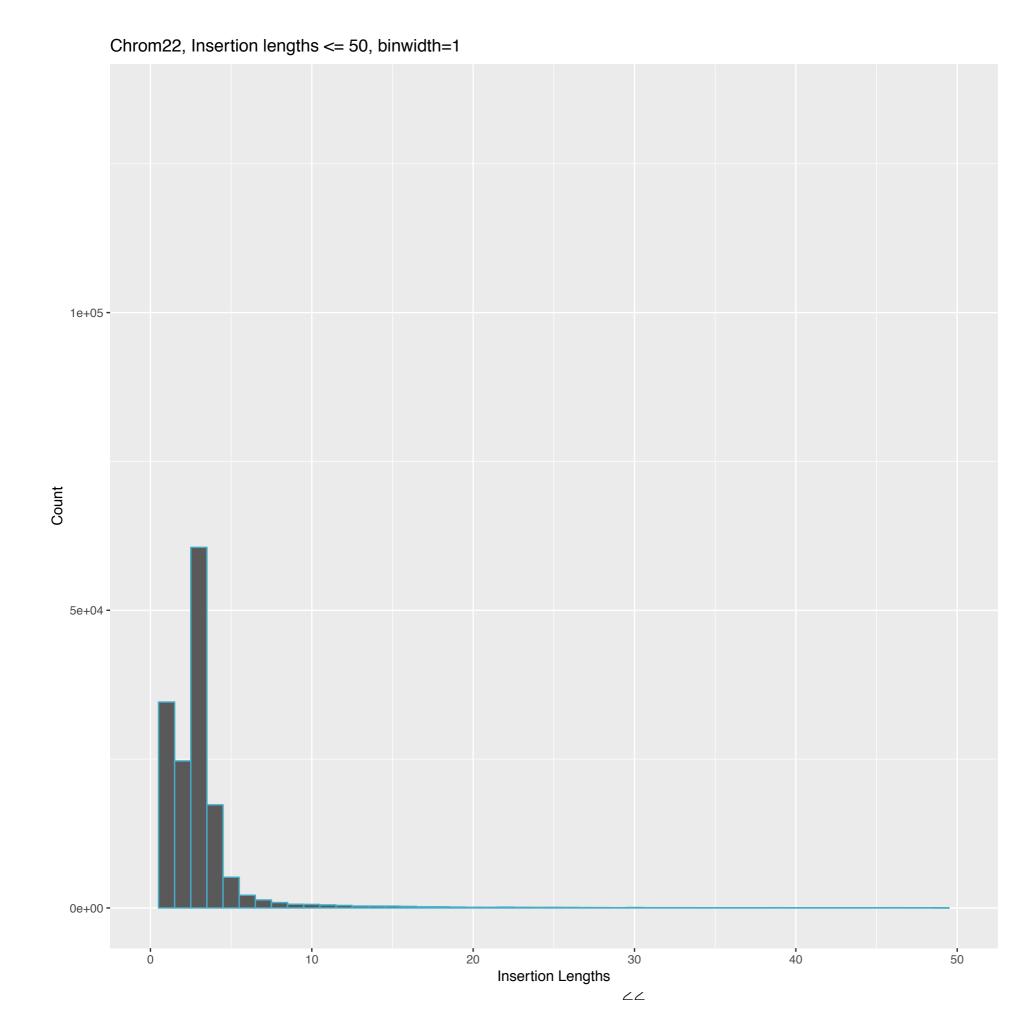


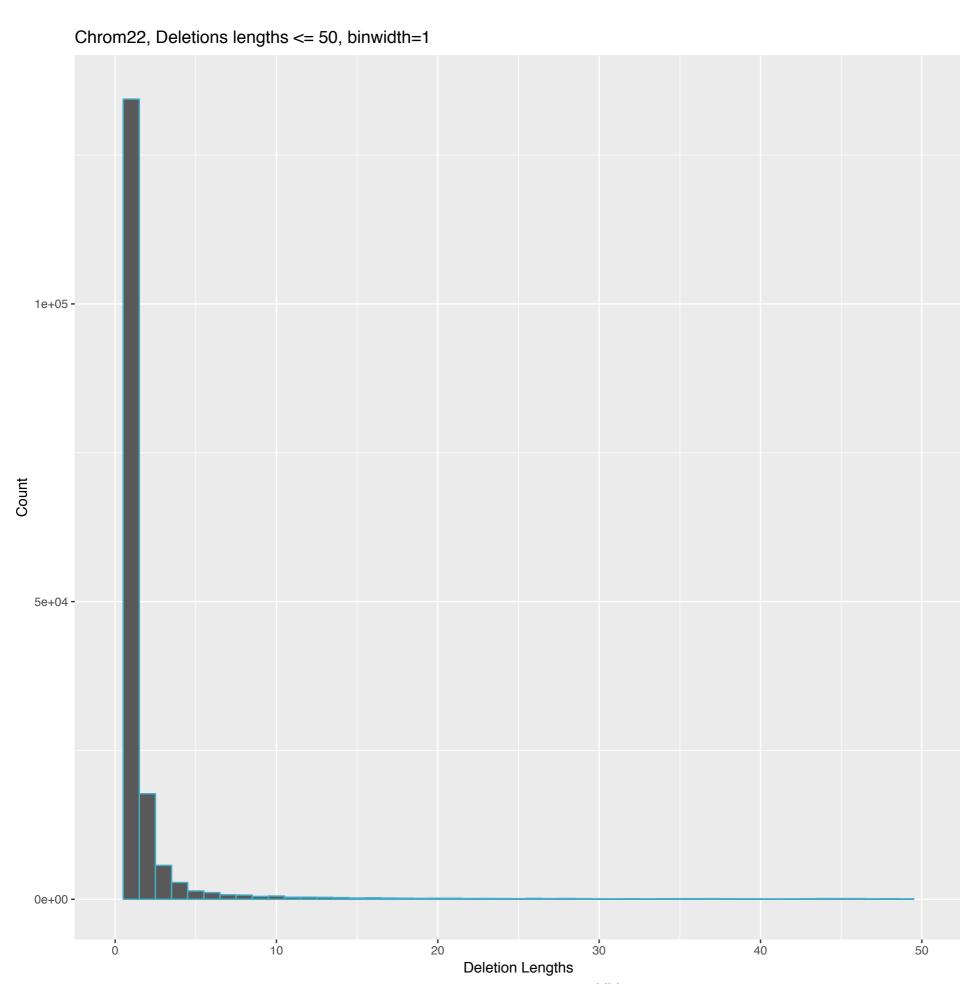


Chrom21, Insertion lengths > 50, binwidth=5

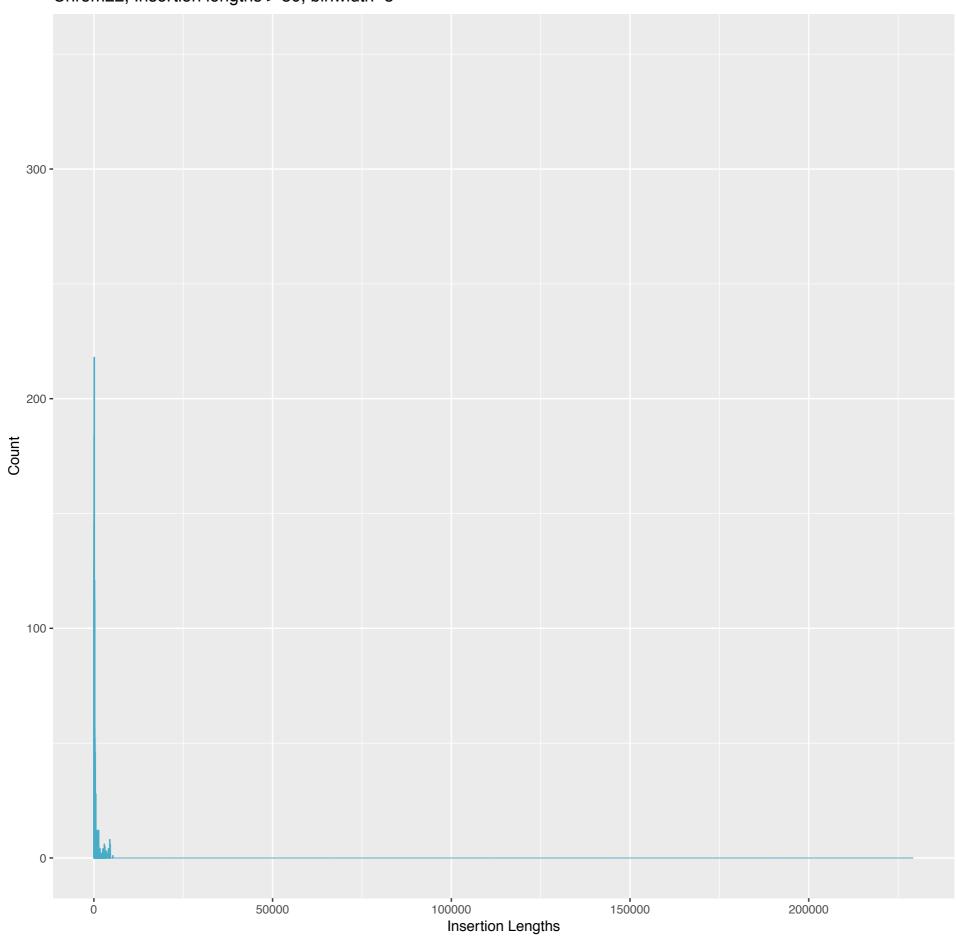








Chrom22, Insertion lengths > 50, binwidth=5



Chrom22, Deletion lengths > 50, binwidth=5 300 -200 -Count 100 -100000 Deletion Lengths 50000 200000 150000

