



Histograms generated from the bedgraph files of each isolate aligned to the reference genome IPO323. Bedgraph files were created with `bedtools genomeCoverageBed -bga -ibam isolate.realign.bam -g Ztritici_bedtools.genome`. Bam files are the final bam files used for SNP calling in GATK. The histogram plots x-axis is limited to 100 for WAI320-329 and to 300 for WAI332, WAI147, WAI55-56.