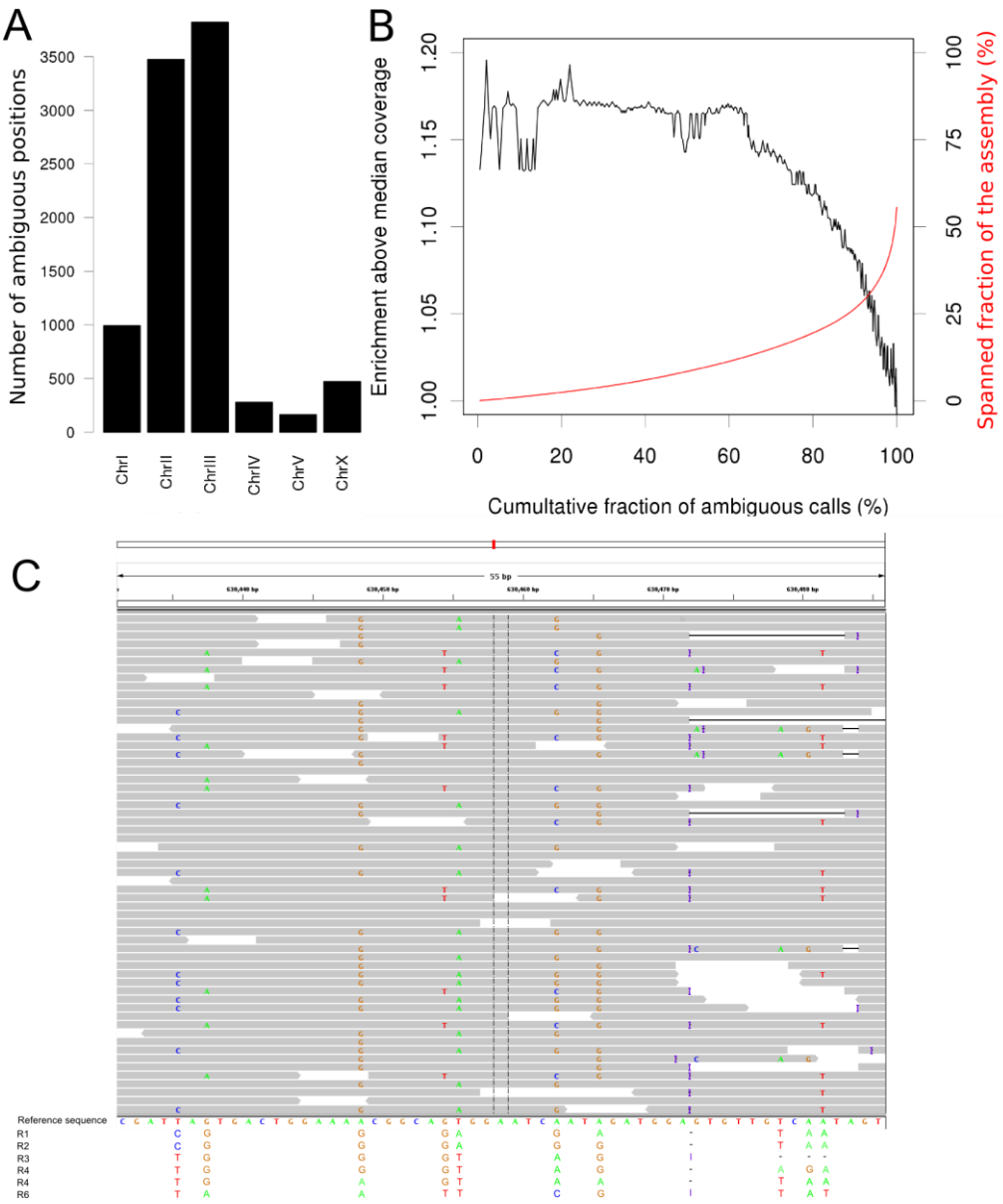

Figure S1 Heterozygosity in the *P. exspectus* assembly. **(A)** Ambiguous sites are present on autosomes and the X chromosome. Shown are the numbers of heterozygous calls per chromosome. *P. exspectatus.* Scaffolds were assigned to chromosomes by blasting *P. pacificus* genetic markers against the *P. exspectatus* assembly. **(B)** Ambiguous sites are associated with increased coverage. Non-overlapping windows of 10kb were ordered by decreasing number of ambiguous sites (x-axis) and the ratio of median coverage within the top X% above the genome-wide median coverage is plotted. At 60-70% of ambiguous sites, the ratio drops to again and reaches a value of one when approaching 100% of ambiguous sites. **(C)** Screenshot from the IGV browser showing realigned *P. exspectatus* reads. One position shows three different genotypes, which cannot be explained by remaining heterozygosity, indicating that reads must originate from highly similar paralogous regions. The alignments suggest that at least six different regions (R1-R6) are required to explain the observed pattern.