**magnifico:Users:talioto:Documents:projects:woodchuck:paula_kmer_analysis.pdf**

**Figure S1. 17-mer analysis of the sequenced genome**

All 17-mers present in the three PE libraries were counted. Thus the number of distinct 17-mers (kmer species) for each depth from 1 to 400 are shown in this plot. The main peak at depth 78 corresponds to unique homozygous sequence. The shoulder on the left corresponds to heterozygous sequence. The periodic waves to the right correspond to multi-copy repetitive sequence in the genome. The high peak at very low depths is caused by sequencing errors.