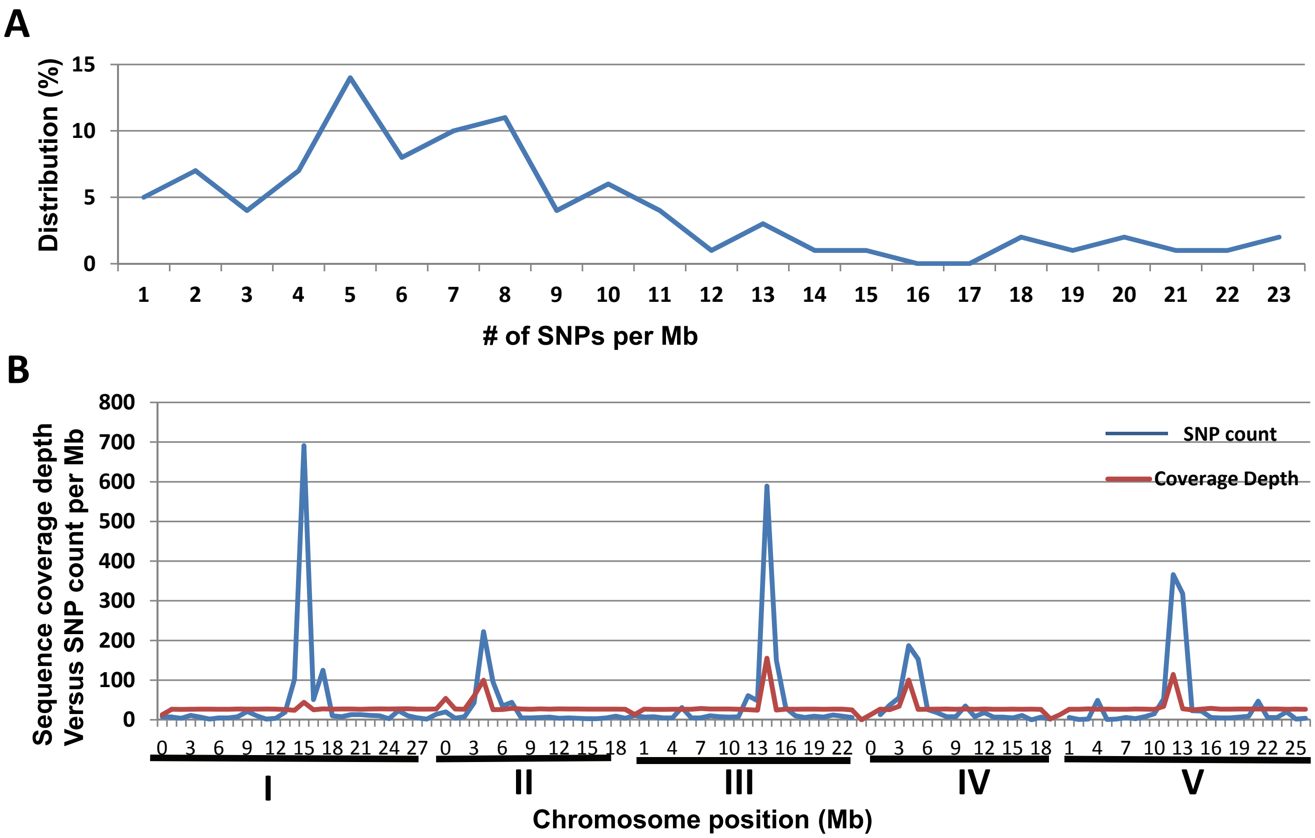

**Figure S2 SNP distribution along the chromosomes. (A) Distribution of SNP count per Mb.** Shown are the number of SNPs identified by SAMtool per Mb (X Axis) and the percentage of chromosome regions with that number of SNP count (Y Axis). The average SNP count is 8 per Mb across all regions. (B) The red line shows sequence coverage depth (sequence reads per site) and blue line shows the SNP count (number per 1 Mb sliding window). Several regions of chromosomes appear to have a high SNP count and most of them correlate with a high coverage depth, indicating a mis-calling of SNPs at the repetitive regions.