Supplementary Figure 1. Zygosity of the evolved mutations. (A) Criteria to classify heterozygous and homozygous mutations. On the x-axis is the allele frequency and on the y-axis is the read depth for each variant called (mean=49X). The red dotted line indicates the cut-off to call homozygous mutations with *p*-values < 0.001. Only 6% of the evolved mutations are homozygotes. We call inconclusive variant if the sequencing depth is below 0.9. (B) Distribution of evolved mutations colored by zygosity. There is an enrichment of homozygous mutations on Chromosome XII. Centromers are represented with a black horizontal line.