

Figure S1: HMY7 Sequence. Read depth (A) and allele frequency (B) after aligning to the *S. cerevisiae* reference genome. Reads were filtered for a quality score above 50 (in Freebayes) and read count between 50-250. There is evidence for aneuploidy at chromosomes 1 and 6, and there appear to be regions of loss of heterozygosity (LOH) on chromosomes 2, 12 and 15. The LOH region on chromosome 12 was previously reported (Magwene et al. 2011)

