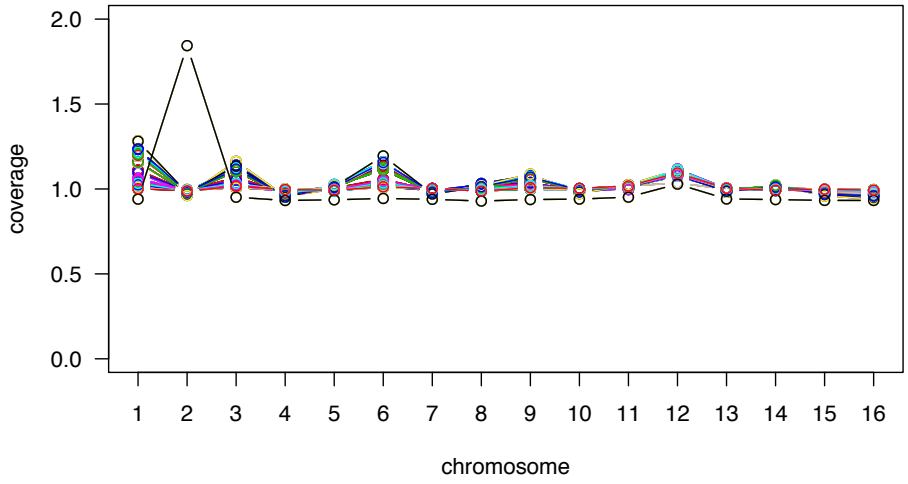

Figure S1 Relative coverage of each chromosome from genomic alignments. Using the Illumina genomic sequence data, the total coverage for each chromosome was calculated as the proportion of sequenced sites mapping to a particular chromosome relative to the proportion of known mapped sites located on that chromosome within the yeast reference genome (as reported by configureBuild.pl in Illumina's CASAVA-1.8.0 package). Examining the coverage data for each chromosome from each BMN line (each line is plotted with a unique colour) indicates only one aneuploidy event - an extra copy of chromosome 2 in BMN27.