Figure S5: Copper tolerance, as measured by $IC_{50}$ after 24 hours of growth in the Bioscreen C for specific spores. Lines were chosen because they had low $CUP1$ copy number and carried either an extra copy of chrII (CBM2 lines), a mutation in $MAM3$ (CBM14 lines), a mutation in $MLP1$ (CBM25 lines), or a mutation in $VTC4$ (CBM34 lines). All mutant lines had a significantly higher $IC_{50}$ than either of the BY controls, and all spores had a significantly lower $IC_{50}$ than their CBM parent. Horizontal bars indicate statistical comparisons, where an asterisk (*) above a bar indicates statistical significance ($p < 0.05$). Among the spores carrying the same allele, only the CBM25 spores differed significantly from one another in $IC_{50}$, and only marginally so if corrected for multiple comparisons. Note that CBM25 t1c also carries the mutation in $ENA5$. Vertical bars represent 95% confidence intervals.