

**Suppl. Figure 3.** Estimation of copy number variation (CNV) and aneuploidy across the evolved clones. Each horizontal band represents a single clone, with points indicating the estimated coverage across chromosomes in windows of 5000 bp and assuming diploidy. All values are standardized relative to the ancestral strain. Dots are colored according to relative estimated ploidy, and the Y-axis tick mark indicates 1.0.