

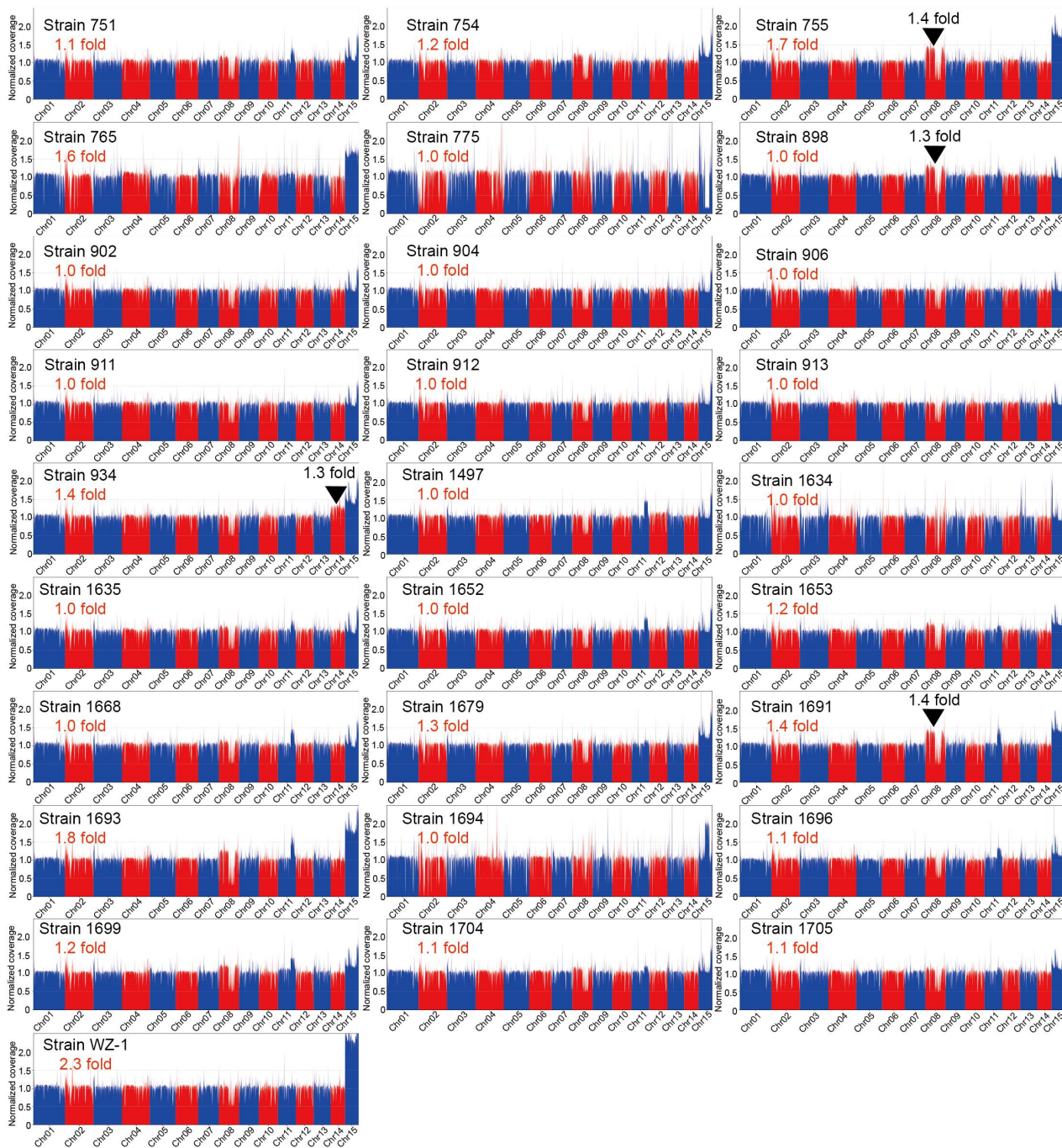


Figure S5. Normalized read depth of the remaining 28 heterokaryotic strains. Strain IDs (black) and copy number of AC (red) inferred from normalized coverage are shown at the top. CC aneuploidy events and inferred copy number are indicated by triangles.