

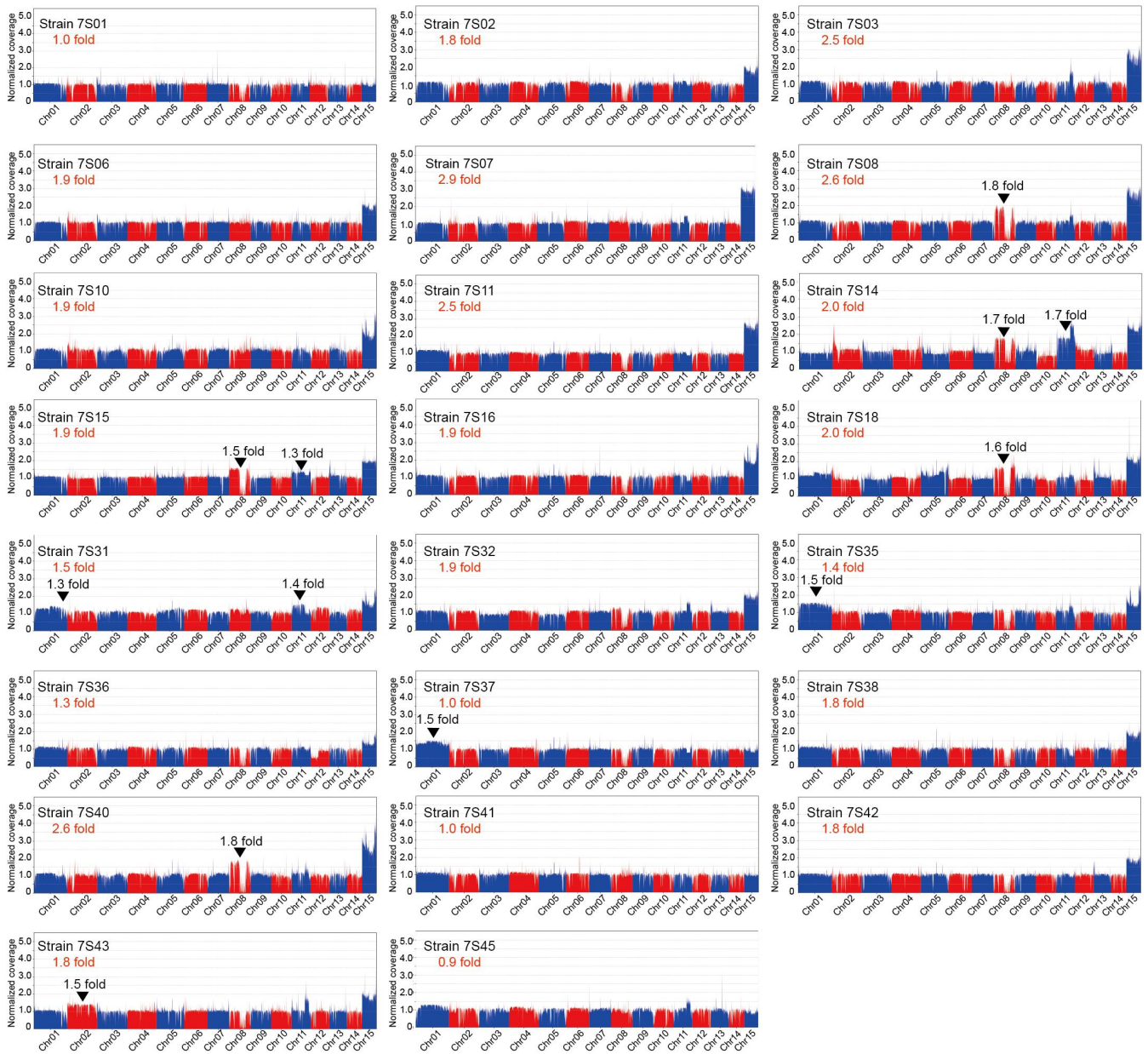


Figure S6. Normalized read depth of the remaining 23 sexual progeny derived from strain 776. Strain IDs (black) and copy number of AC (red) inferred from normalized coverage are shown at the top. CC aneuploidy events and inferred copy number are indicated by triangles.