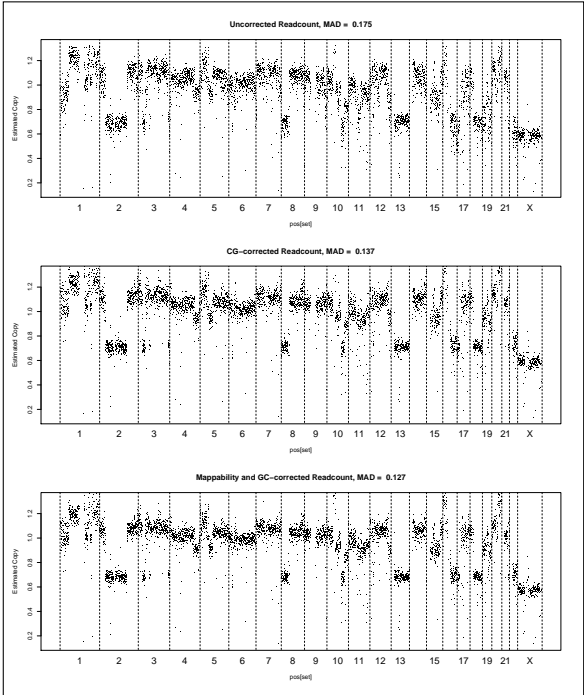
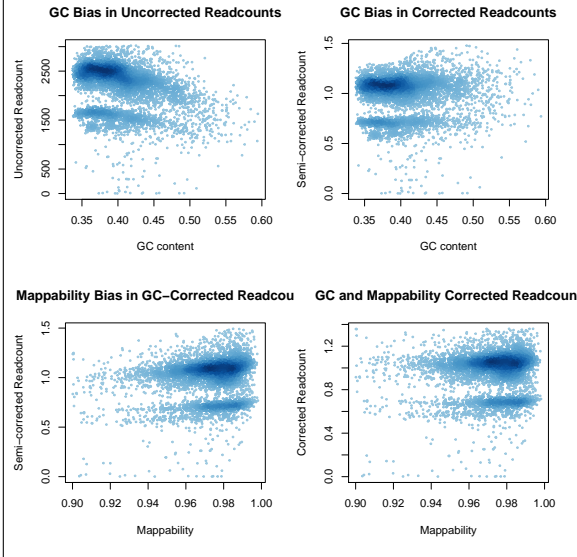


# Bioinformatics Workflow for Ultra-Low-Pass Whole-Genome-Sequencing Data

Reference genome

**bwa**  
Indexing reference genome  
`ULPWgs::index()`



Raw ULP-WGS data

