

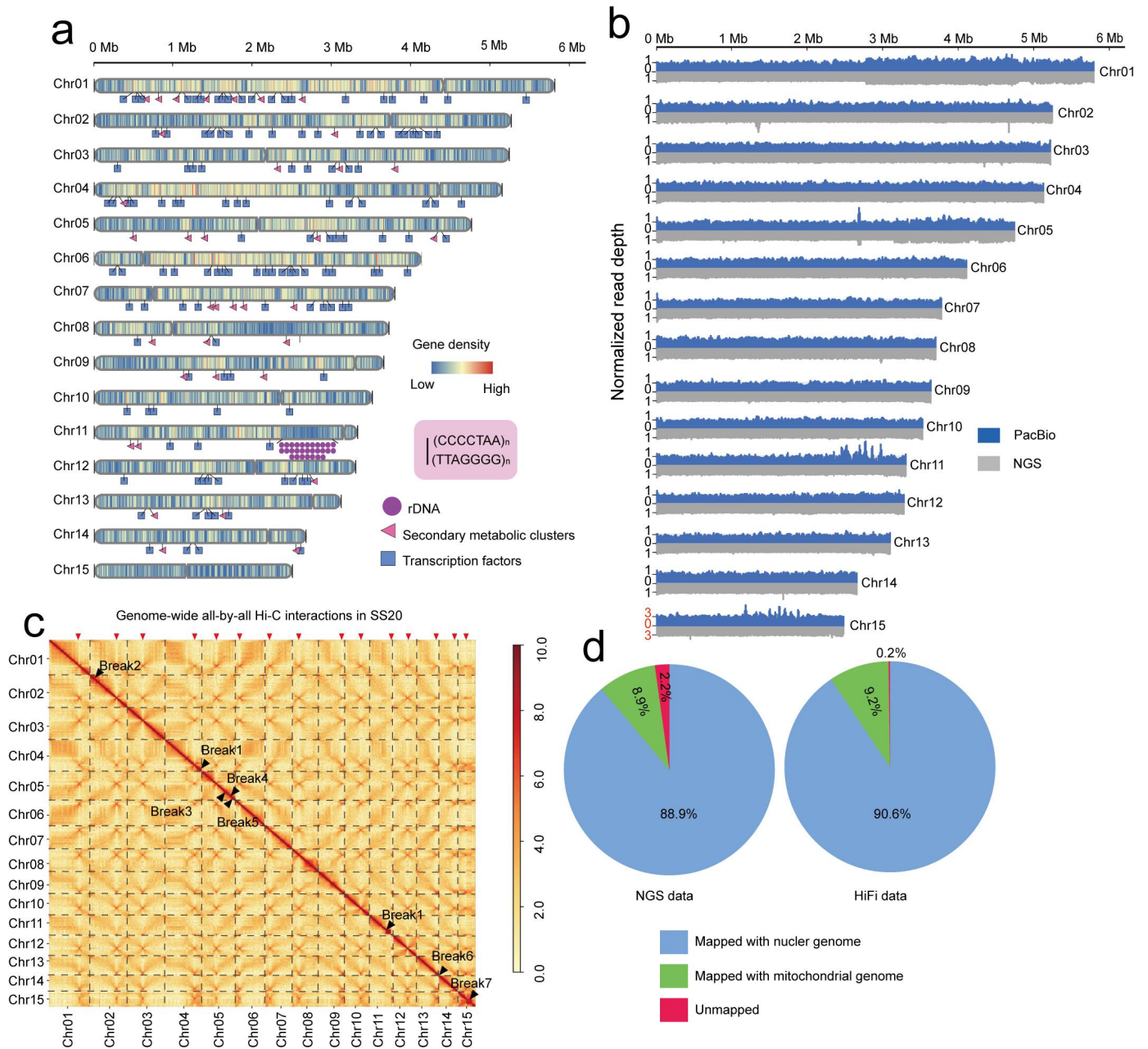


Figure S3. Overview of the SS20 genome. (a), Chromosomal structures of the newly assembled SS20 genome, showing telomeres (black lines), putative centromeres (indentations), and distributions of protein-coding genes, rDNA, transcription factors, and secondary metabolite clusters. (b), Genome-wide read coverage. Chr15 shows ~3-fold elevated read depth relative to the genome average. (c), Hi-C interaction heatmap at 50 kb resolution. Regions with the highest interaction intensities are marked by red triangles (putative centromeres). Breakpoints from the previous assembly are indicated by black triangles. (d), Mapping rates of PacBio and NGS data.