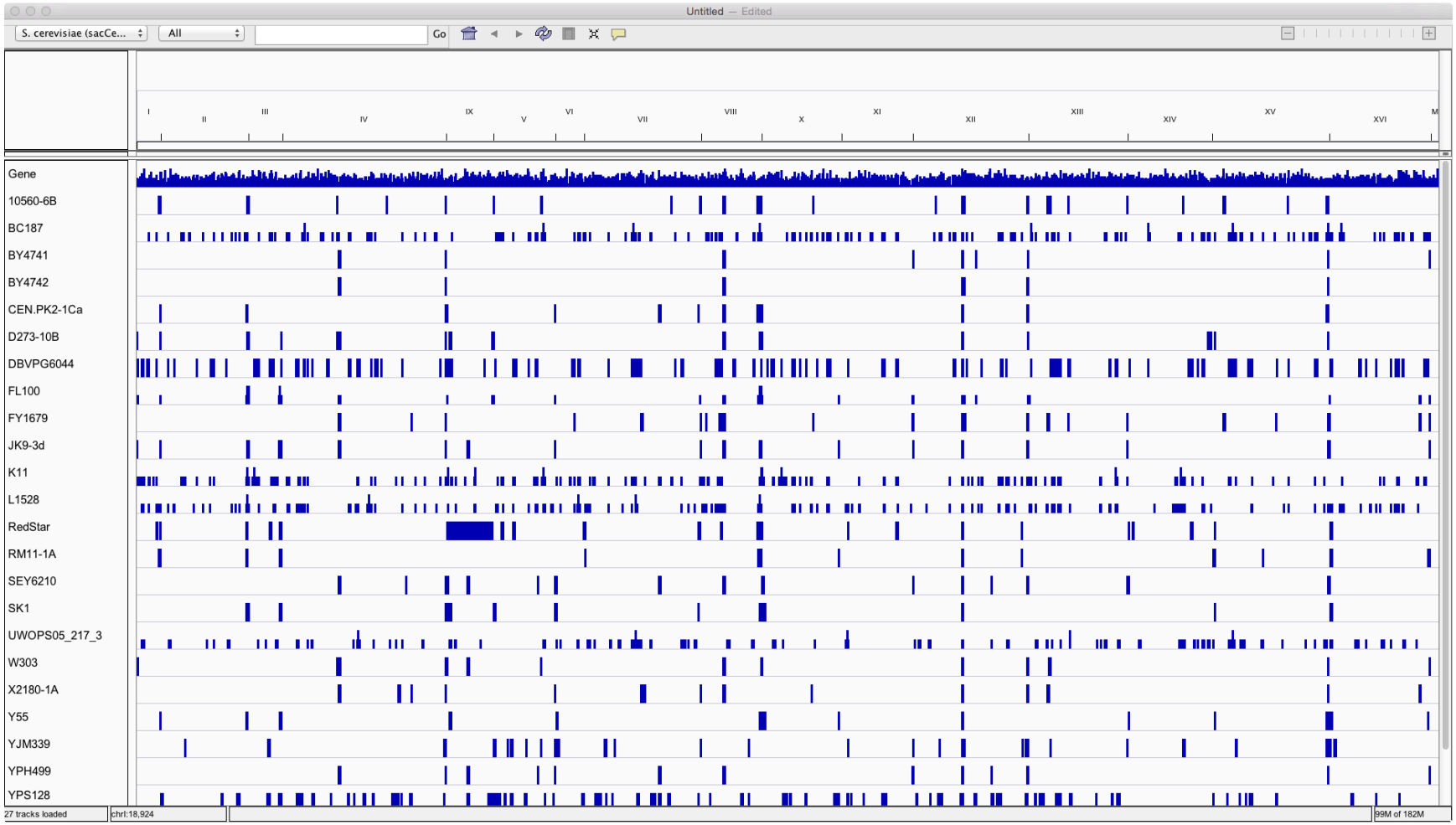

S1 Fig. Copy number variants in *S. cerevisiae*. Copy number variants (CNVs) were called by the program "CNVnator" based on read coverage depth of each strain genome relative to the reference genome (Abyzov *et al*. 2011). Genomic intervals identified as CNVs in each strain were visualized as blue boxes using the IGV (Integrative Genomics Viewer) tool (Thorvaldsdóttir *et al*. 2012).

References

Abyzov A, Urban AE, Snyder M, Gerstein M. (2011) CNVnator: an approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. Genome Res 21(6):974-84.

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