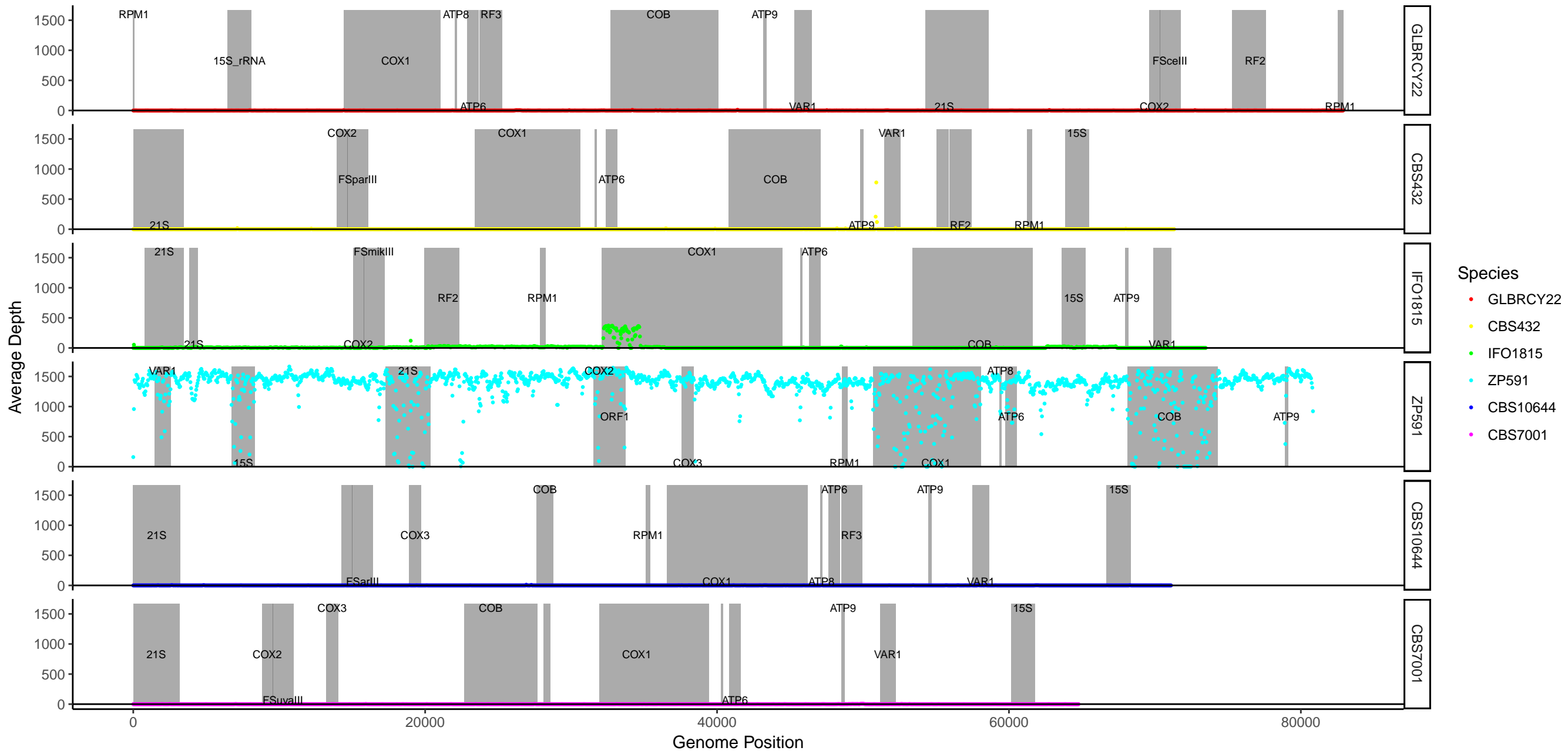


yHRWh4 Avg depth of coverage



The figure displays a genomic map of the mitochondrial genome of *Glomeribacter geophilum*, showing the distribution of genes across six different strains: GLBRCY22, CBS432, IFO1815, ZP591, CBS10644, and CBS7001. The x-axis represents the genomic position in base pairs (bp), ranging from 0 to 80,000. The y-axis represents the relative expression level in Reads Per Million (RPM).

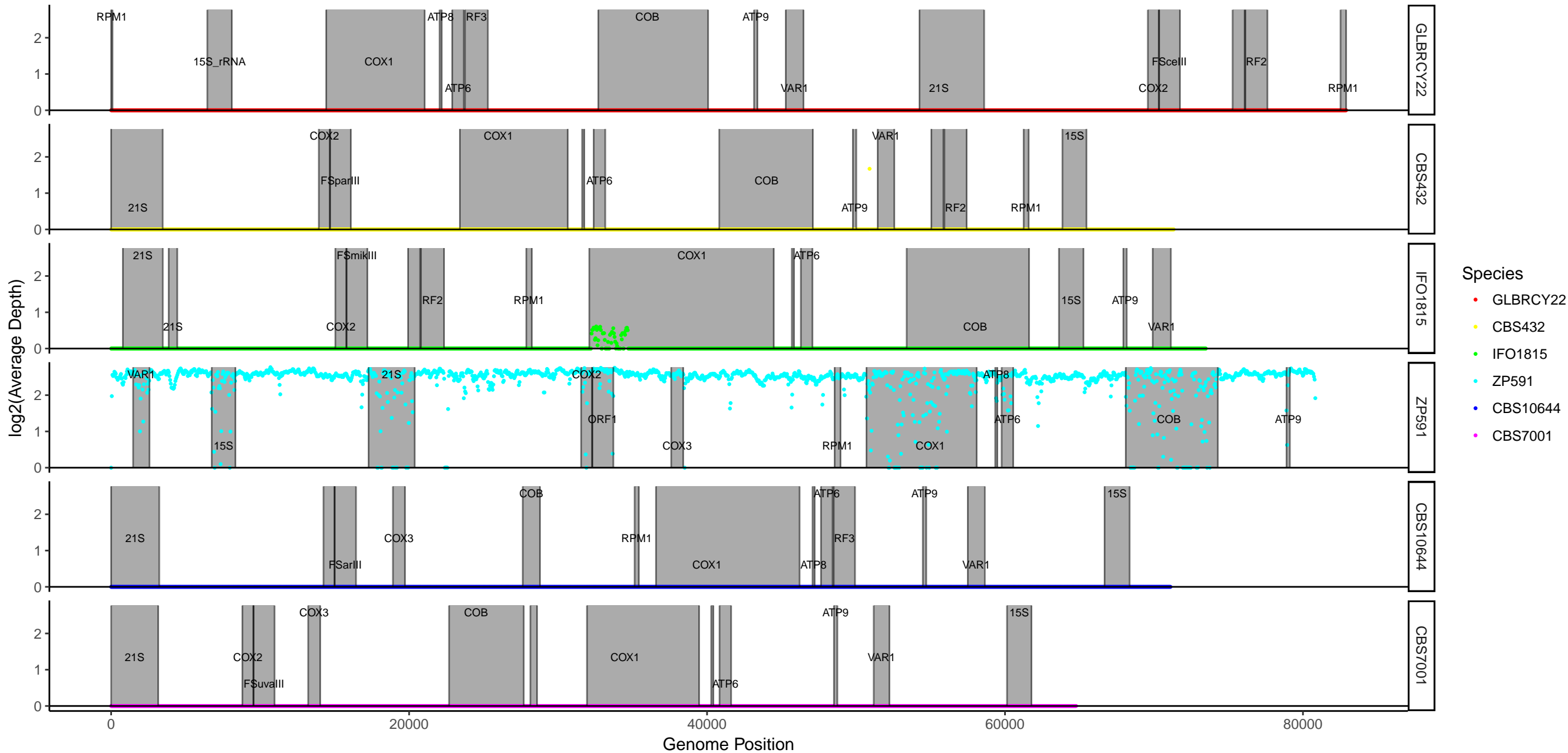
The genes identified in the map include:

- ATP6
- ATP8
- ATP9
- COX1
- COX2
- COX3
- ORF1
- RF2
- RF3
- 15S
- 21S
- VAR1
- FSceIII
- FSparIII
- FSmikIII
- FSarIII
- FSuvallI
- RPM1

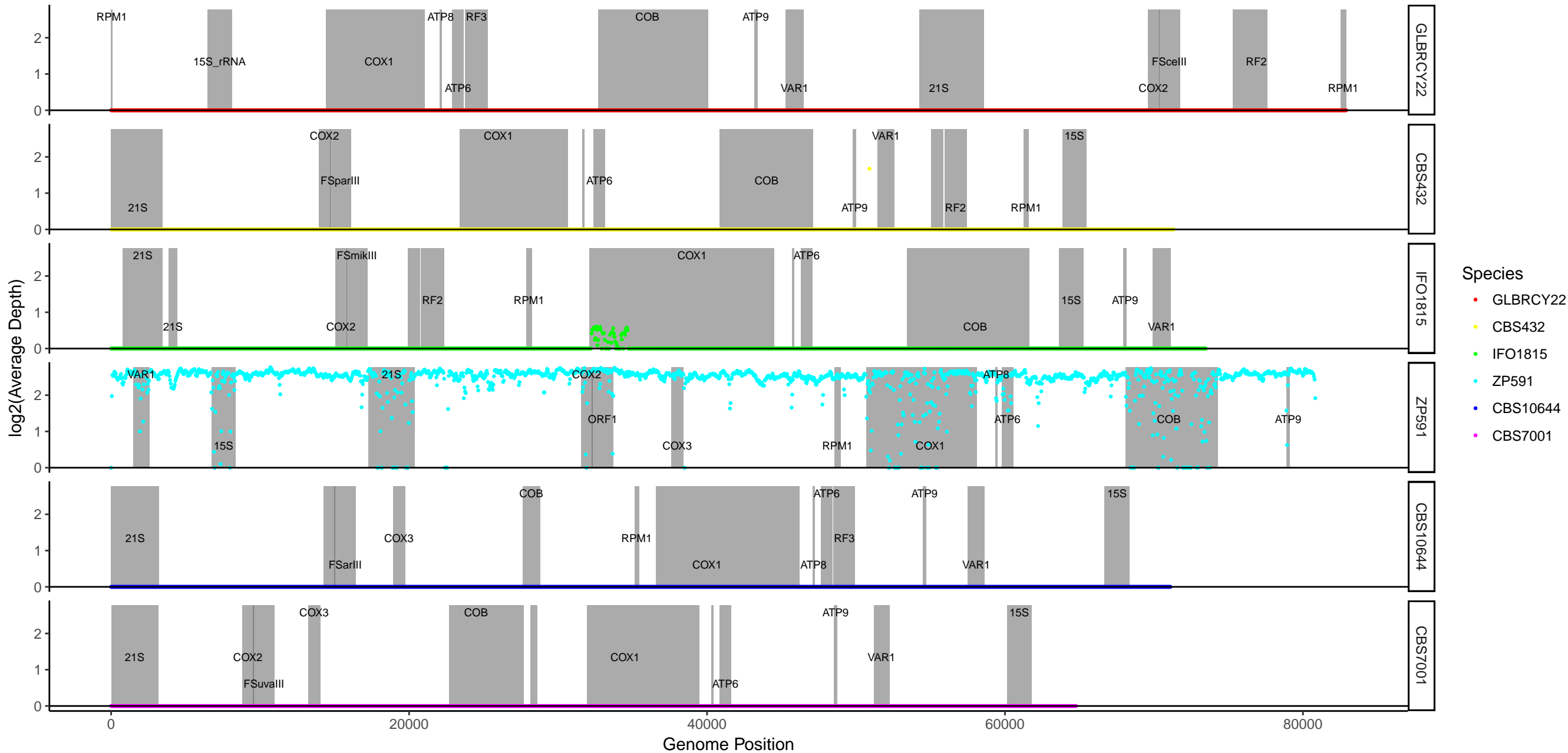
The ZP591 strain shows a distinct cyan signal track across the entire genome, indicating a specific genomic feature or expression profile. The map also includes a scale bar at the bottom indicating the genomic position in base pairs (0, 20,000, 40,000, 60,000, 80,000).

GLBRCY22
CBS432
IFO1815
ZP591
CBS10644
CBS7001

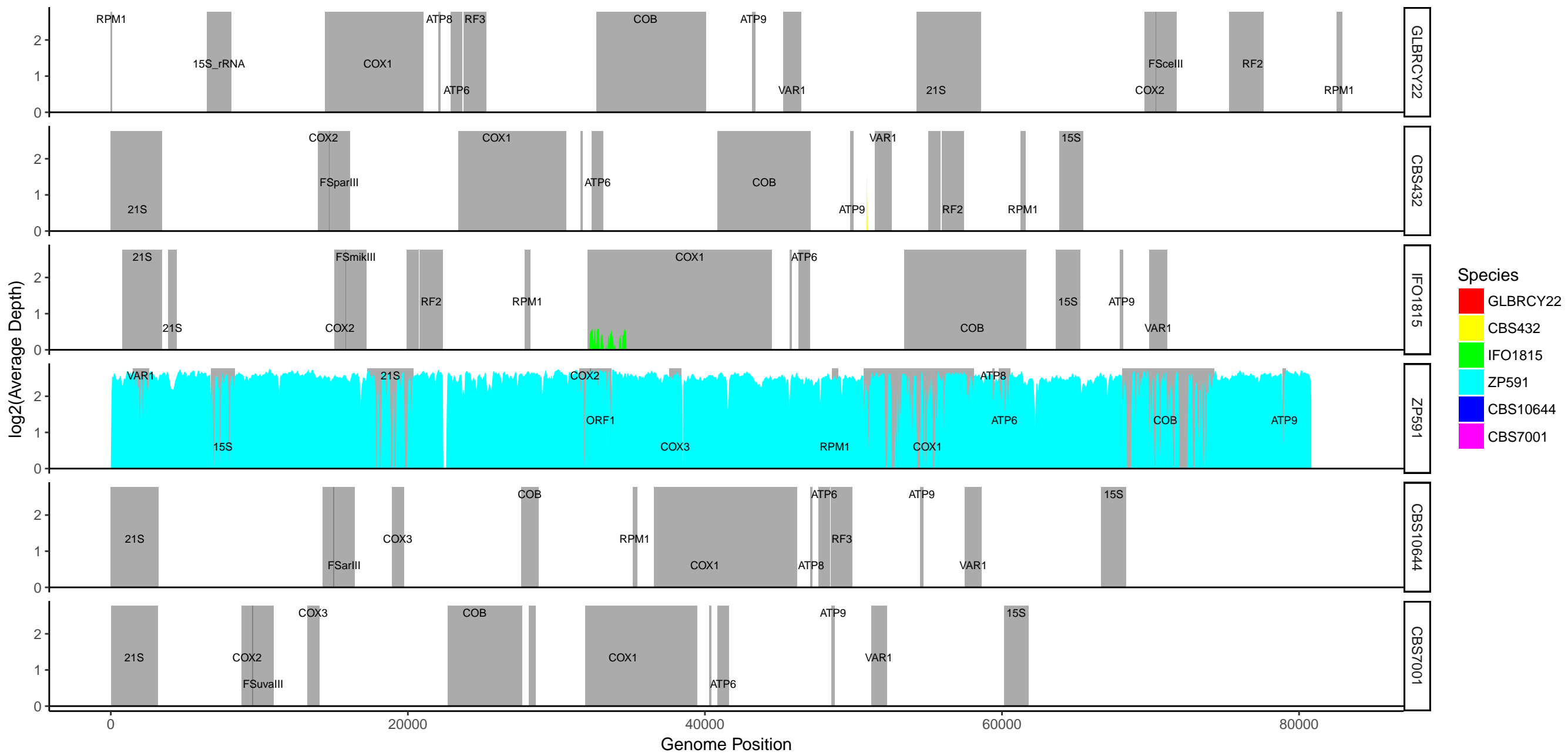
yHRWh4 Log2 Avg depth of coverage



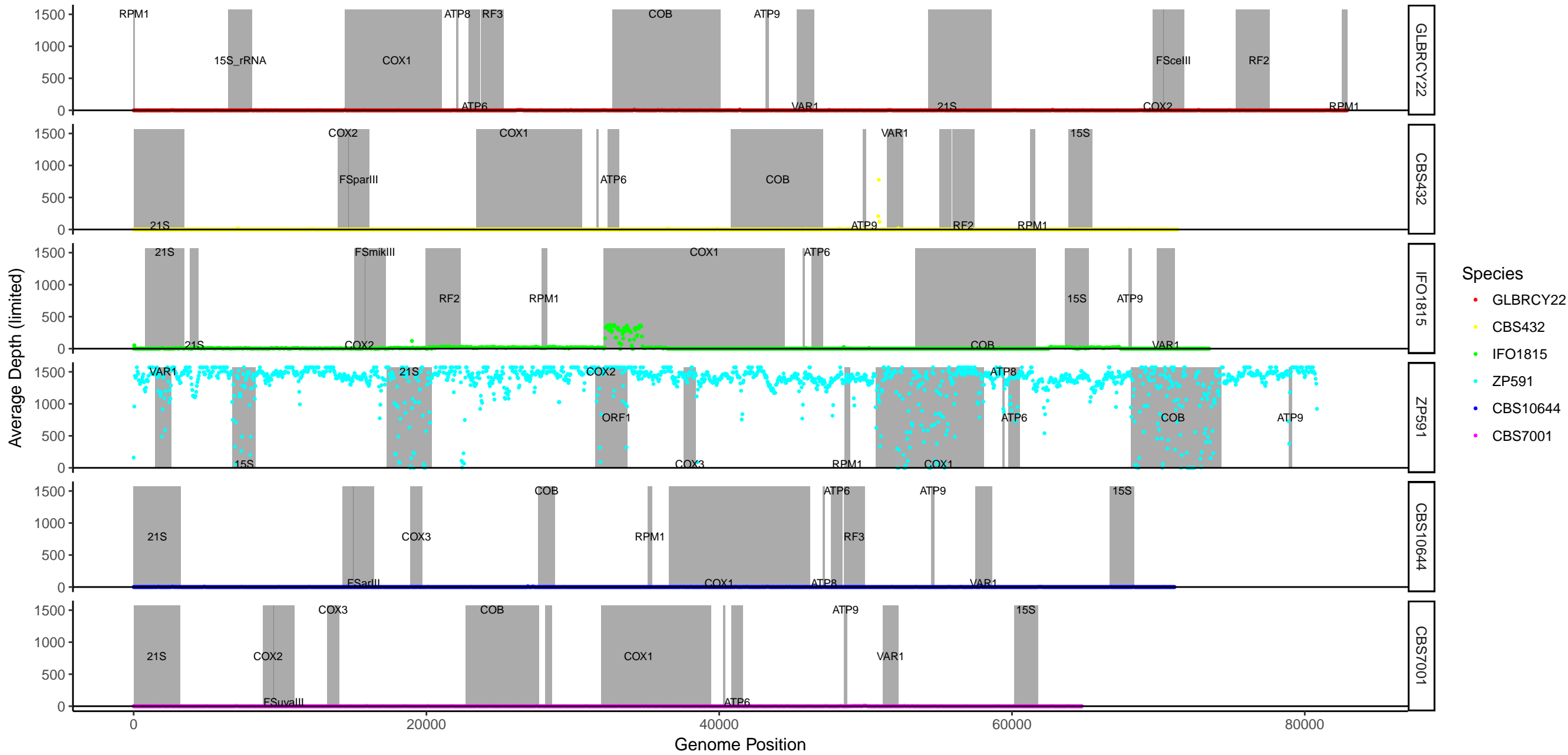
yHRWh4 Log2 Avg depth of coverage



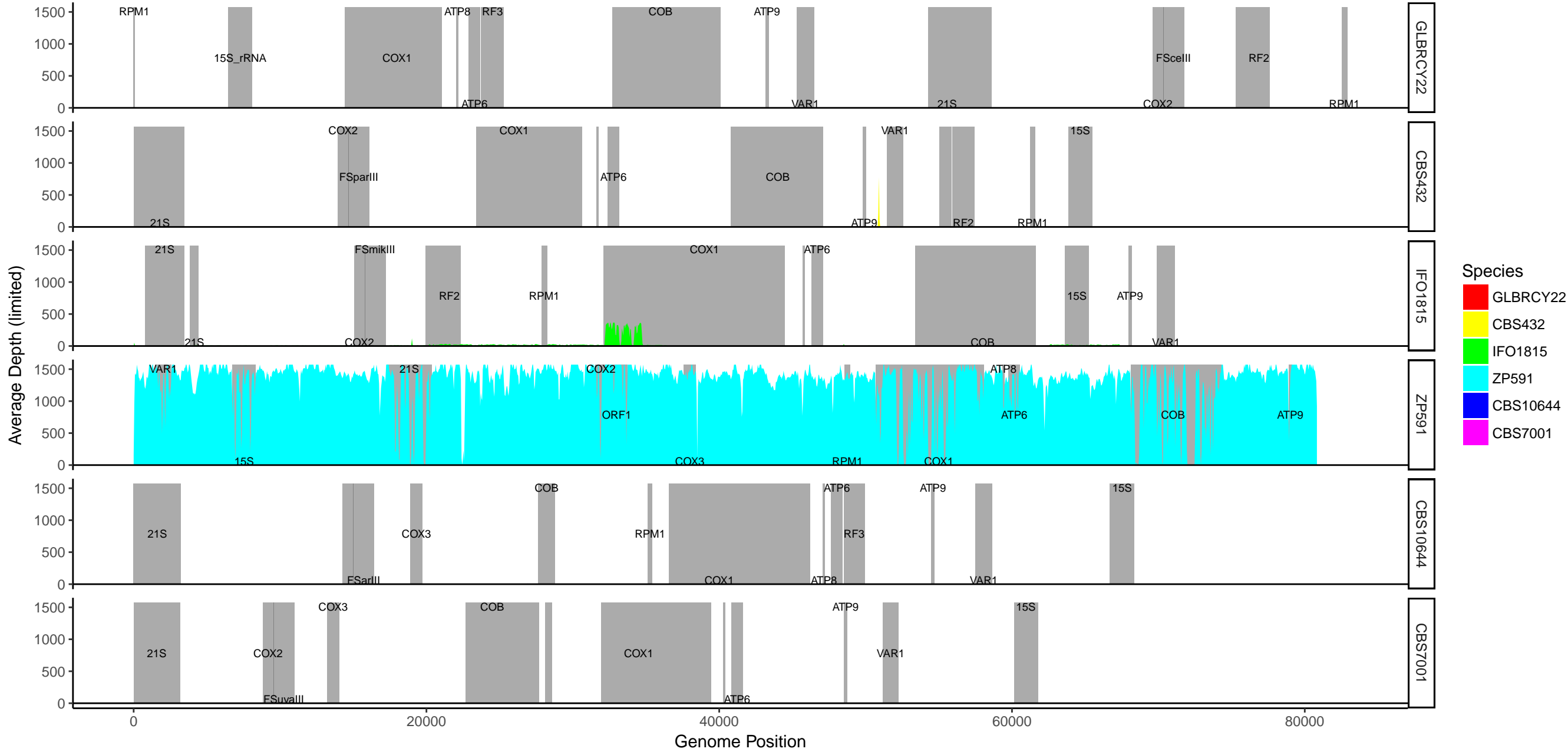
yHRWh4 Avg depth of coverage



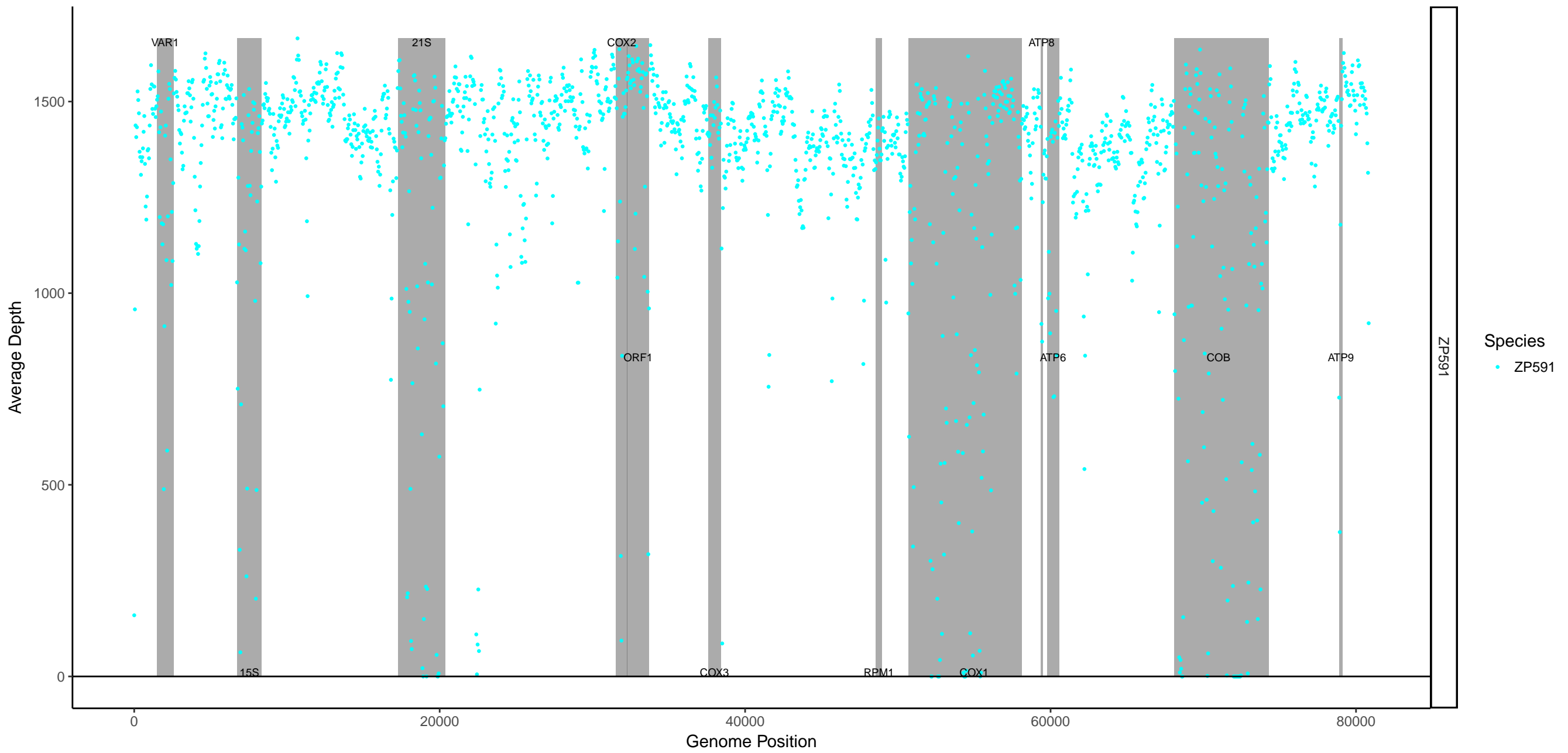
yHRWh4 Avg depth of coverage



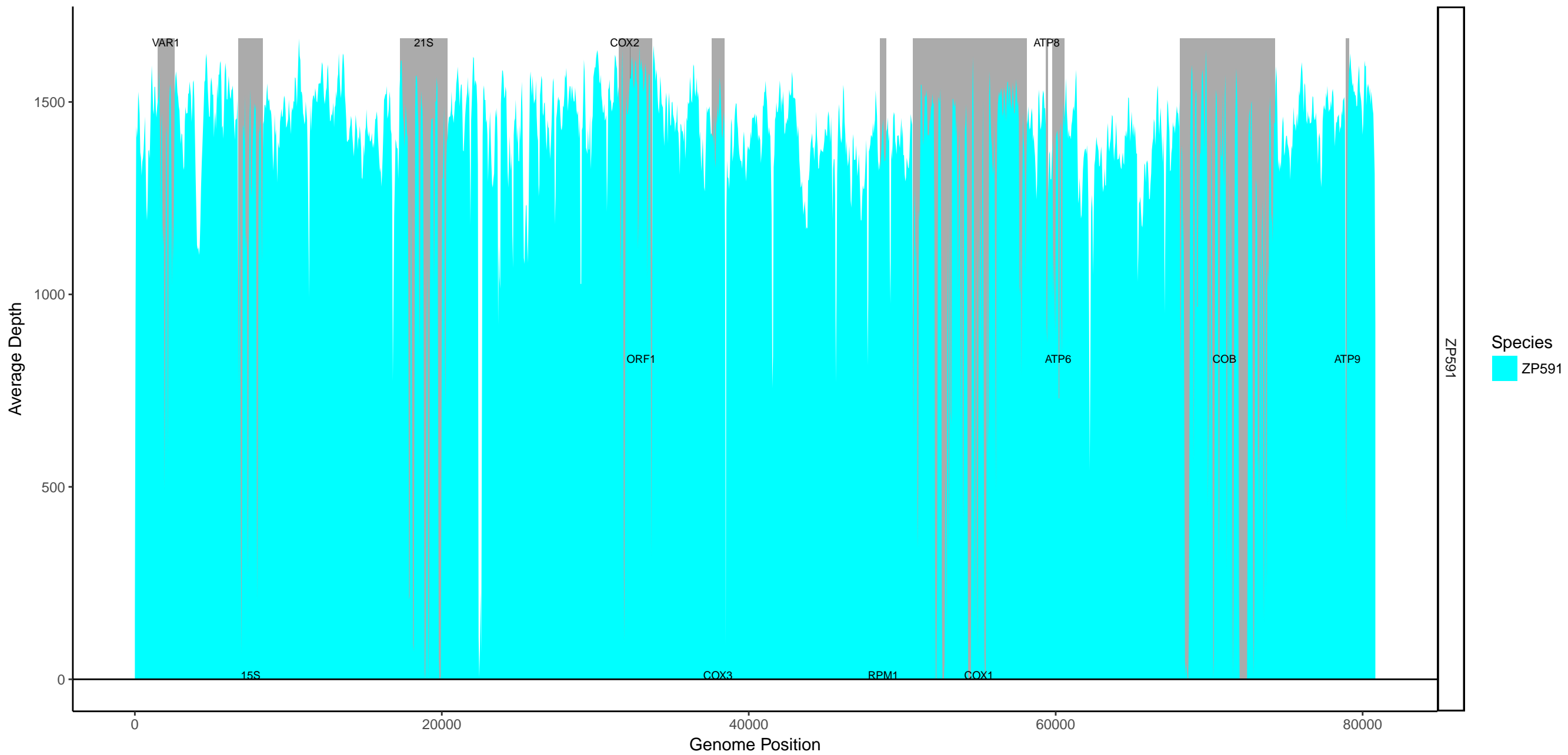
yHRWh4 Avg depth of coverage



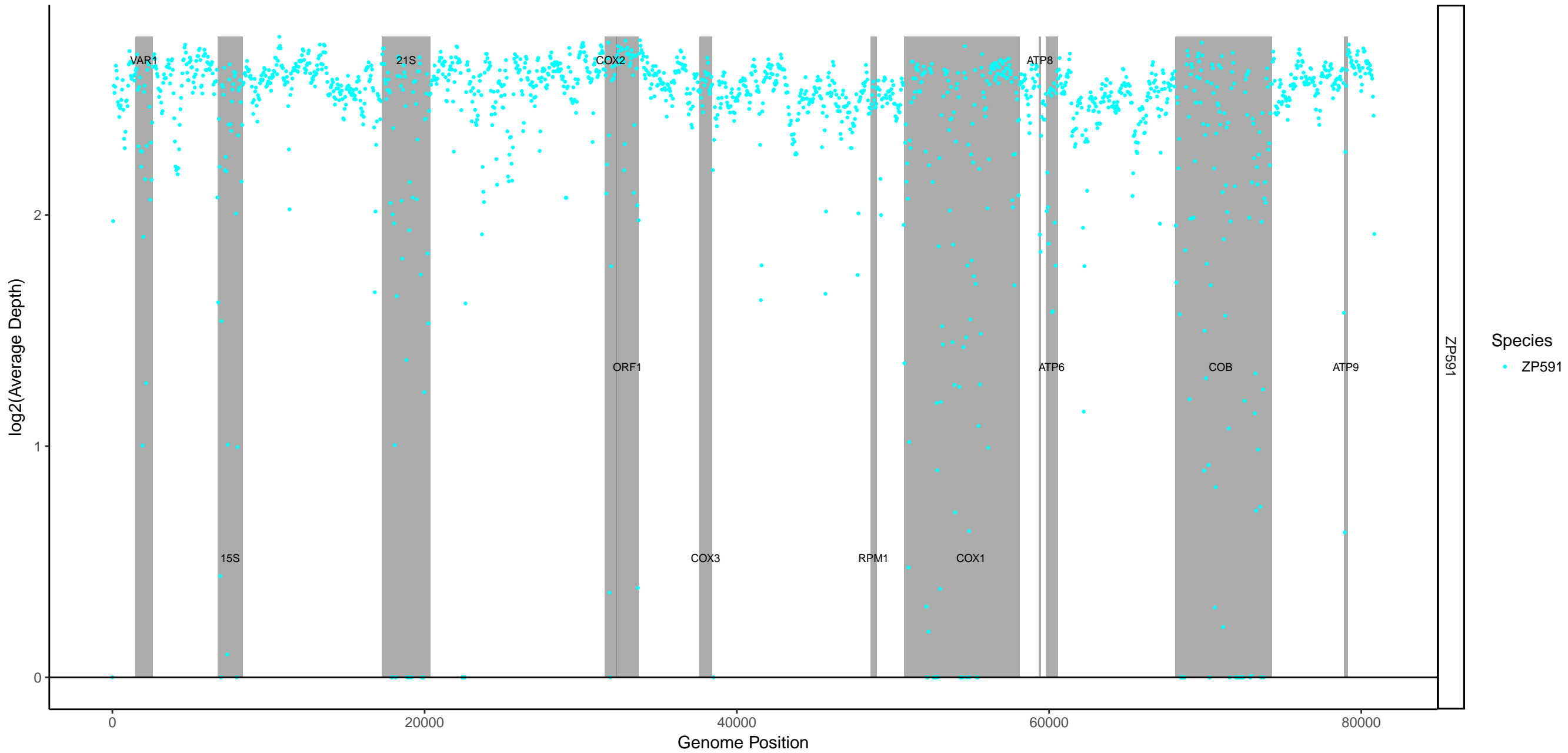
yHRWh4 Avg depth of coverage

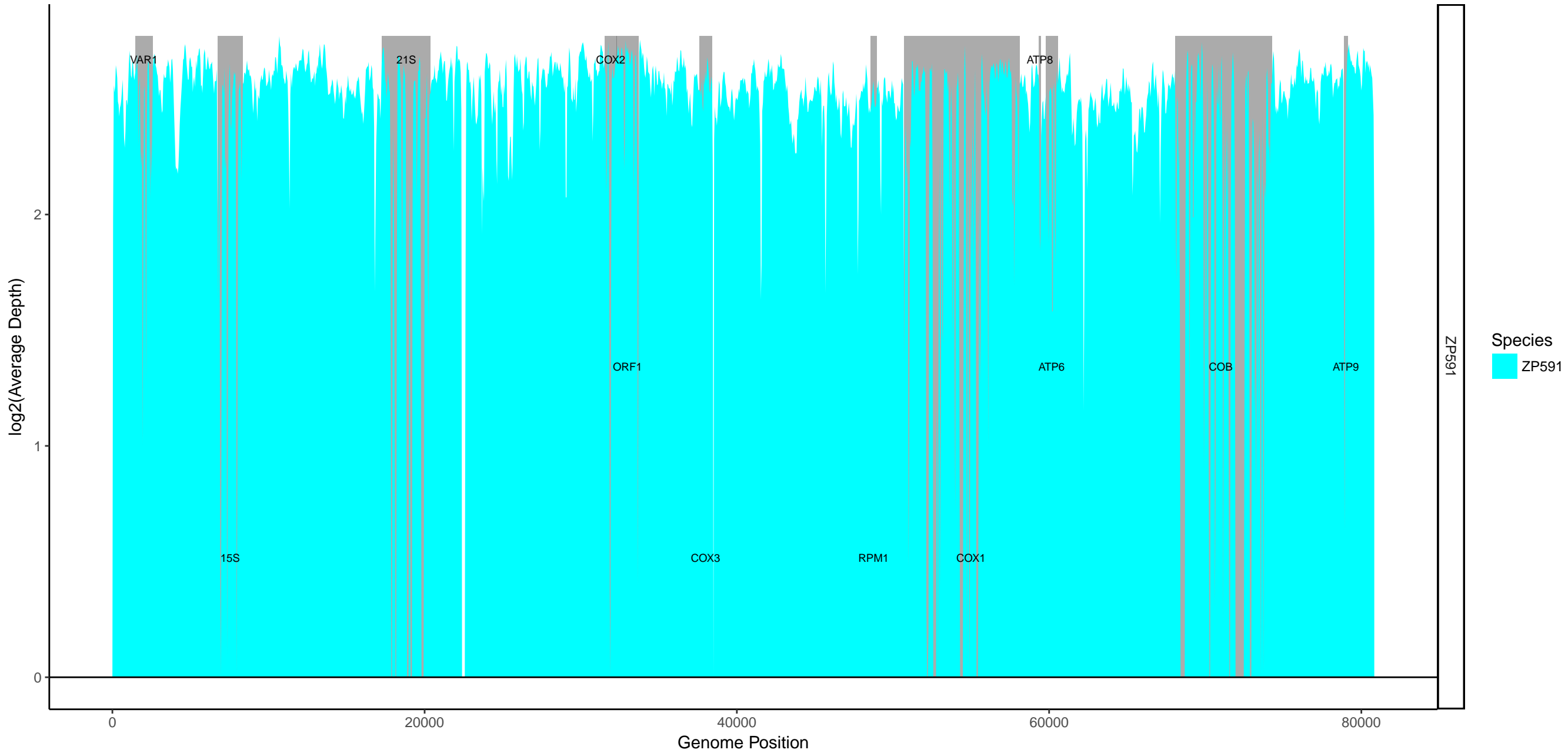


yHRWh4 Avg depth of coverage

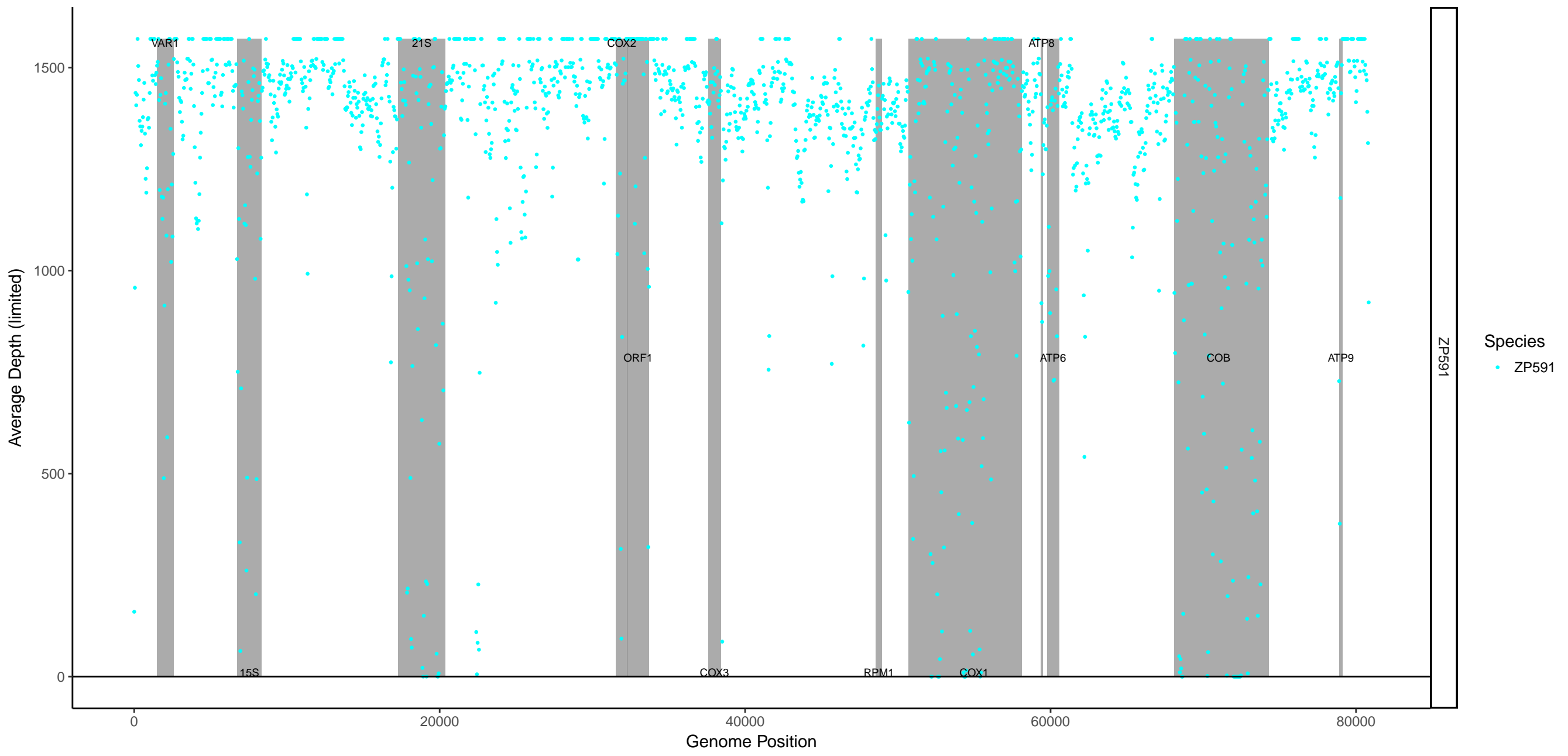


yHRWh4 Avg depth of coverage





yHRWh4 Avg depth of coverage



yHRWh4 Avg depth of coverage

