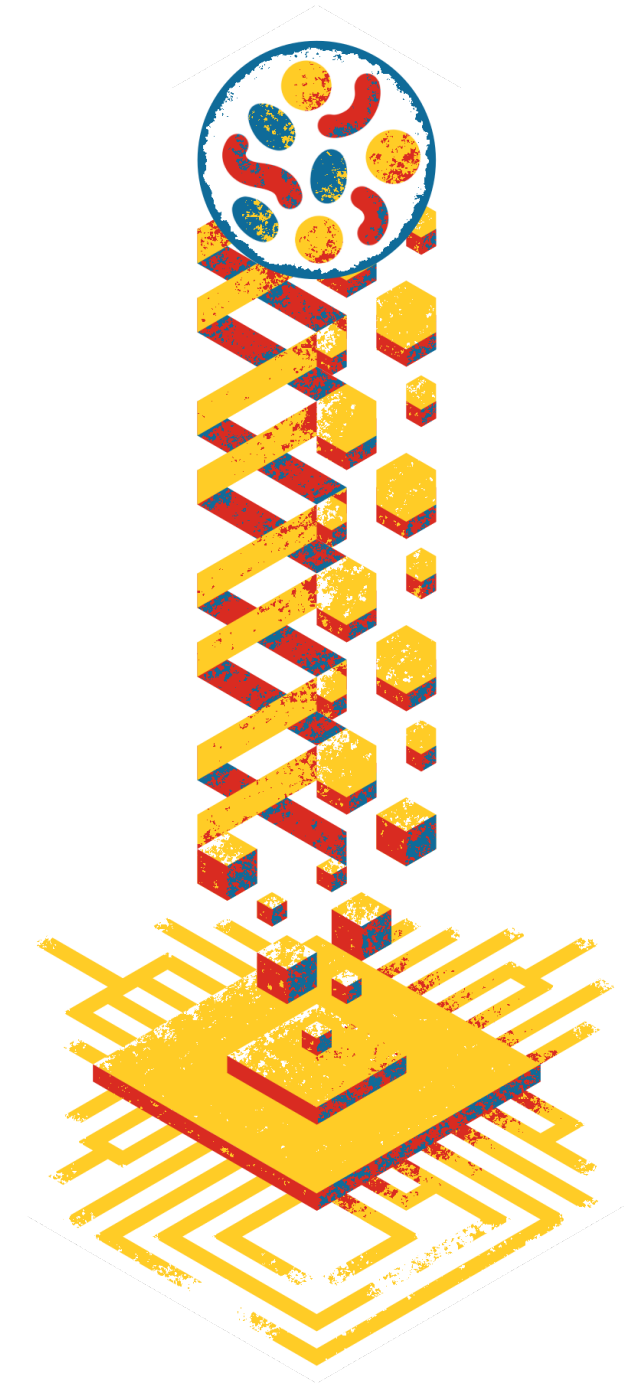
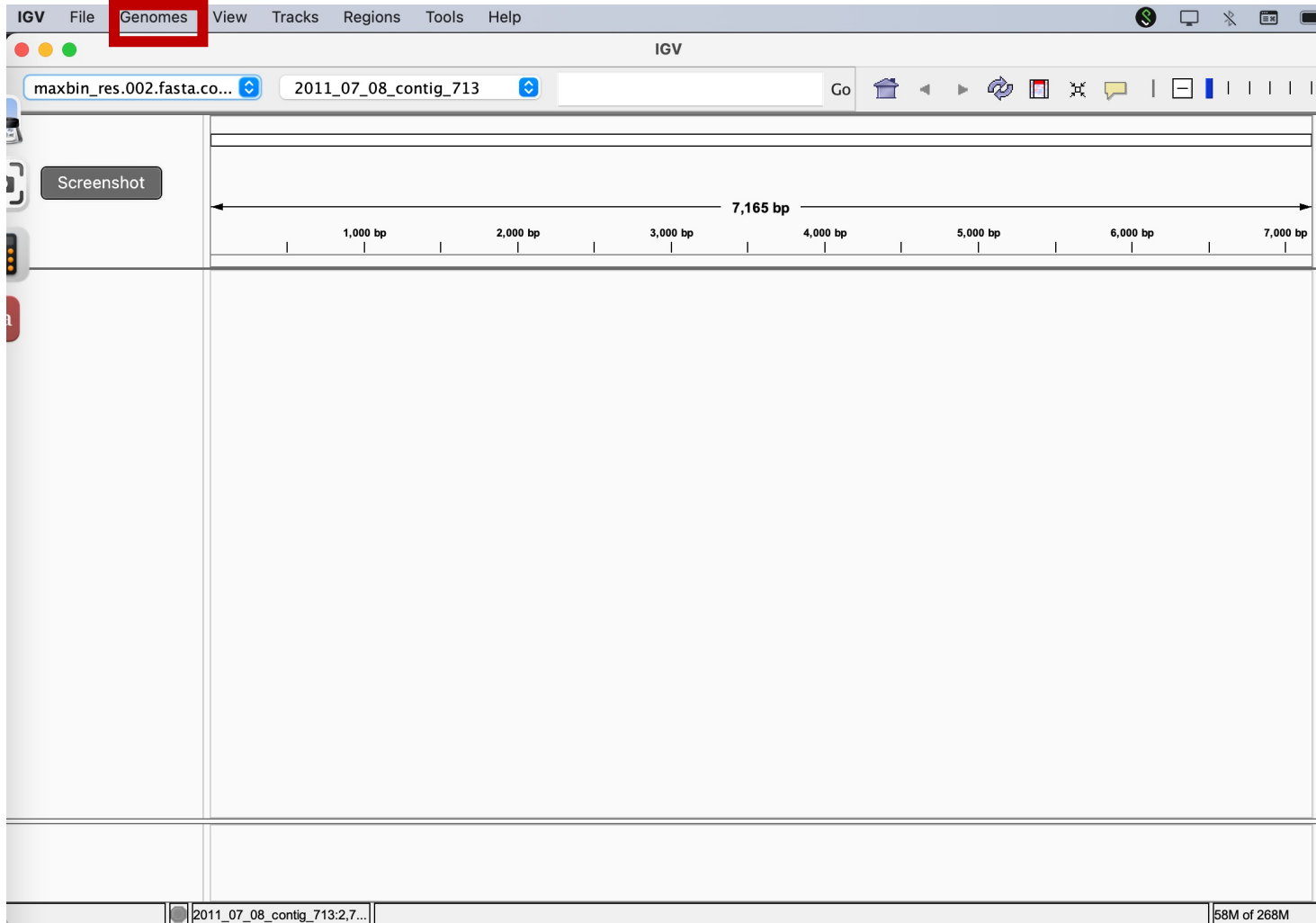
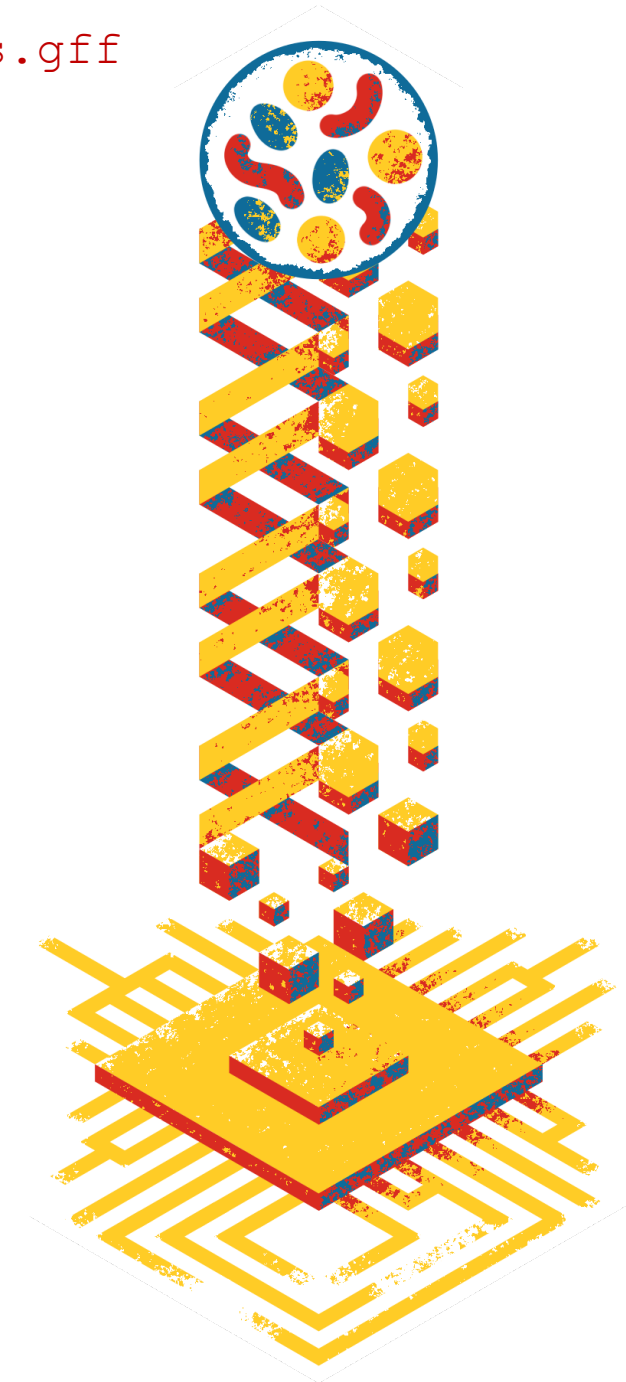
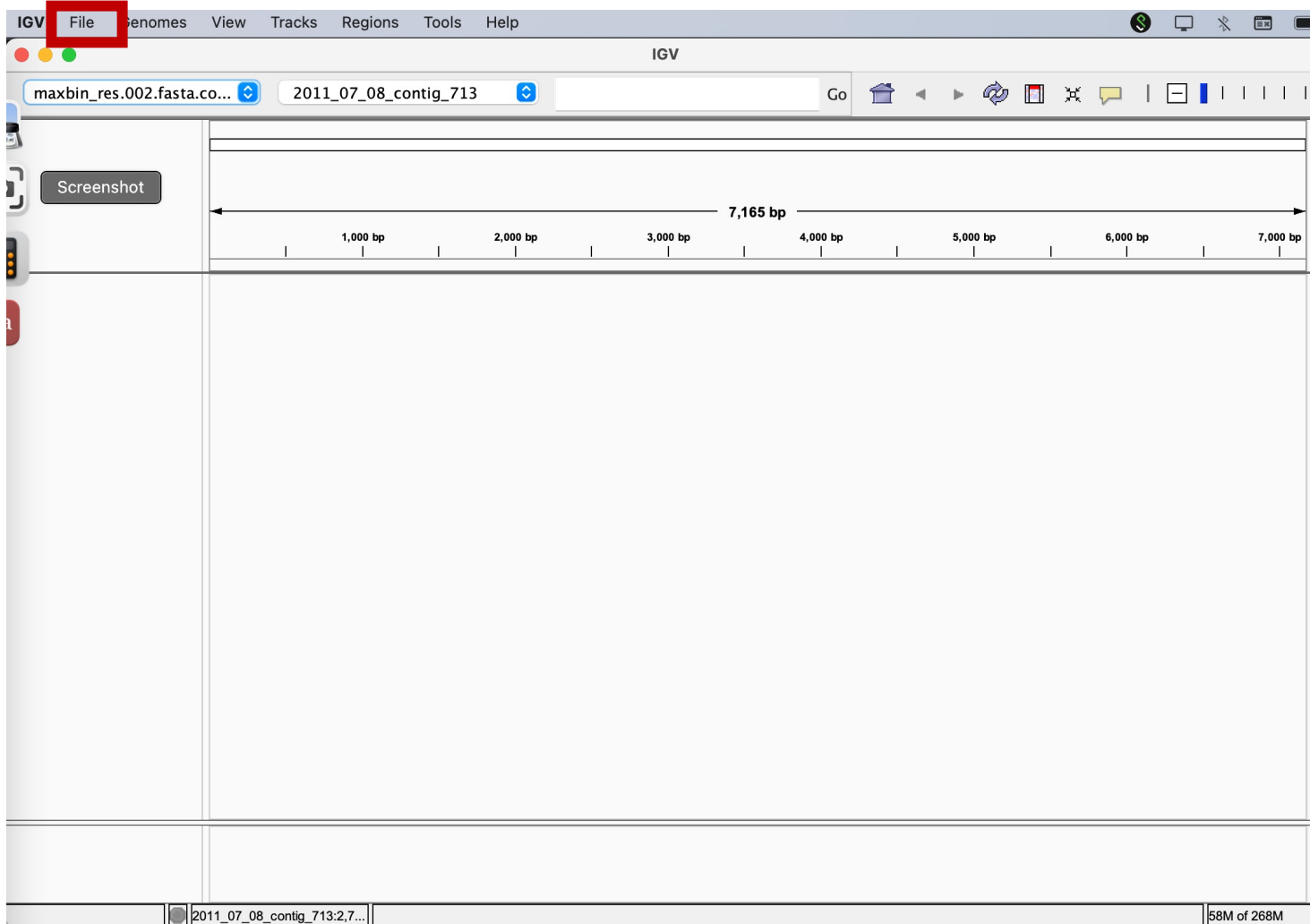
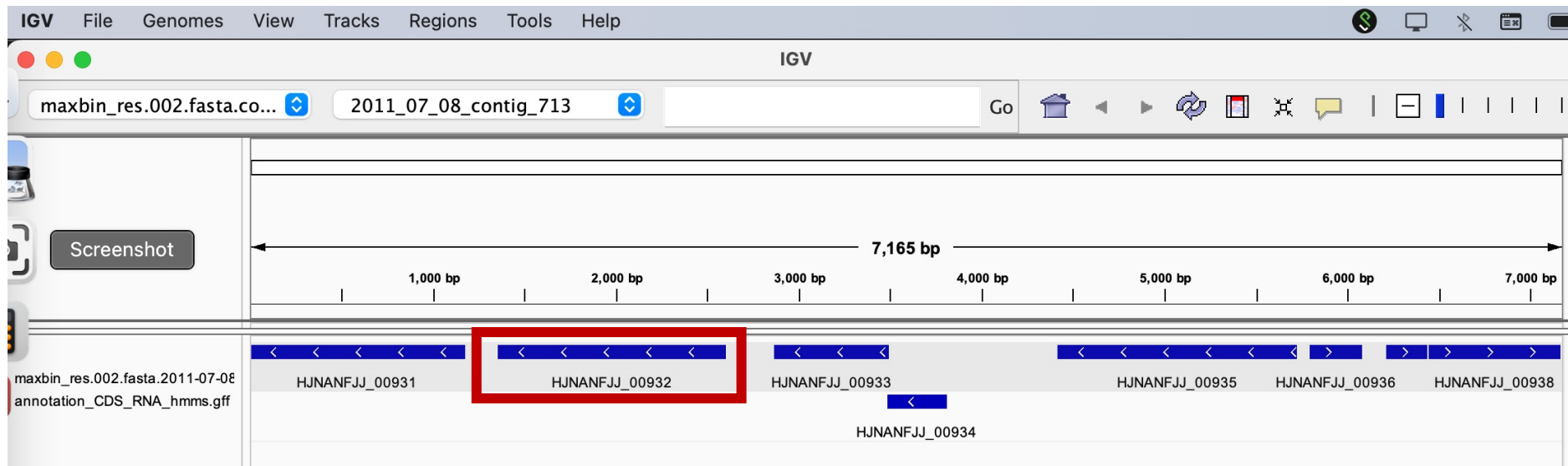


Load genome from file -> select the <MAG>.contigs.fa -file

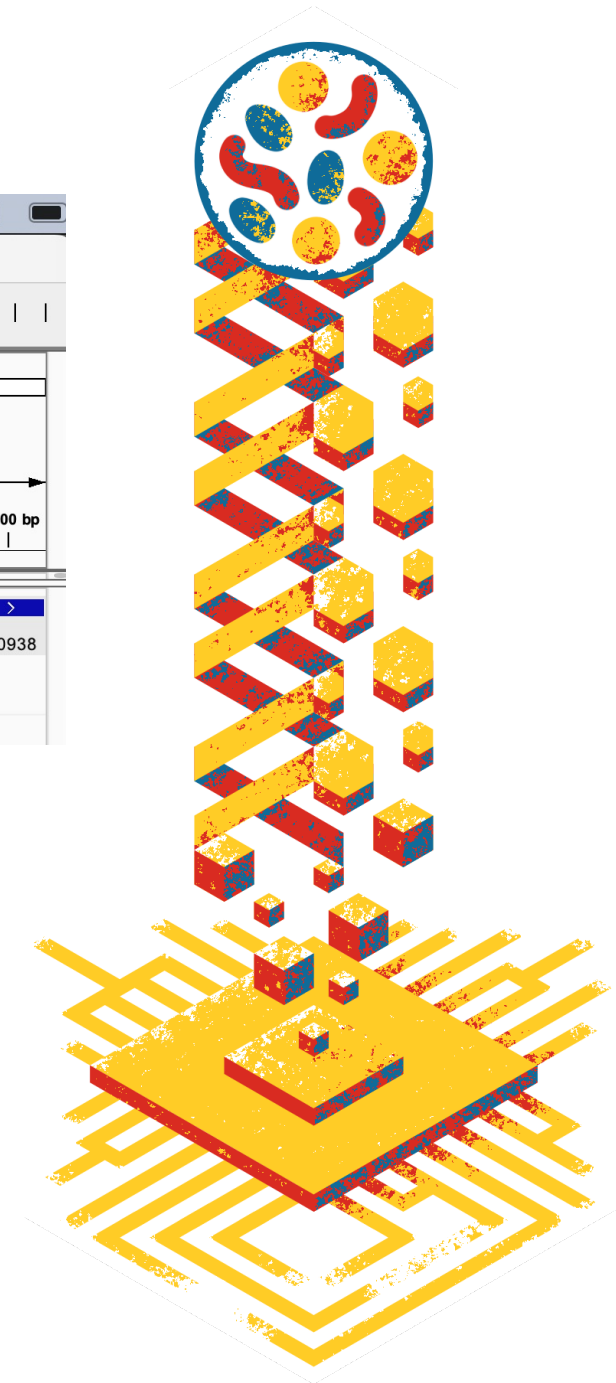


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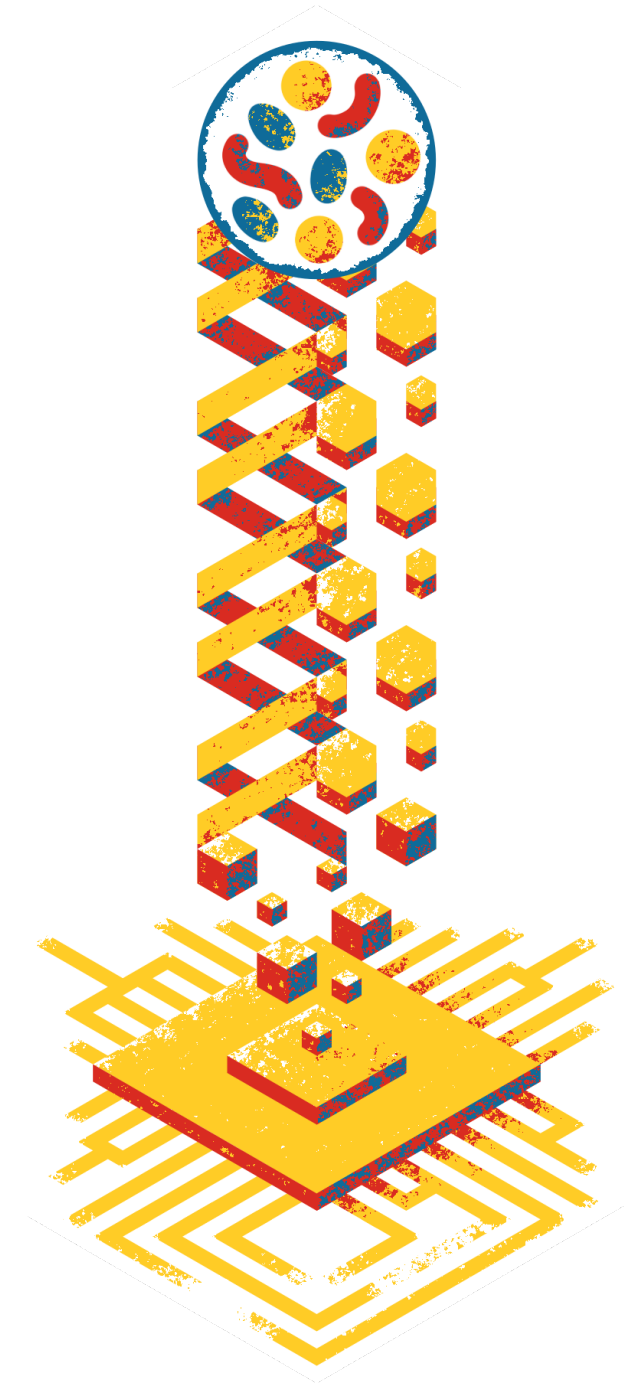
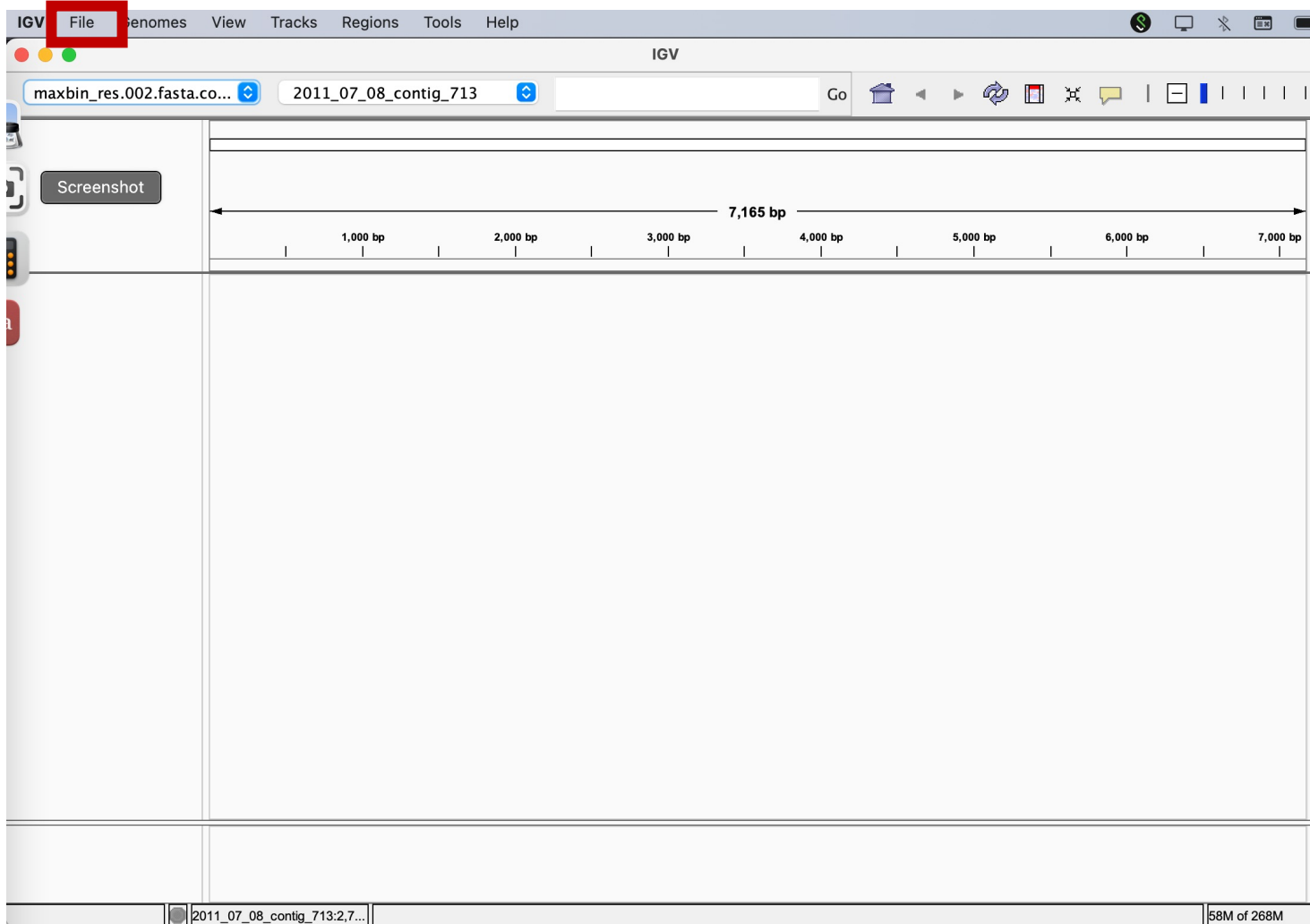


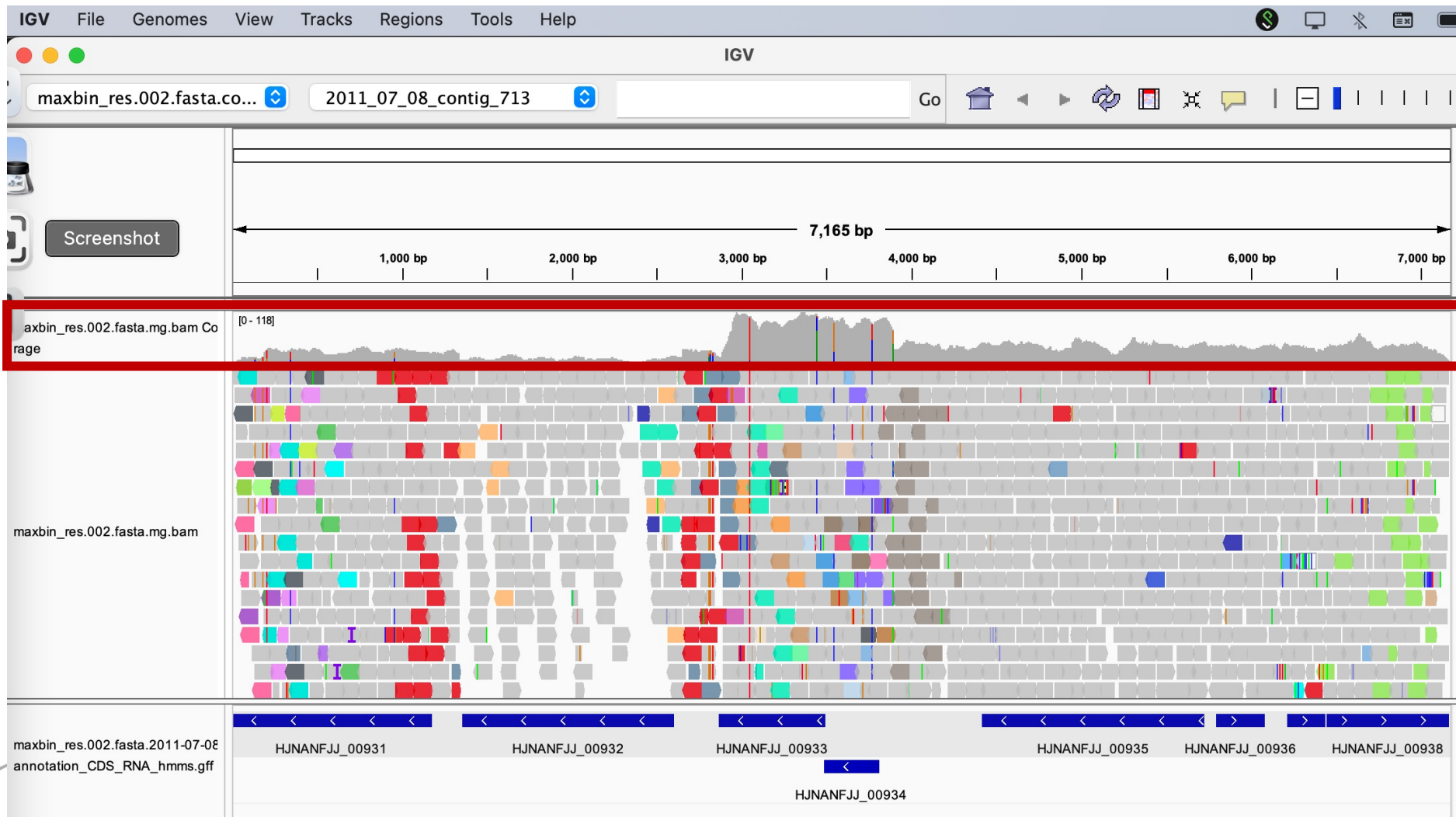


gene representation (arrows are transcription direction),
hover over it to get further annotation



Load from file -> select <MAG> .mg .bam





pile-up of the reads
(coverage depth per
position)

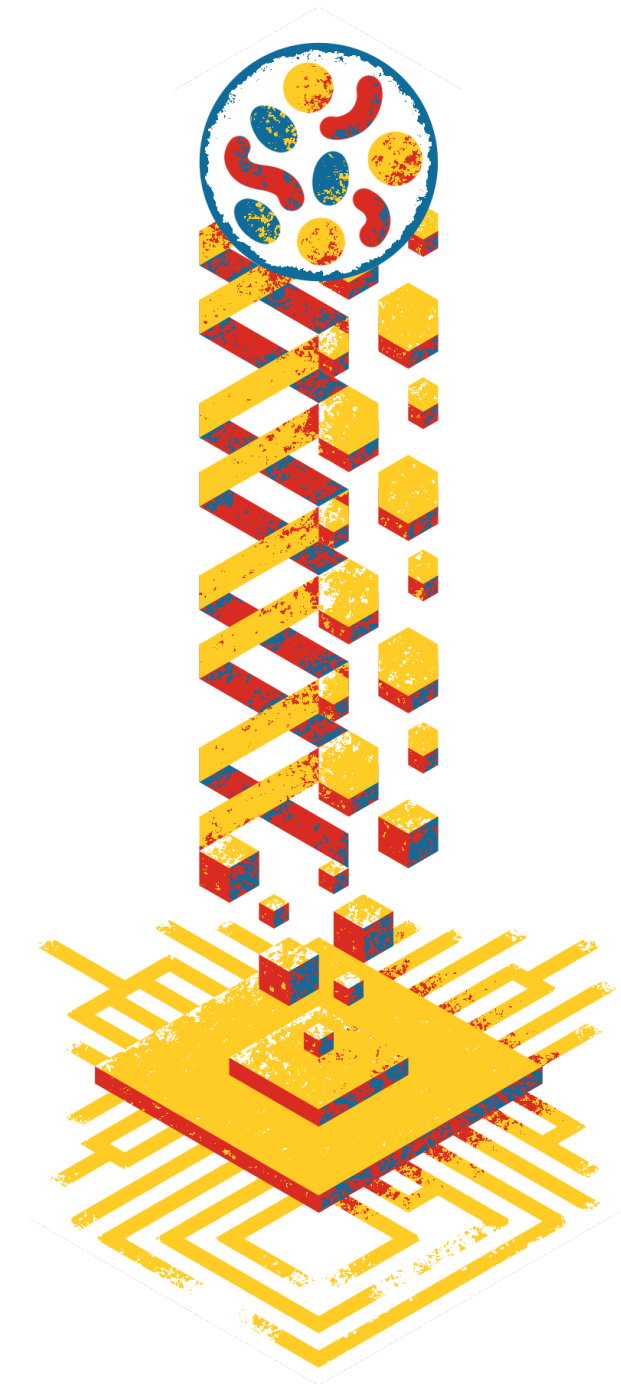
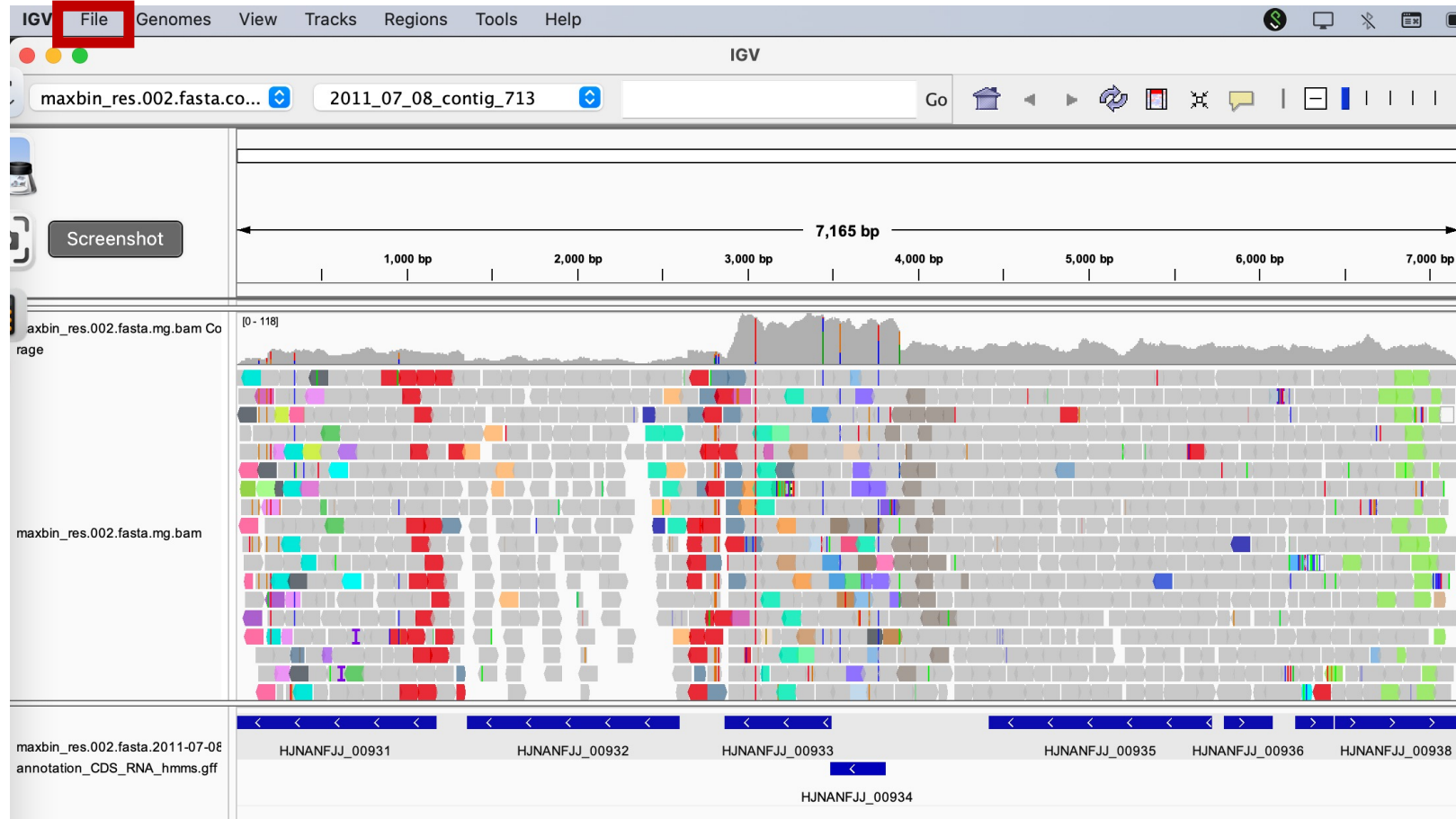
EMBO

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the reads

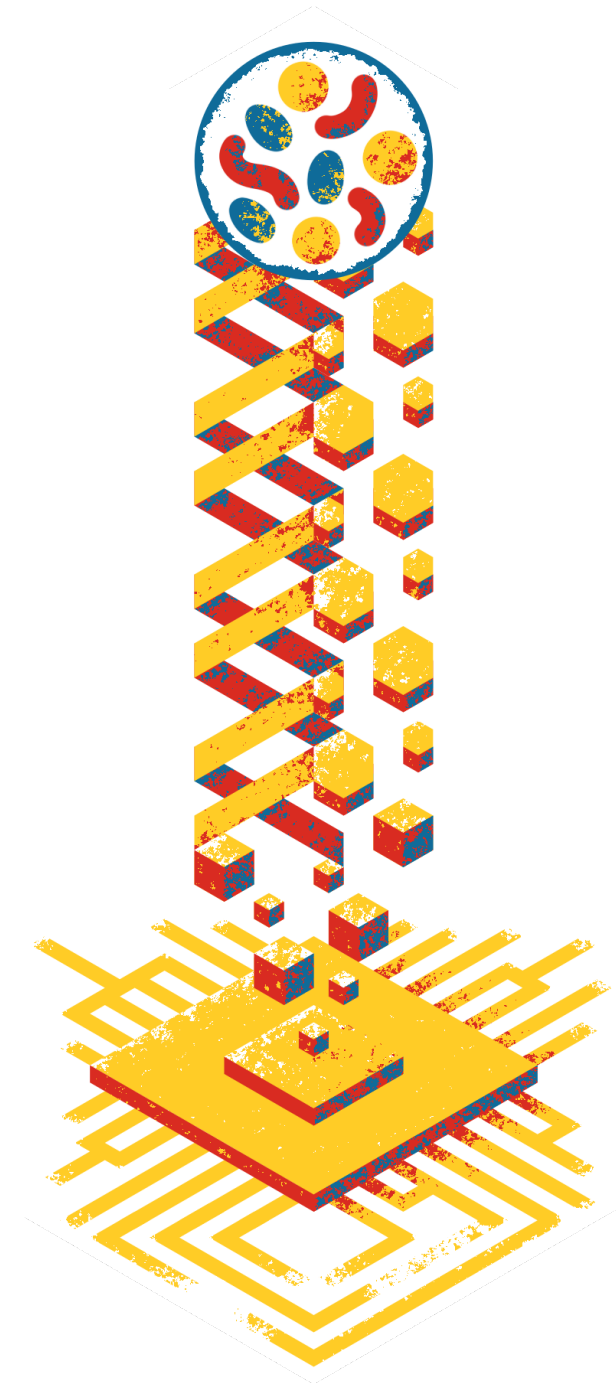
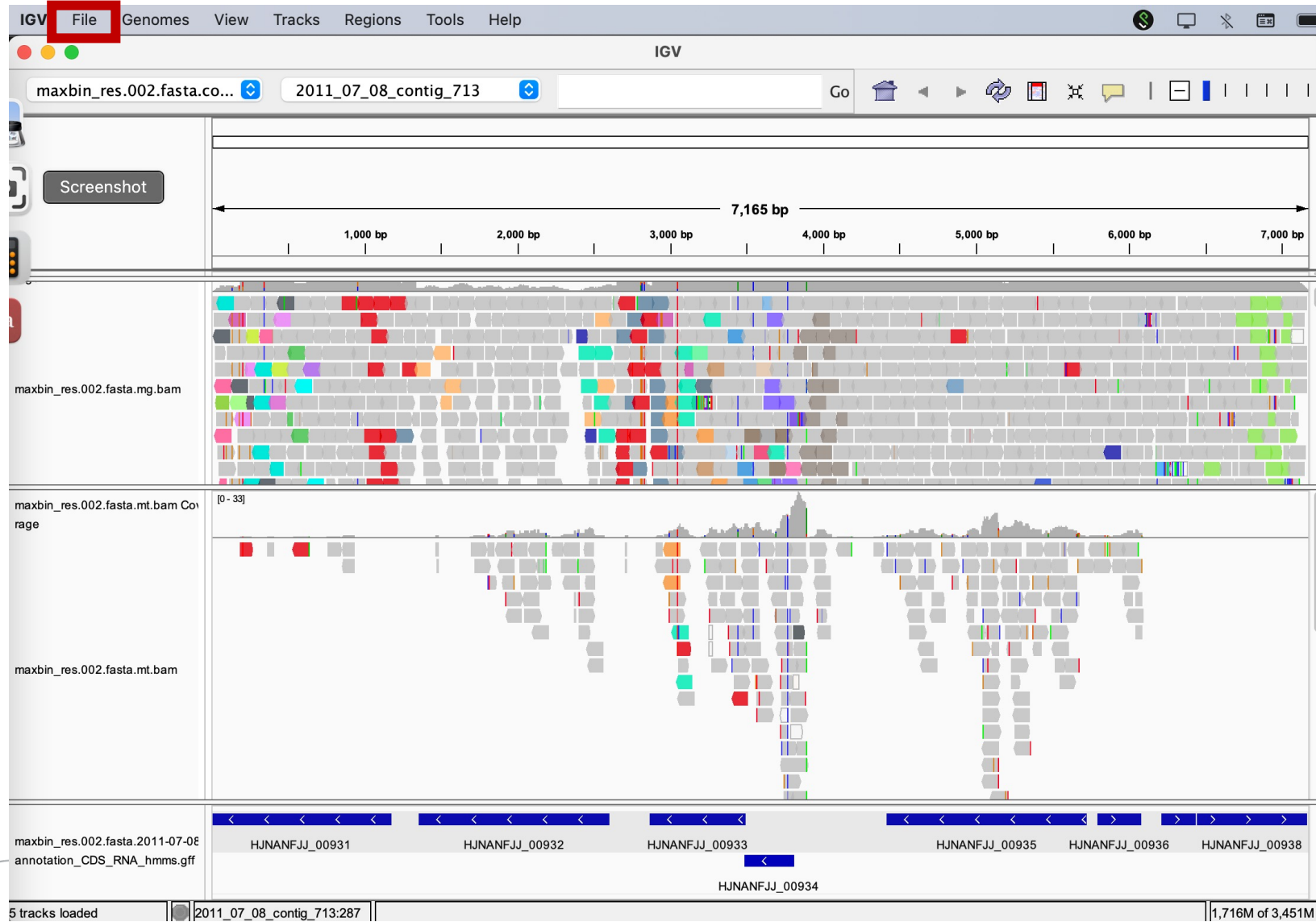
Load from file -> select <MAG> .mt .bam

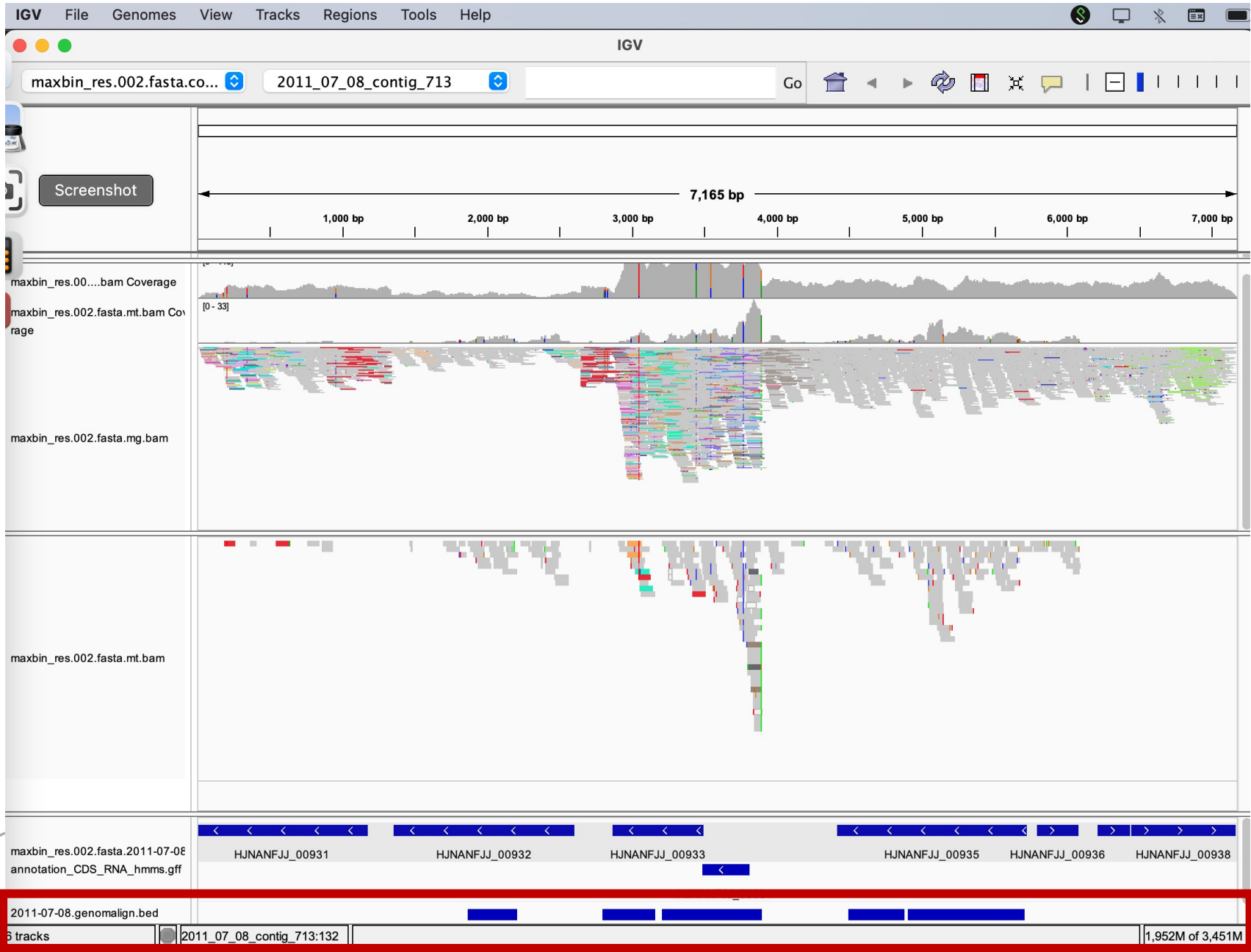




metaT reads

Load from file -> select <SAMPLE>.genomalign.bed



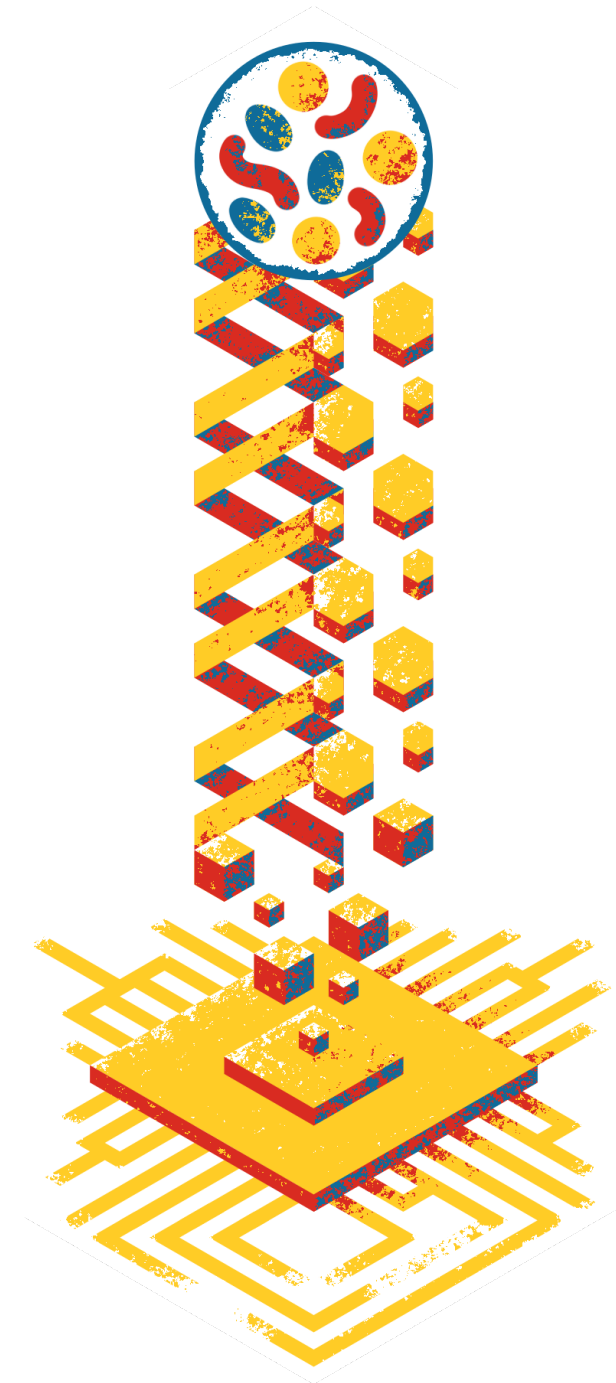


metaT-assembly contigs

choose contigs

search genes

zoom



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