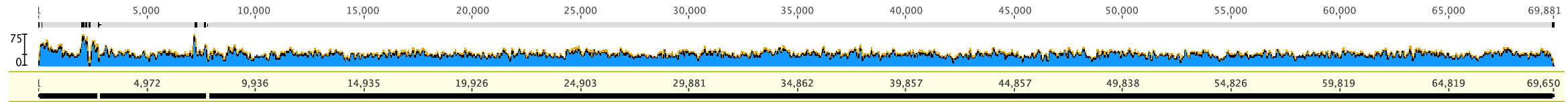
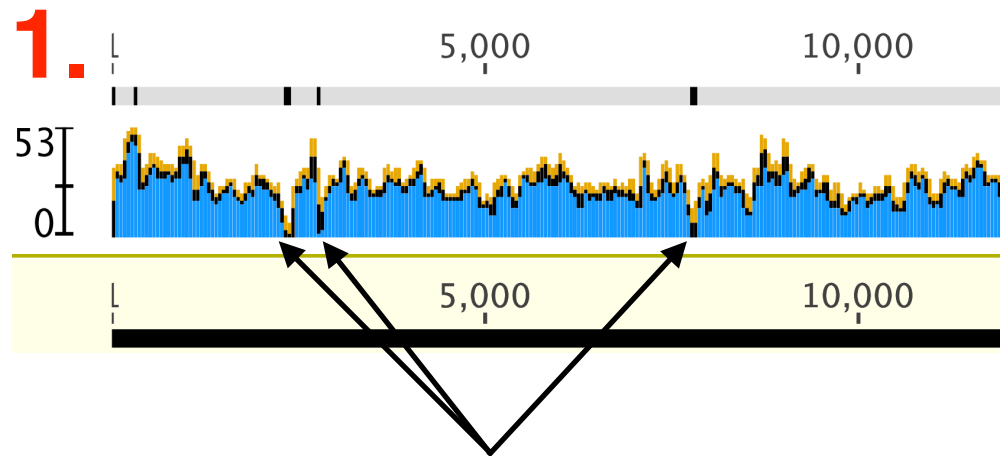
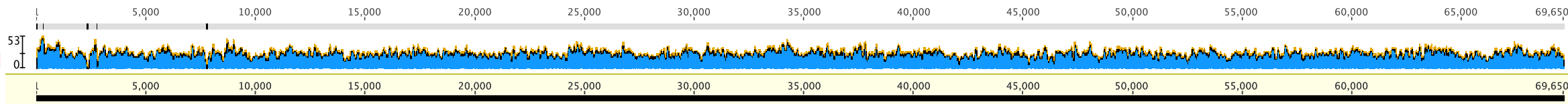


# automated genome error detection and targeted re-assembly

default mapping

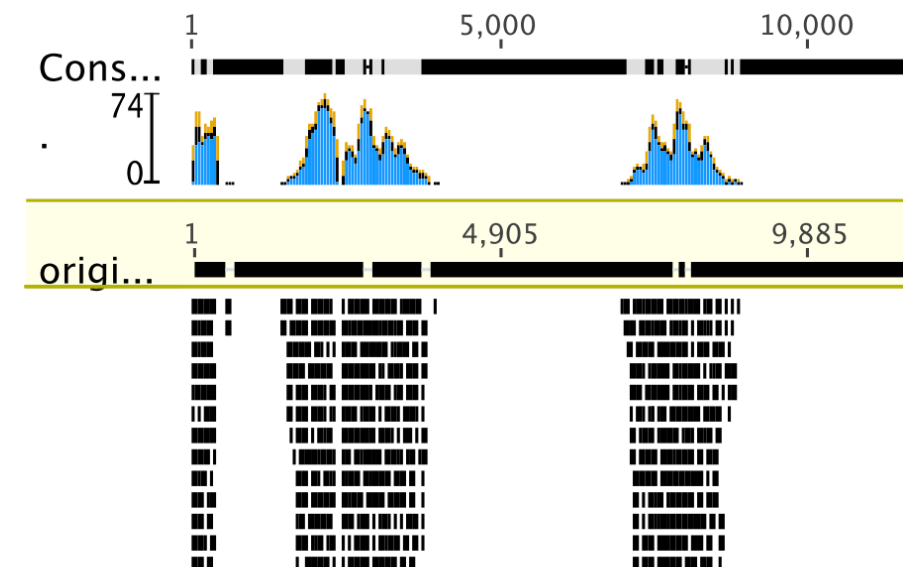


stringent mapping



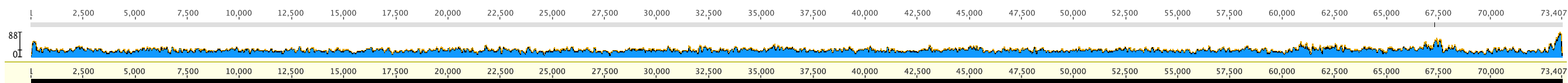
miss-assemblies are identified as regions with zero coverage by stringently mapped paired reads

2. reads are collected from miss-assembled regions based on less-stringent criteria, and independently re-assembled

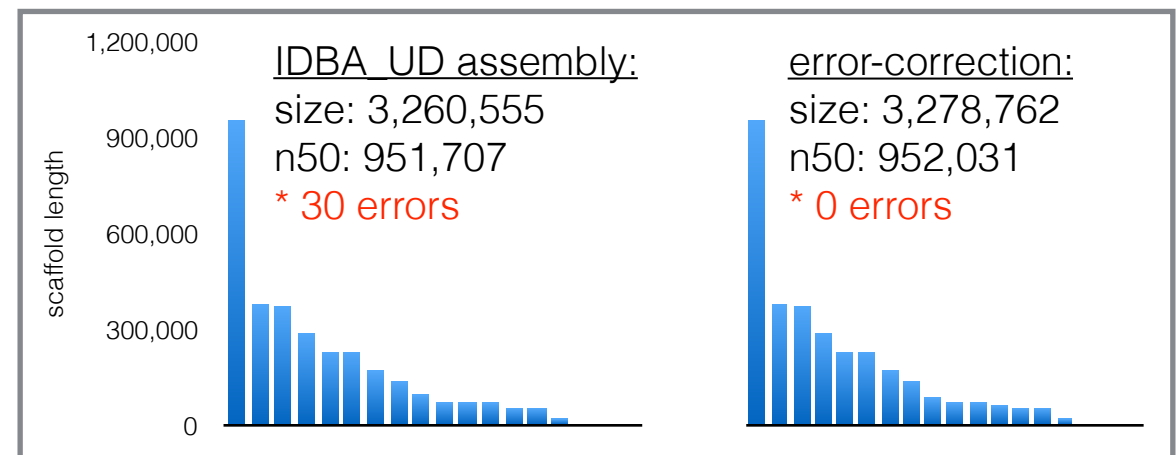


3. zero-coverage regions are removed and replaced with re-assembled regions

4. a final round of mapping can confirm the assembly (not part of ra2.py)

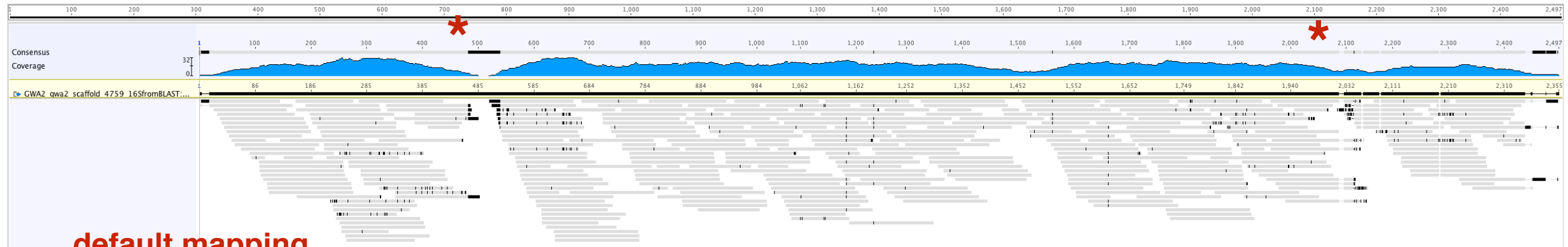


- some misassemblies will not be re-assembled based on the collected reads
- there are different options for handling uncorrected errors (see ``ra2.py -h``)

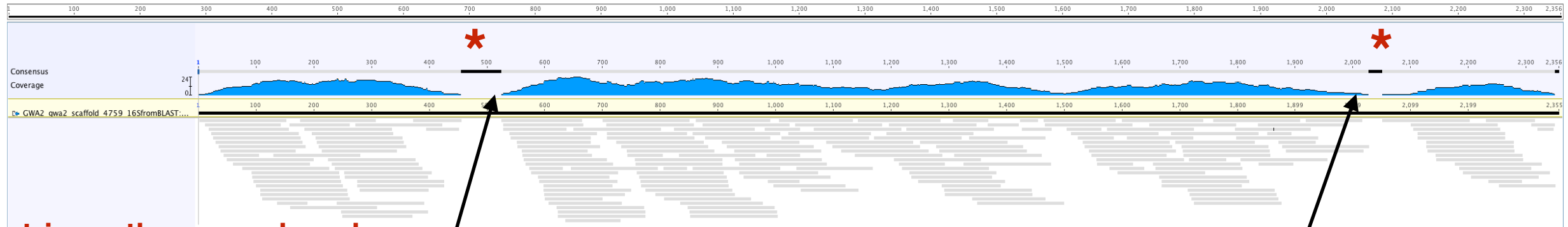


# stringent mapping for scaffolding error detection

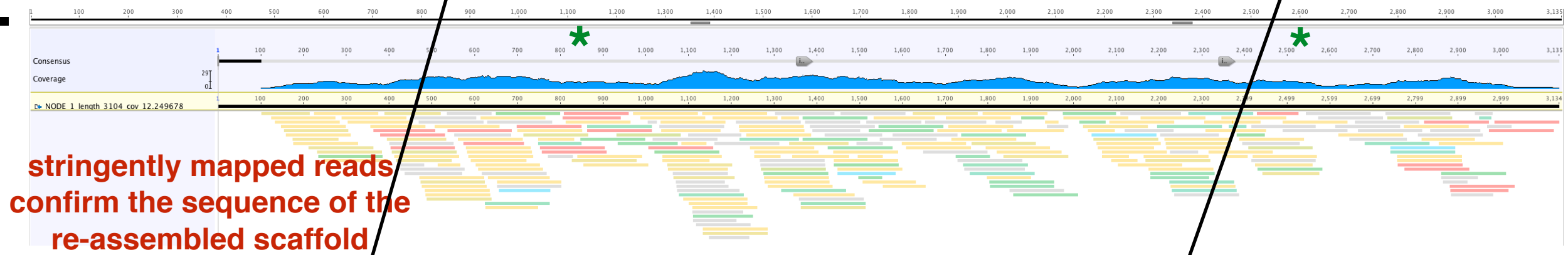
1.



2.



3.



\* = mis-assembly

\* = resolved mis-assembly