

Map reads using STAR aligner

- Highest sensitivity for **both SNPs and indels** among all programs tested
- 2-pass approach described in Pär G Engström et al. “Systematic evaluation of spliced alignment programs for RNA-seq data”. *Nature Methods*, 2013 (see Suppl.I text p. 43 for detailed protocol)
 - First pass identifies splice junctions (SJ)
 - Use the SJ to guide the second round of alignment

