

How do you align to two genomes from one sample?

- Align independently to each genome
 - May have cross alignment
- Make combined genome
 - Bowtie can't do this with large genomes
 - BWA (version 0.6 and newer) can
- Make combined transcriptome
 - Generally sufficient for RNA-Seq, Ribosome Profiling, etc. (assuming good annotation)
- Align to one genome, then align only non-aligned reads to the other

