

Alignments – short reads only

GTF

Novel Transcripts

Remove intronless

Collapse to exons

Keep only internal exons

1. Query transcript alignments
2. Query GENCODE

Novel Exons

TSS support from FANTOM5

Novel tx using alt promoters

Align long reads  
using minimap2

Obtain intron structure

Remove tx that are  
subset of known

1. Query transcript alignments
2. Query long read alignments

