

Processing Short RNA-Seq Reads Mapped to Multiple Loci

1. Choose “Best Loci” based on alignment algorithm (Bowtie)

May misrepresent proportions of expressed families

2. Report all loci as hits

Generate False Positives

3. Do not consider any of the loci,
but classify read as belonging to a given family (Kraken)

Lose location information, but keep information
about expression levels of different families