

## Variant calling in zebrafish (v10)

### 1. Analysis

#### a. Pre-processing

- i. Map reads to reference
- ii. Mark duplicates
- iii. Recalibrate base quality scores
- iv. Indel-base realignment

#### b. Variant discovery

- i. Calling cohorts
- ii. Recalibrate base quality scores
- iii. Genotype refinement
- iv. Annotation and variant evaluation

### 2. Retrieve data from experimental designs

### 3. Generalize into tools

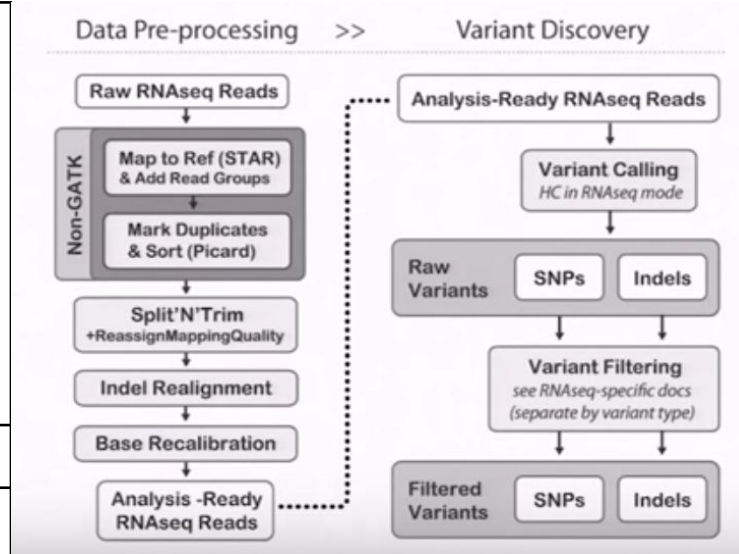
Joint discovery to resolve bias issues

### 4. Assess the scope and limits

```

7 chr10>..294>N>..1>..C>..I
8 chr10>..295>N>..1>..A>..I
9 chr10>..296>N>..1>..T>..I
10 chr10>..297>N>..1>..T>..I
11 chr10>..298>N>..1>..C>..I
12 chr10>..299>N>..1>..A>..I
13 chr10>..300>N>..1>..T>..I
  
```

## RNA-Seq



### New step specific for RNAseq to deal with splicing junctions

