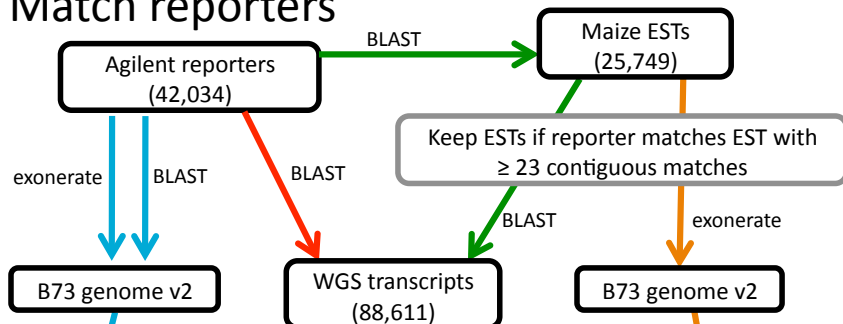
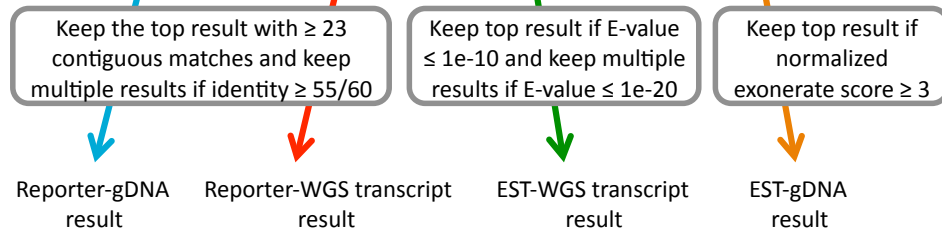


## 1. Match reporters



## 2. Filter results



## 3. Test agreement



## 4. Assign annotation group

- Sense gene model:** Single reporter-gDNA/WGS transcript agreement result
- Antisense gene model:** Single reporter-gDNA/WGS transcript agreement result, but reporter matches the antisense direction of a WGS transcript
- gDNA:** Single reporter-gDNA result, but no reporter-WGS transcript or EST-WGS transcript result; this location is not currently annotated as a gene model
- EST:** Single EST-gDNA/WGS transcript agreement result
- Ambiguous:** More than one reporter-gDNA/WGS transcript agreement or EST-gDNA/WGS transcript agreement result
- Inconclusive:** Reporters without any valid hits, or without any agreement between hits

# Maize Microarray Annotation Database

### Reporter information

- Position on array
- Sequence

### EST information

- Accession number
- Sequence
- Origin maize line
- Functional annotation:
  - GenBank description
  - Walbot lab annotation

### WGS transcript information

- Gene name
- Transcript ID
- Sequence
- Position on B73 genome
- Strand
- Functional annotation:
  - ZmB73\_5a Xref
  - NCBI 'nr' db (Dec 2010)
  - GO terms (Blast2GO)

### Reporter genomic annotation

- Position on B73 genome
- Core bin
- Associated gene:
  - Gene name
  - Sense direction
  - Gene feature (UTR, CDS)

### Evidence (genomic annotation)

- Result type (EST, WGS transcript, gDNA)
- Identity score
- Confidence category
- Annotation group