Anaquin TransQuin Report

Read Alignment

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Summary for dataset: K_RMXA1v2.accepted_hits.sorted.bam

   Unmapped:    0 reads
   Experiment: 36484961 (76.13%) reads
   Synthetic:  11440146 (23.87%) reads

   Reference:  1190 exons
   Reference:  1028 introns
   Reference:  149219 bases

   Query:       84739030 exons
   Query:       27056077 introns
   Query:       153438 bases

   Dilution:    0.238709


   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Exon level is defined by performance per exon. An alignment that
   *** is not mapped entirely within an exon is considered as a FP. The
   *** intron level is similar.
   ***
   *** Base level is defined by performance per nucleotide. A partial
   *** mapped read will have FP and TP.
   ***

   ------------------- Exon level --------------------

   Sensitivity: 0.997479
   Specificity: 0.984404
   Detection:   0.0590086 (R2_33)

   ------------------- Intron level -------------------

   Sensitivity: 0.993191
   Specificity: 1
   Detection:   0.0590086 (R2_33)

   ------------------- Base level --------------------

   Sensitivity: 0.703341
   Specificity: 1
   Detection:   0.0590086 (R2_33)
```

Transctiptome Assembly

```
Summary for dataset: transcripts.gtf

   Experiment: 1897 features
   Synthetic:  799 features

   Reference:  162 exons
   Reference:  1028 introns

   ***
   *** The following statistics are computed for exact and fuzzy.
   ***
   *** The fuzzy level is 10 nucleotides.
   ***

   ------------------- Exon level --------------------

   Sensitivity: 0.547018 (0.566514)
   Specificity: 0.952096 (0.986028)
   Detection:   0.015736 (R2_72_1)

   ------------------- Intron level -------------------

   Sensitivity: 0.521164 (0.52381)
   Specificity: 0.987469 (0.992481)
   Detection:   0.015736 (R2_72_1)

   ------------------- Base level --------------------

   Sensitivity: 0.570883
   Specificity: 0.906859
   Detection:   0.472069 (R2_28)

   ------------------- Transcript level -------------------

   Sensitivity: 0.393939 (0.393939)
   Specificity: 0.555556 (0.555556)

   Missing exons: 385/872 (0.441514)
   Missing introns: 324/756 (0.428571)

   Novel exons: 23/501 (0.0459082)
   Novel introns: 1/399 (0.00250627)
```

Expression Analysis

Differential Analysis