

Anaquin TransQuin Report

Read Alignment

Summary for dataset: K_RMXA1v2.accepted_hits.sorted.bam

Unmapped: 0 alignments
Experiment: 36484961 alignments
Synthetic: 11440146 alignments

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
Accuracy: 0.984404
Detection: 0.0590086 (R2_33)

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

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

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

Sensitivity: 0.703341
Accuracy: 1
Detection: 0.0590086 (R2_33)

- Transcriptome Assembly

- Expression Analysis
- Differential Analysis