

# Anaquin TransQuin Report

## Read Alignment

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

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\*\*\* The following statistics are computed at the exon, intron and base level.

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\*\*\* 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.

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\*\*\* Base level is defined by performance per nucleotide. A partial  
\*\*\* mapped read will have FP and TP.

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----- 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)

# Transcriptome Assembly

Summary for dataset: transcripts.gtf

Experiment: 1897 features

Synthetic: 799 features

Reference: 162 exons

Reference: 1028 introns

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\*\*\* The following statistics are computed for exact and fuzzy.

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\*\*\* The fuzzy level is 10 nucleotides.

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----- 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