Anaquin: TransQuin Report

Contents

TransQuin Alignment

Alignment statistics for: A1

```
Summary for input: K_RMXA1v2.accepted_hits.bam

   ***
   *** Proportion of reads mapped to the synthetic and experiment
   ***

   Unmapped:   0 reads
   Synthetic:  36484961 (76.1291%) reads
   Experiment: 11440146 (23.8709%) reads
   Dilution:   0.761291

   ***
   *** Reference annotation (Synthetic)
   ***

   File: ATR001.v032.gtf

   Synthetic: 1190 exons
   Synthetic: 1028 introns
   Synthetic: 149219 bases

   ***
   *** Reference annotation (Experiment)
   ***

   File: GeneCodeChr1.gtf

   Experiment: 106882 exons
   Experiment: 89631 introns
   Experiment: 12073481 bases

   ***
   *** Input file
   ***

   Synthetic:  85464855 exons
   Synthetic:  32195352 introns
   Synthetic:  161775 bases

   Experiment: 4116941 exons
   Experiment: 1488979 introns
   Experiment: 15859943 bases

   ***
   *** 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.
***
*** Please refer to the paper "Evaluation of gene structure prediction programs" for more details
***

************************************************
***                                          ***
***    Statistics for synthetic chromosome   ***
***                                          ***
************************************************

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

Sensitivity: 0.997479
Specificity: 0.976043
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

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

Sensitivity: 0.993191
Specificity: 0.840372
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

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

Sensitivity: 0.691812
Specificity: 0.932919
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

-------------------- Undetected --------------------

Exon:   0.002521
Intron: 0.006809
Gene:   0.026316

************************************
***                              ***
***    Statistics for experiment ***
***                              ***
************************************

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

Sensitivity: 0.571677
Specificity: 0.915756

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

Sensitivity: 0.493657
Specificity: 0.755703

-------------------- Base level --------------------
```

```
Sensitivity: 0.169268
Specificity: 0.288446

-------------------- Undetected --------------------

Exon:   0.428323
Intron: 0.506343
Gene:   0.832408
```

Alignment statistics for: A2

```
Summary for input: K_RMXA2v2.accepted_hits.bam

   ***
   *** Proportion of reads mapped to the synthetic and experiment
   ***

   Unmapped:   0 reads
   Synthetic:  35066089 (76.6192%) reads
   Experiment: 10700630 (23.3808%) reads
   Dilution:   0.766192

   ***
   *** Reference annotation (Synthetic)
   ***

   File: ATR001.v032.gtf

   Synthetic: 1190 exons
   Synthetic: 1028 introns
   Synthetic: 149219 bases

   ***
   *** Reference annotation (Experiment)
   ***

   File: GeneCodeChr1.gtf

   Experiment: 106882 exons
   Experiment: 89631 introns
   Experiment: 12073481 bases

   ***
   *** Input file
   ***

   Synthetic:  82814262 exons
   Synthetic:  34992686 introns
   Synthetic:  162619 bases

   Experiment: 3629253 exons
   Experiment: 1276494 introns
   Experiment: 15041782 bases

   ***
   *** 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.
```

```
***
*** Please refer to the paper "Evaluation of gene structure prediction programs" for more details
***

************************************************
***                                          ***
***    Statistics for synthetic chromosome   ***
***                                          ***
************************************************

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

Sensitivity: 0.997479
Specificity: 0.974098
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

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

Sensitivity: 0.986381
Specificity: 0.745193
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

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

Sensitivity: 0.691909
Specificity: 0.928206
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

-------------------- Undetected --------------------

Exon:   0.002521
Intron: 0.013619
Gene:   0.026316

************************************
***                              ***
***    Statistics for experiment ***
***                              ***
************************************

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

Sensitivity: 0.561535
Specificity: 0.921506

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

Sensitivity: 0.479243
Specificity: 0.780912

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

Sensitivity: 0.162014
Specificity: 0.291102
```

```
-------------------- Undetected --------------------

Exon:   0.438465
Intron: 0.520757
Gene:   0.837403
```

Alignment statistics for: A3

```
Summary for input: K_RMXA3v2.accepted_hits.bam

   ***
   *** Proportion of reads mapped to the synthetic and experiment
   ***

   Unmapped:   0 reads
   Synthetic:  33232155 (77.2589%) reads
   Experiment: 9781841 (22.7411%) reads
   Dilution:   0.772589

   ***
   *** Reference annotation (Synthetic)
   ***

   File: ATR001.v032.gtf

   Synthetic: 1190 exons
   Synthetic: 1028 introns
   Synthetic: 149219 bases

   ***
   *** Reference annotation (Experiment)
   ***

   File: GeneCodeChr1.gtf

   Experiment: 106882 exons
   Experiment: 89631 introns
   Experiment: 12073481 bases

   ***
   *** Input file
   ***

   Synthetic:  78415783 exons
   Synthetic:  29409848 introns
   Synthetic:  166617 bases

   Experiment: 3801952 exons
   Experiment: 1400763 introns
   Experiment: 15059951 bases

   ***
   *** 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.
```

```
***
*** Please refer to the paper "Evaluation of gene structure prediction programs" for more details
***

************************************************
***                                          ***
***    Statistics for synthetic chromosome   ***
***                                          ***
************************************************

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

Sensitivity: 0.997479
Specificity: 0.971556
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

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

Sensitivity: 0.992218
Specificity: 0.840566
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

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

Sensitivity: 0.696877
Specificity: 0.912440
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

-------------------- Undetected --------------------

Exon:   0.002521
Intron: 0.007782
Gene:   0.026316

************************************
***                              ***
***    Statistics for experiment ***
***                              ***
************************************

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

Sensitivity: 0.550196
Specificity: 0.918023

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

Sensitivity: 0.476598
Specificity: 0.771829

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

Sensitivity: 0.160739
Specificity: 0.288462
```

```
-------------------- Undetected --------------------

Exon:   0.449804
Intron: 0.523402
Gene:   0.838698
```

Alignment statistics for: B1

```
Summary for input: G_RMXB1v2.accepted_hits.bam

   ***
   *** Proportion of reads mapped to the synthetic and experiment
   ***

   Unmapped:   0 reads
   Synthetic:  33694649 (84.2494%) reads
   Experiment: 6299276 (15.7506%) reads
   Dilution:   0.842494

   ***
   *** Reference annotation (Synthetic)
   ***

   File: ATR001.v032.gtf

   Synthetic: 1190 exons
   Synthetic: 1028 introns
   Synthetic: 149219 bases

   ***
   *** Reference annotation (Experiment)
   ***

   File: GeneCodeChr1.gtf

   Experiment: 106882 exons
   Experiment: 89631 introns
   Experiment: 12073481 bases

   ***
   *** Input file
   ***

   Synthetic:  86364151 exons
   Synthetic:  42105718 introns
   Synthetic:  158128 bases

   Experiment: 1697232 exons
   Experiment: 601494 introns
   Experiment: 11657812 bases

   ***
   *** 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.
```

```
***
*** Please refer to the paper "Evaluation of gene structure prediction programs" for more details
***

************************************************
***                                          ***
***    Statistics for synthetic chromosome   ***
***                                          ***
************************************************

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

Sensitivity: 0.993277
Specificity: 0.977562
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

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

Sensitivity: 0.984436
Specificity: 0.793287
Detection Limit: 1.88828 (attomol/ul) (R1_72)

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

Sensitivity: 0.683749
Specificity: 0.943312
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

-------------------- Undetected --------------------

Exon:   0.006723
Intron: 0.015564
Gene:   0.052632

************************************
***                              ***
***    Statistics for experiment ***
***                              ***
************************************

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

Sensitivity: 0.497268
Specificity: 0.905373

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

Sensitivity: 0.399070
Specificity: 0.752942

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

Sensitivity: 0.127187
Specificity: 0.294860
```

```
-------------------- Undetected --------------------

Exon:   0.502732
Intron: 0.600930
Gene:   0.880503
```

Alignment statistics for: B2

```
Summary for input: G_RMXB2v2.accepted_hits.bam

   ***
   *** Proportion of reads mapped to the synthetic and experiment
   ***

   Unmapped:   0 reads
   Synthetic:  33740540 (83.9848%) reads
   Experiment: 6434036 (16.0152%) reads
   Dilution:   0.839848

   ***
   *** Reference annotation (Synthetic)
   ***

   File: ATR001.v032.gtf

   Synthetic: 1190 exons
   Synthetic: 1028 introns
   Synthetic: 149219 bases

   ***
   *** Reference annotation (Experiment)
   ***

   File: GeneCodeChr1.gtf

   Experiment: 106882 exons
   Experiment: 89631 introns
   Experiment: 12073481 bases

   ***
   *** Input file
   ***

   Synthetic:  85746594 exons
   Synthetic:  43266445 introns
   Synthetic:  157833 bases

   Experiment: 1718118 exons
   Experiment: 577019 introns
   Experiment: 11508342 bases

   ***
   *** 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.
```

```
***
*** Please refer to the paper "Evaluation of gene structure prediction programs" for more details
***

************************************************
***                                          ***
***    Statistics for synthetic chromosome   ***
***                                          ***
************************************************

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

Sensitivity: 0.994118
Specificity: 0.976567
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

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

Sensitivity: 0.986381
Specificity: 0.756517
Detection Limit: 1.88828 (attomol/ul) (R1_72)

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

Sensitivity: 0.685982
Specificity: 0.948160
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

-------------------- Undetected --------------------

Exon:   0.005882
Intron: 0.013619
Gene:   0.039474

************************************
***                              ***
***    Statistics for experiment ***
***                              ***
************************************

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

Sensitivity: 0.503237
Specificity: 0.907890

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

Sensitivity: 0.398110
Specificity: 0.785050

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

Sensitivity: 0.126903
Specificity: 0.298024
```

```
-------------------- Undetected --------------------

Exon:   0.496763
Intron: 0.601890
Gene:   0.869774
```

Alignment statistics for: B3

```
Summary for input: G_RMXB3v2.accepted_hits.bam

   ***
   *** Proportion of reads mapped to the synthetic and experiment
   ***

   Unmapped:   0 reads
   Synthetic:  38361013 (82.8492%) reads
   Experiment: 7941201 (17.1508%) reads
   Dilution:   0.828492

   ***
   *** Reference annotation (Synthetic)
   ***

   File: ATR001.v032.gtf

   Synthetic: 1190 exons
   Synthetic: 1028 introns
   Synthetic: 149219 bases

   ***
   *** Reference annotation (Experiment)
   ***

   File: GeneCodeChr1.gtf

   Experiment: 106882 exons
   Experiment: 89631 introns
   Experiment: 12073481 bases

   ***
   *** Input file
   ***

   Synthetic:  98520610 exons
   Synthetic:  50973179 introns
   Synthetic:  157888 bases

   Experiment: 2327740 exons
   Experiment: 812978 introns
   Experiment: 13191197 bases

   ***
   *** 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.
```

```
***
*** Please refer to the paper "Evaluation of gene structure prediction programs" for more details
***

************************************************
***                                          ***
***    Statistics for synthetic chromosome   ***
***                                          ***
************************************************

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

Sensitivity: 0.994958
Specificity: 0.978198
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

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

Sensitivity: 0.983463
Specificity: 0.751422
Detection Limit: 1.88828 (attomol/ul) (R1_72)

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

Sensitivity: 0.684753
Specificity: 0.946133
Detection Limit: 0.0590086 (attomol/ul) (R2_33)

-------------------- Undetected --------------------

Exon:   0.005042
Intron: 0.016537
Gene:   0.052632

************************************
***                              ***
***    Statistics for experiment ***
***                              ***
************************************

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

Sensitivity: 0.525654
Specificity: 0.906386

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

Sensitivity: 0.438052
Specificity: 0.787404

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

Sensitivity: 0.141763
Specificity: 0.290448
```

```
-------------------- Undetected --------------------

Exon:   0.474346
Intron: 0.561948
Gene:   0.867555
```

TransQuin Assembly

Assembly statistics for: A1

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/A1/NotGuided/transcripts.gtf

   ***
   *** Proportion of features mapped to the synthetic and experiment
   ***

   Synthetic:  156131 features
   Experiment: 1955 features

   ***
   *** Reference annotation (Synthetic)
   ***

   File: /Users/tedwong/Desktop/K_562/ATR001.v032.gtf

   Synthetic:  1190 exons
   Synthetic:  1028 introns

   ***
   *** Reference annotation (Experiment)
   ***

   File: /Users/tedwong/Desktop/K_562/GeneCodeChr1.gtf

   Experiment:  106882 exons
   Experiment:  89631 introns

   ***********************************************
   ***                                         ***
   ***    Statistics for synthetic chromosome    ***
   ***                                         ***
   ***********************************************

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

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

   Sensitivity: 1.00 (1.00)
   Specificity: 1.00 (1.00)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)

   -------------------- Base level --------------------
```

```
Sensitivity: 1.00
Specificity: 1.00

-------------------- Intron Chain level --------------------

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 1.00 (0.993939)
Specificity: 1.00 (0.993939)

Missing exons:   0/872 (0.000000)
Missing introns: 3/756 (0.003968)

Novel exons:     0/872 (0.000000)
Novel introns:   0/756 (0.000000)


#####################################
###                               ###
###    Statistics for experiment    ###
###                               ###
#####################################

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

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

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.995505 (1.00)
Specificity: 0.995505 (1.00)

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

Sensitivity: 0.996985
Specificity: 0.999936

-------------------- Intron Chain level --------------------

Sensitivity: 0.968803 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.971469 (0.891616)
```

```
Specificity: 0.996215 (0.914329)

Missing exons:   0/51521 (0.000000)
Missing introns: 140/32924 (0.004252)

Novel exons:   0/50866 (0.000000)
Novel introns: 0/32924 (0.000000)
```

Assembly statistics for: A2

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/A2/NotGuided/transcripts.gtf

   ***
   *** Proportion of features mapped to the synthetic and experiment
   ***

   Synthetic:  144223 features
   Experiment: 1928 features

   ***
   *** Reference annotation (Synthetic)
   ***

   File: /Users/tedwong/Desktop/K_562/ATR001.v032.gtf

   Synthetic:  1190 exons
   Synthetic:  1028 introns

   ***
   *** Reference annotation (Experiment)
   ***

   File: /Users/tedwong/Desktop/K_562/GeneCodeChr1.gtf

   Experiment:  106882 exons
   Experiment:  89631 introns

   ************************************************
   ***                                          ***
   ***    Statistics for synthetic chromosome   ***
   ***                                          ***
   ************************************************

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

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

   Sensitivity: 1.00 (1.00)
   Specificity: 1.00 (1.00)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)

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

   Sensitivity: 1.00
   Specificity: 1.00
```

```
-------------------- Intron Chain level --------------------

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 1.00 (0.993939)
Specificity: 1.00 (0.993939)

Missing exons:   0/872 (0.000000)
Missing introns: 3/756 (0.003968)

Novel exons:     0/872 (0.000000)
Novel introns:   0/756 (0.000000)


#####################################
###                               ###
###    Statistics for experiment    ###
###                               ###
#####################################

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

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

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.995505 (1.00)
Specificity: 0.995505 (1.00)

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

Sensitivity: 0.996985
Specificity: 0.999936

-------------------- Intron Chain level --------------------

Sensitivity: 0.968803 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.971469 (0.891616)
Specificity: 0.996215 (0.914329)
```

```
Missing exons:   0/51521 (0.000000)
Missing introns: 140/32924 (0.004252)

Novel exons:   0/50866 (0.000000)
Novel introns: 0/32924 (0.000000)
```

Assembly statistics for: A3

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/A3/NotGuided/transcripts.gtf

   ***
   *** Proportion of features mapped to the synthetic and experiment
   ***

   Synthetic:  147191 features
   Experiment: 2037 features

   ***
   *** Reference annotation (Synthetic)
   ***

   File: /Users/tedwong/Desktop/K_562/ATR001.v032.gtf

   Synthetic:  1190 exons
   Synthetic:  1028 introns

   ***
   *** Reference annotation (Experiment)
   ***

   File: /Users/tedwong/Desktop/K_562/GeneCodeChr1.gtf

   Experiment:  106882 exons
   Experiment:  89631 introns

   ************************************************
   ***                                          ***
   ***    Statistics for synthetic chromosome   ***
   ***                                          ***
   ************************************************

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

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

   Sensitivity: 1.00 (1.00)
   Specificity: 1.00 (1.00)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)

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

   Sensitivity: 1.00
   Specificity: 1.00
```

```
-------------------- Intron Chain level --------------------

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 1.00 (0.993939)
Specificity: 1.00 (0.993939)

Missing exons:   0/872 (0.000000)
Missing introns: 3/756 (0.003968)

Novel exons:     0/872 (0.000000)
Novel introns:   0/756 (0.000000)


#####################################
###                               ###
###    Statistics for experiment    ###
###                               ###
#####################################

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

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

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.995505 (1.00)
Specificity: 0.995505 (1.00)

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

Sensitivity: 0.996985
Specificity: 0.999936

-------------------- Intron Chain level --------------------

Sensitivity: 0.968803 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.971469 (0.891616)
Specificity: 0.996215 (0.914329)
```

```
Missing exons:   0/51521 (0.000000)
Missing introns: 140/32924 (0.004252)

Novel exons:   0/50866 (0.000000)
Novel introns: 0/32924 (0.000000)
```

Assembly statistics for: B1

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/B1/NotGuided/transcripts.gtf

   ***
   *** Proportion of features mapped to the synthetic and experiment
   ***

   Synthetic:  108316 features
   Experiment: 1691 features

   ***
   *** Reference annotation (Synthetic)
   ***

   File: /Users/tedwong/Desktop/K_562/ATR001.v032.gtf

   Synthetic:  1190 exons
   Synthetic:  1028 introns

   ***
   *** Reference annotation (Experiment)
   ***

   File: /Users/tedwong/Desktop/K_562/GeneCodeChr1.gtf

   Experiment:  106882 exons
   Experiment:  89631 introns

   ************************************************
   ***                                          ***
   ***    Statistics for synthetic chromosome   ***
   ***                                          ***
   ************************************************

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

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

   Sensitivity: 1.00 (1.00)
   Specificity: 1.00 (1.00)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)

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

   Sensitivity: 1.00
   Specificity: 1.00
```

```
-------------------- Intron Chain level --------------------

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 1.00 (0.993939)
Specificity: 1.00 (0.993939)

Missing exons:   0/872 (0.000000)
Missing introns: 3/756 (0.003968)

Novel exons:     0/872 (0.000000)
Novel introns:   0/756 (0.000000)


*************************************
***                               ***
***    Statistics for experiment    ***
***                               ***
*************************************

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

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

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.995505 (1.00)
Specificity: 0.995505 (1.00)

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

Sensitivity: 0.996985
Specificity: 0.999936

-------------------- Intron Chain level --------------------

Sensitivity: 0.968803 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.971469 (0.891616)
Specificity: 0.996215 (0.914329)
```

```
Missing exons:   0/51521 (0.000000)
Missing introns: 140/32924 (0.004252)

Novel exons:   0/50866 (0.000000)
Novel introns: 0/32924 (0.000000)
```

Assembly statistics for: B2

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/B2/NotGuided/transcripts.gtf

   ***
   *** Proportion of features mapped to the synthetic and experiment
   ***

   Synthetic:  107544 features
   Experiment: 1616 features

   ***
   *** Reference annotation (Synthetic)
   ***

   File: /Users/tedwong/Desktop/K_562/ATR001.v032.gtf

   Synthetic:  1190 exons
   Synthetic:  1028 introns

   ***
   *** Reference annotation (Experiment)
   ***

   File: /Users/tedwong/Desktop/K_562/GeneCodeChr1.gtf

   Experiment:  106882 exons
   Experiment:  89631 introns

   ***********************************************
   ***                                         ***
   ***    Statistics for synthetic chromosome    ***
   ***                                         ***
   ***********************************************

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

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

   Sensitivity: 1.00 (1.00)
   Specificity: 1.00 (1.00)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)

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

   Sensitivity: 1.00
   Specificity: 1.00
```

```
-------------------- Intron Chain level --------------------

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 1.00 (0.993939)
Specificity: 1.00 (0.993939)

Missing exons:   0/872 (0.000000)
Missing introns: 3/756 (0.003968)

Novel exons:     0/872 (0.000000)
Novel introns:   0/756 (0.000000)


#####################################
###                               ###
###    Statistics for experiment    ###
###                               ###
#####################################

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

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

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.995505 (1.00)
Specificity: 0.995505 (1.00)

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

Sensitivity: 0.996985
Specificity: 0.999936

-------------------- Intron Chain level --------------------

Sensitivity: 0.968803 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.971469 (0.891616)
Specificity: 0.996215 (0.914329)
```

```
Missing exons:   0/51521 (0.000000)
Missing introns: 140/32924 (0.004252)

Novel exons:   0/50866 (0.000000)
Novel introns: 0/32924 (0.000000)
```

Assembly statistics for: B3

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/B2/NotGuided/transcripts.gtf

   ***
   *** Proportion of features mapped to the synthetic and experiment
   ***

   Synthetic:  107544 features
   Experiment: 1616 features

   ***
   *** Reference annotation (Synthetic)
   ***

   File: /Users/tedwong/Desktop/K_562/ATR001.v032.gtf

   Synthetic:  1190 exons
   Synthetic:  1028 introns

   ***
   *** Reference annotation (Experiment)
   ***

   File: /Users/tedwong/Desktop/K_562/GeneCodeChr1.gtf

   Experiment:  106882 exons
   Experiment:  89631 introns

   ************************************************
   ***                                          ***
   ***    Statistics for synthetic chromosome   ***
   ***                                          ***
   ************************************************

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

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

   Sensitivity: 1.00 (1.00)
   Specificity: 1.00 (1.00)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)

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

   Sensitivity: 1.00
   Specificity: 1.00
```

```
-------------------- Intron Chain level --------------------

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 1.00 (0.993939)
Specificity: 1.00 (0.993939)

Missing exons:   0/872 (0.000000)
Missing introns: 3/756 (0.003968)

Novel exons:     0/872 (0.000000)
Novel introns:   0/756 (0.000000)


*************************************
***                               ***
***    Statistics for experiment    ***
***                               ***
*************************************

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

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

Sensitivity: 1.00 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.995505 (1.00)
Specificity: 0.995505 (1.00)

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

Sensitivity: 0.996985
Specificity: 0.999936

-------------------- Intron Chain level --------------------

Sensitivity: 0.968803 (1.00)
Specificity: 1.00 (1.00)

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

Sensitivity: 0.971469 (0.891616)
Specificity: 0.996215 (0.914329)
```

```
Missing exons:   0/51521 (0.000000)
Missing introns: 140/32924 (0.004252)

Novel exons:   0/50866 (0.000000)
Novel introns: 0/32924 (0.000000)
```

TransQuin Gene Expression

Gene expression summary

```
Summary for input: /Users/tedwong/Desktop/K_562/Cufflinks/A1/genes.fpkm_tracking,/Users/tedwong/Desktop/

   Synthetic:   74.5 ± 0.547723 (0.00122844 ± 9.00928e-06%)
   Experiment:  60571.5 ± 0.547723 (0.998772 ± 9.00928e-06%)

   Reference:   76 ± 0 gene
   Detected:    72.5 ± 0.547723 gene

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 4.72069 ± 5.17125 (R1_62,R1_62,R1_101,R1_72,R1_72,R1_72)

   ***
   *** Before the break
   ***

   Intercept: 4.98514 ± 0.378132
   Slope:     0.217904 ± 0.154108
   R2:        0.17477 ± 0.126267

   ***
   *** After the break
   ***

   Intercept: 2.37852 ± 0.543286
   Slope:     0.934362 ± 0.0937388
   R2:        0.807344 ± 0.116992

   ***
   *** Overall linear regression
   ***

   Correlation: 0.914411 ± 0.0513749
   Slope:       5.06309 ± 1.53683
   R2:          0.838347 ± 0.0939505
   F-statistic: 538.889 ± 357.61
   P-value:     0 ± 0
   SSM:         3.33477e+10 ± 2.17003e+09, DF: 1 ± 0
   SSE:         6.63846e+09 ± 4.11595e+09, DF: 70.5 ± 0.547723
   SST:         3.99862e+10 ± 2.52826e+09, DF: 71.5 ± 0.547723

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.882202 ± 0.0481316
   Slope:       0.667792 ± 0.0375691
   R2:          0.78021 ± 0.0850381
```

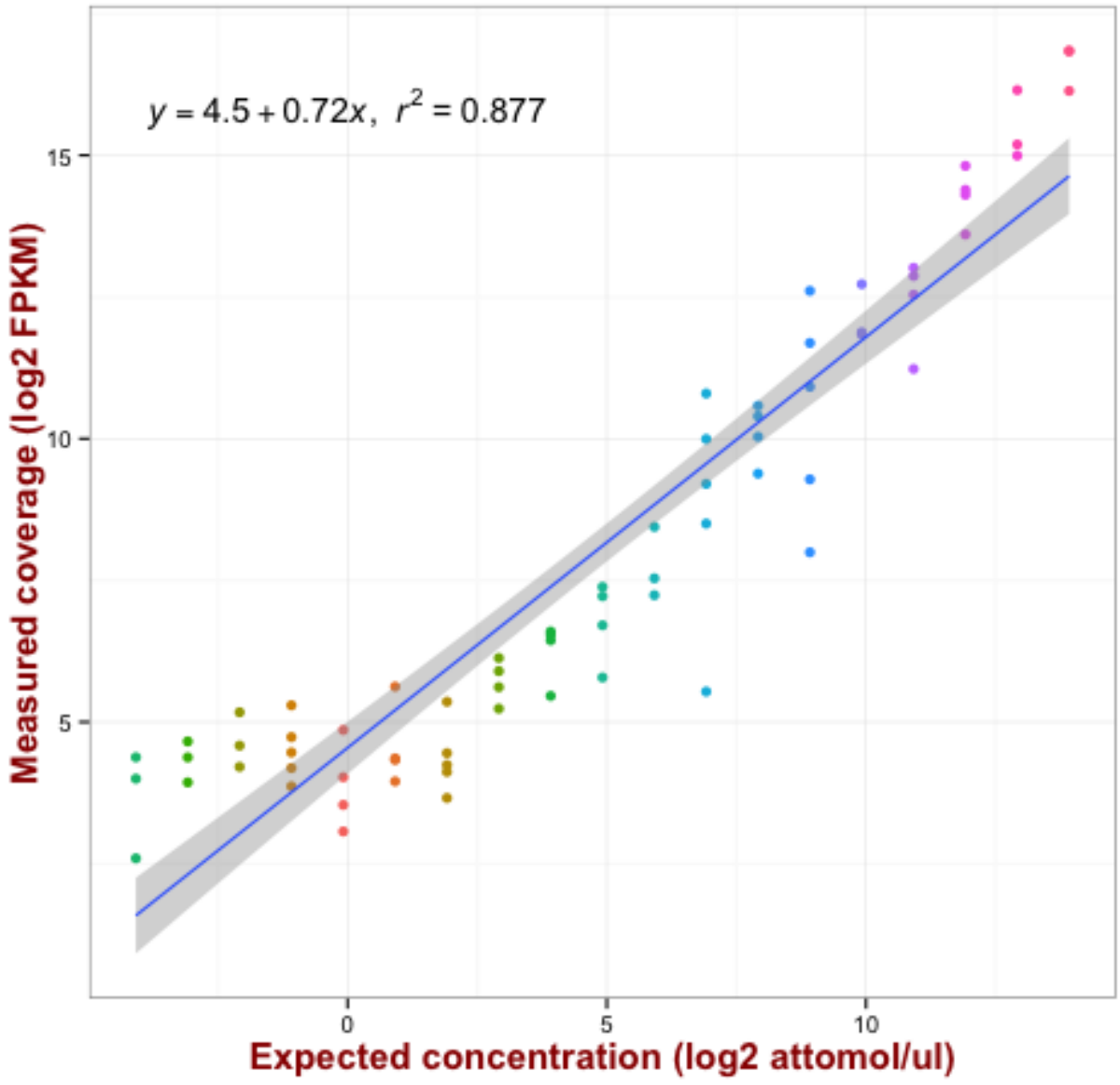
```
F-statistic: 298.912 ± 152.065
P-value:     0 ± 0
SSM:         892.179 ± 94.4268, DF: 1 ± 0
SSE:         252.921 ± 102.486, DF: 70.5 ± 0.547723
SST:         1145.1 ± 54.3084, DF: 71.5 ± 0.547723
```

Gene expression statistics for: A1

```
Summary for input: /Users/tedwong/Desktop/K_562/Cufflinks/A1/genes.fpkm_tracking

   Synthetic:   75 (0.00123666%)
   Experiment:  60572 (0.998763%)

   Reference:   76 gene
   Detected:    73 gene

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 3.77655 (R1_62)

   ***
   *** Before the break
   ***

   Intercept: 4.39067
   Slope:     0.0805742
   R2:        0.0567335

   ***
   *** After the break
   ***

   Intercept: 2.0794
   Slope:     1.00352
   R2:        0.922502

   ***
   *** Overall linear regression
   ***

   Correlation: 0.962825
   Slope:       6.46625
   R2:          0.927032
   F-statistic: 902.032
   P-value:     0
   SSM:         3.50824e+10, DF: 1
   SSE:         2.76138e+09, DF: 71
   SST:         3.78438e+10, DF: 72

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.936306
   Slope:       0.724913
   R2:          0.876669
   F-statistic: 504.686
   P-value:     0
```

```
SSM:          1040.46, DF: 1
SSE:          146.373, DF: 71
SST:          1186.83, DF: 72
```

Gene expression scatter plot for: A1

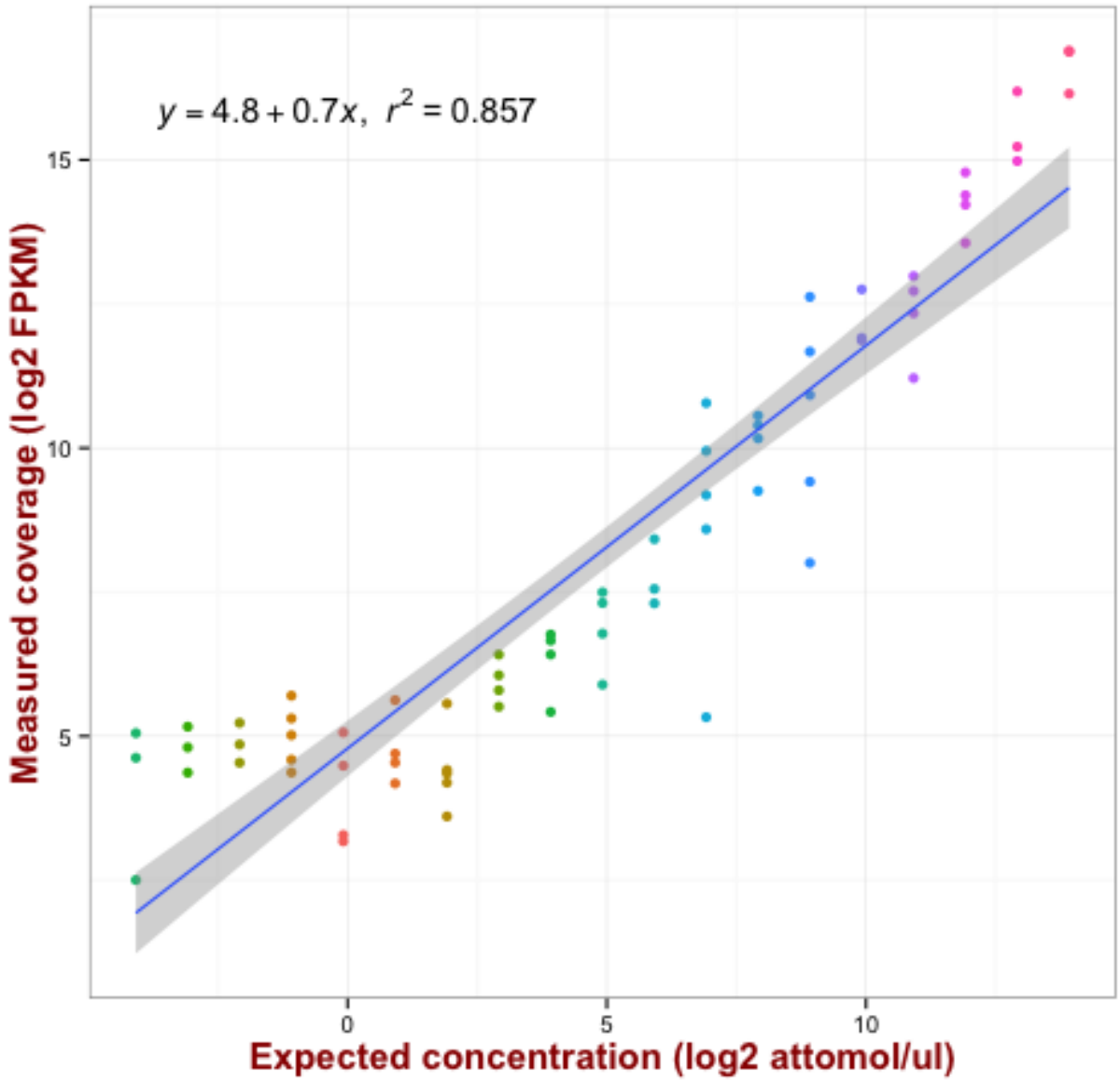


Gene expression statistics for: A2

```
Summary for input: /Users/tedwong/Desktop/K_562/Cufflinks/A2/genes.fpkm_tracking

   Synthetic:   75 (0.00123666%)
   Experiment:  60572 (0.998763%)

   Reference:   76 gene
   Detected:    73 gene

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 3.77655 (R1_62)

   ***
   *** Before the break
   ***

   Intercept: 4.62321
   Slope:     0.0227324
   R2:        0.00360572

   ***
   *** After the break
   ***

   Intercept: 2.20463
   Slope:     0.990951
   R2:        0.91596

   ***
   *** Overall linear regression
   ***

   Correlation: 0.960008
   Slope:       6.60733
   R2:          0.921615
   F-statistic: 834.781
   P-value:     0
   SSM:         3.663e+10, DF: 1
   SSE:         3.11546e+09, DF: 71
   SST:         3.97454e+10, DF: 72

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.925689
   Slope:       0.699133
   R2:          0.8569
   F-statistic: 425.155
   P-value:     0
```

```
SSM:          967.772, DF: 1
SSE:          161.616, DF: 71
SST:          1129.39, DF: 72
```

Gene expression scatter plot for: A2

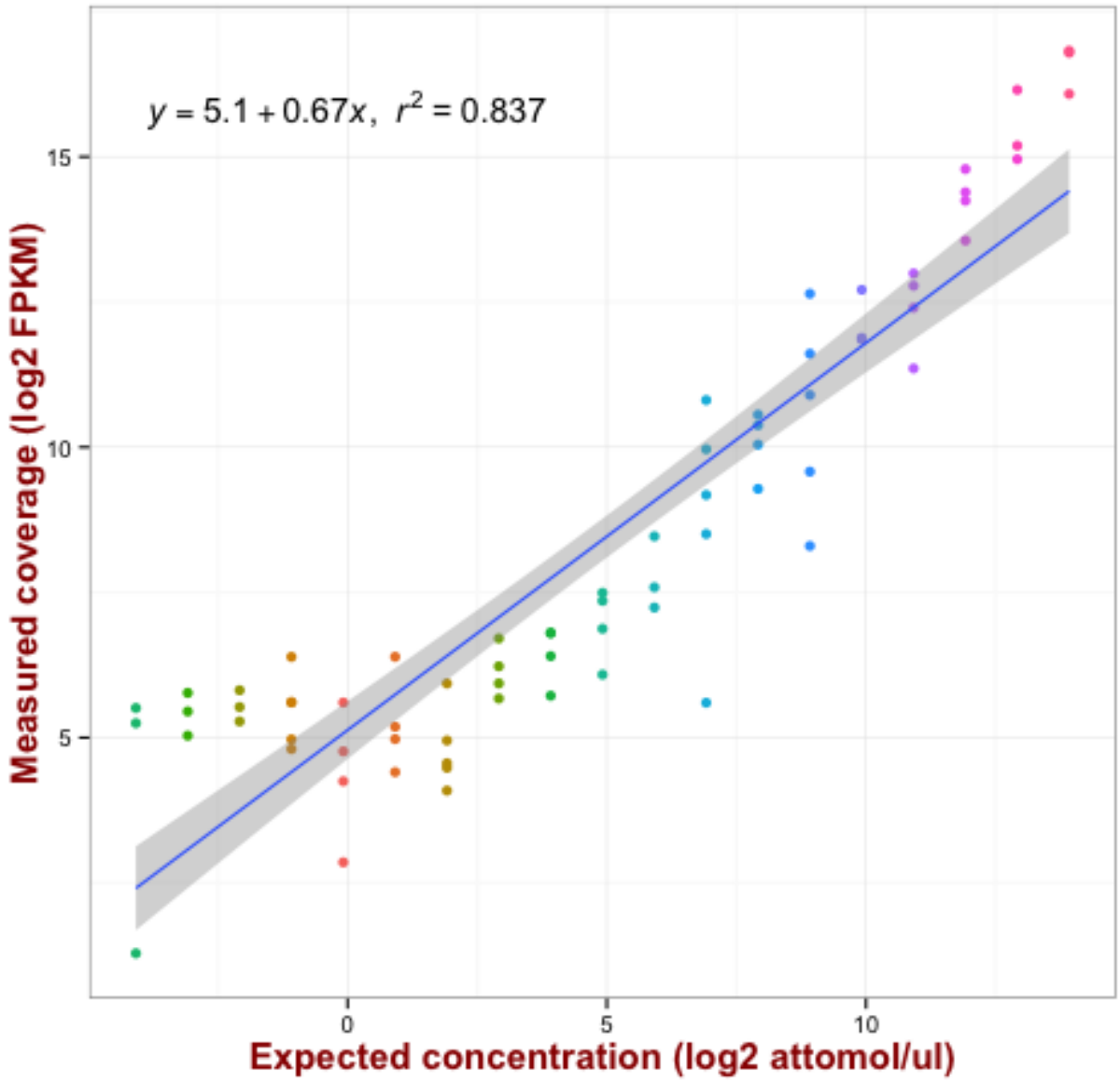


Gene expression statistics for: A3

```
Summary for input: /Users/tedwong/Desktop/K_562/Cufflinks/A3/genes.fpkm_tracking

   Synthetic:   75 (0.00123666%)
   Experiment:  60572 (0.998763%)

   Reference:   76 gene
   Detected:    73 gene

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 15.1062 (R1_101)

   ***
   *** Before the break
   ***

   Intercept: 5.25776
   Slope:     0.16804
   R2:        0.139073

   ***
   *** After the break
   ***

   Intercept: 1.51144
   Slope:     1.05768
   R2:        0.903529

   ***
   *** Overall linear regression
   ***

   Correlation: 0.961001
   Slope:       6.31637
   R2:          0.923522
   F-statistic: 857.371
   P-value:     0
   SSM:         3.34749e+10, DF: 1
   SSE:         2.7721e+09, DF: 71
   SST:         3.6247e+10, DF: 72

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.915017
   Slope:       0.666601
   R2:          0.837255
   F-statistic: 365.266
   P-value:     0
```

```
SSM:          879.802, DF: 1
SSE:          171.015, DF: 71
SST:          1050.82, DF: 72
```

Gene expression scatter plot for: A3

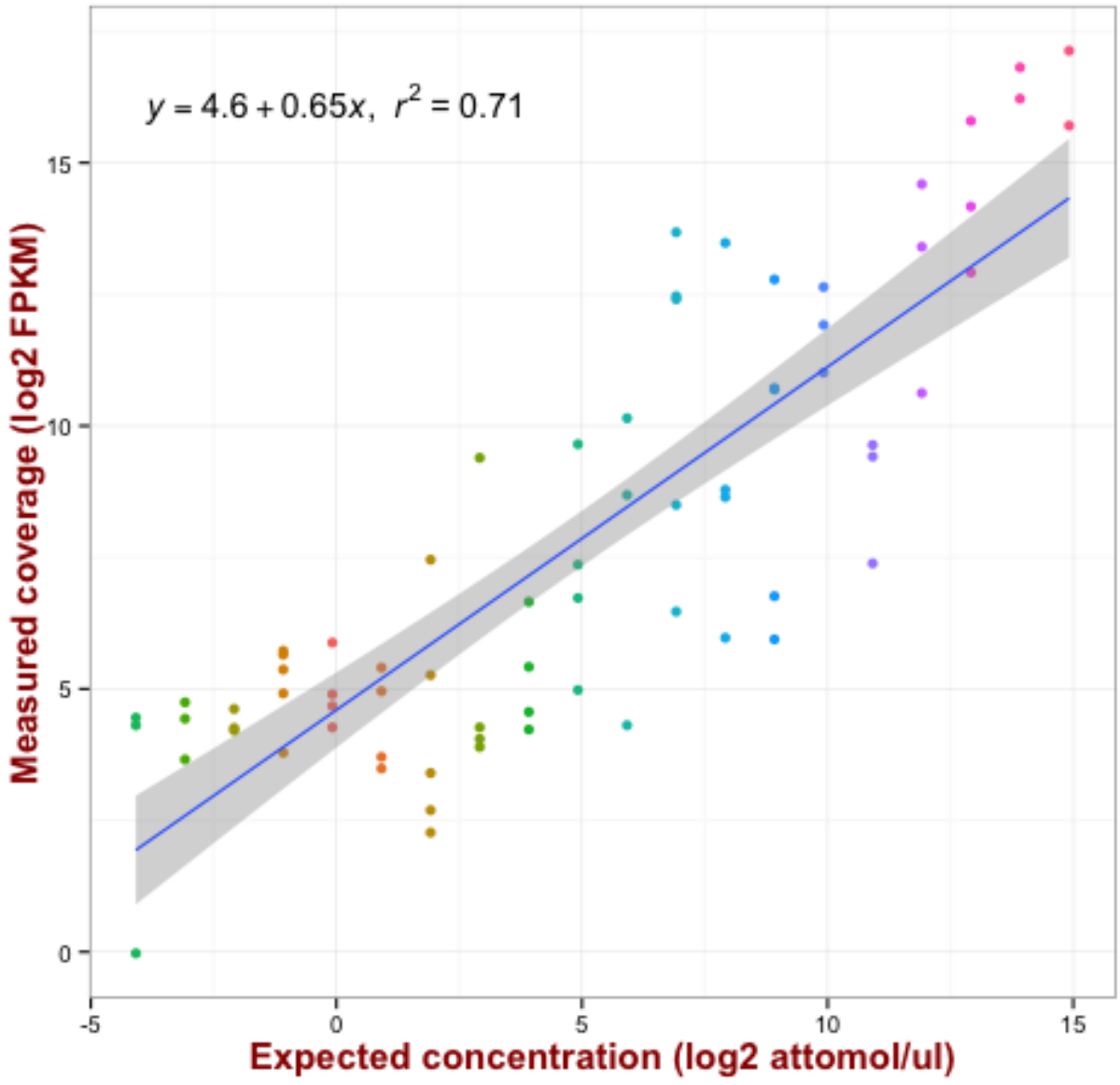


Gene expression statistics for: B1

```
Summary for input: /Users/tedwong/Desktop/K_562/Cufflinks/B1/genes.fpkm_tracking

   Synthetic:   74 (0.00122022%)
   Experiment:  60571 (0.99878%)

   Reference:   76 gene
   Detected:    72 gene

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 1.88828 (R1_72)

   ***
   *** Before the break
   ***

   Intercept: 5.19759
   Slope:     0.42932
   R2:        0.278885

   ***
   *** After the break
   ***

   Intercept: 2.76376
   Slope:     0.857773
   R2:        0.701784

   ***
   *** Overall linear regression
   ***

   Correlation: 0.87057
   Slope:       3.70819
   R2:          0.757893
   F-statistic: 219.128
   P-value:     0
   SSM:         3.24184e+10, DF: 1
   SSE:         1.0356e+10, DF: 70
   SST:         4.27744e+10, DF: 71

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.84233
   Slope:       0.652163
   R2:          0.709519
   F-statistic: 170.98
   P-value:     0
```

```
SSM:          856.494, DF: 1
SSE:          350.653, DF: 70
SST:          1207.15, DF: 71
```

Gene expression scatter plot for: B1

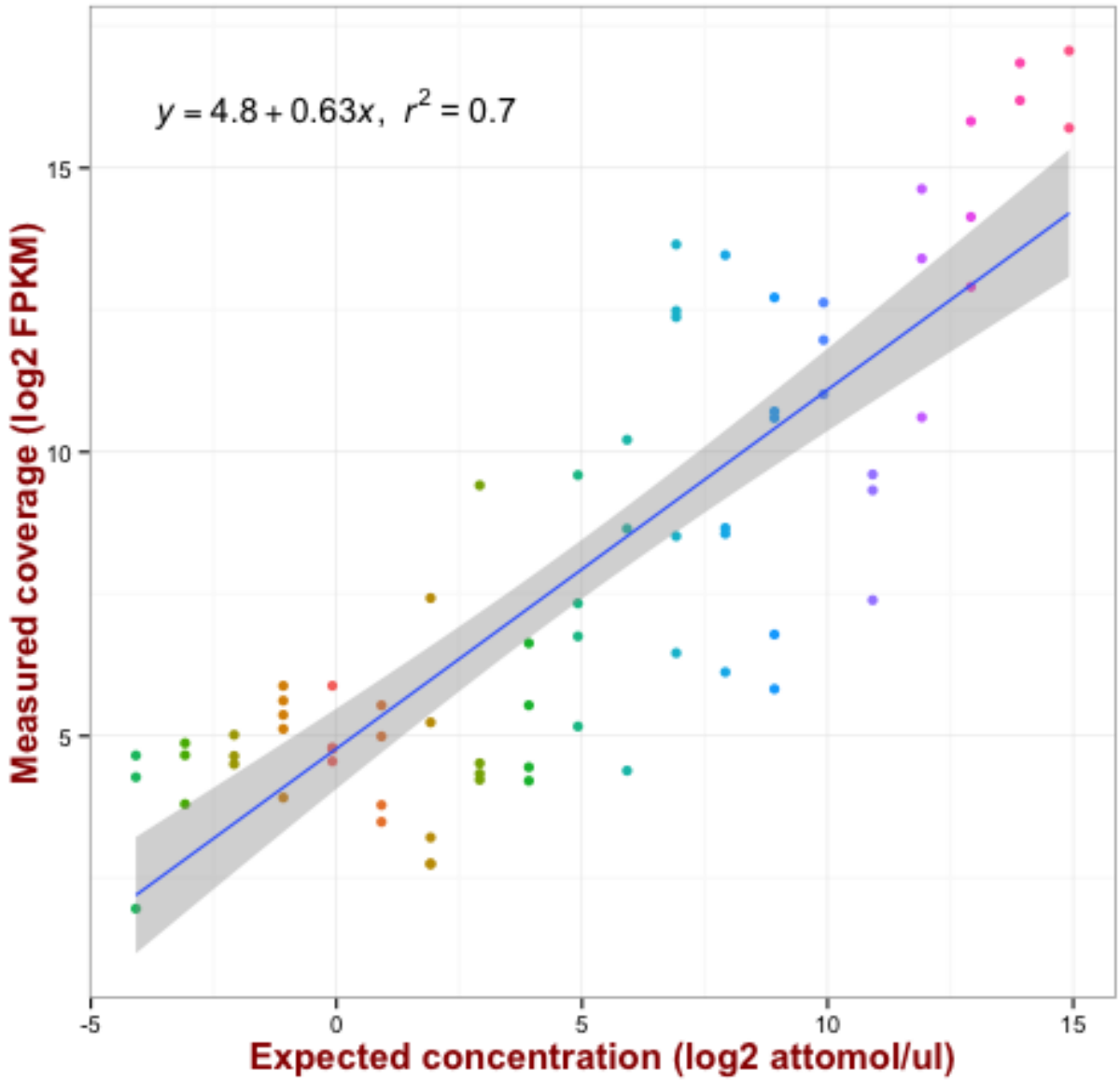


Gene expression statistics for: B2

```
Summary for input: /Users/tedwong/Desktop/K_562/Cufflinks/B2/genes.fpkm_tracking

   Synthetic:   74 (0.00122022%)
   Experiment:  60571 (0.99878%)

   Reference:   76 gene
   Detected:    72 gene

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 1.88828 (R1_72)

   ***
   *** Before the break
   ***

   Intercept: 5.22081
   Slope:     0.303379
   R2:        0.28516

   ***
   *** After the break
   ***

   Intercept: 2.85593
   Slope:     0.848121
   R2:        0.700146

   ***
   *** Overall linear regression
   ***

   Correlation: 0.866031
   Slope:       3.64019
   R2:          0.750009
   F-statistic: 210.01
   P-value:     0
   SSM:         3.12402e+10, DF: 1
   SSE:         1.04129e+10, DF: 70
   SST:         4.16532e+10, DF: 71

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.836934
   Slope:       0.63197
   R2:          0.700459
   F-statistic: 163.691
   P-value:     0
```

```
SSM:          804.275, DF: 1
SSE:          343.936, DF: 70
SST:          1148.21, DF: 71
```

Gene expression scatter plot for: B2

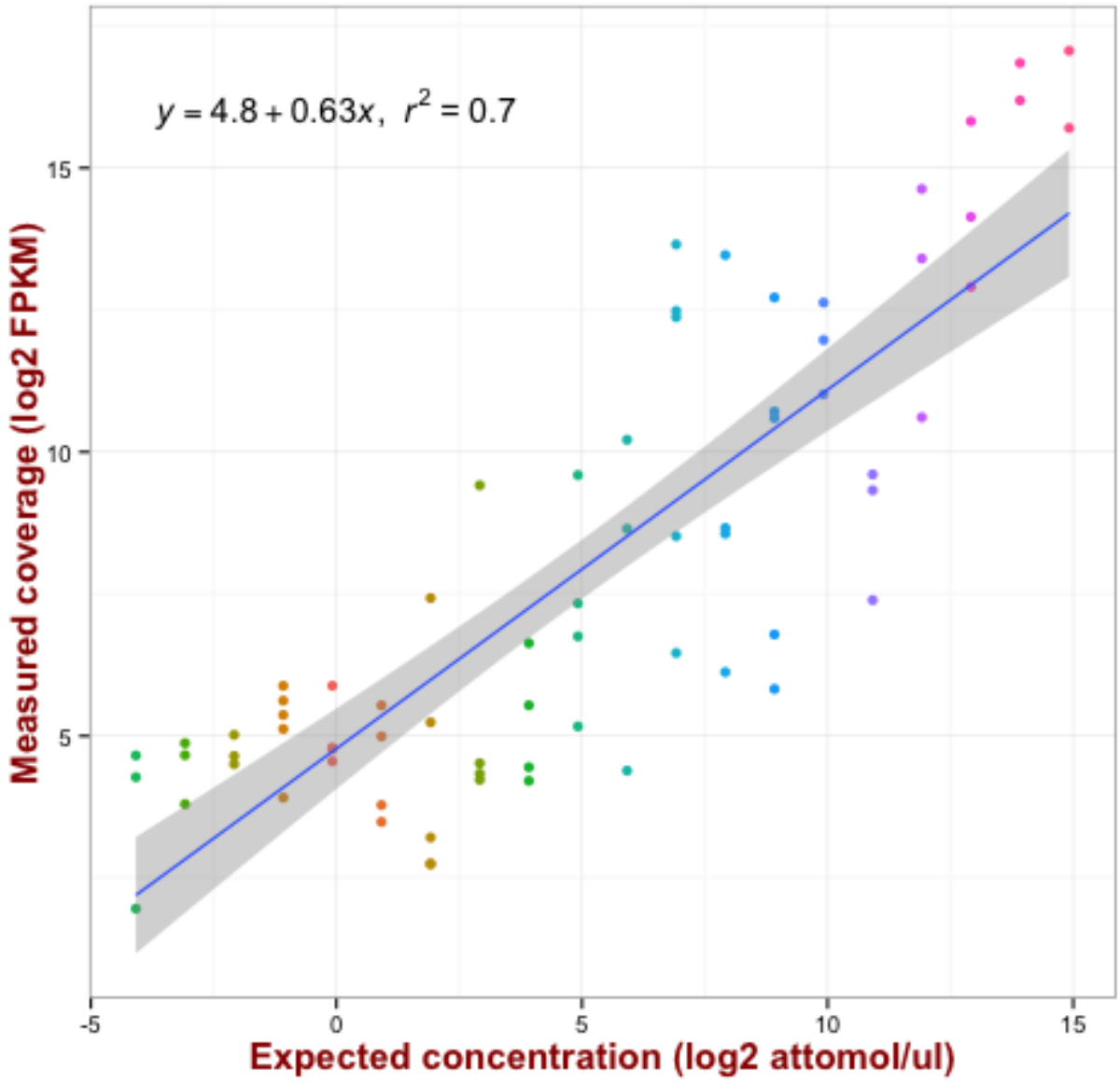


Gene expression statistics for: B3

```
Summary for input: /Users/tedwong/Desktop/K_562/Cufflinks/B3/genes.fpkm_tracking

   Synthetic:   74 (0.00122022%)
   Experiment:  60571 (0.99878%)

   Reference:   76 gene
   Detected:    72 gene

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 1.88828 (R1_72)

   ***
   *** Before the break
   ***

   Intercept: 5.22081
   Slope:     0.303379
   R2:        0.28516

   ***
   *** After the break
   ***

   Intercept: 2.85593
   Slope:     0.848121
   R2:        0.700146

   ***
   *** Overall linear regression
   ***

   Correlation: 0.866031
   Slope:       3.64019
   R2:          0.750009
   F-statistic: 210.01
   P-value:     0
   SSM:         3.12402e+10, DF: 1
   SSE:         1.04129e+10, DF: 70
   SST:         4.16532e+10, DF: 71

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.836934
   Slope:       0.63197
   R2:          0.700459
   F-statistic: 163.691
   P-value:     0
```

```
SSM:          804.275, DF: 1
SSE:          343.936, DF: 70
SST:          1148.21, DF: 71
```

Gene expression scatter plot for: B3



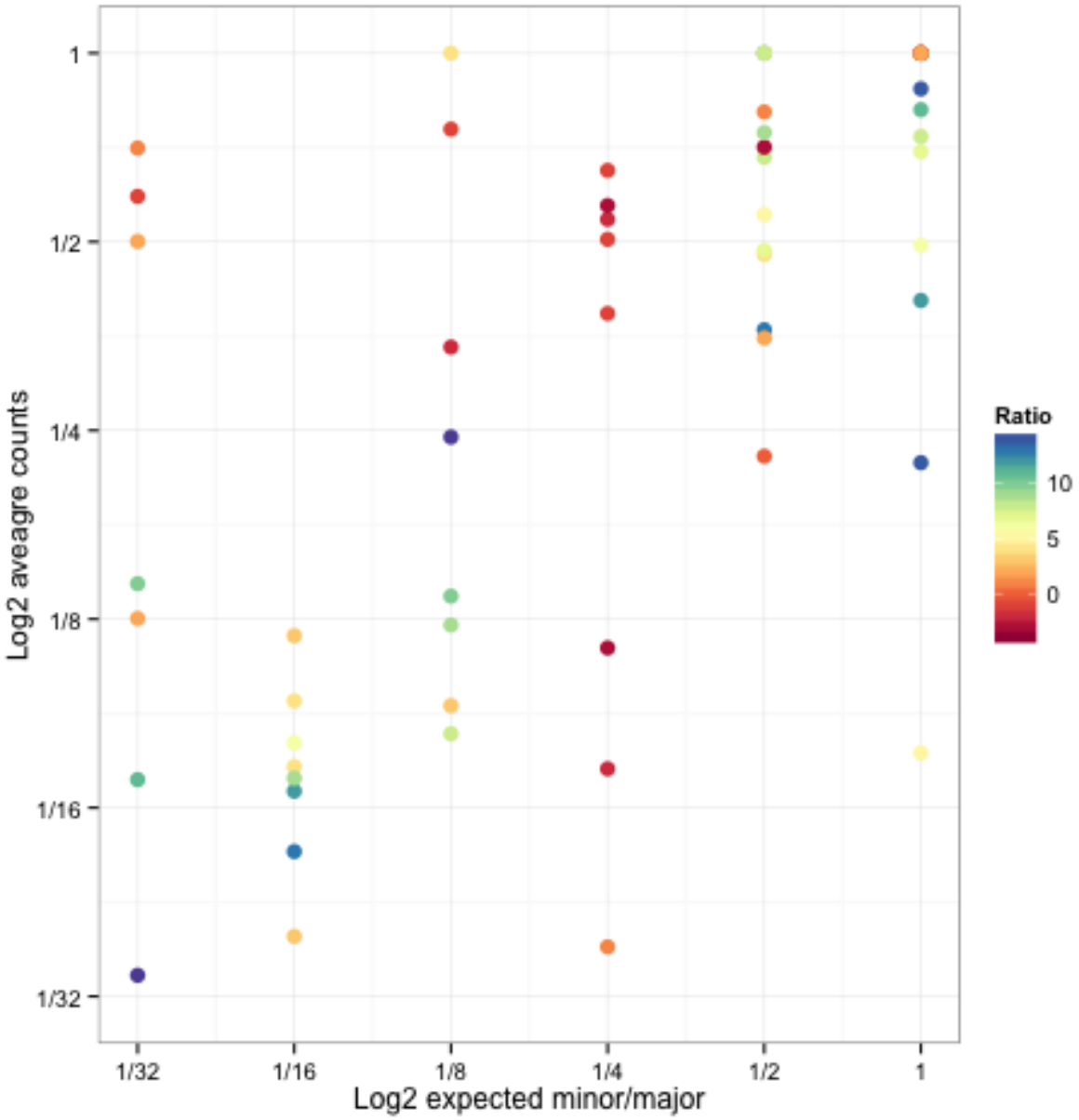
TransQuin Isoform Expression

Isoform expression summary

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab,/Users/tedwong/Desktop/K_562/S

   Synthetic:   164 ± 0 (0.00162484 ± 0%)
   Experiment:  100769 ± 0 (0.998375 ± 1.21619e-16%)

   Reference:   162 ± 0 isoform
   Detected:    162 ± 0 isoform

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 3.5544 ± 0 (R1_32_1,R1_32_1,R1_32_1,R1_32_1,R1_32_1,R1_32_1)

   ***
   *** Before the break
   ***

   Intercept: 1.25307 ± 0
   Slope:     0.157653 ± 0
   R2:        0.0887965 ± 0

   ***
   *** After the break
   ***

   Intercept: 0.825739 ± 0
   Slope:     1.06985 ± 0
   R2:        0.865753 ± 0

   ***
   *** Overall linear regression
   ***

   Correlation: 0.951062 ± 0
   Slope:       5.16984 ± 9.72951e-16
   R2:          0.904519 ± 0
   F-statistic: 1373.62 ± 2.49075e-13
   P-value:     0 ± 0
   SSM:         7.55327e+10 ± 0, DF: 1 ± 0
   SSE:         7.97327e+09 ± 0, DF: 145 ± 0
   SST:         8.35059e+10 ± 0, DF: 146 ± 0

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.940142 ± 1.21619e-16
   Slope:       0.820425 ± 0
   R2:          0.883867 ± 1.21619e-16
```

```
F-statistic: 1103.57 ± 0
P-value:     0 ± 0
SSM:         3387.56 ± 0, DF: 1 ± 0
SSE:         445.096 ± 6.22688e-14, DF: 145 ± 0
SST:         3832.65 ± 0, DF: 146 ± 0
```

Minor/Major plot

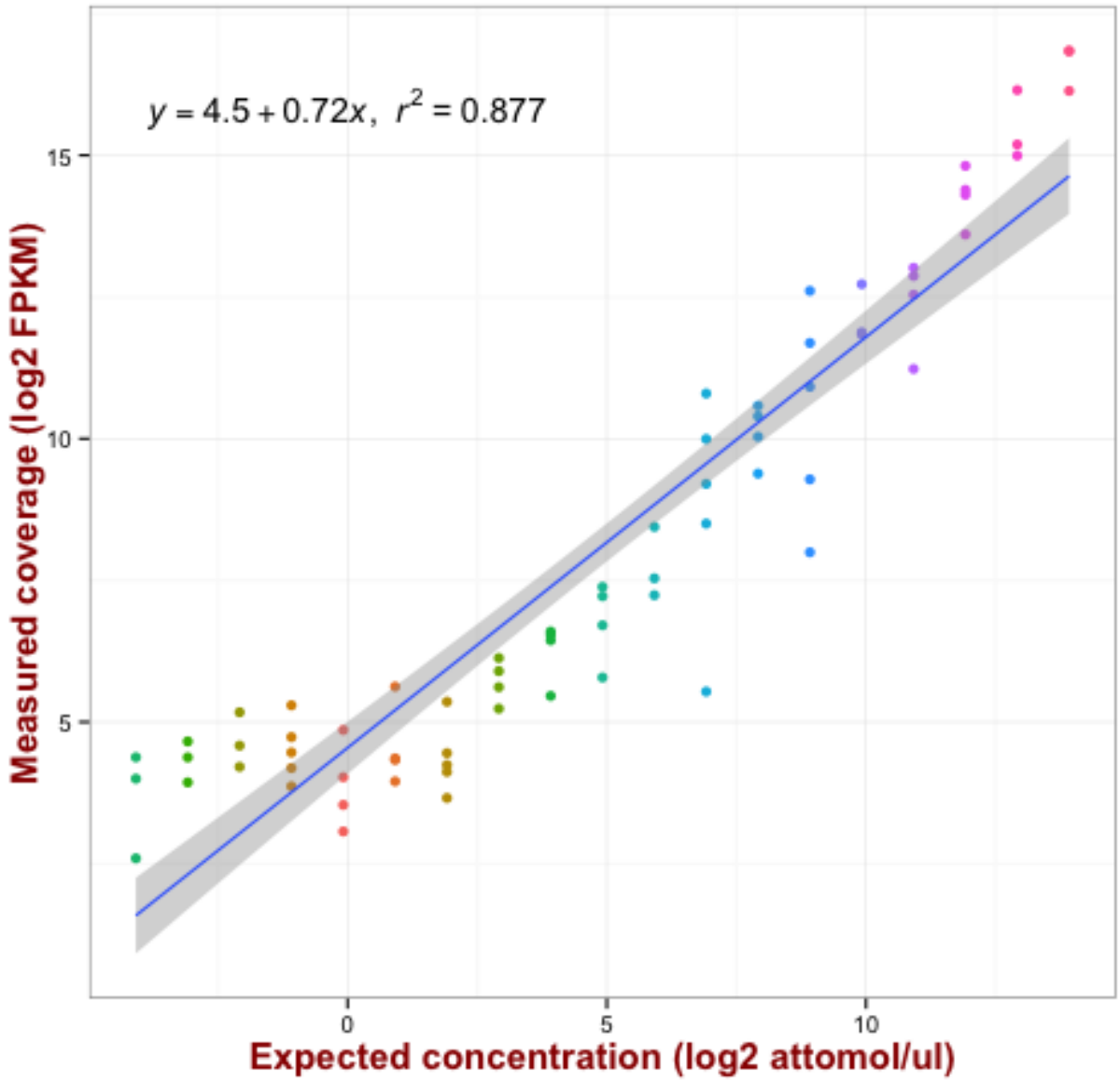


Isoform expression statistics for: A1

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

   Synthetic:   164 (0.00162484%)
   Experiment:  100769 (0.998375%)

   Reference:   162 isoform
   Detected:    162 isoform

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 3.5544 (R1_32_1)

   ***
   *** Before the break
   ***

   Intercept: 1.25307
   Slope:     0.157653
   R2:        0.0887965

   ***
   *** After the break
   ***

   Intercept: 0.825739
   Slope:     1.06985
   R2:        0.865753

   ***
   *** Overall linear regression
   ***

   Correlation: 0.951062
   Slope:       5.16984
   R2:          0.904519
   F-statistic: 1373.62
   P-value:     0
   SSM:         7.55327e+10, DF: 1
   SSE:         7.97327e+09, DF: 145
   SST:         8.35059e+10, DF: 146

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.940142
   Slope:       0.820425
   R2:          0.883867
   F-statistic: 1103.57
   P-value:     0
```

```
SSM:          3387.56, DF: 1
SSE:          445.096, DF: 145
SST:          3832.65, DF: 146
```

Isoform expression scatter plot for: A1

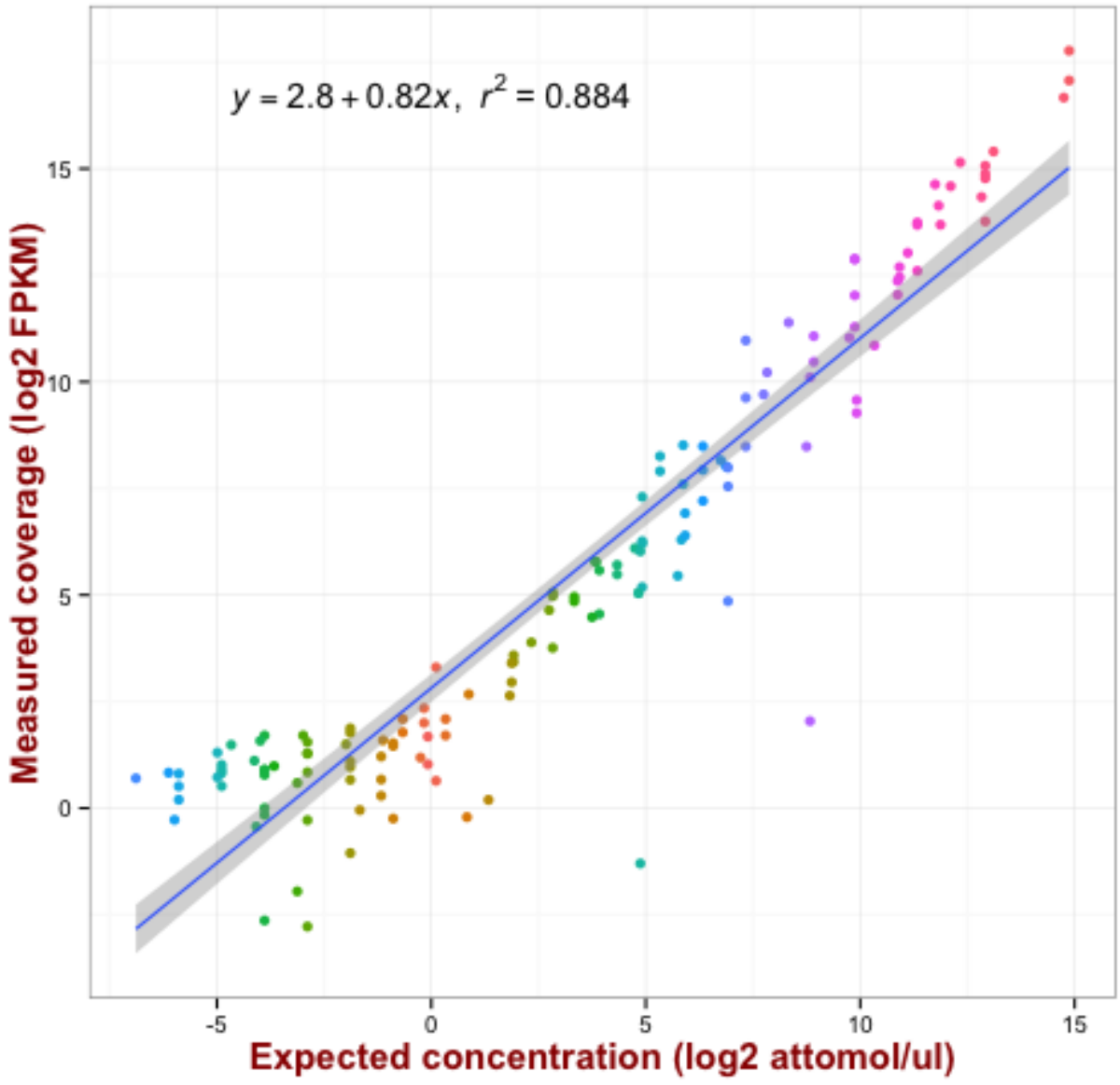


Isoform expression statistics for: A2

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

   Synthetic:   164 (0.00162484%)
   Experiment:  100769 (0.998375%)

   Reference:   162 isoform
   Detected:    162 isoform

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 3.5544 (R1_32_1)

   ***
   *** Before the break
   ***

   Intercept: 1.25307
   Slope:     0.157653
   R2:        0.0887965

   ***
   *** After the break
   ***

   Intercept: 0.825739
   Slope:     1.06985
   R2:        0.865753

   ***
   *** Overall linear regression
   ***

   Correlation: 0.951062
   Slope:       5.16984
   R2:          0.904519
   F-statistic: 1373.62
   P-value:     0
   SSM:         7.55327e+10, DF: 1
   SSE:         7.97327e+09, DF: 145
   SST:         8.35059e+10, DF: 146

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.940142
   Slope:       0.820425
   R2:          0.883867
   F-statistic: 1103.57
   P-value:     0
```

```
SSM:          3387.56, DF: 1
SSE:          445.096, DF: 145
SST:          3832.65, DF: 146
```

Isoform expression scatter plot for: A2

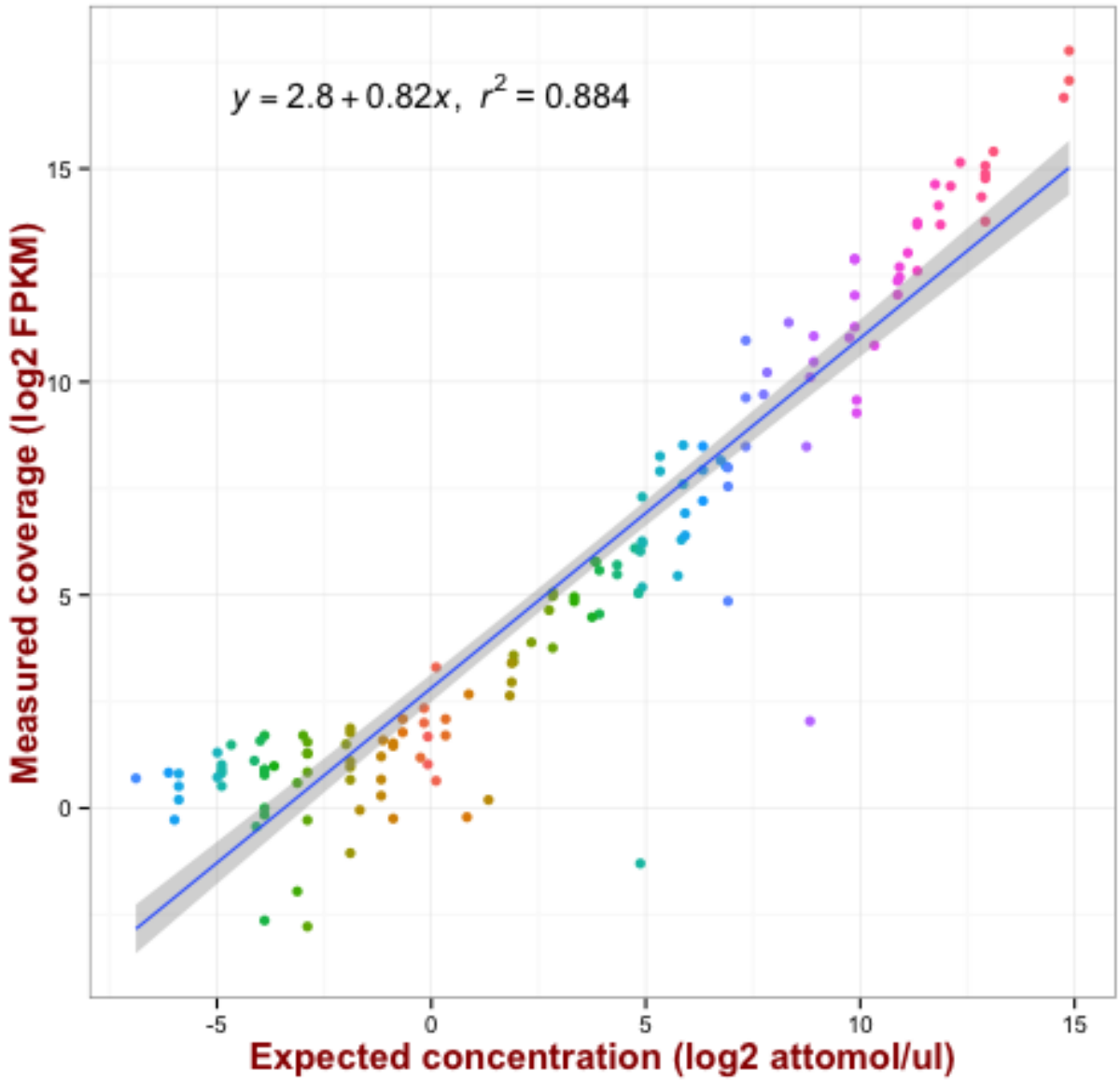


Isoform expression statistics for: A3

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

   Synthetic:   164 (0.00162484%)
   Experiment:  100769 (0.998375%)

   Reference:   162 isoform
   Detected:    162 isoform

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 3.5544 (R1_32_1)

   ***
   *** Before the break
   ***

   Intercept: 1.25307
   Slope:     0.157653
   R2:        0.0887965

   ***
   *** After the break
   ***

   Intercept: 0.825739
   Slope:     1.06985
   R2:        0.865753

   ***
   *** Overall linear regression
   ***

   Correlation: 0.951062
   Slope:       5.16984
   R2:          0.904519
   F-statistic: 1373.62
   P-value:     0
   SSM:         7.55327e+10, DF: 1
   SSE:         7.97327e+09, DF: 145
   SST:         8.35059e+10, DF: 146

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.940142
   Slope:       0.820425
   R2:          0.883867
   F-statistic: 1103.57
   P-value:     0
```

```
SSM:          3387.56, DF: 1
SSE:          445.096, DF: 145
SST:          3832.65, DF: 146
```

Isoform expression scatter plot for: A3

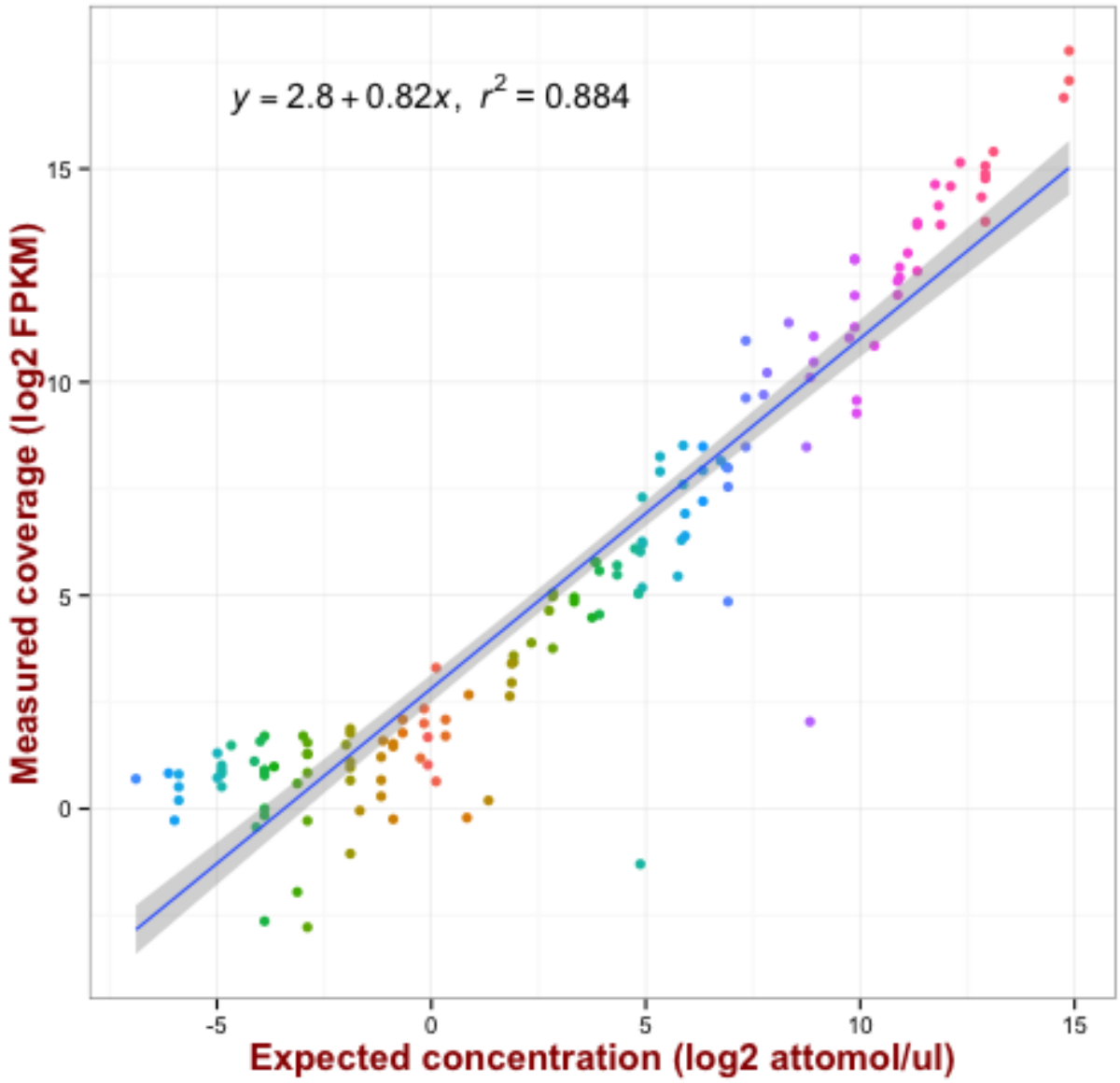


Isoform expression statistics for: B1

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

   Synthetic:   164 (0.00162484%)
   Experiment:  100769 (0.998375%)

   Reference:   162 isoform
   Detected:    162 isoform

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 3.5544 (R1_32_1)

   ***
   *** Before the break
   ***

   Intercept: 1.25307
   Slope:     0.157653
   R2:        0.0887965

   ***
   *** After the break
   ***

   Intercept: 0.825739
   Slope:     1.06985
   R2:        0.865753

   ***
   *** Overall linear regression
   ***

   Correlation: 0.951062
   Slope:       5.16984
   R2:          0.904519
   F-statistic: 1373.62
   P-value:     0
   SSM:         7.55327e+10, DF: 1
   SSE:         7.97327e+09, DF: 145
   SST:         8.35059e+10, DF: 146

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.940142
   Slope:       0.820425
   R2:          0.883867
   F-statistic: 1103.57
   P-value:     0
```

```
SSM:          3387.56, DF: 1
SSE:          445.096, DF: 145
SST:          3832.65, DF: 146
```

Isoform expression scatter plot for: B1

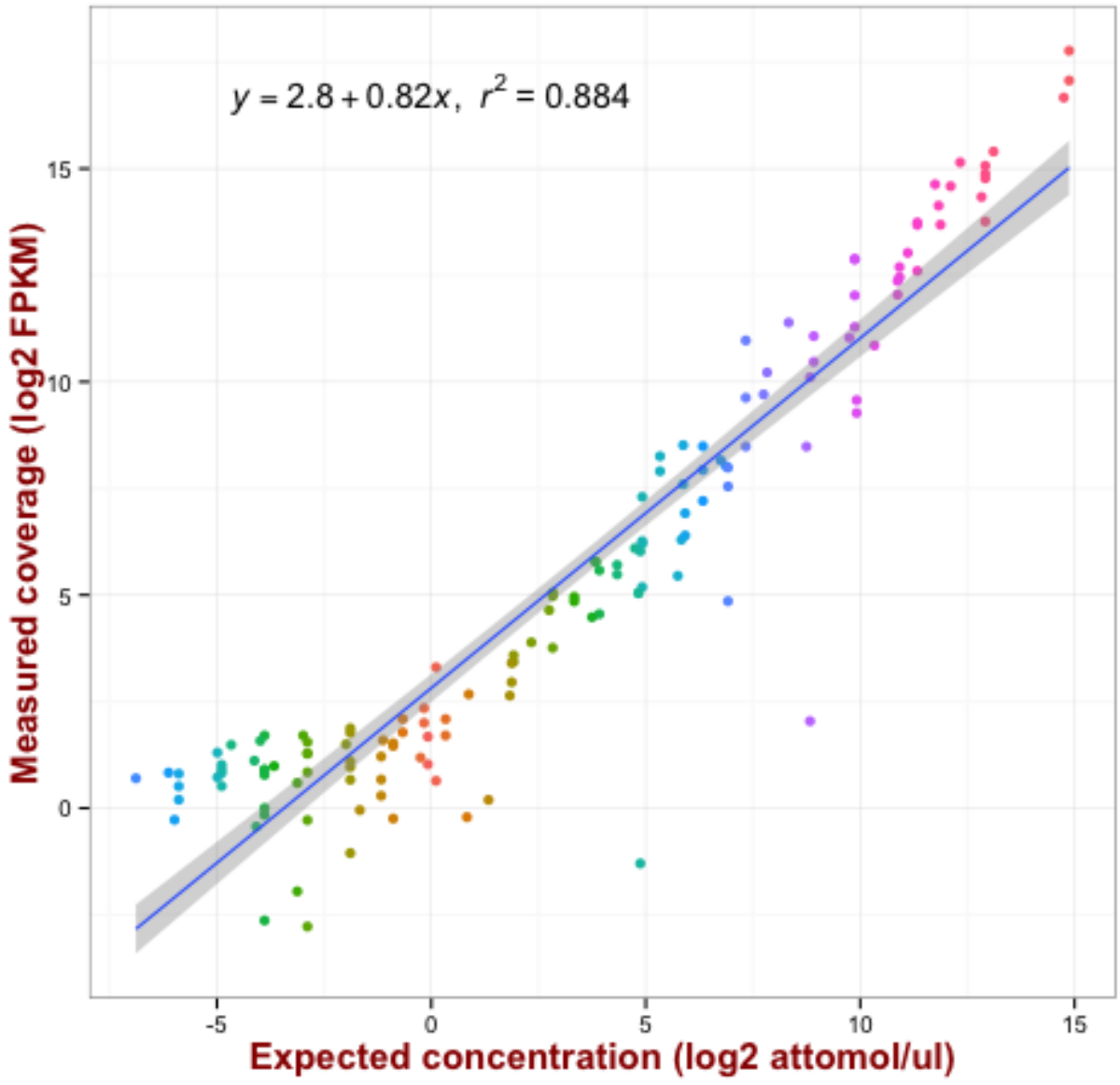


Isoform expression statistics for: B2

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

   Synthetic:   164 (0.00162484%)
   Experiment:  100769 (0.998375%)

   Reference:   162 isoform
   Detected:    162 isoform

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 3.5544 (R1_32_1)

   ***
   *** Before the break
   ***

   Intercept: 1.25307
   Slope:     0.157653
   R2:        0.0887965

   ***
   *** After the break
   ***

   Intercept: 0.825739
   Slope:     1.06985
   R2:        0.865753

   ***
   *** Overall linear regression
   ***

   Correlation: 0.951062
   Slope:       5.16984
   R2:          0.904519
   F-statistic: 1373.62
   P-value:     0
   SSM:         7.55327e+10, DF: 1
   SSE:         7.97327e+09, DF: 145
   SST:         8.35059e+10, DF: 146

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.940142
   Slope:       0.820425
   R2:          0.883867
   F-statistic: 1103.57
   P-value:     0
```

```
SSM:          3387.56, DF: 1
SSE:          445.096, DF: 145
SST:          3832.65, DF: 146
```

Isoform expression scatter plot for: B2

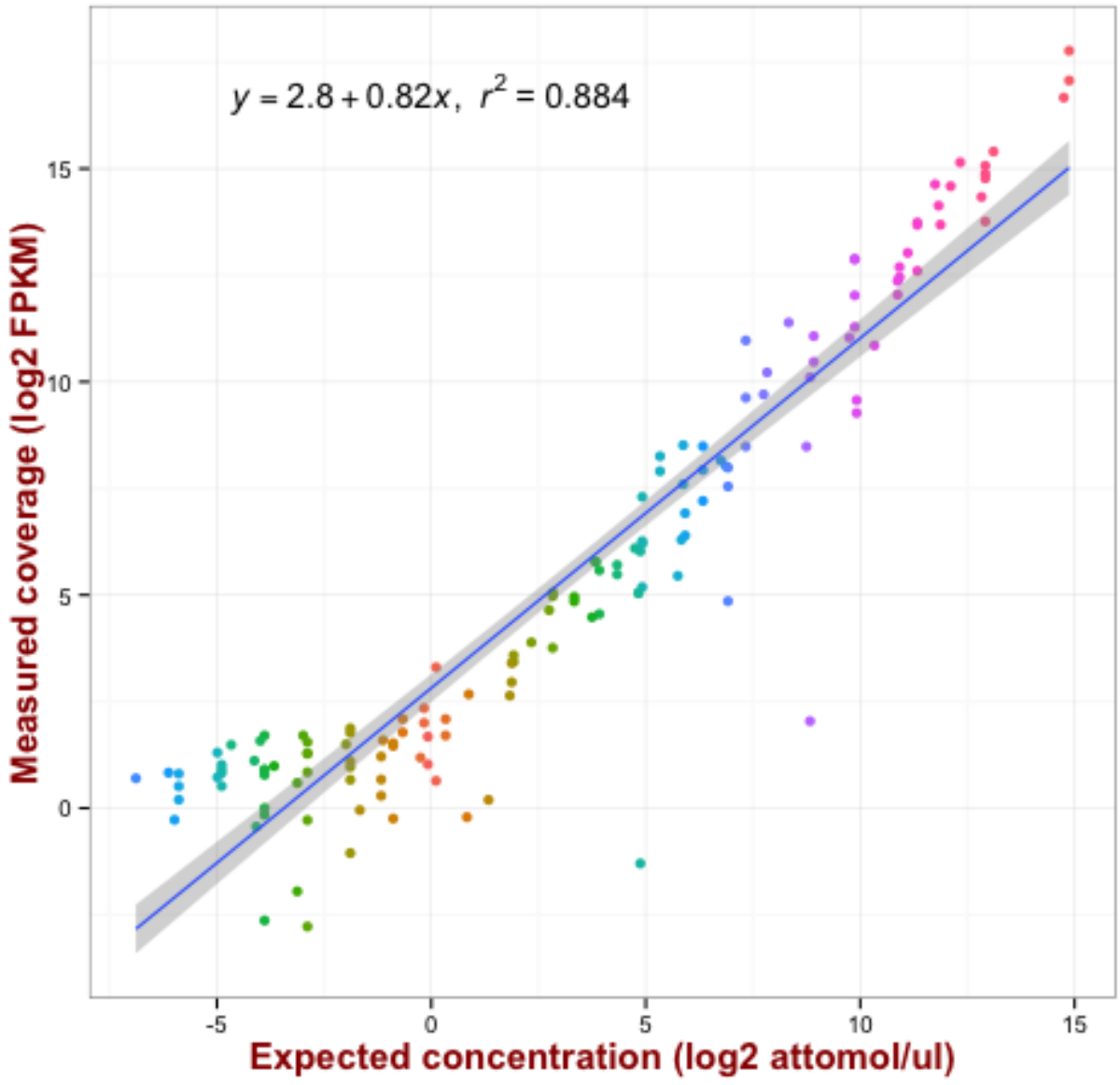


Isoform expression statistics for: B3

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

   Synthetic:   164 (0.00162484%)
   Experiment:  100769 (0.998375%)

   Reference:   162 isoform
   Detected:    162 isoform

   ***
   *** Detection Limit. Estimated by piecewise segmented regression.
   ***

   Break: 3.5544 (R1_32_1)

   ***
   *** Before the break
   ***

   Intercept: 1.25307
   Slope:     0.157653
   R2:        0.0887965

   ***
   *** After the break
   ***

   Intercept: 0.825739
   Slope:     1.06985
   R2:        0.865753

   ***
   *** Overall linear regression
   ***

   Correlation: 0.951062
   Slope:       5.16984
   R2:          0.904519
   F-statistic: 1373.62
   P-value:     0
   SSM:         7.55327e+10, DF: 1
   SSE:         7.97327e+09, DF: 145
   SST:         8.35059e+10, DF: 146

   ***
   *** Overall linear regression (log2 scale)
   ***

   Correlation: 0.940142
   Slope:       0.820425
   R2:          0.883867
   F-statistic: 1103.57
   P-value:     0
```

```
SSM:          3387.56, DF: 1
SSE:          445.096, DF: 145
SST:          3832.65, DF: 146
```

Isoform expression scatter plot for: B3

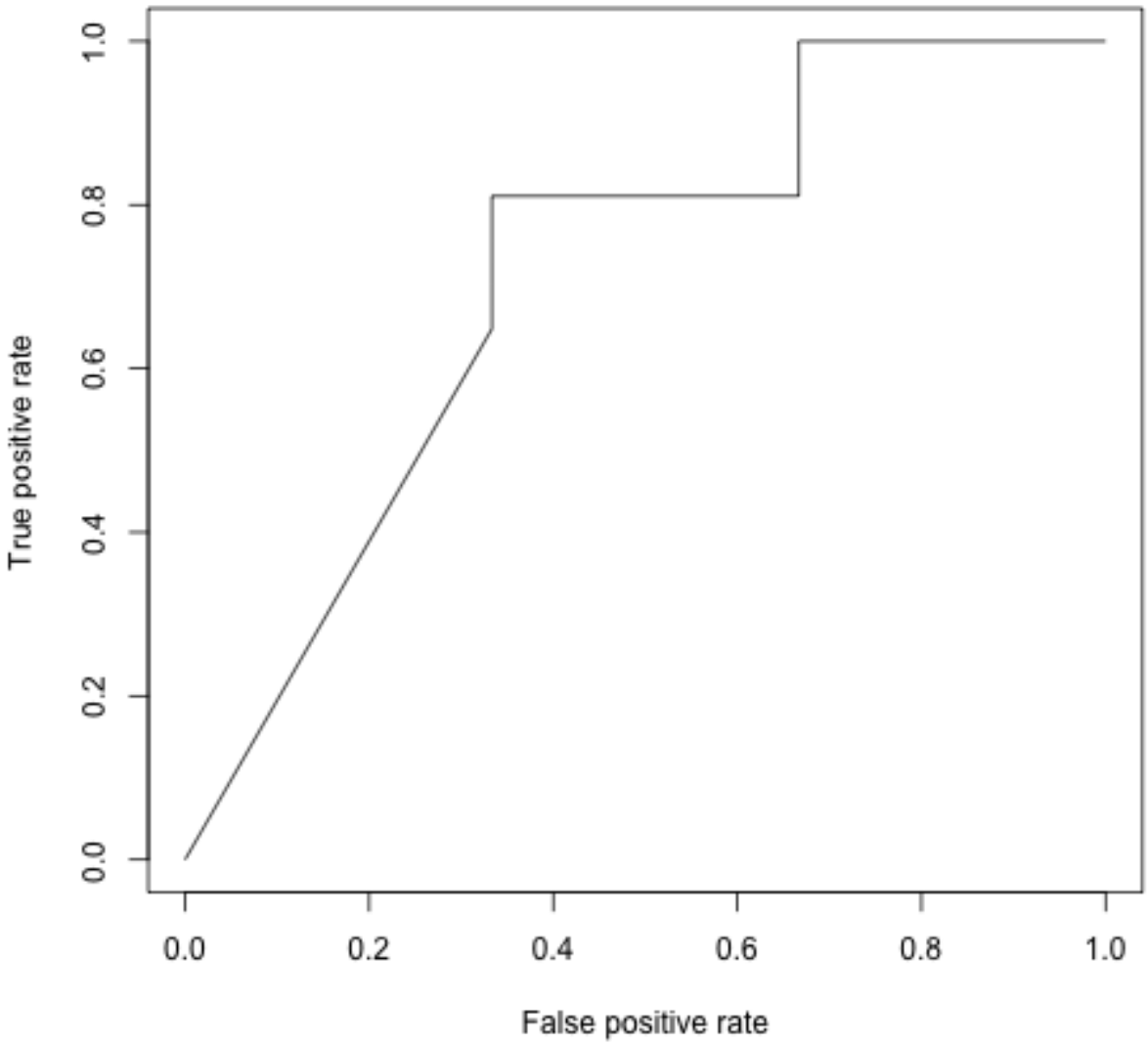


TransQuin Differential

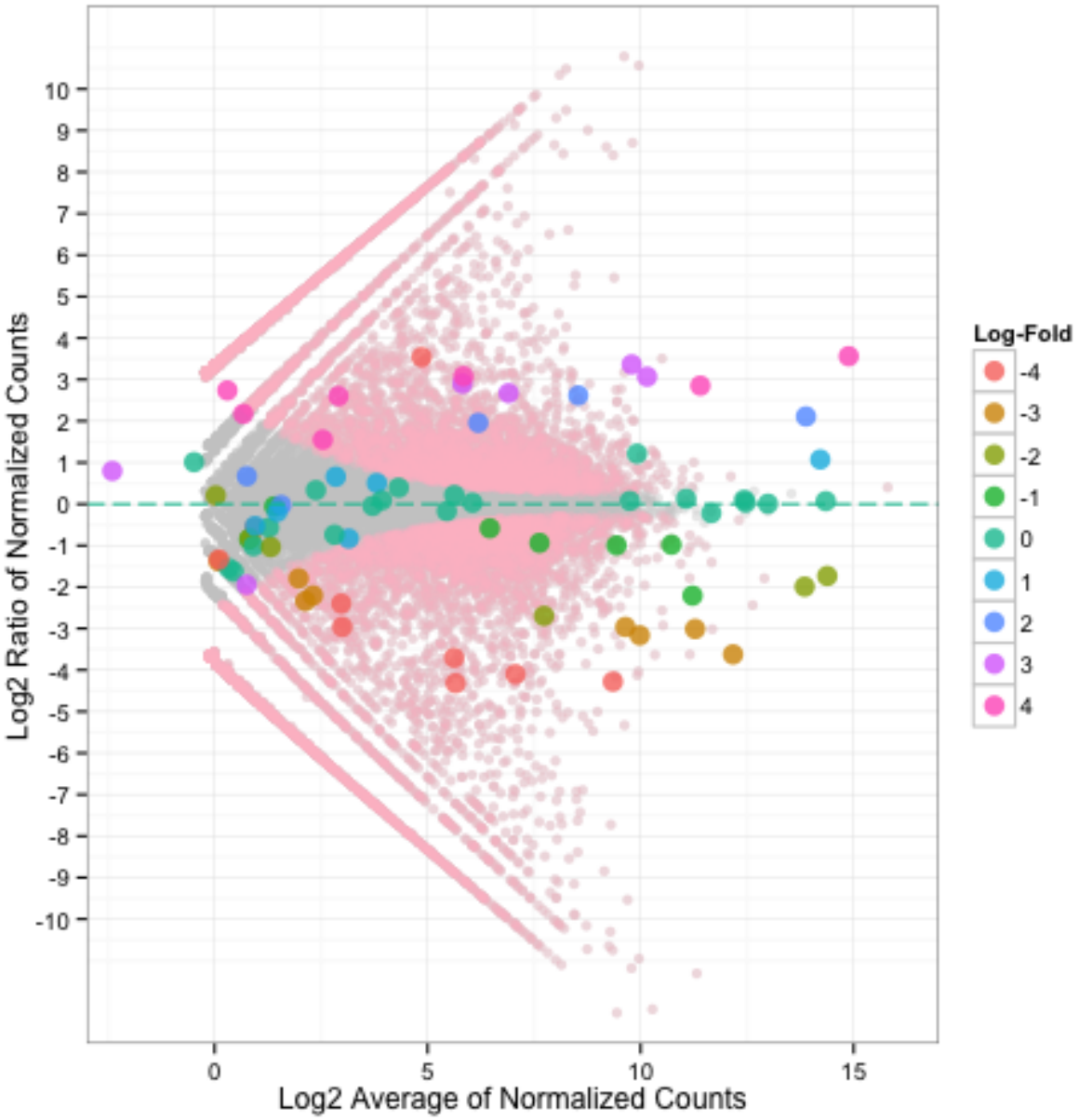
Differential summary statistics

```
Summary for dataset: /Users/tedwong/Desktop/K_562/DESeq2/DESeq2.csv

   Experiment:  60500 gene
   Synthetic:   75 gene

   Reference:   76 gene
   Detected:    75 gene

   ***
   *** Detection Limits
   ***

   Absolute:    0.0590086 (attomol/ul) (R2_38)

   ***
   *** Statistics for linear regression
   ***

   Correlation: 0.707428
   Slope:       0.426606
   R2:          0.500454
   F-statistic: 73.1328
   P-value:     1.29274e-12
   SSM:         302.202, DF: 1
   SSE:         301.653, DF: 73
   SST:         603.855, DF: 74

   ***
   *** Statistics for linear regression (log2 scale)
   ***

   Correlation: 0.790229
   Slope:       0.648599
   R2:          0.624462
   F-statistic: 121.388
   P-value:     0
   SSM:         183.058, DF: 1
   SSE:         110.087, DF: 73
   SST:         293.145, DF: 74
```

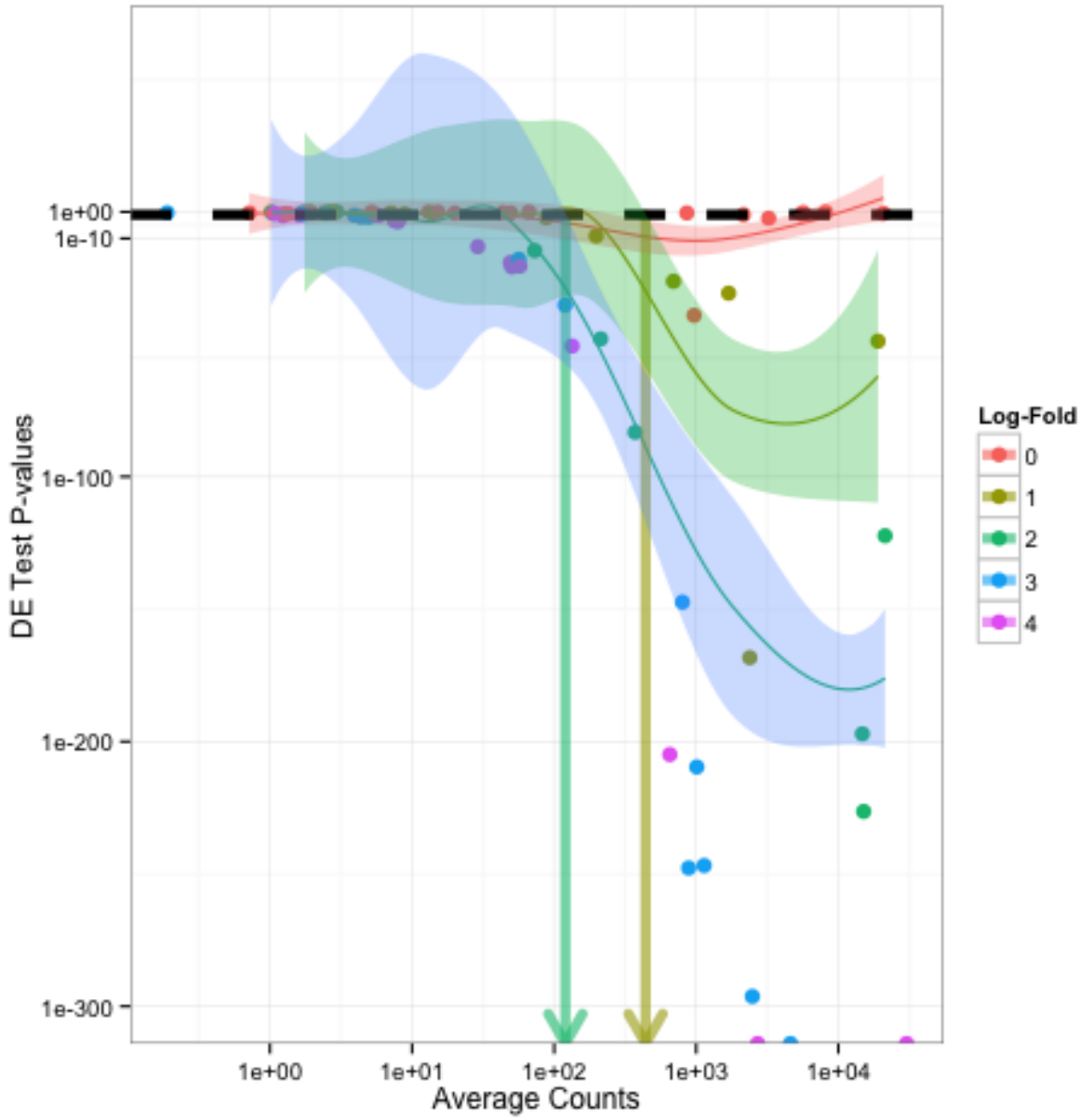
ROC plot


True positive rate
0.0
0.2
0.4
0.6
0.8
1.0
False positive rate
0.0
0.2
0.4
0.6
0.8
1.0

MA plot


Log2 Ratio of Normalized Counts
10
9
8
7
6
5
4
3
2
1
0
-1
-2
-3
-4
-5
-6
-7
-8
-9
-10
0
5
10
15
Log2 Average of Normalized Counts
Log-Fold
-4
-3
-2
-1
0
1
2
3
4

LODR plot


1e+00
1e-10
1e-100
1e-200
1e-300
DE Test P-values
1e+00
1e+01
1e+02
1e+03
1e+04
Average Counts
Log-Fold
0
1
2
3
4

Apprendix: TransQuin Alignment

Sequin statistics for: A1

ID	Abundance (attomol/ul)	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Spe
R1_101	15.1062	0.845083	1	0.999532	1	1
R1_102	15.1062	0.721599	1	0.994156	1	0.901155
R1_103	966.797	0.628255	1	0.995319	1	0.977373
R1_11	241.699	0.645833	1	0.998799	1	0.998818
R1_12	30.2124	0.591978	1	0.992884	1	0.9983
R1_13	7734.38	0.920394	1	0.987685	0.909091	0.946898
R1_14	483.398	1	1	0.999823	--	--
R1_21	30937.5	0.630945	1	0.993234	1	0.916456
R1_22	483.398	0.528054	1	0.998358	1	0.0416689
R1_23	15.1062	0.608499	1	0.988379	1	0.00621383
R1_24	483.398	0.999782	1	0.995249	1	0.998266
R1_31	241.699	0.688293	1	0.995473	1	0.244225
R1_32	60.4248	0.545455	1	0.999737	1	1
R1_33	0.118017	0.899202	1	0.993455	1	0.994169
R1_41	7734.37	0.78125	1	0.996675	1	0.999808
R1_42	7734.38	0.617479	1	0.980681	1	0.976687
R1_43	120.85	0.540369	1	0.990501	0.973684	0.96341
R1_51	1933.59	0.607103	1	0.996288	1	0.999373
R1_52	0.944138	0.622807	1	0.991475	1	1
R1_53	120.85	0.998489	1	0.99784	1	0.370359
R1_61	7.5531	0.679466	1	1	1	1
R1_62	3.77655	0.774336	1	1	1	1
R1_63	3867.19	0.669443	1	0.995492	1	0.971203
R1_71	15468.8	0.740968	1	0.994243	1	0.998708
R1_72	1.88828	0.582844	1	1	1	1
R1_73	1933.59	0.731952	1	0.984041	1	0.98719
R1_81	120.85	0.747244	1	0.99754	1	0.995044
R1_82	3867.19	0.587741	1	0.995744	1	0.992876
R1_83	30.2124	0.644813	1	0.998373	1	0.997866
R1_91	0.472069	0.685055	1	1	1	1
R1_92	241.699	0.777919	1	0.980772	1	0.995753
R1_93	60.4248	0.625086	1	0.996054	1	0.999554
R2_1	0.944138	0.99196	1	1	--	--
R2_105	0.944138	0.874667	1	0.967742	--	--
R2_115	120.85	0.837412	1	0.988931	1	0.996079
R2_116	1.88828	0.584726	1	0.987644	1	1
R2_117	60.4248	0.711066	1	0.999248	1	0.998209
R2_14	15468.8	0.719569	1	0.988252	1	0.987247
R2_150	1933.59	0.835063	1	0.998167	1	0.518953
R2_151	1.88828	0.578303	1	0.983911	1	0.000681453
R2_152	30.2124	0.603856	1	0.99729	1	0.0120943
R2_153	0.944138	0.677873	1	0.995311	1	0.359343
R2_154	3867.19	0.855658	1	0.989621	1	0.547718
R2_18	15468.8	0.628326	1	0.9853	1	0.852844
R2_19	3867.19	0.811493	1	0.992328	1	0.98788
R2_20	30.2124	0.735871	1	0.997986	1	0.997017
R2_24	15.1062	0.586003	0.979592	0.991056	0.957447	0.693273
R2_26	1933.59	0.916638	1	0.994978	1	0.994222
R2_27	7.5531	0.754167	1	0.995777	1	1

```
R2_28   0.472069    0.68506 1   1   1   1   0.68506 1
R2_32   0.472069    0.671486    1   0.98234 1   1   0.671486    0.997715
R2_33   0.0590086   0.879859    1   1   1   0.000191773 0.879859    1
R2_37   0.236034    0.719465    1   0.993295    1   0.982877    0.719465    0.998428
R2_38   0.0590086   0.391233    1   0.989899    1   1   0.391233    0.995805
R2_41   241.699 0.837384    1   0.991692    1   0.995112    0.837384    0.989443
R2_42   0.236034    0.882171    1   0.998311    1   1   0.882171    0.999561
R2_45   0.472069    0.462072    1   1   1   1   0.462072    1
R2_46   0.118017    0.688515    1   0.993056    1   1   0.688515    0.967061
R2_47   120.85  0.887733    1   0.996614    1   0.997939    0.887733    0.998675
R2_53   0.118017    0.396308    1   0.989455    1   0.997009    0.396308    0.997744
R2_54   483.398 0.864703    1   0.982539    1   0.996987    0.864703    0.996936
R2_55   30937.5 0.880804    1   0.987179    1   0.873955    0.880804    0.99142
R2_57   7.5531  0.65303 1   0.996765    1   1   0.65303 0.998819
R2_59   0.472069    0.588824    1   0.988263    1   0.993952    0.588824    0.999726
R2_6    483.398 0.702025    1   0.996212    1   0.990037    0.702025    0.98913
R2_60   7.5531  0.605403    1   0.996636    1   1   0.605403    0.997073
R2_63   966.797 0.879982    1   0.987448    1   0.997983    0.879982    0.997517
R2_65   3.77655 0.995595    1   1   --  --  0.995595    1
R2_66   30937.5 0.529254    1   0.999748    1   0.999936    0.529254    0.985015
R2_67   3.77655 0.959847    1   1   1   1   0.959847    1
R2_68   3.77655 0.705317    1   0.998856    1   1   0.705317    0.999367
R2_7    966.797 0.760474    1   0.994878    1   0.994215    0.760474    0.994466
R2_71   3.77655 0.72861 1   0.986272    1   1   0.72861 0.998168
R2_72   0.236034    0.320416    0.866667    0.993094    0.727273    1   0.320416    0.99815
R2_73   1.88828 0.94562 1   0.988466    1   0.996508    0.94562 0.999279
R2_76   0.0590086   0.470652    1   1   1   1   0.470652    1
```

Sequin statistics for: A2

ID	Abundance (attomol/ul)	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Spe
R1_101	15.1062	0.843342	1	0.997495	1	0.995816	0.843342	0.995889
R1_102	15.1062	0.721599	1	0.995219	1	0.00552418	0.721599	0.998544
R1_103	966.797	0.628532	1	0.995586	1	0.185487	0.628532	0.995612
R1_11	241.699	0.647177	1	0.999245	1	0.0529042	0.647177	0.997927
R1_12	30.2124	0.590595	1	0.9933	0.956522	1	0.590595	0.998247
R1_13	7734.38	0.920394	1	0.988579	0.909091	0.661924	0.920394	0.995082
R1_14	483.398	1	1	0.999844	--	--	1	0.991045
R1_21	30937.5	0.630945	1	0.994394	1	0.942939	0.630945	0.942446
R1_22	483.398	0.527602	1	0.998493	1	0.101617	0.527602	0.994032
R1_23	15.1062	0.604667	1	0.989406	1	0.0153541	0.604667	0.997701
R1_24	483.398	1	1	0.995351	1	0.995767	1	0.99782
R1_31	241.699	0.687823	1	0.994739	1	0.998694	0.687823	0.995916
R1_32	60.4248	0.545455	1	0.998386	1	1	0.545455	0.995772
R1_33	0.118017	0.911321	1	0.998728	1	0.99726	0.911321	0.999676
R1_41	7734.37	0.78125	1	0.996939	1	0.932387	0.78125	0.994695
R1_42	7734.38	0.617479	1	0.981914	1	0.891942	0.617479	0.986842
R1_43	120.85	0.541274	1	0.990613	0.973684	0.989699	0.541274	0.996335
R1_51	1933.59	0.607103	1	0.995118	1	0.988762	0.607103	0.99446
R1_52	0.944138	0.623188	1	0.979032	1	0.992218	0.623188	0.977858
R1_53	120.85	0.998489	1	0.995792	1	0.726932	0.998489	0.996983
R1_61	7.5531	0.676962	1	0.99811	1	0.00262261	0.676962	0.998768
R1_62	3.77655	0.767383	1	0.992147	1	0.00112939	0.767383	0.999177
R1_63	3867.19	0.669964	1	0.995761	1	0.964477	0.669964	0.995745
R1_71	15468.8	0.740968	1	0.993449	1	0.964899	0.740968	0.987705
R1_72	1.88828	0.600451	1	1	1	0.000569401	0.600451	1
R1_73	1933.59	0.732371	1	0.989559	0.96	0.531614	0.732371	0.996583
R1_81	120.85	0.747244	1	0.998029	1	0.994022	0.747244	0.996849
R1_82	3867.19	0.587741	1	0.992549	1	0.995822	0.587741	0.991501
R1_83	30.2124	0.645199	1	0.999418	1	0.999628	0.645199	0.99702
R1_91	0.472069	0.685696	1	1	1	1	0.685696	1
R1_92	241.699	0.781726	1	0.980355	1	0.995561	0.781726	0.995153
R1_93	60.4248	0.625086	1	0.996684	1	0.998378	0.625086	0.996156
R2_1	0.944138	0.98995	1	1	--	--	0.98995	1
R2_105	0.944138	0.68	1	1	--	--	0.68	1
R2_115	120.85	0.840131	1	0.989271	1	0.996256	0.840131	0.99549
R2_116	1.88828	0.524582	1	0.996665	1	1	0.524582	0.998183
R2_117	60.4248	0.710041	1	0.999708	1	0.999328	0.710041	0.997122
R2_14	15468.8	0.719569	1	0.988161	1	0.737964	0.719569	0.991507
R2_150	1933.59	0.835448	1	0.998619	1	0.673702	0.835448	0.991785
R2_151	1.88828	0.565179	1	0.981308	0.85	0.00120631	0.565179	0.998454
R2_152	30.2124	0.603368	1	0.998585	1	0.028801	0.603368	0.997981
R2_153	0.944138	0.669927	1	0.981132	1	1	0.669927	0.999088
R2_154	3867.19	0.855658	1	0.986231	1	0.753071	0.855658	0.994631
R2_18	15468.8	0.628326	1	0.982418	1	0.932695	0.628326	0.986486
R2_19	3867.19	0.811493	1	0.994275	1	0.395306	0.811493	0.998717
R2_20	30.2124	0.732026	1	0.998159	1	0.998462	0.732026	0.998951
R2_24	15.1062	0.586299	0.979592	0.987268	0.957447	0.764632	0.586299	0.998994
R2_26	1933.59	0.916638	1	0.994996	1	0.995074	0.916638	0.997755
R2_27	7.5531	0.750595	1	0.994545	1	1	0.750595	0.999208
R2_28	0.472069	0.686747	1	0.996957	1	1	0.686747	0.979381
R2_32	0.472069	0.671486	1	0.992126	1	1	0.671486	0.998171

R2_33	0.0590086	0.90106	1	1	1	1	0.90106	1	
R2_37	0.236034	0.719239	1	1	1	1	0.719239	1	
R2_38	0.0590086	0.399143	1	0.984831	1	1	0.399143	0.998351	
R2_41	241.699	0.839171	1	0.991918	1	0.998755	0.839171	0.990299	
R2_42	0.236034	0.874031	1	1	1	1	0.874031	1	
R2_45	0.472069	0.464239	1	0.999817	1	0.998319	0.464239	0.999689	
R2_46	0.118017	0.70475	1	0.988748	1	1	0.70475	0.967396	
R2_47	120.85	0.887733	1	0.997391	1	0.998014	0.887733	0.998675	
R2_53	0.118017	0.396487	1	0.997205	1	0.997577	0.396487	0.999097	
R2_54	483.398	0.864703	1	0.983372	1	0.996267	0.864703	0.997191	
R2_55	30937.5	0.880804	1	0.987741	1	0.862818	0.880804	0.990647	
R2_57	7.5531	0.659591	1	0.996748	1	0.00525698	0.659591	0.998248	
R2_59	0.472069	0.583656	1	1	1	1	0.583656	1	
R2_6	483.398	0.702989	1	0.998334	1	0.994613	0.702989	0.995902	
R2_60	7.5531	0.604692	1	0.996744	1	0.00539659	0.604692	0.997069	
R2_63	966.797	0.884363	1	0.984499	1	0.985809	0.884363	0.997037	
R2_65	3.77655	0.995595	1	1	--	--	0.995595	1	
R2_66	30937.5	0.529254	1	0.999748	1	0.999958	0.529254	0.985015	
R2_67	3.77655	0.992352	1	1	1	1	0.992352	1	
R2_68	3.77655	0.707775	1	0.996954	1	1	0.707775	0.999684	
R2_7	966.797	0.760474	1	0.997273	1	0.999218	0.760474	0.993367	
R2_71	3.77655	0.69385	1	0.992081	1	0.992248	0.69385	0.997118	
R2_72	0.236034	0.338827	0.866667	0.985673	0.545455	1	0.338827	0.999124	
R2_73	1.88828	0.950398	1	0.991652	1	0.99652	0.950398	0.975023	
R2_76	0.0590086	0.477536	1	0.99809	1	1	0.477536	0.999242	

Sequin statistics for: A3

ID	Abundance (attomol/ul)	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Spe
R1_101	15.1062	0.844212	1	0.999087	1	1
R1_102	15.1062	0.723352	1	0.995112	1	0.0284201
R1_103	966.797	0.629086	1	0.995227	1	0.535702
R1_11	241.699	0.646505	1	0.998816	1	0.0505829
R1_12	30.2124	0.591978	1	0.993087	1	0.999141
R1_13	7734.38	0.920394	1	0.988092	0.909091	0.909266
R1_14	483.398	1	1	0.999779	--	--
R1_21	30937.5	0.630945	1	0.993913	1	0.951111
R1_22	483.398	0.528054	1	0.998712	1	0.201023
R1_23	15.1062	0.610589	1	0.987265	1	0.0338936
R1_24	483.398	1	1	0.995487	1	0.998898
R1_31	241.699	0.687823	1	0.994534	1	0.998714
R1_32	60.4248	0.544876	1	0.997818	1	1
R1_33	0.118017	0.912504	1	0.997554	1	0.996416
R1_41	7734.37	0.78125	1	0.99667	1	0.999697
R1_42	7734.38	0.617479	1	0.980701	1	0.897666
R1_43	120.85	0.540731	1	0.99053	0.973684	0.984815
R1_51	1933.59	0.607103	1	0.996042	1	0.992969
R1_52	0.944138	0.623951	1	0.989971	1	1
R1_53	120.85	0.998489	1	0.998404	1	0.973515
R1_61	7.5531	0.709516	1	0.993926	1	1
R1_62	3.77655	0.776233	1	1	1	1
R1_63	3867.19	0.669703	1	0.995554	1	0.974728
R1_71	15468.8	0.740968	1	0.993971	1	0.988434
R1_72	1.88828	0.604966	1	1	1	1
R1_73	1933.59	0.731743	1	0.983855	0.96	0.986432
R1_81	120.85	0.747638	1	0.996786	1	0.994027
R1_82	3867.19	0.587741	1	0.992415	1	0.997628
R1_83	30.2124	0.644427	1	0.997372	1	0.996722
R1_91	0.472069	0.684413	1	0.998495	1	1
R1_92	241.699	0.778765	1	0.980597	1	0.995994
R1_93	60.4248	0.625086	1	0.995437	1	0.998834
R2_1	0.944138	0.994975	1	1	--	--
R2_105	0.944138	0.981333	1	0.979167	--	--
R2_115	120.85	0.837955	1	0.989482	1	0.997475
R2_116	1.88828	0.583771	1	0.988752	1	1
R2_117	60.4248	0.709016	1	0.999618	1	0.99934
R2_14	15468.8	0.719569	1	0.989328	1	0.838494
R2_150	1933.59	0.835832	1	0.997978	1	0.821556
R2_151	1.88828	0.589676	1	0.990974	1	0.00596157
R2_152	30.2124	0.603368	1	0.998327	1	0.0588556
R2_153	0.944138	0.685208	1	0.995346	1	0.983165
R2_154	3867.19	0.855658	1	0.986493	1	0.834231
R2_18	15468.8	0.628326	1	0.984271	1	0.935806
R2_19	3867.19	0.811493	1	0.994731	1	0.753652
R2_20	30.2124	0.733948	1	0.996812	1	0.99733
R2_24	15.1062	0.586741	0.979592	0.990687	0.957447	0.842066
R2_26	1933.59	0.916982	1	0.995763	1	0.994951
R2_27	7.5531	0.755357	1	0.993405	1	0.999065
R2_28	0.472069	0.68988	1	0.999127	1	1
R2_32	0.472069	0.671486	1	0.989034	1	1

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R2_33   0.0590086   0.971731    1   0.947368    1   1   0.971731    0.99278
R2_37   0.236034    0.727623    1   0.993796    1   0.993171    0.727623    0.997825
R2_38   0.0590086   0.399473    1   0.995508    1   1   0.399473    0.998353
R2_41   241.699 0.839171    1   0.992037    1   0.998985    0.839171    0.968247
R2_42   0.236034    0.885659    1   0.997419    1   1   0.885659    0.949709
R2_45   0.472069    0.464528    1   0.997782    1   1   0.464528    0.998447
R2_46   0.118017    0.719784    1   0.99254 1   1   0.719784    0.967273
R2_47   120.85  0.888518    1   0.996762    1   0.996155    0.888518    0.998676
R2_53   0.118017    0.397025    1   0.994321    1   0.994027    0.397025    0.997748
R2_54   483.398 0.864703    1   0.982499    1   0.997465    0.864703    0.997446
R2_55   30937.5 0.880804    1   0.988265    1   0.838564    0.880804    0.990647
R2_57   7.5531  0.659205    1   0.99747 1   0.00678764  0.659205    0.99883
R2_59   0.472069    0.596415    1   0.9968  1   0.998424    0.596415    0.999459
R2_6    483.398 0.702025    1   0.995403    1   0.991333    0.702025    0.993179
R2_60   7.5531  0.605759    1   0.995309    1   0.00940813  0.605759    0.997074
R2_63   966.797 0.884801    1   0.985674    1   0.988104    0.884801    0.996547
R2_65   3.77655 0.994493    1   0.997792    --  --  0.994493    0.998894
R2_66   30937.5 0.529254    1   0.988763    1   0.999892    0.529254    0.986
R2_67   3.77655 0.967495    1   1   1   1   0.967495    1
R2_68   3.77655 0.717828    1   0.996747    1   0.998457    0.717828    0.999378
R2_7    966.797 0.76132 1   0.99719 1   0.999558    0.76132 0.994472
R2_71   3.77655 0.916444    1   0.993642    1   0.997036    0.916444    0.986331
R2_72   0.236034    0.347439    0.866667    0.991036    0.727273    1   0.347439    0.997017
R2_73   1.88828 0.943572    1   0.985888    1   0.998646    0.943572    0.999759
R2_76   0.0590086   0.477536    1   0.994867    1   1   0.477536    0.998485
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Sequin statistics for: B1

ID	Abundance (attomol/ul)	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Spe
R1_101	15.1062 0.787641	1	0.996774	1	1	0.787641	0.998896
R1_102	15.1062 0.721248	1	0.98946 1	0.108223	0.721248	0.999514
R1_103	966.797 0.627978	1	0.992978	1	0.959322	0.627978	0.996484
R1_11	241.699 0.644489	1	0.989534	1	1	0.644489	0.997919
R1_12	30.2124 0.569848	1	0.992637	1	0.991467	0.569848	0.998788
R1_13	7734.38 0.920394	1	0.988299	0.909091	0.983353	0.920394	0.995082
R1_14	483.398 0.996988	1	0.999917	--	--	0.996988	0.996988
R1_21	30937.5 0.630945	1	0.993465	1	0.902076	0.630945	0.941599
R1_22	483.398 0.526697	1	0.999028	1	0.0033303	0.526697	0.997429
R1_23	15.1062 0.609892	1	0.983464	1	0.00570884	0.609892	0.997153
R1_24	483.398 0.999345	1	0.995356	1	0.998841	0.999345	0.998472
R1_31	241.699 0.688764	1	0.99394 1	0.997605	0.688764	0.992547
R1_32	60.4248 0.541401	1	1	1	1	0.541401	1
R1_33	0.118017 0.88324	1	0.997831	1	1	0.88324	0.999331
R1_41	7734.37 0.78125 1	0.99979 1	0.997007	0.78125	0.995575
R1_42	7734.38 0.617479	1	0.989977	1	0.975927	0.617479	0.990854
R1_43	120.85 0.541999	1	0.986484	0.973684	0.348855	0.541999	0.996339
R1_51	1933.59 0.603157	1	0.995454	1	0.855858	0.603157	0.995349
R1_52	0.944138 0.622807	1	0.994252	1	1	0.622807	0.998166
R1_53	120.85 0.998993	1	0.997143	1	0.718094	0.998993	0.996985
R1_61	7.5531 0.718698	1	1	1	1	0.718698	1
R1_62	3.77655 0.697219	1	1	1	1	0.697219	1
R1_63	3867.19 0.670484	1	0.994539	1	0.857561	0.670484	0.995748
R1_71	15468.8 0.740968	1	0.99358 1	0.848788	0.740968	0.986694
R1_72	1.88828 0.544921	1	1	1	1	0.544921	1
R1_73	1933.59 0.731115	1	0.991175	0.96	0.993206	0.731115	0.997431
R1_81	120.85 0.747244	1	0.996891	1	0.991853	0.747244	0.996325
R1_82	3867.19 0.587741	1	0.999352	1	0.987979	0.587741	0.992908
R1_83	30.2124 0.647513	1	0.998826	1	0.998681	0.647513	0.998216
R1_91	0.472069 0.66517 1	1	1	1	1	0.66517 1
R1_92	241.699 0.778765	1	0.980861	1	0.995714	0.778765	0.995135
R1_93	60.4248 0.625086	1	0.996681	1	0.99831 0.625086	0.996156
R2_1	0.944138 0.994975	1	1	--	--	0.994975	1
R2_105	0.944138 0.946667	1	0.992857	--	--	0.946667	0.994398
R2_115	120.85 0.842849	1	0.991243	1	0.99245 0.842849	0.923719
R2_116	1.88828 0.573747	1	0.984551	1	1	0.573747	0.999169
R2_117	60.4248 0.71209 1	0.998192	1	0.997355	0.71209 0.994989
R2_14	15468.8 0.719569	1	0.984461	1	0.904376	0.719569	0.991507
R2_150	1933.59 0.831603	1	0.999201	1	0.0928247	0.831603	0.997694
R2_151	1.88828 0.56343 1	1	1	0.000648549 0.56343 1
R2_152	30.2124 0.606541	1	0.99787 1	0.0104632	0.606541	0.997992
R2_153	0.944138 0.680318	1	0.991786	1	1	0.680318	0.988016
R2_154	3867.19 0.853349	1	0.98975 1	0.345297	0.853349	0.994616
R2_18	15468.8 0.628326	1	0.98623 1	0.852354	0.628326	0.986486
R2_19	3867.19 0.811146	1	0.99566 1	0.940862	0.811146	0.999001
R2_20	30.2124 0.733948	1	0.998092	1	0.995501	0.733948	0.997388
R2_24	15.1062 0.586003	0.979592	0.990261	0.957447	0.846247	0.586003	0.998239
R2_26	1933.59 0.916982	1	0.992369	1	0.957098	0.916982	0.997569
R2_27	7.5531 0.752976	1	0.992291	1	1	0.752976	0.99921
R2_28	0.472069 0.689157	1	1	1	1	0.689157	1
R2_32	0.472069 0.66964 1	0.996432	1	1	0.66964 0.998624

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R2_33   0.0590086   0.416961    0.5 1   0   nan 0.416961    1
R2_37   0.236034    0.694992    1   0.994852    1   0.981481    0.694992    0.999348
R2_38   0.0590086   0.379038    1   0.992625    1   1   0.379038    0.997398
R2_41   241.699 0.837026    1   0.993443    1   0.9981  0.837026    0.990694
R2_42   0.236034    0.874031    1   1   1   1   0.874031    1
R2_45   0.472069    0.462216    1   0.996477    1   1   0.462216    0.998439
R2_46   0.118017    0.702646    1   1   1   1   0.702646    1
R2_47   120.85  0.888911    1   0.996626    1   0.995795    0.888911    0.998237
R2_53   0.118017    0.387345    1   0.995233    1   1   0.387345    0.999075
R2_54   483.398 0.864703    1   0.985219    1   0.996922    0.864703    0.997701
R2_55   30937.5 0.880804    1   0.983178    1   0.99546 0.880804    0.990647
R2_57   7.5531  0.625241    1   1   0.941176    1   0.625241    1
R2_59   0.472069    0.553456    1   0.993644    1   0.984615    0.553456    0.999708
R2_6    483.398 0.702989    1   0.996895    1   0.999525    0.702989    0.990489
R2_60   7.5531  0.607892    1   0.997855    1   0.998146    0.607892    0.997085
R2_63   966.797 0.886991    1   0.998694    1   0.999702    0.886991    0.997046
R2_65   3.77655 0.993392    1   1   --  --  0.993392    1
R2_66   30937.5 0.528717    1   0.99979 1   0.999945    0.528717    0.987964
R2_67   3.77655 0.782027    1   1   1   1   0.782027    1
R2_68   3.77655 0.568811    0.846154    0.996553    0.833333    0.998019    0.568811    0.998823
R2_7    966.797 0.76132 1   0.996266    1   0.999624    0.76132 0.994472
R2_71   3.77655 0.77139 1   0.977113    1   0.975684    0.77139 0.99827
R2_72   0.236034    0.313586    0.866667    0.985308    0.636364    1   0.313586    0.99811
R2_73   1.88828 0.921274    1   0.989642    0.952381    0.997619    0.921274    0.999506
R2_76   0.0590086   0.463043    1   0.996114    1   1   0.463043    0.999218
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Sequin statistics for: B2

ID	Abundance (attomol/ul)	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Spe
R1_101	15.1062 0.832898	1	1	1	1	0.832898 1
R1_102	15.1062 0.698107	1	0.985276	1	0.244275	0.698107 0.999498
R1_103	966.797 0.628532	1	0.993265	1	0.970835	0.628532 0.996924
R1_11	241.699 0.644489	1	1	1	1	0.644489 1
R1_12	30.2124 0.590941	1	0.995051	1	1	0.590941 0.998831
R1_13	7734.38 0.920394	1	0.987888	0.909091	0.995075	0.920394 0.995082
R1_14	483.398 1	1	0.999876	--	--	1 0.995502
R1_21	30937.5 0.630945	1	0.99394 1	0.839282	0.630945	0.942446
R1_22	483.398 0.527149	1	0.999506	1	0.0015311	0.527149 0.999142
R1_23	15.1062 0.609892	1	0.986752	1	0.00298525	0.609892 0.997721
R1_24	483.398 0.999563	1	0.995545	1	0.998693	0.999563 0.998037
R1_31	241.699 0.688764	1	0.992008	1	0.997879	0.688764 0.99322
R1_32	60.4248 0.544296	1	1	1	1	0.544296 1
R1_33	0.118017	0.896837	1	0.983193	1	1 0.896837 0.999341
R1_41	7734.37 0.78125 1	0.999876	1	0.874219	0.78125 0.995575	
R1_42	7734.38 0.617479	1	0.990803	1	0.985162	0.617479 0.993884
R1_43	120.85 0.541636	1	0.985438	0.973684	0.803818	0.541636 0.996005
R1_51	1933.59 0.604284	1	0.996225	1	0.0829933	0.604284 0.997209
R1_52	0.944138	0.622807	1	0.994399	1	1 0.622807 0.997557
R1_53	120.85 0.998489	1	0.997344	1	0.0360915	0.998489 0.996482
R1_61	7.5531 0.687813	1	0.986755	1	0.959677	0.687813 0.998788
R1_62	3.77655 0.686473	1	1	0.8 0.8	0.686473	1
R1_63	3867.19 0.670484	1	0.993684	1	0.877702	0.670484 0.996133
R1_71	15468.8 0.740968	1	0.993425	1	0.997341	0.740968 0.984678
R1_72	1.88828 0.600903	1	1	1	0.8	0.600903 1
R1_73	1933.59 0.731115	1	0.991099	0.96	0.985267	0.731115 0.997716
R1_81	120.85 0.748031	1	0.997639	1	0.992314	0.748031 0.996329
R1_82	3867.19 0.587741	1	0.99715 1	0.988495	0.587741	0.9908
R1_83	30.2124 0.647127	1	0.998647	1	0.99802 0.647127	0.998215
R1_91	0.472069	0.668377	1	1	1	1 0.668377 1
R1_92	241.699 0.778342	1	0.983037	1	0.996622	0.778342 0.994595
R1_93	60.4248 0.625086	1	0.996003	1	0.996222	0.625086 0.996156
R2_1	0.944138	0.99397 1	1	--	--	0.99397 1
R2_105	0.944138	0.981333	1	0.954887	--	-- 0.981333 0.994595
R2_115	120.85 0.837412	1	0.99107 1	0.992674	0.837412	0.923261
R2_116	1.88828 0.582339	1	0.99	1	1	0.582339 0.997547
R2_117	60.4248 0.711066	1	0.99903 1	0.997962	0.711066	0.996411
R2_14	15468.8 0.719569	1	0.984606	1	0.928543	0.719569 0.991507
R2_150	1933.59 0.82699 1	0.998974	1	0.046194	0.82699 0.993075	
R2_151	1.88828 0.549431	1	0.996042	1	0.000351715 0.549431	0.996035
R2_152	30.2124 0.603368	1	0.998164	1	0.00536784 0.603368	0.999192
R2_153	0.944138	0.672983	1	1	1	1 0.672983 1
R2_154	3867.19 0.855658	1	0.988501	1	0.339719	0.855658 0.994631
R2_18	15468.8 0.628326	1	0.984501	1	0.951897	0.628326 0.986486
R2_19	3867.19 0.811146	1	0.996182	1	0.957324	0.811146 0.999001
R2_20	30.2124 0.733564	1	0.997507	1	0.994503	0.733564 0.997386
R2_24	15.1062 0.585856	0.979592	0.989461	0.957447	0.828288	0.585856 0.998239
R2_26	1933.59 0.916982	1	0.99228 1	0.640148	0.916982	0.997569
R2_27	7.5531 0.748512	1	0.981896	1	1	0.748512 0.999205
R2_28	0.472069	0.687711	1	1	1	1 0.687711 1
R2_32	0.472069	0.669948	1	0.993046	1	1 0.669948 0.998624

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R2_33   0.0590086   0.95053 1   1   1   1   0.95053 1
R2_37   0.236034    0.706322    1   0.98032 1   0.981481    0.706322    0.998718
R2_38   0.0590086   0.380026    1   0.97554 1   1   0.380026    0.998268
R2_41   241.699 0.836669    1   0.991694    1   0.998627    0.836669    0.995746
R2_42   0.236034    0.851163    1   0.997821    1   1   0.851163    0.999545
R2_45   0.472069    0.461061    1   0.996591    1   0.995166    0.461061    0.999061
R2_46   0.118017    0.694227    1   1   1   1   0.694227    1
R2_47   120.85  0.888518    1   0.996794    1   0.975142    0.888518    0.998456
R2_53   0.118017    0.39111 1   0.999066    1   1   0.39111 0.999542
R2_54   483.398 0.864703    1   0.986481    1   0.997388    0.864703    0.997956
R2_55   30937.5 0.880804    1   0.987022    1   0.998648    0.880804    0.99142
R2_57   7.5531  0.624855    1   0.993583    0.941176    1   0.624855    0.998766
R2_59   0.472069    0.559432    1   1   1   1   0.559432    1
R2_6    483.398 0.702025    1   0.995921    1   0.998458    0.702025    0.990476
R2_60   7.5531  0.607892    1   0.997107    1   0.996965    0.607892    0.995923
R2_63   966.797 0.886991    1   0.998679    1   0.999706    0.886991    0.997046
R2_65   3.77655 0.994493    1   0.984615    --  --  0.994493    0.99779
R2_66   30937.5 0.528717    1   0.999833    1   1   0.528717    0.987964
R2_67   3.77655 0.944551    1   1   1   1   0.944551    1
R2_68   3.77655 0.568811    0.846154    0.995703    0.833333    0.996352    0.568811    0.998431
R2_7    966.797 0.760474    1   0.994988    1   0.999414    0.760474    0.993367
R2_71   3.77655 0.676471    1   0.99635 1   1   0.676471    0.999013
R2_72   0.236034    0.337491    0.866667    0.989529    0.727273    1   0.337491    0.998682
R2_73   1.88828 0.944937    1   0.986542    1   0.998453    0.944937    0.999519
R2_76   0.0590086   0.470652    1   1   1   1   0.470652    1
```

Sequin statistics for: B3

ID	Abundance (attomol/ul)	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Spe
R1_101	15.1062 0.841601	1	0.99403 1	1	0.841601	0.998967
R1_102	15.1062 0.717742	1	0.980746	1	0.0221654	0.717742 0.999024
R1_103	966.797 0.627978	1	0.992148	1	0.835009	0.627978 0.996922
R1_11	241.699 0.645161	1	0.999461	1	1	0.645161 0.998959
R1_12	30.2124 0.590595	1	0.991325	1	0.99781 0.590595	0.99883
R1_13	7734.38 0.920394	1	0.988254	0.909091	0.987014	0.920394 0.995898
R1_14	483.398 1	1	0.999656	--	--	1 0.989568
R1_21	30937.5 0.630945	1	0.993922	1	0.822178	0.630945 0.942446
R1_22	483.398 0.525792	1	1	1	0.00123868	0.525792 1
R1_23	15.1062 0.60815 1		0.98571 1		0.00229028	0.60815 0.997714
R1_24	483.398 0.999563	1	0.995155	1	0.998935	0.999563 0.997819
R1_31	241.699 0.689234	1	0.991529	1	0.983869	0.689234 0.991881
R1_32	60.4248 0.544296	1	1	1	1	0.544296 1
R1_33	0.118017	0.890038	1	0.996205	1	1 0.890038 0.999005
R1_41	7734.37 0.78125 1		0.999946	1	0.996632	0.78125 0.998225
R1_42	7734.38 0.617479	1	0.991638	1	0.949859	0.617479 0.992872
R1_43	120.85 0.541818	1	0.986158	0.973684	0.604672	0.541818 0.996007
R1_51	1933.59 0.60372 1		0.995606	1	0.831258	0.60372 0.996279
R1_52	0.944138	0.62357 1		0.993546	1	0.999107 0.62357 0.997559
R1_53	120.85 0.998489	1	0.99506 1		0.72554 0.998489	0.995982
R1_61	7.5531 0.686144	1	1	1	0.911765	0.686144 1
R1_62	3.77655 0.716182	1	1	1	0.842105	0.716182 1
R1_63	3867.19 0.670484	1	0.9934 1		0.879043	0.670484 0.995363
R1_71	15468.8 0.740968	1	0.991256	1	0.984353	0.740968 0.987705
R1_72	1.88828 0.586456	1	1	1	0.666667	0.586456 1
R1_73	1933.59 0.731325	1	0.99045 0.96		0.991894	0.731325 0.997432
R1_81	120.85 0.749606	1	0.997294	1	0.989216	0.749606 0.996337
R1_82	3867.19 0.587741	1	0.995803	1	0.987377	0.587741 0.991501
R1_83	30.2124 0.644813	1	0.998136	1	0.995882	0.644813 0.998209
R1_91	0.472069	0.679282	1	1	1	1 0.679282 1
R1_92	241.699 0.77665 1		0.97995 1		0.996986	0.77665 0.995122
R1_93	60.4248 0.625086	1	0.996497	1	0.998423	0.625086 0.996156
R2_1	0.944138	0.988945	1	1	--	-- 0.988945 1
R2_105	0.944138	0.984	1	0.983471	--	-- 0.984 0.994609
R2_115	120.85 0.842849	1	0.989942	1	0.993289	0.842849 0.92427
R2_116	1.88828 0.521718	1	0.996266	1	1	0.521718 0.998174
R2_117	60.4248 0.711066	1	0.999352	1	0.997792	0.711066 0.997126
R2_14	15468.8 0.719569	1	0.984373	1	0.944812	0.719569 0.991507
R2_150	1933.59 0.833141	1	0.999017	1	0.0395501	0.833141 0.997698
R2_151	1.88828 0.584864	1	0.997917	1	0.000290904	0.584864 0.999253
R2_152	30.2124 0.603856	1	0.997058	1	0.00392735	0.603856 0.998386
R2_153	0.944138	0.668093	1	0.997268	0.95	1 0.668093 0.99863
R2_154	3867.19 0.855658	1	0.991371	1	0.158151	0.855658 0.994631
R2_18	15468.8 0.628326	1	0.985099	1	0.89836	0.628326 0.986486
R2_19	3867.19 0.811146	1	0.996027	1	0.769173	0.811146 0.998716
R2_20	30.2124 0.732795	1	0.998371	1	0.998409	0.732795 0.997906
R2_24	15.1062 0.586151	0.979592	0.988855	0.957447	0.904814	0.586151 0.99824
R2_26	1933.59 0.916982	1	0.992311	1	0.984013	0.916982 0.997569
R2_27	7.5531 0.749702	1	0.994169	1	1	0.749702 0.99881
R2_28	0.472069	0.686747	1	1	1	1 0.686747 1
R2_32	0.472069	0.667795	1	0.990257	1	1 0.667795 0.997244

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R2_33   0.0590086   0.40636 0.5 1   0   0   0.40636 1
R2_37   0.236034    0.711761    1   0.994798    1   1   0.711761    0.999682
R2_38   0.0590086   0.387607    1   0.9946  1   1   0.387607    0.997455
R2_41   241.699 0.837384    1   0.991778    1   0.985197    0.837384    0.989861
R2_42   0.236034    0.85814 1   1   1   1   0.85814 1
R2_45   0.472069    0.454703    1   0.999465    1   0.98533 0.454703    0.999682
R2_46   0.118017    0.683103    1   1   1   1   0.683103    1
R2_47   120.85  0.888911    1   0.996685    1   0.995092    0.888911    0.998237
R2_53   0.118017    0.385374    1   0.998685    1   1   0.385374    0.999535
R2_54   483.398 0.864703    1   0.982419    1   0.996371    0.864703    0.997446
R2_55   30937.5 0.880804    1   0.989737    1   0.973753    0.880804    0.989875
R2_57   7.5531  0.639907    1   0.99214 0.941176    1   0.639907    0.997593
R2_59   0.472069    0.562177    1   1   1   1   0.562177    1
R2_6    483.398 0.702025    1   0.9962  1   1   0.702025    0.991826
R2_60   7.5531  0.607892    1   0.996822    1   0.998606    0.607892    0.996503
R2_63   966.797 0.886991    1   0.998578    1   1   0.886991    0.996555
R2_65   3.77655 0.995595    1   1   --  --  0.995595    1
R2_66   30937.5 0.527107    1   0.999792    1   0.999952    0.527107    0.986935
R2_67   3.77655 0.804971    1   1   1   1   0.804971    1
R2_68   3.77655 0.597632    0.923077    0.995682    0.875   0.997295    0.597632    0.99888
R2_7    966.797 0.76132 1   0.997063    1   0.99982 0.76132 0.993374
R2_71   3.77655 0.679813    1   0.998536    1   1   0.679813    0.999018
R2_72   0.236034    0.300965    0.866667    0.993569    0.454545    1   0.300965    0.999014
R2_73   1.88828 0.950398    1   0.991451    1   0.997839    0.950398    0.999521
R2_76   0.0590086   0.477536    1   0.990426    1   1   0.477536    0.999242
```