Anaquin: TransQuin Report

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Statistics (TransAlign)

Alignment statistics for: A1

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

   ***
   *** Fraction of reads mapped to the synthetic and experimental chromosomes
   ***

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

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

   Supplied: ATR001.v032.gtf

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

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

   Supplied: GeneCodeChr1.gtf

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

   ***
   *** User Alignments
   ***

   Split reads (Synthetic):      85464855 reads
   Non-split reads (Synthetic):  32195352 reads
   Covered bases (Synthetic):    161775 bases

   Split reads (Experiment):     4116941 reads
   Non-split reads (Experiment): 1488979 reads
   Covered bases (Experiment):   15859943 bases

   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Please refer to the online documentation at www.sequin.xyz for more details.
   ***
```

```
**********************************************
***                                        ***
***    Comparison with synthetic annotation   ***
***                                        ***
**********************************************

-------------------- 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

**************************************************
***                                            ***
***    Comparison with experimental annotation    ***
***                                            ***
**************************************************

-------------------- 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

   ***
   *** Fraction of reads mapped to the synthetic and experimental chromosomes
   ***

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

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

   Supplied: ATR001.v032.gtf

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

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

   Supplied: GeneCodeChr1.gtf

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

   ***
   *** User Alignments
   ***

   Split reads (Synthetic):      82814262 reads
   Non-split reads (Synthetic):  34992686 reads
   Covered bases (Synthetic):    162619 bases

   Split reads (Experiment):     3629253 reads
   Non-split reads (Experiment): 1276494 reads
   Covered bases (Experiment):   15041782 bases

   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Please refer to the online documentation at www.sequin.xyz for more details.
   ***

   ************************************************
   ***                                          ***
   ***    Comparison with synthetic annotation   ***
```

```
***                                              ***
************************************************

-------------------- 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

******************************************************
***                                                ***
***    Comparison with experimental annotation     ***
***                                                ***
******************************************************

-------------------- 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

   ***
   *** Fraction of reads mapped to the synthetic and experimental chromosomes
   ***

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

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

   Supplied: ATR001.v032.gtf

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

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

   Supplied: GeneCodeChr1.gtf

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

   ***
   *** User Alignments
   ***

   Split reads (Synthetic):      78415783 reads
   Non-split reads (Synthetic):  29409848 reads
   Covered bases (Synthetic):    166617 bases

   Split reads (Experiment):     3801952 reads
   Non-split reads (Experiment): 1400763 reads
   Covered bases (Experiment):   15059951 bases

   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Please refer to the online documentation at www.sequin.xyz for more details.
   ***

   ************************************************
   ***                                          ***
   ***    Comparison with synthetic annotation   ***
```

```
***                                              ***
************************************************

-------------------- 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

******************************************************
***                                                ***
***    Comparison with experimental annotation     ***
***                                                ***
******************************************************

-------------------- 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

   ***
   *** Fraction of reads mapped to the synthetic and experimental chromosomes
   ***

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

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

   Supplied: ATR001.v032.gtf

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

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

   Supplied: GeneCodeChr1.gtf

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

   ***
   *** User Alignments
   ***

   Split reads (Synthetic):      86364151 reads
   Non-split reads (Synthetic):  42105718 reads
   Covered bases (Synthetic):    158128 bases

   Split reads (Experiment):     1697232 reads
   Non-split reads (Experiment): 601494 reads
   Covered bases (Experiment):   11657812 bases

   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Please refer to the online documentation at www.sequin.xyz for more details.
   ***

   ************************************************
   ***                                          ***
   ***    Comparison with synthetic annotation   ***
```

```
***                                              ***
************************************************

-------------------- 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

******************************************************
***                                                ***
***    Comparison with experimental annotation     ***
***                                                ***
******************************************************

-------------------- 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

   ***
   *** Fraction of reads mapped to the synthetic and experimental chromosomes
   ***

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

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

   Supplied: ATR001.v032.gtf

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

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

   Supplied: GeneCodeChr1.gtf

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

   ***
   *** User Alignments
   ***

   Split reads (Synthetic):      85746594 reads
   Non-split reads (Synthetic):  43266445 reads
   Covered bases (Synthetic):    157833 bases

   Split reads (Experiment):     1718118 reads
   Non-split reads (Experiment): 577019 reads
   Covered bases (Experiment):   11508342 bases

   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Please refer to the online documentation at www.sequin.xyz for more details.
   ***

   ************************************************
   ***                                          ***
   ***    Comparison with synthetic annotation   ***
```

```
***                                             ***
************************************************

-------------------- 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

****************************************************
***                                              ***
***    Comparison with experimental annotation    ***
***                                              ***
****************************************************

-------------------- 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

   ***
   *** Fraction of reads mapped to the synthetic and experimental chromosomes
   ***

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

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

   Supplied: ATR001.v032.gtf

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

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

   Supplied: GeneCodeChr1.gtf

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

   ***
   *** User Alignments
   ***

   Split reads (Synthetic):      98520610 reads
   Non-split reads (Synthetic):  50973179 reads
   Covered bases (Synthetic):    157888 bases

   Split reads (Experiment):     2327740 reads
   Non-split reads (Experiment): 812978 reads
   Covered bases (Experiment):   13191197 bases

   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Please refer to the online documentation at www.sequin.xyz for more details.
   ***

   ************************************************
   ***                                          ***
   ***    Comparison with synthetic annotation   ***
```

```
***                                             ***
************************************************

-------------------- 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

************************************************
***                                          ***
***    Comparison with experimental annotation    ***
***                                          ***
************************************************

-------------------- 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
```

Statistics (TransAssembly)

Assembly statistics for: A1

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

   ***
   *** Fraction of user assembly mapped to the synthetic and experimental chromosomes
   ***

   Exons (Synthetic):        126716 genes
   Exons (Experiment):       126716 genes

   Transcripts (Synthetic):  31370 transcripts
   Transcripts (Experiment): 31370 transcripts

   ***
   *** 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

   ************************************************************
   ***                                                      ***
   ***    Comparison of assembly to synthetic annotation    ***
   ***                                                      ***
   ************************************************************

   ***
   *** 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)


*****************************************************************
***                                                           ***
***    Comparison of assembly to experimental annotation      ***
***                                                           ***
*****************************************************************

***
*** 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

   ***
   *** Fraction of user assembly mapped to the synthetic and experimental chromosomes
   ***

   Exons (Synthetic):        117285 genes
   Exons (Experiment):       117285 genes

   Transcripts (Synthetic):  28866 transcripts
   Transcripts (Experiment): 28866 transcripts

   ***
   *** 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

   ************************************************************
   ***                                                      ***
   ***    Comparison of assembly to synthetic annotation    ***
   ***                                                      ***
   ************************************************************

   ***
   *** 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)


#################################################################
###                                                           ###
###    Comparison of assembly to experimental annotation      ###
###                                                           ###
#################################################################

***
*** 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

   ***
   *** Fraction of user assembly mapped to the synthetic and experimental chromosomes
   ***

   Exons (Synthetic):        120591 genes
   Exons (Experiment):       120591 genes

   Transcripts (Synthetic):  28637 transcripts
   Transcripts (Experiment): 28637 transcripts

   ***
   *** 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

   ************************************************************
   ***                                                      ***
   ***    Comparison of assembly to synthetic annotation    ***
   ***                                                      ***
   ************************************************************

   ***
   *** 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)


*****************************************************************
***                                                           ***
***    Comparison of assembly to experimental annotation      ***
***                                                           ***
*****************************************************************

***
*** 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

   ***
   *** Fraction of user assembly mapped to the synthetic and experimental chromosomes
   ***

   Exons (Synthetic):        86880 genes
   Exons (Experiment):       86880 genes

   Transcripts (Synthetic):  23127 transcripts
   Transcripts (Experiment): 23127 transcripts

   ***
   *** 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

   ************************************************************
   ***                                                      ***
   ***    Comparison of assembly to synthetic annotation    ***
   ***                                                      ***
   ************************************************************

   ***
   *** 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)


*****************************************************************
***                                                           ***
***    Comparison of assembly to experimental annotation      ***
***                                                           ***
*****************************************************************

***
*** 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

   ***
   *** Fraction of user assembly mapped to the synthetic and experimental chromosomes
   ***

   Exons (Synthetic):        86266 genes
   Exons (Experiment):       86266 genes

   Transcripts (Synthetic):  22894 transcripts
   Transcripts (Experiment): 22894 transcripts

   ***
   *** 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

   ************************************************************
   ***                                                      ***
   ***    Comparison of assembly to synthetic annotation    ***
   ***                                                      ***
   ************************************************************

   ***
   *** 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)


#################################################################
###                                                           ###
###    Comparison of assembly to experimental annotation      ###
###                                                           ###
#################################################################

***
*** 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

   ***
   *** Fraction of user assembly mapped to the synthetic and experimental chromosomes
   ***

   Exons (Synthetic):        86266 genes
   Exons (Experiment):       86266 genes

   Transcripts (Synthetic):  22894 transcripts
   Transcripts (Experiment): 22894 transcripts

   ***
   *** 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

   ************************************************************
   ***                                                      ***
   ***    Comparison of assembly to synthetic annotation    ***
   ***                                                      ***
   ************************************************************

   ***
   *** 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 --------------------
```

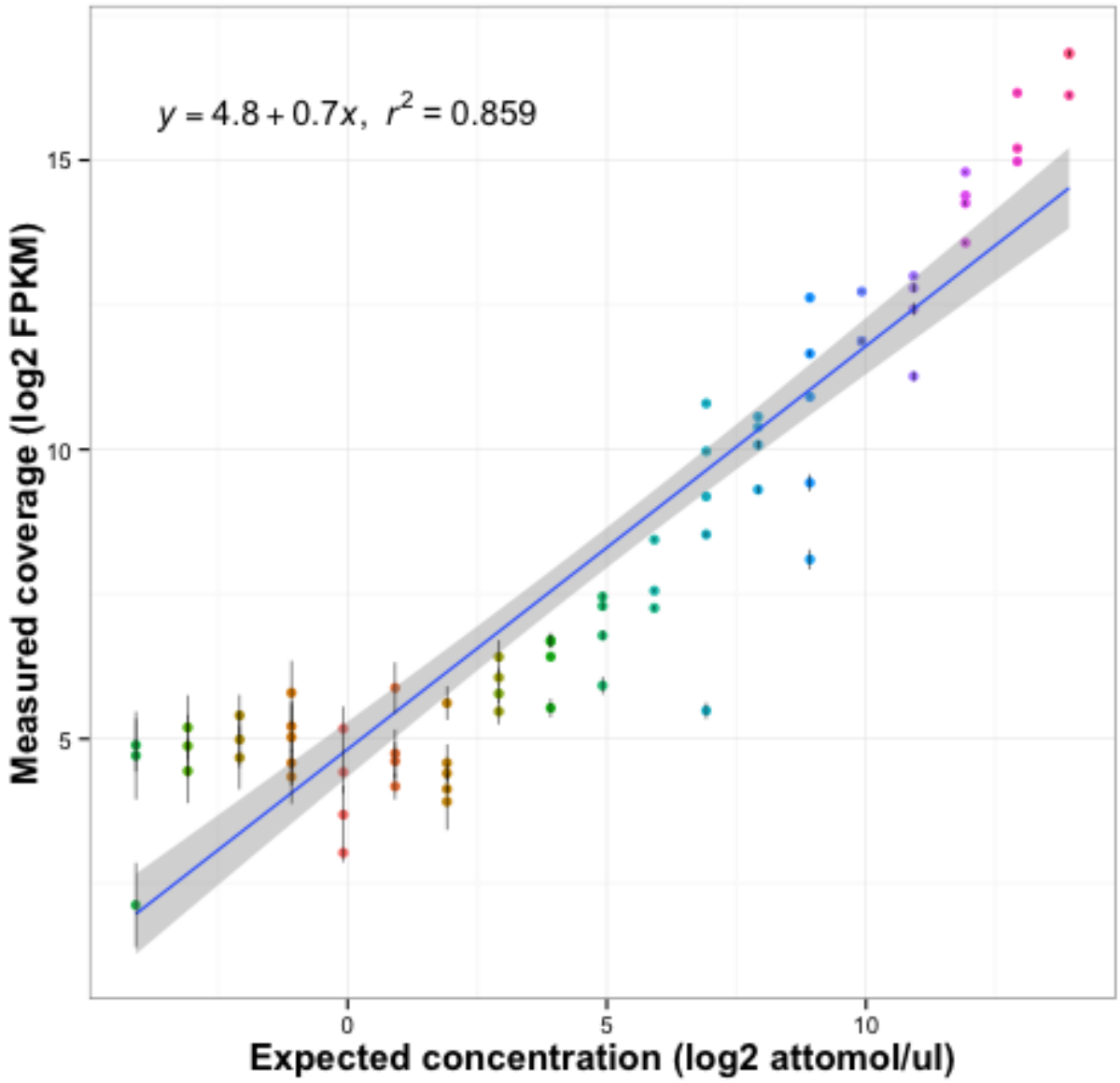
```
Sensitivity: 1.00
Specificity: 1.00

-------------------- 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)


#################################################################
###                                                           ###
###    Comparison of assembly to experimental annotation      ###
###                                                           ###
#################################################################

***
*** 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)
```

Statistics (Gene Expression)

Pooled scatter plot for gene expression

The pooled scatter plot shows the expected abundance against measured abundance on the logarithm scale for all the replicates. This is done by plotting the average and standard deviation. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the gene expression experiment is.



Gene expression summary

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

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 76 ± 0 gene
   Detected:  72.5 ± 0.547723 gene

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

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

   ***
   *** Below LOQ
   ***

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

   ***
   *** Above LOQ
   ***
```

```
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
```

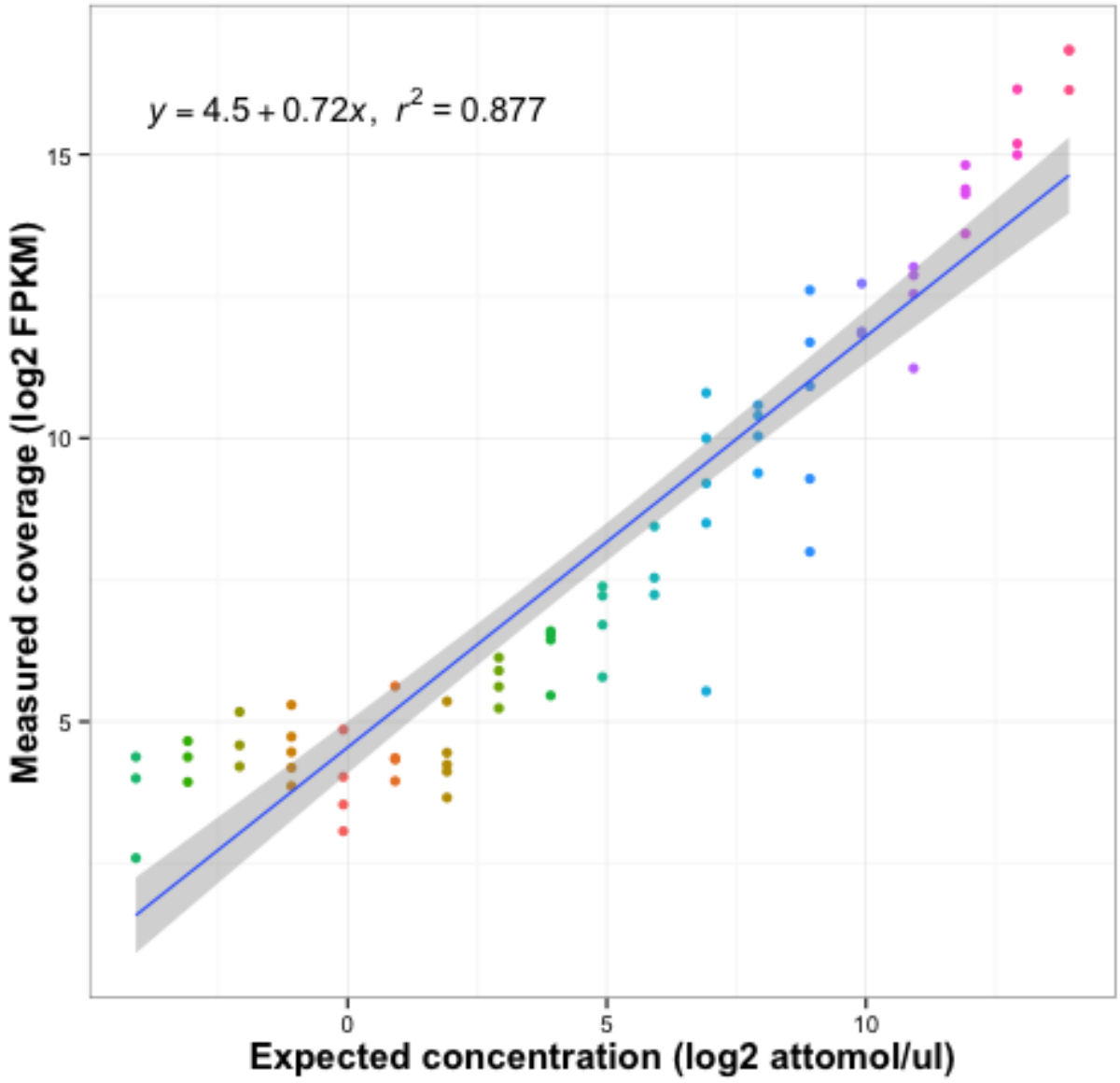
Gene expression statistics for: A1

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

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 76 gene
   Detected:  73 gene

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 3.77655 (R1_62)

   ***
   *** Below LOQ
   ***

   Intercept: 4.39067
   Slope:     0.0805742
   R2:        0.0567335

   ***
   *** Above LOQ
   ***
```

```
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

The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the gene expression experiment is.



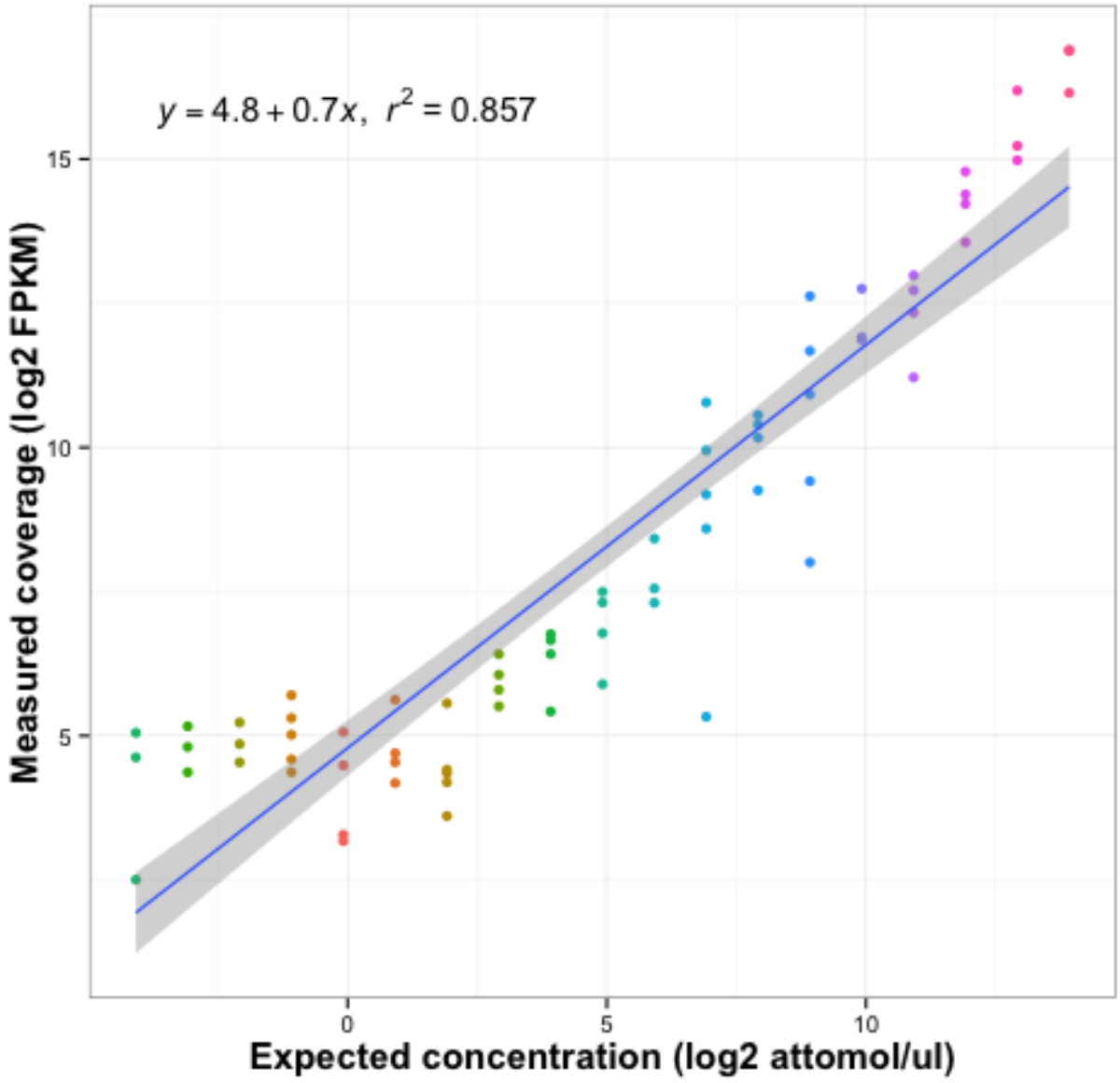
Gene expression statistics for: A2

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

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 76 gene
   Detected:  73 gene

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 3.77655 (R1_62)

   ***
   *** Below LOQ
   ***

   Intercept: 4.62321
   Slope:     0.0227324
   R2:        0.00360572

   ***
   *** Above LOQ
   ***
```

```
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

The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the gene expression experiment is.



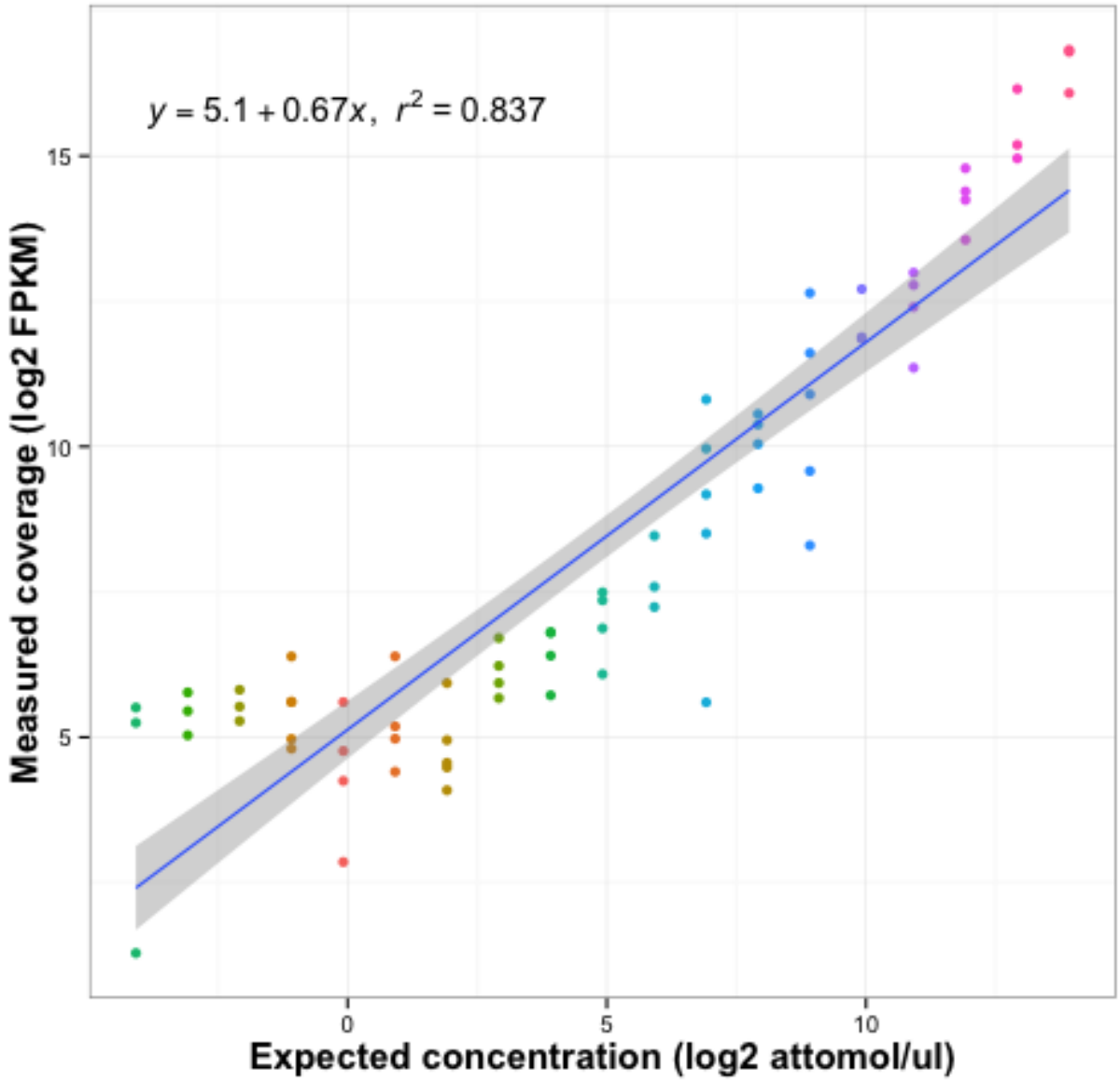
Gene expression statistics for: A3

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

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 76 gene
   Detected:  73 gene

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 15.1062 (R1_101)

   ***
   *** Below LOQ
   ***

   Intercept: 5.25776
   Slope:     0.16804
   R2:        0.139073

   ***
   *** Above LOQ
   ***
```

```
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

The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the gene expression experiment is.



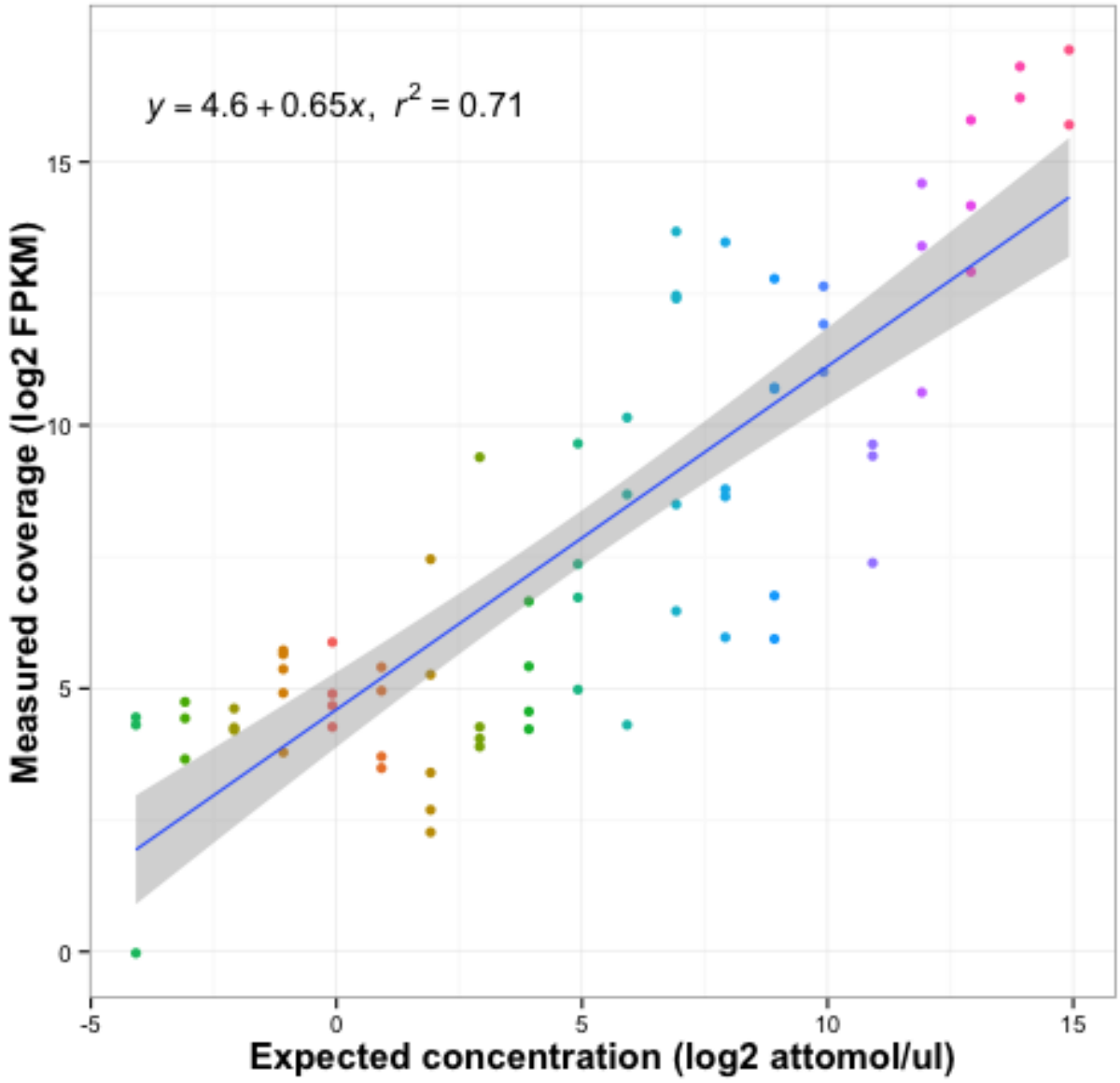
Gene expression statistics for: B1

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

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 76 gene
   Detected:  72 gene

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 1.88828 (R1_72)

   ***
   *** Below LOQ
   ***

   Intercept: 5.19759
   Slope:     0.42932
   R2:        0.278885

   ***
   *** Above LOQ
   ***
```

```
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

The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the gene expression experiment is.



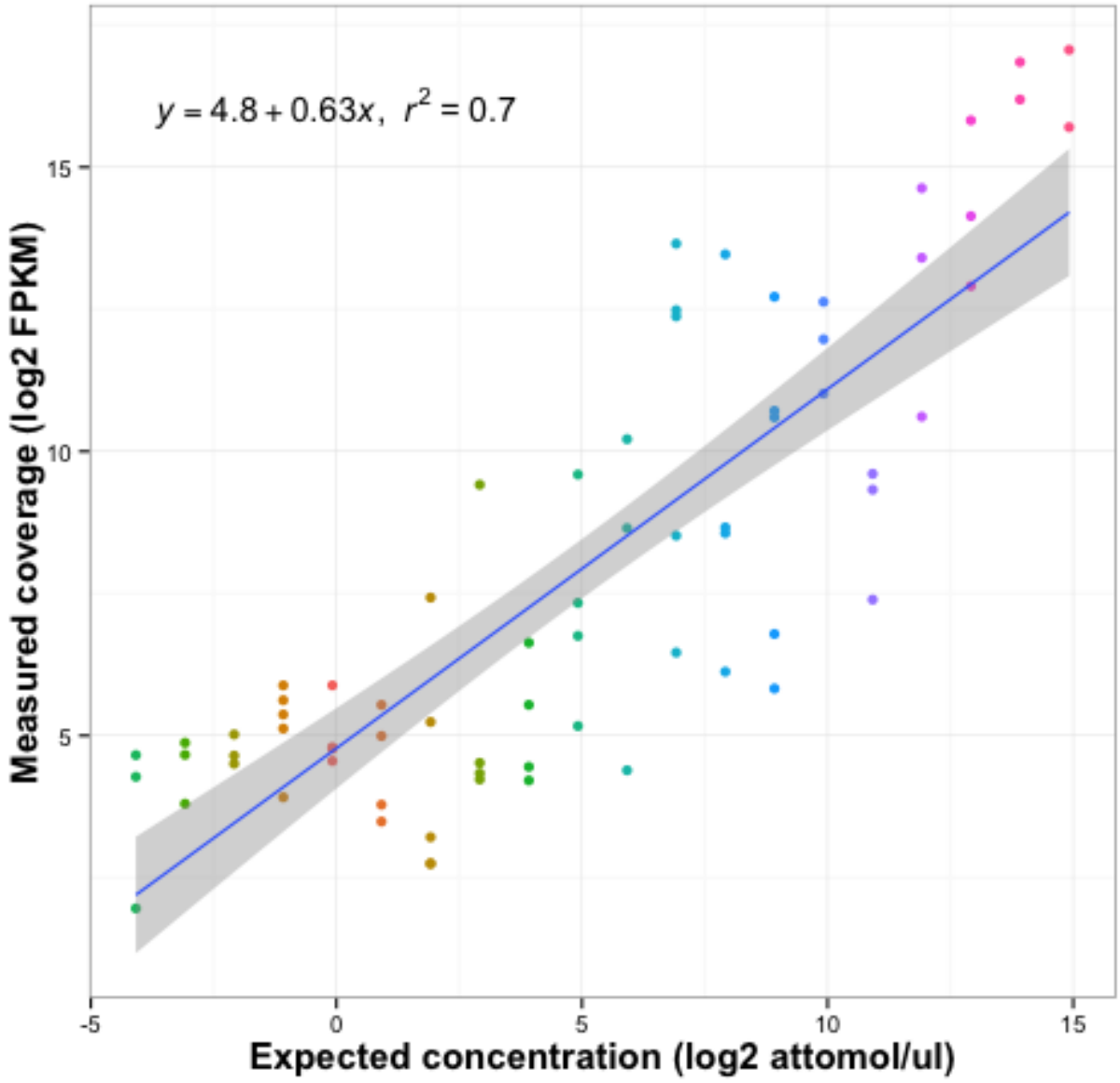
Gene expression statistics for: B2

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

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 76 gene
   Detected:  72 gene

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 1.88828 (R1_72)

   ***
   *** Below LOQ
   ***

   Intercept: 5.22081
   Slope:     0.303379
   R2:        0.28516

   ***
   *** Above LOQ
   ***
```

```
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

The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the gene expression experiment is.



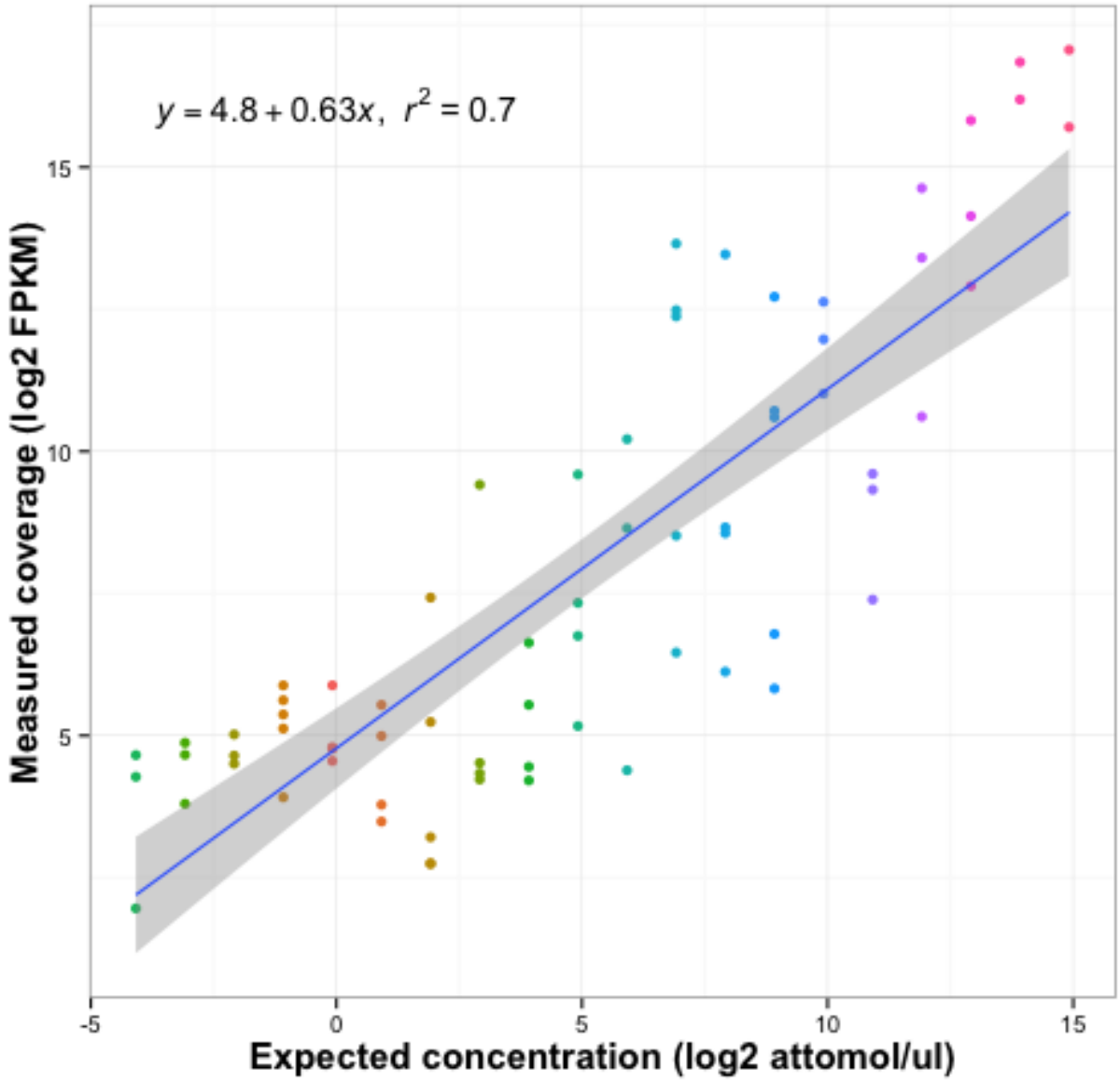
Gene expression statistics for: B3

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

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 76 gene
   Detected:  72 gene

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 1.88828 (R1_72)

   ***
   *** Below LOQ
   ***

   Intercept: 5.22081
   Slope:     0.303379
   R2:        0.28516

   ***
   *** Above LOQ
   ***
```

```
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

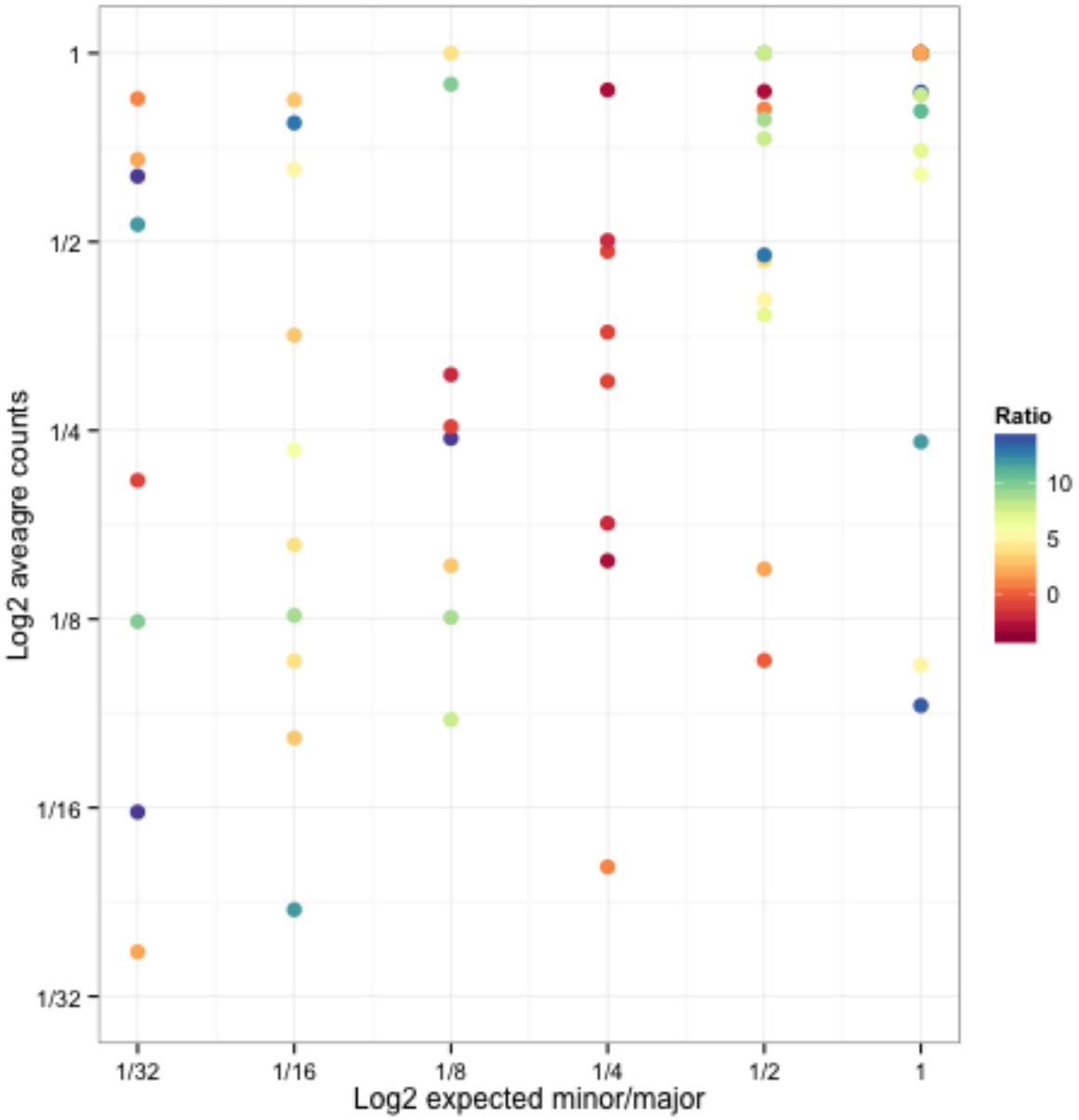
The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the gene expression experiment is.



Statistics (Isoform Expression)

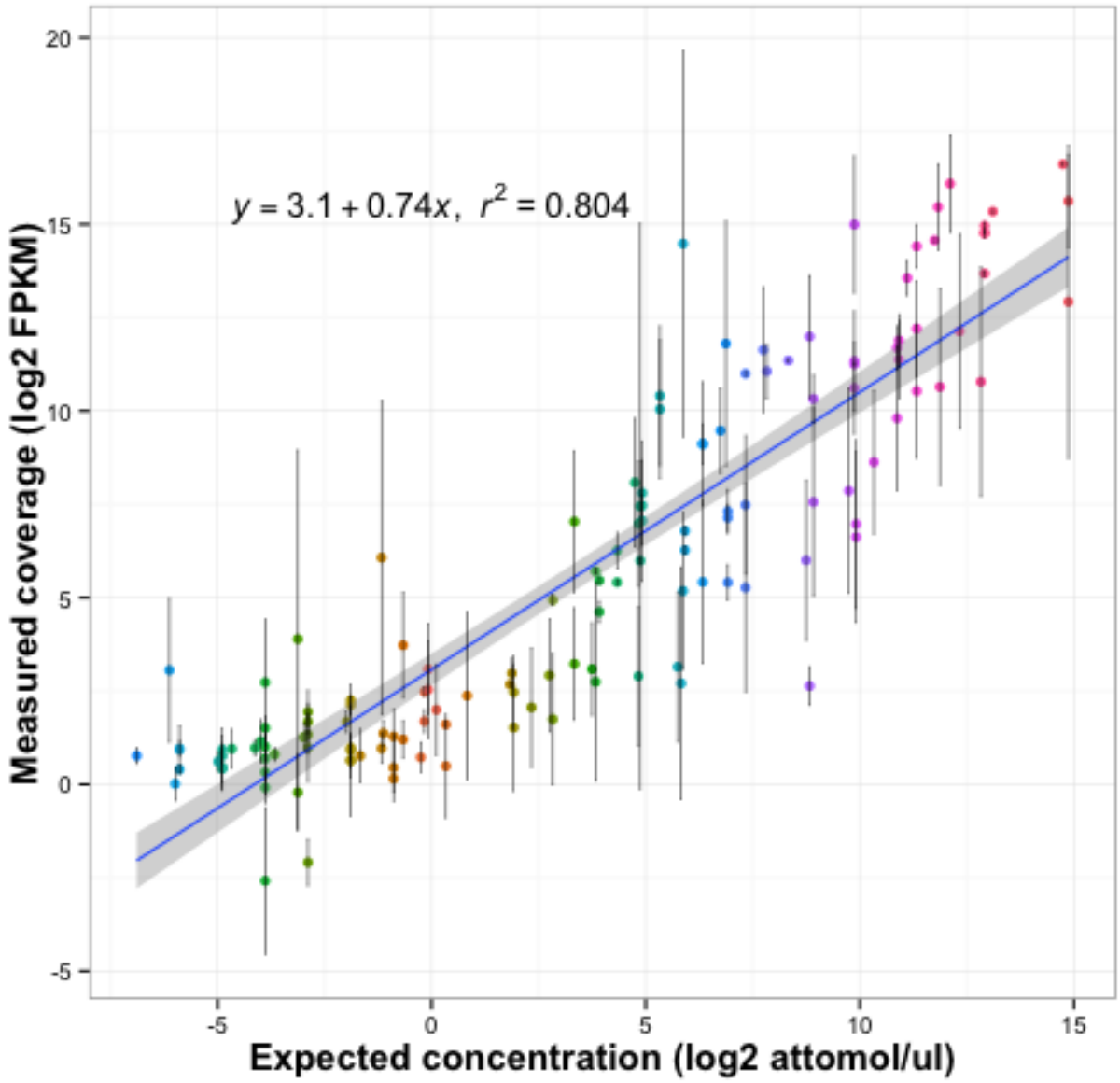
Minor/Major plot

The Minor/Major plot shows the relative quantification of alternative spliced isoforms by measuring the minimum isoform as a fraction of the major isoform for each sequin gene. The accuracy of the quantification is typically dependent on sequence coverage and higher for high abundance genes. The concentration of the gene is shown by colors.



Pooled scatter plot for isoform expression

The pooled scatter plot shows the expected abundance against measured abundance on the logarithm scale for all the replicates. This is done by plotting the average and standard deviation. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the isoform expression experiment is.



Isoform expression summary

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

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 162 ± 0 isoform
   Detected:  162 ± 0 isoform

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 8.5898 ± 5.29196 (R1_32_1,R1_61_2,R2_152_1,R1_61_2,R2_152_1,R1_32_1)

   ***
   *** Below LOQ
   ***

   Intercept: 1.63843 ± 0.455166
   Slope:     0.177731 ± 0.0681607
   R2:        0.0912182 ± 0.0621254

   ***
   *** Above LOQ
   ***
```

```
Intercept: 2.14992 ± 1.06726
Slope:     0.874358 ± 0.154074
R2:        0.526042 ± 0.264914

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

Correlation: 0.546432 ± 0.313433
Slope:       2.84934 ± 1.79749
R2:          0.380455 ± 0.405941
F-statistic: 470.366 ± 699.658
P-value:     1.90628e-05 ± 1.50158e-05
SSM:         3.05358e+10 ± 3.48546e+10, DF: 1 ± 0
SSE:         4.25463e+10 ± 2.67804e+10, DF: 141.333 ± 2.87518
SST:         7.30822e+10 ± 8.07423e+09, DF: 142.333 ± 2.87518

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

Correlation: 0.865583 ± 0.0577629
Slope:       0.744934 ± 0.0594465
R2:          0.752015 ± 0.102148
F-statistic: 571.125 ± 412.436
P-value:     0 ± 0
SSM:         2790.14 ± 469.227, DF: 1 ± 0
SSE:         908.577 ± 361.804, DF: 141.333 ± 2.87518
SST:         3698.72 ± 160.543, DF: 142.333 ± 2.87518
```

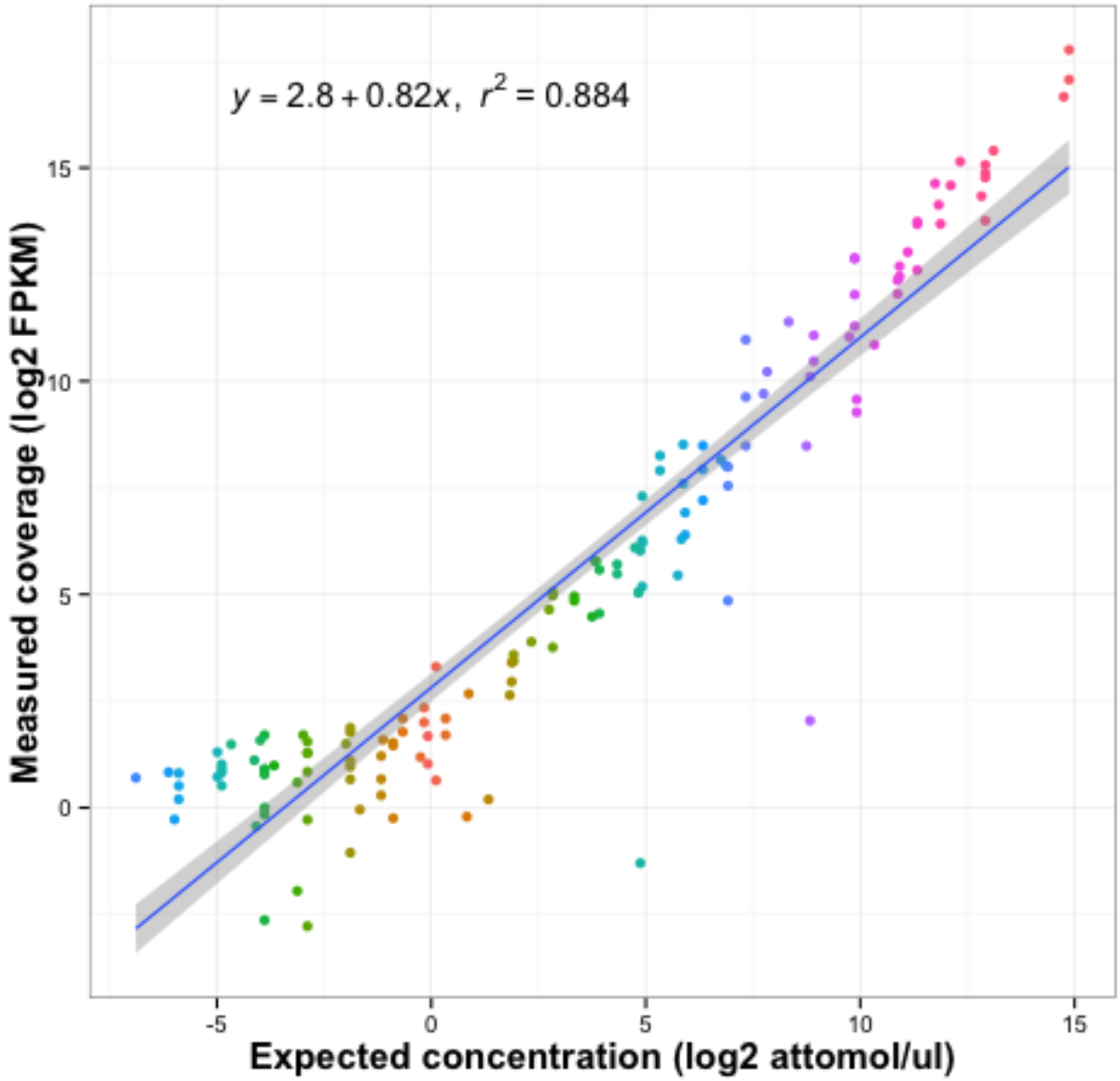
Isoform expression statistics for: A1

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

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 162 isoform
   Detected:  162 isoform

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 3.5544 (R1_32_1)

   ***
   *** Below LOQ
   ***

   Intercept: 1.25307
   Slope:     0.157653
   R2:        0.0887965

   ***
   *** Above LOQ
   ***
```

```
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

The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the isoform expression experiment is.



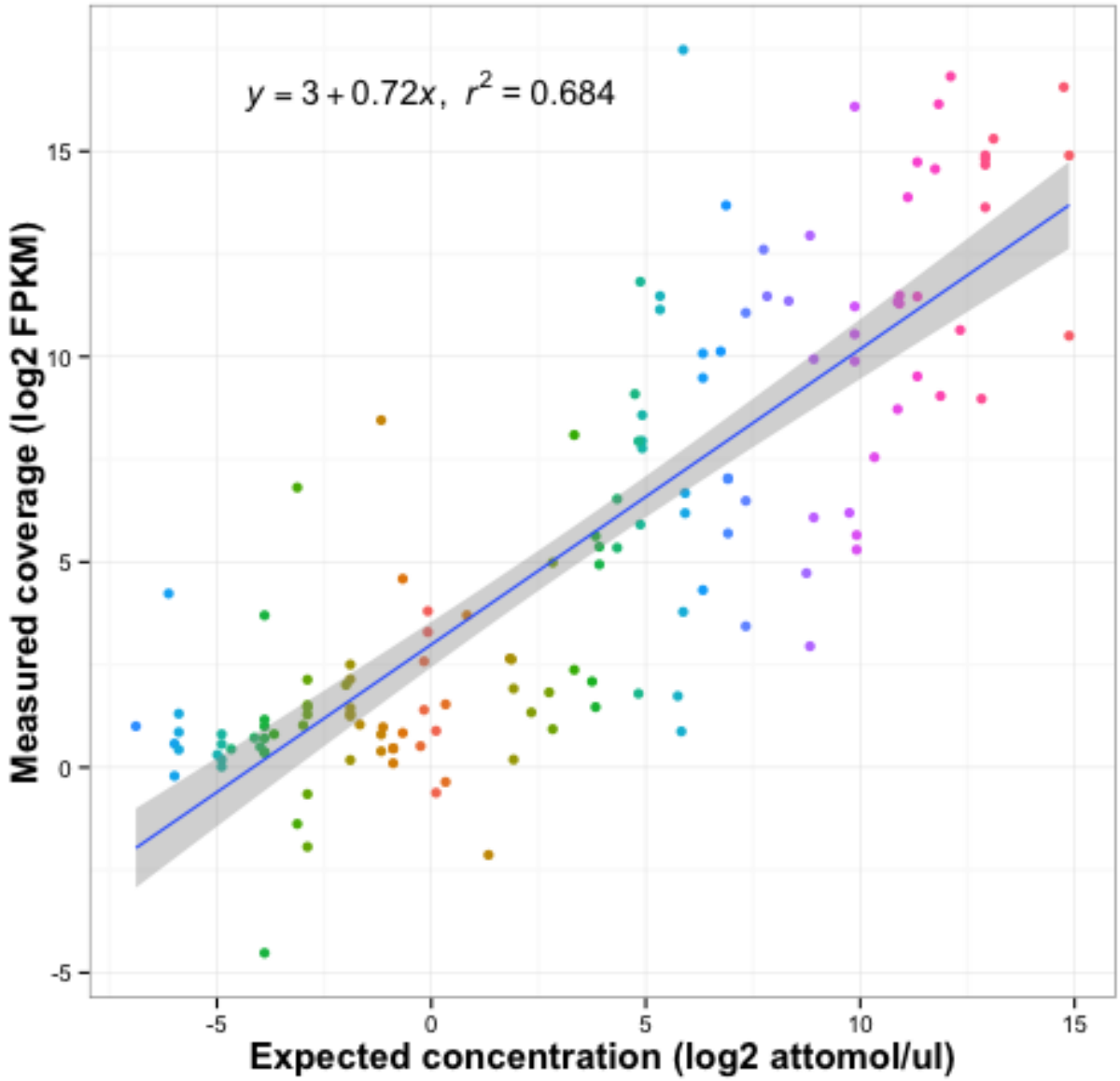
Isoform expression statistics for: A2

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/B1/t_data.ctab

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 162 isoform
   Detected:  162 isoform

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 7.1088 (R1_61_2)

   ***
   *** Below LOQ
   ***

   Intercept: 1.44692
   Slope:     0.113575
   R2:        0.0230025

   ***
   *** Above LOQ
   ***
```

```
Intercept: 2.48232
Slope:     0.808387
R2:        0.390408

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

Correlation: 0.341661
Slope:       1.6768
R2:          0.116732
F-statistic: 18.5023
P-value:     3.16439e-05
SSM:         7.92306e+09, DF: 1
SSE:         5.99508e+10, DF: 140
SST:         6.78739e+10, DF: 141

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

Correlation: 0.827113
Slope:       0.719153
R2:          0.684116
F-statistic: 303.201
P-value:     0
SSM:         2578.25, DF: 1
SSE:         1190.48, DF: 140
SST:         3768.73, DF: 141
```

Isoform expression scatter plot for: A2

The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the isoform expression experiment is.



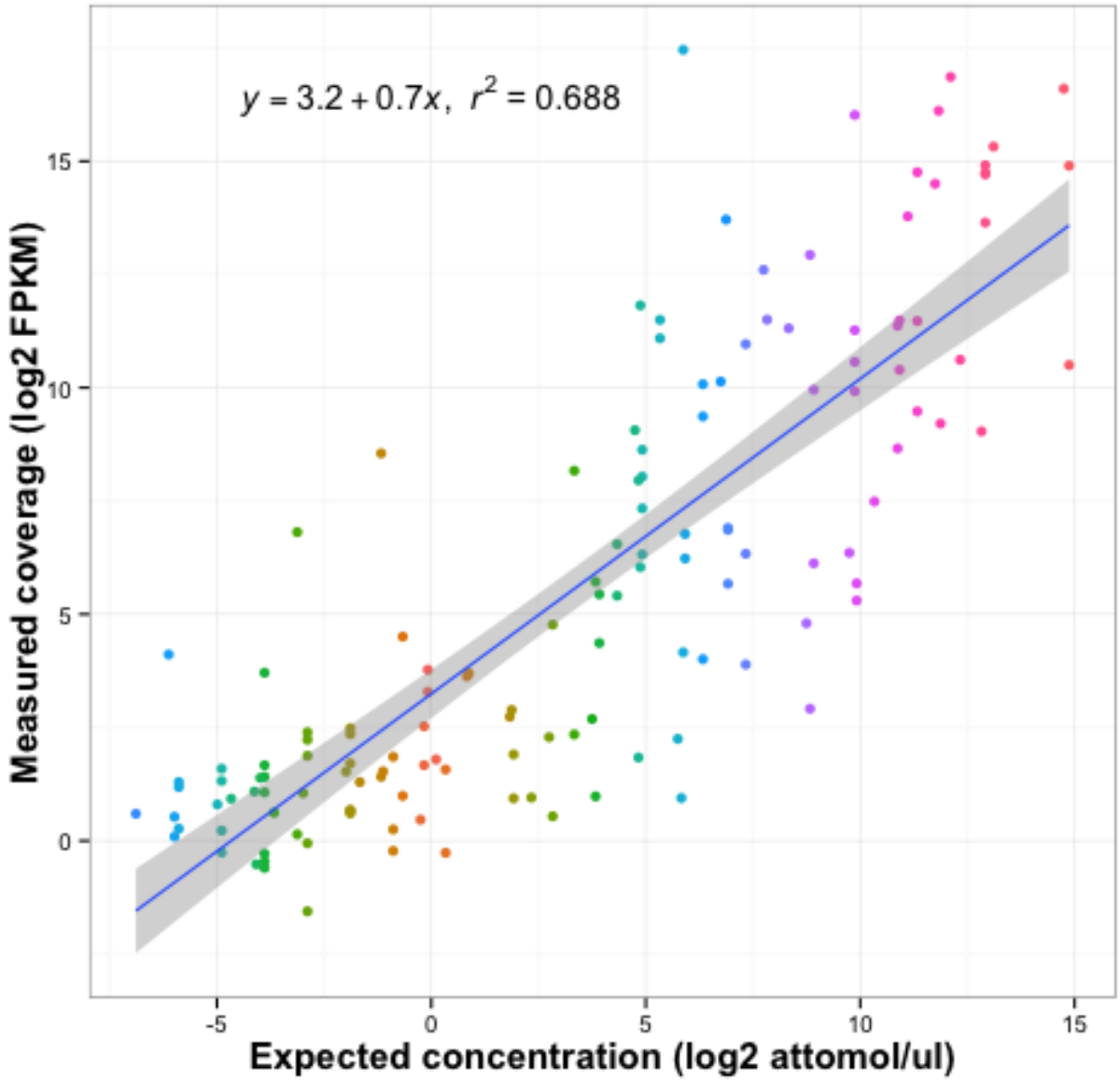
Isoform expression statistics for: A3

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/B2/t_data.ctab

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 162 isoform
   Detected:  162 isoform

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 15.1062 (R2_152_1)

   ***
   *** Below LOQ
   ***

   Intercept: 2.21529
   Slope:     0.261966
   R2:        0.161856

   ***
   *** Above LOQ
   ***
```

```
Intercept: 3.14172
Slope:     0.744835
R2:        0.321964

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

Correlation: 0.346574
Slope:       1.70137
R2:          0.120113
F-statistic: 18.9749
P-value:     2.55445e-05
SSM:         8.15168e+09, DF: 1
SSE:         5.97149e+10, DF: 139
SST:         6.78666e+10, DF: 140

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

Correlation: 0.829495
Slope:       0.695224
R2:          0.688061
F-statistic: 306.601
P-value:     0
SSM:         2404.62, DF: 1
SSE:         1090.15, DF: 139
SST:         3494.77, DF: 140
```

Isoform expression scatter plot for: A3

The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the isoform expression experiment is.



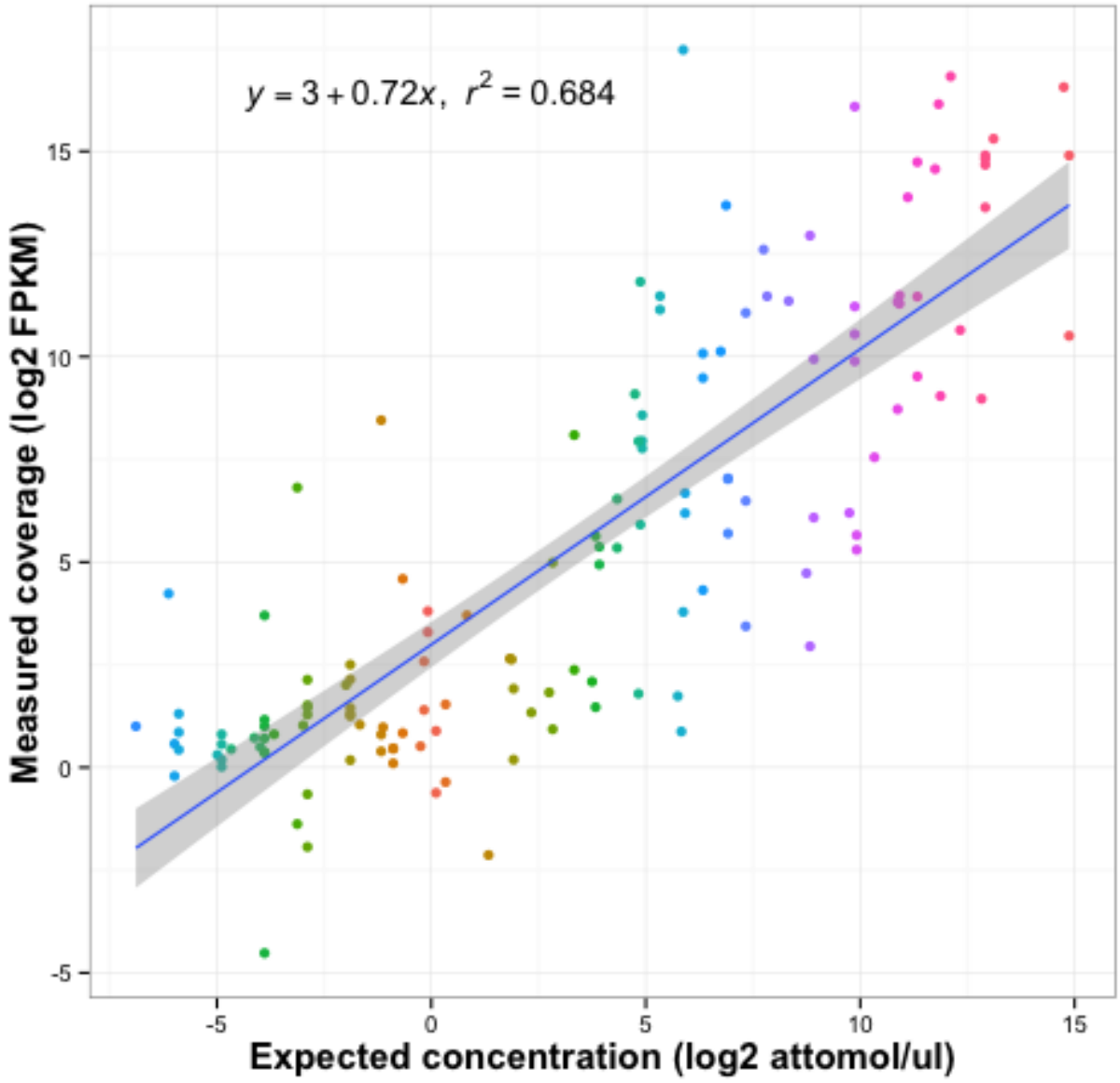
Isoform expression statistics for: B1

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/B1/t_data.ctab

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 162 isoform
   Detected:  162 isoform

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 7.1088 (R1_61_2)

   ***
   *** Below LOQ
   ***

   Intercept: 1.44692
   Slope:     0.113575
   R2:        0.0230025

   ***
   *** Above LOQ
   ***
```

```
Intercept: 2.48232
Slope:     0.808387
R2:        0.390408

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

Correlation: 0.341661
Slope:       1.6768
R2:          0.116732
F-statistic: 18.5023
P-value:     3.16439e-05
SSM:         7.92306e+09, DF: 1
SSE:         5.99508e+10, DF: 140
SST:         6.78739e+10, DF: 141

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

Correlation: 0.827113
Slope:       0.719153
R2:          0.684116
F-statistic: 303.201
P-value:     0
SSM:         2578.25, DF: 1
SSE:         1190.48, DF: 140
SST:         3768.73, DF: 141
```

Isoform expression scatter plot for: B1

The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the isoform expression experiment is.



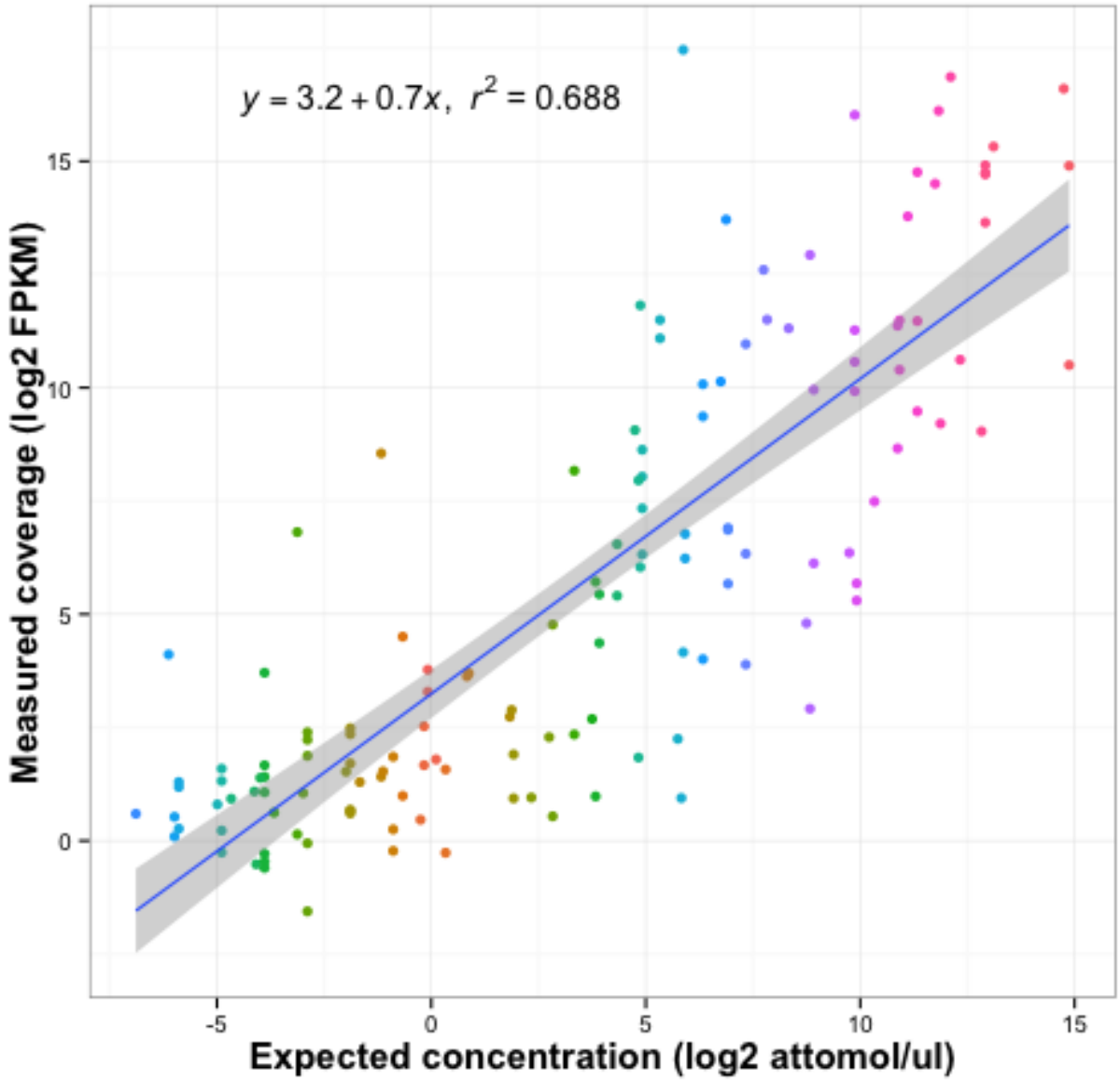
Isoform expression statistics for: B2

```
Summary for input: /Users/tedwong/Desktop/K_562/StringTie/B2/t_data.ctab

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 162 isoform
   Detected:  162 isoform

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 15.1062 (R2_152_1)

   ***
   *** Below LOQ
   ***

   Intercept: 2.21529
   Slope:     0.261966
   R2:        0.161856

   ***
   *** Above LOQ
   ***
```

```
Intercept: 3.14172
Slope:     0.744835
R2:        0.321964

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

Correlation: 0.346574
Slope:       1.70137
R2:          0.120113
F-statistic: 18.9749
P-value:     2.55445e-05
SSM:         8.15168e+09, DF: 1
SSE:         5.97149e+10, DF: 139
SST:         6.78666e+10, DF: 140

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

Correlation: 0.829495
Slope:       0.695224
R2:          0.688061
F-statistic: 306.601
P-value:     0
SSM:         2404.62, DF: 1
SSE:         1090.15, DF: 139
SST:         3494.77, DF: 140
```

Isoform expression scatter plot for: B2

The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the isoform expression experiment is.



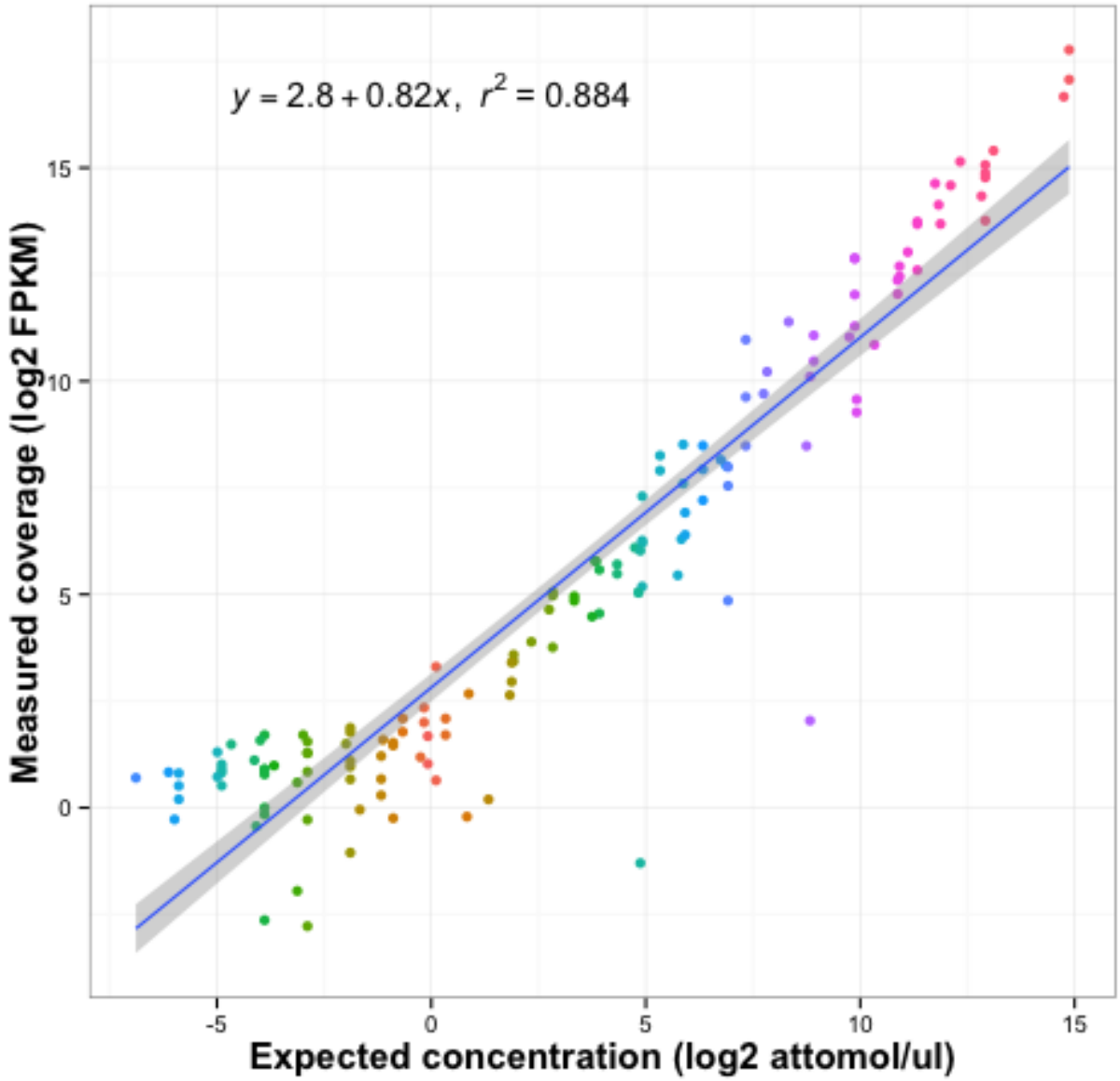
Isoform expression statistics for: B3

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

   ***
   *** The statistics are shown in arithmetic average and standard deviation. For example,
   *** 5.12 ± 0.52 has an arithmetic average of 5.12 and standard deviation 0.52.
   ***

   ***
   *** Fraction of genes for synthetic and experiment relative to all genes detected in the input file
   ***

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

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

   File:      /Users/tedwong/Desktop/K_562/ATR001.v032.gtf
   Reference: 162 isoform
   Detected:  162 isoform

   ***
   *** Please refer to the online documentation for more details on the regression statistics.
   ***
   *** Correlation: Pearson's correlation
   *** Slope:       Regression slope for the regression
   *** R2:          Coefficient of determination for the regression
   *** F-stat:      The F test statistic under the null hypothesis
   *** P-value:     The p-value under the null hypothesis
   *** SSM:         Sum of squares of model in ANOVA
   *** SSE:         Sum of squares of errors in ANOVA
   *** SST:         Total sum of squares in ANOVA
   ***

   ***
   *** Limit of Quantificiation (LOQ). Estimated by piecewise segmented regression.
   ***

   Break: 3.5544 (R1_32_1)

   ***
   *** Below LOQ
   ***

   Intercept: 1.25307
   Slope:     0.157653
   R2:        0.0887965

   ***
   *** Above LOQ
   ***
```

```
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

The scatter plot shows the relationship between expected abundance against measured abundance on the logarithm scale for a single replicate. The line is the fitted linear regression with 95% confidence interval drawn in black. A high R2 is desirable; the higher it is, the more accurate the isoform expression experiment is.



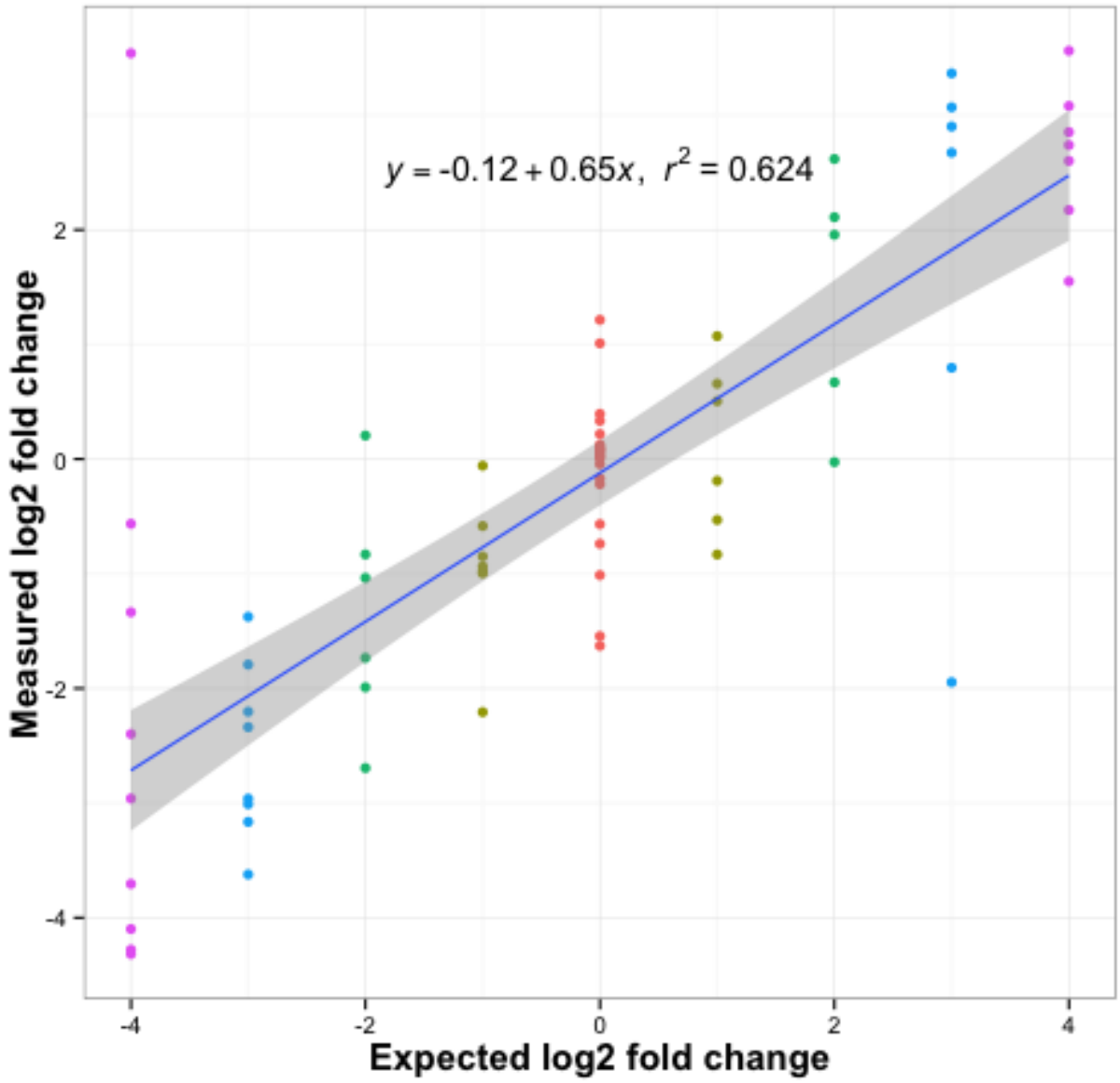
Statistics (Gene Expression Differential)

Differential summary statistics

```
Summary for file: /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
```

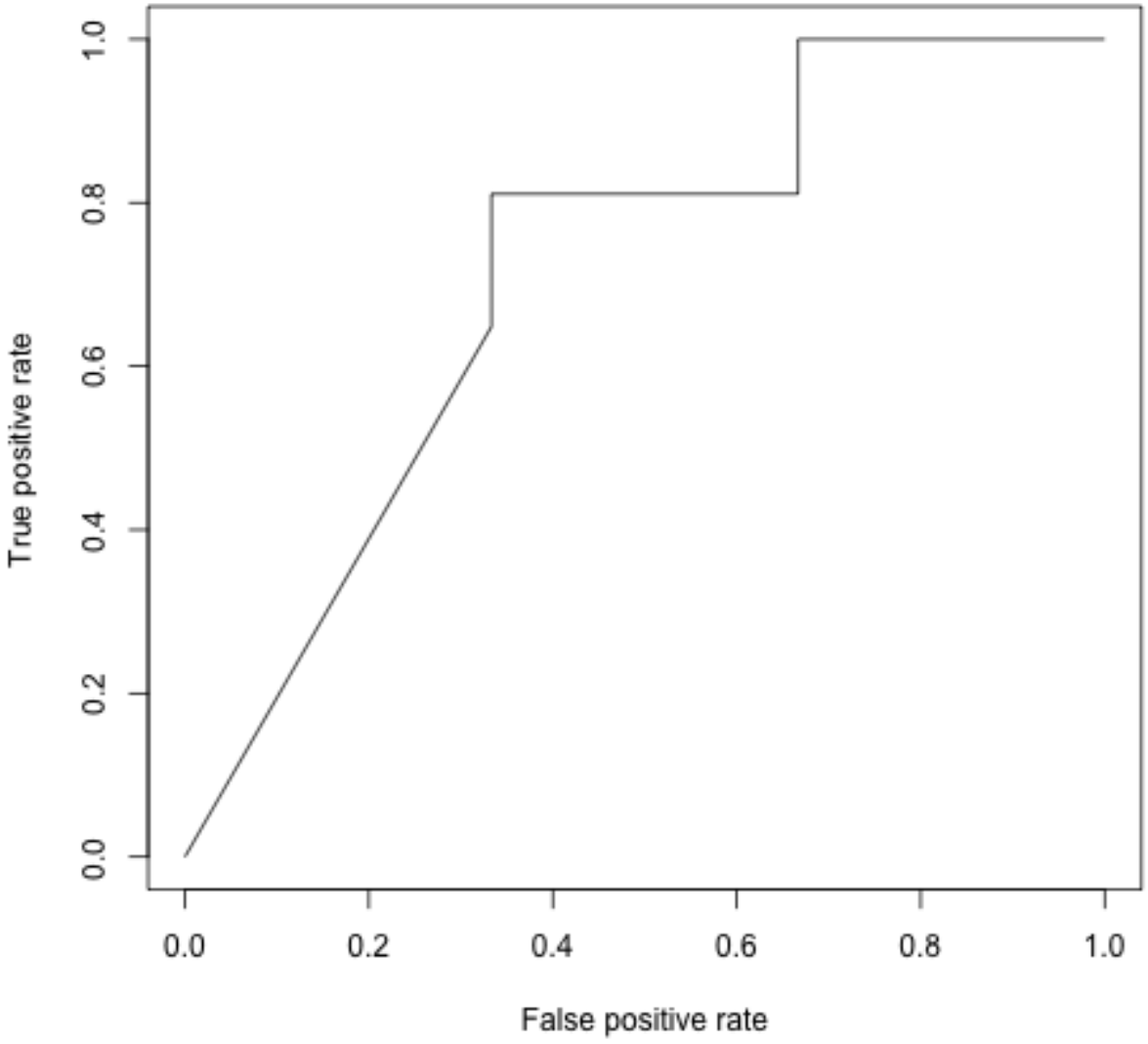
Scatter plot

The scatter plot shows the expected fold-change of genes against their measured fold-change. The more correlated they are the more accurate the experiment is. The R2 statistic measures how accurate the experiment is in detecting fold-changes. Accurate detection of fold-changes is crucial for differential analysis. The accuracy of the quantification is typically dependent on abundance and higher for high abundance genes. The concentration of the gene is shown by colors.



ROC plot

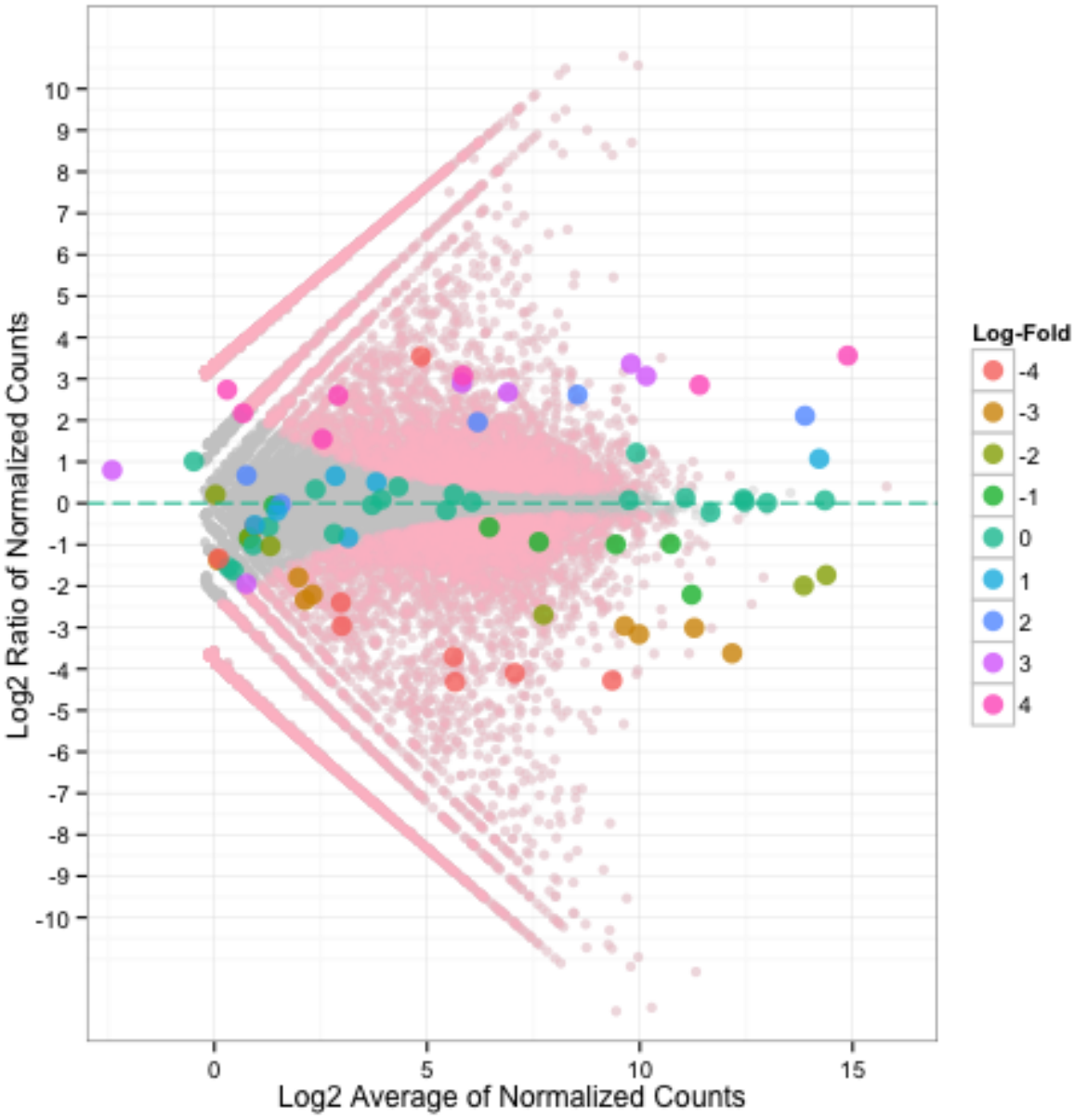
When true differences in expression exist between samples in an experiment, those differences should be detected in differential expression tests; where no differences exist, no difference should be detected. The true-positive and true-negative sequins controls can be used in a receiver operator characteristic (ROC) curve analysis of rank ordered differential expression test P-values.



MA plot

The MA plot is used to study dependences between the log fold-ratio and the average normalized counts. The counts are normalized as they are adjusted for the library size. Typically, the variability is higher for less abundance genes.

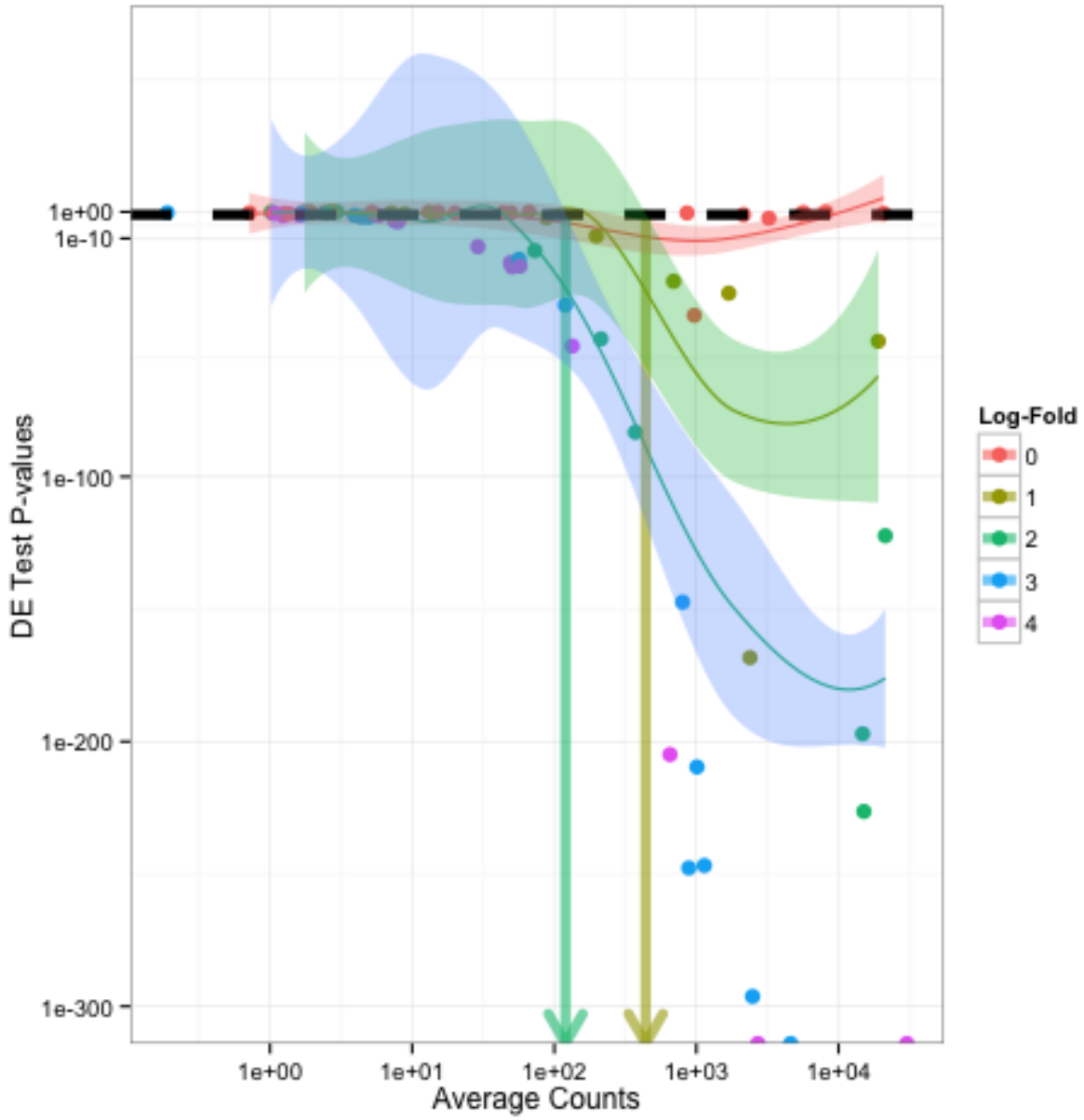
Sequin data points are colored by log-ratio. They represent the mean log-fold changes for a given concentration level. Endogenous genes data points are shown as pink points.



LODR plot

Identifying differentially expressed genes is the objective of differential expression experiments; however, how much information is needed to have confidence that a given fold change in expression of transcripts will be detected? The LODR estimates can inform researchers of diagnostic power at a given fold change.

An LODR estimate for a particular fold change is the minimum signal, above which differentially expressed transcripts can be detected with a specified degree of confidence. The estimate for each ratio group is found based on the intersection of the model upper confidence interval upper bound with the P-value threshold.



Apprendix: Sequin 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
```

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	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
```

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
```