

# Anaquin TransQuin Report

## Contents

Header 1 . . . . .	1
Header 2 . . . . .	1
Read Alignment for accepted_hits.bam (A1)	1
Read Alignment for accepted_hits.bam (A2)	3
Read Alignment for accepted_hits.bam (A3)	4
Read Alignment for accepted_hits.bam (B1)	5
Read Alignment for accepted_hits.bam (B2)	6
Read Alignment for accepted_hits.bam (B3)	7

## Header 1

ssdasd

## Header 2

## Read Alignment for accepted\_hits.bam (A1)

Summary for dataset: A1/TransAlign\_summary.stats

Unmapped: 0 reads  
Experiment: 6635268 (21.5363%) reads  
Synthetic: 24174356 (78.4637%) reads

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

Query: 59421555 exons  
Query: 24855847 introns  
Query: 163383 bases

Dilution: 0.784637

\*\*\*

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

```

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

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

Sensitivity: 0.994958
Specificity: 0.973343
Detection: 0.0590086 (R2_33)

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

Sensitivity: 0.991245
Specificity: 0.821653
Detection: 0.0590086 (R2_33)

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

Sensitivity: 0.692468
Specificity: 0.924613
Detection: 0.0590086 (R2_33)

----- Undetected -----

Exon: 0.005042
Intron: 0.008755
Gene: 0.052632

```

## Read Alignment for accepted\_hits.bam (A2)

Summary for dataset: A2/TransAlign\_summary.stats

Unmapped: 0 reads  
Experiment: 5742035 (20.4187%) reads  
Synthetic: 22379420 (79.5813%) reads

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

Query: 55184443 exons  
Query: 24887760 introns  
Query: 163986 bases

Dilution: 0.795813

\*\*\*

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

\*\*\*

\*\*\* Exon level is defined by performance per exon. An alignment that  
\*\*\* is not mapped entirely within an exon is considered as a FP. The  
\*\*\* intron level is similar.

\*\*\*

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

\*\*\*

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

Sensitivity: 0.996639  
Specificity: 0.975178  
Detection: 0.0590086 (R2\_33)

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

Sensitivity: 0.991245  
Specificity: 0.763722  
Detection: 0.0590086 (R2\_33)

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

Sensitivity: 0.693059  
Specificity: 0.921999  
Detection: 0.0590086 (R2\_33)

----- Undetected -----

Exon: 0.003361  
Intron: 0.008755  
Gene: 0.039474

## Read Alignment for accepted\_hits.bam (A3)

Summary for dataset: A3/TransAlign\_summary.stats

Unmapped: 0 reads  
Experiment: 5803436 (21.0203%) reads  
Synthetic: 21805238 (78.9797%) reads

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

Query: 53748651 exons  
Query: 22830699 introns  
Query: 166153 bases

Dilution: 0.789797

\*\*\*

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

\*\*\*

\*\*\* Exon level is defined by performance per exon. An alignment that  
\*\*\* is not mapped entirely within an exon is considered as a FP. The  
\*\*\* intron level is similar.

\*\*\*

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

\*\*\*

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

Sensitivity: 0.996639  
Specificity: 0.974466  
Detection: 0.0590086 (R2\_33)

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

Sensitivity: 0.992218  
Specificity: 0.811167  
Detection: 0.0590086 (R2\_33)

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

Sensitivity: 0.695741  
Specificity: 0.913495  
Detection: 0.0590086 (R2\_33)

----- Undetected -----

Exon: 0.003361  
Intron: 0.007782  
Gene: 0.039474

## Read Alignment for accepted\_hits.bam (B1)

Summary for dataset: B1/TransAlign\_summary.stats

Unmapped: 0 reads  
Experiment: 3564555 (14.1897%) reads  
Synthetic: 21556180 (85.8103%) reads

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

Query: 57069428 exons  
Query: 26914113 introns  
Query: 158601 bases

Dilution: 0.858103

\*\*\*

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

\*\*\*

\*\*\* Exon level is defined by performance per exon. An alignment that  
\*\*\* is not mapped entirely within an exon is considered as a FP. The  
\*\*\* intron level is similar.

\*\*\*

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

\*\*\*

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

Sensitivity: 0.992437  
Specificity: 0.981463  
Detection: 0.0590086 (R2\_33)

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

Sensitivity: 0.986381  
Specificity: 0.880564  
Detection: 1.88828 (R1\_72)

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

Sensitivity: 0.685079  
Specificity: 0.942327  
Detection: 0.0590086 (R2\_33)

----- Undetected -----

Exon: 0.007563  
Intron: 0.013619  
Gene: 0.065789

## Read Alignment for accepted\_hits.bam (B2)

Summary for dataset: B2/TransAlign\_summary.stats

Unmapped: 0 reads  
Experiment: 3673262 (14.5259%) reads  
Synthetic: 21614486 (85.4741%) reads

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

Query: 57264502 exons  
Query: 28885125 introns  
Query: 160649 bases

Dilution: 0.854741

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

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

Sensitivity: 0.994118  
Specificity: 0.981653  
Detection: 0.0590086 (R2\_33)

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

Sensitivity: 0.984436  
Specificity: 0.818059  
Detection: 0.0590086 (R2\_33)

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

Sensitivity: 0.687879  
Specificity: 0.934117  
Detection: 0.0590086 (R2\_33)

----- Undetected -----

Exon: 0.005882  
Intron: 0.015564  
Gene: 0.052632

## Read Alignment for accepted\_hits.bam (B3)

Summary for dataset: B3/TransAlign\_summary.stats

Unmapped: 0 reads  
Experiment: 4705904 (15.6992%) reads  
Synthetic: 25269549 (84.3008%) reads

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

Query: 67685272 exons  
Query: 37139930 introns  
Query: 162712 bases

Dilution: 0.843008

\*\*\*

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

\*\*\*

\*\*\* Exon level is defined by performance per exon. An alignment that  
\*\*\* is not mapped entirely within an exon is considered as a FP. The  
\*\*\* intron level is similar.

\*\*\*

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

\*\*\*

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

Sensitivity: 0.994958  
Specificity: 0.980831  
Detection: 0.0590086 (R2\_33)

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

Sensitivity: 0.986381  
Specificity: 0.759454  
Detection: 0.0590086 (R2\_33)

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

Sensitivity: 0.688292  
Specificity: 0.922827  
Detection: 0.0590086 (R2\_33)

----- Undetected -----

Exon: 0.005042  
Intron: 0.013619  
Gene: 0.052632

Summary for dataset: /Users/tedwong/Desktop/K\_562/Cuffdiffs/gene\_exp.diff

Experiment: 9682 genes  
Synthetic: 67 genes

Reference: 76 genes  
Detected: 65 genes

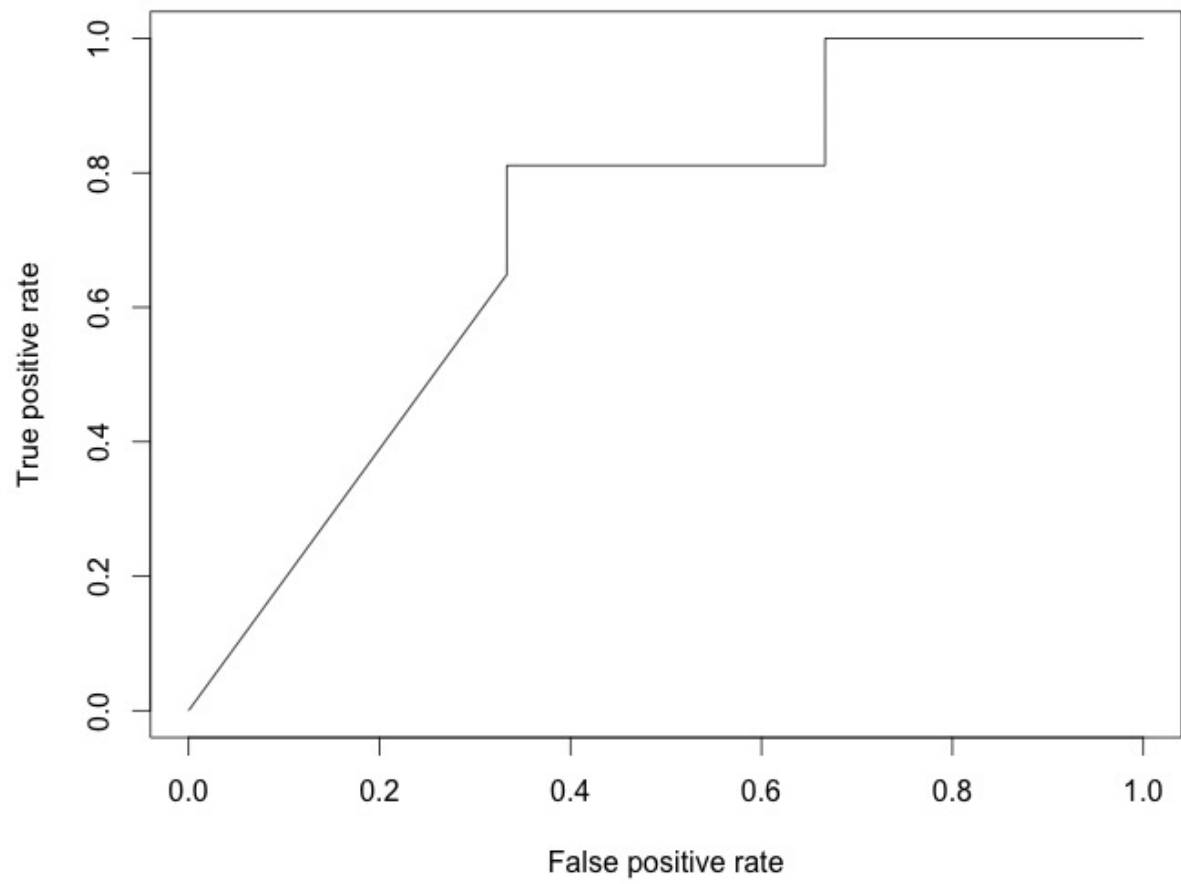
\*\*\*  
\*\*\* Statistics for linear regression  
\*\*\*

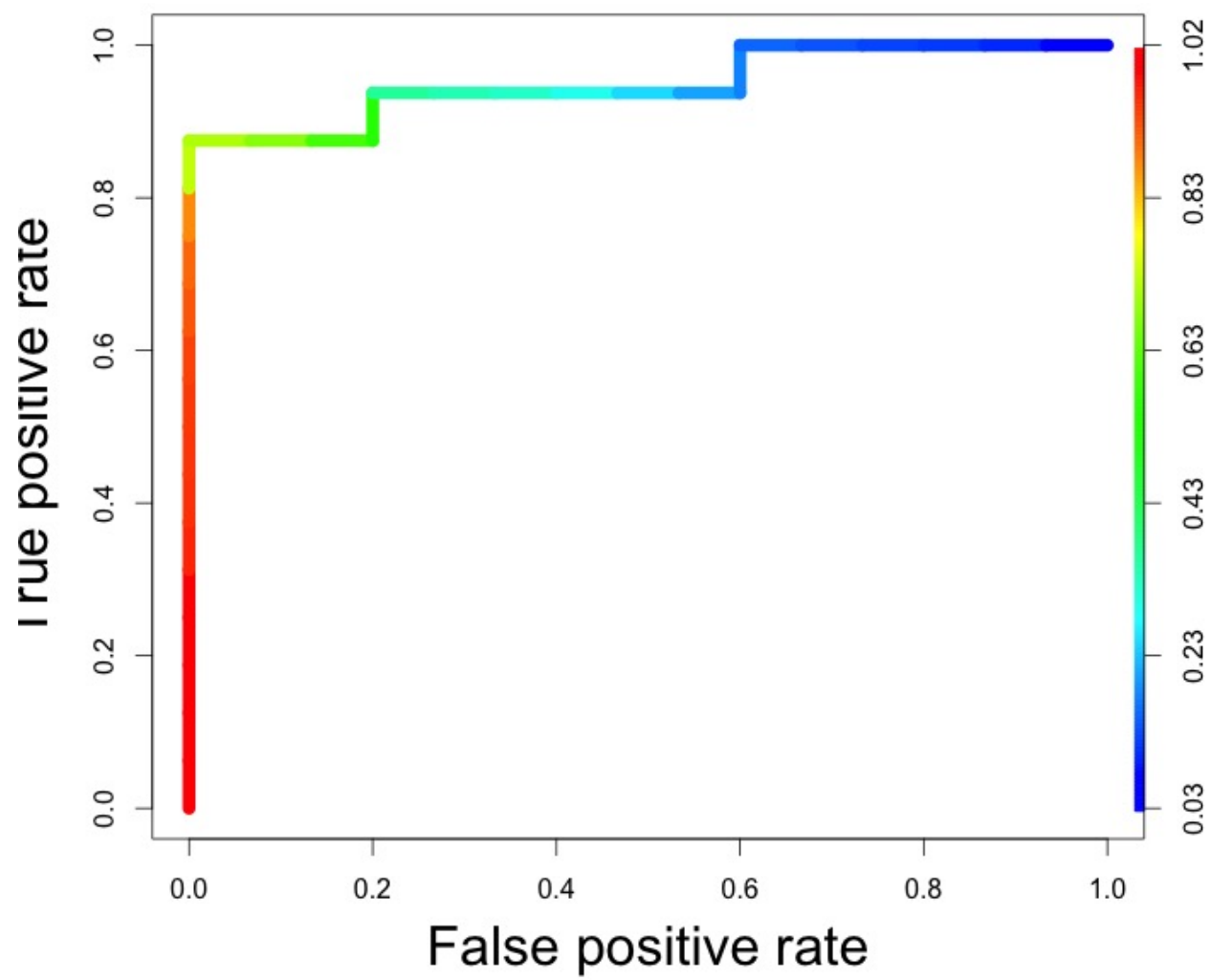
Correlation: 0.56272  
Slope: 0.411349  
R2: 0.316654  
F-statistic: 29.1934  
P-value: 1.06667e-06  
SSM: 244.21, DF: 1  
SSE: 527.011, DF: 63  
SST: 771.221, DF: 64

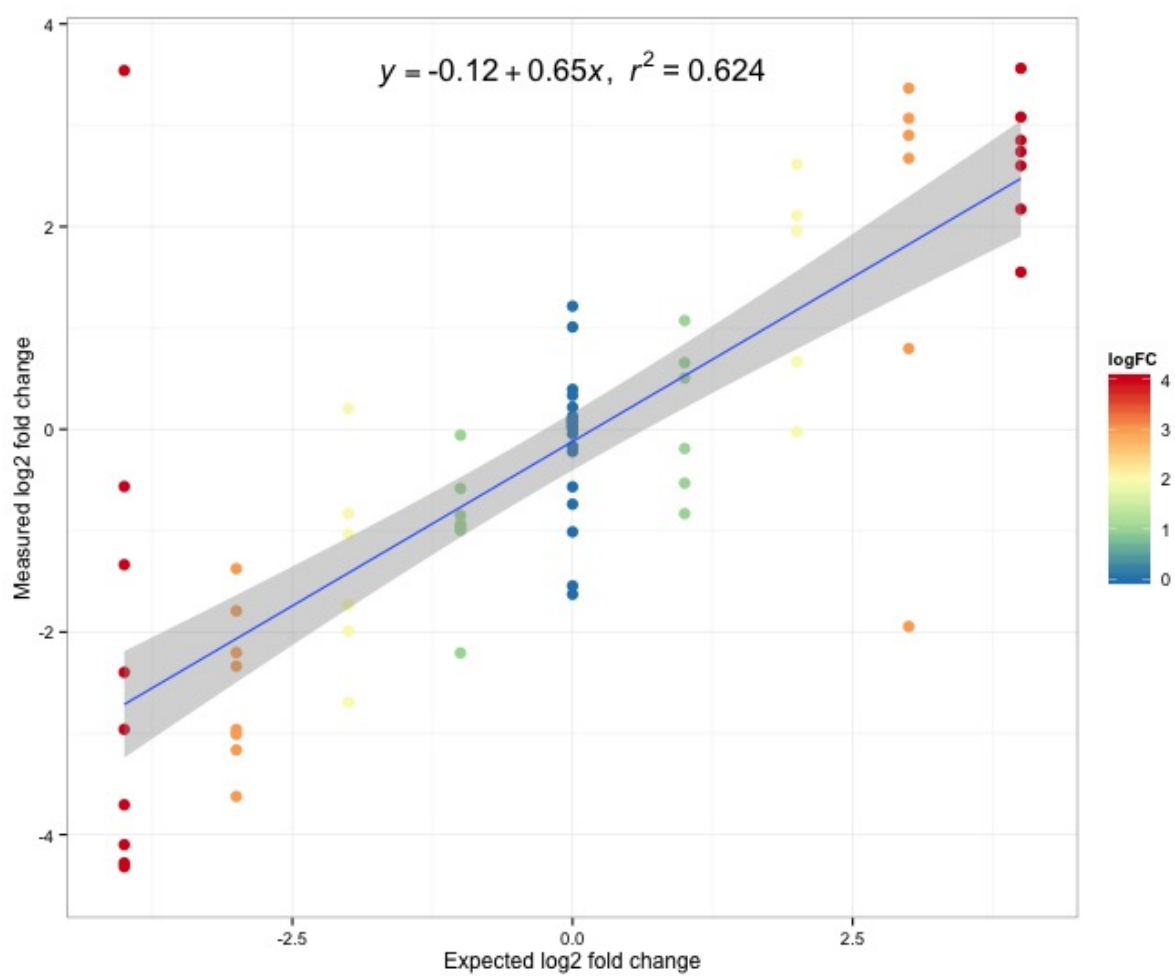
\*\*\*  
\*\*\* Statistics for linear regression (log2 scale)  
\*\*\*

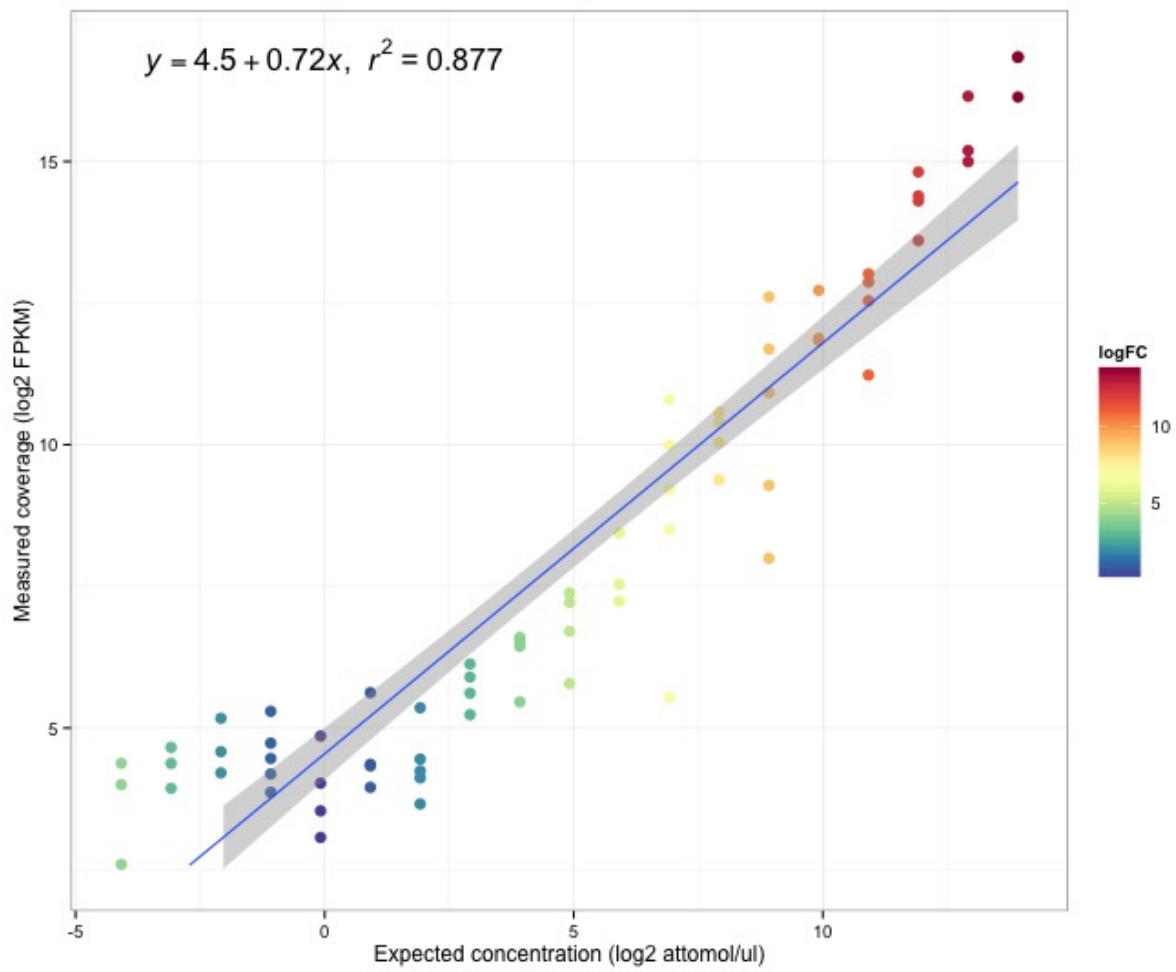
Correlation: 0.769414  
Slope: 0.545994  
R2: 0.591998  
F-statistic: 91.4108  
P-value: 7.00551e-14  
SSM: 116.382, DF: 1  
SSE: 80.21, DF: 63  
SST: 196.592, DF: 64











Summary for dataset: /Users/tedwong/Desktop/K\_562/Cufflinks/A1/genes.fpk\_tracking

Experiment: 60570 gene

Synthetic: 75 gene

Reference: 76 gene

Detected: 4.39067 gene

\*\*\*

\*\*\* Detection Limits

\*\*\*

Break: 3.77655 (R1\_62)

Left:  $4.39067 + 0.0805742x$  ( $R^2 = 0.0567335$ )

Right:  $2.0794 + 1.00352x$  ( $R^2 = 0.922502$ )

\*\*\*

\*\*\* Statistics for 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

\*\*\*

\*\*\* Statistics for 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