Bioconductor Expression Assessment Tool for Affymetrix Oligonucleotide Arrays (affycomp)

June 8, 2011

Contents

In this report only assessment using the **HGU133** spike-In experiment are presetned. Figures 2,3, and 4b are therefore ommited.

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fullname: Rohmatul Fajriyah
method: GCRMA modifikasi
nickname: g14Mb
competition: YES

Overall signal to ratio assessment:

          slope        R2   medianSD Null FC IQR Null FC 99.9% Rank
g14Mb 0.9632645 0.9151095 0.06605897   0.0485874      0.699677    2

Expected Rank (out of 12626) for genes with fold change of 2
when all other genes are not differentially expressed
stratified by nominal concentration.

           g14Mb
0.125:0      707
0.25:0.125   247
0.5:0.25     432
1:0.5          4
2:1            2
4:2            3
8:4            3
16:8           3
32:16          3
64:32          3
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128:64         3
256:128        3
512:256        8
```

Table 1 for Spike-in Data:

	g14Mb
Signal detect slope	0.9632645
Signal detect R2	0.9151095
AUC (FP<10)	0.5202374
AUC (FP<15)	0.5638985
AUC (FP<25)	0.6191639
AUC (FP<100)	0.7860882
AFP, call if fc>2	4.5934066
ATP, call if fc>2	36.2234432
IQR	0.4138010
Obs-intended-fc slope	0.9618646
Obs-(low)int-fc slope	0.6070033
FC=2, AUC (FP<10)	0.3727009
FC=2, AUC (FP<15)	0.4122125
FC=2, AUC (FP<25)	0.4724112
FC=2, AUC (FP<100)	0.6371882
FC=2, AFP, call if fc>2	2.8095238
FC=2, ATP, call if fc>2	19.7619048

Table 2 for Spike-in Data:

	g14Mb
null log-fc IQR	0.04858740
null log-fc 99%	0.42238008
null log-fc 99.9%	0.69967694
low AUC	0.55161088
med AUC	0.80905233
high AUC	0.80598774
weighted avg AUC	0.61594059
25% SD	0.03775136
Median SD	0.06605897
75% SD	0.09649497
99% SD	0.20780811
low.slope	0.61580497
med.slope	0.95843235
high.slope	0.96461266
low.R2	0.37214678

med.R2	0.47644352
high.R2	0.62375552
0.125:0	0.17157649
0.25:0.125	0.27103822
0.5:0.25	0.21821970
1:0.5	0.81270474
2:1	1.26159994
4:2	1.13967289
8:4	1.00927386
16:8	0.86011259
32:16	1.03868385
64:32	1.14199577
128:64	1.19185856
256:128	0.99631989
512:256	0.69509044

Figure 1

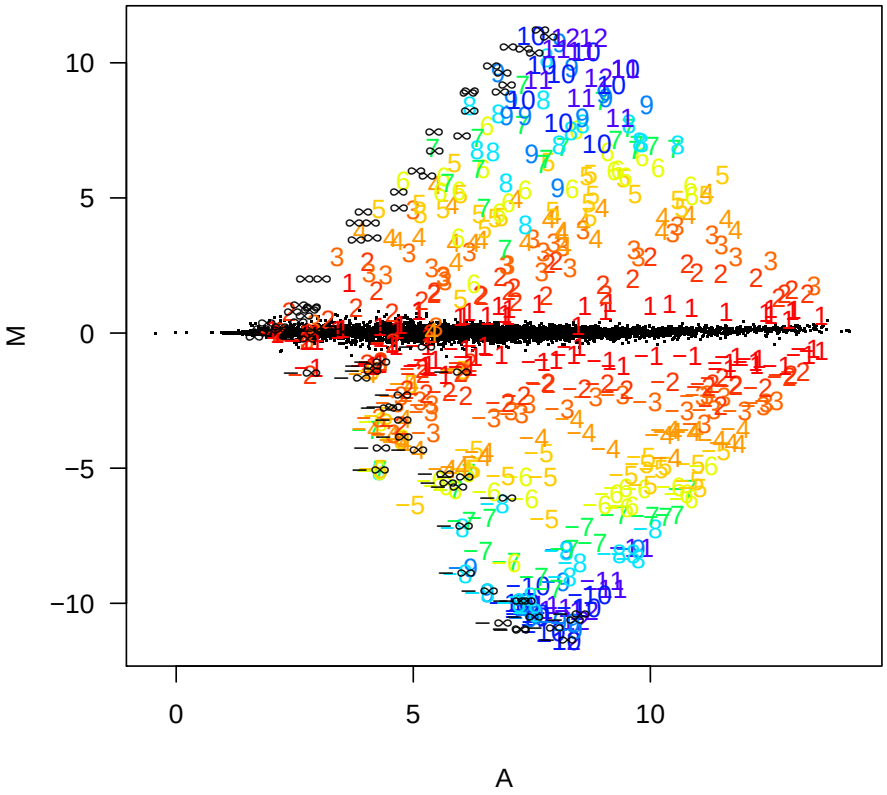

Figure 1: The MA plot shows log fold change as a function of mean log expression level. A set of 14 arrays representing a single experiment from the Affymetrix spike-in data are used for this plot. A total of 13 sets of fold changes are generated by comparing the first array in the set to each of the others. Spiked-in genes are symbolized by numbers representing the nominal $\log_2$ fold change for the gene. Non-differentially expressed genes with observed fold changes larger than 2 are plotted in red. All other probesets are represented with black dots.

Figure 1b

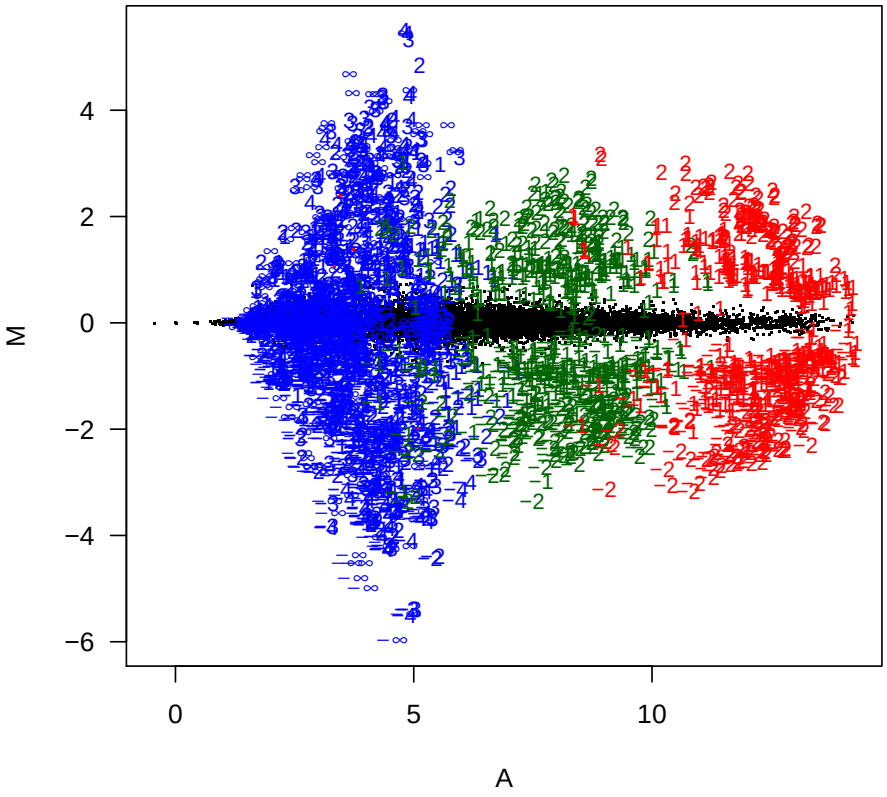

Figure 1b: The MA plot shows log fold change as a function of mean log expression level. A set of 28 arrays representing a single experiment from the Affymetrix spike-in data are used for this plot. Fold changes are generated for all possible comparisons of the the first 14 arrays and the second 14 arrays. Spiked-in genes are symbolized by numbers representing the nominal $\log_2$ fold change for the gene. Of the genes that are spiked to be differentially expressed, only genes with small nominal fold changes are shown. The colors represent four different groups: nominal concentration of genes being compared less than or equal to 2 picoMolar (blue), between 4 and 32 picoMolar (green), greater than or equal to 64 picoMolar (blue). Non-differentially expressed genes with observed fold changes larger than 2 are plotted in red. All other probesets are represented with black dots.

Figure 2b

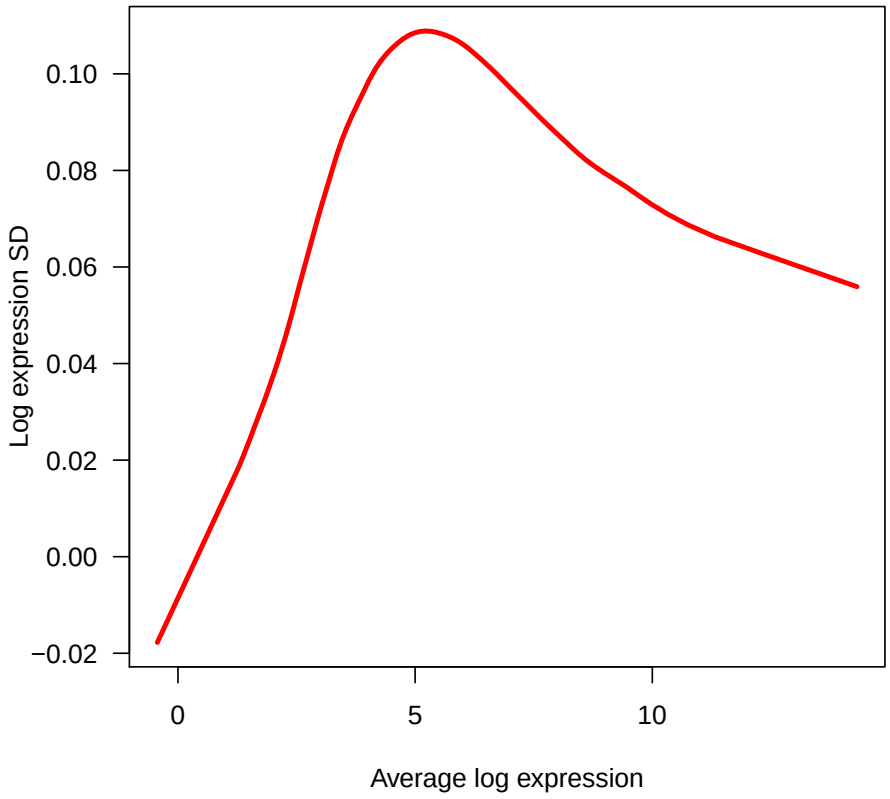

Figure 2b: For each non-spiked-in gene in the 28 arrays used in Figure 1b, we calculate the mean log expression and the observed standard deviation across the 28 replicates. The resulting scatterplot is smoothed to generate a single curve representing mean standard deviation as a function of mean log expression.

Figure 4a

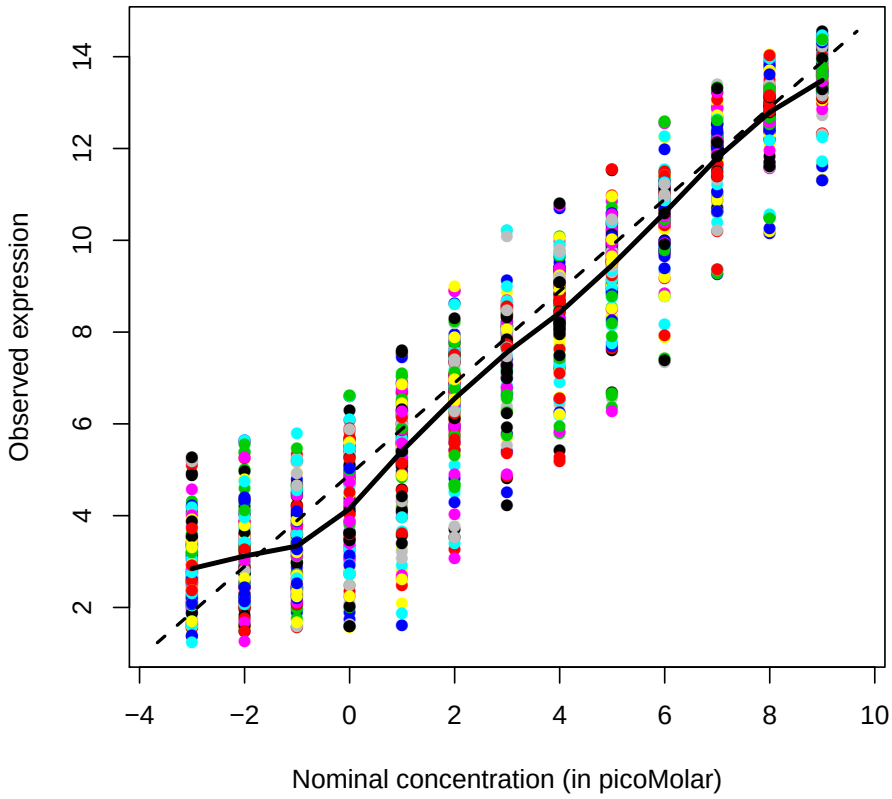

Figure 4a) Average observed log_2 intensity plotted against nominal log_2 concentration for each spiked-in gene for all arrays in Affymetrix spike-In experiment. The dashed line has the ideal slope of 1.

Figure 4c

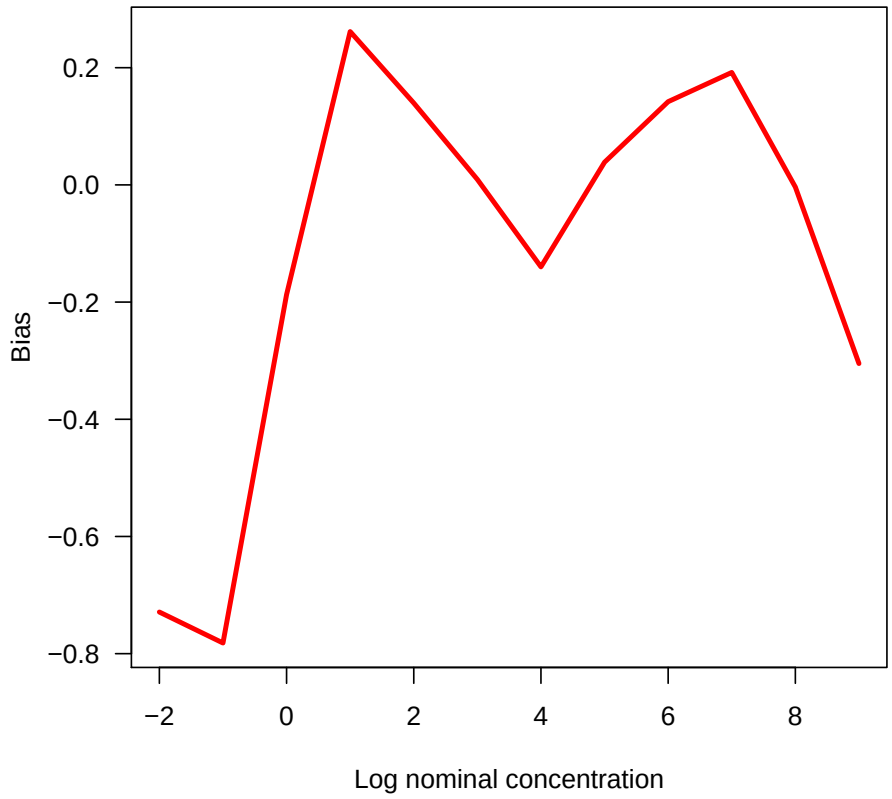

Figure 4c) Using the 28 arrays of Figure 1b, we compute local slopes. As the slopes shown in Figure 4a), the local slopes represent the expected observed log fold-change for probesets with true fold-change of 2 but they are presented as a function of the total nominal probeset concentration in the two samples being compared. In theory the local slopes should be one so we show the bias (difference between the observed local slope and one).

Figure 5a

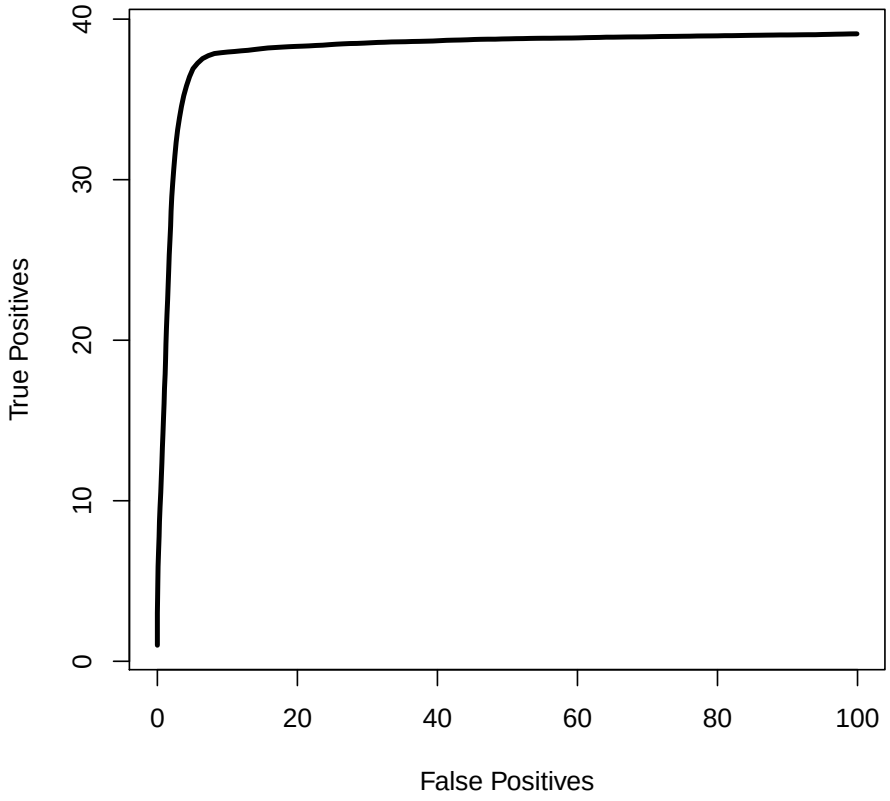

Figure 5a) A typical identification rule for differential expression filters genes with fold change exceeding a given threshold. This figure shows average ROC curves which offer a graphical representation of both specificity and sensitivity for such a detection rule. Average ROC curves based on comparisons with nominal fold changes ranging from 2 to 4096.

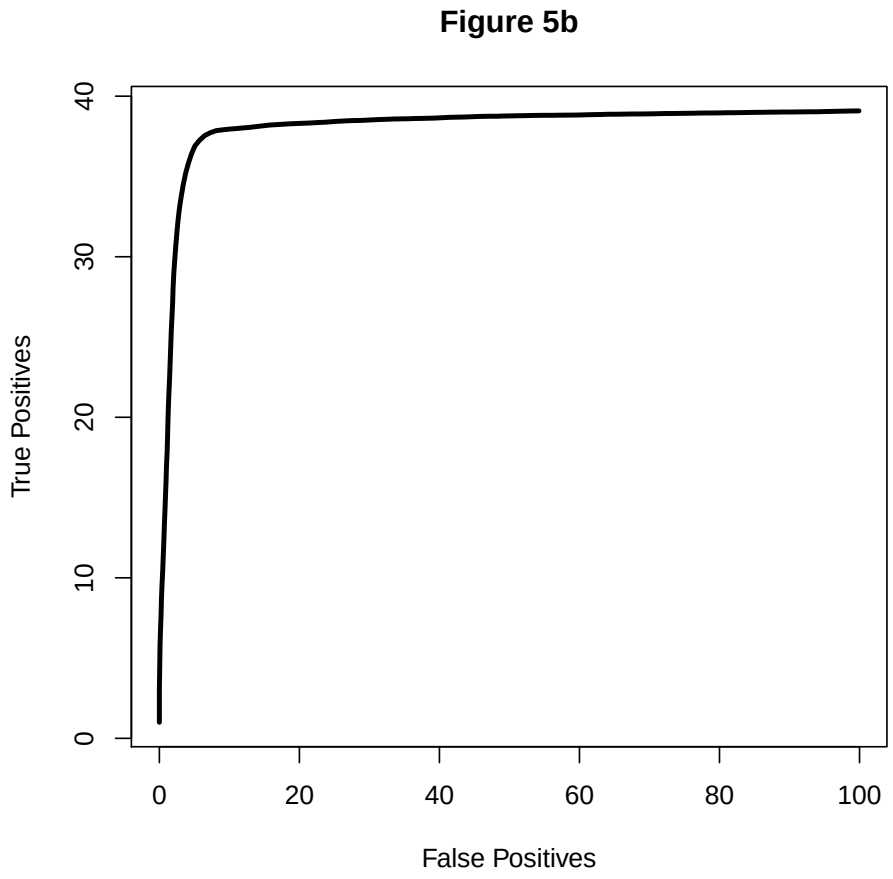

Figure 5b) As 5a) but with nominal fold changes equal to 2.

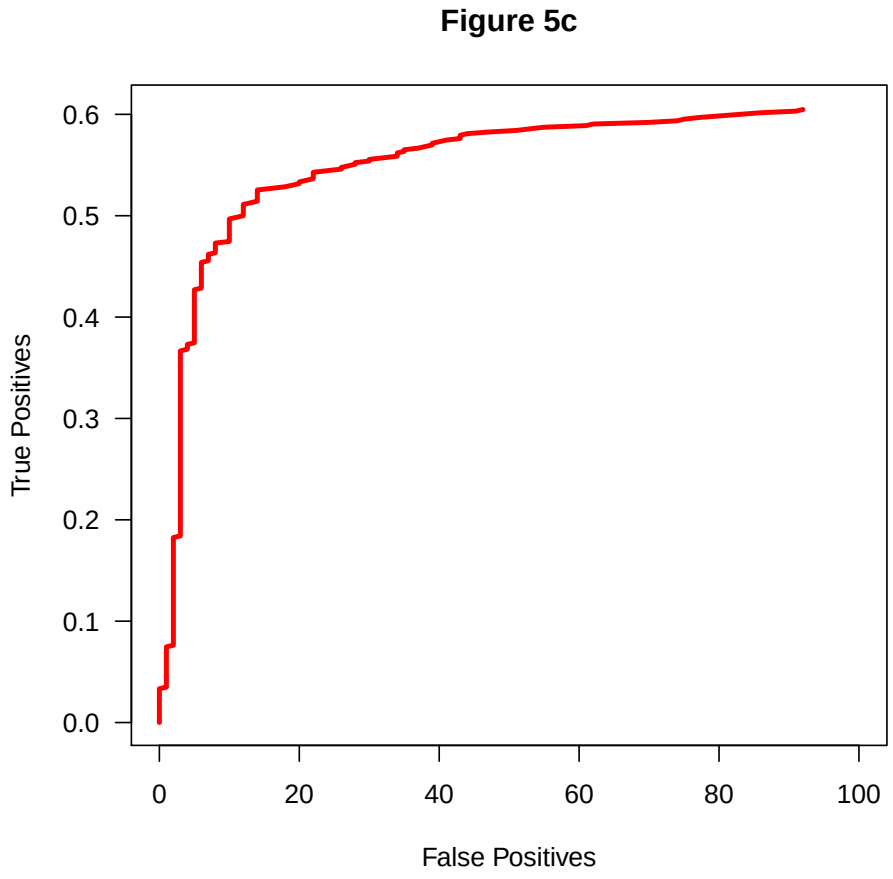

Figure 5c) As 5a) but for comparisons with both nominal concentrations at most 4 picoMolar and nominal fold changes at most 2.

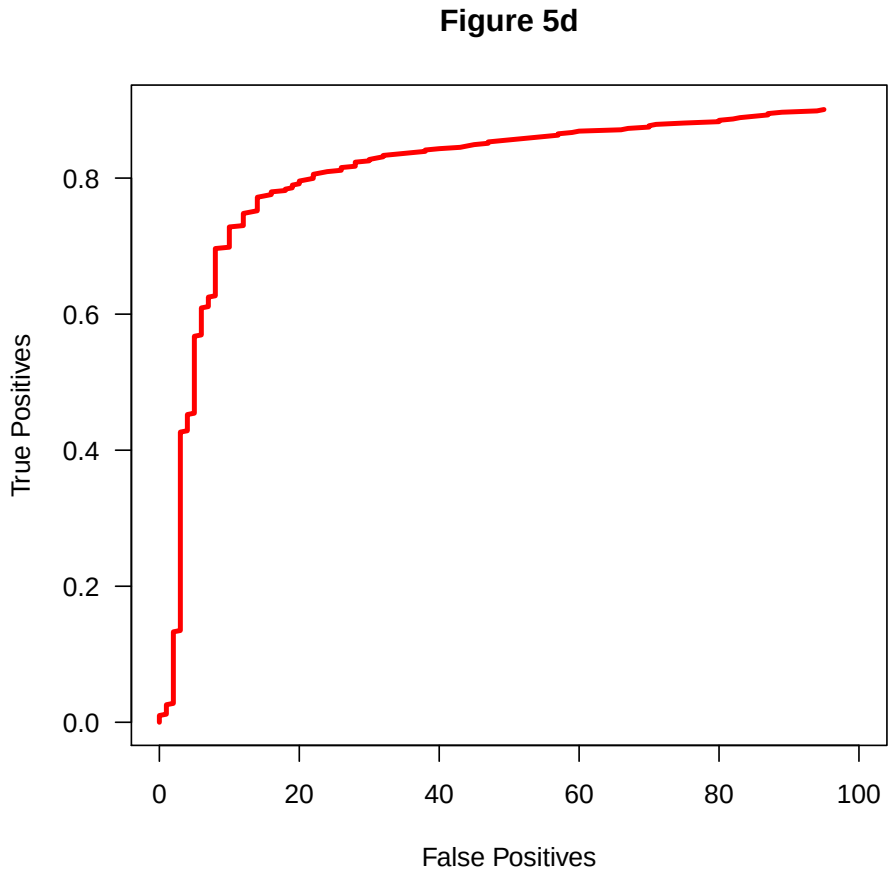

Figure 5d) As 5a) but for comparisons with both nominal concentrations between 4 and 64 picoMolar and nominal fold changes at most 2.

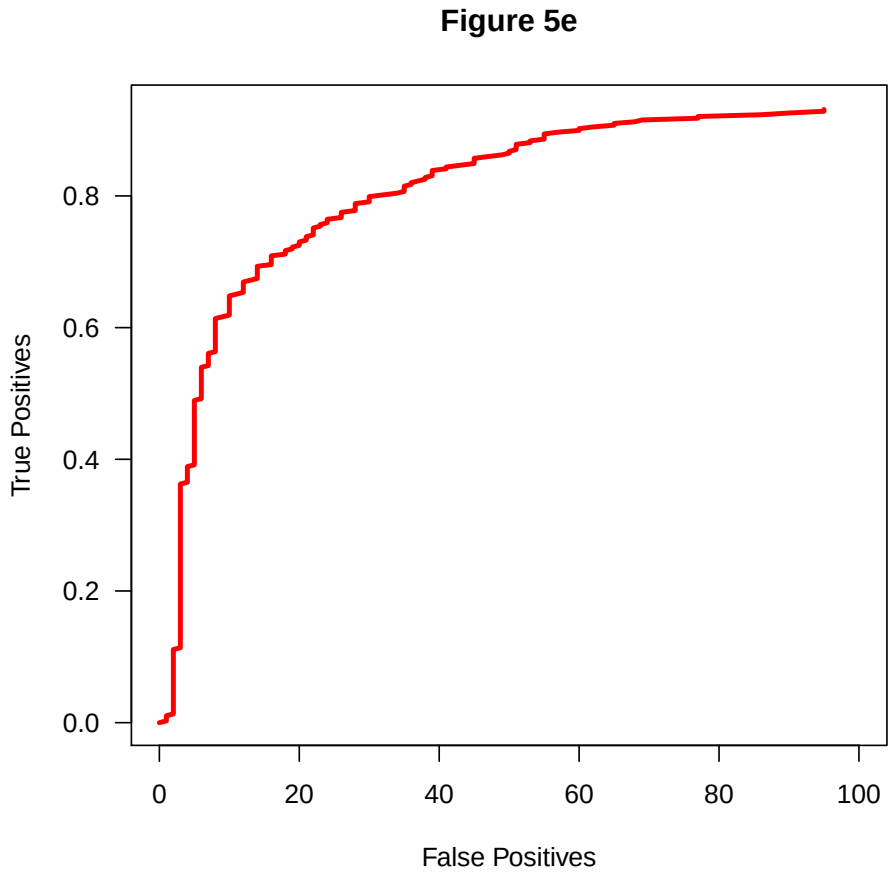

Figure 5e) As 5a) but for comparisons with both nominal concentrations at least 64 and with nominal fold changes at most 2.

Figure 6a

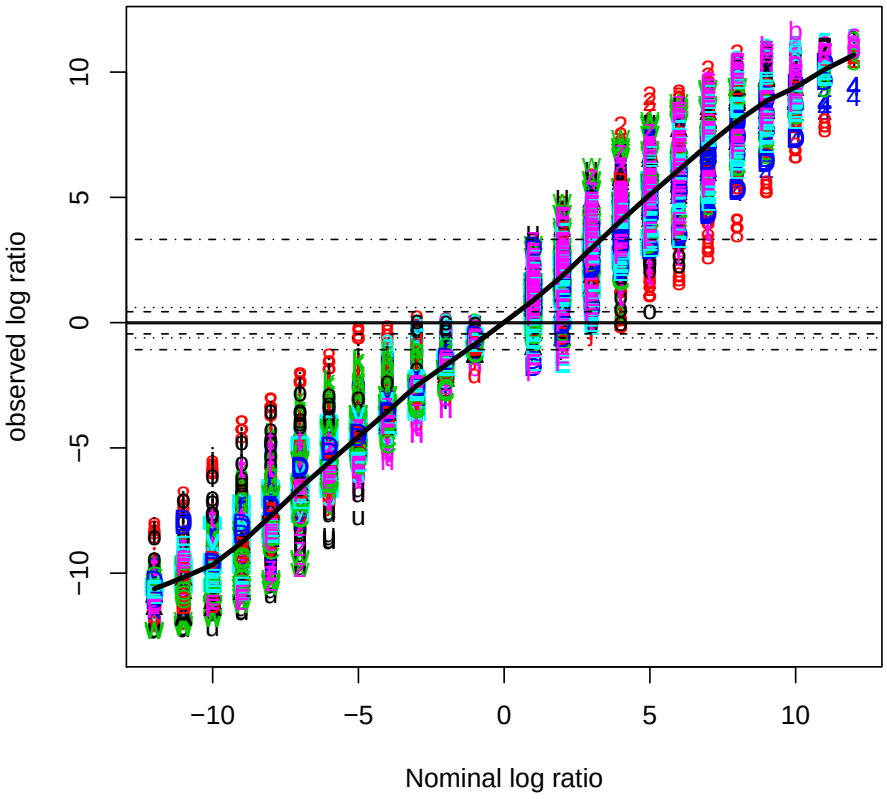

Figure 6a) Observed log fold changes plotted against nominal log fold changes. The dashed lines represent highest, 25th highest, 100th highest, 25th percentile, 75th percentile, smallest 100th, smallest 25th, and smallest log fold change for the genes that were not differentially expressed.

Figure 6b

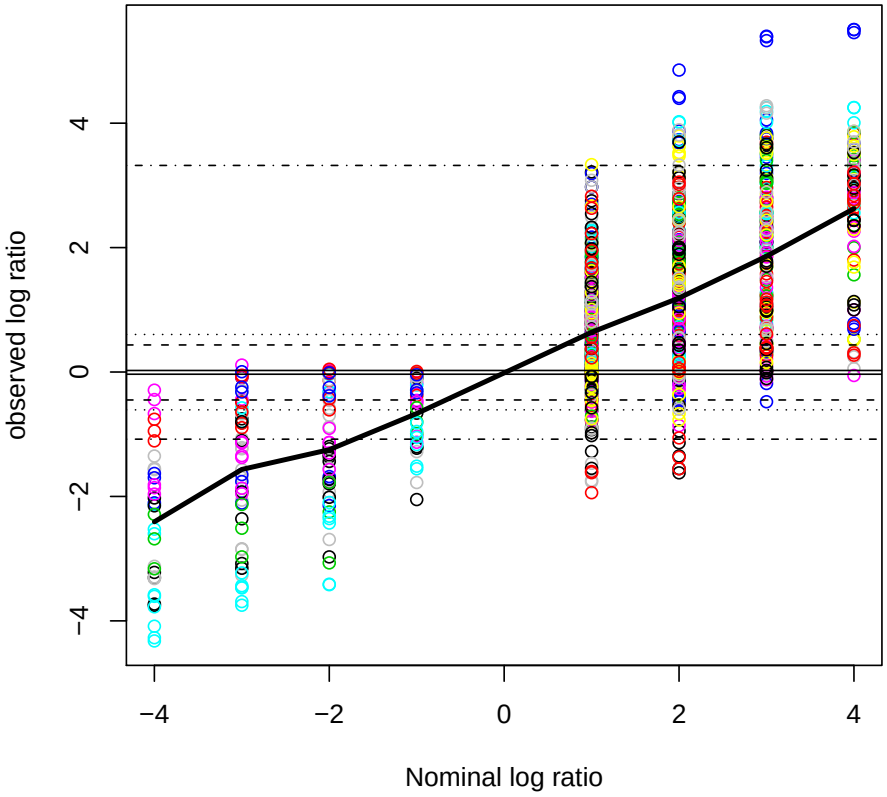

Figure 6b) Like a) but the observed fold changes were calculated for spiked in genes with nominal concentrations no higher than 2pM.