

Bioconductor Expression Assessment Tool for Affymetrix Oligonucleotide Arrays (affycomp)

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Contents

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

fullname: fengxuemei
method: Mas5
nickname: Mas5
competition: YES

Overall signal to ratio assessment:

	slope	R2	medianSD	Null FC	IQR	Null FC	99.9%	Rank
Mas5	0.76688	0.9061658	0.2912686	0.4675374			4.010715	1048

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

	Mas5
0.125:0	1801
0.25:0.125	1882
0.5:0.25	1475
1:0.5	1062
2:1	934
4:2	980
8:4	1153
16:8	1302
32:16	944
64:32	857

128:64	746
256:128	1008
512:256	1691

Table 1 for Spike-in Data:

	Mas5
Signal detect slope	7.668800e-01
Signal detect R2	9.061658e-01
AUC (FP<10)	1.873087e-01
AUC (FP<15)	2.135911e-01
AUC (FP<25)	2.593607e-01
AUC (FP<100)	3.860166e-01
AFP, call if fc>2	2.863348e+03
ATP, call if fc>2	3.544689e+01
IQR	2.662900e+00
Obs-intended-fc slope	7.655332e-01
Obs-(low)int-fc slope	6.419496e-01
FC=2, AUC (FP<10)	6.528723e-02
FC=2, AUC (FP<15)	6.709350e-02
FC=2, AUC (FP<25)	6.903952e-02
FC=2, AUC (FP<100)	7.388327e-02
FC=2, AFP, call if fc>2	2.784571e+03
FC=2, ATP, call if fc>2	1.433333e+01

Table 2 for Spike-in Data:

	Mas5
null log-fc IQR	0.467537422
null log-fc 99%	2.827503395
null log-fc 99.9%	4.010715013
low AUC	0.003756090
med AUC	0.000000000
high AUC	0.000000000
weighted avg AUC	0.002817067
25% SD	0.152465134
Median SD	0.291268609
75% SD	0.636072214
99% SD	1.364764008
low.slope	0.648892846
med.slope	0.713701129
high.slope	0.766467051
low.R2	0.358084277

med.R2	0.541424931
high.R2	0.726321842
0.125:0	0.447159991
0.25:0.125	0.426539443
0.5:0.25	0.554202372
1:0.5	0.757640580
2:1	0.850160360
4:2	0.813908247
8:4	0.702560932
16:8	0.627562170
32:16	0.839693272
64:32	0.909196676
128:64	1.018937340
256:128	0.793091662
512:256	0.478497282

Figure 1

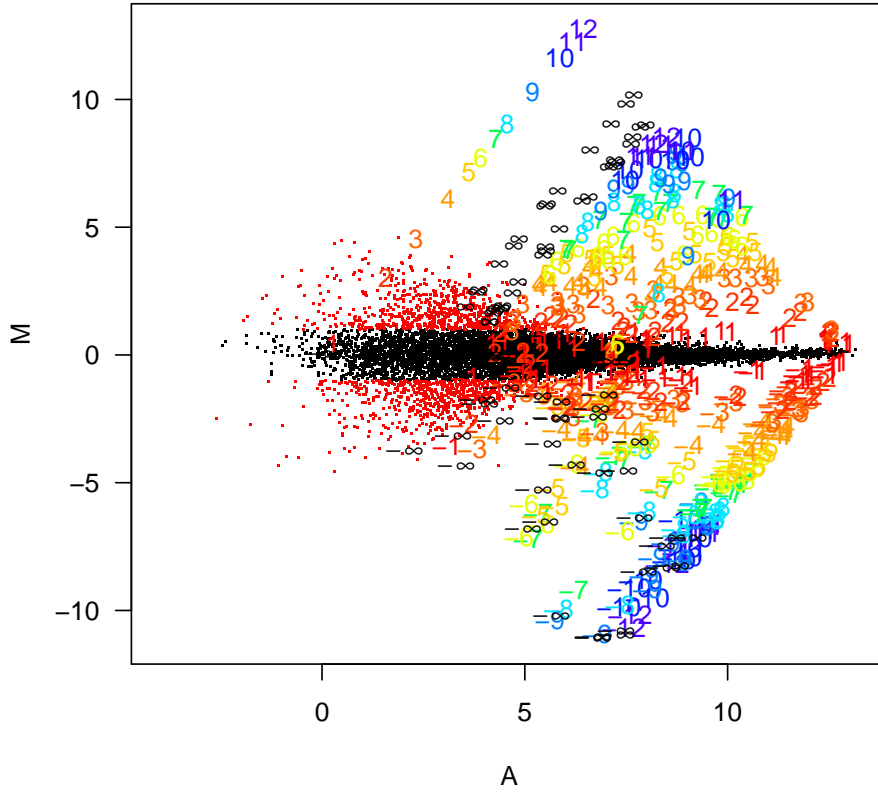


Figure 1: The MA plot shows log fold change as a function of mean log expression level. A set of 14 arrays representing a single experiment from the Affymetrix spike-in data are used for this plot. A total of 13 sets of fold changes are generated by comparing the first array in the set to each of the 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

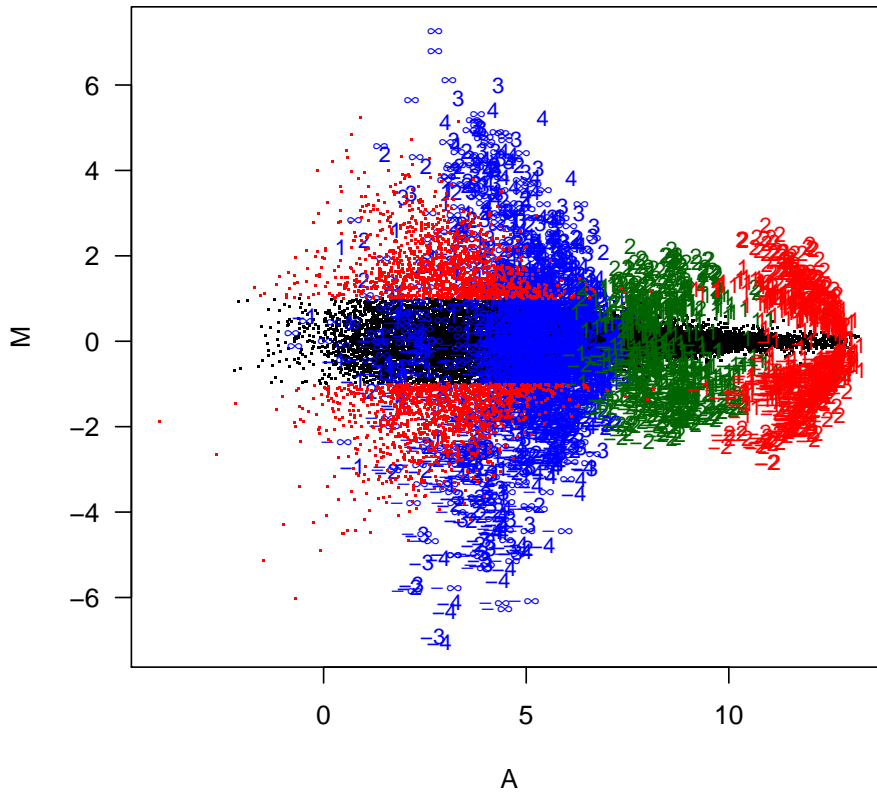


Figure 1b: The MA plot shows log fold change as a function of mean log expression level. A set of 28 arrays representing a single experiment from the Affymetrix spike-in data are used for this plot. Fold changes are generated for all possible comparisons of the the first 14 arrays and the second 14 arrays. 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

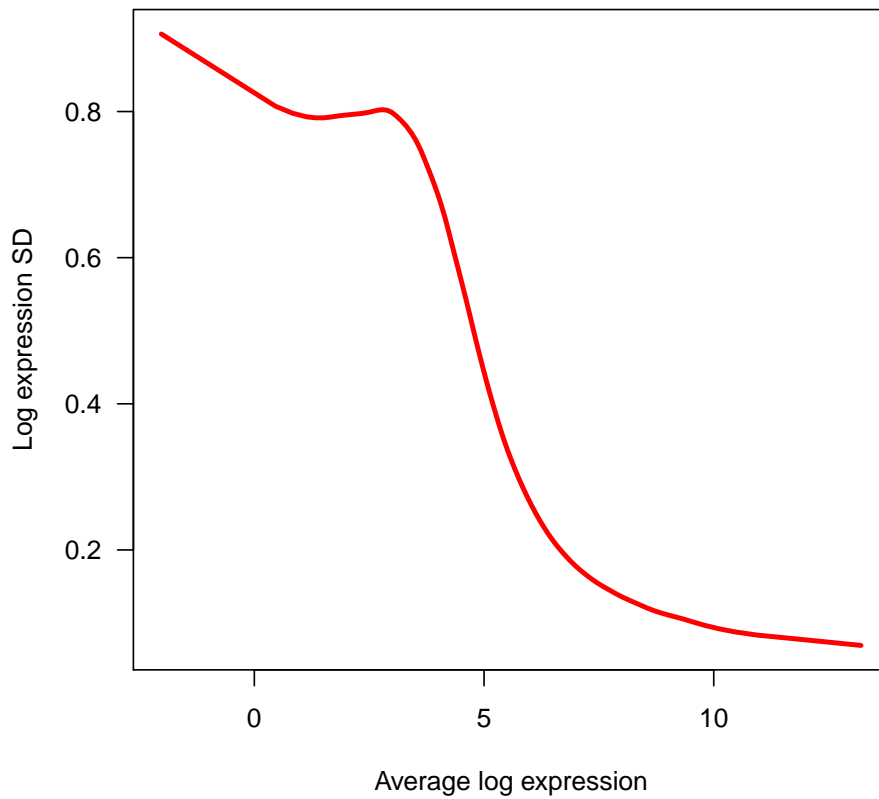


Figure 2b: For each non-spiked-in gene in the 28 arrays used in Figure 1b, we calculate the mean log expression and the observed standard deviation across the 28 replicates. The resulting scatterplot is smoothed to generate a single curve representing mean standard deviation as a function of mean log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

Figure 4a

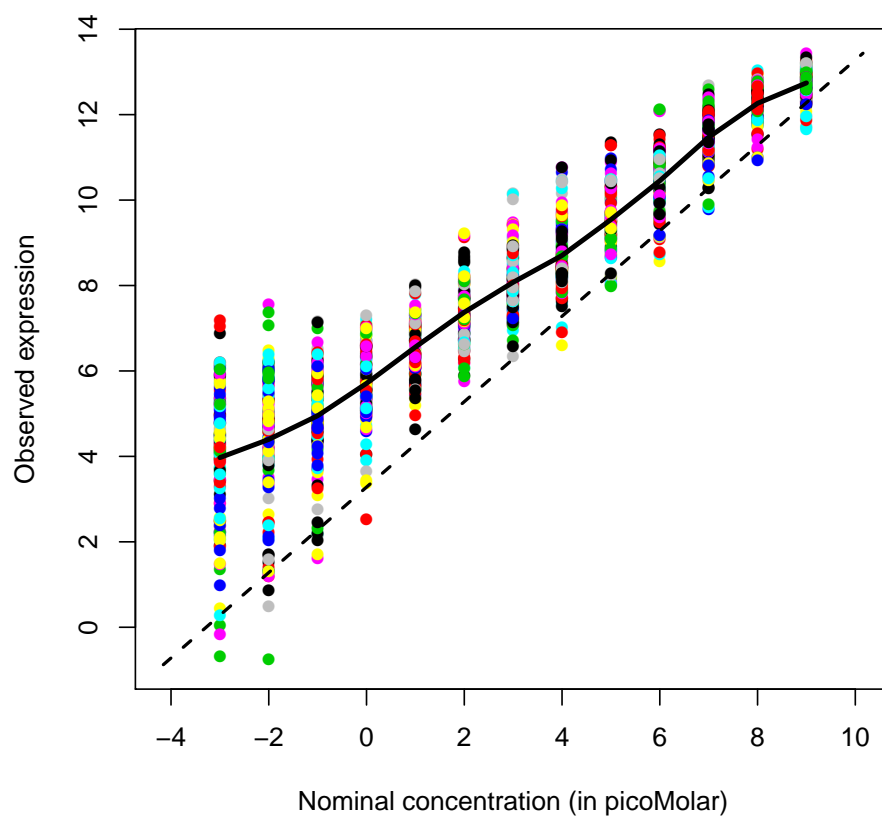


Figure 4a) Average observed \log_2 intensity plotted against nominal \log_2 concentration for each spiked-in gene for all arrays in Affymetrix spike-In experiment. The dashed line has the ideal slope of 1.

Figure 4c

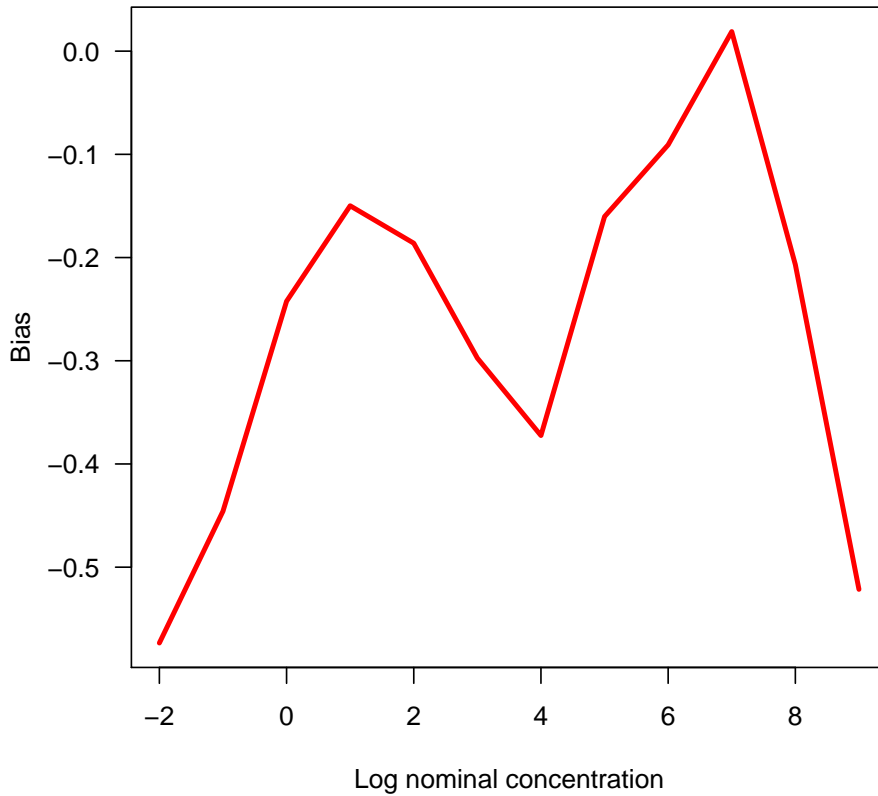


Figure 4c) Using the 28 arrays of Figure 1b, we compute local slopes. As the slopes shown in Figure 4a), the local slopes represent the expected observed log fold-change for probesets with true fold-change of 2 but they are presented as a function of the total nominal probeset concentration in the two 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

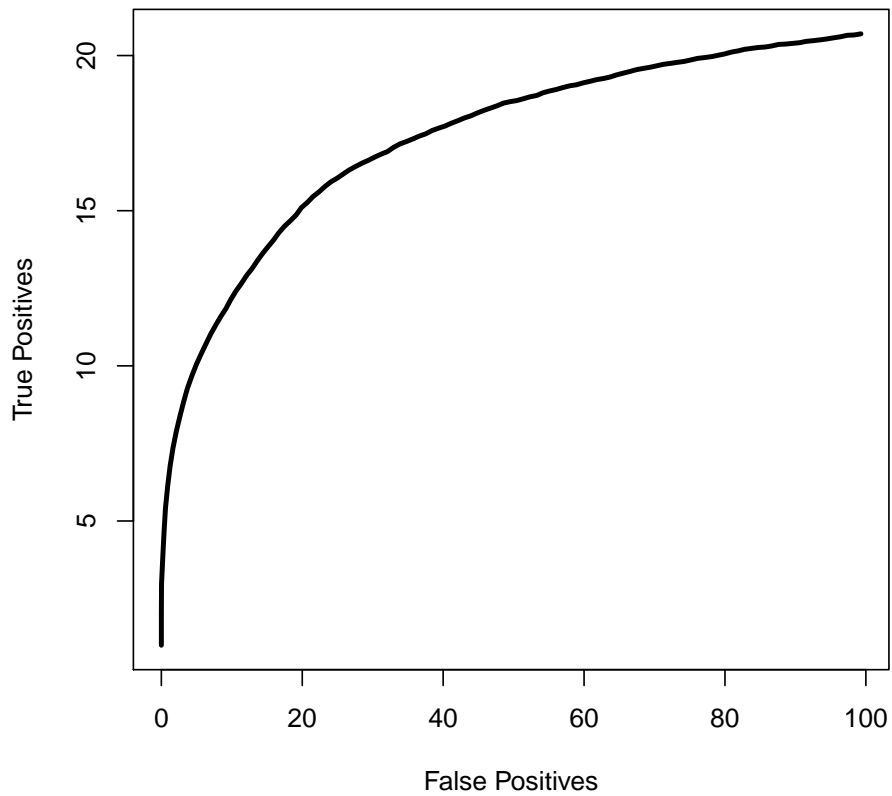


Figure 5a) A typical identification rule for differential expression filters genes with fold change exceeding a given threshold. This figure shows average ROC curves which offer a graphical representation of both specificity and sensitivity for such a detection rule. Average ROC curves based on comparisons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

Figure 5b

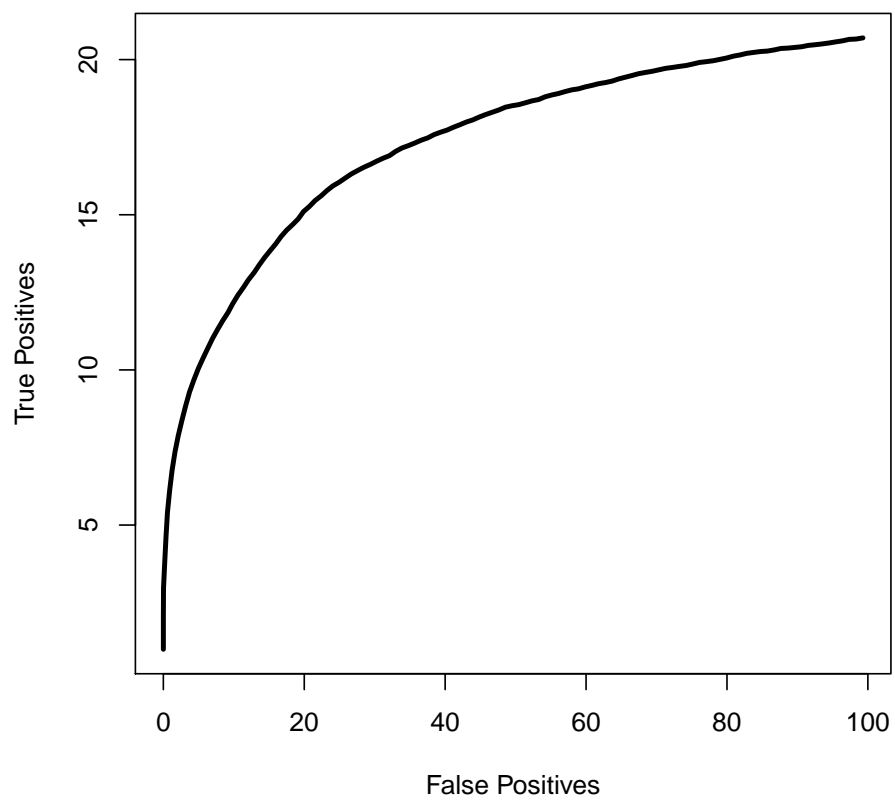


Figure 5b) As 5a) but with nominal fold changes equal to 2.

Figure 5c

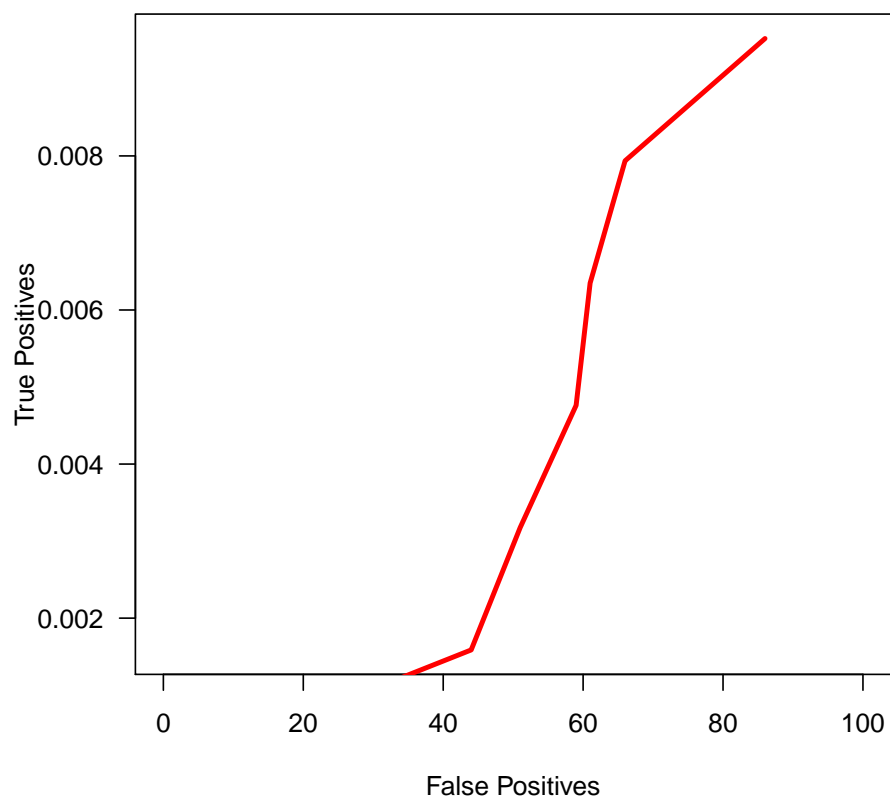


Figure 5c) As 5a) but for comparisons with both nominal concentrations at most 4 picoMolar and nominal fold changes at most 2.

Figure 5d

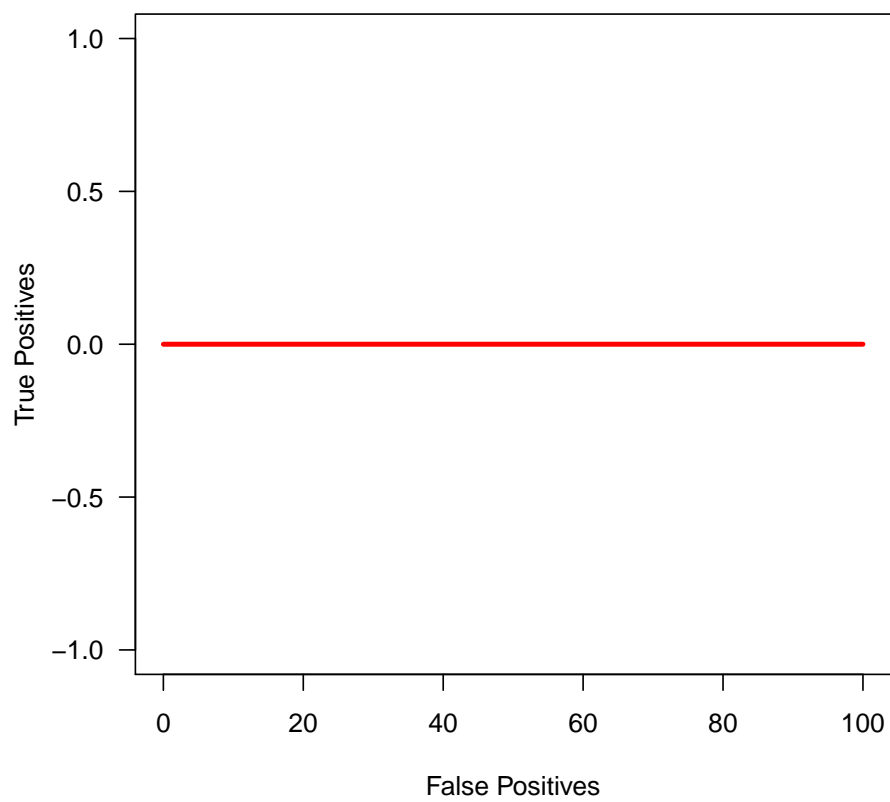


Figure 5d) As 5a) but for comparisons with both nominal concentrations between 4 and 64 picoMolar and nominal fold changes at most 2.

Figure 5e

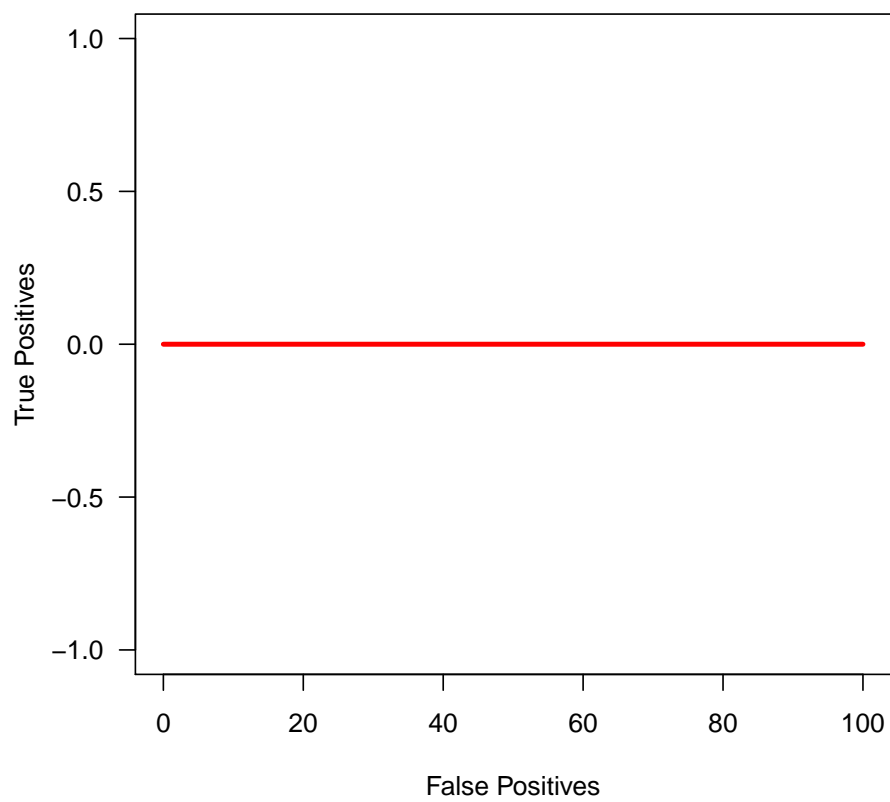


Figure 5e) As 5a) but for comparisons with both nominal concentrations at least 64 and with nominal fold changes at most 2.

Figure 6a

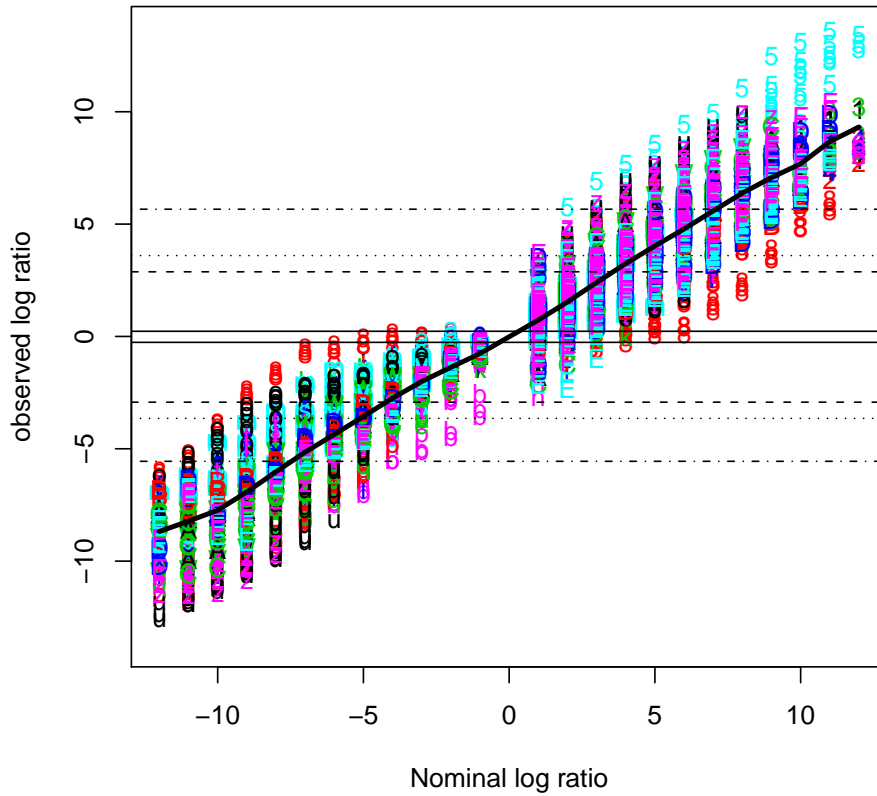


Figure 6a) Observed log fold changes plotted against nominal log fold changes. The dashed lines represent highest, 25th highest, 100th highest, 25th percentile, 75th percentile, smallest 100th, smallest 25th, and smallest log fold change for the genes that were not differentially expressed.

Figure 6b

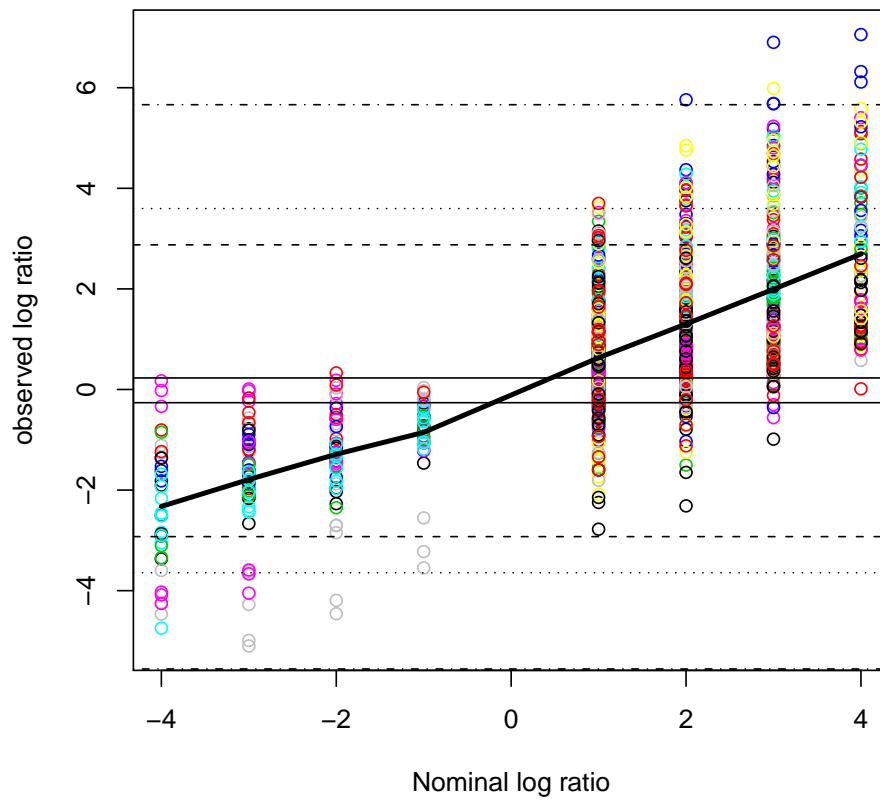


Figure 6b) Like a) but the observed fold changes were calculated for spiked in genes with nominal concentrations no higher than 2pM.