Quality Control & Pre-processing Evaluation

of

lars-test2

REPORT

Array names and grouping

Array.DataFile	SourceName	Factor.Value
GSM288756.CEL.gz	GSM288756.CEL.gz	1
GSM288757.CEL.gz	GSM288757.CEL.gz	1

Array names and grouping

ArrayDataFile	SourceName	FactorValue
GSM286756.CEL.gz	GSM286756.CEL.gz	1
GSM286757.CEL.gz	GSM286757.CEL.gz	1

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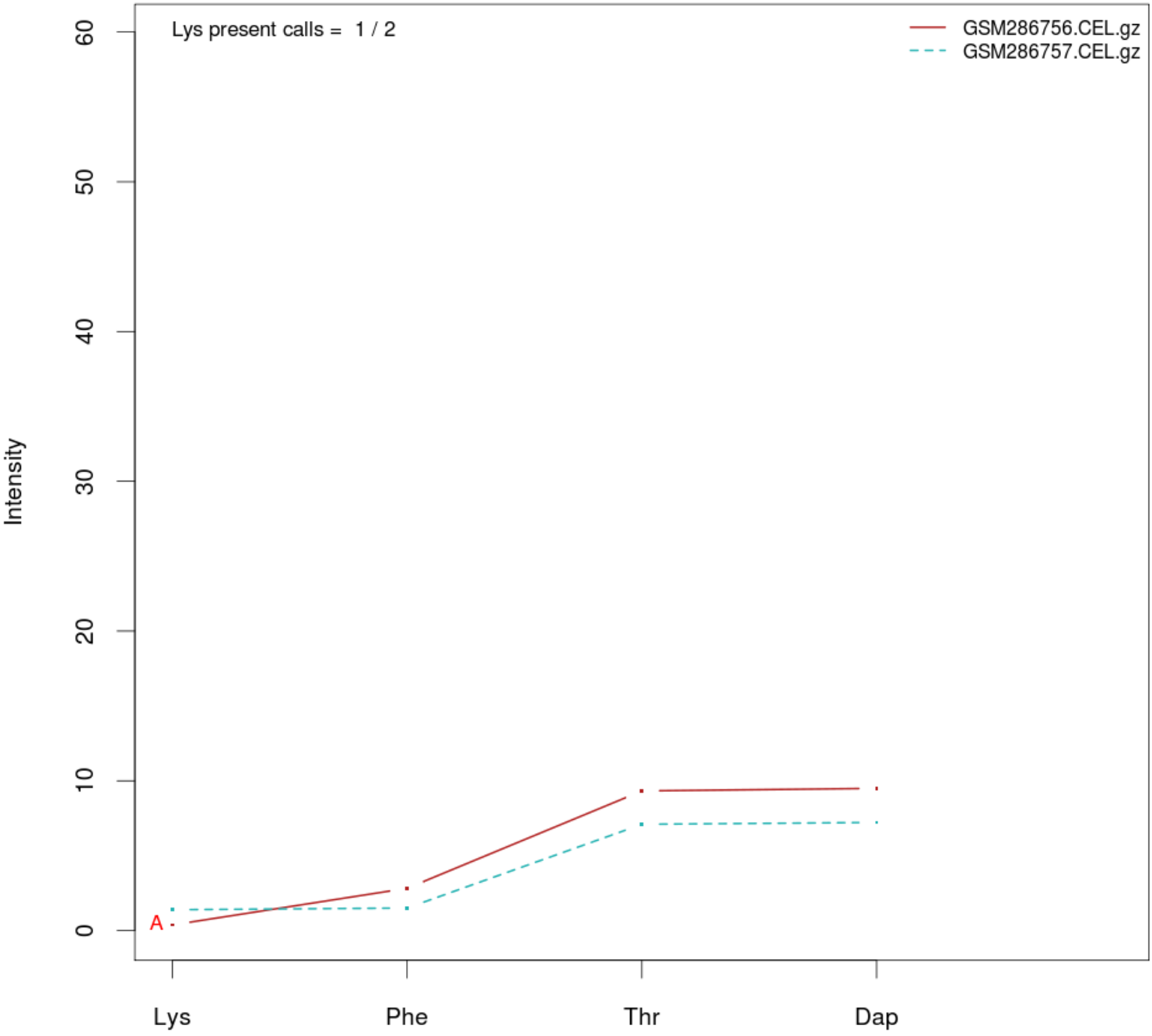
REPORT

Spike-in Sample Prep controls intensities and calls

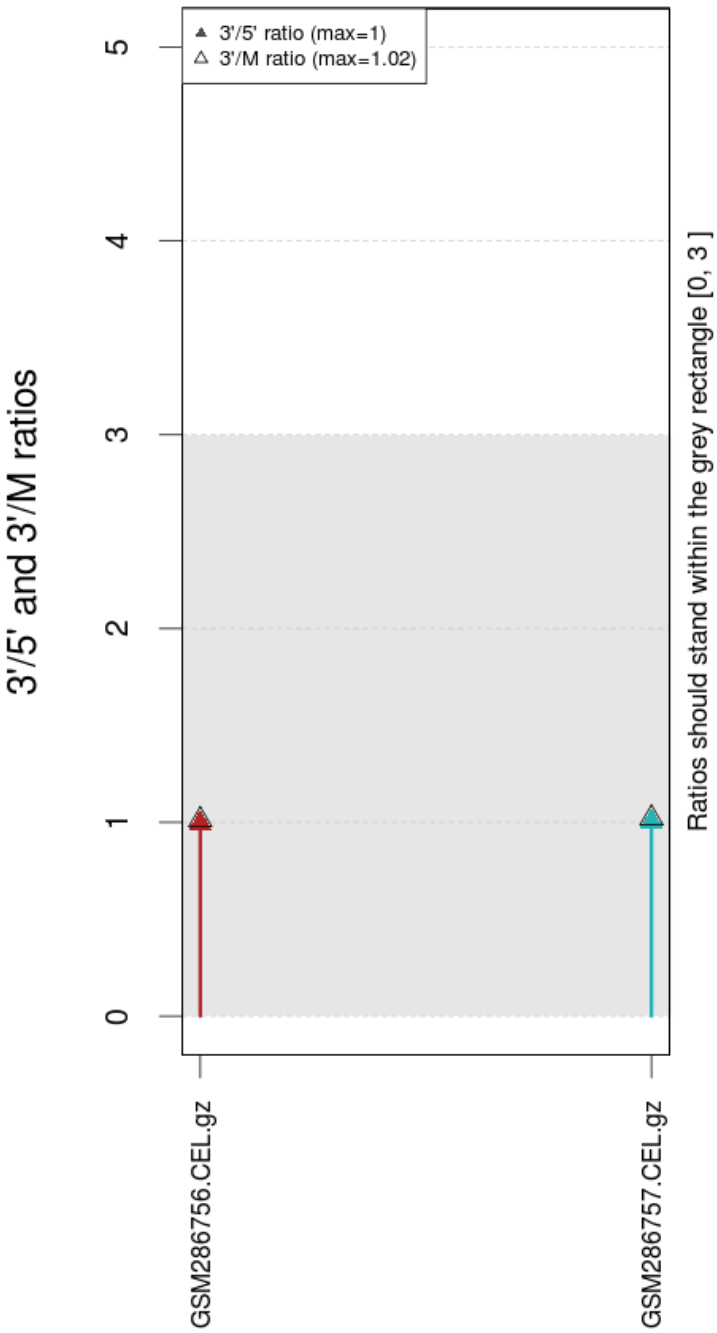


Intensity: OK (Lys < Phe < Thr < Dap for all arrays)

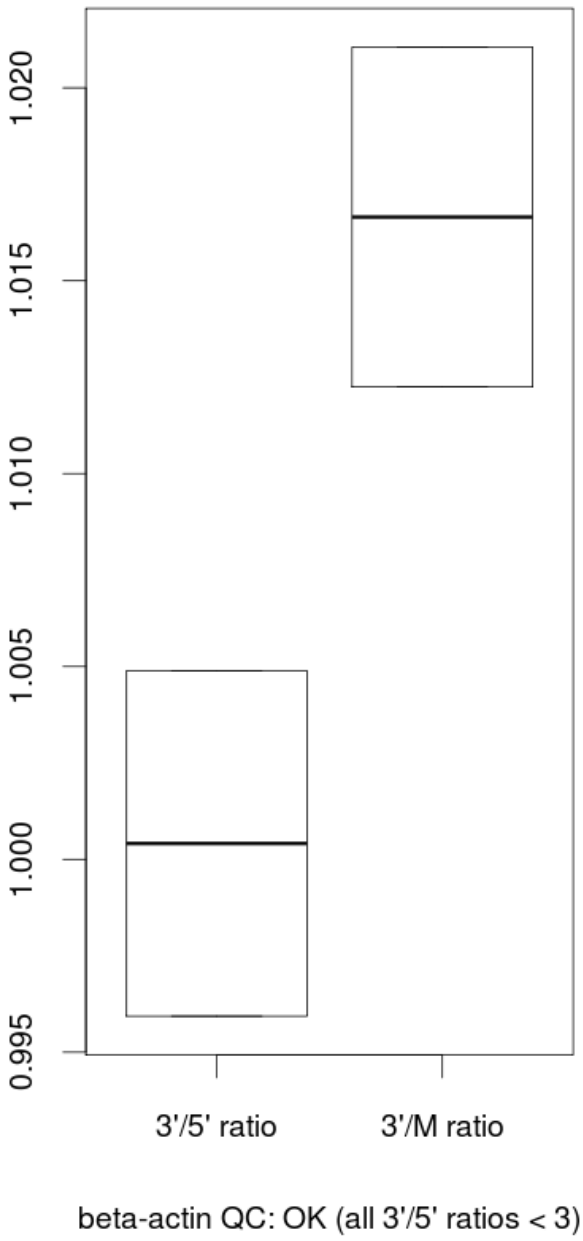
Lys Present calls: 1 Lys not called present

Summary of raw data quality indicators

RNA degradation of beta-actin

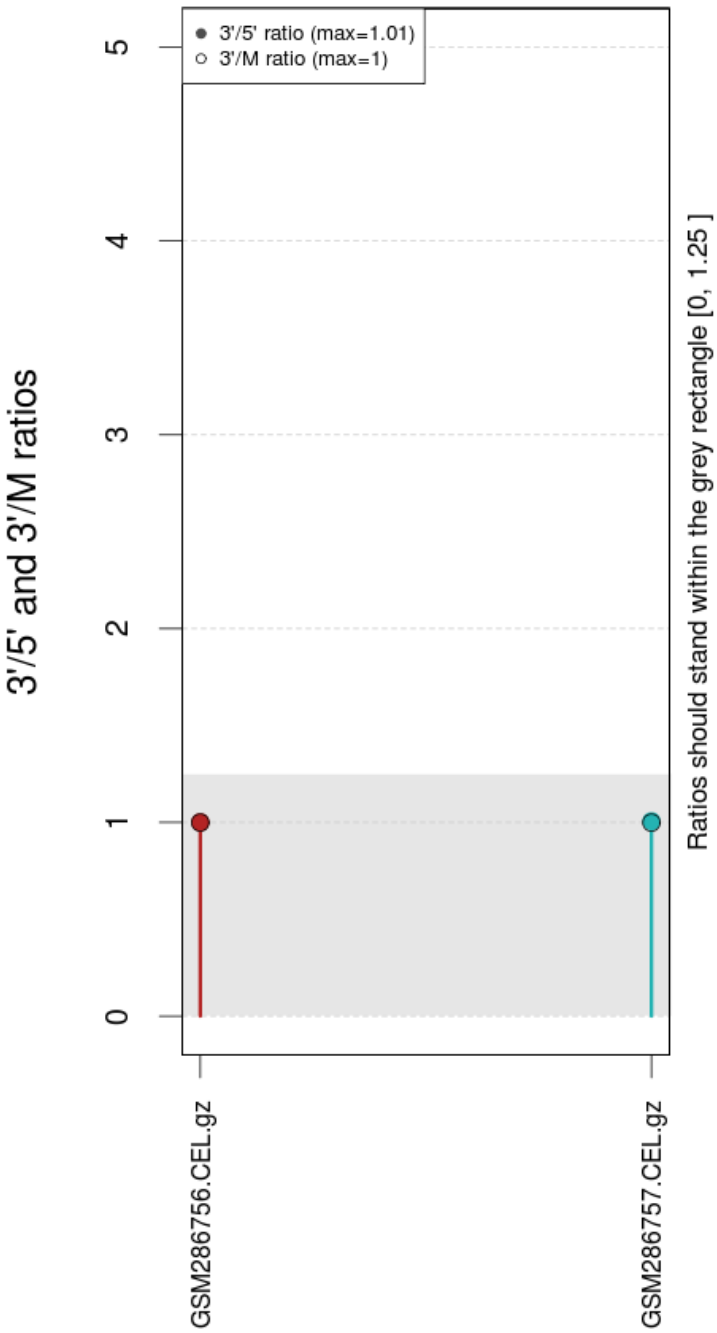


Boxplot of beta-actin ratios

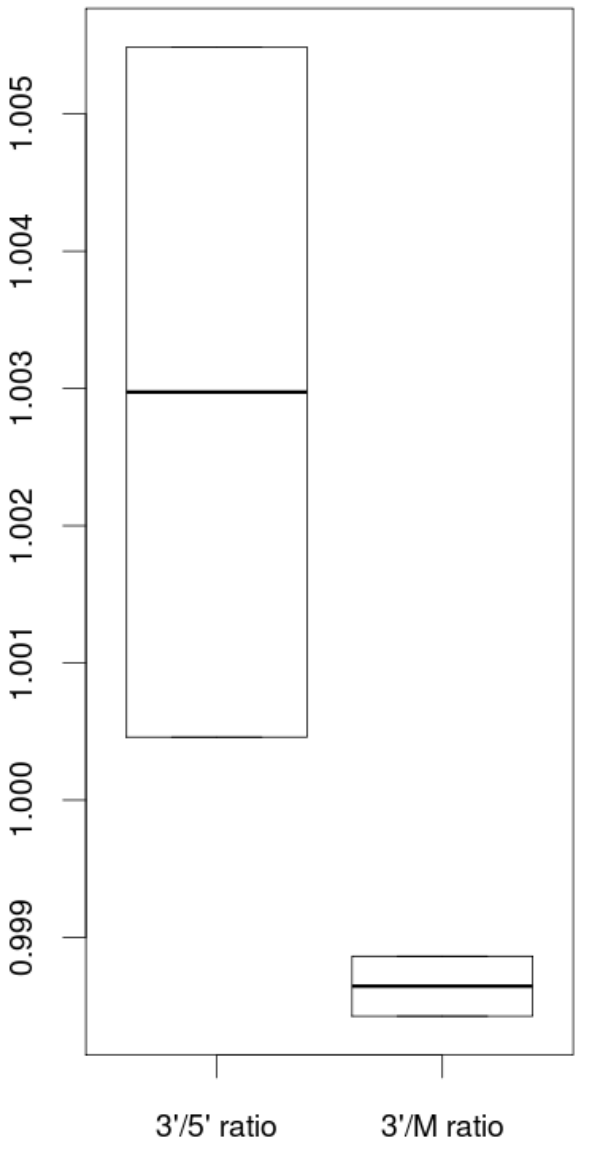


beta-actin QC: OK (all 3'/5' ratios < 3)

RNA degradation of GAPDH

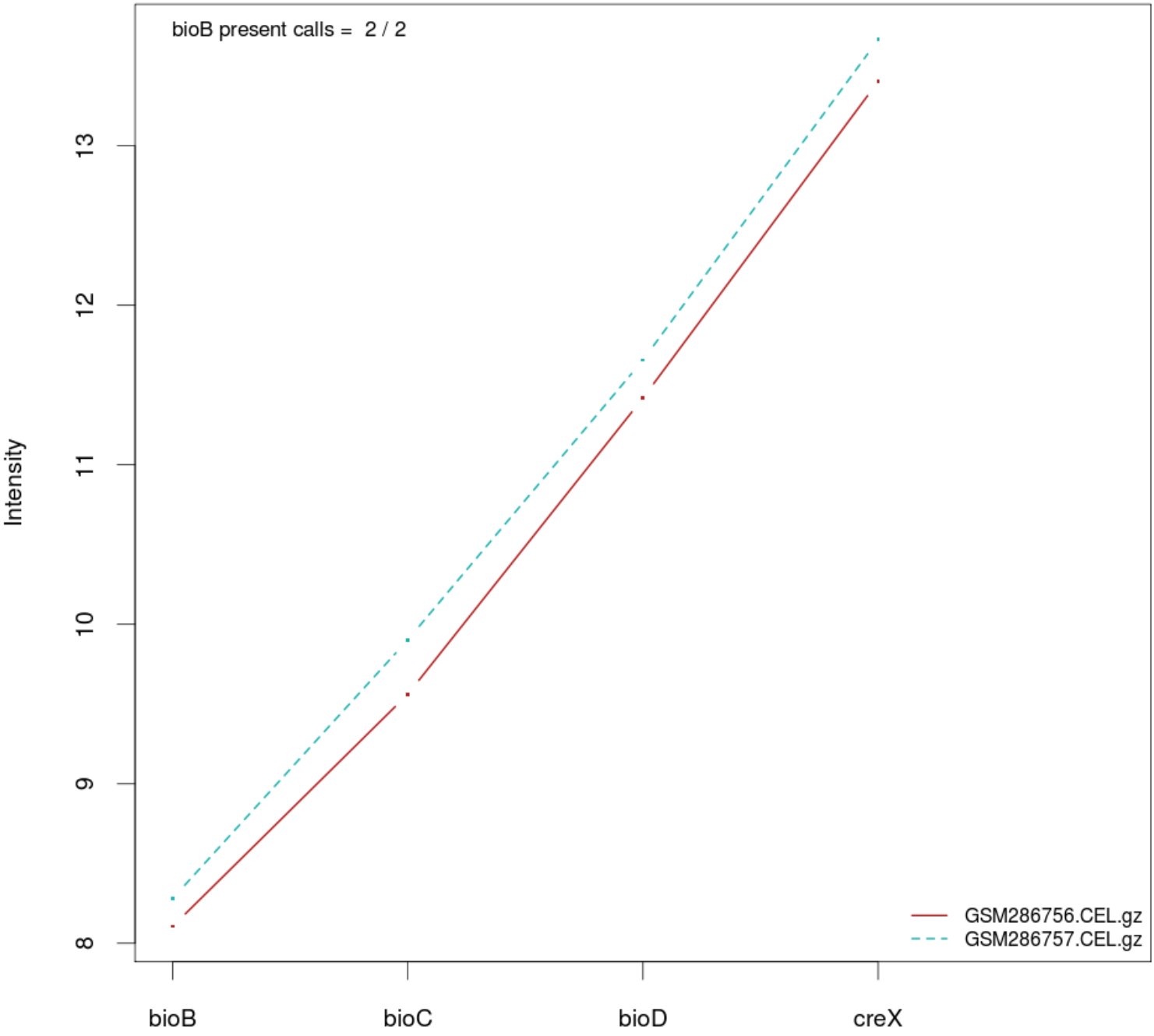


Boxplot of GAPDH ratios



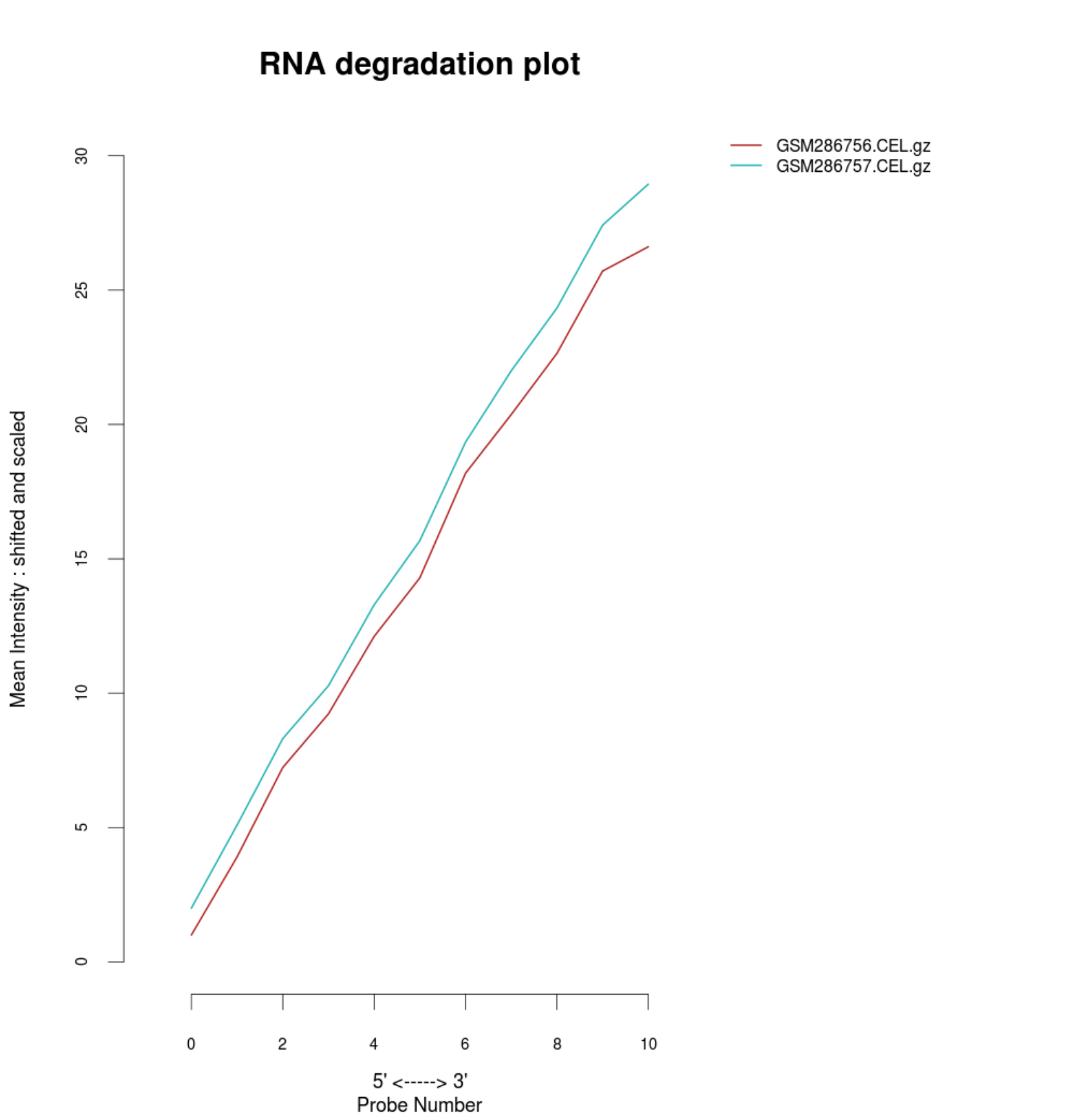
GAPDH QC: OK (all 3'/5' ratios < 1.25)

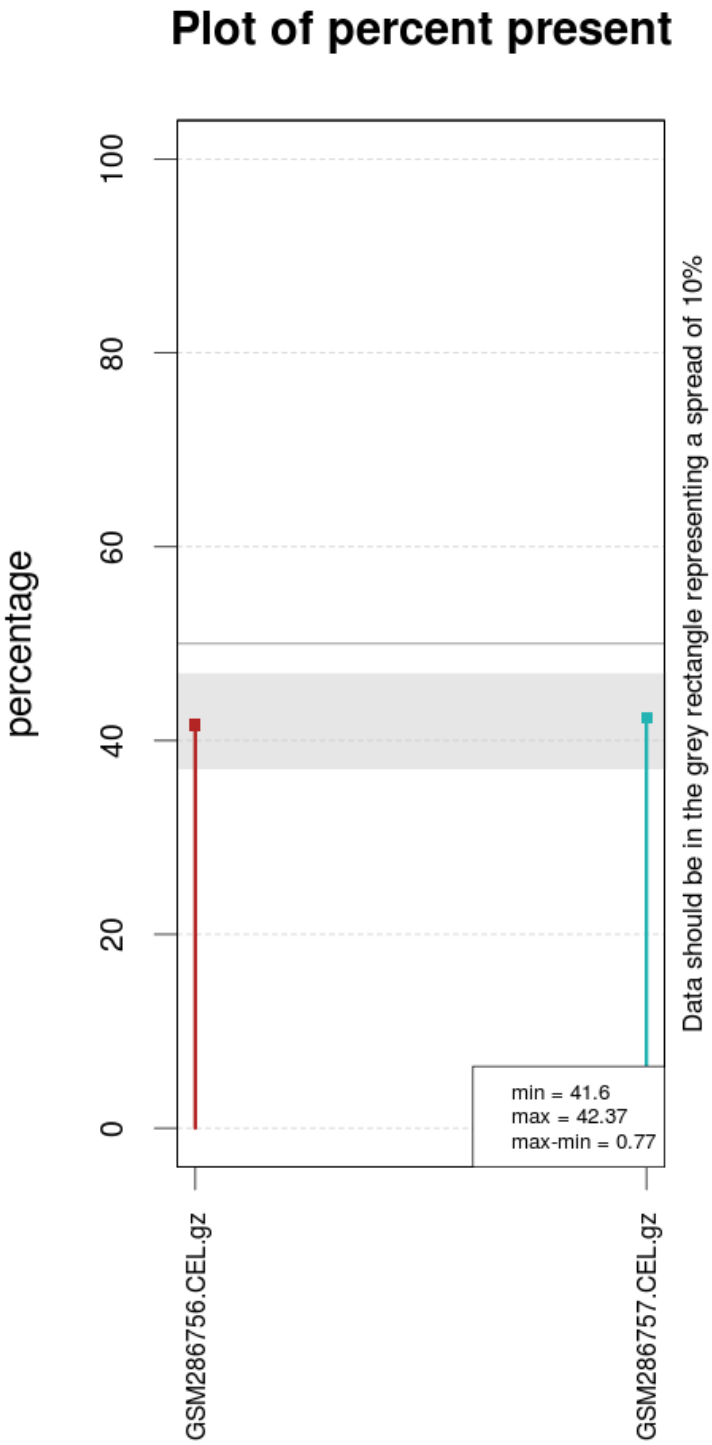
Spike-in Hybridization controls intensities and calls

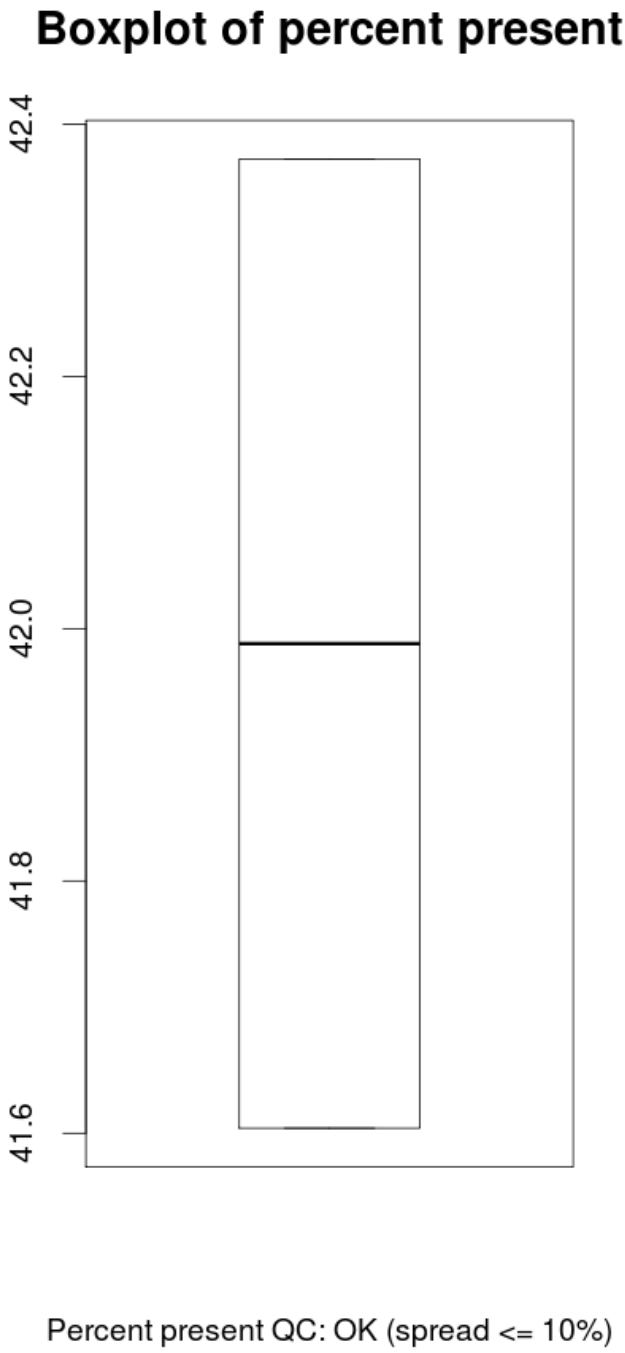


Intensities: OK (bioB < bioC < bioD < creX for all arrays)

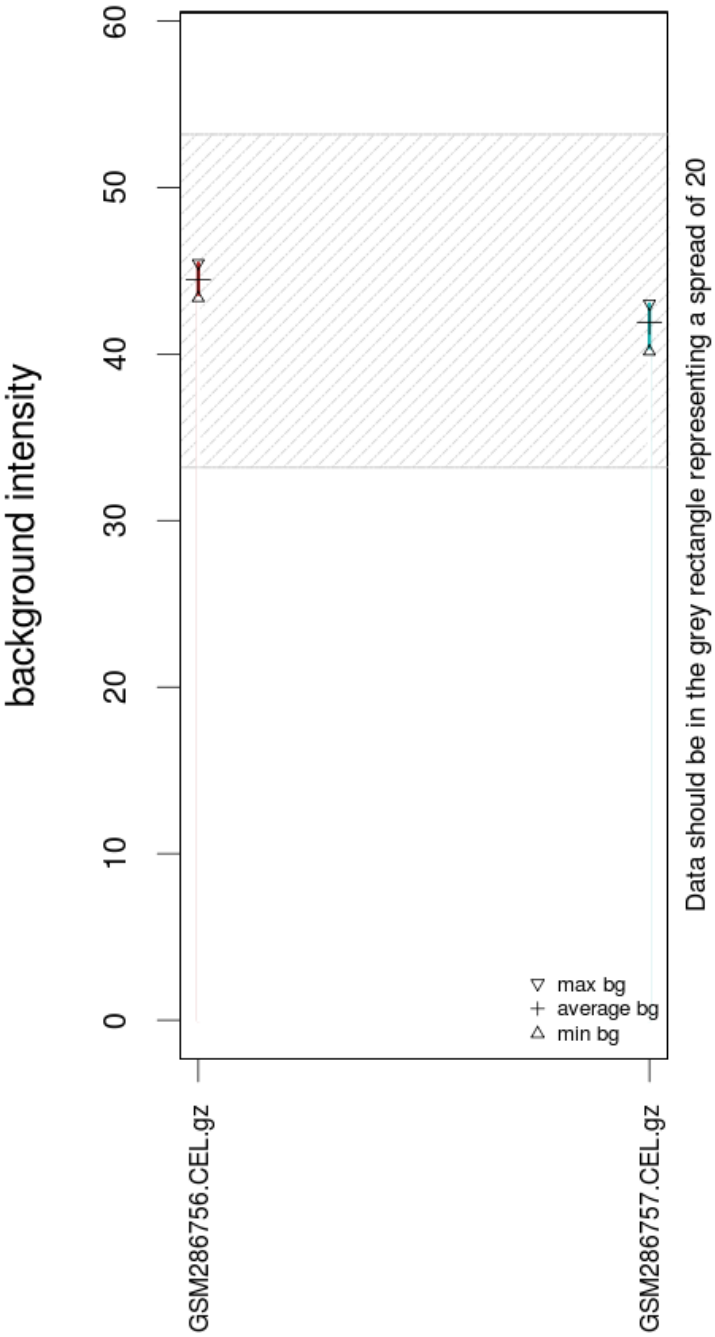
BioB Present calls: OK (indeed all bioB are called present)


RNA degradation plot
GSM286756.CEL.gz
GSM286757.CEL.gz
Mean Intensity : shifted and scaled
0
5
10
15
20
25
30
0
2
4
6
8
10
5' <-----> 3'
Probe Number

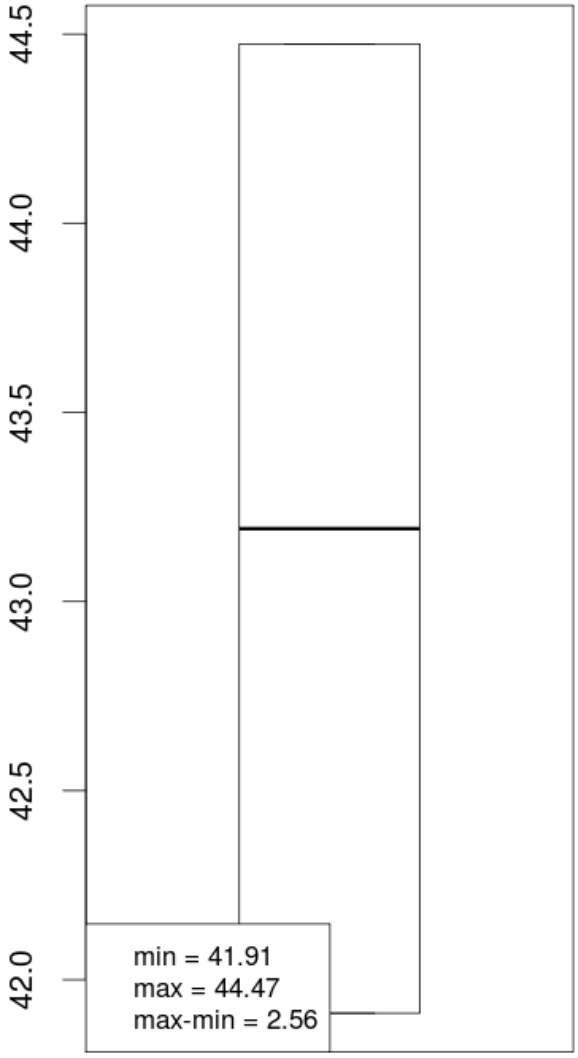

Plot of percent present
percentage
0
20
40
60
80
100
Data should be in the grey rectangle representing a spread of 10%
min = 41.6
max = 42.37
max-min = 0.77
GSM286756.CEL.gz
GSM286757.CEL.gz


Boxplot of percent present
41.6
41.8
42.0
42.2
42.4
Percent present QC: OK (spread <= 10%)

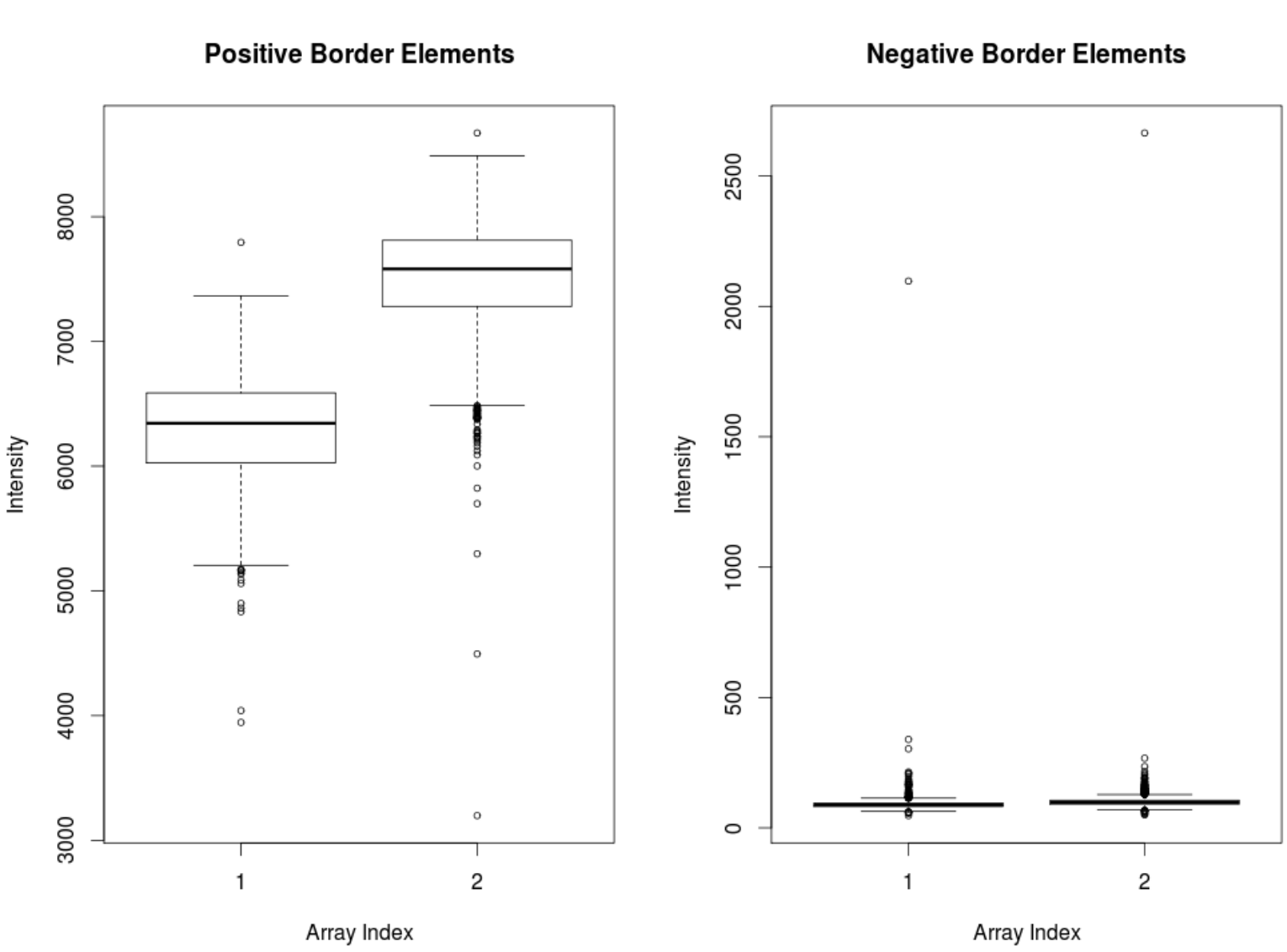
Plot of background intensity



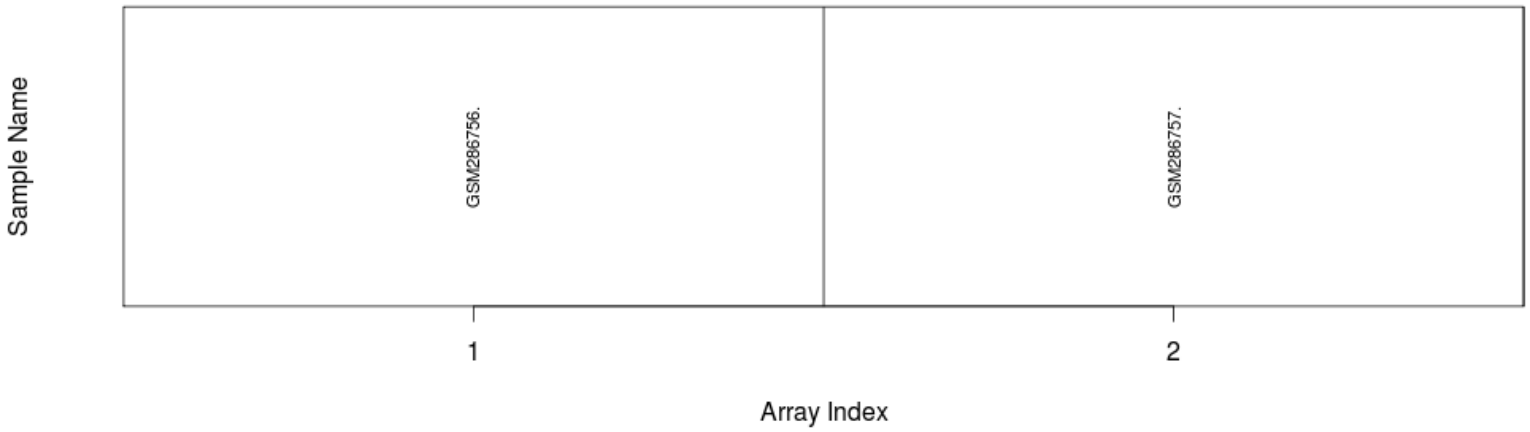
Average background intensity



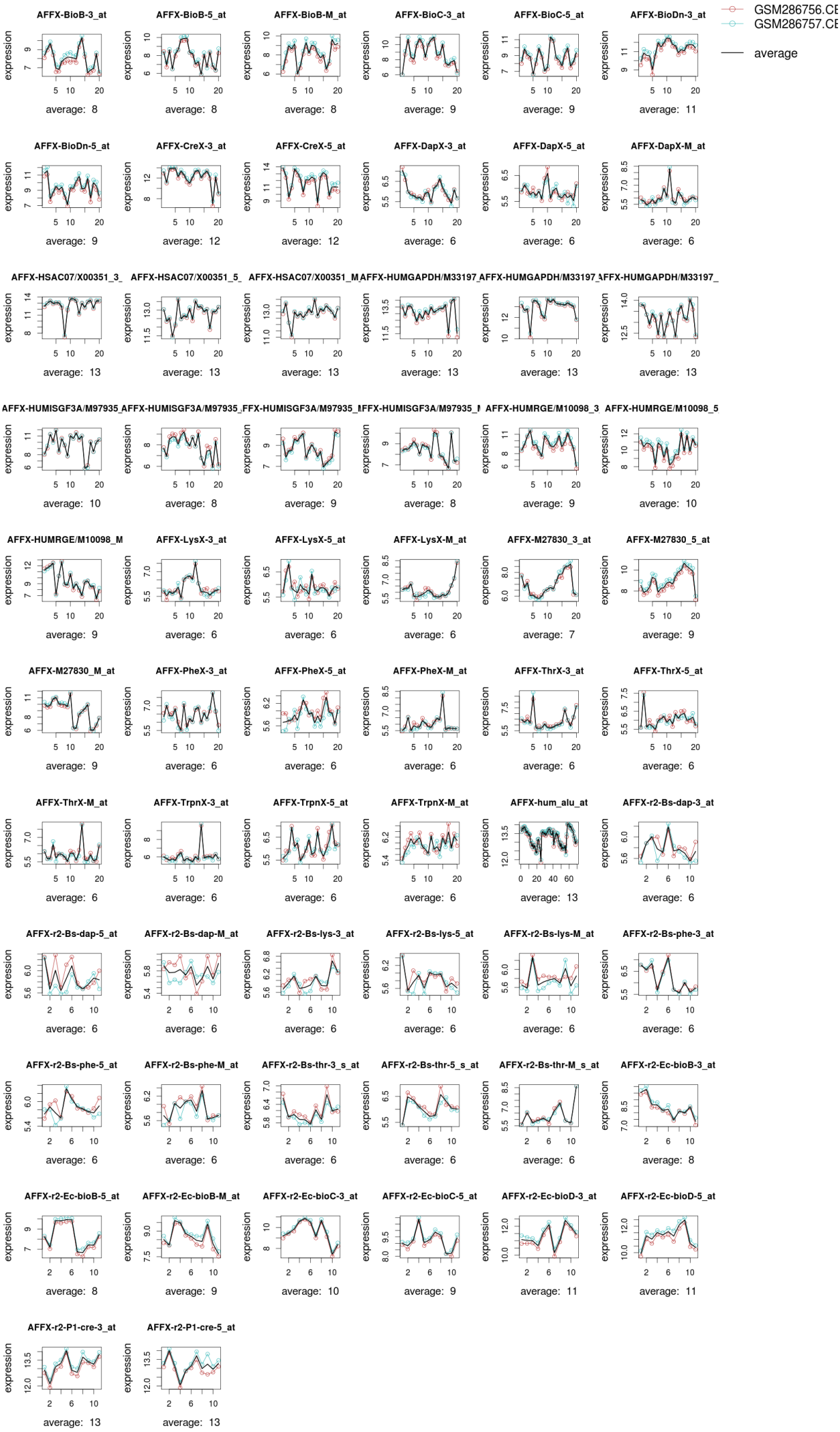
Background QC: OK (spread <= 20)

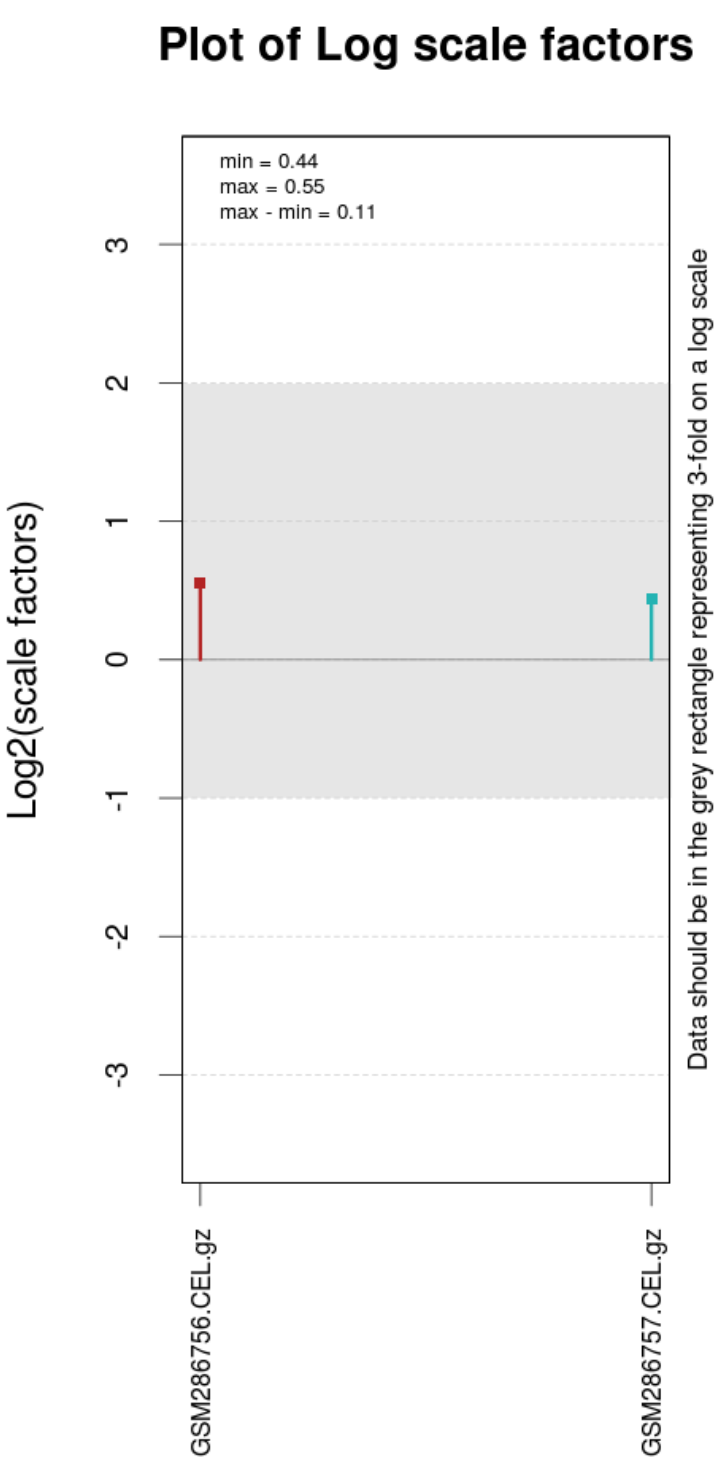


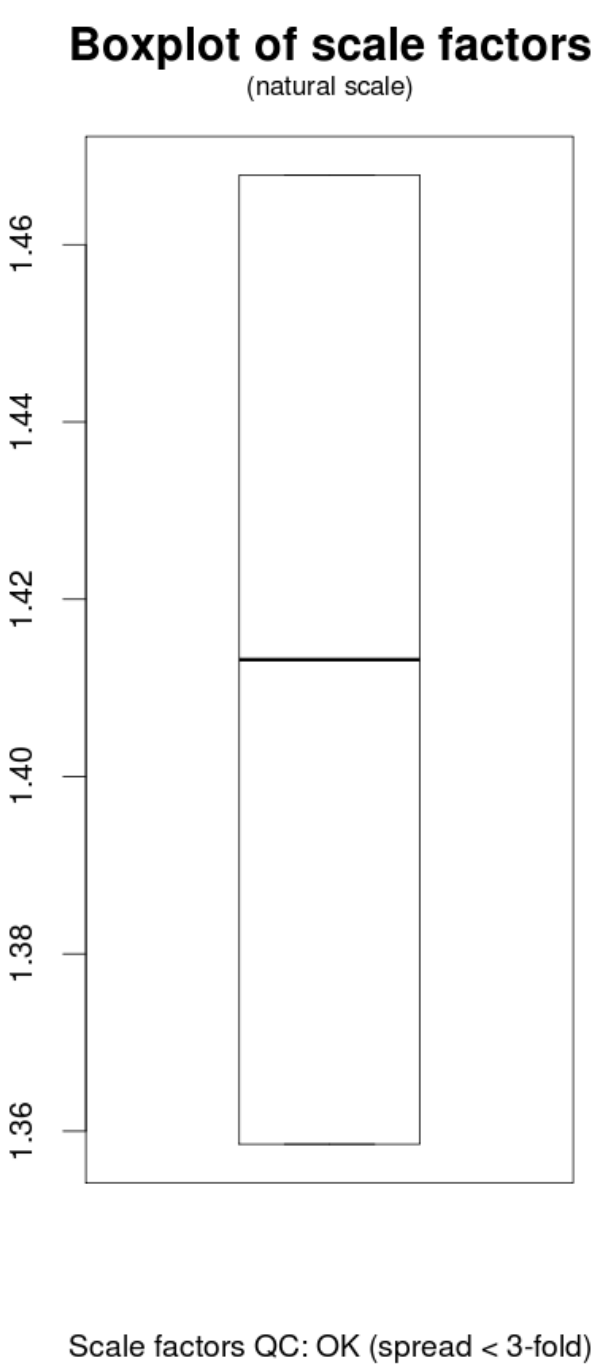
All distributions should be similar and extreme values should not be reached

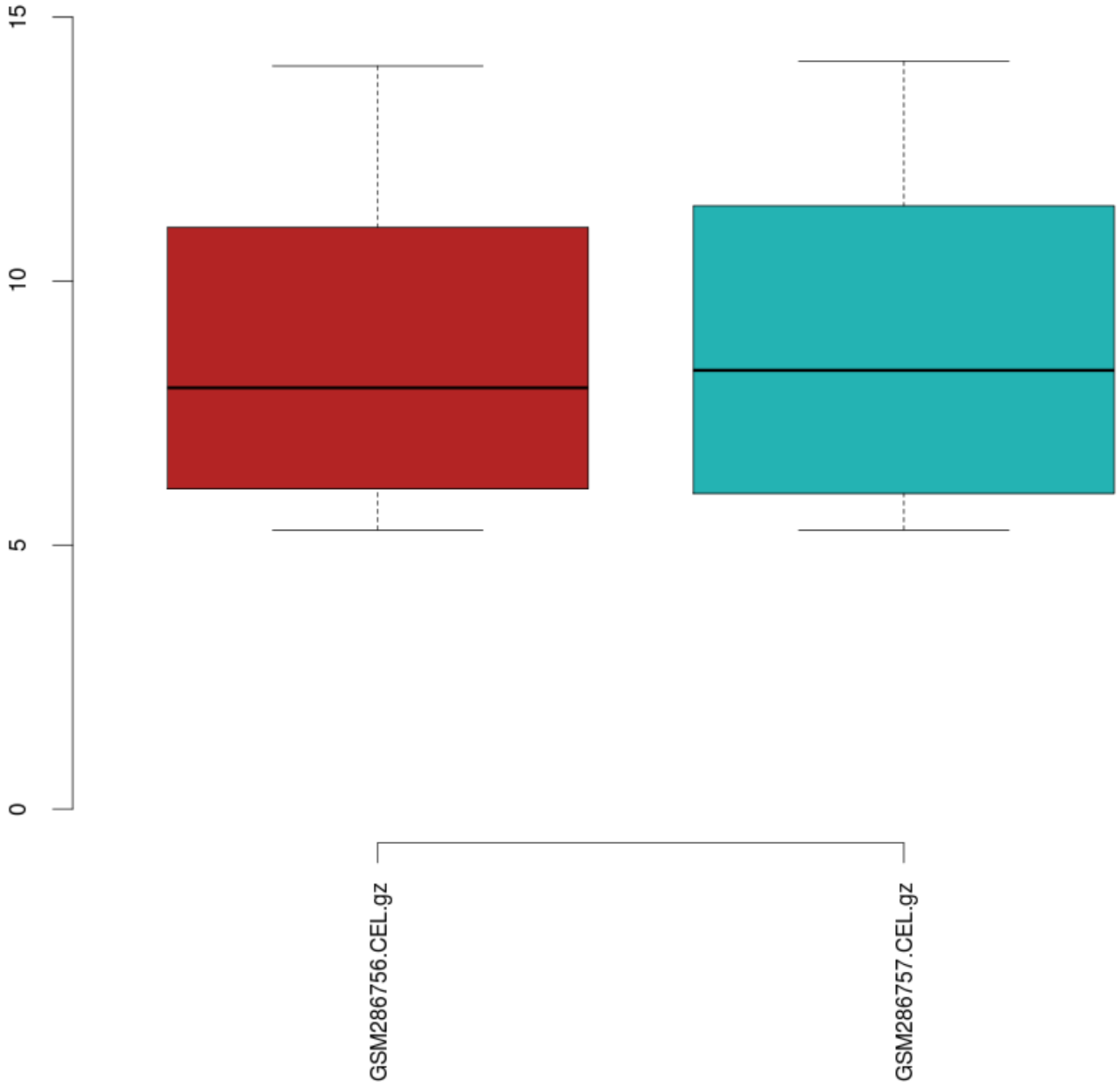


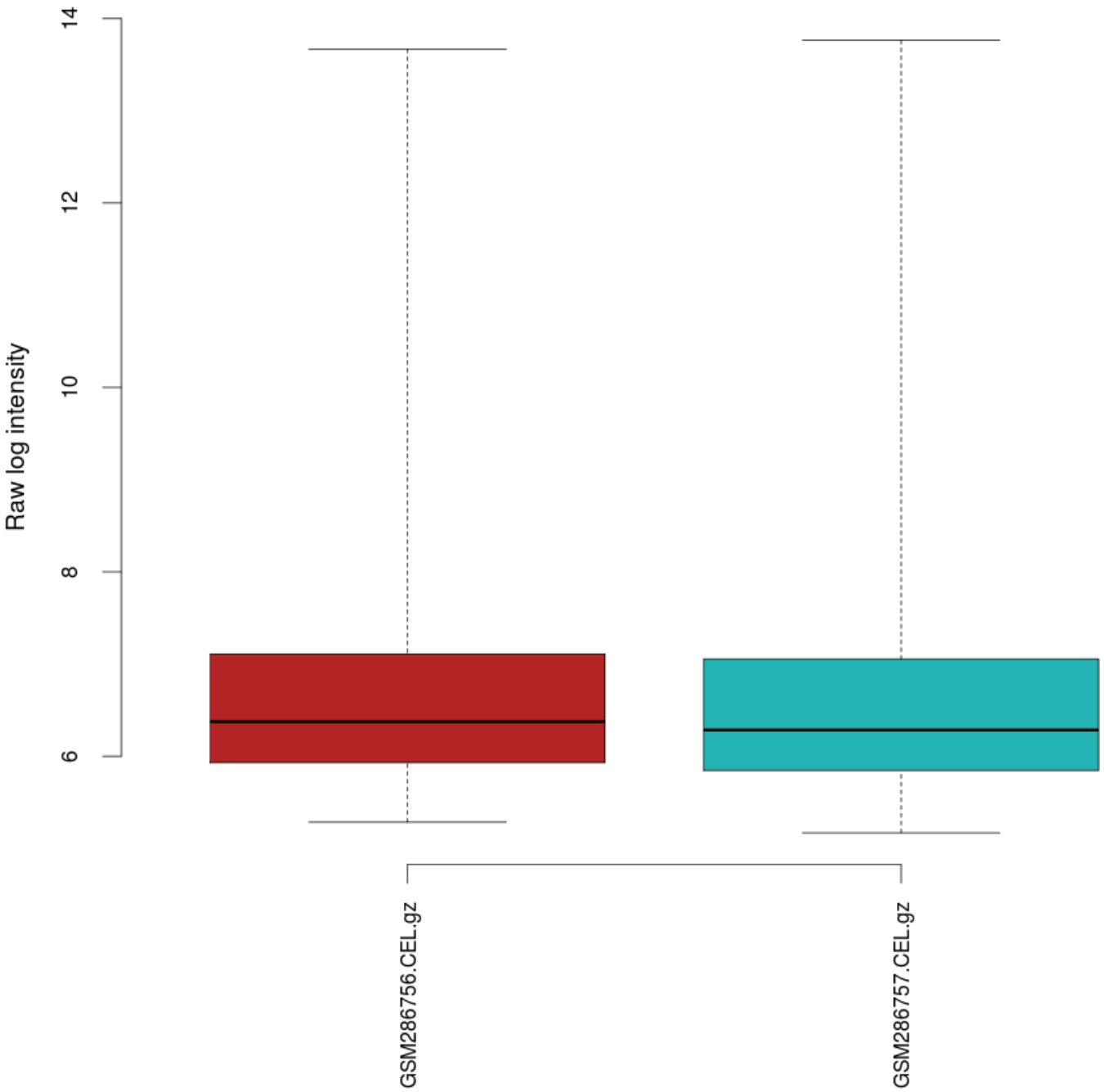
affx control profiles

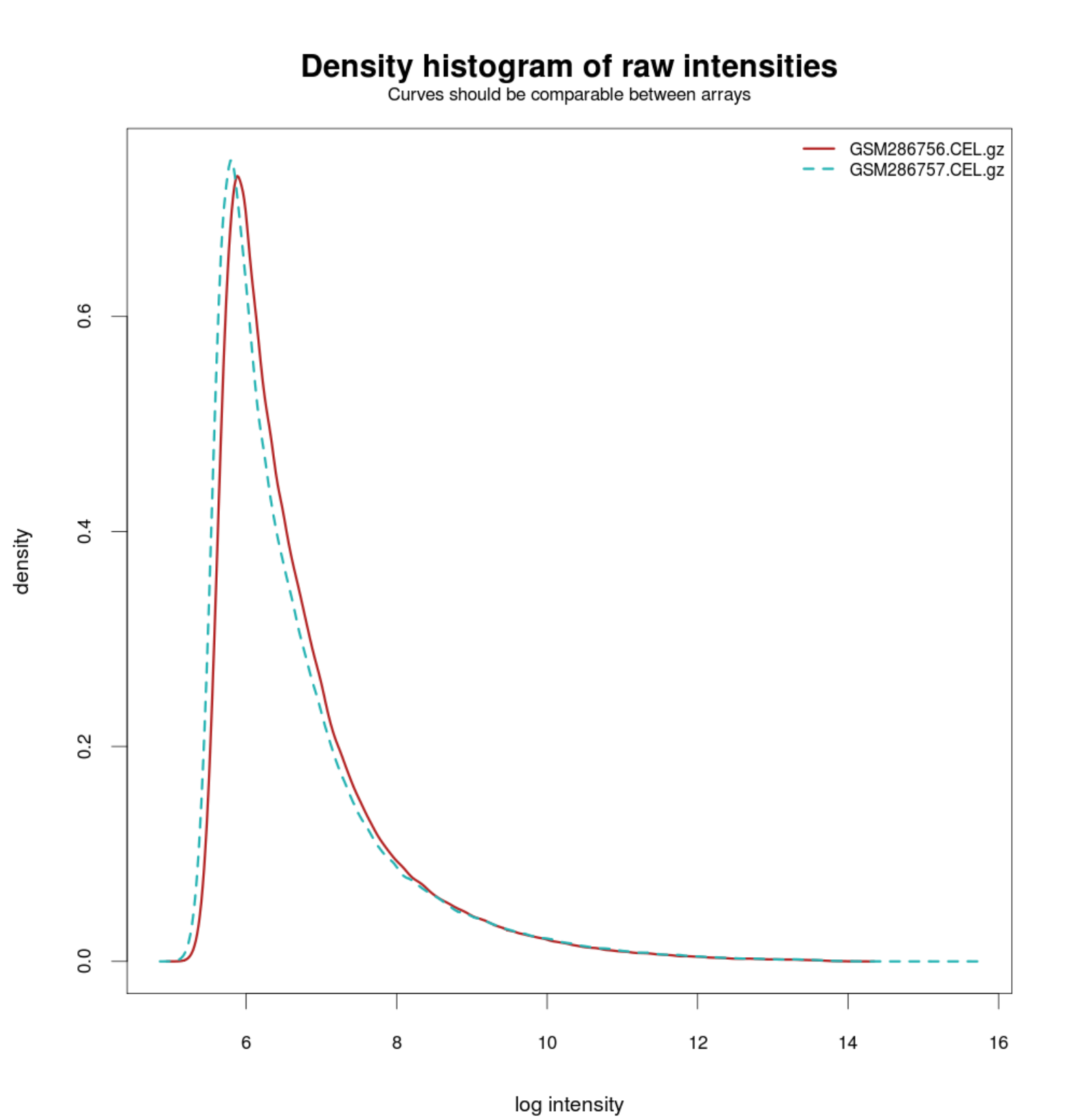



Plot of Log scale factors
min = 0.44
max = 0.55
max - min = 0.11
Log2(scale factors)
3
2
1
0
-1
-2
-3
Data should be in the grey rectangle representing 3-fold on a log scale
GSM286756.CEL.gz
GSM286757.CEL.gz


Boxplot of scale factors
(natural scale)
1.46
1.44
1.42
1.40
1.38
1.36
Scale factors QC: OK (spread < 3-fold)

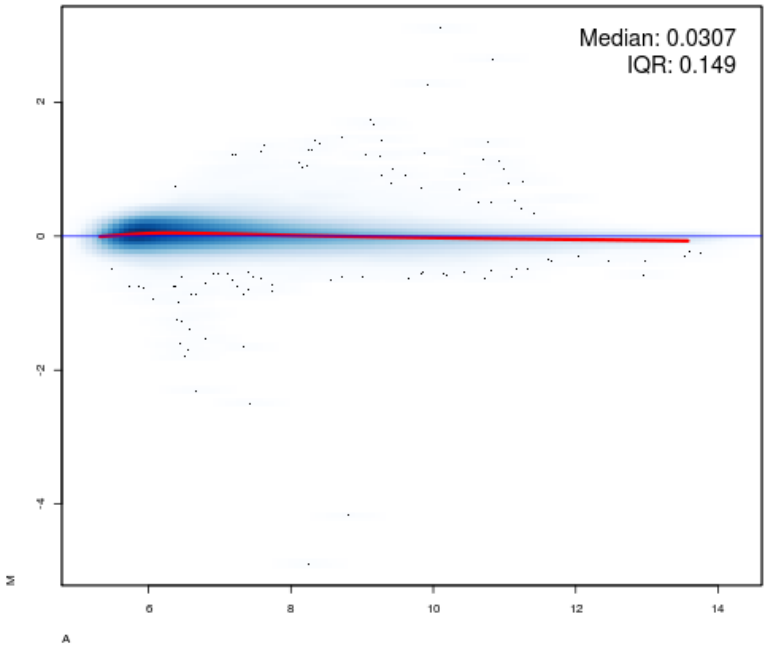

affx controls
15
10
5
0
GSM286756.CEL.gz
GSM286757.CEL.gz


Boxplot of raw intensities
Distributions should be comparable between arrays
Raw log intensity
14
12
10
8
6
GSM286756.CEL.gz
GSM286757.CEL.gz

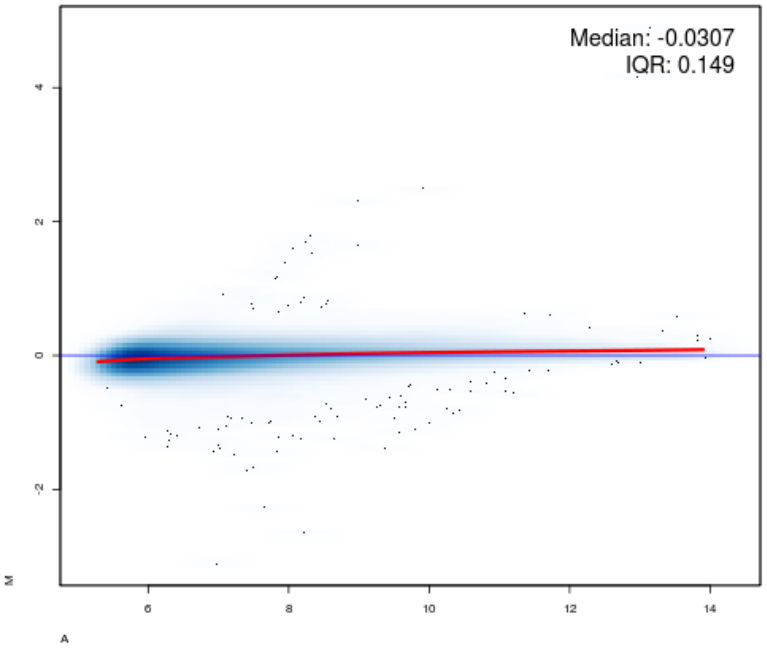

Density histogram of raw intensities
Curves should be comparable between arrays
GSM286756.CEL.gz
GSM286757.CEL.gz
density
0.0
0.2
0.4
0.6
6
8
10
12
14
16
log intensity

MA plots of raw data

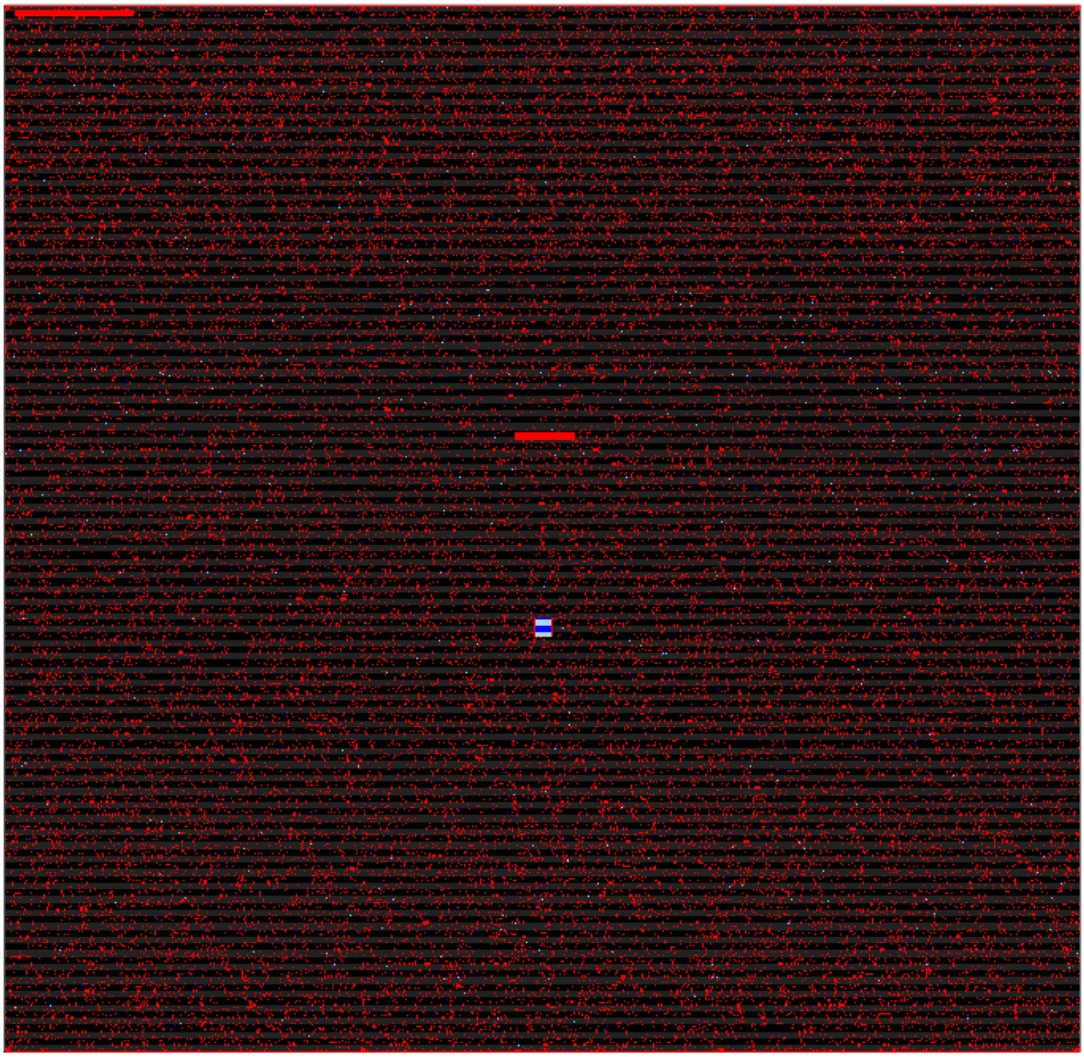
GSM286756.CEL.gz vs pseudo-median reference chip



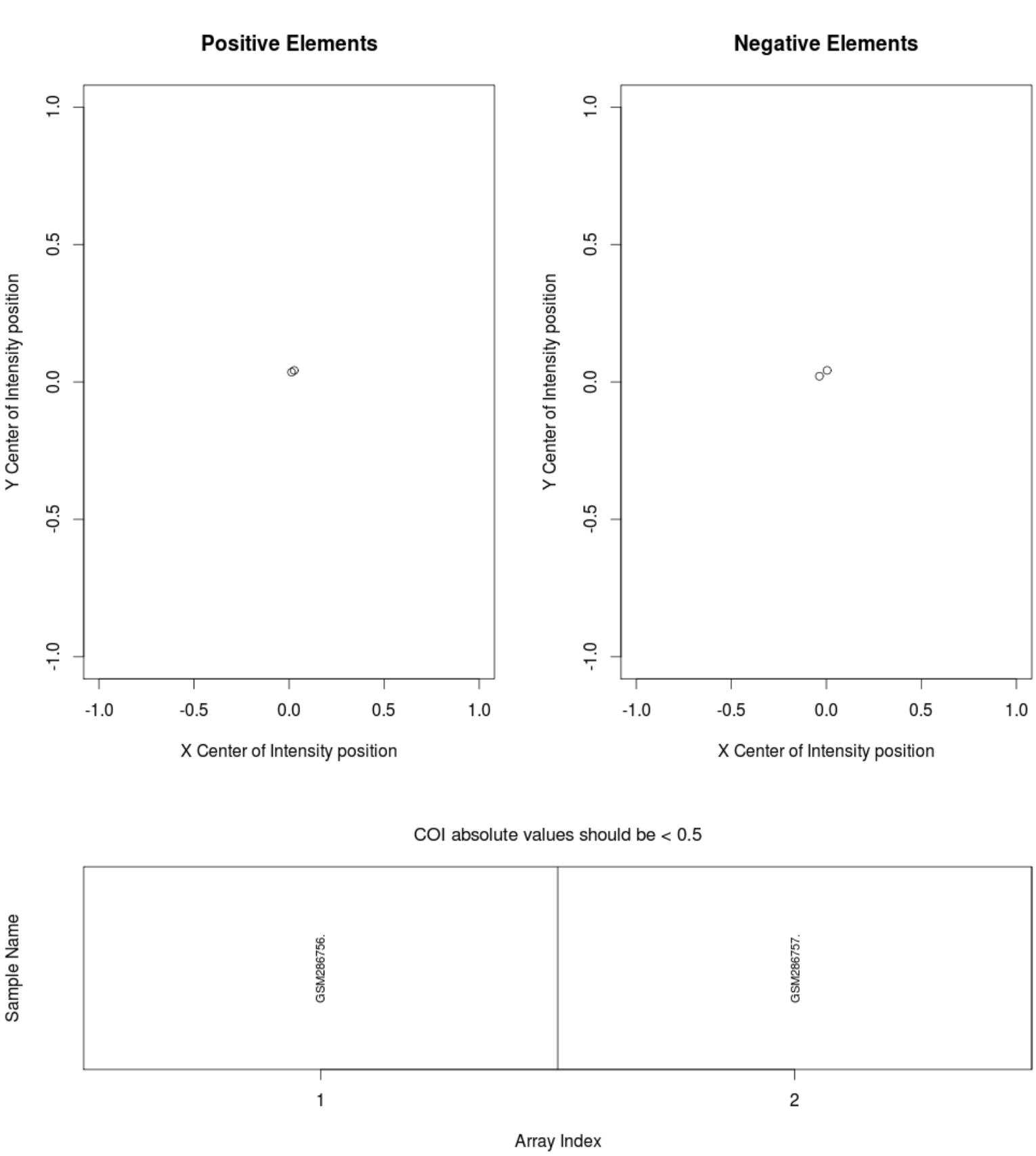
GSM286757.CEL.gz vs pseudo-median reference chip



Array reference layout



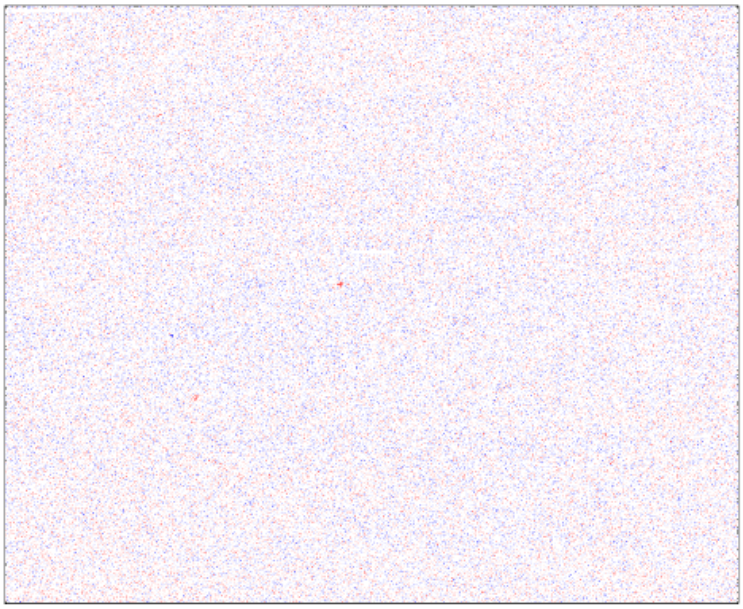
black/gray: regular match/mismatch probe
blue/light blue: control match/mismatch probe
red: unannotated probe (control region)


Positive Elements
Negative Elements
Y Center of Intensity position
X Center of Intensity position
1.0
0.5
0.0
-0.5
-1.0

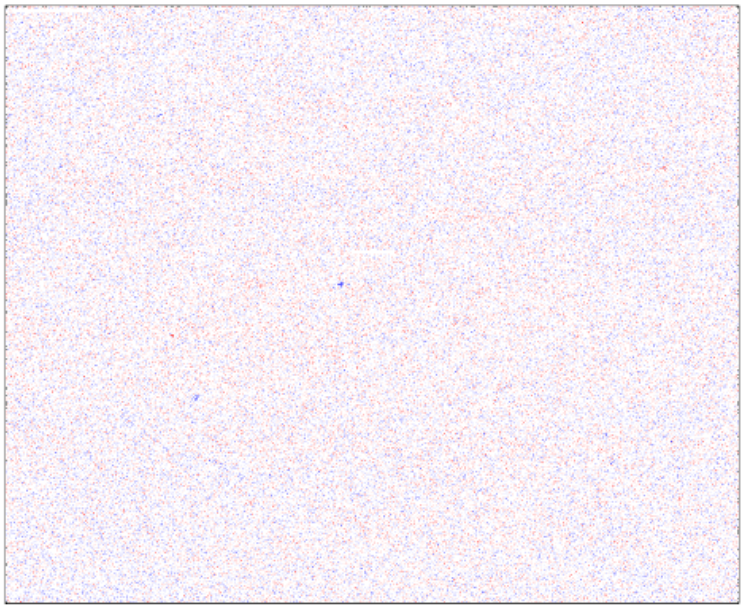
COI absolute values should be < 0.5
Sample Name
GSM286756.
GSM286757.
1
2
Array Index

2D virtual PLM image for model characteristic: resids

GSM286756.CEL.gz

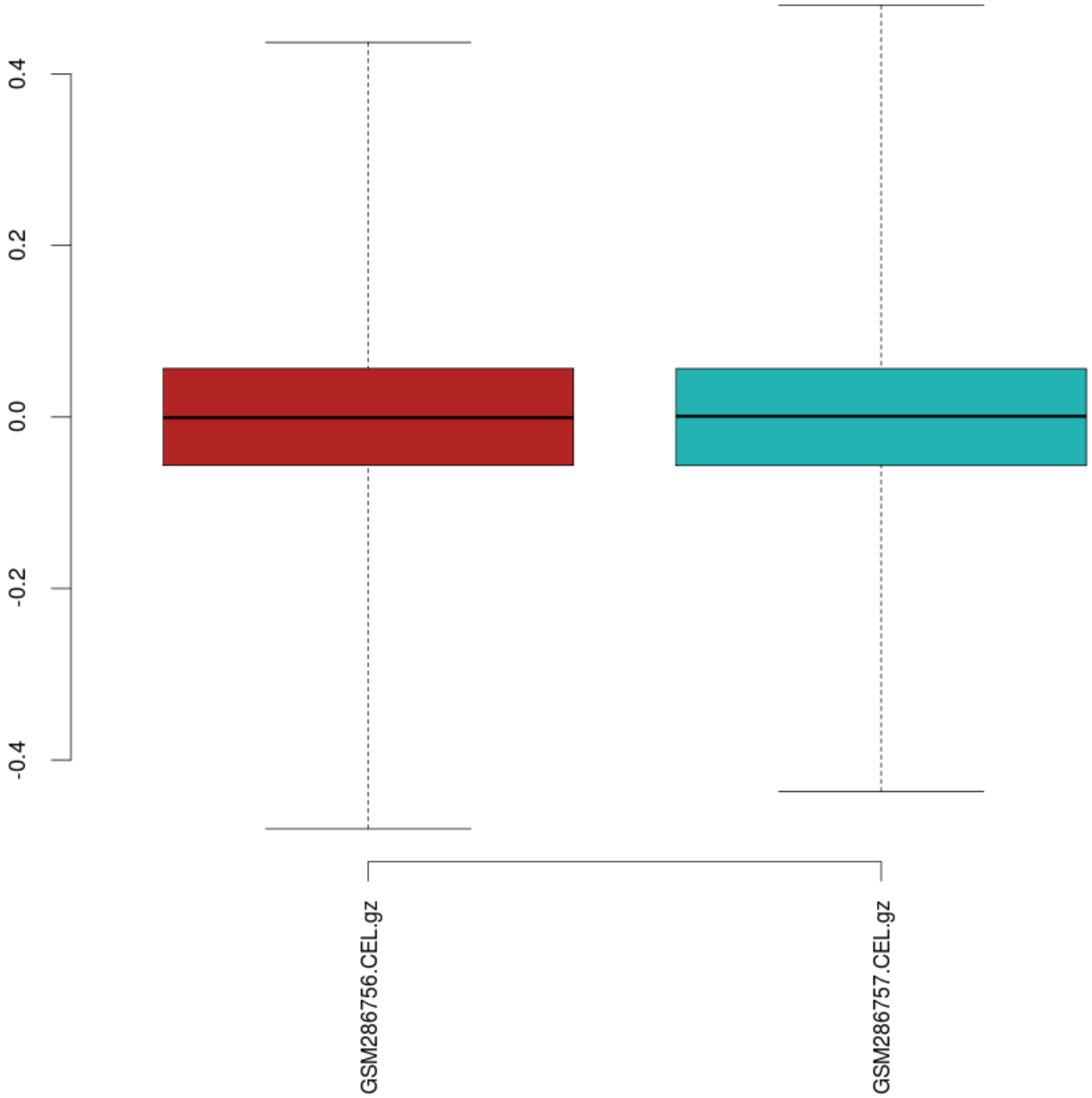


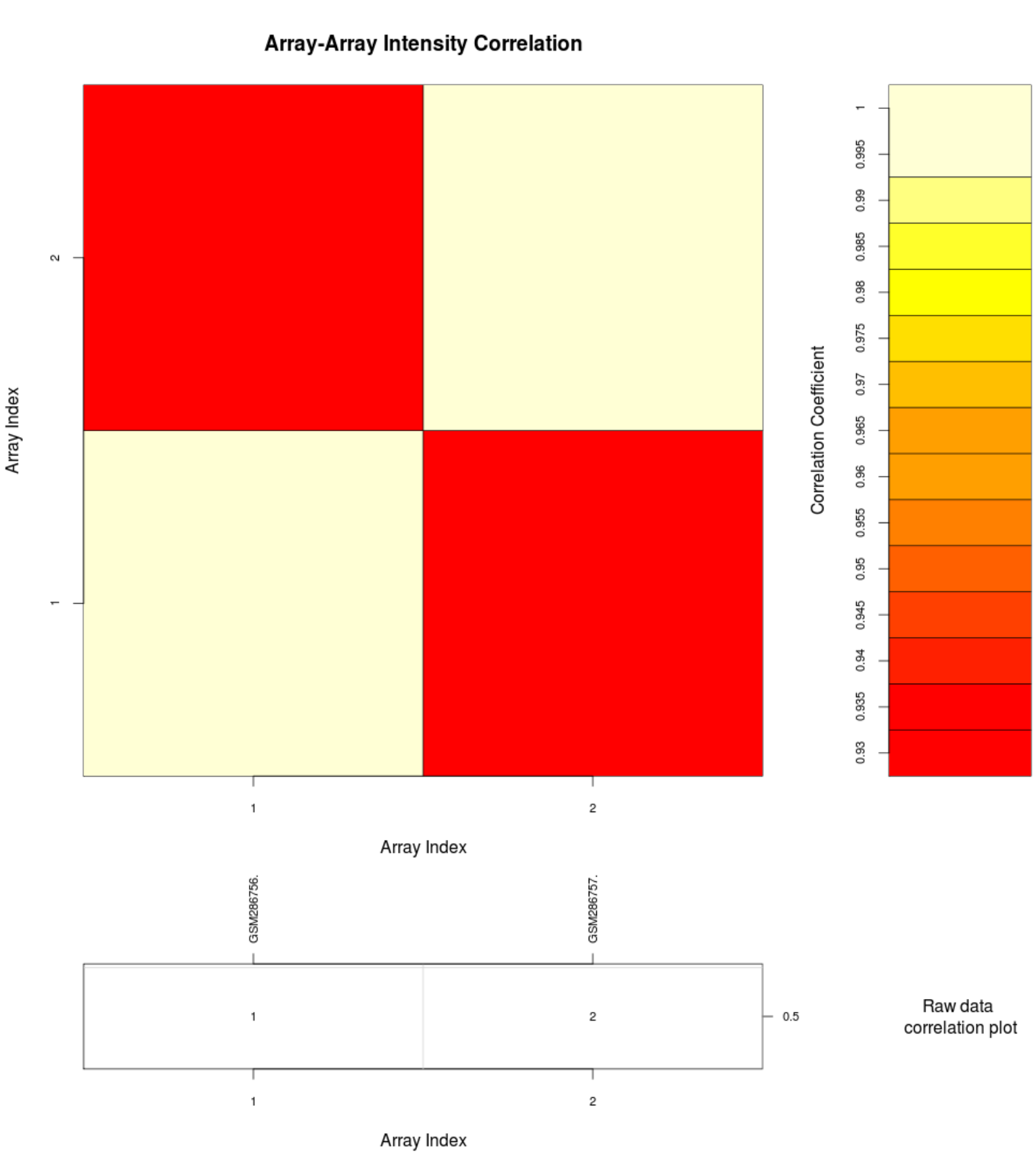
GSM286757.CEL.gz



Relative Log Expression (RLE)

RLE distributions should be centered around 0




Array-Array Intensity Correlation
Array Index
2
1
1
2
Array Index
Correlation Coefficient
1
0.995
0.99
0.985
0.98
0.975
0.97
0.965
0.96
0.955
0.95
0.945
0.94
0.935
0.93
GSM286756.
GSM286757.
1
2
0.5
1
2
Array Index
Raw data
correlation plot