

Quality Control & Pre-processing Evaluation
of
E-GEOD-6955.raw.1_0
REPORT

Array names and grouping

ArrayDataFile	SourceName	FactorValue
GSM160311.CEL	Array1	Group1
GSM160306.CEL	Array2	Group1
GSM160309.CEL	Array3	Group1
GSM160310.CEL	Array4	Group1
GSM160307.CEL	Array5	Group1
GSM160308.CEL	Array6	Group1

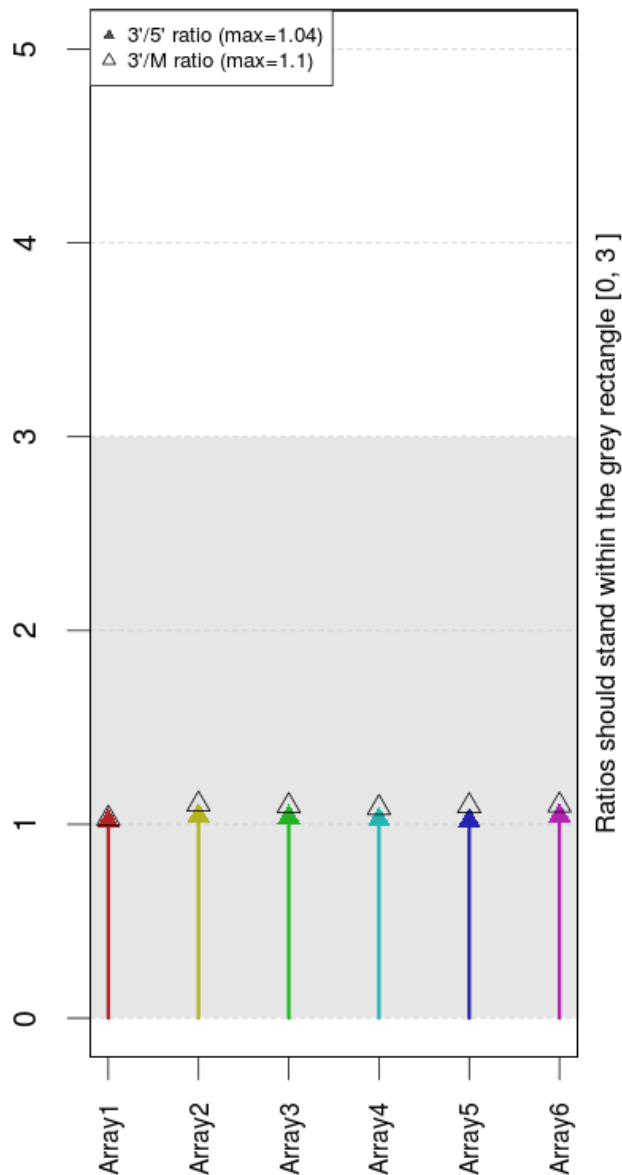
Summary of raw data quality indicators

blue = "within" / red = "out of" recommended cut-off

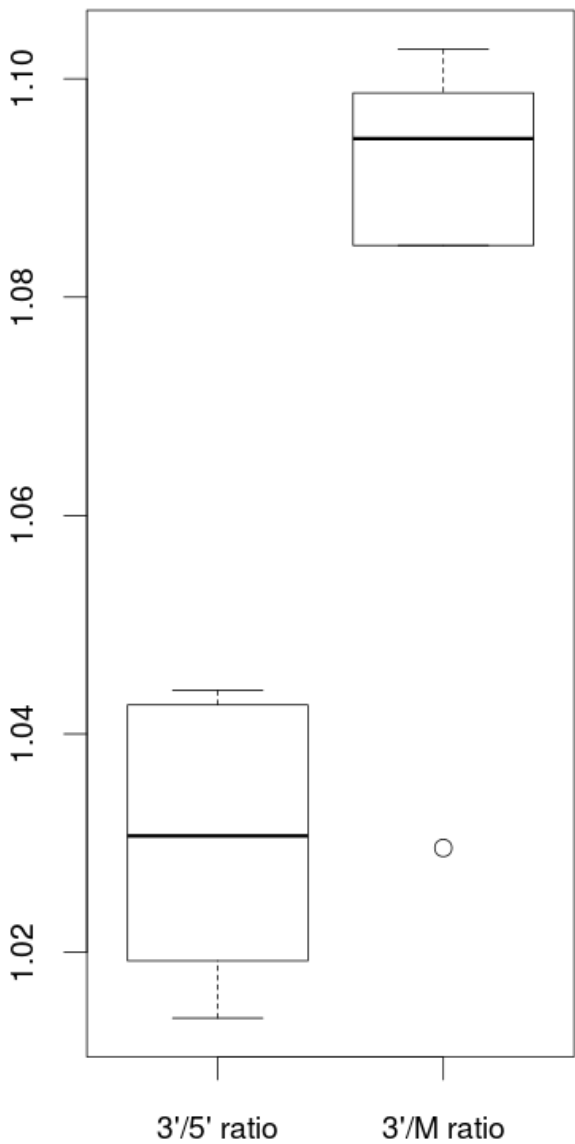
	3'/5' beta-actin (cutoff=3)	3'/5' GAPDH (cutoff= 1.25)	Hybridization BioB<BioC<BioD<CreX	Hybridization BioB=Present	Percent Present spread<= 10%	Background spread<=20%	Log Scale Factor spread<=3
Array1	1.01	0.98	T	P	47 %	77	-0.86
Array2	1.04	1.01	T	P	48 %	67	-0.64
Array3	1.04	1.04	T	P	47 %	46	0.36
Array4	1.02	1.02	T	P	45 %	63	-0.33
Array5	1.02	1.03	T	P	44 %	82	-0.76
Array6	1.04	1.05	T	P	41 %	44	0.52

RNA degradation of beta-actin

3'/5' and 3'/M ratios



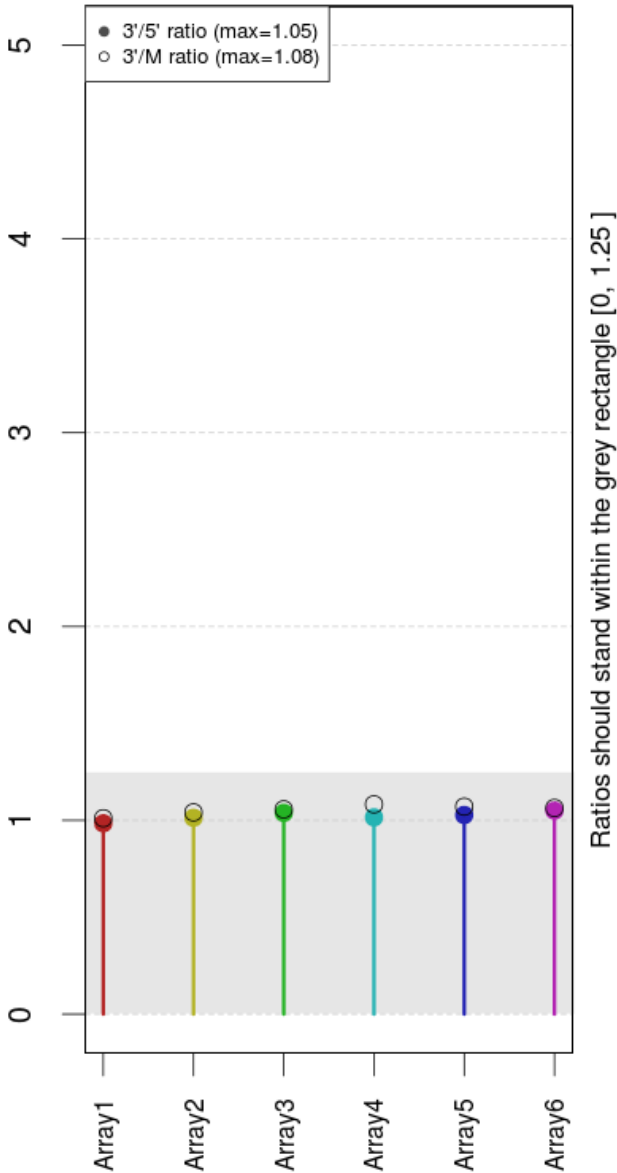
Boxplot of beta-actin ratios



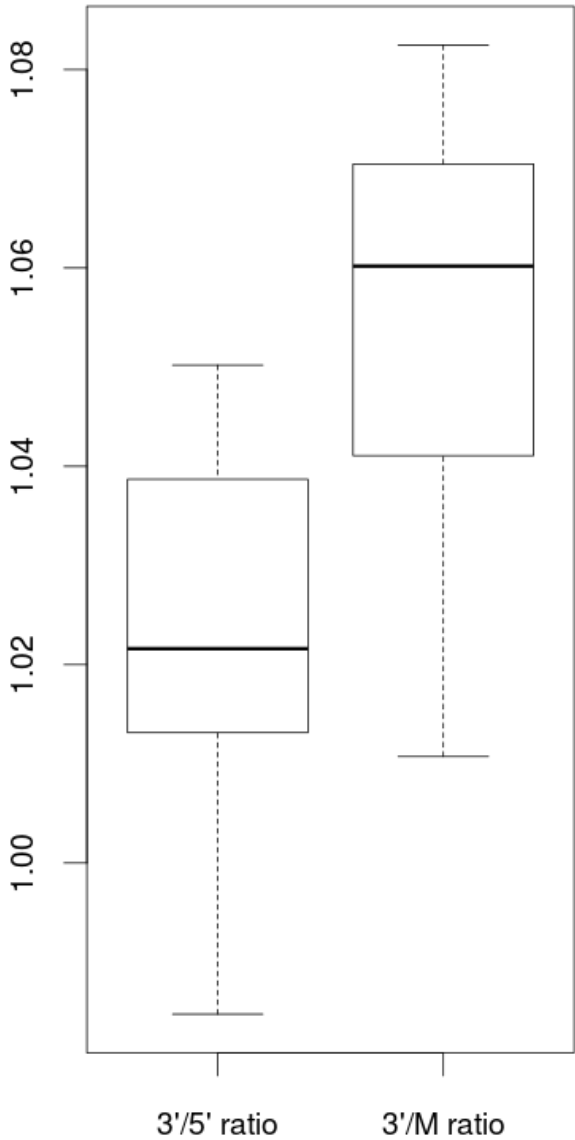
beta-actin QC: OK (all 3'/5' ratios < 3)

RNA degradation of GAPDH

3'/5' and 3'/M ratios

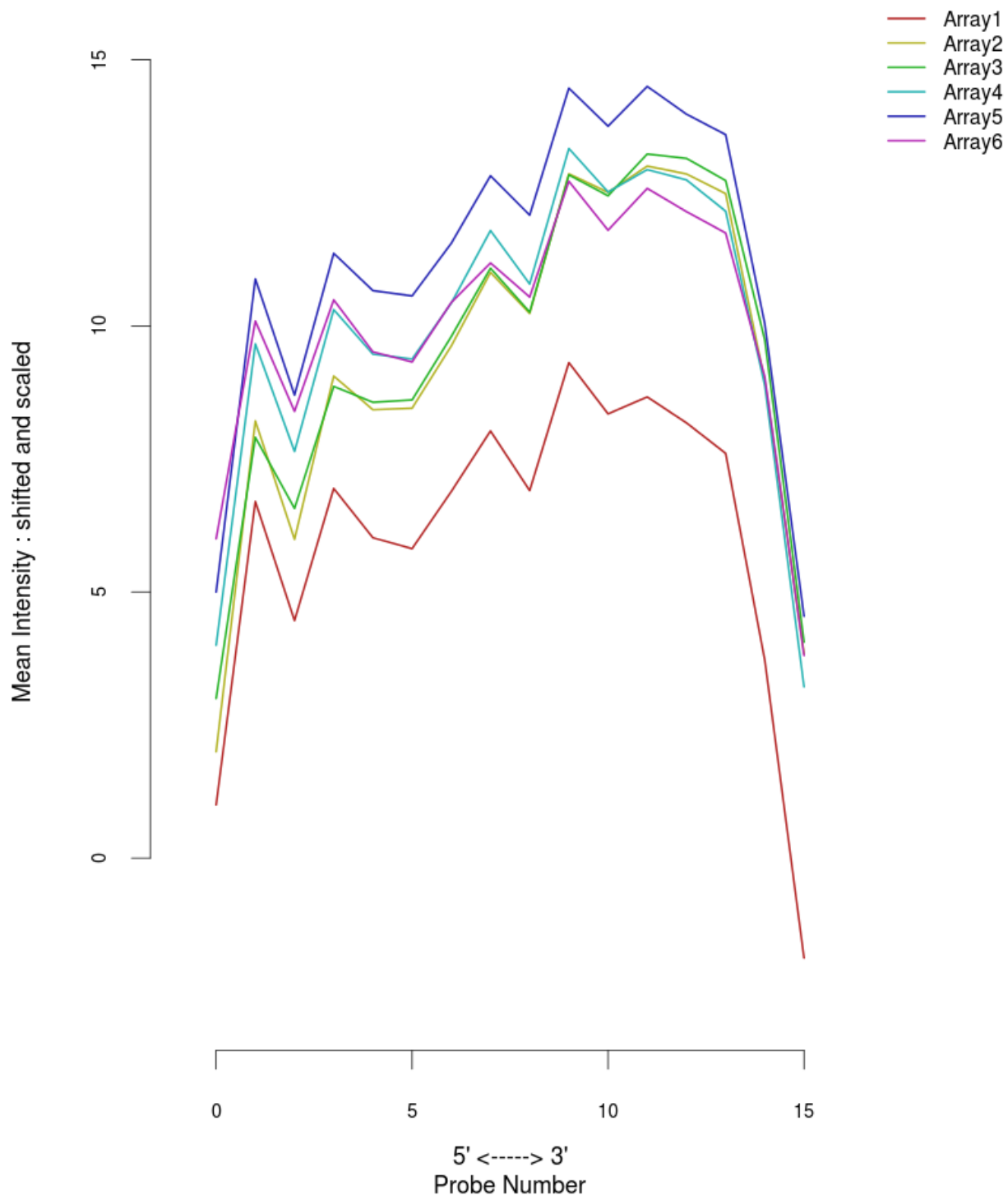


Boxplot of GAPDH ratios

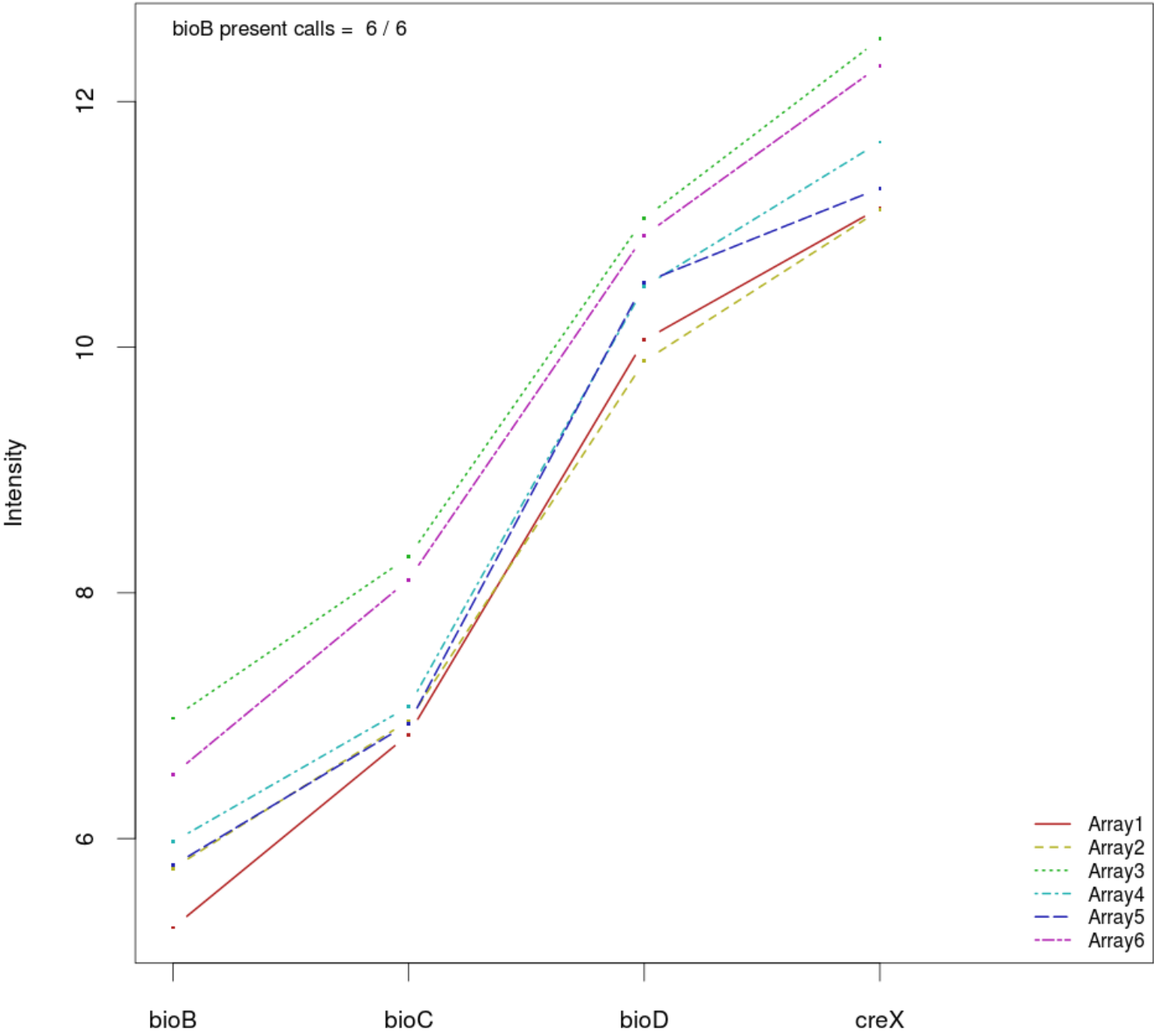


GAPDH QC: OK (all 3'/5' ratios < 1.25)

RNA degradation plot

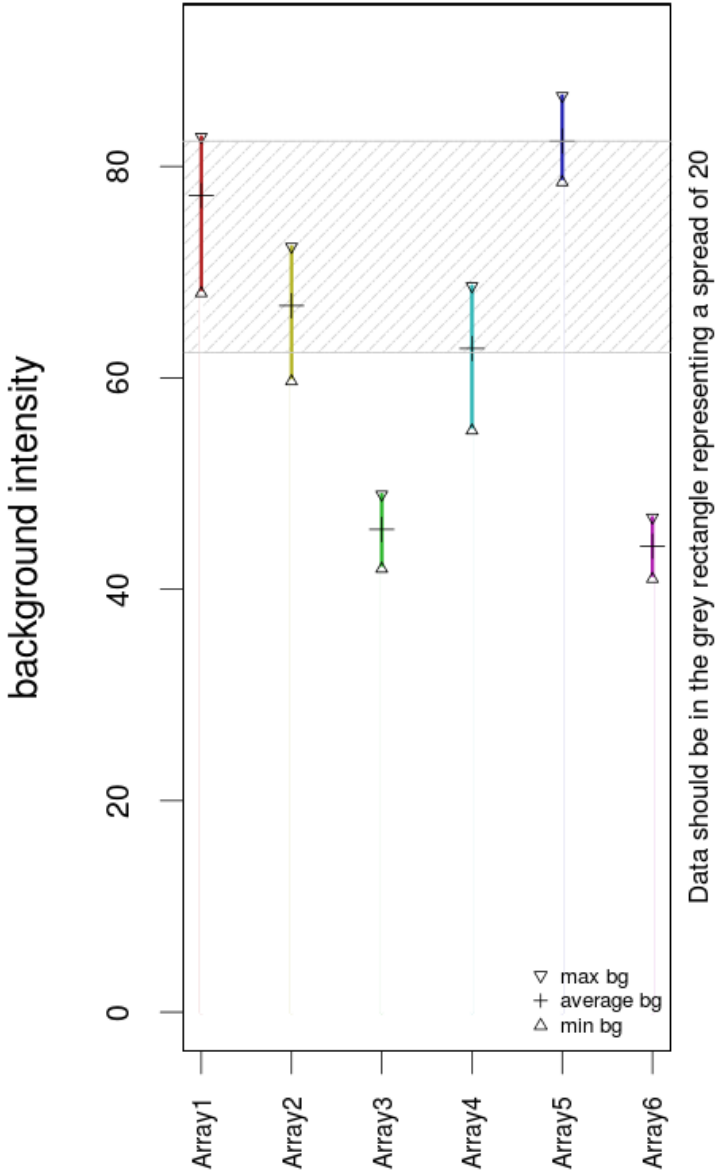


Spike-in Hybridization controls intensities and calls

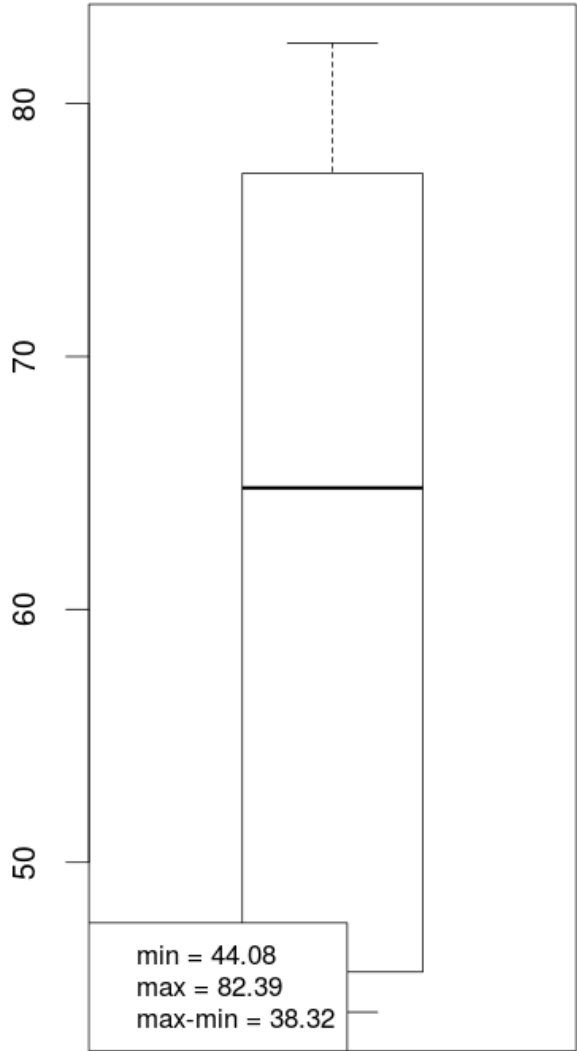


Intensities: OK (bioB < bioC < bioD < creX for all arrays)
BioB Present calls: OK (indeed all bioB are called present)

Plot of background intensity

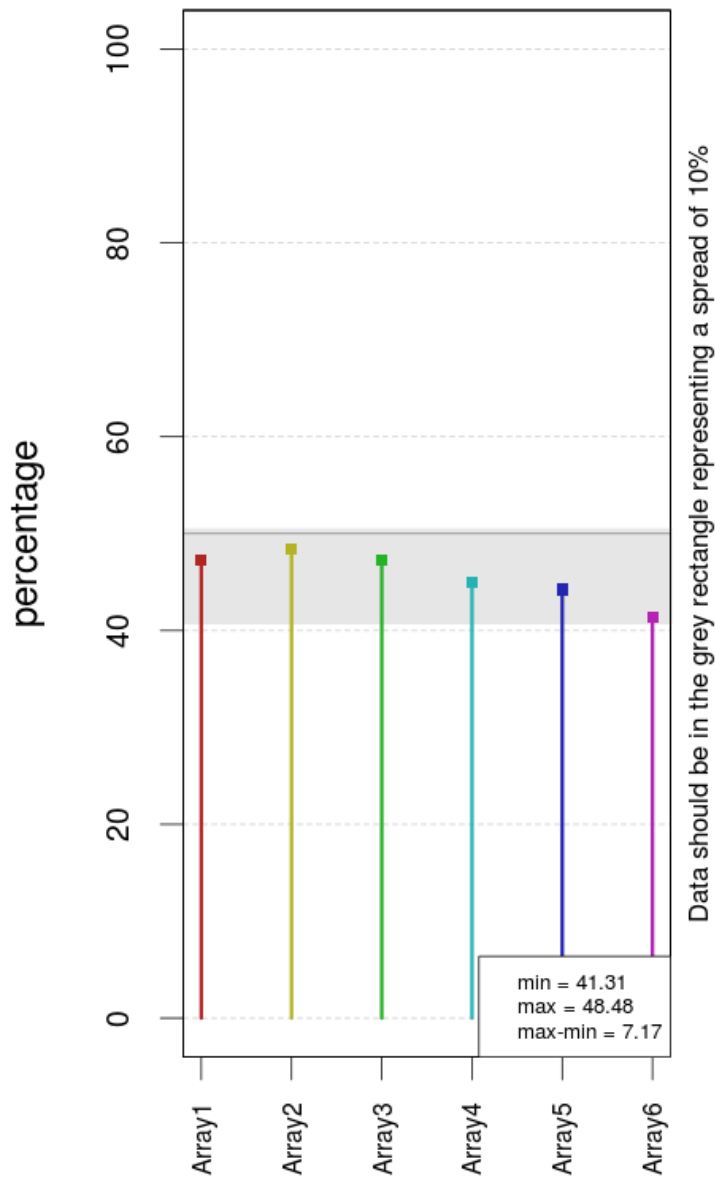


Average background intensity

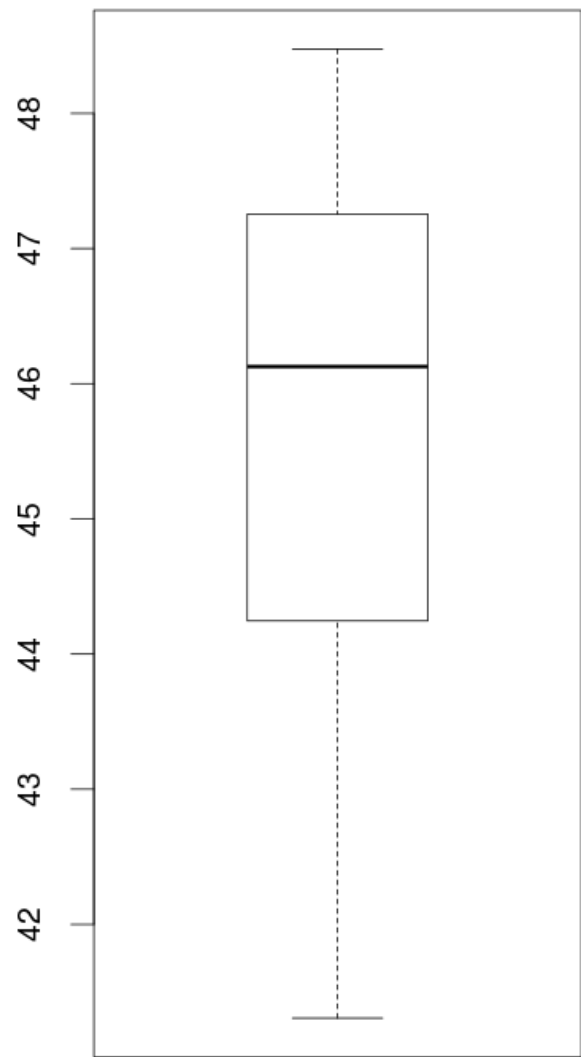


Background QC: not OK (spread > 20)

Plot of percent present

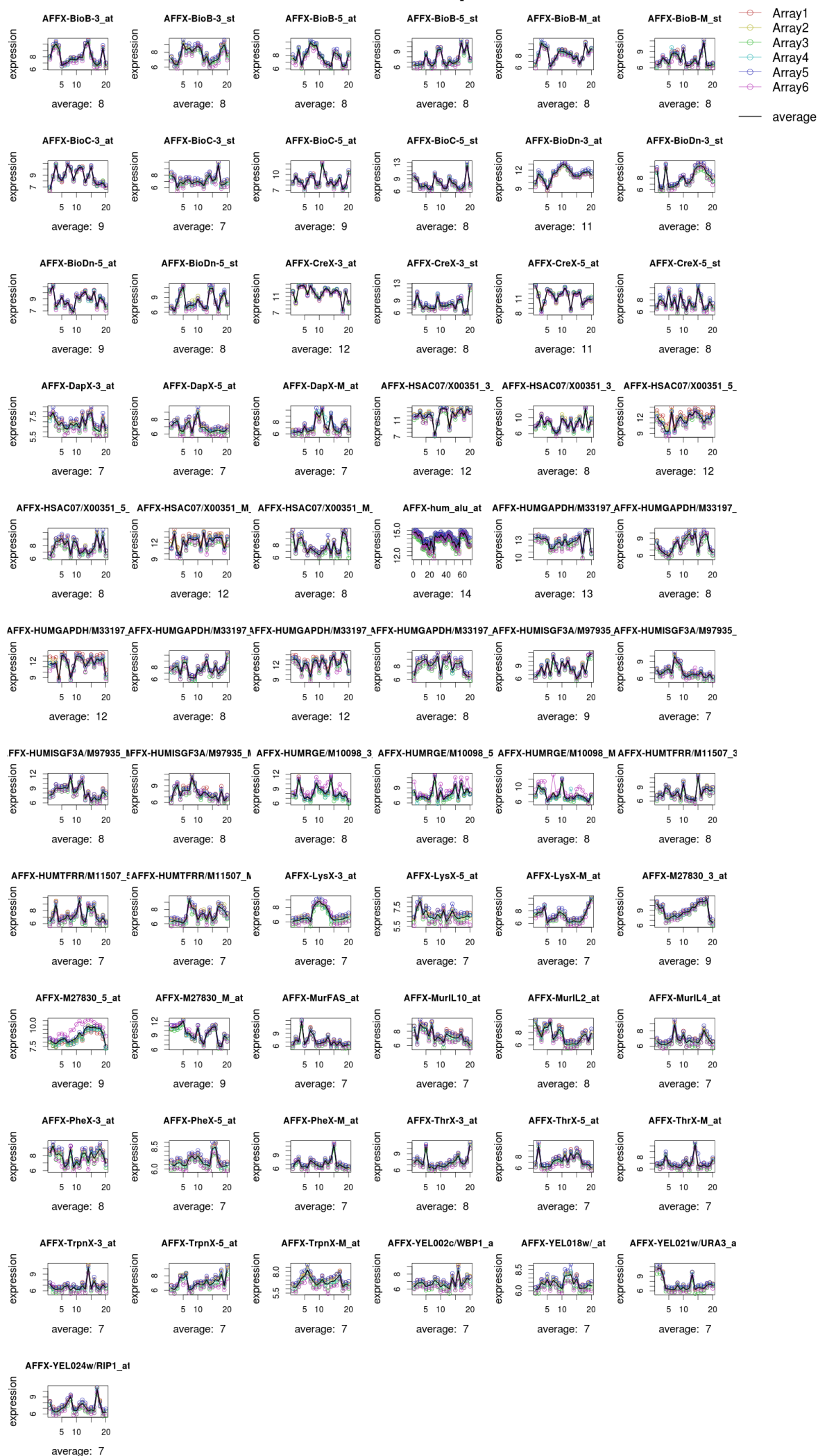


Boxplot of percent present

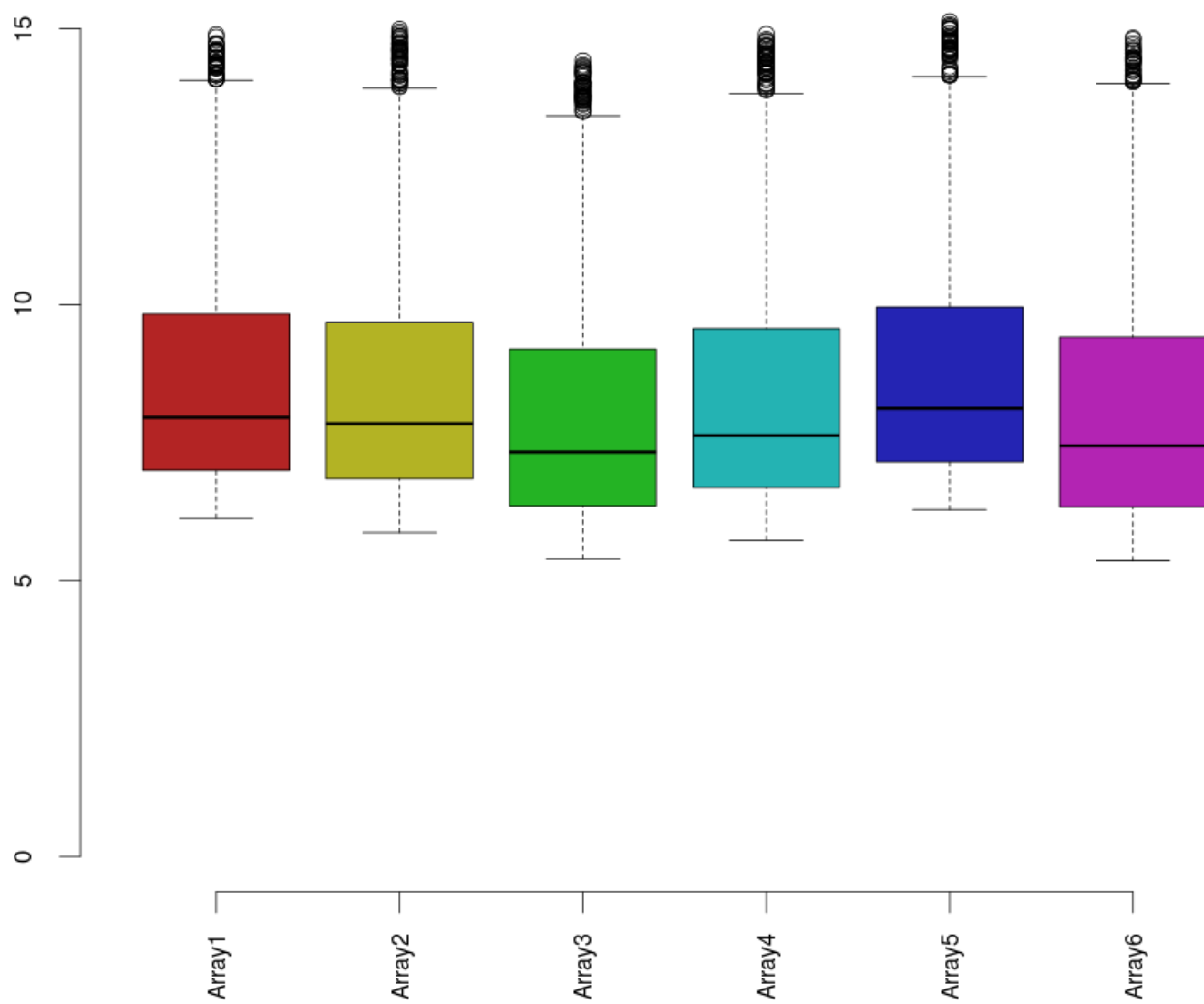


Percent present QC: OK (spread <= 10%)

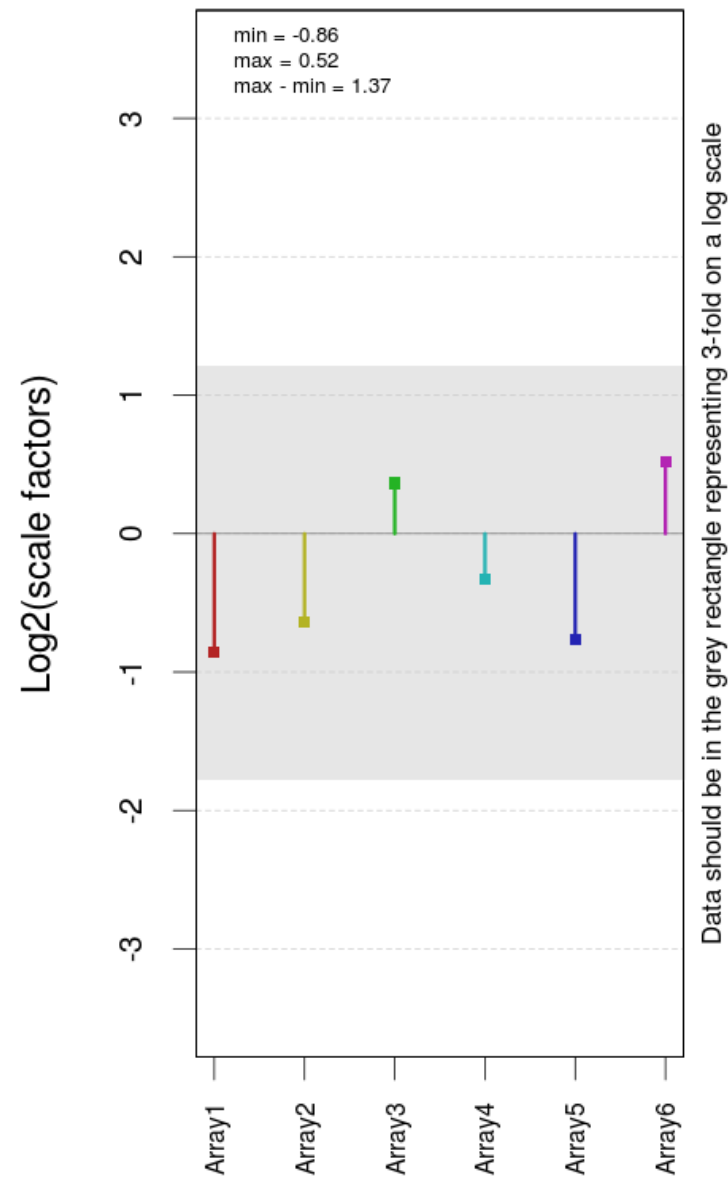
affx control profiles



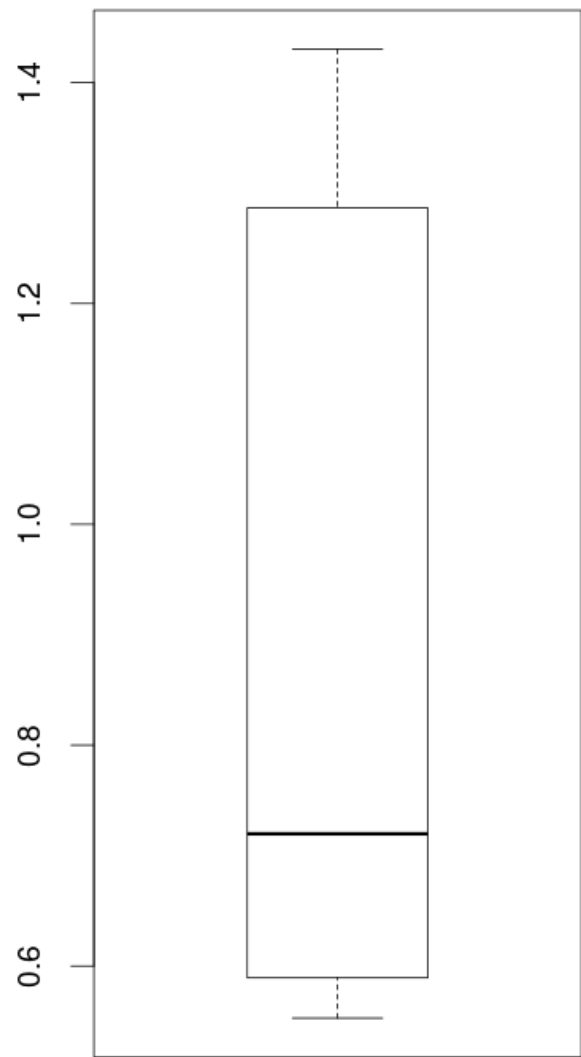
affx controls



Plot of Log scale factors



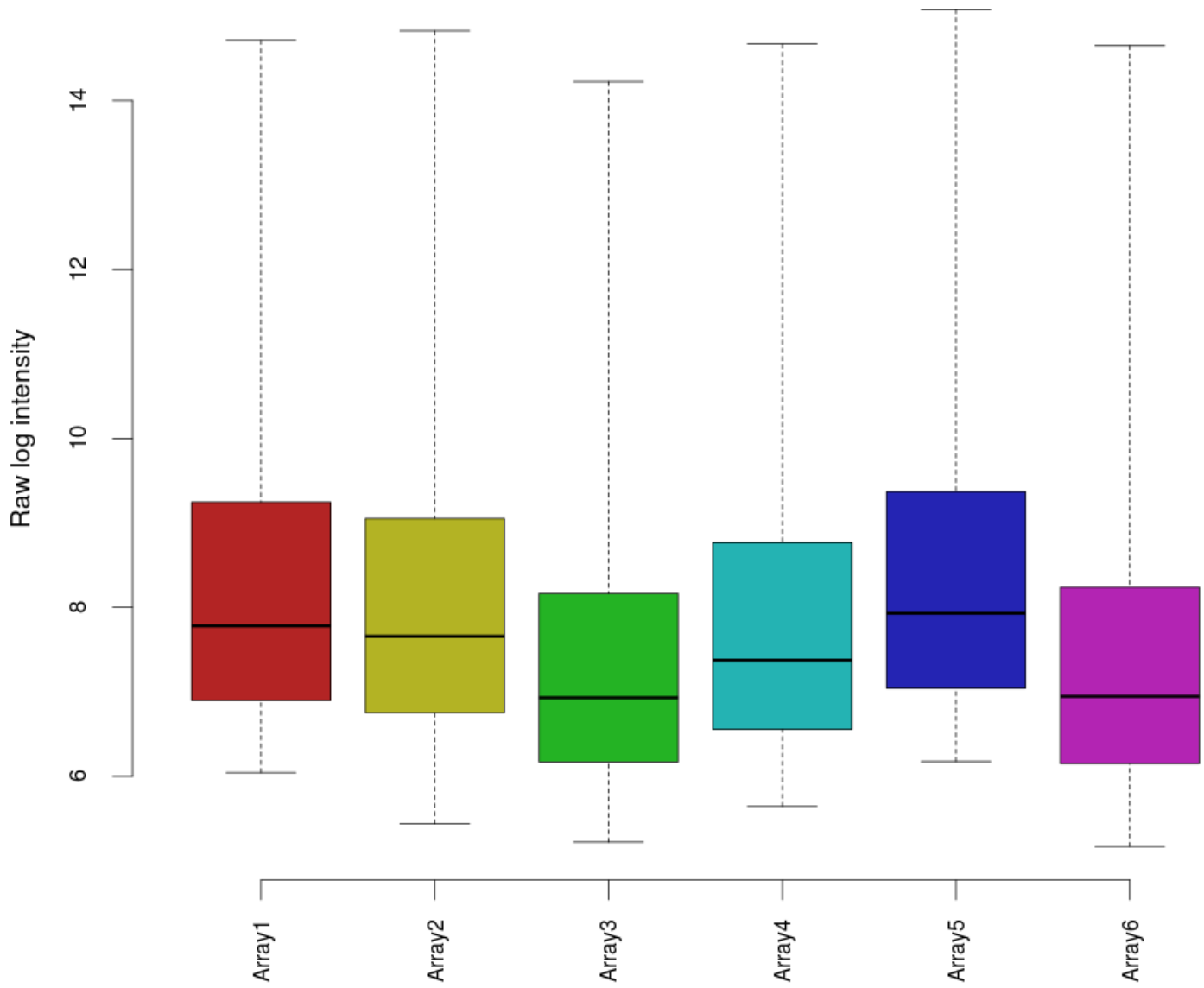
Boxplot of scale factors
(natural scale)



Scale factors QC: OK (spread < 3-fold)

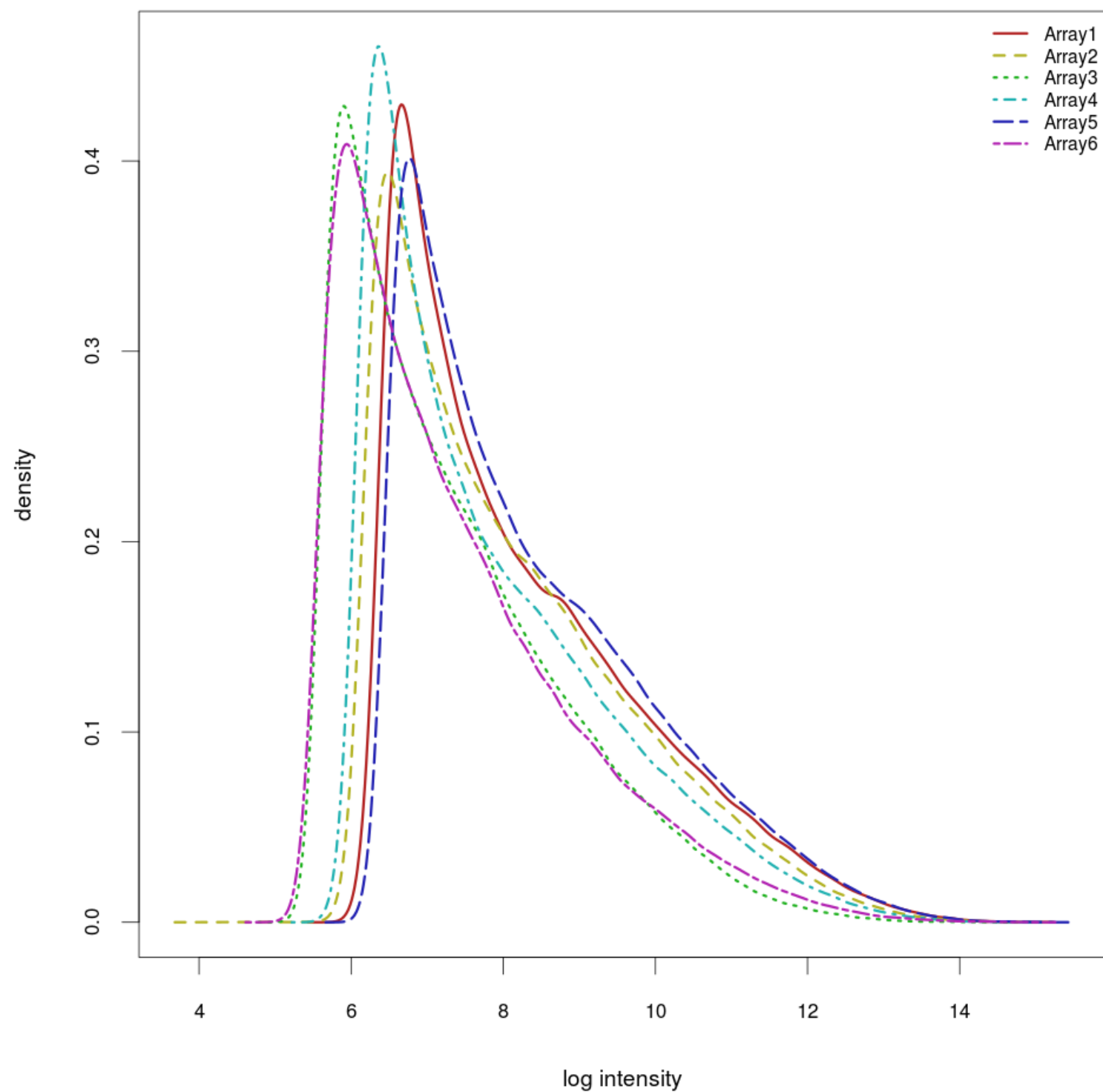
Boxplot of raw intensities

Distributions should be comparable between arrays



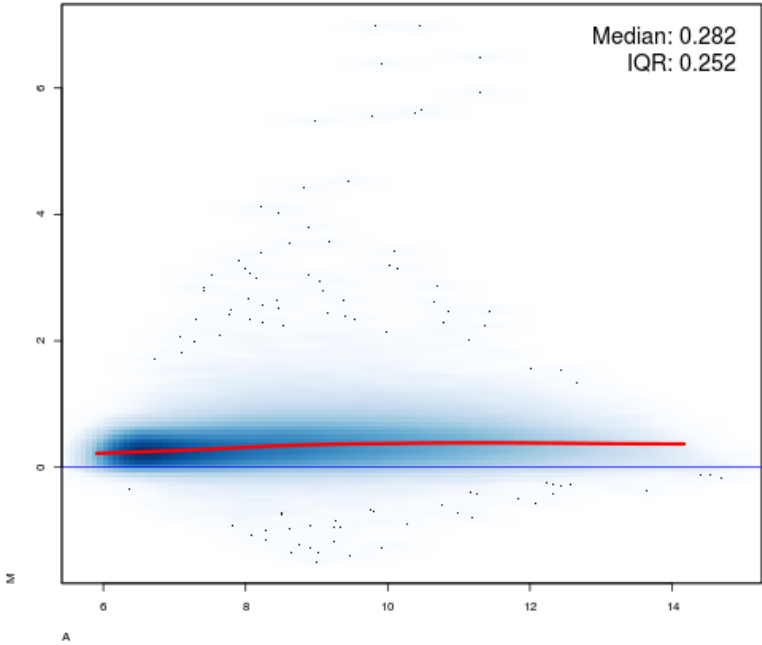
Density histogram of raw intensities

Curves should be comparable between arrays

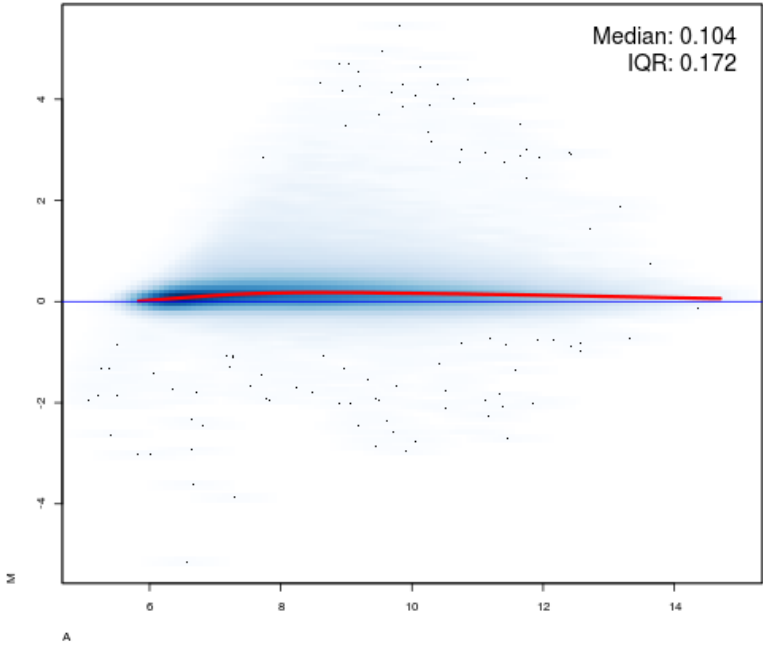


MA plots of raw data

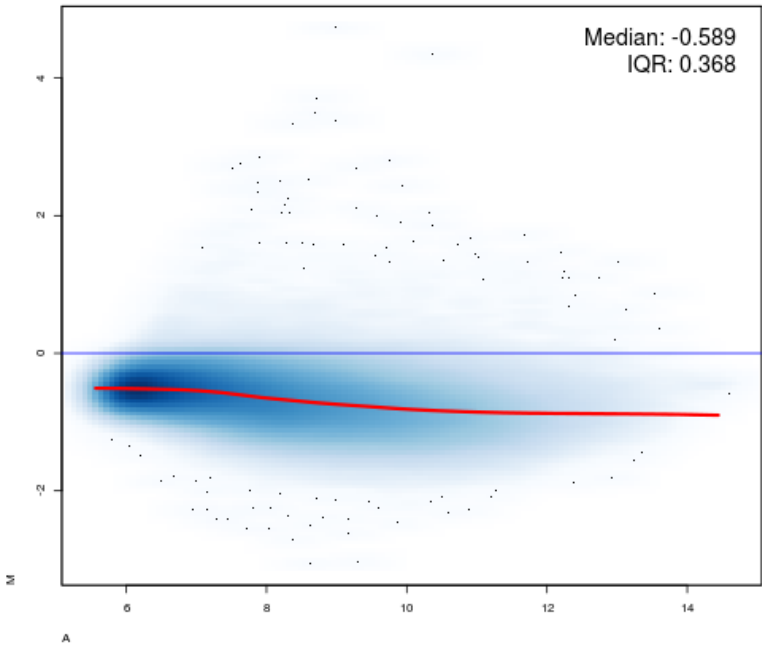
Array1 vs pseudo-median reference chip



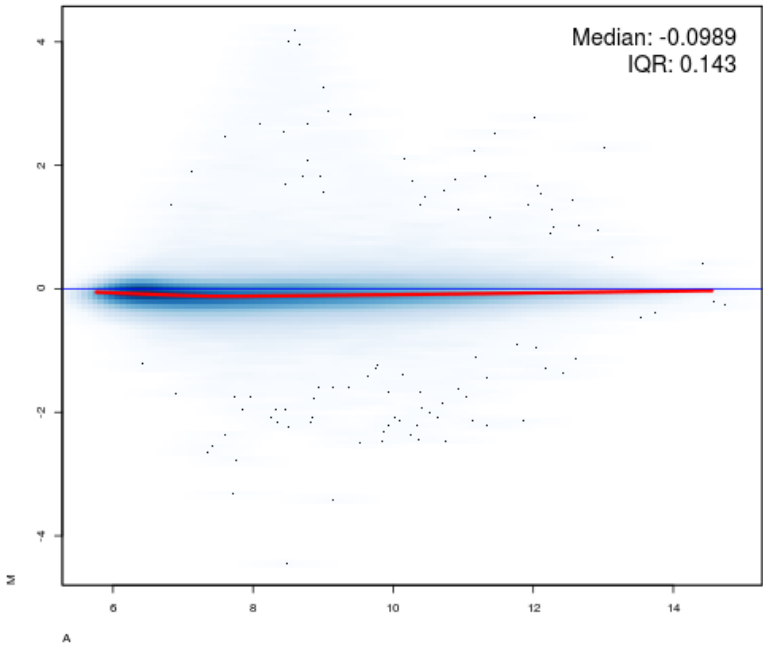
Array2 vs pseudo-median reference chip



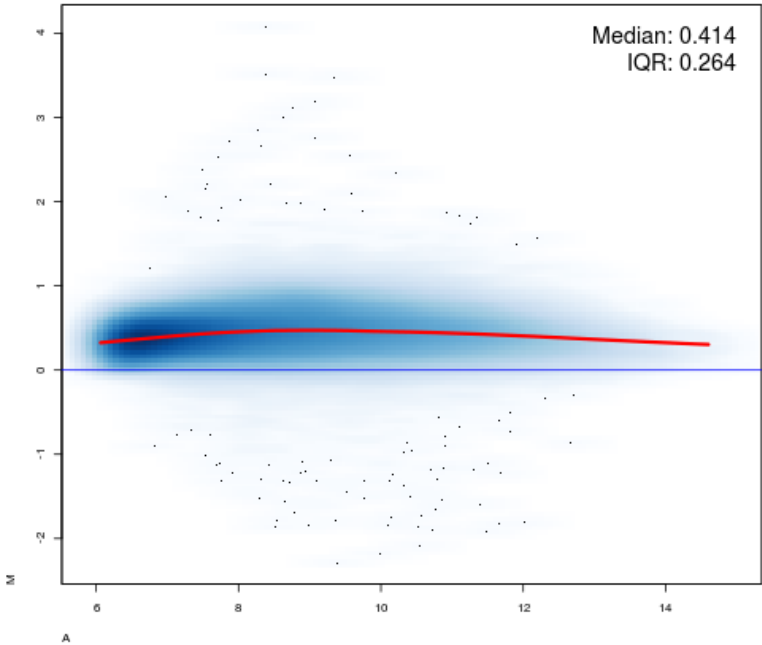
Array3 vs pseudo-median reference chip



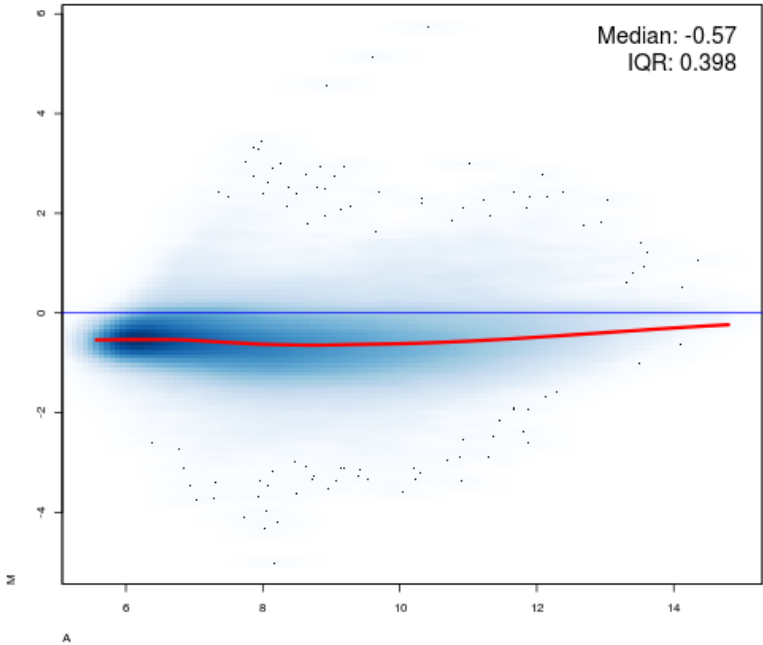
Array4 vs pseudo-median reference chip



Array5 vs pseudo-median reference chip

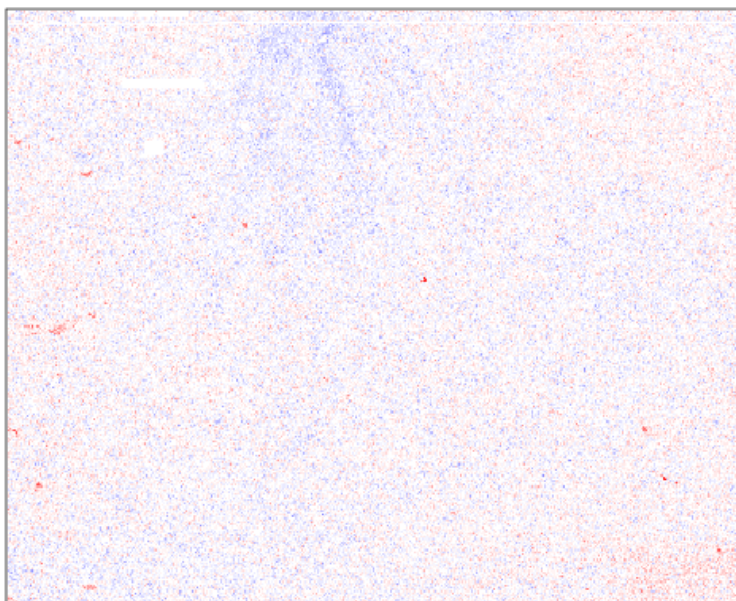


Array6 vs pseudo-median reference chip

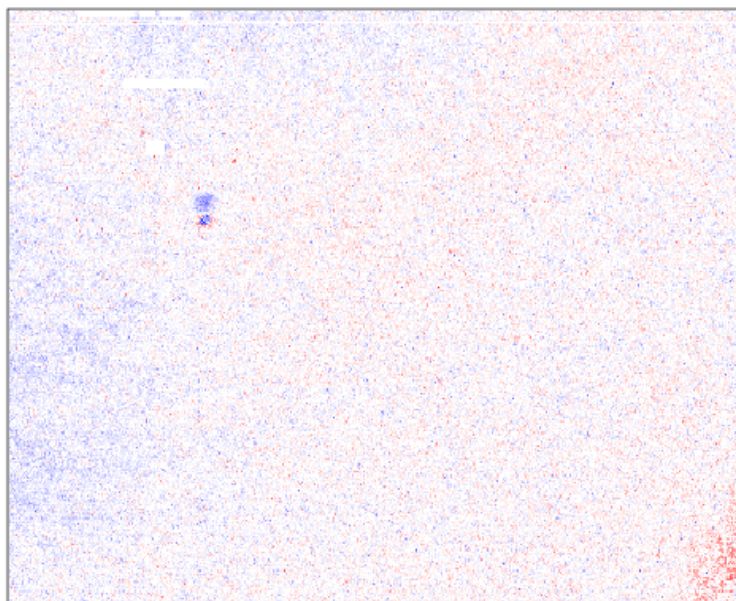


2D virtual PLM image for model characteristic: resids

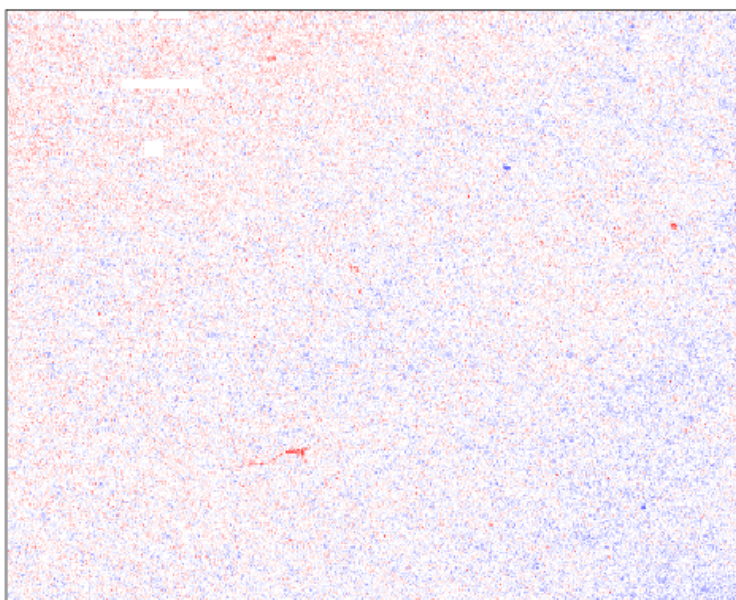
Array1



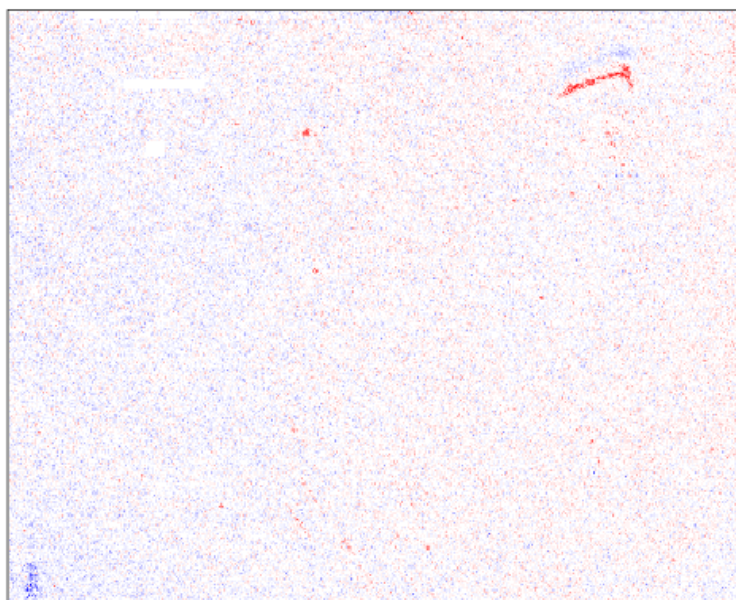
Array2



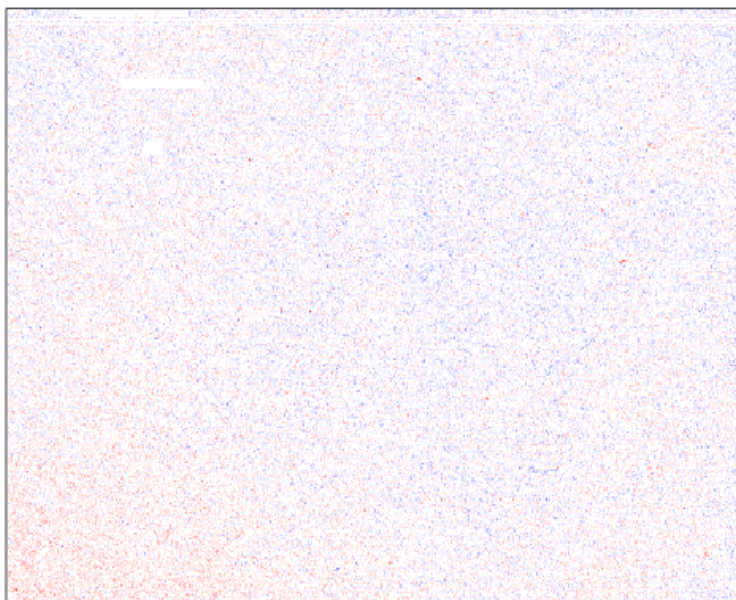
Array3



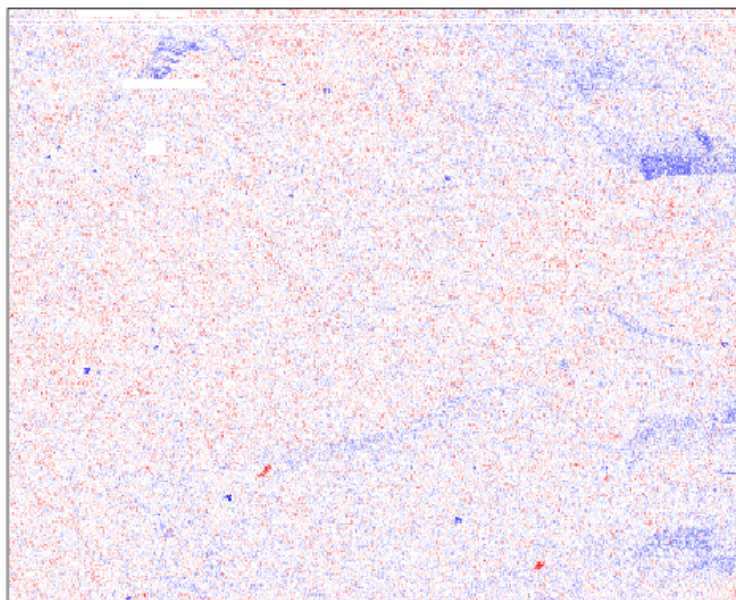
Array4



Array5

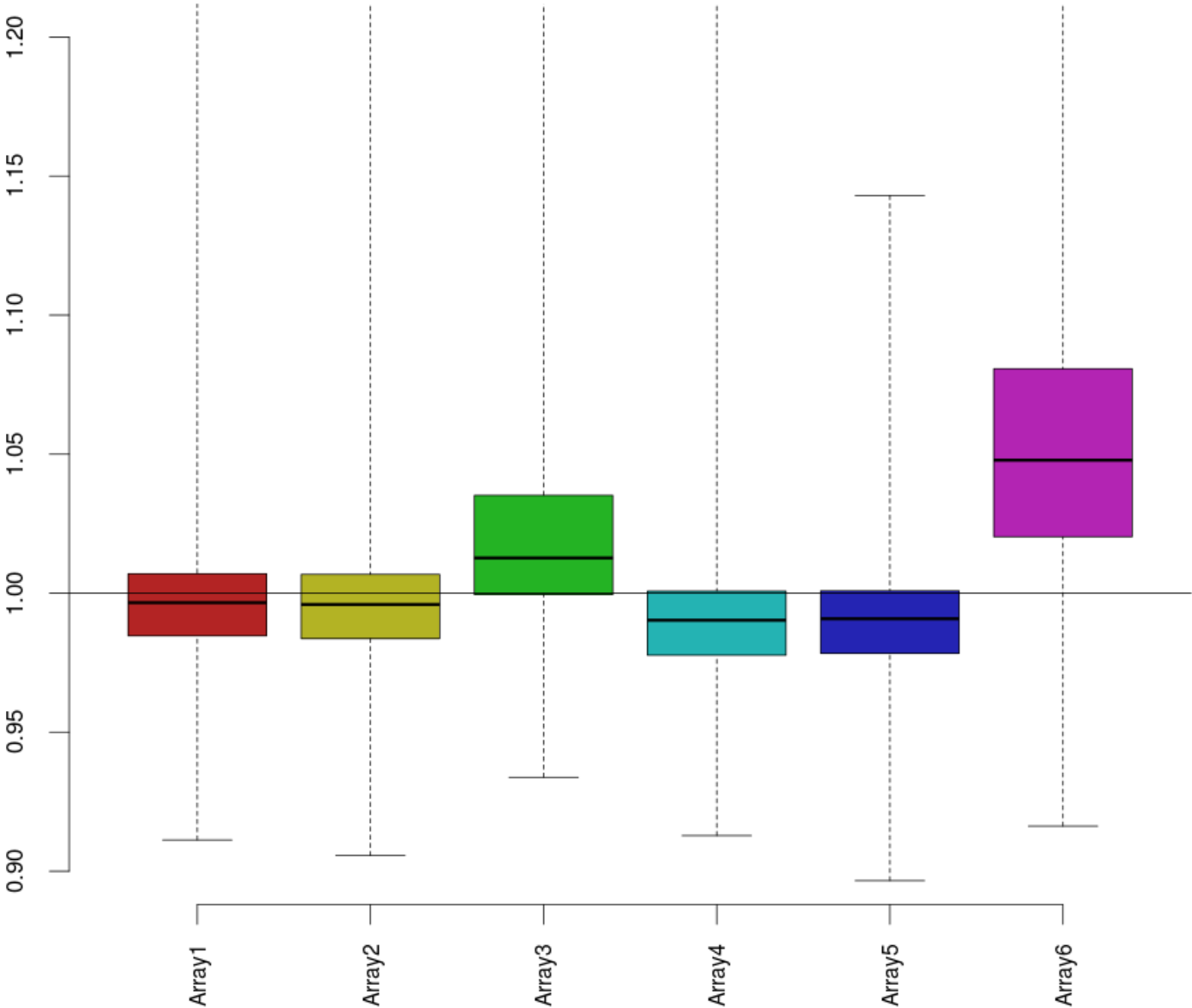


Array6



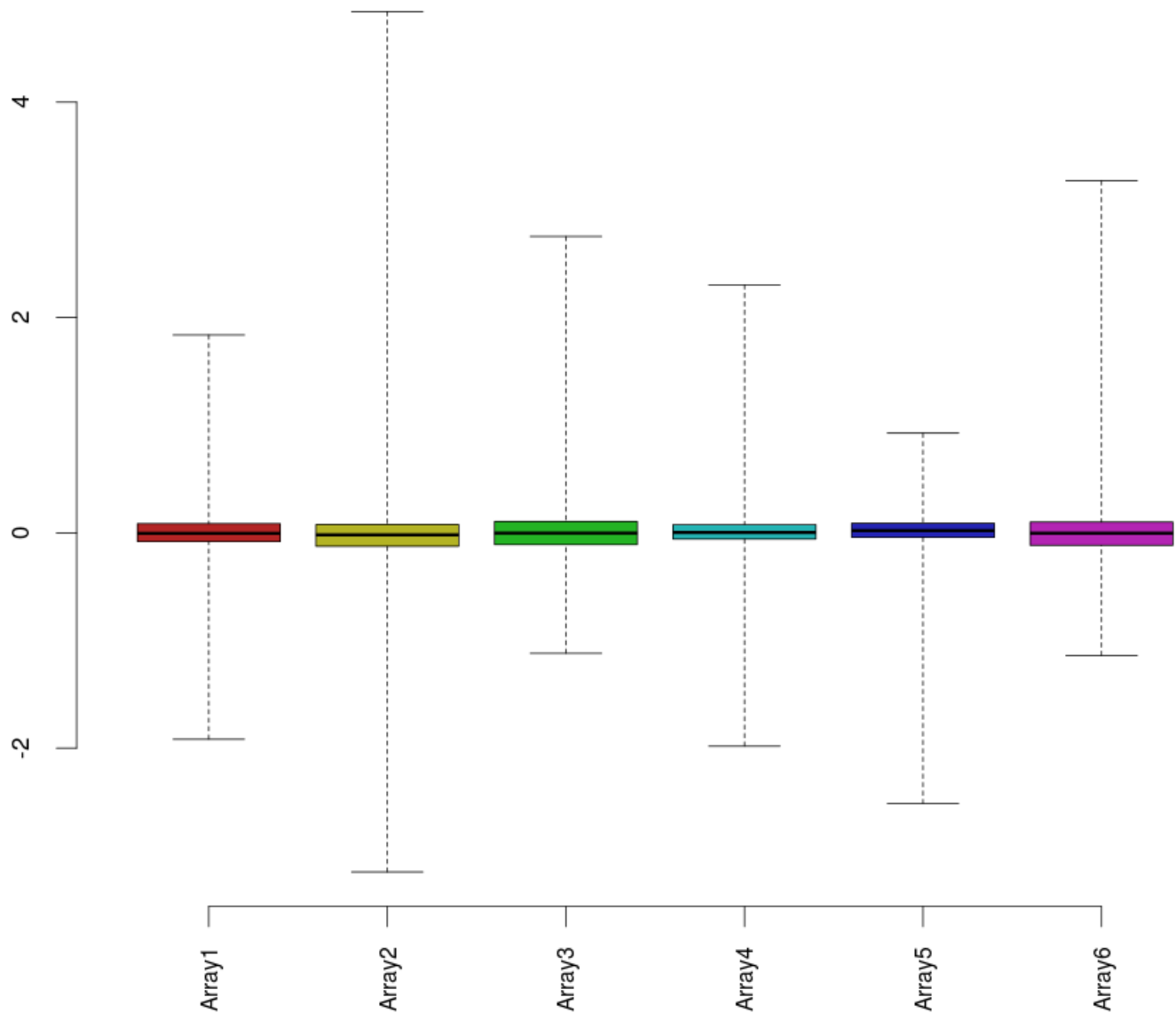
Normalized Unscaled Standard Errors (NUSE)

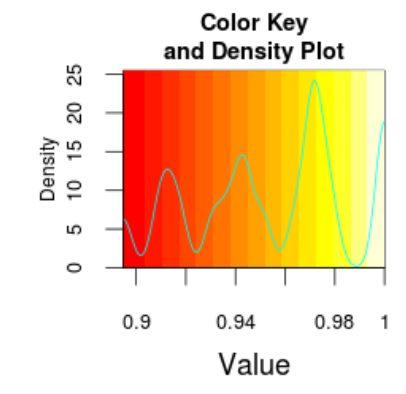
NUSE median value should be < 1.1



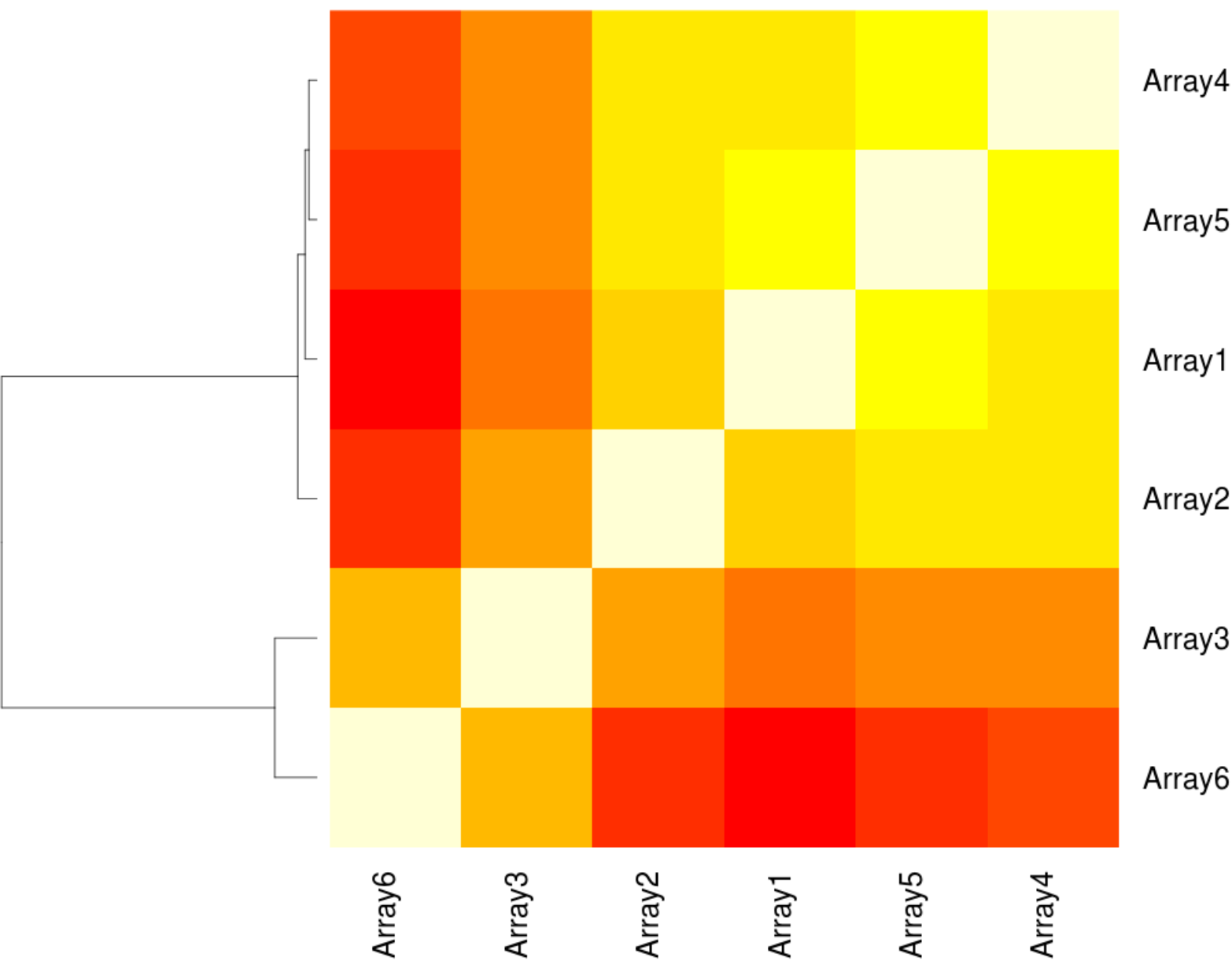
Relative Log Expression (RLE)

RLE distributions should be centered around 0

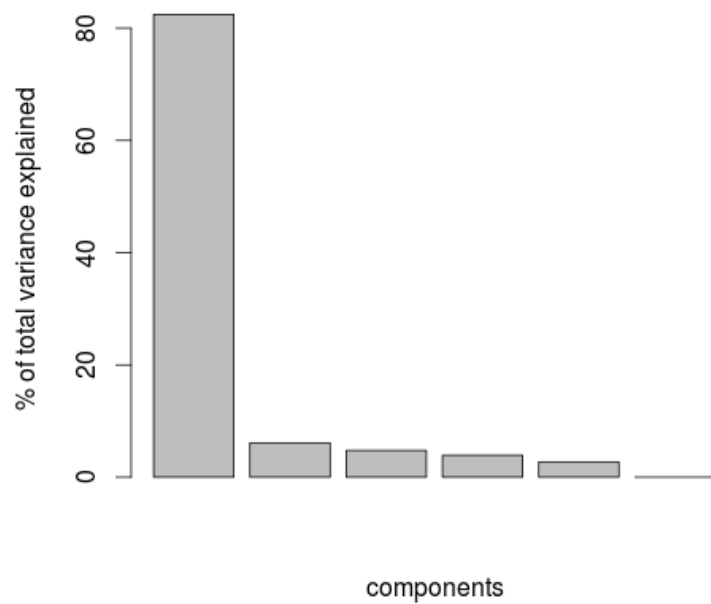
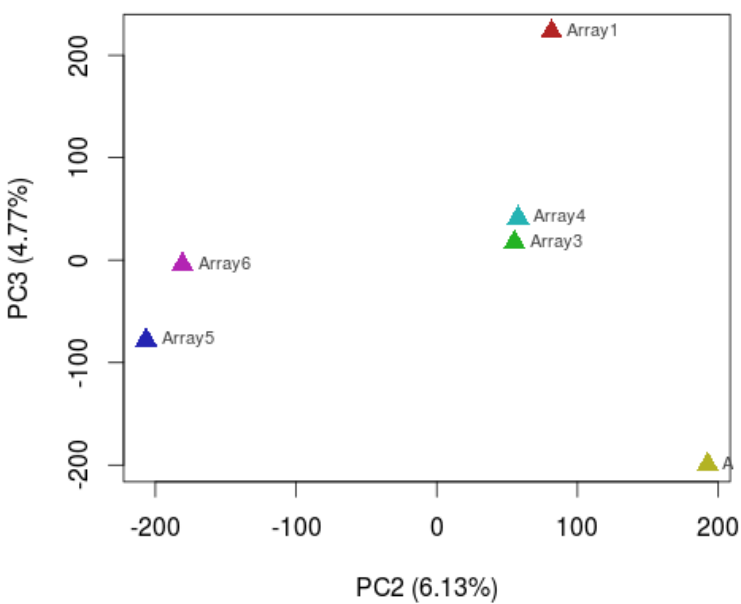
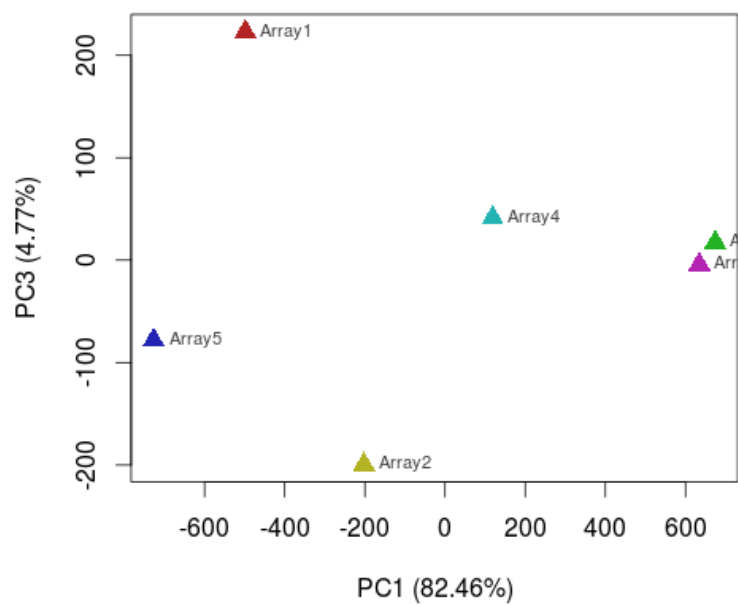
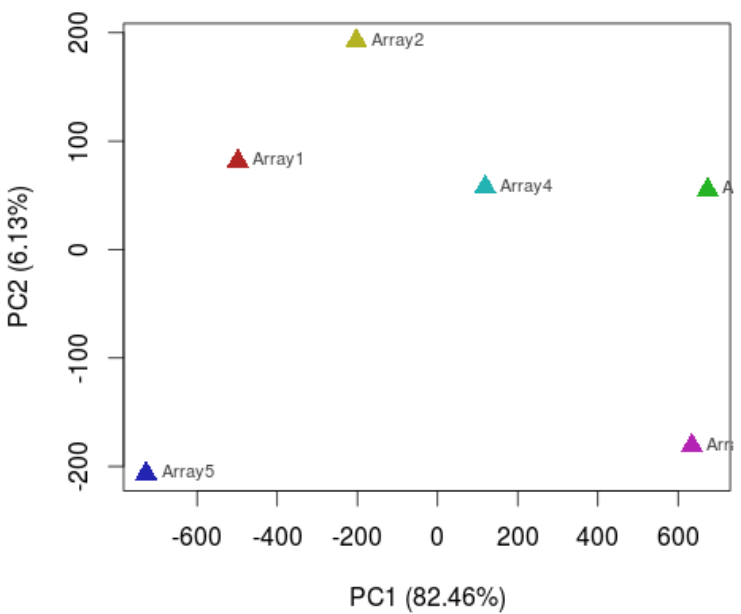




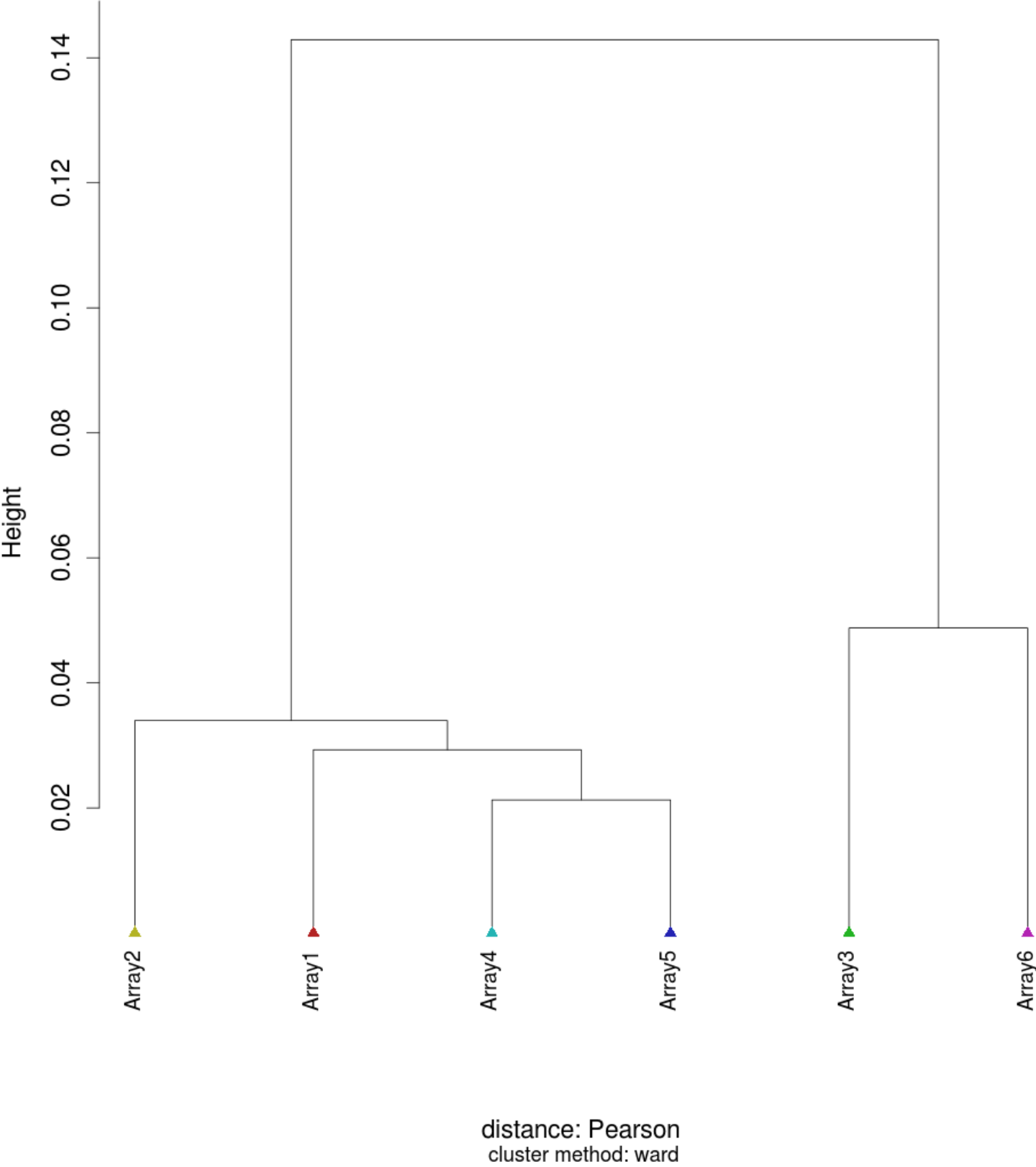
Raw data correlation plot
correlation method: pearson
cluster method: ward



PCA analysis of Raw data



Cluster dendrogram of raw data

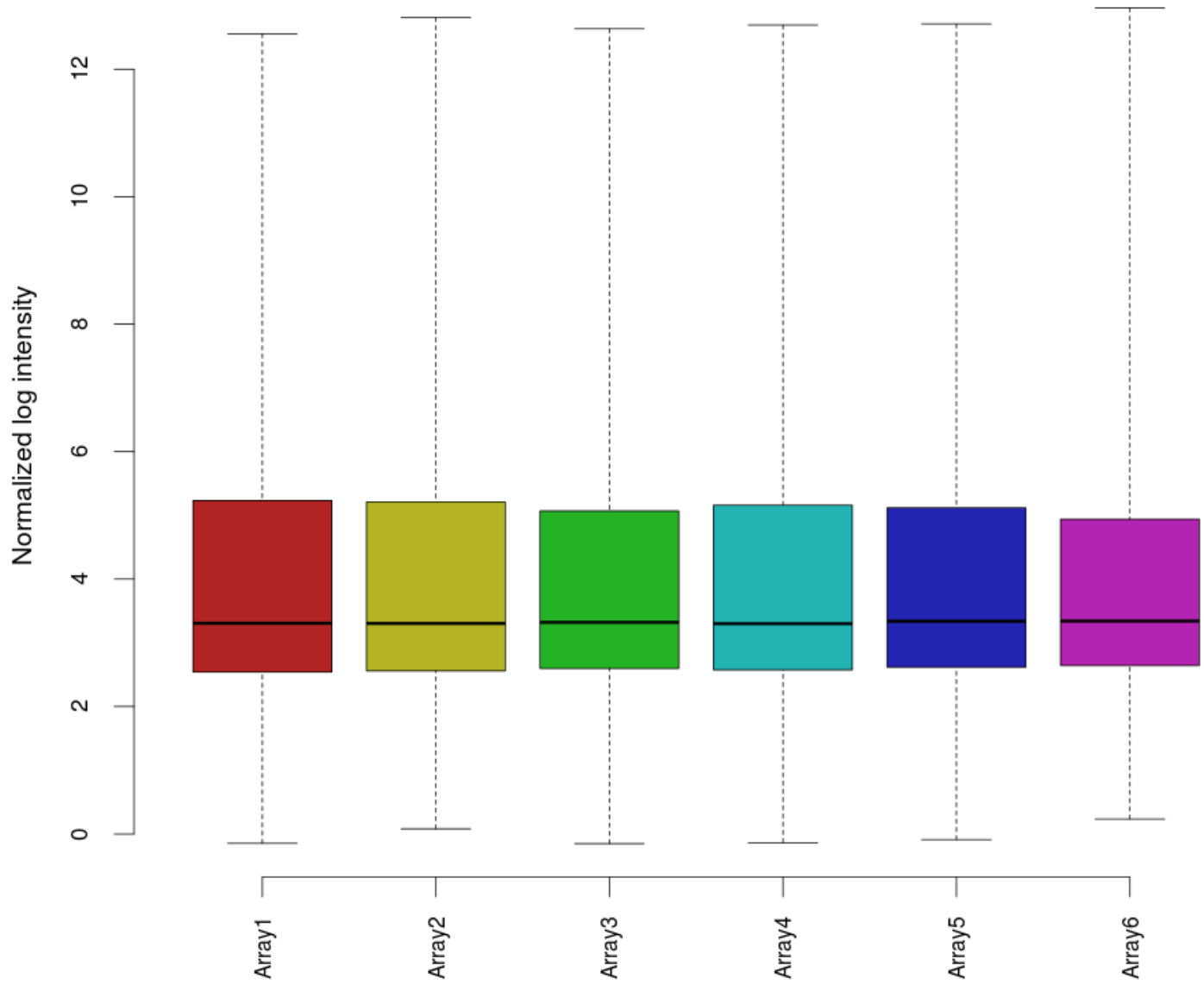


Pre-processing of Raw Data

Method: GCRMA
Annotation: HG_U95Av2

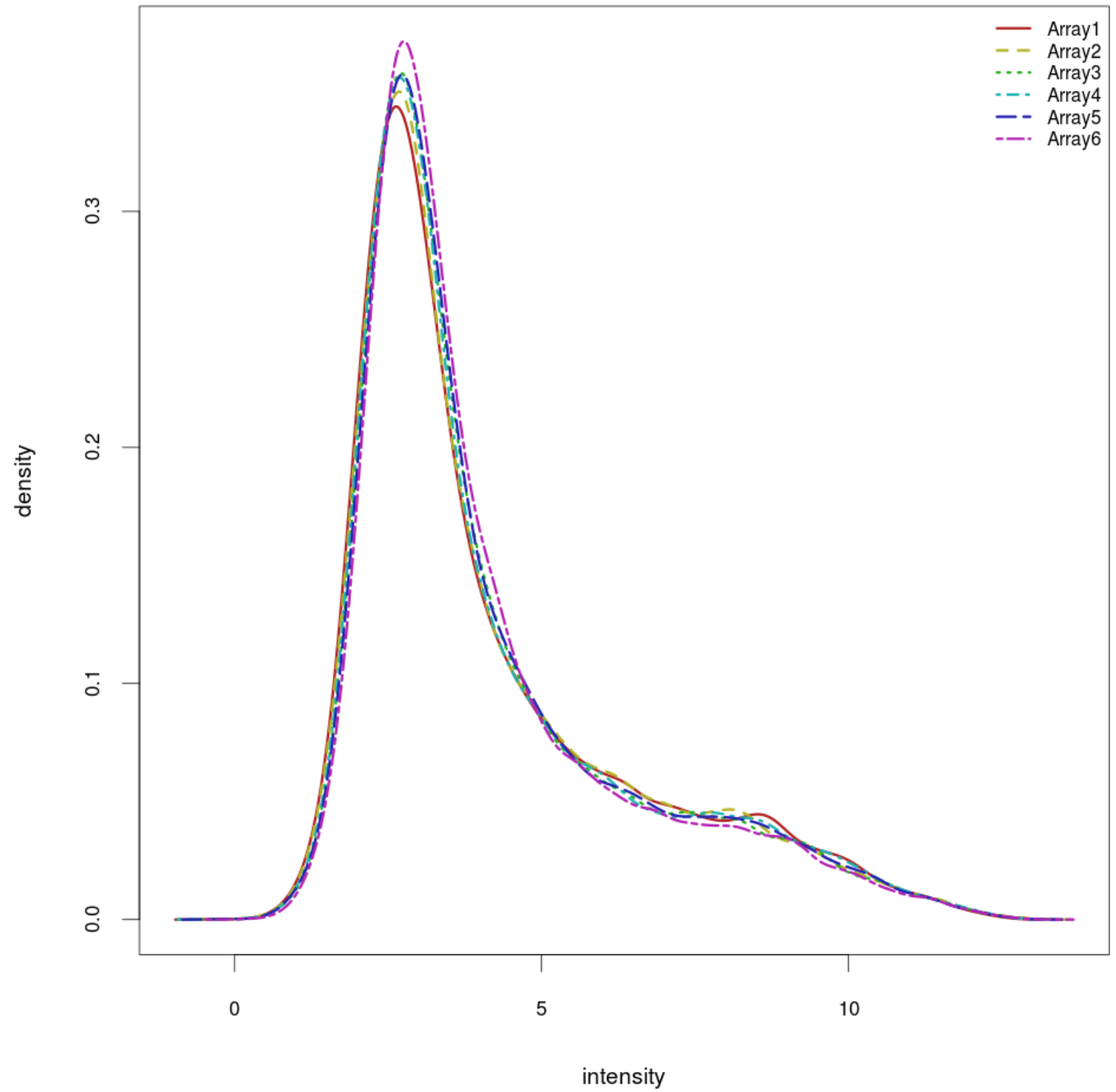
Boxplot after GCRMA

Distributions should be comparable between arrays



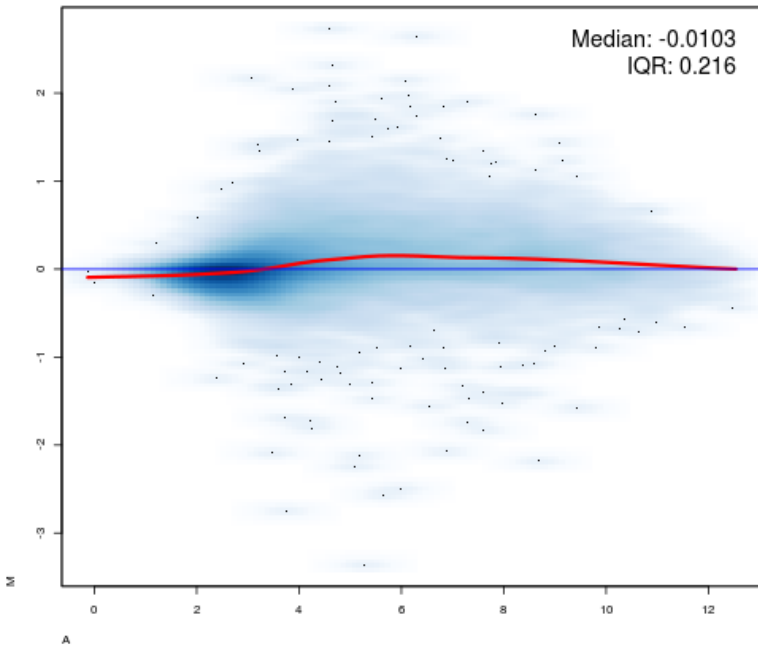
Density histogram after GCRMA

Curves should be comparable between arrays

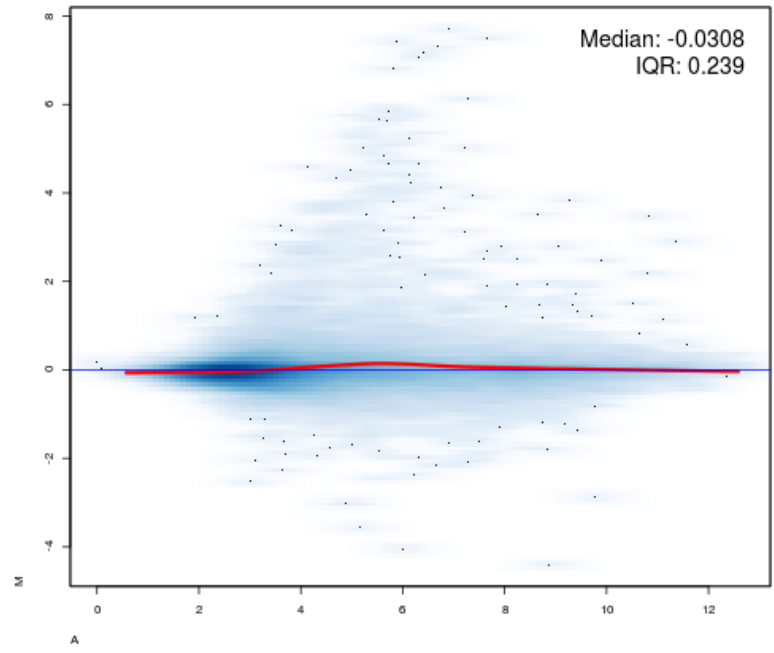


MA plots afterGCRMANormalization

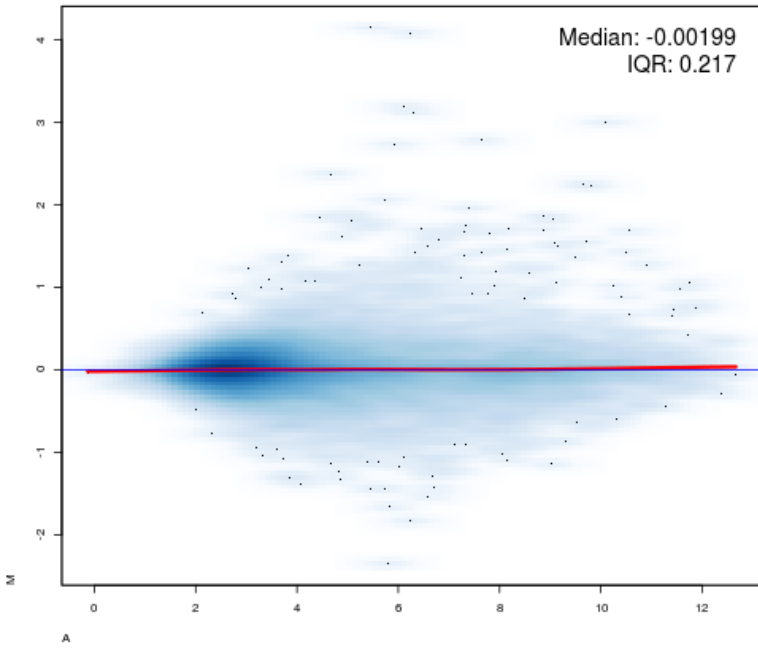
Array1 vs pseudo-median reference chip



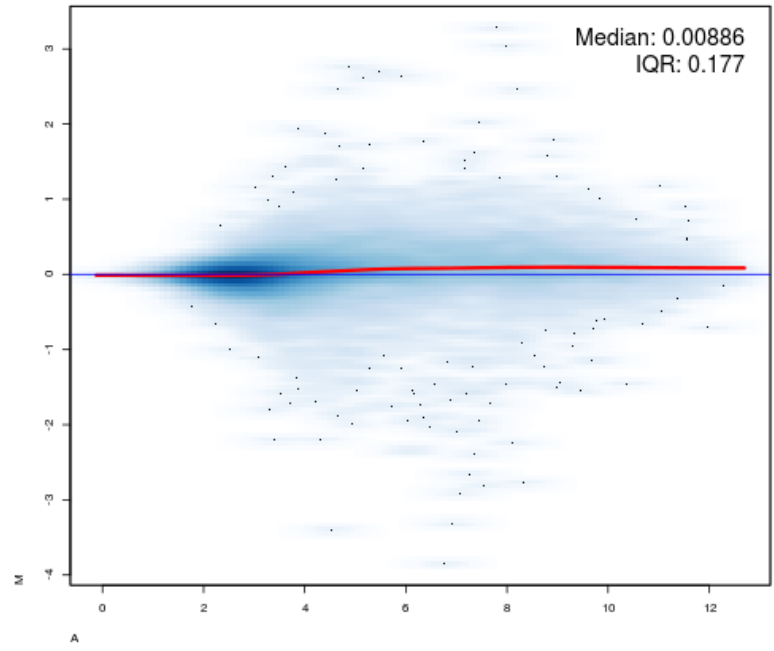
Array2 vs pseudo-median reference chip



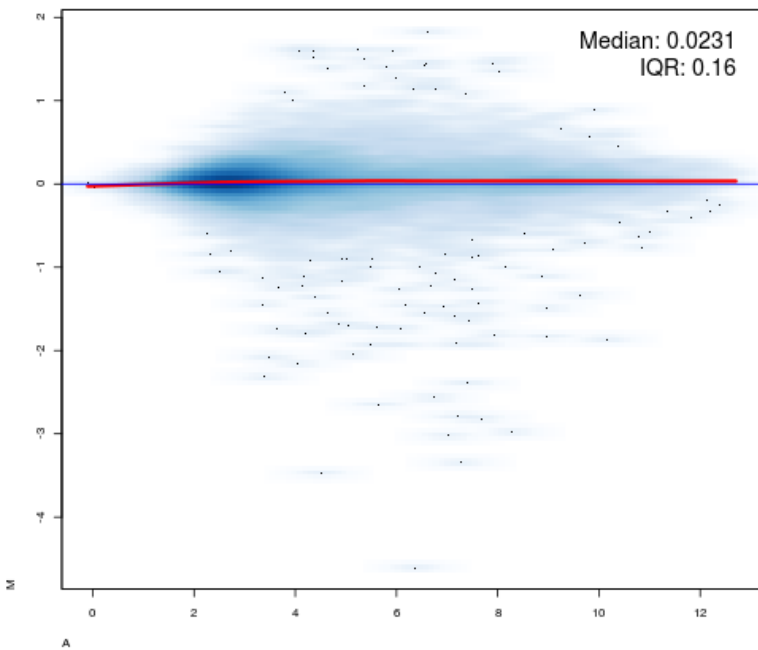
Array3 vs pseudo-median reference chip



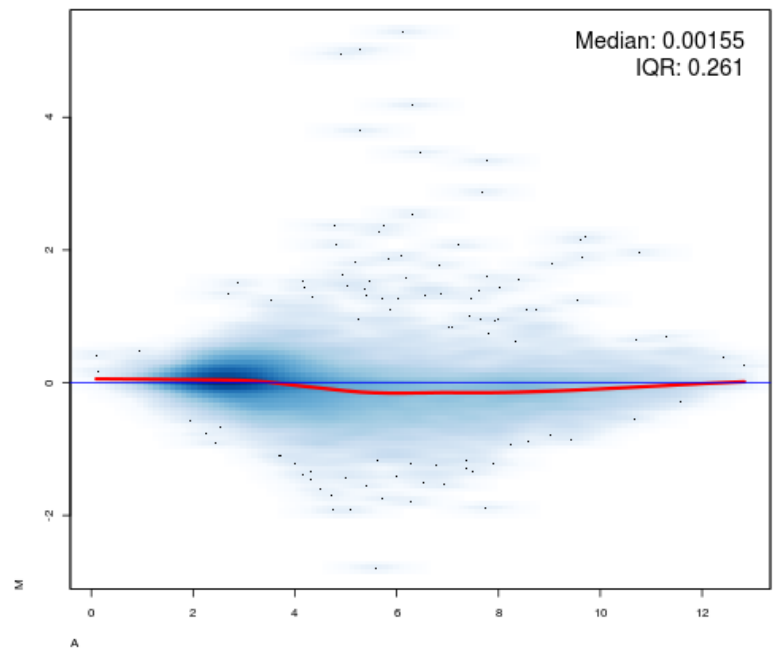
Array4 vs pseudo-median reference chip



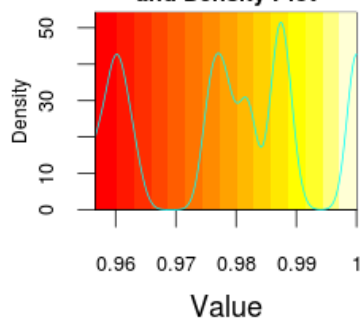
Array5 vs pseudo-median reference chip



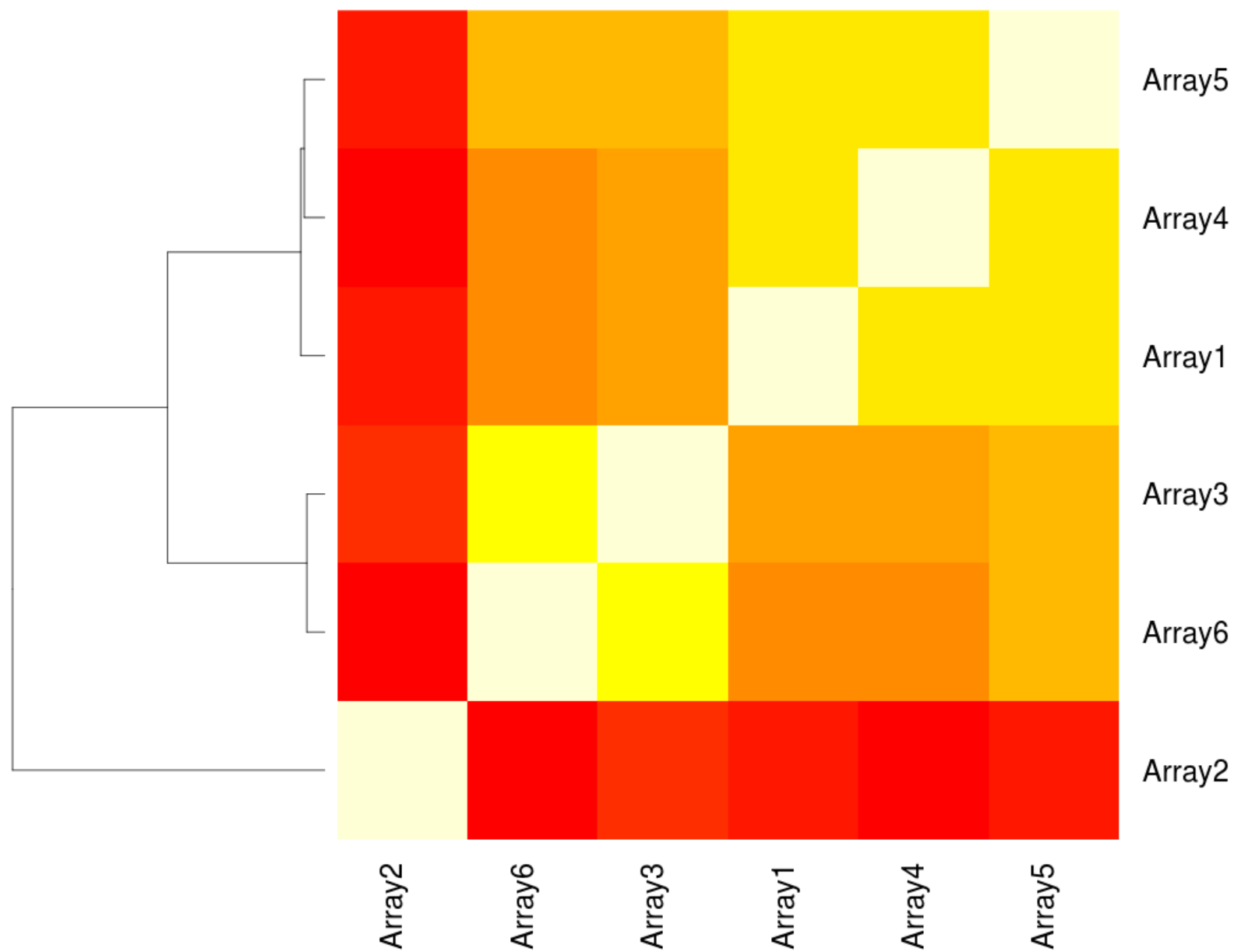
Array6 vs pseudo-median reference chip



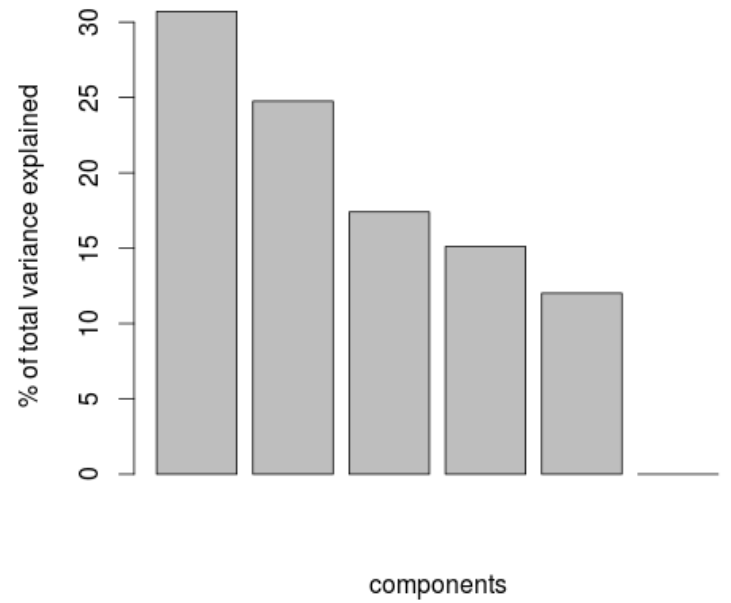
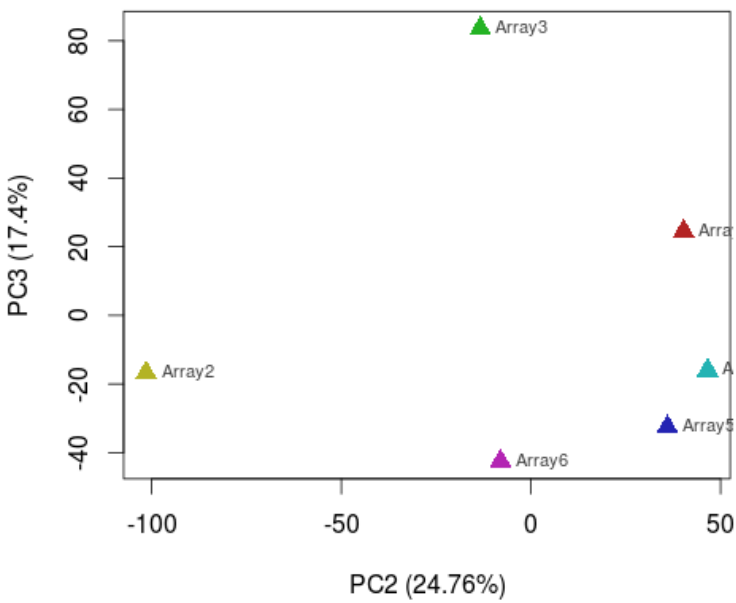
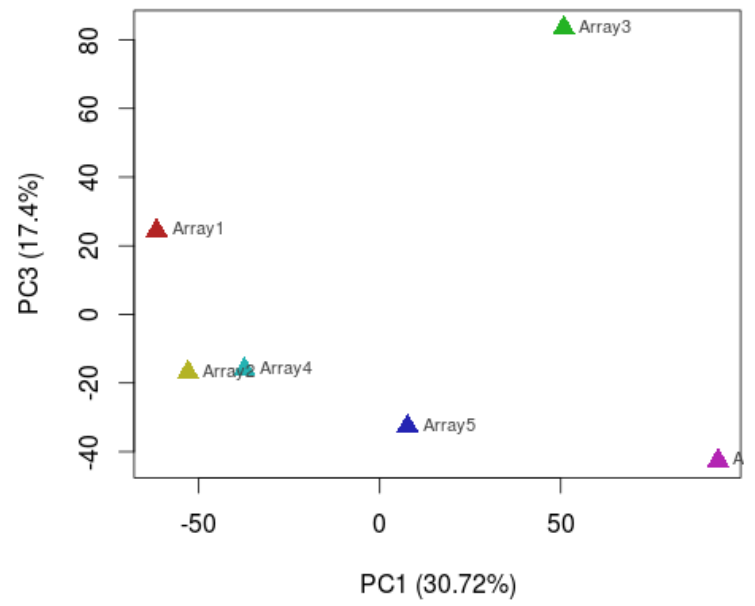
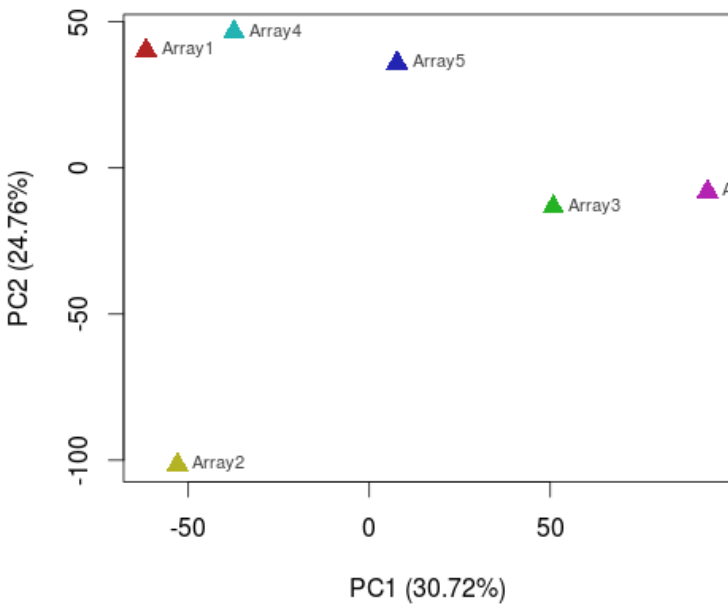
Color Key
and Density Plot



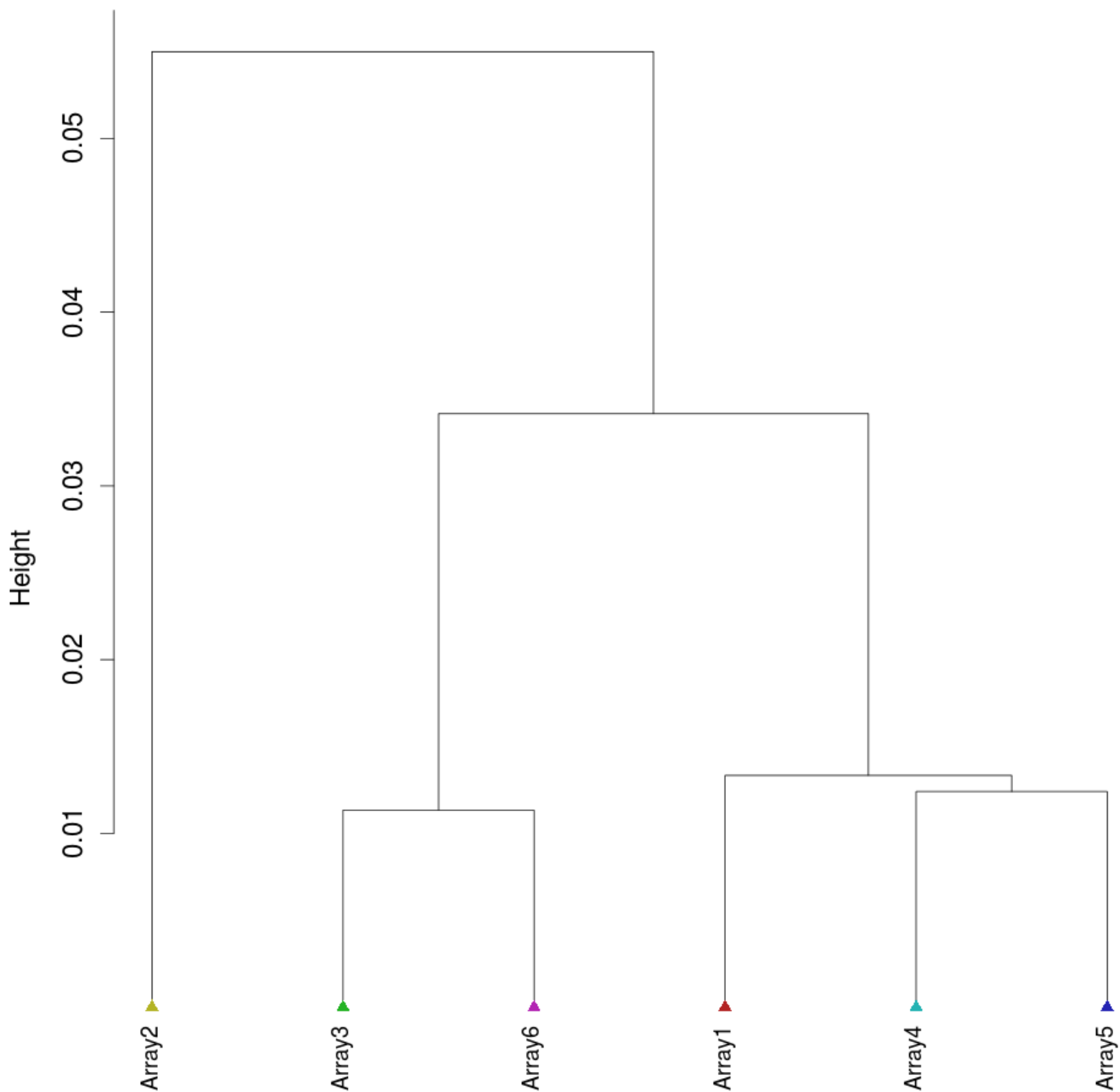
Array correlation plot
after GCRMA normalization
correlation method: pearson
cluster method: ward



PCA analysis after GCRMA normalization



Cluster dendrogram of GCRMA normalized data



distance: Pearson
cluster method: ward