

## Array names and grouping

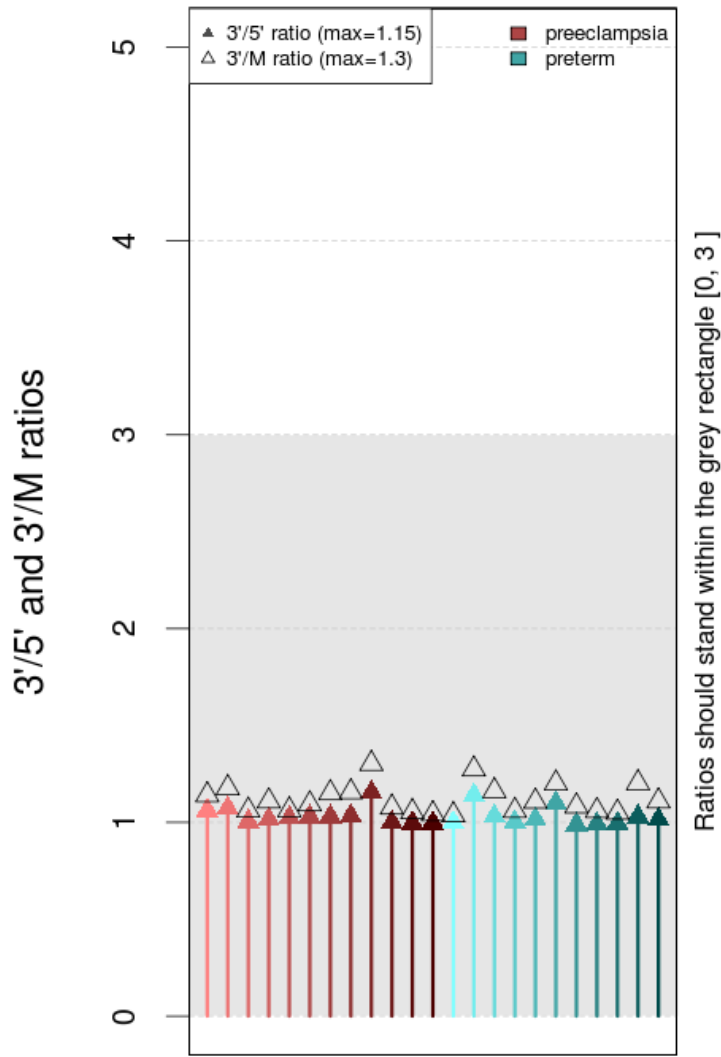
ArrayDataFile	SourceName	FactorValue
GSM367781.CEL	Array1	preterm
GSM367782.CEL	Array2	preterm
GSM367783.CEL	Array3	preterm
GSM367784.CEL	Array4	preterm
GSM367785.CEL	Array5	preterm
GSM367786.CEL	Array6	preterm
GSM367787.CEL	Array7	preterm
GSM367788.CEL	Array8	preterm
GSM367789.CEL	Array9	preterm
GSM367790.CEL	Array10	preterm
GSM367791.CEL	Array11	preterm
GSM367792.CEL	Array12	preeclampsia
GSM367793.CEL	Array13	preeclampsia
GSM367794.CEL	Array14	preeclampsia
GSM367795.CEL	Array15	preeclampsia
GSM367796.CEL	Array16	preeclampsia
GSM367797.CEL	Array17	preeclampsia
GSM367798.CEL	Array18	preeclampsia
GSM367799.CEL	Array19	preeclampsia
GSM367800.CEL	Array20	preeclampsia
GSM367801.CEL	Array21	preeclampsia
GSM367802.CEL	Array22	preeclampsia
GSM367803.CEL	Array23	preeclampsia

Quality Control & Pre-processing Evaluation

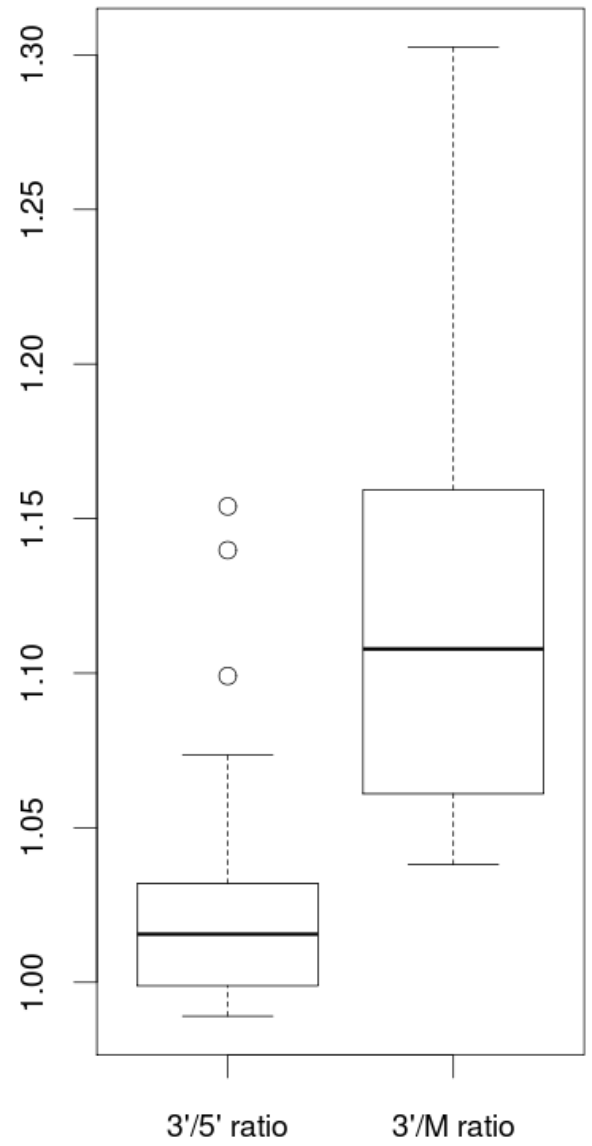
of  
GSE14722\_0

**REPORT**

## RNA degradation of beta-actin



## Boxplot of beta-actin ratios



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

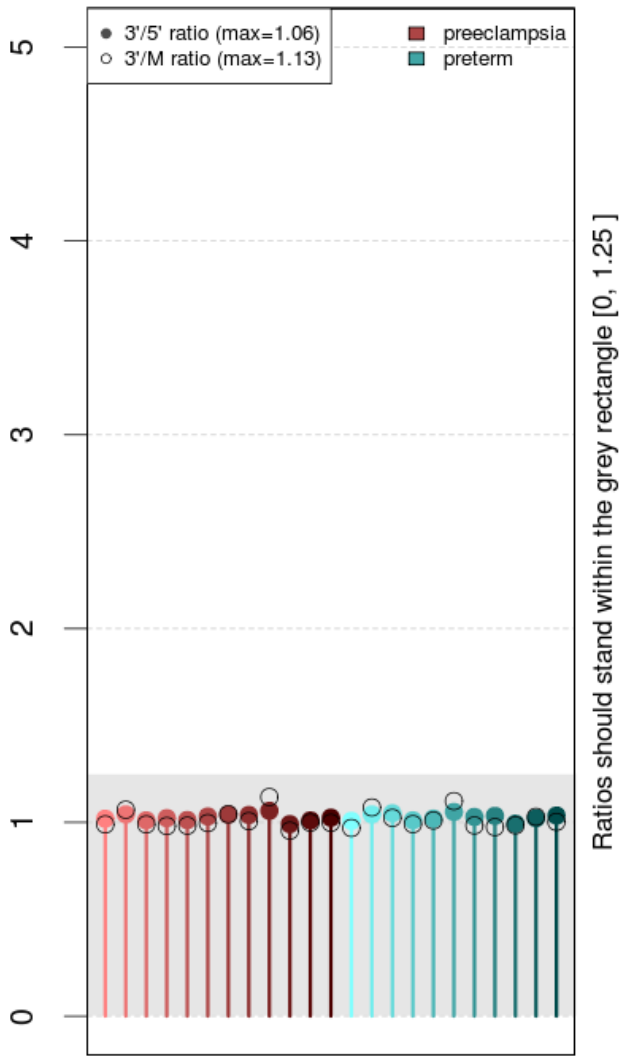
# Summary of raw data quality indicators

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

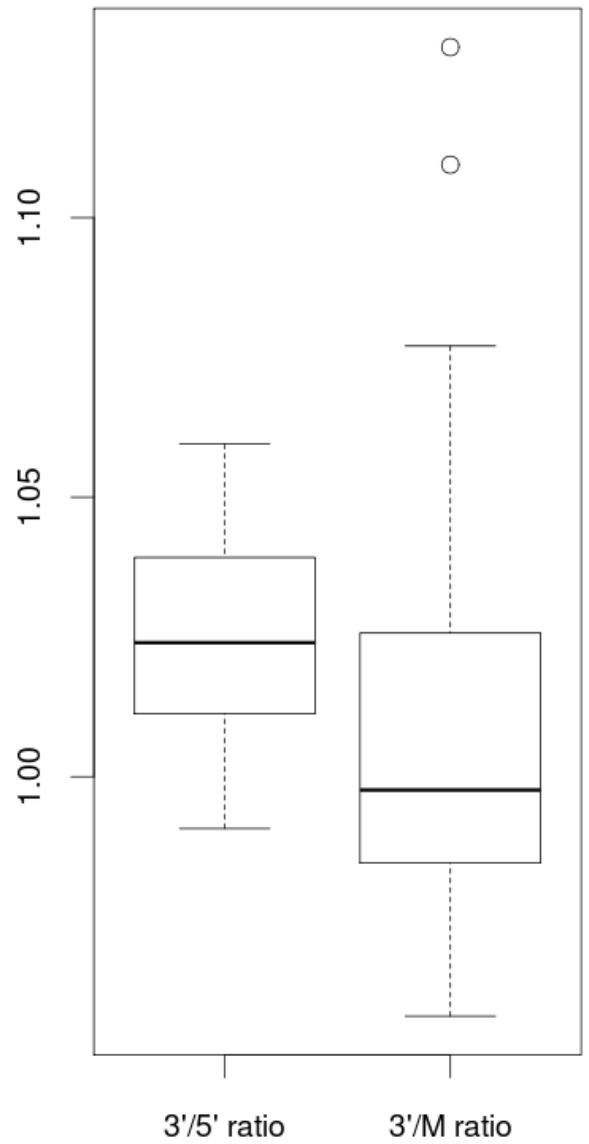
	3'/5' beta-actin (cutoff=3)	3'/5' GAPDH (cutoff=1.25)	Hybridization BioB<BioC<BioD<CreX	Hybridization BioB=Present	Percent Present spread<=10%	Background spread<=20%	Log Scale Factor spread<=3
Array12	1.06	1.02	T	P	43 %	52	-0.41
Array13	1.07	1.04	T	P	41 %	31	1.94
Array14	1	1.01	T	P	42 %	61	-0.72
Array15	1.02	1.02	T	P	47 %	59	-0.63
Array16	1.02	1.01	T	P	45 %	56	-0.71
Array17	1.03	1.03	T	P	47 %	49	-0.63
Array18	1.03	1.04	T	P	50 %	40	-0.21
Array19	1.03	1.04	T	P	44 %	47	-0.29
Array20	1.15	1.06	T	P	28 %	35	3
Array21	1	0.99	T	P	37 %	46	0.17
Array22	1	1.01	T	P	41 %	60	-0.5
Array23	1	1.02	T	P	37 %	60	-0.13
Array1	1	1.01	T	P	43 %	61	-0.77
Array2	1.14	1.04	T	P	36 %	33	2.38
Array3	1.03	1.05	T	P	50 %	47	-1.05
Array4	1	1.01	T	P	44 %	66	-0.98
Array5	1.02	1.02	T	P	49 %	42	-0.02
Array6	1.1	1.05	T	P	36 %	32	2.63
Array7	0.99	1.03	T	P	39 %	58	0.13
Array8	0.99	1.03	T	P	39 %	54	-0.08
Array9	0.99	0.99	T	P	38 %	56	-0.54
Array10	1.03	1.02	T	P	41 %	51	-0.34
Array11	1.02	1.03	T	P	48 %	48	-0.81

# RNA degradation of GAPDH

3'/5' and 3'/M ratios

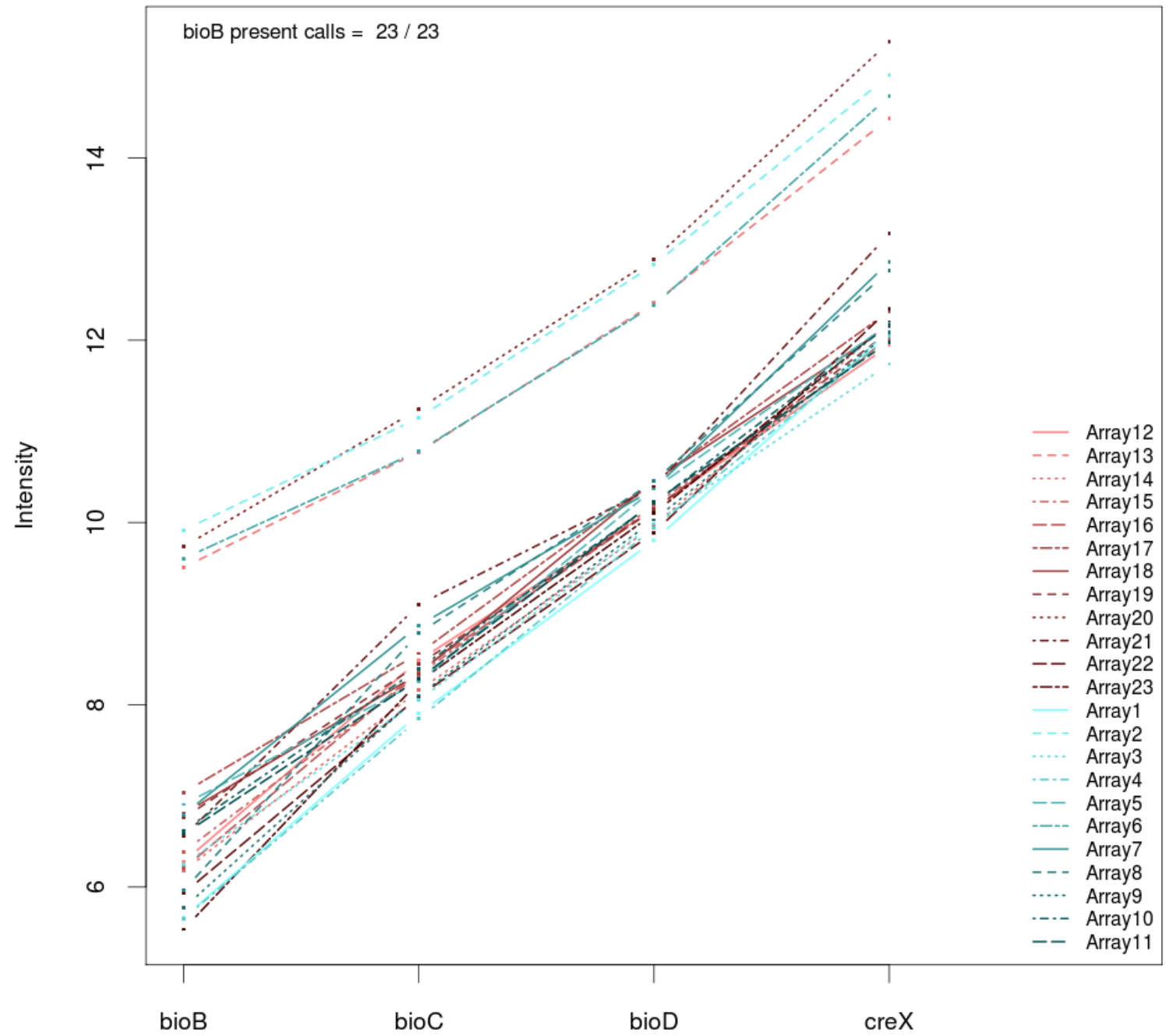


# Boxplot of GAPDH ratios



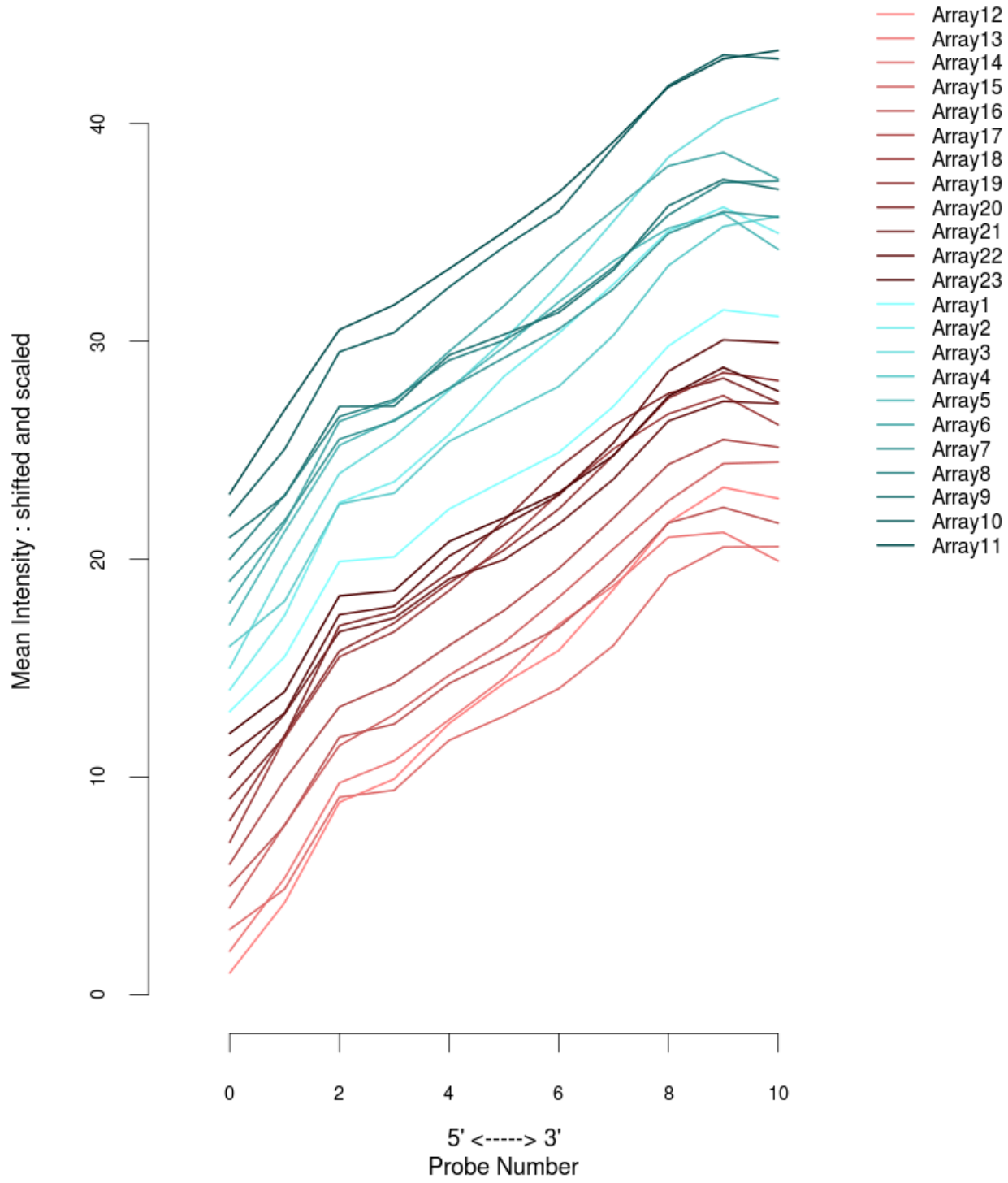
GAPDH QC: OK (all 3'/5' ratios < 1.25)

# Spike-in Hybridization controls intensities and calls

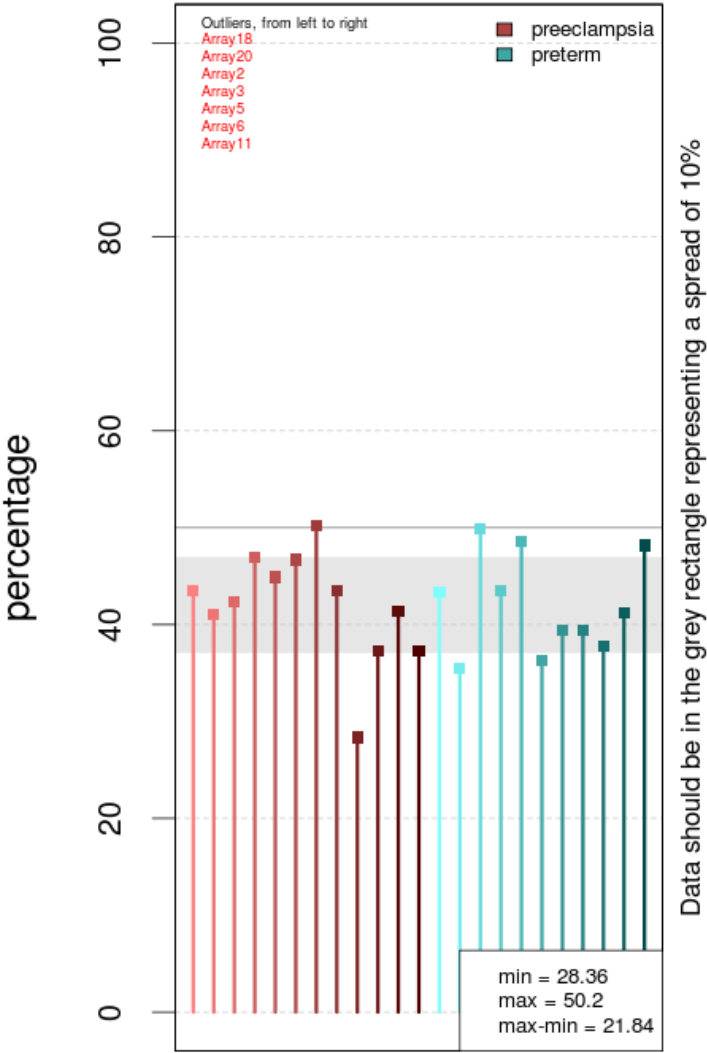


Intensities: OK (bioB < bioC < bioD < creX for all arrays)  
BioB Present calls: OK (indeed all bioB are called present)

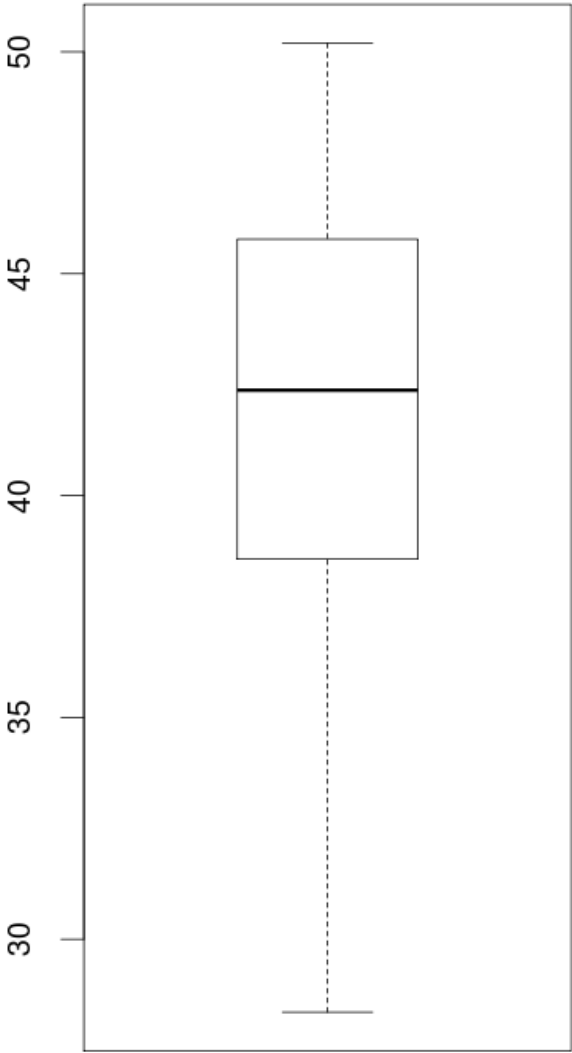
# RNA degradation plot



# Plot of percent present



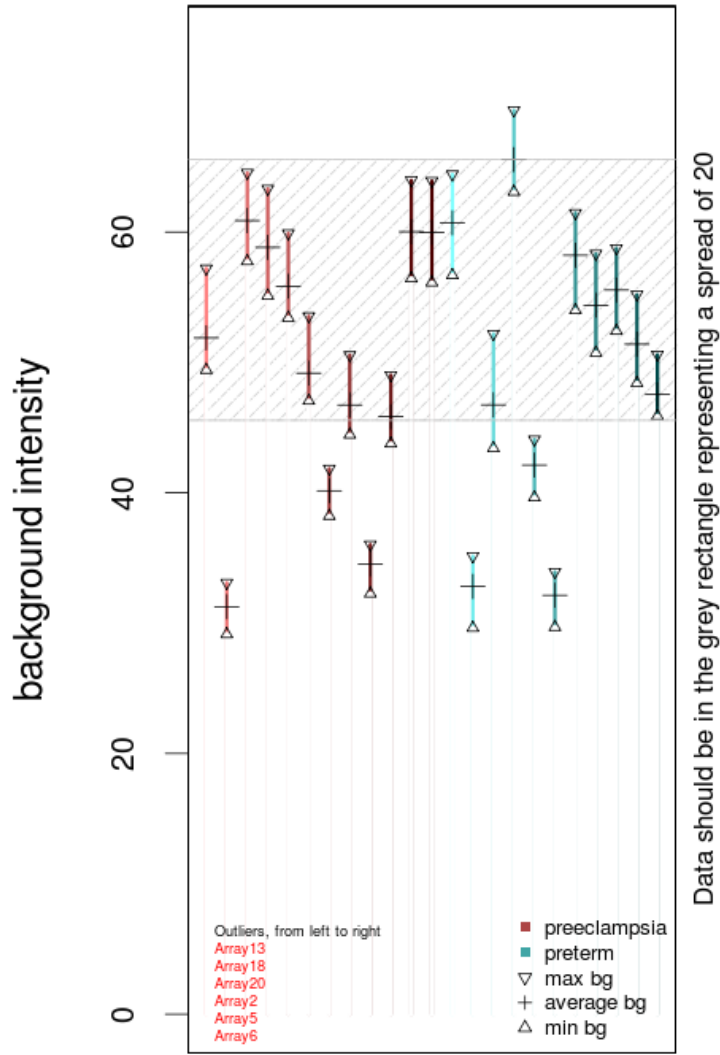
# Boxplot of percent present



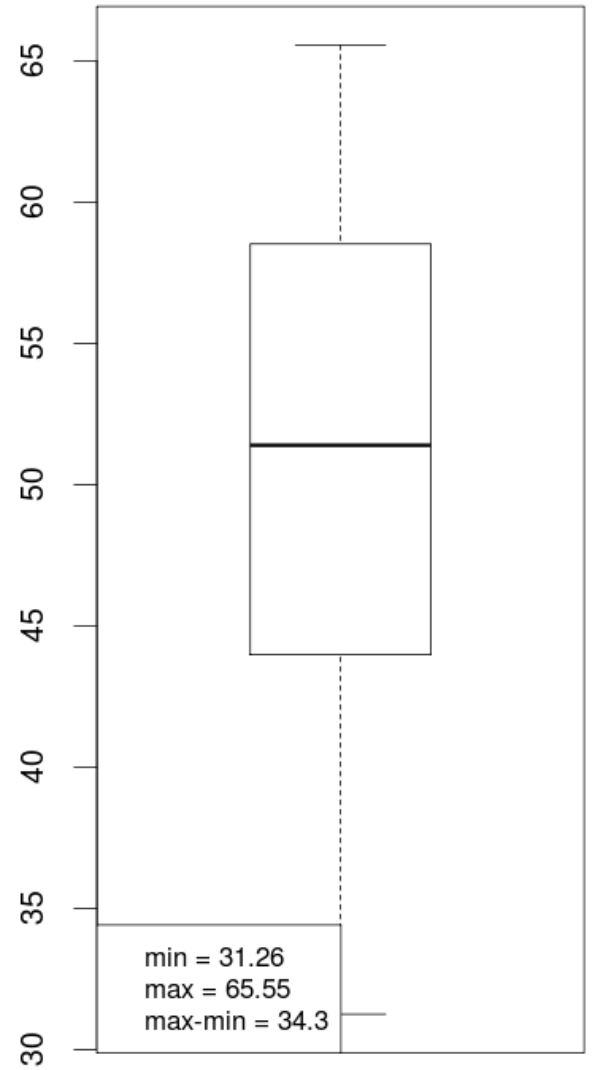
Percent present QC: not OK (spread > 10%)



# Plot of background intensity

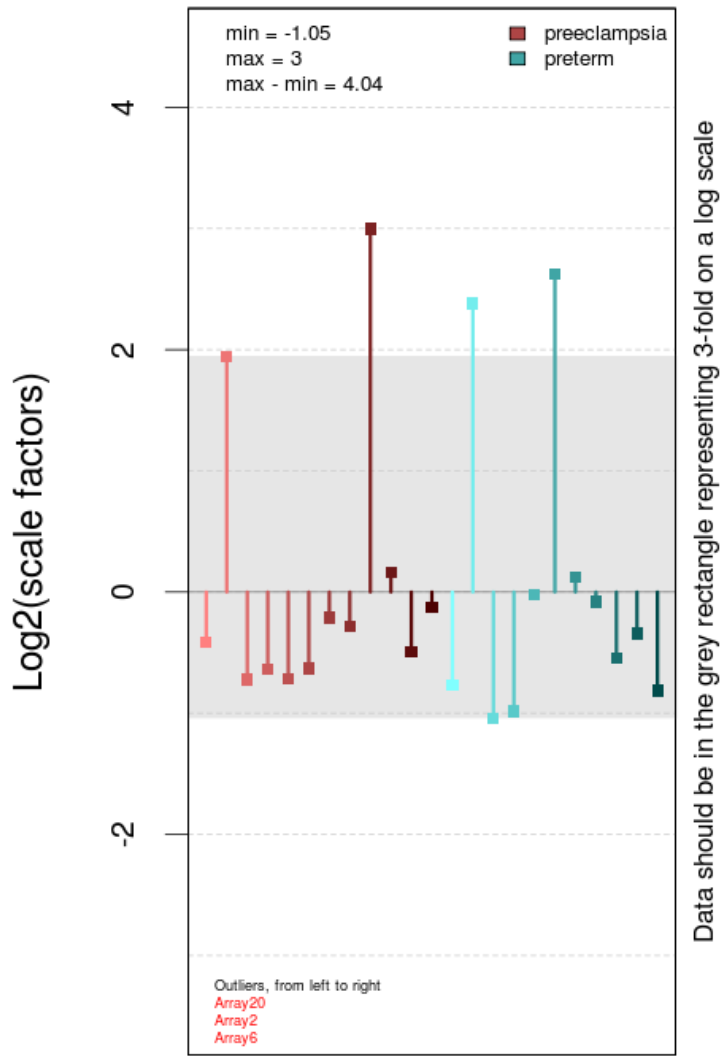


# Average background intensity

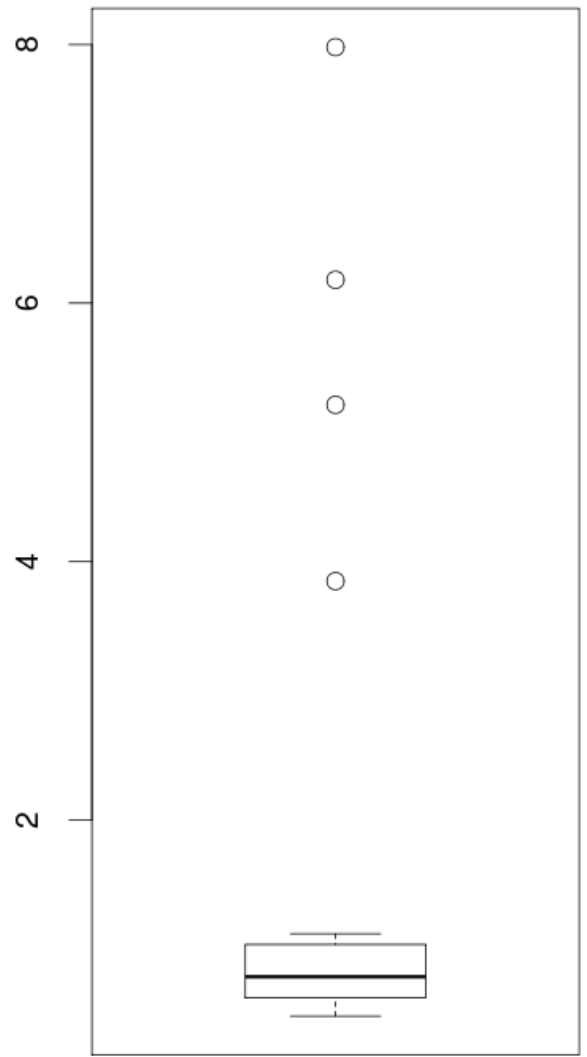


Background QC: not OK (spread > 20)

## Plot of Log scale factors

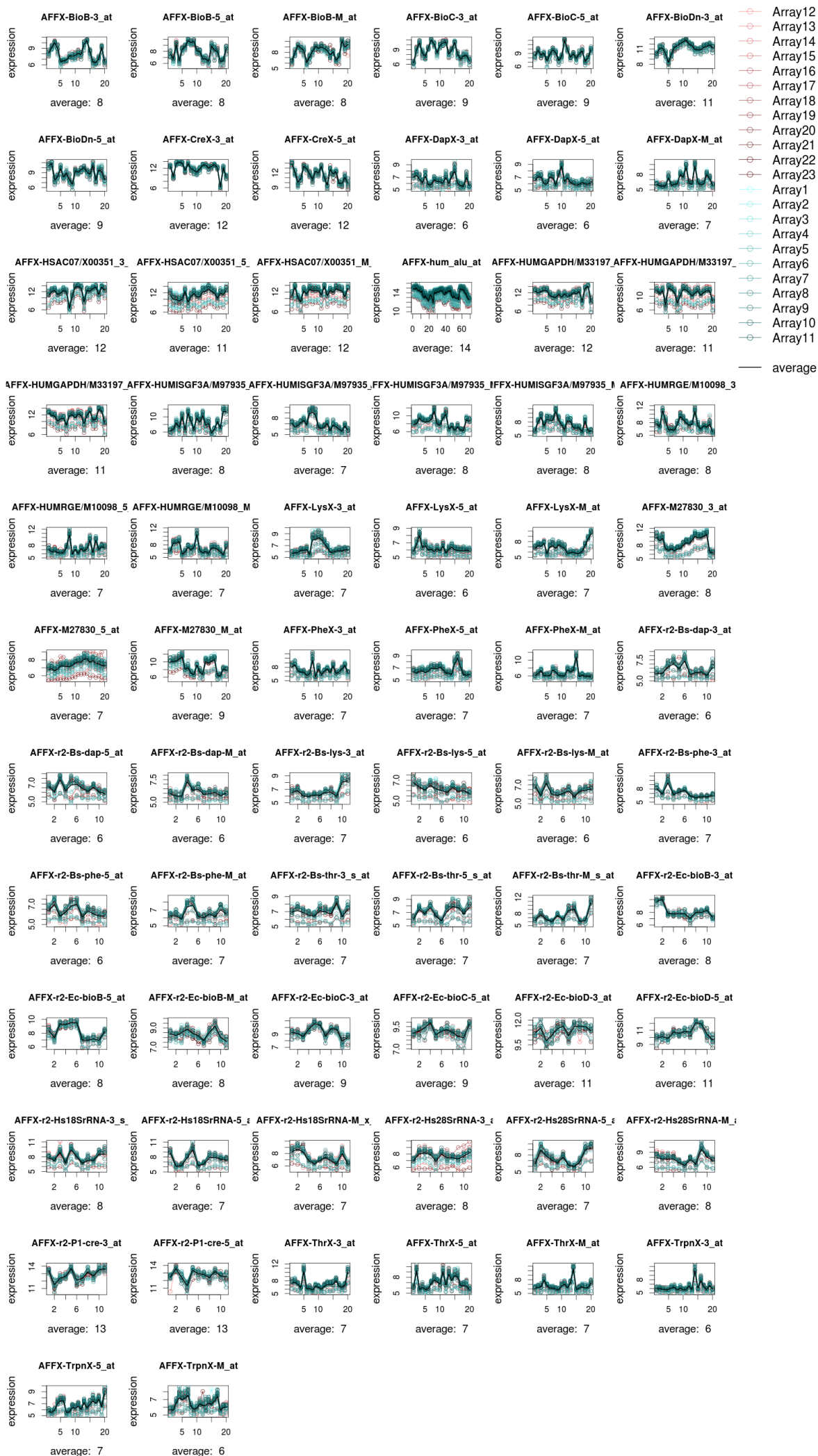


## Boxplot of scale factors (natural scale)

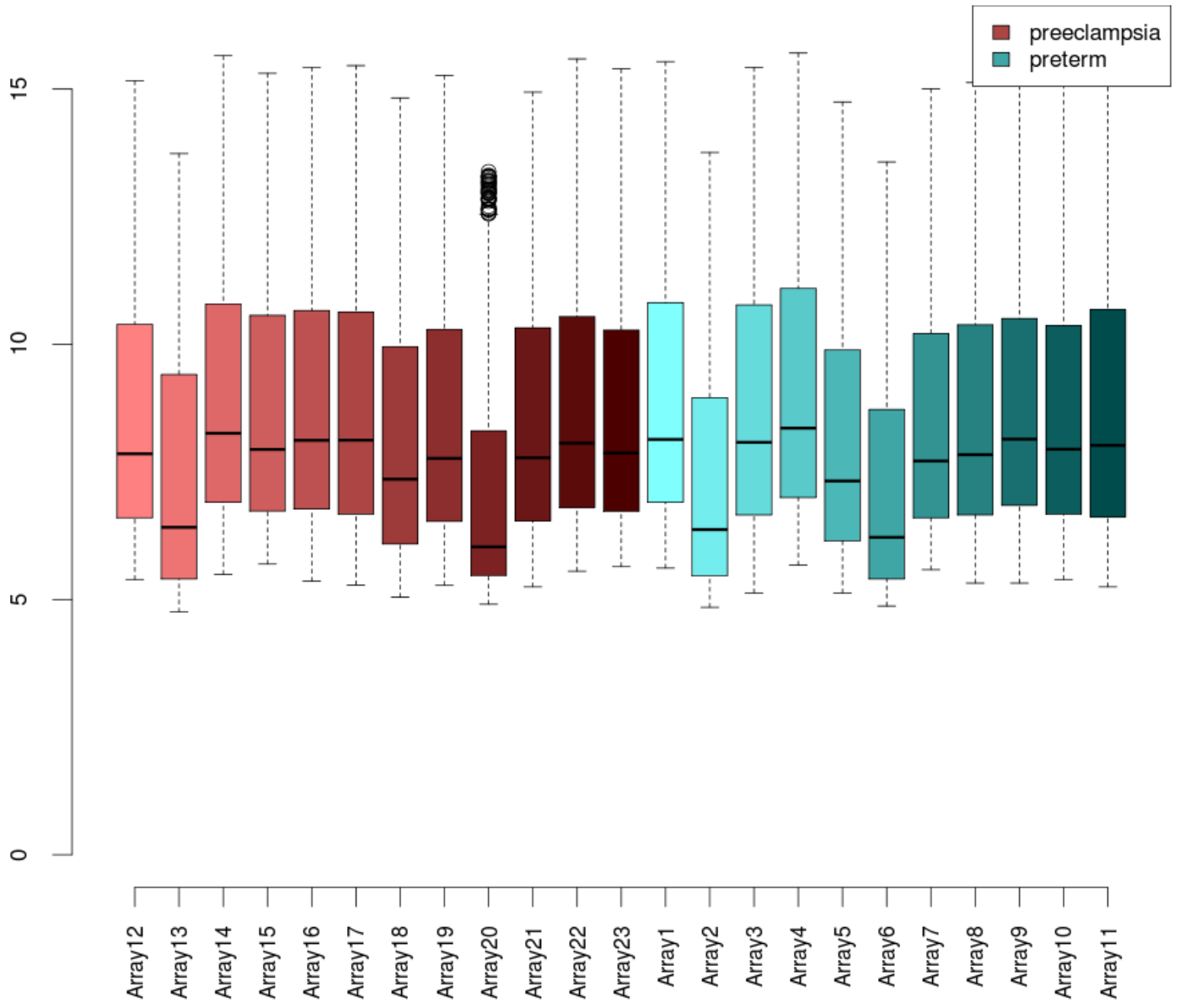


Scale factors QC: not OK (spread > 3-fold)

# affx control profiles

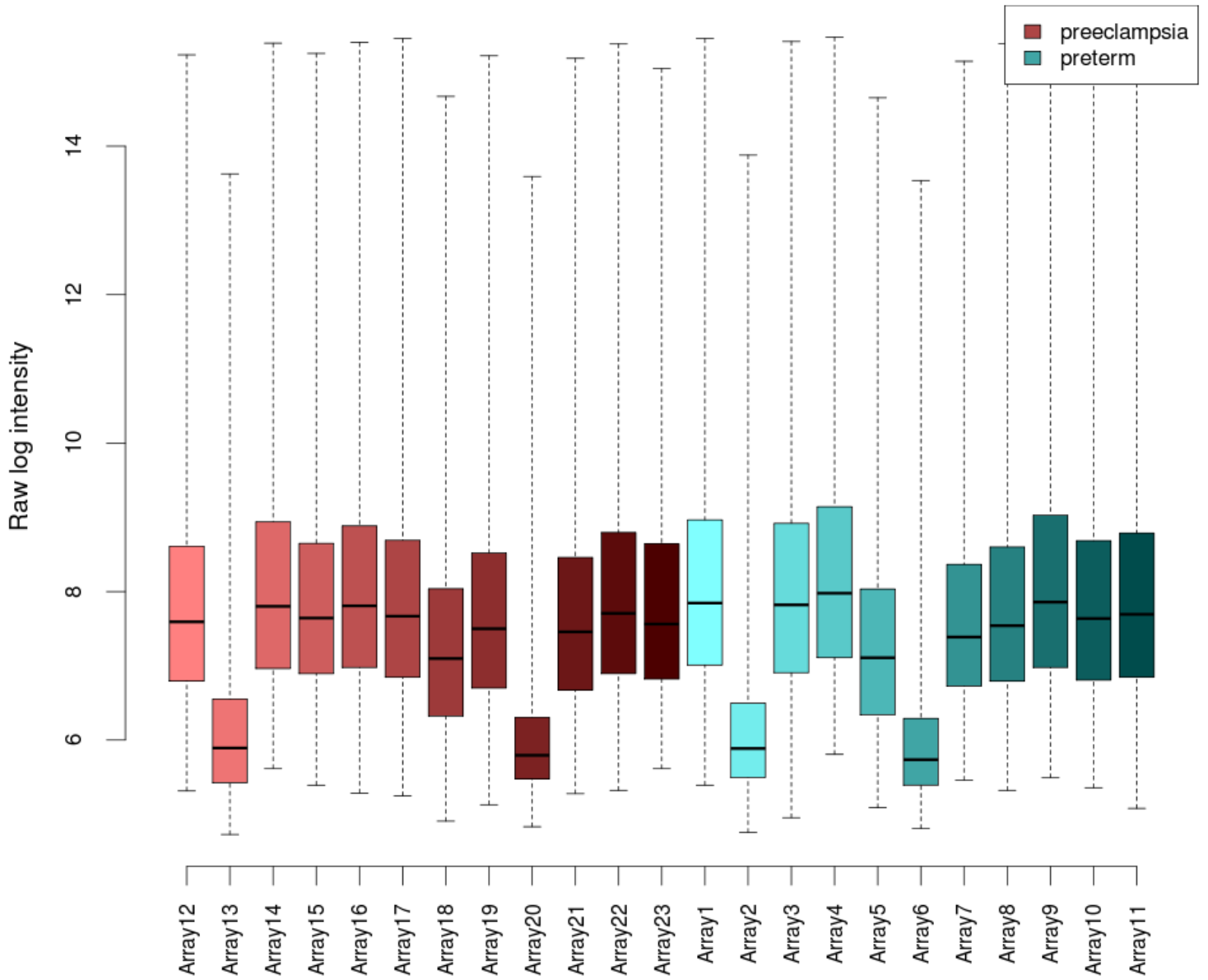


# affx controls



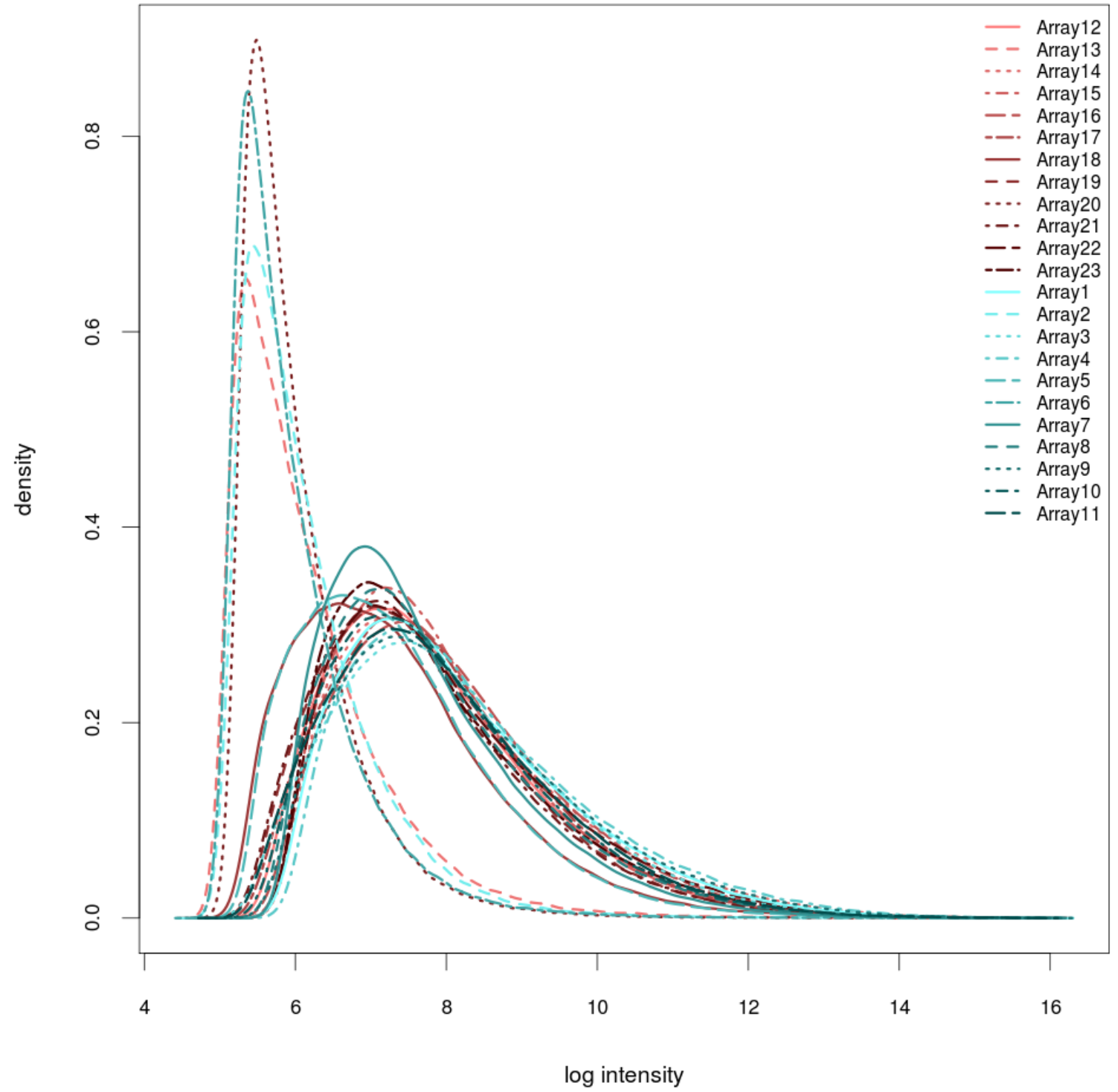
# Boxplot of raw intensities

Distributions should be comparable between arrays



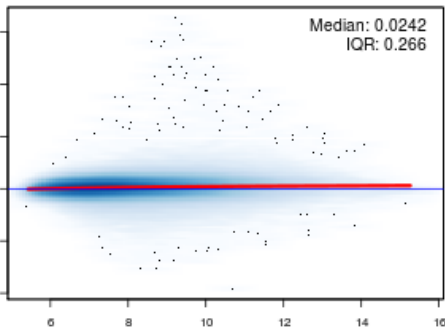
# Density histogram of raw intensities

Curves should be comparable between arrays

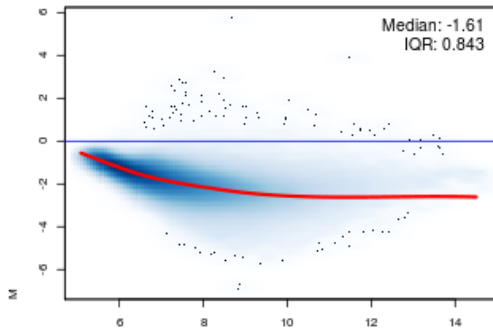


# MA plots of raw data 1 / 2

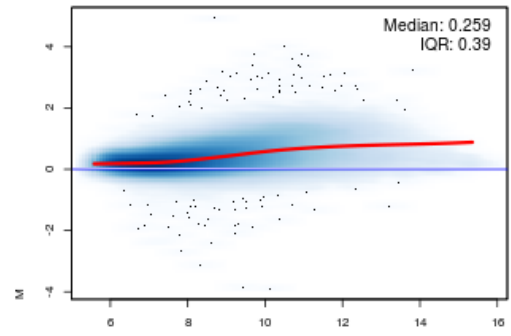
Array12 vs pseudo-median reference chip



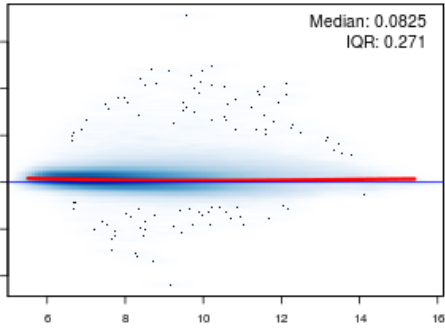
Array13 vs pseudo-median reference chip



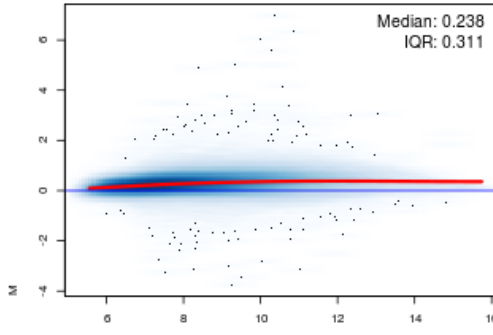
Array14 vs pseudo-median reference chip



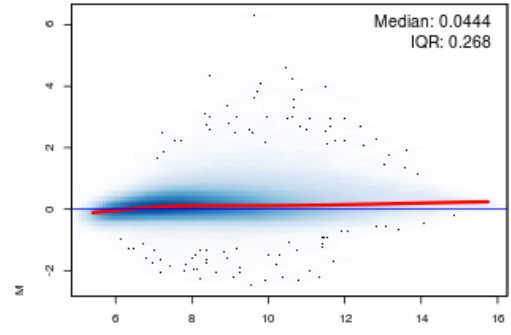
Array15 vs pseudo-median reference chip



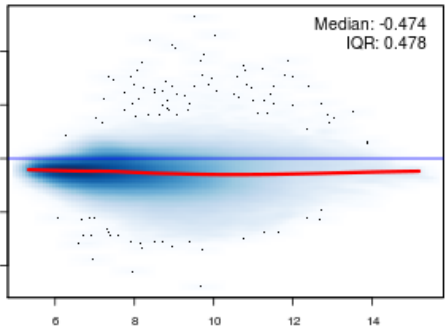
Array16 vs pseudo-median reference chip



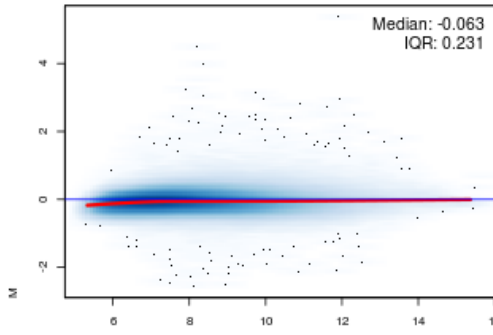
Array17 vs pseudo-median reference chip



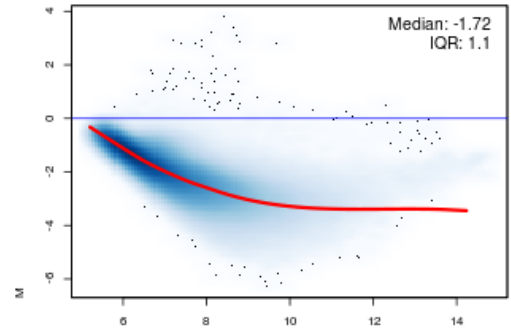
Array18 vs pseudo-median reference chip



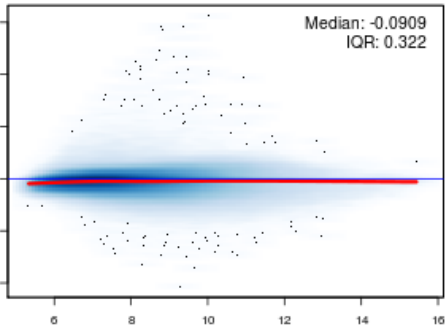
Array19 vs pseudo-median reference chip



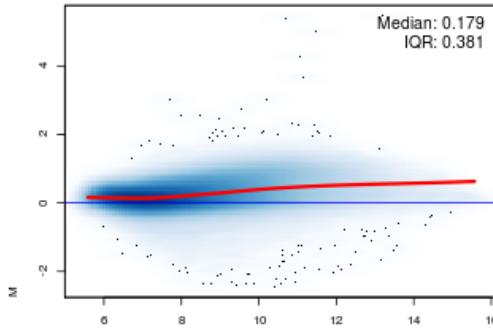
Array20 vs pseudo-median reference chip



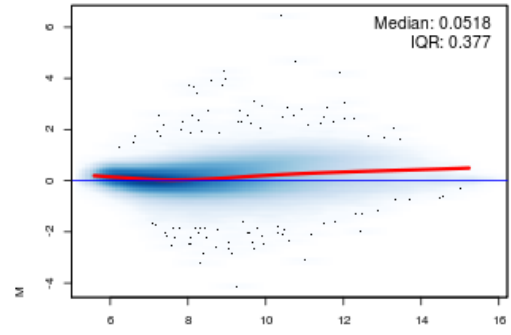
Array21 vs pseudo-median reference chip



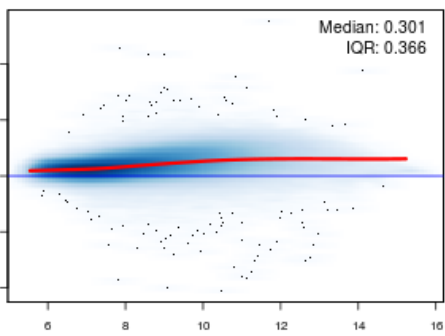
Array22 vs pseudo-median reference chip



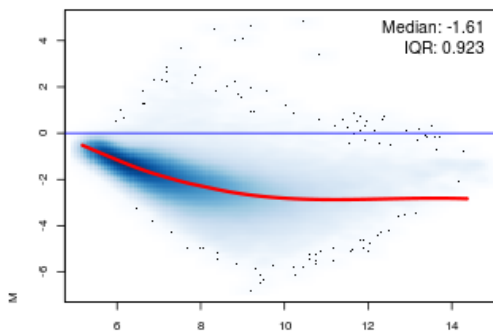
Array23 vs pseudo-median reference chip



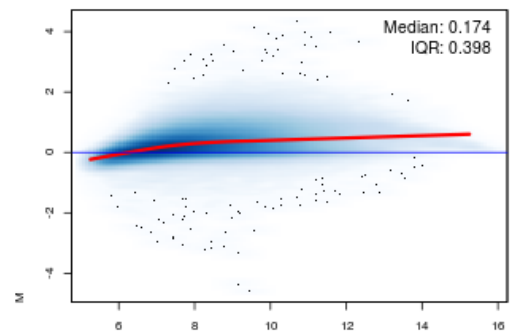
Array1 vs pseudo-median reference chip



Array2 vs pseudo-median reference chip

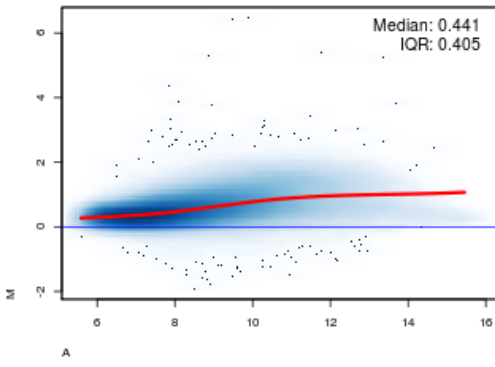


Array3 vs pseudo-median reference chip

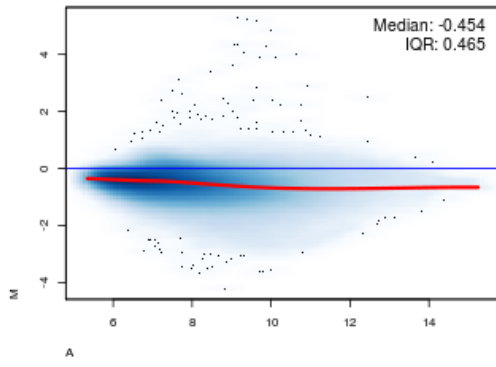


# MA plots of raw data 2 / 2

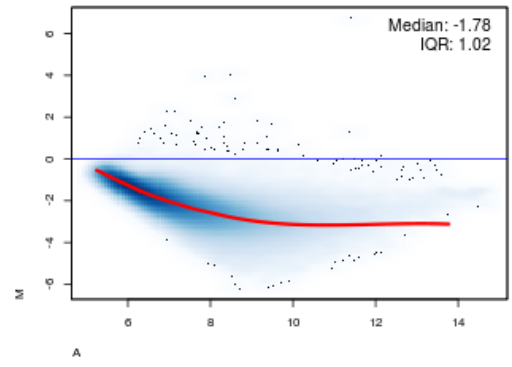
Array4 vs pseudo-median reference chip



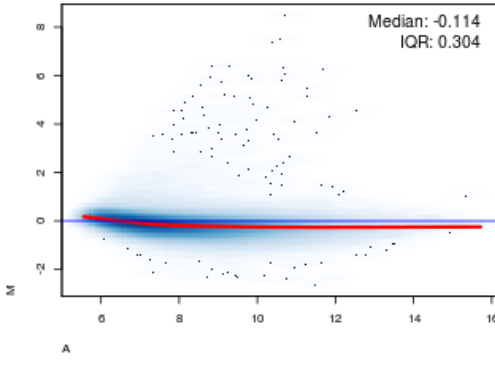
Array5 vs pseudo-median reference chip



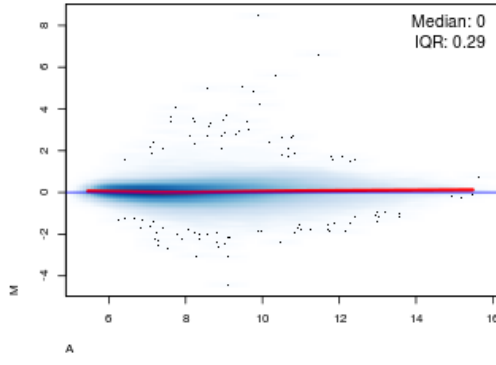
Array6 vs pseudo-median reference chip



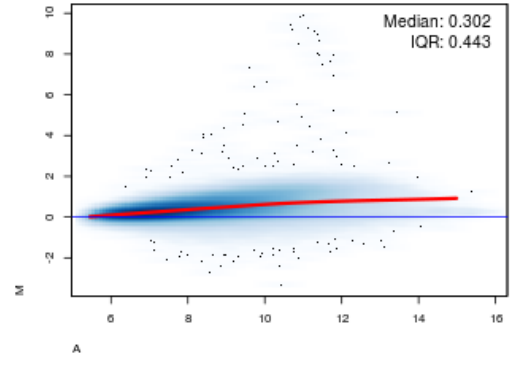
Array7 vs pseudo-median reference chip



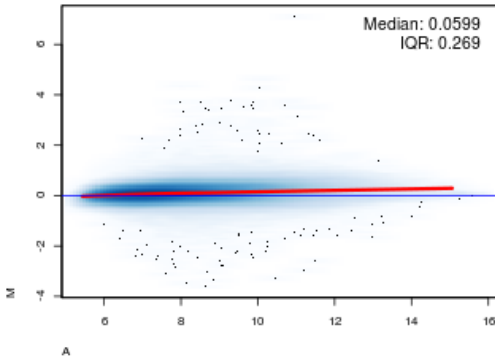
Array8 vs pseudo-median reference chip



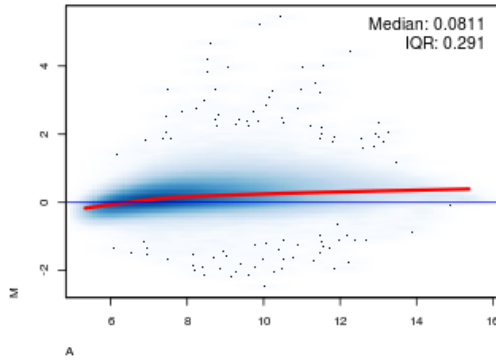
Array9 vs pseudo-median reference chip



Array10 vs pseudo-median reference chip



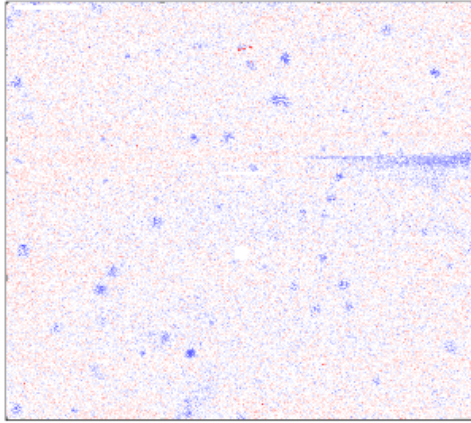
Array11 vs pseudo-median reference chip



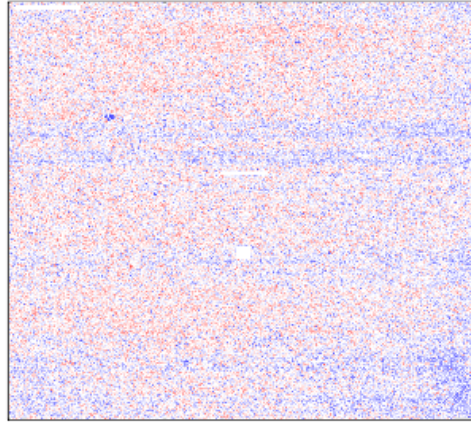


# 2D virtual PLM image for model characteristic: resid 1 / 2

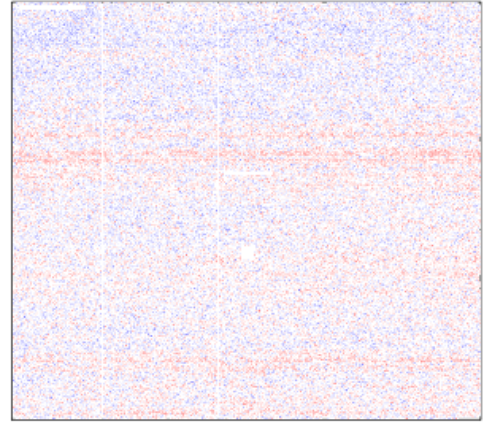
Array12



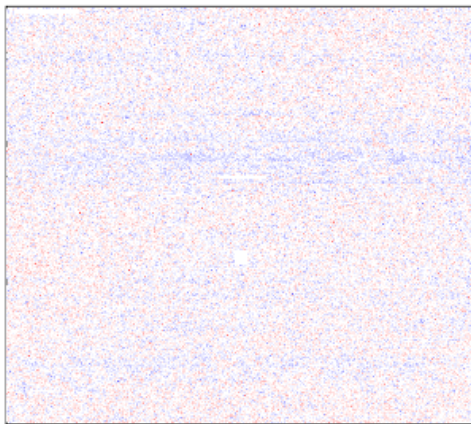
Array13



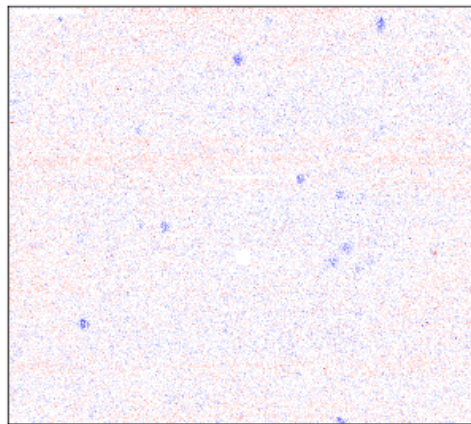
Array14



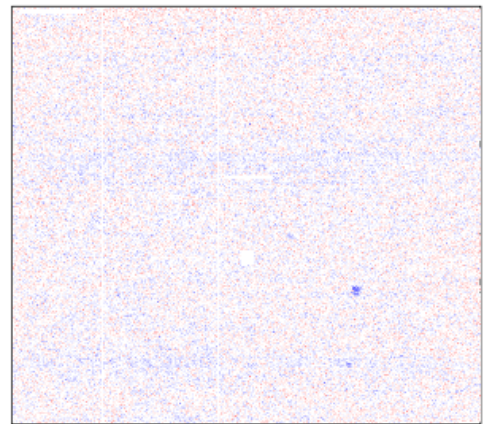
Array15



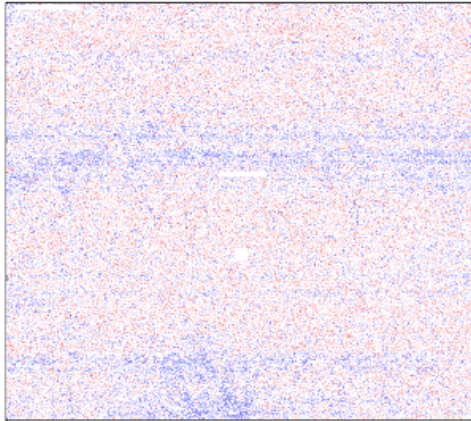
Array16



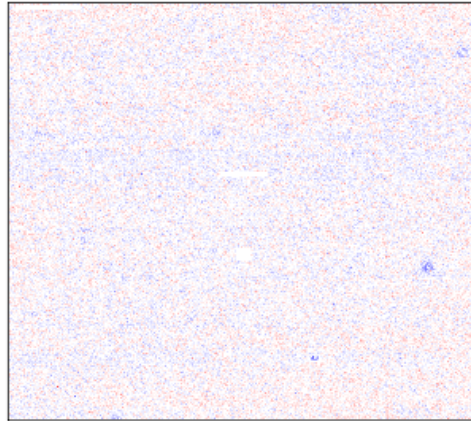
Array17



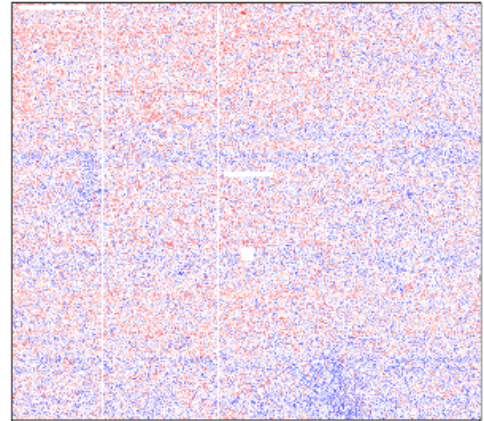
Array18



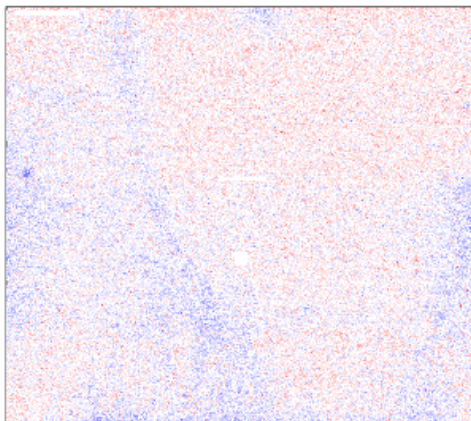
Array19



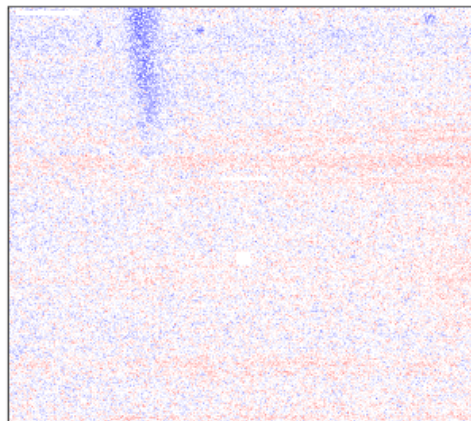
Array20



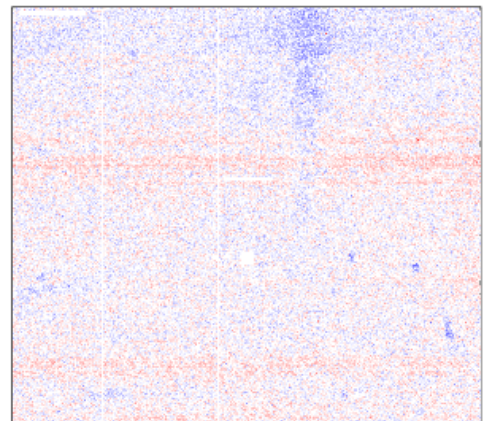
Array21



Array22

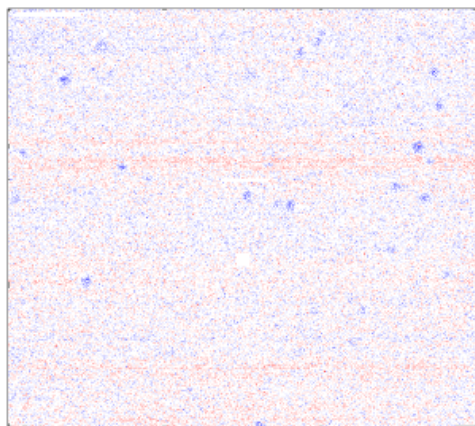


Array23

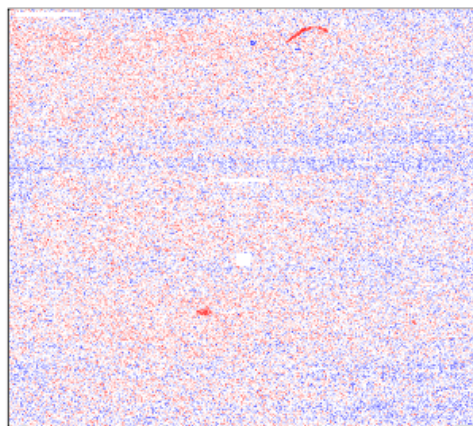


## 2D virtual PLM image for model characteristic: resid 2 / 2

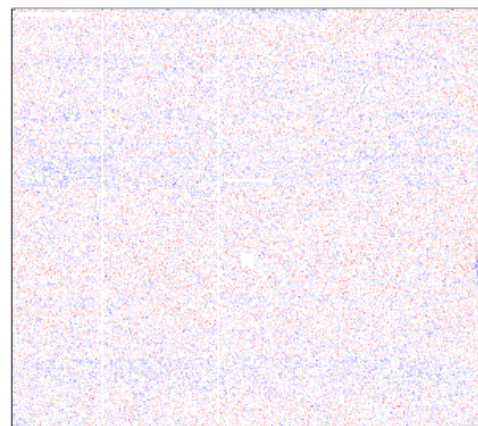
Array1



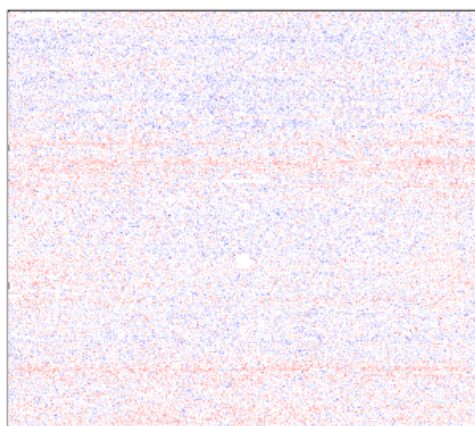
Array2



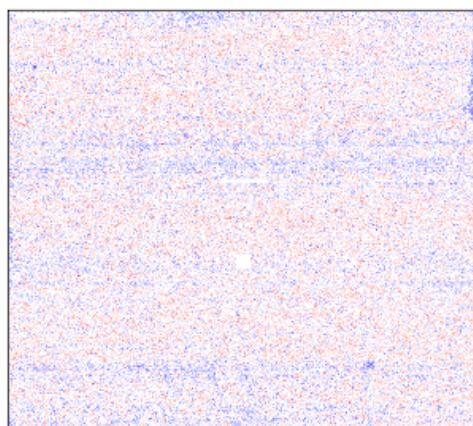
Array3



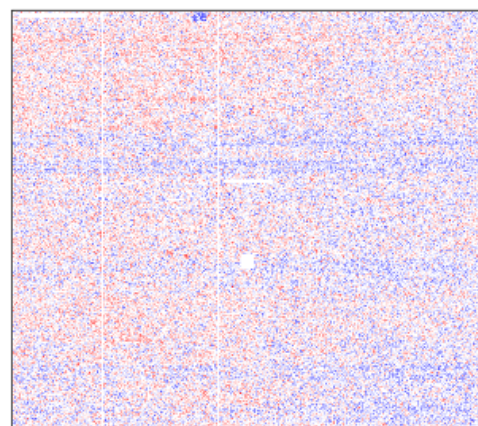
Array4



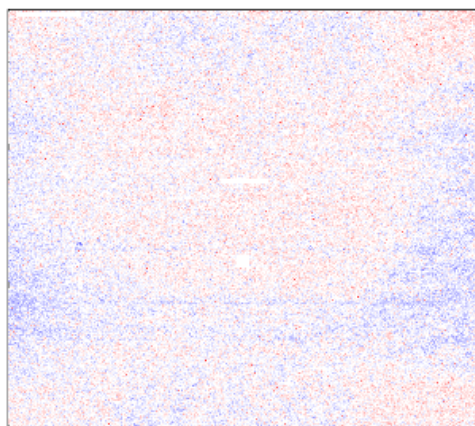
Array5



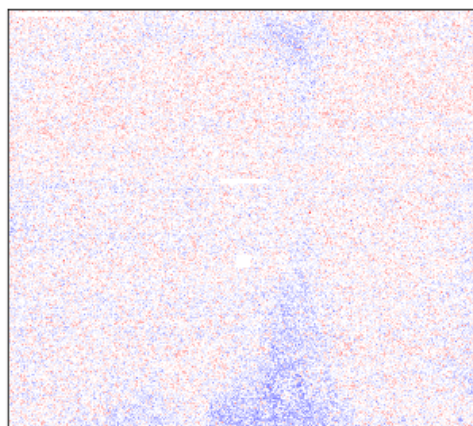
Array6



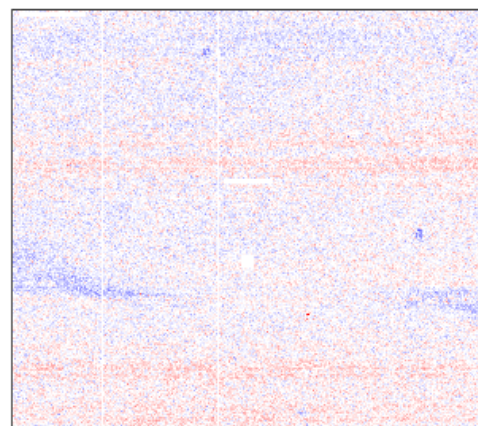
Array7



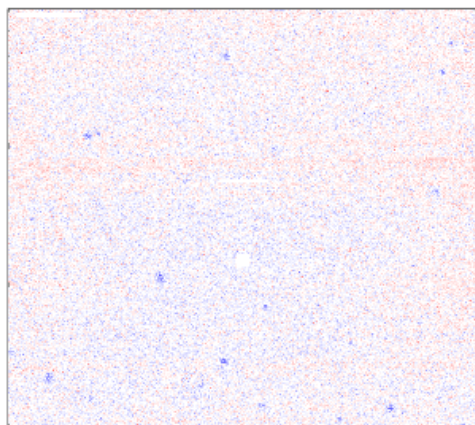
Array8



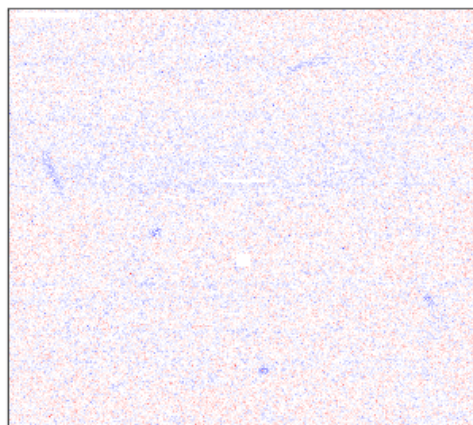
Array9



Array10

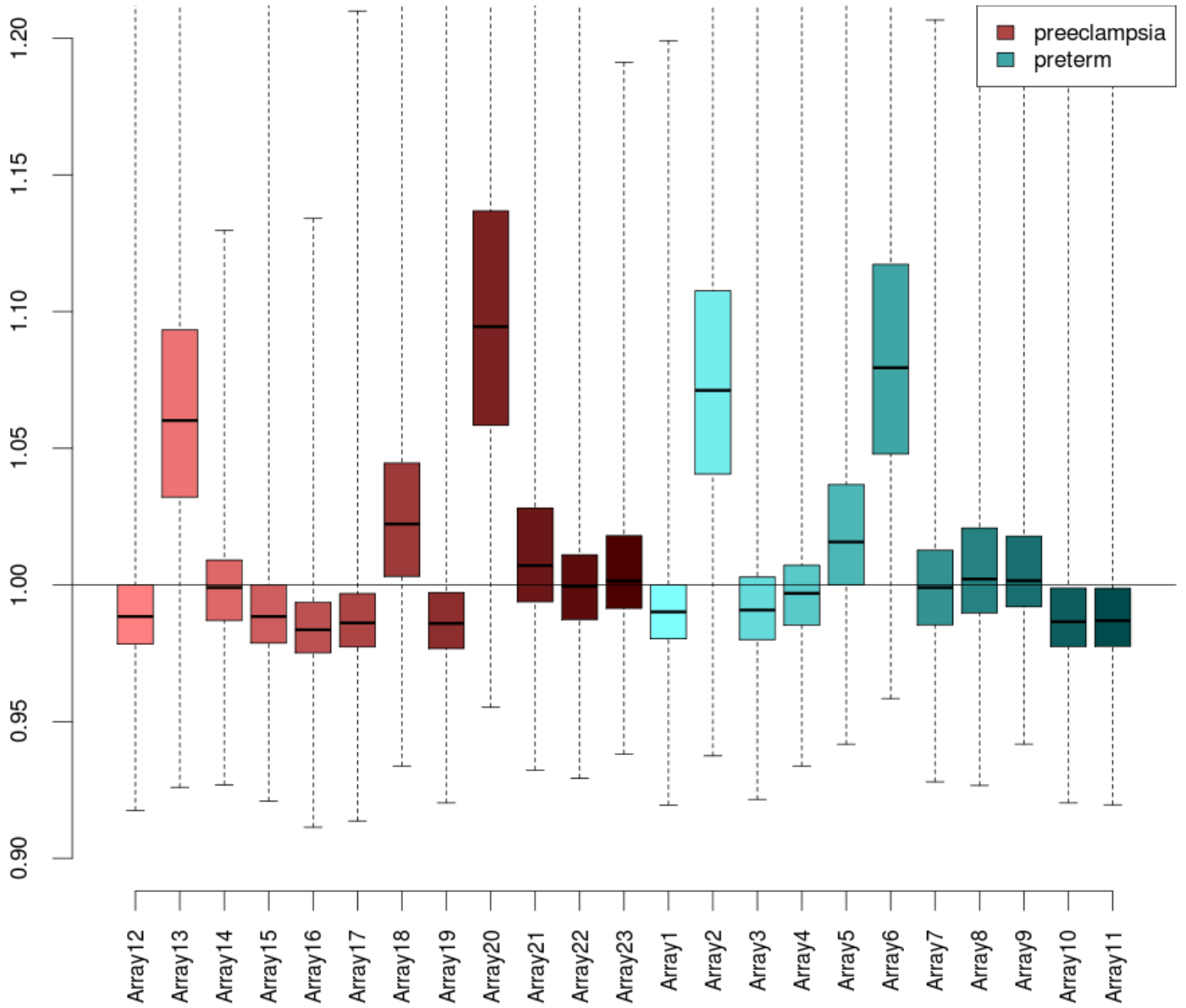


Array11



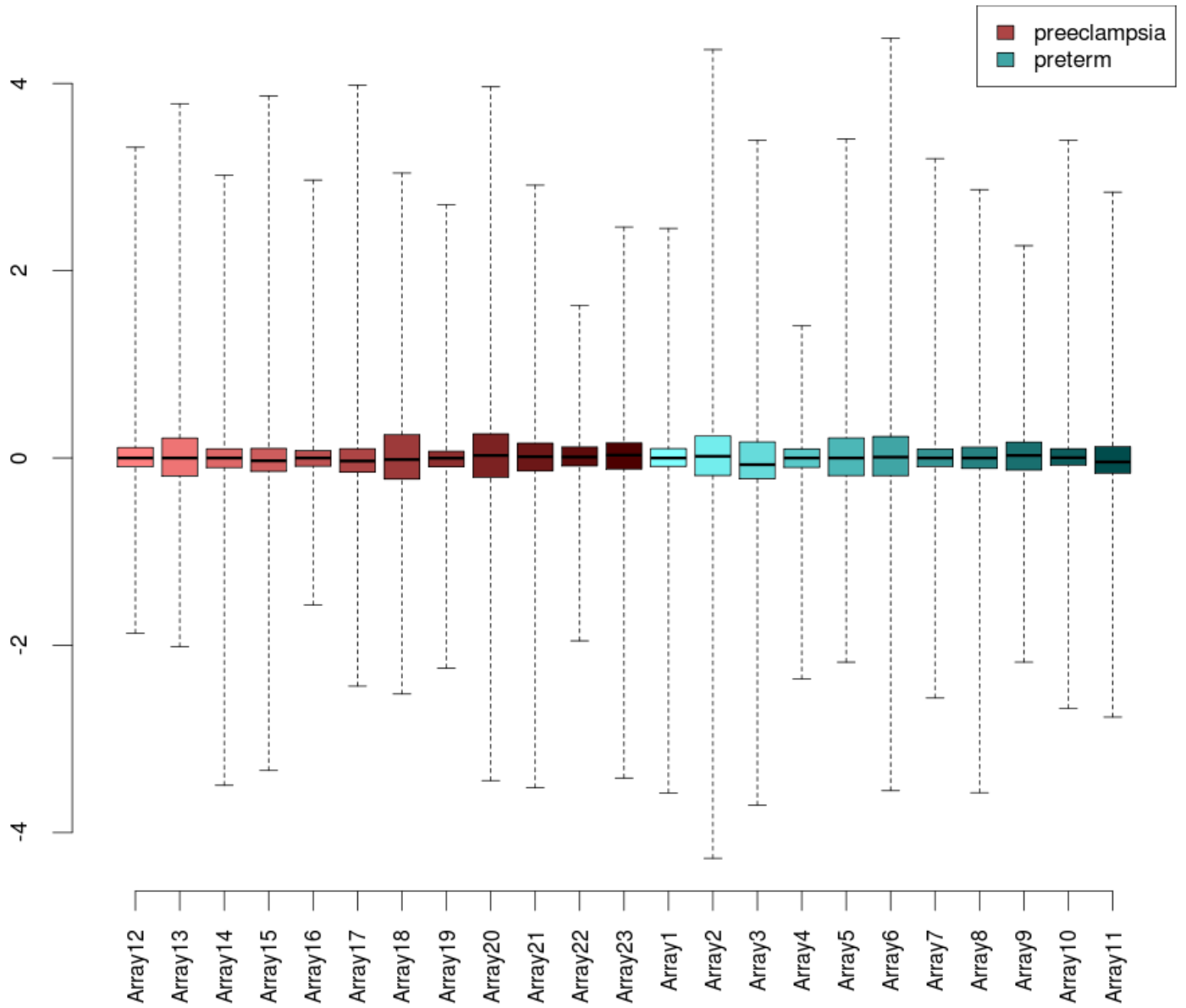
# Normalized Unscaled Standard Errors (NUSE)

NUSE median value should be < 1.1



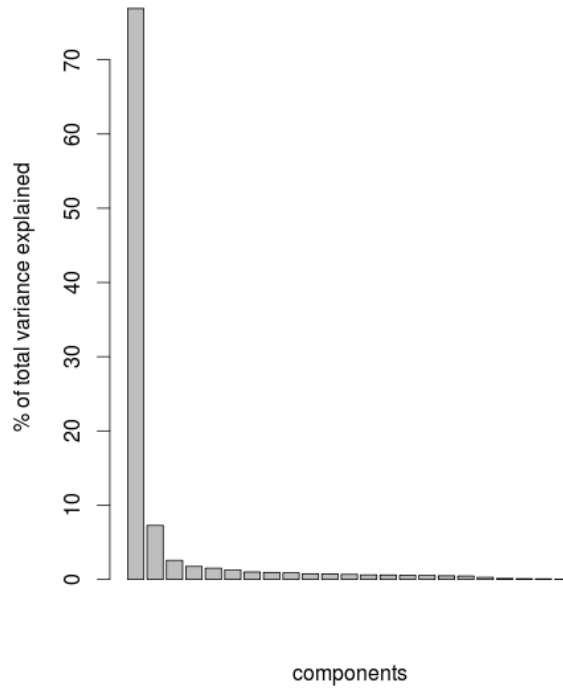
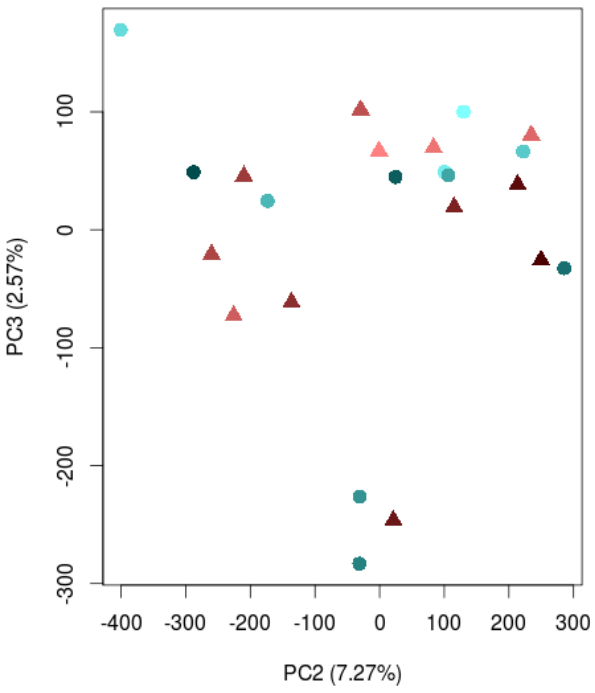
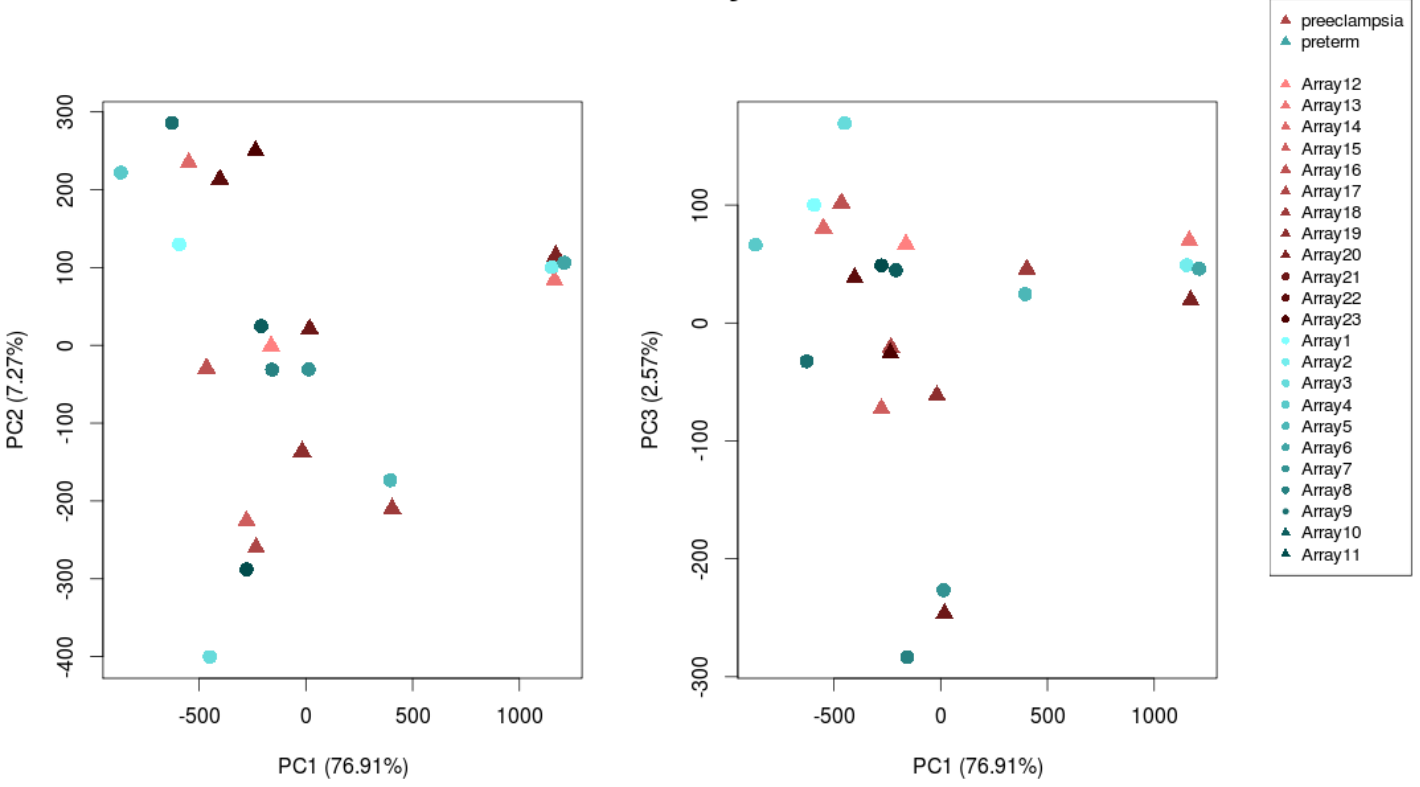
# Relative Log Expression (RLE)

RLE distributions should be centered around 0

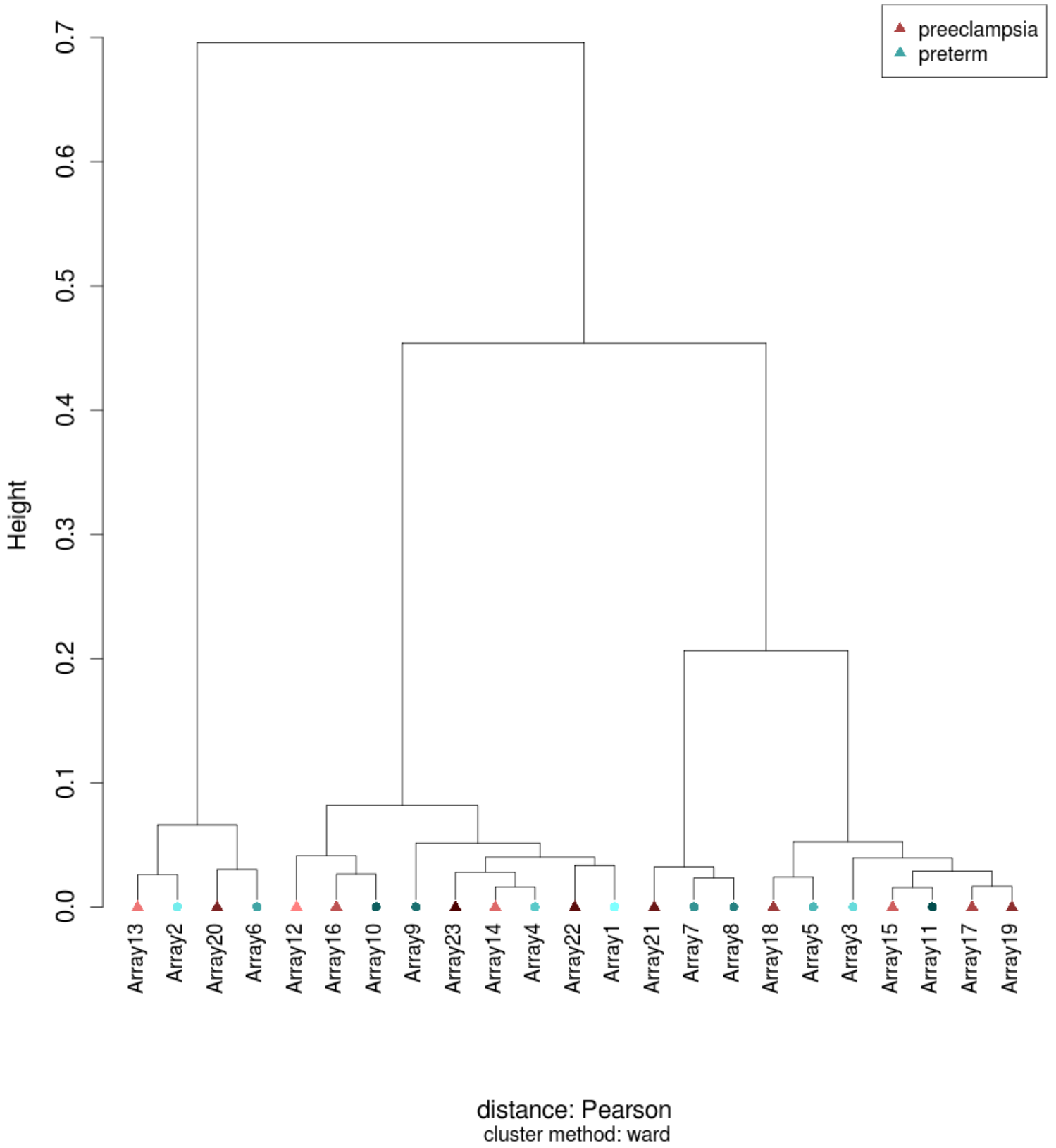




# PCA analysis of Raw data

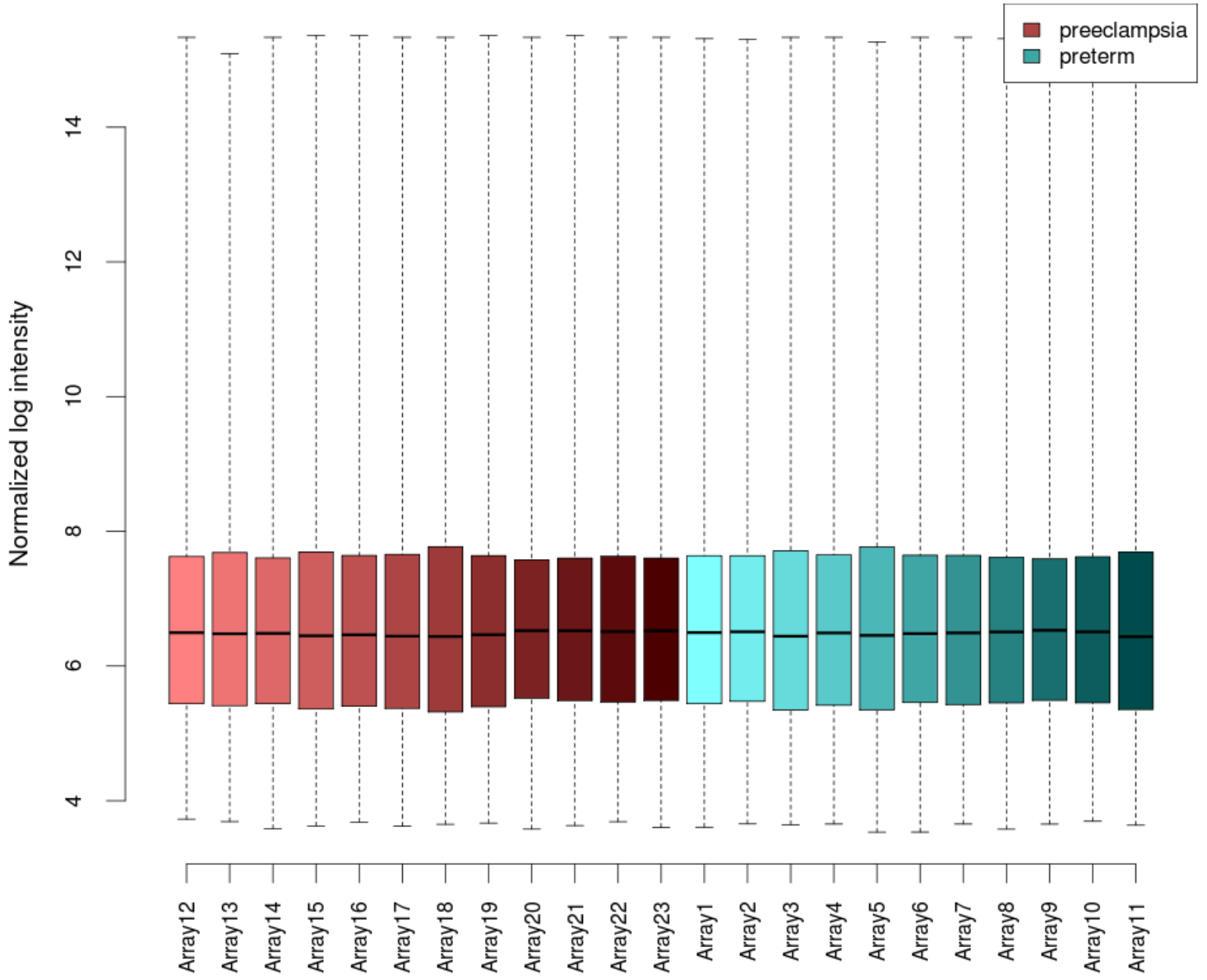


# Cluster dendrogram of raw data



# Boxplot after RMA

Distributions should be comparable between arrays





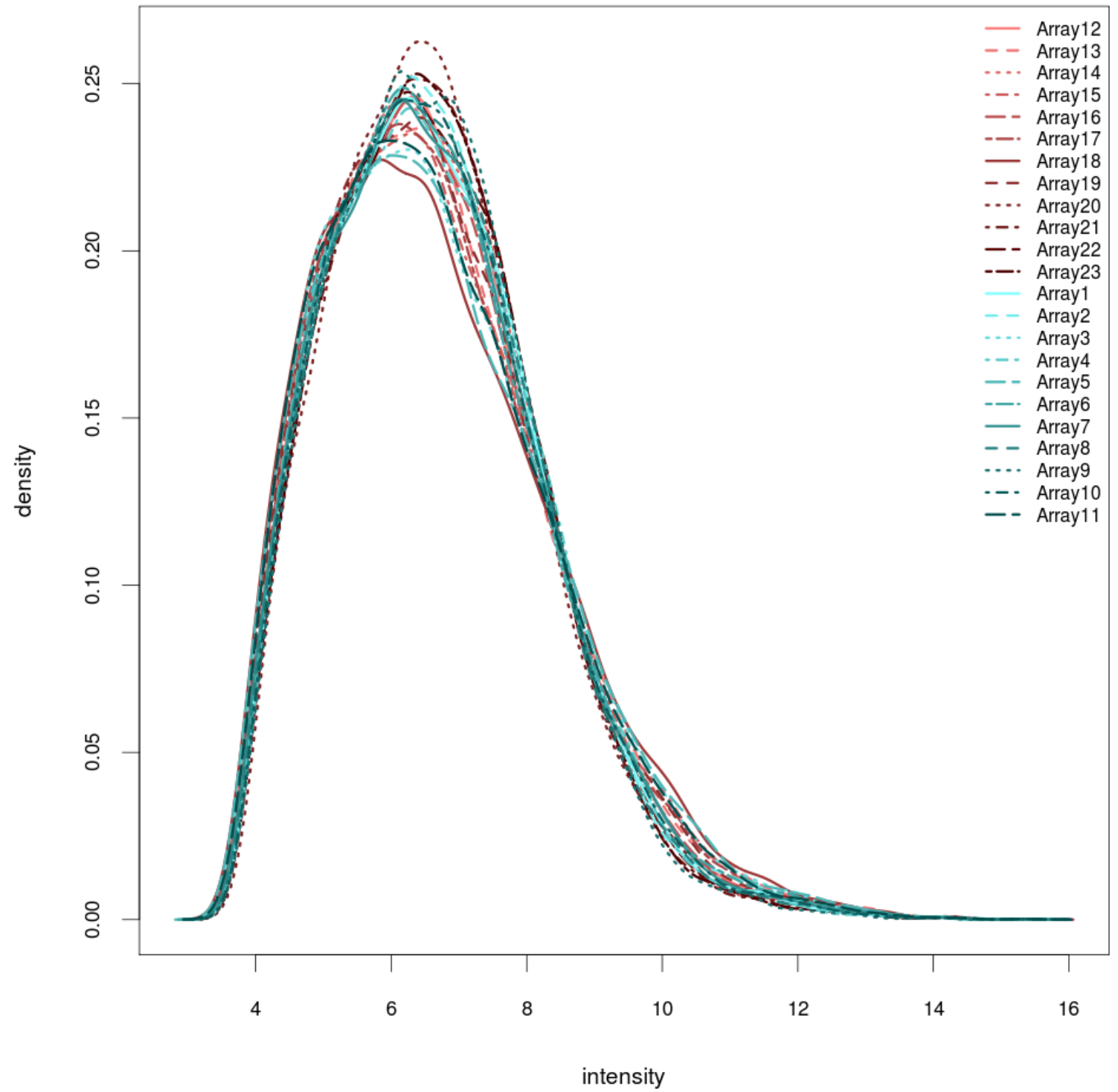
## Pre-processing of Raw Data

Method: RMA

Annotation: hgu133a\_Hs\_ENSG

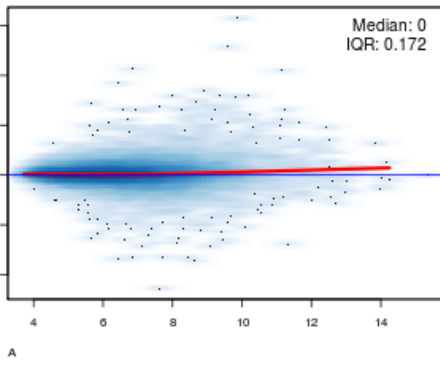
# Density histogram after RMA

Curves should be comparable between arrays

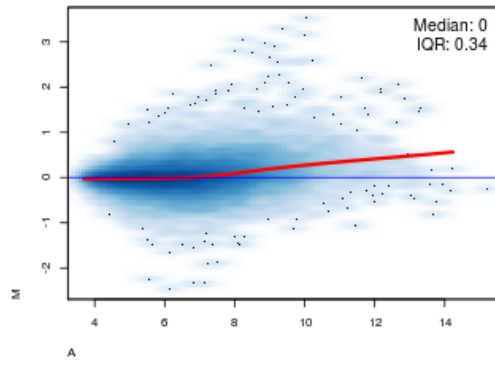


# MA plots after RMA normalization 1 / 2

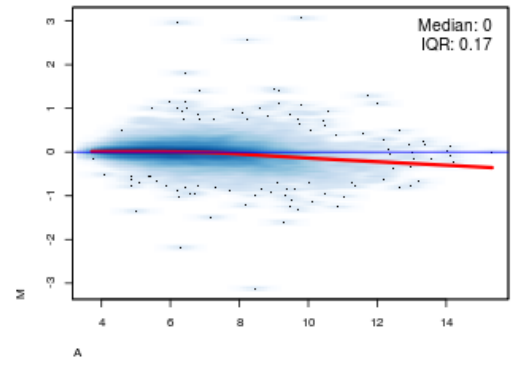
Array12 vs pseudo-median reference chip



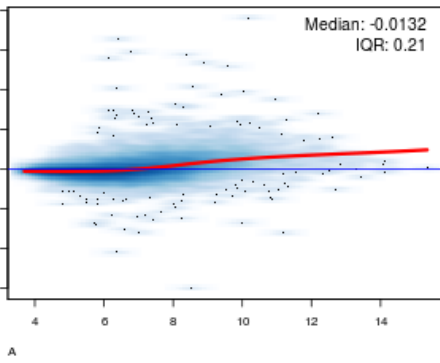
Array13 vs pseudo-median reference chip



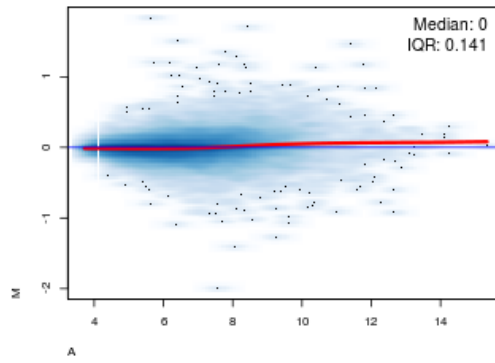
Array14 vs pseudo-median reference chip



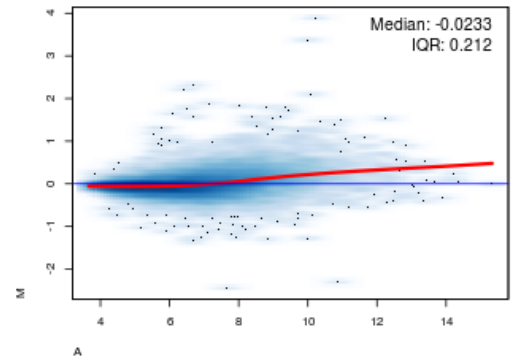
Array15 vs pseudo-median reference chip



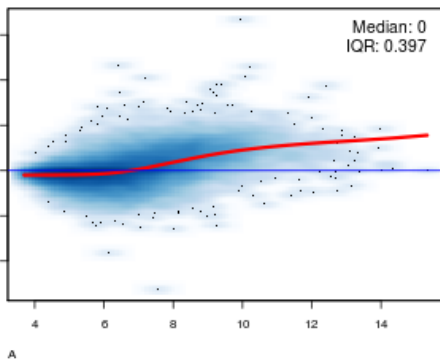
Array16 vs pseudo-median reference chip



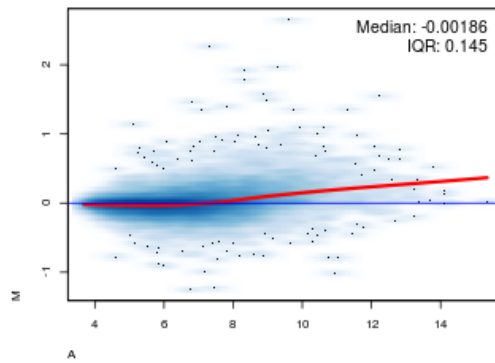
Array17 vs pseudo-median reference chip



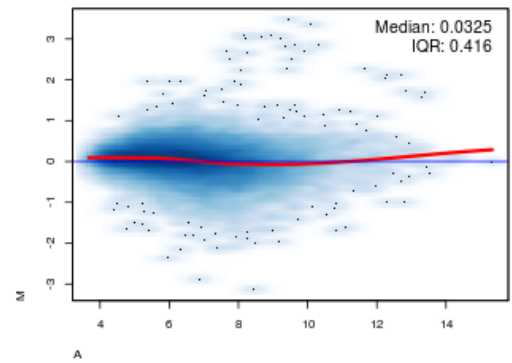
Array18 vs pseudo-median reference chip



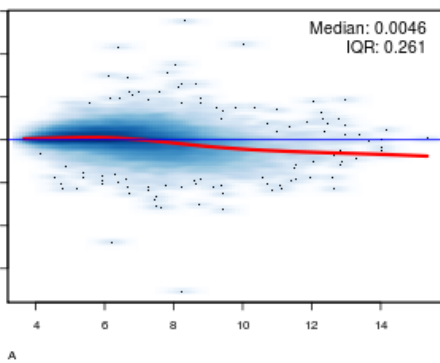
Array19 vs pseudo-median reference chip



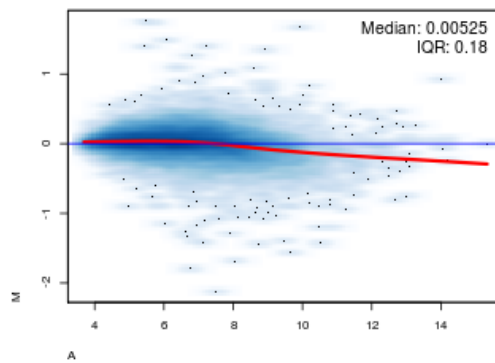
Array20 vs pseudo-median reference chip



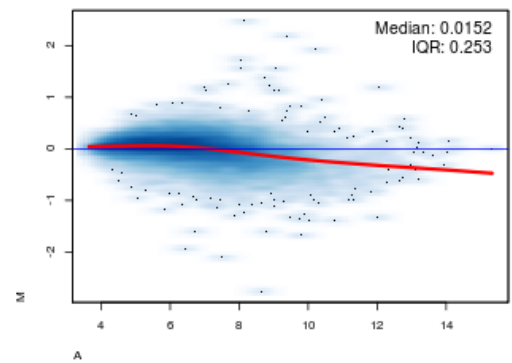
Array21 vs pseudo-median reference chip



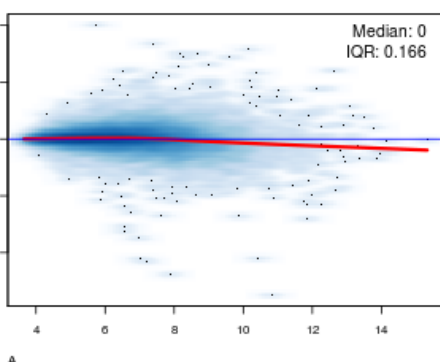
Array22 vs pseudo-median reference chip



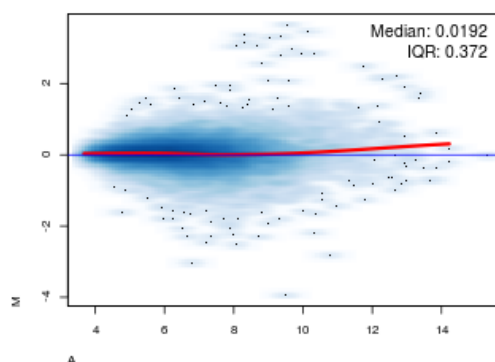
Array23 vs pseudo-median reference chip



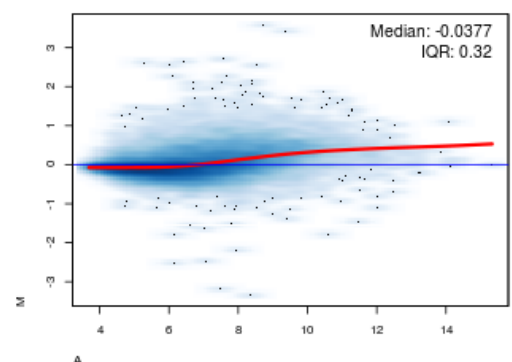
Array1 vs pseudo-median reference chip



Array2 vs pseudo-median reference chip

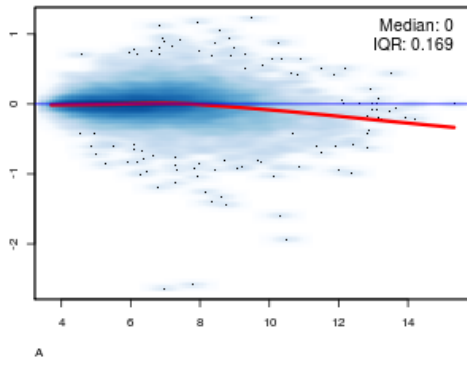


Array3 vs pseudo-median reference chip

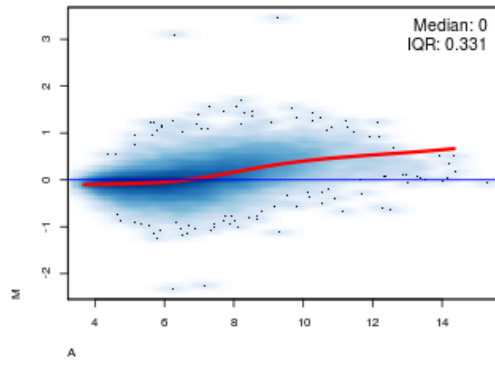


# MA plots after RMA normalization 2 / 2

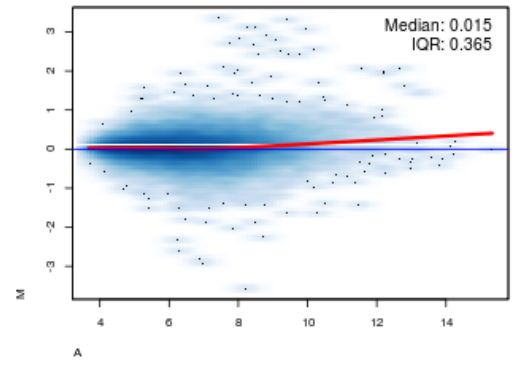
Array4 vs pseudo-median reference chip



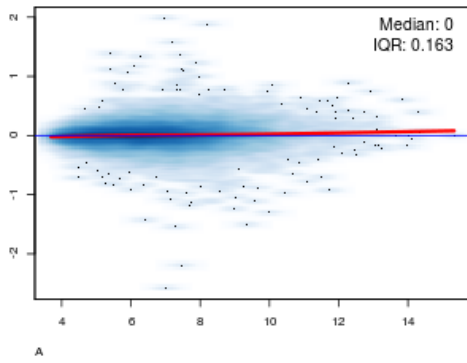
Array5 vs pseudo-median reference chip



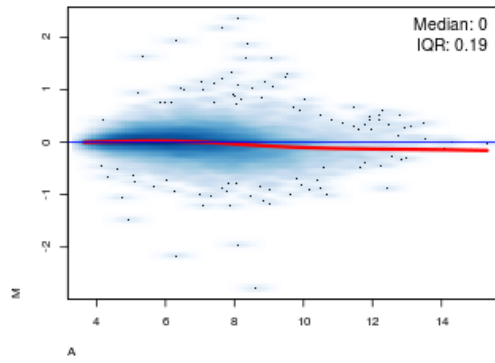
Array6 vs pseudo-median reference chip



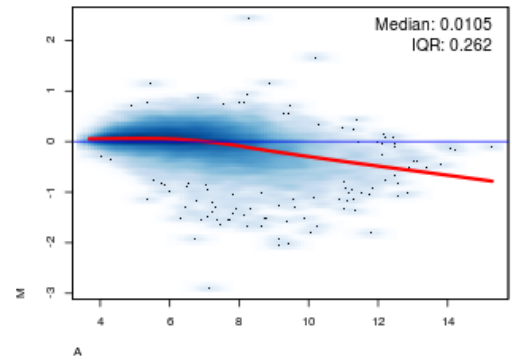
Array7 vs pseudo-median reference chip



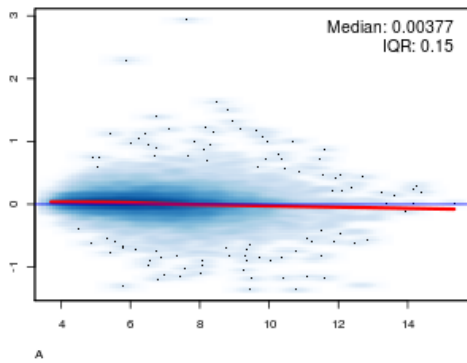
Array8 vs pseudo-median reference chip



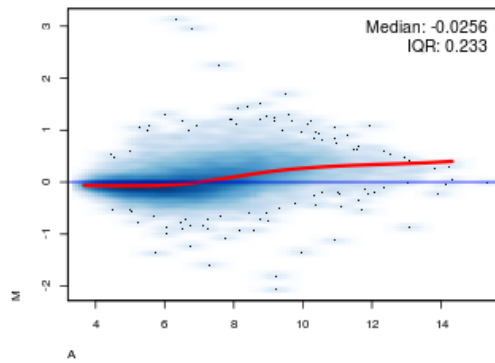
Array9 vs pseudo-median reference chip



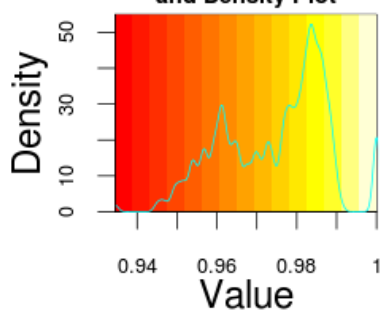
Array10 vs pseudo-median reference chip



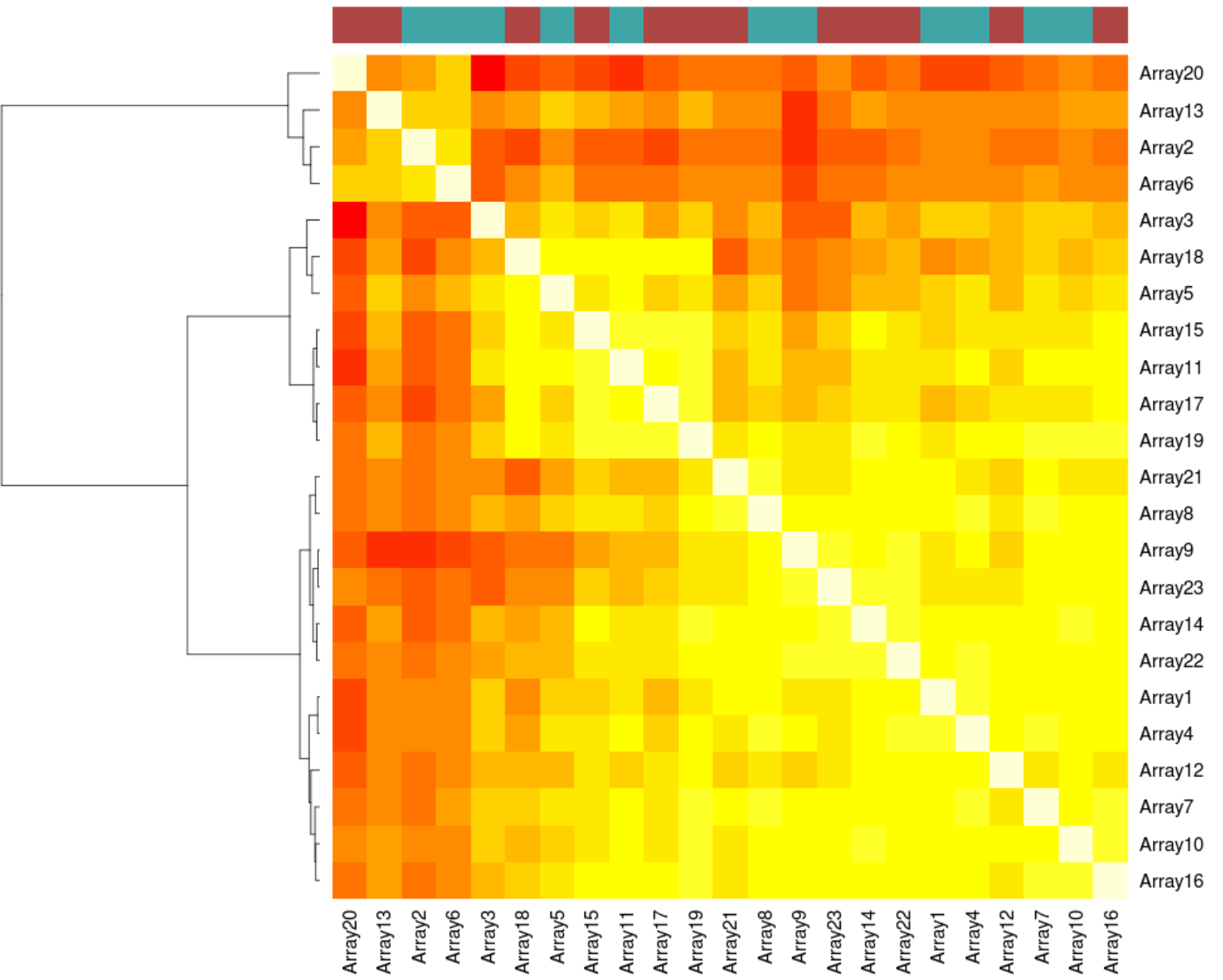
Array11 vs pseudo-median reference chip



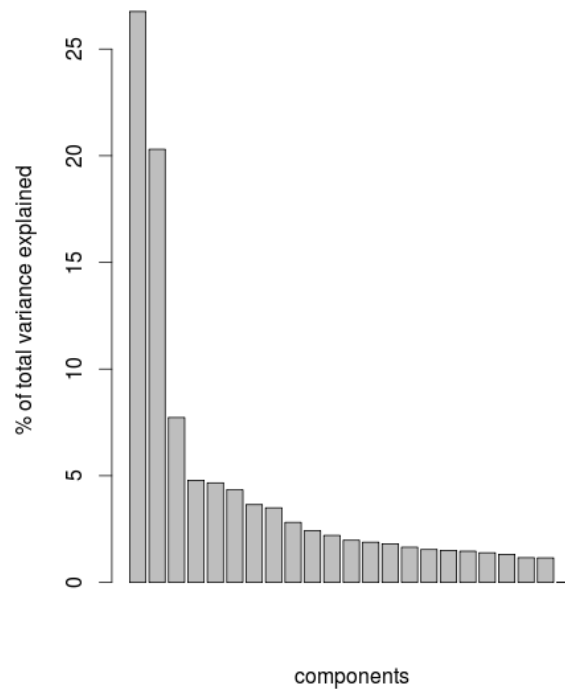
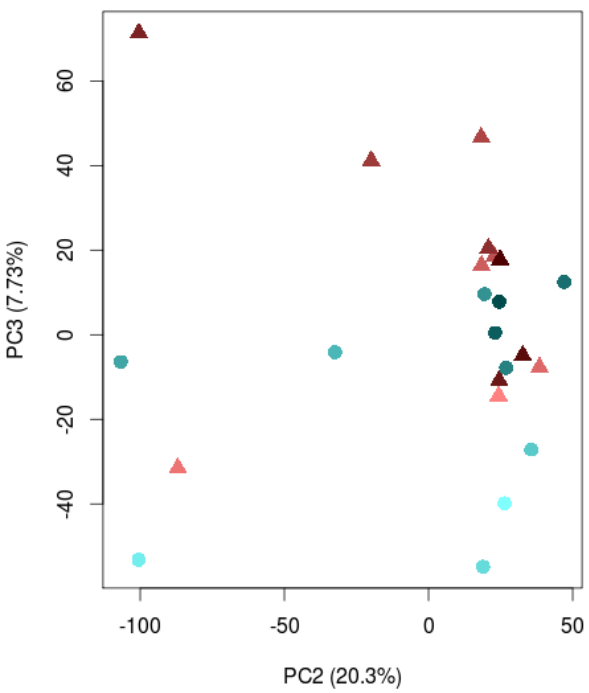
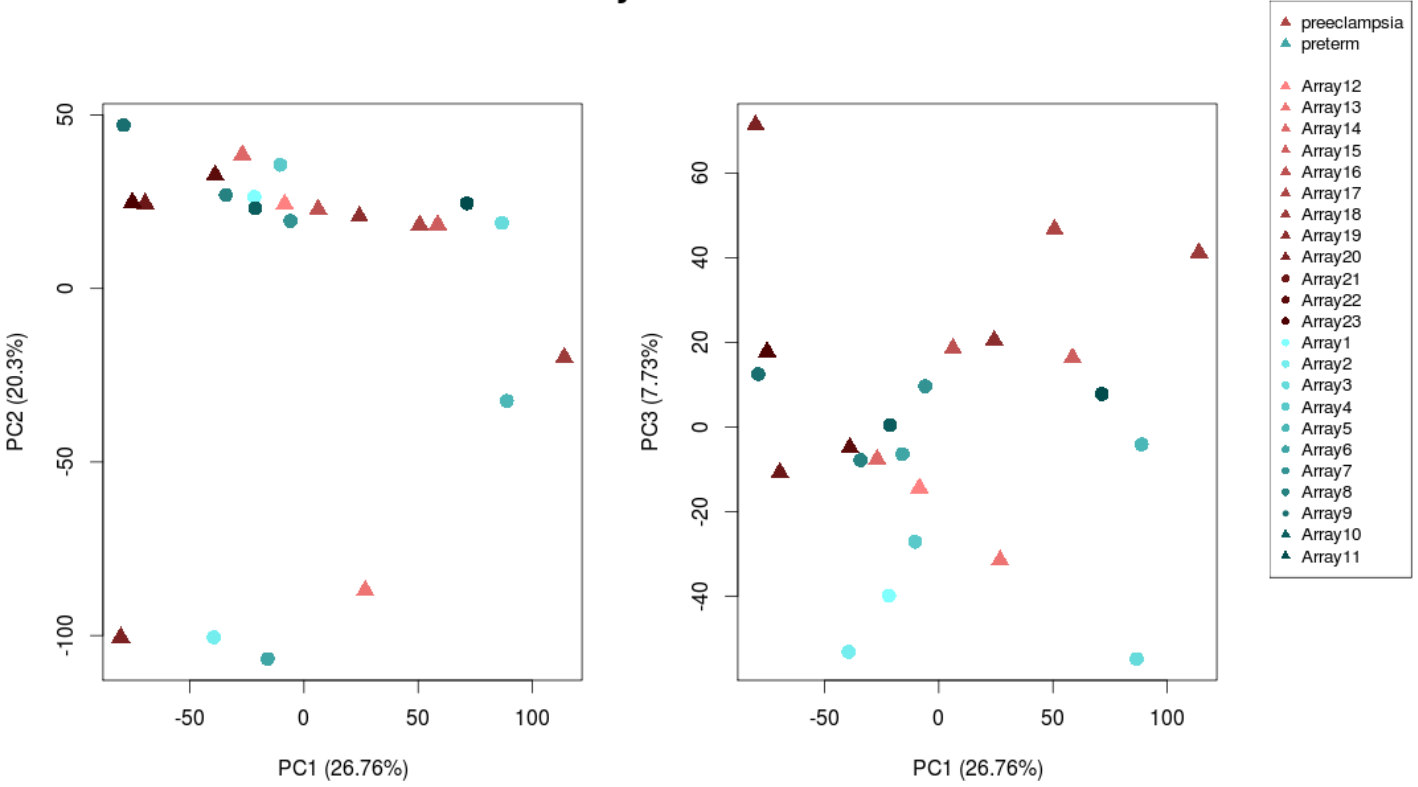
Color Key  
and Density Plot



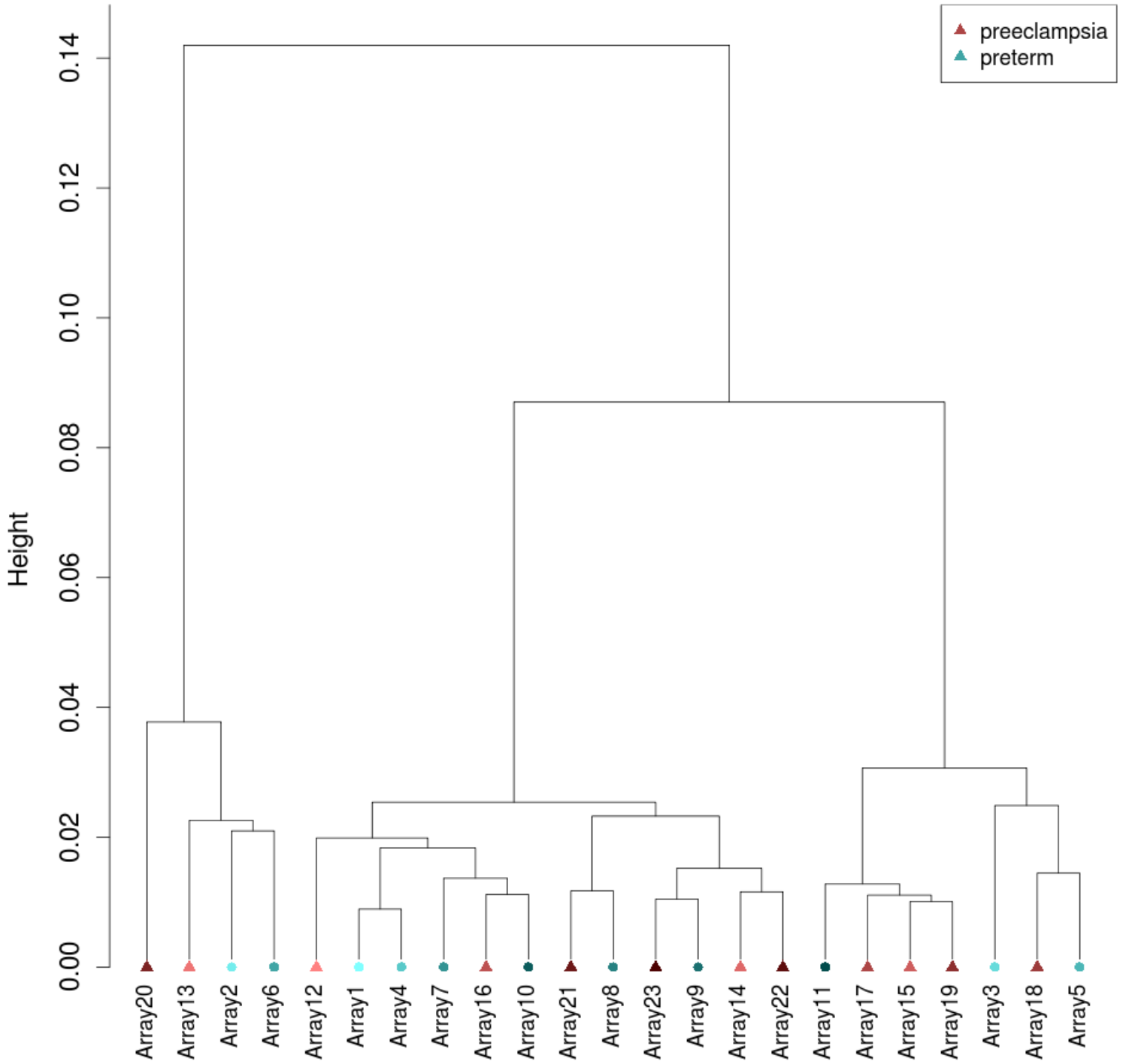
Array correlation plot  
after RMA normalization  
correlation method: pearson  
cluster method: ward



# PCA analysis after RMA normalization



# Cluster dendrogram of RMA normalized data



distance: Pearson  
cluster method: ward