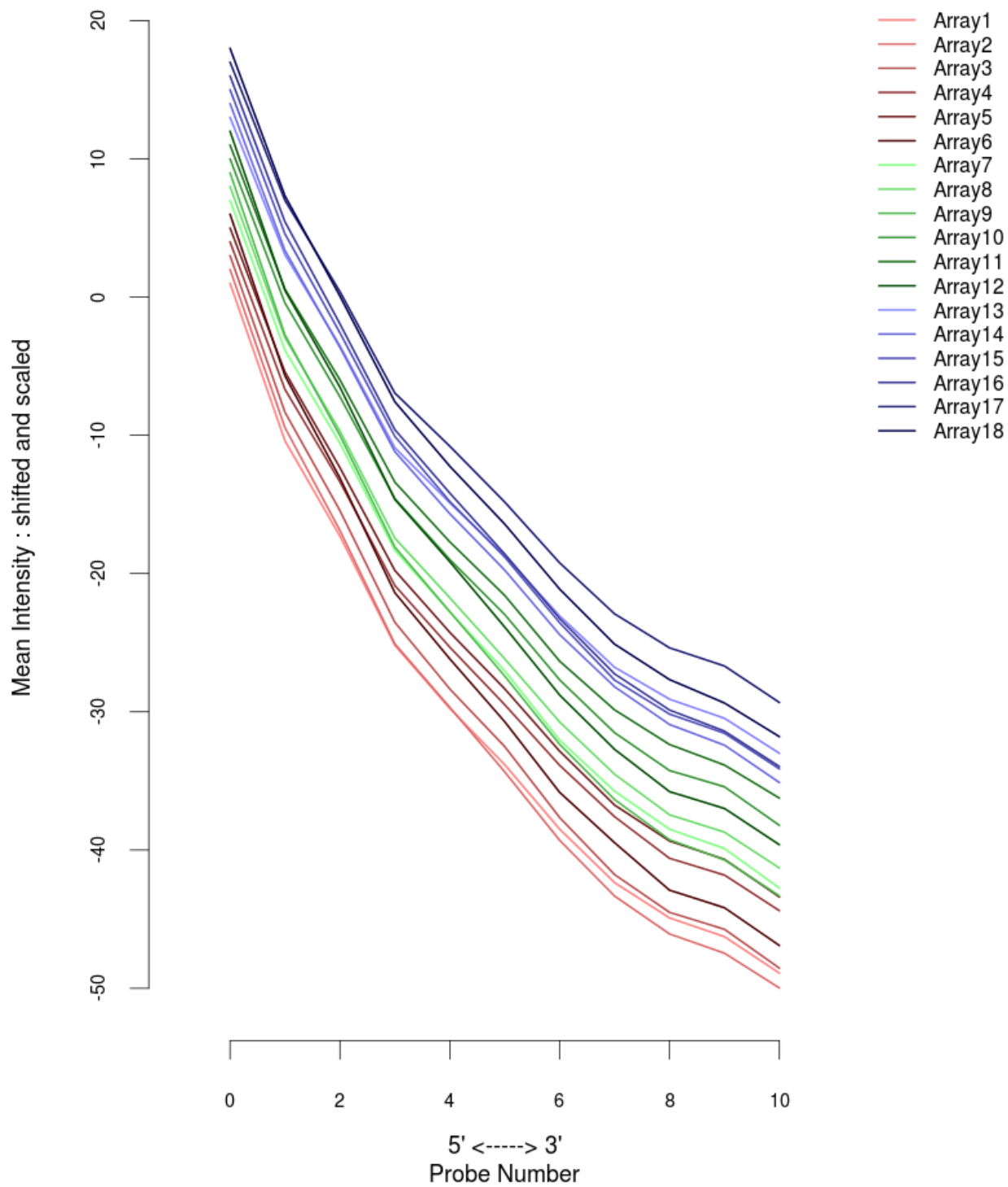


Quality Control & Pre-processing Evaluation
of
E-GEOD-50584.raw.1_0
REPORT

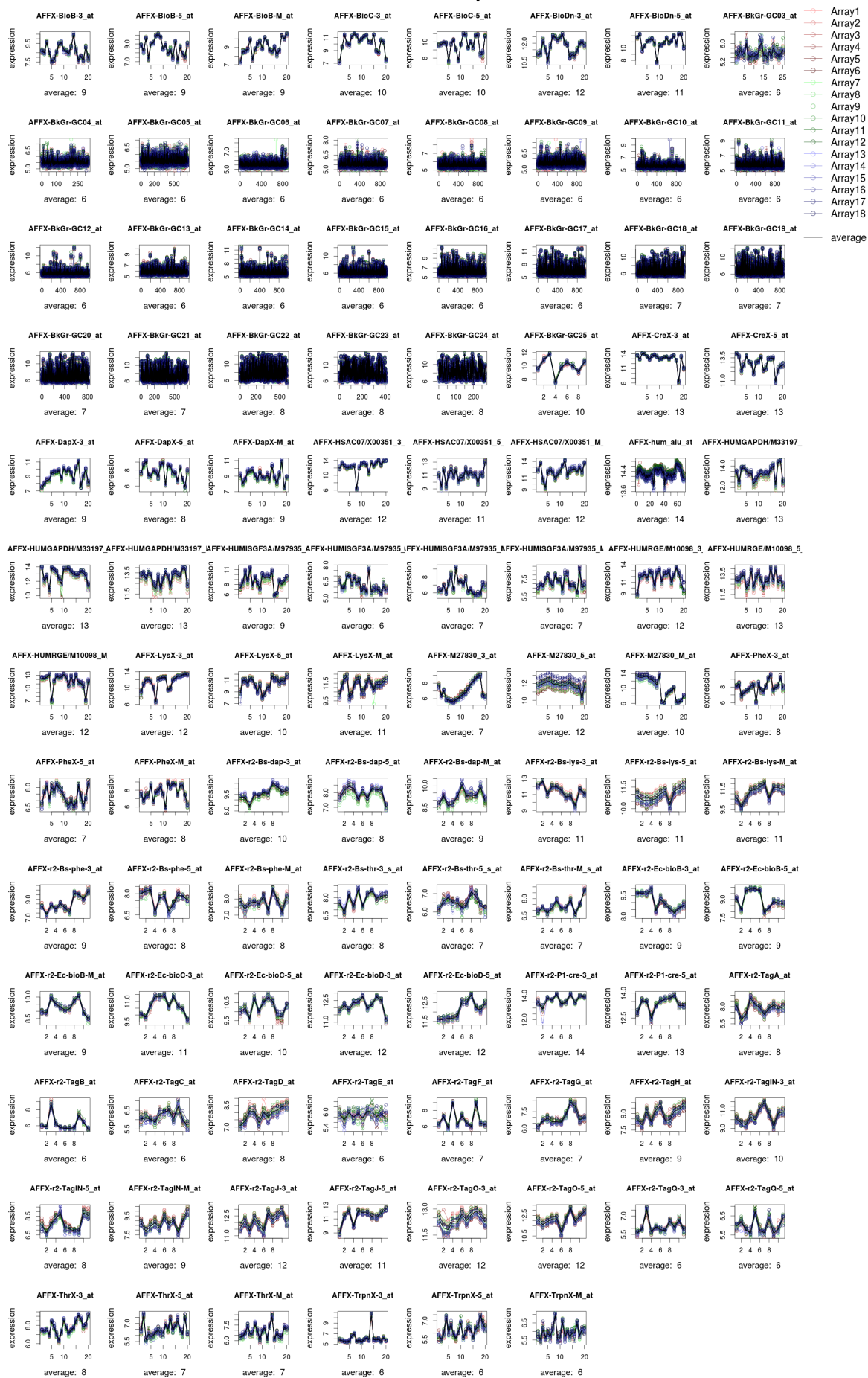
Array names and grouping

ArrayDataFile	SourceName	FactorValue
GSM1223926_WIBR3-Mut2_4wk.CEL	Array1	Group1
GSM1223925_WIBR3-Mut1_4wk.CEL	Array2	Group1
GSM1223924_WIBR1-Mut_4wk.CEL	Array3	Group1
GSM1223923_WIBR3-Con2_4wk.CEL	Array4	Group1
GSM1223922_WIBR3-Con1_4wk.CEL	Array5	Group1
GSM1223921_WIBR1-Con_4wk.CEL	Array6	Group1
GSM1223920_WIBR3-Mut2_2wk.CEL	Array7	Group2
GSM1223919_WIBR3-Mut1_2wk.CEL	Array8	Group2
GSM1223918_WIBR1-Mut_2wk.CEL	Array9	Group2
GSM1223917_WIBR3-Con2_2wk.CEL	Array10	Group2
GSM1223916_WIBR3-Con1_2wk.CEL	Array11	Group2
GSM1223915_WIBR1-Con_2wk.CEL	Array12	Group2
GSM1223914_WIBR3-Mut2_NP.CEL	Array13	Group3
GSM1223913_WIBR3-Mut1_NP.CEL	Array14	Group3
GSM1223912_WIBR1-Mut_NP.CEL	Array15	Group3
GSM1223911_WIBR3-Con2_NP.CEL	Array16	Group3
GSM1223910_WIBR3-Con1_NP.CEL	Array17	Group3
GSM1223909_WIBR1-Con_NP.CEL	Array18	Group3

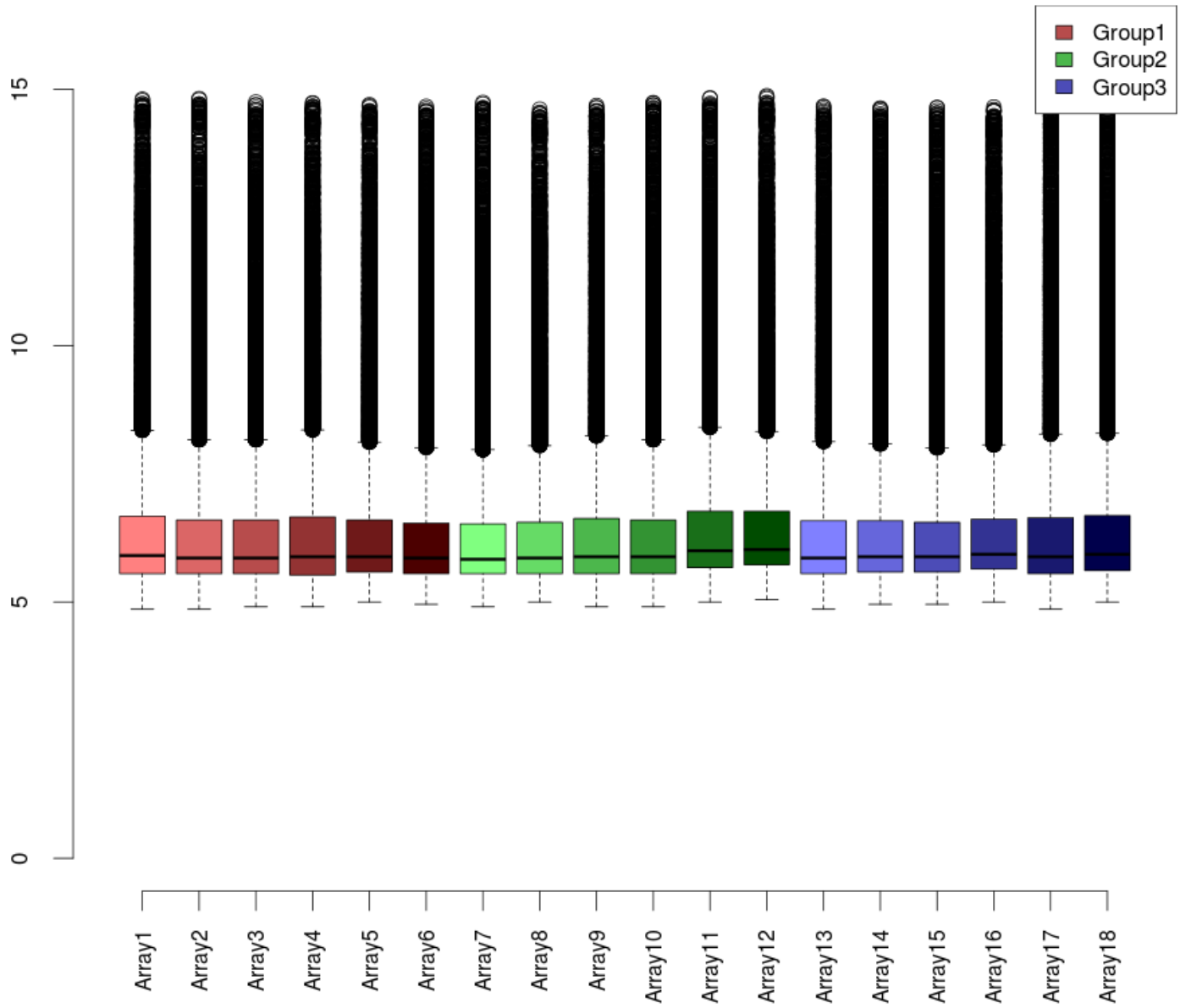
RNA degradation plot



affx control profiles

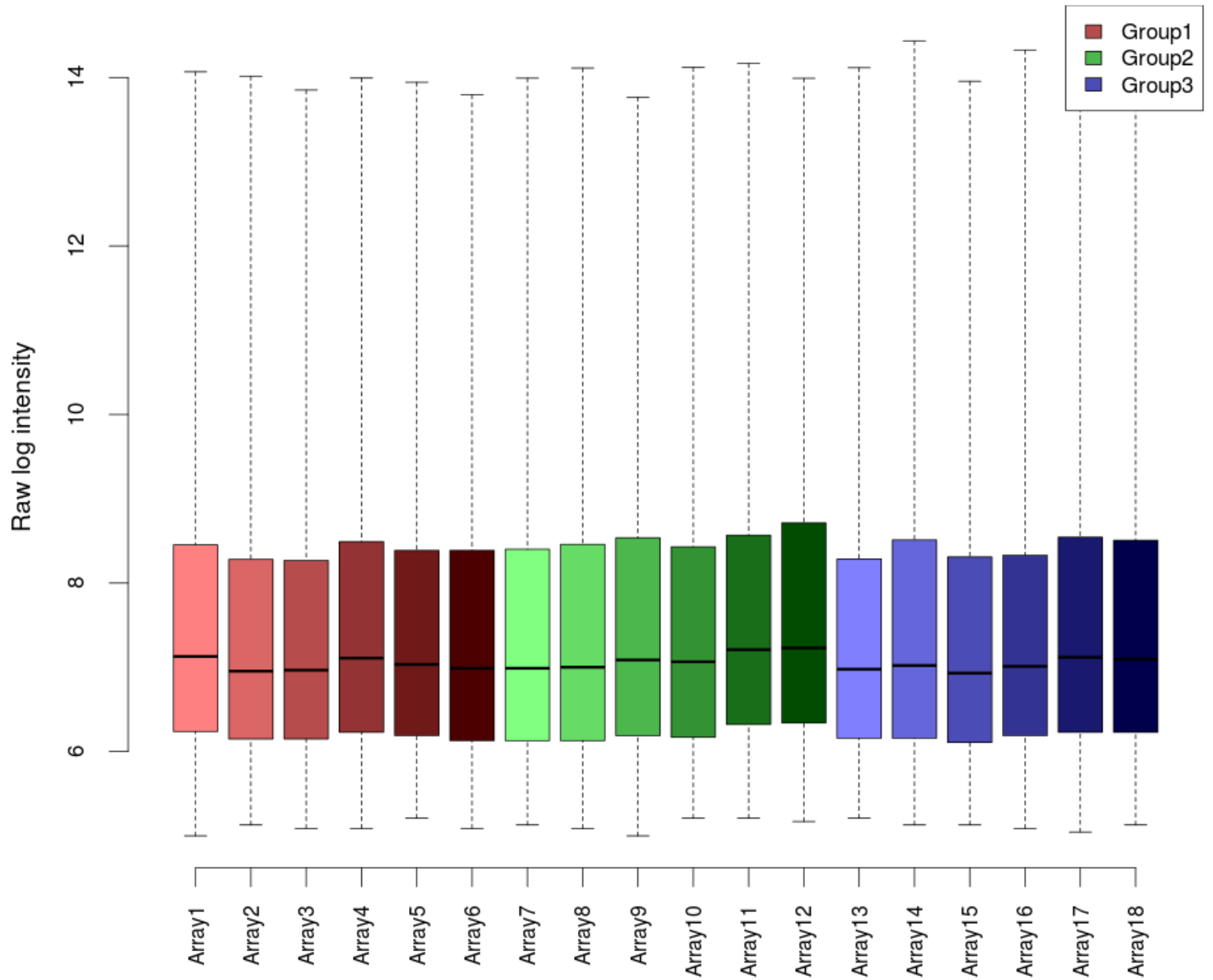


affx controls



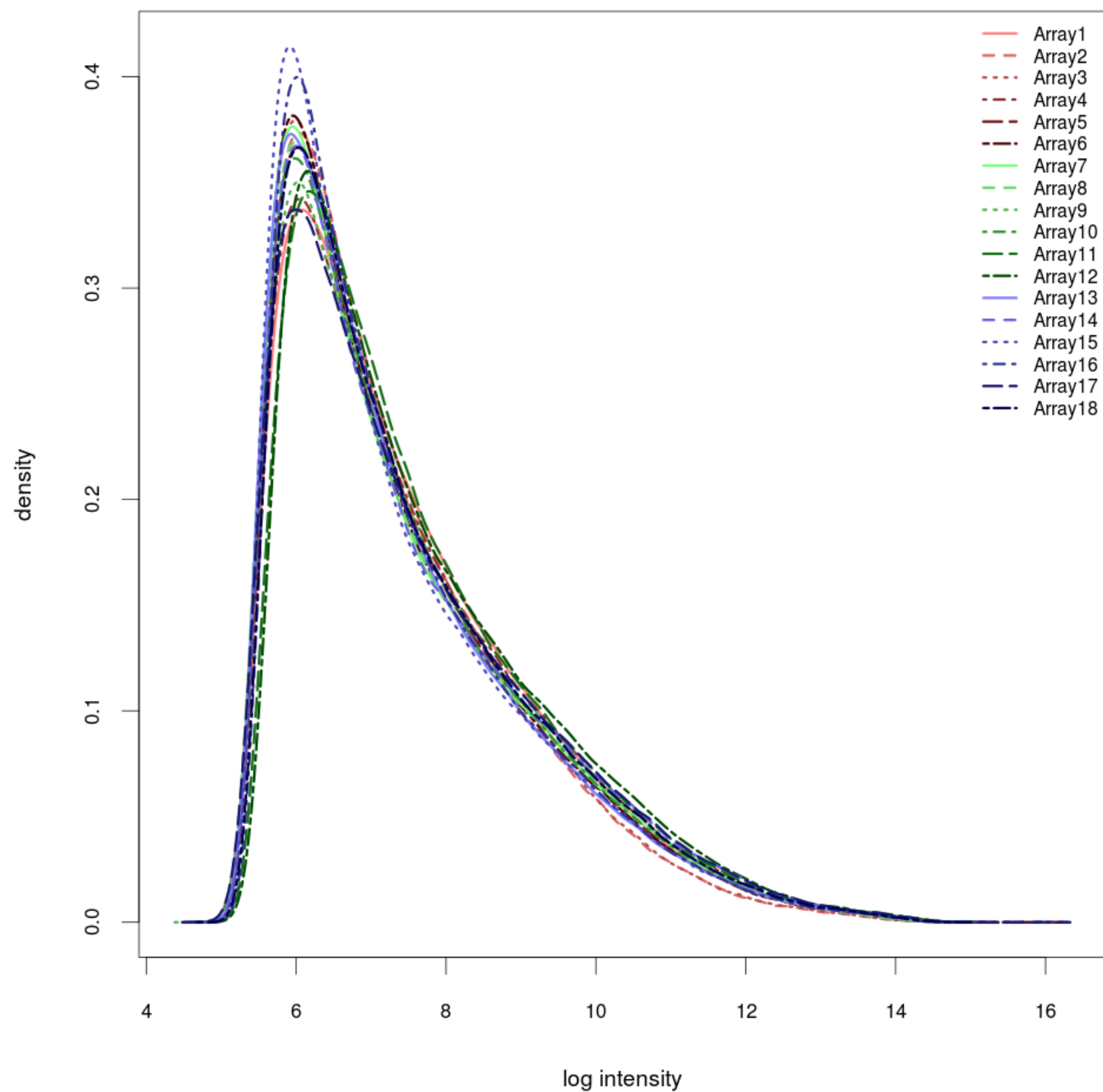
Boxplot of raw intensities

Distributions should be comparable between arrays



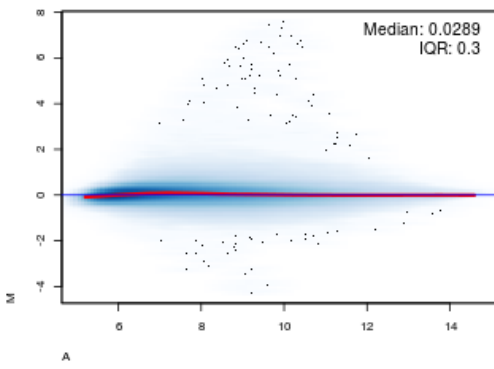
Density histogram of raw intensities

Curves should be comparable between arrays

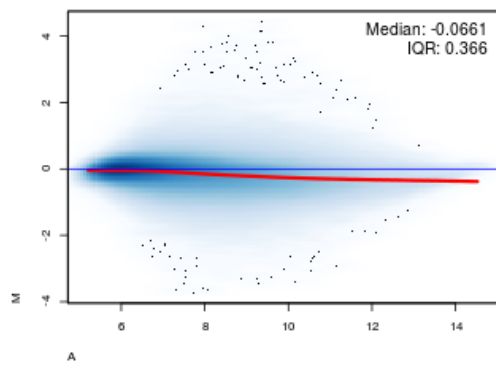


MA plots of raw data 1 / 2

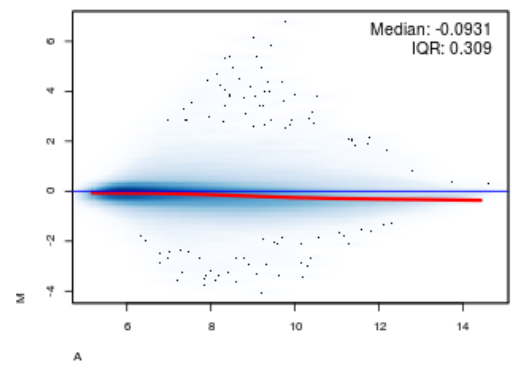
Array1 vs pseudo-median reference chip



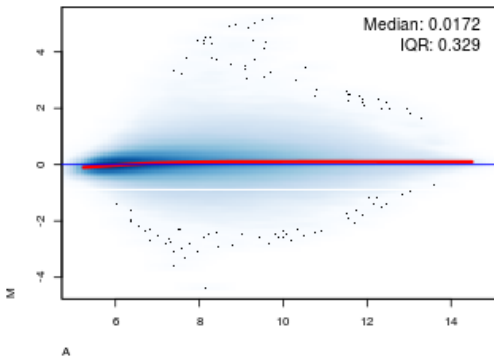
Array2 vs pseudo-median reference chip



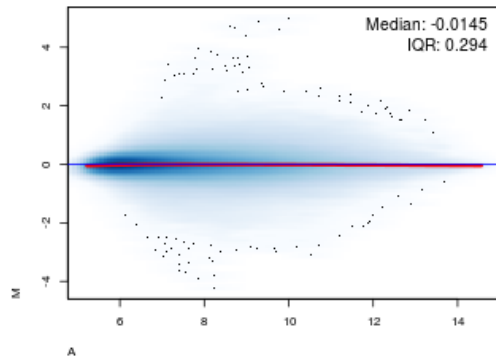
Array3 vs pseudo-median reference chip



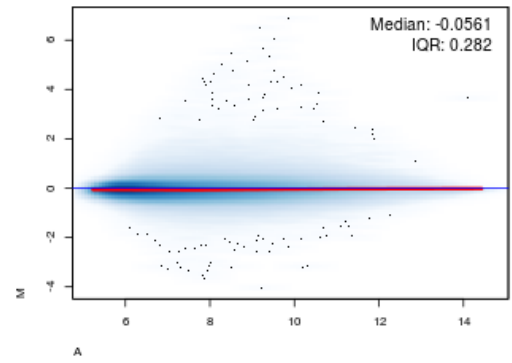
Array4 vs pseudo-median reference chip



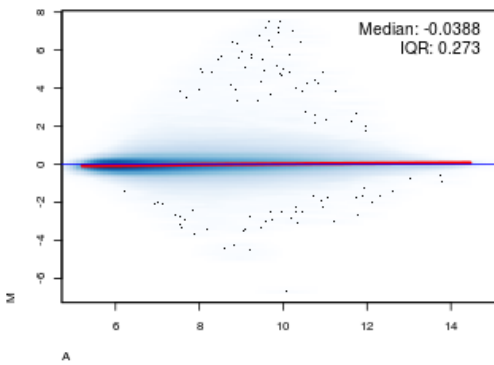
Array5 vs pseudo-median reference chip



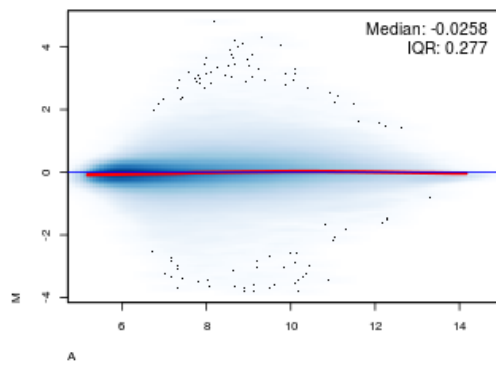
Array6 vs pseudo-median reference chip



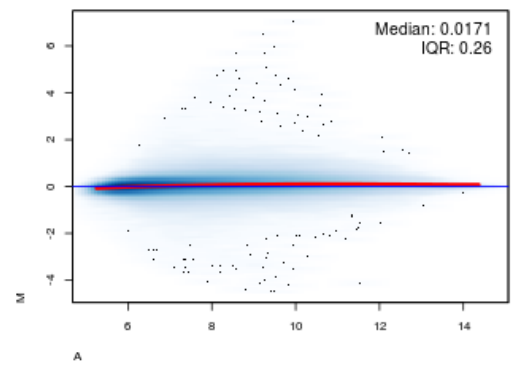
Array7 vs pseudo-median reference chip



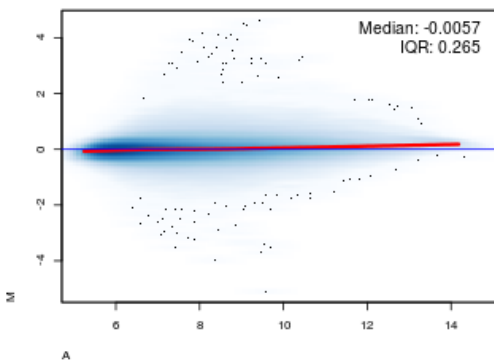
Array8 vs pseudo-median reference chip



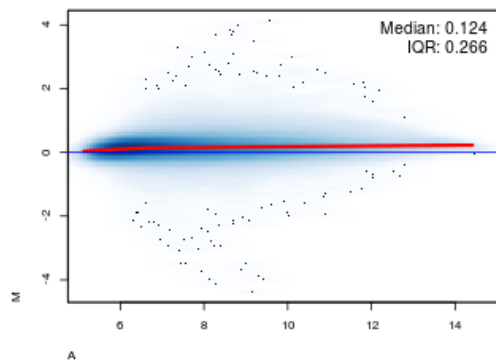
Array9 vs pseudo-median reference chip



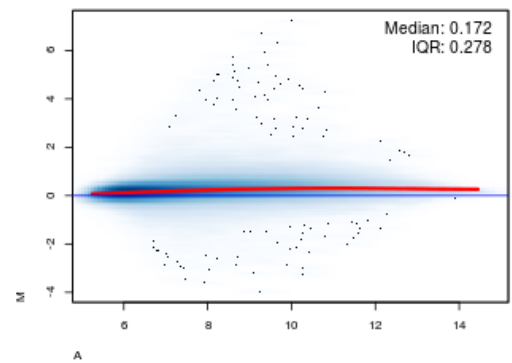
Array10 vs pseudo-median reference chip



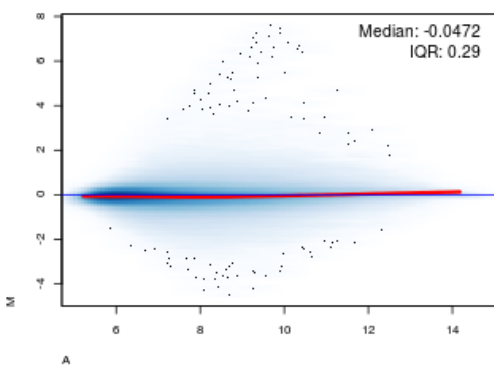
Array11 vs pseudo-median reference chip



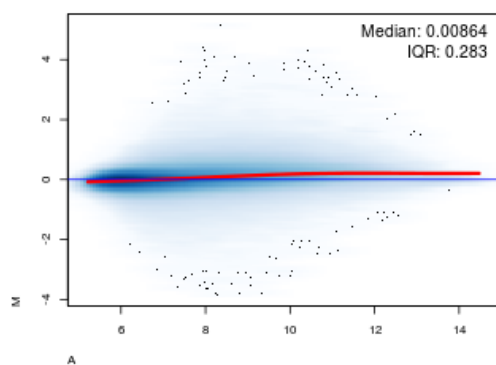
Array12 vs pseudo-median reference chip



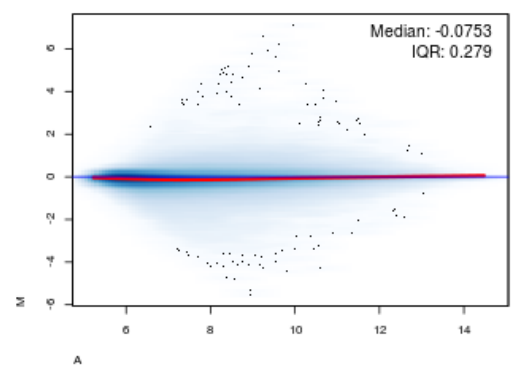
Array13 vs pseudo-median reference chip



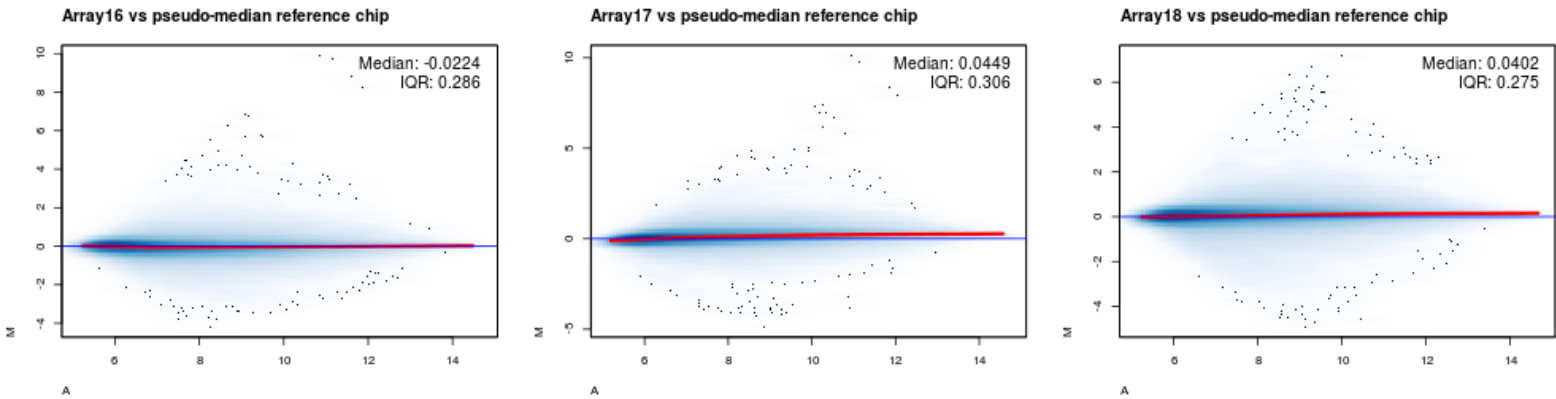
Array14 vs pseudo-median reference chip



Array15 vs pseudo-median reference chip

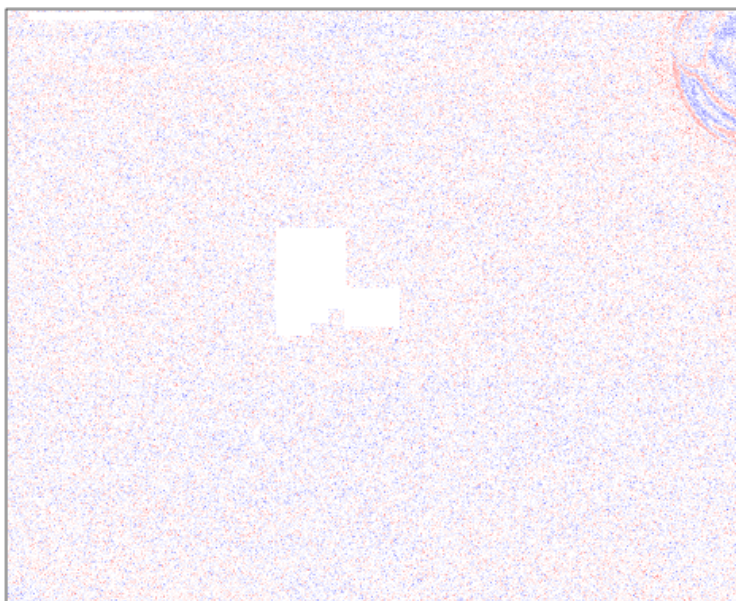


MA plots of raw data 2 / 2

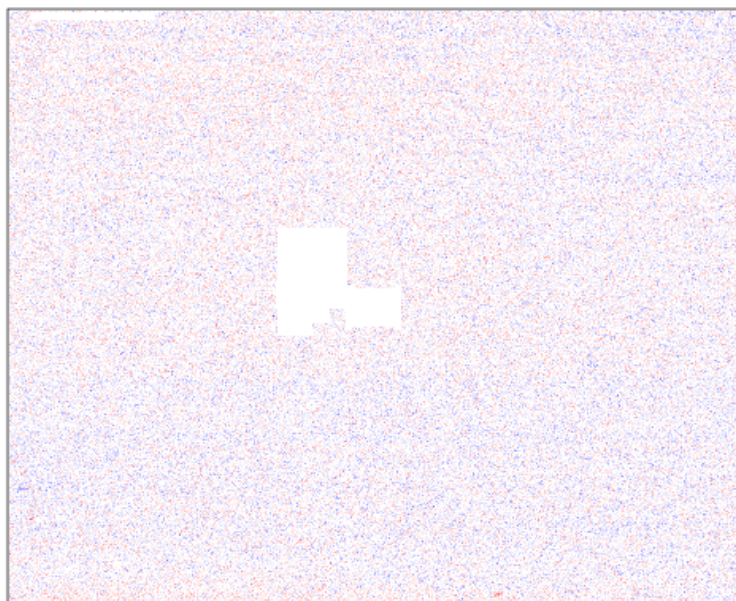


2D virtual PLM image for model characteristic: resid 1 / 3

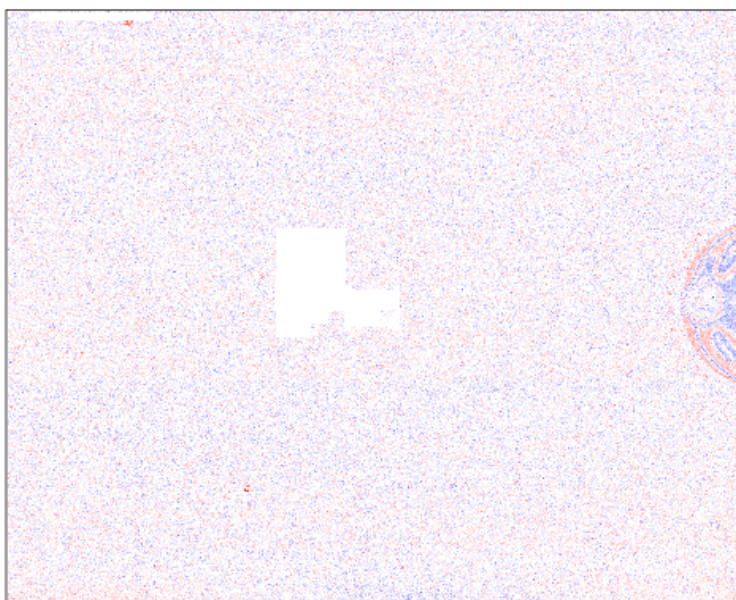
Array1



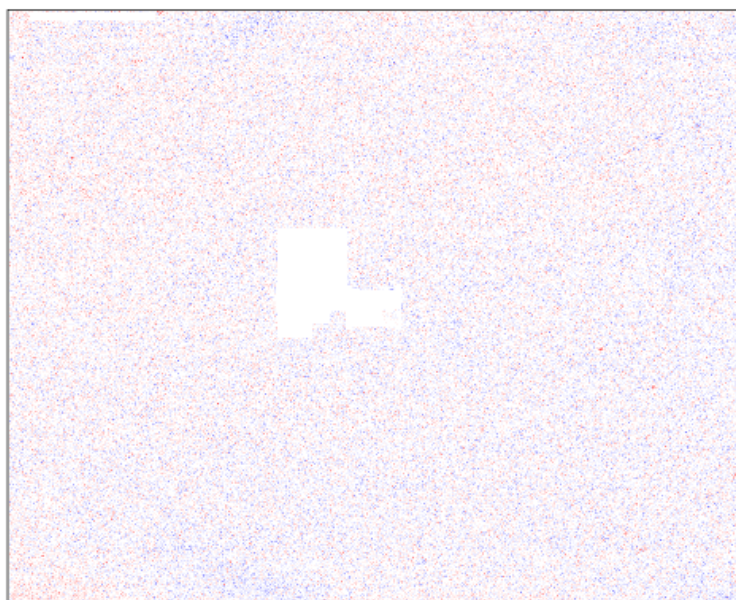
Array2



Array3



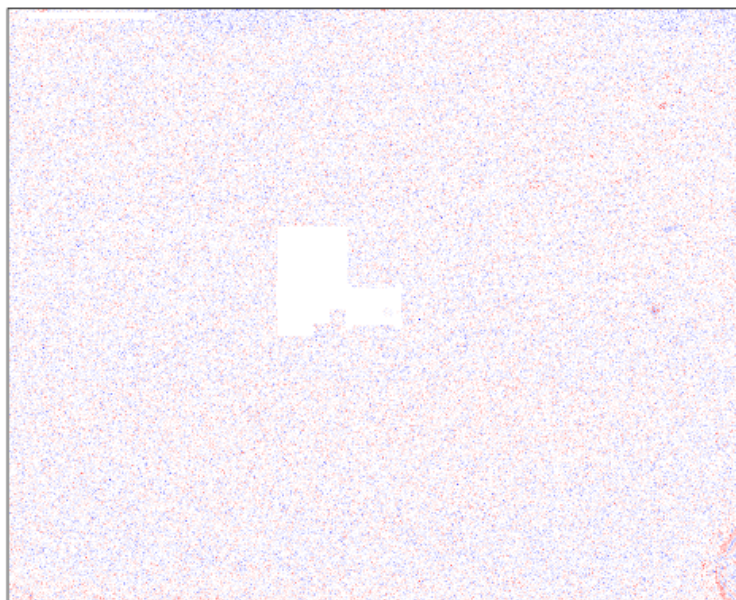
Array4



Array5

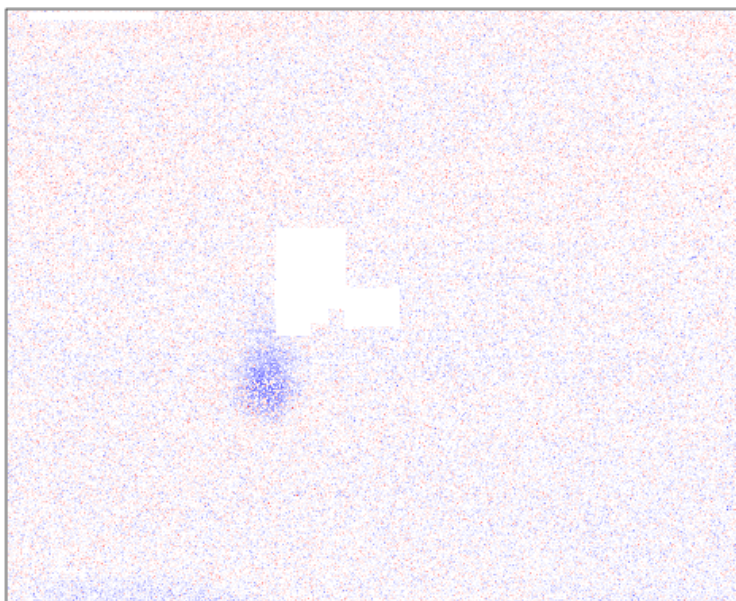


Array6

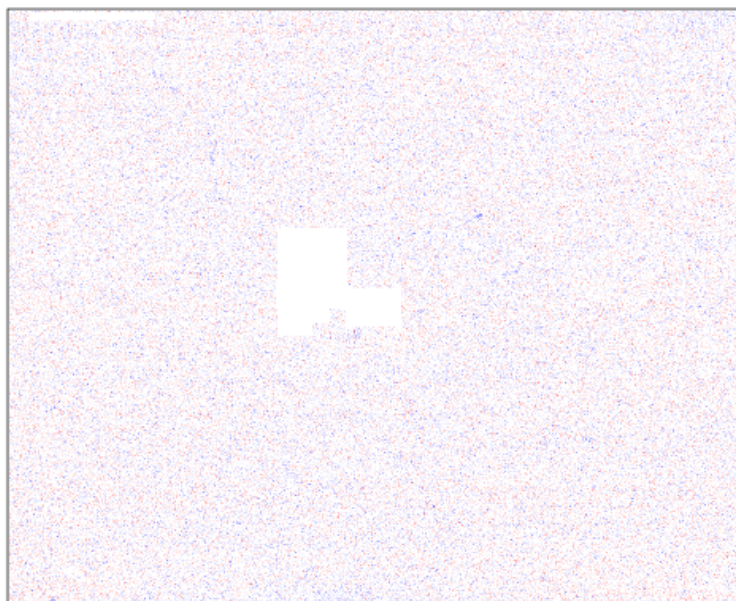


2D virtual PLM image for model characteristic: resid 2 / 3

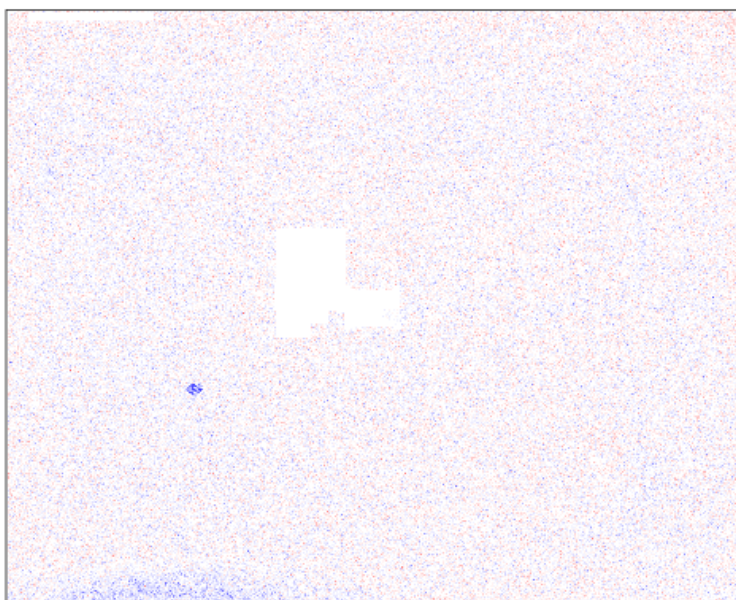
Array7



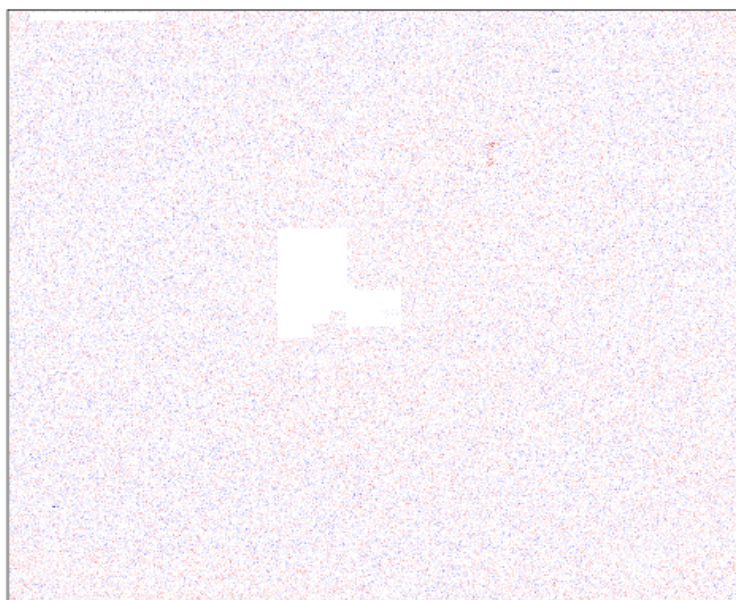
Array8



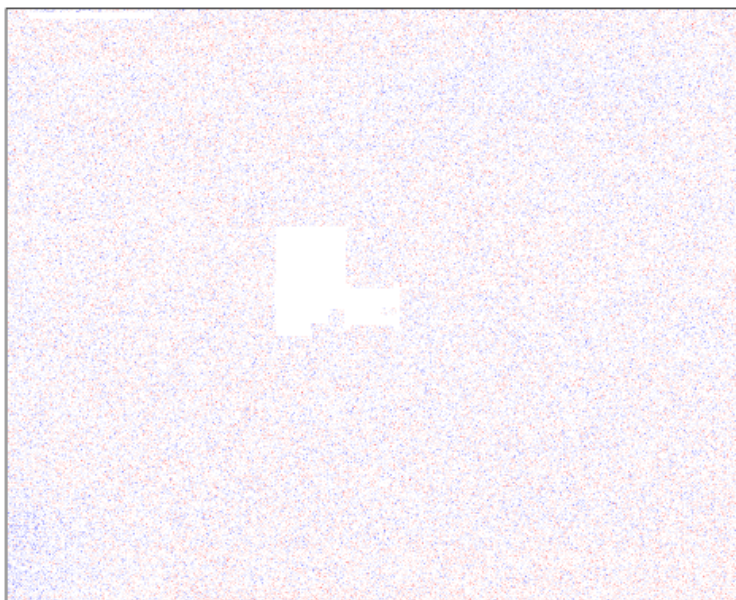
Array9



Array10



Array11

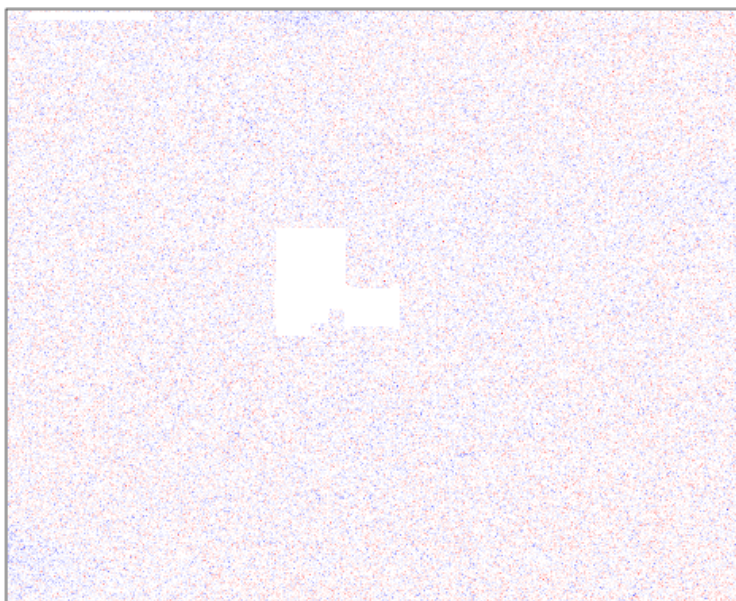


Array12

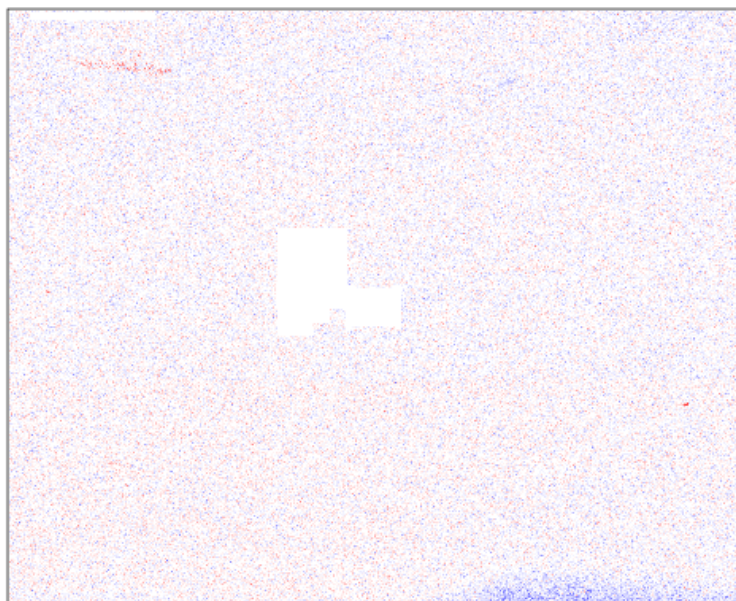


2D virtual PLM image for model characteristic: resid 3 / 3

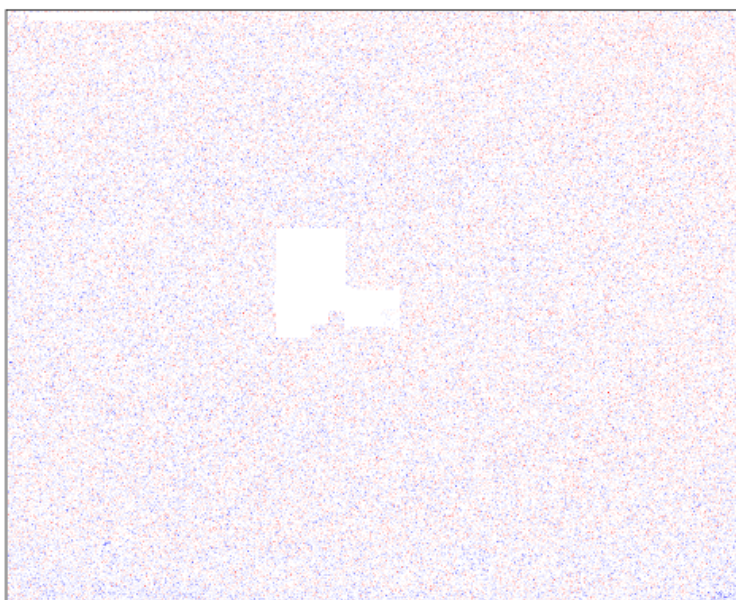
Array13



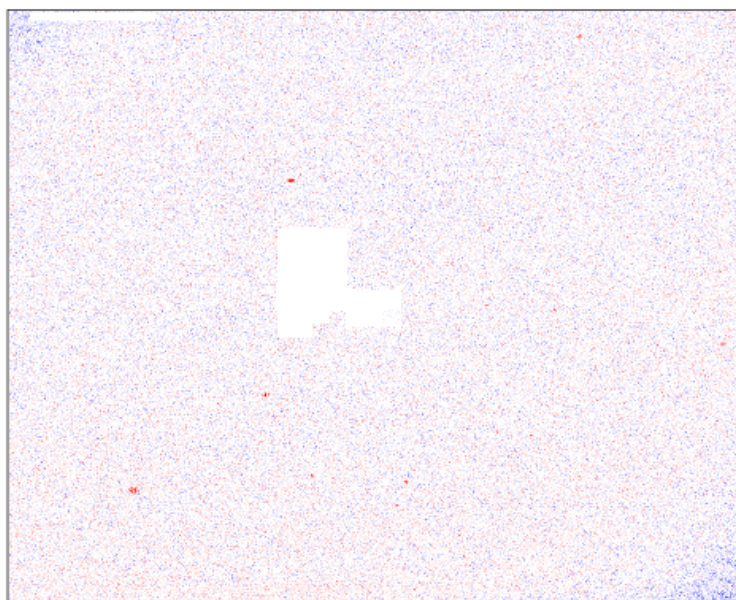
Array14



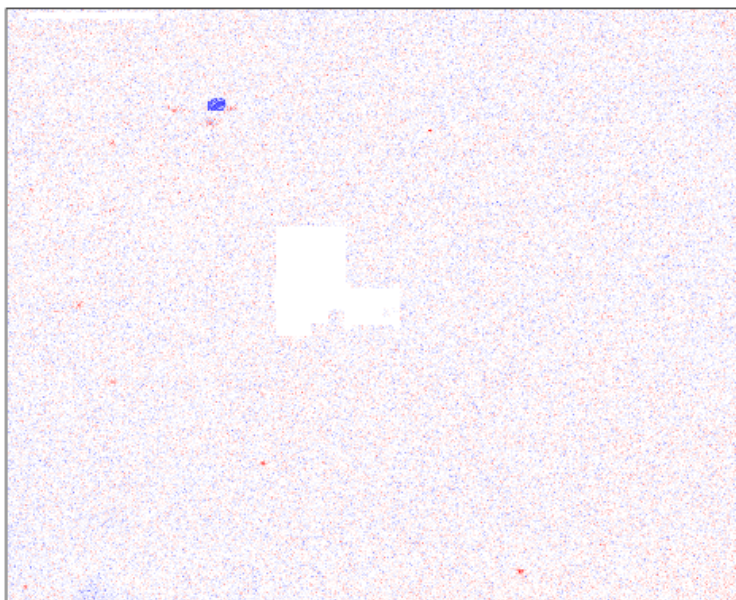
Array15



Array16



Array17

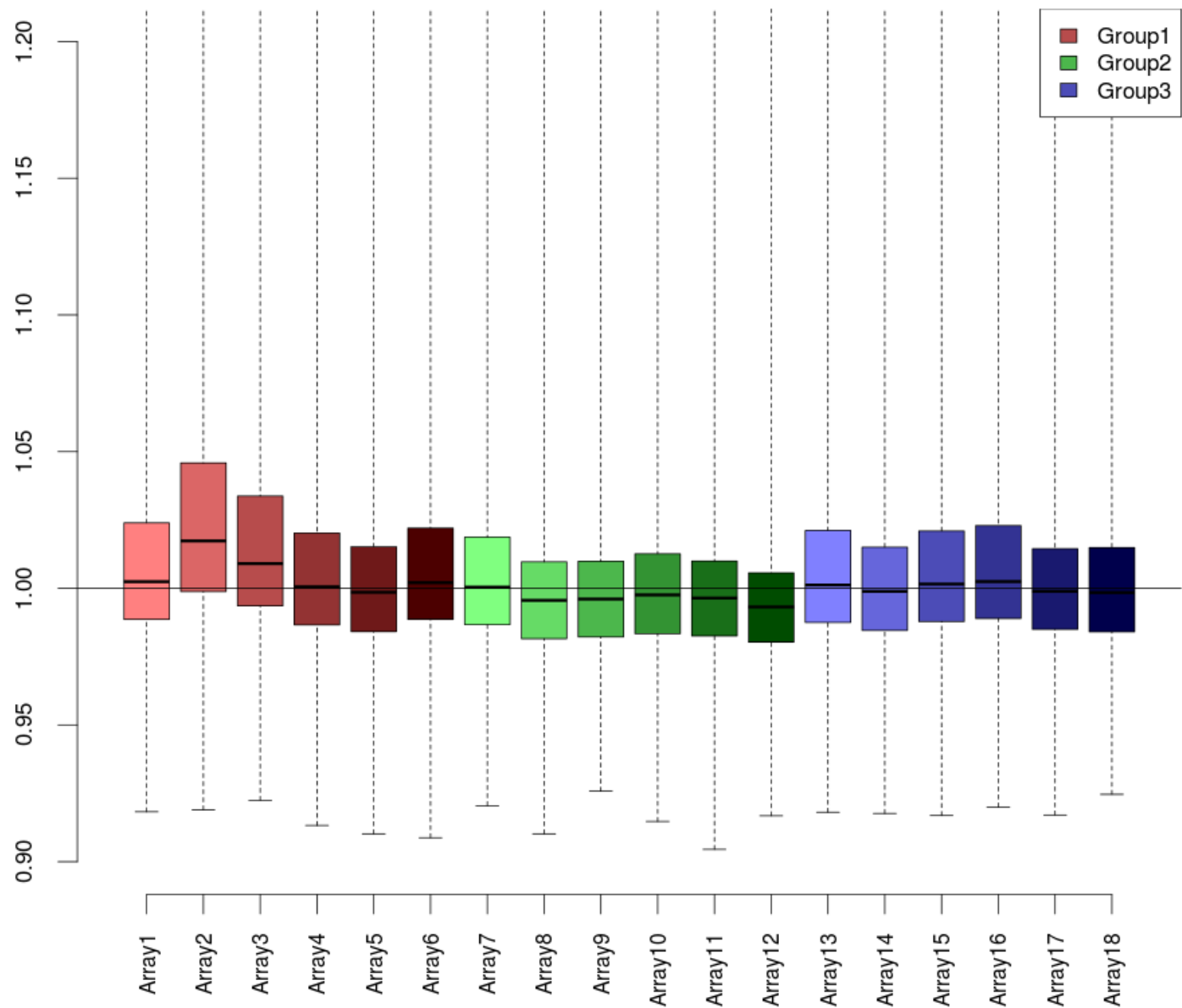


Array18



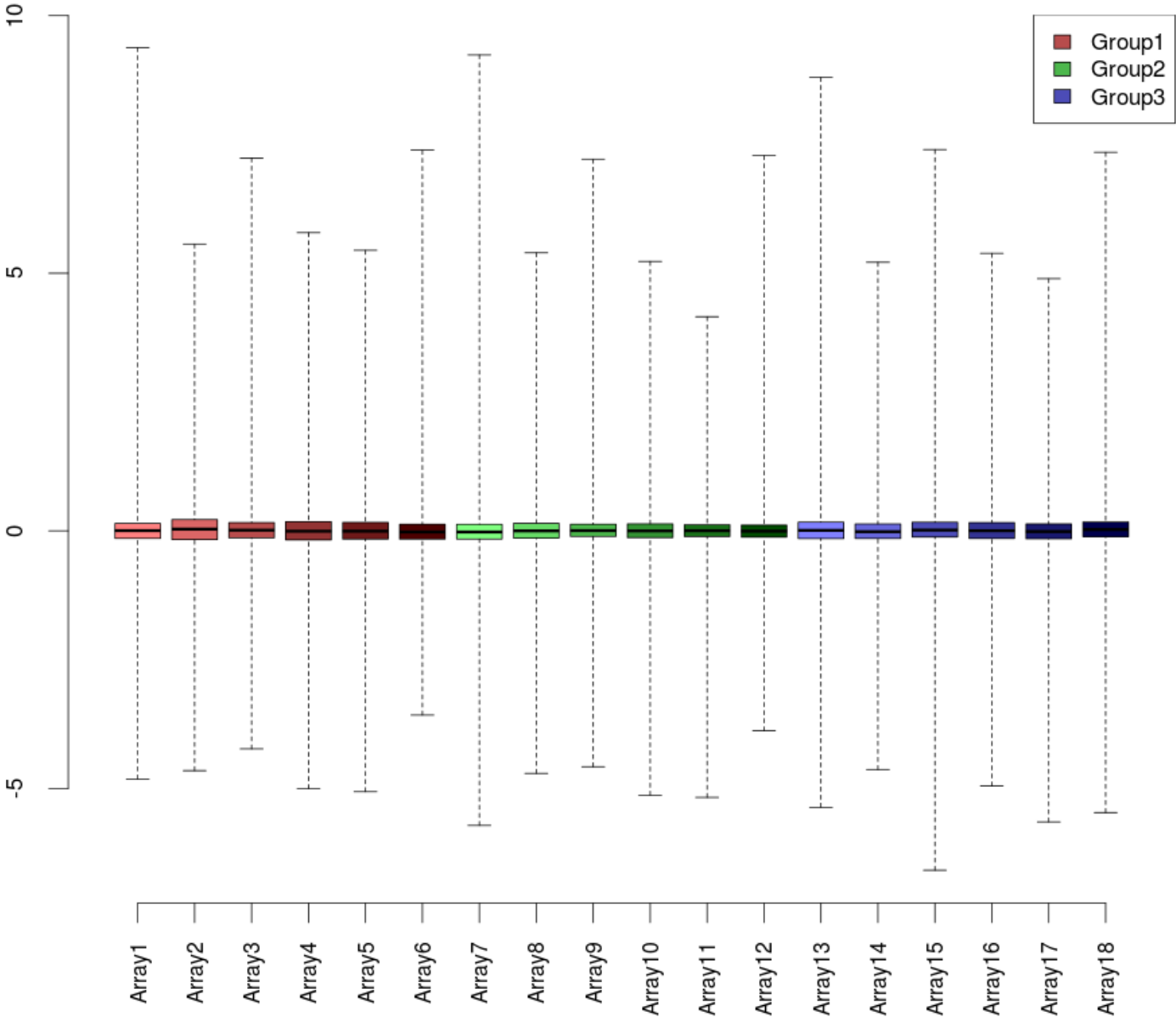
Normalized Unscaled Standard Errors (NUSE)

NUSE median value should be < 1.1



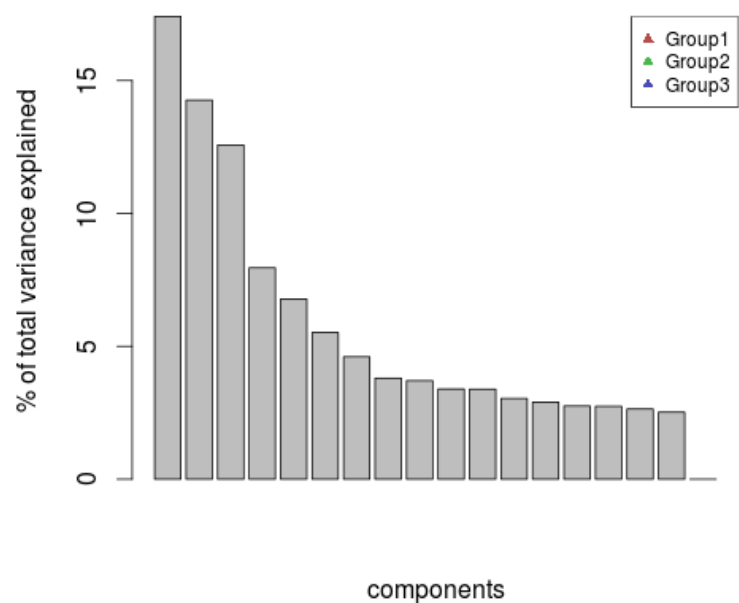
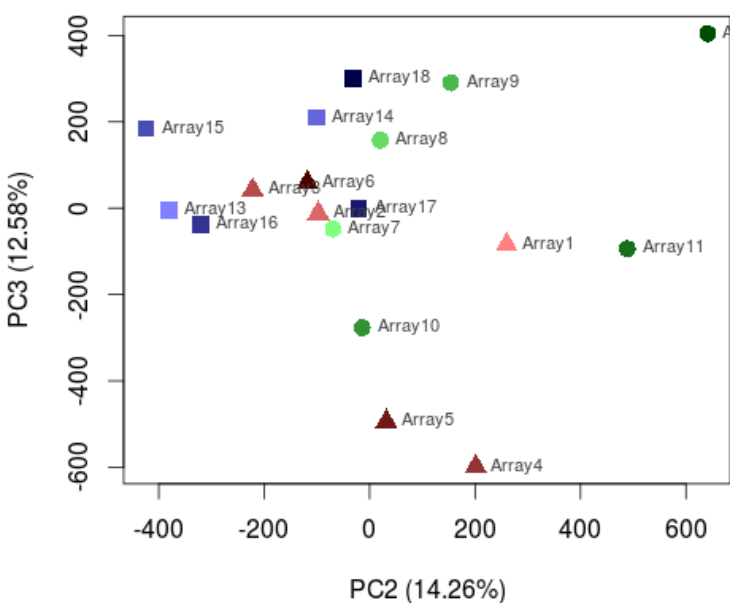
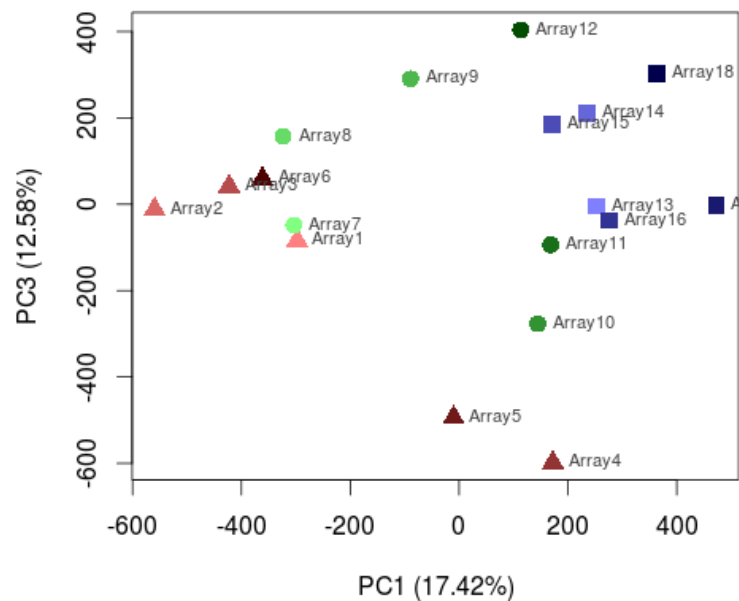
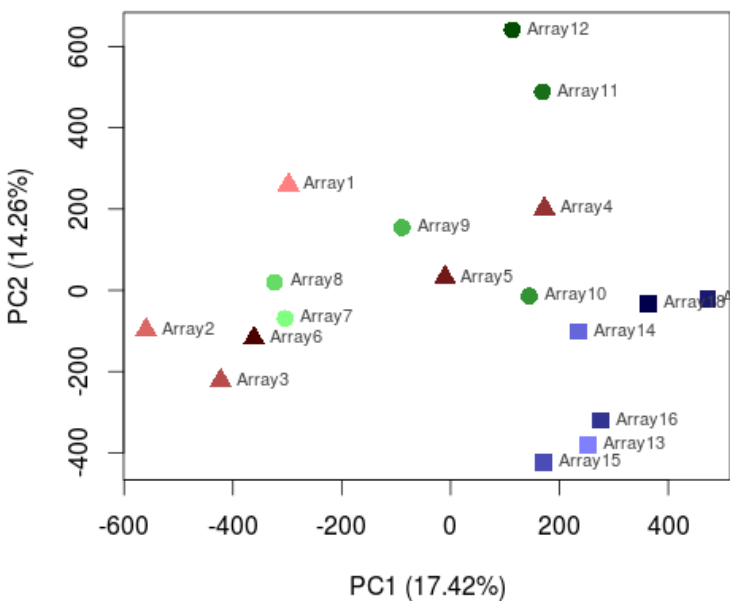
Relative Log Expression (RLE)

RLE distributions should be centered around 0

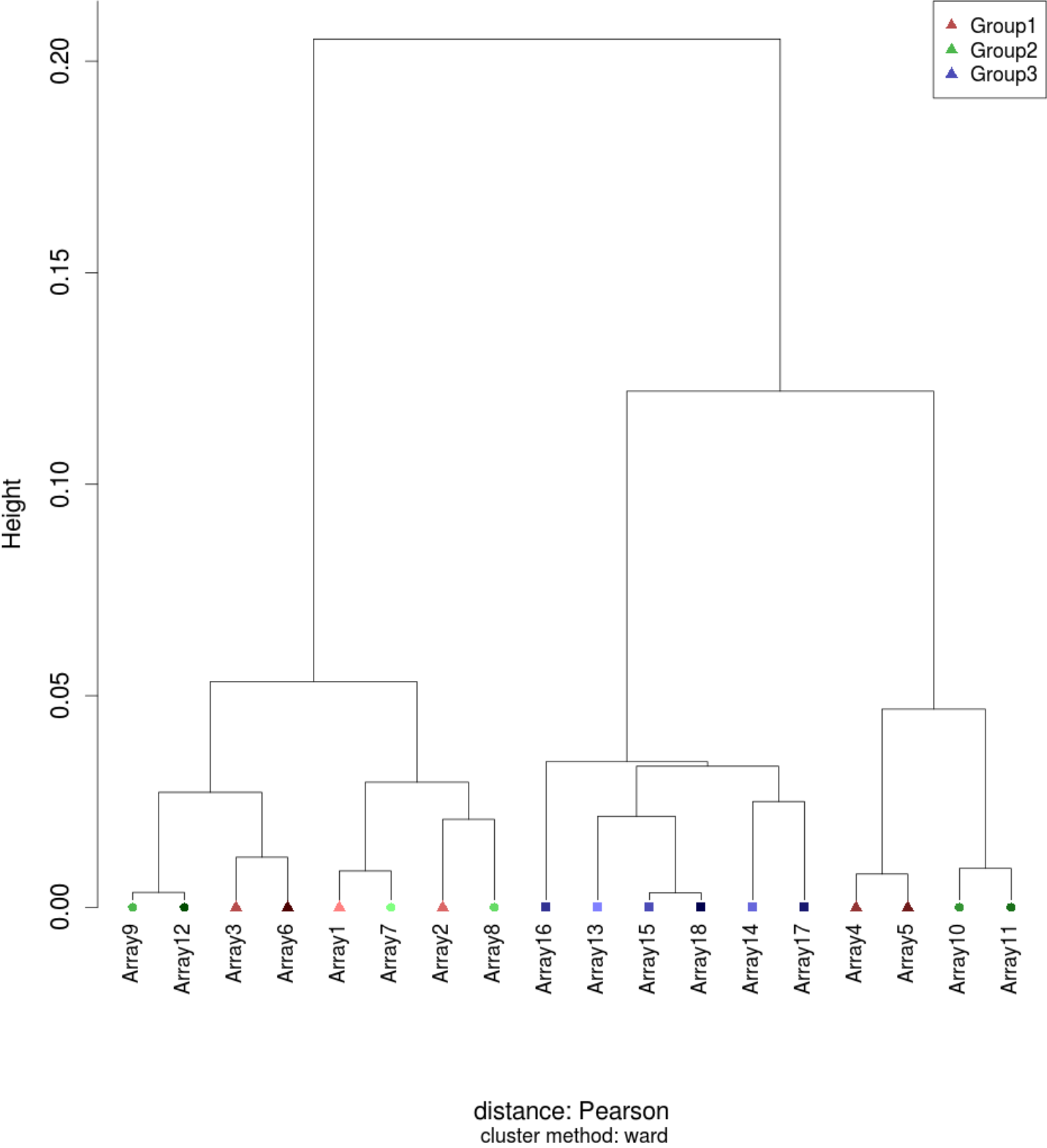


Heatmap visualization of the correlation matrix for 18 arrays. The color scale ranges from dark blue (low correlation) to dark red (high correlation). The diagonal is dark red, indicating perfect self-correlation. The matrix is symmetric. The arrays are ordered as follows: Array9, Array12, Array6, Array3, Array8, Array2, Array1, Array7, Array4, Array5, Array10, Array11, Array16, Array17, Array13, Array14, Array18, Array15.

PCA analysis of Raw data



Cluster dendrogram of raw data



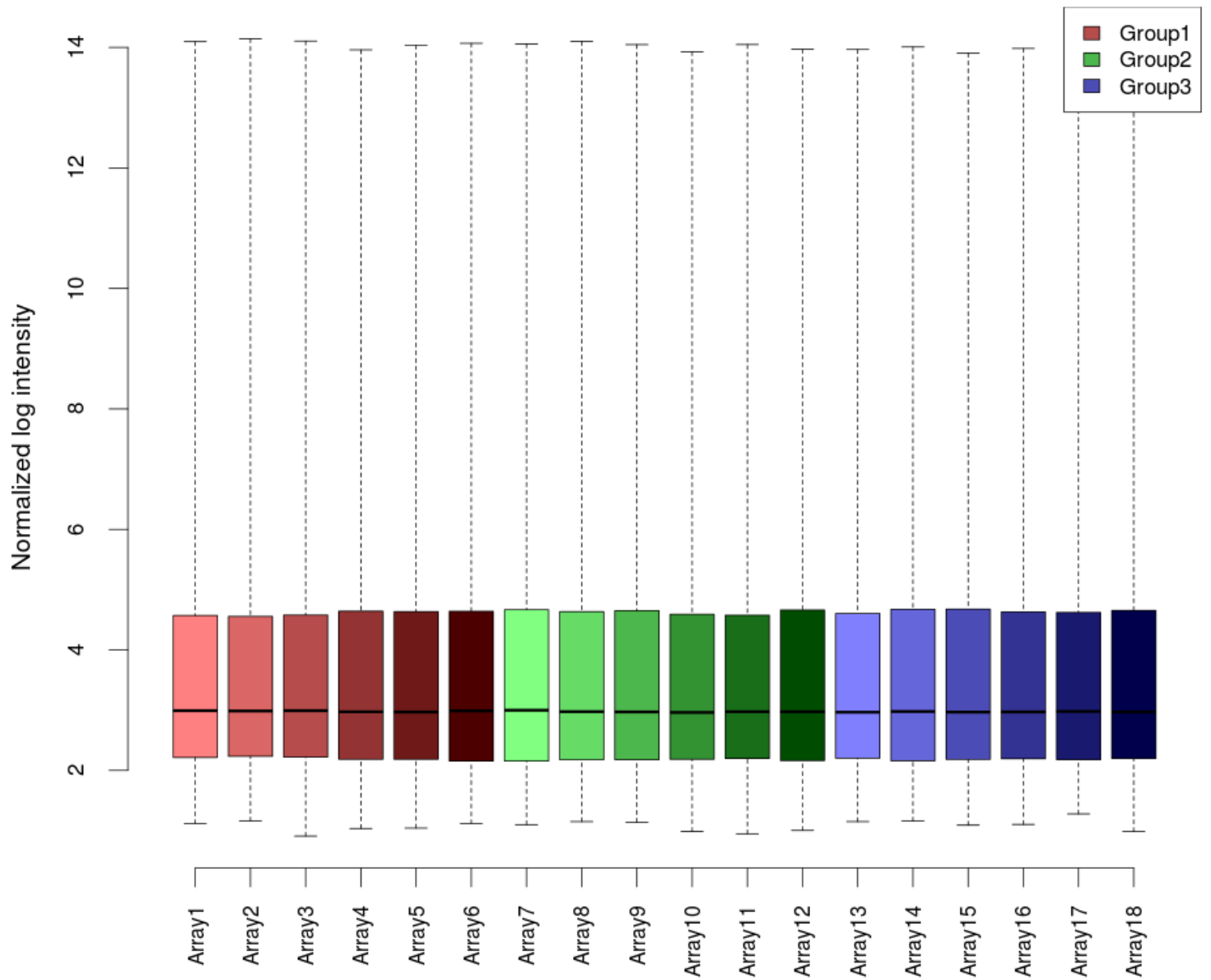
Pre-processing of Raw Data

Method: GCRMA

Annotation: primeview_Hs_ENSG

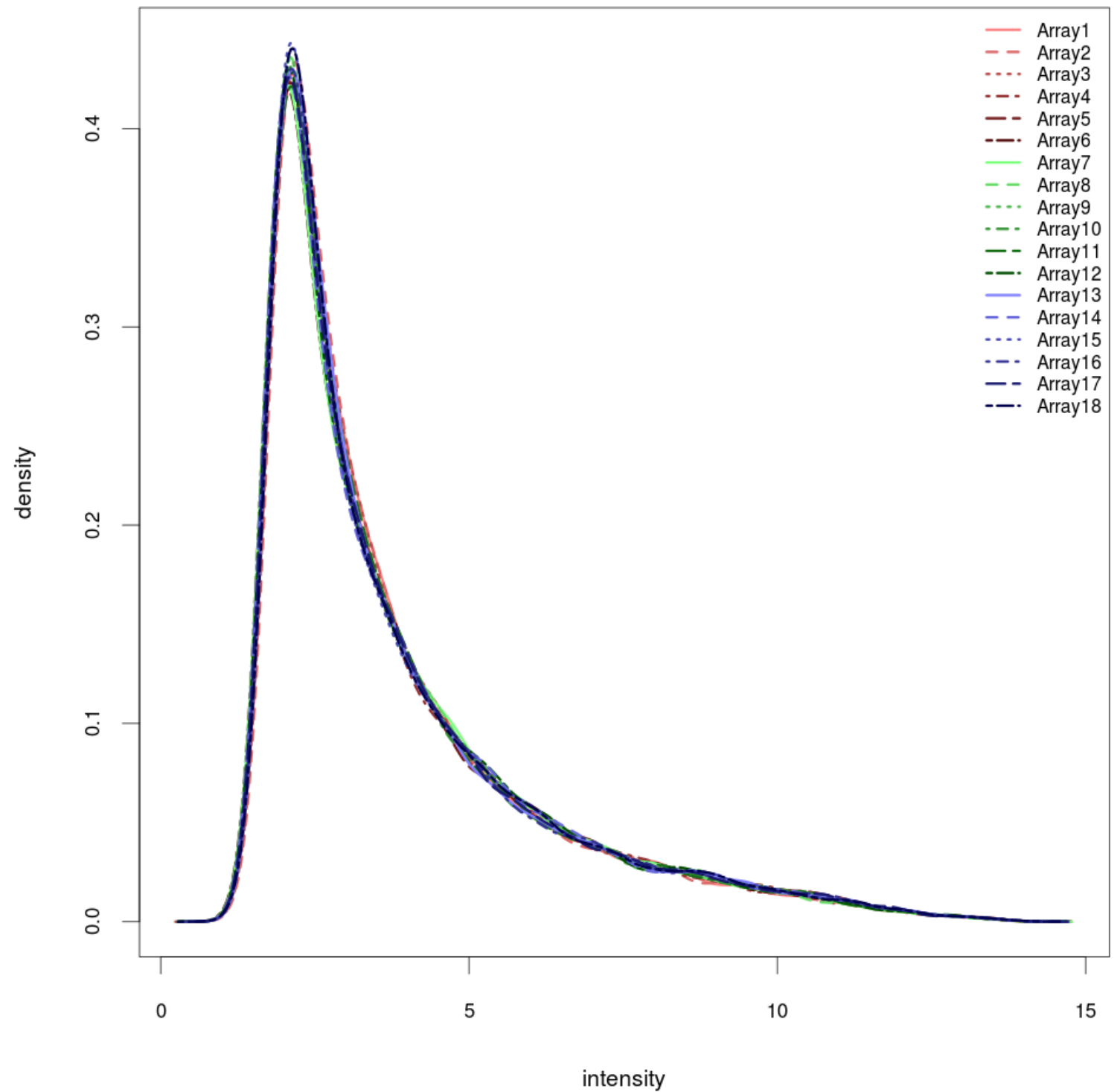
Boxplot after GCRMA

Distributions should be comparable between arrays



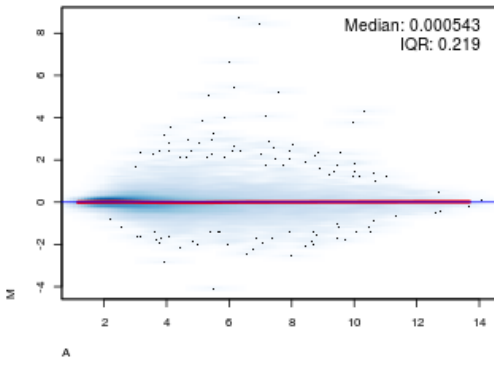
Density histogram after GCRMA

Curves should be comparable between arrays

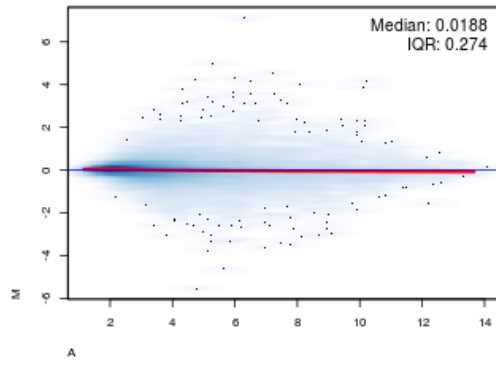


MA plots after GCRMA normalization 1 / 2

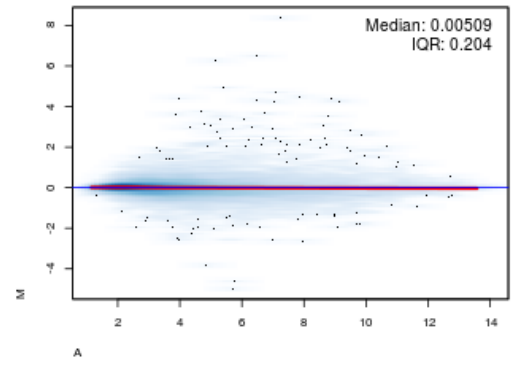
Array1 vs pseudo-median reference chip



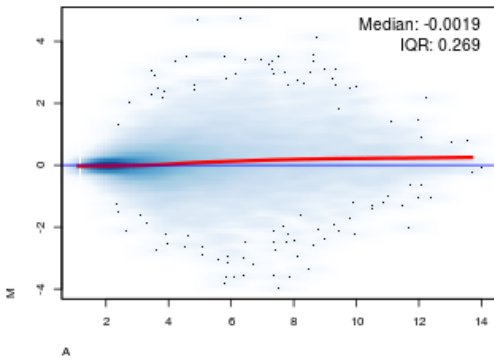
Array2 vs pseudo-median reference chip



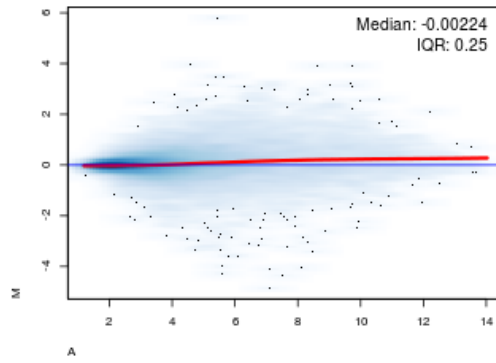
Array3 vs pseudo-median reference chip



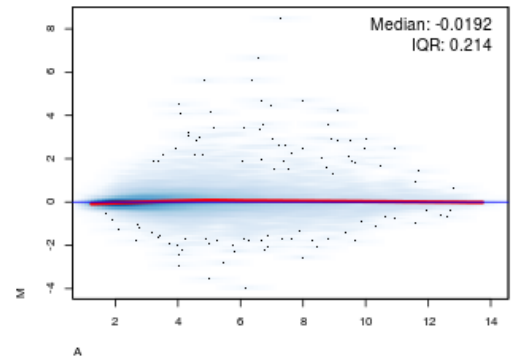
Array4 vs pseudo-median reference chip



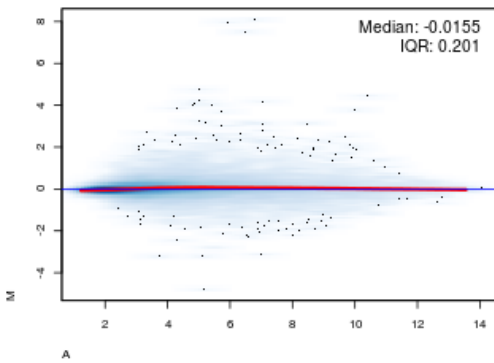
Array5 vs pseudo-median reference chip



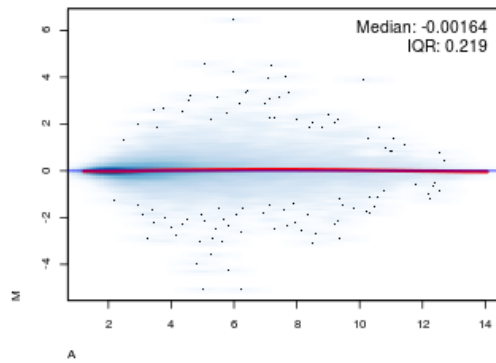
Array6 vs pseudo-median reference chip



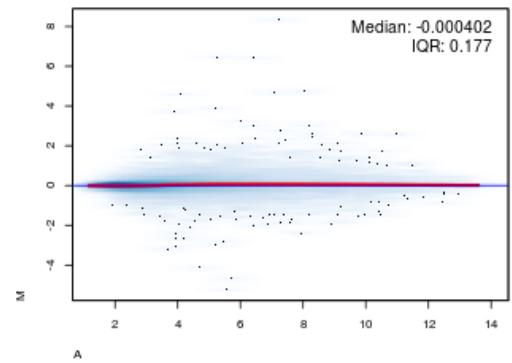
Array7 vs pseudo-median reference chip



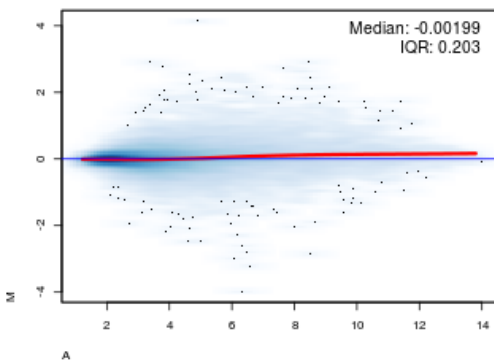
Array8 vs pseudo-median reference chip



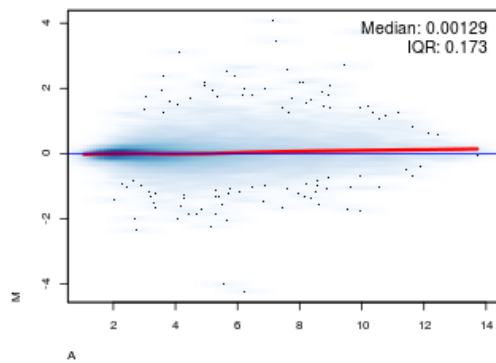
Array9 vs pseudo-median reference chip



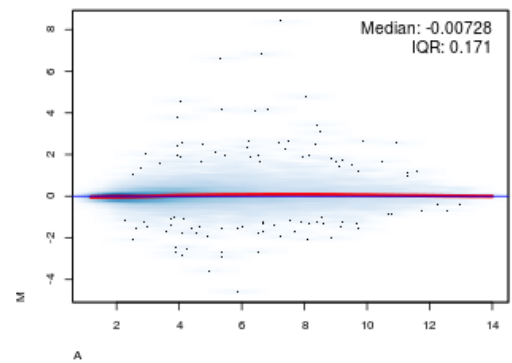
Array10 vs pseudo-median reference chip



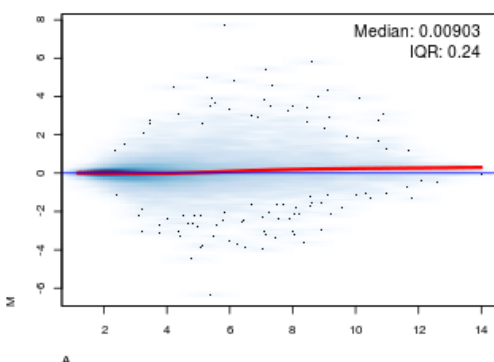
Array11 vs pseudo-median reference chip



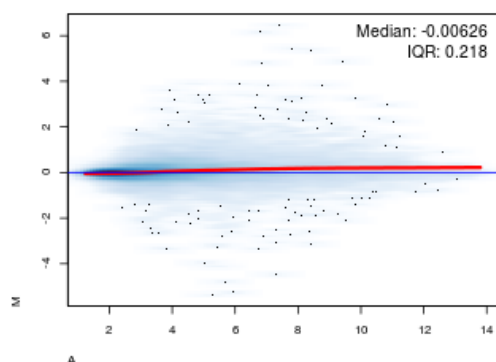
Array12 vs pseudo-median reference chip



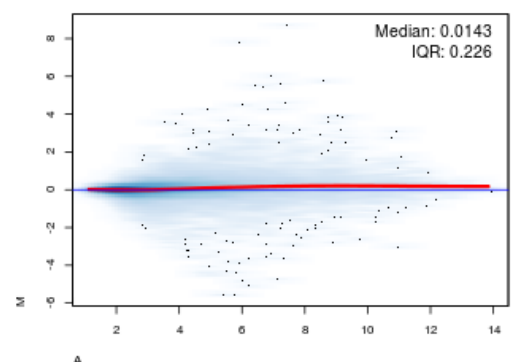
Array13 vs pseudo-median reference chip



Array14 vs pseudo-median reference chip

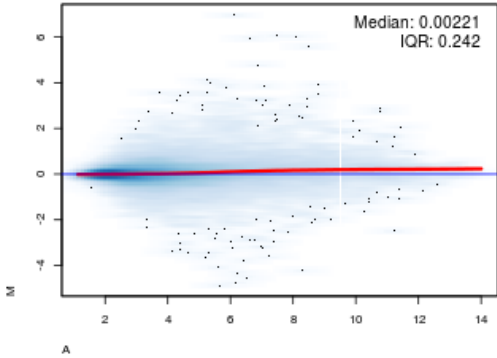


Array15 vs pseudo-median reference chip

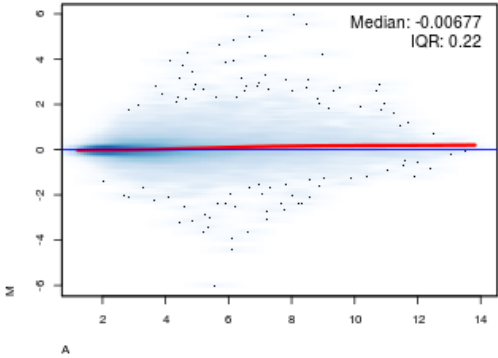


MA plots afterGCRMANormalization 2 / 2

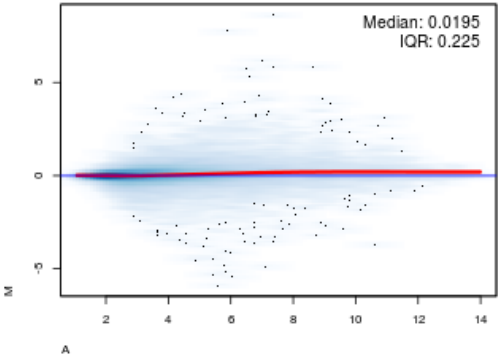
Array16 vs pseudo-median reference chip



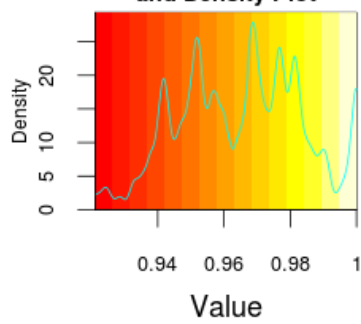
Array17 vs pseudo-median reference chip



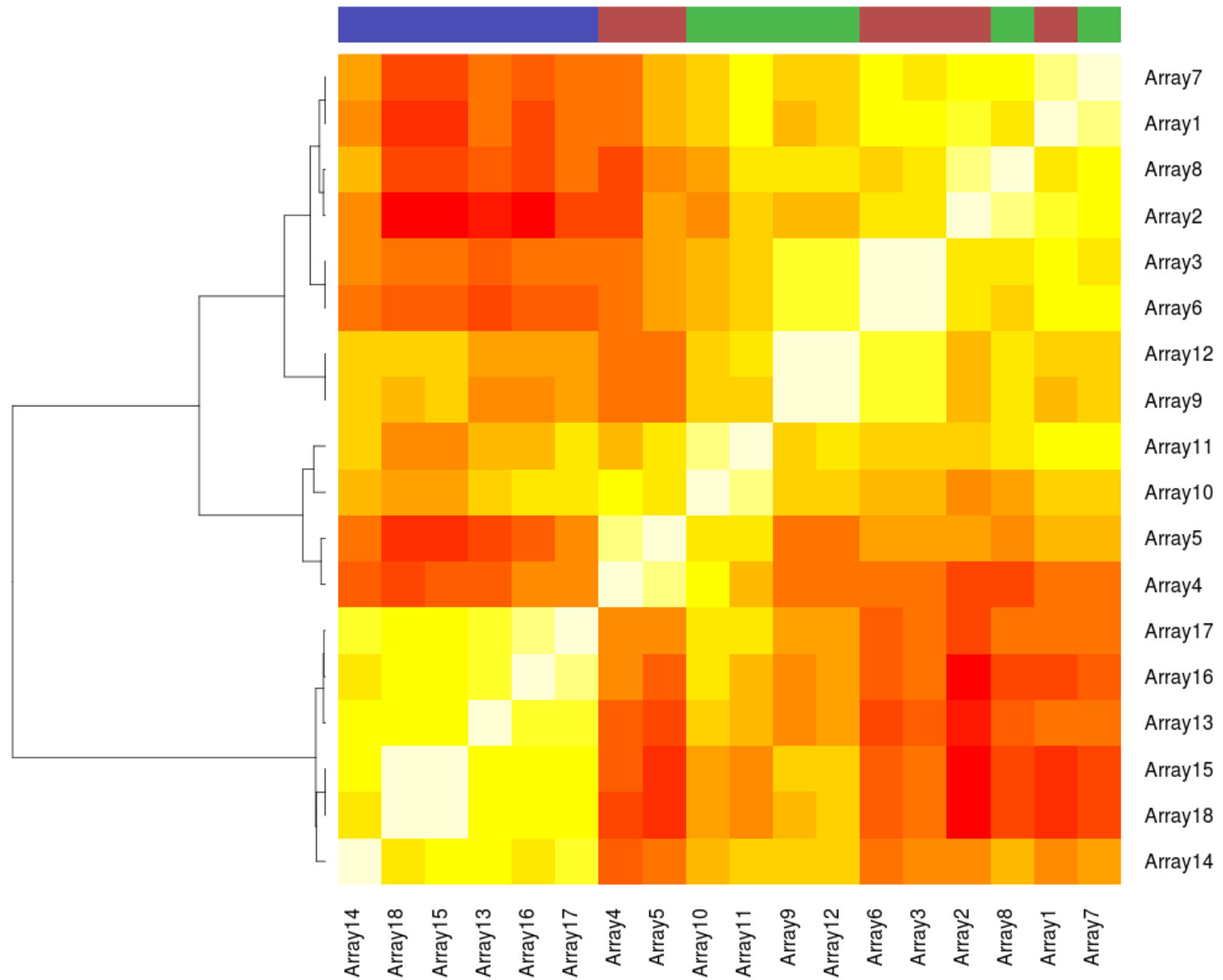
Array18 vs pseudo-median reference chip



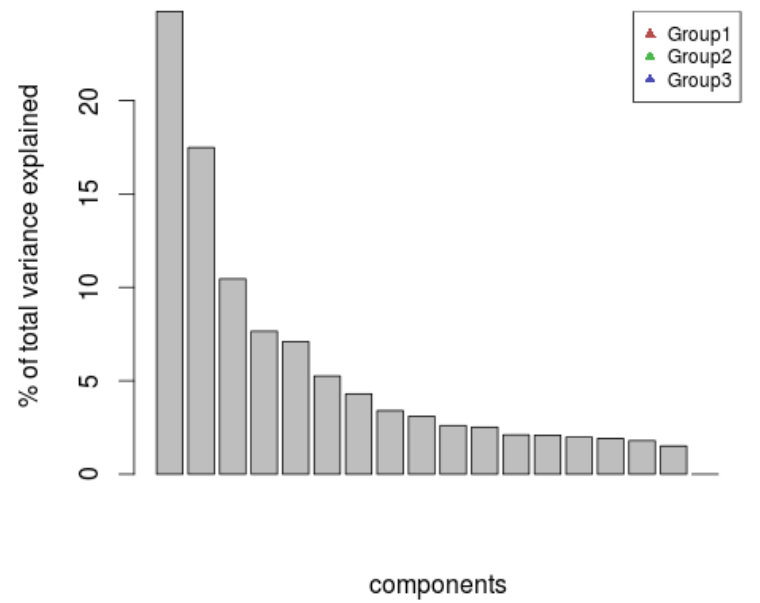
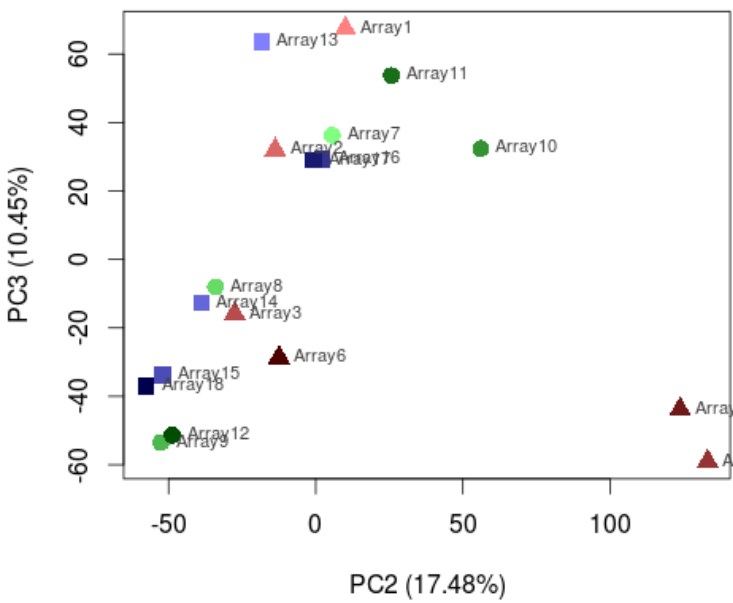
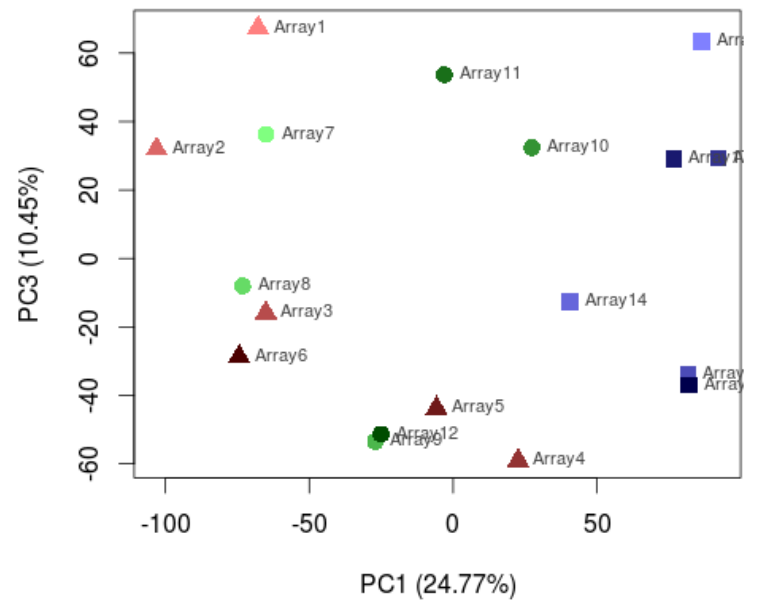
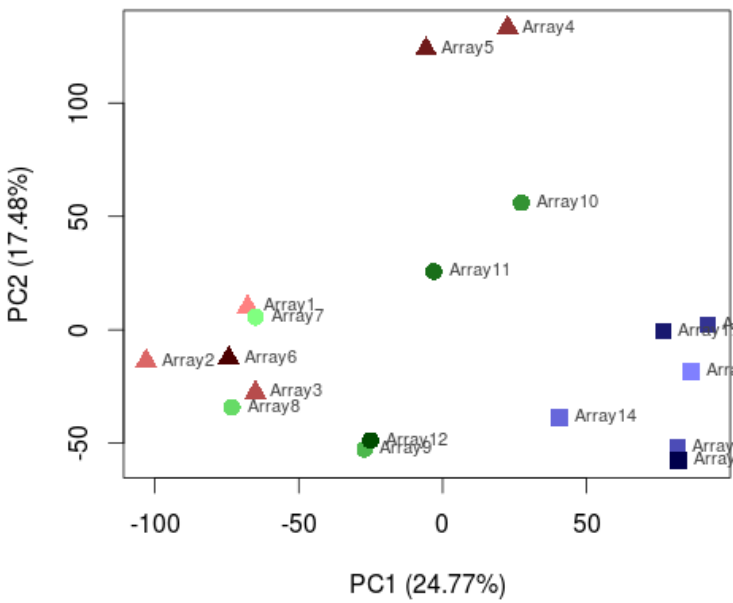
Color Key
and Density Plot



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



PCA analysis after GCRMA normalization



Cluster dendrogram of GCRMA normalized data

