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Appendix A

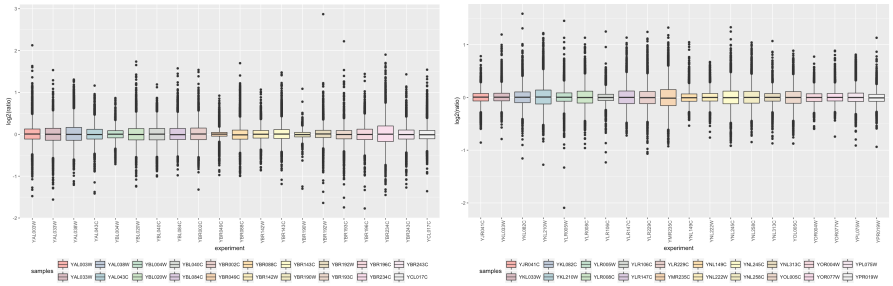
Exploratory Data Analysis

A.1 Initial Analysis of GO Annotations

There are 98,957 protein annotations with 17 variables, for 6381 distinct proteins from SGD database. 5530 distinct GO IDs have been used for annotation. 32,015 annotations were found to be duplicates (32.35% out of all). 232 annotations are explicitly noted as not being associated with the GO term. Under 18 different evidence codes: 25,412 annotations are with experimental evidence code; 5628 are with computational analysis evidence code; 481 are with author statement evidence code; 4838 are with curatorial statement evidence code; and 30,583 annotations are with IEA (Inferred from Electronic Annotation). There are 26,140 Biological Process GO term annotations; 19,129 Molecular Function GO term annotations; and 21,673 Cellular Component GO term annotations, in total. The annotations have been assigned by 8 parties: CACAO, GO Central, GOC, HGNC, InterPro, MGI, SGD and UniProt. Out of them, SGD stands for most of the annotations. All annotations belong to same database object type: 'gene', and the same taxon: 'taxon:559292', which indicates *S. cerevisiae*. Annotations have been made during the time period of 2000 - 2015. Most of the annotations have been made in 2015. All 30,583 IEA annotations have been made in 2015. However, the amount of curated annotations (36,359) surpasses the amount of electronically inferred annotations.

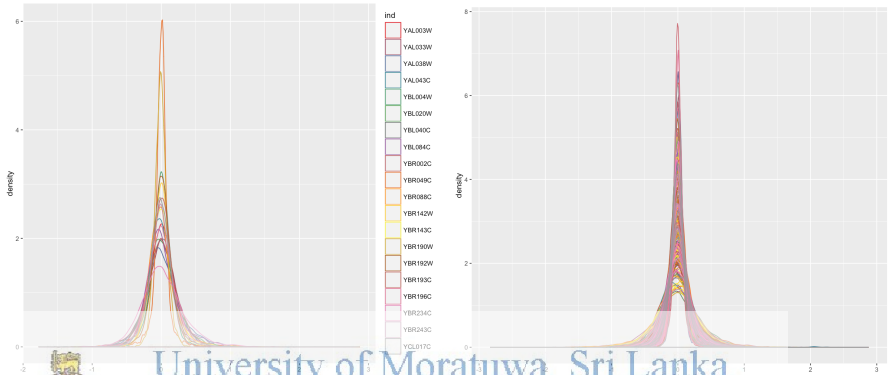
A.2 Data Visualizations

Following data visualizations were obtained using R graphic packages: *ggplot2* and *RColorBrewer*.



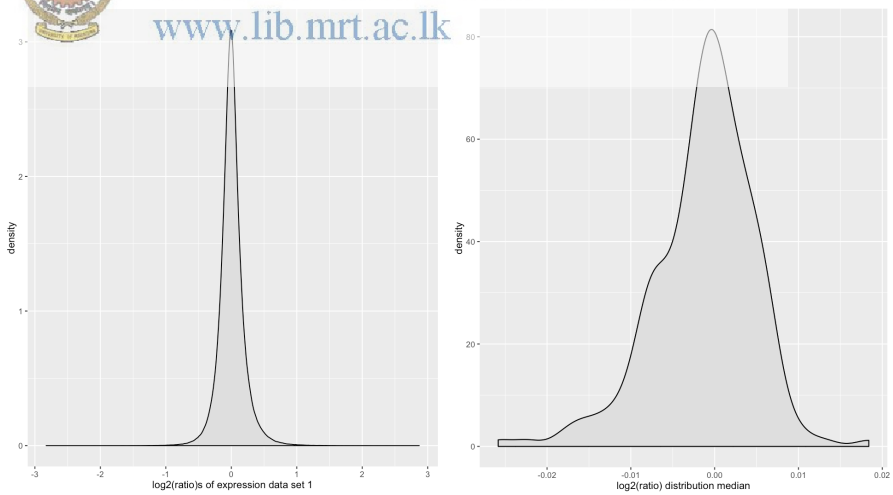
(a) First 20 experiments

(b) Last 20 experiments



(c) First 20 experiments

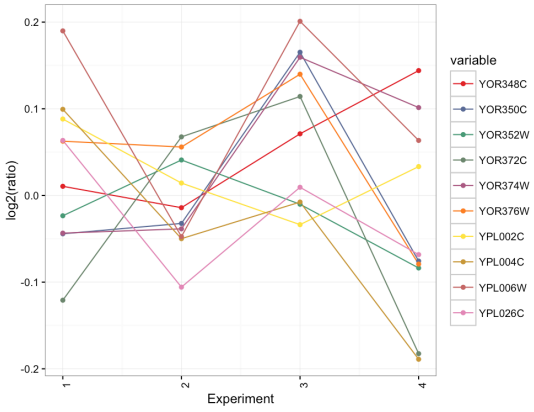
(d) All experiments



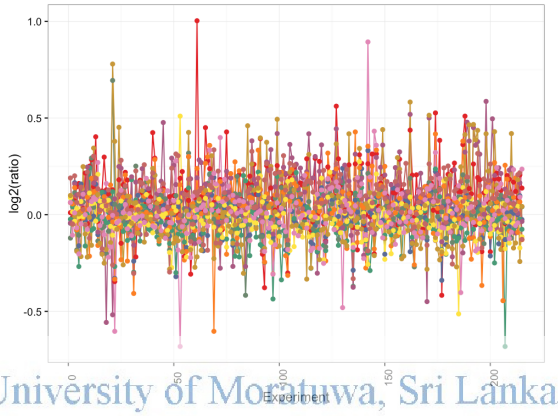
(e) All $\log_2$(ratio) values

(f) Median distribution

Figure A.2.1: Expressions 1 - Before normalization/preprocessing



(a) Expression ratio profiles of first 10 genes for the first 4 experiments



(b) Expression ratio profiles of first 10 genes for all experiments

Figure A.2.2: Expressions 1 - After normalization/preprocessing

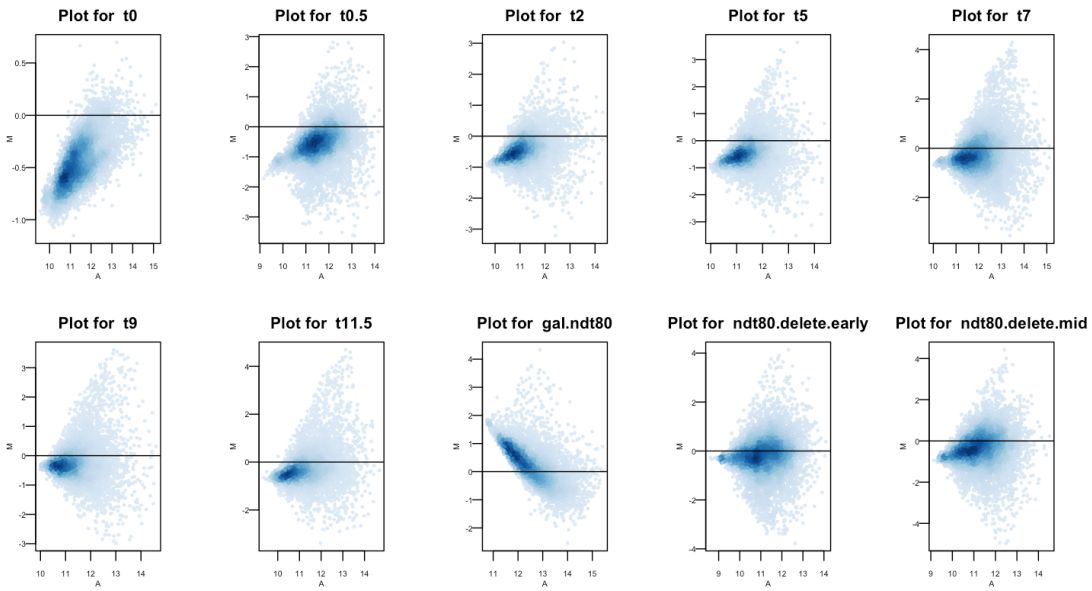


Figure A.2.3: Expressions 2 - MA plots before background correction

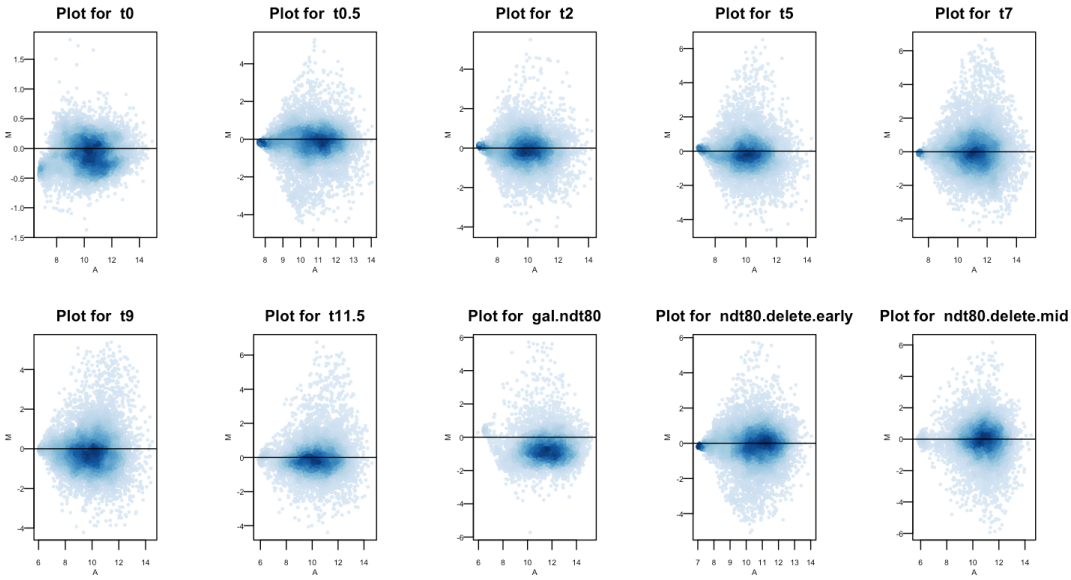


Figure A.2.4: Expressions 2 - MA plots after background correction

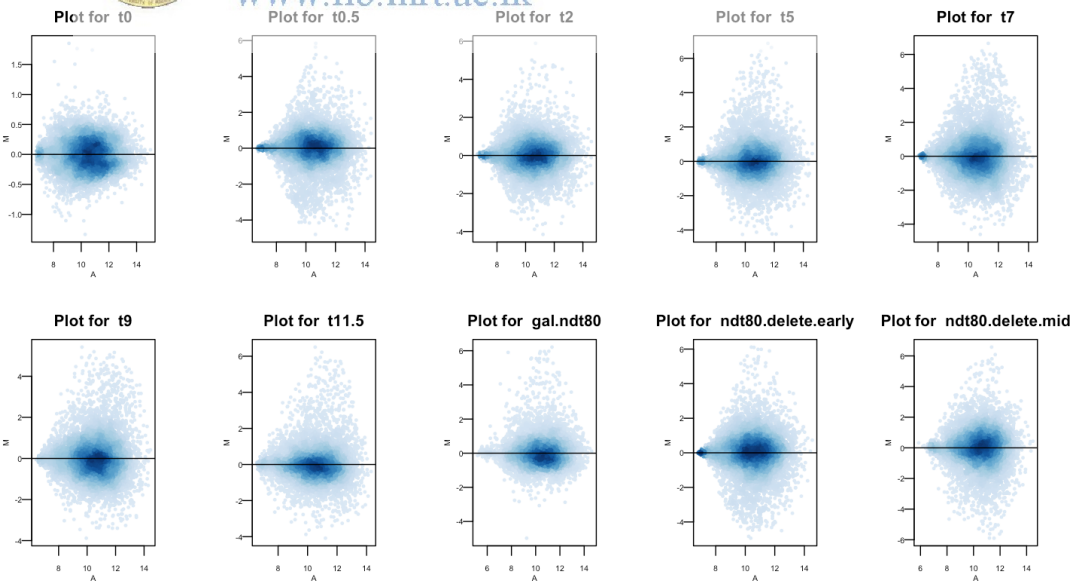
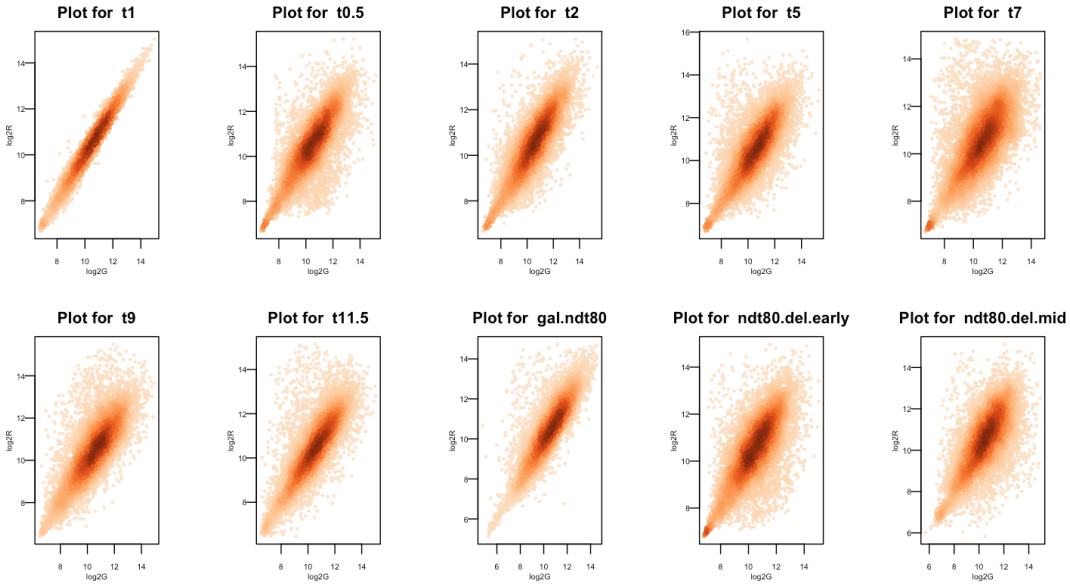
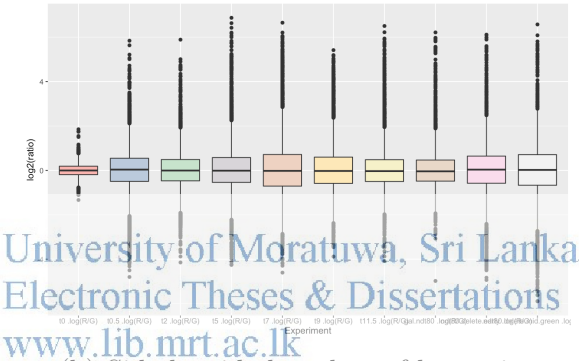


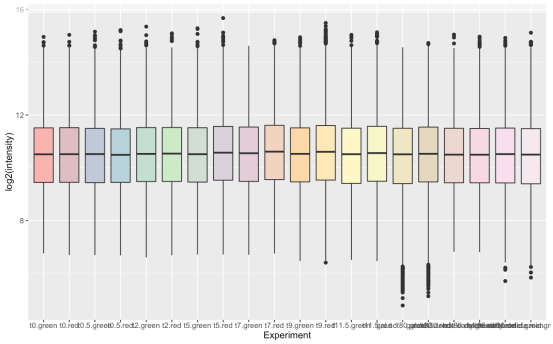
Figure A.2.5: Expressions 2 - MA plots after within/between array normalization



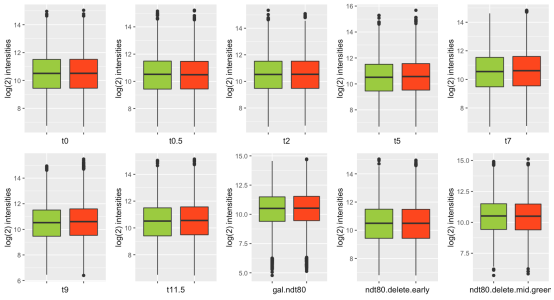
(a) Expressions 2 - log_2(G) vs log_2(R)



(b) Side-by-side boxplots of log ratios

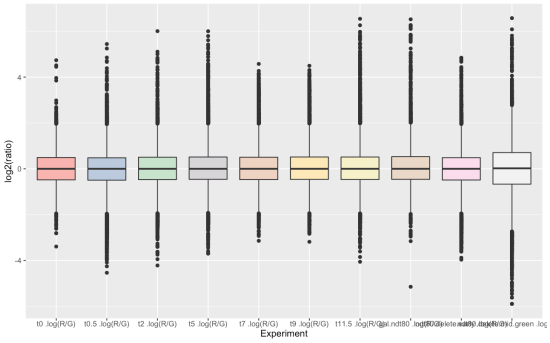


(c) Side-by-side boxplots of log_2(R) and log_2(G)

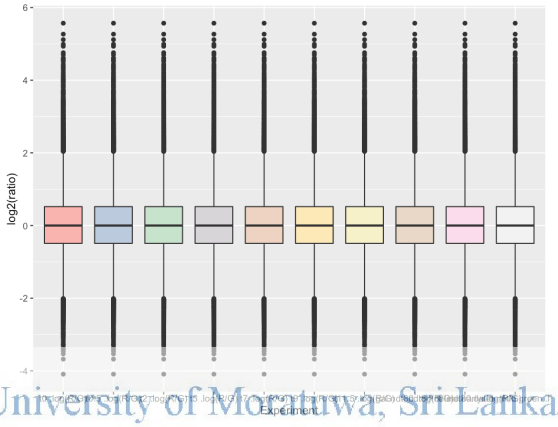


(d) Side-by-side pair boxplots of log_2(R) and log_2(G)

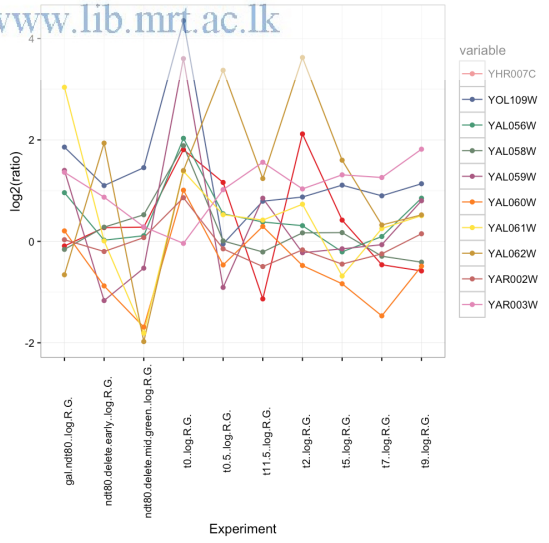
Figure A.2.6: Expressions 2 - After normalization/preprocessing



(a) After median centering and scale normalization

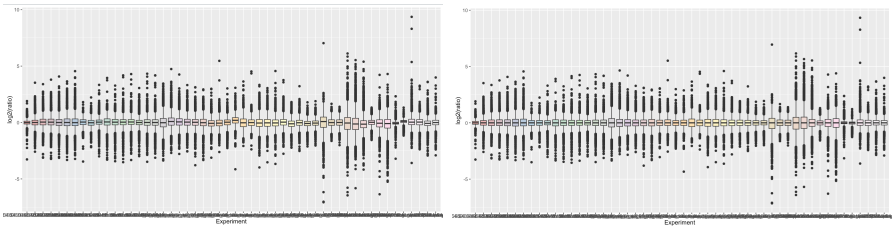


(b) After quantile normalization



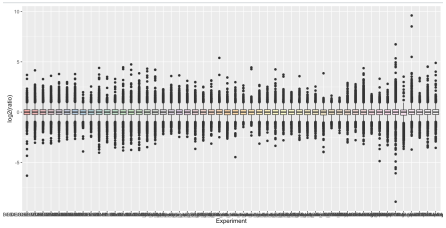
(c) Final Gene expression ratio profiles of first 10 genes

Figure A.2.7: Expressions 2 - After further normalization

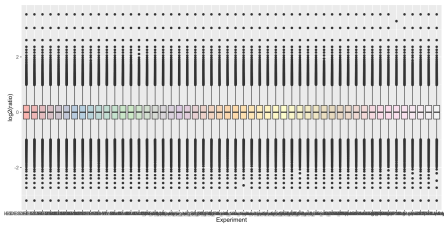


(a) Before normalization

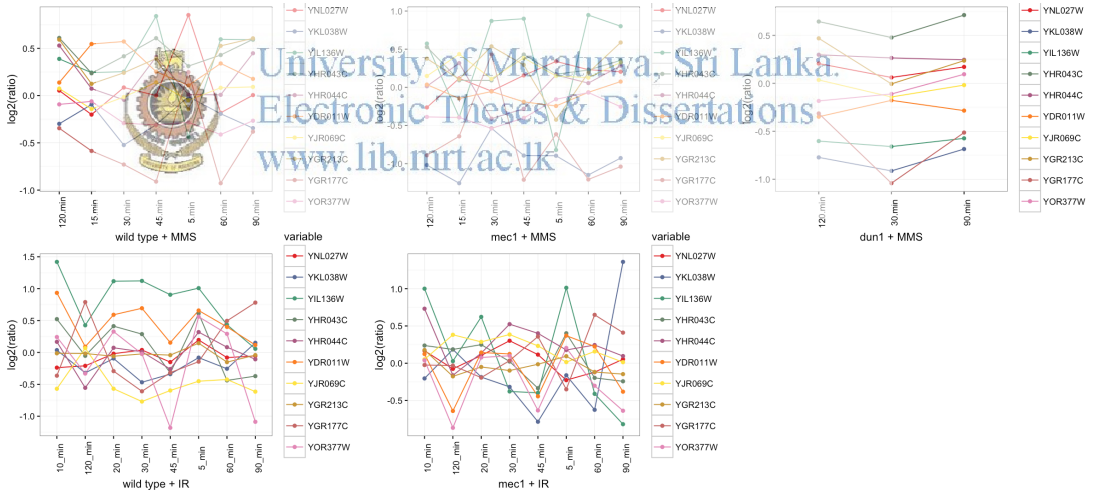
(b) After median centering



(c) After scale normalization

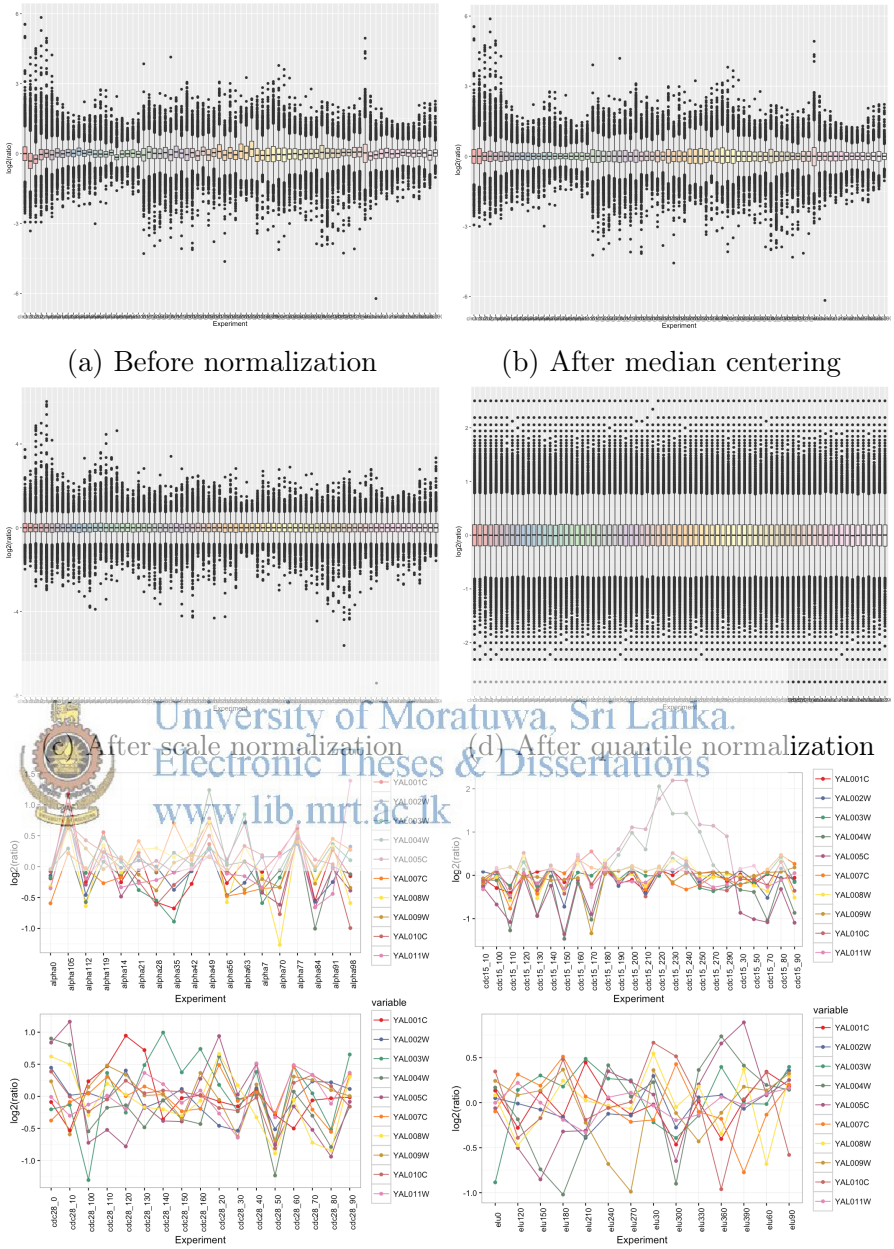


(d) After quantile normalization



(e) After normalization, expression ratio profiles of first 10 genes for the time series over each major experiment

Figure A.2.8: Expressions 3 - before & after normalization/preprocessing



(a) Before normalization

(b) After median centering

(c) After scale normalization

(d) After quantile normalization

(e) After normalization, expression ratio profiles of first 10 genes for the time series over each major experiment

Figure A.2.9: Expressions 4 - Before & after normalization/preprocessing

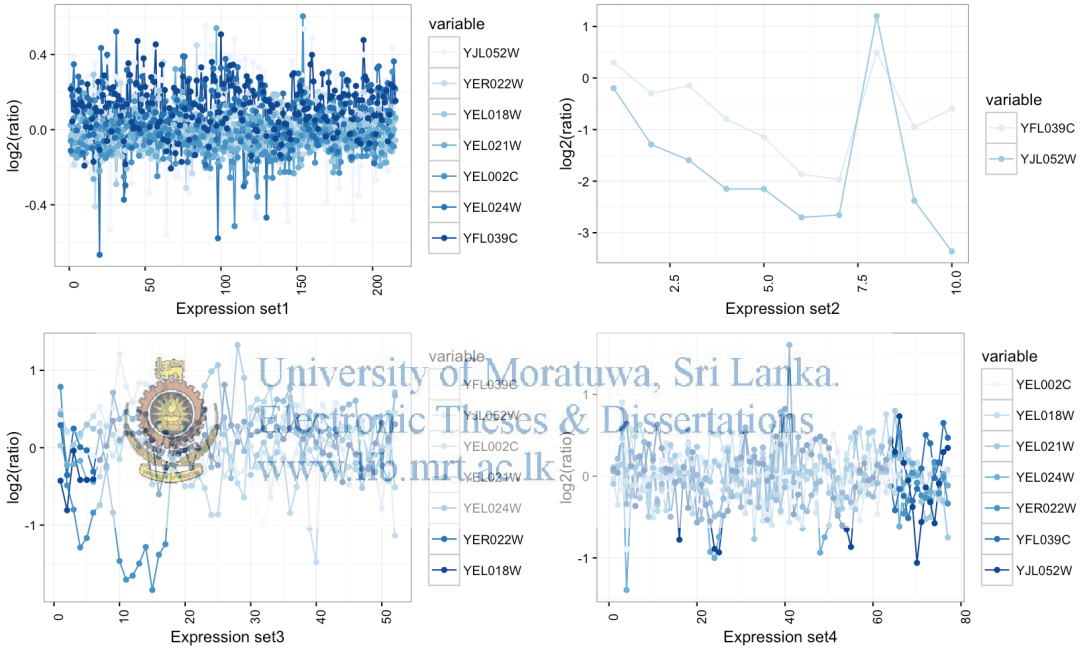


Figure A.2.10: Expression profiles of housekeeping genes

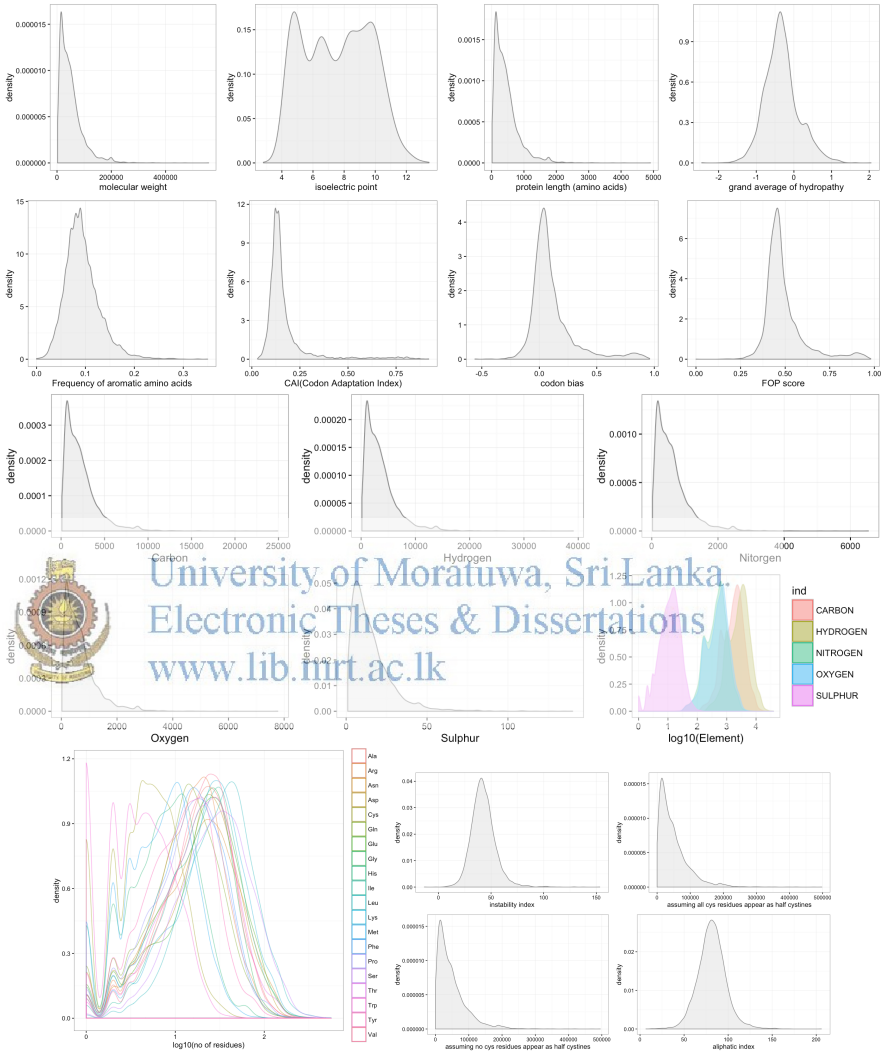


Figure A.2.11: Properties Data