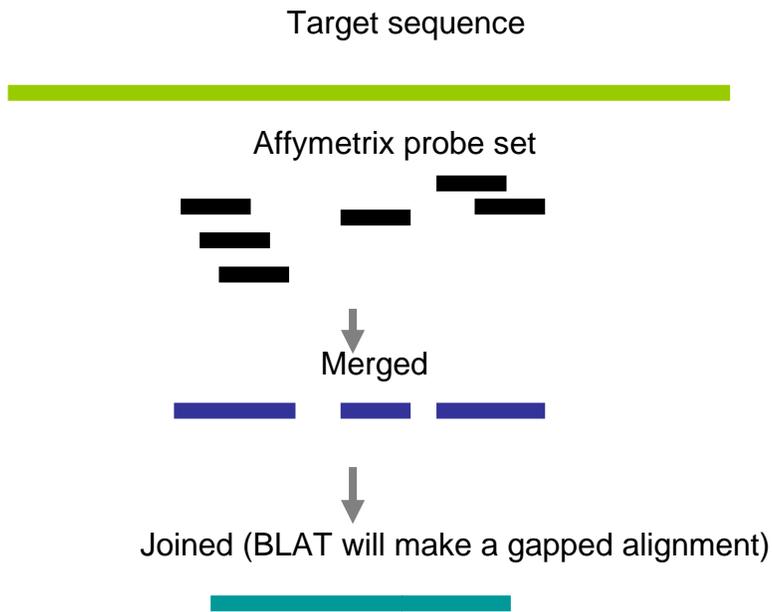


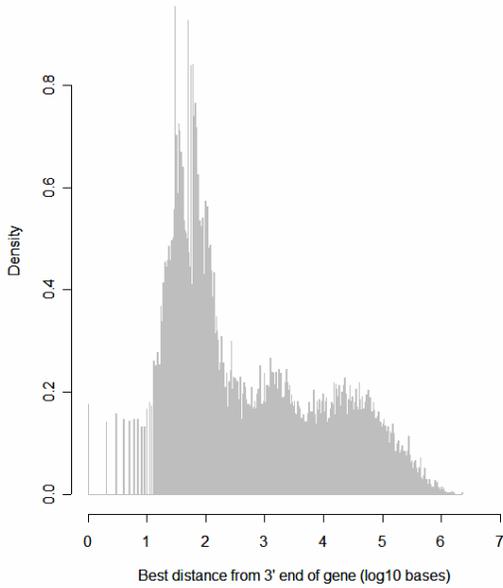
Supplementary figures

Barnes et al.

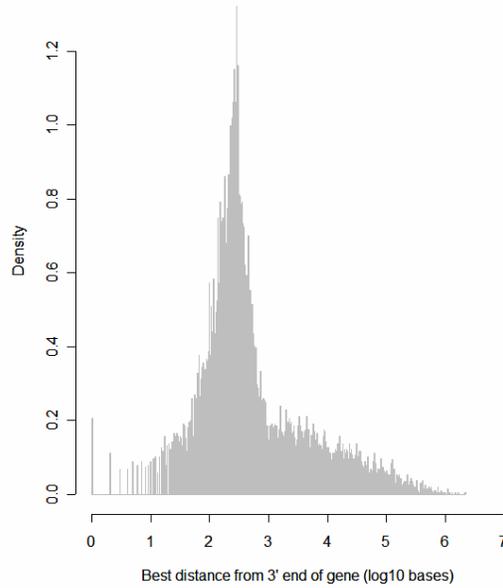


Schematic of the Affymetrix probe merging procedure.

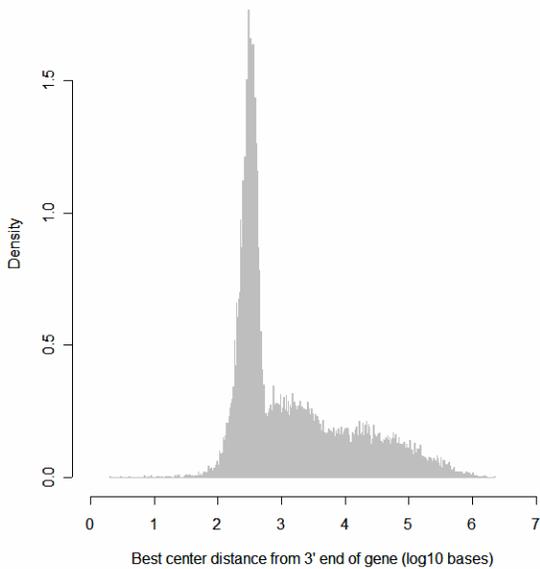
Affymetrix probe locations



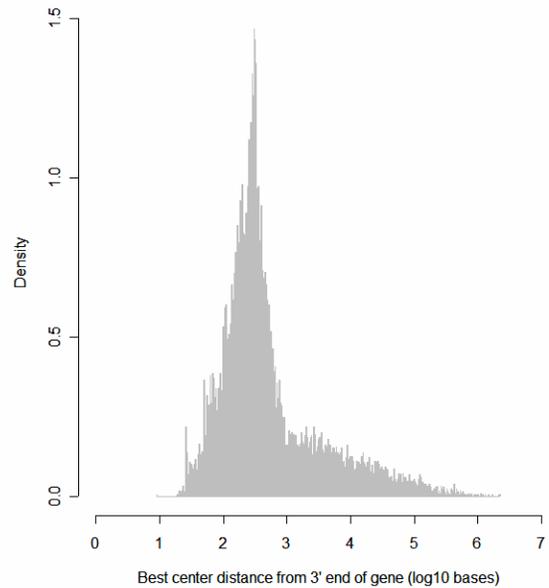
Illumina probe locations



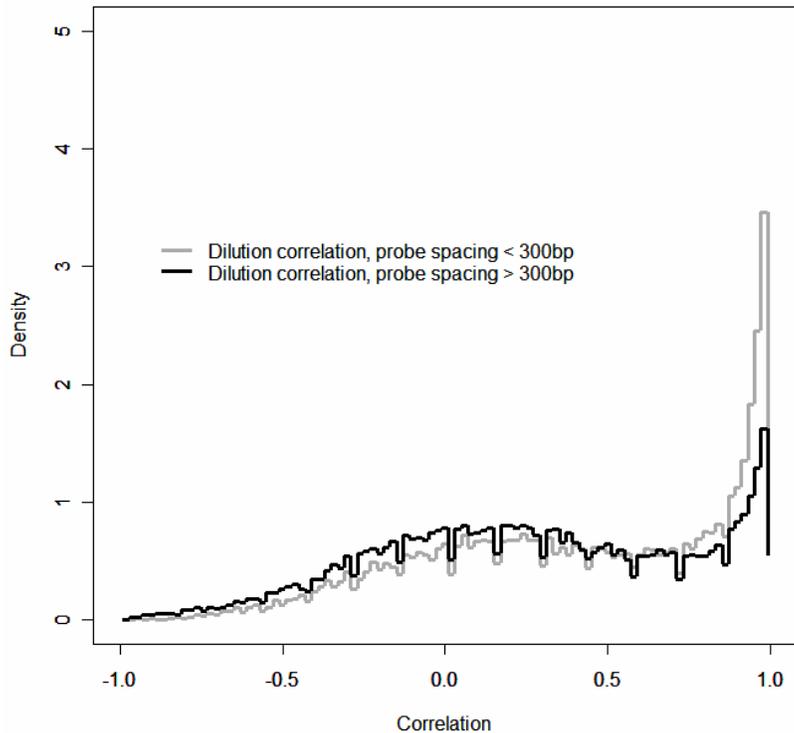
Affymetrix probe locations



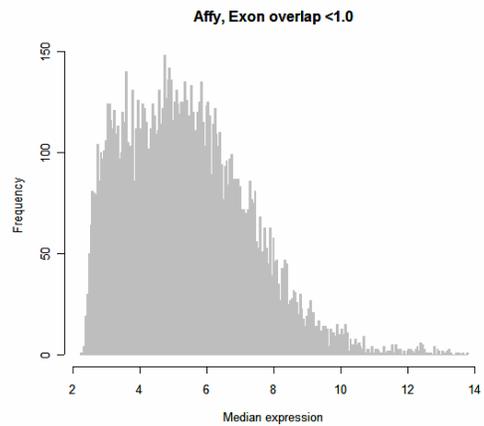
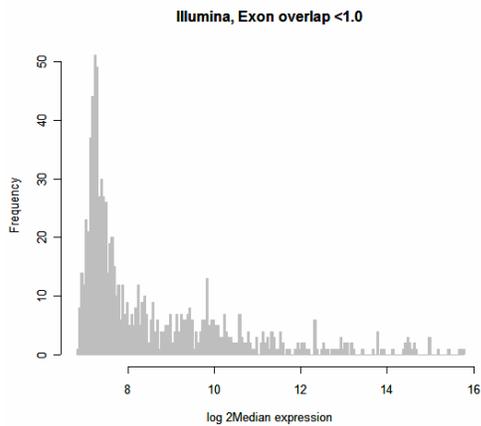
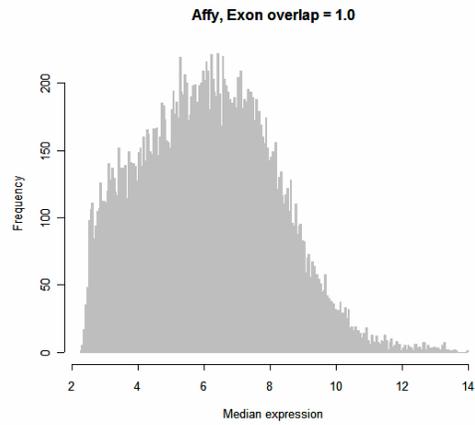
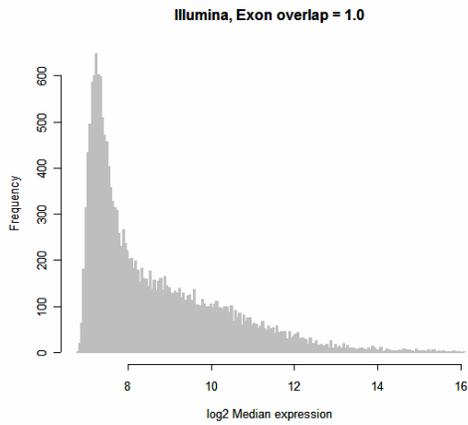
Illumina probe locations



Distribution of probe locations relative to gene 3' ends. Top panels use the 3' end of the probe sequence to compute the distance. Bottom panels use the center.

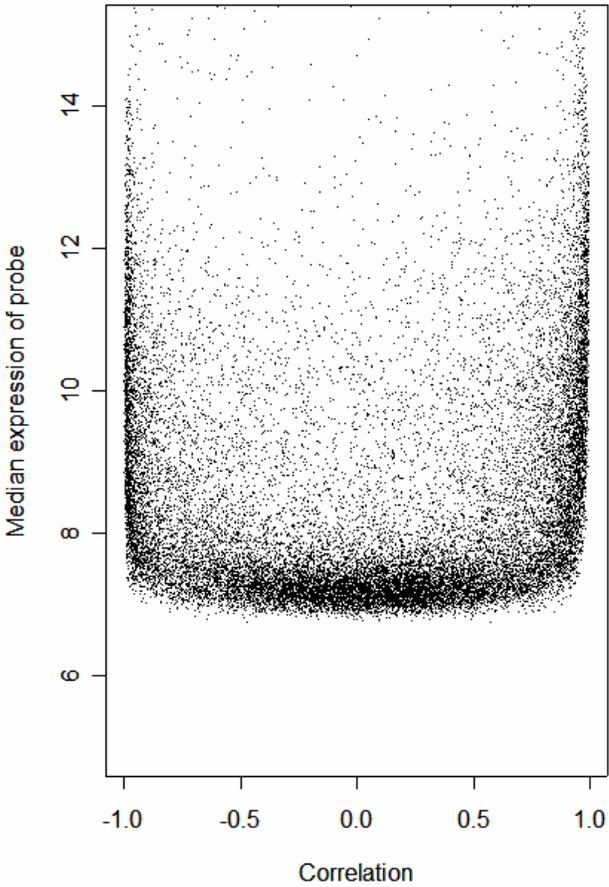


Effect of relative probe location across platforms on agreement across platforms, using the center of the probe instead of the 3' end as the location.

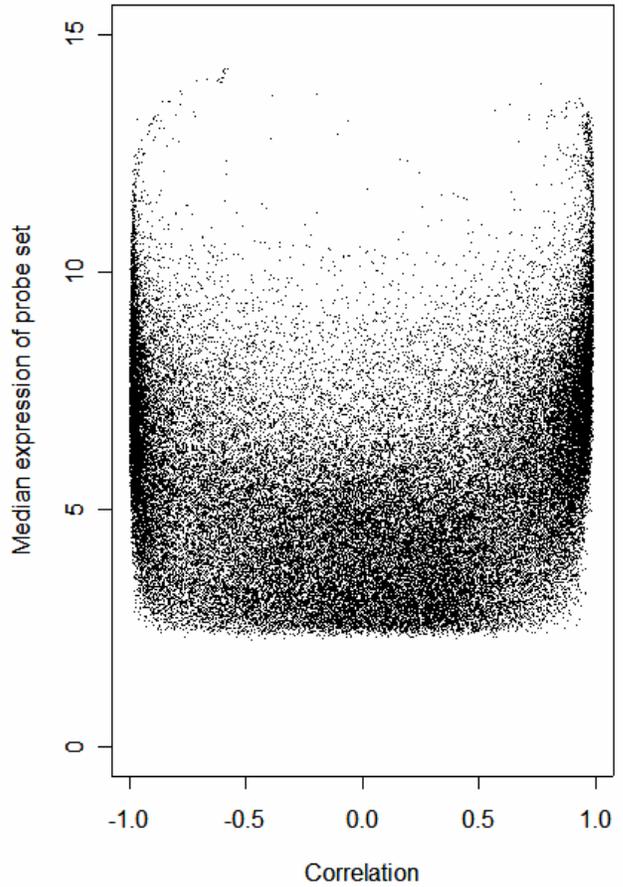


Probes which are not fully contained in known exons are expressed at lower levels on both platforms.

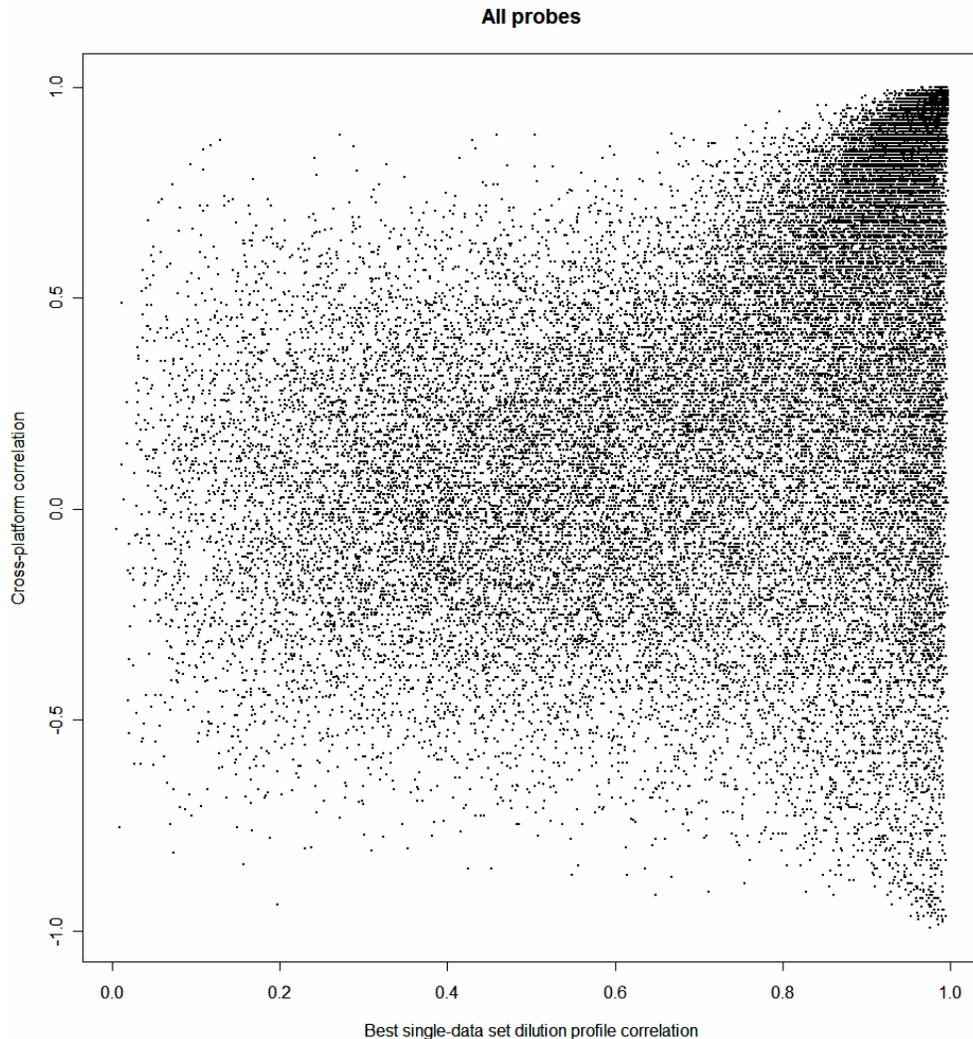
Illumina



Affymetrix

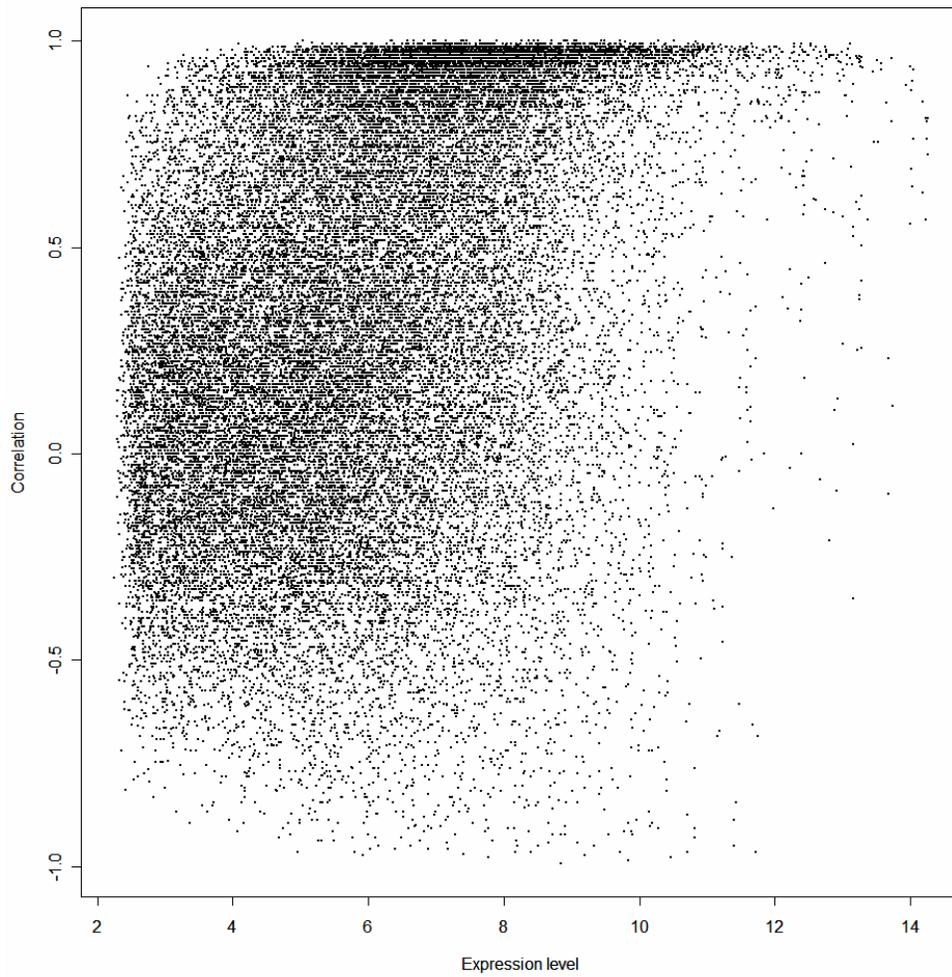


Effect of gene expression level on dilution effect on each platform.

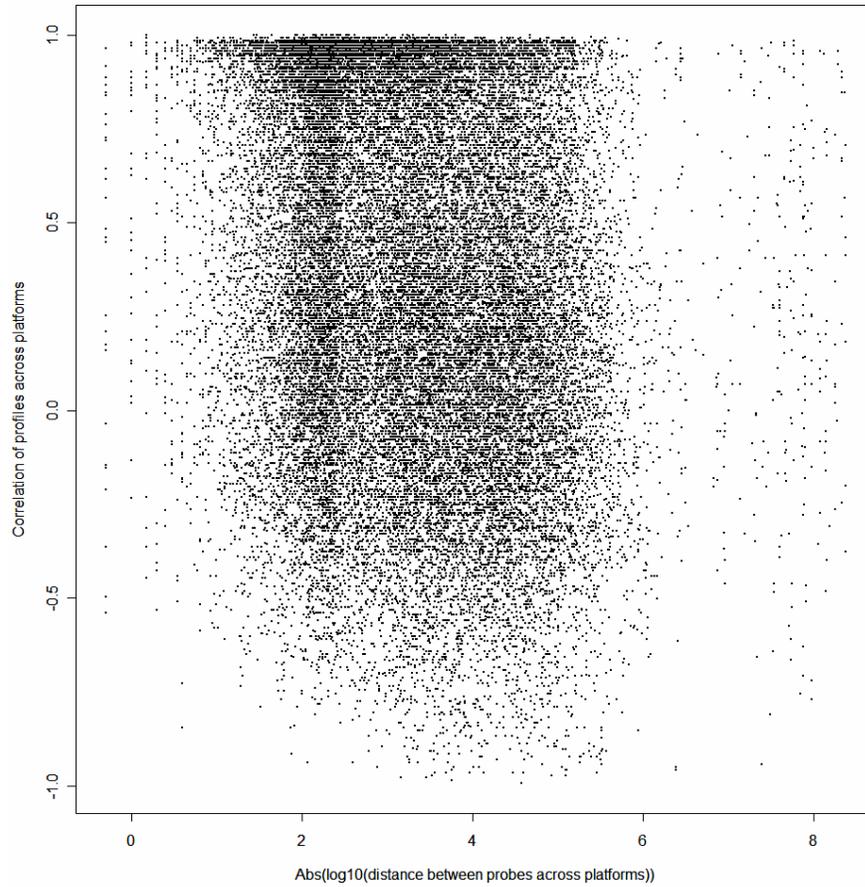


Cross-platform correlation considered as a function of whether the gene shows a dilution effect. The cluster of points at upper right indicates that most probes showing strong cross-platform agreement also show a dilution effect.

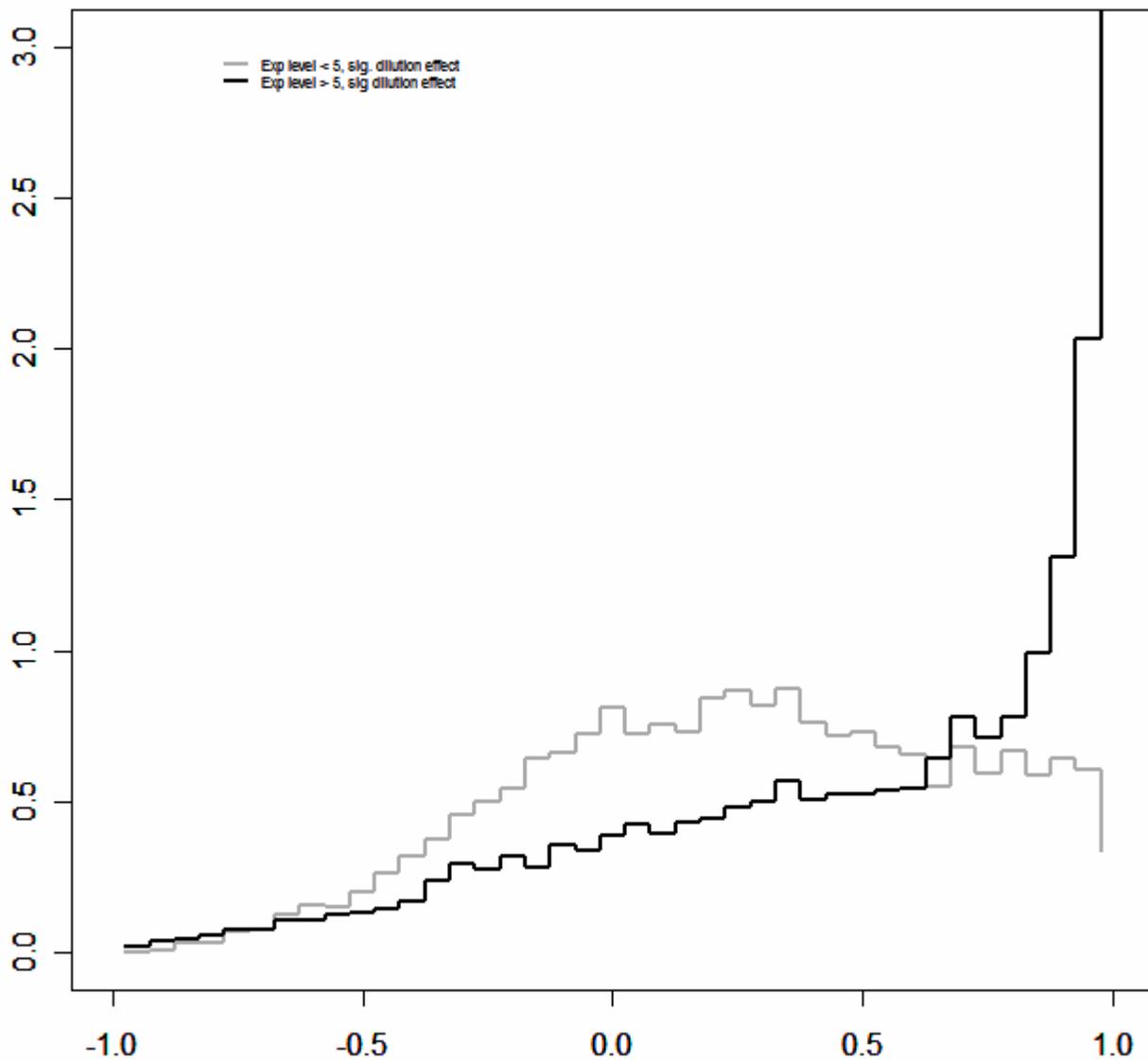
Effect of expression level on cross-platform agreement



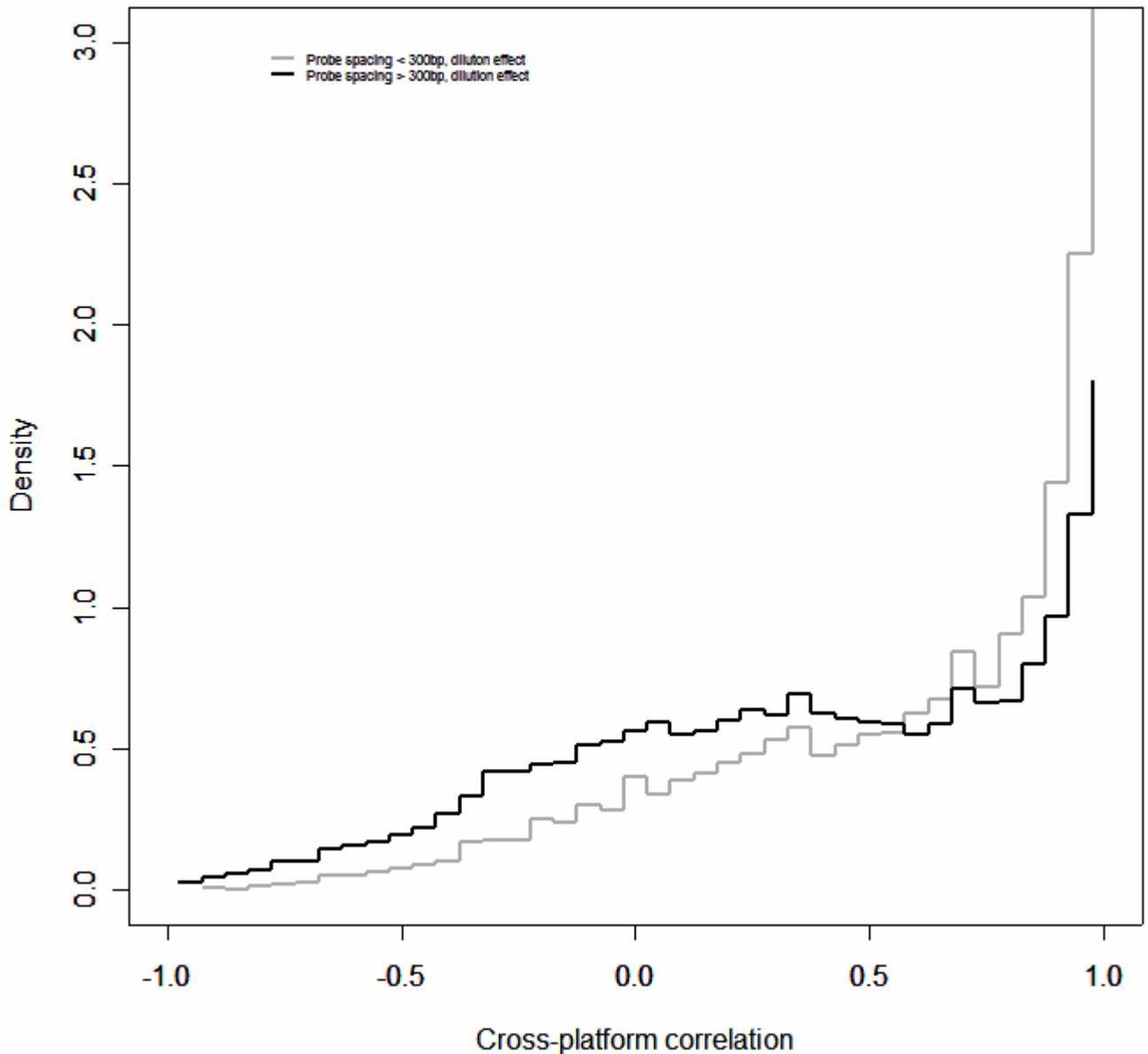
Effect of expression level on cross-platform agreement. Expression is \log_2



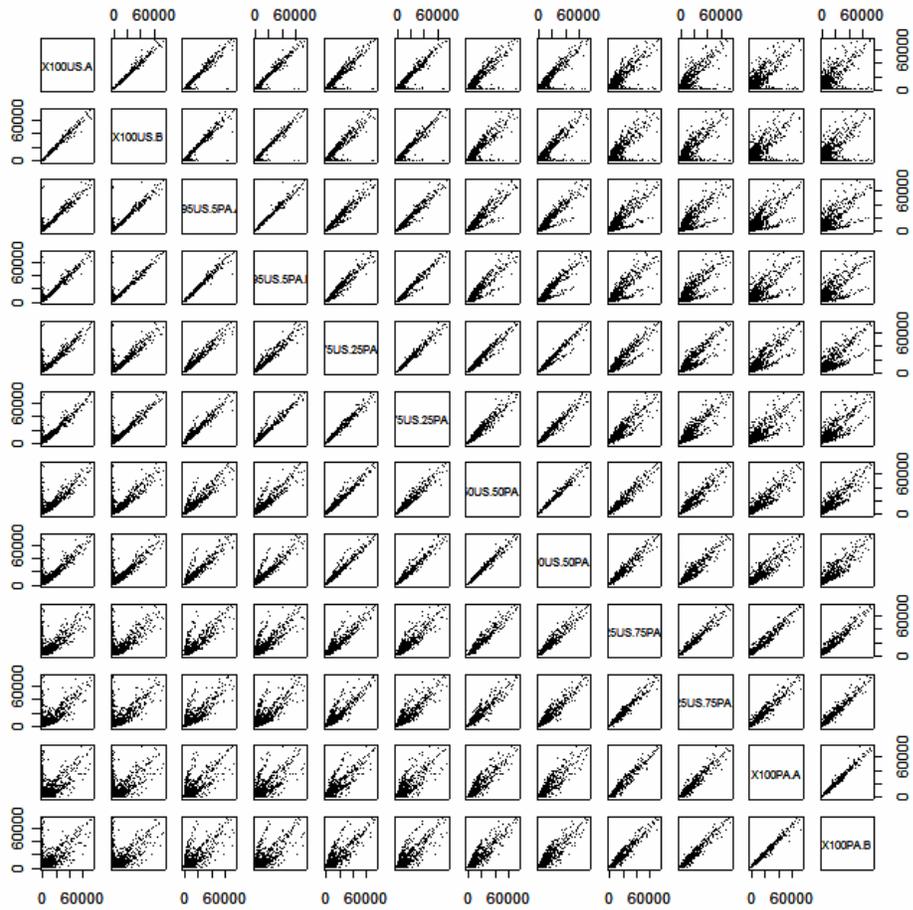
Effect of distance between probes on cross-platform agreement.



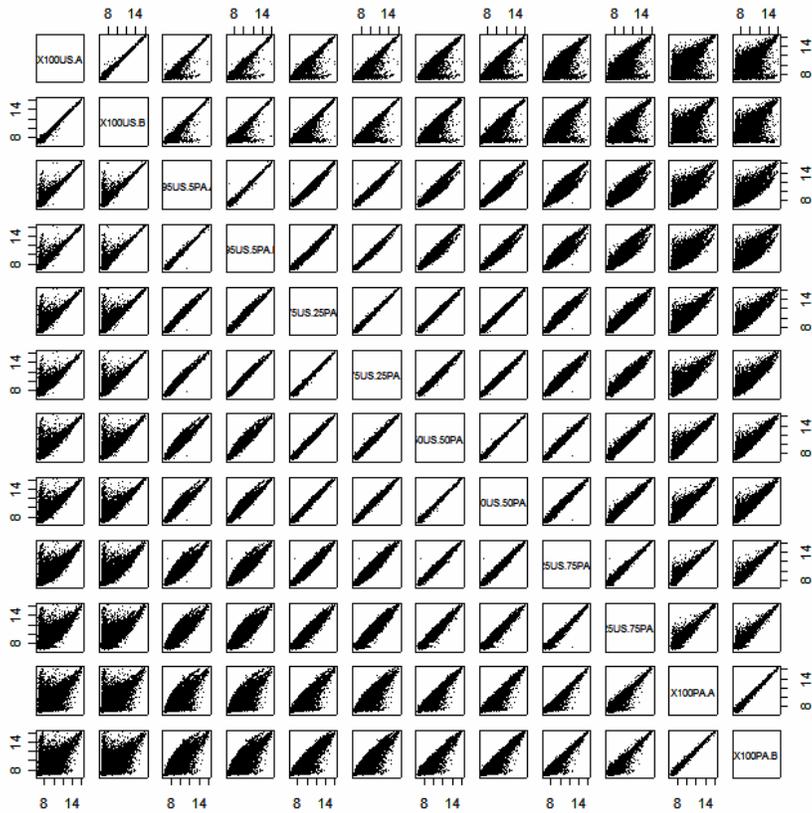
- Expression level effect on cross-platform agreement, after removing probes without a significant dilution effect (in at least one platform)



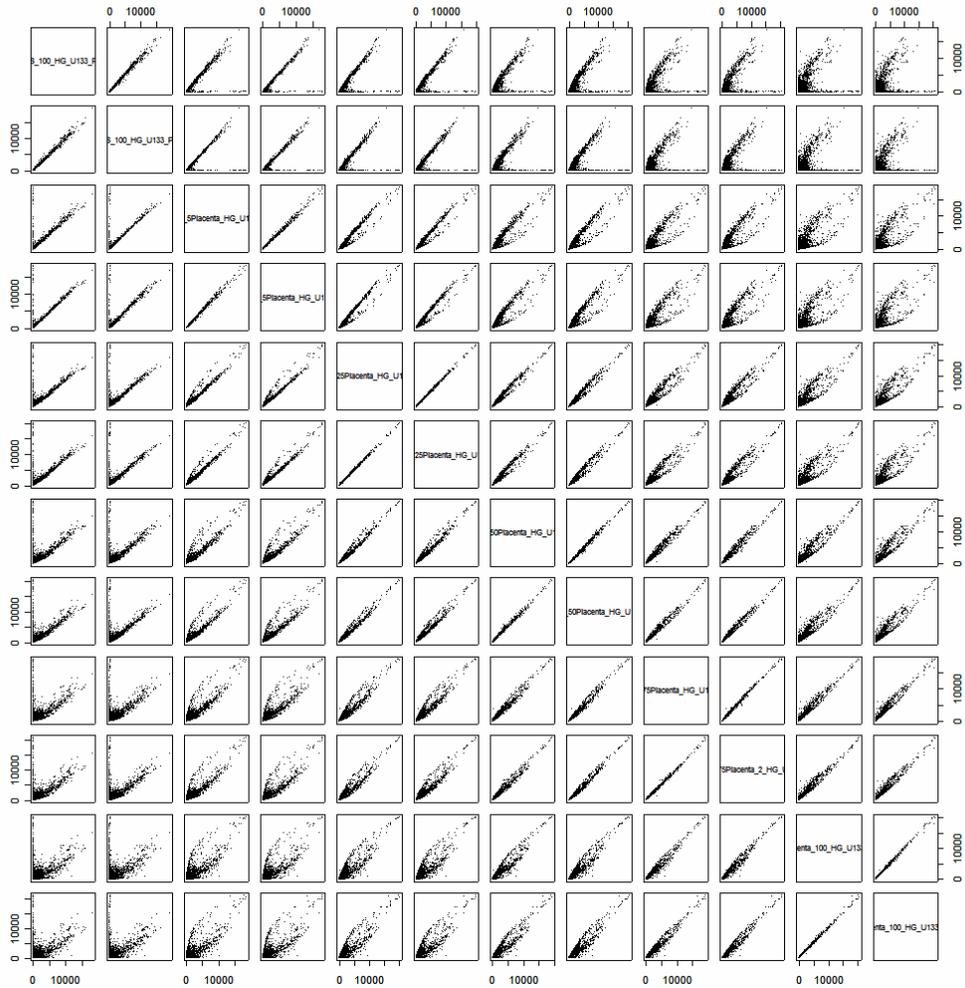
- Probe location effect on cross-platform agreement, after removing probes without a significant dilution effect (in at least one platform)



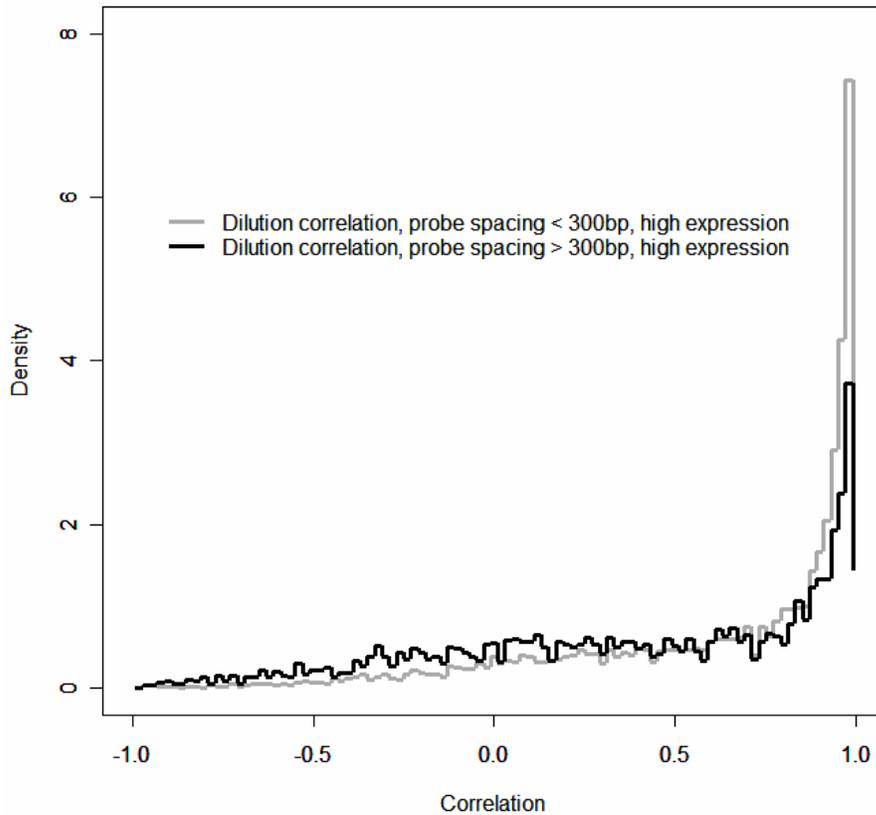
Pairwise graphs of the Illumina data sets (raw scale)



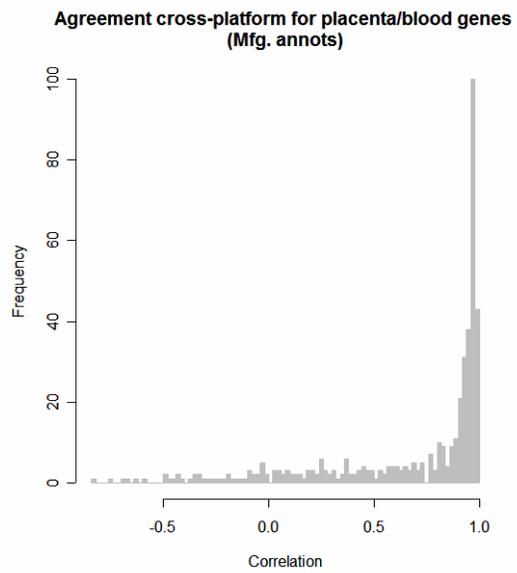
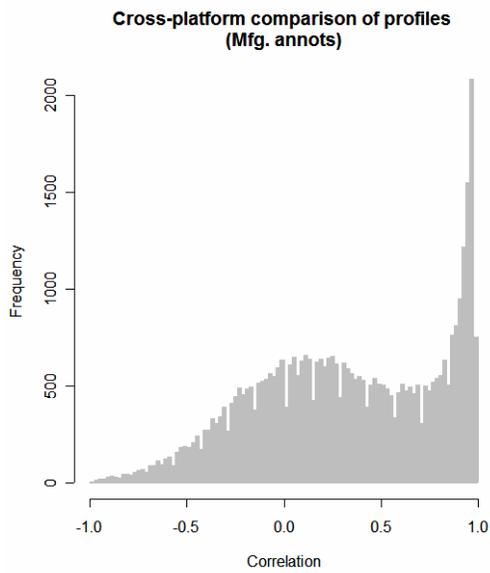
Pairwise graphs of the Illumina data (log scale)



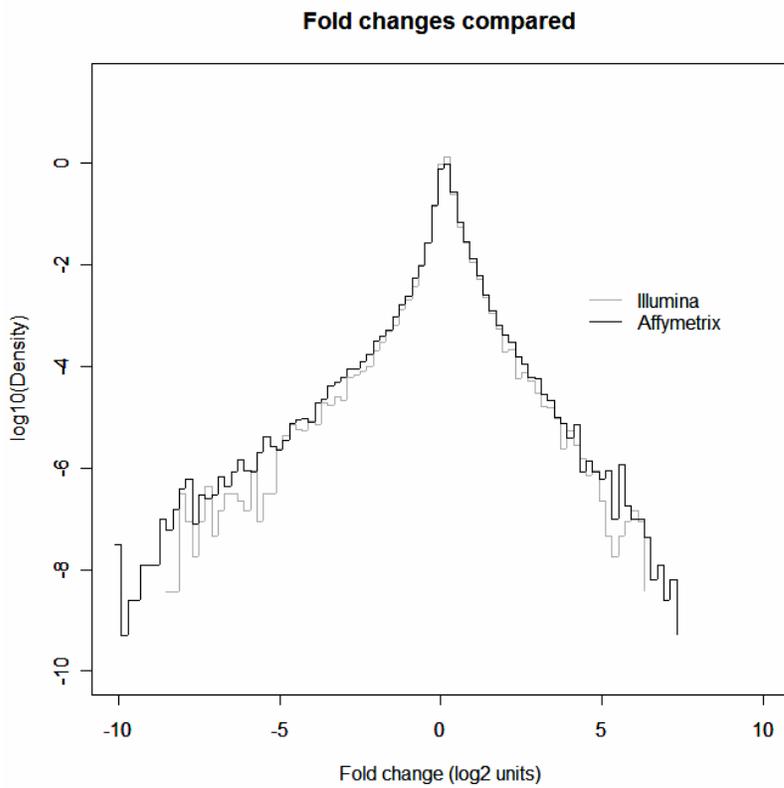
Pairwise graphs for Affymetrix data, raw scale
 (obtained by exponentiating the RMA results)



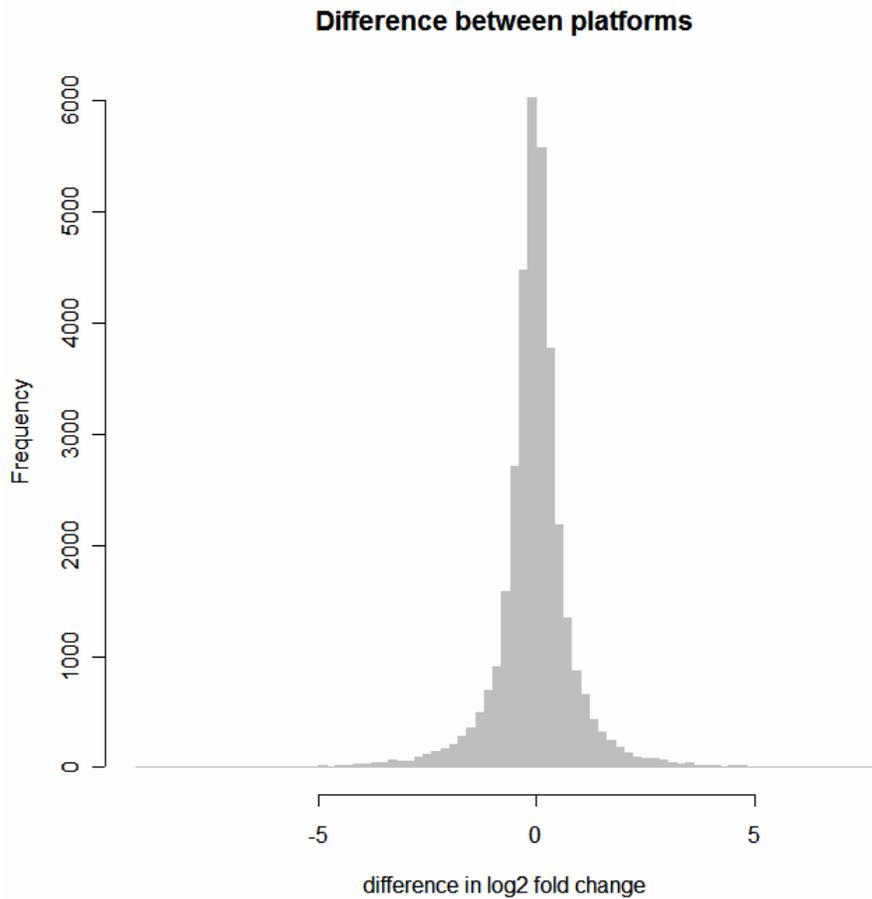
Effect of probe placement on cross-platform agreement, selecting probes expressed at higher levels only.



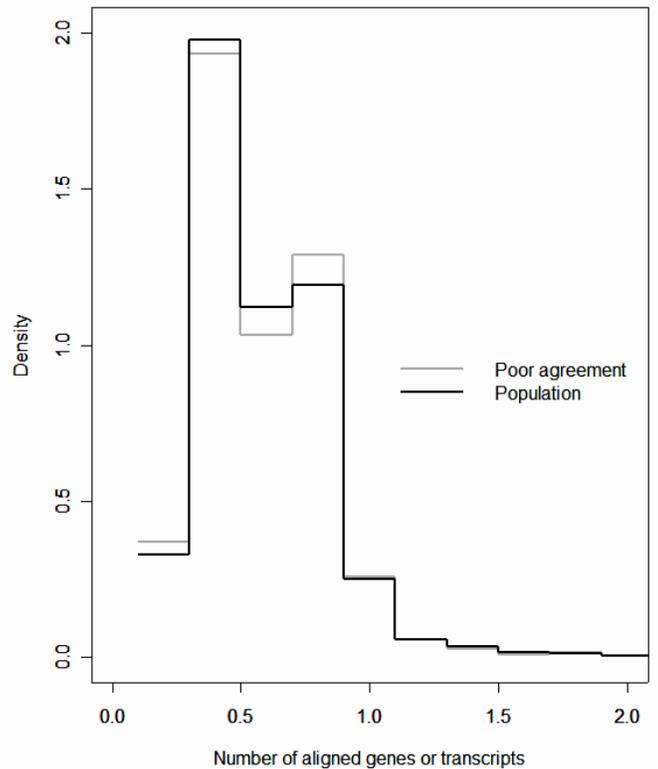
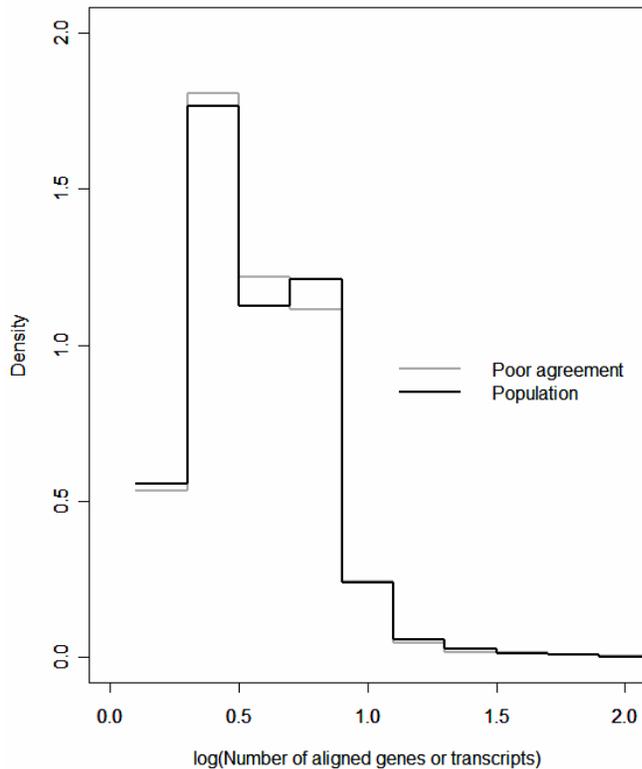
Cross-platform agreement results using manufacturer's gene assignments.



Distribution of fold-change between placenta and blood on each platform.

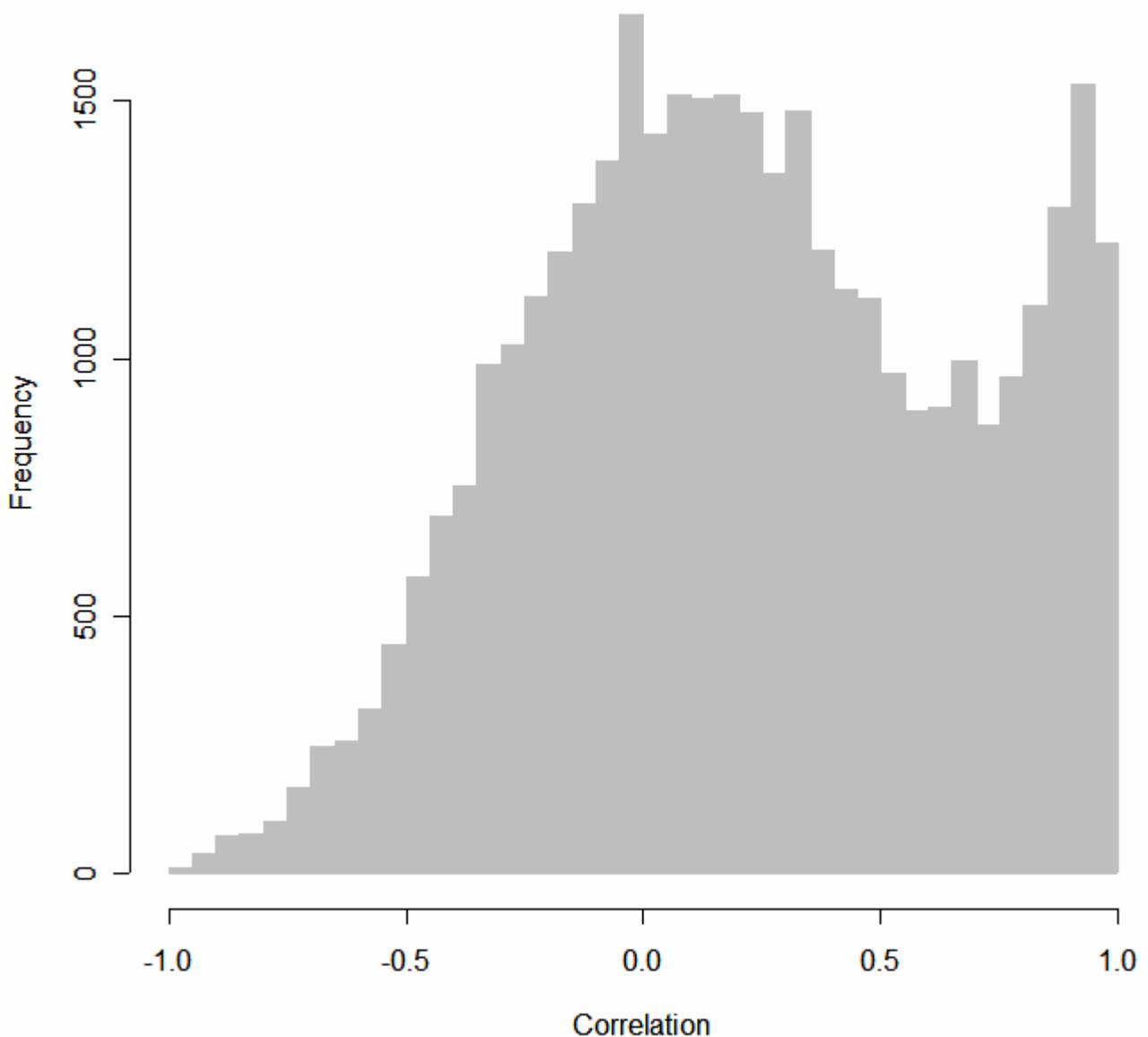


Comparison of fold changes across platforms. Values near zero mean the two platforms agree.



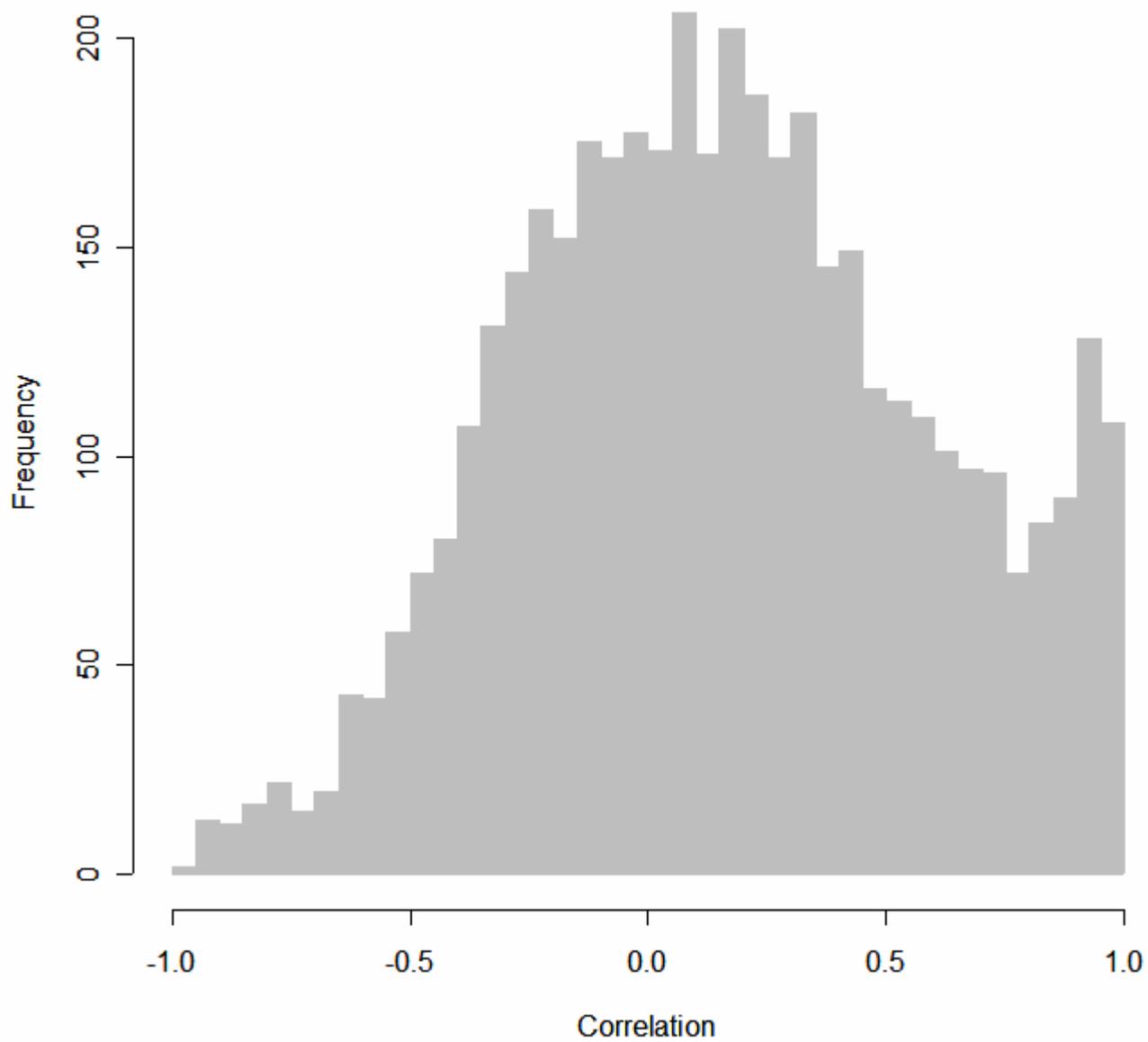
- Probes showing “unexplained” disagreement do not target an unusual distribution of transcripts.
- X axis in both graphs is \log_{10} of the number of transcripts/mRNAs.

Cross-platform comparison of profiles

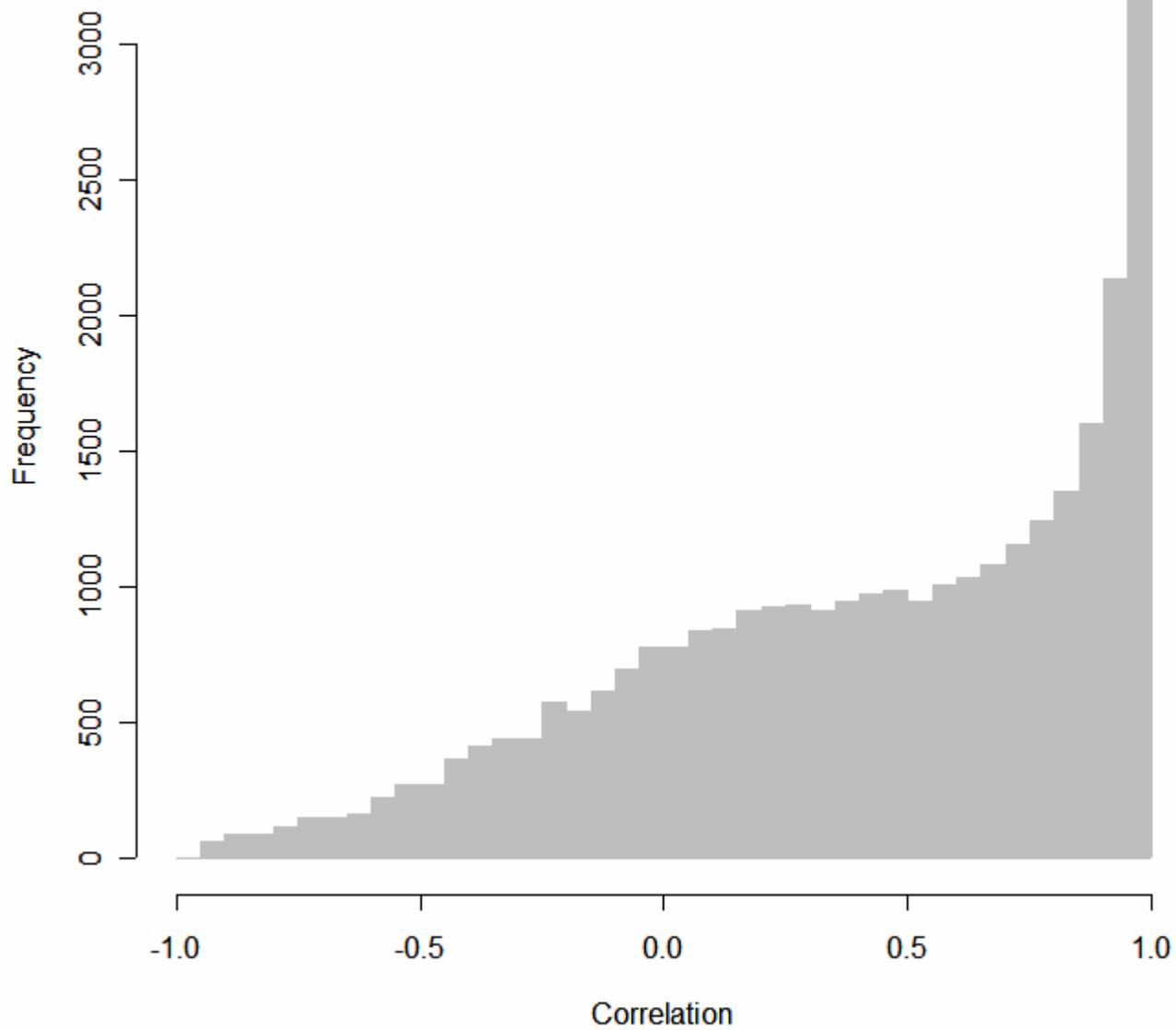


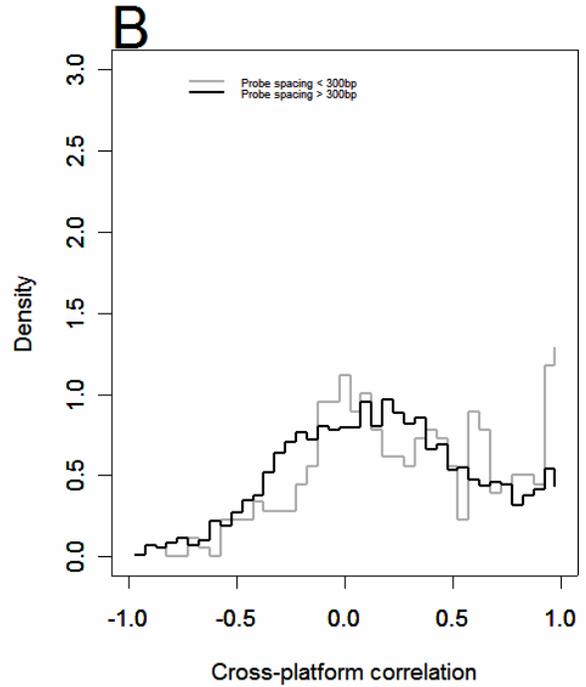
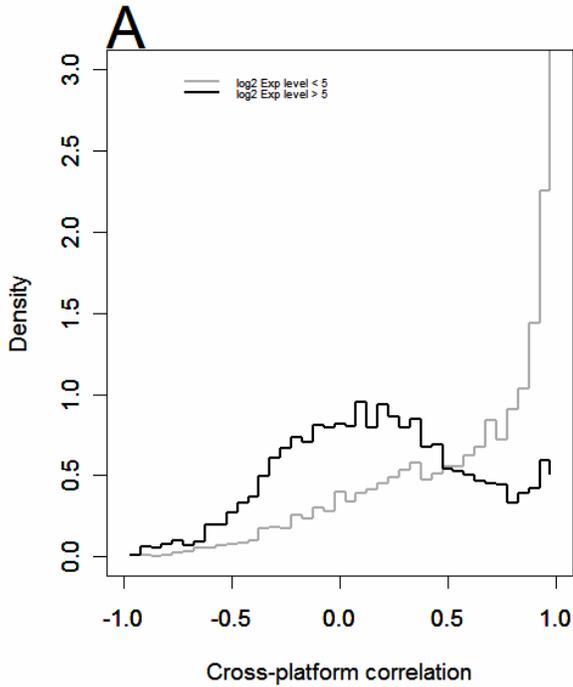
- The Affymetrix data used in this analysis included only the 3'-most probe of each probe set. The results are inferior to those obtained with the full RMA-extracted results.

Within-platform comparison of profiles (Illumina)

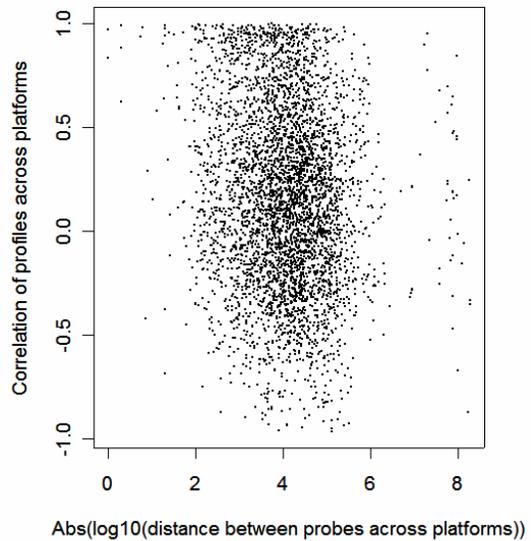
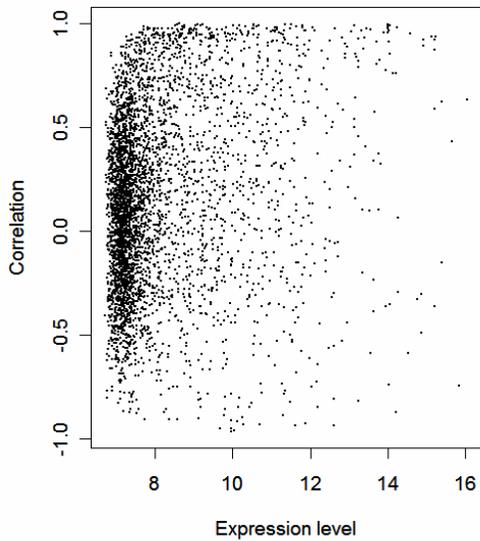


Within-platform comparison of profiles (Affymetrix)

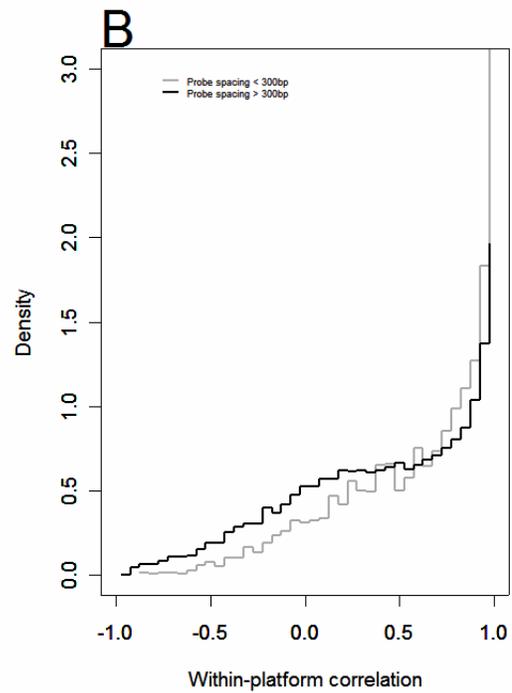
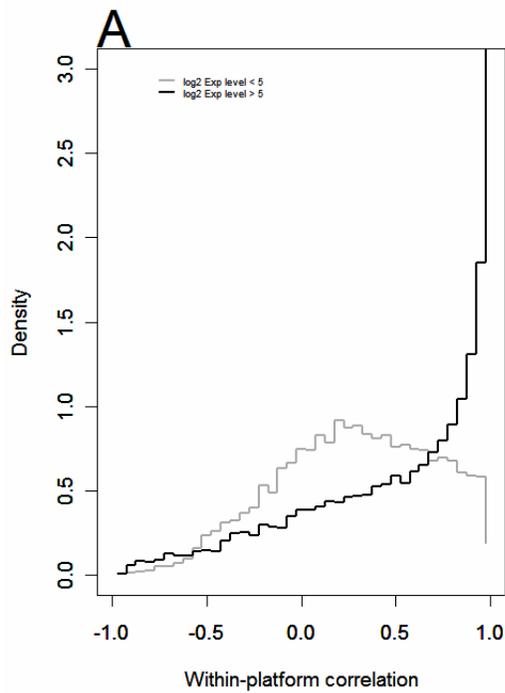




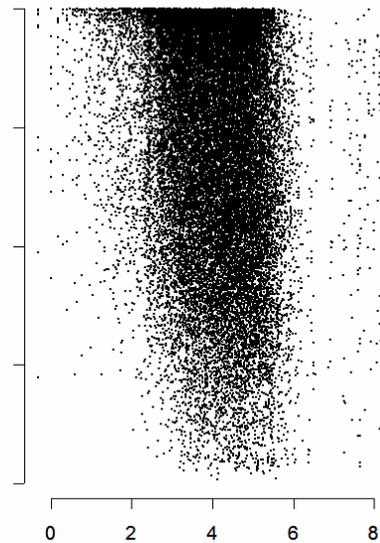
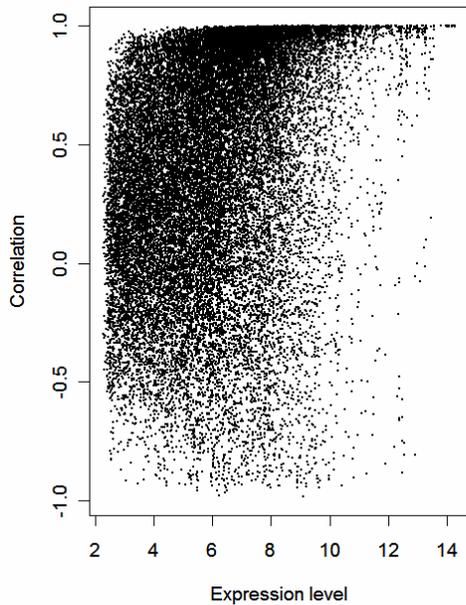
Within-platform reproducibility, stratified by expression level and location (Illumina)



Within-platform reproducibility, full data sets (Illumina)



Within-platform reproducibility, stratified by expression level and location (Affymetrix)



Within-platform reproducibility, full data sets (Affymetrix)