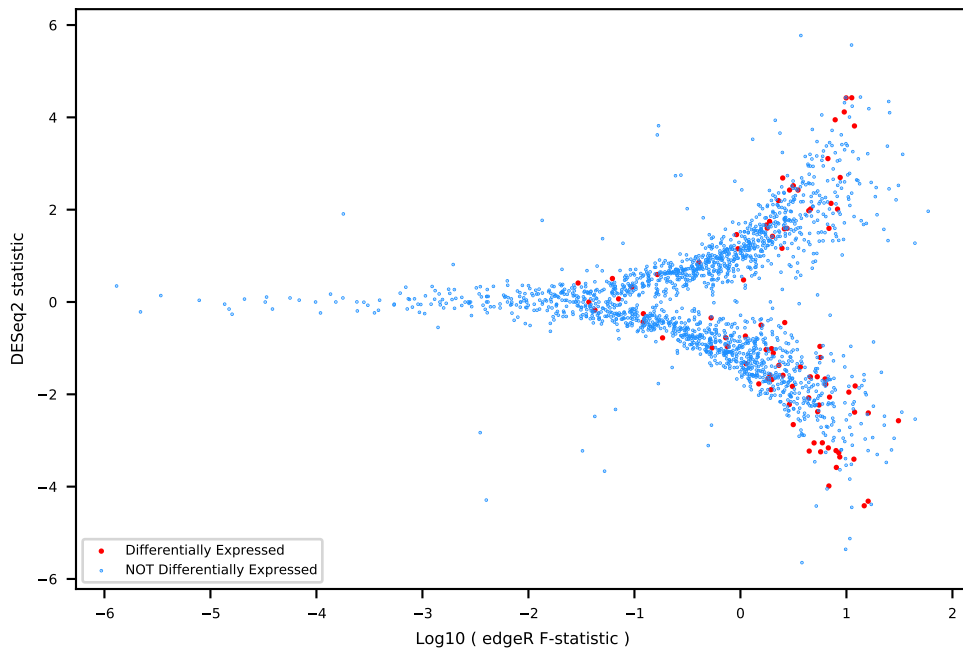
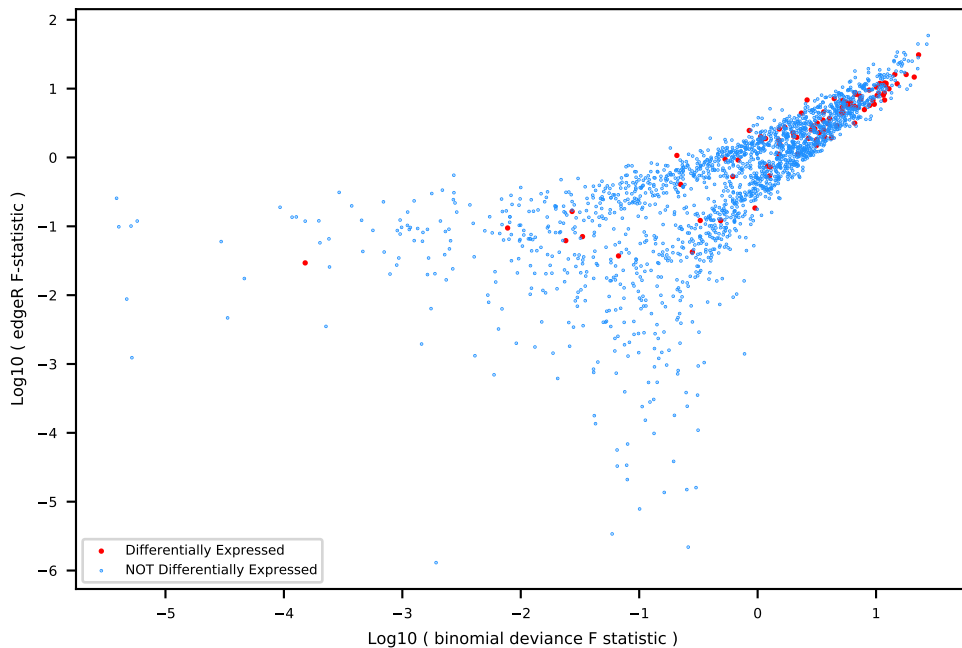


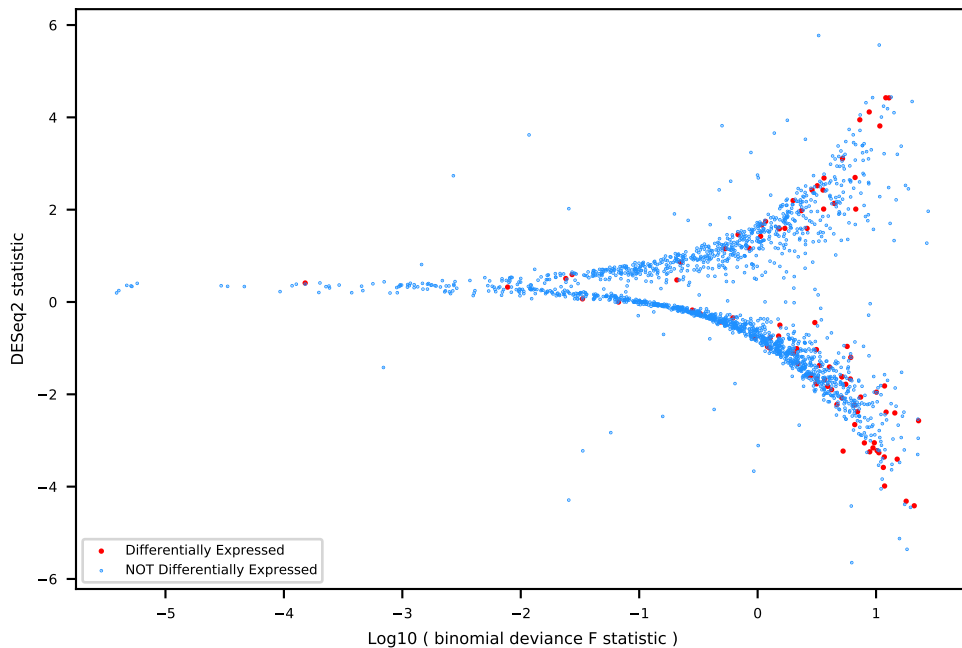
Mou et al. Beta-Poisson simulated data with log fold-change level 1 - Lowly Expressed genes
compare DESeq2 statistic to edgeR F-statistic
1923 genes
(for DESeq2, added pseudo count of 1)



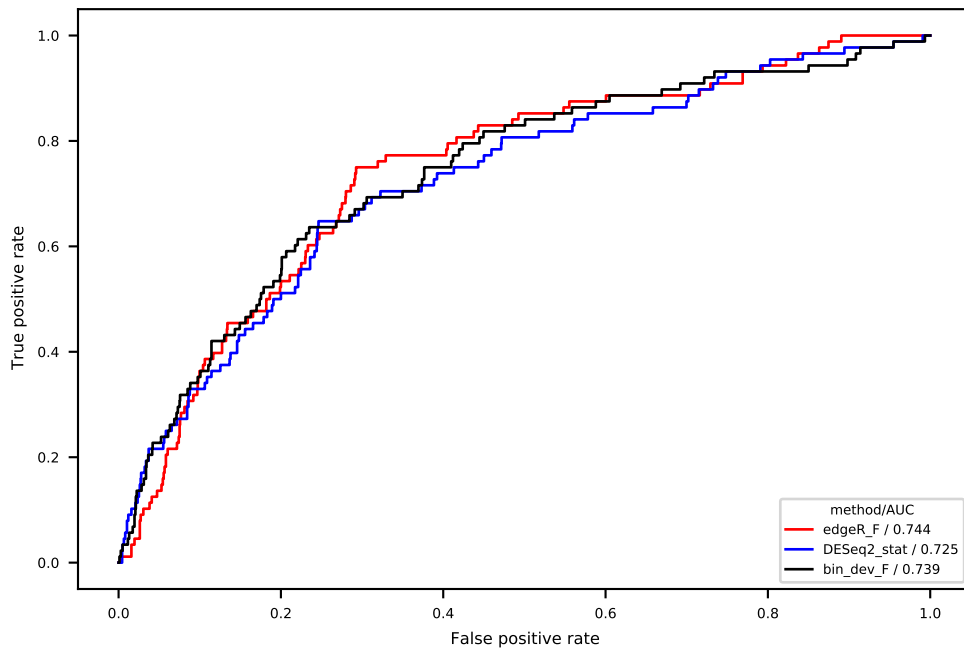
Mou et al. Beta-Poisson simulated data with log fold-change level 1 - Lowly Expressed genes
compare edgeR F-statistic to binomial deviance F statistic
1923 genes



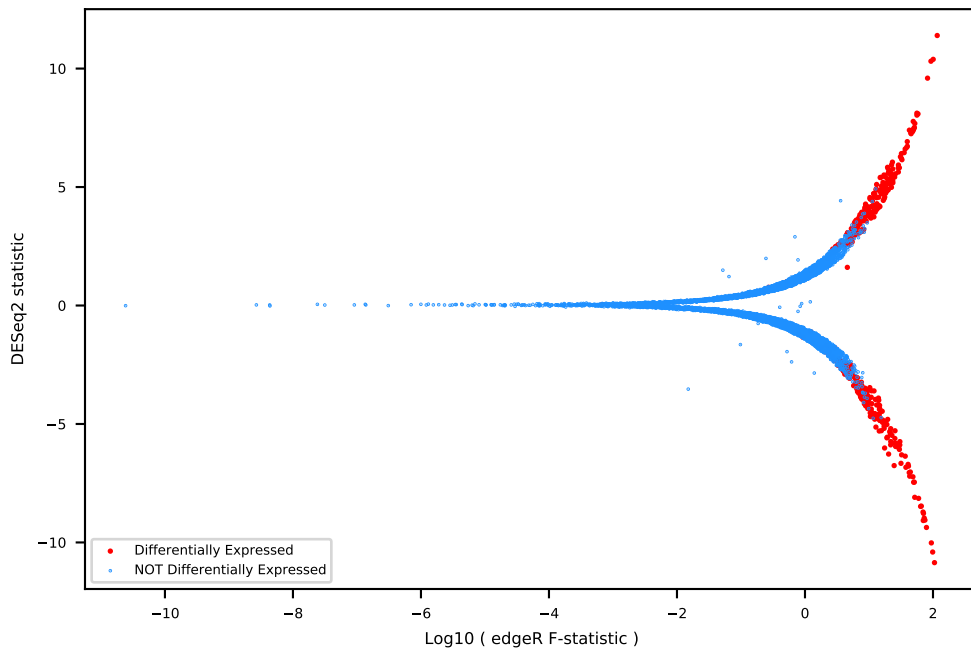
Mou et al. Beta-Poisson simulated data with log fold-change level 1 - Lowly Expressed genes
compare DESeq2 statistic to binomial deviance F statistic
1923 genes
(for DESeq2, added pseudo count of 1)



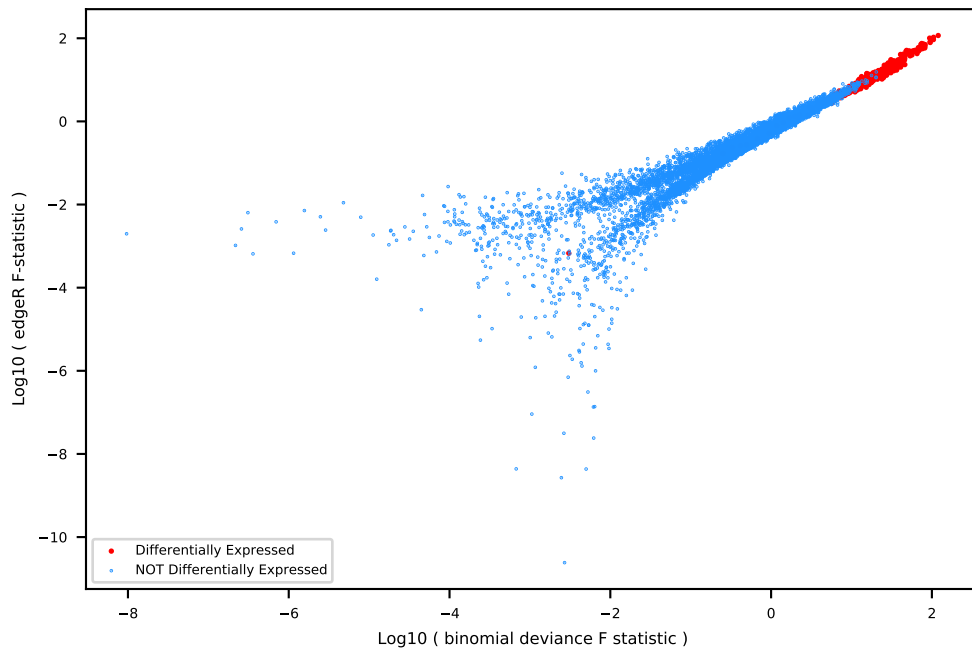
Mou et al. Beta-Poisson simulated data with log fold-change level 1 - Lowly Expressed genes
ROC curves for edgeR, DESeq2, and proposed method
total genes: 1923 number DE: 88



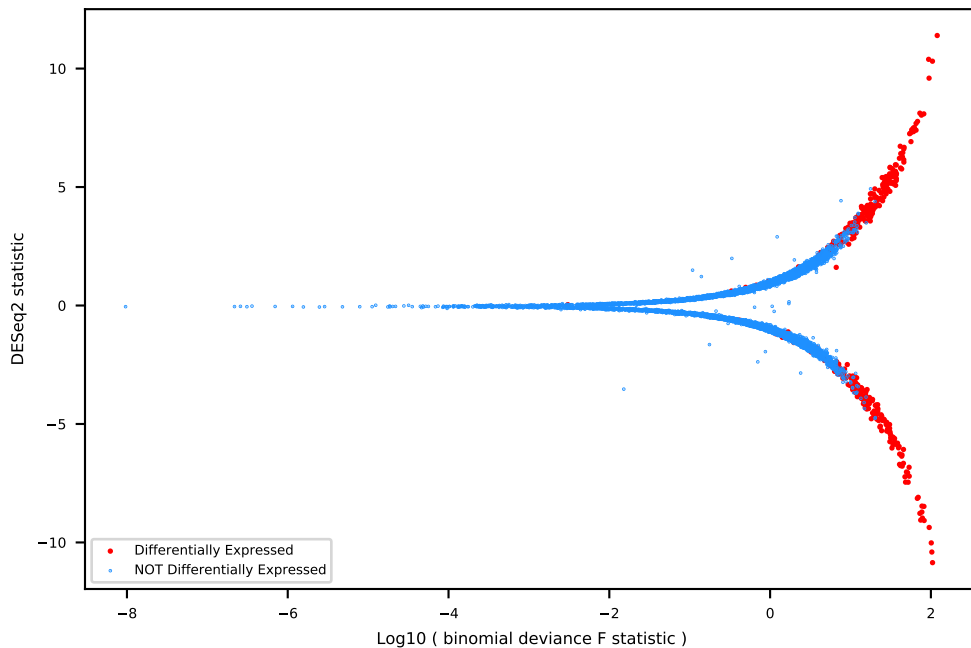
Mou et al. Beta-Poisson simulated data with log fold-change level 1 - Highly Expressed genes
compare DESeq2 statistic to edgeR F-statistic
8077 genes
(for DESeq2, added pseudo count of 1)



Mou et al. Beta-Poisson simulated data with log fold-change level 1 - Highly Expressed genes
compare edgeR F-statistic to binomial deviance F statistic
8077 genes



Mou et al. Beta-Poisson simulated data with log fold-change level 1 - Highly Expressed genes
compare DESeq2 statistic to binomial deviance F statistic
8077 genes
(for DESeq2, added pseudo count of 1)



Mou et al. Beta-Poisson simulated data with log fold-change level 1 - Highly Expressed genes
ROC curves for edgeR, DESeq2, and proposed method
total genes: 8077 number DE: 412

