Results

PCA of using methylation of promoter sites

Promoter methyl distributions

Quantiles plots, rna & methylation

Regression plots. Mse, rsq. We can still see the d-0-2 as outlier

Qusantify within smple hwterogenity. Sine this is fbulk dataset. Different cells types influnces the

Subsequent steps would be to

1. Explain the variability within groups. D-0-2
2. Fit models for groups of genes rather than whole gene sets. Exploring mixed membership models or mixture models
3. Account for sample heterogeneity