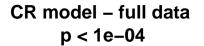
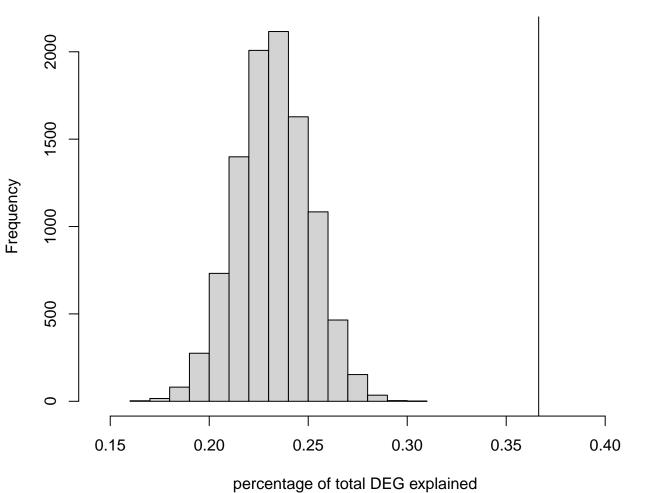
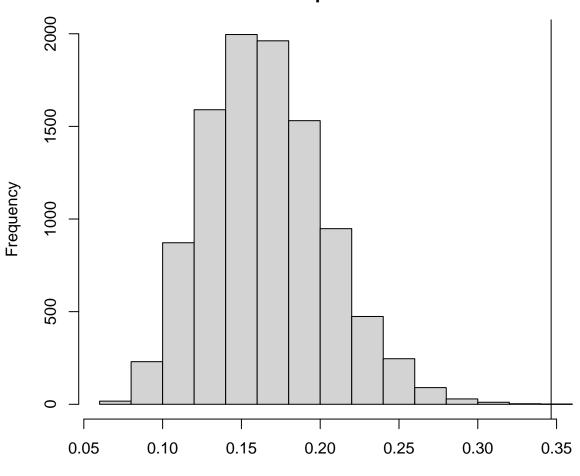


condition-wise average percentage of DEG explained



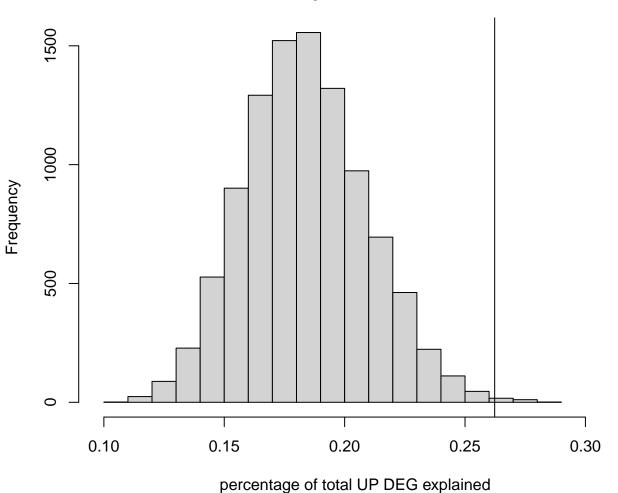


CR model – full data p < 2e-04

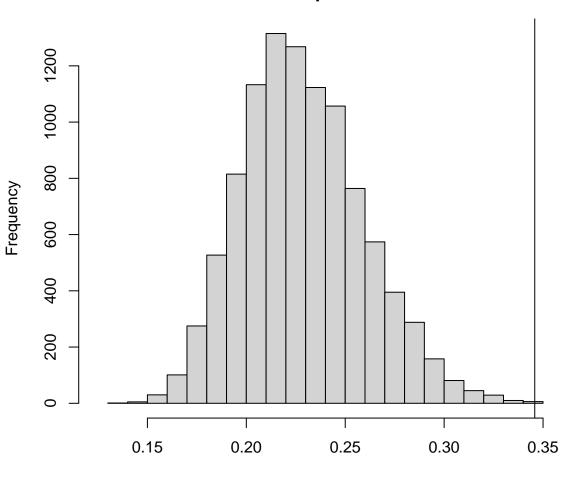


condition-wise average percentage of up DEG explained

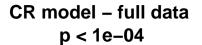
CR model – full data p < 0.0025

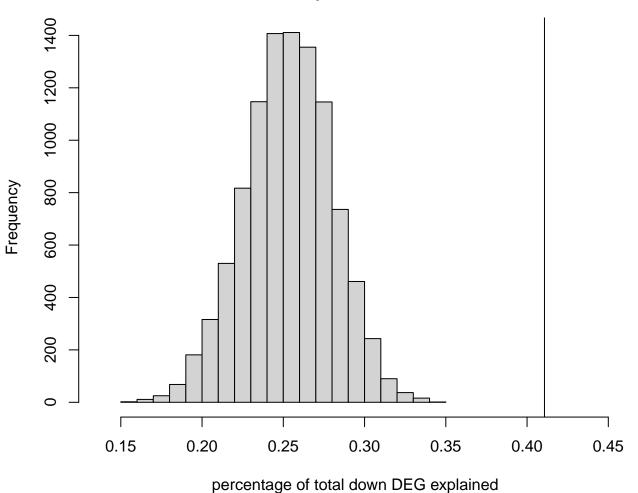


CR model – full data p < 2e-04

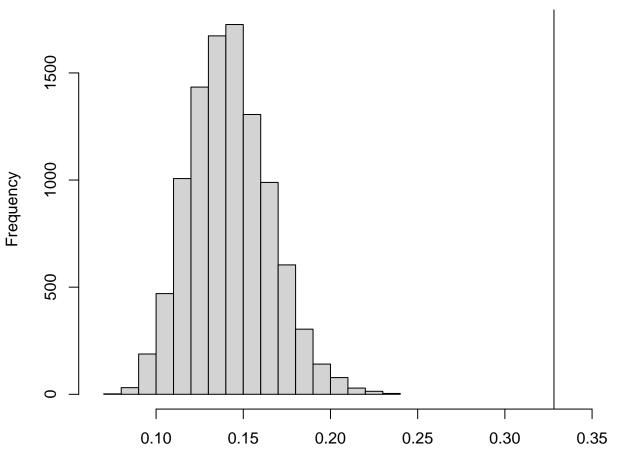


condition-wise average percentage of down DEG explained

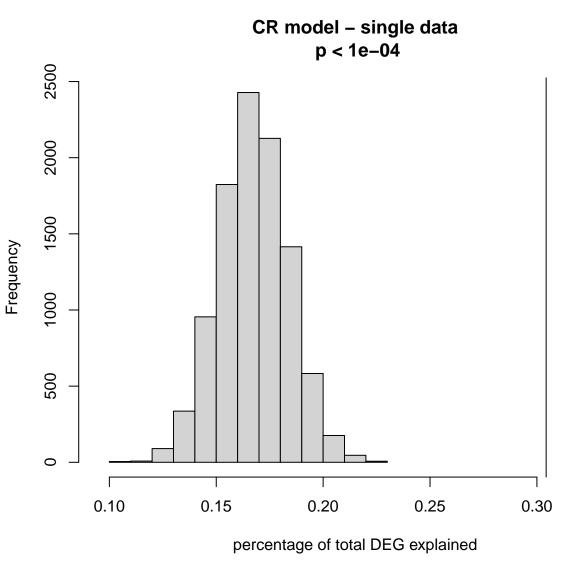




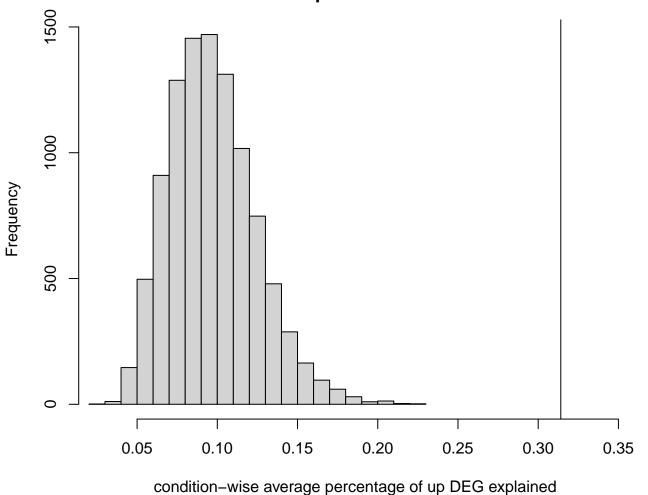
CR model – single data p < 1e-04



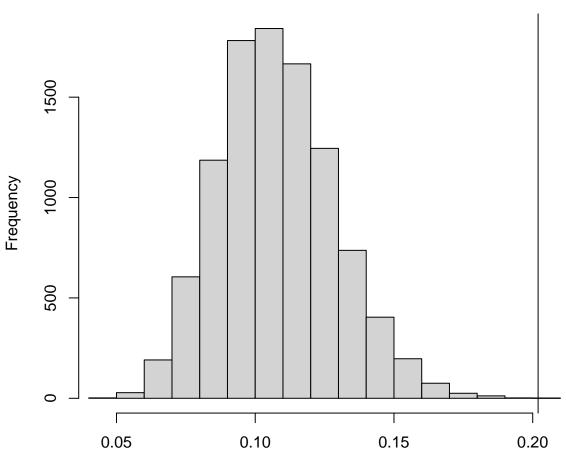
condition-wise average percentage of DEG explained



CR model – single data p < 1e-04

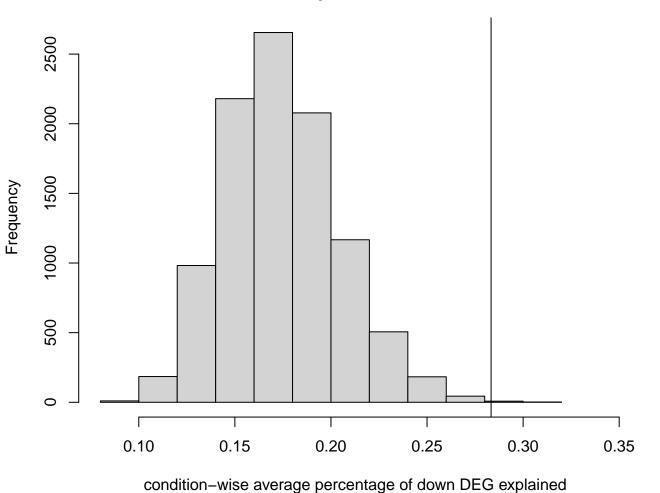


CR model – single data p < 2e-04

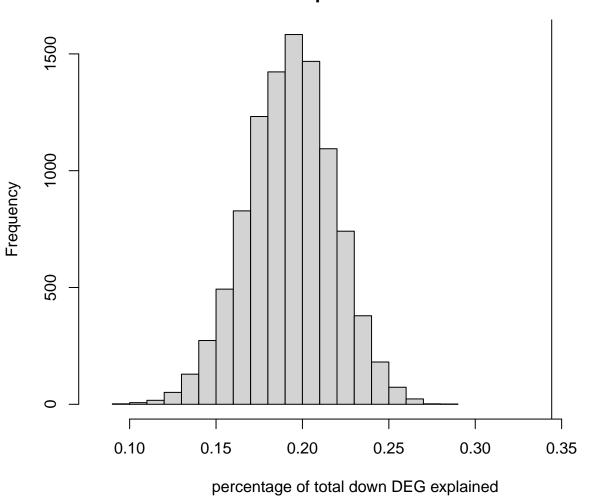


percentage of total UP DEG explained

CR model – single data p < 0.001



CR model – single data p < 1e-04



## single – raw – p < 0.2

energy

Width: 0.56 P-value: 0.062 Width: 0.41 P-value: 0.024

Width: 0.93 With @.96 value: 0.062

Width: 0.69 Width: 22 D value: 0.0089

0.65 -value: 0.12

pro\_modi\_ 0.6 P value: 3e-04

Width: 0.87 value: 0.18

Width: 0.95 P value: 6e-04

Width: 1 P alue: 0.053 Width: 0.75 Value: 1e-04

nucl\_acid\_0.6 P value: 0.0013

## single – normalized – p < 0.2

pro\_modi 65 P-value: 0.017

Width: 0.83 P-value: 0.1

Width: 0.55 P-value: 0.1

nucl\_acid

Width: 0.8 I -value: 0.16 Width: 0.9 P value: 0.051

Width: 1 P-value: 0.053

lipid value: 0.001

Width: 0.95 P-value: 0.14

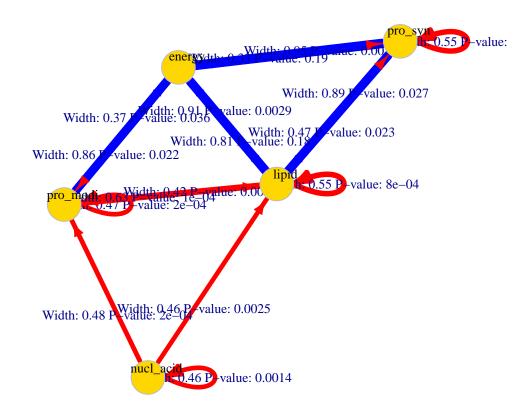
pro\_syn th:-0.871 -value:

Width: 0.97 P value: 0.073

Width: 0.95 P value: 0.0094

energy

## full - raw - p < 0.2



## full – normalized – p < 0.2



Width: 0.88 P-value: 0.076

pro\_sym 1.0.74 P-value: 0.053

Width: 0.96 P-value: 0.0075

Width: 0.88 I

-value: 0.066 Width: 0.87 R-value: 0.079

Width: 0.94 P-value: 0.003

**6:** 0.49 **1** – value:

pro modi

Width: 0.54 P value: 0.002

lipid 1: 4.35 P-value: 3e-04