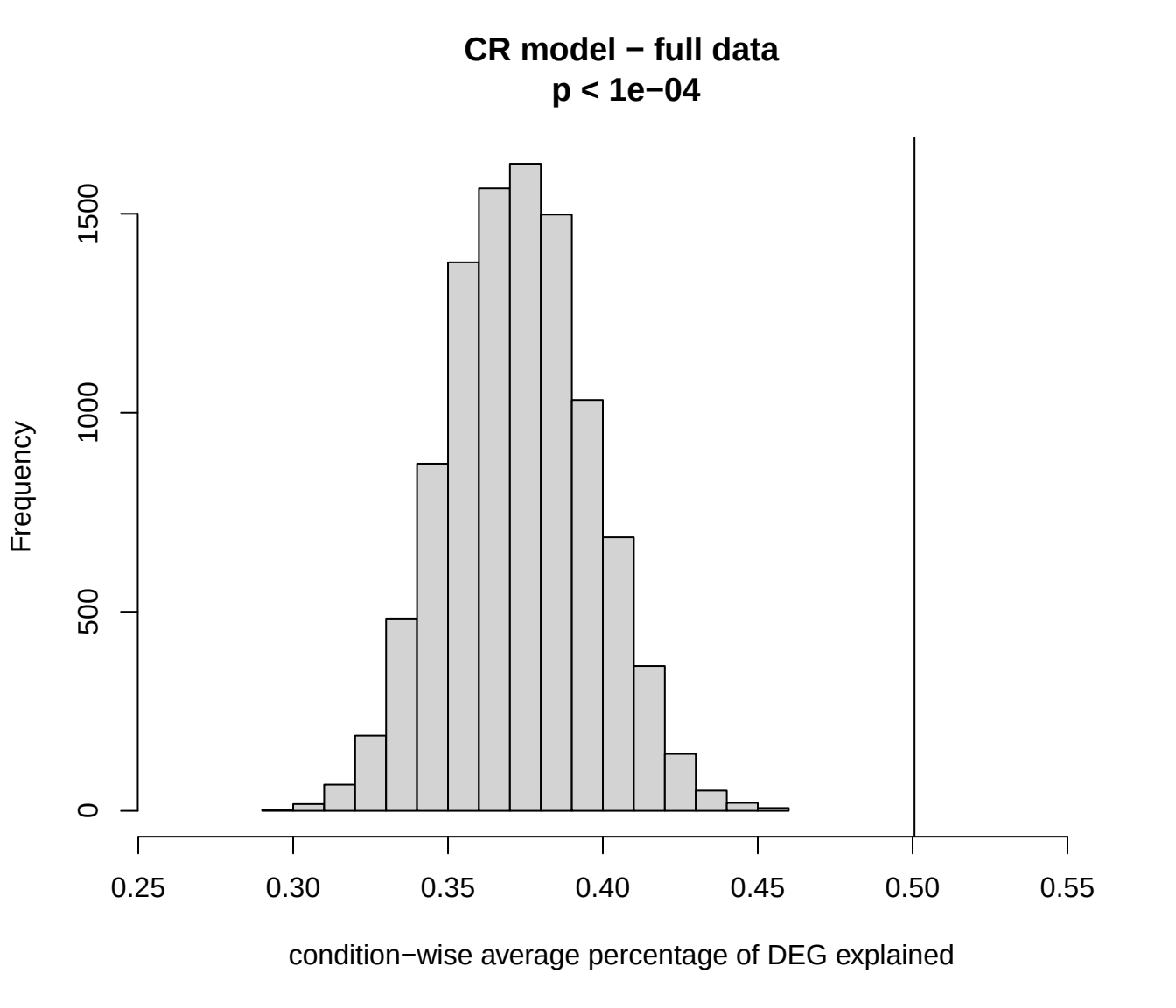
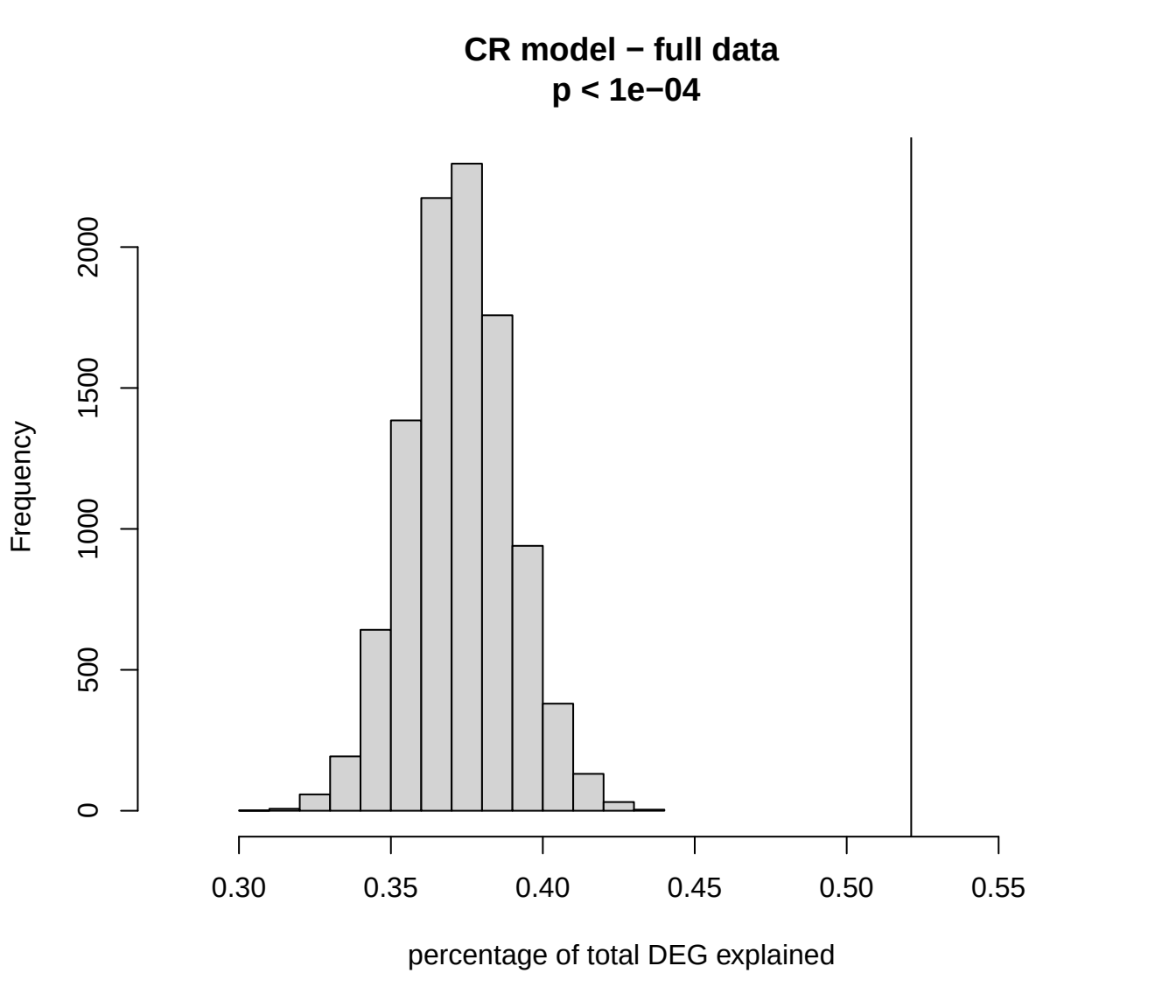
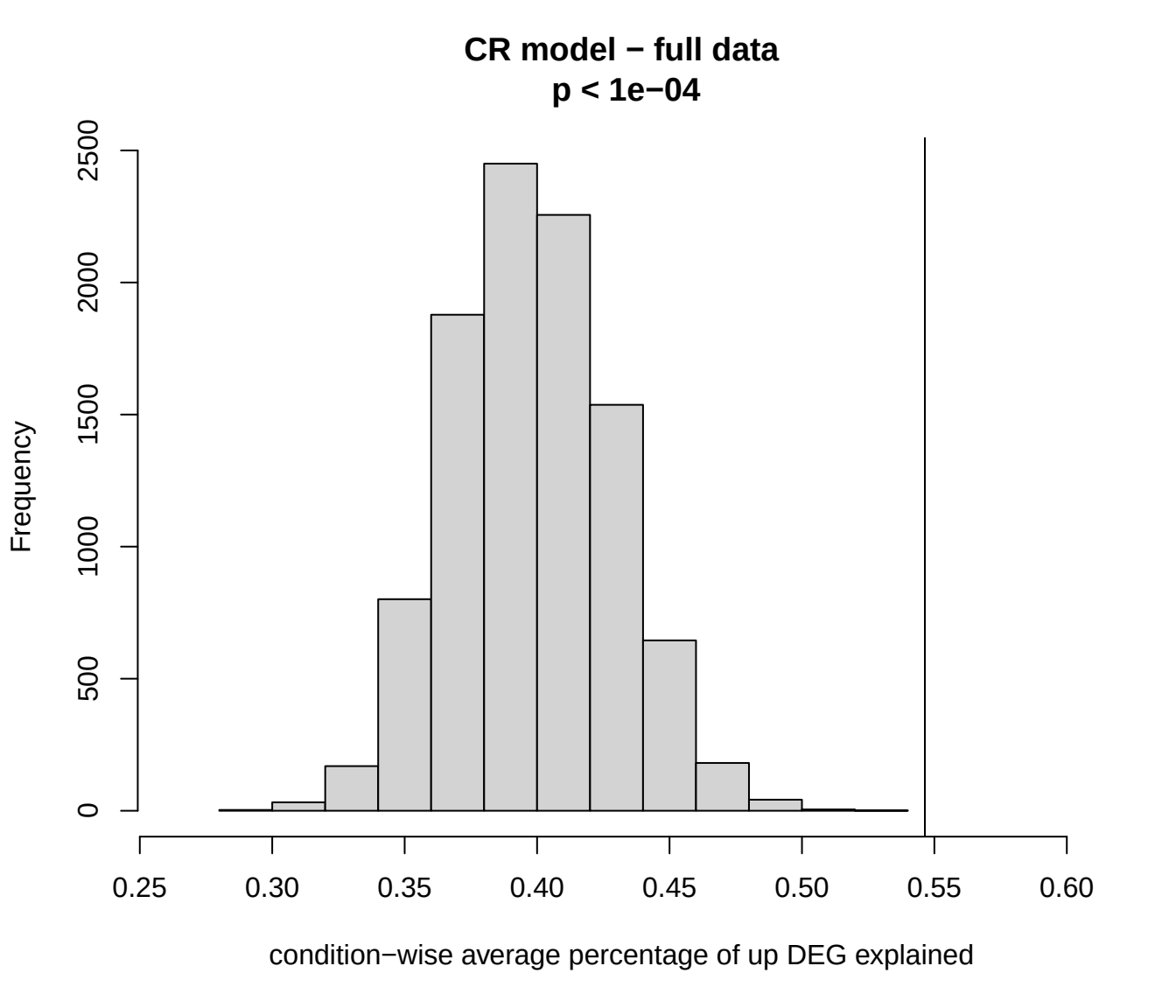
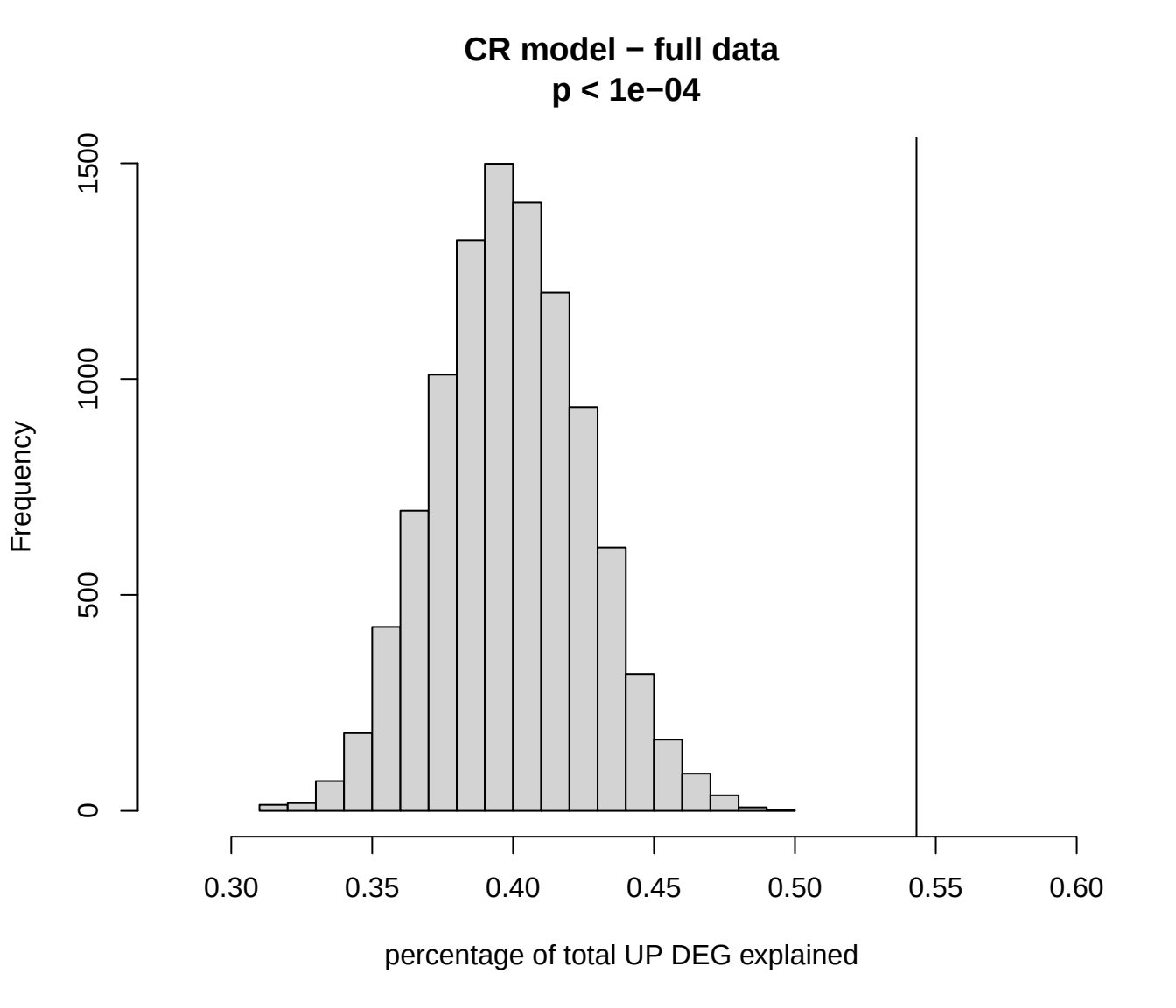
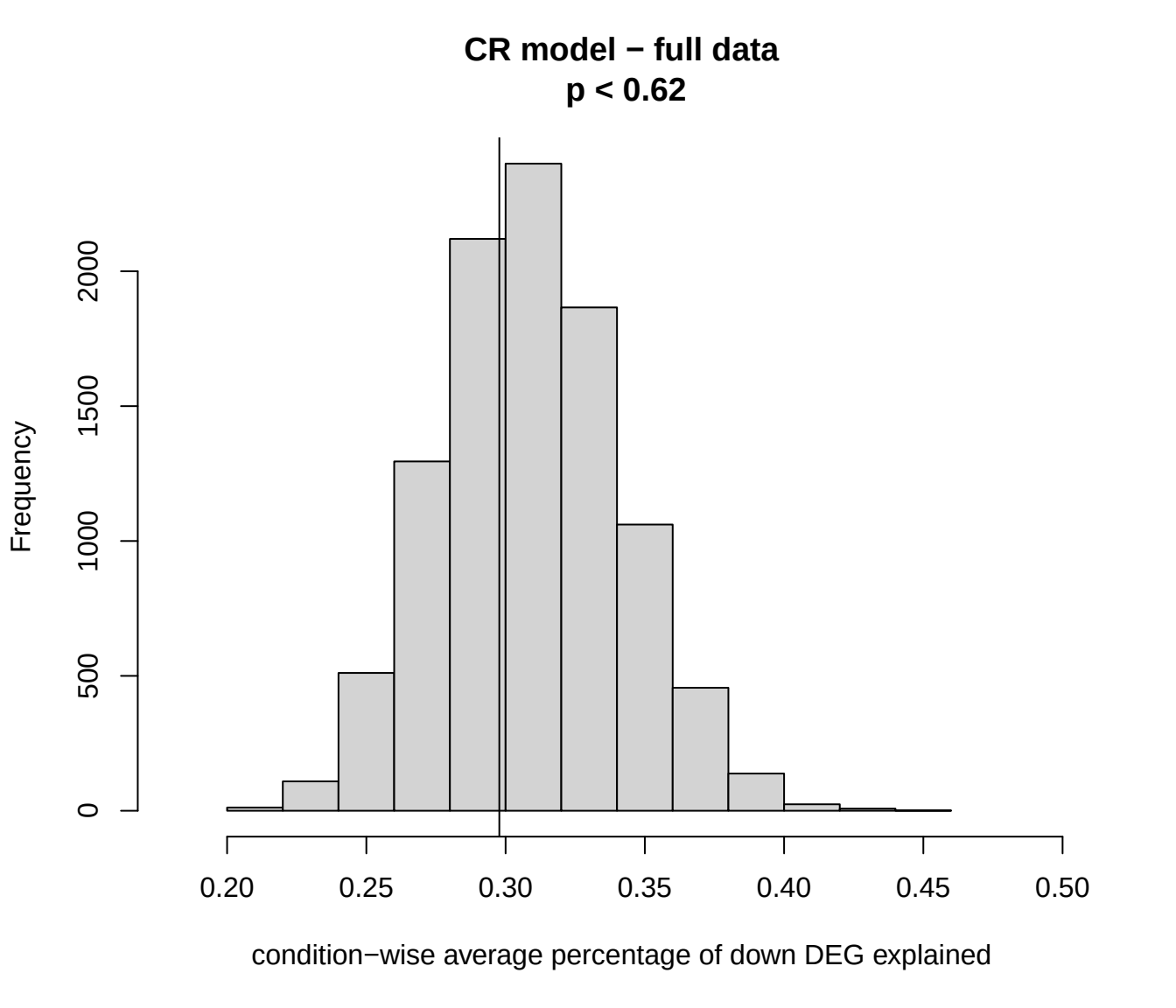
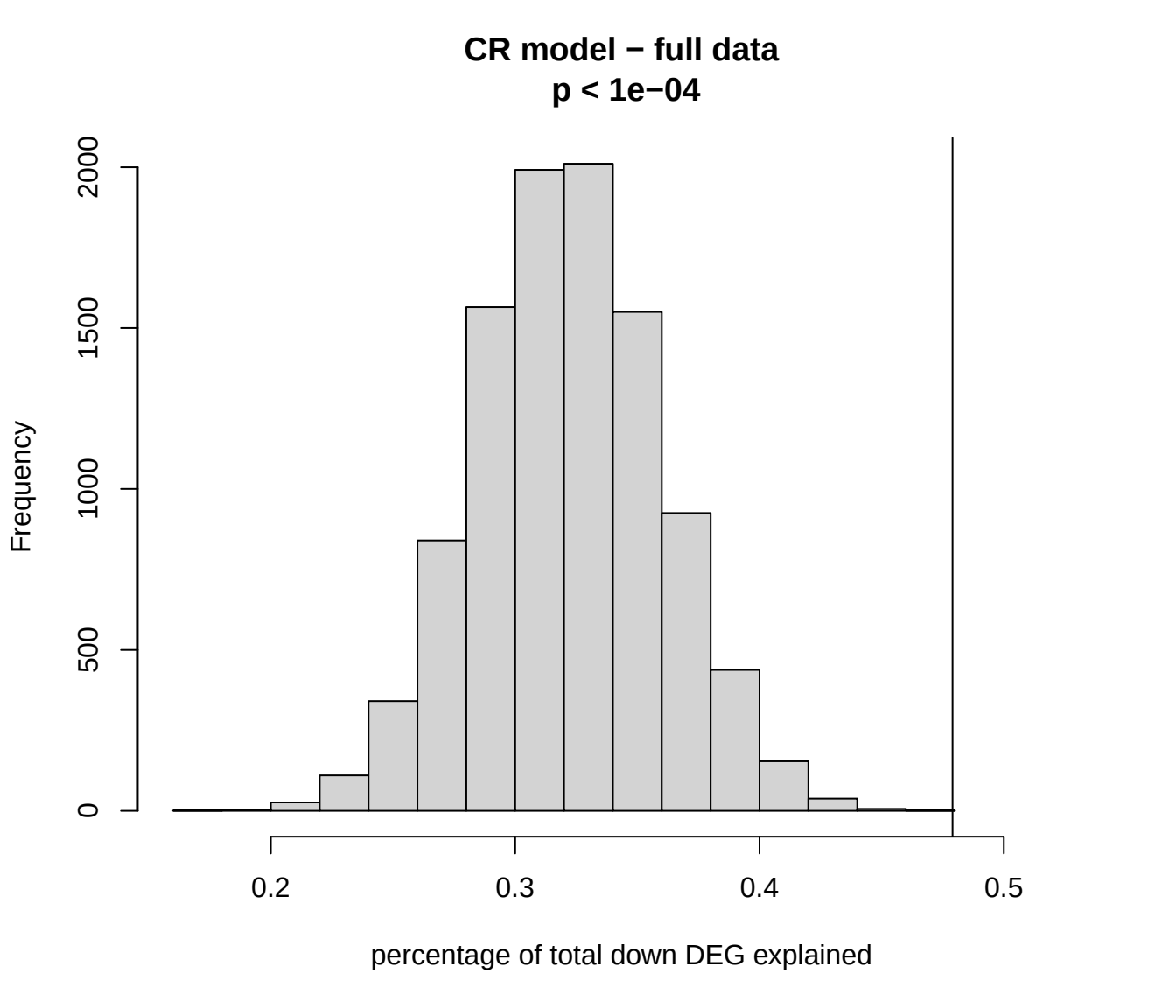

CR model − full data
p < 1e−04
Frequency
0
500
1000
1500
0.25
0.30
0.35
0.40
0.45
0.50
0.55
condition−wise average percentage of DEG explained

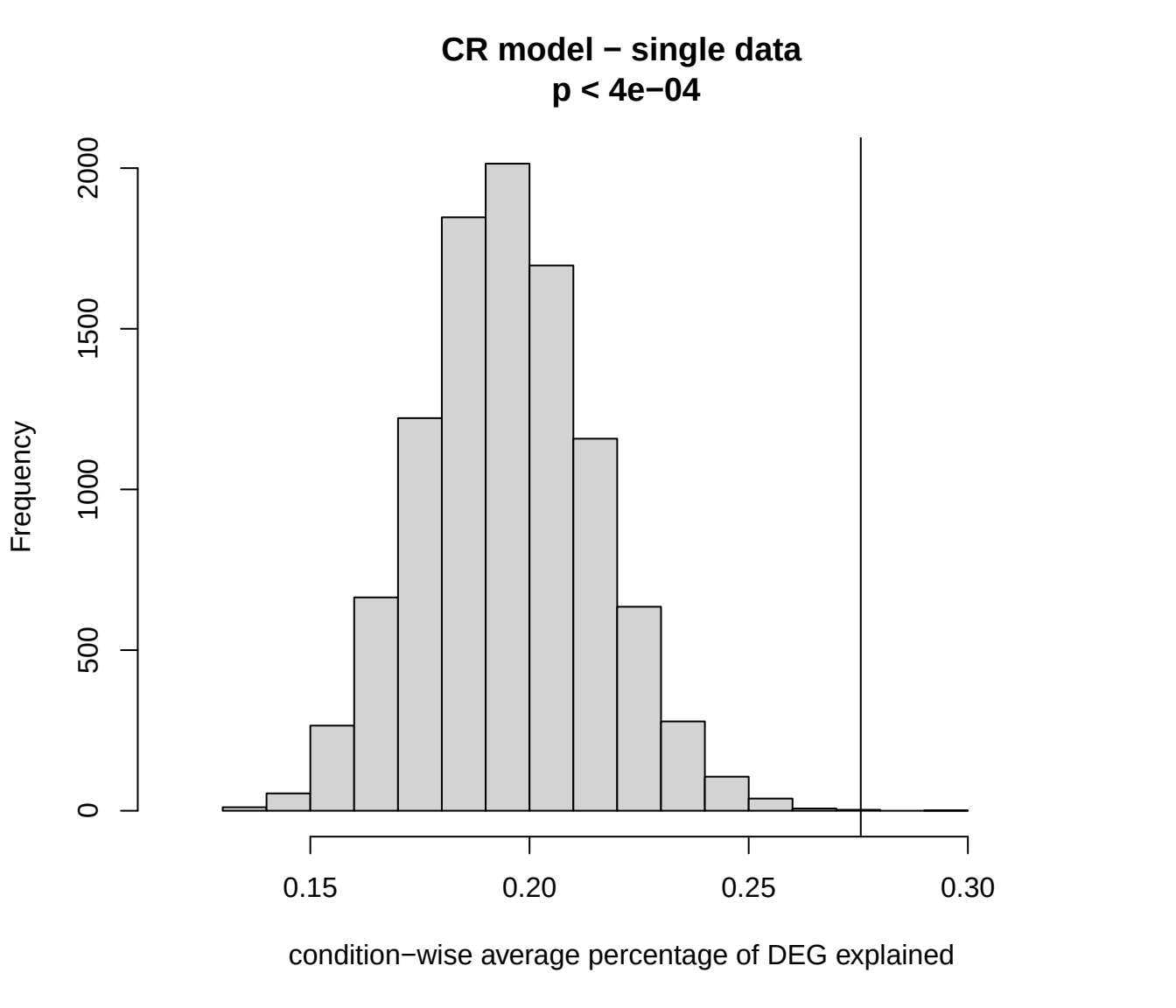

CR model − full data
p < 1e−04
Frequency
0
500
1000
1500
2000
0.30
0.35
0.40
0.45
0.50
0.55
percentage of total DEG explained

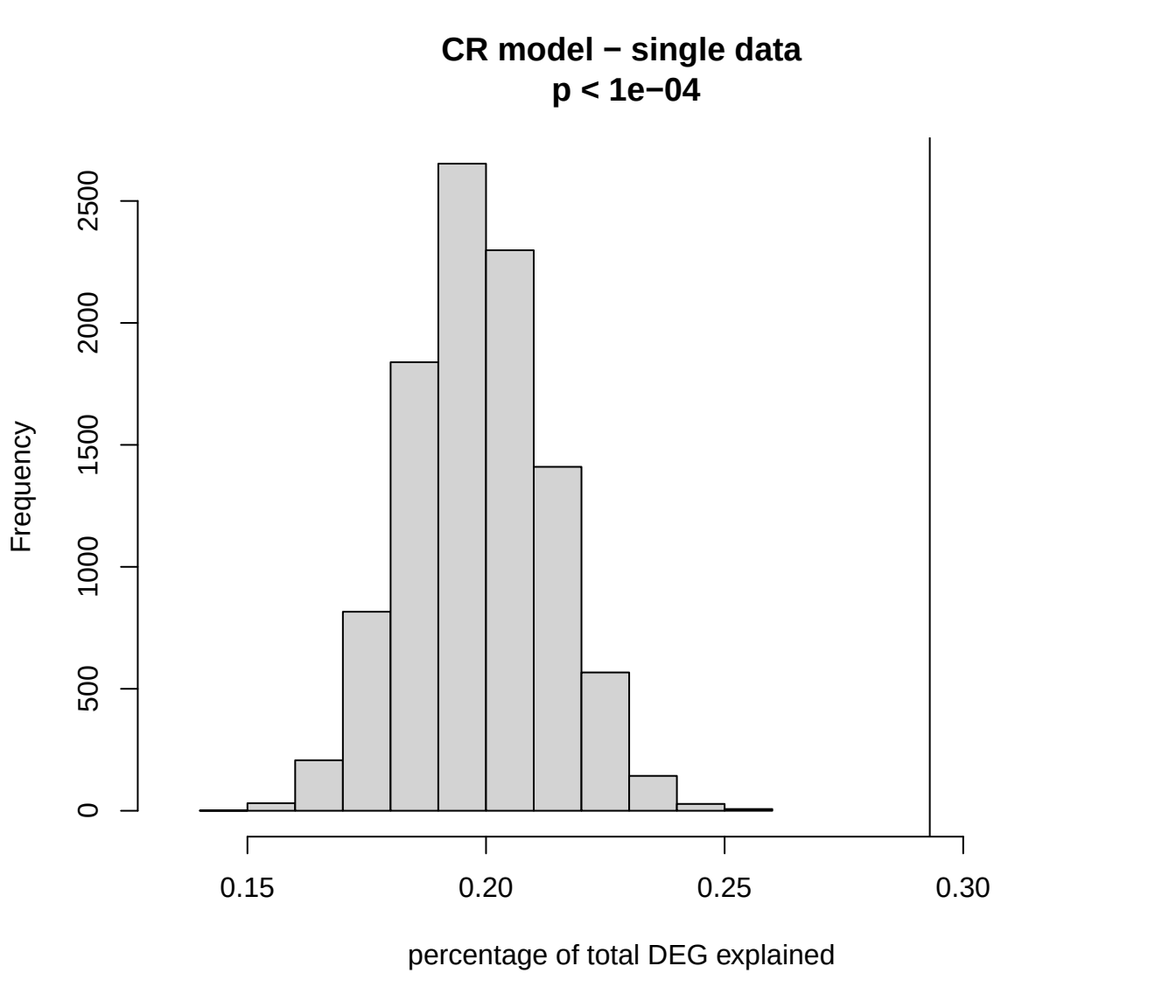

CR model − full data
p < 1e−04
Frequency
0
500
1000
1500
2000
2500
0.25
0.30
0.35
0.40
0.45
0.50
0.55
0.60
condition−wise average percentage of up DEG explained

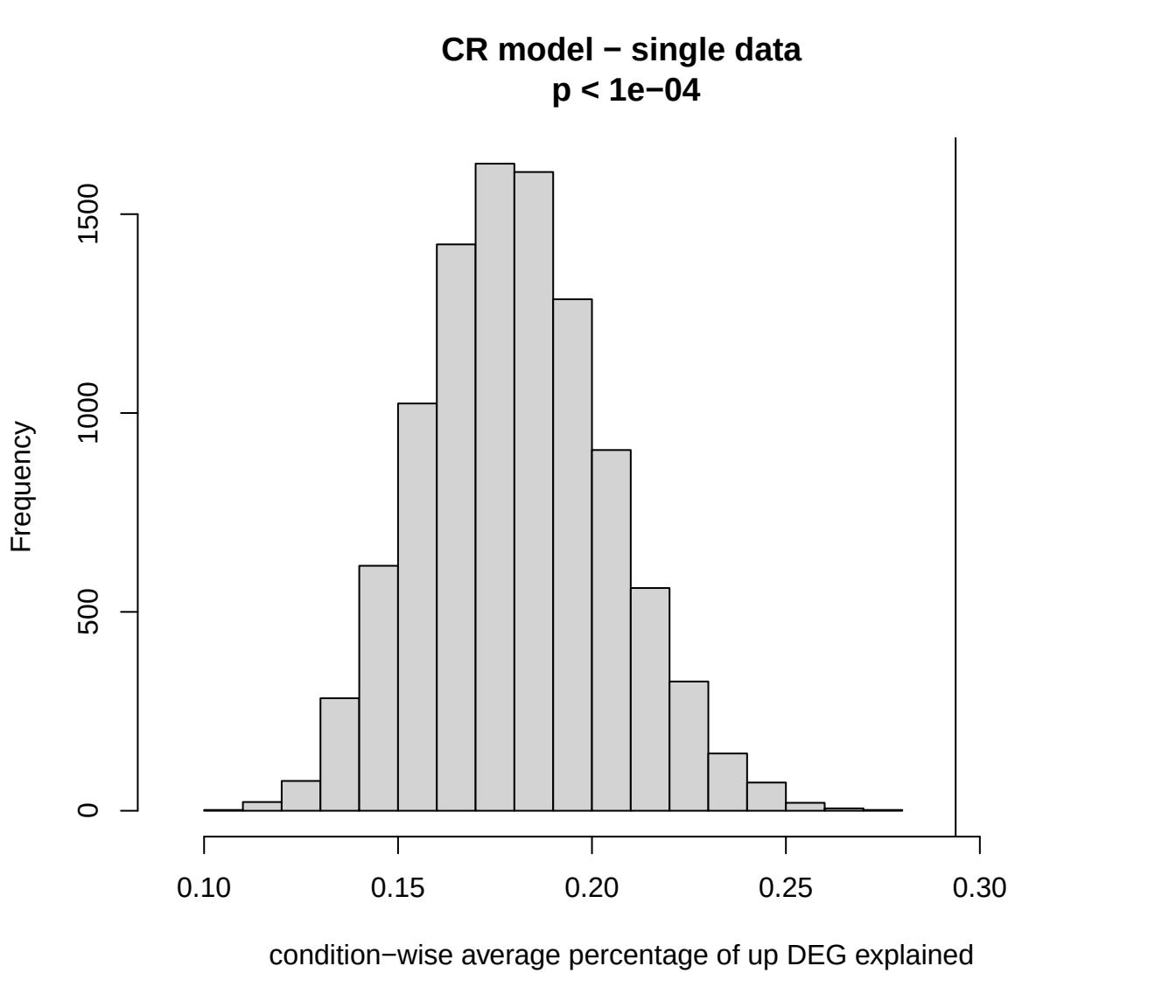

CR model − full data
p < 1e−04
Frequency
0
500
1000
1500
0.30
0.35
0.40
0.45
0.50
0.55
0.60
percentage of total UP DEG explained

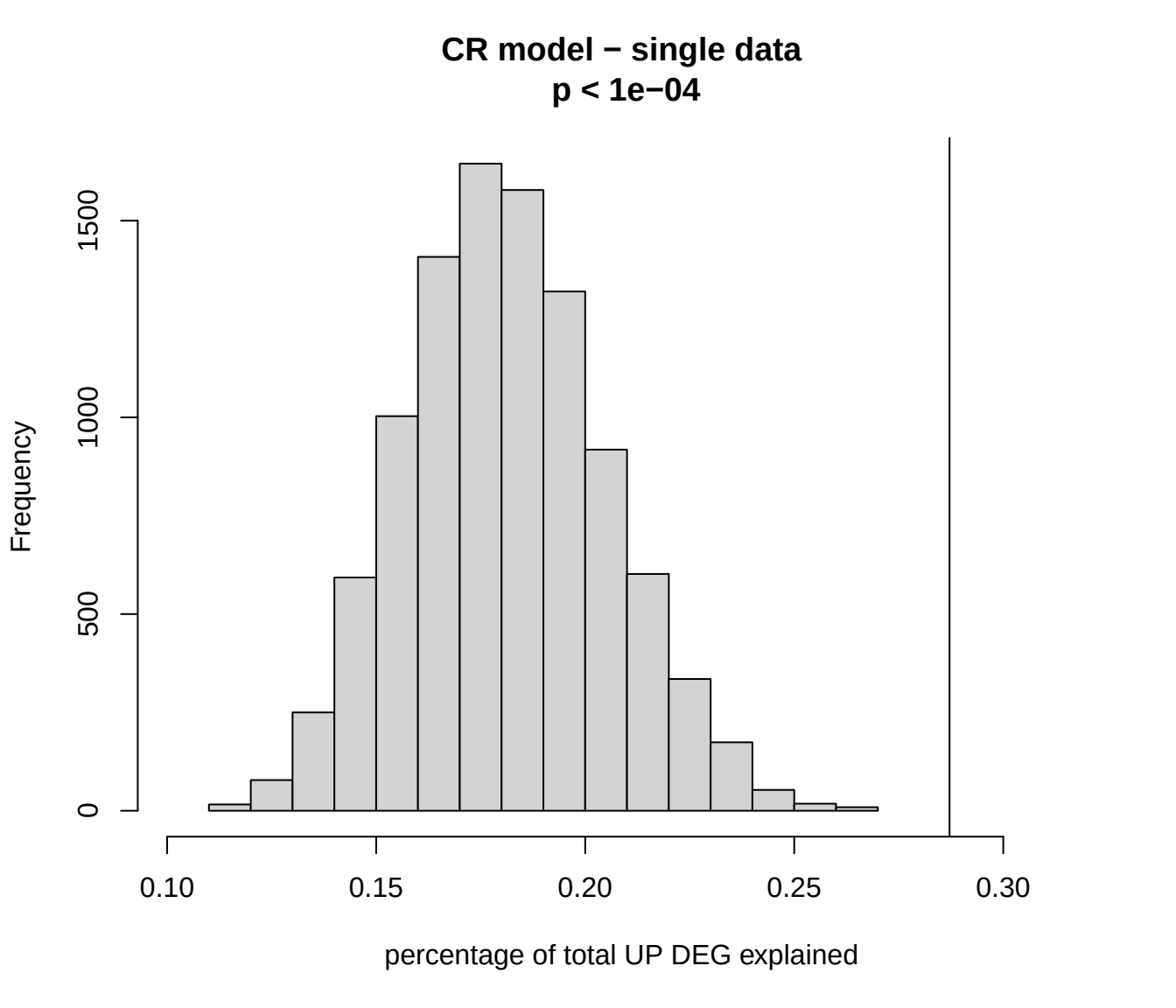

CR model − full data
p < 0.62
Frequency
0
500
1000
1500
2000
0.20
0.25
0.30
0.35
0.40
0.45
0.50
condition−wise average percentage of down DEG explained

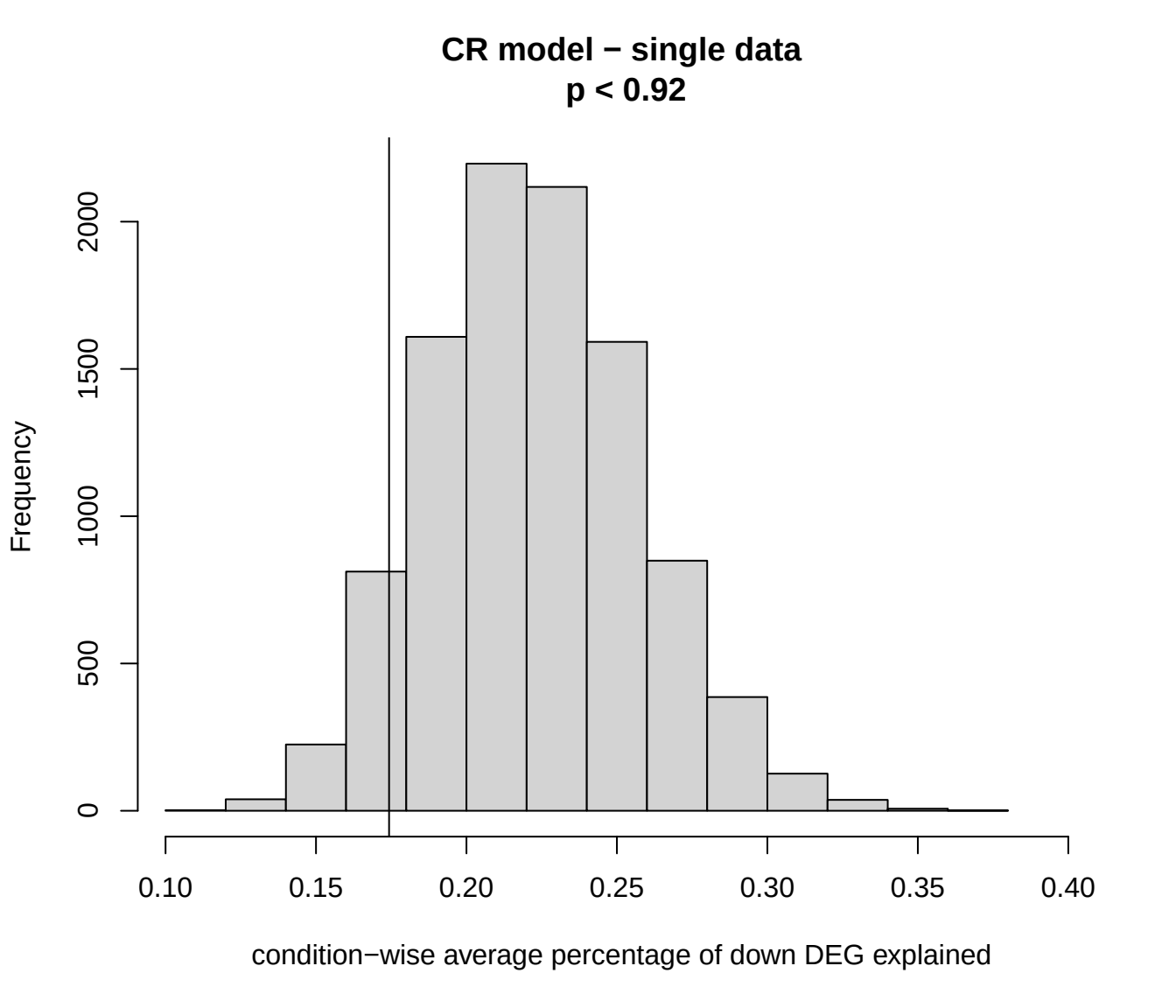

CR model − full data
p < 1e−04
Frequency
0
500
1000
1500
2000
0.2
0.3
0.4
0.5
percentage of total down DEG explained

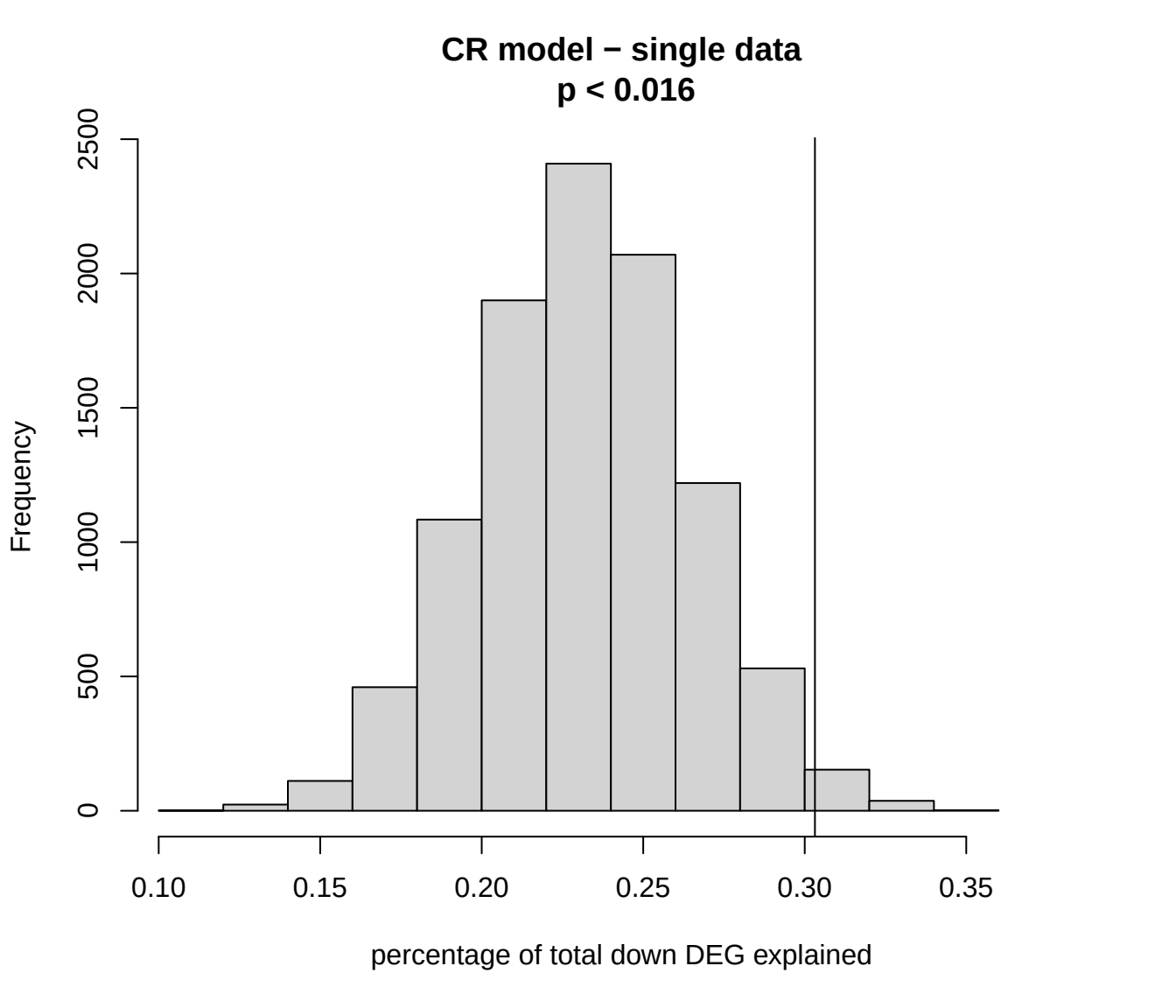

CR model − single data
p < 4e−04
Frequency
0
500
1000
1500
2000
0.15
0.20
0.25
0.30
condition−wise average percentage of DEG explained

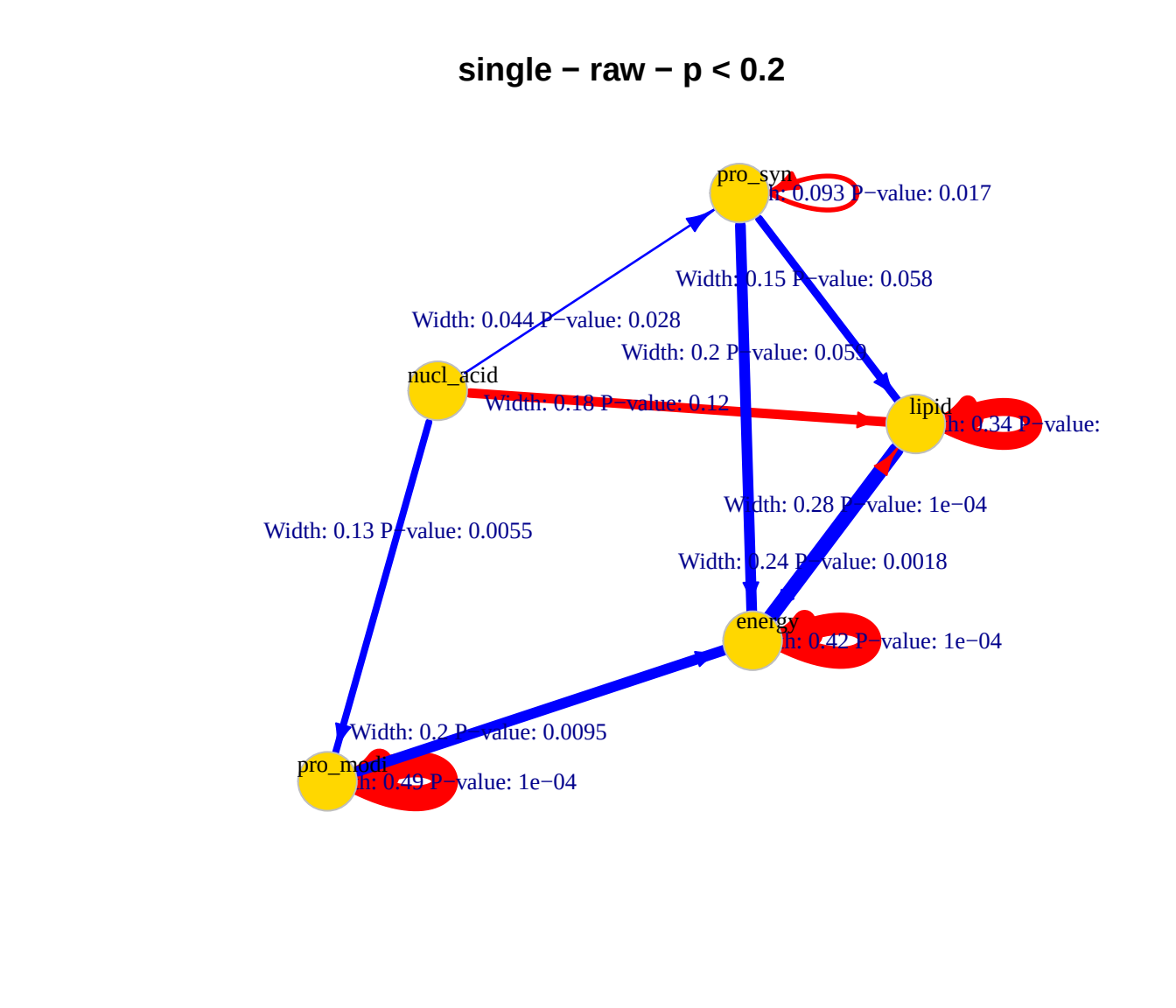

CR model − single data
p < 1e−04
Frequency
0
500
1000
1500
2000
2500
0.15
0.20
0.25
0.30
percentage of total DEG explained


CR model − single data
p < 1e−04
Frequency
0
500
1000
1500
0.10
0.15
0.20
0.25
0.30
condition−wise average percentage of up DEG explained

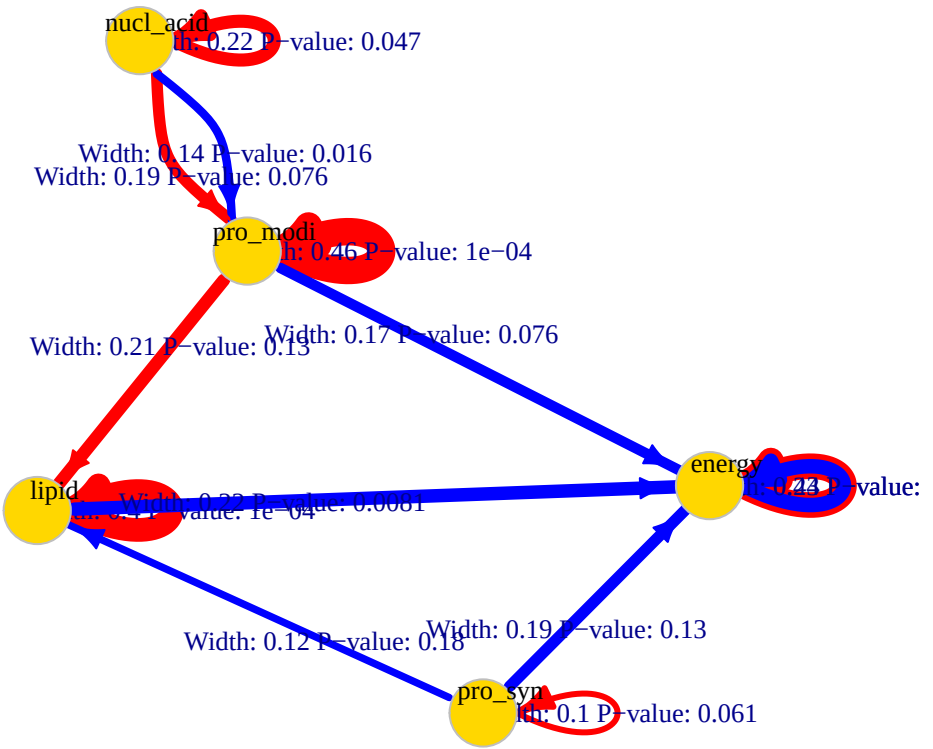

CR model − single data
p < 1e−04
Frequency
0
500
1000
1500
0.10
0.15
0.20
0.25
0.30
percentage of total UP DEG explained


CR model − single data
p < 0.92
Frequency
0
500
1000
1500
2000
0.10
0.15
0.20
0.25
0.30
0.35
0.40
condition−wise average percentage of down DEG explained

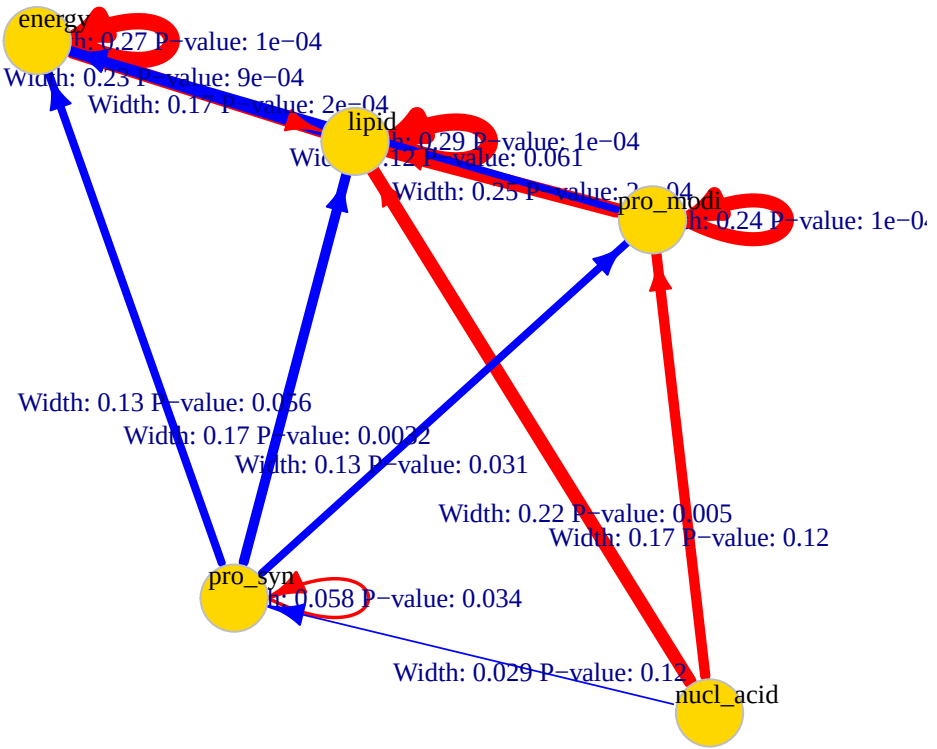
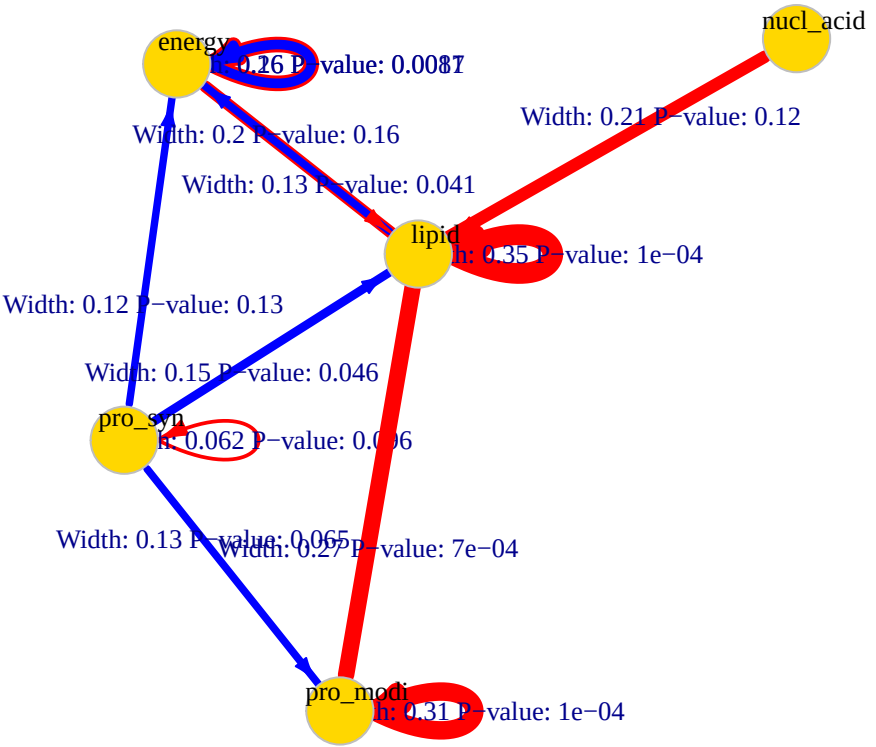

CR model − single data
p < 0.016
Frequency
0
500
1000
1500
2000
2500
0.10
0.15
0.20
0.25
0.30
0.35
percentage of total down DEG explained


single − raw − p < 0.2
pro_syn
h: 0.093 P−value: 0.017
Width: 0.15 P−value: 0.058
Width: 0.044 P−value: 0.028
Width: 0.2 P−value: 0.059
nucl_acid
Width: 0.18 P−value: 0.12
lipid
h: 0.34 P−value:
Width: 0.28 P−value: 1e−04
Width: 0.13 P−value: 0.0055
Width: 0.24 P−value: 0.0018
energy
h: 0.42 P−value: 1e−04
Width: 0.2 P−value: 0.0095
pro_modi
h: 0.49 P−value: 1e−04

single − normalized − p < 0.2



full − raw − p < 0.2


energy
h: 0.27 P−value: 1e−04
Width: 0.23 P−value: 9e−04
Width: 0.17 P−value: 2e−04
lipid
h: 0.29 P−value: 1e−04
Width: 0.25 P−value: 2e−04
pro_modf
h: 0.24 P−value: 1e−04
Width: 0.13 P−value: 0.056
Width: 0.17 P−value: 0.0032
Width: 0.13 P−value: 0.031
Width: 0.22 P−value: 0.005
Width: 0.17 P−value: 0.12
pro_syn
h: 0.058 P−value: 0.034
Width: 0.029 P−value: 0.12
nucl_acid

full − normalized − p < 0.2