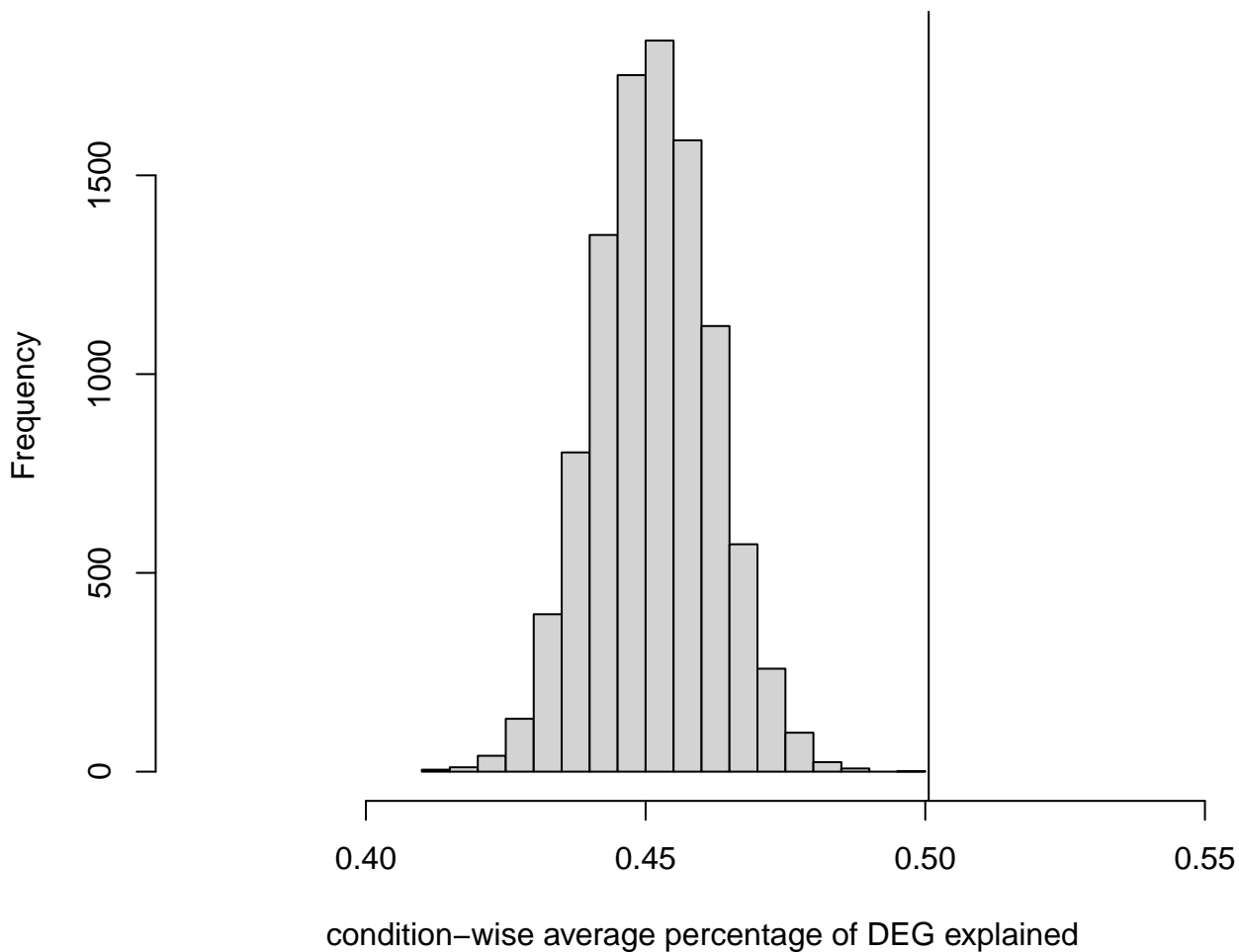
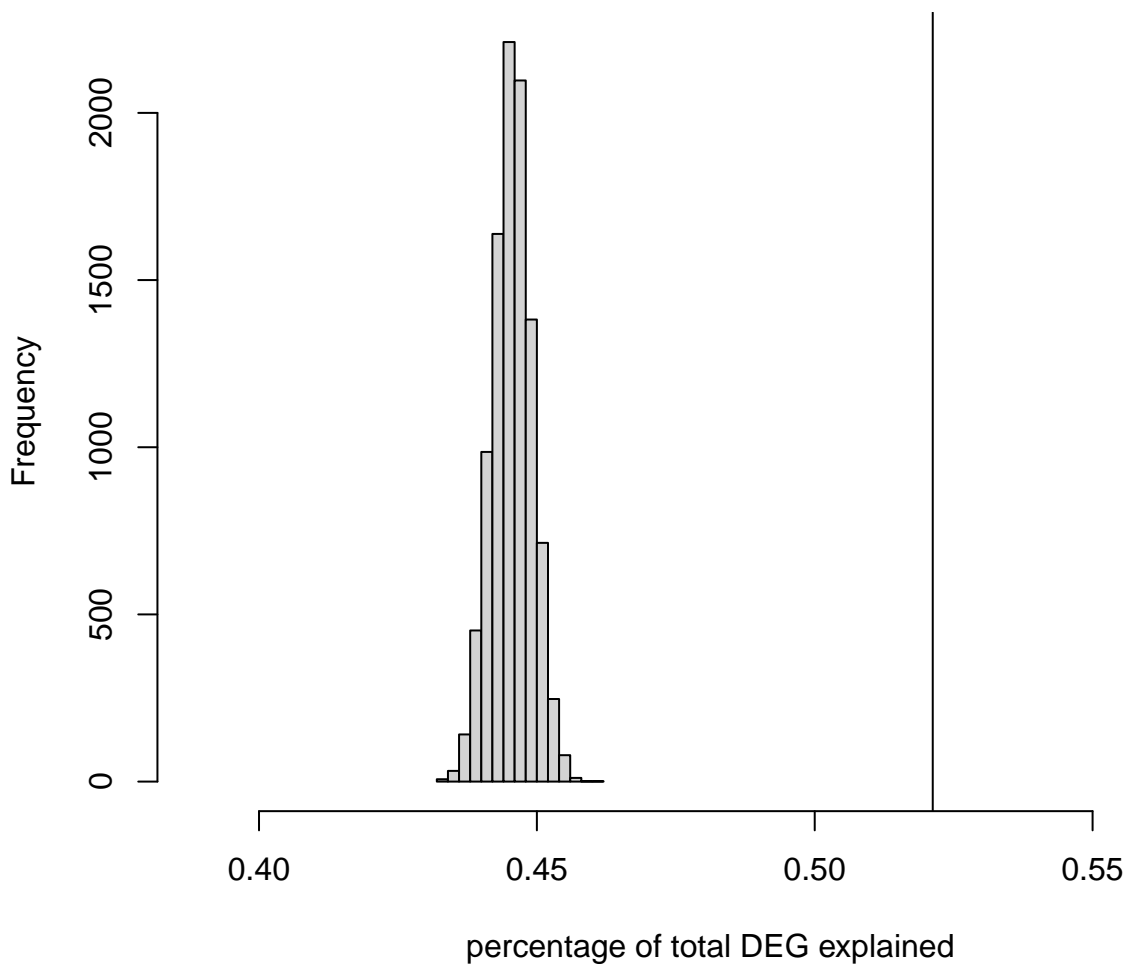


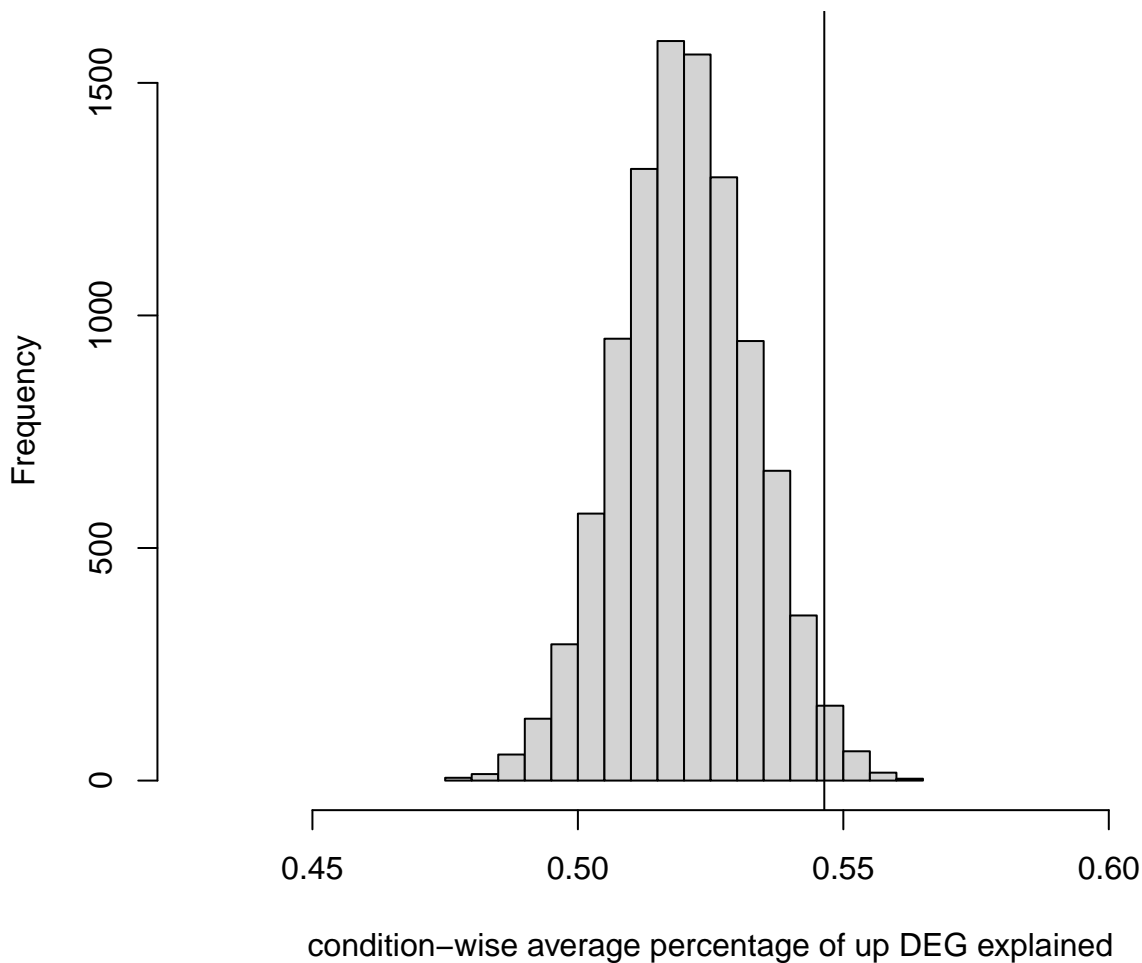
**CR model – full data**  
**p < 1e-04**



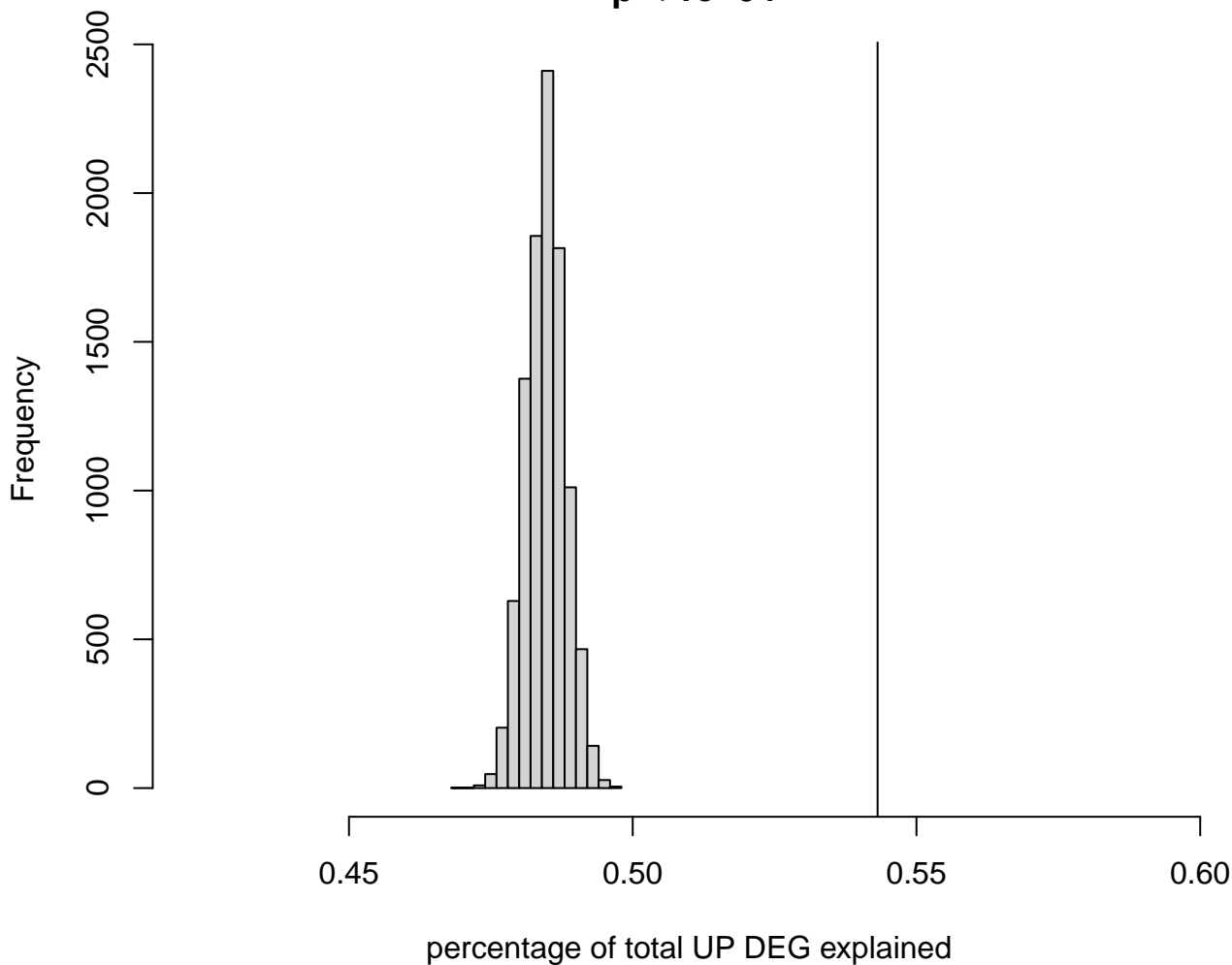
**CR model – full data**  
 **$p < 1e-04$**



**CR model – full data**  
**p < 0.018**

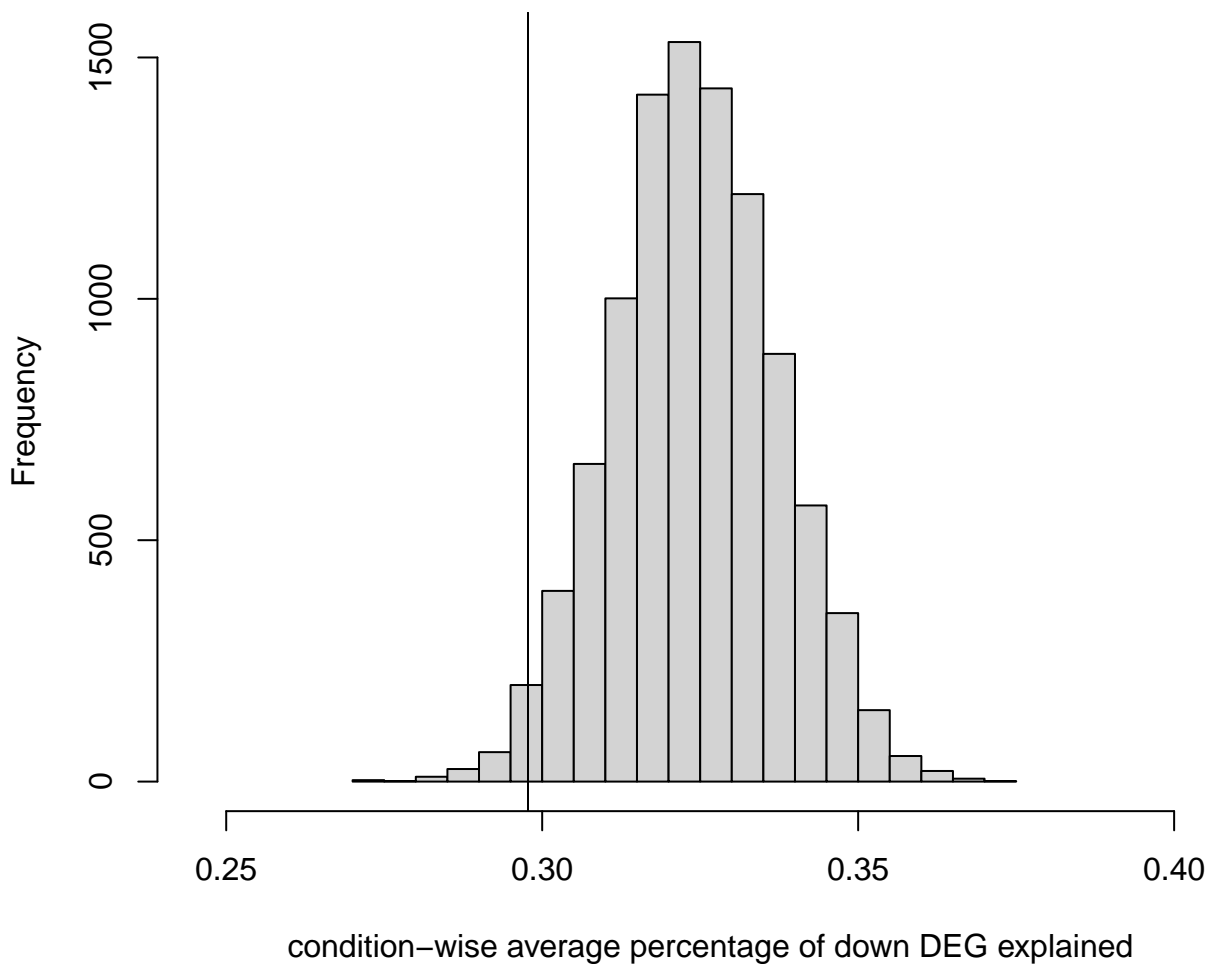


**CR model – full data**  
**p < 1e-04**

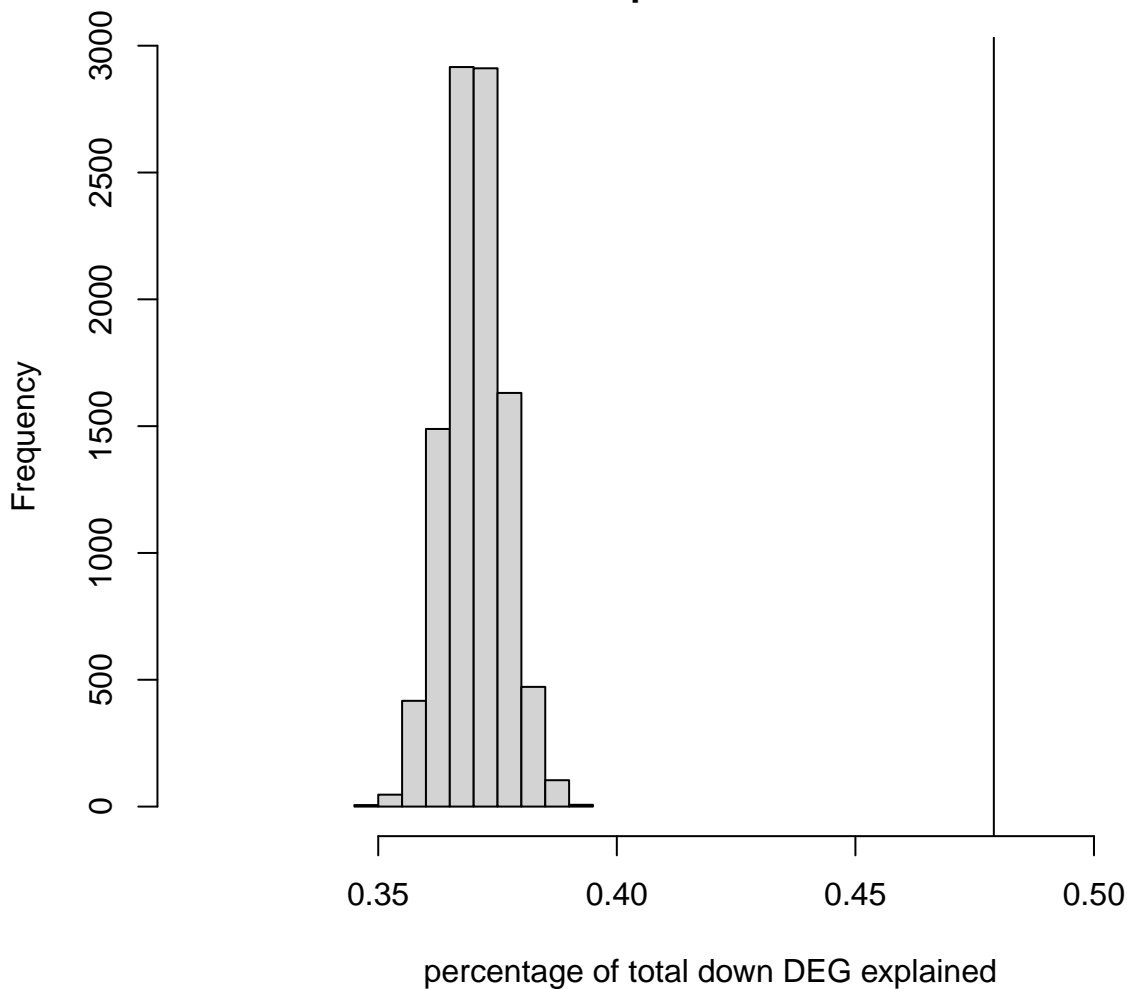


# CR model – full data

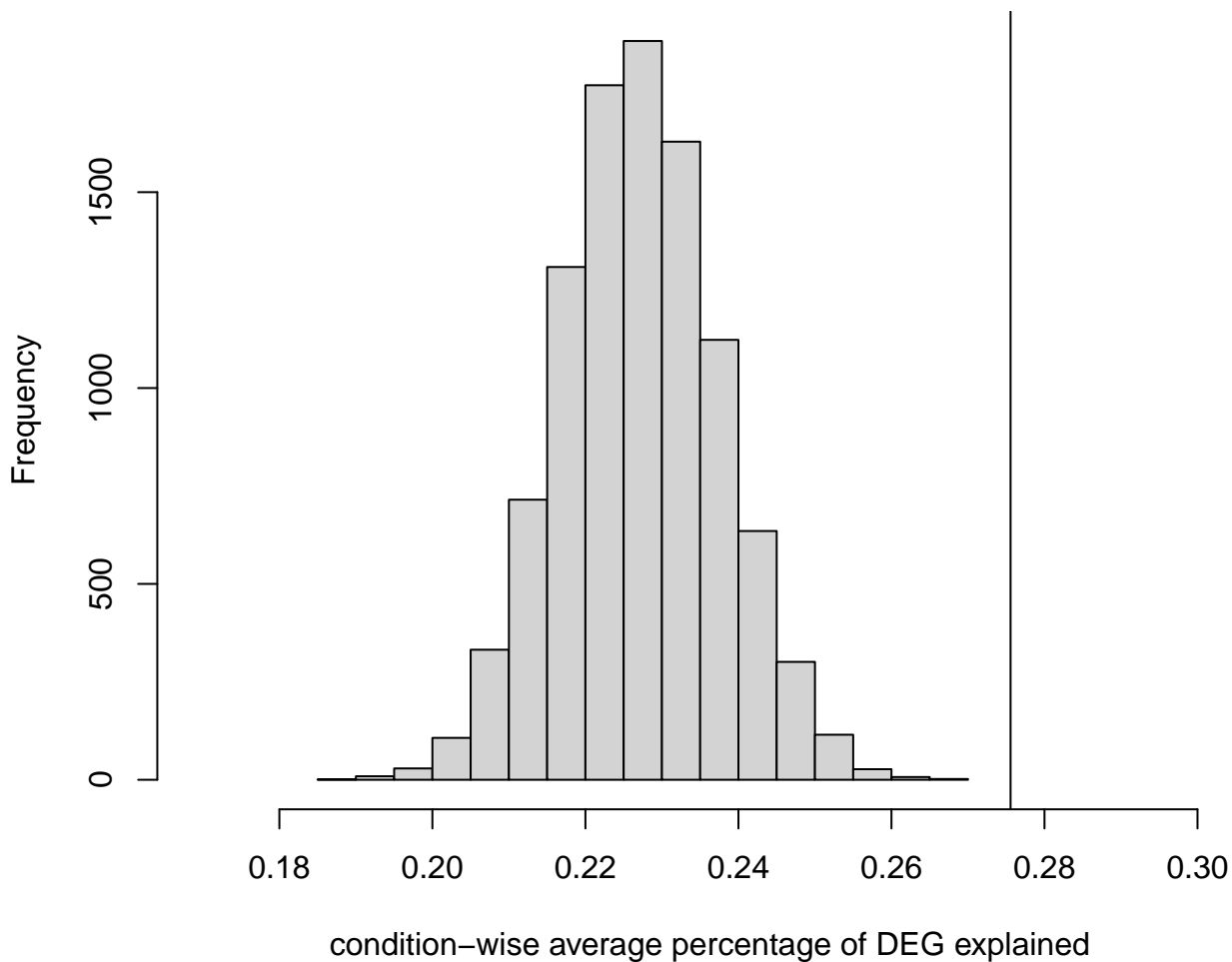
$p < 0.98$



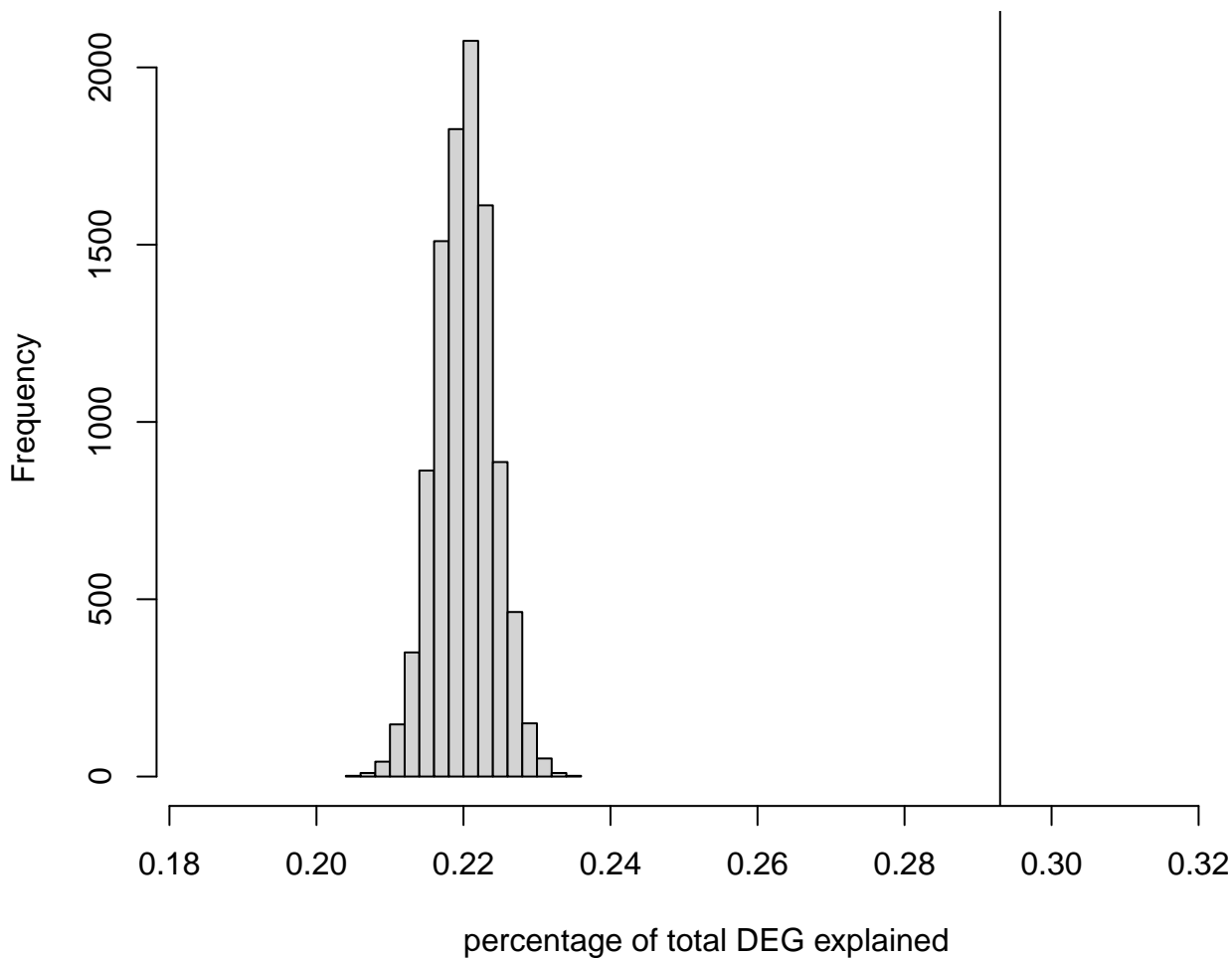
**CR model – full data**  
**p < 1e-04**



**CR model – single data**  
 **$p < 1e-04$**

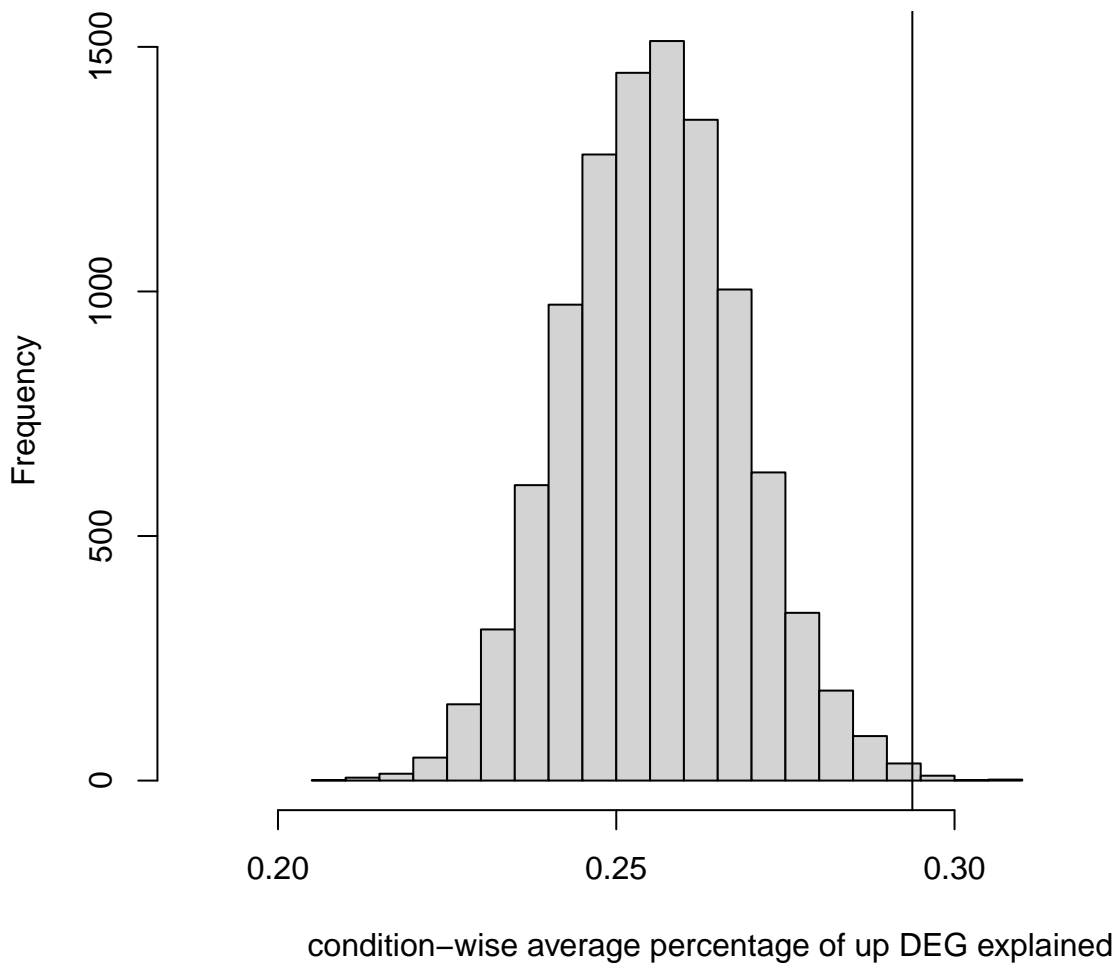


**CR model – single data**  
**p < 1e-04**

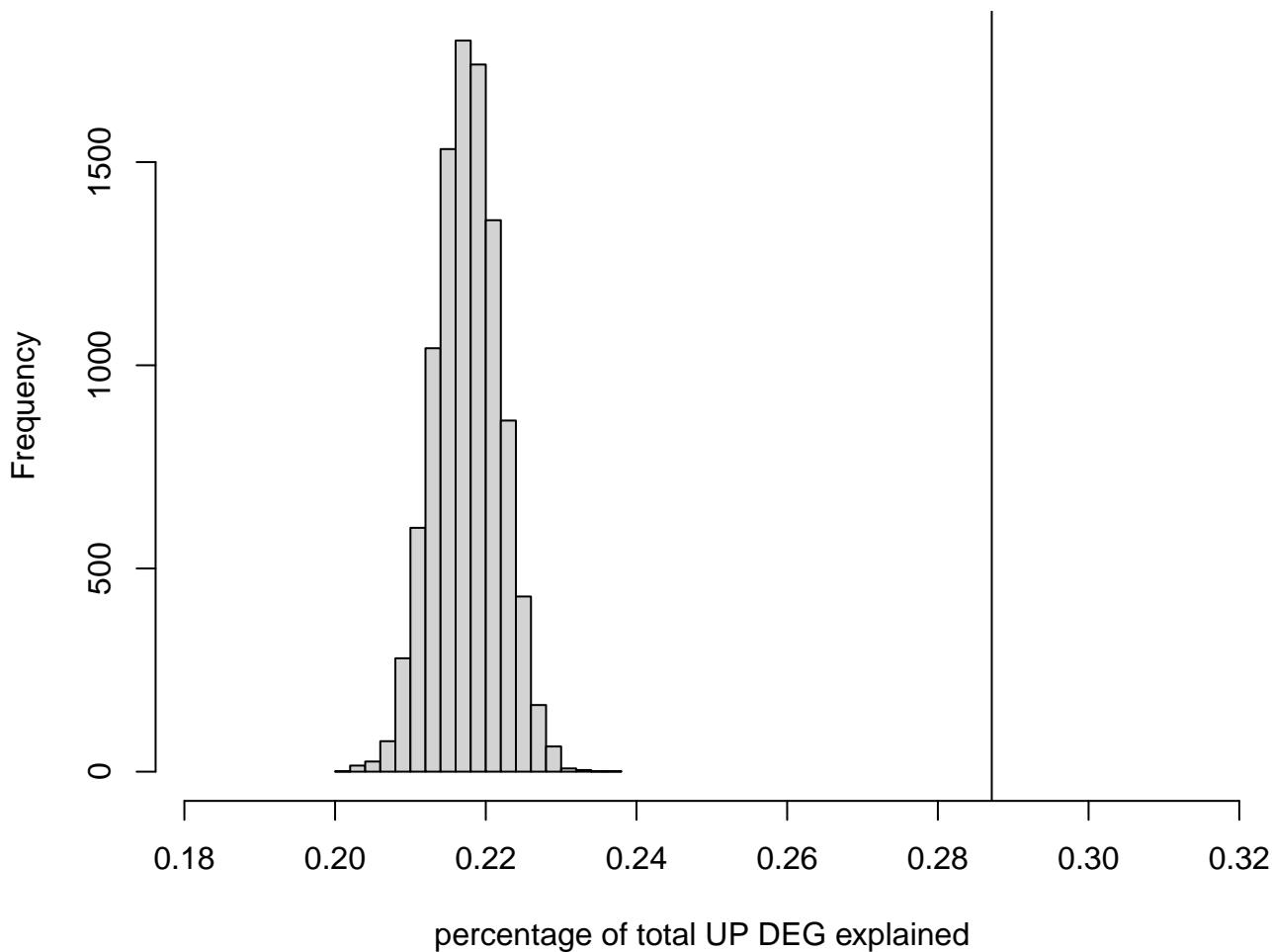




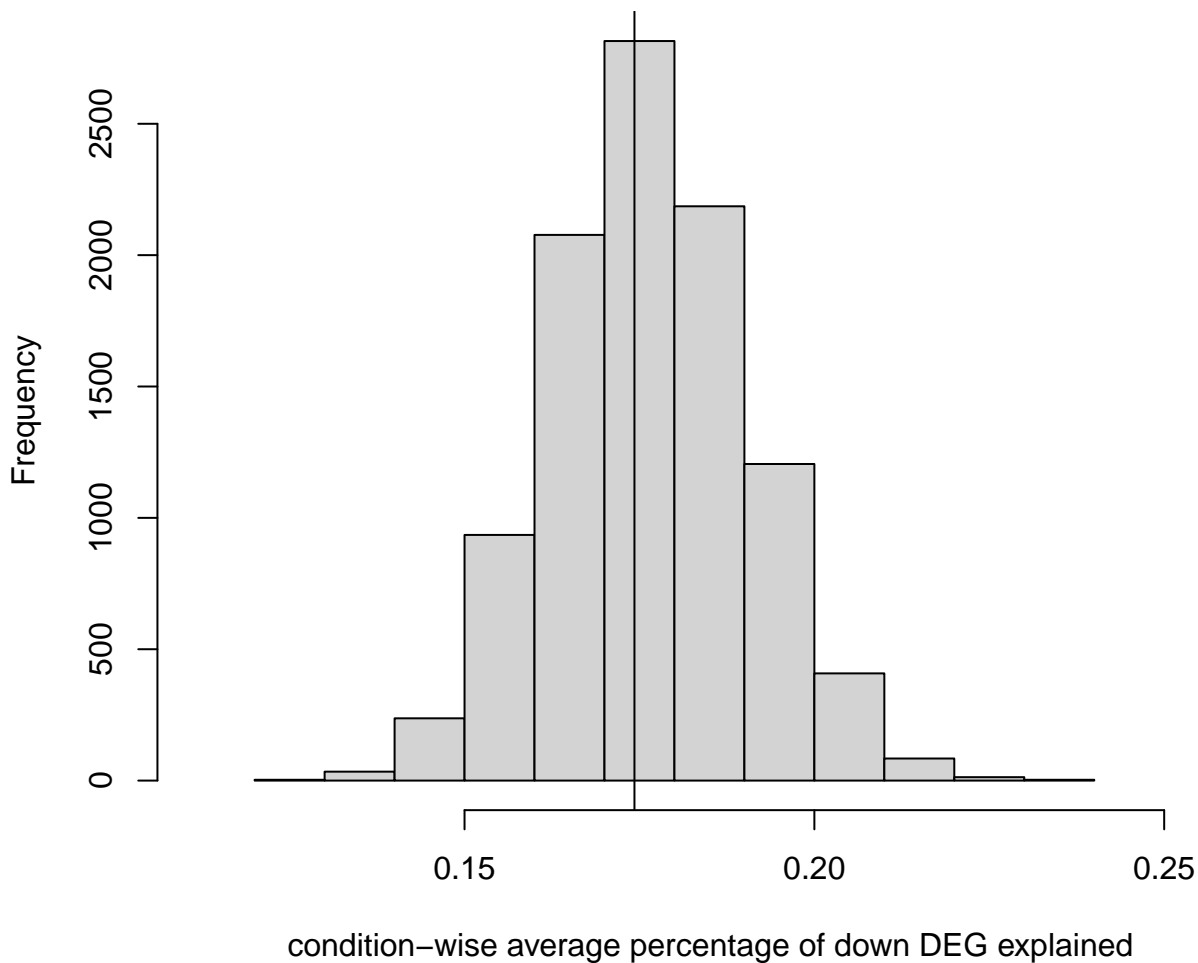
**CR model – single data**  
**p < 0.002**



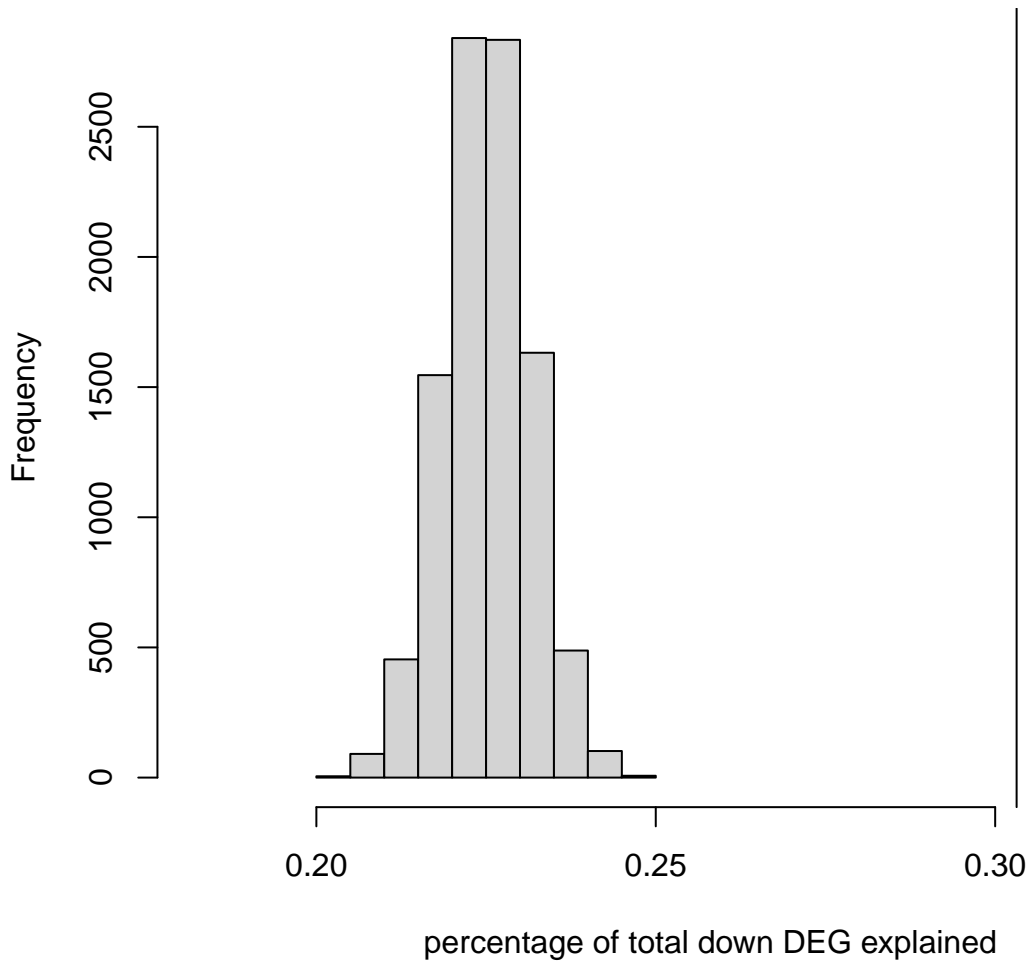
**CR model – single data**  
 **$p < 1e-04$**



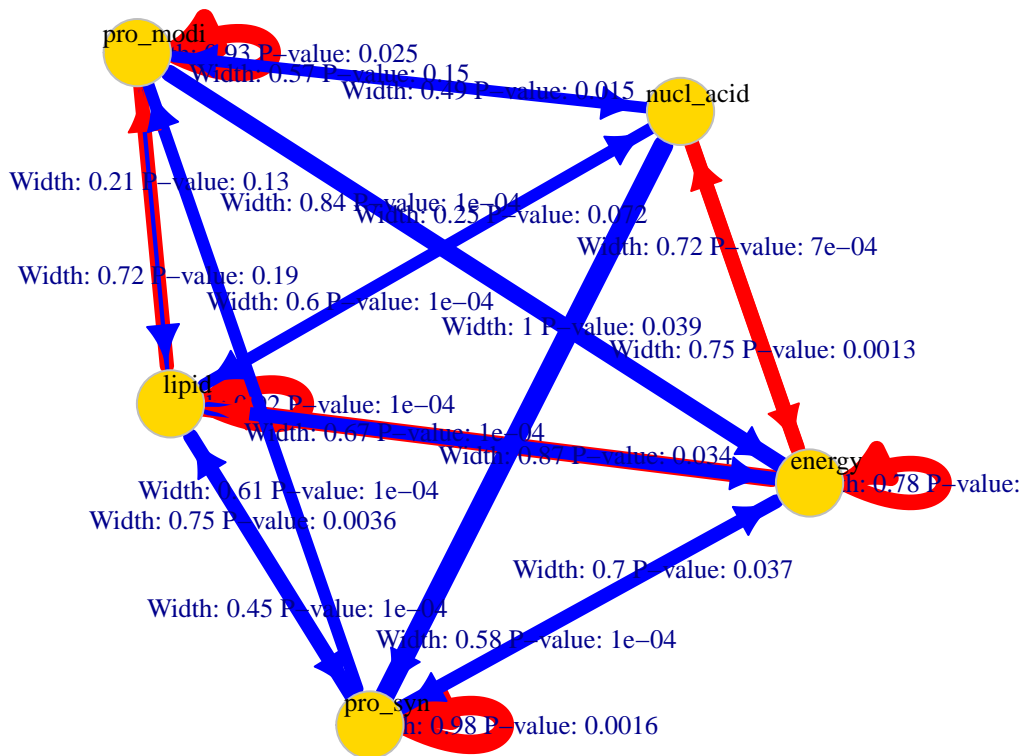
**CR model – single data**  
**p < 0.55**



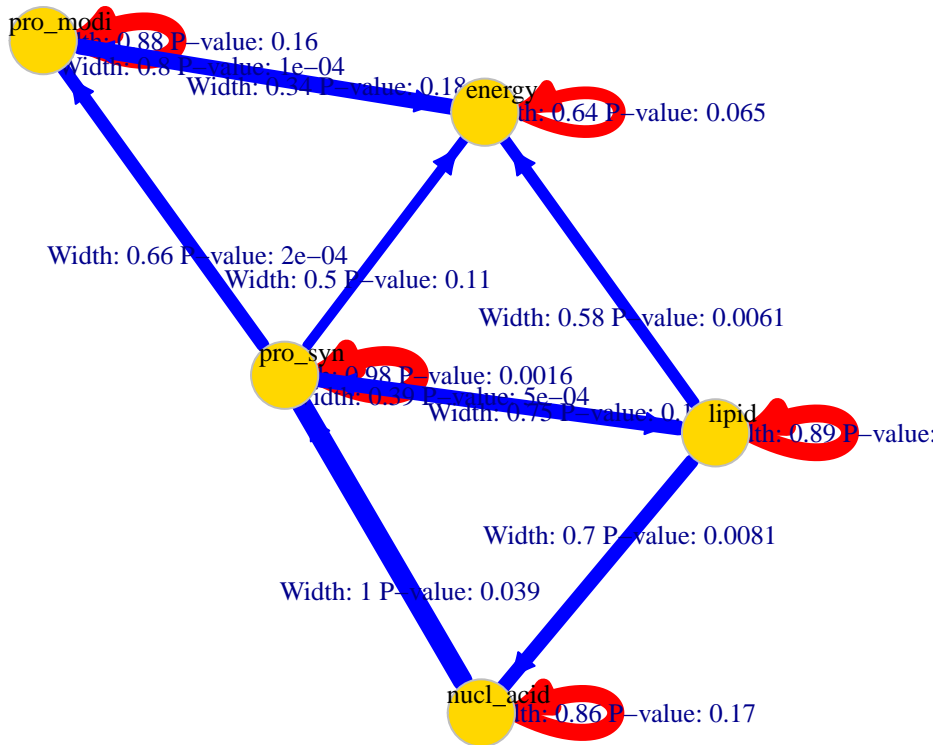
**CR model – single data**  
**p < 1e-04**



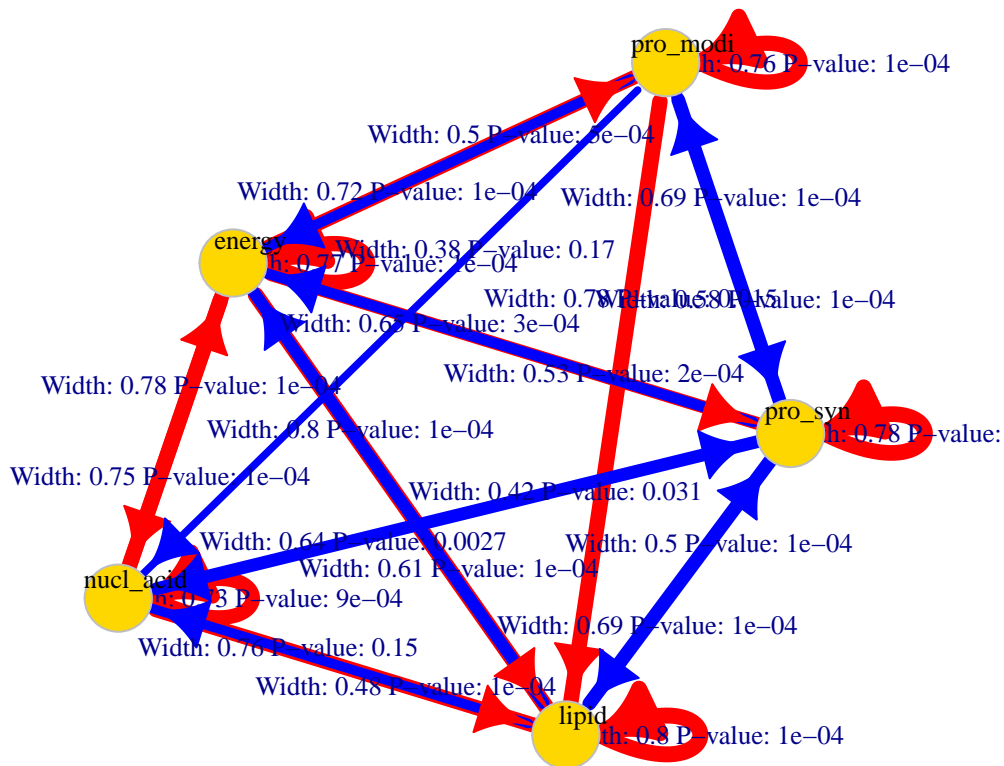
single – raw –  $p < 0.2$



# single – normalized – $p < 0.2$



# full – raw – p < 0.2



# full – normalized – p < 0.2

