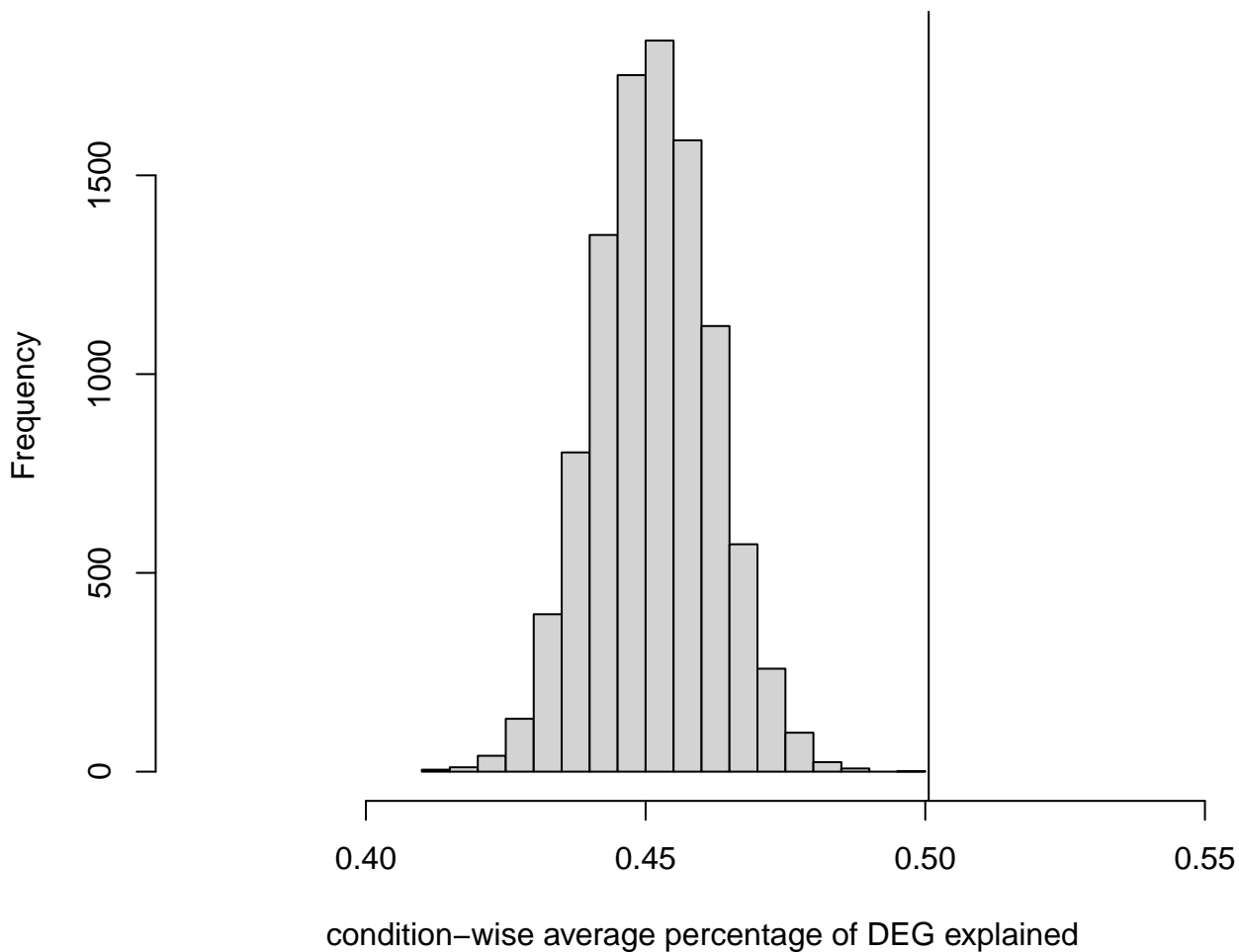
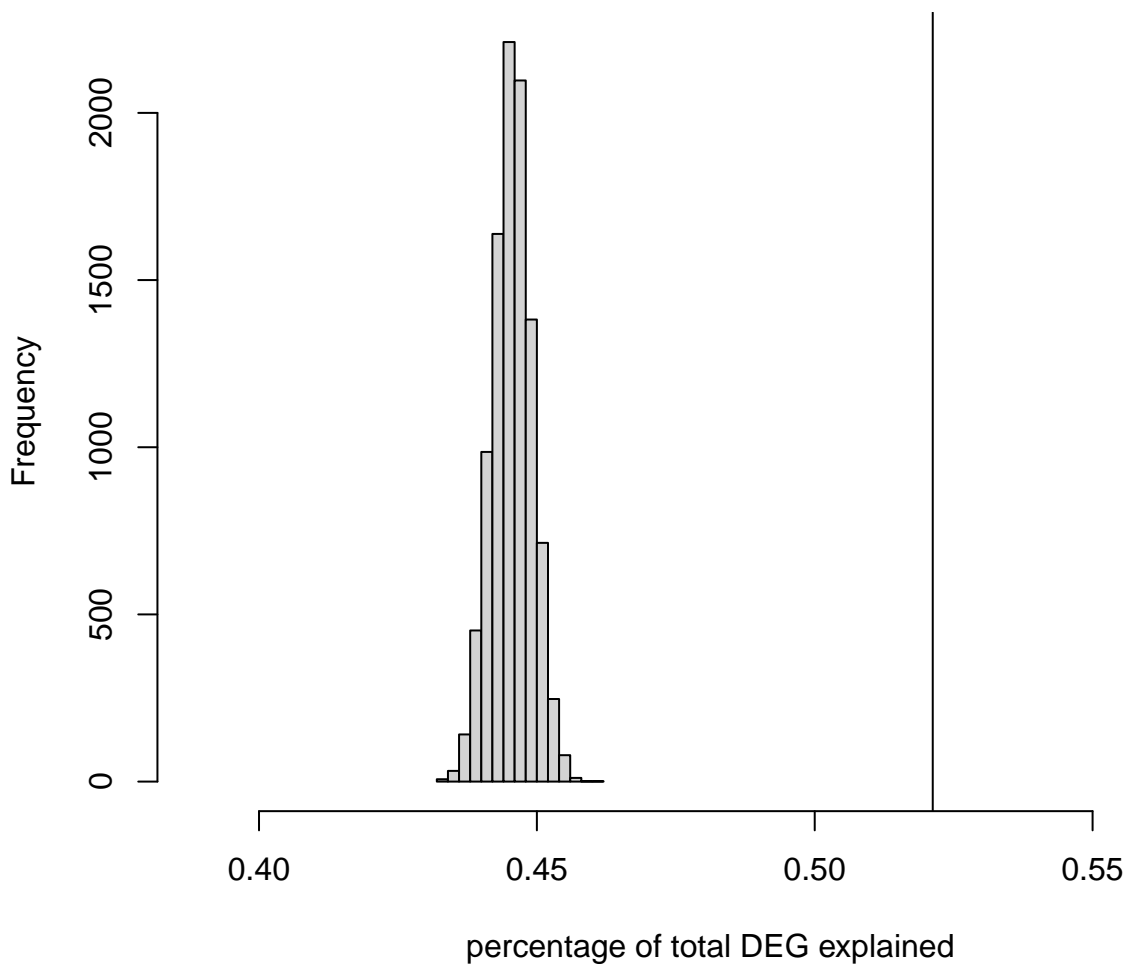


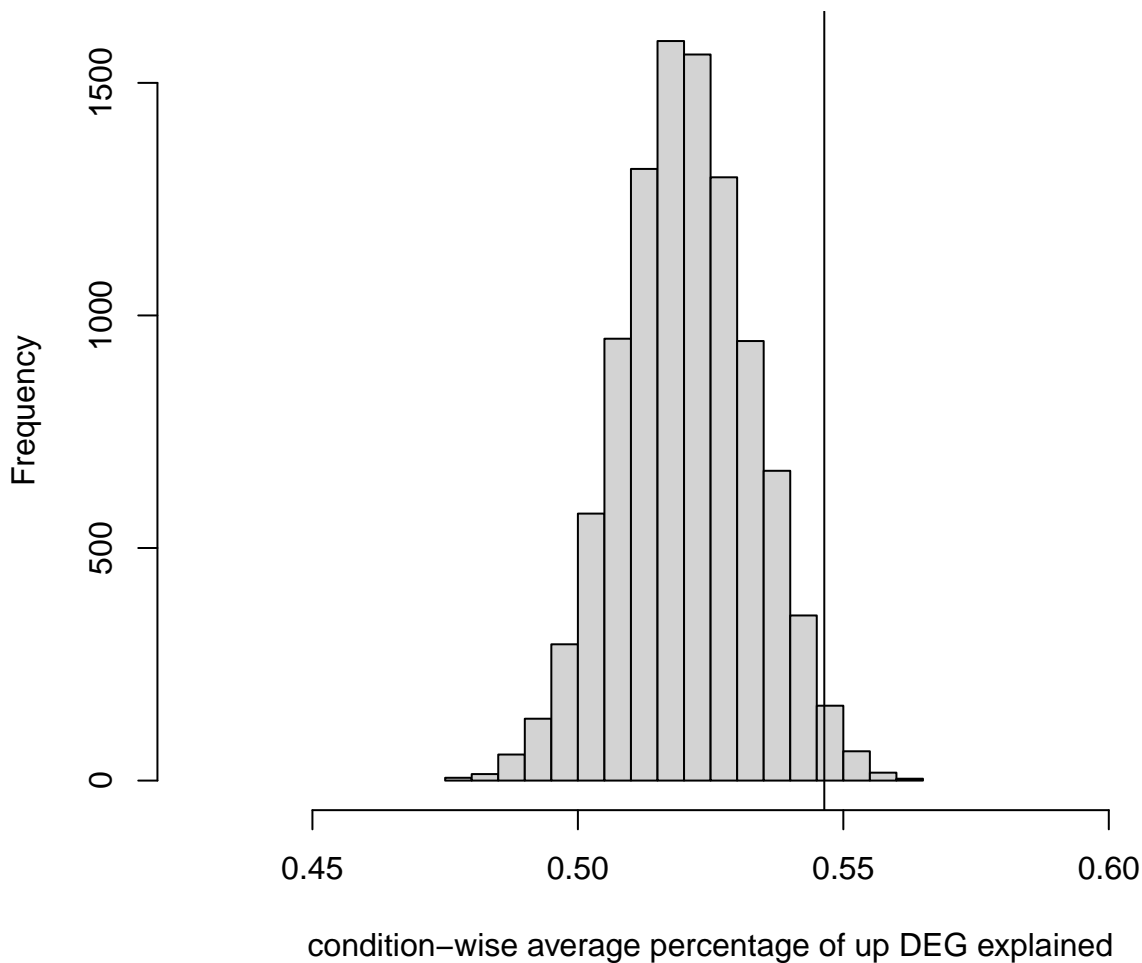
**CR model – full data**  
**p < 1e-04**



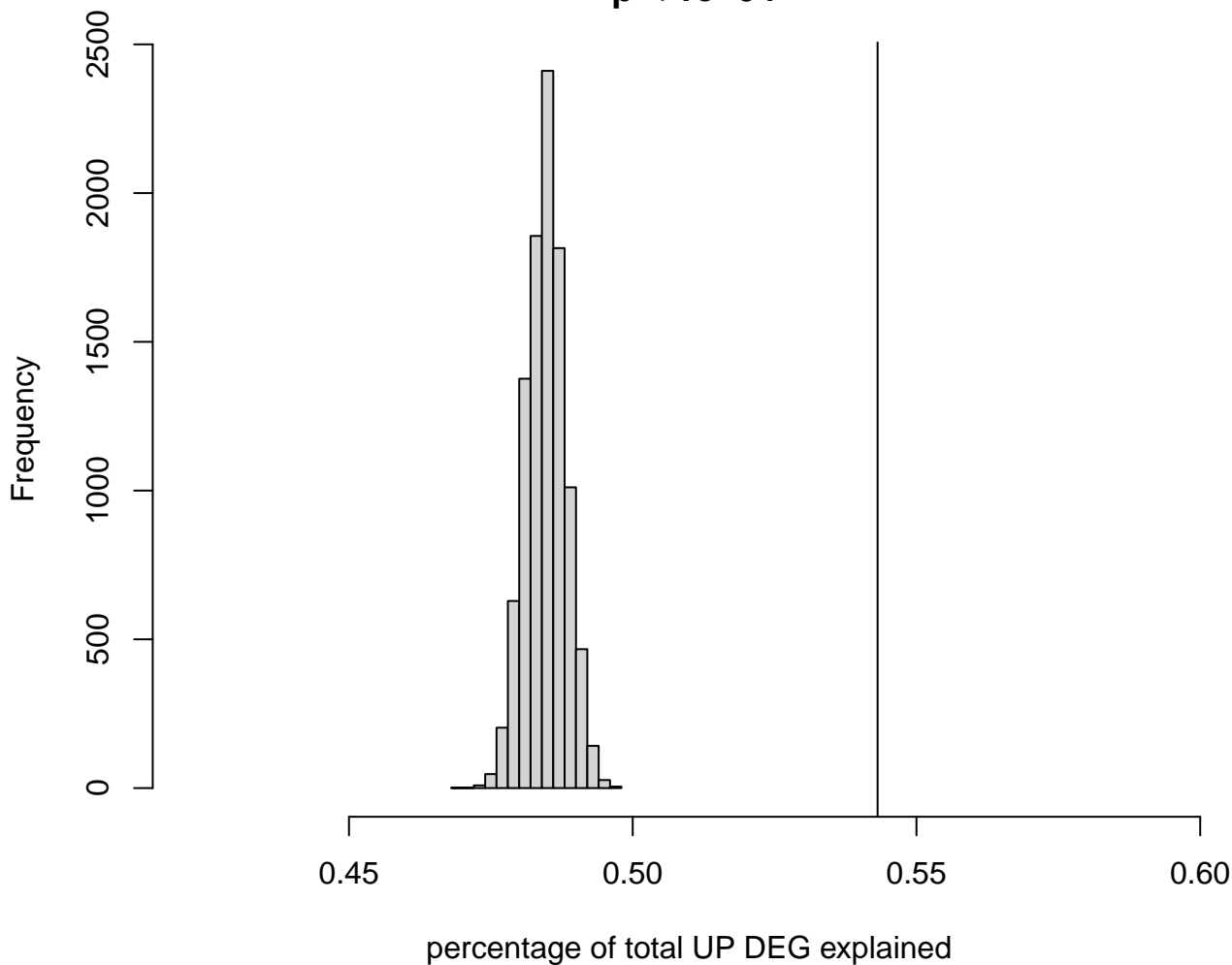
**CR model – full data**  
**p < 1e-04**



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

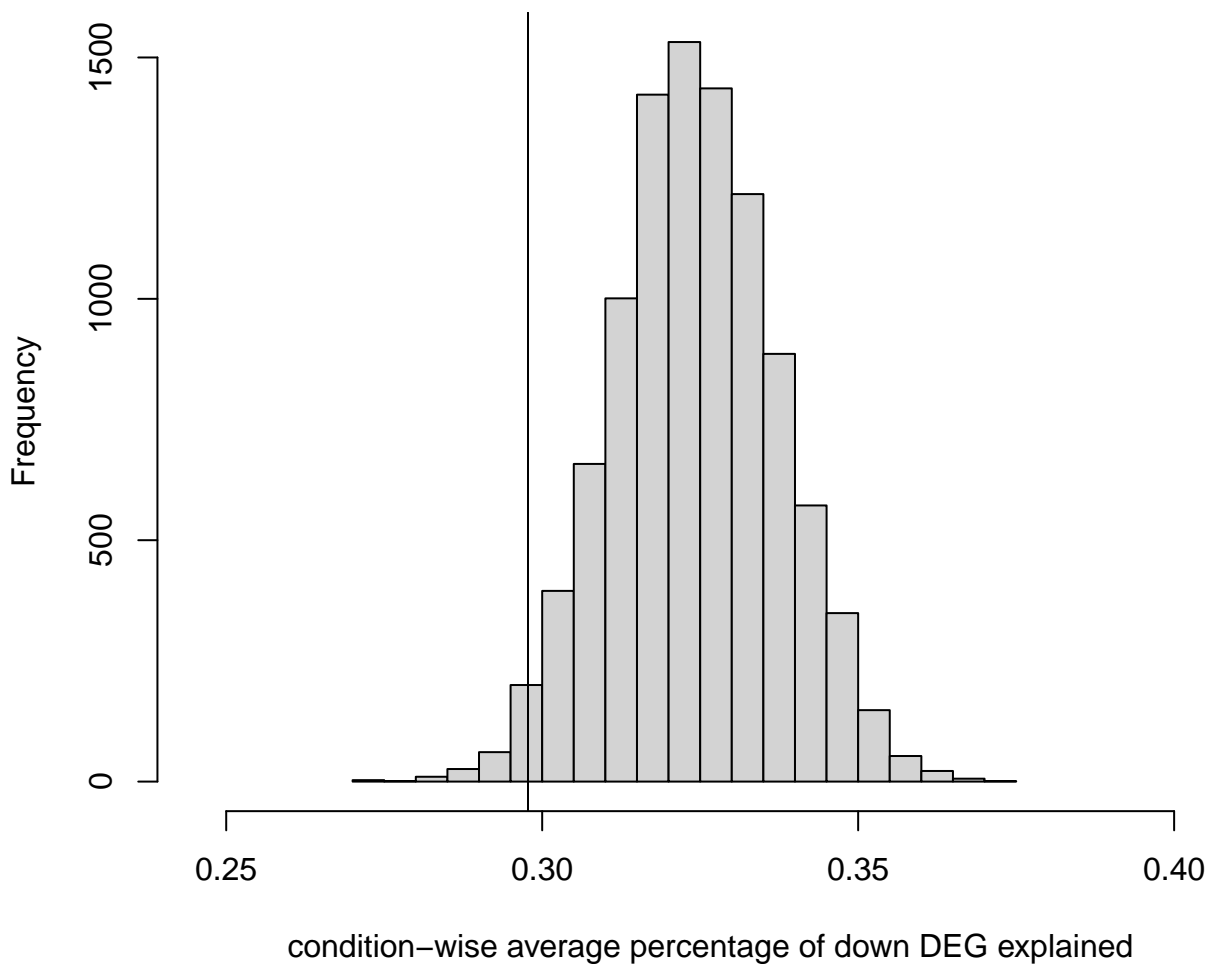


**CR model – full data**  
**p < 1e-04**

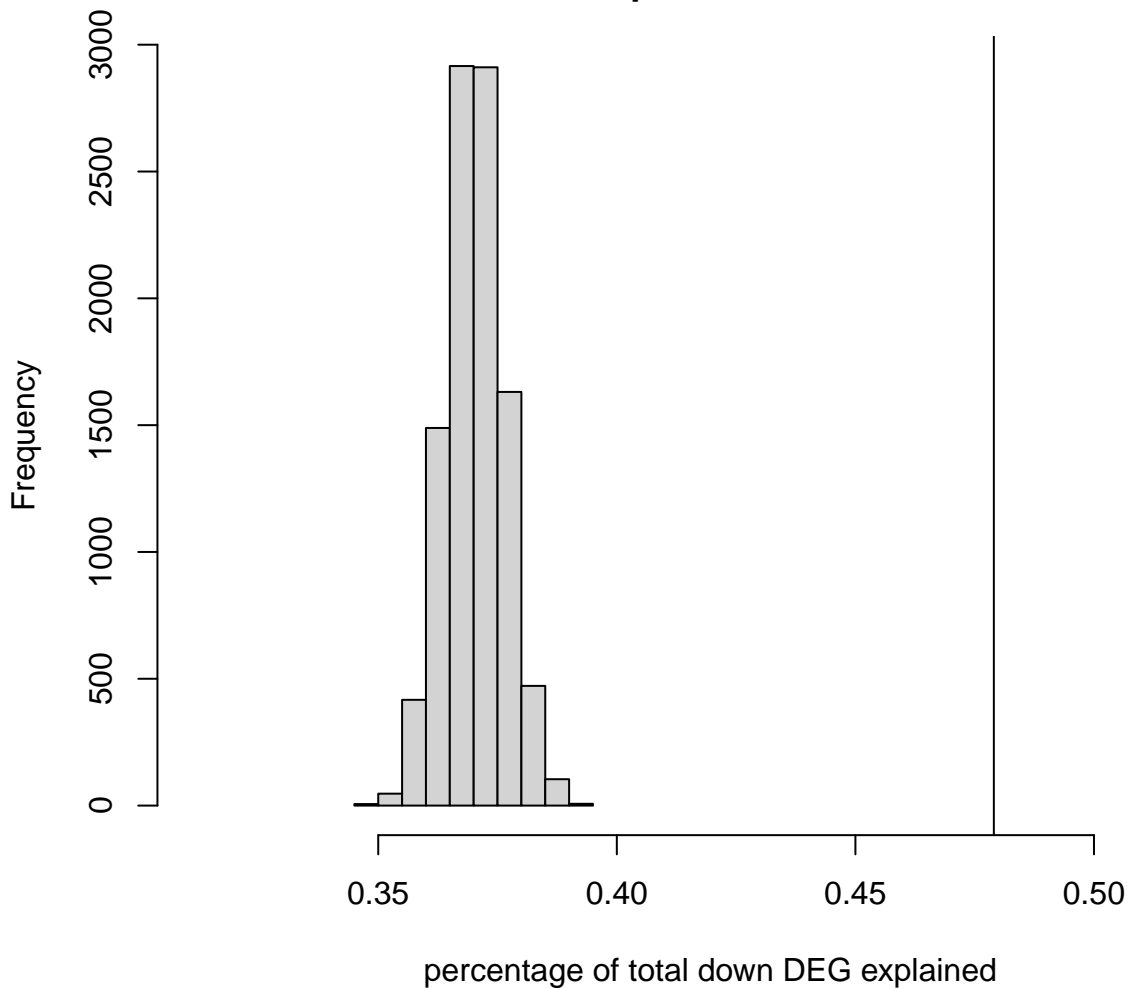


# CR model – full data

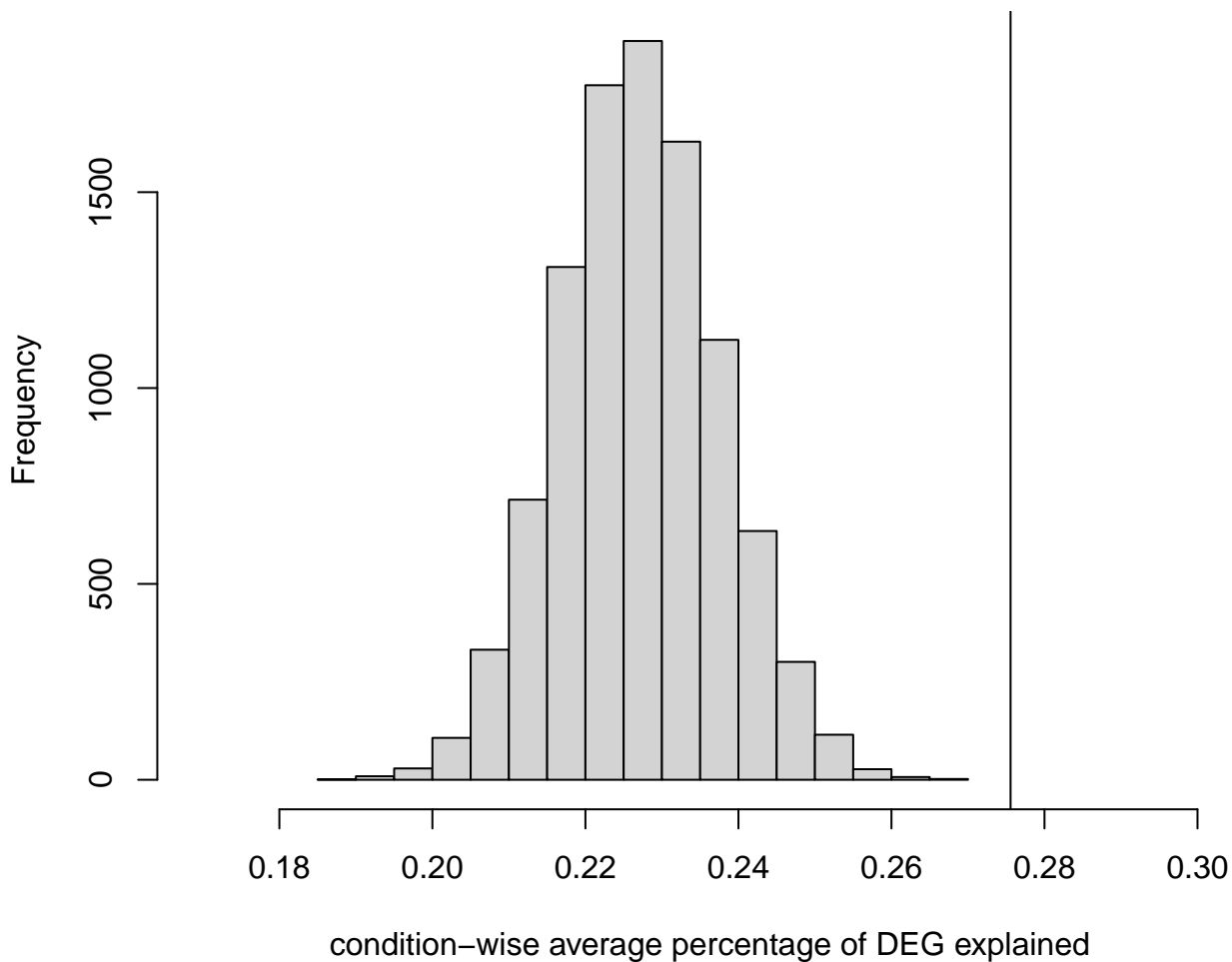
$p < 0.98$



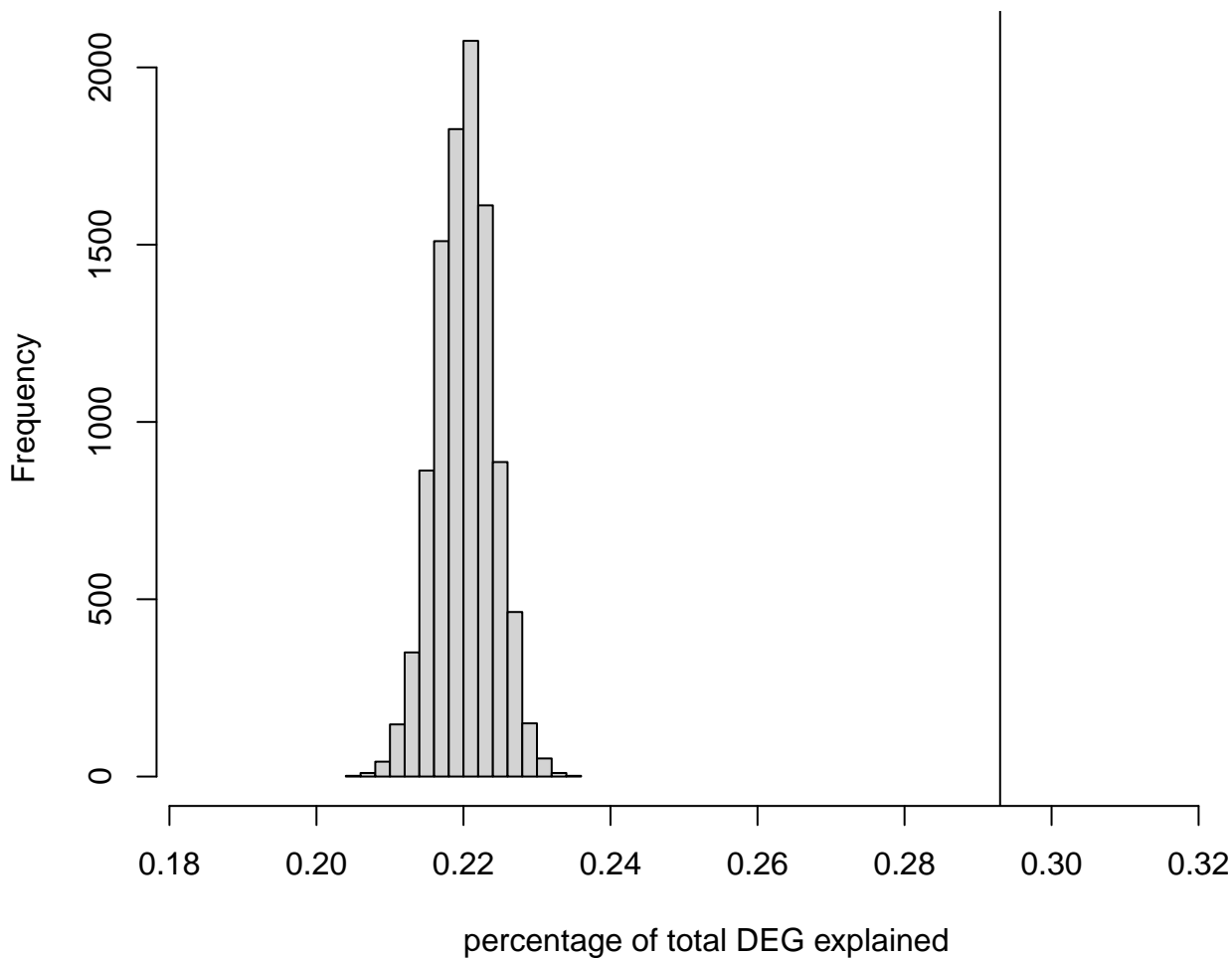
**CR model – full data**  
 **$p < 1e-04$**



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

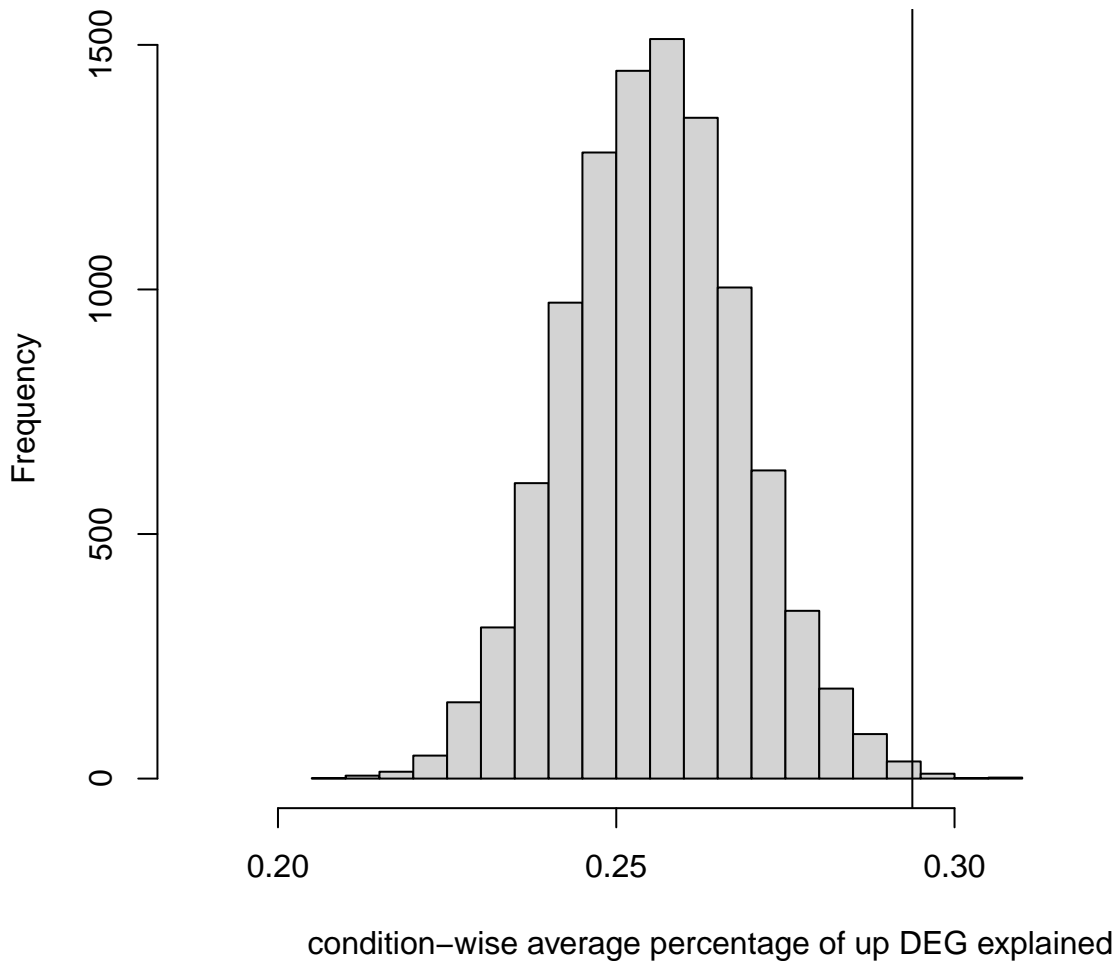


**CR model – single data**  
 **$p < 1e-04$**

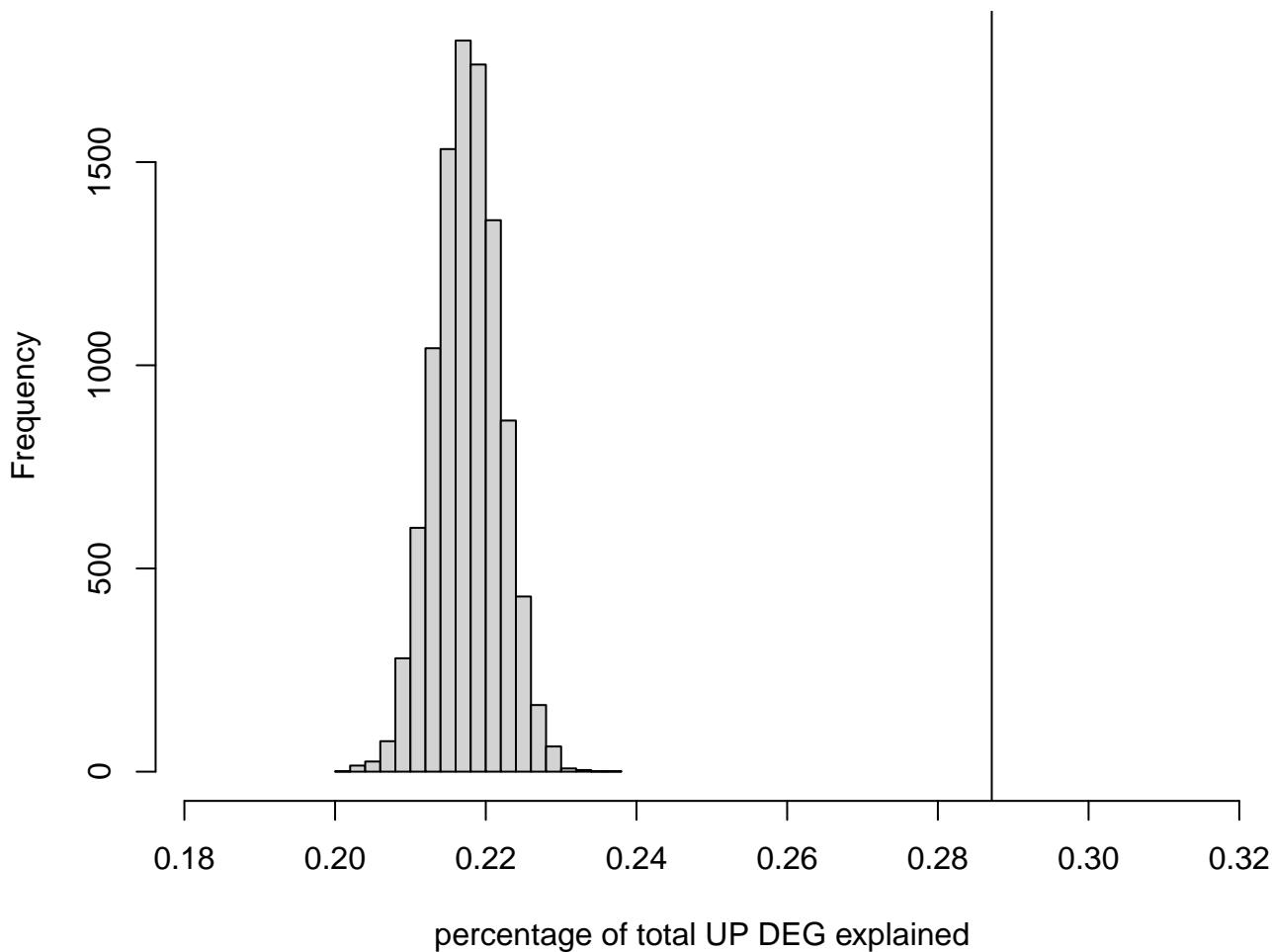




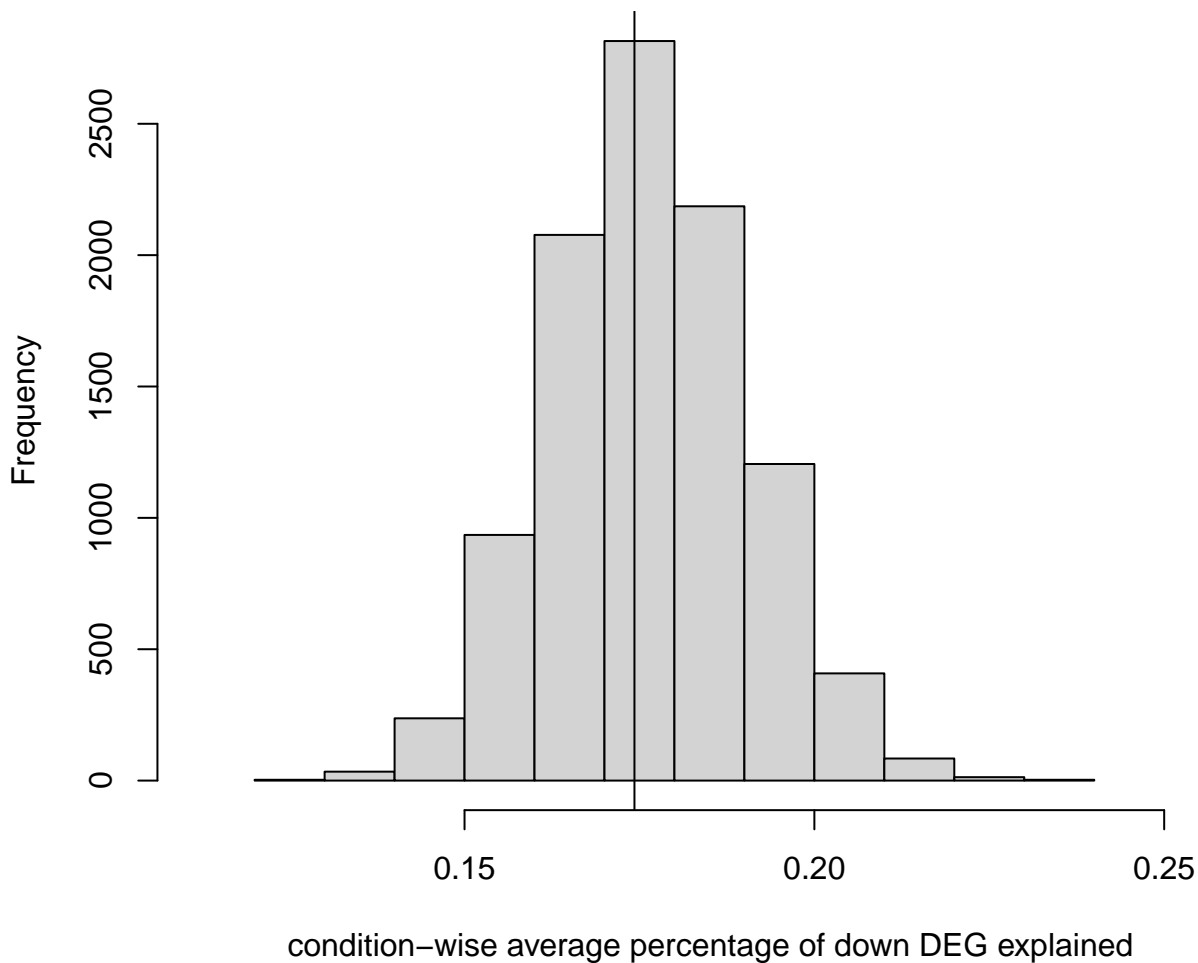
**CR model – single data**  
**p < 0.002**



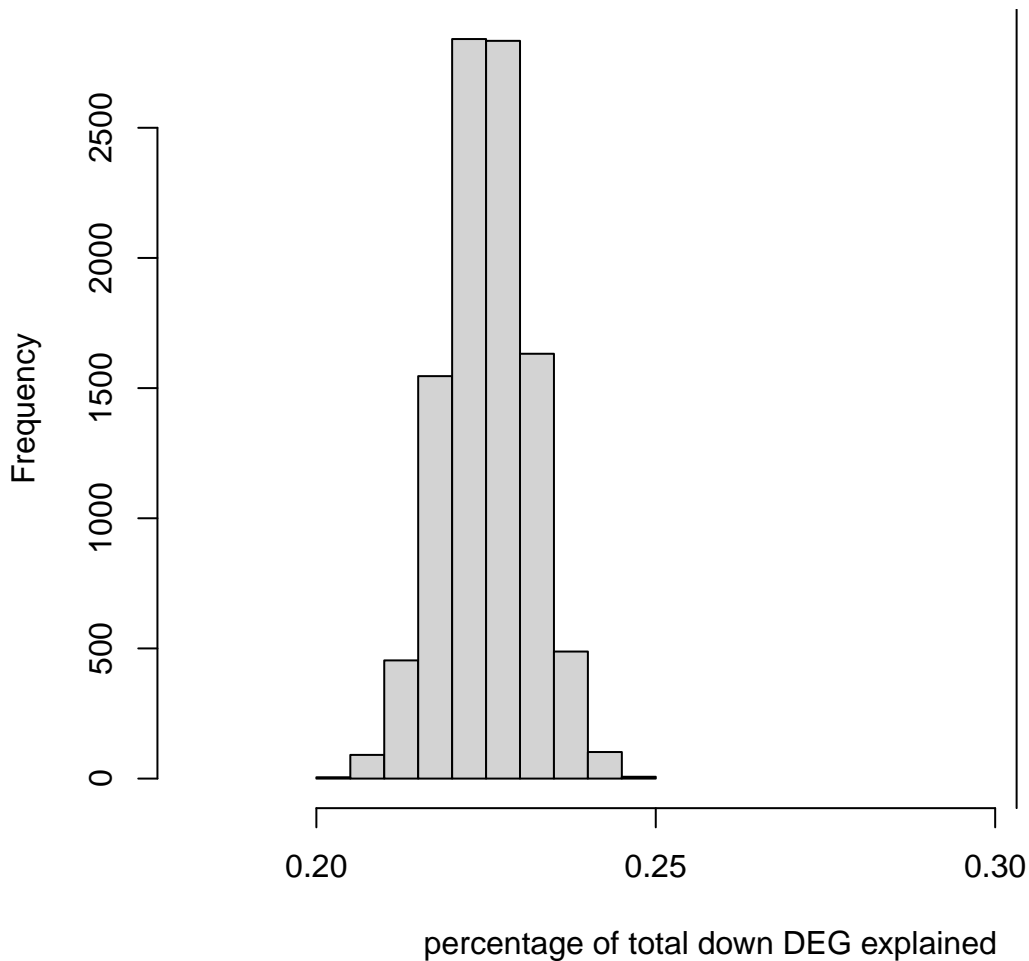
**CR model – single data**  
**p < 1e-04**



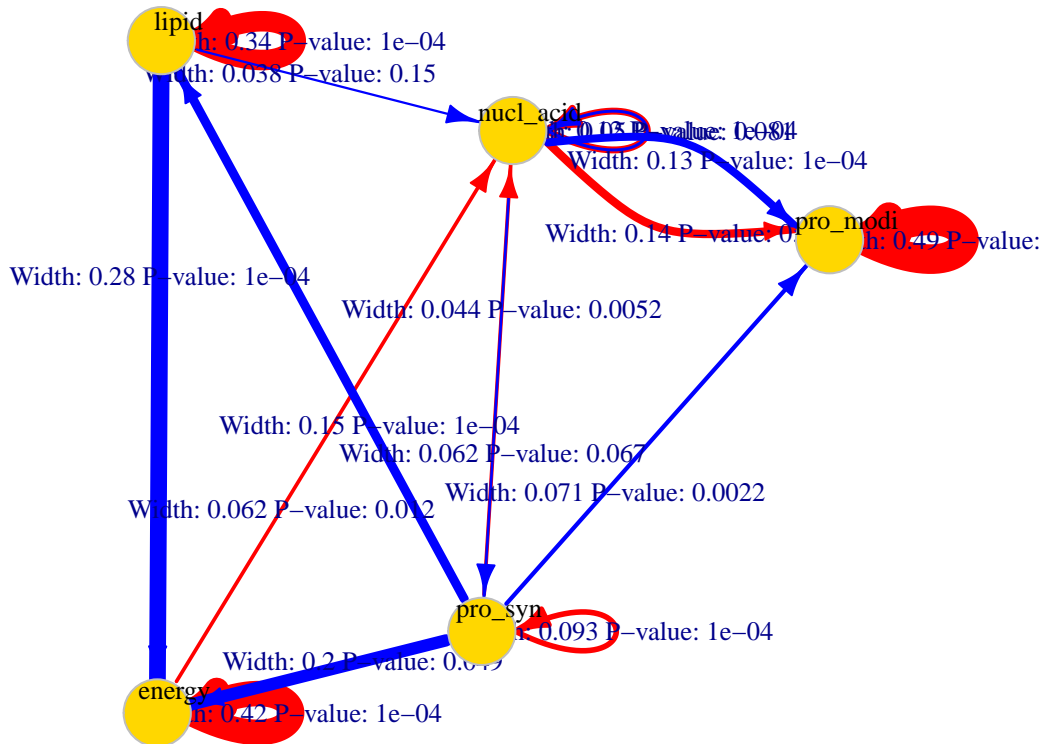
**CR model – single data**  
**p < 0.55**



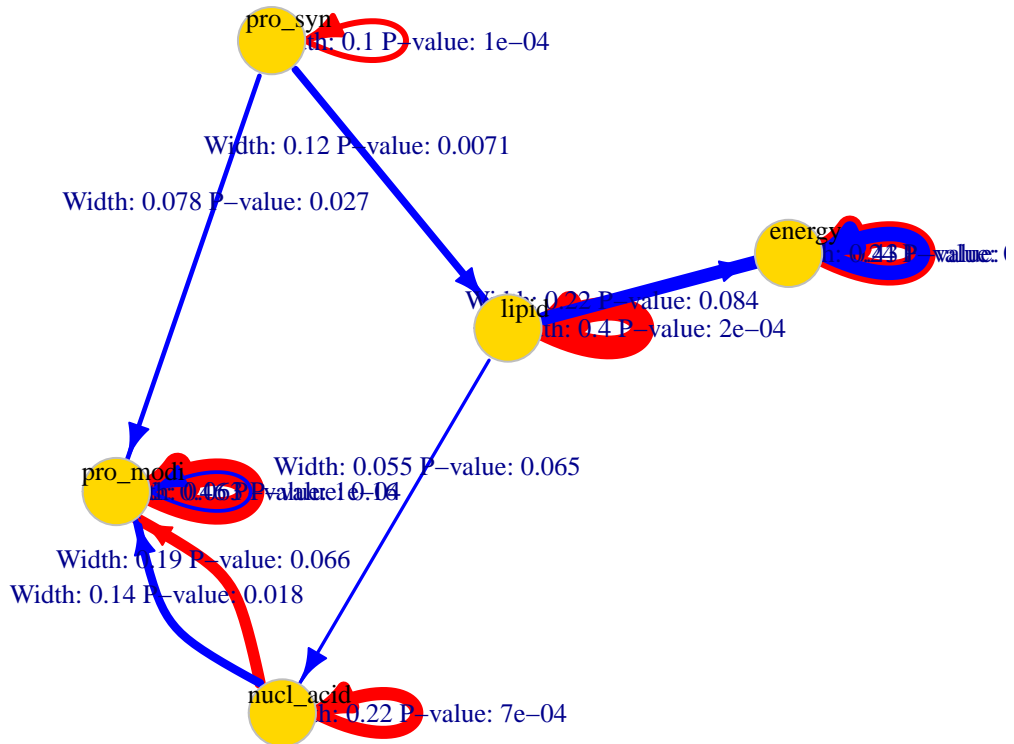
**CR model – single data**  
**p < 1e-04**



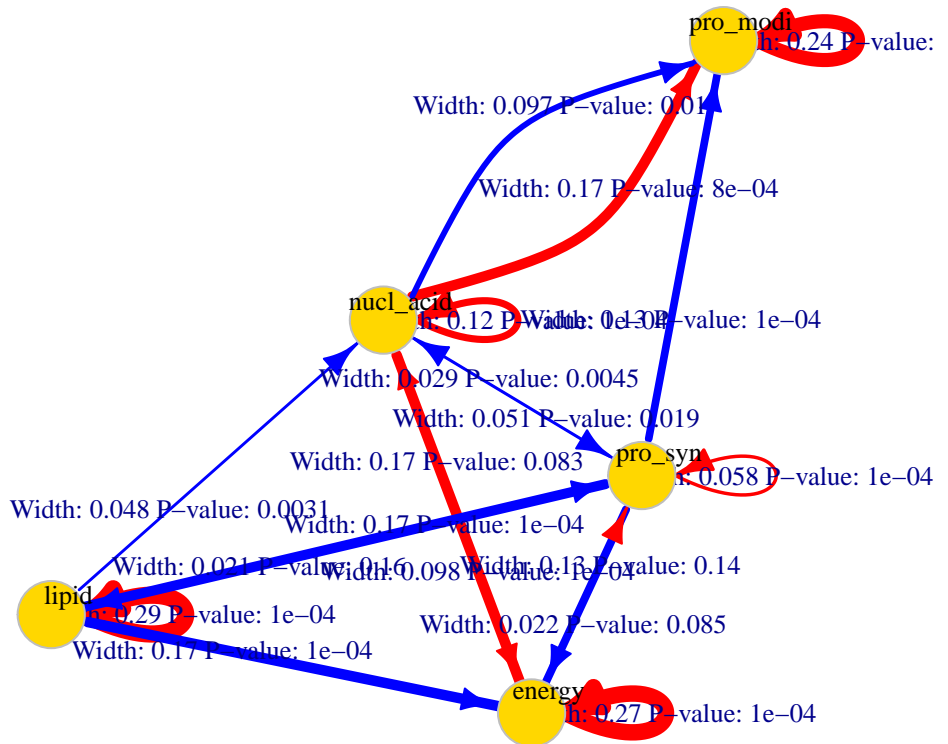
# single – raw – p < 0.2



# single – normalized – $p < 0.2$



**full – raw –  $p < 0.2$**



## full – normalized – $p < 0.2$

