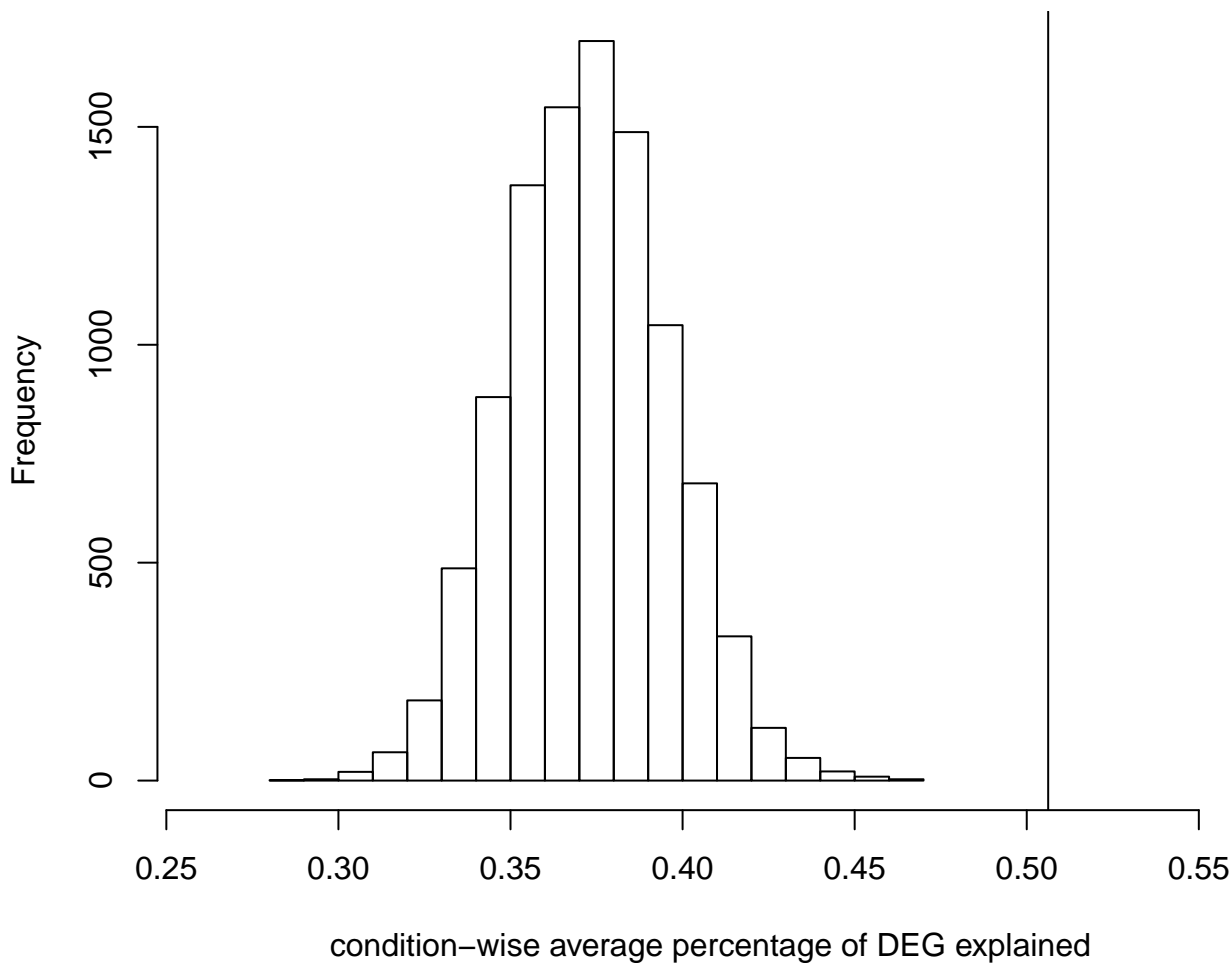
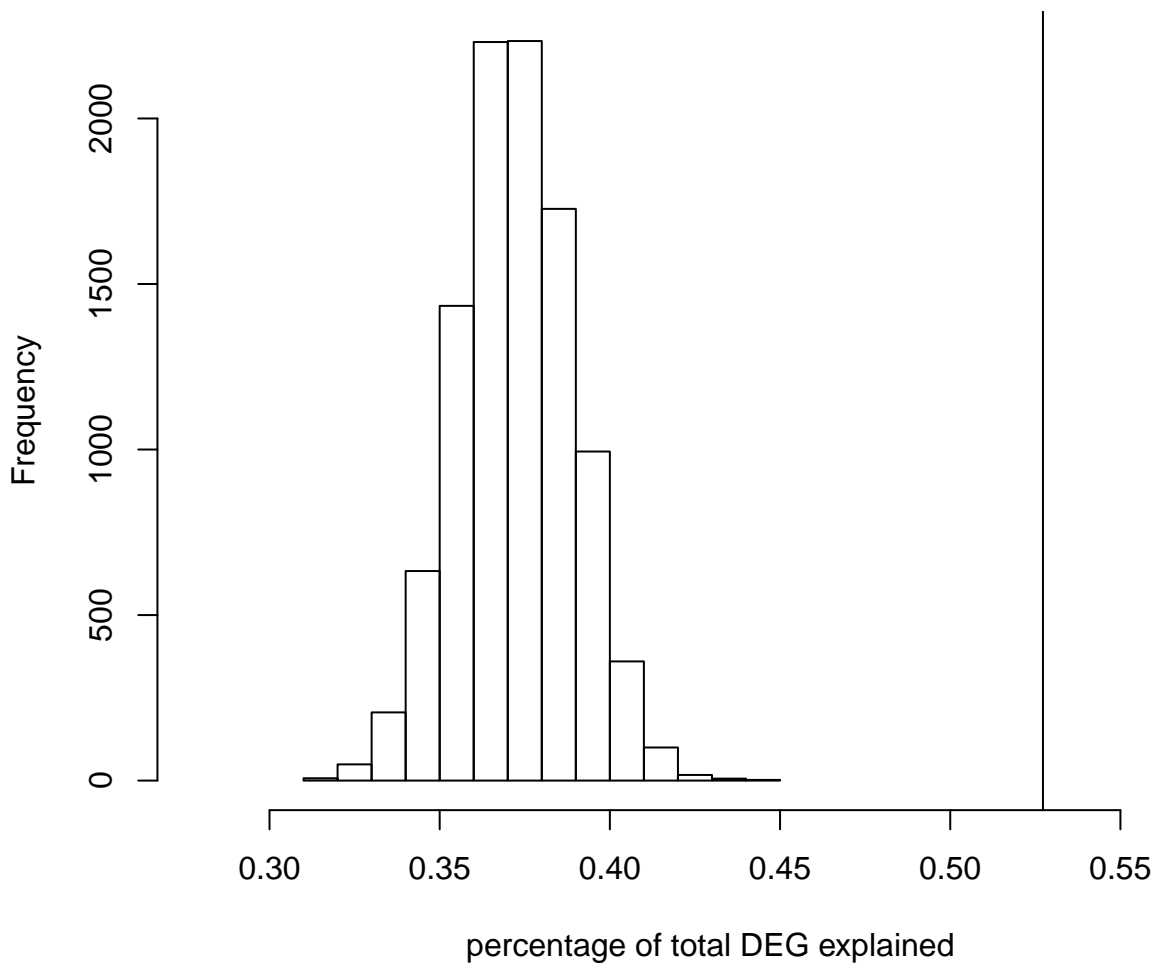


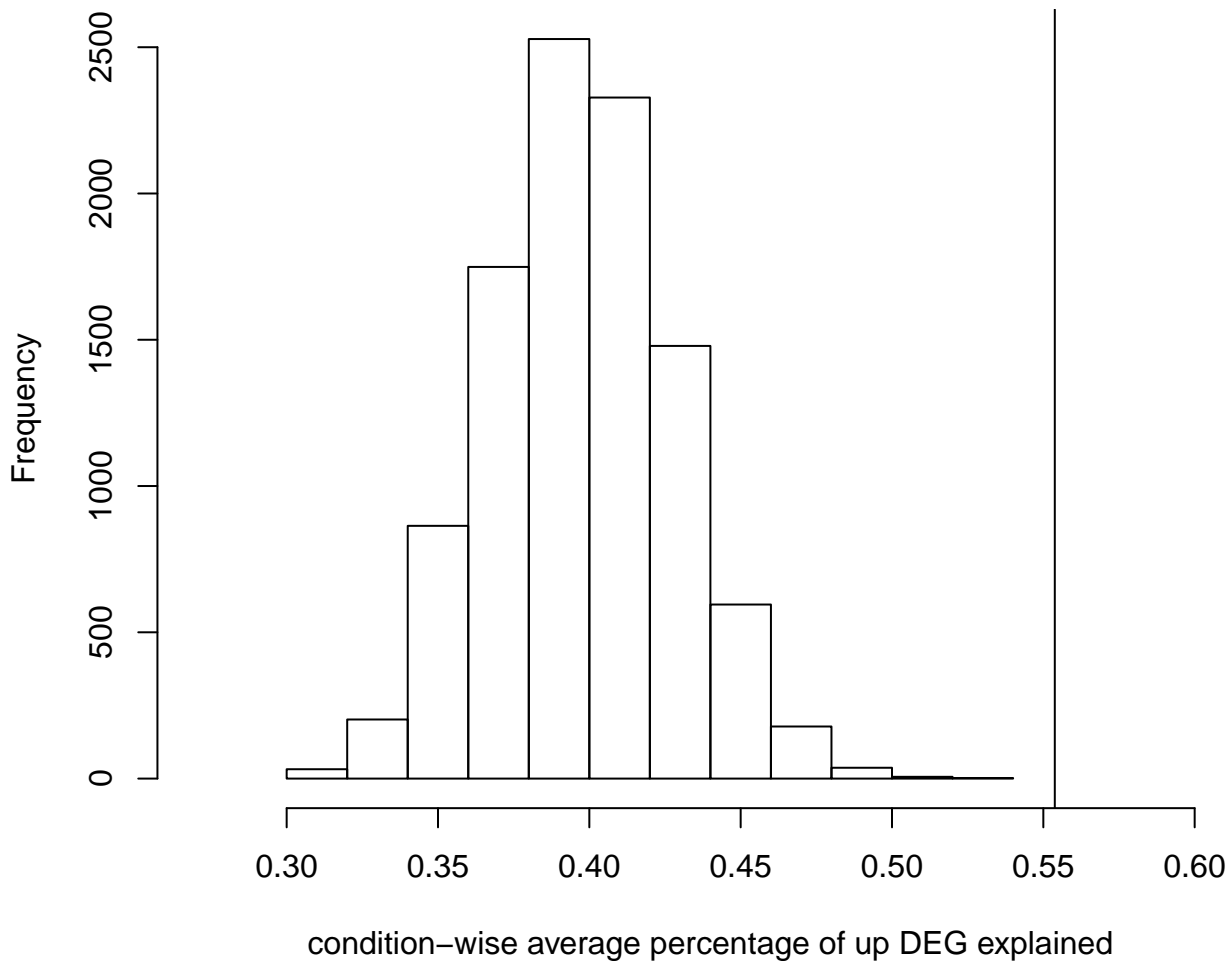
**CR model – full data**  
**p < 1e-04**



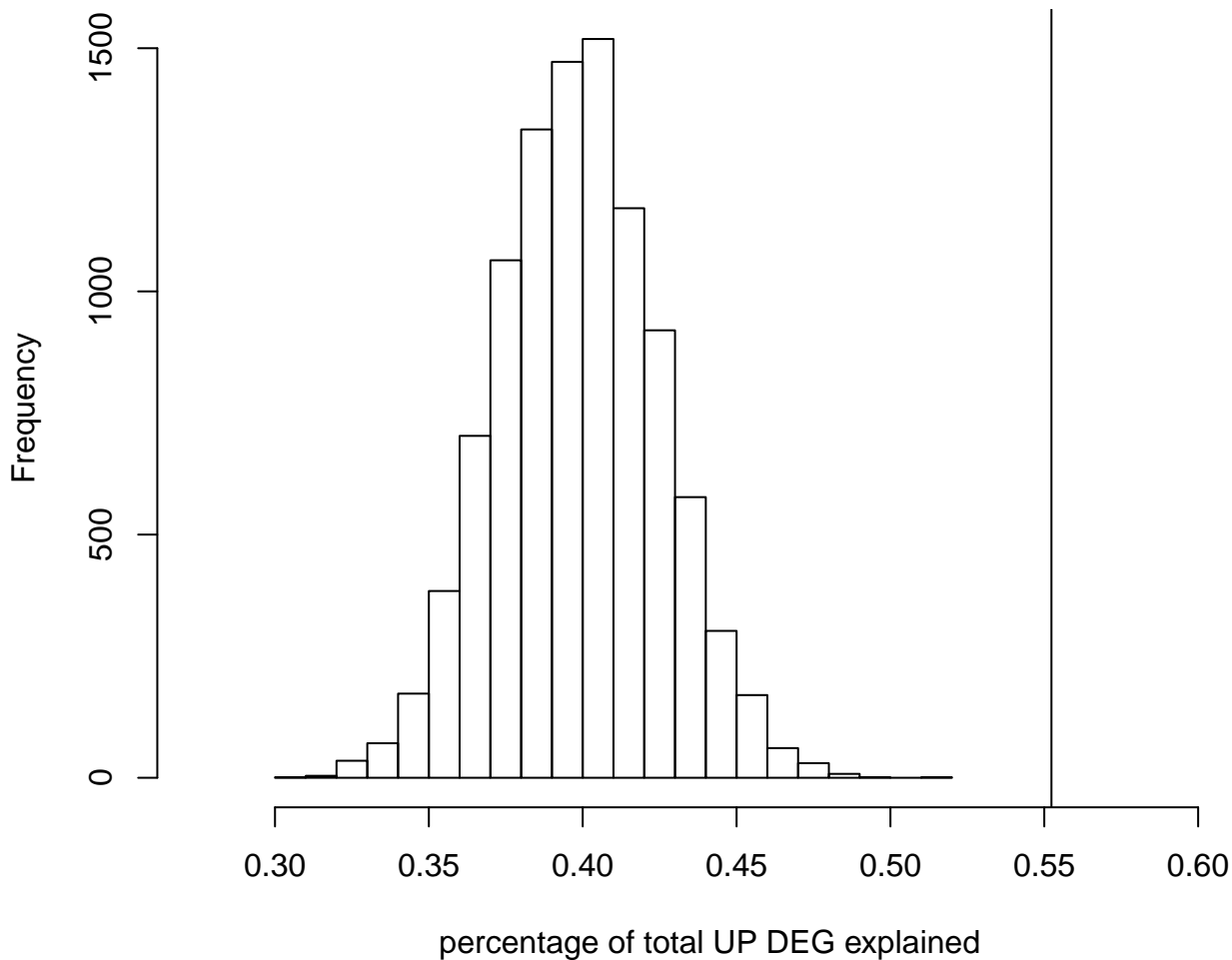
**CR model – full data**  
**p < 1e-04**



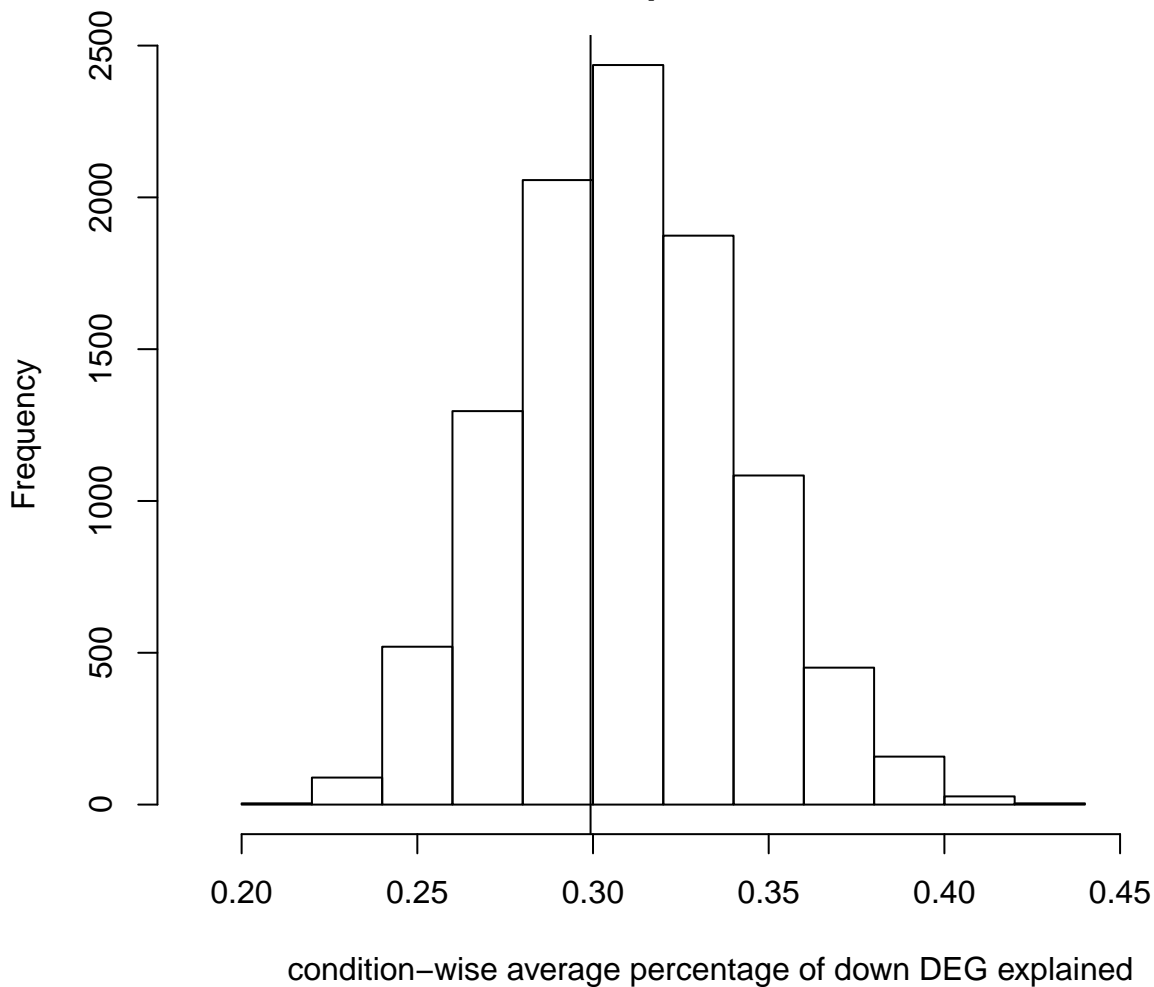
**CR model – full data**  
**p < 1e-04**



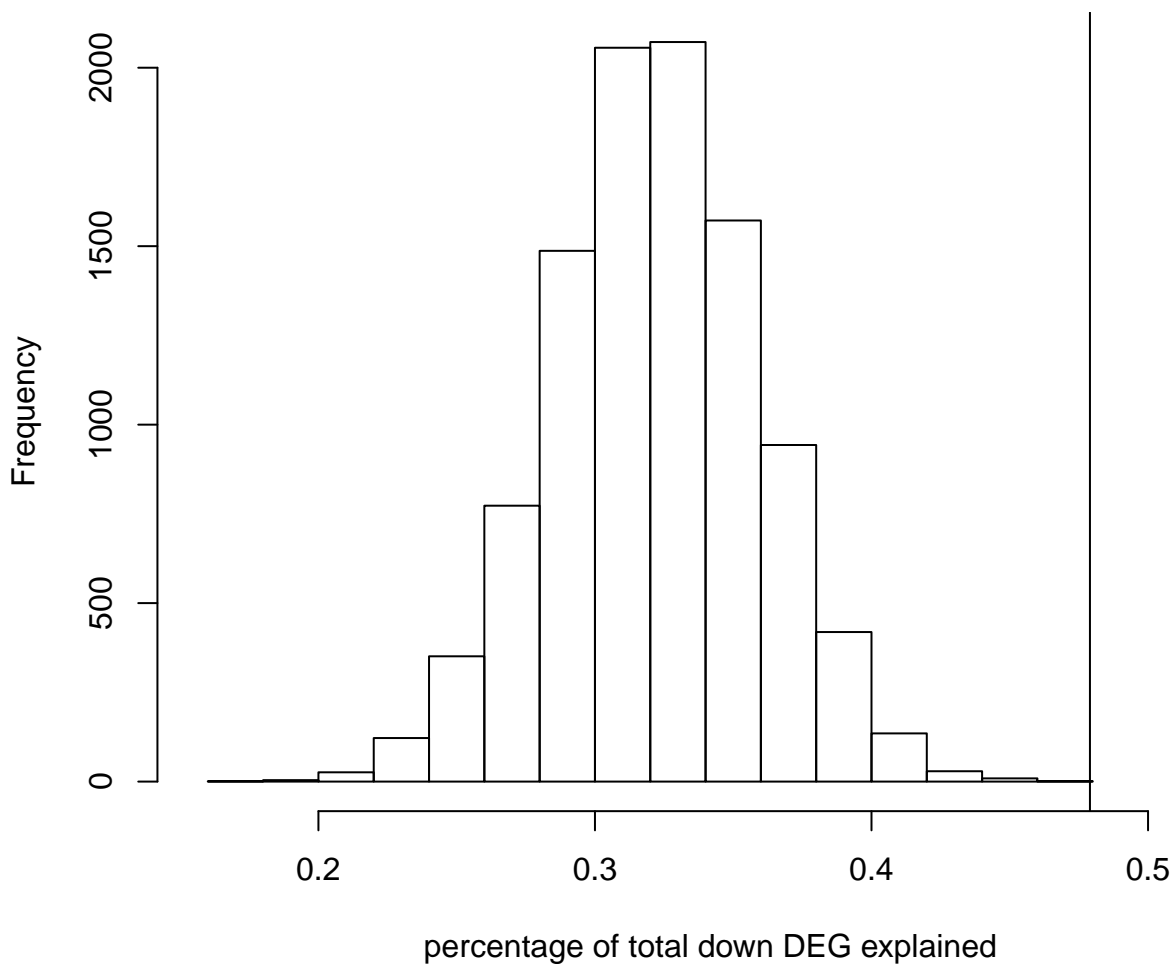
**CR model – full data**  
**p < 1e-04**



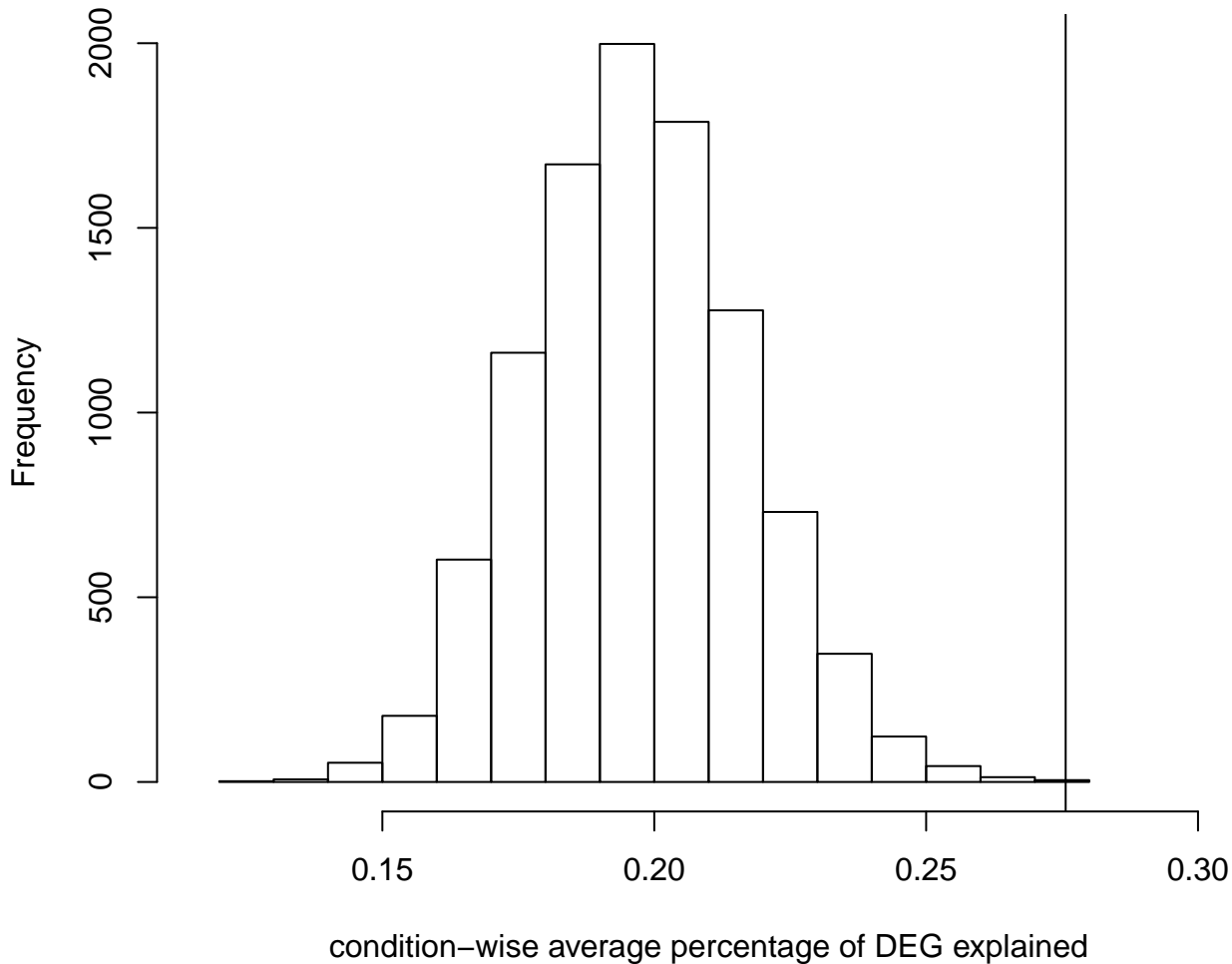
**CR model – full data**  
**p < 0.61**



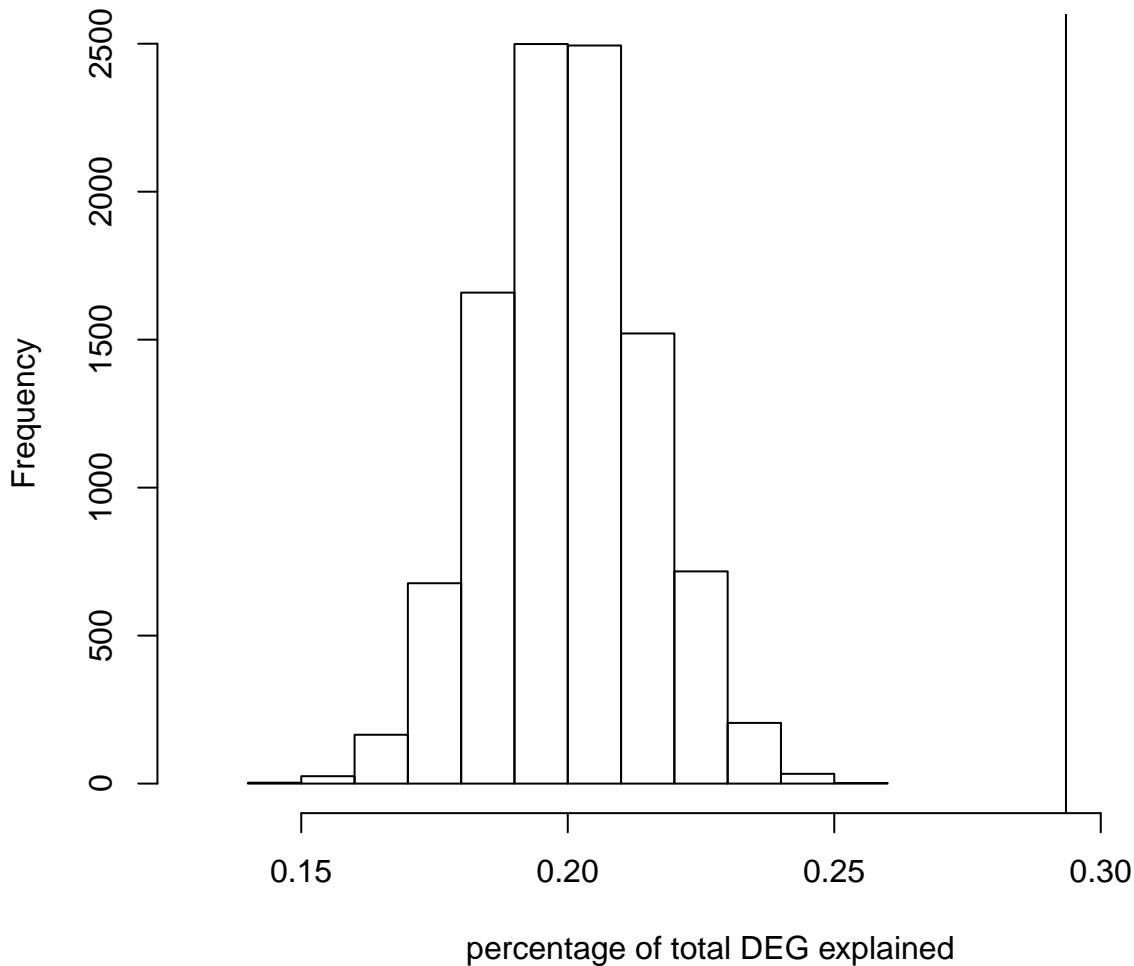
**CR model – full data**  
 **$p < 1e-04$**



**CR model – single data**  
 **$p < 3e-04$**

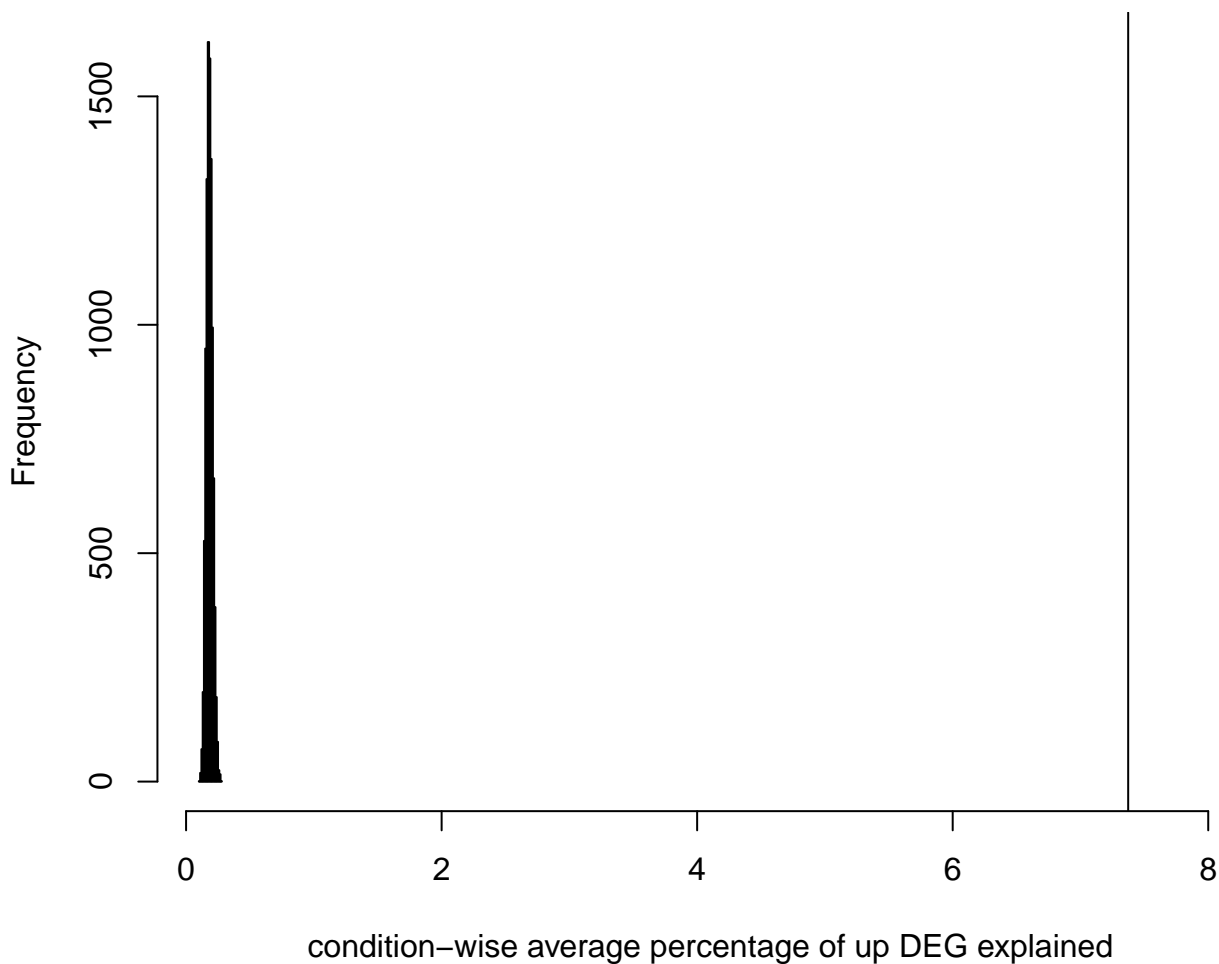


**CR model – single data**  
**p < 1e-04**

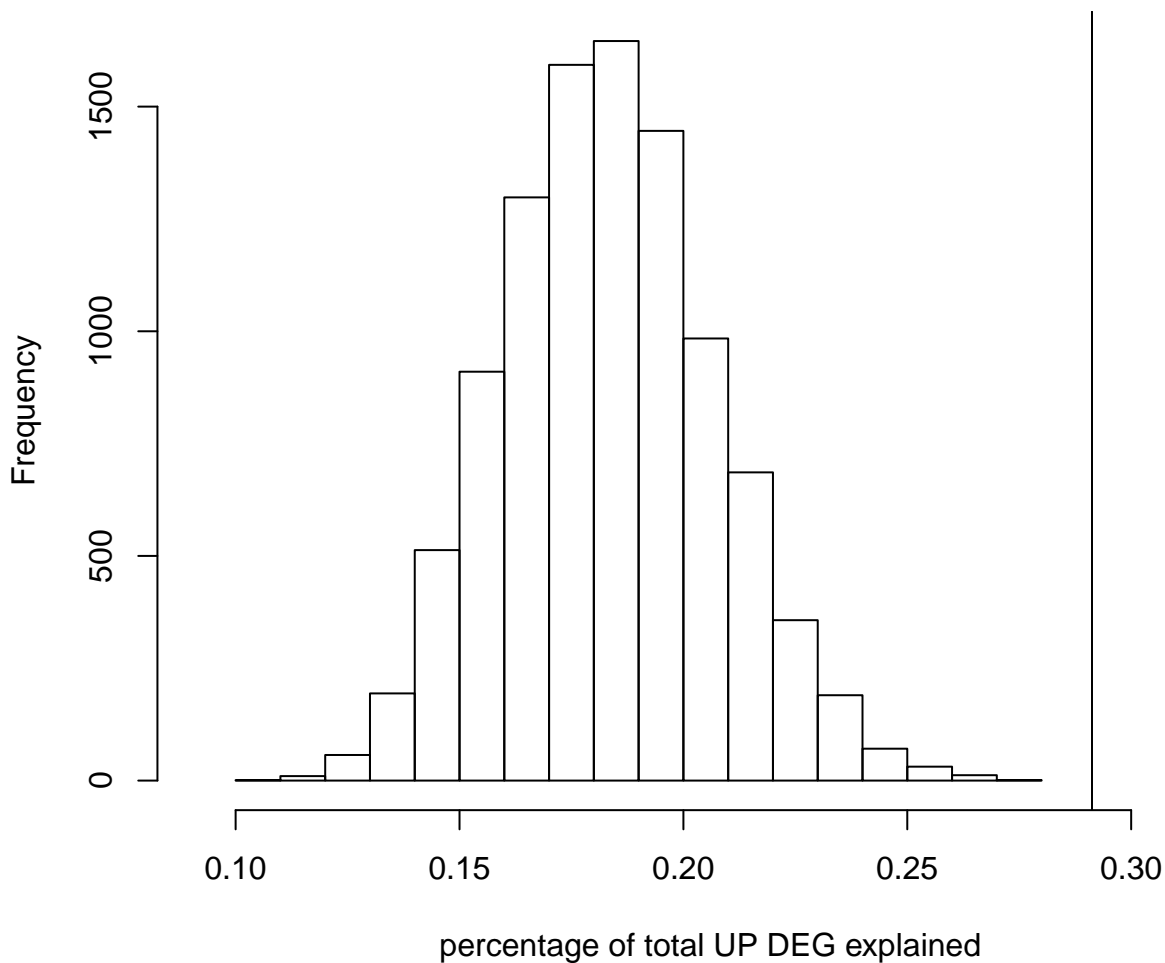




**CR model – single data**  
**p < 1e-04**

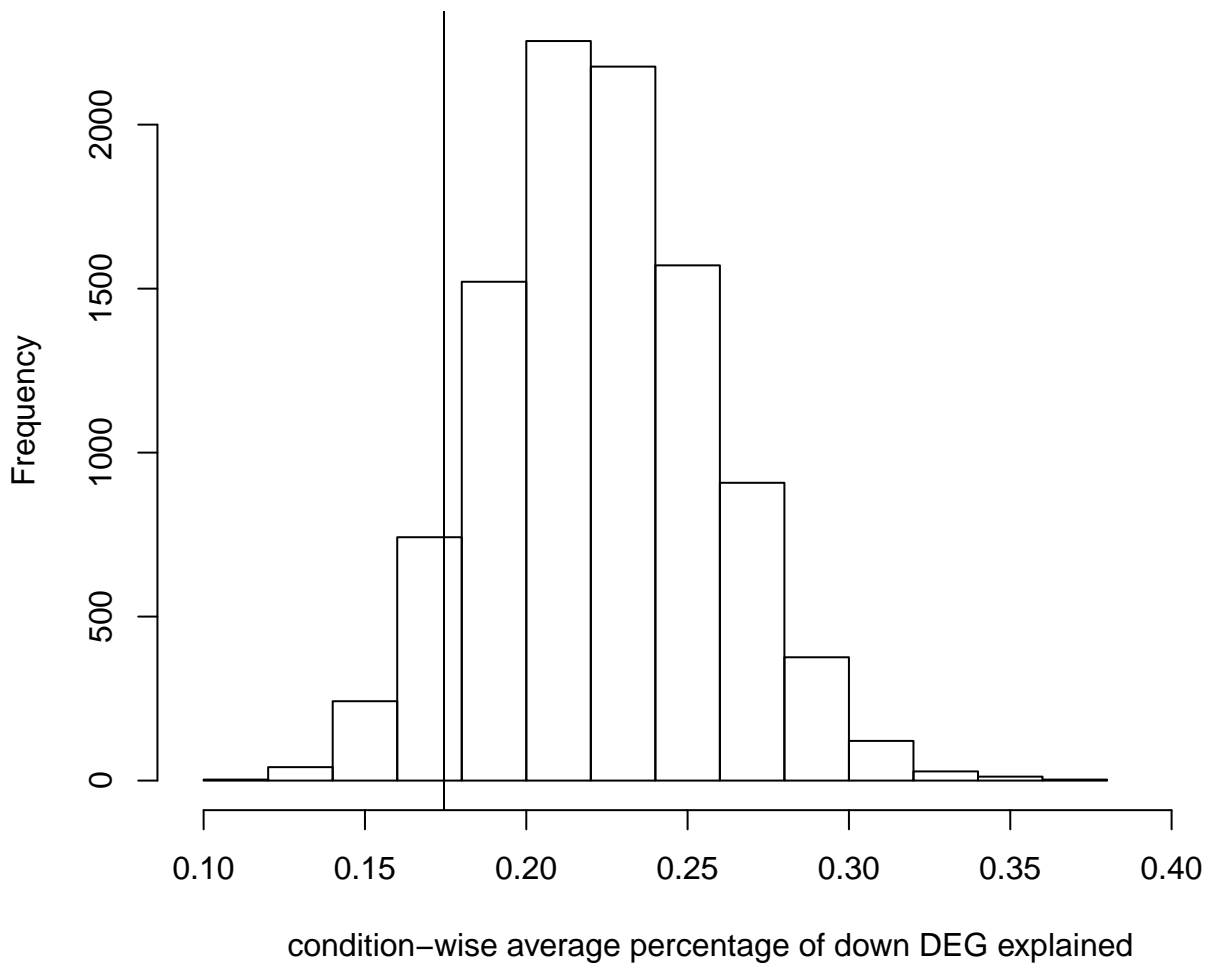


**CR model – single data**  
 **$p < 1e-04$**

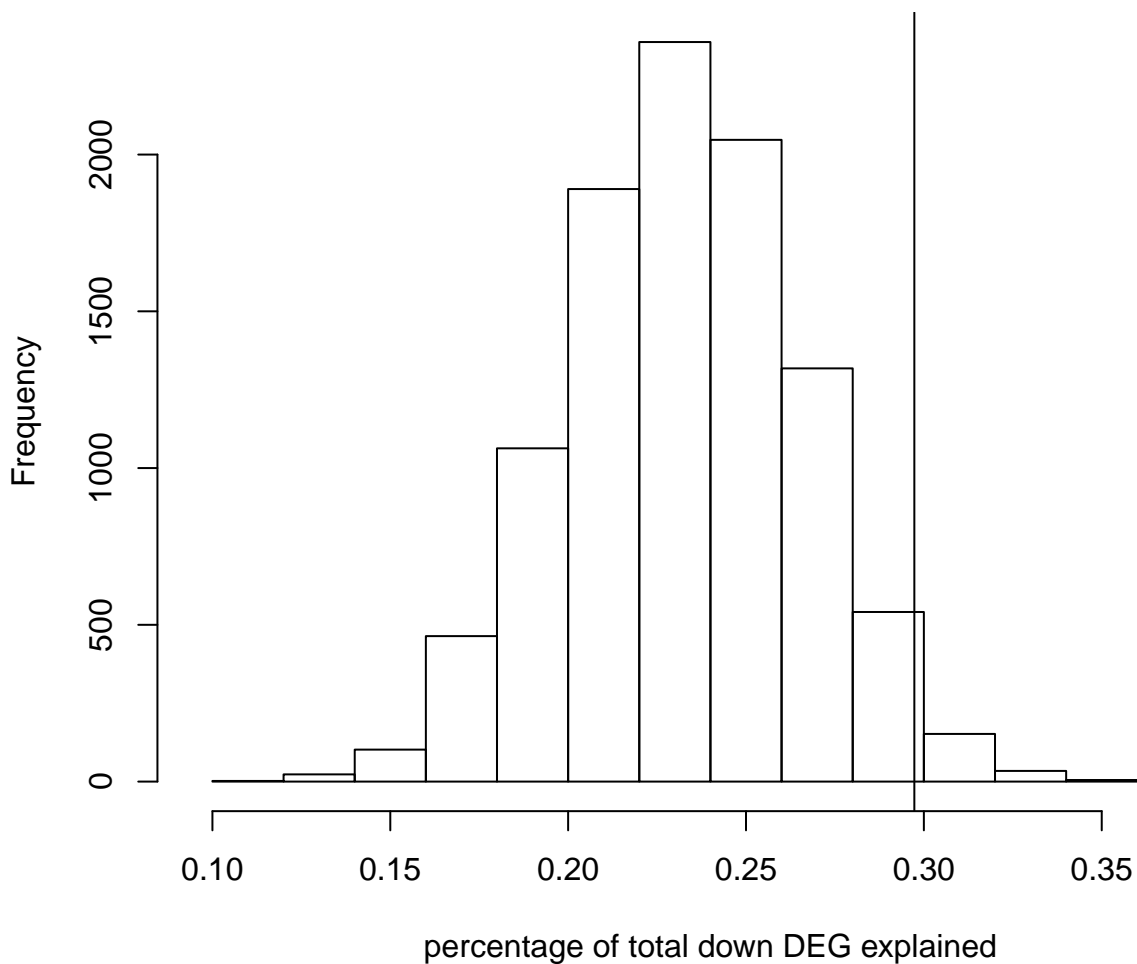


# CR model – single data

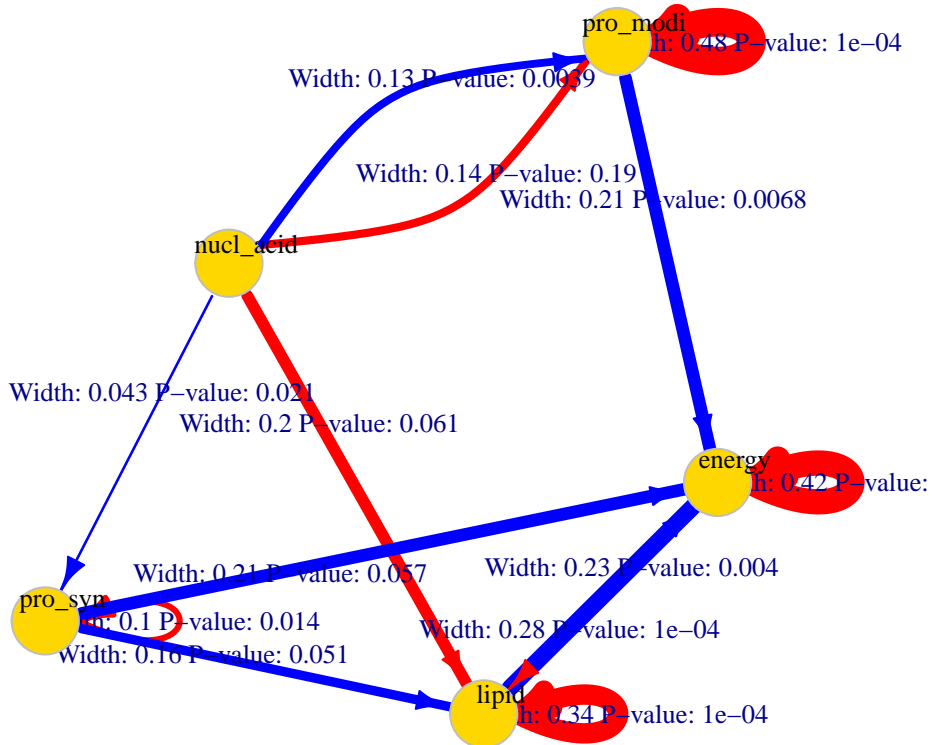
$p < 0.92$



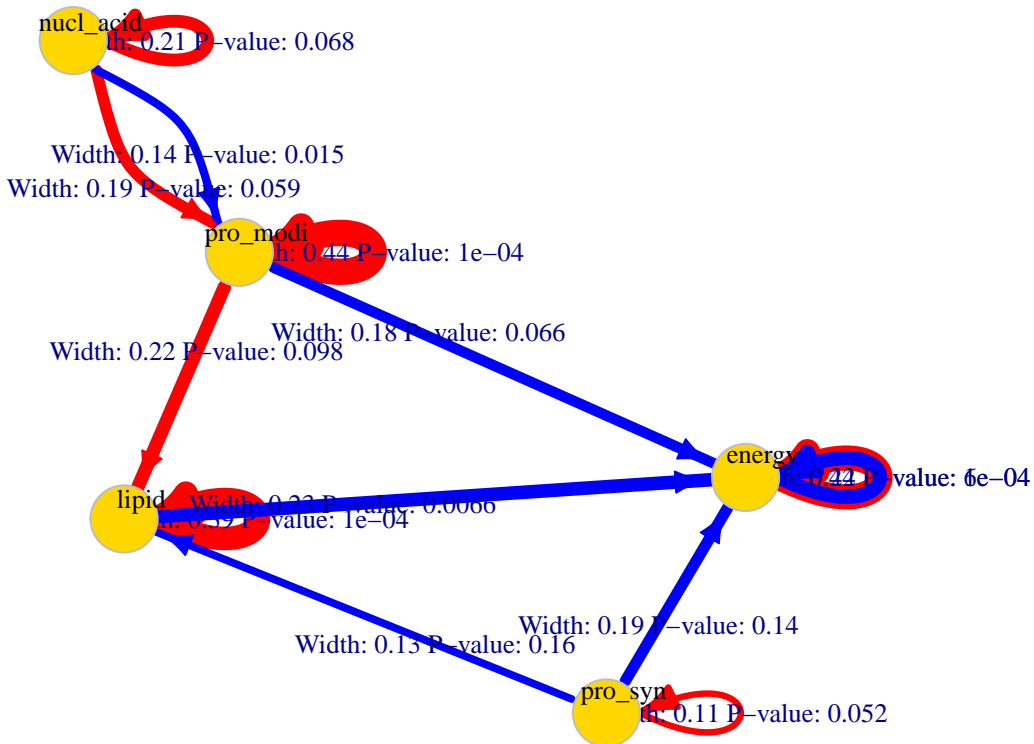
**CR model – single data**  
**p < 0.023**



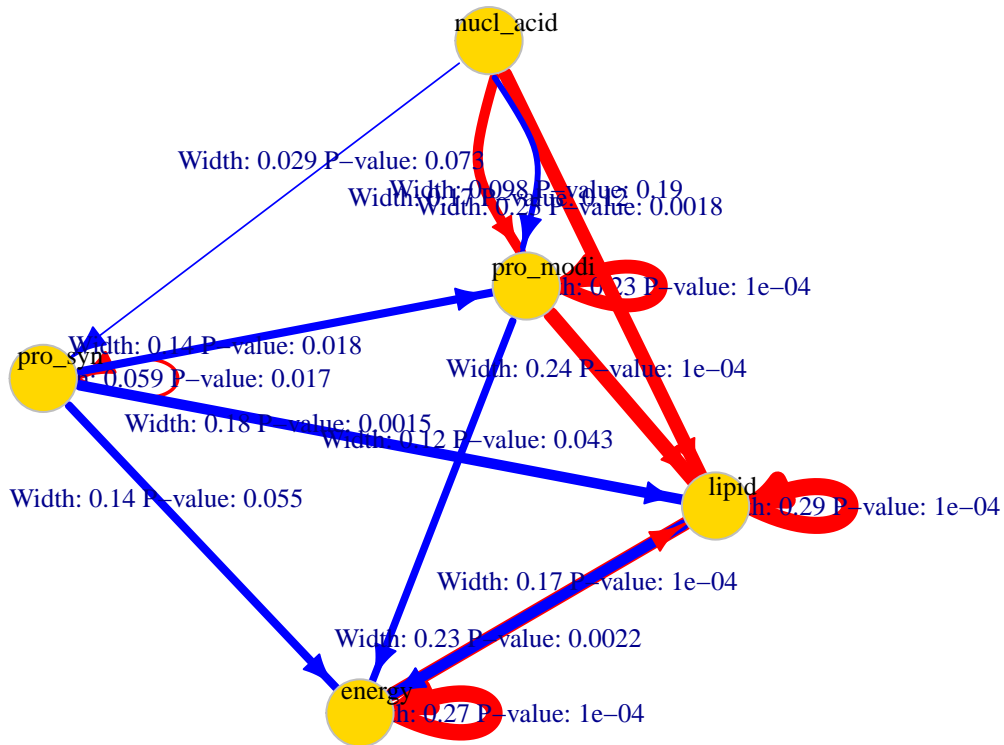
single – raw –  $p < 0.2$



# single – normalized – $p < 0.2$



# full – raw – $p < 0.2$



## full – normalized – $p < 0.2$

