

sim

0.75

0.80

0.85

Count

20

40

60

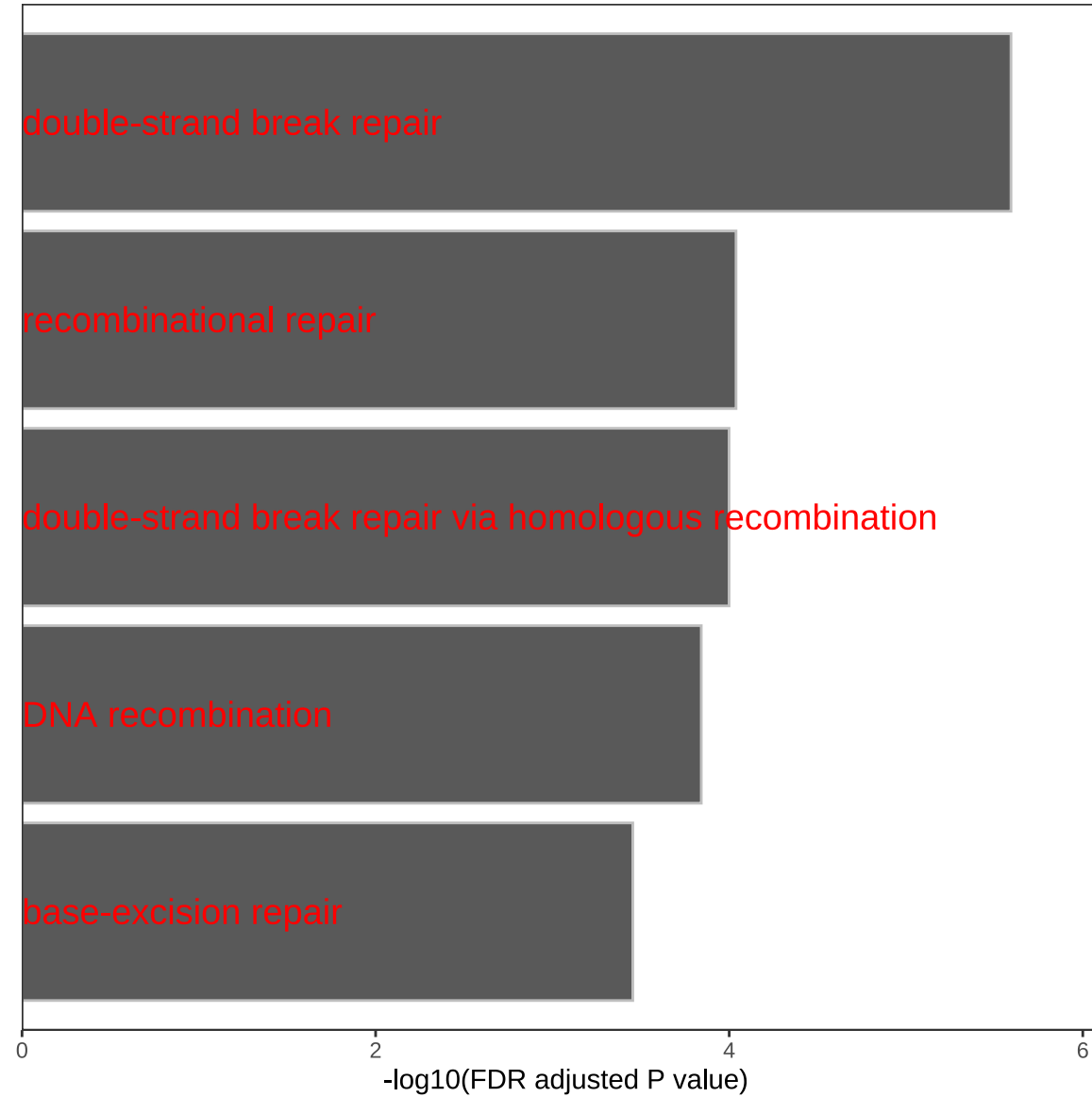
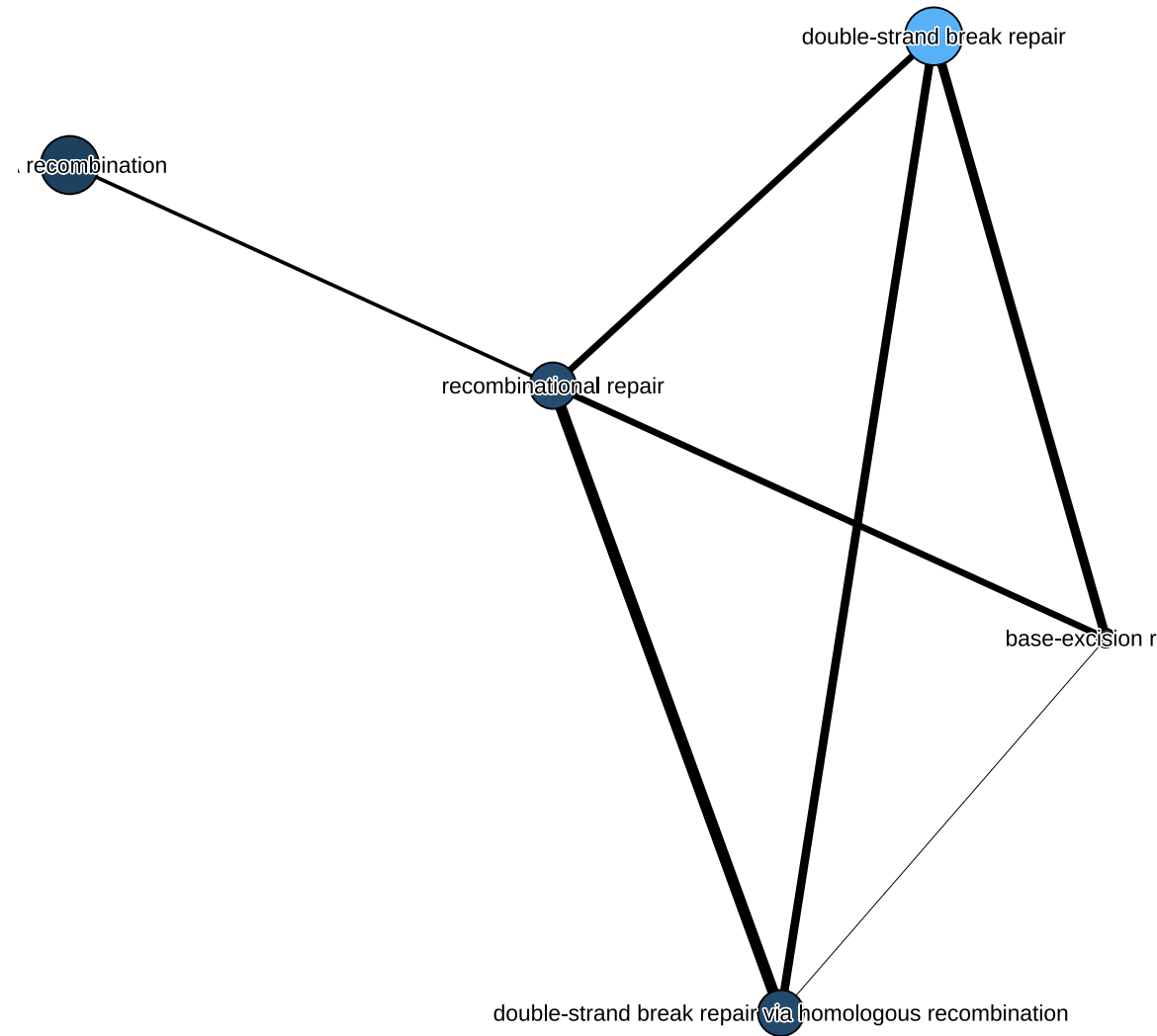
80

$-\log(p.adjust, 10)$

1.75

2.00

2.25



recombination  
homologous break repair  
base-excision  
DNA recombination  
double-strand