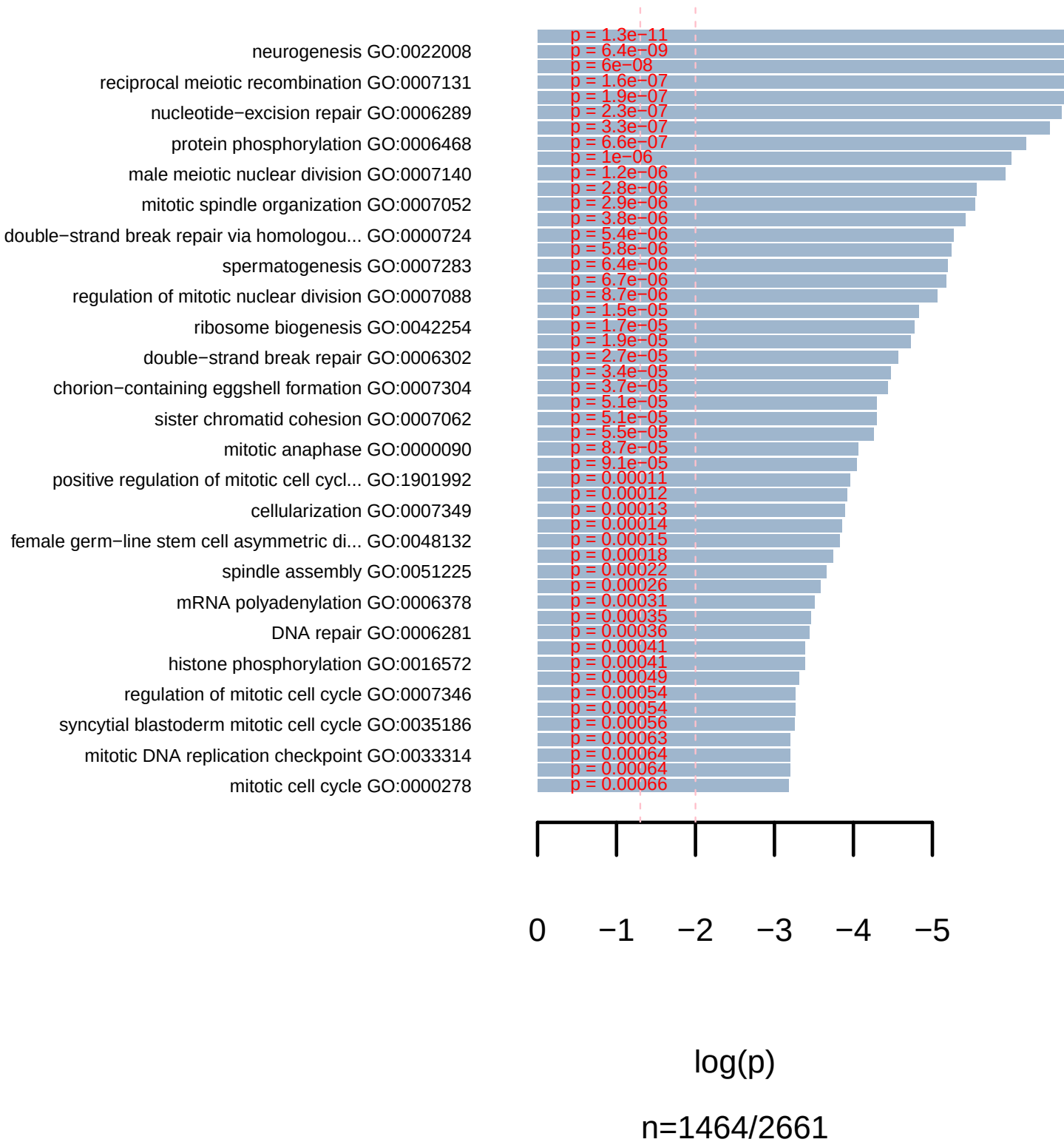
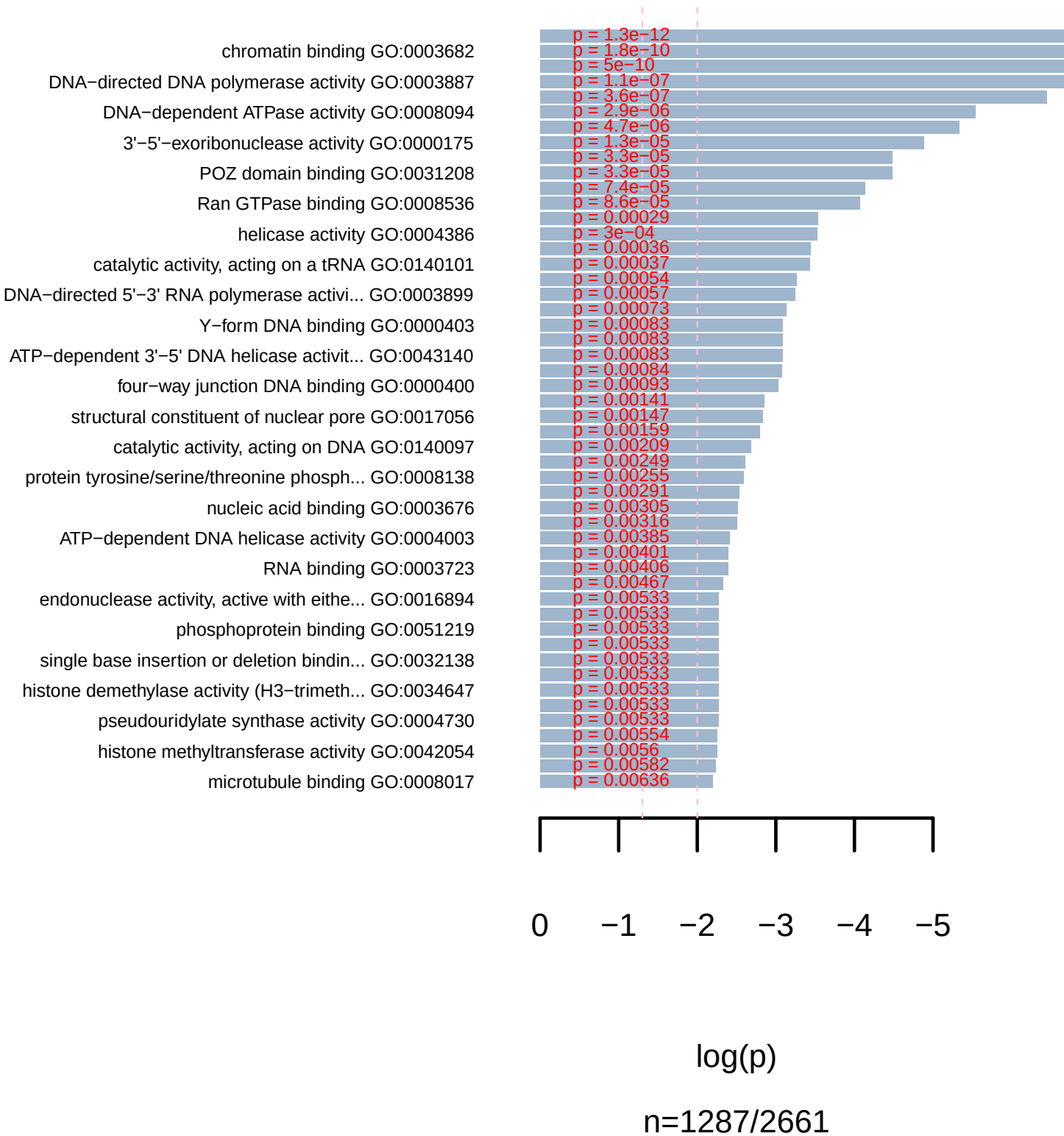
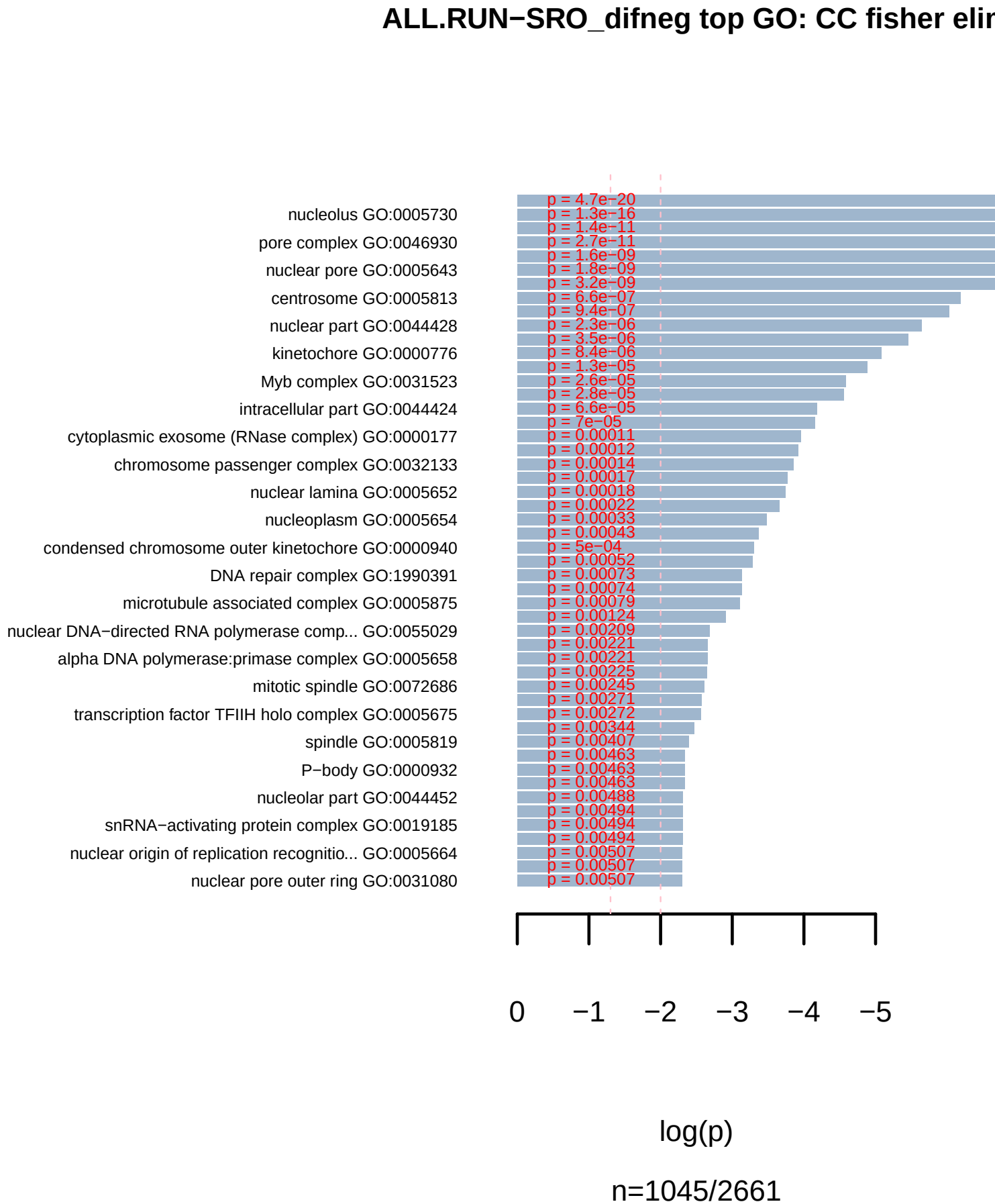
ALL.RUN−SRO_difneg top GO: BP fisher elin



ALL.RUN−SRO_difneg top GO: MF fisher elim




ALL.RUN−SRO_difneg top GO: CC fisher elim
nucleolus GO:0005730
pore complex GO:0046930
nuclear pore GO:0005643
centrosome GO:0005813
nuclear part GO:0044428
kinetochore GO:0000776
Myb complex GO:0031523
intracellular part GO:0044424
cytoplasmic exosome (RNase complex) GO:0000177
chromosome passenger complex GO:0032133
nuclear lamina GO:0005652
nucleoplasm GO:0005654
condensed chromosome outer kinetochore GO:0000940
DNA repair complex GO:1990391
microtubule associated complex GO:0005875
nuclear DNA−directed RNA polymerase comp... GO:0055029
alpha DNA polymerase:primase complex GO:0005658
mitotic spindle GO:0072686
transcription factor TFIIH holo complex GO:0005675
spindle GO:0005819
P−body GO:0000932
nucleolar part GO:0044452
snRNA−activating protein complex GO:0019185
nuclear origin of replication recognitio... GO:0005664
nuclear pore outer ring GO:0031080
p = 4.7e−20
p = 1.3e−16
p = 1.4e−11
p = 2.7e−11
p = 1.6e−09
p = 1.8e−09
p = 3.2e−09
p = 6.6e−07
p = 9.4e−07
p = 2.3e−06
p = 3.5e−06
p = 8.4e−06
p = 1.3e−05
p = 2.6e−05
p = 2.8e−05
p = 6.6e−05
p = 7e−05
p = 0.00011
p = 0.00012
p = 0.00014
p = 0.00017
p = 0.00018
p = 0.00022
p = 0.00033
p = 0.00043
p = 5e−04
p = 0.00052
p = 0.00073
p = 0.00074
p = 0.00079
p = 0.00124
p = 0.00209
p = 0.00221
p = 0.00221
p = 0.00225
p = 0.00245
p = 0.00271
p = 0.00272
p = 0.00344
p = 0.00407
p = 0.00463
p = 0.00463
p = 0.00463
p = 0.00488
p = 0.00494
p = 0.00494
p = 0.00494
p = 0.00507
p = 0.00507
p = 0.00507
0
−1
−2
−3
−4
−5
log(p)
n=1045/2661