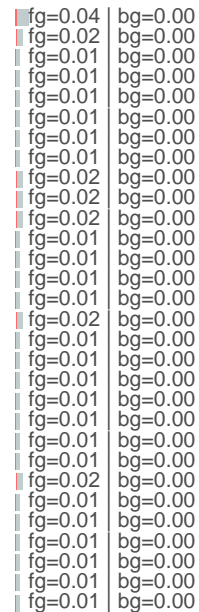


fraction genes in fg and bg



-log₁₀(p)
n=93/97 input genes with annotations