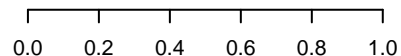
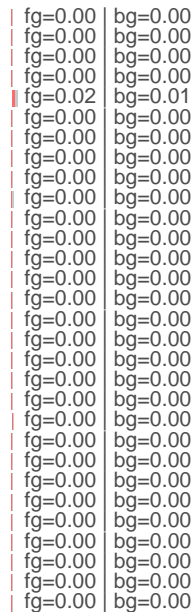


fraction genes in fg and bg



fraction

n=381/310 input genes with annotations