

fraction genes in fg and expected value

| | |
|---------|---------|
| fg=0.50 | bg=0.07 |
| fg=0.08 | bg=0.00 |
| fg=0.08 | bg=0.00 |
| fg=0.08 | bg=0.00 |
| fg=0.08 | bg=0.00 |
| fg=0.08 | bg=0.00 |
| fg=0.08 | bg=0.00 |
| fg=0.08 | bg=0.00 |
| fg=0.08 | bg=0.00 |
| fg=0.08 | bg=0.00 |
| fg=0.12 | bg=0.01 |
| fg=0.08 | bg=0.00 |
| fg=0.08 | bg=0.00 |
| fg=0.08 | bg=0.00 |
| fg=0.08 | bg=0.00 |
| fg=0.04 | bg=0.00 |
| fg=0.08 | bg=0.01 |
| fg=0.08 | bg=0.01 |
| fg=0.04 | bg=0.00 |
| fg=0.04 | bg=0.00 |
| fg=0.04 | bg=0.00 |
| fg=0.08 | bg=0.01 |
| fg=0.08 | bg=0.01 |
| fg=0.04 | bg=0.00 |
| fg=0.08 | bg=0.01 |
| fg=0.08 | bg=0.01 |
| fg=0.04 | bg=0.00 |
| fg=0.04 | bg=0.00 |

A horizontal axis labeled "fraction" with tick marks at 0.0, 0.2, 0.4, 0.6, 0.8, and 1.0.

fraction genes in fg and expected value

[illegible]

fraction genes in fg and expected value

| | |
|---------|---------|
| fg=0.12 | bg=0.01 |
| fg=0.52 | bg=0.25 |
| fg=0.04 | bg=0.00 |
| fg=0.04 | bg=0.00 |
| fg=0.12 | bg=0.02 |
| fg=0.04 | bg=0.00 |
| fg=0.08 | bg=0.01 |
| fg=0.16 | bg=0.04 |
| fg=0.12 | bg=0.02 |
| fg=0.04 | bg=0.00 |
| fg=0.08 | bg=0.01 |
| fg=0.16 | bg=0.05 |
| fg=0.08 | bg=0.01 |
| fg=0.08 | bg=0.01 |
| fg=0.04 | bg=0.00 |
| fg=0.04 | bg=0.00 |
| fg=0.20 | bg=0.08 |
| fg=0.12 | bg=0.03 |
| fg=0.04 | bg=0.00 |
| fg=0.04 | bg=0.00 |
| fg=0.04 | bg=0.00 |
| fg=0.04 | bg=0.00 |
| fg=0.12 | bg=0.04 |
| fg=0.16 | bg=0.07 |
| fg=0.04 | bg=0.00 |
| fg=0.08 | bg=0.02 |
| fg=0.04 | bg=0.01 |
| fg=0.04 | bg=0.01 |

-log(p)

n=25/103 input genes with annotations