

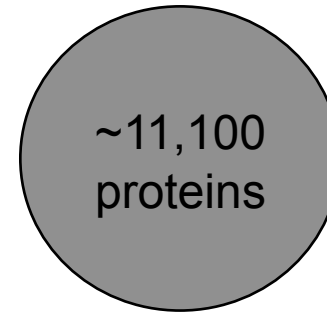
A: proteome-wide ERC calculations

known SP network proteins

SP	CG9997
SPR	CG17575
CG1652	CG1656
seminase	

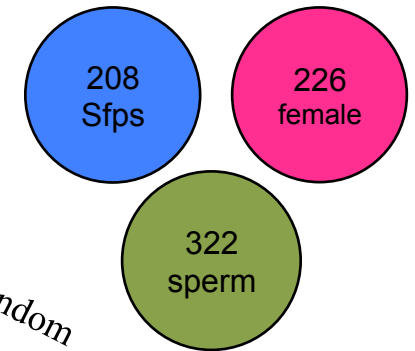
mean corr: 0.3115 $p = 0.000154$

whole proteome



mean corr: 0.0019

664 reprod. proteins*



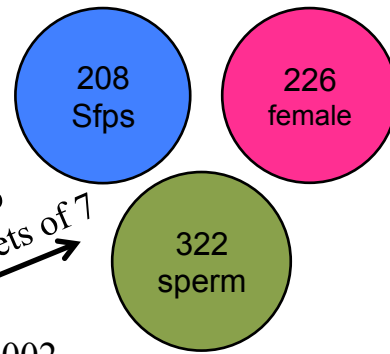
compare to random sets of 664
 $p < 0.0001$
mean corr: 0.0326

B: ERC calculations after controlling for reproductive protein evolution

SP	CG9997
SPR	CG17575
CG1652	CG1656
seminase	

mean corr: 0.2806

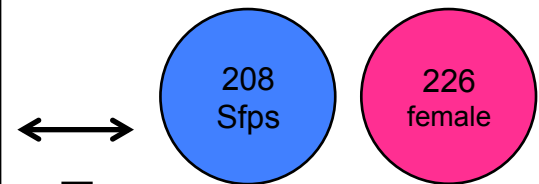
compare to random sets of 7
 $p = 0.001002$



mean corr: 0.0047

C: identify new candidates by screening against Sfps and female sets

SP
CG17575
CG1652
CG1656
CG9997



434 proteins screened

aqrs
antr
intr
frma
hdly

11 with no effect

Esp

1 with no effect

*Numbers in the colored circles sum to 756 proteins, but only 664 had adequate numbers of orthologs to be included in the analysis.