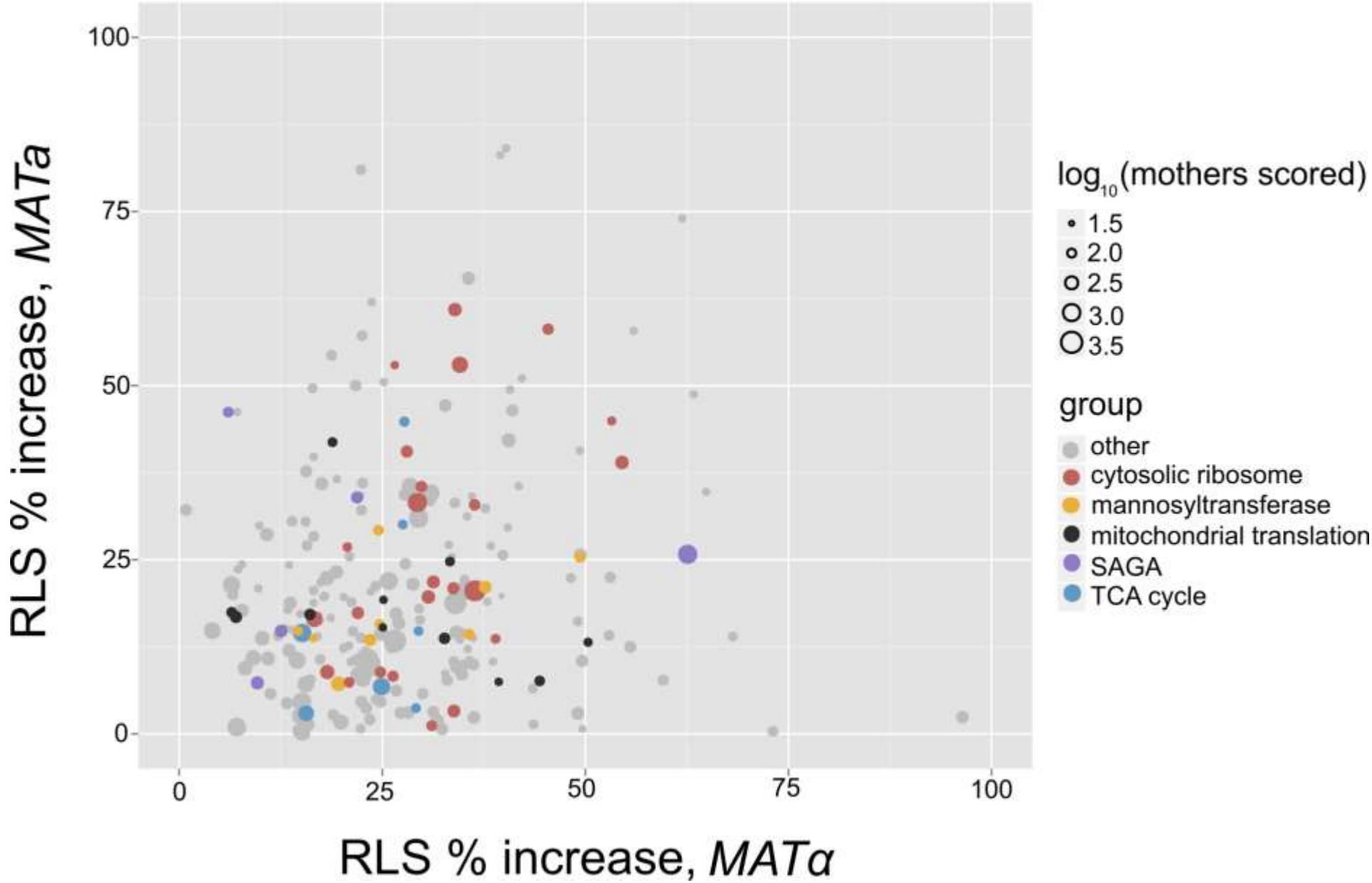
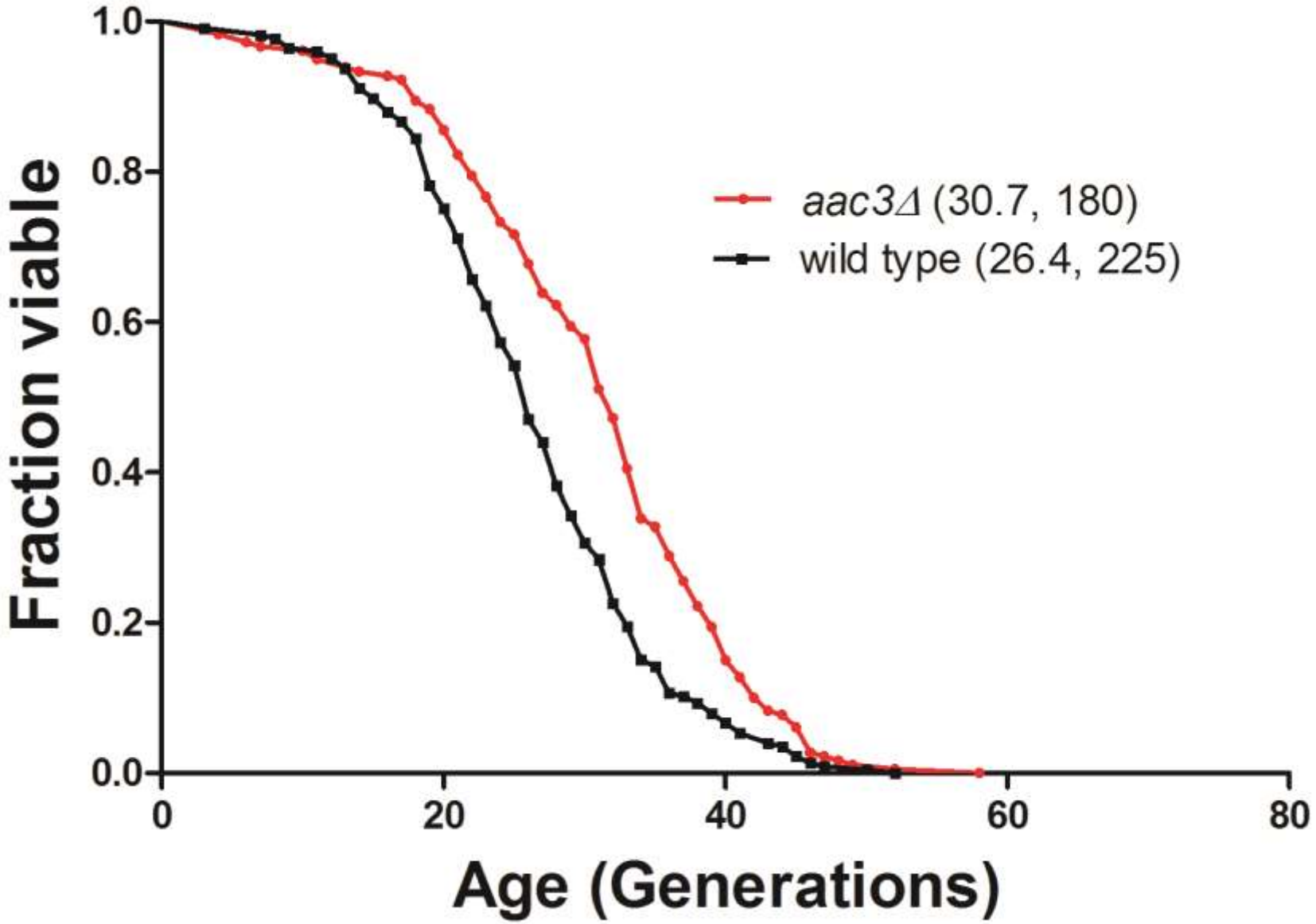
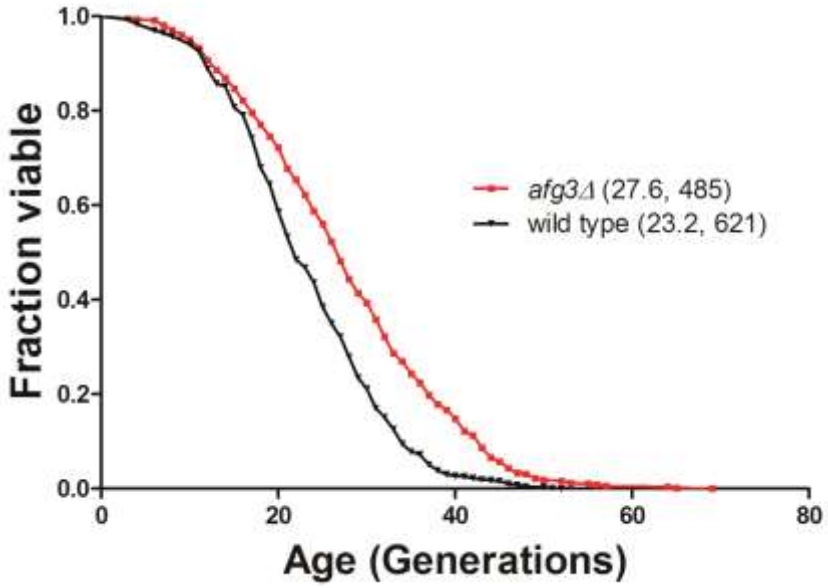
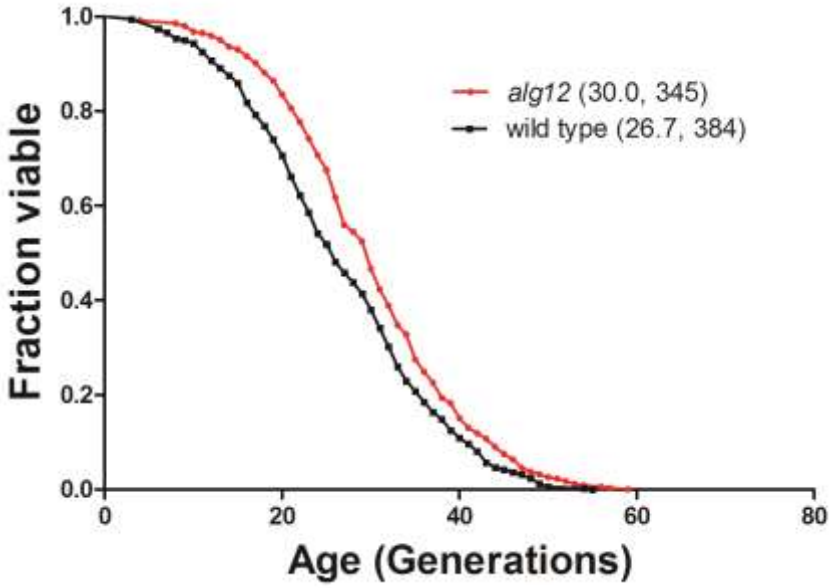
Supplemental Figure S1 A. Graphical RLS by functional group.

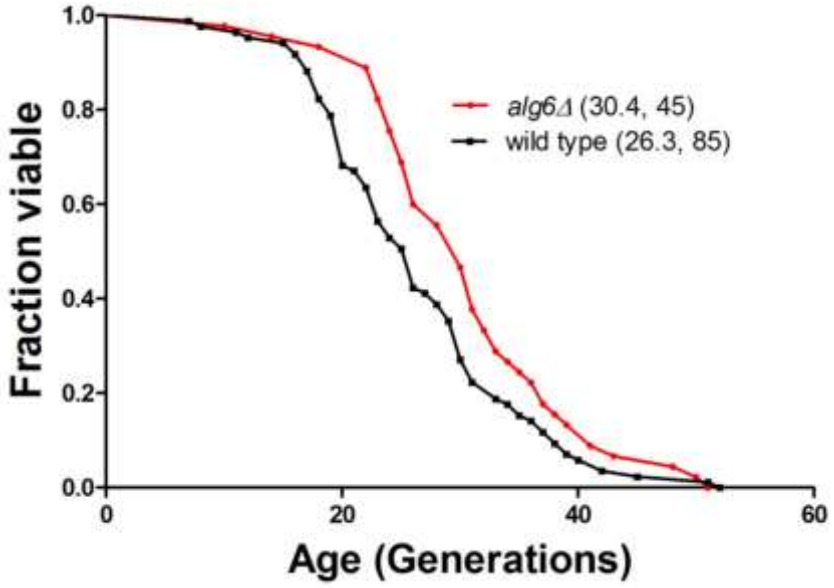


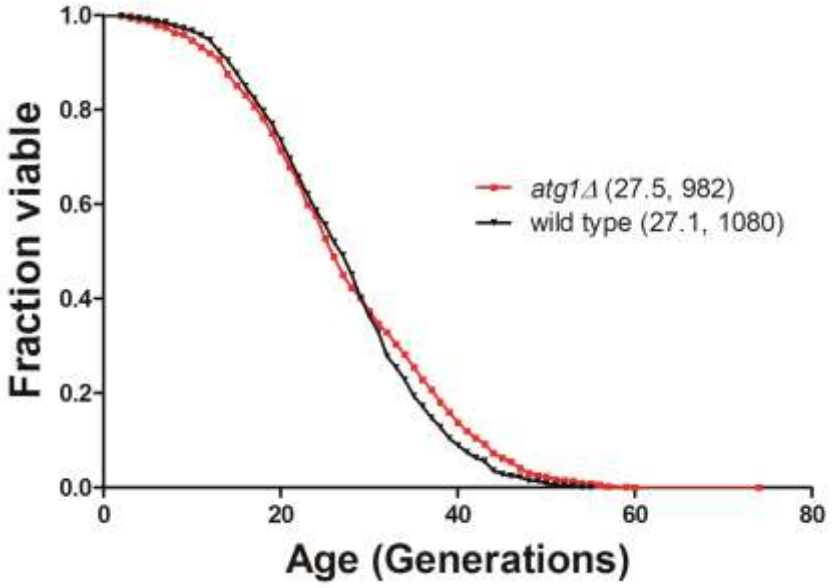
Supplemental Figure S1 B. Lifespans of 238 longlived deletions identified in this screen.

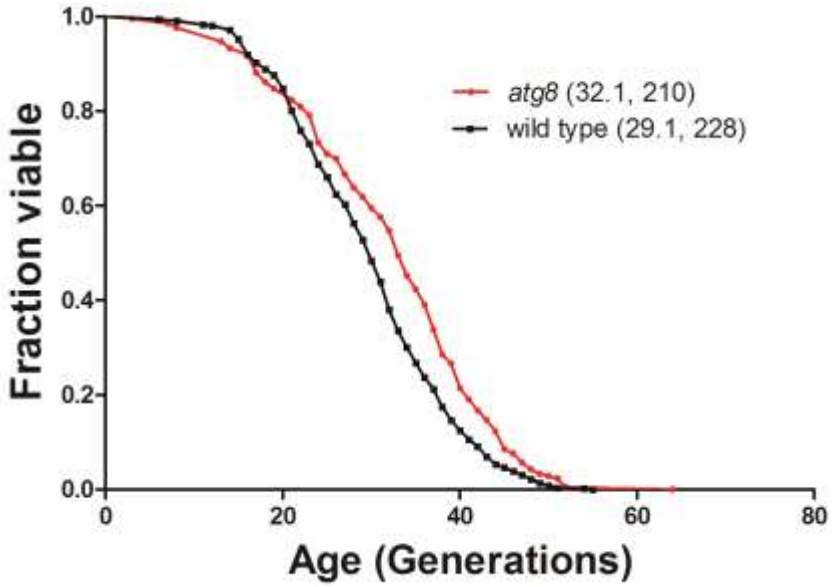


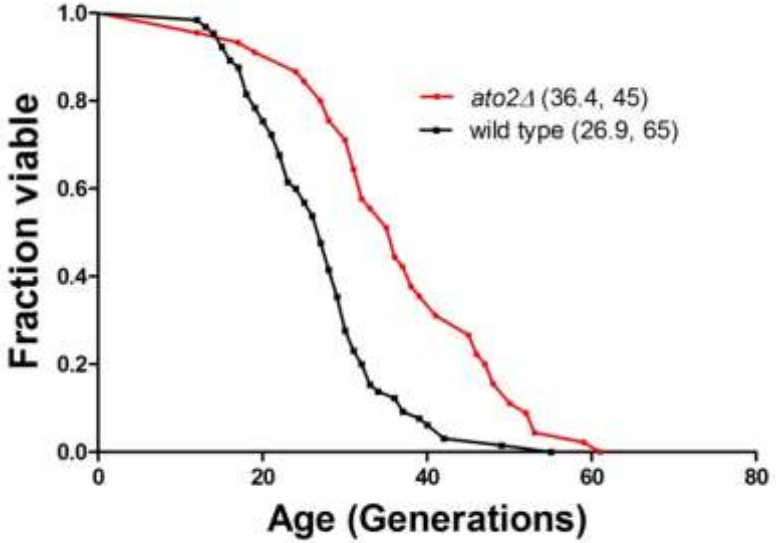

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
afg3Δ (27.6, 485)
wild type (23.2, 621)

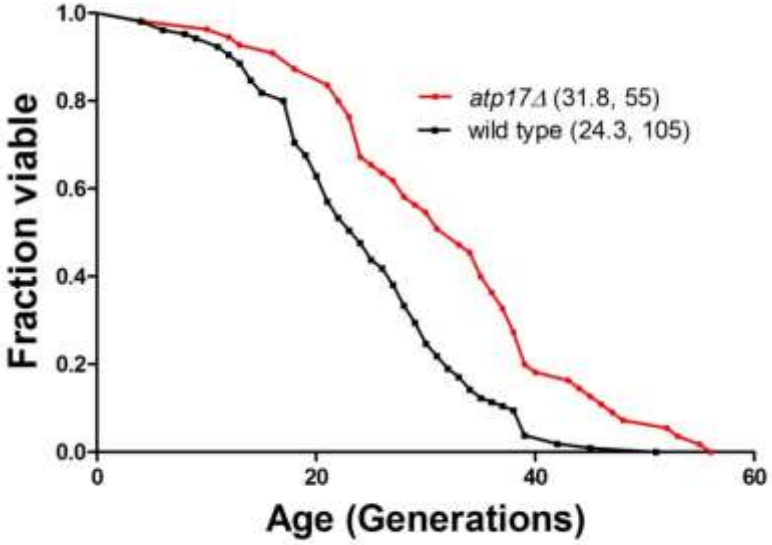

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
alg12 (30.0, 345)
wild type (26.7, 384)

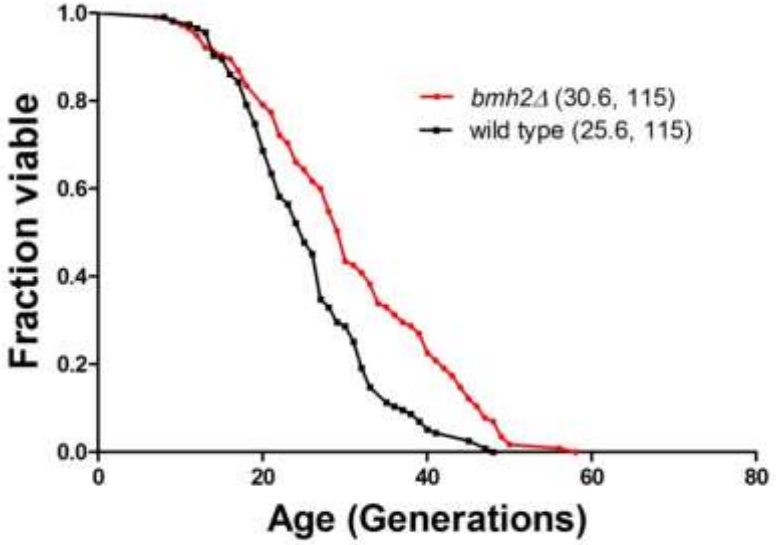

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
alg6Δ (30.4, 45)
wild type (26.3, 85)

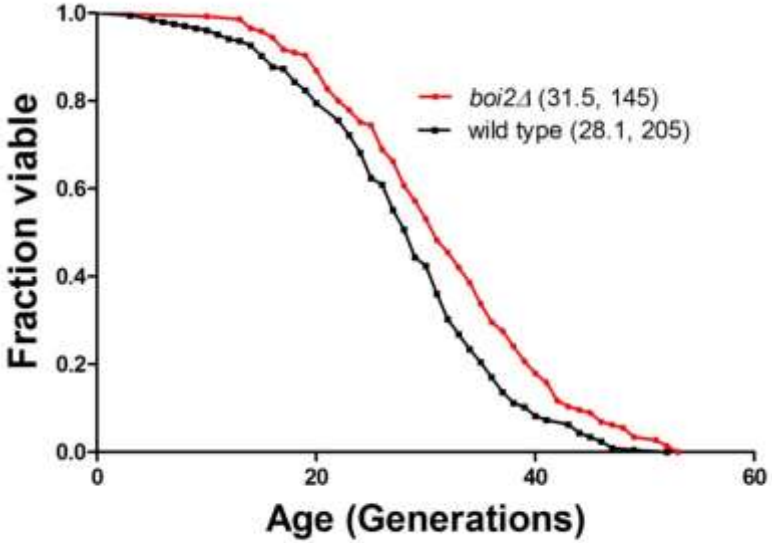

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
atg1Δ (27.5, 982)
wild type (27.1, 1080)

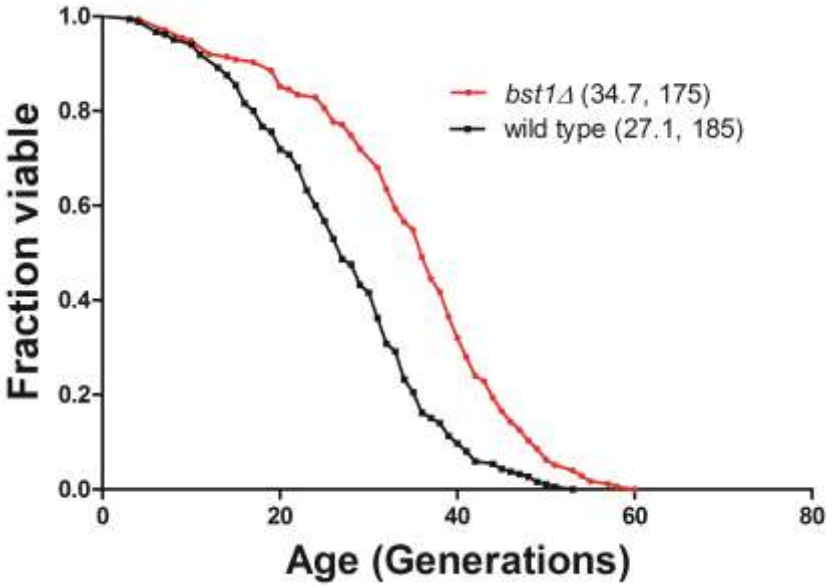

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
atg8 (32.1, 210)
wild type (29.1, 228)

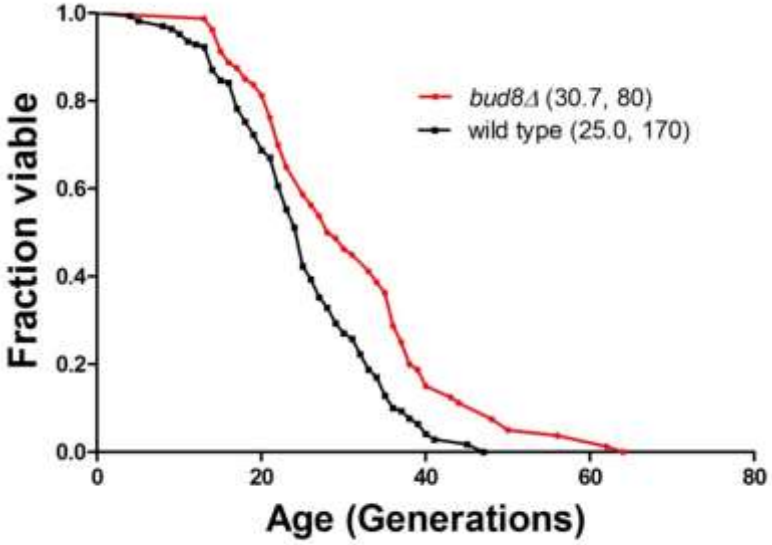

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
ato2Δ (36.4, 45)
wild type (26.9, 65)

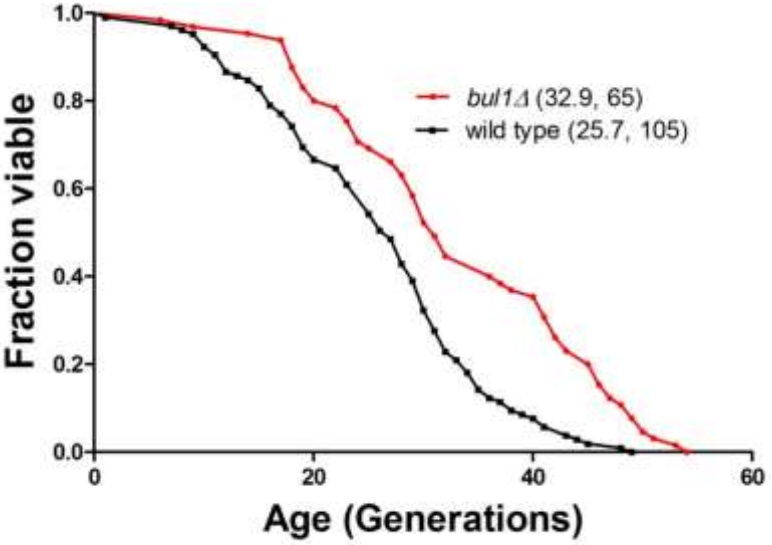

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
atp17Δ (31.8, 55)
wild type (24.3, 105)

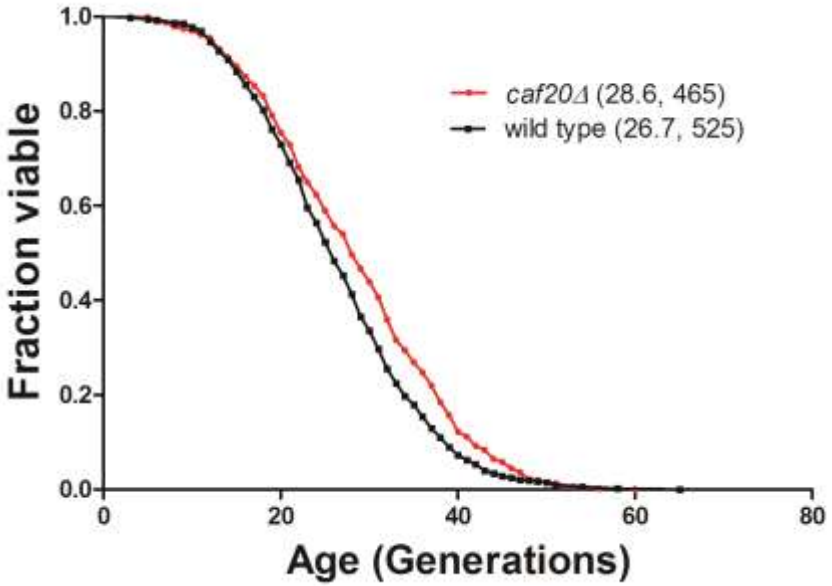

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
bmh2Δ (30.6, 115)
wild type (25.6, 115)

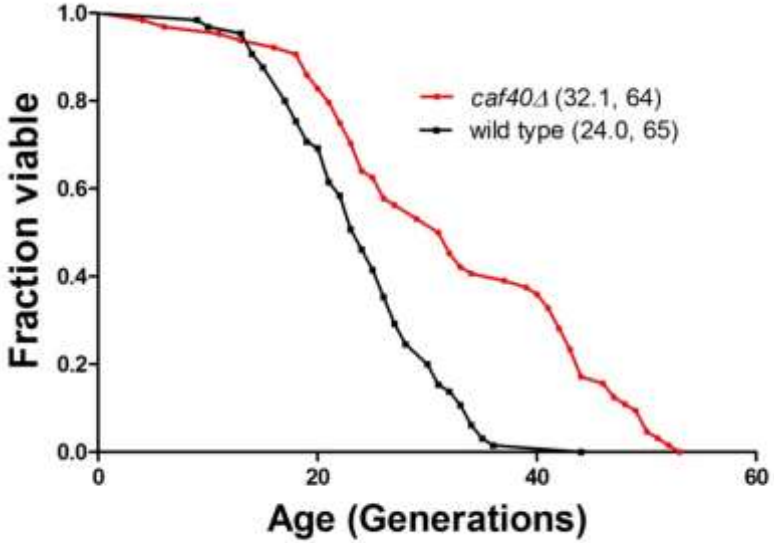

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
boi2Δ (31.5, 145)
wild type (28.1, 205)

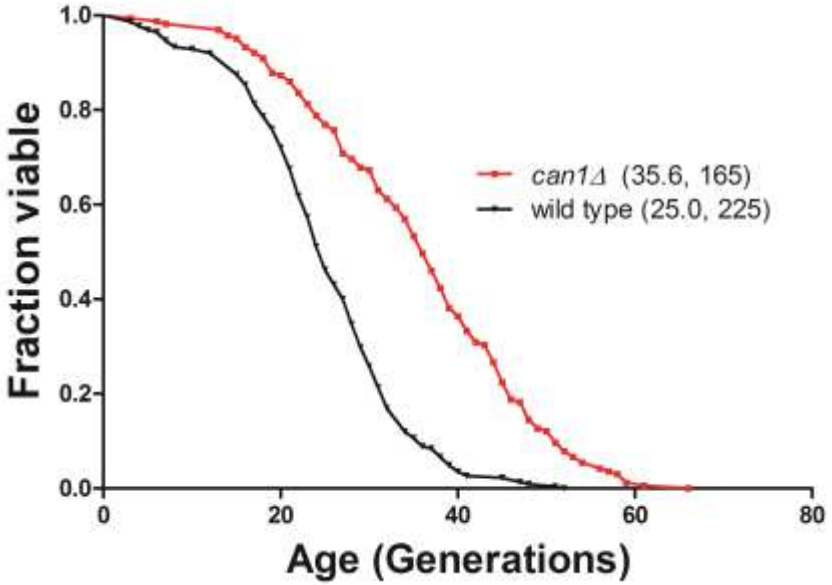

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
bst1Δ (34.7, 175)
wild type (27.1, 185)

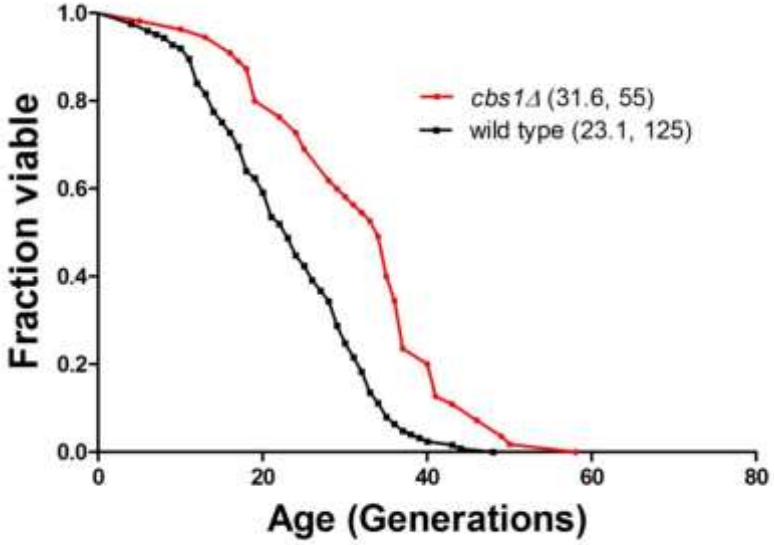

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
bud8Δ (30.7, 80)
wild type (25.0, 170)

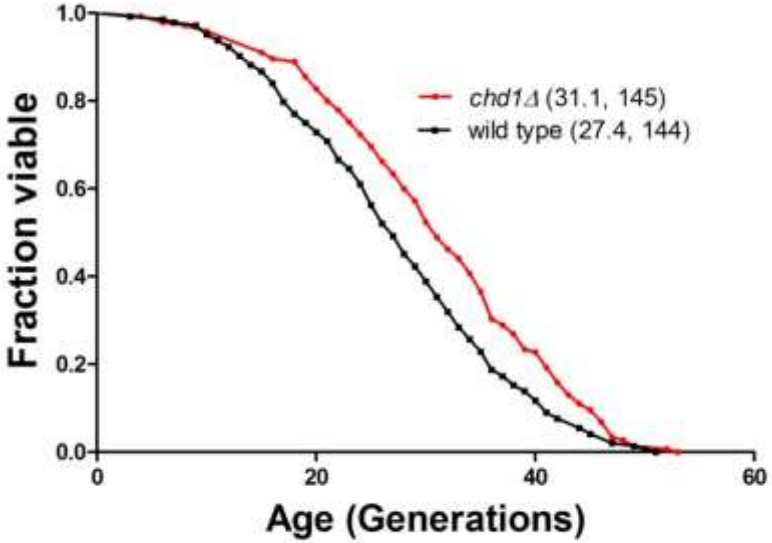

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
bul1Δ (32.9, 65)
wild type (25.7, 105)

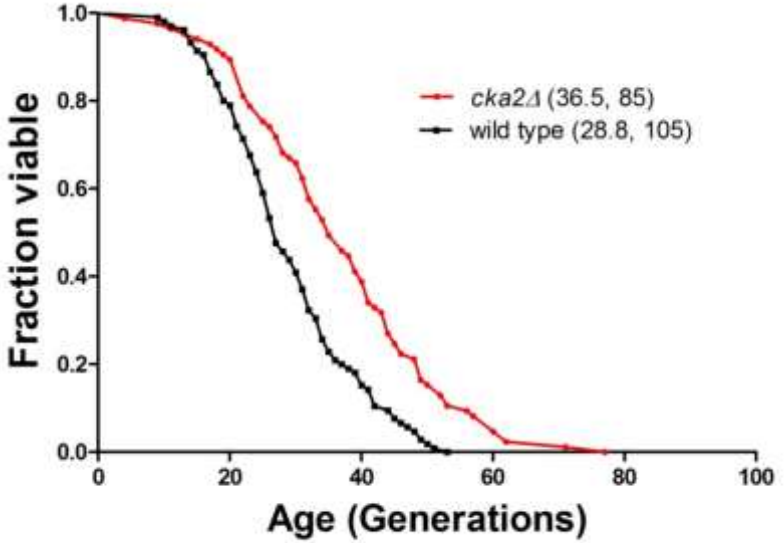

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
caf20Δ (28.6, 465)
wild type (26.7, 525)

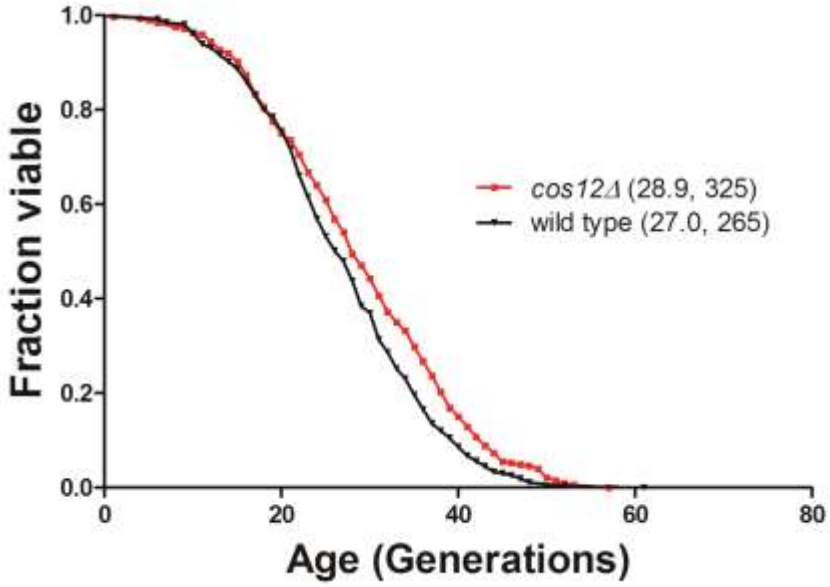

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
caf40Δ (32.1, 64)
wild type (24.0, 65)

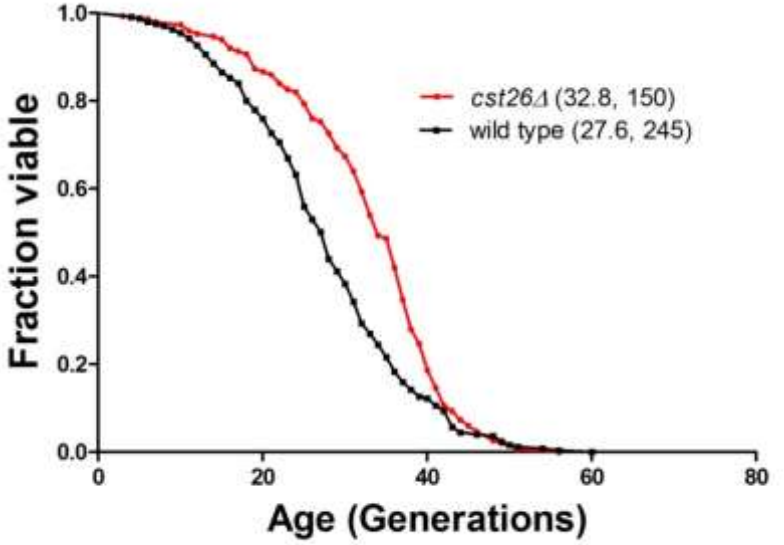

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
can1Δ (35.6, 165)
wild type (25.0, 225)

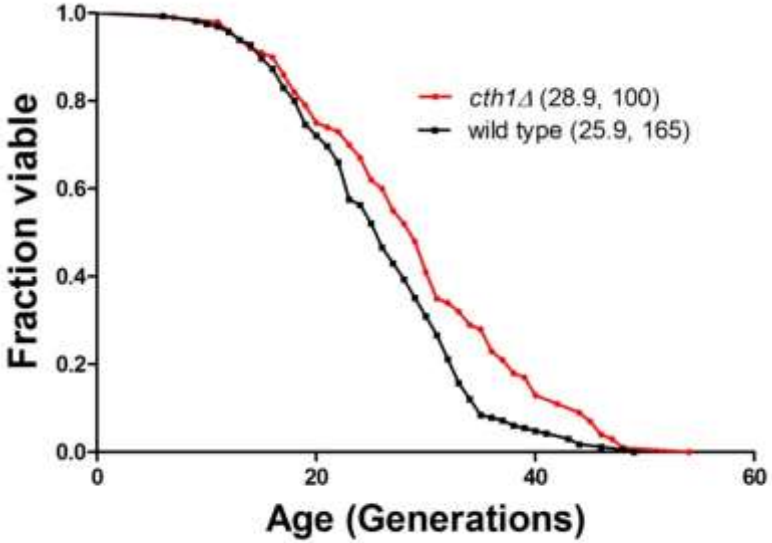

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
cbs1Δ (31.6, 55)
wild type (23.1, 125)

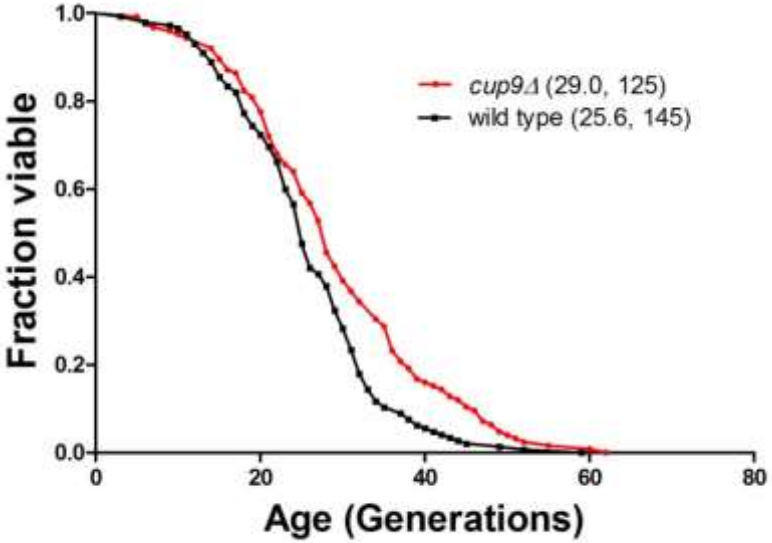

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
chd1Δ (31.1, 145)
wild type (27.4, 144)

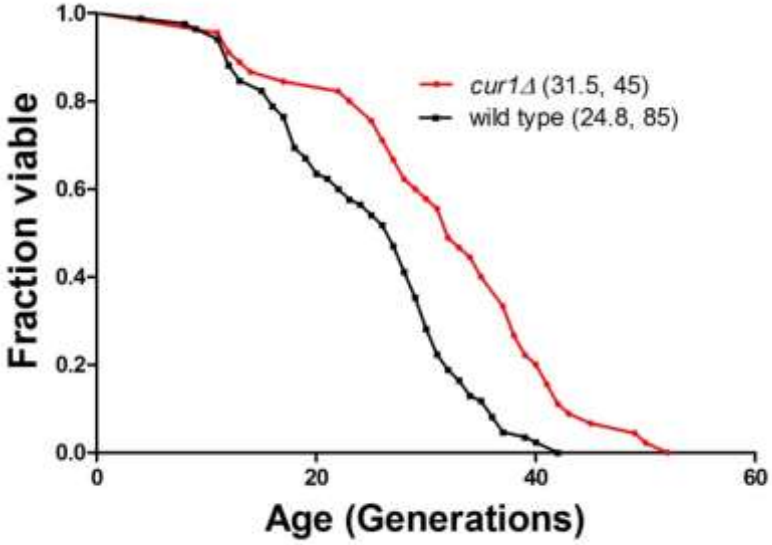

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
Age (Generations)
cka2Δ (36.5, 85)
wild type (28.8, 105)

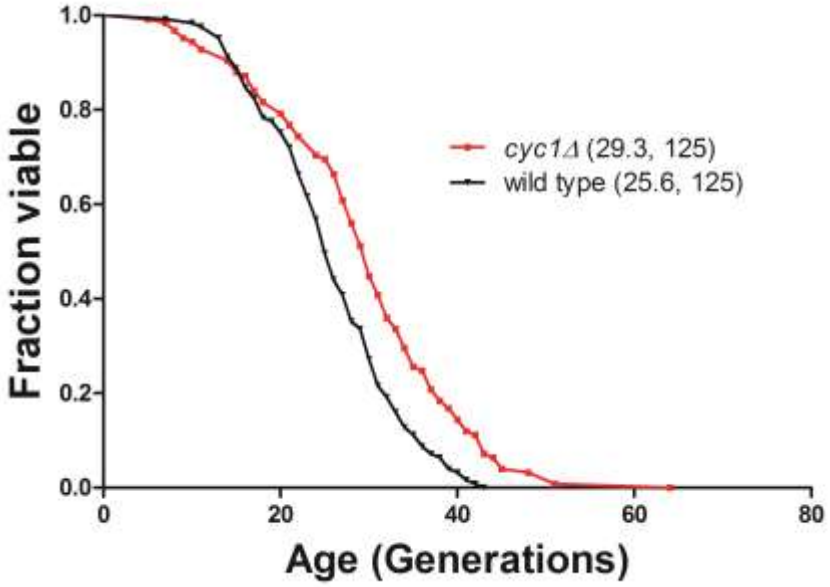

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
cos12Δ (28.9, 325)
wild type (27.0, 265)

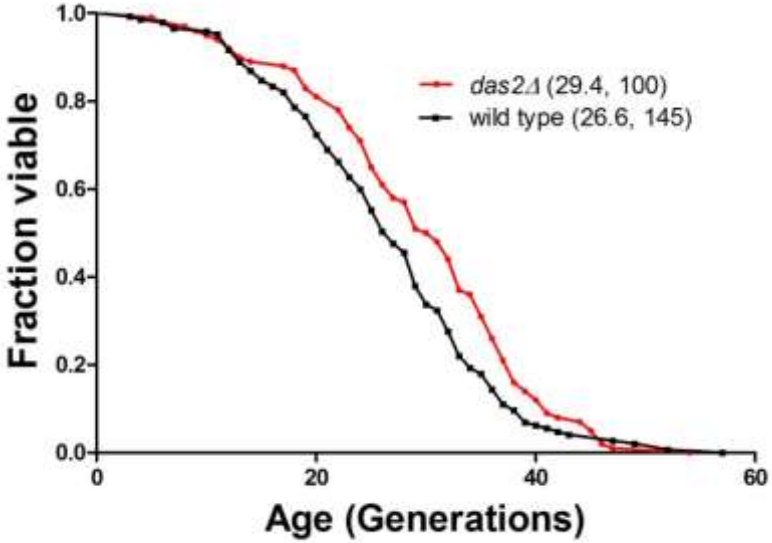

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
cst26Δ (32.8, 150)
wild type (27.6, 245)

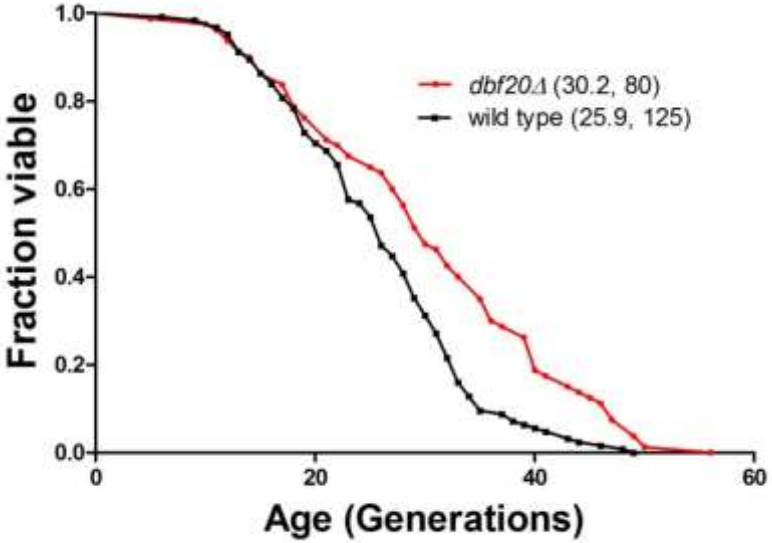

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
cth1Δ (28.9, 100)
wild type (25.9, 165)

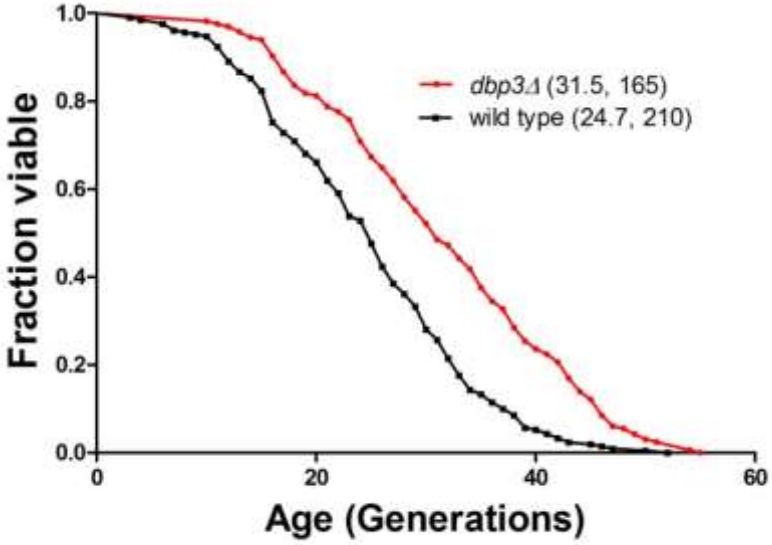

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
cup9Δ (29.0, 125)
wild type (25.6, 145)

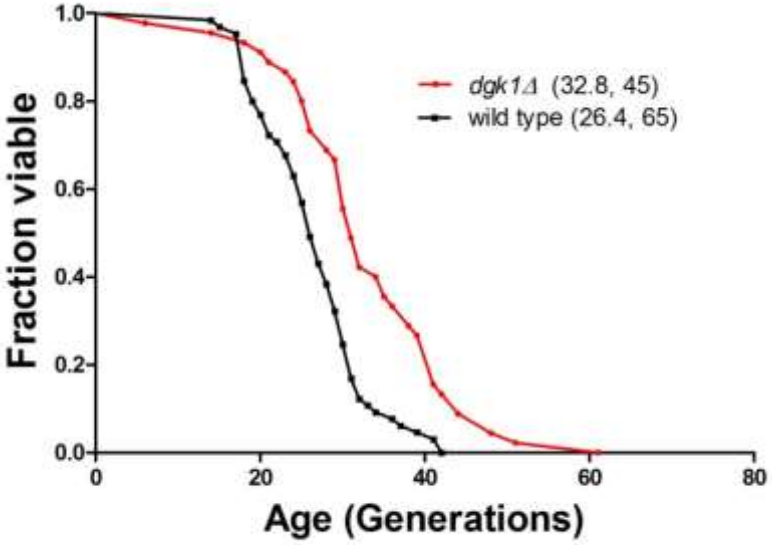

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
cur1Δ (31.5, 45)
wild type (24.8, 85)

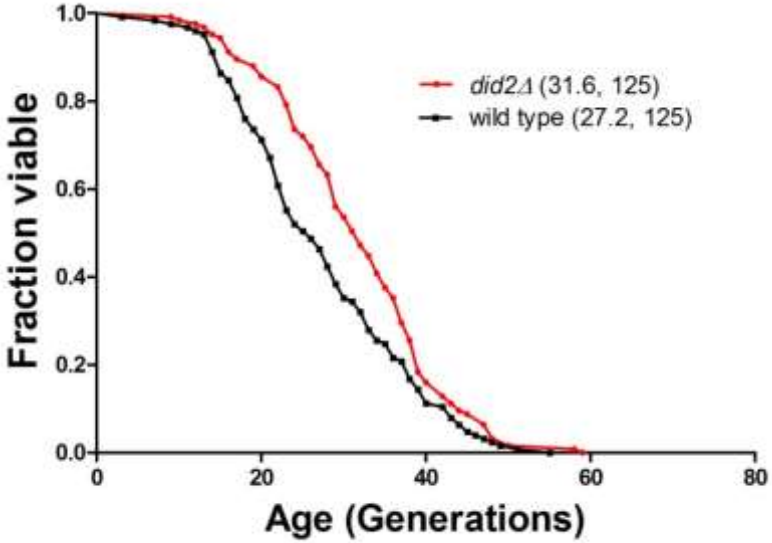

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
cyc1Δ (29.3, 125)
wild type (25.6, 125)

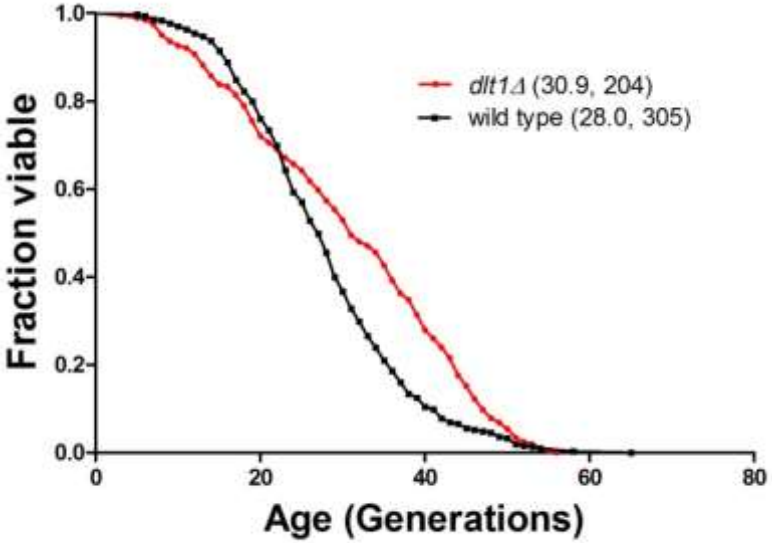

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
das2Δ (29.4, 100)
wild type (26.6, 145)

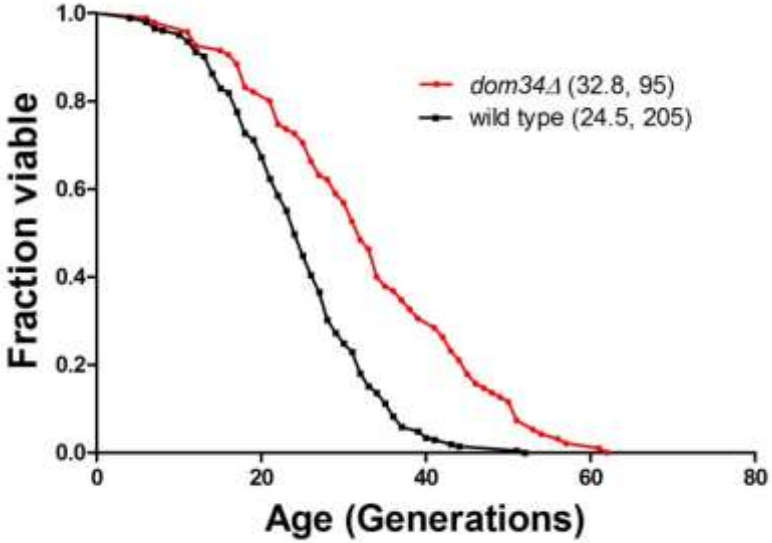

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
dbf20Δ (30.2, 80)
wild type (25.9, 125)

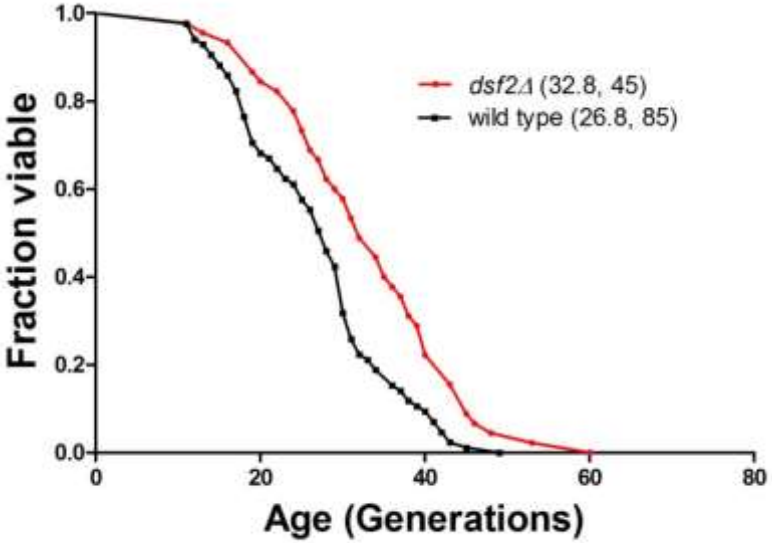

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
dbp3Δ (31.5, 165)
wild type (24.7, 210)

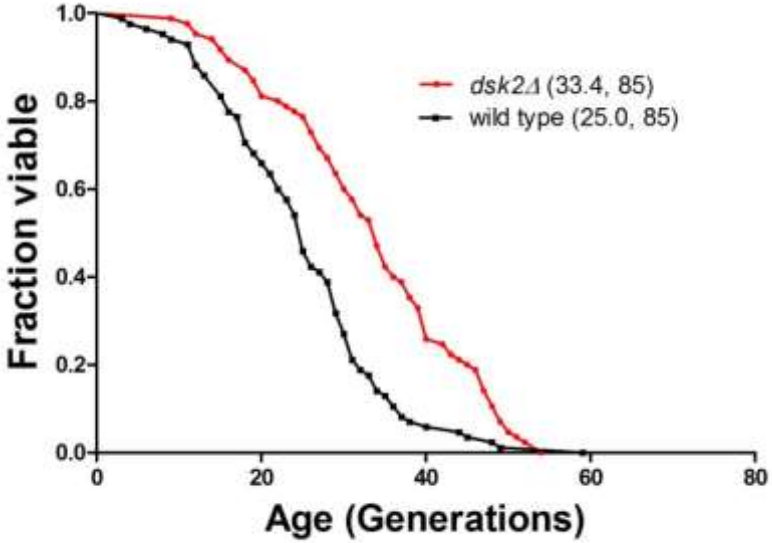

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
dgk1Δ (32.8, 45)
wild type (26.4, 65)

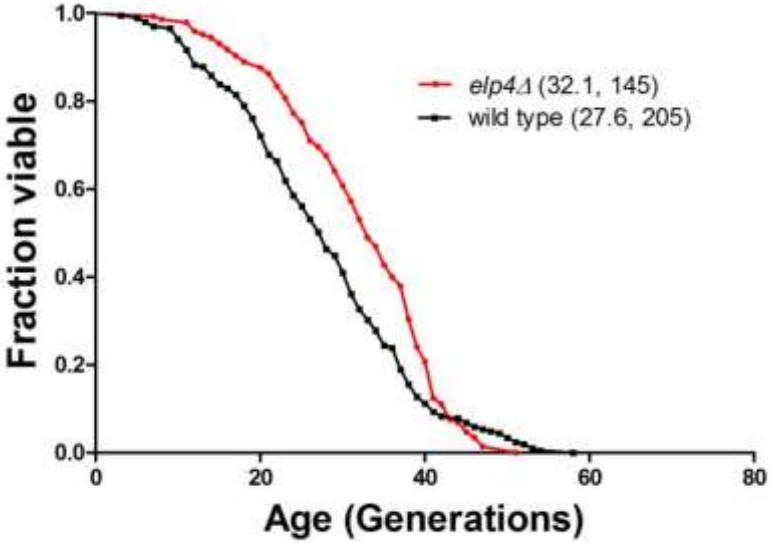

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
did2Δ (31.6, 125)
wild type (27.2, 125)

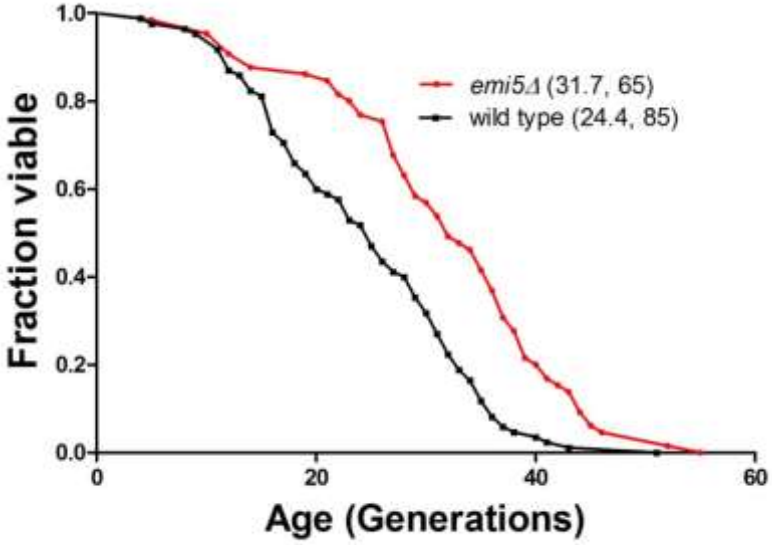

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
dlt1Δ (30.9, 204)
wild type (28.0, 305)

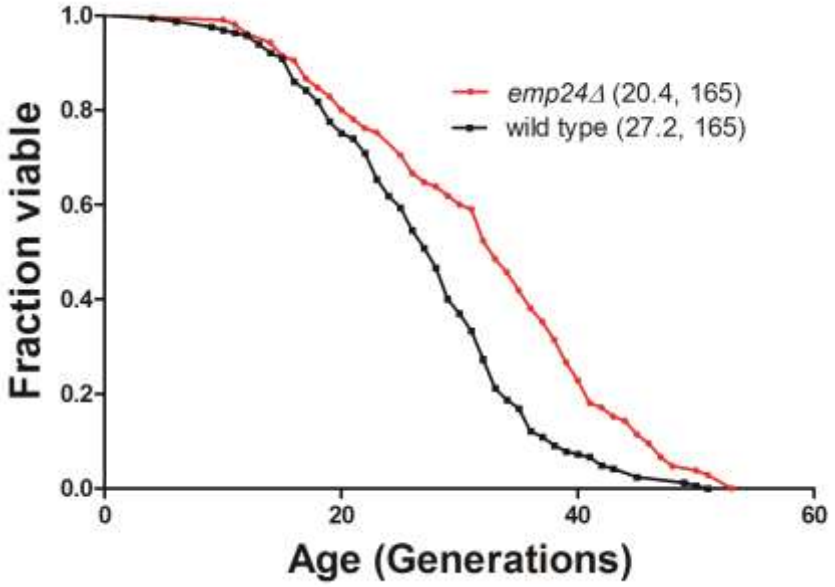

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
dom34Δ (32.8, 95)
wild type (24.5, 205)

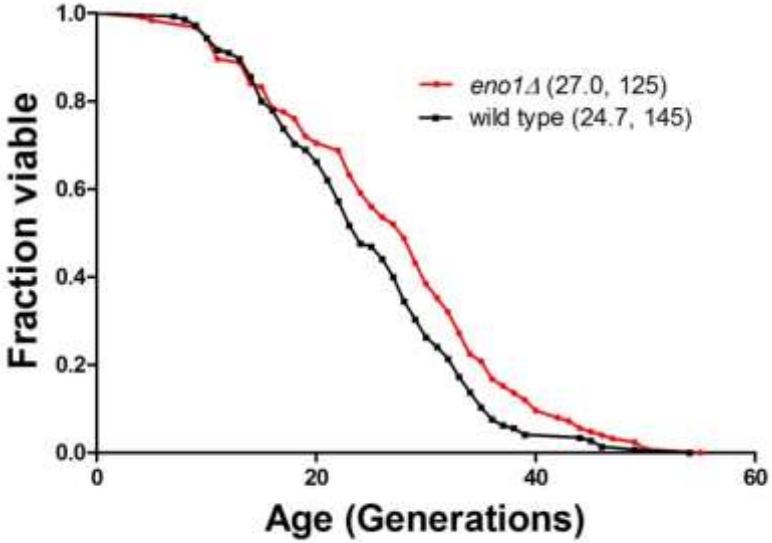

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
dsf2Δ (32.8, 45)
wild type (26.8, 85)

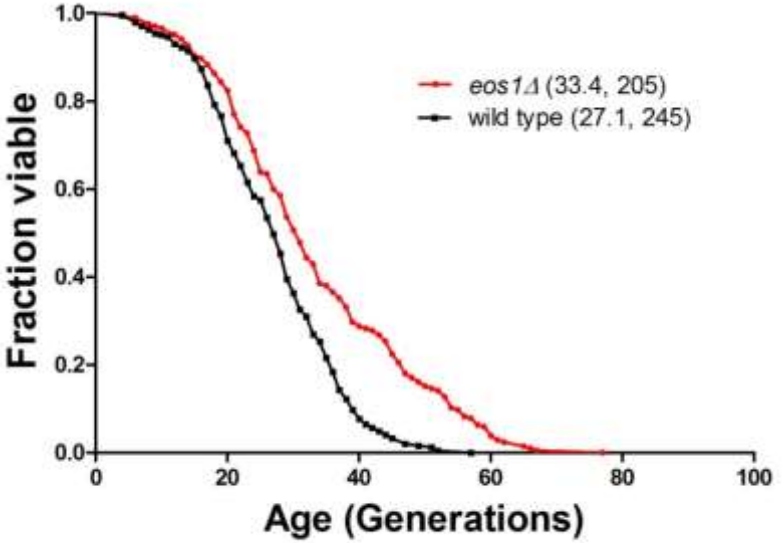

Fraction viable
Age (Generations)
dsk2Δ (33.4, 85)
wild type (25.0, 85)

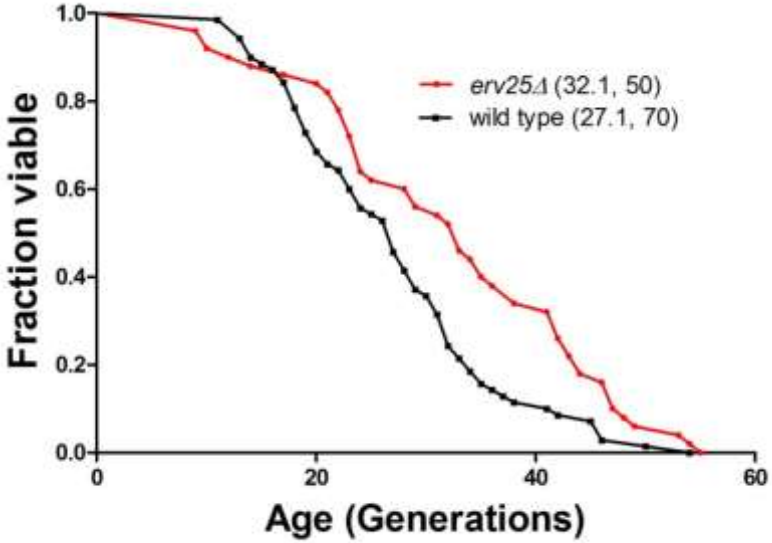

Fraction viable
Age (Generations)
elp4Δ (32.1, 145)
wild type (27.6, 205)

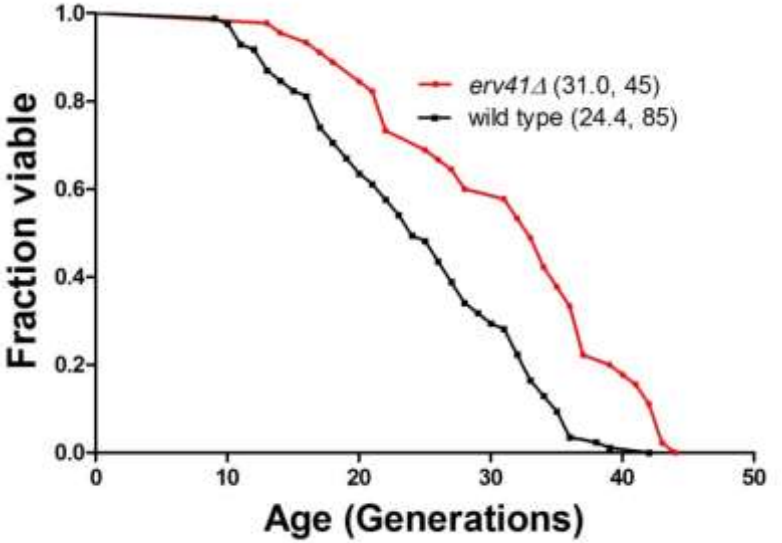

Fraction viable
Age (Generations)
emi5Δ (31.7, 65)
wild type (24.4, 85)

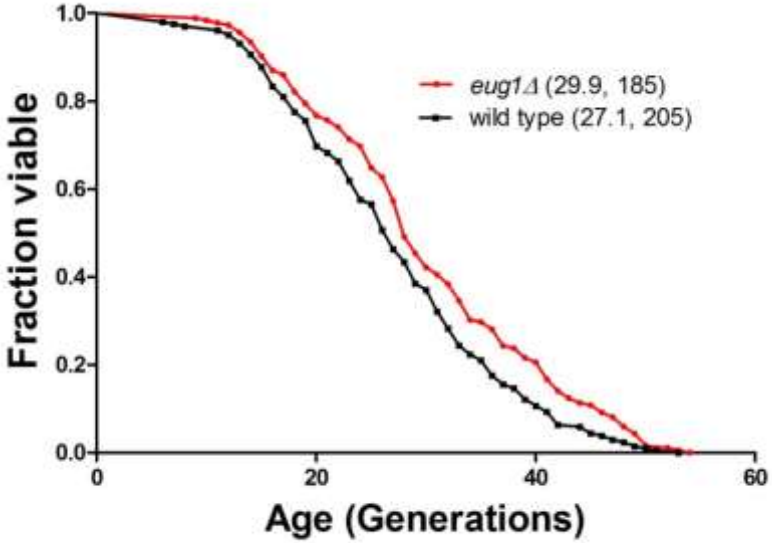

Fraction viable
Age (Generations)
emp24Δ (20.4, 165)
wild type (27.2, 165)

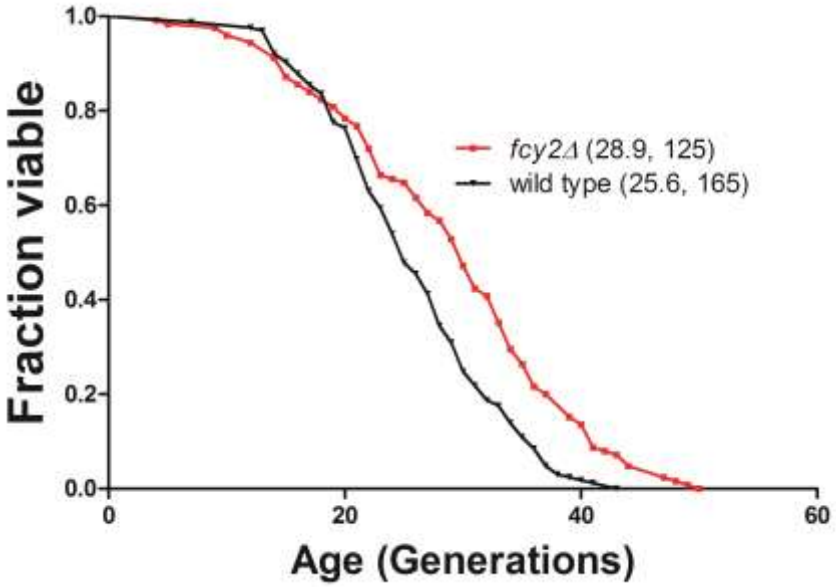

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
eno1Δ (27.0, 125)
wild type (24.7, 145)

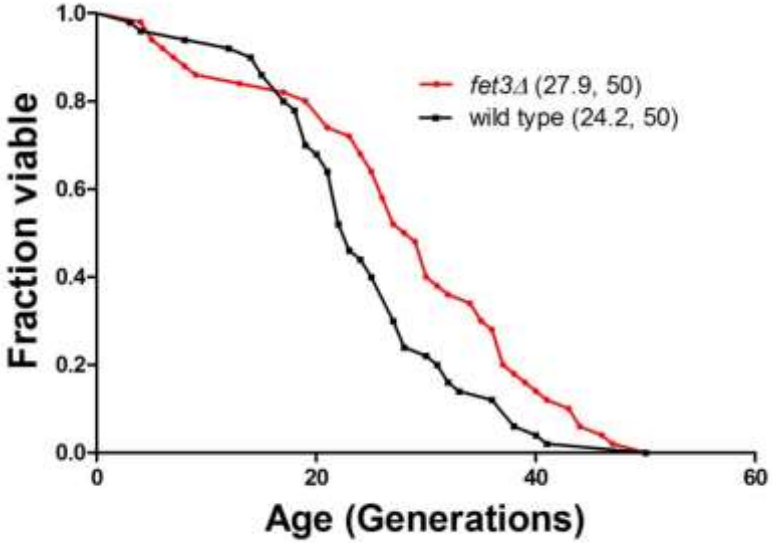

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
Age (Generations)
eos1Δ (33.4, 205)
wild type (27.1, 245)

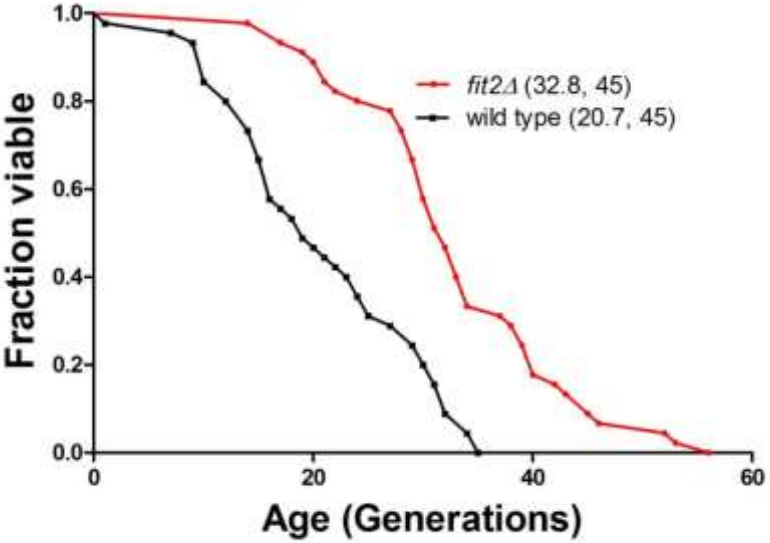

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
erv25Δ (32.1, 50)
wild type (27.1, 70)

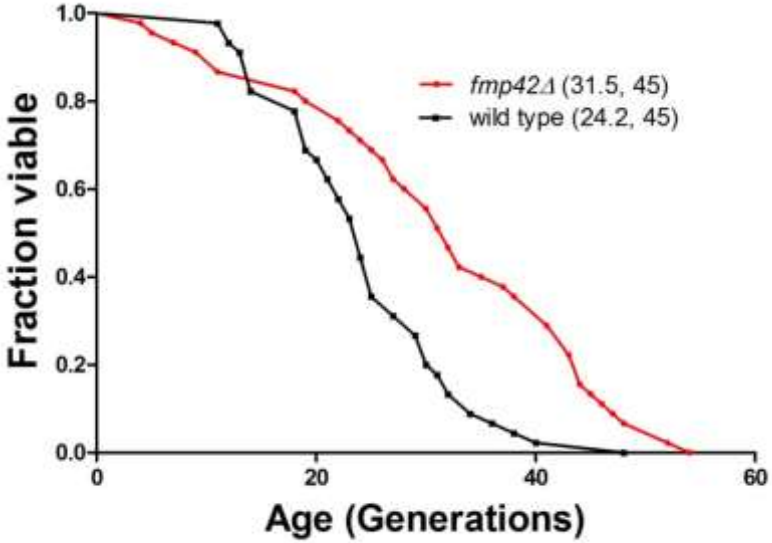

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
Age (Generations)
erv41Δ (31.0, 45)
wild type (24.4, 85)

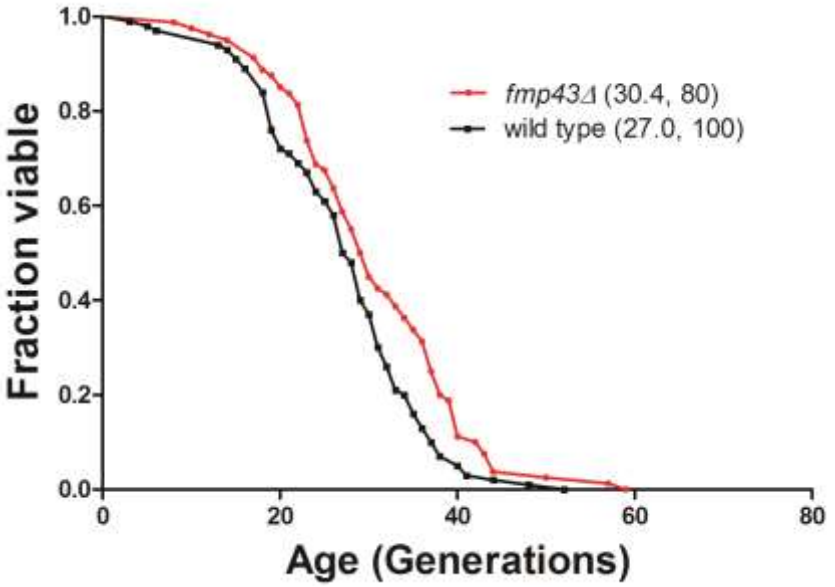

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
eug1Δ (29.9, 185)
wild type (27.1, 205)

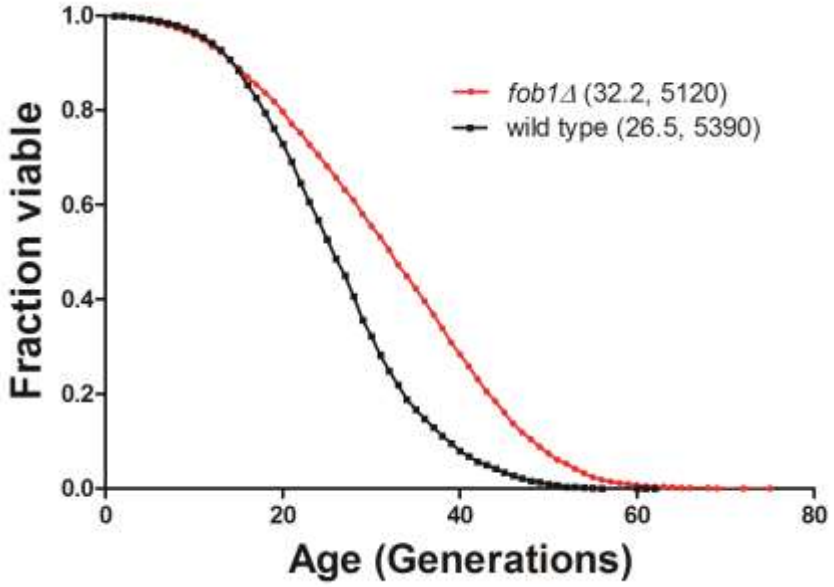

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
fcy2Δ (28.9, 125)
wild type (25.6, 165)

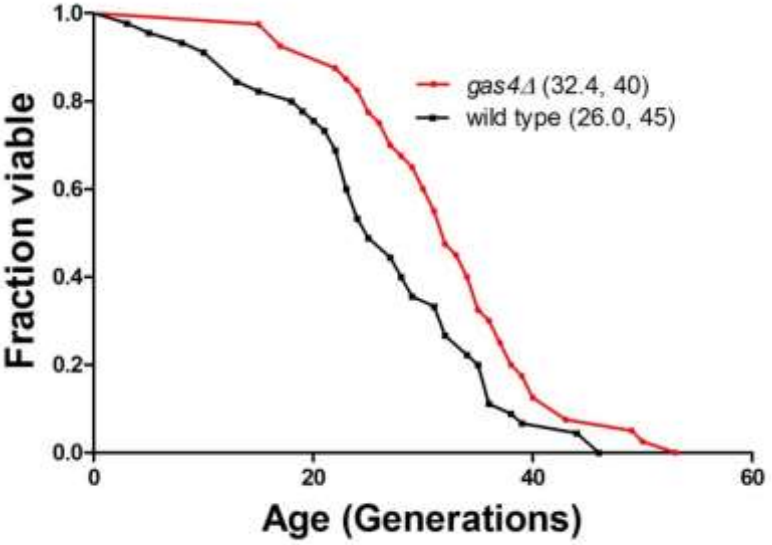

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
fet3Δ (27.9, 50)
wild type (24.2, 50)

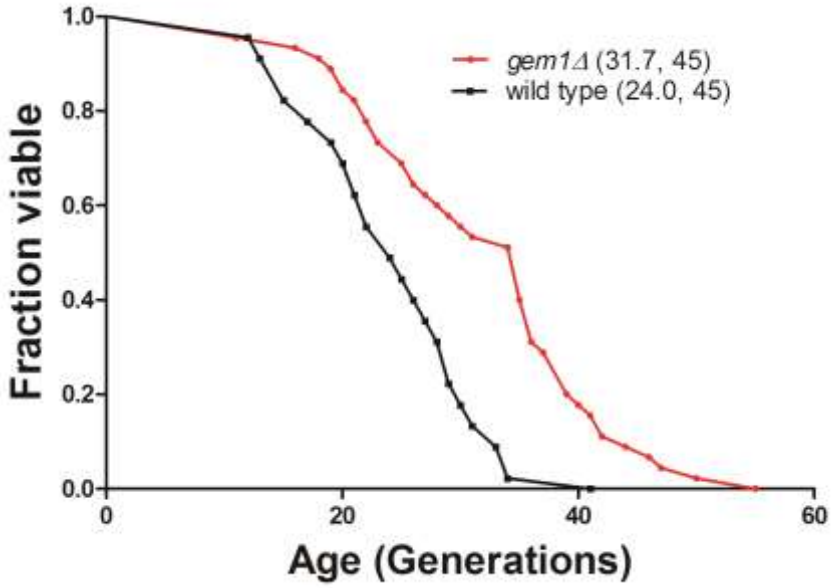

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
fit2Δ (32.8, 45)
wild type (20.7, 45)

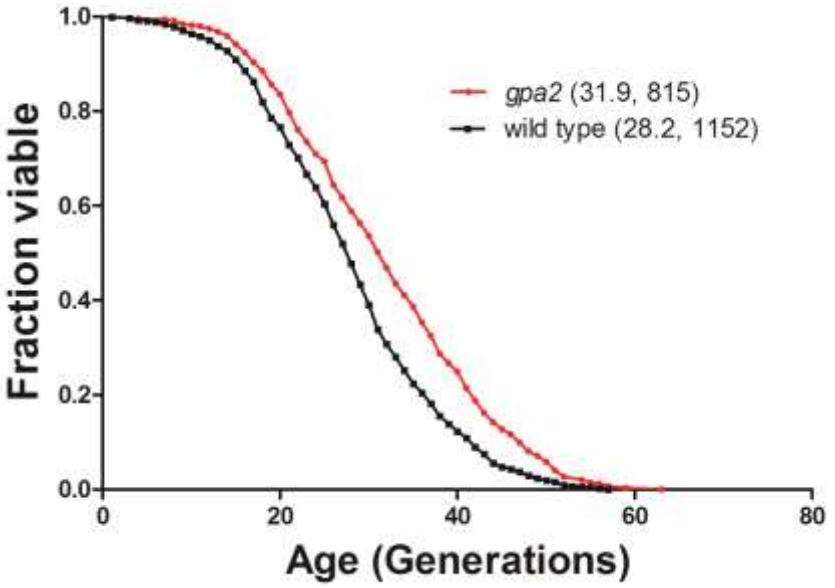

Fraction viable
Age (Generations)
fmp42Δ (31.5, 45)
wild type (24.2, 45)
0.0
0.2
0.4
0.6
0.8
1.0
0
20
40
60

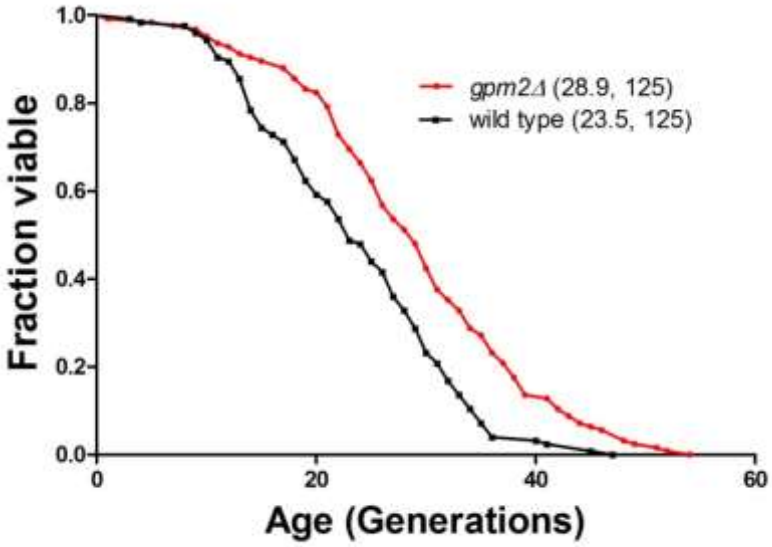

Fraction viable
Age (Generations)
fmp43Δ (30.4, 80)
wild type (27.0, 100)
0.0
0.2
0.4
0.6
0.8
1.0
0
20
40
60
80

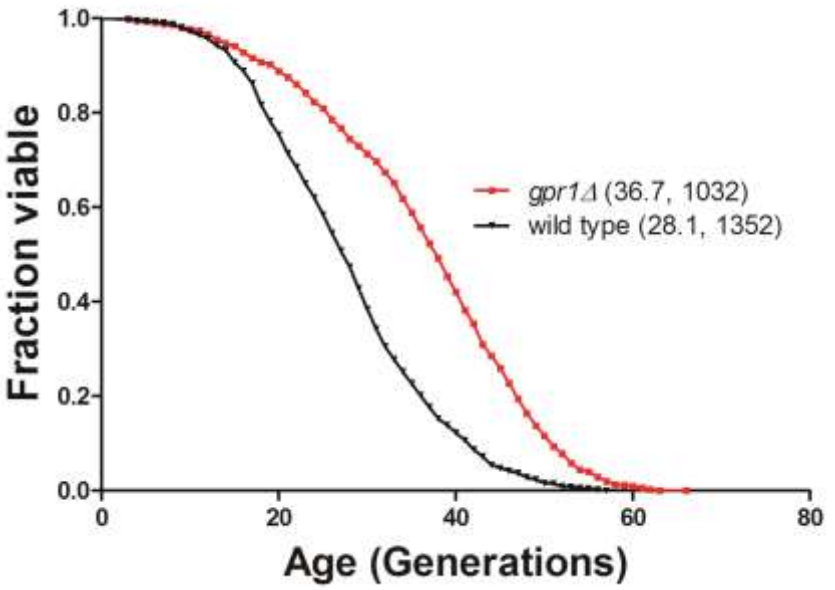

Fraction viable
Age (Generations)
fob1Δ (32.2, 5120)
wild type (26.5, 5390)
0.0
0.2
0.4
0.6
0.8
1.0
0
20
40
60
80

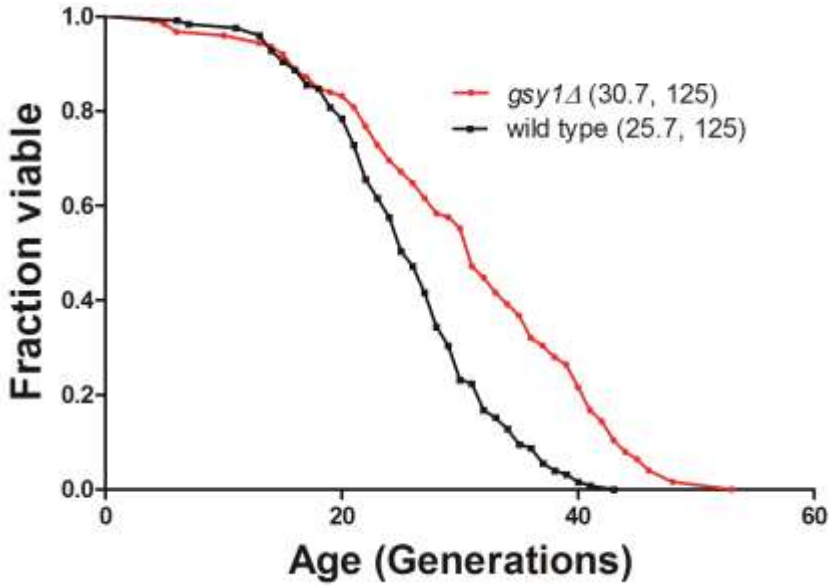

Fraction viable
Age (Generations)
gas4Δ (32.4, 40)
wild type (26.0, 45)
0.0
0.2
0.4
0.6
0.8
1.0
0
20
40
60

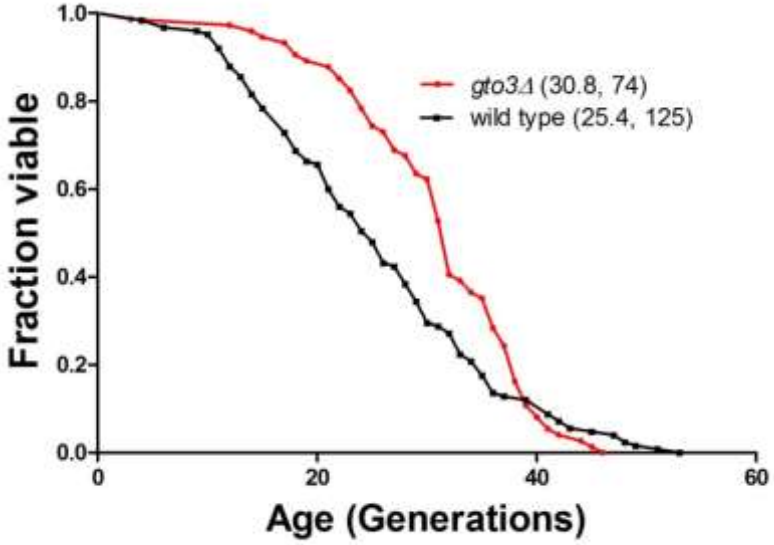

gem1Δ (31.7, 45)
wild type (24.0, 45)
Fraction viable
Age (Generations)

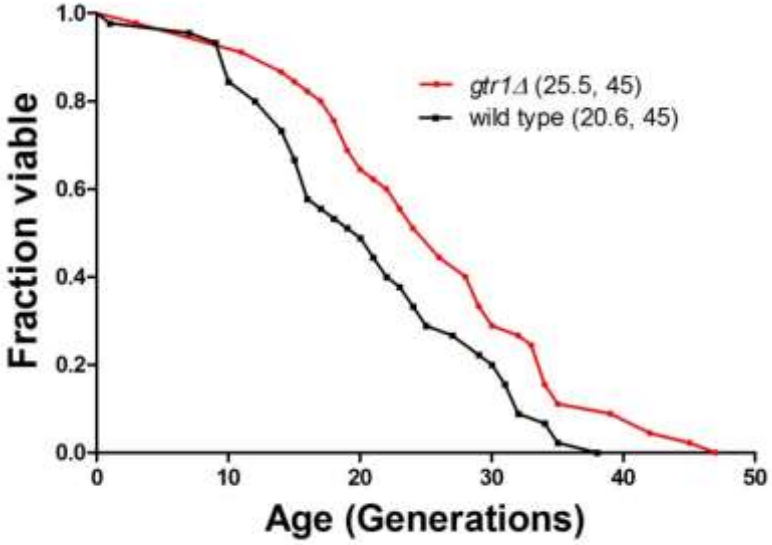

gpa2 (31.9, 815)
wild type (28.2, 1152)
Fraction viable
Age (Generations)

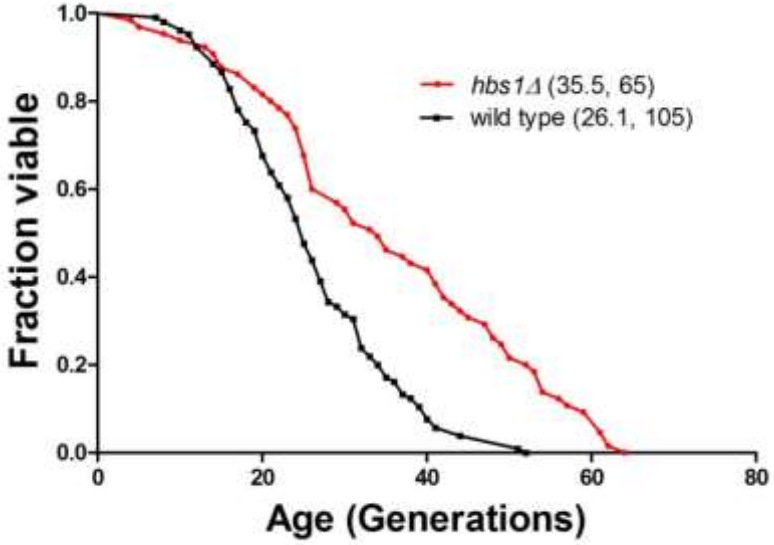

gpm2Δ (28.9, 125)
wild type (23.5, 125)
Fraction viable
Age (Generations)

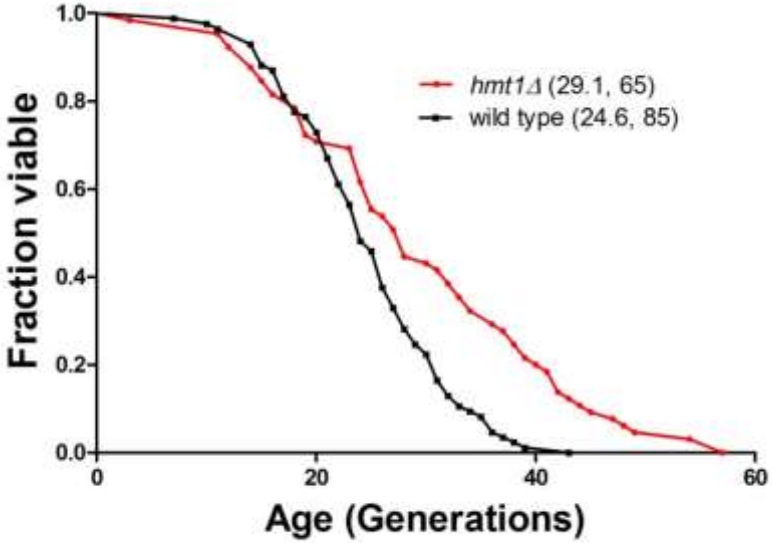

gpr1Δ (36.7, 1032)
wild type (28.1, 1352)
Fraction viable
Age (Generations)

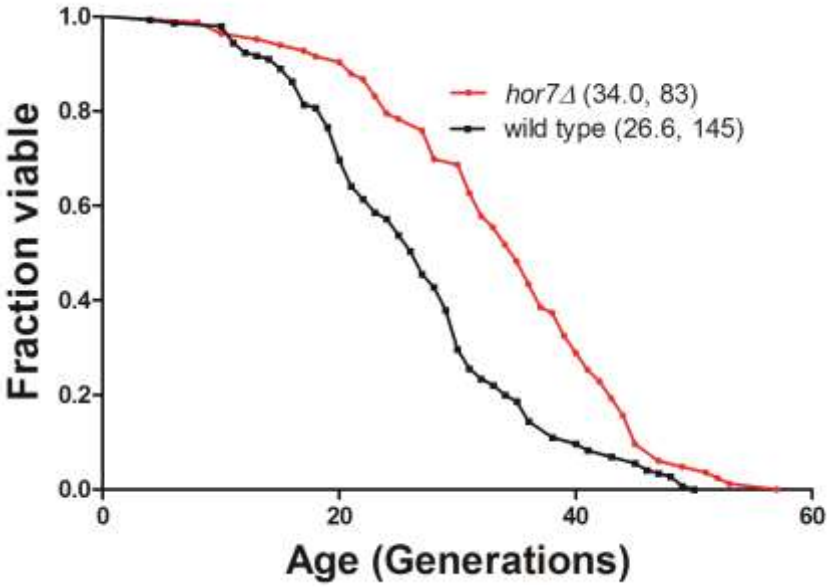

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
gsy1Δ (30.7, 125)
wild type (25.7, 125)

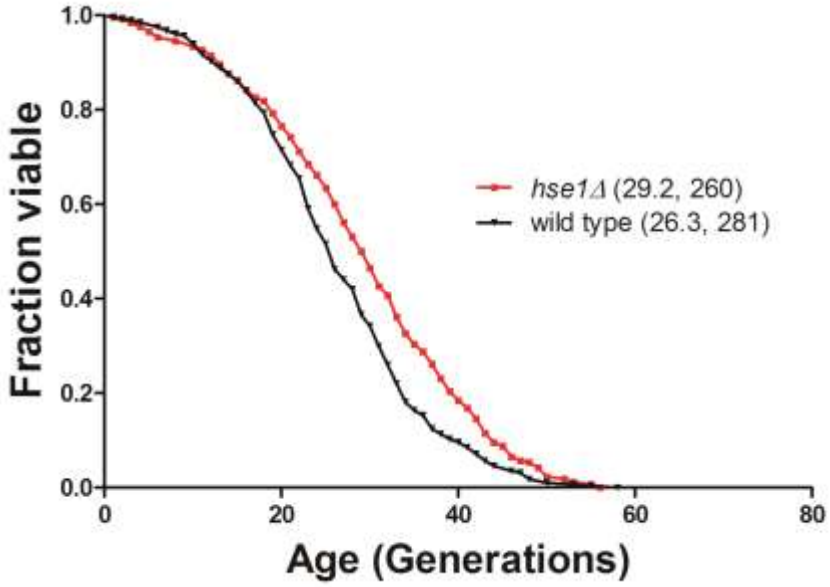

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
gto3Δ (30.8, 74)
wild type (25.4, 125)

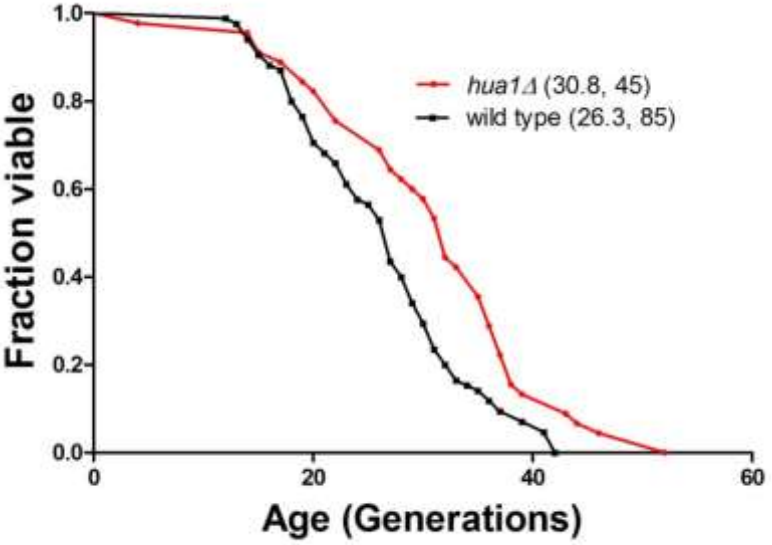

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
Age (Generations)
gtr1Δ (25.5, 45)
wild type (20.6, 45)

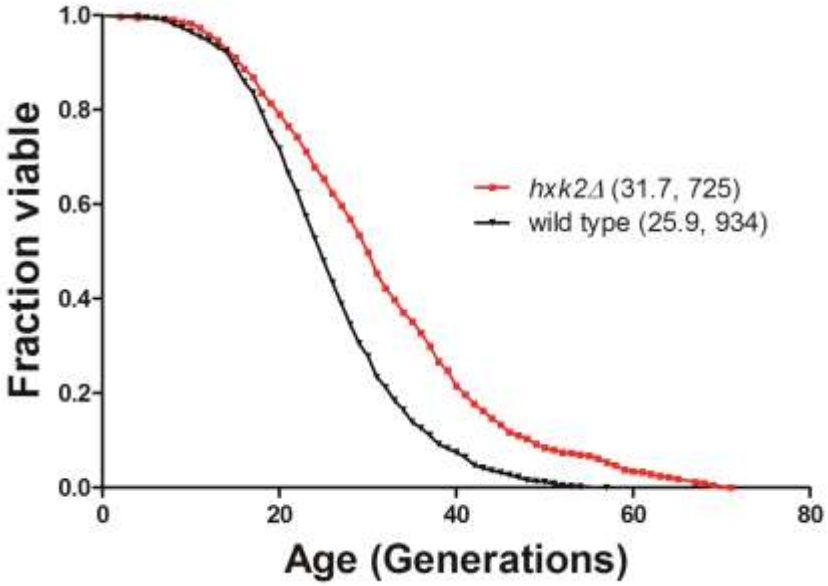

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
hbs1Δ (35.5, 65)
wild type (26.1, 105)

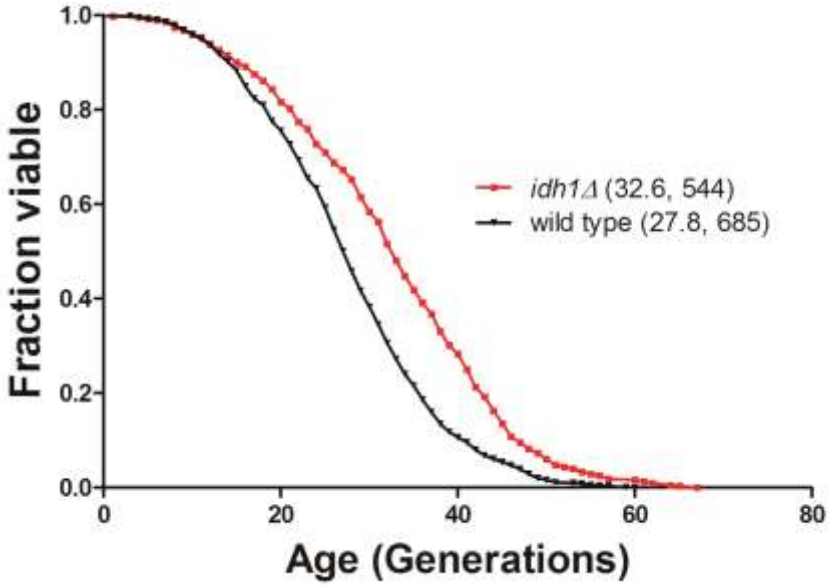

Fraction viable
Age (Generations)
hmt1Δ (29.1, 65)
wild type (24.6, 85)

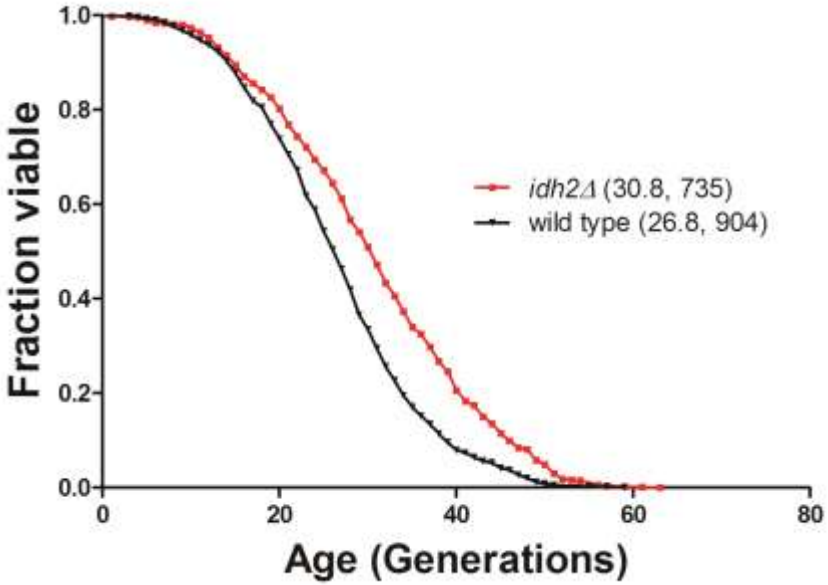

Fraction viable
Age (Generations)
hor7Δ (34.0, 83)
wild type (26.6, 145)

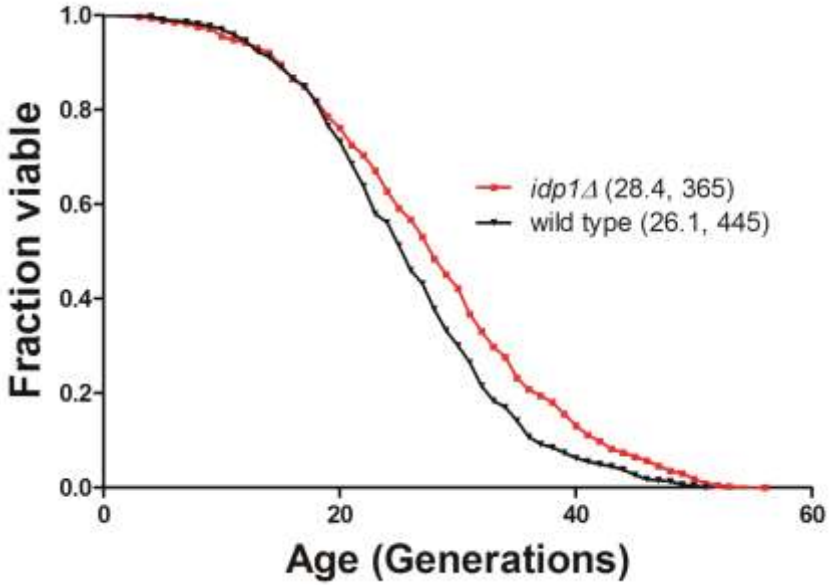

Fraction viable
Age (Generations)
hse1Δ (29.2, 260)
wild type (26.3, 281)

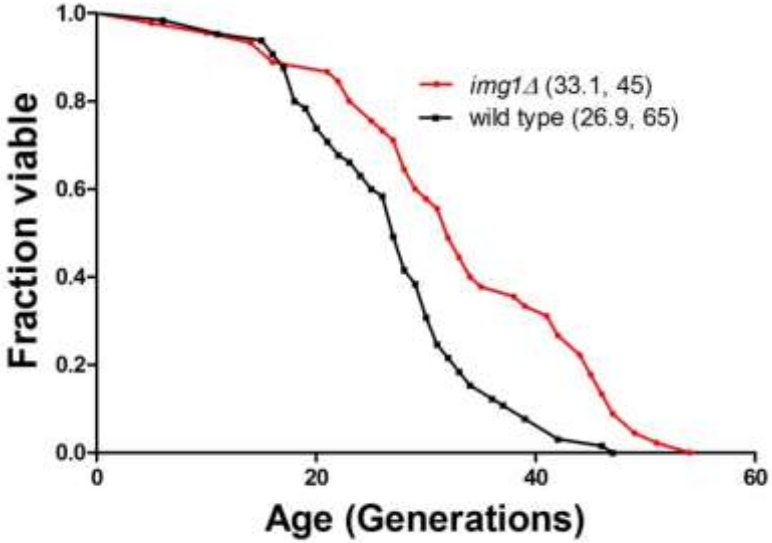

Fraction viable
Age (Generations)
hua1Δ (30.8, 45)
wild type (26.3, 85)

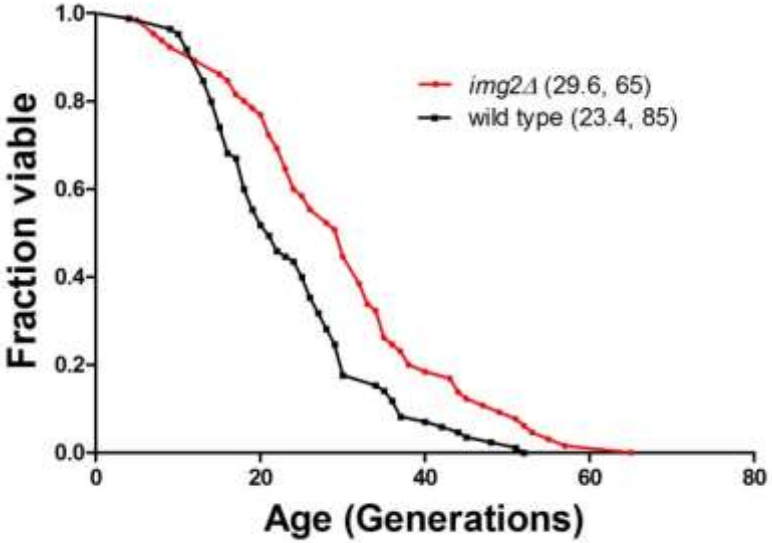

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
hxk2Δ (31.7, 725)
wild type (25.9, 934)

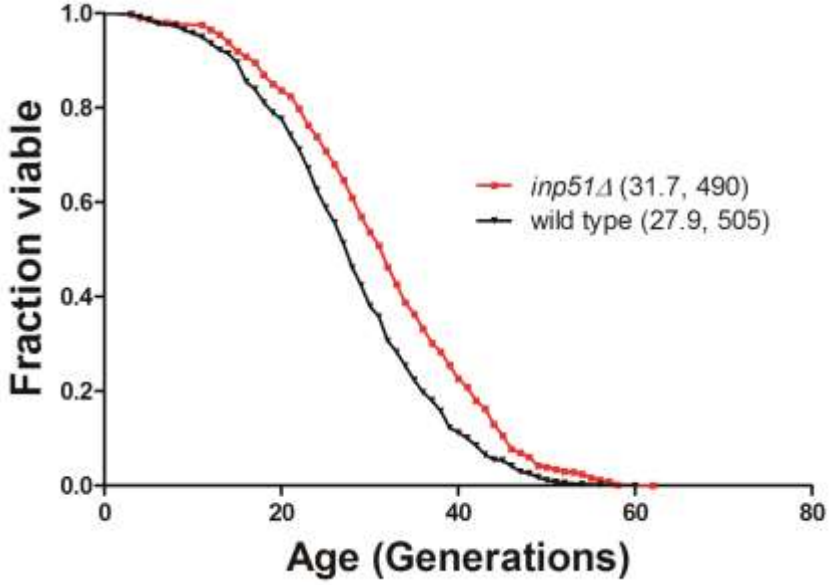

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
idh1Δ (32.6, 544)
wild type (27.8, 685)

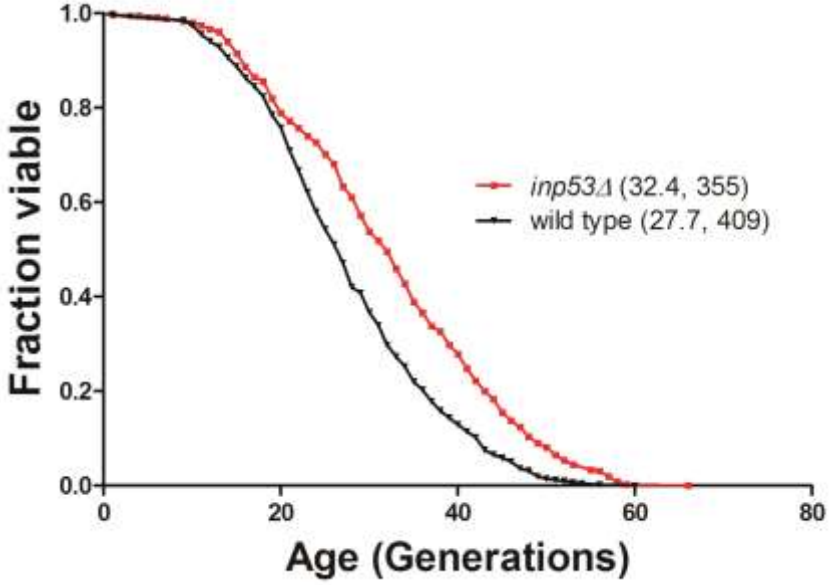

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
idh2Δ (30.8, 735)
wild type (26.8, 904)

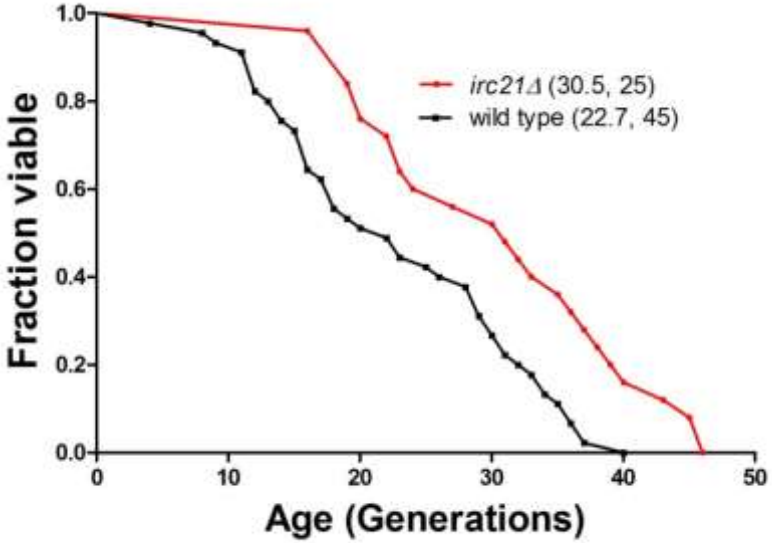

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
idp1Δ (28.4, 365)
wild type (26.1, 445)

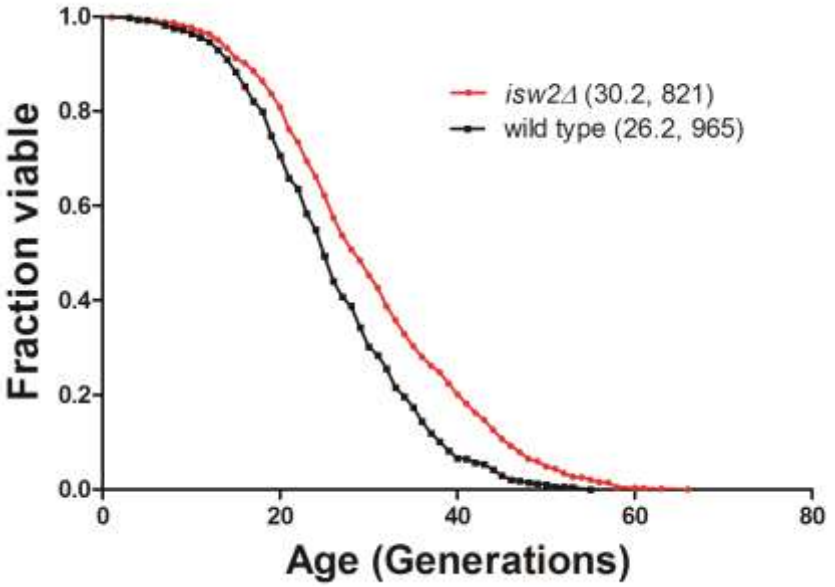

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
img1Δ (33.1, 45)
wild type (26.9, 65)

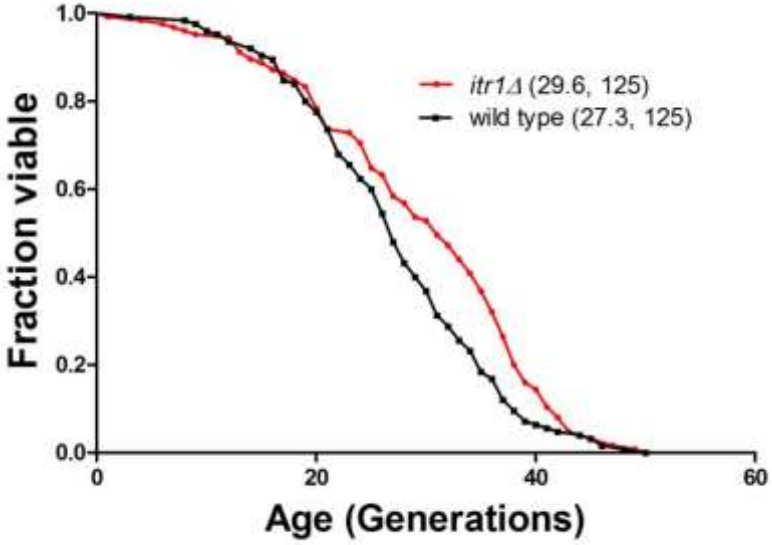

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
img2Δ (29.6, 65)
wild type (23.4, 85)

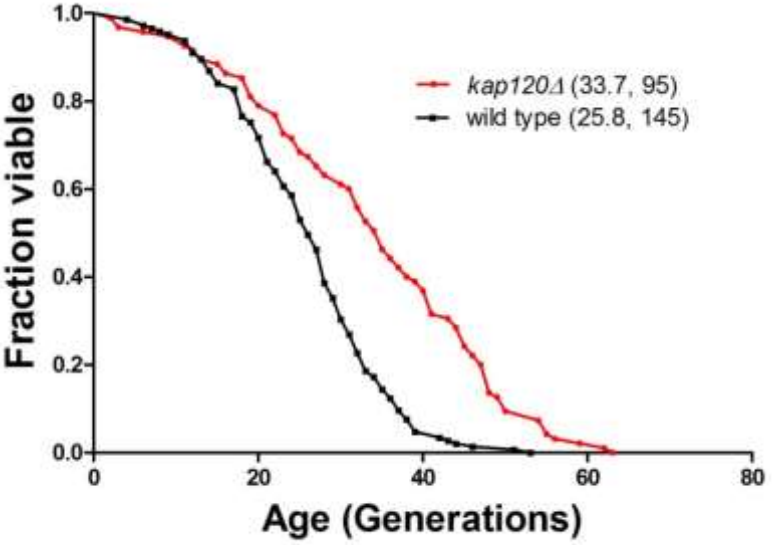

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
inp51Δ (31.7, 490)
wild type (27.9, 505)

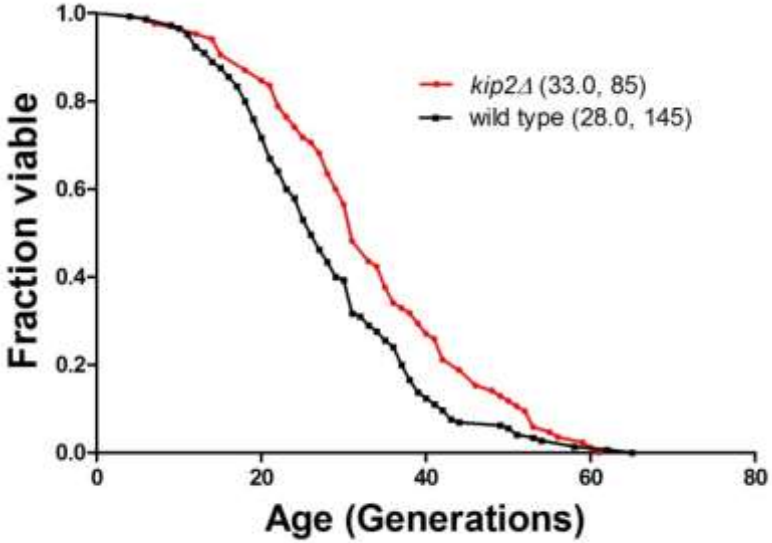

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
inp53Δ (32.4, 355)
wild type (27.7, 409)

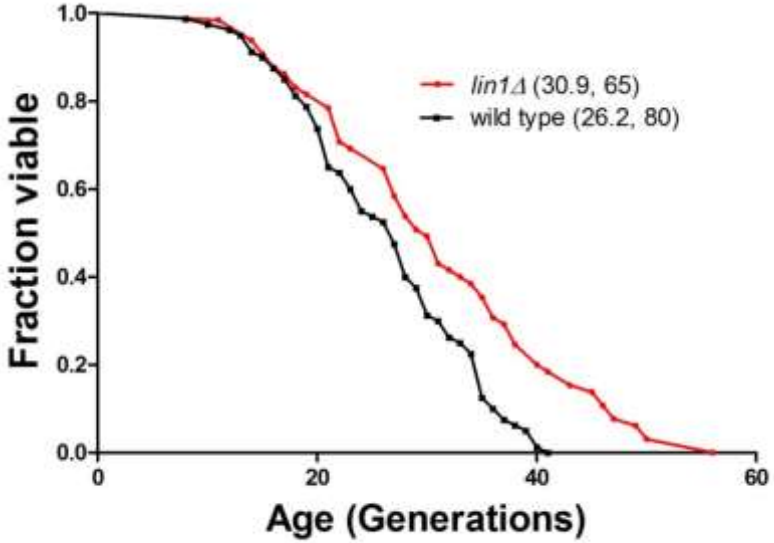

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
Age (Generations)
irc21Δ (30.5, 25)
wild type (22.7, 45)

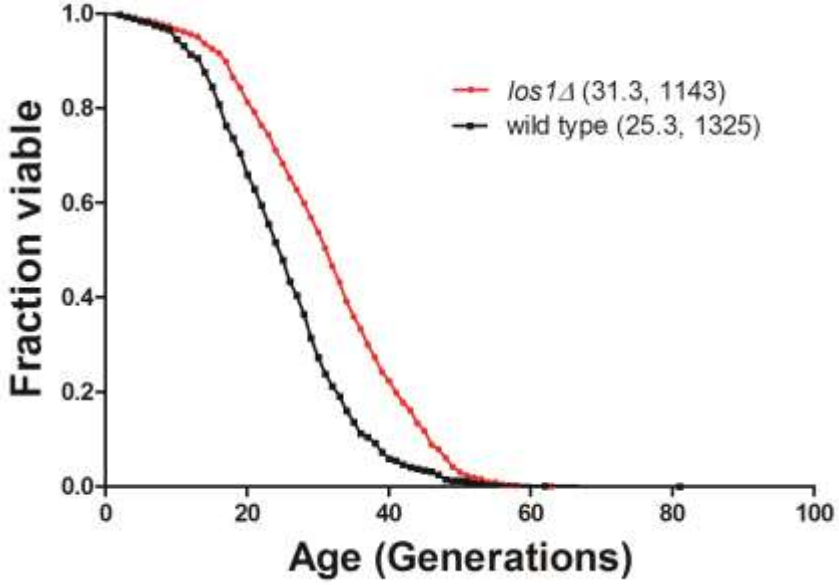

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
isw2Δ (30.2, 821)
wild type (26.2, 965)

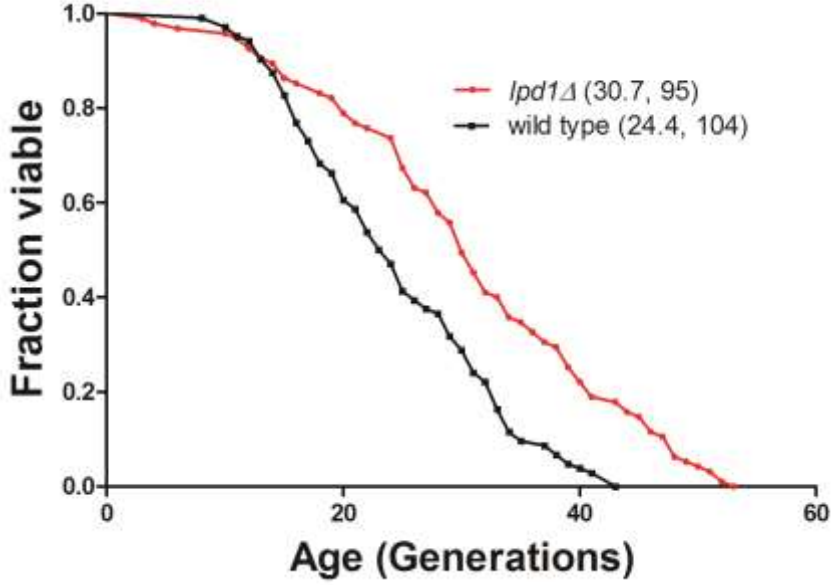

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
itr1Δ (29.6, 125)
wild type (27.3, 125)

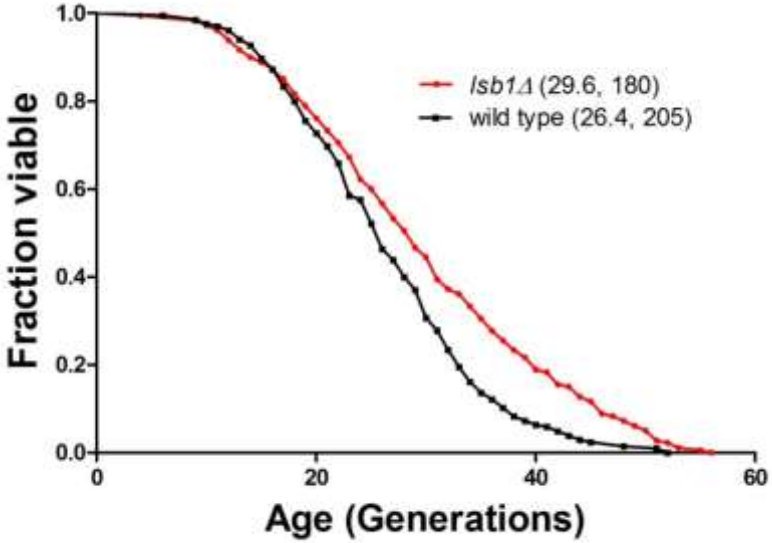

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
kap120Δ (33.7, 95)
wild type (25.8, 145)

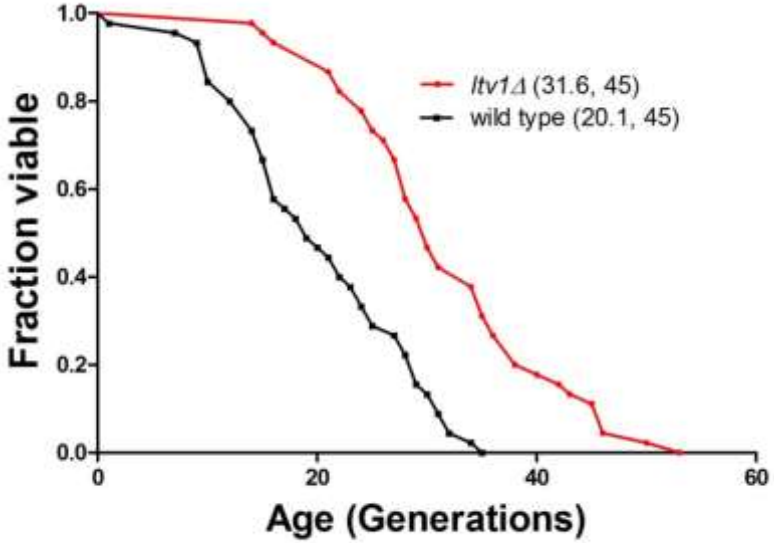

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
kip2Δ (33.0, 85)
wild type (28.0, 145)

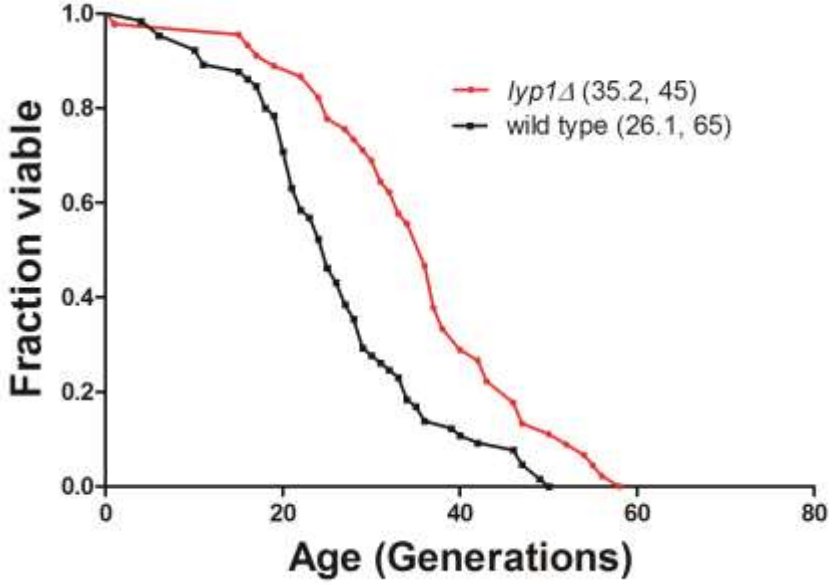

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
lin1Δ (30.9, 65)
wild type (26.2, 80)

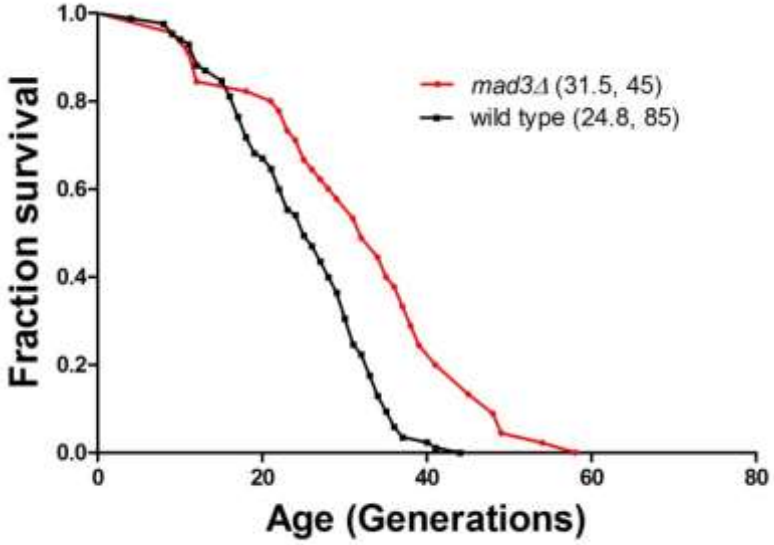

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
Age (Generations)
los1Δ (31.3, 1143)
wild type (25.3, 1325)

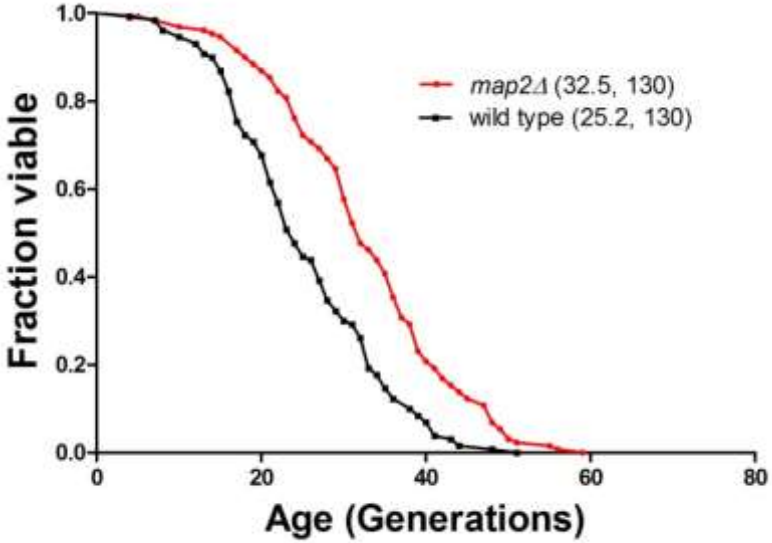

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
lpd1Δ (30.7, 95)
wild type (24.4, 104)

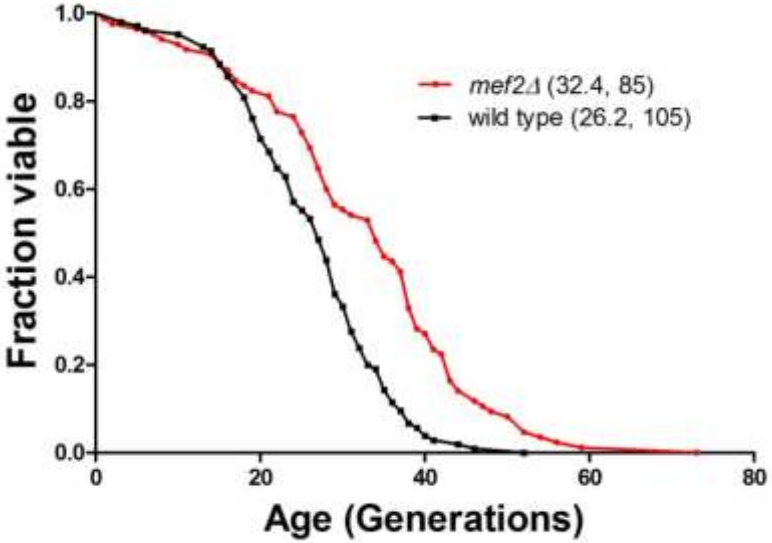

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
lsb1Δ (29.6, 180)
wild type (26.4, 205)

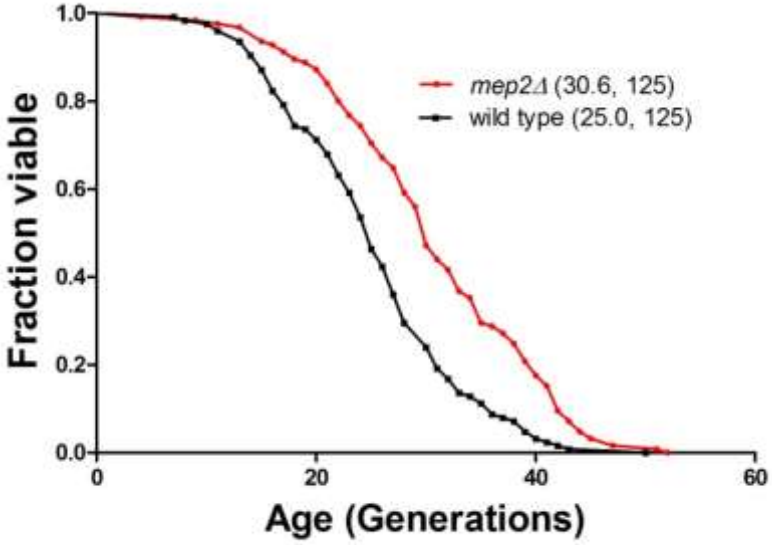

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
ltv1Δ (31.6, 45)
wild type (20.1, 45)

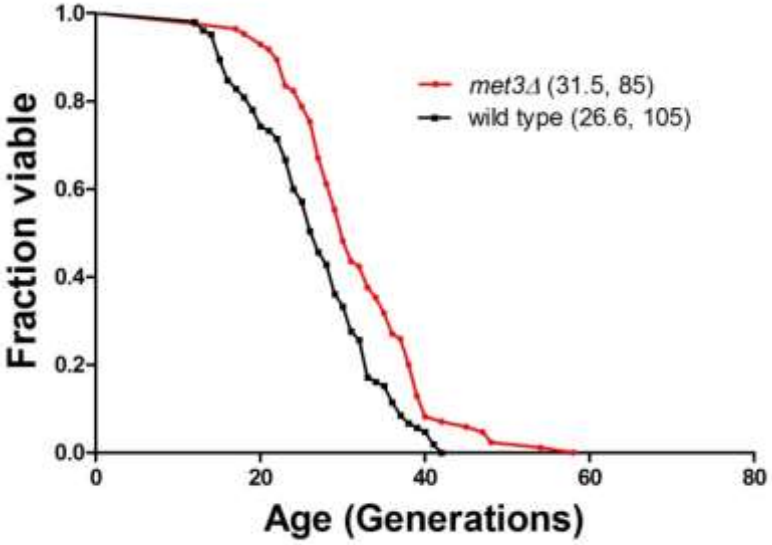

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
lyp1Δ (35.2, 45)
wild type (26.1, 65)

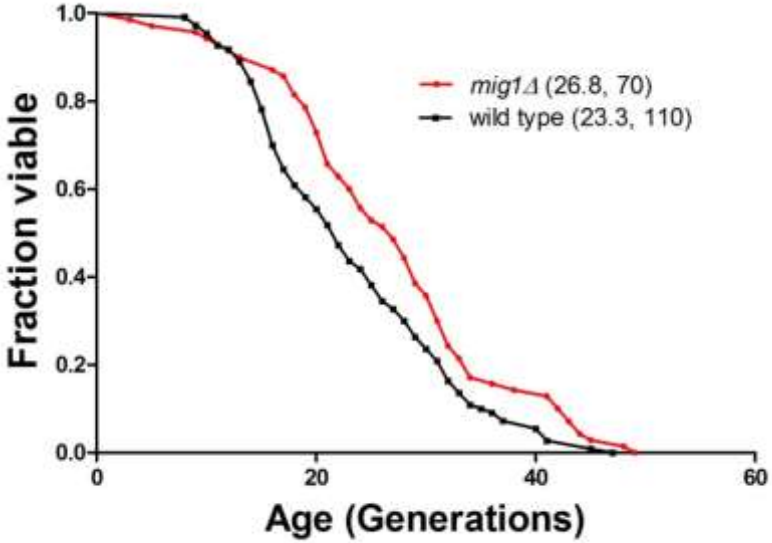

Fraction survival
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
mad3Δ (31.5, 45)
wild type (24.8, 85)

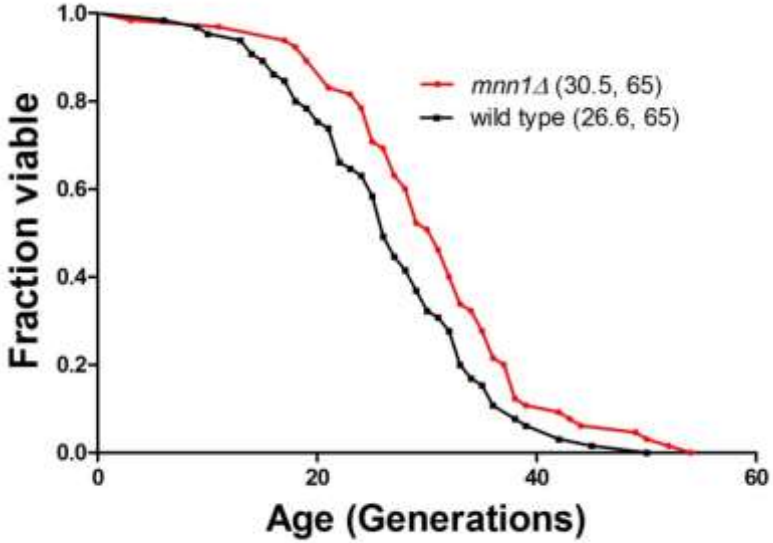

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
map2Δ (32.5, 130)
wild type (25.2, 130)

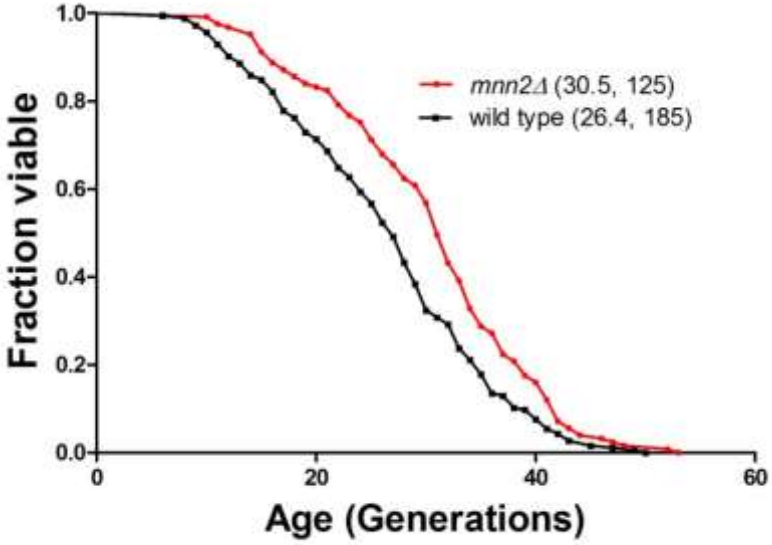

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
mef2Δ (32.4, 85)
wild type (26.2, 105)

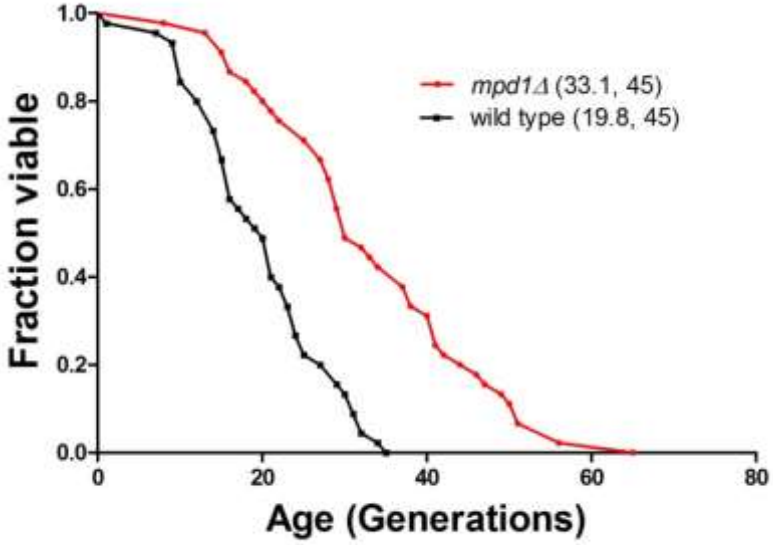

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
mep2Δ (30.6, 125)
wild type (25.0, 125)

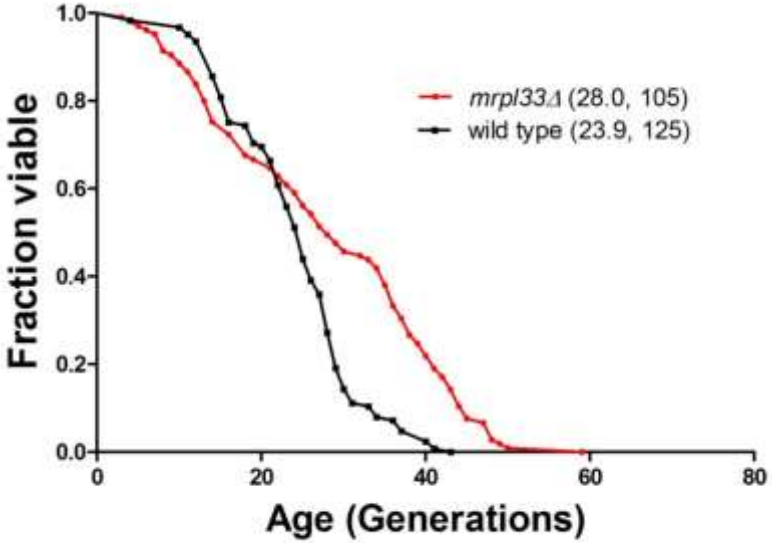

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
met3Δ (31.5, 85)
wild type (26.6, 105)

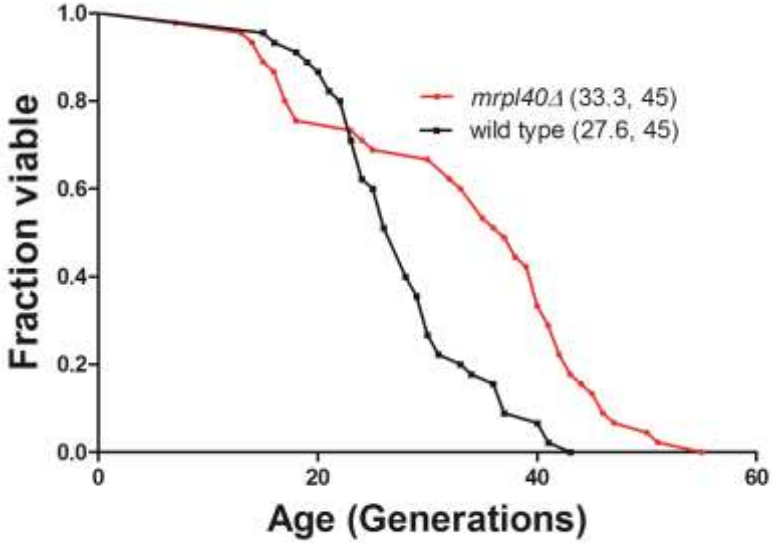

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
mig1Δ (26.8, 70)
wild type (23.3, 110)

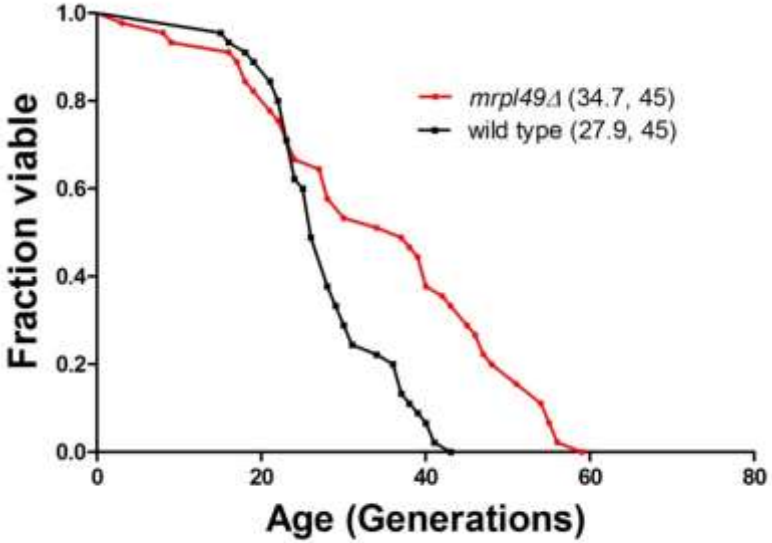

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
mnn1Δ (30.5, 65)
wild type (26.6, 65)

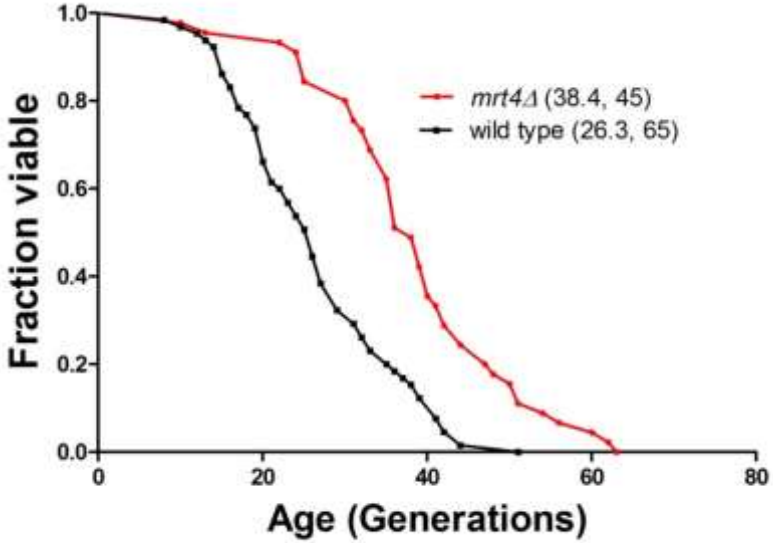

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
mnn2Δ (30.5, 125)
wild type (26.4, 185)

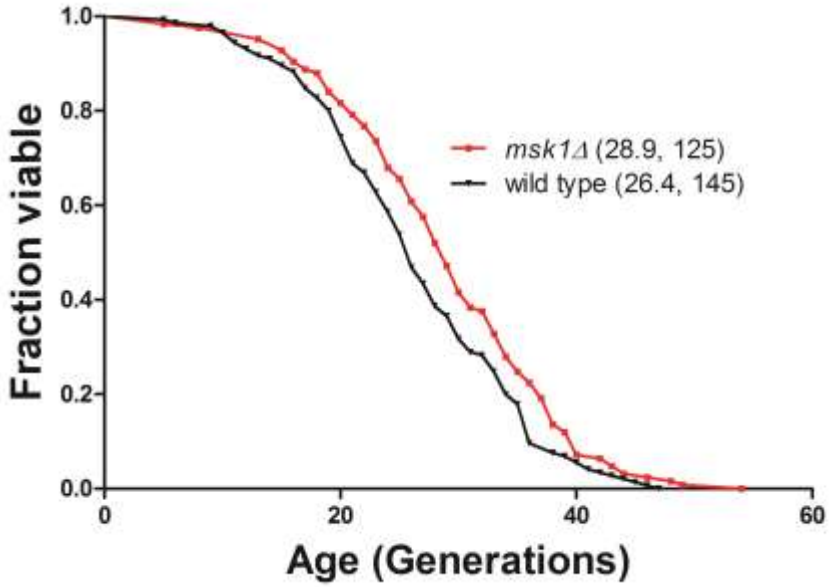

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
mpd1Δ (33.1, 45)
wild type (19.8, 45)

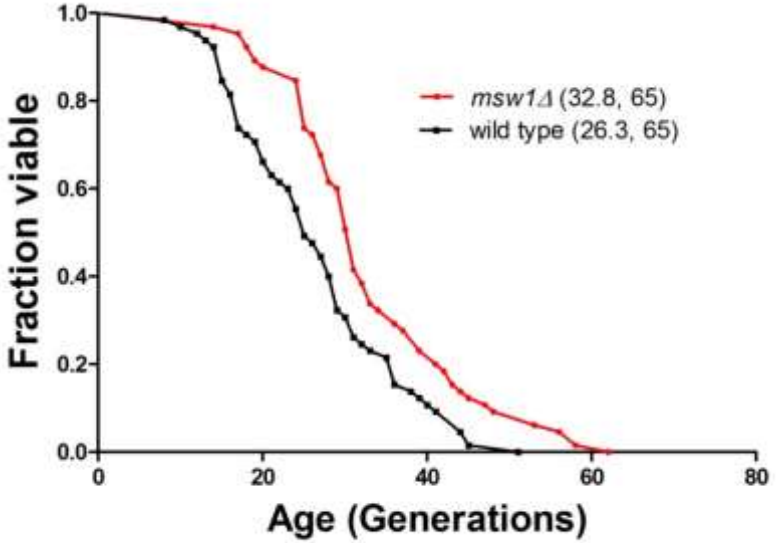

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
mrpl33Δ (28.0, 105)
wild type (23.9, 125)

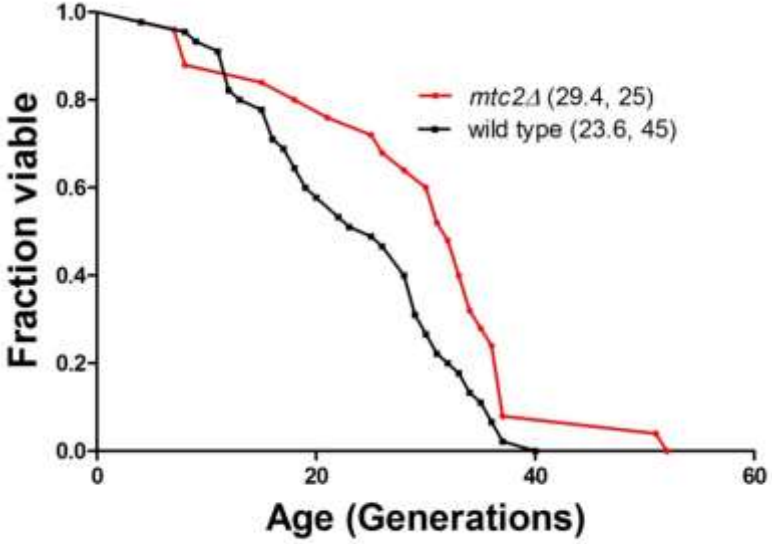

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
mrpl40Δ (33.3, 45)
wild type (27.6, 45)

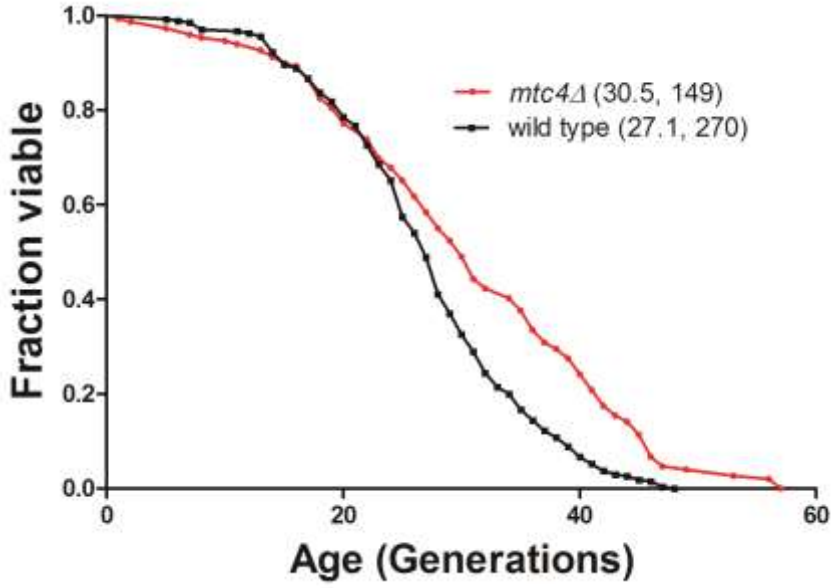

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
mrpl49Δ (34.7, 45)
wild type (27.9, 45)

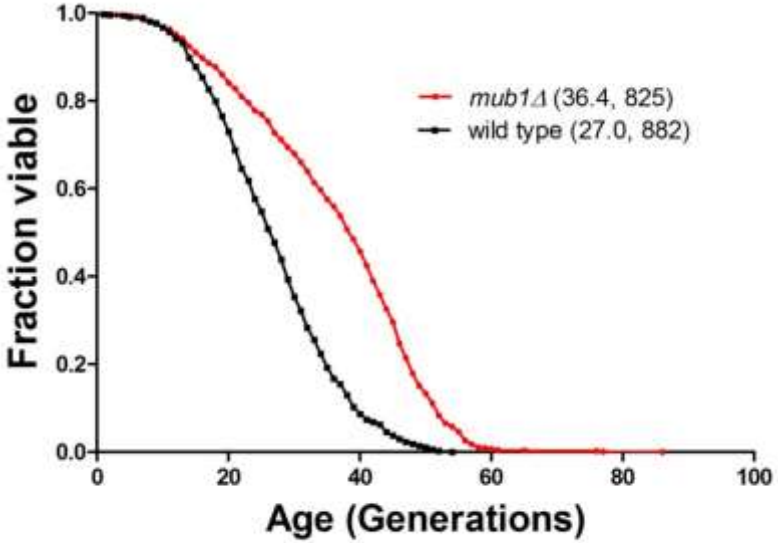

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
mrt4Δ (38.4, 45)
wild type (26.3, 65)

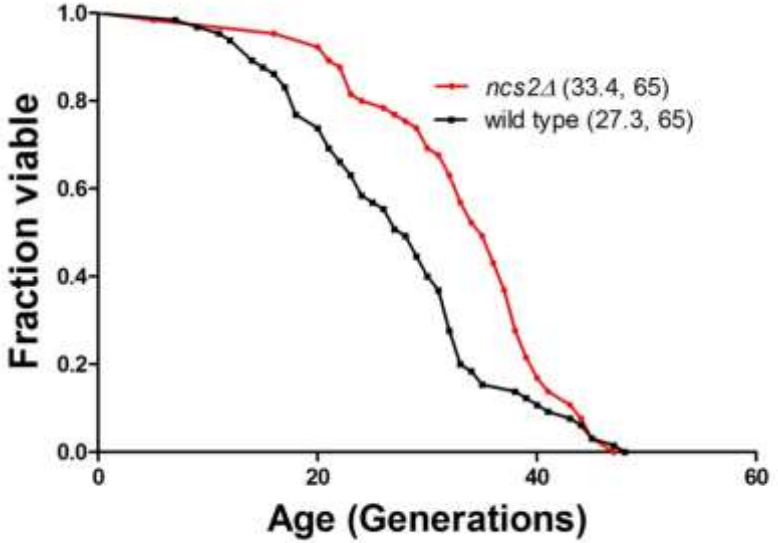

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
msk1Δ (28.9, 125)
wild type (26.4, 145)

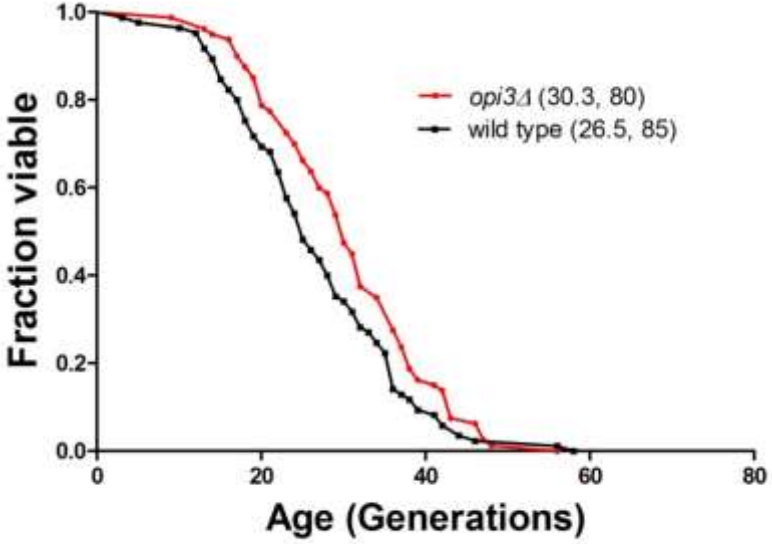

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
msw1Δ (32.8, 65)
wild type (26.3, 65)

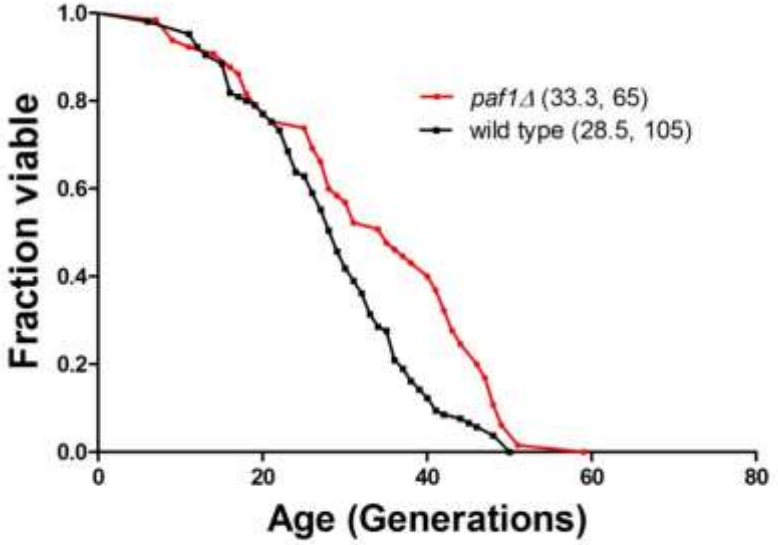

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
mtc2Δ (29.4, 25)
wild type (23.6, 45)

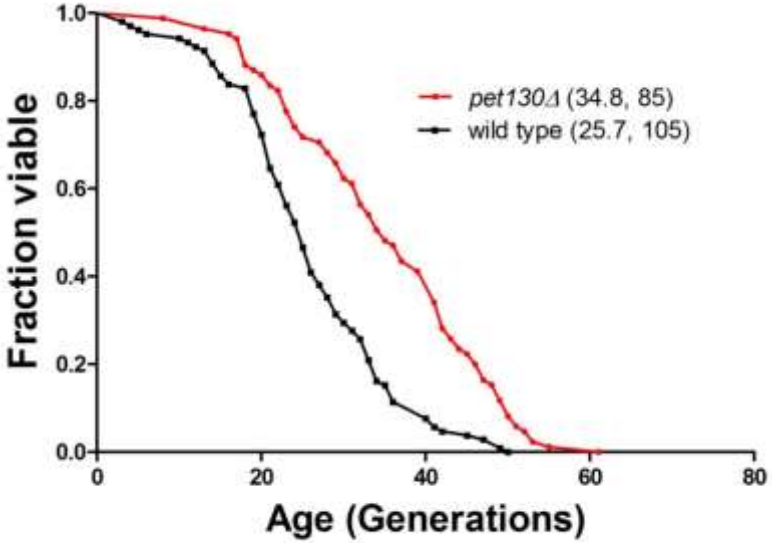

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
mtc4Δ (30.5, 149)
wild type (27.1, 270)

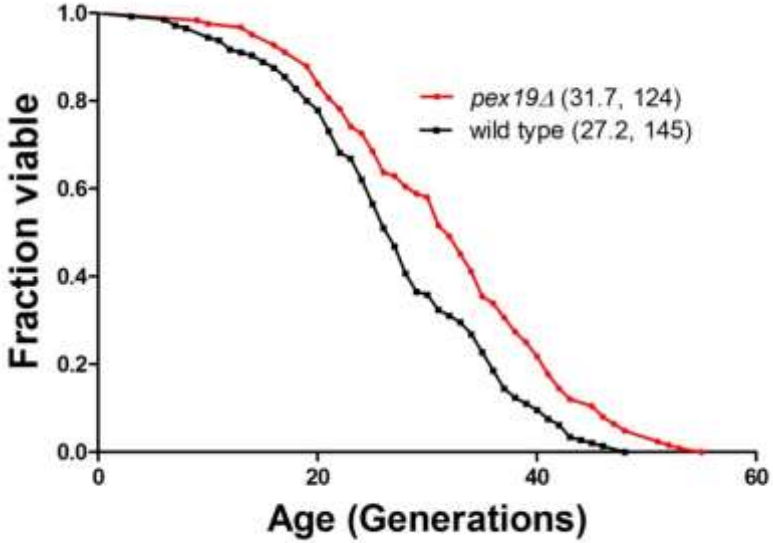

Fraction viable
Age (Generations)
mub1Δ (36.4, 825)
wild type (27.0, 882)

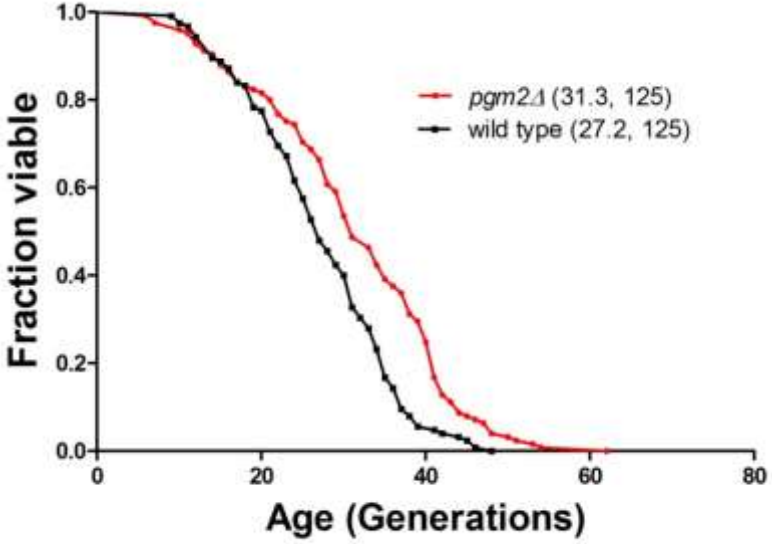

Fraction viable
Age (Generations)
ncs2Δ (33.4, 65)
wild type (27.3, 65)

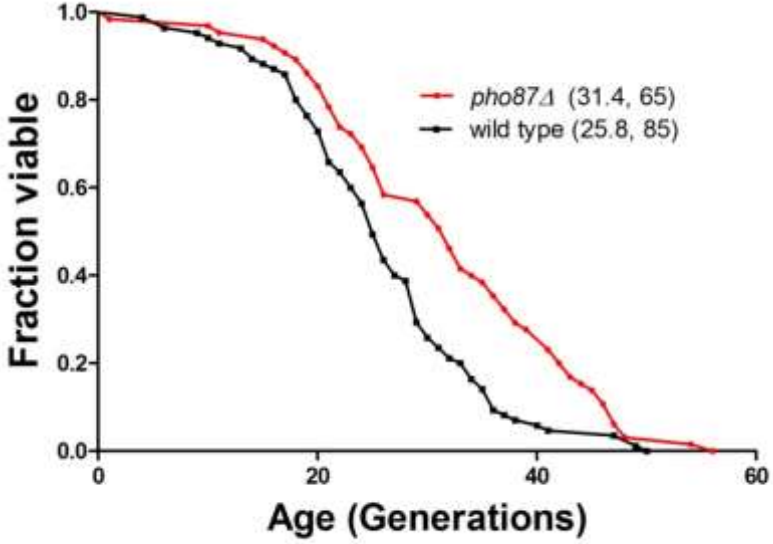

Fraction viable
Age (Generations)
opi3Δ (30.3, 80)
wild type (26.5, 85)

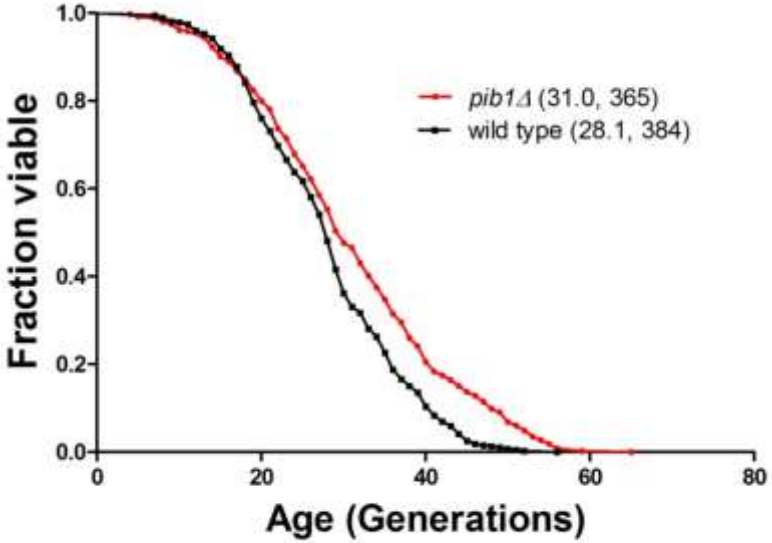

Fraction viable
Age (Generations)
paf1Δ (33.3, 65)
wild type (28.5, 105)

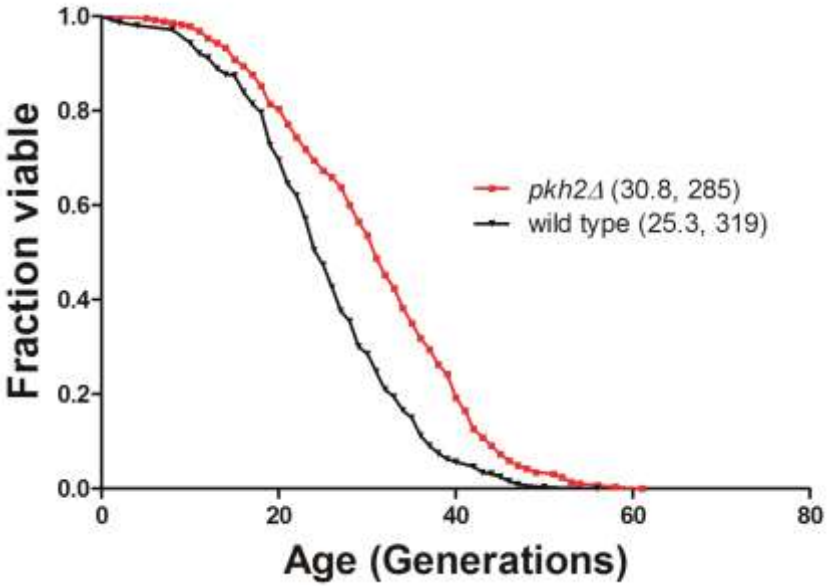

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
pet130Δ (34.8, 85)
wild type (25.7, 105)

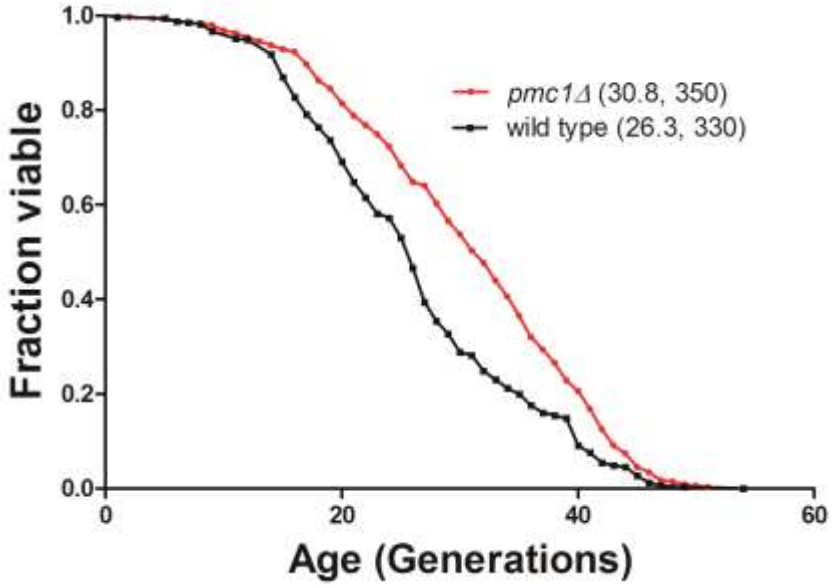

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
pex19Δ (31.7, 124)
wild type (27.2, 145)

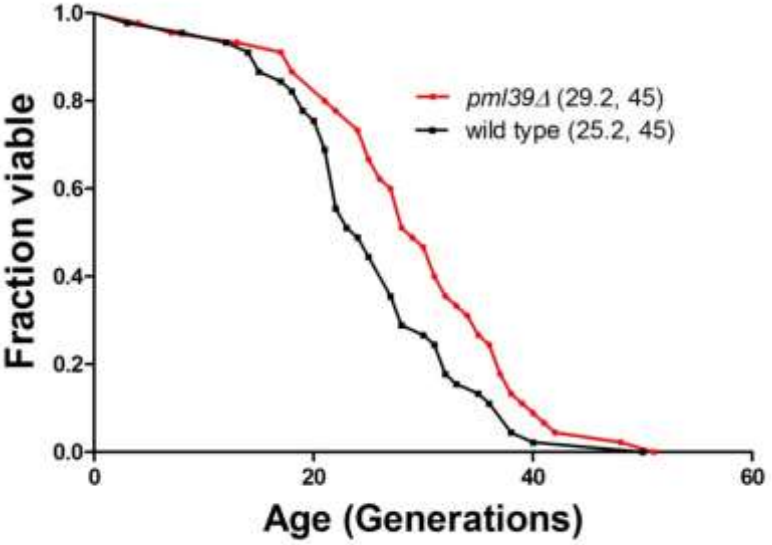

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
pgm2Δ (31.3, 125)
wild type (27.2, 125)

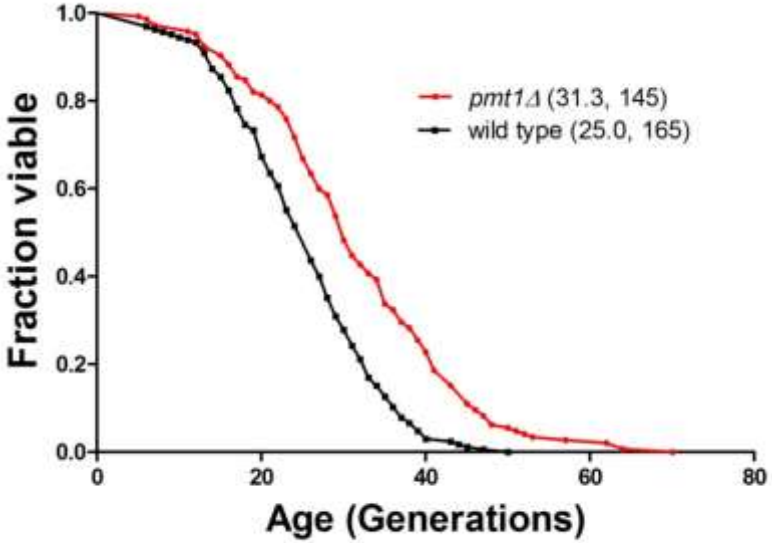

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
pho87Δ (31.4, 65)
wild type (25.8, 85)

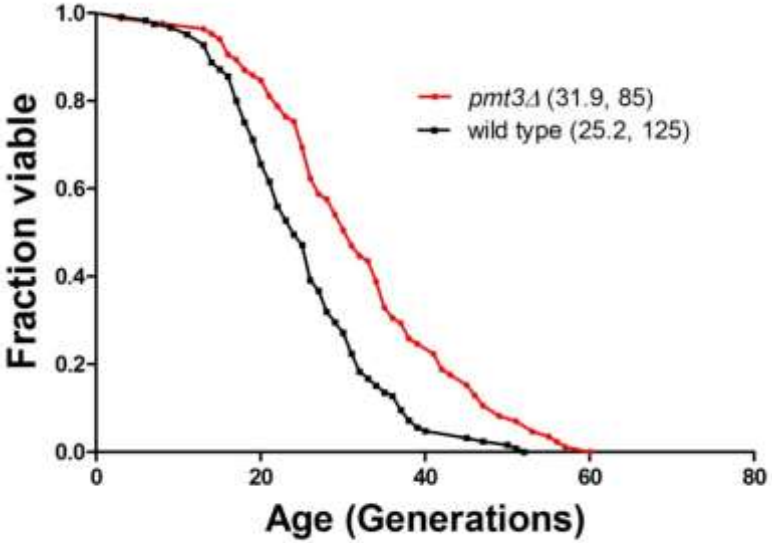

Fraction viable
Age (Generations)
pib1Δ (31.0, 365)
wild type (28.1, 384)

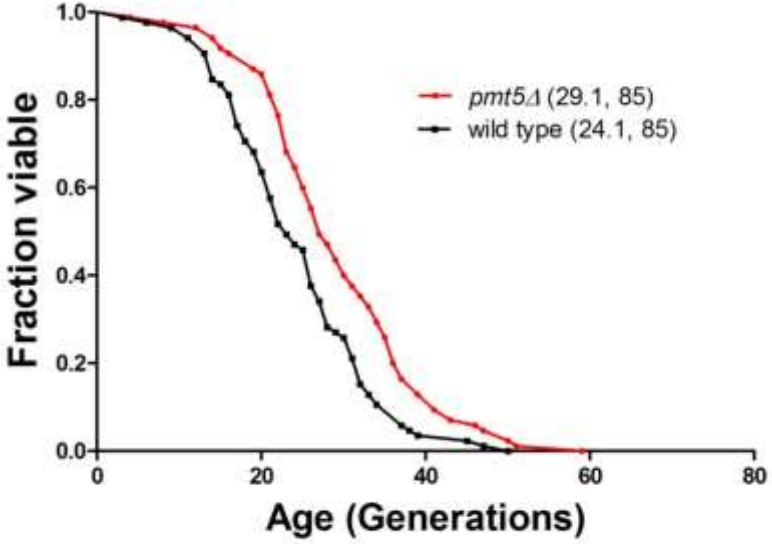

Fraction viable
Age (Generations)
pkh2Δ (30.8, 285)
wild type (25.3, 319)

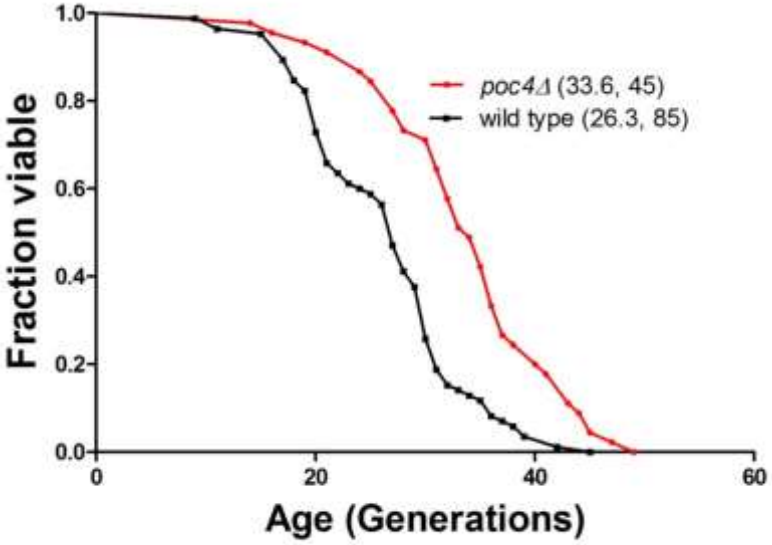

Fraction viable
Age (Generations)
pmc1Δ (30.8, 350)
wild type (26.3, 330)

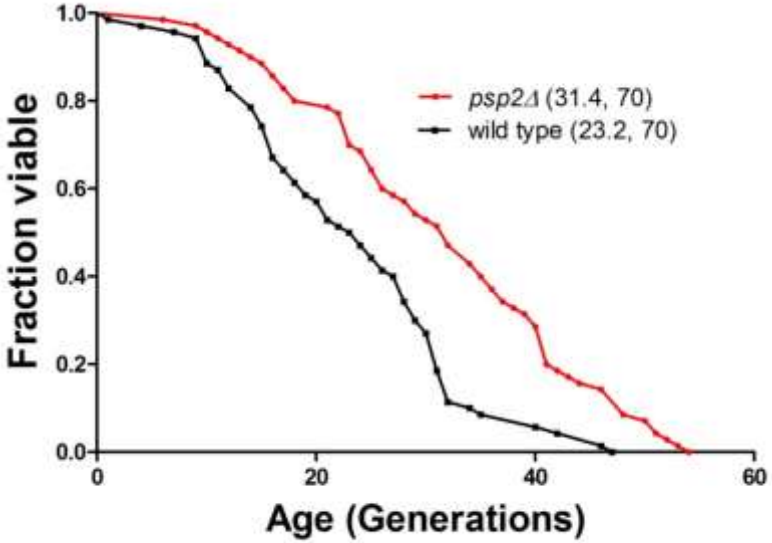

Fraction viable
Age (Generations)
pml39Δ (29.2, 45)
wild type (25.2, 45)

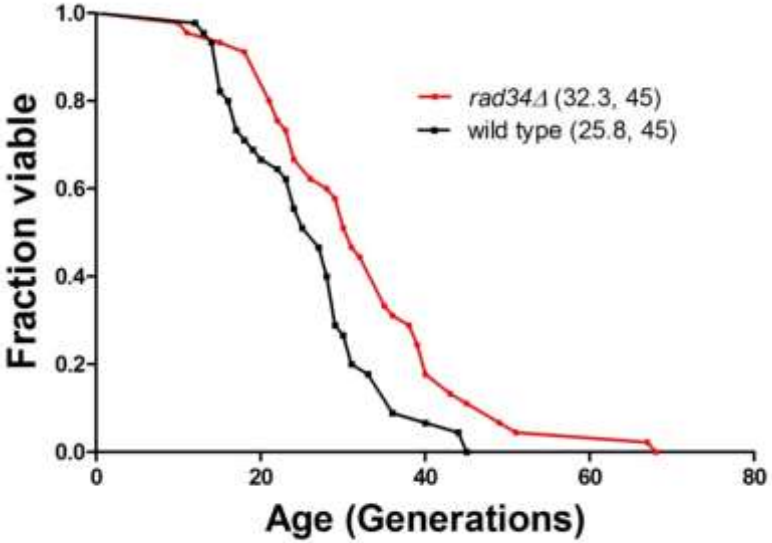

Fraction viable
Age (Generations)
pmt1Δ (31.3, 145)
wild type (25.0, 165)

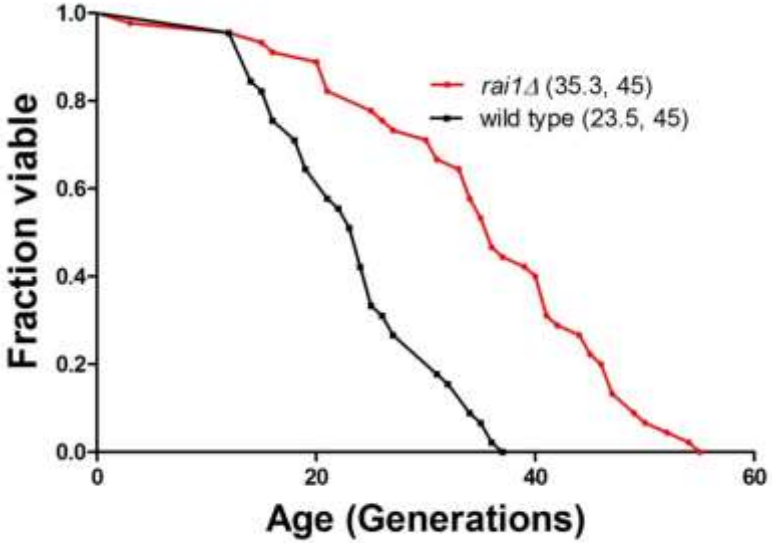

Fraction viable
Age (Generations)
pmt3Δ (31.9, 85)
wild type (25.2, 125)

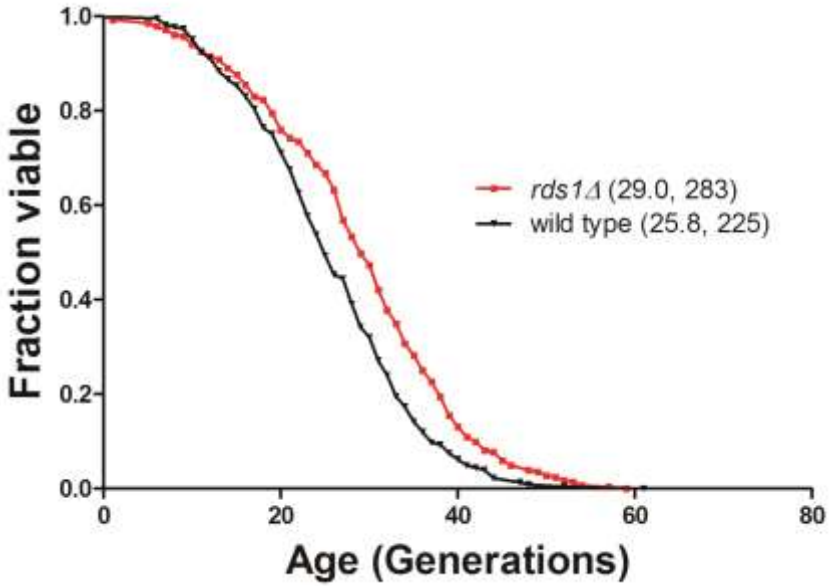

Fraction viable
Age (Generations)
pmt5Δ (29.1, 85)
wild type (24.1, 85)

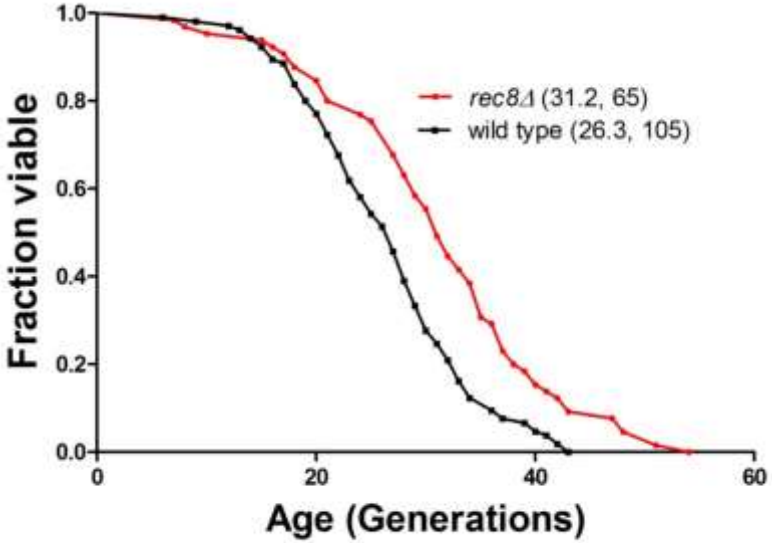

Fraction viable
Age (Generations)
poc4Δ (33.6, 45)
wild type (26.3, 85)

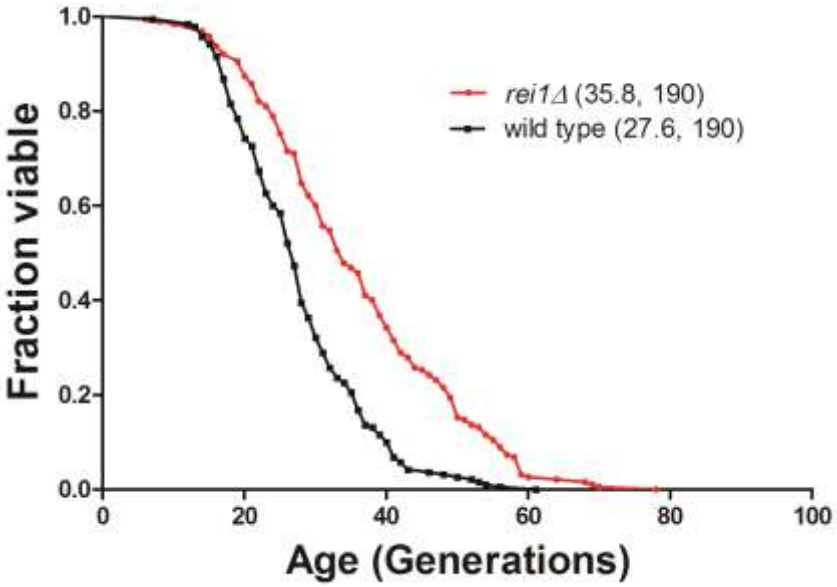

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
psp2Δ (31.4, 70)
wild type (23.2, 70)

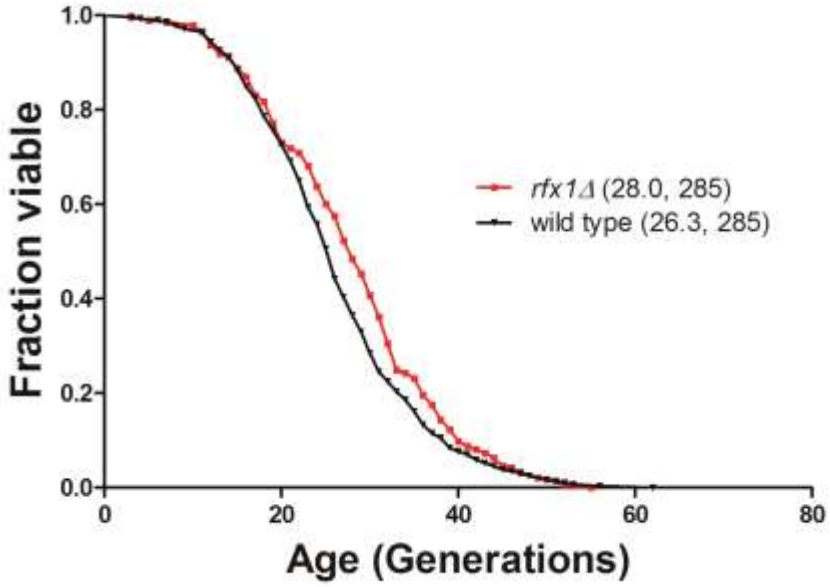

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rad34Δ (32.3, 45)
wild type (25.8, 45)

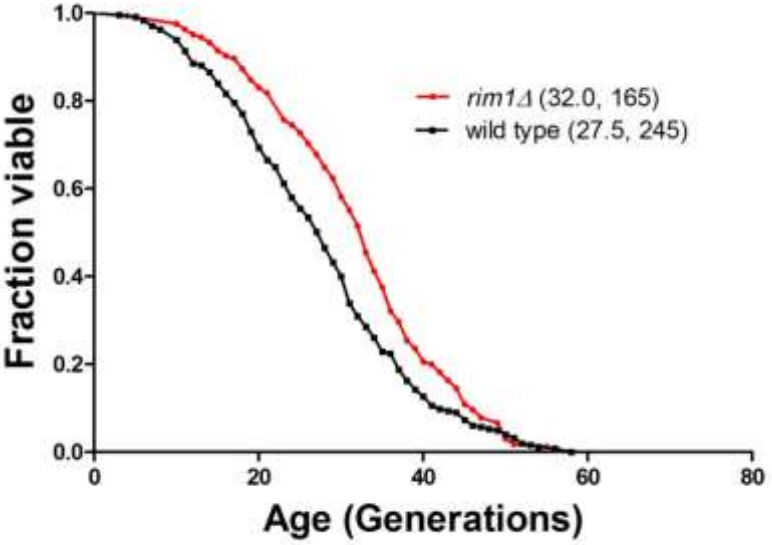

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
rai1Δ (35.3, 45)
wild type (23.5, 45)

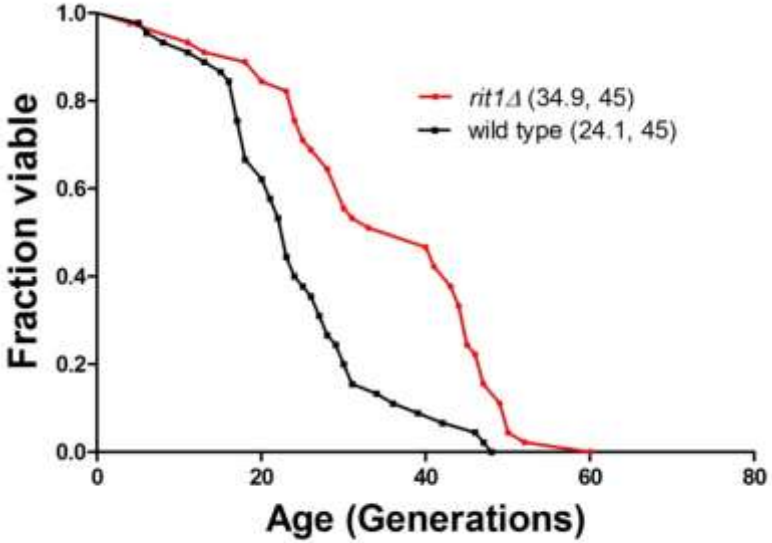

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rds1Δ (29.0, 283)
wild type (25.8, 225)

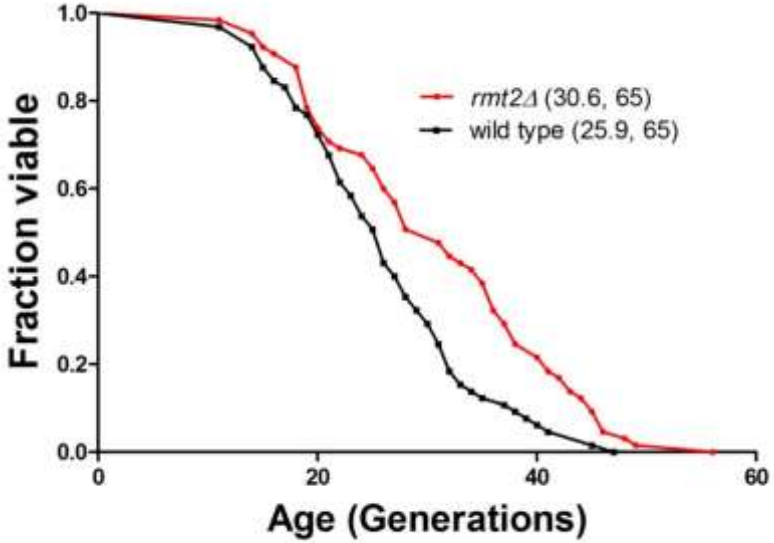

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
rec8Δ (31.2, 65)
wild type (26.3, 105)

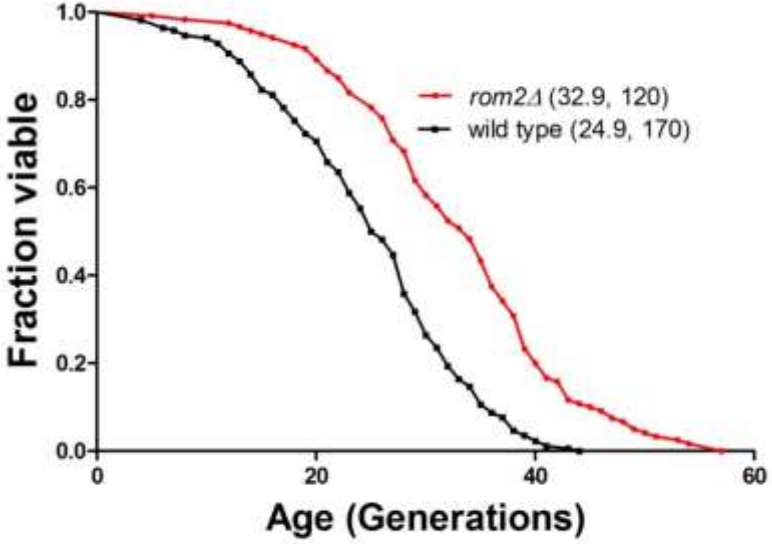

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
Age (Generations)
rei1Δ (35.8, 190)
wild type (27.6, 190)

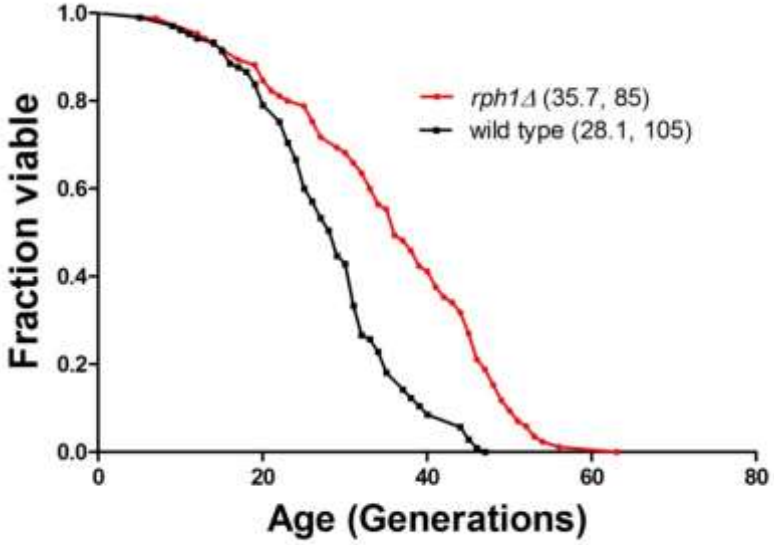

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rfx1Δ (28.0, 285)
wild type (26.3, 285)

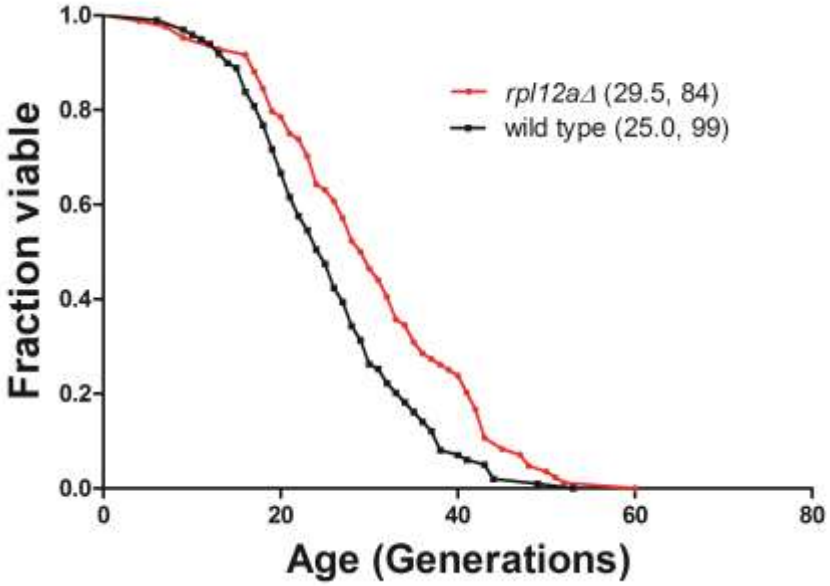

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rim1Δ (32.0, 165)
wild type (27.5, 245)

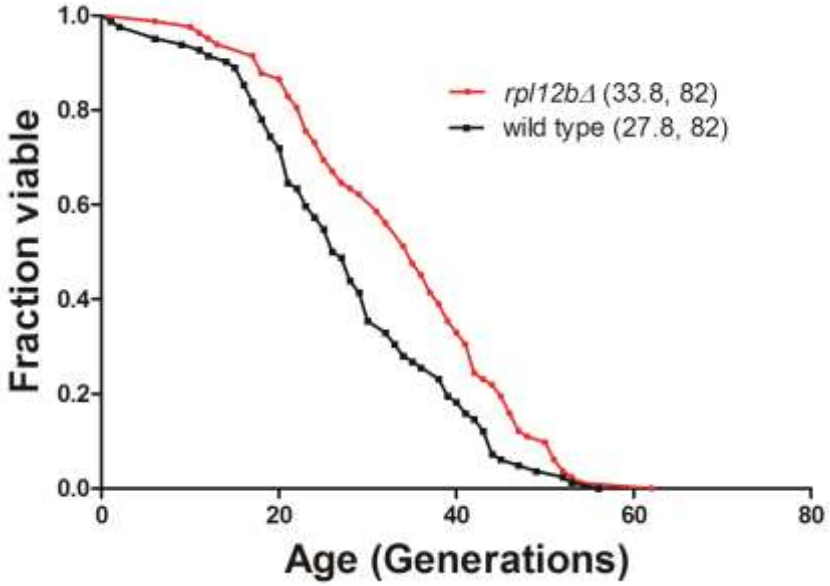

Fraction viable
Age (Generations)
rit1Δ (34.9, 45)
wild type (24.1, 45)

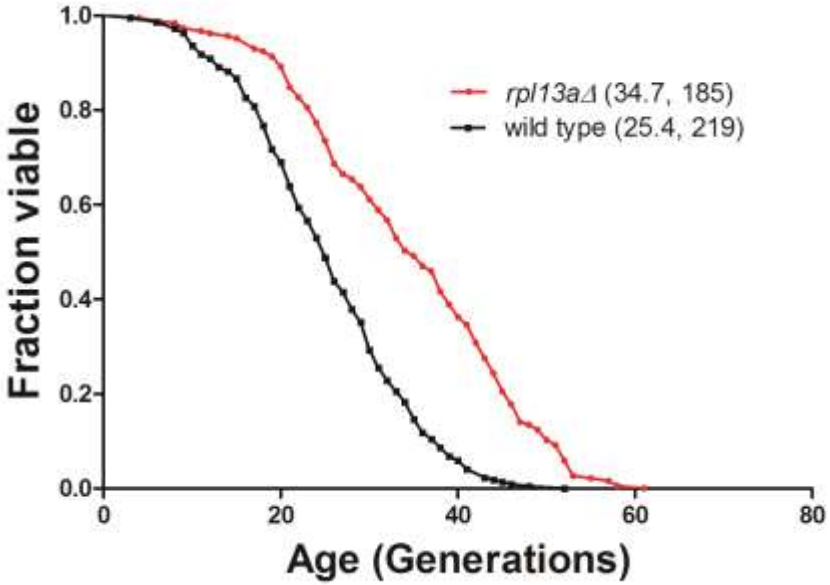

Fraction viable
Age (Generations)
rmt2Δ (30.6, 65)
wild type (25.9, 65)

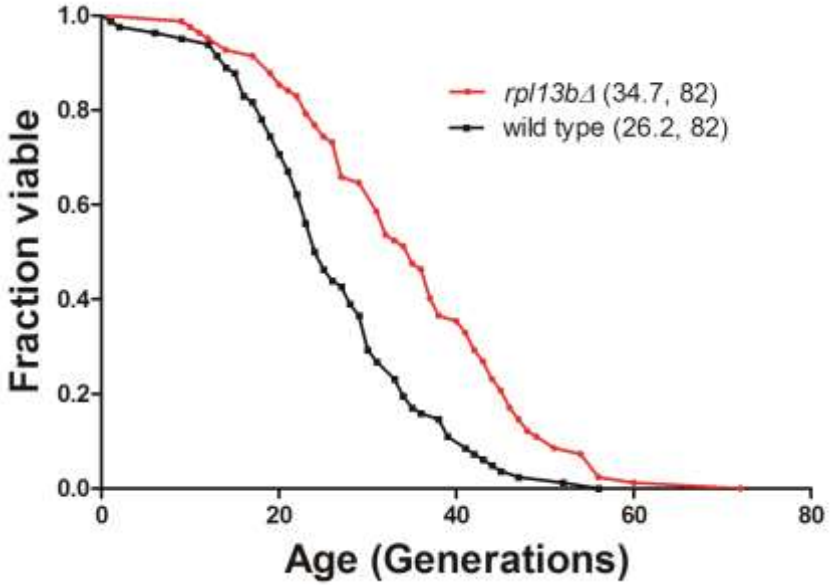

Fraction viable
Age (Generations)
rom2Δ (32.9, 120)
wild type (24.9, 170)

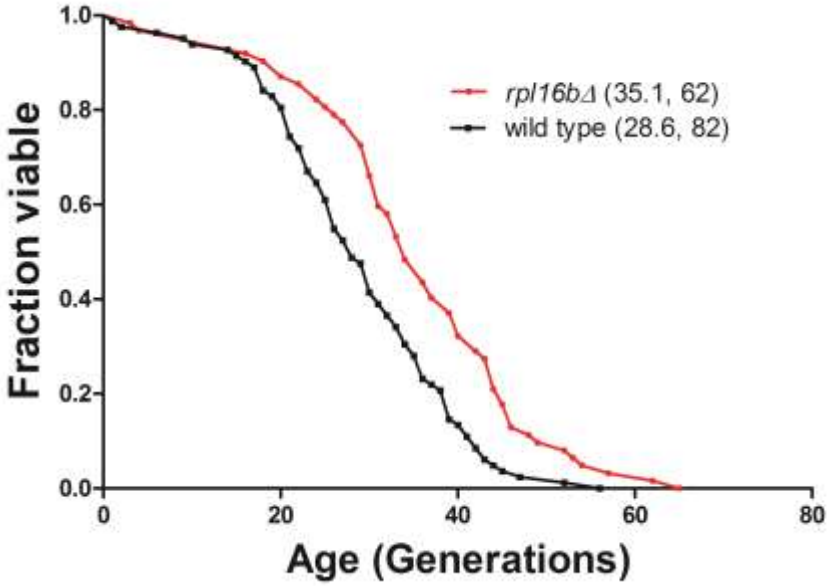

Fraction viable
Age (Generations)
rph1Δ (35.7, 85)
wild type (28.1, 105)

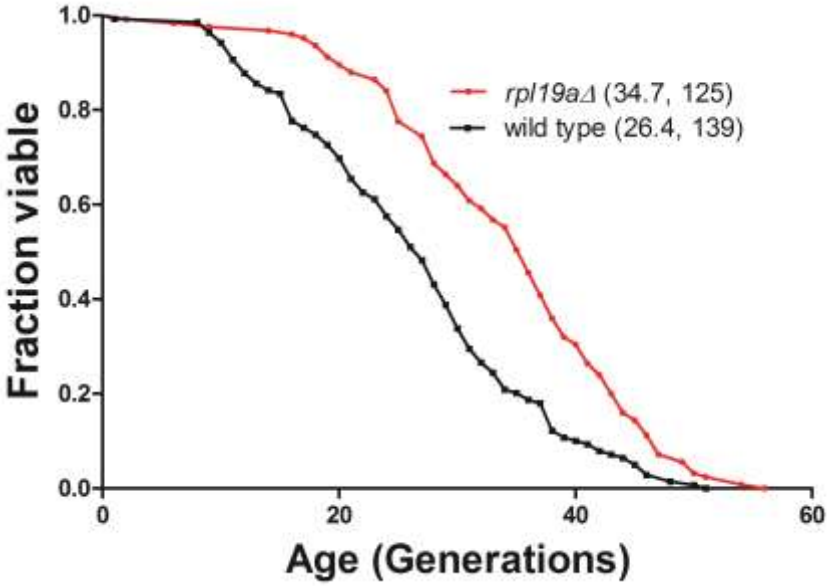

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl12aΔ (29.5, 84)
wild type (25.0, 99)

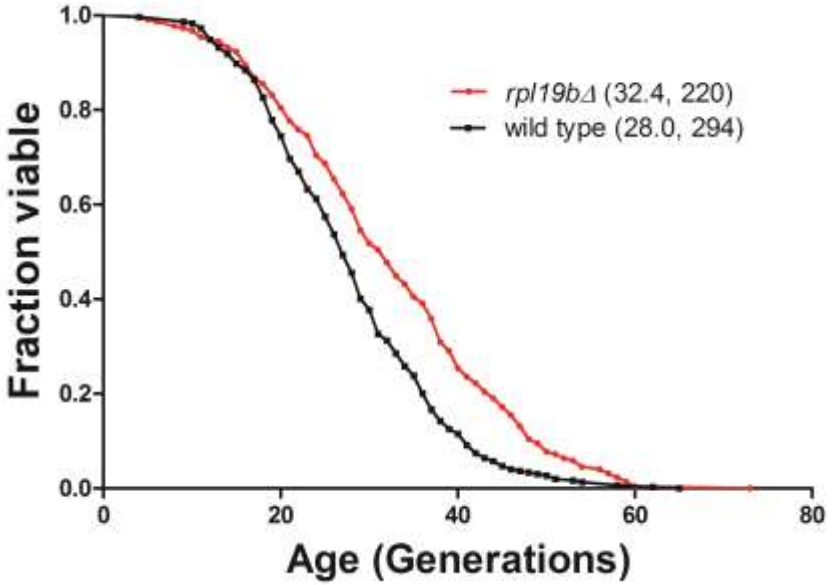

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl12bΔ (33.8, 82)
wild type (27.8, 82)

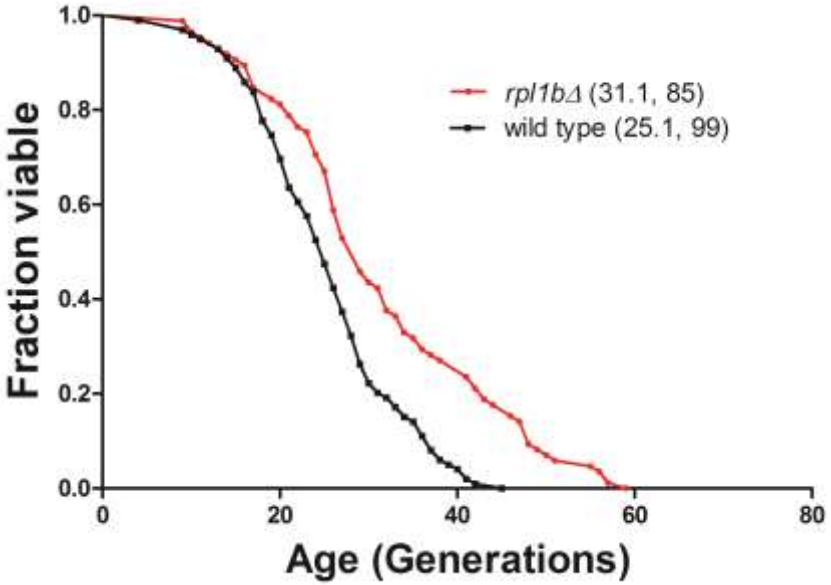

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl13aΔ (34.7, 185)
wild type (25.4, 219)

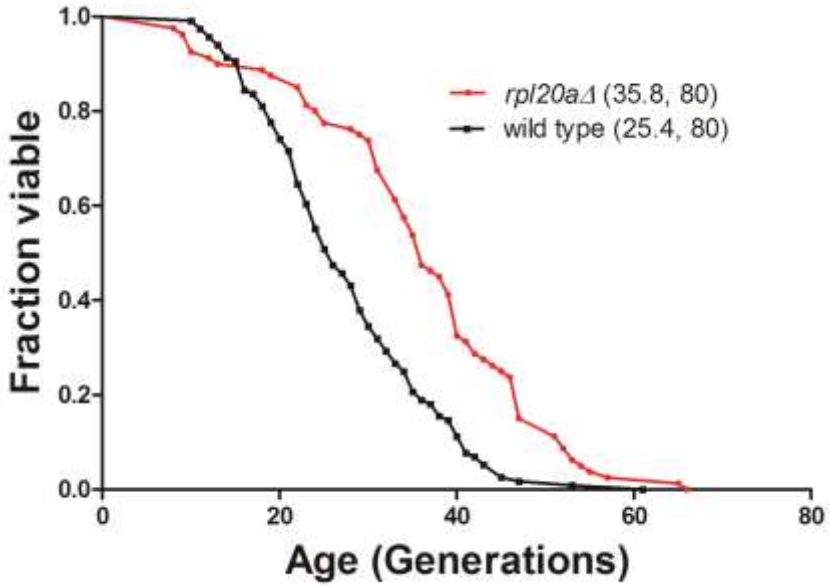

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl13bΔ (34.7, 82)
wild type (26.2, 82)

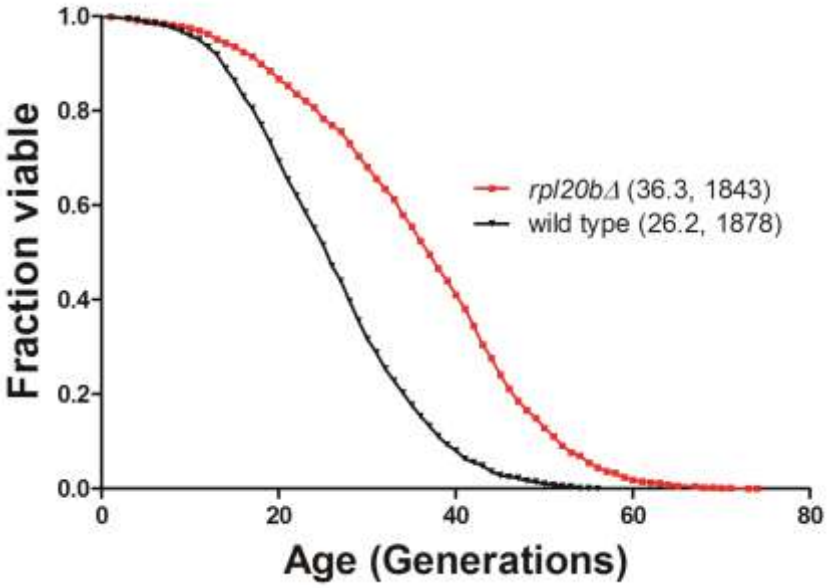

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl16bΔ (35.1, 62)
wild type (28.6, 82)

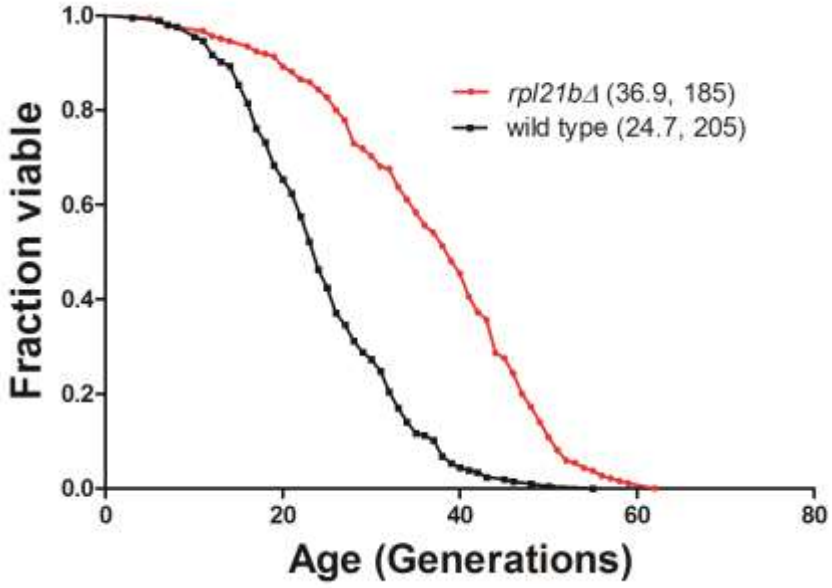

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
rpl19aΔ (34.7, 125)
wild type (26.4, 139)

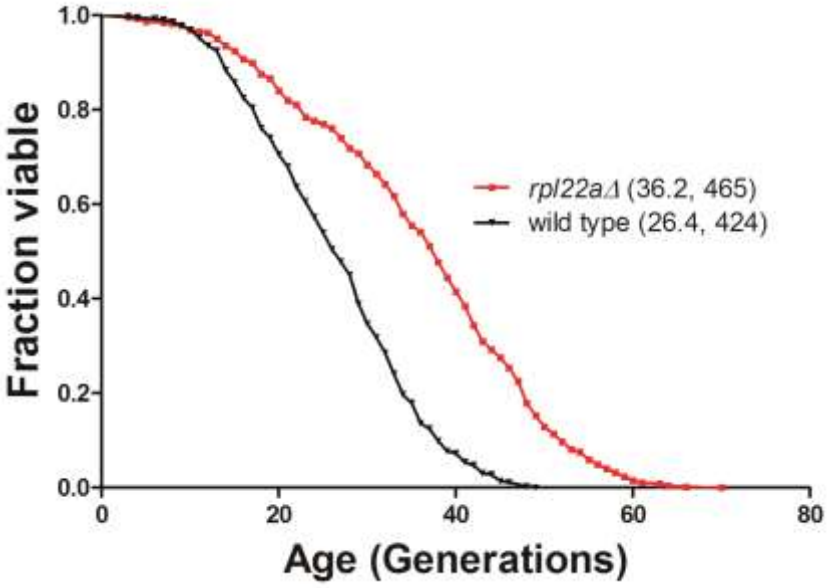

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl19bΔ (32.4, 220)
wild type (28.0, 294)

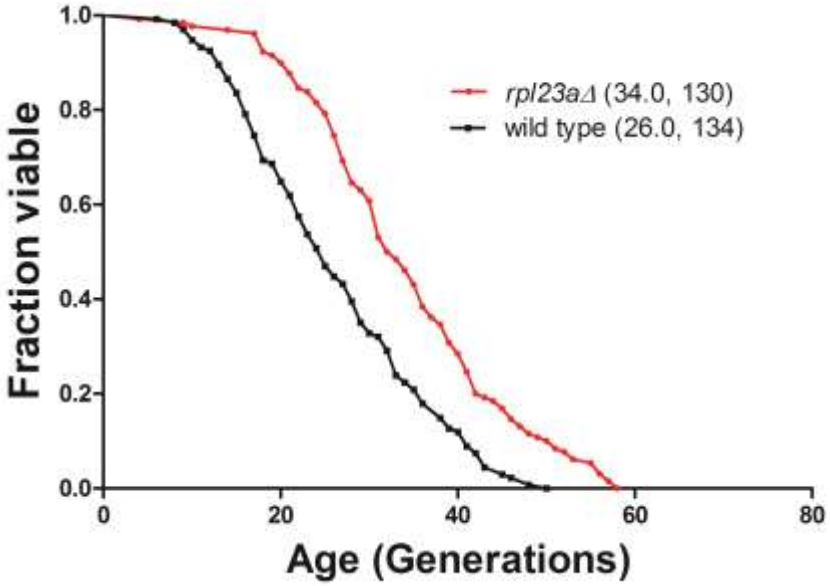

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl1bΔ (31.1, 85)
wild type (25.1, 99)

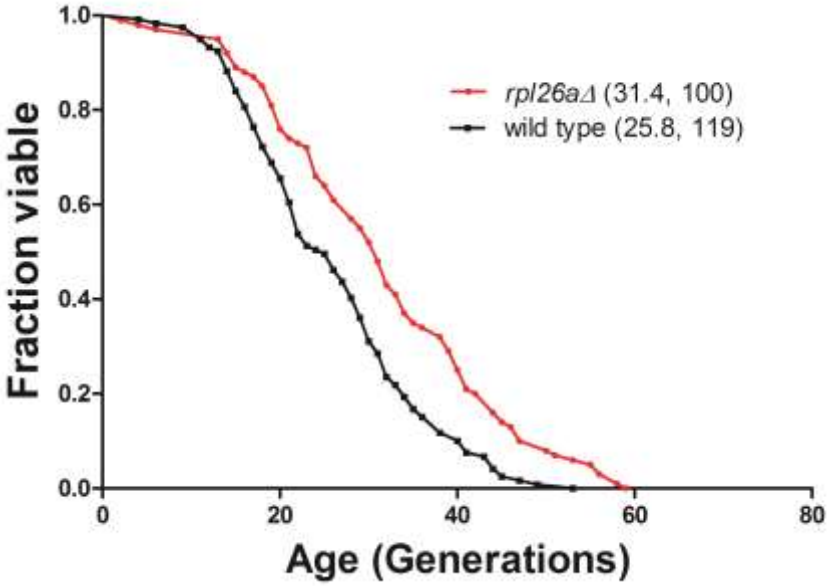

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl20aΔ (35.8, 80)
wild type (25.4, 80)

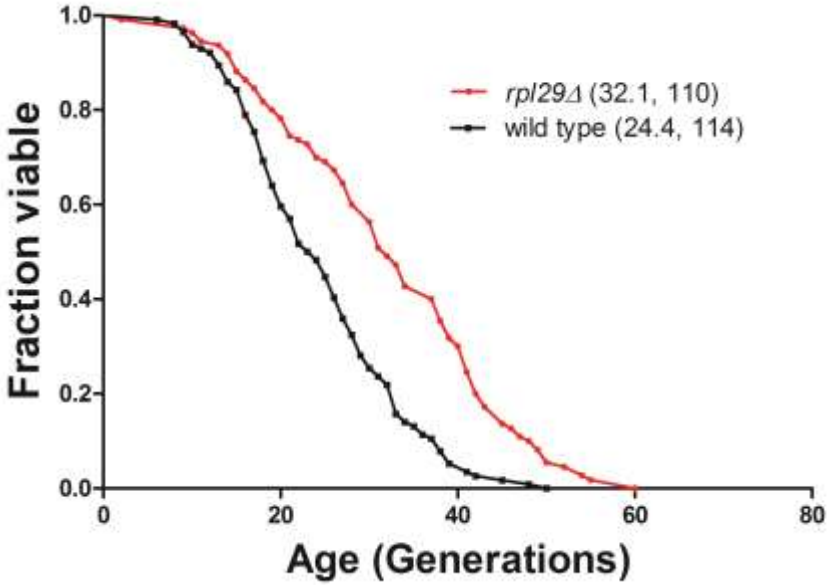

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl20bΔ (36.3, 1843)
wild type (26.2, 1878)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl21bΔ (36.9, 185)
wild type (24.7, 205)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl22aΔ (36.2, 465)
wild type (26.4, 424)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl23aΔ (34.0, 130)
wild type (26.0, 134)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl26aΔ (31.4, 100)
wild type (25.8, 119)


Fraction viable
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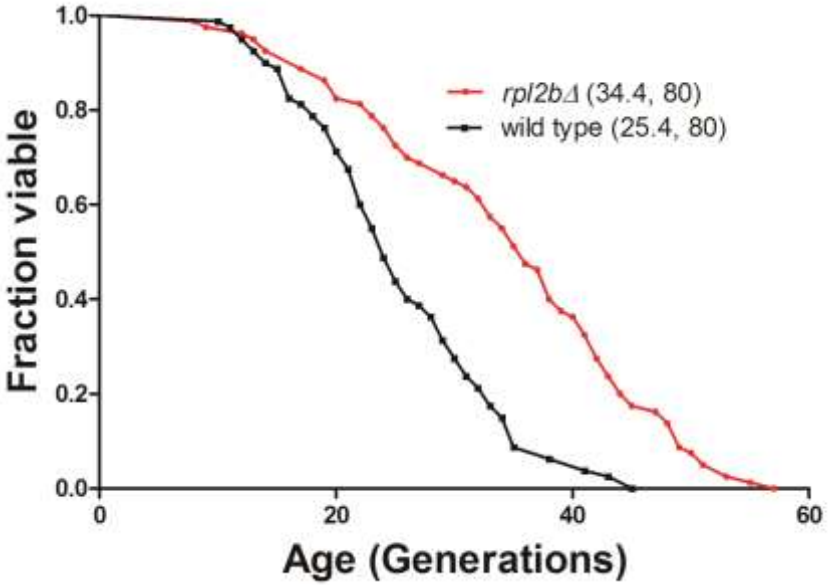
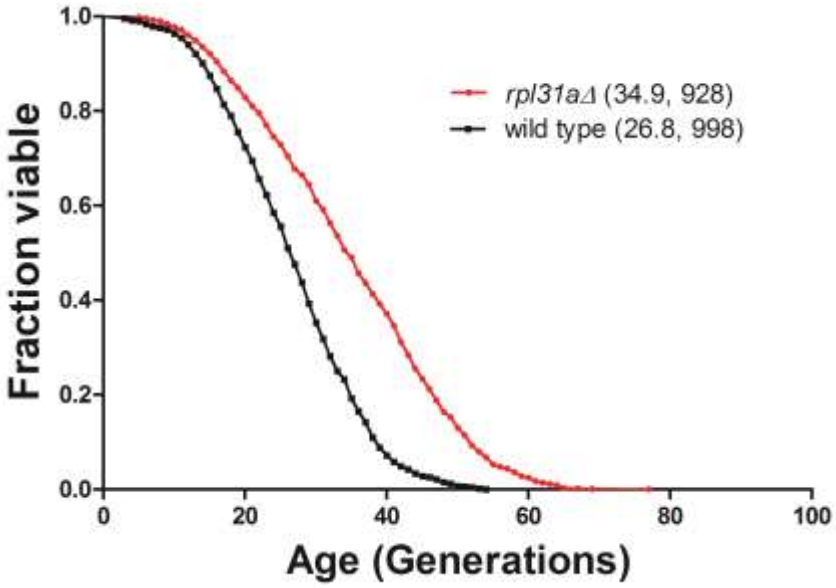
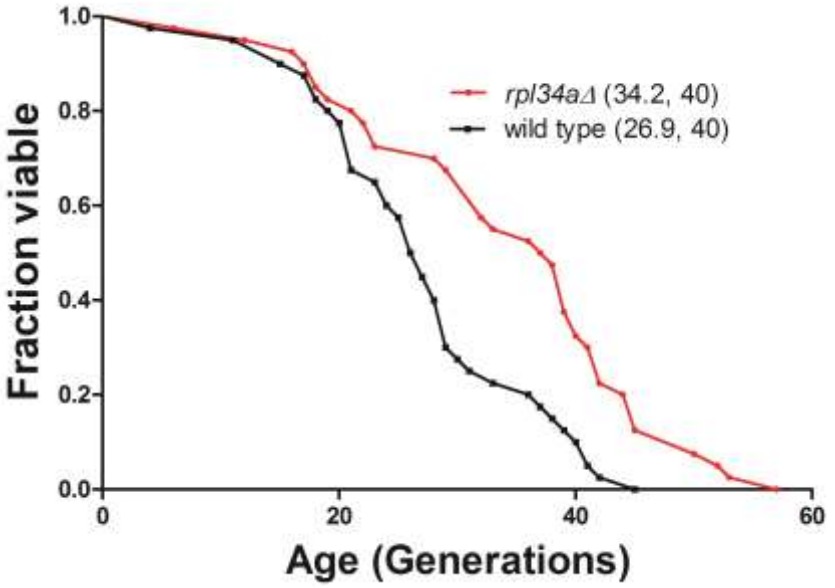
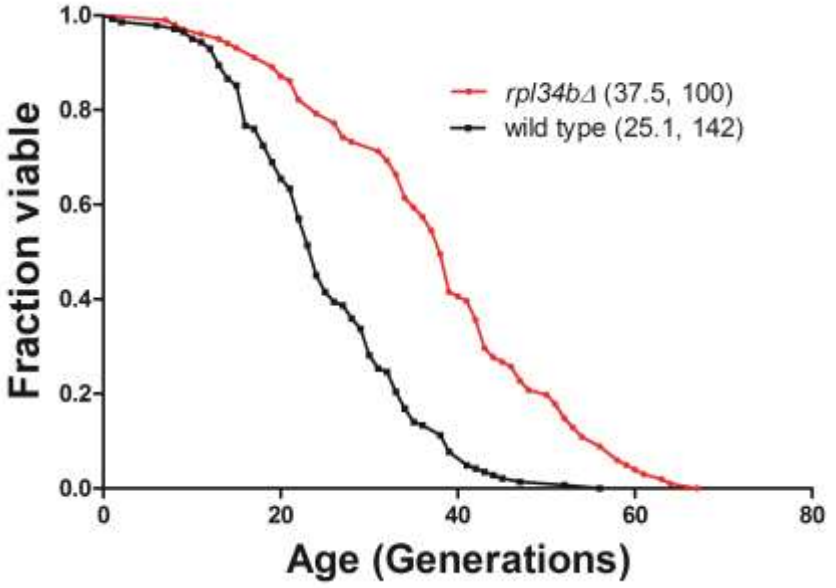
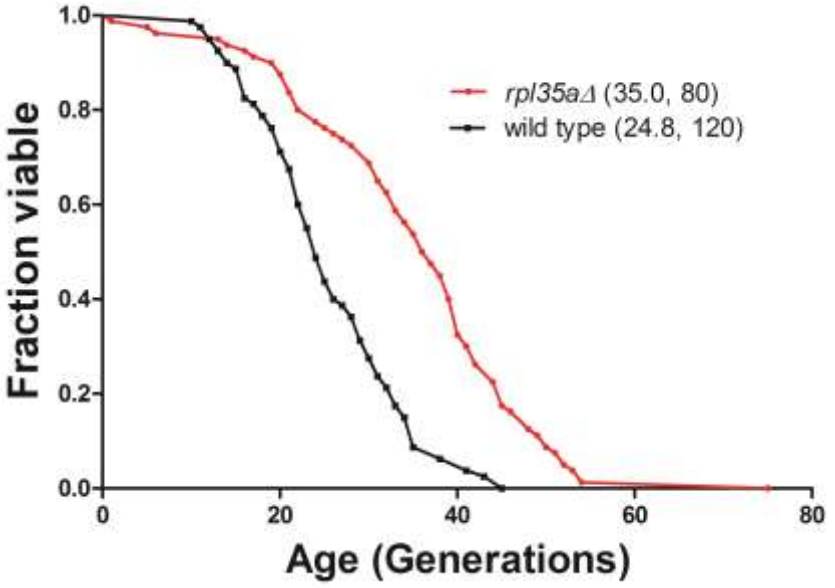
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl29Δ (32.1, 110)
wild type (24.4, 114)

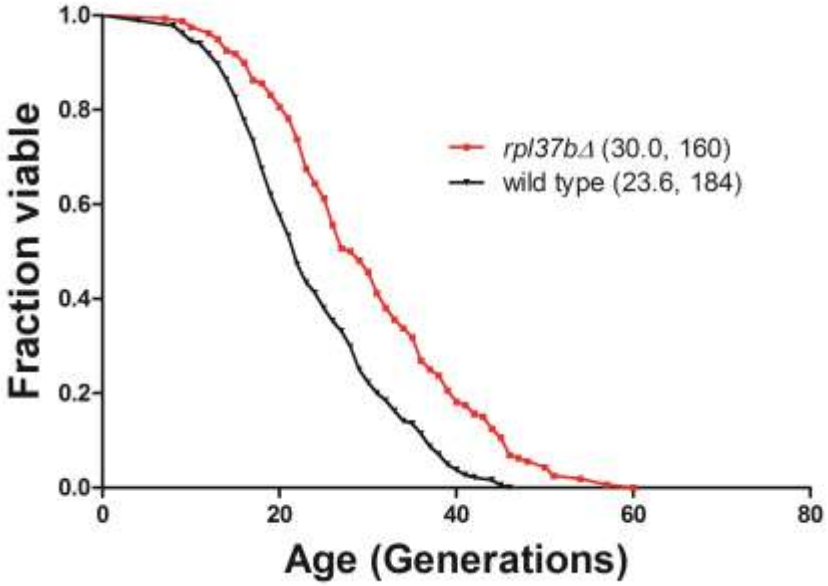

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
rpl2bΔ (34.4, 80)
wild type (25.4, 80)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
Age (Generations)
rpl31aΔ (34.9, 928)
wild type (26.8, 998)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
rpl34aΔ (34.2, 40)
wild type (26.9, 40)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl34bΔ (37.5, 100)
wild type (25.1, 142)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl35aΔ (35.0, 80)
wild type (24.8, 120)


Fraction viable
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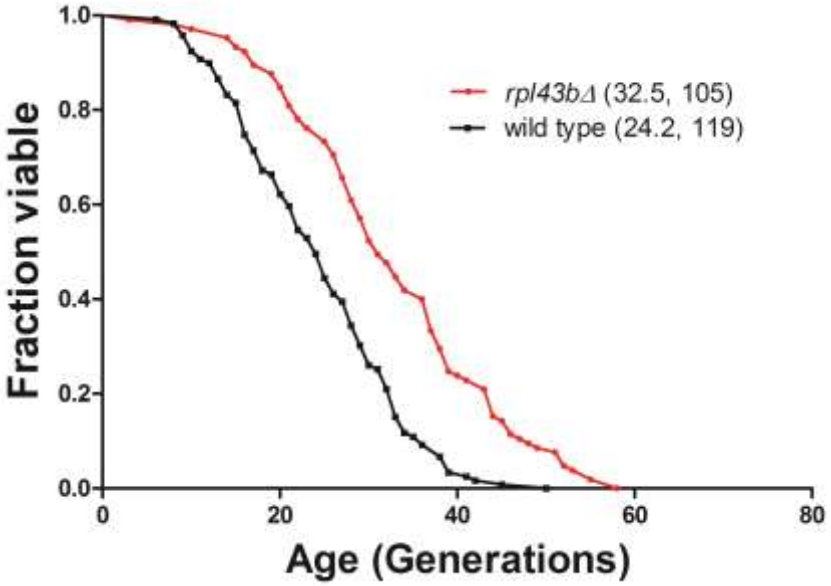
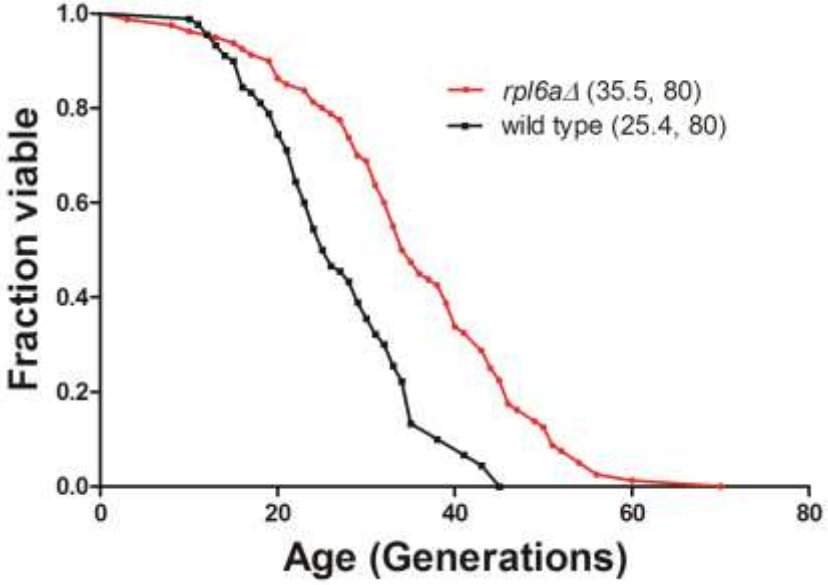
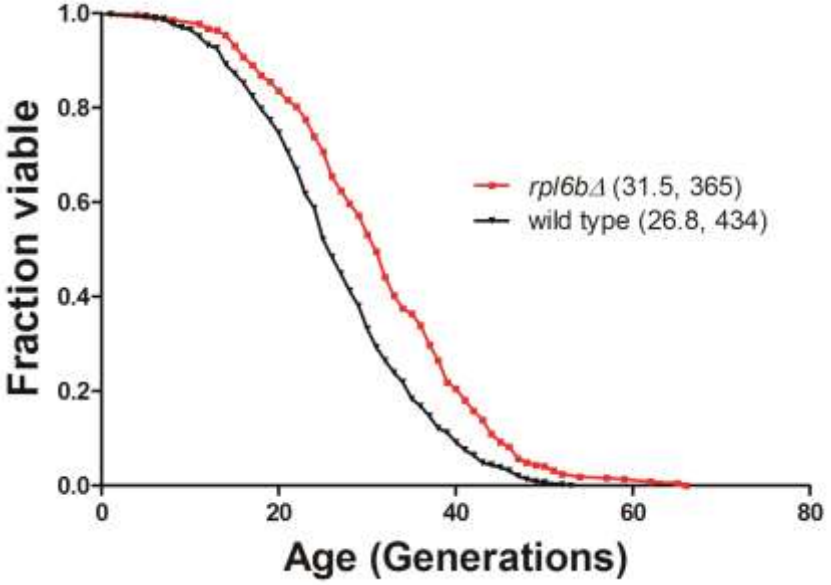
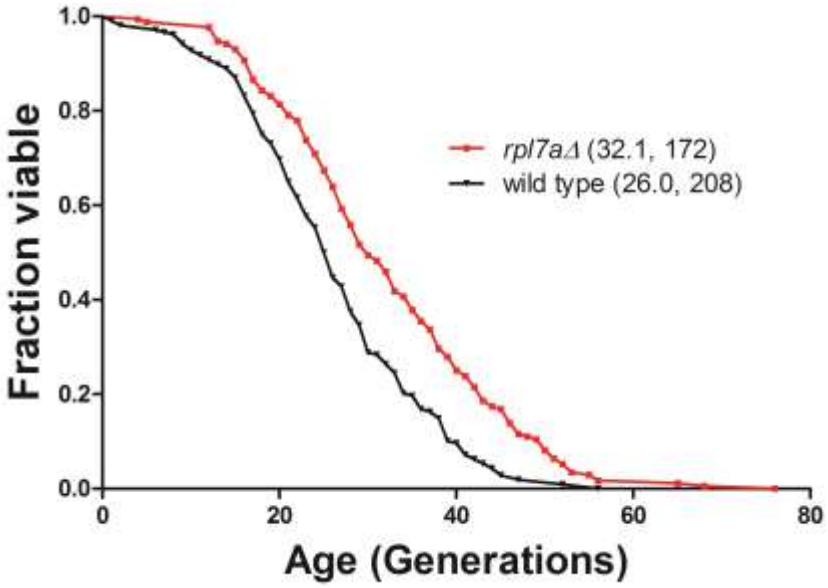
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl37bΔ (30.0, 160)
wild type (23.6, 184)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl43bΔ (32.5, 105)
wild type (24.2, 119)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl6aΔ (35.5, 80)
wild type (25.4, 80)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl6bΔ (31.5, 365)
wild type (26.8, 434)


Fraction viable
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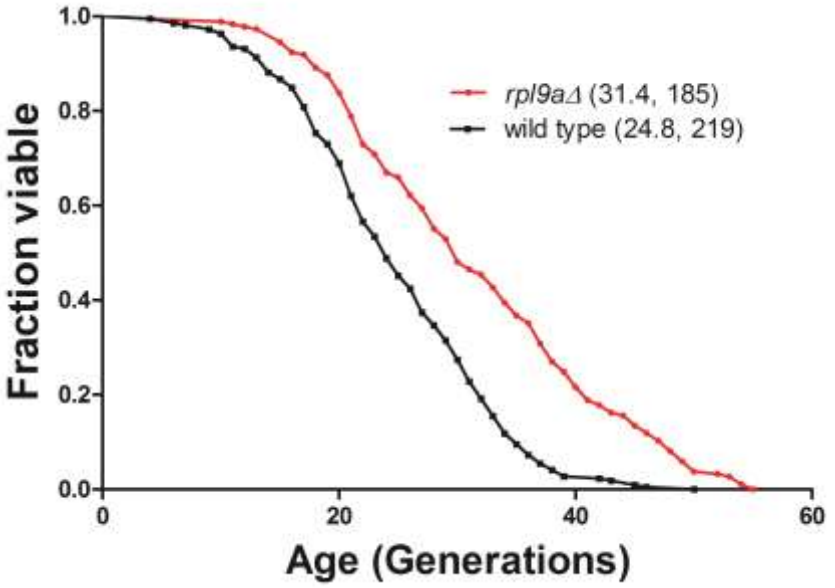
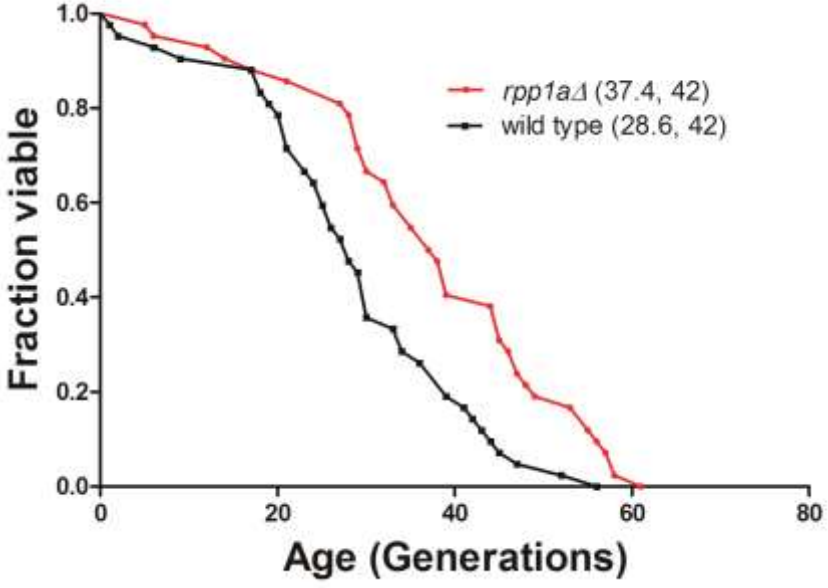
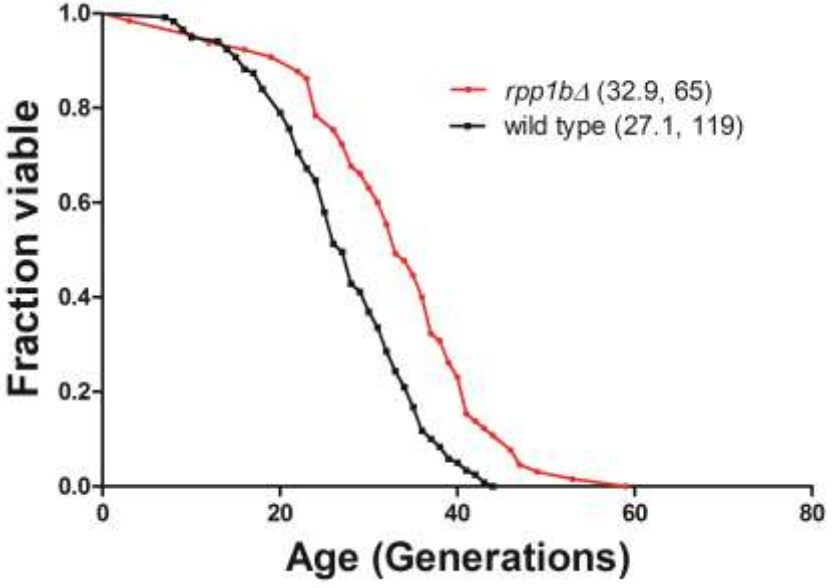
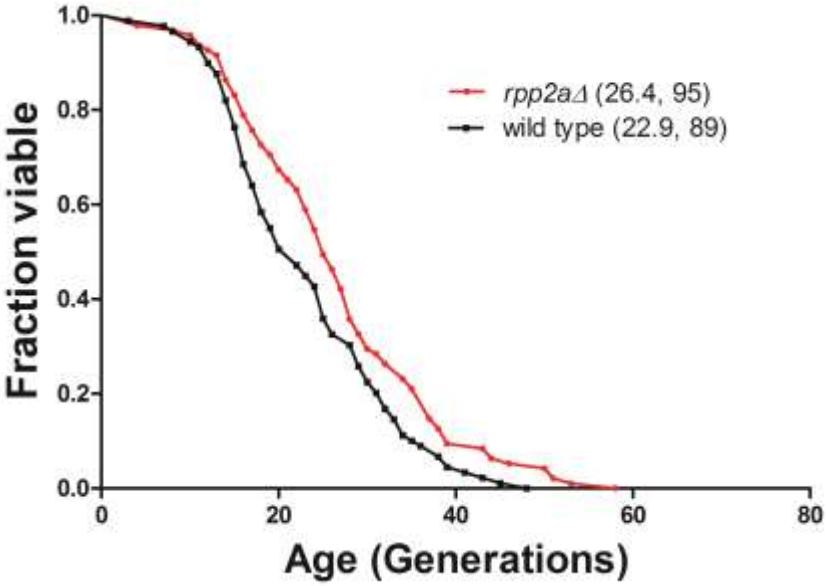
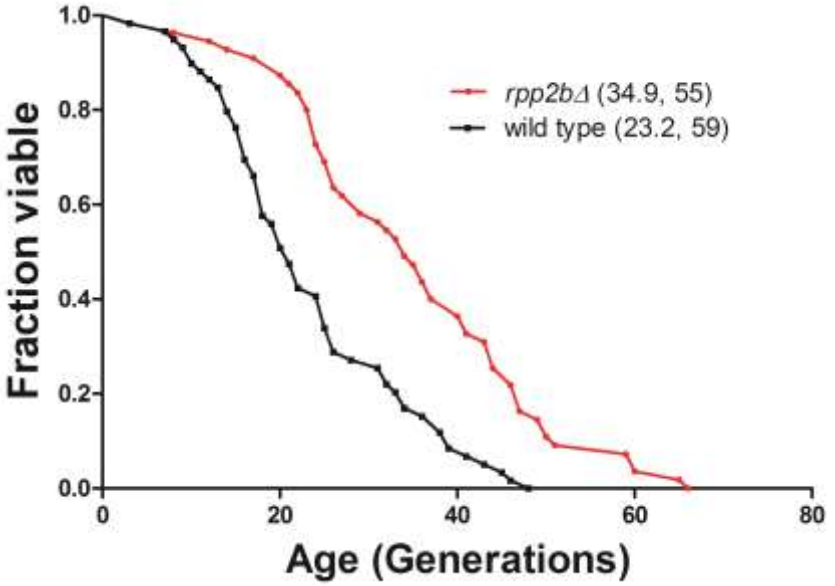
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpl7aΔ (32.1, 172)
wild type (26.0, 208)

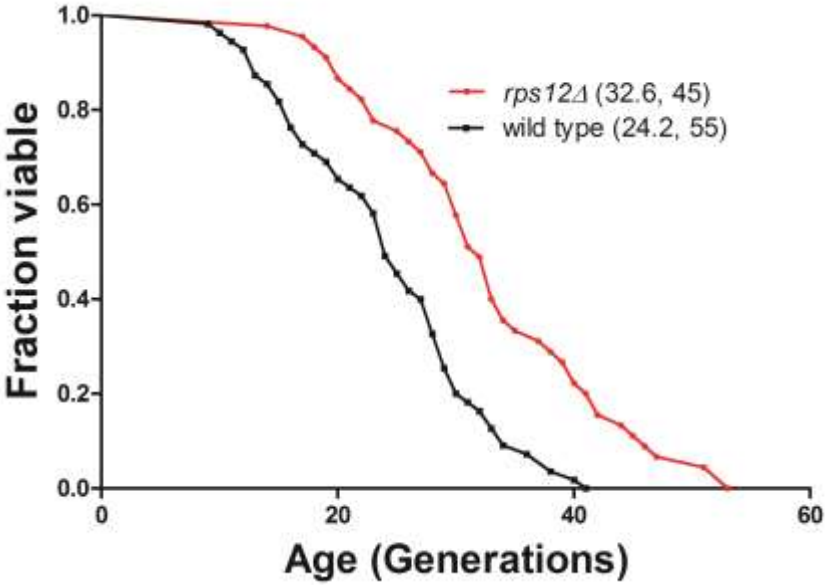

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
rpl9aΔ (31.4, 185)
wild type (24.8, 219)

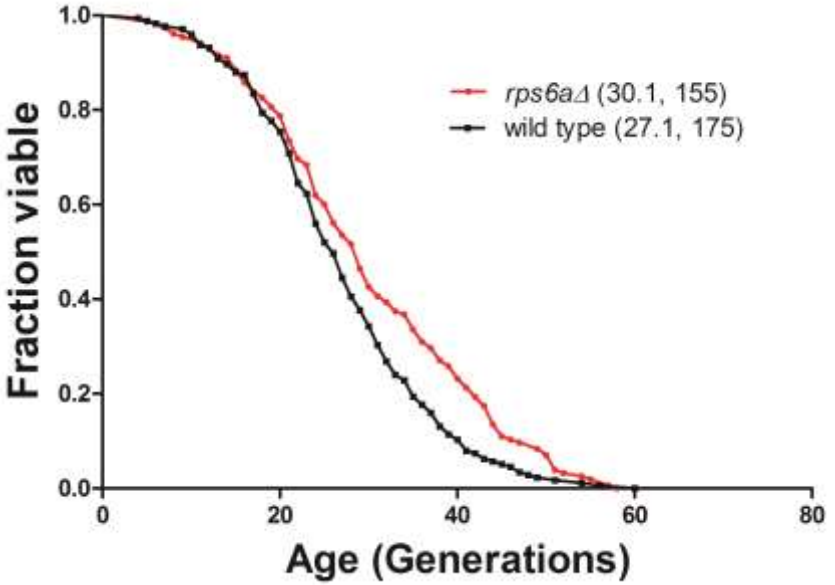

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpp1aΔ (37.4, 42)
wild type (28.6, 42)

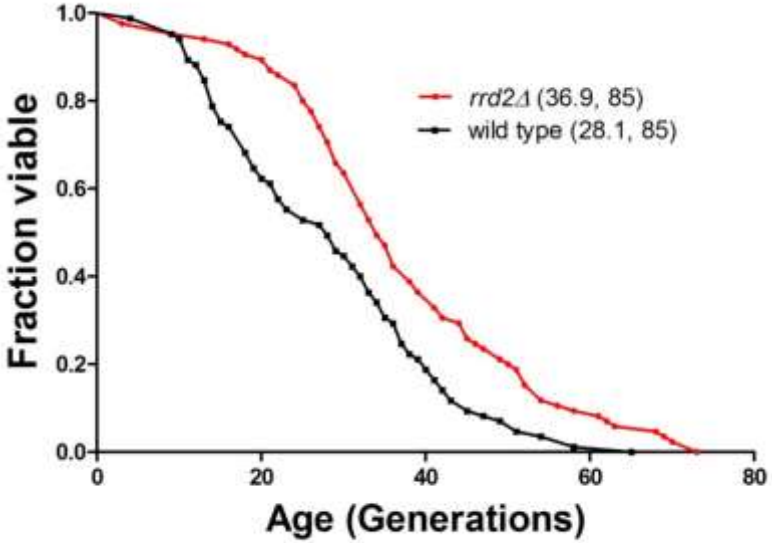

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpp1bΔ (32.9, 65)
wild type (27.1, 119)

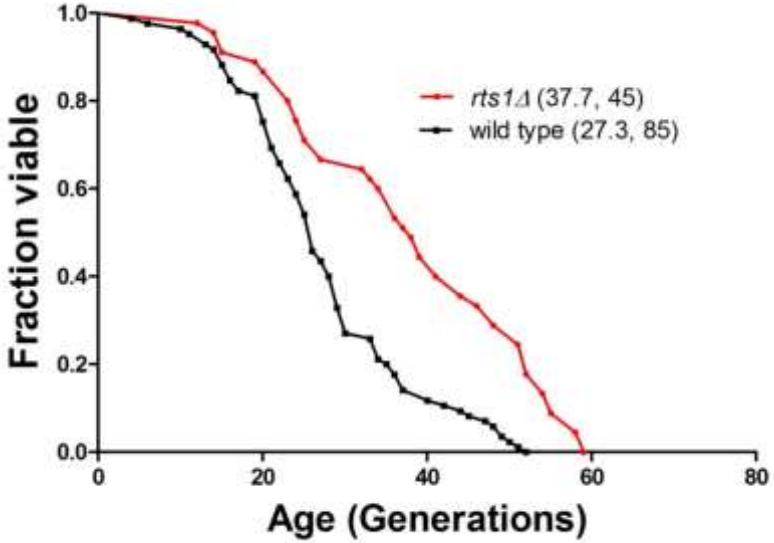

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpp2aΔ (26.4, 95)
wild type (22.9, 89)

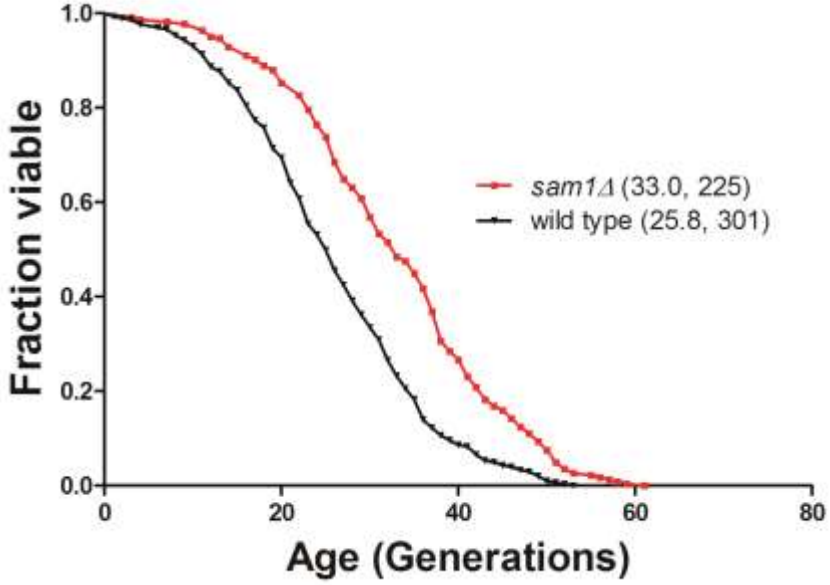

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rpp2bΔ (34.9, 55)
wild type (23.2, 59)

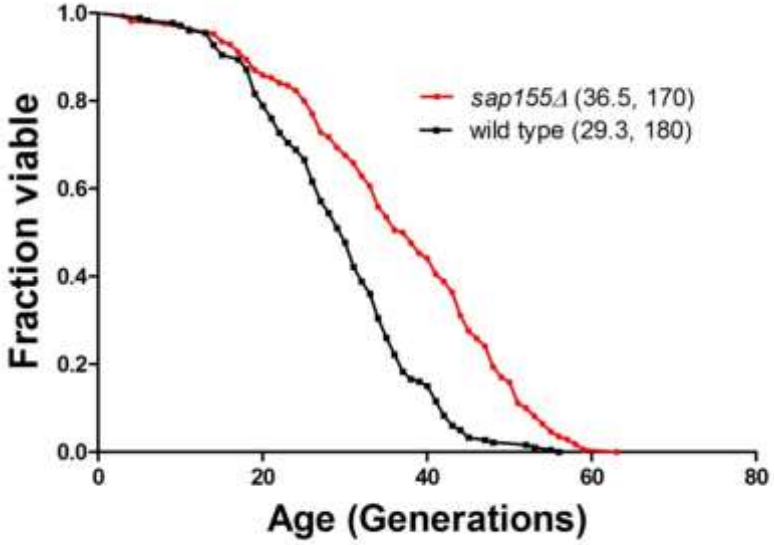

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
rps12Δ (32.6, 45)
wild type (24.2, 55)

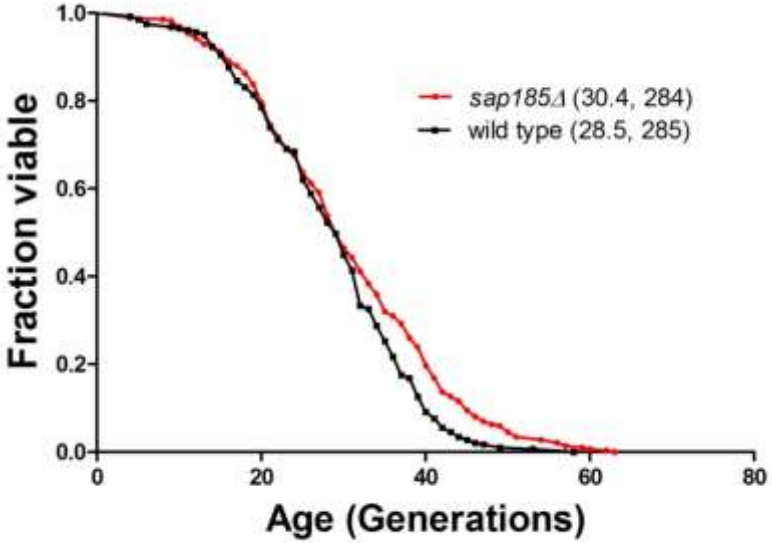

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rps6aΔ (30.1, 155)
wild type (27.1, 175)

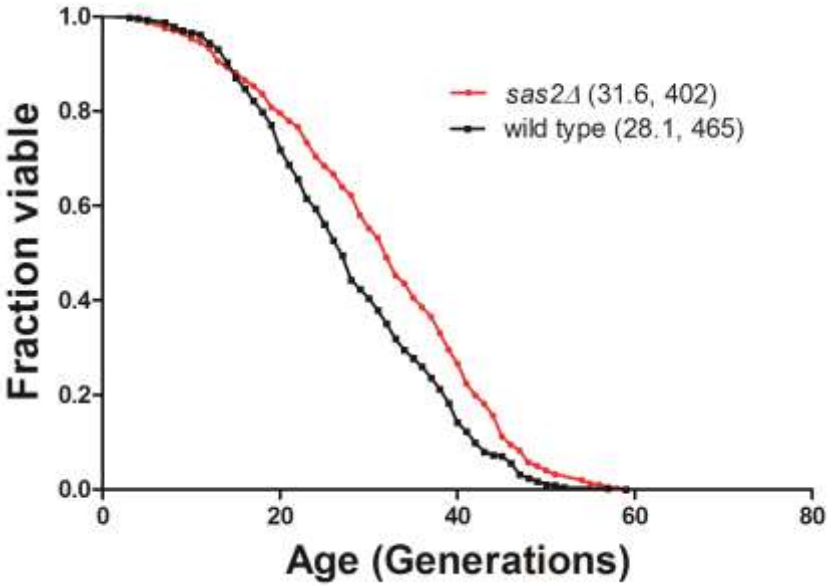

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rrd2Δ (36.9, 85)
wild type (28.1, 85)

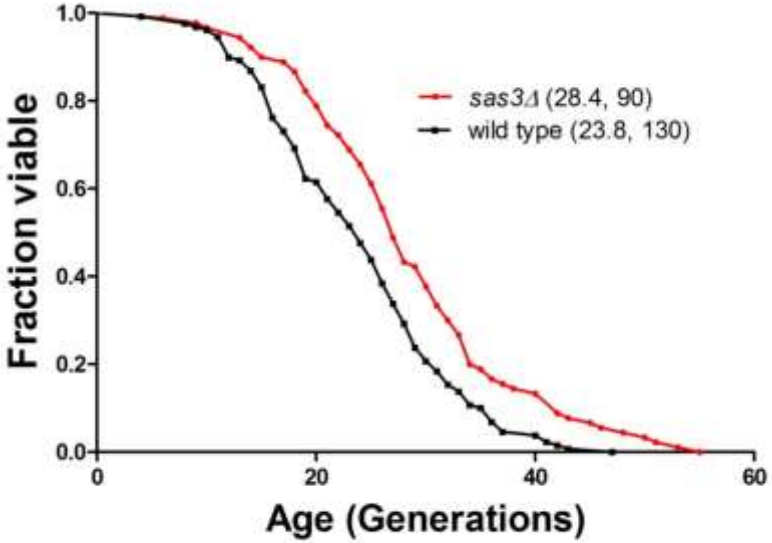

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
rts1Δ (37.7, 45)
wild type (27.3, 85)

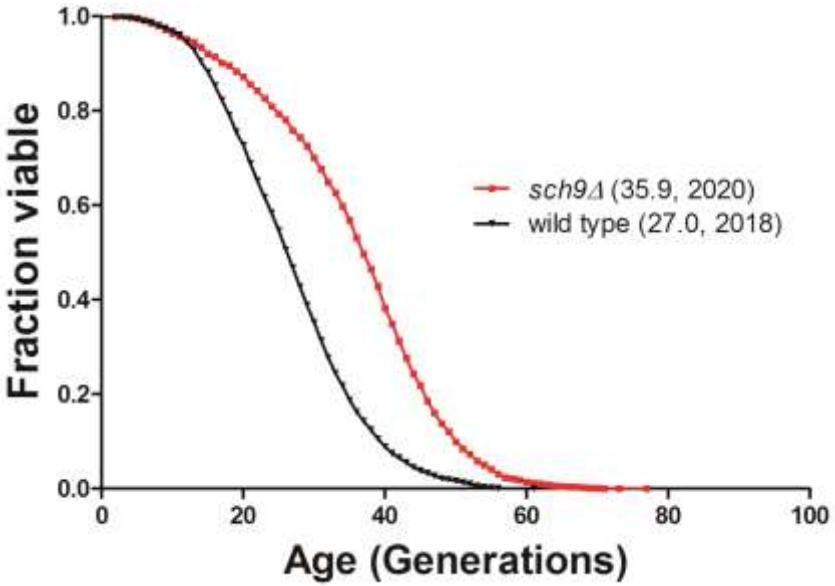

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
sam1Δ (33.0, 225)
wild type (25.8, 301)

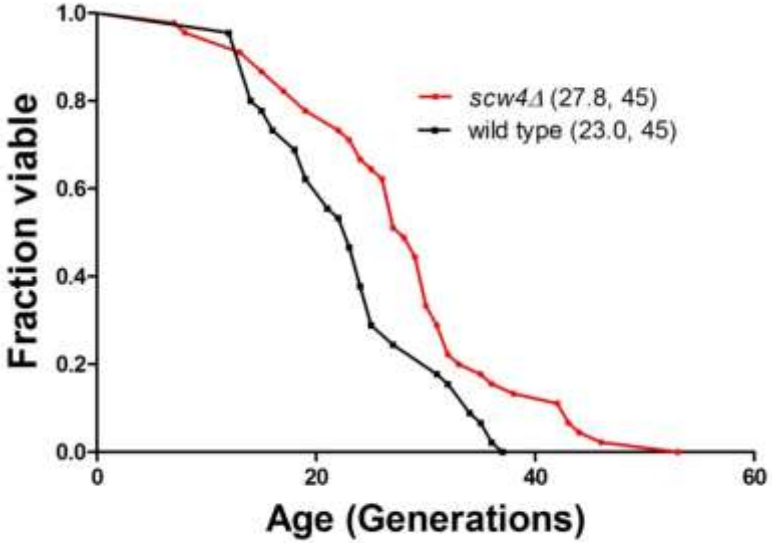

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
sap155Δ (36.5, 170)
wild type (29.3, 180)

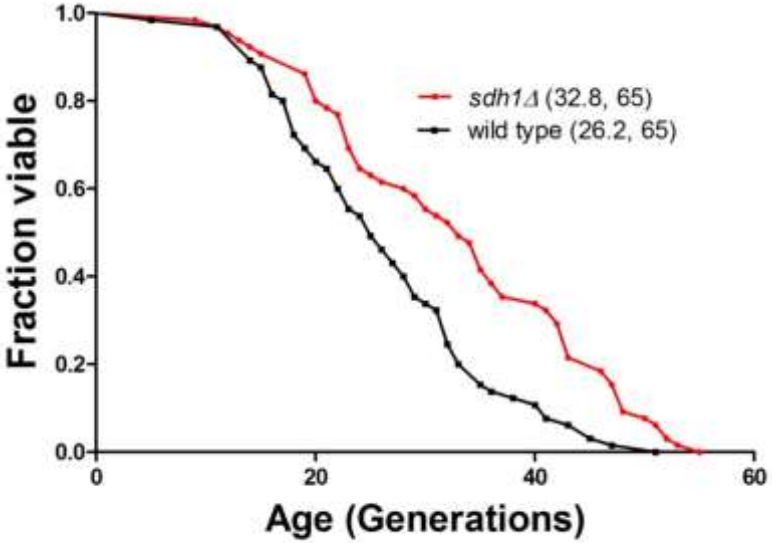

Fraction viable
Age (Generations)
sap185Δ (30.4, 284)
wild type (28.5, 285)

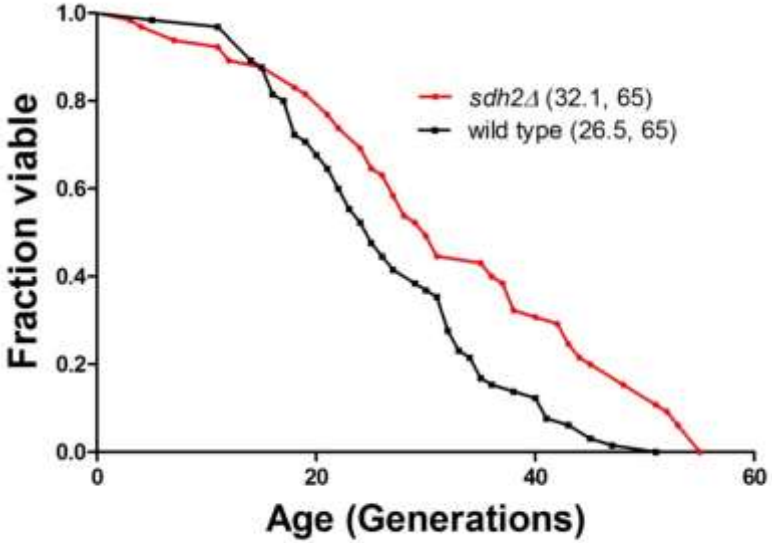

Fraction viable
Age (Generations)
sas2Δ (31.6, 402)
wild type (28.1, 465)

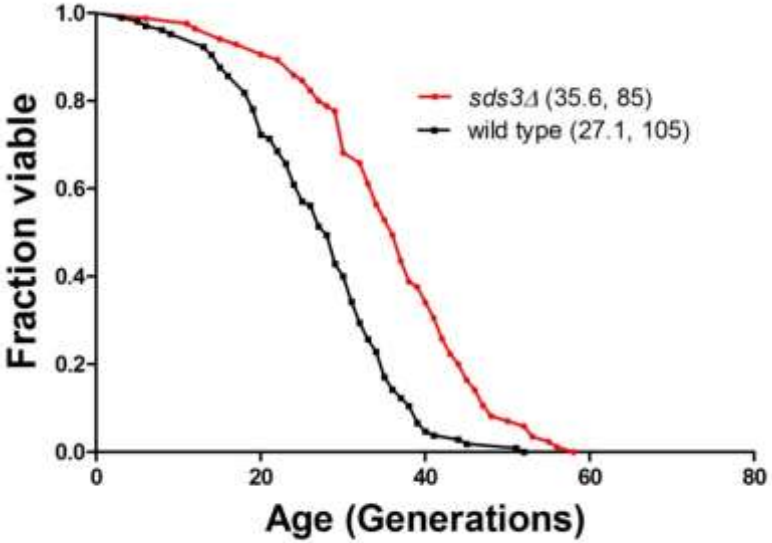

Fraction viable
Age (Generations)
sas3Δ (28.4, 90)
wild type (23.8, 130)

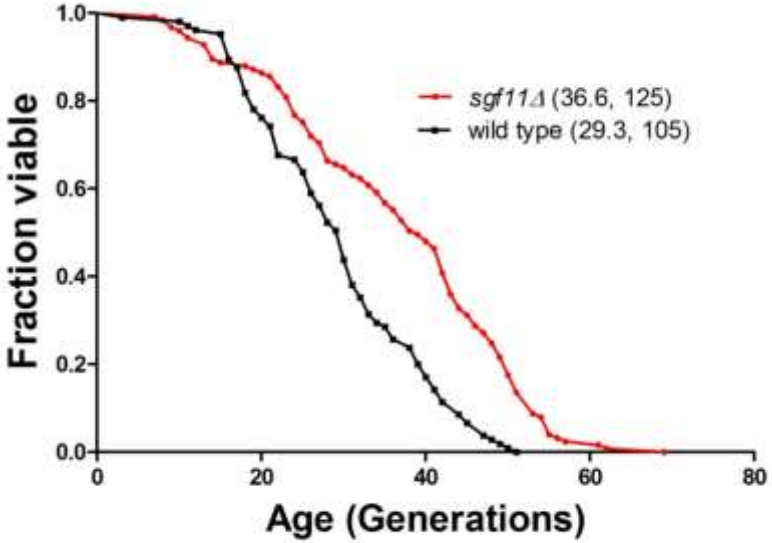

Fraction viable
Age (Generations)
sch9Δ (35.9, 2020)
wild type (27.0, 2018)

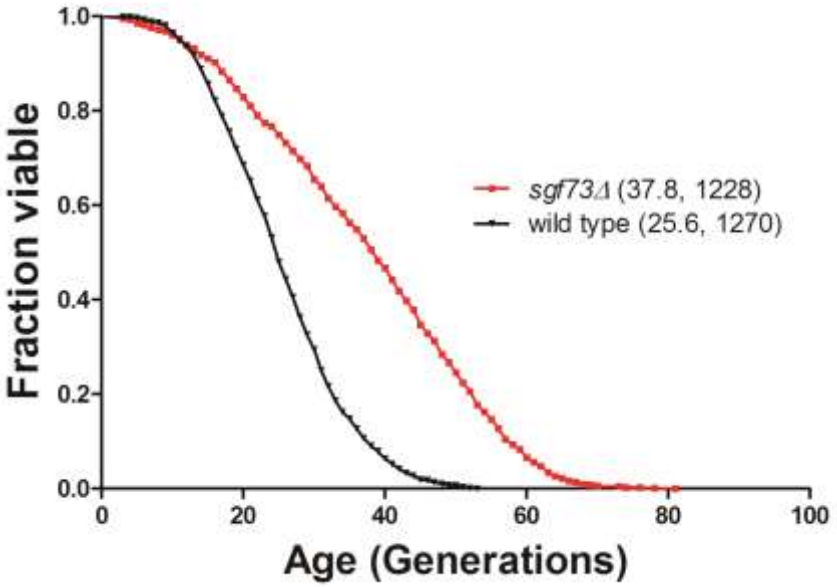

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
scw4Δ (27.8, 45)
wild type (23.0, 45)

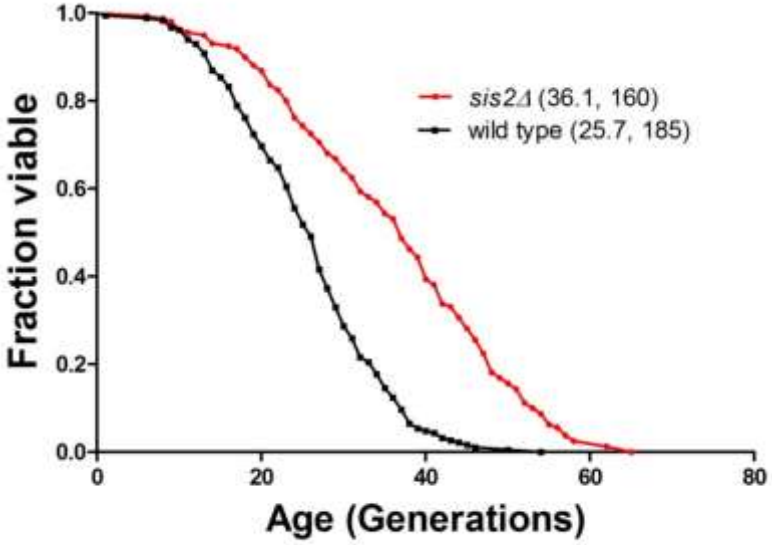

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
sdh1Δ (32.8, 65)
wild type (26.2, 65)

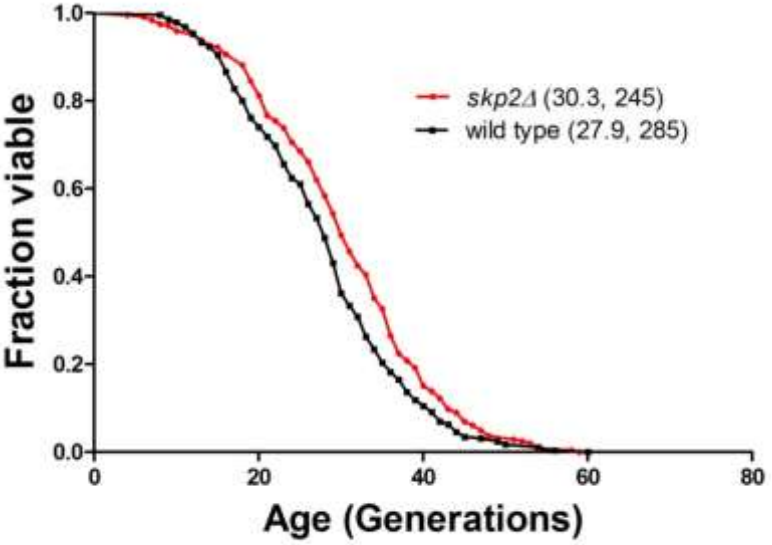

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
sdh2Δ (32.1, 65)
wild type (26.5, 65)

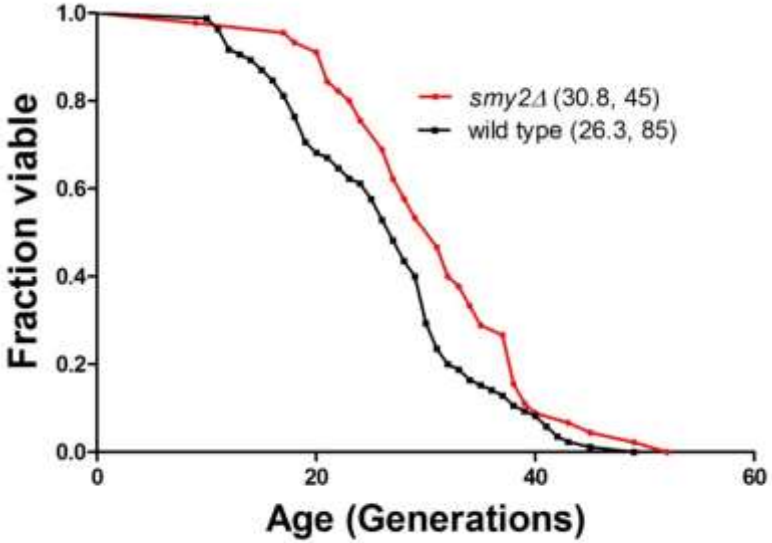

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
sds3Δ (35.6, 85)
wild type (27.1, 105)

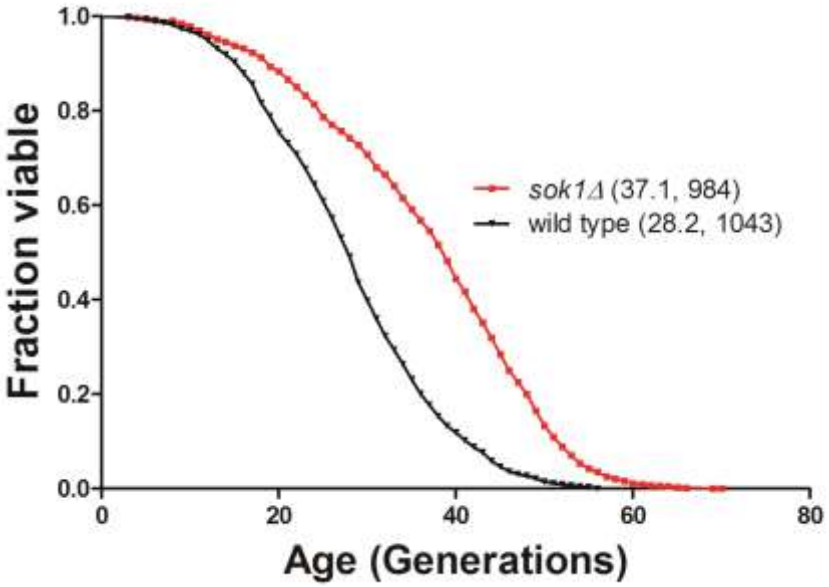

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
sgf11Δ (36.6, 125)
wild type (29.3, 105)

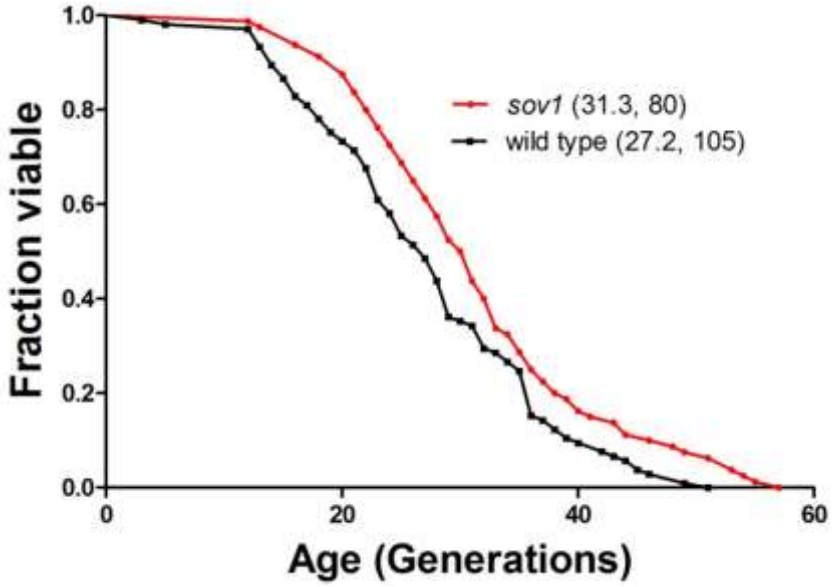

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
Age (Generations)
sgf73Δ (37.8, 1228)
wild type (25.6, 1270)

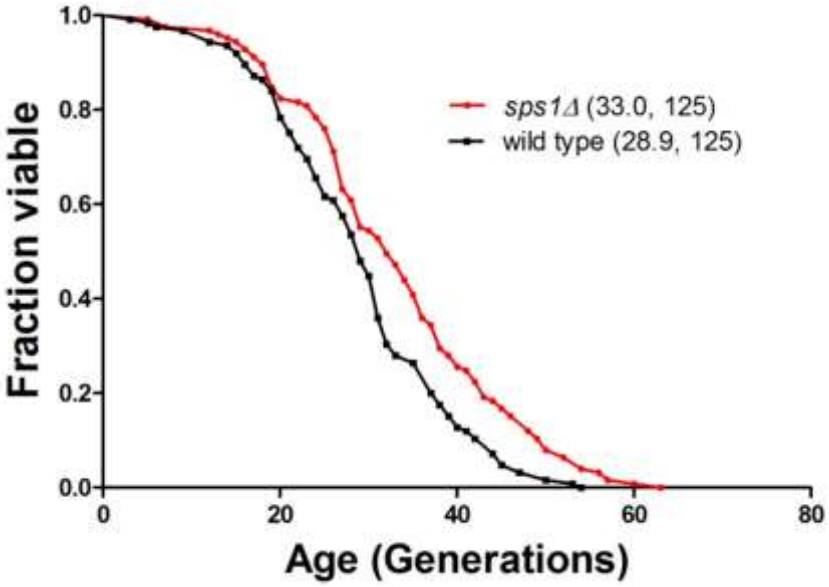

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
sis2Δ (36.1, 160)
wild type (25.7, 185)

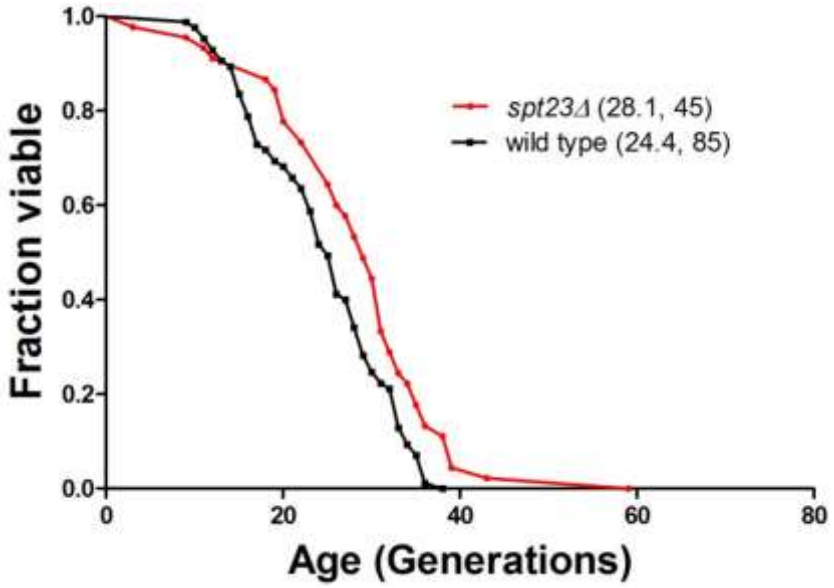

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
skp2Δ (30.3, 245)
wild type (27.9, 285)

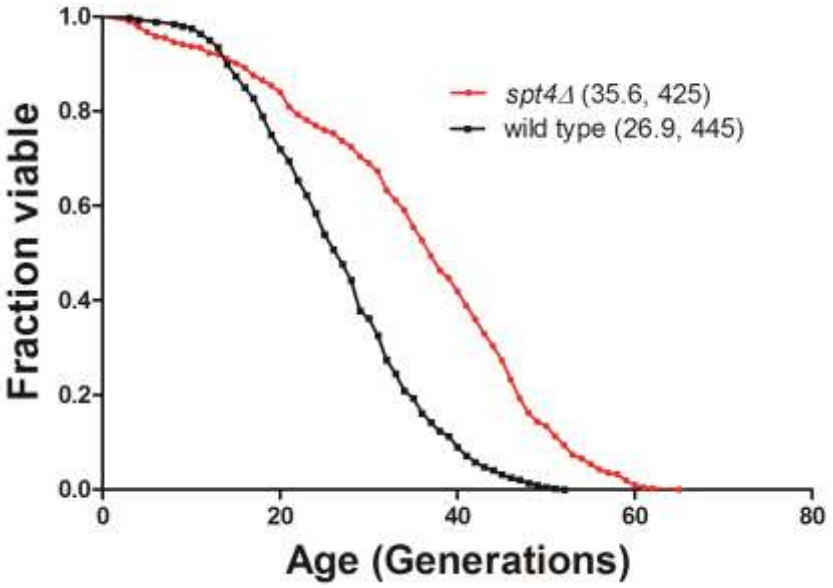

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
smy2Δ (30.8, 45)
wild type (26.3, 85)

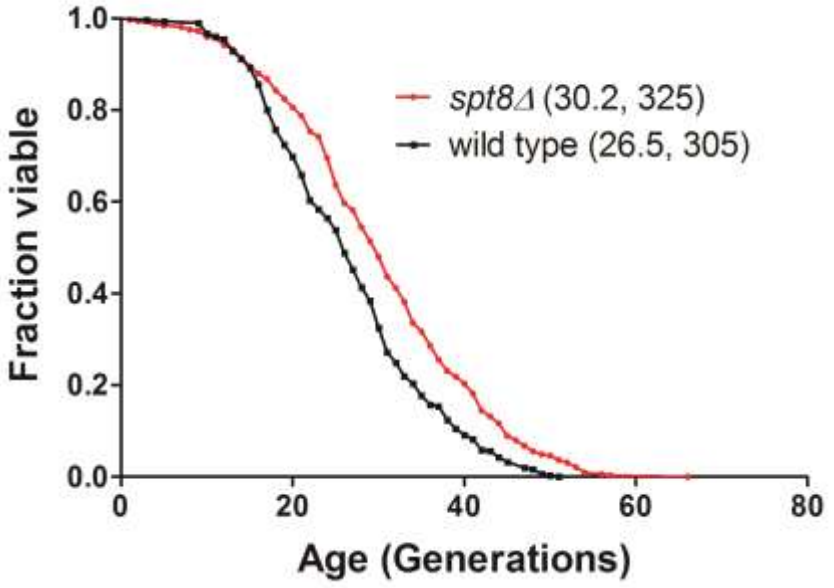

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
sok1Δ (37.1, 984)
wild type (28.2, 1043)

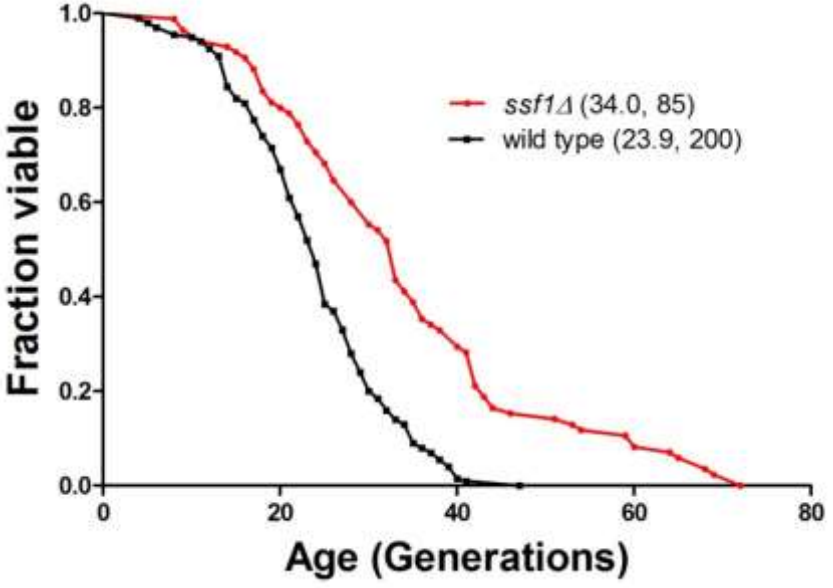

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
sov1 (31.3, 80)
wild type (27.2, 105)

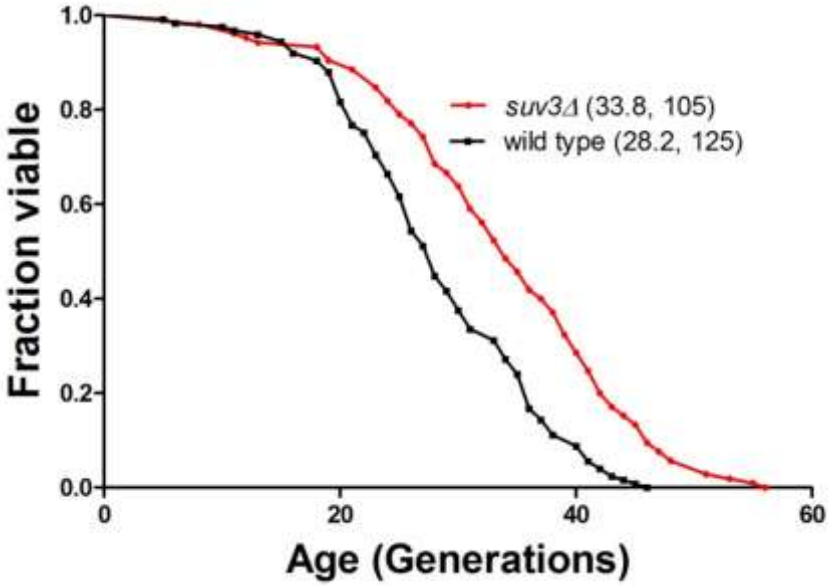

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
sps1Δ (33.0, 125)
wild type (28.9, 125)

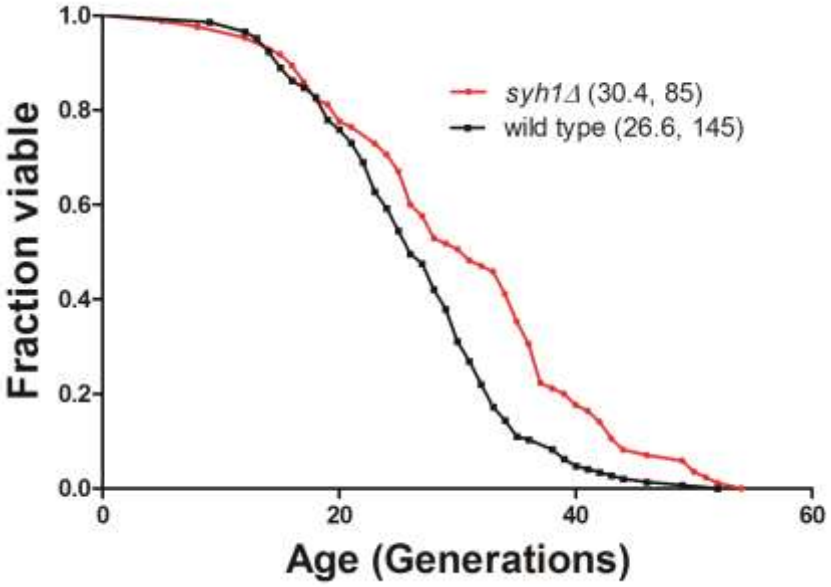

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
spt23Δ (28.1, 45)
wild type (24.4, 85)

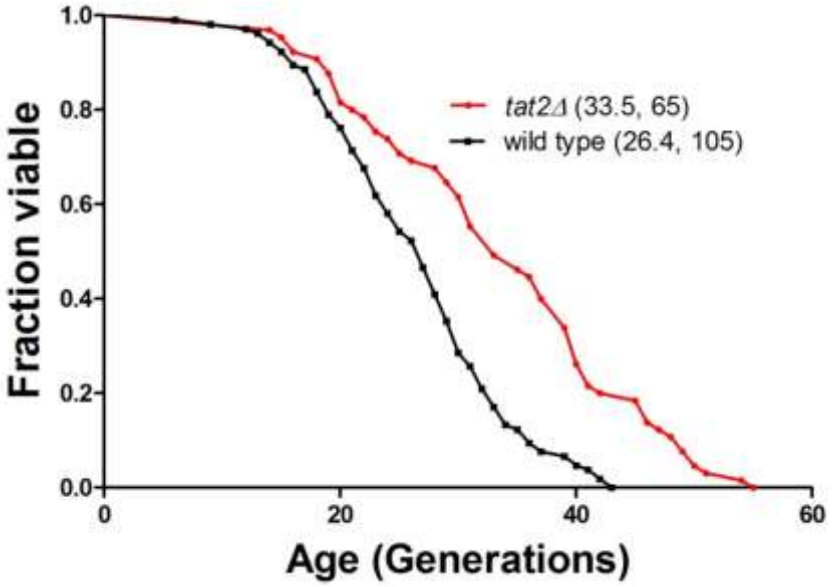

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
spt4Δ (35.6, 425)
wild type (26.9, 445)

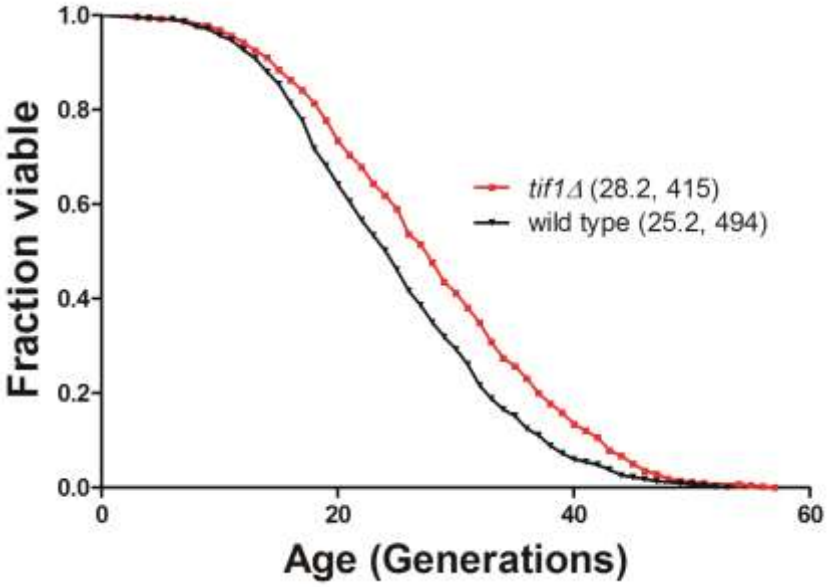

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
spt8Δ (30.2, 325)
wild type (26.5, 305)

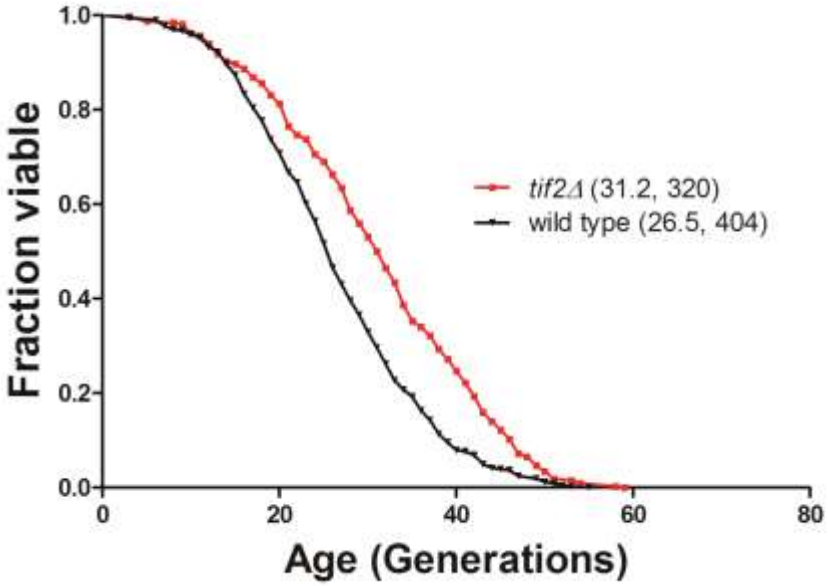

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
ssf1Δ (34.0, 85)
wild type (23.9, 200)

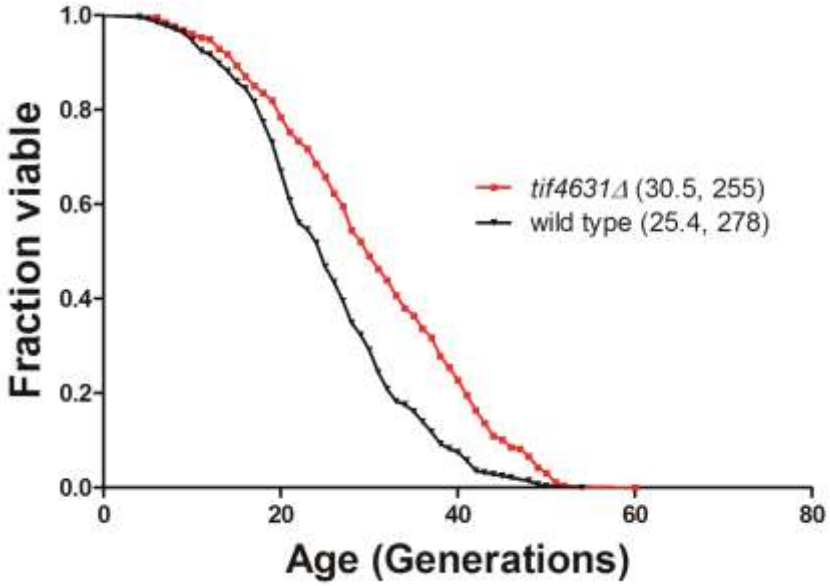

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
suv3Δ (33.8, 105)
wild type (28.2, 125)

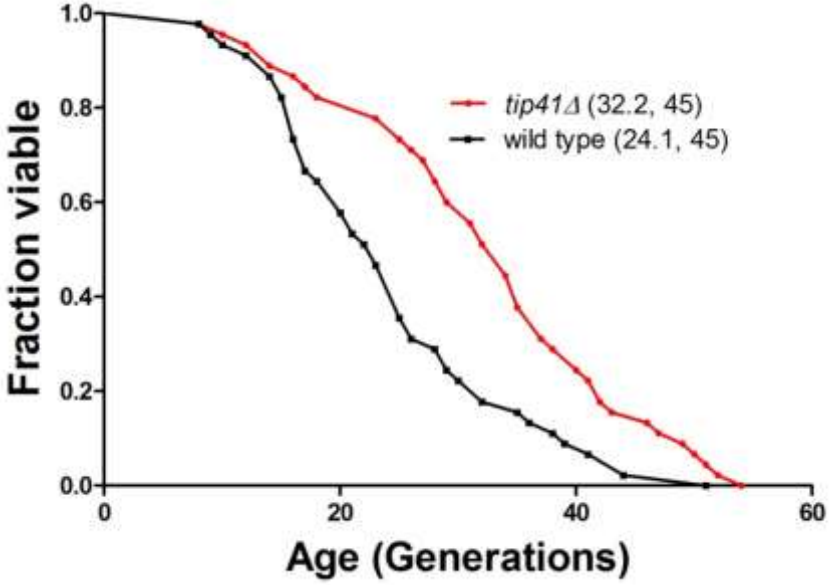

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
syh1Δ (30.4, 85)
wild type (26.6, 145)

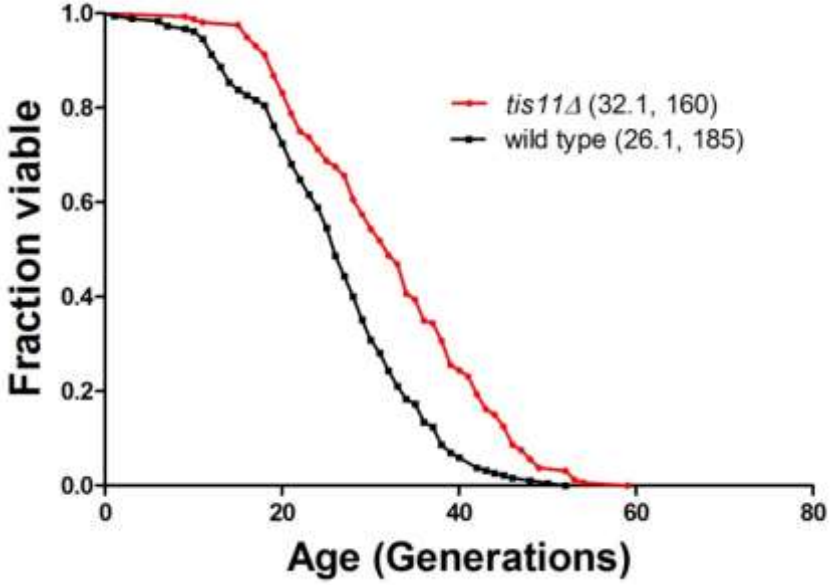

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
tat2Δ (33.5, 65)
wild type (26.4, 105)

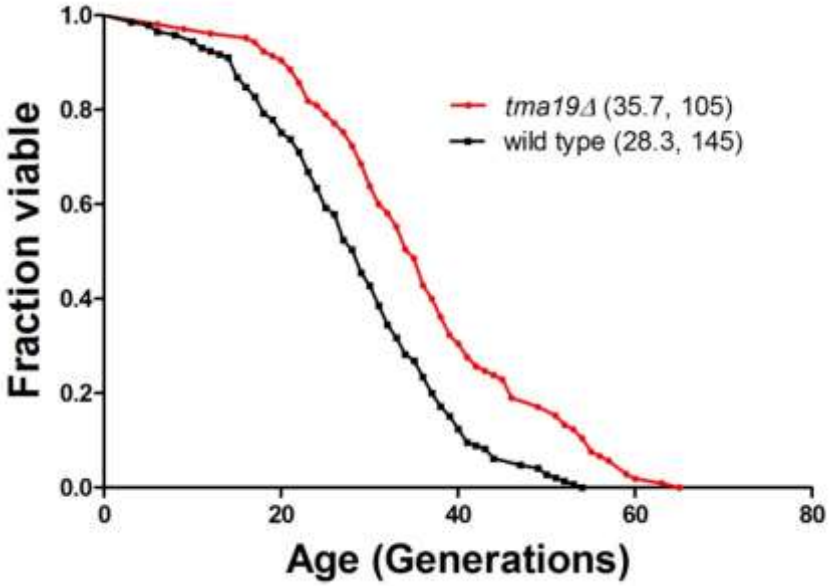

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
tif1Δ (28.2, 415)
wild type (25.2, 494)

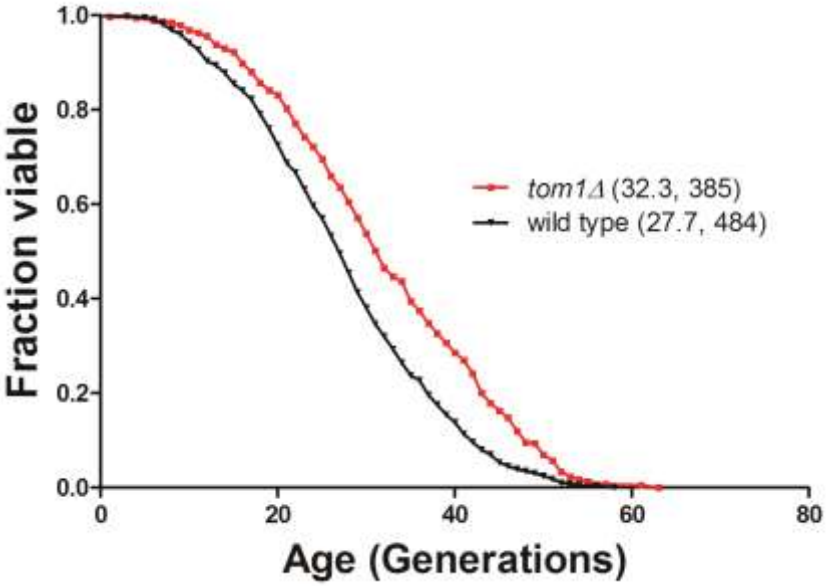

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
tif2Δ (31.2, 320)
wild type (26.5, 404)

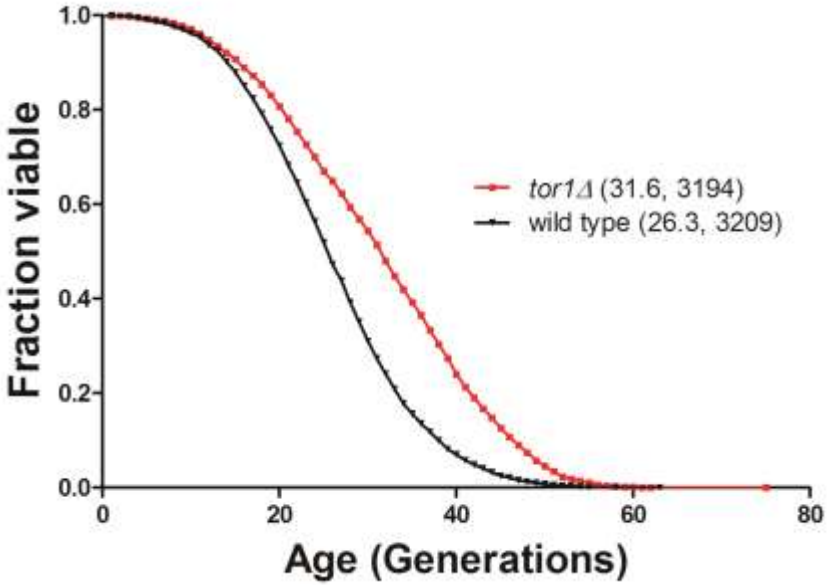

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
tif4631Δ (30.5, 255)
wild type (25.4, 278)

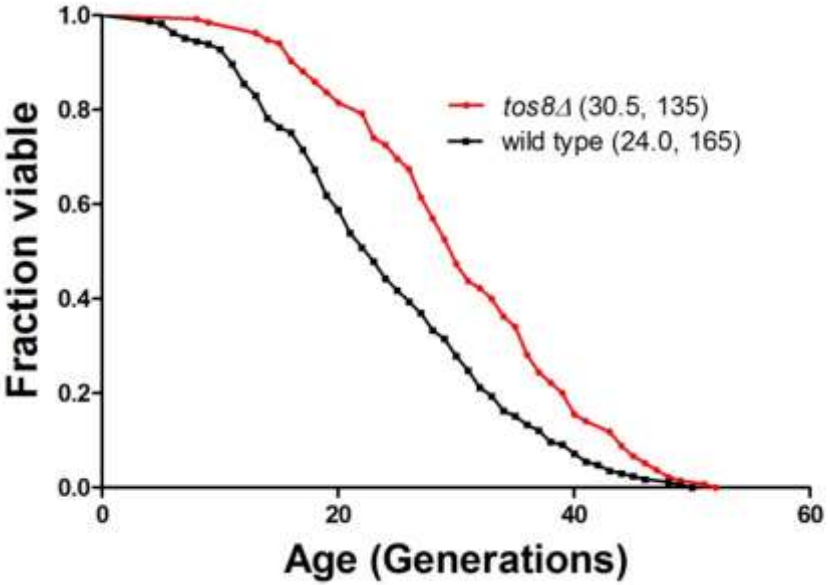

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
tip41Δ (32.2, 45)
wild type (24.1, 45)

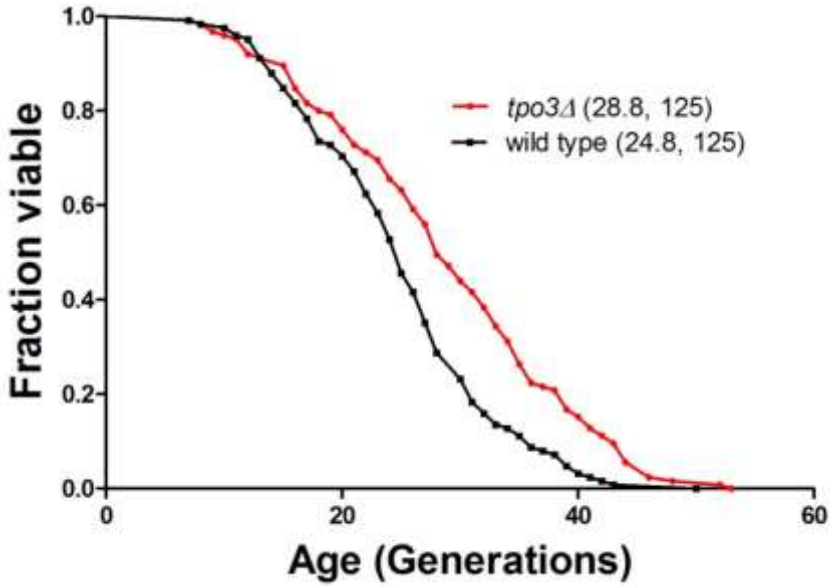

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
tis11Δ (32.1, 160)
wild type (26.1, 185)

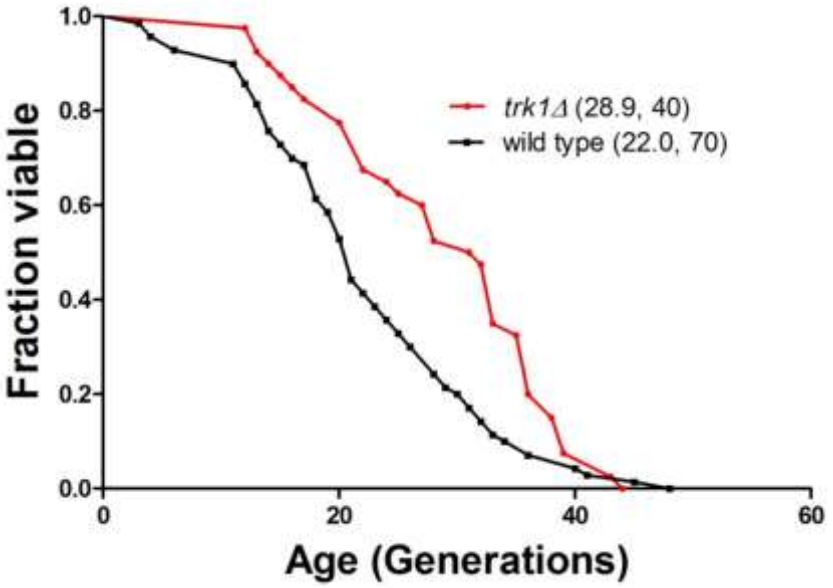

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
tma19Δ (35.7, 105)
wild type (28.3, 145)

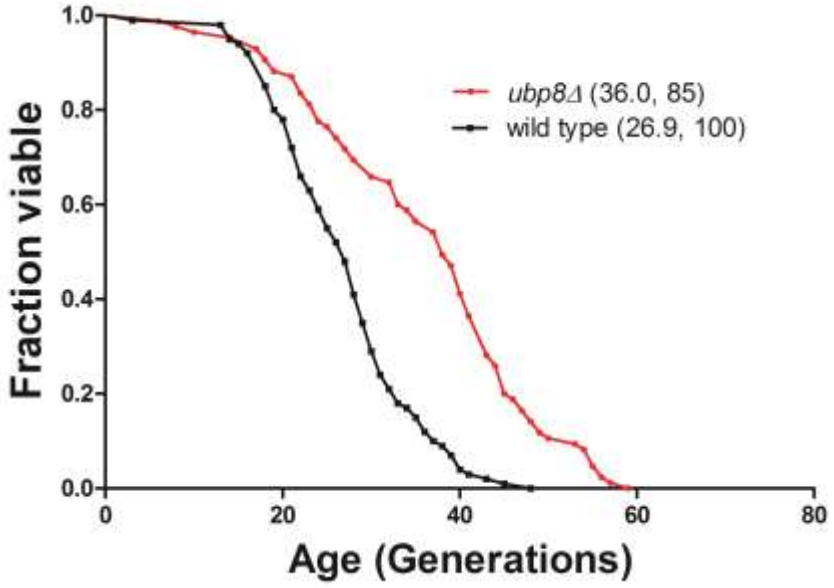

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
tom1Δ (32.3, 385)
wild type (27.7, 484)

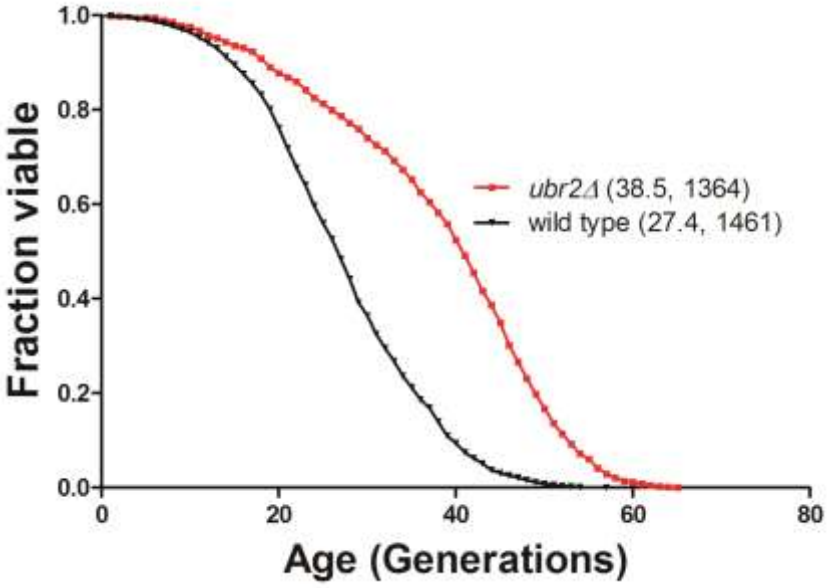

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
tor1Δ (31.6, 3194)
wild type (26.3, 3209)

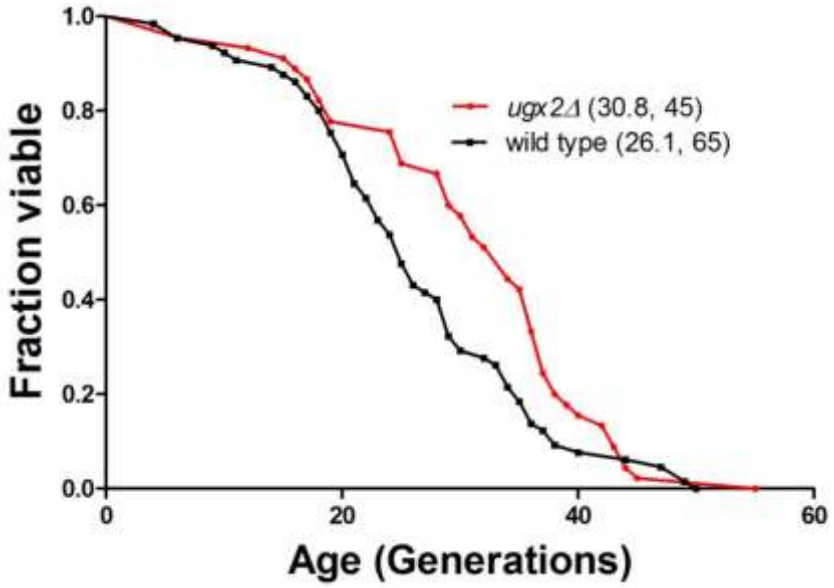

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
tos8Δ (30.5, 135)
wild type (24.0, 165)

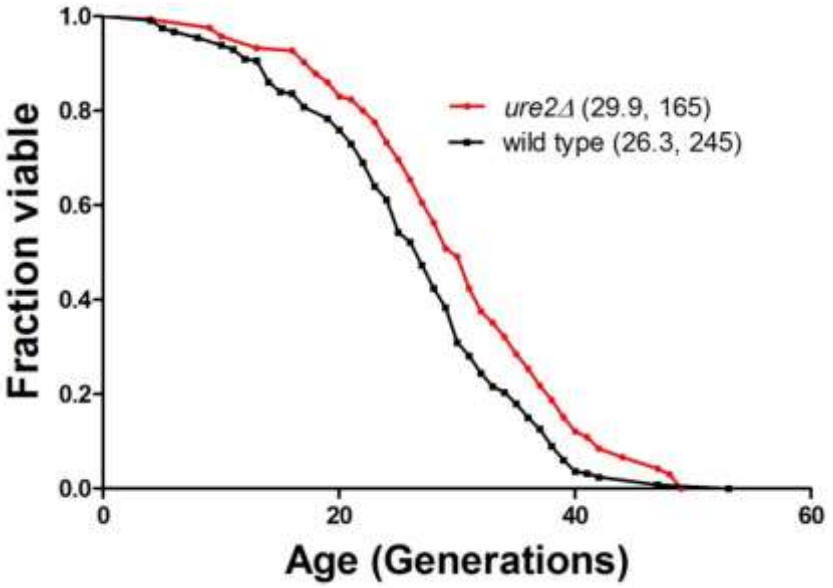

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
tpo3Δ (28.8, 125)
wild type (24.8, 125)

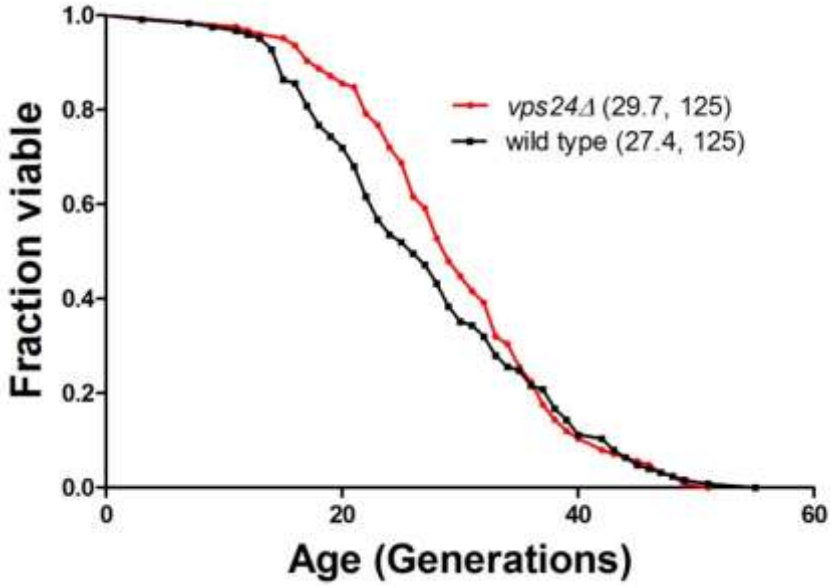

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
trk1Δ (28.9, 40)
wild type (22.0, 70)

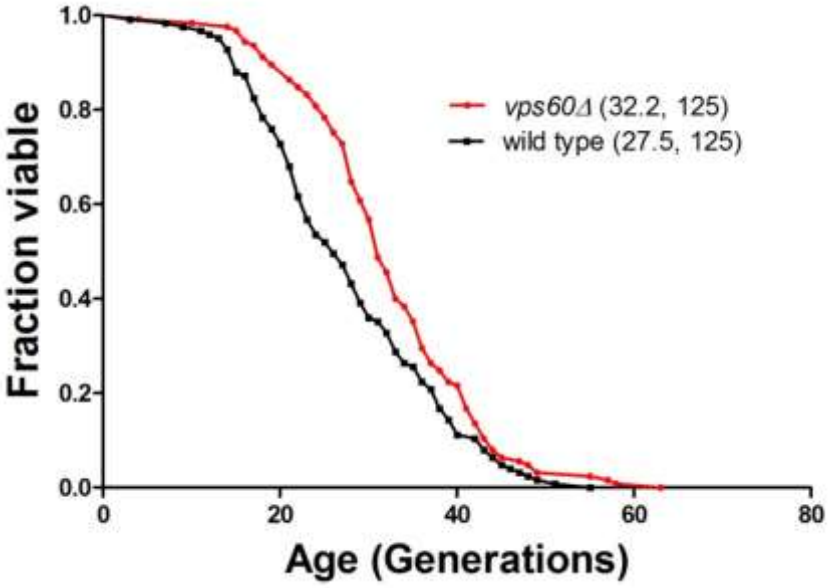

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
ubp8Δ (36.0, 85)
wild type (26.9, 100)

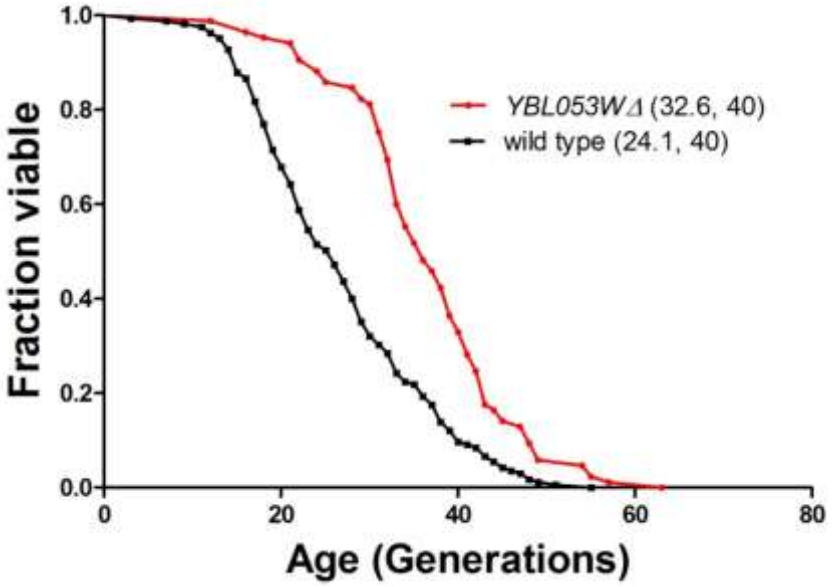

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
ubr2Δ (38.5, 1364)
wild type (27.4, 1461)

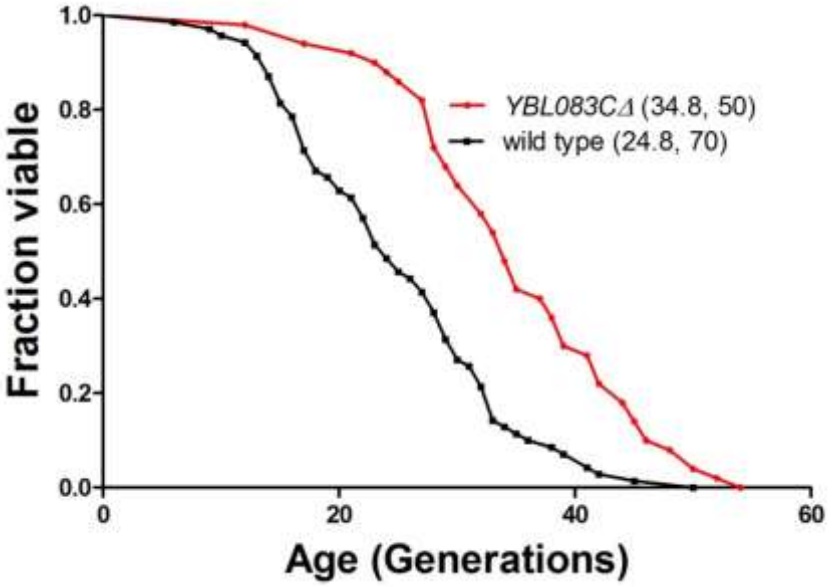

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
ugx2Δ (30.8, 45)
wild type (26.1, 65)

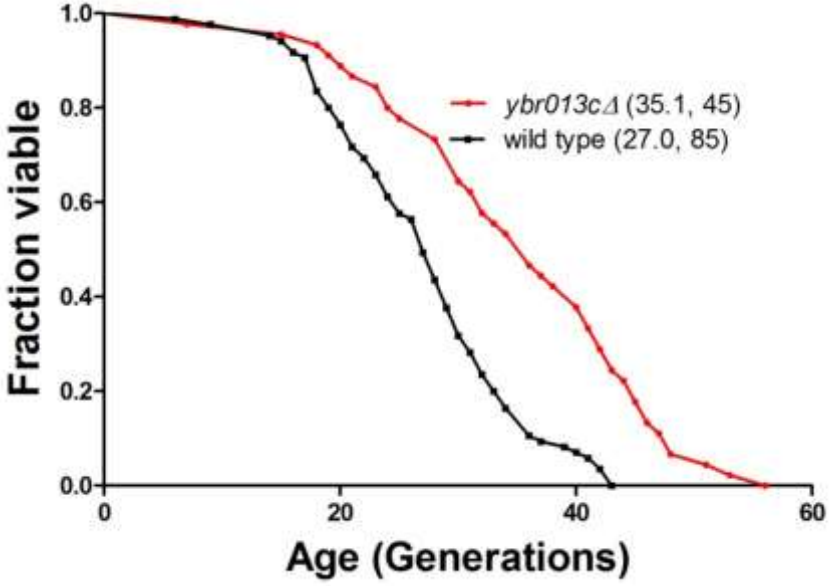

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
ure2Δ (29.9, 165)
wild type (26.3, 245)

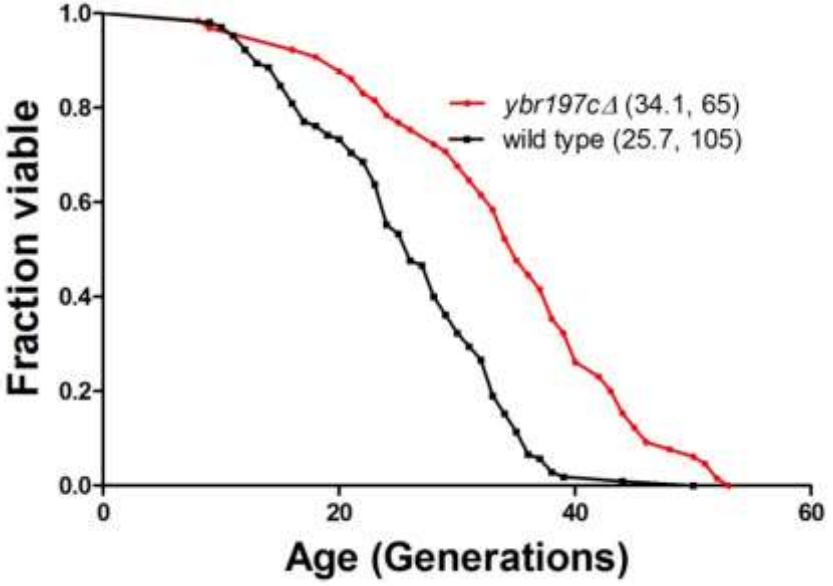

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
vps24Δ (29.7, 125)
wild type (27.4, 125)

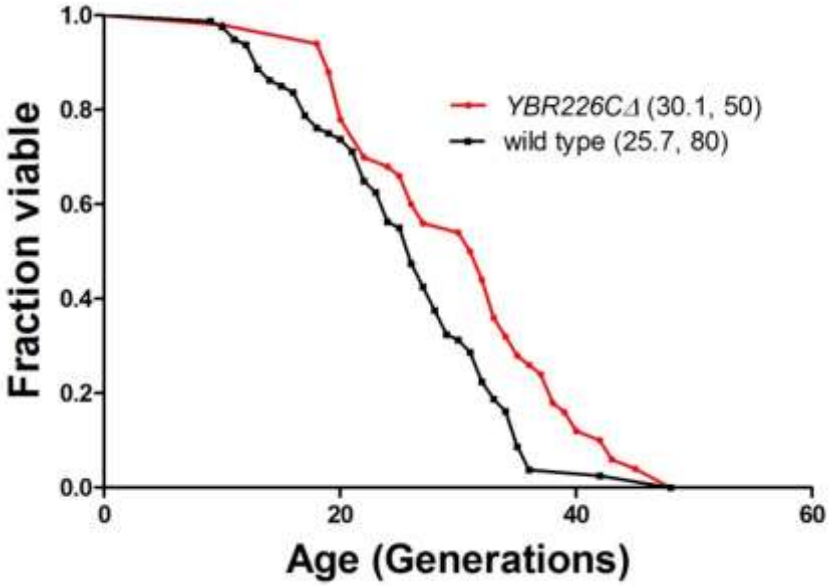

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
vps60Δ (32.2, 125)
wild type (27.5, 125)

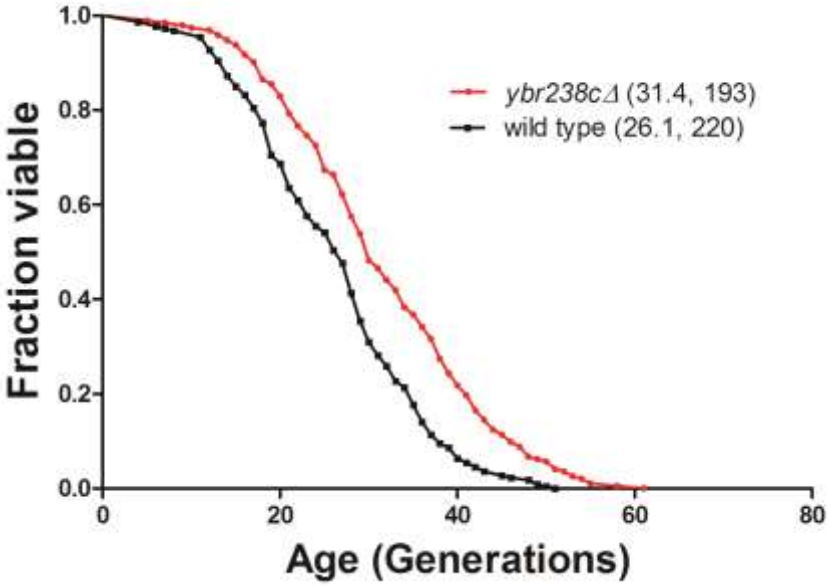

Fraction viable
Age (Generations)
YBL053WΔ (32.6, 40)
wild type (24.1, 40)

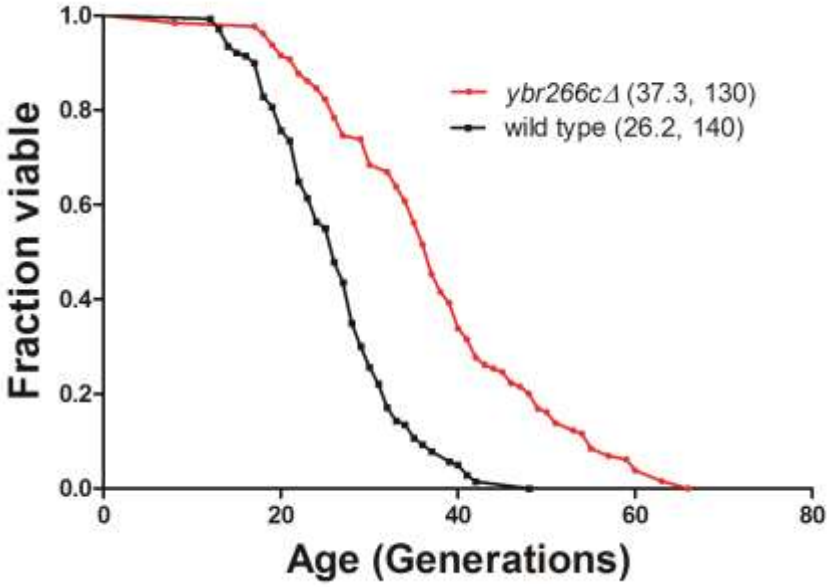

Fraction viable
Age (Generations)
YBL083CΔ (34.8, 50)
wild type (24.8, 70)

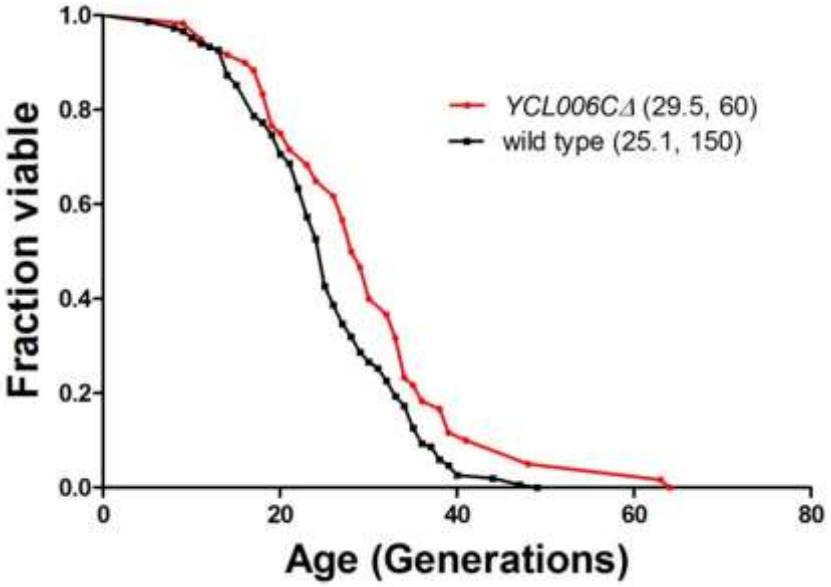

Fraction viable
Age (Generations)
ybr013cΔ (35.1, 45)
wild type (27.0, 85)

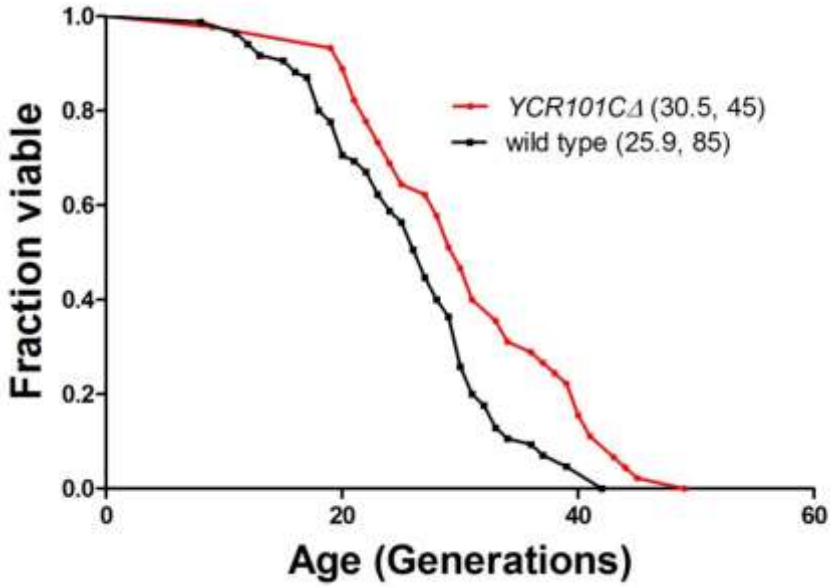

Fraction viable
Age (Generations)
ybr197cΔ (34.1, 65)
wild type (25.7, 105)

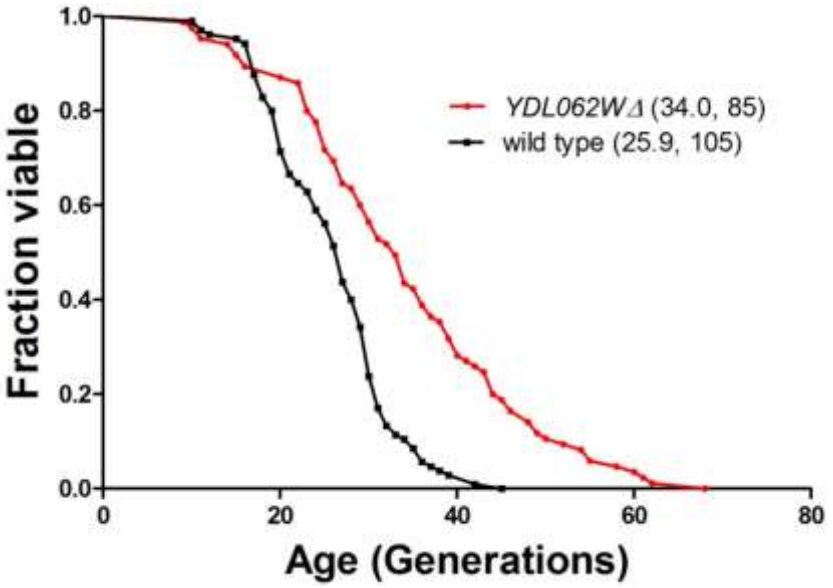

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
YBR226CΔ (30.1, 50)
wild type (25.7, 80)

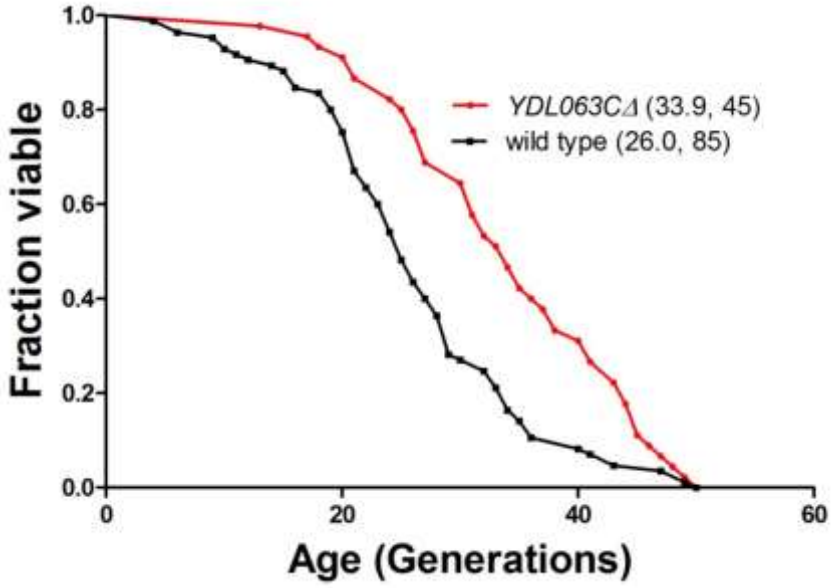

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
ybr238cΔ (31.4, 193)
wild type (26.1, 220)

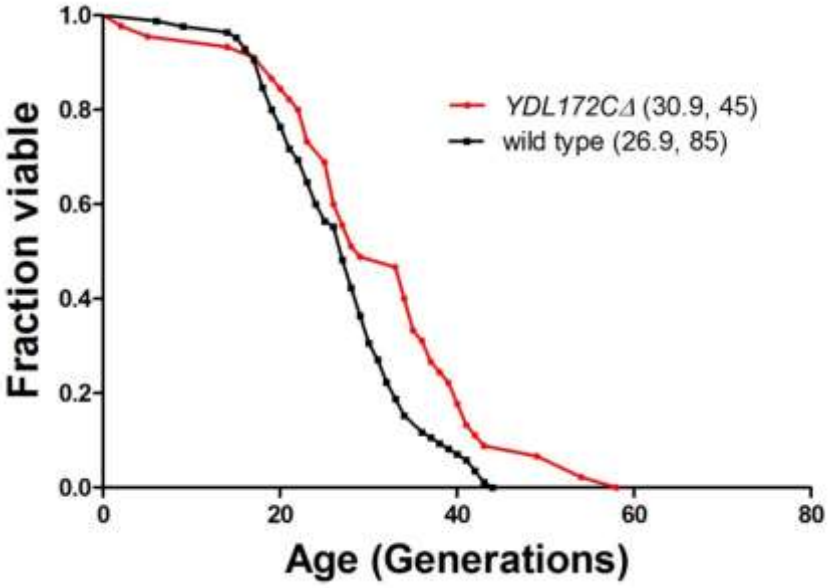

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
ybr266cΔ (37.3, 130)
wild type (26.2, 140)

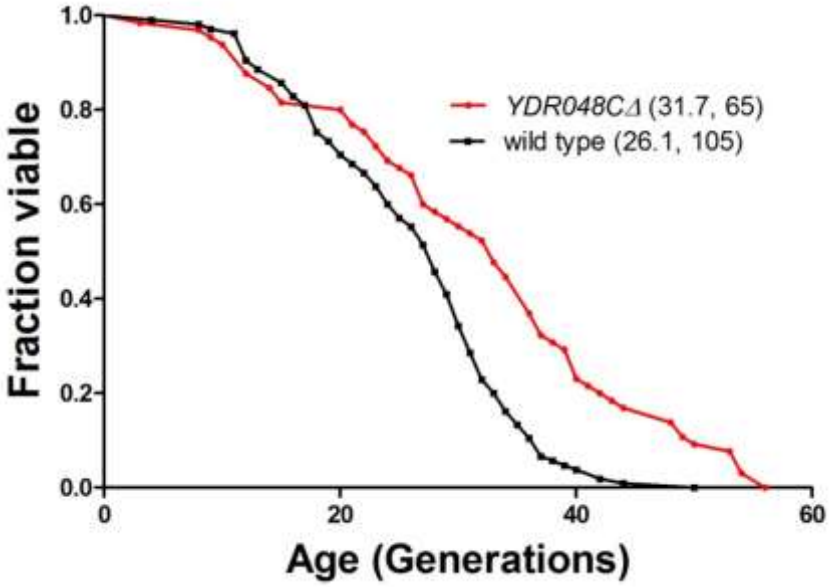

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
YCL006CΔ (29.5, 60)
wild type (25.1, 150)

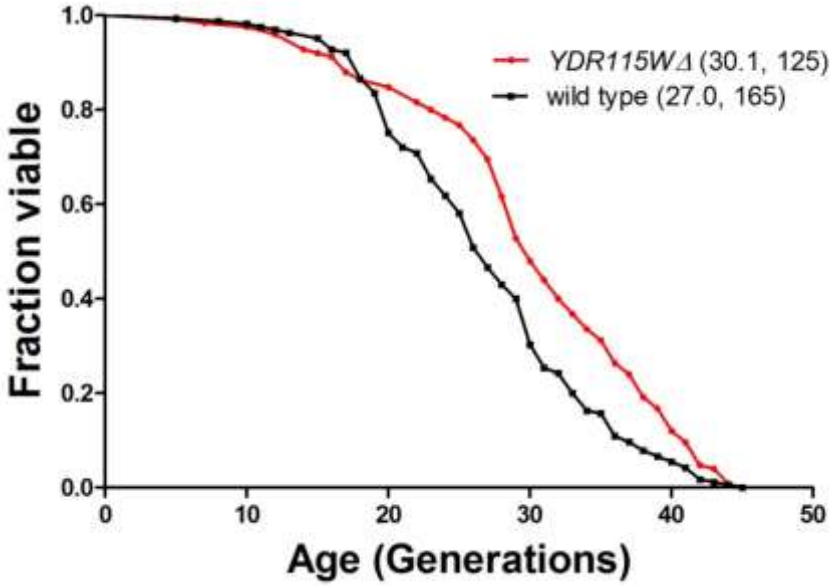

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
YCR101CΔ (30.5, 45)
wild type (25.9, 85)

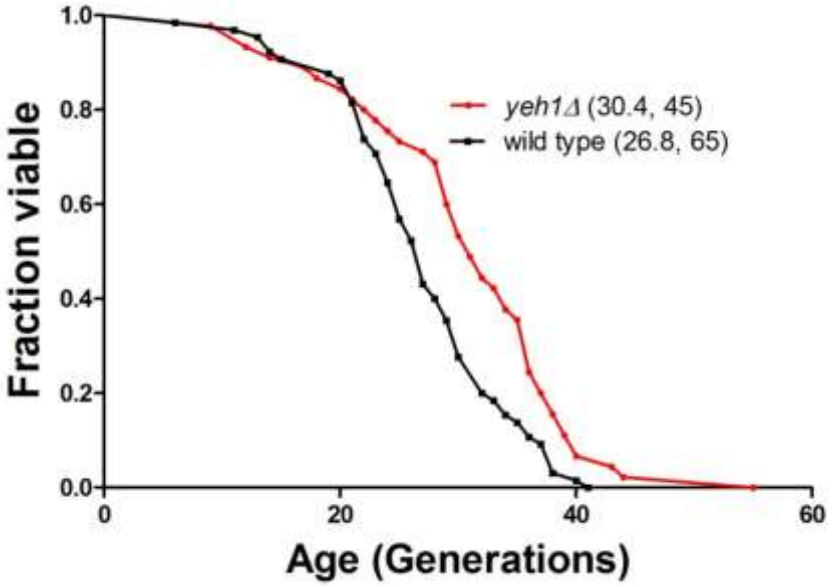

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
YDL062WΔ (34.0, 85)
wild type (25.9, 105)

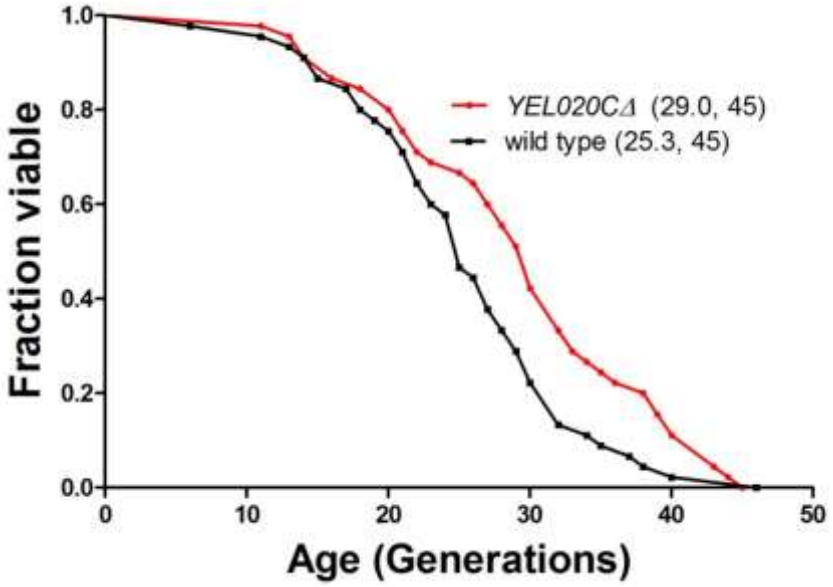

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
YDL063CΔ (33.9, 45)
wild type (26.0, 85)

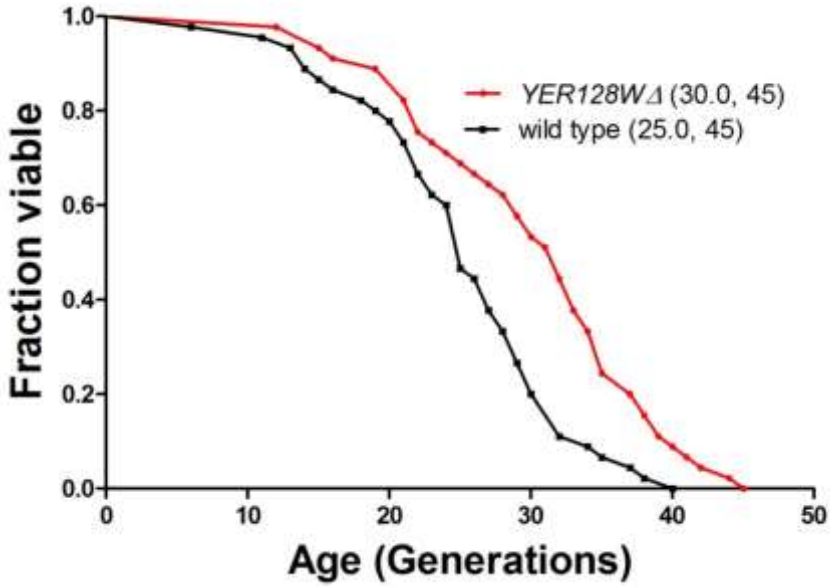

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
YDL172CΔ (30.9, 45)
wild type (26.9, 85)

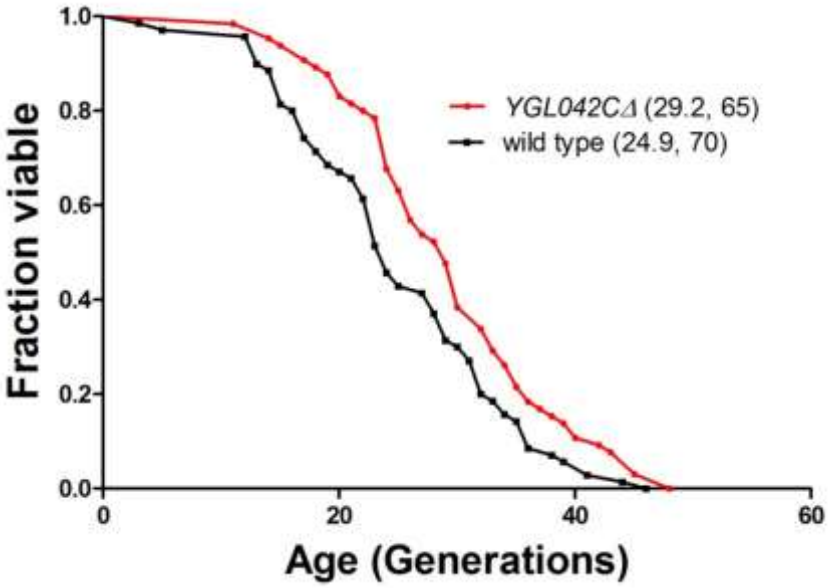

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
YDR048CΔ (31.7, 65)
wild type (26.1, 105)

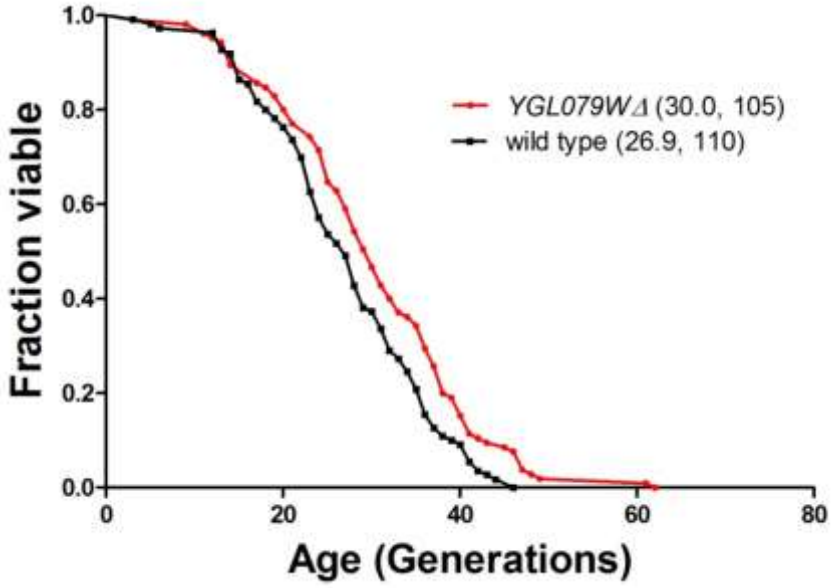

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
Age (Generations)
YDR115WΔ (30.1, 125)
wild type (27.0, 165)

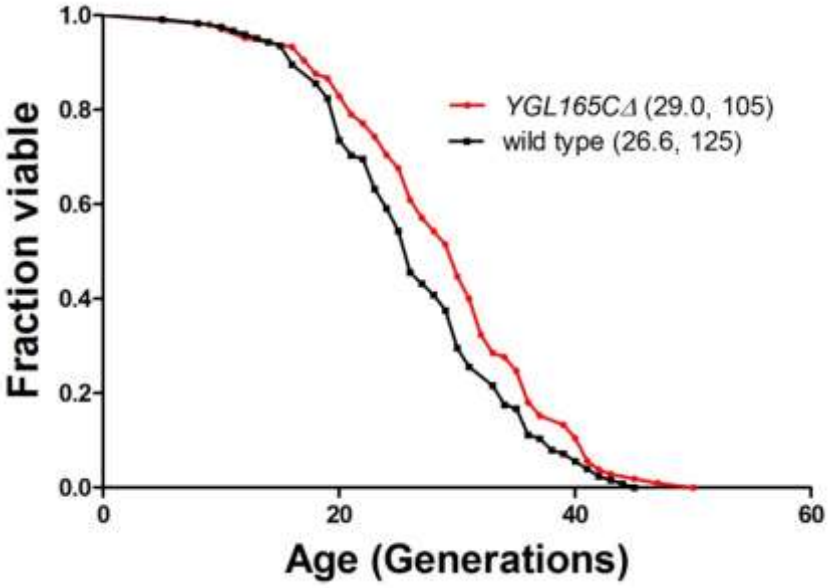

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
yeh1Δ (30.4, 45)
wild type (26.8, 65)

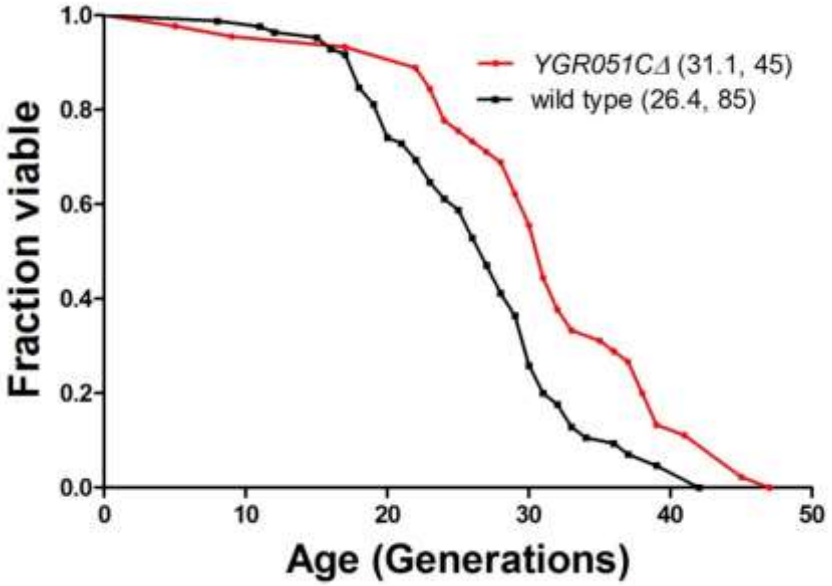

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
Age (Generations)
YEL020CΔ (29.0, 45)
wild type (25.3, 45)

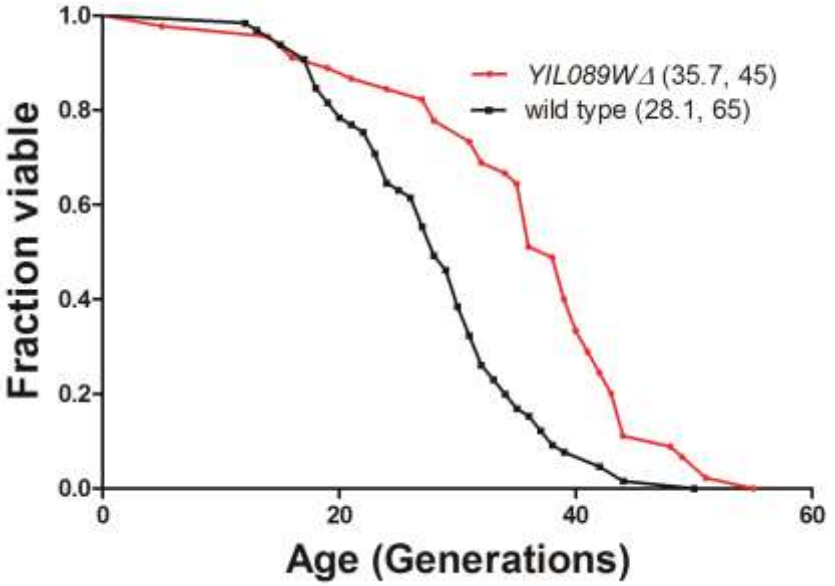

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
Age (Generations)
YER128WΔ (30.0, 45)
wild type (25.0, 45)

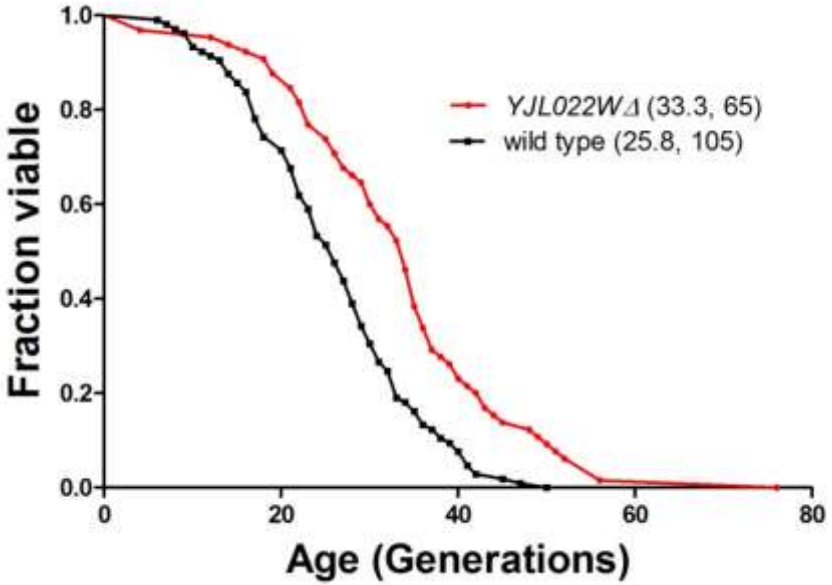

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
YGL042CΔ (29.2, 65)
wild type (24.9, 70)

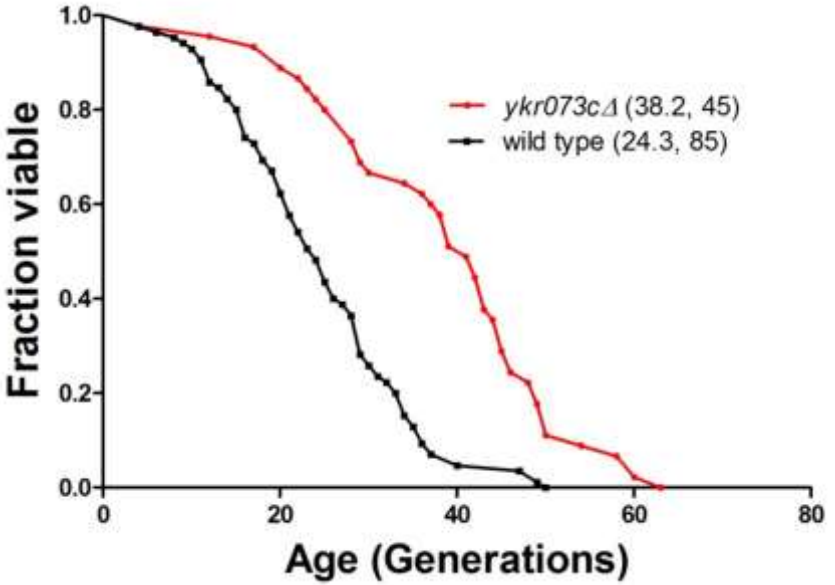

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
YGL079WΔ (30.0, 105)
wild type (26.9, 110)

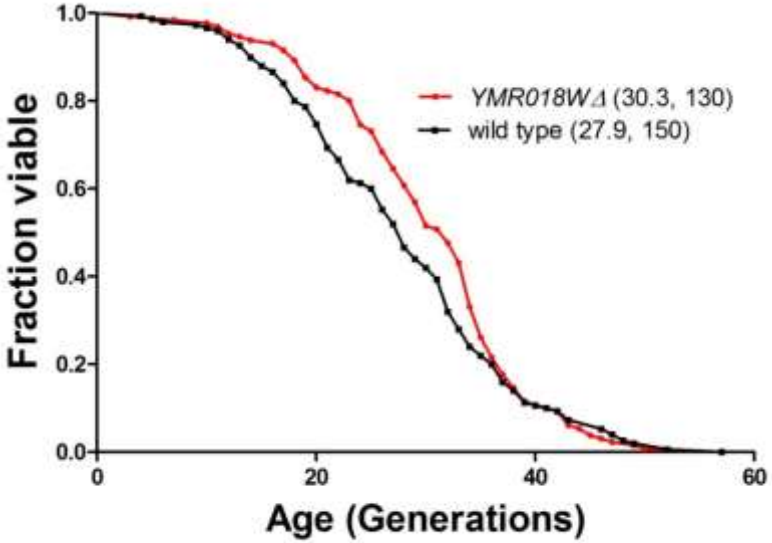

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
YGL165CΔ (29.0, 105)
wild type (26.6, 125)

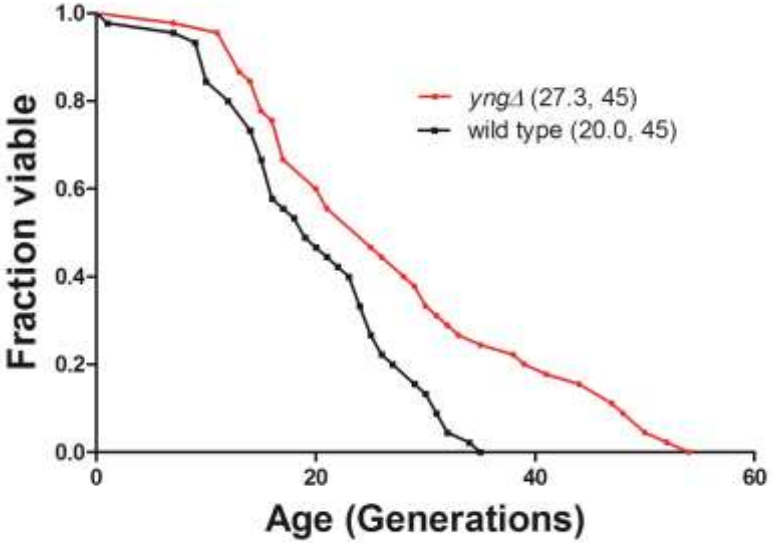

YGR051CΔ (31.1, 45)
wild type (26.4, 85)
Fraction viable
Age (Generations)

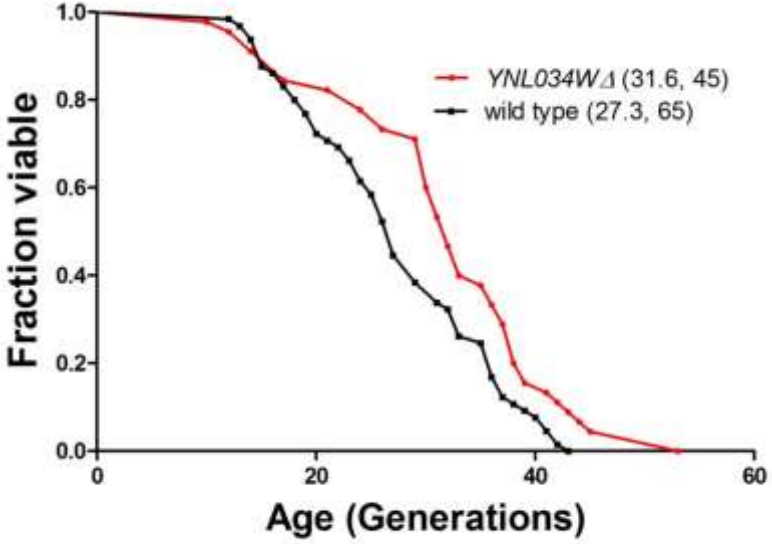

YIL089WΔ (35.7, 45)
wild type (28.1, 65)
Fraction viable
Age (Generations)

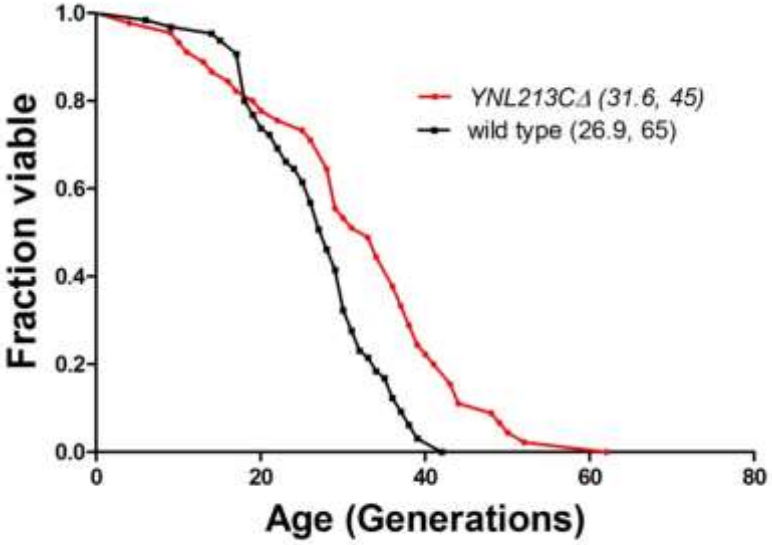

YJL022WΔ (33.3, 65)
wild type (25.8, 105)
Fraction viable
Age (Generations)

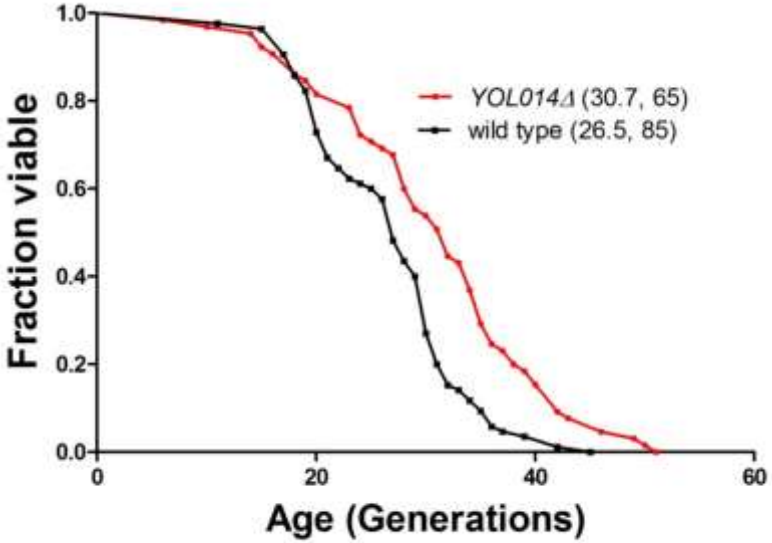

ykr073cΔ (38.2, 45)
wild type (24.3, 85)
Fraction viable
Age (Generations)

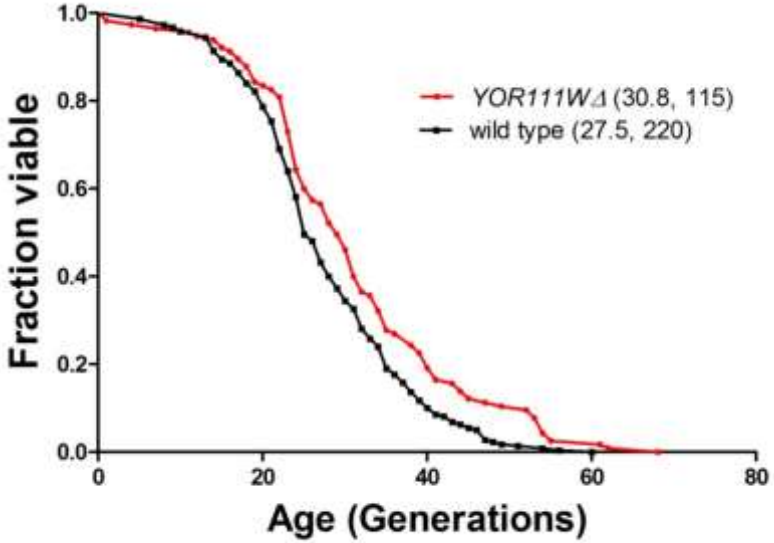

Fraction viable
Age (Generations)
YMR018WΔ (30.3, 130)
wild type (27.9, 150)

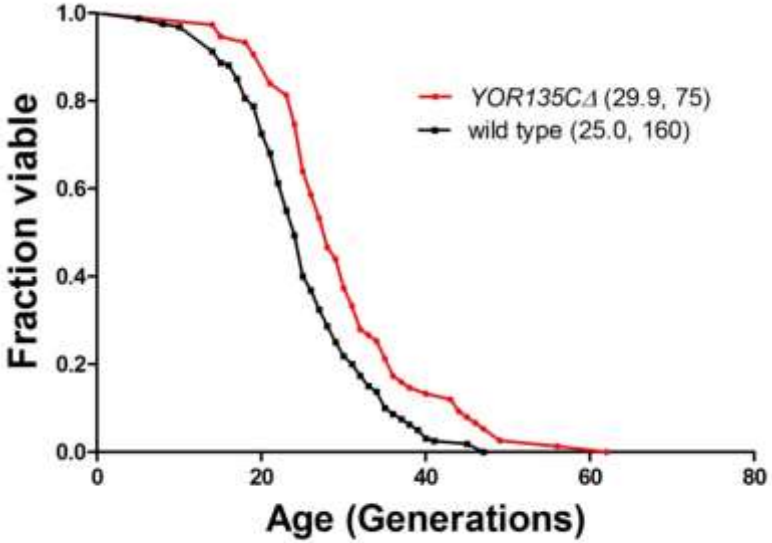

Fraction viable
Age (Generations)
yngΔ (27.3, 45)
wild type (20.0, 45)

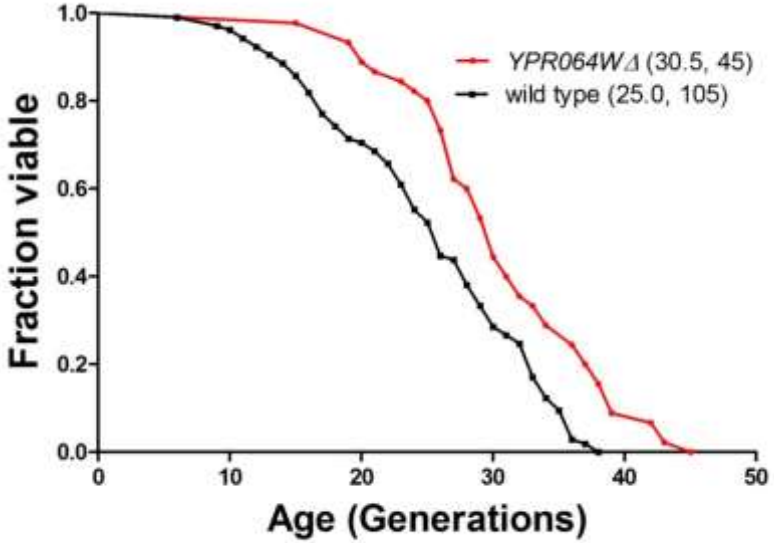

Fraction viable
Age (Generations)
YNL034WΔ (31.6, 45)
wild type (27.3, 65)

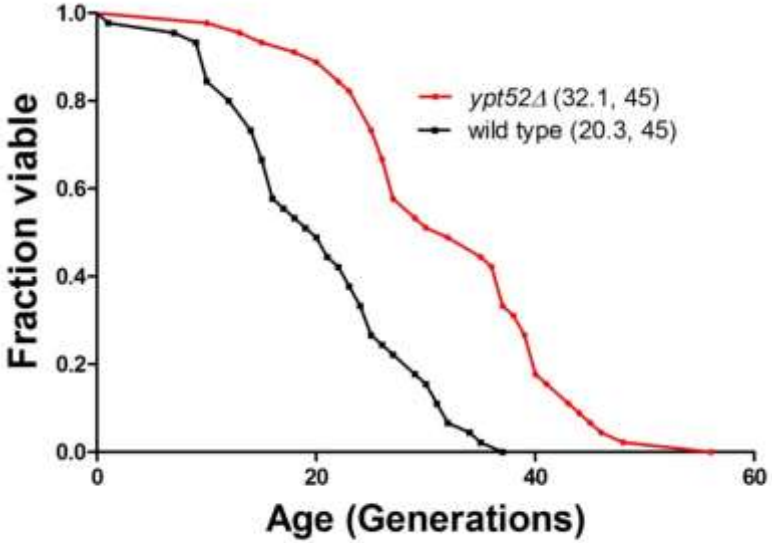

Fraction viable
Age (Generations)
YNL213CΔ (31.6, 45)
wild type (26.9, 65)

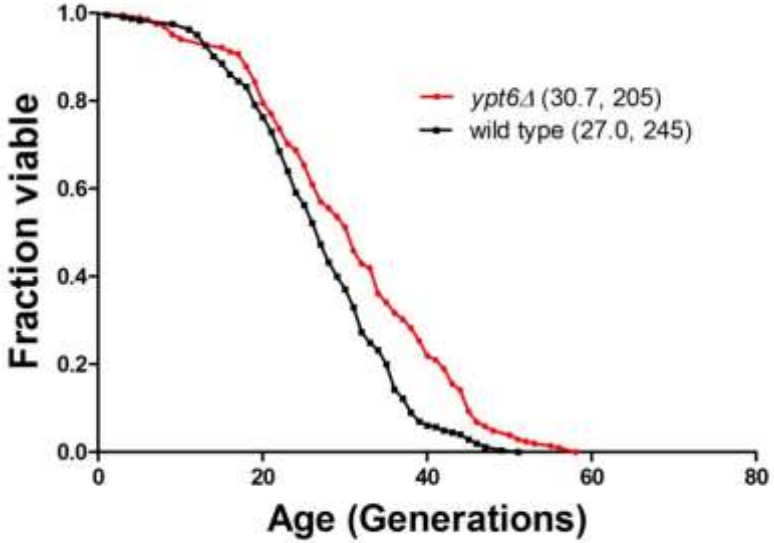

Fraction viable
Age (Generations)
YOL014Δ (30.7, 65)
wild type (26.5, 85)

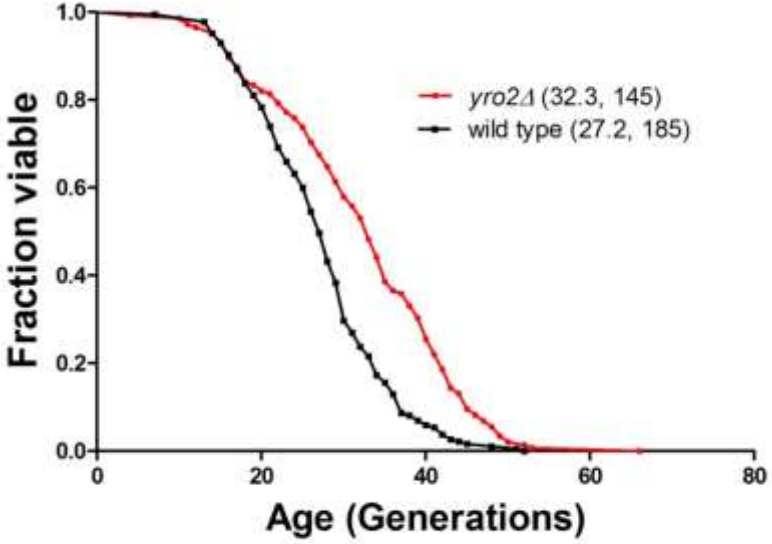

Fraction viable
Age (Generations)
YOR111WΔ (30.8, 115)
wild type (27.5, 220)

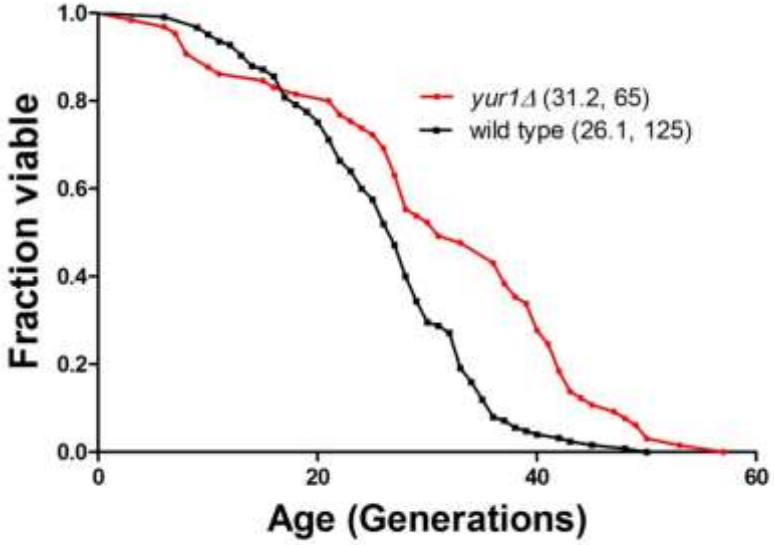

Fraction viable
Age (Generations)
YOR135CΔ (29.9, 75)
wild type (25.0, 160)

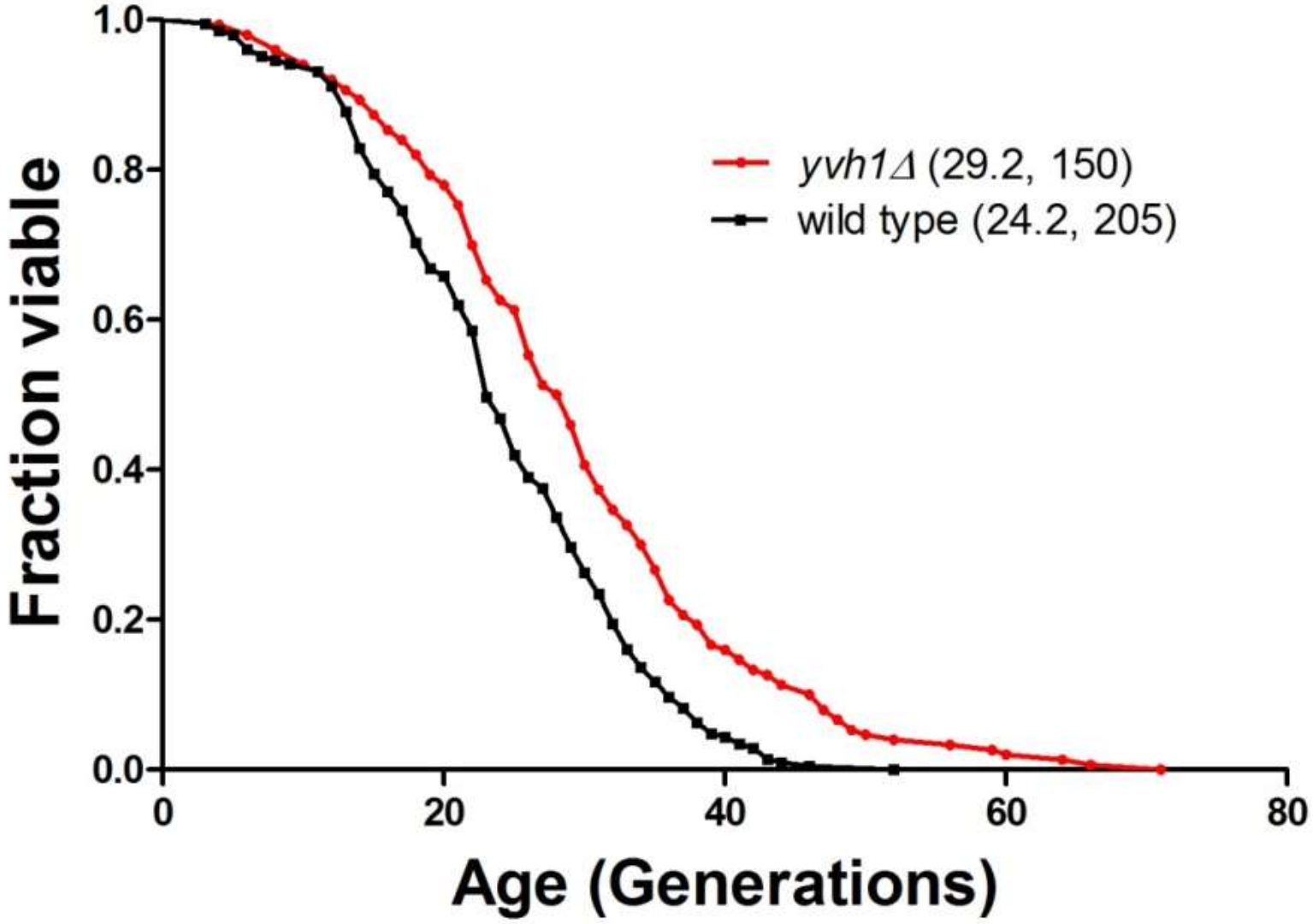

Fraction viable
Age (Generations)
YPR064WΔ (30.5, 45)
wild type (25.0, 105)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
ypt52Δ (32.1, 45)
wild type (20.3, 45)

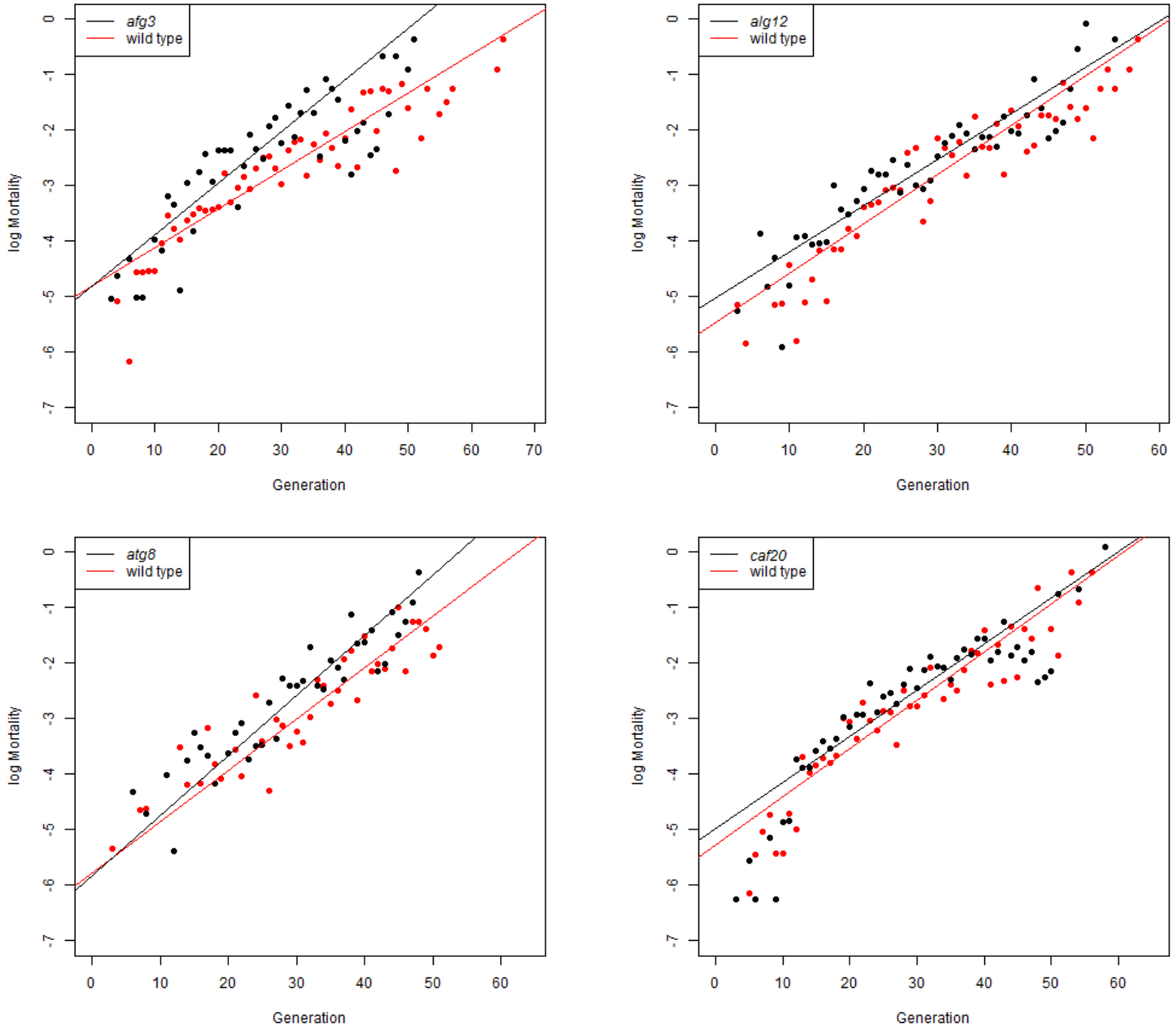

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
ypt6Δ (30.7, 205)
wild type (27.0, 245)

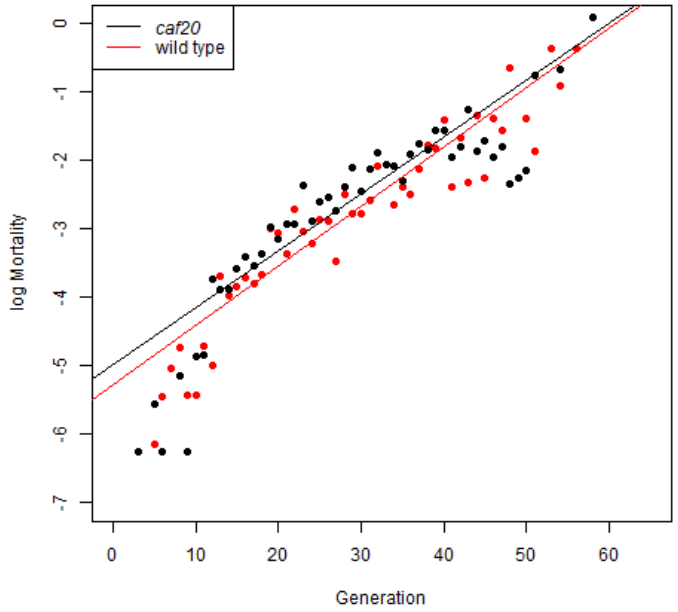

Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
Age (Generations)
yro2Δ (32.3, 145)
wild type (27.2, 185)


Fraction viable
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
Age (Generations)
yur1Δ (31.2, 65)
wild type (26.1, 125)


1.0
0.8
0.6
0.4
0.2
0.0
Fraction viable
0
20
40
60
80
Age (Generations)
yvh1Δ (29.2, 150)
wild type (24.2, 205)

Supplemental Figure S2. Mortality curves for genotypes with over 200 mother cells scored. Lines show maximum likelihood estimation of Gompertz parameters for given mortality data.




caf20
wild type
log Mortality
Generation
0
-1
-2
-3
-4
-5
-6
-7
0
10
20
30
40
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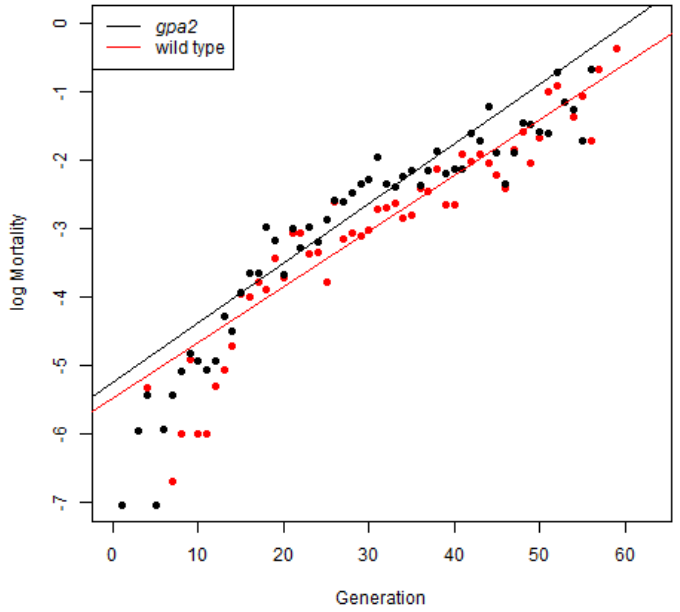
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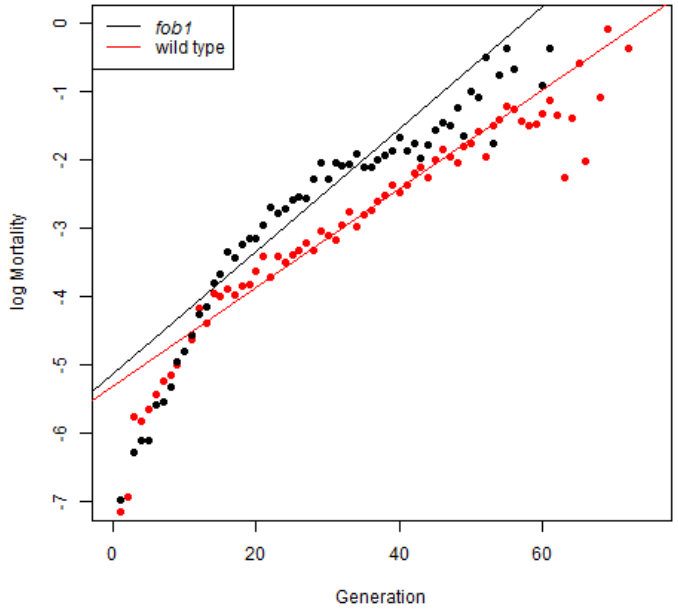
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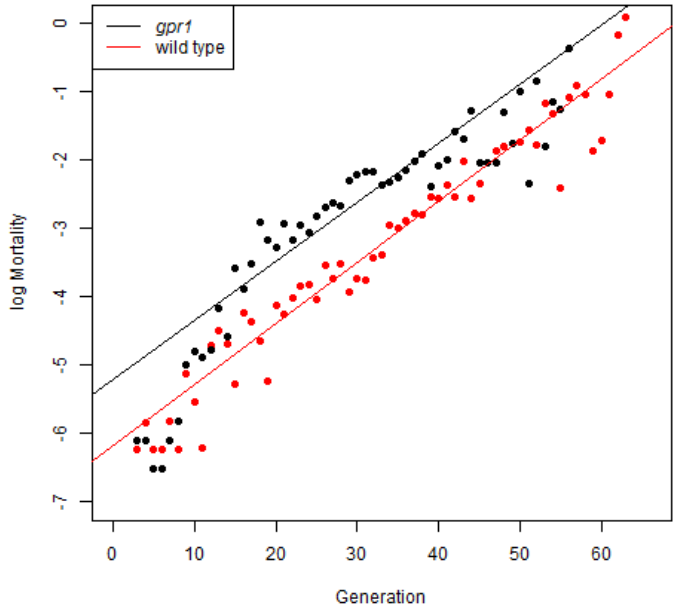
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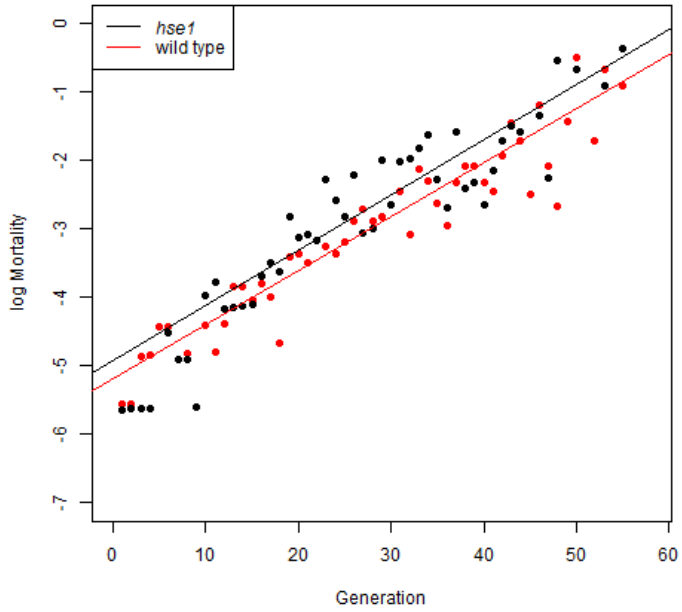
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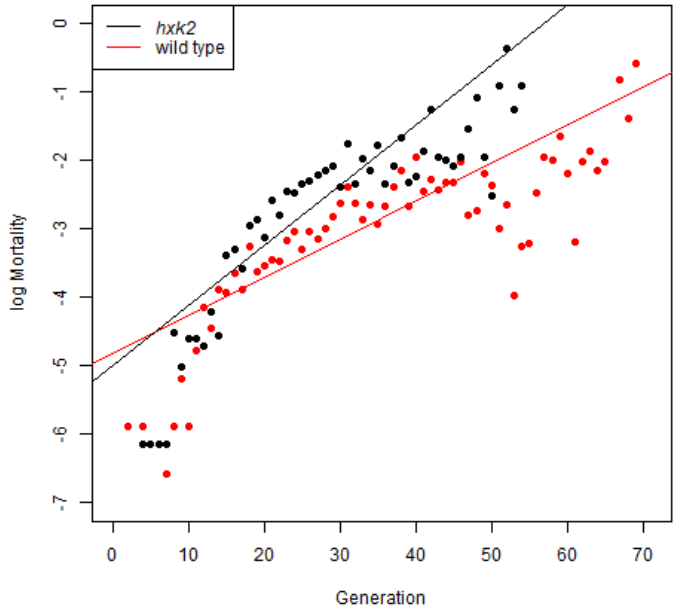
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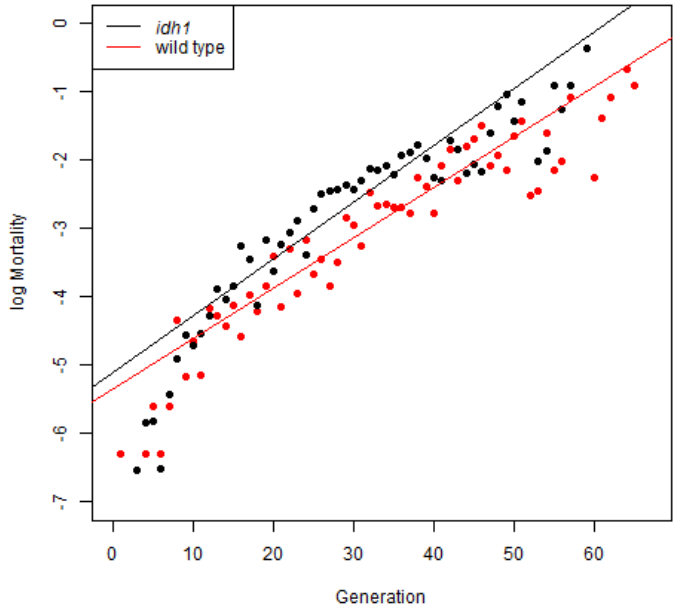
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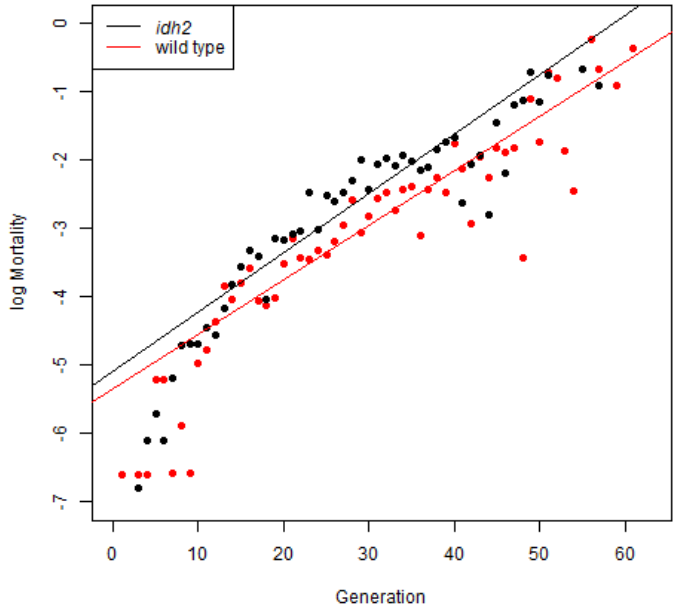
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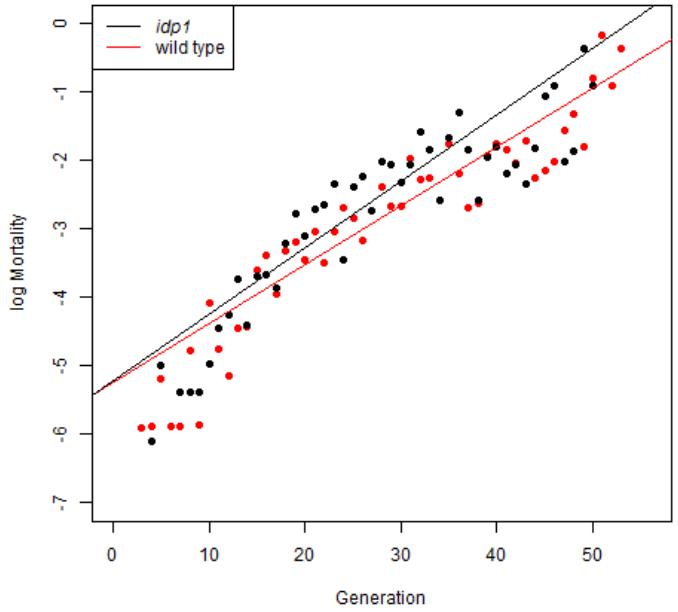
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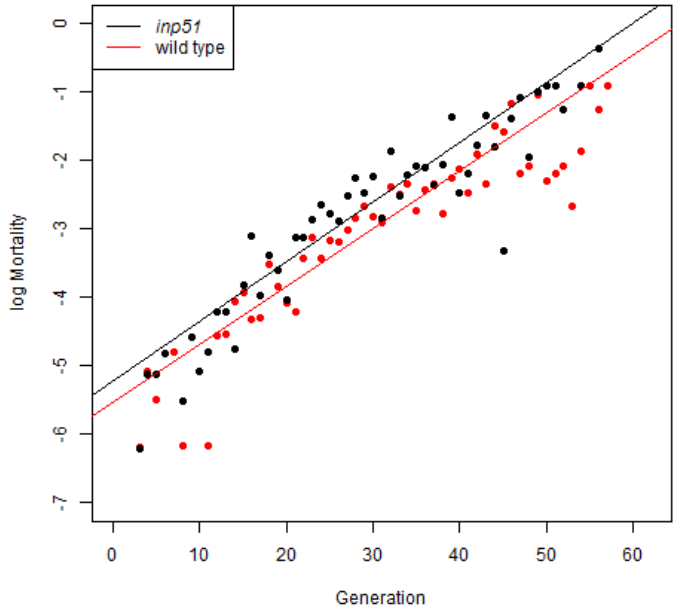
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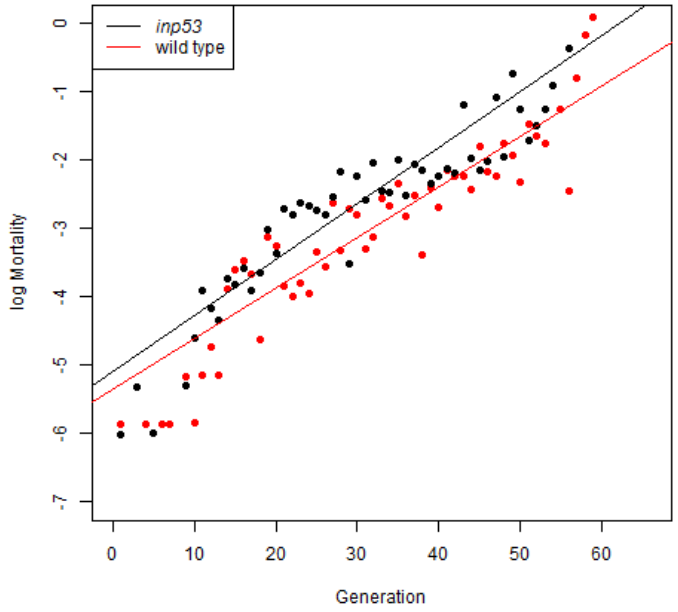
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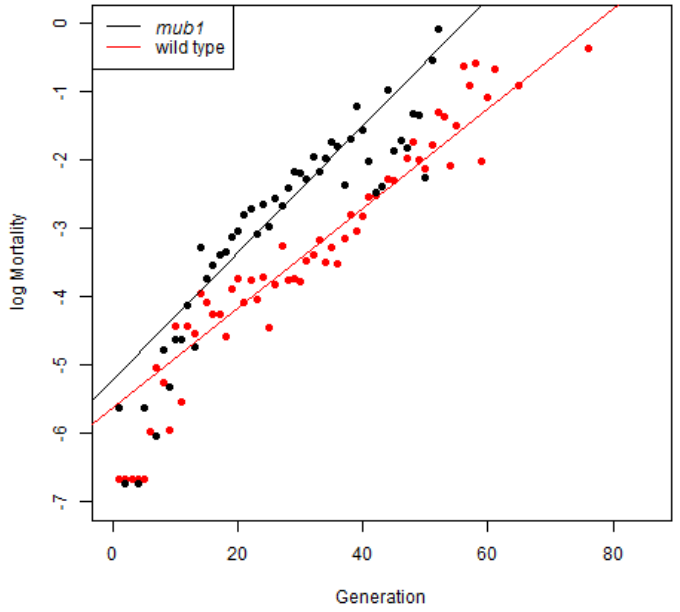
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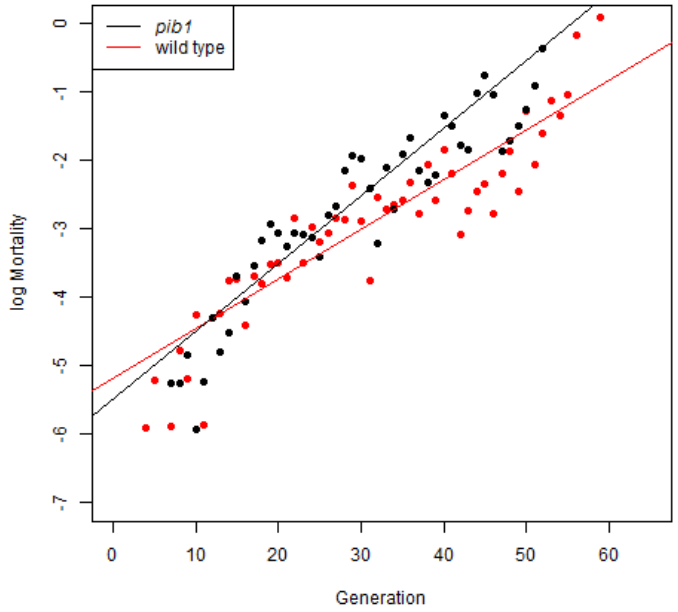
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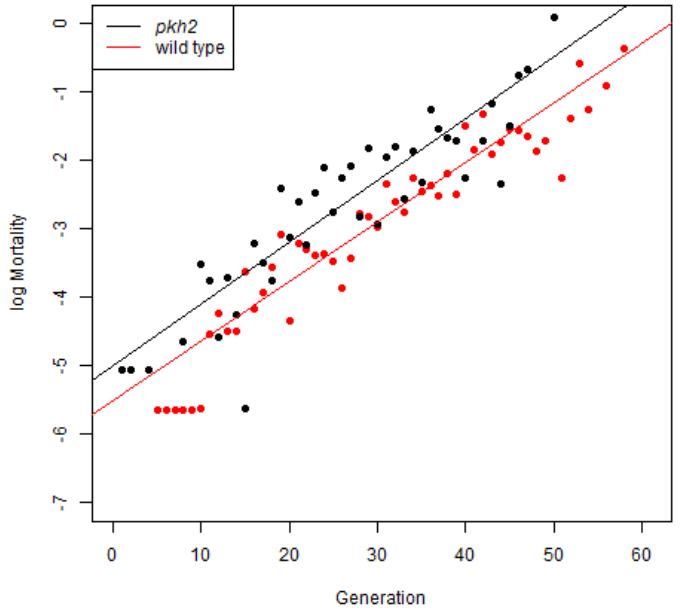
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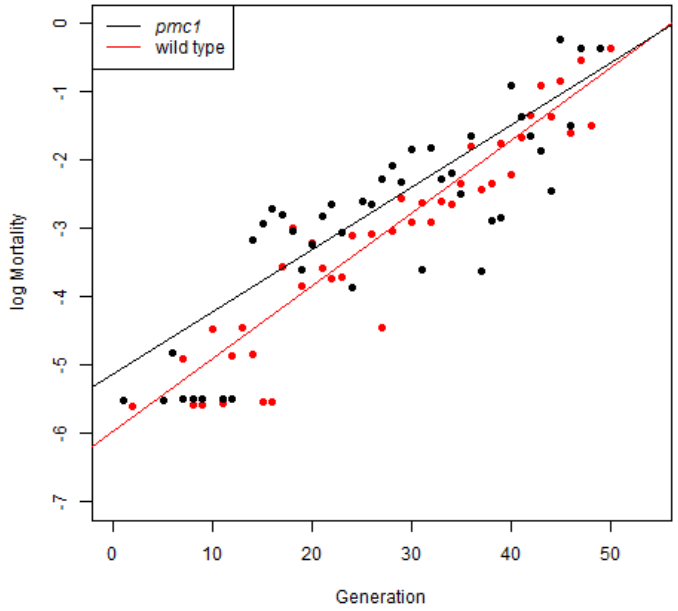
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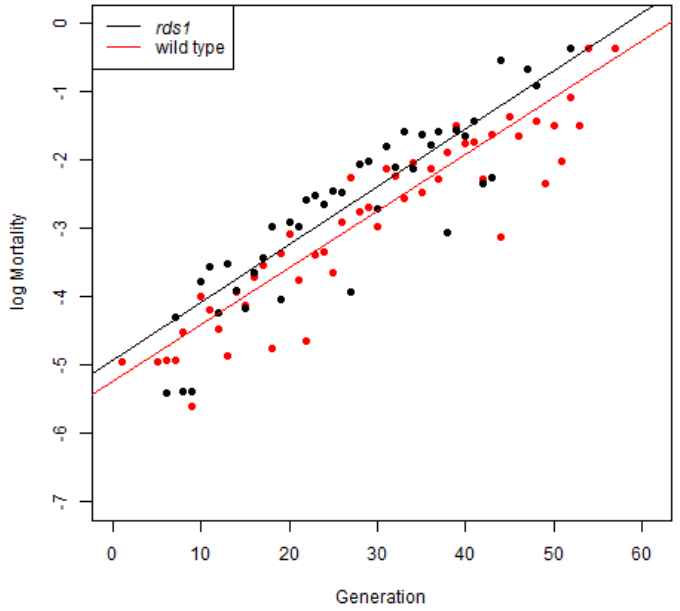
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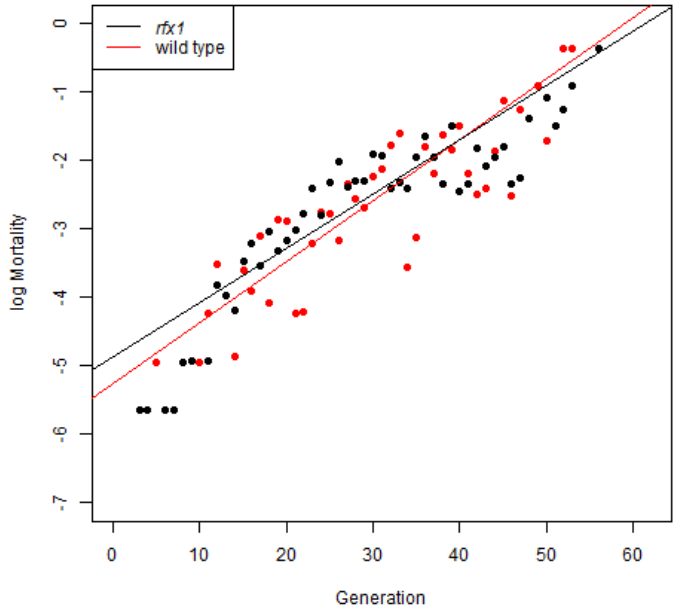
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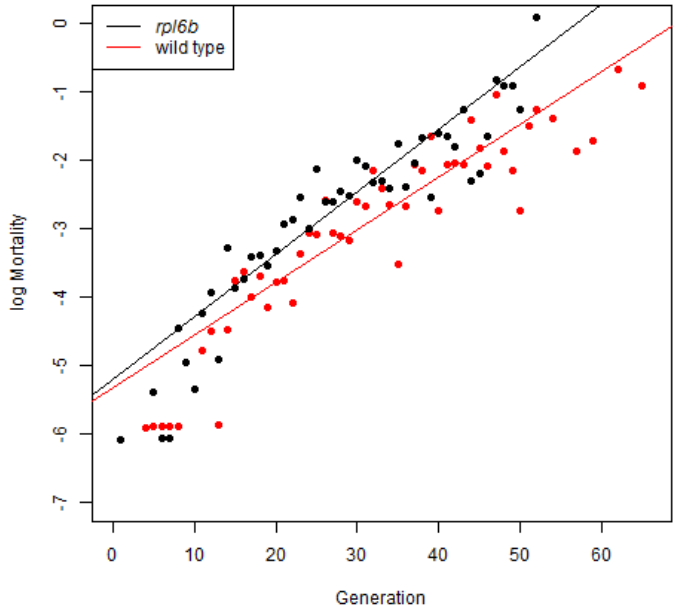
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wild type
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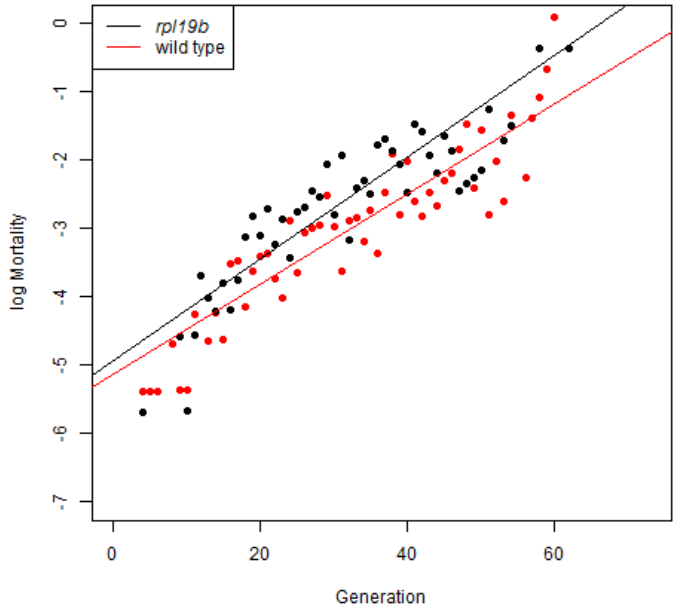
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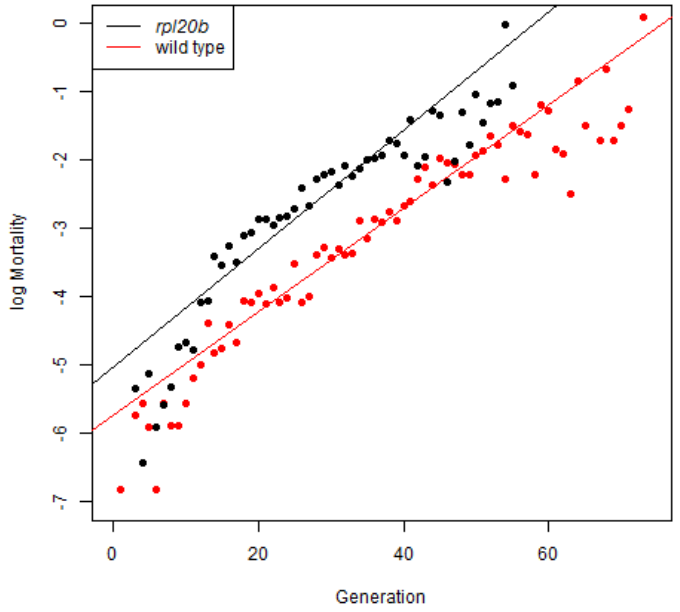
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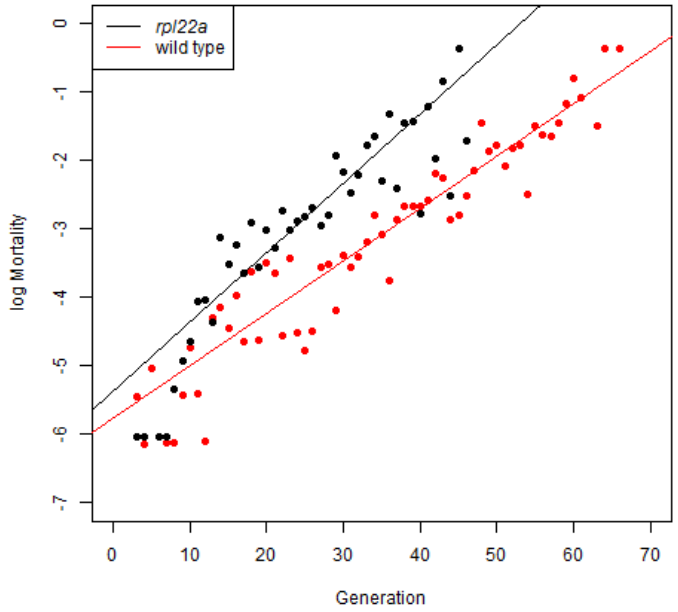
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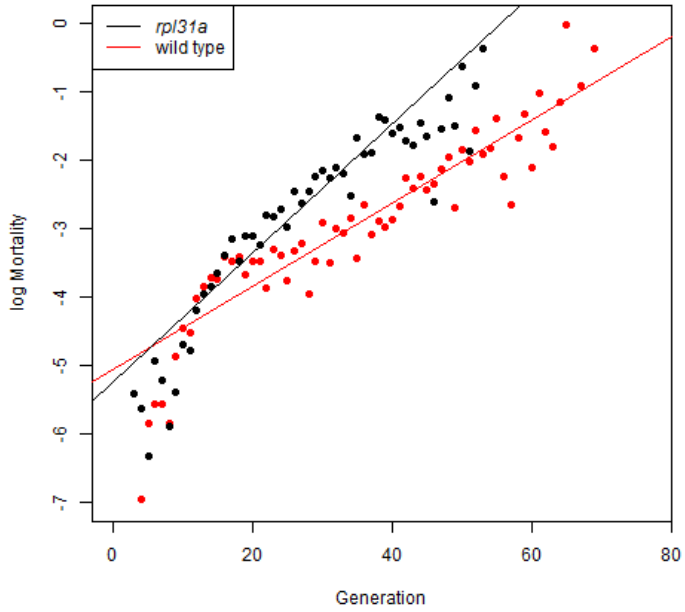
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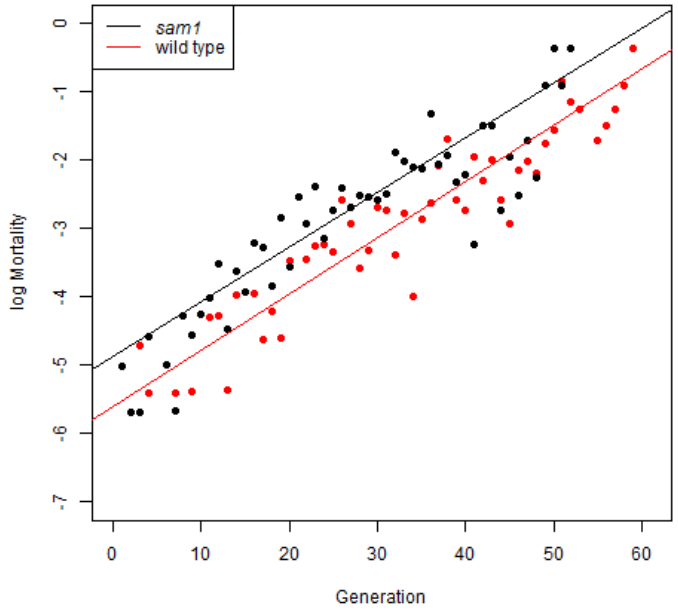
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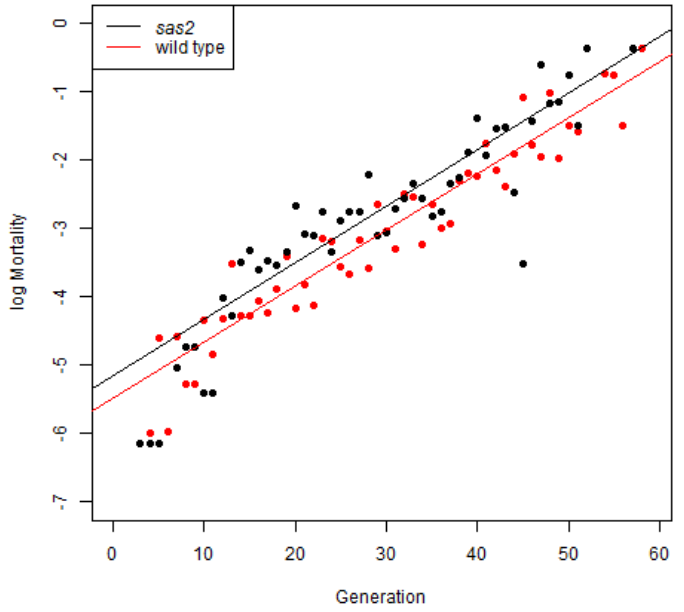
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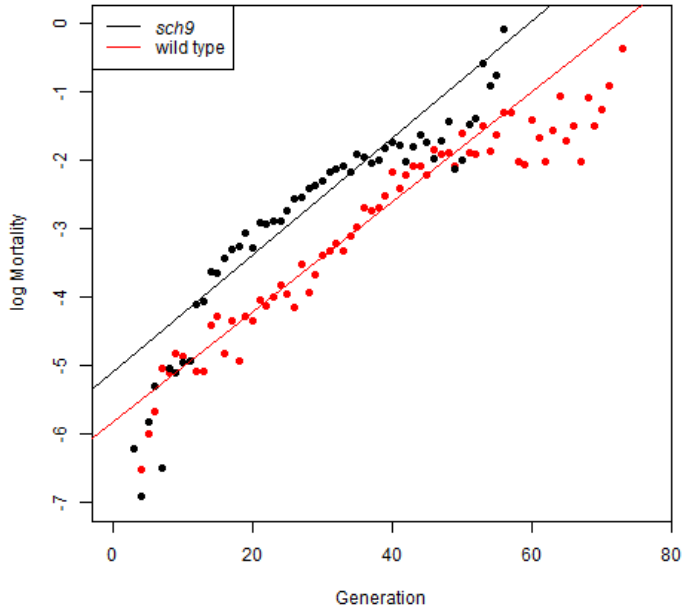
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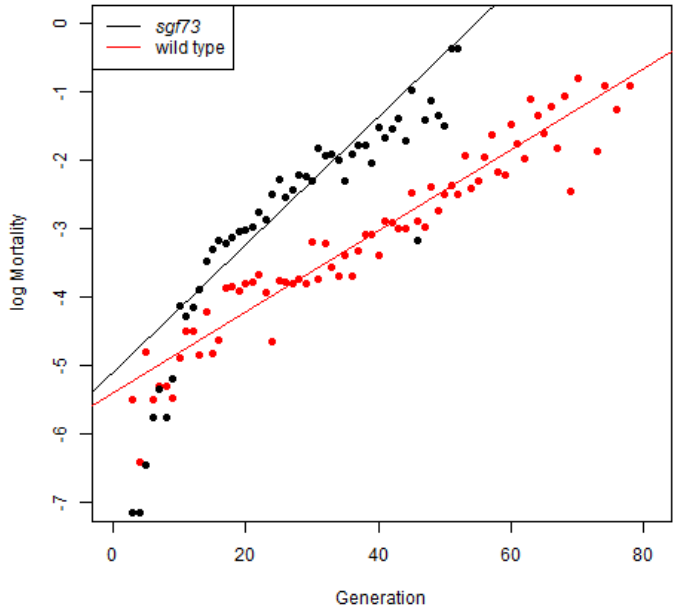
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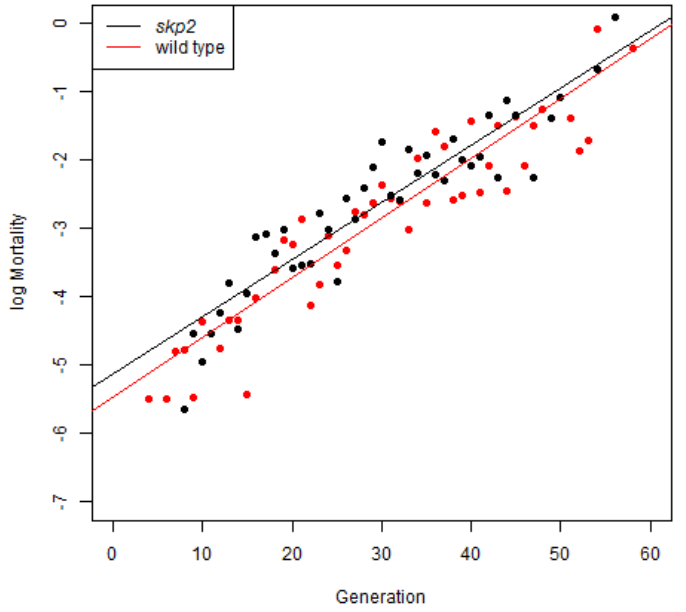
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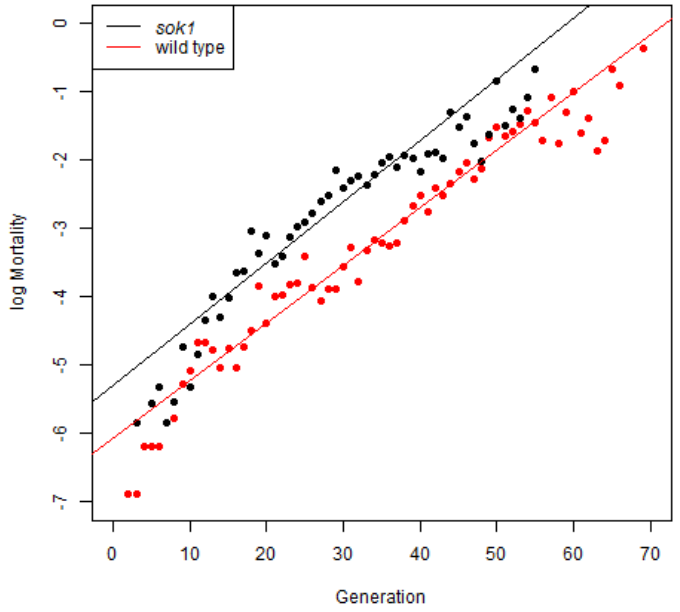
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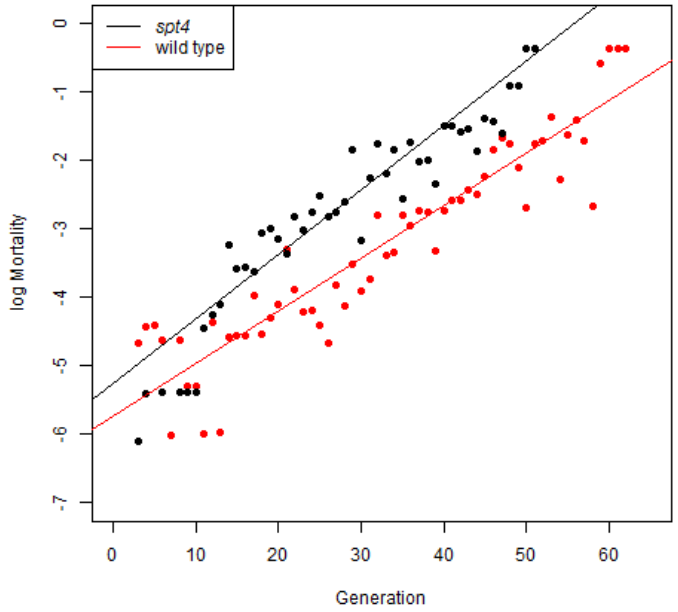
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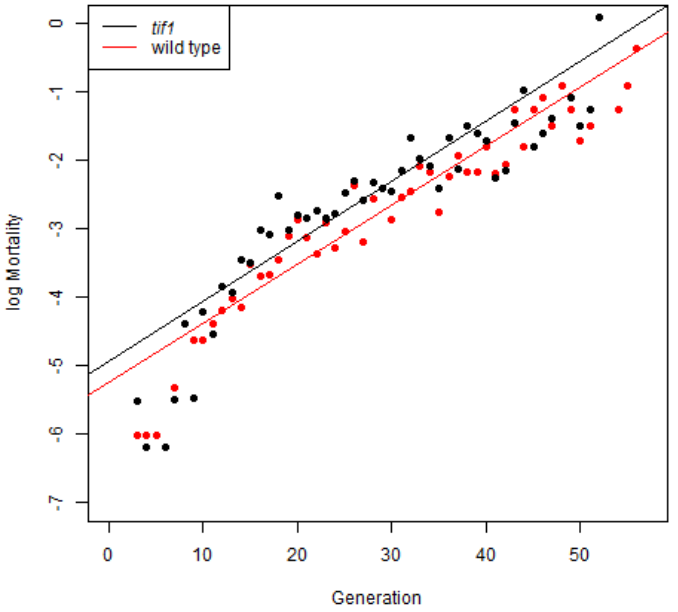
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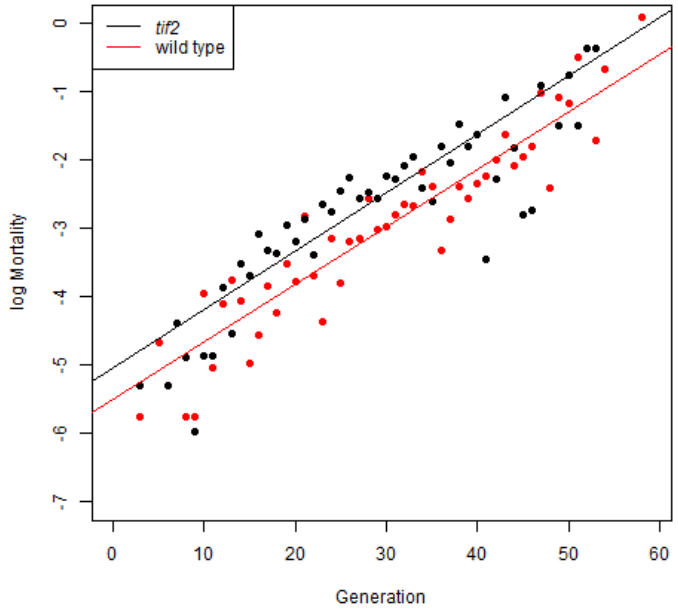
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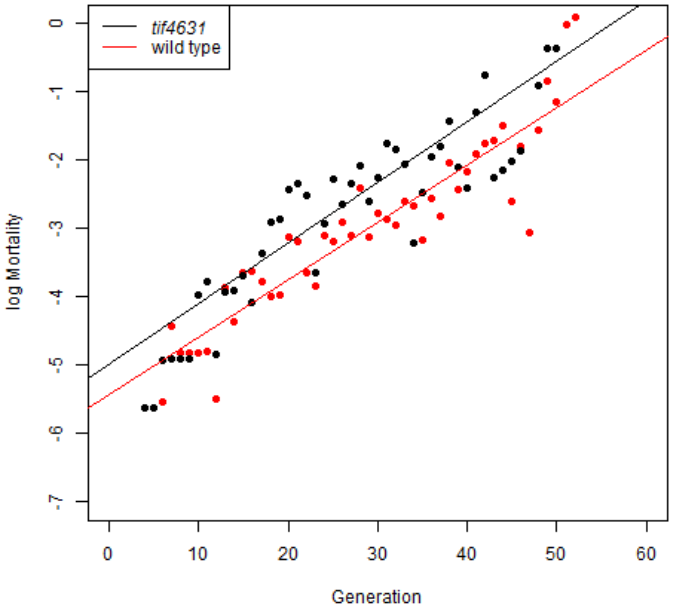
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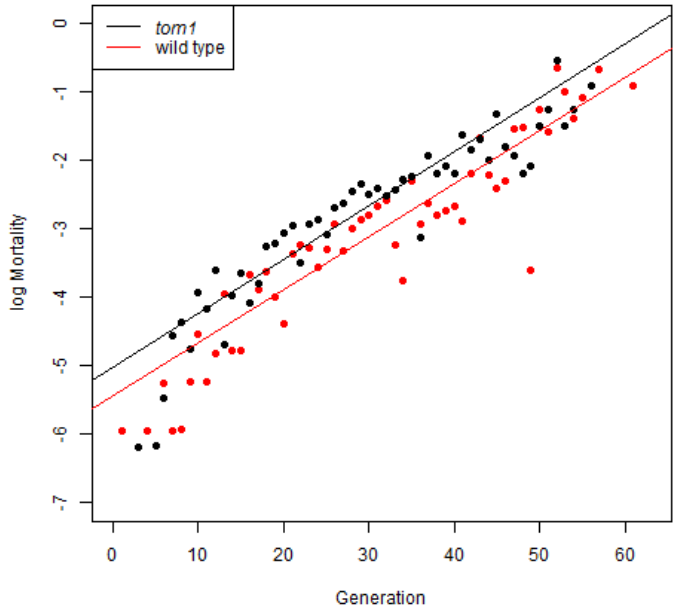
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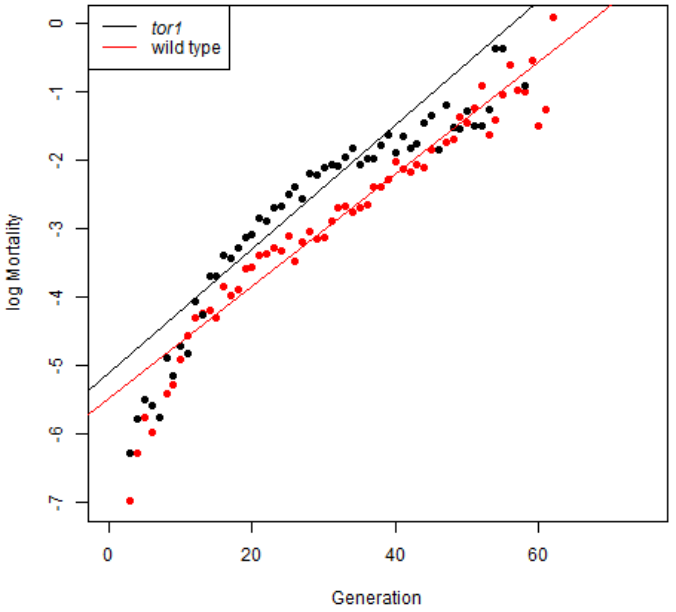
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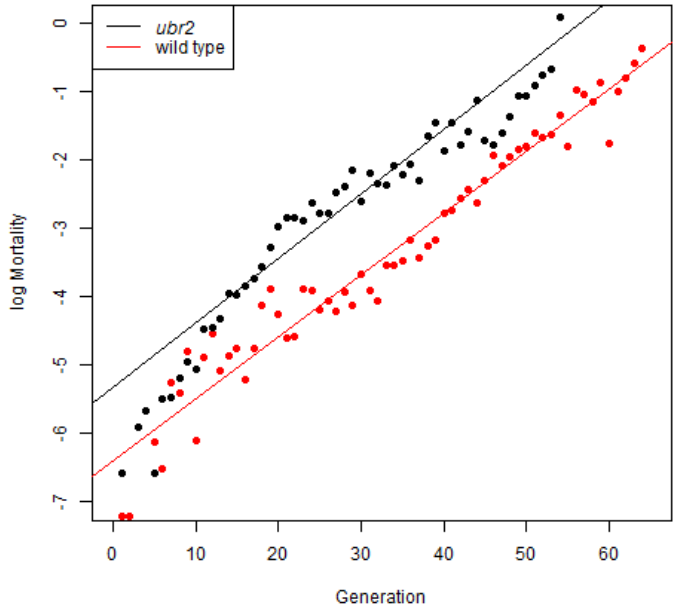
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Supplemental Figure S3.

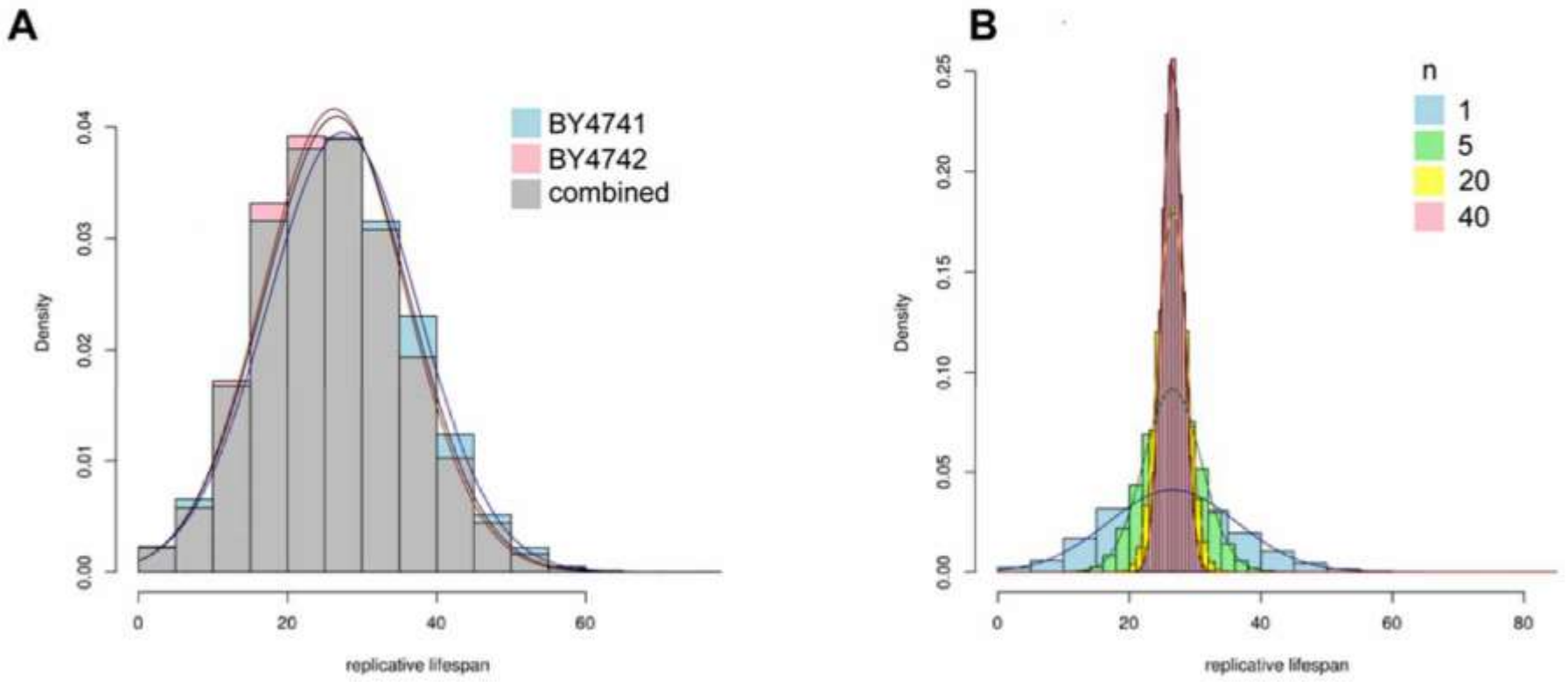
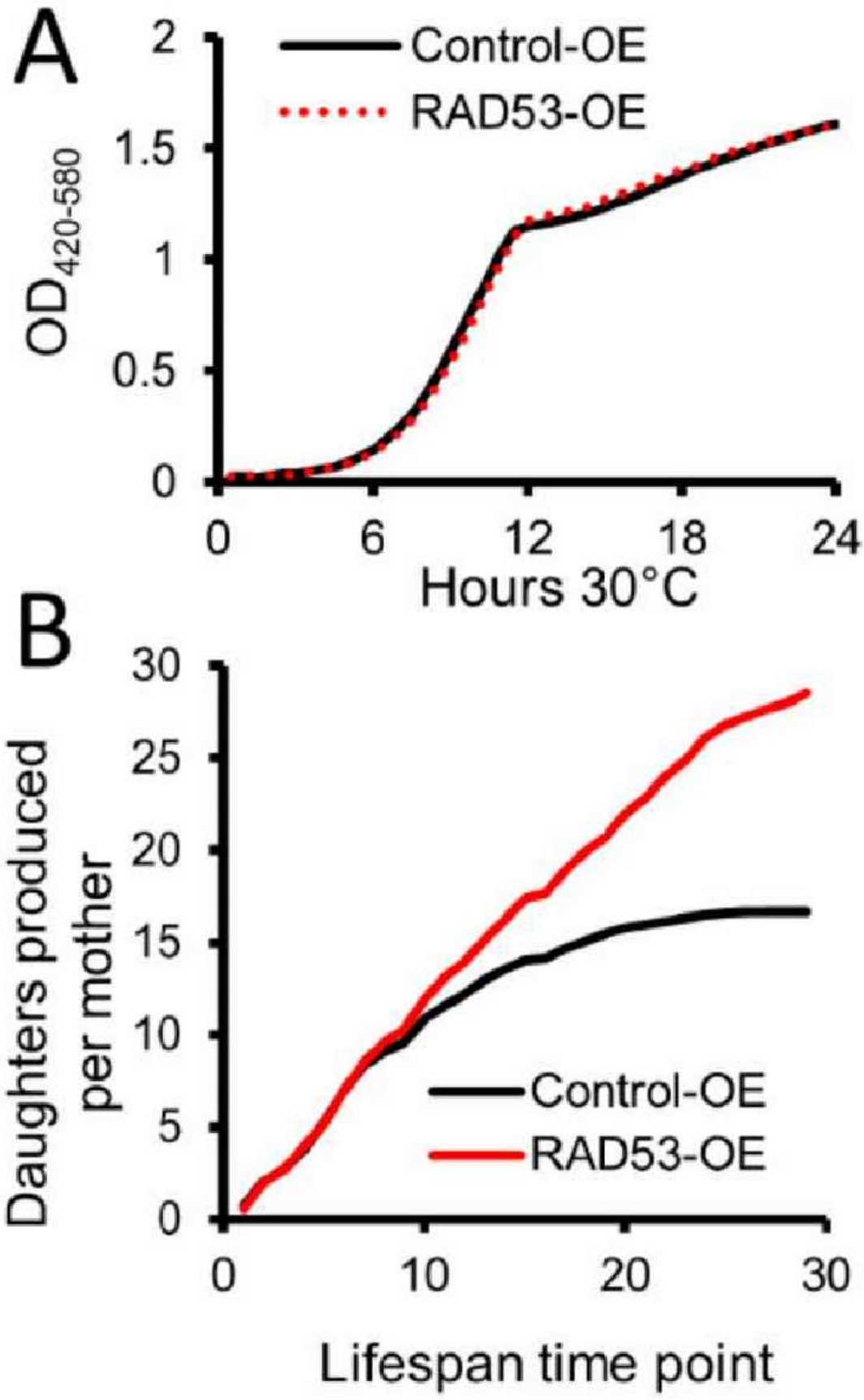


Figure S4



Supplemental Figure S4.

Supplemental Information

Supplemental Figure S1, related to Figure 1. Survival curves of all yeast single gene deletions found to significantly extend replicative lifespan in this study, against experiment-matched wild type control. In all cases the deletion strain is shown in red, and wild type is shown in black. All legends indicate (mean RLS, number of mother cells scored).

Supplemental Figure S2, related to Figure 1. Mortality plots for all yeast single gene deletions found to significantly extend lifespan for which we had more than 200 mother cells of lifespan data. Plots indicate log Mortality vs. generation of mother cell. In all cases deletion strains are shown in black and wild type is shown in red. Overlaid lines are maximum likelihood estimation of Gompertz parameters.

Supplemental Figure S3, related to Figure 2. A. Distribution of wild-type RLS for 220,000 mother cells. Histograms indicate the actual distributions by proportion, of mean RLS for BY4741 *MATa* (light blue), BY4742 *MATα* (pink), and all cells combined (grey). Traces indicate the normal distribution with identical mean and variance to the histogram data in each case. B. Histograms of the actual distributions by proportion, of mean sample RLS for sample sizes of 1 (light blue, for reference) 5 (light green), 20 (yellow), and 40 (pink) mother cells. Generated using 1,000,000 random samples with replacement. Traces indicate normal distribution with identical mean and variance to histogram in each case.

Supplemental Figure S4, related to Figure 5. A. Growth curves of strains used in Figure 4D. No difference was noted. B. The number of daughters produced in the lifespans from Figure 4D as a function of dissection time-point.

Supplemental Table S1, related to Figure 1. List of gene deletions tested in this screen. These are all *S. cerevisiae* ORF deletions that were screened in at least 5 cells in the initial round of the screen. Unique Gene ID, gene name where extant, and a brief description are given for each ORF.

Supplemental Table S2, related to Figure 1. Genes whose deletion extends the replicative lifespan of *S. cerevisiae*. For each genotype, mean RLS, mean RLS of experiment matched control, % increase in mean RLS relative to control, and p-value for increased RLS by Wilcoxon rank-sum are given for *MATa* and *MATα*, respectively. Mean RLS values are highlighted for clarity with a color scale from red (shortest) to green

(longest). p-values are highlighted for clarity with a monochromatic blue color scale proportional to p-value, from low (darkest) to high (lightest).

Supplemental Table S3, related to Figure 2. A. Individual comparison false positive rates for increased RLS vs. wild-type in BY background. The right margin lists sample sizes, n. The top margin lists % RLS increase relative to control in 5% increments. The individual table cells show the proportion of false positives at the given n and % increase estimated by resampling of our actual data one million times for each n and % change. B. Estimated false negative rates at 30% mean RLS increase cutoff, for 5, 10, and 40 cells. For each listed actual % increase in lifespan by genotype, and sample size n, the false negative proportion is given starting with a decision criterion of 30% increased sample RLS vs. control. C. Estimates of undiscovered non-essential genes that alter lifespan in *S. cerevisiae*. Based on our false negative rate estimates and the number of genes identified in the screen, we estimate the number of non-essential genes that remain to be discovered for each range of % increase in RLS relative to wild type, for increases > 25%.

Supplemental Table S4, related to Table 2. Genes reported to exhibit hypomorphic lifespan extension in *C. elegans*. This is the complete list of *C. elegans* ORFS compiled from published findings whose knockdown, deletion, null, or hypomorph extends lifespan, used for comparison to our long-lived *S. cerevisiae* deletions. For each ORF, the wormbase WBGene ID, gene name where extant, and gene and CDS sequence designations are listed.

Supplemental Table S5, related to Figure 4. A. Statistics for replicative lifespans of tRNA synthetase pathway experiments. B. Statistics for microscopy data.

Supplemental Table S6, related to Figure 5. A. List of genes transcriptionally up or down regulated in *los1*Δ and GO annotations enriched in upregulated *los1*Δ genes.

Supplemental Table S7, related to Figure 3. Non-deletion collection strains used in this publication.

Supplemental Table S8, related to Figure 5. Primers used in qPCR experiments.

Extended Experimental Procedures

Strains and plasmids

Prototrophic deletions were made using homologous recombination following amplification of the marker from pRS303, pRS305, or pRS306. All deletions, plasmids, and spore clones were verified by PCR or sequencing

prior to analysis. Additional gene copy plasmids were taken from the Princeton pMoBY collection (Ho et al., 2009) as a generous gift from Maitreya Dunham. These low copy native promoter plasmids were chosen to minimize off-target effects of excessive or mistimed expression that can be found in other expression systems (Minehart and Magasanik, 1991). GFP genomically tagged strains were generated by backcrossing to BY4742 from the collection (Huh et al., 2003); initial GFP strains were a gift from Stan Fields.

Replicative lifespan

In any plasmid containing lifespan, we assured cells began their lifespan with a plasmid by patching onto selective plates prior to analysis, and performed lifespans on mother cells transferred directly from the selective media to YEPD lifespan plates. YEP agar plates (1% yeast extract, 2% bacto-peptone, 2% agar) containing 2% glucose were utilized and strains were grown at 30°C. The control plasmid alone slightly shortened RLS, as previously reported (Falcon and Aris, 2003). Kaplan-Meier survival curves (Kaplan and Meier, 1958) were plotted using Prism (GraphPad, USA).

False positive and negative simulations.

During the course of this screen, we have generated a large amount of data on the distribution of replicative lifespans in wild type yeast in the BY strain background. Using a snapshot of wild-type BY cells grown under standard conditions (YPD solid media at 30C), we can characterize 8,229 *MAT**a*** (BY4741) cells with an RLS mean and standard deviation (SD) of 27.4 and 10.1, and 21,154 *MATα* (BY4742) with an RLS mean and SD of 26.3 and 9.6, whose pooled mean and SD are 26.6 and 9.7 (**Supplemental Figure S3A**). This wild-type data alone represents the manual dissection of over 780,000 individual yeast daughter cells away from their respective mothers, and gives us by far the most comprehensive summary of RLS in a population of laboratory yeast to date. These wild-type replicative lifespans are normally distributed, as shown in **Supplemental Figure S3A**. As such, we might be able to approximate the sampling distributions for samples of size n by assuming perfect normality. However, given the large pool of actual data, we opted to randomly sample the pooled wild-type RLS data 1,000,000 times with replacement, for n of interest using R (R Development Core Team, 2013) to generate actual sampling distributions. Representative sampling distributions for 1, 5, 20, and 40 cells are shown in **Supplemental Figure S3B**. Using these distributions, we can ask the probability of a false-positive sample of size n for specific % increase in RLS. If we had stopped at our screen first pass of 5 cells with a required 30% increase in RLS, for example, our false positive rate would have been 0.037 (implying that for every 100 strains of normal lifespan analyzed in this manner, 3.7 would be falsely scored as long-lived), at 20 cells < 0.0002, and at 40 cells < 1E-6. Individual comparison false positive rates for n of 5, 20, 40, 60, 80, and 120 at increases of 5, 10 … 45 % are displayed (**Supplemental Figure S3C**, **Supplemental Table S3)**.

In order to estimate false negative rates, we can again work from our comprehensive description of the distribution of wild-type RLS, by assuming that the standard deviation or variance of long-lived strains is unchanged, and the mean is adjusted by the % increase described relative to the wild-type mean. Using these sampling distributions, we summarize estimated false negative rates for a 30% increase threshold, for n= 5, 10, and 40, and for actual deletion genotype RLS increases of 30, 35 … 60 % (**Supplemental Figure S3D**, **Supplemental Table S3**). With these estimated false negative rate estimates at a first-pass n of 5, we can use the number of identified deletions exhibiting a given % increase in RLS to conservatively estimate the number of remaining unidentified viable deletions, and thus the total number of viable deletions likely to exhibit a given increase in RLS (**Supplemental Table S3**). These results indicate that the estimated total number of missed viable deletions that extend > 50% relative to wild-type is likely < 1. For a 40% increase in RLS, we estimate ~ 10 additional viable deletions, and for a 30% increase, ~ 58 additional viable deletions.

As described in our results, there is a class of S. cerevisiae genes that are not counted in these false negative estimates; namely essential genes. We might use the fraction of the genome not screened by virtue of being essential (about 20%), multiplied by the number of hits found at each effect level, as a very rough approximation of the possible number of essential genes one would hope to find by screening hypomorphs of non-deleteable genes. Following Table 3, for example, we might estimate 8 essential genes whose knockdown could affect lifespan by 35-45%. However, these approximations are just that, and we do not have the same statistical certainty that we can apply when estimating false negative rates within the non-essential genes themselves.

Fluorescence Microscopy

Cells were grown to log phase by dilute streaking on SC-HIS plates (to select for GFP+ cells) 16 hours prior to analysis. Cells were resuspended in 30µl SC media containing 1µM DAPI and 2.5µl of the cell suspension were used in a Teflon printed slide 6mm well. Pictures were taken using a Zeiss Axiovert 200M fluorescence microscope using AxioVision 4.8 software. Blinded images were analyzed on AxioVision and GFP pixels overlapping strong, nuclear DAPI signals were chosen to measure pixel intensity for nuclear GFP, and a non-vacuolar (and extra-nuclear) GFP pixel was chosen as a cytosolic measurement. A pixel nearby the cell was chosen to subtract background from all measurements. Pictures were analyzed in sets of 20 cells and the results were pooled for statistical analysis, with the pooled statistics shown in **Supplemental Table S5**. Statistics were performed by comparing individual cell fluorescence ratios by Student's t-test.

Flow Cytometry

GFP quantitation by flow cytometry was performed on live cells prepared as in microscopy experiments, except instead of resuspending cells in SC media with DAPI, they were resuspended in ice water and immediately run through the flow cytometer. GFP intensity values were calculated as mean raw GFP intensity subtracted by GFP auto fluorescence of isogenic cells grown under identical conditions. All values were also normalized to relative cell size, as measured by forward scatter. Fold changes were normalized to normal 2% glucose growth conditions of WT (but GFP tagged) cells as an intensity of "1". Values were compared by Student's t-test for statistical analysis. At least 20,000 cells were counted on multiple, independent days. FCS Express was used for flow cytometry data analysis.

Polysome Profiles

125ml of log phase (0.4-0.6 OD, as close to 0.5 OD as possible) yeast were quickly cooled by addition of 60ml frozen YPD containing 133µg/ml cycloheximide to halt translation immediately and prevent ribosomes from dissociating from RNA. Yeast were spun down and then lysed by glass beads and protein-containing fractions were isolated. 20 OD260 units were used for each polysome run by adding the lysate to 7-47% sucrose gradients. Gradients were spun for 2 hours at 39k rpm in a Beckmann ultracentrifuge. The resulting gradients were then fractionated and the A254 read, resulting in the polysome graphs in **Figure 4E**.

Microarrays

Wild type and *los1*Δ cells were inoculated in 5ml YEPD overnight culture. Three genetic isolates of each strain were tested, with six cultures (duplicates) for wild type cells and three cultures for *los1*Δ cells. Overnight cultures were then diluted to <0.05 OD_{600} in 50ml YEPD and shaken at 225 rpm at 30°C until exactly 0.5 OD_{600} was reached. The entire culture was then transferred to conical tubes and centrifuged at 4°C for 2 minutes at 3000g in a counter top centrifuge. Supernatant was removed and resuspended in 1 ml ice cold Martin lysis buffer (40mM KCl, 7.5 mM $MgCl_2$, 1 mM DTT, 25 mM Tris-HCl pH7.5, 0.5 mg/ml heparin, 100µg/ml cycloheximide, in ddH_2O). Suspensions were transferred to microfuge tubes containing 0.4g glass beads (Sigma) and vortexed for 30 seconds, 8 times with 30 seconds on ice between vortex steps. 10µl of 20% triton X-100 and 10µl 20% Na deoxycholate were added to each tube and vortexed for 15 seconds. Lysate was cleared of debris by centrifugation at 17k g in a microcentrifuge at 4°C for 2 minutes. Cleared lysate was then treated by the RNeasy Qiagen RNA prep following the manufacturer's protocol. Integrity of RNA samples was assessed with an Agilent 2100 Bioanalyzer. The Affymetrix 3'-IVT Express Kit was used to process the samples using 100 ng total RNA starting material. Manufacturer protocols were used to process Affymetrix GeneChip Yeast Genome 2.0 Arrays (Santa Clara, CA). Hybridized arrays were scanned with an Affymetrix

GeneChip® 3000 scanner. Image generation and feature extraction were performed using the Affymetrix Gene Chip Command Console (AGCC) software.

Raw microarray data was processed and analyzed with Bioconductor (http://www.bioconductor.org/). The data were normalized with the Bioconductor oligo package (Carvalho and Irizarry, 2010). From the normalized data, genes with significant evidence for differential expression were identified using the Bioconductor limma package (Smyth, 2004). P-values were calculated with a modified t-test in conjunction with an empirical Bayes method to moderate the standard errors of the estimated log-fold changes. P-values were adjusted for multiplicity with the Bioconductor package qvalue (Tusher et al., 2001), which allows for selecting statistically significant genes while controlling the estimated false discovery rate. The microarray data were deposited in the GEO public database, GEO accession number GSE37241.

To check expression by RT-qPCR, cells and RNA were harvested as in the microarray preparations. Superscript III (Invitrogen) reverse transcriptase was used according to manufacturer specifications to synthesize cDNA. SYBR Green (Invitrogen) was used to assay the qPCR steps also according to manufacturer specifications. A Roto-Gene 3000 (Corbett Research) was used to perform the reaction steps and default automated analysis was utilized to calculate Ct values. A single unit difference in Ct was defined as a two-fold change, and fold changes were based on subtracting the Ct values for the housekeeping gene (*PRP8*) to equalize loading between genotypes. At least triplicate runs were performed and mean values are represented on **Figure 5B**. Primers used are listed in **Supplemental Table S8, related to Figure 5**.