**Table S6. Genes contained in both the randomly selected set of 564 single-gene deletion strains and the predicted longevity associated genes in the binding shortest path longevity network**. (**A**) Replicative life span for each haploid deletion (Δ) and experiment matched wild type mother cells are shown as mean replicative life span with number of cells assayed in parentheses. *P*-value is calculated by a Wilcoxon Rank-Sum test. Pooled haploid data refers to pooled *MAT*α and *MAT***a** deletion and wild type data. The binding shortest path longevity network is still enriched for both (**B**) long-lived and **(C)** short-lived deletion strains, relative to the set of randomly selected deleltion strains (R564), when these 11 genes are excluded from the analysis**.** The *p*-value category refers to the results of a Fisher's exact test comparing the frequency of (**B**) increased or (**C**) decreased RLS in the R564 set to the Binding SPLN. *Denotes removal of the 11 overlapping ORFs. Statistical analysis with the 11 overlapping ORFs included is shown in Tables 1 and 2.

## A

| | | ***MAT*α** | | | ***MAT*a** | | | **Pooled haploid mating types** | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **ORF** | **GENE** | **Δ** | **BY4742** | **p-value** | **Δ** | **BY4741** | **p-value** | **Δ** | **WT Pooled** | **p-value** |
| YDR101C | ARX1 | 24.4 (25) | 24.5 (35) | 7.6E-01 | 0 (0) | 0 (0) | 0.0E+00 | 24.4 (25) | 24.5 (35) | 7.6E-01 |
| YER177W | BMH1 | 20.1 (10) | 22.7 (10) | 6.8E-01 | 0 (0) | 0 (0) | 0.0E+00 | 20.1 (10) | 22.7 (10) | 6.8E-01 |
| YDR099W | BMH2 | 26.1 (15) | 28.5 (15) | 3.0E-01 | 0 (0) | 0 (0) | 0.0E+00 | 26.1 (15) | 28.5 (15) | 3.0E-01 |
| YHR142W | CHS7 | 18 (5) | 22.4 (5) | 4.6E-01 | 0 (0) | 0 (0) | 0.0E+00 | 18 (5) | 22.4 (5) | 4.6E-01 |
| YOR144C | ELG1 | 25 (5) | 32.8 (5) | 3.8E-01 | 0 (0) | 0 (0) | 0.0E+00 | 25 (5) | 32.8 (5) | 3.8E-01 |
| YDR283C | GCN2 | 25.7 (495) | 27 (565) | 2.8E-02 | 23.3 (180) | 28.8 (220) | 1.1E-08 | 25.1 (675) | 27.5 (785) | 8.5E-07 |
| YKR048C | NAP1 | 24.6 (45) | 27.2 (45) | 6.3E-02 | 0 (0) | 0 (0) | 0.0E+00 | 24.6 (45) | 27.2 (45) | 6.3E-02 |
| YLR350W | ORM2 | 22.6 (10) | 22.7 (10) | 7.0E-01 | 0 (0) | 0 (0) | 0.0E+00 | 22.6 (10) | 22.7 (10) | 7.0E-01 |
| YGR087C | PDC6 | 24.5 (25) | 24.2 (45) | 7.6E-01 | 0 (0) | 0 (0) | 0.0E+00 | 24.5 (25) | 24.2 (45) | 7.6E-01 |
| YDR129C | SAC6 | 14.7 (30) | 25.8 (60) | 2.4E-05 | 0 (0) | 0 (0) | 0.0E+00 | 14.7 (30) | 25.8 (60) | 2.4E-05 |
| YDR477W | SNF1 | 38.8 (40) | 25.5 (40) | 2.4E-06 | 26.1 (100) | 27 (120) | 3.5E-01 | 29.8 (140) | 26.6 (160) | 4.9E-02 |

**B**

| **Dataset** | **Both Haploid Mating Types** | ***p* - value** | **Pooled < 0.05** | ***p* - value** |
|---|---|---|---|---|
| Binding SPLN* (77) | 9.1 % (7) | - | 16.9% (13) | - |
| R564* (553) | 2.7% (15) | 0.01 | 4.2% (23) | $1.2 \times 10^{-4}$ |

**C**

| **Dataset** | **Mean RLS < 15** | ***p* - value** | **Mean RLS < 20** | ***p* - value** |
|---|---|---|---|---|
| Binding SPLN* (77) | 16.9 % (13) | - | 41.6% (32) | - |
| R564* (553) | 3.4% (19) | $2.6 \times 10^{-5}$ | 17.4% (96) | $4.0 \times 10^{-6}$ |