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 MATα and MATa 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 deletion 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.

<table>
<thead>
<tr>
<th>ORF</th>
<th>GENE</th>
<th>Δ</th>
<th>MATα</th>
<th>p-value</th>
<th>Δ</th>
<th>MATα</th>
<th>p-value</th>
<th>Pooled haploid mating types</th>
<th>Δ</th>
<th>WT Pooled</th>
<th>p-value</th>
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<tbody>
<tr>
<td>YDR101C</td>
<td>ARX1</td>
<td>24.4 (25)</td>
<td>24.5 (35)</td>
<td>7.6E-01</td>
<td>0 (0)</td>
<td>0 (0)</td>
<td>0.0E+00</td>
<td>24.4 (25)</td>
<td>24.5 (35)</td>
<td>7.6E-01</td>
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</tr>
<tr>
<td>YER177W</td>
<td>BMH1</td>
<td>20.1 (10)</td>
<td>22.7 (10)</td>
<td>6.8E-01</td>
<td>0 (0)</td>
<td>0 (0)</td>
<td>0.0E+00</td>
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<td>22.7 (10)</td>
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<tr>
<td>YDR099W</td>
<td>BMH2</td>
<td>26.1 (15)</td>
<td>28.5 (15)</td>
<td>3.0E-01</td>
<td>0 (0)</td>
<td>0 (0)</td>
<td>0.0E+00</td>
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<td>28.5 (15)</td>
<td>3.0E-01</td>
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<tr>
<td>YHR142W</td>
<td>CHS7</td>
<td>18 (5)</td>
<td>22.4 (5)</td>
<td>4.6E-01</td>
<td>0 (0)</td>
<td>0 (0)</td>
<td>0.0E+00</td>
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<tr>
<td>YOR144C</td>
<td>ELG1</td>
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<td>0 (0)</td>
<td>0 (0)</td>
<td>0.0E+00</td>
<td>25 (5)</td>
<td>32.8 (5)</td>
<td>3.8E-01</td>
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<tr>
<td>YDR283C</td>
<td>GCN2</td>
<td>25.7 (495)</td>
<td>27 (565)</td>
<td>2.8E-02</td>
<td>23.3 (180)</td>
<td>28.8 (220)</td>
<td>1.1E-08</td>
<td>25.1 (675)</td>
<td>27.5 (785)</td>
<td>8.5E-07</td>
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<tr>
<td>YKR048C</td>
<td>NAP1</td>
<td>24.6 (45)</td>
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<td>0 (0)</td>
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<tr>
<td>YGR087C</td>
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<td>0.0E+00</td>
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<tr>
<td>YDR129C</td>
<td>SAC6</td>
<td>14.7 (30)</td>
<td>25.8 (60)</td>
<td>2.4E-05</td>
<td>0 (0)</td>
<td>0 (0)</td>
<td>0.0E+00</td>
<td>14.7 (30)</td>
<td>25.8 (60)</td>
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<td>YDR477W</td>
<td>SNF1</td>
<td>38.8 (40)</td>
<td>25.5 (40)</td>
<td>2.4E-06</td>
<td>26.1 (100)</td>
<td>27 (120)</td>
<td>3.5E-01</td>
<td>29.8 (140)</td>
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### B

<table>
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<tr>
<th>Dataset</th>
<th>Both Haploid Mating Types</th>
<th>$p$ - value</th>
<th>Pooled $&lt; 0.05$</th>
<th>$p$ - value</th>
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</thead>
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<tr>
<td>Binding SPLN* (77)</td>
<td>9.1% (7)</td>
<td>-</td>
<td>16.9% (13)</td>
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<tr>
<td>R564* (553)</td>
<td>2.7% (15)</td>
<td>0.01</td>
<td>4.2% (23)</td>
<td>1.2 x $10^{-4}$</td>
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### C

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Mean RLS $&lt; 15$</th>
<th>$p$ - value</th>
<th>Mean RLS $&lt; 20$</th>
<th>$p$ - value</th>
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</thead>
<tbody>
<tr>
<td>Binding SPLN* (77)</td>
<td>16.9% (13)</td>
<td>-</td>
<td>41.6% (32)</td>
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<tr>
<td>R564* (553)</td>
<td>3.4% (19)</td>
<td>2.6 x $10^{-5}$</td>
<td>17.4% (96)</td>
<td>4.0 x $10^{-6}$</td>
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</tbody>
</table>