## Table S1. Unknown and unclassified genes regulated by changes of iron conditions

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<td>Fold changes&lt;sup&gt;\text{*}&lt;/sup&gt; (Wt: L-Fe vs. H-Fe)</td>
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</tbody>
</table>

* Description:

Table S1. Continued

<p>| 6.6949 | 19.3096/19.10608 | no good homologies | -29.3 |
| 6.4418 | 19.4052/19.11534 | no good homologies | -11.3 |
| 6.5180 | 19.9951          | no good homologies | -11.1 |
| 6.2070 | 19.378/19.8011   | no good homologies | -7.0  |
| 6.5407 | 19.6186          | no good homologies | -5.6  |
| 6.1028 | 19.9185          | no good homologies | -5.0  |
| 6.1246 | 19.2452/19.9988  | no good homologies | -4.9  |
| 6.6407 | 19.1549/19.9123  | no good homologies | -4.9  |
| 6.819  | 19.1179          | no good homologies | -4.8  |
| 6.1979 | 19.1953/19.9508  | no good homologies | -4.4  |
| 6.7151 | 19.6887/19.14176 | no good homologies | -4.2  |
| 6.6048 | 19.4942/19.12408 | no good homologies | -3.8  |
| 6.5314 | 19.3716/19.11201 | no good homologies | -3.7  |
| 6.2290 | 19.3773          | no good homologies | -3.6  |
| 6.214  | 19.9351/19.1785  | no good homologies | -3.4  |
| 6.818  | 19.1178/19.8768  | no good homologies | -3.1  |
| 6.805  | 19.11599/19.4117 | no good homologies | -2.9  |
| 6.8565 | 19.7405          | no good homologies | -2.9  |
| 6.6381 | 19.1412/19.8988  | no good homologies | -2.9  |
| 6.3105 | 19.8888/19.1308  | no good homologies | -2.8  |
| 6.6228 | 19.6113/19.13532 | no good homologies | -2.6  |
| 6.9054 | 19.5983/19.13404 | no good homologies | -2.6  |
| 6.8318 | 19.5329/19.12789 | no good homologies | -2.5  |
| 6.8172 | 19.7272          | no good homologies | -2.5  |
| 6.4301 | 19.292/19.7924   | no good homologies | -2.5  |
| 6.7184 | 19.6920          | no good homologies | -2.3  |
| 6.8937 | 19.7589          | no good homologies | -2.2  |
| 6.279  | 19.11989/19.4514 | no good homologies | -2.1  |
| 6.5580 | 19.2328/19.9864  | no good homologies | -2.1  |
| 6.2045 | 19.3587          | no good homologies | -2.1  |</p>
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<tr>
<th>ORF (Assembly6)</th>
<th>ORF &amp; Allele (Assembly19)</th>
<th>Gene name</th>
<th>Description</th>
<th>Fold changes(^a) Wt (L-Fe vs. H-Fe)</th>
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<td>ORF (Assembly6)</td>
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<td>Description</td>
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<td>6.5264</td>
<td>19.6550/19.13903</td>
<td>similar to <em>S. cerevisiae</em></td>
<td>YOR228C</td>
<td>-4.4</td>
</tr>
<tr>
<td>6.1483</td>
<td>19.10685/19.3175</td>
<td>similar to <em>S. cerevisiae</em></td>
<td>YOR356W</td>
<td>-3.9</td>
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</tbody>
</table>
Table S1. Continued

<table>
<thead>
<tr>
<th>ORF (Assembly6)</th>
<th>ORF &amp; Allele (Assembly19)</th>
<th>Gene name</th>
<th>Description</th>
<th>Fold changes&lt;sup&gt;a&lt;/sup&gt; Wt (L-Fe vs. H-Fe)</th>
</tr>
</thead>
<tbody>
<tr>
<td>6.4409</td>
<td>19.11525/19.4043</td>
<td>similar to <em>S. cerevisiae</em> YPR115W</td>
<td>-4.0</td>
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<td>6.6573</td>
<td>19.680/19.8297</td>
<td>similar to <em>S. cerevisiae</em> YPL063W</td>
<td>-2.8</td>
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<tr>
<td>6.7606</td>
<td>19.6062/19.13483</td>
<td>similar to <em>S. cerevisiae</em> YPL098C</td>
<td>-4.1</td>
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<td>6.7082</td>
<td>19.489/19.8119</td>
<td>similar to <em>S. cerevisiae</em> YPL170W</td>
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<td>6.2205</td>
<td>19.12987/19.5541</td>
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<tr>
<td>6.247</td>
<td>19.384/19.8014</td>
<td>similar to <em>S. cerevisiae</em> YPL247C</td>
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<tr>
<td>6.7663</td>
<td>19.5279/19.12744</td>
<td>similar to <em>S. cerevisiae</em> YPR100W</td>
<td>-3.5</td>
<td></td>
</tr>
</tbody>
</table>

<sup>a</sup>Identical or the most closely matched sequences in the assembly 19 of *C. albicans* genome project.

<sup>b</sup>Fold changes are derived from the average of four individual comparisons as described in experimental procedures. The positive and negative (shaded) values represent the transcripts having a higher expression level at the low- and high-iron conditions, respectively.