Table S1. **List and characteristics of the detected pseudogenes in the 8 studied yeast genomes.**

The table is in Additional file 2

Pseudogenes are named according to their position along the chromosome (from left to right end, see text for nomenclature). Chromosomes, coordinates and orientation of pseudogenes are given in columns 2-5. The closest functional homolog among the 8 species studied (bestmatch) and classification of its product into protein families are given in column 6-7. Gene nomenclature refers to (16), family classification refers to (58).

Columns 8-10: characteristics of pseudogene by comparison to its bestmatch.
- **R.L:** relative length of the pseudogene with respect to its bestmatch length.
- **D.A:** amino acid divergence between the pseudogene and its bestmatch (see METHODS).
- **D.N:** nucleotide divergence between the pseudogene and its bestmatch (see METHODS).

Columns 11-12:
- **Stop:** number of in-frame stop codons according to FASTY
- **FS:** number of frameshifts according to FASTY

Column 13: pseudogene(s) of the same family, with the same pattern of disabling mutations. Pseudogenes with an asterisk are part of a larger duplicated region including other genes.

Note that a few pseudogenes were already mentioned in the original annotation of *C. glabrata, D. hansenii, K. lactis* and *Y. lipolytica* (13), and the result of the present work served for the recent updates of their annotation, as well as for the annotation of the newly sequenced genomes of *Z. rouxii, S. kluwyeri* and *K. thermotolerans* (24).
Table S2. **List of gene families (or singletons) with detected pseudogenes.**

The table is in Additional file 2

The phyletic patterns of each family indicate the presence (s, c, r, l, t, k, d, y) or absence (-) of the pseudogene members (column 2) and of the active gene members (column 4) in each species. The one-letter abbreviations are as follows: ‘s’ for *S. cerevisiae*, ‘c’ for *C. glabrata*, ‘r’ for *Z. rouxii*, ‘l’ for *K. lactis*, ‘t’ for *K. thermotolerans*, ‘k’ for *S. kluveri*, ‘d’ for *D. hansenii* and ‘y’ for *Y. lipolytica*.

The general annotation of the *S. cerevisiae* gene members is given in column 7, according to the annotation of the gene indicated in column 6.

The number of pseudogenes is not correlated to the number of their functional paralogs in the same family (from 1 to at least 20 active paralogs can be found per pseudogene). In addition, 61 pseudogenes have been identified by similarity with genes from another species, because they have no paralog and are unique in their genome.
<table>
<thead>
<tr>
<th>Name</th>
<th>Functional homolog</th>
<th>Annotated function in S. cerevisiae or annotation by similarity</th>
</tr>
</thead>
<tbody>
<tr>
<td>SACE0Fp3</td>
<td>DEHA2D01122g</td>
<td>weakly similar to Q899U5 <em>Clostridium tetani</em> Threonine dehydratase</td>
</tr>
<tr>
<td>SACE0Fp2</td>
<td>DEHA2E07282g</td>
<td>similar to Q9J565 <em>Pseudomonas aeruginosa</em> PA0880 Probable ring-cleaving dioxygenase</td>
</tr>
<tr>
<td>SACE0Np2</td>
<td>DEHA2E07282g</td>
<td>similar to Q9J565 <em>Pseudomonas aeruginosa</em> PA0880 Probable ring-cleaving dioxygenase</td>
</tr>
<tr>
<td>CAGL0Lp4</td>
<td>YCR020W-B HTL1</td>
<td>Component of the RSC chromatin remodeling complex</td>
</tr>
<tr>
<td>CAGL0Lp5</td>
<td>YOR043W WHI2</td>
<td>Protein required with binding partner Psr1p for full activation of the general stress response</td>
</tr>
<tr>
<td>CAGL0Mp1</td>
<td>YJR089W BIR1</td>
<td>Essential chromosomal passenger protein involved in coordinating cell cycle events</td>
</tr>
<tr>
<td>ZYRO0Bp8</td>
<td>YDR277C</td>
<td>Protein involved in control of glucose-regulated gene expression</td>
</tr>
<tr>
<td>ZYRO0Bp7</td>
<td>YOR043W WHI2</td>
<td>Protein required with binding partner Psr1p for full activation of the general stress response</td>
</tr>
<tr>
<td>ZYRO0Dp8</td>
<td>YHR084W STE12</td>
<td>Transcription factor, activates genes involved in mating or</td>
</tr>
</tbody>
</table>
pseudohyphal/invasive growth pathways

ZYRO0Gp9 YJR021C REC107 Protein involved in early stages of meiotic recombination

ZYRO0Gp11 YJR089W BIR1 Essential chromosomal passenger protein involved in coordinating cell cycle events

KLTH0Ap7 YCR054C CTR86 Essential protein of unknown function

KLTH0Bp3 YJR021C REC107 Protein involved in early stages of meiotic recombination

KLTH0Cp5 YGL256W ADH4 Alcohol dehydrogenase isoenzyme type IV

KLTH0Dp6 YDL185W TFP1 Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites

KLTH0Ep7 YGL256W ADH4 Alcohol dehydrogenase isoenzyme type IV

KLTH0Ep9 YNR064C Epoxide hydrolase member of the alpha/beta hydrolase fold family

KLTH0Fp3 YLL057C JLP1 Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase involved in sulfonate catabolism

KLTH0Gp3 YDR285W ZIP1 Transverse filament protein of the synaptonemal complex
similar to uniprot|P50505 *Debaryomyces occidentalis* HAK1 high affinity potassium transporter

Proteasome-interacting protein regulatory particle (RP)

Essential UDP-N-acetylglucosamine pyrophosphorylase

DNA repair methyltransferase (6-O-methylguanine-DNA methylase)

Transverse filament protein of the synaptonemal complex

Essential protein required for the DNA integrity checkpoint pathways

Protein involved in bud-site selection nutrient signaling and gene expression

Histone methyltransferase with a role in transcriptional elongation

Protein involved in early stages of meiotic recombination

Transcriptional regulator involved in the repression of GAL genes in the absence of galactose

Epoxide hydrolase member of the alpha/beta hydrolase fold family
SAKL0Fp2     YNR064C  Epoxide hydrolase member of the alpha/beta hydrolase fold family

DEHA2Bp9     YDR280W RRP45  Protein involved in rRNA processing

DEHA2Dp22    YJL085W EXO70  Essential 70kDa subunit of the exocyst complex

DEHA2Ep24    YGL040C HEM2  Delta-aminolevulinate dehydratase

DEHA2Ep15    YDR127W ARO1  Pentafuctional arom protein catalyzes steps 2 through 6 in the biosynthesis of chorismate

DEHA2Ep13    YALI0E11473g similar to uniprot|P50505 Debaryomyces occidentalis HAK1 high affinity potassium transporter

DEHA2Gp11    YOL081W IRA2  GTPase-activating protein that negatively regulates RAS

YALI0Cp8     YOR188W MSB1  Protein involved in positive regulation of both 1,3-beta-glucan synthesis and the Pkc1p-MAPK pathway

YALI0Dp22    YOR274W MOD5  Delta 2-isopentenyl pyrophosphate:tRNA isopentenyl transferase

YALI0Dp8     YHR201C PPX1  Exopolyphosphatase
<table>
<thead>
<tr>
<th>Genes</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>YALI0Fp32</td>
<td>YKL038W RGT1</td>
</tr>
<tr>
<td>YALI0Fp31</td>
<td>YGR112W SHY1</td>
</tr>
<tr>
<td>YALI0Fp5</td>
<td>YGL190C CDC55</td>
</tr>
</tbody>
</table>

*a. pseudogenes without functional paralog (pseudogenes similar to genes with uncharacterized function are not listed).*