

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

Description of Table S2. **List of gene families (or singletons) with detected pseudogenes.**

Table S3. **Lost functions among the eight studied species.** A list of the pseudogenes with no paralog in the different genomes

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. kluyveri* 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. kluyveri*, '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 S3. **Lost functions among the eight studied species.**

| <i>Name<sup>a</sup></i> | <i>Functional homolog</i> | <i>Annotated function in S. cerevisiae or annotation by similarity</i>                            |
|-------------------------|---------------------------|---|
| <i>SACE0Fp3</i>         | <i>DEHA2D01122g</i>       | weakly similar to Q899U5 <i>Clostridium tetani</i> Threonine dehydratase                          |
| <i>SACE0Fp2</i>         | <i>DEHA2E07282g</i>       | similar to Q9I565 <i>Pseudomonas aeruginosa</i> PA0880<br>Probable ring-cleaving dioxygenase      |
| <i>SACE0Np2</i>         | <i>DEHA2E07282g</i>       | similar to Q9I565 <i>Pseudomonas aeruginosa</i> PA0880<br>Probable ring-cleaving dioxygenase      |
| <i>CAGL0Lp4</i>         | <i>YCR020W-B HTL1</i>     | Component of the RSC chromatin remodeling complex   |
| <i>CAGL0Lp5</i>         | <i>YOR043W WHI2</i>       | Protein required with binding partner Psr1p for full activation<br>of the general stress response |
| <i>CAGL0Mp1</i>         | <i>YJR089W BIR1</i>       | Essential chromosomal passenger protein involved in coordinating<br>cell cycle events             |
| <i>ZYRO0Bp8</i>         | <i>YDR277C</i>            | Protein involved in control of glucose-regulated gene expression                                  |
| <i>ZYRO0Bp7</i>         | <i>YOR043W WHI2</i>       | Protein required with binding partner Psr1p for full activation<br>of the general stress response |
| <i>ZYRO0Dp8</i>         | <i>YHR084W STE12</i>      | Transcription factor, activates genes involved in mating or                                       |

pseudohyphal/invasive growth pathways

|                  |                       |   |
|------------------|-----------------------|---|
| <i>ZYRO0Gp9</i>  | <i>YJR021C REC107</i> | Protein involved in early stages of meiotic recombination                                   |
| <i>ZYRO0Gp11</i> | <i>YJR089W BIR1</i>   | Essential chromosomal passenger protein involved in coordinating cell cycle events          |
| <i>KLTH0Ap7</i>  | <i>YCR054C CTR86</i>  | Essential protein of unknown function   |
| <i>KLTH0Bp3</i>  | <i>YJR021C REC107</i> | Protein involved in early stages of meiotic recombination                                   |
| <i>KLTH0Cp5</i>  | <i>YGL256W ADH4</i>   | Alcohol dehydrogenase isoenzyme type IV   |
| <i>KLTH0Dp6</i>  | <i>YDL185W TFP1</i>   | Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites       |
| <i>KLTH0Ep7</i>  | <i>YGL256W ADH4</i>   | Alcohol dehydrogenase isoenzyme type IV   |
| <i>KLTH0Ep9</i>  | <i>YNR064C</i>        | Epoxide hydrolase member of the alpha/beta hydrolase fold family                            |
| <i>KLTH0Fp3</i>  | <i>YLL057C JLP1</i>   | Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase involved in sulfonate catabolism |
| <i>KLTH0Gp3</i>  | <i>YDR285W ZIP1</i>   | Transverse filament protein of the synaptonemal complex                                     |

|                  |                       |   |
|------------------|-----------------------|---|
| <i>KLTH0Hp8</i>  | <i>YALI0C10311g</i>   | similar to uniprot P50505 <i>Debaryomyces occidentalis</i> HAK1 high affinity potassium transporter |
| <i>SAKL0Dp4</i>  | <i>YBR272C HSM3</i>   | Proteasome-interacting protein regulatory particle (RP)   |
| <i>SAKL0Ep17</i> | <i>YDL103C QRI1</i>   | Essential UDP-N-acetylglucosamine pyrophosphorylase   |
| <i>SAKL0Hp7</i>  | <i>YDL200C MGT1</i>   | DNA repair methyltransferase (6-O-methylguanine-DNA methylase)                                      |
| <i>SAKL0Gp7</i>  | <i>YDR285W ZIP1</i>   | Transverse filament protein of the synaptonemal complex   |
| <i>SAKL0Cp4</i>  | <i>YDR499W LCD1</i>   | Essential protein required for the DNA integrity checkpoint pathways                                |
| <i>SAKL0Bp7</i>  | <i>YFL023W BUD27</i>  | Protein involved in bud-site selection nutrient signaling and gene expression                       |
| <i>SAKL0Cp9</i>  | <i>YJL168C SET2</i>   | Histone methyltransferase with a role in transcriptional elongation                                 |
| <i>SAKL0Gp13</i> | <i>YJR021C REC107</i> | Protein involved in early stages of meiotic recombination   |
| <i>SAKL0Dp8</i>  | <i>YML051W GAL80</i>  | Transcriptional regulator involved in the repression of GAL genes in the absence of galactose       |
| <i>SAKL0Bp12</i> | <i>YNR064C</i>        | Epoxide hydrolase member of the alpha/beta hydrolase fold family                                    |

|                  |                      |  |
|------------------|----------------------|--|
| <i>SAKL0Fp2</i>  | <i>YNR064C</i>       | Epoxide hydrolase member of the alpha/beta hydrolase fold family                                     |
| <i>DEHA2Bp9</i>  | <i>YDR280W RRP45</i> | Protein involved in rRNA processing  |
| <i>DEHA2Dp22</i> | <i>YJL085W EXO70</i> | Essential 70kDa subunit of the exocyst complex   |
| <i>DEHA2Ep24</i> | <i>YGL040C HEM2</i>  | Delta-aminolevulinatase  |
| <i>DEHA2Ep15</i> | <i>YDR127W AROI</i>  | Pentafunctional arom protein catalyzes steps 2 through 6 in the biosynthesis of chorismate           |
| <i>DEHA2Ep13</i> | <i>YALI0E11473g</i>  | similar to uniprot P50505 <i>Debaryomyces occidentalis</i> HAK1 high affinity potassium transporter  |
| <i>DEHA2Gp11</i> | <i>YOL081W IRA2</i>  | GTPase-activating protein that negatively regulates RAS  |
| <i>YALI0Cp8</i>  | <i>YOR188W MSB1</i>  | Protein involved in positive regulation of both 1,3-beta-glucan synthesis and the Pkc1p-MAPK pathway |
| <i>YALI0Dp22</i> | <i>YOR274W MOD5</i>  | Delta 2-isopentenyl pyrophosphate:tRNA isopentenyl transferase                                       |
| <i>YALI0Dp8</i>  | <i>YHR201C PPX1</i>  | Exopolyphosphatase   |

*YALI0Fp32*    *YKL038W RGT1*    Glucose-responsive transcription factor

*YALI0Fp31*    *YGR112W SHY1*    Mitochondrial inner membrane protein required for normal respiration

*YALI0Fp5*    *YGL190C CDC55*    Non-essential regulatory subunit B of protein phosphatase 2A

<sup>a</sup>. pseudogenes without functional paralog (pseudogenes similar to genes with uncharacterized function are not listed).