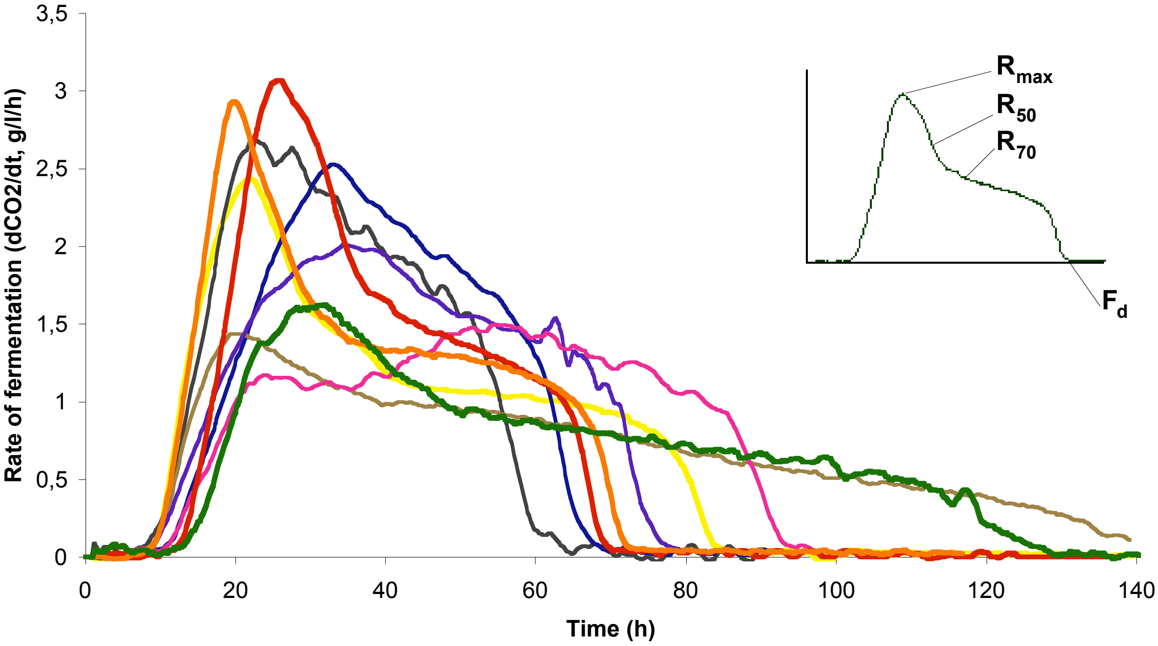
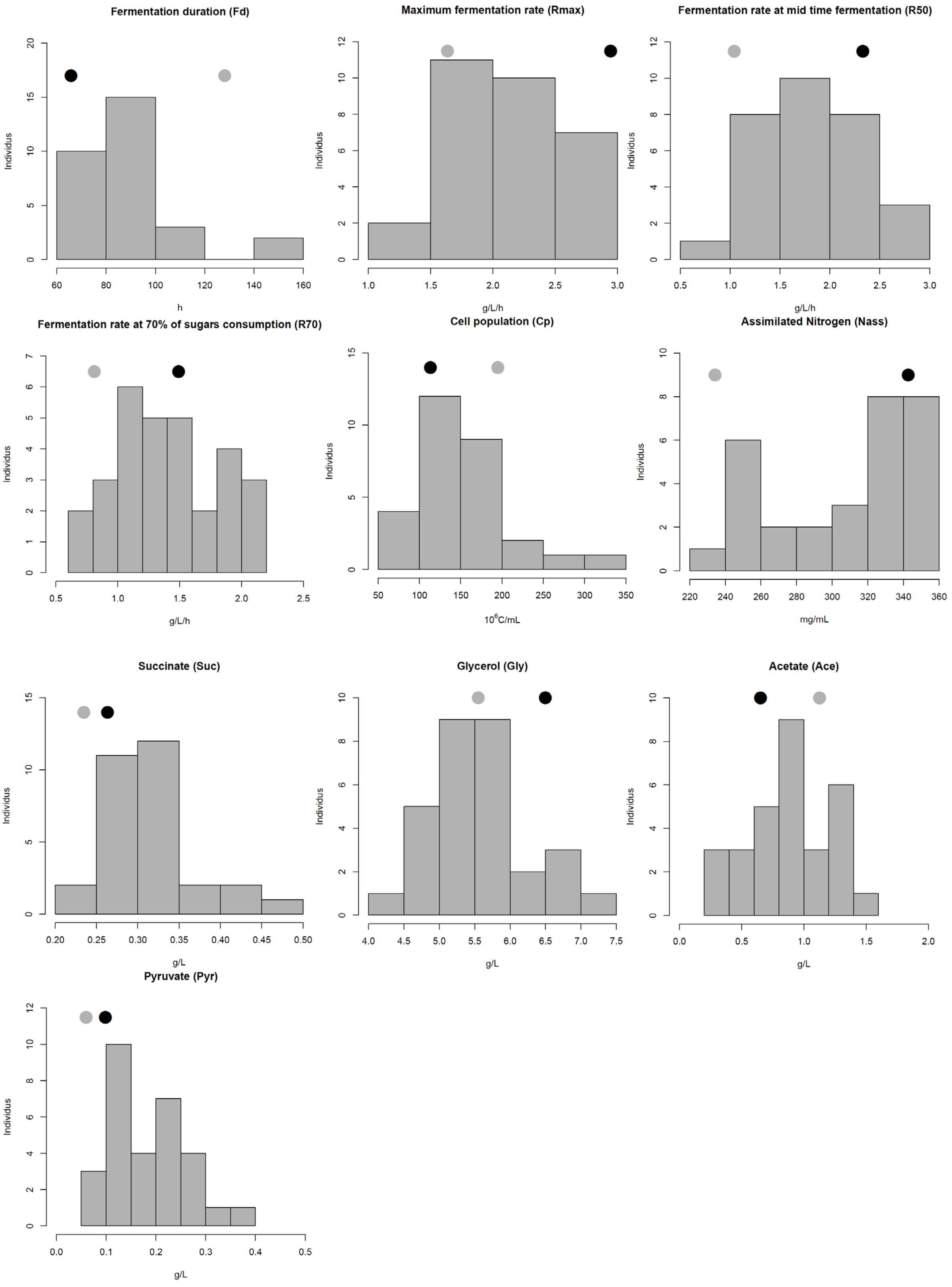


**Figure S1** Fermentation kinetics of EC1118 industrial strain (orange line), S288c laboratory strain (green curve), 59A (red curve), the hybrid Z59S (yellow curve) and some segregants (all other coloured curves). The $CO_2$ production rate was measure in MS300 medium. ($g.L^{-1}.h^{-1}$).



Fermentation duration (Fd)

Maximum fermentation rate (Rmax)

Fermentation rate at mid time fermentation (R50)

Fermentation rate at 70% of sugars consumption (R70)

Cell population (Cp)

Assimilated Nitrogen (Nass)

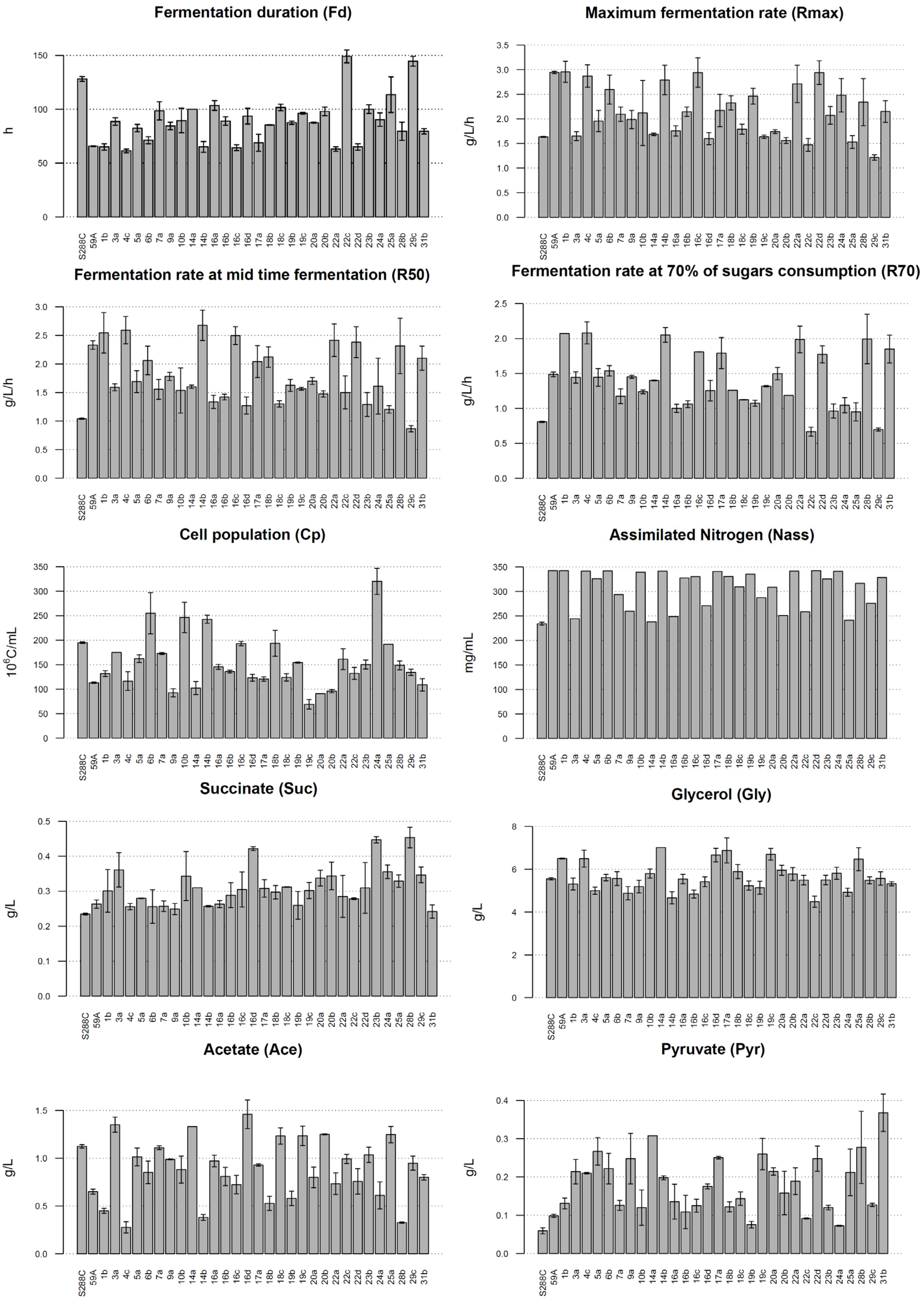
Succinate (Suc)

Glycerol (Gly)

Acetate (Ace)

Pyruvate (Pyr)

**Figure S2** Distribution of fermentation parameters and metabolites production in the 30 segregants. Parent S288c and 59A mean values are shown on the top as grey (S288c) and black (59A) dots.


Fermentation duration (Fd)

Maximum fermentation rate (Rmax)

Fermentation rate at mid time fermentation (R50)

Fermentation rate at 70% of sugars consumption (R70)

Cell population (Cp)

Assimilated Nitrogen (Nass)

Succinate (Suc)

Glycerol (Gly)

Acetate (Ace)

Pyruvate (Pyr)

**Figure S3** Fermentation traits value for each segregant and parental strains. The mean value and the standard deviation for each trait is provided. All traits were measured in two independent biological replicates except Nass measured from one fermentation experiment for the segregants and in five biological replicates for the parental strains and all traits.

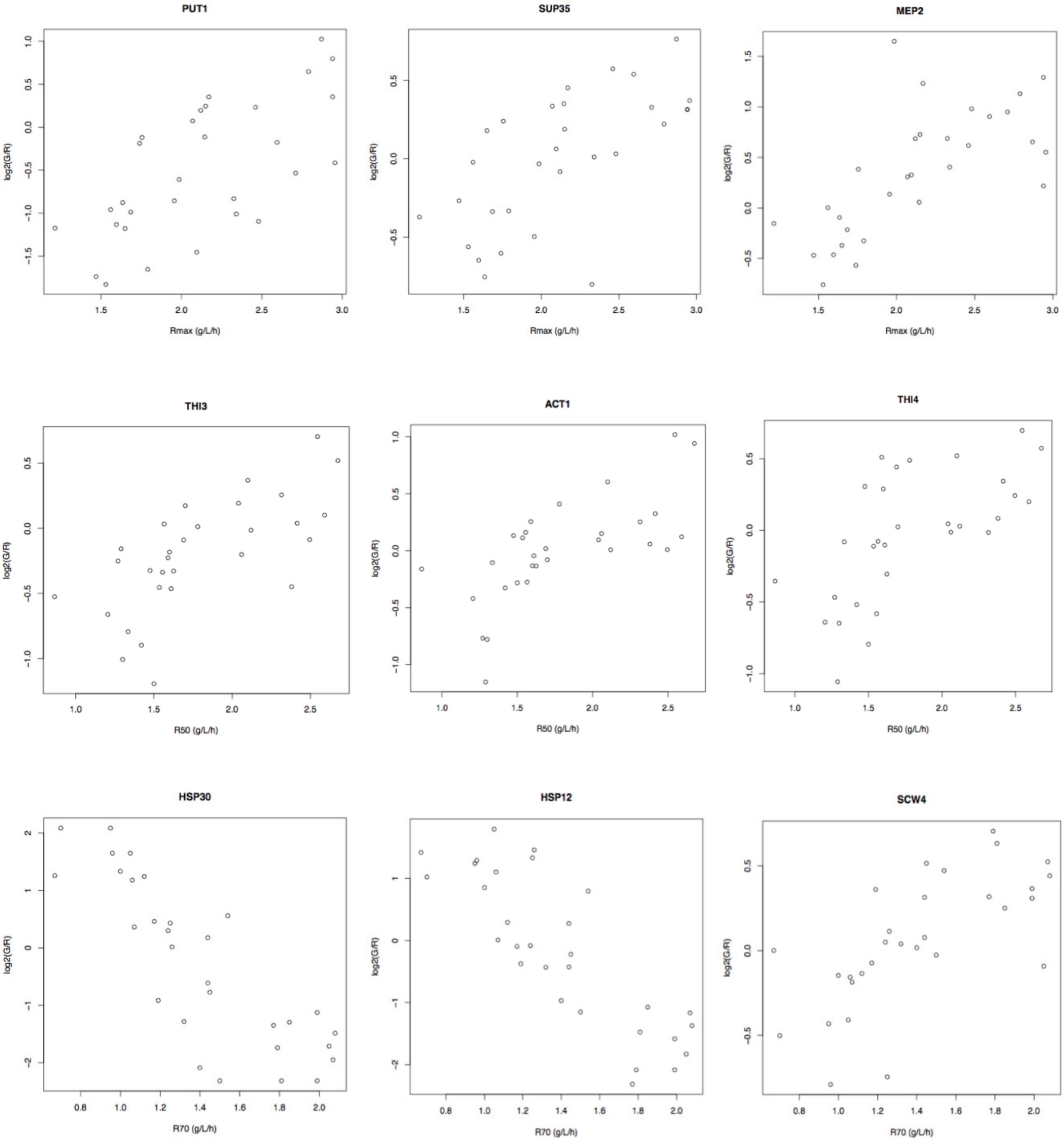


**Figure S4** Correlations between fermentation parameters and the expression ratio of some genes in the population of segregants

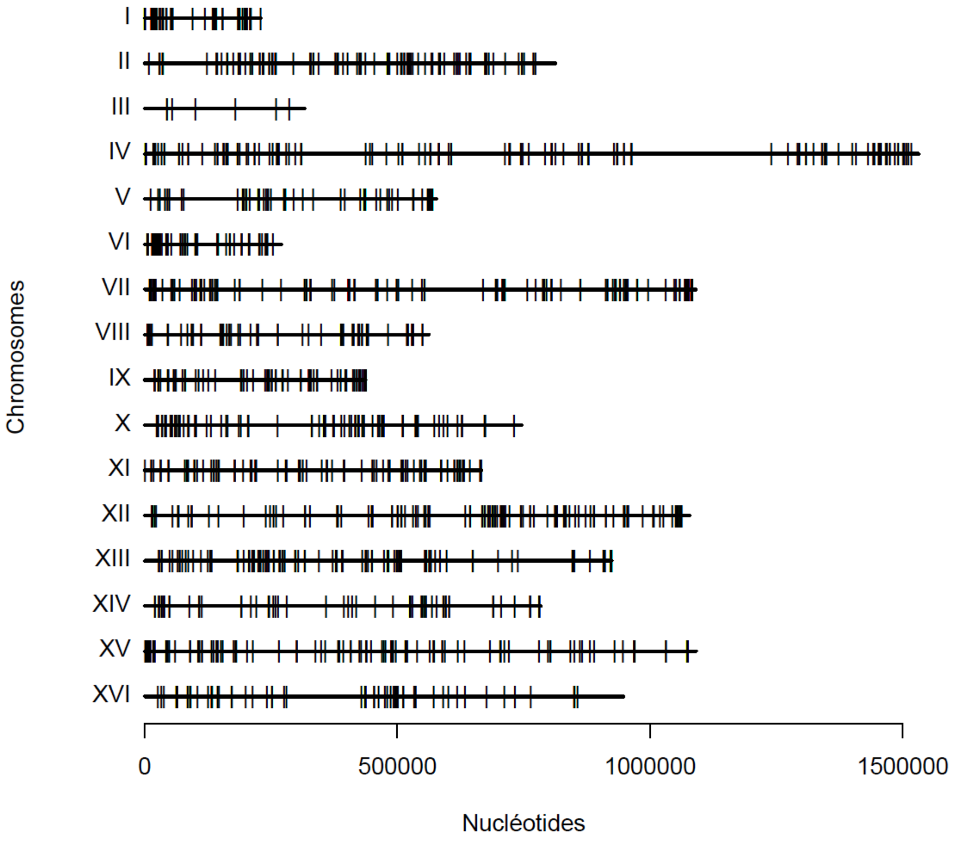


**Figure S5** Microarray-derived marker map. Each vertical tick represents one genetic marker.

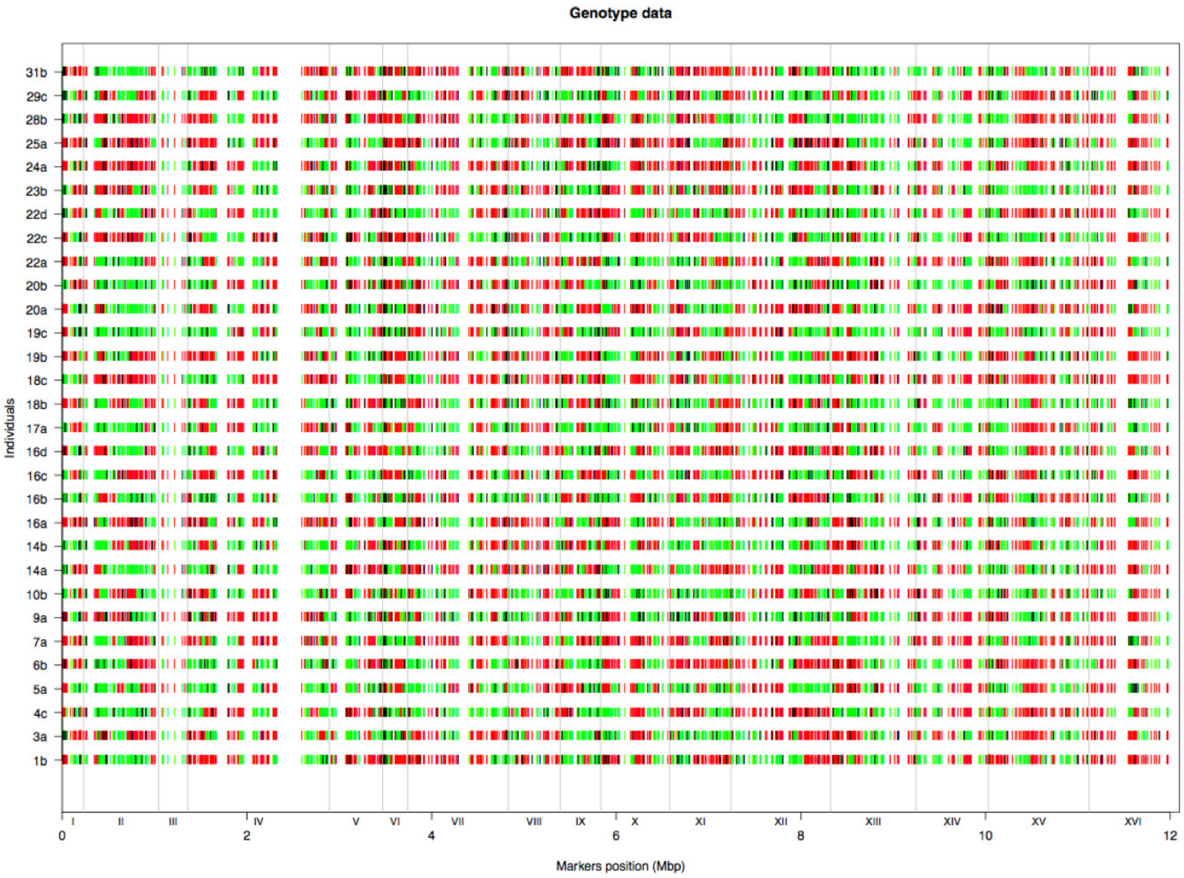


**Figure S6** Markers distribution in the 30 segregants. Each marker position is displayed on the concatenated chromosomes with the colour indicating the parental origin (green 59A, red S288c). Ambiguous markers are indicated by a black bar.

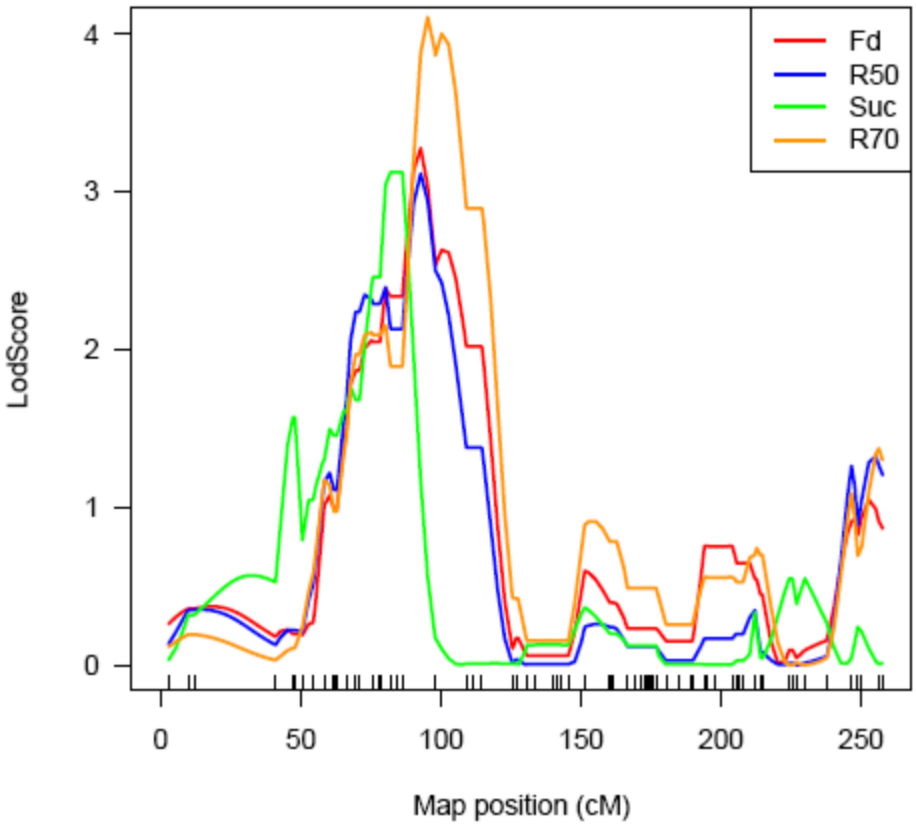


**Figure S7** Overlapping of LOD peak values localised on chromosome II for four phenotypic traits. The x-axis represents the genomic marker localisation and the y-axis represents the LOD score values.

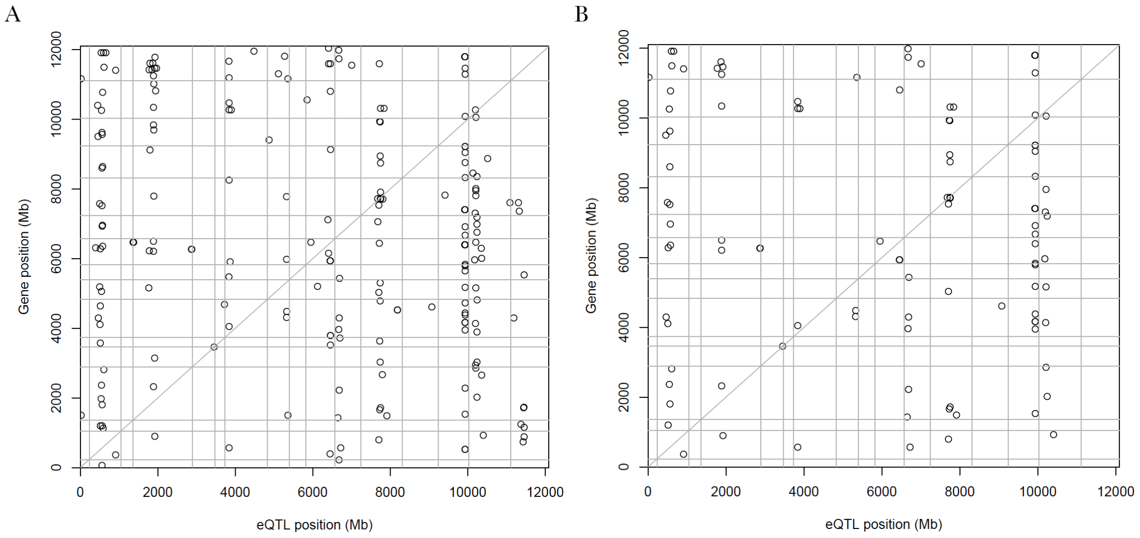


**Figure S8** Genomic distribution of eQTL. Positions of detected eQTL are plotted against the position of the regulated gene. The figure displays eQTL with LOD score higher than 4.0 (A) and higher than 4.5 (B).

| 59 A | R | D | R | E | T |
|---|---|---|---|---|---|
| S. 288C | E N T G E | K K N I K | E F K D I | S V Q E Y | Y N K |
| RM11-1a | E N R G E | K K D I K | E F R D I | S V E E Y | Y T K |
| VIN13 | E N R G E | K K D I K | E F R D I | S V E E Y | Y T K |
| YJM789 | E N R G E | K K D I K | E F R D I | S V E E Y | Y T K |
| Y12 | E N R G E | K K D I K | E F K D I | S V E E Y | Y T K |
| UWOPS87.2421 | E N R G E | K K D I K | E F K D I | S V E E Y | Y T K |
| UWOPS05.217 | E N R G E | K K D I K | E F K D I | S V E E Y | Y T K |
| *S .bayanus* | E N R G E | K K D V E | E F N D I | S V E E Y | Y T K |
| *S. mikatae* | E N R G E | K K D V R | E F N D I | S V E E Y | Y T K |
| *S. paradoxus* | E N R G E | K E D V R | E F N D I | S V E E Y | Y T K |
|  | 313 | 475 | 559 | 650 | 777 |

**Figure S9** Alignment of the Abz1 amino acid modified in the strain 59A with the corresponding region seven other *Saccharomyces cerevisiae* strains and three other *Saccharomyces* species.

**Table S1 Parental strains and segregants fermentation characteristics**

| Strains | Rmax | R50 | R70 | Fd | Cp | Nass |
|---|---|---|---|---|---|---|
| S288C | 1.63 (0.03) | 1.04 (0.02) | 0.81 (0.02) | 128 (4.8) | 194.9 (3.6) | 234 (7) |
| 59A | 2.94 (0.05) | 2.33 (0.17) | 1.49 (0.08) | 66 (0.7) | 113.2 (3.5) | 343 (0) |
| 1b | 2.96 (0.3) | 2.54 (0.5) | 2.07 (NA) | 65 (4.2) | 131.8 (8.3) | 343 (NA) |
| 3a | 1.65 (0.13) | 1.59 (0.08) | 1.44 (0.12) | 88 (4.9) | 175 (0) | 244 (NA) |
| 4c | 2.87 (0.33) | 2.59 (0.34) | 2.08 (0.22) | 61 (2.5) | 116.5 (26.9) | 342 (NA) |
| 5a | 1.96 (0.3) | 1.69 (0.27) | 1.44 (0.18) | 82 (4.9) | 162.2 (11) | 326 (NA) |
| 6b | 2.59 (0.42) | 2.06 (0.35) | 1.54 (0.13) | 71 (4.6) | 255 (59.4) | 342 (NA) |
| 7a | 2.1 (0.21) | 1.55 (0.25) | 1.17 (0.15) | 98 (12) | 172.9 (2.7) | 294 (NA) |
| 9a | 1.98 (0.26) | 1.78 (0.1) | 1.45 (0.03) | 84 (4.9) | 92.7 (11.7) | 260 (NA) |
| 10b | 2.12 (0.93) | 1.53 (0.56) | 1.24 (0.04) | 90 (16.3) | 246.3 (43.7) | 339 (NA) |
| 14a | 1.68 (0.04) | 1.6 (0.04) | 1.4 (0.01) | 100 (0) | 102.3 (18.8) | 238 (NA) |
| 14b | 2.79 (0.42) | 2.67 (0.37) | 2.05 (0.15) | 65 (7.1) | 242.6 (11.5) | 342 (NA) |
| 16a | 1.75 (0.15) | 1.34 (0.16) | 1 (0.08) | 104 (6.4) | 145.4 (7.3) | 249 (NA) |
| 16b | 2.15 (0.13) | 1.42 (0.07) | 1.06 (0.07) | 89 (5.7) | 135.9 (4) | 328 (NA) |
| 16c | 2.94 (0.42) | 2.5 (0.22) | 1.81 (0) | 64 (3.9) | 192.9 (6.2) | 330 (NA) |
| 16d | 1.6 (0.21) | 1.27 (0.26) | 1.25 (0.21) | 94 (10.5) | 123.3 (9.6) | 271 (NA) |
| 17a | 2.17 (0.47) | 2.04 (0.4) | 1.79 (0.32) | 69 (11) | 120.8 (6) | 341 (NA) |
| 18b | 2.33 (0.21) | 2.12 (0.25) | 1.26 (NA) | 85 (0.4) | 193.5 (37.5) | 330 (NA) |
| 18c | 1.79 (0.17) | 1.3 (0.1) | 1.12 (0) | 102 (5.3) | 124.1 (10.6) | 309 (NA) |
| 19b | 2.46 (0.23) | 1.62 (0.15) | 1.07 (0.06) | 88 (2.1) | 154.3 (1.5) | 335 (NA) |
| 19c | 1.64 (0.05) | 1.56 (0.04) | 1.32 (0.01) | 96 (1.1) | 69 (13.8) | 287 (NA) |
| 20a | 1.74 (0.06) | 1.7 (0.08) | 1.5 (0.12) | 88 (0.7) | 90.6 (NA) | 308 (NA) |
| 20b | 1.56 (0.08) | 1.48 (0.08) | 1.19 (NA) | 98 (5.7) | 95.8 (4.5) | 251 (NA) |
| 22a | 2.71 (0.54) | 2.42 (0.4) | 1.99 (0.27) | 63 (2.8) | 161.1 (29.8) | 342 (NA) |
| 22c | 1.47 (0.18) | 1.5 (0.41) | 0.67 (0.09) | 149 (8.5) | 132.2 (17.3) | 258 (NA) |
| 22d | 2.94 (0.34) | 2.38 (0.38) | 1.77 (0.17) | 65 (4.2) | NaN (NA) | 343 (NA) |
| 23b | 2.07 (0.25) | 1.29 (0.3) | 0.96 (0.14) | 100 (5.7) | 150.2 (12.9) | 326 (NA) |
| 24a | 2.48 (0.48) | 1.61 (0.69) | 1.05 (0.15) | 90 (9) | 319.9 (37.6) | 341 (NA) |
| 25a | 1.53 (0.18) | 1.21 (0.09) | 0.95 (0.18) | 114 (23.3) | 191.6 (NA) | 241 (NA) |
| 28b | 2.34 (0.68) | 2.31 (0.69) | 1.99 (0.5) | 80 (12) | 148.6 (12.8) | 316 (NA) |
| 29c | 1.21 (0.08) | 0.86 (0.08) | 0.7 (0.03) | 144 (6.4) | 134.4 (8.9) | 276 (NA) |
| 31b | 2.15 (0.31) | 2.1 (0.3) | 1.85 (0.28) | 80 (3.5) | 108.8 (18) | 328 (NA) |

Standard deviation for each trait is indicated between parentheses.

**Table S2 Parental strains and segregants metabolites production characteristics**

| Strains | Suc | Gly | Ace | Pyr |
|---|---|---|---|---|
| S288C | 0.23 (0.01) | 5.55 (0.12) | 1.12 (0.04) | 0.06 (0.02) |
| 59A | 0.26 (0.03) | 6.5 (0.06) | 0.65 (0.06) | 0.1 (0.01) |
| 1b | 0.3 (0.09) | 5.31 (0.4) | 0.45 (0.04) | 0.13 (0.02) |
| 3a | 0.36 (0.07) | 6.49 (0.56) | 1.35 (0.11) | 0.21 (0.05) |
| 4c | 0.26 (0.01) | 5 (0.24) | 0.28 (0.08) | 0.21 (0) |
| 5a | 0.28 (0) | 5.61 (0.21) | 1.01 (0.13) | 0.27 (0.05) |
| 6b | 0.26 (0.07) | 5.56 (0.45) | 0.85 (0.17) | 0.22 (0.06) |
| 7a | 0.26 (0.02) | 4.88 (0.44) | 1.11 (0.03) | 0.13 (0.02) |
| 9a | 0.25 (0.02) | 5.19 (0.42) | 0.99 (0.01) | 0.25 (0.09) |
| 10b | 0.34 (0.1) | 5.8 (0.3) | 0.88 (0.2) | 0.12 (0.07) |
| 14a | 0.31 (NA) | 7.01 (NA) | 1.33 (NA) | 0.31 (NA) |
| 14b | 0.26 (0) | 4.66 (0.4) | 0.38 (0.04) | 0.2 (0.01) |
| 16a | 0.26 (0.01) | 5.54 (0.31) | 0.97 (0.09) | 0.14 (0.06) |
| 16b | 0.29 (0.05) | 4.84 (0.26) | 0.81 (0.14) | 0.11 (0.06) |
| 16c | 0.3 (0.07) | 5.41 (0.32) | 0.72 (0.14) | 0.12 (0.02) |
| 16d | 0.42 (0.01) | 6.66 (0.44) | 1.46 (0.21) | 0.18 (0.01) |
| 17a | 0.31 (0.04) | 6.88 (0.82) | 0.93 (0.02) | 0.25 (0) |
| 18b | 0.3 (0.03) | 5.89 (0.47) | 0.53 (0.1) | 0.12 (0.02) |
| 18c | 0.31 (0) | 5.23 (0.3) | 1.23 (0.12) | 0.14 (0.02) |
| 19b | 0.26 (0.06) | 5.13 (0.43) | 0.58 (0.11) | 0.08 (0.01) |
| 19c | 0.3 (0.03) | 6.7 (0.38) | 1.23 (0.14) | 0.26 (0.06) |
| 20a | 0.34 (0.03) | 5.95 (0.33) | 0.8 (0.15) | 0.21 (0.01) |
| 20b | 0.34 (0.06) | 5.78 (0.43) | 1.25 (0.01) | 0.16 (0.08) |
| 22a | 0.28 (0.08) | 5.49 (0.32) | 0.73 (0.16) | 0.19 (0.05) |
| 22c | 0.28 (0) | 4.48 (0.37) | 0.99 (0.07) | 0.09 (0) |
| 22d | 0.31 (0.1) | 5.5 (0.32) | 0.76 (0.19) | 0.25 (0.05) |
| 23b | 0.45 (0.01) | 5.81 (0.4) | 1.03 (0.11) | 0.12 (0.01) |
| 24a | 0.36 (0.03) | 4.93 (0.26) | 0.61 (0.2) | 0.07 (0) |
| 25a | 0.33 (0.03) | 6.47 (0.76) | 1.25 (0.12) | 0.21 (0.09) |
| 28b | 0.45 (0.04) | 5.48 (0.23) | 0.33 (0.01) | 0.28 (0.13) |
| 29c | 0.35 (0.03) | 5.57 (0.44) | 0.95 (0.1) | 0.13 (0.01) |
| 31b | 0.24 (0.03) | 5.32 (0.13) | 0.8 (0.04) | 0.37 (0.07) |

Standard deviation for each trait is indicated between parentheses.

**Table S3 Genes showing strong differential expression between the two parental strains. (A) Genes overexpressed in 59A. (B) Genes overexpressed in S288c.**

**A**

| Name | logFC | Ratio | Adj PVal | Function |
|---|---|---|---|---|
| PAU5 | 3.256 | 9.555 | 8.56E-16 | Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions |
| PAU4 | 3.242 | 9.458 | 9.26E-15 | Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions |
| PAU12 | 2.83 | 7.112 | 1.97E-15 | Hypothetical protein |
| PAU20 | 2.827 | 7.094 | 3.61E-15 | Hypothetical protein |
| PAU6 | 2.483 | 5.592 | 1.43E-13 | Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions |
| PAU1 | 2.412 | 5.322 | 1.78E-14 | Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions |
| PAU13 | 2.324 | 5.007 | 8.02E-13 | Putative protein of unknown function |
| INO1 | 2.287 | 4.88 | 1.05E-12 | Inositol 1-phosphate synthase |
| PAU10 | 2.281 | 4.861 | 7.24E-14 | Hypothetical protein |
| PAU14 | 2.239 | 4.721 | 7.27E-14 | Hypothetical protein |
| PAU11 | 2.214 | 4.64 | 7.88E-13 | Putative protein of unknown function |
| PAU8 | 2.133 | 4.385 | 7.85E-12 | Hypothetical protein |
| PAU7 | 2.038 | 4.107 | 3.78E-14 | Part of 23-member seripauperin multigene family |
| PAU18 | 1.973 | 3.926 | 1.96E-12 | Hypothetical protein |
| HXK1 | 1.877 | 3.674 | 2.70E-10 | Hexokinase isoenzyme 1 |
| PAU19 | 1.85 | 3.606 | 3.87E-13 | Hypothetical protein |
| HUG1 | 1.752 | 3.368 | 1.51E-11 | Protein involved in the Mec1p-mediated checkpoint pathway that responds to DNA damage or replication arrest |
| TRK2 | 1.642 | 3.122 | 2.47E-11 | Component of the Trk1p-Trk2p potassium transport system |
| YGR126W | 1.641 | 3.119 | 3.61E-11 | Putative protein of unknown function |
| YNL324W | 1.638 | 3.112 | 2.74E-12 | Dubious ORF unlikely to encode a functional protein |
| YDR102C | 1.589 | 3.008 | 4.15E-12 | Dubious open reading frame |
| YPR126C | 1.558 | 2.945 | 2.35E-14 | Dubious open reading frame unlikely to encode a functional protein |
| DAN3 | 1.549 | 2.925 | 5.89E-10 | Cell wall mannoprotein with similarity to Tir1p |
| DDR48 | 1.544 | 2.917 | 1.37E-07 | DNA damage-responsive protein |
| DAN2 | 1.513 | 2.855 | 1.23E-12 | Cell wall mannoprotein with similarity to Tir1p |
| GPH1 | 1.437 | 2.707 | 1.05E-12 | Non-essential glycogen phosphorylase required for the mobilization of glycogen |
| MFA2 | 1.413 | 2.664 | 4.15E-09 | Mating pheromone a-factor |
| YDL085C-A | 1.402 | 2.643 | 8.24E-09 | Putative protein of unknown function |
| YPR050C | 1.373 | 2.59 | 1.28E-12 | Dubious open reading frame unlikely to encode a protein |
| YDR355C | 1.334 | 2.521 | 9.76E-12 | Dubious: Dubious open reading frame unlikely to encode a protein |
| YIL067C | 1.326 | 2.507 | 5.74E-12 | Uncharacterized protein of unknown function |
| YCL020W | 1.302 | 2.466 | 2.57E-09 | Retrotransposon TYA Gag gene co-transcribed with TYB Pol |
| SOL2 | 1.301 | 2.464 | 9.67E-11 | Protein with a possible role in tRNA export |
| JSN1 | 1.272 | 2.415 | 9.71E-14 | Member of the Puf family of RNA-binding proteins |
| GPM1 | 1.271 | 2.412 | 7.16E-10 | Tetrameric phosphoglycerate mutase |
| MSG5 | 1.256 | 2.389 | 4.09E-10 | Dual-specificity protein phosphatase required for maintenance of a low level of signaling through the cell integrity pathway |
| DBP5 | 1.248 | 2.375 | 3.52E-10 | Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in mRNA export from the nucleus |
| YBR099C | 1.246 | 2.372 | 4.78E-11 | Dubious open reading frame unlikely to encode a protein |
| SDS24 | 1.223 | 2.334 | 1.77E-10 | One of two S |
| HRT1 | 1.221 | 2.33 | 1.20E-11 | RING finger containing subunit of Skp1-Cullin-F-box ubiquitin protein ligases (SCF) |
| PAU17 | 1.218 | 2.326 | 2.77E-09 | Putative protein of unknown function |
| PEX11 | 1.207 | 2.309 | 8.92E-11 | Peroxisomal membrane protein required for peroxisome proliferation and medium-chain fatty acid oxidation |

|  |  |  |  |  |
|---|---|---|---|---|
| MSH6 | 1.206 | 2.307 | 4.89E-09 | Protein required for mismatch repair in mitosis and meiosis |
| FLO5 | 1.205 | 2.306 | 1.71E-13 | Lectin-like cell wall protein (flocculin) involved in flocculation |
| YFL052W | 1.205 | 2.306 | 1.93E-13 | Putative zinc cluster protein that contains a DNA binding domain |
| YKR045C | 1.202 | 2.3 | 2.57E-10 | Putative protein of unknown function |
| YJL127W-A | 1.201 | 2.298 | 1.22E-08 | Dubious open reading frame unlikely to encode a protein |
| DAN1 | 1.2 | 2.297 | 3.92E-10 | Cell wall mannoprotein with similarity to Tir1p |
| ENP1 | 1.189 | 2.28 | 2.20E-08 | Protein associated with U3 and U14 snoRNAs |
| YHR049C-A | 1.188 | 2.279 | 7.03E-11 | Dubious open reading frame unlikely to encode a functional protein |

**B**

| Name | logFC | Ratio | Adj PVal | Function |
|---|---|---|---|---|
| PLC1 | 4.693 | 25.864 | 4.07E-19 | Phospholipase C |
| YNL284C-A* | 4.252 | 19.047 | 1.89E-19 | Retrotransposon TYA Gag gene co-transcribed with TYB Pol |
| AI2* | 4.235 | 18.833 | 3.92E-18 | Reverse transcriptase required for splicing of the COX1 pre-mRNA |
| RTC4 | 3.439 | 10.844 | 3.68E-18 | Putative protein of unknown function |
| CDC5 | 2.857 | 7.246 | 2.82E-17 | Polo-like kinase with similarity to Xenopus Plx1 and S |
| ARH1 | 2.77 | 6.823 | 1.55E-17 | Oxidoreductase of the mitochondrial inner membrane |
| YGR051C | 2.53 | 5.776 | 2.24E-17 | Dubious open reading frame unlikely to encode a protein |
| YER084W | 2.49 | 5.617 | 4.91E-16 | Dubious open reading frame unlikely to encode a protein |
| YNL285W | 2.459 | 5.498 | 1.12E-17 | Dubious open reading frame unlikely to encode a functional protein |
| ELG1 | 2.437 | 5.413 | 1.57E-14 | Protein required for S phase progression and telomere homeostasis |
| ATE1 | 2.41 | 5.316 | 1.89E-19 | Arginyl-tRNA-protein transferase |
| YER138W-A | 2.379 | 5.201 | 5.74E-12 | Putative protein of unknown function |
| SCH9 | 2.365 | 5.152 | 3.30E-16 | Protein kinase involved in transcriptional activation of osmostress-responsive genes |
| YBL107W-A | 2.234 | 4.705 | 6.28E-14 | Dubious open reading frame unlikely to encode a protein |
| RSA1 | 2.204 | 4.609 | 5.55E-18 | Protein involved in the assembly of 60S ribosomal subunits |
| THI80 | 2.157 | 4.459 | 1.55E-16 | Thiamine pyrophosphokinase |
| HSP30 | 2.121 | 4.349 | 3.76E-08 | Hydrophobic plasma membrane localized |
| YBL111C | 2.068 | 4.192 | 9.79E-18 | Helicase-like protein encoded within the telomeric Y element |
| YHR218W | 2.018 | 4.051 | 2.21E-16 | Helicase-like protein encoded within the telomeric Y element |
| YIR014W | 1.93 | 3.809 | 2.68E-15 | Putative protein of unknown function |
| GIN4 | 1.894 | 3.717 | 1.51E-17 | Protein kinase involved in bud growth and assembly of the septin ring |
| HSP12 | 1.885 | 3.695 | 2.94E-14 | Plasma membrane localized protein that protects membranes from desiccation |
| PBP1 | 1.857 | 3.623 | 1.05E-14 | Protein interacting with poly(A)-binding protein Pab1p |
| YHL005C | 1.842 | 3.584 | 6.15E-17 | Dubious open reading frame unlikely to encode a protein |
| AUA1 | 1.801 | 3.485 | 8.96E-09 | Protein required for the negative regulation by ammonia of Gap1p |
| TPO3 | 1.8 | 3.481 | 9.65E-14 | Polyamine transport protein specific for spermine |
| RPL2B | 1.767 | 3.402 | 2.51E-14 | Protein component of the large (60S) ribosomal subunit |
| YER053C-A | 1.745 | 3.352 | 1.89E-06 | Putative protein of unknown function |
| MCM22 | 1.737 | 3.334 | 6.76E-15 | Protein involved in minichromosome maintenance |
| ASP3-1 | 1.734 | 3.326 | 9.66E-15 | Cell-wall L-asparaginase II |
| SPS100 | 1.712 | 3.276 | 1.94E-11 | Protein required for spore wall maturation |
| ASP3-3 | 1.704 | 3.257 | 4.88E-14 | Cell-wall L-asparaginase II |
| NPY1 | 1.669 | 3.18 | 5.89E-15 | NADH diphosphatase (pyrophosphatase) |
| HST1 | 1.665 | 3.172 | 3.56E-15 | NAD(+)-dependent histone deacetylase |
| YLR281C | 1.665 | 3.17 | 1.01E-16 | Putative protein of unknown function |
| SPR3 | 1.644 | 3.125 | 3.61E-15 | Sporulation-specific homolog of the yeast CDC3/10/11/12 family of bud neck microfilament genes |
| ASP3-2 | 1.628 | 3.09 | 1.70E-15 | Cell-wall L-asparaginase II |
| YNL260C | 1.614 | 3.06 | 1.72E-15 | Putative protein of unknown function with similarity to a human protein overexpressed in oral cancers |
| KAR9 | 1.581 | 2.991 | 8.55E-10 | Karyogamy protein required for correct positioning of the mitotic spindle and for orienting cytoplasmic microtubules |
| VIP1 | 1.577 | 2.984 | 8.36E-14 | Inositol hexakisphosphate (IP6) and inositol heptakisphosphate (IP7) kinase |

| | | | | |
|---|---|---|---|---|
| DOT1 | 1.572 | 2.973 | 1.32E-13 | Nucleosomal histone H3-Lys79 methylase |
| AI3 | 1.557 | 2.942 | 1.99E-13 | Endonuclease I-SceIII |
| MRPL13 | 1.54 | 2.909 | 6.20E-13 | Mitochondrial ribosomal protein of the large subunit |
| YLR280C | 1.54 | 2.909 | 5.89E-15 | Dubious open reading frame unlikely to encode a functional protein |
| ASP3-4 | 1.536 | 2.899 | 2.40E-15 | Cell-wall L-asparaginase II |
| ITC1 | 1.519 | 2.865 | 6.51E-14 | Component of the ATP-dependent Isw2p-Itc1p chromatin remodeling complex |
| YIL089W | 1.511 | 2.851 | 6.00E-13 | Putative protein of unknown function |
| RPA49 | 1.498 | 2.824 | 7.21E-06 | RNA polymerase I subunit A49 |
| HXT5 | -1.477 | 2.783 | 3.80 E-15 | Hexose transporter |
| THI72 | -1,477 | 2.783 | 1.71 E-11 | Transporter of thiamine or related compound |

For each gene the $\log_2$ of fold change, the ratio of expression, the adjusted p-value and the function are indicated.
These are Ty1 genes, only one member of each was considered since they cross hybridize.

**Table S4 Genes with eQTL in the 7 hotspots. Hotspot lod > 3.5**

| Hotspot | Gene | | | | |
|---|---|---|---|---|---|
| **Chr II**<br>**87.8 - 125.3 cM**<br>**263400 – 3759000 bp** | YAL044W-A | SSZ1 | YMR031C | PMP3 | MNE1 |
| | FLC2 | SPS100 | NRK1 | HSP12 | ISA2 |
| | TDP1 | CYR1 | RPL42A | FMP37 | PMT6 |
| | HSP30 | HXT8 | COQ10 | YGR079W | ECM12 |
| | NTH1 | SPC1 | GSH2 | CYS4 | GCN3 |
| | YDR053W | OSM1 | DDR2 | PTM1 | EMP46 |
| | TVP23 | GPX1 | MCT1 | YKL165C-A | YMR010W |
| **Chr IV**<br>**161 – 188.2 cM**<br>**483000 – 564600 bp** | SFT2 | STR2 | YOR352W | YJL028W | SWR1 |
| | DAD1 | PNP1 | SMA1 | ISY1 | RHO2 |
| | YDR249C | YNL019C | ELP4 | IZH2 | FMP40 |
| | YPL264C | | | | |
| **Chr XI**<br>**29.2 – 45.5**<br>**87600 – 136500 bp** | YAR069C | TIM21 | YLR104W | YFR016C | SEC4 |
| | MRPL11 | THI4 | SIP3 | FRS1 | |
| | UME6 | POT1 | CSR2 | ORC4 | |
| **Chr XII**<br>**147.7 – 171.6 cM**<br>**443100 – 514800 bp** | CWH43 | RPL43B | CTF18 | SHE10 | YPL034W |
| | MCH1 | ASP3-1 | SSO2 | YOR1 | GSM1 |
| | YDL086W | ASP3-2 | NGL2 | IKI1 | |
| | YEL008W | ASP3-3 | HUB1 | VPS63 | |
| | IOC3 | ASP3-4 | MRPS12 | YUH1 | |
| **Chr XIV**<br>**211.6 - 244 cM**<br>**634800 – 732000 bp** | CDC15 | HAM1 | MTF1 | VOA1 | DDC1 |
| | OLA1 | MOG1 | YMR262W | ENP2 | JID1 |
| | SAS10 | YKL050C | DIA1 | YGR251W | YIL055C |
| | DHH1 | MTR2 | ATG4 | YRF1-3 | RPS24B |
| | PCF11 | SPA2 | RRP40 | LSM12 | MDE1 |
| | PNC1 | YLR012C | YOR021C | YML131W | YJL225C |
| | NSA1 | GAT3 | RPL3 | YMR086W | |
| | PEX14 | RFX1 | YOR289W | MRS1 | |
| | PIL1 | YLR243W | YPL107W | KAR2 | |
| **Chr XV**<br>**51.4 - 71.4 cM**<br>**154200 – 214200 bp** | PGS1 | CDC12 | CHS5 | SWC4 | YOL047C |
| | ESF1 | KRE27 | RSC2 | YGR265W | YOR050C |
| | MUS81 | SNX4 | ATG17 | YHR003C | GCY1 |
| | YDR532C | EXO70 | OGG1 | YLR257W | DSS4 |
| | AFG1 | NNF1 | ALO1 | MEC3 | FRE1 |
| | MST27 | MLP1 | ILV2 | SFH1 | VPS75 |
| | HAP2 | | | | |
| **Chr XVI**<br>**96 – 126 cM**<br>**288000 – 378000 bp** | ATG12 | MRP10 | YEL076C | IDP3 | |
| | YCP4 | MCH1 | ROK1 | YEL008W | |
| | BUD23 | CHL4 | HIS5 | YCR101C | |

Genes which have a LOD score higher than 3.5 in the hotspot are displayed.