

| OS      | Strain        | Geographic, Isolated by, Year and refereces                | Source  |
|---------|---------------|--|---|
| 288/A   | 273614X       | Royal Victoria Infirmary, Newcastle UK, Galloway A         | Clinical isolate (Fecal)  |
| 287/A   | 378604X       | Royal Victoria Infirmary, Newcastle UK, Galloway A         | Clinical isolate (Sputum)   |
| 181     | BC187*        | Napa Valley, Bisson L, USA <sup>Ref</sup>                  | Barrel Fermentation   |
| 150/A   | DBVPG1106*    | Australia, 1947, Fornachon J                               | Grapes  |
| 91/A    | DBVPG1373     | Netherlands, Capriotti A, 1952 <sup>Ref</sup>              | Soil  |
| 84/A    | DBVPG1788     | Turku, Finland, Capriotti A, 1957 <sup>Ref</sup>           | Soil  |
| 92/A    | DBVPG1853     | Ethiopia, Rossi, 1959 <sup>Ref</sup>                       | White Teff  |
| 155/A   | DBVPG6040     | Netherlands, 1947 <sup>Ref</sup>                           | Fermenting fruit juice  |
| 60/A    | DBVPG6044     | West Africa, Guillermond A, 1925 <sup>Ref</sup>            | Bili wine, from <i>Osbeckia grandiflora</i>                           |
| 3/A     | DBVPG6765     | Unknown <sup>Ref</sup>                                     | Unknown   |
| 251/A/A | K11           | Japan, 1981 <sup>Ref</sup>                                 | Shochu sake strain  |
| 220/A   | L-1374*       | Cauquenes, Chile, Ganga A, 1999                            | Fermentation from must País   |
| 21/A    | L-1528*       | Cauquenes, Chile, Ganga A, 1999                            | Fermentation from must Cabernet                                       |
| 247/A   | NCYC110       | West Africa, Guillermond A, pre-1914 <sup>Ref</sup>        | Ginger beer from <i>Z. officinale</i>                                 |
| 96      | S288c         | Merced, California, USA, Mrak E, 1938 <sup>Ref</sup>       | Rotting fig   |
| 17/A    | SK1           | USA, Kane S, pre-1974 <sup>Ref</sup>                       | Soil  |
| 278/A   | UWOPS03-461.4 | Telok Senangin, Malaysia, Wiens F, 2003 <sup>Ref</sup>     | Nectar, Bertram palm  |
| 280/A   | UWOPS05-227.2 | Telok Senangin, Malaysia, Lachance M, 2005                 | <i>Trigona spp</i> (Stringless bee) collected near Bertam palm flower |
| 279/A   | UWOPS05-217.3 | Telok Senangin, Malaysia, Lachance M, 2005                 | Nectar, Bertram palm  |
| 270/A   | UWOPS83-787.3 | Great Inagua Island, Bahamas, 1983, Lachance M             | Fruit, <i>Opuntia stricta</i>   |
| 271/A   | UWOPS87-2421  | Puhelu Road, Maui, Hawaii, Lachance M, 1987                | Cladode, <i>Opuntia megacantha</i>                                    |
| 281     | W303          | Created by Rothstein R by multiple crossing <sup>Ref</sup> | NA  |
| 253/A/A | Y12           | Ivory Cost, pre-1981 <sup>Ref</sup>                        | Palm wine strain  |
| 97/A    | Y55*          | France, Winge Ö, between 1930-60 <sup>Ref</sup>            | Grape   |
| 252/A   | Y9            | Indonesia, pre-1962 <sup>Ref</sup>                         | Ragi (similar to sake wine)   |
| 174     | YIIc17_E5*    | Sauternes, France  | Wine  |
| 308/A   | YJM975*       | Ospedali Riuniti di Bergamo, Italy, 1994-6 <sup>Ref</sup>  | Isolated from vagina of patient suffering from vaginitis              |
| 303/A   | YJM978*       | Ospedali Riuniti di Bergamo, Italy, 1994-6 <sup>Ref</sup>  | Isolated from vagina of patient suffering from vaginitis              |
| 304/A   | YJM981*       | Ospedali Riuniti di Bergamo, Italy, 1994-6 <sup>Ref</sup>  | Isolated from vagina of patient suffering from vaginitis              |
| 182     | YPS606        | Pennsylvania, USA, Sniegowski P, 1999 <sup>Ref</sup>       | Bark of <i>Q.rubra</i>  |
| 258/A/A | YS2           | Australia <sup>Ref</sup>                                   | Baker strain  |
| 259/A/A | YS4           | Netherlands, 1975, Barnett J <sup>Ref</sup>                | Baker strain  |
| 262/A/A | YS9           | Singapore <sup>Ref</sup>                                   | Baker strain  |

**Table S1.** Set of 33 *S.cerevisiae* strains recently sequenced from wine and divers origins (Liti G, Carter DM, Moses AM, Warringer J, Parts L, James SA, Davey RP, Roberts IN, Burt A, Koufopanou V, Tsai IJ, Bergman CM, Bensasson D, O'Kelly MJ, van Oudenaarden A, Barton DB, Bailes E, Nguyen AN, Jones M, Quail MA, Goodhead I, Sims S, Smith F, Blomberg A, Durbin R, Louis EJ, 2009, Nature, 19, 458 (7236) : 337-41). OS column: accession number in the internal collection at the University of Nottingham. OSNNN/A means a single spore was isolated from the original diploid and OSNNN/A/A indicates this process was repeated. The absence of any /A indicates that either the strain was haploid or that a monosporic culture was provided. \*Strains related to wine fermentation

**Table S2.** Set of 35 *S.cerevisiae* strains commonly used in Aquitaine region, as industrial yeast starters in organic and conventional farming.

| Commercial name        | Strain             | Distributor     |
|------------------------|--------------------|-----------------|
| Actiflore cerevisiae   | 522D               | Laffort         |
| Excellence B2          |                    | Lamothe Abiet   |
| Lalvin BM 45           |                    | Lallemand       |
| Levuline CHP           | CIVC8130           | OenoFrance      |
| Lalvin CY 3079         | BourgoBlanc        | Lallemand       |
| Excellence C1 Val oeno |                    | Lamothe Abiet   |
| Zymaflore F10          | FZ 182             | Laffort         |
| Zymaflore F15          |                    | Laffort         |
| Actiflore F33          | F33                | Laffort         |
| Fermol Arome plus      | PB2010             | Spindal         |
| Fermivin               | 7013               | Littorale       |
| Zymaflore FX10         |                    | Laffort         |
| ICV-GRE                | 138 grenache       | ICV             |
| K1                     | Killer non marquée | Lallemand       |
| L.A. L13               | L13                | Lamothe Abiet   |
| Rhône L2226            |                    | Lallemand       |
| Lallferm bio           |                    | IOC / Lallemand |
| Lalvin QA23            | QA23               | Lallemand       |
| Lalvin 71B             | 71B                | Lallemand       |
| Levuline ALS           | EG8                | OenoFrance      |
| Levuline BRG           | UP 30Y5            | OenoFrance      |
| Oenoferm Bio           |                    | Littorale       |
| Vitilevure KD          | R2                 | Martin Vialatte |
| Zymaflore RX60         | rx60               | Laffort         |
| SP organic             |                    | Martin Vialatte |
| Uvaferm CEG            | CEG - Epernay 2    | Lallemand       |
| Achor vin 13           | vin 13             | Littorale       |
| Vitilevure quartz      |                    | Martin Vialatte |
| Zymaflore VL1          | vl1                | Laffort         |
| Zymaflore VL3          | lv3                | Laffort         |
| Zymaflore X16          | x16                | Laffort         |
| Zymaflore X5           | x5                 | Laffort         |
| Zymaflore ST           |                    | Laffort         |
| Zymaflore 011 organiq  |                    | Laffort         |
| UvaFerm BC             |                    | Lallemand       |

**Table S3.**

Characteristics of the microsatellite loci used for *Saccharomyces cerevisiae* genotyping: repeated motif, closest ORF on *S. cerevisiae* genome, primer sequence, fluorescence dye, mix number and concentration used for 8 samples PCR mix preparation for each marker.

| Site name | Motif and type | ORF or coordinates | Primers  | fluorescent dye | Multiplex | Quantity (nM) | Authors |
|-----------|----------------|--------------------|--|-----------------|-----------|---------------|---------|
| ScAAT2    | TAA            | YBL084c            | FW: CAGTCTTATTGCCTTGAACGA<br>RV: GTCTCCATCCTCCAAACAGCC           | PET             | 1         | 100           | 4       |
| ScAAT3    | TAA            | YDR160w            | FW: TGGGAGGAGGGAAATGGACAG<br>RV: TTCAGTTACCCGCACAATCTA           | NED             | 1         | 200           | 1, 3    |
| C5        | GT             | VI-210250/210414   | FW: TGACACAATAGCAATGGCCTTCA<br>RV: GCAAGCGACTAGAACACAATCACA      | VIC             | 1         | 50            | 5       |
| C3        | CAA            | YGL139w            | FW: CTTTTTATTTACGAGCGGGCCAT<br>RV: AAATCTCATGCTGTGAGGGGTAT       | NED             | 1         | 100           | 5       |
| C8        | TAA            | YGL014w            | FW: CAGGTCGTTCTAACGTTGGTAAATG<br>RV: GCTGTTGCTGTTGGTAGCATTACTGT  | 6FAM            | 1         | 25            | 5       |
| C11       | GT             | X-518870/519072    | FW: TTCCATCATAACCGTCTGGGATT<br>RV: TGCTTTTTTCTTAGATGGGCTTTC      | 6FAM            | 1         | 50            | 5       |
| YKR072c   | GAC            | YKR072c            | FW: AGATACAGAAGATAAGAACGAAAA<br>RV: TTATTGATGCTTATCTATTATACC     | PET             | 1         | 50            | 1, 2    |
| SCYOR267c | TGT            | YOR267c            | FW: TACTAACGTCAACACTGCTGCCAA<br>RV: GGATCTACTTGCAGTATACGGG       | VIC             | 1         | 100           | 1, 4    |
| YKL172w   | GAA            | YKL172w            | FW: CAGGACGCTACCGAAGCTCAAAAG<br>RV: ACTTTTGGCCAATTTCTCAAGAT      | 6FAM            | 2         | 25            | 2       |
| ScAAT1    | TTA            | XIII-86902/87140   | FW: AAAGCGTAAGCAATGGTGTAGATACTT<br>RV: CAAGCCTCTTCAAGCATGACCTTT  | VIC             | 2         | 100           | 1, 3, 4 |
| C4        | TAA+TAG        | XV-110701/110935   | FW: AGGAGAAAAATGCTGTTTATTCTGACC<br>RV: TTTTCCTCCGGGACGTGAATA     | NED             | 2         | 200           | 5       |
| C9        | TAA            | YOR156c            | FW: AAGGGTTCGTAAACATATAACTGGCA<br>RV: TATAAGGGAAAAGACGACGATGGC   | NED             | 2         | 100           | 5       |
| ScAAT5    | TAA            | XVI-897051/8970210 | FW: AGCATAATTGGAGGCAGTAAAGCA<br>RV: TCTCCGTCTTTTTGTACTGCGTG      | NED             | 2         | 100           | 5       |
| C6        | CA             | XVI-485898/485996  | FW: GTGGCATCATATCTGTCAATTTTATCAC<br>RV: CAATCAAGCAAAAAGATCGGCCCT | VIC             | 2         | 50            | 5       |
| YPL009c   | CTT            | YPL009c            | FW: AACCCATTGACCTCGTTACTATCGT<br>RV: TTCGATGGCTCTGATAACTCCATTC   | 6FAM            | 2         | 50            | 1, 4    |

Authors:

1. **Field D, Wills C.** 1998. Abundant microsatellite polymorphism in *Saccharomyces cerevisiae*, and the different distributions of microsatellites in eight prokaryotes and *S. cerevisiae*, result from strong mutation pressures and a variety of selective forces. *Proc Natl Acad Sci U S A* **95**:1647–1652.
2. **Hennequin C, Thierry A, Richard GF, Lecointre G, Nguyen HV, Gaillardin C, Dujon B.** 2001. Microsatellite Typing as a New Tool for Identification of *Saccharomyces cerevisiae* Strains. *J Clin Microbiol* **39**:551–559.
3. **Pérez M a., Gallego F j., Martínez I, Hidalgo P.** 2001. Detection, distribution and selection of microsatellites (SSRs) in the genome of the yeast *Saccharomyces cerevisiae* as molecular markers. *Lett Appl Microbiol* **33**:461–466.
4. **González Techera A, Jubany S, Carrau F m., Gaggero C.** 2001. Differentiation of industrial wine yeast strains using microsatellite markers. *Lett Appl Microbiol* **33**:71–75.
5. **Légras J-L, Ruh O, Merdinoglu D, Karst F.** 2005. Selection of hypervariable microsatellite loci for the characterization of *Saccharomyces cerevisiae* strains. *Int J Food Microbiol* **102**:73–83.

a

|   | C             | A             | B             | D             | E             | F             |
|---|---------------|---------------|---------------|---------------|---------------|---------------|
| C | <b>NA</b>     | 0.02 (0.06)   | 0.11 (<0.001) | 0.06 (<0.001) | 0.09 (<0.001) | 0.09 (<0.001) |
| A | 0.02 (0.06)   | <b>NA</b>     | 0.02 (<0.001) | 0.58 (<0.001) | 0.03 (<0.001) | 0.18 (<0.001) |
| B | 0.11 (<0.001) | 0.02 (<0.001) | <b>NA</b>     | 0.09 (<0.001) | 0.04 (<0.001) | 0.10 (<0.001) |
| D | 0.06 (<0.001) | 0.58 (<0.001) | 0.09 (<0.001) | <b>NA</b>     | 0.10 (<0.001) | 0.50 (<0.001) |
| E | 0.09 (<0.001) | 0.03 (<0.001) | 0.04 (<0.001) | 0.10 (<0.001) | <b>NA</b>     | 0.09 (<0.001) |
| F | 0.09 (<0.001) | 0.18 (<0.001) | 0.10 (<0.001) | 0.50 (<0.001) | 0.09 (<0.001) | <b>NA</b>     |

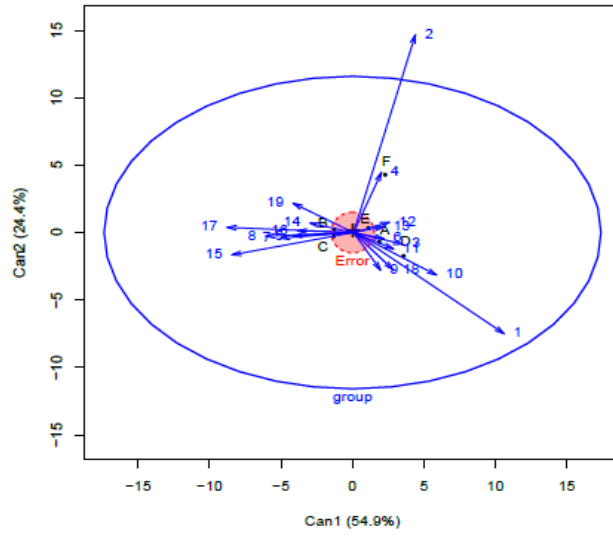
b

|   | A             | C             | B             |
|---|---------------|---------------|---------------|
| A | <b>NA</b>     | 0.11 (<0.001) | 0.10 (<0.001) |
| C | 0.11 (<0.001) | <b>NA</b>     | 0.04 (<0.001) |
| B | 0.10 (<0.001) | 0.04 (<0.001) | <b>NA</b>     |

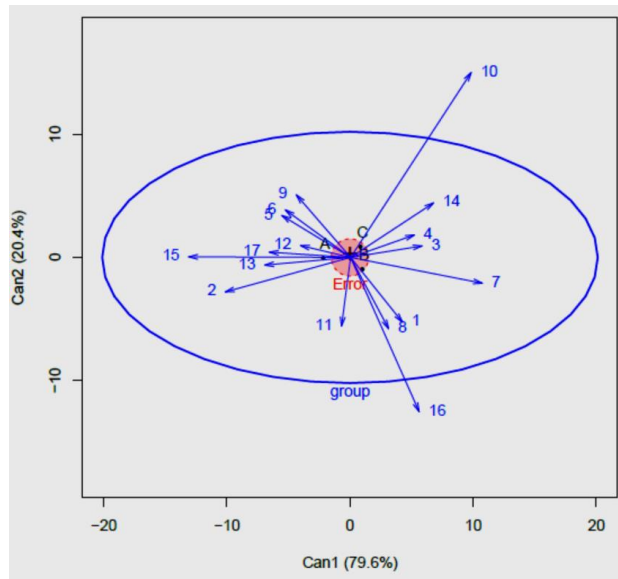
**Table S4.**

Pairwise matrix of R2 values between **a.** the 3 Sauternes and 3 Merlot wine estates and **b.** the only 3 Sauternes wines estates (with P.value).

a.



b.



**Figure S1.** Canonical discriminant analysis on the *Saccharomyces cerevisiae* dataset a. from Sauternes and Merlot and b. only from Sauternes. The HE plot shows the relation of variation of the group means on two variables relative to the error variance. The arrows indicate the position of the inferred populations relative to the axes obtained by the canonical discriminant analysis and red circle reflects the pooled within-group dispersion. The black points indicate predefined populations of wine estate A, B, C, D, E and F while numbers at the arrows indicate inferred populations.