

Strain #	Name	Origin	Phylogenetic group	Habitat
3582	UWOPS87_2421	Americas	Unknown	Wild
3583	W303	Unknown	Unknown	Laboratory
3584	YS9	Asia	Unknown	Baking
3585	273614N	Europe	Unknown	Clinical
3586	YIIC17_E5	Europe	Unknown	Fermentation
3587	322134S	Europe	Unknown	Clinical
3588	Y55	Europe	Unknown	Laboratory
3589	UWOPS83_787_3	Americas	Unknown	Wild
3590	SK1	Americas	Unknown	Laboratory
3591	BC187	Americas	WineEuropean	Fermentation
3592	YJM978	Europe	WineEuropean	Clinical
3593	YJM981	Europe	WineEuropean	Clinical
3594	YJM975	Europe	WineEuropean	Clinical
3595	DBVPG1373	Europe	WineEuropean	Wild
3596	DBVPG1106	Oceania	WineEuropean	Fermentation
3597	DBVPG6765	Unknown	WineEuropean	Unknown
3598	L_1374	Americas	WineEuropean	Fermentation
3599	L_1528	Americas	WineEuropean	Fermentation
3600	DBVPG6044	Africa	WestAfrican	Fermentation
3601	NCYC110	Africa	WestAfrican	Fermentation
3602	UWOPS03_461_4	Asia	Malaysian	Wild
3603	UWOPS05_217_3	Asia	Malaysian	Wild
3604	UWOPS05_227_2	Asia	Malaysian	Wild
3605	Y12	Africa	Sake	Fermentation
3606	YPS606	Americas	NorthAmerican	Wild
3607	YPS128	Americas	NorthAmerican	Wild

**Supp Table 1:** Strain code, name, origin, phylogenetic group, and habitat of the strains used. Extracted from table 1 of (Liti et al. 2009)

Chromosome	Tester	Interval	Lowest strain	Recombination rate cM/kbp	Highest strain	Recombination rate cM/kbp	<i>p</i> -value	Ratio
I	I-R2C3Y4	R2C3	UWOPS83_787_3	0.22	BC187	0.86	5.4e-09	3.84
		C3Y4	UWOPS87_2421	0.19	SK1	0.7	6.4e-07	3.77
VI	VI-C1Y2R3	C1Y2	YIlc17_E5	0.16	Y55	1.09	9.1e-08	6.81
		Y2R3	YIlc17_E5	0.18	Y55	0.66	3.1e-10	3.59
VI	VI-R3Y4C5	R3Y4	UWOPS83_787_3	0.13	Y55	0.39	2.2e-11	2.91
		Y4C5	YIlc17_E5	0.11	DBVPG6044	1.06	4.2e-08	9.46
XI	XI-R1C2Y3	R1C2			Not used			
		C2Y3	YIlc17_E5	0.21	Y12	0.94	7.6e-11	4.46
XI	XI-Y3R4C5	Y3R4	NCYC110	0.13	322134S	0.27	1.3e-09	2.03
		R4C5	YIlc17_E5	0.16	SK1	0.37	4.3e-07	2.32
XI	XI-R4C5Y6	R4C5	YIlc17_E5	0.16	SK1	0.38	5.4e-08	2.37
		C5Y6	YIlc17_E5	0.23	DBVPG6044	0.77	9.6e-11	3.29
XI	VI-Y6C7R8	Y6C7	YIlc17_E5	0.18	Y55	0.58	3.1e-11	3.24
		C7R8	YIlc17_E5	0.17	Y55	0.3	6.3e-09	1.78
XI	VI-R8Y9C10	R8Y9	YIlc17_E5	0.23	Y55	0.79	6.7e-10	3.4
		Y9C10	YIlc17_E5	0.24	DBVPG6044	0.79	3.0e-10	3.3

**Supp Table 2:** Diversity of recombination rate for each interval flanked by fluorescent markers. Lowest strain, highest strain: strains with lowest and highest recombination rates. *p*-value: *p*-value for strain effect (ANOVA). Ratio: ratio between recombination rates of the most and the least recombining strains for each interval.

Genome wide		All intervals		All intervals of a chromosome			Each interval		DSB hotspots within interval		30kb surrounding the interval		
$R^2$	$p$ -value	$R^2$	$p$ -value	Chromosome	$R^2$	$p$ -value	Interval number	$R^2$	$p$ -value	$R^2$	$p$ -value	$R^2$	$p$ -value
0.54	9.5e-05	0.43	9.00e-04	I	0.22	0.034	1	0.24	0.023	0.01	0.66	0.05	0.33
							2	0.15	0.087	0.03	0.43	0.46	0.0007
				VI	0.62	1,00E-05	3	0.74	0	0.44	0.0007	0.53	0.0001
							4	0.26	0.016	0.18	0.045	0.38	0.002
							5	0.04	0.38	0.22	0.029	0.04	0.38
							6	0.45	0.0006	0.34	0.004	0.05	0.34
				XI	0.19	0.044	7	NA	NA	NA	NA	NA	NA
							8	0.01	0.6	0.07	0.23	0.15	0.071
							9	0.03	0.42	0.24	0.019	0.02	0.52
							10 / 11	0.28	0.01	0.02	0.56	0.01	0.73
								0.24	0.02	0.01	0.70	0.01	0.54
							12	0.48	0.0003	0.64	8,00E-06	0.13	0.103
							13	0.69	3,00E-06	0.25	0.022	0.33	0.0065
							14	0.17	0.064	0.18	0.053	0	0.88
							15	0.43	0.0016	0.29	0.014	0.54	0.0002
							16	0.16	0.08	0.3	0.011	0.06	0.306

**Supp Table 3:** Correlation between recombination rate and sequence similarity at different scales. Genome-wide: considering average genome-wide sequence similarity with recombination rate averaged over all intervals. All intervals: considering average sequence similarity within all intervals with recombination rate averaged over all intervals. All intervals of a chromosome: same as before, but for each chromosome separately. Each interval: considering sequence similarity and recombination rate within each interval. DSB hotspots within interval: considering sequence similarity within DSB-rich regions in each interval with recombination rate in the corresponding interval. 30Kb surrounding the interval: considering sequence similarity in 30kb flanking sequences outside each interval on both sides, with recombination rate in the interval.

Cross	Y (cM)	$\mu$	$\alpha S$	GCA		SCA/INB	Residuals (cM)
				P1	P2		
SK1 X SK1	42.6		44.44	-3.2	-3.2	-36.67	0.17
YPS128 X YPS128	55.7	41.4	44.44	-3.4	-3.4	-23.28	0.02
SK1 X YPS128	38.1		1.11	-3.2	-3.4	1.94	-0.25

**Supp Table 4:** Measured recombination rate (Y), and estimated values of the diallele model parameters (see text). SCA/INB: value of SCA for the hybrids or INB for the homozygotes.