Supporting Information for Raghavan *et al.*
Incompatibilities in Mismatch Repair Genes MLH1-PMS1 Contribute to a Wide Range of Mutation Rates in Human Isolates of Baker's Yeast.
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Figure S1 Incompatibility involving the *MLH1* and *PMS1* MMR genes. We proposed a model for an incompatibility involving *MLH1* and *PMS1* (Heck *et al*. 2006). It is based on the hypothesis that ancestral isolates bearing MLH1 Gly 761 and PMS1 Arg 818/822 acquired neutral and beneficial mutations that lead to derived S288c (purple Asp 761, Arg 818/822) and SK1 (green, Gly 761, Lys 818/822) group isolates. Mating between the derived isolates, supported by genetic recombination data presented in Heck *et al.* (2006), yields an incompatible combination (MLH1 Asp 761, PMS1 Lys 818/822) that displays negative epistasis, as shown by a mutator phenotype. Sequences of *MLH1* and *PMS1* genes from a worldwide collection (Peter *et al.* 2018) are shown according to their amino acid residues 761 (G or D) in MLH1 and 818 (R or K) in PMS1 (Bui *et al*. 2017). Only those homozygous for *MLH1* and *PMS1* sequences are shown. Adapted from Bui *et al*. (2017).

Figure S2 DNA sequence, as shown by chromatogram traces, of the *MLH1* incompatibility site (bp 2282, Gly or Asp at amino acid 761) in the indicated isolates and spore clones.

Figure S3 Efficiency of plating of strains transformed with pEAA611, comparing growth on clon-NAT and clon-NAT + G418 plates. Representative images of EAY1369, EAY1370, YJM521, YJS5845 and YJS5885 isolates and YJS5885 spore clones are shown.

Figure S4 Sequencing analysis of G418 resistant revertants and sensitive control colonies. The homopolymeric A-runs in isolates and spore clones transformed with pEAA613

were sequenced (Materials and Method). The sequencing data from G418 resistant (top) and sensitive (bottom) colonies are presented. Only G418 resistant colonies displayed A_{14} to A_{13} frameshift mutations.

Figure S5 Flow cytometry of spore clones. Spore clones of YJS5845 and YJS5885 were prepared for flow cytometry as described in the Materials and Methods. YJS5845 derived spore clones were diploid and YJS5885 derived spore clones were haploid. The black arrows show the position of 1n, 2n, and 4n DNA content. Inset shows the percentage of single cells, small budded and large budded cells in the indicated samples.

Figure S6 Ploidy of YJS5845 and YJS5885 isolates and their spore clones. Whole genome sequencing is presented for YJS5845, YJS5885 and derived spore clones (Materials and Methods). The entire set can be found in Figure 4B and Figure S6.

Table S1 Genotyping of spore clones obtained by dissection of isolate tetrads. *MLH1* and *PMS1* genes were PCR amplified from isolates and derived spore clones and sequenced as described in the Materials and Methods. For YJS5845, three spore clones were genotyped from random spores and 30 were genotyped from spores isolated after tetrad dissection. For YJS5885, all spore clones were genotyped from tetrad dissection. None of the incompatible YJS5845 and YJS5885 spore clones contained the Pro 271 suppressor polymorphism in MLH1 (Demogines *et al*. 2008). For YJM521, 24 spore clones were genotyped from six four-spore viable tetrads. For YJS4806, 24 spore clones were genotyped from random spores with 22 showing the parental genotype for *MLH1*, and two showing a different segregation pattern (2G:2A, 4G:0A). For YJS4810, 24 spore clones were genotyped from random spores, with all showing the parental genotype for *MLH1.*

Table S2 Genotyping of *MLH1* and *PMS1* loci in YJM and YJS isolates and derived spore clones. The sequences for the *MLH1* and *PMS1* open reading frames for each of the two parental chromosomes are shown relative to the S288c and SK1 sequences for YJS5845, YJS5885, and YJM521. The parental chromosomes were genotyped as "c" (S288c) or "k" (SK1) based on the amino acid polymorphisms seen at the incompatibility loci (bp 2282 in *MLH1*, bp 2453 in *PMS1*) in the S288c and SK1 sequences (Materials and Methods). The MLH1-271P suppressor allele is highlighted at bp 812 in *MLH1*. INS = 12 bp insertion in *PMS1*; NO INS = lacking the insertion.

Table S3 Analysis of *HO*, *PHO80* and *STP22* genes in YJS5845 and YJS5885 for variants using SnpEff.

Table S4 Analysis of resistance to 5-FOA in YJS5885 spore clones. The rate of resistance to 5-FOA, presented with 95% confidence intervals (95% C.I.), was determined for n independent cultures of FY90 and the indicated spore clones of YJS5885 as described in the Materials and Methods. The *URA3* open reading frame (ATG =+1) was sequenced from 7, 2, 1, 1, 1 and 1 independent 5-FOA^r colonies from 5885-9a, 5885-15b, 5885-1a, 5885-14a, 5885-16a, and 5885-19a, respectively. [a] Significantly different from FY90 ($p<0.001$, Mann-Whitney test); [b] Significantly different from EAY4087 ($p<0.001$, Mann-Whitney test). YJS5885 compatible and incompatible spore clones are significantly different from each other ($p<0.001$, Mann-Whitney test).

10 of the 13 spore clones contained single mutations in *URA3*, with the following distribution:

5885-9a: Two missense (bp287,A>T; bp542, G>A), One nonsense (bp577, G>T), Two single nucleotide deletions (bp178, A deleted; bp629, G deleted), no changes in ORF for two 5-FOA^r mutants.

5885-15b: One missense (bp205, T>C), one nonsense (bp345 G>A).

5885-1a: One nonsense (bp223 A>T).

5885-14a: One nonsense (bp593 T>A).

5885-16a: No changes in ORF for one 5-FOA^r mutant.

5885-19a: One nonsense (bp310 C>T).

Table S5 Sporulation and Lactate growth phenotype. Spore clones were patched on sporulation media and incubated at 30°C for 6 days after which they were examined for evidence of sporulation by light microscopy. Any samples with dyads, triads and tetrads were marked as being able to sporulate (+). Spore clones were also patched on YP-lactate media and scored as able to grow or not (Lactate$^+$ or $^-$) after 4 days in 30°C. NT: not tested.

Table S6 Assigning MLH1 polymorphisms found in heterozygous genotypes onto the MLH1 structure-function map. A structure function map for MLH1 was created from an analysis of *MLH1* alanine scan and site-specific mutations, and *mlh1* alleles generated based on homology to HNPCC mutations (Pang *et al.* 1997; Shcherbakova and Kunkel 1999; Tran and Liskay 2000; Welz-Voegele *et al.* 2002; Takahashi *et al.* 2007; Wanat *et al.* 2007; Romanova and Crouse 2013; Smith *et al.* 2013; Smith *et al.* 2015). Alleles that conferred a mutator phenotype in a variety of reporter assays are shown. In MLH1, amino acids 1-335 is referred to as that N-terminal/ATP binding domain, 335-509 as the linker domain, and 510-769 as the C-terminal interaction domain (Gueneau *et al.* 2013). See Table S7 for detailed list of the isolates that contain heterozygous polymorphisms that lie on the MLH1 structure-function map (shown here using their standardized names in the 1011 yeast genome project (Peter *et al.* 2018).

Table S7 Amino acid heterozygosities identified in MLH1 in 107 yeast isolates. Amino acid heterozygosities in the MLH1 open reading frame are shown for 107 isolates (relative to the MLH1 S288c sequence; Peter *et al.* 2018).

Literature Cited

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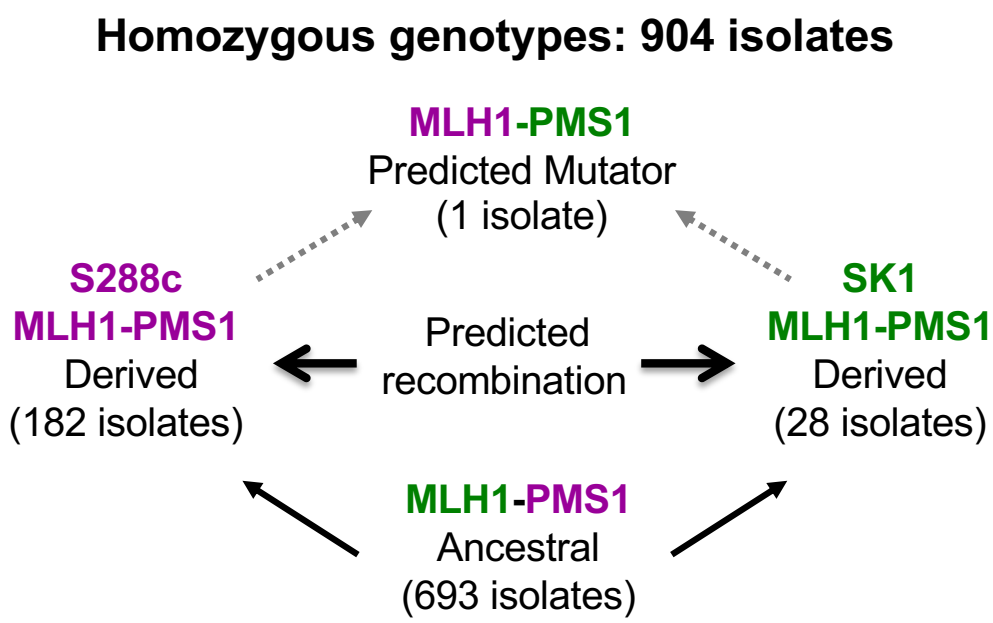
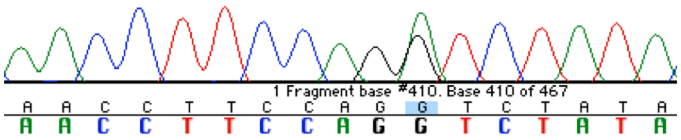
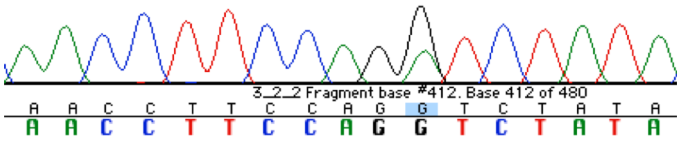

Homozygous genotypes: 904 isolates
MLH1-PMS1
Predicted Mutator
(1 isolate)
S288c
MLH1-PMS1
Derived
(182 isolates)
Predicted
recombination
SK1
MLH1-PMS1
Derived
(28 isolates)
MLH1-PMS1
Ancestral
(693 isolates)

Fig S1

Genotyping at bp 2282 in *MLH1* (G/D at amino acid 761)

YJS5845 1:1 G:A





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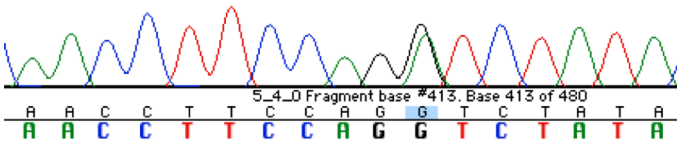
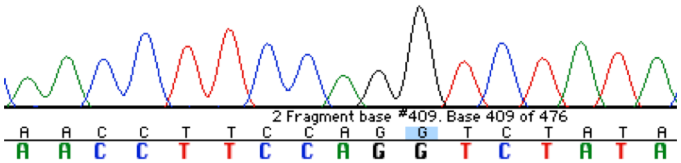
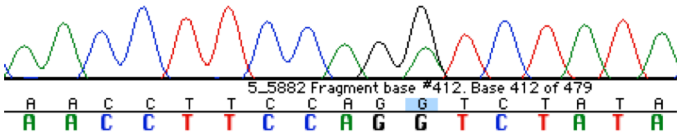


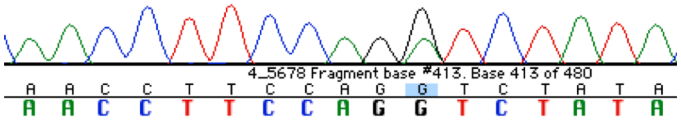
YJS4806 spore clone 2:2 G:A



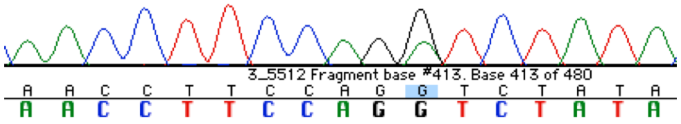
YJS4806 spore clone 4:0 G:A



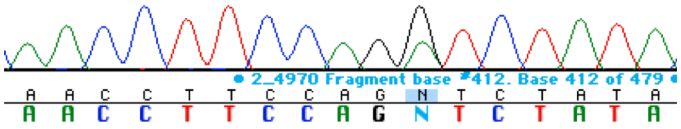
YJS4810 3:1 G:A



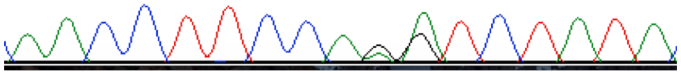
YJS5882 3:1 G:A



YJS5678 3:1 G:A



YJS5512 3:1 G:A



YJS4970 2:2 G:A

Fig S2

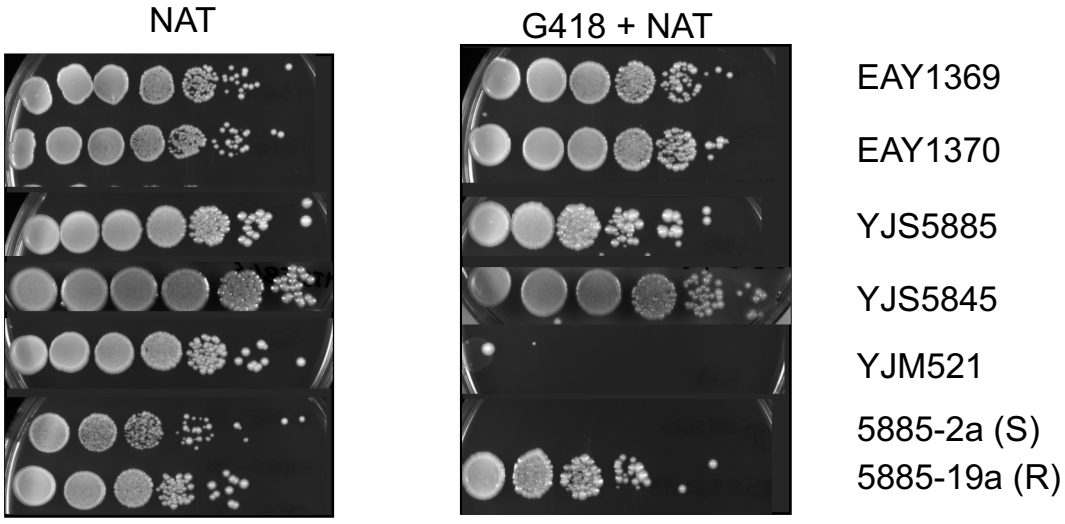
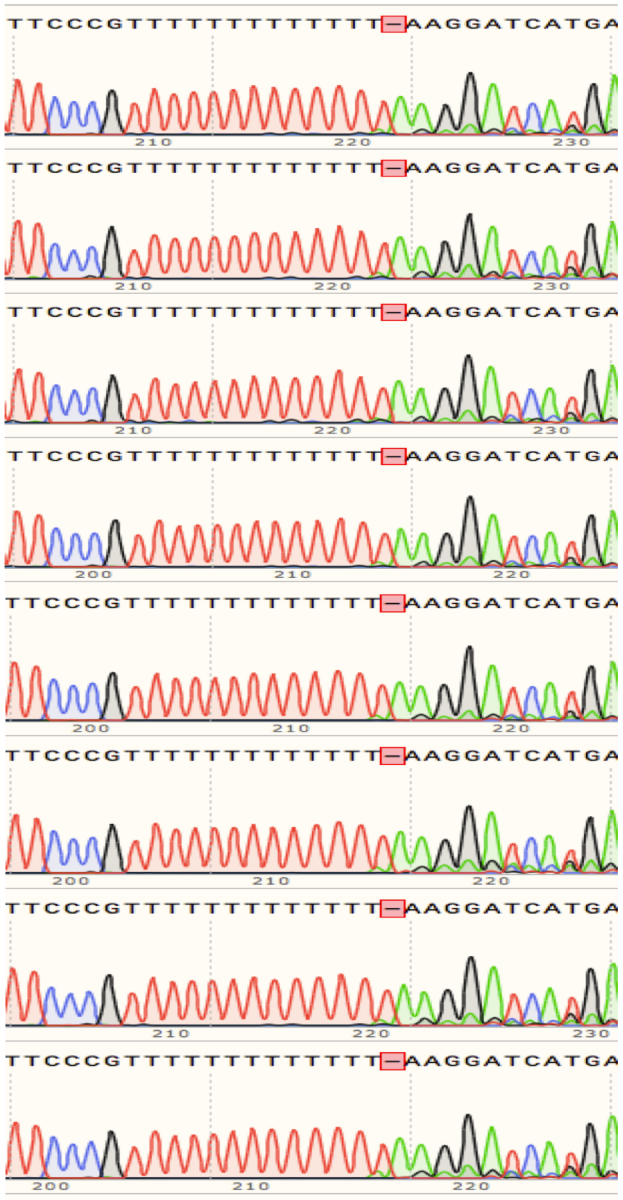

NAT
G418 + NAT
EAY1369
EAY1370
YJS5885
YJS5845
YJM521
5885-2a (S)
5885-19a (R)

Fig S3

Revertants, G418^{r}, NAT^{r}



Controls, NAT^{r}, G418^{s}

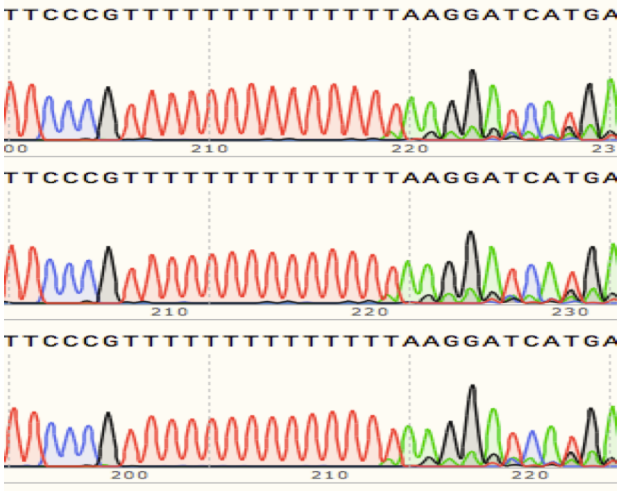
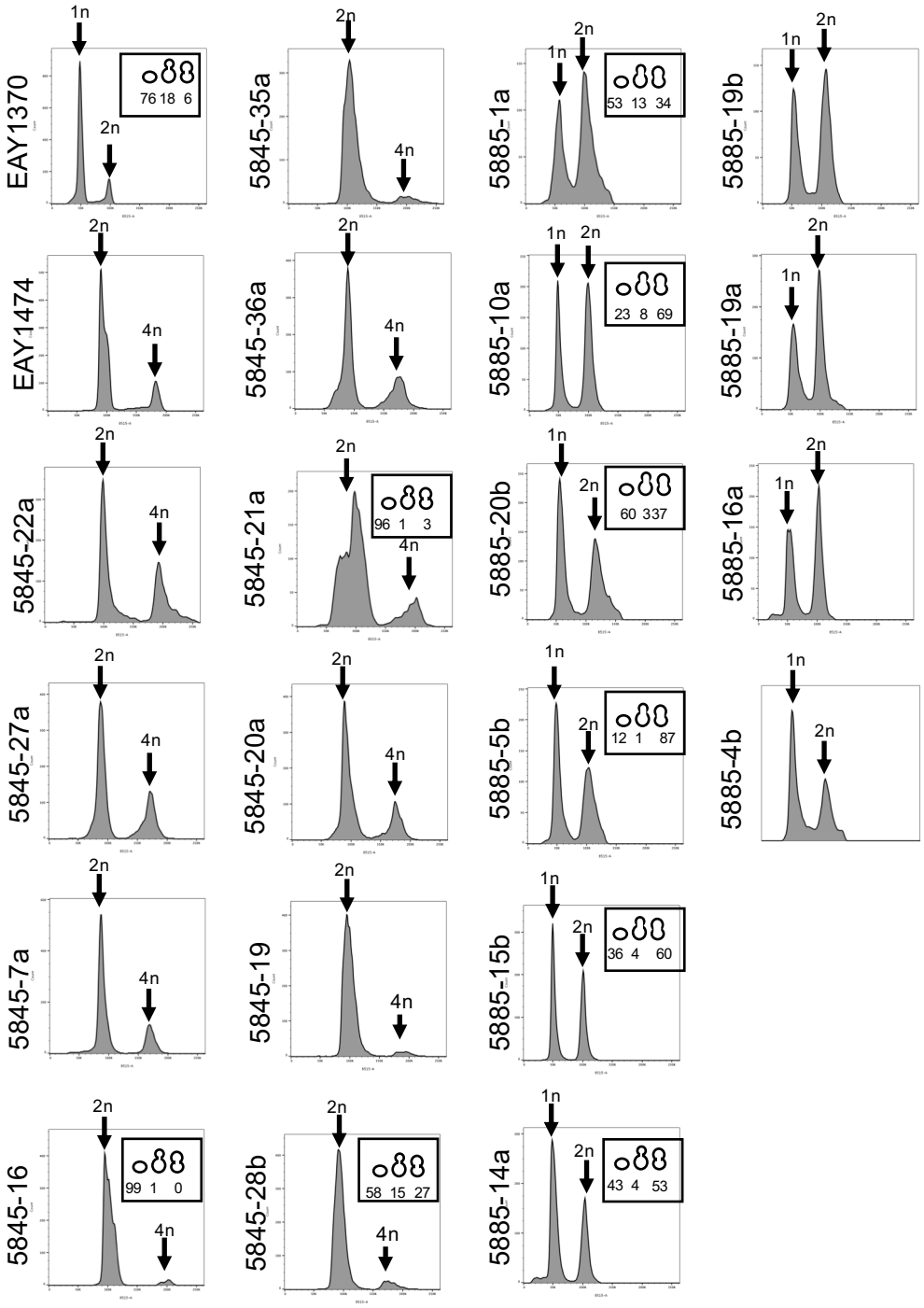


Fig S4


EAY1370
76 18 6
5845-35a
5885-1a
53 13 34
5885-19b
EAY1474
5845-36a
5885-10a
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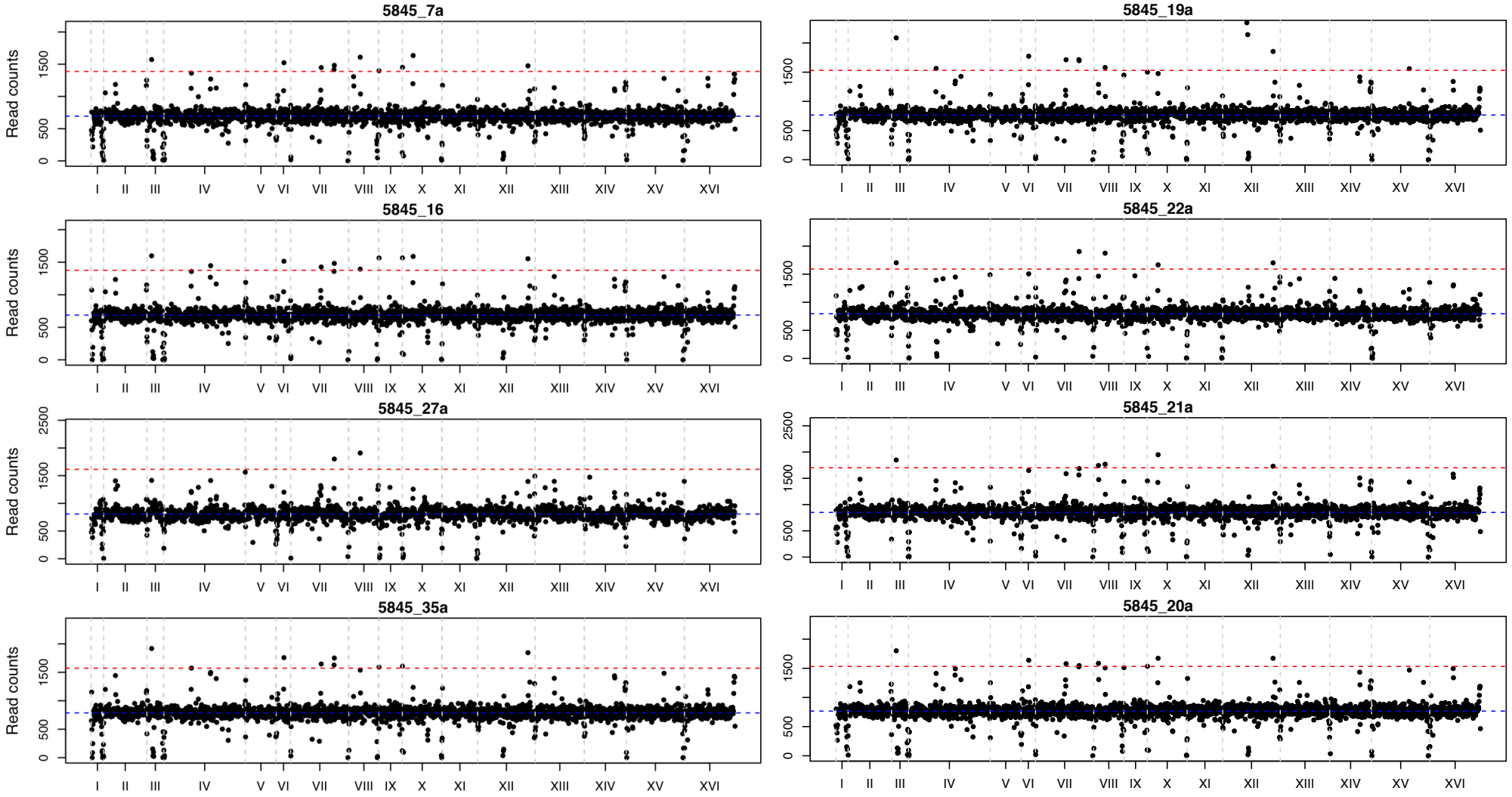
5885-19a
5845-22a
5845-21a
96 1 3
5885-20b
60 337
5885-16a
5845-27a
5845-20a
5885-5b
12 1 87
5885-4b
5845-7a
5845-19
5885-15b
36 4 60
5845-16
99 1 0
5845-28b
58 15 27
5885-14a
43 4 53
1n
2n
4n

Fig S5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5845_20a
Read counts
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500
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IV
V
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XIII
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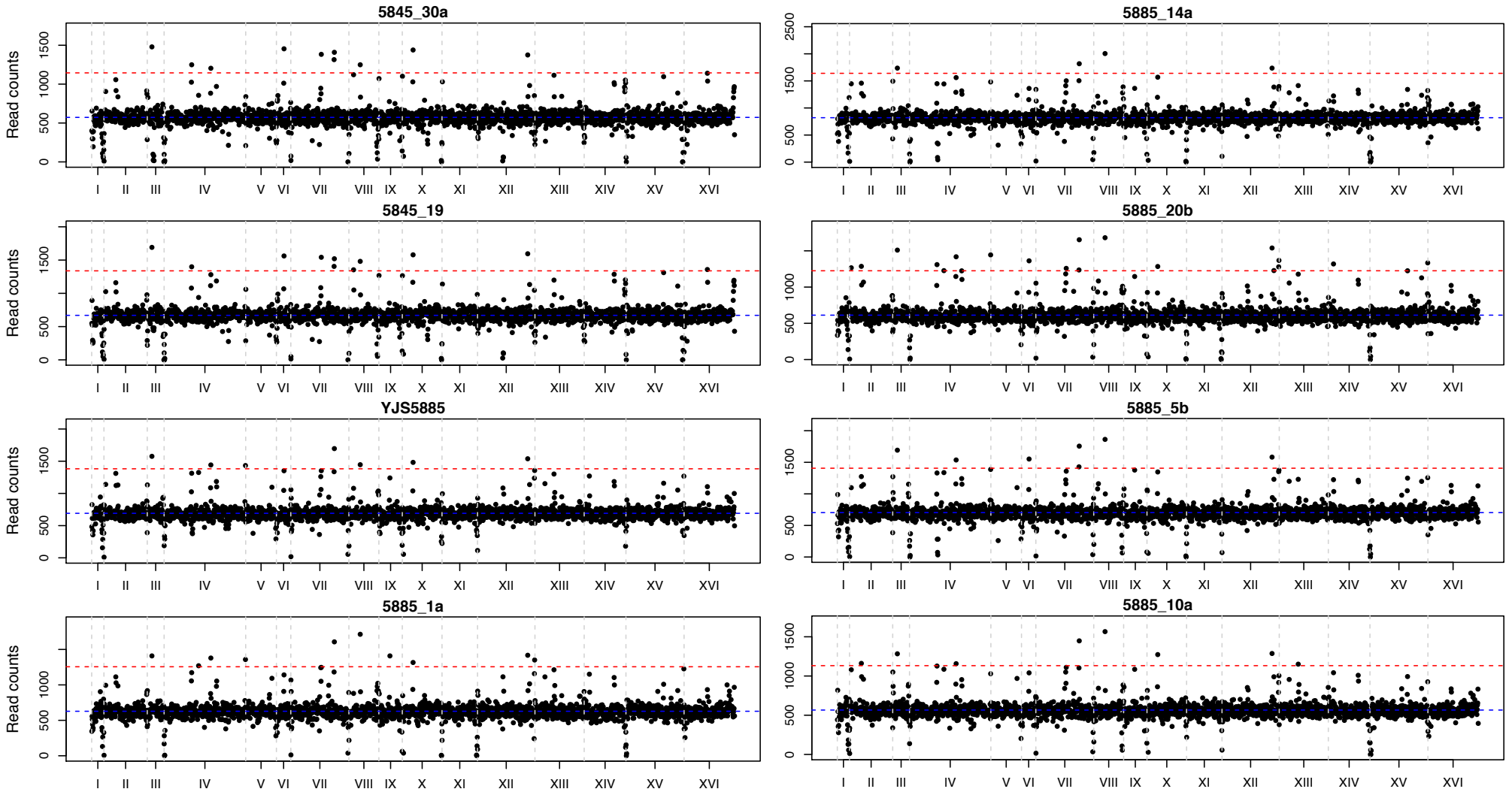
XV
XVI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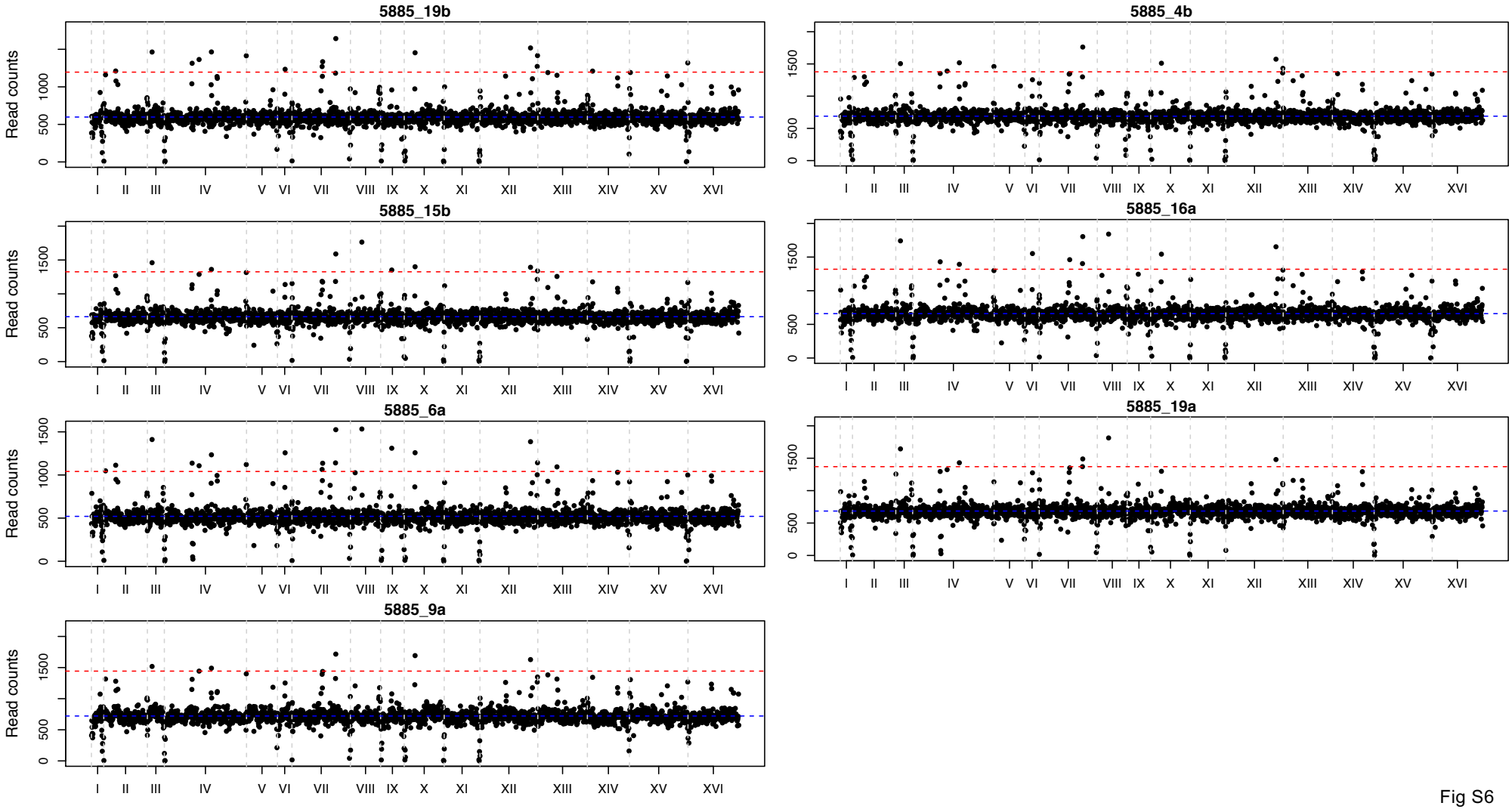
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5885_6a
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5885_9a
Read counts
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500
1000
1500
I II III IV V VI VII VIII IX X XI XII XIII XIV XV XVI

Fig S6

Table S1 Genotyping of spore clones obtained by dissection of isolate tetrads

Lab name	*MLH1* genotype	*PMS1* genotype	Number of spore clones genotyped for *MLH1-PMS1* as: Ancestral	SK1	S288c	Incompatible
YJS5845	SK1/S288c	SK1/S288c	5	17	1	10
YJS5885	SK1/S288c	SK1/S288c	5	6	11	11
YJM521	SK1/S288c	SK1/S288c	5	7	7	5
YJS4806	SK1/S288c (3:1)	SK1	not relevant			
YJS4810	SK1/S288c (3:1)	SK1	not relevant			
YJS5882	SK1/S288c (3:1)	SK1-S288c (2:2)	not relevant			
YJS5678	SK1/S288c (3:1)	SK1/S288c (2:2)	not relevant			
YJS5512	SK1/S288c (3:1)	SK1/S288c (2:2)	not relevant			
YJS4970	SK1/S288c (2:2)	SK1/S288c (2:2)	not relevant			

MLH1 and *PMS1* genes were PCR amplified from isolates and derived spore clones and sequenced as described in the Materials and Methods. For YJS5845, three spore clones were genotyped from random spores and 30 were genotyped from spores isolated after tetrad dissection. For YJS5885, all spore clones were genotyped from tetrad dissection. None of the incompatible YJS5845 and YJS5885 spore clones contained the Pro 271 suppressor polymorphism in MLH1 (Demogines *et al*. 2008). For YJM521, 24 spore clones were genotyped from six four-spore viable tetrads. For YJS4806, 24 spore clones were genotyped from random spores with 22 showing the parental genotype for *MLH1*, and two showing a different segregation pattern (2G:2A, 4G:0A). For YJS4810, 24 spore clones were genotyped from random spores, with all showing the parental genotype for *MLH1.*

Table S2 Genotyping of *MLH1* and *PMS1* loci in YJM and YJS isolates and derived spore clones

base pair	aa	S288c	SK1	YJS5845c	YJS5845k	YJS5885c	YJS5885k	YJM523	YJM521c	YJM521k
MLH1										
486	162	C, ALA	T, ALA	C	C	C	C	C	C	C
552	184	C, SER	C, SER	C	C	C	C	C	T, SER	C
720	240	C, SER	A, ARG	C	C	C	C	C	C	C
812	271	T, LEU	**C, PRO**	T	C	T	C	T	C	C
834	278	C, SER	T, SER	C	T	C	T	C	C	T
997	333	G, GLU	A, LYS	G	G	G	G	G	G	G
1044	348	T, ILE	C, ILE	T	C	T	C	T	T	C
1237	413	T, LEU	C, LEU	T	C	T	C	T	T	C
1393	465	G, ASP	G, ASP	G	G	G	G	G	A, ASN	G
1875	625	T, SER	C, SER	T	C	T	C	T	T	C
2032	678	G, ASP	A, ASN	G	A	G	A	G	G	A
2108	703	C, PRO	T, LEU	C	T	C	T	C	C	T
2282	761	A, ASP	G, GLY	A	G	A	G	A	A	G
PMS1										
122	41	A, ASN	G, SER	G	G	G	G	A	A	A
162	54	T, SER	T, SER	T	T	T	C	T	T	T
177	59	T, ASP	T, ASP	T	T	T	T	C, ASP	T	C, ASP
210	70	G, GLU	G, GLU	G	G	G	G	A, GLU	G	A, GLU
213	71	C, PHE	T, PHE	T	T	T	T	T	C	T
258	86	T, ASP	C, ASP	C	C	C	C	C	C	C
333	111	G, VAL	C, VAL	C	C	C	C	C	C	C
335	112	T, ILE	C, THR	C	C	C	C	T	T	T
465	155	C, PRO	T, PRO	T	T	T	T	T	C	T

552	184	T, ALA	A, ALA	T	A	T	A	T	T	T
558	186	T, ILE	C, ILE	C	C	C	C	C	T	C
708	236	A, LEU	G, LEU	G	G	G	G	G	A	G
711	237	T, ASN	C, ASN	C	C	C	C	C	T	C
810	270	G, SER	C, SER	G	C	G	C	G	G	G
855	285	G, VAL	A, VAL	G	A	G	A	G	G	G
858	286	T, ASN	T, ASN	T	T	T	T	C, ASN	T	C, ASN
918	306	C, PHE	C, PHE	C	C	C	C	C	T, PHE	C
925	309	G, VAL	G, VAL	G	G	G	G	G	T, PHE	G
939	313	T, ALA	A, ALA	A	A	A	A	A	T	A
1150	384	T, PHE	G, VAL	G	G	G	G	G	T	G
1175	392	A, GLU	A, GLU	A	A	A	A	T, ASP	A	T, ASP
1191	397	C, ASN	C, ASN	T, ILE	C	T, ILE	C	T, ILE	C	T, ILE
1199	400	C, THR	G, SER	G	G	G	G	G	C	G
1201	401	G, ALA	G, ALA	T, SER	G	T, SER	G	T, SER	G	T, SER
1249	416	NO INS	INS	INS	INS	INS	INS	INS	NO INS	INS
1329	443	C, ILE	C, ILE	T, ILE	C	C	C	T, ILE	C	T, ILE
1538	513	A, TYR	T, PHE	A	T	A	T	A	A	A
1575	525	G, ALA	C, ALA	G	C	G	C	G	G	G
1691	564	C, ALA	C, ALA	C	C	C	C	T, VAL	C	T, VAL
1782	594	T, TYR	C, TYR	C	C	C	C	C	T	C
1821	607	A, GLU	G, GLU	G	G	G	G	G	A	G
2076	692	T, ASP	T, ASP	C, ASP	T	T	T	T	T	T
2303	768	A, LYS	A, LYS	A	A	A	A	G, ARG	A	G, ARG
2322	774	T, THR	G, THR	G	G	G	G	G	T	G
2364	788	G, LEU	A, LEU	A	A	A	A	A	G	A
2453	818	G, ARG	A, LYS	G	A	G	A	A	G	A

The sequences for the *MLH1* and *PMS1* open reading frames for each of the two parental chromosomes are shown relative to the S288c and SK1 sequences for YJS5845, YJS5885, and YJM521. The parental chromosomes were genotyped as “c” (S288c) or “k” (SK1) based on the amino acid polymorphisms seen at the incompatibility loci (bp 2282 in *MLH1*, bp 2453 in *PMS1*) in the S288c and SK1 sequences (Materials and Methods). The MLH1-271P suppressor allele is highlighted at bp 812 in *MLH1*. INS = 12 bp insertion in *PMS1*; NO INS = lacking the insertion.

Table S3 Analysis of *HO*, *PHO80* and *STP22* genes in YJS5845 and YJS5885 for variants using SnpEff.

YJS5845

Gene Name	Mutation	Type of mutation	Amino acid change	Predicted effect of missense mutation by SnpEff
HO gene in Chromosome IV	1756T>C	missense	Cys586Arg	Deleterious
	1740C>T	synonymous	Asn580Asn	
	1722T>C	synonymous	His574His	
	1718C>T	missense	Pro573Leu	Tolerated
	1710C>T	synonymous	Val570Val	
	1635C>T	synonymous	Gly545Gly	
	1214C>T	missense	Ser405Leu	Tolerated
	1059T>C	synonymous	Val353Val	
	1026C>A	synonymous	Gly342Gly	
	789A>G	synonymous	Leu263Leu	
	667A>G	missense	Ser223Gly	Tolerated
	565G>A	missense	Ala189Thr	Tolerated
	369G>A	synonymous	Arg123Arg	
PHO80 in Chromosome XV	21A>C	missense	Glu7Asp	Tolerated
	111G>A	synonymous	Val37Val	
STP22 in Chromosome III	1000C>A	missense	Gln334Lys	Tolerated
	546A>G	synonymous	Pro182Pro	
	528T>C	synonymous	Asn176Asn	
	525G>A	synonymous	Gln175Gln	
	492C>G	synonymous	Pro164Pro	
	36G>A	synonymous	Ala12Ala	

YJS5885

Gene Name	Mutation	Type of mutation	Amino acid change	Predicted effect of missense mutation by SnpEff
HO gene Chromosome IV	1740C>T	synonymous	Asn580Asn	
	1710C>T	synonymous	Val570Val	
	1635C>T	synonymous	Gly545Gly	
	1424T>A	missense	Leu475His	Tolerated
	1214C>T	missense	Ser405Leu	Tolerated
	667A>G	missense	Ser223Gly	Tolerated
	369G>A	synonymous	Arg123Arg	

YJS5885

Gene Name	Mutation	Type of mutation	Amino acid change	Predicted effect of missense mutation by SnpEff
PHO80 gene in Chromosome XV	21A>C	missense	Glu7Asp	Tolerated
	111G>A	synonymous	Val37Val	
	266C>T	missense	Ser89Phe	Tolerated
	375A>G	synonymous	Thr125Thr	
	739C>T	missense	Pro247Ser	Tolerated
STP22 gene in Chromosome III	1000C>A	missense	Gln334Lys	Tolerated
	528T>C	synonymous	Asn176Asn	
	525G>A	synonymous	Gln175Gln	
	492C>G	synonymous	Pro164Pro	
	123T>A	missense	Asn41Lys	Tolerated
	78C>A	missense	Asn26Lys	Tolerated
	36G>A	synonymous	Ala12Ala	

Table S4 Analysis of resistance to 5-FOA in YJS5885 spore clones.

Strain or spore clone	Incompatible/ Compatible	Rate 5-FOA^r (10^{-7}), (95% C.I.), n	Relative rate
FY90	C	0.79 (0.26-2.6), 22	1
EAY4087 (*mlh1Δ)*	Not applicable	16[a] (9.5-18), 20	20
5885-1a	C	1.9[b] (0.72-5.2), 15	2.4
5885-14a	C	0.98[b] (0.53-2.1), 15	1.2
5885-15b	C	0.48[b] (0.37-3.2), 15	0.61
5885-6a	C	0.68[b] (0.32-1.5), 15	0.86
5885-9a	I	6.0[a, b] (4.7-9.7), 15	7.6
5885-16a	I	1.5[b] (0.92-1.9), 15	1.9
5885-19a	I	6.4[a, b] (2.9-7.9), 15	8.1

The rate of resistance to 5-FOA, presented with 95% confidence intervals (95% C.I.), was determined for n independent cultures of FY90 and the indicated spore clones of YJS5885 as described in the Materials and Methods. The *URA3* open reading frame (ATG =+1) was sequenced from 7, 2, 1, 1, 1 and 1 independent 5-FOA^r colonies from 5885-9a, 5885-15b, 5885-1a, 5885-14a, 5885-16a, and 5885-19a, respectively. [a] Significantly different from FY90 ($p<0.001$, Mann-Whitney test); [b] Significantly different from EAY4087 ($p<0.001$, Mann-Whitney test). YJS5885 compatible and incompatible spore clones are significantly different from each other ($p<0.001$, Mann-Whitney test).

10 of the 13 spore clones contained single mutations in *URA3*, with the following distribution:
5885-9a: Two missense (bp287,A>T; bp542, G>A), One nonsense (bp577, G>T), Two single nucleotide deletions (bp178, A deleted; bp629, G deleted), no changes in ORF for two 5-FOA^r mutants.
5885-15b: One missense (bp205, T>C), one nonsense (bp345 G>A).
5885-1a: One nonsense (bp223 A>T).
5885-14a: One nonsense (bp593 T>A).
5885-16a: No changes in ORF for one 5-FOA^r mutant.
5885-19a: One nonsense (bp310 C>T).

Table S5 Sporulation and lactate growth phenotype

	Sporulation	Lactate+ or -		Sporulation	Lactate + or -
5885-1a	-	+	5845-19a	-	-
5885-6a	-	+	5845-22a	+	+
5885-10a	-	-	5845-27a	+	+
5885-20b	-	+	5845-7a	+	+
5885-5b	-	+	5845-28b	+	+
5885-15b	-	-	5845-29a	+	+
5885-14a	-	+	5845-41a	-	-
5885-19b	-	-	5845-16	+	+
5885-6b	-	+	5845-35a	poor growth- few dyads	+
5885-5a	-	+	5845-18a	+	+
5885-11a	-	+	5845-21a	-	+
5885-12a	-	-	5845-20a	+	+
5885-18a	-	-	5845-30a	+	-
5885-9a	-	-	5845-19	+	+
5885-4b	-	+	5845-36b	+	NT
5885-19a	-	-			
5885-16a	-	-			
5885-3a	-	+			
5885-12b	-	-			
5885-1b	-	NT			
5885-2a	-	NT			
5885-4a	-	NT			
5885-7a	+	NT			
5885-8a	-	NT			
5885-13a	-	NT			
5885-17a	+	NT			

Spore clones were patched on sporulation media and incubated at 30°C for 6 days after which they were examined for evidence of sporulation by light microscopy. Any samples with dyads, triads and tetrads were marked as being able to sporulate (+). Spore clones were also patched on YP-lactate media and scored as able to grow or not (Lactate^{+} or $^{-}$) after 4 days in 30°C. NT: not tested.

Table S6 Assigning MLH1 polymorphisms found in heterozygous genotypes onto the MLH1 structure-function map.

mlh1 allele (Reference)	Amino acid position: isolate(s) with heterozygous genotype
N-terminal/ATP binding	
I22T (Wanat *et al.* 2007)	22-ILE/LEU: APL, CFI, CFN
Linker (Argueso *et al.* 2003)	
R390A,K391A	391-LYS/ASN: BHL, BMQ
K393A,R394A (Argueso *et al.* 2003)	393-LYS/GLU: CPN, CPR
R401A,D403A	402-ILE/LEU: ASN, BGB, BGI, BGM, BGS
C-terminal interaction (Argueso *et al.* 2003)	
E603A,D605A,E606A	605-ASP/ASN: BHL, BMQ
K648A,K650A	650-LYS/THR: ADL, AKT, BFE, BFG, BFM, BML, BMM, BTD, BTE, CKK, CKS, CLA
E680A,D681A,E682A	681-ASP/ASN: CPN, CPR

A structure function map for MLH1 was created from an analysis of *MLH1* alanine scan and site-specific mutations, and *mlh1* alleles generated based on homology to HNPCC mutations (Pang *et al.* 1997; Shcherbakova and Kunkel 1999; Tran and Liskay 2000; Welz-Voegele *et al.* 2002; Takahashi *et al.* 2007; Wanat *et al.* 2007; Romanova and Crouse 2013; Smith *et al.* 2013; Smith *et al.* 2015). Alleles that conferred a mutator phenotype in a variety of reporter assays are shown. In MLH1, amino acids 1-335 is referred to as that N-terminal/ATP binding domain, 335-509 as the linker domain, and 510-769 as the C-terminal interaction domain (Gueneau *et al.* 2013). See Table S7 for detailed list of the isolates that contain heterozygous polymorphisms that lie on the MLH1 structure-function map (shown here using their standardized names in the 1011 yeast genome project (Peter *et al.* 2018).

Table S7 Amino acid heterozygosities identified in MLH1 in 107 yeast isolates

Standardized name	Isolate name	Origin	Position of amino acid heterozygosity (amino acid 1/amino acid 2) in Mlh1																																							
			7	22	215	256	271	283	285	329	366	391	393	400	402	409	417	421	430	436	442	452	465	470	488	489	501	507	542	595	596	605	607	616	650	655	657	678	681	694	703	716	722	761
	S288c		Ala	Ile	Thr	Ile	Leu	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp
	SK1 (SGD)		Ala	Ile	Thr	Ile	PRO	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asn	Asp	Ala	Leu	Glu	Asn	Gly
AAL	CBS1236-a	Bakery, France	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys	Leu	Lys	Asp	Asp	Ala/Ser	Pro	Glu	Asn	Asp/Gly
ABV	DBVPG6861	Water, Brazil	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
ADL	CLIB318_1	Bakery, Netherlands	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys/Thr	Leu	Lys	Asn	Asp	Ala	Leu	Glu	Asn	Gly
ADM	CLIB324_2	Bakery, Vietnam	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
AEB	CBS1171	Beer, Netherlands	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Gly
AEC	CBS1248	Beer	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asn	Asp	Ala	Leu	Glu	Asn	Gly
AEL	CBS1394	Distillery	Ala	Ile	Thr	Ile	Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys	Leu	Lys	Asp	Asp	Ser	Pro	Glu	Asn	Gly
AEV	CBS6216	Water, Netherlands	Ala	Ile	Thr	Ile	Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys	Leu	Lys	Asp/Asn	Asp	Ala/Ser	Pro/Leu	Glu	Asn	Gly
AFC	CBS7764	Rainbow trout, Sweden	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
AFS	CBS1173	Fruit	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Gly
AGG	CBS1480	Distillery	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asn	Asp	Ala	Leu	Glu	Asn	Gly
AIK	C15.1	Palm nuts, Cameroon	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
AKT	CLQCA_10-003	Stingless bee, Equador	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys/Thr	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
ALN	21-4-103	Water, Slovakia	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
ALV	21-4-124	Fruit, Slovakia	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
AMN	SJ5L13	Tree Leaf, Taiwan	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
ANP	UWOPS83-883-2	Drosophila, Navassa Island, S. Amer.	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
APH	M1.1	Distillery, Brazil	Ala	Ile	Thr	Ile	Leu	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe/Ser	Leu	Thr/Lys	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
APL	YS11(E)	Bakery, Turkey	Ala	Ile/Leu	Thr	Ile	Leu/Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys	Leu	Lys	Asp/Asn	Asp	Ala/Ser	Pro/Leu	Glu	Asn	Gly
AQH	CBS7957	Industrial, Brazil	Ala	Ile	Thr	Ile	Leu	Tyr	Pro	Gln	Asp	Lys	Lys	Val/Ala	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala/Ser	Pro	Glu	Asn	Asp/Gly
ARE	CBS1398	Eucalyptus leaf	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ser	Pro	Glu	Asn	Gly
ARN	CBS2246	Sputum, Human clinical, Netherlands	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asn	Asp	Ala	Leu	Glu	Asn	Gly
ASC	CBS4455	Kaffir Beer, South America	Ala	Ile	Thr	Ile	Leu	Tyr	Pro	Gln/Lys	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln/His	Ser	Asp	Pro	Glu	Glu	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp
ASH	CLIB227	Beer, Netherlands	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Gly
ASN	CLIB630	Dairy cheese, France	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile/Leu	Ile	Gln	Phe	Leu/Met	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val/Ile	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu/Gln	Asn	Asp/Gly
ATS	CECT10131	Flower, Spain	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys	Leu	Lys	Asp	Asp	Ala/Ser	Pro	Glu	Asn	Asp/Gly
ATV	CECT1462	Beer, United Kingdom	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp/Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
BBC	CCY_21-4-88	Mushroom fruitbody, Slovakia	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
BBD	CCY_21-4-97	Water, Slovakia	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
BBE	CCY_21-4-98	Water, Slovakia	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
BBG	CCY_21-4-106	Water. Slovakia	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Gly
BBP	1663	Flower, Spain	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys	Leu	Lys	Asp	Asp	Ala/Ser	Pro	Glu	Asn	Asp/Gly
BDA	#34	Evolution Canyon, Israel	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp
BDD	#13	Evolution Canyon, Israel	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp/Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
BFE	EXF-5734	Gooseberry juice	Ala	Ile	Thr	Ile	Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys/Thr	Leu	Lys	Asp/Asn	Asp	Ala/Ser	Pro/Leu	Glu	Asn	Gly
BFG	EXF-5869	Wood	Ala	Ile	Thr	Ile	Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys/Thr	Leu	Lys	Asp/Asn	Asp	Ala/Ser	Pro/Leu	Glu	Asn	Gly
BFM	EXF-6835	Industrial, Slovenia	Ala	Ile	Thr	Ile	Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys/Thr	Leu	Lys	Asp/Asn	Asp	Ala/Ser	Pro/Leu	Glu	Asn	Gly
BGB	CLIB550	Dairy cheese, France	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile/Leu	Ile	Gln	Phe	Leu/Met	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu/Gln	Asn	Asp/Gly
BGI	CLIB557	Dairy cheese, France	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile/Leu	Ile	Gln	Phe	Leu/Met	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val/Ile	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu/Gln	Asn	Asp/Gly
BGM	CLIB560	Dairy cheese, France	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp/Gly	Lys	Lys	Val	Ile/Leu	Ile	Gln	Phe	Leu/Met	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu/Gln	Asn/Ser	Asp/Gly
BGS	CLIB631	Dairy cheese, France	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile/Leu	Ile	Gln	Phe	Leu/Met	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val/Ile	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu/Gln	Asn	Asp/Gly
BHD	CLIB1059	Cider, France	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg/Ile	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
BHL	CLIB1082	Cider, France	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys/Asn	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp/Asn	Leu	Ile	Lys	Leu/Phe	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
BKD	DBVPG1374	Soil, Netherlands	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile/Val	Gln	Phe	Leu	Thr	Gln	Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
BKP	DBVPG1581	Grape must, Italy	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
BMG	NCYC_2925	Sputum, Human clinical, Norway	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys	Leu	Lys	Asp/Asn	Asp	Ala/Ser	Pro/Leu	Glu	Asn	Asp/Gly
BML	NCYC_2780	Vagina, human clinical, Belgium	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys/Thr	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
BMM	2680	Vagina, human clinical, Spain	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys/Thr	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
BMQ	2720	Blood, human clinical, Spain	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys/Asn	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys/Glu	Arg/Ile	Val	Val/Leu	Ile	Val	Asp/Asn	Leu	Ile	Lys	Leu/Phe	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
BNP	DBVPG1714	Grape must, Spain	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile/Val	Gln	Phe	Leu	Thr	Gln	Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
BQH	DBVPG3100	Grape must, Italy	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
BQM	DBVPG4162	Grape must, Italy	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
BRP	DBVPG6694	Beer, Belgium	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp/Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Gly
BRQ	DBVPG6695	Beer, Belgium	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
BRV	DBVPG6874	Human Clinical, USA	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asn	Asp	Ala	Leu	Glu	Asn	Gly
BSI	DBVPG6693	Beer, Belgium	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp/Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Gly
BTA	NCYC_2798	Human clinical, Germany	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Gly
BTB	77	Bakery	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp/Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Gly
BTC	79	Fleischmann baker's yeast	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
BTD	YS5(E)	Canadian baker's eyast	Ala	Ile	Thr	Ile	Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys/Thr	Leu	Lys	Asp/Asn	Asp	Ala/Ser	Pro/Leu	Glu	Asn	Gly
BTE	YS8(E)	Italian baker's yeast	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys/Thr	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
BTV	M.14.1	Distillery, Brazil	Ala	Ile	Thr	Ile	Leu	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe/Ser	Leu	Thr/Lys	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
BVG	SM.9.4.BL2	Bioethanol, Brazil	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe/Ser	Leu	Thr/Lys	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val/Leu	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
BVH	SM.9.4.BR1	Bioethanol, Brazil	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe/Ser	Leu	Thr/Lys	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val/Leu	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CBF	SD-15	Bakery, Italy	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CBL	2	Chalcidoidea insect, Germany	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
CBM	3	Chalcidoidea insect, Germany	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
CBR	NCYC_1187	Beer, United Kingdom	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp/Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Gly
CFC	WLP530	Beer, Belgium	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp/Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala/Ser	Pro/Leu	Glu	Asn	Gly
CFD	WLP001	Beer, USA	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp/Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
CFE	4.9_WLP099	Beer, United Kingdom	Ala	Ile	Thr	Ile	Pro	Tyr/Cys	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp/Asn	Pro	Glu/Lys	Lys	Arg	Val	Val	Ile	Val	Asp	Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
CFG	Safale_S40	Beer, United Kingdom	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp/Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Gly
CFH	WLP039	Beer, United Kingdom	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp/Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Gly
CFI	WLP013	Beer, United Kingdom	Ala	Ile/Leu	Thr	Ile	Leu/Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys	Leu	Lys	Asp/Asn	Asp	Ala/Ser	Pro/Leu	Glu	Asn	Asp/Gly
CFM	WLP090	Beer, San Diego, USA	Ala	Ile	Thr	Ile	Leu	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Gly
CFN	WLP006	Beer	Ala	Ile/Leu	Thr	Ile	Leu/Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys	Leu	Lys	Asp/Asn	Asp	Ala/Ser	Pro/Leu	Glu	Asn	Asp/Gly
CFP	WLP565	Beer	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
CGC	UCD_06-645	Female Olive Fly, Davis, California	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CHE	Lib71	Grape must, Lebanon	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
CHG	324-6C	Bakery, Vietnam	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CHK	Win-8B	Beer, United Kingdom	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys	Leu	Lys	Asp	Asp	Ala/Ser	Pro	Glu	Asn	Asp/Gly
CHQ	B10-1	Bakery, France	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Gly
CHS	SC 32 F.	Feces, human clinical, France	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Ile	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asn	Asp	Ala	Leu	Glu	Asn	Gly
CHT	SC 33 F.	Feces, human clinical, France	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Ile	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asn	Asp	Ala	Leu	Glu	Asn	Gly
CIC	Ponton 11	Mouth, human clinical, Spain	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CIG	PB11	Feces, human clinical, Netherlands	Ala	Ile	Thr	Ile	Leu	Tyr	Pro	Gln	Asp	Lys	Lys	Val/Ala	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala/Ser	Pro	Glu	Asn	Asp/Gly
CII	PB13	Sputum, Human clinical, Netherlands	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val/Ile	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala/Ser	Pro	Glu	Asn	Gly
CIK	PB14	Sputum, Human clinical, Netherlands	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val/Ile	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala/Ser	Pro	Glu	Asn	Gly
CIL	PB15	Feces, human clinical, Netherlands	Ala	Ile	Thr	Ile	Leu	Tyr	Pro	Gln	Asp	Lys	Lys	Val/Ala	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala/Ser	Pro	Glu	Asn	Asp/Gly
CKK	CLI_16	Feces, human clinical, France	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys/Thr	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CKN	CLI_19	Feces, human clinical, France	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CKS	CLI_23	Human clinical, France	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys/Thr	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CLA	CLI_26	Human clinical, France	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln/Glu	Phe	Leu	Thr	Gln	Ser/Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu/Phe	Ile	Lys/Thr	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CMG	RIB6002	Sake, Japan	Ala	Ile	Thr	Ile/Leu	Pro	Tyr	Pro/Ser	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp/Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile/Thr	Lys	Leu	Lys	Asp/Asn	Asp	Ala/Ser	Pro	Glu	Asn	Gly
CNB	SM.8.2.C13	Bioethanol, Brazil	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe/Ser	Leu	Thr/Lys	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val/Leu	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CNE	SM.8.7.L8	Bioethanol, Brazil	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe/Ser	Leu	Thr/Lys	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val/Leu	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CNF	SM.8.7.L9	Bioethanol, Brazil	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe/Ser	Leu	Thr/Lys	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val/Leu	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CNL	SA.9.2.BL3	Bioethanol, Brazil	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe/Ser	Leu	Thr/Lys	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val/Leu	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CNN	SA.9.4.VL4	Bioethanol, Brazil	Ala	Ile	Thr	Ile	Leu/Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe/Ser	Leu	Thr/Lys	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val/Leu	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CNP	SA.9.4.BR2	Bioethanol, Brazil	Ala	Ile	Thr	Ile	Leu	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe/Ser	Leu	Thr/Lys	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp/Asn	Asp	Ala	Pro/Leu	Glu	Asn	Asp/Gly
CPN	LCBG-3Y3	Distillery, Mexico	Ala/Pro	Ile	Ser	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Glu	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Ile	Asp	Asn	Ala	Pro	Glu	Asn	Gly
CPR	LCBG-3Y8	Distillery, Mexico	Ala/Pro	Ile	Ser	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Glu	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Ile	Asp	Asn	Ala	Pro	Glu	Asn	Gly
CRH	L-319	Wine, Chile	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Gly	Asp	Pro	Glu	Lys	Arg	Val/Ile	Val	Ile/Met	Val	Asp	Phe	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp/Gly
SACE_YAN	YJM456	Human clinical, California, USA	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Gly	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp
SACE_YAQ	YJM554	Human clinical, California, USA	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asn	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp
SACE_YAR	YJM555	Human clinical, California, USA	Ala	Ile	Thr	Ile	Leu	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Pro	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asp	Asp	Ala	Pro	Glu	Asn	Asp
SACE_YDK	YJM1592	Sewage, Thailand	Ala	Ile	Thr	Ile	Pro	Tyr	Pro	Gln	Asp	Lys	Lys	Val	Ile	Ile	Gln	Phe	Leu	Thr	Gln	Ser	Asp	Ser	Glu	Lys	Arg	Val	Val	Ile	Val	Asp	Leu	Ile	Lys	Leu	Lys	Asn	Asp	Ala	Leu	Glu	Asn	Gly

Amino acid heterozygosities in the MLH1 open reading frame are shown for 107 isolates (relative to the MLH1 S288c sequence; Peter *et al.* 2018).