

Supplementary Materials.

Figure S1: plasmid maps

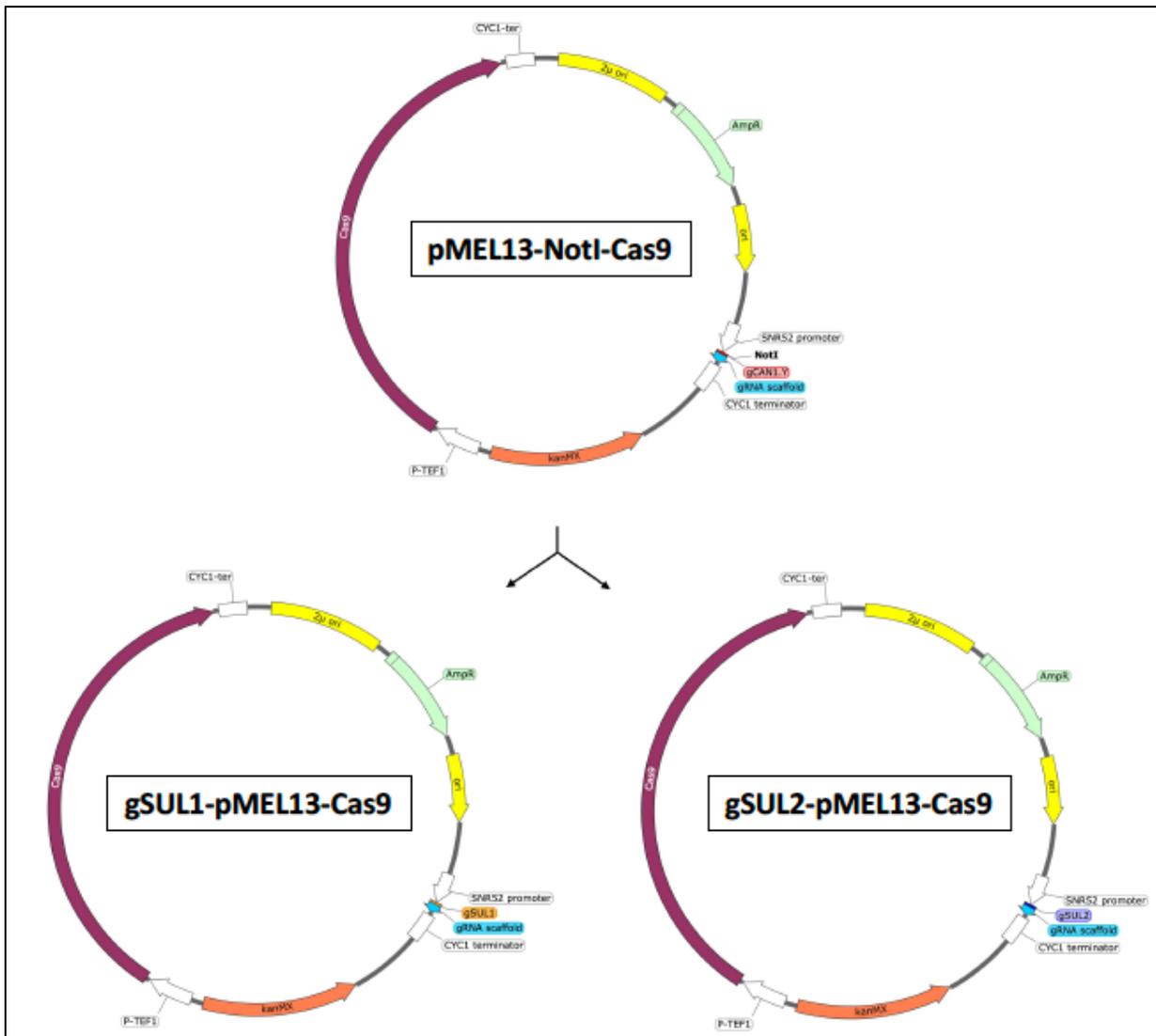
Figure S2: PCR analysis of *SUL1* and *SUL2* loci

Figure S3: genotype analysis by PCR inter-delta assay

Table S1: volatile compounds detected by GC-MS analysis

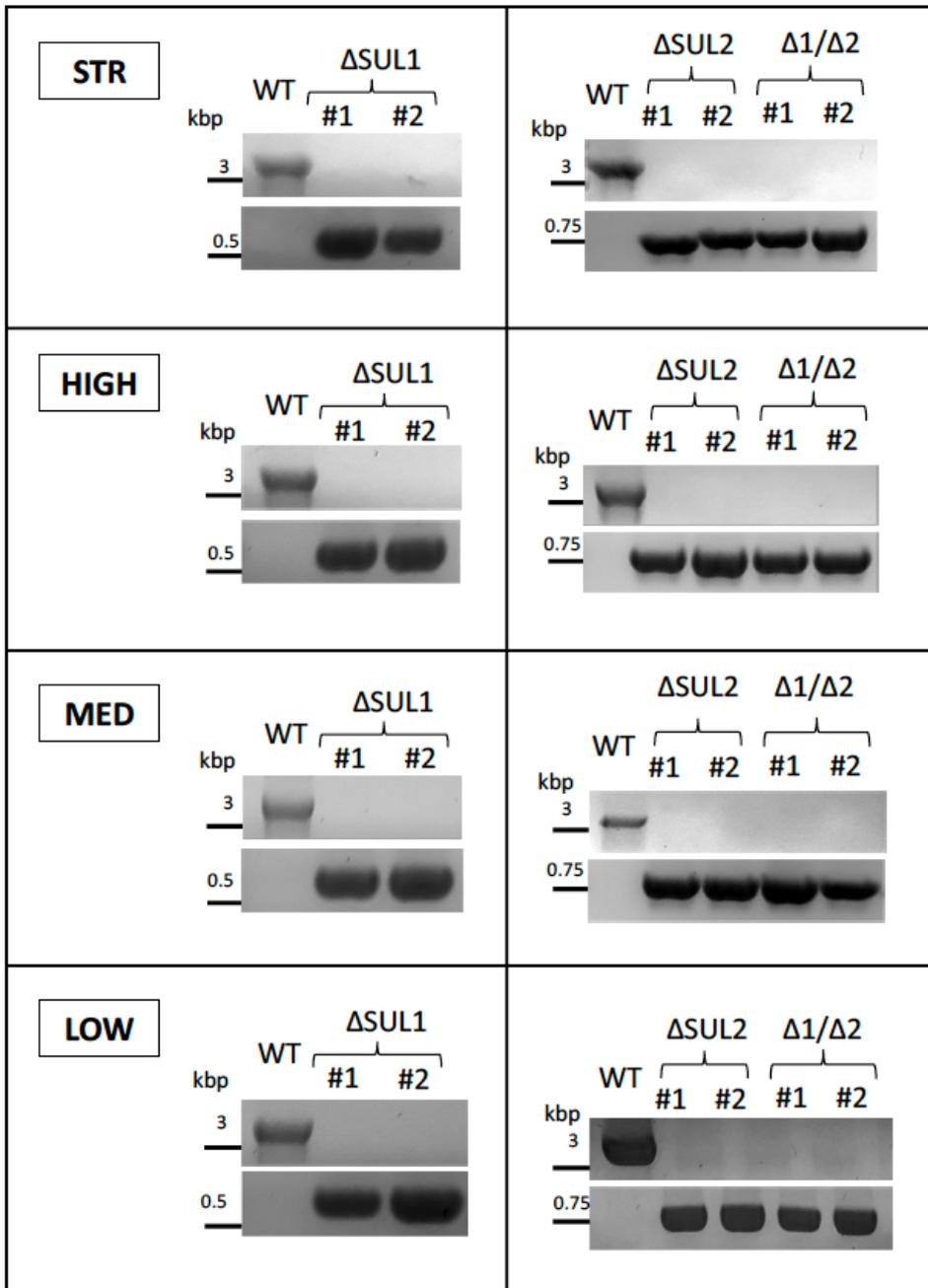
Table S2: plasmids and primers

Table S3: features of natural grape juices



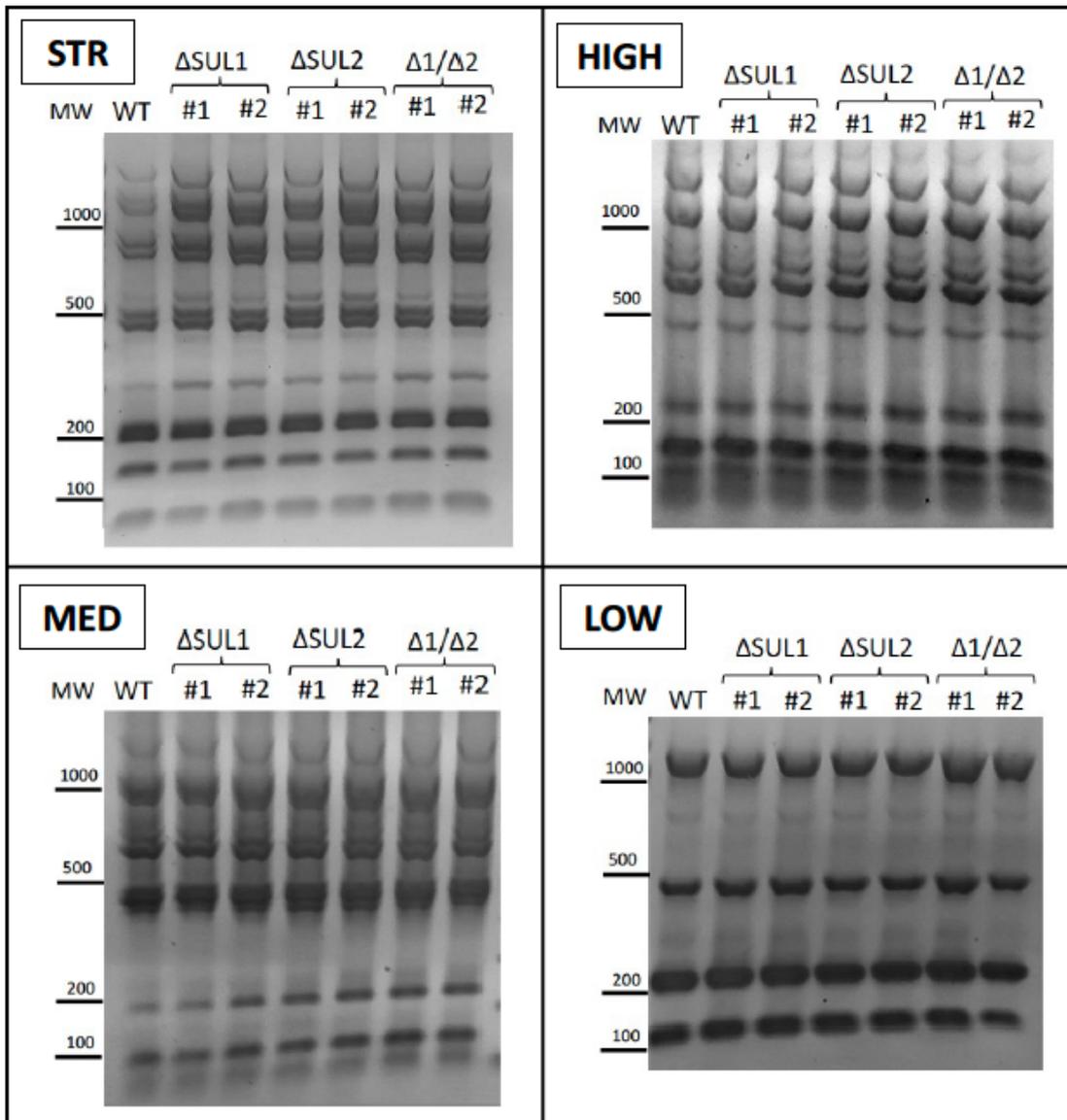
Supplementary Figure S1. Plasmids used.

Maps of the plasmids constructed in this work, representing their main features. By the site-specific replacement of the *gCAN.Y* sequence (including the *NotI* site) with a specific target *gDNA* region (as indicated for *SUL1* or *SUL2* genes), the *gDNA*-pMEL13-Cas9 plasmid can be used to manipulate the genome of any natural yeast strain without the need for specific auxotrophic markers.



Supplementary Figure S2. PCR analysis of *SUL1* and *SUL2* loci

Agarose gel electrophoresis showing PCR amplifications of the genomic DNA, extracted from two different clones (#1, #2) generated by the CRISPR/Cas9-assisted genetic modification of the indicated strains (STR, HIGH, MED, LOW) targeting either *SUL1*, or *SUL2* genes, or both (Δ 1/ Δ 2). Unmodified (WT) strains were used as controls. The PCR were performed using either dgSUL1, or dgSUL2, forward (F) and reverse (R) primers, respectively mapped outside the *SUL1* or the *SUL2* coding sequence. PCR fragments are expected to be sized \sim 3500 bp for the parental alleles, \sim 570 bp for Δ SUL1 and \sim 800 for Δ SUL2 alleles.



Supplementary Figure S3. Genotype analysis by PCR inter-delta assay

Agarose gel electrophoresis showing the inter-Delta profile obtained by PCR amplifications of the genomic DNA from two different clones (#1, #2) of the indicated strains (STR, HIGH, MED, LOW) deleted for either *SUL1*, or *SUL2* genes, or both (Δ 1/ Δ 2). Unmodified (WT) strains were used as controls. The PCR were performed using δ 12 and δ 21 primers as reported (see Materials and Methods)

Supplementary Table S2. List of Plasmid and Primers.

Plasmids generated and primers used		
	Plasmid name	Main features (size; yeast marker; bacterial marker; gDNA)
1)	pMEL13-NotI	6130 bp; KanR; AmpR; gDNA: CAN1.Y-NotI
2)	pMEL13-NotI-Cas9	10969 bp; KanR; AmpR; gDNA: CAN1.Y-NotI; SpCas9 expression
3)	gSUL1-pMEL13-Cas9	10969 bp; KanR; AmpR; gDNA: SUL1; SpCas9 expression
4)	gSUL2-pMEL13-Cas9	10969 bp; KanR; AmpR; gDNA: SUL2; SpCas9 expression
	Primer name	Sequence 5'-3'
1)	pMEL-NotI-F	CTCCGCAGTAAAAGATAAATGATCGATACGCGGCCGCTGGAGGAGTTTTAGAGCTA GAAATAGCAAG
2)	pMEL-NotI-R	CTTGCTATTTCTAGCTCTAAAACCTCTCCAGCGGCCGCGTATCGATCATTTATCTTTC ACTGCGGAG
3)	Cas9-pMEL F	ATTAAGGGTTGTGCGA C AGCTCATAGCTTCAAATGTTTCTACTCC
4)	Cas9-pMEL R	TACGCTGCAGGTCGA C CAAATTAAGCCTTCGAGCGTCCC
5)	6006 F	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAAGGCTAGTC
6)	gSUL1 target R	TTCTAGCTCTAAAACCTAGATTGTATCTCATTATGATCATTATCTTTCCTACTGCGGA GA
7)	gSUL2 target R	TTCTAGCTCTAAAACCTTGATAATTTGTGTAACCGATCATTATCTTTCCTACTGCGGA GA
8)	ssSUL1 repair F	CAATAGCTTTAAAATAAAAATAAATCCCTGCAGAATACTCGGAAAGAATTGTAGT AGATAGTAAGTACTTTAATTACCCCCCTGTTTTAGTTATACA
9)	ssSUL1 repair R	TGTATAACTAAAACAGGGGGGTAATTAAGTACTTACTATCTACTACAATTCTTT CCGAGTATTCTGCAGGGATTTATTTTTATTTTTAAAGCTATTG
10)	ssSUL2 repair F	TCTTTCTTGAGGTGTGTGTGTATAGATTAGCAGGGAATTATCTAAGATCCAATG CATTTACAATGGACATGCAAACATTTATATCATCTCTTTTTTTC
11)	ssSUL2 repair R	GAAAAAAGAGATGATATAAATGTTTGCATGTCCATTGTAATGCATTGGATCTTA GATAATCCCTGCTAATCTATACACACACCTCAAGAAAGA
12)	dgSUL1 control F	AAACTCCACACCTTCCCCAC
13)	dgSUL1 control R	GACCATGTCTTTTCAGCGCC
14)	dgSUL2 control F	ACTAGCAACGTCGGATAGCG
15)	dgSUL2 control R	TAAGTGACATCGGGGATGCC
16)	δ12	TCAACAATGGAATCCCAAC
17)	δ21	CATCTAACACCGTATATGA

Supplementary Table S3. Characterization of natural must types.

	Must	Winery (Italy)	Year	Sugar (g/L)	YAN* (mg/L)	SO₄²⁻ (mg/L)	Free SO₂ (mg/L)	Total SO₂ (mg/L)	pH
1)	Prosecco	<i>Lorenzonetto</i>	2021	124.4	108	390	8.3	37.7	3.37
2)	Gewurztraminer	<i>Caldaro</i>	2020	137.7	167	550	4.4	18.7	3.53
3)	Sauvignon blanc	<i>Masut rive</i>	2021	204	202	480	5.8	27.4	3.35
4)	Prosecco (2)	<i>Vigna vecchia</i>	2020	138	81	124	10.2	28.8	3.35

*: YAN, yeast assimilable nitrogen