

**Table S1.** Phage, bacterial genome and plasmid sequences used in the study.

**Accession numbers of the 134 prophages earlier described [19]**

Strain characteristics	Genome accession number
Lysogens (134)	ACSE01, AJIJ01, AJTO01, ALAD01, ALAE01, ALAG01, ALAH01, ALAJ01, ALAK01, AZHH01, AZIP01, AZJU01, AZJV01, AZJW01, AZJX01, AZJY01, AZKA01, AZKB01, AZKC01, AZKE01, AZKF01, AZKH01, AZKJ01, AZKL01, AZLG01, AZLK01, AZLN01, AZLP01, CP014324, CP027431, CP038451, JPEK01, JPEM01, LKRT01, LKRU01, LKRV01, LKRZ01, LKSA01, LKSB01, LKSC01, LKSD01, LKSE01, LKSR01, MLKP01, MLKQ01, MLKT01, MLKZ01, MLLA01, MLLB01, MLLD01, MLLE01, MLLG01, MLLK01, MLLM01, MLLN01, MLLO01, MLLQ01, MLLS01, MLLU01, MLLX01, MLLZ01, MLMF01, MLMI01, MLMJ01, MLMK01, MLMP01, MLMT01, MLMW01, MLMY01, MLMZ01, MLNA01, MLNC01, MLND01, MLNE01, MLNH01, MLNK01, MLNL01, MLNN01, MLNP01, MLNQ01, MLNS01, MLNU01, MLNV01, MLNX01, MLNY01, MLNZ01, MLOA01, MLOB01, MLOC01, MLOE01, MLOF01, MLOG01, MLOH01, MLOI01, MLOJ01, MLOL01, MLON01, MLOO01, MLOP01, MLOU01, MLOW01, MLOX01, MLOY01, MLPB01, MLPC01, MLPD01, MLPE01, MLPG01, MLPH01, MLPI01, MLPK01, MLPL01, MLPN01, MLPQ01, MLPR01, MLPS01, MLPT01, MLPV01, MLPW01, MLPX01, MLPY01, SNST01, SNSU01, SNSV01, SNSW01, SNSX01, SNSY01, ULFS01, ULFU01, ULFZ01, ULGA01, ULGB01, ULGC01, ULGD01.

**Accession numbers of the selected temperate oenophages used for interspecies CRISPR targeting**

Prophages	Lysogenic strains and GenBank assembly	Accession	Reference
<i>O. oeni</i>			
AWRIB508 <sub>proA</sub>	<i>O. oeni</i> AWRIB508	GCA_001869485.1	19
CRBO14223 <sub>proA</sub>	<i>O. oeni</i> CRBO14223	OP964055	This study
AWRIB422 <sub>proA</sub>	<i>O. oeni</i> AWRIB422	NZ_ALAG000000000	
IOEB1491 <sub>proA</sub>	<i>O. oeni</i> IOEB1491	GCA_000762065.1	
IOEBS161 <sub>proA</sub>	<i>O. oeni</i> IOEBS161	GCA_000762245.1	
IOEBB10 <sub>proB</sub>	<i>O. oeni</i> IOEBB10	GCA_000761865.1	
AWRIB304 <sub>proC</sub>	<i>O. oeni</i> AWRIB304	GCA_000286015.1	
IOEBL26-1 <sub>proB</sub>	<i>O. oeni</i> IOEBL26-1	GCA_000762145.1	
AWRIB847 <sub>proB</sub>	<i>O. oeni</i> AWRIB847	GCA_001869725.1	
AWRIB133 <sub>proB</sub>	<i>O. oeni</i> AWRIB133	GCA_001939345.1	
AWRIB202 <sub>proB</sub>	<i>O. oeni</i> AWRIB202	GCA_000309425.1	19
AWRIB150 <sub>proB</sub>	<i>O. oeni</i> AWRIB150	GCA_001868205.1	
CRBO11105 <sub>proB</sub>	<i>O. oeni</i> CRBO11105	GCA_002462335.1	
IOEB0501 <sub>proA</sub>	<i>O. oeni</i> IOEB0501	GCA_000721875.1	
CRBO14221 <sub>proB</sub>	<i>O. oeni</i> CRBO14221	OP964054	This study
IOEB0205 <sub>proA</sub>	<i>O. oeni</i> IOEB0205	GCA_000721835.1	
CRBO14203 <sub>proA</sub>	<i>O. oeni</i> CRBO14203	GCA_002462565.1	
AWRIB127 <sub>proC</sub>	<i>O. oeni</i> AWRIB127	GCA_001868115.1	
AWRIB424 <sub>proB</sub>	<i>O. oeni</i> AWRIB424	GCA_001868555.1	
CRBO14210 <sub>proB</sub>	<i>O. oeni</i> CRBO14210	GCA_002462395.1	
IOEB0608 <sub>proA</sub>	<i>O. oeni</i> IOEB0608	GCA_000761585.1	
UBOCC315001 <sub>proF</sub>	<i>O. oeni</i> UBOCC315001	GCA_900518825.1	
IOEBS28 <sub>proC</sub>	<i>O. oeni</i> IOEBS28	GCA_000761845.1	
CRBO1384 <sub>proE</sub>	<i>O. oeni</i> CRBO1384	GCA_900518765.1	
IOEB0502 <sub>proA</sub>	<i>O. oeni</i> IOEB0502	GCA_000761575.1	
IOEB9805 <sub>proD</sub>	<i>O. oeni</i> IOEB9805	GCA_000761725.1	19
IOEBS13 <sub>proD</sub>	<i>O. oeni</i> IOEBS13	GCA_000761785.1	
AWRIB418 <sub>proD</sub>	<i>O. oeni</i> AWRIB418	GCA_000286155.1	
AWRIB663 <sub>proE</sub>	<i>O. oeni</i> AWRIB663	GCA_001869605.1	
<i>O. sicerae</i>			

45.3 kb prophage	UCMA15228 <sup>T</sup> (1291631-1337008 bp)	NZ_CP029684	This study
<b>Free phages</b>		<b>Accession number</b>	<b>Reference</b>
OE33PA		<a href="#">MH220877</a>	18
Vinitor162		MF939898	21, 22
Vinitor 27		MT859305	21 22
Vinitor 23		OP964053	21, 22
OE33PA6		OP964052	This study
<b>Other bacterial genomes strains</b>			
<i>L. lactiplantibacillus plantarum</i> QHM38203		CP028334.1	none
<i>Liq. mali</i> LM596		NZ_CP045035.1	none
<i>O. alcoholitolerans</i> UFRJ-M7.2.18 <sup>T</sup>		NR_134780	13
<i>O. kitaharae</i> DSM17330 <sup>T</sup>		NZ_AFVZ00000000	14
<i>O. sicerae</i> OAL24*		NZ_CP029684	16
<i>O. kitaharae</i> CRBO2176		NZ_JANJQP010000000	35
<b>Plasmids</b>		<b>Accession number</b>	<b>Reference</b>
pOeni 1 ( <i>O. oeni</i> ); 18.3 kb; theta-like replication		JX416328	58
pOeni 2 ( <i>O. oeni</i> ); 21.9 kb; theta-like replication		JX416329	58
pRSE2 ( <i>O. oeni</i> ); 2.544 kb; rolling-circle replication		NC_003201	59
pRSE3 ( <i>O. oeni</i> ) ; 3.948 kb; rolling-circle replication		NC_003099	59
pAWRIB429 ( <i>O. oeni</i> )		NZ_CP084702	60

\* the genome of *O. sicerae* OAL24 is a metagenome-assembled genome from water kefir.

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**Table S2.** List of primers used in our study.

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Target	Primers	Phage/lysogenic strain	Sequence	Reference
<i>intA</i>	Int <sub>A</sub> F	IOEB0608	CGAAGTTTTGACTGGAAAAGAAA	19, 24
	Int <sub>A</sub> R		TTGAGCGAAGCTGCTATAAGAAC	
<i>intB</i>	Int <sub>B</sub> F	IOEBB10	AGTTACCACCAAAGGCCATAAAC	
	Int <sub>B</sub> R		GCTCTGACGACTTACCAGCTTTA	
<i>intC</i>	Int <sub>C</sub> F	S28	GGCTATGACGCAGGGCGTG	
	Int <sub>C</sub> R		TGACGGGACGTGCTGGCAAG	
<i>intD</i>	Int <sub>D</sub> F	IOEB9805	CGGAAAATATTATCAAGCACGAG	
	Int <sub>D</sub> R		TTCAGCGTGATCTTTACCAAAAT	
<i>intE</i>	intE F	CRBO1384	GATTTTTTGCCTGTAACGGTG	
	intE R		CGCAGGTATTCATGAGGATTC	
<i>intF</i>	int <sub>F/OC</sub> F	UBOCC31005	GATAGCAACACTGGAATGCC	
	int <sub>F/OC</sub> R		GCTATGGACGGTTATGGCAA	
<i>tmp1</i>	tmp1 F	IOEB B10	TGGAAGTTTGCTTAGTTGCAG	24
	tmp1 R		CAGCGGATGAAAACCATTGAGA	
<i>tmp2</i>	tmp2 F	IOEB L26	GGTTGGATCGGAAATTGCTA	
	tmp2 R		TGCAGCTATGGCTGTAATCG	
<i>tmp3</i>	tmp3 F	IOEB 0608	TGGTTCTGTTGTTCTCTGGTATT	
	tmp3 R		GATTTAGAWGCCAGCTTTGCTA	
<i>tmp4</i>	tmp4 F	IOEB S28	CAACAAGCTGTTTTGGATCGC	
	tmp4 R		TAGCTTCTGCCATACTCTTAGC	
<i>tmp5</i>	tmp5 F	IOEB 9805	GGCCAAGGTACCGCAAAG	
	tmp5 R		CTCTGCTTTTCCAGTTTGCTG	
<i>tmp6</i>	tmp6cri F	Vinitor162	ATTCGCTCACAGGGGCAAAA	This study
	tmp6cri R		CCAAATTAGCAGTTGTCATTGTGCC	
<i>tmp7</i>	tmp7 F	UBOCC31005	TTGCAAGCTGAAGGTAAACAAT	
	tmp7 R		GCAGCTGTTTCATTGACTCTAA	
<i>lm1</i>	LM1_F	IOEB0608	AAAAGCATGATTTCCCGTTG	
	LM1_R		TGGCAATTCTATCAGGCACA	
<i>lm2</i>	LM2_F	IOEB0501	CAATGGATCAGCTTGCAGAA	
	LM2_R		GGTGCATCCATAGCAACTGT	
<i>lm3</i>	LM3_F	IOEB0502	GAAAATGCAGTTCCCGAAAG	
	LM3_R		CGCACGGTTTTATCAAGACA	
<i>lm4</i>	LM4_F	CRBO14203	TGATAAGATCCAAAGTGAAGCG	
	LM4_R		TCATCGGTCATATCAGGATCAG	
<i>lm5</i>	LM5_F	IOEBB10	CTGGTGTAATGTGCTAATCGT	
	LM5_R		CCCGAATCAAGCAACTTCTTAA	
<i>lm6</i>	LM6_F	IOEB9805	AAGACCCAAAATCAGGCAATTT	
	LM6_R		AATTTGTTTCATCAGTGGCACTT	
<i>rep1</i>	Rep1_F	IOEB0608	TGAACAGTGACGAAAAACGA	This study
	Rep1_R		TGCTTTCTCCTCTGTCTTTTCTT	
<i>rep2</i>	Rep2_F	OE33PA	ATTGGAATTGCCAGACGAAG	
	Rep2_R		CTTTCGCAAGCTTAGCGTCT	
<i>rep3</i>	Rep3_F	AWRIB418	ATTACCGATGAAACTTTGACCG	
	Rep3_R		TTCTAATTGCTTGACTCCCTGA	
<i>rep4</i>	Rep4_F	UBOCC31005	ACCAAACTCAGTCAAGACAAC	
	Rep4_R		CTGGTGCTTCTTTACTTTCA	
<i>rep5</i>	Rep5_F	Vinitor 162	AGGCGATATCAAACAAGCAATT	
	Rep5_R		TGTCATCCAGTCACGGGTA	
<i>terS1</i>	TerS1_F	L26-1	TGATCTGCTCGGCAGTAGAA	
	TerS1_R		ACACGCTGGAAGGAAAAGAA	
<i>terS2</i>	TerS2_F	IOEB1491	TCTTAATTCGGGCACCAAAG	
	TerS2_R		TTCAAGATTCCACCGGAAAG	
<i>terS3</i>	TerS3_F	IOEB0608	TTCAAGATTCCACCGGAAAG	

	TerS3_R		TCITTCGGCTGAACGATTTT
<i>terS4</i>	TerS4_F	IOEB0502	GCCATGTGGAGAAAAATCGT
	TerS4_R		TAACCAGCAAAATCCGTTCC
<i>terS5</i>	TerS5_F	IOEB9805	AGACGGCGTAATAGTTGAGTTA
	TerS5_R		CATCTTGATCGCTTTCTTTCCA
<i>terS6</i>	TerS6_F	UBOCC31005	CCTATGGCCATATTCAAAAGCA
	TerS6_R		CCCAACTGACTACCAAGATTG
<i>terS7</i>	TerS7_F	Vinitor 162	ATCAAGCTGGTAAAGACAATGG
	TerS7_R		CTGTTCCATGACTTCGATTGT
<i>doc</i>	Doc_F	IOEB0608	TAACGGCCTTGATAGCGTTT
	Doc_R		TTGAGGCATCCTTCCTCAG

**Table S3.** List of spacers in the four CRISPR loci identified in the *Oenococcus* genus.

**Type II CRISPR in *O. kitaharae* DSM 17330<sup>T</sup>**

K1	TGCACCATGTGCCATATCATCGGCATTGCC
K2	ATAATCACCCAGCTAGGATTTGTACATGGC
K3	AAGAATTCTGTCAAATGCTAAAGACAGATA
K4	CACCACTTTTTACAAGCTCTGTTCTAATGG
K5	GCTATATCGGCCAAACACAAGACCAACAAG
K6	TTGCTTCTGTCTCGGAATGCCGTGACTCAAG
K7	AAAGTTTGGTCAATTTTTTACCTCAATCAT
K8	TTCAAACAAAGCAATTGGTCGAAACATTGG
K9	TGATACGATTGACTTTCAATATCACCAAAC
K10	TAATTGATACAAACGGCGAAGTGTTAAGCA
K11	ACTGTGATTTGCCTGTACGTGTGAAAAACG
K12	TGGAACGGTGCTGAGAACCAATGGTTATGC
K13	GTGATATTTGGATTAGGTGAAACAGAAACG
K14	ACAACCTCAACTATTTGAGTGTTGGCAAGC
K15	GCAACGAATAGGCCGTACCGACCTATTCGT
K16	AAACGGATATTATCAATTTGAGGTAATCGC
K17	TTCAGTGGCTCATAACCCATTGGCATTGT
K18	ATGATTGAAAACAATCTTGCAGATAAAAG
K19	AACGCATTTGCTGGAATTCGGACACGCCAC
K20	AGTACAATACGGATGAAATCAGCATGTCTGA
K21	ATTCATGGGCTTAGGCACACACATGCGAGT
K22	ACAATCGTGTGCTTATCGCCACGCCATGGC
K23	GGTTGGATGACCATAATTTGCTGGGCTTTG
K24	AATCCTTGAGCTAAATTACCGTTAATCGTA
K25	TTTATTACTCCTTTCAAGCTGACTGTTGGG
K26	TAGCTGCACTGGCAGAAACACGGGCATTAA
K27	AAAATATCGTCAATACACAATCAGAAGGTT
K28	TTTCTGTCATCTCGATCCTTTCTAAATTAA
K29	AGAATGCGTTGTTTATCAAGGCTCAAAGTG
K30	AGTTATCAAATCAAAATCGAGAGTATTAAC
K31	GAGACCACTGGCTCTATGATGGAAAAGTAG
K32	CTACTTCTATTGAAGTAGTACTACCAAGCA
K33	AAGTAAATGGTACAAAAGCTCTCACAACGC
K34	TCTTGGCCGGTATCGGAAAGGGCATTGCTA
K35	AATTGCTTAGAGAGCGATTTTCAAACAAT
K36	TACCACATTCTTCAACAGACTATCAGTCCT
K37	AACTAATTTATTCCTTTTAAGGAACATATT

K38	GCGTATATGCTCAAACCGGAGTTCATAGAA	53
K39	ATAGCGACGTTGGCTAAACAACCAAATGGG	54
K40	TTTATCAGGTTTCTCTAAATAGTTCTGCCA	55
K41	TACAAAGCCGTTGGTAATTTATCCGGTTCA	56
K42	TTCACTTCCTCTTTTCTGAGCCCAGAAAAT	57
K43	AAGCGGTGGTTCATGAAGCTCGCCAAAATT	58
K44	CTGATAAACGACGGAATTTTGTCCCTTGAC	59
K45	ATTTCAAAGCAATTTTCGCAAAAAGATCAAA	60
K46	GAAAGCAAATCTTATCTCGTGACGCAGGTG	61
K47	TAGAATCAATCCCCGTGTGCTTCGTCTCTTG	62
K48	GAAGGCTACATCAAGACTGGTGTGCGATCAT	63
K49	CCGTTGGCATGCAACCAGATGCCAACAACC	64
K50	AACCGTTCAGTCCATAAACGCCGGCGCTAT	65
K51	CGGCAAAGCGGAATAATCTTGTCACCTTCG	66
K52	TACAGCTTACAAAATACATAAAAAGTATGCA= K55	67
K53	TTATTTAAAAGCCGGTCAACATCCTTTTAA	68
K54	CATTTTTATCTGTAATGTCACTAAAAATAT	69
K55	TACAGCTTACAAAATACATAAAAAGTATGCA= K52	70
K56	TTTCCCGTGCGTGGGAAAACCCTGATTAA	71
K57	CATGCTGGTCTTGTATGACACCAAACATGA	72

## Type II CRISPR in *O. ciseri* UCMA 15228<sup>†</sup>

S2.1	AGAAATTTTGAATTTATATAATCACAAAG	73
S2.2	GCGGTTCAAAGACTGCGATCAGTTTAATTC = S1.3	74
S2.3	GCGGTTCAAAGACTGCGATCAGTTTAATTC = S1.4	75
S2.4	GGACTGCGAAGACAATCGGCAAGAAATCAC	76
S2.5	GTATCGGTGTCTTCATCAAAGTCTGGTTCG	77
S2.6	GCGGTCTAAGTCGTATTGAAGCCAGTGGCA = S1.7	78
S2.7	GCGGTCTAAGTCGTATTGAAGCCAGTGGCA = S1.6	79
S2.8	TAATAATACCAGCTGCGGGAATATTTAGTT	80
S1.9	GCGATTGATGCGCTCCACCTCGCTGGTGTT	81
S2.10	AGTATCAGCGAGCTTATACCGCTCTGTCAT	82
S2.11	ATCAATGAAAACATGAAAACCCCTTACACT	83
S2.12	CCATTCTGTGACTCCTTTTCTAGCTTTTCTTG	84
S2.13	GAACCTCGGACTTGCTAAATCTTTTTTGTA	85
S2.14	TGGACGTCGAAAATGCACGCTGGCGTATCA	86
S2.15	ATGGTTACGATAACTTGTGGCTGCCTTAG	87
S2.16	GAATATCCGAGCTTCTCTATCACACTTGCG	88
S2.17	ATTTCAAACGAAGCCATCGCAGAATTGACA	89

S2.18	GAGGGAGCTATTGGTAACTTGCAAGCCAAC	95
S2.19	ATGGAATCAACGAAGAGCAAGCCCAAGAG	96
S2.20	TTCATATCATCTATTAAATCACTATATAAA	97
S2.21	TATCTGACGCTGTTGGTATACAAGTCACAA	98
S2.22	CCAACTAATTGCTTTATTGATATTAGCAAT	99
S2.23	TGAAAGACGACTACGTTTACGGACAATTGG	100

### Type I CRISPR in *O. ciseriae* UCMA 15228<sup>T</sup>

S1.1	CTTATAACCAATGACAAAGAAAGCAATGTTAT	105
S1.2	TTATTTTTCAAGGCAAAGATGATGGCCGTTGT	106
S1.3	GCACCGAGTTCGTTGCGCGTTTCGTTTATTTT	107
S1.4	TTTTTGATTTTCGTCATCGATATTTTAAATTGG	108
S1.5	CGATTGACATTGTCGTTTCGGCATGATCCGACT	109
S1.6	TGCTTTTCAAACCGTTTACCCAATTTTCTACC	110
S1.7	TGTGCTGCTCATGGCTTTCGTCATGACTTTACC	S2.17 111
<b>S1.8</b>	TTCATCAAACAGCCCTAATTTTCCATTTGTCC	S2.18 112
S1.9	AATCGTAATATGCGTCGAGCAATCAACTTGCA	113
S1.10	TTTTAAGTATGCCAGCAGGAACATTGGAGCGAC	114
S1.11	TTATAAGCACCTCTTCATTATGCAGGCGGGC	115
S1.12	CAAAATGCTTCTCGAGGCGTGAATGATGGAAT	116
S1.13	ACCTTTTCATGTTTATCTTAACTTTCGGCCAC	117
S1.14	TGGCTATTTTGGCATCTGCCTGGGCTTTTTCT	118
S1.15	CCGCTGATTTACCAGATGATCTAAGTGATAAA	119
S1.16	ACAACGTTGATGAAAAATACGTTGATTGGACT	120
S1.17	TGTGCTGCTCATGGCTTTCGTCATGACTTTACC	S2.7 121
<b>S1.18</b>	TTCATCAAACAGCCCTAATTTTCCATTTGTCC	S2.8 122
S1.19	CTCTTTTTGCGCTTGCGGTTGACCCTCCCACC	123
S1.20	GCAGAGGTTAAGGAACTTTGAAGTTATCATG	124
S1.21	TACATAAATATCAGTATTGCAAGTTTAAACGT	125
S1.22	TTCCATCAGATGAAGTTTTGCCGTTCTAAGCG	126
S1.23	TACACGACAATGACCAGAACTATGAATTATTG	127
S1.24	TGGAACGGTATTATCGTTGTGGCCACGGCCGT	128
S1.25	TCGCCTTTTAAGGTTTTAACGGCGTACTTGCT	129
S1.26	TGGTTGATGCAGCCAAAAATCTGCGCTTAAGC	130
S1.27	ATTCGGCAATATTTTCAATTCATGAATTTTC	131
S1.28	CCACCTTTGACAGCGGTTACTGAAGACTGGCT	132
S1.29	AAGAAAGCCTAACCGAAAAATACCAAAATTAT	133
S1.30	AATGTGCTTGATTCAAGCTATGGCAATGACTC	134
S1.31	TGATTTGCAAATCATCGAGGAGGAAAAAATG	135
S1.32	TTTCATTTAAATATGCATGCTGATGATGACGG	136

S1.33	ACGGTCACATTATCGCCAACATACGATCAGGA		137
S1.34	TCCCATGGGGTTCAGGCCTGAAAAGTGTGCT		138
S1.35	CTTTTCCTGCCGTTTCTGCCATTGCTTGCTCC		139
S1.36	CCCACCAGCTGTCTGGCATTGAGATAGTTCGT		140
S1.37	GTAGTCATGGACAATTCAGCACAGATTCAATC		141
S1.38	GATTCAAAAAATTAGTTTAAATCGTCGTATCA		142
S1.39	GTCATCTAACAAGCTTACAATTTGGTCCCTTA		143
S1.40	TTAATGGTTACTCACAGGGCGAAGCTACATTT		144
S1.41	TTGCACGTTGGCTATGAATAGCACATATAGCC		145
S1.42	CATCATCAGGATCTTCCCGTTCAATTTTGTT		146
S1.43	ATTAAAACGTAAATATAACATTCTAAAAGCAG		147
S1.44	ATGGCCTAACCATACGAATGGGTGGGAAGCCC		148
S1.45	GAATTCAGGTTATGAACCAGAATCTTTGCCAT		149
S1.46	GATCCGTTGCATGATTCTTATGCAGCTGCCTT		150
S1.47	CAAGTTTGATAAGTTAGTTATGTTTAGTGGA		151
S1.48	CAGGAATTTTCCAGAGAACCAGACCTATACCA		152
<b>S1.49</b>	ACGGTACGATTCCGCTCTATCAGTCAACGATT	S1.56 & S1.62	153
<b>S1.50</b>	ATCAGGTGGGCGTTTCTGACGCTATGAACATT	S1.63	154
<b>S1.51</b>	TGACATGCACTGGTCGGAGATGTTTTTTGATG	S1.64	155
<b>S1.52</b>	AAATTCACAGCACCGACCATGTGCGGTCTGAT	S1.65	156
<b>S1.53</b>	TCAGCTTCTCGAGACAAAGGTGCAATCTGATA	S1.66	157
<b>S1.54</b>	AAAAATTAATAATTTTTCGCCAGATTCAGCA	S1.67	158
<b>S1.55</b>	ATTGAGACGGCCCTACATAAAATTTGAAGAG	S1.61	159
<b>S1.56</b>	ACGGTACGATTCCGCTCTATCAGTCAACGATT	S1.49 & S1.62	160
S1.57	ATCGTGTTAATGAAGCCTTATCAGAAGTTACA		161
S1.58	TCAGCTTTGTGATGGCTAACAAGGACTGGCTT		162
S1.59	TAGCTCACGACGAAGGCTTGACAGAGTTTGCC		163
S1.60	TTGCAAGAGGCTTTGGGACAATATTTTGATAA		164
<b>S1.61</b>	ATTGAGACGGCCCTACATAAAATTTGAAGAG	S1.55	165
<b>S1.62</b>	ACGGTACGATTCCGCTCTATCAGTCAACGATT	S1.56 & S1.49	166
<b>S1.63</b>	ATCAGGTGGGCGTTTCTGACGCTATGAACATT	S1.50	167
<b>S1.64</b>	TGACATGCACTGGTCGGAGATGTTTTTTGATG	S1.51	168
<b>S1.65</b>	AAATTCACAGCACCGACCATGTGCGGTCTGAT	S1.52	169
<b>S1.66</b>	TCAGCTTCTCGAGACAAAGGTGCAATCTGATA	S1.53	170
<b>S1.67</b>	AAAAATTAATAATTTTTCGCCAGATTCAGCA	S1.54	171
S1.68	ATTACGTCAATGATTTTCATTGATTGAAGCATT		172
S1.69	TAGCAGCGGCACTAAAAATAGATCCTTGGGAG		173
S1.70	GGTTACTTCAAGGAACAGCTTTTGTGCTGCTA		174
S1.71	CCTCAGCTTTTGTCTTCCGCTGGGCTGCTTCG		175
S1.72	CGTGAGCTGCTGCAGCAAATGTACGGAAAATC		176
S1.73	AAATGACCAAAAAACTTTTTGCGAATCTGGGC		177
S1.74	TGCAATCTTGAGCAATCAGCAGGTAAAGGGT		178



S1.75	CCGTTAGTTTGACTAATTGGGACTTTAGTTGA	179
S1.76	CTACAATTAGATTCTATTCTAGTTATCAAAC	180
S1.77	TCCCATGGGGAATAAATCTGAAAAGTGTGCT	181
S1.78	AACAACCTAACAGAATTAATCGGTGGCCTGTT	182
S1.79	CTAATTTTATTTGTCATTTTGTACCTCTTTA	183
S1.80	AAGCTAGACGAAACACCACTATTGACACTGGC	184
S1.81	TTGTCTCGATGAATACGGTCATATTCAGTTTG	185
S1.82	TATCAGAGTCGACGCTCCCGCTGTAACCGCCG	186
S1.83	TGTGCCTCAAGCCATGAAAAGTTATTTGTTTA	187
S1.84	GGTTTCCTGTCCAGTTTCAAAGAAAACTGTC	188
S1.85	TCAGCCCAGTTCGTCGAAATGAACTGCGAAAT	189
S1.86	ATTTATTAGGACGAGGGACTCCGATGGTGAAC	190
S1.87	ACCATCGTTTGATAAGTCGAGCTCTCAACTTT	191
S1.88	GACTAGCAACAAATCGACAACAAAAGATCCTT	192
S1.89	TTTCTAGTTCTGATAACTAAGTCAGAATTACC	193
S1.90	GAACGGTTAAATTAACACTTAATGGAGTAGTA	194
S1.91	TTCAACAAGACGCTGACAATGCCAACTAGAT	195
S1.92	TTCAAAAAGGGAACGTTAACCCTGCCACAGAT	196
S1.93	AAGCACGTATTTCCGGTTCGCCAGCCATCACG	197
S1.94	TTTGTTTTGGGCTTGTCTATGGGCGTACTGAT	198
S1.95	CTCAGTCATTTTCGACCGTGTATCGCTTGTTAT	199
S1.96	AGCCCTATTTTATCTTTTCCCCGTCAATATAT	200
S1.97	TTTTTTATCAGTCAGCCCAAACAATTCCCGAT	201
S1.98	CAAGAAGTCCACTAATCACTGTCGTCGCAGC	202
S1.99	TTGATTTGCTGCAATGGCTTGTGTTGGCTTAG	203
S1.100	GTTGGCGTGGCAATACTTGCCGTGCCGGTACC	204
S1.101	ATCCTGTTATGTGATTCAATTGTACAGCACACA	205
S1.102	CAAAGCCTTGGGCCATAAAACCCAAGCCTTCCC	206

#### Type I CRISPR in *O. alcoholitolerans* UFRJ-M7.2.18 (chromosomal DNA)

A1	CCCATTTTAATCATTTGCAGATAATCGACT	209
A2	CTAACAGCTAAACAGAACTCTATTGCTAGC	210
A3	CAAAACGGTAAAAGTAACGCCAAAGGGTCA	211
A4	CGTTAGATAAAATCCATCAGCAGGAGAAGT	212
A5	CAAAGTCAGACAACCGTTGTATATATTGGC	213
A6	CATCAATTCATTTAATTTATCATAATCAAT	214
A7	CAACAGTTTCTATCGTACTCAAAGGAACCC	215
A8	CTTGAATTGCCAAAAGAAAAGTGGGCGTTA	216
A9	CTATGGCGATAAATTCAACTGATTCAAATG	217
A10	CTCTAAATATGGTCAACTATGATGCATATG	218
A11	CACCAACTGCCAGCTGTTCCAGAAGTATAA	219

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A12	CGTCACATCGACAAATATAGCTAACGGGCT	221
A13	CCTCGGACTACCTCCACAATGGTGTTGACC	222
A14	CTTATTAAAATGATATATACTTGTTCTCGTT	223
A15	CTGAGAAGTTTGGCGAAATCAAACCCTCTG	224
		225
		226
<b>Miscellaneous in <i>O. alcoholitolerans</i> UFRJ-M7.2.18 (plasmid DNA)</b>		227
Plasmid II		228
	AACGGACGCTAATCGGACGCTAATTAAATAACGAAAGTAGCAAAA	229
		230
Plasmid III		231
	TGGGCGGTCTTGTCAACGGACTTATGCG	232
		233
		234
		235

**Table S4.** Rapid sub-typing scheme amongst oenophages showing 27 distinct patterns.

Prophages	Int A-F	LM 1-6	Rep 1-5	TerS 1-7	TMP 1-7	Doc	Pattern
IOEB0205	A	1	1	1	1	+	1
OE33PA6		1	1	2	1	-	2
IOEB0608		1*	1*	3*	3*	+	3
IOEB1491		2	1	2*	1	-	4
IOEB0501#		2	2*	1	1	-	5
L26-1		2*	2	1*	2*	-	6
AWRI B422		2	2	2	1	+	7
CRBO14223#		2	2	2	1	-	8
S161#		2	2	2	2	-	9
IOEB0502		3*	1	4*	4	-	10
CRBO14203		4*	1	1	1	+	11
AWRIB508#		4	2	2	1	-	12
AWRIB847#		1	2	1	2	-	13
CRBO14210		1	2	3	3	-	14
AWRI B424	B	1	2	3	3	-	15
CRBO14221		4	1	1	1	-	
AWRIB133		4	2	3	1	-	
CRBO11105#		5	2	1	1	-	
AWRI B202#		5	2	1	1	-	17
OE33PA		5	2	1	1	-	
AWRIB150#		5	2	1	1	-	
IOEBB10#		5*	2	2	1*	-	18
AWRIB127*		1	1	1	1	-	19
AWRIB304		1	1	2	2	-	20
S28	D	1	1	3	4*	-	21
IOEB9805		6*	3*	5*	5*	-	22
AWRIB418		6	4	5	5	-	23
CRBO1384	E	1	1	4	4	+	24
AWRI B663		4	3	5	5	-	25
UBOCC31005	F	1	4*	6*	7*	+	26
Vinitor (162, 27, 28)		-	5*	7*	6*	-	27

Phages belonging to clusters I and II are in orange and blue, respectively; #, phages from cluster I.1 which contain several protospacers; \*representative LM, Rep, TerS, TMP and Doc proteins (see Figure 2).