

Table S1 Genomes of lysogenic and non-lysogenic strains of *O. oeni* used in this study.

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, 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.
Non-lysogenic strains (97)	AAUV01, ALAF01, ALAI01, AZJZ01, AZKD01, AZKG01, AZKI01, AZKK01, AZLE01, AZLF01, AZLH01, AZLI01, AZLJ01, AZLL01, AZLM01, AZLO01, AZLQ01, AZLR01, AZLS01, AZLT01, CP008528, JMIS01, JOOH01, JPEJ01, JPEL01, LKRS01, LKRW01, LKRX01, LKRY01, LOBV01, LR031358, MDWO01, MEHP01, MLKR01, MLKS01, MLKU01, MLKV01, MLKW01, MLKX01, MLKY01, MLLC01, MLLF01, MLLH01, MLLI01, MLLJ01, MLLL01, MLLP01, MLLR01, MLLT01, MLLV01, MLLW01, MLLY01, MLMA01, MLMB01, MLMC01, MLMD01, MLME01, MLMG01, MLMH01, MLML01, MLMN01, MLMO01, MLMQ01, MLMR01, MLMS01, MLMU01, MLMV01, MLMX01, MLNB01, MLNF01, MLNG01, MLNI01, MLNJ01, MLNM01, MLNO01, MLNR01, MLNT01, MLNW01, MLOD01, MLOK01, MLOM01, MLOQ01, MLOR01, MLOS01, MLOV01, MLOZ01, MLPA01, MLPF01, MLPJ01, MLPM01, MLPO01, MLPP01, QYTB01, ULFT01, ULFV01, ULFW01, ULFX01.

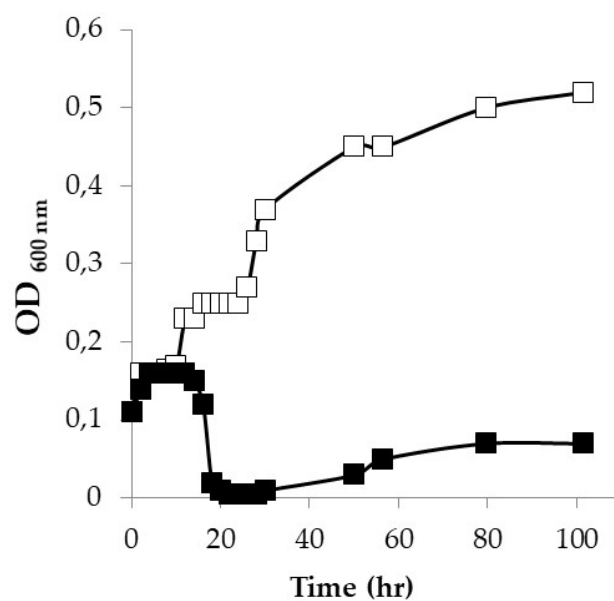


Figure S1 Kinetics of bacteriophage induction from the lysogen *O. oeni* IOEB0608 with (■) and without (□) mitomycin C treatment (1 µg/mL). Each culture was grown in MRS broth to an OD₆₀₀ of 0.2-0.3 and then separated into two aliquots, one of which was induced with mitomycin C.

Int _F	MATIAVQSKTKTYRVQIIITPDHKRVGKSGFHTKTAAKTWLTENQLKIVTGKSEVNSSHEL	60
Int _{B-F}	MASITYQEKVKTYRVQVTTKGHKRVGKSGFRTKTEARKWLTENELKIMTGKSDLIDSSKL	60
Int _F	LSDYFKHWYETYKTNVTDITLDQYKTTYRIIEKYLPHVRLNDFTREKYQKFLNKYGEDHA	120
Int _{B-F}	LSSYFEHWYETYKTNVTDITLDQYKTTYRIIEKKYLPHARLNNFTREYQKFLNKYGDHA	120
Int _F	KETVAKRKTHISACLKDAFADKLISEDITQRITLTGKAGKSSELKFLEYEDFKNLEQYSY	180
Int _{B-F}	KETVAKRKTHISACLKDAFADKLISEDITQRITLTGKAGKSSELKFLEADDFKRLEQYSY	180
Int _F	DHLNNDSQLAIFIAIHTGMRIGEIRALKIKNVDFVHISKITIDKAMDGYGNIKAPKTVASN	240
Int _{B-F}	DHLNNDSQLAIFIAIHTGMRIGEIRALKIKNVDFVQSKITIDKAMDGYGKIKAPKTAASN	240
Int _F	RVIKIDKRLLDVLKGYKRVSGLLVQVTREAINHVLTCDLKHIGAKNVTFFHALRHSASHYL	300
Int _{B-F}	RVIQIDKRLLDVLKRYKRVSGLLVQVTREAINHVLTCDLKKIEAKDVTFFHALRHSASHYL	300
Int _F	LSKGVSIQYVSERLGHSVAITENVYSHLLQTLRENEENKVTDLNMFQ	348
Int _{B-F}	LSKGVSIQYVSERLGHSNVTITENVYSHLLKTLRENEEKKITDLMDFQ	348

Figure S2 Comparisons of the Int_F and Int_B protein sequences. Mutations are in grey. The four conserved amino acids in the C-terminal region (catalytic domain) of all integrases found in *O. oeni* are in red.

Int _F	ATGGCAACAAATTGCTTATCAATCCAAAAACAAAAACATACCGTGTTC-----AGATC	51
PR _F	ATGGCAACCTATATGAAACGTGGTTCAACTTGGCAAGCACGTGTATCA-----	48
Int _D	ATGGCTTCAATTAAAAACGCGGAAAAATATTATCAAGCACGAGTATCCTACAGGGATCCA	60
	***** * * * *	
Int _F	ATTACTCCAGATCATAAGCGTGTGGCAAGTCGGGTTTTCATACAAAAACAGCAGCCAAA	111
PR _F	-----AAGGATAAGCATCGATTCAATAAATCTGGTTTTGCTACCAAAAGAGAAGCAATT	102
Int _D	GTTACCGGAGAAATTCGGACCAAAAAATAAAGTGGTTTTCTTAAAAACAAAGATGCACAA	120
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Int _F	ACATGGCTAACCGAAAAACAGCTTAAAAATTGTTACCGGCAAAATCAGAAGTAAATAGTTCA	171
PR _F	ATTGGGCTTCTAAATAG-----AATTAGGCGAAGAG--AATAAACCAAAAAAT	150
Int _D	ATCTGGGTTGGCCAAGTAT-----TATCTGGGAAACAACAAGAAAAAGAACAGCCT	171
	* * * * *	
Int _F	CACGAATTATTGTCTGATTATTTTAAGCATTGGTATGAAACATATAAAACAAATGTAACG	231
PR _F	AAATTTTATTTTCTGATTATTTTAAAAAATGGTATGAGACATATAAAACAAATCGGACC	210
Int _D	GACATACTTTTATCTGATTACTTTGAGAATTGGTACCTCACATATCGTGTCAACCGATCA	231
	* * * * *	
Int _F	GATATAACGCTCGACCAGTACAAAAACGACTTATCGTATTATTGAAAAATATTTACCACAT	291
PR _F	GATGTCACCTTTATTACAGTACAAAAACACTGACTATGTAAATGATAAATATTTAAAGGT	270
Int _D	AATCAACATATATACAGTATCGAGACACACTTCACACAATTAAGAAGTATTTGCCACAG	291
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Int _F	GTGCGACTGAATGATTTTACCGTGAGAAATATCAGAAATTTTAAACAAATATGGCGAA	351
PR _F	GAAATTTTAAATAAGTAACTTAACCTCGGCTAAATTACAAACATTTATCAATGAATACGGCAA	330
Int _D	ATGACTTTGAAATCGTTCACACGATCTAATTTTCAGACATTATTATAAATTTTGGTAAA	351
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Int _F	GATCAGCTAAAGAACTGTTGCTAAACGAAAAACACACATCTCAGCTTGTTTAAAGAC	411
PR _F	GACCACGCTAAAGAGACTGCTCCAAAAACATAAGGGCATATTATCGCCTG-CTTAAAGAT	389
Int _D	GATCAGCTGAAAAACAGTACAAAAACGCAAGGGTCAAAATTCGCGCGCTTTAAAGAT	411
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Int _F	GCTTTTGCCGATAAAATTAATCAGTGAAGACATAACAACGATTGACCCTAACTGGTAAA	471
PR _F	GCTTATCATGAAGGGCTAATCAAAACAGACGTTACTTTATAGATTGAATCTAGTCTATAAC	449
Int _D	GCCTAGCTGAAGAATTGATAAATAAGGATCCTACTATAAGAATTGGTTTGTGTACAAT	471
	* * * * *	
Int _F	GCCGGCA-----AGTCGTGAGAGCTTAAATCTTGGAGTATGAAGATTTAAGAACTTA	525
PR _F	CAAAAAATATCAAAACCAATCGAAGAAAAATTCCTAGAGGCAGAAAGCAGCATAAATC	509
Int _D	AATGCAACTAAAGTGCTTATTGAAAAATAATTTGGAATTGAATGAAGCTGAAAAATTG	531
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Int _F	GAGCAATATTCATATGATCATCTCAATAACGATTACAGCTGGCTATTTTATAGCTATT	585
PR _F	GTGCTTATTGCGAAAAAGACATCACTA-----GAGGCAACTTTTGTATTCTGACCGGTATT	566
Int _D	ATAGACCTTGTATTAAGAACCTATCTA-----GGGTAATTTTATGATATTAAGTGTCTT	588
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Int _F	CATACAGGCATGCGAATAGGTGAATTAAGCTTTAAAGATTAAAAATGTAGATTTTGTG	645
PR _F	CTATCAGGAGCCAGATTTGGTGAAGTTAGAGCCTTGATTGACAGTGATATAGACCAAG	626
Int _D	CTGTACAGGAGCAAGATTTGGTGAAGCTTCGAGCATTAACCGATGCAGATATCGATACCAA	648
	* * * * *	
Int _F	CATCTCTAAATTAATCTATGATAAGCTATGGACGGTTATGGCAATATCA-----AAGCACCA	702
PR _F	AACCACTATTTAGTATTAACAAGGCTGTTGATAGGCTAACAGGAAAGATAAGGAAACC	686
Int _D	AAACATCTCATCTCTATTACTAAGCAGTTGATAAATTTACCAATAAGGATAAAGCTCCA	708
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Int _F	AAAAACGGTCGCTAGTAACCGTGTAATTAATCGATAAACGATTATTAGACGTATTTAAAG	762
PR _F	AAAAACAAGCAATCCCAAGAAATTATAGCTATGCCGACAGATGGTTTCAATATATAAG	746
Int _D	AAAAACCAAGAAATCGATTAGAGAAATCATAATGCCGATAAATGGTTTGAAGTTTATAGT	768
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Int _F	GGATATAAGCGTGTCTGTTTATGGTACAAGTAACAAGAGAAGCAATTAACACGTT	822
PR _F	AATTACAACCATGATGGAAGACGGCTTTTGACATCAGCTCAAACGCTATCAACAAAGAT	806
Int _D	GATTTCAAGCATAATGACAAGCGACTTTTGACATGACATCTAACGGAATCAACAAAGAC	828
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Int _F	CTAACGAAAGATTTAAAGCACATAGGGGCAAAAAACGTGACCTTTCATGCTTTGCGTCAC	882
PR _F	ATGAGATATATCGCAAGAAAAATCGATATAAAGCCTGTACCTATCACGCTTTAAGGCAC	866
Int _D	TTAAATTTTATGTGAAAACTAGAAATCAAGCAGTTACGTTTTCAGCTTTAAGGCAT	888
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Int _F	AGCCATGCCAGCTATTTATTATCCAAAGGTGTTTCAATTCAATATGTATCCGAACGTTTG	942
PR _F	ACTCAGCTTCAATGCTCTTGCCCAATAACGTTTCAATGCAATATGTTCCGAAAGATTA	926
Int _D	ACGATGCTTCAATGCTATTAGCACATGATATTCAATGCAATATGTGCTGGAAGATTA	948
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Int _F	GGGCAATCCAGTGTGCTATCAGAAAAATGTTTACTCTCATCTACTCAAACGTTTACGG	1002
PR _F	GGACACGCTAATCTATCAATCAGGAAAAAGTCTACTCTCACCTACTTGAAGATAAGAGA	986
Int _D	GGACATGCCAATCTTTCGATAACAGAACAGGTATATTTCGCATCTTTTAGAAGAAAAAGAA	1008
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Int _F	GAAACGAAGAAAAACAGGTCACGTATTTAATGAATTTTCAGTGA	1047
PR _F	AAGAAGAGAAAAAAGGGCGATGGATATTTTAA-----	1022
Int _D	AATCAAGAGAAATGAAGCAATGAAGATATTTAG-----	1044
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Figure S3 Alignments of the nucleotide sequences of the integrase genes from PR_F and Int_F and Int_D prophages. The yellow color represents deletions in *intPR_F* and *intD*, sequences. The blue color represents deletions only observed in the *intF* sequence.