

Supplementary materials for the article:

Liu L. et al. Genomic Analysis of an Excellent Wine-Making Strain *Oenococcus oeni* SD-2a.

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Table SI  
Quality control of DNA samples.

Sample number	Concentration (ng/μl)	OD260/280	OD260/230	Total (μl)	Quality
1	341.6	1.99	1.95	3.41	Qualified
2	255.4	1.94	1.90	2.61	Qualified
3	153.2	1.90	1.85	1.48	Qualified

Table SII  
Statistic of Illumina Hiseq and PacBio data.

	Raw data	Clean data
Pacbio single molecule sequencing		
Total reads number	69,719	
Total bases	268,605,980	
Largest	40,242	
Average length	3,853	
Average coverage	135	
Illumina sequencing		
Total reads number	18,888,710	17,414,843
Total bases	2,833,306,500	2,546,622,389
Reads length	150	
Q20 (%)	92.44	96.58
Average coverage	1424	1279

Table SIII

Predicted proteins related to carbohydrate metabolism in *Oenococcus oeni* SD-2a.

Tracking ID	Gene name	Gene description	Gene length (bp)
<b>PTS sugar transporter</b>			
ORF00177	<i>celB</i>	PTS cellobiose transporter subunit IIC	1,353
ORF00178	<i>celC</i>	PTS cellobiose transporter subunit IIA	324
ORF00179	<i>celA</i>	PTS cellobiose transporter subunit IIB	309
ORF00191	<i>fruB</i>	PTS fructose transporter subunit IIA	414
ORF00301	<i>manX</i>	PTS mannose transporter subunit IIB	492
ORF00302	<i>manY</i>	PTS mannose transporter subunit IIC	936
ORF01118	-	PTS sugar transporter	315
ORF001618	<i>ulaB</i>	PTS lactose transporter subunit IIB	183
<b>Sugar:proton symporter</b>			
ORF01750	<i>fucP</i>	L-fucose:proton symporter	1,347
<b>Sugar ABC transporter</b>			
ORF01785	<i>msmX</i>	maltose ABC transporter ATP-binding protein	1,209
ORF02044	<i>msmG</i>	maltose ABC transporter permease	816
ORF00211	-	sugar ABC transporter substrate-binding protein	1,275
ORF00212	-	sugar ABC transporter permease	933
ORF00708	<i>msmG</i>	ABC-type maltose transporter permease	876
<b>Other carbohydrate related genes</b>			
ORF00830	<i>sacB</i>	levansucrase	2,871
ORF01922	-	sucrose phosphorylase	1,470
ORF02059	-	MFS transporter	1,425

Table SIV

Predicted proteins related to malate metabolism in *Oenococcus oeni* SD-2a.

Tracking ID	Gene name	Gene description	Gene length (bp)
<b><i>mleA</i> and homologous genes</b>			
ORF01700	<i>mleA</i>	malolactic enzyme	1,626
ORF00337	<i>maeA</i>	malate dehydrogenase	1,158
<b><i>mleP</i> and homologous genes</b>			
ORF01699	<i>mleP</i>	malate permease	945
ORF01907	-	permease	951
ORF00338	<i>maeP</i>	malate permease	984
ORF01100	-	transporter	894
ORF01583	-	malate transporter	948

Table SV

Predicted proteins related to citrate metabolism in *Oenococcus oeni* SD-2a.

Tracking ID	Gene name	Gene description	Gene length (bp)
ORF00336	-	citrate lyase	960
ORF00337	<i>maeA</i>	malate dehydrogenase	1,158
ORF00338	<i>maeP</i>	malate permease	984
ORF00339	<i>citC</i>	citrate lyase synthetase	1,047
ORF00340	<i>citD</i>	citrate lyase ACP	294
ORF00341	<i>citE</i>	citrate lyase	915
ORF00342	<i>citF</i>	citrate lyase subunit alpha	1,539
ORF00343	<i>citX</i>	CitXG protein	552
ORF00344	<i>citG</i>	triphosphoribosyl-dephospho-CoA synthase	825
ORF00591	<i>butA</i>	acetoin reductase	780
ORF00037	<i>butC</i>	diacetyl reductase	783
ORF01844	<i>alsD</i>	$\alpha$ -acetolactate decarboxylase	717
ORF01843	<i>alsS</i>	acetolactate synthase	1,683
ORF00279	<i>pdhA</i>	pyruvate dehydrogenase E1 subunit alpha	1,137
ORF00280	<i>pdhB</i>	pyruvate dehydrogenase E1 subunit beta	981
ORF00281	<i>pdhC</i>	dihydrolipoamide acetyltransferase	1,347
ORF00282	<i>pdhD</i>	dihydrolipoamide dehydrogenase	1,422
ORF01085	<i>ldhA</i>	lactate dehydrogenase	996
ORF01231	<i>ldh</i>	L-lactate dehydrogenase	924

Table SVI  
Stress genes characterized in *Oenococcus oeni* SD-2a.

Tracking ID	Gene name	Gene description	References
ORF00243	<i>hsp20</i>	heat shock protein Hsp20	Guzzo et al. (2011)
ORF01760	<i>trxA</i>	thioredoxine	Guzzo et al. (2011); Margalef-Català et al. (2017a)
ORF01842	<i>trxA</i>	thioredoxine	Guzzo et al. (2011); Margalef-Català et al. (2017a)
ORF00476	<i>trxB1</i>	thioredoxine reductase	Margalef-Català et al. (2017a)
ORF00127	<i>trxB2</i>	ferredoxine reductase	Margalef-Català et al. (2017a)
ORF01869	<i>clpX</i>	regulatory ATPase subunit of ClpP	Olguin et al. (2009)
ORF00480	<i>clpP</i>	ClpP protease	Beltramo et al. (2004)
ORF00426	<i>ctsR</i>	repressor	Grandvalet et al. (2005)
ORF01079	<i>cfa</i>	cyclopropane fatty acid synthase	Silveira et al. (2004)
ORF01585	<i>rmlB</i>	dtdP-glucose-4,6-dehydratase	Olguin et al. (2009)
ORF01995	<i>ggpps</i>	geranylgeranyl pyrophosphate synthase	Cafaro et al. (2016)
ORF00152	<i>ftsH</i>	membrane protease	Bourdineaud et al. (2003)
ORF00427	<i>clpC</i>	regulatory ATPase subunit of ClpP	Grandvalet et al. (2005)
ORF00482	<i>clpL</i>	Clp ATPase protein	Beltramo et al. (2004)
ORF00563	<i>atpB</i>	ATPase F1F0 $\beta$ -subunit	Fortier et al. (2003)
ORF00547	<i>clpE</i>	ATP-binding subunit of Clp protease	Grandvalet et al. (2005)
ORF01022	<i>arcA</i>	arginine deiminase	Tonon et al. (2001)
ORF00834	<i>argG</i>	argininosuccinate synthase	Zhao et al. (2019)
ORF01523	<i>groEL</i>	molecular chaperone GroEL	Seydlova et al. (2012)
ORF01094	<i>gsR</i>	glutathione reductase	Olguin et al. (2015)
ORF01216	<i>dnaK</i>	molecular chaperone DnaK	Seydlova et al. (2012)

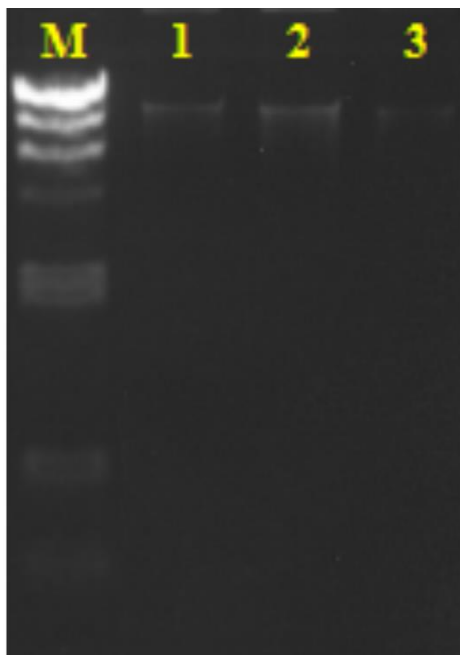


Fig. S1. Agarose electrophoresis of DNA samples. The M lane are  $\lambda$  DNA-HindIII digest fragments. The 1–3 lanes are DNA samples used to genome sequencing.

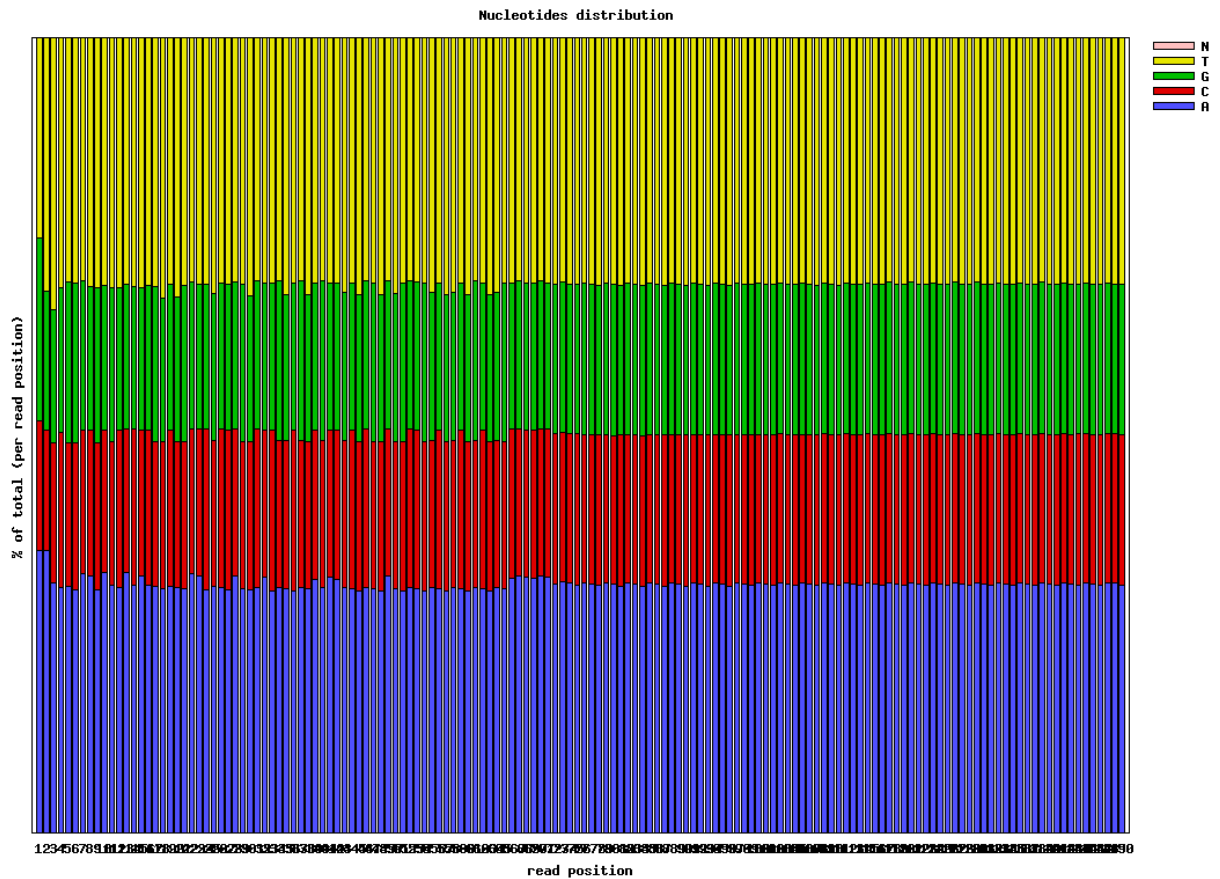


Fig. S2. Nucleotides distribution of the Illumina raw data. Abscissa is read base coordinate. The ordinate is the percentage of A, C, G, T, and N bases of all reads.

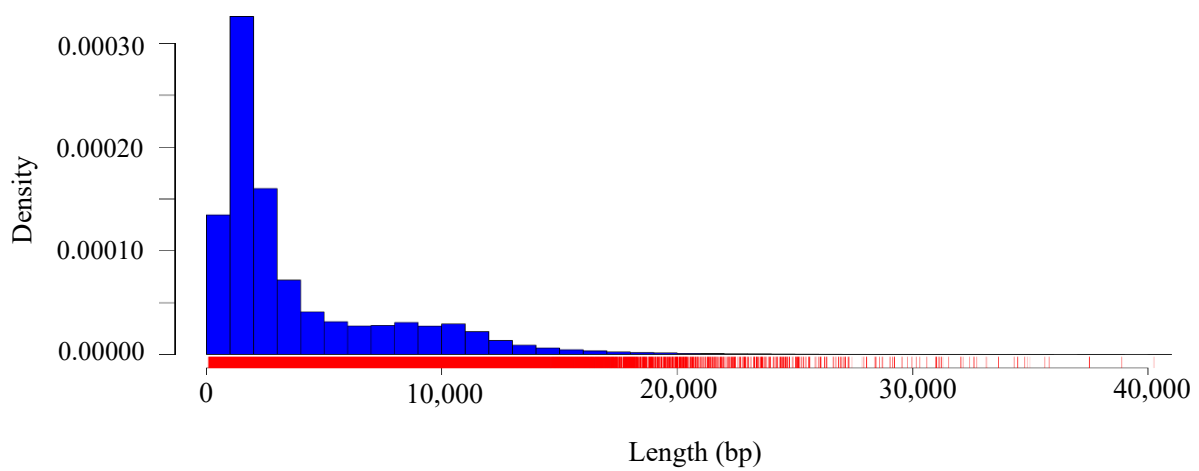


Fig. S3. Distrubution of reads length in Pacbio clean data.

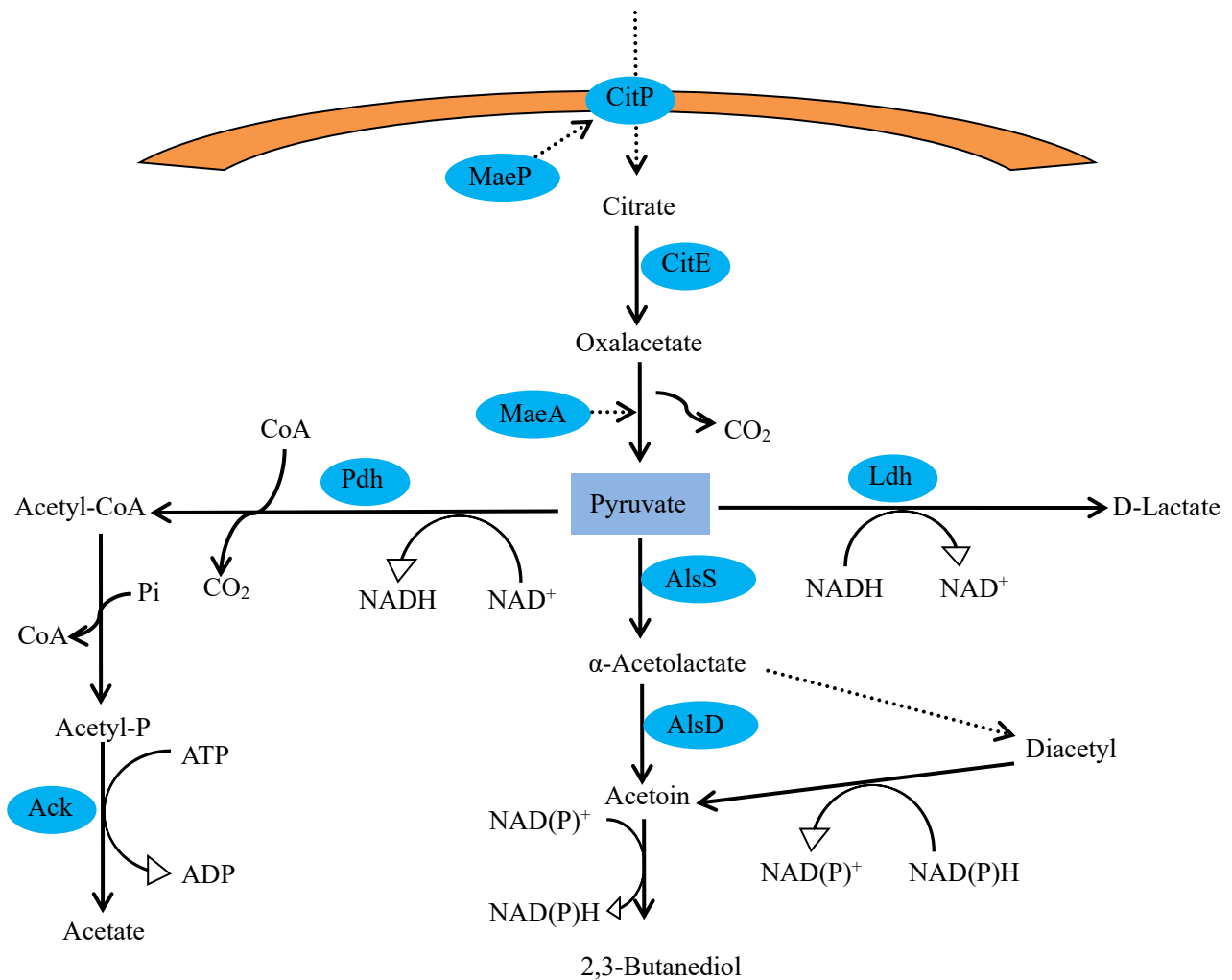


Fig . S4. Main pathways for citrate metabolism by *Oenococcus oeni*. Citrate is transported to *O. oeni* cells through citrate permease (CitP) or malate permease (MaeP). Citrate is catalyzed to oxalacetate through citrate lyase (CitE). Oxaloacetate is catalyzed to pyruvate through oxaloacetate decarboxylase. Malate dehydrogenase (MaeA) is involved in this reaction. Pyruvate produces a variety of metabolites due to various enzymes activity. It is ultimately catalyzed to acetate through pyruvate dehydrogenase (Pdh) complex and acetate kinase (Ack), or to D-Lactate through lactate dehydrogenase, or to acetoin, diacetyl and 2,3-butanediol through  $\alpha$ -acetolactate synthase (AlsS) and  $\alpha$ -acetolactate decarboxylase (AlsD). The solid arrow indicates that it has been proved experimentally, while the dashed arrow indicates that it needs to be proved experimentally.



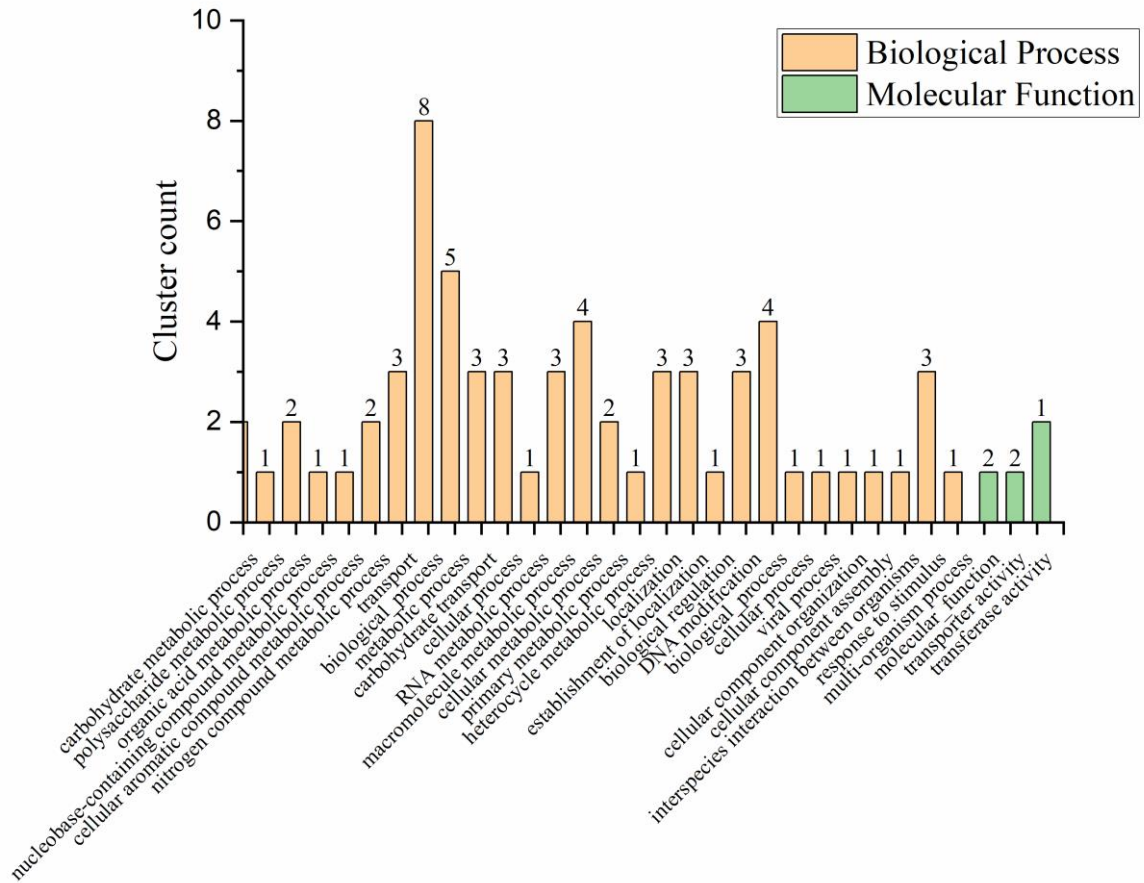


Fig. S5. GO analysis of the specific gene clusters in *Oenococcus oeni* SD-2a. These gene clusters are enriched into the GO terms shown in the figure.