

Supplemental Data for:

Zepeda-Mendoza ML, Kruse Edwards N, Madsen MG, Abel-Kistrup M, Puetz L, Sicheritz-Ponten T and Swiegers JH. 2018. Influence of *Oenococcus oeni* and *Brettanomyces bruxellensis* on wine microbial taxonomic and functional potential profile. Am J Enol Vitic 69:321-333. doi: 10.5344/ajev.2018.17092

Supplemental Table 1 Reads abundance statistics and number of microbial species identifications.

Sample ^a	Total # of reads (as in single end)	# of cleaned reads	% clean	Unmapped reads	Unmapped reads (%)	Archaea all identifications	Archaea filtered identifications	Virus all identifications	Virus filtered identifications	Fungi all identifications	Fungi filtered identifications	Plasmid all identifications	Plasmid filtered identifications	Bacteria all identifications	Bacteria filtered identifications
Control_1	3421248	3317232	96.96	696747	21.00	74	3	41	1	26	18	262	33	857	127
Control_2	5333498	5195056	97.40	791042	15.23	86	6	33	1	26	18	269	37	895	131
BA_3	4198426	4107740	97.84	350774	8.54	29	0	6	0	26	12	130	6	478	24
BA_4	6826122	6695169	98.08	562946	8.41	44	0	9	1	27	16	175	24	703	52
BB_5	2813322	2761092	98.14	57432	2.08	39	1	8	3	26	15	97	23	529	33
BB_6	11167246	10993754	98.45	224209	2.04	66	2	10	3	26	16	157	32	818	109
BC_7	14101228	13827278	98.06	449032	3.25	134	4	19	3	27	20	209	42	1049	193
BC_8	2098266	2054860	97.93	89441	4.35	19	0	5	2	26	9	78	17	341	15
OEP-BA_9	8242260	8067295	97.88	637483	7.90	71	6	24	3	27	19	204	25	833	78
OEP-BA_10	66840514	65488400	97.98	3629752	5.54	219	15	31	4	576	277	274	56	3488	475
OEP-BB_11	60828644	59758655	98.24	1141361	1.91	147	6	14	4	322	67	173	38	1918	165
OEP-BB_12	20275512	19900342	98.15	377115	1.90	97	2	24	3	27	18	235	30	948	134
OEP-BC_13	39792638	39001458	98.01	1401496	3.59	139	5	18	4	387	103	181	39	2231	196
OEN-BA_15	44811824	43950984	98.08	1876831	4.27	220	13	53	9	27	22	314	67	1288	400
OEN-BA_16	6873158	6728890	97.90	684784	10.18	49	1	12	0	27	14	207	23	756	74
OEN-BB_17	37900104	37224934	98.22	789714	2.12	142	5	33	5	27	18	239	57	1096	281
OEN-BB_18	162426646	159467366	98.18	3318148	2.08	21	21	38	4	433	115	244	61	2787	328
OEN-BC_19	6594040	6443410	97.72	413225	6.41	46	0	14	0	26	14	183	12	643	48
OEN-BC_20	6577992	6458253	98.18	399616	6.19	79	1	28	3	27	16	229	39	940	102
OEP_21	6726974	6547785	97.34	767769	11.73	86	6	42	3	27	18	282	45	953	143
OEP_22	6583580	6451292	97.99	590629	9.16	84	5	40	2	27	18	271	44	907	129
OEN_23	1899372	1831535	96.43	933872	50.99	90	6	43	1	25	10	300	50	997	181
OEN_24	7802650	7664243	98.23	275737	3.60	54	1	21	3	27	17	221	32	861	88

^a*B. bruxellensis* strains CBS 73 (BA), CBS 2336 (BB), and CBS 2499 (BC). *O. oeni* strains esterase positive (OEP) and esterase negative (OEN).

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Supplemental Table 2 Differentially abundant pathways with putative relation to microbial survival/interactions in enological conditions with different inoculations of *Oenococcus oeni* and *Brettanomyces bruxellensis* strains.^a

Pathway	Only in the comparisons all vs. controls		Only in the comparisons OEP-B. <i>bruxellensis</i> vs. OEP		Only in the comparisons OEN-B. <i>bruxellensis</i> vs. OEN		Only in the comparison of the <i>O. oeni</i> strains		Only in the comparisons <i>O. oeni</i> -BA vs. BA		Only in the comparisons <i>O. oeni</i> -BB vs. BB		Only in the comparisons <i>O. oeni</i> -BC vs. BC		
	Higher abundance	Less abundance	Higher abundance	Less abundance	Higher abundance	Less abundance	Higher abundance	Less abundance	Higher abundance	Less abundance	Higher abundance	Less abundance	Higher abundance	Less abundance	
Alanine, aspartate, and glutamate metabolism															x
Aminoacyl-tRNA biosynthesis															x
Amino sugar and nucleotide sugar metabolism															x
AMPK signaling pathway															x
Antigen processing and presentation	x			x											
Ascorbate and aldarate metabolism														x	
Biosynthesis of amino acids															x
Biosynthesis of secondary metabolites															x
Biotin metabolism		x													
Butanoate metabolism														x	
C5-Branched dibasic acid metabolism															x
Citrate cycle (TCA cycle)														x	
Collecting duct acid secretion							x								
D-Glutamine and D-glutamate metabolism															x
Fatty acid biosynthesis															x
Fc gamma R-mediated phagocytosis	x														
Fructose and mannose metabolism														x	
Galactose metabolism															x
Glycerophospholipid metabolism															x
Glycolysis / Gluconeogenesis															x
Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	x														x
Insulin signaling pathway															x
Lysine biosynthesis													x	x	
MAPK signaling pathway	x														
MAPK signaling pathway - yeast															x
Methane metabolism														x	
Mismatch repair											x				
N-Glycan biosynthesis	x														
One carbon pool by folate											x				x
Other glycan degradation											x				
Pantothenate and CoA biosynthesis														x	

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Supplemental Table 2 (continued) Differentially abundant pathways with putative relation to microbial survival/interactions in enological conditions with different inoculations of *Oenococcus oeni* and *Brettanomyces bruxellensis* strains.^a

Pathway	Only in the comparisons all vs. controls		Only in the comparisons OEP- <i>B. bruxellensis</i> vs. OEP		Only in the comparisons OEN- <i>B. bruxellensis</i> vs. OEN		Only in the comparison of the <i>O. oeni</i> strains		Only in the comparisons <i>O. oeni</i> -BA vs. BA		Only in the comparisons <i>O. oeni</i> -BB vs. BB		Only in the comparisons <i>O. oeni</i> -BC vs. BC	
	Higher abundance	Less abundance	Higher abundance	Less abundance	Higher abundance	Less abundance	Higher abundance	Less abundance	Higher abundance	Less abundance	Higher abundance	Less abundance	Higher abundance	Less abundance
Pentose and glucuronate interconversions														x
Pentose phosphate pathway														x
Peptidoglycan biosynthesis														x
Peroxisome	x													x
Phagosome														x
Phenylpropanoid biosynthesis		x											x	
Phosphonate and phosphinate metabolism							x	x						
PI3K-Akt signaling pathway														x
Polyketide sugar unit biosynthesis													x	x
Porphyrin and chlorophyll metabolism	x													x
Propanoate metabolism													x	
Proteasome	x													
Protein processing in endoplasmic reticulum														x
Purine metabolism												x		
Pyrimidine metabolism							x							
Pyruvate metabolism														x
Ras signaling pathway														x
Regulation of actin cytoskeleton	x													x
Regulation of mitophagy - yeast														x
RNA degradation	x													
RNA transport														x
SNARE interactions in vesicular transport	x													
Sphingolipid signaling pathway														x
Starch and sucrose metabolism														x
Steroid biosynthesis	x													x
Synthesis and degradation of ketone bodies												x		
Ubiquitin mediated proteolysis														x
Valine, leucine and isoleucine biosynthesis												x		x
Various types of N-glycan biosynthesis	x													x
Wnt signaling pathway														x

^a*B. bruxellensis* strains CBS 73 (BA), CBS 2336 (BB), and CBS 2499 (BC). *O. oeni* strains esterase positive (OEP) and esterase negative (OEN).

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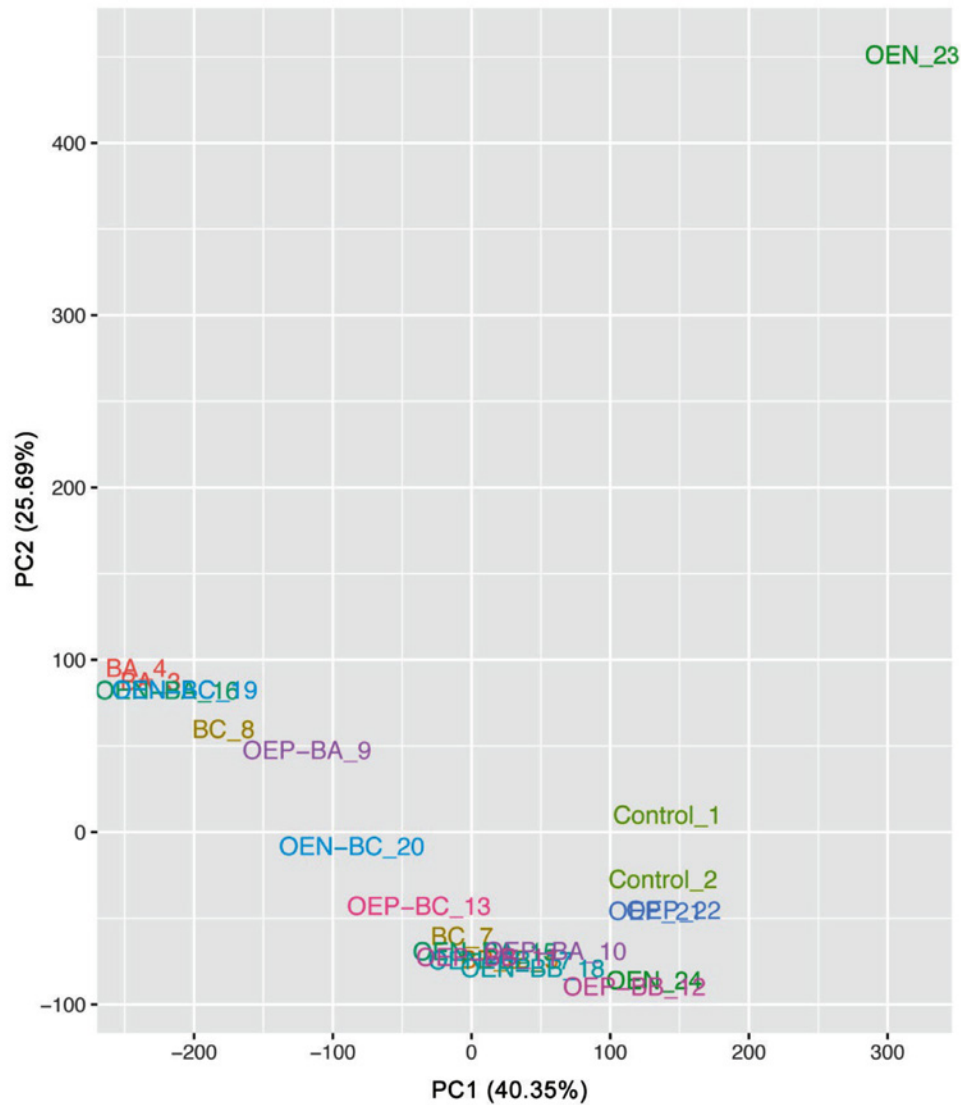
Supplemental Table 3				
Top 10 abundant nt-database microbial identifications of the unmapped reads from sample Control_1				
Name	Reads	Coverage	Depth	Abundance (%)
<i>Saccharomyces cerevisiae</i>	1447388	0.026	0.071	56.267
<i>Apteryx australis</i>	121596	0.017	0.141	4.727
<i>Bradyrhizobium sp. BTAi1</i>	60192	0.303	0.589	2.34
<i>Oenococcus oeni</i>	47704	0.705	2.138	1.855
<i>Marmota marmota</i>	37316	0.733	6.735	1.451
<i>Pseudomonas mendocina</i>	13886	0.05	0.082	0.54
<i>Rhodanobacter denitrificans</i>	7438	0.067	0.158	0.289
<i>Torulaspora microellipsoides</i>	4984	0.852	7.199	0.194
<i>Zygosaccharomyces bailii</i>	4002	0.103	1.421	0.156
<i>Pseudomonas pseudoalcaligenes</i>	3268	0.02	0.032	0.127

Top 10 abundant nt-database microbial identifications of the unmapped reads from sample Control_2				
Name	Reads	Coverage	Depth	Abundance (%)
<i>S. cerevisiae</i>	2620922	0.038	0.129	64.881
<i>A. australis</i>	216886	0.016	0.204	5.369
<i>O. oeni</i>	79784	0.791	3.386	1.975
<i>M. marmota</i>	64458	0.781	11.371	1.596
<i>Bradyrhizobium sp. BTAi1</i>	44190	0.22	0.402	1.094
<i>P. mendocina</i>	19094	0.069	0.112	0.473
<i>Z. bailii</i>	8526	0.052	1.432	0.211
<i>T. microellipsoides</i>	6524	0.886	9.361	0.162
<i>R. denitrificans</i>	6474	0.064	0.138	0.16
<i>P. pseudoalcaligenes</i>	4246	0.027	0.041	0.105

Top 10 abundant nt-database microbial identifications of the unmapped reads from sample OEN_23				
Name	Reads	Coverage	Depth	Abundance (%)
<i>S. cerevisiae</i>	258768	0.007	0.013	17.47
<i>Bradyrhizobium sp. BTAi1</i>	76568	0.349	0.726	5.169
<i>A. australis</i>	25706	0.003	0.01	1.735
<i>P. mendocina</i>	14266	0.05	0.083	0.963
<i>O. oeni</i>	10826	0.279	0.495	0.731
<i>M. marmota</i>	7738	0.609	1.533	0.522
<i>R. denitrificans</i>	5630	0.059	0.12	0.38
<i>Burkholderia ubonensis</i>	3786	0.004	0.007	0.256
<i>Pseudomonas fluorescens</i>	3320	0.001	0.002	0.224
<i>P. pseudoalcaligenes</i>	3290	0.02	0.032	0.222

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Supplemental Figure 1 Principal component analysis (PCA) of the functional potential profile of all samples. *Brettanomyces bruxellensis* strains CBS 73 (BA), CBS 2336 (BB), and CBS 2499 (BC). *Oenococcus oeni* strains esterase positive (OEP) and esterase negative (OEN). PCA of the counts of all filtered assembled genes from all samples, including those with lowest (OEN_23) and deepest (OEN-BB_18) sequencing.

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