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BMC Genomics

ERRATUM

Erratum to: 'Consensus pan-genome assembly of the specialised wine bacterium *Oenococcus oeni*'

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Unfortunately, the version of this article as originally published [1] contained an error. The quality of Figs. 1, 2, 3, 4, 5, 6 and 7 were affected due to an error in sampling the original images and an incorrect version of the article being used during the production process. For the sake of clarity, the legible Figs. 1, 2, 3, 4, 5, 6 and 7 have been included below.

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Reference

1. Sternes PR, Borneman AR. Consensus pan-genome assembly of the specialised wine bacterium *Oenococcus oeni*. BMC Genomics. 2016;17:308.

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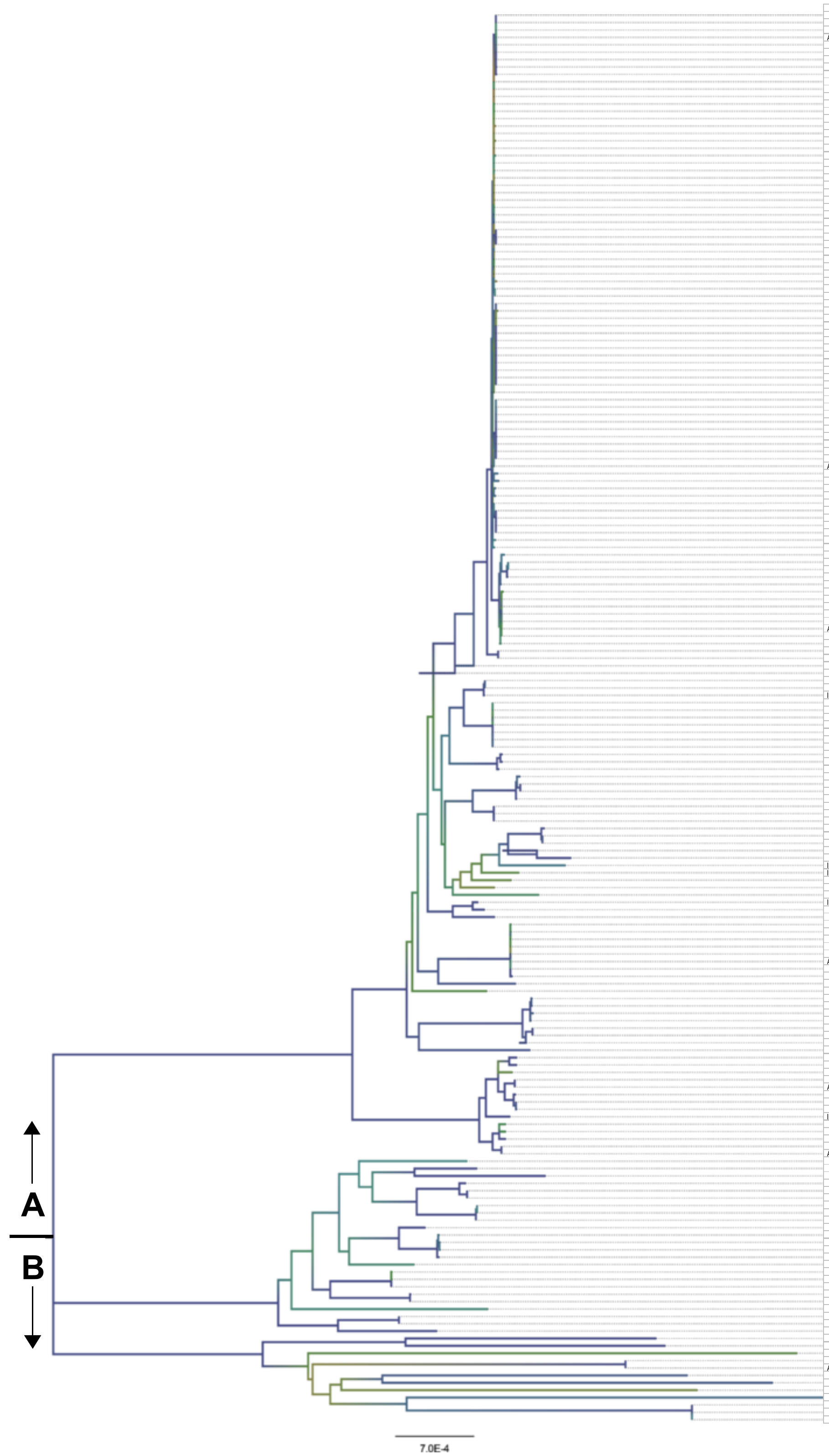


Strain ID	Region	Isolated	Variety
AWRIB821	-	-	-
AWRIB344	Australia	1982	Shiraz
AWRIB216	-	-	-
AWRIB1118	-	-	-
AWRIB873	-	1986/1984	-
AWRIB217	Australia	1984	Red
AWRIB215	Australia	1984	Red
AWRIB863	-	1986	-
AWRIB328	Australia	1981	Red
AWRIB461	Australia	2002	-
AWRIB460	Australia	2002	-
AWRIB446	-	2002	CabSauv
AWRIB345	Australia	1982	Shiraz
AWRIB331	Australia	1981	Shiraz
AWRIB124	Australia	1988	-
AWRIB326	Australia	1981	Red
AWRIB117	Australia	1981/2	Red
AWRIB424	Australia	2002	CabSauv
AWRIB342	Australia	1981	Shiraz
AWRIB335	Australia	1981	Shiraz
AWRIB900	Australia	-	-
AWRIB346	Australia	1981	Red
AWRIB141	Australia	1980's	-
AWRIB203	Australia	1993	-
AWRIB148	Australia	-	-
AWRIB949	-	1990	-
AWRIB883	Australia	1990	-
AWRIB465	Australia	2003	PinotNoir
AWRIB323	Australia	-	-
AWRIB132	Australia	1970's	-
AWRIB899	Australia	-	-
AWRIB150	Australia	1980's	Chardonnay
AWRIB897	-	-	-
AWRIB334	Australia	1982	PinotNoir
AWRIB330	Australia	1982	Chardonnay
AWRIB333	Australia	1982	Chardonnay
AWRIB131	-	-	-
AWRIB889	Australia	-	-
AWRIB868	-	1980's	-
S28	France	2009	Red
IOEB_CiNe	-	-	-
AWRIB304	Australia	1999	Zinfandel
AWRIB634	Australia	2009	Sparkling
AWRIB629	Australia	2009	Sparkling
AWRIB625	Australia	2009	Sparkling
AWRIB619	Australia	2009	Sparkling
AWRIB540	Australia	2006	Shiraz
AWRIB432	Australia	2002	CabSauv
AWRIB431	Australia	2002	CabSauv
AWRIB621	Australia	2009	Sparkling
AWRIB433	Australia	2002	CabSauv
AWRIB879	-	1980's	-
AWRIB576	Australia	2008	Chardonnay
AWRIB568	Australia	2008	Chardonnay
AWRIB858	Australia	2012	Chardonnay
AWRIB583	Australia	2008	Chardonnay
AWRIB565	Australia	2008	Chardonnay
AWRIB509	Australia	2004	Grenache
AWRIB984	Australia	2011	Chardonnay
AWRIB503	Australia	2004	Grenache
AWRIB950	Australia	2012	PinotNoir
AWRIB1059	Australia	2014	Chardonnay
S11	France	2008	Sparkling
AWRIB147	Switzerland	-	-
S23	England	2009	White
IOEB_0608	France	2006	Red
AWRIB853	Australia	2012	Chardonnay
AWRIB402	Australia	2001	Chardonnay
AWRIB401	Australia	2001	Chardonnay
AWRIB151	Australia	-	White
AWRIB118	Australia	1988	-
AWRIB794	USA	-	-
AWRIB214	Switzerland	-	-
AWRIB318	-	1964	-
AWRIB887	-	1986	-
AWRIB867	-	1986	-
AWRIB316	-	-	-
AWRIB708	Australia	2009	Merlot
AWRIB202	Australia	1994	CabSauv
AWRIB447	-	2002	CabSauv
AWRIB130	-	1984	PinotNoir
AWRIB127	-	1992	Red
AWRIB126	-	1992	Red
AWRIB1116	-	1992	Red
AWRIB819	Australia	-	-
AWRIB442	-	2002	Merlot
AWRIB714	Australia	2009	Shiraz
AWRIB706	-	2009	Red
AWRIB898	-	1994	-
AWRIB869	-	1986	-
IOEB_VF	France	-	-
AWRIB419	France	-	-
IOEB_S436a	France	-	Red
AWRIB494	Australia	2004	Chardonnay
AWRIB430	Australia	2002	CabSauv
AWRIB398	Australia	2001	Chardonnay
AWRIB394	Australia	2001	Red
AWRIB713	-	2009	Shiraz
AWRIB712	-	2009	CabSauv
AWRIB710	Australia	2009	CabSauv
AWRIB847	Australia	2012	Chardonnay
AWRIB438	-	2001	CabSauv
AWRIB121	-	1980's	-
S19	France	2009	Red
AWRIB541	Australia	2006	CabSauv
AWRIB445	-	2002	Shiraz
IOEB_1491	France	-	Red
AWRIB134	-	-	-
AWRIB337	Australia	1981	Shiraz
AWRIB336	Australia	1982	Shiraz
S161	France	-	Red
S15	France	2009	Red
IOEB_S277	France	-	-
AWRIB436	Australia	2002	Red
AWRIB441	-	2002	CabSauv
IOEB_L40_4	Lebanon	-	Red
IOEB_L18_3	Lebanon	-	Red
AWRIB553	France	-	-
IOEB_B10	France	-	-
AWRIB129	France	-	-
IOEB_L65_2	Lebanon	-	Red
IOEB_9517	France	-	-
AWRIB581	Australia	2008	Chardonnay
PSU-1	USA	-	Red
AWRIB884	-	-	-
AWRIB459	Australia	2002	-
AWRIB845	-	-	-
AWRIB332	Australia	1981	Shiraz
AWRIB1119	Australia	1982	CabSauv
AWRIB322	Australia	1982	CabSauv
AWRIB888	-	1985	-
S14	France	2009	Red
IOEB_S450	France	-	-
IOEB_B16	France	-	Champagne
AWRIB454	Australia	2002	White
IOEB_0205	France	-	Champagne
AWRIB548	France	-	Champagne
AWRIB422	France	-	Champagne
AWRIB490	Australia	2004	Chardonnay
AWRIB492	Australia	2004	Chardonnay
AWRIB156	Australia	1988	CabSauv
S25	France	2009	Red
AWRIB508	Australia	2004	Grenache
IOEB_0607	France	-	Red
AWRIB885	-	1986	-
AWRIB1064	Australia	2014	CabSauv
AWRIB138	-	1984	CabSauv
AWRIB462	Australia	2002	CabSauv
AWRIB133	-	-	-
IOEB_L26_1	Lebanon	-	Red
S22	France	2009	Sparkling
AWRIB467	Australia	2002	PinotNoir
AWRIB128	-	1992	Red
AWRIB882	-	1994	-
AWRIB1063	Australia	2014	CabSauv
S13	France	2009	Red
S12	France	2009	White
BAA1163	France	1984	Red
AWRIB787	Australia	1982	-
AWRIB392	Australia	2001	Shiraz
AWRIB391	Australia	2001	Shiraz
AWRIB343	Australia	1982	PinotNoir
AWRIB329	-	-	-
AWRIB327	Australia	1982	PinotNoir
IOEB_0501	France	2005	Red
AWRIB338	-	-	-
AWRIB324	-	1981	CabSauv
AWRIB875	USA	-	-
AWRIB791	-	-	-
AWRIB864	-	1986	-
IOEB_9805	France	-	Red
IOEB_9803	France	-	Red
IOEB_8417	France	-	Red
AWRIB418	USA	-	-
AWRIB816	-	-	-
IOEB_0502	France	-	Red
IOEB_C28	France	-	Cider
IOEB_9304	France	1993	Cider
IOEB_C23	France	-	Cider
AWRIB435	Australia	2002	CabSauv
AWRIB341	Australia	1981	Shiraz
AWRIB683	Australia	2009	PinotGris
AWRIB880	-	1994	-
AWRIB1062	Australia	2014	Chardonnay
IOEB_C52	France	-	Cider
AWRIB670	Australia	2009	PinotGris
AWRIB663	Australia	2009	Viognier
AWRIB661	Australia	2009	PinotGris
AWRIB241	Australia	1996	SauvBlanc
AWRIB240	Australia	1996	Red
AWRIB136	-	-	-

Fig. 1 Neighbour-joining phylogeny based on whole-genome alignments of 191 *O. oeni* strains. The strain ID, region of isolation, date of isolation and the grape variety are as indicated. The tree was characterised into two broad genetic groups

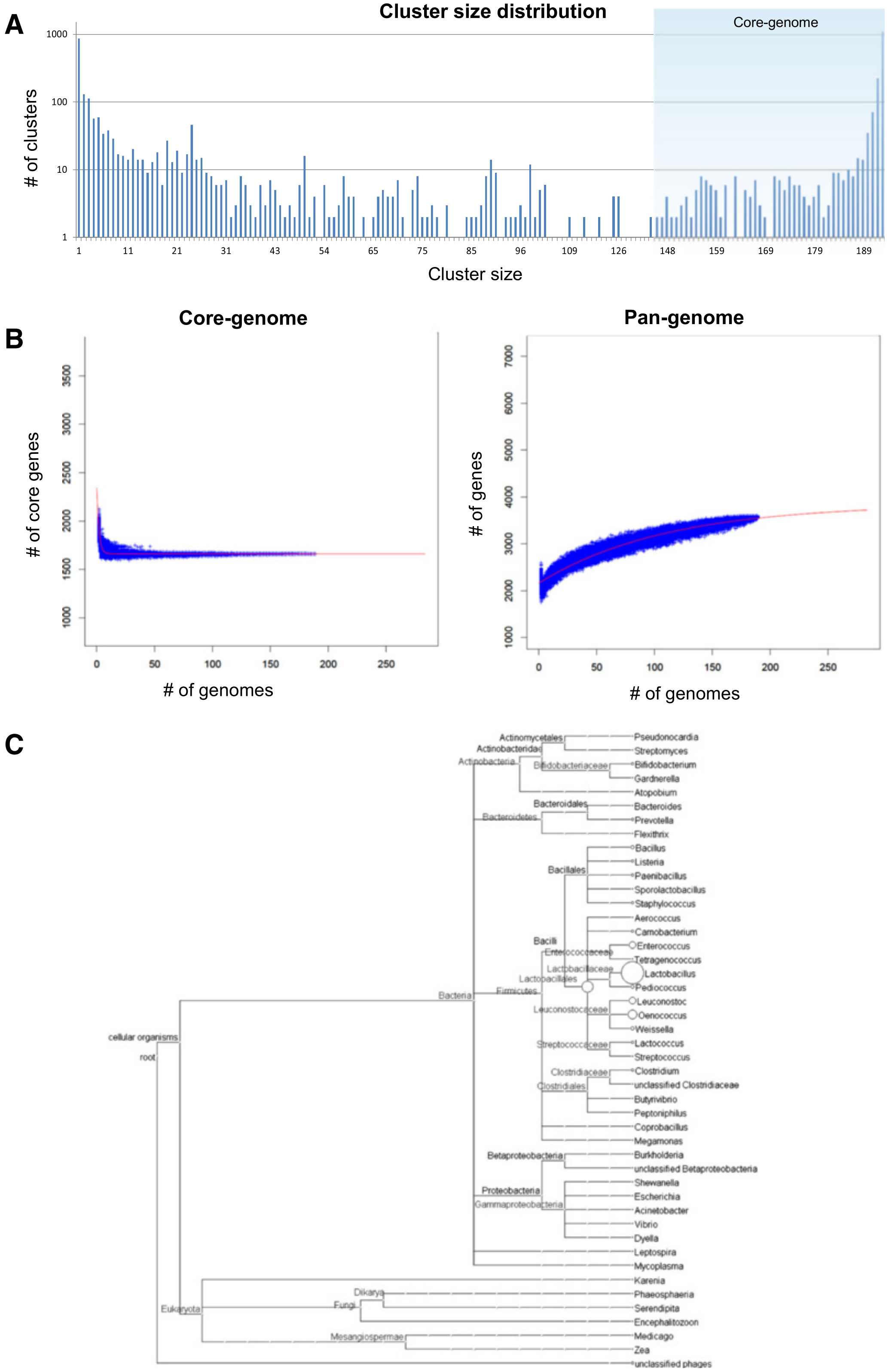


Fig. 2 The core- and pan-genomes of *O. oeni*. **a** Distribution of protein cluster sizes generated from the comparison of 191 genomes. **b** Calculation of core- and pan-genome sizes including exponential law models to fit the medians. **c** Distribution of BLAST best-hits by genus for clusters with no *O. oeni* match in the NCBI non-redundant dataset. The size of the circles represents the number of assigned hits

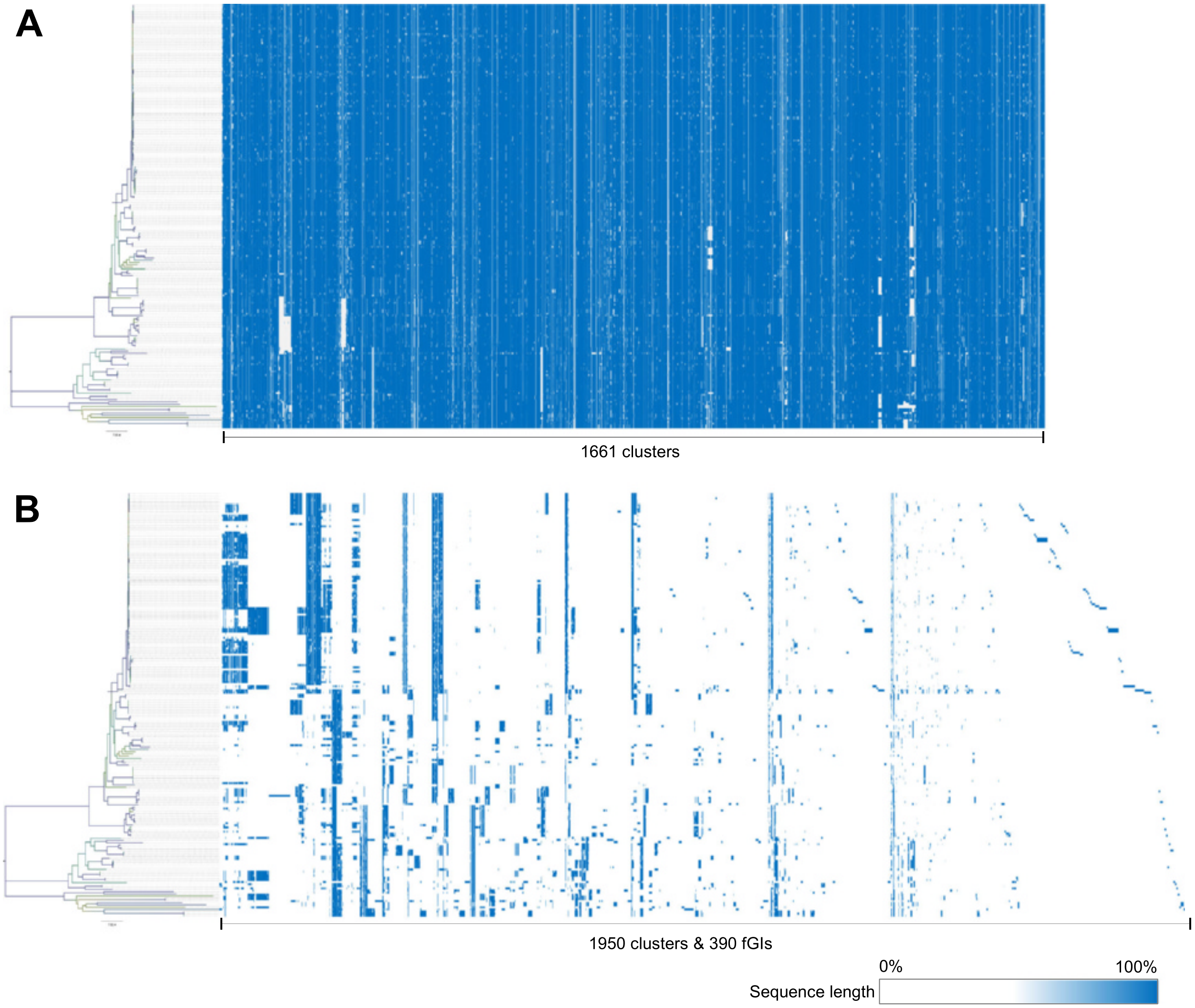


Fig. 3 Visualisation of the core-genome and fGI assemblies. Full versions of the annotated assemblies are available in Additional file 3. **a** Core-genome assembly of 1661 clusters. **b** Concatenated fGI assemblies of 1950 clusters into 390 fGIs

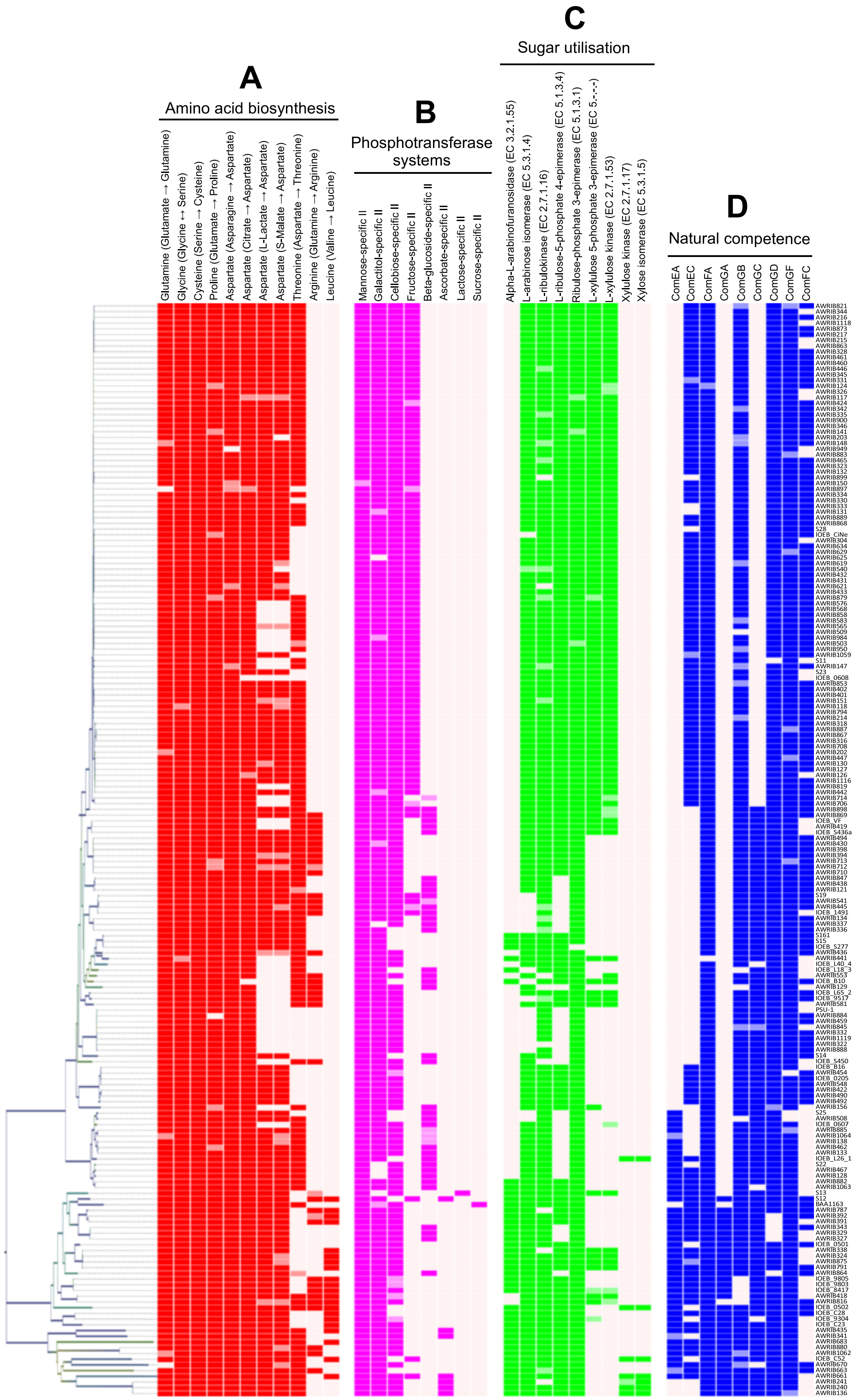


Fig. 4 (See legend on next page.)

(See figure on previous page.)

Fig. 4 Intra-specific differences in amino acid biosynthesis, sugar transport and utilisation and natural competence. ORFs which contained a contig break are shaded in a lighter colour. **a** Intra-specific differences in amino acid biosynthesis. Each pathway requires multiple enzymes, as described by their KEGG module numbers. **b** Intra-specific differences in PTS components. Each sugar-specific system requires multiple subunits (typically IIA, IIB, IIC and occasionally IID). **c** Intra-specific differences in the genes involved in five-carbon sugar utilisation, as described in Fig. 6. **d** Intra-specific differences in the genes encoding natural competence proteins

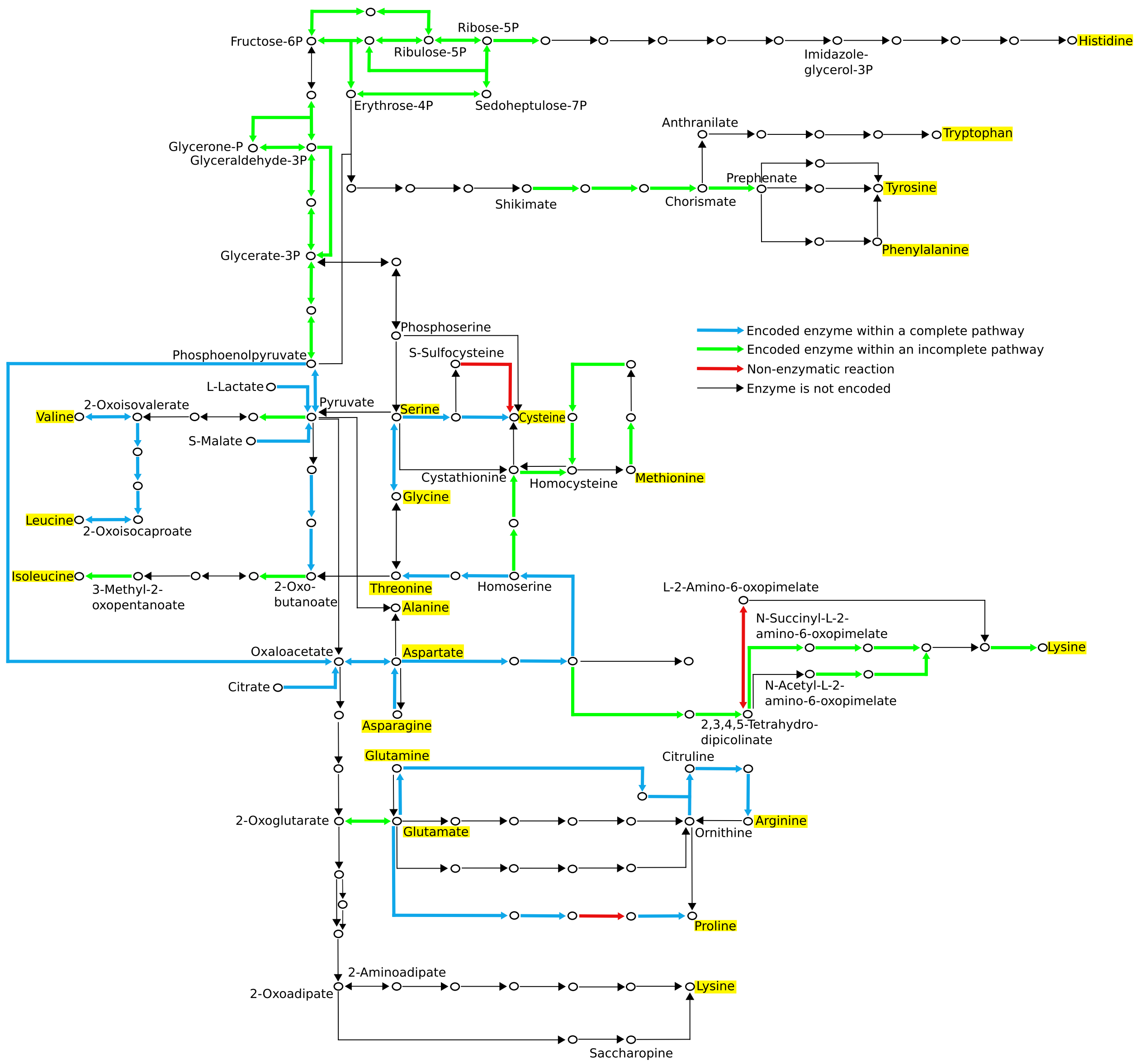


Fig. 5 Overview of amino acid biosynthesis pathways in *O. oeni*. KEGG, RAST and BLAST annotations were used determine the presence of ORFs associated with amino acid biosynthesis across 191 strains. Pathways containing the full set of required genes, mostly between two amino acids (highlighted in yellow), are highlighted in blue and represented in Fig. 4a. ORFs forming incomplete pathways are highlighted in green. Pathways to make nine different amino acids were observed

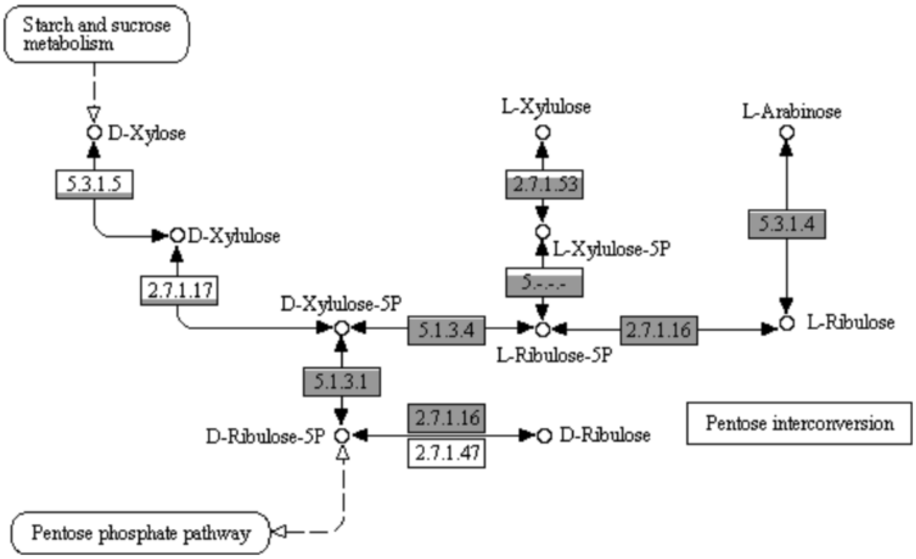
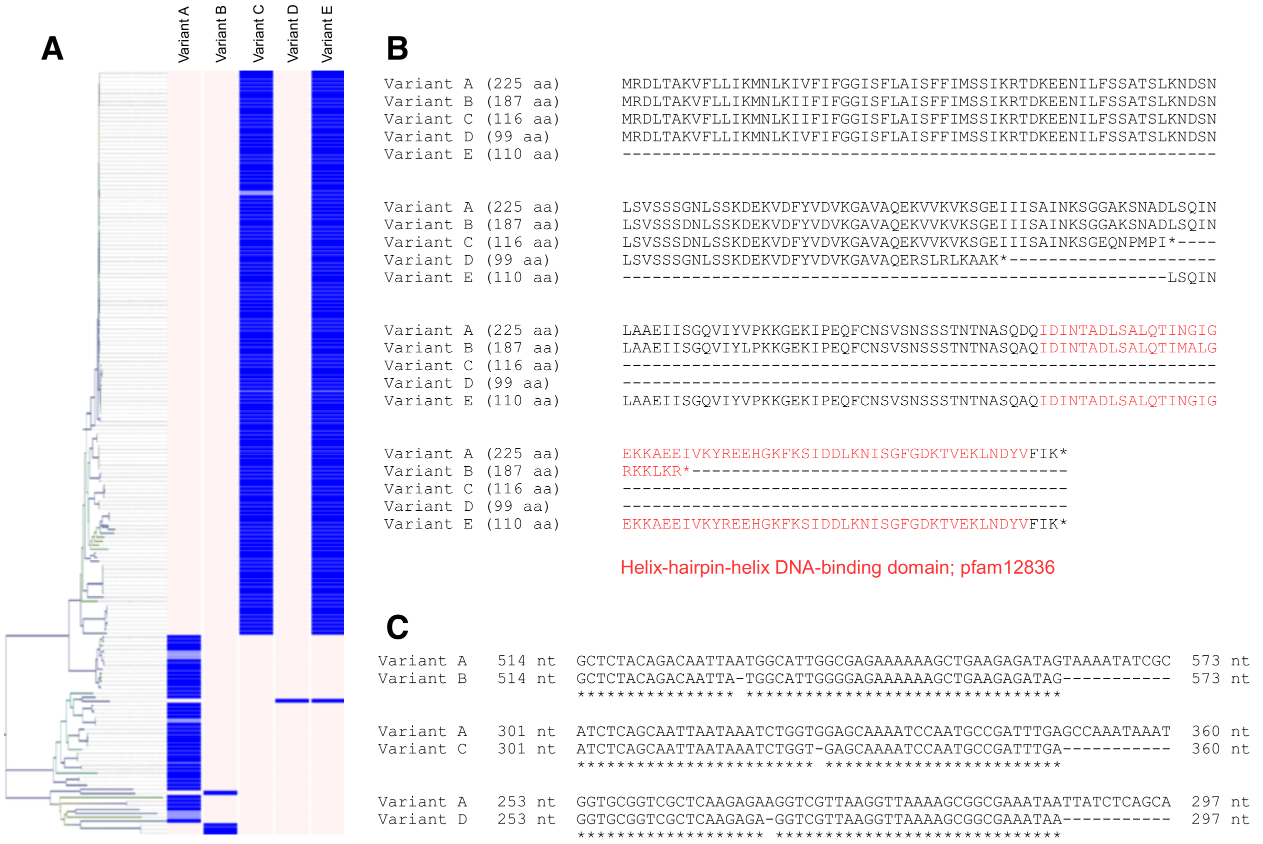


Fig. 6 Variations in five-carbon sugar utilisation in *O. oeni*. The predicted pathways for the assimilation of xylose, arabinose and xylulose and the individual enzymatic steps with their corresponding EC numbers are indicated. The grey shading represents the number of strains out of 191 which contain that enzyme. The boxes are shaded relative to each other on a square-root scale. EC 2.7.1.16 was most common, present in 176 strains



```
Variant A (225 aa)      MRDLTAKVFLLIKMNLKIVFIFGGISFLAISFFIMSSIKRTDKEENILFSSATSLKNDSN
Variant B (187 aa)      MRDLTAKVFLLIKMNLKIIFIFGGISFLAISFFIMSSIKRTDKEENILFSSATSLKNDSN
Variant C (116 aa)      MRDLTAKVFLLIKMNLKIIFIFGGISFLAISFFIMSSIKRTDKEENILFSSATSLKNDSN
Variant D (99 aa)       MRDLTAKVFLLIKMNLKIVFIFGGISFLAISFFIMSSIKRTDKEENILFSSATSLKNDSN
Variant E (110 aa)      ------------------------------------------------------------

Variant A (225 aa)      LSVSSSGNLSSKDEKVDFYVDVKGAVAQEKVVKVKSGEIIISAINKSGGAKSNADLSQIN
Variant B (187 aa)      LSVSSSDNLSSKDEKVDFYVDVKGAVAQEKVVKVKSGEIIISAINKSGGAKSNADLSQIN
Variant C (116 aa)      LSVSSSDNLSSKDEKVDFYVDVKGAVAQEKVVKVKSGEIIISAINKSGEQNPMPI*----
Variant D (99 aa)       LSVSSSGNLSSKDEKVDFYVDVKGAVAQERSLRLKAAK*---------------------
Variant E (110 aa)      -------------------------------------------------------LSQIN

Variant A (225 aa)      LAAEIISGQVIYVPKKGEKIPEQFCNSVSNSSSTNTNASQDQIDINTADLSALQTINGIG
Variant B (187 aa)      LAAEIISGQVIYLPKKGEKIPEQFCNSVSNSSSTNTNASQAQIDINTADLSALQTIMALG
Variant C (116 aa)      ------------------------------------------------------------
Variant D (99 aa)       ------------------------------------------------------------
Variant E (110 aa)      LAAEIISGQVIYVPKKGEKIPEQFCNSVSNSSSTNTNASQAQIDINTADLSALQTINGIG

Variant A (225 aa)      EKKAEEIVKYREEHGKFKSIDDLKNISGFGDKTVEKLNDYVFIK*
Variant B (187 aa)      RKKLKR*--------------------------------------
Variant C (116 aa)      ---------------------------------------------
Variant D (99 aa)       ---------------------------------------------
Variant E (110 aa)      EKKAEEIVKYREEHGKFKSIDDLKNISGFGDKTVEKLNDYVFIK*
```

Helix-hairpin-helix DNA-binding domain; pfam12836

```
Variant A   514 nt  GCTCTACAGACAATTAATGGCATTGGCGAGAAAAAAGCTGAAGAGATAGTAAAATATCGC  573 nt
Variant B   514 nt  GCTCTACAGACAATTA-TGGCATTGGGGAGAAAAAAGCTGAAGAGATAG-----------  573 nt
                    **************** ********************************

Variant A   301 nt  ATCTCAGCAATTAATAAATCTGGTGGAGCAAAATCCAATGCCGATTTGAGCCAAATAAAT  360 nt
Variant C   301 nt  ATCTCAGCAATTAATAAATCTGGT-GAGCAAAATCCAATGCCGATTTGA-----------  360 nt
                    ************************ ************************

Variant A   253 nt  GGTGCGGTCGCTCAAGAGAAGGTCGTTAAGGTTAAAGCGGCGAAATAATTATCTCAGCA  297 nt
Variant D   253 nt  GGTGCGGTCGCTCAAGAGA-GGTCGTTAAGGTTAAAGCGGCGAAATAA-----------  297 nt
                    ******************* *****************************
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Fig. 7 Intra-specific variation in the gene encoding the ComEA transmembrane DNA receptor. **a** Five variants were found to map to specific branches of the genetic relatedness dendrogram. Strains which contained a contig break in the ORF encoding ComEA are shaded in light blue and assigned to the likely variant category. **b** Alignment of predicted ComEA peptide sequences showing full-length (Variant A) and truncated (Variants B to E) versions. Variants B, C and D contained frameshift mutations resulting in prematurely-encoded stop codons which resulted in an additional ORF being predicted *in silico* (Variant E). The C-terminal DNA-binding motif is highlighted in red and is not encoded by Variants C and D. Variant B contains a premature stop within the DNA-binding domain and still corresponds with genetically-distant strains. Variant D represents a frameshift mutation unique to the BAA-1163 strain. **c** Nucleotide sequence alignment highlighting single nucleotide deletions causing frameshift mutations and truncation of the ComEA peptide sequence