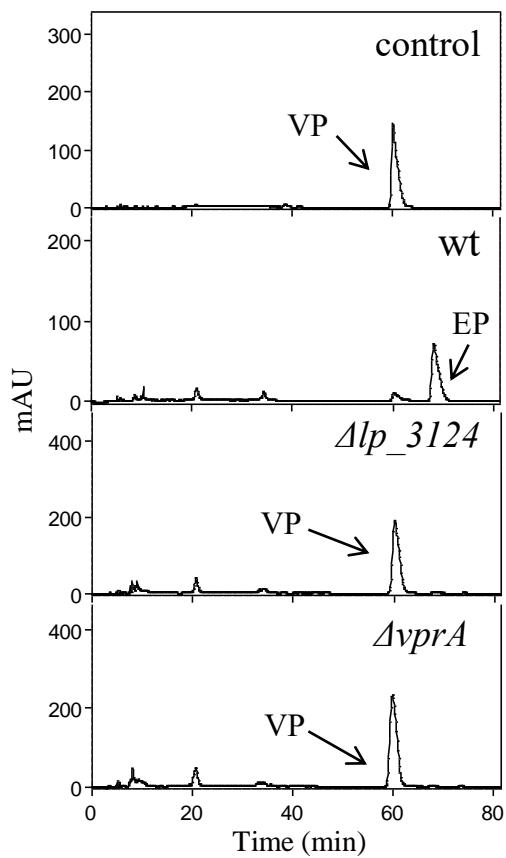


Figure S1



**FIG S1** Effect of disruption of *lp\_3124* (*vprR*), and *lp\_3125* (*vprA*) on vinylphenol reductase activity in *L. plantarum* WCFS1. HPLC chromatograms of *L. plantarum* cultures incubated in 1.5 mM 4-vinylphenol are shown for *L. plantarum* WCFS1 (wild type [wt]), *L. plantarum* WCFS1 (pUCE191-*vprR*) ( $\Delta lp\_3124$  mutant), and *L. plantarum* WCFS1 (pUCE191-*vprA*) ( $\Delta lp\_3125$  mutant). Results for uninoculated medium are also shown (control). The 4-vinylphenol (VP) and 4-ethylphenol (EP) detected are indicated. Chromatograms were recorded at 280 nm.

**Figure S2**

**A**

VprA	MTLAHKDSYDIVVVGTGAAGTAAALEAAQHGASVLLKEGRHTGGSSNYTEGLFAVDSYL
DBVR	-----
VprA	QKAQNINVSATDVLKEEVVDYSKYRADSRIWRRYLDSDANTVQWLKDQGVEYEGVQAMGAG
DBVR	-----
VprA	EATWHIYKGMGQAVLHDALQPQAQKLGVELLTSTTAITLHQATDGAI TGVMIQSAATNET
DBVR	-----
VprA	QVINTAAVILATGGYLNNPDMMQKLTHYDTRRLIPVSSGKGTGDGLRLAWQAGAQGYGTG
DBVR	-----
VprA	MAMLFGGYLKDPSEPSFKYMASQMETAAGQQPLLWLNEHGERFVDEAVVYNFSYAGNALY
DBVR	-----
VprA	TQNQVFSILDQGVINKMAQDGFMGLGVYVRRGEKMTKLQAE-----IDA AVAA
DBVR	-----MVKAVAVVRGDSTVKGVVTFEQTSESEPTTIXNIEG * . * * : . . * . * : .
VprA	NKPFIFKANTIEALATKMHLPWDQVTHSIQTYNQYCDNGQDDDFGKNPEYLVKVSQGPFY
DBVR	NDPNALRGFH-----IHT-----FGDNTNG--CTSAGPHF * . * : : . * : * . * . :
VprA	-GFELNVGA-----FCTMGLKVTTNN-----EVLDTTGQ-PIT---GLYAAGND
DBVR	NPFGKTHGAPTDENRHVGDLGNIKTDANGVAKGTIKDKLVKLIGXNSIIGRTVVVHAGTD * . * * . : * . : * . : * . : * . : * . : * . : * . :
VprA	AAGLTGDTYGPNMPGTCVGYAFYSGRNSGRHAAQYTHQQSIVSH
DBVR	DLGKGGDAG-S-----LQTGNAGGRPACGVIGLSA--- * * * : : : * . . * * . . :

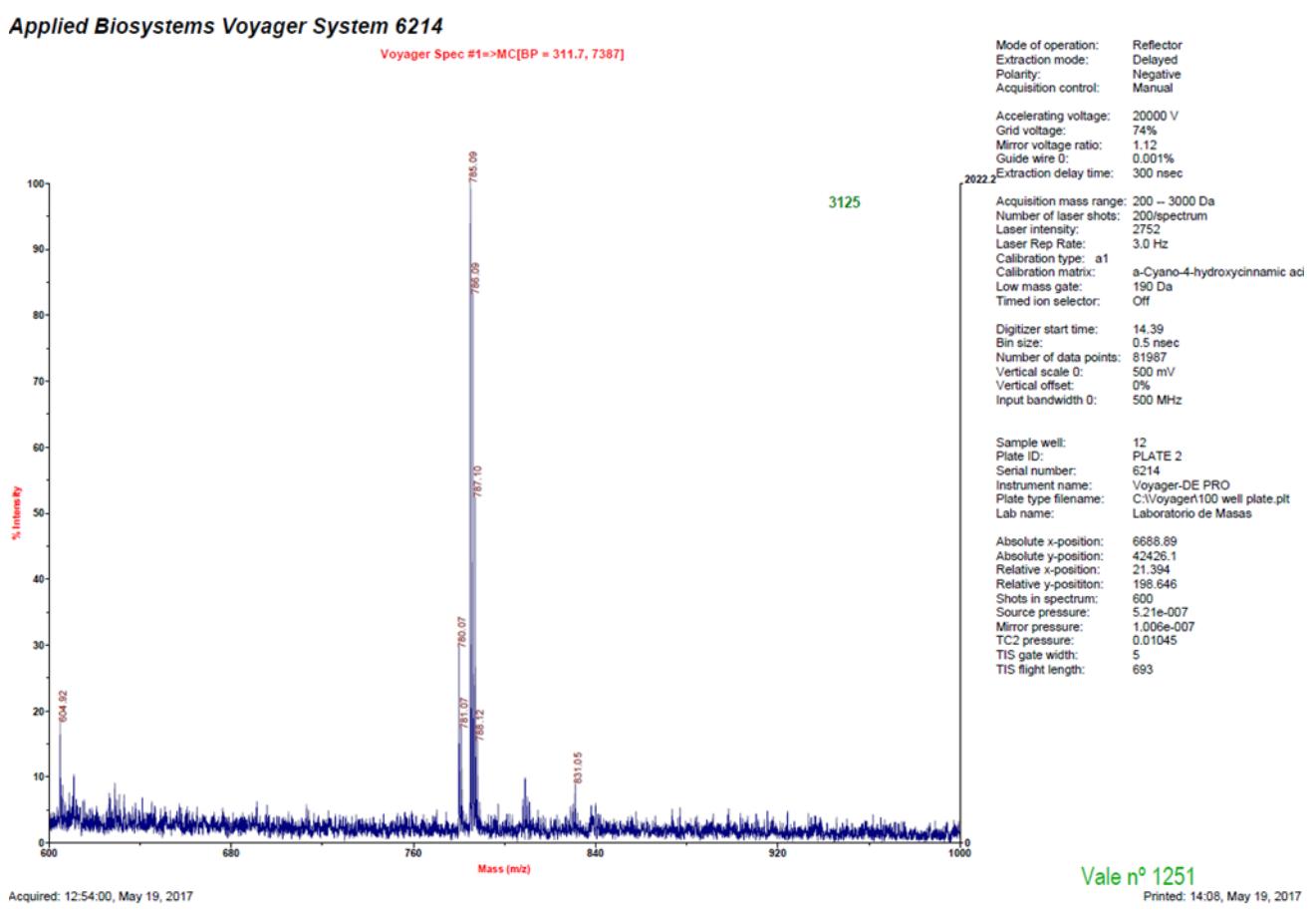
**B**

VprA	-----
HcrB	MKFVGIVGTNAQHSYNRMLLEFMQRHFATQAEIEILELTDVPMFDESNDQTDSTIIQNFA
VprA	-----
HcrB	TKIATADGVIIASPEHNHSVPSALKSIIIEWLSFKIHPLDGQAVMIVGASYSVQGSSRAQL
VprA	-----
HcrB	HLRQILDAPGVNASVMPGSEFLGRAQTAFFDDQGNLKVGQTVDFLDSCFAKFQKFATIVA

VprA	-----
HcrB	EMRAPEALSFAPGTYQVTATGHNGELPMRVTLSADRIENIEIDTSSETQGIADVAFERIP
VprA	-----MTLAKHDS
HcrB	KEIIAGQTLAVDAISGASITSHGVIDVARAVKEAGANPDDLKKRRATKQVAQPAVKEVT . * . :
VprA	YDIVVVGTGAAGTAAALEAAQHGASVLLEKGRHTGGSSNYTEGLFA-----
HcrB	TDVVVVGACGAGMTAAAKVLQAGHQAVVLEKFPAVGGNTVRAGGPMAADPDWQRQFAAL *:****:.*.* :** :. * * .. :*** .***. : * :
VprA	-----VDSYLQKAQNINVS--ATDVLK-----
HcrB	PGEKQTLKDLSERDESTIAPEYRADFRKLKQQIDAYLTANTNQKTLFDSTLLHRIQTYL :*** * : : : :*:
VprA	----EEVDYSKYRADSRIWRRYLDLDSANTVQWLKDQGVEYEGVQAMGAGEATWHIYK-GM
HcrB	GGQRTDLNGQEIHGQYDLVKELTDNALDSVKWLQSIGVKFDESQVTMPVGAIWRRGHKPM ::: . : . : . * : :* :**:. **::: * . * * : : * *
VprA	GQAVL--HDALQPQAQKLGVELLTSTTAITLHQATDGAITGVMIQSAATNETQVINTAAV
HcrB	GDLGFAYIKTLRAFVEQQGGTIMTE-TPVKELLVTDGQVRGVIAAT-AAHEKVIVHADAV *: : . :*: . :* * : :*. * : . *** : **: . * :*. :: : **
VprA	I LATGGYLNNPDMMQKLTHYDTRR---LIPVSSGKGTGDGLRLAWQAGAQGYGTGMAMLF
HcrB	I LASGGFAANTKMLQKYNTYWTAI DDDVKTTPAMTGDGIRLGTSVGAALVGMGFSQMM ***:***: * .*:*** . * * : . ..* ***:***. .** * * : : :
VprA	GGYLKDPSFPSFKYMASQMETAAGQQPLLWLNEHGERFVDEAVVYNFSYAGNALYTQNQV
HcrB	PV----SDPETGELFSGLQ--VPPANFVMVNQQGKRFVNEYGSRDEL--TQAAIDNGSL *:*. . : * : . : . :* :* :***: * : : * : : :
VprA	FSILDQGVINKMAQDGFMGLGVYVRRGEKMTLQAEIDAAVAANKPFIFKANTIEALAT
HcrB	FYLIADDEIKKT-----AYNTTQAKIDQQVA--NGTLFRADTLTDLAQ * : : . :* : * .. * : **:***: * : : * :* :* : **
VprA	KMHLPVDQVTHSIQTYNQYCDNGQDDDFGKNPPEYLVKVSQGPFYGFELNVGAFC
HcrB	TMGLK QIGMDPAALTKTIADYNRYVDAGEDPEFHKT-AFDLKVAAPFYATPRKPATHHTMGLK :: : :*: * **: * * :* : * . : :***: * **. : . . . *****
VprA	VTTNNEVLDTTGQPITGLYAAAGNDAAGLTDYGPNCPTCVGYAFYSGRNSGRHAAQYT
HcrB	IDSDAHVLNTDGQVIDGLYAAAGEVAGGIHAG---NRLGGNSLSDI
	FTFGRIAAAHAVAEEH : : : . * :* * * : * . . : * . . * . . * . . * . . * .
VprA	HQQSIVSH
HcrB	-VDPVTA- : . . :

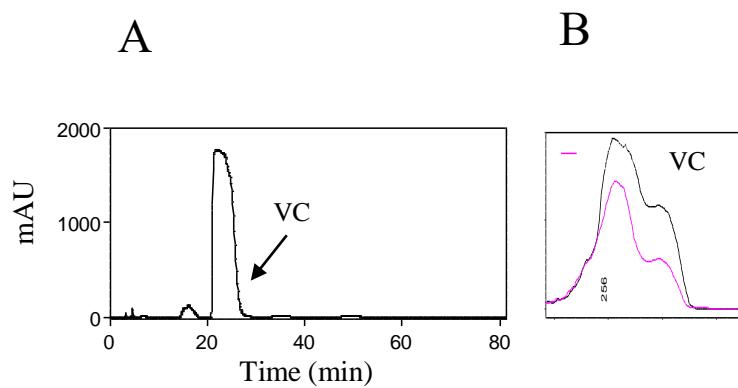
**FIG S2** Comparison of amino acid sequences of *L. plantarum* WCFS1 VprA protein and vinylphenol reductase from *D. bruxellensis* (DBVR, I2JWC1) (A) or to *L. plantarum* WCFS1 hydroxycinnamate reductase (HcrB) (B). Multiple alignments were done using the programs ClustalOmega after retrieval of sequences from BLAST homology searches. Residues that are identical (\*), conserved (: ) or semiconserved (.) in all sequences are indicated. Dashes indicated gaps introduced to maximize similarities. The Rossmann-fold GXGXXG motif is highlighted in green.

Figure S3



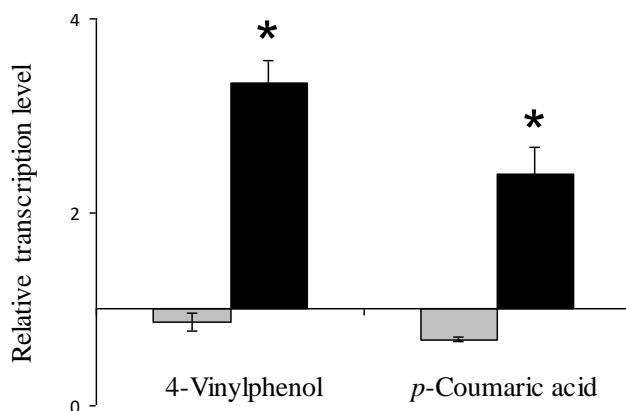
**FIG S3.** Mass spectra of FAD. The yellow VprA protein was subjected to mass spectrometry analysis and the FAD flavin cofactor (785.09 Da) was identified.

Figure S4



**FIG S4** Production of 4-vinylcatechol from *p*-coumaric acid. (A) Chromatograms of supernatants from *E. coli* cells bearing pURI3-pdc plasmid overexpressing the *pdc* gene from *L. plantarum* (Rodríguez et al., 2008. J Agric Food Chem 56:3068) grown in the presence of caffeic acid. Chromatogram was recorded at 280 nm. (B) Comparison between spectra of the compound produced and 4-vinylcatechol identified previously by LC-DAD/ESI-MS (Rodríguez et al., 2008. J Agric Food Chem 56:3068). The same *E.coli* strain was used previously to produce vinyl derivatives from alkaline hydrolysates of corn cobs (Salgado et al., 2012. Bioresource Technol 117:274-285; Salgado et al., 2014. Enz Microb Technol 58-59, 22-28).

Figure S5



**FIG S5** Relative transcriptional expression of *vpr* genes in *L. plantarum* WCFS1 in response to the presence of two hydroxycinnamic derivatives, 4-vinylphenol and *p*-coumaric acid. *L. plantarum* cultures were exposed during 10 min at 1.5 mM of 4-vinylphenol or *p*-coumaric acid. Expression levels were calculated with the 7500 Fast System relative quantification software using *L. plantarum* *ldh* gene as endogenous gene and the growth in the absence of phenolic compound as growth condition calibrator. Expression level of *vprR* and *vprA* genes are represented by grey or black colour bars, respectively. The experiments were done in triplicate. The mean value and the standard error are shown. Asterisks indicate a *p* value <0.1.

Figure S6

LFA	LAE LAE KLN LP-----
LCO	LEELA TKL GLAK-----
LRO	IEELA QKM GPSEQLM QT MTKY NQ DC EL QG DS LF GK DP KY MR PINE GP FV GF SL NV GA FC
LBI	IEAL AQA MG MSET AL TQ TL VLT YN QF CA AG VD QDF GKA QQ YL LV P VTK GPF Y GF KLN NV GA FC
LSI	IEAL AEK MN VP DV DQL TKT IT D YND Y CEAG DD KF AK GD TE YL LV KVA EGP FV GF KLN NV GA FC
LPC	IDAL AKE KM GL PV KV VE TI KT YNG CDA KED GDF GKN PE YL V KV AK GP FV GF E LN NV GA FC
LPL	IEAL AKE TM HLP L P D QV TH S I QTY N QY CD NG Q DDD FG K N P E YL V KV S QGP FV GF E LN NV GA FC
LPE	IEEL AAK M HLP L P D QV T R S I QTY N QY CD NG Q DNE FG K DPA YL V KV D QGP FV GF E LN NV GA FC
LPA	I D E L A A K M HLP L P D QV T K S V Q T Y N QY CD NG Q DAD FG K N P D YL V KV AT GP Y Y G F E LN NV GA FC
	: * * : : : : * * * : * : : * * : * . * * : * . * * : * . * * :
LFA	AL GGL RVD NQNA V L ND HG YP V P GL YAV G NDA AG ML VGD TYA V T LPG STAG YAA FSG RNA V
LCO	AL GG IRV SDD NEV L ND HG YP V P GL YA AG NDA AG ML VGD TYA V T LPG STAG YAA FSG RNA V
LRO	TM GG L QV NP NN V E L N N N Q A I A GL YA AG NDA AG - LT GDT YGP NM PG TC VGY AF YSG RN AG
LBI	TM GG L QV T D N A V L T N A G T P I P GL YA AG NDA AG - LT GDT YGP NM PG TC VGY AF YSG RN AG
LSI	TM GG L QV T S N E V L A E N G L P V A GL YA AG NDA AG - LT GDT YGP NM PG TC VGY AF YSG RN SG
LPC	TM GG L QV T T E N V L D D M G D K I G GL YA AG NDA AG - LAG DT YGP NM PG TC VGY AY YSG RN SG
LPL	TM GG L K V T T N N E V L D T T Q P I P GL YA AG NDA AG - LT GDT YGP NM PG TC VGY AF YSG RN SG
LPE	TM GG L K V T T A N E V L D T E G T P I P GL YA AG NDA AG - LT GDT YGP NM PG TC VGY AF YSG RN SG
LPA	TM GG L K V T T A N E V L D T T G N T I Q GL YA AG NDA AG - LT GDT YGP NM PG TC VGY AF YSG RN SG
	: * * : * * : * : * * * * * : * . * * . . : * : . * * : * : * * :
	1658
LFA	LSMV NAS -----
LCO	ANM -----
LRO	LHA AMT VS DE LE DN -
LBI	HHA AQA -----
LSI	KHAA AY KA G VTA --
LPC	KHA ASY TK GL KITE -
LPL	RHA A QY TH QQ SIV SH
LPE	RNA V T YL NND V A V TD
LPA	RHA ASY ANH -----

**FIG S6** Comparison of amino acid sequences of putative VprA proteins from lactic acid bacteria. Multiple alignments were done using the program ClustalOmega after retrieval of sequences from BLAST homology searches. The VprA proteins are from *Lactobacillus plantarum* WCFS1 (LPL) (lp\_3125), *Lactobacillus paraplantarum* DSM 10667 (LPA) (A0A0R1RBK3), *Lactobacillus pentosus* DSM 10667 (LPE) (A0A0R1FK87), *Lactobacillus fabifermentans* DSM 21115 (LFA) (A0A0R2NSN6), *Lactobacillus collinoides* DSM 20515 (LCO) (A0A0R2BBL2), *Lactobacillus paracollinoides* DSM 15502 (LPC) (A0A0R1T9H1), *Lactobacillus bifermentans* DSM 20003 (LBI) (A0A0R16M13), *Lactobacillus similis* DSM 23365 (LSI) (A0A0R2F9E3), and *Lactobacillus rossiae* DSM 15814 (LRO) (A0A0R1RHT0). Residues that are identical (\*), conserved (:) or semiconserved (.) in all sequences are indicated. Dashes indicated gaps introduced to maximize similarities. The Rossmann-fold GXGXXG motif is highlighted in green. Degenerate primers were designed on the conserved domains yellow highlighted.