

**Supplementary Table and Figure****Table S1. Characteristics of the reads from Cinnamaldehyde treated or untreated libraries in *P. carotovorum* BP201601.**

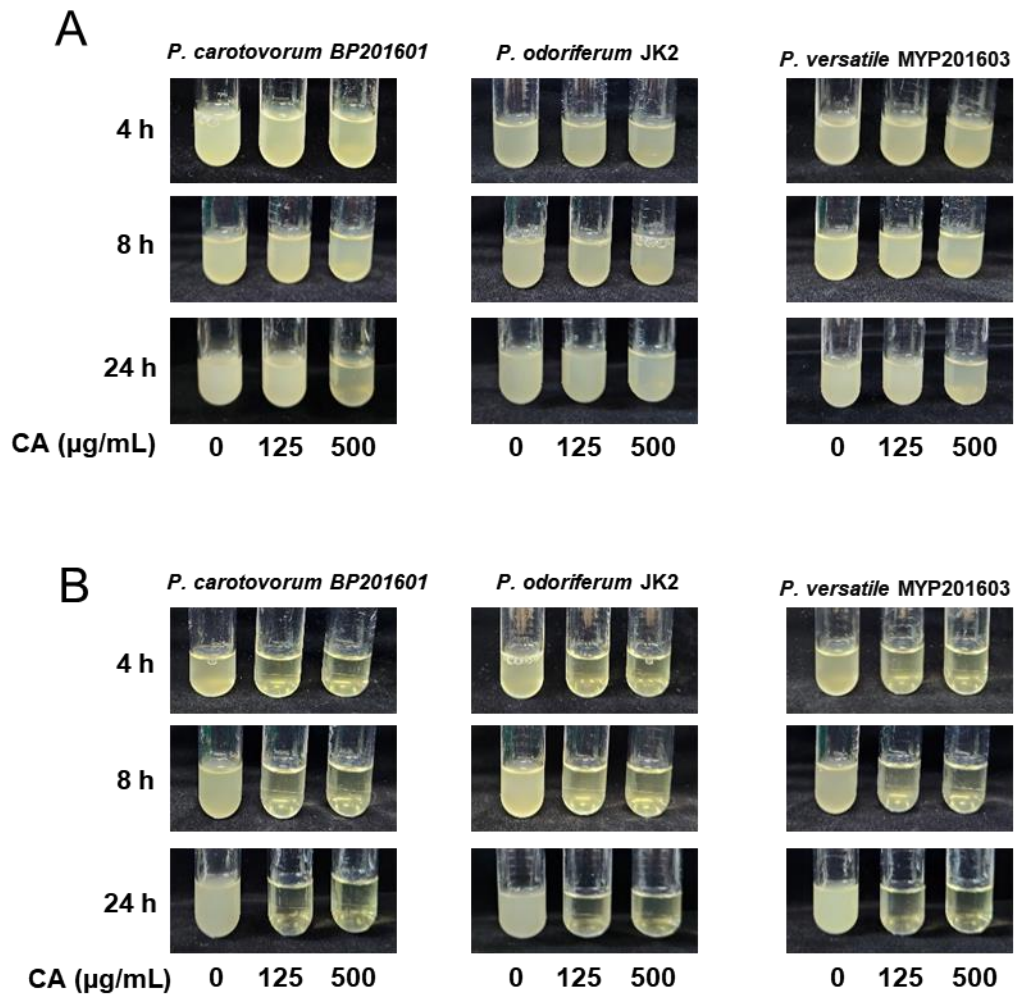
Sample id	Raw Data		Trimmed Data		GC(%)	Q20(%)	Q30(%)
	Total read bases	Total reads	Total read bases	Total reads			
Control_1	2,477,476,066	24,529,466	2,442,723,772	24,285,292	46.48	99.09	96.65
Control_4	2,204,472,258	21,826,458	2,174,337,119	21,610,870	45	99.08	96.57
Control_5	3,700,367,098	36,637,298	3,649,263,753	36,287,172	47.07	99.02	96.36
CA_500_3	2,493,741,308	24,690,508	2,171,545,627	21,799,246	47.6	98.95	96.22
CA_500_4	2,360,851,164	23,374,764	1,955,194,234	19,778,542	48.18	98.96	96.22
CA_500_5	3,111,102,798	30,802,998	705,590,814	7,247,982	44.16	98.74	95.75

**Table S2. Summary of RNA-seq alignment.**

Sample ID	Processed reads	Mapped reads	Failed to align reads	Multiplemapped reads
Control_1	24,285,292	23,123,778 (95.22%)	1,116,866 (4.60%)	44,648 (0.18%)
Control_4	21,610,870	20,634,372 (95.48%)	919,922 (4.26%)	56,576 (0.26%)
Control_5	36,287,172	34,334,400 (94.62%)	1,890,938 (5.21%)	61,834 (0.17%)
CA_500_3	21,799,246	17,843,922 (81.86%)	3,838,866 (17.61%)	116,458 (0.53%)
CA_500_4	19,778,542	15,136,864 (76.53%)	4,546,598 (22.99%)	95,080 (0.48%)
CA_500_5	7,247,982	4,591,230 (63.34%)	2,641,490 (36.44%)	15,262 (0.21%)

**Table S3. Primers used in this study.**

Gene	Forwards	Reverse
<i>16S rRNA</i>	GGCAGCAGTGGGGAATATTG	CTTTACGCCCAGTCATTCCG
<i>narX</i>	GATGCCGATCCTGAACGAAC	CGCCATATTGCCCGTGTITA
<i>narL</i>	GGACCCGGATTTGATTCTGC	GCAGCCAGTAAATCTTCCGG
<i>narH</i>	TGAAACGTATGCTGGCGATG	TGAATTTGGTATCGCTGCCG
<i>narJ</i>	GACTACCTGCCGCTGTATCT	ACCTGTTCTCTTCCCACAC
<i>sucA</i>	GACTCCGTGCTATCCGAAGA	CTCTGGACCTTGACCTTCGT
<i>odhB</i>	GCGTCTTTGGCTCTCTGATG	TCCAGCATCTCTTTCACCGT

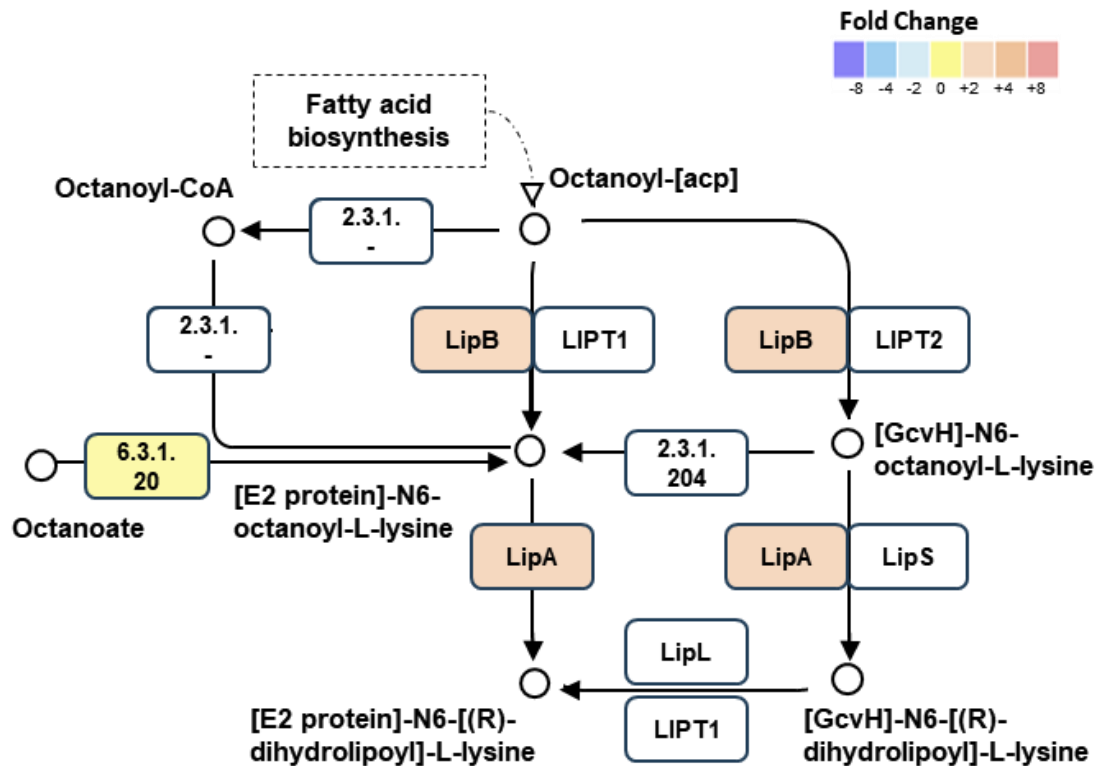


**Supplementary Fig. S1. Bactericidal effect of cinnamaldehyde on**

*Pectobacterium* spp. bactericidal effect of cinnamaldehyde on *P. carotovorum*

BP201601, *P. odoriferum* JK2 and *P. versatile* MYP201603 based on different

concentration values of  $1 \times 10^8$  CFU/mL (**A**) and  $1 \times 10^7$  CFU/mL (**B**).



## Lipoic acid metabolism

**Supplementary Fig. 2. Pathways highlighting the differentially expressed genes identified in this study.** Up-regulated genes in the “Lipoic acid metabolism” pathway in RNA-seq. The scale represents the average fold change (FC) values between samples treated with cinnamaldehyde and the controls. The gene depicted in this figure are detailed in Supplementary File4.