

**Response and degradation of indole-3-acetic acid by the plant
growth-promoting rhizobacteria *Variovorax boronicumulans***

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27 **Table Caption**

28 **Table S1** KEGG pathway up-regulated protein of *V. boronicumulans* CGMCC 4969

29 **Table S2** Down-regulated Proteins from KEGG Analysis (FC<0.83)

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33 **Figure Caption**

34 **Fig. S1** IAA metabolic pathway

35 **Fig. S2** Protein quantification and variance analysis results

36 **Fig. S3** GO Annotation statistics of differentially expressed proteins (Level 2)

37 **Fig. S4** Network diagram of differentially expressed protein interactions

38 **Fig. S5** Expression levels of key IAA-degrading genes in *V. boronicumulans* CGMCC

39 4969 under lb and lb with 1 mmol/l IAA culture conditions

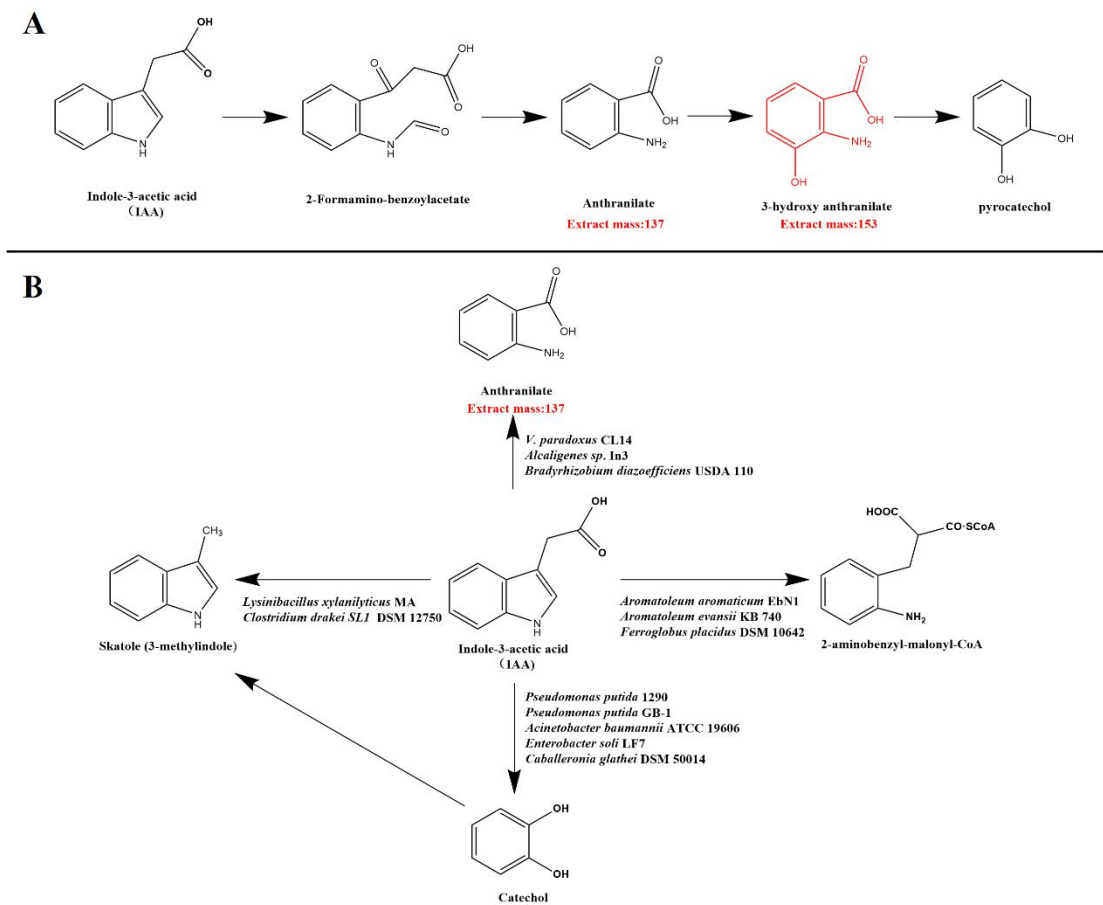
40 **Table S1** KEGG pathway up-regulated protein of *V. boronicumulans* CGMCC 4969

KEGG pathway	ID	Protein	Amino acids length	Fold change
Quorum sensing (ko02024)	ATA51874.1	ABC transporter permease	290	2.41
	ATA51875.1	ABC transporter permease	391	1.47
ABC transporters (ko02010) (except ATA57166.1)	ATA52143.1	Branched-chain amino acid ABC transporter permease	329	1.30
	ATA56139.1	Branched-chain amino acid ABC transporter substrate-binding protein	387	3.19
	ATA52145.1	ABC transporter substrate-binding protein	401	1.67
	ATA52142.1	ABC transporter ATP-binding protein	251	1.39
	ATA56137.1	Metal-dependent hydrolase	595	2.61
	ATA56136.1	ABC transporter ATP-binding protein	243	1.82
	ATA56142.1	Branched-chain amino acid ABC transporter substrate-binding protein	380	4.56
	ATA56143.1	Branched-chain amino acid ABC transporter substrate-binding protein	388	4.50
	ATA56138.1	Branched-chain amino acid ABC transporter permease	351	1.47
	ATA57166.1	Long-chain fatty acid-CoA ligase	654	1.31
	ATA52144.1	Branched-chain amino acid ABC transporter permease	309	1.39
Benzoate degradation (ko00362)	ATA56157.1	3-hydroxybutyryl-CoA dehydrogenase	334	2.06
	ATA57522.1	Benzoyl-CoA oxygenase component A	430	2.42
	ATA51899.1	Glutaryl-CoA dehydrogenase (ETF)	399	1.61
	ATA51882.1	Benzoyl-CoA 2,3-epoxidase subunit BoxB	475	2.20
	ATA51877.1	4-hydroxybenzoate--CoA ligase	517	1.70
	ATA51881.1	Benzoyl-CoA-dihydrodiol lyase	557	2.43
	ATA53551.1	Acetyl-CoA C-acyltransferase	394	1.31
	ATA56131.1	4-hydroxybenzoyl-CoA thioesterase	155	1.56
	ATA51878.1	3,4-dehydroadipyl-CoA semialdehyde dehydrogenase	516	1.50

Biosynthesis of cofactors (ko01240)	ATA53544.1	Dihydrolipoyl dehydrogenase	581	1.47
	CKY39_32335	Adenylosuccinate lyase	459	-
	ATA53020.1	GTP cyclohydrolase I	243	1.25
	ATA54951.1	3-oxoacyl-[acyl-carrier-protein] reductase	260	1.32
	ATA56134.1	Short-chain dehydrogenase	249	2.50
	ATA56144.1	Short-chain dehydrogenase	244	2.87
	ATA56133.1	3-hydroxyacyl-CoA dehydrogenase	258	2.20
	ATA57189.1	Oxidoreductase	302	1.28
Fatty acid biosynthesis (ko00061)	ATA54951.1	3-oxoacyl-[acyl-carrierprotein] reductase	260	1.32
	ATA56134.1	Short-chain dehydrogenase	249	2.50
	ATA56144.1	Short-chain dehydrogenase	244	2.87
	ATA56133.1	3-hydroxyacyl-CoA dehydrogenase	258	2.20
	ATA57166.1	Long-chain fatty acid-CoA ligase	654	1.31
	ATA57189.1	Oxidoreductase	302	1.28

42 **Table S2 Down-regulated proteins from KEGG Analysis (FC<0.83)**

KEGG pathways	ID	Protein	Amino acids	Fold change
Biosynthesis of cofactors	ATA52721.1	3-demethoxyubiquinol 3-hydroxylase	209	0.82
	ATA57786.1	Dihydropteroate synthase	306	0.71
	ATA55673.1	6,7-dimethyl-8-ribityllumazine synthase	170	0.79
	ATA56418.1	Dihydrothymine dehydrogenase	436	0.71
	ATA51988.1	Nicotinamidase	241	0.71
	ATA53366.1	3-oxoacyl-[acyl-carrier-protein] synthase 1	406	0.83
Propanoate metabolism	ATA53232.1	Citrate synthase	385	0.80
	ATA55325.1	Methylmalonyl-CoA mutase	721	0.82
	ATA54260.1	Methylmalonate-semialdehyde dehydrogenase (CoA acylating)	507	0.70
	ATA55268.1	Propionate--CoA ligase	637	0.71



46 **Fig. S1** IAA metabolic pathway.

47 New products discovered in the study are shown in red. (A) *V. boronicumulans*
48 CGMCC 4969 hypothesised pathway for degrading IAA. (B) Reported IAA metabolic
49 pathways. Only the end product is shown. Next to the arrows are the bacteria that
50 carry out the metabolic pathway.

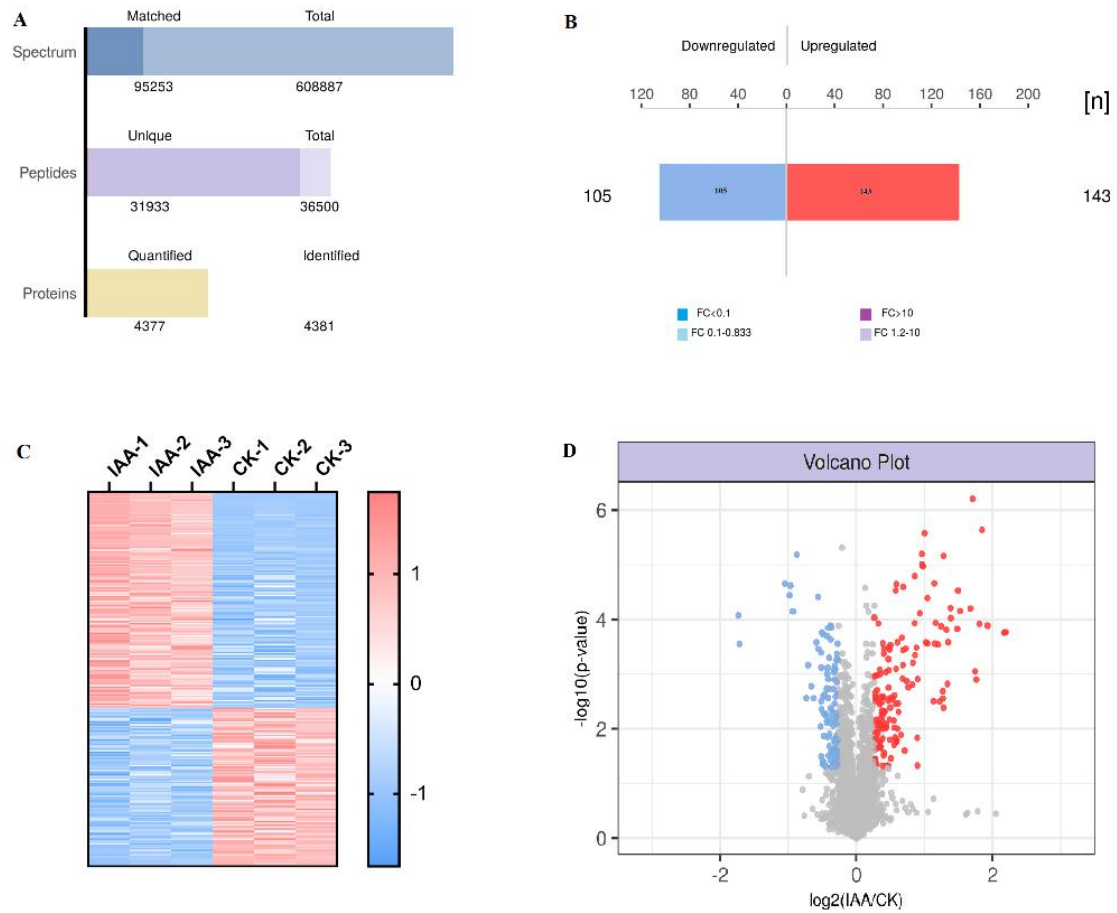


Fig. S2 Protein quantification and variance analysis results.

(A) Histogram of identification and quantification results. (B) Histogram of quantitative protein difference results. (C) Results of cluster analysis of differentially expressed proteins. The $\log_2$ method was used to normalise the expression of various proteins in different samples. The results were visualized as a heatmap, with red, blue, and white representing significant up-regulation, significant down-regulation, and non-quantifiable protein expression, respectively (D) Volcano map of the proteins, significantly downregulated proteins (FC < 0.83, $p < 0.05$) are marked in blue, while significantly upregulated proteins (FC > 1.2, $p < 0.05$) are highlighted in red, non-significant proteins ($p \geq 0.05$) are displayed in grey.

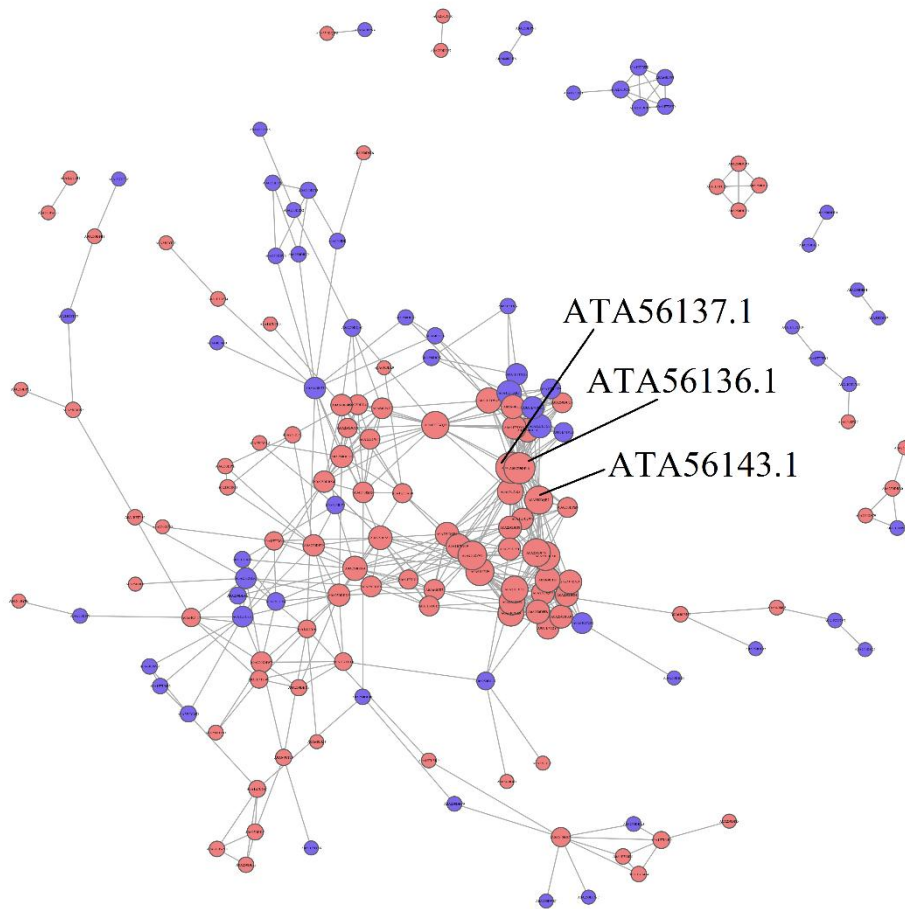


Fig. S3 Network diagram of DEPs.

The circle nodes in the figure indicate differentially expressed proteins and the lines indicate protein-protein interactions. The color of the circle indicates the differential expression of the protein (downregulation is marked in blue, upregulation in red), and the size of the circle indicates the connectivity of the protein (the number of proteins that directly interact with a protein).

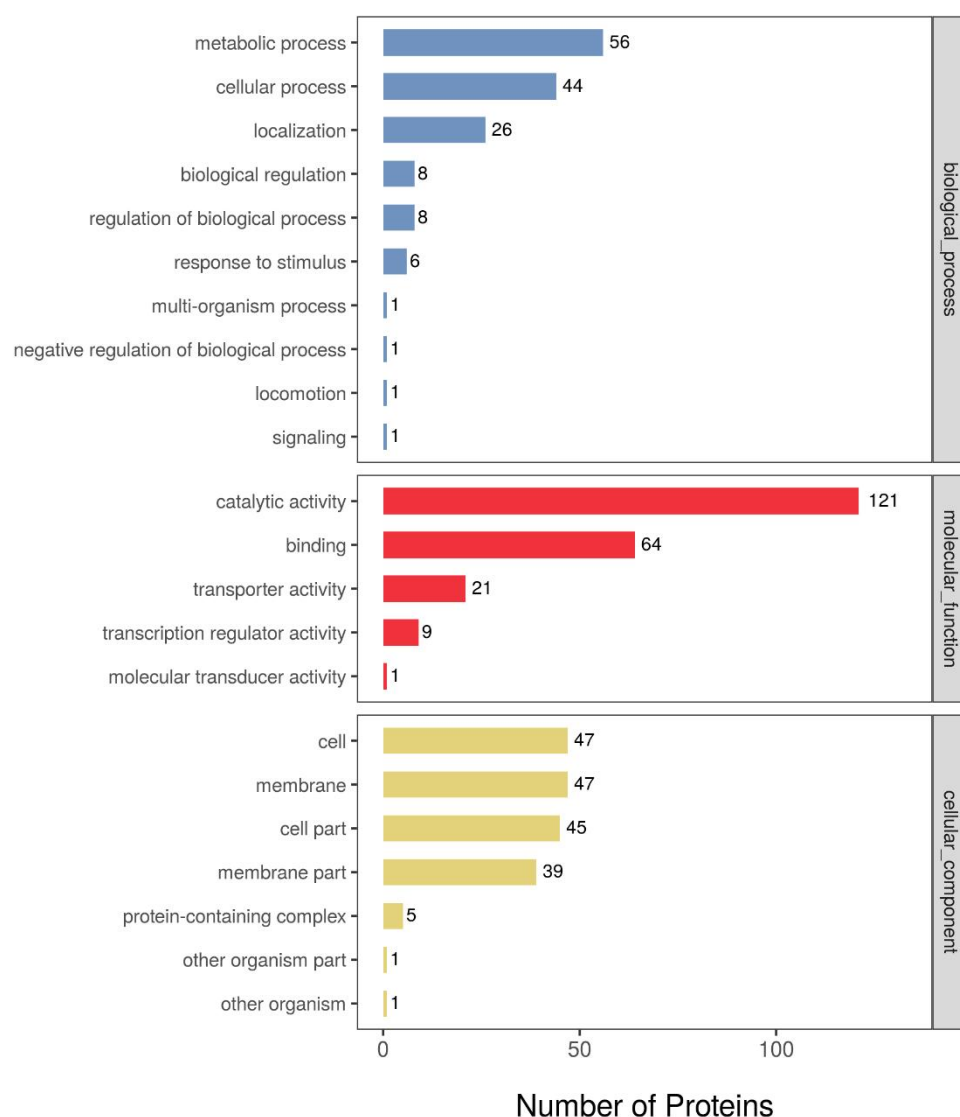


Fig. S4 GO annotation statistics of DEPs (Level 2).

The graph's vertical axis displays GO Level 2 functional annotation information, comprising Biological Process, Molecular Function, and Cellular Component. These are distinguished by blue, red, and yellow. The horizontal axis represents the number of differentially expressed proteins under each functional category. Upon each functional category, the number of differentially expressed proteins is portrayed. The x-axis signifies the quantity of proteins with differential expression within each functional category.

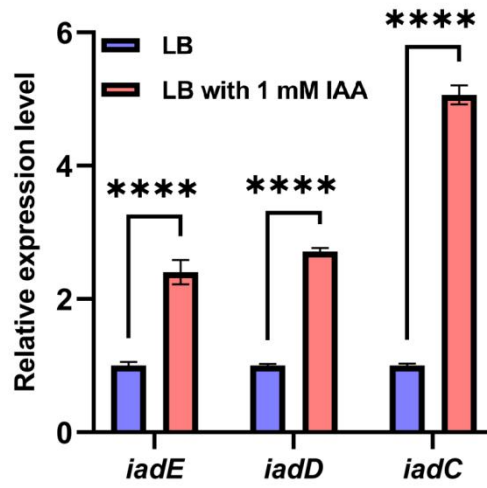


Fig. S5 Expression levels of key IAA-degrading genes in *V. boronicumulans* CGMCC 4969 under LB and LB with 1 mmol/L IAA culture conditions.