

Figure S1 a. Time course of LR initiation in response to PS01. At time point 0 d, bacteria were inoculated on the plates. The values represent means \pm SD ($n = 15$). Asterisks indicate statistically significant differences compared with untreated roots (Student's t test; $p < 0.05$).

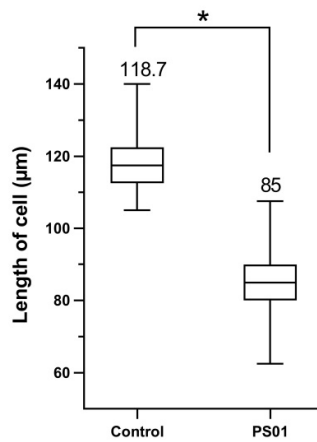
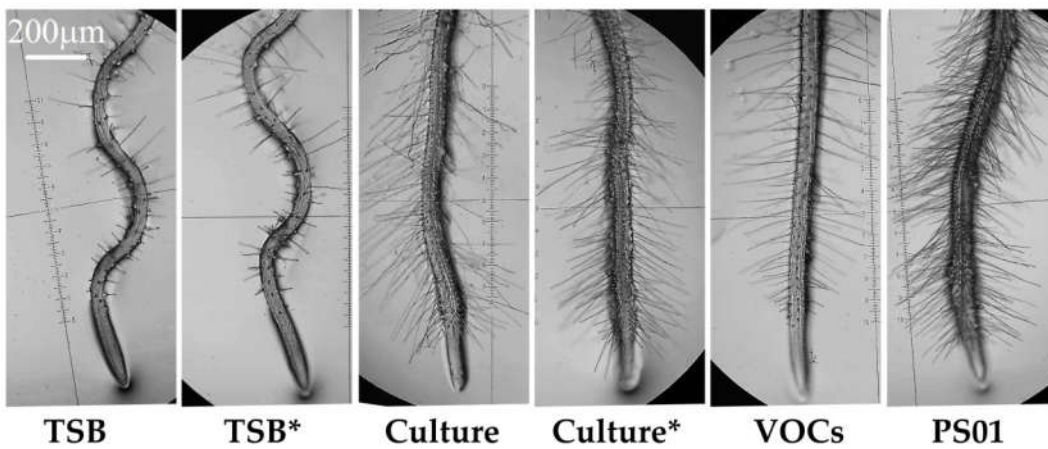


Figure S1 b. Inhibition of root cell elongation in differentiation zone by PS01. Length of cells were observed and measured under a 40 X microscope. Bars represent average lengths \pm SD of 75 cells in each developmental zone ($n = 15$). Asterisks indicate statistically significant differences compared with non-inoculated roots (Student's t test; $p < 0.05$).



(a)



(b)

Figure S2. Different secreted metabolites produced by PS01 implicated in RSA of *Arabidopsis*. (a) Split plate assay; (b) Effect of VOCs blend and diffusible compounds on RH development. Photos were taken after 7 days of inoculation.

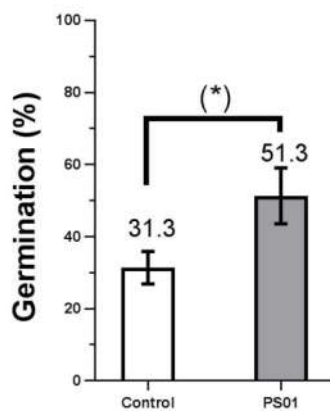


Figure S3. *Pseudomonas* PS01 improves germination rate in *Zea mays*. The germination rate was evaluated after 2 days incubation (100 seeds). Bars represent average values ($n = 3$). Asterisks indicate statistically significant differences compared with non-inoculated roots (Student's t test; $p < 0.05$)

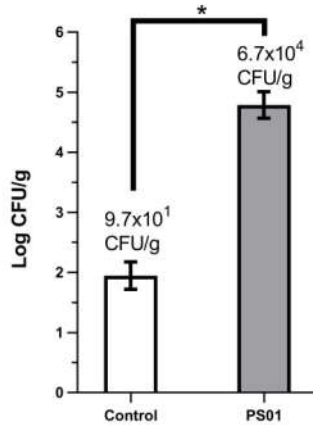


Figure S4. Root colonization of maize plants by PS01. The number of *Pseudomonas* sp. per gram of root was determined at 30 th day. Bars represent average of log CFU g⁻¹ ± SD (*n* = 15). Asterisks indicate statistically significant differences compared with non-inoculated roots (Student's *t* test; *p* < 0.05)

Table S1. Accession number, name, description, and primer sequences used for quantitative RT-PCR [43]

AGI Code	Name	Description	Fw/Rv primers
At3	AIR12	Auxin-responsive protein	5'-TGAATCAGGTATGGCAGATCGG-3'(F) 5'-TGAAACTCAACACACCGTGGG-3'(R)
g07390	DFL1	IAA-amido synthase that conjugates Ala, Asp, Phe, and Trp to auxin	5'-CACAAAGATCGCAGCTTTG-3'(F) 5'-ATCATCTGCGTTTCGTGTCAC-3'(R)
At1	NAC1	Transcription factor involved in shoot apical meristem formation and auxin mediated Lateral root formation	5'-GCCTCCGGGATTTCAGATTCA-3'(F) 5'-TCAGGACAAGAGGTGGTCGATG-3'(R)
g56010	AUX1	Auxin permease	5'-AAGGGCTTTGGCTAGATTGCC-3'(F) 5'-CAAGAAGAGCACCACAGCG-3'(R)
At2	IAA3/SHY2	Regulates multiple auxin responses in roots, induced by IAA	5'-GCCAAAGGTTTAGGCTGTGTG-3'(F) 5'-TAGATCTTGCCCGAGAAACCCG-3'(R)
g38120	PIN1	Auxin efflux carrier involved in shoot and root development	5'-CGCTTCAGAGTTCAGAAACCC-3'(F) 5'-CACAGCTTCTCCAGGACCAAAG-3'(R)
At1	PIN2/EIR1	Auxin efflux carrier	5'-CCAATGTTACGGGGTCAACG-3'(F) 5'-GAAGCACTCGAACTCCACACG-3'(R)
g73590	AAO1	Arabidopsis aldehyde oxidase 1 with the specificity for indole-3-acetaldehyde	5'-TGTGGCGAAGGTGGTTGTGG-3'(F) 5'-GCTGCGAGGAGGTGGATGAG-3'(R)
At5	ASA1	Anthranilate synthase alpha subunit 1	5'-GCGTTGGTCGTTATAGCGTTG-3'(F) 5'-TGGGATCTCCATTGGATCTTCG-3'(R)
g57090	TSA1	Tryptophan synthase alpha chain	5'-CGTTGGAGAGGGGAACAAC-3'(F) 5'-TTGGTGTGGTTGGTGTAGTGAG-3'(R)
At3	YUCCA5	Flavin mono-oxygenase	5'-TGTGTCCAGTCTGCTCGATACG-3'(F) 5'-CCCCTGCCACCACCTAACC-3'(R)
g20960	CYP79 B2	Cytochrome P450 that is involved in tryptophan metabolism	5'-CCATGCAGAGACAACAGAAACC-3'(F) 5'-AGGTGCTAAAGGACGATGTTTC-3'(R)
At4	CYP83 B1	Cytochrome P450 mono-oxygenase 83 B1	5'-ACGAGACGCAAGCACITTTGG-3'(F) 5'-GGGCGTTAGGGTCAAGAGTC-3'(R)
g31500	IGPS	Indole-3-glycerol-phosphate synthase	5'-GGACATTTGAGTTGAGATTGC-3'(F) 5'-CCTAAGAGCCCCAACAAAATCC-3'(R)
At2			
g04400			

Table S2. Gene annotations of PS01 genome related to its IAA- and VOCs-producing ability.

Trait	Contig ID	Peptide ID	Gene annotation	KO/gene ID	KEGG gene name	EC number
IAA biosynthesis TAM pathway	NODE_382	fig 286.823.pcg.23 19	Tryptophan decarboxylase	K01593	DDC, TDC	4.1.1.28
	NODE_30	fig 286.823.pcg.19 39	monoamine oxidase	k00274	MAO, aofH	1.4.3.4
	NODE_446	fig 286.823.pcg.28 40	aldehyde dehydrogenase (NAD ⁺)	K00128	ALDH	1.2.1.3
IAA biosynthesis IAM pathway	NODE_157	fig 286.823.pcg.42 9	Tryptophan 2-monooxygenase	K00466	iaaM	1.13.12.3
	NODE_16	fig 286.823.pcg.69 3	amidase	K01426	amiE	3.5.1.4
	NODE_382	fig 286.823.pcg.21 79	amidase	K01426	amiE	3.5.1.4

(R)-2-Acetoin	NODE_101	fig 286.823.peg.62	acetolactate synthase I/II/III large subunit	K01652	ilvB, ilvG, ilvI	2.2.1.6
	NODE_152	fig 286.823.peg.367	acetolactate synthase I/II/III large subunit	K01652	ilvB, ilvG, ilvI	2.2.1.6
	NODE_293	fig 286.823.peg.1591	acetolactate synthase I/II/III large subunit	K01652	ilvB, ilvG, ilvI	2.2.1.6
	NODE_76	fig 286.823.peg.3854	acetolactate synthase I/II/III large subunit	K01652	ilvB, ilvG, ilvI	2.2.1.6
	NODE_76	fig 286.823.peg.3855	acetolactate synthase I/III small subunit	K01653	ilvH, ilvN	2.2.1.6
	NODE_209	fig 286.823.peg.1000	(R,R)-butanediol dehydrogenase / meso-butanediol dehydrogenase / diacetyl reductase	K00004	BDH, butB	1.1.1.-
2,3-butanediol	NODE_209	fig 286.823.peg.1000	(R,R)-butanediol dehydrogenase / meso-butanediol dehydrogenase / diacetyl reductase	K00004	BDH, butB	1.1.1.-
						1.1.1.4 1.1.1.303
4-hydroxybenzoate	NODE_446	fig 286.823.peg.2897	chorismate-pyruvate lyase	K03181	ubiC	4.1.3.40