

Supplementary Table 1. Primers for amplification and sequencing using housekeeping genes (*atpD/recA*)

Gene	Usage of primer	Primer name and sequences (5'-3')	Position	Amplicon size (bp)	Annealing temperature (°C)	
<i>atpD</i>	Amplification	<i>atpDPF</i> GTCGGCGACTTCACCAAGGGCAAGGTGTTCAACACC	283-318	998	63	
		<i>atpDPR</i> GTGAACTGCTTGGCGACGTGGGTGTTCTGGGACAGGAA	1,243-1,280			
	Sequencing	<i>atpDF</i> ACCAAGGGCAAGGTGTTCAA	295-314	-	-	
		<i>atpDR</i> GCCGGGTAGATGCCCTTCTC	1,027-1,046			
		Amplification	<i>recAPF</i> CCGCRCTCGCACAGATTGAACGSCAATTC	35-63	913	60
			<i>recAPR</i> GCSAGGTCGGGGTTGTCCTTSAGGAAGTTGCG	916-947		
Sequencing	<i>recAF</i> ACAGATTGAACGGCAATTCG	45-64	-	-		
	<i>recAR</i> ACCTGTTCTTGACCACCTT	733-752				

Supplementary Table 2. Microbes isolation and selection of anti-Psa strains from rhizosphere soil, sap and pollen of kiwifruit

	Rhizosphere	Sap	Pollen
Isolated microbes	1,175	768	1,080
1st screening	56	156	106
2nd screening	15	35	2
3rd screening	9	0	2

Psa, *Pseudomonas syringae* pv. *actinidiae*.

Supplementary Table 3. GenBank accession numbers for genome sequencing

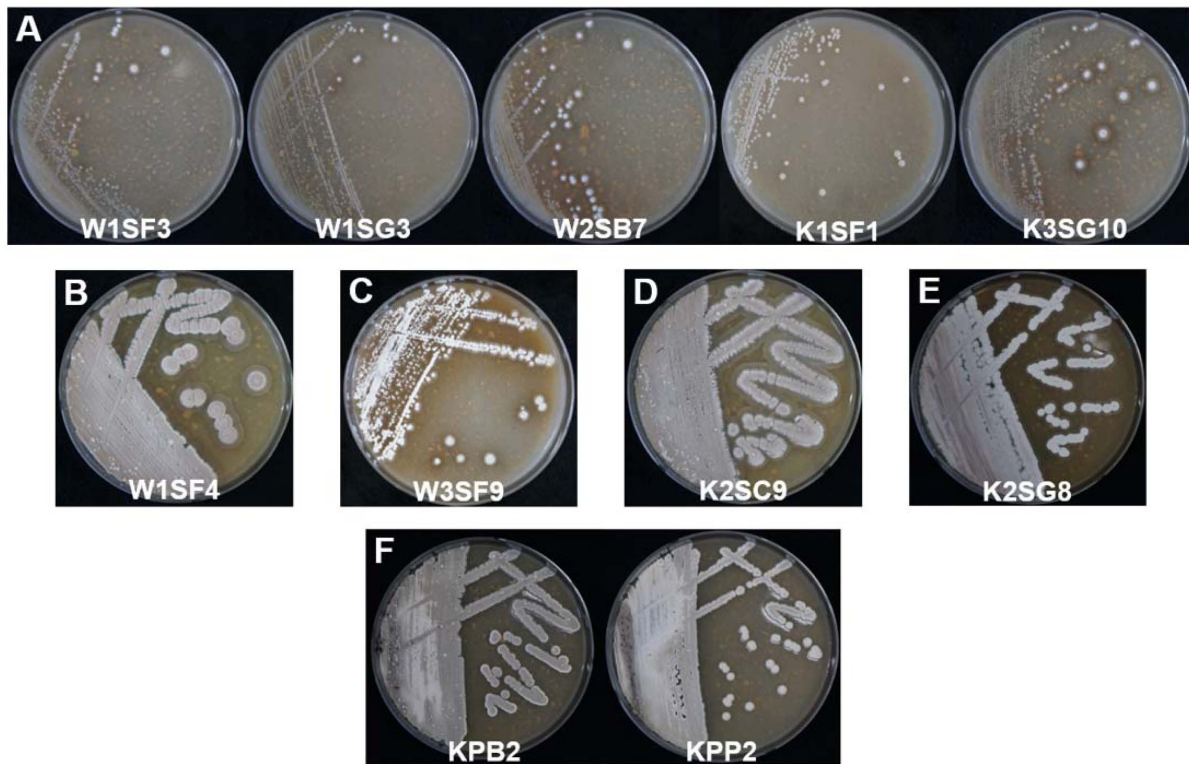
Bacteria strain		SRA	BioProject	Biosample	Genome
<i>Streptomyces racemochromogenes</i> . W1SF4	Chromosome	SRP172801	PRJNA487679	SAMN09908039	CP34350.0
	Plasmid 1	SRP172801	PRJNA487679	SAMN09908039	CP034351.1
	Plasmid 2	SRP172801	PRJNA487679	SAMN09908039	CP034352.1
<i>Streptomyces parvulus</i> KPB2	Chromosome	SRP172808	PRJNA487680	SAMN09908040	CP034353.1

Supplementary Table 4. Gene ontology analysis in *Streptomyces* sp. W1SF4 by EggNOG

Eggnog	Description	Count	Ratio (%)
A	RNA processing and modification	1	0.0139
B	Chromatin structure and dynamics	1	0.0139
C	Energy production and conversion	319	4.423
D	Cell cycle control, cell division, chromosome partitioning	34	0.4735
E	Amino acid transport and metabolism	405	5.6399
F	Nucleotide transport and metabolism	96	1.3369
G	Carbohydrate transport and metabolism	317	4.4144
H	Coenzyme transport and metabolism	149	2.0749
I	Lipid transport and metabolism	206	2.8687
J	Translation, ribosomal structure and biogenesis	187	2.6041
K	Transcription	557	7.7566
L	Replication, recombination and repair	180	2.5066
M	Cell wall/membrane/envelope biogenesis	202	2.813
N	Cell motility	1	0.0139
O	Posttranslational modification, protein turnover, chaperones	158	2.2003
P	Inorganic ion transport and metabolism	261	3.6346
Q	Secondary metabolites biosynthesis, transport and catabolism	165	2.2977
R	General function prediction only	1318	18.354
S	Function unknown	2141	29.8148
T	Signal transduction mechanisms	328	4.5676
U	Intracellular trafficking, secretion, and vesicular transport	34	0.4735
V	Defense mechanisms	119	1.6572
Z	Cytoskeleton	2	0.0279
Total	-	7181	100

Supplementary Table 5. Gene assigned of ontology in *Streptomyces* sp. KPB2 with EggNOG

Eggnog	Description	Count	Ratio (%)
A	RNA processing and modification	1	0.0141
B	Chromatin structure and dynamics	1	0.0141
C	Energy production and conversion	330	4.6499
D	Cell cycle control, cell division, chromosome partitioning	26	0.3664
E	Amino acid transport and metabolism	406	5.7207
F	Nucleotide transport and metabolism	99	1.395
G	Carbohydrate transport and metabolism	464	6.538
H	Coenzyme transport and metabolism	151	2.1277
I	Lipid transport and metabolism	170	2.3954
J	Translation, ribosomal structure and biogenesis	194	2.7335
K	Transcription	598	8.4261
L	Replication, recombination and repair	207	2.9167
M	Cell wall/membrane/envelope biogenesis	226	3.1844
O	Posttranslational modification, protein turnover, chaperones	141	1.9868
P	Inorganic ion transport and metabolism	293	4.1285
Q	Secondary metabolites biosynthesis, transport and catabolism	159	2.2404
R	General function prediction only	1147	16.1618
S	Function unknown	2006	28.2655
T	Signal transduction mechanisms	317	4.4667
U	Intracellular trafficking, secretion, and vesicular transport	31	0.4368
V	Defense mechanisms	130	1.8318
Total	-	7097	100



Supplementary Fig. 1. Phenotypes of selected anti-*Pseudomonas syringae* pv. *actinidiae* (Psa) strains on mannitol-soya (MS) agar. Selected 11 anti-Psa strains were cultured to sporulation fully on MS media at 30°C for 5 days. The phenotypic characteristics on MS are distinguished as 6 types according to colony color, shape or color change around the colony. The A types produce powdery and poor sporulating white colony with ocher halo (A), the B type produces powdery and abundant light pink colony (B), the C type produces powdery and rough surfaced white colony with brown halo (C), and the D type produces powdery and flat light pink colony (D). The E type produces powdery and smooth pink colony (E) and the F types produce powdery and smooth dusky pink colony (F). The A types are grouped with W1SF3, W1SG3, W2SB7, K1SF1 and K3SG10. The B, C, D and E type are grouped with W1SF4, W3SF9, K2SC9 and K2SG8 individually. The F types are grouped with KPB2 and KPP2.