

Supplementary file for

Mangrove sediments-associated bacterium (*Bacillus* sp. SW7) with multiple plant growth-promoting traits promotes the growth of tomato (*Solanum Lycopersicum*)

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Result S1

Among the COG categories, amino acid transport and metabolism accounted for 338 genes, general function prediction and unknown function accounted for 13.08%, transcription accounted for 8.8%, and signal transduction mechanisms accounted for 5.38% (Figure. S1). Similarly, the number of CDSs assigned to the Kyoto Encyclopedia of Genes and Genomes (KEGG) database was 2,469, and the major pathways were global and overview maps (59.13%), carbohydrate metabolism (22.8%), amino acid metabolism (20.65%), environmental information processing (9.1%), genetic information processing (7.9%), and energy transport (5.38%). The SW7 genome consists of Enzymatic (Reactions) Commission numbers (EC) for transferases (92), hydrolases (93), lyases (18), oxidoreductases (40), isomerases (12), ligases

(35), and translocase (19). Interproscan showed the *Bacillus* sp. SW7 genome had Gene Ontology for abiotic, biotic, and stress response GO terms, and also has GO for iron-sulfur cluster binding (Magotra et al., 2021).

Table S1. Morphological, biochemical and plant growth-promoting (PGP) characteristics of *Bacillus* sp. SW7.

Morphological, biochemical and PGP features	<i>Bacillus</i> sp. SW7
Colony shape	Circular, Cream
Colony diameter, Colony elevation, Colony margin	7 nm, Raised, Undulate
Gram reaction	Gram-positive
Catalase, oxidase, ONPG (Beta-galactosidase)	+
Arginine (Arginine dihydrolase)	+
Citrate (Citrate utilization), Na thiosulfate (H ₂ S production), Urea (Urea hydrolysis)	-
Tryptophan (Deaminase), Na pyruvate (Acetoin production),	+
Charcoal gelatin (Gelatinase)	+
Glucose, Mannitol, Inositol (Fermentation/oxidation)	+
Sorbitol, Rhamnose, Sucrose, Melibiose, Amygdalin (Fermentation/oxidation)	-
Arabinose (Fermentation/oxidation)	+
Nitrogen fixation, Hydrogen cyanide	+
Siderophore production	-
Indole Acetic Acid (IAA)	3.60 ±0.44 ppm
Ammonia Production (ppm)	0.5 ppm
Phosphate Solubilization (SI)	83.3 g/L ⁻¹
Potassium Solubilization (KI)	39.6 g/L ⁻¹

Table S2. Pairwise comparisons of *Bacillus* sp. SW7 with reference genome of *Bacillus anthracis* str. Ames, *B. cereus* along with the 11 *Bacillus* isolated from the international space station using GBDP algorithm and GGDC calculated digital DDH value and confidence interval (C.I) and G+C content difference.

Query strain	Subject strain	dDDH (d0, in %)	C.I. (d0, in%)	dDDH (d4, in%)	C.I. (d4, in %)	dDDH (d6, in%)	C.I. (d6, in%)	G+C content difference (in %)
<i>Bacillus-cereus</i> -W-gcontig	<i>Bacillus</i> sp. SW7	80.8	[76.9 - 84.2]	75.8	[72.8 - 78.6]	82.9	[79.5 - 85.7]	0.33
<i>Bacillus cereus</i> strain ISSFR-3F	<i>Bacillus</i> sp. SW7	82	[78.1 - 85.3]	75.7	[72.7 - 78.5]	83.8	[80.5 -86.6]	0.23
<i>Bacillus</i> sp.JEM-1	<i>Bacillus</i> sp. SW7	80.8	[76.9 - 84.2]	75.7	[72.7 - 78.4]	82.8	[79.5 - 85.7]	0.54
<i>Bacillus cereus</i> strain ISSFR-9F	<i>Bacillus</i> sp. SW7	82	[78.1 - 85.3]	75.7	[72.7 - 78.5]	83.8	[80.5 -86.6]	0.24
<i>Bacillus cereus</i> -strain-ISSFR-23F	<i>Bacillus</i> sp. SW7	81.6	[77.7 - 84.9]	75.6	[72.5 - 78.3]	83.4	[80.1 - 86.3]	0.26
<i>Bacillus-cereus</i> -strain-JEM-2	<i>Bacillus</i> sp. SW7	82.1	[78.2 - 85.4]	75.6	[72.6 - 78.4]	83.9	[80.6 -86.7]	0.21
<i>Bacillus</i> sp.S1-R4H1-FB	<i>Bacillus</i> sp. SW7	82.8	[78.9 - 86.0]	75.4	[72.4 - 78.2]	84.4	[81.2 -87.2]	0.17
<i>Bacillus</i> sp.S2-R3J1-FB-BA1	<i>Bacillus</i> sp. SW7	82	[78.1 - 85.3]	75.3	[72.3 - 78.1]	83.8	[80.5 -86.6]	0.26
<i>Bacillus</i> sp.ISSFR-25F	<i>Bacillus</i> sp. SW7	75.2	[71.2 - 78.8]	75.1	[72.1 - 77.9]	77.9	[74.5 - 81.0]	1.84
<i>Bacillus anthracis</i> str.A0248	<i>Bacillus</i> sp. SW7	79	[75.0 - 82.5]	75	[72.0 - 77.8]	81.2	[77.8 - 84.1]	0.07
<i>Bacillus</i> sp.S1-R1J2-FB	<i>Bacillus</i> sp. SW7	82.3	[78.4 - 85.6]	75	[72.0 - 77.8]	83.9	[80.7 -86.7]	0.27
<i>Bacillus</i> sp. SW7	<i>Bacillus anthracis</i> ATCC 14578	79	[75.0 - 82.5]	75	[72.0 - 77.8]	81.2	[77.8 - 84.1]	0.07
<i>Bacillus anthracis</i> str Ames	<i>Bacillus</i> sp. SW7	83.4	[79.6 - 86.6]	75	[72.0 - 77.8]	84.9	[81.7 -87.6]	0.2
<i>Bacillus anthracis</i> strain HYU01	<i>Bacillus</i> sp. SW7	79	[75.1 - 82.5]	74.9	[71.9 - 77.7]	81.2	[77.8 - 84.1]	0.06
<i>Bacillus</i> sp.S1-R2T1-FB	<i>Bacillus</i> sp. SW7	81.2	[77.3 - 84.6]	74.9	[71.8 - 77.6]	83	[79.7 - 85.9]	0.39

<i>Bacillus</i> sp.S1-R5C1-FB	<i>Bacillus</i> sp. SW7	82	[78.1 - 85.3]	74.5	[71.4 - 77.3]	83.6	[80.3 -86.4]	0.39
	<i>Bacillus</i>							
	<i>paranthracis</i>							
<i>Bacillus</i> sp. SW7	MCCC-1A00395	77.4	[73.4 - 81.0]	65.5	[62.5 - 68.3]	77.8	[74.4 - 80.9]	0.01
<i>Bacillus cereus</i> strain FSL W8-0003	<i>Bacillus</i> sp. SW7	72.8	[68.8 - 76.4]	64.4	[61.4 - 67.2]	73.6	[70.1 - 76.8]	0.11
<i>Bacillus cereus</i> Q1	<i>Bacillus</i> sp. SW7	74.3	[70.3 - 77.9]	63.4	[60.5 - 66.2]	74.6	[71.2 - 77.8]	0.29
<i>Bacillus cereus</i> ATCC 4342	<i>Bacillus</i> sp. SW7	81.8	[78.0 - 85.2]	61.9	[59.0 - 64.7]	80.7	[77.3 - 83.7]	0.03
	<i>Bacillus tropicus</i>							
<i>Bacillus</i> sp. SW7	N24	79.4	[75.5 - 82.9]	59.3	[56.5 - 62.0]	78	[74.5 - 81.1]	0.03
	<i>Bacillus pacificus</i>							
<i>Bacillus</i> sp. SW7	MCCC 1A06182	70	[66.1 - 73.7]	57.7	[54.9 - 60.4]	69.6	[66.1 - 72.8]	0.03
	<i>Bacillus dicomae</i>							
<i>Bacillus</i> sp. SW7	MHSD28T	77	[73.0 - 80.5]	55.4	[52.6 - 58.1]	74.8	[71.3 - 78.0]	0.03
	<i>Bacillus basilensis</i>							
<i>Bacillus</i> sp. SW7	403507-21	71.9	[67.9 - 75.5]	55.2	[52.5 - 57.9]	70.5	[67.0 - 73.7]	0.02
	<i>Bacillus fungorum</i>							
<i>Bacillus</i> sp. SW7	17-SMS-01	59.9	[56.2 - 63.4]	53.7	[51.0 - 56.4]	59.7	[56.5 - 62.9]	0.2
	<i>Bacillus albus</i>							
<i>Bacillus</i> sp. SW7	N35-10-2	68.1	[64.3 - 71.8]	52.8	[50.1 - 55.4]	66.6	[63.2 - 69.9]	0.24
	<i>Bacillus</i>							
	<i>wiedmannii</i> FSL							
<i>Bacillus</i> sp. SW7	W8-0169	73	[69.1 - 76.7]	51.7	[49.0 - 54.3]	70.4	[66.9 - 73.6]	0.02
	<i>Bacillus pretiosus</i>							
<i>Bacillus</i> sp. SW7	SAICEU11T	72.5	[68.6 - 76.2]	51.4	[48.7 - 54.0]	69.9	[66.5 - 73.1]	0.12
	<i>Bacillus mobilis</i>							
<i>Bacillus</i> sp. SW7	MCCC 1A05942	66.6	[62.8 - 70.3]	50.1	[47.4 - 52.7]	64.5	[61.2 - 67.8]	0.1
	<i>Streptomyces</i>							
	<i>microflavus</i> JCM							
<i>Bacillus</i> sp. SW7	4496	12.5	[9.8 - 15.7]	46.2	[43.6 - 48.8]	12.9	[10.6 - 15.6]	36.06
<i>Bacillus cereus</i> strain FSL W8-0268	<i>Bacillus</i> sp. SW7	66.6	[62.7 - 70.2]	44.9	[42.3 - 47.4]	62.8	[59.5 - 66.0]	0.14
<i>Bacillus cereus</i> AH676	<i>Bacillus</i> sp. SW7	67.9	[64.1 - 71.6]	44.9	[42.3 - 47.4]	63.9	[60.6 - 67.1]	0.19

<i>Bacillus</i> sp. SW7	<i>Bacillus cereus</i> ATCC 14579	70.6	[66.7 - 74.3]	44.8	[42.3 - 47.4]	66.1	[62.7 - 69.3]	0.11
<i>Bacillus cereus</i> strain AFS099306	<i>Bacillus</i> sp. SW7	71.2	[67.2 - 74.8]	44.7	[42.2 - 47.3]	66.4	[63.0 - 69.7]	0.18
<i>Bacillus</i> sp. SW7	<i>Bacillus luti</i> MCCC 1A00359	67.2	[63.3 - 70.8]	44.6	[42.0 - 47.1]	63.2	[59.9 - 66.4]	0.27
<i>Bacillus</i> sp. RZ2MS9	<i>Bacillus</i> sp. SW7	70.2	[66.3 - 73.9]	44.6	[42.1 - 47.2]	65.7	[62.3 - 68.9]	0.05
<i>Bacillus cereus</i> strain ET31	<i>Bacillus</i> sp. SW7	64.1	[60.3 - 67.7]	44.6	[42.1 - 47.2]	60.7	[57.4 - 63.9]	0.27
<i>Bacillus</i> sp. SW7	<i>Bacillus</i> <i>thuringiensis</i> ATCC 10792	61	[57.3 - 64.6]	44.3	[41.8 - 46.9]	58.1	[54.9 - 61.2]	0.35
<i>Bacillus cereus</i> strain FSL K6- 0043	<i>Bacillus</i> sp. SW7	66.8	[62.9 - 70.4]	44.2	[41.7 - 46.8]	62.8	[59.4 - 66.0]	0.25
<i>Bacillus</i> sp. SW7	<i>Bacillus toyonensis</i> NCIMB 14858	66	[62.2 - 69.7]	42.8	[40.2 - 45.3]	61.6	[58.3 - 64.8]	0.38
<i>Bacillus cereus</i> -Rock4-2	<i>Bacillus</i> sp. SW7	61.3	[57.6 - 64.9]	42.5	[40.0 - 45.1]	57.7	[54.5 - 60.9]	0.19
<i>Bacillus cereus</i> Rock3-29	<i>Bacillus</i> sp. SW7	60.5	[56.8 - 64.1]	42.5	[40.0 - 45.0]	57	[53.9 - 60.2]	0.24
<i>Bacillus cereus</i> strain FSL H8- 0488	<i>Bacillus</i> sp. SW7	61.2	[57.5 - 64.8]	42.5	[40.0 - 45.1]	57.6	[54.4 - 60.8]	0.24
<i>Bacillus</i> sp. SW7	<i>Bacillus</i> <i>nitratreducens</i> 4049	62.5	[58.8 - 66.1]	39.8	[37.3 - 42.3]	57.6	[54.4 - 60.8]	0.13
<i>Bacillus</i> sp. SW7	<i>Bacillus</i> <i>proteolyticus</i> MCCC 1A00365	57.9	[54.3 - 61.4]	39.5	[37.0 - 42.1]	53.9	[50.8 - 57.0]	0.03
<i>Bacillus</i> sp. SW7	<i>Bacillus</i> <i>weihenstephanensis</i> is NBRC 101238	60.4	[56.8 - 64.0]	38.2	[35.7 - 40.7]	55.4	[52.3 - 58.5]	0.03
<i>Bacillus</i> sp. SW7	<i>Bacillus</i> <i>paramycoides</i> NH24A2	55	[51.5 - 58.5]	37.1	[34.6 - 39.6]	50.8	[47.7 - 53.8]	0.02
<i>Bacillus</i> sp. SW7	<i>Bacillus arachidis</i> - SY8	28.3	[24.9 - 31.9]	26.7	[24.3 - 29.2]	26.8	[23.9 - 29.9]	0.16

<i>Bacillus</i> sp. SW7	<i>Bacillus</i> <i>paralicheniformis</i> KJ-16	12.6	[9.9 - 15.9]	21.8	[19.6 - 24.3]	13	[10.7 - 15.8]	10.59
<i>Bacillus</i> sp. SW7	<i>Bacillus</i> <i>licheniformis</i> ATCC 14580	12.6	[10.0 - 15.9]	21.4	[19.1 - 23.8]	13	[10.7 - 15.8]	11.02
<i>Bacillus</i> sp. SW7	<i>Neobacillus</i> <i>ginsengisoli</i> DSM 27594	12.6	[10.0 - 15.9]	21.1	[18.8 - 23.5]	13	[10.7 - 15.8]	2.91
<i>Bacillus</i> sp. SW7	<i>Bacillus</i> <i>weihaiensis</i> Alg07	12.7	[10.0 - 16.0]	20.9	[18.7 - 23.3]	13.1	[10.8 - 15.9]	1.3
<i>Bacillus</i> sp. SW7	<i>Bacillus</i> <i>wudalianchiensis</i> FJAT-27215	12.6	[10.0 - 15.9]	20.5	[18.3 - 22.9]	13	[10.7 - 15.8]	6.01
<i>Bacillus</i> sp. SW7	<i>Priestia</i> <i>megaterium</i> ATCC 14581	12.8	[10.1 - 16.1]	20.2	[18.0 - 22.6]	13.2	[10.9 - 16.0]	2.65
<i>Bacillus</i> sp. SW7	<i>Robertmurraya</i> <i>yapensis</i> XXST-01	12.7	[10.0 - 16.0]	20.1	[17.9 - 22.5]	13.1	[10.8 - 15.8]	2.97
<i>Bacillus-megaterium</i> -QM-B1551	<i>Bacillus</i> sp. SW7	12.9	[10.2 - 16.2]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	3.08
<i>Bacillus</i> sp. SW7	<i>Cytobacillus</i> <i>oceanisediminis</i> CGMCC 1.10115	12.7	[10.0 - 15.9]	20	[17.8 - 22.4]	13	[10.7 - 15.8]	5.7
<i>Bacillus</i> sp. SW7	<i>Bacillus</i> <i>pinisoli</i> GXH0341T	12.7	[10.0 - 16.0]	19.9	[17.7 - 22.3]	13.1	[10.8 - 15.9]	1.78
<i>Bacillus</i> sp. SW7	<i>Priestia</i> <i>veravalensis</i> DSM28242T	12.8	[10.1 - 16.1]	19.8	[17.6 - 22.2]	13.2	[10.9 - 16.0]	2.52
<i>Bacillus</i> sp. SW7	<i>Priestia</i> <i>aryabhatai</i> JCM 13839	12.8	[10.1 - 16.1]	19.8	[17.6 - 22.2]	13.2	[10.8 - 15.9]	2.8
<i>Bacillus</i> sp. SW7	<i>Priestia flexa</i> NBRC 15715	12.8	[10.1 - 16.1]	19.6	[17.4 - 22.0]	13.2	[10.8 - 15.9]	2.47
<i>Bacillus</i> sp. SW7	<i>Metabacillus</i> <i>iocasae</i> DSM 104297	12.9	[10.2 - 16.2]	19.6	[17.4 - 22.0]	13.2	[10.9 - 16.0]	2.42

<i>Bacillus</i> sp. SW7	<i>Sutcliffeiella halmapala</i> DSM 8723	12.8	[10.1 - 16.1]	19.5	[17.3 - 21.9]	13.2	[10.8 - 16.0]	2.41
<i>Bacillus</i> sp. SW7	<i>Solibacillus merdavius</i> Sa1YVA6	12.6	[10.0 - 15.9]	19.5	[17.3 - 21.9]	13	[10.7 - 15.8]	1.83
<i>Bacillus</i> sp. SW7	<i>Pseudoneobacillus rhizosp.haerae</i> CIP 111885T	12.7	[10.0 - 16.0]	19.4	[17.2 - 21.8]	13.1	[10.8 - 15.8]	1.49
<i>Bacillus aryabhattai</i> strain D5	<i>Bacillus</i> sp. SW7	12.7	[10.0 - 15.9]	19.3	[17.1 - 21.6]	13	[10.7 - 15.8]	1.75
<i>Bacillus</i> sp. SW7	<i>Bacillus suaedaesalsae</i> RD4P76	12.8	[10.1 - 16.0]	18.8	[16.7 - 21.2]	13.1	[10.8 - 15.9]	1.03
<i>Bacillus</i> sp. SW7	<i>Kurthia huakuii</i> LAM0618	12.7	[10.0 - 16.0]	18.6	[16.4 - 20.9]	13.1	[10.7 - 15.8]	4.74
<i>Bacillus</i> sp. SW7	<i>Ornithinibacillus scapharcae</i> TW25	12.7	[10.0 - 15.9]	18.5	[16.4 - 20.9]	13	[10.7 - 15.8]	1.53
<i>Bacillus</i> sp. SW7	<i>Priestia endophytica</i> DSM 13796	12.8	[10.1 - 16.1]	18.2	[16.0 - 20.5]	13.2	[10.8 - 16.0]	1.32
<i>Bacillus</i> sp. SW7	<i>Kurthia huakuii</i> DSM 103359	12.7	[10.0 - 16.0]	17.9	[15.7 - 20.2]	13.1	[10.7 - 15.8]	4.58

Table S3. ANI comparison values along and number of fragments mapped against *Bacillus* sp. SW7 with the closest related *Bacillus* species.

Query	Reference	ANI(%)	Number of fragments mapped	Total number of query fragments
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus</i> sp.RZ2MS9.fna	91.6173	1478	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus anthracis</i> str.A0248.fna	97.189	1549	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus anthracis</i> str. Ames.fna	97.196	1546	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus anthracis</i> strain HYU01.fna	97.2111	1545	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus aryabhatai</i> strain D5.fasta	74.3509	1929	5155
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> AH676.fna	91.6791	1485	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> ATCC 4342.fna	95.3621	1525	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> Q1.fna	95.5874	1508	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> Rock3-29.fna	90.6862	1475	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> -Rock4-2.fna	90.8371	1472	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> strain AFS099306.fasta	91.6633	1447	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> strain ET31.fasta	91.6864	1475	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> strain FSL H8-0488.fasta	90.8954	1435	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> strain FSL K6-0043.fasta	91.587	1472	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> strain FSL W8-0003.fasta	95.76	1480	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> strain FSL W8-0268.fasta	91.8208	1466	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> strain ISSFR-3F.fna	97.3072	1537	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> -strain-ISSFR-23F.fna	97.2927	1524	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus cereus</i> strain ISSFR-9F.fna	97.292	1532	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus-cereus</i> -strain-JEM-2.fna	97.2722	1541	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus-cereus</i> -W-gcontig.fasta	97.2763	1495	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus aryabhatai</i> strain D5.fasta	74.3509	1929	5155
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus</i> sp.ISSFR-25F.fna	97.2133	1241	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus</i> sp.JEM-1.fna	97.3199	1508	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus</i> sp.S1-R1J2-FB.fna	97.2922	1526	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus</i> sp.S1-R2T1-FB.fna	97.3236	1528	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus</i> sp.S1-R4H1-FB.fna	97.3107	1476	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus</i> sp.S1-R5C1-FB.fna	97.3158	1521	1718
<i>Bacillus</i> sp. SW7.fasta	<i>Bacillus</i> sp.S2-R3J1-FB-BA1.fna	97.347	1519	1718

Figure S1. The influence of strain *Bacillus* sp. SW7 on the tomato plant shoot height in comparison with control.

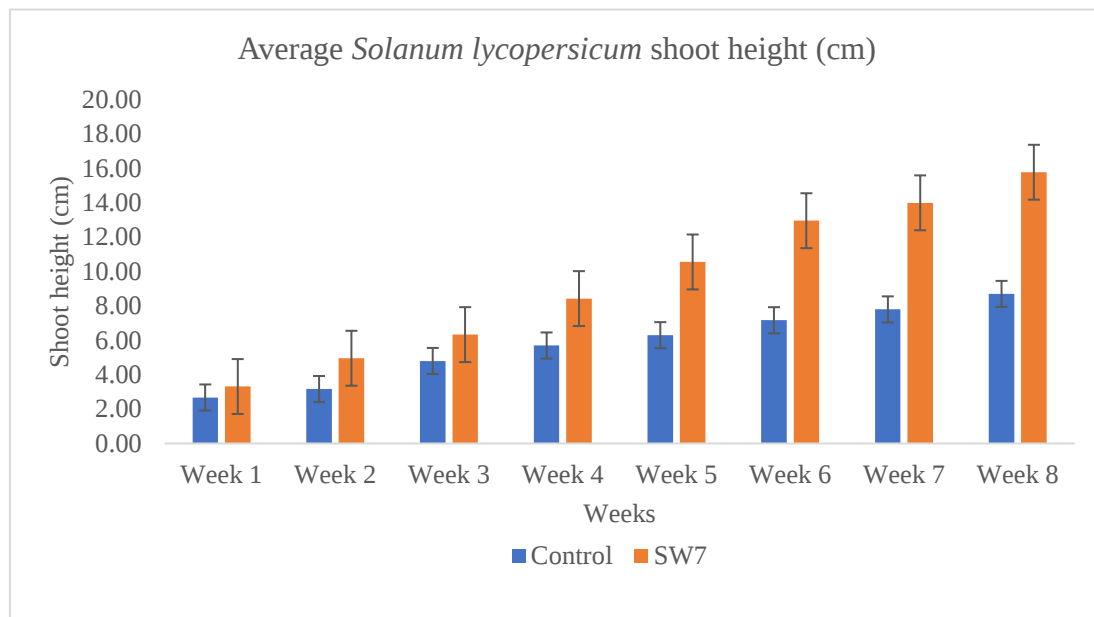


Figure S2. Cluster of genes (COG) assigned to the CDS of isolate *Bacillus* sp. SW7.

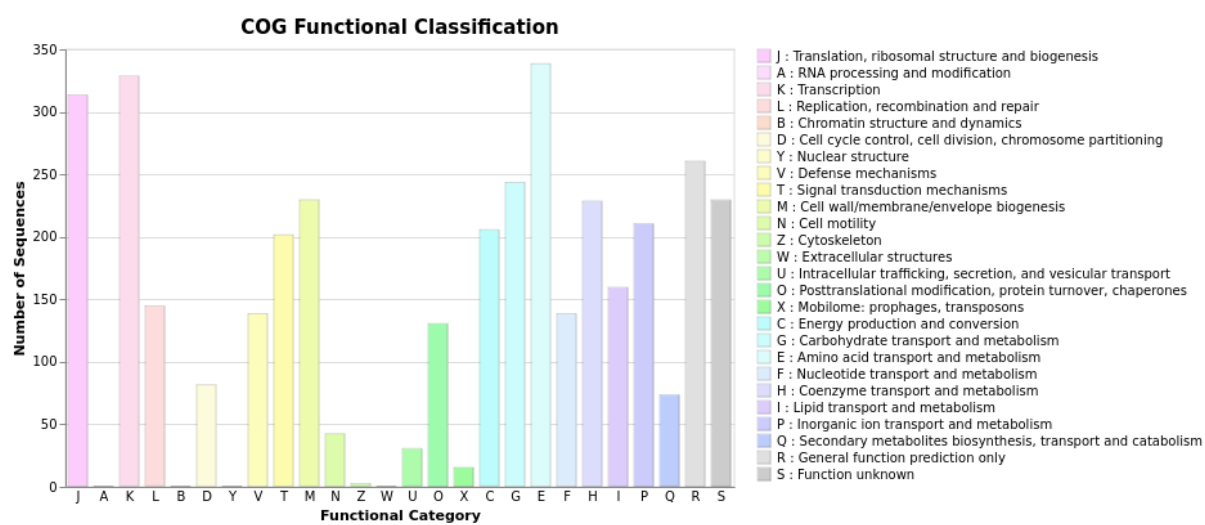


Figure S3. Pairwise alignment using mauve aligner (Darling et al., 2010) of *Bacillus* sp. SW7 A) with *Bacillus* sp. S1_R2T1-FB demonstrating a high ANI value B) with non-pathogenic *Bacillus cereus* Q1, C) with plasmidless *Bacillus anthracis* str. Ames and D) with plant growth-promoting (PGP) *Bacillus* sp. RZ2MS9 (PGPB). The colored block indicates the homologous region between the genomes.

