Table S1. Analysis of variance for the Box-Behnken experimental design of strain F65.

Source	Sum of squares	df	Mean aquare	F-value	p-value
Model	0.8402	9	0.0934	33.29	< 0.0001
X_1-Temperature	0.1145	1	0.1145	40.82	0.0004
X_2-Salinity	0.0000	1	0.0000	0.0026	0.9604
X_3-pH	0.2861	1	0.2861	102.05	0.0001
$X_1 X_2$	0.0006	1	0.0006	0.2071	0.6628
$X_1 X_3$	0.0177	1	0.0177	6.30	0.0404
$X_2 X_3$	0.0006	1	0.0006	0.2097	0.6609
X_1^2	0.0813	1	0.0813	28.99	0.0010
X_2^2	0.0464	1	0.0464	16.54	0.0048
X_3^2	0.2557	1	0.2557	91.18	0.0001
Residual	0.0196	7	0.0028		
Lack of fit	0.0122	3	0.0041	2.20	0.2303
Pure error	0.0074	4	0.0019		
Cor. total	0.8598	16			
R_{pre}^2	0.7590				
R_{adj}^2	0.9478				
C.V. %	14.83				

Note: The Model F-value of 33.29 indicates the statistical significance of the model, with a negligible probability (0.01%) that such a large F-value could occur by chance alone. *P*-values less than 0.0500 indicate significant model terms. The Lack of fit F-value of 2.20 suggests that the Lack of fit is not statistically significant relative to pure error, with a moderate probability (23.03%) that this value could arise due to noise; non-significant lack of fit is desirable as it indicates good model fitting performance. The Predicted R^2 value (0.7590) agrees reasonably well with the adjusted R^2 value (0.9478), differing by less than 0.2.

Table S2. Analysis of variance for the Box-Behnken experimental design of strain G84.

Source	Sum of squares	df	Mean aquare	F-value	p-value
Model	0.0545	9	0.0061	10.85	0.0024
X_1-Temperature	0.0020	1	0.0020	3.66	0.0973
X_2-Salinity	0.0021	1	0.0021	3.77	0.0933
X_3-pH	0.0008	1	0.0008	1.45	0.2684
X_1X_2	0.0009	1	0.0009	1.59	0.2474
X_1X_3	0.0019	1	0.0019	3.41	0.1074
X_2X_3	0.0001	1	0.0001	0.1373	0.7220
X_1^2	0.0352	1	0.0352	63.08	0.0001
X_2^2	0.0014	1	0.0014	2.44	0.1621
X_3^2	0.0070	1	0.0070	12.53	0.0095
Residual	0.0039	7	0.0006		
Lack of fit	0.0002	3	0.0001	0.0816	0.9666
Pure error	0.0037	4	0.0009		
Cor. total	0.0584	16			
R^2_{pre}	0.8398				
R^2_{adj}	0.8471				
C.V. %	4.73				

Note: The Model F-value of 10.85 indicates the statistical significance of the model, with a negligible probability (0.24%) that such a large F-value could occur by chance alone. p-values less than 0.0500 indicate significant model terms. The Lack of fit F-value of 0.08 suggests that the Lack of fit is not statistically significant relative to the pure error, with a moderate probability (96.99%) that this value could arise due to noise, non-significant lack of fit is desirable as it indicates good model fitting performance. The Predicted R^2 value (0.8398) agrees reasonably well with the Adjusted R^2 value (0.8471), differing by less than 0.2.

Table S3. Analysis of variance for the Box-Behnken experimental design of strain G85.

Source	Sum of squares	df	Mean aquare	F-value	*p*-value
Model	0.6340	9	0.0704	27.93	0.0001
X_1-Temperature	0.0997	1	0.0997	39.51	0.0004
X_2-Salinity	0.0046	1	0.0046	1.81	0.2201
X_3-pH	0.2118	1	0.2118	83.96	< 0.0001
X_1X_2	0.0063	1	0.0063	2.51	0.1568
X_1X_3	0.0018	1	0.0018	0.7292	0.4218
X_2X_3	0.0158	1	0.0158	6.24	0.0411
X_1^2	0.0952	1	0.0952	37.75	0.0005
X_2^2	0.0915	1	0.0915	36.27	0.0005
X_3^2	0.0765	1	0.0765	30.31	0.0009
Residual	0.0177	7	0.0025		
Lack of fit	0.0044	3	0.0015	0.4424	0.7356
Pure error	0.0133	4	0.0033		
Cor. total	0.6517	16			
R^2_{pre}	0.8602				
R^2_{adj}	0.9381				
C.V. %	13.30				

Note: The Model F-value of 27.93 indicates the statistical significance of the model, with a negligible probability (0.01%) that such a large F-value could occur by chance alone. P-values less than 0.0500 indicate significant model terms. The Lack of fit F-value of 0.44 suggests that the Lack of fit is not statistically significant relative to pure error, with a moderate probability (73.56%) that this value could arise due to noise; non-significant lack of fit is desirable as it indicates good model fitting performance. The Predicted R^2 value (0.8602) agrees reasonably well with the adjusted R^2 value (0.9381), differing by less than 0.2.

Table S4. Analysis of variance for the Box-Behnken experimental design of strain G86.

Source	Sum of squares	df	Mean aquare	F-value	p-value
Model	0.4173	9	0.0464	22.89	0.0002
X_1-Temperature	0.0551	1	0.0551	27.18	0.0012
X_2-Salinity	0.0709	1	0.0709	35.02	0.0006
X_3-pH	0.0266	1	0.0266	13.15	0.0084
$X_1 X_2$	0.0174	1	0.0174	8.61	0.0219
$X_1 X_3$	0.0007	1	0.0007	0.33	05858
$X_2 X_3$	0.0000	1	0.0000	0.02	0.8901
X_1^2	0.0367	1	0.0367	18.12	0.0038
X_2^2	0.0281	1	0.0281	13.89	0.0074
X_3^2	0.1607	1	0.1607	79.35	<.0001
Residual	0.0142	7	0.0020		
Lack of fit	0.0066	3	0.0022	1.18	0.4231
Pure error	0.0075	4	0.0019		
Cor. total	0.4315	16			
R_{pre}^2	0.7262				
R_{adj}^2	0.9249				
C.V. %	10.70				

Note: The Model F-value of 22.89 indicates the statistical significance of the model, with a negligible probability (0.02%) that such a large F-value could occur by chance alone. P-values less than 0.0500 indicate significant model terms. The Lack of fit F-value of 1.18 suggests that the Lack of fit is not statistically significant relative to pure error, with a moderate probability (42.31%) that this value could arise due to noise; non-significant lack of fit is desirable as it indicates good model fitting performance. The Predicted R^2 value (0.7262) agrees reasonably well with the adjusted R^2 value (0.9249), differing by less than 0.2.

Table S5. Analysis of variance for the Box-Behnken experimental design of strain I109.

Source	Sum of squares	df	Mean aquare	F-value	p-value
Model	0.8962	9	0.0996	39.73	< 0.0001
X_1-Temperature	0.1366	1	0.1366	54.49	0.0002
X_2-Salinity	0.0012	1	0.0012	0.4839	0.5091
X_3-pH	0.4078	1	0.4078	162.70	< 0.0001
X_1X_2	0.0042	1	0.0042	1.67	0.2369
X_1X_3	0.0182	1	0.0182	7.26	00309
X_2X_3	0.0000	1	0.0000	0.00	0.9985
X_1^2	0.1132	1	0.1132	45.16	0.0003
X_2^2	0.0651	1	0.0651	25.98	0.0014
X_3^2	0.1161	1	0.1161	46.31	0.0003
Residual	0.0175	7	0.0025		
Lack of fit	0.0134	3	0.0045	4.35	0.0949
Pure error	0.0041	4	0.0010		
Cor. total	0.9138	16			
R_{pre}^2	0.7579				
R_{adj}^2	0.9561				
C.V. %	14.19				

Note: The Model F-value of 39.73 indicates the statistical significance of the model, with a negligible probability (0.02%) that such a large F-value could occur by chance alone. P-values less than 0.0500 indicate significant model terms. The Lack of fit F-value of 4.35 suggests that the Lack of fit is not statistically significant relative to pure error, with a moderate probability (9.49%) that this value could arise due to noise; non-significant lack of fit is desirable as it indicates good model fitting performance. The Predicted R^2 value (0.7579) agrees reasonably well with the adjusted R^2 value (0.9561), differing by less than 0.2.

Table S6. Classification of bacterial from the rhizospheres of *Zostera marina*.

Isolate	Database			
	NCBI	GenBank accession no.	E-value	SI (%)
A1	*Hydrogenophaga taeniospiralis*	NR_114131.1	0.0	98.65
A2	*Qipengyuania xiapuensis*	NR_181836.1	0.0	99.64
A9	*Sutcliffiella halmapala*	NR_026144.1	0.0	98.18
B16	*Rossellomorea aquimaris*	NR_025241.1	0.0	97.59
B17	*Thalassospira lucentensis*	NR_115011.1	0.0	98.84
B19	*Pseudoalteromonas shioyasakiensis*	NR_125458.1	0.0	99.44
C24	*Altericroceibacterium indicum*	NR_043783.1	0.0	99.93
C26	*Flavobacterium haoranii*	NR_117422.1	0.0	96.64
C27	*Lutibacter maritimus*	NR_116738.1	0.0	97.50
D33	*Pseudodonghicola xiamenensis*	NR_043565.1	0.0	98.30
E41	*Paracoccus homiensis*	MZ276322.1	0.0	99.79
E46	*Euzebyella saccharophila*	NR_117007.1	0.0	99.64
E47	*Mesobacillus boroniphilus*	NR_041275.1	0.0	99.58
F55	*Rheinheimera aquimaris*	NR_044068.1	0.0	99.08
F56	*Pseudalkalibacillus hwajinpoensis*	NR_025264.1	0.0	99.65
F59	*Alteromonas portus*	MG994978.1	0.0	99.65
F61	*Exiguobacterium aquaticum*	NR_109413.1	0.0	99.24
F-63	*Klebsiella oxytoca*	NR_112010.1	0.0	99.58
F65	*Raoultella ornithinolytica*	NR_114736.1	0.0	99.65
F66	*Thioclava pacifica*	KX618934.1	0.0	97.05
F67	*Rhizobium rosettiformans*	MZ276328.1	0.0	99.64
F70	*Loktanella agnita*	NR_043097.1	0.0	98.81
G71	*Enterobacter cloacae subsp.*	KJ847720.1	0.0	99.36
G74	*Alishewanella agri*	NR_116499.1	0.0	98.72
G79	*Shewanella basaltis*	NR_044418.1	0.0	99.65
G81	*Simiduia agarivorans*	NR_074853.1	0.0	99.09
G84	*Pantoea cypripedii*	NR_118394.1	0.0	98.66
G85	*Klebsiella variicola*	NR_025635.1	0.0	99.86
G86	*Novosphingobium profundi*	NR_164872.1	0.0	98.83
H95	*Paenibacillus pocheonensis*	NR_112565.1	0.0	98.46
H99	*Neobacillus bataviensis*	NR_114093.1	0.0	98.99
I101	*Thalassospira profundimaris*	NR_042766.1	0.0	99.27
I104	*Bacillus pumilus*	OQ876682.1	0.0	99.79
I105	*Mycolicibacterium vanbaalenii*	NR_074572.1	0.0	99.15
I106	*Aeromonas enteropelogenes*	NR_116026.1	0.0	99.37

Isolate	Database		E-value	SI (%)
	NCBI	**GenBank accession no.**		
I107	*Microbacterium testaceum*	NR_026163.1	0.0	98.68
I108	*Rhizobium panacihumi*	NR_179174.1	0.0	99.05
I109	*Klebsiella pneumoniae*	OM403526.1	0.0	99.54
J111	*Gallaecimonas pentaromativorans*	NR_116926.1	0.0	99.65
J112	*Thioclava atlantica*	KX618919.1	0.0	95.81
J113	*Marinomonas posidonica*	NR_074719.1	0.0	99.43
J119	*Pseudomonas khazarica*	NR_169334.1	0.0	99.06
J120	*Thioclava dalianensis*	NR_118422.1	0.0	94.54
K123	*Vibrio diazotrophicus*	NR_114217.1	0.0	99.09