

**Table S1.** Morphological description of the 27 putative nitrogen-fixing bacterial (NFB) strains identified from pea embryos.

Strain No.	Size	Shape	Edge	Texture	Color	Raised/Flat	Transparency
S18P01-1	Small	Round	Smooth	Dry	White	Flat	Opaque
S18P01-2	Medium	Round	Smooth	Wet	None	Raised	Transparent
S18P02-1	Small	Round	Smooth	Wet	White	Raised	Translucent
S18P02-2	Medium	Round	Smooth	Wet	Yellowish	Raised	Transparent
S18P02-3	Large	Round	Smooth	Wet	Milky	Raised	Translucent
S18P03-1	Medium	Round	Smooth	Wet	Milky	Raised	Translucent
S18P03-2	Medium	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P04-1	Medium	Round	Smooth	Wet	Light yellow	Raised	Transparent
S18P04-2	Large	Round	Smooth	Wet	Yellow	Raised	Translucent
S18P04-3	Medium	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P05-1	Small	Round	Smooth	Dry	White	Raised	Opaque
S18P05-2	Small	Round	Smooth	Wet	None	Raised	Transparent
S18P06-1	Small	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P06-2	Small	Round	Smooth	Wet	Light yellow	Raised	Opaque
S18P06-3	Small	Round	Smooth	Wet	Light yellow	Raised	Transparent
S18P07-1	Large	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P07-2	Small	Round	Smooth	Wet	White	Raised	Translucent
S18P07-3	Medium	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P08-1	Medium	Round	Smooth	Wet	Light yellow	Raised	Opaque
S18P08-2	Medium	Round	Smooth	Wet	Milky	Raised	Opaque
S18P08-3	Small	Round	Smooth	Wet	White	Raised	Translucent
S18P09	Small	Round	Smooth	Wet	Milky	Raised	Translucent
S18P10	Medium	Round	Smooth	Wet	Light yellow	Raised	Transparent
S18P11-1	Medium	Round	Smooth	Wet	Milky	Raised	Opaque
S18P11-2	Medium	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P12-1	Medium	Round	Smooth	Wet	Milky	Raised	Translucent
S18P12-2	Medium	Round	Smooth	Wet	Milky	Raised	Translucent

**Table S2.** Summary of effective DNA sequencing reads from endophytic bacteria in pea embryos and derived operational taxonomic units (OTUs).

Sample No.	Effective reads	OTUs	Sample No.	Effective reads	OTUs
S18P01.1	25236	690	S18P11.1	34886	301
S18P01.2	36987	362	S18P11.2	36418	283
S18P02.1	33292	271	S18P12.1	31574	311
S18P02.2	33984	334	S18P12.2	33842	310
S18P03.1	36059	360	S18P13.1	31849	406
S18P03.2	33734	379	S18P13.2	35615	418
S18P04.1	33225	433	S18P14.1	36546	514
S18P04.2	34204	483	S18P14.2	33946	488
S18P05.1	32964	332	S18P15.1	35856	399
S18P05.2	35107	341	S18P15.2	36085	423
S18P06.1	31884	358	S18P16.1	32335	338
S18P06.2	23449	323	S18P16.2	34855	446
S18P07.1	33543	460	S18P17.1	36774	374
S18P07.2	33656	604	S18P17.2	37104	354
S18P08.1	34236	367	S18P18.1	35905	604
S18P08.2	36669	335	S18P18.2	27585	452
S18P09.1	35348	453	S18P19.1	35176	297
S18P09.2	35535	329	S18P19.2	34399	395
S18P10.1	35810	343	S18P20.1	34660	342
S18P10.2	34477	278	S18P20.2	35954	387

**Table S3.** Sequencing depths and diversity indexes of endophytic bacterial samples in pea embryos.

Sample No.	Sequencing depth	Diversity index		
		Chao1	Shannon	Simpson
S18P02.1	0.9993	239.39	6.91	0.98
S18P02.2	0.9990	300.41	6.45	0.94
S18P03.1	0.9988	300.93	7.13	0.98
S18P03.2	0.9992	302.72	7.14	0.98
S18P04.1	0.9987	346.90	7.31	0.99
S18P04.2	0.9985	394.01	7.42	0.99
S18P05.1	0.9991	284.61	7.21	0.99
S18P05.2	0.9983	312.30	6.62	0.96
S18P06.1	0.9986	305.09	7.01	0.98
S18P06.2	0.9992	268.86	6.68	0.97
S18P08.1	0.9990	305.40	7.05	0.98
S18P08.2	0.9990	301.90	6.49	0.95
S18P10.1	0.9993	288.42	5.89	0.88
S18P10.2	0.9991	239.01	5.61	0.89
S18P11.1	0.9989	262.95	6.34	0.94
S18P11.2	0.9982	226.26	1.20	0.20
S18P12.1	0.9989	276.76	7.20	0.99
S18P12.2	0.9991	245.85	7.19	0.99