Figure S1 Morphological features of 58 endophytic strains (Red box: SH-1.2-R-15).
| NO. | Strains | Host plant | Parts | Closest sequences by BlastN | Percent Identity | Genbank accession |
|-----|---------|------------|-------|-----------------------------|-----------------|------------------|
| 1   | SH-1.1-R-1 |  | Root | Bacillus sp. (in: Bacteria) strain 12D6 | 97.14% | MN784185 |
| 2   | SH-1.1-R-2 |  | Root | Stenotrophomonas rhizophila strain PgBE58 | 99.72% | MN784186 |
| 3   | SH-1.1-R-3 |  | Root | Bacillus sp. BS98 | 99.90% | MN784187 |
| 4   | SH-1.1-R-4 |  | Root | Streptomyces sp. strain SHP 1-2 | 99.80% | MN784188 |
| 5   | SH-1.1-R-5 |  | Root | Streptomyces sp. strain H9 | 100.00% | MN784189 |
| 6   | SH-1.1-R-6 |  | Root | Streptomyces sp. SR3-82 gene | 99.85% | MN784190 |
| 7   | SH-1.1-R-7 |  | Root | Bacillus thuringiensis strain ZLynn1000-39 | 97.59% | MN784191 |
| 8   | SH-1.1-R-8 |  | Root | Same as 5 | - | - |
| 9   | SH-1.1-R-9 |  | Root | Aerococcus viridans strain NBRC 12219 | 99.78% | MN784192 |
| 10  | SH-1.1-L-1 | Leaf | Leaf | Bacillus cereus strain BC2 | 99.90% | MN784193 |
| 11  | SH-1.1-L-2 | Leaf | Leaf | Bacillus thuringiensis strain GA-A07 | 99.90% | MN784194 |
| 12  | SH-1.1-L-3 |  | Leaf | Same as 58 | - | - |
| 13  | SH-1.1-S-1 | Stem | Stem | Stenotrophomonas sp. Strain FB14 | 99.93% | MN784195 |
| 14  | SH-1.2-R-1 | Root | Root | Streptomyces sp. NK04104 | 96.58% | MN784196 |
| 15  | SH-1.2-R-2 | Root | Root | Streptomyces sp. CdTB01 | 97.13% | MN784197 |
| 16  | SH-1.2-R-3 | Root | Root | Pseudomonas sp. BMS12 | 99.33% | MN784198 |
| 17  | SH-1.2-R-4 | Root | Root | Streptomyces sp. g2b | 99.79% | MN784199 |
| 18  | SH-1.2-R-5 | Root | Root | Streptomyces sp. HF-2 | 96.82% | MN784200 |
| 19  | SH-1.2-R-6 | Root | Root | Pseudomonas sp. Strain IAE244 | 99.92% | MN784201 |
| 20  | SH-1.2-R-7 | Root | Root | Streptomyces sp. LCB 0297 | 97.94% | MN784202 |
| 21  | SH-1.2-R-8 | Root | Root | Streptomyces sp. strain QJSt8 | 97.47% | MN784203 |
| 22  | SH-1.2-R-9 | Root | Root | Same as 7 | - | - |
| 23  | SH-1.2-R-10 | Root | Root | Same as 8 | - | - |
| 24  | SH-1.2-R-11 | Root | Root | Same as 21 | - | - |
| 25  | SH-1.2-R-12 | Root | Root | Bacillus cereus strain ULT15 | 99.60% | MN784204 |
| 26  | SH-1.2-R-13 | Root | Root | Streptomyces sp. TM-74 | 97.51% | MN784205 |
| 27  | SH-1.2-R-14 | Root | Root | Streptomyces fulvissimus strain DSM 40593 | 97.64% | MN784206 |
| 28  | SH-1.2-R-15 | Root | Root | Streptomyces chartreusis strain ISP 5085 | 99.21% | MN784207 |
| 29  | SH-1.2-R-16 | Root | Root | Streptomyces variabilis strain NRRL B-3984 | 97.52% | MN784208 |
| 30  | SH-1.2-R-17 | Root | Root | Streptomyces sp. strain TM-A158 | 99.86% | MN784209 |
| 31  | SH-1.2-R-18 | Root | Root | Bacillus thuringiensis strain GA-A07 chromosome | 99.93% | MN784210 |
| 32  | SH-1.2-R-19 | Root | Root | Same as 58 | - | - |
| 33  | SH-1.2-L-1 | Leaf | Leaf | Micromonospora aurantiaca strain IMB16-201 | 99.92% | MN784211 |
| 34  | SH-3.1-R-1 | Root | Root | Bacillus sp. (in: Bacteria) strain 12D6 | 98.67% | MN784212 |
| 35  | SH-3.1-R-2 | Root | Root | Same as 36 | - | - |
| 36  | SH-3.1-R-3 | Root | Root | Streptomyces sp. GSENDO-0578 | 96.80% | MN784213 |
| 37  | SH-3.1-R-4 | Root | Root | Same as 50 | - | - |
| 38  | SH-3.1-R-5 | Root | Root | Streptomyces sp. 13-22 | 96.92% | MN784214 |
| 39  | SH-3.1-R-6 | Root | Root | Streptomyces sp. MI02-7b | 99.58% | MN784215 |
| 40  | SH-3.1-R-7 | Root | Root | Streptomyces anulatus strain 174456 | 97.06% | MN784216 |
| 41  | SH-3.1-R-8 | Root | Root | Same as 38 | - | - |
| 42  | SH-3.1-R-9 | Root | Root | Streptomyces sp. DSM 40835 clone K12 | 99.70% | MN784217 |
| 43  | SH-3.1-R-10 | Root | Root | Bacillus thuringiensis strain JW-1 | 99.81% | MN784218 |
| 44  | SH-3.1-R-11 | Root | Root | Bacillus thuringiensis strain GA-A07 | 100.00% | MN784219 |

**Table S1 16S rRNA analysis of 58 endophytic strains.**
|   |   |   |   |   |
|---|---|---|---|---|
|   |   |   |   |   |
| **45** | SH-3.1-R-12 | Root | Same as 66 | - | - |
| **46** | SH-3.1-R-13 | Root | *Bacillus* sp. JAS24-2 chromosome | 100.00% | MN784220 |
| **47** | SH-3.1-R-14 | Root | *Streptomyces* sp. strain MUSC11 | 98.46% | MN784221 |
| **48** | SH-3.1-R-15 | Root | Same as 66 | - | - |
| **49** | SH-3.1-R-16 | Root | *Streptomyces* sp. strain BOR09 | 93.69% | MN784222 |
| **50** | SH-3.1-R-17 | Root | *Viridibacillus* sp. strain TM-B117 | 99.69% | MN784223 |
| **51** | SH-3.1-R-19 | Root | *Streptomyces* sp. SR3-82 | 96.17% | MN784224 |
| **52** | SH-3.1-R-20 | Root | *Bacillus thuringiensis* strain GCU1 | 99.79% | MN784225 |
| **53** | SH-3.1-R-21 | Root | *Streptomyces prunicolor* NBRC 13075 | 99.80% | MN784226 |
| **54** | SH-3.1-R-22 | Root | *Streptomyces* sp. strain GDMCC 60254 | 96.51% | MN784227 |
| **55** | SH-3.1-L-1 | Leaf | Same as 59 | - | - |
| **56** | SH-3.1-L-2 | Leaf | Same as 65 | - | - |
| **57** | SH-3.1-L-3 | Leaf | Same as 60 | - | - |
| **58** | SH-3.1-S-1 | Stem | *Streptomyces* sp. strain GDMCC 60254 | 96.92% | MN784228 |
| **59** | SH-3.1-S-2 | Stem | *Bacillus cereus* strain NRRL B-23957 | 98.73% | MN784229 |
| **60** | SH-3.1-S-3 | Stem | *Streptomyces* sp. SM17 | 99.31% | MN784230 |
| **61** | SH-3.1-S-4 | Stem | Same as 65 | - | - |
| **62** | SH-3.2-R-1 | Dendrobium officinale - three years old-2 | Root | *Bacillus* sp. HT-Z74-B2 | 98.55% | MN784231 |
| **63** | SH-3.2-R-2 | Root | Same as 50 | - | - |
| **64** | SH-3.2-R-3 | Root | Same as 60 | - | - |
| **65** | SH-3.2-R-4 | Root | *Bacillus cereus* strain GE16 | 98.78% | MN784232 |
| **66** | SH-3.2-R-5 | Root | *Streptomyces* sp. GKY 867 | 100.00% | MN784233 |
| **67** | SH-3.2-R-6 | Root | *Bacillus thuringiensis* strain QZL38 chromosome | 100.00% | MN784234 |
| **68** | SH-3.2-R-7 | Root | *Streptomyces rochei* 7434AN4 DNA | 99.79% | MN784235 |
| **69** | SH-3.2-R-8 | Root | *Streptomyces* sp. Endophyte N2 chromosome | 100.00% | MN784236 |
| **70** | SH-3.2-R-9 | Root | *Bacillus cereus* strain Sneb2000 | 100.00% | MN784237 |
| **71** | SH-3.2-R-10 | Root | *Brevundimonas* sp. strain 7002-176 | 100.00% | MN784238 |
| **72** | SH-3.2-R-11 | Root | *Corynebacterium* sp. strain ABYHD3-2 | 99.85% | MN784239 |
| **73** | SH-3.2-R-12 | Root | *Streptomyces* sp. TJ-27 | 97.98% | MN784240 |
| **74** | SH-3.2-R-13 | Root | *Bacillus* sp. AR4-2 chromosome | 100.00% | MN784241 |
| **75** | SH-3.2-L-1 | Leaf | *Bacillus thuringiensis* strain GA-A07 | 100.00% | MN784242 |
Figure S2 Scatterplot of 75 cultured endophytic strains screened in triplicate at 25 or 50 µg/mL in Hep3B2.1-7 cell viability assay. Data are shown normalized to percent max response of the high control (Medium only group). Each data point represents the mean and standard deviation of three replicates in 96 wells. The hit cutoff calculated as the average percent inhibition plus three times the standard deviation of the low control wells, is shown as the black line at 11.7%.

Table S2. Strains showed inhibition against Hep3B2.1-7 cell more than the hit cutoff (>11.7%).

| No. | Endophytic strains | %Inhibition | No. | Endophytic strains | %Inhibition |
|-----|--------------------|-------------|-----|--------------------|-------------|
| 2   | SH-1.1-R-2         | 22.14±4.46  | 54  | SH-3.1-R-22        | 35.74±2.31  |
| 4   | SH-1.1-R-4         | 44.24±1.39  | 56  | SH-3.1-L-2         | 18.64±1.16  |
| 16  | SH-1.2-R-3         | 14.67±1.99  | 58  | SH-3.1-S-1         | 14.87±3.17  |
| 18  | SH-1.2-R-5         | 97.24±0.38  | 59  | SH-3.1-S-2         | 47.80±0.99  |
| 19  | SH-1.2-R-6         | 89.27±9.58  | 61  | SH-3.1-S-4         | 12.00±1.38  |
| 24  | SH-1.2-R-11        | 23.97±4.63  | 62  | SH-3.2-R-1         | 33.77±2.22  |
| 27  | SH-1.2-R-14        | 98.44±0.36  | 63  | SH-3.2-R-2         | 41.40±1.71  |
| 28  | SH-1.2-R-15        | 20.30±3.76  | 64  | SH-3.2-R-3         | 31.27±4.01  |
| 31  | SH-1.2-R-18        | 34.47±2.74  | 65  | SH-3.2-R-4         | 12.30±3.31  |
| 33  | SH-1.2-L-1         | 14.47±1.28  | 66  | SH-3.2-R-5         | 47.07±1.86  |
| 42  | SH-3.1-R-9         | 23.14±1.77  | 67  | SH-3.2-R-6         | 62.20±6.76  |
| 43  | SH-3.1-R-10        | 26.37±2.21  | 68  | SH-3.2-R-7         | 98.67±0.62  |
| 44  | SH-3.1-R-11        | 12.17±4.47  | 69  | SH-3.2-R-8         | 89.50±2.46  |
| 47  | SH-3.1-R-14        | 45.34±1.71  | 73  | SH-3.2-R-12        | 49.97±1.41  |
Figure S3 Scatterplot of 75 cultured endophytic strains screened in triplicate at 25 or 50 µg/mL in *S. aureus* inhibitory assay. Data are shown normalized to percent max response of the high control (Bacterial treated with 100 µg/mL Ampicillin). Each data point represents the mean and standard deviation of three replicates in 96 wells. The hit cutoff calculated as the average percent inhibition plus three times the standard deviation of the low control wells, is shown as the black line at 36.2%.

Table S3 Strains showed inhibition against *S. aureus* more than the hit cutoff (>36.2%).

| No. | Endophytic strains | %Inhibition | No. | Endophytic strains | %Inhibition |
|-----|--------------------|-------------|-----|--------------------|-------------|
| 12  | SH-1.1-L-3         | 41.86±3.50  | 37  | SH-3.1-R-4         | 51.50±1.96  |
| 13  | SH-1.1-S-1         | 50.13±5.59  | 44  | SH-3.1-R-11        | 41.81±8.64  |
| 14  | SH-1.2-R-1         | 36.70±6.74  | 48  | SH-3.1-R-15        | 40.45±21.15 |
| 15  | SH-1.2-R-2         | 40.17±5.94  | 50  | SH-3.1-R-17        | 48.24±15.86 |
| 18  | SH-1.2-R-5         | 95.12±3.34  | 52  | SH-3.1-R-20        | 47.21±7.18  |
| 23  | SH-1.2-R-10        | 54.04±7.21  | 56  | SH-3.1-L-2         | 46.37±3.41  |
| 24  | SH-1.2-R-11        | 72.75±6.14  | 57  | SH-3.1-L-3         | 38.59±3.27  |
| 26  | SH-1.2-R-13        | 51.38±3.27  | 68  | SH-3.2-R-7         | 100.00±0.24 |
| 27  | SH-1.2-R-14        | 99.66±0.58  | 69  | SH-3.2-R-8         | 99.32±0.53  |
| 28  | SH-1.2-R-15        | 100.12±0.09 | 70  | SH-3.2-R-9         | 51.01±6.67  |
| 29  | SH-1.2-R-16        | 40.21±5.97  |
Figure S4 Scatterplot of 75 samples screened in triplicate at 25 or 50 µg/mL in *E. coli* inhibitory assay. Data are shown normalized to percent max response of the high control (Bacterial treated with 100 µg/mL Ampicillin). Each data point represents the mean and standard deviation of three replicates in 96 wells. The hit cutoff calculated as the average percent inhibition plus three times the standard deviation of the low control wells, is shown as the black line at 26.4%.

Table S4 Strains showed inhibition against *E. coli* more than the hit cutoff (>26.4%).

| No. | Endophytic strains | %Inhibition    |
|-----|--------------------|---------------|
| 59  | SH-3.1-S-2         | 31.49±6.86    |
Scheme S1 Work-up scheme for the *Streptomyces* sp. SH-1.2-R-15.

*Streptomyces* sp. 1.2-R-15
8 L (shaker), using Medium Bran
7 days (28°C, 200 rpm)

Culture broth → Centrifugation

**Supernatant**
XAD-16 RESIN (4%), mixing 6-8 hours
Filtration
Extraction with MeOH (3 x 500 mL)
evap. in vac.

54.8 g of brown crude extract

**Mycelium**
MeOH (3 x 2 L) evap. in vac.

82.3 g crude extract

MCI (9 x 40 cm, aqueous MeOH: 20%-100%)

**A (49.6 g)**

B (1.51 g) C (0.99 g) D (1.95 g) E (3.13 g) F (1.24 g) G (0.57 g) H (0.99 g) I (3.44 g)

Sephadex LH-20 5x110cm, 80% MeOH

**B (1.51 g)**

Bl (1.47 g) B2 (1.74 g)

HPLC
5 (2 mg) 6 (3 mg)

**C (0.99 g)**

D (1.95 g)

Sephadex LH-20 5x110cm, MeOH

**D (1.95 g)**

D1 (120 mg) D2 (206 mg)

HPLC
4 (29 mg)

1 (1 mg) 2 (16 mg)
Figure S5. (+) and (−)-ESI-MS of compound 1.

Figure S6. HRESI-MS spectrum of compound 1.
Figure S7. $^1$H NMR (500 MHz, DMSO-$d_6$) spectrum of compound 1.

Figure S8. $^1$H NMR (500 MHz, CDCl$_3$) spectrum of compound 1.
Figure S9. $^{13}$C NMR (125 MHz, CDCl$_3$) spectrum of compound 1.

Figure S10. $^1$H-$^1$H COSY (500 MHz, CDCl$_3$) spectrum of compound 1.
**Figure S11.** HSQC (500 MHz, CDCl₃) spectrum of compound 1.

**Figure S12.** HMBC (500 MHz, CDCl₃) spectrum of compound 1.
Figure S13. ROESY (500 MHz, CDCl₃) spectrum of compound 1.

Figure S14. (+) and (−)-ESI-MS of compound 2.
Figure S15. HRESI-MS spectrum of compound 2.

Figure S16. $^1$H NMR (500 MHz, DMSO-$d_6$) spectrum of compound 2.
Figure S17. $^1$H NMR (500 MHz, CDCl$_3$) spectrum of compound 2.

Figure S18. $^{13}$C NMR (125 MHz, CDCl$_3$) spectrum of compound 2.
Figure S19. $^1$H-$^1$H COSY (500 MHz, CDCl$_3$) spectrum of compound 2.

Figure S20. HSQC (500 MHz, CDCl$_3$) spectrum of compound 2.
Figure S21. HMBC (500 MHz, CDCl₃) spectrum of compound 2.

Figure S22. ROESY (500 MHz, CDCl₃) spectrum of compound 2.
Figure S23. (+) and (−)-ESI-MS of compound 3.

Figure S24. HRESI-MS spectrum of compound 3.
Figure S25. $^1$H NMR (500 MHz, DMSO-$d_6$) spectrum of compound 3.

Figure S26. $^{13}$C NMR (125 MHz, DMSO-$d_6$) spectrum of compound 3.
Figure S27. $^1$H-$^1$H COSY (500 MHz, DMSO-$d_6$) spectrum of compound 3.

Figure S28. HSQC (500 MHz, DMSO-$d_6$) spectrum of compound 3.
Figure S29. HMBC (500 MHz, DMSO-d$_6$) spectrum of compound 3.

Figure S30. (+) and (−)-ESI-MS of compound 4.
Figure S31. HRESI-MS spectrum of compound 4.

Figure S32. $^1$H NMR (500 MHz, DMSO-$d_6$) spectrum of compound 4.
Figure S33. $^{13}$C NMR (125 MHz, DMSO-$d_6$) spectrum of compound 4.
Figure S34. (+) and (‒)-ESI-MS of compound 5.
Figure S35. HRESI-MS spectrum of compound 5.

Figure S36. $^1$H NMR (500 MHz, CDOD$_3$) spectrum of compound 5.
**Figure S37.** $^{13}$C NMR (125 MHz, CDOD$_3$) spectrum of compound 5.
Figure S38. (+) and (‒)-ESI-MS of compound 6.
Figure S39. HRESI-MS spectrum of compound 6.

Figure S40. $^1$H NMR (500 MHz, CDOD$_3$) spectrum of compound 6.
Figure S41. $^{13}$C NMR (125 MHz, CDOD$_3$) spectrum of compound 6.

Figure S42. (+) and (‒)-ESI-MS of compound 7.
Figure S43. HRESI-MS spectrum of compound 7.

Figure S44. $^1$H NMR (500 MHz, DMSO-$d_6$) spectrum of compound 7.
Figure S45. $^{13}$C NMR (125 MHz, DMSO-$d_6$) spectrum of compound 7.