**Table S1.** PCR reaction system of endophytic bacteria LSR7

| Gene sequence | Reaction System | Amount of reaction |
|---|---|---|
| - | 2×Taq PCR Master Mix (Vazyme) | 25 μL |
| 16S rDNA | 27F (5′ - AGAGTTTGATCCTGGCTCAG -3′) | 1 μL |
| | 1492R (5′ - GGTTACCTTGTTACGACTT -3′) | 1 μL |
| *gyrB* gene | UP1 (5′-GAAGTCATCATGACCGTTCTGCAYGCNGGNGGNAARTTYGA-3′) | 1 μL |
| | UP2r (5′-AGCAGGGTACGGATGTGCGAGCCRTCNACRTCNGCRTCNGTCAT-3′) | 1 μL |
| - | DNA template | 2 μL |
| - | dd $H_2O$ | 21μL |

**Table S2.** PCR reaction procedure of endophytic bacteria LSR7

| Reaction conditions | Reaction time | Number of cycles |
|---|---|---|
| 95°C (Predenaturation) | 3 min | |
| 95°C | 1 min | |
| 58°C | 1 min | 35 |
| 72°C | 1 min 30 s | |
| 72℃(Terminal extension) | 10 min | |
| 4°C | store | |

**Table S3.** qPCR reaction system of endophytic bacteria LSR7

| Reaction System | Amount of reaction |
|---|---|
| 2× Q3 SYBR qPCR Master Mix (Cellagen Technology, San Diego, CA, USA) | 10.0 μL |
| ACT (forward: 5′-CATCGAGCACGGTATTGTCA-3′) | 0.5 μL |
| ACT (reverse: 5′-TCTCGAACATGATTTGGGTC-3′) | 0.5 μL |
| 18S rRNA (forward: 5′-ACGAAGGTTAGGGGATCGAAA-3′) | 0.5 μL |
| 18S rRNA (reverse: 5′-CGAGCGACACATAAGATTGAGG-3′) | 0.5 μL |
| DNA template | 2 μL |
| dd $H_2O$ | 7 μL |

**Table S4**. qPCR reaction system of endophytic bacteria LSR7

| Reaction conditions | Reaction time | Number of cycles |
|---|---|---|
| 95°C (Predenaturation) | 3 min | |
| 95°C | 30 s | |
| 55°C | 30 s | 35 |
| 72°C | 1 min s | |
| 72℃(Terminal extension) | 10 min | |
| 4°C | store | |

**Table S5**. Genome feature of strain LSR7

| **Type** | **Number** | **Total_len** | **Average_len** | **Percentage of genome (%)** |
|---|---|---|---|---|
| Gene | 3,908 | 3,517,808 | 900 | 90.01 |
| CDS | 3,711 | 34,575,554 | 932 | 88.47 |
| tRNA | 86 | 6,665 | 78 | 0.17 |
| 23S rRNA | 9 | 26,334 | 2,926 | 0.67 |
| 16S rRNA | 9 | 13,923 | 1,547 | 0.36 |
| 5S rRNA | 9 | 999 | 111 | 0.03 |
| tm RNA | 1 | 360 | 360 | 0.01 |

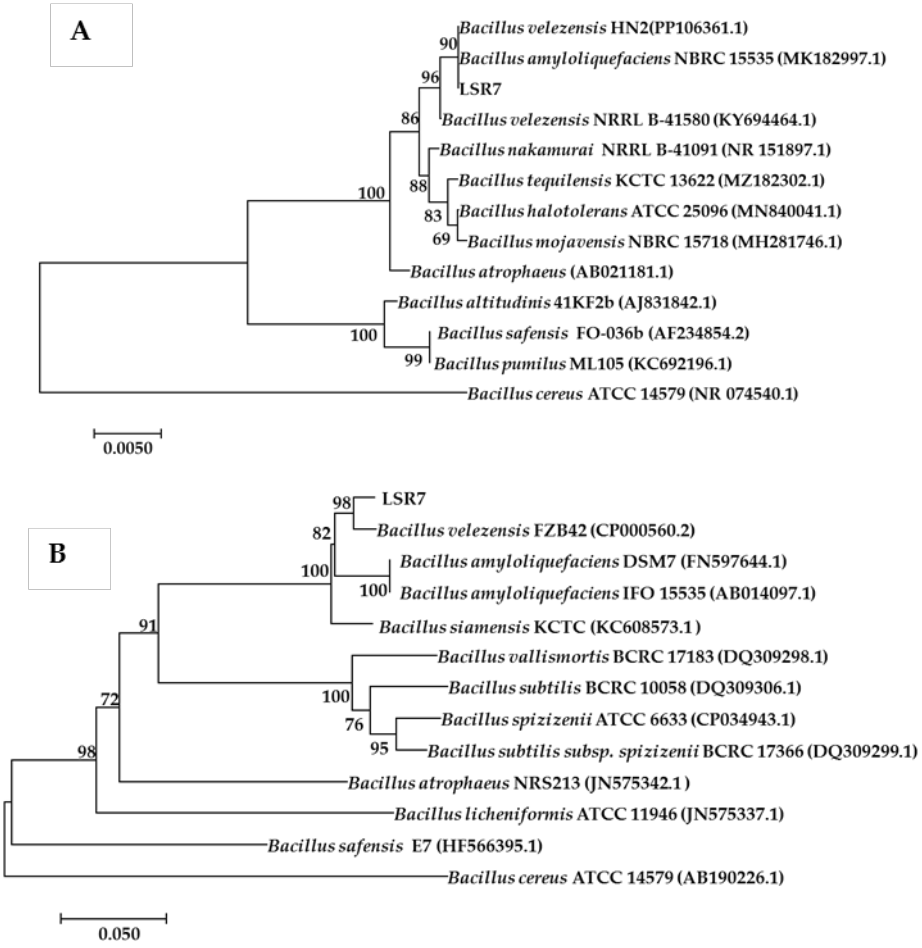



**Figure S1.** Phylogenetic trees based on the 16S rDNA sequence (A) and *gyrB* sequence (B) of LSR7 and their homologous sequences. Phylogenetic trees were constructed by the Neighbor-joining method of MEGA 7.0 with bootstrap values based on 1000 replications. *B. cereus* ATCC 14579 was chosen as the out-group. Gene bank accession numbers of bacterial strains are shown in parentheses. The scale bar represents the number of substitutions per base position.

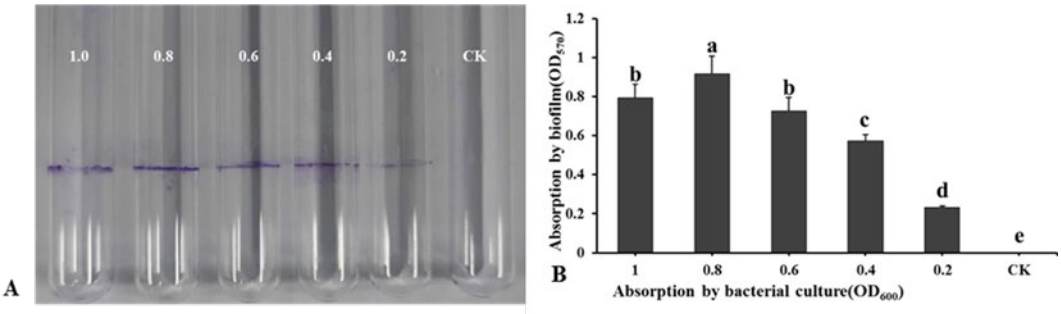



**Figure S2.** Biofilm formation. **(A)** Biofilms developing on glass tubes were stained with 0.1% crystal violet. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article). **(B)** The mean amount of biofilm produced by different concentrations culture ($OD_{600}$ = 0.2, 0.4, 0.6, 0.8, 1.0). Error bars represent the standard error of the average value, and the letter denotes significant differences at $p < 0.05$.

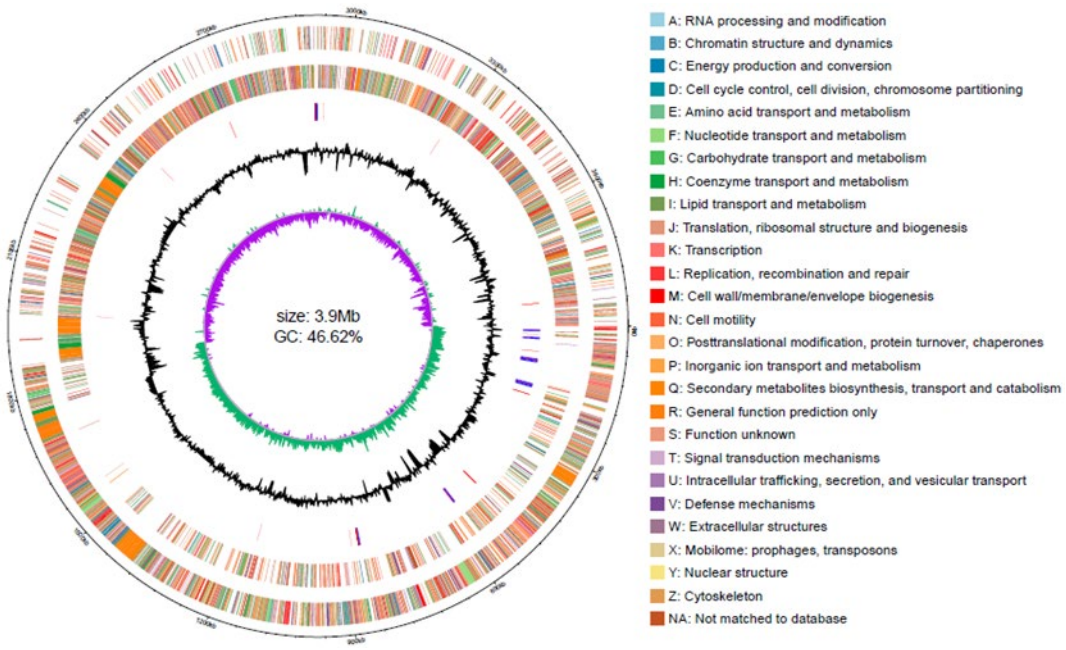



**Figure S3.** Circular map of strain LSR7 genome

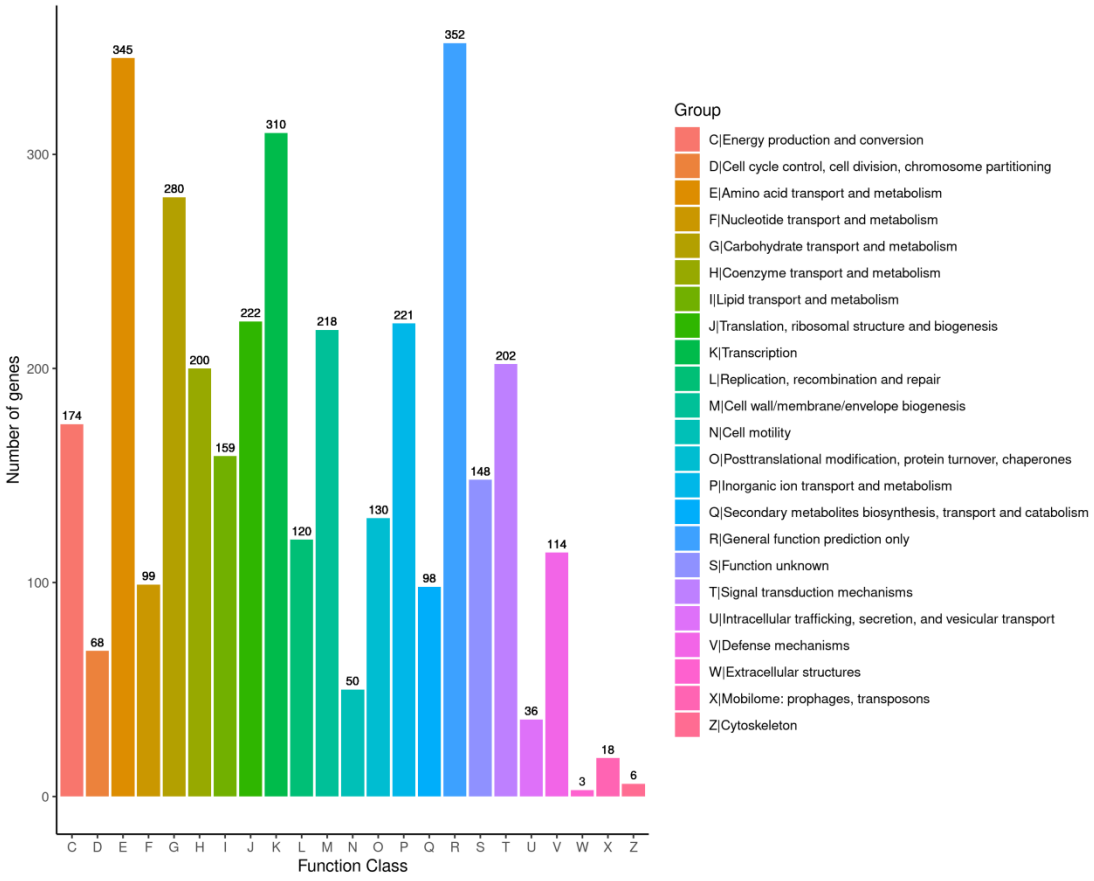



**Figure S4.** COG annotation of the strain LSR7 genome

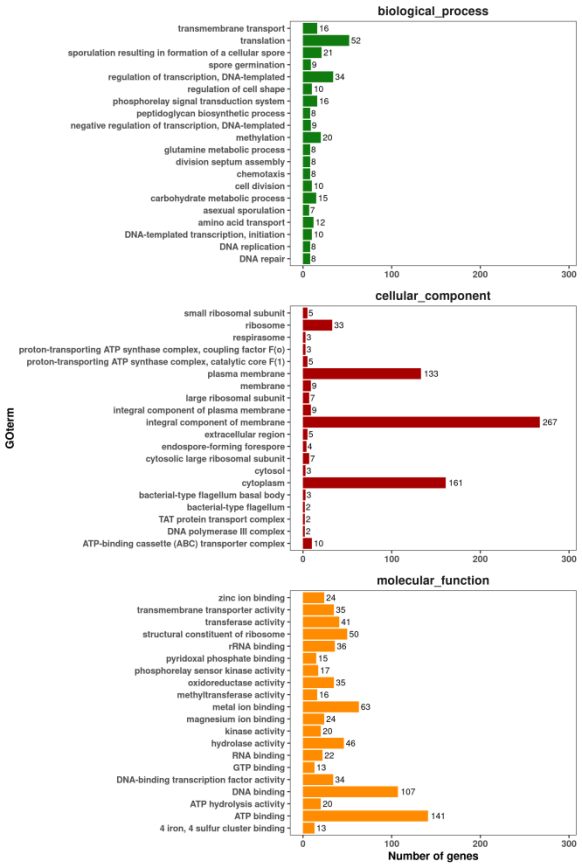



**Figure S5.** GO annotation of the strain LSR7 genome

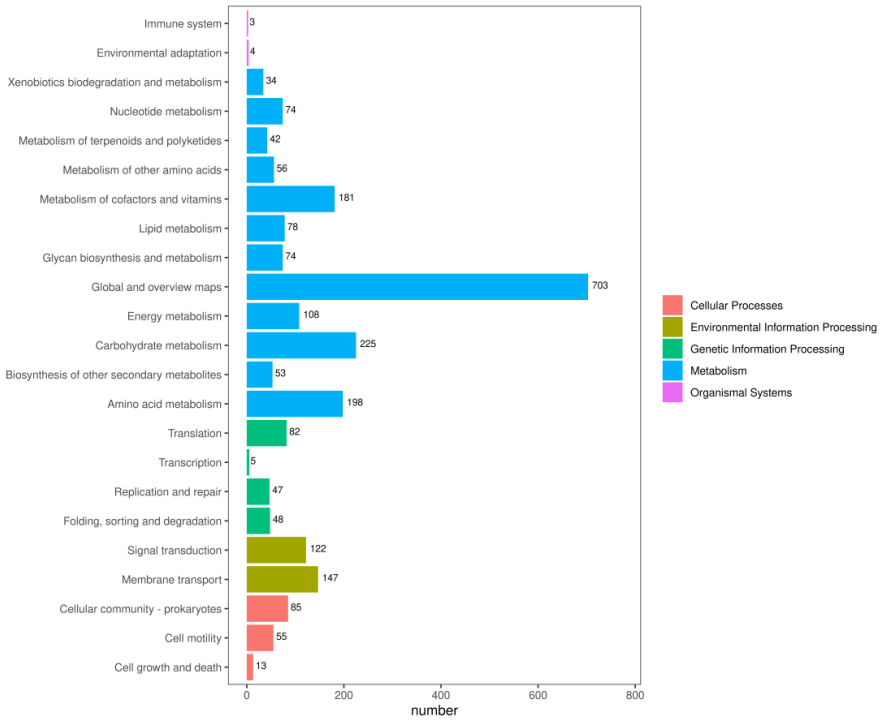



**Figure S6.** KEGG passageway annotation of the strain LSR7 genome

| Region | Type | From | To | Most similar known cluster | | Similarity |
|---|---|---|---|---|---|---|
| Region 1.1 | NRPS | 304,769 | 370,176 | surfactin | NRP:Lipopeptide | 82% |
| Region 1.2 | thiopeptide , LAP | 571,106 | 600,219 | kijanimicin | Polyketide | 4% |
| Region 1.3 | RRE-containing , LAP | 686,677 | 709,854 | plantazolicin | RiPP:LAP | 91% |
| Region 1.4 | PKS-like | 921,711 | 962,955 | butirosin A/butirosin B | Saccharide | 7% |
| Region 1.5 | terpene | 1,044,996 | 1,065,736 | | | |
| Region 1.6 | transAT-PKS | 1,370,516 | 1,458,725 | macrolactin H | Polyketide | 100% |
| Region 1.7 | transAT-PKS , T3PKS , NRPS | 1,680,080 | 1,790,203 | bacillaene | Polyketide+NRP | 100% |
| Region 1.8 | NRPS , transAT-PKS , betalactone | 1,852,134 | 1,989,968 | fengycin | NRP | 100% |
| Region 1.9 | terpene | 2,012,534 | 2,034,417 | | | |
| Region 1.10 | T3PKS | 2,105,183 | 2,146,283 | | | |
| Region 1.11 | transAT-PKS | 2,261,793 | 2,367,962 | difficidin | Polyketide | 100% |
| Region 1.12 | NRPS | 2,855,620 | 2,899,573 | bacillothiazol A/bacillothiazol B/bacillothiazol C/bacillothiazol D/bacillothiazol E/bacillothiazol F/bacillothiazol G/bacillothiazol H/bacillothiazol I/bacillothiazol J/bacillothiazol K/bacillothiazol L/bacillothiazol M/bacillothiazol N | NRP | 100% |
| Region 1.13 | NRP-metallophore , NRPS , RiPP-like | 3,000,164 | 3,051,957 | bacillibactin | NRP | 100% |
| Region 1.14 | other | 3,563,166 | 3,604,584 | bacilysin | Other | 100% |

**Figure S7.** Prediction information of BCGs in strain LSR7 genome by antiSMASH online tool (https://antismash.secondarymetabolites.org/).

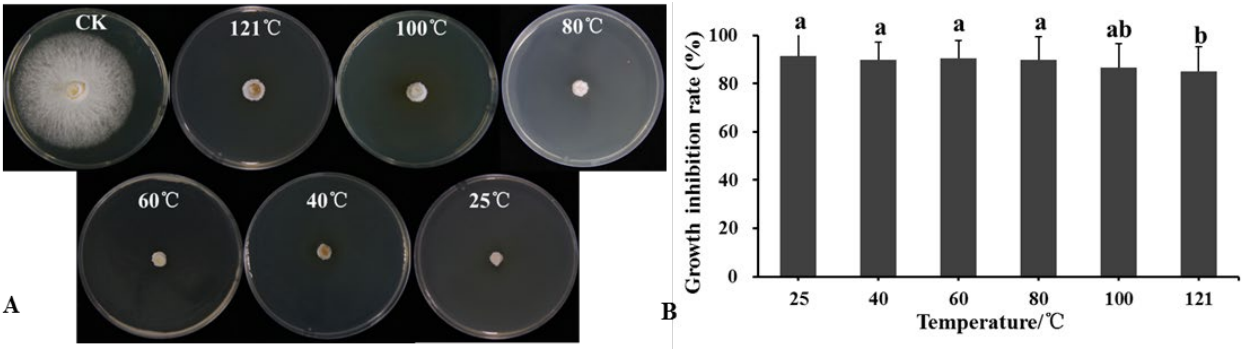



**Figure S8.** (A, B) Effect of temperature on antifungal activity of LSR7. Bars indicate the standard error of the mean. Columns marked with the same letter are not significantly different according to Duncan' s Multiple Range Test at $p<0.05$.