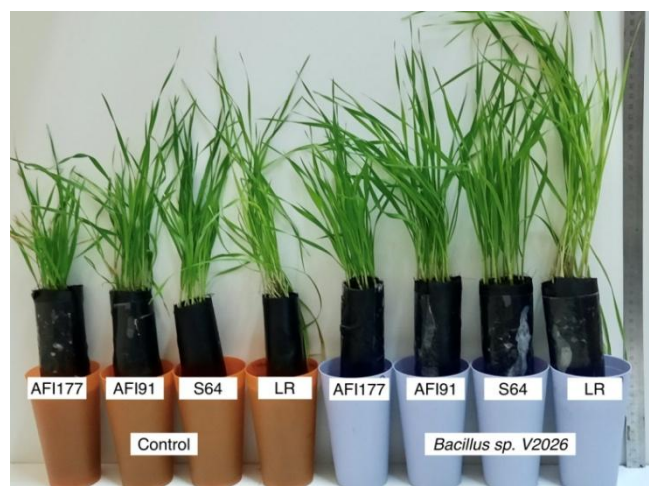
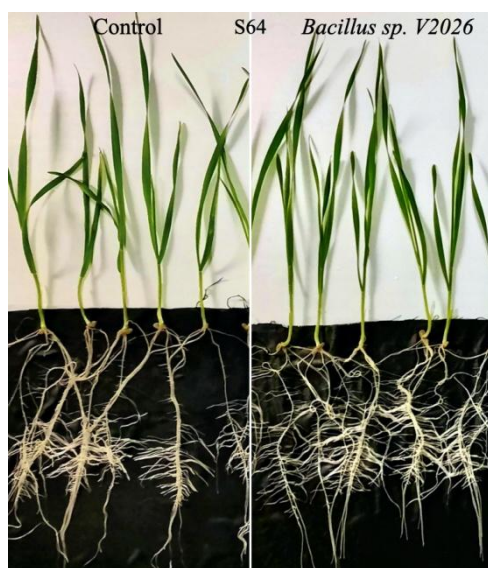


Figure S1. Identification of dominant (288 b.p.) and recessive (414 b.p.) alleles of *Ppd-D1* gene(a), dominant (715+624 b.p.) and recessive (484 b.p.) alleles of *Vrn-A1* gene(b), dominant (1124 b.p.) allele of *Vrn-B1* gene(c), and dominant (1671 b.p.) allele of *Vrn-D1* gene(d), in wheat varieties by PCR with allele-specific markers. Wheat varieties: 1- AFI-177, 2- AFI-91, 3- Leningradskaya rannya, 4- Sonora-64; M-DNA ladder.



(a)



(b)



(c)



(d)



(e)

Figure S2. Effect of inoculation with *Bacillus* sp. V2026 on wheat seedlings of early-maturing genotypes (a): 14-day old wheat seedlings in hydroponic experiments; (b): plants of cv.S64 without treatment (control) and inoculated with *Bacillus* sp. V2026; (c): ultra-early-maturing line AFI91 without treatment (control) and inoculated with *Bacillus* sp. V2026 plants; (d): ultra-early-maturing line AFI177 without treatment (control) and inoculated with *Bacillus* sp. V2026 plants; (e): plants of cv.LR without treatment (control) and inoculated with *Bacillus* sp. V2026.

Table S1. Morphological, physiological and biochemical characteristics of the studied strain

| Characteristics | <i>Bacillus sp. V2026</i> |
|-----------------------------|----------------------------------|
| Gram staining | + |
| Cell shape | Rod |
| Spore-forming | + |
| Morphology of colonies | Round, white, smooth |
| Motile | + |
| Oxidase | + |
| Catalase | - |
| Indole | - |
| H ₂ S | - |
| Growth at 5 ⁰ C | + |
| Growth at 40 ⁰ C | + |
| Growth on 6% NaCl | + |
| Voges-Proskauer | - |
| Utilization of | |
| Glucose | + |
| Sucrose | + |
| xylose | + |
| arabinose | + |
| maltose | + |
| sorbitol | + |
| mannitol | + |

Table S2. Analysis of variance (ANOVA) for genotype and *Bacillus sp.* V2026 effect on various traits four spring wheat genotypes

| Trait | Source of Variation | df | MS | F-value | P-value |
|---------------------------------|----------------------|----|---------|---------|---------|
| Productivity Wheat yield traits | | | | | |
| Plant height | Genotype | 3 | 14090.0 | 1251.2 | 0.001 |
| | Treatment | 1 | 81.9 | 7.27 | 0.01 |
| | Genotype x Treatment | 3 | 36.9 | 3.28 | 0.05 |
| Spike length | Genotype | 3 | 70.39 | 275.81 | 0.001 |
| | Treatment | 1 | 9.03 | 35.39 | 0.001 |
| | Genotype x Treatment | 3 | 0.66 | 2.60 | ns |
| Number of productive tillers | Genotype | 3 | 24.73 | 20.79 | 0.001 |
| | Treatment | 1 | 63.85 | 53.69 | 0.001 |
| | Genotype x Treatment | 3 | 1.62 | 1.361 | ns |
| Number of spikelets/ spike | Genotype | 3 | 215.3 | 239.33 | 0.001 |
| | Treatment | 1 | 51.01 | 56.70 | 0.001 |
| | Genotype x Treatment | 3 | 0.75 | 0.84 | ns |
| Number of grains/ spike | Genotype | 3 | 894.2 | 78.19 | 0.001 |
| | Treatment | 1 | 816.1 | 71.36 | 0.001 |
| | Genotype x Treatment | 3 | 43.8 | 3.83 | 0.05 |
| Grain weight/ spike | Genotype | 3 | 0.108 | 6.20 | 0.001 |
| | Treatment | 1 | 1.621 | 93.36 | 0.001 |
| | Genotype x Treatment | 3 | 0.023 | 1.30 | ns |
| Number of grains/ plant | Genotype | 3 | 56698 | 82.49 | 0.001 |
| | Treatment | 1 | 67896 | 98.79 | 0.001 |
| | Genotype x Treatment | 3 | 10830 | 15.76 | 0.001 |
| Grain yield | Genotype | 3 | 8.39 | 14.08 | 0.001 |
| | Treatment | 1 | 72.92 | 122.35 | 0.001 |
| | Genotype x Treatment | 3 | 1.81 | 3.04 | 0.05 |
| Harvest index | Genotype | 3 | 0.060 | 94.28 | 0.001 |
| | Treatment | 1 | 0.062 | 98.58 | 0.001 |
| | Genotype x Treatment | 3 | 0.010 | 15.82 | 0.001 |
| 1000 grain weight | Genotype | 3 | 1169.4 | 103.73 | 0.001 |
| | Treatment | 1 | 303.5 | 26.92 | 0.001 |
| | Genotype x Treatment | 3 | 34.0 | 3.02 | 0.05 |
| Straw yield | Genotype | 3 | 38.30 | 47.06 | 0.001 |
| | Treatment | 1 | 33.33 | 40.95 | 0.001 |
| | Genotype x Treatment | 3 | 0.30 | 0.37 | ns |
| Chaff to grain ratio | Genotype | 3 | 0.008 | 7.41 | 0.001 |
| | Treatment | 1 | 0.193 | 185.17 | 0.001 |
| | Genotype x Treatment | 3 | 0.006 | 5.97 | 0.001 |
| Onthogenesis | | | | | |
| Seedling-tillering | Genotype | 3 | 9.93 | 33.86 | 0.001 |
| | Treatment | 1 | 25.92 | 88.36 | 0.001 |
| | Genotype x Treatment | 3 | 0.41 | 1.41 | ns |
| Tillering-stem elongation | Genotype | 3 | 109.50 | 177.69 | 0.001 |
| | Treatment | 1 | 60.50 | 98.17 | 0.001 |
| | Genotype x Treatment | 3 | 4.70 | 7.63 | 0.001 |
| Seedling-stem elongation | Genotype | 3 | 69.71 | 129.90 | 0.001 |
| | Treatment | 1 | 165.62 | 308.61 | 0.001 |
| | Genotype x Treatment | 3 | 7.13 | 13.28 | 0.001 |

| | | | | | |
|--|----------------------|---|----------|---------|-------|
| Stem elongation-heading | Genotype | 3 | 715.36 | 725.03 | 0.001 |
| | Treatment | 1 | 3.38 | 3.43 | ns |
| | Genotype x Treatment | 3 | 1.41 | 1.43 | ns |
| Seedling-heading | Genotype | 3 | 1076.4 | 1400.9 | 0.001 |
| | Treatment | 1 | 214.2 | 278.8 | 0.001 |
| | Genotype x Treatment | 3 | 8.2 | 10.7 | 0.001 |
| Heading-maturing | Genotype | 3 | 385.6 | 205.24 | 0.001 |
| | Treatment | 1 | ns | 0.01 | ns |
| | Genotype x Treatment | 3 | ns | 1.49 | ns |
| Seedling-maturing | Genotype | 3 | 242.5 | 104.1 | 0.001 |
| | Treatment | 1 | 210.1 | 90.2 | 0.001 |
| | Genotype x Treatment | 3 | 3.3 | 1.4 | ns |
| Protein and macronutrient/micronutrient content in grain | | | | | |
| N | Genotype | 3 | 0.5027 | 188.8 | 0.001 |
| | Treatment | 1 | 1.1008 | 413.5 | 0.001 |
| | Genotype x Treatment | 3 | 0.0597 | 22.4 | 0.001 |
| P | Genotype | 3 | 0.009126 | 64.42 | 0.001 |
| | Treatment | 1 | 0.005704 | 40.26 | 0.001 |
| | Genotype x Treatment | 3 | 0.001471 | 10.38 | 0.001 |
| K | Genotype | 3 | 0.06110 | 293.30 | 0.001 |
| | Treatment | 1 | 0.06510 | 312.50 | 0.001 |
| | Genotype x Treatment | 3 | 0.00265 | 12.71 | 0.001 |
| Mg | Genotype | 3 | 0.000555 | 41.3 | 0.001 |
| | Treatment | 1 | 0.000081 | 6.0 | 0.05 |
| | Genotype x Treatment | 3 | 0.000377 | 28.1 | 0.001 |
| Fe | Genotype | 3 | 677.08 | 223.37 | 0.001 |
| | Treatment | 1 | 124.22 | 40.98 | 0.001 |
| | Genotype x Treatment | 3 | 50.66 | 16.71 | 0.001 |
| Mn | Genotype | 3 | 18.33 | 9.28 | 0.001 |
| | Treatment | 1 | 45.65 | 23.11 | 0.001 |
| | Genotype x Treatment | 3 | 2.88 | 1.46 | ns |
| Zn | Genotype | 3 | 162.92 | 83.49 | 0.001 |
| | Treatment | 1 | 9.13 | 4.68 | 0.05 |
| | Genotype x Treatment | 3 | 5.97 | 3.06 | ns |
| Protein | Genotype | 3 | 19.64 | 188.8 | 0.001 |
| | Treatment | 1 | 43.00 | 413.5 | 0.001 |
| | Genotype x Treatment | 3 | 2.33 | 22.4 | 0.001 |
| Hormones | | | | | |
| IAA in roots | Genotype | 3 | 618.73 | 52.00 | 0.001 |
| | Treatment | 1 | 532.04 | 44.72 | 0.001 |
| | Genotype x Treatment | 3 | 91.90 | 7.72 | 0.01 |
| IAA in shoots | Genotype | 3 | 115.42 | 25.31 | 0.001 |
| | Treatment | 1 | 1159.26 | 254.15 | 0.001 |
| | Genotype x Treatment | 3 | 73.97 | 16.22 | 0.001 |
| GA in roots | Genotype | 3 | 199.79 | 100.43 | 0.001 |
| | Treatment | 1 | 2398.00 | 1205.42 | 0.001 |
| | Genotype x Treatment | 3 | 173.40 | 87.16 | 0.001 |
| GA in shoots | Genotype | 3 | 84.43 | 136.50 | 0.001 |
| | Treatment | 1 | 133.58 | 215.96 | 0.001 |

| | | | | | |
|--------------|----------------------|---|--------|---------|-------|
| | Genotype x Treatment | 3 | 9.78 | 15.81 | 0.001 |
| tZ in roots | Genotype | 3 | 97.52 | 187.623 | 0.001 |
| | Treatment | 1 | 98.29 | 189.11 | 0.001 |
| | Genotype x Treatment | 3 | 199.95 | 384.69 | 0.001 |
| tZ in shoots | Genotype | 3 | 10.959 | 144.77 | 0.001 |
| | Treatment | 1 | 0.788 | 10.412 | 0.01 |
| | Genotype x Treatment | 3 | 10.344 | 136.64 | 0.001 |

Table S3. Primers used in the study

| Plants primers | | | |
|-------------------|---|----------------------|--------------------|
| Allel | Allele-specific primers (5’-3’) | Fragment length, bp | Reference |
| <i>Ppd-D1a</i> | <i>Ppd-D1AF</i> ACGCCTCCCACTACACTG | 288 | Beales et al.,2007 |
| <i>Ppd-D1b</i> | <i>Ppd-D1/R1</i> GTTGGTTCAAACAGAGAGC | 414 | |
| | <i>Ppd-D1/R2</i> CACTGGTGGTAGCTGAGATT | | |
| <i>Vrn-A1a</i> | VRN1AF GAAAGGAAAAATTCTGCTCG | 715 + 624 | Yan et al., 2004 |
| <i>vrn-A1</i> | VRN1-1R TGCACCTTCCCCCGCCCCAT | 484 | |
| <i>Vrn-B1a</i> | Intr1 ATCATCTTCTCCACCAAGGG | 1124 | Fu et al., 2005 |
| | Intr1/B/R3 CTCATGCCAAAAATTGAAGATGA | | |
| <i>Vrn-D1</i> | Intr1/D/F GTTGTCTGCCTCATCAAATCC | 1671 | Fu et al., 2005 |
| | Intr1/D/R3 GGTCACTGGTGGTCTGTGC | | |
| Bacterial primers | | | |
| Genome fragment | Primers (5’-3’) | Reference | |
| 16S rRNA | 27f AGAGTTTGATCMTGGCTCAG 1525r AAGGAGGTGWTCCARCC | Lane, 1991 | |
| ITS | FGPL132-38 CCGGGTTTCCCCATTCGG FGPS1490-72 TGCGGCTGGATCACCTCCTT | Normand et al., 1992 | |