

Figure S1. Relationship between SOC and organic carbon content of different soil aggregate sizes at 0–60 cm soil layer. Blank: bare land; control: full film-mulched (FM) ridge-furrow tillage typical for maize production in the Loess Plateau using local standard chemical fertilizer doses of 150 kg ha<sup>-1</sup> N, 120 kg ha<sup>-1</sup> P<sub>2</sub>O<sub>5</sub>, and 75 kg ha<sup>-1</sup> K<sub>2</sub>O; humate: FM with combined organic–inorganic fertilizer using active humic acid organic fertilizer (granules) of 1500 kg.ha<sup>-1</sup> (organic matter/dry base matter ≥45.0–55%, free humic acid/dry base matter ≥20.0%); and straw: FM plus 7500 kg ha<sup>-1</sup> air-dried maize straw. Figure a, b, c, d, and e represents the relationship between the total SOC content and the organic carbon content in > 5 mm, 2 < d < 5 mm, 1 < d < 2 mm, 0.25 < d < 1 mm, and d < 0.25 mm soil aggregate size fractions in 0–60 cm soil layer, respectively.

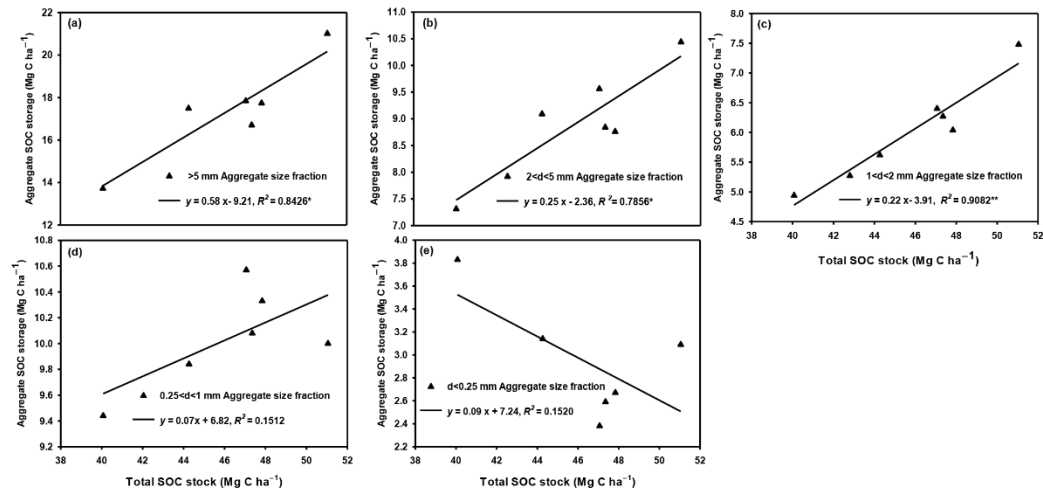


Figure S2. Correlation between total SOC stock and the different fractions of soil organic C at 0–60 cm soil layer. Figures a, b, c, d, and e represents the relationship between the SOC and the SOC stocks in > 5 mm, 2 < d < 5 mm, 1 < d < 2 mm, 0.25 < d < 1 mm, and d < 0.25 mm soil aggregate size fractions in 0–60 cm soil layer, respectively.

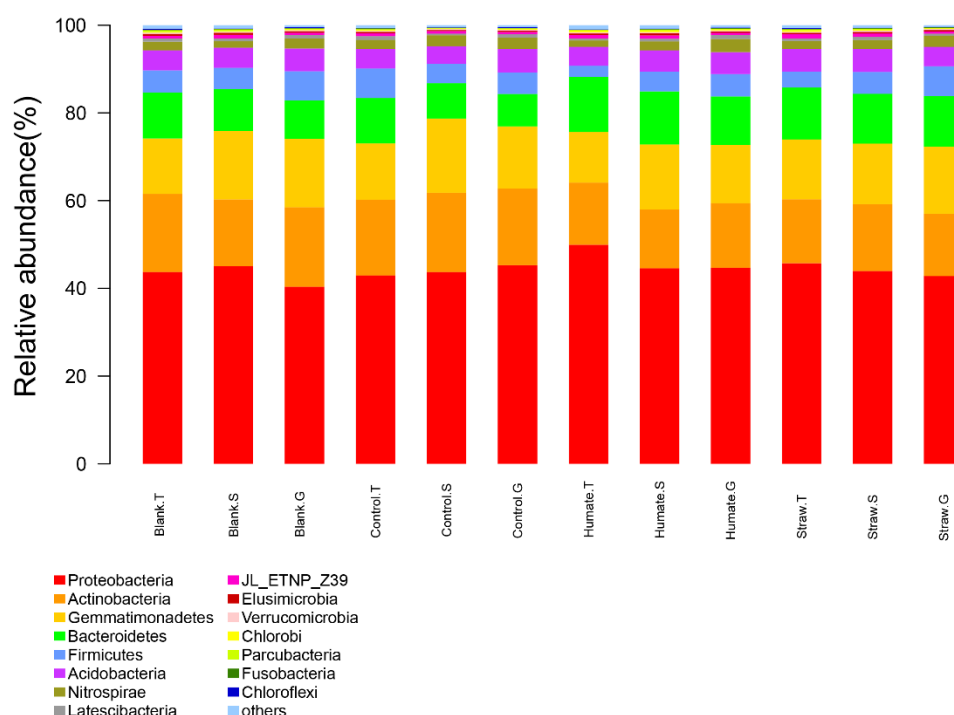


Figure S3. The relative abundance of the top 15 soil bacteria at phylum level under different treatments determined by using High-throughput 16S rRNA sequencing in 2018 (by OE Biotech Co., Ltd., Shanghai, China). Blank: bare land; control: full film-mulched (FM) ridge-furrow tillage typical for maize production in the Loess Plateau using local standard chemical fertilizer doses of 150 kg ha<sup>-1</sup> N, 120 kg ha<sup>-1</sup> P<sub>2</sub>O<sub>5</sub>, and 75 kg ha<sup>-1</sup> K<sub>2</sub>O; humate: FM with combined organic-inorganic fertilizer using active humic acid organic fertilizer (granules) of 1500 kg ha<sup>-1</sup> (organic matter/dry base matter ≥45.0–55%, free humic acid/dry base matter ≥20.0%); and straw: FM plus 7500 kg ha<sup>-1</sup> air-dried maize straw. The letters T, S, and G after the treatment stand for 0–20 cm, 20–40 cm and 40–60 cm soil layer, respectively.

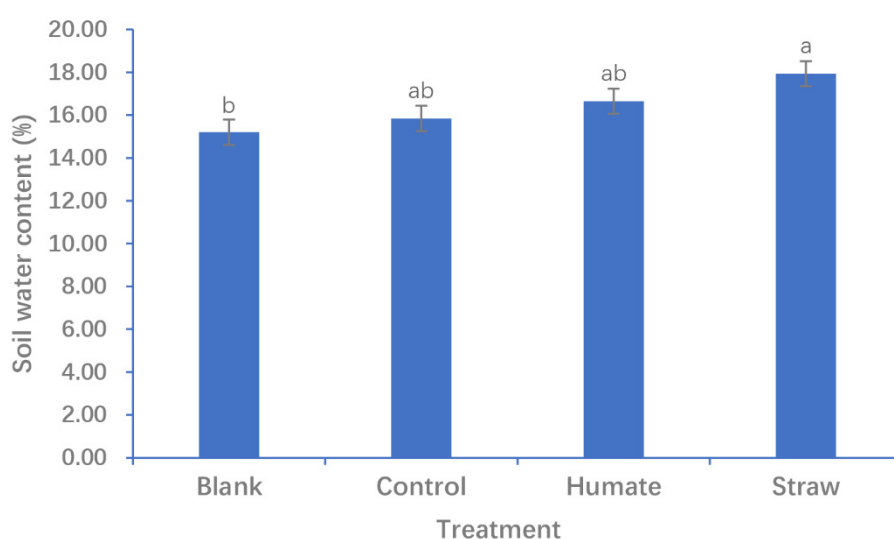


Figure S4. The average soil water content of 0–100 cm soil layer in the period 2016–2018. Different letters (a, ab, b) in the bars indicate significantly different means according to LSD test at  $p < 0.05$  level.

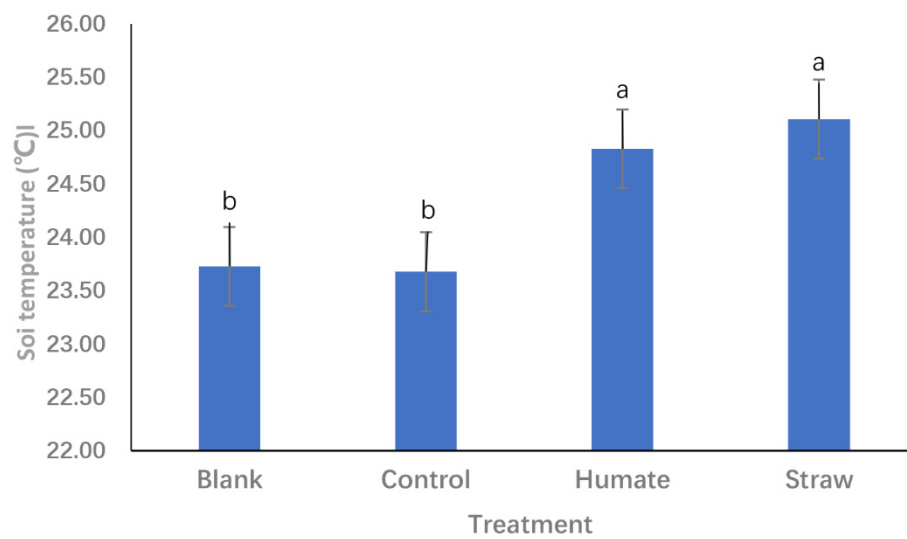


Figure S5. The average soil temperature of the top 5 cm soil layer in the period 2016–2018. Different letters (a, b) in the bars indicate significantly different means according to LSD test at  $p < 0.05$  level. Table S1. The Chao1, Shannon and Simpson indices of alpha diversity of soil bacteria as affected by the treatments determined using High-throughput 16S rDNA sequencing in 2018 (by OE Biotech Co., Ltd., Shanghai, China)

Treatments	chao1	shannon	simpson
Blank	2376.90	9.14	0.99
Control	1745.50	7.07	0.94
Humate	1782.90	7.31	0.95
Straw	1848.70	6.98	0.90

Table S2. The relative abundance of the top 15 soil bacteria at the phylum level under different treatments determined by High-throughput 16S rDNA sequencing in 2018 (by OE Biotech Co., Ltd., Shanghai, China)

Taxonomy	Blank	Control	Humate	Straw
Proteobacteria	43.82%	42.98%	50.08%	45.79%
Firmicutes	4.97%	6.70%	2.45%	3.55%
Actinobacteria	17.87%	17.13%	14.12%	14.56%
Gemmatimonadetes	12.65%	12.93%	11.47%	13.71%
Bacteroidetes	10.39%	10.40%	12.70%	11.86%
Acidobacteri	4.59%	4.43%	4.26%	5.17%
Nitrospirae	1.94%	2.06%	1.43%	1.76%
JL_ETNP_Z39	0.63%	0.66%	0.71%	0.91%
Latescibacteria	0.67%	0.86%	0.46%	0.60%
Elusimicrobia	0.47%	0.33%	0.41%	0.34%

Verrucomicrobia	0.27%	0.19%	0.25%	0.22%
Chlorobi	0.17%	0.27%	0.32%	0.36%
Fusobacteria	0.11%	0.19%	0.05%	0.11%
Parcubacteria	0.40%	0.17%	0.23%	0.22%
Chloroflexi	0.23%	0.11%	0.07%	0.18%
Other	0.25%	0.07%	0.18%	0.18%