

# Supplementary Materials

**Table S1.** Yield, biomass, shoot and grain N content of four maize cultivars in response to nitrate and mixed N

Cultivars	N treatment	Grain yield (kg ha <sup>-1</sup> )	Shoot biomass (g plant <sup>-1</sup> )	Shoot N content (g plant <sup>-1</sup> )	Grain N content (g plant <sup>-1</sup> )
<b>2018</b>					
<b>ZD958</b>	NO <sub>3</sub> <sup>-</sup> -N	9459b	110.7b	3.2b	2.0b
	(NH <sub>4</sub> <sup>+</sup> +NO <sub>3</sub> <sup>-</sup> )-N	10480a	124.9a	3.6a	2.3a
<b>WK702</b>	NO <sub>3</sub> <sup>-</sup> -N	10466b	105.6b	3.2b	2.1b
	(NH <sub>4</sub> <sup>+</sup> +NO <sub>3</sub> <sup>-</sup> )-N	11218a	123.4a	3.8a	2.3a
<b>DH605</b>	NO <sub>3</sub> <sup>-</sup> -N	10409a	112.6a	3.7a	2.5a
	(NH <sub>4</sub> <sup>+</sup> +NO <sub>3</sub> <sup>-</sup> )-N	10117a	104.3a	3.5b	2.2b
<b>LP206</b>	NO <sub>3</sub> <sup>-</sup> -N	10813a	126.8a	3.9a	2.7a
	(NH <sub>4</sub> <sup>+</sup> +NO <sub>3</sub> <sup>-</sup> )-N	10261b	121.6a	3.8a	2.6a
<b>2019</b>					
<b>ZD958</b>	NO <sub>3</sub> <sup>-</sup> -N	10354b	101.9a	3.3b	2.3a
	(NH <sub>4</sub> <sup>+</sup> +NO <sub>3</sub> <sup>-</sup> )-N	11887a	114.2b	3.7a	2.6b
<b>WK702</b>	NO <sub>3</sub> <sup>-</sup> -N	12315b	106.9b	3.4b	2.3a
	(NH <sub>4</sub> <sup>+</sup> +NO <sub>3</sub> <sup>-</sup> )-N	13146a	121.6a	3.8a	2.7b
<b>DH605</b>	NO <sub>3</sub> <sup>-</sup> -N	11337a	117.2a	3.7a	2.6b
	(NH <sub>4</sub> <sup>+</sup> +NO <sub>3</sub> <sup>-</sup> )-N	10551b	112.1a	3.4b	2.2a
<b>LP206</b>	NO <sub>3</sub> <sup>-</sup> -N	11448a	111.1a	3.5a	2.4a
	(NH <sub>4</sub> <sup>+</sup> +NO <sub>3</sub> <sup>-</sup> )-N	10796a	106.9a	3.3a	2.2a
<b>Source of variation</b>					
<b>Year</b>		**	*	NS	NS
<b>N form</b>		*	*	*	*
<b>Cultivar</b>		**	NS	*	*
<b>Year × N form</b>		NS	NS	NS	NS
<b>Year × cultivar</b>		**	**	**	**
<b>N form × cultivar</b>		**	**	**	**
<b>Year × cultivar × N form</b>		NS	NS	NS	NS

supply over two years. Three-way ANOVA followed by an LSD test was performed using R software. Different letters indicate significant differences within each cultivar or year ( $P < 0.05$ ). NS: not significant ( $P > 0.05$ ). \* Significant at  $P < 0.05$ . \*\* Significant at  $P < 0.01$ .

**Figure S1** Boxplots for maize root weight (A), root area (B) and root angle (C) of ZD958 and DH605 in response to nitrate and mixed N supply in 2019. One-way ANOVA followed by an LSD test was performed using R software. NS: not significant ( $P > 0.05$ ). \* Significant at  $P < 0.05$ . \*\* Significant at  $P < 0.01$ .

**Figure S2** Shannon index of (A) rhizospheric bacteria, (B) endophytic bacteria, (C) rhizospheric fungi and (D) endophytic fungi for ZD958 and DH605 under nitrate and mixed N supply. The horizontal bars within boxes represent medians. The tops and bottoms of boxes represent the 75th and 25th percentiles, respectively. The whiskers mark the range of the data. One-way ANOVA followed by an LSD test was performed using R software. NS: not significant ( $P > 0.05$ ). \* Significant at  $P < 0.05$ . \*\* Significant at  $P < 0.01$ .

**Figure S3** Heatmap of correlation analysis between dominant rhizospheric bacterial phyla of ZD958 (A) and DH605 (B) and multiple important phenotypic traits based on Pearson correlation coefficients; heatmap of correlation analysis between dominant rhizospheric fungal phyla of ZD958 (C) and DH605 (D) and multiple important phenotypic traits based on Pearson correlation coefficient. Color values above or below zero indicate positive or negative relationships between microbial phyla and differential metabolites. \* Significant at  $P < 0.05$ . \*\* Significant at  $P < 0.01$ . \*\*\* Significant at  $P < 0.001$ .

**Figure S4** Volcanic plot of differential root metabolite of ZD958 (A) and DH605 (B) under nitrate and mixed N supply.

**Figure S5** Heat map of differential metabolites detected by GC-MS for ZD958 (A) and DH605 (B) under nitrate and mixed N supply.

**Figure S6** Heatmap of correlation analysis between dominant rhizospheric bacterial phyla of ZD958 (A) and DH605 (B) and differential root metabolites based on Pearson correlation coefficients; heatmap of correlation analysis between dominant rhizospheric fungal phyla of ZD958 (C) and DH605 (D) based on Pearson correlation coefficients. Color values above or below zero indicate positive or negative relationships between microbial phyla and differential metabolites. \* Significant at  $P < 0.05$ . \*\* Significant at  $P < 0.01$ . \*\*\* Significant at  $P < 0.001$ .

**Figure S1**

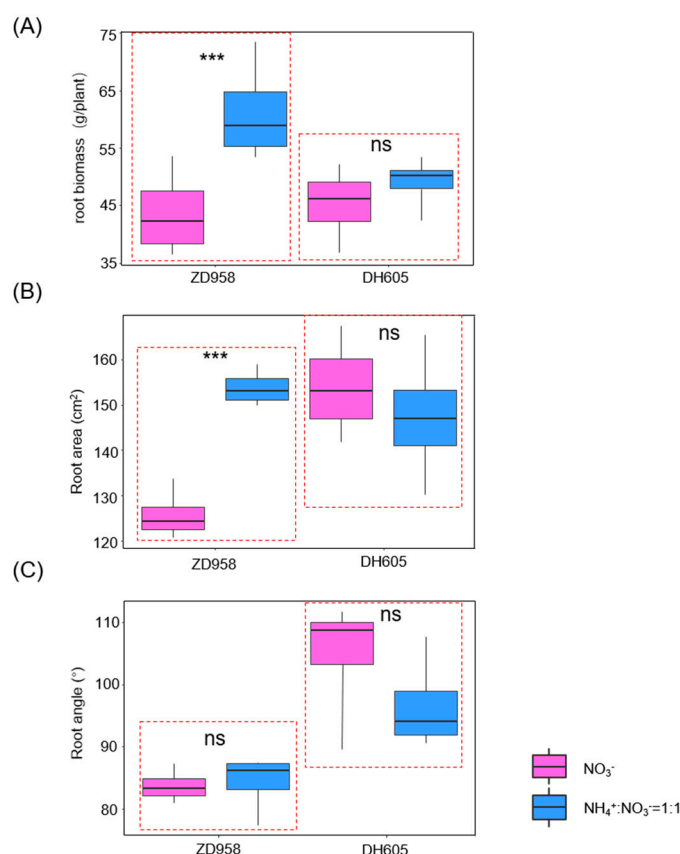


Figure S2

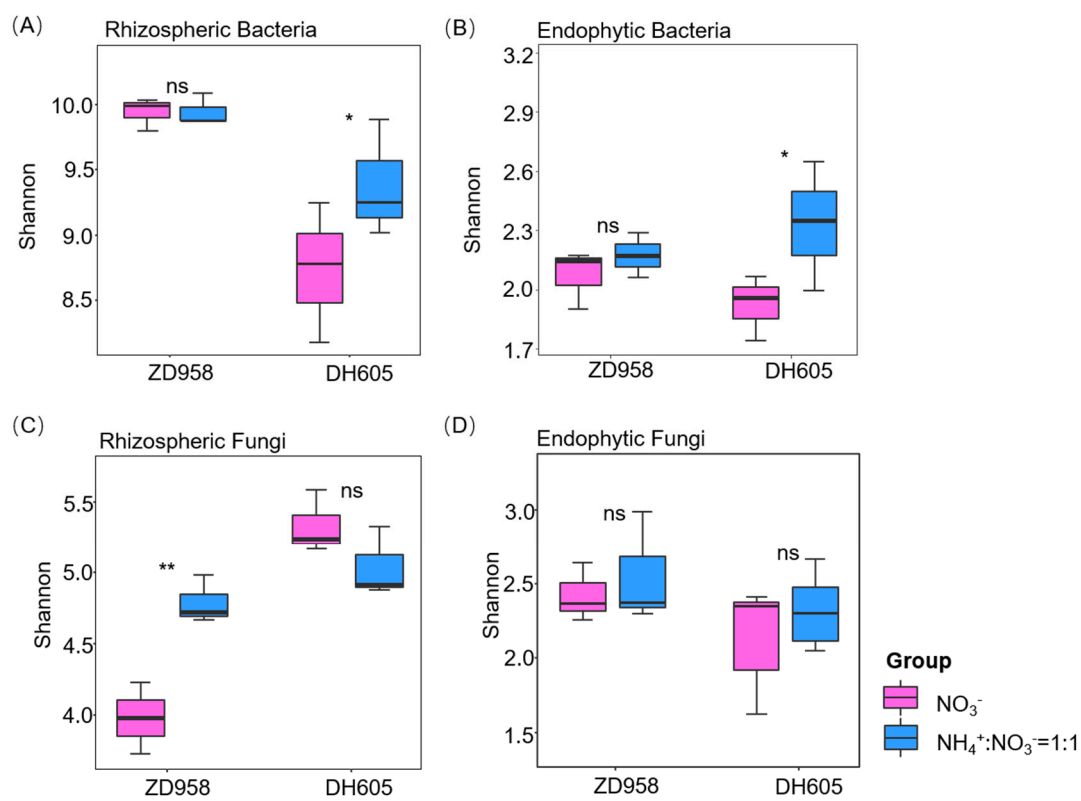
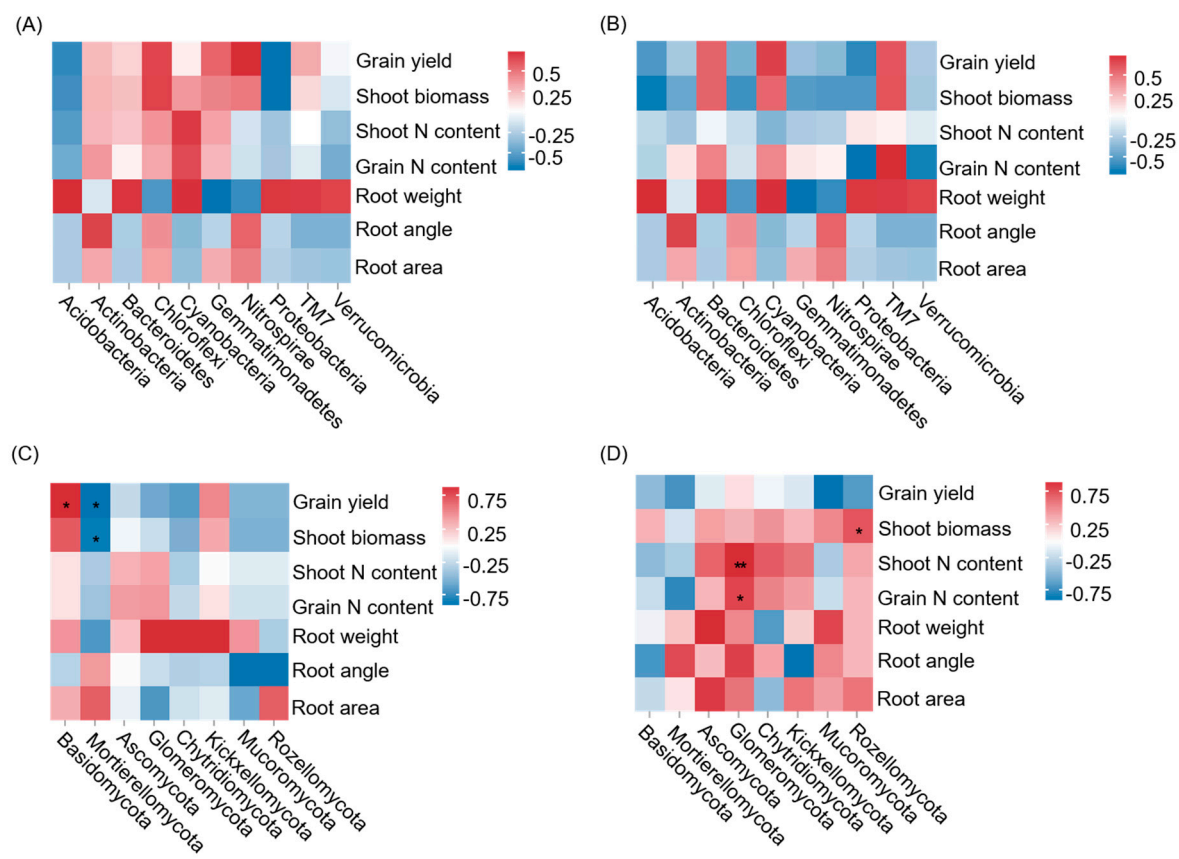
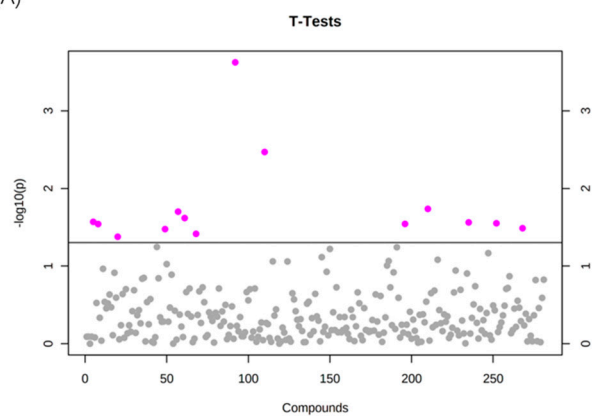


Figure S3

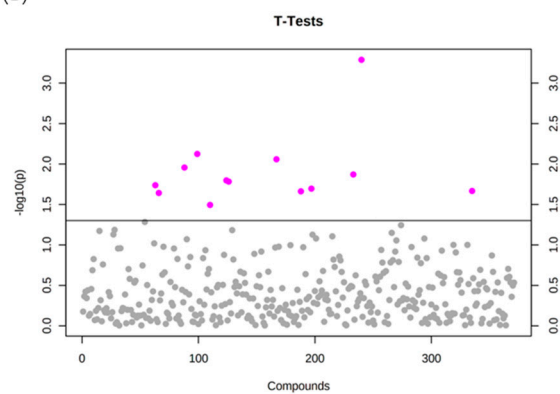


**Figure S4**

(A)

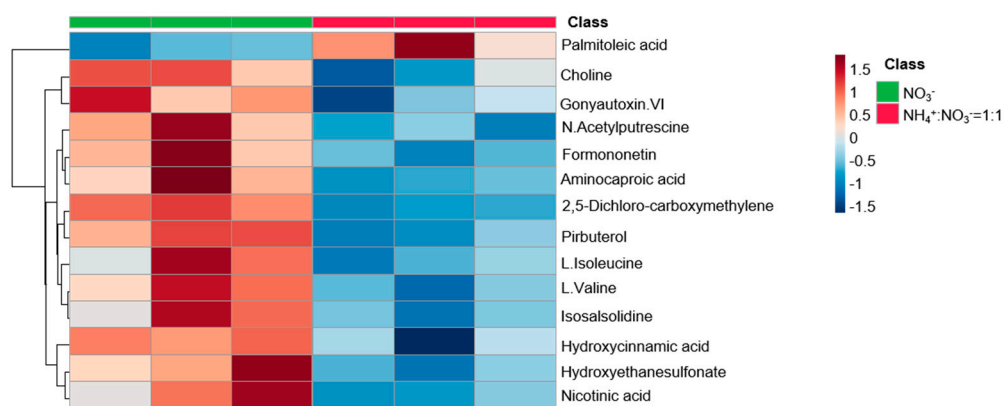


(B)

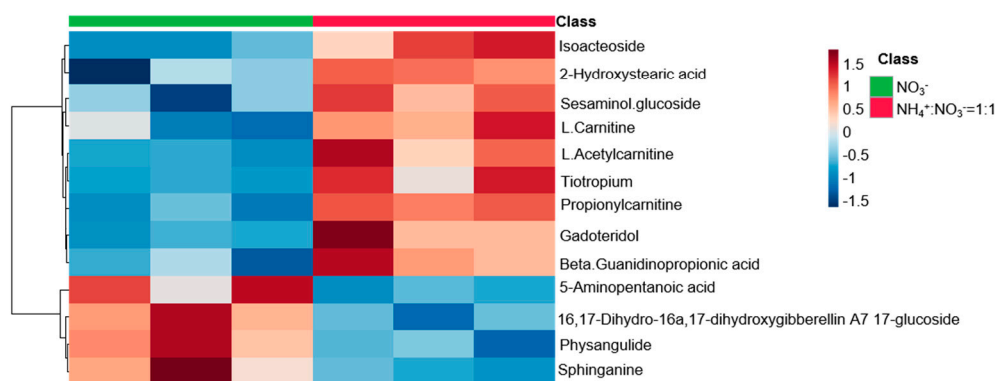


**Figure S5**

(A)



(B)



**Figure S6**

