

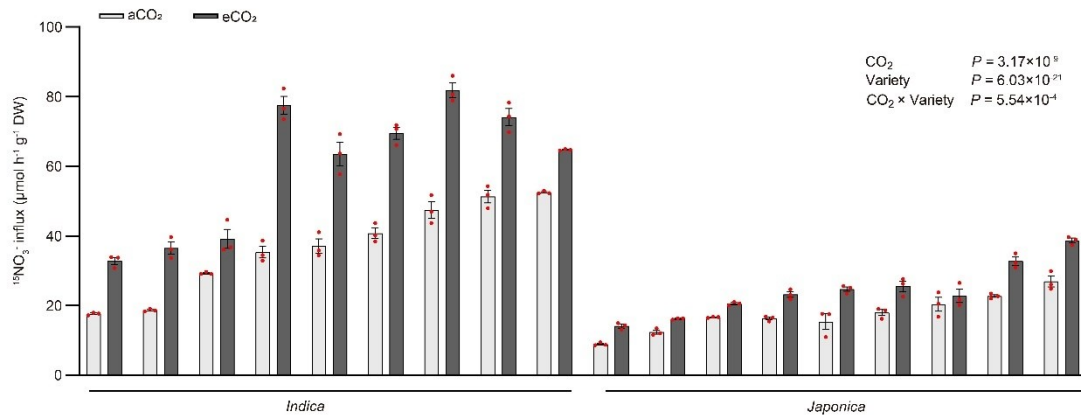
## Supplementary Materials

### Supplementary method

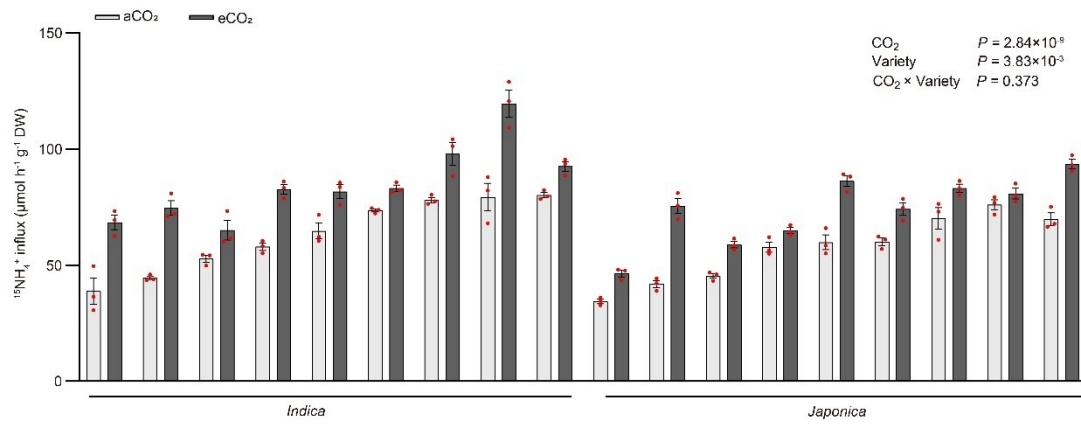
To evaluate genetic variations between *indica* and *japonica* and their responses to eCO<sub>2</sub>, we planted a typical *indica* variety, Yangdao 6 (YD6) and a typical *japonica* variety Zhonghua 11 (ZH11) in the FACE system. The plots for each treatment were sized at 2 m × 2.5 m, with planting spaced at 15 cm × 25 cm intervals. Nitrogen fertilizer, in the form of urea, was applied at a total rate of 225 kg N ha<sup>-1</sup>. This was divided into three applications: 40% at soil tillage, 30% at the tillering stage, and the remaining 30% at the jointing stage. Phosphorus fertilizer, at a rate of 120 kg P<sub>2</sub>O<sub>5</sub> ha<sup>-1</sup>, was applied at soil tillage, while potassium fertilizer, at 160 kg K<sub>2</sub>O ha<sup>-1</sup>, was split equally between the soil tillage and jointing stages. All other agronomic practices were conducted in accordance with local agricultural recommendations. At heading stage, rice flag leaves were collected, immediately frozen and stored at -80°C for subsequent RNA extraction and sequencing (See sampling and methods).

## Supplementary Figures

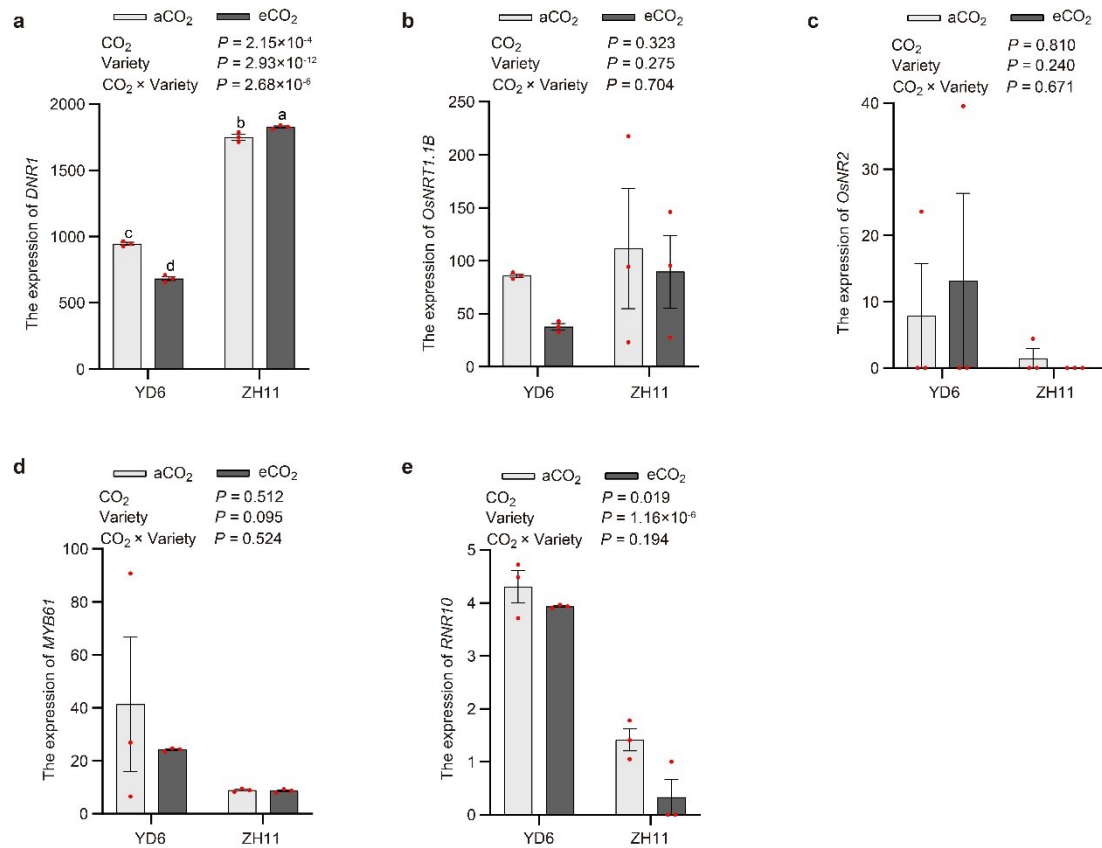
**a**



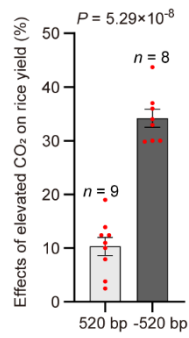
**b**



**Supplementary Fig. 1 | The influx of  $^{15}\text{NO}_3^-$  and  $^{15}\text{NH}_4^+$  absorption in *indica* and *japonica* subspecies under ambient CO<sub>2</sub> and elevated CO<sub>2</sub> conditions. a-b,  $^{15}\text{NO}_3^-$  uptake (a) and  $^{15}\text{NH}_4^+$  uptake (b), in roots of 18 *indica* and *japonica* varieties labeled with 2.5 mM  $^{15}\text{N}$ . DW, dry weight. aCO<sub>2</sub> and eCO<sub>2</sub> indicate ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) condition, respectively. Data are mean  $\pm$  s.e.m. ( $n = 3$  biological replicates).  $P$ -values were generated from two-way ANOVA. Source data are provided as a Source Data file.**

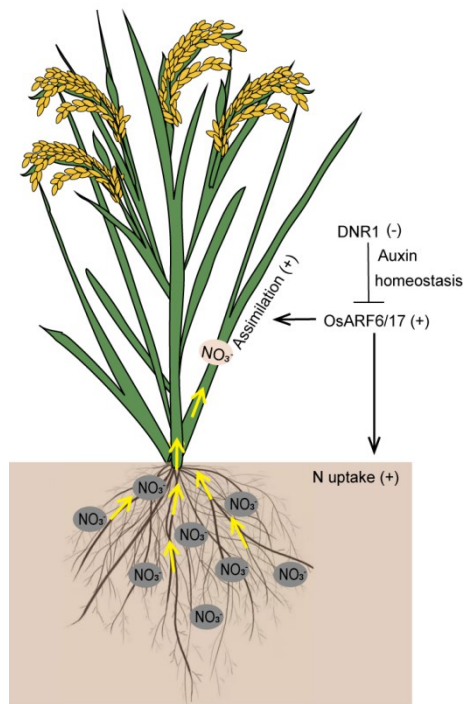


**Supplementary Fig. 2 | The expression levels of *DNR1*, *OsNRT1.1B*, *OsNR2*, *MYB61*, *RNR10* in *indica* variety Yangdao 6 and *japonica* variety Zhonghua 11 under ambient CO<sub>2</sub> and elevated CO<sub>2</sub> conditions. a-e, *DNR1* (a), *OsNRT1.1B* (b), *OsNR2* (c), *MYB61* (d), *RNR10* (e) transcript abundances in flag leaf at heading stage under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions. YD6 and ZH11 indicate *indica* variety Yangdao 6 and *japonica* variety Zhonghua 11, respectively. Data are mean ± s.e.m. ( $n = 3$  biological replicates).  $P$ -values were generated from two-way ANOVA. a, Different letters indicate significant differences among groups ( $P < 0.05$ ). Source data are provided as a Source Data file.**

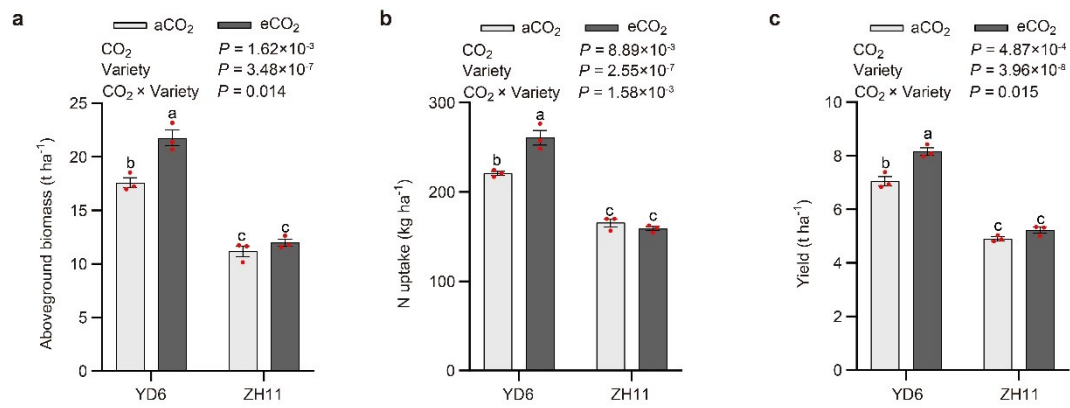


**Supplementary Fig. 3 | Differences in the effect of elevated CO<sub>2</sub> on rice yields between rice varieties carrying the *japonica* *DNRI* allele (520 bp) or *indica* *DNRI* allele (-520 bp) in FACE experiments.** *P*-values were generated from two-sided Student's *t* tests. Source data are provided as a Source Data file.

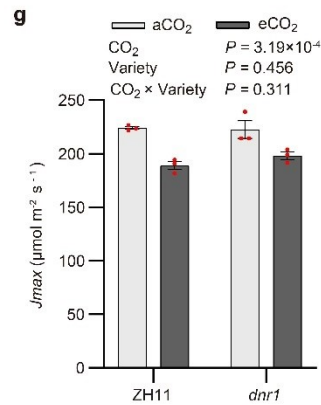
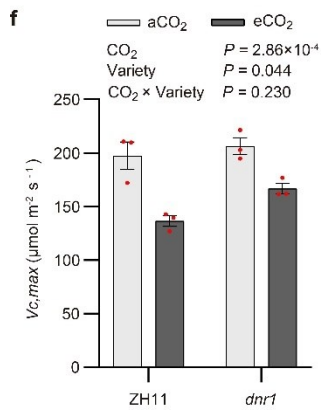
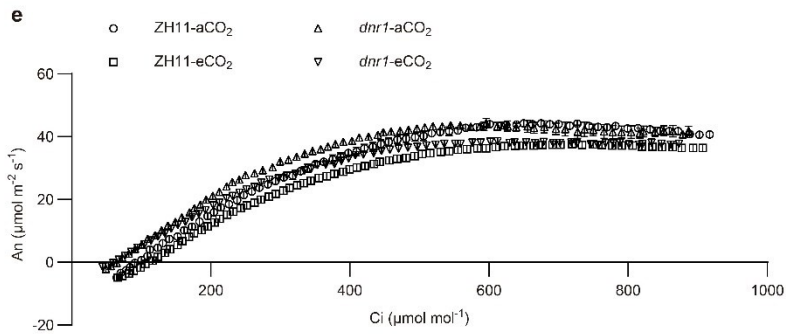
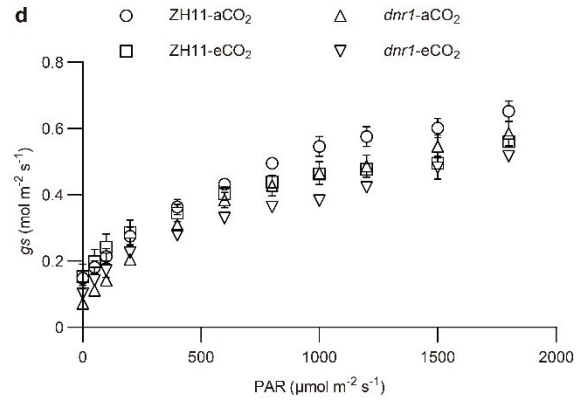
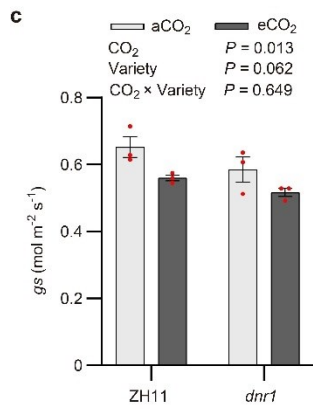
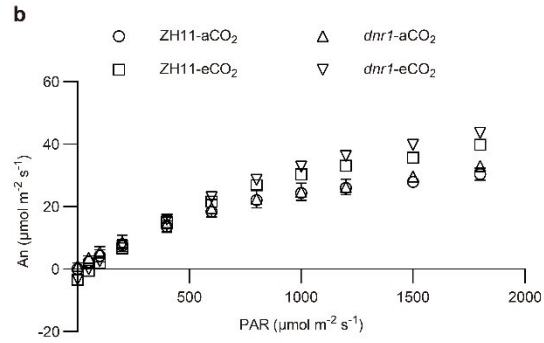
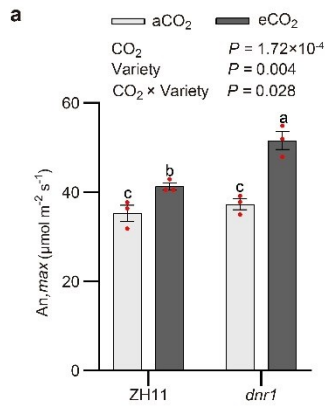
*Indica vs. Japonica*



**Supplementary Fig. 4 | Schematic overview of the differences in nitrate use efficiency between *indica* and *japonica* rice, as regulated by DNR1. + and - indicate positive and negative differences in *indica* compared to *japonica*, respectively.**

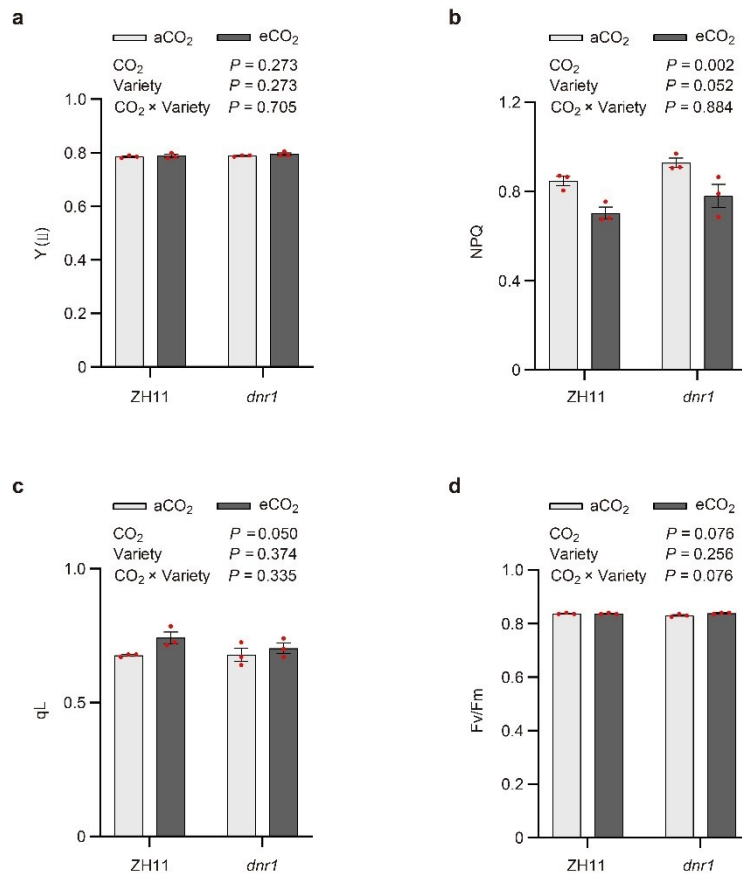


**Supplementary Fig. 5 | Different responses of *indica* variety Yangdao 6 and *japonica* variety Zhonghua 11 to elevated CO<sub>2</sub>.** a-c, Aboveground biomass (a), N uptake (b), and yield (c) under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions were measured at maturity stage. YD6 and ZH11 indicate *indica* variety Yangdao 6 and *japonica* variety Zhonghua 11, respectively. Data are mean ± s.e.m ( $n = 3$  biological replicates).  $P$ -values were generated from two-way ANOVA. Different letters indicate significant differences among groups ( $P < 0.05$ ). Source data are provided as a Source Data file.

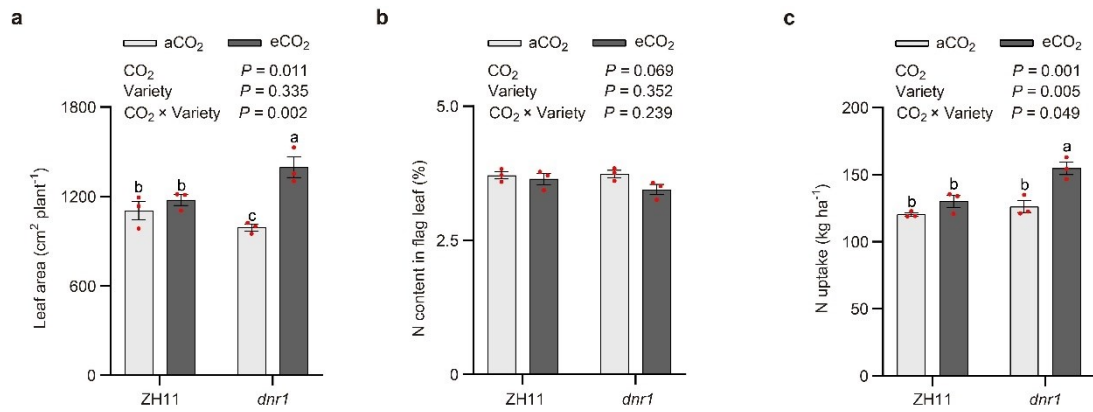


**Supplementary Fig. 6 | The responses of photosynthetic parameters to elevated CO<sub>2</sub>.** **a**, Light-saturated net photosynthesis rate. Different letters indicate significant differences among groups ( $P < 0.05$ ). **b**, Light response of net photosynthesis rate (An). **c**, Light-saturated stomatal conductance (gs). **d**, Light response of stomatal conductance (gs). **e**, CO<sub>2</sub> response of net photosynthesis rate (An). **f**, Maximum rate of RuBP carboxylation ( $V_{c,max}$ ). **g**, Maximum rate of electron transport driving RuBP regeneration ( $J_{max}$ ). ZH11 and *dnr1* indicate *japonica* variety Zhonghua 11 and its *dnr1* mutants mimicking the *indica* *DNR1* allele, respectively. aCO<sub>2</sub> and eCO<sub>2</sub> indicate ambient CO<sub>2</sub> and elevated CO<sub>2</sub> condition, respectively. **a**, **c**, **f-g**, Data are mean  $\pm$  s.e.m. ( $n = 3$  biological replicates).  $P$ -values were generated from two-way ANOVA. Source data are provided as a Source Data file.

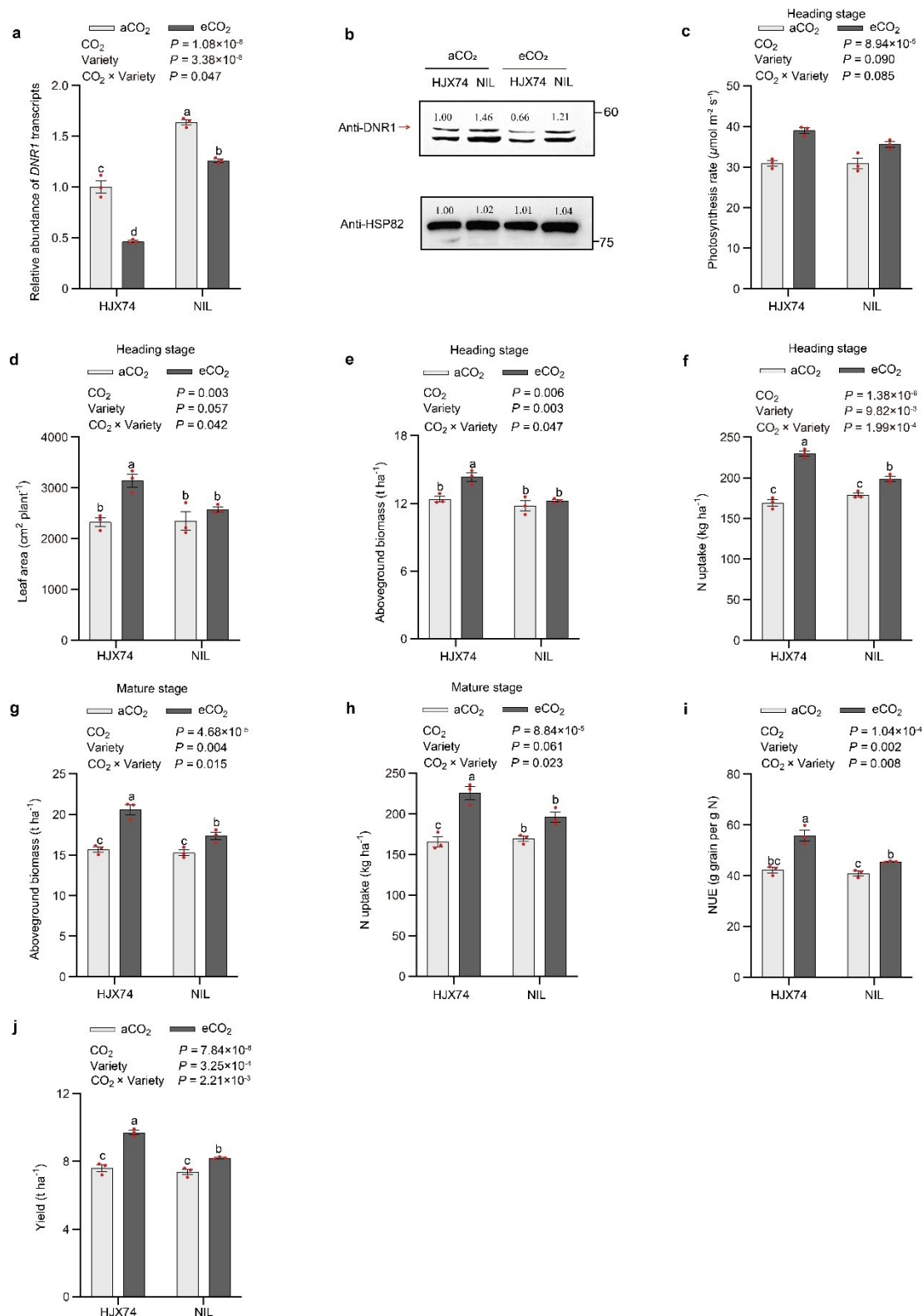




**Supplementary Fig. 7 | The responses of chlorophyll fluorescence parameters to elevated CO<sub>2</sub>.** **a**, Quantum yield of Photosystem II (Y(II)). **b**, Non-photochemical quenching (NPQ). **c**, Photochemical quenching coefficient (qL). **d**, Maximum photochemical quantum yield of Photosystem II (Fv/Fm). ZH11 and *dnr1* indicate *japonica* variety Zhonghua 11 and its *dnr1* mutants mimicking the *indica* *DNRI* allele, respectively. aCO<sub>2</sub> and eCO<sub>2</sub> indicate ambient CO<sub>2</sub> and elevated CO<sub>2</sub> condition, respectively. **a-d**, Data are mean ± s.e.m. ( $n = 3$  biological replicates).  $P$ -values were generated from two-way ANOVA. Source data are provided as a Source Data file.

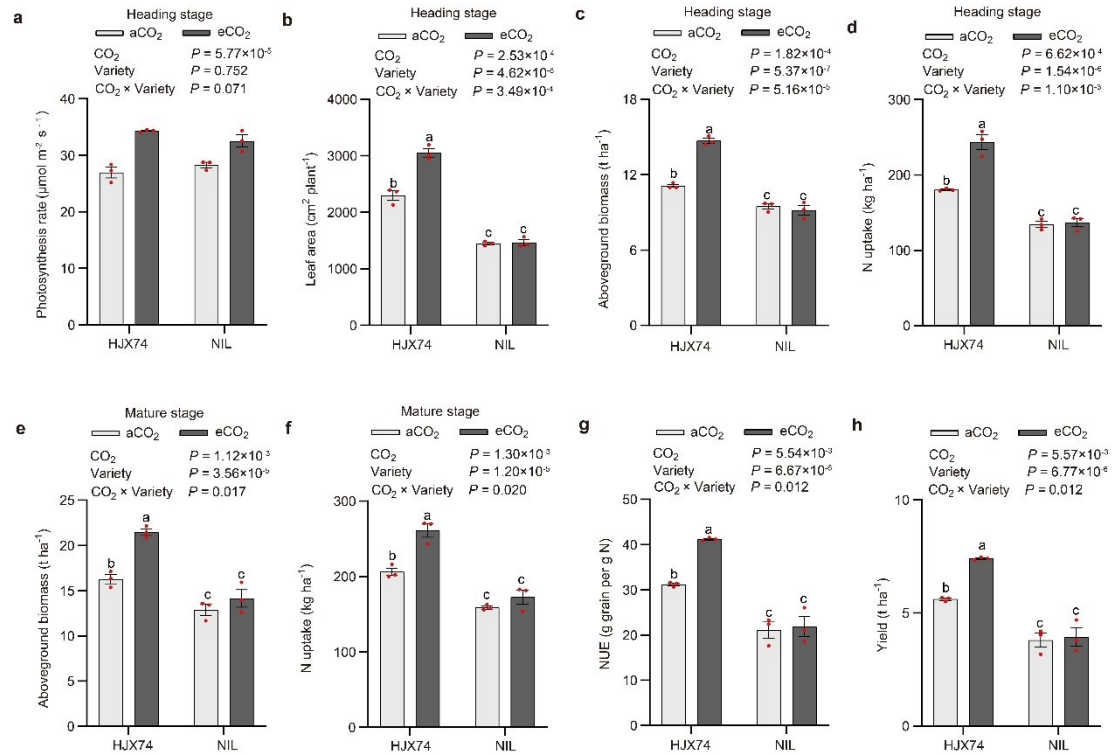


**Supplementary Fig. 8 | Different responses of *japonica* variety Zhonghua 11 and its *dnr1* mutants mimicking the *indica* *DNR1* allele to elevated CO<sub>2</sub>.** a-c, Total leaf area per plant (a), flag leaf N content (b), and N uptake (c) under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions. All these variables were measured at the heading stage. ZH11 and *dnr1* indicate *japonica* variety Zhonghua 11 and its *dnr1* mutants, respectively. Data are mean ± s.e.m. ( $n = 3$  biological replicates).  $P$ -values were generated from two-way ANOVA. a, c, Different letters indicate significant differences among groups ( $P < 0.05$ ). Source data are provided as a Source Data file.

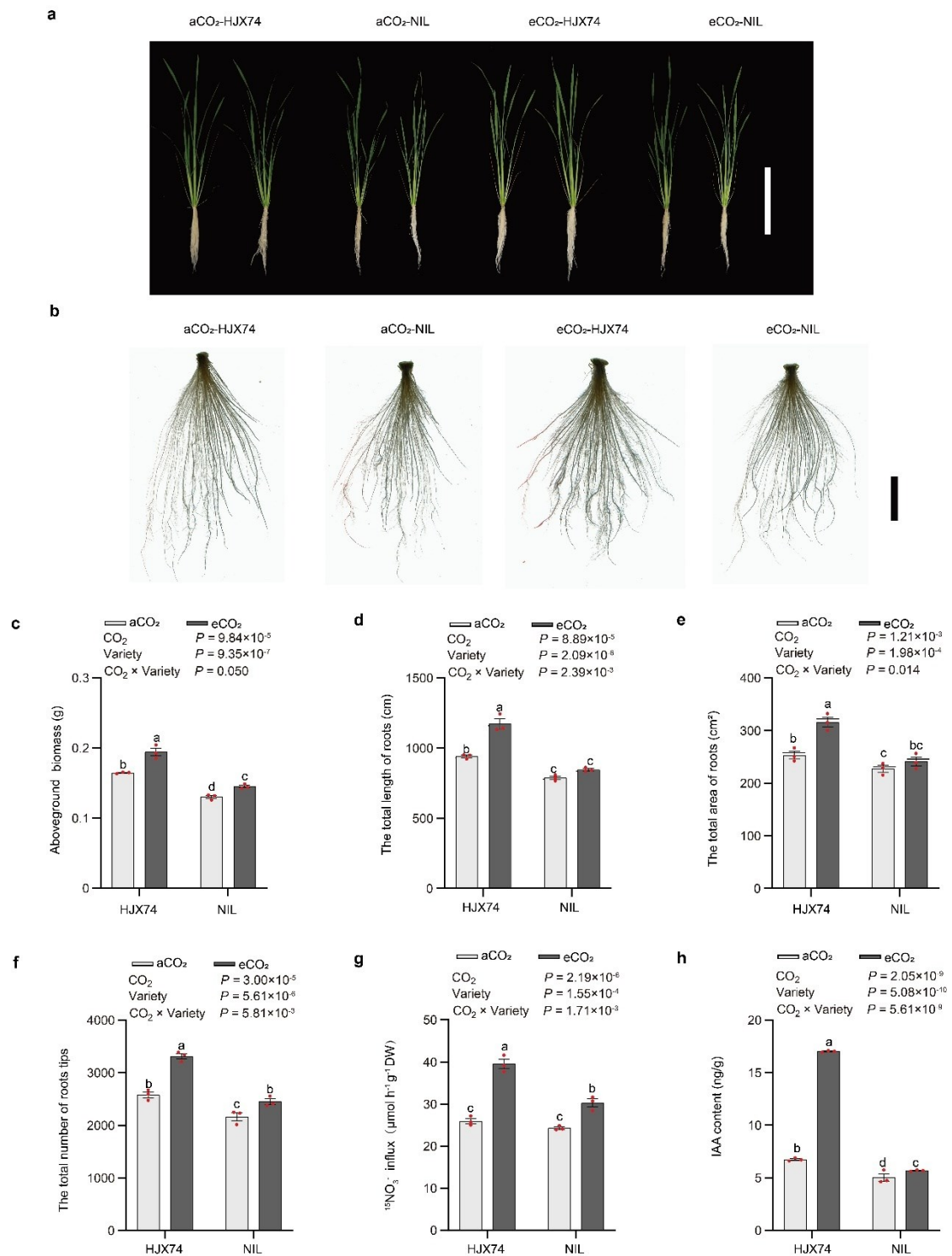


**Supplementary Fig. 9 | Different responses of *indica* variety Hua-Jing-Xian 74 and the near-isogenic line carrying the *japonica* *DNR1* allele to elevated  $CO_2$  in 2023. a**, *DNR1* transcript abundance in shoots under ambient  $CO_2$  (aCO<sub>2</sub>) and elevated  $CO_2$  (eCO<sub>2</sub>) conditions, respectively. Transcript abundance was measured relative to Hua-Jing-Xian 74 under aCO<sub>2</sub> (set to 1). **b**, *DNR1* protein abundance in shoots. HSP82 serves as a loading control. The red arrowhead indicates the

DNR1 bands. **c-f**, Net photosynthesis rate of flag leaves (**c**), total leaf area per plant (**d**), aboveground biomass (**e**), and N uptake (**f**) under aCO<sub>2</sub> and eCO<sub>2</sub> conditions were measured at heading stage. **g-j**, Aboveground biomass (**g**), N uptake (**h**), N-use efficiency (**i**), yield (**j**) under aCO<sub>2</sub> and eCO<sub>2</sub> conditions were measured at maturity. HJX74 and NIL indicate *indica* variety Hua-Jing-Xian 74 and the near-isogenic line carrying the *japonica DNR1* allele, respectively. **a, c-j**, Data are mean ± s.e.m. ( $n = 3$  biological replicates). *P*-values were generated from two-way ANOVA. **a, d-j**, Different letters indicate significant differences among groups ( $P < 0.05$ ). Source data are provided as a Source Data file.

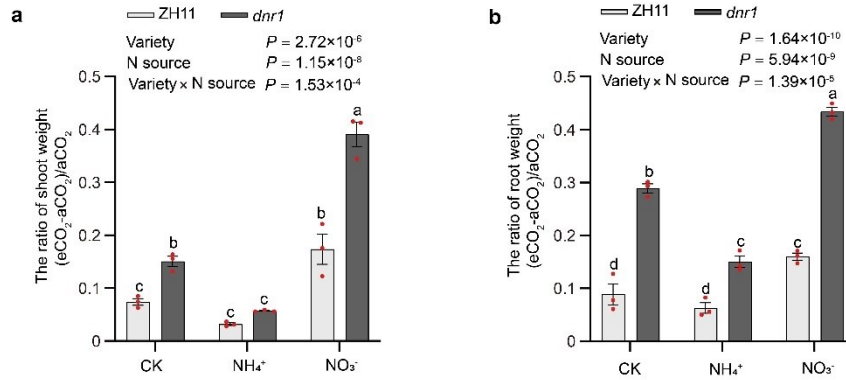


**Supplementary Fig. 10 | Different responses of *indica* variety Hua-Jing-Xian 74 and the near-isogenic line carrying the *japonica DNRI* allele to elevated CO<sub>2</sub> in 2022.** **a-d**, Net photosynthesis rate of flag leaves (**a**), total leaf area per plant (**b**), aboveground biomass (**c**), and N uptake (**d**) under aCO<sub>2</sub> and eCO<sub>2</sub> conditions were measured at heading stage. **e-h**, Aboveground biomass (**e**), N uptake (**f**), N-use efficiency (**g**) and yield (**h**) under aCO<sub>2</sub> and eCO<sub>2</sub> conditions were measured at maturity. HJX74 and NIL indicate *indica* variety Hua-Jing-Xian 74 and the near-isogenic line carrying the *japonica DNRI* allele, respectively. **a-h**, Data are mean  $\pm$  s.e.m. ( $n = 3$  biological replicates).  $P$ -values were generated from two-way ANOVA. **b-h**, Different letters indicate significant differences among groups ( $P < 0.05$ ). Source data are provided as a Source Data file.



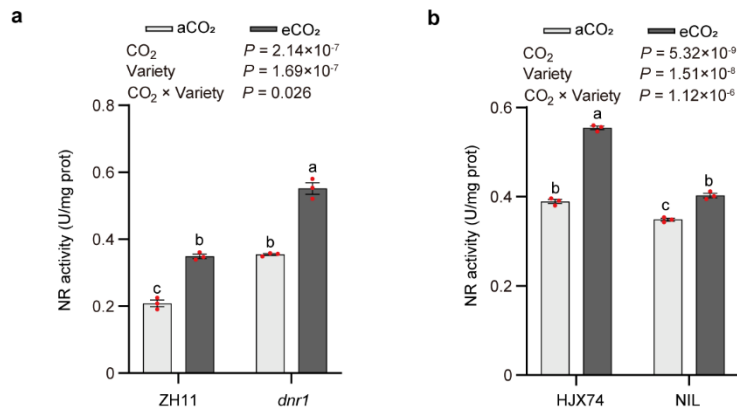
**Supplementary Fig. 11 | Differences in root development in response to elevated CO<sub>2</sub> between *indica* variety Hua-Jing-Xian 74 (HJX74) and the near-isogenic line (NIL) carrying the *japonica DNR1* allele. a, b, 14-day-old *indica* HJX74 and NIL rice plants grown under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions, respectively. Morphology of plants (a), root systems (b). a, Scale bar, 20 cm. b, Scale bar, 5 cm. c, Aboveground biomass. d-f, Root statistics of total length of visible roots (d), total area of visible roots (e), and number of root tips (f). g, h, <sup>15</sup>NO<sub>3</sub><sup>-</sup> uptake rates (g) and root free IAA content (h) of *indica* HJX74 and NIL under aCO<sub>2</sub> and eCO<sub>2</sub>**

conditions. **c-h**, Data are mean  $\pm$  s.e.m. ( $n = 3$  biological replicates).  $P$ -values were generated from two-way ANOVA. Different letters indicate significant differences among groups ( $P < 0.05$ ). Source data are provided as a Source Data file.

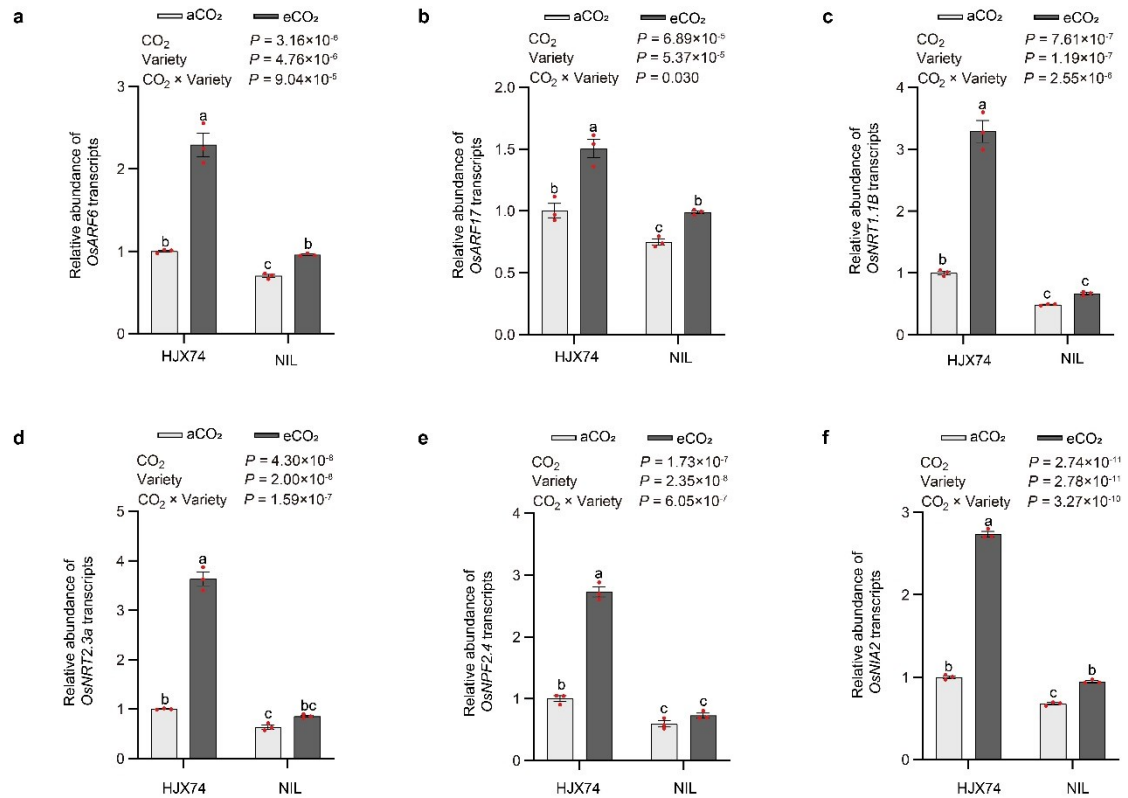


**Supplementary Fig. 12 | The response of Zhonghua 11 and *dnr1* plants to elevated CO<sub>2</sub> under different nitrogen source conditions. a-b**, 14-day-old *japonica* variety Zhonghua 11 (ZH11) and its *dnr1* mutants (*dnr1*) conducted hydroponic experiments using NH<sub>4</sub>NO<sub>3</sub> (CK), (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> (NH<sub>4</sub><sup>+</sup> N) or KNO<sub>3</sub> (NO<sub>3</sub><sup>-</sup> N) as the N source, respectively. The ratio of shoot weight (**a**), and the ratio of root weight (**b**). Data are mean  $\pm$  s.e.m. ( $n = 3$  biological replicates).  $P$ -values were generated from two-way ANOVA. Different letters indicate significant differences among groups ( $P < 0.05$ ). Source data are provided as a Source Data file.

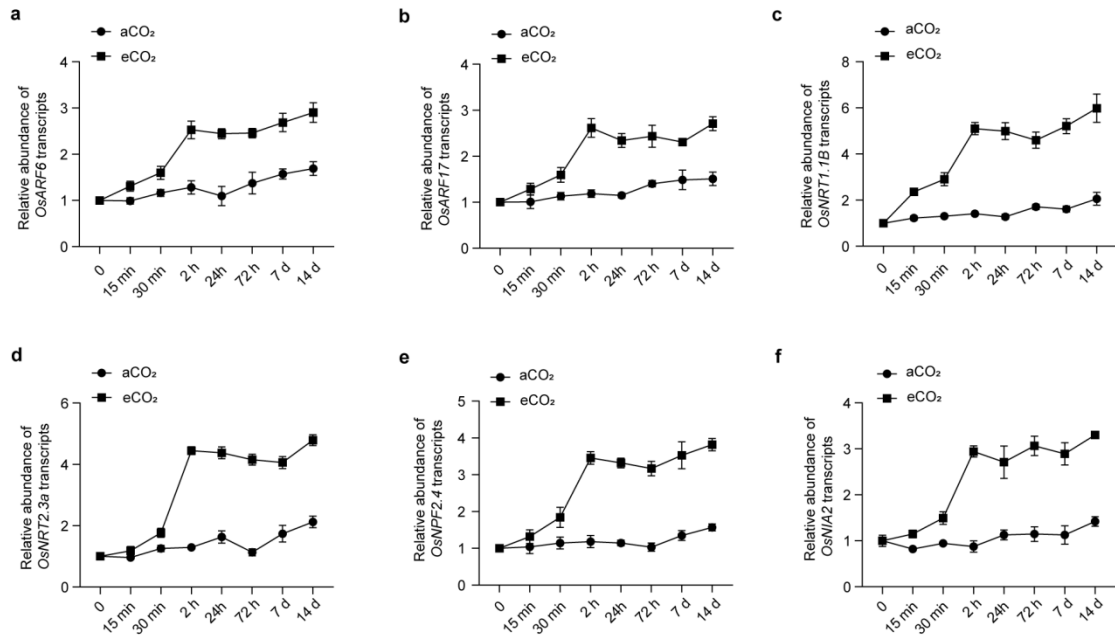




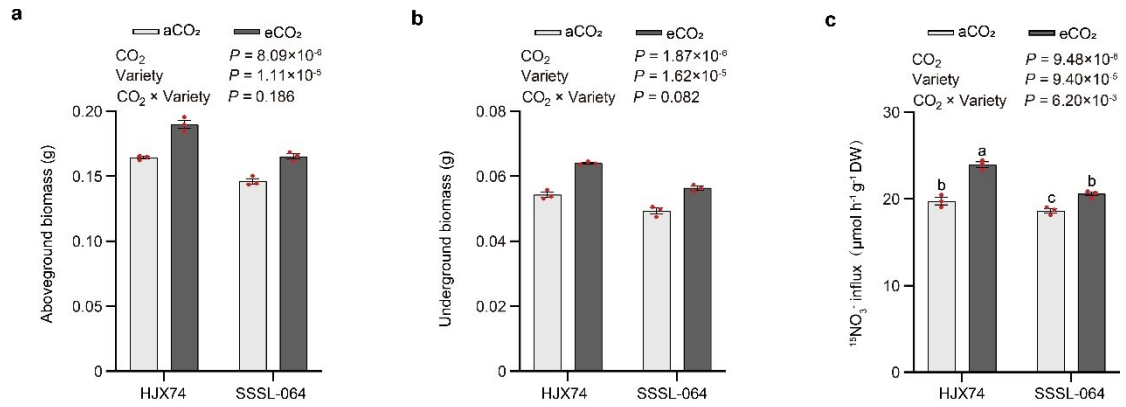
**Supplementary Fig. 13 | The responses of nitrate reductase activity to elevated CO<sub>2</sub>. a-b,** Nitrate reductase (NR) activities in *japonica* variety Zhonghua 11 (ZH11) and its *dnr1* mutants (*dnr1*) mimicking the *indica* *DNRI* allele (**a**), and *indica* variety Hua-Jing-Xian 74 (HJX74) and the near-isogenic line (NIL) carrying the *japonica* *DNRI* allele (**b**) grown under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions. Data are mean ± s.e.m. ( $n = 3$  biological replicates).  $P$ -values were determined by two-way ANOVA. Different letters indicate significant differences among groups ( $P < 0.05$ ). Source data are provided as a Source Data file.



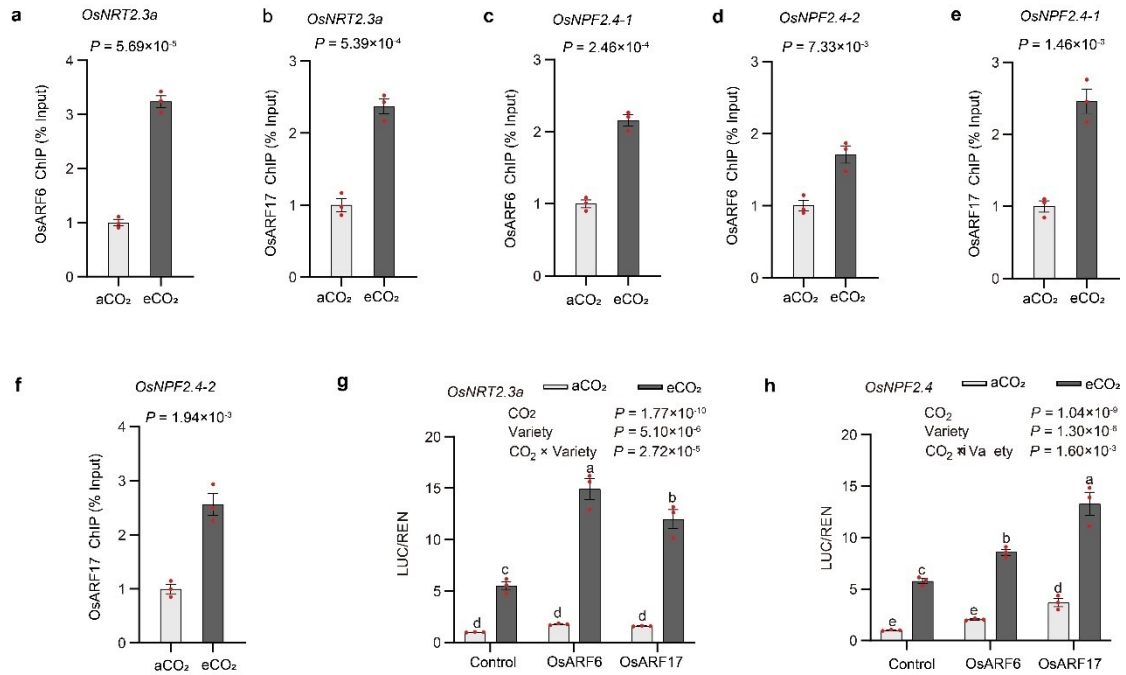
**Supplementary Fig. 14 | Elevated CO<sub>2</sub> enhances the expression levels of genes related to NO<sub>3</sub><sup>-</sup> metabolism in *indica* variety Hua-Jing-Xian 74 and the near-isogenic line carrying the *japonica DNRI* allele. a-b, Shoot mRNA abundances of *OsARF6* (a) and *OsARF17* (b) under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions relative to HJX74 under aCO<sub>2</sub> (set to 1). c-d, Root mRNA abundances of *OsNRT1.1B* (c) and *OsNRT2.3a* (d) under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions relative to HJX74 under aCO<sub>2</sub> (set to 1). e-f, Shoot mRNA abundances of *OsNPF2.4* (e) and *OsNIA2* (f) under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions relative to HJX74 under aCO<sub>2</sub> (set to 1). HJX74 and NIL indicate *indica* variety Hua-Jing-Xian 74 and the near-isogenic line carrying the *japonica DNRI* allele, respectively. a-f, Data are mean ± s.e.m. ( $n = 3$  biological replicates).  $P$ -values were determined by two-way ANOVA. Different letters indicate significant differences among groups ( $P < 0.05$ ). Source data are provided as a Source Data file.**



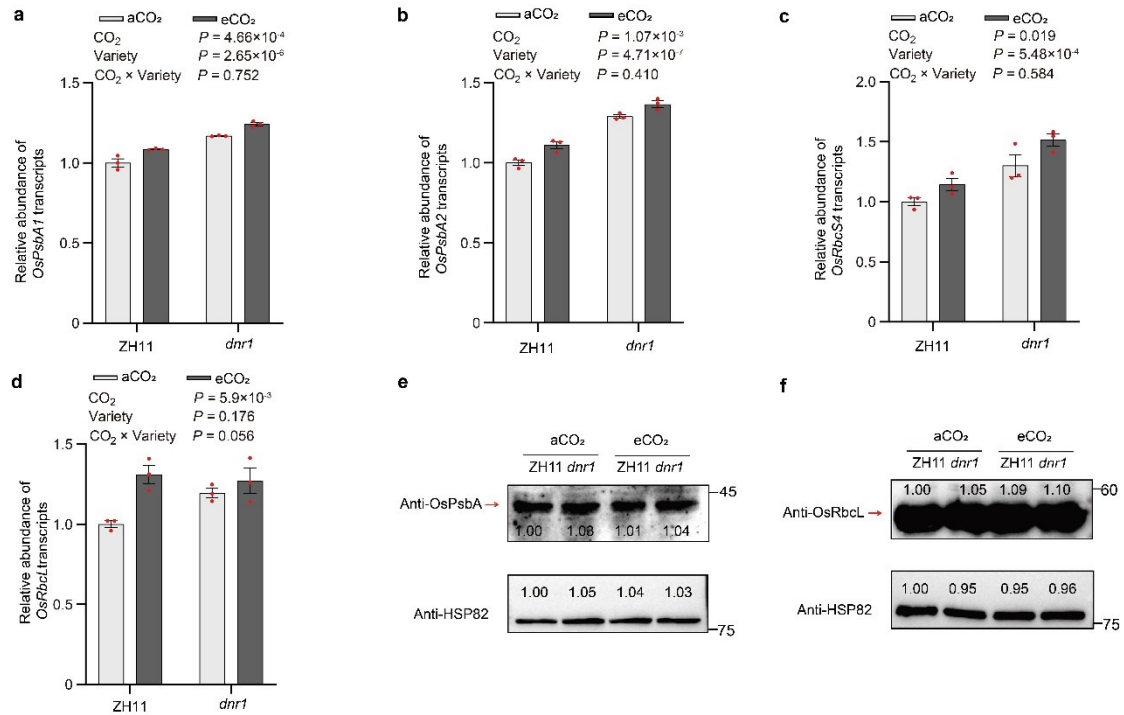
**Supplementary Fig. 15 | Elevated CO<sub>2</sub> enhances the expression levels of nitrogen-related genes through *OsARFs*.** **a-f**, The time course expression levels of *OsARF6* (**a**), *OsARF17* (**b**), *OsNRT1.1B* (**c**), *OsNRT2.3a* (**d**), *OsNPF2.4* (**e**), and *OsNIA2* (**f**) in Zhonghua 11 under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions relative to 0 (set to 1). Data are mean ± s.e.m. ( $n = 3$  biological replicates). Source data are provided as a Source Data file.



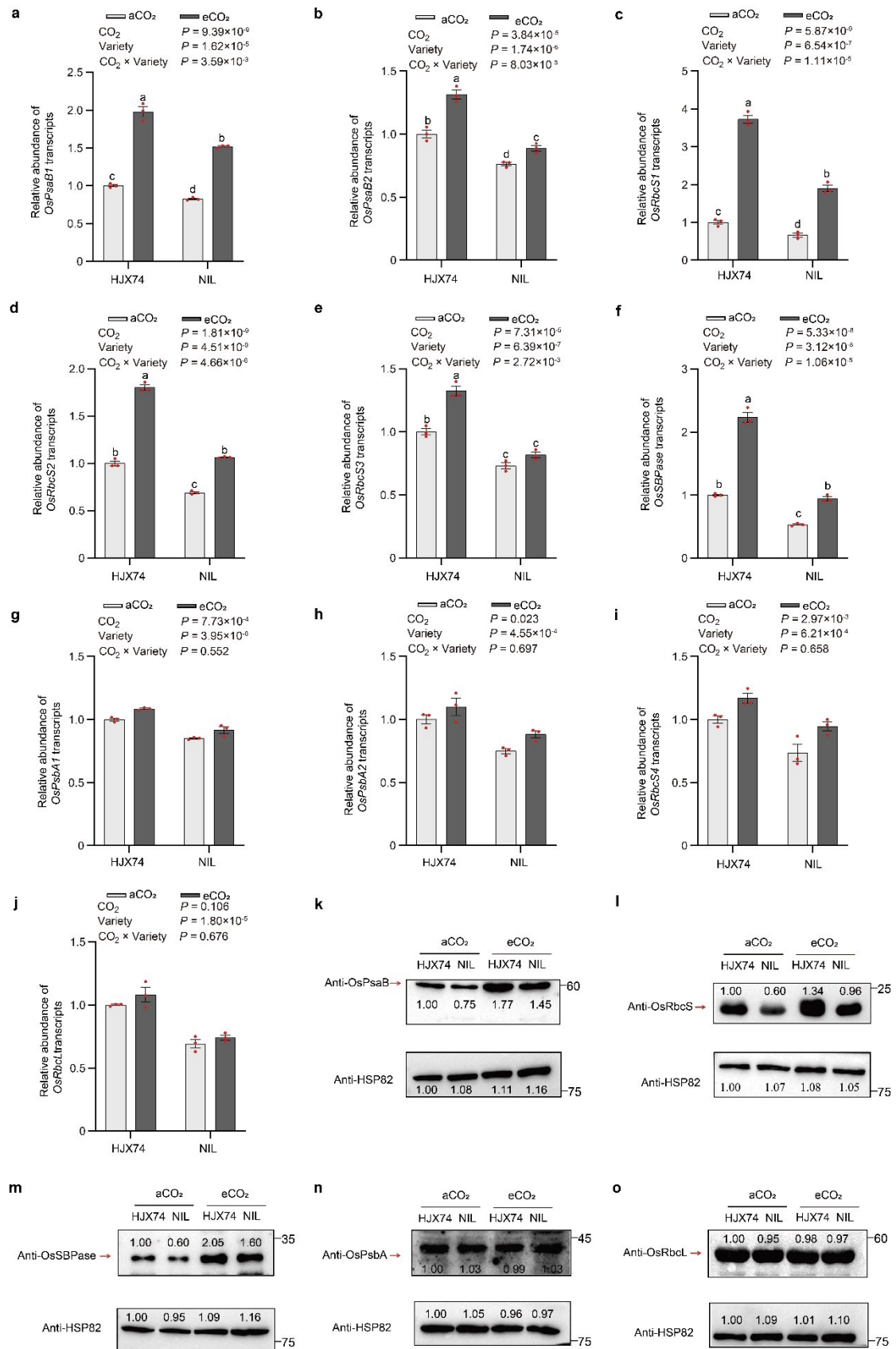
**Supplementary Fig. 16 | Differences in biomass and <sup>15</sup>NO<sub>3</sub><sup>-</sup> influx in responses to elevated CO<sub>2</sub> of Hua-Jing-Xian 74 and the near-isogenic line carrying the *japonica OsNRT1.1B* allele. a-c, 14-day-old *indica* Hua-Jing-Xian 74 (HJX74) and near-isogenic line (SSSL-064) rice plants grown under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions, respectively. Aboveground biomass (a), underground biomass (b), and <sup>15</sup>NO<sub>3</sub><sup>-</sup> influx (c). Data are mean ± s.e.m. ( $n = 3$  biological replicates).  $P$ -values were determined by two-way ANOVA. c, Different letters indicate significant differences among groups ( $P < 0.05$ ). Source data are provided as a Source Data file.**



**Supplementary Fig. 17 | eCO<sub>2</sub> promotes OsARF6 and OsARF17-mediated CHIP-qPCR enrichment and transactivation on N metabolism-related genes.** **a-f**, Extent of OsARF6 and OsARF17-mediated CHIP-qPCR enrichment (relative to Input) of TGTCTC-containing promoter fragments from *OsNRT2.3a* (**a, b**) and *OsNPF2.4* (**c-f**) under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions. *P*-values were generated from two-sided Student's *t* tests. **g, h**, OsARF6 and OsARF17 activate promoter-luciferase fusion constructs *OsNRT2.3a* (**g**) and, *OsNPF2.4* (**h**) in transient transactivation assays. The luciferase (LUC)/renilla (REN) activity obtained from a co-transfection with an empty effector construct and indicated reporter constructs under ambient CO<sub>2</sub> was set to 1. *P*-values were generated from two-way ANOVA. Different letters indicate significant differences among groups (*P* < 0.05). **a-h**, Data are mean ± s.e.m. (*n* = 3 biological replicates). Source data are provided as a Source Data file.



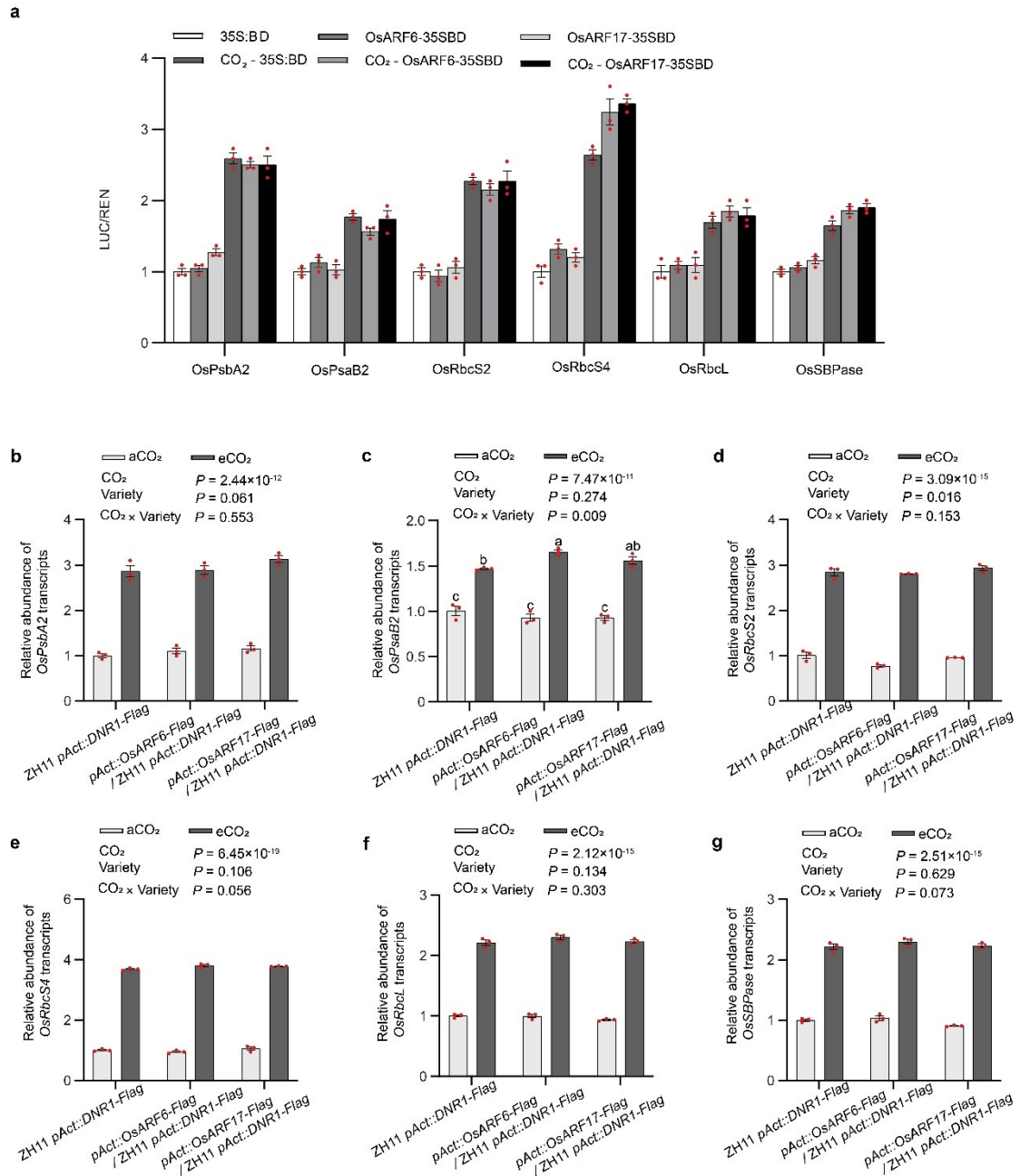
**Supplementary Fig. 18 | The expression of photosynthetic genes in *japonica* variety Zhonghua 11 and its *dnr1* mutants mimicking the *indica* *DNRI* allele under ambient CO<sub>2</sub> and elevated CO<sub>2</sub>. a-d**, Shoot mRNA abundances of *OsPsbA1* (a), *OsPsbA2* (b), *OsRbcS4* (c), and *OsRbcL* (d) grown ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions, respectively, relative to Zhonghua 11 under aCO<sub>2</sub> (set to 1). *P*-values were generated from two-way ANOVA. Data are mean ± s.e.m. (*n* = 3 biological replicates). **e-f**, OsPsaA (e) and OsRbcL (f) protein abundances in shoots. HSP82 serves as a loading control. The red arrows indicate the OsPsaA, and OsRbcL bands, respectively. Data are representative of three independent experiments, with similar results. Source data are provided as a Source Data file.



**Supplementary Fig. 19 | Elevated CO<sub>2</sub> affects the abundances of photosynthetic-related genes in *indica* variety Hua-Jing-Xian 74 and the near-isogenic line carrying the *japonica* DNR1**

**allele. a-j,** The expression levels of *OsPsaB1* (**a**), *OsPsaB2* (**b**), *OsRbcS1* (**c**), *OsRbcS2* (**d**), *OsRbcS3* (**e**), *OsSBPase* (**f**), *OsPsbA1* (**g**), *OsPsbA2* (**h**), *OsRbcS4* (**i**), *OsRbcL* (**j**) in plants grown under ambient CO<sub>2</sub> (aCO<sub>2</sub>) and elevated CO<sub>2</sub> (eCO<sub>2</sub>) conditions, relative to Hua-Jing-Xian 74 (HJX74) under aCO<sub>2</sub> (set to 1). Data are mean ± s.e.m. ( $n = 3$  biological replicates).  $P$ -values were generated from two-way ANOVA. **k-o,** *OsPsaB* (**k**), *OsRbcS* (**l**), *OsSBPase* (**m**), *OsPsbA* (**n**) and *OsRbcL* (**o**) protein abundances in leaves. HSP82 serves as a loading control. The red arrows indicate the *OsPsaB*, *OsRbcS*, *OsSBPase*, *OsPsbA*, and *OsRbcL* bands, respectively. Data are representative of three independent experiments, with similar results. **a-f,** Different letters indicate significant differences among groups ( $P < 0.05$ ). Source data are provided as a Source Data file.





**Supplementary Fig. 20 | The effect of elevated CO<sub>2</sub> on the expression of photosynthetic genes may not be mediated by OsARFs.** (a) OsARF6 and OsARF17 do not activate promoter-luciferase fusion constructs *OsPsbA2*, *OsPsaB2*, *OsRbcS2*, *OsRbcS4*, *OsRbcL* and *OsSBPase* in transient transactivation assays. The luciferase (LUC)/renilla (REN) activity obtained from a co-transfection with an empty effector construct and indicated reporter constructs under ambient CO<sub>2</sub> (aCO<sub>2</sub>) was set to 1. **b-g**, Shoot mRNA abundances of *OsPsbA2* (b), *OsPsaB2* (c), *OsRbcS2* (d), *OsRbcS4* (e), *OsRbcL* (f), and *OsSBPase* (g) in plants overexpressing *OsARF6* and *OsARF17* within the ZH11/*pAct::DNR1-Flag* background with either aCO<sub>2</sub> or elevated CO<sub>2</sub> (eCO<sub>2</sub>) treatment, relative to ZH11 *pAct::DNR1-Flag* under aCO<sub>2</sub> (set to 1). **a-g**, Data are mean ± s.e.m. (*n* = 3 biological replicates). *P*-values were generated from two-way ANOVA. **c**, Different letters indicate significant differences among groups (*P* < 0.05). Source data are provided as a Source Data file.

## Supplementary Tables

**Supplementary Table 1 | The allelic variations of five genes involved in NO<sub>3</sub><sup>-</sup> use efficiency between *indica* and *japonica*.**

Location	<i>Indica</i>	<i>Japonica</i>
<i>OsNRT1.1B</i>	c.980 T	c.980 C
<i>OsNR2</i>	Arg783	Trp779
<i>DNR1</i>	-	p -1728 ~ -1209, 520 bp insertion
<i>RNR10</i>	-	p -3645 ~ -150, 3496 bp insertion
<i>MYB61</i>	-	helitron element

**Supplementary Table 2 | Detailed information on genes regulated by DNR1.**

Gene name	Gene ID	Crop biological function(s)
<i>OsNRT1.1B</i>	LOC_Os10g40600	dual-affinity nitrate transporter
<i>OsNRT2.3a</i>	LOC_Os01g50820	high-affinity nitrate transporter
<i>OsNPF2.4</i>	LOC_Os03g48180	root to shoot nitrate transporter
<i>OsNIA2</i>	LOC_Os08g36500	NADH-dependent nitrate reductase
<i>OsARF6</i>	LOC_Os02g06910	auxin-responsive transcription factor promoting nitrate metabolism
<i>OsARF17</i>	LOC_Os06g46410	auxin-responsive transcription factor promoting nitrate metabolism

**Supplementary Table 3 | Rice varieties in FACE experiments exhibiting *DNRI* allelic variations.**

Varieties	520 bp	<i>indica/japonica</i>
No8	+	<i>japonica</i>
Koshi	+	<i>japonica</i>
Aikoku	+	<i>japonica</i>
Akita	+	<i>japonica</i>
Nipponbare	+	<i>japonica</i>
Nanjing 9108	+	<i>japonica</i>
Wuxiangjing 14	+	<i>japonica</i>
Wuyunjing 21	+	<i>japonica</i>
Wuyunjing 23	+	<i>japonica</i>
YD6	-	<i>indica</i>
IR24	-	<i>indica</i>
Ilyou 084	-	<i>indica</i>
Shanyou 63	-	<i>indica</i>
Liangyoupei 9	-	<i>indica</i>
Huajingxian 74	-	<i>indica</i>

**Supplementary Table 4 | Detailed information on photosynthetic genes.**

Gene name	Gene ID	Crop biological function(s)
<i>OsPsbA1</i>	LOC_Os04g16770.1	photosynthetic reaction center protein, putative, expressed
<i>OsPsbA2</i>	LOC_Os08g35420	photosynthetic reaction center protein, putative, expressed
<i>OsPsbA3</i>	LOC_Os10g21192	photosystem Q, putative, expressed
<i>OsPsbA4</i>	LOC_Os10g39880	photosynthetic reaction center protein, putative, expressed
<i>OsPsbA5</i>	LOC_Os12g19580	photosynthetic reaction center protein, putative, expressed
<i>OsPsaB1</i>	LOC_Os01g57962	photosystem I P700 chlorophyll a apoprotein A2, putative, expressed
<i>OsPsaB2</i>	LOC_Os01g57964	photosystem I P700 chlorophyll a apoprotein A1, putative, expressed
<i>OsPsaB3</i>	LOC_Os04g16760	photosystem I P700 chlorophyll a apoprotein A1, putative
<i>OsPsaB4</i>	LOC_Os05g01675	photosystem I P700 chlorophyll a apoprotein A1, putative
<i>OsPsaB5</i>	LOC_Os10g21248	photosystem I P700 chlorophyll a apoprotein A2, putative
<i>OsPsaB6</i>	LOC_Os10g21250	photosystem I P700 chlorophyll a apoprotein A1, putative
<i>OsPsaB7</i>	LOC_Os10g38229	photosystem I P700 chlorophyll a apoprotein A1, putative
<i>OsPsaB8</i>	LOC_Os10g38234	photosystem I P700 chlorophyll a apoprotein A2, putative
<i>OsRbcS1</i>	LOC_Os02g05830	small subunit of Rubisco
<i>OsRbcS2</i>	LOC_Os12g17600	small subunit of Rubisco
<i>OsRbcS3</i>	LOC_Os12g19381	small subunit of Rubisco
<i>OsRbcS4</i>	LOC_Os12g19470	small subunit of Rubisco
<i>OsRbcL</i>	LOC_Os10g21268	ribulose biphosphate carboxylase large chain precursor
<i>OsSBPase</i>	LOC_Os04g16680	sedoheptulose 1,7-bisphosphatase

**Supplementary Table 5 | 13 transcription factors respond to both eCO<sub>2</sub> and DNR1.**

Gene_id	Gene_name	Gene_description	Annotation
Os01g0619900	OsTCL2	TCL2_ARATH MYB-like transcription factor TCL2	
Os01g0603300	Os01g0603300	KUA1_ARATH Transcription factor KUA1	
Os06g0166400	OsERF#007	ERF08_ARATH Ethylene-responsive transcription factor ERF008	
Os10g0562900	DERF12	EF102_ARATH Ethylene-responsive transcription factor 5	Up-regulated by
Os12g0116600	OsWRKY95	WRK46_ARATH Probable WRKY transcription factor 46	both eCO <sub>2</sub> and
Os12g0618600	OsHAP2F	NFYA6_ARATH Nuclear transcription factor Y subunit A-6	null- <i>DNR1</i> allele
Os11g0117600	OsWRKY50	RK19_ORYSJ Transcription factor WRKY19	
Os07g0158500	OsHAP2J	NFYAA_ARATH Nuclear transcription factor Y subunit A-10	
Os03g0366800	OsHsfB4d	HFB4D_ORYSJ Heat stress transcription factor B-4d	
Os04g0541100	GT-2	DF1_ARATH Trihelix transcription factor DF1	Down-regulated
Os04g0381700	OsBHLH156	BH156_ORYSJ Transcription factor BHLH156	by both eCO <sub>2</sub> and
Os04g0686200	Os04g0686200	PRAF1_ARATH PH, RCC1 and FYVE domains-containing protein 1	null- <i>DNR1</i> allele
Os08g0483900	OsBHLH047	BH094_ARATH Transcription factor bHLH94	

**Supplementary Table 6 | Effects of elevated CO<sub>2</sub> and varieties on rice yield composition.**

Treatment		Panicles per ha (10 <sup>4</sup> )	Spikelets per panicle	Grain filling rate (%)	1000-grain weight (g)
ZH11	aCO <sub>2</sub>	215.1±6.4	137.3±3.0	82.1±0.6	28.6±0.2
	eCO <sub>2</sub>	220.4±6.4	141.7±0.9	82.7±1.0	27.9±0.1
<i>dnr1</i>	aCO <sub>2</sub>	227.6±1.8	150.0±0.6	80.4±1.4	26.3±0.2
	eCO <sub>2</sub>	248.9±4.7	158.8±2.3	87.8±0.2	25.6±0.1
	CO <sub>2</sub>	0.033	0.010	0.003	0.001
<i>P</i> -value	Variety	0.004	6.5×10 <sup>-5</sup>	0.108	2.3×10 <sup>-7</sup>
	CO <sub>2</sub> ×Variety	0.161	0.296	0.006	0.770
HJX74	aCO <sub>2</sub>	245.3±5.3	170.0±5.7	86.7±0.6	24.6±0.2
	eCO <sub>2</sub>	284.4±7.7	182.6±4.4	93.3±0.1	23.9±0.2
NIL	aCO <sub>2</sub>	216.9±8.9	164.2±3.3	82.5±0.9	29.0±0.1
	eCO <sub>2</sub>	231.1±6.4	165.7±2.9	83.1±1.3	29.3±0.3
	CO <sub>2</sub>	0.006	0.136	0.003	0.423
<i>P</i> -value	Variety	4.7×10 <sup>-4</sup>	0.028	3.2×10 <sup>-5</sup>	2.0×10 <sup>-8</sup>
	CO <sub>2</sub> ×Variety	0.123	0.226	0.008	0.056

ZH11 and *dnr1* indicate *japonica* variety Zhonghua 11 and its *dnr1* mutants mimicking the *indica* *DNR1* allele, respectively. HJX74 and NIL indicate *indica* variety Hua-Jing-Xian 74 and the near-isogenic line carrying the *japonica* *DNR1* allele, respectively. aCO<sub>2</sub> and eCO<sub>2</sub> indicate ambient CO<sub>2</sub> and elevated CO<sub>2</sub> condition, respectively. Data are mean ± s.e.m. (*n* = 3 biological replicates). *P*-values were generated from two-way ANOVA. Source data are provided as a Source Data file.

**Supplementary Table 7 | Primer sequences used for qPCR assays used in this study.**

Primers	Forward sequence (5'-3')	Reverse sequence (5'-3')	Annotation
OsActin2	AGCAGCATGAAGATCAAGGTGGTC	CCTTGGCAATCCACATCTGCTG	
DNR1	TGCAAACAAGCATGGTGTGG	TCACAAGTTCTTGCAAGCCG	
OsNRT1.1B	GGCAGGCTCGACTACTTCTA	AGGCGCTTCTCCTTGTAGAC	
OsNRT2.3a	CTCATCCGCGACACCCCTC	GATGGAGGAGCAGTACACCG	
OsNPF2.4	TAGGATTAAGTGGGTGAGG	GTCAAACAGCAAGTAGCG	
OsNIA2	GTTACGAACCAAGGGGGAT	AATCTCCACGGGCCACCATA	
OsARF6	CCACATCCAACCTCCTTAGC	ACAGAGACGTACAGAACTGG	
OsARF17	GGATCAAGATGGGAACTCTG	TAGTCATCACAGCTGCTACC	
OsPsbA-Primer 1	TGCAGCTGCTACTGCTGTTT	CACTAAATAGGGAACCGCCG	For <i>OsPsbA1-3</i>
OsPsbA--Primer 2	TTTGGGAAGCTGCATCTGTT	AGAAAACAGCAGTAGCAGCT	For <i>OsPsbA1-5</i>
OsPsaB--Primer 1	CCACTCAAGGAGCGGAACTG	GAGCAATATCGGTCAGCCACAAAC	For <i>OsPsaB1, 5, 8</i>
OsPsaB--Primer 2	TATTTGCTCGCAGTTCCCGT	TACCCCAAACATCCGACTGC	For <i>OsPsaB2, 3, 4, 6, 7</i>
OsRbcS1	ATGCCATTGCCATCCCAAGT	ATGTCGCCGGAGTAGAGAGT	
OsRbcS2	CCCTCTCCTACCTGCCACCG	GACGAATGCATCAGGGTACG	
OsRbcS3	GCATCATCGGCTTCGACAAC	TTAGTTTCCGCCGACTCCT	
OsRbcS4	CTCTGTCTACTTGCCGCCAT	AACGAAGGCATCAGGGTATG	
OsRbcL	AAACTTTCCAAGGTCCGCCT	ACAAAACGGTCCCTCCAACG	
OsSBPase	AAACAGTCGGTGCTGGACAA	GAGTCTCCTCGAACCGGATG	
ChIP-OsNRT1.1B	CGGTGGCTTCATCACAGCAT	TTGTAGTCCCACGCTCCGT	
ChIP-OsNRT2.3a	CGGCCAGCTCAAGGAACTT	CCATGGCTTCTCATGCTCTG	
ChIP-OsNPF2.4-1	CTGACGACTAGTACGAATCG	TCTCACCAACCACCACCTCT	
ChIP-OsNPF2.4-2	CGCATCCGCATCCGTACATT	CTCTCCCTTCACTGCGTC	
ChIP-OsNIA2	ATGTGTGCATGTTGTGTACG	TTCAGCTCAGCTACAGCTCG	



**Supplementary Table 8 | Primer sequences used for luciferase activity assays.**

Primers	Sequence (5'-3')
OsARF6-sem-BamHI-F	TCGCCGTCTAGAACTAGTGAATGAAGCTCTCGCCGTCGGCC
OsARF6-sem-EcoRI-R	GTATCGATAAGCTTGATATCGTTTCAGAACTCAACTGAGCCCA
OsARF17-sem-BamHI-F	TCGCCGTCTAGAACTAGTGAATGAGGCTTTCGTCGTCGTC
OsARF17-sem-EcoRI-R	GTATCGATAAGCTTGATATCGTTTCAGAATCAACTGAGCCGA
OsNRT1.1B-sem-EcoRV-F	TGGATTGATGTGATATCAAGGGCATCGTCTGAGTCTG
OsNRT1.1B-sem-XbaII-R	CTTGACAGATCCTCTAGAATCAACAACAACAAGCTCGA
OsNRT2.3a-sem-EcoRV-F	TGGATTGATGTGATATCTGTTGCCAGGAATTGCTTG
OsNRT2.3a-sem-XbaII-R	CTTGACAGATCCTCTAGACTCCAACACGTGGTAGCAAG
OsNPF2.4-sem-EcoRV-F	TGGATTGATGTGATATCTGGAAGGAGGGTTTTGGCCAG
OsNPF2.4-sem-XbaII-R	CTTGACAGATCCTCTAGACCTCTCTACCAACCACCACCT
OsNIA2-sem-EcoRV-F	TGGATTGATGTGATATCGAATCCCACAATTATTTTC
OsNIA2-sem-XbaII-R	CTTGACAGATCCTCTAGAGCTTGGTGTTCGGTTCTGCGT
OsPsbA2-sem-EcoRV-F	TGGATTGATGTGATATCGGGAGGAAGGTCTCGGACAA
OsPsbA2-sem-XbaII-R	CTTGACAGATCCTCTAGACTTTCTCCGAGTCCCAATA
OsPsaB2-sem-EcoRV-F	TGGATTGATGTGATATCAATGACGGTAGCTTGCGAAT
OsPsaB2-sem-XbaII-R	CTTGACAGATCCTCTAGATAAGTCTCTCTTTCCGGA
OsRbcS2-sem-EcoRV-F	TGGATTGATGTGATATCGTATTGCTGATGCCCTTATT
OsRbcS2-sem-XbaII-R	CTTGACAGATCCTCTAGACTCTGCAGCTCACCAAGCTC
OsRbcS4-sem-EcoRV-F	TGGATTGATGTGATATCTGTCACTGGCAGTCTATGA
OsRbcS4-sem-XbaII-R	CTTGACAGATCCTCTAGATGCTAGCTTGCTAGGAGCTA
OsRbcL-sem-EcoRV-F	TGGATTGATGTGATATCCCCAAATAATTCGCTTAGGA
OsRbcL-sem-XbaII-R	CTTGACAGATCCTCTAGAACAGGGTCTACTCGATATGG
OsSBPase-sem-EcoRV-F	TGGATTGATGTGATATCTCATGAGCCTGCACAGATAG
OsSBPase-sem-XbaII-R	CTTGACAGATCCTCTAGACCGCCTAGCTAGTTAGTTA