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Supplementary Information for

OsPDCD5 negatively regulates plant architecture and grain yield in rice

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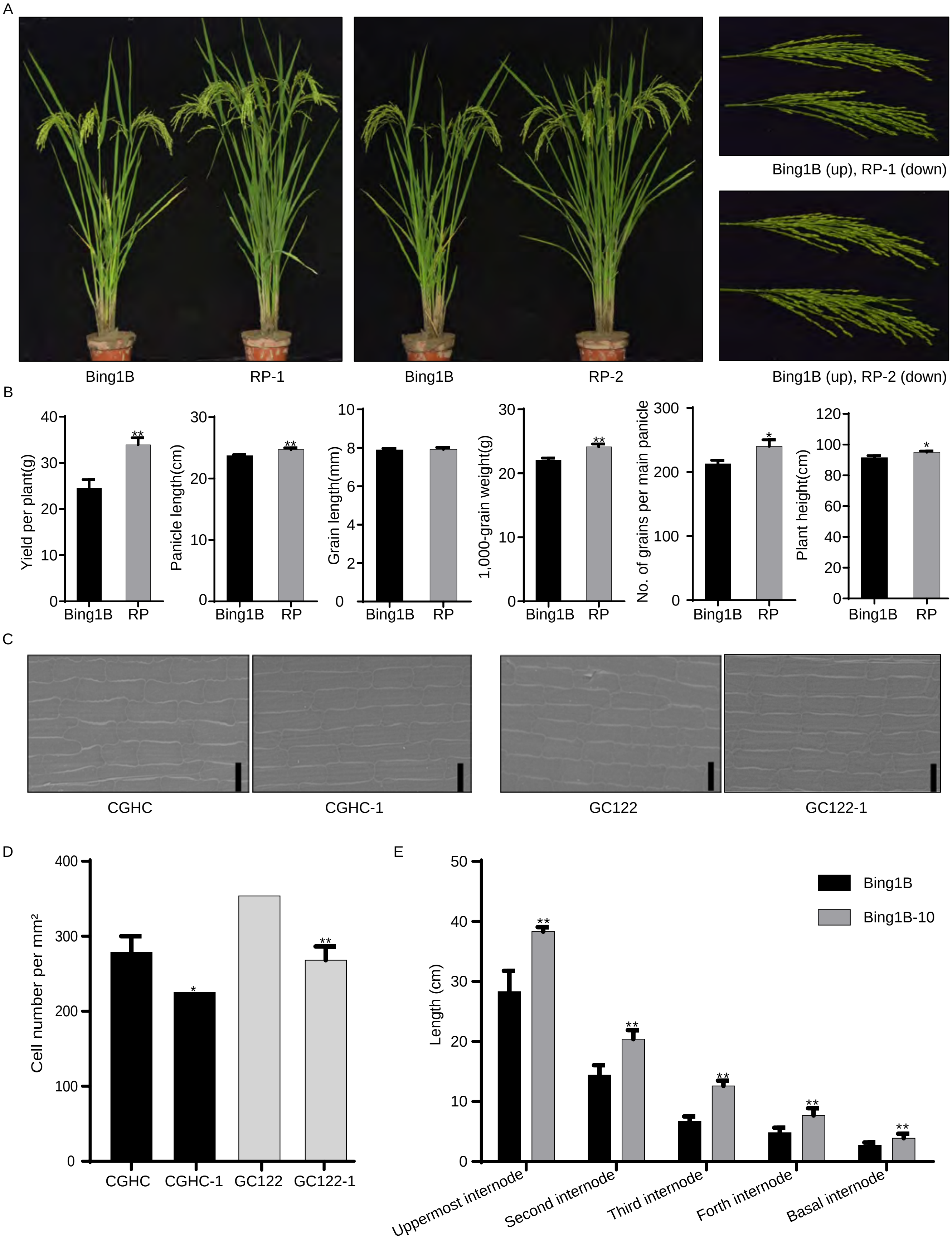
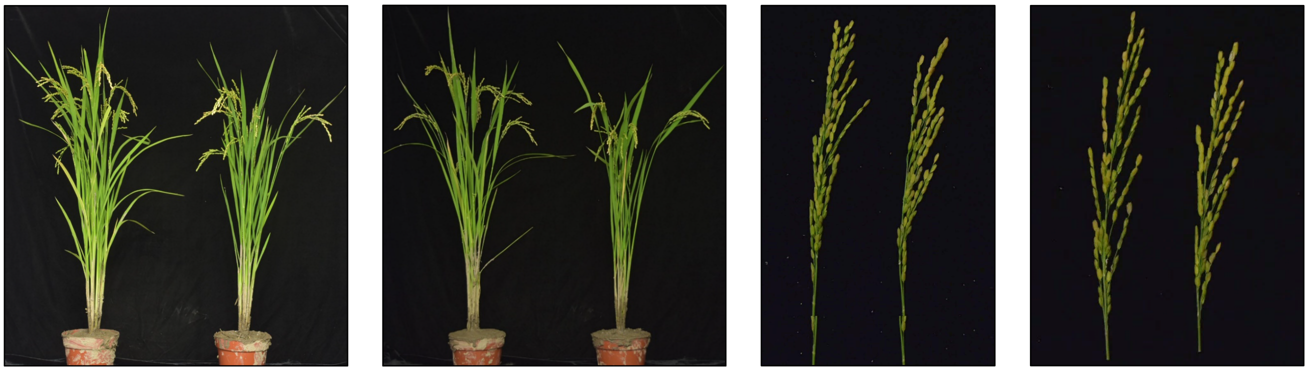
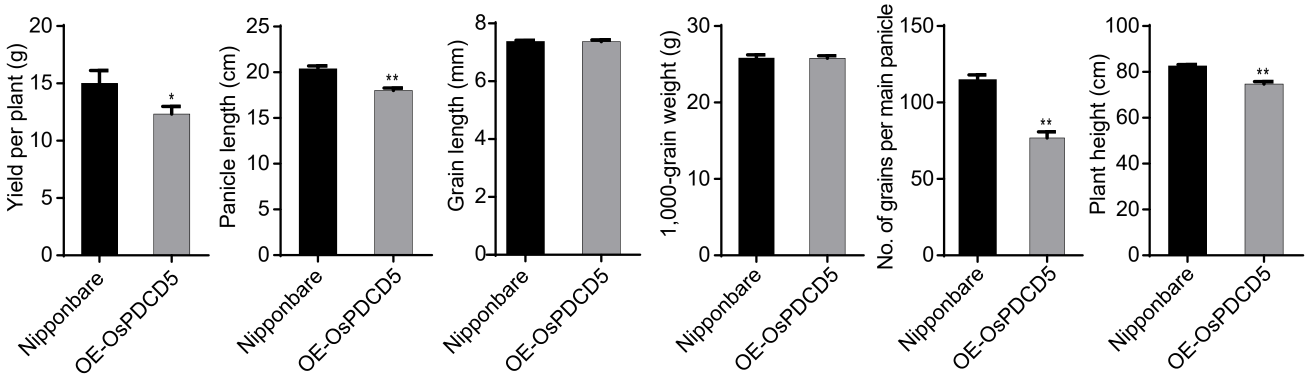

A
Bing1B
RP-1
Bing1B
RP-2
Bing1B (up), RP-1 (down)
Bing1B (up), RP-2 (down)
B
Yield per plant(g)
0
10
20
30
40
**
Bing1B
RP
Panicle length(cm)
0
10
20
30
**
Bing1B
RP
Grain length(mm)
0
2
4
6
8
10
Bing1B
RP
1,000-grain weight(g)
0
10
20
30
**
Bing1B
RP
No. of grains per main panicle
0
100
200
300
*
Bing1B
RP
Plant height(cm)
0
20
40
60
80
100
120
*
Bing1B
RP
C
CGHC
CGHC-1
GC122
GC122-1
D
Cell number per mm²
0
100
200
300
400
*
**
CGHC
CGHC-1
GC122
GC122-1
E
Length (cm)
0
10
20
30
40
50
Bing1B
Bing1B-10
**
**
**
**
**
Uppermost internode
Second internode
Third internode
Forth internode
Basal internode

F



Nipponbare OE-*OsPDCD5*-1 Nipponbare OE-*OsPDCD5*-2 Nipponbare OE-*OsPDCD5*-1 Nipponbare OE-*OsPDCD5*-2

G



H

Target site on *OsPDCD5*

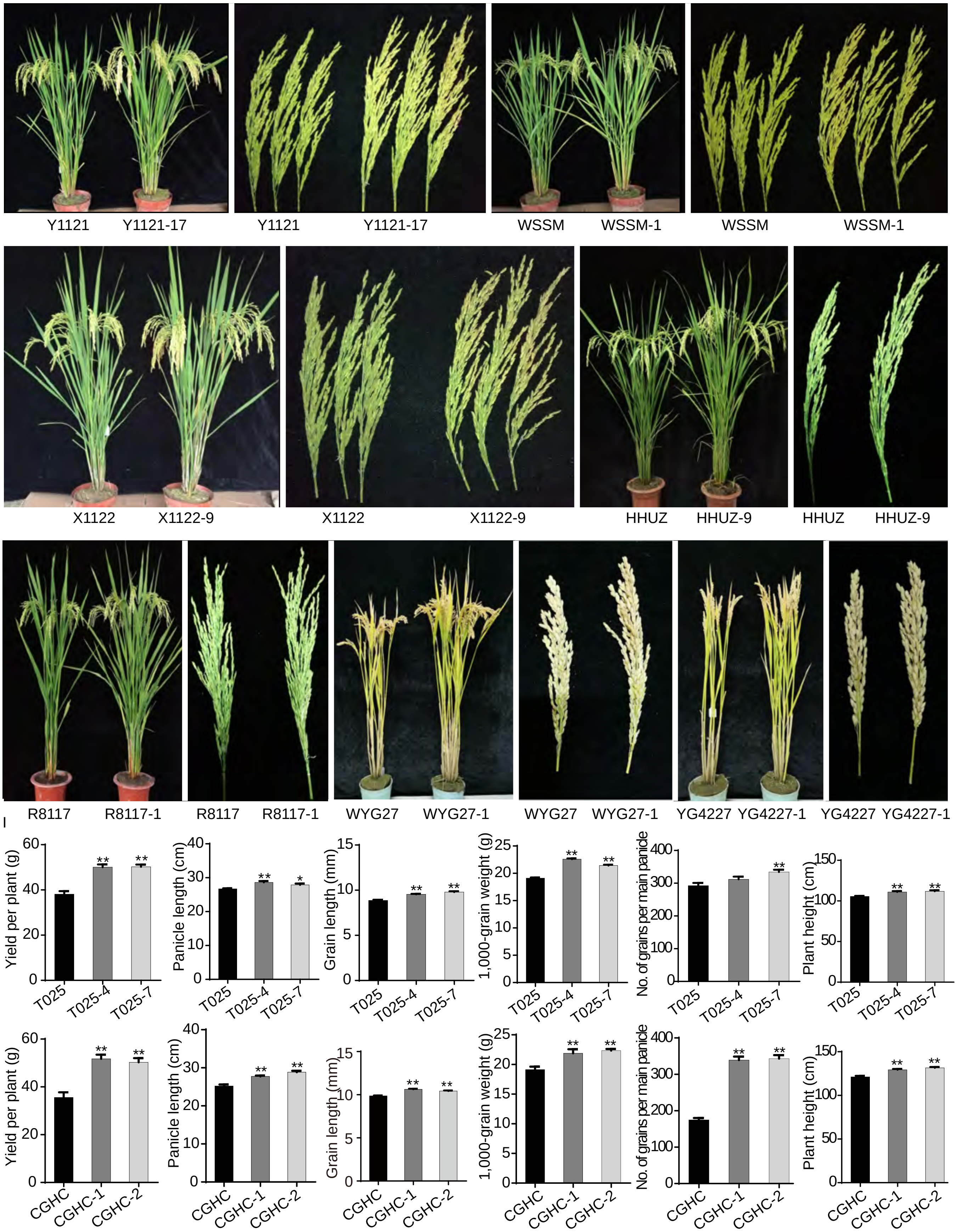
5' …ACCCAGAGTTGGAAGCTATCAGGCAGAGG… 3' T025
5' …ACCCAGAGTTGGAA----TCAGGCAGAGG… 3' T025-7

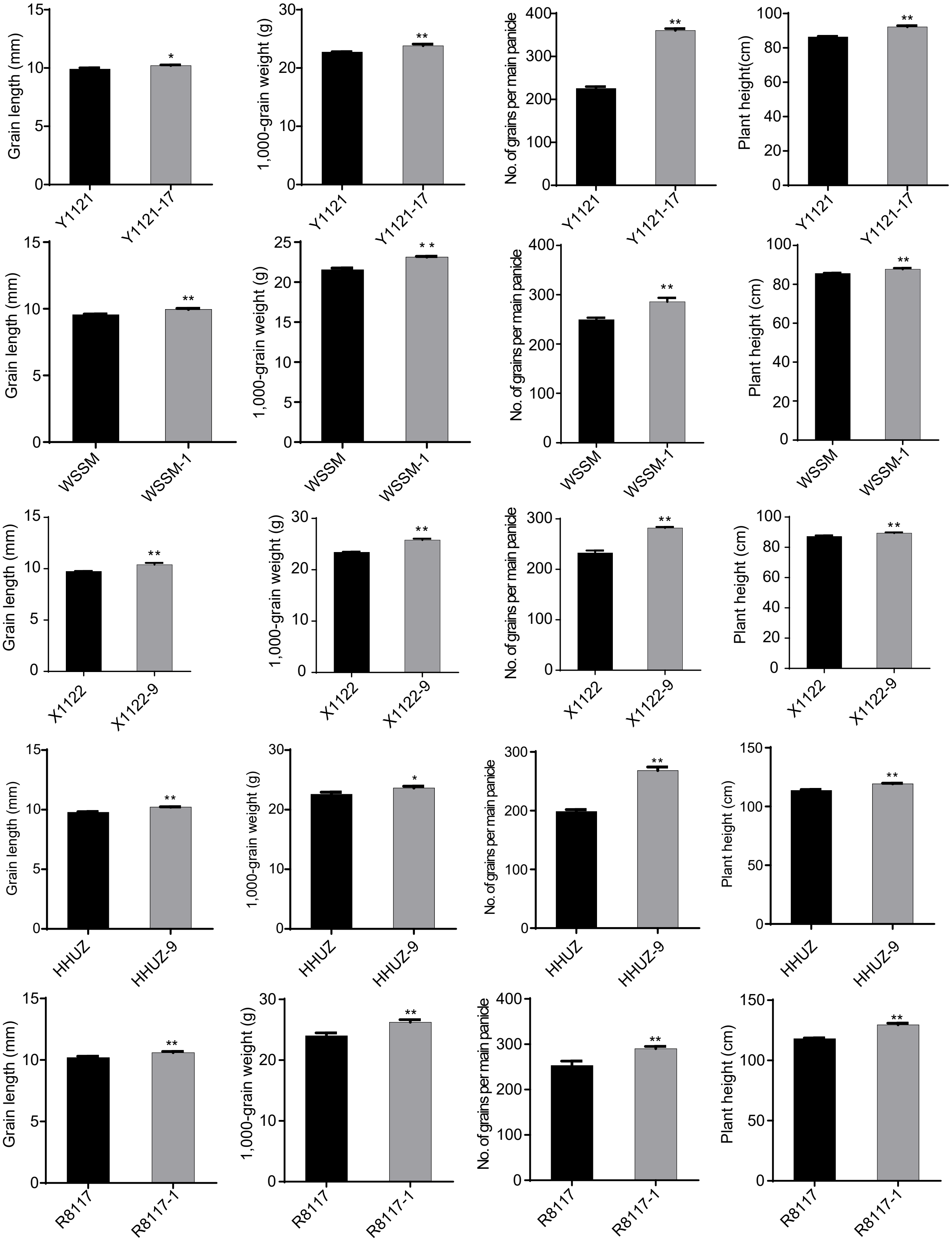
T025 T025-7 T025 T025-7 T025 T025-7 T025 T025-7

Target site on *OsPDCD5*

5' …ACCCAGAGTTGGAAGCTATCAGGCAGAGG… 3' CGHC
5' …ACCCAGAGTTGGAAGCTATCAGGC-GAGG… 3' CGHC-2

CGHC CGHC-2 CGHC CGHC-2 CGHC CGHC-2 CGHC CGHC-2


Y1121
Y1121-17
Y1121
Y1121-17
WSSM
WSSM-1
WSSM
WSSM-1
X1122
X1122-9
X1122
X1122-9
HHUZ
HHUZ-9
HHUZ
HHUZ-9
R8117
R8117-1
R8117
R8117-1
WYG27
WYG27-1
WYG27
WYG27-1
YG4227
YG4227-1
YG4227
YG4227-1
I
Yield per plant (g)
0
20
40
60
**
**
T025
T025-4
T025-7
Panicle length (cm)
0
10
20
30
40
**
*
T025
T025-4
T025-7
Grain length (mm)
0
5
10
15
**
**
T025
T025-4
T025-7
1,000-grain weight (g)
0
5
10
15
20
25
**
**
T025
T025-4
T025-7
No. of grains per main panicle
0
100
200
300
400
**
T025
T025-4
T025-7
Plant height (cm)
0
50
100
150
**
**
T025
T025-4
T025-7
Yield per plant (g)
0
20
40
60
**
**
CGHC
CGHC-1
CGHC-2
Panicle length (cm)
0
10
20
30
40
**
**
CGHC
CGHC-1
CGHC-2
Grain length (mm)
0
5
10
15
**
**
CGHC
CGHC-1
CGHC-2
1,000-grain weight (g)
0
5
10
15
20
25
**
**
CGHC
CGHC-1
CGHC-2
No. of grains per main panicle
0
100
200
300
400
**
**
CGHC
CGHC-1
CGHC-2
Plant height (cm)
0
50
100
150
**
**
CGHC
CGHC-1
CGHC-2


Grain length (mm)
1,000-grain weight (g)
No. of grains per main panicle
Plant height(cm)
Y1121
Y1121-17
*
**
Grain length (mm)
1,000-grain weight (g)
No. of grains per main panicle
Plant height (cm)
WSSM
WSSM-1
**
* *
Grain length (mm)
1,000-grain weight (g)
No. of grains per main panicle
Plant height (cm)
X1122
X1122-9
**
Grain length (mm)
1,000-grain weight (g)
No. of grains per main panicle
Plant height (cm)
HHUZ
HHUZ-9
**
*
Grain length (mm)
1,000-grain weight (g)
No. of grains per main panicle
Plant height (cm)
R8117
R8117-1
**
0
5
10
15
20
25
30
40
50
60
80
100
150
200
300
400

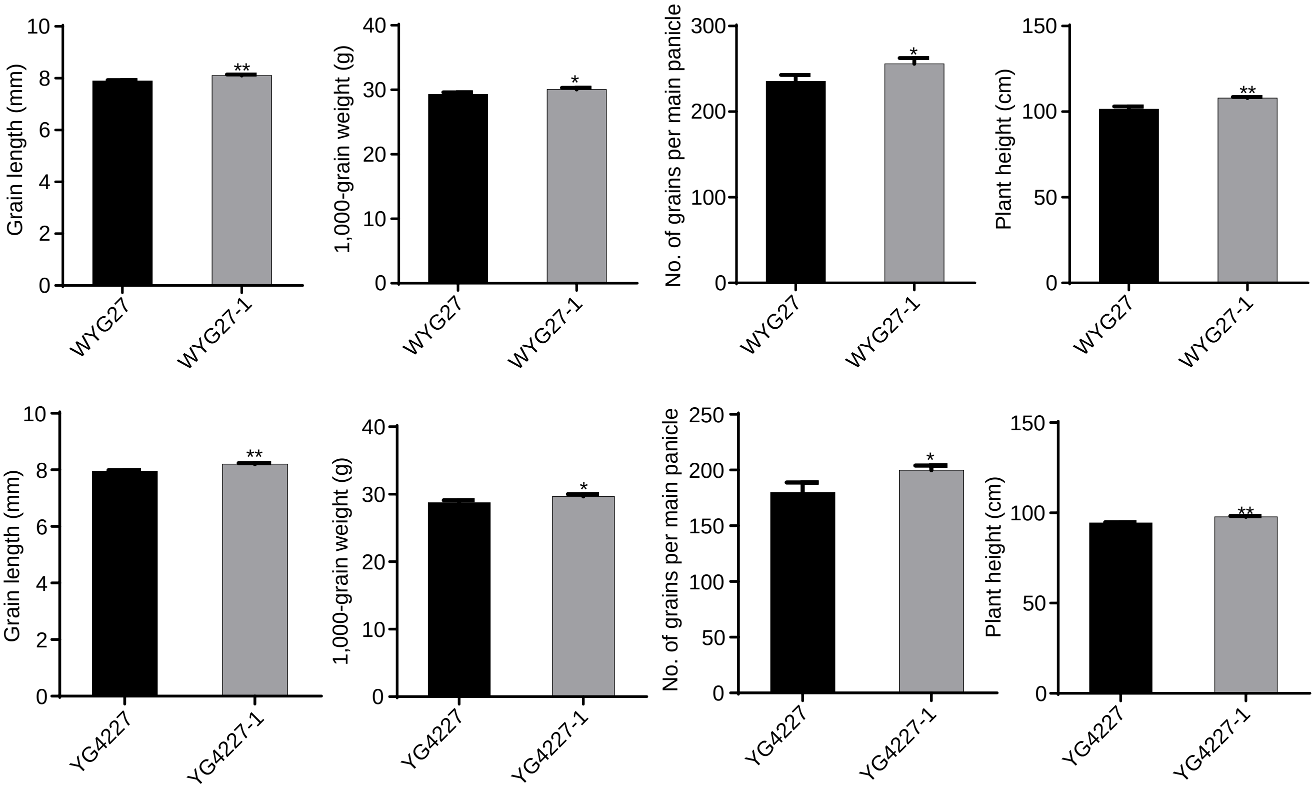


Fig. S1. Phenotypes of RNAi-*OsPDCD5*-RNAi lines (RP), *OsPDCD5* knockout lines and OE-*OsPDCD5* (transgenic line overexpressing *OsPDCD5*). (*A*) Plant architecture and panicles of Bing1B (wildtype) and RP-1 and RP-2 plants. RP-1 and RP-2 are individual plants of the same RNAi-*OsPDCD5* line. (*B*) Phenotypic traits of Bing1B and RP. (*C*) Scanning electron and light microscope photographs of the glume inner surfaces of mature seeds from wildtype and knockout lines CGHC, CGHC-1, GC122 and GC122-1. Scale bars are 50 µm. (*D*) Cell density per square millimeter on the glume inner surfaces of CGHC, CGHC-1, GC122 and GC122-1. (*E*) Internode length of Bing1B and Bing1B-10. (*F*) Plant architecture and panicles of Nipponbare (wildtype) and OE-*OsPDCD5*-1 and OE-*OsPDCD5*-2 plants. (*G*) Phenotypic traits of Nipponbare and OE-*OsPDCD5*. OE-*OsPDCD5*-1 and OE-*OsPDCD5*-2 are individual plants of the same OE-*OsPDCD5* line. (*H*) Target site in the *OsPDCD5* sequence in *OsPDCD5* knockout line T025-7 and CGHC-2. Field state, plant architecture, panicles and grains of T025 (wildtype) and T025-7, CGHC (wildtype) and CGHC-2. Plant architecture and panicles of Y1121 (wildtype) and Y1121-17 (knockout), WSSM (wildtype) and WSSM-1 (knockout), X1122 (wildtype) and X1122-9 (knockout), HHUZ (wildtype) and HHUZ-9 (knockout), R8117 (wildtype) and R8117-1 (knockout), WYG27 (wildtype) and WYG27-1 (knockout), YG4227 (wildtype) and YG4227-1 (knockout). (*I*) Phenotypic traits of T025 and T025-7, CGHC and CGHC-2, Y1121 and Y1121-17, WSSM and WSSM-1, X1122 and X1122-9, HHUZ and HHUZ-9, R8117 and R8117-1, WYG27 and WYG27-1, YG4227 and YG4227-1.The data are the means ± SEM (three replicates in *D* and *E*; over six replicates in *B*, *G* and *I*). *P <0.05, **P <0.01 (Student's *t*-test).

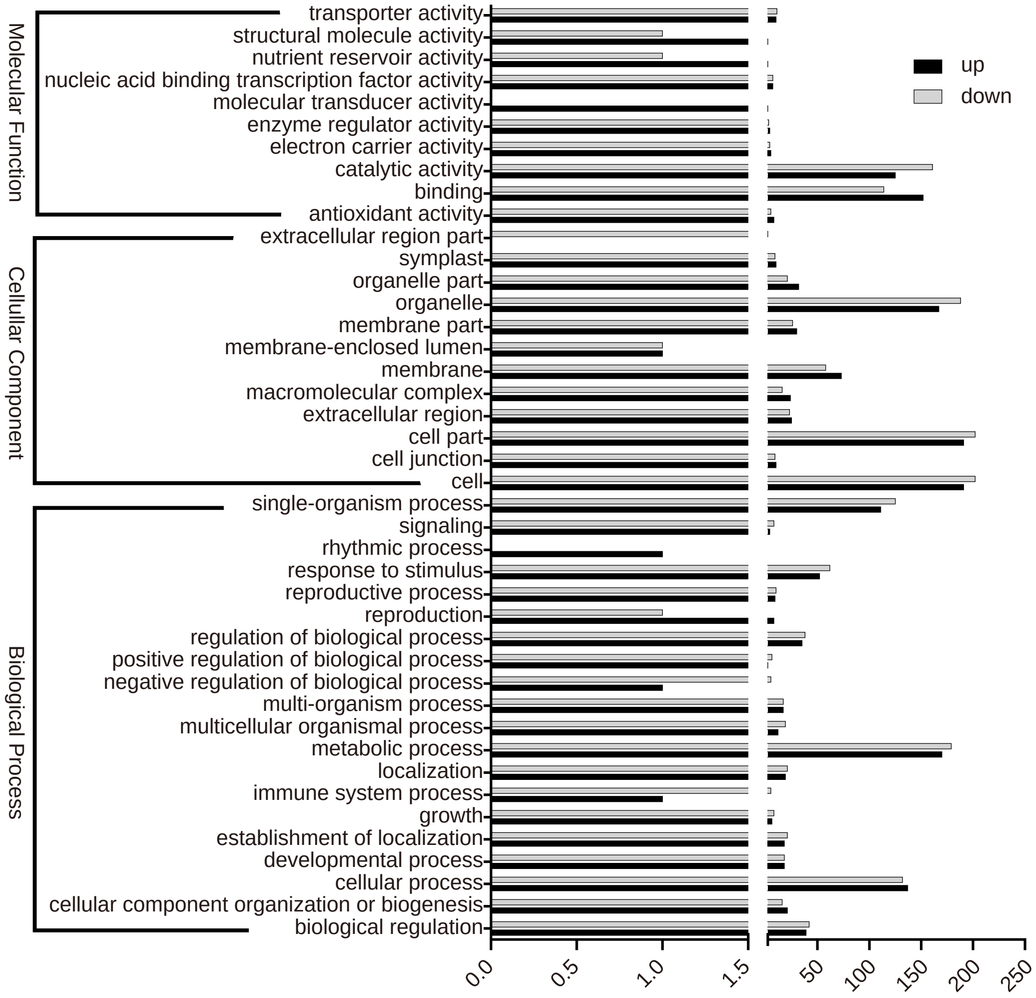


Fig.S2. GO functional enrichment analyzes of DEGs.

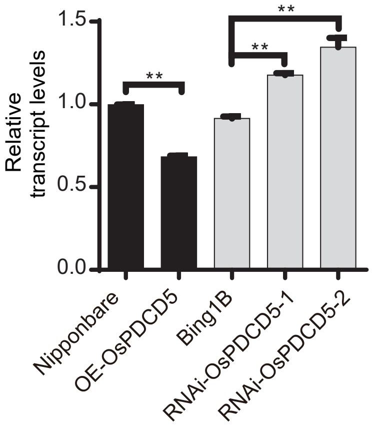


Fig.S3. Expression levels of *OsAGAP* in OE-*OsPDCD5* (transgenic line overexpressing *OsPDCD5*) and RNAi-*OsPDCD5* lines and the corresponding wildtypes Nipponbare and Bing1B by qPCR (three replicates). *Tubulin* was used as the loading control.The data are the means ± SEM. *P <0.05, **P <0.01 (Student's *t*-test).

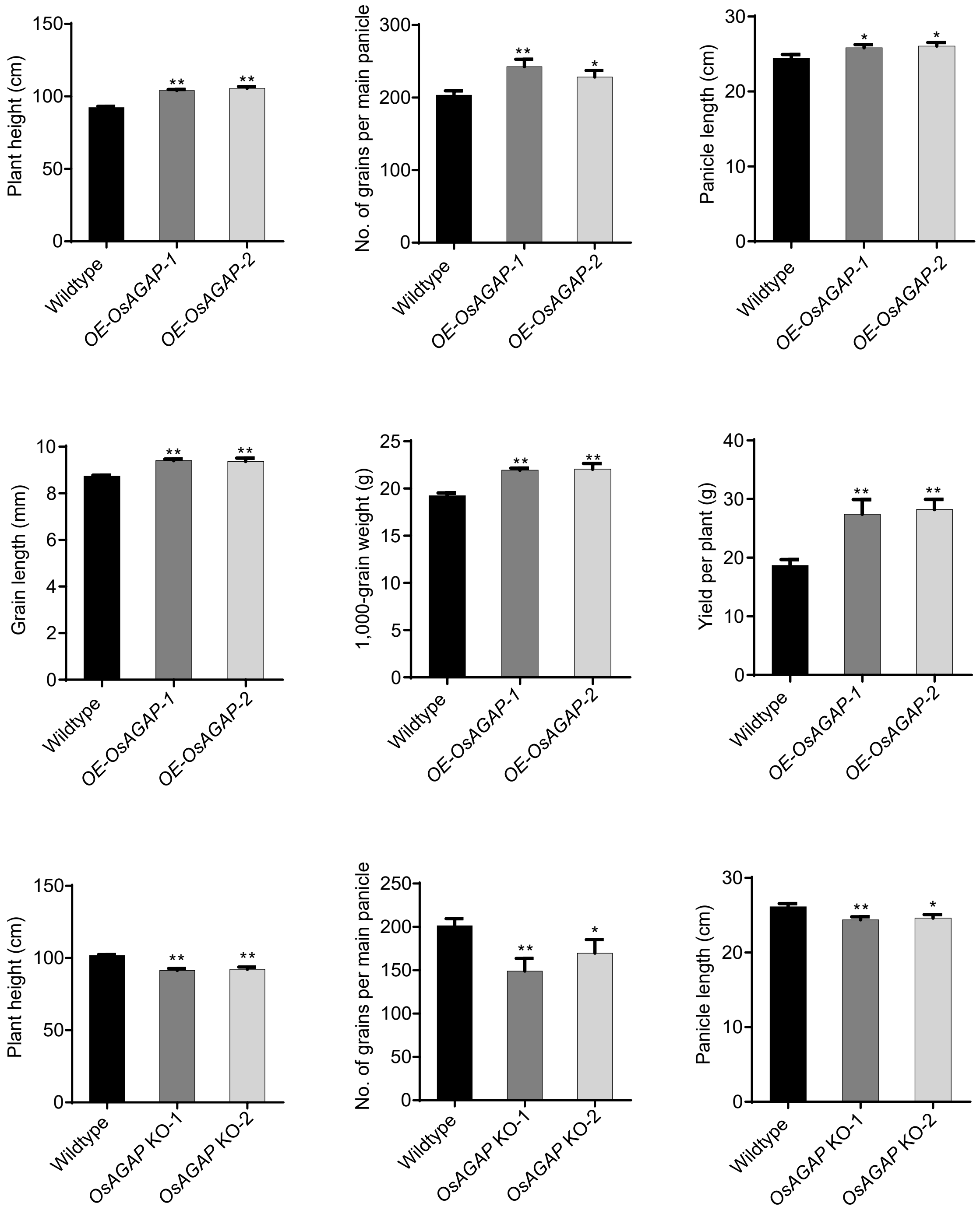
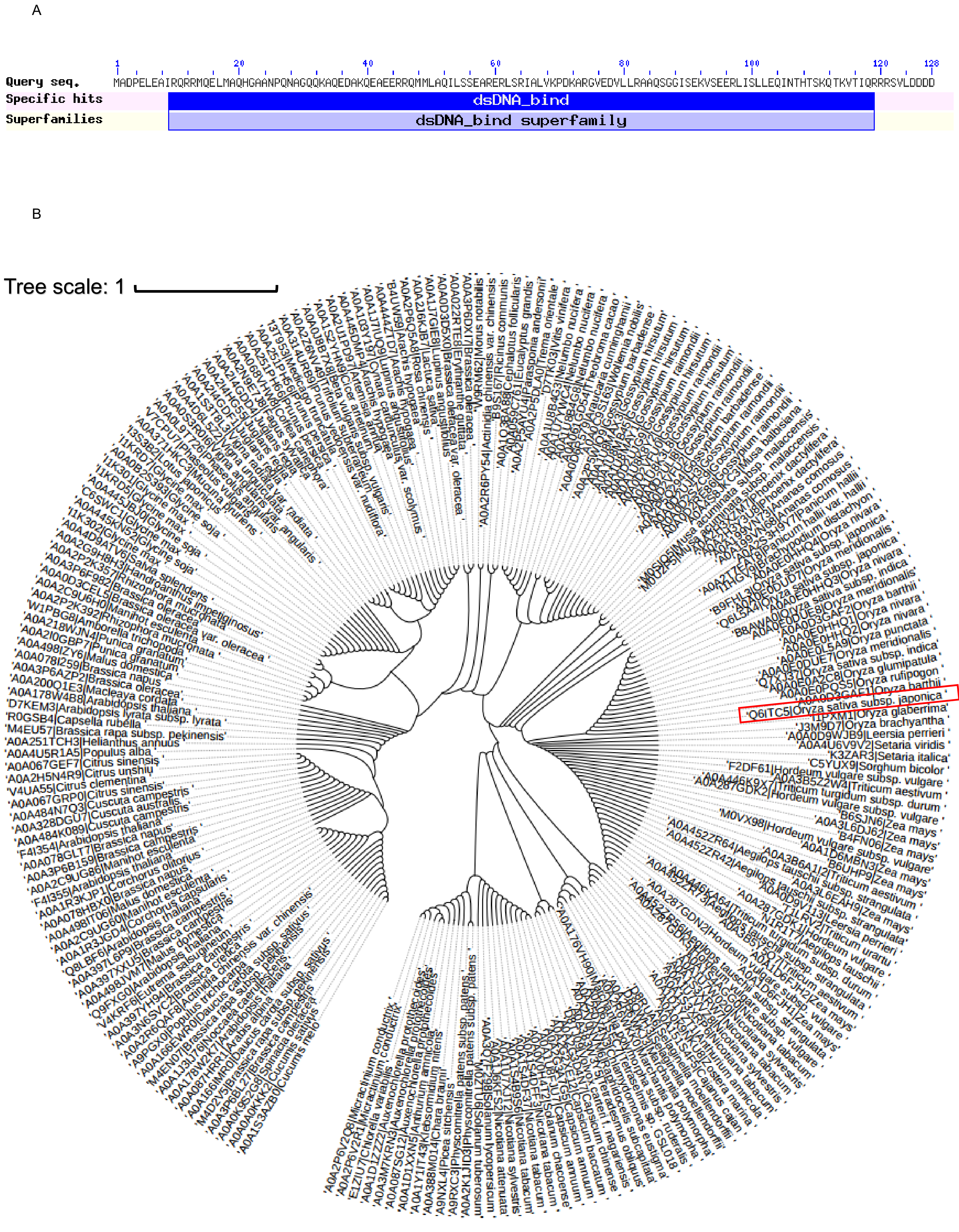


Fig.S4. Phenotypic traits of transgenic lines overexpressing *OsAGAP* (OE-*OsAGAP*-1 and OE-*OsAGAP*-2) and wildtype Bing1B (seven replicates). *OsAGAP* knockout lines (*OsAGAP* KO-1 and *OsAGAP* KO-2) and wildtype CGHC (over ten replicates). The data are the means ± SEM. **P* <0.05, ***P* <0.01 (Student's *t*-test).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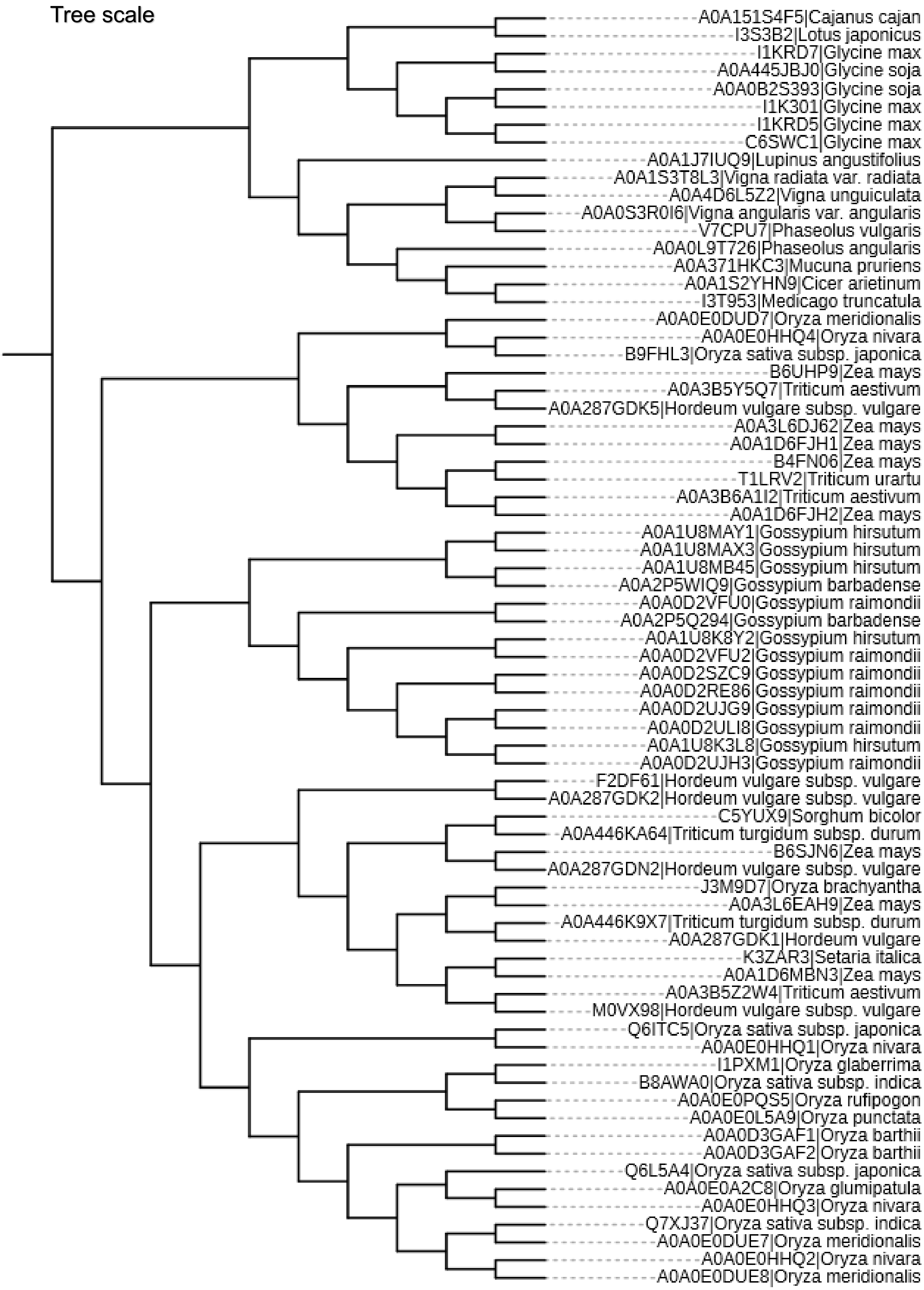
1
20
40
60
80
100
120
128
Specific hits
dsDNA_bind
Superfamilies
dsDNA_bind superfamily
B
Tree scale: 1
'Q6ITC5|Oryza sativa subsp. japonica'

C


Tree scale
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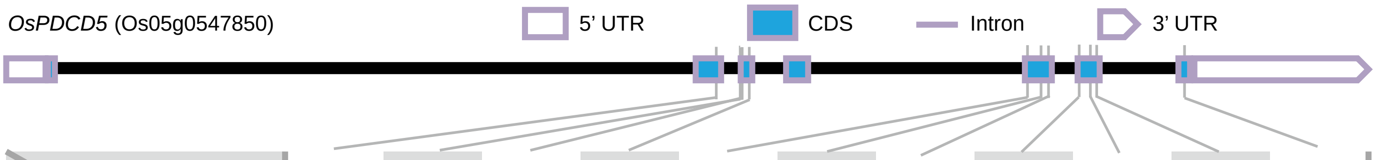
I3S3B2|Lotus japonicus
I1KRD7|Glycine max
A0A445JBJ0|Glycine soja
A0A0B2S393|Glycine soja
I1K301|Glycine max
I1KRD5|Glycine max
C6SWC1|Glycine max
A0A1J7IUQ9|Lupinus angustifolius
A0A1S3T8L3|Vigna radiata var. radiata
A0A4D6L5Z2|Vigna unguiculata
A0A0S3R0I6|Vigna angularis var. angularis
V7CPU7|Phaseolus vulgaris
A0A0L9T726|Phaseolus angularis
A0A371HKC3|Mucuna pruriens
A0A1S2YHN9|Cicer arietinum
I3T953|Medicago truncatula
A0A0E0DUD7|Oryza meridionalis
A0A0E0HHQ4|Oryza nivara
B9FHL3|Oryza sativa subsp. japonica
B6UHP9|Zea mays
A0A3B5Y5Q7|Triticum aestivum
A0A287GDK5|Hordeum vulgare subsp. vulgare
A0A3L6DJ62|Zea mays
A0A1D6FJH1|Zea mays
B4FN06|Zea mays
T1LRV2|Triticum urartu
A0A3B6A1I2|Triticum aestivum
A0A1D6FJH2|Zea mays
A0A1U8MAY1|Gossypium hirsutum
A0A1U8MAX3|Gossypium hirsutum
A0A1U8MB45|Gossypium hirsutum
A0A2P5WIQ9|Gossypium barbadense
A0A0D2VFU0|Gossypium raimondii
A0A2P5Q294|Gossypium barbadense
A0A1U8K8Y2|Gossypium hirsutum
A0A0D2VFU2|Gossypium raimondii
A0A0D2SZC9|Gossypium raimondii
A0A0D2RE86|Gossypium raimondii
A0A0D2UJG9|Gossypium raimondii
A0A0D2ULI8|Gossypium raimondii
A0A1U8K3L8|Gossypium hirsutum
A0A0D2UJH3|Gossypium raimondii
F2DF61|Hordeum vulgare subsp. vulgare
A0A287GDK2|Hordeum vulgare subsp. vulgare
C5YUX9|Sorghum bicolor
A0A446KA64|Triticum turgidum subsp. durum
B6SJN6|Zea mays
A0A287GDN2|Hordeum vulgare subsp. vulgare
J3M9D7|Oryza brachyantha
A0A3L6EAH9|Zea mays
A0A446K9X7|Triticum turgidum subsp. durum
A0A287GDK1|Hordeum vulgare
K3ZAR3|Setaria italica
A0A1D6MBN3|Zea mays
A0A3B5Z2W4|Triticum aestivum
M0VX98|Hordeum vulgare subsp. vulgare
Q6ITC5|Oryza sativa subsp. japonica
A0A0E0HHQ1|Oryza nivara
I1PXM1|Oryza glaberrima
B8AWA0|Oryza sativa subsp. indica
A0A0E0PQS5|Oryza rufipogon
A0A0E0L5A9|Oryza punctata
A0A0D3GAF1|Oryza barthii
A0A0D3GAF2|Oryza barthii
Q6L5A4|Oryza sativa subsp. japonica
A0A0E0A2C8|Oryza glumipatula
A0A0E0HHQ3|Oryza nivara
Q7XJ37|Oryza sativa subsp. indica
A0A0E0DUE7|Oryza meridionalis
A0A0E0HHQ2|Oryza nivara
A0A0E0DUE8|Oryza meridionalis

D



SNP pos. (bp) Accessions	27181409	27181299	27181298	27181284	27180332	27180300	27180288	27180164	27180143	27180135	27179808
Haplotype3	t	a	c	t	t	t	g	a	g	t	a
Nipponare	t	a	c	t	t	t	g	a	g	t	a
Wuyungeng27	t	a	c	t	t	t	g	a	g	t	a
Yanggeng4227	t	a	c	t	t	t	g	a	g	t	a
Haplotype4	c	g	c	c	t	t	g	a	g	t	-
Bing1B	c	g	c	c	t	t	g	a	g	t	g
R8117	c	g	c	c	t	t	g	a	g	t	g
T025	c	g	t	c	t	t	g	a	g	t	g
CGHC	c	g	t	c	t	t	g	a	g	t	g
GC122	c	g	t	c	t	t	g	a	g	t	g
Y1121	c	g	t	c	t	t	g	a	g	t	g
X1122	c	g	t	c	t	t	g	a	g	t	g
HHUZ	c	g	t	c	t	t	g	a	g	t	g
WSSM	c	g	t	c	t	t	g	a	g	t	g

E

```
Bing1B      MADPELEAIRQRRMQELMAQRGAANPQNAGQQKAQEDAKQEAEERRQMMLAQILSSEARERLSRIALVKPDKARGVEDVL  80
Haplotype4  MADPELEAIRQRRMQELMAQRGAANPQNAGQQKAQEDAKQEAEERRQMMLAQILSSEARERLSRIALVKPDKARGVEDVL  80

Bing1B      LRAAQSGGISEKVSEERLISLLEQINTHTSKQTKVTIQRRRSVLDDDD* - - - - - - - - - - - - - - - -   129
Haplotype4  LRAAQSGGISEKVSEERLISLLEQINTHTSKQTKVTIQRRRSVLDEMTSCMCVVCTMSWWRSLL*  145
```

Fig. S5. *OsPDCD5* gene structure and conservation. (*A*) Predicted double-stranded DNA-binding domain of *OsPDCD5*. (*B, C*) OsPDCD5 homologs are present in a large number of species (*B*) and in many common crops (*C*). *OsPDCD5* is marked by the red box. (*D*) Comparison of *OsPDCD5* haplotype3,4 and *OsPDCD5* in rice varieties edited in this study. (*E*) OsPDCD5 protein alignment of Bing1B and Haplotype4 using the CLC sequence viewer7 multiple sequence alignment tool.

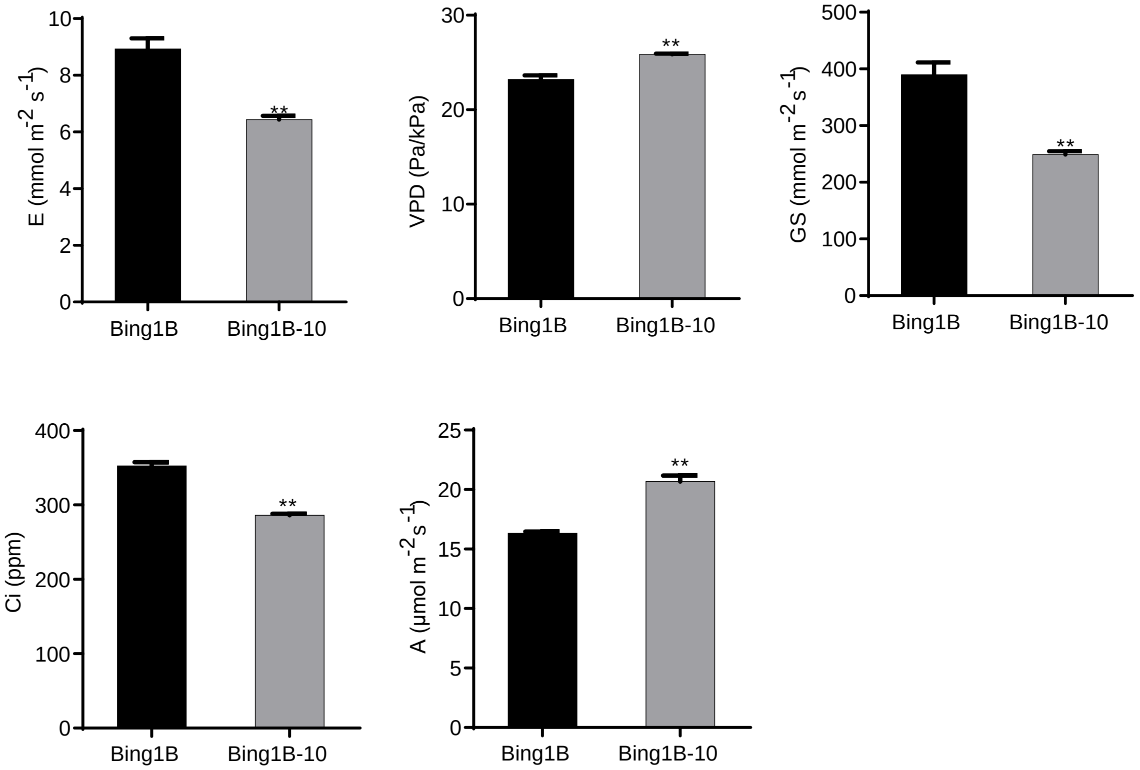


Fig. S6. Photosynthetic parameters of *OsPDCD5* knockout line Bing1B-10 and wildtype Bing1B at the tillering stage. E, transpiration rate; VPD, water pressure saturation deficit; GS, stomatal conductance; Ci, intercellular CO2 concentration; A, net photosynthetic rate. The data are the means ± SEM (three replicates). *P <0.05, **P <0.01 (Student's *t*-test).

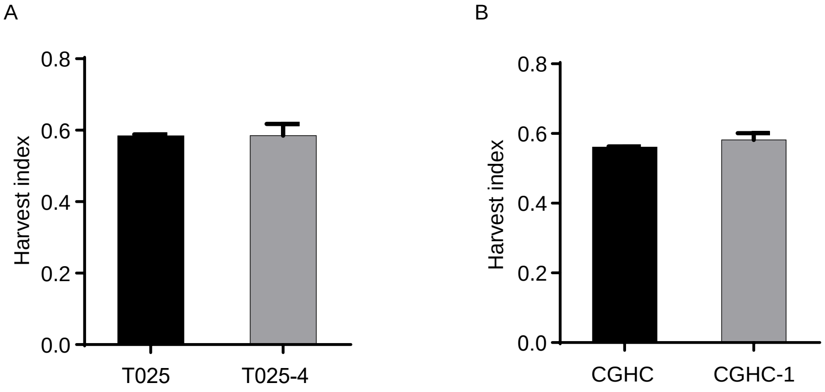


Fig. S7. Harvest index of *OsPDCD5* knockout lines. (*A*) Harvest index of T025 (wildtype) and T025-4 (knockout). (*B*) Harvest index of CGHC (wildtype) and CGHC-1 (knockout). (five replicates in *A* and *B*).

Table. S1 Conservation of OsPDCD5 amino acid sequences among various plant species

Entry name	Organism	Identity	Score	E-value
I1PXM1	Oryza glaberrima	100.00%	611	8.00E-80
A0A0D3GAF1	Oryza barthii	100.00%	611	1.20E-79
B9FHL3	Oryza sativa subsp. japonica	98.50%	317	1.3E-35
Q7XJ37	Oryza sativa subsp. indica	98.40%	605	6.80E-79
K3ZAR3	Setaria italica	97.70%	601	2.80E-78
J3M9D7	Oryza brachyantha	96.90%	599	5.80E-78
C5YUX9	Sorghum bicolor	96.10%	590	1.30E-76
A0A287GDK5	Hordeum vulgare subsp. vulgare	95.50%	312	6.10E-35
A0A3B6A1I2	Triticum aestivum	93.70%	556	2.10E-71
B6SJN6	Zea mays	93.00%	564	1.10E-72
A0A0D2UJG9	Gossypium raimondii	86.70%	537	1.60E-68
A0A1S3T8L3	Vigna radiata var. radiata	82.80%	520	6.20E-66
A0A151S4F5	Cajanus cajan	79.50%	503	2.50E-63
………………	………………	……..	…….	………
I3S3B2	Lotus japonicus	77.30%	489	3.40E-61

Table. S2 Primers used to confirm knockout mutants

Name	Primers (5'-3')	Gene Name
OsU6-JC-S	CCTGGCTGTATTTGGTGGTT	*OsU6*
OsU6-JC-A	AGTTAGCTGGGCAATGTGGT	*OsU6*
Cas9-OsU6-F	GATGTGCAGTCAGGGACCAT	*Cas9*
Cas9-RNAi-R	GACTCGGTGCCACTTTTTCA	*Cas9*
PCD-Exon2,3,4-F	ACCATGTAACTTCTCCTGATGGAAC	*OsPDCD5*
PCD-Exon2,3,4-R	GTTCAACAAAAATGACATCAAC	*OsPDCD5*
hyg (280)+	ACGGTGTCGTCCATCACAGTTTGCC	*hygr*
hyg (280)-	TTCCGGAAGTGCTTGACATTGGGGA	*hygr*
Kana (270)+	CGGCTATGACTGGGCACAACAGACAAT	*Kana*
Kana (270)-	CTCGGCAGGAGCAAGGTGAGATGAC	*Kana*
35S-CX-S	ATCCTTCGCAAGACCCTTCCTC	

Table. S3 List of rice cultivars used in this study

Type	Original producing area	Name on paper	Full name	Corresponding transgenic lines
Xian/Indica	China	Bing1B	Bing1B	Bing1B-10 (knockout line), RP-1, RP-2 (RNAi lines)
Xian/Indica	China	T025	Changhui T025	T025-1, T025-4, T025-7, T025-8, T025-10 (knockout lines)
Xian/Indica	China	CGHC	Changguihuicang	CGHC-1, CGHC-2 (knockout lines)
Xian/Indica	China	Y1121	Yeyue1121	Y1121-17 (knockout line)
Xian/Indica	China	WSSM	Wushansimiao	WSSM-1(knockout line)
Xian/Indica	China	X1122	Xin1121	X1122-9 (knockout line)
Xian/Indica	China	GC122	Guangchao122	GC122-1, GC122-2 (knockout lines)
Xian/Indica	China	HHUZ	Huanghuazhan	HHUZ-9 (knockout line)
Xian/Indica	China	R8117	R8117	R8117-1 (knockout line)
Geng/japonica	Japan	Nipponbare	Nipponbare	OE-*OsPDCD5*-1, OE-*OsPDCD5*-2 (over-expression transgenic lines)
Geng/japonica	China	YG4227	YangGeng4227	YG4227-1(knockout line)
Geng/japonica	China	WYG27	WuYuGeng27	WYG27-1(knockout line)

Table. S4 Primers used to construct vectors

Name	Primers (5'-3')	Gene Name
pPCD-5-SalI	GGgtcgacAGAAGAAGATGGAACAATAG	*OsPDCD5*
pPCD-3-BglII	ATAagatctACCATGGCTTCCCCCGCGCGCTCA	*OsPDCD5*
PCD-GFP-NcoI	TATccatggATGGCTGACCCAGAGTTGG	*OsPDCD5*
PCD-GFP-SpeI	GGactagtGTCATCGTCGTCAAGGACGC	*OsPDCD5*
PCD-GFPC-EcoRI	TATgaattcATGGCTGACCCAGAGTTGG	*OsPDCD5*
PCD-GFPC-KpnI	GGggtaccGGTCATCGTCGTCAAGGACGC	*OsPDCD5*
PCD-RNAi5-BamHI	CGggatccATGGCTGACCCAGAGTTGG	*OsPDCD5*
PCD-RNAi5-KpnI	GGggtaccCTAGTCATCGTCGTCAAGGAC	*OsPDCD5*
PCD-RNAi3-SpeI	GGactagtCTAGTCATCGTCGTCAAGGAC	*OsPDCD5*
PCD-RNAi3-SacI	GGgagctcATGGCTGACCCAGAGTTGG	*OsPDCD5*
PCD-GFPN-EcoRI	TATgaattcTATGGCTGACCCAGAGTTGG	*OsPDCD5*
PCD-GFPN-KpnI	GGggtaccCTAGTCATCGTCGTCAAGGA	*OsPDCD5*
M13R	CAGGAAACAGCTATGACC	
M13F	TGTAAAACGACGGCCAGT	
NGFP-Sequence	ATGGTCCGGACTCAGATCTCGA	*GFP*
GFPC-Sequence	CCATGGGCACTAGTATGGTC	*GFP*

Table. S5 Primers used for the qPCRs

Name	Primers (5’-3’)	Gene Name
Actin-F	TCTGGCATCACACCTTCTACA	*Actin*
Actin-R	GGAAGGCTGGAAGAGGAC	*Actin*
Tubulin-F	TACCGTGCCCTTACTGTTCC	*Tubulin*
Tubulin-R	CGGTGGAATGTCACAGACAC	*Tubulin*
OsPDCD5-S2	CTGAGGAACGGCGGCAGATGAT	*OsPDCD5*
OsPDCD5-A2	GGTATTGATTTGCTCCAGAAGTG	*OsPDCD5*
OsAGAP-F	GAAGGAGCTATTGCACAG	*OsAGAP*
OsAGAP-R	CATATATAGCATTGGCGTG	*OsAGAP*
OsEXPA1-F	ACATGCCTCCTCTGGAAC	*OsEXPA1*
OsEXPA1-R	GTACATCACCGGCACGAT	*OsEXPA1*
OsEXPA5-F	CTTGTATCACCCGCCAAAAT	*OsEXPA5*
OsEXPA5-R	TAAGCAGCACACAGGGCATA	*OsEXPA5*
OsEXPA10-F	GAACACCTTTGGAGCCAT	*OsEXPA10*
OsEXPA10-R	ATCTTCTCGAAGGACTGGAT	*OsEXPA10*
OsEXPA16-F	GTGAAGGTGAAAGGGTCGAG	*OsEXPA16*
OsEXPA16-R	CAAGAATGACACCCACATCG	*OsEXPA16*
06g47360-F	CACCTTCTACACCGTTTACAC	*LOC_Os06g47360*
06g47360-R	GTCGACGATCTTGACGGTGAC	*LOC_Os06g47360*
08g37930-F	CATCTGGAGTCGCCACCTTCTACAC	*LOC_Os08g37930*
08g37930-R	GTTGTCGACCATCTTCACGGTGAC	*LOC_Os08g37930*
06g03970-F	ATATTGCTCTGCGTTCTGCTG	*LOC_Os06g03970*
06g03970-R	ACAAGTGGCTGTGGTTGATTTG	*LOC_Os06g03970*
OsGA20ox1-S	TACGCCAGCAGCTTCACGG	*OsGA20ox1*
OsGA20ox1-A	TCCATCAGCTCCAGCGACA	*OsGA20ox1*
OsGA20ox3-S	CGCTCACCTTCTTCCTCAACC	*OsGA20ox3*
OsGA20ox3-A	AGCCATTCCTTTGCTTGATCCA	*OsGA20ox3*
OsGA2ox3-S	TCGTTGCAGGTTCTGACCA	*OsGA2ox3*
OsGA2ox3-A	CCTGTTGTCTCCAAGCCTT	*OsGA2ox3*
OsGA2ox4-S	CTCCTTCCTCGTCATCGTC	*OsGA2ox4*
OsGA2ox4-A	GCAGCCTTCTTGTACTCCC	*OsGA2ox4*
OsGA2ox5-S	CCAGCACCCTCATCGTCA	*OsGA2ox5*
OsGA2ox5-A	TGCTTCCTGTACTCGCCGAA	*OsGA2ox5*
OsGA2ox6-S	GACTTCCTCACCGTCCTG	*OsGA2ox6*
OsGA2ox6-A	GCACCTTCTTCCTGTACTCC	*OsGA2ox6*
OsGA3ox1-S	GATCTCTTCCATGTGCTCACC	*OsGA3ox1*
OsGA3ox1-A	GAATCATGCTCAACGCCGAT	*OsGA3ox1*

Name	Primers (5’-3’)	Gene Name
OsGA3ox2-S	TCCAAGCTCATGTGGTCCGA	*OsGA3ox2*
OsGA3ox2-A	TCCTCTCCGCCTCGACTC	*OsGA3ox2*
EUI-F2	CTTCTCCTTCGATGTGATATCGC	*OsEUI*
EUI-R2	ACGCTGGTCTCCGACATGAG	*OsEUI*
OsGID1-F2	CAAGAGCCTCATCATCGTGT	*OsGID1*
OsGID1-R2	CATTGGACAACCTTGACGTG	*OsGID1*
OsGID2-F2	CTATCTCAGAGCTGGACACT	*OsGID2*
OsGID2-R2	CCTCCTGTTTCCGACAAATC	*OsGID2*
OsSPY-F	ATCGTCCTCTGGTCATTGGC	*OsSPY*
OsSPY-R	TCTCTTACCAAGCTAGCAACC	*OsSPY*
SLR1-F1	GACGTCAACGAACGCTCAATT	*OsSLR1*
SLR1-R1	CGGAGTCCAGTCGTCGATCT	*OsSLR1*
OsYUC3-F	CTGGTGACATCAAGGTACGG	*OsYUC3*
OsYUC3-R	ACTCCCGGTCCTTTAACCAG	*OsYUC3*
OsYUC9-F	CTGGCTCAAGAGTGATGACG	*OsYUC9*
OsYUC9-R	TCCTCGTAGCTGCCGTAGAT	*OsYUC9*
OsTAR2-F	CGCCCTACTACTCGTCATACC	*OsTAR2*
OsTAR2-R	GATTGTTCGGGGAGCAGAC	*OsTAR2*
OsIPT9-F	ACACCCGAACAACCATCGAA	*OsIPT9*
OsIPT9--R	GTCGACCCCACTTCTCTGTG	*OsIPT9*
OsIPT10-F	CTGCCTTCTCCTTGCCCTAC	*OsIPT10*
OsIPT10-R	CAGCATCTCTTCGCACCTCA	*OsIPT10*
LOG-F	CGGTTTGCTGATGCGTTCAT	*OsLOG*
LOG-R	TCGCTGACAGCCATGTCAAT	*OsLOG*
OsCKX4-F	GACCGACTACCTCCATCTCACA	*OsCKX4*
OsCKX4-R	GGTTGACATTGCTGACCTGC	*OsCKX4*
OsRR9/10-F	TCATGAGGACAGCCCAATTTCTA	*OsRR9/10*
OsRR9/10-R	TGCAGTAGTCTGTGATGATCAGGTT	*OsRR9/10*
OHK4-F	CAAGAACATATTGGTAGTTG	*OsOHK4*
OHK4-R	CCTTCCCTTCCATTGCTCGT	*OsOHK4*
OsAHP1-F	CAGAGATGGGTGCCTCAAGAC	*OsAHP1*
OsAHP1-R	CGCGCCAGTTTAATGTTTAGG	*OsAHP1*
OsAHP2-F	GCGCAACAAGTTTCAGACTATGC	*OsAHP2*
OsAHP2-R	GATCACATGCAGCTACACTCTTTTG	*OsAHP2*
OHK2-F	AGGGATGCTCCAAATGCTCA	*OsOHK2*
OHK2-R	AGATCAAAGGGCACCGTCTC	*OsOHK2*

Name	Primers (5’-3’)	Gene Name
OHK3b-RT-F	CCTGCTTCTTGGTGTCTTAG	*OsOHK3b*
OHK3b-RT-R	AGCATCCTAGCTCTCTCATCA	*OsOHK3b*