

Table S1 Markers used for fine mapping of *DNRL1*

Primer	Forward sequence	Reverse sequence
S1	5'-TTCGATGTGACATGGTGA-3'	5'-TCTTCGTGCGAGTAGGTT -3'
S5	5'-GGTTGGTACGCCTACGTC-3'	5'-GGGGCTTTTGATGATGGG-3'
S11	5'-AGGGTCGGTGGGGTAGGT-3'	5'-GAGGAGGCCGGTGAAATT-3'
RM21981	5'-TTAATCCAGCTCCTCTGACTTTGG-3'	5'-TGGCGGCTTAGGAGTGTTTATAGG-3'
RM21985	5'-GTCGGTATCTGCGCGTACTTGG-3'	5'-GGCCCTGTAATGAGACGACAAGC-3'
RM21989	5'-AGGTGCAGGTGAGGTGACTCC-3'	5'-CACCTTCCTTCCATTCGACTCC-3'
RM18	5'-TTCCCTCTCATGAGCTCCAT-3'	5'-GAGTGCCTGGCGCTGTAC-3'
RM8261	5'-GACGACTGGATGGTACGAC-3'	5'-TGCTTCTCCTGCAAACAC-3'

Table S2 Performance of agronomic traits in IR64, *dnrl1*, complementation and overexpression lines

Material	Plant height(cm)	No.of panicles	Seed-setting rate (%)	1000-grain weight(g)
IR64	109.1 ±1.2	22.7 ±2.3	65.8 ±3.3	26.3 ±0.3
<i>dnrl1</i>	83.1 ±2.8**	17.3 ±2.5	67.5 ±0.4	22.8 ±0.7**
dnrl1-c1	84.0 ±1.1**	19.3 ±2.9	41.5 ±6.4*	22.1 ±0.3**
dnrl1-c3	81.7 ±2.1**	21.7 ±1.5	67.2 ±4.3	22.2 ±0.3**
dnrl1-ox3	82.1 ±0.9**	21.3 ±1.5	52 ±1.7*	22.1 ±0.2**
dnrl1-ox7	82.6 ±1.5**	21.7 ±1.5	55.7 ±3.9	22.8 ±0.7*

Values are means ± SD (n=3), * indicates significance at $P \leq 0.05$; ** indicates significance at $P \leq 0.01$; dnrl1-c1 and dnrl1-c3 are complementation lines;

dnrl1-ox3 and dnrl1-ox7 are overexpression lines.

Table S3. List of genes used for qRT- PCR analysis

Gene	Forward primer (5'–3')	Reverse primer (5'–3')	Accession No.
<i>OsCAO1</i>	GATCCATACCCGATCGACAT	CGAGAGACATCCGGTAGAGC	J013116K15
<i>OsRpoTp</i>	ATTTCTCCTGCTCTTC	TGACTTGCTGCGTATGTG	AK058530
<i>HEMA1</i>	CGCTATTTCTGATGCTATGGGT	TCTTGGGTGATGATTGTTTGG	J013000F15
<i>OsPORA</i>	TGTACTGGAGCTGGAACAACAA	GAGCACAGCAAAATCCTAGACG	AK065236
<i>PPR1</i>	CTAAGACCGAATGACAAATGC	GCACTGCCAACAAGAATACC	AY584749
<i>psaA</i>	GCGAGCAAATAAAACACCTTTC	GTACCAGCTTAACGTGGGGAG	AAS46121
<i>psbA</i>	CCCTCATTAGCAGATTCGTTTT	ATGATTGTATTCCAGGCAGAGC	AAS46104
<i>rpoA</i>	ACGGAAGTCAGAAAGAAC	TACGAGAAGCCTCATAAA	NC_001320
<i>SPP</i>	CGGAGAGGAAACATAATGAC	ATAGGCATTGTCTTTGTCTC	AK066566
<i>YGL1</i>	AACCTTACCGTCCTATTCCTT	CCATACATCTAACAGAGCACCC	EF432576
<i>OscpSRP54</i>	AGATGTGAGTCTCCAGT	TCAGATACTTCTCCACCC	AY050999
<i>DNRL1</i>	CACAGCGAACAAGGAGACAGG	AGAGGAGGCACTCATGGGATG	AB122082.1
<i>NAL1</i>	TTGGTATGGAATCTATGCTGGAA	TGAGGCTATTGAGCGGACACT	EU093963
<i>NRL1</i>	ACCACAACCTCGTCTTCTTCG	TCTTCTTGCCCATGCTCTTCT	AK242601
<i>OsCOW1</i>	TAGGTTTCTACTCCTCGTTGC	CTTGATGTTTCCCGATTGAT	AK072466
<i>TDD1</i>	TTTTGGTGTCTGCATGGGTCT	CTCCTCATCGTAGCGAACTGG	AK107879
<i>ubq</i>	GCTCCGTGGCGGTATCAT	CGGCAGTTGACAGCCCTAG	AF184280
<i>LYL1</i>	ACGAGTACATCGGCATGGTC	TGTAGTGCACCACGTACGAC	KF305678
<i>OsCAO2</i>	AGACTGTTGCAAGACGGAGG	TTGTTCAAAAACGGGACGC	AK063367
<i>OsChlD</i>	CATAGCAATGGCCCGAATC	TACGTCCAACATCACCGCTC	AK072463
<i>OsPORB</i>	GGGTGTACTGGAGCTGGAAC	ACTGATCGTGATCGGCCAAG	AK068143
<i>YL1</i>	AACTCTGCCGGTGGATTTCAT	GGAGCGAGCCCATTGTCATA	AK061136
<i>YGL8</i>	GCAGTTCCTCAACGACTGGA	TGTTGTGCGGTTGGTCTCAA	AK059435

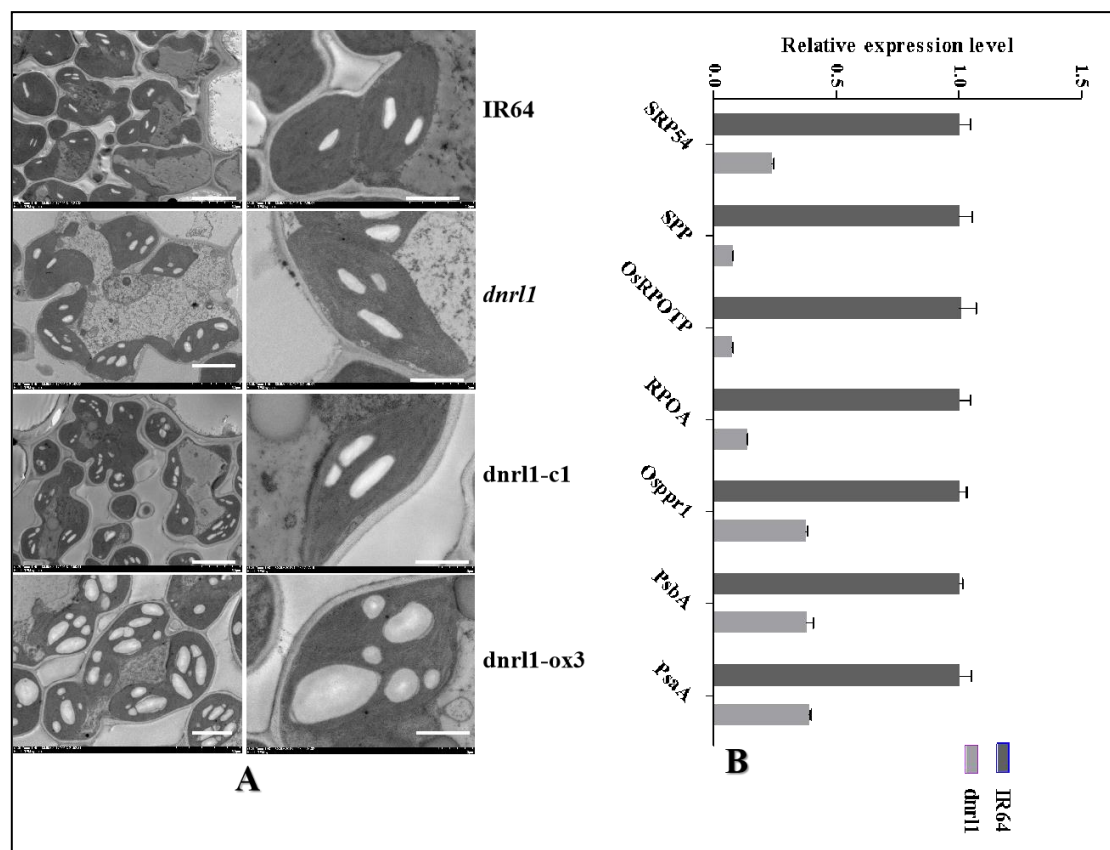


Figure S1. Ultrastructure of chloroplast and qRT-PCR analysis of photosynthesis-related genes

A, Chloroplast ultrastructure of IR64, *dnr11*, *dnr11-c1* and *dnr11-ox3*, for the left column bar=50 um, for the right column bar=20um; B, qRT-PCR analysis of 7 photosynthesis- related genes .