

Table 1 Suppl. Water use efficiency and yield related traits of parents IR64 and INRC10192 ($n = 5$) and recombinant inbred lines (RILs; $n = 153$) under control conditions and a reduced moisture supply (treatment). RWC - relative water content, SLA - specific leaf area, CID - carbon isotope discrimination ($\Delta^{13}\text{C}$), LLN - leaf length, LWD - leaf width, SHLN - shoot length, RTLN - root length, SPF - spikelet fertility, PNO - number of panicles, NFG - number of filled grains, TMT - test mass, TYLD - total yield per plant, SD - standard deviation, Range - (minimum) - (maximum), TS - transgressive segregation [%], SKEW - skewness.

Traits	Control							Treatment						
	INRC	IR64	RILs	SD	Range	TS	SKEW	INRC	IR64	RILs	SD	Range	TS	SKEW
RWC [%]	94.1	88.9	88.82	6.35	67.0-104.0	72.5	-0.52	90.3	82.4	85.95	6.78	67.0-99.0	58.8	-0.11
SLA [$\text{cm}^2 \text{g}^{-1}$]	58.9	78.3	105.86	32.01	31.8-226.8	83.6	0.96	53.2	64.9	82.57	27.25	32.7-179.2	80.3	1.07
CID [%]	19.3	20.5	19.78	0.64	17.7-20.9	22.2	-0.58	-	-	-	-	-	-	-
LLN [cm]	46.0	28.0	52.33	8.79	32.5-73.0	62.7	0.23	45.0	23.0	50.80	8.70	35.0-69.5	72.5	-0.20
LWD [cm]	9.5	8.5	9.83	2.17	5.5-17.5	64.7	0.99	9.3	8.2	9.10	2.13	6.5-15.5	71.8	0.64
SHLN [cm]	113.0	66.5	122.16	19.39	67.0-178.5	71.2	-0.30	105.0	64.5	119.48	15.97	77.5-168.5	81.0	0.00
RTLN [cm]	33.5	25.0	32.88	5.37	17.5-51.0	50.9	0.06	32.0	24.0	32.88	5.08	20.5-53.0	57.5	0.65
SPF [%]	86.0	87.0	82.25	9.57	50.8-98.1	92.1	-0.83	84.0	83.0	79.79	7.64	58.5-97.0	89.5	-0.21
PNO	8.5	9.0	5.95	1.81	2.0-12.5	95.4	0.48	6.5	7.5	5.37	1.58	3.0-12.0	80.3	1.17
NFG	103.0	150.0	98.23	24.32	30.0-149.0	58.1	-0.32	100.0	120.0	96.83	24.61	25.0-135.0	75.8	0.47
TMT [g]	17.8	24.0	21.84	2.63	15.6-30.5	20.2	0.52	15.0	19.0	21.57	2.48	14.9-28.1	43.7	0.27
TYLD [g]	12.4	18.0	10.69	4.20	4.2-26.5	72.5	0.74	10.6	8.1	7.73	2.44	2.2-14.1	20.2	0.44

Table 2 Suppl. Correlation coefficients (* - $P < 0.05$, ** - $P < 0.01$) among water use efficiency and yield related traits under control (C) conditions. For abbreviations see Table 1.

	RWC-C	SLA-C	CID-C	LLN-C	LWD-C	SHLN-C	RTLN-C	SPF-C	PNO-C	NFG-C	TWT-C	TYLD-C
RWC-C	1											
SLA-C	-0.077	1										
CID-C	-0.059	-0.176*	1									
LLN-C	0.066	0.082	-0.080	1								
LWD-C	0.074	0.038	0.199*	0.000	1							
SHLN-C	0.026	-0.074	0.061	0.200*	0.016	1						
RTLN-C	-0.033	-0.160	-0.135	0.064	-0.079	0.055	1					
SPF-C	-0.058	0.112	-0.023	0.221*	0.0818	0.001	-0.028	1				
PNO-C	-0.080	-0.073	-0.002	0.006	0.166	-0.053	0.026	-0.159	1			
NFG-C	-0.027	0.057	0.059	0.226*	0.101	0.118	-0.056	0.485**	-0.012	1		
TWT-C	-0.076	-0.012	0.030	-0.030	0.041	0.245*	0.127	0.030	-0.061	-0.045	1	
TYLD-C	-0.076	-0.079	0.050	0.046	0.192*	0.230*	0.0735	0.114	0.286*	0.142	0.299*	1

Table 3 Suppl. Correlation coefficients (* - $P < 0.05$, ** - $P < 0.01$) among water use efficiency and yield related traits under treatment (T) conditions. For abbreviations see Table 1.

	RWC-T	SLA-T	CID	LLN-T	LWD-T	SHLN-T	RTLN-T	SPF-T	PNO-T	NFG-T	TWT-T	TYLD-T
RWC-T	1											
SLA-T	0.044	1										
CID	-0.081	-0.154	1									
LLN-T	-0.162	-0.008	0.010	1								
LWD-T	0.229*	0.158	-0.119	0.099	1							
SHLN-T	-0.130	-0.008	0.078	0.218*	-0.154	1						
RTLN-T	0.099	-0.136	-0.069	-0.025	-0.127	0.081	1					
SPF-T	-0.186*	-0.093	0.112	0.129	-0.019	-0.123	-0.084	1				
PNO-T	0.190*	-0.058	-0.176	-0.119	0.129	-0.113	0.161	-0.140	1			
NFG-T	-0.009	0.055	0.087	0.042	0.101	0.018	0.018	0.347**	-0.050	1		
TWT-T	0.068	-0.0004	-0.020	-0.024	0.167	0.117	-0.035	0.031	-0.014	0.105	1	
TYLD-T	-0.029	-0.028	-0.124	0.064	0.240*	0.033	-0.144	-0.012	0.246*	0.139	0.304**	1

Table 4 Suppl. Transcriptomic analysis, *PosMed*, and genomic variations within QTL regions. Infl - inflorescence; el - early; em - emerging; lea 20a, lea 20b - 20-d-old leaves in two replications; sh - shoots 1-, 5-, and 10-d-old; SNP - single nucleotide polymorphism; nsSNP - non synonymous single nucleotide polymorphism.

No.	RAP Os ID	Gene/TF	PosMed	Infl (el)	Infl (em)	lea 20a	lea 20b	Sh 1d	Sh 5d	Sh 10d	SNPs	ns SNP
1	Os01g0818000	RM486-RM6703 (CID) auxin efflux carrier component putative expressed	no	11.23	48.94	34.12	64.35	56.75	57.64	60.18	34	4
2	Os01g0819900	HEAT repeat family protein putative expressed	no	48.03	37.53	24.33	29.69	34.10	35.87	35.64	47	4
3	Os01g0819500	ubiquitin-conjugating enzyme putative expressed	yes	274.75	320.01	128.20	154.86	263.66	265.45	194.69	1	0
										total	82	8
1	Os01g0658400	RM6703-RM11484 (SLA-C,SLA-T, LWD-C, LWD-T, PNO-T) ubiquitin-conjugating enzyme putative expressed	yes	202.70	247.24	99.89	315.54	322.26	319.846	314.358	15	0
2	Os01g0809300	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor putative expressed	no	171.75	213.71	36.70	86.66	152.00	151.52	138.58	20	0
3	Os01g0675700	OsIAA5 - auxin-responsive Aux/IAA gene family member expressed	yes	59.44	49.27	70.15	46.54	49.65	48.46	39.70	25	2
4	Os01g0805700	proline-rich family protein putative expressed	yes	32.71	28.52	9.84	14.88	25.48	26.98	19.94	28	1
5	Os01g0672400	drought induced 19 protein putative expressed	yes	22.88	29.36	60.90	37.14	38.65	32.65	30.30	12	4
6	Os01g0749400	trehalose synthase putative expressed	yes	15.64	23.61	42.73	41.82	40.91	44.86	25.80	22	2
7	Os01g0810300	calmodulin-binding protein putative expressed	yes	11.77	87.88	272.13	86.51	59.52	61.21	59.01	51	4
8	Os01g0837900	serine/threonine-protein kinase AFC1 putative expressed	yes	16.31	18.21	10.87	19.49	21.26	19.48	18.74	44	2
9	Os01g0750100	WRKY13 expressed	yes	2.37	8.42	59.81	14.91	10.06	13.69	14.38	13	2
10	Os01g0723800	ABC transporter ATP-binding protein putative expressed	yes	3.05	3.76	7.81	7.90	14.40	18.24	12.94	19	3
11	Os01g0733200	HSF-type DNA-binding domain containing protein expressed	yes	0.42	9.56	1.13	0.30	0.00	0.4169	0.36	11	4
12	Os01g0649100	lactate/malate dehydrogenase putative expressed	yes	223.91	193.17	57.47	40.31	118.54	111.61	89.53	15	0
13	Os01g0773700	photosystem II reaction center W protein chloroplast precursor putative expressed	no	141.28	434.87	1303.08	912.55	1259.2	1022.0	1269.6	3	1
14	Os01g0720500	chlorophyll A-B binding protein putative expressed	no	245.90	1858.7	4141.8	1857.1	2068.7	1635.6	3458.4	3	0
										total	281	25
1	Os01g0557500	RM488-RM11069 (SHLNC, TWTT, TWTC) sodium/calcium exchanger protein putative expressed	no	105.03	73.98	145.01	68.30	30.06	34.98	54.40	28	0
2	Os01g0583100	protein phosphatase 2C putative expressed	yes	40.11	42.90	56.62	59.47	24.53	23.05	50.39	43	1
3	Os01g0570800	calmodulin-binding protein putative expressed	no	1.28	4.85	127.66	18.36	14.99	13.75	13.02	73	6
4	Os01g0590900	serine/threonine-protein kinase AFC3 putative expressed	yes	107.20	10.84	8.77	11.17	13.74	11.08	8.98	25	3
5	Os01g0591300	aldehyde dehydrogenase putative expressed	yes	0.20	3.62	17.38	10.78	8.69	11.37	15.08	154	13
6	Os01g0603300	Myb transcription factor putative expressed	no	7.11	5.13	17.84	25.42	21.70	25.40	29.72	32	3
										total	355	26
1	Os08g0374100	RM404-RM447 (SLAC, SLAT, LWDC) ubiquitin-conjugating enzyme putative expressed	yes	45.26	77.49	31.33	62.05	59.70	54.22	43.58	101	2

2	Os08g0517200	calcium-transporting ATPase 9 plasma membrane-type putative expressed	no	17.14	18.42	5.96	8.93	13.30	16.03	10.67	38	0	
3	Os08g0398000	ABC transporter ATP-binding protein putative expressed	yes	4.31	4.63	4.93	6.27	3.73	5.31	3.88	47	6	
4	Os08g0445700	trehalose-6-phosphate synthase putative expressed	yes	7.73	2.78	3.62	0.60	0.89	1.58	1.11	24	5	
5	Os08g0359500	co-chaperone protein SBA1 putative expressed	no	376.11	273.32	43.22	48.18	134.95	118.20	65.32	51	3	
6	Os08g0408500	ethylene-responsive transcription factor putative expressed	yes	23.20	19.35	59.79	20.78	13.37	15.49	20.47	15	2	
7	Os08g0434300	lactate/malate dehydrogenase putative expressed	yes	30.55	44.85	62.99	27.69	38.80	39.38	57.05	27	7	
8	Os08g0500300	protein phosphatase 2C putative expressed	yes	25.99	17.67	9.46	19.82	27.43	27.28	23.85	21	1	
9	Os08g0500700	heat shock protein putative expressed	no	357.17	226.40	83.16	213.05	172.00	193.10	167.73	31	1	
10	Os08g0504700	AN1-like zinc finger domain containing protein expressed	no	13.77	21.37	290.75	34.09	74.50	67.61	54.92	3	0	
											total	358	27
1	Os08g0249400	RM1384-RM556 (LLNT, LLNC) proline rich protein 3 putative expressed	no	32.87	24.43	13.52	16.6	17.14	18.53	18.87	125	4	
2	Os08g0224100	serine/threonine-protein kinase HT1 putative expressed	yes	32.57	51.33	23.67	43.99	27.60	33.30	38.03	19	0	
3	Os08g0250900	heat shock protein-related putative expressed	yes	6.42	10.40	37.72	46.77	39.081	42.88	64.04	37	11	
4	Os08g0191000	auxin efflux carrier component putative expressed	no	27.58	39.865	26.30	10.68	12.52	16.85	15.95	69	5	
											total	250	20
RM24879-RM171 (RWCC, SLAC)													
1	Os10g0478200	lactate/malate dehydrogenase putative expressed	no	507.80	521.81	406.28	345.51	437.65	470.31	355.54	25	0	
2	Os10g0445400	zinc finger RING-type putative expressed	no	16.48	44.85	26.072	2.60	1.91	2.27	0.36	14	3	
3	Os10g0447100	ubiquitin-conjugating enzyme putative expressed	yes	64.31	99.60	23.48	64.42	80.74	83.31	58.43	30	0	
4	Os10g0375600	calmodulin-binding transcription activator putative expressed	no	29.41	36.30	30.14	53.15	40.00	49.70	35.83	68	13	
5	Os10g0476600	serine/threonine-protein phosphatase 2A regulatory subunit B subunitbeta putative expressed	no	42.01	30.27	14.48	25.63	32.17	30.09	21.71	26	0	
6	Os10g0346600	vacuolar-sorting receptor precursor no putative expressed	no	98.57	103.28	34.60	45.47	58.37	66.85	41.64	42	3	
7	Os10g0442800	tyrosine protein kinase domain containing protein putative expressed	yes	9.12	20.17	12.39	17.06	17.72	18.44	21.71	50	4	
											Total	255	23
1	Os11g0167800	RM229-RM332 (RWCT, TWTT) abscisic acid?? stress-ripening putative expressed	no	1270.9	3333.9	2243.5	1178.0	1004.8	982.62	1420.8	3	0	
2	Os11g0186200	aldehyde dehydrogenase putative expressed	yes	18.37	82.68	55.95	29.06	36.54	40.55	36.13	64	3	
3	Os11g0171500	CAMK_CAMK_like.43 - CAMK includes calcium/calmodulin depedent protein kinases expressed	yes	83.95	90.74	17.63	9.34	16.77	19.73	12.01	24	0	
4	Os11g0199600	zinc finger CCHC domain-containing protein 10 putative expressed	no	39.46	41.41	13.39	20.00	21.40	19.78	23.44	46	2	
5	Os11g0454300	Similar to water-stress inducible protein RAB21.	yes	0.20	1.27	24.24	31.87	2.36	0.19	0.34	20	1	
											total	157	6