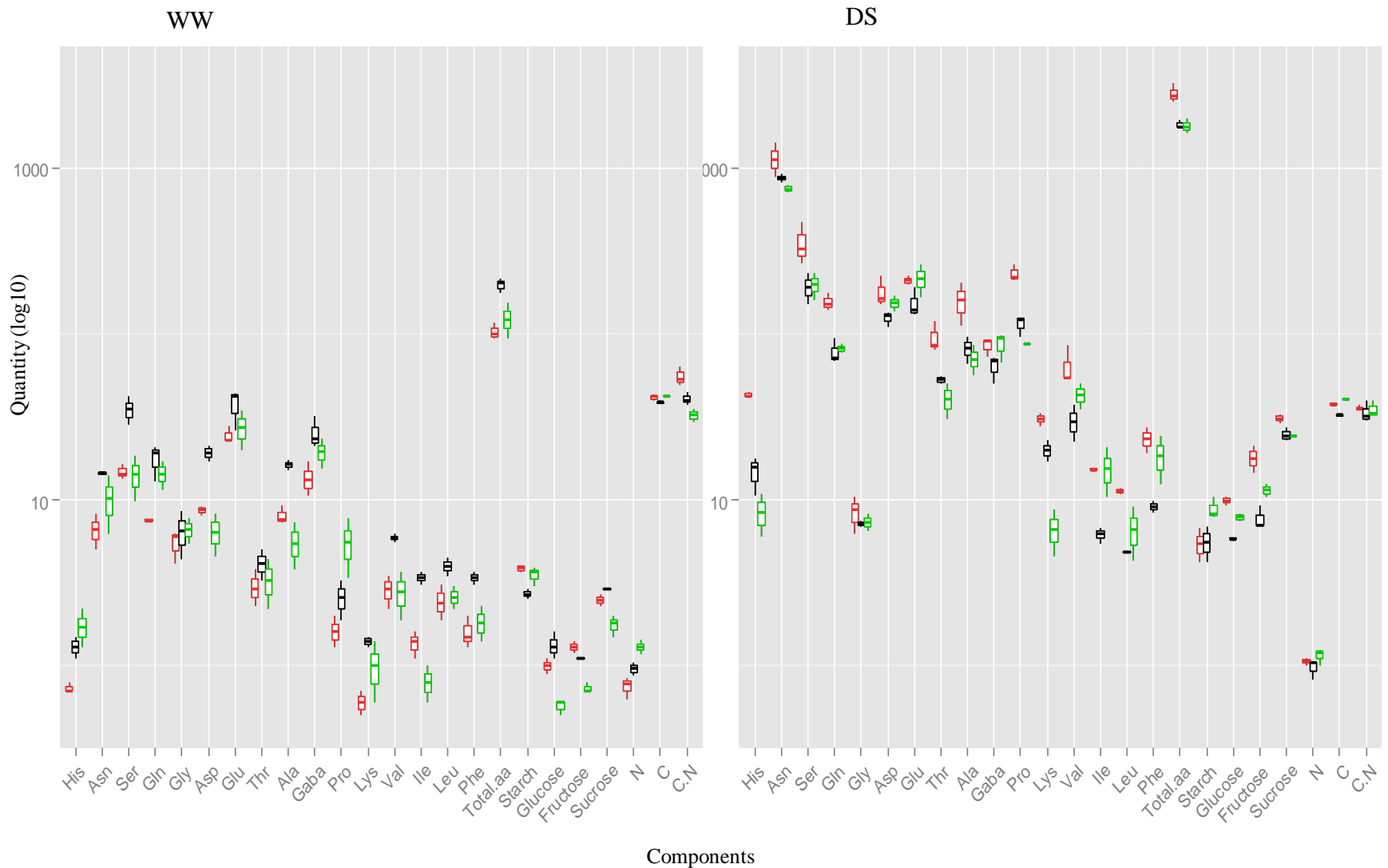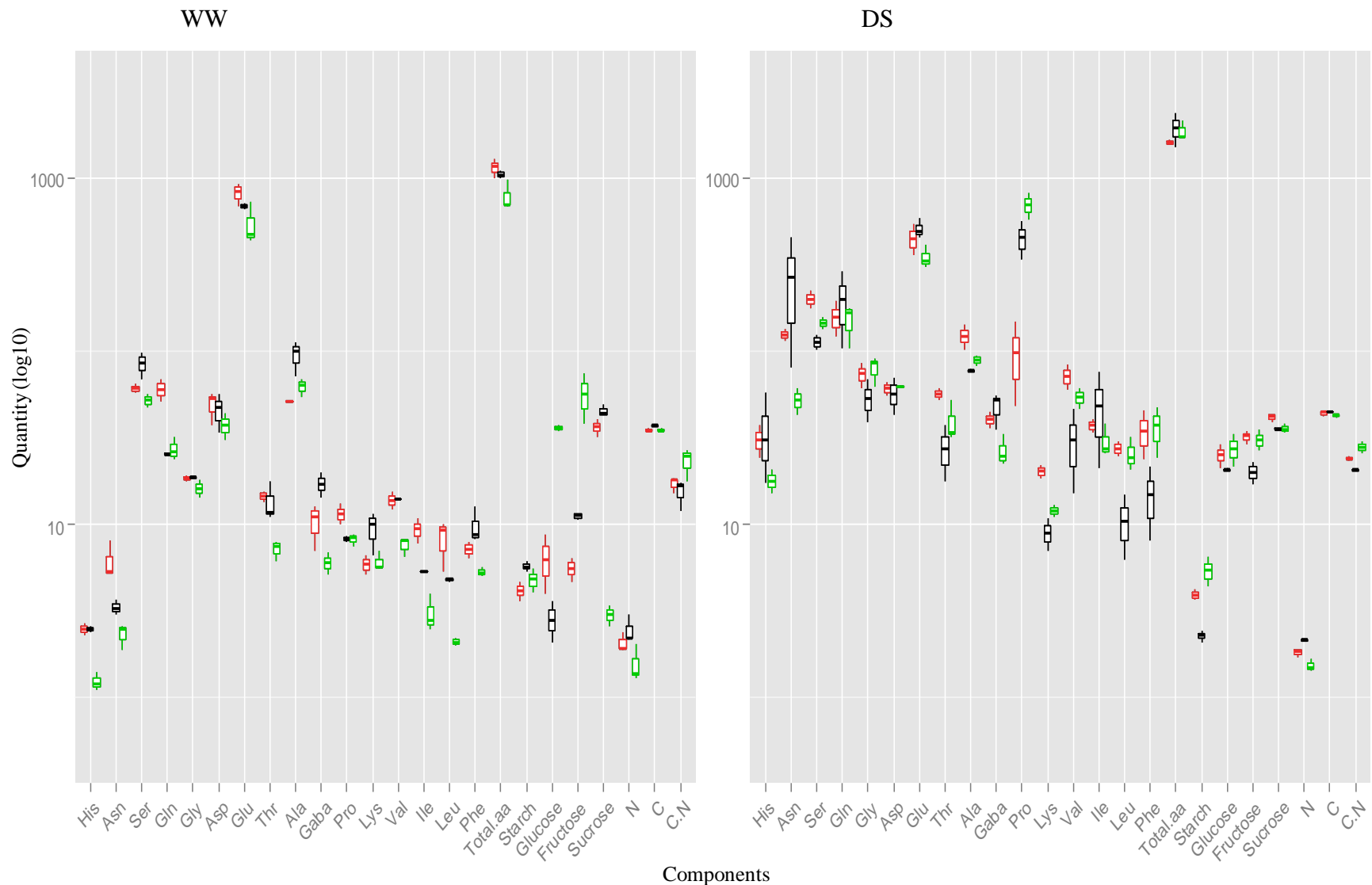**Supplementary Figure 1. Proline content estimation:** Amount of proline measured in micrograms per milligram of tissue dry weight in the stem and root of the three genotypes under drought revealed greatest amount in the 481-B stem and root. This data suggested movement of proline from the flag leaf to the root.
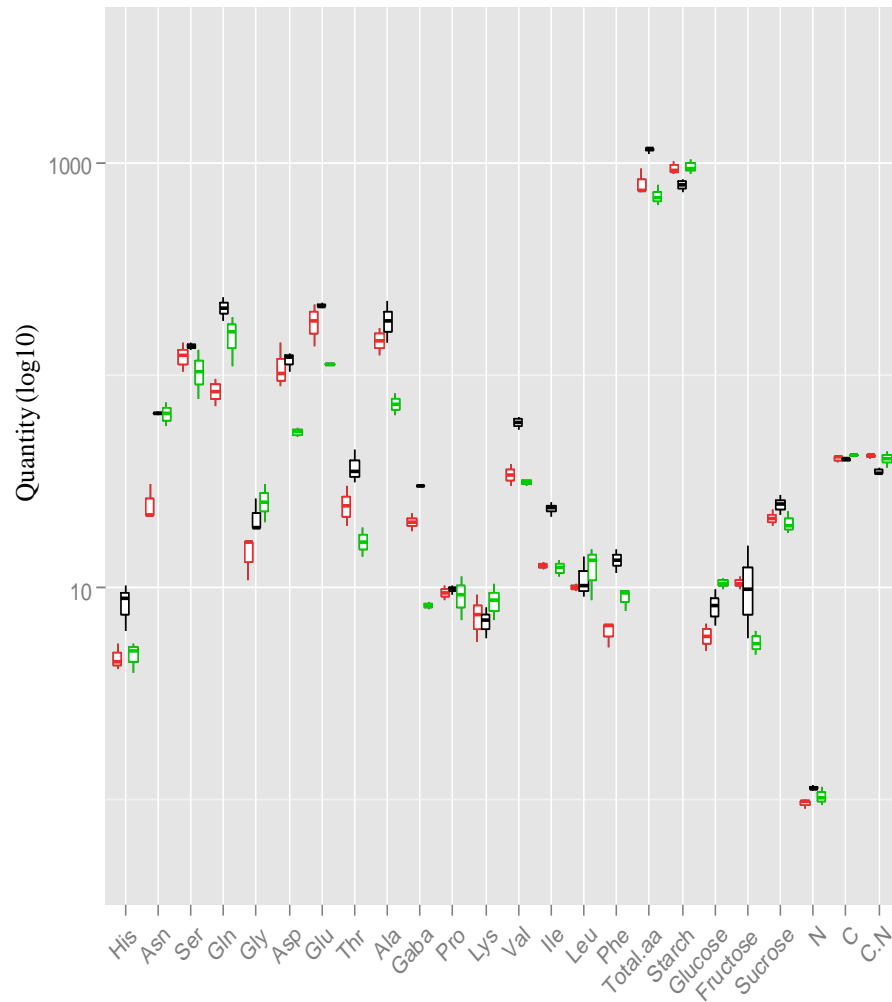
Supplementary Figure 1: Boxplots for metabolite contents in roots. Boxplots represent all metabolites grouped by genotype. The left and the right panels represent well-watered (WW) and drought stress (DS) conditions. Metabolites are represented on the horizontal axis and quantities on the vertical axis. The data is represented on a log10 scale to accommodate different unit magnitudes in one representation. The horizontal white lines represent the values 1, 10, 100 and 1000. Each vertical white line represents a metabolite, and the 3 boxes closest to it are the 3 genotypes: Vandana on the white line is coded in black, 481-B on the left of the line is in red, and Way Rarem on the right is in green. In each box, the horizontal line represents the median of the data, the upper quartile represents the 75th percentiles and the lower quartile represents the 25th percentile. The whiskers represented the 95% and 5% of the data and the circles, when present, signified the outliers. The amino acids were measured in pmol/mg; starch, glucose, fructose and sucrose in μmol/gr fresh weight; and N and C in %, where C/N is their ratio.

Supplementary Figure 2: Boxplots for metabolite contents in flag leaves. Boxplots represent all metabolites grouped by genotype. The left and the right panels represent well-watered (WW) and drought stress (DS) conditions. Metabolites are represented on the horizontal axis and quantities on the vertical axis. The data is represented on a log10 scale to accommodate different unit magnitudes in one representation. The horizontal white lines represent the values 1, 10, 100 and 1000. Each vertical white line represents a metabolite, and the 3 boxes closest to it are the 3 genotypes: Vandana on the white line is coded in black, 481-B on the left of the line is in red, and Way Rarem on the right is in green. In each box, the horizontal line represents the median of the data, the upper quartile represents the 75th percentiles and the lower quartile represents the 25th percentile. The whiskers represented the 95% and 5% of the data and the circles, when present, signified the outliers. The amino acids were measured in pmol/mg; starch, glucose, fructose and sucrose in µmol/gr fresh weight; and N and C in %, where C/N is their ratio.
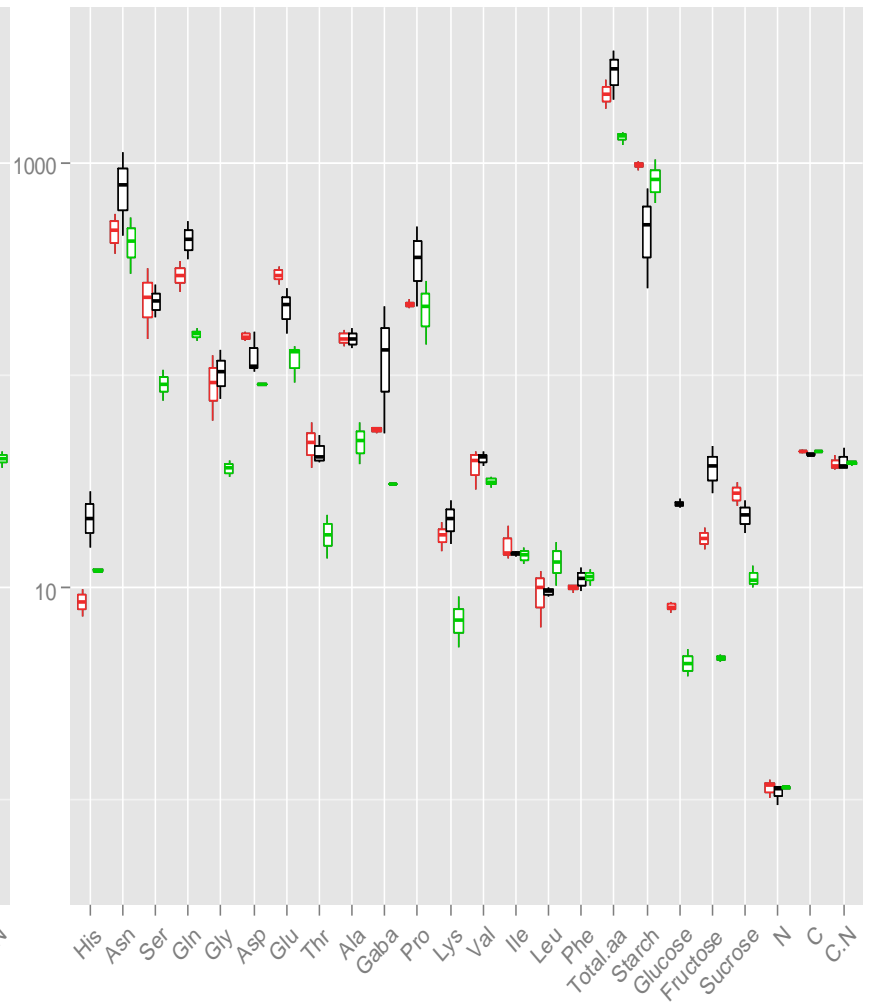
Supplementary Figure 3: Boxplots for metabolite contents in spikelets. Boxplots represent all metabolites grouped by genotype. The left and the right panels represent well-watered (WW) and drought stress (DS) conditions. Metabolites are represented on the horizontal axis and quantities on the vertical axis. The data is represented on a log10 scale to accommodate different unit magnitudes in one representation. The horizontal white lines represent the values 1, 10, 100 and 1000. Each vertical white line represents a metabolite, and the 3 boxes closest to it are the 3 genotypes: Vandana on the white line is coded in black, 481-B on the left of the line is in red, and Way Rarem on the right is in green. In each box, the horizontal line represents the median of the data, the upper quartile represents the 75th percentiles and the lower quartile represents the 25th percentile. The whiskers represented the 95% and 5% of the data and the circles, when present, signified the outliers. The amino acids were measured in pmol/mg; starch, glucose, fructose and sucrose in μmol/gr fresh weight; and N and C in %, where C/N is their ratio.

1 **Comparison of variation in primary metabolites between the parental and near-isogenic lines of the rice**

2 **QTL *qDTY$_{12.1}$* for yield under drought: changes in roots and flag leaves help maintain spikelet characters**

3

4 Molecular Breeding

5

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1 **Supplementary Information**
2
3 **Supplementary Table 1: One-way ANOVA outputs for each metabolite in roots, flag leaves and spikelets.**
4 Each table contains the output values for each metabolite in root tissue. The table describes the treatment
5 significance (T), the genotype significance (G), the genotype x treatment (GxE) interaction significance and Res
6 for the residuals. The first column represents the degrees of freedom, the second the sum of squares, the third
7 the mean of the sum of squares, the fourth one is the F test and the last is the p for the F test.
8
9 **Flag Leaf**

His

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	3031.6	3031.6	38.407	4.61E-05
G	2	288	144	1.824	0.203
GxE	2	210.7	105.4	1.335	0.3
Res	12	947.2	78.9		

Gly

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	11817	11817	120.895	1.27E-07
G	2	486	243	2.487	0.1248
GxE	2	655	328	3.351	0.0698
Res	12	1173	98		

Val

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	7288	7288	101.697	3.27E-07
G	2	1240	620	8.649	0.00472
GxE	2	1342	671	9.362	0.00355
Res	12	860	72		

Ala

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	3110	3110	20.006	0.000762
G	2	483	241.7	1.555	0.250877
GxE	2	5896	2948.2	18.965	0.000193
Res	12	1865	155.5		

Pro

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	748313	748313	148.22	4.12E-08
G	2	273041	136520	27.04	3.59E-05
GxE	2	279414	139707	27.67	3.20E-05
Res	12	60583	5049		

Lys

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	194.04	194.04	77.64	1.38E-06
G	2	61.94	30.97	12.39	0.00121
GxE	2	165.28	82.64	33.06	1.31E-05
Res	12	29.99	2.5		

Ser

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	34357	34357	189.85	1.02E-08
G	2	3986	1993	11.01	0.00192
GxE	2	9246	4623	25.55	4.74E-05
Res	12	2172	181		

Thr

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	3854	3854	91.981	5.61E-07
G	2	759	380	9.058	0.004
GxE	2	600	300	7.158	0.00899
Res	12	503	42		

Glu

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	277140	277140	28.203	0.000185
G	2	119081	59541	6.059	0.015171
GxE	2	33828	16914	1.721	0.220183
Res	12	117918	9827		

Asp

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	1156.8	1156.8	14.134	0.00272
G	2	81.1	40.5	0.495	0.62134
GxE	2	198.3	99.2	1.212	0.3317
Res	12	982.1	81.8		

Ile

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	4812	4812	36.282	6.00E-05
G	2	316	158	1.191	0.337
GxE	2	242	121	0.913	0.428

Leu

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	1181	1181	108.61	2.29E-07
G	2	317.1	158.6	14.58	0.000614
GxE	2	258.4	129.2	11.88	0.001428

Rice primary metabolites variation under drought

Res	12	1591	133		

1

Gln

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	34357	34357	189.85	1.02E-08
G	2	3986	1993	11.01	0.00192
GxE	2	9246	4623	25.55	4.74E-05
Res	12	2172	181		

Gaba

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	3278	3278	107.393	2.43E-07
G	2	766	383	12.555	0.00114
GxE	2	88	44	1.445	0.27388
Res	12	366	31		

Total aa

	Df	Sum S	q Mean S	q F valu	Pr(>F)
T	1	2982415	2982415	59.503	5.45E-06
G	2	91218	45609	0.91	0.4286
GxE	2	313046	156523	3.123	0.0809
Res	12	601462	50122		

Glucose

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	401.4	401.4	43.58	2.53E-05
G	2	1325.7	662.8	71.97	2.08E-07
GxE	2	709.1	354.6	38.5	6.01E-06
Res	12	110.5	9.2		

Sucrose

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	407.1	407.1	59.79	5.32E-06
G	2	1630.5	815.3	119.75	1.18E-08
GxE	2	1402.7	701.4	103.02	2.78E-08
Res	12	81.7	6.8		

C

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	269.11	269.11	408.291	1.24E-10
G	2	12.58	6.29	9.545	0.00331
GxE	2	1.49	0.74	1.128	0.35559
Res	12	7.91	0.66		

Res	12	130.5	10.9		

Asn

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	93283	93283	16.172	0.0017
G	2	35655	17827	3.091	0.0827
GxE	2	35474	17737	3.075	0.0835
Res	12	69220	5768		

Phe

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	2005.6	2005.6	39.964	3.82E-05
G	2	287.4	143.7	2.863	0.0962
GxE	2	595.3	297.6	5.931	0.0162
Res	12	602.2	50.2		

Starch

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	4.621	4.621	12.5	0.004108
G	2	4.866	2.433	6.58	0.01177
GxE	2	13.852	6.926	18.73	0.000204
Res	12	4.437	0.37		

Fructose

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	47	47	0.755	0.401926
G	2	2815.7	1407.8	22.595	8.53E-05
GxE	2	2091.7	1045.8	16.785	0.000333
Res	12	747.7	62.3		

N

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	0.1824	0.1824	2.149	0.16839
G	2	1.7539	0.877	10.333	0.00246
GxE	2	0.0664	0.0332	0.391	0.68469
Res	12	1.0184	0.0849		

C/N

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	140.89	140.89	21.383	0.000586
G	2	173.51	86.75	13.167	0.000941
GxE	2	3.89	1.94	0.295	0.749713
Res	12	79.06	6.59		

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1 **Roots**

His

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	1949	1949	522.8	2.91E-11
G	2	966.3	483.1	129.6	7.50E-09
GxE	2	1073	536.5	143.9	4.11E-09
Res	12	44.7	3.7		

Gly

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	9.68	9.68	4.668	0.0517
G	2	0.058	0.029	0.014	0.9862
GxE	2	5.293	2.647	1.276	0.3144
Res	12	24.887	2.074		

Ala

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	39640	39640	93.98	5.00E-07
G	2	6731	3366	7.98	0.00625
GxE	2	7330	3665	8.69	0.00464
Res	12	5061	422		

Val

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	7846	7846	109.491	2.19E-07
G	2	779	390	5.438	0.02083
GxE	2	1067	534	7.447	0.00789
Res	12	860	72		

Asp

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	89973	89973	268.834	1.40E-09
G	2	1612	806	2.409	0.132
GxE	2	3372	1686	5.038	0.0258
Res	12	4016	335		

Glu

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	121393	121393	189.518	1.03E-08
G	2	2265	1133	1.768	0.2123
GxE	2	4954	2477	3.867	0.0506
Res	12	7686	641		

Lys

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	1483.3	1483.3	432.38	8.85E-11
G	2	424.6	212.3	61.88	4.77E-07
GxE	2	450.6	225.3	65.67	3.44E-07
Res	12	41.2	3.4		

Pro

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	89747	89747	518.39	3.06E-11
G	2	16722	8361	48.29	1.82E-06
GxE	2	18237	9119	52.67	1.14E-06
Res	12	2078	173		

Ser

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	233085	233085	98.581	3.87E-07
G	2	22819	11409	4.826	0.029
GxE	2	29566	14783	6.252	0.0138
Res	12	28373	2364		

Thr

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	16080	16080	169.29	1.95E-08
G	2	2453	1226	12.91	0.00102
GxE	2	2562	1281	13.49	0.000852
Res	12	1140	95		

Gln

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	38411	38411	359.23	2.61E-10
G	2	4530	2265	21.18	0.000116
GxE	2	7119	3559	33.29	1.27E-05
Res	12	1283	107		

Asn

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	3736922	3736922	310.566	6.08E-10
G	2	119207	59603	4.953	0.027
GxE	2	125267	62634	5.205	0.0236
Res	12	144391	12033		

Rice primary metabolites variation under drought

Leu

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	93.85	93.85	85.97	8.06E-07
G	2	22.52	11.26	10.32	0.00247
GxE	2	48.64	24.32	22.28	9.12E-05
Res	12	13.1	1.09		

Ile

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	490.9	490.9	110.353	2.10E-07
G	2	47.4	23.7	5.333	0.022019
GxE	2	133.2	66.6	14.967	0.000549
Res	12	53.4	4.4		

Phe

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	966.5	966.5	106.97	2.49E-07
G	2	117.7	58.8	6.512	0.01216
GxE	2	200.2	100.1	11.079	0.00188
Res	12	108.4	9		

Gaba

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	15506	15506	161.02	2.59E-08
G	2	210	105	1.09	0.3674
GxE	2	974	487	5.06	0.0255
Res	12	1156	96		

Total aa

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	18041023	18041023	585.07	1.50E-11
G	2	911074	455537	14.77	0.000581
GxE	2	1133757	566879	18.38	0.000222
Res	12	370030	30836	36	

Starch

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	47.86	47.86	53.605	9.20E-06
G	2	13.99	7	7.837	0.00665
GxE	2	11.07	5.54	6.201	0.01415
Res	12	10.71	0.89		

Glucose

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	212.87	212.87	2152.59	6.56E-15
G	2	10.77	5.39	54.48	9.54E-07
GxE	2	14.92	7.46	75.44	1.60E-07
Res	12	1.19	0.1		

Fructose

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	574.6	574.6	260.33	1.68E-09
G	2	82.4	41.2	18.67	0.000207
GxE	2	73.8	36.9	16.72	0.000339
Res	12	26.5	2.2		

Sucrose

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	2642.6	2642.6	1780.22	2.04E-14
G	2	46.7	23.3	15.72	0.000445
GxE	2	40.6	20.3	13.68	0.000802
Res	12	17.8	1.5		

N

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	0.0154	0.01542	1.301	0.276325
G	2	0.3499	0.17493	14.756	0.000584
GxE	2	0.1585	0.07924	6.684	0.011203
Res	12	0.1423	0.01186		

C

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	63.89	63.89	125.93	1.02E-07
G	2	92.93	46.46	91.58	5.40E-08
GxE	2	16.73	8.37	16.49	0.000361
Res	12	6.09	0.51		

C/N

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	284.9	284.91	15.64	0.00191
G	2	448.7	224.35	12.32	0.00123
GxE	2	379.6	189.8	10.42	0.00238
Res	12	218.5	18.21		

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1 Spikelets

His

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	296.87	296.87	36.605	5.76E-05
G	2	235.36	117.68	14.511	0.000627
GxE	2	67.11	33.56	4.138	0.042984
Res	12	97.32	8.11		

Gly

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	14849	14849	48.892	1.45E-05
G	2	3249	1624	5.348	0.02184
GxE	2	4862	2431	8.004	0.00618
Res	12	3645	304		

Ala

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	1338	1338	2.804	0.12
G	2	37385	18693	39.169	5.49E-06
GxE	2	1059	529	1.109	0.361
Res	12	5727	477		

Val

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	115.5	115.5	6.058	0.02997
G	2	1149.4	574.7	30.135	2.10E-05
GxE	2	444.2	222.1	11.646	0.00155
Res	12	228.8	19.1		

Pro

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	285743	285743	64.986	3.48E-06
G	2	21558	10779	2.451	0.128
GxE	2	21318	10659	2.424	0.131
Res	12	52764	4397		

Lys

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	257.64	257.64	37.151	5.38E-05
G	2	121.45	60.72	8.756	0.004519
GxE	2	200.08	100.04	14.426	0.000642
Res	12	83.22	6.94		

Asn

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	1190836	1190836	50.366	1.25E-05
G	2	129755	64877	2.744	0.104
GxE	2	107997	53998	2.284	0.144
Res	12	283724	23644		

Gln

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	99488	99488	46.06	1.94E-05
G	2	95508	47754	22.11	9.45E-05
GxE	2	48063	24031	11.13	0.00185
Res	12	25917	2160		

Asp

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	3744	3744	11.241	0.005751
G	2	12092	6046	18.152	0.000235
GxE	2	1016	508	1.525	0.256927
Res	12	3997	333		

Glu

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	7581	7581	7.953	0.01546
G	2	49352	24676	25.887	4.44E-05
GxE	2	13657	6829	7.164	0.00897
Res	12	11439	953		

Ser

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	17323	17323	10.089	0.00798
G	2	27190	13595	7.918	0.00642
GxE	2	13493	6746	3.929	0.04869
Res	12	20605	1717		

Thr

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	503.5	503.5	10.769	0.006561
G	2	1870.5	935.3	20.003	0.000151
GxE	2	409	204.5	4.374	0.037429
Res	12	561.1	46.8		

Rice primary metabolites variation under drought

Leu

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	0.85	0.845	0.145	0.7095
G	2	32.72	16.362	2.817	0.0993 .
GxE	2	4.12	2.062	0.355	0.7083
Res	12	69.69	5.808		

Ile

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	8.41	8.41	3.149	0.101343
G	2	111.57	55.79	20.898	0.000123
GxE	2	138.65	69.33	25.97	4.37E-05
Res	12	32.03	2.67		

Phe

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	6.24	6.242	4.856	0.047831
G	2	52.5	26.251	20.42	0.000137
GxE	2	31.35	15.677	12.195	0.001286
Res	12	15.43	1.286		

Gaba

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	12715	12715	12.212	0.00443
G	2	11983	5991	5.754	0.01769
GxE	2	5506	2753	2.644	0.11184
Res	12	12494	1041		

Total aa

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	6065064	6065064	60.911	4.84E-06
G	2	2499274	1249637	12.55	0.00115
GxE	2	712552	356276	3.578	0.06043
Res	12	1194868	99572		

Starch

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	68882	68882	3.616	0.0815
G	2	330909	165454	8.686	0.00465
GxE	2	72498	36249	1.903	0.1915
Res	12	228588	19049		

Glucose

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	83.2	83.21	88.05	7.09E-07
G	2	349.7	174.84	185.01	9.61E-10
GxE	2	398.7	199.33	210.93	4.48E-10
Res	12	11.3	0.94		

Fructose

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	527	527	28.02	0.00019
G	2	1054.2	527.1	28.02	3.01E-05
GxE	2	604.7	302.3	16.07	0.000403
Res	12	225.7	18.8		

Sucrose

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	13.69	13.69	1.758	0.209529
G	2	273.61	136.81	17.566	0.000272
GxE	2	183.65	91.83	11.79	0.001472
Res	12	93.46	7.79		

N

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	0.02431	0.024315	3.548	0.0841
G	2	0.00911	0.004555	0.665	0.5324
GxE	2	0.04437	0.022185	3.237	0.0751
Res	12	0.08223	0.006853		

C

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	31.24	31.24	52.71	1.00E-05
G	2	6.848	3.424	5.777	0.0175
GxE	2	1.981	0.991	1.671	0.2289
Res	12	7.112	0.593		

C/N

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
T	1	0.34	0.34	0.04	0.8441
G	2	20.15	10.077	1.198	0.3355
GxE	2	53.29	26.644	3.167	0.0786
Res	12	100.94	8.412		

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Supplementary Table 2: Tukey's HSD test outputs for the pairwise analysis of each metabolite in the 3 different genotypes in root, flag leaf and spikelets. Vandana (V), WayRarem (WR) and 481-B. Each table contains the difference between the 2 sample means in the first column (diff), the lower (lwr) and upper (upr) bounds of the 95% confidence interval, and the adjusted probability for the difference test (adj p).

Flag leaf

Ala

			diff	lwr	upr	p adj
Drought	V	481-B	-44.900	-79.094	-10.706	0.009
Drought	WR	481-B	-33.400	-67.594	0.794	0.057
Drought	WR	V	11.500	-22.694	45.694	0.860

Val

			diff	lwr	upr	p adj
Drought	V	481-B	-40.700	-63.917	-17.483	0.001
Drought	WR	481-B	-17.433	-40.651	5.784	0.192
Drought	WR	V	23.267	0.049	46.484	0.049

Pro

			diff	lwr	upr	p adj
Drought	V	481-B	353.033	158.165	547.901	0.001
Drought	WR	481-B	604.000	409.132	798.868	0.000
Drought	WR	V	250.967	56.099	445.835	0.010

Lys

			diff	lwr	upr	p adj
Drought	V	481-B	-11.267	-15.603	-6.931	0.000
Drought	WR	481-B	-8.200	-12.536	-3.864	0.000
Drought	WR	V	3.067	-1.269	7.403	0.238

Ser

			diff	lwr	upr	p adj
Drought	V	481-B	-86.867	-123.760	-49.973	0.000
Drought	WR	481-B	-53.800	-90.694	-16.906	0.004
Drought	WR	V	33.067	-3.827	69.960	0.089

Thr

			diff	lwr	upr	p adj
Drought	V	481-B	-28.867	-46.620	-11.113	0.002
Drought	WR	481-B	-16.967	-34.720	0.787	0.064
Drought	WR	V	11.900	-5.854	29.654	0.284

Leu

			diff	lwr	upr	p adj
Drought	V	481-B	-16.967	-26.010	-7.923	0.000
Drought	WR	481-B	-1.867	-10.910	7.177	0.979
Drought	WR	V	15.100	6.057	24.143	0.001

Gly

			diff	lwr	upr	p adj
Drought	V	481-B	-20.267	-47.381	6.848	0.195
Drought	WR	481-B	5.900	-21.215	33.015	0.974
Drought	WR	V	26.167	-0.948	53.281	0.061

Gln

			diff	lwr	upr	p adj
Drought	V	481-B	39.900	-81.673	161.473	0.871
Drought	WR	481-B	-8.133	-129.706	113.440	1.000
Drought	WR	V	-48.033	-169.606	73.540	0.766

Asn

			diff	lwr	upr	p adj
Drought	V	481-B	141.300	-66.995	349.595	0.274
Drought	WR	481-B	-72.800	-281.095	135.495	0.841
Drought	WR	V	-214.100	-422.395	-5.805	0.043

Phe

			diff	lwr	upr	p adj
Drought	V	481-B	-19.800	-39.228	-0.372	0.045
Drought	WR	481-B	1.567	-17.862	20.995	1.000
Drought	WR	V	21.367	1.938	40.795	0.028

Total

			diff	lwr	upr	p adj
Drought	V	481-B	346.100	-267.899	960.099	0.450
Drought	WR	481-B	267.733	-346.266	881.732	0.691
Drought	WR	V	-78.367	-692.366	535.632	0.998

Rice primary metabolites variation under drought

Starch

			diff	lwr	upr	p adj
Drought	V	481-B	-1.653	-3.321	0.014	0.052
Drought	WR	481-B	1.503	-0.164	3.171	0.087
Drought	WR	V	3.157	1.489	4.824	0.000

Glucose

			diff	lwr	upr	p adj
Drought	V	481-B	-4.467	-12.790	3.856	0.499
Drought	WR	481-B	2.333	-5.990	10.656	0.928
Drought	WR	V	6.800	-1.523	15.123	0.136

Fructose

			diff	lwr	upr	p adj
Drought	V	481-B	-12.067	-33.715	9.582	0.461
Drought	WR	481-B	-1.200	-22.848	20.448	1.000
Drought	WR	V	10.867	-10.782	32.515	0.564

Sucrose

			diff	lwr	upr	p adj
Drought	V	481-B	-5.867	-13.023	1.289	0.134
Drought	WR	481-B	-5.467	-12.623	1.689	0.180
Drought	WR	V	0.400	-6.756	7.556	1.000

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1 **Roots**

His

			diff	lwr	upr	p adj
Drought	V	481-B	-28.300	-33.595	-23.005	0.000
Drought	WR	481-B	-34.600	-39.895	-29.305	0.000
Drought	WR	V	-6.300	-11.595	-1.005	0.017

Gly

			diff	lwr	upr	p adj
Drought	V	481-B	-1.267	-5.216	2.683	0.881
Drought	WR	481-B	-1.100	-5.050	2.850	0.929
Drought	WR	V	0.167	-3.783	4.116	1.000

Ser

			diff	lwr	upr	p adj
Drought	V	481-B	-163.400	-296.757	-30.043	0.014
Drought	WR	481-B	-157.467	-290.824	-24.110	0.018
Drought	WR	V	5.933	-127.424	139.290	1.000

Thr

			diff	lwr	upr	p adj
Drought	V	481-B	-42.767	-69.496	-16.037	0.002
Drought	WR	481-B	-55.067	-81.796	-28.337	0.000
Drought	WR	V	-12.300	-39.029	14.429	0.645

Ala

			diff	lwr	upr	p adj
Drought	V	481-B	-77.433	-133.757	-21.109	0.006
Drought	WR	481-B	-88.100	-144.424	-31.776	0.002
Drought	WR	V	-10.667	-66.991	45.657	0.986

Val

			diff	lwr	upr	p adj
Drought	V	481-B	-34.567	-57.783	-11.351	0.003
Drought	WR	481-B	-21.500	-44.716	1.716	0.076
Drought	WR	V	13.067	-10.149	36.283	0.451

Leu

			diff	lwr	upr	p adj
Drought	V	481-B	-6.467	-9.332	-3.601	0.000
Drought	WR	481-B	-4.667	-7.532	-1.801	0.002
Drought	WR	V	1.800	-1.065	4.665	0.344

Ile

			diff	lwr	upr	p adj
Drought	V	481-B	-9.067	-14.851	-3.282	0.002
Drought	WR	481-B	0.267	-5.518	6.051	1.000
Drought	WR	V	9.333	3.549	15.118	0.002

Pro

			diff	lwr	upr	p adj
Drought	V	481-B	-116.533	-152.619	-80.448	0.000
Drought	WR	481-B	-143.600	-179.686	-107.514	0.000
Drought	WR	V	-27.067	-63.152	9.019	0.193

Lys

			diff	lwr	upr	p adj
Drought	V	481-B	-10.833	-15.913	-5.754	0.000
Drought	WR	481-B	-24.100	-29.180	-19.020	0.000
Drought	WR	V	-13.267	-18.346	-8.187	0.000

Asp

			diff	lwr	upr	p adj
Drought	V	481-B	-56.033	-106.206	-5.861	0.026
Drought	WR	481-B	-28.000	-78.173	22.173	0.460
Drought	WR	V	28.033	-22.139	78.206	0.459

Glu

			diff	lwr	upr	p adj
Drought	V	481-B	-56.600	-126.011	12.811	0.138
Drought	WR	481-B	4.367	-65.044	73.777	1.000
Drought	WR	V	60.967	-8.444	130.377	0.098

Gln

			diff	lwr	upr	p adj
Drought	V	481-B	-77.567	-105.926	-49.208	0.000
Drought	WR	481-B	-73.900	-102.259	-45.541	0.000
Drought	WR	V	3.667	-24.692	32.026	0.998

Asn

			diff	lwr	upr	p adj
Drought	V	481-B	-272.000	-572.839	28.839	0.085
Drought	WR	481-B	-394.267	-695.106	-93.428	0.009
Drought	WR	V	-122.267	-423.106	178.572	0.746

Rice primary metabolites variation under drought

Gaba

			diff	lwr	upr	p adj
Drought	V	481-B	-21.433	-48.346	5.480	0.152
Drought	WR	481-B	1.200	-25.713	28.113	1.000
Drought	WR	V	22.633	-4.280	49.546	0.120

Phe

			diff	lwr	upr	p adj
Drought	V	481-B	-14.200	-22.444	-5.956	0.001
Drought	WR	481-B	-4.900	-13.144	3.344	0.397
Drought	WR	V	9.300	1.056	17.544	0.024

Total aa

			diff	lwr	upr	p adj
Drought	V	481-B	-988.500	-1470.095	-506.905	0.000
Drought	WR	481-B	-1025.400	-1506.995	-543.805	0.000
Drought	WR	V	-36.900	-518.495	444.695	1.000

Starch

			diff	lwr	upr	p adj
Drought	V	481-B	0.137	-2.455	2.728	1.000
Drought	WR	481-B	3.457	0.865	6.048	0.008
Drought	WR	V	3.320	0.729	5.911	0.010

Glucose

			diff	lwr	upr	p adj
Drought	V	481-B	-4.067	-4.929	-3.204	0.000
Drought	WR	481-B	-2.000	-2.862	-1.138	0.000
Drought	WR	V	2.067	1.204	2.929	0.000

Fructose

			diff	lwr	upr	p adj
Drought	V	481-B	-10.067	-14.141	-5.992	0.000
Drought	WR	481-B	-6.400	-10.475	-2.325	0.002
Drought	WR	V	3.667	-0.408	7.741	0.087

Sucrose

			diff	lwr	upr	p adj
Drought	V	481-B	-6.267	-9.608	-2.925	0.000
Drought	WR	481-B	-6.767	-10.108	-3.425	0.000
Drought	WR	V	-0.500	-3.841	2.841	0.995

N

			diff	lwr	upr	p adj
Drought	V	481-B	-0.082	-0.381	0.216	0.932
Drought	WR	481-B	0.095	-0.204	0.394	0.884
Drought	WR	V	0.177	-0.121	0.476	0.398

C

			diff	lwr	upr	p adj
Drought	V	481-B	-5.386	-7.339	-3.432	0.000
Drought	WR	481-B	2.334	0.380	4.287	0.017
Drought	WR	V	7.720	5.766	9.673	0.000

C/N

			diff	lwr	upr	p adj
Drought	V	481-B	-2.074	-13.778	9.630	0.989
Drought	WR	481-B	-0.663	-12.367	11.041	1.000
Drought	WR	V	1.411	-10.293	13.115	0.998

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1 **Spikelets**

His

			diff	lwr	upr	p adj
Drought	V	481-B	13.067	5.256	20.877	0.001
Drought	WR	481-B	3.433	-4.377	11.244	0.684
Drought	WR	V	-9.633	-17.444	-1.823	0.013

Gly

			diff	lwr	upr	p adj
Drought	V	481-B	11.567	-36.229	59.363	0.960
Drought	WR	481-B	-56.367	-104.163	-8.571	0.018
Drought	WR	V	-67.933	-115.729	-20.137	0.005

Gln

			diff	lwr	upr	p adj
Drought	V	481-B	144.400	16.946	271.854	0.024
Drought	WR	481-B	-138.800	-266.254	-11.346	0.030
Drought	WR	V	-283.200	-410.654	-155.746	0.000

Glu

			diff	lwr	upr	p adj
Drought	V	481-B	-87.733	-172.407	-3.059	0.041
Drought	WR	481-B	-177.800	-262.474	-93.126	0.000
Drought	WR	V	-90.067	-174.741	-5.393	0.035

Ser

			diff	lwr	upr	p adj
Drought	V	481-B	-7.833	-121.478	105.811	1.000
Drought	WR	481-B	-143.600	-257.244	-29.956	0.011
Drought	WR	V	-135.767	-249.411	-22.122	0.017

Thr

			diff	lwr	upr	p adj
Drought	V	481-B	-4.300	-23.053	14.453	0.968
Drought	WR	481-B	-30.400	-49.153	-11.647	0.002
Drought	WR	V	-26.100	-44.853	-7.347	0.005

Val

			diff	lwr	upr	p adj
Drought	V	481-B	2.967	-9.010	14.943	0.956
Drought	WR	481-B	-6.133	-18.110	5.843	0.545
Drought	WR	V	-9.100	-21.076	2.876	0.184

Lys

			diff	lwr	upr	p adj
Drought	V	481-B	3.400	-3.822	10.622	0.624
Drought	WR	481-B	-10.533	-17.756	-3.311	0.004
Drought	WR	V	-13.933	-21.156	-6.711	0.000

Ile

			diff	lwr	upr	p adj
Drought	V	481-B	-1.567	-6.048	2.914	0.841
Drought	WR	481-B	-1.833	-6.314	2.648	0.741
Drought	WR	V	-0.267	-4.748	4.214	1.000

Phe

			diff	lwr	upr	p adj
Drought	V	481-B	1.100	-2.010	4.210	0.834
Drought	WR	481-B	1.400	-1.710	4.510	0.664
Drought	WR	V	0.300	-2.810	3.410	0.999

Total aa

			diff	lwr	upr	p adj
Drought	V	481-B	583.833	-281.580	1449.247	0.278
Drought	WR	481-B	-799.300	-1664.713	66.113	0.077
Drought	WR	V	-1383.133	-2248.547	-517.720	0.002

Starch

			diff	lwr	upr	p adj
Drought	V	481-B	-468.933	-847.454	-90.412	0.013
Drought	WR	481-B	-137.300	-515.821	241.221	0.820
Drought	WR	V	331.633	-46.888	710.154	0.099

Glucose

			diff	lwr	upr	p adj
Drought	V	481-B	16.833	14.167	19.499	0.000
Drought	WR	481-B	-3.667	-6.333	-1.001	0.006
Drought	WR	V	-20.500	-23.166	-17.834	0.000

Fructose

			diff	lwr	upr	p adj
Drought	V	481-B	19.933	8.039	31.827	0.001
Drought	WR	481-B	-12.533	-24.427	-0.639	0.037
Drought	WR	V	-32.467	-44.361	-20.573	0.000

Sucrose

			diff	lwr	upr	p adj
Drought	V	481-B	-5.900	-13.554	1.754	0.173
Drought	WR	481-B	-16.633	-24.287	-8.980	0.000
Drought	WR	V	-10.733	-18.387	-3.080	0.005

N

			diff	lwr	upr	p adj
Drought	V	481-B	-0.065	-0.292	0.162	0.920
Drought	WR	481-B	-0.002	-0.229	0.225	1.000
Drought	WR	V	0.064	-0.163	0.291	0.927

C/N

			diff	lwr	upr	p adj
Drought	V	481-B	1.402	-6.552	9.356	0.990
Drought	WR	481-B	-0.076	-8.031	7.878	1.000
Drought	WR	V	-1.479	-9.433	6.476	0.987

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1   **Supplementary Table 3:** List of primers used for qRT-PCR.

Locus ID	Gene Name	Primer Name	Primer Sequence (5'-3')
Os08g01770	adenylate kinase	08AK_CF3	CCCAAGAAGCTATTCGCAAG
		08AK_CR3	ATCAAGCCGTCTCCCAACTA
Os07g42490	sucrose synthase	07SucroSy_CF2	CTACAGCCCCACCAGATCAT
		07SucroSy_CR2	AGGGACACTCAGCTCCTCAA
Os01g71990	pyrroline-5-carboxylate reductase	1P5CR_CF2	ATCTCTGTGAAGCCGCAGAT
		1P5CR_CR2	CAACAGCTGAAGGGGTGTTT
Os05g38150	pyrroline-5-carboxylate synthase	5P5CS_CF2	CAGTTTAGCAGGACTGTTGG
		5P5CS_CR2	TGTCATGCCTCCTCTACCTA
Os04g55720	D-3-phosphoglycerate dehydrogenase	04PGDH_CF2	ATCTTGTTGGATGGCTCACC
		04PGDH_CR2	CAAGCTCACATCAACCTGGA
Os01g64630	actin	01Act qCF1	ACTCCCGCATGCTATTCTTCGAC
		01Act qCR1	TGAAGGAGTAACCCCTCTCTGTGA
Os07g38730	tubulin	07Tub qCF2	CCTCTGTTGTCCCTGGTGGTGA
		07Tub qCR2	GGTCGATGCGCGAGAAAACCTC
Os07g01760	glutamate glyoxylate aminotransferase	07AmTrans qCF2	ACCCGCTTTATTCTGCTGCCATTT
		07AmTrans qCR2	CGAAGTCAAGTCCCCAGTTAGCCT
Os08g39300	alanine-glyoxylate aminotransferase	08AmTrans qCF1	TCTACAAGATGGGCACCTACTGGC
		08AmTrans qCR1	CTTCCTCGAAGATGAGGTCGAGGG
Os07g46460	Fd-GOGAT	07FGDS qCF1	CAATATTGTCCGGGATGCCCTTGT
		07FGDS qCR1	TGAACCGTCACCGGAGTCATTGTC
Os02g50240	glutamine synthase	02GluSyn qCF2	ATTGAGCAAGAGTACACCCTCC
		02GluSyn qCR2	TAGTAAGGACCCTGAGGACCAG
Os08g25734	gluc-1-phosphate adenylyltransferase	08G1PAT qCF1	CTTGACGACGTGAGGGCAAAAGAA
		08G1PAT qCR1	TCACGGAGGAGCTGAAGCATTACA
Os02g02890	cyclophilin 2	OsCyclo_qCF1	GTGGTGTTAGTCTTTTTATGAGTTCGT
		OsCyclo_qCR1	ACCAAACCATGGGCGATCT

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