

Supplementary Material

Genome-wide association studies identifies genetic loci related to fatty acid and branched-chain amino acid metabolism and histone modifications under varying nitrogen treatments in safflower (*Carthamus tinctorius*)

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Table S1. List of safflower genotypes.

S.No	Country Origin	Plant ID
Genotype1	Afghanistan	P1-253764
Genotype 2	Afghanistan	P1-304592
Genotype3	Afghanistan	PI 220647
Genotype4	Argentina	P1-367833
Genotype5	Australia	PI 235660
Genotype6	Austria	PI 253519
Genotype7	Austria	BVAL-901352
Genotype8	Bangladesh	PI-401472
Genotype9	Bangladesh	PI-401478
Genotype10	Bangladesh	PI-401480
Genotype11	Bangladesh	PI 401470
Genotype12	China	P1-262452
Genotype13	China	P1-262453
Genotype14	China	PI 543979
Genotype15	China	PI 543982
Genotype16	China	PI 544001
Genotype17	China	PI 568809
Genotype18	China	PI 568874
Genotype19	Egypt	P1-250082
Genotype20	Egypt	P1-250528
Genotype21	Egypt	P1-250532
Genotype22	Egypt	P1-250540
Genotype23	Egypt	P1-250605
Genotype24	Egypt	P1-250608
Genotype25	France	PI 576985
Genotype26	Hungary	PI 288983
Genotype27	India	P1-250601
Genotype28	India	P1-305195
Genotype29	India	P1-306926
Genotype30	India	P1-306941
Genotype31	India	P1-306976
Genotype32	India	PI 199878
Genotype33	Iran	P1-250720
Genotype34	Iran	P1-304444
Genotype35	Iran	P1-304448
Genotype36	Iran	P1-405958
Genotype37	Iran	P1-405967
Genotype38	Iran	PI 250840
Genotype39	Iran	PI 406010

Genotype40	Israel	P1-198990
Genotype41	Israel	P1-253386
Genotype42	Israel	P1-253892
Genotype43	Israel	PI 251290
Genotype44	Iraq	P1-253761
Genotype45	Iraq	P1-253762
Genotype46	Jordan	P1-251284
Genotype47	Jordan	P1-251285
Genotype48	Jordan	PI 251265
Genotype49	Jordan	PI 251267
Genotype50	Jordan	PI 251268
Genotype51	Kazakhstan	P1-314650
Genotype52	Libya	PI 393499
Genotype53	Morocco	P1-239042
Genotype54	Morocco	P1-253560
Genotype55	Pakistan	P1-250194
Genotype56	Pakistan	P1-250201
Genotype57	Pakistan	P1-250345
Genotype58	Pakistan	P1-250346
Genotype59	Pakistan	P1-250351
Genotype60	Pakistan	P1-250353
Genotype61	Pakistan	P1-250481
Genotype62	Pakistan	PI 250474
Genotype63	Pakistan	PI 250478
Genotype64	Pakistan	PI 426521
Genotype65	Pakistan	Thori-78
Genotype66	Portugal	P1-253553
Genotype67	Portugal	P1-253556
Genotype68	Portugal	P1-253564
Genotype69	Portugal	P1-253569
Genotype70	Portugal	P1-253571
Genotype71	Portugal	P1-258412
Genotype72	Romania	P1-209287
Genotype73	Russia	P1-305535
Genotype74	Spain	P1-253388
Genotype75	Spain	P1-253391
Genotype76	Spain	P1-253394
Genotype77	Spain	P1-253395
Genotype78	Syria	P1-253898
Genotype79	Syria	P1-253900
Genotype80	Syria	P1-386174
Genotype81	Thailand	P1-387821

Genotype82	Turkey	P1-304498
Genotype83	Turkey	P1-304502
Genotype84	Turkey	P1-304504
Genotype85	Turkey	P1-304505
Genotype86	Turkey	P1-340086
Genotype87	Turkey	PI 237538
Genotype88	Turkey	PI 251978
Genotype89	Turkey	PI 251984
Genotype90	Turkey	PI 406701
Genotype91	Turkey	PI 406702
Genotype92	Uzbekistan	P1-262435
Genotype93	Uzbekistan	P1-369846
Genotype94	Uzbekistan	P1-369853

Table S2. Summary statistics for all the studied traits across four treatments.

Treatment	Variable	Mean	SE Mean	Minimum	Maximum
T1	BY	1.19	0.10	0.37	0.98
	C	0.37	0.01	0.16	0.75
	CA	0.42	0.01	0.16	0.71
	CB	0.29	0.01	0.10	0.87
	CT	1.08	0.03	0.45	1.72
	FSW	0.42	0.02	0.14	0.96
	NOL	7.10	0.10	5.00	10.67
	PH	1.76	0.02	0.97	2.12
	RL	15.18	0.47	7.37	31.33
	RW	0.68	0.03	0.17	2.30
T2	BY	1.39	0.06	0.63	3.31
	C	0.47	0.01	0.18	0.79
	CA	0.48	0.01	0.12	0.84
	CB	0.35	0.01	0.11	0.55
	CT	1.31	0.03	0.44	2.04
	FSW	0.51	0.02	0.26	1.44
	NOL	8.12	0.13	6.33	13.00
	PH	1.83	0.02	1.27	2.20
	RL	16.13	0.39	8.55	27.43
	RW	0.88	0.04	0.31	2.62
T3	BY	1.66	0.06	0.58	3.41
	C	0.49	0.02	0.15	0.89
	CA	0.51	0.01	0.15	0.83
	CB	0.38	0.01	0.13	0.67
	CT	1.37	0.03	0.55	2.19
	FSW	0.63	0.02	0.23	1.42
	NOL	9.02	0.15	6.67	15.00
	PH	1.86	0.02	1.35	2.29
	RL	16.90	0.34	8.72	28.87
	RW	1.02	0.05	0.26	2.58
T4	BY	1.48	0.07	0.43	3.30
	C	0.55	0.02	0.12	0.91
	CA	0.52	0.02	0.13	0.96
	CB	0.36	0.01	0.11	0.64
	CT	1.44	0.04	0.53	2.40
	FSW	0.57	0.02	0.18	1.40
	NOL	8.73	0.13	6.33	12.33
	PH	1.82	0.02	1.02	2.20
	RL	16.66	0.43	8.04	27.52
	RW	0.91	0.05	0.17	2.22

CA	0.1153	0.5466**								
CB	0.1413	0.533**	0.5522**							
CT	0.0842	0.8414**	0.8604**	0.7955**						
FRW	0.9702**	-0.0445	0.0916	0.1011	0.0548					
FSW	0.8582**	-0.007	0.127	0.1779	0.1114	0.7156**				
NOL	0.2261*	0.0867	0.2094*	0.2276*	0.2044*	0.2127*	0.2027*			
PH	0.3061**	0.1986	0.0614	0.15	0.1597	0.2482*	0.3623**	0.2127*		
RL	0.4755**	-0.0864	-0.0211	0.1009	-0.0139	0.4547**	0.4048**	0.2942**	0.2311*	

Table S4. Marker-associated loci under T1, T2, T3 and T4 treatments.

Treatment	Trait	Marker	AGI	Abbreviation	Loci Name
T1	NOL	DArT-45481731	AT1G68530	<i>KCS6/CER6/ CUT1/POP1</i>	<i>3-KETOACYL-COA SYNTHASE6 / CUTICULAR1 / ECERIFERUM6 / POLLEN-PISTIL INCOMPATIBILITY1</i>
	NOL	DArT-45483063	AT3G29160	<i>KIN11 / SNRK1.2</i>	<i>SNF1 KINASE HOMOLOG 11 / SNF1-RELATED PROTEIN KINASE 1.2</i>
	NOL	DArT-38079559	AT5G07260	-	START (StAR-related lipid-transfer) lipid-binding domain- containing protein
	NOL	DArT-45485734	AT5G05600	<i>JAO2/JOX2</i>	<i>JASMONATE-INDUCED OXYGENASE2 / JASMONIC ACID OXIDASE2</i>
	FRW	DArT-17812864	AT5G11530	<i>EMF1</i>	<i>EMBRYONIC FLOWER1</i>
	FRW	DArT-22762716	AT5G45260	<i>WRKY52/ RRS1/SLH1</i>	<i>WRKY DOMAIN PROTEIN52 / RESISTANT TO RALSTONIA SOLANACEARUM1 / SENSITIVE TO LOW HUMIDITY1</i>
	CT	DArT-15670677	AT5G37660	<i>PDLP7</i>	<i>PLASMODESMATA-LOCATED PROTEIN7</i>
	BY	DArT-38083567	AT2G33847	-	Hypothetical protein
	BY	DArT-17812864	AT5G11530	<i>EMF1</i>	<i>EMBRYONIC FLOWER1</i>
	BY	DArT-22761898	AT3G53970	<i>PTRE1</i>	<i>PROTEASOME REGULATOR1</i>
T2	FSW	DArT-100046395	AT4G29190	<i>OZF2/TZF3</i>	<i>OXIDATION-RELATED ZINC FINGER2 / TANDEM ZINC FINGER 3</i>
	FSW	DArT-38083554	AT3G54540	<i>ABCF4/GCN4</i>	<i>ATP-BINDING CASSETTE F4 / GENERAL CONTROL NON- DEREPRESSIBLE4</i>
	NOL	DArT-22764463	AT1G31800	<i>CYP97A3/LUT5</i>	<i>CYTOCHROME P450 FAMILY 97 SUBFAMILY A POLYPEPTIDE3 / LUTEIN DEFICIENT5</i>
	NOL	DArT-45478831	AT4G00730	<i>ANL2</i>	<i>ANTHOCYANINLESS 2</i>
	NOL	DArT-45481731	AT1G68530	<i>KCS6/CER6/ CUT1/POP1</i>	<i>3-KETOACYL-COA SYNTHASE6 / CUTICULAR1 / ECERIFERUM6 / POLLEN-PISTIL INCOMPATIBILITY1</i>
	RL	DArT-15670186	AT3G16920	<i>CTL2</i>	<i>CHITINASE-LIKE PROTEIN 2</i>
	FRW	DArT-45483148	AT2G18040	<i>PINIAT</i>	<i>PEPTIDYLPROLYL CIS/TRANS ISOMERASE NIMA- INTERACTING1</i>
	FRW	DArT-45487501	AT2G20860	<i>LIP1</i>	<i>LIPOIC ACID SYNTHASE 1</i>
	FRW	DArT-15670279	AT5G65780	<i>BCAT5</i>	<i>BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE5</i>
	BY	DArT-15670279	AT5G65780	<i>BCAT5</i>	<i>BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE5</i>

	BY	DArT-45483151	AT3G17680	-	Kinase interacting (KIP1-like) family protein
	FSW	DArT-100005164	AT2G01430	<i>HB17</i>	<i>HOMEBOX-LEUCINE ZIPPER PROTEIN17</i>
T3	FRW	DArT-45482737	AT1G45050	<i>UBC15</i>	<i>UBIQUITIN-CONJUGATING ENZYME15</i>
	BY	DArT-45482737	AT1G45050	<i>UBC15</i>	<i>UBIQUITIN-CONJUGATING ENZYME15</i>
	FSW	DArT-100002034	AT1G53470	<i>MSL4</i>	<i>MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE4</i>
	FSW	DArT-45485354	AT1G07720	<i>KCS3</i>	<i>3-KETOACYL-COA SYNTHASE3</i>
	FSW	DArT-45487831	AT1G07720	<i>KCS3</i>	<i>3-KETOACYL-COA SYNTHASE3</i>
	RL	DArT-45478819	AT2G36145	-	Hypothetical protein
T4	FRW	DArT-15672551	AT1G62000	<i>TBA1</i>	<i>TESTA ABUNDANTI</i>
	FRW	DArT-15674217	AT5G51150	-	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein
	FRW	DArT-45480200	AT1G09130	<i>CLPR3</i>	<i>ATP-DEPENDENT CASEINOLYTIC (CLP) PROTEASE/CROTONASE3</i>
	BY	DArT-45487918	AT1G51450	<i>ASH2R/TRO</i>	<i>ASH2 RELATIVE / TRAUCO</i>

Shared markers between different treatments are given in bold.