

Supplementary Figures

Stem replicates

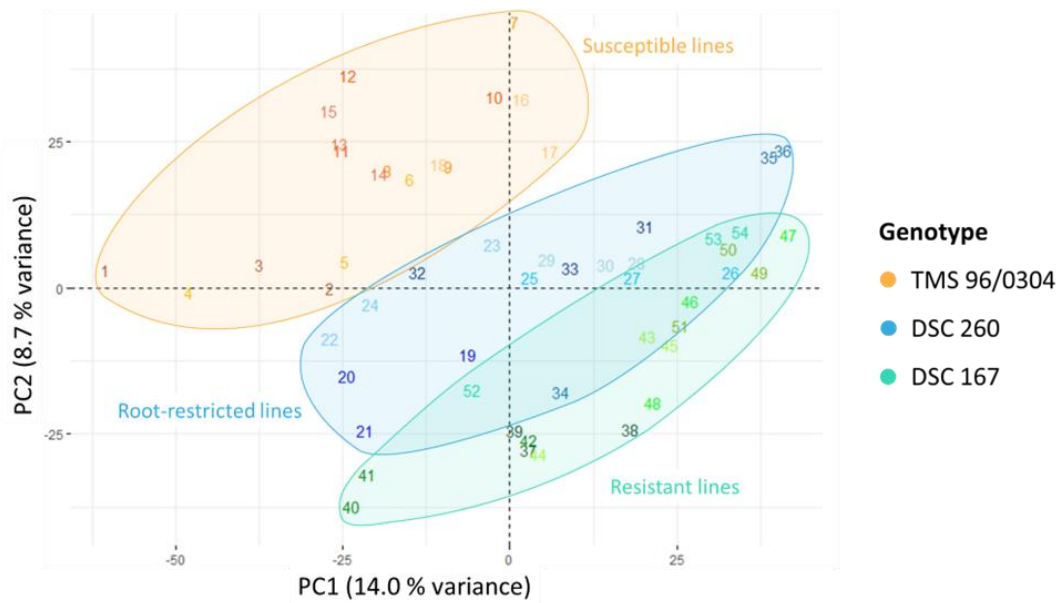


Figure S1: PCA plot of RNA-seq stem replicates grouped by genotype. Each number corresponds to an individual biological replicate of healthy control cassava plants and CBSV-Mo83-infected cassava plants sampled at 1, 5, and 10 DAI. Orange, susceptible TMS 96/0304 (number 1-18); blue, root-restricted DSC 260 (number 19-36); green, resistant DSC 167 (number 37-54). PC1 is 14.0 % variance; PC2 is 8.7 % variance.

Root replicates

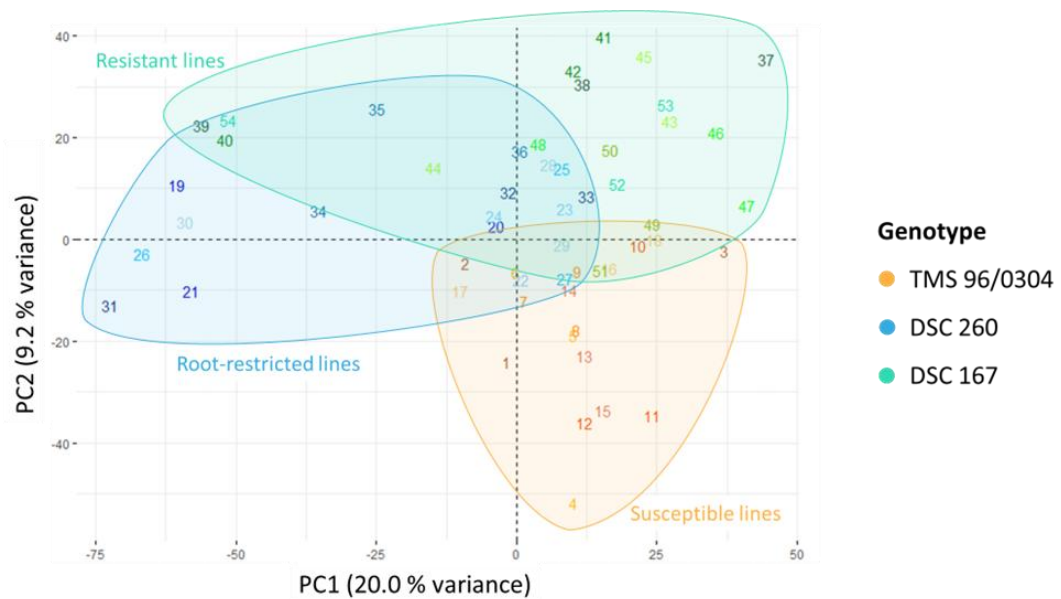


Figure S2: PCA plot of RNA-seq root replicates grouped by genotype. Each number corresponds to an individual biological replicate of healthy control cassava plants and CBSV-Mo83-infected cassava plants sampled at 1, 5, and 10 DAI. Orange, susceptible TMS 96/0304 (number 1-18); blue, root-restricted DSC 260 (number 19-36); green, resistant DSC 167 (number 37-54). PC1 is 20.0 % variance; PC2 is 9.2 % variance.

YL replicates

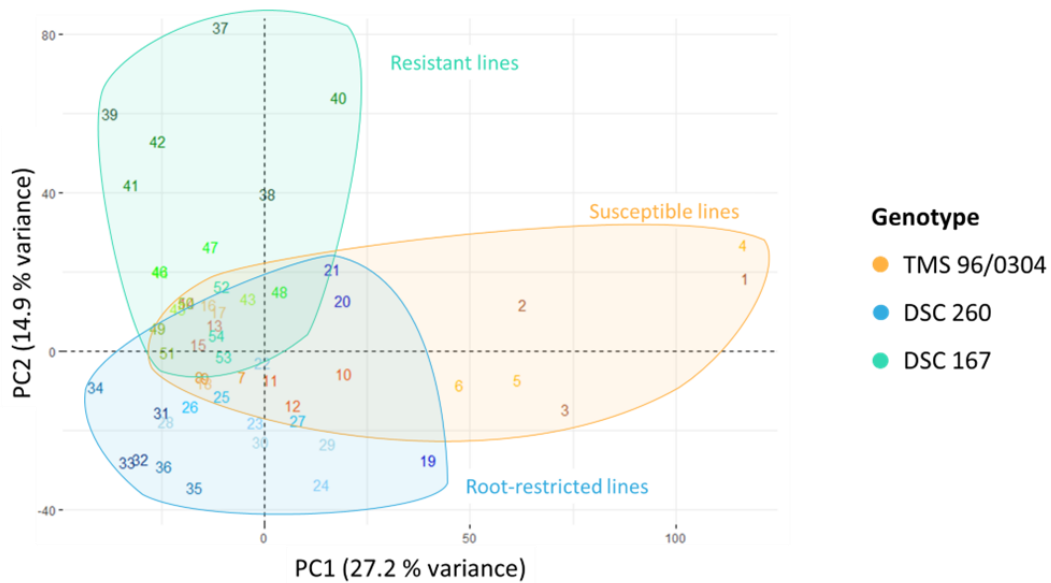


Figure S3: PCA plot of RNA-seq young leaf (YL) replicates grouped by genotype. Each number corresponds to an individual biological replicate of healthy control cassava plants and CBSV-Mo83-infected cassava plants sampled at 1, 5, and 10 DAI. Replicates: orange = susceptible TMS 96/0304 (number 1-18); blue, root-restricted DSC 260 (number 19-36); green, resistant DSC 167 (number 37-54). PC1 is 27.2 % variance; PC2 is 14.9 % variance.

OL replicates

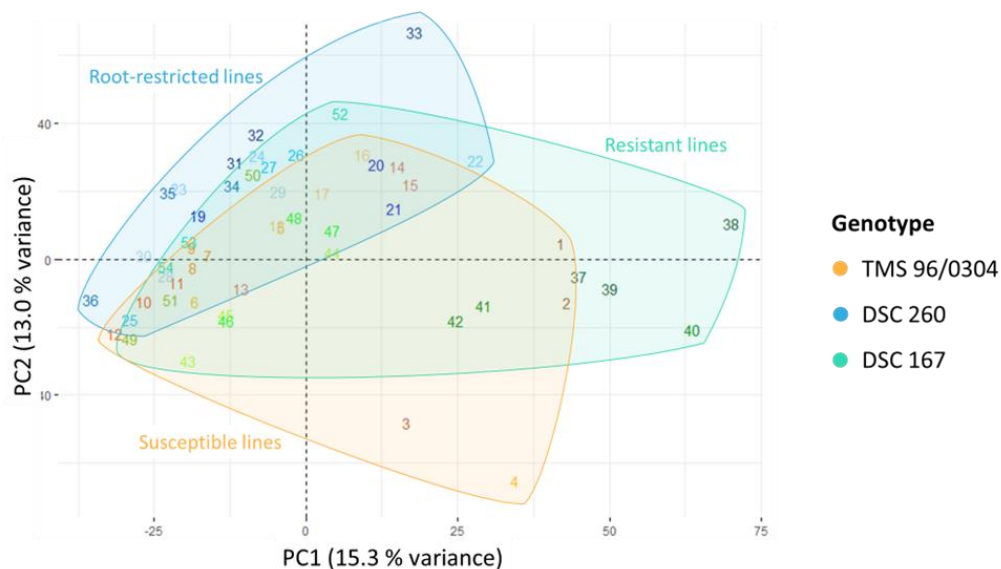


Figure S4: PCA plot of RNA-seq old leaf (OL) replicates grouped by genotype. Each number corresponds to an individual biological replicate of healthy control cassava plants and CBSV-Mo83-infected cassava plants sampled at 1, 5, and 10 DAI. Replicates: orange = susceptible TMS 96/0304 (number 1-18); blue, root-restricted DSC 260 (number 19-36); green, resistant DSC 167 (number 37-54). PC1 is 15.3 % variance; PC2 is 13.0 % variance.

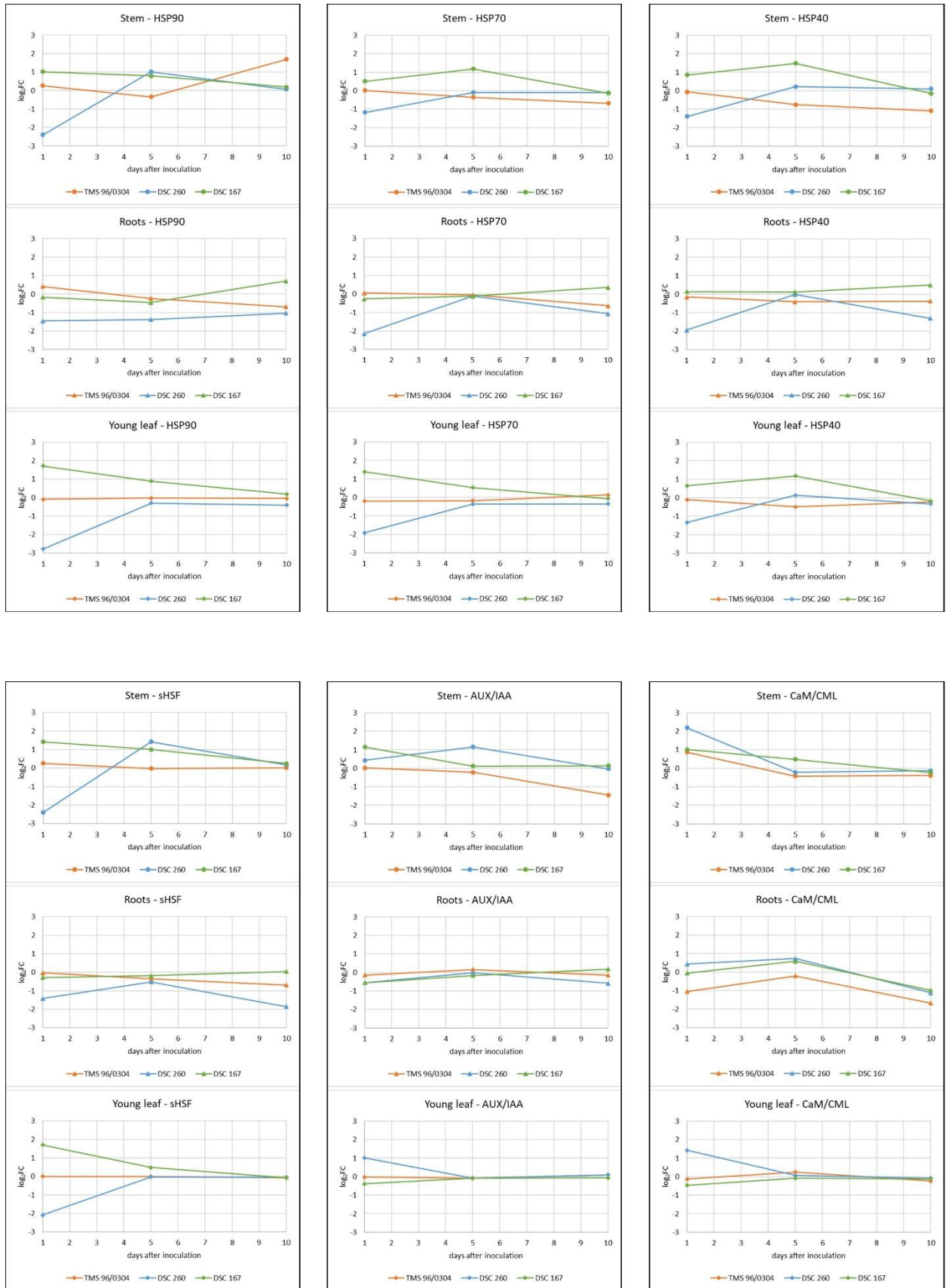


Figure S5 : Temporal expression pattern plots of protein candidates based on the log₂FC at 1, 5, and 10 days after inoculation.

Supplementary Tables

Table S1: Sampling strategy

Time Points of Sampling	Plant genotype					
	Susceptible Cassava Plants (TMS 96/0304)		Root-Restricted Cassava Plants (DSC 260)		Resistant Cassava Plants (DSC 167)	
	Healthy	Infected	Healthy	Infected	Healthy	Infected
1 DAI	9	9	9	9	9	9
5 DAI	9	9	9	9	9	9
10 DAI	9	9	9	9	9	9
Total No. of Plants	27	27	27	27	27	27
	54		54		54	

Table S2 : qRT-PCR results for replicates sampled at 10 and 30 days after inoculation(+, presence of virus; -, absend of presence)

STEM at 10 days after inoculation			
Genotype	Condition	Replicate	qRT-PCR
TMS 96/0304	healthy	A	-
TMS 96/0304	healthy	B	-
TMS 96/0304	healthy	C	-
TMS 96/0304	infected	A	-
TMS 96/0304	infected	B	-
TMS 96/0304	infected	C	-
DSC 260	healthy	A	-
DSC 260	healthy	B	-
DSC 260	healthy	C	-
DSC 260	infected	A	-
DSC 260	infected	B	-
DSC 260	infected	C	-
DSC 167	healthy	A	-
DSC 167	healthy	B	-
DSC 167	healthy	C	-
DSC 167	infected	A	-
DSC 167	infected	B	-
DSC 167	infected	C	-

ROOTS at 10 days after inoculation			
Genotype	Condition	Replicate	qRT-PCR
TMS 96/0304	healthy	A	-
TMS 96/0304	healthy	B	-
TMS 96/0304	healthy	C	-
TMS 96/0304	infected	A	+
TMS 96/0304	infected	B	+
TMS 96/0304	infected	C	-
DSC 260	healthy	A	-
DSC 260	healthy	B	-
DSC 260	healthy	C	-
DSC 260	infected	A	-
DSC 260	infected	B	-
DSC 260	infected	C	-
DSC 167	healthy	A	-
DSC 167	healthy	B	-
DSC 167	healthy	C	-
DSC 167	infected	A	-
DSC 167	infected	B	-
DSC 167	infected	C	-

YOUNG LEAF at 10 days after inoculation			
Genotype	Condition	Replicate	qRT-PCR
TMS 96/0304	healthy	A	-
TMS 96/0304	healthy	B	-
TMS 96/0304	healthy	C	-
TMS 96/0304	infected	A	-
TMS 96/0304	infected	B	-
TMS 96/0304	infected	C	-
DSC 260	healthy	A	-
DSC 260	healthy	B	-
DSC 260	healthy	C	-
DSC 260	infected	A	-
DSC 260	infected	B	-
DSC 260	infected	C	-
DSC 167	healthy	A	-
DSC 167	healthy	B	-
DSC 167	healthy	C	-
DSC 167	infected	A	-
DSC 167	infected	B	-
DSC 167	infected	C	-

OLD LEAF at 10 days after inoculation			
Genotype	Condition	Replicate	qRT-PCR
TMS 96/0304	healthy	A	-
TMS 96/0304	healthy	B	-

TMS 96/0304	healthy	C	-
TMS 96/0304	infected	A	-
TMS 96/0304	infected	B	-
TMS 96/0304	infected	C	-
DSC 260	healthy	A	-
DSC 260	healthy	B	-
DSC 260	healthy	C	-
DSC 260	infected	A	-
DSC 260	infected	B	-
DSC 260	infected	C	-
DSC 167	healthy	A	-
DSC 167	healthy	B	-
DSC 167	healthy	C	-
DSC 167	infected	A	-
DSC 167	infected	B	-
DSC 167	infected	C	-

STEM at 1 month after virus inoculation			
Genotype	Condition	Plant	qRT-PCR
TMS 96/0304	infected	1	+
TMS 96/0304	infected	2	+
TMS 96/0304	infected	3	+
DSC 260	infected	1	-
DSC 260	infected	2	-
DSC 260	infected	3	-
DSC 167	infected	1	-
DSC 167	infected	2	-
DSC 167	infected	3	-

LEAF at 1 month after virus inoculation			
Genotype	Condition	Plant	qRT-PCR
TMS 96/0304	infected	1	+
TMS 96/0304	infected	2	+
TMS 96/0304	infected	3	+

Table S3: Raw reads and mapping of stem samples

Sample number	Clean reads	GC %	Reads mapped to CBSV genome sequence	Reads mapped to cassava genome sequence
1	15,039,750	46.2	0	14,867,303
2	64,293,016	51.3	0	63,935,390
3	24,313,190	44.4	0	23,994,340
4	36,114,744	50.5	0	35,883,291
5	43,846,208	50.5	0	43,571,134
6	51,899,068	52.9	0	50,547,717
7	30,773,516	53.6	0	30,718,092
8	16,024,920	51.3	0	15,954,289
9	27,727,090	51.8	0	27,543,609
10	32,336,866	53.0	0	32,192,600
11	28,867,872	49.3	0	28,619,295
12	30,240,488	44.2	0	29,760,439
13	28,145,456	44.6	0	27,727,109
14	41,372,494	51.1	0	41,122,835
15	27,938,132	46.8	0	27,634,590
16	22,527,422	52.6	2,001	22,439,860
17	39,557,338	54.5	970	39,464,977
18	60,635,596	51.0	0	58,831,097
19	48,443,244	53.9	0	48,312,480
20	45,446,974	53.7	0	45,273,460
21	35,124,890	51.2	0	34,907,494
22	37,417,870	44.0	0	36,851,959
23	24,297,802	53.6	0	24,217,157
24	26,038,948	45.8	0	25,724,277
25	26,490,172	51.3	0	26,225,122
26	4,143,898	52.8	0	4,115,979
27	48,489,504	53.4	0	48,234,757
28	33,717,496	52.6	0	33,533,983
29	24,243,572	49.1	0	23,971,595
30	56,922,866	51.9	0	56,462,675
31	23,398,210	53.5	0	23,280,740
32	39,557,740	51.2	0	39,260,728

33	28,747,382	53.3	0	28,570,004
34	33,185,016	53.4	0	33,043,246
35	28,376,452	55.0	0	28,283,017
36	35,988,118	54.1	0	35,842,757
37	34,515,210	53.4	0	34,356,758
38	40,503,922	54.0	0	40,376,489
39	29,282,044	51.6	0	29,133,296
40	25,062,570	44.4	0	24,740,475
41	36,268,590	46.9	0	35,866,248
42	66,478,650	53.1	0	66,173,332
43	88,888,578	53.8	0	88,553,623
44	51,493,240	52.0	0	51,068,654
45	91,202,328	53.1	0	90,746,118
46	60,428,878	53.3	0	60,200,785
47	70,881,398	53.9	0	70,574,691
48	66,820,580	51.6	0	66,458,815
49	35,568,480	54.6	0	35,488,566
50	36,009,972	55.1	0	35,945,616
51	97,195,718	53.5	0	96,933,994
52	68,776,654	54.0	78,492	68,442,145
53	48,188,218	54.5	0	48,035,085
54	43,128,712	54.2	0	43,013,968

Table S4: Raw reads and mapping of root samples

Sample number	Clean reads	GC %	Reads mapped to CBSV genome sequence	Reads mapped to cassava genome sequence
1	15,549,880	48.7	0	13,803,962
2	16,145,632	53.9	0	15,923,010
3	25,126,712	52.1	0	24,694,486
4	25,817,152	53.4	0	25,563,009
5	25,335,182	51.9	0	25,074,691
6	32,146,744	53.9	0	31,646,174
7	28,901,754	51.5	0	28,656,705
8	30,262,474	51.2	0	30,038,209

9	30,341,608	50.9	0	30,012,251
10	23,928,958	51.6	0	23,709,490
11	30,915,118	52.1	0	30,663,778
12	29,430,470	46.2	0	29,015,031
13	37,735,558	47.3	0	37,236,215
14	25,289,522	48.9	0	25,005,542
15	21,999,010	50.7	0	21,765,065
16	26,725,808	50.0	14,894	26,356,761
17	33,804,342	52.8	17,614	33,463,593
18	21,661,700	53.5	0	21,478,930
19	21,079,544	50.6	0	20,816,619
20	27,987,742	53.3	0	27,478,334
21	14,046,844	54.1	0	13,944,030
22	23,749,592	53.5	0	23,436,042
23	22,951,656	53.3	0	22,754,860
24	29,639,712	53.0	0	29,227,894
25	28,817,344	52.4	0	28,495,378
26	13,386,824	52.8	0	13,300,388
27	38,915,250	52.8	0	38,486,693
28	128,522,134	52.7	0	127,034,367
29	26,543,164	53.4	0	26,511,788
30	12,942,656	50.8	0	12,816,215
31	14,236,566	52.6	0	14,100,034
32	32,639,418	52.6	0	29,777,473
33	28,416,294	52.9	0	27,819,805
34	25,404,546	54.6	0	25,154,415
35	24,340,494	54.4	0	23,549,173
36	26,819,836	54.2	0	26,467,424
37	22,521,394	51.0	0	22,291,895
38	24,383,530	48.6	0	24,117,051
39	22,103,670	50.7	0	21,748,269
40	23,104,298	53.4	0	22,844,611
41	27,776,714	53.8	0	27,612,655
42	22,454,038	53.9	0	22,315,165
43	25,248,432	52.8	0	25,027,452

44	26,260,506	54.3	0	25,814,141
45	50,054,340	52.6	0	49,651,950
46	31,005,540	53.1	0	30,771,924
47	25,339,926	51.0	0	25,029,787
48	27,549,642	52.5	0	26,477,405
49	33,268,750	51.4	0	32,883,925
50	149,479,810	53.7	0	148,504,514
51	35,404,658	53.8	0	35,172,439
52	38,902,910	53.3	1,192	38,294,210
53	34,603,076	53.7	0	34,387,504
54	28,699,852	53.8	0	28,493,514

Table S5: Raw reads and mapping of YL samples

Sample number	Clean reads	GC %	Reads mapped to CBSV genome sequence	Reads mapped to cassava genome sequence
1	25,134,390	46.6	0	24,858,146
2	57,483,816	44.6	0	56,740,970
3	32,905,432	46.6	0	32,503,181
4	23,840,518	48.7	0	23,610,938
5	30,391,704	45.5	0	30,043,282
6	18,427,702	50.8	0	18,321,688
7	33,975,406	50.2	0	33,780,034
8	11,779,354	51.9	0	11,733,484
9	31,182,592	48.5	0	30,920,480
10	21,477,704	50.7	0	21,339,788
11	45,102,916	47.1	0	44,667,882
12	24,846,818	48.7	0	24,630,386
13	26,072,222	45.7	0	25,776,401
14	26,128,650	45	0	25,812,141
15	19,482,678	45.1	0	19,253,206
16	24,502,562	46.7	0	24,276,319
17	41,744,616	48.5	0	41,400,059
18	30,604,444	47.2	0	30,322,521
19	32,475,360	46.6	0	32,133,501
20	52,173,832	45.3	0	51,542,658
21	32,504,256	45.5	0	32,121,289
22	36,853,248	44.6	0	36,395,043
23	49,284,552	45.7	0	48,079,622
24	53,245,034	45.6	0	52,609,950
25	26,207,936	47.4	0	25,619,281
26	15,927,248	45.3	0	15,839,533
27	25,553,208	45.2	0	25,214,080
28	24,576,422	47.8	0	24,293,778
29	33,202,748	45.8	0	32,892,184
30	24,855,316	47.1	0	24,543,557
31	28,425,328	46.7	0	28,066,885
32	31,737,838	45.9	0	31,232,606

33	12,801,904	46.3	0	12,610,865
34	14,392,284	51.1	0	14,226,088
35	13,988,418	49.8	0	13,783,290
36	16,678,758	50.1	0	16,502,884
37	16,335,164	50.4	0	16,074,216
38	16,509,632	45.5	0	16,362,443
39	23,175,334	50.7	0	22,931,644
40	21,991,812	49.7	0	21,832,752
41	25,942,274	50.5	0	25,738,195
42	23,419,074	50.4	0	23,294,410
43	81,350,378	47.0	0	80,350,577
44	22,275,482	50.2	0	21,984,823
45	22,066,784	50.1	0	21,819,246
46	24,259,256	48.5	0	24,184,188
47	23,601,196	49.3	0	23,204,884
48	34,616,634	44.2	0	34,326,338
49	26,693,024	50.1	0	26,442,886
50	27,876,498	45.4	0	27,552,183
51	25,848,136	51.4	0	25,598,524
52	29,337,102	48.5	0	29,024,614
53	31,570,116	49.4	0	31,388,976
54	32,111,540	50.1	0	32,021,065

Table S6: Raw reads and mapping of OL samples

Sample number	Clean reads	GC %	Reads mapped to CBSV genome sequence	Reads mapped to cassava genome sequence
1	27,311,890	49.8	0	27,091,462
2	23,308,534	45.9	0	23,003,262
3	34,874,904	50.1	0	34,521,096
4	32,482,960	53.0	0	32,303,367
5	31,041,912	46.8	0	30,700,346
6	29,521,644	53.9	0	29,445,149
7	42,014,104	52.6	0	41,869,262
8	30,301,300	52.1	0	30,183,518
9	38,962,956	52.3	0	38,762,798
10	28,631,758	53.4	0	28,492,312
11	24,137,738	53.1	0	24,006,886
12	26,172,926	54.8	0	26,080,411
13	31,188,114	47.2	0	30,863,274
14	28,471,480	45.3	0	28,088,101
15	27,189,442	45.6	0	26,855,875
16	28,293,082	46.5	0	27,997,261
17	35,415,920	51.1	0	35,189,842
18	34,720,016	49.7	0	34,463,126
19	35,851,098	49.9	0	35,593,104
20	32,134,500	49.6	0	31,858,731
21	18,856,280	49.3	0	18,696,746
22	19,143,176	46.4	0	18,898,812
23	27,204,814	52.0	0	27,076,614
24	22,977,754	51.2	0	22,841,719
25	21,417,716	54.0	0	21,367,084
26	20,483,180	46.2	0	20,232,061
27	24,640,084	46.8	0	24,358,060
28	20,187,480	53.4	0	20,116,315
29	26,222,922	48.7	0	25,996,374
30	22,842,964	52.2	0	22,743,141
31	23,163,450	52.1	0	23,034,320
32	22,118,820	50.7	0	21,971,842

33	16,520,428	48.3	0	16,341,619
34	26,587,076	53.4	0	26,476,801
35	26,364,368	52.0	0	26,206,887
36	24,616,238	54.0	0	24,549,743
37	29,196,282	52.5	0	29,073,355
38	26,325,338	46.1	0	26,020,641
39	39,169,310	53.3	0	39,034,680
40	40,923,056	51.5	0	40,729,017
41	50,566,616	52.0	0	50,351,157
42	44,480,506	52.1	0	44,268,671
43	38,663,556	53.1	0	38,543,129
44	38,184,062	52.7	0	38,010,437
45	32,535,476	53.9	0	32,417,575
46	31,882,264	52.0	0	31,733,500
47	35,869,796	50.7	0	35,644,566
48	58,211,950	44.0	0	57,441,666
49	37,894,322	54.5	0	37,828,902
50	60,648,616	45.5	0	59,960,717
51	44,408,096	54.1	0	44,309,498
52	45,190,722	49.9	0	44,857,093
53	40,510,340	53.6	0	40,378,544
54	46,284,964	53.7	0	46,180,086

Table S7: Number of DEGs

Tissue	TMS 96/0304			DSC 260			DSC 167		
	1 DAI	5 DAI	10 DAI	1 DAI	5 DAI	10 DAI	1 DAI	5 DAI	10 DAI
Stem	43	74	737	335	20	22	436	21	9
Roots	47	6	834	398	47	37	16	20	15
Young leaf	0	14	80	405	0	0	135	57	14
Old leaf	47	86	1124	109	5	149	124	492	19

Table S8: List of gene names and functions

Genotype	tissue	DAI	Gene ID	Protein ID	log ₂ FC	adj. p-value	Chromosome	Putative Function	Gene group			
TMS 96/0304	stem	1	LOC110629547	XP_021632259.1	-1.972	1.95045E-08	13	ethylene-response factor C3	ethylene			
			LOC110610662	XP_021606389.1	-1.116	0.041237636	3	auxin-responsive protein IAA4	auxin			
			LOC110614146	XP_043812975.1	-1.714	3.11025E-06	5	transcription factor BEE 3	BEE 3			
			LOC110623008	XP_021623512.1	-1.084	0.045864768	1	transcription factor BEE 3	BEE 3			
			LOC110621693	XP_021621664.1	-1.046	0.048118015	8	probable E3 ubiquitin-protein ligase WAVH2 isoform X1	E3 ubiquitin			
			LOC110621693	XP_021621665.1	-1.044	0.048118015	8	probable E3 ubiquitin-protein ligase WAVH2 isoform X2	E3 ubiquitin			
			LOC110620832	XP_021620436.1	-1.109	0.048118015	8	WAT1-related protein At2g37460	WAT1			
			LOC110608515	XP_021603452.2	1.269	0.013408329	2	WAT1-related protein At5g47470	WAT1			
			LOC110629040	XP_043805134.1	-1.363	0.010541734	13	cellulose synthase-like protein H1 isoform X3	cell-wall			
			LOC110629040	XP_043805133.1	-1.351	0.010541734	13	cellulose synthase-like protein H1 isoform X2	cell-wall			
			LOC110629040	XP_043805132.1	-1.351	0.010541734	13	cellulose synthase-like protein H1 isoform X1	cell-wall			
			LOC110624589	XP_021625482.1	-1.223	0.006098614	10	expansin-A8	expansin			
			LOC110599873	XP_043813512.1	-1.179	0.037874948	1	plasmodesmata-located protein 7 isoform X2	cell-wall			
			LOC110620868	XP_021620494.1	-1.080	0.04964999	8	putative pectinesterase/pectinesterase inhibitor 22 isoform X1	pectinesterase			
			LOC110613960	XP_021611089.1	1.127	0.018110579	4	phenylalanine ammonia-lyase isoform X1	cell-wall			
			LOC110613960	XP_021611090.1	1.174	0.018110579	4	phenylalanine ammonia-lyase isoform X2	cell-wall			
			LOC110624589	XP_021625482.1	-1.223	0.006098614	10	expansin-A8	expansin			
			LOC110620868	XP_021620494.1	-1.080	0.04964999	8	putative pectinesterase/pectinesterase inhibitor 22 isoform X1	pectinesterase			
			TMS 96/0304	stem	5	LOC110629328	XP_021631932.1	-1.457	7.43357E-07	13	ethylene-responsive transcription factor 9	ethylene
						LOC110606096	XP_021600540.1	-1.259	0.012492256	18	pathogen-related protein	ethylene
LOC110618698	XP_021617607.1	-1.216				0.004823435	1	ethylene-responsive transcription factor 2	ethylene			
LOC110606363	XP_021600828.1	-1.206				0.032943412	18	ethylene-responsive transcription factor ERF014	ethylene			
LOC110616467	XP_021614518.1	-1.181				0.002968513	6	ethylene-responsive transcription factor ERF105	ethylene			
LOC110612806	XP_021609304.1	1.110				0.000374177	4	auxin response factor 10	auxin			
LOC110611351	XP_021607320.1	1.137				0.009545474	1	auxin-induced protein 22D	auxin			
LOC110621914	XP_021621905.1	1.229				0.004823435	1	auxin-induced protein AUX28	auxin			
LOC110614786	XP_021612140.1	1.017				0.039837401	5	probable WRKY transcription factor 12 isoform X1	WRKY			
LOC110614786	XP_021612141.1	1.154				0.009679383	5	probable WRKY transcription factor 12 isoform X2	WRKY			
LOC110607083	XP_021601831.1	-1.095				0.035839283	18	zinc finger protein ZAT10	zinc finger			
LOC110602254	XP_021595420.1	-1.033				0.009884409	15	RING-H2 finger protein ATL2	zinc finger			
LOC110610270	XP_021605844.1	1.052				0.005700199	1	RING-H2 finger protein ATL8	zinc finger			
LOC110621983	XP_021621997.1	-1.068				0.00839027	9	aquaporin PIP2-4	aquaporin			
LOC122724502	XP_043815583.1	-1.135				0.002511486	9	NDR1/HIN1-like protein 10	NDR1/HIN1			
LOC110600003	XP_021592360.2	-1.202				7.10578E-06	14	leucine-rich repeat receptor-like serine/threonine/tyrosine-protein kinase SOBIR1	LRR			
LOC110609777	XP_021605264.1	-1.482				9.78829E-05	2	E3 ubiquitin ligase PQT3-like	E3 ubiquitin			
LOC110622109	XP_021622192.1	-1.092				0.001847011	9	E3 ubiquitin-protein ligase ATL6	E3 ubiquitin			
LOC110602254	XP_021595420.1	-1.033				0.009884409	15	RING-H2 finger protein ATL2	RING-H2			
LOC110610270	XP_021605844.1	1.052				0.005700199	1	RING-H2 finger protein ATL8	RING-H2			
LOC110629370	XP_021631999.1	1.305				1.5433E-05	13	probable xyloglucan endotransglucosylase/hydrolase protein 6	cell-wall			
LOC110623596	XP_021624284.2	1.596				2.65852E-05	9	probable pectinesterase 8	pectinesterase			
LOC110623596	XP_021624284.2	1.596				2.65852E-05	9	probable pectinesterase 8	pectinesterase			
LOC110614572	XP_021611827.1	1.571				8.56716E-06	5	very-long-chain aldehyde decarboxylase CER1	CER1			
LOC110605987	XP_021600380.1	-1.538				0.00049239	18	serine/threonine-protein kinase-like protein CCR4	serine/threonine			
LOC110600003	XP_021592360.2	-1.202				7.10578E-06	14	leucine-rich repeat receptor-like serine/threonine/tyrosine-protein kinase SOBIR1	serine/threonine			
TMS 96/0304	stem	5				LOC110610982	XP_021606759.1	-1.690	2.46867E-07	3	pathogen-related protein	ethylene
						LOC110611493	XP_021607567.2	-1.341	0.002345307	9	peroxidase 21, partial	ethylene
						LOC110629429	XP_021632089.1	-1.111	0.007594963	13	peroxidase 17	ethylene
						LOC110610896	XP_021606660.1	1.073	0.002243044	3	ethylene-responsive transcription factor RAP2-3	ethylene
			LOC110605960	XP_021600348.1	1.212	0.046435203	18	ethylene-responsive transcription factor ABR1 isoform X2	ethylene			
			LOC122721339	XP_043804565.1	1.236	0.014091843	12	peroxidase 3-like	ethylene			
			LOC110602651	XP_021595914.1	1.244	0.00215638	15	peroxidase 15	ethylene			
			LOC110618124	XP_021616874.1	1.263	0.024914783	6	peroxidase 11	ethylene			
			LOC110624455	XP_021625302.1	1.324	0.015749462	10	ethylene-responsive transcription factor WR11	ethylene			
			LOC110612377	XP_021608842.1	1.333	0.009821369	3	peroxidase 24	ethylene			
			LOC110600304	XP_021592812.1	1.417	0.015997061	14	peroxidase 11	ethylene			
			LOC110629052	XP_021631591.1	1.442	0.002493939	13	ethylene-responsive transcription factor ERF053	ethylene			
			LOC110610900	XP_021606663.1	1.476	0.001440564	3	1-aminocyclopropane-1-carboxylate oxidase 1	ethylene			
			LOC110619476	XP_021618646.1	1.506	0.002028073	7	peroxidase 4	ethylene			
			LOC110601389	XP_021594194.1	1.597	0.000258961	15	peroxidase 55	ethylene			
			LOC110611351	XP_021607320.1	-1.505	4.81305E-05	1	auxin-induced protein 22D	auxin			
			LOC110610819	XP_021606590.1	-1.451	7.99884E-08	3	auxin-responsive protein IAA27	auxin			
			LOC110600709	XP_021593241.1	-1.089	4.87897E-06	15	auxin-responsive protein IAA14	auxin			
			LOC110629707	XP_021632489.1	-1.025	0.003869923	13	auxin-responsive protein SAUR36	auxin			
			LOC110610670	XP_021606399.1	-1.004	0.035830332	3	auxin-responsive protein IAA14	auxin			
			LOC110629170	XP_043805338.1	1.178	0.012929171	13	probable jasmonic acid carboxyl methyltransferase 2	jasmonic acid			
			LOC110613421	XP_021610227.1	1.062	0.015762144	1	WRKY transcription factor 23	WRKY			
			LOC110608207	XP_021603111.1	1.087	0.02221684	16	probable WRKY transcription factor 65	WRKY			
			LOC110601388	XP_021594193.1	1.252	0.020938899	15	probable WRKY transcription factor 31	WRKY			
			LOC110621275	XP_021621183.1	1.336	0.000134935	8	WRKY transcription factor 44	WRKY			
			LOC110615072	XP_021612474.1	1.381	0.007713693	1	probable WRKY transcription factor 43	WRKY			
			LOC110615593	XP_021613248.1	1.602	5.84898E-06	5	WRKY transcription factor 23	WRKY			
			LOC110604559	XP_021598481.1	1.663	8.29242E-05	17	probable WRKY transcription factor 31	WRKY			
			LOC110616186	XP_021614226.1	1.747	0.000200634	5	probable WRKY transcription factor 43	WRKY			
			LOC110618720	XP_021617634.1	-1.048	0.010319523	7	transcription factor bHLH51	bHLH			
			LOC110612840	XP_021609351.1	-1.017	0.004175975	4	transcription factor bHLH63 isoform X1	bHLH			
			LOC110612840	XP_021609352.1	-1.017	0.004175975	4	transcription factor bHLH63 isoform X2	bHLH			
			LOC110616901	XP_021615112.1	1.155	0.012020631	6	transcription factor bHLH137	bHLH			
			LOC110624679	XP_021625605.1	1.250	0.024635181	10	transcription factor bHLH25 isoform X2	bHLH			
			LOC110624679	XP_021625603.1	1.256	0.023630543	10	transcription factor bHLH25 isoform X1	bHLH			
			LOC110611785	XP_021607958.1	1.983	5.67698E-09	1	transcription factor bHLH42	bHLH			
			LOC110631036	XP_021634430.1	-1.405	0.005157681	14	myb-related protein 306	myb-related			
			LOC110626832	XP_043817691.1	-1.068	0.013062247	11	transcription factor MYB59	myb-related			
			LOC110620100	XP_021619373.1	-1.062	0.02357947	8	myb-related protein 2	myb-related			
			LOC110623298	XP_021623916.1	1.170	0.036421295	1	transcription repressor MYB6 isoform X2	myb-related			
LOC110623298	XP_021623909.1	1.178	0.034771554	1	transcription factor MYB8 isoform X1	myb-related						
LOC110601742	XP_021594698.1	1.196	0.021906357	15	transcription repressor MYB5	myb-related						
LOC110604571	XP_021598494.1	1.233	0.000441091	17	myb family transcription factor MOF1	myb-related						
LOC110612424	XP_021608897.1	1.238	0.024787854	3	myb-related protein 308	myb-related						
LOC110604279	XP_021598137.1	1.240	0.029953742	16	transcription factor MYB86	myb-related						
LOC110627470	XP_021629490.1	1.286	0.028904108	12	transcription factor MYB30	myb-related						

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LOC110629321	XP_021631920.2	1.291	0.018219289	13	transcription factor MYB102	MYB	
LOC110603387	XP_021596793.1	1.305	0.010683574	16	transcription factor MYB102		
LOC110623638	XP_021624330.1	1.322	0.010906491	9	transcription repressor MYB5		
LOC110604642	XP_021598594.1	1.354	0.0003755	17	transcription factor MYB102		
LOC110615013	XP_021612408.1	1.365	0.011710536	5	myb-related protein 308		
LOC110607055	XP_021601802.1	1.378	0.01432526	18	transcription factor MYB93		
LOC110607422	XP_021602216.1	1.410	0.00739946	13	transcription factor MYB92		
LOC110610671	XP_021606400.1	1.548	7.35658E-06	3	transcription factor MYB123		
LOC110621722	XP_043815246.1	1.568	0.007746037	8	transcription factor MYB93 isoform X1		
LOC110609873	XP_021605390.1	1.570	0.002538654	2	transcription factor MYB93		
LOC110601109	XP_021593815.1	1.588	0.001136487	15	transcription factor MYB102	zinc finger	
LOC110621722	XP_021621702.1	1.664	0.003440536	8	transcription factor MYB93 isoform X2		
LOC110600922	XP_021593546.1	1.700	5.19205E-07	15	myb family transcription factor MOF1		
LOC110630890	XP_021634223.1	-1.120	0.000545808	1	zinc finger protein CONSTANS-LIKE 2		
LOC110604729	XP_021598705.1	-1.027	0.001448854	2	zinc finger protein CONSTANS-LIKE 2		
LOC110610666	XP_021606393.1	-1.017	0.04991848	3	GATA transcription factor 15		
LOC110625106	XP_021626334.1	1.175	0.038566237	10	zinc finger protein ZAT11		
LOC110608235	XP_021603135.1	1.236	0.004226638	12	zinc finger protein CONSTANS-LIKE 9		
LOC110608761	XP_021603741.1	-1.194	0.006613225	2	transcription factor BEE 3 isoform X1		
LOC110608761	XP_021603742.1	-1.193	0.006613225	2	transcription factor BEE 1 isoform X2		
LOC110629593	XP_021632319.1	-1.255	0.015530574	13	small heat shock protein, chloroplastic	HSP	
LOC110621494	XP_021621464.1	-1.064	0.03984978	8	18.1 kDa class I heat shock protein		
LOC110603605	XP_021597086.2	1.681	0.000454907	2	heat shock protein 83	DNAJ	
LOC110627121	XP_021629057.1	-1.088	0.000830341	11	dnaj protein homolog		
LOC110629988	XP_021632942.1	1.256	9.74361E-06	13	chaperone protein dnaj C76, chloroplastic	calmodulin	
LOC110615897	XP_043812755.1	-1.850	4.93597E-08	5	calmodulin-like protein 2		
LOC110606090	XP_021600533.1	-1.882	1.54809E-06	18	probable calcium-binding protein CML28 isoform X2	calcium-binding	
LOC110606090	XP_021600532.1	-1.845	1.68113E-06	18	probable calcium-binding protein CML28 isoform X1		
LOC110611166	XP_021607011.1	-1.413	0.006205819	3	probable leucine-rich repeat receptor-like protein kinase At1g35710	LRR	
LOC110603621	XP_021597107.1	-1.079	9.5165E-06	16	probable LRR receptor-like serine/threonine-protein kinase		
LOC110601759	XP_021594737.1	1.164	0.000193108	15	phytosulfokine receptor 2		
LOC110600025	XP_021592398.1	1.274	0.004439861	14	leucine-rich repeat receptor protein kinase HPCA1 isoform X1		
LOC110600025	XP_021592399.1	1.274	0.004439861	14	leucine-rich repeat receptor protein kinase HPCA1 isoform X2		
LOC110608443	XP_021603351.1	-1.199	0.016979707	2	probable E3 ubiquitin-protein ligase RHA4A	E3 ubiquitin	
LOC110630125	XP_021633142.1	-1.119	0.018716898	13	E3 ubiquitin-protein ligase RMA1H1		
LOC110630125	XP_021633143.1	-1.119	0.018716898	13	E3 ubiquitin-protein ligase RMA1H1		
LOC110631024	XP_021634414.1	1.115	0.014670992	14	E3 ubiquitin-protein ligase ORTHRUS 2 isoform X1		
LOC110631024	XP_043805969.1	1.132	0.012228872	14	E3 ubiquitin-protein ligase ORTHRUS 2 isoform X2		
LOC110609115	XP_021604155.1	1.206	0.032368823	2	E3 ubiquitin ligase BIG BROTHER-related		
LOC110629373	XP_021632001.1	1.322	0.000140269	13	probable E3 ubiquitin-protein ligase XERICO		
LOC110628002	XP_021630126.1	1.824	0.000106692	12	E3 ubiquitin-protein ligase APD2		
LOC110616744	XP_021614915.1	1.007	0.037490276	6	RING-H2 finger protein AT1L13		RING-H2
LOC110620832	XP_021620436.1	-1.735	7.43536E-05	8	WAT1-related protein At2g37460		
LOC110620526	XP_021619991.1	-1.688	6.93508E-08	8	WAT1-related protein At5g07050	WAT1	
LOC110630534	XP_021633761.2	-1.651	2.29593E-05	1	WAT1-related protein At3g30340		
LOC110625087	XP_021626304.1	-1.360	0.000120517	10	WAT1-related protein At2g39510		
LOC110624625	XP_021625528.1	-1.262	0.003142737	10	WAT1-related protein At1g25270 isoform X2		
LOC110605754	XP_021600072.1	-1.218	0.000407845	2	WAT1-related protein At4g08300		
LOC110624625	XP_021625527.1	-1.146	0.007091364	10	WAT1-related protein At1g25270 isoform X1		
LOC110627422	XP_021629414.1	-1.096	0.038970643	12	WAT1-related protein At5g64700		
LOC110614367	XP_021611578.1	1.179	0.037729435	5	WAT1-related protein At5g40240		
LOC110612870	XP_021609395.1	-2.020	1.96602E-11	4	probable pectinesterase/pectinesterase inhibitor 35		
LOC110611067	XP_021606873.1	-1.999	1.23598E-06	3	pectinesterase		
LOC110629370	XP_021631999.1	-1.554	5.93337E-06	13	probable xyloglucan endotransglucosylase/hydrolase protein 6	cell-wall	
LOC110631132	XP_021634549.1	-1.268	0.023500353	14	xyloglucan endotransglucosylase/hydrolase protein 22		
LOC122721686	XP_043806018.1	-1.213	0.02199418	14	xyloglucan endotransglucosylase/hydrolase protein 22-like		
LOC110608269	XP_021603175.2	-1.193	0.000454907	2	putative wall-associated receptor kinase-like 16		
LOC122721683	XP_043806007.1	-1.167	0.02403676	14	probable xyloglucan endotransglucosylase/hydrolase protein 23		
LOC110630964	XP_021634322.1	-1.166	0.027009109	14	probable xyloglucan endotransglucosylase/hydrolase protein 23		
LOC110627031	XP_021628944.1	-1.157	0.003452114	11	fasciclin-like arabinogalactan protein 12		
LOC122721685	XP_043806011.1	-1.152	0.026145072	14	probable xyloglucan endotransglucosylase/hydrolase protein 23		
LOC110630961	XP_021634319.1	-1.142	0.031992318	14	probable xyloglucan endotransglucosylase/hydrolase protein 23		
LOC122721684	XP_043806008.1	-1.141	0.030986451	14	probable xyloglucan endotransglucosylase/hydrolase protein 23		
LOC110627066	XP_021628989.1	-1.118	0.00300318	11	fasciclin-like arabinogalactan protein 12		
LOC110627084	XP_021629011.1	-1.115	0.005459936	11	fasciclin-like arabinogalactan protein 12		
LOC110602230	XP_021595383.1	-1.096	0.04052596	15	pectinesterase		
LOC110609580	XP_021604952.1	-1.080	0.011297909	1	lysine-rich arabinogalactan protein 19		
LOC122723367	XP_043811387.1	-1.080	0.013159996	3	fasciclin-like arabinogalactan protein 12		
LOC110627064	XP_021628987.1	-1.021	0.012268877	11	fasciclin-like arabinogalactan protein 12		
LOC110600929	XP_021593557.1	1.099	0.007778862	15	cinnamoyl-CoA reductase-like SNL6		
LOC110628216	XP_043804550.1	1.168	0.045932622	12	callose synthase 5		
LOC110630043	XP_021633048.1	1.200	0.00136971	1	expansin-A15 isoform X2		
LOC110630909	XP_021634242.1	1.203	0.000850103	14	cinnamoyl-CoA reductase-like SNL6		
LOC110626127	XP_021627577.1	1.204	0.005027859	11	xyloglucan endotransglucosylase/hydrolase protein 31		
LOC110601094	XP_043806868.1	1.207	0.02439845	15	vegetative cell wall protein gp1 isoform X2		
LOC110601094	XP_043806867.1	1.207	0.02439845	15	vegetative cell wall protein gp1 isoform X1		
LOC110630043	XP_021633042.1	1.221	0.000848088	1	expansin-A15 isoform X1		
LOC110601112	XP_021593818.1	1.240	0.022793461	15	probable xyloglucan galactosyltransferase GT17		
LOC110606389	XP_043808927.1	1.267	0.025184742	18	wall-associated receptor kinase 3		
LOC110609261	XP_021604408.2	1.289	0.006683765	2	cellulose synthase-like protein G3		
LOC110610854	XP_021606625.1	1.330	0.011785915	1	pectinesterase QRT1		
LOC110604605	XP_021598539.1	1.348	0.002782972	17	probable xyloglucan endotransglucosylase/hydrolase protein 30		
LOC110626819	XP_021628626.1	1.366	0.0003382	11	beta-fructofuranosidase, cell wall isozyme isoform X1		
LOC110619169	XP_021618132.1	1.603	0.008076307	7	polygalacturonase QRT2		
LOC110613289	XP_021610033.1	1.626	5.35926E-05	4	cinnamoyl-CoA reductase 1		
LOC110611158	XP_021606999.1	1.687	1.57848E-05	3	polygalacturonase QRT3		
LOC110618558	XP_021617395.1	1.795	1.83861E-06	7	expansin-A8		
LOC110622267	XP_021622419.2	1.937	1.36699E-07	9	phenylalanine ammonia-lyase		
LOC110608586	XP_021603545.1	2.190	4.05596E-06	2	cinnamoyl-CoA reductase-like SNL6		
LOC110630043	XP_021633048.1	1.200	0.00136971	1	expansin-A15 isoform X2	expansin	
LOC110630043	XP_021633042.1	1.221	0.000848088	1	expansin-A15 isoform X1		
LOC110618558	XP_021617395.1	1.795	1.83861E-06	7	expansin-A8		

LOC110612870	XP_021609395.1	-2.020	1.96602E-11	4	probable pectinesterase/pectinesterase inhibitor 35	pectinesterase	
LOC110611067	XP_021606873.1	-1.999	1.23598E-06	3	pectinesterase		
LOC110602230	XP_021595383.1	-1.096	0.04052596	15	pectinesterase		
LOC110610854	XP_021606625.1	1.330	0.011785915	1	pectinesterase QRT1		
LOC110625160	XP_021626402.1	1.308	0.016634644	10	protein PELPK1	PELPK1	
LOC110619615	XP_021618820.1	2.120	4.35912E-05	7	protein PELPK1		
LOC110624270	XP_021625070.1	2.161	2.35549E-07	10	protein PELPK1		
LOC110619131	XP_021618075.1	2.339	1.05022E-06	7	protein PELPK1-like		
LOC110624269	XP_021625069.1	2.382	3.68774E-08	10	protein PELPK1	serine/threonine	
LOC12724939	XP_043817236.1	2.548	3.82052E-11	10	protein PELPK1-like		
LOC110623324	XP_021623932.1	-1.525	1.07386E-06	9	G-type lectin S-receptor-like serine/threonine-protein kinase CES101		
LOC110612119	XP_021608493.1	-1.352	9.22117E-05	3	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290		
LOC110625819	XP_043818134.1	-1.153	0.032694936	11	serine/threonine-protein kinase-like protein ACR4	serine/threonine	
LOC110624496	XP_021625369.1	-1.139	0.001261303	10	putative serine/threonine-protein kinase-like protein CCR3		
LOC110603621	XP_021597107.1	-1.079	9.5165E-06	16	probable LRR receptor-like serine/threonine-protein kinase		
LOC110629967	XP_021632903.1	1.075	0.006269055	13	G-type lectin S-receptor-like serine/threonine-protein kinase		
LOC110602000	XP_021595122.2	1.116	0.000368667	15	CBL-interacting serine/threonine-protein kinase 23 isoform X1		
LOC110611814	XP_021608001.1	1.122	0.0014643	3	serine/threonine-protein kinase RUNKEL		
LOC110605105	XP_021599119.1	1.132	0.000441091	17	CBL-interacting serine/threonine-protein kinase 23 isoform X2		
LOC110607766	XP_021602622.1	1.147	0.001396252	6	G-type lectin S-receptor-like serine/threonine-protein kinase		
LOC110602000	XP_043807361.1	1.165	0.00010539	15	CBL-interacting serine/threonine-protein kinase 23 isoform X2		
LOC110605105	XP_021599119.1	1.173	0.000110978	17	CBL-interacting serine/threonine-protein kinase 23 isoform X1		
LOC110603117	XP_021596490.1	1.426	0.005805452	16	serine/threonine-protein kinase RIPK		
LOC110626213	XP_021627690.1	1.501	0.00524157	11	putative serine/threonine-protein kinase isoform X2		
LOC110605310	XP_043808298.1	1.522	0.000745243	17	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X4		
LOC110605310	XP_021599473.1	1.522	0.000745243	17	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X3		
LOC110605310	XP_021599472.1	1.522	0.000745243	17	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X2		
LOC110605310	XP_021599471.1	1.522	0.000745243	17	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X1		
LOC110626213	XP_021627688.1	1.593	0.002714815	11	putative serine/threonine-protein kinase isoform X1		
LOC110619107	XP_021618053.1	2.050	0.000121476	7	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK3		
LOC110607888	XP_021602745.1	-1.454	0.000847696	14	peroxidase 16		ethylene
LOC110628776	XP_021631268.1	1.105	0.043681837	12	ethylene-responsive transcription factor ERF053		
LOC110610790	XP_021606557.1	1.182	0.000820048	3	ethylene-responsive transcription factor 4		
LOC110611378	XP_021607363.1	1.263	0.000113562	3	1-aminocyclopropane-1-carboxylate oxidase homolog 1		
LOC110600617	XP_021593177.1	1.923	1.54233E-08	14	ethylene-responsive transcription factor ERF105		
LOC110616467	XP_021614518.1	2.157	7.2456E-15	6	ethylene-responsive transcription factor ERF105		
LOC110621326	XP_021621263.1	2.457	3.27706E-19	1	ethylene-responsive transcription factor 5		
LOC110611162	XP_021607005.1	2.876	7.5627E-17	3	ethylene-responsive transcription factor ERF017		
LOC110610587	XP_021606261.1	3.112	2.70049E-20	3	ethylene-responsive transcription factor ERF017		
LOC110609410	XP_021604658.2	3.150	5.7739E-17	2	ethylene-responsive transcription factor 6		
LOC110630961	XP_021634319.1	1.659	3.03452E-05	14	auxin-repressed 12.5 kDa protein	auxin	
LOC110617882	XP_021616578.1	1.666	2.11989E-07	6	probable WRKY transcription factor 53	WRKY	
LOC110617083	XP_021615382.1	1.842	2.49429E-11	1	probable WRKY transcription factor 53		
LOC110621299	XP_021621222.1	-1.402	0.030781165	8	transcription factor MYB15	MYB	
LOC110600317	XP_021592835.1	-1.117	0.028711367	14	transcription factor MYB62		
LOC110611129	XP_021606963.1	1.126	0.03154962	3	transcription factor MYB30		
LOC110601117	XP_021593824.1	1.546	0.001112061	15	transcription factor MYB30		
LOC110629654	XP_021632420.1	1.600	0.000128487	13	transcription factor MYB14	zinc finger	
LOC110606942	XP_021601650.2	-1.186	0.049800917	18	zinc finger protein DOF1.6		
LOC110614052	XP_021611192.1	1.024	0.019948992	4	GATA transcription factor 5		
LOC110617714	XP_021616374.1	1.082	0.009875024	6	zinc finger protein CONSTANS-LIKE 6		
LOC110614331	XP_021611535.1	1.193	0.011989759	5	zinc finger protein ZAT10		
LOC110616763	XP_021614935.1	1.240	0.00019018	6	GATA zinc finger domain-containing protein 10		
LOC110606164	XP_021600622.1	1.260	0.002057664	2	FCS-Like Zinc finger 5		
LOC110624430	XP_021625251.1	1.300	0.016146952	10	zinc finger protein ZAT10		
LOC110618858	XP_021617821.1	1.338	0.000424954	7	zinc finger CCCH domain-containing protein 29		
LOC110607083	XP_021601831.1	1.343	4.51248E-05	18	zinc finger protein ZAT10		
LOC110622056	XP_021622101.1	1.384	0.000568515	9	zinc finger AN1 and C2H2 domain-containing stress-associated protein	HSP	
LOC110613196	XP_021609904.1	1.685	1.13385E-05	4	zinc finger CCCH domain-containing protein 29 isoform X1		
LOC110624629	XP_021625534.1	1.702	4.77083E-07	10	zinc finger CCCH domain-containing protein 29 isoform X2		
LOC110610459	XP_021606079.1	1.929	3.9486E-10	3	RING-H2 finger protein ATL2		
LOC110602254	XP_021595420.1	2.062	1.00041E-10	15	RING-H2 finger protein ATL2		
LOC110607327	XP_021602110.1	-2.865	6.97163E-15	2	17.3 kDa class I heat shock protein		
LOC110611125	XP_043811369.1	-2.762	7.52835E-22	3	heat shock factor protein HSF30 isoform X2		
LOC110631094	XP_021634501.1	-2.739	1.55911E-13	14	17.3 kDa class I heat shock protein		
LOC110611125	XP_043811367.1	-2.735	1.91754E-21	3	heat shock factor protein HSF30 isoform X1		
LOC110605018	XP_021599004.1	-2.708	2.92109E-13	2	17.3 kDa class I heat shock protein		
LOC110631209	XP_021634648.1	-2.632	1.67383E-12	14	17.5 kDa class I heat shock protein		
LOC110616446	XP_021614483.1	-2.406	1.73701E-14	6	23.6 kDa heat shock protein, mitochondrial		
LOC110631276	XP_021634739.1	-2.398	1.55911E-13	14	23.6 kDa heat shock protein, mitochondrial		
LOC110600163	XP_021592620.1	-2.394	4.0422E-16	14	heat shock protein 83		
LOC110628332	XP_021630642.1	-2.297	8.86769E-11	12	small heat shock protein, chloroplastic		
LOC110618796	XP_021617731.1	-2.265	1.4879E-07	7	22.0 kDa class IV heat shock protein		
LOC110617718	XP_021616382.1	-2.030	3.50672E-11	6	heat shock protein 83		
LOC110631253	XP_021634711.1	-2.019	7.4299E-07	14	17.3 kDa class I heat shock protein		
LOC110603775	XP_021597369.1	-1.932	3.50614E-06	16	17.3 kDa class II heat shock protein		
LOC110613482	XP_021610330.1	-1.854	3.61788E-08	4	17.4 kDa class I heat shock protein		
LOC110603467	XP_021596894.1	-1.668	0.000598574	16	18.1 kDa class I heat shock protein		
LOC127271693	XP_043806094.1	-1.633	0.000170416	14	17.3 kDa class I heat shock protein-like		
LOC110619449	XP_021618593.1	-1.612	0.000894867	7	18.2 kDa class I heat shock protein		
LOC110603158	XP_021596549.1	-1.386	7.51414E-05	2	18.1 kDa class I heat shock protein		
LOC110620193	XP_021619516.1	-1.351	0.001492546	1	small heat shock protein, chloroplastic		
LOC110607779	XP_021602638.1	-1.257	0.040793972	18	16.9 kDa class I heat shock protein 1		
LOC110626448	XP_043817917.1	-1.248	0.030123329	11	17.4 kDa class III heat shock protein isoform X1		
LOC110626448	XP_021628049.1	-1.218	0.03380323	11	17.4 kDa class III heat shock protein isoform X2		

DSC 260	stem	1	LOC110619469	XP_021618635.1	-1.173	0.003712688	7	heat shock cognate 70 kDa protein 2	
			LOC110627121	XP_021629057.1	-1.392	8.3318E-05	11	dnaJ protein homolog	
			LOC110608517	XP_021603454.1	-1.183	0.009915139	2	chaperone protein dnaJ 11, chloroplast	
			LOC110614088	XP_021611255.1	-1.166	8.28506E-05	4	dnaJ protein homolog	
			LOC110602863	XP_021596139.1	-1.127	8.20825E-05	16	dnaJ homolog subfamily B member 13	
			LOC110613943	XP_043812166.1	1.044	0.026957843	4	dnaJ homolog subfamily B member 7 isoform X2	DNAJ
			LOC110613943	XP_021611061.1	1.057	0.022254801	4	dnaJ homolog subfamily B member 6 isoform X3	
			LOC110613943	XP_021611060.1	1.073	0.019948992	4	dnaJ homolog subfamily B member 6 isoform X1	
			LOC110629988	XP_021632942.1	1.222	0.00607154	13	chaperone protein dnaJ C76, chloroplast	
			LOC110609477	XP_021604759.1	1.310	0.000149026	2	chaperone protein dnaJ 49 isoform X2	
			LOC110613224	XP_021609940.1	-1.450	0.000190681	4	aquaporin TIP1-1	
			LOC110621983	XP_021621997.1	-1.088	0.026241739	9	aquaporin PIP2-4	aquaporin
			LOC110619660	XP_021618883.1	-1.087	0.013379506	7	probable aquaporin PIP-type 7a	
			LOC110622410	XP_021622596.1	1.050	0.001703503	9	calmodulin-binding protein 25	
			LOC110621796	XP_021621792.1	1.094	0.001804542	8	calmodulin-binding protein 25	calmodulin
			LOC110605140	XP_021599176.1	1.121	0.016081465	17	calmodulin-binding receptor kinase CaMRLK	
			LOC110612131	XP_021608514.1	1.885	9.61345E-08	3	calcium-binding protein KRP1	calcium-binding
			LOC110608491	XP_021603425.1	2.190	2.12345E-07	2	probable calcium-binding protein CML23	
			LOC110625743	XP_021627059.1	1.503	1.35744E-05	11	NDR1/HIN1-like protein 13	NDR1/HIN1
			LOC110630964	XP_021634322.1	1.678	2.54223E-05	14	NDR1/HIN1-like protein 13	
			LOC110620125	XP_021619411.1	1.050	5.97224E-05	8	probable LRR receptor-like serine/threonine-protein kinase	
			LOC110620125	XP_021619412.1	1.050	5.97224E-05	8	probable LRR receptor-like serine/threonine-protein kinase	
			LOC110628130	XP_021630328.1	1.055	0.002354949	12	leucine-rich repeat receptor-like serine/threonine-protein kinase	
			LOC110620125	XP_043815007.1	1.057	5.97224E-05	8	probable LRR receptor-like serine/threonine-protein kinase	LRR
			LOC110620125	XP_043815008.1	1.058	5.97224E-05	8	probable LRR receptor-like serine/threonine-protein kinase	
			LOC110611166	XP_021607011.1	1.284	0.005683052	3	probable leucine-rich repeat receptor-like protein kinase At1g35710	
			LOC110600003	XP_021592360.2	1.999	1.61311E-10	14	leucine-rich repeat receptor-like serine/threonine/tyrosine-protein kinase SOBIR1	
			LOC110622109	XP_021622192.1	1.209	0.000158805	9	E3 ubiquitin-protein ligase ATL6	E3 ubiquitin
			LOC110609586	XP_021604963.1	1.865	3.62508E-07	2	E3 ubiquitin-protein ligase RDU1	
			LOC110609777	XP_021605264.1	2.507	3.45097E-09	2	E3 ubiquitin ligase PQT3-like	
			LOC110610459	XP_021606079.1	1.929	3.9486E-10	3	RING-H2 finger protein ATL2	RING-H2
			LOC110602254	XP_021595420.1	2.062	1.00041E-10	15	RING-H2 finger protein ATL2	
			LOC110620526	XP_021619991.1	-1.353	0.037234745	8	WAT1-related protein At5g07050	WAT1
			LOC110602376	XP_021595569.1	-1.467	0.003375801	15	cell wall / vacuolar inhibitor of fructosidase 1	
			LOC110627041	XP_021628957.1	-1.353	0.001492546	1	expansin-like B1	
			LOC122724074	XP_043814505.1	-1.158	0.046480343	7	glycine-rich cell wall structural protein 2-like	
			LOC110630931	XP_043806063.1	-1.067	0.045507811	14	putative glycine-rich cell wall structural protein 1 isoform X2	
			LOC110603002	XP_021596330.1	1.014	0.000301561	16	probable pectinesterase/pectinesterase inhibitor 12	
			LOC110612933	XP_021609487.1	1.236	0.000876232	4	vegetative cell wall protein gp1	
			LOC122721688	XP_043806055.1	1.313	0.005156703	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
			LOC110613363	XP_021610134.1	1.518	0.000214725	4	putative wall-associated receptor kinase-like 11	
			LOC110616307	XP_021614386.1	1.671	3.30933E-06	5	probable xyloglucan endotransglucosylase/hydrolase protein 23	
			LOC122721686	XP_043806018.1	1.743	3.51501E-05	14	xyloglucan endotransglucosylase/hydrolase protein 22-like	
			LOC122721684	XP_043806008.1	1.768	2.85918E-05	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
			LOC122721685	XP_043806011.1	1.795	2.31779E-05	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
			LOC122721683	XP_043806007.1	1.826	1.51195E-05	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
			LOC110630940	XP_021634284.1	2.990	2.45246E-16	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
			LOC110627041	XP_021628957.1	-1.353	0.001492546	1	expansin-like B1	expansin
			LOC110603002	XP_021596330.1	1.014	0.000301561	16	probable pectinesterase/pectinesterase inhibitor 12	pectinesterase
			LOC110610980	XP_021606757.1	-1.144	0.036188506	3	G-type lectin 5-receptor-like serine/threonine-protein kinase LECRK3	
LOC110620796	XP_021620359.1	-1.081	0.024500183	8	probable serine/threonine-protein kinase WNK9				
LOC110620125	XP_021619411.1	1.050	5.97224E-05	8	probable LRR receptor-like serine/threonine-protein kinase				
LOC110620125	XP_021619412.1	1.050	5.97224E-05	8	probable LRR receptor-like serine/threonine-protein kinase				
LOC110628130	XP_021630328.1	1.055	0.002354949	12	leucine-rich repeat receptor-like serine/threonine-protein kinase				
LOC110620125	XP_043815007.1	1.057	5.97224E-05	8	probable LRR receptor-like serine/threonine-protein kinase	serine/threonine			
LOC110620125	XP_043815008.1	1.058	5.97224E-05	8	probable LRR receptor-like serine/threonine-protein kinase				
LOC110607627	XP_043807875.1	1.367	0.011198988	16	G-type lectin 5-receptor-like serine/threonine-protein kinase				
LOC110610252	XP_021605783.1	1.493	0.000246756	3	serine/threonine-protein kinase RIPK				
LOC110600003	XP_021592360.2	1.999	1.61311E-10	14	leucine-rich repeat receptor-like serine/threonine/tyrosine-protein kinase SOBIR1				
LOC110605987	XP_021600380.1	2.133	1.29312E-06	18	serine/threonine-protein kinase-like protein CCR4				
LOC110599929	XP_021592248.1	1.157	0.039127192	14	auxin-responsive protein IAA9	auxin			
LOC110599654	XP_021591848.1	-1.898	5.90852E-08	14	transcription factor MYB28	MYB			
LOC110630767	XP_021634029.1	1.321	0.01303934	14	transcription factor MYB1				
LOC110630687	XP_021633924.1	-1.174	0.007141448	14	zinc finger protein CO3 isoform X3	zinc finger			
LOC110630687	XP_021633922.1	-1.120	0.01303934	14	putative zinc finger protein CONSTANS-LIKE 11 isoform X2				
LOC110600163	XP_021592620.1	1.020	0.046509111	14	heat shock protein 83	HSP			
LOC110631276	XP_021634739.1	1.426	0.002714869	14	23.6 kDa heat shock protein, mitochondrial				
LOC110608641	XP_021603607.1	1.158	0.001377686	2	ethylene-responsive transcription factor ERF014	ethylene			
LOC110606363	XP_021600828.1	1.181	0.004020278	18	ethylene-responsive transcription factor ERF014				
LOC110609129	XP_021604178.1	-1.057	0.015889377	2	pectinesterase inhibitor 10	cell-wall			
LOC110604516	XP_021598401.1	1.043	0.002806285	17	xyloglucan glucosyltransferase 4				
LOC110609129	XP_021604178.1	-1.057	0.015889377	2	pectinesterase inhibitor 10	pectinesterase			
LOC122722376	XP_043808950.1	1.272	0.031292708	2	ethylene-responsive transcription factor 2-like				
LOC110603497	XP_021596937.1	1.329	0.002778589	16	endoglucanase 16	ethylene			
LOC110607385	XP_021602177.1	1.646	0.003062087	2	ethylene-responsive transcription factor ABR1				
LOC110615035	XP_021612434.1	-1.218	0.007006014	5	auxin-responsive protein SAUR50	auxin			
LOC110599929	XP_021592248.1	1.157	0.039127192	14	auxin-responsive protein IAA9				
LOC110624547	XP_021625434.1	1.171	0.029061784	10	linoleate 13S-lipoxygenase 2-1, chloroplast				
LOC110618536	XP_021617370.1	1.217	0.015265214	7	linoleate 13S-lipoxygenase 2-1, chloroplast				
LOC122722370	XP_043808919.1	1.311	0.029042723	18	allene oxide synthase-like	jasmonic acid			
LOC110601354	XP_021594149.1	1.444	0.000482109	15	allene oxide synthase 3				
LOC110606023	XP_021600430.2	1.484	0.005886591	18	allene oxide synthase				
LOC110622714	XP_021623008.1	1.722	3.57529E-05	9	jasmonate-induced oxygenase 2				
LOC110627831	XP_021629893.1	-1.604	6.30584E-08	12	transcription factor bHLH93	bHLH			
LOC110629534	XP_021632246.1	-1.156	0.000196364	13	transcription factor bHLH62				
LOC110622399	XP_021622582.1	-1.044	6.13705E-06	9	transcription factor bHLH94				
LOC110599654	XP_021591848.1	-1.898	5.90852E-08	14	transcription factor MYB28				
LOC110616910	XP_043813177.1	-1.439	0.00117432	6	MYB-like transcription factor ODO1				
LOC110616910	XP_043813178.1	-1.439	0.00117432	6	MYB-like transcription factor ODO1				

DSC 167	stem	1	LOC110605537	XP_021599855.1	1.099	0.008350022	2	transcription repressor MYB6	MYB			
			LOC110613514	XP_021610371.1	1.291	0.000174757	4	transcription factor MYB53				
			LOC110630767	XP_021634029.1	1.321	0.01303934	14	transcription factor MYB1				
			LOC110606627	XP_021601217.1	1.347	0.021846519	2	transcription factor MYB106				
			LOC110616246	XP_021614299.1	-1.386	0.00329689	5	zinc finger protein 6				
			LOC110630687	XP_021633924.1	-1.174	0.007141448	14	zinc finger protein CO3 isoform X3				
			LOC110630687	XP_021633922.1	-1.120	0.01303934	14	putative zinc finger protein CONSTANS-LIKE 11 isoform X2	zinc finger			
			LOC110604032	XP_021597761.1	1.020	0.019460773	16	zinc finger CCCH domain-containing protein 20				
			LOC110618025	XP_043806144.1	1.109	0.028903458	1	RING-H2 finger protein ATL79 isoform X2				
			LOC110603731	XP_021597347.1	1.149	0.018833103	1	zinc-finger homeodomain protein 11				
			LOC110623008	XP_021623512.1	1.652	0.000261695	1	transcription factor BEE 3	BEE 3			
			LOC110600163	XP_021592620.1	1.020	0.046509111	14	heat shock protein 83				
			LOC110625070	XP_021626275.1	1.116	0.031737812	10	18.1 kDa class I heat shock protein				
			LOC110630152	XP_021633190.1	1.356	0.001438405	13	heat shock factor protein HSF24	HSP			
			LOC110631276	XP_021634739.1	1.426	0.002714869	14	23.6 kDa heat shock protein, mitochondrial				
			LOC110626966	XP_021628863.1	1.023	0.042939584	11	chaperone protein dnaJ 8, chloroplastic				
			LOC110608517	XP_021603454.1	1.113	0.028249251	2	chaperone protein dnaJ 11, chloroplastic	DNAJ			
			LOC110612776	XP_043811592.1	1.363	0.000823199	4	chaperone protein dnaJ 8, chloroplastic isoform X2				
			LOC110612776	XP_021609256.1	1.456	0.00022259	4	chaperone protein dnaJ 8, chloroplastic isoform X1				
			LOC110629517	XP_021632215.1	1.014	0.019523813	13	probable calcium-binding protein CML41	calcium-binding			
			LOC110615346	XP_043812593.1	-1.261	1.17806E-09	5	probable LRR receptor-like serine/threonine-protein kinase				
			LOC110615346	XP_043812594.1	-1.261	1.17806E-09	5	probable LRR receptor-like serine/threonine-protein kinase				
			LOC110615346	XP_043812595.1	-1.199	2.10972E-06	5	probable LRR receptor-like serine/threonine-protein kinase	LRR			
			LOC110610829	XP_021606597.1	-1.186	0.000143298	3	leucine-rich repeat extensin-like protein 4				
			LOC110614421	XP_021611641.1	-1.117	1.65108E-09	5	somatic embryogenesis receptor kinase 2				
			LOC110621467	XP_043814710.1	1.194	0.005402417	8	E3 ubiquitin-protein ligase WAV3	E3 ubiquitin			
			LOC110618025	XP_043806144.1	1.109	0.028903458	1	RING-H2 finger protein ATL79 isoform X2	RING-H2			
			LOC110616367	XP_021614463.1	-1.515	0.003403456	5	WAT1-related protein At1g70260				
			LOC110616367	XP_021614464.1	-1.515	0.003403456	5	WAT1-related protein At1g70260				
			LOC110624625	XP_021625528.1	-1.355	0.000728366	10	WAT1-related protein At1g25270 isoform X2				
			LOC110624625	XP_021625527.1	-1.337	0.001469886	10	WAT1-related protein At1g25270 isoform X1	WAT1			
			LOC110606419	XP_021600909.1	-1.312	0.017315525	18	WAT1-related protein At1g43650 isoform X1				
			LOC110606419	XP_021600910.1	-1.260	0.035747164	18	WAT1-related protein At1g43650 isoform X2				
			LOC110624658	XP_021625611.1	-1.102	0.036638845	1	WAT1-related protein At3g30340				
			LOC110609262	XP_021604409.2	-1.718	0.00145323	2	cellulose synthase-like protein G3				
			LOC110603035	XP_021596376.2	-1.438	1.57513E-10	16	probable pectinesterase 53				
			LOC110605784	XP_021600122.1	-1.068	0.028048	2	expansin-A5 isoform X2				
			LOC110605784	XP_021600115.1	-1.060	0.028249251	2	expansin-A10 isoform X1				
			LOC122722380	XP_043808974.1	1.063	9.29499E-08	18	extensin-3				
			LOC110599873	XP_021592156.1	1.065	0.03870929	1	plasmodesmata-located protein 7 isoform X1				
			LOC110622267	XP_021622419.2	1.098	0.000424878	9	phenylalanine ammonia-lyase	cell-wall			
			LOC110599873	XP_043813512.1	1.140	0.028903458	1	plasmodesmata-located protein 7 isoform X2				
			LOC110626036	XP_021627458.1	1.435	0.003088464	11	agmatine hydroxycinnamoyltransferase 1				
			LOC110601094	XP_043806868.1	1.445	0.003497602	15	vegetative cell wall protein gp1 isoform X2				
			LOC110601094	XP_043806867.1	1.445	0.003497602	15	vegetative cell wall protein gp1 isoform X1				
			LOC110615287	XP_021612783.1	1.779	0.00036458	5	pectinesterase 2				
			LOC110605784	XP_021600122.1	-1.068	0.028048	2	expansin-A5 isoform X2	expansin			
			LOC110605784	XP_021600115.1	-1.060	0.028249251	2	expansin-A10 isoform X1				
			LOC110603035	XP_021596376.2	-1.438	1.57513E-10	16	probable pectinesterase 53	pectinesterase			
			LOC110615287	XP_021612783.1	1.779	0.00036458	5	pectinesterase 2				
			LOC110614939	XP_021612323.1	1.184	0.010586468	5	very-long-chain aldehyde decarboxylase CER1	CER1			
			LOC110615004	XP_021612399.1	1.740	0.000217137	5	very-long-chain aldehyde decarboxylase CER1				
			LOC110615346	XP_043812593.1	-1.261	1.17806E-09	5	probable LRR receptor-like serine/threonine-protein kinase				
			LOC110615346	XP_043812594.1	-1.261	1.17806E-09	5	probable LRR receptor-like serine/threonine-protein kinase				
			LOC110615346	XP_043812595.1	-1.199	2.10972E-06	5	probable LRR receptor-like serine/threonine-protein kinase	serine/threonine			
			LOC110601054	XP_021593743.1	-1.198	0.019637151	15	putative serine/threonine-protein kinase				
			LOC110618309	XP_021617157.1	1.111	0.034699263	6	G-type lectin 5-receptor-like serine/threonine-protein kinase				
			LOC110631276	XP_021634739.1	1.007	0.042947168	14	23.6 kDa heat shock protein, mitochondrial	HSP			
			LOC110609185	XP_021604285.1	1.184	0.000169941	8	heat shock cognate 70 kDa protein 2				
			LOC110627121	XP_021629057.1	1.478	2.50398E-11	11	dnaJ protein homolog	DNAJ			
			LOC110601183	XP_021593922.1	1.103	0.016362602	15	calcium-binding protein KRP1	calcium-binding			
			LOC110620832	XP_021620436.1	-1.027	0.0256879	8	WAT1-related protein At2g37460	WAT1			
			LOC110630964	XP_021634322.1	1.083	0.020503685	14	probable xyloglucan endotransglucosylase/hydrolase protein 23				
			LOC110630961	XP_021634319.1	1.086	0.020503685	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	cell-wall			
			LOC110630940	XP_021634284.1	1.138	0.008194403	14	probable xyloglucan endotransglucosylase/hydrolase protein 23				
			DSC 167	stem	10	LOC110602080	XP_043808616.1	-1.321	4.86273E-07	15	glycine-rich cell wall structural protein 1.8	cell-wall
						LOC110621326	XP_021621263.1	-1.115	3.28091E-05	1	ethylene-responsive transcription factor 5	
						LOC110609410	XP_021604658.2	-1.093	0.004883864	2	ethylene-responsive transcription factor 6	ethylene
						LOC110627552	XP_021629594.1	-1.070	0.021849995	1	1-aminocyclopropane-1-carboxylate synthase	
						LOC110613515	XP_021610372.1	1.419	0.004955101	4	26.5 kDa heat shock protein, mitochondrial	
						LOC110601421	XP_021594236.1	1.506	0.00194145	15	class I heat shock protein	HSP
						LOC110619449	XP_021618593.1	1.620	0.001737282	7	18.2 kDa class I heat shock protein	
						LOC110619449	XP_021625360.1	1.849	2.85177E-06	10	17.3 kDa class I heat shock protein	
						LOC110619449	XP_021609940.1	-2.309	3.87666E-11	4	aquaporin TIP1-1	
						LOC110619449	XP_021621997.1	-2.053	7.51007E-15	9	aquaporin PIP2-4	
						LOC110619449	XP_021603457.1	-1.590	0.000205628	2	probable aquaporin TIP-type	
						LOC110619449	XP_021624817.1	-1.589	5.96322E-05	10	aquaporin TIP1-3	aquaporin
						LOC110619449	XP_021629159.1	-1.475	0.014613219	11	aquaporin PIP2-1	
						LOC110619449	XP_021627763.1	-1.448	0.015574357	11	probable aquaporin TIP1-2	
						LOC110619449	XP_021618883.1	-1.423	0.000236217	7	probable aquaporin PIP-type 7a	
						LOC110619449	XP_021622562.1	-1.280	0.019936256	9	E3 ubiquitin-protein ligase PUB23	E3 ubiquitin
						LOC110619449	XP_021609656.1	1.263	0.00030028	4	WAT1-related protein At5g07050	WAT1
						LOC110619449	XP_021610131.1	-1.382	0.044343449	4	wall-associated receptor kinase-like 1	
						LOC110619449	XP_021598401.1	-1.372	0.014446912	17	xyloglucan glycosyltransferase 4	cell-wall
			TMS 96/0304	roots	5	LOC122722380	XP_043808974.1	-1.338	3.28587E-05	18	extensin-3	cell-wall
						LOC110611162	XP_021607005.1	-2.172	3.4401E-07	3	ethylene-responsive transcription factor ERF017	
						LOC110629619	XP_021632366.1	-2.030	2.38272E-14	13	peroxidase 47	
						LOC110616697	XP_021614849.1	-1.756	1.15475E-07	6	ethylene-responsive transcription factor CRF4	
						LOC110624639	XP_021625546.1	-1.644	0.008959864	10	ethylene-responsive transcription factor ERF109	
						LOC110631040	XP_021634435.1	-1.625	0.010654085	14	ethylene-responsive transcription factor ERF027	
						LOC110609282	XP_021604440.1	-1.616	0.011510522	2	ethylene-responsive transcription factor ERF061	
						LOC110600617	XP_021593177.1	-1.588	3.72775E-05	14	ethylene-responsive transcription factor ERF105	
						LOC110629328	XP_021631932.1	-1.551	7.89244E-07	13	ethylene-responsive transcription factor 9	

LOC110609410	XP_021604658.2	-1.526	0.000404803	2	ethylene-responsive transcription factor 6	
LOC110616467	XP_021614518.1	-1.487	3.87315E-06	6	ethylene-responsive transcription factor ERF105	
LOC110621326	XP_021621263.1	-1.454	5.97039E-05	1	ethylene-responsive transcription factor 5	
LOC110607097	XP_021601843.2	-1.418	0.012579211	18	ethylene-responsive transcription factor ERF021	
LOC110621419	XP_021621391.1	-1.417	2.57577E-06	8	ethylene-responsive transcription factor ERN1	
LOC110608641	XP_021603607.1	-1.391	0.004505263	2	ethylene-responsive transcription factor ERF014	
LOC110606363	XP_021600828.1	-1.339	0.012420597	18	ethylene-responsive transcription factor ERF014	ethylene
LOC110609408	XP_021604656.2	-1.335	0.009680652	2	ethylene-responsive transcription factor 6	
LOC110604212	XP_021598041.1	-1.304	0.010894632	16	ethylene-responsive transcription factor ERF017	
LOC110627552	XP_021629594.1	-1.101	1.5561E-07	1	1-aminocyclopropane-1-carboxylate synthase	
LOC110618538	XP_021617371.1	-1.096	0.041079079	7	ethylene-responsive transcription factor 3	
LOC110628297	XP_021630596.1	-1.052	9.42197E-05	12	ethylene-responsive transcription factor RAP2-4	
LOC110627991	XP_021630111.1	-1.032	0.004074903	12	peroxidase 17	
LOC110619675	XP_021618904.1	1.146	0.039174795	7	basic form of pathogenesis-related protein 1	
LOC110611244	XP_021607133.1	1.167	0.035750633	3	ethylene receptor 2	
LOC110611244	XP_021607134.1	1.167	0.035750633	3	ethylene receptor 2	
LOC110611244	XP_021607135.1	1.167	0.035750633	3	ethylene receptor 2	
LOC110602651	XP_021595914.1	1.312	0.010638331	15	peroxidase 15	
LOC110629547	XP_021632259.1	1.453	0.007449976	13	ethylene-response factor C3	
LOC110600800	XP_021593377.1	1.667	0.000461296	15	ethylene-responsive transcription factor 1B	
LOC110610031	XP_021605593.1	2.000	0.000577572	2	peroxidase 12	
LOC110614563	XP_021611815.1	1.079	0.021950769	5	auxin-responsive protein SAUR32	
LOC122722417	XP_043809051.1	1.082	0.046771212	18	auxin-responsive protein SAUR50-like	auxin
LOC110621914	XP_021621905.1	1.203	0.037842009	1	auxin-induced protein AUX28	
LOC110604848	XP_021598846.1	1.532	1.19928E-09	2	auxin transporter-like protein 3	
LOC110615035	XP_021612434.1	2.021	4.86466E-06	5	auxin-responsive protein SAUR50	
LOC110623720	XP_021624431.1	1.209	0.011435065	9	probable linoleate 9S-lipoxygenase 5	jasmonic acid
LOC110606314	XP_021600759.2	1.619	0.001378402	18	defensin-like protein	
LOC110617083	XP_021615382.1	-2.068	1.40545E-07	1	probable WRKY transcription factor 53	
LOC110619370	XP_021618466.1	-1.446	4.91208E-07	1	WRKY transcription factor 22	
LOC110617016	XP_021615285.1	-1.362	0.000368693	6	probable WRKY transcription factor 27	
LOC110623521	XP_021624193.1	-1.134	0.01516013	9	probable WRKY transcription factor 30	WRKY
LOC110616151	XP_021614182.1	-1.120	2.40059E-07	5	probable WRKY transcription factor 7	
LOC110615501	XP_021613059.1	-1.091	0.013921591	5	WRKY transcription factor 22	
LOC110612123	XP_021608498.1	-1.477	0.000415166	3	transcription factor bHLH123 isoform X1	
LOC110612123	XP_021608499.1	-1.477	0.000415166	3	transcription factor bHLH123 isoform X2	
LOC110602806	XP_021596056.1	-1.174	0.002048986	16	transcription factor bHLH112 isoform X2	
LOC110602806	XP_021596055.1	-1.157	0.002637871	16	transcription factor bHLH112 isoform X1	bHLH
LOC110627945	XP_021630052.1	1.763	0.000189573	12	transcription factor bHLH94	
LOC110608708	XP_021603678.1	1.791	0.004220943	2	transcription factor bHLH96	
LOC110606323	XP_021600770.1	2.044	5.08306E-08	18	transcription factor bHLH93	
LOC110628584	XP_021631021.1	-1.964	3.98261E-14	12	transcription factor MYB44	
LOC110606842	XP_021601521.2	-1.778	3.78459E-05	18	transcription factor MYB73-like	
LOC110606940	XP_021601648.1	-1.594	2.88178E-09	18	transcription factor MYB44	
LOC110619160	XP_021618117.1	-1.374	0.002184168	7	myb family transcription factor PHL5 isoform X2	
LOC110619160	XP_021618116.1	-1.374	0.002184168	7	myb family transcription factor PHL5 isoform X1	
LOC110611129	XP_021606663.1	-1.321	0.004105121	3	transcription factor MYB30	
LOC110615580	XP_021613222.1	-1.262	0.006200401	5	transcription factor MYB44	MYB
LOC110629654	XP_021632420.1	-1.242	0.044938393	13	transcription factor MYB14	
LOC110620470	XP_021619909.1	-1.179	0.001837366	8	myb family transcription factor PHL5 isoform X2	
LOC110620470	XP_021619908.1	-1.179	0.001837366	8	myb family transcription factor PHL5 isoform X1	
LOC110622339	XP_021622514.1	-1.164	0.000162448	9	myb family transcription factor PHL5	
LOC110613514	XP_021610371.1	-1.088	3.85805E-06	4	transcription factor MYB53	
LOC110625465	XP_021626756.1	1.439	0.006196355	11	transcription factor MYB1	
LOC110613853	XP_021610903.1	-2.366	7.02273E-08	4	zinc finger protein ZAT11	
LOC110624629	XP_021625533.1	-2.329	1.84466E-09	10	zinc finger CCCH domain-containing protein 29 isoform X1	
LOC110624629	XP_021625534.1	-2.329	1.84466E-09	10	zinc finger CCCH domain-containing protein 29 isoform X2	
LOC110618858	XP_021617821.1	-1.973	4.07262E-07	7	zinc finger CCCH domain-containing protein 29	
LOC110614052	XP_021611192.1	-1.937	1.49729E-08	4	GATA transcription factor 5	
LOC110630476	XP_021633682.1	-1.894	9.91182E-08	13	RING-H2 finger protein ATL78	
LOC110626977	XP_021628881.1	-1.868	0.00022871	11	zinc finger protein ZAT12	
LOC110618678	XP_021617583.1	-1.845	4.93793E-05	7	zinc finger protein ZAT10	
LOC110607083	XP_021601831.1	-1.667	5.36982E-06	18	zinc finger protein ZAT10	
LOC110602254	XP_021595420.1	-1.589	2.97695E-06	15	RING-H2 finger protein ATL2	
LOC110611024	XP_021606815.1	-1.560	0.001691745	3	zinc finger protein 3	
LOC110622056	XP_021622101.1	-1.427	7.04746E-05	9	zinc finger AN1 and C2H2 domain-containing stress-associated protein	
LOC110626687	XP_021628427.1	-1.418	0.000117877	1	RING-H2 finger protein ATL5	
LOC110604729	XP_021598705.1	-1.379	4.66714E-06	2	zinc finger protein CONSTANS-LIKE 2	
LOC110601044	XP_021593727.1	-1.338	1.43096E-06	15	B-box zinc finger protein 19	zinc finger
LOC110614331	XP_021611535.1	-1.282	0.026134576	5	zinc finger protein ZAT10	
LOC110618040	XP_021616745.1	-1.137	5.99535E-10	6	zinc finger protein CONSTANS-LIKE 5	
LOC110600274	XP_021592778.1	-1.133	4.60093E-07	14	zinc finger protein CONSTANS-LIKE 5	
LOC110617353	XP_021615778.1	-1.115	0.006068486	6	RING-H2 finger protein ATL22	
LOC110625483	XP_021626783.1	-1.042	0.006196355	11	B-box zinc finger protein 19 isoform X2	
LOC110625483	XP_021626785.1	-1.042	0.006196355	11	B-box zinc finger protein 19 isoform X2	
LOC110625483	XP_021626786.1	-1.042	0.006196355	11	B-box zinc finger protein 19 isoform X2	
LOC110625483	XP_021626787.1	-1.042	0.006196355	11	B-box zinc finger protein 19 isoform X2	
LOC110630890	XP_021634223.1	-1.041	0.044377016	1	zinc finger protein CONSTANS-LIKE 2	
LOC110616539	XP_021614624.1	-1.034	0.001039555	6	dof zinc finger protein DOF5.4	
LOC110625483	XP_021626780.1	-1.026	0.006780229	11	B-box zinc finger protein 19 isoform X1	
LOC110625483	XP_021626781.1	-1.026	0.006780229	11	B-box zinc finger protein 19 isoform X1	
LOC110625483	XP_021626782.1	-1.026	0.006780229	11	B-box zinc finger protein 19 isoform X1	
LOC110606570	XP_043809264.1	-1.021	0.007377018	18	zinc finger CCCH domain-containing protein 6 isoform X1	
LOC110627919	XP_021630010.1	1.119	2.15549E-06	12	zinc finger protein MAGPIE	
LOC110607716	XP_021602558.1	-1.180	0.034658114	1	transcription factor BEE 3	BEE 3
LOC110618796	XP_021617731.1	-1.859	0.003471828	7	22.0 kDa class IV heat shock protein	
LOC110628332	XP_021630642.1	-1.837	0.00055925	12	small heat shock protein, chloroplastic	
LOC110613515	XP_021610372.1	-1.351	0.03292707	4	26.5 kDa heat shock protein, mitochondrial	HSP
LOC110625873	XP_021627250.1	-1.340	0.014569311	11	heat shock cognate 70 kDa protein	
LOC110629593	XP_021632319.1	-1.237	0.039217325	13	small heat shock protein, chloroplastic	
LOC110603158	XP_021596549.1	-1.078	0.032910252	2	18.1 kDa class I heat shock protein	
LOC110608909	XP_021603884.1	-1.104	4.09926E-06	1	dnaJ homolog subfamily B member 4	DNAJ

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LOC110624056	XP_021624817.1	-1.590	0.000651507	10	aquaporin TIP1-3	
LOC110613224	XP_021609940.1	-1.443	0.000319126	4	aquaporin TIP1-1	
LOC110621983	XP_021621997.1	-1.378	3.6852E-05	9	aquaporin PIP2-4	
LOC110619997	XP_021619227.1	-1.269	2.30418E-06	8	aquaporin PIP2-4	aquaporin
LOC110608519	XP_021603457.1	-1.208	8.34777E-05	2	probable aquaporin TIP-type	
LOC110622032	XP_021622073.1	-1.083	0.020775388	1	aquaporin NIP2-1	
LOC110622032	XP_043812672.1	-1.083	0.020775388	1	aquaporin NIP2-1	
LOC110619660	XP_021618883.1	-1.071	0.000505717	7	probable aquaporin PIP-type 7a	
LOC110623384	XP_021624003.1	-1.046	0.020775388	1	probable aquaporin TIP-type	
LOC110620650	XP_021620152.1	-1.590	0.000705852	8	calmodulin-binding protein 60 D	calmodulin
LOC110628683	XP_021631167.1	-1.448	0.009521354	12	calmodulin-like protein 3	
LOC110614734	XP_021612063.1	-2.103	1.19613E-09	5	calcium-binding protein CML37	
LOC110601183	XP_021593922.1	-2.092	9.15001E-09	15	calcium-binding protein KRP1	
LOC110610096	XP_021605659.2	-1.676	0.00063474	2	probable calcium-binding protein CML44, partial	
LOC110606929	XP_021601631.1	-1.674	0.000305178	18	probable calcium-binding protein CML41	
LOC110608491	XP_021603425.1	-1.365	0.008219965	2	probable calcium-binding protein CML23	
LOC110613812	XP_021610836.1	-1.326	0.023902981	4	probable calcium-binding protein CML48	
LOC110601763	XP_021594743.1	-1.301	0.014442574	15	calcium-binding protein CML38	calcium-binding
LOC110612131	XP_021608514.1	-1.210	0.035750633	3	calcium-binding protein KRP1	
LOC110622425	XP_021622610.1	-1.204	0.005342409	9	probable calcium-binding protein CML43	
LOC110620505	XP_021619965.1	-1.133	0.019094258	8	probable calcium-binding protein CML43	
LOC110617801	XP_021616500.1	-1.087	0.012061045	1	probable calcium-binding protein CML23	
LOC110616940	XP_021615165.1	-1.029	0.012699009	6	probable calcium-binding protein CML27	
LOC110607632	XP_021602480.1	1.092	0.041670978	16	calcium-binding protein PBP1	
LOC110625743	XP_021627059.1	-1.748	1.72693E-11	11	NDR1/HIN1-like protein 13	
LOC122724502	XP_043815583.1	-1.408	0.005721152	9	NDR1/HIN1-like protein 10	NDR1/HIN1
LOC110613196	XP_021609904.1	-1.244	0.046643634	4	NDR1/HIN1-like protein 13	
LOC110605523	XP_021599830.1	-1.364	7.57612E-05	17	LRR receptor-like serine/threonine-protein kinase FLS2	
LOC110619506	XP_021618701.2	-1.318	6.87274E-09	7	phytosulfokine receptor 1, partial	
LOC110620510	XP_043814775.1	-1.207	4.11368E-06	8	leucine-rich repeat protein 1 isoform X2	
LOC110606488	XP_021601001.1	-1.194	7.24687E-05	18	LRR receptor-like serine/threonine-protein kinase RGI1	
LOC110620510	XP_021619974.1	-1.187	2.57577E-06	8	leucine-rich repeat protein 1 isoform X1	LRR
LOC110611166	XP_021607011.1	-1.019	0.029258605	3	probable leucine-rich repeat receptor-like protein kinase At1g35710	
LOC110606932	XP_021601639.2	1.030	0.040990851	2	putative leucine-rich repeat-containing protein DDB_G0290503	
LOC110623937	XP_021624652.2	1.037	0.014322431	10	leucine-rich repeat extensin-like protein 3	
LOC110601159	XP_021593887.1	1.135	0.017494015	15	leucine-rich repeat extensin-like protein 6	
LOC110627398	XP_021629381.1	1.211	0.003223121	12	leucine-rich repeat extensin-like protein 3	
LOC110609777	XP_021605264.1	-2.243	5.5323E-05	2	E3 ubiquitin ligase PQT3-like	
LOC110609586	XP_021604963.1	-1.972	5.89285E-09	2	E3 ubiquitin-protein ligase RDUF1	
LOC110613011	XP_021609604.1	-1.652	4.28635E-10	4	probable BDI-related E3 ubiquitin-protein ligase 2	
LOC110619982	XP_021619204.1	-1.528	5.09896E-06	8	E3 ubiquitin-protein ligase ATL31	
LOC110620557	XP_021620037.1	-1.470	0.006546504	8	E3 ubiquitin-protein ligase PUB23	
LOC110619415	XP_043814502.1	-1.426	0.004553703	7	E3 ubiquitin-protein ligase HERC2 isoform X2	
LOC110622109	XP_021622192.1	-1.283	0.001253007	9	E3 ubiquitin-protein ligase ATL6	E3 ubiquitin
LOC110622386	XP_021622562.1	-1.257	0.021071648	9	E3 ubiquitin-protein ligase PUB23	
LOC110619779	XP_021619020.1	-1.238	0.002857075	7	probable E3 ubiquitin-protein ligase RHY1A	
LOC110613156	XP_021609841.1	-1.156	0.001202853	1	E3 ubiquitin-protein ligase MARCHF1	
LOC110603491	XP_021596926.1	-1.144	0.025980202	16	E3 ubiquitin ligase PQT3-like	
LOC110600714	XP_021593247.1	-1.112	0.039105511	15	E3 ubiquitin-protein ligase CIP8	
LOC110630476	XP_021633682.1	-1.894	9.91182E-08	13	RING-H2 finger protein ATL78	
LOC110602254	XP_021595420.1	-1.589	2.97695E-06	15	RING-H2 finger protein ATL2	RING-H2
LOC110604729	XP_021598705.1	-1.379	4.66714E-06	2	zinc finger protein CONSTANS-LIKE 2	
LOC110617353	XP_021615778.1	-1.115	0.006068486	6	RING-H2 finger protein ATL22	
LOC110625087	XP_021626304.1	-2.313	1.72119E-07	10	WAT1-related protein At2g39510	
LOC110618767	XP_021617697.1	-1.352	1.68313E-05	7	WAT1-related protein At2g39510	
LOC110619108	XP_021618054.1	-1.126	0.008408702	1	WAT1-related protein At1g43650	
LOC110618768	XP_021617698.1	-1.042	0.017838915	7	WAT1-related protein At2g39510 isoform X1	WAT1
LOC110618768	XP_043813992.1	-1.037	0.018689949	7	WAT1-related protein At2g39510 isoform X2	
LOC110620526	XP_021619991.1	-1.024	1.79075E-05	8	WAT1-related protein At5g07050	
LOC110616367	XP_021614463.1	1.178	0.00701536	5	WAT1-related protein At1g70260	
LOC110616367	XP_021614464.1	1.178	0.00701536	5	WAT1-related protein At1g70260	
LOC122721688	XP_043806055.1	-3.606	1.03949E-24	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
LOC122721684	XP_043806008.1	-3.517	5.0777E-23	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
LOC110607806	XP_043806385.1	-3.508	1.62484E-20	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
LOC122721685	XP_043806011.1	-3.456	1.62484E-20	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
LOC122721683	XP_043806007.1	-3.420	1.94565E-20	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
LOC122721686	XP_043806018.1	-3.355	1.23383E-18	14	xyloglucan endotransglucosylase/hydrolase protein 22-like	
LOC110630961	XP_021634319.1	-2.881	1.26477E-17	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
LOC110630964	XP_021634322.1	-2.873	2.0045E-17	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
LOC110630940	XP_021634284.1	-2.737	3.84656E-15	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
LOC110615049	XP_021612447.1	-2.674	1.19613E-09	5	probable xyloglucan endotransglucosylase/hydrolase protein 23	
LOC110631062	XP_021634464.1	-2.518	3.8676E-11	14	xyloglucan endotransglucosylase/hydrolase protein 22	
LOC110604516	XP_021598401.1	-2.505	1.67427E-12	17	xyloglucan glycosyltransferase 4	
LOC110613004	XP_021609595.1	-2.084	5.88836E-14	4	expansin-like A2	
LOC110631116	XP_021634526.1	-2.041	0.000155918	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
LOC110609346	XP_021604559.1	-1.768	8.20916E-08	1	probable galacturonosyltransferase-like 9	cell-wall
LOC110612933	XP_021609487.1	-1.730	3.66575E-07	4	vegetative cell wall protein gp1	
LOC110631132	XP_021634549.1	-1.579	4.60097E-06	14	xyloglucan endotransglucosylase/hydrolase protein 22	
LOC110630931	XP_021634273.1	-1.523	3.72775E-05	14	putative glycine-rich cell wall structural protein 1 isoform X1	
LOC110613360	XP_021610131.1	-1.513	0.018204242	4	wall-associated receptor kinase-like 1	
LOC110629415	XP_021632071.1	-1.510	7.89244E-07	13	classical arabinogalactan protein 4	
LOC110626821	XP_021628628.1	-1.477	3.36082E-06	11	pectinesterase 3	
LOC110630931	XP_043806063.1	-1.344	0.002031248	14	putative glycine-rich cell wall structural protein 1 isoform X2	
LOC110602222	XP_021595376.1	-1.263	6.44646E-13	15	xyloglucan 6-xylosyltransferase 2	
LOC122724872	XP_043816733.1	-1.258	0.000162957	10	putative glycine-rich cell wall structural protein 1	
LOC110606598	XP_021601167.1	-1.224	0.001378402	18	probable xyloglucan glycosyltransferase 12	
LOC110628606	XP_021631058.2	-1.154	0.000997951	12	xyloglucan galactosyltransferase MUR3	
LOC110626938	XP_021628825.1	-1.010	0.046703738	11	wall-associated receptor kinase-like 22	
LOC110618558	XP_021617395.1	1.429	0.001021917	7	expansin-A8	
LOC110620705	XP_021620217.1	1.565	0.004723587	8	probable pectinesterase/pectinesterase inhibitor 17	
LOC110613004	XP_021609595.1	-2.084	5.88836E-14	4	expansin-like A2	
LOC110618558	XP_021617395.1	1.429	0.001021917	7	expansin-A8	expansin

			LOC110626821	XP_021628628.1	-1.477	3.36082E-06	11	pectinesterase 3	pectinesterase
			LOC110620705	XP_021620217.1	1.565	0.004723587	8	probable pectinesterase/pectinesterase inhibitor 17	
			LOC110609198	XP_021604310.1	-1.929	0.000265509	2	serine/threonine-protein kinase-like protein CCR4	
			LOC110627556	XP_021629597.1	-1.915	0.000223832	12	G-type lectin 5-receptor-like serine/threonine-protein kinase At2g19130	
			LOC110610252	XP_021605783.1	-1.608	0.000100296	3	serine/threonine-protein kinase RIPK	
			LOC110605523	XP_021599830.1	-1.364	7.57612E-05	17	LRR receptor-like serine/threonine-protein kinase FLS2	
			LOC110611082	XP_021606886.1	-1.312	0.020365975	3	G-type lectin 5-receptor-like serine/threonine-protein kinase	
			LOC110603117	XP_021596490.1	-1.281	0.00508019	16	serine/threonine-protein kinase RIPK	
			LOC110612719	XP_021609181.1	-1.246	0.000175889	4	probable serine/threonine-protein kinase PBL5	
			LOC110627934	XP_021630031.1	-1.208	0.003526898	12	putative serine/threonine-protein kinase	
			LOC110606488	XP_021601001.1	-1.194	7.24687E-05	18	LRR receptor-like serine/threonine-protein kinase RG11	
			LOC110613331	XP_043811802.1	-1.182	0.004983226	4	serine/threonine-protein kinase STY46 isoform X5	
			LOC110613331	XP_043811801.1	-1.172	0.004737235	4	serine/threonine-protein kinase STY46 isoform X4	
			LOC110613331	XP_021610097.1	-1.171	0.003466382	4	serine/threonine-protein kinase STY46 isoform X1	
			LOC110613331	XP_021610098.1	-1.151	0.003466382	4	serine/threonine-protein kinase STY46 isoform X2	
			LOC110613331	XP_043811800.1	-1.142	0.004275572	4	serine/threonine-protein kinase STY46 isoform X3	
			LOC110609578	XP_021604950.1	-1.141	0.004306104	2	CBL-interacting serine/threonine-protein kinase 3 isoform X3	
			LOC110609578	XP_043810106.1	-1.126	0.005731024	2	CBL-interacting serine/threonine-protein kinase 3 isoform X1	
			LOC110609578	XP_043810107.1	-1.126	0.005731024	2	CBL-interacting serine/threonine-protein kinase 3 isoform X1	
			LOC110609578	XP_043810108.1	-1.126	0.005731024	2	CBL-interacting serine/threonine-protein kinase 3 isoform X1	
			LOC110609578	XP_021604947.1	-1.126	0.005731024	2	CBL-interacting serine/threonine-protein kinase 3 isoform X2	
			LOC110631167	XP_021634596.1	1.081	0.013810849	14	serine/threonine-protein kinase UCNL	
			LOC110616880	XP_021615082.1	1.234	0.011374231	6	CBL-interacting serine/threonine-protein kinase 21 isoform X1	
			LOC110619974	XP_021619194.1	1.424	0.011970155	8	serine/threonine-protein kinase-like protein CCR1	
			LOC110616880	XP_021615083.1	1.427	0.001039555	6	CBL-interacting serine/threonine-protein kinase 21 isoform X2	
			LOC110625277	XP_021626578.1	-1.726	0.017358761	10	pathogenesis-related protein 1C	
			LOC110617088	XP_021615388.1	-1.603	0.000448427	6	pathogenesis-related protein PR-1	
			LOC110603388	XP_021596794.1	-1.572	0.01092483	16	ethylene-responsive transcription factor ERF018	
			LOC110600889	XP_021593495.1	-1.015	0.006125228	15	ethylene-responsive transcription factor RAP2-3	
			LOC110616175	XP_021614214.1	1.253	0.015503568	5	chitinase 10	
			LOC110621409	XP_021621382.1	1.699	0.007757216	8	peroxidase 2	
			LOC110607019	XP_021601755.1	1.937	2.23808E-08	18	1-aminocyclopropane-1-carboxylate oxidase 5	
			LOC110607098	XP_021601845.2	2.493	2.454E-13	18	pathogen-related protein	
			LOC110601468	XP_021594309.1	-1.768	0.007371456	15	probable WRKY transcription factor 75	
			LOC110610262	XP_021605796.1	1.024	0.041962475	3	probable WRKY transcription factor 40	
			LOC110609837	XP_021605353.1	1.099	0.000916925	2	probable WRKY transcription factor 26	
			LOC110609254	XP_021604396.1	1.179	0.001250204	2	probable WRKY transcription factor 53	
			LOC110602513	XP_021595743.1	1.613	0.010215922	15	probable WRKY transcription factor 72	
			LOC110606323	XP_021600770.1	-1.619	0.010182213	18	transcription factor bHLH93	
			LOC110610132	XP_021605692.1	-2.097	5.35803E-06	2	transcription factor MYB2	
			LOC110602691	XP_021595959.1	-1.826	0.000686837	15	transcription factor MYB2	
			LOC110608493	XP_021603427.1	-1.505	0.003791427	2	transcription factor MYB20	
			LOC110612998	XP_021609582.1	-1.364	0.034897389	4	Myb-related protein 308	
			LOC122723500	XP_043811717.1	1.039	0.028343938	4	transcription factor MYB59-like isoform X1	
			LOC110620470	XP_021619909.1	1.898	0.000926813	8	myb family transcription factor PHL5 isoform X2	
			LOC110620470	XP_021619908.1	1.898	0.000926813	8	myb family transcription factor PHL5 isoform X1	
			LOC110601235	XP_021593988.1	-1.401	0.029442713	15	FCS-Like Zinc finger 1 isoform X1	
			LOC110601235	XP_021593989.1	-1.397	0.029442713	15	FCS-Like Zinc finger 1 isoform X2	
			LOC110614198	XP_021611399.1	-1.392	0.026775112	4	B-box zinc finger protein 24	
			LOC110622855	XP_021623231.1	1.200	0.004532296	9	zinc finger protein JACKDAW	
			LOC110617643	XP_021616261.1	1.799	1.7042E-07	6	zinc finger protein BRUTUS-like At1g18910	
			LOC110618796	XP_021617731.1	-3.936	1.17001E-19	7	22.0 kDa class IV heat shock protein	
			LOC110613482	XP_021610330.1	-3.827	1.28463E-21	4	17.4 kDa class I heat shock protein	
			LOC110613257	XP_021609991.1	-3.475	1.59921E-16	4	17.4 kDa class I heat shock protein	
			LOC110625072	XP_021626276.1	-3.216	2.00657E-14	10	17.3 kDa class I heat shock protein	
			LOC110603775	XP_021597369.1	-3.145	1.61033E-12	16	17.3 kDa class II heat shock protein	
			LOC110616446	XP_021614483.1	-3.024	4.97821E-14	6	23.6 kDa heat shock protein, mitochondrial	
			LOC110600777	XP_021593335.1	-2.660	1.14587E-07	15	heat shock 70 kDa protein 8	
			LOC110603158	XP_021596549.1	-2.349	6.68895E-06	2	18.1 kDa class I heat shock protein	
			LOC110619469	XP_021618635.1	-2.152	9.73516E-08	7	heat shock cognate 70 kDa protein 2	
			LOC110631153	XP_021634576.1	-1.880	0.002305976	14	heat shock 70 kDa protein	
			LOC110605018	XP_021599004.1	-1.820	0.007543733	2	17.3 kDa class I heat shock protein	
			LOC110622990	XP_021623478.1	-1.744	0.002267248	1	17.3 kDa class I heat shock protein	
			LOC110628332	XP_021630642.1	-1.711	0.021281504	12	small heat shock protein, chloroplastic	
			LOC110623419	XP_021624052.1	-1.653	4.26593E-05	9	hsp70 nucleotide exchange factor fes1	
			LOC110630943	XP_021634293.1	-1.498	0.00025393	14	18.1 kDa class I heat shock protein	
			LOC110631276	XP_021634739.1	-1.415	0.049282281	14	23.6 kDa heat shock protein, mitochondrial	
			LOC110628482	XP_021630847.1	-1.340	2.29656E-07	12	Heat shock protein 90-6, mitochondrial isoform X1	
			LOC110628482	XP_021630848.1	-1.331	2.29656E-07	12	Heat shock protein 90-6, mitochondrial isoform X2	
			LOC110626210	XP_021627683.1	-1.142	0.010621581	11	heat shock 70 kDa protein 15	
			LOC110624683	XP_021625610.1	-1.109	0.034281508	10	heat shock cognate 70 kDa protein 2	
			LOC110599687	XP_021591904.1	-1.090	6.87185E-05	14	heat shock protein 90-5, chloroplastic	
			LOC110604755	XP_021598737.1	-5.167	1.22901E-34	17	chaperone protein DnaJ	
			LOC110614088	XP_021611255.1	-2.140	8.92287E-08	4	dnaJ protein homolog	
			LOC110627121	XP_021629057.1	-1.940	3.91976E-05	11	dnaJ protein homolog	
			LOC110602863	XP_021596139.1	-1.861	1.25155E-06	16	dnaJ homolog subfamily B member 13	
			LOC110620651	XP_021620153.1	-1.131	0.005397748	8	dnaJ homolog subfamily B member 6 isoform X2	
			LOC110621983	XP_021621997.1	-1.456	0.00995751	9	Aquaporin PIP2-4	
			LOC110629492	XP_021632171.1	-1.227	0.011802243	13	calmodulin-like protein 30	
			LOC110627073	XP_021628999.1	1.775	2.32556E-05	11	calcium/calmodulin-regulated receptor-like kinase 1	
			LOC110611166	XP_021607011.1	1.490	0.002130339	3	probable leucine-rich repeat receptor-like protein kinase At1g35710	
			LOC110626327	XP_043817605.1	1.808	0.002900584	11	putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g04300 isoform X1	
			LOC110620645	XP_043814771.1	1.822	0.001240529	8	probable LRR receptor-like serine/threonine-protein kinase At5g37450 isoform X2	LRR
			LOC110620645	XP_021620146.1	1.827	0.001240529	8	probable LRR receptor-like serine/threonine-protein kinase At5g37450 isoform X1	
			LOC110626327	XP_021627846.1	2.285	1.07425E-05	11	LRR receptor-like serine/threonine-protein kinase IOS1 isoform X2	
			LOC110630988	XP_021634355.1	-1.266	0.017872719	14	E3 ubiquitin-protein ligase RHA2A	
			LOC110615229	XP_021612699.1	-1.264	0.049260267	5	E3 ubiquitin-protein ligase MPSR1	
			LOC110611498	XP_021607581.1	-1.063	0.010135717	1	E3 ubiquitin-protein ligase MPSR1	E3 ubiquitin

			LOC110605009	XP_021598990.1	-3.215	3.36703E-10	17	expansin-like B1	
			LOC110622470	XP_021622663.1	-1.708	2.42241E-05	9	probable xyloglucan endotransglucosylase/hydrolase protein 32	
			LOC110602256	XP_021595422.1	-1.685	0.004014484	15	membrane protein PM19L	
			LOC110618558	XP_021617395.1	-1.418	0.002649173	7	Expansin-A8	cell-wall
			LOC122724074	XP_043814505.1	-1.221	0.035008428	7	glycine-rich cell wall structural protein 2-like	
			LOC110607806	XP_043806385.1	1.094	0.043267765	14	probable xyloglucan endotransglucosylase/hydrolase protein 23	
			LOC110600342	XP_043806105.1	1.219	4.27111E-06	14	extensin-2-like	
			LOC110605009	XP_021598990.1	-3.215	3.36703E-10	17	expansin-like B1	
			LOC110618558	XP_021617395.1	-1.418	0.002649173	7	Expansin-A8	expansin
			LOC110616882	XP_021615086.1	-1.125	0.02353049	6	serine/threonine-protein kinase UCNL	
			LOC110622878	XP_021623266.1	1.136	0.044244532	9	probable serine/threonine-protein kinase WNK4 isoform X2	
			LOC110622878	XP_021623265.1	1.146	0.032181015	9	probable serine/threonine-protein kinase WNK5 isoform X1	
			LOC110626213	XP_021627690.1	1.152	0.014847944	11	putative serine/threonine-protein kinase isoform X2	
			LOC110626213	XP_021627688.1	1.225	0.010621581	11	putative serine/threonine-protein kinase isoform X1	
			LOC110625458	XP_021626747.2	1.405	0.037488507	11	putative serine/threonine-protein kinase	
			LOC110626327	XP_043817605.1	1.808	0.002900584	11	putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g04300 isoform X1	serine/threonine
			LOC110620645	XP_043814771.1	1.822	0.001240529	8	probable LRR receptor-like serine/threonine-protein kinase At5g37450 isoform X2	
			LOC110620645	XP_021620146.1	1.827	0.001240529	8	probable LRR receptor-like serine/threonine-protein kinase At5g37450 isoform X1	
			LOC110626327	XP_021627846.1	2.285	1.07425E-05	11	LRR receptor-like serine/threonine-protein kinase IOS1 isoform X2	
			LOC110621319	XP_021621244.1	-2.333	3.53521E-07	8	L-ascorbate peroxidase 2, cytosolic	
			LOC110601492	XP_021594337.2	-1.232	0.044719198	1	peroxidase 5	ethylene
			LOC110611162	XP_021607005.1	1.574	0.000535542	3	ethylene-responsive transcription factor ERF017	
			LOC110624639	XP_021625546.1	1.616	0.001414835	10	ethylene-responsive transcription factor ERF109	
			LOC110610132	XP_021605692.1	-1.426	0.008688347	2	transcription factor MYB2	MYB
			LOC110601044	XP_021593727.1	-1.473	4.27295E-07	15	B-box zinc finger protein 19	zinc finger
			LOC110601421	XP_021594236.1	-2.860	4.86888E-12	15	class I heat shock protein	
			LOC110624489	XP_021625360.1	-2.821	4.37105E-12	10	17.3 kDa class I heat shock protein	
			LOC110601288	XP_021594063.1	-2.797	1.10606E-11	15	22.0 kDa class IV heat shock protein	
			LOC110613515	XP_021610372.1	-2.552	1.41285E-10	4	26.5 kDa heat shock protein, mitochondrial	
			LOC110613257	XP_021609991.1	-2.427	1.0431E-09	4	17.4 kDa class I heat shock protein	
			LOC122724330	XP_043814740.1	-2.278	4.85881E-07	8	class I heat shock protein-like	
			LOC110625241	XP_021626537.1	-2.237	2.94833E-07	10	22.0 kDa class IV heat shock protein	
			LOC110619449	XP_021618593.1	-2.211	7.78705E-07	7	18.2 kDa class I heat shock protein	
			LOC110620193	XP_021619516.1	-2.190	6.08274E-09	1	small heat shock protein, chloroplastic	HSP
			LOC110620636	XP_021620134.1	-2.107	5.58858E-06	8	class I heat shock protein	
			LOC110624613	XP_021625513.1	-1.844	9.54217E-05	10	22.0 kDa class IV heat shock protein	
			LOC110603775	XP_021597369.1	-1.824	0.000148909	16	17.3 kDa class II heat shock protein	
			LOC110600777	XP_021593335.1	-1.726	0.000237739	15	heat shock 70 kDa protein 8	
			LOC110613482	XP_021610330.1	-1.683	0.000342764	4	17.4 kDa class I heat shock protein	
			LOC110607779	XP_021602638.1	-1.616	0.003204886	18	16.9 kDa class I heat shock protein 1	
			LOC110626592	XP_021628289.1	-1.546	0.001987736	11	heat shock 70 kDa protein 5	
			LOC110603605	XP_021597086.2	-1.378	0.029729221	2	heat shock protein 83	
			LOC110613196	XP_021609904.1	1.292	0.001287463	4	NDR1/HIN1-like protein 13	NDR1/HIN1
			LOC110622386	XP_021622562.1	1.223	0.009536582	9	E3 ubiquitin-protein ligase PUB23	E3 ubiquitin
			LOC122723212	XP_043810679.1	1.500	0.025335452	3	E3 ubiquitin-protein ligase RING1-like	
			LOC110618512	XP_021617347.1	1.626	0.026903397	7	peroxidase P7	ethylene
			LOC110606164	XP_021600622.1	1.318	0.044186049	2	FCS-Like Zinc finger 5	zinc finger
			LOC110607327	XP_021602110.1	-2.243	1.09885E-05	2	17.3 kDa class I heat shock protein	
			LOC110611125	XP_043811369.1	-1.889	0.000220486	3	heat shock factor protein HSF30 isoform X2	
			LOC110631276	XP_021634739.1	-1.856	0.000189776	14	23.6 kDa heat shock protein, mitochondrial	HSP
			LOC110618796	XP_021617731.1	-1.828	0.01954617	7	22.0 kDa class IV heat shock protein	
			LOC110605018	XP_021599004.1	-1.773	0.003821524	2	17.3 kDa class I heat shock protein	
			LOC110611125	XP_043811367.1	-1.551	0.018307975	3	heat shock factor protein HSF30 isoform X1	
			LOC110627121	XP_021629057.1	-1.310	0.02044571	11	dnaJ protein homolog	DNAJ
			LOC110622460	XP_043815513.1	-1.405	0.007020608	9	calcium-binding protein CBP	calcium-binding
			LOC110604202	XP_021598028.1	-1.678	0.004361121	16	pectinesterase	
			LOC122722147	XP_043808073.1	1.150	0.011611348	16	non-classical arabinogalactan protein 31-like	cell-wall
			LOC110623277	XP_021623912.1	1.181	0.027860452	1	expansin-A4	expansin
			LOC110623277	XP_021623912.1	1.181	0.027860452	1	expansin-A4	expansin
			LOC110604202	XP_021598028.1	-1.678	0.004361121	16	pectinesterase	pectinesterase
			LOC110616575	XP_021614684.1	-1.123	0.000762554	6	plasma membrane ATPase 4	
			LOC110615734	XP_021613480.1	1.158	0.006652045	5	cellulose synthase-like protein D5	cell-wall
			LOC110623126	XP_021623718.1	1.486	0.000900281	9	bark storage protein B	
			LOC110622339	XP_021622514.1	-1.014	0.000337273	9	myb family transcription factor PHL5	MYB
			LOC110626130	XP_021627580.1	-1.315	6.96429E-07	11	zinc finger protein 1	zinc finger
			LOC110628158	XP_021630369.1	1.235	0.010037984	12	probable E3 ubiquitin-protein ligase XERICO	E3 ubiquitin
			LOC110601065	XP_021593757.1	-1.042	0.030441744	15	extensin	cell-wall
			LOC110608713	XP_021603684.1	1.297	0.013590059	2	peroxidase 72	ethylene
			LOC110605844	XP_021600197.1	1.523	0.046283833	18	peroxidase 4	
			LOC110604559	XP_021598481.1	1.703	0.005719983	17	probable WRKY transcription factor 31	WRKY
			LOC110620675	XP_021620181.1	1.964	3.00645E-07	8	E3 ubiquitin-protein ligase WAV3	E3 ubiquitin
			LOC110624589	XP_021625482.1	1.122	0.002543421	10	expansin-A8	
			LOC110613106	XP_021609747.1	1.595	0.00223259	4	probable xyloglucan endotransglucosylase/hydrolase protein 5	cell-wall
			LOC110615287	XP_021612783.1	1.746	0.000284642	5	pectinesterase 2	
			LOC110624589	XP_021625482.1	1.122	0.002543421	10	expansin-A8	expansin
			LOC110615287	XP_021612783.1	1.746	0.000284642	5	pectinesterase 2	pectinesterase
			LOC110617088	XP_021615388.1	-1.411	1.30395E-23	6	pathogenesis-related protein PR-1	ethylene
			LOC110629429	XP_021632089.1	1.053	0.000412565	13	peroxidase 17	ethylene
			LOC110613514	XP_021610371.1	-1.020	2.65553E-06	4	transcription factor MYB53	MYB
			LOC110626052	XP_021627481.1	1.156	0.000153812	18	zinc finger protein CONSTANS-LIKE 6 isoform X3	
			LOC110626052	XP_021627479.1	1.185	0.000100106	18	zinc finger protein CONSTANS-LIKE 6 isoform X1	zinc finger
			LOC110626052	XP_021627480.1	1.190	0.000100106	18	zinc finger protein CONSTANS-LIKE 6 isoform X2	
			LOC110608678	XP_021603650.1	1.299	6.15933E-08	2	zinc finger protein CONSTANS-LIKE 7	
			LOC110620896	XP_021620539.1	1.273	1.27419E-05	1	small heat shock protein, chloroplastic isoform X1	HSP
			LOC110626549	XP_021628210.1	1.092	5.22865E-06	11	dnaJ homolog subfamily B member 6 isoform X1	DNAJ
			LOC110626549	XP_021628211.1	1.105	5.22865E-06	11	dnaJ homolog subfamily B member 6 isoform X2	
			LOC110602376	XP_021595569.1	-1.084	1.73345E-06	15	cell wall / vacuolar inhibitor of fructosidase 1	
			LOC110631163	XP_021634589.1	1.016	0.001425663	14	xyloglucan endotransglucosylase/hydrolase protein 24	cell-wall
			LOC110619476	XP_021618646.1	-2.287	6.92226E-05	7	peroxidase 4	
			LOC110601389	XP_021594194.1	-1.947	0.002595701	15	peroxidase 55	

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LOC110627264	XP_021629204.1	-1.762	0.004884379	12	1-aminocyclopropane-1-carboxylate oxidase	ethylene
LOC110600304	XP_021592812.1	-1.671	0.00132759	14	peroxidase 11	
LOC110604630	XP_021598578.1	-1.442	0.046403042	17	ethylene-responsive transcription factor 4	
LOC110630305	XP_021633426.1	-1.384	0.011542946	13	auxin-induced in root cultures protein 12	auxin
LOC110600709	XP_021593241.1	1.012	5.26436E-05	15	auxin-responsive protein IAA14	
LOC110606798	XP_021601480.1	-1.782	6.59253E-05	18	putative 12-oxophytodienoate reductase 11 isoform X1	jasmonic acid
LOC110606798	XP_043808806.1	-1.661	0.00024483	18	putative 12-oxophytodienoate reductase 11 isoform X2	
LOC110626614	XP_021628322.1	-1.411	0.006603546	11	probable WRKY transcription factor 40	WRKY
LOC110615501	XP_021613059.1	-1.085	0.025357333	5	WRKY transcription factor 22	
LOC110607873	XP_021602729.1	-1.857	0.000698611	13	transcription factor MYB15	MYB
LOC110626760	XP_021628528.1	1.095	0.005450769	1	myb-related protein 306	
LOC110629575	XP_021632299.1	1.127	0.001464716	13	MYB-like transcription factor ETC1	
LOC110625106	XP_021626334.1	-1.960	0.011287815	10	zinc finger protein ZAT11	
LOC110630954	XP_021634306.2	-1.153	0.047322686	14	LOW QUALITY PROTEIN: zinc finger CCCH domain-containing protein	zinc finger
LOC110620938	XP_021620585.1	1.104	0.003730733	1	zinc finger protein ZAT9	
LOC110616246	XP_021614299.1	1.391	0.039971123	5	zinc finger protein 6	
LOC110608678	XP_021603650.1	1.480	0.001157982	2	zinc finger protein CONSTANS-LIKE 7	
LOC110600163	XP_021592620.1	-2.780	3.60874E-18	14	heat shock protein 83	
LOC110605018	XP_021599004.1	-2.740	1.13483E-12	2	17.3 kDa class I heat shock protein	
LOC110613482	XP_021610330.1	-2.536	2.79354E-18	4	17.4 kDa class I heat shock protein	
LOC110603775	XP_021597369.1	-2.307	1.32695E-05	16	17.3 kDa class II heat shock protein	
LOC110607779	XP_021602638.1	-2.245	0.000139588	18	16.9 kDa class I heat shock protein 1	
LOC110611125	XP_043811369.1	-2.221	0.000129453	3	heat shock factor protein HSF30 isoform X2	
LOC110618796	XP_021617731.1	-2.132	5.37559E-05	7	22.0 kDa class IV heat shock protein	
LOC110611125	XP_043811367.1	-2.125	0.000236226	3	heat shock factor protein HSF30 isoform X1	
LOC110631276	XP_021634739.1	-2.088	1.82981E-06	14	23.6 kDa heat shock protein, mitochondrial	
LOC110616446	XP_021614483.1	-2.068	1.88926E-05	6	23.6 kDa heat shock protein, mitochondrial	HSP
LOC110626448	XP_021628049.1	-2.042	6.91083E-05	11	17.4 kDa class III heat shock protein isoform X2	
LOC110626448	XP_043817916.1	-1.998	7.01989E-05	11	17.4 kDa class III heat shock protein isoform X1	
LOC110607327	XP_021602110.1	-1.983	0.001430114	2	17.3 kDa class I heat shock protein	
LOC110619469	XP_021618635.1	-1.918	0.001235285	7	heat shock cognate 70 kDa protein 2	
LOC110628248	XP_021630509.1	-1.661	0.007680227	12	heat shock factor protein HSF24	
LOC110631253	XP_021634711.1	-1.521	0.002775459	14	17.3 kDa class I heat shock protein	
LOC110617718	XP_021616382.1	-1.516	0.020099508	6	heat shock protein 83	
LOC110603158	XP_021596549.1	-1.450	0.009272511	2	18.1 kDa class I heat shock protein	
LOC110628332	XP_021630642.1	-1.438	0.028889144	12	small heat shock protein, chloroplastic	
LOC110631209	XP_021634648.1	-1.112	0.046599359	14	17.5 kDa class I heat shock protein	
LOC110627121	XP_021629057.1	-1.341	5.57942E-08	11	dnaJ protein homolog	DNAJ
LOC110614088	XP_021611255.1	-1.039	0.003455576	4	dnaJ protein homolog	
LOC110619660	XP_021618883.1	-2.601	2.26318E-10	7	probable aquaporin PIP-type 7a	aquaporin
LOC110613224	XP_021609940.1	-1.398	0.005503798	4	aquaporin TIP1-1	
LOC110623980	XP_021624708.1	-1.202	0.019191403	10	probable aquaporin PIP1-2	
LOC110601024	XP_021593691.1	-1.406	0.000132412	15	calcium-binding protein CP1	calcium-binding
LOC110622425	XP_021622610.1	1.423	0.029432297	9	probable calcium-binding protein CML43	
LOC110613196	XP_021609904.1	1.474	0.004252299	4	NDR1/HIN1-like protein 13	NDR1/HIN1
LOC110624717	XP_021625675.1	-2.115	0.004040556	10	probable LRR receptor-like serine/threonine-protein kinase At3g47570	LRR
LOC110605178	XP_021599237.1	-1.335	0.046403042	17	probable LRR receptor-like serine/threonine-protein kinase	
LOC110619415	XP_043814502.1	-1.907	0.001691032	7	E3 ubiquitin-protein ligase HERC2 isoform X2	E3 ubiquitin
LOC110606419	XP_021600909.1	1.259	0.035380287	18	WAT1-related protein At1g43650 isoform X1	WAT1
LOC110606419	XP_021600910.1	1.265	0.031976234	18	WAT1-related protein At1g43650 isoform X2	
LOC110630931	XP_043806063.1	-1.873	1.66267E-14	14	putative glycine-rich cell wall structural protein 1 isoform X2	
LOC110630931	XP_021634273.1	-1.803	1.5263E-12	14	putative glycine-rich cell wall structural protein 1 isoform X1	
LOC110627987	XP_021630107.1	-1.753	0.003994084	12	probable pectinesterase/pectinesterase inhibitor 51	
LOC110629415	XP_021632071.1	-1.615	0.006901281	13	classical arabinogalactan protein 4	
LOC122724872	XP_043816733.1	-1.555	0.002015886	10	putative glycine-rich cell wall structural protein 1	cell-wall
LOC110619641	XP_021618857.1	-1.519	0.034670596	7	classical arabinogalactan protein 1	
LOC110631132	XP_021634549.1	-1.505	0.003690479	14	xyloglucan endotransglucosylase/hydrolase protein 22	
LOC110609580	XP_021604952.1	1.062	3.31989E-10	1	lysine-rich arabinogalactan protein 19	
LOC122724500	XP_043815572.1	1.083	0.000230499	9	arabinogalactan protein 13-like	
LOC110625794	XP_021627137.1	1.449	0.012185591	11	wall-associated receptor kinase-like 8	
LOC110627987	XP_021630107.1	-1.753	0.003994084	12	probable pectinesterase/pectinesterase inhibitor 51	pectinesterase
LOC110619183	XP_021618150.1	-2.957	1.05172E-11	7	protein PELPK1	
LOC110619598	XP_021618801.1	-2.670	1.05172E-11	7	protein PELPK1	
LOC110619117	XP_021618060.1	-2.604	7.77217E-09	7	protein PELPK1	
LOC110619131	XP_021618075.1	-2.549	1.49786E-06	7	protein PELPK1-like	
LOC110619130	XP_021618074.1	-2.180	1.37185E-05	7	protein PELPK1	
LOC122724829	XP_043816639.1	-2.137	0.004040556	10	protein PELPK2-like	PELPK1
LOC110624537	XP_021625424.1	-2.103	0.000179724	10	protein PELPK1	
LOC110619615	XP_021618820.1	-1.922	0.001706482	7	protein PELPK1	
LOC110624536	XP_021625423.1	-1.882	0.011353445	10	protein PELPK1	
LOC110619118	XP_021618061.1	-1.882	0.003128867	7	protein PELPK1	
LOC110618992	XP_021617949.1	-1.804	0.003736979	7	protein PELPK1 isoform X1	
LOC110618992	XP_043814525.1	-1.804	0.003736979	7	protein PELPK1 isoform X2	
LOC110624717	XP_021625675.1	-2.115	0.004040556	10	probable LRR receptor-like serine/threonine-protein kinase At3g47570	
LOC110609692	XP_021605155.1	-1.846	0.003940264	2	serine/threonine-protein kinase PBL27 isoform X5	
LOC122722120	XP_043807878.1	-1.652	0.028931081	16	G-type lectin S-receptor-like serine/threonine-protein kinase At1g61370	
LOC122722119	XP_043807876.1	-1.618	0.025710248	16	G-type lectin S-receptor-like serine/threonine-protein kinase At1g61370	
LOC110627503	XP_021629542.2	-1.571	0.010617494	12	serine/threonine-protein kinase OXI1	
LOC110604514	XP_021598400.1	-1.401	0.046403042	17	G-type lectin S-receptor-like serine/threonine-protein kinase	serine/threonine
LOC110604514	XP_021598397.1	-1.369	0.046403042	17	G-type lectin S-receptor-like serine/threonine-protein kinase	
LOC110604514	XP_043808771.1	-1.369	0.046403042	17	G-type lectin S-receptor-like serine/threonine-protein kinase	
LOC110604514	XP_021598398.1	-1.364	0.046403042	17	G-type lectin S-receptor-like serine/threonine-protein kinase	
LOC110613953	XP_021611079.1	-1.351	0.041922423	4	probable serine/threonine-protein kinase PIX13	
LOC110605178	XP_021599237.1	-1.335	0.046403042	17	probable LRR receptor-like serine/threonine-protein kinase	
LOC110630721	XP_021633965.1	-1.323	0.016754061	14	G-type lectin S-receptor-like serine/threonine-protein kinase RKS1	
LOC110630721	XP_043806213.1	-1.320	0.016754061	14	G-type lectin S-receptor-like serine/threonine-protein kinase RKS1	
LOC110620002	XP_021619231.1	-1.236	0.030985827	8	serine/threonine-protein kinase AtPK2/AtPK19	
LOC110628776	XP_021631268.1	1.264	0.031243179	12	ethylene-responsive transcription factor ERF053	ethylene

DSC 167	young leaf	1	LOC110622560	XP_021622803.1	-1.533	0.006656597	9	auxin efflux carrier component 5	auxin
			LOC110614935	XP_021612319.1	2.109	0.001213971	5	transcription factor MYC2	bHLH
			LOC110621662	XP_021621624.1	-1.842	0.00412221	8	zinc finger protein ZAT5	zinc finger
			LOC110608235	XP_021603135.1	-1.144	0.036186215	12	zinc finger protein CONSTANS-LIKE 9	
			LOC110620193	XP_021619516.1	1.345	0.008857801	1	small heat shock protein, chloroplastic	HSP
			LOC110619469	XP_021618635.1	1.391	7.81812E-14	7	heat shock cognate 70 kDa protein 2	
			LOC110613482	XP_021610330.1	1.580	9.59672E-05	4	17.4 kDa class I heat shock protein	
			LOC110616446	XP_021614483.1	1.708	5.56975E-07	6	23.6 kDa heat shock protein, mitochondrial	
			LOC110615064	XP_021612462.1	1.765	0.02194715	5	heat stress transcription factor A-7a	
			LOC110629373	XP_021632001.1	1.514	0.000679032	13	probable E3 ubiquitin-protein ligase XERICO	E3 ubiquitin
			LOC110611396	XP_021607390.2	1.815	4.49738E-09	3	probable E3 ubiquitin-protein ligase RZFP34 isoform X3	
			LOC110611396	XP_043810849.1	1.820	4.49738E-09	3	probable E3 ubiquitin-protein ligase RZFP34 isoform X4	
			LOC110611396	XP_021607389.2	1.851	2.31606E-09	3	probable E3 ubiquitin-protein ligase RZFP34 isoform X2	
			LOC110611396	XP_021607388.2	1.851	2.31606E-09	3	probable E3 ubiquitin-protein ligase RZFP34 isoform X1	
			LOC110611498	XP_021607581.1	1.872	1.06833E-05	1	E3 ubiquitin-protein ligase MPSR1	RING-H2
			LOC110618025	XP_043806144.1	1.244	0.014291922	1	RING-H2 finger protein ATL79 isoform X2	
			LOC110618025	XP_021616732.2	1.263	0.007382215	1	RING-H2 finger protein ATL79 isoform X1	cell-wall
			LOC110629370	XP_021631999.1	-1.411	0.034245361	13	probable xyloglucan endotransglucosylase/hydrolase protein 6	
			LOC110620853	XP_021620473.2	1.494	0.007289656	8	expansin-A8	expansin
			LOC110620853	XP_021620473.2	1.494	0.007289656	8	expansin-A8	
LOC110622242	XP_021622387.1	1.472	0.004572114	9	serine/threonine-protein phosphatase PP1 isozyme 1	serine/threonine			
DSC 167	young leaf	5	LOC110625037	XP_021626224.1	-1.120	1.51515E-05	10	ethylene-responsive transcription factor RAP2-7 isoform X2	ethylene
			LOC110616028	XP_021614017.1	1.997	2.96673E-18	5	ninja-family protein AFP2	jasmonic acid
			LOC110608678	XP_021603650.1	-1.170	2.29977E-05	2	zinc finger protein CONSTANS-LIKE 7	zinc finger
			LOC110620193	XP_021619516.1	1.080	9.64843E-05	1	small heat shock protein, chloroplastic	HSP
			LOC110627121	XP_021629057.1	1.179	7.57146E-05	11	dnaj protein homolog	DNAJ
			LOC110601277	XP_043807286.1	-1.287	5.46132E-12	15	calmodulin-like protein 11	calmodulin
			LOC110609262	XP_021604409.2	1.046	2.29977E-05	2	cellulose synthase-like protein G3	cell-wall
			LOC110612870	XP_021609395.1	1.183	2.97918E-07	4	probable pectinesterase/pectinesterase inhibitor 35	
			LOC110612870	XP_021609395.1	1.183	2.97918E-07	4	probable pectinesterase/pectinesterase inhibitor 35	pectinesterase
			DSC 167	young leaf	10	LOC110617088	XP_021615388.1	-1.144	5.4321E-09
LOC110610868	XP_021606638.1	-1.031				4.65062E-05	3	zinc finger protein CONSTANS-LIKE 4	zinc finger
LOC110628816	XP_021631316.1	-1.016				0.001514414	12	zinc finger protein CONSTANS-LIKE 4	
LOC110630896	XP_021634229.1	1.120				1.11777E-07	14	zinc finger protein CONSTANS-LIKE 6 isoform X2	
LOC110630896	XP_021634228.1	1.132				9.93197E-08	14	zinc finger protein CONSTANS-LIKE 6 isoform X1	aquaporin
LOC110621983	XP_021621997.1	-1.011				8.86268E-11	9	aquaporin PIP2-4	
LOC110602376	XP_021595569.1	-1.372				2.29701E-12	15	cell wall / vacuolar inhibitor of fructosidase 1	cell-wall

Table S9: Protein ID, log₂ fold change, adjusted p-value, and protein function of DEGs after two-factor DESeq2 analyses. Analysis of 1 and 10 DAI of stem and root tissues of the three genotypes.

A- Stem, 1 DAI, DSC 260 vs. TMS 96/0304

protein ID	log ₂ FC	adjusted p-value	protein function
XP_043816518.1	-8.446645052	0.034237032	protein SOSEKI 1 isoform X1
XP_021620219.1	-8.416046294	0.045838447	germin-like protein subfamily 1 member 13
XP_043804901.1	-7.617526371	0.003551763	RNA-directed DNA methylation 4 isoform X2
XP_021634880.1	-7.010139899	0.022303382	zinc finger A20 and AN1 domain-containing stress-associated protein 8
XP_021615023.1	-6.812694148	0.000806791	60S ribosomal protein L34
XP_021592887.1	-6.556925469	1.41E-06	uncharacterized protein LOC110600355
XP_043812548.1	-6.458728235	0.014710581	inactive glucose-1-phosphate adenylyltransferase small subunit 2, chloroplastic isoform X3
XP_021607564.1	-6.449486623	0.033437716	uncharacterized protein LOC110611490
XP_021621558.1	-5.412606437	0.007178221	rRNA 2'-O-methyltransferase fibrillarin
XP_021600889.2	-5.200150517	0.034039209	tetratricopeptide repeat protein SKI3 isoform X2
XP_021626810.1	-5.154006774	0.034237032	SH3 domain-containing protein 2
XP_021626808.1	-5.117316841	0.03807028	vesicle transport protein GOT1
XP_021592749.1	-4.950228167	0.018656879	HVA22-like protein a
XP_021622791.1	-4.709156248	0.017238475	CASP-like protein 2B1 isoform X3
XP_021625363.1	-4.294872566	0.00983851	shaggy-related protein kinase kappa
XP_043806250.1	-4.182155327	0.007140268	glyceraldehyde-3-phosphate dehydrogenase GAPCP2, chloroplastic isoform X1
XP_021606000.1	-3.978304086	0.000587454	pre-mRNA-processing protein 40C isoform X2
XP_021634306.2	-3.962747439	0.000378011	LOW QUALITY PROTEIN: zinc finger CCCH domain-containing protein 56-like
XP_021634307.1	-3.943291782	0.003551763	heterogeneous nuclear ribonucleoprotein H2 isoform X3
XP_043806374.1	-3.915341742	0.004173223	heterogeneous nuclear ribonucleoprotein F isoform X2

XP_021609899.1	-3.866689479	9.74E-07	LOB domain-containing protein 1
XP_021609897.1	-3.794037118	1.95E-06	pentatricopeptide repeat-containing protein At4g02750
XP_043805936.1	-3.793679557	7.71E-05	copper-transporting ATPase HMA4 isoform X1
XP_043809759.1	-3.793357127	0.000463932	uncharacterized protein LOC122723072
XP_021624125.1	-3.677816275	0.00891203	uncharacterized protein LOC110623473 isoform X1
XP_021630023.1	-3.655448139	0.013277817	photosystem II core complex proteins psbY, chloroplastic
XP_043806251.1	-3.631393191	7.71E-05	glyceraldehyde-3-phosphate dehydrogenase GAPCP2, chloroplastic isoform X2
XP_021633704.1	-3.323819797	9.25E-06	thioredoxin 1
XP_043806161.1	-3.299461741	0.004400993	uncharacterized protein LOC122721709
XP_021608340.1	-3.197417934	0.039076036	beta-galactosidase isoform X1
XP_021608341.1	-3.157153422	0.041623538	beta-galactosidase isoform X2
XP_021631956.1	-3.109801352	0.046720704	SPX and EXS domain-containing protein 1 isoform X2
XP_021617446.1	-2.856857487	7.71E-05	regulator of nonsense transcripts UPF2
XP_021634356.1	-2.661135009	0.036178099	40S ribosomal protein S11
XP_021622520.1	-2.550956901	0.034439146	uncharacterized protein LOC110622344
XP_043807847.1	-2.51625742	0.012075755	pyruvate kinase, cytosolic isozyme isoform X1
XP_021619161.1	-2.450318266	0.001290608	transcription factor bHLH140
XP_043806601.1	-2.336489157	0.038150664	uncharacterized protein LOC110630714 isoform X3
XP_021633956.1	-2.259619196	0.033237137	uncharacterized protein LOC110630714 isoform X1
XP_043805206.1	-2.24843963	0.031499749	uncharacterized protein LOC110611039 isoform X3
XP_021599374.2	-1.996196554	0.003551763	vacuolar-processing enzyme
XP_043807862.1	-1.957695257	0.003551763	uncharacterized vacuolar membrane protein YML018C isoform X3
XP_021611748.1	-1.883583799	0.045838447	protein ABIL2
XP_021607662.1	1.503666775	0.019555235	uncharacterized protein LOC110611581
XP_021602326.1	1.511958387	0.032282499	suppressor of disruption of TFIS
XP_021598461.1	1.515731883	0.022303382	uncharacterized protein LOC110604550 isoform X7

XP_021602346.1	1.538756353	0.023876911	cyclin-D4-2
XP_021601915.2	1.548878593	0.014609217	enoyl-CoA hydratase 2, peroxisomal
XP_021601917.1	1.549916885	0.014609217	uncharacterized protein LOC110607145
XP_043807440.1	1.551069085	0.00891203	disease resistance protein RPS2 isoform X2
XP_021602322.1	1.551134377	0.013277817	abscisic acid 8'-hydroxylase 2 isoform X2
XP_021602336.1	1.551961643	0.024275617	transmembrane protein 18
XP_021601918.2	1.558406361	0.014609217	cytochrome P450 714C2
XP_043809378.1	1.568657746	0.00891203	abscisic acid 8'-hydroxylase 2 isoform X1
XP_021606798.1	1.614771618	0.034237032	paired amphipathic helix protein Sin3-like 5
XP_043807753.1	1.710011739	0.034237032	uncharacterized protein LOC110626934
XP_021612500.1	1.759136168	0.019668873	kinesin-like protein KIN-8A isoform X1
XP_021611235.1	1.817673006	0.016231493	auxin-induced protein 15A
XP_021603432.1	1.825518685	0.041623538	probable methyltransferase PMT10
XP_021624260.1	1.891873512	0.007856571	uncharacterized protein LOC110623573
XP_021595497.1	1.947465007	0.015843951	carbonic anhydrase, chloroplastic isoform X1
XP_043805151.1	1.986643747	0.02271829	putative inactive glutathione hydrolase 4 isoform X3
XP_021633085.1	2.029652858	0.014005795	GLABRA2 expression modulator isoform X1
XP_021624332.1	2.055042558	0.018936748	uncharacterized protein LOC110623640
XP_021606204.1	2.098044297	0.038612729	peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic isoform X1
XP_021607143.1	2.110923616	0.019641007	putative E3 ubiquitin-protein ligase RF298 isoform X2
XP_021607134.1	2.186498426	0.000628976	ethylene receptor 2
XP_021617505.1	2.193812146	0.043678203	nuclear transcription factor Y subunit A-1
XP_021634909.1	2.200172305	0.008614843	methionyl-tRNA formyltransferase isoform X2
XP_021634921.1	2.205199724	0.008460259	heavy metal-associated isoprenylated plant protein 21
XP_021603128.1	2.218900663	0.003551763	uncharacterized protein LOC110608224
XP_021631975.1	2.22701688	0.004585493	GDP-mannose transporter GONST3

XP_043808776.1	2.233080365	0.019668873	uncharacterized protein LOC110605224 isoform X2
XP_021631974.1	2.241237847	0.004400993	uncharacterized protein LOC110629355
XP_021631058.2	2.265927487	0.015843951	xyloglucan galactosyltransferase MUR3
XP_021631057.1	2.293542584	0.015843951	probable calcium-binding protein CML41
XP_021617842.1	2.334798496	0.047515034	protein ESKIMO 1
XP_021612189.2	2.364969011	0.012075755	uncharacterized protein LOC110614822
XP_021604018.1	2.433795133	0.009628063	uncharacterized protein LOC110609020
XP_043814928.1	2.446526853	0.004999603	probable E3 ubiquitin-protein ligase ZFP1 isoform X1
XP_021625976.1	2.546909229	0.001817546	UDP-glycosyltransferase TURAN isoform X1
XP_021613045.1	2.555021216	0.044150268	uncharacterized protein LOC110615495
XP_021624213.1	2.556777286	0.039359113	calmodulin-2/4 isoform X1
XP_021594345.1	2.565626199	0.030394789	WAT1-related protein At5g40240 isoform X4
XP_043808505.1	2.648557315	0.000374271	uncharacterized protein LOC110607353 isoform X1
XP_021634386.1	2.73728102	0.008168983	putative fasciclin-like arabinogalactan protein 20
XP_021634387.1	2.737362173	0.00891203	probable ribose-5-phosphate isomerase 2
XP_043804430.1	2.763697734	0.016963113	uncharacterized mitochondrial protein AtMg00810-like
XP_043814801.1	2.868259809	0.017978305	uncharacterized protein LOC122724336
XP_043809743.1	2.873287378	0.043032913	prostatic spermine-binding protein-like
XP_021598083.1	2.973819332	0.004173223	uncharacterized protein LOC110604244 isoform X1
XP_021604868.1	3.027312223	5.27E-05	disease resistance RPP13-like protein 4 isoform X6
XP_021613165.1	3.028705407	0.004345507	delta(8)-fatty-acid desaturase 2
XP_021620273.1	3.076021585	0.046720704	protein BONZAI 3 isoform X2
XP_043815082.1	3.077353507	0.046720704	protein BONZAI 3 isoform X1
XP_021627696.1	3.14694736	0.003551763	endochitinase EP3
XP_021606298.1	3.157836531	0.018830794	actin-related protein 2/3 complex subunit 4
XP_021604105.1	3.302739075	0.002383475	bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT

XP_043815174.1	3.357024021	0.005068216	snRNA-activating protein complex subunit isoform X1
XP_021604156.1	3.770439109	0.000374271	protease Do-like 7
XP_043809303.1	3.948577952	0.046720704	uncharacterized protein LOC110606542 isoform X1
XP_021602171.1	3.956949968	0.045257045	probable WRKY transcription factor 32
XP_021599836.1	3.975127308	0.034237032	uncharacterized protein LOC110605525 isoform X4
XP_043808740.1	3.981393745	0.034237032	uncharacterized protein LOC110605525 isoform X8
XP_021592033.1	4.030962229	0.032282499	probable polygalacturonase
XP_021607522.1	4.053185202	0.033480476	long chain acyl-CoA synthetase 6, peroxisomal isoform X1
XP_043818236.1	4.183843314	0.027637145	L-cysteine desulhydrase
XP_021592540.1	4.347891869	0.005714726	LON peptidase N-terminal domain and RING finger protein 1 isoform X2
XP_021619164.1	4.594398401	0.005068216	nicotinate N-methyltransferase 1
XP_043809304.1	4.907325646	0.014609217	uncharacterized protein LOC110606542 isoform X2
XP_043817781.1	6.36679051	0.034237032	PH, RCC1 and FYVE domains-containing protein 1 isoform X3
XP_021599671.1	21.78775928	3.74E-10	plant cysteine oxidase 4
XP_021603861.1	21.85196766	1.66E-05	isoflavone 3'-hydroxylase
XP_043815012.1	22.0967671	1.85E-08	mediator of RNA polymerase II transcription subunit 27
XP_021626517.1	22.68813797	2.62E-10	probable E3 ubiquitin ligase SUD1 isoform X1

B- Stem, 1 DAI, DSC 167 vs. DSC 260

protein ID	log₂FC	adjusted p-value	protein function
XP_021597928.1	-38.47692558	0.000159525	dof zinc finger protein DOF1.5 isoform X1
XP_043815012.1	-19.91828813	6.84E-07	mediator of RNA polymerase II transcription subunit 27
XP_021599671.1	-17.40261837	3.32E-06	plant cysteine oxidase 4
XP_021603861.1	-17.11361835	0.001559309	isoflavone 3'-hydroxylase
XP_021626517.1	-15.98152265	0.000115761	probable E3 ubiquitin ligase SUD1 isoform X1
XP_043810190.1	-9.351195505	0.043257216	uncharacterized protein LOC110609790 isoform X2
XP_021611721.1	-7.571588558	0.00253334	4-hydroxy-tetrahydrodipicolinate reductase 1, chloroplastic isoform X1
XP_043807019.1	-6.544977028	0.019408006	mitogen-activated protein kinase 15 isoform X2
XP_021621039.1	-6.107465877	0.018803027	uncharacterized protein LOC110621192
XP_021630149.1	-5.821553881	0.045782335	cytochrome P450 71AU50
XP_021592540.1	-5.27648491	5.79E-05	LON peptidase N-terminal domain and RING finger protein 1 isoform X2
XP_043807845.1	-5.057834847	0.003491733	SPX domain-containing membrane protein At4g22990 isoform X1
XP_021606385.2	-4.832289689	0.036294245	protein transport protein Sec24-like At3g07100
XP_021607522.1	-4.455979426	0.004244955	long chain acyl-CoA synthetase 6, peroxisomal isoform X1
XP_043818236.1	-4.43128921	0.009817872	L-cysteine desulfhydrase
XP_043817414.1	-4.298357441	0.030070812	probable magnesium transporter NIPA8 isoform X2
XP_021612229.1	-4.254158961	0.030489804	L-cysteine desulfhydrase
XP_021612230.1	-4.054261105	0.04792422	L-cysteine desulfhydrase
XP_021631246.1	-3.98792154	0.024847238	uncharacterized protein LOC110628756 isoform X3
XP_043809973.1	-3.94336725	0.021526001	uncharacterized protein LOC110609013
XP_021611720.1	-3.882117182	0.026644961	probable 1-acyl-sn-glycerol-3-phosphate acyltransferase 4 isoform X2
XP_043806597.1	-3.880579093	0.029887535	reticulon-like protein B21 isoform X2
XP_021602173.1	-3.873358733	0.024500612	probable LRR receptor-like serine/threonine-protein kinase At2g24230
XP_021602171.1	-3.871487419	0.022521318	probable WRKY transcription factor 32

XP_021602172.1	-3.836561853	0.025486491	reticulon-like protein B21 isoform X1
XP_021632909.1	-3.711886199	0.029885599	uncharacterized protein LOC110629969 isoform X1
XP_021606281.1	-3.699861066	0.015644184	farnesyl pyrophosphate synthase 2 isoform X4
XP_021593170.1	-3.611024333	0.00893607	citrate synthase, glyoxysomal
XP_021620714.1	-3.554186221	0.001540404	tRNAse Z TRZ4, mitochondrial isoform X6
XP_021592033.1	-3.504264817	0.041388133	probable polygalacturonase
XP_021613426.1	-3.407472335	0.039123109	nucleolin isoform X1
XP_021605966.1	-3.374430242	0.028485072	pre-mRNA cleavage factor Im 25 kDa subunit 1
XP_021630984.1	-3.319357472	0.047068921	photosystem I reaction center subunit IV A, chloroplastic
XP_021613045.1	-3.22134108	0.001074844	uncharacterized protein LOC110615495
XP_021599388.1	-3.176378817	0.012582955	telomerase Cajal body protein 1 isoform X1
XP_043805786.1	-3.16281664	0.018500365	WD40 repeat-containing protein HOS15 isoform X1
XP_043809743.1	-3.121311364	0.007325852	prostatic spermine-binding protein-like
XP_021603859.1	-3.108702767	0.020201582	protein MAIN-LIKE 2-like
XP_021593309.1	-3.058148024	0.000253037	small ubiquitin-related modifier 1
XP_021627696.1	-3.04870198	0.001766668	endochitinase EP3
XP_043807993.1	-3.040425959	0.033744307	plant cysteine oxidase 4 isoform X4
XP_021608505.1	-3.019351785	0.040437178	NAD(P)H dehydrogenase (quinone) FQR1 isoform X1
XP_021596753.1	-3.016644681	0.0485857	cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG8
XP_043806447.1	-2.988575405	0.033744307	transcription factor BIM1 isoform X1
XP_043816841.1	-2.987662297	0.019408006	uncharacterized protein LOC110624697 isoform X44
XP_021630985.1	-2.976049314	0.0485857	uncharacterized protein LOC110628563 isoform X1
XP_021606797.1	-2.949322351	3.76E-08	uncharacterized protein LOC110611008
XP_021607000.1	-2.934829915	0.031102669	3-isopropylmalate dehydratase large subunit, chloroplastic isoform X1
XP_043814927.1	-2.925432049	0.000206509	probable E3 ubiquitin-protein ligase ZFP1 isoform X1
XP_021607001.1	-2.873846037	0.025486491	3-isopropylmalate dehydratase large subunit, chloroplastic isoform X2

XP_021606998.1	-2.856940167	0.020397041	receptor-like cytosolic serine/threonine-protein kinase RBK2 isoform X2
XP_021601278.1	-2.849573452	0.017402943	alkylbase DNA glycosidase-like protein mag2
XP_021596921.1	-2.807643325	0.033690528	putative transcription factor bHLH041 isoform X2
XP_021606997.1	-2.80312419	0.028836842	receptor-like cytosolic serine/threonine-protein kinase RBK2 isoform X1
XP_021599879.1	-2.771541292	0.015150682	vacuolar protein sorting-associated protein 55 homolog
XP_043808524.1	-2.754071062	0.018297278	glycosyltransferase BC10 isoform X5
XP_021626055.1	-2.740049254	0.0003212	putative disease resistance protein RGA3
XP_021608954.1	-2.705630037	0.036497438	NADPH:quinone oxidoreductase
XP_043816799.1	-2.679949439	0.040676071	nuclear envelope pore membrane protein POM 121 isoform X5
XP_043817024.1	-2.664510508	0.003239677	eukaryotic translation initiation factor 3 subunit A isoform X2
XP_021605831.1	-2.640250309	1.41E-05	protein GRAVITROPIC IN THE LIGHT 1
XP_043807283.1	-2.62039386	2.48E-05	uncharacterized protein LOC110601486
XP_043816121.1	-2.553451832	0.033744307	mitogen-activated protein kinase kinase kinase 20-like
XP_043808505.1	-2.545735503	0.000200571	uncharacterized protein LOC110607353 isoform X1
XP_021613165.1	-2.5416797	0.012900324	delta(8)-fatty-acid desaturase 2
XP_021629919.1	-2.484218849	0.017635444	lysM domain receptor-like kinase 4
XP_021630081.1	-2.477424394	0.039229946	uncharacterized protein LOC110627969 isoform X1
XP_021594328.1	-2.447441088	0.000185961	uncharacterized protein LOC110601486
XP_021628588.1	-2.409611914	0.009817872	transcription factor PRE6
XP_043816817.1	-2.395169345	0.049151346	uncharacterized protein LOC110624697 isoform X22
XP_021631975.1	-2.390156311	0.000560818	GDP-mannose transporter GONST3
XP_021615258.1	-2.385954512	0.015752113	serine/threonine-protein kinase Nek6 isoform X1
XP_043806956.1	-2.37755364	0.022423675	ABC transporter F family member 4 isoform X1
XP_021594327.1	-2.35666547	0.000560818	loganic acid O-methyltransferase
XP_021615784.1	-2.336854561	0.012800971	uncharacterized protein LOC110617357 isoform X3
XP_021631974.1	-2.317950577	0.00099467	uncharacterized protein LOC110629355

XP_021628603.1	-2.317805822	0.020397041	rab GTPase-activating protein 22
XP_021607884.1	-2.312760003	0.027269677	protein NPGR2
XP_021591818.1	-2.311966784	0.031737619	diacylglycerol kinase 1
XP_043814834.1	-2.310711599	0.002947302	uncharacterized protein LOC122724347
XP_043808300.1	-2.308569009	0.001147139	TORTIFOLIA1-like protein 2
XP_021593700.1	-2.287259804	0.022521318	3-ketoacyl-CoA synthase 20
XP_021619354.1	-2.256328646	0.006607813	dnaJ protein P58IPK homolog
XP_021628955.1	-2.250878637	0.022521318	dynein light chain 1, cytoplasmic
XP_021604018.1	-2.20821099	0.01257029	uncharacterized protein LOC110609020
XP_021627546.2	-2.203984693	0.042016556	uncharacterized protein LOC110626107
XP_021595705.1	-2.198341181	0.00037587	60S ribosomal protein L32-1
XP_021627787.1	-2.158823003	0.004113624	uncharacterized protein LOC110626278
XP_021617505.1	-2.149806481	0.021785969	nuclear transcription factor Y subunit A-1
XP_021592165.2	-2.147023251	0.017644626	uncharacterized protein LOC110599881 isoform X1
XP_021619207.1	-2.104888201	0.039229946	uncharacterized protein LOC110619985
XP_043807450.1	-2.100172483	0.003354385	light-mediated development protein DET1 isoform X1
XP_021599451.2	-2.0910482	0.020397041	hepatoma-derived growth factor-related protein 2 isoform X1
XP_043816960.1	-2.088397342	0.014150033	putative disease resistance RPP13-like protein 1 isoform X1
XP_043808177.1	-2.086535877	0.047409519	WAT1-related protein At5g40240
XP_021630123.1	-2.08193638	0.012346199	nucleobase-ascorbate transporter 11 isoform X1
XP_043805943.1	-2.080007791	0.023936218	uncharacterized protein LOC110599881 isoform X3
XP_043814827.1	-2.076791001	0.041388133	BEL1-like homeodomain protein 1
XP_021592164.1	-2.072860042	0.024587556	elongation factor Tu, chloroplastic
XP_043814901.1	-2.06485769	0.02183673	uncharacterized protein LOC110620828 isoform X2
XP_021592161.1	-2.045885973	0.006297547	probable boron transporter 2 isoform X1
XP_043816959.1	-2.043835347	0.018297278	putative disease resistance RPP13-like protein 1 isoform X1

XP_043814363.1	-2.041207791	0.015508747	uncharacterized protein LOC110619219 isoform X1
XP_021602121.2	-2.032902531	0.006917201	receptor-like protein EIX2, partial
XP_021628073.2	-2.024147913	0.009524017	putative Peroxidase 48
XP_021595280.1	-2.020459427	0.000364391	beta-glucosidase 18
XP_021631309.1	-1.994440611	0.002975344	transcription factor VOZ1
XP_021595140.1	-1.988870171	0.047581263	rRNA (cytosine-C(5))-methyltransferase NOP2C isoform X3
XP_043805835.1	-1.95849528	0.00235558	probable mannitol dehydrogenase isoform X2
XP_021605308.1	-1.954218012	0.000635773	uncharacterized protein LOC110609800
XP_043809379.1	-1.95010436	0.036675918	low affinity sulfate transporter 3 isoform X2
XP_043817279.1	-1.949975143	0.009686808	uncharacterized protein LOC110625209 isoform X8
XP_021598133.1	-1.91417821	4.93E-05	uncharacterized protein LOC110604276 isoform X1
XP_021628900.1	-1.91057185	0.025193575	protein BASIC PENTACYSTEINE4
XP_021610613.1	-1.895960448	0.005306348	probable inactive receptor kinase At5g10020 isoform X1
XP_021596423.1	-1.895217798	0.032977904	transcriptional corepressor LEUNIG isoform X1
XP_021602706.2	-1.881303325	0.015930244	phenylacetaldehyde reductase isoform X1
XP_021617602.1	-1.879261869	0.000759844	60S ribosomal protein L35
XP_021634292.1	-1.879165447	0.000825513	RHOMBOID-like protein 12, mitochondrial
XP_021599799.1	-1.863960602	0.024755806	mavicyanin
XP_043815370.1	-1.840613429	0.015905453	small polypeptide DEVIL 16-like
XP_043815352.1	-1.823353546	0.02105896	uncharacterized protein LOC122724452
XP_043806880.1	-1.820832227	0.015508747	putative pentatricopeptide repeat-containing protein At1g53330 isoform X2
XP_021599367.1	-1.818836696	0.012891241	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8-B, mitochondrial
XP_021634921.1	-1.817194088	0.025800659	heavy metal-associated isoprenylated plant protein 21
XP_021634909.1	-1.81644458	0.02590472	methionyl-tRNA formyltransferase isoform X2
XP_021598739.1	-1.809621929	0.041106922	uncharacterized protein LOC110604753
XP_021602809.1	-1.809318995	0.002664367	cytochrome b561 and DOMON domain-containing protein At5g47530

XP_021607143.1	-1.797326623	0.038647141	putative E3 ubiquitin-protein ligase RF298 isoform X2
XP_043808066.1	-1.783601995	0.003698501	uncharacterized protein LOC110603064
XP_021633439.1	-1.776203003	5.96E-06	uncharacterized protein LOC110630315
XP_043811510.1	-1.765944435	0.003917714	probable E3 ubiquitin-protein ligase MARCHF10 isoform X3
XP_043814158.1	-1.75939034	0.039229946	phenylacetaldehyde reductase-like
XP_021625976.1	-1.757824253	0.046620663	UDP-glycosyltransferase TURAN isoform X1
XP_043808584.1	-1.752501485	0.044375103	uncharacterized protein LOC110605587
XP_021596480.1	-1.740382937	0.029885599	probable transcriptional regulatory protein At2g25830
XP_021601614.1	-1.736641072	0.015931339	uncharacterized protein LOC110606917 isoform X1
XP_021620874.1	-1.730100496	0.00047482	UPF0161 protein At3g09310
XP_021603128.1	-1.72427293	0.022521318	uncharacterized protein LOC110608224
XP_043811624.1	-1.710390393	0.020201582	transcription factor TCP20
XP_021599404.1	-1.707132225	0.035974061	nicotinate-nucleotide pyrophosphorylase [carboxylating], chloroplastic isoform X1
XP_043809492.1	-1.697907197	0.024225439	calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X7
XP_021616107.1	-1.697621033	0.006263277	probable serine/threonine-protein kinase At1g54610
XP_021628563.1	-1.697118164	0.008470589	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like isoform X1
XP_021610637.1	-1.680031686	0.00882466	acyltransferase-like protein At3g26840, chloroplastic isoform X1
XP_021605876.1	-1.677559544	0.041226384	coatomer subunit beta-1
XP_021594466.1	-1.649878311	0.006817754	probable disease resistance protein At4g27220
XP_021609492.1	-1.63130859	0.028442291	dof zinc finger protein DOF3.1
XP_021598123.1	-1.631095921	0.033171309	triose phosphate/phosphate translocator, chloroplastic isoform X2
XP_021628066.1	-1.626396296	0.011333103	phytochrome-associated serine/threonine-protein phosphatase isoform X2
XP_043806021.1	-1.620621302	0.002180642	uncharacterized protein LOC110599817
XP_043807602.1	-1.615688708	0.002965038	linoleate 13S-lipoxygenase 3-1, chloroplastic-like isoform X1
XP_021616403.1	-1.596760409	0.042506236	protection of telomeres protein 1a isoform X1
XP_021597570.1	-1.59652124	0.013092064	uncharacterized protein LOC110603890 isoform X2

XP_021602346.1	-1.580266937	0.009817872	cyclin-D4-2
XP_021624139.1	-1.578015078	0.021568947	uncharacterized protein LOC110623484
XP_043807440.1	-1.568619068	0.004034942	disease resistance protein RPS2 isoform X2
XP_021620878.1	-1.560704945	0.001843924	60S ribosomal protein L18-2
XP_021633499.1	-1.55370553	0.029887535	homeobox-leucine zipper protein HDG2 isoform X1
XP_021591795.1	-1.552530568	0.023739314	protein decapping 5
XP_043812838.1	-1.54906086	0.012710393	uncharacterized protein LOC110615637 isoform X1
XP_021602326.1	-1.544177459	0.013835692	suppressor of disruption of TFIIIS
XP_043807437.1	-1.540631864	0.006917201	disease resistance protein At4g27190 isoform X1
XP_021610976.1	-1.533533463	0.022521318	transcription factor 25
XP_043809378.1	-1.529642025	0.006440069	abscisic acid 8'-hydroxylase 2 isoform X1
XP_021602336.1	-1.528296367	0.015349397	transmembrane protein 18
XP_021620458.1	-1.525962024	0.002588474	folylpolyglutamate synthase isoform X1
XP_021620459.1	-1.506321763	0.001859883	folylpolyglutamate synthase isoform X2
XP_043814875.1	-1.502448538	0.001565076	folylpolyglutamate synthase isoform X3
XP_043812813.1	-1.501756329	0.018484911	ARM REPEAT PROTEIN INTERACTING WITH ABF2-like isoform X1
XP_021620461.1	-1.501487489	0.001672215	folylpolyglutamate synthase isoform X3
XP_043809132.1	1.502200777	0.040478889	MLO-like protein 1 isoform X3
XP_043807862.1	1.514691422	0.028568301	uncharacterized vacuolar membrane protein YML018C isoform X3
XP_021616321.1	1.526983686	0.049309452	FGGY carbohydrate kinase domain-containing protein isoform X2
XP_043812220.1	1.534750952	0.007233689	AP-2 complex subunit alpha-1 isoform X5
XP_021616319.1	1.5484341	0.039229946	ribulose-phosphate 3-epimerase, chloroplastic isoform X2
XP_043808977.1	1.571384637	0.02183673	protein DETOXIFICATION 27 isoform X1
XP_021623529.1	1.581872547	0.017695294	B3 domain-containing transcription repressor VAL2 isoform X2
XP_043810022.1	1.587953578	0.010085464	transcription factor bHLH110 isoform X3
XP_043815403.1	1.591050468	0.027435687	uncharacterized protein LOC110622260

XP_021631954.1	1.603997073	0.031484356	SPX and EXS domain-containing protein 1 isoform X1
XP_043817550.1	1.622595903	2.60E-05	uncharacterized protein LOC110626004
XP_043811811.1	1.626616856	0.031317313	cell division control protein 48 homolog B isoform X4
XP_021609323.1	1.641104466	0.001464659	AP-2 complex subunit alpha-1 isoform X4
XP_021622616.1	1.656398245	0.046401288	AP-2 complex subunit alpha-1 isoform X4
XP_021594716.1	1.665651938	0.013450423	translationally-controlled tumor protein homolog isoform X2
XP_021598431.1	1.706738998	0.023158018	translationally-controlled tumor protein homolog isoform X2
XP_021601213.1	1.709634708	0.01667079	stress response protein NST1
XP_021623209.1	1.719714726	0.016330058	RRP12-like protein isoform X3
XP_021601212.1	1.72257926	0.018876669	ubiquitin carboxyl-terminal hydrolase MINDY-3
XP_021593984.1	1.745935685	0.017382534	uncharacterized protein LOC110601229
XP_043815353.1	1.769538132	0.029461806	probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC
XP_021629709.1	1.772600103	9.03E-07	uncharacterized protein LOC110627674
XP_021613367.1	1.774296256	0.046585304	protein PHOSPHATE-INDUCED 1
XP_021613044.1	1.781448395	0.003688297	uncharacterized protein LOC110615495
XP_021609753.1	1.793241154	0.040676071	uncharacterized protein LOC110613110
XP_021601500.2	1.8091985	0.036497438	DIS3-like exonuclease 2 isoform X3
XP_043817342.1	1.812800522	0.004666104	LOW QUALITY PROTEIN: receptor-like protein 56
XP_021632247.1	1.822919995	3.79E-08	mitochondrial import receptor subunit TOM7-1
XP_021633693.1	1.823919191	0.004649823	ethylene-responsive transcription factor ESR2
XP_021613043.1	1.830534562	0.002664367	glycine--tRNA ligase, chloroplastic/mitochondrial 2
XP_043815279.1	1.832786696	0.001074844	LOW QUALITY PROTEIN: probable LRR receptor-like serine/threonine-protein kinase At3g47570
XP_021611102.1	1.833067186	0.02196312	protein ELC-like
XP_043817344.1	1.840124803	0.006297547	receptor like protein 21
XP_021613236.1	1.855255557	0.006806569	metal-nicotianamine transporter YSL3
XP_021600044.1	1.886082325	0.021907887	protein DMR6-LIKE OXYGENASE 2

XP_021595365.1	1.903462598	0.000149934	RAN GTPase-activating protein 2 isoform X2
XP_021622301.1	1.920694091	0.007364019	putative DNA (cytosine-5)-methyltransferase CMT1 isoform X1
XP_021621609.1	1.924661107	0.000568259	protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 1
XP_043812547.1	1.92771411	3.55E-05	inactive glucose-1-phosphate adenylyltransferase small subunit 2, chloroplastic isoform X1
XP_021616080.1	1.932629229	0.024413812	uncharacterized protein LOC110617533
XP_043814802.1	1.948677162	0.001788178	uncharacterized protein LOC122724336
XP_043809385.1	1.956725819	0.047919842	40S ribosomal protein S29-like
XP_021616082.1	1.960385921	0.01852053	uncharacterized protein LOC110617533
XP_021595091.1	1.975808553	0.000265846	cyclin-dependent kinase inhibitor 5 isoform X4
XP_043809384.1	2.006567927	0.044785138	40S ribosomal protein S29-like
XP_021611428.1	2.023570894	0.037206461	dehydration-responsive element-binding protein 2D
XP_043815258.1	2.024965668	0.018500365	ATP-dependent zinc metalloprotease FTSH 7, chloroplastic isoform X3
XP_021622606.1	2.031211455	0.012777476	lectin-domain containing receptor kinase VI.3
XP_043810051.1	2.036608372	0.028610503	putative pre-16S rRNA nuclease isoform X2
XP_021614178.1	2.045329799	0.015508747	ATP-dependent zinc metalloprotease FTSH 9, chloroplastic isoform X4
XP_021618855.1	2.050350434	0.008245809	uncharacterized protein LOC110619639
XP_043810737.1	2.080172649	0.021967058	callose synthase 3 isoform X2
XP_021630055.1	2.089275338	0.046598758	putative disease resistance protein RGA3
XP_021614952.1	2.090266082	0.015349397	histone H3.2
XP_021608064.1	2.090737898	0.040457757	histone deacetylase 19
XP_021630056.1	2.092946898	0.046598758	FRIGIDA-like protein 3
XP_021610207.1	2.110008831	0.027269677	probable phospholipid-transporting ATPase 4
XP_021607187.1	2.116367615	0.026127905	casein kinase 1-like protein 1
XP_021622405.1	2.138166322	0.013142823	thioredoxin-like 3-1, chloroplastic
XP_021607189.1	2.141132864	0.027090412	ultraviolet-B receptor UVR8 isoform X2
XP_021625299.1	2.141887999	0.040457757	ABC transporter B family member 25, mitochondrial

XP_021631196.1	2.179117985	0.021859109	probable pectate lyase 5
XP_021602813.1	2.189369132	0.034324173	cytochrome b561 and DOMON domain-containing protein At2g04850
XP_021597443.1	2.20431864	1.23E-07	actin-related protein 2/3 complex subunit 2A isoform X1
XP_021631210.1	2.214168795	0.048842832	cytochrome b561 and DOMON domain-containing protein At5g35735
XP_021601116.2	2.219141419	0.047068921	calcium-dependent protein kinase 29 isoform X2
XP_021599505.1	2.224659033	0.04792422	protein trichome birefringence-like 38
XP_021600980.1	2.233456362	0.000206509	probable protein phosphatase 2C 12
XP_043806024.1	2.241137376	0.009130097	UPF0565 protein C2orf69 homolog isoform X2
XP_021618582.1	2.256022035	0.008997987	protein IQ-DOMAIN 3
XP_021599510.1	2.257431973	0.033744307	plant UBX domain-containing protein 7 isoform X2
XP_021599508.1	2.25829698	0.034686186	senescence-specific cysteine protease SAG39
XP_043806894.1	2.268385315	0.002664367	ABC transporter D family member 1-like isoform X2
XP_021603522.1	2.268683483	0.042025993	calcium-dependent protein kinase 11 isoform X2
XP_021599506.1	2.275229586	0.033744307	50S ribosomal protein L34, chloroplastic
XP_021599509.1	2.275411146	0.033744307	plant UBX domain-containing protein 7 isoform X1
XP_021617860.1	2.297533856	0.019549317	alpha-L-fucosidase 2 isoform X1
XP_043813209.1	2.306281987	0.024225439	calcium-transporting ATPase 10, plasma membrane-type
XP_021601114.2	2.317086622	0.025800659	calcium-dependent protein kinase 29 isoform X1
XP_021622382.1	2.321818882	0.030726705	50S ribosomal protein L18
XP_021612281.1	2.349340743	0.041658652	RING-H2 finger protein ATL47
XP_021596081.1	2.366558481	0.036226088	glucan endo-1,3-beta-glucosidase 1
XP_021599511.1	2.372120637	0.04792422	probable ADP-ribosylation factor GTPase-activating protein AGD8 isoform X1
XP_043812516.1	2.383679185	0.024500612	RING-H2 finger protein ATL47
XP_021633956.1	2.386830932	0.008770958	uncharacterized protein LOC110630714 isoform X1
XP_021607860.1	2.389352043	0.033744307	cyclin-dependent kinase F-1
XP_021592562.1	2.432753137	0.007233689	tetraspanin-8

XP_043817060.1	2.437506363	0.0485857	putative receptor-like protein kinase At3g47110
XP_021596692.1	2.49268282	0.00261909	TLC domain-containing protein 4-B isoform X1
XP_021627141.1	2.495871299	0.045992976	putative Peroxidase 48
XP_043806601.1	2.507149828	0.009817872	uncharacterized protein LOC110630714 isoform X3
XP_021601113.2	2.512574272	0.015508747	L-ascorbate oxidase homolog
XP_021600979.1	2.553565713	5.70E-06	probable protein phosphatase 2C 12
XP_043812715.1	2.575538066	4.65E-05	uncharacterized protein LOC122723683
XP_021604087.1	2.576793906	0.026906923	eukaryotic translation initiation factor 5
XP_021597227.1	2.603474942	0.03980587	uncharacterized protein LOC110603577 isoform X2
XP_021606614.1	2.618551306	0.001018081	uncharacterized protein LOC110610847
XP_021627838.1	2.622306926	1.41E-05	transportin-1 isoform X1
XP_021633630.1	2.636675675	0.00239488	ras-related protein Rab11D
XP_021605824.1	2.720468683	0.039324843	acyl-lipid (9-3)-desaturase
XP_021594352.1	2.728986951	0.016330058	SWI/SNF complex subunit SWI3D isoform X2
XP_021631934.2	2.787154419	0.001046019	tyrosine-protein phosphatase DSP1 isoform X1
XP_021634395.1	2.788553437	0.032974918	F-box/kelch-repeat protein At1g22040
XP_021634668.1	2.79796368	0.015644184	uncharacterized protein LOC110631225 isoform X2
XP_043807514.1	2.807387393	0.006297547	dymeclin isoform X3
XP_021624125.1	2.814450581	0.049149658	uncharacterized protein LOC110623473 isoform X1
XP_021614242.1	2.822068423	0.000144423	F-box protein At1g47056
XP_021614319.1	2.824668327	0.000759844	pentatricopeptide repeat-containing protein At2g46050, mitochondrial
XP_043809888.1	2.838908468	0.002135826	bifunctional adenosine 5'-phosphosulfate phosphorylase/adenylylsulfatase HINT4 isoform X2
XP_021610345.1	2.869190634	0.012800971	pleiotropic drug resistance protein 1
XP_021632345.1	2.895504486	0.039842762	50S ribosomal protein L30
XP_021603156.1	2.91371393	0.004360182	BTB/POZ domain-containing protein At1g04390 isoform X10
XP_043805324.1	2.926908168	0.000199138	pupal cuticle protein 36-like, partial

XP_021603150.1	2.937326518	0.003211768	BTB/POZ domain-containing protein At1g04390 isoform X4
XP_021606607.2	2.937505737	0.00037587	AT-hook motif nuclear-localized protein 20, partial
XP_021606051.1	2.939223638	0.033744307	uncharacterized protein LOC110610438 isoform X2
XP_043811511.1	2.952955055	0.014685071	uncharacterized protein LOC122723432
XP_021603152.1	2.96881081	0.002149176	BTB/POZ domain-containing protein At1g04390 isoform X6
XP_043813064.1	2.977241309	0.002664367	E3 ubiquitin-protein ligase UPL2 isoform X1
XP_043807847.1	2.978153662	0.0003548	pyruvate kinase, cytosolic isozyme isoform X1
XP_043805313.1	2.996289573	0.0006798	uncharacterized protein LOC122721522
XP_021603961.1	3.020856061	0.002664367	uncharacterized protein LOC110608978 isoform X1
XP_043805206.1	3.044834356	0.000253037	uncharacterized protein LOC110611039 isoform X3
XP_021592984.1	3.060790996	0.026644961	plant intracellular Ras-group-related LRR protein 6
XP_043807904.1	3.065343432	0.041106922	protein NAP1 isoform X2
XP_021596102.1	3.073721098	0.040676071	protein NAP1 isoform X1
XP_043810555.1	3.093453759	0.029444559	uncharacterized protein LOC110610757 isoform X2
XP_021618719.1	3.107365564	0.006169558	protein MID1-COMPLEMENTING ACTIVITY 1 isoform X4
XP_021620367.1	3.205304216	0.000206509	pentatricopeptide repeat-containing protein At2g41720 isoform X4
XP_021622596.1	3.232860049	0.000185996	calmodulin-binding protein 25
XP_021621981.1	3.244662989	0.028485072	vacuolar cation/proton exchanger 3 isoform X1
XP_021619315.1	3.26093995	0.000206509	heavy metal-associated isoprenylated plant protein 39 isoform X1
XP_021619291.1	3.274208539	0.000202424	probable methyltransferase PMT27
XP_021619302.1	3.274210605	0.000202424	protein SHI RELATED SEQUENCE 1
XP_021620344.1	3.305187642	0.020201582	uncharacterized protein LOC110620786 isoform X1
XP_043811631.1	3.333871248	0.028429752	uncharacterized protein LOC110613056
XP_021609670.1	3.339239278	0.028429752	uncharacterized protein LOC110613056
XP_021619161.1	3.370939794	4.82E-08	transcription factor bHLH140
XP_021609076.1	3.474123613	0.021204215	uncharacterized protein LOC110612606

XP_043808617.1	3.50862503	0.041388133	3-isopropylmalate dehydratase large subunit-like
XP_021634407.1	3.515892196	0.020201582	uncharacterized protein LOC110631018 isoform X1
XP_021634410.1	3.517561898	0.020201582	serine/threonine-protein kinase AFC2 isoform X2
XP_021613334.1	3.527317698	0.00023127	uncharacterized protein LOC110615649
XP_021622028.1	3.537809645	0.000560818	pyruvate kinase 1, cytosolic isoform X1
XP_043816422.1	3.58778831	0.00635383	uncharacterized protein LOC110622321 isoform X3
XP_021622029.1	3.611484831	0.000599413	transducin beta-like protein 3 isoform X1
XP_021595771.1	3.67182688	0.038489548	MLP-like protein 43
XP_021595666.1	3.799404989	0.019408006	choline transporter protein 1 isoform X1
XP_021603731.1	3.827019124	0.009510722	basic leucine zipper 43
XP_021617446.1	3.854121819	4.76E-10	regulator of nonsense transcripts UPF2
XP_043806251.1	3.869243871	0.000110527	glyceraldehyde-3-phosphate dehydrogenase GAPCP2, chloroplastic isoform X2
XP_021634307.1	3.89375843	0.008119318	heterogeneous nuclear ribonucleoprotein H2 isoform X3
XP_021628071.1	3.957224627	0.047855577	ATP-dependent DNA helicase DDX11 isoform X1
XP_043806374.1	3.986666866	0.007233689	heterogeneous nuclear ribonucleoprotein F isoform X2
XP_021621455.1	3.988333637	0.009817872	NAC domain-containing protein 7
XP_021623045.1	4.007716878	0.000306506	uncharacterized protein LOC110622744
XP_021618339.1	4.020712353	0.028429752	malate dehydrogenase [NADP], chloroplastic
XP_021621465.1	4.021309813	0.008119318	probable calcium-binding protein CML46
XP_021618341.1	4.02496967	0.028356259	malate dehydrogenase [NADP], chloroplastic
XP_043813967.1	4.04480265	0.007507316	auxin response factor 6 isoform X3
XP_021634306.2	4.053430854	0.000909639	LOW QUALITY PROTEIN: zinc finger CCCH domain-containing protein 56-like
XP_021614794.1	4.07471439	0.003069391	heme-binding-like protein At3g10130, chloroplastic isoform X3
XP_043813966.1	4.147547006	0.004002446	auxin response factor 21 isoform X2
XP_021617691.1	4.149043899	0.004113624	structure-specific endonuclease subunit slx1 isoform X1
XP_021617690.1	4.162021965	0.004034942	mitogen-activated protein kinase kinase kinase 18

XP_021621903.1	4.283160749	0.012900324	protein RETICULATA-RELATED 3, chloroplastic
XP_021624249.1	4.332652594	0.023565294	tubulin-folding cofactor B
XP_021633704.1	4.362790023	4.76E-10	thioredoxin 1
XP_021606013.1	4.379288585	0.012053854	gamma-glutamyl hydrolase 2 isoform X5
XP_021609653.1	4.415844611	0.029444559	60S ribosomal protein L30
XP_021607257.1	4.418090169	0.038154765	protein S-acyltransferase 10 isoform X1
XP_021592615.1	4.450382889	0.03770005	calcium-dependent protein kinase 8 isoform X1
XP_043809759.1	4.452015413	3.42E-06	uncharacterized protein LOC122723072
XP_021629405.1	4.50332257	0.000160012	APO protein 4, mitochondrial isoform X1
XP_043806250.1	4.532037438	0.006458113	glyceraldehyde-3-phosphate dehydrogenase GAPCP2, chloroplastic isoform X1
XP_043809248.1	4.613592549	0.002364351	disease resistance protein RPM1 isoform X5
XP_021609899.1	4.62497575	4.76E-10	LOB domain-containing protein 1
XP_021609897.1	4.635653708	4.76E-10	pentatricopeptide repeat-containing protein At4g02750
XP_021630023.1	4.650143892	0.000202424	photosystem II core complex proteins psbY, chloroplastic
XP_043809249.1	4.654661409	0.001868217	disease resistance protein RPM1 isoform X6
XP_043809247.1	4.656345698	0.001859883	disease resistance protein RPM1 isoform X2
XP_043811024.1	4.690430123	0.033870786	glycine-rich cell wall structural protein-like
XP_021597451.1	4.705880934	0.033744307	uncharacterized protein LOC110603827
XP_021598192.2	4.743918344	0.001565076	uncharacterized protein LOC110604363
XP_021598181.1	4.754164318	0.001486343	uncharacterized protein LOC110604343
XP_021612261.1	4.778928809	0.042399559	calcium-binding protein KIC
XP_021634739.1	4.881829731	0.046298345	23.6 kDa heat shock protein, mitochondrial
XP_043813701.1	4.882913041	0.007348981	uncharacterized protein LOC110617863
XP_021606421.1	4.901298747	0.037854142	major allergen Pru ar 1
XP_021606000.1	4.90503031	1.17E-06	pre-mRNA-processing protein 40C isoform X2
XP_021606533.1	4.914513272	0.043130163	protein AGENET DOMAIN (AGD)-CONTAINING P1 isoform X3

XP_021627587.1	5.143983896	0.018521858	actin-depolymerizing factor 5
XP_021620704.1	5.169099212	0.000233916	uncharacterized protein LOC110621020
XP_021619973.1	5.172805951	0.035616373	B3 domain-containing protein At2g36080
XP_021622791.1	5.279815764	0.001550831	CASP-like protein 2B1 isoform X3
XP_021603242.1	5.328604578	0.023158018	pentatricopeptide repeat-containing protein At2g26790, mitochondrial
XP_043805936.1	5.347794598	4.76E-10	copper-transporting ATPase HMA4 isoform X1
XP_021621558.1	5.380303999	0.006190437	rRNA 2'-O-methyltransferase fibrillarin
XP_043810597.1	5.439205546	0.003529706	DNA-directed RNA polymerases II and IV subunit 5A isoform X1
XP_043817023.1	5.52264469	0.011250548	heat stress transcription factor A-6b isoform X1
XP_021625514.1	5.582812617	0.018289545	2-oxoglutarate dehydrogenase, mitochondrial
XP_021610946.1	5.612622502	0.027068623	uncharacterized protein Osl_027940
XP_043811657.1	5.634379571	4.21E-05	kinesin-like protein KIN-13B isoform X3
XP_021603222.1	5.652785532	0.009817872	pentatricopeptide repeat-containing protein At2g26790, mitochondrial
XP_043814252.1	5.794144892	0.008916181	aminoacyl tRNA synthase complex-interacting multifunctional protein 1-like isoform X4
XP_021625198.1	5.808502476	0.002018587	purine permease 3
XP_021620711.1	5.843461217	0.000206509	tRNase Z TRZ4, mitochondrial isoform X4
XP_043813719.1	5.847980849	0.018342822	uncharacterized protein LOC110617918
XP_043815938.1	5.876751921	0.000827378	probable inactive leucine-rich repeat receptor-like protein kinase At3g03770
XP_021623201.1	5.916531399	0.000784139	probable inactive leucine-rich repeat receptor-like protein kinase At3g03770
XP_021602310.1	6.016827492	0.006805074	probable inactive purple acid phosphatase 28
XP_021607564.1	6.244756155	0.019408006	uncharacterized protein LOC110611490
XP_021627633.1	6.283392559	0.018500365	glyoxylate/hydroxypyruvate/pyruvate reductase 2KGR
XP_021624112.1	6.321968762	0.012979854	probable linoleate 9S-lipoxygenase 5
XP_021592259.1	6.360422451	0.024413812	HIPL1 protein isoform X1
XP_021615023.1	6.366192711	0.007766897	60S ribosomal protein L34
XP_021615764.1	6.486145331	0.00789433	60S ribosomal protein L34

XP_043817061.1	6.5415463	0.000825513	monooxygenase 2-like
XP_043805332.1	6.607017898	0.00459693	aquaporin SIP1-1-like
XP_021592887.1	6.641328984	1.18E-05	uncharacterized protein LOC110600355
XP_021618435.1	6.788296973	0.017233382	sm-like protein LSM4
XP_043809984.1	6.799879349	0.035746397	pre-mRNA splicing factor SR-like 1 isoform X2
XP_021600889.2	6.849967407	0.000299786	tetratricopeptide repeat protein SKI3 isoform X2
XP_043814187.1	7.150106083	0.007325852	uroporphyrinogen decarboxylase, chloroplastic isoform X3
XP_021629064.1	7.204237589	0.02329874	histone H2B
XP_021633970.1	7.259925357	0.001944279	probable WRKY transcription factor 27
XP_021592945.1	7.394640161	0.006715491	26S proteasome non-ATPase regulatory subunit 6 homolog
XP_043815344.1	7.467867632	0.045206033	flagellar attachment zone protein 1
XP_043816260.1	7.474033832	0.003066192	pentatricopeptide repeat-containing protein At1g63330-like
XP_021622220.1	7.764481909	0.033744307	bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic
XP_021608602.1	7.768672002	0.001805264	protein translation factor SUI1 homolog 2
XP_021620132.1	7.81638366	0.004824149	transcription factor ORG2 isoform X1
XP_021615355.1	8.458403162	0.009686808	uncharacterized protein LOC110617065 isoform X2
XP_021592749.1	9.087829831	3.46E-06	HVA22-like protein a
XP_043818240.1	9.240525768	0.0076426	uncharacterized protein LOC122725266
XP_021591800.1	12.40967319	0.030866435	uncharacterized protein LOC110599632 isoform X3
XP_021611560.1	12.58698199	0.001565076	uncharacterized protein LOC110614349
XP_021604091.1	14.38946954	0.00599866	integrator complex subunit 3 homolog isoform X1
XP_043813615.1	22.50270046	0.008282827	uncharacterized protein LOC110618294 isoform X5
XP_021618399.1	24.72725801	8.07E-08	LOB domain-containing protein 21

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protein ID	log₂FC	adjusted p-value	protein function
XP_021601174.1	-9.129930369	0.0288271	SET and MYND domain-containing protein 4 isoform X1
XP_043804899.1	-5.922453427	0.013210959	pentatricopeptide repeat-containing protein At4g33990
XP_021632909.1	-3.857832488	0.037180632	uncharacterized protein LOC110629969 isoform X1
XP_021624426.1	-3.271698077	0.045131026	receptor-like protein kinase ANXUR1 isoform X2
XP_043815392.1	-3.271698077	0.045131026	ubiquitin-like protein 5
XP_021633476.1	-2.43767671	0.031227982	probable galacturonosyltransferase 13 isoform X1
XP_021633485.1	-2.426460107	0.033329795	probable galacturonosyltransferase 14 isoform X2
XP_021633501.1	-2.397333465	0.034134649	probable galacturonosyltransferase 14 isoform X4
XP_021595705.1	-1.779997895	0.03319091	60S ribosomal protein L32-1
XP_021610637.1	-1.653287287	0.047570595	acyltransferase-like protein At3g26840, chloroplastic isoform X1
XP_021629067.1	-1.600349442	0.03051115	disease resistance protein RPV1
XP_021593760.1	1.524737021	0.008584714	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8-B, mitochondrial
XP_021625428.1	1.533601922	0.045131026	FT-interacting protein 1
XP_021633967.1	1.631666844	0.004247313	uncharacterized protein LOC110630722 isoform X2
XP_021633869.2	1.810464785	0.01438457	uncharacterized protein slr0889
XP_021611733.1	1.929764706	0.004247313	glutathione S-transferase
XP_021613044.1	1.952344033	0.005914539	uncharacterized protein LOC110615495
XP_043812715.1	1.953375217	0.03319091	uncharacterized protein LOC122723683
XP_021611735.1	1.996048021	0.003461052	putative UDP-rhamnose:rhamnosyltransferase 1
XP_021613043.1	2.012916028	0.004247313	glycine--tRNA ligase, chloroplastic/mitochondrial 2
XP_021593984.1	2.179724506	0.005914539	uncharacterized protein LOC110601229
XP_021603132.1	2.244260554	0.022921225	uncharacterized protein LOC110608230
XP_043805669.1	2.286989784	0.013210959	uncharacterized protein LOC110629996 isoform X2
XP_021606614.1	2.288804323	0.037180632	uncharacterized protein LOC110610847

XP_021624442.1	2.299028349	0.013210959	secoisolariciresinol dehydrogenase
XP_021602667.1	2.634224691	0.037869556	pumilio homolog 5 isoform X2
XP_043808626.1	2.833965421	0.038668226	protein farnesyltransferase subunit beta-like isoform X5
XP_021614035.1	3.018778775	0.018866683	uncharacterized protein LOC110616039
XP_043810508.1	3.155352675	0.042114267	rRNA N6-adenosine-methyltransferase METTL5 isoform X2
XP_021620367.1	3.170470508	0.002877917	pentatricopeptide repeat-containing protein At2g41720 isoform X4
XP_043810127.1	3.408598785	0.037180632	calcium-dependent protein kinase 17
XP_043809081.1	3.452826744	0.045131026	polygalacturonase-like
XP_021623045.1	3.755033306	0.01094866	uncharacterized protein LOC110622744
XP_021597227.1	3.775899665	0.004019333	uncharacterized protein LOC110603577 isoform X2
XP_021615301.1	3.827516295	0.037180632	recQ-mediated genome instability protein 1
XP_043808398.1	4.195748128	0.045131026	putative uncharacterized protein DDB_G0290521
XP_021620704.1	4.274584398	0.03051115	uncharacterized protein LOC110621020
XP_021614915.1	4.569132678	0.042114267	RING-H2 finger protein ATL13
XP_021614484.1	4.705739178	0.018699818	uncharacterized protein LOC110616447
XP_021614485.1	4.705739178	0.018699818	uncharacterized protein LOC110616448
XP_021615428.1	5.234302718	0.017079498	mannosyl-oligosaccharide 1,2-alpha-mannosidase MNS1 isoform X1
XP_043809304.1	5.62842913	0.004824222	uncharacterized protein LOC110606542 isoform X2
XP_021604105.1	5.702784947	1.72E-05	bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT
XP_021630782.1	6.730750073	0.014216764	F-box/kelch-repeat protein At1g67480
XP_021625208.1	7.77123852	0.037180632	protein SEMI-ROLLED LEAF 2
XP_021599566.1	29.86793568	3.09E-16	carboxyl-terminal-processing peptidase 1, chloroplastic isoform X1

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protein ID	log₂FC	adjusted p-value	protein function
XP_021624284.2	-7.473153249	0.017637233	probable pectinesterase 8
XP_043814751.1	-6.64754373	0.044716631	germin-like protein subfamily 1 member 13
XP_021605449.1	-5.865595781	0.041049416	GDSL esterase/lipase At1g29670
XP_021608842.1	-5.445716711	0.009702719	peroxidase 24
XP_043817798.1	-5.32811938	0.00282284	U-box domain-containing protein 34, partial
XP_021595994.1	-4.934678837	0.00555184	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2
XP_021594332.1	-4.892162547	0.00282284	loganic acid O-methyltransferase
XP_021606785.1	-4.536182781	0.016196742	thermospermine synthase ACAULIS5
XP_021625069.1	-4.434870572	0.000309844	protein PELPK1
XP_021608957.1	-4.382244462	0.008359984	probable 2-oxoglutarate-dependent dioxygenase AOP1
XP_021618053.1	-4.35938936	0.00028779	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK3
XP_021595870.1	-4.215402101	0.001180807	ABC transporter G family member 10
XP_021608704.1	-4.194663794	0.020786883	peroxidase 24
XP_021595702.1	-4.138092049	0.000986486	3-ketoacyl-CoA synthase 20
XP_021605390.1	-4.093466183	0.01993036	transcription factor MYB93
XP_021613935.1	-4.049124268	0.021016524	type IV inositol polyphosphate 5-phosphatase 11
XP_021605595.2	-3.899979759	0.019840668	LOW QUALITY PROTEIN: WRKY transcription factor 22
XP_021614226.1	-3.896807631	0.00282284	probable WRKY transcription factor 43
XP_021606625.1	-3.88339376	0.011002974	pectinesterase QRT1
XP_021601218.1	-3.85186148	0.010514373	aldehyde oxidase GLOX
XP_021616508.2	-3.847549601	0.014319701	putative receptor protein kinase ZmPK1
XP_021627690.1	-3.836518717	0.012713848	putative serine/threonine-protein kinase isoform X2
XP_021600257.2	-3.812338045	0.008005433	dihydroflavonol 4-reductase
XP_021625070.1	-3.790659332	0.000189251	protein PELPK1

XP_021611090.1	-3.778017665	0.001353515	phenylalanine ammonia-lyase isoform X2
XP_021622566.2	-3.758101711	0.000114136	bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic
XP_021627688.1	-3.736793263	0.010292565	putative serine/threonine-protein kinase isoform X1
XP_021611089.1	-3.722545205	0.002494596	phenylalanine ammonia-lyase isoform X1
XP_043817236.1	-3.711631316	0.000366957	protein PELPK1-like
XP_021614132.1	-3.710547312	0.001737978	non-specific lipid transfer protein GPI-anchored 5
XP_021609389.1	-3.701287931	0.014599405	chalcone synthase 2
XP_021594193.1	-3.645446714	0.011551355	probable WRKY transcription factor 31
XP_021618820.1	-3.628372765	0.009616229	protein PELPK1
XP_021609574.2	-3.594284046	0.000685083	omega-hydroxypalmitate O-feruloyl transferase
XP_021605381.1	-3.580348456	0.045040417	non-specific lipid-transfer protein B
XP_021598733.1	-3.567764944	0.00282284	protein SRG1
XP_021595652.1	-3.547315593	0.009893974	non-specific lipid transfer protein GPI-anchored 20
XP_021615183.1	-3.492050233	0.000838685	cytochrome P450 86A1
XP_021618075.1	-3.463244472	0.000685083	protein PELPK1-like
XP_021594194.1	-3.460290615	0.001737978	peroxidase 55
XP_021623956.1	-3.441156265	0.012634712	probable lysophospholipase BODYGUARD 3
XP_021603611.1	-3.437929718	0.005806611	ABC transporter G family member 23
XP_021620403.1	-3.435469533	0.019796159	non-specific lipid-transfer protein 2
XP_021618139.1	-3.435244655	0.002583558	glycerol-3-phosphate acyltransferase 5
XP_021620078.1	-3.419009758	0.004516191	ABC transporter G family member 20
XP_021619481.1	-3.417599947	0.011271989	germin-like protein subfamily 1 member 13
XP_021593818.1	-3.412618376	0.021706058	probable xyloglucan galactosyltransferase GT17
XP_021631825.2	-3.384529208	0.037497011	flavonoid 3',5'-hydroxylase 2
XP_021616908.1	-3.361754113	0.008743266	stellacyanin
XP_021601982.1	-3.359701158	0.003273873	CASP-like protein 1C1

XP_021618074.1	-3.357629366	0.00282284	protein PELPK1
XP_021592812.1	-3.347680305	0.001180807	peroxidase 11
XP_021616874.1	-3.31268359	0.00757	peroxidase 11
XP_021617732.1	-3.312167759	0.004439647	ABC transporter G family member 6
XP_021621841.1	-3.307582936	0.005218871	cytochrome b561 and DOMON domain-containing protein At5g47530
XP_021614044.1	-3.295338408	0.005559579	non-specific lipid transfer protein GPI-anchored 5
XP_021625424.1	-3.293688693	0.014978048	protein PELPK1
XP_043813659.1	-3.289395645	0.008807028	putative receptor protein kinase ZmPK1
XP_021627812.1	-3.286805385	0.003728645	omega-hydroxypalmitate O-feruloyl transferase
XP_021625423.1	-3.285058249	0.006025954	protein PELPK1
XP_021625302.1	-3.283732333	0.001492269	ethylene-responsive transcription factor WRI1
XP_021608749.1	-3.279100654	0.029118467	CASP-like protein 1B1
XP_021615437.1	-3.271997411	0.002778894	uncharacterized protein LOC110617135
XP_021630581.1	-3.25792174	0.036637411	leucoanthocyanidin dioxygenase
XP_021615448.1	-3.244757322	0.041049416	omega-hydroxypalmitate O-feruloyl transferase
XP_021620064.1	-3.241649224	0.047646453	uncharacterized protein LOC110620577
XP_021607718.1	-3.238039731	0.005080604	non-specific lipid transfer protein GPI-anchored 16
XP_021607962.1	-3.237056109	0.004132647	receptor like protein kinase S.2
XP_021602139.1	-3.214123524	0.018777378	NAC domain-containing protein 100
XP_043808304.1	-3.208470792	0.034728764	D-galacturonate reductase isoform X1
XP_021596793.1	-3.20171071	0.01433689	transcription factor MYB102
XP_021618819.1	-3.194385383	0.007705463	serine carboxypeptidase-like 28
XP_043814525.1	-3.190459056	0.016543849	protein PELPK1 isoform X2
XP_021617075.1	-3.188028195	0.003730134	heptahelical transmembrane protein 1
XP_021632540.1	-3.181328947	0.001180807	GDSL esterase/lipase At2g23540
XP_021591842.1	-3.177816995	0.001693266	omega-hydroxypalmitate O-feruloyl transferase

XP_021632303.1	-3.174736897	0.001190885	septum-promoting GTP-binding protein 1
XP_021618150.1	-3.154839159	0.004048453	protein PELPK1
XP_021626402.1	-3.153677142	0.002778894	protein PELPK1
XP_021625581.1	-3.138641259	0.047646453	GDSL esterase/lipase At5g03610
XP_021622172.1	-3.136916497	0.002561865	glycerol-3-phosphate 2-O-acyltransferase 6
XP_021621548.1	-3.133250466	0.00347267	uncharacterized protein LOC110621583
XP_021632542.1	-3.125999209	0.016895315	stemmadenine O-acetyltransferase
XP_021611580.1	-3.12498385	0.023016821	probable carboxylesterase 5
XP_021612474.1	-3.124743684	0.005806611	probable WRKY transcription factor 43
XP_021603146.1	-3.113148828	0.002778894	stearoyl-[acyl-carrier-protein] 9-desaturase 6, chloroplastic
XP_021598637.1	-3.111824446	0.008807028	MLP-like protein 28
XP_043804597.1	-3.103657434	0.00304318	rhamnogalacturonate lyase isoform X2
XP_021603659.1	-3.102679933	0.020710681	probable lysophospholipase BODYGUARD 3
XP_021603684.1	-3.08184695	0.044358364	peroxidase 72
XP_021618061.1	-3.063765334	0.029118467	protein PELPK1
XP_021603640.1	-3.063304513	0.000189251	protein DETOXIFICATION 41
XP_021625441.1	-3.059582575	0.006025954	nucleobase-ascorbate transporter 4
XP_043817133.1	-3.058534409	0.008840648	non-specific lipid transfer protein GPI-anchored 15
XP_021615500.2	-3.038520483	0.029118467	LOW QUALITY PROTEIN: G-type lectin S-receptor-like serine/threonine-protein kinase RKS1
XP_021602216.1	-3.038449909	0.033716689	transcription factor MYB92
XP_021621613.1	-3.031150635	0.00829981	respiratory burst oxidase homolog protein A
XP_021633765.1	-3.015353588	0.020710681	patatin-like protein 3
XP_021617615.1	-3.005423384	0.000838685	chalcone isomerase-like protein 2
XP_021602431.1	-3.001207895	0.049364097	probable amidase At4g34880
XP_021619116.1	-2.978884624	0.010802131	gallate 1-beta-glucosyltransferase 84A24
XP_021597983.1	-2.971690645	0.010905113	phospholipase A1-IIgamma

XP_021600935.1	-2.9638886	0.014722135	transcription factor RAX3
XP_021611180.1	-2.962624816	0.045682275	non-specific lipid transfer protein GPI-anchored 30
XP_021598238.1	-2.960392434	0.018777378	protein JINGUBANG
XP_021627705.1	-2.958976331	0.007865678	cytochrome P450 86B1
XP_043804542.1	-2.946743023	0.045682275	uncharacterized protein LOC122721328
XP_021617395.1	-2.946441656	0.000333211	expansin-A8
XP_021618060.1	-2.942897308	0.019757608	protein PELPK1
XP_043816639.1	-2.930738132	0.018521701	protein PELPK2-like
XP_021608748.1	-2.930047905	0.008743266	uncharacterized protein LOC110612305
XP_021610640.1	-2.923633366	0.042327828	protein NODULATION SIGNALING PATHWAY 1
XP_021618918.1	-2.919098626	0.036699301	protein SOB FIVE-LIKE 5
XP_021615451.1	-2.9045828	0.007865678	GDSL esterase/lipase At1g74460
XP_021623015.1	-2.903782094	0.010859433	epoxide hydrolase 4
XP_021610027.1	-2.898096989	0.009349182	uncharacterized protein LOC110613282
XP_021618132.1	-2.891099997	0.039639845	polygalacturonase QRT2
XP_021618823.1	-2.88781575	0.004439647	NAC domain-containing protein 100
XP_021602531.1	-2.874518284	0.036699301	beta-1,2-xylosyltransferase XYXT1 isoform X4
XP_021630155.1	-2.873261123	0.016944704	coniferyl alcohol acyltransferase
XP_021600654.2	-2.866620037	0.00304318	protein ECERIFERUM 26-like
XP_021631234.1	-2.86408408	0.001293452	zinc finger protein 6
XP_021603552.1	-2.858695539	0.029976029	putative laccase-9
XP_021625416.1	-2.858320696	0.010802131	serine carboxypeptidase-like 18
XP_021630126.1	-2.842052454	0.003381742	E3 ubiquitin-protein ligase APD2
XP_021597588.2	-2.830203008	0.036816745	protein trichome birefringence-like 19
XP_043817637.1	-2.827113809	0.019757608	phosphatidylinositol/phosphatidylcholine transfer protein SFH3 isoform X1
XP_021605137.1	-2.816747166	0.008743266	naringenin,2-oxoglutarate 3-dioxygenase

XP_021598021.1	-2.808112156	0.022139465	exocyst complex component EXO70I
XP_021614037.1	-2.777479109	0.011369801	stress-related protein
XP_021612097.1	-2.770140781	0.004194528	cytochrome P450 86A8
XP_021620832.1	-2.755733824	0.001118941	non-specific lipid transfer protein GPI-anchored 7
XP_021610990.1	-2.751242579	0.00028779	ATPase 10, plasma membrane-type
XP_021611134.1	-2.743381468	0.045682275	transcription factor RAX2
XP_021630889.1	-2.739707636	0.023647909	uncharacterized protein At5g48480
XP_021601802.1	-2.731952863	0.013168506	transcription factor MYB93
XP_021627945.1	-2.730160635	0.019757608	phosphatidylinositol/phosphatidylcholine transfer protein SFH3 isoform X3
XP_021592863.2	-2.706612707	0.018867671	palmitoyl-acyl carrier protein thioesterase, chloroplastic
XP_021626234.1	-2.681403494	0.035068408	linoleate 13S-lipoxygenase 2-1, chloroplastic
XP_021596210.1	-2.680017713	0.00028779	anthocyanidin reductase ((2S)-flavan-3-ol-forming)
XP_021630096.1	-2.661867647	0.021016524	rhamnogalacturonate lyase isoform X1
XP_021627264.1	-2.657168206	0.003044796	chalcone synthase
XP_021628946.1	-2.637809303	0.043150702	transcription factor RAX2
XP_021619906.1	-2.63735286	0.031204632	laccase-7
XP_021623184.1	-2.628871023	0.003730134	4-coumarate--CoA ligase 2
XP_021610002.1	-2.626430727	0.004064858	fatty acyl-CoA reductase 3
XP_021611776.1	-2.602891576	0.017637233	uncharacterized protein LOC110614528
XP_021596563.1	-2.558568897	0.042327828	internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial
XP_021629746.1	-2.547799823	0.015893647	alcohol dehydrogenase 2
XP_021596490.1	-2.517270212	0.036699301	serine/threonine-protein kinase RIPK
XP_021622639.1	-2.508420947	0.02751838	WD repeat-containing protein LWD1 isoform X2
XP_021622638.1	-2.497358172	0.022999873	WD repeat-containing protein LWD2 isoform X1
XP_021634788.1	-2.481744445	0.036816745	GDSL esterase/lipase At1g74460
XP_021598501.1	-2.456382414	0.00948057	probable CoA ligase CCL6

XP_021620730.1	-2.443048846	0.014815678	glutathione S-transferase F9
XP_021627577.1	-2.42653197	0.037076251	xyloglucan endotransglucosylase/hydrolase protein 31
XP_021606999.1	-2.416744916	0.029553003	polygalacturonase QRT3
XP_021592900.1	-2.413923068	0.037497011	probable carboxylesterase 2
XP_043811662.1	-2.394347542	0.042327828	CASP-like protein 1F2
XP_021598604.1	-2.391877146	0.002781254	protein SRG1
XP_021605520.1	-2.350932954	0.036816745	zinc finger protein 6
XP_021612194.1	-2.33981959	0.002716508	phospholipase A1-lgamma1, chloroplastic
XP_021596493.1	-2.335103563	0.007926707	cytochrome P450 86A1
XP_021632282.1	-2.290665182	0.029118467	cysteine proteinase COT44
XP_021612481.1	-2.278201813	0.031672554	GDSL esterase/lipase EXL3
XP_021633426.1	-2.270605738	0.005265574	auxin-induced in root cultures protein 12
XP_021606229.1	-2.258101209	0.022405527	ABC transporter B family member 11
XP_021631476.1	-2.252514999	0.027453759	uncharacterized protein LOC110628963
XP_021601668.1	-2.248802337	0.041049416	uncharacterized protein LOC110606959
XP_021628924.1	-2.233155636	0.045446689	alcohol-forming fatty acyl-CoA reductase
XP_021613248.1	-2.232646065	0.002781254	WRKY transcription factor 23
XP_043805978.1	-2.222620949	0.002778894	scopoletin 8-hydroxylase-like
XP_021607958.1	-2.188031352	0.010802131	transcription factor BHLH42
XP_043810585.1	-2.187688669	0.035068408	probable amino acid permease 7 isoform X2
XP_021617696.1	-2.144739261	0.007926707	laccase-5
XP_021603452.2	-2.120566907	0.023336927	WAT1-related protein At5g47470
XP_043808298.1	-2.110140692	0.033867047	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X4
XP_021599472.1	-2.103808718	0.034128348	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X2
XP_021618646.1	-2.103102927	0.027453759	peroxidase 4
XP_021610472.1	-2.086759593	0.028844595	ABC transporter G family member 29

XP_021598728.1	-2.081761218	0.036543776	oligopeptide transporter 7
XP_021603692.1	-2.071746961	0.014804537	uncharacterized protein LOC110608720
XP_021602464.1	-2.059868631	0.045682275	G-type lectin S-receptor-like serine/threonine-protein kinase B120 isoform X1
XP_021606129.1	-2.011792673	0.029118467	receptor-like protein 7
XP_043807108.1	-2.001960938	0.045682275	non-specific lipid transfer protein GPI-anchored 5
XP_021609221.1	-1.994724344	0.021673923	uncharacterized protein At5g01610
XP_021606400.1	-1.994496707	0.020332458	transcription factor MYB123
XP_021634670.1	-1.980103246	0.026358062	short-chain dehydrogenase TIC 32 B, chloroplastic
XP_021598774.1	-1.97295274	0.030670083	pectin acetylerase 7 isoform X1
XP_043808237.1	-1.969734495	0.029118467	pectin acetylerase 7 isoform X2
XP_021628626.1	-1.953997398	0.026804744	beta-fructofuranosidase, cell wall isozyme isoform X1
XP_021597746.1	-1.914449572	0.002114298	low-temperature-induced cysteine proteinase
XP_021619703.1	-1.886440108	0.041163553	probable aldo-keto reductase 1
XP_021616292.1	-1.87817401	0.032497074	respiratory burst oxidase homolog protein C
XP_021598776.1	-1.840808569	0.048242715	pectin acetylerase 7 isoform X3
XP_021634242.1	-1.809868585	0.007705463	cinnamoyl-CoA reductase-like SNL6
XP_021632101.1	-1.807128753	0.001118941	U-box domain-containing protein 19
XP_021633997.1	-1.796701076	0.004885177	leucoanthocyanidin reductase
XP_021615058.1	-1.753839834	0.031672554	probable galactinol--sucrose galactosyltransferase 6
XP_021601261.1	-1.746256728	0.01993036	pathogenesis-related thaumatin-like protein 3.5
XP_021616288.1	-1.740515438	0.020332458	flavonoid 3'-monooxygenase
XP_021598494.1	-1.738108802	0.049664687	myb family transcription factor MOF1
XP_021612278.1	-1.730547839	0.000838685	protein MIZU-KUSSEI 1
XP_021596544.1	-1.717405768	0.020710681	dehydration-responsive element-binding protein 3
XP_021609079.1	-1.7133348	0.028448258	uncharacterized protein LOC110612609
XP_021628541.1	-1.706379205	0.010802131	subtilisin-like protease SBT1.5

XP_043807618.1	-1.691768579	0.009882157	ent-kaurene synthase TSP4, chloroplastic
XP_021633725.1	-1.681746198	0.048242715	uncharacterized protein LOC110630508
XP_021606660.1	-1.660977911	0.032267143	ethylene-responsive transcription factor RAP2-3
XP_021611817.1	-1.62287453	0.014777977	cyclin-D3-1 isoform X2
XP_021595770.1	-1.617762212	0.038204801	probable protein phosphatase 2C 24
XP_021612913.1	-1.615096475	0.029118467	probable glycerol-3-phosphate acyltransferase 8
XP_021601488.2	-1.603757603	0.040870781	deoxyuridine 5'-triphosphate nucleotidohydrolase
XP_043808508.1	-1.596422281	0.010802131	CBL-interacting serine/threonine-protein kinase 23 isoform X2
XP_021594737.1	-1.596260826	0.002114298	phytosulfokine receptor 2
XP_021610730.1	-1.586700708	0.028448258	phospholipase D alpha 1
XP_021611816.1	-1.584939808	0.018867671	cyclin-D3-1 isoform X1
XP_021609491.1	-1.583131383	0.001415311	protein BIG GRAIN 1-like B
XP_021606909.1	-1.570800092	0.028073593	lachrymatory-factor synthase-like
XP_021599119.1	-1.554880947	0.009879072	CBL-interacting serine/threonine-protein kinase 23 isoform X1
XP_043805992.1	-1.514995483	0.030489787	probable pectate lyase 5
XP_021611260.1	1.502833432	0.016247733	protein LNK3
XP_021618540.1	1.50819662	0.004132647	probable protein phosphatase 2C 63
XP_021598003.1	1.596462726	0.035879125	zinc transporter 4, chloroplastic
XP_021601648.1	1.612625685	0.022139465	transcription factor MYB44
XP_021609595.1	1.627347489	8.12E-05	expansin-like A2
XP_021634042.1	1.628388957	0.027142275	heat stress transcription factor B-2b
XP_021617424.1	1.638355885	0.037936719	anthranilate synthase alpha subunit 1, chloroplastic
XP_021620493.1	1.71838444	0.031672554	uncharacterized protein LOC110620867 isoform X1
XP_021625369.1	1.733479625	0.045682275	putative serine/threonine-protein kinase-like protein CCR3
XP_021594496.2	1.738412159	0.008807028	uncharacterized protein LOC110601610, partial
XP_021607112.1	1.758498602	0.03680156	uncharacterized protein LOC110611231

XP_021615465.1	1.779792373	0.027437738	zinc finger CCCH domain-containing protein 55 isoform X1
XP_021624777.1	1.830614758	0.00553974	uncharacterized protein LOC110624032
XP_021629903.1	1.881089333	0.029157173	probable trehalose-phosphate phosphatase J
XP_021628680.1	1.918428454	0.047646453	uncharacterized protein LOC110626856
XP_021633848.2	1.921991687	0.003730134	heavy metal-associated isoprenylated plant protein 7
XP_021615468.1	1.941598738	0.014649773	zinc finger CCCH domain-containing protein 55 isoform X2
XP_043813283.1	1.960469013	0.014648913	zinc finger CCCH domain-containing protein 55 isoform X3
XP_021606610.1	1.962579064	0.003896555	uncharacterized protein LOC110610844
XP_021607213.1	1.991376418	0.038692578	BURP domain protein RD22 isoform X2
XP_043810482.1	2.014283034	0.034128348	BURP domain protein RD22 isoform X3
XP_021609857.1	2.023735716	0.040118842	protein NRT1/ PTR FAMILY 5.4
XP_021600549.2	2.095306642	0.037720293	blue copper protein
XP_021627753.1	2.109354104	6.57E-06	inositol oxygenase 1
XP_021613577.1	2.143617363	0.003896555	uncharacterized protein LOC110615787
XP_021604024.1	2.29399803	0.049968205	receptor-like protein kinase FERONIA
XP_021634319.1	2.32503577	0.040101332	probable xyloglucan endotransglucosylase/hydrolase protein 23
XP_021602134.1	2.326667511	0.018777378	protein EXORDIUM-like 5
XP_021634322.1	2.387004255	0.032270508	probable xyloglucan endotransglucosylase/hydrolase protein 23
XP_021619675.1	2.427918268	0.049968205	DNA ligase 1 isoform X2
XP_021602965.1	2.436079711	0.0042993	vascular-related unknown protein 1
XP_043814735.1	2.447934927	0.00948057	heavy metal-associated isoprenylated plant protein 7
XP_021620436.1	2.462621115	0.007865678	WAT1-related protein At2g37460
XP_043812755.1	2.517861316	0.001693266	calmodulin-like protein 2
XP_021619674.1	2.523743753	0.02600125	DNA ligase 1 isoform X1
XP_021615407.1	2.532998842	0.036574314	bidirectional sugar transporter SWEET10
XP_021625528.1	2.538192664	0.024264119	WAT1-related protein At1g25270 isoform X2

XP_021595709.1	2.553878692	0.00304318	MLP-like protein 28
XP_021618142.1	2.562021077	0.005388921	BURP domain-containing protein BNM2A
XP_021634233.1	2.605714861	0.014150996	cytochrome P450 78A5
XP_021593785.1	2.642039348	0.045682275	uncharacterized protein LOC110601082
XP_021629414.1	2.652400727	0.015215657	WAT1-related protein At5g64700
XP_021603607.1	2.701028532	0.026482516	ethylene-responsive transcription factor ERF014
XP_021600061.1	2.710024569	0.000986486	protein PHOSPHATE-INDUCED 1
XP_021627268.1	2.731887638	0.018086613	rust resistance kinase Lr10
XP_021605177.1	2.753768465	0.003050499	ABC transporter G family member 11
XP_021609395.1	2.80680681	0.009834341	probable pectinesterase/pectinesterase inhibitor 35
XP_021632114.1	2.859541125	0.00042938	transcription activator GLK1
XP_043811061.1	2.894844828	0.013144623	glycine-rich cell wall structural protein
XP_021593692.1	2.906348954	0.036699301	epidermis-specific secreted glycoprotein EP1
XP_043816693.1	2.933947537	0.007986324	abscisic acid 8'-hydroxylase CYP707A2-like
XP_021619046.1	2.953629478	0.00028779	uncharacterized protein LOC110619799
XP_021593980.1	3.026856071	0.019744368	epidermis-specific secreted glycoprotein EP1
XP_021632193.1	3.084057869	0.044881354	uncharacterized protein LOC110629501
XP_043816563.1	3.148249972	0.024264119	abscisic acid 8'-hydroxylase CYP707A2
XP_021601100.1	3.159132135	0.007705463	protein PHOSPHATE-INDUCED 1
XP_021601617.1	3.223892713	0.039972668	protein PHOSPHATE-INDUCED 1
XP_043808081.1	3.307782537	0.042957261	metal transporter Nramp5-like
XP_021614983.1	3.348598873	0.013168506	cytochrome P450 78A5
XP_021629932.1	3.356680082	0.034128348	probable xyloglucan endotransglucosylase/hydrolase protein 33
XP_021629976.1	3.361496219	0.002642732	BTB/POZ domain-containing protein DOT3 isoform X2
XP_021629975.1	3.492039182	0.000986486	BTB/POZ domain-containing protein DOT3 isoform X1
XP_043804863.1	3.686031433	0.000986486	BTB/POZ domain-containing protein DOT3 isoform X3

XP_021601842.1	4.181385083	0.033867047	agamous-like MADS-box protein AGL12
XP_021614886.1	4.776125165	0.032931832	very-long-chain aldehyde decarbonylase CER3
XP_043810413.1	4.848957198	0.049364097	GDSL esterase/lipase EXL3-like
XP_021614785.1	5.12411914	0.004681716	myb-related protein 306
XP_021634715.1	6.108568547	0.036897309	dehydration-responsive element-binding protein 1A
XP_043808844.1	7.219691761	0.017637233	GDSL esterase/lipase EXL3
XP_021595893.1	16.98299523	0.000986486	MLP-like protein 328

D- Stem, 10 DAI, DSC 167 vs. DSC 260

protein ID	log ₂ FC	adjusted p-value	protein function
XP_043808844.1	-8.10585636	0.045004977	GDSL esterase/lipase EXL3
XP_021613577.1	-2.130738312	0.022942827	uncharacterized protein LOC110615787
XP_021614386.1	-2.041952308	0.020705947	probable WRKY transcription factor 53
XP_021609359.1	-1.812737119	0.039621558	L-ascorbate oxidase homolog
XP_021611561.1	-1.587862799	0.025624793	D-aminoacyl-tRNA deacylase
XP_021607267.1	1.549952727	0.012509083	uncharacterized protein LOC110611325
XP_021615991.1	1.586304248	0.048384734	uncharacterized protein LOC110617485
XP_021612691.1	1.595110969	0.046457277	glutamyl-tRNA reductase 1, chloroplastic
XP_021604301.1	1.634378733	0.025624793	disease resistance protein UNI
XP_021599266.1	1.701685301	0.039621558	chlorophyll a-b binding protein of LHCII type 1
XP_021593667.1	1.709917378	0.045004977	protochlorophyllide reductase, chloroplastic isoform X1
XP_021621616.1	1.802824179	0.039621558	chlorophyll a-b binding protein CP29.1, chloroplastic
XP_021633556.1	1.813430376	0.022942827	photosystem II core complex proteins psbY, chloroplastic
XP_021622228.1	1.859646466	0.022942827	protein SRC1
XP_021631529.1	1.871499955	0.042152053	chlorophyll a-b binding protein 8, chloroplastic
XP_021605804.1	1.913049866	0.022942827	protochlorophyllide reductase, chloroplastic
XP_021628863.1	1.977682298	0.039621558	chaperone protein dnaJ 8, chloroplastic
XP_021609254.1	2.008329838	0.044709359	photosystem I reaction center subunit VI-1, chloroplastic
XP_021593162.1	2.07164536	0.02541936	chlorophyll a-b binding protein CP24 10A, chloroplastic
XP_021614907.1	2.10706054	0.012509083	alkane hydroxylase MAH1
XP_021596314.1	2.119885403	0.032643957	uncharacterized protein LOC110602986
XP_021609387.1	2.134924873	0.022942827	anthocyanidin 3-O-glucosyltransferase 6
XP_021613006.1	2.204346835	0.022942827	photosystem II reaction center W protein, chloroplastic
XP_021629713.1	2.278162549	0.022942827	transcription factor HHO5

XP_021620961.1	2.366199813	0.045004977	uncharacterized protein LOC110621150
XP_021630984.1	2.493363155	0.027844182	photosystem I reaction center subunit IV A, chloroplastic
XP_021616411.1	2.696465524	0.022942827	photosystem II 5 kDa protein, chloroplastic
XP_021615431.1	3.009739046	0.048384734	uncharacterized protein LOC110617128

E- Stem, 10 DAI, DSC 167 vs. TMS 96/0304

protein ID	log ₂ FC	adjusted p-value	protein function
XP_021622793.1	-4.486217921	0.033468891	endoglucanase CX
XP_021595870.1	-4.445215951	0.000389872	ABC transporter G family member 10
XP_021625069.1	-4.018601044	0.001305522	protein PELPK1
XP_021622581.1	-3.900280629	0.009582786	secoisolariciresinol dehydrogenase
XP_021630581.1	-3.810228975	0.006265921	leucoanthocyanidin dioxygenase
XP_021607757.1	-3.727785913	0.030696985	early nodulin-75
XP_021622566.2	-3.699059015	5.23E-05	bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic
XP_043817236.1	-3.690700343	0.000344155	protein PELPK1-like
XP_021595652.1	-3.64976947	0.006265921	non-specific lipid transfer protein GPI-anchored 20
XP_021611090.1	-3.566278939	0.002302217	phenylalanine ammonia-lyase isoform X2
XP_021607758.2	-3.551848744	0.022300482	early nodulin-75
XP_021608257.1	-3.54086388	0.013673908	non-specific lipid transfer protein GPI-anchored 5
XP_021593662.1	-3.525770425	0.003135202	NAC domain-containing protein 71
XP_021611089.1	-3.524961634	0.003332052	phenylalanine ammonia-lyase isoform X1
XP_021618075.1	-3.479991167	0.000389872	protein PELPK1-like
XP_021611776.1	-3.398449617	0.000389872	uncharacterized protein LOC110614528
XP_021607962.1	-3.380170348	0.002525944	receptor like protein kinase S.2
XP_021615437.1	-3.371887503	0.001765603	uncharacterized protein LOC110617135

XP_021595702.1	-3.371074454	0.010948204	3-ketoacyl-CoA synthase 20
XP_021626402.1	-3.318807187	0.001305522	protein PELPK1
XP_021600257.2	-3.266899143	0.026565175	dihydroflavonol 4-reductase
XP_021618820.1	-3.253200056	0.02565118	protein PELPK1
XP_021609389.1	-3.236503755	0.033468891	chalcone synthase 2
XP_021631825.2	-3.199013095	0.040745169	flavonoid 3',5'-hydroxylase 2
XP_021618139.1	-3.183426252	0.005446908	glycerol-3-phosphate acyltransferase 5
XP_021626234.1	-3.180830007	0.005685936	linoleate 13S-lipoxygenase 2-1, chloroplastic
XP_021625302.1	-3.171237793	0.001911404	ethylene-responsive transcription factor WRI1
XP_021629051.1	-3.153586821	0.020964171	dirigent protein 23
XP_021624241.1	-3.152242802	0.037893863	transcription factor MYB92
XP_021612474.1	-3.11458395	0.005702646	probable WRKY transcription factor 43
XP_021625070.1	-3.102740447	0.002912459	protein PELPK1
XP_021607958.1	-3.083905581	2.86E-05	transcription factor BHLH42
XP_021631591.1	-3.0604185	0.006649328	ethylene-responsive transcription factor ERF053
XP_021606185.1	-3.001342858	0.04681829	NAC domain-containing protein JA2L
XP_021618061.1	-2.980263323	0.026438145	protein PELPK1
XP_021625441.1	-2.92454524	0.008613342	nucleobase-ascorbate transporter 4
XP_021603611.1	-2.923440017	0.024858639	ABC transporter G family member 23
XP_021607718.1	-2.915522171	0.014224628	non-specific lipid transfer protein GPI-anchored 16
XP_021627705.1	-2.914091785	0.007373237	cytochrome P450 86B1
XP_021616874.1	-2.882427065	0.023201794	peroxidase 11
XP_021598238.1	-2.870525941	0.019980112	protein JINGUBANG
XP_043814525.1	-2.865011559	0.033591883	protein PELPK1 isoform X2
XP_021617395.1	-2.860437335	0.000389872	expansin-A8
XP_021623015.1	-2.850025368	0.011297774	epoxide hydrolase 4

XP_021611580.1	-2.813412221	0.039536149	probable carboxylesterase 5
XP_021619116.1	-2.809937009	0.016048721	gallate 1-beta-glucosyltransferase 84A24
XP_021620078.1	-2.80820337	0.026565175	ABC transporter G family member 20
XP_021609574.2	-2.801476444	0.011419907	omega-hydroxypalmitate O-feruloyl transferase
XP_021617732.1	-2.773787129	0.022754396	ABC transporter G family member 6
XP_021592863.2	-2.772761547	0.012123551	palmitoyl-acyl carrier protein thioesterase, chloroplastic
XP_021625424.1	-2.769083044	0.045572562	protein PELPK1
XP_021632540.1	-2.766337044	0.005914923	GDSL esterase/lipase At2g23540
XP_021622172.1	-2.765136362	0.00888175	glycerol-3-phosphate 2-O-acyltransferase 6
XP_021618074.1	-2.715451082	0.022300482	protein PELPK1
XP_021603640.1	-2.699242426	0.001107265	protein DETOXIFICATION 41
XP_043813659.1	-2.64658399	0.04681829	putative receptor protein kinase ZmPK1
XP_021592812.1	-2.641126254	0.015945311	peroxidase 11
XP_021618060.1	-2.639311978	0.036460832	protein PELPK1
XP_021617615.1	-2.631182309	0.003403067	chalcone isomerase-like protein 2
XP_021627812.1	-2.627843492	0.027755434	omega-hydroxypalmitate O-feruloyl transferase
XP_021610990.1	-2.615944791	0.000389872	ATPase 10, plasma membrane-type
XP_021623184.1	-2.61263887	0.003332052	4-coumarate--CoA ligase 2
XP_021605137.1	-2.570922681	0.017223621	naringenin,2-oxoglutarate 3-dioxygenase
XP_021614044.1	-2.57053181	0.043399822	non-specific lipid transfer protein GPI-anchored 5
XP_021621841.1	-2.563377324	0.042898909	cytochrome b561 and DOMON domain-containing protein At5g47530
XP_021611557.1	-2.547405731	0.045572562	cytochrome P450 CYP82D47 isoform X2
XP_021610472.1	-2.54004189	0.003137923	ABC transporter G family member 29
XP_043817133.1	-2.523154234	0.038977931	non-specific lipid transfer protein GPI-anchored 15
XP_021618150.1	-2.502883357	0.031844979	protein PELPK1
XP_021593472.1	-2.50158025	0.043873012	protein ALTERED XYLOGLUCAN 4-like

XP_021615183.1	-2.489566876	0.027160898	cytochrome P450 86A1
XP_021628924.1	-2.47991469	0.015179823	alcohol-forming fatty acyl-CoA reductase
XP_021591842.1	-2.467187404	0.022158901	omega-hydroxypalmitate O-feruloyl transferase
XP_021632101.1	-2.45258976	2.53E-06	U-box domain-containing protein 19
XP_021625416.1	-2.433322992	0.031714831	serine carboxypeptidase-like 18
XP_021610027.1	-2.420214636	0.038336071	uncharacterized protein LOC110613282
XP_021633939.1	-2.407249995	0.017071674	probable CoA ligase CCL9
XP_021610002.1	-2.401633074	0.009520487	fatty acyl-CoA reductase 3
XP_021618823.1	-2.398507695	0.026337701	NAC domain-containing protein 100
XP_021615451.1	-2.391932929	0.03656782	GDSL esterase/lipase At1g74460
XP_021600227.2	-2.369374415	0.044810354	putative receptor-like protein kinase At3g47110
XP_021621548.1	-2.361527378	0.041901995	uncharacterized protein LOC110621583
XP_021598501.1	-2.292837396	0.015945311	probable CoA ligase CCL6
XP_021626115.1	-2.291983266	0.001653289	N-(5'-phosphoribosyl)anthranilate isomerase 1, chloroplastic
XP_021629019.1	-2.287299676	0.008518941	ATPase 10, plasma membrane-type
XP_021629987.1	-2.269041468	0.047921774	caffeoyl-CoA O-methyltransferase
XP_021596210.1	-2.248413528	0.003141752	anthocyanidin reductase ((2S)-flavan-3-ol-forming)
XP_021603146.1	-2.240379773	0.047441369	stearoyl-[acyl-carrier-protein] 9-desaturase 6, chloroplastic
XP_021613248.1	-2.233641874	0.003135202	WRKY transcription factor 23
XP_021627264.1	-2.211354942	0.018324371	chalcone synthase
XP_021632303.1	-2.190560882	0.044787455	septum-promoting GTP-binding protein 1
XP_021634050.1	-2.17317886	0.023062671	protein LATERAL ROOT PRIMORDIUM 1
XP_021615574.1	-2.121068584	0.012707454	alpha-xylosidase 1
XP_021616292.1	-2.118160991	0.00888175	respiratory burst oxidase homolog protein C
XP_021620832.1	-2.110911998	0.018753249	non-specific lipid transfer protein GPI-anchored 7
XP_043812367.1	-2.099987848	0.033468891	F-box/kelch-repeat protein At5g43190-like

XP_021596493.1	-2.099396851	0.018931271	cytochrome P450 86A1
XP_021597484.1	-2.082409661	0.035827227	arogenate dehydratase/prephenate dehydratase 1, chloroplastic
XP_021634670.1	-2.071080314	0.012578836	short-chain dehydrogenase TIC 32 B, chloroplastic
XP_021634610.1	-2.042960491	0.044409881	universal stress protein YxiE
XP_021632282.1	-2.041430691	0.04681829	cysteine proteinase COT44
XP_021603452.2	-2.039084241	0.020572289	WAT1-related protein At5g47470
XP_021622431.1	-2.038376319	0.017291643	transcription repressor OFP1
XP_021628626.1	-2.016606693	0.015945311	beta-fructofuranosidase, cell wall isozyme isoform X1
XP_043807108.1	-2.009930855	0.037651221	non-specific lipid transfer protein GPI-anchored 5
XP_021597746.1	-1.979165577	0.001145084	low-temperature-induced cysteine proteinase
XP_021617696.1	-1.956949362	0.016240253	laccase-5
XP_021632903.1	-1.950308326	0.013220159	G-type lectin S-receptor-like serine/threonine-protein kinase At1g34300
XP_021633997.1	-1.914919903	0.001911404	leucoanthocyanidin reductase
XP_021598728.1	-1.889256348	0.049795441	oligopeptide transporter 7
XP_021633426.1	-1.88733612	0.032771037	auxin-induced in root cultures protein 12
XP_021618646.1	-1.882667403	0.044309403	peroxidase 4
XP_021621183.1	-1.849889049	0.003403067	WRKY transcription factor 44
XP_021598142.1	-1.845234497	0.01932373	respiratory burst oxidase homolog protein E
XP_021596544.1	-1.82260771	0.011419907	dehydration-responsive element-binding protein 3
XP_021606580.1	-1.811834925	0.009582786	type IV inositol polyphosphate 5-phosphatase 7
XP_021627833.1	-1.799260386	0.031844979	ABC transporter G family member 29
XP_043811930.1	-1.790060544	0.019645616	histidine protein methyltransferase 1 homolog
XP_021619781.2	-1.777565813	0.031844979	transcription factor MYB56
XP_021603951.2	-1.772125365	0.033468891	transcription factor GLABRA 3 isoform X1
XP_021628546.1	-1.768518791	0.006028263	uncharacterized protein LOC110626778
XP_021617740.2	-1.767103513	0.018931271	cysteine proteinase RD21A

XP_021611567.1	-1.765428719	0.045147286	expansin-A1 isoform X2
XP_021610730.1	-1.759627092	0.00840987	phospholipase D alpha 1
XP_021593691.1	-1.735076336	0.026153708	calcium-binding protein CP1
XP_021603950.2	-1.734024555	0.042796191	transcription factor GLABRA 3 isoform X2
XP_021603692.1	-1.728864414	0.045584289	uncharacterized protein LOC110608720
XP_021594052.1	-1.724382857	0.039276654	protein TORNADO 1
XP_021594737.1	-1.71708889	0.000647678	phytosulfokine receptor 2
XP_021606400.1	-1.716526206	0.044481744	transcription factor MYB123
XP_021624539.1	-1.700737596	0.021420288	cysteine proteinase RD21A
XP_021616900.1	-1.675976712	0.045572562	disease resistance protein RPV1
XP_021593557.1	-1.66307855	0.035827227	cinnamoyl-CoA reductase-like SNL6
XP_021628541.1	-1.661086413	0.013560304	subtilisin-like protease SBT1.5
XP_021597616.1	-1.658150019	0.044239507	CTP synthase
XP_021626907.1	-1.656205896	0.04681829	expansin-A1
XP_021593337.1	-1.652179072	0.036107796	uncharacterized protein LOC110600779
XP_021610233.1	-1.636625306	0.015464708	uncharacterized protein LOC110613427
XP_021616486.1	-1.632294842	0.037556097	uncharacterized protein LOC110617795
XP_043807618.1	-1.630280775	0.013870886	ent-kaurene synthase TSP4, chloroplastic
XP_021622193.1	-1.629629385	0.017071674	protein OCTOPUS
XP_021615710.1	-1.628451847	0.044481744	probable methyltransferase PMT15
XP_021627237.1	-1.626325613	0.042898909	two-component response regulator-like APRR9 isoform X1
XP_021599119.1	-1.617251512	0.005870016	CBL-interacting serine/threonine-protein kinase 23 isoform X1
XP_021610410.1	-1.612632108	0.009032534	beta-galactosidase 8
XP_021614728.1	-1.60026759	0.040627186	phosphoenolpyruvate carboxylase 4
XP_021606691.1	-1.588451752	0.014594175	SEC14 cytosolic factor
XP_043811908.1	-1.556290787	0.01932373	uncharacterized protein LOC110613571

XP_043808797.1	-1.555773502	0.017071674	cysteine-rich receptor-like protein kinase 26
XP_043808508.1	-1.544739339	0.013220159	CBL-interacting serine/threonine-protein kinase 23 isoform X2
XP_021610785.1	1.501670739	0.02565118	protein SRG1 isoform X1
XP_021594742.1	1.508479673	0.025746221	probable adenylate kinase 7, mitochondrial
XP_021605157.1	1.524479544	0.03805926	2-oxoisovalerate dehydrogenase subunit alpha 1, mitochondrial
XP_021631132.1	1.538350832	0.00888175	zinc finger CCCH domain-containing protein 18 isoform X3
XP_021631130.1	1.539166565	0.00888175	zinc finger CCCH domain-containing protein 18 isoform X1
XP_043809753.1	1.546839912	0.033372417	disease resistance protein At4g27190
XP_043811707.1	1.54872678	0.02451045	putative proline-rich receptor-like protein kinase PERK6 isoform X2
XP_021633556.1	1.548768073	0.026153708	photosystem II core complex proteins psbY, chloroplastic
XP_021595014.1	1.551342477	0.017223621	ABC transporter B family member 2 isoform X1
XP_021627740.1	1.557845963	0.025609649	structural maintenance of chromosomes protein 1A
XP_021609756.1	1.563070312	0.013560304	putative proline-rich receptor-like protein kinase PERK6 isoform X3
XP_021629207.1	1.577190839	0.042400777	photosystem I reaction center subunit N, chloroplastic
XP_021619366.1	1.586040188	0.049795441	fructose-1,6-bisphosphatase, chloroplastic
XP_021618613.1	1.587222398	0.031844979	cilia- and flagella-associated protein 251
XP_021598601.1	1.58779518	0.026438145	abscisic acid receptor PYR1
XP_043807365.1	1.589309907	0.015098843	ABC transporter B family member 2 isoform X2
XP_021618786.1	1.592309519	0.001591287	ubiquitin-conjugating enzyme E2 14 isoform X1
XP_021618788.1	1.593866989	0.001591287	ubiquitin-conjugating enzyme E2 14 isoform X3
XP_043810276.1	1.59415674	0.048592509	sucrose transport protein SUC2
XP_021618787.1	1.599813598	0.003197094	ubiquitin-conjugating enzyme E2 14 isoform X2
XP_021619299.1	1.607148033	0.010057815	uncharacterized protein LOC110620046
XP_021599916.1	1.608440243	0.010057815	uncharacterized protein LOC110605595
XP_021606175.1	1.609271767	0.015811477	metallothionein-like protein type 3
XP_021615991.1	1.61152532	0.015811477	uncharacterized protein LOC110617485

XP_021599827.1	1.630821839	0.038336071	uncharacterized protein LOC110605520 isoform X2
XP_021599826.1	1.638041767	0.031844979	uncharacterized protein LOC110605520 isoform X1
XP_021598533.1	1.645600182	0.019880119	uncharacterized protein LOC110604600
XP_021609755.1	1.661795325	0.010994421	proline-rich receptor-like protein kinase PERK1 isoform X1
XP_021614332.1	1.664412166	0.019010295	ribosome-binding factor PSRP1, chloroplastic
XP_021609532.1	1.666195072	0.039276654	mediator of RNA polymerase II transcription subunit 9 isoform X2
XP_021634244.1	1.668426147	0.015098843	transcription factor TCP14
XP_021617166.1	1.681055872	0.027942941	rhodanese-like domain-containing protein 14, chloroplastic
XP_021601171.1	1.683202133	0.010057815	catalase isozyme 1 isoform X2
XP_021614907.1	1.685477135	0.016239647	alkane hydroxylase MAH1
XP_021609947.2	1.687296165	0.004923243	uncharacterized protein LOC110613232
XP_021603807.1	1.6912811	0.017223621	glycine, alanine and asparagine-rich protein
XP_021620450.1	1.691675304	0.009605262	photosystem II reaction center W protein, chloroplastic
XP_021632489.1	1.706545299	0.009392807	auxin-responsive protein SAUR36
XP_021627587.1	1.721827644	0.006821486	actin-depolymerizing factor 5
XP_021613115.1	1.729466024	0.005662784	uncharacterized protein LOC110615533
XP_043810587.1	1.729699354	0.042111587	desmethyl-deoxy-podophyllotoxin synthase-like isoform X1
XP_021614174.1	1.738521225	0.022300482	uncharacterized isomerase BH0283
XP_021600480.1	1.740696422	0.026337701	uncharacterized protein LOC110606054
XP_021594496.2	1.745594915	0.006540565	uncharacterized protein LOC110601610, partial
XP_021628863.1	1.747106089	0.039429981	chaperone protein dnaJ 8, chloroplastic
XP_021609254.1	1.751660255	0.04849977	photosystem I reaction center subunit VI-1, chloroplastic
XP_021634555.1	1.760011485	2.86E-05	protein indeterminate-domain 16
XP_021596160.1	1.780737066	0.013560304	ABC transporter F family member 4
XP_021599132.1	1.783723808	0.016886759	WAT1-related protein At3g28050
XP_021610060.1	1.80122304	0.039279333	bidirectional sugar transporter SWEET17 isoform X1

XP_021600182.1	1.817086085	0.032430432	fructose-1,6-bisphosphatase, cytosolic isoform X1
XP_021593999.1	1.824722233	0.034498889	glycine cleavage system H protein, mitochondrial
XP_021598859.1	1.825457541	0.038655471	uncharacterized protein LOC110604865
XP_021592796.1	1.829450431	0.044183214	peptidyl-prolyl cis-trans isomerase FKBP17-2, chloroplastic
XP_043807177.1	1.832716506	0.003956547	metallothionein-like protein type 3
XP_043810482.1	1.844817065	0.040745169	BURP domain protein RD22 isoform X3
XP_021608559.1	1.846504261	0.029237001	inter alpha-trypsin inhibitor, heavy chain 4 isoform X1
XP_043805402.1	1.848718049	0.012237456	serine/arginine-rich splicing factor SR45a
XP_021607213.1	1.849768417	0.042400777	BURP domain protein RD22 isoform X2
XP_021599655.1	1.851045994	0.032200105	E3 ubiquitin-protein ligase AIRP2 isoform X1
XP_021605513.1	1.853164468	0.026297369	protein PLASTID TRANSCRIPTIONALLY ACTIVE 16, chloroplastic
XP_021607701.2	1.864565639	0.040627186	BURP domain protein RD22
XP_021617841.1	1.880665441	0.032522752	LOB domain-containing protein 38
XP_021622543.2	1.905601045	0.025609649	protein CHUP1, chloroplastic
XP_021615032.1	1.91440776	0.027755434	signal peptide peptidase-like 2 isoform X1
XP_021622230.1	1.919364527	0.013074238	uncharacterized protein LOC110622132
XP_021633848.2	1.926475237	0.003141752	heavy metal-associated isoprenylated plant protein 7
XP_021593877.1	1.930155298	0.005902584	calcium/calmodulin-regulated receptor-like kinase 2 isoform X1
XP_021593883.1	1.936005802	0.003403067	calcium/calmodulin-regulated receptor-like kinase 2 isoform X2
XP_021622544.1	1.941988223	0.017223621	cysteine proteinase inhibitor 5
XP_021630395.1	1.943515498	0.022300482	cytochrome P450 81Q32
XP_021614663.1	1.983591675	0.035827227	autophagy-related protein 16
XP_021621871.1	2.002400389	0.022402715	F-box/kelch-repeat protein At1g15670
XP_021601443.1	2.005992022	0.045205551	cinnamoyl-CoA reductase 1
XP_021615035.1	2.019836178	0.023931858	signal peptide peptidase-like 2 isoform X2
XP_021630984.1	2.044663562	0.049795441	photosystem I reaction center subunit IV A, chloroplastic

XP_021619574.1	2.048188244	0.028168549	metallothionein-like protein type 2
XP_021612362.1	2.049070851	0.036460832	2-alkenal reductase (NADP(+)-dependent)
XP_043811909.1	2.057495579	0.026834069	E3 ubiquitin-protein ligase RZFP34
XP_021629304.1	2.087045019	0.048600666	LOB domain-containing protein 37 isoform X1
XP_021629305.1	2.098438422	0.044220501	LOB domain-containing protein 37 isoform X2
XP_021622039.1	2.098764103	0.039804819	light-regulated protein 1, chloroplastic
XP_021592777.1	2.099106528	0.009137005	mitochondrial outer membrane protein porin of 36 kDa
XP_021614380.1	2.112545106	0.003141752	homeobox-leucine zipper protein ATHB-13
XP_021626304.1	2.130909185	0.026716736	WAT1-related protein At2g39510
XP_021606590.1	2.155276428	0.003443478	auxin-responsive protein IAA27
XP_021627753.1	2.155435189	1.63E-06	inositol oxygenase 1
XP_021597819.1	2.164773254	0.000333754	sulfite exporter TauE/SafE family protein 2 isoform X3
XP_021609857.1	2.200808265	0.016277711	protein NRT1/ PTR FAMILY 5.4
XP_021597817.1	2.216857183	0.000154325	sulfite exporter TauE/SafE family protein 5 isoform X1
XP_021595709.1	2.22260933	0.012293758	MLP-like protein 28
XP_021601006.1	2.223948377	0.033070706	shewanella-like protein phosphatase 1
XP_021597818.1	2.230960561	0.00014772	sulfite exporter TauE/SafE family protein 5 isoform X2
XP_021609754.1	2.232447257	0.022754396	photosystem I subunit O
XP_021634380.1	2.251463255	0.001801593	beta-carotene hydroxylase 2, chloroplastic
XP_021606610.1	2.29644398	0.001305522	uncharacterized protein LOC110610844
XP_043804824.1	2.316106822	0.012123551	uncharacterized protein LOC122721358
XP_021616411.1	2.316714189	0.021420288	photosystem II 5 kDa protein, chloroplastic
XP_021629824.2	2.373426791	0.027160898	methylesterase 10
XP_021619675.1	2.404271198	0.040379174	DNA ligase 1 isoform X2
XP_021608413.1	2.421391918	0.006249292	uncharacterized protein LOC110612066 isoform X2
XP_021607112.1	2.460874285	0.000757353	uncharacterized protein LOC110611231

XP_021608412.1	2.462086837	0.007395615	uncharacterized protein LOC110612066 isoform X1
XP_021593875.1	2.470905742	0.003141752	uncharacterized protein LOC110601147
XP_021619674.1	2.499958202	0.021539008	DNA ligase 1 isoform X1
XP_021606236.1	2.503004808	0.021763022	probable aspartic proteinase GIP2
XP_021619568.1	2.505306171	0.006350495	cytochrome P450 78A9
XP_021634233.1	2.538309118	0.017071674	cytochrome P450 78A5
XP_021602965.1	2.574182675	0.003255985	vascular-related unknown protein
XP_021605177.1	2.722058279	0.005900945	ABC transporter G family member 11
XP_021614983.1	2.823196908	0.04849977	cytochrome P450 78A5
XP_043812755.1	2.872036257	0.000166529	calmodulin-like protein 2
XP_021620961.1	3.023551105	0.001305522	uncharacterized protein LOC110621150
XP_021618804.1	3.141893372	0.045572562	MLO-like protein 12 isoform X1
XP_021629713.1	3.150924638	2.82E-05	transcription factor HHO5
XP_021620960.1	3.151836133	0.037749119	amino acid transporter AVT1D isoform X2
XP_043815181.1	3.18166168	0.026153708	amino acid transporter AVT1D isoform X3
XP_021620959.1	3.295404308	0.026153708	amino acid transporter AVT1D isoform X1
XP_021625417.1	3.411747715	0.012384533	flavonol sulfotransferase-like
XP_043808081.1	3.525335456	0.018753249	metal transporter Nramp5-like
XP_021598791.1	3.742186811	0.003956547	uncharacterized protein LOC110604791

F- Roots, 1 DAI, DSC 260 vs. TMS 96/0304

protein ID	log ₂ FC	adjusted p-value	protein function
XP_021629035.1	-16.26849399	0.013000335	cytosolic sulfotransferase 15
XP_021617731.1	-8.438292645	0.038717091	22.0 kDa class IV heat shock protein
XP_021609991.1	-8.238342058	0.01399323	17.4 kDa class I heat shock protein
XP_021592997.1	-6.866132259	0.036742729	bidirectional sugar transporter SWEET12
XP_021604097.2	-6.559889383	0.017008582	expansin-like B1
XP_021597369.1	-6.550514349	0.010944613	17.3 kDa class II heat shock protein
XP_021610330.1	-6.364942643	0.013000335	17.4 kDa class I heat shock protein
XP_021630299.1	-6.32594613	0.044214841	non-specific lipid transfer protein GPI-anchored 1
XP_021605659.2	-5.895179167	0.00499341	probable calcium-binding protein CML44, partial
XP_021604129.2	-5.74369964	0.022282377	protein phosphatase 2C 51
XP_021622483.1	-5.63601363	0.026247839	zeatin O-glucosyltransferase
XP_021612364.1	-5.607363758	0.001826221	BAG family molecular chaperone regulator 6
XP_021612371.1	-5.607363758	0.001826221	BAG family molecular chaperone regulator 6
XP_021622320.1	-5.254158278	0.002181144	ferritin-3, chloroplastic
XP_043817570.1	-5.052175338	0.027967861	ubiquitin-like protein 5
XP_021609722.1	-5.000682418	0.009972392	pyridoxal 5'-phosphate synthase-like subunit PDX1.2
XP_021616943.1	-4.849625168	0.034938828	bidirectional sugar transporter SWEET10
XP_021622201.2	-4.80020864	0.015515184	uncharacterized protein LOC110622114
XP_021613499.1	-4.673304248	0.005979378	protein NRT1/ PTR FAMILY 2.13
XP_021628785.1	-4.644367595	0.014457953	elicitor-responsive protein 3
XP_021626276.1	-4.594371558	0.011521328	17.3 kDa class I heat shock protein
XP_021624116.1	-4.067506566	0.02084571	11 kDa late embryogenesis abundant protein
XP_021605572.2	-4.009473302	0.033141576	uncharacterized protein LOC110610018
XP_021605448.1	-3.654855025	0.002989958	uncharacterized protein LOC110609917

XP_021610308.1	-3.621401347	0.03224074	putative low molecular weight protein-tyrosine-phosphatase slr0328 isoform X1
XP_021610309.1	-3.568767129	0.034385706	putative low molecular weight protein-tyrosine-phosphatase slr0328 isoform X2
XP_021634257.1	-3.553005677	0.036578672	nifU-like protein 3, chloroplastic
XP_021602292.2	-3.533108549	0.046525437	LOW QUALITY PROTEIN: homeobox-leucine zipper protein ATHB-40
XP_021619574.1	-3.403698876	0.046770375	metallothionein-like protein type 2
XP_021617303.1	-3.263127455	0.026837743	protein GRAVITROPIC IN THE LIGHT 1
XP_021620148.1	-3.077322702	0.038717091	cytochrome P450 709B2
XP_043809565.1	-2.913275984	0.043225447	probable protein phosphatase 2C 26 isoform X2
XP_021620073.1	-2.821940986	0.007135019	protein SRC2 homolog
XP_021609582.1	-2.740018154	0.049261052	myb-related protein 308
XP_021595355.1	-2.627468565	0.028370336	uncharacterized protein LOC110602205
XP_021606591.1	-2.625008254	0.046770375	uncharacterized protein LOC110610820
XP_021598214.1	-2.502933412	0.038717091	3-ketoacyl-CoA synthase 4
XP_021612000.1	-2.407272134	0.048169378	indole-3-acetic acid-induced protein ARG2
XP_021624294.2	-2.376037388	0.001826221	sulfite exporter TauE/SafE family protein 4 isoform X2
XP_021624293.2	-2.376037388	0.001826221	sulfite exporter TauE/SafE family protein 4 isoform X1
XP_021598665.1	-2.288965731	0.033511307	probable peroxygenase 4 isoform X1
XP_043815422.1	-2.287525667	0.00302015	sulfite exporter TauE/SafE family protein 4 isoform X3
XP_021608516.2	-1.972786243	0.005080157	uncharacterized protein LOC110612133
XP_021615086.1	-1.931020159	0.044214841	serine/threonine-protein kinase UCNL
XP_021623028.1	-1.671202489	0.03224074	superoxide dismutase [Cu-Zn] isoform X2
XP_021621239.1	-1.619287336	0.038717091	two-component response regulator ARR8
XP_021622937.1	1.547992306	0.019779098	scarecrow-like protein 33
XP_043816921.1	1.633485518	0.034019822	probable sugar phosphate/phosphate translocator At3g11320
XP_021617668.1	1.820739721	0.011521328	heat stress transcription factor A-4c
XP_021604899.1	1.838372282	0.045120011	probable ribose-5-phosphate isomerase 2

XP_043804611.1	1.849200272	0.002021195	cytochrome b561 and DOMON domain-containing protein At5g47530-like
XP_021624607.1	1.850158905	0.022171969	probable E3 ubiquitin-protein ligase RHC1A
XP_021605405.1	1.853111906	0.042232382	putative glucuronosyltransferase PGSIP8
XP_043817944.1	1.896567634	0.044214841	uncharacterized protein LOC110626939
XP_021615172.1	1.917854001	0.005979378	3-ketoacyl-CoA synthase 11
XP_021620139.1	1.961341904	0.011521328	bZIP transcription factor TGA10 isoform X1
XP_021616094.1	1.986907168	0.017008582	tetraspanin-8
XP_043816985.1	1.993939215	0.041442801	hippocampus abundant transcript-like protein 1 isoform X2
XP_021626069.1	2.023244838	0.036199559	hippocampus abundant transcript-like protein 1 isoform X1
XP_021605354.2	2.034891959	0.034385706	BTB/POZ domain-containing protein At5g41330
XP_021605335.1	2.037003605	0.015515184	U-box domain-containing protein 5 isoform X1
XP_021624769.1	2.072881897	0.022282377	putative serine/threonine-protein kinase-like protein CCR3 isoform X1
XP_021619016.1	2.072973579	0.034385706	S-adenosyl-L-methionine-dependent uroporphyrinogen III methyltransferase, chloroplastic isoform X1
XP_021605353.1	2.091785636	0.047334816	probable WRKY transcription factor 26
XP_021619019.1	2.109192772	0.038717091	S-adenosyl-L-methionine-dependent uroporphyrinogen III methyltransferase, chloroplastic isoform X2
XP_021623265.1	2.172618642	0.038717091	probable serine/threonine-protein kinase WNK5 isoform X1
XP_021602811.2	2.246701697	0.011521328	cytochrome b561 and DOMON domain-containing protein At5g47530
XP_021617334.1	2.282767819	0.032407541	uncharacterized protein LOC110618503
XP_021617383.2	2.345553277	0.004482909	uncharacterized protein LOC110618547 isoform X2
XP_043814256.1	2.353229556	0.004380024	uncharacterized protein LOC110618547 isoform X1
XP_021626531.2	2.360629188	0.038717091	probable receptor-like protein kinase At1g11050
XP_043804514.1	2.431527455	0.038717091	cytochrome b561 and DOMON domain-containing protein At5g47530-like
XP_021605783.1	2.465684295	0.011521328	serine/threonine-protein kinase RIPK
XP_021595994.1	2.50443682	0.036742729	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2
XP_021624325.1	2.591298976	0.022171969	protein DETOXIFICATION 24

XP_043804493.1	2.667627355	0.002768021	cytochrome b561 and DOMON domain-containing protein At5g35735
XP_021624734.1	2.715372004	0.013000335	aspartic proteinase PCS1
XP_021616072.1	2.755650623	0.046770375	glucosamine inositolphosphorylceramide transferase 1 isoform X1
XP_021604396.1	2.812781726	0.001826221	probable WRKY transcription factor 53
XP_021621313.1	2.857110484	0.011521328	oligopeptide transporter 3
XP_021619909.1	2.961358417	0.026247839	myb family transcription factor PHL5 isoform X2
XP_021615181.1	3.047569721	0.045120011	gamma-glutamyl peptidase 5
XP_021627108.1	3.12565191	0.01554744	proline-rich receptor-like protein kinase PERK5
XP_043809312.1	3.255588466	0.011521328	nitrate reductase [NADH] isoform X1
XP_021634749.2	3.262835468	0.026017128	high-affinity nitrate transporter 3.1
XP_043809313.1	3.301903369	0.005979378	nitrate reductase [NADH] isoform X2
XP_021606416.1	3.340836065	0.011521328	pleiotropic drug resistance protein 1
XP_021614214.1	3.405534388	0.005979378	chitinase 10
XP_021616261.1	3.56836528	0.033124237	zinc finger protein BRUTUS-like At1g18910
XP_021626801.1	3.722975811	0.025468774	laccase-11
XP_021610131.1	3.791170921	0.038717091	wall-associated receptor kinase-like 1
XP_021618054.1	3.801518141	0.009466494	WAT1-related protein At1g43650
XP_021627899.1	4.573158222	0.017969985	uncharacterized protein LOC110626366
XP_021595743.1	4.707112635	0.002181144	probable WRKY transcription factor 72
XP_021598088.1	5.19221101	0.005979378	metal tolerance protein 9
XP_021622847.1	5.640128502	0.005979378	potassium transporter 5
XP_021594312.1	7.79264585	0.011884793	pleiotropic drug resistance protein 3
XP_043808936.1	8.014799618	0.048169378	metal transporter Nramp5-like
XP_043816734.1	8.136613701	0.038717091	7-deoxyloganetin glucosyltransferase isoform X2
XP_021625530.1	8.146707169	0.038717091	7-deoxyloganetin glucosyltransferase isoform X1
XP_021602057.1	11.82377341	0.013000335	fe(2+) transport protein 1

XP_043812482.1	12.26220301	0.002419153	uncharacterized protein LOC110614799
XP_021596409.1	21.86276446	0.002247228	2-oxoglutarate-dependent dioxygenase 19

G- Roots, 1 DAI, DSC 167 vs. DSC 260

protein ID	log ₂ FC	adjusted p-value	protein function
XP_021617831.1	-20.64213732	0.038153321	beta-glucosidase 12
XP_021595743.1	-4.306373111	0.007175504	probable WRKY transcription factor 72
XP_021634749.2	-3.734218661	0.007550138	high-affinity nitrate transporter 3.1
XP_021600897.2	-2.074572876	0.007175504	cytochrome P450 734A1
XP_021605335.1	-2.041416809	0.025312878	U-box domain-containing protein 5 isoform X1
XP_021633847.1	-1.541272476	0.036500919	methionine aminopeptidase 1B, chloroplastic
XP_021602795.1	1.522829982	0.009738462	D-3-phosphoglycerate dehydrogenase 3, chloroplastic
XP_021604462.1	1.67680322	0.036500919	beta-galactosidase 3
XP_021621239.1	1.723145257	0.036500919	two-component response regulator ARR8
XP_021618573.1	1.84280636	0.036500919	D-3-phosphoglycerate dehydrogenase 1, chloroplastic
XP_021605792.1	2.133484352	0.038153321	uncharacterized protein LOC110610257
XP_021610028.1	2.176737411	0.022045474	GEM-like protein 4
XP_043806303.1	2.328321306	0.036500919	protein LNK1 isoform X2
XP_043809810.1	2.39469497	0.036500919	arabinogalactan protein 41-like
XP_021594006.1	2.415769787	0.036500919	uncharacterized protein LOC110601248
XP_021607270.1	2.42523547	0.028385152	2-oxoglutarate-dependent dioxygenase DAO
XP_021630901.1	2.521640899	0.007175504	peptidyl-prolyl cis-trans isomerase FKBP62
XP_021592826.1	2.541165322	0.043203503	protein LNK1 isoform X1
XP_021602326.1	2.547587358	0.025312878	suppressor of disruption of TFIS
XP_021605066.1	2.662298213	0.036500919	cytochrome P450 71B34

XP_043805014.1	2.808768628	0.043203503	arabinogalactan protein 20-like
XP_021593989.1	2.812988316	0.036734988	FCS-Like Zinc finger 1 isoform X2
XP_021617184.1	2.872256496	0.045850938	protein phosphatase 2C 51
XP_021593988.1	2.946751037	0.036500919	FCS-Like Zinc finger 1 isoform X1
XP_021605448.1	3.151143044	0.033098265	uncharacterized protein LOC110609917
XP_021623718.1	3.228620178	0.007175504	bark storage protein B
XP_021595770.1	3.326384644	0.036500919	probable protein phosphatase 2C 24
XP_021597530.1	3.45132042	0.03862046	protein PHOSPHATE-INDUCED 1
XP_021615058.1	3.687866795	0.036500919	probable galactinol--sucrose galactosyltransferase 6
XP_021621420.1	3.716951963	0.045850938	GDSL esterase/lipase At4g01130
XP_043815152.1	3.807778547	0.007175504	probable galactinol--sucrose galactosyltransferase 2 isoform X2
XP_021620353.1	3.838768361	0.007175504	probable galactinol--sucrose galactosyltransferase 2 isoform X1
XP_021620354.1	3.838768361	0.007175504	probable galactinol--sucrose galactosyltransferase 2 isoform X1
XP_021620148.1	3.85227676	0.007175504	cytochrome P450 709B2
XP_043806418.1	3.982276266	0.045850938	14 kDa proline-rich protein DC2.15-like
XP_021624116.1	4.275579938	0.022045474	11 kDa late embryogenesis abundant protein
XP_043809104.1	4.637428869	0.007175504	acidic endochitinase WIN6.2C-like
XP_021592525.1	5.190060258	0.022045474	photosystem I reaction center subunit psaK, chloroplastic
XP_021612462.1	5.377363946	0.022045474	heat stress transcription factor A-7a
XP_021622483.1	5.752691127	0.020766233	zeatin O-glucosyltransferase
XP_043814290.1	5.844242288	0.007175504	beta-glucosidase 12-like
XP_021601186.1	7.425254671	0.043252124	thioredoxin M-type, chloroplastic
XP_021619979.1	9.956533497	0.047484437	respiratory burst oxidase homolog protein B
XP_021598121.1	10.875594	0.009738462	bark storage protein A isoform X1
XP_043808072.1	11.13127943	0.024522189	bark storage protein A isoform X2

H- Roots, 1 DAI, DSC 167 vs. TMS 96/0304

protein ID	log₂FC	adjusted p-value	protein function
XP_043805374.1	-19.32983781	0.004957285	trans-resveratrol di-O-methyltransferase-like
XP_021620134.1	-12.52188387	0.029208845	class I heat shock protein
XP_021625513.1	-11.68879415	0.042326168	22.0 kDa class IV heat shock protein
XP_043814740.1	-11.48293692	0.044388826	class I heat shock protein-like
XP_021625360.1	-9.084466326	0.027486492	17.3 kDa class I heat shock protein
XP_021609991.1	-8.100568014	0.042736604	17.4 kDa class I heat shock protein
XP_021614058.1	-7.554599271	0.042326168	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial
XP_021624294.2	-2.451061482	0.001329227	sulfite exporter TauE/SafE family protein 4 isoform X2
XP_021624293.2	-2.451061482	0.001329227	sulfite exporter TauE/SafE family protein 4 isoform X1
XP_043815422.1	-2.404462357	0.00201373	sulfite exporter TauE/SafE family protein 4 isoform X3
XP_021618424.1	1.795793318	0.027486492	uncharacterized protein LOC110619344
XP_021596490.1	1.851153278	0.042736604	serine/threonine-protein kinase RIPK
XP_021627256.1	1.951630742	0.001831905	transcription factor bHLH63
XP_021609486.1	2.136909234	0.042736604	probable amidase At4g34880
XP_021622610.1	2.222056209	0.012558836	probable calcium-binding protein CML43
XP_021605354.2	2.329274028	0.029208845	BTB/POZ domain-containing protein At5g41330
XP_021592360.2	2.576717493	0.03013239	leucine-rich repeat receptor-like serine/threonine/tyrosine-protein kinase SOBIR1
XP_021603446.1	2.76760078	0.029208845	L-Ala-D/L-amino acid epimerase isoform X1
XP_021603447.1	2.777508398	0.03013239	L-Ala-D/L-amino acid epimerase isoform X2
XP_021622562.1	2.825088946	0.042736604	E3 ubiquitin-protein ligase PUB23
XP_021622469.1	3.612375148	0.038907582	U-box domain-containing protein 9 isoform X1
XP_021625403.1	3.634600615	0.001963422	mitochondrial uncoupling protein 5
XP_021625430.1	4.032987145	0.03013239	mitochondrial uncoupling protein 5
XP_021609710.1	4.425842334	0.03013239	exocyst complex component EXO70H1

XP_021596409.1	23.0012545	0.001831905	2-oxoglutarate-dependent dioxygenase 19
XP_021618096.1	24.45560134	0.038907582	pathogenesis-related protein 1

I- Roots, 10 DAI, DSC 260 vs. TMS 96/0304

protein ID	log ₂ FC	adjusted p-value	protein function
XP_043814599.1	-35.23355433	0.002597821	beta-glucosidase 12
XP_021634176.1	-30.48873338	3.31E-10	non-specific lipid-transfer protein
XP_021597898.1	-30.09903456	0.029430274	probable flavin-containing monooxygenase 1
XP_021613333.1	-29.73364737	3.26E-11	glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic
XP_021626861.1	-29.11404443	2.14E-11	proline-rich protein 4
XP_021611811.1	-28.65890051	2.31E-09	protein CURVATURE THYLAKOID 1B, chloroplastic
XP_021593834.2	-22.83169531	7.06E-06	chlorophyll a-b binding protein CP26, chloroplastic
XP_021629416.1	-21.71622479	3.26E-11	chlorophyll a-b binding protein, chloroplastic
XP_021630114.1	-21.52300978	0.000124258	perakine reductase
XP_021593252.1	-18.03621212	0.001098199	chlorophyll a-b binding protein CP26, chloroplastic
XP_021610153.2	-15.95756051	0.01945529	cytochrome P450 CYP82D47
XP_021615231.1	-13.06318134	0.000253692	berberine bridge enzyme-like 18
XP_021630014.1	-11.3748202	0.009616571	cytochrome P450 CYP82D47
XP_021629795.2	-10.96368242	0.008339189	cytochrome P450 CYP82D47
XP_043807618.1	-9.116579085	0.009152486	ent-kaurene synthase TSP4, chloroplastic
XP_021601745.2	-8.060145419	0.000445765	cytochrome P450 CYP82D47
XP_021610011.1	-6.605640079	0.008339189	lysine histidine transporter-like 8
XP_021634672.1	-6.37264358	0.009577813	class V chitinase
XP_021621599.1	-5.305505121	0.012452966	germin-like protein subfamily 1 member 17
XP_021623665.2	-4.661511646	0.017037449	cullin-1 isoform X1

XP_043815643.1	-4.611565189	0.029164639	cullin-1 isoform X2
XP_021595914.1	-4.325863765	0.043137617	peroxidase 15
XP_021594339.1	-3.382055422	0.03362549	cytochrome P450 716B1
XP_021609177.1	-2.913328679	0.000681157	superoxide dismutase [Cu-Zn], chloroplastic
XP_021598846.1	-2.723346493	1.64E-05	auxin transporter-like protein 3
XP_021617617.1	-2.69426228	0.000859731	probable sodium/metabolite cotransporter BASS1, chloroplastic
XP_021623028.1	-2.222678825	0.000447512	superoxide dismutase [Cu-Zn] isoform X2
XP_043816443.1	-1.882338857	0.006395365	superoxide dismutase [Cu-Zn] 1 isoform X3
XP_043816442.1	-1.869792366	0.003873927	superoxide dismutase [Cu-Zn] 1 isoform X1
XP_021629746.1	-1.645417289	0.03362549	alcohol dehydrogenase 2
XP_021614763.1	-1.580086352	0.009152486	uncharacterized protein LOC110616638
XP_021614182.1	1.584230938	0.003873927	probable WRKY transcription factor 7
XP_043806171.1	1.597500933	0.039069879	copper methylamine oxidase isoform X3
XP_021611101.1	1.649008522	0.033006583	protein LATE ELONGATED HYPOCOTYL isoform X2
XP_021603106.1	1.657108038	0.006490048	protein NRT1/ PTR FAMILY 5.8
XP_021616115.1	1.694703154	0.033785993	protein LNK1 isoform X1
XP_021596909.1	1.898633866	0.028002096	LOB domain-containing protein 4
XP_021617334.1	2.16420548	0.03362549	uncharacterized protein LOC110618503
XP_043806962.1	2.189384518	0.043137617	CLAVATA3/ESR (CLE)-related protein 25
XP_021619046.1	2.439705943	0.026150806	uncharacterized protein LOC110619799
XP_021620641.1	2.522060376	0.006909173	transcription repressor OFP4
XP_021614753.1	2.880440759	3.55E-05	cyclic dof factor 3
XP_021617273.1	2.931555099	0.010509229	uncharacterized protein LOC110618449
XP_021601886.1	2.999638516	0.003980817	SPX domain-containing protein 1
XP_021622761.1	3.378438246	0.008339189	cationic amino acid transporter 6, chloroplastic
XP_021598401.1	4.293023644	0.009152486	xyloglucan glycosyltransferase 4

XP_021627829.1	4.684399089	0.019929212	high affinity nitrate transporter 2.4
XP_021601617.1	4.812346458	0.002597821	protein PHOSPHATE-INDUCED 1
XP_021622677.1	5.400053706	0.049343614	cyclic dof factor 3 isoform X2

J- Roots, 10 DAI, DSC 167 vs. DSC 260

protein ID	log ₂ FC	adjusted p-value	protein function
XP_043808730.1	-3.358957512	0.046725826	type IV inositol polyphosphate 5-phosphatase 9 isoform X2
XP_021600014.1	-3.181050969	0.021607201	type IV inositol polyphosphate 5-phosphatase 9 isoform X1
XP_021619985.1	-2.186827829	2.17E-05	uncharacterized protein LOC110620519
XP_021614753.1	-2.128462281	0.034650616	cyclic dof factor 3
XP_021624198.1	1.589774092	0.005800192	uncharacterized protein At2g37660, chloroplastic isoform X1
XP_021624199.1	1.627371512	0.005702297	uncharacterized protein At2g37660, chloroplastic isoform X2
XP_021618896.1	1.874659856	0.005800192	triosephosphate isomerase, cytosolic
XP_021598846.1	2.261743404	0.003065461	auxin transporter-like protein 3
XP_021629057.1	2.289056333	0.014266927	dnaJ protein homolog
XP_021619906.1	3.113414489	0.020675683	laccase-7
XP_021599002.1	3.7441057	0.007330294	CBS domain-containing protein CBSX5
XP_021592620.1	4.684361142	0.048478962	heat shock protein 83
XP_021615066.1	5.870748479	0.029598903	thylakoid lumenal 16.5 kDa protein, chloroplastic
XP_021627250.1	6.059246818	0.014266927	heat shock cognate 70 kDa protein
XP_021606413.1	6.993332061	0.007330294	probable aspartic proteinase GIP2
XP_021608894.1	7.05807475	0.015187242	sugar transport protein 13
XP_021596790.1	7.725526792	0.009916617	L-ascorbate oxidase homolog
XP_021629892.1	8.919425316	0.014963067	cytochrome P450 CYP82D47

XP_021634609.1	9.12254333	0.019590887	berberine bridge enzyme-like 8
XP_021634648.1	9.418489422	0.029598903	17.5 kDa class I heat shock protein
XP_021615231.1	10.61933514	0.004639435	berberine bridge enzyme-like 18
XP_021592898.1	14.96201977	0.019070824	stellacyanin
XP_021629416.1	19.94122139	6.48E-09	chlorophyll a-b binding protein, chloroplastic
XP_021626570.1	22.95705717	0.005800192	beta-glucosidase 24
XP_021593834.2	23.02643996	1.25E-05	chlorophyll a-b binding protein CP26, chloroplastic
XP_021593252.1	41.1671806	3.58E-21	chlorophyll a-b binding protein CP26, chloroplastic
XP_021593253.1	41.1671806	3.58E-21	chlorophyll a-b binding protein CP26, chloroplastic
XP_043814599.1	47.99294045	3.68E-07	beta-glucosidase 12

K- Roots, 10 DAI, DSC 167 vs. TMS 96/0304

protein ID	log ₂ FC	adjusted p-value	protein function
XP_021626861.1	-24.32484796	2.10E-06	proline-rich protein 4
XP_021634176.1	-24.32321145	5.71E-05	non-specific lipid-transfer protein
XP_021611811.1	-23.84630189	5.71E-05	protein CURVATURE THYLAKOID 1B, chloroplastic
XP_021613333.1	-23.45429667	3.62E-05	glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic
XP_021596276.1	-17.75401363	0.06220229	wound-induced protein 1
XP_021622365.1	-16.44453435	0.003044511	GDSL esterase/lipase At5g33370
XP_021610153.2	-15.27731631	0.098066455	cytochrome P450 CYP82D47
XP_021632366.1	2.798816609	0.06220229	peroxidase 47
XP_021604656.2	3.132704801	0.098066455	ethylene-responsive transcription factor 6
XP_021611800.1	6.517555897	0.093782669	galactinol synthase 1
XP_021602057.1	6.802162757	0.00568206	fe(2+) transport protein 1
XP_021598606.1	23.6552436	0.06220229	protein SRG1

Table S10: Number DEGs_DESeq2_2factor_LRT_3factor

A- STEM 1 DAI		
Comparison	DEGs in total	upregulated ↑ / downregulated ↓
DSC 260 vs. TMS 96/0304	115	↑ 72
		↓ 43
DSC 167 vs. DSC 260	411	↑ 240
		↓ 171
DSC 167 vs. TMS 96/0304	46	↑ 35
		↓ 11

B- ROOTS 1 DAI		
Comparison	DEGs in total	upregulated ↑ / downregulated ↓
DSC 260 vs. TMS 96/0304	103	↑ 57
		↓ 46
DSC 167 vs. DSC 260	45	↑ 39
		↓ 6
DSC 167 vs. TMS 96/0304	26	↑ 16
		↓ 10

C- STEM 10 DAI		
Comparison	DEGs in total	upregulated ↑ / downregulated ↓
DSC 260 vs. TMS 96/0304	291	↑ 70
		↓ 221
DSC 167 vs. DSC 260	28	↑ 23
		↓ 5
DSC 167 vs. TMS 96/0304	271	↑ 121
		↓ 150

D- ROOTS 10 DAI		
Comparison	DEGs in total	upregulated ↑ / downregulated ↓
DSC 260 vs. TMS 96/0304	49	↑ 18
		↓ 31
DSC 167 vs. DSC 260	28	↑ 24
		↓ 4
DSC 167 vs. TMS 96/0304	12	↑ 5
		↓ 7

Table S11: Protein ID, log2 fold change of DSC 260, log2 fold change of DSC 167, adjusted p-value, and protein function of DEGs after three-factor DESeq2-LRT analyses. Analysis of 1 and 10 DAI of stem and root tissues of the three genotypes. Susceptible genotype TMS 96/0304 was the basis of the three-factor analysis.

A- Stem, 1 DAI, DSC 260 and DSC 167 vs. TMS 96/0304

protein ID	adjusted p-value	log ₂ FC DSC 260	log ₂ FC DSC 167	protein function
XP_043810755.1	0.013268605	-4.217570755	-8.83486821	trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1
XP_043812548.1	0.004784749	-6.458703467	-5.930586888	inactive glucose-1-phosphate adenylyltransferase small subunit 2, chloroplastic isoform X3
XP_043804899.1	0.015901413	-3.652766386	-5.922440241	pentatricopeptide repeat-containing protein At4g33990
XP_043804901.1	0.014210475	-7.617496674	-4.331744153	RNA-directed DNA methylation 4 isoform X2
XP_021632909.1	0.011216352	-0.145944403	-3.857830602	uncharacterized protein LOC110629969 isoform X1
XP_043807845.1	0.009008862	1.260025613	-3.797809235	SPX domain-containing membrane protein At4g22990 isoform X1
XP_021624426.1	0.030120503	-2.169160993	-3.271695187	receptor-like protein kinase ANXUR1 isoform X2
XP_043815392.1	0.030120503	-2.169160993	-3.271695187	ubiquitin-like protein 5
XP_021624396.1	0.04032774	-1.604248853	-3.099734266	GDSL esterase/lipase At5g33370
XP_021611721.1	0.006325069	4.733870075	-2.837718483	4-hydroxy-tetrahydrodipicolinate reductase 1, chloroplastic isoform X1
XP_021606281.1	0.045091289	1.161648382	-2.538212684	farnesyl pyrophosphate synthase 2 isoform X4
XP_021633476.1	0.01437066	-0.666712097	-2.437676369	probable galacturonosyltransferase 13 isoform X1
XP_043810581.1	0.046368581	-1.263422103	-2.432138722	60S ribosomal protein L37-1
XP_021633485.1	0.015059996	-0.620848945	-2.426459777	probable galacturonosyltransferase 14 isoform X2
XP_021633501.1	0.015478853	-0.611404376	-2.397333152	probable galacturonosyltransferase 14 isoform X4
XP_043808177.1	0.018915937	-0.286781155	-2.373317033	WAT1-related protein At5g40240
XP_043806161.1	0.003609137	-3.299459601	-2.330772037	uncharacterized protein LOC122721709
XP_043808524.1	0.04025969	0.555745475	-2.198325588	glycosyltransferase BC10 isoform X5
XP_021599879.1	0.034964288	0.584298641	-2.187242651	vacuolar protein sorting-associated protein 55 homolog

XP_021620714.1	0.008350493	1.545406122	-2.008780099	tRNase Z TRZ4, mitochondrial isoform X6
XP_021593309.1	0.001434445	1.099728022	-1.958420001	small ubiquitin-related modifier 1
XP_021630123.1	0.011846077	0.255130201	-1.826806179	nucleobase-ascorbate transporter 11 isoform X1
XP_021626055.1	0.0014423	0.923618081	-1.816431173	putative disease resistance protein RGA3
XP_021599799.1	0.024089974	0.081864454	-1.782096149	mavicyanin
XP_021595705.1	0.000550158	0.418343182	-1.779997998	60S ribosomal protein L32-1
XP_021593170.1	0.030349385	1.91091269	-1.700111643	citrate synthase, glyoxysomal
XP_021628955.1	0.046368581	0.592408807	-1.65846983	dynein light chain 1, cytoplasmic
XP_021610637.1	0.006510557	0.026744286	-1.6532874	acyltransferase-like protein At3g26840, chloroplastic isoform X1
XP_043807283.1	0.000156116	0.992236808	-1.628157052	uncharacterized protein LOC110601486
XP_021629067.1	0.005659499	-0.286805672	-1.60034926	disease resistance protein RPV1
XP_021594328.1	0.000898847	0.875445517	-1.571995571	uncharacterized protein LOC110601486
XP_021605831.1	0.000116273	1.087566506	-1.552683803	protein GRAVITROPIC IN THE LIGHT 1
XP_021592165.2	0.043322471	0.613772477	-1.533250774	uncharacterized protein LOC110599881 isoform X1
XP_021610613.1	0.010261621	0.373053157	-1.522907291	probable inactive receptor kinase At5g10020 isoform X1
XP_021611720.1	0.046368581	2.392928095	-1.489189087	probable 1-acyl-sn-glycerol-3-phosphate acyltransferase 4 isoform X2
XP_021594327.1	0.00246991	0.867852372	-1.488813098	loganic acid O-methyltransferase
XP_043815753.1	0.04436076	-0.396806513	-1.467108055	pentatricopeptide repeat-containing protein At1g63330-like
XP_043817508.1	7.5754E-06	-0.164003758	-1.424190936	exportin-T isoform X1
XP_021628493.1	5.73665E-06	-0.152558884	-1.403047064	phototropin-1
XP_021592163.1	0.026249652	0.634982321	-1.389159475	V-type proton ATPase catalytic subunit A
XP_043805786.1	0.046368581	1.810221244	-1.352595397	WD40 repeat-containing protein HOS15 isoform X1
XP_021592161.1	0.020805904	0.696602409	-1.349283564	probable boron transporter 2 isoform X1
XP_043806495.1	0.020805904	0.696602409	-1.349283564	probable boron transporter 2 isoform X3
XP_021606797.1	3.94578E-07	1.614771183	-1.334551168	uncharacterized protein LOC110611008
XP_021606798.1	3.94578E-07	1.614771183	-1.334551168	paired amphipathic helix protein Sin3-like 5

XP_021627787.1	0.015973896	0.897258523	-1.26156448	uncharacterized protein LOC110626278
XP_021612353.1	0.046368581	-0.000655037	-1.243802547	UDP-galactose/UDP-glucose transporter 3 isoform X1
XP_021612364.1	0.046368581	-0.000655037	-1.243802547	BAG family molecular chaperone regulator 6
XP_021612371.1	0.046368581	-0.000655037	-1.243802547	BAG family molecular chaperone regulator 6
XP_021612383.1	0.046368581	-0.000655037	-1.243802547	uncharacterized protein LOC110614988 isoform X1
XP_021612391.1	0.046368581	-0.000655037	-1.243802547	uncharacterized protein LOC110614988 isoform X2
XP_021612402.1	0.046368581	-0.000655037	-1.243802547	LOW QUALITY PROTEIN: protein ABIL1
XP_043805079.1	0.046368581	-0.000655037	-1.243802547	F-box/kelch-repeat protein At3g61590
XP_043816321.1	0.046368581	-0.000655037	-1.243802547	UDP-galactose/UDP-glucose transporter 3 isoform X2
XP_021634292.1	0.003380432	0.642881655	-1.236283792	RHOMBOID-like protein 12, mitochondrial
XP_021622526.1	0.037995292	-1.152665327	-1.217157783	ADP-ribosylation factor GTPase-activating protein AGD3 isoform X1
XP_021633634.1	0.022930903	-0.229021867	-1.181586464	uncharacterized protein LOC110630435
XP_043817024.1	0.013164244	1.485669066	-1.178841442	eukaryotic translation initiation factor 3 subunit A isoform X2
XP_043816960.1	0.044813689	0.924692725	-1.163704617	putative disease resistance RPP13-like protein 1 isoform X1
XP_021614482.1	0.04089149	0.29781002	-1.162655949	plant intracellular Ras-group-related LRR protein 7
XP_021610215.1	0.046368581	-0.161810177	-1.111528059	stachyose synthase
XP_021602809.1	0.010193335	0.700699308	-1.108619687	cytochrome b561 and DOMON domain-containing protein At5g47530
XP_021602811.2	0.010193335	0.700699308	-1.108619687	cytochrome b561 and DOMON domain-containing protein At5g47530
XP_021629598.1	0.024703503	0.289516022	-1.088633563	zinc finger CCCH domain-containing protein 2
XP_021604782.1	0.044451183	0.019964841	-1.064652922	non-specific lipid transfer protein GPI-anchored 7 isoform X1
XP_021604784.1	0.044451183	0.019964841	-1.064652922	non-specific lipid transfer protein GPI-anchored 7 isoform X3
XP_043814834.1	0.012754684	1.250881213	-1.059830386	uncharacterized protein LOC122724347
XP_021599367.1	0.039047503	0.770173014	-1.048663682	NADH dehydrogenase
XP_021599369.1	0.039047503	0.770173014	-1.048663682	protein NONRESPONDING TO OXYLIPINS 2, mitochondrial isoform X2
XP_021606683.1	0.020301555	0.424109613	-1.046268074	dynamamin-related protein 3A isoform X1
XP_021608329.1	0.008484811	0.454469525	-1.025776361	uncharacterized protein LOC110612014

XP_043812838.1	0.034964288	0.529806387	-1.019254473	uncharacterized protein LOC110615637 isoform X1
XP_043808300.1	0.005659499	1.290652361	-1.017916648	TORTIFOLIA1-like protein 2
XP_021628563.1	0.025211444	0.680041869	-1.017076295	tRNA-dihydrouridine(47) synthase
XP_021615258.1	0.048206919	1.438667988	-0.947286525	serine/threonine-protein kinase Nek6 isoform X1
XP_043805835.1	0.010168991	1.013646611	-0.944848668	probable mannitol dehydrogenase isoform X2
XP_021613884.1	0.026249652	-0.196703699	-0.934454279	protein SHORT ROOT IN SALT MEDIUM 1 isoform X1
XP_043807602.1	0.011631351	0.683820073	-0.931868635	linoleate 13S-lipoxygenase 3-1, chloroplastic-like isoform X1
XP_043807604.1	0.011631351	0.683820073	-0.931868635	linoleate 13S-lipoxygenase 3-1, chloroplastic-like isoform X3
XP_021592540.1	0.000266161	4.34788936	-0.928595551	LON peptidase N-terminal domain and RING finger protein 1 isoform X2
XP_021628588.1	0.024089974	1.481341941	-0.928269973	transcription factor PRE6
XP_021605308.1	0.003397843	1.031802634	-0.922415377	uncharacterized protein LOC110609800
XP_043817279.1	0.033348678	1.033050148	-0.916924995	uncharacterized protein LOC110625209 isoform X8
XP_043807019.1	0.037055249	5.635972643	-0.909004385	mitogen-activated protein kinase 15 isoform X2
XP_021625363.1	0.010520931	-4.294869314	-0.907681272	shaggy-related protein kinase kappa
XP_021595046.1	0.024166368	0.041689716	-0.905403512	60S ribosomal protein L29-1-like
XP_043812813.1	0.048522693	0.606698851	-0.895057478	ARM REPEAT PROTEIN INTERACTING WITH ABF2-like isoform X1
XP_021619354.1	0.022191765	1.362525734	-0.893802912	dnaJ protein P58IPK homolog
XP_043807450.1	0.013617226	1.208849891	-0.891322592	light-mediated development protein DET1 isoform X1
XP_021625205.1	0.011452532	-1.187671482	-0.880730009	uncharacterized protein LOC110624398 isoform X3
XP_021626810.1	0.038772125	-5.154003009	-0.867017566	SH3 domain-containing protein 2
XP_021624125.1	0.009025195	-3.677814706	-0.863364126	uncharacterized protein LOC110623473 isoform X1
XP_021598133.1	0.000270842	1.054253958	-0.859924253	uncharacterized protein LOC110604276 isoform X1
XP_021613592.1	0.036118591	0.510764231	-0.859643301	bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase
XP_021628066.1	0.036236263	0.773343299	-0.853052997	phytochrome-associated serine/threonine-protein phosphatase isoform X2
XP_021627279.1	0.022911873	-0.437215846	-0.852504439	protein DOWNY MILDEW RESISTANCE 6
XP_021634880.1	0.024089974	-7.010128662	-0.848967561	zinc finger A20 and AN1 domain-containing stress-associated protein 8

XP_021620458.1	0.009907888	0.698138736	-0.827823288	folylpolyglutamate synthase isoform X1
XP_043814875.1	0.006452073	0.674668756	-0.827779782	folylpolyglutamate synthase isoform X3
XP_021620459.1	0.007530082	0.679657152	-0.826664611	folylpolyglutamate synthase isoform X2
XP_021620461.1	0.00680533	0.679163877	-0.822323611	folylpolyglutamate synthase isoform X3
XP_043809114.1	0.015312729	0.45615369	-0.816402139	bZIP transcription factor 27-like isoform X1
XP_021602121.2	0.022913823	1.231039344	-0.801863188	receptor-like protein EIX2, partial
XP_021618870.1	0.013237614	0.69891163	-0.797242966	NDR1/HIN1-like protein 13
XP_021606685.1	0.045795352	-1.446389041	-0.792474345	dynamamin-related protein 3A isoform X2
XP_021606686.1	0.045795352	-1.446389041	-0.792474345	lariat debranching enzyme
XP_021606973.1	0.0218195	0.502758997	-0.785947862	NAC domain-containing protein 21/22
XP_021599353.1	0.004946747	-1.996196558	-0.771088578	serine acetyltransferase 2 isoform X2
XP_021599374.2	0.004946747	-1.996196558	-0.771088578	vacuolar-processing enzyme
XP_021621119.1	0.034371094	0.337565279	-0.770245843	probable gamma-aminobutyrate transaminase 3, mitochondrial
XP_021633439.1	3.7553E-05	1.0145807	-0.761622303	uncharacterized protein LOC110630315
XP_043816123.1	0.007546772	0.602617365	-0.738368016	cell surface glycoprotein 1-like
XP_043816841.1	0.039564696	2.254979404	-0.732682893	uncharacterized protein LOC110624697 isoform X44
XP_021594265.1	0.00012164	0.573737723	-0.730211195	dirigent protein 19
XP_021594268.1	0.00012164	0.573737723	-0.730211195	transcription factor GTE8 isoform X1
XP_043807016.1	0.00012164	0.573737723	-0.730211195	transcription factor GTE8 isoform X2
XP_043807154.1	0.00012164	0.573737723	-0.730211195	outer envelope pore protein 16-2, chloroplastic isoform X2
XP_043815593.1	0.001183859	0.689678312	-0.709941754	protein DETOXIFICATION 42-like
XP_043814363.1	0.045091289	1.33198294	-0.709224851	uncharacterized protein LOC110619219 isoform X1
XP_021617602.1	0.002548856	1.176650796	-0.702611074	60S ribosomal protein L35
XP_021604578.1	0.045795352	0.692647548	-0.698426733	zinc finger CCCH domain-containing protein 46 isoform X1
XP_021620874.1	0.001987907	1.03966	-0.690440496	UPF0161 protein At3g09310
XP_021621120.1	0.011357086	0.591816147	-0.667267922	isocitrate dehydrogenase

XP_021599388.1	0.029633776	2.509249829	-0.667128988	telomerase Cajal body protein 1 isoform X1
XP_021613045.1	0.002290919	2.55502052	-0.66632056	uncharacterized protein LOC110615495
XP_021615524.1	0.039499598	-0.079901014	-0.661733984	protein KINESIN LIGHT CHAIN-RELATED 3
XP_021628603.1	0.032120713	1.667486554	-0.650319268	rab GTPase-activating protein 22
XP_021594075.1	0.040289427	1.188104996	-0.632727231	FCS-Like Zinc finger 2 isoform X1
XP_021594077.1	0.040289427	1.188104996	-0.632727231	probable protein phosphatase 2C 39
XP_043806880.1	0.040289427	1.188104996	-0.632727231	putative pentatricopeptide repeat-containing protein At1g53330 isoform X2
XP_021628073.2	0.022005828	1.396841214	-0.627306699	putative Peroxidase 48
XP_021606974.1	0.04025969	0.594183156	-0.624401039	kinesin-related protein 4
XP_021595280.1	0.001310149	1.397578577	-0.62288085	beta-glucosidase 18
XP_021620878.1	0.007438088	0.941787312	-0.618917634	60S ribosomal protein L18-2
XP_021622196.1	0.04025969	-1.163773123	-0.595091946	nuclear transcription factor Y subunit B-10 isoform X3
XP_043811654.1	0.024783448	0.66087316	-0.575493679	cytochrome P450 714C2-like isoform X2
XP_021598277.1	0.044813689	0.472117669	-0.574835595	glucan endo-1,3-beta-glucosidase 1
XP_021618509.1	0.024089974	0.193185668	-0.552387769	uncharacterized protein LOC110619396
XP_043814207.1	0.024089974	0.193185668	-0.552387769	uncharacterized protein LOC110619395 isoform X2
XP_043814206.1	0.023474394	0.19379653	-0.550456276	uncharacterized protein LOC110619395 isoform X1
XP_043815370.1	0.04025969	1.2985846	-0.542028829	small polypeptide DEVIL 16-like
XP_021626808.1	0.03721448	-5.11731361	-0.528065469	vesicle transport protein GOT1
XP_021626809.1	0.03721448	-5.11731361	-0.528065469	probable 2-carboxy-D-arabinitol-1-phosphatase
XP_021608340.1	0.038267815	-3.197416642	-0.507924427	beta-galactosidase isoform X1
XP_021633495.1	0.035276215	0.976700282	-0.507904793	60S ribosomal protein L17-2
XP_043806956.1	0.046368581	1.876536745	-0.501016896	ABC transporter F family member 4 isoform X1
XP_021601376.2	0.000671555	0.867362091	-0.485161109	E3 ubiquitin-protein ligase WAV3
XP_021601377.2	0.000671555	0.867362091	-0.485161109	protein LAZ1 homolog 1 isoform X1
XP_043814927.1	0.00013423	2.446526144	-0.478905905	probable E3 ubiquitin-protein ligase ZFP1 isoform X1

XP_043814928.1	0.00013423	2.446526144	-0.478905905	probable E3 ubiquitin-protein ligase ZFP1 isoform X1
XP_021633750.1	0.007072971	0.816500615	-0.470711727	axial regulator YABBY 4 isoform X3
XP_021626065.1	0.005291359	-1.184577698	-0.457691646	putative disease resistance protein RGA3
XP_021616107.1	0.014210475	1.24417693	-0.453444103	probable serine/threonine-protein kinase At1g54610
XP_021615023.1	0.001221087	-6.812689767	-0.446497056	60S ribosomal protein L34
XP_043807862.1	0.002343353	-1.957695268	-0.443003846	uncharacterized vacuolar membrane protein YML018C isoform X3
XP_043814113.1	0.008254474	1.055533513	-0.439579307	protein NRT1/ PTR FAMILY 5.4-like isoform X3
XP_043814114.1	0.008254474	1.055533513	-0.439579307	protein NRT1/ PTR FAMILY 5.4-like isoform X4
XP_043809973.1	0.039564696	3.504802971	-0.438564279	uncharacterized protein LOC110609013
XP_021631309.1	0.007053308	1.556046035	-0.438394576	transcription factor VOZ1
XP_021614953.1	0.036118591	-0.901367966	-0.420067795	RING-H2 finger protein ATL56
XP_043807649.1	0.046368581	0.958549179	-0.419826678	putative transcription factor bHLH041 isoform X1
XP_021626492.1	5.73665E-06	1.09538763	-0.411564619	phosphoglucan phosphatase DSP4, amyloplastic isoform X1
XP_043808066.1	0.008296925	1.373268069	-0.410333926	uncharacterized protein LOC110603064
XP_021600544.1	0.025386367	0.340772737	-0.406974022	uncharacterized protein LOC110606098 isoform X2
XP_021601614.1	0.034964288	1.332304449	-0.404336623	uncharacterized protein LOC110606917 isoform X1
XP_021607522.1	0.009046239	4.053183184	-0.402796242	long chain acyl-CoA synthetase 6, peroxisomal isoform X1
XP_021608341.1	0.035276215	-3.157152322	-0.389637987	beta-galactosidase isoform X2
XP_021615784.1	0.019372893	1.949309723	-0.387544838	uncharacterized protein LOC110617357 isoform X3
XP_021600452.1	0.001978783	0.732534396	-0.377341554	probable arabinosyltransferase ARAD1
XP_043811510.1	0.008350493	1.397137234	-0.368807201	probable E3 ubiquitin-protein ligase MARCHF10 isoform X3
XP_043805429.1	0.001987907	0.775498578	-0.367700519	uncharacterized protein LOC122721552
XP_021623340.1	0.011631351	-1.13385484	-0.364164494	DNA gyrase subunit B, chloroplastic/mitochondrial isoform X1
XP_043806021.1	0.005091014	1.260092136	-0.360529167	uncharacterized protein LOC110599817
XP_043805428.1	0.001959717	0.779746174	-0.357260653	uncharacterized protein LOC122721551
XP_021622778.1	0.024783448	-0.987196566	-0.350077676	tyrosine-specific transport protein

XP_021624682.1	0.028946562	0.465003552	-0.34208196	uncharacterized protein LOC110623954 isoform X1
XP_021628900.1	0.046368581	1.573375415	-0.337196435	protein BASIC PENTACYSTEINE4
XP_021606998.1	0.033111847	2.529041306	-0.327898861	receptor-like cytosolic serine/threonine-protein kinase RBK2 isoform X2
XP_021606999.1	0.033111847	2.529041306	-0.327898861	polygalacturonase QRT3
XP_043813723.1	0.001152961	0.937686558	-0.327750955	nucleolin-like
XP_021632555.1	0.022000408	0.904995963	-0.31650058	B3 domain-containing transcription factor ABI3
XP_021632558.1	0.022000408	0.904995963	-0.31650058	putative ETHYLENE INSENSITIVE 3-like 4 protein
XP_021632559.1	0.022000408	0.904995963	-0.31650058	putative ETHYLENE INSENSITIVE 3-like 4 protein
XP_043805459.1	0.022000408	0.904995963	-0.31650058	uncharacterized acetyltransferase At3g50280
XP_043805526.1	0.022000408	0.904995963	-0.31650058	casein kinase II subunit alpha-2 isoform X2
XP_021610976.1	0.045064703	1.219388381	-0.314145082	transcription factor 25
XP_021618536.1	0.022516222	-0.750124457	-0.29516256	ultraviolet-B receptor UVR8 isoform X1
XP_043813303.1	0.001152961	0.951133539	-0.293739037	uncharacterized protein LOC110617922 isoform X1
XP_021621039.1	0.024130837	5.815302889	-0.292162988	uncharacterized protein LOC110621192
XP_021593678.1	0.006452073	1.188314379	-0.288733817	DExH-box ATP-dependent RNA helicase DEXH3 isoform X1
XP_021597570.1	0.024835491	1.309806981	-0.286714259	uncharacterized protein LOC110603890 isoform X2
XP_021593669.1	0.007053308	1.181382261	-0.281061548	uncharacterized protein LOC110600998
XP_021616061.1	0.037995292	0.933905879	-0.278772791	acyl-protein thioesterase 2 isoform X5
XP_043814922.1	0.030763488	1.148556781	-0.267235149	probable E3 ubiquitin-protein ligase ZFP1 isoform X1
XP_043814921.1	0.048882238	1.107943511	-0.267232053	probable E3 ubiquitin-protein ligase ZFP1 isoform X1
XP_043814920.1	0.033502214	1.165336466	-0.263313995	probable E3 ubiquitin-protein ligase ZFP1 isoform X1
XP_043814919.1	0.033709783	1.165324325	-0.262438896	probable E3 ubiquitin-protein ligase ZFP1 isoform X1
XP_021616219.1	0.038319669	0.780962861	-0.256758969	uncharacterized protein LOC110617614 isoform X2
XP_043810892.1	0.013743901	-0.961619688	-0.254088065	probable cytokinin riboside 5'-monophosphate phosphoribohydrolase LOGL10 isoform X2
XP_021611332.1	0.022121658	1.093589668	-0.251594384	scarecrow-like protein 3

XP_043809743.1	0.010193335	2.873286311	-0.248025053	prostatic spermine-binding protein-like
XP_043818236.1	0.010943685	4.183836679	-0.247452532	L-cysteine desulfhydrase
XP_021629729.1	0.034596272	-1.214276703	-0.245056396	isovalerate--CoA ligase CCL2
XP_021606997.1	0.041606296	2.561717889	-0.241406301	receptor-like cytosolic serine/threonine-protein kinase RBK2 isoform X1
XP_043817999.1	0.037046932	1.25822163	-0.241159292	putative protease Do-like 14
XP_021607001.1	0.037277136	2.639668958	-0.234177079	3-isopropylmalate dehydratase large subunit, chloroplastic isoform X2
XP_021602706.2	0.024089974	1.649288161	-0.232015163	phenylacetaldehyde reductase isoform X1
XP_021624402.1	0.000285071	-1.325548706	-0.231278668	cyclic dof factor 1
XP_021596175.1	0.038659365	-0.858182104	-0.230579913	uncharacterized protein LOC110602897 isoform X2
XP_043806941.1	0.022832269	0.758844679	-0.230488204	uncharacterized protein LOC122721910
XP_021632836.1	0.042792187	0.646465054	-0.225166164	iron-sulfur assembly protein IscA, chloroplastic isoform X1
XP_043815541.1	0.014912885	-0.556847147	-0.224552224	serine/threonine-protein kinase CTR1 isoform X2
XP_021619095.1	0.007516317	-0.980133128	-0.221886196	protein GDAP2 homolog
XP_021596174.1	0.039564696	-0.850253433	-0.21767841	uncharacterized protein LOC110602897 isoform X1
XP_021628271.1	0.042040336	1.139755279	-0.215386803	BON1-associated protein 2
XP_021607564.1	0.030955043	-6.449474448	-0.204718293	uncharacterized protein LOC110611490
XP_021594466.1	0.007893299	1.445800637	-0.204077675	probable disease resistance protein At4g27220
XP_021620327.1	0.045795352	-0.887120573	-0.201808462	uncharacterized protein LOC110620776 isoform X2
XP_043815222.1	0.045795352	-0.887120573	-0.201808462	uncharacterized protein LOC110620776 isoform X1
XP_043816924.1	0.046368581	-2.04553506	-0.199696806	uncharacterized protein LOC110625009 isoform X2
XP_043804845.1	0.035658899	-1.087714773	-0.196376722	uncharacterized protein LOC110610937
XP_021595706.1	0.00521536	1.238331843	-0.189251309	60S ribosomal protein L32-1
XP_021631975.1	0.000469031	2.227016226	-0.163140085	GDP-mannose transporter GONST3
XP_043817416.1	0.019775405	1.138820726	-0.159875549	uncharacterized protein LOC122725054
XP_043815719.1	0.017212369	1.31708018	-0.138487721	pentatricopeptide repeat-containing protein At1g62930, chloroplastic-like
XP_021615216.1	0.017986469	1.317237412	-0.135280381	replication protein A 70 kDa DNA-binding subunit B

XP_021615217.1	0.017986469	1.317237412	-0.135280381	telomere-associated protein RIF1
XP_021611746.1	0.034964288	-1.883584006	-0.133614116	pectinesterase 3
XP_021611747.1	0.034964288	-1.883584006	-0.133614116	thioredoxin-like fold domain-containing protein MRL7L, chloroplastic
XP_021611748.1	0.034964288	-1.883584006	-0.133614116	protein ABIL2
XP_021625350.1	0.007530082	-1.35723175	-0.13133576	histone deacetylase 6
XP_021607000.1	0.039564696	2.805121494	-0.129708421	3-isopropylmalate dehydratase large subunit, chloroplastic isoform X1
XP_021627445.2	0.04969806	0.741305414	-0.120423642	MDIS1-interacting receptor like kinase 2-like
XP_043809379.1	0.045583092	1.832325128	-0.117779232	low affinity sulfate transporter 3 isoform X2
XP_021623949.1	0.039390337	1.17377792	-0.112981189	36.4 kDa proline-rich protein
XP_021609492.1	0.034964288	1.519133268	-0.112175322	dof zinc finger protein DOF3.1
XP_021615087.1	0.041082756	-0.86363607	-0.101170725	U6 snRNA phosphodiesterase
XP_043812816.1	0.046368581	1.15982337	-0.099382721	UDP-glycosyltransferase 83A1
XP_021615088.1	0.043734202	-0.855208053	-0.098933174	protein QUIRKY
XP_021595017.1	0.046368581	1.371149191	-0.097083876	folate-biopterin transporter 1, chloroplastic isoform X3
XP_043816207.1	0.037799179	-0.771019578	-0.09486483	iron-sulfur assembly protein IscA-like 1, mitochondrial isoform X1
XP_021623956.1	0.043687102	1.172114201	-0.082212464	probable lysophospholipase BODYGUARD 3
XP_021631974.1	0.000671555	2.241237103	-0.076713474	uncharacterized protein LOC110629355
XP_043816361.1	0.000156116	-1.328721456	-0.076226863	myosin-binding protein 1 isoform X1
XP_043816362.1	0.000156116	-1.328721456	-0.076226863	myosin-binding protein 1 isoform X2
XP_021607771.1	0.03040763	1.189310101	-0.065091569	protein transport protein SEC13 homolog B
XP_021602173.1	0.030955043	3.813818624	-0.059540109	probable LRR receptor-like serine/threonine-protein kinase At2g24230
XP_021634307.1	0.000847351	-3.943291688	-0.049533259	heterogeneous nuclear ribonucleoprotein H2 isoform X3
XP_043814870.1	0.011566192	1.080452624	-0.043144842	probable galacturonosyltransferase 4 isoform X1
XP_021602346.1	0.006977802	1.538755997	-0.04151094	cyclin-D4-2
XP_021603631.1	0.046368581	-1.140422486	-0.04126648	ubiquitin-conjugating enzyme E2 30 isoform X2
XP_043814609.1	0.045583092	-1.760843688	-0.037375634	DNA-(apurinic or apyrimidinic site) endonuclease 2 isoform X2

XP_021623671.1	0.012035395	-0.865004668	-0.035478695	putative deoxyribonuclease TATDN1 isoform X1
XP_021623672.1	0.012035395	-0.865004668	-0.035478695	putative deoxyribonuclease TATDN1 isoform X2
XP_021621558.1	0.005639315	-5.412603818	-0.032299819	rRNA 2'-O-methyltransferase fibrillarin
XP_021602326.1	0.010168991	1.511958022	-0.032219437	suppressor of disruption of TFIIIS
XP_021594338.1	0.007546772	1.376164531	-0.027652307	uncharacterized protein LOC110601496
XP_021612752.1	0.022005828	1.471662344	-0.02611748	receptor-like protein kinase FERONIA
XP_043806597.1	0.037993364	3.854735284	-0.025843809	reticulon-like protein B21 isoform X2
XP_043807863.1	0.004567084	0.687958144	-0.023060026	cysteine-rich receptor-like protein kinase 10 isoform X2
XP_021624105.1	0.046368581	-0.933059467	-0.021288926	pentatricopeptide repeat-containing protein At5g18390, mitochondrial
XP_043807440.1	0.001951452	1.551068768	-0.0175503	disease resistance protein RPS2 isoform X2
XP_021607884.1	0.026952241	2.296302974	-0.016457029	protein NPGR2
XP_043811434.1	0.000671555	-0.868589899	-0.01446454	rhamnogalacturonate lyase B-like
XP_043814158.1	0.038571205	1.755738673	-0.003651668	phenylacetaldehyde reductase-like
XP_021612750.1	0.024089974	1.454761788	-0.001923512	receptor-like protein kinase FERONIA
XP_021622515.1	0.019372893	-2.550956679	0.002110605	squamosa promoter-binding-like protein 9 isoform X1
XP_021622516.1	0.019372893	-2.550956679	0.002110605	squamosa promoter-binding-like protein 9 isoform X2
XP_021622517.1	0.019372893	-2.550956679	0.002110605	UBP1-associated protein 2A
XP_021622518.1	0.019372893	-2.550956679	0.002110605	myb family transcription factor PHL5
XP_021622520.1	0.019372893	-2.550956679	0.002110605	uncharacterized protein LOC110622344
XP_021612751.1	0.022005828	1.474906141	0.002620477	cytochrome P450 CYP749A22
XP_021614385.1	0.010943685	-0.976009424	0.005651152	probable glutathione S-transferase
XP_021602322.1	0.003575969	1.551134031	0.010502167	abscisic acid 8'-hydroxylase 2 isoform X2
XP_043807437.1	0.003575969	1.551134031	0.010502167	disease resistance protein At4g27190 isoform X1
XP_043816121.1	0.032529927	2.564672199	0.011220367	mitogen-activated protein kinase kinase kinase 20-like
XP_021602336.1	0.00921736	1.551961254	0.023664887	transmembrane protein 18
XP_021633499.1	0.024089974	1.584986013	0.031280483	homeobox-leucine zipper protein HDG2 isoform X1

XP_021633529.1	0.011216352	-0.898916792	0.031505654	conserved oligomeric Golgi complex subunit 1 isoform X3
XP_021633530.1	0.011216352	-0.898916792	0.031505654	WAT1-related protein At1g43650
XP_021598519.1	0.003444041	1.332152239	0.03235129	uncharacterized protein LOC110604589 isoform X2
XP_021598517.1	0.005291359	1.329176629	0.035467417	40S ribosomal protein S7
XP_021607662.1	0.006109963	1.503666393	0.038130372	uncharacterized protein LOC110611581
XP_021593399.1	0.046368581	0.952476796	0.038679737	WD repeat-containing protein 26 homolog
XP_043809378.1	0.002549724	1.568657416	0.03901539	abscisic acid 8'-hydroxylase 2 isoform X1
XP_021617505.1	0.018360029	2.193811521	0.04400504	nuclear transcription factor Y subunit A-1
XP_043808822.1	0.039564696	-0.750356382	0.064348108	nitrate regulatory gene2 protein-like
XP_021598518.1	0.009615451	1.310383534	0.065181441	uncharacterized protein LOC110604589 isoform X1
XP_021632917.1	0.027515608	-1.210326581	0.069986533	AT-hook motif nuclear-localized protein 17 isoform X1
XP_021632930.1	0.027515608	-1.210326581	0.069986533	protein STRICTOSIDINE SYNTHASE-LIKE 10
XP_043806374.1	0.000898847	-3.915341734	0.071325133	heterogeneous nuclear ribonucleoprotein F isoform X2
XP_043812311.1	0.025211444	-0.637842635	0.073340744	MADS-box protein SOC1 isoform X1
XP_021620772.1	0.024554611	0.580899327	0.076189346	uncharacterized protein LOC110621053 isoform X1
XP_043818194.1	0.035658899	0.533984124	0.076837347	uncharacterized protein LOC110627907
XP_021632943.1	0.025211444	-1.204871792	0.078639368	LRR receptor-like serine/threonine-protein kinase RGI3
XP_021632957.1	0.025211444	-1.204871792	0.078639368	regulatory protein RecX isoform X1
XP_021632966.1	0.025211444	-1.204871792	0.078639368	regulatory protein RecX isoform X2
XP_021632433.1	0.018568616	1.138106142	0.079802243	YTH domain-containing protein ECT1 isoform X2
XP_043816876.1	8.53204E-05	-0.812941896	0.083876431	LOW QUALITY PROTEIN: mitogen-activated protein kinase kinase kinase 1-like
XP_043812312.1	0.031470699	-0.62323535	0.084096638	MADS-box protein SOC1 isoform X1
XP_021592887.1	6.70798E-09	-6.556918896	0.084410088	uncharacterized protein LOC110600355
XP_021602172.1	0.026249652	3.921084388	0.084522535	reticulon-like protein B21 isoform X1
XP_021602171.1	0.022913823	3.956947012	0.085459593	probable WRKY transcription factor 32

XP_021634306.2	4.71545E-05	-3.96274742	0.090683434	LOW QUALITY PROTEIN: zinc finger CCCH domain-containing protein 56-like
XP_043806373.1	4.71545E-05	-3.96274742	0.090683434	heterogeneous nuclear ribonucleoprotein F isoform X1
XP_021614011.1	0.039564696	-0.611446399	0.092981513	probable metal-nicotianamine transporter YSL7 isoform X1
XP_021622971.1	0.000167167	-1.127799424	0.095718368	uncharacterized protein LOC110622683
XP_021606019.1	0.034592764	1.038220524	0.09686065	uncharacterized protein LOC110610411
XP_021627696.1	0.000898847	3.146946015	0.098244034	endochitinase EP3
XP_043808505.1	3.90288E-05	2.648556608	0.102821105	uncharacterized protein LOC110607353 isoform X1
XP_021594716.1	0.01437066	-1.556934275	0.108717662	translationally-controlled tumor protein homolog isoform X2
XP_021623903.1	0.018360029	0.85205318	0.118538121	FRIGIDA-like protein 4a
XP_021633956.1	0.010078253	-2.259619215	0.127211717	uncharacterized protein LOC110630714 isoform X1
XP_043812289.1	0.000263077	1.265166818	0.127723365	transcription factor MYB17 isoform X2
XP_021632189.1	0.006220587	-1.247295013	0.153189017	MADS-box transcription factor 23 isoform X1
XP_043806601.1	0.012353226	-2.336489167	0.170660661	uncharacterized protein LOC110630714 isoform X3
XP_021592329.1	0.001918531	1.113004937	0.171000287	zinc finger protein 4
XP_021627420.1	0.005032851	-1.086981986	0.172189972	uncharacterized protein LOC110626004
XP_021602216.1	0.004946747	1.0936099	0.176388218	transcription factor MYB92
XP_021629982.1	0.009025195	-0.952259005	0.185519684	nicotianamine aminotransferase 1
XP_043804540.1	0.009025195	-0.952259005	0.185519684	membrane protein of ER body 2 isoform X2
XP_021630139.1	0.033913148	-0.730817471	0.201456384	39S ribosomal protein L47, mitochondrial
XP_043805882.1	0.04412594	1.552153481	0.210081856	uncharacterized protein LOC122721620
XP_021630985.1	0.035276215	3.189457973	0.213408659	uncharacterized protein LOC110628563 isoform X1
XP_021630986.1	0.035276215	3.189457973	0.213408659	uncharacterized protein LOC110628563 isoform X2
XP_021631830.1	0.048242461	-0.553341419	0.221254606	uncharacterized protein LOC110629224
XP_043807710.1	0.04412594	1.100015367	0.224696494	probable terpene synthase 13 isoform X2
XP_021604018.1	0.004868973	2.433794054	0.225583064	uncharacterized protein LOC110609020
XP_043807033.1	0.034940874	-0.657985153	0.228340972	uncharacterized protein LOC110601507

XP_021627865.1	0.019100575	0.955927618	0.23010224	uncharacterized protein At4g10930 isoform X2
XP_043807753.1	0.025618234	1.710011254	0.237829907	uncharacterized protein LOC110626934
XP_043806251.1	5.73665E-06	-3.631393352	0.23785052	glyceraldehyde-3-phosphate dehydrogenase GAPCP2, chloroplastic isoform X2
XP_021628376.1	0.008350493	1.409182697	0.241551657	factor of DNA methylation 1 isoform X2
XP_043816380.1	0.008254474	-0.71312061	0.248380781	adenylyl-sulfate kinase 3 isoform X1
XP_043814776.1	0.039564696	1.716443592	0.249330816	1,4-alpha-glucan-branching enzyme 2-2, chloroplastic/amyloplastic isoform X1
XP_043814239.1	0.034046961	-0.747662043	0.260227369	dynamamin-related protein 3A isoform X2
XP_021631196.1	0.038319669	-1.913588548	0.265529437	probable pectate lyase 5
XP_021612500.1	0.012293136	1.759135762	0.269372911	kinesin-like protein KIN-8A isoform X1
XP_021598651.1	0.013237614	1.268082434	0.275611288	uncharacterized protein LOC110604690 isoform X1
XP_021596959.1	0.043541199	1.314442336	0.287428714	probable apyrase 6
XP_021632100.1	0.035658899	-0.970893636	0.304671706	haloacid dehalogenase-like hydrolase domain-containing protein At4g39970
XP_021607143.1	0.013877939	2.110922523	0.313595901	putative E3 ubiquitin-protein ligase RF298 isoform X2
XP_021625475.1	0.022005828	0.957670138	0.319060858	uncharacterized protein LOC110624585
XP_021600044.1	0.035829821	-1.566111865	0.31997046	protein DMR6-LIKE OXYGENASE 2
XP_043817550.1	2.09198E-05	-1.296087949	0.326507954	uncharacterized protein LOC110626004
XP_043816314.1	0.002798354	-0.861945416	0.334239851	transcription factor MYB124 isoform X1
XP_021619524.1	0.038340303	-0.352139228	0.340789622	proactivator polypeptide-like 1
XP_021619526.1	0.039564696	-0.349808545	0.340798863	metal tolerance protein 4
XP_021619527.1	0.039564696	-0.349808545	0.340798863	protein MKS1
XP_021634308.1	0.000912784	-4.182155324	0.349882114	heterogeneous nuclear ribonucleoprotein H2 isoform X4
XP_021634309.1	0.000912784	-4.182155324	0.349882114	chaperonin-like RbcX protein 2, chloroplastic isoform X1
XP_021634311.1	0.000912784	-4.182155324	0.349882114	chaperonin-like RbcX protein 2, chloroplastic isoform X2
XP_043806250.1	0.000912784	-4.182155324	0.349882114	glyceraldehyde-3-phosphate dehydrogenase GAPCP2, chloroplastic isoform X1

XP_021607027.1	0.010261621	-0.725645818	0.349941151	pentatricopeptide repeat-containing protein At5g18950 isoform X3
XP_021600419.1	0.033348678	-0.260770822	0.350361041	ER lumen protein-retaining receptor erd-2.2
XP_043815365.1	0.003424903	-1.416172752	0.351043908	uncharacterized protein LOC110620863 isoform X2
XP_021596844.1	0.004946747	-0.814150885	0.352457564	RNA-binding KH domain-containing protein RCF3
XP_021610921.1	0.022000408	-0.669076826	0.359207647	jacalin-related lectin 19
XP_043814423.1	0.013056484	-1.099427461	0.359942575	uncharacterized protein sll0005 isoform X5
XP_021610924.1	0.022911873	-0.663272849	0.361815143	IAA-amino acid hydrolase ILR1-like 4
XP_021609323.1	0.00217968	-1.279043382	0.362061084	AP-2 complex subunit alpha-1 isoform X4
XP_043814424.1	0.013617226	-1.093103669	0.36246002	uncharacterized protein sll0005 isoform X6
XP_043815258.1	0.030955043	-1.656927238	0.368038429	ATP-dependent zinc metalloprotease FTSH 7, chloroplastic isoform X3
XP_043814422.1	0.010193335	-1.055504277	0.369585492	uncharacterized protein slr1919 isoform X4
XP_021616080.1	0.045795352	-1.561430077	0.371199152	uncharacterized protein LOC110617533
XP_021593734.1	0.032565186	-0.500934885	0.375292468	GDSL esterase/lipase At5g55050
XP_043812220.1	0.013743901	-1.158698791	0.376052161	AP-2 complex subunit alpha-1 isoform X5
XP_043809888.1	0.006072743	-2.461218217	0.377690251	bifunctional adenosine 5'-phosphosulfate phosphorylase/adenylylsulfatase HINT4 isoform X2
XP_021634909.1	0.006202741	2.200171435	0.383726855	methionyl-tRNA formyltransferase isoform X2
XP_021634921.1	0.006072743	2.205198852	0.388004765	heavy metal-associated isoprenylated plant protein 21
XP_021614102.1	0.025618234	-1.648676097	0.396653702	ATP-dependent zinc metalloprotease FTSH 7, chloroplastic isoform X2
XP_021614178.1	0.025618234	-1.648676097	0.396653702	ATP-dependent zinc metalloprotease FTSH 9, chloroplastic isoform X4
XP_021616082.1	0.036428328	-1.559414734	0.400971187	uncharacterized protein LOC110617533
XP_021616724.1	0.000266161	-0.565536594	0.403486703	AP2-like ethylene-responsive transcription factor PLT2 isoform X1
XP_021616081.1	0.036419455	-1.55930519	0.408756114	uncharacterized protein LOC110617533
XP_021604958.1	0.000847351	-0.711032906	0.41186146	probable prolyl 4-hydroxylase 10 isoform X1
XP_021614952.1	0.033502214	-1.668930701	0.42133538	histone H3.2
XP_021602621.1	0.046368581	-0.594562493	0.430879014	uncharacterized protein LOC110607765

XP_043811511.1	0.024783448	-2.501062942	0.451892113	uncharacterized protein LOC122723432
XP_043807847.1	0.000693012	-2.516258039	0.461895623	pyruvate kinase, cytosolic isozyme isoform X1
XP_043810783.1	0.00591969	1.056113123	0.46289052	3-deoxy-manno-octulosonate cytidyltransferase, mitochondrial
XP_021621609.1	0.00148452	-1.45817262	0.466488487	protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 1
XP_043805633.1	0.046368581	-0.944004832	0.468695542	DDT domain-containing protein DDB_G0282237 isoform X4
XP_043805634.1	0.046368581	-0.943471372	0.468696114	DDT domain-containing protein DDB_G0282237 isoform X5
XP_021622229.1	0.024783448	1.420353333	0.475083256	B3 domain-containing protein At2g32645
XP_021622230.1	0.024783448	1.420353333	0.475083256	uncharacterized protein LOC110622132
XP_021622231.1	0.024783448	1.420353333	0.475083256	uncharacterized protein LOC110622133
XP_021622232.1	0.024783448	1.420353333	0.475083256	probable serine/threonine-protein kinase PBL25
XP_021613165.1	0.00217968	3.028704113	0.487024413	delta(8)-fatty-acid desaturase 2
XP_021597024.1	0.039691888	1.772398514	0.492936322	starch synthase 3, chloroplastic/amyloplastic isoform X1
XP_021622233.1	0.026520965	1.450034017	0.493474174	putative gamma-glutamylcyclotransferase At3g02910
XP_021603128.1	0.00246991	2.218899858	0.494626928	uncharacterized protein LOC110608224
XP_021622234.1	0.029633776	1.442904626	0.499675579	BTB/POZ domain and ankyrin repeat-containing protein NOOT2
XP_021622235.1	0.029633776	1.442904626	0.499675579	probable F-box protein At2g36090
XP_021604955.1	0.000266161	-0.265734807	0.524333508	probable prolyl 4-hydroxylase 10 isoform X1
XP_021592033.1	0.024783448	4.030958606	0.526693789	probable polygalacturonase
XP_021596305.1	0.006547831	-0.405693794	0.535428655	2-hydroxy-6-oxononadienedioate/2-hydroxy-6-oxononatrienedioate hydrolase isoform X3
XP_021595365.1	0.00038545	-1.366790674	0.536671925	RAN GTPase-activating protein 2 isoform X2
XP_021594634.1	0.029343466	1.166374159	0.541334149	uncharacterized protein sll0005
XP_021623282.1	0.046338652	-0.785718814	0.545421099	ubiquitin carboxyl-terminal hydrolase 8
XP_043816159.1	0.000898847	1.208006693	0.547355504	serine/threonine-protein kinase STY13
XP_021594636.1	0.039228091	1.190713505	0.549308964	tubulin alpha-5 chain
XP_021615482.1	0.0218195	1.042328428	0.552561147	uncharacterized protein LOC110617173 isoform X2

XP_043812547.1	0.00012164	-1.375096283	0.552617827	inactive glucose-1-phosphate adenylyltransferase small subunit 2, chloroplastic isoform X1
XP_043813858.1	0.026133544	1.155332459	0.554535821	BURP domain-containing protein 12
XP_021609028.1	0.00855137	0.796294446	0.563081365	uncharacterized protein LOC110612560
XP_021594517.1	0.035276215	-0.379310558	0.565474171	uncharacterized protein LOC110601623
XP_021617860.1	0.045091289	-1.727641847	0.56989201	alpha-L-fucosidase 2 isoform X1
XP_021622791.1	0.004651338	-4.709153876	0.570661887	CASP-like protein 2B1 isoform X3
XP_021595497.1	0.015973896	1.947464281	0.572924934	carbonic anhydrase, chloroplastic isoform X1
XP_021614562.1	0.034975685	1.013883298	0.574829952	bidirectional sugar transporter SWEET10
XP_043816422.1	0.013617226	-3.012221124	0.575567186	uncharacterized protein LOC110622321 isoform X3
XP_021620273.1	0.039047503	3.076019423	0.576225343	protein BONZAI 3 isoform X2
XP_043815082.1	0.039047503	3.077351343	0.576239704	protein BONZAI 3 isoform X1
XP_043816178.1	0.004945764	-0.398458362	0.576493946	2-hydroxy-6-oxononadienedioate/2-hydroxy-6-oxononatrienedioate hydrolase isoform X4
XP_043810605.1	0.034317733	1.491007339	0.583044106	pentatricopeptide repeat-containing protein At5g21222 isoform X2
XP_021623281.1	0.032308104	-0.807879312	0.586587535	histone-lysine N-methyltransferase SUVR3
XP_043806471.1	0.04032774	1.403177027	0.590031547	5'-deoxynucleotidase HDDC2 isoform X2
XP_021632103.1	0.04412594	1.308585713	0.596677494	transcription factor TCP20
XP_043813064.1	0.006956382	-2.370320614	0.606920695	E3 ubiquitin-protein ligase UPL2 isoform X1
XP_021623209.1	0.045760898	-1.105613517	0.614101209	RRP12-like protein isoform X3
XP_021604744.1	0.048242461	-0.16450069	0.616417254	zinc finger MYND domain-containing protein 15 isoform X3
XP_021622301.1	0.0218195	-1.29836528	0.622328811	putative DNA (cytosine-5)-methyltransferase CMT1 isoform X1
XP_021623896.1	0.037995292	-0.599650075	0.629444985	uncharacterized protein LOC110623286
XP_043817344.1	0.020164544	-1.191540681	0.648584122	receptor like protein 21
XP_021633816.1	0.024783448	1.986642969	0.648615121	glutathione hydrolase 1 isoform X1
XP_021633818.1	0.024783448	1.986642969	0.648615121	glutathione hydrolase 1 isoform X2
XP_043805151.1	0.024783448	1.986642969	0.648615121	putative inactive glutathione hydrolase 4 isoform X3

XP_043809759.1	7.69527E-06	-3.793356641	0.658658772	uncharacterized protein LOC122723072
XP_043810022.1	0.031005347	-0.92390796	0.664045618	transcription factor bHLH110 isoform X3
XP_021618582.1	0.024783448	-1.585463869	0.670558166	protein IQ-DOMAIN 3
XP_043806682.1	5.98887E-05	-0.641257323	0.670799655	isochorismate synthase 2, chloroplastic isoform X3
XP_021616780.1	0.048359719	-0.660707584	0.676843452	uncharacterized protein LOC110618063 isoform X2
XP_021616784.1	0.048359719	-0.660707584	0.676843452	auxin-responsive protein IAA31
XP_021616785.2	0.048359719	-0.660707584	0.676843452	ankyrin repeat-containing protein At5g02620
XP_021616786.1	0.048359719	-0.660707584	0.676843452	uncharacterized protein LOC110618068
XP_021607922.1	0.039564696	-0.261060203	0.681448237	diacylglycerol O-acyltransferase 1 isoform X2
XP_021616787.1	0.046368581	-0.648118438	0.685358228	gamma carbonic anhydrase-like 2, mitochondrial
XP_021623897.1	0.015312729	-0.5402388	0.695275734	exopolygalacturonase
XP_021608816.1	0.009008862	-0.738580437	0.695489537	uncharacterized protein LOC110612347 isoform X1
XP_021596132.2	0.015349513	-0.538784666	0.710448292	NADP-dependent malic enzyme
XP_021607134.1	0.000898847	2.18649776	0.710577699	ethylene receptor 2
XP_021629709.1	6.04373E-06	-1.057463828	0.715136275	uncharacterized protein LOC110627674
XP_021629222.1	0.020041805	-0.116312179	0.715959254	probable GABA transporter 2
XP_021606204.1	0.046368581	2.098043287	0.716177872	peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic isoform X1
XP_021606206.1	0.046368581	2.098043287	0.716177872	peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic isoform X3
XP_021606207.1	0.046368581	2.098043287	0.716177872	protein TIFY 4B isoform X1
XP_021606208.1	0.046368581	2.098043287	0.716177872	protein TIFY 4B isoform X3
XP_021606209.1	0.046368581	2.098043287	0.716177872	uncharacterized protein LOC110610546
XP_043811435.1	0.046368581	2.098043287	0.716177872	protein TIFY 4B isoform X2
XP_043811436.1	0.046368581	2.098043287	0.716177872	protein TIFY 4B isoform X4
XP_021629231.1	0.046368581	-0.134255278	0.726845628	probable GABA transporter 2
XP_021624332.1	0.024089974	2.055041563	0.72801641	uncharacterized protein LOC110623640
XP_043814802.1	0.007336006	-1.210605956	0.738071206	uncharacterized protein LOC122724336

XP_021602641.2	0.016520293	-1.057202724	0.755597798	AAA-ATPase ASD, mitochondrial
XP_043817342.1	0.016520293	-1.057202724	0.755597798	LOW QUALITY PROTEIN: receptor-like protein 56
XP_021609899.1	9.29449E-10	-3.866689188	0.758286562	LOB domain-containing protein 1
XP_021609900.1	9.29449E-10	-3.866689188	0.758286562	signal recognition particle 14 kDa protein
XP_021627867.1	0.039424774	-0.529926705	0.761104848	guanine nucleotide-binding protein subunit gamma 3
XP_021627868.1	0.039424774	-0.529926705	0.761104848	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
XP_043817433.1	0.039424774	-0.529912803	0.761496857	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
XP_043813694.1	0.033348678	1.265304042	0.766508019	hsc70-interacting protein
XP_021591960.1	0.045153564	-0.545436802	0.773622572	mRNA cap guanine-N7 methyltransferase 1
XP_021596490.1	0.034046961	-0.65641327	0.779087702	serine/threonine-protein kinase RIPK
XP_021632520.1	0.010168991	0.337498993	0.781747872	uncharacterized protein LOC110629734
XP_021625976.1	0.001918531	2.546908319	0.789084066	UDP-glycosyltransferase TURAN isoform X1
XP_021618855.1	0.027250076	-1.257215151	0.793135284	uncharacterized protein LOC110619639
XP_043805206.1	0.000777943	-2.248439847	0.796394509	uncharacterized protein LOC110611039 isoform X3
XP_043811043.1	0.019372893	-0.531759665	0.798221061	desmethyl-deoxy-podophyllotoxin synthase-like
XP_021624260.1	0.011631351	1.891872628	0.804798621	uncharacterized protein LOC110623573
XP_021598461.1	0.032120713	1.515731163	0.808185899	uncharacterized protein LOC110604550 isoform X7
XP_021593637.1	0.032308104	-0.431573555	0.815324367	SAGA-associated factor 29 homolog A isoform X1
XP_043815174.1	0.005480459	3.357021795	0.817606682	snRNA-activating protein complex subunit isoform X1
XP_021601915.2	0.01885327	1.548878162	0.821321427	enoyl-CoA hydratase 2, peroxisomal
XP_021601917.1	0.018915937	1.549916453	0.823143755	uncharacterized protein LOC110607145
XP_043815279.1	0.005291359	-1.000761866	0.83202483	LOW QUALITY PROTEIN: probable LRR receptor-like serine/threonine-protein kinase At3g47570
XP_021601918.2	0.018654642	1.558405922	0.833829773	cytochrome P450 714C2
XP_021596489.1	0.037433398	-0.595809167	0.838821222	probable terpene synthase 13
XP_021609897.1	1.02435E-09	-3.794036908	0.8416168	pentatricopeptide repeat-containing protein At4g02750

XP_021601213.1	0.048242461	-0.857217163	0.852417545	stress response protein NST1
XP_043808776.1	0.026364833	2.233079224	0.860474493	uncharacterized protein LOC110605224 isoform X2
XP_021607159.1	0.046368581	-0.306677026	0.882601109	non-lysosomal glucosylceramidase isoform X1
XP_021632247.1	3.28368E-07	-0.932166634	0.890753361	mitochondrial import receptor subunit TOM7-1
XP_021611235.1	0.02173068	1.817672268	0.893224207	auxin-induced protein 15A
XP_021594352.1	0.048359719	-1.821412416	0.907574535	SWI/SNF complex subunit SWI3D isoform X2
XP_021607161.1	0.033320088	-0.259299878	0.914534965	non-lysosomal glucosylceramidase isoform X3
XP_021619161.1	2.90209E-07	-2.450318336	0.920621458	transcription factor bHLH140
XP_021606000.1	2.16241E-06	-3.9783035	0.926726809	pre-mRNA-processing protein 40C isoform X2
XP_021633085.1	0.02066258	2.029651892	0.930379068	GLABRA2 expression modulator isoform X1
XP_021602692.1	0.010584891	0.110626273	0.941682252	aspartic proteinase Asp1 isoform X2
XP_021615689.1	0.043732718	-0.340291508	0.943463225	uncharacterized protein LOC110617293
XP_043813276.1	0.043732718	-0.340291508	0.943463225	uncharacterized protein LOC110617293
XP_021597443.1	1.26389E-06	-1.258301583	0.946017057	actin-related protein 2/3 complex subunit 2A isoform X1
XP_021595091.1	0.00148452	-1.003537819	0.972270734	cyclin-dependent kinase inhibitor 5 isoform X4
XP_021598773.1	0.022930903	0.768262384	0.972942133	cinnamoyl-CoA reductase-like SNL6 isoform X1
XP_021634117.1	0.014288016	0.006072154	0.976663443	pentatricopeptide repeat-containing protein At5g61400
XP_021630023.1	0.000600915	-3.655447616	0.994696276	photosystem II core complex proteins psbY, chloroplastic
XP_021617446.1	3.78362E-09	-2.856857942	0.997263877	regulator of nonsense transcripts UPF2
XP_021633704.1	1.00822E-09	-3.323819871	1.038970151	thioredoxin 1
XP_021621903.1	0.036118591	-3.242383376	1.040777372	protein RETICULATA-RELATED 3, chloroplastic
XP_021601113.2	0.048623069	-1.462764428	1.049809843	L-ascorbate oxidase homolog
XP_021627838.1	0.000114538	-1.571632483	1.050674443	transportin-1 isoform X1
XP_021625198.1	0.012969159	-4.756862373	1.051640103	purine permease 3
XP_021622606.1	0.040811247	-0.967248071	1.063963384	lectin-domain containing receptor kinase VI.3
XP_021599912.1	0.043193705	0.83477667	1.086242856	pyridoxine/pyridoxamine 5'-phosphate oxidase 1, chloroplastic isoform X2

XP_021613334.1	0.001281782	-2.410676682	1.116641016	uncharacterized protein LOC110615649
XP_021606298.1	0.024667869	3.157834794	1.125355304	actin-related protein 2/3 complex subunit 4
XP_043816245.1	0.005291359	-0.07548742	1.128124569	putative pentatricopeptide repeat-containing protein At1g12700, mitochondrial
XP_021620131.1	0.045153564	0.310675081	1.139221873	protein yippee-like
XP_043816536.1	0.046368581	0.756477459	1.1642368	alpha/beta hydrolase domain-containing protein 17C isoform X5
XP_021603416.1	0.03721448	0.081837296	1.174181875	NAC domain-containing protein 17 isoform X1
XP_021604009.1	0.020301555	0.350704912	1.180711175	lisH domain-containing protein C1711.05 isoform X2
XP_021623529.1	0.03841955	-0.391598864	1.190273682	B3 domain-containing transcription repressor VAL2 isoform X2
XP_021596674.1	0.013953694	0.115335976	1.266729505	peptidyl-prolyl cis-trans isomerase Pin1
XP_021603432.1	0.046368581	1.825517724	1.26924788	probable methyltransferase PMT10
XP_021603433.1	0.046368581	1.825517724	1.26924788	integrin-linked protein kinase 1
XP_021604766.1	0.037995292	0.090933558	1.272691399	uncharacterized protein LOC110609483 isoform X1
XP_021600980.1	0.000671555	-0.956897568	1.276558794	probable protein phosphatase 2C 12
XP_021596620.1	0.025211444	0.17948347	1.287301114	protein arginine N-methyltransferase 1.6
XP_021631934.2	0.006036834	-1.495297528	1.29185689	tyrosine-protein phosphatase DSP1 isoform X1
XP_021598083.1	0.006647382	2.973817127	1.293282265	uncharacterized protein LOC110604244 isoform X1
XP_043814252.1	0.033348678	-4.482500292	1.311644601	aminoacyl tRNA synthase complex-interacting multifunctional protein 1-like isoform X4
XP_021593881.1	0.043497157	-0.017936799	1.31693109	uncharacterized protein LOC110601152 isoform X2
XP_021600979.1	1.51106E-05	-1.229112449	1.324453264	probable protein phosphatase 2C 12
XP_043811934.1	0.037799179	1.335999867	1.339713286	OVARIAN TUMOR DOMAIN-containing deubiquitinating enzyme 6 isoform X1
XP_043814597.1	0.045583092	0.279608377	1.339865227	uncharacterized protein LOC122724105
XP_021614794.1	0.014870039	-2.733071697	1.341642693	heme-binding-like protein At3g10130, chloroplastic isoform X3
XP_021628924.1	0.046368581	0.293519355	1.346193477	alcohol-forming fatty acyl-CoA reductase
XP_021628925.1	0.046368581	0.293519355	1.346193477	glutaredoxin-C5

XP_021628926.1	0.046368581	0.293519355	1.346193477	trimethyltridecatetraene synthase
XP_021628928.1	0.046368581	0.293519355	1.346193477	E3 ubiquitin-protein ligase PUB24
XP_021613236.1	0.016242447	-0.486256103	1.368999454	metal-nicotianamine transporter YSL3
XP_021619950.1	0.046368581	0.785350303	1.379245998	exosome complex component RRP43
XP_043814801.1	0.022005828	2.868257749	1.396291838	uncharacterized protein LOC122724336
XP_043806024.1	0.028949121	-0.84174436	1.399393016	UPF0565 protein C2orf69 homolog isoform X2
XP_021605792.1	0.04068273	1.196028802	1.407754852	uncharacterized protein LOC110610257
XP_021592562.1	0.02213932	-0.965835696	1.466917441	tetraspanin-8
XP_021614319.1	0.004784749	-1.355924738	1.468743589	pentatricopeptide repeat-containing protein At2g46050, mitochondrial
XP_021613173.1	0.001152961	0.17609537	1.474535164	nucleolin isoform X3
XP_021610345.1	0.04412594	-1.364215479	1.504975155	pleiotropic drug resistance protein 1
XP_021610346.1	0.04412594	-1.364215479	1.504975155	1-phosphatidylinositol-3-phosphate 5-kinase FAB1B isoform X1
XP_021593760.1	0.000655786	1.49209195	1.524736515	NADH dehydrogenase
XP_021625428.1	0.032120713	0.686643236	1.533601267	FT-interacting protein 1
XP_043805936.1	1.57017E-09	-3.79367912	1.554115478	copper-transporting ATPase HMA4 isoform X1
XP_021604156.1	0.000847351	3.770436088	1.565879216	protease Do-like 7
XP_043817023.1	0.046368581	-3.950825605	1.571819085	heat stress transcription factor A-6b isoform X1
XP_021619315.1	0.001281782	-1.670988692	1.589951258	heavy metal-associated isoprenylated plant protein 39 isoform X1
XP_021619291.1	0.001183859	-1.670988126	1.603220413	probable methyltransferase PMT27
XP_021619302.1	0.001183859	-1.663542737	1.610667869	protein SHI RELATED SEQUENCE 1
XP_021633967.1	0.002007418	0.610620113	1.631666339	uncharacterized protein LOC110630722 isoform X2
XP_021633693.1	0.005468906	-0.178336262	1.645582929	ethylene-responsive transcription factor ESR2
XP_021600889.2	0.001310149	-5.200150658	1.64981675	tetratricopeptide repeat protein SKI3 isoform X2
XP_021631058.2	0.015210519	2.265926022	1.68014274	xyloglucan galactosyltransferase MUR3
XP_021633630.1	0.009970631	-0.955776441	1.680899234	ras-related protein Rab11D
XP_021633631.1	0.009970631	-0.955776441	1.680899234	protein HEADING DATE 3A

XP_021631057.1	0.015059996	2.293541069	1.703406149	probable calcium-binding protein CML41
XP_021596692.1	0.009128852	-0.769569031	1.723113789	TLC domain-containing protein 4-B isoform X1
XP_021634386.1	0.011415692	2.737278962	1.74858972	putative fasciclin-like arabinogalactan protein 20
XP_043806894.1	0.006566703	-0.517688743	1.750696572	ABC transporter D family member 1-like isoform X2
XP_021614242.1	0.000655786	-1.062737896	1.759330528	F-box protein At1g47056
XP_021634387.1	0.0126977	2.737360067	1.770355863	probable ribose-5-phosphate isomerase 2
XP_021626548.1	0.046368581	2.170521552	1.786181604	probable cinnamyl alcohol dehydrogenase 1
XP_021634640.1	0.045091289	2.052877959	1.7875996	DNA-directed RNA polymerase 3B, chloroplastic isoform X1
XP_021619521.1	0.033348678	0.473764131	1.809772154	UPF0481 protein At3g47200
XP_021633869.2	0.0096661	0.971693403	1.810464005	uncharacterized protein slr0889
XP_021612189.2	0.00922045	2.364967551	1.862020064	uncharacterized protein LOC110614822
XP_021617132.1	0.04025969	0.576010617	1.882012687	uncharacterized protein LOC110618289 isoform X2
XP_021607187.1	0.039047503	-0.23256835	1.883799264	casein kinase 1-like protein 1
XP_021622405.1	0.01885327	-0.234135283	1.90403104	thioredoxin-like 3-1, chloroplastic
XP_043805314.1	0.000898847	-1.022789091	1.904119077	uncharacterized protein LOC122721523
XP_043805315.1	0.000898847	-1.022789091	1.904119077	uncharacterized protein LOC122721524
XP_043805320.1	0.000898847	-1.022789091	1.904119077	uncharacterized mitochondrial protein AtMg00860-like
XP_043805324.1	0.000898847	-1.022789091	1.904119077	pupal cuticle protein 36-like, partial
XP_021607188.1	0.039564696	-0.228433201	1.912699663	ultraviolet-B receptor UVR8 isoform X1
XP_021607189.1	0.039564696	-0.228433201	1.912699663	ultraviolet-B receptor UVR8 isoform X2
XP_021611733.1	0.002148106	1.125581786	1.929763974	glutathione S-transferase
XP_043809384.1	0.04969806	-0.069031882	1.937536045	40S ribosomal protein S29-like
XP_021613044.1	0.000981123	0.170895229	1.952343624	uncharacterized protein LOC110615495
XP_043812715.1	0.000130409	-0.622163672	1.953374394	uncharacterized protein LOC122723683
XP_043813209.1	0.040811247	-0.332148669	1.974133318	calcium-transporting ATPase 10, plasma membrane-type
XP_021629405.1	0.001311667	-2.510568931	1.992753639	APO protein 4, mitochondrial isoform X1

XP_021611735.1	0.0015823	1.148657068	1.996047256	putative UDP-rhamnose:rhamnosyltransferase 1
XP_021613043.1	0.000671555	0.182381041	2.012915603	glycine--tRNA ligase, chloroplastic/mitochondrial 2
XP_021600887.2	0.046368581	0.357920332	2.014514027	tetratricopeptide repeat protein SKI3 isoform X1
XP_021609307.1	0.02213932	1.789302591	2.021721488	protein ROLLING AND ERECT LEAF 2
XP_043812516.1	0.042590108	-0.357137802	2.026541383	RING-H2 finger protein ATL47
XP_043805313.1	0.002999601	-0.954267679	2.042021894	uncharacterized protein LOC122721522
XP_021604719.1	0.04068273	1.238957284	2.046868998	histone H4
XP_021604868.1	0.000114538	3.027310614	2.05575471	disease resistance RPP13-like protein 4 isoform X6
XP_021593512.1	0.045091289	1.056769068	2.060072081	two-pore potassium channel 3 isoform X2
XP_021622022.1	0.001918531	-1.466800639	2.071009006	uncharacterized protein LOC110621997 isoform X2
XP_021622023.1	0.001918531	-1.466800639	2.071009006	pentatricopeptide repeat-containing protein At3g03580
XP_021622024.1	0.001918531	-1.466800639	2.071009006	probable glutathione S-transferase
XP_021622025.1	0.001918531	-1.466800639	2.071009006	glutathione S-transferase L3 isoform X1
XP_021622027.1	0.001918531	-1.466800639	2.071009006	glutathione S-transferase L3 isoform X2
XP_021622028.1	0.001918531	-1.466800639	2.071009006	pyruvate kinase 1, cytosolic isoform X1
XP_043816410.1	0.001918531	-1.466800639	2.071009006	pyruvate kinase 1, cytosolic isoform X2
XP_043816450.1	0.001918531	-1.466800639	2.071009006	uncharacterized protein LOC110621997 isoform X1
XP_021619164.1	0.005238617	4.594393276	2.088004513	nicotinate N-methyltransferase 1
XP_021608602.1	0.019372893	-5.668782152	2.09988985	protein translation factor SUI1 homolog 2
XP_043810597.1	0.024554611	-3.336745398	2.102460148	DNA-directed RNA polymerases II and IV subunit 5A isoform X1
XP_021603961.1	0.009652199	-0.915980833	2.104875228	uncharacterized protein LOC110608978 isoform X1
XP_021598194.1	0.035973487	0.929957478	2.111527895	zinc finger protein GIS2
XP_043809248.1	0.015553879	-2.486705158	2.126887391	disease resistance protein RPM1 isoform X5
XP_043809249.1	0.01338461	-2.514964185	2.139697224	disease resistance protein RPM1 isoform X6
XP_043809247.1	0.013237614	-2.514705376	2.141640323	disease resistance protein RPM1 isoform X2
XP_043812379.1	0.043205971	1.318809894	2.149062329	probable LRR receptor-like serine/threonine-protein kinase At2g16250

XP_043807514.1	0.015627733	-0.651565365	2.155822028	dymeclin isoform X3
XP_021622029.1	0.001986004	-1.453872855	2.157611977	transducin beta-like protein 3 isoform X1
XP_021622030.1	0.001986004	-1.453872855	2.157611977	transducin beta-like protein 3 isoform X2
XP_021593984.1	0.001918531	0.433787982	2.179723667	uncharacterized protein LOC110601229
XP_021592945.1	0.013743901	-5.176618065	2.218022096	26S proteasome non-ATPase regulatory subunit 6 homolog
XP_021606013.1	0.045151816	-2.149535224	2.229753361	gamma-glutamyl hydrolase 2 isoform X5
XP_021602813.1	0.027388162	0.040768369	2.230137501	cytochrome b561 and DOMON domain-containing protein At2g04850
XP_021634446.1	0.049849225	1.505541534	2.231362922	ethylene-responsive transcription factor ERF115
XP_043813967.1	0.033348678	-1.807217821	2.237584828	auxin response factor 6 isoform X3
XP_021603132.1	0.015901413	1.119509129	2.244258729	uncharacterized protein LOC110608230
XP_043804430.1	0.012969159	2.763694837	2.245968677	uncharacterized mitochondrial protein AtMg00810-like
XP_043817170.1	0.033334442	1.524568756	2.247953161	dicarboxylate transporter 2.1, chloroplastic
XP_021617691.1	0.021365575	-1.888135868	2.260908031	structure-specific endonuclease subunit slx1 isoform X1
XP_021618435.1	0.020805904	-4.518522969	2.269774004	sm-like protein LSM4
XP_021617690.1	0.020807066	-1.890561298	2.271460667	mitogen-activated protein kinase kinase kinase 18
XP_043813966.1	0.020479413	-1.868018627	2.279528379	auxin response factor 21 isoform X2
XP_021618719.1	0.016520293	-0.826384767	2.280980797	protein MID1-COMPLEMENTING ACTIVITY 1 isoform X4
XP_043814451.1	0.016520293	-0.826384767	2.280980797	protein MID1-COMPLEMENTING ACTIVITY 1 isoform X5
XP_043805669.1	0.006169246	1.610470625	2.286988569	uncharacterized protein LOC110629996 isoform X2
XP_021606614.1	0.001400397	-0.329748515	2.288802791	uncharacterized protein LOC110610847
XP_021624442.1	0.00941137	1.049723874	2.2990267	secoisolariciresinol dehydrogenase
XP_021622596.1	0.000671555	-0.932302327	2.300557722	calmodulin-binding protein 25
XP_021606607.2	0.000939493	-0.618772917	2.31873282	AT-hook motif nuclear-localized protein 20, partial
XP_021617842.1	0.020697948	2.334796186	2.332132146	protein ESKIMO 1
XP_021594345.1	0.013617226	2.565623773	2.378576319	WAT1-related protein At5g40240 isoform X4
XP_043808740.1	0.039564696	3.981387679	2.387465388	uncharacterized protein LOC110605525 isoform X8

XP_021599836.1	0.039652015	3.975121257	2.387493384	uncharacterized protein LOC110605525 isoform X4
XP_021603746.1	0.036118591	1.456542374	2.389561314	RNA-binding protein 38 isoform X2
XP_043815938.1	0.009907888	-3.48718236	2.389569561	probable inactive leucine-rich repeat receptor-like protein kinase At3g03770
XP_021603156.1	0.00941137	-0.512290434	2.401423496	BTB/POZ domain-containing protein At1g04390 isoform X10
XP_021621460.1	0.035658899	-1.612186207	2.409123606	pentatricopeptide repeat-containing protein At3g14580, mitochondrial
XP_021621465.1	0.035658899	-1.612186207	2.409123606	probable calcium-binding protein CML46
XP_021621455.1	0.039652015	-1.569678092	2.418655546	NAC domain-containing protein 7
XP_021634668.1	0.022913823	-0.361574808	2.436388872	uncharacterized protein LOC110631225 isoform X2
XP_021603150.1	0.006956382	-0.500379473	2.436947045	BTB/POZ domain-containing protein At1g04390 isoform X4
XP_021603152.1	0.004946747	-0.529186234	2.439624575	BTB/POZ domain-containing protein At1g04390 isoform X6
XP_021623201.1	0.0096661	-3.462422348	2.454109051	probable inactive leucine-rich repeat receptor-like protein kinase At3g03770
XP_021623202.1	0.0096661	-3.462422348	2.454109051	probable inactive leucine-rich repeat receptor-like protein kinase At3g03770
XP_043813701.1	0.039564696	-2.323484486	2.559428556	uncharacterized protein LOC110617863
XP_021620711.1	0.000652802	-3.256874906	2.586586311	tRNase Z TRZ4, mitochondrial isoform X4
XP_021625514.1	0.006504914	-2.996170554	2.586642063	2-oxoglutarate dehydrogenase, mitochondrial
XP_021634395.1	0.045091289	-0.181871924	2.606681513	F-box/kelch-repeat protein At1g22040
XP_021602667.1	0.019455464	0.639722162	2.634222337	pumilio homolog 5 isoform X2
XP_021602310.1	0.005659499	-3.34661144	2.670216052	probable inactive purple acid phosphatase 28
XP_043808626.1	0.02742636	1.159712757	2.833963284	protein farnesyltransferase subunit beta-like isoform X5
XP_021621981.1	0.046368581	-0.406573129	2.838089861	vacuolar cation/proton exchanger 3 isoform X1
XP_043805332.1	0.018654642	-3.745280788	2.86173711	aquaporin SIP1-1-like
XP_021614035.1	0.015039404	1.44824482	3.018776344	uncharacterized protein LOC110616039
XP_021598192.2	0.010063434	-1.644435504	3.09948284	uncharacterized protein LOC110604363
XP_021598181.1	0.009615451	-1.629004834	3.125159484	uncharacterized protein LOC110604343

XP_043810508.1	0.01744931	2.378515373	3.155349617	rRNA N6-adenosine-methyltransferase METTL5 isoform X2
XP_021620367.1	0.000114538	-0.034835674	3.170468543	pentatricopeptide repeat-containing protein At2g41720 isoform X4
XP_021605862.1	0.045795352	2.108992973	3.186985599	2-oxoglutarate-Fe(II) type oxidoreductase hxnY
XP_021603222.1	0.045795352	-2.445787154	3.206998378	pentatricopeptide repeat-containing protein At2g26790, mitochondrial
XP_043810127.1	0.022342361	1.480206899	3.408595967	calcium-dependent protein kinase 17
XP_043811657.1	0.00038545	-2.214983768	3.419395803	kinesin-like protein KIN-13B isoform X3
XP_043809081.1	0.031026426	1.021954361	3.452821705	polygalacturonase-like
XP_021626494.1	0.042375148	0.291994113	3.532976507	protein RMD5 homolog
XP_021603731.1	0.01151361	-0.086800178	3.740218946	basic leucine zipper 43
XP_021623045.1	0.000167167	-0.252684363	3.755032515	uncharacterized protein LOC110622744
XP_021597227.1	0.002066375	1.172420725	3.775895667	uncharacterized protein LOC110603577 isoform X2
XP_021615301.1	0.0218195	2.899145554	3.827509701	recQ-mediated genome instability protein 1
XP_043809303.1	0.018219607	3.948569573	3.924980985	uncharacterized protein LOC110606542 isoform X1
XP_043814936.1	0.044813689	0.600797874	4.004759937	probable E3 ubiquitin-protein ligase ZFP1 isoform X3
XP_021592749.1	2.90209E-07	-4.950228295	4.137601536	HVA22-like protein a
XP_043817781.1	0.01744931	6.366767249	4.149107203	PH, RCC1 and FYVE domains-containing protein 1 isoform X3
XP_021620708.1	0.038659365	2.732911429	4.184160307	tRNAse Z TRZ4, mitochondrial isoform X3
XP_043808398.1	0.02819019	3.261570404	4.195739619	putative uncharacterized protein DDB_G0290521
XP_021615764.1	0.016208643	-2.257734495	4.228410836	sulfhydryl oxidase 2 isoform X1
XP_021620132.1	0.014729142	-3.561022939	4.25536072	transcription factor ORG2 isoform X1
XP_021620704.1	0.001094058	-0.894520337	4.274578876	uncharacterized protein LOC110621020
XP_043812749.1	0.046368581	1.781171942	4.283551759	protein FAM98B-like
XP_043816260.1	0.01087263	-3.150546433	4.323487399	pentatricopeptide repeat-containing protein At1g63330-like
XP_043817145.1	0.048242461	4.492087974	4.356459349	organelle RRM domain-containing protein 1, chloroplastic isoform X2
XP_043817061.1	0.010168991	-2.126704797	4.414841503	monooxygenase 2-like
XP_021614915.1	0.039564696	1.952505345	4.56912355	RING-H2 finger protein ATL13

XP_021614484.1	0.014870039	1.299117746	4.705730856	uncharacterized protein LOC110616447
XP_021614485.1	0.014870039	1.299117746	4.705730856	uncharacterized protein LOC110616448
XP_021606421.1	0.043456623	-0.182551904	4.718746843	major allergen Pru ar 1
XP_021615428.1	0.016026969	2.371217439	5.234293019	mannosyl-oligosaccharide 1,2-alpha-mannosidase MNS1 isoform X1
XP_021633970.1	0.017375253	-1.719237688	5.540687669	probable WRKY transcription factor 27
XP_021611560.1	0.049849225	-6.975037737	5.611944252	uncharacterized protein LOC110614349
XP_043809304.1	0.000898847	4.907313059	5.628416564	uncharacterized protein LOC110606542 isoform X2
XP_021604105.1	2.24944E-07	3.302735042	5.70277923	bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT
XP_021629064.1	0.040551867	-0.534929278	6.669308311	histone H2B
XP_021593413.1	0.035829821	2.36275695	6.67055108	uncharacterized protein LOC110600830
XP_021630782.1	0.019779008	1.964473116	6.730729668	F-box/kelch-repeat protein At1g67480
XP_021625208.1	0.012604042	5.16050699	7.771194023	protein SEMI-ROLLED LEAF 2
XP_021622220.1	0.034964288	0.925006624	8.689488533	bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic

B- Stem, 10 DAI, DSC 260 and DSC 167 vs. TMS 96/0304

protein ID	adjusted p-value	log ₂ FC DSC 260	log ₂ FC DSC 167	protein function
XP_021618904.1	0.013228232	-1.045021332	-8.589971843	basic form of pathogenesis-related protein 1
XP_021605449.1	0.011260946	-5.865542441	-6.947534983	GDSL esterase/lipase At1g29670
XP_021595870.1	0.000375907	-4.215396435	-4.445210195	ABC transporter G family member 10
XP_021604408.2	0.049961914	-2.039334266	-4.091923683	cellulose synthase-like protein G3
XP_021625069.1	0.000259068	-4.434864819	-4.01859523	protein PELPK1
XP_021618918.1	0.001628969	-2.919094345	-3.968274535	protein SOB FIVE-LIKE 5
XP_021622581.1	0.02957872	-1.379906932	-3.900277549	secoisolariciresinol dehydrogenase
XP_021630581.1	0.010973181	-3.257917695	-3.81022494	leucoanthocyanidin dioxygenase
XP_021632971.1	0.019336052	-2.982853423	-3.700393184	protein DOWNY MILDEW RESISTANCE 6
XP_021622566.2	2.08E-05	-3.758098845	-3.699056144	bifunctional 3-dehydroquinone hydratase/shikimate dehydrogenase, chloroplastic
XP_043817236.1	0.000124071	-3.711627923	-3.690696896	protein PELPK1-like
XP_021603583.1	0.010969658	-2.450594823	-3.665263662	uncharacterized protein LOC110608623
XP_021613935.1	0.024179201	-4.049115581	-3.657246506	type IV inositol polyphosphate 5-phosphatase 11
XP_021595652.1	0.006410298	-3.547311074	-3.649764894	non-specific lipid transfer protein GPI-anchored 20
XP_021611090.1	0.000981159	-3.778014319	-3.566275613	phenylalanine ammonia-lyase isoform X2
XP_021608257.1	0.026919311	-2.844939637	-3.540859949	non-specific lipid transfer protein GPI-anchored 5
XP_021593662.1	0.007348574	-2.439709368	-3.525768478	NAC domain-containing protein 71
XP_021611089.1	0.001628969	-3.722541769	-3.524958212	phenylalanine ammonia-lyase isoform X1
XP_021618075.1	0.000173351	-3.46324203	-3.479988723	protein PELPK1-like
XP_021605390.1	0.029117991	-4.093459101	-3.428132002	transcription factor MYB93
XP_021611776.1	0.000981159	-2.602889831	-3.398447893	uncharacterized protein LOC110614528
XP_021607962.1	0.001739826	-3.237053454	-3.380167633	receptor like protein kinase S.2
XP_021615437.1	0.001052681	-3.271994653	-3.371884693	uncharacterized protein LOC110617135
XP_021595702.1	0.001628969	-4.138087512	-3.371069787	3-ketoacyl-CoA synthase 20

XP_021626402.1	0.000973236	-3.153674561	-3.318804561	protein PELPK1
XP_021608957.1	0.020599766	-4.38223598	-3.31642576	probable 2-oxoglutarate-dependent dioxygenase AOP1
XP_021600257.2	0.011478085	-3.812334618	-3.266895717	dihydroflavonol 4-reductase
XP_021618820.1	0.012214007	-3.62836805	-3.253195151	protein PELPK1
XP_021609389.1	0.019006276	-3.701283878	-3.236499713	chalcone synthase 2
XP_021606970.1	0.043451642	-2.597343997	-3.234463447	RING-H2 finger protein ATL16
XP_021618053.1	0.000859899	-4.359384858	-3.207884662	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK3
XP_021631825.2	0.034819742	-3.384525783	-3.199009673	flavonoid 3',5'-hydroxylase 2
XP_021618139.1	0.001967672	-3.435241793	-3.183423372	glycerol-3-phosphate acyltransferase 5
XP_021626234.1	0.008516028	-2.681401383	-3.180827877	linoleate 13S-lipoxygenase 2-1, chloroplastic
XP_021625302.1	0.000859899	-3.283730031	-3.171235481	ethylene-responsive transcription factor WRI1
XP_021608704.1	0.042889472	-4.194655668	-3.166962283	peroxidase 24
XP_021629051.1	0.031211305	-2.672594226	-3.153583719	dirigent protein 23
XP_021612474.1	0.003653026	-3.124740979	-3.114581213	probable WRKY transcription factor 43
XP_021625070.1	0.000215118	-3.790656381	-3.102737491	protein PELPK1
XP_021607958.1	0.000111961	-2.188030352	-3.0839046	transcription factor BHLH42
XP_021631591.1	0.014335127	-2.26344751	-3.060416801	ethylene-responsive transcription factor ERF053
XP_021627690.1	0.025136356	-3.836512088	-3.034099553	putative serine/threonine-protein kinase isoform X2
XP_021618061.1	0.022790445	-3.063762298	-2.980260269	protein PELPK1
XP_021627688.1	0.021170227	-3.736787393	-2.962999799	putative serine/threonine-protein kinase isoform X1
XP_021595994.1	0.019822539	-4.934669297	-2.95654457	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2
XP_021622639.1	0.004510482	-2.508418682	-2.927599809	WD repeat-containing protein LWD1 isoform X2
XP_021625441.1	0.004867032	-3.059580302	-2.924542959	nucleobase-ascorbate transporter 4
XP_021603611.1	0.008390093	-3.437926552	-2.923436823	ABC transporter G family member 23
XP_021599708.1	0.007166206	-1.793846091	-2.922492518	uncharacterized protein LOC110605428

XP_021607718.1	0.005997319	-3.238036715	-2.915519112	non-specific lipid transfer protein GPI-anchored 16
XP_021627705.1	0.005122895	-2.958974183	-2.914089627	cytochrome P450 86B1
XP_021616874.1	0.008649524	-3.312680736	-2.882424179	peroxidase 11
XP_021598238.1	0.01404234	-2.960389603	-2.870523036	protein JINGUBANG
XP_021617949.1	0.01895915	-3.190455838	-2.86500826	protein PELPK1 isoform X1
XP_043814525.1	0.01895915	-3.190455838	-2.86500826	protein PELPK1 isoform X2
XP_021617395.1	9.45E-05	-2.946440731	-2.860436395	expansin-A8
XP_021623015.1	0.007348574	-2.903779728	-2.850022975	epoxide hydrolase 4
XP_021611580.1	0.024535241	-3.124981084	-2.813409436	probable carboxylesterase 5
XP_021619116.1	0.008649524	-2.978882389	-2.809934765	gallate 1-beta-glucosyltransferase 84A24
XP_021620078.1	0.007348574	-3.419007027	-2.808200626	ABC transporter G family member 20
XP_021609574.2	0.001102154	-3.5942817	-2.801474082	omega-hydroxypalmitate O-feruloyl transferase
XP_021630126.1	0.001389202	-2.842050627	-2.779243755	E3 ubiquitin-protein ligase APD2
XP_021617732.1	0.007034303	-3.312165268	-2.773784629	ABC transporter G family member 6
XP_021592863.2	0.00979463	-2.70661057	-2.772759388	palmitoyl-acyl carrier protein thioesterase, chloroplastic
XP_021622638.1	0.005740039	-2.497356091	-2.772489428	WD repeat-containing protein LWD2 isoform X1
XP_021625424.1	0.021674013	-3.293685419	-2.769079737	protein PELPK1
XP_021623956.1	0.020774482	-3.44115267	-2.768203469	probable lysophospholipase BODYGUARD 3
XP_021632540.1	0.001176561	-3.181327143	-2.766335228	GDSL esterase/lipase At2g23540
XP_021622172.1	0.002240882	-3.136914299	-2.765134128	glycerol-3-phosphate 2-O-acyltransferase 6
XP_021618074.1	0.004991331	-3.35762684	-2.715448553	protein PELPK1
XP_021603640.1	9.45E-05	-3.063303361	-2.699241271	protein DETOXIFICATION 41
XP_043813659.1	0.01666935	-3.289391935	-2.646580209	putative receptor protein kinase ZmPK1
XP_021592812.1	0.00183043	-3.347678159	-2.641124074	peroxidase 11
XP_021618060.1	0.021426398	-2.942894794	-2.639309451	protein PELPK1
XP_021617615.1	0.000717052	-3.005422288	-2.631181214	chalcone isomerase-like protein 2

XP_021627812.1	0.006623381	-3.286803225	-2.627841325	omega-hydroxypalmitate O-feruloyl transferase
XP_021610990.1	9.45E-05	-2.751241735	-2.615943954	ATPase 10, plasma membrane-type
XP_021623184.1	0.001757184	-2.628869903	-2.612637748	4-coumarate--CoA ligase 2
XP_021594193.1	0.026354193	-3.645442156	-2.587041445	probable WRKY transcription factor 31
XP_021601802.1	0.011272918	-2.731950553	-2.578229336	transcription factor MYB93
XP_021605137.1	0.008065259	-2.816745891	-2.570921406	naringenin,2-oxoglutarate 3-dioxygenase
XP_021614044.1	0.0100975	-3.29533584	-2.570529223	non-specific lipid transfer protein GPI-anchored 5
XP_021621841.1	0.00946701	-3.307580382	-2.563374762	cytochrome b561 and DOMON domain-containing protein At5g47530
XP_021618819.1	0.011409716	-3.194382751	-2.543434891	serine carboxypeptidase-like 28
XP_021610472.1	0.004510482	-2.086758826	-2.540041113	ABC transporter G family member 29
XP_021603552.1	0.032057722	-2.858692711	-2.532982658	putative laccase-9
XP_021593818.1	0.03608545	-3.412614609	-2.524186418	probable xyloglucan galactosyltransferase GT17
XP_043817133.1	0.012816082	-3.058532032	-2.523151833	non-specific lipid transfer protein GPI-anchored 15
XP_021594332.1	0.008632444	-4.892152701	-2.517732907	loganic acid O-methyltransferase
XP_021618150.1	0.007166206	-3.154837107	-2.502881294	protein PELPK1
XP_021625423.1	0.011803914	-3.285055924	-2.492939099	protein PELPK1
XP_021615183.1	0.001699108	-3.492048176	-2.489564794	cytochrome P450 86A1
XP_021617075.1	0.006623877	-3.188025815	-2.488710049	heptahelical transmembrane protein 1
XP_021628924.1	0.018809407	-2.233154302	-2.479913341	alcohol-forming fatty acyl-CoA reductase
XP_021591842.1	0.002858018	-3.177815282	-2.467185675	omega-hydroxypalmitate O-feruloyl transferase
XP_021606625.1	0.029800976	-3.883387398	-2.459709371	pectinesterase QRT1
XP_021614132.1	0.005221948	-3.710544261	-2.458403605	non-specific lipid transfer protein GPI-anchored 5
XP_021632101.1	4.33E-06	-1.807128421	-2.45258938	U-box domain-containing protein 19
XP_021619906.1	0.024609941	-2.637350565	-2.445134458	laccase-7
XP_021616908.1	0.01895915	-3.361751281	-2.441373024	stellacyanin
XP_021625416.1	0.012320583	-2.858318831	-2.433321162	serine carboxypeptidase-like 18

XP_021598021.1	0.025400521	-2.808109991	-2.427497173	exocyst complex component EXO70I
XP_021610027.1	0.012694201	-2.898094947	-2.42021255	uncharacterized protein LOC110613282
XP_021631476.1	0.00889766	-2.252513876	-2.408707361	uncharacterized protein LOC110628963
XP_021633939.1	0.046017643	-1.332717629	-2.40724922	probable CoA ligase CCL9
XP_021610002.1	0.003606102	-2.62642964	-2.401631983	fatty acyl-CoA reductase 3
XP_021622094.1	0.027762865	0.264221629	-2.399001602	transcription factor CSA
XP_021618823.1	0.006672432	-2.887813704	-2.398505603	NAC domain-containing protein 100
XP_021600935.1	0.022289588	-2.963886358	-2.395481106	transcription factor RAX3
XP_021615451.1	0.010638822	-2.904581013	-2.391931115	GDSL esterase/lipase At1g74460
XP_021601982.1	0.008065259	-3.359698533	-2.36460413	CASP-like protein 1C1
XP_021621548.1	0.007166206	-3.133248578	-2.361525477	uncharacterized protein LOC110621583
XP_021619481.1	0.026408114	-3.41759652	-2.331706662	germin-like protein subfamily 1 member 13
XP_021598501.1	0.007348574	-2.45638133	-2.292836301	probable CoA ligase CCL6
XP_021626115.1	0.004510482	-0.881405944	-2.291982927	N-(5'-phosphoribosyl)anthranilate isomerase 1, chloroplastic
XP_021629019.1	0.021813626	-1.52456913	-2.287298897	ATPase 10, plasma membrane-type
XP_021602139.1	0.035525895	-3.214120282	-2.267133625	NAC domain-containing protein 100
XP_043816639.1	0.029117991	-2.930735874	-2.258470745	protein PELPK2-like
XP_021596210.1	0.000218702	-2.680017109	-2.248412918	anthocyanidin reductase ((2S)-flavan-3-ol-forming)
XP_021603146.1	0.005997319	-3.113147061	-2.240377982	stearoyl-[acyl-carrier-protein] 9-desaturase 6, chloroplastic
XP_021603659.1	0.038446569	-3.102677274	-2.240337951	probable lysophospholipase BODYGUARD 3
XP_021613248.1	0.001044172	-2.232645453	-2.233641228	WRKY transcription factor 23
XP_021633765.1	0.036415056	-3.015350939	-2.231528402	patatin-like protein 3
XP_021627264.1	0.004054802	-2.657167516	-2.211354254	chalcone synthase
XP_021632303.1	0.00253124	-3.174735372	-2.19055926	septum-promoting GTP-binding protein 1
XP_043804597.1	0.007348574	-3.103655519	-2.136299206	rhamnogalacturonate lyase isoform X2
XP_021620403.1	0.045617406	-3.43546764	-2.135340406	non-specific lipid-transfer protein 2

XP_021614037.1	0.019213928	-2.777477253	-2.125405397	stress-related protein
XP_021615574.1	0.033507415	-1.167172533	-2.121068342	alpha-xylosidase 1
XP_021616292.1	0.009426827	-1.87817334	-2.1181603	respiratory burst oxidase homolog protein C
XP_021620832.1	0.001628969	-2.755732761	-2.110910928	non-specific lipid transfer protein GPI-anchored 7
XP_021630096.1	0.030488629	-2.661865884	-2.109633439	rhamnogalacturonate lyase isoform X1
XP_043812367.1	0.044848957	-1.863890005	-2.099986824	F-box/kelch-repeat protein At5g43190-like
XP_021596493.1	0.007195539	-2.335102708	-2.099395983	cytochrome P450 86A1
XP_021601218.1	0.029935078	-3.851856097	-2.092128636	aldehyde oxidase GLOX
XP_021597484.1	0.039167155	-1.974650766	-2.082408551	arogenate dehydratase/prephenate dehydratase 1, chloroplastic
XP_021634670.1	0.009319533	-1.980102791	-2.071079862	short-chain dehydrogenase TIC 32 B, chloroplastic
XP_021630889.1	0.037704269	-2.739705793	-2.0677535	uncharacterized protein At5g48480
XP_021606999.1	0.034819742	-2.416743447	-2.045013547	polygalacturonase QRT3
XP_021632282.1	0.027895052	-2.290664255	-2.041429762	cysteine proteinase COT44
XP_021603452.2	0.013827106	-2.120566057	-2.03908341	WAT1-related protein At5g47470
XP_021612097.1	0.008121608	-2.770139289	-2.038990421	cytochrome P450 86A8
XP_021622431.1	0.02774298	-1.666352154	-2.038375842	transcription repressor OFP1
XP_021628626.1	0.012553483	-1.953996644	-2.016605918	beta-fructofuranosidase, cell wall isozyme isoform X1
XP_043807108.1	0.030106068	-2.00196	-2.009929869	non-specific lipid transfer protein GPI-anchored 5
XP_021627577.1	0.048277432	-2.426530989	-1.987516783	xyloglucan endotransglucosylase/hydrolase protein 31
XP_021594194.1	0.0057796	-3.460288182	-1.982007676	peroxidase 55
XP_021597746.1	0.000433038	-1.91444931	-1.979165312	low-temperature-induced cysteine proteinase
XP_021617696.1	0.006617097	-2.144738786	-1.956948884	laccase-5
XP_021632903.1	0.024857695	-1.47203676	-1.950308174	G-type lectin S-receptor-like serine/threonine-protein kinase At1g34300
XP_021614226.1	0.008649524	-3.896804202	-1.940171268	probable WRKY transcription factor 43
XP_021633997.1	0.001127487	-1.796700813	-1.914919643	leucoanthocyanidin reductase
XP_021598728.1	0.030488629	-2.081760393	-1.889255514	oligopeptide transporter 7

XP_021633426.1	0.007195539	-2.27060496	-1.88733528	auxin-induced in root cultures protein 12
XP_021618646.1	0.025136356	-2.103102556	-1.88266703	peroxidase 4
XP_021598637.1	0.022610148	-3.11182212	-1.850143627	MLP-like protein 28
XP_021621183.1	0.006537433	-1.42602359	-1.849888798	WRKY transcription factor 44
XP_021598142.1	0.025998354	-1.594124857	-1.845234044	respiratory burst oxidase homolog protein E
XP_021600654.2	0.007882867	-2.866618778	-1.843947714	protein ECERIFERUM 26-like
XP_021596544.1	0.008065259	-1.717405482	-1.822607399	dehydration-responsive element-binding protein 3
XP_021606580.1	0.026565376	-0.954047024	-1.811834672	type IV inositol polyphosphate 5-phosphatase 7
XP_021632542.1	0.039167155	-3.125996987	-1.796025103	stemmadenine O-acetyltransferase
XP_021610474.1	0.030106068	-1.373260352	-1.790060231	histidine protein methyltransferase 1 homolog
XP_021610475.1	0.030106068	-1.373260352	-1.790060231	histidine protein methyltransferase 1 homolog
XP_043811930.1	0.030106068	-1.373260352	-1.790060231	histidine protein methyltransferase 1 homolog
XP_021621613.1	0.022213584	-3.031148748	-1.784518109	respiratory burst oxidase homolog protein A
XP_021603951.2	0.030106068	-1.663805315	-1.772125034	transcription factor GLABRA 3 isoform X1
XP_021628546.1	0.017381626	-0.609320377	-1.7685187	uncharacterized protein LOC110626778
XP_021617740.2	0.018572325	-0.0526493	-1.767103519	cysteine proteinase RD21A
XP_021610730.1	0.008065259	-1.586700578	-1.759626959	phospholipase D alpha 1
XP_021603950.2	0.039167155	-1.654016424	-1.734024225	transcription factor GLABRA 3 isoform X2
XP_021603692.1	0.01666935	-2.071746396	-1.728863846	uncharacterized protein LOC110608720
XP_021594737.1	0.000285591	-1.596260701	-1.717088758	phytosulfokine receptor 2
XP_021606400.1	0.021500443	-1.994496137	-1.716525649	transcription factor MYB123
XP_021631234.1	0.003653026	-2.864083064	-1.713724604	zinc finger protein 6
XP_021608748.1	0.022870713	-2.930046317	-1.705415422	uncharacterized protein LOC110612305
XP_021624539.1	0.030106068	-1.393858937	-1.700737403	cysteine proteinase RD21A
XP_021628541.1	0.006614353	-1.706379165	-1.661086359	subtilisin-like protease SBT1.5
XP_021596793.1	0.030577705	-3.201708199	-1.659048735	transcription factor MYB102

XP_021600971.1	0.02410987	1.929355382	-1.658042375	protein EXORDIUM-like 2
XP_021606229.1	0.036446787	-2.258100277	-1.648478435	ABC transporter B family member 11
XP_021610233.1	0.014335127	-1.420169811	-1.636625113	uncharacterized protein LOC110613427
XP_043807618.1	0.00660839	-1.691768407	-1.630280586	ent-kaurene synthase TSP4, chloroplastic
XP_021622193.1	0.029117991	-0.291333521	-1.629629346	protein OCTOPUS
XP_021599119.1	0.003578538	-1.554880785	-1.617251344	CBL-interacting serine/threonine-protein kinase 23 isoform X1
XP_021610410.1	0.022314132	-1.039084332	-1.612632201	beta-galactosidase 8
XP_021606691.1	0.015856544	-1.354244213	-1.588451514	SEC14 cytosolic factor
XP_021612194.1	0.005337799	-2.339818915	-1.583211924	phospholipase A1-lgamma1, chloroplastic
XP_021619703.1	0.047511852	-1.88643968	-1.562207919	probable aldo-keto reductase 1
XP_043811908.1	0.045210512	-0.545636082	-1.55629071	uncharacterized protein LOC110613571
XP_043808797.1	0.044070413	-0.793596181	-1.555773455	cysteine-rich receptor-like protein kinase 26
XP_043808508.1	0.006431508	-1.596422094	-1.544739144	CBL-interacting serine/threonine-protein kinase 23 isoform X2
XP_021620730.1	0.029935078	-2.443048264	-1.542398576	glutathione S-transferase F9
XP_021634242.1	0.008649524	-1.809868335	-1.479612681	cinnamoyl-CoA reductase-like SNL6
XP_021615686.1	0.040916043	-1.528458007	-1.472791098	UDP-arabinopyranose mutase 3
XP_021606129.1	0.044524622	-2.011792098	-1.464025716	receptor-like protein 7
XP_021595770.1	0.03479297	-1.617761888	-1.451848013	probable protein phosphatase 2C 24
XP_021630155.1	0.039167155	-2.873259434	-1.448209321	coniferyl alcohol acyltransferase
XP_021595964.1	0.012115213	-1.461468345	-1.434014077	KIN14B-interacting protein At4g14310 isoform X2
XP_021599524.1	0.004040575	-1.326727288	-1.419411116	pyruvate kinase, cytosolic isozyme
XP_043807361.1	0.043022241	-1.355165663	-1.391252921	CBL-interacting serine/threonine-protein kinase 23 isoform X2
XP_021594488.1	0.00316959	-1.353437338	-1.387593907	adagio protein 3
XP_021609221.1	0.037704269	-1.994723858	-1.376626645	uncharacterized protein At5g01610
XP_021599371.1	0.030106068	-0.367274052	-1.346474596	uncharacterized protein LOC110605251
XP_021618729.1	0.019006276	-1.303124007	-1.343884787	protein phosphatase 2C 37

XP_021595963.1	0.008632444	-1.486712162	-1.338216274	KIN14B-interacting protein At4g14310 isoform X1
XP_021599136.1	0.010759454	-0.842862067	-1.336117589	phosphoglucomutase, cytoplasmic
XP_021616288.1	0.029117991	-1.740515325	-1.321341606	flavonoid 3'-monooxygenase
XP_043805992.1	0.029117991	-1.514995543	-1.319024901	probable pectate lyase 5
XP_021610669.1	0.017926877	-0.854864355	-1.306079798	protein argonaute 5
XP_021632370.1	0.014756986	-1.38804942	-1.2977286	dof zinc finger protein DOF3.4
XP_021593310.1	0.034264276	-1.100384529	-1.29364158	3-hydroxyisobutyryl-CoA hydrolase-like protein 5
XP_021633433.1	0.03276092	-1.197345906	-1.284441227	inositol-3-phosphate synthase
XP_021629388.1	0.010573182	-1.100298184	-1.281026896	ATP-citrate synthase alpha chain protein 1
XP_021614460.1	0.004510482	-0.053624338	-1.260057062	transcription factor bHLH62 isoform X1
XP_021614461.1	0.004510482	-0.053624338	-1.260057062	transcription factor bHLH62 isoform X2
XP_043805978.1	0.007195539	-2.222620721	-1.249755033	scopoletin 8-hydroxylase-like
XP_021611817.1	0.018908898	-1.622874251	-1.248876086	cyclin-D3-1 isoform X2
XP_021630822.1	0.004602716	-0.59048609	-1.244409384	asparagine synthetase
XP_021598604.1	0.007531428	-2.391876645	-1.243853667	protein SRG1
XP_021606660.1	0.043007825	-1.66097766	-1.240491397	ethylene-responsive transcription factor RAP2-3
XP_043817182.1	0.007348574	-1.026992533	-1.237783158	pyruvate kinase 1, cytosolic
XP_021611816.1	0.022610148	-1.584939536	-1.235394029	cyclin-D3-1 isoform X1
XP_021612278.1	0.001102154	-1.730547781	-1.227410281	protein MIZU-KUSSEI 1
XP_021614386.1	0.008065259	0.819439277	-1.22251303	probable WRKY transcription factor 53
XP_021599401.1	0.025136356	-1.188214067	-1.197529581	polyol transporter 5
XP_043813632.1	0.047948746	-0.55258576	-1.181280209	phosphoenolpyruvate/phosphate translocator 1, chloroplastic
XP_021603477.1	0.014844323	-1.090000029	-1.180608609	long chain acyl-CoA synthetase 4
XP_021595657.1	0.009426827	-0.887346379	-1.15539422	ATP-citrate synthase beta chain protein 2
XP_021595658.1	0.009426827	-0.887346379	-1.15539422	ATP-citrate synthase beta chain protein 2
XP_021595659.1	0.009426827	-0.887346379	-1.15539422	ATP-citrate synthase beta chain protein 2

XP_021595660.1	0.009426827	-0.887346379	-1.15539422	ATP-citrate synthase beta chain protein 2
XP_021592944.1	0.030572135	-0.180136833	-1.154106461	phosphoglucomutase, chloroplastic
XP_043814831.1	0.032244671	0.285994965	-1.144215283	phosphoinositide phosphatase SAC6 isoform X3
XP_043814829.1	0.030106068	0.385765787	-1.07667012	phosphoinositide phosphatase SAC6 isoform X2
XP_021612913.1	0.049940058	-1.615096391	-1.075883122	probable glycerol-3-phosphate acyltransferase 8
XP_021601261.1	0.038829528	-1.746256624	-1.073907404	pathogenesis-related thaumatin-like protein 3.5
XP_021629236.1	0.04352706	-1.06811089	-1.073632033	probable pectinesterase/pectinesterase inhibitor 51
XP_021624848.1	0.029267969	-1.292986127	-1.069161993	biotin carboxyl carrier protein of acetyl-CoA carboxylase
XP_021622086.1	0.023195935	-0.366172638	-1.05559886	uncharacterized protein LOC110622045
XP_021599262.2	0.032716627	0.396544617	-1.054766125	phosphoinositide phosphatase SAC6 isoform X1
XP_021601825.2	0.030106068	-1.335954079	-1.037428505	UDP-glycosyltransferase 91C1
XP_021629494.1	0.041654701	-1.132269233	-1.02607815	acetyl-CoA acetyltransferase, cytosolic 1
XP_021629495.1	0.041654701	-1.132269233	-1.02607815	acetyl-CoA acetyltransferase, cytosolic 1
XP_043818154.1	0.041654701	-1.132269233	-1.02607815	acetyl-CoA acetyltransferase, cytosolic 1
XP_021621648.1	0.024921886	-1.139716332	-1.023064278	flocculation protein FLO11
XP_021609359.1	0.043330954	0.811117766	-1.001619354	L-ascorbate oxidase homolog
XP_021629746.1	0.030919005	-2.547798639	-0.99571211	alcohol dehydrogenase 2
XP_021622776.2	0.002638653	-1.231213677	-0.989670427	probable pectate lyase 12
XP_043809454.1	0.017058292	-1.292312078	-0.982594562	uncharacterized protein LOC110606424
XP_021618844.1	0.020897784	-1.497172848	-0.953859669	chalcone--flavanone isomerase
XP_021611759.1	0.041654701	-1.259107044	-0.928604542	sterol carrier protein 2
XP_043816921.1	0.024033843	0.616119987	-0.916681708	probable sugar phosphate/phosphate translocator At3g11320
XP_021604587.1	0.037871943	-0.85786209	-0.904832377	dynammin-related protein 5A
XP_021611561.1	0.024179201	0.700837661	-0.887025137	D-aminoacyl-tRNA deacylase
XP_043808844.1	0.016359777	7.219659028	-0.886197332	GDSL esterase/lipase EXL3
XP_021621889.1	0.007065939	0.744782598	-0.864464394	mucin-5AC

XP_021597625.1	0.022870713	-0.369394819	-0.848950911	pyruvate decarboxylase 1
XP_021617261.1	0.029117991	-1.193829295	-0.844563865	secoisolariciresinol dehydrogenase-like
XP_043814350.1	0.029117991	-1.193829295	-0.844563865	secoisolariciresinol dehydrogenase-like
XP_043814351.1	0.029117991	-1.193829295	-0.844563865	secoisolariciresinol dehydrogenase-like
XP_043814352.1	0.029117991	-1.193829295	-0.844563865	secoisolariciresinol dehydrogenase-like
XP_021616729.1	0.030919005	-1.316045444	-0.843877767	cationic amino acid transporter 1
XP_021616213.1	0.003578538	-1.136781387	-0.829705028	dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic
XP_021618695.1	0.015308655	-1.411890214	-0.827014549	7-deoxyloganetin glucosyltransferase
XP_021632464.1	0.030768645	-0.42172064	-0.826810639	phospholipid-transporting ATPase 2 isoform X1
XP_021633075.1	0.042889472	-0.133635897	-0.789436296	cystathionine gamma-synthase 1, chloroplastic
XP_021597983.1	0.020599766	-2.971689021	-0.770414822	phospholipase A1-IIgamma
XP_021619343.2	0.012816082	0.942728558	-0.765807661	bifunctional TH2 protein, mitochondrial
XP_021601946.1	0.038829528	-0.453553761	-0.725411719	PH, RCC1 and FYVE domains-containing protein 1
XP_021594583.1	0.009019262	-1.105057959	-0.686617842	pyruvate kinase isozyme G, chloroplastic
XP_021607577.2	0.005161035	0.709347167	-0.664465344	leucine-rich repeat extensin-like protein 4
XP_043817637.1	0.029117991	-2.82711252	-0.636327568	phosphatidylinositol/phosphatidylcholine transfer protein SFH3 isoform X1
XP_043817638.1	0.029117991	-2.82711252	-0.636327568	phosphatidylinositol/phosphatidylcholine transfer protein SFH3 isoform X2
XP_021633727.1	0.029358882	-1.194092845	-0.597768873	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase PASTICCINO 2 isoform X1
XP_021627945.1	0.028332697	-2.730159588	-0.56788321	phosphatidylinositol/phosphatidylcholine transfer protein SFH3 isoform X3
XP_043817919.1	0.028108187	0.348756194	-0.539675922	DNA-directed RNA polymerase I subunit rpa49-like
XP_021595062.1	0.029117991	1.033658691	-0.501958496	protein argonaute 10
XP_021595063.1	0.029117991	1.033658691	-0.501958496	protein argonaute 10
XP_021595064.1	0.029117991	1.033658691	-0.501958496	protein argonaute 10

XP_021604737.1	0.047948746	-0.653930558	-0.491754356	uncharacterized protein LOC110609464 isoform X1
XP_021620893.1	0.04645719	-0.545471172	-0.486292541	monodehydroascorbate reductase
XP_021598733.1	0.003578476	-3.567763287	-0.477635144	protein SRG1
XP_021604700.1	0.039445158	-0.874404899	-0.447946964	biotin carboxylase 1, chloroplastic
XP_021595801.1	0.008649524	-1.211121143	-0.442462425	probable glutathione S-transferase
XP_021619146.1	0.034091779	1.284847468	-0.441531391	uncharacterized protein LOC110619931
XP_021601842.1	0.017961197	4.181379677	-0.418083552	agamous-like MADS-box protein AGL12
XP_043805905.1	0.029800976	-1.128612845	-0.334776394	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase PASTICCINO 2 isoform X2
XP_021624777.1	0.001389202	1.830614339	-0.308027773	uncharacterized protein LOC110624032
XP_021607407.1	0.025731208	1.030600313	-0.246678287	putative methyltransferase C9orf114
XP_021601668.1	0.045113409	-2.248801758	-0.239908495	uncharacterized protein LOC110606959
XP_021609079.1	0.026733148	-1.713334648	-0.212239435	uncharacterized protein LOC110612609
XP_021596564.1	0.022704123	-1.176116967	-0.197292677	thioredoxin-related transmembrane protein 2
XP_021597424.1	0.04427587	-0.792592024	-0.163182647	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
XP_021609491.1	0.000981159	-1.583131437	-0.158164433	protein BIG GRAIN 1-like B
XP_021603040.1	0.022870713	0.667460791	-0.156044794	ultraviolet-B receptor UVR8
XP_021631454.1	0.034628215	0.611797096	-0.150521268	copper methylamine oxidase isoform X2
XP_021631453.1	0.031030322	0.602483519	-0.138216591	copper methylamine oxidase isoform X1
XP_021624573.1	0.001389202	-1.299700821	-0.124167043	glutathione S-transferase DHAR2
XP_043812307.1	0.029800976	1.069045251	-0.077173327	O-fucosyltransferase 29
XP_021598056.1	0.003615793	-0.9150726	-0.071060921	peroxiredoxin-2
XP_021630737.2	0.030600059	-0.790652739	-0.05753493	farnesylcysteine lyase
XP_021592794.1	0.021813626	0.799539979	-0.017162456	probable serine/threonine-protein kinase SIS8 isoform X1
XP_021613577.1	0.00183043	2.143616271	0.012877958	uncharacterized protein LOC110615787
XP_021605792.1	0.014268967	-0.926343622	0.02274087	uncharacterized protein LOC110610257

XP_043809692.1	0.030889345	-2.095280657	0.034154259	heavy metal-associated isoprenylated plant protein 39 isoform X1
XP_021599764.1	0.026156543	-0.674729667	0.098937968	formate dehydrogenase, mitochondrial
XP_021599256.1	0.01895915	1.113769653	0.152755934	uncharacterized protein At2g34460, chloroplastic
XP_021598700.1	0.043837729	-1.856347634	0.162042477	vacuolar protein 8
XP_021593011.1	9.45E-05	1.214424035	0.231036073	uncharacterized protein LOC110600458 isoform X1
XP_021593012.1	0.005221948	1.171385269	0.27836194	uncharacterized protein LOC110600458 isoform X2
XP_021593013.1	0.005221948	1.171385269	0.27836194	uncharacterized protein LOC110600458 isoform X2
XP_021592193.1	0.049256052	1.30770113	0.296527905	copper methylamine oxidase isoform X1
XP_021606909.1	0.005382776	-1.570800034	0.30426771	lachrymatory-factor synthase-like
XP_043806170.1	0.044666832	1.317628864	0.312801247	copper methylamine oxidase isoform X2
XP_021629594.1	0.047957114	1.359342829	0.341941198	1-aminocyclopropane-1-carboxylate synthase
XP_021618540.1	0.006672432	1.508196307	0.347233171	probable protein phosphatase 2C 63
XP_021591902.1	0.019932937	-0.643196585	0.347826505	protein S-acyltransferase 24
XP_021615465.1	0.040420526	1.779791801	0.363029995	zinc finger CCCH domain-containing protein 55 isoform X1
XP_021622228.1	0.010020881	-1.487231769	0.372414697	protein SRC1
XP_021610587.1	0.024544201	-0.43674309	0.382483386	protein NCA1
XP_021620493.1	0.048083782	1.718383828	0.391399222	uncharacterized protein LOC110620867 isoform X1
XP_021615468.1	0.024060839	1.94159811	0.410296176	zinc finger CCCH domain-containing protein 55 isoform X2
XP_043813283.1	0.024389311	1.960468365	0.442984956	zinc finger CCCH domain-containing protein 55 isoform X3
XP_043816693.1	0.008121608	2.933946141	0.462452193	abscisic acid 8'-hydroxylase CYP707A2-like
XP_021611260.1	0.030106068	1.502832899	0.486752107	protein LNK3
XP_021601648.1	0.036687146	1.612625037	0.510482119	transcription factor MYB44
XP_021604509.1	0.030577705	-0.605470335	0.543800766	cysteine proteinase inhibitor
XP_021605407.1	0.01917019	1.227610658	0.651028855	root phototropism protein 2
XP_021612134.1	0.025183679	-0.676332314	0.671041345	pentatricopeptide repeat-containing protein At4g01030, mitochondrial
XP_021601100.1	0.012618383	3.159129212	0.676872389	protein PHOSPHATE-INDUCED 1

XP_021618711.1	0.003653026	1.422998044	0.728676889	omega-3 fatty acid desaturase, chloroplastic
XP_021620703.1	0.044958364	0.689031303	0.732604096	GATA transcription factor 5
XP_021617747.1	0.010020881	1.260139862	0.767591641	telomere repeat-binding protein 3
XP_043814215.1	0.010020881	1.260139862	0.767591641	telomere repeat-binding protein 3
XP_021618142.1	0.011581758	2.562019467	0.774726107	BURP domain-containing protein BNM2A
XP_021610875.1	0.017961197	1.488610593	0.775274541	dolichol kinase EVAN
XP_021617737.1	0.032716627	-0.490314769	0.796019022	nicotinamidase 1
XP_043814483.1	0.032716627	-0.490314769	0.796019022	nicotinamidase 1
XP_021595699.1	0.007166206	-0.010295153	0.806782137	vesicle-associated protein 4-1
XP_021611524.1	0.028848163	0.710996152	0.812830802	homeobox protein knotted-1-like 2
XP_043807438.1	0.048083782	0.530363687	0.831424097	small EDRK-rich factor 2-like
XP_021603607.1	0.043837729	2.701026615	0.87402165	ethylene-responsive transcription factor ERF014
XP_021609591.1	0.033507415	0.069021508	0.901146319	protein EARLY RESPONSIVE TO DEHYDRATION 15
XP_043813300.1	0.049961914	0.74934733	0.917144821	alpha/beta hydrolase domain-containing protein 17B isoform X2
XP_021600061.1	0.002072667	2.710023009	0.933358213	protein PHOSPHATE-INDUCED 1
XP_021627268.1	0.03147927	2.731885888	0.937888166	rust resistance kinase Lr10
XP_021609595.1	9.81E-05	1.627347215	0.955542522	expansin-like A2
XP_021601511.1	0.022213584	0.134420702	0.959002098	transcription factor TCP22
XP_021597666.1	0.043007825	-0.183981918	0.963014544	zinc finger protein CONSTANS-LIKE 4
XP_021614719.1	0.03479297	-0.11054901	0.963625241	transcription factor bHLH79
XP_021595752.1	0.028848163	1.441789268	1.007354793	homocysteine S-methyltransferase 3 isoform X1
XP_021612412.1	0.013827106	-0.436130295	1.01468751	uncharacterized protein LOC110615014
XP_021607441.1	0.038917536	-0.341665816	1.019102896	zinc finger protein CONSTANS-LIKE 4
XP_021591763.1	0.049056771	0.102280239	1.025962966	uncharacterized protein LOC110599609
XP_021628737.1	0.042468964	0.221534492	1.037065397	uncharacterized protein LOC110626876
XP_021621658.1	0.032057722	1.320366669	1.05363368	superoxide dismutase

XP_021611825.1	0.040427775	0.014194848	1.054103856	uncharacterized protein LOC110614569 isoform X2
XP_021621859.1	0.048893738	1.414279156	1.062729867	F-box protein At2g26850
XP_021598911.1	0.022978197	0.376995435	1.072893957	probable mannitol dehydrogenase
XP_021597332.1	0.020774482	-0.344108415	1.073436239	uncharacterized protein LOC110603749
XP_021595753.1	0.012011111	1.434229122	1.079236088	homocysteine S-methyltransferase 3 isoform X2
XP_021613723.1	0.046460651	1.315107449	1.092151906	uncharacterized protein C24B11.05 isoform X2
XP_021613724.1	0.046460651	1.315107449	1.092151906	uncharacterized protein C24B11.05 isoform X2
XP_021619046.1	0.000772278	2.953627807	1.097491603	uncharacterized protein LOC110619799
XP_021607204.1	0.019336052	1.377743233	1.100294857	28 kDa heat- and acid-stable phosphoprotein
XP_021595278.1	0.048083782	0.328206855	1.101985095	uncharacterized protein LOC110602150
XP_021601750.1	0.039467054	0.955571863	1.104185004	beta-carotene isomerase D27, chloroplastic
XP_043816563.1	0.047948746	3.148246681	1.109803773	abscisic acid 8'-hydroxylase CYP707A2
XP_021598577.1	0.004041935	0.586921361	1.112465248	TBC1 domain family member 5 homolog B
XP_021612691.1	0.044848957	-0.467923047	1.127187922	glutamyl-tRNA reductase 1, chloroplastic
XP_021607267.1	0.003578476	-0.407399349	1.142553378	uncharacterized protein LOC110611325
XP_021592702.1	0.024060839	1.388459636	1.14400392	probable LRR receptor-like serine/threonine-protein kinase At1g07650 isoform X1
XP_021604043.1	0.004510482	0.687500355	1.150258342	E3 ubiquitin-protein ligase SINAT5
XP_021624533.1	0.025183679	1.032911443	1.159359763	probable galactinol--sucrose galactosyltransferase 2 isoform X1
XP_021605804.1	0.012173656	-0.753077719	1.159972147	protochlorophyllide reductase, chloroplastic
XP_021624534.1	0.023502979	1.040832566	1.168077872	probable galactinol--sucrose galactosyltransferase 2 isoform X2
XP_021605619.1	0.024033843	-0.140246668	1.170662096	RNA polymerase II transcriptional coactivator KELP isoform X1
XP_021619507.1	0.030750028	1.089704462	1.176361338	heavy metal-associated isoprenylated plant protein 35
XP_021607123.1	0.029893842	-0.141641726	1.180631943	probable plastid-lipid-associated protein 12, chloroplastic
XP_021593469.1	0.041654701	0.413504566	1.18082262	protein CREG1
XP_021616362.1	0.028848163	0.103782269	1.182616065	ferredoxin--NADP reductase, leaf isozyme, chloroplastic

XP_021604301.1	0.013813015	-0.445732102	1.188646631	disease resistance protein UNI
XP_021615850.1	0.00304864	0.577991281	1.190810666	uncharacterized protein LOC110617407
XP_021593667.1	0.04287234	-0.515865016	1.194052362	protochlorophyllide reductase, chloroplastic isoform X1
XP_021631529.1	0.043586459	-0.662251371	1.209248584	chlorophyll a-b binding protein 8, chloroplastic
XP_021628803.1	0.022314132	0.122509779	1.213637954	solute carrier family 25 member 44
XP_021609387.1	0.019075834	-0.917353656	1.217571217	anthocyanidin 3-O-glucosyltransferase 6
XP_021632114.1	0.001179676	2.859539868	1.225416938	transcription activator GLK1
XP_021598003.1	0.048083782	1.596461848	1.236176178	zinc transporter 4, chloroplastic
XP_021632972.1	0.02618661	0.753146087	1.238456094	RNA-binding protein 25 isoform X1
XP_021616025.1	0.012700436	-0.063924024	1.245486612	uncharacterized protein LOC110617502
XP_021625213.1	0.029358882	-0.072474892	1.257107688	partner of Y14 and mago
XP_021621616.1	0.03608545	-0.539485084	1.263339095	chlorophyll a-b binding protein CP29.1, chloroplastic
XP_021602134.1	0.038541686	2.32666583	1.269634052	protein EXORDIUM-like 5
XP_021616746.1	0.003653026	0.832550093	1.275748662	transcription factor HHO3
XP_021613931.1	0.03479297	0.236433314	1.281921417	(+)-neomenthol dehydrogenase
XP_021634769.1	0.027643545	0.994405004	1.284665592	F-box/kelch-repeat protein At1g55270
XP_021623179.1	0.039594392	-0.089904609	1.288094987	photosystem II reaction center W protein, chloroplastic
XP_021599266.1	0.030106068	-0.398157739	1.303527562	chlorophyll a-b binding protein of LHClI type 1
XP_021596351.1	0.029870265	-0.065530025	1.313467987	cationic amino acid transporter 5
XP_021618845.1	0.00694606	0.118345563	1.313940972	uncharacterized protein At2g23090
XP_021618640.1	0.014756986	1.023770927	1.319825598	protein C2-DOMAIN ABA-RELATED 4
XP_021629903.1	0.044415286	1.881088237	1.337079458	probable trehalose-phosphate phosphatase J
XP_043814735.1	0.022213584	2.447933288	1.362044063	heavy metal-associated isoprenylated plant protein 7
XP_021632603.1	0.01895915	0.106051514	1.372248579	UV-B-induced protein At3g17800, chloroplastic
XP_021622135.1	0.002639394	0.16448867	1.376048352	zinc finger protein 593
XP_021608683.1	0.021813626	0.932555934	1.380127531	vicilin-like seed storage protein At2g18540

XP_021623768.1	0.038829528	0.735869542	1.386913492	amidase 1 isoform X1
XP_021596257.1	0.026733148	1.279036584	1.397269098	homeobox protein SBH1
XP_021604086.1	0.033507415	0.204069636	1.398740191	uncharacterized protein LOC110609070
XP_043807005.1	0.034423367	0.845460846	1.401954307	potassium transporter 8 isoform X2
XP_021602697.1	0.036446787	0.862049031	1.402520484	potassium transporter 8 isoform X1
XP_021593162.1	0.01895915	-0.618445284	1.453200076	chlorophyll a-b binding protein CP24 10A, chloroplastic
XP_021610371.1	0.006127436	0.610492527	1.454702563	transcription factor MYBS3
XP_021610786.1	0.049118786	0.108172436	1.460458442	protein SRG1 isoform X2
XP_043807006.1	0.013156021	0.874401945	1.463204182	potassium transporter 8 isoform X3
XP_043808834.1	0.015486348	0.932573553	1.466449238	ferredoxin--NADP reductase, leaf isozyme, chloroplastic
XP_021634434.1	0.009837744	0.238149621	1.48422318	uncharacterized protein LOC110631039
XP_021608820.1	0.000906371	1.48862664	1.494187743	uncharacterized protein LOC110612361
XP_021608821.1	0.000906371	1.48862664	1.494187743	uncharacterized protein LOC110612361
XP_021610785.1	0.038446569	0.238470751	1.501670189	protein SRG1 isoform X1
XP_021593516.1	0.041466939	-0.343668131	1.513288148	protein TIC 20-v, chloroplastic
XP_021593508.1	0.04427587	-0.480797524	1.535902547	pentatricopeptide repeat-containing protein At1g31920 isoform X2
XP_021631132.1	0.022870713	0.857815903	1.538350372	zinc finger CCCH domain-containing protein 18 isoform X3
XP_021631130.1	0.022940664	0.85527116	1.539166104	zinc finger CCCH domain-containing protein 18 isoform X1
XP_021631131.1	0.022940664	0.85527116	1.539166104	zinc finger CCCH domain-containing protein 18 isoform X2
XP_043809753.1	0.041654701	1.310233372	1.546839515	disease resistance protein At4g27190
XP_021633556.1	0.008121608	-0.264663032	1.548767345	photosystem II core complex proteins psbY, chloroplastic
XP_021595014.1	0.024179201	1.288434011	1.551341709	ABC transporter B family member 2 isoform X1
XP_021627740.1	0.043837729	0.335720485	1.557845311	structural maintenance of chromosomes protein 1A
XP_021609756.1	0.03265901	0.814146151	1.563069827	putative proline-rich receptor-like protein kinase PERK6 isoform X3
XP_021620436.1	0.015856544	2.462619044	1.571203847	WAT1-related protein At2g37460
XP_021598601.1	0.043837729	1.165927922	1.587794297	abscisic acid receptor PYR1

XP_021629414.1	0.029358882	2.652398976	1.588458352	WAT1-related protein At5g64700
XP_043807365.1	0.020819477	1.312961154	1.589309125	ABC transporter B family member 2 isoform X2
XP_043804872.1	0.029117991	-0.928143274	1.590223429	LOW QUALITY PROTEIN: tryptamine 5-hydroxylase-like
XP_021630969.1	0.026565376	-0.338466316	1.59039021	uncharacterized protein LOC110628552
XP_021618786.1	0.002638653	0.387913943	1.592309029	ubiquitin-conjugating enzyme E2 14 isoform X1
XP_021618788.1	0.002639394	0.387438049	1.593866498	ubiquitin-conjugating enzyme E2 14 isoform X3
XP_021618787.1	0.006270092	0.367657218	1.599813078	ubiquitin-conjugating enzyme E2 14 isoform X2
XP_021596314.1	0.025850691	-0.517379165	1.602506238	uncharacterized protein LOC110602986
XP_021619299.1	0.023449504	0.4606303	1.607147458	uncharacterized protein LOC110620046
XP_021599916.1	0.007166206	-0.052884661	1.608439887	uncharacterized protein LOC110605595
XP_021606175.1	0.024234686	1.306514883	1.609270733	metallothionein-like protein type 3
XP_021615991.1	0.014301394	0.025220402	1.61152465	uncharacterized protein LOC110617485
XP_021609395.1	0.024179201	2.806803165	1.644244694	probable pectinesterase/pectinesterase inhibitor 35
XP_021598533.1	0.032244671	0.303703791	1.645599598	uncharacterized protein LOC110604600
XP_021609755.1	0.029099785	0.880717663	1.661794733	proline-rich receptor-like protein kinase PERK1 isoform X1
XP_021614332.1	0.020251912	0.113412899	1.664411444	ribosome-binding factor PSRP1, chloroplastic
XP_021634244.1	0.024179201	0.230642983	1.668425554	transcription factor TCP14
XP_021613006.1	0.012553483	-0.534447374	1.669899461	photosystem II reaction center W protein, chloroplastic
XP_043811061.1	0.029800976	2.894840581	1.67153453	glycine-rich cell wall structural protein
XP_021601171.1	0.023729627	0.535297563	1.683201369	catalase isozyme 1 isoform X2
XP_021614907.1	0.002638653	-0.42158402	1.685476519	alkane hydroxylase MAH1
XP_021609351.1	0.041654701	1.809045463	1.686066634	transcription factor bHLH63 isoform X1
XP_021609352.1	0.041654701	1.809045463	1.686066634	transcription factor bHLH63 isoform X2
XP_021609947.2	0.012249782	1.011654956	1.68729564	uncharacterized protein LOC110613232
XP_021603807.1	0.039967451	0.533022296	1.691280621	glycine, alanine and asparagine-rich protein
XP_021620450.1	0.013827106	0.27434454	1.691674334	photosystem II reaction center W protein, chloroplastic

XP_021616113.1	0.036446787	-0.275658081	1.696646957	acyl carrier protein 1, chloroplastic
XP_021632489.1	0.021813626	1.024354161	1.706544705	auxin-responsive protein SAUR36
XP_021593980.1	0.038869219	3.026852082	1.713019879	epidermis-specific secreted glycoprotein EP1
XP_021627587.1	0.01331393	0.452494186	1.721827085	actin-depolymerizing factor 5
XP_021613115.1	0.014537728	1.035579622	1.729465158	uncharacterized protein LOC110615533
XP_043810587.1	0.037602271	-0.038951895	1.729698569	desmethyl-deoxy-podophyllotoxin synthase-like isoform X1
XP_021614174.1	0.038344745	0.318829685	1.738520277	uncharacterized isomerase BH0283
XP_021594496.2	0.003930603	1.738411259	1.745594013	uncharacterized protein LOC110601610, partial
XP_021628863.1	0.019822539	-0.230577165	1.747105133	chaperone protein dnaJ 8, chloroplastic
XP_021609254.1	0.025183679	-0.256670971	1.751658867	photosystem I reaction center subunit VI-1, chloroplastic
XP_021634555.1	9.45E-05	0.483984122	1.760011171	protein indeterminate-domain 16
XP_021596160.1	0.032137382	0.668479285	1.780736236	ABC transporter F family member 4
XP_021634560.1	0.029117991	1.701214494	1.783334891	uncharacterized protein LOC110631145 isoform X1
XP_021634561.1	0.029117991	1.701214494	1.783334891	uncharacterized protein LOC110631145 isoform X1
XP_021634562.1	0.029117991	1.701214494	1.783334891	uncharacterized protein LOC110631145 isoform X1
XP_021599132.1	0.01917019	1.517748867	1.783722902	WAT1-related protein At3g28050
XP_021634566.1	0.027988812	1.710744556	1.793122281	uncharacterized protein LOC110631145 isoform X2
XP_021606223.1	0.020605621	0.090669179	1.811696416	uncharacterized protein LOC110610554
XP_043807177.1	0.012115213	0.844557484	1.832715509	metallothionein-like protein type 3
XP_021625528.1	0.033201036	2.538190511	1.834980245	WAT1-related protein At1g25270 isoform X2
XP_043810482.1	0.024932587	2.014281813	1.844815852	BURP domain protein RD22 isoform X3
XP_043805402.1	0.022213584	1.390102456	1.848717105	serine/arginine-rich splicing factor SR45a
XP_021607213.1	0.028108187	1.99137518	1.849767187	BURP domain protein RD22 isoform X2
XP_021605513.1	0.027804838	0.093064808	1.853163163	protein PLASTID TRANSCRIPTIONALLY ACTIVE 16, chloroplastic
XP_021622543.2	0.046379781	0.364453757	1.905600244	protein CHUP1, chloroplastic
XP_021615032.1	0.048083782	1.486359715	1.914406906	signal peptide peptidase-like 2 isoform X1

XP_021622230.1	0.018908898	0.279071548	1.919363722	uncharacterized protein LOC110622132
XP_021633848.2	0.001384363	1.921990571	1.926474115	heavy metal-associated isoprenylated plant protein 7
XP_021593877.1	0.014815951	0.834301495	1.930154571	calcium/calmodulin-regulated receptor-like kinase 2 isoform X1
XP_021596373.1	0.012341722	0.938669119	1.931558541	uncharacterized protein LOC110603033
XP_021593883.1	0.009235147	0.893377938	1.936005129	calcium/calmodulin-regulated receptor-like kinase 2 isoform X2
XP_021622544.1	0.024041202	0.27508475	1.941987245	cysteine proteinase inhibitor 5
XP_021630395.1	0.027895052	0.125504722	1.943514545	cytochrome P450 81Q32
XP_021621871.1	0.03704139	0.383599983	2.002399207	F-box/kelch-repeat protein At1g15670
XP_021615035.1	0.038291986	1.578987071	2.019835229	signal peptide peptidase-like 2 isoform X2
XP_021630984.1	0.019336052	-0.448701641	2.044661514	photosystem I reaction center subunit IV A, chloroplastic
XP_021619574.1	0.026261767	0.027363109	2.048186834	metallothionein-like protein type 2
XP_021622039.1	0.047511852	0.102937332	2.098761957	light-regulated protein 1, chloroplastic
XP_021592777.1	0.024179201	1.39947955	2.099105608	mitochondrial outer membrane protein porin of 36 kDa
XP_021614380.1	0.008632444	0.942150466	2.112544291	homeobox-leucine zipper protein ATHB-13
XP_021614381.1	0.008632444	0.942150466	2.112544291	homeobox-leucine zipper protein ATHB-13
XP_021614382.1	0.008632444	0.942150466	2.112544291	homeobox-leucine zipper protein ATHB-13
XP_021614383.1	0.008632444	0.942150466	2.112544291	homeobox-leucine zipper protein ATHB-13
XP_043813051.1	0.008632444	0.942150466	2.112544291	homeobox-leucine zipper protein ATHB-13
XP_021615407.1	0.043330954	2.532995706	2.12892512	bidirectional sugar transporter SWEET10
XP_021606590.1	0.007348574	1.565884454	2.155274959	auxin-responsive protein IAA27
XP_021627753.1	6.71E-08	2.109353488	2.155434572	inositol oxygenase 1
XP_021597819.1	0.000859899	1.103117033	2.164772819	sulfite exporter TauE/SafE family protein 2 isoform X3
XP_021604024.1	0.022589357	2.29399595	2.188133588	receptor-like protein kinase FERONIA
XP_021609857.1	0.017705419	2.023734194	2.200806728	protein NRT1/ PTR FAMILY 5.4
XP_021597817.1	0.000405485	1.117578388	2.21685675	sulfite exporter TauE/SafE family protein 5 isoform X1
XP_021595709.1	0.002858018	2.553876676	2.222607304	MLP-like protein 28

XP_021597818.1	0.000375907	1.110806137	2.230960129	sulfite exporter TauE/SafE family protein 5 isoform X2
XP_021609754.1	0.030577705	0.279335556	2.232445091	photosystem I subunit O
XP_021606222.1	0.003578538	0.502498222	2.238208824	cation/calcium exchanger 4
XP_021634380.1	0.005337799	1.081938818	2.251462142	beta-carotene hydroxylase 2, chloroplastic
XP_021606610.1	0.000433038	1.962578089	2.296442926	uncharacterized protein LOC110610844
XP_021633380.1	0.005122895	-1.013614881	2.304068552	uncharacterized protein LOC110630279
XP_043804824.1	0.029800976	0.938457579	2.316105192	uncharacterized protein LOC122721358
XP_021616411.1	0.007195539	-0.379753023	2.316712502	photosystem II 5 kDa protein, chloroplastic
XP_021618056.1	0.02947674	1.438613328	2.318422805	transcription factor DIVARICATA
XP_021618057.1	0.02947674	1.438613328	2.318422805	transcription factor DIVARICATA
XP_021629976.1	0.004510482	3.361493541	2.363505846	BTB/POZ domain-containing protein DOT3 isoform X2
XP_021629824.2	0.049961914	0.397214295	2.373424945	methylesterase 10
XP_021629975.1	0.001618927	3.492036643	2.373765476	BTB/POZ domain-containing protein DOT3 isoform X1
XP_043807402.1	0.01917019	-0.140698	2.375919647	probable peroxygenase 4 isoform X1
XP_021619675.1	0.029117991	2.427915749	2.404268645	DNA ligase 1 isoform X2
XP_021619677.1	0.029117991	2.427915749	2.404268645	DNA ligase 1 isoform X2
XP_021634463.1	0.035525895	1.931851627	2.417576447	uncharacterized protein LOC110631061
XP_021608413.1	0.01895915	1.228559594	2.421390215	uncharacterized protein LOC110612066 isoform X2
XP_021608826.1	0.022213584	1.61069879	2.447390807	protein SPEAR3
XP_021607112.1	0.001378536	1.75849739	2.46087306	uncharacterized protein LOC110611231
XP_021608412.1	0.022940664	1.285694896	2.462084923	uncharacterized protein LOC110612066 isoform X1
XP_021593875.1	0.008690369	1.398328142	2.470904088	uncharacterized protein LOC110601147
XP_021619674.1	0.012618383	2.523741371	2.499955793	DNA ligase 1 isoform X1
XP_021619568.1	0.01895915	1.569258107	2.505304412	cytochrome P450 78A9
XP_021622567.1	0.040183673	0.576699008	2.530058806	uncharacterized protein LOC110622390
XP_021634233.1	0.009019262	2.605712405	2.538306615	cytochrome P450 78A5

XP_021602965.1	0.001378536	2.43607771	2.574180479	vascular-related unknown protein 1
XP_043804863.1	0.001176561	3.686028501	2.644434836	BTB/POZ domain-containing protein DOT3 isoform X3
XP_021605177.1	0.001463562	2.753765716	2.722055348	ABC transporter G family member 11
XP_021614983.1	0.01895915	3.348594339	2.823192146	cytochrome P450 78A5
XP_021612322.2	0.007348574	1.857074286	2.852586489	amino acid transporter AVT1l
XP_043812755.1	0.000124071	2.517859856	2.872034767	calmodulin-like protein 2
XP_043807961.1	0.007195539	2.200705716	2.87968249	receptor-like protein kinase HSL1
XP_021634612.1	0.029117991	-0.359653644	2.966434124	uncharacterized protein PAM68-like
XP_021620961.1	0.002638653	0.657348843	3.023548656	uncharacterized protein LOC110621150
XP_021614785.1	0.009319533	5.124106699	3.072660618	myb-related protein 306
XP_021607210.2	0.007195539	-1.216441861	3.112894758	MDIS1-interacting receptor like kinase 2
XP_021629713.1	9.45E-05	0.872760683	3.150923233	transcription factor HHO5
XP_021625417.1	0.032812359	1.207217162	3.411743291	flavonol sulfotransferase-like
XP_021598791.1	0.012695595	1.57638852	3.742182097	uncharacterized protein LOC110604791
XP_021600533.1	0.014843229	1.538142812	3.789921807	probable calcium-binding protein CML28 isoform X2
XP_021600532.1	0.012698802	1.495638996	3.798488788	probable calcium-binding protein CML28 isoform X1
XP_043810481.1	0.043296257	1.14058228	4.174863907	BURP domain protein RD22 isoform X1

C- Roots, 1 DAI, DSC 260 and DSC 167 vs. TMS 96/0304

protein ID	adjusted p-value	log ₂ FC DSC 260	log ₂ FC DSC 167	protein function
XP_021609991.1	0.047487531	-8.238293448	-8.100519381	17.4 kDa class I heat shock protein
XP_021614058.1	0.035854335	-2.817351095	-7.554582073	NADH dehydrogenase
XP_021622024.1	0.024912158	-5.518950081	-6.260201354	probable glutathione S-transferase
XP_021610414.1	0.048916834	0.131251953	-5.847949859	receptor like protein 21-like
XP_021612364.1	0.011470313	-5.607356643	-3.629185853	BAG family molecular chaperone regulator 6
XP_021612371.1	0.011470313	-5.607356643	-3.629185853	BAG family molecular chaperone regulator 6
XP_043809565.1	0.018863963	-2.913273678	-3.21221872	probable protein phosphatase 2C 26 isoform X2
XP_021613499.1	0.023891822	-4.67329884	-3.005132019	protein NRT1/ PTR FAMILY 2.13
XP_021622320.1	0.014740203	-5.254153516	-2.898399053	ferritin-3, chloroplastic
XP_021610309.1	0.044388668	-3.568761338	-2.842335657	putative low molecular weight protein-tyrosine-phosphatase slr0328 isoform X2
XP_021610308.1	0.04180551	-3.621395486	-2.822919381	putative low molecular weight protein-tyrosine-phosphatase slr0328 isoform X1
XP_043813743.1	0.017919733	5.438231603	-2.79192583	uncharacterized protein LOC110617977, partial
XP_021624293.2	0.000225426	-2.376036998	-2.451060583	sulfite exporter TauE/SafE family protein 4 isoform X1
XP_043815422.1	0.001003744	-2.287525267	-2.404461483	sulfite exporter TauE/SafE family protein 4 isoform X3
XP_021604129.2	0.019177759	-5.743694111	-2.260293776	protein phosphatase 2C 51
XP_021628785.1	0.03677926	-4.644361038	-2.121369104	elicitor-responsive protein 3
XP_021614046.1	0.035854335	2.996902507	-2.087709845	probable alkaline/neutral invertase B
XP_021600739.1	0.03677926	-6.798645496	-1.798212198	acidic endochitinase WIN6.2C
XP_043809106.1	0.03677926	-6.798645496	-1.798212198	acidic endochitinase WIN6.2C-like
XP_021609722.1	0.035854335	-5.000677781	-1.689287691	pyridoxal 5'-phosphate synthase-like subunit PDX1.2
XP_021633847.1	0.045935178	0.38120439	-1.160068086	methionine aminopeptidase 1B, chloroplastic
XP_021605659.2	0.018979053	-5.895176337	-0.973552318	probable calcium-binding protein CML44, partial
XP_021626276.1	0.030639153	-4.594369263	-0.806563215	17.3 kDa class I heat shock protein
XP_021600897.2	0.014740203	1.451783457	-0.622789418	cytochrome P450 734A1
XP_021622201.2	0.023891822	-4.800203867	-0.605193623	uncharacterized protein LOC110622114

XP_021622203.2	0.023891822	-4.800203867	-0.605193623	uncharacterized protein LOC110622114
XP_021622913.1	0.045935178	0.300893768	-0.552409198	transcription factor TGA2.3
XP_021620073.1	0.017478391	-2.821940756	-0.550880578	protein SRC2 homolog
XP_021595355.1	0.047604405	-2.627468498	-0.505719374	uncharacterized protein LOC110602205
XP_021605448.1	0.006339174	-3.654854242	-0.503711198	uncharacterized protein LOC110609917
XP_021634749.2	0.011683215	3.26283209	-0.471386571	high-affinity nitrate transporter 3.1
XP_021608516.2	0.011470313	-1.97278619	-0.393690132	uncharacterized protein LOC110612133
XP_021604201.2	0.039405736	1.205938909	-0.28335003	homeobox protein BEL1 homolog
XP_021591904.1	0.03581678	-1.219641792	-0.168930481	heat shock protein 90-5, chloroplastic
XP_021615086.1	0.049961497	-1.931020316	-0.165262459	serine/threonine-protein kinase UCNL
XP_021623028.1	0.033575714	-1.671202623	-0.160210987	superoxide dismutase
XP_021625568.1	0.011807068	1.420554546	-0.077285089	calcium and calcium/calmodulin-dependent serine/threonine-protein kinase
XP_021593296.1	0.014740203	-1.424767181	-0.052028378	calcyclin-binding protein
XP_021606591.1	0.035854335	-2.625007995	-0.008404887	uncharacterized protein LOC110610820
XP_021605335.1	0.010980135	2.037002945	-0.004413864	U-box domain-containing protein 5 isoform X1
XP_043814340.1	0.035854335	1.745429839	0.015660917	phenylacetaldehyde reductase
XP_021622698.1	0.042710402	-3.949083698	0.068509798	microtubule-binding protein TANGLED
XP_021621239.1	0.023527564	-1.619287522	0.103857736	two-component response regulator ARR8
XP_021622483.1	0.021069673	-5.636003494	0.116687633	zeatin O-glucosyltransferase
XP_021593066.1	0.035854335	-1.639053426	0.131894076	uncharacterized protein LOC110600516
XP_043816985.1	0.042710402	1.993938332	0.145120481	hippocampus abundant transcript-like protein 1 isoform X2
XP_021626069.1	0.037511859	2.023243919	0.182052713	hippocampus abundant transcript-like protein 1 isoform X1
XP_021624116.1	0.018979053	-4.067507144	0.208072794	11 kDa late embryogenesis abundant protein
XP_021620139.1	0.014740203	1.961341239	0.252804434	bZIP transcription factor TGA10 isoform X1
XP_021601705.1	0.00550042	-1.173398749	0.262109221	probable L-ascorbate peroxidase 6, chloroplastic/mitochondrial isoform X2
XP_021604102.1	0.00550042	1.299615691	0.276934488	auxin response factor 9

XP_021601704.1	0.00165031	-1.161825044	0.278015922	probable L-ascorbate peroxidase 6, chloroplastic/mitochondrial isoform X1
XP_021595770.1	0.032802803	-3.009371298	0.317013346	probable protein phosphatase 2C 24
XP_021619908.1	0.034135648	2.961356445	0.320138904	myb family transcription factor PHL5 isoform X1
XP_021594006.1	0.035854335	-2.087573795	0.328195992	uncharacterized protein LOC110601248
XP_021627352.1	0.03093241	1.19158523	0.350362637	NAC domain-containing protein 91
XP_021617184.1	0.047604405	-2.510633541	0.361622955	protein phosphatase 2C 51
XP_021618573.1	0.035854335	-1.466127372	0.376678988	D-3-phosphoglycerate dehydrogenase 1, chloroplastic
XP_021624325.1	0.035854335	2.591297421	0.381470711	protein DETOXIFICATION 24
XP_021595743.1	0.001003744	4.707108106	0.400734995	probable WRKY transcription factor 72
XP_021622937.1	0.04180551	1.547991767	0.472453134	scarecrow-like protein 33
XP_021593988.1	0.03581678	-2.463198361	0.483552676	FCS-Like Zinc finger 1 isoform X1
XP_021593989.1	0.039036068	-2.310281117	0.502707199	FCS-Like Zinc finger 1 isoform X2
XP_021621313.1	0.022298181	2.857108554	0.510994172	oligopeptide transporter 3
XP_021623718.1	0.007937537	-2.594839909	0.633780269	bark storage protein B
XP_021617383.2	0.011986983	2.345552205	0.680317829	uncharacterized protein LOC110618547 isoform X2
XP_043814256.1	0.011807068	2.353228482	0.681012974	uncharacterized protein LOC110618547 isoform X1
XP_021626811.1	0.042710402	1.34851454	0.722696101	protein argonaute 5
XP_021620148.1	0.011470313	-3.077323133	0.774953627	cytochrome P450 709B2
XP_021617668.1	0.03093241	1.820739083	0.829128229	heat stress transcription factor A-4c
XP_043804611.1	0.006339174	1.849199774	0.82962247	cytochrome b561 and DOMON domain-containing protein At5g47530-like
XP_021630901.1	0.012729034	-1.681976455	0.839664444	peptidyl-prolyl cis-trans isomerase FKBP62
XP_021627108.1	0.040158083	3.125649075	0.919296018	proline-rich receptor-like protein kinase PERK5
XP_021624734.1	0.033575714	2.71537043	0.940917209	aspartic proteinase PCS1
XP_021612635.1	0.04710248	-0.456408354	0.951167957	heat shock cognate protein 80
XP_043814615.1	0.00550042	-0.098215701	0.961129673	uncharacterized protein LOC110621336
XP_021614214.1	0.019177759	3.405531614	1.167836586	chitinase 10

XP_021610609.1	0.032802803	1.087149313	1.259294608	putative disease resistance protein RGA3
XP_021618054.1	0.02550052	3.801514155	1.312685656	WAT1-related protein At1g43650
XP_021602811.2	0.030572483	2.246700546	1.38074324	cytochrome b561 and DOMON domain-containing protein At5g47530
XP_021610028.1	0.033038259	-0.756772772	1.419964638	GEM-like protein 4
XP_021616094.1	0.03677926	1.986906072	1.444311782	tetraspanin-8
XP_021604396.1	0.00550042	2.812780252	1.471601925	probable WRKY transcription factor 53
XP_021602795.1	0.005565691	-0.048452932	1.47437705	D-3-phosphoglycerate dehydrogenase 3, chloroplastic
XP_043815152.1	0.023527564	-2.281297215	1.526481332	probable galactinol--sucrose galactosyltransferase 2 isoform X2
XP_021606416.1	0.037816091	3.340832819	1.537097361	pleiotropic drug resistance protein 1
XP_021620353.1	0.023527564	-2.291358702	1.547409659	probable galactinol--sucrose galactosyltransferase 2 isoform X1
XP_021615172.1	0.011470313	1.917853189	1.564817438	3-ketoacyl-CoA synthase 11
XP_021598088.1	0.02550052	5.192202214	1.600430284	metal tolerance protein 9
XP_021602326.1	0.039405736	-0.933137685	1.614449673	suppressor of disruption of TFIS
XP_043809100.1	0.023527564	-2.941265579	1.673679083	acidic endochitinase WIN6.2C-like
XP_043804493.1	0.011470313	2.667625618	1.707986006	cytochrome b561 and DOMON domain-containing protein At5g35735
XP_021624769.1	0.035854335	2.072880825	1.711066966	putative serine/threonine-protein kinase-like protein CCR3 isoform X1
XP_043809312.1	0.03677926	3.255583972	1.752595113	nitrate reductase
XP_021618424.1	0.023527564	0.901403317	1.795791482	uncharacterized protein LOC110619344
XP_021596490.1	0.024902001	1.461987511	1.851151048	serine/threonine-protein kinase RIPK
XP_021613939.1	0.03581678	1.564831809	1.856385296	glycosyltransferase family 92 protein RCOM_0530710
XP_043809313.1	0.023891822	3.301899225	1.917586959	nitrate reductase
XP_021604899.1	0.026030353	1.838371057	1.930335651	probable ribose-5-phosphate isomerase 2
XP_021627256.1	0.00550042	0.9132538	1.951632999	transcription factor bHLH63
XP_021607270.1	0.02928055	-0.454504738	1.970730733	2-oxoglutarate-dependent dioxygenase DAO
XP_021609486.1	0.042710402	1.274940286	2.136907918	probable amidase At4g34880
XP_021622610.1	0.014740203	1.286610474	2.222055051	probable calcium-binding protein CML43

XP_021605354.2	0.011986983	2.034890376	2.3292725	BTB/POZ domain-containing protein At5g41330
XP_021605783.1	0.011807068	2.465682261	2.353624663	serine/threonine-protein kinase RIPK
XP_021624303.1	0.035854335	1.979754653	2.504486348	BAHD acyltransferase DCR
XP_021592360.2	0.023527564	1.926574918	2.576715322	leucine-rich repeat receptor-like serine/threonine/tyrosine-protein kinase SOBIR1
XP_021626531.2	0.024052101	2.360627349	2.589177554	probable receptor-like protein kinase At1g11050
XP_021603446.1	0.018492225	2.260772382	2.767599236	L-Ala-D/L-amino acid epimerase isoform X1
XP_021603447.1	0.021439953	2.269967541	2.777506736	L-Ala-D/L-amino acid epimerase isoform X2
XP_021622562.1	0.048916834	1.548390221	2.825086726	E3 ubiquitin-protein ligase PUB23
XP_021622847.1	0.035854335	5.640115063	2.873352707	potassium transporter 5
XP_021634685.1	0.02550052	0.347391535	2.999677629	RING-H2 finger protein ATL40
XP_021626801.1	0.03618264	3.722970158	3.08026889	laccase-11
XP_021622470.1	0.02550052	2.565553606	3.416306947	U-box domain-containing protein 9 isoform X2
XP_021622469.1	0.018218031	2.703053317	3.612386047	U-box domain-containing protein 9 isoform X1
XP_021625403.1	0.00550042	1.953726761	3.634597287	mitochondrial uncoupling protein 5
XP_021625430.1	0.032802803	1.347556066	4.032982057	mitochondrial uncoupling protein 5
XP_043814290.1	0.019177759	-1.471451242	4.372791045	beta-glucosidase 12-like
XP_021609710.1	0.035854335	3.0676615	4.425833428	exocyst complex component EXO70H1
XP_021592525.1	0.02108258	-0.711516574	4.478543684	photosystem I reaction center subunit psaK, chloroplastic
XP_021610025.1	0.04354499	4.90027717	5.189234203	UPF0481 protein At3g47200
XP_043812482.1	0.023891822	12.26210609	7.13769864	uncharacterized protein LOC110614799

D-Roots, 10 DAI, DSC 260 and DSC 167 vs. TMS 96/0304

protein ID	adjusted p-value	log ₂ FC DSC 260	log ₂ FC DSC 167	protein function
XP_021601745.2	0.020416884	-8.060120149	-4.565223193	cytochrome P450 CYP82D47
XP_021594339.1	0.046583639	-3.382050526	-3.205106101	cytochrome P450 716B1
XP_021615231.1	0.017659154	-13.06304677	-2.443711622	berberine bridge enzyme-like 18
XP_021609177.1	0.004818799	-2.913327874	-2.034166409	superoxide dismutase [Cu-Zn], chloroplastic
XP_021610011.1	0.037084788	-6.605630159	-1.744180649	lysine histidine transporter-like 8
XP_021617617.1	0.007691374	-2.694261642	-1.45289206	probable sodium/metabolite cotransporter BASS1, chloroplastic
XP_021619985.1	0.00037575	1.43321623	-0.753611599	uncharacterized protein LOC110620519
XP_021614763.1	0.046583639	-1.580086288	-0.641814258	uncharacterized protein LOC110616638
XP_021600014.1	0.043482803	2.56477268	-0.616278289	type IV inositol polyphosphate 5-phosphatase 9 isoform X1
XP_021623028.1	0.003483825	-2.222678766	-0.56190206	superoxide dismutase [Cu-Zn] isoform X2
XP_021633795.1	0.046583639	-1.403454392	-0.55735739	60S ribosomal protein L13a-4
XP_021598846.1	0.000134109	-2.723346083	-0.461602679	auxin transporter-like protein 3
XP_043812418.1	0.04927429	3.998018779	-0.387762063	protein RADIALIS-like 3 isoform X2
XP_043816442.1	0.012818997	-1.86979233	-0.323073132	superoxide dismutase [Cu-Zn] 1 isoform X1
XP_043816443.1	0.017659154	-1.882338815	-0.315043745	superoxide dismutase [Cu-Zn] 1 isoform X3
XP_021612586.1	0.00045813	0.967502788	-0.247285347	uncharacterized protein LOC110615168
XP_021626454.1	0.037084788	1.043304748	-0.026441679	uncharacterized protein LOC110625191
XP_021593302.1	0.000520026	0.985929744	0.112222851	far upstream element-binding protein 2
XP_021633549.1	0.008318036	-0.754988157	0.132923849	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
XP_043815733.1	0.008663737	0.757189619	0.220297815	uncharacterized protein LOC110623326
XP_021592369.1	0.025209037	1.161381603	0.386020835	scarecrow-like protein 8
XP_021603106.1	0.025209037	1.657107552	0.431567245	protein NRT1/ PTR FAMILY 5.8
XP_021594721.1	0.037084788	1.082434585	0.460108956	alpha/beta hydrolase domain-containing protein 17B isoform X1
XP_021624199.1	0.017659154	-1.132115789	0.495255723	uncharacterized protein At2g37660, chloroplastic isoform X2
XP_021624198.1	0.020440382	-1.077589828	0.512184263	uncharacterized protein At2g37660, chloroplastic isoform X1

XP_043812552.1	0.04927429	-0.562795852	0.60953129	palmitoyl-protein thioesterase 1 isoform X1
XP_021614182.1	0.023588026	1.584230438	0.618402325	probable WRKY transcription factor 7
XP_021618896.1	0.021445811	-1.18559117	0.689068686	triosephosphate isomerase, cytosolic
XP_021614753.1	0.000444826	2.880439563	0.751977282	cyclic dof factor 3
XP_021614220.1	0.044162977	-0.019151783	0.785388962	uncharacterized calcium-binding protein At1g02270
XP_021620641.1	0.034941867	2.522059434	0.968456539	transcription repressor OFP4
XP_021629057.1	0.04927429	-1.284931808	1.004124525	dnaJ protein homolog
XP_021615066.1	0.015410036	-4.848896364	1.021852114	thylakoid lumenal 16.5 kDa protein, chloroplastic
XP_021609286.1	0.037987407	1.072621081	1.03297456	trihelix transcription factor ASIL2
XP_021601886.1	0.02704992	2.999636517	1.092409681	SPX domain-containing protein 1
XP_021629594.1	0.007691374	1.446293637	1.414829491	1-aminocyclopropane-1-carboxylate synthase
XP_043809573.1	0.037084788	1.750702602	1.778454788	uncharacterized protein LOC122722542
XP_021622761.1	0.046583639	3.378435326	2.103756982	cationic amino acid transporter 6, chloroplastic
XP_021617273.1	0.042136525	2.931552118	2.266394794	uncharacterized protein LOC110618449
XP_021599002.1	0.028137419	-1.088560903	2.655544797	CBS domain-containing protein CBSX5
XP_021632366.1	0.025209037	2.273774589	2.798814179	peroxidase 47
XP_021601617.1	0.025209037	4.812336907	3.033254399	protein PHOSPHATE-INDUCED 1
XP_021598401.1	0.049272341	4.293014794	3.108122713	xyloglucan glycosyltransferase 4
XP_021604656.2	0.021304274	-0.614747513	3.132702644	ethylene-responsive transcription factor 6
XP_021627250.1	0.022956375	-1.085522679	4.973724138	heat shock cognate 70 kDa protein
XP_021602057.1	0.015410036	3.616455401	6.802148013	fe(2+) transport protein 1