

Supplementary Information

Supplementary Tables S1-S4

Supplementary Table S1. Low-mapping CL153 RNA-seq libraries retained for QC-aware interpretation.

CL153 libraries with Salmon mapping rates below 50%. These libraries were retained to preserve the balanced genotype-specific factorial design but were flagged in downstream interpretation, particularly for severe-heat and recovery-stage CL153 results.

Sample ID	Run accession	Genotype	Water	Stage	Replicate	Processed fragments	Mapped fragments	Percent mapped
CL153 SWD T42 R1	SRR29823144	CL153	SWD	T42	1	22543647	7245251	32.14
CL153 SWD REC14 R3	SRR29823143	CL153	SWD	REC14	3	21429606	8818571	41.15
CL153 WW REC14 R3	SRR28347734	CL153	WW	REC14	3	26566229	11474540	43.19
CL153 WW REC14 R2	SRR28347733	CL153	WW	REC14	2	19979216	8691441	43.5
CL153 SWD T42 R2	SRR29823145	CL153	SWD	T42	2	17338479	8438993	48.67

Supplementary Table S2. Full functional-module enrichment results for non-additive genes.

Complete module-by-stage enrichment statistics for each genotype. Module counts are reported relative to the genotype-specific non-additive set and feature background, with hypergeometric p -values and Benjamini-Hochberg FDR values. The compact significant/suggestive subset is summarized in Main Table 3. FDR class indicates whether each module-stage test was significant ($\text{FDR} < 0.05$), suggestive ($0.05 \leq \text{FDR} < 0.10$), or not significant ($\text{FDR} \geq 0.10$).

Genotype	Stage	Module	Non-additive genes in module	Total non-additive genes in stage	Background module genes	Background total genes	Enrichment ratio	p -value	FDR	FDR class
<i>C. arabica</i> Icatu	REC14	Other or Unannotated	599	719	44317	54602	1.026	0.0743	0.7426	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	REC14	TF / Hormone Crosstalk	29	719	1870	54602	1.178	0.2085	0.7817	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	REC14	Dehydration / LEA / Osmoprotection	14	719	1039	54602	1.023	0.5026	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	REC14	Protease / Vacuole / Ubiquitin	25	719	1881	54602	1.009	0.5096	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	REC14	ABA Signaling	39	719	3569	54602	0.83	0.9044	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	REC14	ROS / Redox	7	719	781	54602	0.681	0.8901	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	REC14	Proteostasis / HSP / Chaperone	3	719	424	54602	0.537	0.9188	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	REC14	Water Transport / Aquaporin	1	719	147	54602	0.517	0.8579	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	REC14	Lipid / Membrane	2	719	357	54602	0.425	0.9497	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	REC14	Photosynthesis	0	719	217	54602	0	1	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T37	Photosynthesis	17	2680	217	54602	1.596	0.0397	0.5954	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T37	Other or Unannotated	2211	2680	44317	54602	1.016	0.0359	0.5954	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T37	TF / Hormone Crosstalk	102	2680	1870	54602	1.111	0.1453	0.7817	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T37	Water Transport / Aquaporin	9	2680	147	54602	1.247	0.2965	0.8748	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T37	Lipid / Membrane	20	2680	357	54602	1.141	0.3037	0.8748	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T37	Protease / Vacuole / Ubiquitin	97	2680	1881	54602	1.051	0.3208	0.8748	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T37	ROS / Redox	39	2680	781	54602	1.017	0.4792	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T37	Dehydration / LEA / Osmoprotection	48	2680	1039	54602	0.941	0.6884	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T37	Proteostasis / HSP / Chaperone	15	2680	424	54602	0.721	0.9287	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T37	ABA Signaling	122	2680	3569	54602	0.696	1	1	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T42	Proteostasis / HSP / Chaperone	10	947	424	54602	1.36	0.2048	0.7817	Not significant ($\text{FDR} \geq 0.10$)
<i>C. arabica</i> Icatu	T42	Dehydration / LEA / Osmoprotection	22	947	1039	54602	1.221	0.1985	0.7817	Not significant ($\text{FDR} \geq 0.10$)

Genotype	Stage	Module	Non-additive genes in module	Total non-additive genes in stage	Background module genes	Background total genes	Enrichment ratio	p-value	FDR	FDR class
<i>C. arabica</i> Icatu	T42	Other or Unannotated	779	947	44317	54602	1.014	0.2045	0.7817	Not significant (FDR $\geq$ 0.10)
<i>C. arabica</i> Icatu	T42	Photosynthesis	4	947	217	54602	1.063	0.5207	1	Not significant (FDR $\geq$ 0.10)
<i>C. arabica</i> Icatu	T42	Protease / Vacuole / Ubiquitin	32	947	1881	54602	0.981	0.5698	1	Not significant (FDR $\geq$ 0.10)
<i>C. arabica</i> Icatu	T42	Lipid / Membrane	6	947	357	54602	0.969	0.5868	1	Not significant (FDR $\geq$ 0.10)
<i>C. arabica</i> Icatu	T42	ABA Signaling	59	947	3569	54602	0.953	0.6686	1	Not significant (FDR $\geq$ 0.10)
<i>C. arabica</i> Icatu	T42	TF / Hormone Crosstalk	25	947	1870	54602	0.771	0.9283	1	Not significant (FDR $\geq$ 0.10)
<i>C. arabica</i> Icatu	T42	ROS / Redox	10	947	781	54602	0.738	0.8713	1	Not significant (FDR $\geq$ 0.10)
<i>C. arabica</i> Icatu	T42	Water Transport / Aquaporin	0	947	147	54602	0	1	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	REC14	Photosynthesis	7	668	35	20285	6.073	0.000122	0.0033	Significant (FDR < 0.05)
<i>C. canephora</i> CL153	REC14	Water Transport / Aquaporin	2	668	16	20285	3.796	0.0959	0.5177	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	REC14	TF / Hormone Crosstalk	1	668	12	20285	2.531	0.331	0.934	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	REC14	ABA Signaling	105	668	3103	20285	1.028	0.3958	0.934	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	REC14	Other or Unannotated	551	668	17001	20285	0.984	0.8412	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	REC14	Dehydration / LEA / Osmoprotection	2	668	73	20285	0.832	0.6981	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	REC14	Protease / Vacuole / Ubiquitin	0	668	2	20285	0	1	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	REC14	Proteostasis / HSP / Chaperone	0	668	40	20285	0	1	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	REC14	ROS / Redox	0	668	3	20285	0	1	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T37	Water Transport / Aquaporin	2	165	16	20285	15.367	0.0073	0.0989	Suggestive (0.05 $\leq$ FDR < 0.10)
<i>C. canephora</i> CL153	T37	Photosynthesis	1	165	35	20285	3.513	0.2488	0.934	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T37	Dehydration / LEA / Osmoprotection	1	165	73	20285	1.684	0.4497	0.934	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T37	Other or Unannotated	138	165	17001	20285	0.998	0.5753	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T37	ABA Signaling	23	165	3103	20285	0.911	0.7186	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T37	Protease / Vacuole / Ubiquitin	0	165	2	20285	0	1	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T37	Proteostasis / HSP / Chaperone	0	165	40	20285	0	1	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T37	ROS / Redox	0	165	3	20285	0	1	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T37	TF / Hormone Crosstalk	0	165	12	20285	0	1	1	Not significant (FDR $\geq$ 0.10)

Genotype	Stage	Module	Non-additive genes in module	Total non-additive genes in stage	Background module genes	Background total genes	Enrichment ratio	p-value	FDR	FDR class
<i>C. canephora</i> CL153	T42	Photosynthesis	4	650	35	20285	3.567	0.0249	0.2242	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T42	Water Transport / Aquaporin	2	650	16	20285	3.901	0.0915	0.5177	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T42	Proteostasis / HSP / Chaperone	3	650	40	20285	2.341	0.1358	0.6112	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T42	TF / Hormone Crosstalk	1	650	12	20285	2.601	0.3236	0.934	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T42	Dehydration / LEA / Osmoprotection	3	650	73	20285	1.283	0.4159	0.934	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T42	ABA Signaling	102	650	3103	20285	1.026	0.405	0.934	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T42	Other or Unannotated	535	650	17001	20285	0.982	0.8663	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T42	Protease / Vacuole / Ubiquitin	0	650	2	20285	0	1	1	Not significant (FDR $\geq$ 0.10)
<i>C. canephora</i> CL153	T42	ROS / Redox	0	650	3	20285	0	1	1	Not significant (FDR $\geq$ 0.10)

Supplementary Table S3. Top interaction candidates in *Coffea arabica* Icatu.

Top 50 Icatu gene/transcript candidates ranked by interaction support and non-additivity score. The table reports target stage, response class, functional module assignment, product annotation, non-additivity score, and FDR for candidate-level interpretation and validation prioritization.

Gene/transcript ID	Stage	Class	Module	Product annotation	Non-additive score	FDR
XM_027214964.1	T37	Synergistic Positive	Other or Unannotated	protein REVEILLE 8, transcript variant X2	7.82	5.66e-21
XM_027218966.1	T42	Antagonistic or Buffered	Other or Unannotated	alpha-1,4 glucan phosphorylase L-1 isozyme, chloroplastic/amyloplastic, transcript variant X1	-2.181	1.73e-20
XM_027265798.1	T37	Synergistic Positive	Other or Unannotated	uncharacterized LOC113738558, transcript variant X4	1.532	6.02e-20
XM_027238646.1	T37	Synergistic Positive	ROS / Redox	sucrose transport protein SUC4-like, transcript variant X1	1.56	4.68e-19
XR_003447948.1	T37	Synergistic Positive	TF / Hormone Crosstalk	transcription termination factor MTERF9, chloroplastic-like, transcript variant X19	6.726	8.45e-19
XM_027265454.1	T37	Synergistic Positive	Other or Unannotated	glucose-1-phosphate adenylyltransferase large subunit 3, chloroplastic/amyloplastic-like	5.272	8.45e-19
XM_027212216.1	T37	Synergistic Positive	Other or Unannotated	protein N-lysine methyltransferase METTL21A-like, transcript variant X12	3.641	1.48e-18
XM_027243758.1	T37	Synergistic Positive	Other or Unannotated	beta-carotene isomerase D27, chloroplastic-like, transcript variant X2	2.162	1.48e-18
XR_003458857.1	T37	Synergistic Positive	Dehydration / LEA / Osmoprotection	5'-3' exoribonuclease 4-like, transcript variant X1	1.049	1.48e-18
XM_027222865.1	T37	Synergistic Positive	Other or Unannotated	leucine-rich repeat extensin-like protein 3	6.996	2.38e-18
XM_027260682.1	T37	Synergistic Positive	Other or Unannotated	actin-related protein 9, transcript variant X2	8.852	3.93e-18
XM_027225669.1	T37	Synergistic Positive	Other or Unannotated	deacetylvinidoline O-acetyltransferase-like	7.154	6.46e-18
XM_027214964.1	T42	Synergistic Positive	Other or Unannotated	protein REVEILLE 8, transcript variant X2	1.836	9.25e-18
XM_027263249.1	T37	Synergistic Positive	Other or Unannotated	reticulon-like protein B13, transcript variant X1	2.102	1.27e-17
XM_027214642.1	T37	Not Significant or Small	Other or Unannotated	homeobox protein knotted-1-like 11, transcript variant X3	0.939	1.79e-17
XM_027225752.1	T37	Synergistic Positive	Other or Unannotated	monooxygenase 2-like, transcript variant X3	3.056	2.28e-17
XM_027236135.1	T37	Synergistic Positive	TF / Hormone Crosstalk	carboxymethylenebutenolidase homolog, transcript variant X1	5.552	2.35e-17
XM_027216788.1	T37	Synergistic Positive	Other or Unannotated	cyclic nucleotide-gated ion channel 17-like	1.888	2.35e-17
XM_027263750.1	T37	Synergistic Positive	Other or Unannotated	inositol transporter 1-like, transcript variant X1	1.797	2.35e-17
XM_027224325.1	T37	Synergistic Positive	Other or Unannotated	protein SPA1-RELATED 2-like, transcript variant X6	1.344	2.35e-17
XM_027255469.1	T37	Synergistic Positive	Protease / Vacuole / Ubiquitin	vacuolar protein sorting-associated protein 60.2-like, transcript variant X1	2.003	2.38e-17
XM_027270362.1	T37	Synergistic Positive	Other or Unannotated	40S ribosomal protein SA-like, transcript variant X1	1.907	2.38e-17
XR_003454925.1	T37	Not Significant or Small	Dehydration / LEA / Osmoprotection	U5 small nuclear ribonucleoprotein 40 kDa protein-like, transcript variant X2	0.641	2.67e-17
XM_027233866.1	T37	Synergistic Positive	Protease / Vacuole / Ubiquitin	autophagy-related protein 8C-like, transcript variant X1	1.611	2.72e-17
XM_027257433.1	T42	Antagonistic or Buffered	Other or Unannotated	zinc finger CCCH domain-containing protein 40-like, transcript variant X2	-7.548	3.66e-17
XM_027257303.1	T37	Synergistic Positive	Lipid / Membrane	probable plastid-lipid-associated protein 4, chloroplastic, transcript variant X4	2.525	3.73e-17

Gene/transcript ID	Stage	Class	Module	Product annotation	Non-additive score	FDR
XM_027257433.1	T37	Synergistic Positive	Other or Unannotated	zinc finger CCCH domain-containing protein 40-like, transcript variant X2	2.172	6.33e-17
XM_027206314.1	T37	Synergistic Positive	Other or Unannotated	pyridoxal phosphate homeostasis protein-like, transcript variant X1	1.862	6.57e-17
XM_027255433.1	T37	Synergistic Positive	Other or Unannotated	7-methylguanosine phosphate-specific 5'-nucleotidase A-like, transcript variant X2	2.276	7.72e-17
XM_027236135.1	REC14	Synergistic Positive	TF / Hormone Crosstalk	carboxymethylenebutenolidase homolog, transcript variant X1	6.077	8.03e-17
XM_027235440.1	T37	Synergistic Positive	Other or Unannotated	UDP-xylose transporter 3	1.151	9.32e-17
XM_027248384.1	T37	Synergistic Positive	Other or Unannotated	uncharacterized LOC113725291	2.213	1.22e-16
XM_027263043.1	T37	Synergistic Positive	Lipid / Membrane	plastid-lipid-associated protein 6, chloroplastic-like	2.388	1.53e-16
XM_027216200.1	T37	Not Significant or Small	Other or Unannotated	protein COP1 SUPPRESSOR 2-like, transcript variant X1	0.402	1.85e-16
XR_003450742.1	T37	Synergistic Positive	ABA Signaling	PREDICTED: Coffea arabica uncharacterized LOC113700691 (LOC113700691), transcript variant X15, ncRNA	1.459	2.24e-16
XM_027230745.1	T37	Not Significant or Small	Other or Unannotated	E3 SUMO-protein ligase SIZ1-like, transcript variant X1	0.964	2.35e-16
XM_027256695.1	T37	Synergistic Positive	ABA Signaling	bZIP transcription factor 46-like, transcript variant X3	1.931	2.54e-16
XM_027254120.1	T37	Not Significant or Small	Other or Unannotated	uncharacterized LOC113729838, transcript variant X1	0.837	3.16e-16
XM_027247749.1	T37	Synergistic Positive	ABA Signaling	protein ABIL3-like, transcript variant X4	7.126	3.57e-16
XM_027225564.1	T37	Not Significant or Small	Other or Unannotated	60S ribosomal protein L5-like	0.727	5.01e-16
XM_027265269.1	T37	Not Significant or Small	Other or Unannotated	eukaryotic translation initiation factor 2 subunit gamma-like, transcript variant X1	0.647	5.02e-16
XM_027219789.1	REC14	Antagonistic or Buffered	Other or Unannotated	protein PIN-LIKES 3-like, transcript variant X3	-7.24	6.69e-16
XM_027263396.1	T37	Synergistic Positive	Other or Unannotated	glycine-rich cell wall structural protein-like, transcript variant X1	15.744	7.63e-16
XM_027242394.1	T37	Synergistic Positive	Other or Unannotated	zinc finger protein BRUTUS-like, transcript variant X1	1.848	7.63e-16
XM_027255917.1	T37	Synergistic Positive	Other or Unannotated	uncharacterized LOC113730923, transcript variant X2	1.803	8.21e-16
XM_027267721.1	T37	Not Significant or Small	Other or Unannotated	selenium-binding protein 1-like, transcript variant X1	0.728	8.21e-16
XM_027269828.1	T37	Not Significant or Small	Other or Unannotated	uncharacterized LOC113742114, transcript variant X2	0.802	8.3e-16
XM_027240907.1	T37	Not Significant or Small	Other or Unannotated	ribosome-recycling factor, chloroplastic, transcript variant X1	0.842	1.07e-15
XM_027268047.1	T37	Synergistic Positive	Other or Unannotated	CBBY-like protein, transcript variant X1	1.146	1.08e-15
XM_027216684.1	T37	Synergistic Positive	Other or Unannotated	pentatricopeptide repeat-containing protein At1g56690, mitochondrial-like, transcript variant X1	2.529	1.17e-15

Supplementary Table S4. Top interaction candidates in Coffea canephora CL153.

Top 50 CL153 gene/transcript candidates ranked by interaction support and non-additivity score. The table reports target stage, response class, functional module assignment, product annotation, annotation source where available, non-additivity score, and FDR for candidate-level interpretation and validation prioritization.

Gene/transcript ID	Stage	Class	Module	Product annotation	Source organism	Non-additive score	FDR
GSCOC_T00035262001	REC14	Synergistic Positive	Other or Unannotated	unannotated		6.688	2.8e-09
GSCOC_T00035723001	T42	Synergistic Positive	Other or Unannotated	unannotated		8.734	8.34e-08
GSCOC_T00003937001	T42	Synergistic Positive	ABA Signaling	Probable carboxylesterase 8	<i>Arabidopsis thaliana</i> AT2G45600 (UniProt O64640)	4.31	2.93e-07
GSCOC_T00011816001	REC14	Synergistic Positive	Other or Unannotated	unannotated		8.532	6.2e-07
GSCOC_T00039583001	T37	Antagonistic or Buffered	ABA Signaling	Expansin	<i>Arabidopsis thaliana</i> AT3G29030 (UniProt Q1ECM3)	-1.244	6.3e-07
GSCOC_T00032911001	T37	Antagonistic or Buffered	Other or Unannotated	unannotated		-8.87	6.44e-07
GSCOC_T00029696001	T37	Antagonistic or Buffered	Other or Unannotated	unannotated		-3.465	6.44e-07
GSCOC_T00023375001	T37	Antagonistic or Buffered	ABA Signaling	Glycerol-3-phosphate 2-O-acyltransferase 6	<i>Arabidopsis thaliana</i> AT2G38110 (UniProt O80437)	-2.844	7.64e-07
GSCOC_T00027825001	T42	Synergistic Positive	Other or Unannotated	unannotated		7.017	1.08e-06
GSCOC_T00031728001	T42	Synergistic Positive	Other or Unannotated	unannotated		4.632	1.46e-06
GSCOC_T00034556001	T42	Synergistic Positive	Other or Unannotated	Endoplasmic reticulum (ER) membrane protein, Early tapetum development and meiosis	<i>Oryza sativa</i> Os07g0622900	1.875	1.46e-06
GSCOC_T00010080001	REC14	Synergistic Positive	Other or Unannotated	unannotated		5.118	1.61e-06
GSCOC_T00030125001	T42	Synergistic Positive	Other or Unannotated	unannotated		3.315	1.73e-06
GSCOC_T00037111001	REC14	Synergistic Positive	Other or Unannotated	unannotated		7.422	2.61e-06
GSCOC_T00021256001	REC14	Antagonistic or Buffered	Water Transport / Aquaporin	Early nodulin-like protein 2	<i>Arabidopsis thaliana</i> AT4G27520 (UniProt Q9T076)	-3.488	3.42e-06
GSCOC_T00021256001	T37	Antagonistic or Buffered	Water Transport / Aquaporin	Early nodulin-like protein 2	<i>Arabidopsis thaliana</i> AT4G27520 (UniProt Q9T076)	-3.419	4.29e-06
GSCOC_T00042324001	REC14	Synergistic Positive	Other or Unannotated	unannotated		10.359	4.87e-06
GSCOC_T00030352001	REC14	Synergistic Positive	Other or Unannotated	unannotated		7.533	4.87e-06
GSCOC_T00040373001	REC14	Synergistic Positive	Other or Unannotated	unannotated		5.069	4.87e-06
GSCOC_T00022250001	REC14	Antagonistic or Buffered	Other or Unannotated	unannotated		-3.787	4.87e-06
GSCOC_T00035723001	REC14	Synergistic Positive	Other or Unannotated	unannotated		8.531	5.1e-06
GSCOC_T00030125001	REC14	Synergistic Positive	Other or Unannotated	unannotated		3.55	5.1e-06
GSCOC_T00040308001	T42	Synergistic Positive	Other or Unannotated	unannotated		10.498	6.27e-06
GSCOC_T00019798001	REC14	Synergistic Positive	ABA Signaling	Syntaxin-21	<i>Arabidopsis thaliana</i> AT5G16830 (UniProt Q39233)	7.234	7.18e-06
GSCOC_T00034556001	REC14	Synergistic Positive	Other or Unannotated	Endoplasmic reticulum (ER) membrane protein, Early tapetum development and meiosis	<i>Oryza sativa</i> Os07g0622900	1.544	7.18e-06
GSCOC_T00018044001	T42	Synergistic Positive	Other or Unannotated	unannotated		8.349	7.56e-06
GSCOC_T00004713001	T42	Synergistic Positive	Other or Unannotated	unannotated		6.156	7.56e-06
GSCOC_T00014902001	T42	Synergistic Positive	ABA Signaling	Basic blue protein	<i>Arabidopsis thaliana</i> AT2G02850 (UniProt Q8LG89)	5.281	7.56e-06
GSCOC_T00036149001	REC14	Synergistic Positive	Other or Unannotated	unannotated		5.249	7.69e-06
GSCOC_T00030194001	T42	Synergistic Positive	Other or Unannotated	unannotated		6.79	1.02e-05
GSCOC_T00011537001	REC14	Synergistic Positive	Other or Unannotated	unannotated		4.858	1.21e-05
GSCOC_T00039726001	REC14	Synergistic Positive	Other or Unannotated	unannotated		4.065	1.21e-05

Gene/transcript ID	Stage	Class	Module	Product annotation	Source organism	Non-additive score	FDR
GSCOC_T00030127001	T42	Synergistic Positive	Other or Unannotated	unannotated		2.506	1.41e-05
GSCOC_T00003937001	REC14	Synergistic Positive	ABA Signaling	Probable carboxylesterase 8	<i>Arabidopsis thaliana</i> AT2G45600 (UniProt O64640)	3.344	1.53e-05
GSCOC_T00036867001	T37	Not Significant or Small	Other or Unannotated	unannotated		-0.529	2.61e-05
GSCOC_T00028412001	REC14	Synergistic Positive	Other or Unannotated	unannotated		8.096	2.85e-05
GSCOC_T00018049001	T42	Synergistic Positive	Other or Unannotated	unannotated		7.786	3.2e-05
GSCOC_T00028476001	T42	Synergistic Positive	ABA Signaling	LSH6	<i>Arabidopsis thaliana</i> AT1G07090 (UniProt A0A178WE41)	2.459	3.2e-05
GSCOC_T00039786001	T42	Synergistic Positive	Other or Unannotated	unannotated		5.59	3.36e-05
GSCOC_T00008464001	REC14	Synergistic Positive	Other or Unannotated	unannotated		7.028	3.7e-05
GSCOC_T00011816001	T42	Synergistic Positive	Other or Unannotated	unannotated		6.064	4.06e-05
GSCOC_T00032445001	T42	Synergistic Positive	Other or Unannotated	unannotated		2.928	4.06e-05
GSCOC_T00022168001	T42	Synergistic Positive	Other or Unannotated	unannotated		2.92	4.06e-05
GSCOC_T00017742001	T37	Antagonistic or Buffered	ABA Signaling	Cytochrome P450 like protein	<i>Arabidopsis thaliana</i> AT1G11600 (UniProt Q9SAB7)	-2.549	4.18e-05
GSCOC_T00022683001	T42	Synergistic Positive	ABA Signaling	MPB2C	<i>Arabidopsis thaliana</i> AT5G08120 (UniProt A0A178UL06)	3.104	4.52e-05
GSCOC_T00036482001	T42	Synergistic Positive	Other or Unannotated	unannotated		3.094	4.69e-05
GSCOC_T00004701001	REC14	Synergistic Positive	Other or Unannotated	unannotated		7.272	5.07e-05
GSCOC_T00022889001	T42	Synergistic Positive	Other or Unannotated	unannotated		4.295	5.77e-05
GSCOC_T00004701001	T42	Synergistic Positive	Other or Unannotated	unannotated		8.067	6.42e-05
GSCOC_T00022272001	T42	Antagonistic or Buffered	Other or Unannotated	unannotated		-7.783	6.42e-05