

SUPPLEMENTARY MATERIALS

The following table and figures provide further insight into the co-expression analysis discussed for the CsSEOR gene family within chapter 3 of the accompanying master's thesis.

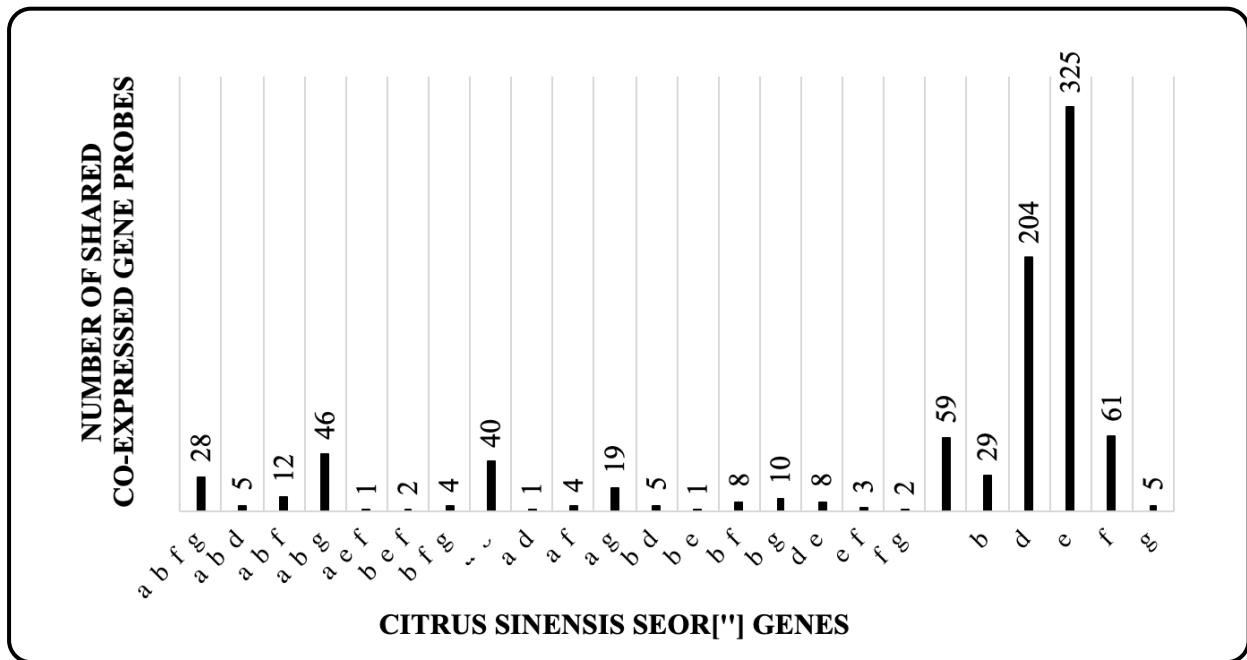


Figure S1. Frequency of common and unique co-expressed genes (i.e., NiCCE probe sets) when compared to all other *CsSEOR* gene probe sets respectively. The top 100 co-expressed genes were pulled for all 12 probe sets that correspond to the *CsSEOR* gene family members. The 12 ‘top 100 co-expressed genes’ lists were compared for common and unique probe sets. The chart above displays how the probe sets were partitioned into a relationship with a single *CsSEOR* gene or into an *CsSEOR* gene grouping. Group *CsSEOR*a,b,f,&g represents the grouping that contains the highest number of *CsSEOR* genes, while *CsSEOR*e contains the largest number of uniquely occurring co-expressed genes. See Supplemental Figure 1 for details regarding the commonly co-expressed genes shared across *CsSEOR*a,b,f,g genes.

Table S1. Commonly Co-Expressed Genes Shared Among *CsSEORa,b,f,&g* Genes

NiCCE GENE PROBE SETS	P-VALUE	BEST Cs MATCH	BEST At MATCH	SYMBOL IN NiCCE	At FUNCTION	Cs FUNCTION
**CIT.23911.1.S1_AT	0.849	Cs3g07110.1	AT3G01680	AtSEOR1	Phloem filament formation	Putative uncharacterized protein
CIT.37174.1.S1_AT	0.839	Cs2g07310.1	AT4G21310	DEAL2, DESIGUAL2	DUF1218 family protein/leaf bilateral symmetry	Putative uncharacterized protein Sb02g035630
CIT.7736.1.S1_AT	0.829	Cs5g01160.1	AT1G63310	N/A	unknown	Putative uncharacterized protein At1g63310
***CIT.7276.1.S1_AT	0.809	Cs2g26900.1	AT3G01670	AtSEOR2	Phloem filament formation	Putative uncharacterized protein (Fragment)
CIT.7727.1.S1_AT	0.7999	orange1.1t03414.1	AT3G20570	plastocyanin-like	plastocyanin-like domain-containing protein	Early nodulin-like protein 1
CIT.34966.1.S1_AT	0.798	N/A	AT1G70990	proline-rich gibberellin-regulated	proline-rich family protein	N/A
CIT.9890.1.S1_S_AT	0.79	Cs8g04550.1	AT2G14900		gibberellin-regulated family protein	Snakin-1
***CIT.28865.1.S1_AT	0.7899	Cs3g07110.1	AT3G01680	AtSEOR1	Phloem filament formation	Putative uncharacterized protein
CIT.29883.1.S1_A_AT	0.789	Cs4g08170.1	AT3G44730	kinesin motor	kinesin motor protein-related	Kinesin-4
CIT.5132.1.S1_AT	0.78	Cs5g15150.1	AT1G17200	integral membrane	CASP-like protein 2A1, putative	Putative uncharacterized protein fl5 (Fragment)
CIT.13973.1.S1_AT	0.78	Cs3g10920.2	AT5G43700	IAA4	ATAUX2-11 (AUXIN INDUCIBLE 2-11)	Indole-3-acetic acid inducible 3 (Fragment)
CIT.29749.1.S1_S_AT	0.78	Cs3g23940.1	AT5G42680	N/A	MIZU-KUSSEI-like protein	Plant-specific domain TIGR01570 family protein
***CIT.15924.1.S1_AT	0.7799	Cs2g26900.1	AT3G01670	AtSEOR2	Phloem filament formation	Putative uncharacterized protein (Fragment)
CIT.16404.1.S1_AT	0.77	Cs4g08170.1	AT3G44730	kinesin motor	kinesin motor protein-related	Kinesin-4
CIT.381.1.S1_S_AT	0.77	Cs4g20530.1	AT5G11330	monooxygenase	monooxygenase family protein	3-hydroxybenzoate 6-hydroxylase
CIT.29717.1.S1_S_AT	0.77	Cs5g15150.1	AT1G17200	integral membrane	CASP-like protein 2A1, putative	Putative uncharacterized protein fl5 (Fragment)
CIT.14470.1.S1_AT	0.76	Cs5g33170.1	AT3G62820	invertase	invertase/pectin methylesterase inhibitor family protein	21 kDa protein
CIT.31368.1.S1_AT	0.758	Cs6g06770.1	AT5G02140	thaumatin-like	thaumatin-like protein, putative	Thaumatin-like protein
CIT.29576.1.S1_S_AT	0.758	Cs2g10440.1	AT5G15780	extensin	pollen Ole allergen & extensin family protein	N/A
CIT.26839.1.S1_AT	0.758	Cs3g07250.1	AT1G31880	NLM9	BRX (BREVIS RADIX)	Putative uncharacterized protein Sb01g048205
CIT.21512.1.S1_AT	0.75	N/A	N/A	N/A	N/A	N/A
CIT.23791.1.S1_S_AT	0.7499	N/A	AT4G05220	HIN1-related	harpin-induced protein-related/ HIN1-related	N/A
CIT.15469.1.S1_AT	0.749	N/A	AT1G23530	N/A	unknown protein	N/A
CIT.31001.1.S1_AT	0.748	Cs6g10970.1	AT3G02700	NC	NC domain-containing protein	Putative uncharacterized protein OJ1323_A06.34
CIT.25025.1.S1_S_AT	0.7399	Cs5g16700.1	AT1G73370	SUS6	SUS6 (SUCROSE SYNTHASE 6)	Sucrose synthase 2
CIT.15049.1.S1_AT	0.7299	Cs3g10680.1	AT3G22910	ACA13	calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA13)	Calcium-transporting ATPase 13, plasma membrane-type, putative, expressed
CIT.36825.1.S1_AT	0.7299	Cs4g06600.1	AT5G20870	hydrolase	glycosyl hydrolase family 17 protein	Glucan endo-1,3-beta-glucosidase 5
CIT.635.1.S1_AT	0.728	Cs3g17810.1	AT1G22480	plastocyanin-like	plastocyanin-like domain-containing protein	Blue copper protein

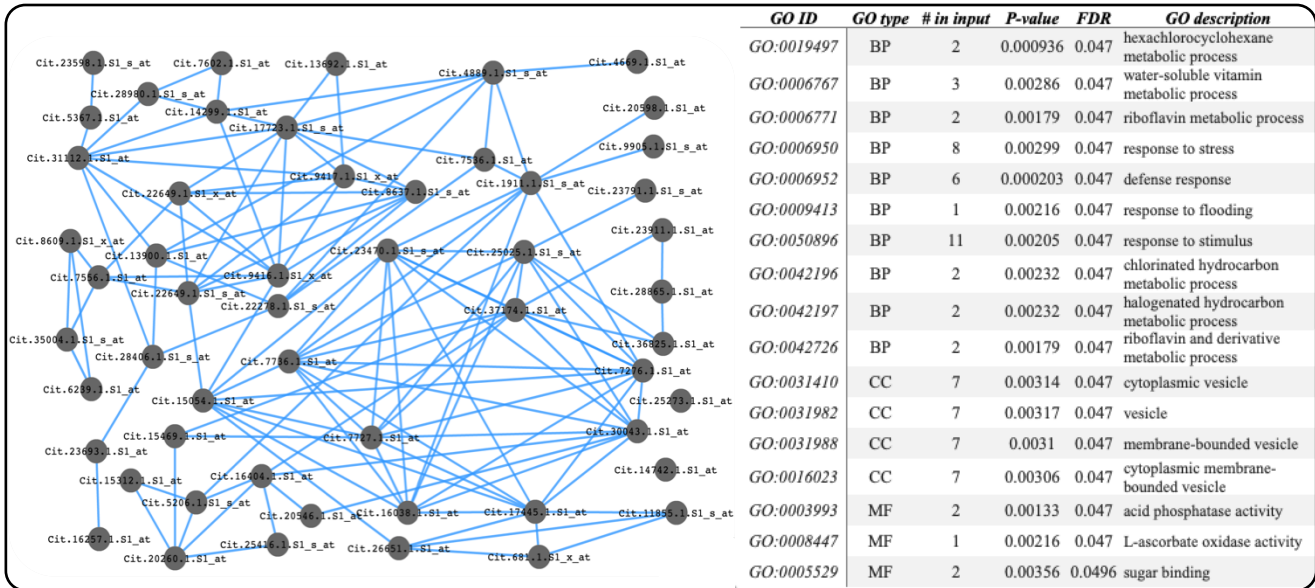


Figure S3. Co-expression network inferring biological relevance to stress response for the *CsSEORabfg* gene grouping. MCL stress-specific cluster 58 comprises 54 nodes with 317 edges and contains member genes over-represented with GO terms. Biological Process (BP), Cellular Component (CC), and Molecular Function (MF). The MCL stress cluster 58 network as well as the GO annotation list was retrieved directly from the NicCE database.

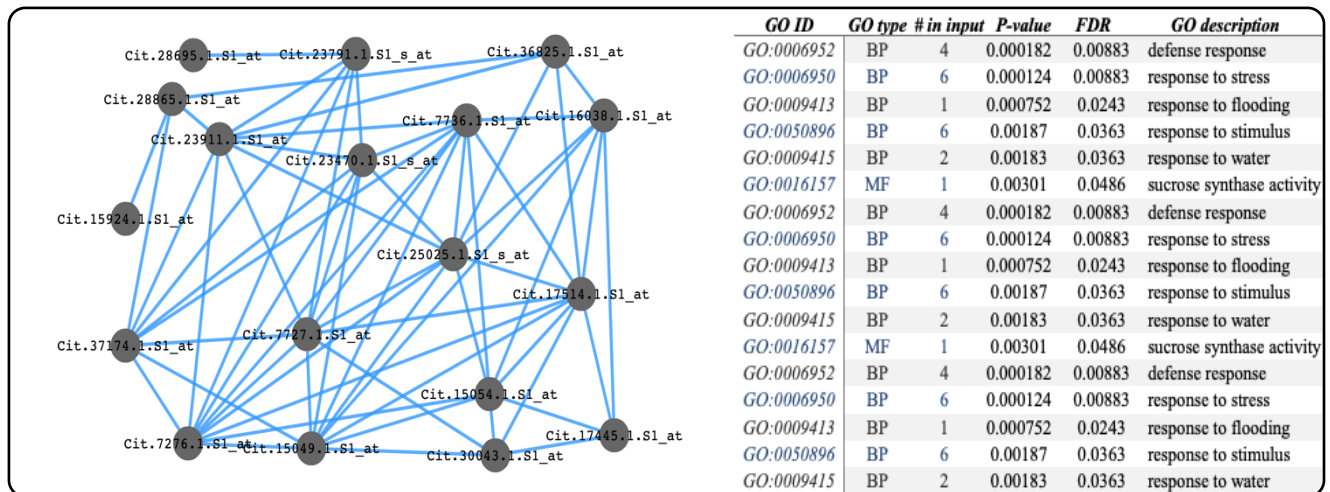


Figure S4. Co-expression network inferring biological relevance to *Citrus sinensis* leaves for the *CsSEORabfg* gene grouping. MCL leaf-specific cluster 535 comprises 18 nodes with 123 edges and contains member genes over-represented with GO terms enriched in stress response. Biological Process (BP), Cellular Component (CC), and Molecular Function (MF). The MCL leaf cluster 535 network as well as the GO annotation list was retrieved directly from the NicCE database.