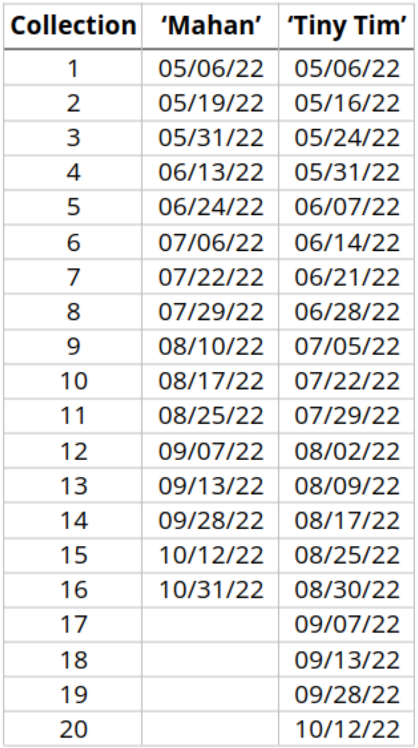
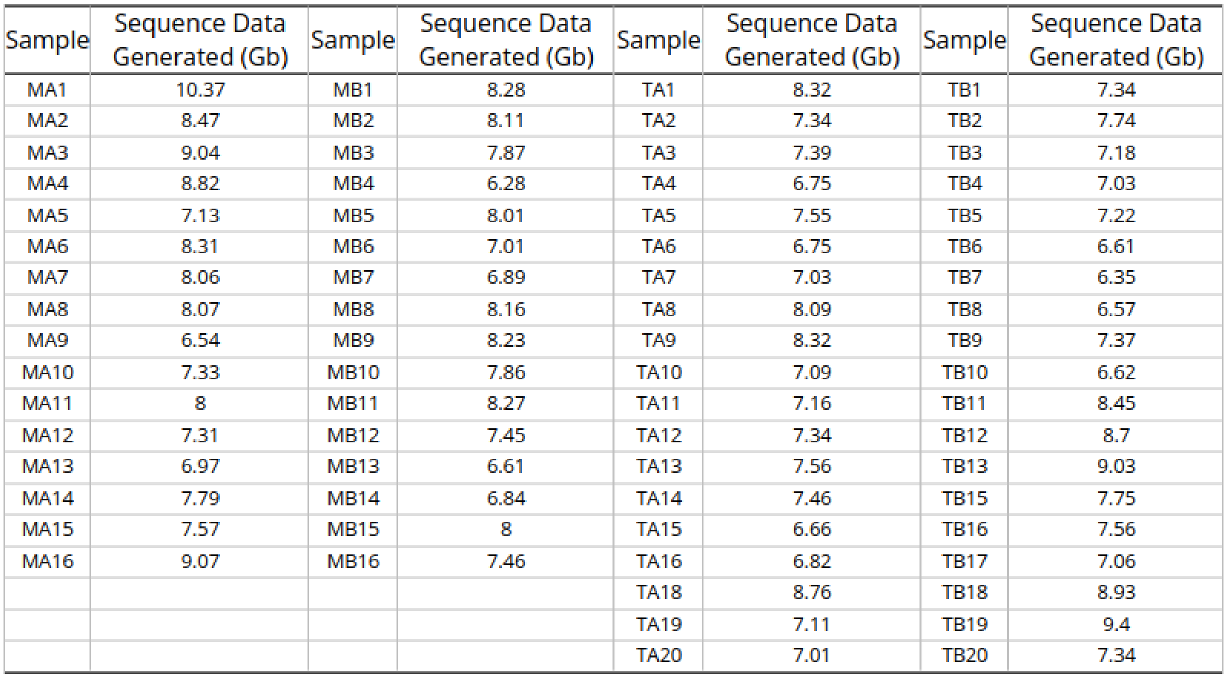
Supplementary Data



Collection	'Mahan'	'Tiny Tim'
1	05/06/22	05/06/22
2	05/19/22	05/16/22
3	05/31/22	05/24/22
4	06/13/22	05/31/22
5	06/24/22	06/07/22
6	07/06/22	06/14/22
7	07/22/22	06/21/22
8	07/29/22	06/28/22
9	08/10/22	07/05/22
10	08/17/22	07/22/22
11	08/25/22	07/29/22
12	09/07/22	08/02/22
13	09/13/22	08/09/22
14	09/28/22	08/17/22
15	10/12/22	08/25/22
16	10/31/22	08/30/22
17		09/07/22
18		09/13/22
19		09/28/22
20		10/12/22

Table S1. Collection dates of samples.



Sample	Sequence Data Generated (Gb)	Sample	Sequence Data Generated (Gb)	Sample	Sequence Data Generated (Gb)	Sample	Sequence Data Generated (Gb)
MA1	10.37	MB1	8.28	TA1	8.32	TB1	7.34
MA2	8.47	MB2	8.11	TA2	7.34	TB2	7.74
MA3	9.04	MB3	7.87	TA3	7.39	TB3	7.18
MA4	8.82	MB4	6.28	TA4	6.75	TB4	7.03
MA5	7.13	MB5	8.01	TA5	7.55	TB5	7.22
MA6	8.31	MB6	7.01	TA6	6.75	TB6	6.61
MA7	8.06	MB7	6.89	TA7	7.03	TB7	6.35
MA8	8.07	MB8	8.16	TA8	8.09	TB8	6.57
MA9	6.54	MB9	8.23	TA9	8.32	TB9	7.37
MA10	7.33	MB10	7.86	TA10	7.09	TB10	6.62
MA11	8	MB11	8.27	TA11	7.16	TB11	8.45
MA12	7.31	MB12	7.45	TA12	7.34	TB12	8.7
MA13	6.97	MB13	6.61	TA13	7.56	TB13	9.03
MA14	7.79	MB14	6.84	TA14	7.46	TB15	7.75
MA15	7.57	MB15	8	TA15	6.66	TB16	7.56
MA16	9.07	MB16	7.46	TA16	6.82	TB17	7.06
				TA18	8.76	TB18	8.93
				TA19	7.11	TB19	9.4
				TA20	7.01	TB20	7.34

Table S2. Quantity of sequencing data for each sample measured in billions of base pairs (gigabases/Gb).

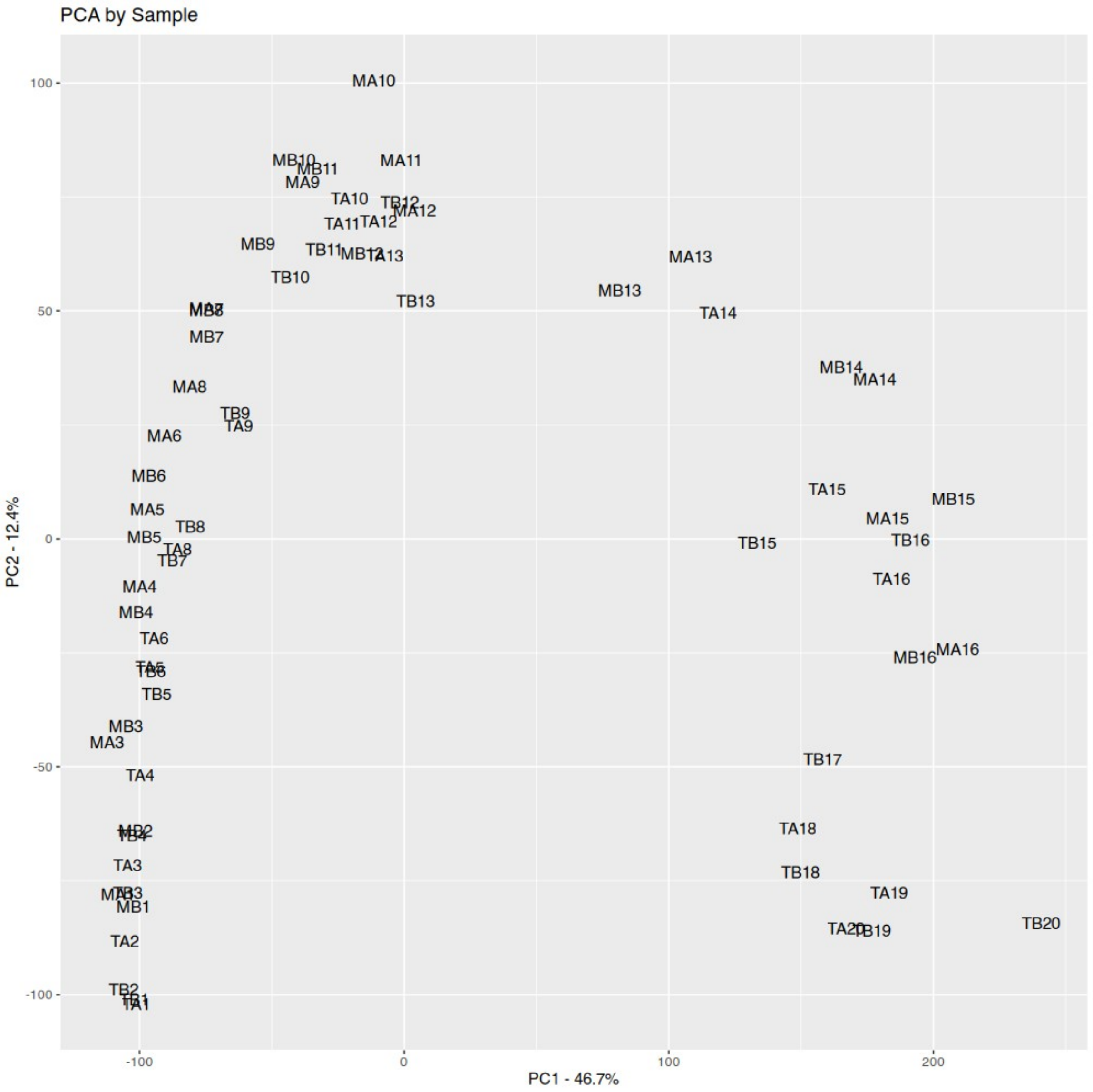


Figure S1. Principal components analysis of TPM and log2 normalized gene expression data. Two outliers, MA2 and TA7, have been removed due to the effect of sample degradation on data reliability.

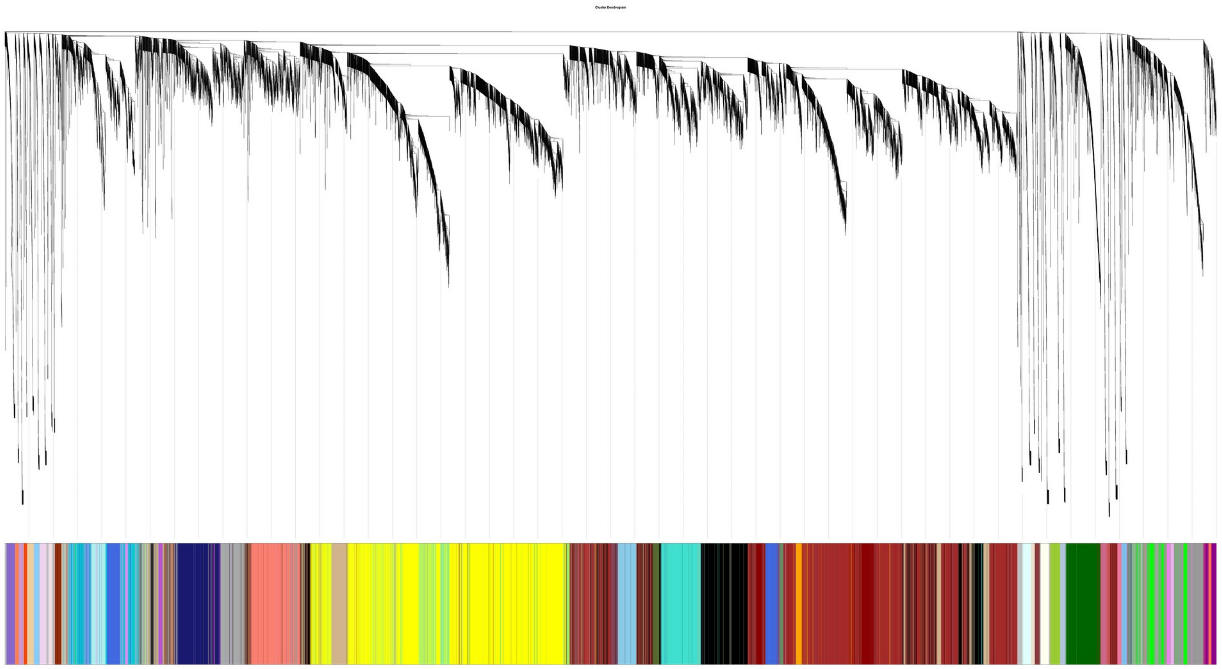
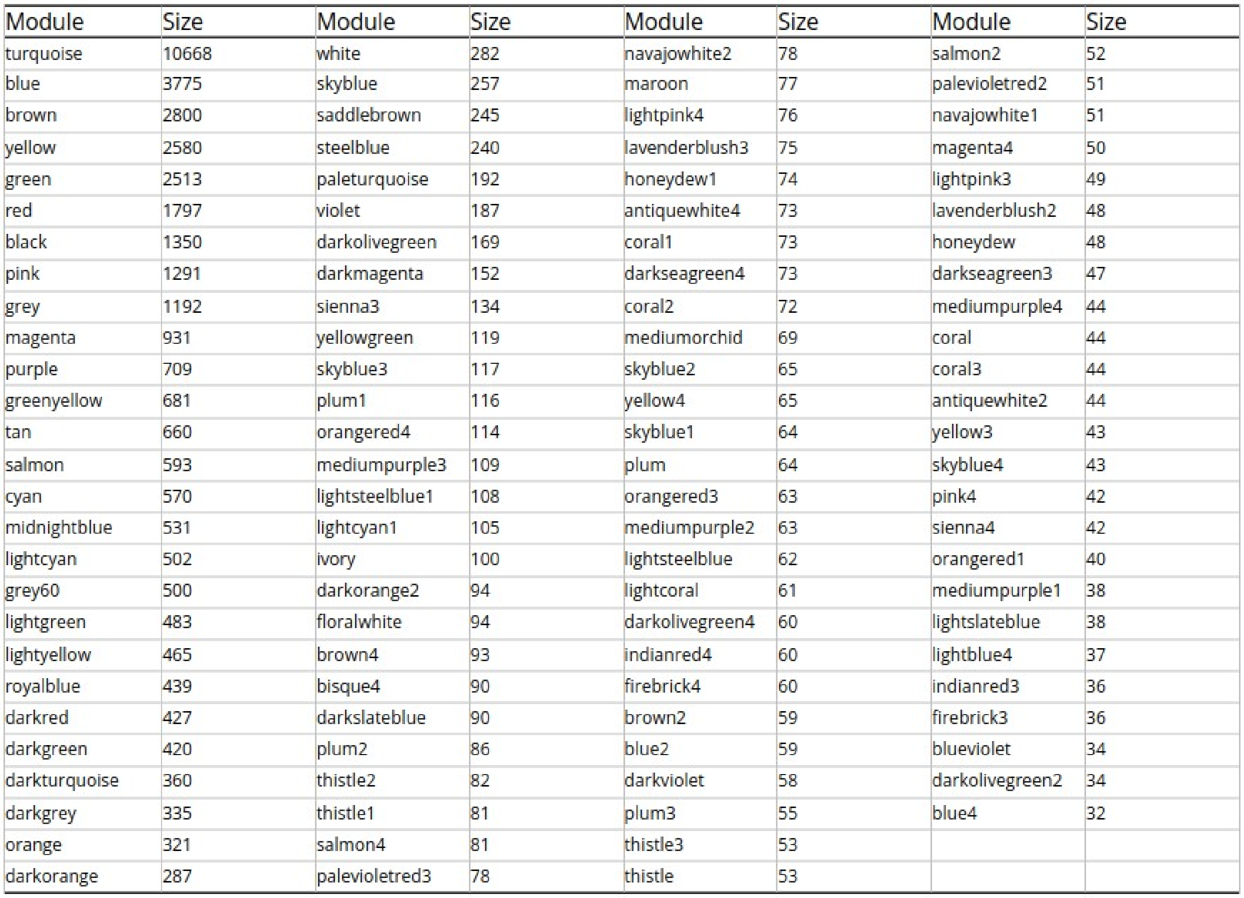
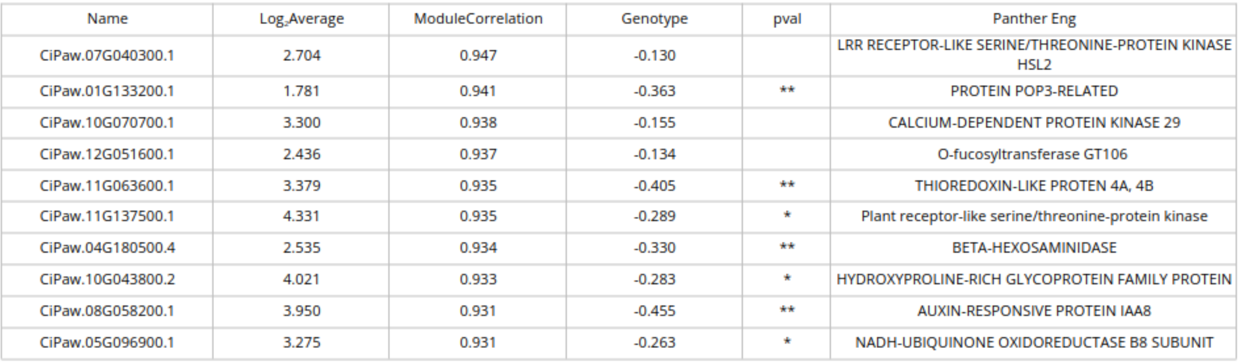


Figure S2. Cluster dendrogram describing the co-expression network constructed from gene expression data. Colors correspond to modules of correlated genes, and genes not assigned to any module are left grey.



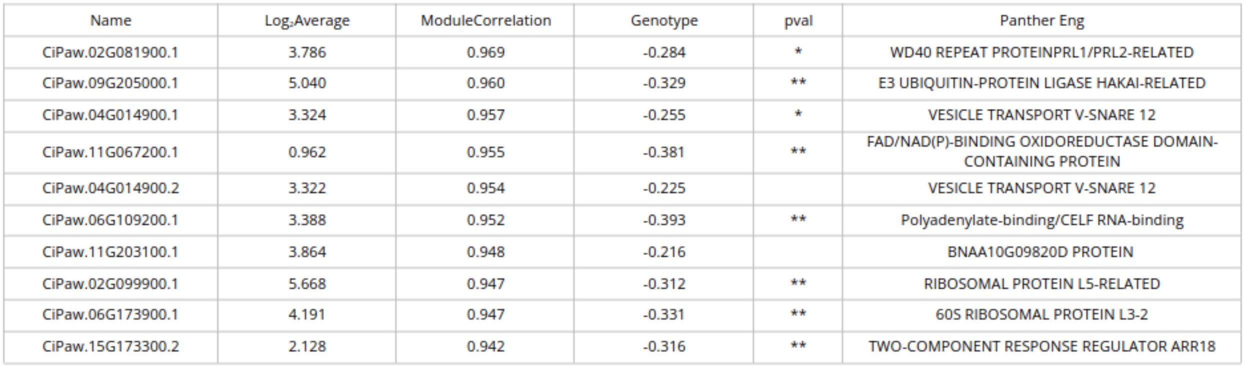
Module	Size	Module	Size	Module	Size	Module	Size
turquoise	10668	white	282	navajowhite2	78	salmon2	52
blue	3775	skyblue	257	maroon	77	palevioletred2	51
brown	2800	saddlebrown	245	lightpink4	76	navajowhite1	51
yellow	2580	steelblue	240	lavenderblush3	75	magenta4	50
green	2513	paleturquoise	192	honeydew1	74	lightpink3	49
red	1797	violet	187	antiquewhite4	73	lavenderblush2	48
black	1350	darkolivegreen	169	coral1	73	honeydew	48
pink	1291	darkmagenta	152	darkseagreen4	73	darkseagreen3	47
grey	1192	sienna3	134	coral2	72	mediumpurple4	44
magenta	931	yellowgreen	119	mediumorchid	69	coral	44
purple	709	skyblue3	117	skyblue2	65	coral3	44
greenyellow	681	plum1	116	yellow4	65	antiquewhite2	44
tan	660	orangered4	114	skyblue1	64	yellow3	43
salmon	593	mediumpurple3	109	plum	64	skyblue4	43
cyan	570	lightsteelblue1	108	orangered3	63	pink4	42
midnightblue	531	lightcyan1	105	mediumpurple2	63	sienna4	42
lightcyan	502	ivory	100	lightsteelblue	62	orangered1	40
grey60	500	darkorange2	94	lightcoral	61	mediumpurple1	38
lightgreen	483	floralwhite	94	darkolivegreen4	60	lightslateblue	38
lightyellow	465	brown4	93	indianred4	60	lightblue4	37
royalblue	439	bisque4	90	firebrick4	60	indianred3	36
darkred	427	darkslateblue	90	brown2	59	firebrick3	36
darkgreen	420	plum2	86	blue2	59	blueviolet	34
darkturquoise	360	thistle2	82	darkviolet	58	darkolivegreen2	34
darkgrey	335	thistle1	81	plum3	55	blue4	32
orange	321	salmon4	81	thistle3	53		
darkorange	287	palevioletred3	78	thistle	53		

Table S3. Size of each module in number of transcripts.



Name	Log$_2$Average	ModuleCorrelation	Genotype	pval	Panther Eng
CiPaw.07G040300.1	2.704	0.947	-0.130		LRR RECEPTOR-LIKE SERINE/THREONINE-PROTEIN KINASE HSL2
CiPaw.01G133200.1	1.781	0.941	-0.363	**	PROTEIN POP3-RELATED
CiPaw.10G070700.1	3.300	0.938	-0.155		CALCIUM-DEPENDENT PROTEIN KINASE 29
CiPaw.12G051600.1	2.436	0.937	-0.134		O-fucosyltransferase GT106
CiPaw.11G063600.1	3.379	0.935	-0.405	**	THIOREDOXIN-LIKE PROTEN 4A, 4B
CiPaw.11G137500.1	4.331	0.935	-0.289	*	Plant receptor-like serine/threonine-protein kinase
CiPaw.04G180500.4	2.535	0.934	-0.330	**	BETA-HEXOSAMINIDASE
CiPaw.10G043800.2	4.021	0.933	-0.283	*	HYDROXYPROLINE-RICH GLYCOPROTEIN FAMILY PROTEIN
CiPaw.08G058200.1	3.950	0.931	-0.455	**	AUXIN-RESPONSIVE PROTEIN IAA8
CiPaw.05G096900.1	3.275	0.931	-0.263	*	NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT

Table S4. Top 10 transcripts in Module Orange by module correlation.



Name	Log$_2$Average	ModuleCorrelation	Genotype	pval	Panther Eng
CiPaw.02G081900.1	3.786	0.969	-0.284	*	WD40 REPEAT PROTEINPRL1/PRL2-RELATED
CiPaw.09G205000.1	5.040	0.960	-0.329	**	E3 UBIQUITIN-PROTEIN LIGASE HAKAI-RELATED
CiPaw.04G014900.1	3.324	0.957	-0.255	*	VESICLE TRANSPORT V-SNARE 12
CiPaw.11G067200.1	0.962	0.955	-0.381	**	FAD/NAD(P)-BINDING OXIDOREDUCTASE DOMAIN-CONTAINING PROTEIN
CiPaw.04G014900.2	3.322	0.954	-0.225		VESICLE TRANSPORT V-SNARE 12
CiPaw.06G109200.1	3.388	0.952	-0.393	**	Polyadenylate-binding/CELF RNA-binding
CiPaw.11G203100.1	3.864	0.948	-0.216		BNAA10G09820D PROTEIN
CiPaw.02G099900.1	5.668	0.947	-0.312	**	RIBOSOMAL PROTEIN L5-RELATED
CiPaw.06G173900.1	4.191	0.947	-0.331	**	60S RIBOSOMAL PROTEIN L3-2
CiPaw.15G173300.2	2.128	0.942	-0.316	**	TWO-COMPONENT RESPONSE REGULATOR ARR18

Table S5. Top 10 Transcripts in Module Darkred by module correlation.