

1 **Table S1** Primer sequences used in qRT-PCR for the validation of dual RNA-seq data.

Gene ID	Sequence (5'–3')
CmEF1 α -F	TCAGGTCATCATCATGAACCA
CmEF1 α -R	AAGAGGTGGGTACTCAGCAA
CL11098.Contig2_All-F	GAGCATAGGAAGAAAGTGCTG CTAAACATAGCTTGACCAGGC
CL1653.Contig1_All-R	GAAGCAGTAGCAGTAGCAATCG ATGTTGAGATCACCCACGGTTG
CL5572.Contig1_All	GGATAAACACTCCAGAAGAGCG CTGAGCAGGGTTGTATGGATTC
Unigene47090_All	CCTCATTGCCAAAGCAGCTTGATC GAACCTCATTAGAGGCGTCAGAC
CL3907.Contig2_All	CTGGTCCATCATACGCCAATTC GTGCTCTCCACCAACAACCTTG
CL11265.Contig3_All	GAAGCTCAGTTAAGAGTCGC GTCCAAATGCAGAGAACGAC
CC77DRAFT_1036704	CTGCAATATCACAGGTGACTG CCTGTCCAGTTGTAGTTTGTC
CC77DRAFT_779096	GAACACCACACTACGGATATG AGTAACTTCTGTTCCTTGGC
CC77DRAFT_598231	CACAACTCTTTCCCGTACTTC CAGTAACGCTTGGAGTTCTC
CC77DRAFT_950634	GTGGCGATTACTACAATGTTCG GAAGATCTCGTTTCGCTTCAAC
CC77DRAFT_945175	CTATGGCTCTCAAGGAACTAG GAACTGGCTCATCATTGAAGC
CC77DRAFT_1044312	G TTCAGCGTTGGATCAGTAC GGCTAGCTTGATCAGTGATG

3 **Table S2** Summary statistics of chrysanthemum raw reads and clean reads.

Sample	Total Raw Reads (Mb)	Total Clean Reads (Mb)	Total Clean Bases (Gb)	Clean Reads Q20 (%)	Clean Reads Q30 (%)	Clean Reads Ratio (%)
	107.38	107.38	10.74	97.62	90.69	100
CK1h	107.14	107.14	10.71	97.67	90.94	100
	107.53	107.53	10.75	97.61	90.69	100
	110.9	110.9	11.09	98.54	93.17	100
CK12h	108.61	108.61	10.86	98.62	93.53	100
	110	110	11	98.42	92.69	100
	110.74	110.74	11.07	98.53	93.15	100
CK24h	108.48	108.48	10.85	98.47	92.86	100
	108.1	108.1	10.81	98.46	92.86	100
Average	108.76	108.76	10.88	98.22	92.29	100
	45.3	45.3	4.53	98.39	92.75	100
In1h	47.92	47.92	4.79	98.47	93.11	100
	37.97	37.97	3.8	98.37	92.84	100
	37.14	37.14	3.71	98.2	92.24	100
In12h	35.74	35.74	3.57	98.32	92.73	100
	38.55	38.55	3.85	98.26	92.43	100
	43.62	43.62	4.36	98.16	92.05	100
In24h	40.88	40.88	4.09	97.95	91.47	100
	43.66	43.66	4.37	98.34	92.72	100
Average	41.20	41.20	4.12	98.27	92.48	100

5 **Table S3** Summary statistics of *A. alternata* raw reads and clean reads.

Sample	Total Raw Reads (Mb)	Total Clean Reads (Mb)	Total Clean Bases (Gb)	Clean Reads Q20 (%)	Clean Reads Q30 (%)	Clean Reads Ratio (%)
	114.94	106.92	10.69	97.31	89.88	93.02
Aa1h	114.94	107	10.7	97.44	90.27	93.09
	112.44	104.06	10.41	97.27	89.72	92.54
	114.94	110.31	11.03	98.09	91.57	95.97
Aa12h	114.94	110.38	11.04	98.15	91.8	96.03
	114.88	110.71	11.07	98.25	92.12	96.37
	114.94	110	11	98.09	91.62	95.7
Aa24h	112.44	108.19	10.82	98.31	92.44	96.22
	114.94	110.22	11.02	98.21	92.09	95.89
Average	114.38	108.64	10.86	97.90	91.28	94.98
	112.44	108.87	10.89	98.31	92.32	96.83
In1h	114.94	111.19	11.12	98.45	92.88	96.74
	114.94	111.05	11.11	98.38	92.62	96.62
	114.94	110.43	11.04	98.28	92.29	96.07
In12h	114.94	110.54	11.05	98.41	92.79	96.17
	112.44	108.07	10.81	98.28	92.26	96.11
	110.37	106.32	10.63	98.06	91.59	96.33
In24h	107.86	103.38	10.34	97.91	91.17	95.85
	114.94	110.53	11.05	98.33	92.48	96.16
Average	113.09	108.93	10.89	98.27	92.27	96.32

7 **Table S4** Summary of the assembly results of chrysanthemum.

Sample	Total Number	Total Length	Mean Length	N50	N70	N90	GC(%)
	51399	39924269	776	1081	715	366	40.54
	60991	49686251	814	1157	757	376	40.47
CK1h	53787	43655213	811	1160	746	370	40.65
	58005	45650884	787	1106	723	366	40.49
	54057	41965352	776	1095	706	356	40.58
CK12h	57455	46808244	814	1156	747	371	40.61
	52786	39322987	744	1016	685	356	40.45
	47458	36032467	759	1064	692	347	40.7
CK24h	55099	43194881	783	1098	721	362	40.48
Average	54560	42915616	785	1104	721	363	40.55
	46920	34616729	737	1045	664	332	42.53
	44278	29364412	663	869	598	322	42.07
In1h	37543	24138023	642	865	556	296	43.11
	22195	14571366	656	901	556	298	45.37
	24461	16613962	679	944	585	304	45.01
In12h	27980	20133835	719	1042	636	315	44.02
	37071	27465624	740	1081	661	323	42.97
	36335	25713984	707	1008	620	312	43.82
In24h	45808	33355888	728	1047	644	321	43.12
Average	35843	25108203	697	978	613	314	43.56

9 **Table S5** Unigene annotation overview of chrysanthemum.

Values	NR	NT	Swissprot	KEGG	KOG	Pfam	GO	Overall
Number	89,889	55,679	61,156	64,705	64,694	60,671	68,727	94,961
Percentage	72.62%	44.98%	49.41%	52.27%	52.26%	49.01%	55.52%	76.72%

11 **Table S6** Summary of clean read mapping to *A. alternata* genomic database.

Sample	Total Clean Reads (Mb)	Total Mapping(%)	Uniquely Mapping(%)
	106.92	86.92	67.93
Aa1h	107	86.53	68.21
	104.06	86.66	67.69
	110.31	87.73	70.89
Aa12h	110.38	88.11	71.58
	110.71	87.34	69.98
	110	88.87	71.67
Aa24h	108.19	89.21	72.76
	110.22	88.23	71.43
Average	108.64	87.73	70.24
	108.87	58.4	47.5
In1h	111.19	56.9	46.7
	111.05	65.81	53.62
	110.43	66.37	54.11
In12h	110.54	67.67	55.09
	108.07	64.33	52.29
	106.32	58.97	47.23
In24h	103.38	60.46	48.69
	110.53	60.5	49.33
Average	108.93	62.16	50.51

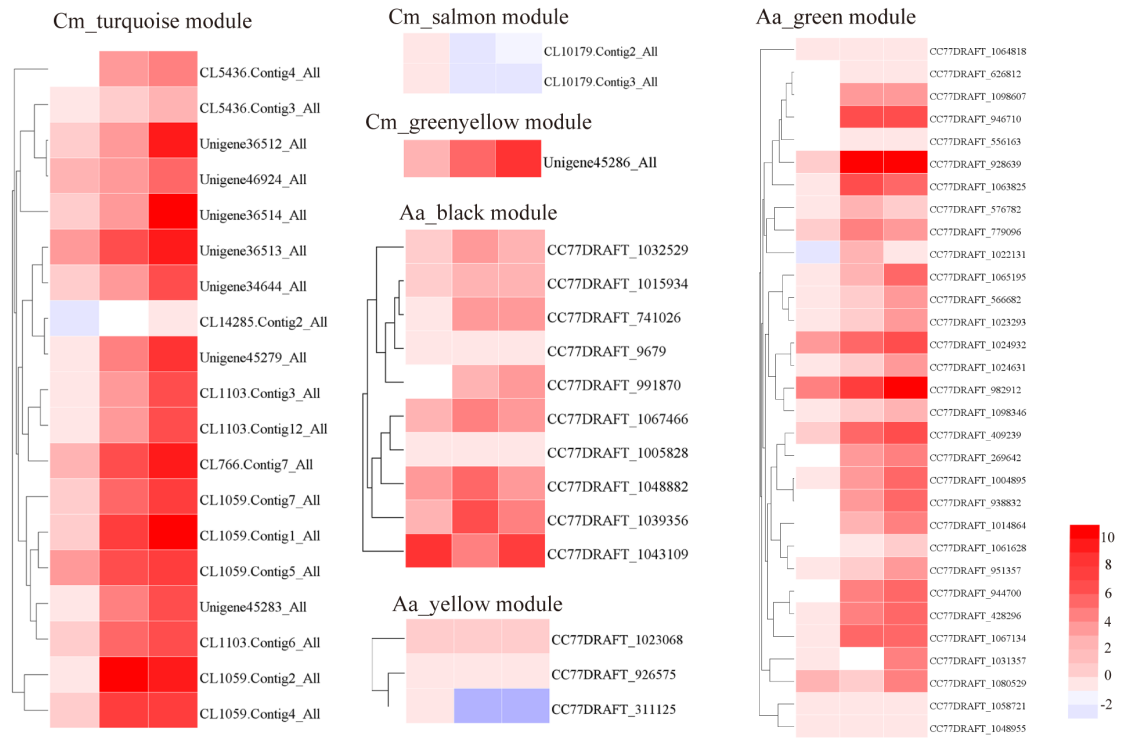
13 **Table S7** Results of kyoto encyclopedia of genes and genomes (KEGG) pathway
 14 enrichment analysis of chrysanthemum.

Pathway ID	Pathway Name	Number of genes with pathway annotation	Number of DEGs at each individual time point		
			1 HPI	12 HPI	24 HPI
ko04626	Plant-pathogen interaction	2100	509	1337	986
ko04075	Plant hormone signal transduction	1725	375	1215	774
ko04016	MAPK signaling pathway - plant	1647	409	1077	776
ko01200	Carbon metabolism	1556	372	1033	812
ko04141	Protein processing in endoplasmic reticulum	1788	318	1022	753
ko01230	Biosynthesis of amino acids	1505	297	1004	716
ko00940	Phenylpropanoid biosynthesis	1196	427	849	714
ko04144	Endocytosis	1588	285	935	644
ko00500	Starch and sucrose metabolism	1134	250	737	489
ko04120	Ubiquitin-mediated proteolysis	992	156	606	351
ko00270	Cysteine and methionine metabolism	570	130	409	268
ko00460	Cyanoamino acid metabolism	522	141	345	257
ko04145	Phagosome	565	123	324	233
ko03030	DNA replication	541	69	386	181
ko02010	ABC transporters	437	108	283	228
ko00260	Glycine, serine, and threonine metabolism	405	110	297	210
ko00592	alpha-Linolenic acid metabolism	384	148	238	204
ko00480	Glutathione metabolism	421	90	270	199
ko00380	Tryptophan metabolism	342	114	238	175
ko00360	Phenylalanine metabolism	313	129	226	192
ko00906	Carotenoid biosynthesis	269	110	211	145
ko00900	Terpenoid backbone biosynthesis	315	77	199	146

ko00310	Lysine degradation	247	54	155	127
ko00945	Stilbenoid, diarylheptanoid, and gingerol biosynthesis	171	63	125	109
ko00330	Arginine and proline metabolism	322	96	214	163
ko00909	Sesquiterpenoid and triterpenoid biosynthesis	183	55	118	87
ko00591	Linoleic acid metabolism	127	59	88	77
ko00100	Steroid biosynthesis	172	33	121	69
ko04130	SNARE interactions in vesicular transport	167	30	103	53
ko00072	Synthesis and degradation of ketone bodies	63	15	34	36

16 **Table S8** Results of Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway
 17 enrichment analysis of *A. alternata*.

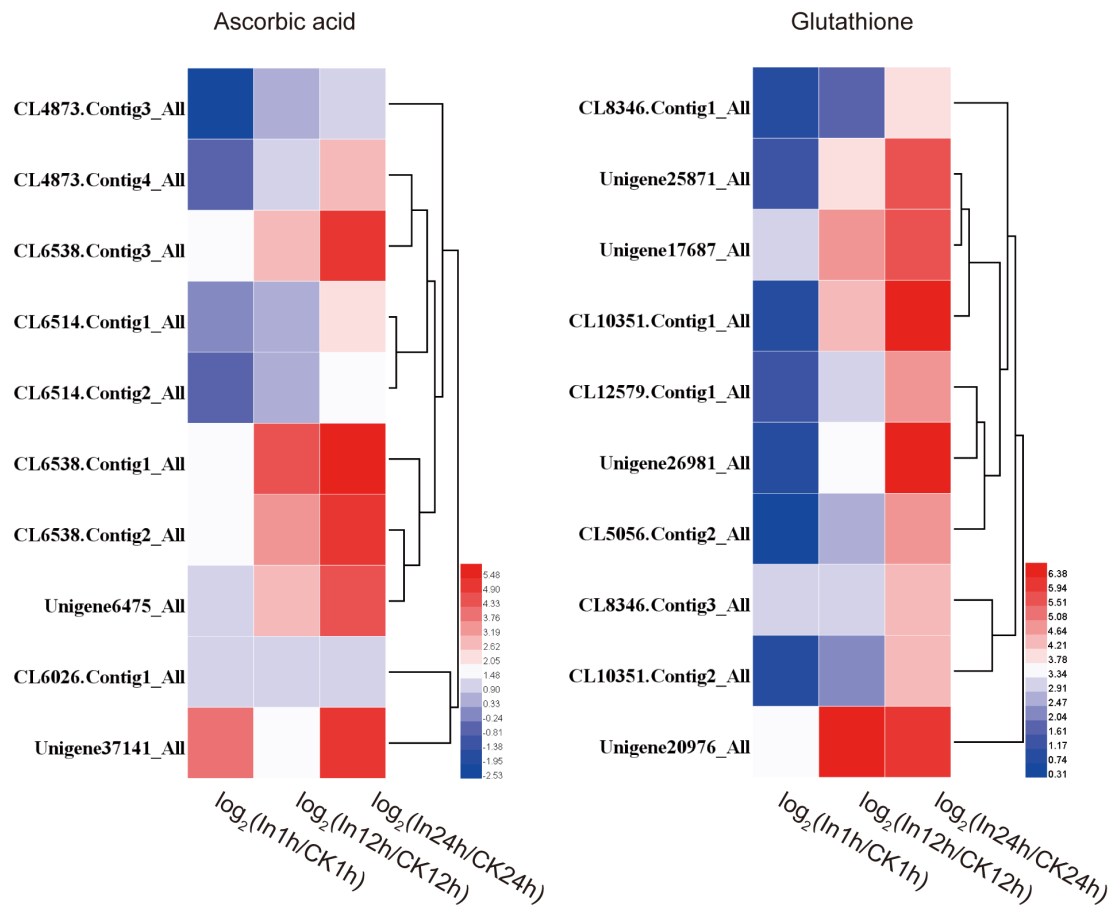
Pathway ID	Pathway Name	Number of genes with pathway annotation	Number of DEGs at each individual time point		
			1HPI	12HPI	24HPI
ko01130	Biosynthesis of antibiotics	833	312	430	390
ko04011	MAPK signaling pathway - yeast	585	154	218	196
ko00520	Amino sugar and nucleotide sugar metabolism	395	103	161	159
ko00260	Glycine, serine and threonine metabolism	262	107	124	127
ko01200	Carbon metabolism	239	95	129	121
ko04146	Peroxisome	194	83	118	116
ko00500	Starch and sucrose metabolism	226	87	120	113
ko01230	Biosynthesis of amino acids	252	87	112	107
ko00230	Purine metabolism	260	78	113	106
ko00350	Tyrosine metabolism	180	84	97	103
ko03013	RNA transport	277	69	90	96
ko00010	Glycolysis / Gluconeogenesis	169	79	101	94
ko00380	Tryptophan metabolism	188	77	100	94
ko04141	Protein processing in endoplasmic reticulum	230	63	79	94
ko00040	Pentose and glucuronate interconversions	146	73	96	93
ko00564	Glycerophospholipid metabolism	200	61	101	93
ko00071	Fatty acid degradation	144	66	86	85
ko00620	Pyruvate metabolism	154	66	88	82
ko04144	Endocytosis	279	71	96	82
ko00051	Fructose and mannose metabolism	123	69	77	76



19
20 **Figure S1** Heatmap of genes involved in cell wall reinforcement and disassembly.

21 Expression values are presented as log₂ fold-change value (red represents up-regulation;
22 blue represents down-regulation).

23



24

25 **Figure S2** Heatmap of genes involved in ascorbic acid and glutathione synthesis.

26 Expression values are presented as \log_2 fold-change value (red represents up-regulation;
 27 blue represents down-regulation).