Table S3: qPCR analysis of expression in LSo, SSo, and SSi leaves in response to simulated herbivory at 2 h, 6 h, and 24 h post-treatment*.

Clone ID [Genome model] (annotation)	Local Treated Source (LSo)						Systemic Source (SSo)						Systemic Sink (SSi)					
	2hrs		6hrs		24hrs		2hrs		6hrs		24hrs		2hrs		6hrs		24hrs	
	FC	P	FC	P	FC	P	FC	P	FC	P	FC	P	FC	P	FC	P	FC	P
WS0158_D14 [POPTR_0009s15160] (histone deacetylase)	4.77	< 0.001	4.48	0.001	5.18	< 0.001	3.48	0.004	1.38	0.437	1.73	0.187	0.15	< 0.001	0.67	0.330	1.23	0.611
	0.812	0.060	0.871	0.211	1.09	0.425	0.994	0.990	1.24	0.652	1.06	0.900	1.26	0.621	1.81	0.210	3.39	0.011
WS0147_P16 [POPTR_0019s12320] (9-*cis*-epoxycarotenoid dioxygenase)	0.37	0.007	0.55	0.091	1.63	0.162	3.06	0.002	0.85	0.636	1.12	0.739	202.71	< 0.001	1.67	0.145	4.56	< 0.001
	0.47	<0.001	0.46	<0.001	0.81	0.008	1.13	0.706	1.28	0.455	0.95	0.874	7.76	<0.001	1.87	0.059	1.52	0.201
WS0124_D16 [POPTR_0014s11710] (universal stress protein)	1.12	0.766	1.44	0.332	2.33	0.027	3.62	0.001	1.51	0.271	0.87	0.708	504.90	< 0.001	1.29	0.488	0.87	0.709
	0.60	<0.001	0.68	<0.001	0.73	0.002	1.07	0.805	0.86	0.545	0.68	0.125	20.94	<0.001	1.39	0.194	0.97	0.890
WS0205_I02 [POPTR_0002s14800] (LRR transmembrane protein kinase)	0.73	0.485	0.60	0.255	0.28	0.007	1301.08	< 0.001	87.40	< 0.001	4.42	0.002	0.07	< 0.001	0.07	< 0.001	0.02	< 0.001
	0.74	0.112	1.93	0.001	18.32	<0.001	0.89	0.705	0.59	0.075	21.812	<0.001	0.79	0.427	1.06	0.856	2.61	0.002
WS0212_I21 [POPTR_0006s24090] (aminopeptidase M)	2.32	0.046	1.10	0.822	2.04	0.087	14.51	< 0.001	1.31	0.511	0.79	0.562	2.26	0.053	0.99	0.970	1.85	0.138
	1.95	<0.001	3.28	<0.001	12.06	<0.001	1.16	0.446	0.72	0.094	12.11	<0.001	1.88	0.001	1.72	0.006	9.53	<0.001
WS0214_H20 [POPTR_0001s22060] (serine carboxypeptidase S28)	2.48	0.071	27.31	< 0.001	11.77	< 0.001	19.90	< 0.001	11.95	< 0.001	21.55	< 0.001	3.17	0.024	0.76	0.579	64.45	< 0.001
	2.42	<0.001	4.88	<0.001	1.42	0.006	1.22	0.429	1.39	0.200	1.44	0.151	1.62	0.059	1.21	0.455	6.51	<0.001
WS0143_A03 [POPTR_0009s14420] (endochitinase)	2.48	0.046	8.86	< 0.001	320.77	< 0.001	16.53	< 0.001	0.85	0.722	7.15	< 0.001	0.87	0.751	2.61	0.035	123.67	< 0.001
	2.36	<0.001	8.42	<0.001	10.89	<0.001	1.05	0.800	1.94	0.002	15.09	<0.001	1.15	0.502	1.82	0.004	5.57	<0.001
WS0134_G14 [POPTR_0010s01150] (Kunitz protease inhibitor)	3.04	< 0.001	25.05	< 0.001	1857.27	< 0.001	1.85	0.026	0.21	< 0.001	79.67	< 0.001	2.89	< 0.001	1.83	0.029	296.05	< 0.001
	1.92	0.001	3.53	<0.001	14.11	<0.001	1.01	0.959	0.69	0.082	9.63	<0.001	1.78	0.007	1.32	0.181	10.21	<0.001
PPO [POPTR_0001s39660] (polyphenol oxidase)	2.97	0.009	283.78	< 0.001	607.31	< 0.001	1.28	0.534	2.59	0.021	794.12	< 0.001	1.42	0.381	5.53	< 0.001	2234.94	< 0.001
	1.37	0.087	6.54	<0.001	4.32	<0.001	0.92	0.754	1.18	0.528	2.00	0.008	1.37	0.222	1.39	0.202	8.43	<0.001
TPS1 [POPTR_0001s44080] ((−)-germacrene-*D* synthase)	2.55	0.010	41.66	< 0.001	9.37	< 0.001	2.17	0.032	13.61	< 0.001	16.62	< 0.001	10.30	< 0.001	2.00	0.052	50.73	< 0.001
	1.69	0.031	4.50	<0.001	1.89	0.009	1.05	0.902	2.86	0.006	2.44	0.020	2.93	0.005	1.05	0.896	6.25	<0.001

* Values represent fold-change (FC) relative to control trees. Values obtained by qPCR represent the mean of three or more independent technical replicates, each consisting of pooled RNA from five biological replicates. A Student's *t*-test (two-sample, unpaired, one-sided) was performed to test significance (*P*) of up- or down-regulation of each transcript between treated and control plants. For each transcript, qPCR data is shaded light-grey, with the corresponding microarray data provided below (see Table S1 for the complete microarray dataset). Abbreviations: LRR, leucine-rich repeat.