

Table S6: qPCR analysis of GOLS systemic gene expression in LSo, SSo, and SSi leaves in response to simulated herbivory at 2 h, 6 h, and 24 h post-treatment*.

Clone ID	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
PtdGOLS1.2	0.32	0.078	0.15	0.005	0.34	0.096	2.58	0.143	1.27	0.704	1.43	0.574	234.61	<0.001	0.75	0.656	1.66	0.431
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PtdGOLS2.1	1.75	0.001	1.82	<0.001	1.32	0.073	1.69	0.001	0.79	0.115	0.40	<0.001	305.34	<0.001	1.52	0.008	2.29	<0.001
	0.89	0.506	0.84	0.300	0.63	0.007	0.67	0.193	1.05	0.877	0.77	0.403	8.23	<0.001	1.16	0.636	1.06	0.806
PtGOLS3.1	0.05	<0.001	<0.01	<0.001	<0.01	<0.001	414.86	<0.001	52.07	<0.001	3.03	0.008	1.48	0.326	0.13	<0.001	0.10	<0.001
	0.79	<0.001	0.39	<0.001	0.43	<0.001	1.22	0.397	1.12	0.635	0.73	0.177	1.17	0.504	1.66	0.031	1.35	0.200
PtdGOLS6.1	12.75	<0.001	1.35	0.275	1.42	0.210	16.45	<0.001	5.47	<0.001	0.59	0.065	1.87	0.028	11.53	<0.001	0.37	0.001
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* 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 are shaded light-grey, with the corresponding microarray data provided below (see Table S1 for the complete microarray dataset). '--' indicates that this gene is not represented on the 15.5K microarray.