Supplementary Information

The molecular genetic basis of herbivory between butterflies and their host-plants

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Supplementary Table 1. List of 96 *A. thaliana* accessions used in *Arabidopsis* GWAS.

Accession name	**country**	**Stockparent**	**collector**	**Collection date**	**country**	**Latitude**	**Longitude**	**Site**
Ag-0	France	CS22630	Albert Kranz	NA	France	45	1.3	Ag
An-1	Belgium	CS22626	Albert Kranz	NA	Belgium	51.2167	4.4	An
Bay-0	Germany	CS22633	Albert Kranz	NA	Germany	49	11	Bay
Bil-5	Sweden	CS22578	Magnus Nordborg	6/25/2000	Sweden	63.324	18.484	Bil
Bil-7	Sweden	CS22579	Magnus Nordborg	6/25/2000	Sweden	63.324	18.484	Bil
Bor-1	Czech	CS22590	Jirina Relichová	5/31/2000	Czech Republic	49.4013	16.2326	Bor
Bor-4	Czech	CS22591	Jirina Relichová	5/31/2000	Czech Republic	49.4013	16.2326	Bor
Br-0	Czech	CS22628	Albert Kranz	NA	Czech Republic	49.2	16.6166	Br
Bur-0	Ireland	CS22656	Albert Kranz	NA	Ireland	54.1	-6.2	Bur
C24	Portugal	CS22620	Brigitte Damm	NA	Portugal	40.2077	-8.42639	Co
CIBC-17	UK	CS22603	Mick Crawley	5/21/1993	United Kingdom	51.4083	-0.6383	CIBC
CIBC-5	UK	CS22602	Mick Crawley	5/21/1993	United Kingdom	51.4083	-0.6383	CIBC
Col-0	USA	CS22625	Albert Kranz	NA	USA	38.3	-92.3	Col
Ct-1	Italy	CS22639	Albert Kranz	NA	Italy	37.3	15	Ct
Cvi-0	Cape Verde	CS22614	Albert Kranz	NA	Cape Verde	15.1111	-23.6167	Cvi

Eden-1	Sweden	CS22572	Magnus Nordborg	6/25/2000	Sweden	62.877	18.177	Eden
Eden-2	Sweden	CS22573	Magnus Nordborg	6/25/2000	Sweden	62.877	18.177	Eden
Edi-0	UK	CS22657	Albert Kranz	NA	United Kingdom	55.949444	-3.160278	Edi
Ei-2	Germany	CS22616	Albert Kranz	NA	Germany	50.3	6.3	Ei
Est-1	Russia	CS22629	Albert Kranz	NA	Russia	58.3	25.3	Est
Fäb-2	Sweden	CS22576	Magnus Nordborg	6/25/2000	Sweden	63.0165	18.3174	Fäb
Fäb-4	Sweden	CS22577	Magnus Nordborg	6/25/2000	Sweden	63.0165	18.3174	Fäb
Fei-0	Portugal	CS22645	Carlos Alonso-Blanco	NA	Portugal	40.5	-8.32	Fei
Ga-0	Germany	CS22634	Albert Kranz	NA	Germany	50.3	8	Ga
Got-22	Germany	CS22609	Gerhard Röbbelen	NA	Germany	51.5338	9.9355	GOT
Got-7	Germany	CS22608	Gerhard Röbbelen	NA	Germany	51.5338	9.9355	GOT
Gu-0	Germany	CS22617	Albert Kranz	NA	Germany	50.3	8	Gu
Gy-0	France	CS22631	Albert Kranz	NA	France	49	2	Gy
HR-10	UK	CS22597	Mick Crawley	5/21/1993	United Kingdom	51.4083	-0.6383	HR
HR-5	UK	CS22596	Mick Crawley	5/21/1993	United Kingdom	51.4083	-0.6383	HR
Kas-2	India	CS6751	Shauna Somerville	1/1/1976	India	35	77	Kas

Kin-0	USA	CS22654	Albert Kranz	NA	USA	44.46	-85.37	Kin
Kno-10	USA	CS22566	Joy Bergelson	34111	USA	41.2816	-86.621	Knox
Kno-18	USA	CS22567	Joy Bergelson	34111	USA	41.2816	-86.621	Knox
Kondara	Tajikistan	CS22651	Igor Vizir	NA	Tajikistan	38.48	68.49	Kondara
Kz-1	Kazakhstan	CS22606	Ihsan Al-Shehbaz	6/7/1994	Kazakhstan	49.5	73.1	KZ
Kz-9	Kazakhstan	CS22607	Ihsan Al-Shehbaz	6/7/1994	Kazakhstan	49.5	73.1	KZ
Ler-1	Germany	CS22618	Eric Holub	NA	Germany	47.984	10.8719	Ler
LL-0	Spain	CS22650	Albert Kranz	NA	Spain	41.59	2.49	Ll
Löv-1	Sweden	CS22574	Magnus Nordborg	6/25/2000	Sweden	62.801	18.079	Löv
Löv-5	Sweden	CS22575	Magnus Nordborg	6/25/2000	Sweden	62.801	18.079	Löv
Lp2-2	Czech	CS22594	Ivo Cetl	NA	Czech Republic	49.38	16.81	Lp2
Lp2-6	Czech	CS22595	Ivo Cetl	NA	Czech Republic	49.38	16.81	Lp2
Lz-0	France	CS22615	Albert Kranz	NA	France	46	3.3	Lz
Mr-0	Italy	CS22640	Albert Kranz	NA	Italy	44.15	9.65	Mr
Mrk-0	Germany	CS22635	Albert Kranz	NA	Germany	49	9.3	Mrk
Ms-0	Russia	CS22655	Albert Kranz	NA	Russia	55.7522	37.6322	Ms
Mt-0	Libya	CS22642	Albert Kranz	NA	Libya	32.34	22.46	Mt

Mz-0	Germany	CS22636	Albert Kranz	NA	Germany	50.3	8.3	Mz
N13	Russia	CS22491	Andy Savushkin	NA	Russia	61.36	34.15	Konchezero
Nd-1	Switzerland	CS22619	Eric Holub	NA	Switzerland	50	10	Nd
NFA-10	UK	CS22599	Mick Crawley	5/21/1993	United Kingdom	51.4083	-0.6383	NFA
NFA-8	UK	CS22598	Mick Crawley	5/21/1993	United Kingdom	51.4083	-0.6383	NFA
Nok-3	Netherlands	CS22643	Albert Kranz	NA	Netherlands	52.24	4.45	Nok
ÖMö2-1	Sweden	CS22584	Magnus Nordborg	5/14/2000	Sweden	56.1481	15.821214	ÖMö2
ÖMö2-3	Sweden	CS22585	Magnus Nordborg	5/14/2000	Sweden	56.147363	15.814587	ÖMö2
Oy-0	Norwegia	CS22658	Albert Kranz	NA	Norway	60.385543	6.193019	Oy
Pna-10	USA	CS22571	Joy Bergelson	NA	USA	42.0945	-86.3253	PNA
Pna-17	USA	CS22570	Joy Bergelson	NA	USA	42.0945	-86.3253	PNA
Pro-0	Spain	CS22649	Joy Bergelson	NA	Spain	43.25	-6	Pro
Pu2-23	Czech	CS22593	Ivo Cetl	NA	Czech Republic	49.42	16.36	Pu2
Pu2-7	Czech	CS22592	Ivo Cetl	NA	Czech Republic	49.42	16.36	Pu2
Ra-0	France	CS22632	Albert Kranz	NA	France	46	3.3	Ra
Ren-1	France	CS22610	Gerhard Röbbelen	NA	France	48.5	-1.41	REN
Ren-11	France	CS22611	Gerhard Röbbelen	NA	France	48.5	-1.41	REN

Rmx-A02	USA	CS22568	Joy Bergelson	NA	USA	42.036	-86.511	RMX
Rmx-A180	USA	CS22569	Joy Bergelson	NA	USA	42.036	-86.511	RMX
RRS-10	USA	CS22565	Joy Bergelson	NA	USA	41.5609	-86.4251	RRS
RRS-7	USA	CS22564	Joy Bergelson	NA	USA	41.5609	-86.4251	RRS
Se-0	Spain	CS22646	Albert Kranz	NA	Spain	38.3333	-3.53333	Se
Shahdara	Tajikistan	CS22652	Igor Vizir	NA	Tajikistan	38.35	68.48	Sha
Sorbo	Tajikistan	CS22653	Igor Vizir	NA	Tajikistan	38.35	68.48	Sorbo
Spr1-2	Sweden	CS22582	Magnus Nordborg	5/15/2000	Sweden	58.4168	14.1612	Spr1
Spr1-6	Sweden	CS22583	Magnus Nordborg	5/15/2000	Sweden	58.4168	14.1612	Spr1
Sq-1	UK	CS22600	Mick Crawley	5/21/1993	United Kingdom	51.4083	-0.6383	SQ
Sq-8	UK	CS22601	Mick Crawley	5/21/1993	United Kingdom	51.4083	-0.6383	SQ
Tamm-2	Finland	CS22604	Outi Savolainen	NA	Finland	60	23.5	Tamm
Tamm-27	Finland	CS22605	Outi Savolainen	NA	Finland	60	23.5	Tamm
Ts-1	Spain	CS22647	Albert Kranz	NA	Spain	41.7194	2.93056	Ts
Ts-5	Spain	CS22648	Albert Kranz	NA	Spain	41.7194	2.93056	Ts
Tsu-1	Japan	CS22641	Eric Holub	NA	Japan	34.43	136.31	Tsu
Ull2-3	Sweden	CS22587	Magnus Nordborg	5/14/2000	Sweden	56.0648	13.9707	Ull2

Ull2-5	Sweden	CS22586	Magnus Nordborg	5/14/2000	Sweden	56.0648	13.9707	Ull2
Uod-1	Austria	CS22612	Marcus Koch	6/23/2000	Austria	48.3	14.45	Uod
Uod-7	Austria	CS22613	Marcus Koch	6/23/2000	Austria	48.3	14.45	Uod
Van-0	Canada	CS22627	Albert Kranz	NA	Canada	49.2655	-123.206	Van
Vår2-1	Sweden	CS22580	Magnus Nordborg	6/1/2000	Sweden	55.58	14.334	V?r2
Vår2-6	Sweden	CS22581	Magnus Nordborg	6/1/2000	Sweden	55.58	14.334	V?r2
Wa-1	Poland	CS22644	Albert Kranz	NA	Poland	52.3	21	Wa
Wei-0	Switzerland	CS22622	Alan Slusarenko	NA	Switzerland	47.25	8.26	Wei
Ws-0	Russia	CS22623	Albert Kranz	NA	Russia	52.3	30	Ws
Ws-2	Russia	CS22659	Kenneth Feldmann	NA	Russia	52.3	30	Ws
Wt-5	Germany	CS22637	Albert Kranz	NA	Germany	52.3	9.3	Wt
Yo-0	USA	CS22624	Albert Kranz	NA	USA	37.45	-119.35	Yo
Zdr-1	Czech	CS22588	Jirina Relichová	5/31/2000	Czech Republic	49.3853	16.2544	Zdr
Zdr-6	Czech	CS22589	Jirina Relichová	5/31/2000	Czech Republic	49.3853	16.2544	Zdr

Supplementary Table 2. List of 96 *P. rapae* individuals used in *Pieris* GWAS

Sample ID	Location	# Reads	Sequencing Depth (X)	SNPs per sample	Breadth of genome coverage
SN1-1	University of Chicago, IL	16,835,642	10.42	3,831,390	0.91
SN1-2	University of Chicago, IL	16,690,476	10.33	3,499,432	0.89
SN1-3	University of Chicago, IL	26,957,598	16.68	4,262,071	0.94
SN1-4	University of Chicago, IL	18,250,528	11.29	3,792,942	0.91
SN1-5	Schaumburg, IL	28,371,122	17.56	3,778,816	0.92
SN1-6	University of Chicago, IL	25,206,968	15.60	4,120,740	0.93
SN1-7	University of Chicago, IL	23,495,440	14.54	4,199,475	0.93
SN1-8	University of Chicago, IL	28,485,402	17.63	4,328,932	0.94
SN1-9	University of Chicago, IL	15,116,196	9.35	3,686,801	0.90
SN1-10	University of Chicago, IL	19,030,478	11.78	4,565,351	0.93
SN1-11	University of Chicago, IL	27,052,932	16.74	5,358,852	0.95
SN1-12	University of Chicago, IL	14,893,910	9.22	2,928,379	0.80
SN1-13	University of Chicago, IL	18,059,212	11.18	3,828,798	0.91
SN1-14	University of Chicago, IL	22,820,320	14.12	3,983,847	0.92
SN1-15	University of Chicago, IL	36,021,418	22.29	4,356,063	0.94
SN1-16	University of Chicago, IL	12,271,404	7.59	3,419,565	0.87
SN1-17	University of Chicago, IL	26,675,546	16.51	4,189,629	0.94
SN1-18	University of Chicago, IL	22,361,262	13.84	3,926,289	0.92
SN1-19	University of Chicago, IL	18,815,332	11.64	3,919,399	0.91
SN1-20	University of Chicago, IL	21,906,464	13.56	4,663,772	0.94
SN1-21	University of Chicago, IL	18,279,550	11.31	3,771,071	0.90
SN1-22	University of Chicago, IL	11,794,858	7.30	4,002,105	0.88
SN1-23	University of Chicago, IL	18,078,476	11.19	3,817,351	0.91
SN1-24	University of Chicago, IL	26,813,358	16.59	4,215,037	0.94
SN2-1	University of Chicago, IL	35,502,330	21.97	4,404,469	0.95
SN2-2	University of Chicago, IL	26,399,338	16.34	4,418,141	0.94
SN2-3	University of Chicago, IL	12,114,480	7.50	3,369,810	0.87
SN2-4	University of Chicago, IL	30,325,014	18.77	4,340,905	0.94
SN2-5	University of Chicago, IL	28,937,674	17.91	4,257,918	0.94
SN2-6	University of Chicago, IL	24,441,562	15.13	4,098,097	0.93
SN2-7	University of Chicago, IL	14,409,634	8.92	3,298,740	0.87
SN2-8	University of Chicago, IL	17,851,616	11.05	3,686,303	0.90
SN2-9	University of Chicago, IL	29,575,908	18.30	4,242,049	0.94
SN2-10	University of Chicago, IL	25,206,240	15.60	4,170,416	0.93
SN2-11	University of Chicago, IL	12,842,508	7.95	3,354,444	0.87
SN2-12	University of Chicago, IL	28,153,206	17.42	4,421,812	0.94
SN2-13	University of Chicago, IL	16,721,526	10.35	3,738,070	0.90

SN2-14	University of Chicago, IL	25,174,770	15.58	4,145,893	0.93
SN2-15	University of Chicago, IL	23,191,436	14.35	3,917,609	0.92
SN2-16	University of Chicago, IL	30,018,634	18.58	4,213,145	0.94
SN2-17	University of Chicago, IL	23,429,212	14.50	4,058,390	0.93
SN2-18	University of Chicago, IL	31,742,776	19.64	4,156,959	0.93
SN2-19	University of Chicago, IL	24,448,420	15.13	4,052,921	0.93
SN2-20	University of Chicago, IL	18,959,980	11.73	3,722,312	0.90
SN2-21	University of Chicago, IL	39,691,768	24.56	4,830,783	0.95
SN2-22	University of Chicago, IL	24,922,346	15.42	4,264,440	0.94
SN2-23	University of Chicago, IL	39,987,340	24.75	4,401,123	0.95
SN2-24	University of Chicago, IL	34,115,436	21.11	4,447,627	0.94
SN2-25	University of Chicago, IL	16,194,606	10.02	3,468,528	0.88
SN2-26	University of Chicago, IL	17,365,278	10.75	3,814,271	0.91
SN2-27	University of Chicago, IL	15,122,652	9.36	4,306,601	0.90
SN2-28	Schaumburg, IL	31,841,314	19.71	4,374,753	0.94
SN2-29	Schaumburg, IL	17,495,634	10.83	3,694,208	0.90
SN2-30	Schaumburg, IL	14,902,966	9.22	3,780,863	0.89
SN2-31	Schaumburg, IL	15,245,638	9.43	3,839,257	0.91
SN2-32	University of Chicago, IL	45,800,742	28.34	4,341,145	0.94
SN2-33	Schaumburg, IL	24,533,058	15.18	4,160,031	0.93
SN2-34	Schaumburg, IL	29,684,602	18.37	4,194,515	0.93
SN2-35	Schaumburg, IL	27,851,996	17.24	4,270,839	0.94
SN2-36	Schaumburg, IL	22,625,152	14.00	4,080,784	0.93
SN2-37	Schaumburg, IL	14,306,364	8.85	3,057,695	0.88
SN2-38	Schaumburg, IL	18,849,984	11.67	3,790,211	0.90
SN2-39	Schaumburg, IL	23,002,558	14.24	3,844,742	0.91
SN2-40	Schaumburg, IL	15,183,264	9.40	3,780,936	0.90
SN3-1	Schaumburg, IL	15,620,068	9.67	3,785,333	0.90
SN3-2	Schaumburg, IL	29,512,116	18.26	4,169,538	0.93
SN3-3	Schaumburg, IL	21,037,624	13.02	3,917,810	0.91
SN3-4	University of Chicago, IL	24,676,850	15.27	4,088,482	0.93
SN3-5	Schaumburg, IL	14,681,648	9.09	3,434,508	0.87
SN3-6	Chicago downtown, IL	21,271,010	13.16	4,081,587	0.92
SN3-7	Schaumburg, IL	14,866,824	9.20	3,781,025	0.89
SN3-8	University of Chicago, IL	17,898,040	11.08	3,798,314	0.91
SN3-9	Schaumburg, IL	17,474,592	10.81	3,845,304	0.91
SN3-10	University of Chicago, IL	21,455,300	13.28	4,018,951	0.92
SN3-11	Carolina Biological Supply, NC	18,661,246	11.55	3,221,765	0.90
SN3-12	Chicago downtown, IL	25,666,124	15.88	4,148,584	0.93
SN3-13	University of Chicago, IL	19,371,456	11.99	3,879,331	0.91

SN3-14	University of Chicago, IL	38,173,414	23.62	4,341,148	0.94
SN3-15	Chicago downtown, IL	17,197,960	10.64	3,831,755	0.91
SN3-16	University of Chicago, IL	19,148,234	11.85	3,923,953	0.92
SN3-17	Langdon, ND	10,667,446	6.60	3,327,261	0.86
SN3-18	Langdon, ND	15,693,070	9.71	3,689,625	0.89
SN3-19	Langdon, ND	20,140,606	12.46	3,912,035	0.91
SN3-20	Langdon, ND	34,623,120	21.43	4,438,222	0.94
SN3-21	Langdon, ND	23,224,660	14.37	4,108,532	0.93
SN3-22	Langdon, ND	20,277,212	12.55	3,997,092	0.92
SN3-23	Langdon, ND	21,832,814	13.51	3,815,381	0.90
SN3-24	Langdon, ND	17,669,434	10.93	3,513,475	0.88
SN3-25	Langdon, ND	10,645,710	6.59	3,397,642	0.84
SN3-26	Langdon, ND	16,729,946	10.35	3,739,124	0.90
SN3-27	Langdon, ND	15,135,064	9.37	3,651,243	0.89
SN3-28	Langdon, ND	28,124,188	17.40	4,454,347	0.94
SN3-29	Langdon, ND	34,790,408	21.53	4,421,381	0.95
SN3-30	Langdon, ND	18,450,192	11.42	3,960,058	0.92
SN3-31	Langdon, ND	11,127,958	6.89	3,287,501	0.85
SN3-32	Langdon, ND	15,590,884	9.65	3,720,455	0.90

Supplementary Table 3. Individual values, means, and statistical tests for *Arabidopsis* SALK T-DNA mutants shown in Fig. 1c. For each mutant, we used Student's t-test to compare to control (Col-0). Shaded *p*-values indicate statistical significance after Bonferroni correction.

Larval weight gain (mg)

SALK mutant	**Rep1**	**Rep2**	**Rep3**	**Rep4**	**Rep5**	**Rep6**	**Mean**	**s.e.m.**	***p*-value**
AT4G20320	6.1	5.4	6.2	7.4	6.4	7.5	6.50	0.33	3.23E-05
IMPA-1	6.4	6.3	6.1	6.4	6.3	6.2	6.30	0.05	1.29E-13
CYP79B2	6.7	6.6	6.4	5.8	5	6.7	6.20	0.28	1.62E-05
CYP705A33	6.2	4.5	6.9	5.7	6.8	5.9	6.00	0.36	9.36E-05
PROPEP1	4.5	4.4	4.6	4.5	4.5	4.2	4.45	0.06	5.12E-11
PROPEP3	5.5	2.6	5.3	3.7	2.6	4.6	4.05	0.53	0.014571
PAI3	3.5	3.3	3.5	3.4	3.5	3.5	3.45	0.03	2.49E-08
AT1G29470	3.4	3	3.2	3.3	3.1	3.3	3.22	0.06	1.24E-07
RABE1b	2.2	2.5	2.4	2.3	2.3	2.1	2.30	0.06	0.064648
TRX z	1.8	1.9	1.8	1.7	1.7	1.8	1.78	0.03	0.000635
AT1G47530	0.9	1.1	1	1.2	1.3	1.1	1.10	0.06	1.52E-07
AT3G26510	0.9	1.1	1.1	1	1.1	1.1	1.05	0.03	1.21E-07
Col-0	2.2	2.1	2.3	1.9	2.1	2.2	2.13	0.06	

Leaf material eaten (cm^2)

SALK mutant	**Rep1**	**Rep2**	**Rep3**	**Mean**	**s.e.m.**	***p*-value**
AT4G20320	3.094	3.275	3.194	3.188	0.052	4.06E-05
IMPA-1	3.053	3.163	3.216	3.144	0.048	3.39E-05
CYP79B2	4.888	4.926	4.987	4.934	0.029	3.5E-06
CYP705A33	2.968	2.867	2.855	2.897	0.036	6.66E-05
PROPEP1	3.247	3.102	3.212	3.187	0.044	2.5E-05
PROPEP3	2.760	2.566	2.606	2.644	0.059	0.000459
PAI3	2.743	2.578	2.681	2.667	0.048	0.00019
AT1G29470	3.083	2.871	2.995	2.983	0.062	0.000165
RABE1b	1.457	1.425	1.531	1.471	0.031	0.00681
TRX z	1.720	1.761	1.685	1.722	0.022	0.299914
AT1G47530	0.998	1.093	1.182	1.091	0.053	0.000649
AT3G26510	1.467	1.514	1.403	1.461	0.032	0.006075
Col-0	1.807	1.698	1.852	1.786	0.046	

Supplementary Table 4. List of various time points for RNA-seq sample collection

Time points	**Host Plants (Treatment)**	**Host Plants (Control)**	**Butterflies (Treatment)**	**Butterflies (Control)**
72 h after oviposition	leaves with eggs	control leaves without eggs (*entire plant not exposed*)	eggs deposited on leaves	eggs deposited on wax paper
24 h of larval feeding, age of larvae ~48h	leaves after 24 h of larval feeding from plants previously exposed to eggs	control leaves never exposed to eggs or larvae (*entire plant not exposed*)	larvae after 24 h of feeding on leaves from plants exposed to eggs (*larvae from eggs laid on plants*)	larvae after 24 h of feeding on artificial diet (*larvae from eggs laid on wax paper*)
	leaves after 24 h of larval feeding from plants not previously exposed to eggs (*entire plant not exposed*)		larvae after 24 h of feeding on leaves from plants not exposed to eggs (*larvae from eggs laid on wax paper*)	
24 h after mechanical wounding	leaves 24 h after mechanical wounding		n/a	n/a

Supplementary Table 5. RNA-seq based expression values (fragments per kilobase of transcript per million fragments mapped, or FPKM), means, s.e.m, and results of Tukey (HSD) test for all pairwise comparisons of treatments for each herbivory candidate gene identified in *Arabidopsis thaliana* and *Pieris rapae* GWAS in Figure 3.

Figure 3a

AT4G20320									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
leaves with eggs	4.38	4.121	3.787	4.096	0.171640127			C	
leaf ctrl for eggs	9.021	3.753	4.637	5.803666667	1.628781685		B	C	
leaves with larvae	15.049	13.683	13.528	14.08666667	0.483242635	A	B		
leaves with larvae+eggs	19.901	13.872	13.228	15.667	2.125147132	A			
leaf ctrl for larvae	7.753	13.858	12.806	11.47233333	1.884299723	A	B	C	
wounded leaves	19.506	11.214	10.476	13.732	2.89484991	A	B		
CYP705A33									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
leaves with eggs	1.916	2.796	3.066	2.593	0.34719511		B	C	
leaf ctrl for eggs	1.169	0.368	1.353	0.963	0.302368612			C	
leaves with larvae	2.081	4.147	4.421	3.55	0.738580922	A	B		
leaves with larvae+eggs	4.496	5.298	6.351	5.382	0.537123925	A			
leaf ctrl for larvae	1.391	0.173	0.277	0.614	0.389824462			C	
wounded leaves	1.379	1.278	1.108	1.255	0.079071697			C	
PROPEP3									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
leaves with eggs	2.719	2.164	2.008	2.297	0.215752173	A			
leaf ctrl for eggs	0.654	0.382	0.322	0.453	0.102145865	A			
leaves with larvae	1.866	2.248	2.727	2.28	0.249074509	A			
leaves with larvae+eggs	7.362	1.964	1.497	3.608	1.882001269	A			
leaf ctrl for larvae	0.133	0.735	1.279	0.716	0.330962905	A			
wounded leaves	0.965	1.505	2.158	1.543	0.344904012	A			

PROPEP1									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
leaves with eggs	3.515	4.058	3.76	3.778	0.156999292	A			
leaf ctrl for eggs	0.919	0.171	0.455	0.515	0.218003058				D
leaves with larvae	2.618	2.823	4.436	3.292	0.574887332	A	B		
leaves with larvae+eggs	2.028	1.415	1.052	1.498	0.284811244			C	D
leaf ctrl for larvae	1.11	1.157	1.002	1.09	0.045885122			C	D
wounded leaves	2.227	1.566	2.805	2.199	0.357935904		B	C	
CYP79B2									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
leaves with eggs	3.302	3.649	3.874	3.608	0.166369402			C	
leaf ctrl for eggs	38.547	18.726	25.587	27.62	5.811420566		B	C	
leaves with larvae	54.229	99.085	99.018	84.111	14.94084585	A	B		
leaves with larvae+eggs	80.51	108.677	105.335	98.174	8.884535497	A			
leaf ctrl for larvae	80.505	14.106	13.531	36.047	22.22945306		B	C	
wounded leaves	6.294	20.875	10.732	12.634	4.315230482			C	
AT1G29470									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
leaves with eggs	10.463	9.699	10.113	10.092	0.220805596		B		
leaf ctrl for eggs	23.679	18.094	15.835	19.203	2.331232888	A			
leaves with larvae	11.963	13.362	13.405	12.91	0.473662679	A	B		
leaves with larvae+eggs	16.042	16.06	16.128	16.077	0.026187359	A	B		
leaf ctrl for larvae	16.099	15.344	14.251	15.231	0.536437736	A	B		
wounded leaves	8.137	18.723	11.362	12.741	3.132698003	A	B		
IMPA-1									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
leaves with eggs	11.184	10.281	10.174	10.54633333	0.320326049			C	
leaf ctrl for eggs	19.851	13.212	14.2	15.75433333	2.06809448		B	C	
leaves with larvae	18.323	18.202	17.402	17.97566667	0.288952322	A	B		

leaves with larvae+eggs	20.964	15.743	15.55	17.419	1.773375407	A	B	C	
leaf ctrl for larvae	17.637	12.809	13.094	14.51333333	1.563998757		B	C	
wounded leaves	20.844	26.733	22.479	23.352	1.75515213	A			
PAI3									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
leaves with eggs	1.922	2.421	3.214	2.519	0.376173276	A			
leaf ctrl for eggs	0.766	0.619	1.165	0.85	0.163116523		B		
leaves with larvae	1.769	1.86	2.595	2.075	0.261489537	A			
leaves with larvae+eggs	1.638	1.313	2.099	1.683	0.22802802	A	B		
leaf ctrl for larvae	0.769	0.886	1.002	0.886	0.067261513		B		
wounded leaves	1.261	1.893	1.19	1.448	0.223442013	A	B		
TRX z									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
leaves with eggs	75	75.95	73	74.65	0.869386757	A			
leaf ctrl for eggs	72	73	91	78.667	7.348469228	A			
leaves with larvae	52	96	79	75.667	12.8105859	A			
leaves with larvae+eggs	117	132	87	112	13.22875656	A			
leaf ctrl for larvae	141	107	88	112	15.50268794	A			
wounded leaves	124	89	77	96.667	14.09885732	A			
RABE1b									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
leaves with eggs	1195	1098	812	1035	114.9623127		B		
leaf ctrl for eggs	2162	1831.98	1924	1972.66	98.32623726		B		
leaves with larvae	1318	2201	1495	1671.333333	269.7173418		B		
leaves with larvae+eggs	1925	2958	1848	2243.666667	357.8576688		B		
leaf ctrl for larvae	4664	3175	3872.99	3903.996667	430.116771	A			
wounded leaves	2287	2109	1768	2054.666667	152.2654845		B		
AT1G47530									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			

leaves with eggs	335	307	190	277.333	44.40845765	A			
leaf ctrl for eggs	275	183	259	239	28.37839554	A			
leaves with larvae	401	522	379	434	44.45597073	A			
leaves with larvae+eggs	392	796	447	545	126.5003294	A			
leaf ctrl for larvae	239	391	509	379.667	78.14800772	A			
wounded leaves	441	200	254	298.333	73.01674085	A			
AT3G26510									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
leaves with eggs	173	191	192	185.333	6.173419726		B		
leaf ctrl for eggs	85	159	303	182.333	64.00347213		B		
leaves with larvae	150.78	281	209	213.593	37.66136895		B		
leaves with larvae+eggs	461	817.99	495	591.33	113.7542185	A			
leaf ctrl for larvae	195	312	332	279.667	42.72522024		B		
wounded leaves	457	225	300	327.333	68.35284274	A	B		

Figure 3b

Ppro								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	5.294	6.646	6.856	6.265	6.265	A		
eggs on plants	2.514	2.29	2.943	2.582	2.582		B	
larvae on artificial diet	3.728	3.772	3.479	3.660	3.660		B	
larvae on plants	6.871	6.41	4.978	6.086	6.086	A		
larvae on plants with eggs	4.728	3.467	2.871	3.689	3.689		B	
pupa	4	NA	NA	NA	NA	NA		
adult male	4	NA	NA	NA	NA	NA		
adult female	5	NA	NA	NA	NA	NA		
NPHS1								

Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	0.739	0.502	0.724	0.655	0.655		B	
eggs on plants	1.13	0.469	1.158	0.919	0.919		B	
larvae on artificial diet	3.14	3.262	4.343	3.582	3.582	A		
larvae on plants	3.89	5.87	3.72	4.493	4.493	A		
larvae on plants with eggs	4.551	5.177	5.288	5.005	5.005	A		
pupa	3859.86	NA	NA	NA	NA	NA		
adult male	1	NA	NA	NA	NA	NA		
adult female	1	NA	NA	NA	NA	NA		
slc5a9								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	15.548	10.071	12.316	12.645	12.645	A		
eggs on plants	9.136	6.162	9.854	8.384	8.384		B	
larvae on artificial diet	2.452	2.067	2.966	2.495	2.495			C
larvae on plants	3.347	3.453	3.064	3.288	3.288			C
larvae on plants with eggs	2.387	2.968	2.568	2.641	2.641			C
pupa	7	NA	NA	NA	NA	NA		
adult male	3	NA	NA	NA	NA	NA		
adult female	4	NA	NA	NA	NA	NA		
NATT4_2								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	7.889	8.213	8.454	8.185	8.185	A		
eggs on plants	8.432	4.849	8.281	7.187	7.187	A	B	
larvae on artificial diet	8.131	8.665	7.469	8.088	8.088	A		

larvae on plants	8.478	5.544	8.6	7.541	7.541	A	B	
larvae on plants with eggs	5.034	4.35	4.556	4.647	4.647		B	
pupa	10	NA	NA	NA	NA	NA		
adult male	8	NA	NA	NA	NA	NA		
adult female	6	NA	NA	NA	NA	NA		
rnf168								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	1.608	2.085	2.017	1.903	1.903	A		
eggs on plants	0.868	0.054	0.571	0.498	0.498		B	
larvae on artificial diet	0.213	0.523	0.907	0.548	0.548		B	
larvae on plants	0.776	0.81	0.996	0.861	0.861		B	
larvae on plants with eggs	0.847	0.77	0.814	0.810	0.810		B	
pupa	56	NA	NA	NA	NA	NA		
adult male	62	NA	NA	NA	NA	NA		
adult female	48	NA	NA	NA	NA	NA		
pelA_2								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	28	35	40	34.333	3.480		B	
eggs on plants	44	58	34	45.333	6.960		B	
larvae on artificial diet	85	89	110	94.667	7.753	A		
larvae on plants	115	98	95	102.667	6.227	A		
larvae on plants with eggs	110	104	87	100.333	6.888	A		
pupa	56	NA	NA	NA	NA	NA		
adult male	62	NA	NA	NA	NA	NA		
adult female	48	NA	NA	NA	NA	NA		
resilin_7								

Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	23	28	20	23.667	2.333			C
eggs on plants	33	30	21	28.000	3.606		B	C
larvae on artificial diet	68	64	61	64.333	2.028		B	
larvae on plants	90	126	130	115.333	12.719	A		
larvae on plants with eggs	152	138	111	133.667	12.032	A		
pupa	64	NA	NA	NA	NA	NA		
adult male	68	NA	NA	NA	NA	NA		
adult female	53	NA	NA	NA	NA	NA		
POLX								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	1034	781	928	914.333	73.354	A		
eggs on plants	1162	898	897	985.667	88.167	A		
larvae on artificial diet	891	1036	924	950.333	43.880	A		
larvae on plants	844	1082	997	974.333	69.633	A		
larvae on plants with eggs	812	1014	819	881.667	66.197	A		
pupa	951	NA	NA	NA	NA	NA		
adult male	910	NA	NA	NA	NA	NA		
adult female	889	NA	NA	NA	NA	NA		
Obfc1								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	166	150	154	156.667	4.807			C
eggs on plants	164	99	110	124.333	20.086			C
larvae on artificial diet	309	320	268	299.000	15.822	A		
larvae on plants	229	231	240	233.333	3.383		B	

larvae on plants with eggs	259	270	242	257.000	8.145	A	B	
pupa	98	NA	NA	NA	NA	NA		
adult male	110	NA	NA	NA	NA	NA		
adult female	121	NA	NA	NA	NA	NA		
DHX35								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	620	526	628	591.333	32.748		B	
eggs on plants	623	674	576	624.333	28.298	A	B	
larvae on artificial diet	770	716	725	737.000	16.703	A		
larvae on plants	796	697	727	740.000	29.309	A		
larvae on plants with eggs	727	717	766	736.667	14.948	A		
pupa	653	NA	NA	NA	NA	NA		
adult male	540	NA	NA	NA	NA	NA		
adult female	631	NA	NA	NA	NA	NA		
Glo1								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	1123	1038	1016	1059.000	32.624			C
eggs on plants	1179	1157	1138	1158.000	11.846		B	C
larvae on artificial diet	1397	1486	1389	1424.000	31.086	A	B	
larvae on plants	1761	1539	1324	1541.333	126.156	A		
larvae on plants with eggs	1433	1684	1347	1488.000	101.096	A	B	
pupa	1152	NA	NA	NA	NA	NA		
adult male	1259	NA	NA	NA	NA	NA		
adult female	1180	NA	NA	NA	NA	NA		
thap11								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		

eggs on wax paper	2630	2009	2180	2273.000	185.200		B	
eggs on plants	2636	2592	2195	2474.333	140.243		B	
larvae on artificial diet	5245	5003	4100	4782.667	348.409	A		
larvae on plants	4698	4142	3220	4020.000	431.000	A	B	
larvae on plants with eggs	4625	6528	4147	5100.000	727.211	A		
pupa	2331	NA	NA	NA	NA	NA		
adult male	3041	NA	NA	NA	NA	NA		
adult female	2865	NA	NA	NA	NA	NA		
MYLK2DHX35								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	9.354	13.496	12.346	11.732	1.234	A		
eggs on plants	6.981	7.501	6.661	7.048	0.245		B	
larvae on artificial diet	8.581	9.051	7.736	8.456	0.385		B	
larvae on plants	6.151	7.692	6.16	6.668	0.512		B	
larvae on plants with eggs	6.257	7.228	7.02	6.835	0.295		B	
pupa	493.49	NA	NA	NA	NA	NA		
adult male	0	NA	NA	NA	NA	NA		
adult female	0	NA	NA	NA	NA	NA		
Hmcn2HMCN1								
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*		
eggs on wax paper	0.751	0.596	0.523	0.623	0.067		B	
eggs on plants	1.227	0.643	0.978	0.949	0.169		B	
larvae on artificial diet	2.889	2.801	3.425	3.038	0.195	A		
larvae on plants	3.236	5.308	3.184	3.909	0.699	A		

larvae on plants with eggs	4.022	4.09	4.463	4.192	0.137	A		
pupa	323.06	NA	NA	NA	NA	NA		
adult male	0	NA	NA	NA	NA	NA		
adult female	0	NA	NA	NA	NA	NA		

Figure 3c

Xpac									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	12.215	15.33	15.348	14.298	1.041	A			
eggs on plants	13.355	28.919	14.285	18.853	0.661	A			
larvae on artificial diet	14.985	14.318	11.022	13.442	4.890	A			
larvae on plants	8.057	7.569	10.11	8.579	5.040	A			
larvae on plants with eggs	7.668	8.349	8.217	8.078	4.766	A			
pupa	1093.12	NA	NA	NA	NA	NA			
adult male	0	NA	NA	NA	NA	NA			
adult female	0	NA	NA	NA	NA	NA			
Beg									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	15.859	17.579	19.217	17.552	0.969	A			
eggs on plants	19.057	37.17	20.116	25.448	0.521	A			
larvae on artificial diet	21.465	22.995	21.394	21.951	6.011	A			

larvae on plants	15.505	20.535	20.898	18.979	5.869	A			
larvae on plants with eggs	17.477	17.435	18.479	17.797	5.474	A			
pupa	37.96	NA	NA	NA	NA	NA			
adult male	0	NA	NA	NA	NA	NA			
adult female	0	NA	NA	NA	NA	NA			
Acadvl									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	15.859	17.579	19.217	17.552	0.969	A			
eggs on plants	19.057	37.17	20.116	25.448	0.521	A			
larvae on artificial diet	21.465	22.995	21.394	21.951	6.011	A			
larvae on plants	15.505	20.535	20.898	18.979	5.869	A			
larvae on plants with eggs	17.477	17.435	18.479	17.797	5.474	A			
pupa	0	NA	NA	NA	NA	NA			
adult male	0	NA	NA	NA	NA	NA			
adult female	0	NA	NA	NA	NA	NA			
LCMT1									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	4.903	7.445	7.603	6.650	0.875	A			
eggs on plants	5.993	13.676	6.708	8.792	0.512	A			
larvae on artificial diet	5.491	6.026	4.396	5.304	2.339	A			
larvae on plants	4.355	4.274	4.749	4.459	2.451	A			

larvae on plants with eggs	3.728	3.999	4.451	4.059	2.550	A			
pupa	588.81	NA	NA	NA	NA	NA			
adult male	0	NA	NA	NA	NA	NA			
adult female	0	NA	NA	NA	NA	NA			
INTS9									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	6.35	6.865	6.722	6.646	0.153	A			
eggs on plants	5.776	20.695	6.324	10.932	0.342	A			
larvae on artificial diet	7.455	8.242	6.701	7.466	4.823	A			
larvae on plants	5.752	6.804	6.762	6.439	4.884	A			
larvae on plants with eggs	5.104	5.053	5.276	5.144	4.613	A			
pupa	67.56	NA	NA	NA	NA	NA			
adult male	0	NA	NA	NA	NA	NA			
adult female	0	NA	NA	NA	NA	NA			
G103827									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	0	0	0	0.000	0.000	A			
eggs on plants	0	0	0	0.000	0.000	A			
larvae on artificial diet	0	0	0	0.000	0.000	A			
larvae on plants	0	0	0.46	0.153	0.000	A			
larvae on plants with eggs	0.294	0.238	0	0.177	0.000	A			
pupa	0	NA	NA	NA	NA	NA			

adult male	0	NA	NA	NA	NA	NA			
adult female	0	NA	NA	NA	NA	NA			
Cyt-b5_2									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	53.038	56.844	56.305	55.396	1.189			C	D
eggs on plants	24.07	40.171	24.836	29.692	10.836				D
larvae on artificial diet	203.802	200.745	168.154	190.900	9.305	A	B		
larvae on plants	141.924	142.421	123.257	135.867	5.244		B	C	
larvae on plants with eggs	292.456	167.289	226.568	228.771	57.271	A			
pupa	1083.5	NA	NA	NA	NA	NA			
adult male	0	NA	NA	NA	NA	NA			
adult female	0	NA	NA	NA	NA	NA			
Ceacam1									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	0.869	1.317	0.956	1.047	0.137		B		
eggs on plants	2.903	4.139	2.818	3.287	0.598	A			
larvae on artificial diet	0.863	0.722	0.992	0.859	0.926		B		
larvae on plants	0.853	1.316	1.149	1.106	0.427		B		
larvae on plants with eggs	1.129	1.382	0.999	1.170	0.952		B		
pupa	95.67	NA	NA	NA	NA	NA			
adult male	4	NA	NA	NA	NA	NA			
adult female	3	NA	NA	NA	NA	NA			

dpr6									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	182	204	208	198.000	8.083	A			
eggs on plants	212	232	225	223.000	5.859	A			
larvae on artificial diet	315	282	216	271.000	29.103	A			
larvae on plants	369	273	240	294.000	38.691	A			
larvae on plants with eggs	295	280	251	275.333	12.914	A			
pupa	208	NA	NA	NA	NA	NA			
adult male	190	NA	NA	NA	NA	NA			
adult female	186	NA	NA	NA	NA	NA			
aldB_2									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	0.906	0.815	0.874	0.865	0.027		B		
eggs on plants	2.492	3.242	2.434	2.723	0.549	A			
larvae on artificial diet	0.988	0.772	0.95	0.903	0.699		B		
larvae on plants	1.142	1.586	1.411	1.380	0.260		B		
larvae on plants with eggs	1.211	1.257	1.627	1.365	0.659		B		
pupa	95.67	NA	NA	NA	NA	NA			
adult male	4	NA	NA	NA	NA	NA			
adult female	3	NA	NA	NA	NA	NA			
Plscr1									

Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	0.23	0.259	0.157	0.215	0.030		B		
eggs on plants	0.412	0	0.564	0.325	0.074		B		
larvae on artificial diet	0.801	0.672	0.523	0.665	0.120		B		
larvae on plants	1.939	1.856	1.215	1.670	0.168	A			
larvae on plants with eggs	1.752	1.473	1.685	1.637	0.238	A			
pupa	6	NA	NA	NA	NA	NA			
adult male	0	NA	NA	NA	NA	NA			
adult female	1	NA	NA	NA	NA	NA			
CRYAB									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	1.123	2.288	2.255	1.889	0.383		B		
eggs on plants	1.212	2.532	1.894	1.879	0.353		B		
larvae on artificial diet	2.539	1.942	1.686	2.056	0.402		B		
larvae on plants	43.411	65.497	95.4	68.103	0.381	A			
larvae on plants with eggs	27.462	49.381	41.932	39.592	0.214	A			
pupa	178.35	NA	NA	NA	NA	NA			
adult male	1	NA	NA	NA	NA	NA			
adult female	0	NA	NA	NA	NA	NA			
panC_2									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			

eggs on wax paper	0.081	0.055	0.067	0.068	0.008		B		
eggs on plants	0.209	0.147	0.172	0.176	0.049		B		
larvae on artificial diet	23.504	28.897	21.842	24.748	0.041	A			
larvae on plants	11.847	27.159	31.512	23.506	0.018	A			
larvae on plants with eggs	15.113	19.666	18.967	17.915	7.782	A			
pupa	0	NA	NA	NA	NA	NA			
adult male	1	NA	NA	NA	NA	NA			
adult female	1	NA	NA	NA	NA	NA			
Nomo1									
Treatment	*rep1*	*rep2*	*rep3*	*mean*	*std. error*	*Tukey (HSD) Groups*			
eggs on wax paper	16.92	13.935	16.102	15.652	0.891		B		
eggs on plants	22.962	10.997	21.822	18.594	2.721		B		
larvae on artificial diet	35.574	34.375	39.171	36.373	3.466	A			
larvae on plants	29.158	29.566	31.928	30.217	3.813	A			
larvae on plants with eggs	34.471	34.711	35.563	34.915	7.112	A			
pupa	3426.76	NA	NA	NA	NA	NA			
adult male	0	NA	NA	NA	NA	NA			
adult female	0	NA	NA	NA	NA	NA			

Supplementary Table 6. Individual values, means, and statistical test (Tukey's HSD test) summaries for all pairwise comparisons of the *Osiris 9E* fold changes across developmental stages shown in Supplementary Fig. 5.

Pieris rapae								
Developmental stage	**rep1**	**rep2**	**rep3**	**mean**	**s.e.m.**	**Tukey (HSD) Groups**		
24h larvae	0.0030553	0.0027584	0.003472	0.0030952	0.000207			C
48h larvae	0.0111659	0.0328474	0.042801	0.0289381	0.0093391			C
72h larvae	0.1990372	0.1845324	0.0244288	0.1359995	0.0559423		B	C
2nd instar	0.8467595	0.6366519	1.0936835	0.8590316	0.1320763	A	B	
3rd instar	1.1591234	0.9780164	1.1282862	1.0884753	0.0559423	A		C
4th instar	0.3604731	0.1423509	0.3436663	0.2821634	0.0700744		B	
5th instar	0.9148744	0.9423553	0.7866263	0.8812853	0.0479897	A	B	
prepupa	1.2875207	0.7287369	2.1228102	1.3796893	0.4050643	A		
pupa	0.1133886	NA	NA	0.1133886	NA	NA		
adult female	0.014935	NA	NA	0.014935	NA	NA		
Colias eurytheme								
Developmental stage	**rep1**	**rep2**	**rep3**	**mean**	**s.e.m.**	**Tukey (HSD) Groups**		
24h larvae	9.883E-05	7.376E-05	0.0001001	9.091E-05	8.582E-06		B	
48h larvae	0.6794347	0.3236686	0.5700031	0.5243688	0.105205	A		
72h larvae	0.0261241	0.0112276	0.0074933	0.0149483	0.0056909		B	
2nd instar	0.7882852	0.1967747	0.380937	0.4553323	0.174759	A		
3rd instar	0.0132865	0.0415419	0.0550586	0.036629	0.0123062		B	
4th instar	NA	NA	0.0074369	0.0074369	NA	NA		
5th instar	0.0030519	0.003122	0.0007403	0.0023047	0.0007825		B	
prepupa	0.0006229	0.0006766	0.0004756	0.0005917	6.008E-05		B	
pupa	NA	NA	NA	NA	NA	NA		
adult female	0.0022773	0.0034614	0.0044445	0.0033944	0.0006265		B	
Papilio polytes								
Developmental stage	**rep1**	**rep2**	**rep3**	**mean**	**s.e.m.**	**Tukey (HSD) Groups**		
24h larvae	0.0042847	0.0060155	0.0079452	0.0060818	0.0010572		B	
48h larvae	NA	0.0002822	0.0001192	0.0002007	6.656E-05		B	
72h larvae	NA	NA	2.873E-05	2.873E-05	NA	NA		
2nd instar	NA	0.0908007	0.0390395	0.0649201	0.0211314		B	
3rd instar	0.0122871	0.0314087	0.0458392	0.029845	0.0097171		B	

4th instar	0.1205018	0.5004385	0.4381417	0.3530273	0.1176454		B	
5th instar	1.4504244	1.4805875	0.3666173	1.0992097	0.3663997	A		
prepupa	1.477E-06	3.011E-08	1.818E-07	5.63E-07	1.53E-07		B	
pupa	6.409E-06	2.418E-06	4.795E-06	4.541E-06	1.159E-06		B	
adult female	5.98E-06	4.648E-06	3.976E-06	4.868E-06	5.888E-07		B	
Heliconius cydno								
Developmental stage	**rep1**	**rep2**	**rep3**	**mean**	**s.e.m.**	**Tukey (HSD) Groups**		
24h larvae	0.0001748	8.81E-05	7.004E-05	0.000111	3.232E-05		B	
48h larvae	2.976E-05	3.639E-05	3.005E-05	3.207E-05	2.165E-06		B	
72h larvae	0.0013058	0.0038315	0.0020306	0.0023893	0.0007508		B	
2nd instar	0.0012627	0.0026182	0.0013451	0.001742	0.0004387		B	
3rd instar	0.1434532	0.2239242	0.4180106	0.261796	0.0814885	A		
4th instar	0.1584838	0.207667	0.4286732	0.2649413	0.083088	A		
5th instar	0.0094337	0.0151617	0.0399316	0.021509	0.0093585		B	
prepupa	1.759E-05	5.732E-05	9.753E-05	5.748E-05	2.308E-05		B	
pupa	0.034641	0.0078983	0.0266907	0.0230767	0.0079286		B	
adult female	0.0205087	0.0235544	0.0251669	0.0051803	0.0013658		B	

Supplementary Table 7. Individual values, means, and statistical test (Tukey's HSD test) summary for the comparisons of *Osiris 9E* fold changes across various tissues of *P. rapae* third instar larvae shown in Supplementary Fig. 6.

Tissue	rep1	rep2	rep3	mean	s.e.m.	Tukey HSD Groups	
Foregut	1.8817	1.3643	NA	1.6230	0.2587	A	
Midgut	1.3577	1.1214	1.3405	1.2732	0.0932	A	
Skin	0.0575	0.0496	NA	0.0535	0.0040		B

Supplementary Table 8. Single copy ortholog content was assessed using BUSCO (version 3.0.2) with insecta lineage protein set from Ortholog Database (version 9, creation date 2016-02-13), BLAST (version 2.3.0), and Augustus (version 3.3).

BUSCOs	**Prapae allpaths scaffolds**	**Prapae HiRise scaffolds**	**Prapae Chromosomes and unplaced scaffolds**	**Prapae Chromosomes only**
Complete	1555 (93.8%)	1589 (95.9%)	1587 (95.7%)	1452 (87.5%)
Complete and single copy	1375 (82.9%)	1432 (86.4%)	1428 (86.1%)	1360 (82.0%)
Complete and duplicated	180 (10.9%)	157 (9.5%)	159 (9.6%)	92 (5.5%)
Fragmented	56 (3.4%)	30 (1.8%)	30 (1.8%)	33 (2.0%)
Missing	47 (2.8%)	39 (2.3%)	41 (2.5%)	173 (10.5%)
Total Searched	1658	1658	1658	1658

Supplemental Table 9. RNA-seq data from plant and butterfly species

RNA-seq reads from plant treatments	***A. thaliana***		***M. sativa***		***C. microcarpa***		***P. oerstedii***	
	PE100 reads	SR50 reads	PE100 reads	SR50 reads	PE100 reads	SR50 reads	PE100 reads	SR50 reads
leaves after 72h oviposition (Rep1)		21,639,196		26,858,839		27,896,344		22,763,741
leaves after 72h oviposition (Rep2)		22,438,375		36,693,096		28,539,350		22,623,340
leaves after 72h oviposition (Rep3)		14,941,355		30,231,556		19,894,497		24,959,732
control leaves for 72h oviposition (Rep1)	76,129,862	19,364,500	78,973,496	30,498,283	91,412,840	25,353,096	80,271,576	27,032,270
control leaves for 72h oviposition (Rep2)		22,532,746		24,553,867		28,606,745		26,642,181
control leaves for 72h oviposition (Rep3)		22,259,053		24,683,116		25,798,401		22,077,161
leaves after 24h larval feeding (Rep1)		22,312,484		29,600,842		38,948,895		34,843,393

leaves after 24h larval feeding (Rep2)		19,993,693		9,457,426		34,499,506		28,488,412
leaves after 24h larval feeding (Rep3)		23,015,788		25,757,440		33,470,124		29,895,097
leaves with eggs after 24h larval feeding (Rep1)		24,126,638		29,393,154		31,478,959		38,146,566
leaves with eggs after 24h larval feeding (Rep2)		27,405,885		32,592,609		31,945,118		32,441,898
leaves with eggs after 24h larval feeding (Rep3)		32,846,908		22,831,046		40,478,517		35,107,655
control leaves for 24h larval feeding (Rep1)		19,307,208		31,493,122		33,057,620		35,728,964
control leaves for 24h larval feeding(Rep2)		15,247,207		25,445,840		36,357,523		36,710,010
control leaves for 24h larval feeding (Rep3)		28,278,897		25,680,542		32,830,868		33,291,937

leaves after 24h wounding (Rep1)		23,137,056		25,943,823		34,815,190		36,098,418
leaves after 24h wounding (Rep2)		15,708,770		33,566,017		37,242,158		32,359,870
leaves after 24h wounding (Rep3)		15,139,341		33,676,797		32,036,477		30,635,188
RNA-seq reads from butterfly treatments	***P. rapae***		***C. eurytheme***		***P. polytes***		***H. cydno***	
	PE100 reads	SR50 reads	PE100 reads	SR50 reads	PE100 reads	SR50 reads	PE100 reads	SR50 reads
eggs on leaves after 72h oviposition (Rep1)	51,284,958	26,189,771	69,706,332	28,983,275	65,934,998	31,706,333	75,509,498	25,978,394
eggs on leaves after 72h oviposition (Rep2)		13,639,140		27,606,177		23,990,652		28,733,262
eggs on leaves after 72h oviposition (Rep3)		23,225,446		28,421,623		28,459,252		23,432,067

eggs on wax paper after 72h oviposition (Rep1)		22,615,848		25,429,477		28,152,911		26,367,632
eggs on wax paper after 72h oviposition (Rep2)		20,753,366		33,402,631		25,904,895		30,869,940
eggs on wax paper after 72h oviposition (Rep3)		17,549,302		26,197,572		28,617,920		30,547,665
larvae on leaves after 24h feeding (Rep1)		17,841,901		21,684,935		33,603,426		34,539,669
larvae on leaves after 24h feeding (Rep2)		15,970,738		24,829,703		29,788,442		29,345,527
larvae on leaves after 24h feeding (Rep3)		31,116,237		29,608,766		31,713,851		20,813,092
larvae on leaves with eggs after 24h feeding (Rep1)	41,731,336	38,238,647	58,505,982	18,396,988	56,095,998	34,228,342	55,131,042	34,874,271
larvae on leaves with eggs after		23,463,201		41,944,678		35,932,927		28,741,649

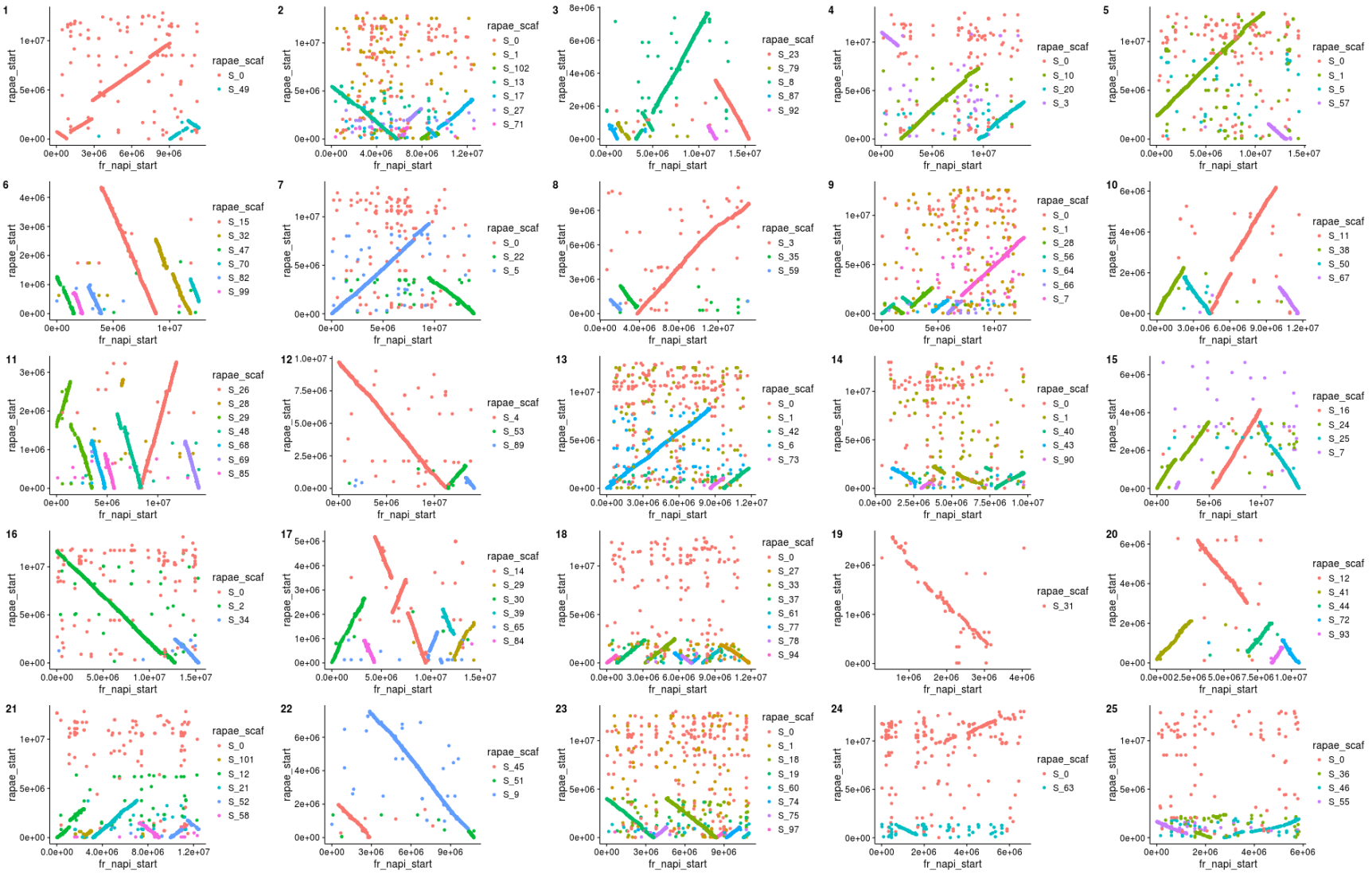
24h feeding (Rep2)								
larvae on leaves with eggs after 24h feeding (Rep3)		27,648,012		32,583,736		34,730,888		35,992,224
larvae on artificial diet after 24h feeding (Rep1)		20,259,852		20,689,227		29,104,773		27,525,825
larvae on artificial diet after 24h feeding(Rep2)		17,132,971		46,524,562		32,380,255		31,087,478
larvae on artificial diet after 24h feeding (Rep3)		22,139,037		37,819,789		26,477,204		28,877,256

Supplementary Table 10. Comparison of the RNA-seq results from the two different analysis methods for *Pieris rapae* and *Arabidopsis thaliana*.

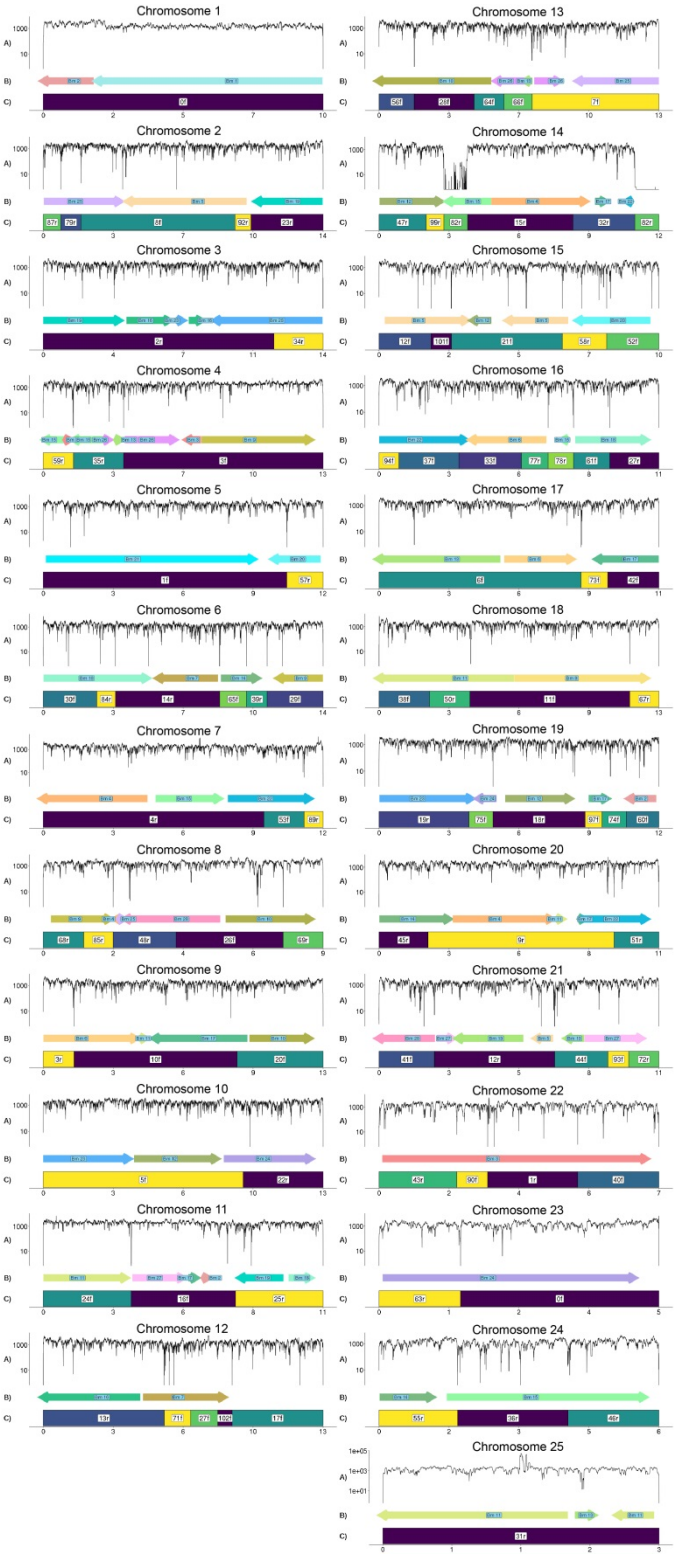
Treatment	**Common**	**Trinity only**	**Cuffdiff only**
Leaves with eggs	11558	1538	3005
Leaves with larvae, eggs	833	0	921
Leaves with larvae	1033	0	1035
Wounded leaves	1074	0	1370
Eggs on leaves	763	260	56
Larvae on leaves with eggs	397	174	60
Larvae on leaves without eggs	586	67	33

Supplementary Table 11. Primer sequences for cDNA synthesis for *Osiris 9E* spatial and temporal expression patterns

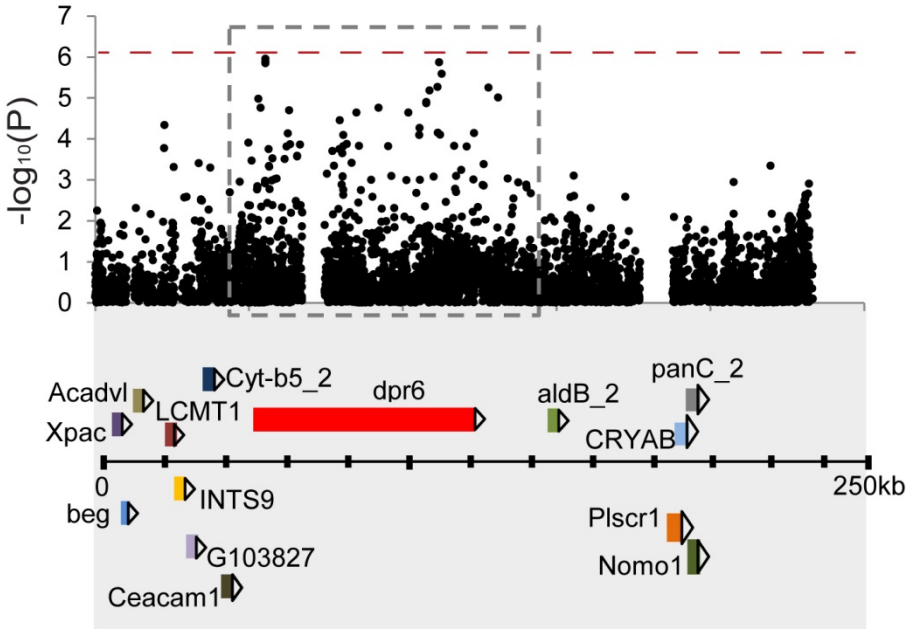
P. rapae	
Osiris_9E_PR_left primer	TCGCGGTCTATTGCCATTGT
Osiris_9E_PR_right primer	TGTCTCTGGCGATAGGGTCA
EF1a_PR_left primer	ACAAAACCCCTCTGCGTTGA
EF1a_PR_right primer	TTGATGACTCCCACAGCGAC
C. eurytheme	
Osiris_9E_CE_left primer	GACCGCTAAGATTGCTCTGG
Osiris_9E_CE_right primer	CGTATGTCGTCTTGGTGTGG
EF1a_CE_left primer	AAGGTTGACCGTCGTACTGG
EF1a_CE_right primer	GGGAACTCCTGGAAGGACTC
H. cydno	
Osiris_9E_HC_left primer	GCGCCAGGAATATTGTGATT
Osiris_9E_HC_right primer	ACTTCGGCATCTCTTGCTGT
EF1a_HC_left primer	TCGACAAACGTACCATCGAA
EF1a_HC_right primer	GCTCAGCCTTCAGTTTGTCC
P. polytes	
Osiris_9E_PP_left primer	GACCGCTAAGATTGCTCTGG
Osiris_9E_PP_right primer	CGTATGTCGTCTTGGTGTGG
EF1a_PP_left primer	AACATTGTCGTCATCGGACA
EF1a_PP_right primer	GGCCTCCTTCTCGAACTTCT


1
rapae_start
fr_napi_start
rapae_scaf
S_0
S_49
2
rapae_scaf
S_0
S_1
S_102
S_13
S_17
S_27
S_71
3
rapae_scaf
S_23
S_79
S_8
S_87
S_92
4
rapae_scaf
S_0
S_10
S_20
S_3
5
rapae_scaf
S_0
S_1
S_5
S_57
6
rapae_scaf
S_15
S_32
S_47
S_70
S_82
S_99
7
rapae_scaf
S_0
S_22
S_5
8
rapae_scaf
S_3
S_35
S_59
9
rapae_scaf
S_0
S_1
S_28
S_56
S_64
S_66
S_7
10
rapae_scaf
S_11
S_38
S_50
S_67
11
rapae_scaf
S_26
S_28
S_29
S_48
S_68
S_69
S_85
12
rapae_scaf
S_4
S_53
S_89
13
rapae_scaf
S_0
S_1
S_42
S_6
S_73
14
rapae_scaf
S_0
S_1
S_40
S_43
S_90
15
rapae_scaf
S_16
S_24
S_25
S_7
16
rapae_scaf
S_0
S_2
S_34
17
rapae_scaf
S_14
S_29
S_30
S_39
S_65
S_84
18
rapae_scaf
S_0
S_27
S_33
S_37
S_61
S_77
S_78
S_94
19
rapae_scaf
S_31
20
rapae_scaf
S_12
S_41
S_44
S_72
S_93
21
rapae_scaf
S_0
S_101
S_12
S_21
S_52
S_58
22
rapae_scaf
S_45
S_51
S_9
23
rapae_scaf
S_0
S_1
S_18
S_19
S_60
S_74
S_75
S_97
24
rapae_scaf
S_0
S_63
25
rapae_scaf
S_0
S_36
S_46
S_55

Supplementary Figure 1: Alignment of *P. rapae* scaffolds to *P. napi* chromosomes. The 102 largest scaffolds in the *P. rapae* assembly were aligned to the 25 chromosomes of *P. napi* using LAST (version 714). Each panel depicts a *P. napi* chromosome and the *P. rapae* HiRise scaffolds that aligned to it. 82 of the 102 scaffolds in the *P. rapae* assembly mapped in full to the *P. napi* chromosomes. Coordinates of the mapped scaffolds and scaffold segments were used to place the *P. rapae* HiRise assembly in a chromosomal context using a custom R script (Supplementary Material finalPrapae.agp), assuming conservation of synteny between *P. napi* and *P. rapae*. While there may be some differences in chromosomal organization between the two species, the completeness of scaffolds mapping to chromosomes combined with mate pairs spanning junctions between scaffolds lend support to this *P. rapae* chromosomal model.

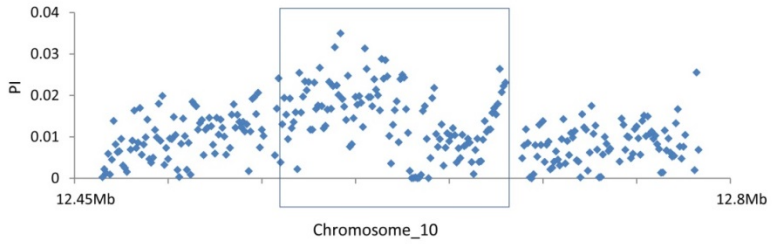

Chromosome 1
Chromosome 2
Chromosome 3
Chromosome 4
Chromosome 5
Chromosome 6
Chromosome 7
Chromosome 8
Chromosome 9
Chromosome 10
Chromosome 11
Chromosome 12
Chromosome 13
Chromosome 14
Chromosome 15
Chromosome 16
Chromosome 17
Chromosome 18
Chromosome 19
Chromosome 20
Chromosome 21
Chromosome 22
Chromosome 23
Chromosome 24
Chromosome 25

Supplementary Figure 2: Chromosomal assembly of butterfly *Pieris rapae* genome. (a) Read pairs from the 3 kbp, 7 kbp, and 40 kbp insert size mate pair libraries were mapped to the *P. rapae* chromosomes and the number of times a position was flanked by read pair mapped in the proper orientation with a mapq > 20 for both reads was counted. A count of zero occurs at a position where no mate pairs span which can be caused by either a misassembly or a high density repetitive sequence. (b) Orthologous genes from *Bombyx mori* occur in blocks along the *P. rapae* chromosomes and their *B. mori* chromosome of origin and orientation are shown above (c) the number and direction, forward or reverse, of the component scaffold used to construct the chromosome. A chromosome misassembly is less likely to occur within a scaffold, within a syntenic block, or where mate pair spanning is high. Taken together we regard a scaffold join that is spanned by an average number of mate pairs and a syntenic block from *B. mori* to be correct.

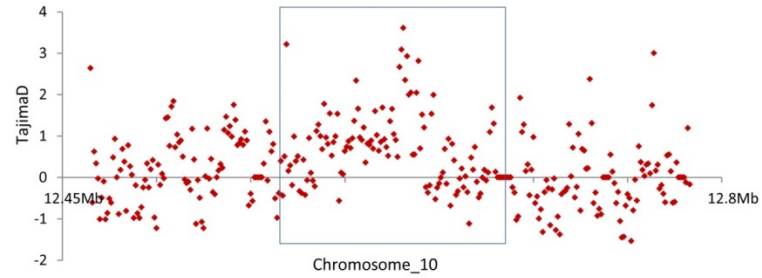


Supplementary Figure 3: Chromosome 15 peak region. Zoom-in on the chromosome 15 region (boxed) associated with herbivory in the *P. rapae* genome. A gene map below shows the underlying genes found in the associated and the adjoining regions.

a



b



c

	pelA_2	**Resilin**	**POLX**	**Obfc1**	**DHX 35**	**Glo1**	**thap11**	NPHS1	slc5a9	Hmcn2HMCN1
Obs. polymorphic sites	25	138	18	46	35	58	47	121	26	134
Obs. fixed divergent sites	51	63	32	21	84	24	26	168	40	179

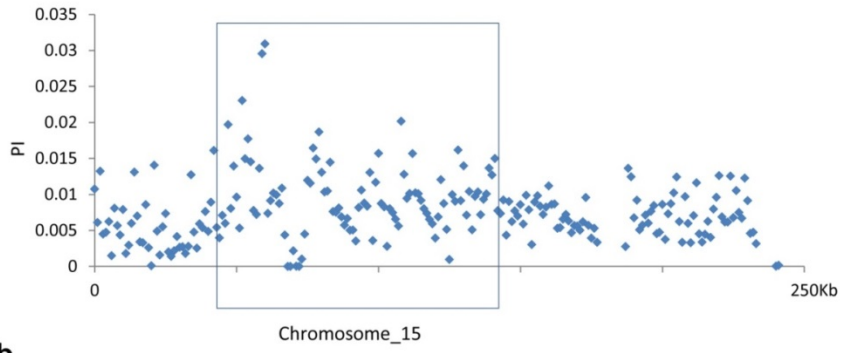
d

	NPHS1	slc5a9	Hmcn2HMCN1
pelA_2	0.057	1.352	2.467
Resilin	4.024*	5.159*	5.762*
POLX	0.028	0.167	0.531
Obfc1	6.364*	4.892*	4.127*
DHX35	1.572	0.639	1.067
Glo1	5.936*	6.017*	5.158*
thap11	4.757*	4.016*	4.524*
NPHS1		0.036	0.014
slc5a9	0.036		0.149
Hmcn2HMCN1	0.014	0.149	

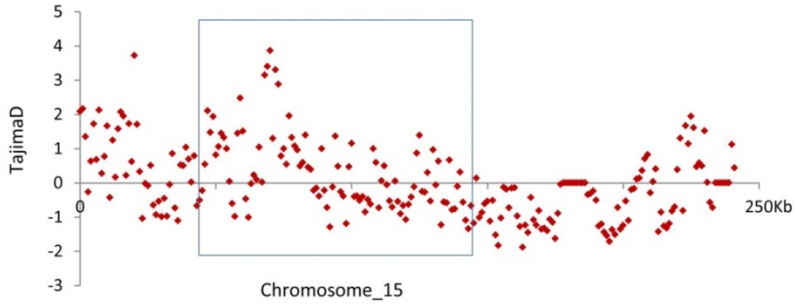
* 0.01<P<0.05

Supplementary Figure 4: Chromosome 10 peak selection scans. Population genetic scans for evidence of natural selection across the herbivory associated region on *P. rapae* chromosome 10. (a) Nucleotide diversity (π) in the herbivory associated region (boxed) and 100 kbp upstream and downstream. (b) Tajima's D values in the herbivory associated region (boxed) and 100 kbp upstream and downstream. (c) The observed number of polymorphic and fixed divergent sites found in the CDS of genes in the herbivory associated region (bold) and neighboring genes. (d) HKA test results.

a



b



c

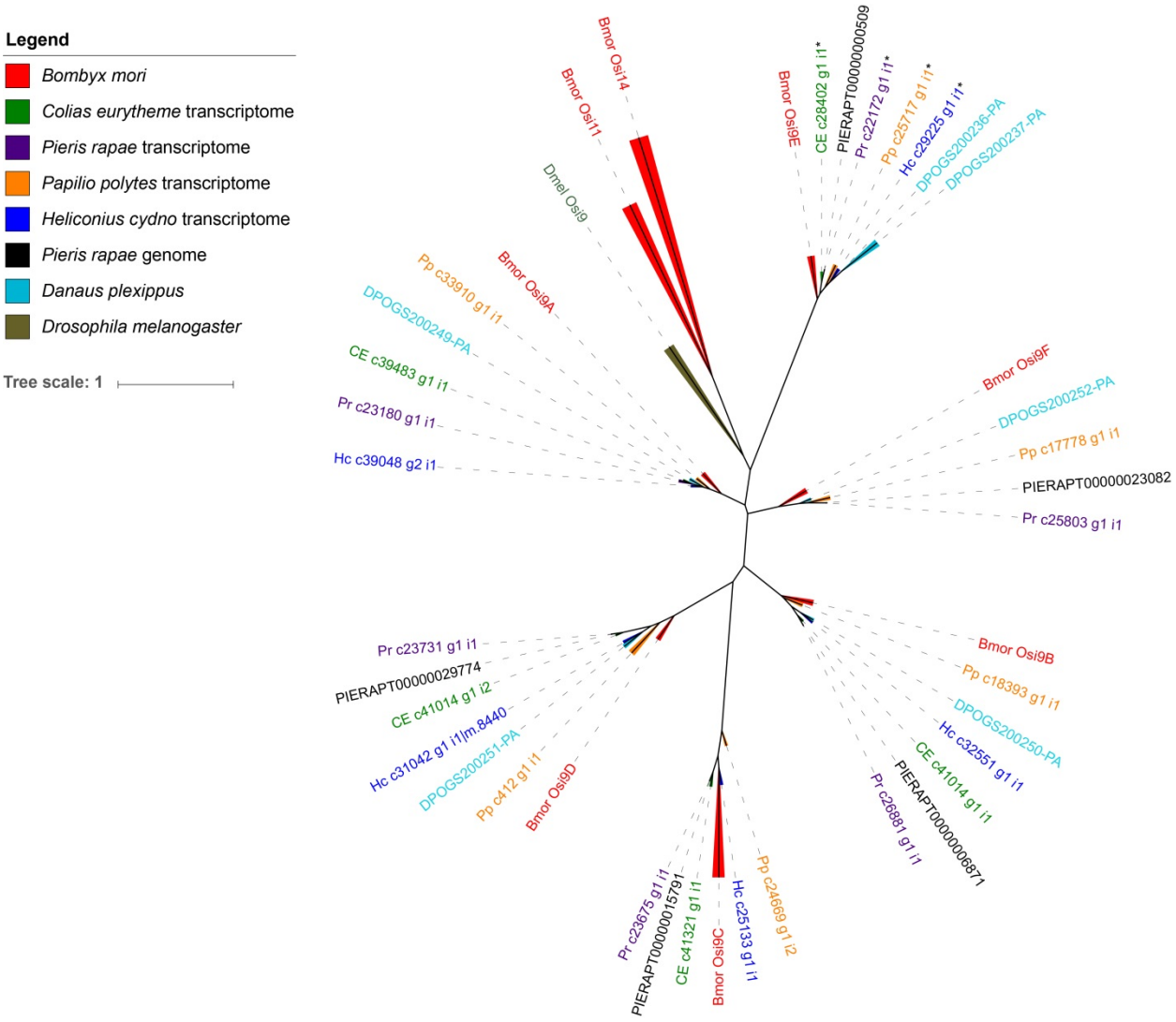
	dpr6	Nomo1	Plscr1	panC_2
Obs. polymorphic sites	23	87	23	15
Obs. fixed divergent sites	52	109	34	26

d

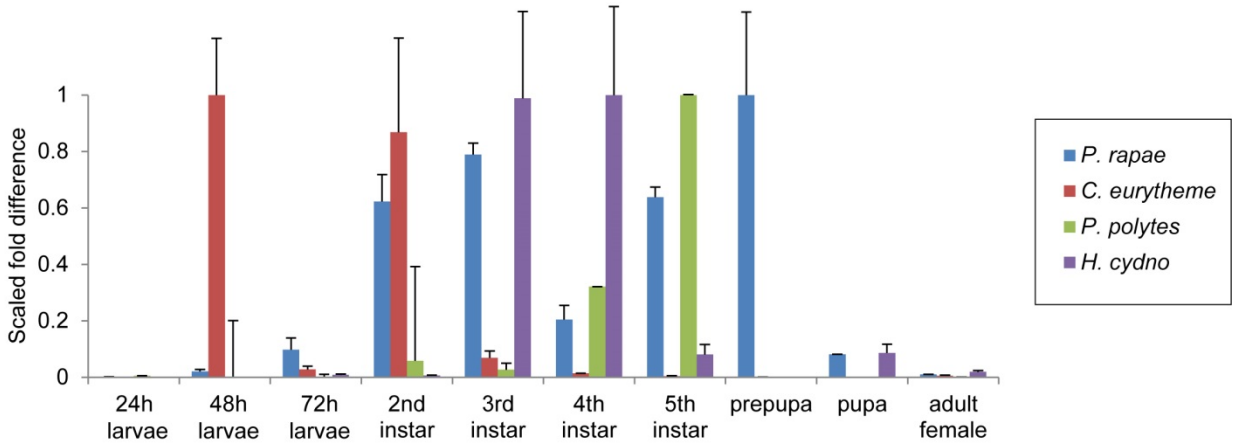
	Nomo1	Plscr1	panC_2
dpr6	2.015	1.873	1.364
Nomo1		0.157	1.078
Plscr1	0.157		0.035
panC_2	1.078	0.035	

* 0.01<P<0.05

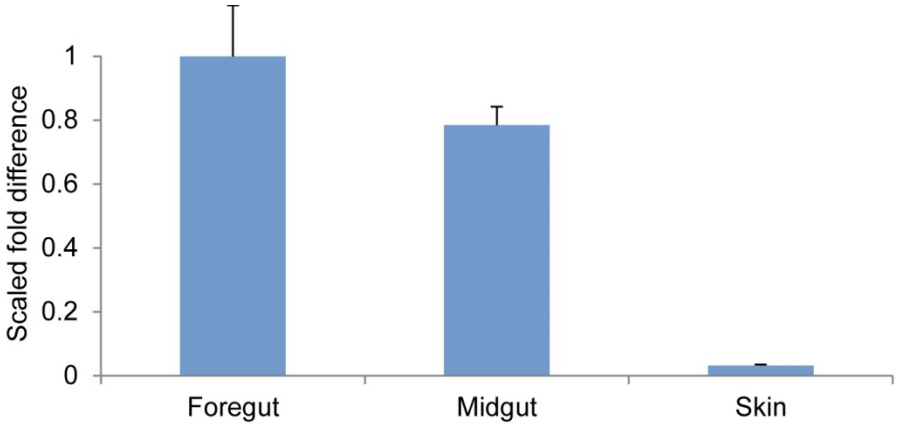
Supplementary Figure 5: Chromosome 15 peak selection scans. Population genetic scans for evidence of natural selection across the herbivory associated region on *P. rapae* chromosome 15. (a) Nucleotide diversity (π) in the herbivory associated region (boxed) and 100 kbp upstream and downstream. (b) Tajima's D values in the herbivory associated region (boxed) and 100 kbp upstream and downstream. (c) The observed number of polymorphic and fixed divergent sites found in the CDS of genes in the herbivory associated region (bold) and neighboring genes. (d) HKA test results.



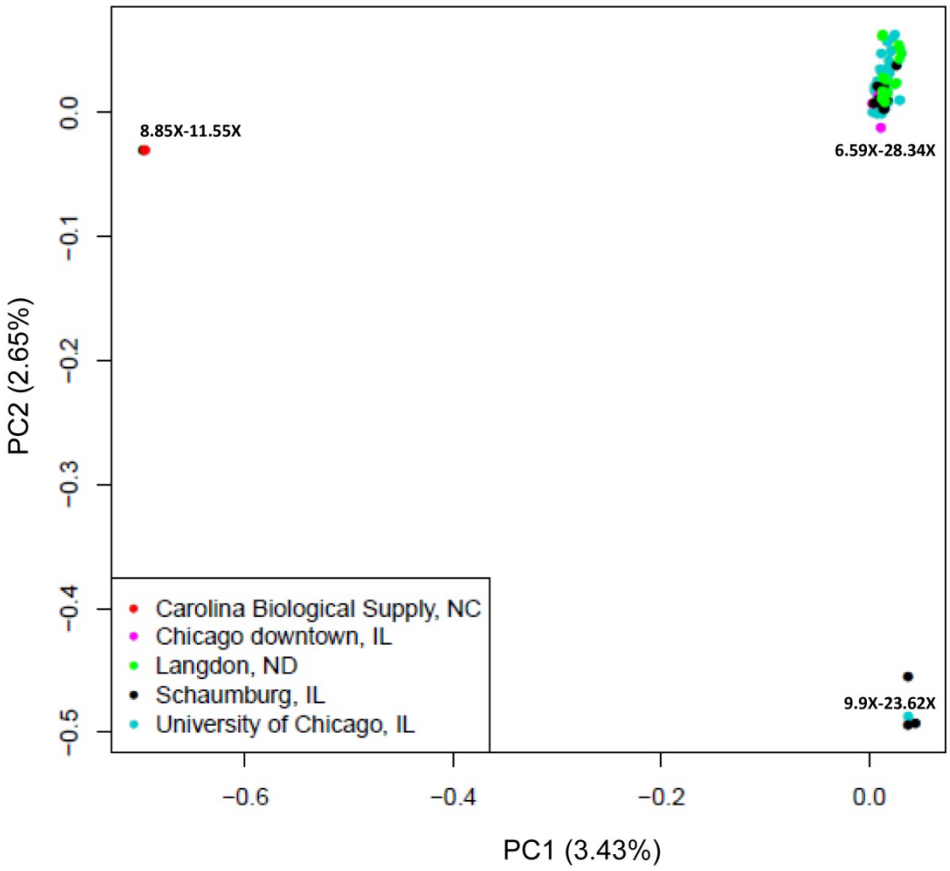
Supplementary Figure 6: Osiris 9 protein Tree. Tree of *Osiris 9* protein sequences extracted from the *Pieris rapae* genome and each of the four assembled transcriptomes—*Colias eurytheme*, *Pieris rapae*, *Papilio polytes*, and *Heliconius cydno*. These are combined with *Osiris 9* protein sequences from *Drosophila melanogaster*, *Bombyx mori*, and *Danaus plexippus*, as well as *Osiris 11* and *Osiris 14* from *B. mori*. While *Osi9* is clearly a multi-copy gene across the Lepidoptera, we found one copy to be up-regulated in larvae of all four butterfly species when feeding on leaves with prior exposure to eggs (Supplementary data 10). These genes are marked with an asterisk and the *Osi9* tree shows that they are all *Osi9E*.



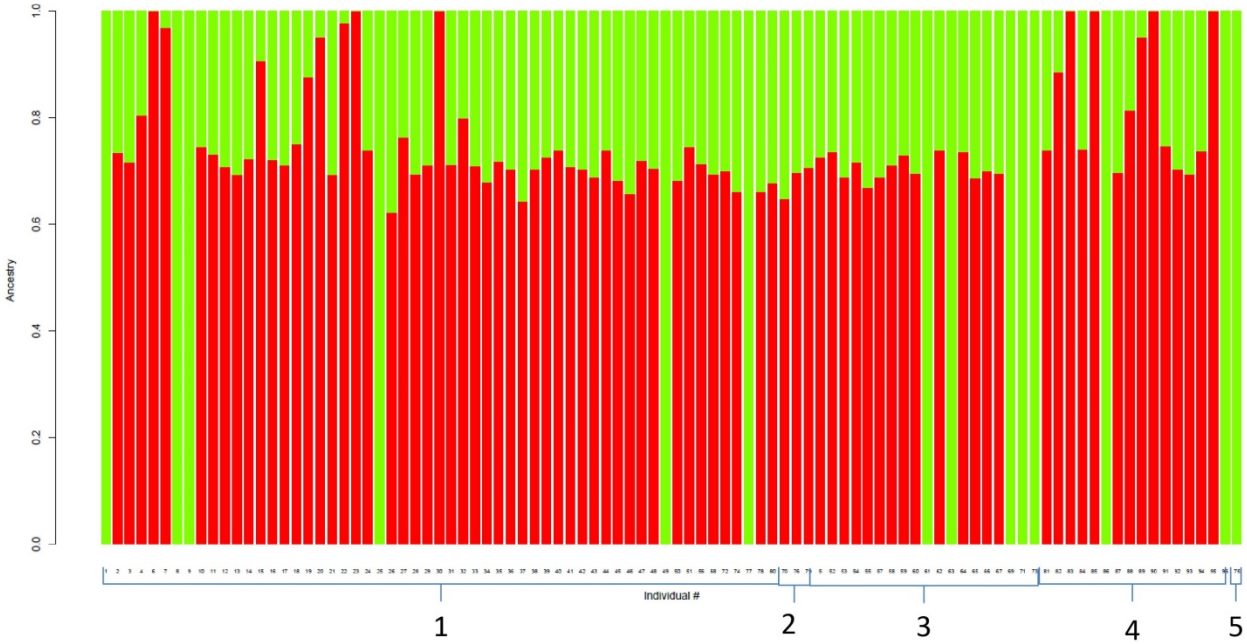
Supplementary Figure 7: Temporal expression patterns of *Osiris 9E*. Temporal expression patterns of *Osiris 9E* with positive standard error of the mean for all the three biological replicates in a given developmental stage. Developmental stages are represented along the x-axis with gene expression, fold difference of *Osi9E* relative to control gene *EF1α*, along the y-axis. Plots show mean ± s.e.m., scaled to the highest value for each species. Individual values, means, and statistical tests are in Supplementary Table 6.



Supplementary Figure 8: Spatial expression patterns of *Osiris 9E*. Spatial expression patterns of *Osiris 9E* with positive standard error of the mean for all the three biological replicates in the larval 3rd instar of *P. rapae*. Various parts of the body are represented along the x-axis with gene expression, fold difference of *Osi9E* relative to control gene *EF1α*, along the y-axis. Plots show mean ± s.e.m., scaled to the highest value. Individual values, means, and statistical tests are in Supplementary Table 7.

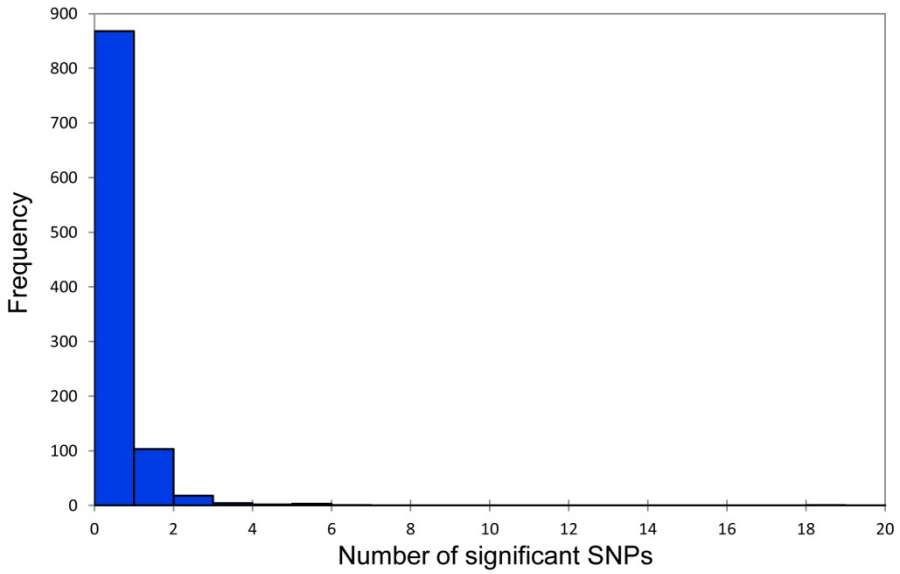


Supplementary Figure 9: *P. rapae* GWAS samples PCA plot. A PCA plot of the *P. rapae* samples used in the GWAS shows evidence of some population genetic structure but not associated with sampling location or sequencing coverage. The minimum and maximum sequencing coverage depth is shown for each group.



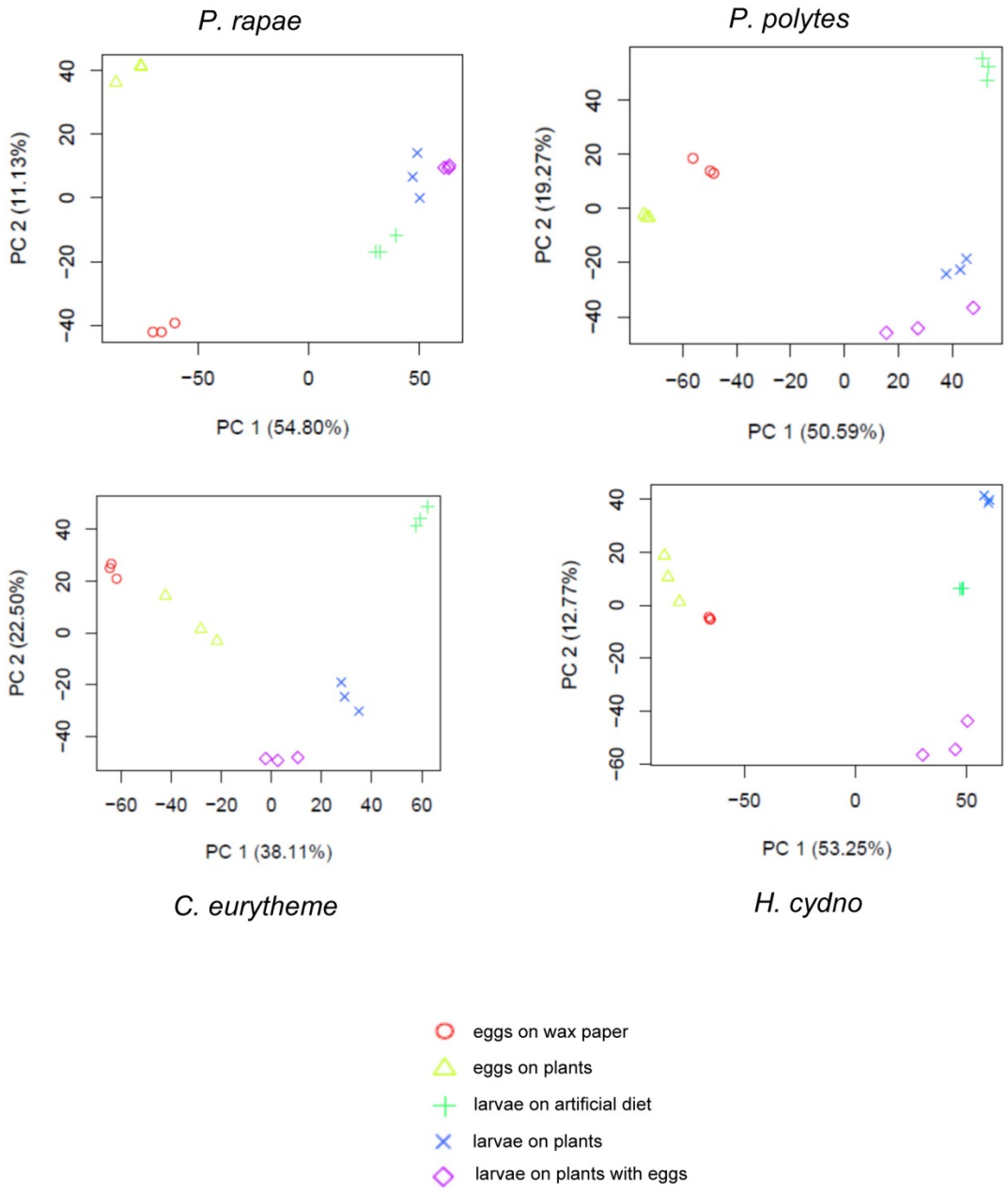
Group#	Location	Mean Sequencing Depth (X)	Std Sequencing Depth (X)
1	University of Chicago, IL	14.5407	4.759554
2	Chicago downtown, IL	13.22667	2.620636
3	Schaumburg, IL	12.93421	3.777232
4	Langdon, ND	12.1725	4.642329
5	Carolina Biological Supply, NC	11.55	NA
Green	NA	11.95143	3.753931
Red	NA	14.0639	4.607565

Supplementary Figure 10: *P. rapae* GWAS samples Admixture plot. An Admixture plot of the *P. rapae* samples used in the GWAS shows evidence of some population genetic structure but not associated with sampling location or sequencing coverage. The plot was generated using K =2, which had the lowest cross-validation error compared to other values of K. The samples are grouped according to sampling location, and the mean and the standard deviation of the sequencing coverage of every group are shown.

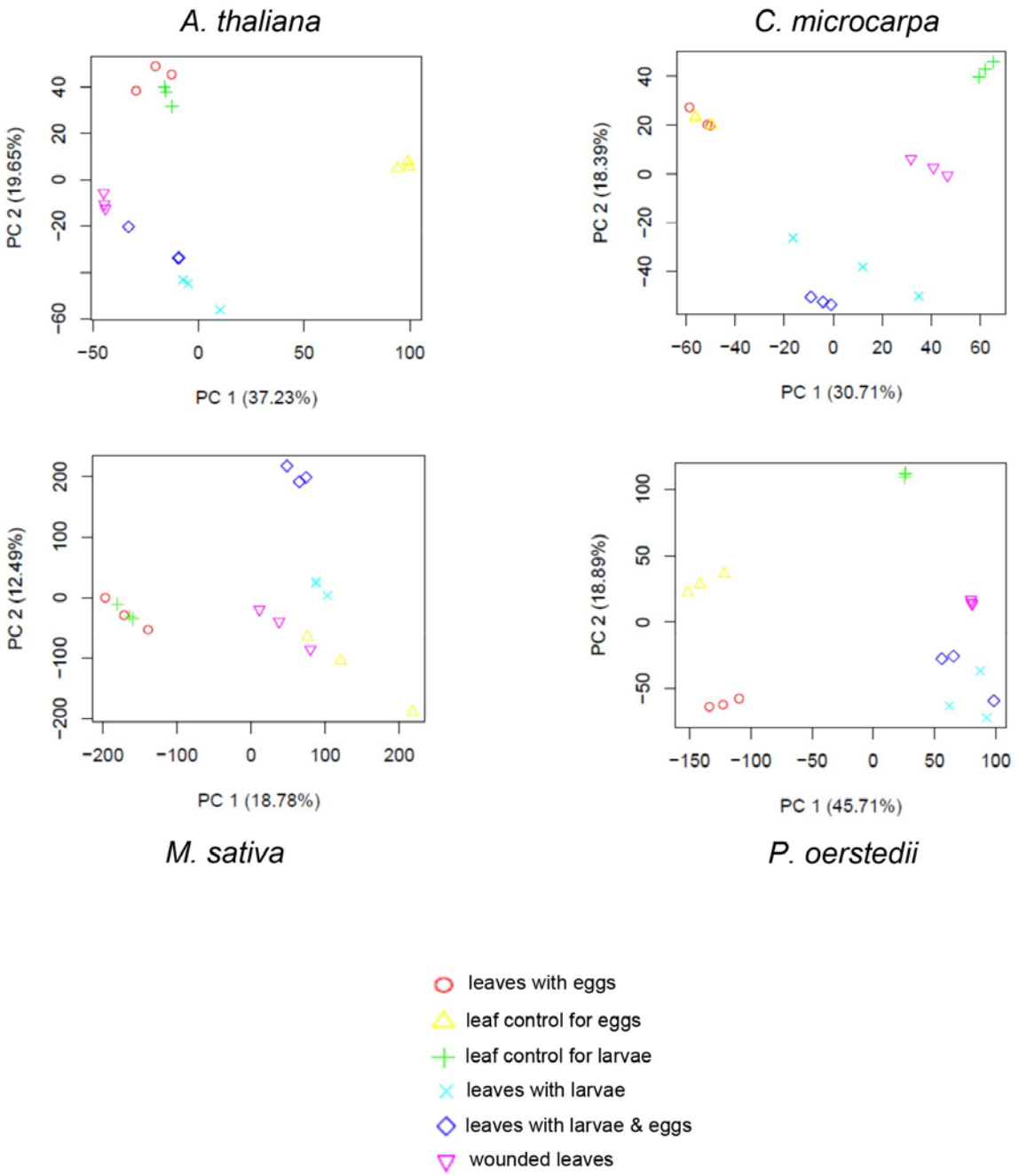


Number significant SNPs	Frequency
0	868
1	103
2	18
3	4
4	2
5	3
6	1
7	0
8	0
9	0
10	0
11	0
12	0
13	0
14	0
15	0
16	0
17	0
18	1

Supplementary Figure 11: *P. rapae* GWAS permutation test. Number of significant SNPs at our empirical significance threshold from association tests that were repeated 1,000 times with randomized phenotype data.



Supplementary Figure 12: PCA plots of plant RNA-seq data. PCA plots displaying the correlation among samples and treatments from the RNA-seq experiments from all four plants species.



Supplementary Figure 13: PCA plots of butterfly RNA-seq data. PCA plots displaying the correlation among samples and treatments from the RNA-seq experiments from all four butterfly species.