

Supplementary Materials: Comparisons of Transcriptional Profiles of Gut Genes between Cry1Ab-Resistant and Susceptible Strains of *Ostrinia nubilalis* Revealed Genes Possibly Related to the Adaptation of Resistant Larvae to Transgenic Cry1Ab Corn

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Table S1. The complete list of gut genes in R- and S-strain larvae of *O. nubilalis* with significantly differential expression after fed transgenic Cry1Ab corn leaves as compared with those fed non-transgenic corn (control) leaves.

EST ID	GenBank EST ID #	E-Value	Sequence Description	Expression Ratio *	
				S:Cry1Ab Corn	R:Cry1Ab Corn
Trypsin, chymotrypsin					
Contig[0039]	GH997464.1	0.0	trypsin serine protease (<i>Ostrinia furnacalis</i>)	-3.63	-2.01
Contig[0113]	GH998291	2.45 × 10 ⁻⁶⁹	trypsin (<i>Helicoverpa armigera</i>)		-4.67
Contig[0130]	GH999462.1	1.07 × 10 ⁻⁸⁸	chymotrypsin-like protease C3 (<i>Heliothis virescens</i>)	-2.95	
Contig[0147]	GH998279.1	7.20 × 10 ⁻¹⁰⁴	chymotrypsin (<i>Helicoverpa armigera</i>)	-2.28	
Contig[0243]	GH998064.1	1 × 10 ⁻¹⁷⁴	trypsin-like serine protease 12 (<i>Ostrinia nubilalis</i>)	-9.02	-5.89
Contig[2151]	GH996088.1	1.26 × 10 ⁻³⁹	larval chymotrypsin-like protein precursor (<i>Aedes aegypti</i>)	-3.71	
Contig[0293]	GH997809	7.89 × 10 ⁻⁷¹	trypsin-like serine proteinase t26	-3.22	
Contig[0573]	GH999314.1	3.39 × 10 ⁻⁸⁴	chymotrypsin-like serine protease	-2.47	
Contig[0578]	GH996481.1	4.69 × 10 ⁻¹⁰⁰	trypsin-like serine proteinase t26	-4.68	-2.52
Contig[1519]	GH999020.1	8.46 × 10 ⁻⁸⁴	chymotrypsin-like protease		-2.26
Contig[3118]	GH990367	4.65 × 10 ⁻⁵⁷	trypsin-like serine proteinase t26	-3.05	
Contig[3466]	GH997407	1.69 × 10 ⁻⁵⁵	trypsin-like serine protease	-2.88	
ECB-C-18_B11	GH994018	7.13 × 10 ⁻¹¹⁴	silk gland derived serine protease	-3.00	
Contig[4021]	GH987247.1	1.03 × 10 ⁻¹⁰⁹	chymotrypsin-like serine protease	-2.57	
ECB-C-13_A03	GH993568.1	5.60 × 10 ⁻⁷	chymotrypsin-C-like (<i>Meleagris gallopavo</i>)		-2.30
J-ECB-52_A02	GH987844.1	3.93 × 10 ⁻⁸	serine protease inhibitor 3 (<i>Tabanus yao</i>)	10.71	
J-ECB-08_D11	GH992096.1	3.97 × 10 ⁻²⁷	putative protease inhibitor 4 (<i>Lonomia obliqua</i>)	19.48	
Contig[1913]	GH997417.1	4.00 × 10 ⁻¹²⁰	serpin-2 (<i>Bombyx mandarina</i>)	2.13	
aminopeptidase					
Contig[1398]	GH993761.1	0.0	aminopeptidase N	-2.32	2.05
Contig[4776]	GH998970.1	0.0	aminopeptidase N	2.59	2.31
Contig[5112]	GH997440.1	0.0	aminopeptidase N	-2.90	-2.32
ECB-V-02_D07	GH994338	2.20 × 10 ⁻⁹⁹	aminopeptidase N	-3.50	

ECB-V-05_D12	GH994609	2.03×10^{-112}	aminopeptidase N	-3.28	
J-ECB-41_F04	GH988241	2.06×10^{-61}	aminopeptidase N		2.09
carboxylesterase and carboxypeptidase					
Contig[0266]	GH999150.1	2.63×10^{-170}	carboxylesterase-11	-2.61	
Contig[0115]	GH997328.1	2.13×10^{-80}	carboxylesterase (<i>Loxostege sticticalis</i>)	25.18	
Contig[1179]	GH995965.1	1.22×10^{-75}	carboxylesterase		-2.84
Contig[3820]	GH999448.1	1.80×10^{-99}	carboxylesterase	-2.67	
Contig[4729]	GH992299.1	4.59×10^{-70}	carboxylesterase	-17.96	
Contig[5372]	GH998289.1	1.90×10^{-98}	carboxylesterase-11	-2.69	
Contig[5691]	GH990344.1	6×10^{-56}	carboxyl/choline esterase (<i>Helicoverpa armigera</i>)	-10.91	-4.57
ECB-V-21_D08	GH995856.1	1.14×10^{-21}	carboxylesterase	-4.55	
J-ECB-07_G03	GH991809.1	1.95×10^{-7}	carboxylesterase	16.37	
J-ECB-09_D02	GH992373.1	4.32×10^{-105}	carboxylesterase (<i>Spodoptera litura</i>)	-2.86	
Contig[5791]	EL929195.1	3.92×10^{-39}	carboxyl/choline esterase CCE021b (<i>Helicoverpa armigera</i>)		-2.87
ECB-27_F04	GH999378.1	3.26×10^{-86}	carboxyl choline esterase cce006b	-2.71	
Contig[2666]	GH990614.1	2.47×10^{-83}	carboxypeptidase A		-2.82
Contig[3400]	GH997499.1	5.15×10^{-52}	zinc carboxypeptidase A 1	-2.79	
Contig[3637]	GH997603.1	5.71×10^{-75}	carboxypeptidase C (<i>Culicoides sonorensis</i>)	-2.35	
Contig[3784]	GH997291.1	4.64×10^{-76}	midgut carboxypeptidase (<i>Loxostege sticticalis</i>)	-2.21	
ECB-V-29_E10	GH996536.1	3×10^{-20}	midgut carboxypeptidase 2 (<i>Danaus plexippus</i>)	-17.64	-4.19
J-ECB-42_B07	GH988427.1	6.87×10^{-40}	zinc carboxypeptidase A 1 (<i>Culex quinquefasciatus</i>)	-2.37	
Contig[0077]	GH998660.1	1.94×10^{-165}	carboxypeptidase 4 (<i>Mamestra configurata</i>)	-2.12	
Contig[0009]	GH992549.1	8×10^{-78}	zinc carboxypeptidase A 1 (<i>Danaus plexippus</i>)	-3.85	-2.09
Contig[0019]	GH998697.1	3×10^{-106}	plasma glutamate carboxypeptidase (<i>Danaus plexippus</i>)	-6.65	-2.28
Contig[3603]	GH993634.1	1.37×10^{-115}	cathepsin b	2.98	
Chitin related transcripts					
Contig[0505]	GH998325.1	0.0	chitin binding PM protein (<i>Helicoverpa armigera</i>)	-3.3	-2.43
Contig[0188]	GH997506.1	0.0	chitinase (<i>Ostrinia nubilalis</i>)	-6.00	
Contig[4654]	GH996835.1	2.28×10^{-65}	peritrophic membrane chitin binding protein (<i>Loxostege sticticalis</i>)	-2.39	
Contig[0233]	GH989367.1	1.25×10^{-66}	chitin deacetylase 2 (<i>Mamestra brassicae</i>)	-2.60	-2.44
ECB-C-05_D05	GH992955.1	6.25×10^{-21}	glucosamine-fructose-6-phosphate aminotransferase 2 (<i>Culex quinquefasciatus</i>)	-2.88	-2.10
Contig[4598]	GH998948.1	4.98×10^{-95}	glucosamine-6-phosphate N-acetyltransferase (<i>Bombyx mori</i>)		2.26
Signal transduction					
Contig[3760]	GH992475.1	5.95×10^{-96}	small GTP-binding protein (<i>Bombyx mori</i>)	2.24	
ECB-14_B10	GH998220.1	2.17×10^{-16}	protein kinase c inhibitor (<i>Bombyx mori</i>)		3.48
J-ECB-37_F07	GH991243.1	1.50×10^{-56}	receptor for activated protein kinase C (<i>Helicoverpa armigera</i>)	2.76	

J-ECB-33_E10	GH989160.1	4.58×10^{-51}	ATP-binding cassette sub-family B member 1 (<i>Trichoplusia ni</i>)	2.59	
J-ECB-10_B09	GH988438.1	4.06×10^{-22}	Oxidative stress-induced growth inhibitor 1 (<i>Camponotus floridanus</i>)	-2.36	
ECB-V-27_D10	GH996357.1	9.61×10^{-64}	Hypoxia up-regulated protein 1 (<i>Acromyrmex echinator</i>)		-2.59
Contig[5194]	GH993661.1	8.21×10^{-79}	signal sequence receptor (<i>Biston betularia</i>)		-2.18
ECB-30_C02	GH999600.1	4.24×10^{-79}	signal sequence receptor β subunit (<i>Bombyx mori</i>)		-2.35
Transcription regulator factors					
Contig[5330]	GH990640.1	2.39×10^{-54}	Rho GTPase activating protein, putative (<i>Pediculus humanus corporis</i>)		2.94
Contig[3833]	GH993952.1	8.94×10^{-20}	DNA-binding nuclear protein p8 (<i>Simulium guianense</i>)		3.78
ECB-09_F07	GH997837.1	1.68×10^{-65}	Rho GTPase-activating protein 12-like (<i>Acyrtosiphon pisum</i>)	2.70	2.76
ECB-V-14_D07	GH995295.1	5×10^{-11}	Reverse transcriptase (<i>Ostrinia nubilalis</i>)	2.30	2.22
Heat shock protein					
Contig[0227]	GH997898.1	0.0	heat shock protein 70	2.36	2.06
Contig[2669]	GH990174.1	6.38×10^{-99}	heat shock cognate 70 protein		-2.65
gi_133905913	EL928755	1.21×10^{-17}	heat shock cognate 70 protein (<i>Loxostege sticticalis</i>)		-2.97
J-ECB-29_F11	GH992461.1	5.73×10^{-75}	heat shock protein hsp23.7 (<i>Bombyx mori</i>)		-14.3
Transporter					
Contig[0814]	GH998546.1	1×10^{-27}	sodium-bile acid cotransporter	-14.14	-4.21
Contig[1314]	GH993616.1	2×10^{-73}	putative amino acid transporter (<i>Danaus plexippus</i>)	-3.80	-2.52
Contig[4763]	GH998142.1	2×10^{-65}	sodium-bile acid cotransporter	-10.83	-6.56
Contig[5496]	GH998547.1	2×10^{-103}	sugar transporter	-2.66	-2.36
Contig[5743]	GH993678.1	7×10^{-97}	sodium chloride dependent amino acid transporter	-3.96	-2.55
ECB-16_F07	GH998441.1	4.45×10^{-57}	sodium-dependent phosphate transporter	-5.51	2.83
ECB-21_C09	GH998857.1	6.29×10^{-30}	sugar transporter	-4.90	-2.12
ECB-22_H11	GH998995.1	1.20×10^{-78}	Sodium- and chloride-dependent glycine transporter 2 (<i>Harpegnathos saltator</i>)		-2.45
ECB-V-21_D11	GH995859.1	1.47×10^{-26}	monocarboxylate transporter		-2.21
ECB-V-22_E06	GH995942.1	1.46×10^{-83}	GDP-fucose transporter, putative (<i>Nasonia vitripennis</i>)	2.02	2.39
gi_133906576	EL929414	3.68×10^{-30}	ATP-binding cassette transporter subfamily B (<i>Bombyx mori</i>)		-2.39
J-ECB-39_E12	GH992066.1	3.41×10^{-15}	sugar transporter (<i>Anopheles darlingi</i>)	-9.56	-4.34
J-ECB-52_H10	GH988032.1	3.05×10^{-17}	monocarboxylate transporter	-3.30	-2.13
J-ECB-42_F09	GH988676.1	3.01×10^{-7}	zinc transporter foi-like isoform 2 (<i>Apis mellifera</i>)		6.84
J-ECB-55_E04	GH988996.1	6.00×10^{-38}	monocarboxylate transporter	-3.62	-3.88
Contig[3828]	GH993919.1	2.85×10^{-22}	transport protein Sec61 γ subunit (<i>Bombyx mori</i>)		-2.07
Xenobiotics detoxification enzyme					
Contig[4722]	GH997947.1	1.40×10^{-87}	cytochrome P450 CYP6AB4 (<i>Bombyx mandarina</i>)	-2.93	
Contig[5056]	GH995380.1	7.10×10^{-25}	cytochrome P450		2.14

Contig[5080]	GH996933.1	9.88×10^{-95}	cytochrome P450 monooxygenase cyp4m5		3.84
ECB-C-03_D08	GH992802.1	3×10^{-106}	cytochrome P450 (<i>Spodoptera litura</i>)		2.62
J-ECB-10_F11	GH988695.1	3.50×10^{-50}	cytochrome P450	2.38	
J-ECB-21_B02	GH988756.1	2.52×10^{-99}	cytochrome P450	-3.34	
Contig[0004]	GH992504.1	4.79×10^{-52}	glutathione S-transferase (<i>Choristoneura fumiferana</i>)	-8.76	-2.95
Contig[0012]	GH987677.1	5.36×10^{-54}	microsomal glutathione transferase (<i>Heliothis virescens</i>)		-2.59
Antibacterial related proteins					
gi_133905829	EL928679	1.82×10^{-13}	hinnavin II (<i>Pieris rapae</i>)	11.84	
Contig[5720]	GH993782.1	1.08×10^{-93}	immune-related Hdd13 (<i>Hyphantria cunea</i>)	-2.41	
Contig[4668]	GH989903.1	5.75×10^{-63}	peptidoglycan recognition protein		-2.84
J-ECB-60_D07	GH987186.1	1.88×10^{-24}	antibacterial protein (<i>Heliothis virescens</i>)		3.49
Other metabolic enzymes					
BM2_D02	GH992543.1	6.85×10^{-60}	lipase	-2.90	
Contig[0016]	GH997476.1	1.25×10^{-84}	lipase 1 precursor	-2.56	
Contig[0029]	GH998728.1	2.12×10^{-104}	gastric lipase-like protein (<i>Epiphyas postvittana</i>)	-5.44	
Contig[0140]	GH998810.1	7×10^{-136}	pancreatic lipase-related protein 2-like (<i>Bombyx mori</i>)		-11.58
Contig[0450]	GH997309.1	1.24×10^{-121}	lipase	-4.71	
Contig[0923]	GH999509.1	7.84×10^{-80}	lipase	-7.96	-10.45
Contig[1081]	GH998825.1	6.98×10^{-55}	pancreatic lipase-like protein (<i>Epiphyas postvittana</i>)	-4.83	-5.02
Contig[2857]	GH998380.1	2.58×10^{-124}	lipase	-3.19	
Contig[4980]	GH998599.1	1.22×10^{-55}	lipase 1 precursor		-2.69
Contig[5664]	GH997481.1	1.40×10^{-47}	lipase	-4.33	
ECB-07_C04	GH997675.1	4.43×10^{-23}	Lipase 1 (<i>Camponotus floridanus</i>)	-4.64	
J-ECB-56_D02	GH989456.1	2.80×10^{-21}	Gastric triacylglycerol lipase (<i>Camponotus floridanus</i>)	-4.57	
Contig[1486]	GH997709.1	1.25×10^{-63}	c-5 sterol desaturase erg32-like (<i>Bombyx mori</i>)	-7.75	-2.79
Contig[1897]	GH997709.1	9.20×10^{-92}	c-5 sterol desaturase erg32-like (<i>Bombyx mori</i>)	-7.03	-2.13
ECB-V-05_B10	GH994560.1	7.96×10^{-116}	acyl-CoA-Δ9-3a-desaturase (<i>Dendrolimus punctatus</i>)		-2.19
ECB-C-20_B10	GH994173.1	1.50×10^{-68}	carbohydrate kinase-like (<i>Tribolium castaneum</i>)	-2.37	
J-ECB-61_C03	GH987254.1	7.52×10^{-47}	UDP-glucosyltransferase (<i>Bombyx mori</i>)	2.57	2.08
ECB-V-19_F07	GH995711.1	1.06×10^{-52}	UDP-glucosyltransferase (<i>Bombyx mori</i>)	2.87	
J-ECB-30_H09	GH988109.1	1×10^{-120}	Myrosinase 1 (<i>Papilio xuthus</i>)	-4.16	
ECB-C-14_E07	GH993705.1	2.07×10^{-77}	β-glucosidase precursor (<i>Spodoptera frugiperda</i>)	-5.25	
J-ECB-15_G11	GH990690.1	3.69×10^{-43}	putative 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (<i>Danaus plexippus</i>)	2.65	2.42
Contig[0075]	GH997236.1	5.55×10^{-143}	glycoside hydrolases	-3.44	
Contig[0700]	GH998843.1	2.36×10^{-121}	sucrose-6-phosphate hydrolase	-2.98	
Contig[0911]	GH999492.1	3.62×10^{-153}	juvenile hormone epoxide hydrolase	-2.39	
Contig[4515]	GH987646.1	2.23×10^{-70}	γ-glutamyl hydrolase	-2.56	-2.49

Contig[4896]	GH998937.1	3×10^{-134}	epoxide hydrolase 3-like (<i>Plutella xylostella</i>)	-2.65	
Contig[5232]	GH987506.1	8.08×10^{-57}	glycoside hydrolases	-29.36	
Contig[4425]	GH988573.1	4.78×10^{-105}	enolase	-2.36	
J-ECB-46_D03	GH990544.1	4.07×10^{-54}	ubiquitin carboxyl-terminal hydrolase 14-like isoform 1 (<i>Bombus terrestris</i>)	2.42	
J-ECB-33_G12	GH989302.1	1.24×10^{-95}	juvenile hormone epoxide hydrolase-like protein 1 (<i>Bombyx mori</i>)	-6.20	
J-ECB-50_D10	GH987676.1	9.67×10^{-85}	glycoside hydrolases	-5.16	
J-ECB-58_H02	GH990678.1	1.85×10^{-115}	platelet-activating factor acetyl-hydrolase isoform 1b α subunit (<i>Aedes aegypti</i>)	2.16	
BM2_B12	GH992538.1	2.23×10^{-48}	hydroxysteroid (17- β) dehydrogenase 8	-2.24	-2.30
Contig[0022]	GH992601.1	2.89×10^{-53}	alcohol dehydrogenase	-6.41	-2.36
Contig[0030]	GH997149.1	0.0	aldehyde dehydrogenase, mitochondrial	-2.88	
Contig[0231]	GH997486.1	3.12×10^{-64}	short-chain dehydrogenase		-3.25
Contig[1778]	GH994839.1	1.56×10^{-57}	acyl-CoA dehydrogenase	-2.50	-2.63
Contig[3532]	GH997374.1	0.0	Isocitrate dehydrogenase (NADP), mitochondrial (<i>Papilio xuthus</i>)	-3.13	
Contig[3814]	GH994966.1	2.32×10^{-112}	alcohol dehydrogenase (<i>Bombyx mori</i>)	-3.07	
Contig[4310]	GH997290.1	1.82×10^{-56}	3-hydroxybutyrate dehydrogenase type 2	-2.11	
Contig[5289]	GH990630.1	9.57×10^{-26}	isovaleryl coenzyme A dehydrogenase (<i>Heliothis virescens</i>)	-5.68	
ECB-01_G12	GH997221.1	4.02×10^{-146}	zinc-containing alcohol dehydrogenase (<i>Bombyx mori</i>)		2.17
ECB-14_D05	GH998238.1	8.51×10^{-63}	aldehyde dehydrogenase (<i>Heliothis virescens</i>)	-3.09	
gi_133906638	EL929475	8.18×10^{-30}	retinol dehydrogenase (<i>Heliothis virescens</i>)	-10.53	-10.95
Contig[0362]	GH997850.1	2.85×10^{-89}	carbonyl reductase	-4.82	-2.14
Contig[1032]	GH999460.1	5.61×10^{-15}	γ -interferon inducible lysosomal thiol reductase (<i>Glossina morsitans</i>)	-2.48	
Contig[2754]	GH997997.1	2.30×10^{-79}	carbonyl reductase	2.51	
Contig[4521]	GH989023.1	8.07×10^{-98}	aldo-keto reductase		-27.07
Contig[5655]	GH996386.1	3.83×10^{-79}	lysosomal thiol reductase IP30 isoform 2 (<i>Bombyx mori</i>)		-2.29
Others					
Contig[0308]	GH997849.1	1.26×10^{-21}	peritrophin type-A domain protein 2 (<i>Mamestra configurata</i>)		-5.72
Contig[0218]	GH998427.1	1.48×10^{-117}	NADPH cytochrome b5 reductase (<i>Spodoptera exigua</i>)	-2.14	-2.02
Contig[5933]	GH997219.1	2.23×10^{-07}	Abhydrolase domain-containing protein 4 (<i>Harpegnathos saltator</i>)	2.38	
Contig[3484]	GH987848.1	3.95×10^{-54}	mitochondrial cytochrome c (<i>Bombyx mori</i>)		-2.65
Contig[1432]	GH994698.1	5.19×10^{-133}	catalase (<i>Bombyx mori</i>)	-2.36	
Contig[1310]	GH993550.1	1.51×10^{-78}	uridine phosphorylase (<i>Aedes aegypti</i>)	-2.30	
Contig[5679]	GH988679.1	3.47×10^{-81}	phosphoserine aminotransferase	-4.08	-3.26

Contig[0098]	EL929505.1	2.72×10^{-6}	JHBP-like protein (<i>Diploptera punctata</i>)	-3.76	
Contig[0165]	GH998248.1	1.66×10^{-78}	actin depolymerizing factor	2.26	
Contig[0241]	GH997622.1	6.80×10^{-12}	conserved hypothetical protein (<i>Culex quinquefasciatus</i>)	2.16	
Contig[0382]	GH998342.1	0.0	β -1,3-glucanase (<i>Helicoverpa armigera</i>)	-2.21	
Contig[0407]	GH997662.1	3.18×10^{-31}	sensory appendage protein 3 (<i>Manduca sexta</i>)		-57.87
Contig[0535]	GH990867.1	4.20×10^{-8}	hypothetical protein AaeL_AAEL009036 (<i>Aedes aegypti</i>)	-2.71	-2.53
Contig[0810]	GH999215.1	2.25×10^{-150}	calreticulin (<i>Galleria mellonella</i>)		-3.37
Contig[0827]	GH996906.1	2.72×10^{-21}	Ankyrin repeat domain protein Wolbachia endosymbiont of (<i>Culex quinquefasciatus</i>)	-3.26	
Contig[0924]	GH999510.1	4.70×10^{-46}	carbonic anhydrase (<i>Aedes aegypti</i>)	-2.12	
Contig[0976]	GH987290.1	1.92×10^{-120}	ferritin (<i>Manduca sexta</i>)	-2.33	
Contig[1250]	GH992423.1	3.90×10^{-44}	aquaporin	-2.47	
Contig[1305]	GH998434.1	0.0	angiotensin converting enzyme (<i>Spodoptera littoralis</i>)	-2.19	
Contig[1573]	GH997739.1	9.41×10^{-14}	hypothetical conserved protein	2.27	2.76
Contig[1640]	GH991677.1	7.33×10^{-26}	fatty acid-binding protein-like (<i>Bombus terrestris</i>)	-2.76	
Contig[1868]	GH995418.1	1.16×10^{-43}	ER protein reticulon (<i>Aedes aegypti</i>)	2.74	2.21
Contig[1880]	GH995131.1	1.46×10^{-6}	adipokinetic 3 (<i>Helicoverpa armigera</i>)	5.46	4.09
Contig[1953]	GH997798.1	3×10^{-145}	prostaglandin reductase 1-like (<i>Papilio xuthus</i>)	-2.71	-2.51
Contig[2576]	GH992555.1	5×10^{-91}	hypothetical protein g.11100 (<i>Pectinophora gossypiella</i>)	-3.03	
Contig[2896]	GH987914.1	4.35×10^{-58}	lipid storage droplets surface binding protein 2	2.98	
Contig[2947]	GH992278.1	3.52×10^{-52}	high-affinity copper uptake protein	-5.88	
Contig[3004]	GH990119.1	2.66×10^{-89}	β lactamase domain	-5.38	
Contig[3035]	GH997788.1	7.67×10^{-47}	anterior fat body protein	-12.82	
Contig[3237]	GH992782.1	5.35×10^{-86}	dipeptidyl peptidase 4	-2.74	
Contig[3266]	GH987418.1	2×10^{-6}	hypothetical protein RR48_06180 (<i>Papilio machaon</i>)	-3.02	
Contig[3372]	GH987678.1	2.75×10^{-15}	macrophage migration inhibitory factor	4.26	
Contig[3454]	GH987480.1	4.99×10^{-15}	α 1,3-fucosyltransferase C (<i>Apis mellifera</i>)	2.30	
Contig[3515]	GH994781.1	3.96×10^{-18}	uncharacterized protein LOC101737697 (<i>Bombyx mori</i>)	-3.17	-2.37
Contig[3585]	GH988106.1	7.56×10^{-91}	glutathione peroxidase	2.14	
Contig[3619]	GH992525.1	2.24×10^{-6}	takeout/JHBP-like protein (<i>Diploptera punctata</i>)	-3.65	
Contig[3674]	GH998445.1	5.16×10^{-60}	bcr-associated protein, bap (<i>Aedes aegypti</i>)	3.15	
Contig[3708]	GH991311.1	4.46×10^{-95}	muscle protein 20-like protein (<i>Papilio xuthus</i>)	2.15	
Contig[3740]	GH988393.1	2.25×10^{-89}	FK506-binding protein (<i>Bombyx mori</i>)		-3.83
Contig[5365]	GH993317.1	6.23×10^{-69}	tetraspanin 2A, isoform A (<i>Drosophila melanogaster</i>)	2.22	
Contig[5386]	GH996141.1	2.52×10^{-32}	tetraspanin E118 (<i>Bombyx mori</i>)	2.34	2.04
ECB-C-04_H06	GH992916.1	4.23×10^{-75}	tetraspanin d107	4.16	2.99
Contig[3869]	GH997175.1	4.22×10^{-49}	creg1 precursor(Cellular repressor of E1A-stimulated genes 1) (<i>Tribolium castaneum</i>)		-2.18

Contig[4000]	GH997153.1	1.31×10^{-59}	ryanodine receptor-like protein (<i>Phlebotomus papatasi</i>)	2.28	
Contig[4287]	GH991765.1	3.21×10^{-125}	β -tubulin (<i>Bombyx mori</i>)	2.56	
Contig[4527]	GH989618.1	1.58×10^{-17}	conserved hypothetical protein (<i>Culex quinquefasciatus</i>)	-15.05	-5.28
Contig[4714]	GH990109.1	3.94×10^{-21}	similar to X box binding protein-1 CG9415-PA (<i>Tribolium castaneum</i>)	2.73	2.28
Contig[4784]	GH992658.1	1.55×10^{-60}	leucine repeat-rich protein (<i>Heliconius melpomene melpomene</i>)		2.83
Contig[4916]	GH990108.1	4.27×10^{-16}	hypothetical protein TcasGA2_TC002334 (<i>Tribolium castaneum</i>)		3.60
Contig[5038]	GH991382.1	2.82×10^{-20}	MBF2 (<i>Samia cynthia</i>)		2.39
Contig[5045]	GH998223.1	5.41×10^{-84}	ubiquitin-conjugating enzyme rad6 (<i>Aedes aegypti</i>)	2.02	
Contig[5050]	GH993665.1	9.36×10^{-10}	salivary secreted peptide-like (<i>Bombyx mori</i>)	2.94	4.92
Contig[5114]	GH997529.1	4.37×10^{-100}	xaa-pro dipeptidase peptidase (<i>Aedes aegypti</i>)	-2.08	
Contig[5119]	GH997971.1	7.17×10^{-58}	similar to CG3625 CG3625-PB isoform 2 (<i>Tribolium castaneum</i>)	-2.63	-3.78
Contig[5123]	GH998229.1	1.19×10^{-69}	Abl interactor 2 (<i>Harpegnathos saltator</i>)		2.41
Contig[5133]	GH999457.1	9.52×10^{-78}	myosin light chain 2 (<i>Antheraea pernyi</i>)	2.98	
Contig[5136]	GH992820.1	2.79×10^{-101}	ceramidase (<i>Aedes aegypti</i>)	-2.90	
Contig[5143]	GH995296.1	3.51×10^{-49}	ctl2 (<i>Aedes aegypti</i>)	2.25	2.17
Contig[5148]	GH992405.1	7.10×10^{-42}	Coronin-2B (<i>Harpegnathos saltator</i>)	2.79	
Contig[5168]	GH989763.1	4.13×10^{-124}	tropomyosin-1 (<i>Bombyx mori</i>)	3.64	
Contig[5228]	GH988628.1	1.21×10^{-130}	putative C1A cysteine protease precursor (<i>Manduca sexta</i>)	2.31	3.42
Contig[5259]	GH997723.1	6.74×10^{-40}	dipeptidyl-peptidase (<i>Aedes aegypti</i>)	-3.10	
Contig[5301]	GH998943.1	1.45×10^{-48}	insect intestinal mucin 3 (<i>Helicoverpa armigera</i>)	-2.40	
Contig[5397]	GH991289.1	9.12×10^{-61}	astacin (<i>Mamestra configurata</i>)	-4.06	
Contig[5632]	GH989110.1	1.98×10^{-9}	GH18999 (<i>Drosophila grimshawi</i>)		5.40
Contig[5707]	GH994232.1	3.54×10^{-91}	myosin light polypeptide 9 isoform B (<i>Bombyx mori</i>)	2.28	2.53
Contig[5715]	GH997945.1	1.68×10^{-151}	alkaline nuclease (<i>Bombyx mori</i>)	-3.70	-2.54
Contig[5729]	GH990820.1	6.31×10^{-78}	SEC14-like protein 2-like (<i>Apis mellifera</i>)	-4.23	-2.79
Contig[5744]	GH997656.1	1.27×10^{-06}	363_100_1 protein (<i>Mamestra configurata</i>)		-2.67
Contig[5800]	GH991870.1	1.26×10^{-16}	larval cuticle protein 14 (<i>Manduca sexta</i>)	3.14	
Contig[5826]	GH999419.1	7.07×10^{-68}	troponin I (<i>Loxostege sticticalis</i>)	2.57	
Contig[5837]	GH992838.1	6.81×10^{-15}	unknown unsecreted protein (<i>Papilio xuthus</i>)	2.54	3.09
Contig[5838]	GH993157.1	2.23×10^{-18}	canopy-1-like (<i>Apis mellifera</i>)		-2.83
Contig[5872]	GH990179.1	7.76×10^{-125}	suppressor of profilin 2 (<i>Papilio polytes</i>)	2.73	2.20
Contig[5929]	GH990692.1	3.96×10^{-5}	unknown (<i>Picea sitchensis</i>)	3.98	2.45
Contig[5975]	GH996882.1	4.78×10^{-5}	SocE (<i>Bacillus cereus</i> W)		-2.94
Contig[6042]	GH996189.1	2.64×10^{-36}	chemosensory protein (<i>Papilio xuthus</i>)	6.71	
ECB-01_G02	GH997211.1	4×10^{-141}	putative actin-related protein 2/3 complex subunit 2 (<i>Papilio xuthus</i>)	2.45	2.10
ECB-02_H03	GH997311.1	4.48×10^{-102}	saposin-like protein (<i>Bombyx mori</i>)	2.84	2.87

ECB-03_E12	GH997370.1	4.71×10^{-64}	DUF233 protein (<i>Heliothis virescens</i>)	9.52	
ECB-11_E02	GH997992.1	5.91×10^{-7}	lipoyltransferase 1, mitochondrial-like isoform X1 (<i>Bombyx mori</i>)	-3.47	-2.34
ECB-11_E06	GH997996.1	2.71×10^{-18}	peroxisomal membrane protein 11C-like (<i>Bombyx mori</i>)	-5.13	-2.69
ECB-12_D10	GH998071.1	1.38×10^{-48}	putative WD repeat domain 13 (Wdr13) (<i>Heliconius melpomene</i>)		2.27
ECB-14_B03	GH998214.1	3.08×10^{-125}	ubiquitin conjugating enzyme E2 (<i>Danaus plexippus</i>)	2.54	2.72
ECB-15_C06	GH998316.1	8.43×10^{-74}	translocon-associated protein γ isoform 2 (<i>Bombyx mori</i>)		-2.54
ECB-16_E08	GH998430.1	3.12×10^{-49}	mitochondrial aminotransferase (<i>Camponotus floridanus</i>)		-2.94
ECB-17_C10	GH998499.1	2.35×10^{-56}	protein disulfide isomerase (<i>Helicoverpa armigera</i>)		-2.60
ECB-18_C11	GH998591.1	3.21×10^{-152}	β -tubulin (<i>Bombyx mori</i>)	3.74	
ECB-18_E05	GH998608.1	1.32×10^{-113}	thioredoxin (<i>Bombyx mori</i>)	2.35	
ECB-19_A07	GH998655.1	6.22×10^{-69}	astacin (<i>Mamestra configurata</i>)	-3.34	
ECB2_C08	GH996766.1	1.76×10^{-26}	farnesyl diphosphate synthase (<i>Bombyx mori</i>)	-2.96	-2.64
ECB-21_E01	GH998872.1	8.95×10^{-13}	CG12926-PA-like protein (<i>Helicoverpa armigera</i>)	-2.48	
ECB-23_E01	GH999038.1	1.57×10^{-30}	α -tocopherol transfer protein-like (<i>Bombus terrestris</i>)	3.63	2.87
ECB-25_G02	GH999219.1	3.13×10^{-38}	CG3862-PA-like protein (<i>Plutella xylostella</i>)	2.09	
ECB-26_F04	GH999292.1	2.98×10^{-74}	Arp2/3 complex p21 subunit (<i>Spodoptera frugiperda</i>)	2.42	
ECB-26_F05	GH999293.1	9.83×10^{-4}	spaghetti squash (<i>Papilio xuthus</i>)	2.26	2.57
ECB-27_B09	GH999338.1	5.92×10^{-33}	ankyrin repeat domain protein	-2.86	
ECB-C-02_F10	GH992743.1	2.71×10^{-108}	Rab32 (<i>Helicoverpa armigera</i>)	2.45	
ECB-C-03_G05	GH992827.1	9.31×10^{-17}	conserved hypothetical protein (<i>Culex quinquefasciatus</i>)	3.32	
ECB-C-04_A08	GH992850.1	3.23×10^{-18}	β -1 tubulin (<i>Spodoptera frugiperda</i>)	3.33	
ECB-C-05_C05	GH992946.1	1.41×10^{-5}	lysine-specific demethylase 6A-like (<i>Bombyx mori</i>)	6.49	5.50
ECB-C-06_B02	GH993009.1	3.22×10^{-15}	hypothetical protein KGM_13045 (<i>Danaus plexippus</i>)	-3.50	-2.68
ECB-C-11_A06	GH993413.1	9.75×10^{-4}	hypothetical protein KGM_21983 (<i>Danaus plexippus</i>)	-4.22	-3.00
ECB-C-12_E09	GH993531.1	7.65×10^{-33}	kinesin-associated protein, putative (<i>Aedes aegypti</i>)	2.14	
ECB-C-13_F05	GH993625.1	1.91×10^{-79}	heterogeneous nuclear ribonucleoprotein A1 (<i>Bombyx mori</i>)	2.28	
ECB-C-14_B06	GH993671.1	1.54×10^{-6}	glycolipid transfer protein (<i>Bombyx mori</i>)		2.55
ECB-C-14_D01	GH993689.1	1.12×10^{-5}	hypothetical protein AND_12479 (<i>Anopheles darlingi</i>)	-2.85	
ECB-C-17_F04	GH993969.1	2.37×10^{-53}	rrm-containing protein seb-4, putative (<i>Pediculus humanus corporis</i>)	-2.12	
ECB-C-20_C09	GH994183.1	5.77×10^{-20}	conserved hypothetical protein (<i>Culex quinquefasciatus</i>)	2.26	
ECB-V-02_E10	GH994349.1	3.62×10^{-60}	scavenger mRNA-decapping enzyme DcpS-like isoform 1 (<i>Apis mellifera</i>)	2.17	
ECB-V-05_D03	GH994574.1	1.09×10^{-43}	Adhesion-regulating molecule 1 precursor (<i>Pediculus humanus corporis</i>)	3.25	2.68
ECB-V-05_G12	GH994609.1	5.33×10^{-45}	ecdysteroid UDP-glucosyltransferase	3.54	
ECB-V-07_C07	GH994728.1	5.67×10^{-10}	hypothetical protein KGM_13882 (<i>Danaus plexippus</i>)	3.37	2.19

ECB-V-07_D03	GH994735.1	2.69×10^{-34}	similar to CG6040 (<i>Papilio polytes</i>)	6.60	6.08
ECB-V-08_G01	GH994850.1	2.44×10^{-66}	conserved hypothetical protein (<i>Culex quinquefasciatus</i>)	2.07	
ECB-V-08_G03	GH994852.1	3.61×10^{-61}	ecdysteroid UDP-glucosyltransferase	3.17	
ECB-V-09_A03	GH994876.1	5.51×10^{-85}	Mps one binder kinase activator-like 1 (<i>Harpegnathos saltator</i>)	2.84	
ECB-V-12_E11	GH995156.1	2.43×10^{-49}	Dipeptidyl peptidase 4 (<i>Harpegnathos saltator</i>)	-3.57	
ECB-V-14_C12	GH995289.1	8.09×10^{-64}	vacuolar protein sorting 37b	2.30	2.82
ECB-V-15_B06	GH995352.1	4.97×10^{-6}	visgun, isoform A (<i>Drosophila melanogaster</i>)	3.52	
ECB-V-15_E06	GH995381.1	8.36×10^{-19}	Receptor expression-enhancing protein 1 (<i>Harpegnathos saltator</i>)	2.18	
ECB-V-18_A08	GH995588.1	1.09×10^{-6}	fatty acid binding protein		-2.79
ECB-V-19_E04	GH995700.1	3.15×10^{-42}	sialic acid synthase-like (<i>Xenopus tropicalis</i>)		2.16
ECB-V-22_G04	GH995962.1	1.42×10^{-9}	CG42837 (<i>Drosophila melanogaster</i>)	-3.14	
ECB-V-23_A09	GH995988.1	3.96×10^{-21}	fatty acid transport protein (<i>Ostrinia scapularis</i>)	-2.41	
ECB-V-23_C10	GH996010.1	8.68×10^{-88}	putative growth hormone regulated TBC protein 1 (<i>Danaus plexippus</i>)	2.27	2.10
ECB-V-23_H01	GH996053.1	3.19×10^{-42}	WW domain binding protein wBP-2 (<i>Glossina morsitans morsitans</i>)	2.42	
ECB-V-25_C10	GH996179.1	6.84×10^{-7}	hypothetical protein CAEBREN_00117 (<i>Caenorhabditis brenneri</i>)	5.91	6.27
ECB-V-25_F09	GH996208.1	2.97×10^{-42}	presqualene diphosphate phosphatase-like (<i>Bombyx mori</i>)	3.46	3.21
ECB-V-26_H03	GH996306.1	1.59×10^{-16}	AMP dependent CoA ligase (<i>Aedes aegypti</i>)	-5.28	
ECB-V-29_B10	GH996506.1	4.72×10^{-57}	farnesyltransferase/geranylgeranyltransferase type I α subunit (<i>Bombyx mori</i>)	2.28	
ECB-V-29_G10	GH996557.1	1.35×10^{-72}	acyl-CoA oxidase (<i>Heliothis virescens</i>)		-2.42
gi_133905779	EL928629	5.08×10^{-16}	vanin-like protein 1	-9.20	-5.67
gi_133906199	EL929039	1.13×10^{-7}	hypothetical protein KGM_15512 (<i>Danaus plexippus</i>)	3.17	2.58
gi_133906407	EL929247	8.35×10^{-35}	kynureninase (<i>Bombyx mori</i>)		-3.30
gi_133906419	EL929259	8.96×10^{-5}	lipophorin receptor protein (<i>Spodoptera litura</i>)	2.63	2.44
gi_133906904	EL929734	1.57×10^{-57}	GK17133 (<i>Drosophila willistoni</i>)	2.12	
gi_133906913	EL929743	3.03×10^{-5}	similar to CG3823 CG3823-PA (<i>Tribolium castaneum</i>)	4.37	
J-ECB-04_E11	GH990310.1	7.43×10^{-77}	sorting nexin (<i>Culex quinquefasciatus</i>)		3.06
J-ECB-05_E12	GH990826.1	9.99×10^{-34}	actin 3 isoform, putative (<i>Tribolium castaneum</i>)		2.38
J-ECB-06_D11	GH991264.1	8.49×10^{-69}	aquaporin (<i>Bombyx mori</i>)	-9.45	-3.20
J-ECB-08_B02	GH991953.1	2.43×10^{-31}	sensory appendage protein 3 (<i>Manduca sexta</i>)		-71.78
J-ECB-11_C08	GH988987.1	5.76×10^{-75}	ADP ribosylation factor-like protein (<i>Phlebotomus papatasi</i>)	2.14	
J-ECB-14_D04	GH989986.1	7.87×10^{-19}	CG2765 CG2765-PA (<i>Tribolium castaneum</i>)		2.49
J-ECB-14_H06	GH990255.1	4.44×10^{-4}	similar to CG14661-PA (<i>Apis mellifera</i>)	6.28	
J-ECB-17_A10	GH991305.1	7.05×10^{-46}	ras-related protein Rab-18-like (<i>Bombyx mori</i>)	2.42	2.36
J-ECB-21_F05	GH989017.1	1.27×10^{-12}	Kunitz-type protease inhibitor precursor (<i>Galleria mellonella</i>)		-4.66
J-ECB-21_G07	GH989088.1	2.34×10^{-26}	leucine-rich repeat-containing protein 70-like (<i>Bombyx mori</i>)	2.55	2.33

J-ECB-24_F10	GH990510.1	1.68×10^{-71}	p94-like protein		3.83
J-ECB-24_G10	GH990570.1	1.75×10^{-32}	putative midgut protein (<i>Phlebotomus perniciosus</i>)	4.16	
J-ECB-25_A10	GH990720.1	7.12×10^{-37}	2-acylglycerol O-acyltransferase 1 (<i>Harpegnathos saltator</i>)	-2.23	
J-ECB-25_D01	GH990842.1	1.34×10^{-43}	myelin proteolipid (<i>Biston betularia</i>)	2.29	
J-ECB-29_G03	GH992468.1	5.86×10^{-69}	IST1 homolog (<i>Bombyx mori</i>)	5.72	6.66
J-ECB-29_H09	GH992490.1	1.19×10^{-49}	Inhibitor of growth protein 3 (<i>Camponotus floridanus</i>)	2.59	
J-ECB-33_D08	GH989092.1	3.78×10^{-104}	pyridoxine 5'-phosphate oxidase (<i>Bombyx mori</i>)	-2.38	
J-ECB-33_G10	GH989292.1	1.29×10^{-26}	transmembrane protein 205-like (<i>Bombyx mori</i>)	2.66	3.41
J-ECB-35_F06	GH990233.1	6.66×10^{-48}	heme oxygenase (<i>Bombyx mori</i>)	2.29	2.22
J-ECB-37_E05	GH991174.1	1.10×10^{-43}	oxidoreductase (<i>Acromyrmex echinator</i>)	-2.77	
J-ECB-38_B03	GH991444.1	2.09×10^{-33}	inhibitor of growth protein 3	2.75	2.06
J-ECB-39_F07	GH992097.1	1.35×10^{-69}	cytidylate kinase	-2.21	
J-ECB-39_H09	GH992207.1	4.65×10^{-70}	extracellular domains-containing protein CG31004-like isoform X1 (<i>Bombyx mori</i>)	3.36	2.67
J-ECB-40_D07	GH987842.1	3.45×10^{-73}	troponin C (<i>Bombyx mori</i>)	2.22	
J-ECB-41_A03	GH988071.1	1.06×10^{-17}	ankyrin-2-like (<i>Bombyx mori</i>)	3.23	3.65
J-ECB-41_H07	GH988338.1	1.46×10^{-81}	G10 protein (<i>Bombyx mori</i>)		2.05
J-ECB-42_A08	GH988386.1	2.15×10^{-21}	RGS-GAIP interacting protein GIPC (<i>Bombyx mori</i>)		2.24
J-ECB-42_C06	GH988476.1	9.42×10^{-25}	glucosylceramidase-like (<i>Monodelphis domestica</i>)	-3.45	
J-ECB-43_F12	GH989190.1	4.24×10^{-70}	EF-hand domain-containing protein CG10641-like (<i>Bombyx mori</i>)	8.91	7.79
J-ECB-47_A02	GH990851.1	3.71×10^{-39}	hepatocyte growth factor-regulated tyrosine kinase substrate-like (<i>Bombyx mori</i>)	3.77	3.78
J-ECB-49_C04	GH991887.1	1.10×10^{-110}	actin (<i>Spodoptera exigua</i>)	2.18	
J-ECB-49_H10	GH992172.1	1.28×10^{-19}	cystathionine γ -lyase (<i>Bombyx mori</i>)	6.29	2.97
J-ECB-50_C10	GH987666.1	4.80×10^{-76}	S-adenosylmethionine decarboxylase proenzyme (<i>Camponotus floridanus</i>)		2.46
J-ECB-50_F10	GH987698.1	2.36×10^{-32}	elongation factor-1 α (<i>Corcyra cephalonica</i>)	-2.08	
J-ECB-53_A10	GH988057.1	1.07×10^{-21}	hypothetical protein TcasGA2_TC008350 (<i>Tribolium castaneum</i>)	2.21	
J-ECB-54_F04	GH988562.1	6.00×10^{-25}	troponin T transcript variant A (<i>Bombyx mandarina</i>)	4.03	
J-ECB-58_A02	GH990235.1	2.89×10^{-45}	cuticular protein RR-1 motif 23 (<i>Bombyx mori</i>)	19.61	
J-ECB-58_A11	GH990291.1	7.31×10^{-104}	innexin 2 (<i>Heliothis virescens</i>)		2.49
J-ECB-60_B03	GH987159.1	9.42×10^{-43}	pyroglutamyl-peptidase 1-like (<i>Apis mellifera</i>)	-2.33	
J-ECB-60_C07	GH987175.1	5.23×10^{-43}	probable 4-coumarate--CoA ligase 3-like isoform 2 (<i>Acyrtosiphon pisum</i>)	-5.18	
J-ECB-60_H07	GH987229.1	1.45×10^{-35}	disulfide-isomerase A6 (<i>Culex tarsalis</i>)		-2.48

* S:Cry1Ab corn and R:Cry1Ab corn denote S- and R-strain larvae fed transgenic corn leaves expressing Cry1Ab toxin, respectively. # Each contig sequence has multiple Genbank EST ID and the listed ID represents the ID of the longest EST sequence in GenBank.

Table S2. List of 48 common differentially expressed gut genes in S-strain larvae fed artificial diet containing Cry1Ab protoxin as compared with those fed artificial diet without Cry1Ab protoxin, and S- and R-strain larvae fed transgenic corn leaves expressing Cry1Ab toxin as compared with those fed non-transgenic corn leaves.

EST ID	GenBank EST ID #	Sequence Description	Expression Ratio *		
			S:protoxin	S:Cry1Ab Corn	R:Cry1Ab Corn
BM2_B12	GH992538	hypothetical protein TcasGA2_TC011405 (<i>Tribolium castaneum</i>)	-2.07	-2.24	-2.30
Contig[0004]	GH992504	glutathione S-transferase (<i>Choristoneura fumiferana</i>)	-3.53	-8.76	-2.95
Contig[0009]	GH992549	putative carboxypeptidase A-like (<i>Nasonia vitripennis</i>)	-2.19	-3.85	-2.09
Contig[0019]	GH998697	glutamate carboxypeptidase-like isoform 1 (<i>Apis mellifera</i>)	-3.14	-6.64	-2.28
Contig[0243]	GH998064	trypsin (<i>Helicoverpa armigera</i>)	-2.45	-9.02	-5.89
Contig[0814]	GH998546	sodium/bile acid cotransporter (<i>Tribolium castaneum</i>)	-5.03	-14.14	-4.21
Contig[1081]	GH998825	pancreatic lipase-like protein (<i>Epiphyas postvittana</i>)	-2.57	-4.83	-5.01
Contig[1314]	GH993616	amino acid transporter (<i>Bombyx mori</i>)	-4.68	-3.80	-2.51
Contig[1486]	GH997709	C-5 sterol desaturase-like (<i>Acyrtosiphon pisum</i>)	-4.96	-7.75	-2.79
Contig[1897]	GH997709	C-5 sterol desaturase-like (<i>Acyrtosiphon pisum</i>)	-4.48	-7.03	-2.13
Contig[1953]	GH997798	NADP-dependent oxidoreductase (<i>Bombyx mori</i>)	-3.27	-2.71	-2.51
Contig[4527]	GH989618	conserved hypothetical protein (<i>Culex quinquefasciatus</i>)	-7.89	-15.05	-5.28
Contig[4763]	GH998142	sodium-bile acid cotransporter (<i>Aedes aegypti</i>)	-4.39	-10.83	-6.56
Contig[5679]	GH988679	phosphoserine aminotransferase (<i>Antheraea pernyi</i>)	-2.18	-4.08	-3.26
Contig[5743]	GH993678	amino acid transporter (<i>Bombyx mori</i>)	-5.40	-3.96	-2.55
ECB-02_H03	GH997311	saposin-like protein (<i>Bombyx mori</i>)	-2.02	2.84	2.87
ECB-14_E05	GH998249	n/a	-3.62	3.27	2.56
ECB-C-04_H06	GH992916	tetraspanin D107 (<i>Bombyx mori</i>)	-2.70	4.16	2.99
ECB-C-11_A06	GH993413	hypothetical protein EAI_08582 (<i>Harpegnathos saltator</i>)	-2.86	-4.22	-3.00
gi_133905779	EL928629	Vanin-like protein 1 (<i>Culex quinquefasciatus</i>)	-3.35	-9.20	-5.67
gi_133906638	EL929475	retinol dehydrogenase (<i>Heliothis virescens</i>)	-3.61	-10.53	-10.95
J-ECB-39_E12	GH992066	sugar transporter (<i>Culex quinquefasciatus</i>)	-2.65	-9.57	-4.35
J-ECB-55_E04	GH988996	monocarboxylate transporter (<i>Aedes aegypti</i>)	-3.4	-3.62	-3.88
Contig[1263]	GH996374	n/a	4.74	2.32	2.91
Contig[1573]	GH997739	n/a	2.07	2.27	2.76
Contig[4776]	GH998970	SXSS-APN2 (<i>Ostrinia furnacalis</i>)	2.17	-2.59	2.31
Contig[5143]	GH995296	ctl2 (<i>Aedes aegypti</i>)	2.32	2.25	2.17
Contig[5262]	GH993421	n/a	5.52	3.58	4.86
Contig[5386]	GH996141	tetraspanin E118 (<i>Bombyx mori</i>)	2.33	2.34	2.04
Contig[5414]	GH997359	Ubiquitin-63E, isoform A (<i>Drosophila melanogaster</i>)	2.73	2.49	2.04
Contig[5929]	GH990692	n/a	2.60	3.98	2.45
Contig[6000]	GH998341	n/a	2.14	2.48	2.82
ECB-11_E06	GH997996	GD21009 (<i>Drosophila simulans</i>)	2.21	-5.13	-2.69

ECB-14_H12	GH998287	n/a	2.13	5.29	5.16
ECB-17_F12	GH998536	n/a	16.41	24.46	6.87
ECB-18_B07	GH998575	n/a	3.99	2.71	2.44
ECB-21_C09	GH998857	sugar transporter protein 3 (<i>Bombyx mori</i>)	2.52	-4.90	-2.12
ECB-C-05_D05	GH992955	glucosamine-fructose-6-phosphate aminotransferase 2 (<i>Culex quinquefasciatus</i>)	2.24	-2.88	-2.10
ECB-V-07_D03	GH994735	similar to CG6040 (<i>Papilio polytes</i>)	2.66	6.60	6.08
ECB-V-16_B02	GH995433	n/a	2.36	2.35	2.07
ECB-V-25_C10	GH996179	hypothetical protein (<i>Aedes aegypti</i>)	2.29	5.91	6.27
gi_133907290	EL930112	n/a	4.37	5.14	3.90
J-ECB-25_H03	GH991098	n/a	4.21	6.25	4.84
J-ECB-29_G03	GH992468	IST1 homolog (<i>Bombus terrestris</i>)	2.18	5.72	6.66
J-ECB-39_H09	GH992207	Extracellular domains-containing protein (<i>Acromyrmex echinator</i>)	2.15	3.36	2.67
J-ECB-47_A02	GH990851	hepatocyte growth factor-regulated tyrosine kinase substrate (hgs) (<i>Tribolium castaneum</i>)	3.09	3.77	3.78

“*” S:protoxin denotes the S-strain larvae fed artificial diet containing Cry1Ab protoxin at the LC₅₀ concentration; S:Cry1Ab corn and R:Cry1Ab denote the S- and R-strain larvae fed transgenic corn leaves expressing Cry1Ab, respectively. “#” Each contig sequence has multiple Genbank EST IDs and the listed ID represents the ID of the longest EST sequence in GenBank. “n/a” The sequence does not have functional descriptions in NCBI database.

Table S3. List of differentially expressed gut genes in S and R-strain larvae fed non-transgenic corn leaves.

EST ID	Sequence Description	Expression Ratio $\pm$ SE (R/S)
Serine protease		
Contig[2883]	chymotrypsin	-3.01 ± 0.24
Contig[5043]	chymotrypsin 7	-2.73 ± 0.16
Contig[0147]	chymotrypsin-like serine protease	-2.50 ± 0.00
Contig[4021]	chymotrypsin-like serine protease	-2.21 ± 0.12
Contig[0573]	chymotrypsin-like serine protease	-2.44 ± 0.09
Contig[1519]	chymotrypsin-like serine protease	3.21 ± 0.31
ECB-V-27_E08	chymotrypsin-like serine protease partial	-23.76 ± 2.21
Contig[0027]	serine protease	-2.69 ± 0.15
Contig[3118]	serine protease 24	-5.30 ± 0.16
ECB-05_D02	serine protease inhibitor dipetalogastin-like	5.97 ± 0.34
J-ECB-50_G05	serine protease partial	-42.35 ± 2.30
Contig[1207]	serine protease precursor	-14.06 ± 0.33
Contig[5740]	trypsin β -like	-3.36 ± 0.45
Contig[0344]	trypsin-like serine protease	-4.48 ± 0.42
Contig[3704]	trypsin-like serine protease	-2.38 ± 0.04
Contig[4768]	trypsin-like serine protease	-5.50 ± 0.16
Aminopeptidase/ABC/ALP		
ECB-V-10_H10	aminopeptidase	2.36 ± 0.09
Contig[1398]	aminopeptidase	-2.45 ± 0.03
Contig[4776]	aminopeptidase	4.34 ± 0.08
Contig[5190]	V-type proton ATPase subunit B	2.17 ± 0.05
Contig[1309]	V-type proton ATPase subunit e 2-like	2.25 ± 0.14
J-ECB-37_G01	V-type proton ATPase subunit S1	2.64 ± 0.04
Contig[3154]	alkaline phosphatase-like	3.24 ± 0.21
Transporter		
Contig[5496]	Facilitated trehalose transporter Tret1	-2.47 ± 0.21
ECB-16_F07	inorganic phosphate cotransporter	-5.78 ± 1.16
ECB-V-21_D11	monocarboxylate transporter 5	2.25 ± 0.07
ECB-C-20_C03	Organic cation transporter	-6.28 ± 0.33
ECB-22_H11	sodium- and chloride-dependent glycine transporter 1-like	3.25 ± 0.18
Contig[5211]	facilitated trehalose transporter Tret1-like	4.74 ± 0.39
Detoxification or detoxification-related genes		
Contig[4729]	truncated carboxylesterase	-2.69 ± 0.10
Contig[0115]	esterase CXE14	4.97 ± 0.29
J-ECB-07_G03	esterase CXE14	7.47 ± 0.82
Contig[5372]	esterase FE4-like	2.50 ± 0.15
Contig[0448]	cytochrome b561 domain-containing 2	2.04 ± 0.01
Contig[6043]	cytochrome b5-like	-2.26 ± 0.10
Contig[4079]	cytochrome b-c1 complex subunit 10	2.23 ± 0.05
J-ECB-50_C06	cytochrome c oxidase assembly factor 4 mitochondrial	-2.30 ± 0.16
J-ECB-33_D09	cytochrome P450	14.02 ± 0.32
ECB5_D02	Cytochrome P450 6B4	-4.64 ± 0.11
Contig[5056]	cytochrome P450 6k1-like	-2.57 ± 0.18
J-ECB-04_G10	cytochrome P450 6k1-like	-3.83 ± 0.23
Contig[4426]	cytochrome P450 CYP12A2-like	3.32 ± 0.17
ECB-V-17_G09	cytochrome P450 CYP12A2-like	3.36 ± 1.22
Contig[2821]	NADPH cytochrome P450 reductase	7.60 ± 0.35
ECB-12_F03	NADPH--cytochrome P450 reductase	3.91 ± 0.29

Contig[0643]	glutathione S-transferase 1-1-like	3.65 ± 1.30
Contig[1881]	glutathione S-transferase-like	3.05 ± 0.95
Others		
Contig[3650]	10 kDa secreted protein	−22.50 ± 1.00
ECB-C-15_C10	15-hydroxyprostaglandin dehydrogenase (NAD ⁺)-like	−4.46 ± 0.38
J-ECB-25_A10	2-acylglycerol O-acyltransferase 2-A-like	2.48 ± 0.14
Contig[5545]	3-oxoacyl-(acyl-carrier-) reductase -like	3.08 ± 0.18
ECB-V-26_H03	4-coumarate-- ligase 1-like	3.33 ± 0.16
ECB-V-22_H03	4-hydroxybutyrate coenzyme A transferase	3.21 ± 0.29
ECB-C-17_G01	5-demethoxyubiquinone mitochondrial	−2.42 ± 0.13
ECB-V-27_D07	5-formyltetrahydrofolate cyclo-ligase	2.52 ± 0.08
Contig[5728]	AAEL004564- partial	2.33 ± 0.07
ECB-17_C04	AAEL017413- partial	−4.74 ± 1.42
Contig[0031]	acyl-Δ ¹¹ desaturase	9.08 ± 0.80
ECB-V-05_B10	acyl-desaturase Z9-1	3.23 ± 0.37
ECB-13_A01	adipocyte plasma membrane-associated	2.72 ± 0.31
Contig[0030]	aldehyde dehydrogenase mitochondrial-like	2.36 ± 0.06
ECB-C-18_H09	aldose reductase-like isoform X1	5.78 ± 0.23
J-ECB-35_D11	alkaline ceramidase	−2.12 ± 0.01
Contig[0635]	alkaline C-like	8.36 ± 0.65
Contig[1659]	alkaline C-like	2.78 ± 0.00
Contig[5759]	alkaline C-like	3.58 ± 0.17
J-ECB-33_F11	alkaline C-like	5.53 ± 0.36
J-ECB-29_C01	α-(1,3)-fucosyltransferase 10-like	−2.24 ± 0.09
Contig[3475]	α-(1,3)-fucosyltransferase C-like	−2.49 ± 0.08
ECB-30_C09	α-amylase 1-like	−2.25 ± 0.17
ECB-28_F03	α-tocopherol transfer-like	2.06 ± 0.02
ECB-27_B09	Ankyrin repeat domain	2.06 ± 0.06
J-ECB-06_D11	aquaporin isoform X2	−2.54 ± 0.33
Contig[3920]	armadillo repeat-containing 6 homolog	−8.85 ± 0.92
Contig[0915]	arylphorin subunit α-like	−5.00 ± 0.41
Contig[2890]	asteroid log 1	−28.20 ± 1.28
J-ECB-24_E07	ATP-binding cassette sub-family G member 1-like	−2.31 ± 0.07
ECB-C-16_D12	ATP-dependent RNA helicase DHX30	−3.37 ± 0.24
ECB-V-30_D11	bifunctional 3 -phosphoadenosine 5 -phosphosulfate synthase	2.71 ± 0.09
Contig[2754]	carbonyl reductase (NADPH) 1-like	2.14 ± 0.11
Contig[0362]	carbonyl reductase (NADPH) 3-like	2.66 ± 0.19
ECB-V-29_E10	carboxypeptidase B-like	−3.05 ± 0.27
Contig[5228]	cathepsin L	−4.20 ± 0.21
Contig[0407]	chemosensory	67.54 ± 20.30
Contig[0505]	chitin deacetylase 1	−2.50 ± 0.49
Contig[5328]	chitinase 3	2.86 ± 0.14
J-ECB-48_H08	cleft lip and palate transmembrane 1 homolog	2.31 ± 0.14
ECB-15_G12	coiled-coil domain-containing 47	−2.18 ± 0.13
Contig[1382]	collagenase-like	−266.68 ± 9.01
Contig[0578]	collagenase-like	−2.04 ± 0.00
Contig[0245]	collagenase-like	3.32 ± 0.08
Contig[5126]	collagenase-like	2.70 ± 0.32
ECB-C-06_B02	cueball	−2.12 ± 0.08
Contig[0348]	cyclic GMP-AMP synthase-like	−2.62 ± 0.37
Contig[3758]	cyclic GMP-AMP synthase-like	−6.91 ± 1.22

J-ECB-08_G07	cyclic GMP-AMP synthase-like	−29.87 ± 9.22
ECB-V-07_H04	DALR anticodon-binding domain-containing 3	−2.29 ± 0.24
ECB-03_A08	DEAD-box helicase Dbp80	2.18 ± 0.13
Contig[6024]	defense 1	4.97 ± 0.35
Contig[1719]	Δ ²⁴ -sterol reductase-like	3.35 ± 1.24
ECB-28_E04	diamine acetyltransferase 2-like	2.89 ± 0.16
J-ECB-42_H12	DNA-directed RNA polymerase II subunit GRINL1A	−2.77 ± 0.15
ECB-V-11_B08	DNAJ homolog 1	−2.15 ± 0.04
Contig[3724]	dTDP-glucose 4,6-dehydratase	−2.13 ± 0.07
J-ECB-01_D10	Dynein heavy chain axonemal	2.55 ± 0.39
J-ECB-53_E04	dynein light chain roadblock-type 2	−4.89 ± 1.44
Contig[4781]	E3 ubiquitin- ligase sina-like isoform X3	−6.67 ± 0.73
ECB-V-14_B03	E3 ubiquitin- ligase Su(Dx)	−2.26 ± 0.13
J-ECB-04_B07	ecdysteroid 22-kinase	−2.47 ± 0.33
ECB-11_F07	ecdysteroid-regulated 16 kDa	4.23 ± 0.49
J-ECB-43_F12	EF-hand domain-containing D2 homolog	2.44 ± 0.11
Contig[6042]	ejaculatory bulb-specific 3-like	3.06 ± 0.15
Contig[5715]	Endonuclease mitochondrial	−2.50 ± 0.26
Contig[2154]	endonuclease-reverse transcriptase	−6.90 ± 4.68
J-ECB-47_A03	endonuclease-reverse transcriptase	3.73 ± 1.45
Contig[5481]	epidermal retinol dehydrogenase 2-like	2.79 ± 0.26
Contig[1610]	epididymal secretory E1-like	−2.59 ± 0.11
ECB-V-19_H05	estrogen sulfotransferase	3.71 ± 0.15
Contig[5427]	eukaryotic translation initiation factor 4E-like	−14.84 ± 0.83
Contig[0615]	fas-associated death domain	−6.16 ± 0.22
Contig[0347]	Fatty acid-binding 2	−8.20 ± 0.85
Contig[0566]	fatty acid-binding 2	4.69 ± 0.43
Contig[1085]	flexible cuticle 12-like	10.37 ± 1.15
ECB-20_C07	GATA zinc finger domain-containing 14-like	−13.84 ± 2.02
Contig[1778]	glutaryl- mitochondrial	2.33 ± 0.21
ECB-05_B10	glycerophosphodiester phosphodiesterase	−2.19 ± 0.05
Contig[0111]	hatching enzyme	−2.39 ± 0.07
Contig[5397]	hatching enzyme	2.59 ± 0.08
ECB-22_B05	helicase SKI2W	11.26 ± 8.11
J-ECB-08_H05	Hematopoietically-expressed homeobox hhex	−2.20 ± 0.07
Contig[5984]	histidine triad nucleotide-binding 1	−2.29 ± 0.19
ECB-15_A08	histidine-rich glyco -like	3.55 ± 0.59
ECB-V-03_C02	hsc70-interacting-like	−2.38 ± 0.08
Contig[5654]	hydroxylysine kinase	3.52 ± 0.16
Contig[5010]	hypothetical protein g.12871	−2.32 ± 0.08
J-ECB-12_A05	hypothetical protein g.14421	−3.24 ± 0.16
ECB-12_A06	hypothetical protein g.8449	−2.41 ± 0.08
Contig[5666]	hypothetical protein OBRU01_04590	−77.68 ± 3.96
J-ECB-56_E05	hypothetical protein RR48_07032	−2.47 ± 0.16
Contig[0251]	hypothetical protein RR48_12366	−37.90 ± 3.08
Contig[1427]	hypothetical protein RR48_12366	−7.56 ± 4.53
Contig[5720]	immune-related Hdd13	−4.57 ± 0.21
J-ECB-53_B03	integrator complex subunit 1 isoform X2	−3.10 ± 0.46
Contig[3532]	isocitrate dehydrogenase (NADP) cytoplasmic-like	2.30 ± 0.01
ECB-V-26_D03	isopentenyl-diphosphate Δ-isomerase 1	−4.09 ± 0.47
ECB-03_E12	juvenile hormone binding	9.79 ± 0.56
Contig[3727]	larval cuticle 1-like	13.46 ± 1.19

Contig[5800]	larval cuticle LCP-17-like	3.88 ± 0.35
gi_133905657	lipase 1-like	−3.64 ± 0.54
J-ECB-56_D02	lipase 1-like	−10.87 ± 0.48
ECB-07_C04	lipase 1-like	4.09 ± 0.42
Contig[4980]	lipase 3-like	−2.34 ± 0.06
J-ECB-12_D03	lipid storage droplets surface-binding 2	2.49 ± 0.30
ECB-V-22_G04	Lipoate ligase	2.18 ± 0.04
ECB-11_E02	lipoyltransferase mitochondrial isoform X1	4.35 ± 2.12
ECB-V-23_A09	long-chain fatty acid transport 4-like	−4.33 ± 0.77
Contig[0685]	lysosomal acid phosphatase-like	3.02 ± 0.21
Contig[1923]	lysozyme 1	2.06 ± 0.04
Contig[2229]	Maltase 1	−2.82 ± 0.44
Contig[3279]	maltase A1-like	2.58 ± 0.12
Contig[0738]	membrane alanyl aminopeptidase-like	2.75 ± 0.17
ECB-C-05_H08	Mitochondrial import inner membrane translocase subunit Tim9	2.16 ± 0.04
J-ECB-33_E10	multidrug resistance 1A-like	59.13 ± 9.42
J-ECB-01_C01	multiple epidermal growth factor-like domains 10	−4.17 ± 0.24
Contig[5453]	Myophilin	3.37 ± 0.05
gi_133905748	myosin light chain smooth muscle-like	−2.28 ± 0.18
Contig[5133]	myosin regulatory light chain 2	2.79 ± 0.09
Contig[5707]	myosin regulatory light chain sqh	−2.41 ± 0.29
ECB-26_F05	myosin regulatory light chain sqh	−3.16 ± 0.44
J-ECB-30_H09	myrosinase 1-like	−2.37 ± 0.17
Contig[1061]	NADH dehydrogenase (ubiquinone) 1β subcomplex subunit mitochondrial	2.29 ± 0.25
J-ECB-01_B08	NFX1-type zinc finger-containing 1-like	−4.85 ± 0.50
ECB-19_H01	nose resistant to fluoxetine 6-like	−4.00 ± 0.97
ECB-27_E07	nuclease HARBI1	2.30 ± 0.11
J-ECB-10_B09	oxidative stress-induced growth inhibitor 1-like	−2.48 ± 0.18
J-ECB-24_F10	p94	−3.36 ± 0.53
Contig[0112]	pancreatic triacylglycerol lipase-like	−5.04 ± 1.12
Contig[0450]	pancreatic triacylglycerol lipase-like	−6.49 ± 0.43
Contig[3472]	pancreatic triacylglycerol lipase-like	−3.42 ± 0.10
Contig[2388]	peptidoglycan recognition -like	3.09 ± 0.52
Contig[2223]	peptidoglycan-recognition LB-like	−2.73 ± 0.16
Contig[1391]	peptidoglycan-recognition LB-like	10.90 ± 0.43
Contig[5021]	peritrophin type-A domain 2	−6.79 ± 0.68
Contig[1195]	phosphatidylethanolamine-binding homolog-like	−10.20 ± 1.44
J-ECB-55_A05	probable 2-oxoglutarate dehydrogenase E1 component DHKTD1 mitochondrial	−6.05 ± 1.26
ECB-05_H12	probable citrate synthase mitochondrial	2.13 ± 0.11
Contig[3585]	probable phospholipid hydroperoxide glutathione peroxidase	2.24 ± 0.08
Contig[5679]	probable phosphoserine aminotransferase	−5.73 ± 0.33
Contig[5038]	probable salivary secreted peptide	5.83 ± 1.18
Contig[5205]	probable salivary secreted peptide	4.55 ± 0.13
Contig[0619]	proline-rich extensin EPR1	2.62 ± 0.44
J-ECB-08_D11	protease inhibitor 4	11.51 ± 1.82
ECB-10_C01	pyridoxal kinase	3.42 ± 0.38
J-ECB-60_B03	Pyroglutamyl-peptidase 1	−4.84 ± 2.49
J-ECB-24_C06	regucalcin-like	−3.69 ± 0.48

Contig[3035]	regucalcin-like	3.77 ± 0.01
J-ECB-04_F11	regucalcin-like (<i>Papilio xuthus</i>)	3.81 ± 0.06
Contig[5349]	regulation of enolase 1-like	−8.76 ± 2.90
J-ECB-54_C04	reticulocyte-binding 2 homolog a-like	−35.47 ± 1.27
ECB-C-04_B10	retrovirus-related Pol poly from transposon TNT 1-94	2.34 ± 0.12
ECB-C-17_F04	RNA-binding 24-B-like	−2.53 ± 0.26
Contig[0105]	RNA-directed DNA polymerase from transposon partial	2.33 ± 0.14
ECB-05_E11	RNMT-activating mini	3.06 ± 0.04
J-ECB-07_H02	RPII140-upstream gene	2.47 ± 0.01
ECB-C-20_B10	sedoheptulokinase-like isoform X2	−2.20 ± 0.12
Contig[4387]	seleno K-like	−2.29 ± 0.11
J-ECB-24_D12	selT	−2.85 ± 0.10
Contig[0813]	SET and MYND domain-containing 4-like	−3.35 ± 0.15
ECB-V-22_F04	SET and MYND domain-containing 4-like	−3.89 ± 0.18
Contig[5961]	short-chain dehydrogenase reductase	−3.36 ± 0.17
ECB-C-11_A06	Signal CUB and EGF-like domain-containing 2	3.05 ± 0.53
Contig[0068]	single domain major allergen	−4.45 ± 0.53
Contig[4763]	solute carrier family 10 member 6-like	3.07 ± 0.24
ECB-V-07_H05	solute carrier family riboflavin member 3-A-like	14.64 ± 0.77
Contig[6015]	SUMO-conjugating enzyme UBC9-B	−2.16 ± 0.00
Contig[3086]	superoxide dismutase (Cu-Zn)	−7.44 ± 2.87
Contig[6056]	synaptic vesicle glyco 2C-like	−10.37 ± 0.40
gi_133906571	testin	−2.60 ± 0.34
Contig[0408]	tetraspanin E118	−3.64 ± 0.54
Contig[0010]	thioredoxin-2	2.16 ± 0.01
Contig[4717]	Threonine dehydratase	2.65 ± 0.29
J-ECB-41_A03	transient receptor potential channel pyrexia-like isoform X2	−5.09 ± 1.08
ECB-C-15_H04	Translation elongation factor 2	14.76 ± 3.62
ECB-28_F07	transmembrane 42	−2.38 ± 0.13
J-ECB-40_D07	troponin C	2.14 ± 0.14
J-ECB-54_F04	troponin T	3.14 ± 0.28
ECB-C-04_A08	tubulin β chain	2.68 ± 0.09
ECB-18_C11	tubulin β-1 chain	2.22 ± 0.09
Contig[5247]	Tudor domain-containing 1	−2.99 ± 0.42
J-ECB-33_E12	U11 U12 small nuclear ribonucleo 25 kDa	2.55 ± 0.15
ECB-V-29_H03	ubiquitin carboxyl-terminal hydrolase 46	−2.63 ± 0.10
ECB-V-05_G12	UDP-glucuronosyltransferase 2B15-like	6.47 ± 0.68
Contig[5837]	uncharacterized LOC106121242	−2.50 ± 0.12
Contig[4263]	uncharacterized oxidoreductase TM_0325-like	2.38 ± 0.07
Contig[5802]	uncharacterized protein LOC105842367 isoform X2 (<i>Bombyx mori</i>)	−5.67 ± 0.79
J-ECB-11_E05	uridine 5 -monophosphate synthase	2.43 ± 0.08
gi_133905779	vanin 2 isoform X2	4.14 ± 0.25
ECB-V-12_E11	venom dipeptidyl peptidase 4-like isoform X1	−2.52 ± 0.08
Contig[2624]	YIF1B	−7.17 ± 0.72
ECB-C-05_F02	zinc finger CCHC domain-containing 24-like	−68.49 ± 7.89
ECB-03_F06	zinc finger CCHC domain-containing partial	−5.34 ± 0.50
J-ECB-15_E12	zinc finger CCHC domain-containing partial	−39.00 ± 3.57

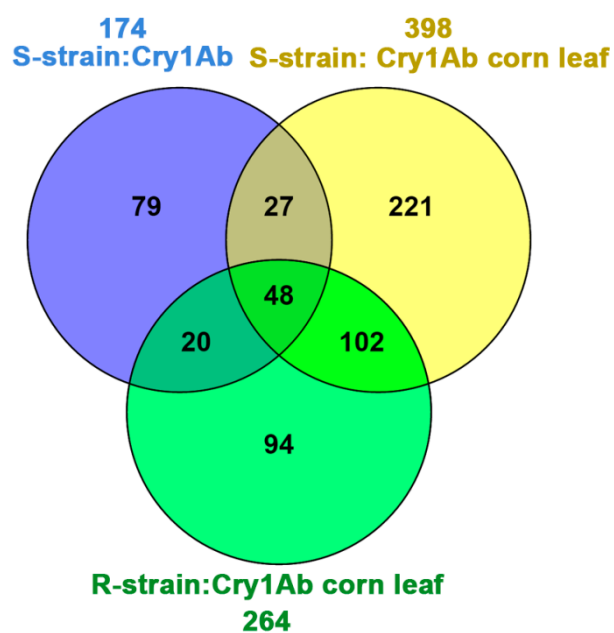


Figure S1. A Venn diagram showing the number of differentially expressed gut genes in S- and R-strain larvae of *O. nubilalis* fed transgenic corn leaves expressing Cry1Ab toxin and in S-strain larvae fed artificial diet containing Cry 1Ab protoxin. S-strain:Cry1Ab (slate blue) denotes S-strain larvae fed artificial diet containing Cry1Ab protoxin (LC₅₀) [18], whereas S-strain:Cry1Ab corn leaf (yellow) and R-strain:Cry1Ab corn leaf (green) denote S- and R-strain larvae fed transgenic corn leaves expressing Cry1Ab, respectively.