

# Supplementary Tables

**Table S1 Primers used for RT-qPCR experiment**

Gene ID	Gene	Primer	Primer Sequences	Product size
ncbi_114357739	UDP	Forward	ACCTTGGTGGGATGCATCAG	223
		Reverse	GGAGTGCGTCCAGGTAGTTC	
ncbi_114355278	ABCG1u	Forward	CGGACACCAGCCACCATATT	151
		Reverse	ATATCACGGTGCCCATCGAC	
ncbi_114360773	GST1	Forward	ACGCTCTGTACCCAACTGAC	204
		Reverse	ACGGTGAGACTGAAGCCAAG	
ncbi_114356024	ABCG1d	Forward	GTTGGGCCTTCTAGTTGGTTC	170
		Reverse	AGAGTCCGTAGCGGAGGTAT	
ncbi_114363214	ABCA2	Forward	TAGCGACTGCAGCATACGAG	225
		Reverse	CGGCTAACGAAGTGGCAATG	
ncbi_114361254	ABCG4	Forward	GGAAAGGGGGAGATCATAGA	149
		Reverse	ACCCTGTGGTAGGTTTCATCA	
ncbi_114362710	MBALP	Forward	TTTGAGGAAAAACGCAGCCG	230
		Reverse	TCCACGAACAGGAAGAAGCC	
ncbi_114354725	HSP68	Forward	CGTGTGTTGGAGTTTGGCAG	201
		Reverse	TCTTCGGGTCGTGCAACTTG	
ncbi_114349629	PNLIP	Forward	ACGCTGGATTGTCAGACTGG	197
		Reverse	AGTGTGGATCGCTTCAACGT	

**Table S2 A subset of the differentially expressed genes up- or down-regulated in ACB-IeR or –FR compared with ACB-BtS strain.**

Gene ID	Description	log2(fc) (FDR)	log2(fc) (FDR)
Cadherin		ACB-IeR	ACB-FR
MSTRG.22659	LOW QUALITY PROTEIN: cadherin-99C-like [ <i>Ctenocephalides felis</i> ]	+0.14(8.42e-01)	+0.23(7.48e-01)
MSTRG.7252	Cadherin EGF LAG seven-pass G-type receptor 1 [ <i>Papilio machaon</i> ]	-1.82(1.00e+00)	-9.42(1.00e+00)
ncbi_114350636	protocadherin Fat 3-like isoform X1 [ <i>Bicyclus anynana</i> ]	+0.21(4.44e-01)	-0.53(4.07e-01)
ncbi_114350637	protocadherin Fat 3-like isoform X1 [ <i>Bicyclus anynana</i> ]	-0.17(9.18e-01)	-0.48(1.24e-01)
ncbi_114350687	cadherin EGF LAG seven-pass G-type receptor 2 [ <i>Ostrinia furnacalis</i> ]	+0.00(1.00e+00)	+0.00(1.00e+00)
ncbi_114351342	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	-0.59(8.80e-01)	-1.66(2.83e-01)
ncbi_114351362	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	-0.17(9.83e-01)	-0.90(2.81e-01)
ncbi_114352029	neural-cadherin-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	+0.00(1.00e+00)	+3.74(1.00e+00)
ncbi_114352171	cadherin-86C isoform X1 [ <i>Ostrinia furnacalis</i> ]	-3.17(1.00e+00)	-0.85(1.00e+00)
ncbi_114353392	cadherin [ <i>Ostrinia nubilalis</i> ]	+0.57(3.31e-02)	-0.74(8.85e-02)
ncbi_114353394	protocadherin Fat 1-like [ <i>Ostrinia furnacalis</i> ]	-0.09(9.56e-01)	-0.10(9.64e-01)
ncbi_114355216	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	-3.20(3.28e-02)	-1.17(1.04e-06)
ncbi_114355389	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	-1.69(2.66e-01)	-1.12(5.28e-01)
ncbi_114355497	cadherin-related tumor suppressor [ <i>Ostrinia furnacalis</i> ]	-1.46(5.43e-01)	-1.87(2.31e-01)
ncbi_114355663	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	-1.02(7.36e-01)	-0.97(6.48e-01)
ncbi_114355667	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	-1.05(2.97e-01)	-0.97(2.48e-01)
ncbi_114355939	Mutant cadherin [ <i>Operophtera brumata</i> ]	+0.70(3.61e-01)	+1.32(1.59e-02)
ncbi_114355983	Mutant cadherin [ <i>Operophtera brumata</i> ]	-0.61(4.15e-01)	-0.11(9.77e-01)
ncbi_114356045	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	+4.06(1.00e+00)	+5.64(1.00e+00)
ncbi_114356126	cadherin-23 [ <i>Ostrinia furnacalis</i> ]	-2.46(1.21e-01)	-1.70(3.16e-01)
ncbi_114356128	Cadherin-23 [ <i>Papilio machaon</i> ]	+0.00(1.00e+00)	+0.00(1.00e+00)
ncbi_114356360	LOW QUALITY PROTEIN: fat-like cadherin-related tumor suppressor homolog	-0.07(9.71e-01)	-0.04(9.68e-01)

	[ <i>Ostrinia furnacalis</i> ]		
ncbi_114356615	cadherin-23 [ <i>Ostrinia furnacalis</i> ]	-0.53(5.29e-01)	-0.35(6.96e-01)
ncbi_114357327	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	-2.27(1.10e-01)	+0.08(9.19e-01)
ncbi_114357759	cadherin-24-like [ <i>Ostrinia furnacalis</i> ]	+0.00(1.00e+00)	+0.00(1.00e+00)
ncbi_114358153	Mutant cadherin [Operophtera brumata]	+0.00(1.00e+00)	+5.32(1.00e+00)
ncbi_114358900	protocadherin-like wing polarity protein stan [ <i>Ostrinia furnacalis</i> ]	-1.32(4.21e-02)	-0.64(4.42e-01)
ncbi_114359978	neural-cadherin-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	-2.58(1.00e+00)	-4.32(1.00e+00)
ncbi_114360023	Protocadherin Fat 1 [ <i>Papilio machaon</i> ]	-0.26(1.00e+00)	-0.82(8.39e-01)
ncbi_114360982	cadherin-87A-like, partial [ <i>Ostrinia furnacalis</i> ]	+2.46(1.00e+00)	+3.39(1.00e+00)
ncbi_114361932	Cadherin-related tumor suppressor [ <i>Papilio machaon</i> ]	-0.24(1.00e+00)	-0.83(1.00e+00)
ncbi_114362503	protocadherin Fat 3-like isoform X1 [Bicyclus anynana]	-0.03(7.74e-01)	-0.38(1.51e-01)
ncbi_114362562	DE-cadherin [ <i>Ostrinia furnacalis</i> ]	+0.03(7.52e-01)	+0.07(7.72e-01)
ncbi_114362815	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	+0.73(7.80e-01)	-0.98(1.00e+00)
ncbi_114362981	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	-0.79(8.39e-01)	-0.32(9.72e-01)
ncbi_114363449	Mutant cadherin, partial [Operophtera brumata]	+4.54(1.00e+00)	+0.00(1.00e+00)
ncbi_114363888	cadherin-87A-like, partial [ <i>Ostrinia furnacalis</i> ]	+1.58(1.00e+00)	+3.21(1.00e+00)
ncbi_114364807	cadherin-89D [ <i>Ostrinia furnacalis</i> ]	-4.06(1.00e+00)	-4.06(1.00e+00)
ncbi_114365074	Mutant cadherin [Operophtera brumata]	+7.67(1.00e+00)	+7.54(1.00e+00)
ncbi_114365286	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	+0.53(8.10e-01)	-1.33(1.00e+00)
ncbi_114365466	Mutant cadherin [Operophtera brumata]	+0.90(6.01e-01)	+1.47(2.26e-01)
ncbi_114365945	cadherin-99C, partial [ <i>Ostrinia furnacalis</i> ]	+1.49(5.72e-01)	-0.81(1.00e+00)
ncbi_114366173	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	-0.92(2.60e-01)	-1.80(1.71e-03)
ncbi_114366269	cadherin-99C-like [ <i>Ostrinia furnacalis</i> ]	+1.43(4.05e-01)	-0.05(9.98e-01)
ncbi_114366536	fat-like cadherin-related tumor suppressor homolog [ <i>Spodoptera litura</i> ]	+0.12(1.00e+00)	-2.13(1.00e+00)
<b>ABC</b>			

ncbi_114366205	ABC transporter G family member 20-like, partial [ <i>Ostrinia furnacalis</i> ]	-0.25(9.41e-01)	-1.61(1.52e-01)
ncbi_114351228	PREDICTED: DNA-directed RNA polymerases I, II, and III subunit RPABC1 [ <i>Papilio xuthus</i> ]	+0.05(7.63e-01)	+0.38(1.69e-01)
ncbi_114351209	ABC transporter G family member 23-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	-0.87(6.57e-01)	-1.63(2.25e-01)
ncbi_114353021	DNA-directed RNA polymerases I, II, and III subunit RPABC3 [ <i>Ostrinia furnacalis</i> ]	+0.11(6.48e-01)	+0.28(3.30e-01)
ncbi_114364630	DNA-directed RNA polymerases I, II, and III subunit RPABC2 [ <i>Ostrinia furnacalis</i> ]	+0.33(2.89e-01)	+0.24(3.54e-01)
ncbi_114366330	ABC transporter G family member 23 isoform X1 [ <i>Ostrinia furnacalis</i> ]	-0.33(9.18e-01)	-0.63(6.11e-01)
ncbi_114365778	DNA-directed RNA polymerases I, II, and III subunit RPABC4 [ <i>Ostrinia furnacalis</i> ]	-0.97(4.41e-01)	-0.59(6.24e-01)
ncbi_114366309	ABC transporter G family member 20-like [ <i>Ostrinia furnacalis</i> ]	-1.53(4.91e-01)	-0.98(6.81e-01)
ncbi_114351142	ABC transporter G family member 20 isoform X1 [ <i>Ostrinia furnacalis</i> ]	-1.20(3.72e-01)	-0.47(7.75e-01)
ncbi_114353871	ABC transporter G family member 7-like [ <i>Trichoplusia ni</i> ]	-0.79(1.00e+00)	-0.55(8.91e-01)
ncbi_114352409	DNA-directed RNA polymerases I, II, and III subunit RPABC5 [ <i>Melipona quadrifasciata</i> ]	+0.02(9.23e-01)	-0.10(9.96e-01)
ncbi_114362695	Excinuclease ABC, A subunit, partial [ <i>Operophtera brumata</i> ]	-0.81(1.00e+00)	-3.54(1.00e+00)
ncbi_114365993	ABC transporter A family member 4-like [ <i>Ostrinia furnacalis</i> ]	+4.32(1.00e+00)	+2.74(1.00e+00)
ncbi_114358164	ABC-type transporter, integral membrane subunit [ <i>Operophtera brumata</i> ]	+0.00(1.00e+00)	+4.74(1.00e+00)
ncbi_114350490	phospholipid-transporting ATPase ABCA7 isoform X3 [ <i>Galleria mellonella</i> ]	+0.00(1.00e+00)	+0.00(1.00e+00)
ncbi_114357341	ABC transporter ATP-binding protein, partial [ <i>Operophtera brumata</i> ]	+0.00(1.00e+00)	+0.00(1.00e+00)
ncbi_114358663	ABC transporter permease [ <i>Operophtera brumata</i> ]	+0.00(1.00e+00)	+0.00(1.00e+00)
ncbi_114363764	Multidrug resistance ABC transporter ATP-binding and permease protein [ <i>Operophtera brumata</i> ]	+0.00(1.00e+00)	+0.00(1.00e+00)
<b>ALP</b>			
ncbi_114352782	membrane-bound alkaline phosphatase-like [ <i>Ostrinia furnacalis</i> ]	-0.32(1.00e+00)	+0.49(1.00e+00)
ncbi_114355041	alkaline phosphatase, tissue-nonspecific isozyme-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	-0.06(9.81e-01)	+0.36(8.39e-01)
ncbi_114355045	alkaline phosphatase, tissue-nonspecific isozyme-like [ <i>Ostrinia furnacalis</i> ]	+4.74(1.00e+00)	+6.20(1.00e+00)

ncbi_114355362	alkaline phosphatase [ <i>Ostrinia furnacalis</i> ]	-0.20(7.66e-01)	-0.13(9.14e-01)
ncbi_114355386	Alkaline phosphatase, tissue-nonspecific isozyme [ <i>Papilio machaon</i> ]	+0.56(1.00e+00)	-1.09(1.00e+00)
ncbi_114356329	alkaline phosphatase-like [ <i>Ostrinia furnacalis</i> ]	+0.00(1.00e+00)	+0.00(1.00e+00)
ncbi_114362708	membrane-bound alkaline phosphatase-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	-0.28(6.93e-01)	-0.03(9.25e-01)
ncbi_114362709	membrane-bound alkaline phosphatase-like [ <i>Ostrinia furnacalis</i> ]	-0.33(4.05e-01)	+0.05(6.53e-01)
ncbi_114362710	membrane-bound alkaline phosphatase-like [ <i>Ostrinia furnacalis</i> ]	-1.37(5.77e-04)	-0.14(9.87e-01)
<b>APN</b>			
ncbi_114361315	membrane alanyl aminopeptidase-like [ <i>Ostrinia furnacalis</i> ]	+0.41(6.80e-06)	+0.54(2.37e-06)
ncbi_114353834	methionine aminopeptidase 2 [ <i>Ostrinia furnacalis</i> ]	-0.06(9.16e-01)	+0.35(1.84e-02)
ncbi_114361548	membrane alanyl aminopeptidase-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	+0.01(5.77e-01)	+0.26(3.26e-02)
ncbi_114361563	membrane alanyl aminopeptidase-like [ <i>Ostrinia furnacalis</i> ]	+0.03(4.75e-01)	+0.20(1.11e-01)
ncbi_114365886	methionine aminopeptidase 1, partial [ <i>Ostrinia furnacalis</i> ]	-0.30(6.61e-01)	+0.27(1.56e-01)
ncbi_114361414	aminopeptidase N-like [ <i>Ostrinia furnacalis</i> ]	-0.05(9.10e-01)	+0.14(1.75e-01)
ncbi_114365560	xaa-Pro aminopeptidase 3-like [ <i>Ostrinia furnacalis</i> ]	+0.37(2.12e-01)	+0.38(2.06e-01)
ncbi_114361386	Membrane alanyl aminopeptidase [ <i>Papilio xuthus</i> ]	-0.04(7.74e-01)	+0.12(2.07e-01)
ncbi_114361449	membrane alanyl aminopeptidase-like [ <i>Ostrinia furnacalis</i> ]	-0.23(7.71e-01)	+0.13(4.07e-01)
ncbi_114361372	aminopeptidase N3c [ <i>Ostrinia nubilalis</i> ]	-0.69(1.48e-01)	-0.33(5.20e-01)
ncbi_114350973	leucyl-cystinyl aminopeptidase-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	+0.04(8.23e-01)	-0.36(5.57e-01)
ncbi_114353229	xaa-Pro aminopeptidase ApepP-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	-0.11(9.84e-01)	-0.21(7.97e-01)
ncbi_114356040	dipeptidyl aminopeptidase-like protein 6 [ <i>Ostrinia furnacalis</i> ]	-0.51(9.33e-01)	-0.74(8.21e-01)
ncbi_114361949	glutamyl aminopeptidase-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	+0.03(7.26e-01)	-0.19(8.43e-01)
ncbi_114365491	cytosol aminopeptidase-like [ <i>Ostrinia furnacalis</i> ]	-0.38(9.31e-01)	-0.47(8.70e-01)
ncbi_114366310	aminopeptidase N-like [ <i>Ostrinia furnacalis</i> ]	+0.48(3.72e-01)	+0.08(8.88e-01)
ncbi_114361327	aminopeptidase N-like [ <i>Ostrinia furnacalis</i> ]	-0.17(9.83e-01)	-0.30(8.96e-01)
ncbi_114363130	probable aminopeptidase NPEPL1 isoform X4 [ <i>Ostrinia furnacalis</i> ]	+0.02(7.31e-01)	-0.14(9.35e-01)

MSTRG.22364	xaa-Pro aminopeptidase 1-like [ <i>Centruroides sculpturatus</i> ]	-0.79(8.50e-01)	-0.27(9.44e-01)
ncbi_114361393	aminopeptidase N-like isoform X2 [ <i>Ostrinia furnacalis</i> ]	-0.81(6.24e-01)	+0.14(9.51e-01)
ncbi_114350952	xaa-Pro aminopeptidase 3-like, partial [ <i>Ostrinia furnacalis</i> ]	+0.42(7.03e-01)	+0.06(9.54e-01)
ncbi_114353253	xaa-Pro aminopeptidase ApepP-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	-0.13(9.95e-01)	-0.12(9.58e-01)
ncbi_114361540	membrane alanyl aminopeptidase-like [ <i>Ostrinia furnacalis</i> ]	-0.22(7.32e-01)	-0.09(9.61e-01)
ncbi_114361612	puromycin-sensitive aminopeptidase isoform X1 [ <i>Ostrinia furnacalis</i> ]	+0.04(7.24e-01)	-0.10(9.66e-01)
ncbi_114361404	membrane alanyl aminopeptidase-like [ <i>Ostrinia furnacalis</i> ]	+0.29(2.42e-02)	-0.06(9.82e-01)
ncbi_114365752	methionine aminopeptidase 1D, mitochondrial isoform X1 [ <i>Ostrinia furnacalis</i> ]	-0.14(9.81e-01)	-0.08(9.93e-01)
ncbi_114350764	aminopeptidase N isoform X1 [ <i>Ostrinia furnacalis</i> ]	+0.00(1.00e+00)	-0.51(1.00e+00)
ncbi_114361861	xaa-Pro aminopeptidase 1 [ <i>Ostrinia furnacalis</i> ]	-0.49(1.00e+00)	-2.22(1.00e+00)
ncbi_114362805	glutamyl aminopeptidase-like isoform X4 [ <i>Ostrinia furnacalis</i> ]	+0.00(1.00e+00)	+0.00(1.00e+00)
ncbi_114365049	cytosol aminopeptidase-like, partial [ <i>Ostrinia furnacalis</i> ]	+0.00(1.00e+00)	+0.00(1.00e+00)
<b>Others</b>			
MSTRG.14142	UDP-glucuronosyltransferase 2B15-like [ <i>Ostrinia furnacalis</i> ]	+1.44(6.34e-05)	+2.31(8.21e-13)
MSTRG.14366	PREDICTED: nuclear transcription factor Y subunit gamma-like [ <i>Amyeloidis transitella</i> ]	+2.03(1.21e-07)	+2.46(1.59e-09)
MSTRG.23526	retinol dehydrogenase 14-like [ <i>Vanessa tameamea</i> ]	-1.00(7.05e-03)	+0.87(7.28e-03)
ncbi_114349629	pancreatic triacylglycerol lipase-like [ <i>Ostrinia furnacalis</i> ]	+3.98(3.11e-11)	+1.98(1.66e-03)
ncbi_114349639	pancreatic triacylglycerol lipase-like [ <i>Ostrinia furnacalis</i> ]	-1.43(1.29e-05)	-0.97(2.66e-01)
ncbi_114351935	trypsin, alkaline C-like [ <i>Ostrinia furnacalis</i> ]	+2.08(2.03e-20)	+0.36(1.60e-01)
ncbi_114351936	trypsin, alkaline C-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	+2.95(1.20e-08)	+1.29(1.33e-05)
ncbi_114351939	trypsin, alkaline C-like [ <i>Ostrinia furnacalis</i> ]	+1.79(3.27e-03)	+1.33(3.15e-06)
ncbi_114351942	trypsin, alkaline B-like [ <i>Ostrinia furnacalis</i> ]	+3.34(5.79e-10)	+1.22(5.59e-02)
ncbi_114352259	trypsin, alkaline B-like [ <i>Ostrinia furnacalis</i> ]	-1.33(5.98e-07)	-0.42(1.92e-01)
ncbi_114352777	protein lethal(2)essential for life-like [ <i>Ostrinia furnacalis</i> ]	-0.15(9.98e-01)	-2.55(4.34e-03)
ncbi_114353127	proton-coupled amino acid transporter-like protein pathetic isoform X1 [ <i>Ostrinia</i> ]	-1.09(9.67e-06)	-0.02(9.06e-01)

	<i>furnacalis</i> ]		
ncbi_114353674	pancreatic lipase-related protein 2-like [ <i>Ostrinia furnacalis</i> ]	-3.04(2.09e-03)	-2.87(2.80e-01)
ncbi_114353764	protein lethal(2)essential for life-like [ <i>Ostrinia furnacalis</i> ]	-0.08(9.65e-01)	-1.50(6.22e-10)
ncbi_114354259	heat shock protein 68-like [ <i>Ostrinia furnacalis</i> ]	-0.60(7.36e-01)	-2.32(5.31e-13)
ncbi_114354720	next to BRCA1 gene 1 protein-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	+0.30(5.42e-01)	-1.53(9.98e-08)
ncbi_114354721	protein lethal(2)essential for life-like [ <i>Ostrinia furnacalis</i> ]	+0.13(6.98e-01)	-1.57(1.77e-08)
ncbi_114354725	heat shock protein 68-like [ <i>Ostrinia furnacalis</i> ]	-0.42(8.97e-01)	-3.26(3.26e-06)
ncbi_114354906	chymotrypsin-1-like [ <i>Ostrinia furnacalis</i> ]	+1.08(4.58e-22)	-0.00(7.75e-01)
ncbi_114355297	proton-coupled amino acid transporter-like protein pathetic [ <i>Ostrinia furnacalis</i> ]	-1.30(3.53e-08)	-0.49(1.32e-01)
ncbi_114356221	heat shock protein 68-like [ <i>Ostrinia furnacalis</i> ]	-0.34(9.18e-01)	-1.56(1.57e-12)
ncbi_114356222	protein lethal(2)essential for life-like [ <i>Ostrinia furnacalis</i> ]	-0.55(8.27e-01)	-2.68(5.34e-04)
ncbi_114357580	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase-like isoform X3 [ <i>Ostrinia furnacalis</i> ]	+2.33(1.80e-02)	+2.65(4.86e-03)
ncbi_114357646	trypsin, alkaline C-like [ <i>Ostrinia furnacalis</i> ]	+3.04(2.61e-03)	+1.07(2.37e-01)
ncbi_114357736	UDP-glucuronosyltransferase 2B14-like [ <i>Ostrinia furnacalis</i> ]	+3.38(2.16e-03)	+1.67(2.97e-01)
ncbi_114357739	UDP-glucuronosyltransferase 2B14-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	+2.45(6.40e-03)	+1.62(2.10e-01)
ncbi_114357991	pancreatic triacylglycerol lipase-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	-1.47(7.36e-04)	-0.07(9.98e-01)
ncbi_114358382	protein lethal(2)essential for life-like [ <i>Ostrinia furnacalis</i> ]	-0.39(9.10e-01)	-2.36(1.81e-13)
ncbi_114358386	protein lethal(2)essential for life-like [ <i>Ostrinia furnacalis</i> ]	-0.05(9.21e-01)	-1.48(2.36e-07)
ncbi_114358387	protein lethal(2)essential for life-like [ <i>Ostrinia furnacalis</i> ]	-0.19(9.54e-01)	-1.82(1.26e-16)
ncbi_114359074	carboxypeptidase B-like [ <i>Ostrinia furnacalis</i> ]	+2.38(2.08e-18)	+1.00(1.39e-05)
ncbi_114359077	carboxypeptidase B-like [ <i>Ostrinia furnacalis</i> ]	+1.88(5.10e-12)	+1.07(5.23e-04)
ncbi_114359798	chymotrypsin-like elastase family member 2A [ <i>Ostrinia furnacalis</i> ]	+1.04(2.94e-04)	+0.12(7.03e-01)
ncbi_114359801	collagenase-like [ <i>Ostrinia furnacalis</i> ]	+1.81(6.67e-41)	+0.94(5.02e-10)
ncbi_114360123	short-chain dehydrogenase/reductase family 16C member 6 [ <i>Ostrinia furnacalis</i> ]	-4.96(1.90e-05)	-4.23(2.58e-05)
ncbi_114360499	trypsin, alkaline A-like [ <i>Ostrinia furnacalis</i> ]	+10.93(8.66e-03)	+10.67(5.24e-03)

ncbi_114360773	glutathione S-transferase 1-like [ <i>Ostrinia furnacalis</i> ]	+1.91(3.46e-02)	+2.75(8.12e-11)
ncbi_114361580	heat shock protein Hsp-12.2-like [ <i>Ostrinia furnacalis</i> ]	-0.73(7.31e-01)	-2.85(2.01e-26)
ncbi_114362420	acetylcholinesterase-like [ <i>Ostrinia furnacalis</i> ]	+1.55(6.75e-03)	+0.75(8.24e-02)
ncbi_114362872	alpha-amylase 2-like isoform X3 [ <i>Ostrinia furnacalis</i> ]	-1.91(2.25e-11)	-0.66(9.86e-02)
ncbi_114363240	trypsin theta-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	+1.15(1.65e-08)	+0.20(3.11e-01)
ncbi_114363773	heat shock protein 68-like [ <i>Ostrinia furnacalis</i> ]	-0.06(9.75e-01)	-2.90(1.61e-02)
ncbi_114364477	proton-coupled amino acid transporter-like protein CG1139 [ <i>Ostrinia furnacalis</i> ]	-1.25(2.91e-03)	+0.25(4.74e-01)
ncbi_114365341	glutathione S-transferase-like [ <i>Ostrinia furnacalis</i> ]	-1.66(3.11e-11)	-1.33(7.81e-05)
ncbi_114366668	UDP-glucuronosyltransferase 2B1-like isoform X3 [ <i>Ostrinia furnacalis</i> ]	-1.35(6.12e-03)	-0.84(6.99e-02)
ncbi_114366687	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 [ <i>Ostrinia furnacalis</i> ]	+0.21(6.24e-01)	-1.10(1.12e-02)
ncbi_114366714	GTP-binding protein SAR1b [ <i>Ostrinia furnacalis</i> ]	-0.16(9.79e-01)	+1.02(3.23e-04)



**Table S3 Gene ontology analysis of *Ostrinia furnacalis* transcriptome**

<b>GO ID (Ontology)</b>	<b>GO Term (level1)</b>	<b>GO ID (GO-terms)</b>	<b>GO Term (level2)</b>	<b>Number of genes</b>	<b>up</b>	<b>down</b>
<b>ACB-BtS vs.ACB-FR</b>						
GO:0003674	Molecular Function	GO:0003824	catalytic activity	100	42	58
GO:0003674	Molecular Function	GO:0005488	binding	72	22	50
GO:0003674	Molecular Function	GO:0005215	transporter activity	7	1	6
GO:0003674	Molecular Function	GO:0005198	structural molecule activity	4	3	1
GO:0003674	Molecular Function	GO:0098772	molecular function regulator	4	1	3
GO:0003674	Molecular Function	GO:0060089	molecular transducer activity	4	1	3
GO:0003674	Molecular Function	GO:0004871	signal transducer activity	3	1	2
GO:0003674	Molecular Function	GO:0000988	transcription factor activity, protein binding	2	1	1
GO:0003674	Molecular Function	GO:0016209	antioxidant activity	1	0	1
GO:0003674	Molecular Function	GO:0001071	nucleic acid binding transcription factor activity	1	0	1
GO:0008150	Biological Process	GO:0044699	single-organism process	91	27	64
GO:0008150	Biological Process	GO:0009987	cellular process	90	22	68
GO:0008150	Biological Process	GO:0008152	metabolic process	88	27	61
GO:0008150	Biological Process	GO:0065007	biological regulation	55	13	42
GO:0008150	Biological Process	GO:0050789	regulation of biological process	52	13	39
GO:0008150	Biological Process	GO:0050896	response to stimulus	45	9	36
GO:0008150	Biological Process	GO:0032501	multicellular organismal process	45	12	33
GO:0008150	Biological Process	GO:0032502	developmental process	43	13	30
GO:0008150	Biological Process	GO:0051179	localization	30	11	19
GO:0008150	Biological Process	GO:0023052	signaling	20	5	15

GO:0008150	Biological Process	GO:0071840	cellular component organization or biogenesis	20	5	15
GO:0008150	Biological Process	GO:0007610	behavior	12	4	8
GO:0008150	Biological Process	GO:0048519	negative regulation of biological process	11	4	7
GO:0008150	Biological Process	GO:0051704	multi-organism process	11	3	8
GO:0008150	Biological Process	GO:0002376	immune system process	10	2	8
GO:0008150	Biological Process	GO:0022414	reproductive process	9	2	7
GO:0008150	Biological Process	GO:0000003	reproduction	9	2	7
GO:0008150	Biological Process	GO:0048518	positive regulation of biological process	8	3	5
GO:0008150	Biological Process	GO:0040007	growth	6	2	4
GO:0008150	Biological Process	GO:0040011	locomotion	6	2	4
GO:0008150	Biological Process	GO:0099531	presynaptic process involved in synaptic transmission	1	0	1
GO:0008150	Biological Process	GO:0022610	biological adhesion	1	0	1
GO:0005575	Cellular Component	GO:0044464	cell part	68	19	49
GO:0005575	Cellular Component	GO:0005623	cell	68	19	49
GO:0005575	Cellular Component	GO:0043226	organelle	56	16	40
GO:0005575	Cellular Component	GO:0016020	membrane	34	11	23
GO:0005575	Cellular Component	GO:0044422	organelle part	23	8	15
GO:0005575	Cellular Component	GO:0032991	macromolecular complex	19	4	15
GO:0005575	Cellular Component	GO:0044425	membrane part	14	5	9
GO:0005575	Cellular Component	GO:0031974	membrane-enclosed lumen	8	4	4
GO:0005575	Cellular Component	GO:0045202	synapse	5	2	3
GO:0005575	Cellular Component	GO:0005576	extracellular region	5	2	3
GO:0005575	Cellular Component	GO:0044456	synapse part	4	2	2
GO:0005575	Cellular Component	GO:0044421	extracellular region part	4	2	2

GO:0005575	Cellular Component	GO:0030054	cell junction	2	0	2
<b>ACB-BtS vs. ACB-IeR</b>						
GO:0003674	Molecular Function	GO:0003824	catalytic activity	78	39	39
GO:0003674	Molecular Function	GO:0005488	binding	57	22	35
GO:0003674	Molecular Function	GO:0005215	transporter activity	4	3	1
GO:0003674	Molecular Function	GO:0004871	signal transducer activity	3	1	2
GO:0003674	Molecular Function	GO:0060089	molecular transducer activity	3	1	2
GO:0003674	Molecular Function	GO:0016209	antioxidant activity	1	0	1
GO:0003674	Molecular Function	GO:0005198	structural molecule activity	1	1	0
GO:0003674	Molecular Function	GO:0098772	molecular function regulator	1	0	1
GO:0003674	Molecular Function	GO:0001071	nucleic acid binding transcription factor activity	1	1	0
GO:0008150	Biological Process	GO:0044699	single-organism process	67	24	43
GO:0008150	Biological Process	GO:0009987	cellular process	58	23	35
GO:0008150	Biological Process	GO:0008152	metabolic process	52	21	31
GO:0008150	Biological Process	GO:0065007	biological regulation	36	13	23
GO:0008150	Biological Process	GO:0050896	response to stimulus	35	11	24
GO:0008150	Biological Process	GO:0050789	regulation of biological process	34	11	23
GO:0008150	Biological Process	GO:0032501	multicellular organismal process	33	14	19
GO:0008150	Biological Process	GO:0032502	developmental process	28	12	16
GO:0008150	Biological Process	GO:0051179	localization	21	12	9
GO:0008150	Biological Process	GO:0023052	signaling	17	6	11
GO:0008150	Biological Process	GO:0071840	cellular component organization or biogenesis	14	6	8
GO:0008150	Biological Process	GO:0051704	multi-organism process	11	3	8
GO:0008150	Biological Process	GO:0002376	immune system process	8	5	3
GO:0008150	Biological Process	GO:0022414	reproductive process	8	3	5

GO:0008150	Biological Process	GO:0000003	reproduction	8	3	5
GO:0008150	Biological Process	GO:0048518	positive regulation of biological process	8	5	3
GO:0008150	Biological Process	GO:0007610	behavior	6	4	2
GO:0008150	Biological Process	GO:0040011	locomotion	6	2	4
GO:0008150	Biological Process	GO:0048519	negative regulation of biological process	4	0	4
GO:0008150	Biological Process	GO:0040007	growth	3	1	2
GO:0008150	Biological Process	GO:0022610	biological adhesion	2	1	1
GO:0008150	Biological Process	GO:0044848	biological phase	1	1	0
GO:0005575	Cellular Component	GO:0044464	cell part	55	20	35
GO:0005575	Cellular Component	GO:0005623	cell	55	20	35
GO:0005575	Cellular Component	GO:0043226	organelle	44	17	27
GO:0005575	Cellular Component	GO:0016020	membrane	28	12	16
GO:0005575	Cellular Component	GO:0044422	organelle part	20	9	11
GO:0005575	Cellular Component	GO:0032991	macromolecular complex	14	8	6
GO:0005575	Cellular Component	GO:0044425	membrane part	12	6	6
GO:0005575	Cellular Component	GO:0031974	membrane-enclosed lumen	9	2	7
GO:0005575	Cellular Component	GO:0005576	extracellular region	6	4	2
GO:0005575	Cellular Component	GO:0044421	extracellular region part	4	3	1
GO:0005575	Cellular Component	GO:0044456	synapse part	3	3	0
GO:0005575	Cellular Component	GO:0045202	synapse	3	3	0
GO:0005575	Cellular Component	GO:0030054	cell junction	3	1	2
GO:0005575	Cellular Component	GO:0031012	extracellular matrix	1	1	0

**Table S4 Significantly enriched KEGG pathways in *Ostrinia furnacalis***

Pathway ID	Pathway	Pvalue	Differentially expressed genes with pathway annotation	All genes with pathway annotation
<b>ACB-BtS vs.ACB-FR</b>			<b>Totally 130</b>	<b>Totally 4856</b>
ko04213	Longevity regulating pathway - multiple species	0.000000	13 (10%)	85 (1.75%)
ko04141	Protein processing in endoplasmic reticulum	0.000036	14 (10.77%)	149 (3.07%)
ko04612	Antigen processing and presentation	0.000232	5 (3.85%)	22 (0.45%)
ko05134	Legionellosis	0.000518	6 (4.62%)	39 (0.8%)
ko00830	Retinol metabolism	0.005906	6 (4.62%)	62 (1.28%)
ko02010	ABC transporters	0.005906	6 (4.62%)	62 (1.28%)
ko01523	Antifolate resistance	0.008812	4 (3.08%)	31 (0.64%)
ko00980	Metabolism of xenobiotics by cytochrome P450	0.011320	6 (4.62%)	71 (1.46%)
ko04974	Protein digestion and absorption	0.011457	10 (7.69%)	163 (3.36%)
ko00982	Drug metabolism - cytochrome P450	0.021452	5 (3.85%)	60 (1.24%)
ko04972	Pancreatic secretion	0.037338	10 (7.69%)	197 (4.06%)
ko05204	Chemical carcinogenesis	0.038542	5 (3.85%)	70 (1.44%)
ko04975	Fat digestion and absorption	0.040604	5 (3.85%)	71 (1.46%)
ko04071	Sphingolipid signaling pathway	0.042732	5 (3.85%)	72 (1.48%)
ko04915	Estrogen signaling pathway	0.044927	5 (3.85%)	73 (1.5%)
<b>ACB-BtS vs. ACB-IeR</b>			<b>Totally 94</b>	<b>Totally 4856</b>
ko04972	Pancreatic secretion	0.000000	19 (20.21%)	197 (4.06%)
ko04974	Protein digestion and absorption	0.000000	16 (17.02%)	163 (3.36%)
ko00980	Metabolism of xenobiotics by cytochrome P450	0.000394	7 (7.45%)	71 (1.46%)
ko00982	Drug metabolism - cytochrome P450	0.000967	6 (6.38%)	60 (1.24%)

ko00830	Retinol metabolism	0.001151	6 (6.38%)	62 (1.28%)
ko05164	Influenza A	0.001210	9 (9.57%)	137 (2.82%)
ko05204	Chemical carcinogenesis	0.002168	6 (6.38%)	70 (1.44%)
ko04080	Neuroactive ligand-receptor interaction	0.002177	9 (9.57%)	149 (3.07%)
ko00040	Pentose and glucuronate interconversions	0.005361	5 (5.32%)	59 (1.21%)
ko02010	ABC transporters	0.006622	5 (5.32%)	62 (1.28%)
ko00561	Glycerolipid metabolism	0.006787	6 (6.38%)	88 (1.81%)
ko00140	Steroid hormone biosynthesis	0.007063	4 (4.26%)	40 (0.82%)
ko04975	Fat digestion and absorption	0.011631	5 (5.32%)	71 (1.46%)
ko00983	Drug metabolism - other enzymes	0.014218	6 (6.38%)	103 (2.12%)
ko00053	Ascorbate and aldarate metabolism	0.015376	4 (4.26%)	50 (1.03%)
ko00860	Porphyrin and chlorophyll metabolism	0.017555	4 (4.26%)	52 (1.07%)
ko01100	Metabolic pathways	0.031157	36 (38.3%)	1407 (28.97%)
ko04976	Bile secretion	0.049927	4 (4.26%)	72 (1.48%)

**Table S5 Differentially expressed genes among ACB-BtS, ACB-FR and ACB-IeR**

Gene ID	Description	log2(fc)	PValue	FDR
<b>ACB-BtS vs.ACB-FR</b>				
MSTRG.10516	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Trichinella sp. T9]	-1.73	5.84e-04	8.45e-03
MSTRG.11204	-	-1.29	6.23e-04	8.84e-03
MSTRG.11721	polyprotein [Operophtera brumata]	+2.54	1.48e-08	1.76e-06
MSTRG.12449	uncharacterized protein LOC114363438 [Ostrinia furnacalis]	-1.05	5.04e-05	1.30e-03
MSTRG.12462	uncharacterized protein LOC114363310 [Ostrinia furnacalis]	-1.56	1.09e-04	2.38e-03
MSTRG.1319	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Papilio machaon]	-2.48	2.57e-05	7.66e-04
MSTRG.13843	gag-pol polyprotein [Lasius niger]	+2.96	7.65e-06	2.95e-04
MSTRG.14142	UDP-glucuronosyltransferase 2B15-like [Ostrinia furnacalis]	+2.31	1.05e-15	8.21e-13
MSTRG.14366	PREDICTED: nuclear transcription factor Y subunit gamma-like [Amyeloidis transitella]	+2.46	5.14e-12	1.59e-09
MSTRG.14429	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like, partial [Papilio machaon]	-1.28	1.37e-04	2.84e-03
MSTRG.14691	-	+3.28	1.53e-18	2.00e-15
MSTRG.14718	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Eumeta japonica]	-1.08	1.81e-03	1.99e-02
MSTRG.14779	-	+2.95	4.84e-03	4.02e-02
MSTRG.14792	carboxylesterase, partial [Ostrinia furnacalis]	-1.24	7.27e-11	1.62e-08
MSTRG.14891	protein cps3-like [Manduca sexta]	+1.01	4.78e-03	3.99e-02
MSTRG.15032	polyprotein [Antheraea mylitta]	+2.44	2.13e-05	6.58e-04
MSTRG.15192	-	-1.20	7.59e-07	4.39e-05
MSTRG.15302	Histone-lysine N-methyltransferase SETMAR [Eumeta japonica]	+3.29	2.19e-03	2.28e-02
MSTRG.16274	-	-1.00	1.94e-03	2.09e-02
MSTRG.17777	arylphorin subunit alpha-like [Ostrinia furnacalis]	-5.71	1.91e-03	2.06e-02
MSTRG.18395	-	+2.77	6.64e-09	8.69e-07

MSTRG.18486	-	-2.63	2.25e-03	2.32e-02
MSTRG.1876	-	+1.59	6.43e-05	1.60e-03
MSTRG.18991	seminal fluid protein HACP044 [Danaus plexippus plexippus]	-1.98	1.00e-03	1.28e-02
MSTRG.19083	THAP domain-containing protein 2-like [Ostrinia furnacalis]	-1.67	4.47e-05	1.18e-03
MSTRG.19665	Transposable element Tc3 transposase [Eumeta japonica]	-1.17	8.12e-04	1.08e-02
MSTRG.19724	reverse transcriptase [Ostrinia nubilalis]	-3.34	1.07e-11	2.84e-09
MSTRG.1988	Histone-lysine N-methyltransferase SETMAR [Eumeta japonica]	+3.65	8.53e-04	1.12e-02
MSTRG.20008	PREDICTED: retrovirus-related Pol polyprotein from transposon 17.6 isoform X1 [Tribolium castaneum]	+1.49	2.29e-03	2.35e-02
MSTRG.20601	-	-1.20	3.18e-03	3.02e-02
MSTRG.20602	MULE domain-containing protein [Aphis craccivora]	-9.22	1.76e-04	3.46e-03
MSTRG.21164	ectopic P granules protein 5 homolog [Hyposmocoma kahamanoa]	-1.12	1.68e-03	1.88e-02
MSTRG.2161	-	-1.26	1.91e-09	2.88e-07
MSTRG.21877	-	-1.48	8.89e-05	2.04e-03
MSTRG.21950	rna-directed dna polymerase from mobile element jockey-like protein [Lasius niger]	+3.51	3.19e-03	3.02e-02
MSTRG.21972	-	-1.15	1.86e-07	1.47e-05
MSTRG.22677	Retrovirus-related Pol polyprotein from transposon 297 [Araneus ventricosus]	-1.87	2.57e-03	2.57e-02
MSTRG.23031	hypothetical protein evm_011585 [Chilo suppressalis]	-2.48	5.83e-03	4.62e-02
MSTRG.23064	-	-1.11	4.75e-04	7.24e-03
MSTRG.23493	hypothetical protein evm_000661 [Chilo suppressalis]	-2.26	2.25e-03	2.32e-02
MSTRG.23630	transmembrane protein adipocyte-associated 1 homolog isoform X2 [Hyposmocoma kahamanoa]	-1.60	5.37e-07	3.46e-05
MSTRG.24953	PREDICTED: vesicle transport protein GOT1B-like [Plutella xylostella]	-1.07	4.17e-03	3.65e-02
MSTRG.2537	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Eumeta japonica]	-1.74	5.55e-04	8.15e-03
MSTRG.25409	gamma-tubulin complex component 2-like isoform X2 [Ostrinia furnacalis]	-1.49	6.53e-04	9.15e-03
MSTRG.25437	uncharacterized protein LOC114351417 [Ostrinia furnacalis]	+2.02	9.49e-06	3.48e-04



MSTRG.25513	-	-1.04	4.39e-06	1.88e-04
MSTRG.25630	uncharacterized protein LOC114350796 [Ostrinia furnacalis]	+2.80	6.61e-05	1.64e-03
MSTRG.25758	-	-1.68	3.88e-05	1.05e-03
MSTRG.25972	gag-pol polyprotein [Lasius niger]	+2.54	7.00e-07	4.21e-05
MSTRG.25973	pol polyprotein-like protein [Leptotrombidium deliense]	+2.82	6.76e-05	1.66e-03
MSTRG.26169	uncharacterized protein LOC114362841 isoform X2 [Ostrinia furnacalis]	+3.33	1.43e-03	1.67e-02
MSTRG.26200	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R1 [Eumeta japonica]	-1.22	3.50e-10	6.44e-08
MSTRG.26234	extensin-like [Bombyx mandarina]	-1.23	1.46e-05	4.87e-04
MSTRG.26321	retroelement polyprotein [Glyptapanteles flavicoxis]	+4.17	1.72e-03	1.91e-02
MSTRG.26453	nephrin-like [Ostrinia furnacalis]	-4.29	5.88e-04	8.51e-03
MSTRG.2646	hypothetical protein evm_006816 [Chilo suppressalis]	-1.26	6.91e-05	1.69e-03
MSTRG.26467	equilibrative nucleoside transporter 1 isoform X3 [Ostrinia furnacalis]	+1.31	3.79e-04	6.10e-03
MSTRG.2777	Transposon Tf2-6 polyprotein [Eumeta japonica]	-3.21	9.37e-05	2.13e-03
MSTRG.2994	reverse transcriptase [Anguilla japonica]	+2.04	7.29e-07	4.30e-05
MSTRG.3070	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like isoform X1 [Amyelois transitella]	-1.95	4.28e-03	3.71e-02
MSTRG.3632	PREDICTED: neutral ceramidase [Papilio xuthus]	-2.51	3.60e-05	9.93e-04
MSTRG.4415	-	-5.47	7.72e-06	2.97e-04
MSTRG.4860	src substrate cortactin [Spodoptera litura]	-1.58	6.67e-06	2.61e-04
MSTRG.5318	Transposon Tf2-6 polyprotein [Eumeta japonica]	-2.21	1.52e-13	8.12e-11
MSTRG.625	DNA transposase THAP9 [Araneus ventricosus]	-1.07	2.95e-03	2.86e-02
MSTRG.6300	microtubule-associated serine/threonine-protein kinase 4 [Ostrinia furnacalis]	-4.57	1.83e-06	9.02e-05
MSTRG.6385	-	+1.58	3.20e-06	1.46e-04
MSTRG.6636	hypothetical protein evm_003645 [Chilo suppressalis]	+1.59	1.49e-04	3.05e-03
MSTRG.7260	gag-pol polyprotein [Lasius niger]	+1.11	8.50e-05	1.97e-03

MSTRG.8248	-	+2.85	1.27e-03	1.52e-02
MSTRG.9028	-	-1.44	4.88e-03	4.05e-02
MSTRG.9141	THAP domain-containing protein 2-like [Ostrinia furnacalis]	-1.59	3.96e-03	3.51e-02
MSTRG.9260	-	+11.37	3.15e-05	8.82e-04
MSTRG.9261	-	-1.58	1.31e-03	1.56e-02
MSTRG.9381	-	-1.79	1.83e-04	3.57e-03
MSTRG.9428	Intraflagellar transport protein 81 [Folsomia candida]	+5.39	9.59e-05	2.15e-03
ncbi_114349548	glycerol-3-phosphate dehydrogenase, mitochondrial-like isoform X4 [Ostrinia furnacalis]	+1.73	3.12e-22	7.35e-19
ncbi_114349570	centromere protein I-like [Ostrinia furnacalis]	-1.15	7.32e-04	1.00e-02
ncbi_114349603	pancreatic lipase-related protein 2-like [Ostrinia furnacalis]	+1.78	1.21e-03	1.47e-02
ncbi_114349629	pancreatic triacylglycerol lipase-like [Ostrinia furnacalis]	+1.98	6.78e-05	1.66e-03
ncbi_114349648	AAEL013537-PB [Aedes aegypti]	+2.20	6.00e-03	4.72e-02
ncbi_114349651	cyclic nucleotide-gated cation channel beta-3 isoform X1 [Ostrinia furnacalis]	+2.32	3.53e-09	5.07e-07
ncbi_114349707	Kynurenine formamidase [Danaus plexippus plexippus]	-1.28	1.92e-03	2.07e-02
ncbi_114349711	Formin-like protein 2 [Papilio machaon]	-1.06	1.15e-03	1.42e-02
ncbi_114349888	ribonucleoside-diphosphate reductase large subunit [Ostrinia furnacalis]	-1.09	8.05e-06	3.07e-04
ncbi_114349930	PREDICTED: ice nucleation protein-like [Amyeloidis transitella]	+5.55	4.87e-04	7.38e-03
ncbi_114349932	ATP-binding cassette sub-family A member 1-like [Ostrinia furnacalis]	+4.03	2.27e-06	1.08e-04
ncbi_114349935	diacylglycerol kinase theta [Hyposmocoma kahamanoa]	+6.00	1.63e-07	1.33e-05
ncbi_114350009	nuclease HARBI1-like [Acyrtosiphon pisum]	-2.18	5.92e-04	8.53e-03
ncbi_114350010	myb/SANT-like DNA-binding domain-containing protein 4, partial [Photinus pyralis]	-1.03	1.05e-04	2.32e-03
ncbi_114350169	asparagine synthetase [glutamine-hydrolyzing] [Ostrinia furnacalis]	+1.40	5.53e-13	2.41e-10
ncbi_114350216	kynureninase [Bombyx mori]	-2.07	1.08e-04	2.37e-03
ncbi_114350246	tyramine beta-hydroxylase isoform X1 [Ostrinia furnacalis]	-3.49	1.86e-03	2.02e-02
ncbi_114350299	Retrovirus-related Pol polyprotein from transposon 297 [Eumeta japonica]	-9.81	1.11e-03	1.38e-02

ncbi_114350307	Gag-pol polyprotein [Operophtera brumata]	+2.11	4.62e-04	7.10e-03
ncbi_114350454	larval cuticle protein LCP-17-like [Ostrinia furnacalis]	+1.35	1.54e-07	1.28e-05
ncbi_114350455	double-stranded RNA-specific editase 1-like [Ostrinia furnacalis]	-1.21	1.06e-10	2.19e-08
ncbi_114350508	probable basic-leucine zipper transcription factor G [Bombyx mori]	-1.44	3.16e-03	3.00e-02
ncbi_114350515	piggyBac transposable element-derived protein 4-like isoform X1 [Ostrinia furnacalis]	-1.07	2.08e-05	6.46e-04
ncbi_114350530	protein unc-93 homolog A [Helicoverpa armigera]	-1.56	8.04e-04	1.07e-02
ncbi_114350533	Probable RNA-directed DNA polymerase from transposon BS [Eumeta japonica]	+2.55	3.09e-07	2.15e-05
ncbi_114350537	Endonuclease-reverse transcriptase [Operophtera brumata]	-1.86	3.30e-19	4.86e-16
ncbi_114350556	PREDICTED: LOW QUALITY PROTEIN: transmembrane protein 53-like [Plutella xylostella]	+1.29	1.08e-11	2.84e-09
ncbi_114350635	tetraspanin-33-like [Ostrinia furnacalis]	-1.29	3.15e-04	5.30e-03
ncbi_114350651	uncharacterized protein LOC114350651 [Ostrinia furnacalis]	-1.68	5.74e-09	7.68e-07
ncbi_114350698	cytochrome P450 CYP12A2-like [Ostrinia furnacalis]	-1.19	3.75e-07	2.49e-05
ncbi_114350734	Ribonuclease H-like domain,Integrase, catalytic core,Reverse transcriptase domain [Cinara cedri]	-2.31	3.22e-03	3.03e-02
ncbi_114350784	THAP domain-containing protein 2 [Eumeta japonica]	-1.68	2.66e-04	4.75e-03
ncbi_114350885	cubilin homolog [Ostrinia furnacalis]	+3.36	9.39e-05	2.13e-03
ncbi_114351007	transcription factor Adf-1-like [Trichoplusia ni]	-1.30	5.01e-03	4.14e-02
ncbi_114351014	testis-specific serine/threonine-protein kinase 3-like [Ostrinia furnacalis]	+9.00	1.47e-03	1.70e-02
ncbi_114351044	gag-pol polyprotein precursor [Lasius niger]	-1.44	1.01e-03	1.29e-02
ncbi_114351064	xenotropic and polytropic retrovirus receptor 1-like, partial [Ostrinia furnacalis]	-1.23	7.15e-05	1.73e-03
ncbi_114351300	mucin-5AC-like isoform X1 [Ostrinia furnacalis]	+5.02	1.04e-26	3.07e-23
ncbi_114351333	caspase Drnc [Ostrinia furnacalis]	-1.07	1.05e-03	1.32e-02
ncbi_114351347	Gag-pol polyprotein [Operophtera brumata]	+2.97	1.53e-03	1.75e-02
ncbi_114351356	AGAP003808-PA [Anopheles gambiae str. PEST] [Anopheles gambiae]	-1.46	6.40e-03	4.97e-02
ncbi_114351397	kunitz-type U19-barytoxin-T11a-like isoform X1 [Ostrinia furnacalis]	+1.31	5.48e-06	2.26e-04
ncbi_114351477	succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial [Ostrinia furnacalis]	-1.01	2.07e-06	1.02e-04

ncbi_114351540	kinesin-like protein KIF18A isoform X1 [Ostrinia furnacalis]	-1.02	3.19e-03	3.02e-02
ncbi_114351572	Zinc finger DNA binding protein [Operophtera brumata]	-2.94	3.67e-11	8.81e-09
ncbi_114351648	AAEL012860-PA [Aedes aegypti]	+1.48	5.45e-06	2.25e-04
ncbi_114351652	PREDICTED: alpha-glucosidase 2-like [Papilio xuthus]	-1.35	9.85e-06	3.58e-04
ncbi_114351683	Apolipophorin [Papilio xuthus]	-2.24	2.27e-06	1.08e-04
ncbi_114351695	voltage-dependent calcium channel subunit alpha-2/delta-3 isoform X1 [Ostrinia furnacalis]	-5.13	2.05e-03	2.18e-02
ncbi_114351743	mitochondrial enolase superfamily member 1-like [Ostrinia furnacalis]	-1.28	3.47e-04	5.69e-03
ncbi_114351758	Sortilin-related receptor [Papilio xuthus]	+1.27	4.30e-03	3.72e-02
ncbi_114351915	transmembrane protease serine 9-like [Ostrinia furnacalis]	+1.07	5.74e-11	1.33e-08
ncbi_114351936	trypsin, alkaline C-like isoform X1 [Ostrinia furnacalis]	+1.29	1.64e-07	1.33e-05
ncbi_114351939	trypsin, alkaline C-like [Ostrinia furnacalis]	+1.33	2.86e-08	3.15e-06
ncbi_114351953	monocarboxylate transporter 9-like [Ostrinia furnacalis]	-2.15	6.74e-05	1.66e-03
ncbi_114351970	mucin-5AC-like [Ostrinia furnacalis]	-4.44	5.95e-07	3.77e-05
ncbi_114352033	CD109 antigen-like [Ostrinia furnacalis]	+1.13	9.72e-04	1.25e-02
ncbi_114352176	myosin-binding protein H-like [Bombyx mandarina]	-1.11	3.19e-07	2.21e-05
ncbi_114352248	WD repeat-containing protein 7-like [Ostrinia furnacalis]	-1.19	1.89e-03	2.05e-02
ncbi_114352314	tigger transposable element-derived protein 6-like isoform X1 [Manduca sexta]	-5.35	5.00e-18	5.36e-15
ncbi_114352315	Integrase catalytic domain-containing protein [Aphis craccivora]	+2.37	7.48e-12	2.15e-09
ncbi_114352321	delta(24)-sterol reductase-like isoform X2 [Ostrinia furnacalis]	+1.37	5.27e-13	2.39e-10
ncbi_114352435	ras GTPase-activating protein 1-like [Ostrinia furnacalis]	-1.02	1.46e-03	1.70e-02
ncbi_114352487	collagenase-like [Ostrinia furnacalis]	+1.18	2.15e-18	2.53e-15
ncbi_114352553	trypsin, alkaline A-like [Ostrinia furnacalis]	+2.29	4.01e-04	6.39e-03
ncbi_114352599	RING finger protein 145 [Papilio xuthus]	-1.22	6.24e-04	8.84e-03
ncbi_114352631	UDP-glucuronosyltransferase 2B15-like [Ostrinia furnacalis]	+7.07	2.98e-07	2.10e-05
ncbi_114352700	pickpocket protein 28-like isoform X1 [Aphis craccivora]	-5.27	7.74e-06	2.97e-04

ncbi_114352709	zinc finger protein 468-like [Ostrinia furnacalis]	-1.45	4.19e-03	3.66e-02
ncbi_114352740	SMC domain protein [Heliothis subflexa]	-6.43	3.79e-06	1.67e-04
ncbi_114352770	ommochrome-binding protein-like [Spodoptera litura]	-1.23	2.53e-03	2.54e-02
ncbi_114352777	protein lethal(2)essential for life-like [Ostrinia furnacalis]	-2.55	2.38e-04	4.34e-03
ncbi_114352796	uncharacterized protein LOC114352796 [Ostrinia furnacalis]	+2.16	3.84e-03	3.44e-02
ncbi_114352816	proline-rich extensin-like protein EPR1 isoform X1 [Ostrinia furnacalis]	-1.01	6.42e-04	9.05e-03
ncbi_114352834	ATP-dependent RNA helicase DDX54 [Ostrinia furnacalis]	+1.17	1.55e-06	7.81e-05
ncbi_114352883	alpha-tocopherol transfer protein-like [Ostrinia furnacalis]	+2.03	9.50e-05	2.14e-03
ncbi_114352885	probable kinetochore protein NDC80 [Bicyclus anynana]	-3.61	1.03e-06	5.54e-05
ncbi_114352903	L-lactate dehydrogenase B chain-like [Ostrinia furnacalis]	-7.57	4.19e-04	6.60e-03
ncbi_114352955	nicotinic acid-CoA ligase pyr1-like [Ostrinia furnacalis]	+1.12	3.46e-07	2.34e-05
ncbi_114352982	piggyBac transposable element-derived protein 4-like [Ostrinia furnacalis]	-1.55	1.23e-03	1.48e-02
ncbi_114352989	retinal-specific ATP-binding cassette transporter-like [Ostrinia furnacalis]	+3.10	1.66e-05	5.44e-04
ncbi_114353006	serine hydrolase-like protein [Ostrinia furnacalis]	+1.43	1.38e-06	7.11e-05
ncbi_114353036	polyprotein [Antheraea mylitta]	+1.30	1.29e-06	6.77e-05
ncbi_114353077	cytochrome P450 9e2-like [Ostrinia furnacalis]	-2.52	9.89e-05	2.20e-03
ncbi_114353086	Cytochrome P450 9e2 [Papilio xuthus]	-1.35	2.31e-08	2.57e-06
ncbi_114353206	lipase member I-like [Ostrinia furnacalis]	-1.85	3.73e-03	3.37e-02
ncbi_114353277	pancreatic lipase-related protein 2-like [Ostrinia furnacalis]	+1.81	1.82e-03	2.00e-02
ncbi_114353390	synaptic vesicle glycoprotein 2C-like isoform X1 [Ostrinia furnacalis]	-1.86	1.73e-03	1.92e-02
ncbi_114353417	synaptotagmin 1 isoform X1 [Ostrinia furnacalis]	-1.12	1.01e-04	2.23e-03
ncbi_114353454	probable cytochrome P450 301a1, mitochondrial [Ostrinia furnacalis]	-1.72	4.13e-05	1.11e-03
ncbi_114353474	neutral ceramidase, partial [Ostrinia furnacalis]	-1.59	5.30e-04	7.87e-03
ncbi_114353522	synaptic vesicle glycoprotein 2A-like [Ostrinia furnacalis]	-1.34	1.59e-05	5.25e-04
ncbi_114353646	testis-expressed protein 10-like [Ostrinia furnacalis]	+1.14	9.68e-04	1.24e-02

ncbi_114353653	protein maternal effect lethal 26-like [Ostrinia furnacalis]	-1.33	3.46e-06	1.56e-04
ncbi_114353764	protein lethal(2)essential for life-like [Ostrinia furnacalis]	-1.50	1.74e-12	6.22e-10
ncbi_114353955	uncharacterized protein LOC114353955 [Ostrinia furnacalis]	+10.92	1.22e-04	2.60e-03
ncbi_114354032	protein PFC0760c-like [Vanessa tameamea]	-1.77	2.43e-04	4.41e-03
ncbi_114354065	solute carrier family 2, facilitated glucose transporter member 1-like [Ostrinia furnacalis]	-3.34	4.27e-04	6.67e-03
ncbi_114354101	laccase-2 [Ostrinia furnacalis]	-2.44	5.26e-03	4.31e-02
ncbi_114354259	heat shock protein 68-like [Ostrinia furnacalis]	-2.32	6.31e-16	5.31e-13
ncbi_114354277	facilitated trehalose transporter Tret1-like [Ostrinia furnacalis]	-2.49	6.30e-03	4.91e-02
ncbi_114354284	PREDICTED: cilia- and flagella-associated protein 45-like [Papilio machaon]	-4.53	1.12e-03	1.39e-02
ncbi_114354285	ATP-binding cassette sub-family G member 5 isoform X1 [Ostrinia furnacalis]	-2.60	4.92e-04	7.42e-03
ncbi_114354289	multidrug resistance-associated protein 4-like [Ostrinia furnacalis]	-1.71	4.25e-04	6.65e-03
ncbi_114354309	multidrug resistance-associated protein 4-like [Galleria mellonella]	-9.37	5.80e-07	3.69e-05
ncbi_114354320	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase hpo-8 [Ostrinia furnacalis]	-1.01	4.83e-06	2.03e-04
ncbi_114354442	acetylcholine receptor subunit alpha-like [Ostrinia furnacalis]	+3.01	4.31e-03	3.72e-02
ncbi_114354545	Reverse transcriptase and recombinase [Operophtera brumata]	-1.60	1.33e-03	1.57e-02
ncbi_114354689	cell wall protein DAN4-like [Hyposmocoma kahamanoa]	-4.83	2.31e-03	2.37e-02
ncbi_114354720	next to BRCA1 gene 1 protein-like isoform X1 [Ostrinia furnacalis]	-1.53	5.74e-10	9.98e-08
ncbi_114354721	protein lethal(2)essential for life-like [Ostrinia furnacalis]	-1.57	8.10e-11	1.77e-08
ncbi_114354725	heat shock protein 68-like [Ostrinia furnacalis]	-3.26	3.00e-08	3.26e-06
ncbi_114354966	tyramine receptor 1 [Ostrinia furnacalis]	+1.54	4.43e-03	3.78e-02
ncbi_114355040	Uncharacterized 50 kDa protein in type I retrotransposable element R1DM [Eumeta japonica]	-1.40	5.29e-04	7.85e-03
ncbi_114355095	GDP-fucose protein O-fucosyltransferase 2-like [Ostrinia furnacalis]	-1.02	3.81e-03	3.42e-02
ncbi_114355216	fat-like cadherin-related tumor suppressor homolog [Spodoptera litura]	-1.17	8.45e-09	1.04e-06
ncbi_114355250	uncharacterized protein LOC114355250, partial [Ostrinia furnacalis]	+2.24	1.76e-03	1.95e-02
ncbi_114355390	protein kinase C isoform X2 [Ostrinia furnacalis]	-1.45	2.80e-03	2.75e-02

ncbi_114355439	Integrase catalytic domain-containing protein, partial [ <i>Aphis craccivora</i> ]	-3.73	3.05e-05	8.61e-04
ncbi_114355467	trypsin, alkaline C-like [ <i>Ostrinia furnacalis</i> ]	+2.54	2.68e-04	4.76e-03
ncbi_114355559	fungal protease inhibitor-1-like [ <i>Ostrinia furnacalis</i> ]	-1.60	3.15e-03	2.99e-02
ncbi_114355671	inter-alpha-trypsin inhibitor heavy chain H4-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	-1.06	2.39e-03	2.44e-02
ncbi_114355715	C-type lectin [ <i>Heliothis virescens</i> ]	+1.68	3.44e-03	3.19e-02
ncbi_114355741	Integrase catalytic domain-containing protein [ <i>Aphis craccivora</i> ]	-1.84	2.05e-11	5.03e-09
ncbi_114355779	Retrovirus-related Pol polyprotein from transposon 297 [ <i>Eumeta japonica</i> ]	-3.93	1.60e-05	5.28e-04
ncbi_114355780	Zinc finger DNA binding protein [ <i>Operophtera brumata</i> ]	-5.48	9.76e-13	3.83e-10
ncbi_114355784	transcription factor Sox-12-like [ <i>Ostrinia furnacalis</i> ]	-1.54	3.02e-08	3.26e-06
ncbi_114355894	Armadillo-type fold,Armadillo-like helical [ <i>Cinara cedri</i> ]	-1.77	1.00e-03	1.28e-02
ncbi_114355939	Mutant cadherin [ <i>Operophtera brumata</i> ]	+1.32	1.34e-03	1.59e-02
ncbi_114355963	kynurenine formamidase isoform X1 [ <i>Ostrinia furnacalis</i> ]	-1.09	1.70e-08	1.96e-06
ncbi_114355992	Retrovirus-related Pol polyprotein from transposon 412 [ <i>Eumeta japonica</i> ]	+3.05	8.38e-05	1.95e-03
ncbi_114356144	trypsin-like [ <i>Ostrinia furnacalis</i> ]	-1.13	4.24e-03	3.68e-02
ncbi_114356174	Zinc finger DNA binding protein [ <i>Operophtera brumata</i> ]	-1.39	1.70e-04	3.39e-03
ncbi_114356221	heat shock protein 68-like [ <i>Ostrinia furnacalis</i> ]	-1.56	2.53e-15	1.57e-12
ncbi_114356222	protein lethal(2)essential for life-like [ <i>Ostrinia furnacalis</i> ]	-2.68	1.62e-05	5.34e-04
ncbi_114356285	histone acetyltransferase KAT6A-like [ <i>Manduca sexta</i> ]	-7.54	1.86e-03	2.02e-02
ncbi_114356356	uncharacterized protein LOC114356356 [ <i>Ostrinia furnacalis</i> ]	-1.43	2.63e-05	7.80e-04
ncbi_114356426	flexible cuticle protein 12-like [ <i>Ostrinia furnacalis</i> ]	+2.24	1.43e-08	1.72e-06
ncbi_114356505	ankyrin3 [ <i>Culex quinquefasciatus</i> ]	-1.11	1.27e-09	2.03e-07
ncbi_114356515	optineurin isoform X1 [ <i>Ostrinia furnacalis</i> ]	-1.05	1.29e-06	6.77e-05
ncbi_114356554	DNA-directed RNA polymerase I subunit RPA2 [ <i>Ostrinia furnacalis</i> ]	+1.30	9.14e-07	5.10e-05
ncbi_114356560	zinc finger HIT domain-containing protein 2 [ <i>Trichoplusia ni</i> ]	-1.68	1.63e-03	1.84e-02
ncbi_114356594	RNA exonuclease 5 [ <i>Ostrinia furnacalis</i> ]	-1.01	1.13e-03	1.40e-02

ncbi_114356609	oxidative stress-responsive serine-rich protein 1 [Helicoverpa armigera]	-1.35	3.08e-04	5.21e-03
ncbi_114356611	formin-A-like [Ostrinia furnacalis]	+2.62	5.19e-03	4.26e-02
ncbi_114356687	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like isoform X1 [Amyeloidis transitella]	+2.80	1.32e-03	1.57e-02
ncbi_114356758	sorting nexin-4-like isoform X1 [Ostrinia furnacalis]	-1.04	2.37e-07	1.76e-05
ncbi_114356863	ORF [Drosophila melanogaster]	-1.21	3.08e-03	2.94e-02
ncbi_114356943	Gag-pol polyprotein [Operophtera brumata]	+2.05	1.92e-04	3.71e-03
ncbi_114356982	Jerky-like, partial [Aphis craccivora]	-3.58	3.67e-03	3.34e-02
ncbi_114357156	lipid droplet localized protein-like [Ostrinia furnacalis]	-3.24	4.38e-03	3.76e-02
ncbi_114357161	organic cation transporter protein-like, partial [Ostrinia furnacalis]	+1.03	2.88e-05	8.37e-04
ncbi_114357207	uncharacterized protein LOC114357207 [Ostrinia furnacalis]	-1.23	1.02e-03	1.29e-02
ncbi_114357236	zinc finger DNA binding protein [Danaus plexippus plexippus]	-2.26	1.66e-06	8.30e-05
ncbi_114357237	probable sodium-coupled neutral amino acid transporter 6 [Ostrinia furnacalis]	+1.65	1.11e-04	2.41e-03
ncbi_114357324	secretory phospholipase A2 receptor-like [Ostrinia furnacalis]	-5.52	6.12e-04	8.73e-03
ncbi_114357385	nucleolar protein 58 [Ostrinia furnacalis]	+1.06	2.28e-10	4.32e-08
ncbi_114357436	Reverse transcriptase and recombinase [Operophtera brumata]	-5.41	3.74e-03	3.37e-02
ncbi_114357451	organic cation transporter protein-like [Ostrinia furnacalis]	-2.36	5.30e-28	2.08e-24
ncbi_114357498	Gag-pol polyprotein [Operophtera brumata]	+1.03	1.08e-03	1.35e-02
ncbi_114357556	Integrase catalytic domain-containing protein, partial [Aphis craccivora]	-2.97	2.46e-03	2.49e-02
ncbi_114357558	sulfotransferase family cytosolic 1B member 1-like [Ostrinia furnacalis]	+1.28	5.67e-05	1.43e-03
ncbi_114357580	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase-like isoform X3 [Ostrinia furnacalis]	+2.65	2.76e-04	4.86e-03
ncbi_114357591	Integrase catalytic domain-containing protein, partial [Aphis craccivora]	+1.65	2.44e-04	4.42e-03
ncbi_114357630	Pogo transposable element with KRAB domain [Papilio machaon]	-2.61	8.44e-08	7.71e-06
ncbi_114357743	protein NYNRIN-like [Hypomocoma kahamanoa]	-2.66	7.28e-12	2.14e-09
ncbi_114357777	cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A-like [Ostrinia furnacalis]	-3.06	9.09e-04	1.18e-02



ncbi_114357858	A disintegrin and metalloproteinase with thrombospondin motifs 7 [Ostrinia furnacalis]	+1.40	3.27e-12	1.07e-09
ncbi_114357864	testisin [Ostrinia furnacalis]	+2.38	9.72e-04	1.25e-02
ncbi_114357904	Retrovirus-related Pol polyprotein from transposon opus [Eumeta japonica]	-2.55	2.07e-04	3.90e-03
ncbi_114357933	sorting nexin-2 [Ostrinia furnacalis]	-1.05	2.19e-09	3.26e-07
ncbi_114357956	DNA polymerase nu-like [Helicoverpa armigera]	-3.35	6.82e-05	1.67e-03
ncbi_114357985	toll-like receptor 6 [Ostrinia furnacalis]	-1.31	1.04e-10	2.18e-08
ncbi_114358032	sulfotransferase family cytosolic 1B member 1-like [Ostrinia furnacalis]	+3.01	2.40e-06	1.13e-04
ncbi_114358252	NADPH oxidase 5, partial [Ostrinia furnacalis]	-5.28	1.33e-04	2.79e-03
ncbi_114358258	ATP-sensitive inward rectifier potassium channel 1-like [Ostrinia furnacalis]	-1.62	6.00e-10	1.02e-07
ncbi_114358284	synaptonemal complex protein 1-like [Ostrinia furnacalis]	-2.92	3.91e-03	3.48e-02
ncbi_114358317	reticulocyte-binding protein 2 homolog a-like [Bombyx mandarina]	-1.60	1.52e-03	1.74e-02
ncbi_114358381	GATA zinc finger domain-containing protein 10-like [Spodoptera litura]	+2.03	2.56e-03	2.56e-02
ncbi_114358382	protein lethal(2)essential for life-like [Ostrinia furnacalis]	-2.36	1.99e-16	1.81e-13
ncbi_114358386	protein lethal(2)essential for life-like [Ostrinia furnacalis]	-1.48	1.52e-09	2.36e-07
ncbi_114358387	protein lethal(2)essential for life-like [Ostrinia furnacalis]	-1.82	6.41e-20	1.26e-16
ncbi_114358448	Endonuclease-reverse transcriptase [Operophtera brumata]	-2.43	4.43e-08	4.24e-06
ncbi_114358494	attacin-like [Ostrinia furnacalis]	+2.51	3.41e-03	3.17e-02
ncbi_114358595	Integrase catalytic domain-containing protein [Aphis craccivora]	+3.97	4.21e-04	6.61e-03
ncbi_114358601	CLUMA_CG019058, isoform A [Clunio marinus]	-1.72	2.19e-04	4.06e-03
ncbi_114358603	phospholipase A1 VesT1.02-like [Ostrinia furnacalis]	-1.02	5.79e-03	4.61e-02
ncbi_114358606	sulfotransferase family cytosolic 1B member 1-like [Ostrinia furnacalis]	-1.20	1.74e-06	8.62e-05
ncbi_114358612	testis-expressed protein 2 [Galleria mellonella]	-1.08	4.47e-09	6.13e-07
ncbi_114358650	YqaJ domain-containing protein [Aphis craccivora]	+9.18	3.52e-07	2.37e-05
ncbi_114358671	reverse transcriptase [Anopheles gambiae]	-1.17	1.30e-03	1.55e-02
ncbi_114358690	collagenase-like [Ostrinia furnacalis]	+1.73	4.65e-13	2.19e-10

ncbi_114358723	collagenase-like [Ostrinia furnacalis]	+1.44	1.31e-16	1.28e-13
ncbi_114358734	collagenase-like [Ostrinia furnacalis]	+1.26	3.25e-09	4.72e-07
ncbi_114358757	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Amyeloides transitella]	+1.57	6.71e-04	9.33e-03
ncbi_114358775	larval cuticle protein LCP-17-like [Ostrinia furnacalis]	+1.86	3.90e-09	5.53e-07
ncbi_114358820	ATP-dependent DNA helicase PIF1 [Eumeta japonica]	-1.39	3.35e-03	3.13e-02
ncbi_114358879	uncharacterized protein LOC114358879 [Ostrinia furnacalis]	+1.37	5.76e-10	9.98e-08
ncbi_114358890	Envelope fusion protein-like Protein [Tribolium castaneum]	-1.37	1.52e-06	7.80e-05
ncbi_114358899	lysoplasmalogenase [Ostrinia furnacalis]	-1.37	4.60e-03	3.88e-02
ncbi_114359071	Pro-Pol polyprotein [Folsomia candida]	+4.84	2.63e-04	4.70e-03
ncbi_114359074	carboxypeptidase B-like [Ostrinia furnacalis]	+1.00	1.72e-07	1.39e-05
ncbi_114359077	carboxypeptidase B-like [Ostrinia furnacalis]	+1.07	1.58e-05	5.23e-04
ncbi_114359082	peptide transporter family 1-like [Ostrinia furnacalis]	-1.41	9.88e-07	5.39e-05
ncbi_114359083	carboxypeptidase B-like [Ostrinia furnacalis]	-1.13	9.57e-05	2.15e-03
ncbi_114359099	saccharopine dehydrogenase-like oxidoreductase [Ostrinia furnacalis]	-3.87	3.32e-13	1.63e-10
ncbi_114359229	proton-coupled folate transporter-like [Ostrinia furnacalis]	-1.34	4.83e-03	4.02e-02
ncbi_114359336	polyprotein [Antheraea mylitta]	+1.67	1.34e-11	3.42e-09
ncbi_114359399	sarcoplasmic calcium-binding proteins I, III, and IV-like, partial [Nilaparvata lugens]	-1.23	1.12e-10	2.27e-08
ncbi_114359533	Pre-mRNA-processing factor 17 [Operophtera brumata]	+3.21	1.80e-03	1.98e-02
ncbi_114359657	shavenoid [Papilio xuthus]	-3.40	6.26e-07	3.92e-05
ncbi_114359671	arylphorin subunit alpha-like [Ostrinia furnacalis]	-6.70	6.15e-03	4.82e-02
ncbi_114359766	zinc metalloproteinase nas-13-like [Ostrinia furnacalis]	+1.29	5.72e-06	2.29e-04
ncbi_114359791	calsequestrin-1-like [Spodoptera litura]	-4.74	9.14e-06	3.40e-04
ncbi_114359847	tektin-3-like isoform X1 [Ostrinia furnacalis]	+5.10	3.37e-04	5.55e-03
ncbi_114359874	gamma-glutamyl hydrolase-like [Ostrinia furnacalis]	-2.18	2.09e-05	6.47e-04
ncbi_114359889	annulin-like isoform X1 [Ostrinia furnacalis]	-2.32	2.79e-04	4.89e-03

ncbi_114360063	piggyBac transposable element-derived protein 3-like, partial [Danaus plexippus plexippus]	+1.60	6.64e-05	1.64e-03
ncbi_114360122	epidermal retinol dehydrogenase 2-like [Ostrinia furnacalis]	-1.06	1.67e-04	3.35e-03
ncbi_114360123	short-chain dehydrogenase/reductase family 16C member 6 [Ostrinia furnacalis]	-4.23	3.90e-07	2.58e-05
ncbi_114360125	MORN repeat-containing protein 4-like isoform X1 [Ostrinia furnacalis]	-2.29	9.18e-07	5.10e-05
ncbi_114360162	1-acyl-sn-glycerol-3-phosphate acyltransferase beta-like [Ostrinia furnacalis]	-1.12	5.10e-05	1.31e-03
ncbi_114360250	Integrase catalytic domain-containing protein, partial [Aphis craccivora]	-1.97	7.57e-04	1.02e-02
ncbi_114360251	Gag-pol polyprotein [Operophtera brumata]	-1.30	2.79e-04	4.89e-03
ncbi_114360286	Retrovirus-related Pol polyprotein from transposon 297 [Eumeta japonica]	-10.16	2.54e-04	4.58e-03
ncbi_114360325	alpha-scruin [Bicyclus anynana]	-2.21	8.70e-06	3.26e-04
ncbi_114360387	torso-like protein isoform X5 [Ostrinia furnacalis]	-1.22	9.68e-05	2.16e-03
ncbi_114360401	conserved oligomeric Golgi complex subunit 7 [Ostrinia furnacalis]	+1.67	1.51e-04	3.09e-03
ncbi_114360499	trypsin, alkaline A-like [Ostrinia furnacalis]	+10.67	3.10e-04	5.24e-03
ncbi_114360511	esterase FE4-like [Ostrinia furnacalis]	-3.37	4.26e-03	3.70e-02
ncbi_114360532	retinol-binding protein [Culex quinquefasciatus]	+2.58	4.84e-03	4.02e-02
ncbi_114360624	eukaryotic translation initiation factor 4E-like [Ostrinia furnacalis]	-1.21	7.69e-09	9.67e-07
ncbi_114360773	glutathione S-transferase 1-like [Ostrinia furnacalis]	+2.75	1.46e-13	8.12e-11
ncbi_114360790	venom serine carboxypeptidase [Ostrinia furnacalis]	+1.30	3.47e-12	1.10e-09
ncbi_114360800	gag-pol polyprotein precursor [Lasius niger]	+2.33	4.41e-03	3.77e-02
ncbi_114360807	chymotrypsin-like elastase family member 2A [Ostrinia furnacalis]	-1.27	1.78e-04	3.48e-03
ncbi_114360825	calphotin-like [Ostrinia furnacalis]	-1.31	2.41e-19	4.05e-16
ncbi_114360831	ankyrin repeat and LEM domain-containing protein 1-like isoform X1 [Galleria mellonella]	-1.12	3.26e-07	2.25e-05
ncbi_114360837	coatomer subunit epsilon-like [Ostrinia furnacalis]	-1.01	8.08e-04	1.07e-02
ncbi_114360920	lachesin-like [Ostrinia furnacalis]	-3.63	1.99e-03	2.13e-02
ncbi_114360950	ORF1p [Operophtera brumata]	-1.27	6.10e-04	8.73e-03
ncbi_114361117	collagen alpha-1(III) chain-like [Ostrinia furnacalis]	+1.54	5.80e-03	4.61e-02

ncbi_114361136	uncharacterized protein LOC114361136 [Ostrinia furnacalis]	-1.08	6.07e-06	2.41e-04
ncbi_114361175	tyrosine-protein kinase Src64B-like [Ostrinia furnacalis]	-1.08	3.06e-04	5.20e-03
ncbi_114361190	rho guanine nucleotide exchange factor 5 isoform X1 [Trichoplusia ni]	-1.08	2.14e-07	1.63e-05
ncbi_114361273	alpha,alpha-trehalose-phosphate synthase [UDP-forming] [Ostrinia furnacalis]	+1.01	3.25e-04	5.38e-03
ncbi_114361322	CD63 antigen-like [Ostrinia furnacalis]	-1.28	3.36e-03	3.14e-02
ncbi_114361430	blastopia polypeptide [Lasius niger]	-1.42	4.78e-03	3.99e-02
ncbi_114361495	luciferin 4-monooxygenase-like isoform X1 [Ostrinia furnacalis]	-3.78	4.15e-03	3.63e-02
ncbi_114361498	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Papilio machaon]	+1.95	9.90e-06	3.59e-04
ncbi_114361500	nephrin-like [Ostrinia furnacalis]	+1.33	1.39e-05	4.69e-04
ncbi_114361507	PREDICTED: probable salivary secreted peptide [Amyelois transitella]	+1.00	8.11e-05	1.89e-03
ncbi_114361580	heat shock protein Hsp-12.2-like [Ostrinia furnacalis]	-2.85	3.41e-30	2.01e-26
ncbi_114361602	Microtubule binding protein, partial [Operophtera brumata]	+2.34	1.16e-03	1.43e-02
ncbi_114361606	dual specificity protein phosphatase 23-like isoform X1 [Ostrinia furnacalis]	-2.30	7.77e-04	1.05e-02
ncbi_114361691	speckle-type POZ protein-like isoform X1 [Ostrinia furnacalis]	-1.16	5.37e-03	4.37e-02
ncbi_114361809	thrombospondin type-1 domain-containing protein 7A-like [Ostrinia furnacalis]	-3.81	2.95e-03	2.86e-02
ncbi_114361890	PREDICTED: hemicentin-1-like [Plutella xylostella]	+3.72	4.80e-03	4.00e-02
ncbi_114362061	protein turtle-like [Ostrinia furnacalis]	+3.91	1.59e-10	3.13e-08
ncbi_114362092	trichohyalin-like [Trichoplusia ni]	-1.21	1.09e-09	1.76e-07
ncbi_114362108	furin-like protease 1, partial [Ostrinia furnacalis]	-1.08	9.23e-12	2.59e-09
ncbi_114362189	proline-rich extensin-like protein EPR1 [Galleria mellonella]	-1.53	3.72e-06	1.65e-04
ncbi_114362207	Integrase catalytic domain-containing protein, partial [Aphis craccivora]	-1.73	1.45e-05	4.86e-04
ncbi_114362231	Efflux transporter, RND family, partial [Operophtera brumata]	+4.70	4.39e-03	3.76e-02
ncbi_114362367	MyD88 [Spodoptera frugiperda]	-1.10	9.40e-07	5.17e-05
ncbi_114362382	Cytochrome c oxidase polypeptide Vb [Operophtera brumata]	-3.90	4.46e-09	6.13e-07
ncbi_114362427	activin receptor type-1-like, partial [Ostrinia furnacalis]	-1.07	1.20e-03	1.46e-02

ncbi_114362441	DNA-directed RNA polymerase II subunit GRINL1A [Ostrinia furnacalis]	-1.07	4.75e-06	2.02e-04
ncbi_114362465	adenosine kinase [Ostrinia furnacalis]	+1.00	2.55e-07	1.86e-05
ncbi_114362479	uncharacterized protein LOC114362479 [Ostrinia furnacalis]	+5.35	5.99e-03	4.72e-02
ncbi_114362482	Pro-Pol polyprotein [Folsomia candida]	+4.96	3.43e-07	2.34e-05
ncbi_114362510	saccharopine dehydrogenase-like oxidoreductase [Ostrinia furnacalis]	-1.02	2.08e-05	6.46e-04
ncbi_114362514	gag-pol polyprotein precursor [Lasius niger]	-1.20	1.99e-05	6.25e-04
ncbi_114362551	PREDICTED: max-binding protein MNT-like [Papilio machaon]	-1.32	6.63e-04	9.25e-03
ncbi_114362572	O-acyltransferase like protein-like [Ostrinia furnacalis]	+3.25	3.32e-05	9.21e-04
ncbi_114362585	uncharacterized protein LOC114362585 [Ostrinia furnacalis]	-9.42	2.05e-03	2.18e-02
ncbi_114362605	UNC93-like protein MFSD11 [Ostrinia furnacalis]	-1.08	5.69e-06	2.29e-04
ncbi_114362618	TD and POZ domain-containing protein 4 [Papilio machaon]	-1.06	3.86e-05	1.05e-03
ncbi_114362670	MADF domain-containing protein, partial [Aphis craccivora]	+1.04	3.51e-04	5.74e-03
ncbi_114362699	F-box/LRR-repeat protein 20-like [Ostrinia furnacalis]	-1.61	6.18e-03	4.84e-02
ncbi_114362704	testis-expressed protein 2-like isoform X1 [Ostrinia furnacalis]	-1.03	3.11e-06	1.43e-04
ncbi_114362736	cuticle protein 1-like [Ostrinia furnacalis]	+9.85	4.35e-03	3.75e-02
ncbi_114362756	short-chain dehydrogenase/reductase family 16C member 6-like [Ostrinia furnacalis]	+2.85	4.01e-06	1.74e-04
ncbi_114362928	peroxisomal membrane protein 11C-like [Ostrinia furnacalis]	+2.12	5.12e-05	1.31e-03
ncbi_114363007	organic cation transporter protein-like [Ostrinia furnacalis]	+1.17	2.09e-06	1.02e-04
ncbi_114363023	ATP-dependent DNA helicase PIF1 [Eumeta japonica]	-1.39	4.09e-05	1.11e-03
ncbi_114363053	solute carrier family 25 member 35-like isoform X1 [Ostrinia furnacalis]	+1.53	1.59e-04	3.23e-03
ncbi_114363104	fatty acid-binding protein 1-like [Ostrinia furnacalis]	+1.32	1.28e-13	7.55e-11
ncbi_114363204	DNA-directed RNA polymerase I subunit RPA43 [Ostrinia furnacalis]	-1.04	2.45e-03	2.49e-02
ncbi_114363286	proteoglycan 4-like [Ostrinia furnacalis]	-1.90	1.99e-15	1.30e-12
ncbi_114363287	P94 protein [Danaus plexippus plexippus]	-1.85	1.19e-15	8.76e-13
ncbi_114363298	Fanconi anemia group D2 protein [Ostrinia furnacalis]	-1.19	7.60e-07	4.39e-05

ncbi_114363299	Apolipoprotein of lipid transfer particle-III [Operophtera brumata]	+2.52	7.59e-05	1.80e-03
ncbi_114363343	Jerky-like, partial [Aphis craccivora]	-3.49	6.44e-03	4.98e-02
ncbi_114363471	PREDICTED: GATA zinc finger domain-containing protein 14-like [Amyeloidis transitella]	-1.59	3.40e-08	3.45e-06
ncbi_114363654	NHP2-like protein 1 [Ostrinia furnacalis]	+1.03	8.12e-08	7.48e-06
ncbi_114363699	uncharacterized protein LOC114363699 [Ostrinia furnacalis]	+8.96	2.45e-03	2.49e-02
ncbi_114363709	adenylate kinase-like [Ostrinia furnacalis]	+1.61	7.49e-10	1.24e-07
ncbi_114363715	beta-hexosaminidase subunit alpha-like isoform X1 [Ostrinia furnacalis]	-1.10	5.01e-04	7.51e-03
ncbi_114363760	nuclear pore complex protein Nup133 [Hypomocoma kahamanoa]	-1.95	1.10e-04	2.39e-03
ncbi_114363773	heat shock protein 68-like [Ostrinia furnacalis]	-2.90	1.37e-03	1.61e-02
ncbi_114363785	myosin-9-like [Ostrinia furnacalis]	-4.29	6.70e-12	2.02e-09
ncbi_114363794	dynein heavy chain 12, axonemal [Ostrinia furnacalis]	-1.37	2.43e-03	2.47e-02
ncbi_114363798	mitochondrial import inner membrane translocase subunit Tim29 [Ostrinia furnacalis]	+1.79	2.67e-03	2.64e-02
ncbi_114363810	alanine--glyoxylate aminotransferase 2-like [Ostrinia furnacalis]	-1.64	1.68e-15	1.16e-12
ncbi_114363814	decaprenyl-diphosphate synthase subunit 1 [Ostrinia furnacalis]	+1.09	3.06e-08	3.28e-06
ncbi_114363843	Integrase catalytic domain-containing protein [Aphis craccivora]	+3.09	2.53e-05	7.57e-04
ncbi_114363884	peroxidase-like [Ostrinia furnacalis]	+8.04	4.36e-03	3.76e-02
ncbi_114363893	KH domain-containing protein 3-like [Ostrinia furnacalis]	-1.23	2.38e-07	1.76e-05
ncbi_114363909	cell cycle checkpoint protein RAD1 isoform X1 [Ostrinia furnacalis]	+1.57	1.17e-07	1.02e-05
ncbi_114363921	mucin-5AC isoform X2 [Helicoverpa armigera]	-4.29	3.21e-03	3.03e-02
ncbi_114363979	uncharacterized protein LOC114363979 [Ostrinia furnacalis]	-1.20	4.84e-03	4.02e-02
ncbi_114363995	Retrovirus-related Pol polyprotein from transposon 17.6 [Operophtera brumata]	-4.54	7.17e-07	4.25e-05
ncbi_114364020	leucine-rich melanocyte differentiation-associated protein-like isoform X1 [Ostrinia furnacalis]	-1.04	3.90e-03	3.48e-02
ncbi_114364072	long-chain-fatty-acid--CoA ligase 4 [Ostrinia furnacalis]	+1.05	2.11e-08	2.37e-06
ncbi_114364098	C-type lectin 4 isoform X2 [Bombyx mori]	+2.05	9.51e-06	3.48e-04
ncbi_114364123	transposase, partial [Helicoverpa zea]	-1.09	1.24e-05	4.28e-04

ncbi_114364179	glutamate receptor ionotropic, NMDA 2B [Ostrinia furnacalis]	-3.73	2.24e-06	1.08e-04
ncbi_114364204	protein N-lysine methyltransferase FAM173B-like [Ostrinia furnacalis]	+1.12	4.39e-03	3.76e-02
ncbi_114364316	uncharacterized protein LOC114364316 [Ostrinia furnacalis]	+1.76	1.17e-03	1.43e-02
ncbi_114364367	vitellogenin receptor protein [Ostrinia furnacalis]	+3.44	6.12e-03	4.80e-02
ncbi_114364369	calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1-like isoform X1 [Ostrinia furnacalis]	+1.44	3.68e-05	1.01e-03
ncbi_114364428	ATP-dependent DNA helicase PIF1 [Eumeta japonica]	+2.16	6.79e-13	2.86e-10
ncbi_114364584	dual oxidase isoform X1 [Ostrinia furnacalis]	-1.91	1.05e-03	1.32e-02
ncbi_114364591	NK-tumor recognition protein-like [Bombyx mandarina]	+2.93	2.96e-04	5.10e-03
ncbi_114364620	TRAS3 [Bombyx mori]	+7.93	1.88e-03	2.03e-02
ncbi_114364654	indole-3-acetaldehyde oxidase-like isoform X1 [Ostrinia furnacalis]	-1.27	6.35e-07	3.95e-05
ncbi_114364671	F-box/LRR-repeat protein 7-like [Ostrinia furnacalis]	-1.12	1.09e-03	1.36e-02
ncbi_114364698	proline-rich protein 36-like, partial [Ostrinia furnacalis]	-1.12	3.37e-03	3.14e-02
ncbi_114364789	Si:dkey-56d12.4 protein [Operophtera brumata]	-1.51	1.04e-06	5.58e-05
ncbi_114364831	pickpocket protein 28-like [Ostrinia furnacalis]	-2.24	1.44e-04	2.99e-03
ncbi_114364876	probable cytochrome P450 304a1 isoform X1 [Ostrinia furnacalis]	-3.91	1.37e-03	1.61e-02
ncbi_114365145	PREDICTED: serine/threonine-protein kinase BRSK2-like [Plutella xylostella]	+1.75	1.33e-03	1.57e-02
ncbi_114365229	dynein heavy chain 10, axonemal, partial [Ostrinia furnacalis]	-2.10	1.59e-04	3.23e-03
ncbi_114365282	cytochrome P450 6B5-like [Ostrinia furnacalis]	-1.05	6.30e-06	2.48e-04
ncbi_114365293	headcase protein [Ostrinia furnacalis]	-1.12	5.35e-05	1.36e-03
ncbi_114365341	glutathione S-transferase-like [Ostrinia furnacalis]	-1.33	1.55e-06	7.81e-05
ncbi_114365479	odorant receptor [Ostrinia scapulalis]	-4.89	1.17e-05	4.13e-04
ncbi_114365487	olfactory receptor 3 [Ostrinia furnacalis]	-5.20	1.06e-03	1.33e-02
ncbi_114365542	flocculation protein FLO11-like [Manduca sexta]	+8.34	9.08e-04	1.18e-02
ncbi_114365545	aldo-keto reductase AKR2E4-like [Ostrinia furnacalis]	+9.01	4.92e-04	7.41e-03

ncbi_114365566	fasciclin-2-like [Ostrinia furnacalis]	+3.42	4.92e-03	4.08e-02
ncbi_114365584	arf-GAP with dual PH domain-containing protein 1-like isoform X1 [Ostrinia furnacalis]	-1.14	5.68e-03	4.55e-02
ncbi_114365595	nitric oxide synthase-like protein [Ostrinia furnacalis]	+1.84	2.75e-06	1.28e-04
ncbi_114365597	cysteine synthase-like [Ostrinia furnacalis]	-1.31	1.19e-12	4.53e-10
ncbi_114365688	AGAP004199-PA [Anopheles gambiae str. PEST] [Anopheles gambiae]	+1.65	3.38e-07	2.32e-05
ncbi_114365702	chymotrypsin-1-like [Ostrinia furnacalis]	+1.43	7.12e-04	9.80e-03
ncbi_114365747	uncharacterized protein LOC114365747 [Ostrinia furnacalis]	-1.12	7.38e-05	1.76e-03
ncbi_114365751	pancreatic triacylglycerol lipase-like [Ostrinia furnacalis]	+2.06	1.91e-03	2.07e-02
ncbi_114365762	microvitellogenin-like [Ostrinia furnacalis]	+1.10	1.49e-03	1.72e-02
ncbi_114365835	biogenesis of lysosome-related organelles complex 1 subunit 3-like [Bombyx mandarina]	-2.08	9.60e-05	2.15e-03
ncbi_114365850	mpv17-like protein isoform X1 [Ostrinia furnacalis]	+1.08	1.81e-07	1.45e-05
ncbi_114365912	uncharacterized protein LOC114365912 [Ostrinia furnacalis]	+5.75	2.03e-89	2.39e-85
ncbi_114365951	PREDICTED: protein Dok-7-like [Papilio machaon]	-4.67	5.31e-03	4.34e-02
ncbi_114366046	BRCA1-associated ATM activator 1 [Operophtera brumata]	-1.11	9.28e-07	5.13e-05
ncbi_114366053	PREDICTED: protein unc-13 homolog C-like [Amyelois transitella]	-2.69	1.30e-03	1.54e-02
ncbi_114366060	protein scarlet isoform X1 [Ostrinia furnacalis]	-1.10	1.38e-03	1.62e-02
ncbi_114366090	fructose-bisphosphate aldolase-like [Ostrinia furnacalis]	-1.08	5.67e-03	4.54e-02
ncbi_114366114	organic cation transporter protein-like [Ostrinia furnacalis]	+2.29	1.82e-05	5.83e-04
ncbi_114366120	lysosomal thioesterase PPT2 homolog [Ostrinia furnacalis]	-1.35	1.03e-03	1.31e-02
ncbi_114366128	glutamic acid-rich protein-like [Ostrinia furnacalis]	+1.15	7.89e-04	1.06e-02
ncbi_114366173	fat-like cadherin-related tumor suppressor homolog [Spodoptera litura]	-1.80	7.02e-05	1.71e-03
ncbi_114366235	clavesin-2-like isoform X2 [Ostrinia furnacalis]	-1.24	1.31e-04	2.76e-03
ncbi_114366244	probable chitinase 2 [Ostrinia furnacalis]	+1.01	1.19e-07	1.02e-05
ncbi_114366246	probable chitinase 2 [Ostrinia furnacalis]	+1.85	4.54e-08	4.31e-06
ncbi_114366292	prostaglandin reductase 1-like isoform X1 [Ostrinia furnacalis]	+1.12	3.38e-08	3.45e-06



ncbi_114366345	tenascin-like isoform X6 [ <i>Pieris rapae</i> ]	-1.04	1.97e-05	6.24e-04
ncbi_114366431	C-type lectin 5 precursor [ <i>Bombyx mori</i> ]	+1.89	5.83e-06	2.33e-04
ncbi_114366439	Ecdysteroid 22-kinase [ <i>Operophtera brumata</i> ]	-1.47	3.03e-07	2.13e-05
ncbi_114366442	Protein Flattop homolog [ <i>Eumeta japonica</i> ]	+1.32	4.02e-11	9.47e-09
ncbi_114366470	facilitated trehalose transporter Tret1-like [ <i>Ostrinia furnacalis</i> ]	-2.06	1.75e-03	1.93e-02
ncbi_114366503	cytochrome P450 302a1, mitochondrial [ <i>Ostrinia furnacalis</i> ]	-1.62	9.25e-05	2.11e-03
ncbi_114366552	pupal cuticle protein 36-like [ <i>Ostrinia furnacalis</i> ]	-5.81	6.31e-05	1.58e-03
ncbi_114366654	AGAP001610-PA-like protein [ <i>Anopheles sinensis</i> ]	+2.76	7.12e-07	4.24e-05
ncbi_114366669	UDP-glucuronosyltransferase 2B2-like [ <i>Ostrinia furnacalis</i> ]	+1.30	6.26e-06	2.47e-04
ncbi_114366672	beta-1,3-glucan-binding protein-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	-2.53	5.05e-09	6.84e-07
ncbi_114366687	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 [ <i>Ostrinia furnacalis</i> ]	-1.10	8.58e-04	1.12e-02
ncbi_114366714	GTP-binding protein SAR1b [ <i>Ostrinia furnacalis</i> ]	+1.02	8.54e-06	3.23e-04
ncbi_114366745	transferrin [ <i>Ostrinia furnacalis</i> ]	-1.45	9.01e-04	1.17e-02
<b>ACB-BtS vs. ACB-IeR</b>				
MSTRG.11721	polyprotein [ <i>Operophtera brumata</i> ]	+2.51	8.28e-06	3.89e-04
MSTRG.12072	-	-1.32	5.45e-04	1.12e-02
MSTRG.12593	polyprotein [ <i>Antheraea mylitta</i> ]	+10.02	3.16e-04	7.36e-03
MSTRG.12887	-	-1.19	2.93e-03	3.94e-02
MSTRG.13629	mitogen-activated protein kinase kinase kinase 5-like, partial [ <i>Manduca sexta</i> ]	-2.11	3.62e-03	4.57e-02
MSTRG.13644	-	-1.28	2.41e-03	3.45e-02
MSTRG.13843	gag-pol polyprotein [ <i>Lasius niger</i> ]	+3.64	6.63e-12	1.62e-09
MSTRG.14142	UDP-glucuronosyltransferase 2B15-like [ <i>Ostrinia furnacalis</i> ]	+1.44	9.59e-07	6.34e-05
MSTRG.14273	-	+1.58	1.31e-03	2.22e-02
MSTRG.14336	Tyrosine-protein kinase BAZ1B [ <i>Folsomia candida</i> ]	+4.14	9.92e-04	1.81e-02
MSTRG.14366	PREDICTED: nuclear transcription factor Y subunit gamma-like [ <i>Amyeloidis transitella</i> ]	+2.03	8.11e-10	1.21e-07

MSTRG.1441	-	-1.98	2.39e-13	7.45e-11
MSTRG.14629	-	-1.39	6.29e-05	2.08e-03
MSTRG.14691	-	+1.80	2.53e-06	1.45e-04
MSTRG.14718	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Eumeta japonica]	-1.07	8.07e-04	1.54e-02
MSTRG.14792	carboxylesterase, partial [Ostrinia furnacalis]	-1.12	1.59e-04	4.28e-03
MSTRG.15192	-	-1.15	1.99e-06	1.18e-04
MSTRG.15302	Histone-lysine N-methyltransferase SETMAR [Eumeta japonica]	+3.81	3.47e-04	7.97e-03
MSTRG.15495	Transposable element P transposase-like Protein [Tribolium castaneum]	-1.23	4.61e-04	9.99e-03
MSTRG.15983	-	-2.63	2.03e-03	3.06e-02
MSTRG.16057	Copia protein, partial [Trachymyrmex cornetzi]	-1.64	1.43e-03	2.38e-02
MSTRG.17496	-	-3.16	3.24e-03	4.26e-02
MSTRG.18395	-	+2.07	4.12e-05	1.47e-03
MSTRG.1876	-	+1.32	5.08e-04	1.07e-02
MSTRG.18901	-	-1.48	1.87e-03	2.92e-02
MSTRG.19620	-	-1.28	1.96e-03	3.00e-02
MSTRG.19800	-	+2.79	2.62e-07	2.07e-05
MSTRG.1988	Histone-lysine N-methyltransferase SETMAR [Eumeta japonica]	+4.25	1.46e-04	3.94e-03
MSTRG.19983	Transposable element P transposase [Papilio xuthus]	-1.56	2.87e-15	1.22e-12
MSTRG.20185	-	-1.20	1.15e-04	3.28e-03
MSTRG.20799	reverse transcriptase and recombinase [Glyptapanteles indiensis]	-1.01	4.61e-05	1.60e-03
MSTRG.20845	uncharacterized protein LOC114356336 [Ostrinia furnacalis]	-1.27	7.73e-07	5.36e-05
MSTRG.2091	Integrase catalytic domain-containing protein, partial [Aphis craccivora]	-1.48	2.90e-03	3.92e-02
MSTRG.21492	-	-2.71	2.10e-03	3.15e-02
MSTRG.21877	-	-1.58	3.92e-05	1.41e-03
MSTRG.21972	-	-1.14	4.13e-07	3.06e-05

MSTRG.21975	Probable RNA-directed DNA polymerase from transposon BS [ <i>Eumeta japonica</i> ]	-1.09	2.18e-06	1.27e-04
MSTRG.22088	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [ <i>Acropora digitifera</i> ]	-3.75	2.62e-03	3.64e-02
MSTRG.22193	uncharacterized protein LOC114363438 [ <i>Ostrinia furnacalis</i> ]	+1.08	2.47e-04	6.13e-03
MSTRG.22677	Retrovirus-related Pol polyprotein from transposon 297 [ <i>Araneus ventricosus</i> ]	-2.97	5.10e-05	1.76e-03
MSTRG.22788	ORF1p [ <i>Operophtera brumata</i> ]	-1.23	1.38e-09	1.94e-07
MSTRG.22839	PREDICTED: uncharacterized protein LOC106137436 [ <i>Amyeloides transitella</i> ]	-1.50	1.54e-03	2.52e-02
MSTRG.23064	-	-1.42	4.28e-06	2.27e-04
MSTRG.23526	retinol dehydrogenase 14-like [ <i>Vanessa tameamea</i> ]	-1.00	2.99e-04	7.05e-03
MSTRG.2455	-	-6.72	1.38e-05	6.01e-04
MSTRG.2456	piggyBac transposable element-derived protein 2-like [ <i>Bicyclus anynana</i> ]	-4.09	4.29e-04	9.47e-03
MSTRG.2477	-	-1.89	9.56e-04	1.75e-02
MSTRG.24877	Yokozuna [ <i>Bombyx mori</i> ]	-1.03	1.52e-06	9.30e-05
MSTRG.25018	-	+1.98	1.99e-04	5.12e-03
MSTRG.25147	CLIP-associating protein-like [ <i>Ostrinia furnacalis</i> ]	+10.57	1.06e-05	4.78e-04
MSTRG.2537	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [ <i>Eumeta japonica</i> ]	-2.38	1.87e-05	7.57e-04
MSTRG.25513	-	-1.13	1.89e-15	8.36e-13
MSTRG.25630	uncharacterized protein LOC114350796 [ <i>Ostrinia furnacalis</i> ]	+3.74	4.92e-08	4.93e-06
MSTRG.25758	-	-1.75	1.66e-05	6.86e-04
MSTRG.25915	-	-1.12	3.47e-03	4.43e-02
MSTRG.25972	gag-pol polyprotein [ <i>Lasius niger</i> ]	+1.91	8.72e-04	1.63e-02
MSTRG.26114	reverse transcriptase [ <i>Ostrinia nubilalis</i> ]	+1.25	2.44e-07	1.95e-05
MSTRG.2643	Maltase A1 [ <i>Eumeta japonica</i> ]	-1.09	4.55e-06	2.37e-04
MSTRG.2646	hypothetical protein evm_006816 [ <i>Chilo suppressalis</i> ]	-1.82	3.57e-11	7.61e-09
MSTRG.2994	reverse transcriptase [ <i>Anguilla japonica</i> ]	+1.82	7.08e-08	6.57e-06
MSTRG.3110	reverse transcriptase [ <i>Ostrinia nubilalis</i> ]	+1.45	5.79e-13	1.71e-10

MSTRG.3528	Activity-regulated cytoskeleton associated protein 2 [Eumeta japonica]	-1.52	2.53e-17	1.45e-14
MSTRG.3530	activity-regulated cytoskeleton associated protein 1-like [Ostrinia furnacalis]	-3.74	9.90e-05	2.91e-03
MSTRG.3877	-	-1.27	9.99e-07	6.53e-05
MSTRG.4352	-	+5.02	4.49e-04	9.82e-03
MSTRG.4353	-	-1.57	3.16e-06	1.76e-04
MSTRG.4559	chymotrypsin-like serine protease [Ostrinia nubilalis]	+1.31	3.67e-13	1.11e-10
MSTRG.4713	-	-1.08	3.61e-03	4.56e-02
MSTRG.4860	src substrate cortactin [Spodoptera litura]	-2.15	2.19e-10	3.70e-08
MSTRG.5947	N-terminal kinase-like protein [Manduca sexta]	-1.15	7.96e-07	5.49e-05
MSTRG.6385	-	+2.70	3.85e-10	6.33e-08
MSTRG.6440	hypothetical protein B5X24_HaOG210684 [Helicoverpa armigera]	-1.59	2.94e-07	2.26e-05
MSTRG.6632	gag-pol protein, partial [Lasius niger]	-1.90	3.32e-04	7.67e-03
MSTRG.6933	-	-3.85	4.54e-04	9.87e-03
MSTRG.8144	-	+11.05	6.36e-04	1.27e-02
MSTRG.8195	pol polyprotein [Lasius niger]	-1.50	8.39e-05	2.57e-03
MSTRG.840	Gag-pol polyprotein, partial [Operophtera brumata]	-1.37	1.03e-05	4.69e-04
MSTRG.9141	THAP domain-containing protein 2-like [Ostrinia furnacalis]	-2.26	1.88e-03	2.92e-02
MSTRG.9261	-	-2.06	2.69e-03	3.71e-02
ncbi_114349549	probable glycerol-3-phosphate dehydrogenase, mitochondrial isoform X1 [Ostrinia furnacalis]	+1.97	1.30e-06	8.38e-05
ncbi_114349592	phospholipase A1 member A-like [Ostrinia furnacalis]	+1.42	9.99e-07	6.53e-05
ncbi_114349600	lipoprotein lipase-like [Ostrinia furnacalis]	+1.09	5.60e-08	5.46e-06
ncbi_114349603	pancreatic lipase-related protein 2-like [Ostrinia furnacalis]	+2.79	1.23e-09	1.79e-07
ncbi_114349618	uncharacterized protein LOC114349618 [Ostrinia furnacalis]	+5.38	3.35e-06	1.85e-04
ncbi_114349629	pancreatic triacylglycerol lipase-like [Ostrinia furnacalis]	+3.98	9.20e-14	3.11e-11
ncbi_114349639	pancreatic triacylglycerol lipase-like [Ostrinia furnacalis]	-1.43	1.50e-07	1.29e-05

ncbi_114349648	AAEL013537-PB [ <i>Aedes aegypti</i> ]	+2.32	2.02e-03	3.05e-02
ncbi_114349651	cyclic nucleotide-gated cation channel beta-3 isoform X1 [ <i>Ostrinia furnacalis</i> ]	+1.42	3.59e-03	4.54e-02
ncbi_114349707	Kynurenine formamidase [ <i>Danaus plexippus plexippus</i> ]	-2.68	4.29e-10	6.77e-08
ncbi_114349797	dynein heavy chain 8, axonemal [ <i>Ostrinia furnacalis</i> ]	+4.25	4.28e-04	9.47e-03
ncbi_114349834	DNA helicase MCM8 isoform X1 [ <i>Ostrinia furnacalis</i> ]	+1.70	1.67e-04	4.46e-03
ncbi_114349846	agrin-like [ <i>Ostrinia furnacalis</i> ]	+2.10	4.45e-04	9.77e-03
ncbi_114349898	THAP-type domain-containing protein, partial [ <i>Aphis craccivora</i> ]	-1.09	1.63e-03	2.63e-02
ncbi_114349957	Ring canal kelch-like [ <i>Papilio xuthus</i> ]	-1.75	1.26e-09	1.82e-07
ncbi_114350040	leucine-rich repeats and immunoglobulin-like domains protein 2 [ <i>Ostrinia furnacalis</i> ]	+4.19	2.77e-07	2.15e-05
ncbi_114350090	transmembrane protease serine 3-like [ <i>Ostrinia furnacalis</i> ]	+1.40	5.34e-25	6.15e-22
ncbi_114350216	kynureninase [ <i>Bombyx mori</i> ]	-1.11	5.66e-04	1.16e-02
ncbi_114350246	tyramine beta-hydroxylase isoform X1 [ <i>Ostrinia furnacalis</i> ]	-3.40	3.14e-03	4.17e-02
ncbi_114350359	titin-like [ <i>Ostrinia furnacalis</i> ]	+2.38	5.11e-04	1.08e-02
ncbi_114350361	CLUMA_CG007896, isoform C [ <i>Clunio marinus</i> ]	-1.06	9.51e-05	2.82e-03
ncbi_114350447	cuticle collagen 1-like [ <i>Ostrinia furnacalis</i> ]	+4.16	4.17e-07	3.07e-05
ncbi_114350537	Endonuclease-reverse transcriptase [ <i>Operophtera brumata</i> ]	-2.08	9.74e-17	4.67e-14
ncbi_114350635	tetraspanin-33-like [ <i>Ostrinia furnacalis</i> ]	-1.31	4.76e-04	1.02e-02
ncbi_114350648	probable maleylacetoacetate isomerase 1 [ <i>Ostrinia furnacalis</i> ]	-1.84	3.97e-03	4.88e-02
ncbi_114350651	uncharacterized protein LOC114350651 [ <i>Ostrinia furnacalis</i> ]	-1.21	3.01e-05	1.14e-03
ncbi_114350692	THAP domain-containing protein 2-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	-1.12	3.30e-03	4.30e-02
ncbi_114350784	THAP domain-containing protein 2 [ <i>Eumeta japonica</i> ]	-1.73	2.91e-04	6.90e-03
ncbi_114350785	fatty acyl-CoA reductase wat-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	-3.18	6.00e-04	1.22e-02
ncbi_114350848	5'-AMP-activated protein kinase catalytic subunit alpha-2-like [ <i>Ostrinia furnacalis</i> ]	-1.15	3.98e-07	2.98e-05
ncbi_114350993	Integrase catalytic domain-containing protein, partial [ <i>Aphis craccivora</i> ]	-1.30	1.84e-07	1.53e-05
ncbi_114351005	senecionine N-oxygenase isoform X1 [ <i>Ostrinia furnacalis</i> ]	-3.57	3.51e-05	1.29e-03

ncbi_114351044	gag-pol polyprotein precursor [ <i>Lasius niger</i> ]	-1.35	1.04e-03	1.87e-02
ncbi_114351145	Integrase catalytic domain-containing protein, partial [ <i>Aphis craccivora</i> ]	+1.14	7.48e-05	2.36e-03
ncbi_114351183	multidrug resistance protein 1A isoform X1 [ <i>Ostrinia furnacalis</i> ]	-1.92	5.17e-22	4.25e-19
ncbi_114351190	prostaglandin reductase 1-like [ <i>Ostrinia furnacalis</i> ]	-1.29	2.48e-16	1.14e-13
ncbi_114351223	alpha-tocopherol transfer protein-like [ <i>Ostrinia furnacalis</i> ]	-1.68	9.69e-11	1.83e-08
ncbi_114351224	alpha-tocopherol transfer protein-like [ <i>Ostrinia furnacalis</i> ]	-1.10	9.94e-04	1.81e-02
ncbi_114351296	J protein JJJ1-like isoform X1 [ <i>Danaus plexippus plexippus</i> ]	-1.02	2.07e-05	8.27e-04
ncbi_114351422	sodium-dependent phosphate transporter [ <i>Danaus plexippus plexippus</i> ]	-1.19	7.14e-07	5.04e-05
ncbi_114351480	cytochrome b5-related protein-like [ <i>Ostrinia furnacalis</i> ]	-3.15	2.81e-03	3.82e-02
ncbi_114351538	proteasome assembly chaperone 2 [ <i>Ostrinia furnacalis</i> ]	-1.07	1.91e-04	4.96e-03
ncbi_114351551	lymphocyte expansion molecule-like [ <i>Galleria mellonella</i> ]	+3.99	4.71e-06	2.43e-04
ncbi_114351572	Zinc finger DNA binding protein [ <i>Operophtera brumata</i> ]	-3.75	8.75e-12	2.05e-09
ncbi_114351648	AAEL012860-PA [ <i>Aedes aegypti</i> ]	+1.28	7.23e-05	2.30e-03
ncbi_114351683	Apolipophorin [ <i>Papilio xuthus</i> ]	-1.72	6.44e-04	1.28e-02
ncbi_114351809	pancreatic triacylglycerol lipase-like [ <i>Ostrinia furnacalis</i> ]	+1.07	2.21e-08	2.51e-06
ncbi_114351842	cyclin-J-like [ <i>Ostrinia furnacalis</i> ]	-1.19	1.61e-09	2.23e-07
ncbi_114351909	alpha-tocopherol transfer protein-like, partial [ <i>Ostrinia furnacalis</i> ]	+1.32	1.21e-03	2.09e-02
ncbi_114351915	transmembrane protease serine 9-like [ <i>Ostrinia furnacalis</i> ]	+3.17	7.36e-05	2.33e-03
ncbi_114351935	trypsin, alkaline C-like [ <i>Ostrinia furnacalis</i> ]	+2.08	2.11e-23	2.03e-20
ncbi_114351936	trypsin, alkaline C-like isoform X1 [ <i>Ostrinia furnacalis</i> ]	+2.95	5.85e-11	1.20e-08
ncbi_114351939	trypsin, alkaline C-like [ <i>Ostrinia furnacalis</i> ]	+1.79	1.14e-04	3.27e-03
ncbi_114351942	trypsin, alkaline B-like [ <i>Ostrinia furnacalis</i> ]	+3.34	2.06e-12	5.79e-10
ncbi_114351970	mucin-5AC-like [ <i>Ostrinia furnacalis</i> ]	-6.08	9.52e-07	6.34e-05
ncbi_114352033	CD109 antigen-like [ <i>Ostrinia furnacalis</i> ]	+1.60	7.43e-08	6.80e-06
ncbi_114352048	exonuclease mut-7 homolog [ <i>Ostrinia furnacalis</i> ]	-1.12	1.78e-03	2.82e-02

ncbi_114352104	lipase 1-like [Ostrinia furnacalis]	+1.47	1.12e-06	7.30e-05
ncbi_114352113	peptidoglycan-recognition protein LB-like [Ostrinia furnacalis]	-1.20	4.00e-09	5.23e-07
ncbi_114352176	myosin-binding protein H-like [Bombyx mandarina]	-1.18	1.38e-06	8.78e-05
ncbi_114352259	trypsin, alkaline B-like [Ostrinia furnacalis]	-1.33	4.62e-09	5.98e-07
ncbi_114352314	tigger transposable element-derived protein 6-like isoform X1 [Manduca sexta]	-5.43	4.58e-17	2.51e-14
ncbi_114352437	E3 ubiquitin-protein ligase znrf2-like [Ostrinia furnacalis]	+1.17	1.71e-06	1.03e-04
ncbi_114352487	collagenase-like [Ostrinia furnacalis]	+2.41	7.09e-41	1.63e-37
ncbi_114352537	malate dehydrogenase, mitochondrial-like [Ostrinia furnacalis]	-1.35	1.94e-06	1.17e-04
ncbi_114352594	protein snakeskin-like [Diabrotica virgifera virgifera]	+1.10	3.67e-08	3.95e-06
ncbi_114352603	Endonuclease-reverse transcriptase [Operophtera brumata]	-1.55	1.98e-03	3.00e-02
ncbi_114352700	pickpocket protein 28-like isoform X1 [Aphis craccivora]	-9.59	6.51e-08	6.19e-06
ncbi_114352740	SMC domain protein [Heliothis subflexa]	-2.26	3.07e-03	4.09e-02
ncbi_114352840	Pro-Pol polyprotein [Folsomia candida]	-1.54	7.15e-05	2.29e-03
ncbi_114352903	L-lactate dehydrogenase B chain-like [Ostrinia furnacalis]	-5.82	2.25e-04	5.69e-03
ncbi_114353077	cytochrome P450 9e2-like [Ostrinia furnacalis]	-2.33	7.27e-15	2.99e-12
ncbi_114353127	proton-coupled amino acid transporter-like protein pathetic isoform X1 [Ostrinia furnacalis]	-1.09	1.08e-07	9.67e-06
ncbi_114353130	probable multidrug resistance-associated protein lethal(2)03659 [Ostrinia furnacalis]	-1.12	2.47e-05	9.62e-04
ncbi_114353264	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like isoform X1 [Papilio machaon]	-2.17	2.68e-03	3.70e-02
ncbi_114353293	uncharacterized protein LOC114353293 [Ostrinia furnacalis]	-1.79	3.42e-05	1.27e-03
ncbi_114353333	midgut protein Lsti99 [Loxostege sticticalis]	-1.08	3.10e-14	1.15e-11
ncbi_114353390	synaptic vesicle glycoprotein 2C-like isoform X1 [Ostrinia furnacalis]	-1.69	2.74e-03	3.75e-02
ncbi_114353413	synaptic vesicle 2-related protein-like [Ostrinia furnacalis]	-1.59	1.93e-10	3.36e-08
ncbi_114353440	ommochrome-binding protein-like [Helicoverpa armigera]	-4.10	1.38e-05	6.01e-04
ncbi_114353478	mucin-5AC-like [Ostrinia furnacalis]	+6.64	1.74e-94	9.99e-91

ncbi_114353519	GPN-loop GTPase 1 [Ostrinia furnacalis]	-1.30	1.13e-03	1.99e-02
ncbi_114353634	brachyurin-like [Ostrinia furnacalis]	-1.19	4.17e-10	6.66e-08
ncbi_114353646	testis-expressed protein 10-like [Ostrinia furnacalis]	-1.55	9.53e-04	1.74e-02
ncbi_114353648	protein DPCD [Ostrinia furnacalis]	-1.48	1.37e-03	2.31e-02
ncbi_114353649	nucleolar protein 16 [Ostrinia furnacalis]	-1.19	3.65e-03	4.60e-02
ncbi_114353653	protein maternal effect lethal 26-like [Ostrinia furnacalis]	-1.19	2.84e-05	1.09e-03
ncbi_114353674	pancreatic lipase-related protein 2-like [Ostrinia furnacalis]	-3.04	6.33e-05	2.09e-03
ncbi_114353709	organic cation transporter protein-like [Ostrinia furnacalis]	-1.57	5.92e-10	9.09e-08
ncbi_114353728	reverse transcriptase [Operophtera brumata]	-2.75	1.51e-03	2.47e-02
ncbi_114353731	armadillo repeat-containing protein 6 homolog [Ostrinia furnacalis]	-1.01	1.36e-05	5.96e-04
ncbi_114353788	multidrug resistance protein 1A-like [Ostrinia furnacalis]	-3.34	4.50e-04	9.82e-03
ncbi_114353859	phenoloxidase-activating factor 2-like [Ostrinia furnacalis]	+3.77	5.05e-09	6.45e-07
ncbi_114354003	DNA polymerase nu-like isoform X1 [Ostrinia furnacalis]	-1.08	4.03e-03	4.92e-02
ncbi_114354118	leucine-rich repeat LGI family member 3-like [Ostrinia furnacalis]	+5.25	2.85e-08	3.15e-06
ncbi_114354181	tyrosine-protein kinase transmembrane receptor Ror [Ostrinia furnacalis]	-1.11	3.39e-03	4.38e-02
ncbi_114354340	programmed cell death protein 2 isoform X1 [Ostrinia furnacalis]	-1.36	1.19e-04	3.37e-03
ncbi_114354373	fatty acid synthase-like [Ostrinia furnacalis]	-1.34	8.48e-04	1.60e-02
ncbi_114354442	acetylcholine receptor subunit alpha-like [Ostrinia furnacalis]	+4.41	9.39e-06	4.30e-04
ncbi_114354482	integrator complex subunit 10 [Ostrinia furnacalis]	-1.12	3.52e-04	8.06e-03
ncbi_114354525	5'-AMP-activated protein kinase subunit gamma-2-like [Ostrinia furnacalis]	-1.04	8.09e-05	2.49e-03
ncbi_114354545	Reverse transcriptase and recombinase [Operophtera brumata]	-3.16	1.51e-05	6.37e-04
ncbi_114354906	chymotrypsin-1-like [Ostrinia furnacalis]	+1.08	3.58e-25	4.58e-22
ncbi_114354911	cytochrome c oxidase subunit 6C-like [Ostrinia furnacalis]	+1.12	3.50e-07	2.65e-05
ncbi_114355012	endoplasmin [Ostrinia furnacalis]	+1.08	1.92e-19	1.16e-16
ncbi_114355021	ribosome maturation protein SBDS [Ostrinia furnacalis]	-1.00	1.90e-04	4.94e-03



ncbi_114355026	glucose dehydrogenase [FAD, quinone]-like isoform X1 [Ostrinia furnacalis]	-1.16	1.58e-05	6.58e-04
ncbi_114355056	Integrase catalytic domain-containing protein, partial [Aphis craccivora]	-1.20	1.58e-07	1.34e-05
ncbi_114355077	cytochrome P450 4c3-like [Bicyclus anynana]	+2.07	1.18e-03	2.05e-02
ncbi_114355216	fat-like cadherin-related tumor suppressor homolog [Spodoptera litura]	-3.20	2.23e-03	3.28e-02
ncbi_114355250	uncharacterized protein LOC114355250, partial [Ostrinia furnacalis]	+1.99	1.45e-03	2.40e-02
ncbi_114355297	proton-coupled amino acid transporter-like protein pathetic [Ostrinia furnacalis]	-1.30	2.05e-10	3.53e-08
ncbi_114355428	brefeldin A-inhibited guanine nucleotide-exchange protein 3 [Ostrinia furnacalis]	+1.32	2.21e-04	5.60e-03
ncbi_114355482	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Amyelois transitella]	+3.66	3.87e-03	4.81e-02
ncbi_114355646	keratin-associated protein 19-2-like [Ostrinia furnacalis]	-1.28	1.59e-08	1.86e-06
ncbi_114355704	activity-regulated cytoskeleton associated protein 1-like [Ostrinia furnacalis]	-1.45	6.93e-04	1.36e-02
ncbi_114355741	Integrase catalytic domain-containing protein [Aphis craccivora]	-1.26	8.18e-06	3.86e-04
ncbi_114355759	proclotting enzyme-like isoform X2 [Ostrinia furnacalis]	-1.34	2.11e-03	3.15e-02
ncbi_114355779	Retrovirus-related Pol polyprotein from transposon 297 [Eumeta japonica]	-4.77	5.65e-06	2.80e-04
ncbi_114355827	hemiceitin-1-like, partial [Ostrinia furnacalis]	+2.68	5.05e-04	1.07e-02
ncbi_114355931	probable chitinase 2 isoform X1 [Ostrinia furnacalis]	-1.48	9.52e-07	6.34e-05
ncbi_114355974	UPF0587 protein GA18326-like [Ostrinia furnacalis]	+1.50	4.52e-05	1.58e-03
ncbi_114355992	Retrovirus-related Pol polyprotein from transposon 412 [Eumeta japonica]	+4.00	9.62e-10	1.42e-07
ncbi_114356009	glucose dehydrogenase [FAD, quinone]-like [Ostrinia furnacalis]	+1.12	1.80e-08	2.09e-06
ncbi_114356174	Zinc finger DNA binding protein [Operophtera brumata]	-1.76	1.03e-07	9.21e-06
ncbi_114356250	PREDICTED: protein son of sevenless-like [Plutella xylostella]	-1.47	2.48e-03	3.50e-02
ncbi_114356307	prostatic acid phosphatase-like [Ostrinia furnacalis]	-2.34	6.24e-25	6.53e-22
ncbi_114356322	tubulin polyglutamylase TTLL13-like [Ostrinia furnacalis]	+9.06	4.34e-06	2.27e-04
ncbi_114356422	neurexin-4-like [Ostrinia furnacalis]	-1.56	7.85e-04	1.51e-02
ncbi_114356497	cytochrome P450 6B6-like [Ostrinia furnacalis]	-1.15	6.96e-05	2.25e-03
ncbi_114356560	zinc finger HIT domain-containing protein 2 [Trichoplusia ni]	-1.77	8.14e-04	1.55e-02

ncbi_114356609	oxidative stress-responsive serine-rich protein 1 [Helicoverpa armigera]	-1.30	1.86e-03	2.91e-02
ncbi_114356634	PREDICTED: coiled-coil domain-containing protein 39 [Amyeloidis transitella]	+1.48	1.80e-04	4.74e-03
ncbi_114356668	histone-lysine N-methyltransferase 2D-like isoform X1 [Ostrinia furnacalis]	+1.01	7.05e-04	1.37e-02
ncbi_114356845	Cysteine string protein [Papilio xuthus]	-1.34	1.06e-05	4.78e-04
ncbi_114356945	zinc transporter ZIP1-like [Ostrinia furnacalis]	+2.44	7.22e-05	2.30e-03
ncbi_114357040	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Acropora digitifera]	-5.11	1.08e-03	1.92e-02
ncbi_114357150	glutamate dehydrogenase, mitochondrial-like isoform X2 [Ostrinia furnacalis]	+1.80	3.42e-03	4.38e-02
ncbi_114357213	proto-oncogene tyrosine-protein kinase ROS [Ostrinia furnacalis]	-1.44	2.36e-03	3.40e-02
ncbi_114357236	zinc finger DNA binding protein [Danaus plexippus plexippus]	-3.46	7.49e-12	1.80e-09
ncbi_114357324	secretory phospholipase A2 receptor-like [Ostrinia furnacalis]	-4.79	2.68e-03	3.71e-02
ncbi_114357451	organic cation transporter protein-like [Ostrinia furnacalis]	-1.68	4.00e-08	4.14e-06
ncbi_114357458	ATP-binding cassette sub-family A member 1-like [Ostrinia furnacalis]	-2.51	9.51e-04	1.74e-02
ncbi_114357532	alpha-crystallin B chain-like [Ostrinia furnacalis]	+1.80	2.24e-11	4.95e-09
ncbi_114357580	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase-like isoform X3 [Ostrinia furnacalis]	+2.33	9.87e-04	1.80e-02
ncbi_114357630	Pogo transposable element with KRAB domain [Papilio machaon]	-1.33	2.11e-03	3.15e-02
ncbi_114357646	trypsin, alkaline C-like [Ostrinia furnacalis]	+3.04	8.62e-05	2.61e-03
ncbi_114357736	UDP-glucuronosyltransferase 2B14-like [Ostrinia furnacalis]	+3.38	6.59e-05	2.16e-03
ncbi_114357739	UDP-glucuronosyltransferase 2B14-like isoform X1 [Ostrinia furnacalis]	+2.45	2.64e-04	6.40e-03
ncbi_114357777	cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A-like [Ostrinia furnacalis]	-3.01	4.25e-04	9.45e-03
ncbi_114357817	xanthine dehydrogenase-like [Ostrinia furnacalis]	-1.11	2.28e-04	5.73e-03
ncbi_114357821	cytochrome P450 6B6-like [Ostrinia furnacalis]	-1.21	5.88e-04	1.20e-02
ncbi_114357956	DNA polymerase nu-like [Helicoverpa armigera]	-5.57	6.79e-06	3.27e-04
ncbi_114357981	dual specificity protein phosphatase MPK-4-like isoform X2 [Ostrinia furnacalis]	-1.66	5.74e-05	1.96e-03
ncbi_114357991	pancreatic triacylglycerol lipase-like isoform X1 [Ostrinia furnacalis]	-1.47	1.80e-05	7.36e-04
ncbi_114358018	Serine/threonine-protein phosphatase, partial [Aphis craccivora]	+3.05	3.11e-12	8.14e-10

ncbi_114358032	sulfotransferase family cytosolic 1B member 1-like [Ostrinia furnacalis]	+2.93	9.69e-52	3.72e-48
ncbi_114358161	zinc carboxypeptidase-like [Ostrinia furnacalis]	-1.02	9.68e-09	1.20e-06
ncbi_114358317	reticulocyte-binding protein 2 homolog a-like [Bombyx mandarina]	-1.45	3.75e-03	4.70e-02
ncbi_114358336	LINE-1 reverse transcriptase homolog [Eumeta japonica]	-2.09	2.28e-04	5.74e-03
ncbi_114358375	phospholipase A-2-activating protein-like [Ostrinia furnacalis]	-1.10	1.78e-04	4.69e-03
ncbi_114358448	Endonuclease-reverse transcriptase [Operophtera brumata]	-3.40	2.87e-11	6.24e-09
ncbi_114358491	attacin-like [Ostrinia furnacalis]	+4.32	8.36e-06	3.91e-04
ncbi_114358539	Zinc finger DNA binding protein [Operophtera brumata]	+1.54	4.57e-05	1.59e-03
ncbi_114358601	CLUMA_CG019058, isoform A [Clunio marinus]	-1.74	1.81e-04	4.75e-03
ncbi_114358643	polyprotein [Antheraea mylitta]	+2.13	1.92e-07	1.58e-05
ncbi_114358670	ADP-ribose pyrophosphatase, mitochondrial isoform X1 [Ostrinia furnacalis]	+1.06	6.36e-05	2.09e-03
ncbi_114358690	collagenase-like [Ostrinia furnacalis]	+3.43	2.70e-12	7.23e-10
ncbi_114358723	collagenase-like [Ostrinia furnacalis]	+2.85	1.01e-25	1.45e-22
ncbi_114358734	collagenase-like [Ostrinia furnacalis]	+2.79	1.32e-08	1.60e-06
ncbi_114358804	chorion peroxidase isoform X1 [Ostrinia furnacalis]	+1.86	1.45e-04	3.94e-03
ncbi_114358820	ATP-dependent DNA helicase PIF1 [Eumeta japonica]	-2.49	1.73e-06	1.04e-04
ncbi_114358859	apoptosis-inducing factor 1, mitochondrial-like isoform X1 [Ostrinia furnacalis]	-2.92	4.00e-03	4.90e-02
ncbi_114358879	uncharacterized protein LOC114358879 [Ostrinia furnacalis]	+1.20	1.39e-03	2.33e-02
ncbi_114358900	protocadherin-like wing polarity protein stan [Ostrinia furnacalis]	-1.32	3.18e-03	4.21e-02
ncbi_114358964	lipase 3-like [Ostrinia furnacalis]	+2.88	3.39e-03	4.38e-02
ncbi_114359044	lysosomal-associated transmembrane protein 4A [Ostrinia furnacalis]	-1.00	4.30e-08	4.38e-06
ncbi_114359063	prefoldin subunit 6 [Ostrinia furnacalis]	-1.35	8.56e-05	2.60e-03
ncbi_114359074	carboxypeptidase B-like [Ostrinia furnacalis]	+2.38	2.71e-21	2.08e-18
ncbi_114359075	uncharacterized protein LOC114359075 [Ostrinia furnacalis]	-1.36	1.39e-07	1.21e-05
ncbi_114359077	carboxypeptidase B-like [Ostrinia furnacalis]	+1.88	1.29e-14	5.10e-12

ncbi_114359099	saccharopine dehydrogenase-like oxidoreductase [Ostrinia furnacalis]	-3.11	5.26e-09	6.65e-07
ncbi_114359315	RNase H and integrase-like protein, partial [Bombyx mori]	+1.59	2.58e-03	3.61e-02
ncbi_114359336	polyprotein [Antheraea mylitta]	+1.25	8.09e-05	2.49e-03
ncbi_114359575	gustatory receptor 68a-like [Ostrinia furnacalis]	+3.62	3.17e-03	4.19e-02
ncbi_114359657	shavenoid [Papilio xuthus]	-2.02	2.24e-03	3.29e-02
ncbi_114359718	PREDICTED: ankyrin repeat domain-containing protein 11-like [Plutella xylostella]	-1.16	3.53e-03	4.49e-02
ncbi_114359766	zinc metalloproteinase nas-13-like [Ostrinia furnacalis]	+2.15	2.54e-20	1.62e-17
ncbi_114359768	astacin-like metalloprotease toxin 5 [Ostrinia furnacalis]	+1.20	1.30e-20	9.33e-18
ncbi_114359791	calsequestrin-1-like [Spodoptera litura]	-4.24	1.70e-05	6.99e-04
ncbi_114359798	chymotrypsin-like elastase family member 2A [Ostrinia furnacalis]	+1.04	6.00e-06	2.94e-04
ncbi_114359801	collagenase-like [Ostrinia furnacalis]	+1.81	2.32e-44	6.67e-41
ncbi_114359847	tektin-3-like isoform X1 [Ostrinia furnacalis]	+5.35	2.72e-04	6.56e-03
ncbi_114359850	transport and Golgi organization protein 6 homolog isoform X1 [Ostrinia furnacalis]	-1.19	1.16e-03	2.03e-02
ncbi_114360123	short-chain dehydrogenase/reductase family 16C member 6 [Ostrinia furnacalis]	-4.96	2.34e-07	1.90e-05
ncbi_114360158	NFATC2-interacting protein [Operophtera brumata]	-1.09	5.24e-04	1.09e-02
ncbi_114360241	Retrovirus-related Pol polyprotein from transposon 17.6 [Araneus ventricosus]	-1.33	7.58e-04	1.46e-02
ncbi_114360250	Integrase catalytic domain-containing protein, partial [Aphis craccivora]	-2.20	1.59e-05	6.58e-04
ncbi_114360251	Gag-pol polyprotein [Operophtera brumata]	-1.49	4.31e-06	2.27e-04
ncbi_114360286	Retrovirus-related Pol polyprotein from transposon 297 [Eumeta japonica]	-10.16	2.57e-04	6.28e-03
ncbi_114360434	general transcription factor 3C polypeptide 4 isoform X2 [Cryptotermes secundus]	-1.15	3.94e-03	4.87e-02
ncbi_114360485	Kv channel-interacting protein 4-like isoform X1 [Ostrinia furnacalis]	-1.66	3.30e-04	7.64e-03
ncbi_114360499	trypsin, alkaline A-like [Ostrinia furnacalis]	+10.93	3.86e-04	8.66e-03
ncbi_114360549	uncharacterized protein LOC114360549 [Ostrinia furnacalis]	-2.34	1.90e-10	3.36e-08
ncbi_114360595	Gag-Pol polyprotein [Folsomia candida]	-1.34	3.33e-08	3.62e-06
ncbi_114360773	glutathione S-transferase 1-like [Ostrinia furnacalis]	+1.91	2.43e-03	3.46e-02

ncbi_114360825	calphotin-like [Ostrinia furnacalis]	-1.11	5.34e-05	1.83e-03
ncbi_114360920	lachesin-like [Ostrinia furnacalis]	-3.72	1.78e-03	2.82e-02
ncbi_114360950	ORF1p [Operophtera brumata]	-2.97	1.89e-08	2.18e-06
ncbi_114360986	Integrase catalytic domain-containing protein, partial [Aphis craccivora]	-1.94	3.17e-03	4.20e-02
ncbi_114361102	high affinity copper uptake protein 1-like [Ostrinia furnacalis]	+2.02	6.98e-32	1.34e-28
ncbi_114361117	collagen alpha-1(III) chain-like [Ostrinia furnacalis]	+1.67	1.87e-03	2.92e-02
ncbi_114361122	juvenile hormone esterase-like isoform X1 [Ostrinia furnacalis]	-1.96	1.74e-03	2.77e-02
ncbi_114361130	paired box protein Pax-1-like [Ostrinia furnacalis]	+2.38	8.14e-04	1.55e-02
ncbi_114361313	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Papilio machaon]	+1.67	1.88e-03	2.92e-02
ncbi_114361498	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Papilio machaon]	+1.22	3.20e-03	4.22e-02
ncbi_114361500	nephrin-like [Ostrinia furnacalis]	+1.05	1.27e-03	2.16e-02
ncbi_114361507	PREDICTED: probable salivary secreted peptide [Amyelois transitella]	+1.06	1.06e-13	3.48e-11
ncbi_114361766	myrosinase 1-like [Ostrinia furnacalis]	-1.20	4.62e-08	4.66e-06
ncbi_114361845	Lysocardiolipin acyltransferase 1, partial [Operophtera brumata]	-1.65	8.48e-04	1.60e-02
ncbi_114362131	PiggyBac transposable element-derived protein 3 [Eumeta japonica]	-2.21	1.23e-03	2.11e-02
ncbi_114362146	MADF domain-containing protein [Aphis craccivora]	-1.28	3.57e-03	4.53e-02
ncbi_114362322	polyprotein [Antheraea mylitta]	-1.87	5.67e-06	2.80e-04
ncbi_114362336	tigger transposable element-derived protein 4-like isoform X1 [Ostrinia furnacalis]	+4.30	3.84e-06	2.08e-04
ncbi_114362420	acetylcholinesterase-like [Ostrinia furnacalis]	+1.55	2.82e-04	6.75e-03
ncbi_114362457	tyrosine-protein phosphatase non-receptor type 13-like [Ostrinia furnacalis]	-1.27	1.05e-03	1.88e-02
ncbi_114362479	uncharacterized protein LOC114362479 [Ostrinia furnacalis]	+3.30	2.66e-03	3.68e-02
ncbi_114362482	Pro-Pol polyprotein [Folsomia candida]	+4.56	3.96e-07	2.98e-05
ncbi_114362538	chymotrypsin BI-like [Ostrinia furnacalis]	+4.55	1.91e-14	7.33e-12
ncbi_114362546	piggyBac transposable element-derived protein 1-like, partial [Spodoptera litura]	-5.81	1.02e-11	2.36e-09
ncbi_114362577	formin-like protein 14 [Vanessa tameamea]	+1.81	4.32e-06	2.27e-04

ncbi_114362585	uncharacterized protein LOC114362585 [Ostrinia furnacalis]	-9.42	2.52e-03	3.55e-02
ncbi_114362672	ATP-dependent DNA helicase PIF1 [Eumeta japonica]	-1.84	3.52e-06	1.94e-04
ncbi_114362710	membrane-bound alkaline phosphatase-like [Ostrinia furnacalis]	-1.37	1.31e-05	5.77e-04
ncbi_114362735	janus kinase and microtubule-interacting protein 1-like [Ostrinia furnacalis]	-2.51	1.44e-03	2.39e-02
ncbi_114362757	polyprotein [Mizuhopecten yessoensis]	-1.37	3.67e-04	8.29e-03
ncbi_114362872	alpha-amylase 2-like isoform X3 [Ostrinia furnacalis]	-1.91	6.25e-14	2.25e-11
ncbi_114363023	ATP-dependent DNA helicase PIF1 [Eumeta japonica]	-2.64	2.08e-11	4.68e-09
ncbi_114363240	trypsin theta-like isoform X1 [Ostrinia furnacalis]	+1.15	8.63e-11	1.65e-08
ncbi_114363286	proteoglycan 4-like [Ostrinia furnacalis]	-1.94	1.45e-20	9.84e-18
ncbi_114363287	P94 protein [Danaus plexippus plexippus]	-1.68	5.27e-12	1.32e-09
ncbi_114363298	Fanconi anemia group D2 protein [Ostrinia furnacalis]	-1.55	2.58e-12	7.07e-10
ncbi_114363342	Integrase catalytic domain-containing protein, partial [Aphis craccivora]	-1.09	8.75e-06	4.06e-04
ncbi_114363457	uncharacterized protein LOC114363457 isoform X1 [Ostrinia furnacalis]	-3.25	1.85e-05	7.53e-04
ncbi_114363590	keratin, type II cytoskeletal 2 epidermal-like [Ostrinia furnacalis]	-2.44	2.14e-06	1.26e-04
ncbi_114363699	uncharacterized protein LOC114363699 [Ostrinia furnacalis]	+9.86	7.57e-05	2.37e-03
ncbi_114363785	myosin-9-like [Ostrinia furnacalis]	-3.65	2.32e-08	2.61e-06
ncbi_114363829	CLUMA_CG003690, isoform A [Clunio marinus]	+3.75	2.42e-03	3.46e-02
ncbi_114363830	structural maintenance of chromosomes protein 3-like isoform x2 protein [Lasius niger]	+4.69	1.62e-03	2.61e-02
ncbi_114363843	Integrase catalytic domain-containing protein [Aphis craccivora]	+3.42	3.83e-05	1.38e-03
ncbi_114363909	cell cycle checkpoint protein RAD1 isoform X1 [Ostrinia furnacalis]	+1.31	1.19e-03	2.07e-02
ncbi_114364123	transposase, partial [Helicoverpa zea]	-1.42	5.18e-07	3.77e-05
ncbi_114364375	3-ketoacyl-CoA thiolase, mitochondrial-like [Ostrinia furnacalis]	-1.51	6.92e-17	3.62e-14
ncbi_114364384	probable protein BRICK1-A [Bombyx mori]	+1.04	7.06e-11	1.40e-08
ncbi_114364477	proton-coupled amino acid transporter-like protein CG1139 [Ostrinia furnacalis]	-1.25	9.95e-05	2.91e-03
ncbi_114364789	Si:dkey-56d12.4 protein [Operophtera brumata]	-1.12	9.20e-04	1.70e-02

ncbi_114364874	probable cytochrome P450 304a1 [Ostrinia furnacalis]	-1.19	3.23e-04	7.51e-03
ncbi_114364949	forkhead box protein J1-A-like [Ostrinia furnacalis]	-2.60	6.81e-04	1.34e-02
ncbi_114365248	glycine-rich cell wall structural protein-like [Ostrinia furnacalis]	-2.77	1.79e-03	2.83e-02
ncbi_114365282	cytochrome P450 6B5-like [Ostrinia furnacalis]	-1.54	8.62e-11	1.65e-08
ncbi_114365306	polyprotein [Antheraea mylitta]	+6.60	5.04e-237	5.80e-233
ncbi_114365322	cis, cis-muconate transporter protein [Bombyx mori]	-3.42	2.43e-03	3.46e-02
ncbi_114365341	glutathione S-transferase-like [Ostrinia furnacalis]	-1.66	9.05e-14	3.11e-11
ncbi_114365395	multiple inositol polyphosphate phosphatase 1-like [Ostrinia furnacalis]	+8.65	2.86e-05	1.09e-03
ncbi_114365409	G2/M phase-specific E3 ubiquitin-protein ligase [Bombyx mori]	-1.54	5.17e-04	1.08e-02
ncbi_114365566	fasciclin-2-like [Ostrinia furnacalis]	+3.72	2.49e-03	3.50e-02
ncbi_114365597	cysteine synthase-like [Ostrinia furnacalis]	-1.85	4.10e-28	6.74e-25
ncbi_114365702	chymotrypsin-1-like [Ostrinia furnacalis]	+3.47	8.53e-17	4.27e-14
ncbi_114365712	NICE-3 family member [Aedes aegypti]	+1.02	1.13e-04	3.24e-03
ncbi_114365715	alpha-2-macroglobulin-like protein 1 [Ostrinia furnacalis]	-2.94	3.33e-06	1.85e-04
ncbi_114365747	uncharacterized protein LOC114365747 [Ostrinia furnacalis]	-1.25	1.42e-05	6.09e-04
ncbi_114365855	elongation of very long chain fatty acids protein 4-like [Ostrinia furnacalis]	-2.37	1.29e-03	2.19e-02
ncbi_114365912	uncharacterized protein LOC114365912 [Ostrinia furnacalis]	+7.11	1.13e-07	9.97e-06
ncbi_114366090	fructose-bisphosphate aldolase-like [Ostrinia furnacalis]	-1.55	6.05e-04	1.22e-02
ncbi_114366113	organic cation transporter-like protein [Ostrinia furnacalis]	-1.51	1.49e-05	6.32e-04
ncbi_114366264	angiotensin-converting enzyme-like [Ostrinia furnacalis]	+1.91	7.61e-06	3.62e-04
ncbi_114366439	Ecdysteroid 22-kinase [Operophtera brumata]	-1.56	1.42e-06	8.89e-05
ncbi_114366528	piggyBac transposable element-derived protein 2-like [Trichoplusia ni]	-1.36	3.37e-05	1.25e-03
ncbi_114366552	pupal cuticle protein 36-like [Ostrinia furnacalis]	+2.08	1.57e-03	2.55e-02
ncbi_114366668	UDP-glucuronosyltransferase 2B1-like isoform X3 [Ostrinia furnacalis]	-1.35	2.46e-04	6.12e-03
ncbi_114366672	beta-1,3-glucan-binding protein-like isoform X1 [Ostrinia furnacalis]	-1.86	4.22e-04	9.40e-03

ncbi_114366725	X-ray repair cross-complementing protein 5-like [Ostrinia furnacalis]	-1.17	1.59e-08	1.86e-06
ncbi_114366797	zinc transporter 7-like isoform X1 [Ostrinia furnacalis]	+1.81	8.55e-05	2.60e-03



**Table S6 Transcript data about heat shock protein, and P-Value $\leq$ 0.05.**

Gene ID	Description	log2(fc)	P-Value	FDR
<b>ACB-BtS vs.ACB-FR</b>				
ncbi_114354725	heat shock protein 68-like [Ostrinia furnacalis]	-3.26	3.00e-08	3.26e-06
ncbi_114363773	heat shock protein 68-like [Ostrinia furnacalis]	-2.90	1.37e-03	1.61e-02
ncbi_114361580	heat shock protein Hsp-12.2-like [Ostrinia furnacalis]	-2.85	3.41e-30	2.01e-26
ncbi_114354259	heat shock protein 68-like [Ostrinia furnacalis]	-2.32	6.31e-16	5.31e-13
ncbi_114356221	heat shock protein 68-like [Ostrinia furnacalis]	-1.56	2.53e-15	1.57e-12
ncbi_114356220	heat shock protein 83 [Ostrinia furnacalis]	+0.25	1.75e-02	1.03e-01
ncbi_114358080	heat shock protein 30C isoform X1 [Helicoverpa armigera]	+0.34	2.51e-02	1.34e-01
ncbi_114362461	heat shock protein 60A-like [Ostrinia furnacalis]	+0.61	6.39e-07	3.95e-05
ncbi_114365590	10 kDa heat shock protein, mitochondrial [Ostrinia furnacalis]	+0.67	3.13e-05	8.81e-04
<b>ACB-BtS vs.ACB-IeR</b>				
ncbi_114365089	heat shock protein 75 kDa, mitochondrial [Ostrinia furnacalis]	-0.40	3.92e-02	2.25e-01
ncbi_114362461	heat shock protein 60A-like [Ostrinia furnacalis]	+0.29	2.78e-03	3.79e-02
ncbi_114365590	10 kDa heat shock protein, mitochondrial [Ostrinia furnacalis]	+0.57	6.38e-07	4.56e-05

**Table S7 Transcript data about UDP-glucuronosyltransferase, and P-Value≤0.05.**

Gene ID	Description	log2(fc)	P-Value	FDR
<b>ACB-BtS vs.ACB-FR</b>				
ncbi_114360717	UDP-glucuronosyltransferase 2B20-like [Ostrinia furnacalis]	-1.34	8.69e-03	6.24e-02
ncbi_114366668	UDP-glucuronosyltransferase 2B1-like isoform X3 [Ostrinia furnacalis]	-0.84	1.01e-02	6.99e-02
ncbi_114365422	UDP-glucuronosyltransferase 2B1-like [Ostrinia furnacalis]	-0.68	2.39e-05	7.22e-04
ncbi_114350603	UDP-glucuronosyltransferase 1-6 [Habropoda laboriosa]	-0.44	1.60e-02	9.70e-02
ncbi_114350074	UDP-glucuronosyltransferase 2B10-like [Ostrinia furnacalis]	-0.43	2.44e-02	1.31e-01
ncbi_114353020	UDP-glucuronosyltransferase 1-7C-like isoform X1 [Ostrinia furnacalis]	+0.33	4.14e-03	3.63e-02
ncbi_114366667	UDP-glucuronosyltransferase 2B1-like isoform X1 [Ostrinia furnacalis]	+0.40	3.11e-04	5.25e-03
ncbi_114357098	UDP-glucuronosyltransferase 2B15-like [Ostrinia furnacalis]	+0.41	3.07e-04	5.21e-03
ncbi_114358977	UDP-glucuronosyltransferase 2B1-like [Ostrinia furnacalis]	+0.53	6.45e-03	4.99e-02
ncbi_114357101	UDP-glucuronosyltransferase 2B15-like isoform X1 [Ostrinia furnacalis]	+0.63	2.08e-02	1.17e-01
ncbi_114357080	UDP-glucuronosyltransferase 2B2-like [Ostrinia furnacalis]	+0.65	1.56e-04	3.18e-03
ncbi_114358082	UDP-glucuronosyltransferase 3A1-like [Ostrinia furnacalis]	+0.77	1.87e-09	2.86e-07
ncbi_114350056	UDP-glucuronosyltransferase 2B1-like [Ostrinia furnacalis]	+0.88	2.64e-10	4.93e-08
ncbi_114352649	UDP-glucuronosyltransferase 2B20-like isoform X1 [Vanessa tameamea]	+0.92	1.99e-04	3.79e-03
ncbi_114357102	UDP-glucuronosyltransferase 2B15-like [Ostrinia furnacalis]	+0.93	7.74e-04	1.04e-02
ncbi_114364052	UDP-glucuronosyltransferase 2B30-like [Ostrinia furnacalis]	+0.96	3.73e-05	1.02e-03
ncbi_114366669	UDP-glucuronosyltransferase 2B2-like [Ostrinia furnacalis]	+1.30	6.26e-06	2.47e-04
ncbi_114357739	UDP-glucuronosyltransferase 2B14-like isoform X1 [Ostrinia furnacalis]	+1.62	4.99e-02	2.10e-01
MSTRG.14142	UDP-glucuronosyltransferase 2B15-like [Ostrinia furnacalis]	+2.31	1.05e-15	8.21e-13
ncbi_114352631	UDP-glucuronosyltransferase 2B15-like [Ostrinia furnacalis]	+7.07	2.98e-07	2.10e-05
<b>ACB-BtS vs.ACB-IeR</b>				

MSTRG.14142	UDP-glucuronosyltransferase 2B15-like [ <i>Ostrinia furnacalis</i> ]	-1.35	2.46e-04	6.12e-03
ncbi_114364052	UDP-glucuronosyltransferase 2B30-like [ <i>Ostrinia furnacalis</i> ]	-0.68	5.38e-03	6.09e-02
ncbi_114357098	UDP-glucuronosyltransferase 2B15-like [ <i>Ostrinia furnacalis</i> ]	-0.54	1.46e-02	1.21e-01
ncbi_114350603	UDP-glucuronosyltransferase 1-6 [ <i>Habropoda laboriosa</i> ]	-0.40	2.03e-02	1.48e-01
ncbi_114366668	UDP-glucuronosyltransferase 2B1-like isoform X3 [ <i>Ostrinia furnacalis</i> ]	+0.37	2.94e-03	3.96e-02
ncbi_114350056	UDP-glucuronosyltransferase 2B1-like [ <i>Ostrinia furnacalis</i> ]	+0.92	7.28e-13	2.09e-10
ncbi_114360717	UDP-glucuronosyltransferase 2B20-like [ <i>Ostrinia furnacalis</i> ]	+1.44	9.59e-07	6.34e-05
ncbi_114358082	UDP-glucuronosyltransferase 3A1-like [ <i>Ostrinia furnacalis</i> ]	+2.45	2.64e-04	6.40e-03
ncbi_114357736	UDP-glucuronosyltransferase 2B14-like [ <i>Ostrinia furnacalis</i> ]	+3.38	6.59e-05	2.16e-03

**Table S8 Transcript data about trypsin alkaline C-like, and P-Value $\leq$ 0.05.**

Gene ID	Description	log2(fc)	P-Value	FDR
<b>ACB-BtS vs.ACB-FR</b>				
ncbi_114351933	trypsin, alkaline C-like [Ostrinia furnacalis]	+2.54	2.68e-04	4.76e-03
ncbi_114351935	trypsin, alkaline C-like [Ostrinia furnacalis]	+1.33	2.86e-08	3.15e-06
ncbi_114351936	trypsin, alkaline C-like isoform X1 [Ostrinia furnacalis]	+1.29	1.64e-07	1.33e-05
ncbi_114355419	trypsin, alkaline C-like [Ostrinia furnacalis]	+0.57	8.74e-03	6.26e-02
ncbi_114355420	trypsin, alkaline C-like [Ostrinia furnacalis]	+0.36	3.31e-02	1.60e-01
<b>ACB-BtS vs.ACB-IeR</b>				
ncbi_114351933	trypsin, alkaline C-like [Ostrinia furnacalis]	+2.07	3.67e-02	2.15e-01
ncbi_114351935	trypsin, alkaline C-like [Ostrinia furnacalis]	+1.79	1.14e-04	3.27e-03
ncbi_114351936	trypsin, alkaline C-like isoform X1 [Ostrinia furnacalis]	+2.95	5.85e-11	1.20e-08
ncbi_114351939	trypsin, alkaline C-like [Ostrinia furnacalis]	+3.04	8.62e-05	2.61e-03
ncbi_114355419	trypsin, alkaline C-like [Ostrinia furnacalis]	+0.77	6.51e-04	1.29e-02
ncbi_114355420	trypsin, alkaline C-like [Ostrinia furnacalis]	+2.08	2.11e-23	2.03e-20
ncbi_114355467	trypsin, alkaline C-like [Ostrinia furnacalis]	+0.17	1.62e-02	1.29e-01

**Table S9 Transcript data about glutathione S-transferase, and P-Value $\leq$ 0.05.**

Gene ID	Description	log2(fc)	P-Value	FDR
<b>ACB-BtS vs.ACB-FR</b>				
ncbi_114365341	glutathione S-transferase-like [Ostrinia furnacalis]	-1.33	1.55e-06	7.81e-05
ncbi_114357527	glutathione S-transferase theta-1-like [Ostrinia furnacalis]	+0.34	8.87e-04	1.16e-02
ncbi_114358125	glutathione S-transferase omega-1-like [Ostrinia furnacalis]	+0.24	1.58e-02	9.59e-02
ncbi_114360536	glutathione S-transferase C-terminal domain-containing protein homolog [Ostrinia furnacalis]	+0.87	9.29e-03	6.53e-02
ncbi_114360773	glutathione S-transferase 1-like [Ostrinia furnacalis]	+2.75	1.46e-13	8.12e-11
ncbi_114363146	glutathione S-transferase 1-like [Ostrinia furnacalis]	-0.84	4.24e-04	6.64e-03
ncbi_114359748	glutathione S-transferase 1-1-like [Ostrinia furnacalis]	+0.38	5.01e-03	4.14e-02
<b>ACB-BtS vs.ACB-IeR</b>				
ncbi_114365341	glutathione S-transferase-like [Ostrinia furnacalis]	-1.66	9.05e-14	3.11e-11
ncbi_114364484	glutathione S-transferase 2-like [Ostrinia furnacalis]	-0.66	2.12e-03	3.16e-02
MSTRG.22972	glutathione S-transferase 1-like [Ostrinia furnacalis]	+1.91	2.43e-03	3.46e-02
ncbi_114358125	glutathione S-transferase 1-like [Ostrinia furnacalis]	+0.27	1.74e-02	1.34e-01
ncbi_114365321	glutathione S-transferase 1-like [Ostrinia furnacalis]	-0.98	1.97e-03	3.00e-02