

Table S1. The number of identified unigenes in *de novo* database and their proportion

Sample name	Identified expressed unigenes	Proportion in <i>de novo</i> database (%)
CK1	29146	85.34
CK2	31163	91.24
CK3	30282	88.66
CH_6h1	31087	91.02
CH_6h2	30350	88.86
CH_6h3	30746	90.02
CH_48h1	30785	90.14
CH_48h2	30840	90.30
CH_48h3	31022	90.83
CL_6h1	31355	91.80
CL_6h2	30301	88.72
CL_6h3	31467	92.13
CL_48h1	30895	90.46
CL_48h2	31092	91.03
CL_48h3	30509	89.33

CK: control; CH_6: Chlorpyrifos treated 6 hours; CH_48h: Chlorpyrifos treated 48 hours; CL_6h: Clothianidin treated 6 hours; CL_48h: Clothianidin treated 48 h.

Table S2: GO categories of DEUs.

	CH6h VS CK	CH48h VS CK	CL6h VS CK	CL48h VS CK
Behavior	1	2	1	3
Biological adhesion	1	0	1	2
Biological regulation	12	17	17	31
Cell component organization or biogenesis	10	14	12	16
Cellular process	30	40	47	64
Developmental process	12	17	14	29
Growth	1	1	1	8
Immune system process	1	4	3	6
Localization	11	10	14	18
Locomotion	6	6	7	11
Metabolic process	27	48	56	67
Multicellular organismal process	10	15	13	27
Multi-organismal process	3	4	4	7
Negative regulation of biological process	4	6	5	8
Positive regulation of biological process	2	4	3	8
Regulation of biological process	11	14	15	28
Reproduction	4	4	5	13
Reproductive process	4	4	5	7
response to stimulus	7	11	12	21
signaling	2	4	6	21
Single-organism process	22	42	42	59
Cell	22	27	25	46
Cell junction	3	3	2	3
Cell part	22	27	25	46
Extracellular Matrix	1	0	1	1

Extracellular Matrix component	1	0	1	1
Extracellular region	2	3	6	2
Extracellular region part	1	0	1	1
Macromolecular complex	9	8	9	19
Membrane	6	8	17	19
Membrane-enclosed lumen	2	4	2	4
Membrane part	4	5	12	12
Organelle	19	21	19	36
Organelle part	14	17	15	26
Supramolecular fiber	1	2	1	1
Antioxidant activity	1	3	1	3
binding	36	44	64	78
Catalytic activity	33	70	71	80
Electron carrier activity	0	1	2	2
Molecular function regulator	1	1	1	2
Molecular transducer activity	1	0	1	2
Nucleic acid binding transcription factor activity	1	1	1	2
Signal transducer activity	1	0	1	2
Structural molecule activity	6	6	6	13
Transcription factor activity protein binding	0	1	0	2
Transporter activity	2	1	5	6
total	370	520	572	863

Table S3. DEUs' percentage assigned into three main GO categories.

Main Categories	CH6h VS CK	CH48h VS CK	CL6h VS CK	CL48h VS CK	CL6h VS CH6h	CL48h VS CH48h	CH48h VS CH6h	CL48h VS CL6h
biological process	48.92	51.35	49.48	52.61	40.91	41.18	38.46	51.56
cellular component	28.92	24.04	23.78	25.14	22.73	32.77	24.48	24.00
molecular function	22.16	24.62	26.75	22.25	36.36	26.05	37.06	24.44

CK: Control; CH: Chlorpyrifos; CL: Clothianidin; 6h: treated 6 h; 48h: treated 48 h.

Table S4. KEGG pathway identification of DEUs

Pathway Identification	CH6h VS CK	CH48h VS CK	CL6h VS CK	CL48h VS CK
Cell growth and death	5	9	6	6
Cell motility	38	44	46	52
Cellular community	51	54	56	69
Transport and catabolism	42	58	60	64
Membrane transport	1	0	1	1
Signaling molecules and interaction	27	47	43	47
Signal transduction	66	74	98	101
Folding, sorting and degradation	18	25	35	32
Replication and repair	1	2	3	3
Transcription	26	52	43	33

Translation	13	20	24	39
Cancers: Overview	63	71	100	100
Cancers: Specific types	32	37	49	46
Cardiovascular diseases	41	47	47	53
Endocrine and metabolic diseases	12	19	24	21
Immune diseases	7	8	11	9
Infectious diseases: Bacterial	65	82	87	93
Infectious diseases: Parasitic	40	41	52	44
Infectious diseases: Viral	36	76	77	66
Neurodegenerative diseases	35	57	57	53
Substance dependence	3	6	7	6
Amino acid metabolism	13	35	29	31
Biosynthesis of other secondary metabolism	0	1	1	1
Carbohydrate metabolism	21	38	50	34
Energy metabolism	6	3	10	13
Global and overview maps	55	108	126	105
Glycan biosynthesis and metabolism	1	4	3	2
Lipid metabolism	17	26	40	32
Metabolism of cofactors and vitamins	8	9	17	23
Metabolism of other amino acids	10	14	20	17
Metabolism of terpenoids and polyketides	4	6	8	8
Nucleotide metabolism	19	41	39	25
Xenobiotics biodegradation and metabolism	10	10	24	20
Circulatory system	23	25	29	32
Development	23	23	26	28
Digestive system	30	57	57	62
Endocrine system	54	74	95	87
Environmental adaptation	5	6	9	7
Excretory system	7	6	10	9
Immune system	46	62	64	68
Nervous system	11	23	30	28
Sensory system	2	9	10	6
Total	987	1409	1623	1576

Table S5. RNA-Seq samples' value detected by Agilent 2100.

Sample name	concentration (ng/ μ L)	volume (μ L)	total amount (μ g)	RNA Integrated Number
egg	579	60	34.7	7.2
2 nd instar larva	714	300	214.2	7.2
4 th instar larva	1056	200	211.2	7.1
pupa	1096	80	87.7	6.9
adult	624	120	74.9	7.2
CK-1	562	60	33.72	6.4
CK-2	428	80	34.24	6.7
CK-3	476	60	28.56	6.5
CH_6h-1	832	80	66.56	6.9
CH_6h-2	732	80	58.56	7.1

CH_6h-3	525	160	84.00	7.0
CH_48h-1	600	60	36.00	7.0
CH_48h-2	573	80	45.84	7.0
CH_48h-3	657	60	39.42	7.0
CL_6h-1	450	160	72.00	7.0
CL_6h-2	744	80	59.52	7.0
CL_6h-3	603	160	96.48	7.0
CL_48h-1	748	60	44.88	6.9
CL_48h-2	708	60	42.48	6.9
CL_48h-3	868	40	34.72	6.9

CK: Control; CH: Chlorpyrifos; CL: Clothianidin; 6h and 48h: treatment with Chlorpyrifos or Clothianidin after 6 or 48 h.

Table S6. The primers to confirm unigenes and RT-qPCR.

	Gene name	Unigene number	accession number in NCBI		PCR product size (bp)
Primers to confirm unigenes	P450	CL2656.Contig1	KY997061	F: ATACTTCTTGGCGTTATTTCAAAT	1554
		Unigene17178	KY997062	R: CATGGGTCTCCTATTCAGTGATAC	2098
				F: TGGATTGCGTTCGAAACATT	
		Unigene 6476	KY997063	R: AATTCACGTAATTCGGCACG	682
				F: TTCGCTCAAAGGTGTGTTACAA	
	CL1542.Contig2	CL1542.Contig2	KY997064	R: ATATGACGTGTTGCAAAAGATGA	1450
				F: CTGCTGTAAAGTTGATCTGTTATC	
		CL276.Contig2	KY997065	R: TCAGACGAGGTTAAGATGAGTGC	357
				F: CGGATTATCTGACCTCAAATACG	
				R: GAAATGTGGCGAATCGCATA	
	GST	Unigene2860	KY997066	F:	898
				TTTGATTACTGTAAAAAGGAGAACC	
		Unigene16851	KY997067	R: AATGTTATCCGACGTTAGTATTC	764
				F: CATTTTTTCCACACCATTGT	
		Unigene8896	KY997068	R: TTGGTTTCTATCTATTGAACGTGAA	846
				F: TGTAATGCAAAATCTACGCACAG	
Primers for RT-qPCR	Carboxylesterases	Unigene1880	KY997069	R: TTAGTATTCGTAGCGGTCCGA	1899
				F:	
		CL2626.Contig1	KY997070	ACAGATACACGATCAGTTATCGTGA	1593
				R: TCGTTGCTACTAATCAGTTGAACC	
		Unigene12260	MG407793	F: TTATGTGCTCTACGTTTCTGAAT	927
				R: CATACTAGCAGTTACGAGTTCG	
	Cuticle protein	Unigene1844	MG407794	F:	974
				TCTAAAAGATCAAGTTGAAGCTTTG	
		CL2724.Contig1	MG407795	R: GCAAAATTGTAGTACATATCGACG	718
				F: GTTGCAAGGCACGCTTATAAT	
		Unigene15206	MG407796	R: TCGATGAAATAGTCCAGCCG	693
				F:	
	GAPDH	Unigene19803	KY997073	TAAGGAAATAAAATCTTTTACGCA	1425
				R: TACAACTGTGAATATGCAATTGTTG	
		Unigene19803	KY997073	F: AAAATGGCATTCAAGTTTTTGAC	160
				R: GTTTTCAAACAGTTTGTTCAAAGAC	
		Unigene19803	KY997073	F: TTATCTTCTCAGAAATTTGCCCTT	106
				R: TATTCTATAACACGGTTTTAATGCC	
Primers for RT-qPCR	P450	CL2656.Contig1	KY997061	F: ATATGGCTGTTCCCTTTTCC	146
				R: CAACTGTCCTATGATGCTGTTAGT	
		Unigene17178	KY997062	F: TTGCTCCAGCTTTTCATCAG	126
				R: AACACTTTGCCACCTCTTT	
		Unigene 6476	KY997063	F: TGTTGCTCAAAGGTGTGTT	131
				R: TTCGTGTGTTAAATTGGCAGG	
	CL1542.Contig2	CL1542.Contig2	KY997064	F: AACAGACGGATGCAATCGA	196
				R: CAAGACAAGGCAAGGGAAG	
		CL276.Contig2	KY997065	F: GTCATCATACCTGTCTACTCGCT	157
				R: GGAAGGAATACACTGCTGTCTTT	
		Unigene2860	KY997066	F: TCATCCAGATAATCGGCAATA	197
				R: CATACTGCTCAGCGAACACAC	
	GST	Unigene16851	KY997067	F: TACTCGGAGACTTCGGGTAGA	106
				R: AATTCGGAGGCAATAATCATG	
		Unigene8896	KY997068	F: TTCATCCAGATAATCGGCAA	159
				R: CATACTGCTCAGCGAACACA	
		Unigene1880	KY997069	F: ATTGAGACTGCTTCTCTTCTGC	130
				R: GGTGTTGTTTTTTATGTTCCG	
Primers for RT-qPCR	CL2626.Contig1	CL2626.Contig1	KY997070	F: GGTTACCAGACGTCCAGACAC	130
				R: GACCCACCTACGACAATCAAT	
		Unigene12260	MG407793	F: GCTGGTGGTAGTAGTGTTCATTT	130
		Unigene12260	MG407793		
	Carboxylesterases	Unigene12260	MG407793		130
		Unigene12260	MG407793		130
		Unigene12260	MG407793		130

	Unigene1844	MG40779 4	R: GAGCTTTTCTCTTGGTTTTTG F: CTTAAGTTCGTTTTGCGGTC	124
Cuticle protein	CL2724.Contig1	MG40779 5	R: TAGTCTCTTCCATGCTTTGGTT F: GCCCTTGTTTCTTTTATTGCT	200
	Unigene15206	MG40779 6	R: GATCGGGTTTCCTGTTGATT F: AAGACGGTTTGACGGGTG	184
GAPDH	Unigene19803	KY997073	R: GCTGCTACGATTTTTCG F: CGAAATCGTTGAAGGTCTGA R: CTGGAATGATGTTTGCTGG	122

F: forward; R: reverse; PCR: polymerase chain reaction; RT-qPCR: reverse transcription quantitative. Confirm unigenes PCR primer T_m were set 58°C and RT-qPCR primer were set 56°C. GAPDH was considered as reference gene.

Table S7. The amplification efficiencies of primers for qRT-PCR

<i>Gene name</i>	Unigene number	Curve fitting linear	R²	amplification efficiencies
<i>P450</i>	CL2656.Contig1	Y=3.33x+16.80	0.99	1.99
	Unigene17178	Y=3.25x+21.42	0.99	2.05
	Unigene 6476	Y=3.32x+17.95	0.99	1.99
	CL1542.Contig2	Y=3.40x+13.24	0.99	1.96
	CL276.Contig2	Y=3.46x+17.45	0.99	1.95
<i>GST</i>	Unigene2860	Y=3.44x+14.40	0.99	1.95
	Unigene16851	Y=3.36x+15.48	0.99	1.98
	Unigene8896	Y=3.46x+14.37	0.99	1.95
	Unigene1880	Y=3.50x+16.52	0.99	1.93
	CL2626.Contig1	Y=3.50x+14.06	0.99	1.93
<i>Carboxylesterases</i>	Unigene12260	Y=3.59x+18.11	0.99	1.90
	Unigene1844	Y=3.35x+19.94	0.99	1.99
<i>Cuticle protein</i>	CL2724.Contig1	Y=3.57x+18.54	0.99	1.91
	Unigene15206	Y=3.48x+17.35	0.99	1.94
<i>GAPDH</i>	Unigene19803	Y=3.41x+12.03	0.99	1.96