

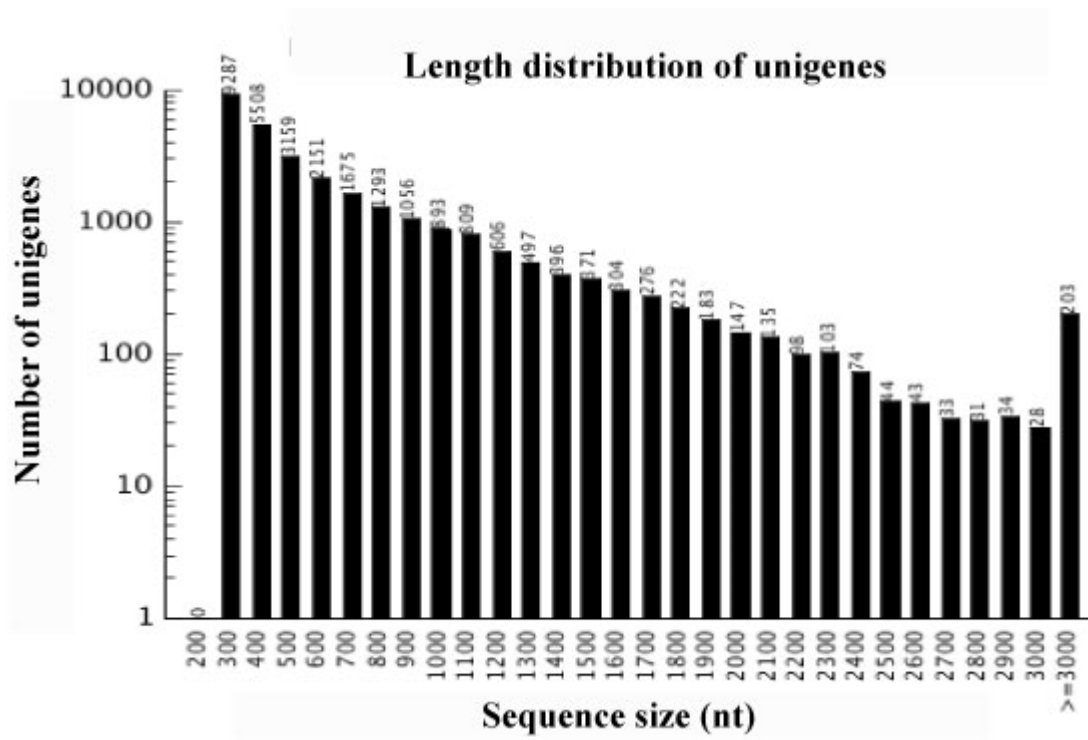
**The *de novo* transcriptome and its analysis of the worldwide vegetable pest, *Delia antiqua*
(Diptera: Anthomyiidae)**

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File S1 Length distribution of unigenes in *D. antiqua*.

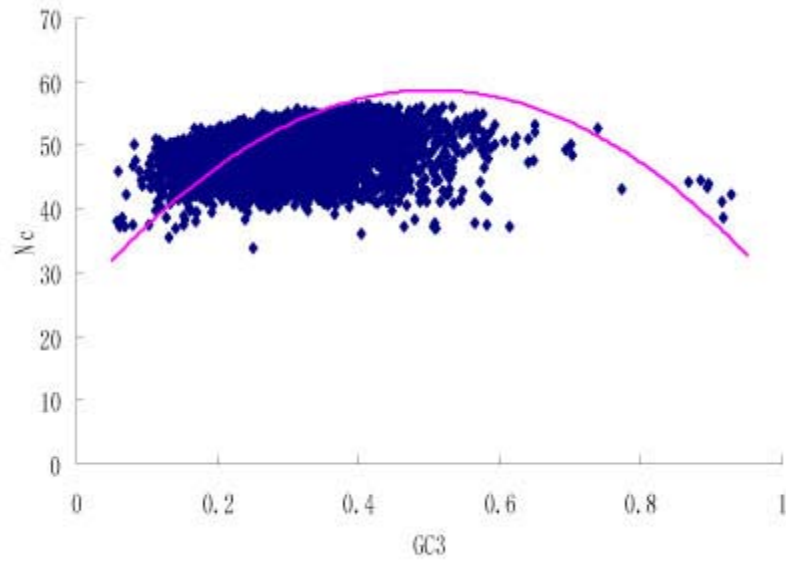
File S2 Total codon usage and codon usage bias in *De. antiqua* transcriptome. A total of 20578 ORF containing 3913673 codons in the *De. antiqua* transcriptome were used in the calculation of codon usage bias measured by RSCU.

Codon	Amino Acid	Total codon counts	RSCU	Codon	Amino Acid	Total codon counts	RSCU
CGU	R	81490	2.037	UCC	S	43072	0.737
UUA	L	118878	1.808	GGA	G	44472	0.733
GGU	G	111980	1.623	CGC	R	27367	0.686
UUG	L	104910	1.477	GUG	V	43091	0.657
GAU	D	172863	1.342	UCG	S	39066	0.644
AAU	N	177112	1.333	CUA	L	37341	0.569
GCU	A	105216	1.299	UGG	W	38282	0.549
GAA	E	202421	1.286	CUU	L	34950	0.532
CAA	Q	147888	1.271	CGA	R	18777	0.525
GUU	V	83193	1.247	GUC	V	30508	0.445
AAA	K	195467	1.234	UUC	F	43668	0.435
UAU	Y	99910	1.223	AGC	S	25606	0.430
ACA	T	87752	1.199	AAG	K	72085	0.417
CCA	P	73462	1.188	CUG	L	26604	0.393
CAU	H	75842	1.159	CCG	P	22061	0.384
UUU	F	107042	1.159	UGC	C	21035	0.382
UCA	S	69422	1.143	ACG	T	25727	0.368
AGA	R	41095	1.142	CAG	Q	44046	0.363
AGU	S	64397	1.112	CAC	H	23232	0.358
AUU	I	104368	1.112	GAG	E	55560	0.351
AUA	I	89316	1.024	UAC	Y	29080	0.348
ACU	T	73298	1.014	AUC	I	31938	0.348
UCU	S	59447	0.971	AAC	N	46335	0.328
GCC	A	75178	0.970	GAC	D	37400	0.287
GUA	V	62064	0.961	AGG	R	9837	0.282
UGU	C	52258	0.950	GCG	A	18599	0.267
CCC	P	53246	0.912	CUC	L	16359	0.244
GCA	A	57320	0.798	CGG	R	7571	0.206
CCU	P	48604	0.795	GGG	G	8038	0.140
GGC	G	51205	0.778	UAA	*	685	0.029
ACC	T	54346	0.753	UGA	*	679	0.023
AUG	M	89348	0.744	UAG	*	264	0.011

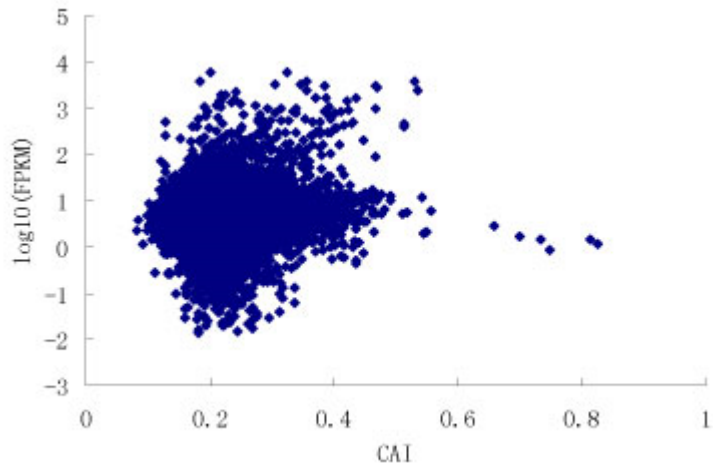
File S3

The ID and FPKM of unigenes, and the CAI, Nc and GC3 of ORFs in each unigene in *D. antiqua*.

File S3 is available for download as an Excel file at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.113.009779/-/DC1>



File S4 A plot of N_c versus GC3 (Nc-plot) for *D. antiqua* ORFs. The pink-dotted curve represents the expected curve between GC3 and N_c under random codon usage. A blue dot each indicates corresponding ORFs of each unigene.



File S5 Relationship between CAI (Codon Adaptation Index) and expression level (Log10 (FPKM)) of all *D. antiqua* transcriptome unigenes.

File S6

SSR identification of *D. antiqua* unigenes.

File S6 is available for download as an Excel file at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.113.009779/-/DC1>