Table S1. Summary statistics for *D. v. virgifera* transcriptome sequencing and assembly.

egg 0-10 day total RNA (Illumina, paired-end)	
Total number of paired-end reads before filtering (length)	38,657,737 (2,899,330,275 bp)
Number of paired-end reads that entered assembly after > Q20 filtering (length)	15,162,017 (1,137,151,275 bp)
Assembly program used	Trinity (2013-02-25)
Total number of contigs	72,638
Average contig length (range)	825 bp (201 – 13,911 bp)
N50 length	1,357 bp
Assembly program used	Velvet/Oasis (ver. 1.2.03)
Total number of contigs	56,135
Average contig length (range)	583 bp (100 – 10,434 bp)
N50 length	850 bp
Assembly program used	Mira (ver. 3.4.0)
Total number of contigs	69,815
Average contig length (range)	520 bp (100 – 13,526 bp)
N50 length	850 bp
Third larval midgut RNA (Illumina, paired-end)	
Total number of paired-end reads before filtering (length)	76,202,715 (5,715,203,625 bp)
Number of paired-end reads that entered assembly after > Q20 filtering (length)	44,852,488 (3,363,936,600 bp)
Assembly program used	Trinity (2013-02-25)
Total number of contigs	72,325
Average contig length (range)	859 bp (201 – 17,831 bp)
N50 length	1,435 bp
Assembly program used	Velvet/Oasis (ver. 1.2.03)
Total number of contigs	96,215
Average contig length (range)	635 bp (100 – 17,673 bp)
N50 length	1,180 bp
Third larval midgut RNA (Roche 454)	
Total number of reads before filtering (length)	664,431 (361,187,777 bp)
Number of reads that entered assembly after filtering (removing the adapters and > Q20)	415,742 (210,423,467 bp)
Assembly program used	Trinity (2013-02-25)
Total number of contigs	37,181
Average contig length (range)	614 bp (201 – 5,044 bp)
N50 length	743 bp

Assembly program used	Newbler (ver. 2.5)
Total number of contigs	45,994
Average contig length (range)	535 bp (51 – 4,098)
N50 length	595 bp
Assembly program used	Velvet/Oasis (ver. 1.2.03)
Total number of contigs	165,361
Average contig length (range)	322 bp (100 – 5,807 bp)
N50 length	481 bp
Assembly program used	Mira (ver. 3.4.0)
Total number of contigs	57,923
Average contig length (range)	762 bp (100 – 3,032 bp)
N50 length	853 bp
Neonates RNA (Illumina Hi-seq, paired-end)	
Total number of paired-end reads before filtering (length)	1,347,291,731 (136,076,464,831 bp)
Number of paired-end reads that entered assembly after > Q30 filtering (length)	721,697,288 (72,891,426,088 bp)
Assembly program used	Trinity
Total number of contigs	155,787
Average contig length (range)	937 bp (201 – 25,737 bp)
N50 length	1,817 bp