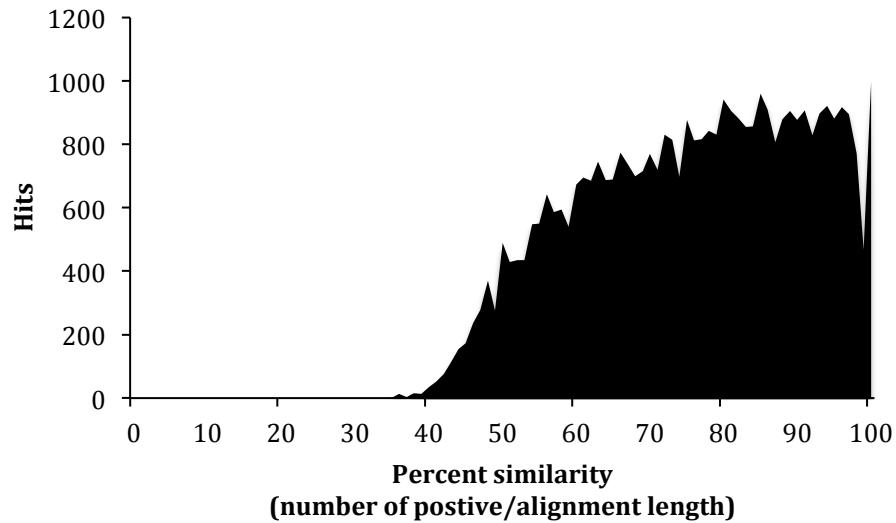
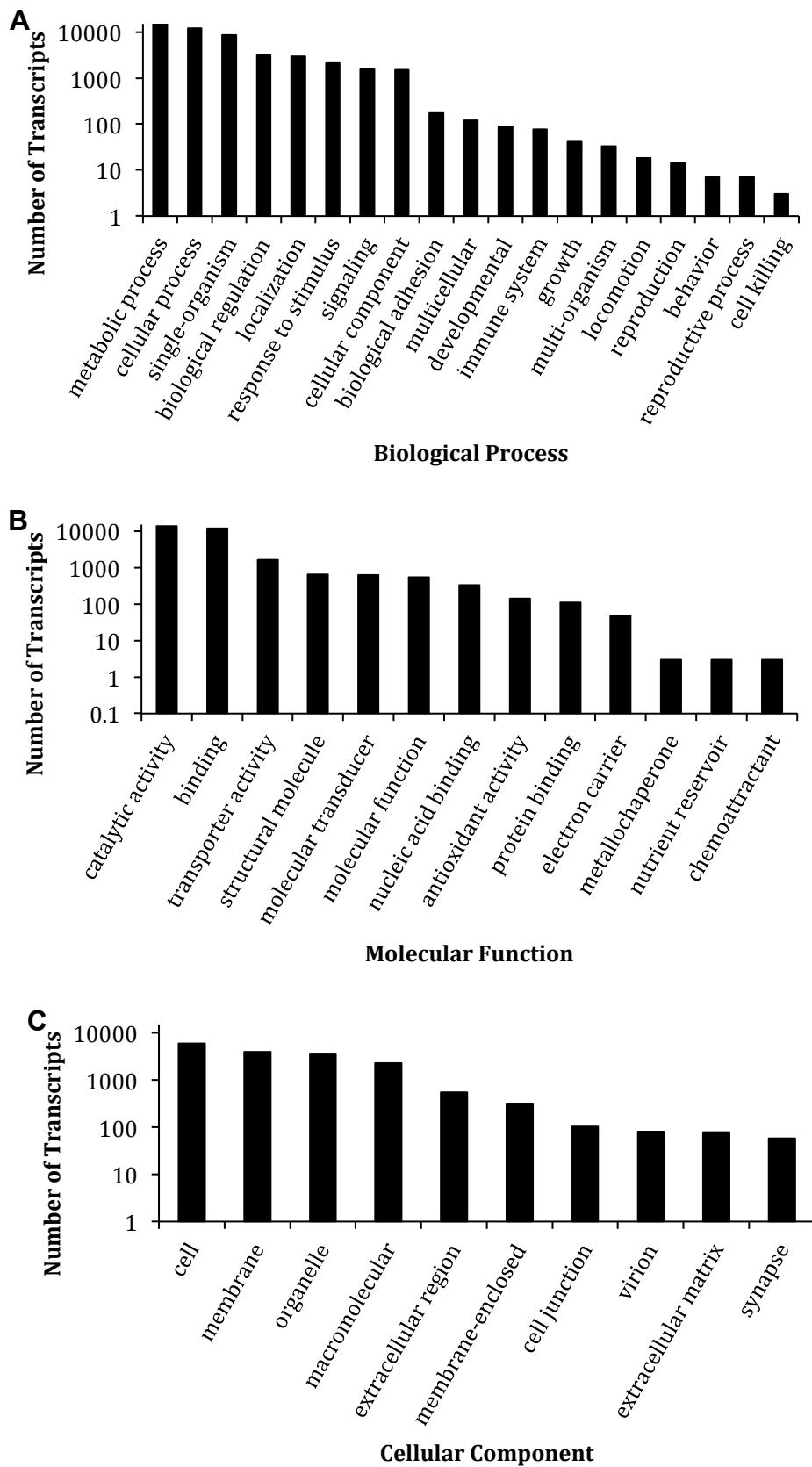


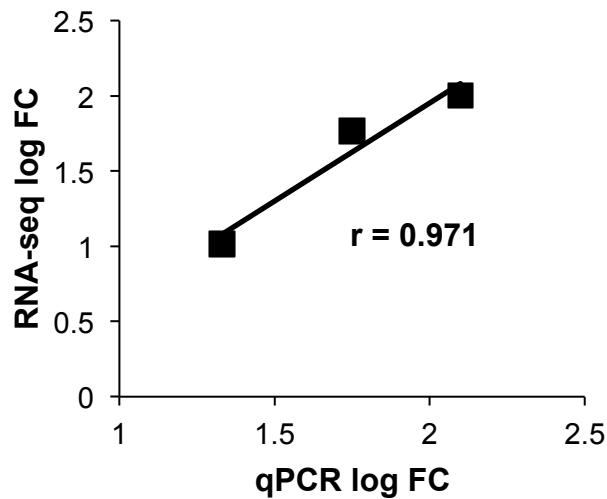
Supplementary Figure 1. Lengths of contiguous nucleotide sequences (contigs) from *de novo* assembly of transcriptome from *D. variabilis*. Assembly of RNA-seq data was performed with Trinity with a minimum contig length of 150 followed by open reading frame determination with TransDecoder with a minimum amino acid length of 100.



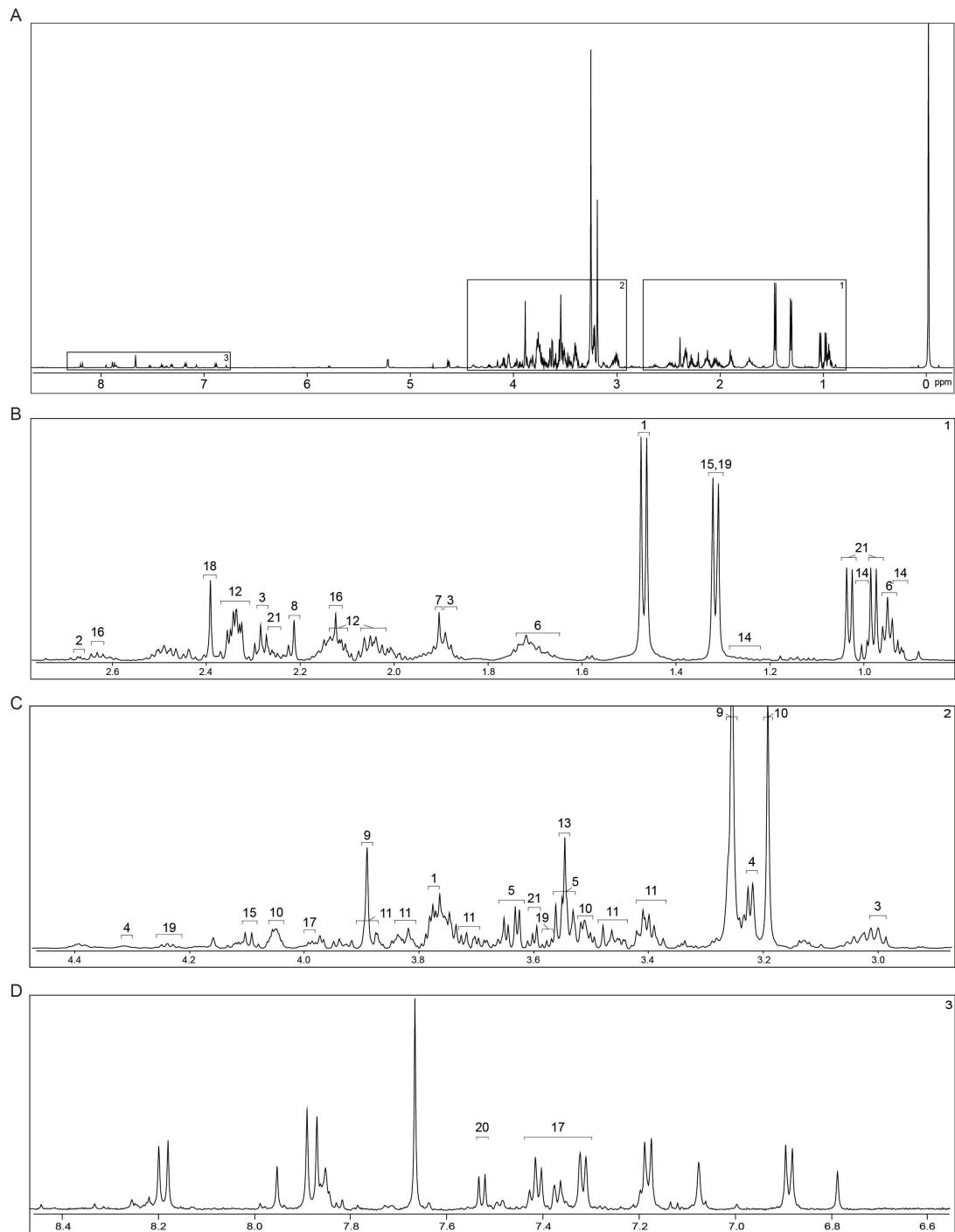
Supplementary Figure 2. Summary of the percent sequence similarity of the contigs of the transcriptome of *D. variabilis* with NCBI's arthropod nr protein database.



Supplementary Figure 3.  
Distribution of gene ontology (GO) terms assigned to the transcriptome of *D. variabilis*. Mapping, annotation, and InterPro Scan tools in the Blast2GO software were used to annotate the contigs with BLAST hits. Sequences were categorized into (A) biological process, (B) molecular function, and (C) cellular component using GO level 2 terms.



Supplementary Figure 4. Results of qPCR validation experiment. Log fold changes obtained by RNA-seq and qPCR for each gene plotted with the best-fit regression line. For qPCR, fold changes were determined using the  $\Delta\Delta C_q$  method with  $\beta$ -actin as a reference gene. Pearson correlation coefficient ( $r$ ) is shown.



Supplementary Figure 5. (A) Representative  $^1\text{H}$  NMR spectrum of tick homogenates. (B-D) Magnification of spectral regions with metabolites identified. 1-Alanine, 2-Aspartate, 3-GABA, 4-Glycerophosphocholine, 5-Glycerol, 6-Leucine, 7-Acetate, 8-Acetone, 9-Betaine, 10-Choline, 11-Glucose, 12-Glutamate, 13-Glycine, 14-Isoleucine, 15-Lactate, 16-Methionine, 17-Phenylalanine, 18-Succinate, 19-Threonine, 20-Uracil, 21-Valine.

Table S1. Primers used for qPCR gene expression analysis

Gene	Sequence
<i>Superoxide dismutase</i>	Forward 5- CCTCACACAGGAACCATAAA -3 Reverse 5- TTCAGTCCGGTCACGTTTC-3
<i>β-actin</i>	Forward 5-TCC ACG AGA CCA CCT ACA A -3 Reverse 5-TGC ATA CGGTG GCA ATA C -3
<i>Glutathione-S-transferase</i>	Forward 5- GAGAAGTACGCACCGGAATC-3 Reverse 5- CCTGACCCTTGAACCACTTT-3
<i>Cysteine dioxygenase 1</i>	Forward 5- GAGTGACTGACCGGAAACAG-3 Reverse 5- AGCGATATTGTCACCACCTTC-3

Table S2.

[Click here to Download Table S2](#)

Table S3: DAVID analysis of differentially expressed genes in control vs dehydrated *Dermacentor variabilis*

Category	Term	Count	P-value	Fold Enrichment
<b>Upregulated</b>				
<i>I. scapularis</i>				
BP	sulfur amino acid metabolic process	3	0.0222	12.61
MF	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	5	0.0029	8.19
MF	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	6	0.0092	4.60
MF	protein dimerization activity	4	0.0220	6.55
MF	gamma-butyrobetaine dioxygenase activity	2	0.0324	60.62
INTERPRO	Basic-leucine zipper (bZIP) transcription factor	3	0.0198	13.54
INTERPRO	Taurine catabolism dioxygenase TauD/TfdA	2	0.0312	63.18
<i>D. melanogaster</i>				
BP	sulfur amino acid metabolic process	4	0.0008	20.80
BP	oxidation reduction	18	0.0040	2.11
BP	cellular amino acid biosynthetic process	4	0.0069	10.04
BP	organic acid biosynthetic process	5	0.0110	5.69
BP	carboxylic acid biosynthetic process	5	0.0110	5.69
BP	sulfur metabolic process	4	0.0136	7.87
BP	chromatin modification	6	0.0181	3.90
BP	regulation of RNA metabolic process	17	0.0205	1.83
BP	transcription	13	0.0217	2.06
BP	regulation of protein modification process	4	0.0217	6.62
BP	organic acid catabolic process	4	0.0230	6.47
BP	carboxylic acid catabolic process	4	0.0230	6.47
BP	amine biosynthetic process	4	0.0258	6.20
BP	instar larval or pupal development	12	0.0264	2.09
BP	negative regulation of cell cycle process	3	0.0297	10.92
BP	R7 cell fate commitment	3	0.0297	10.92
BP	regulation of cellular protein metabolic process	6	0.0319	3.36
BP	histone methylation	3	0.0326	10.40

BP	post-embryonic development	12	0.0335	2.01
BP	histone modification	4	0.0386	5.30
BP	covalent chromatin modification	4	0.0386	5.30
BP	olfactory behavior	5	0.0402	3.83
BP	regulation of histone methylation	2	0.0403	48.54
BP	epithelium development	8	0.0408	2.48
BP	regulation of transcription	18	0.0412	1.64
BP	negative regulation of cell cycle	3	0.0417	9.10
BP	establishment or maintenance of apical/basal cell polarity	3	0.0482	8.40
MF	sequence-specific DNA binding	9	0.0254	2.52
MF	rDNA binding	2	0.0306	64.37
MF	transition metal ion binding	30	0.0360	1.43
INTERPRO	Zinc finger, RING-type, conserved site	5	0.0203	4.77
INTERPRO	Basic-leucine zipper (bZIP) transcription factor	3	0.0466	8.58
<b>Downregulated</b>				
<i>D. melanogaster</i>				
MF	endopeptidase inhibitor activity	3	0.0187	13.50
MF	peptidase inhibitor activity	3	0.0200	13.01
MF	enzyme inhibitor activity	3	0.0327	10.00

Gene ontology terms BP - biological process and MF - molecular function (Ashburner et al., 2000). INTERPRO - InterPro protein domains (McDowall and Hunter, 2011).

Table S4. CLC Genomics Workbench Gene Set Enrichment Analysis of all annotated genes in control and dehydrated ticks.

Description	Count	p value
<b>Over-represented in control</b>		
<b>Biological process</b>		
nucleic acid phosphodiester bond hydrolysis	279	<0.001
peptidoglycan catabolic process	23	<0.001
RNA phosphodiester bond hydrolysis, endonucleolytic	227	<0.001
DNA integration	282	<0.001
sodium ion transport	16	<0.001
conversion of methionyl-tRNA to N-formyl-methionyl-tRNA	10	<0.001
negative regulation of endopeptidase activity	214	<0.001
DNA replication	94	<0.001
DNA ligation	16	<0.001
RNA-dependent DNA replication	535	<0.001
phosphatidylcholine metabolic process	11	0.001
DNA recombination	22	0.001
DNA repair	186	0.002
mannose metabolic process	42	0.004
innate immune response	60	0.004
vesicle-mediated transport	205	0.004
ganglioside catabolic process	14	0.005
transposition, DNA-mediated	17	0.007
oxidation-reduction process	2229	0.008
DNA replication initiation	25	0.008
chromatin modification	16	0.01
<b>Molecular function</b>		
serine-type endopeptidase inhibitor activity	136	<0.001
ribonuclease H activity	184	<0.001
endonuclease activity	195	<0.001
methionyl-tRNA formyltransferase activity	10	<0.001
metalloendopeptidase activity	436	<0.001
DNA ligase (NAD <sup>+</sup> ) activity	16	<0.001
RNA-directed DNA polymerase activity	535	<0.001
beta-N-acetylhexosaminidase activity	24	<0.001
alcohol sulfotransferase activity	110	<0.001
nucleic acid binding	2401	<0.001
DNA clamp loader activity	16	<0.001
carbohydrate binding	139	<0.001
N-acetylmuramoyl-L-alanine amidase activity	23	<0.001
retinal dehydrogenase activity	27	<0.001
serine-type exopeptidase activity	13	0.002
zinc ion binding	2060	0.002
protein tyrosine/serine/threonine phosphatase activity	39	0.003

DNA-directed DNA polymerase activity	67	0.004
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	71	0.004
transposase activity	17	0.004
monooxygenase activity	61	0.006
methanol dehydrogenase activity	11	0.008
NADH dehydrogenase activity	17	0.008
alpha-mannosidase activity	40	0.008
thiamine pyrophosphate binding	13	0.009
lysophospholipase activity	20	0.009
<b>Over-represented in dehydrated</b>		
<b>Biological process</b>		
signal transduction	334	<0.001
ion transport	40	<0.001
regulation of transcription, DNA-dependent	604	<0.001
neurotransmitter transport	81	<0.001
cell adhesion	103	0.001
biosynthetic process	111	0.001
histone lysine methylation	101	0.001
purine ribonucleoside monophosphate biosynthetic process	15	0.001
small GTPase mediated signal transduction	203	0.002
lipid transport	236	0.003
long-chain fatty acid metabolic process	23	0.003
sensory perception of sound	12	0.003
DNA-dependent transcription, initiation	24	0.004
multicellular organismal development	21	0.005
regulation of translational initiation	43	0.005
dephosphorylation	278	0.005
Wnt receptor signaling pathway	21	0.005
formation of translation preinitiation complex	48	0.005
activation of MAPKK activity	55	0.006
regulation of cell growth	17	0.006
actin filament organization	34	0.008
proteolysis involved in cellular protein catabolic process	15	0.009
termination of G-protein coupled receptor signaling pathway	33	0.009
gamma-aminobutyric acid metabolic process	10	0.009
ubiquitin-dependent protein catabolic process	186	0.01
mitosis	38	0.01
<b>Molecular function</b>		
poly(A)-specific ribonuclease activity	29	<0.001
glutathione transferase activity	50	<0.001
cytoskeletal protein binding	27	<0.001
N-acetylgalactosamine-4-sulfatase activity	36	<0.001
kinase activity	306	<0.001
translation initiation factor activity	257	<0.001

myosin heavy chain kinase activity	111	<0.001
sequence-specific DNA binding	167	<0.001
neurotransmitter:sodium symporter activity	79	<0.001
actin filament binding	83	<0.001
retinol dehydrogenase activity	10	0.001
phosphoprotein phosphatase activity	161	0.001
long-chain fatty acid-CoA ligase activity	23	0.001
sphingomyelin phosphodiesterase activity	68	0.001
histone-lysine N-methyltransferase activity	115	0.002
hydrolase activity	572	0.002
fatty acid synthase activity	12	0.003
transferase activity, transferring acyl groups	65	0.003
magnesium ion binding	122	0.003
[acyl-carrier-protein] S-acetyltransferase activity	31	0.004
3-oxoacyl-[acyl-carrier-protein] synthase activity	31	0.004
3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity	31	0.004
enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity	31	0.004
oleoyl-[acyl-carrier-protein] hydrolase activity	31	0.004
N,N-dimethylaniline monooxygenase activity	13	0.004
chloride channel activity	15	0.004
myristoyl-[acyl-carrier-protein] hydrolase activity	31	0.004
palmitoyl-[acyl-carrier-protein] hydrolase activity	31	0.004
threonine-type endopeptidase activity	32	0.004
inositol-1,4,5-trisphosphate 3-kinase activity	12	0.005
lipid transporter activity	208	0.005
MAP kinase kinase kinase activity	55	0.005
glucose-6-phosphatase activity	14	0.006
peroxidase activity	57	0.006
insulin-like growth factor binding	17	0.006
[acyl-carrier-protein] S-malonyltransferase activity	32	0.008
dipeptidase activity	10	0.008
carnitine O-palmitoyltransferase activity	10	0.008
GTP binding	440	0.008
gamma-glutamyltransferase activity	24	0.009
manganese ion binding	19	0.01

Table S5. Mean Survival times ( $\pm$  SEM, days) of ticks injected with insect Ringer's (control), glycerol, or GABA solutions at several relative humidities.

	Ringer's	Glycerol	GABA	P
0%	6.4 $\pm$ 0.9	6.4 $\pm$ 0.7	n.d.	0.999
70%	6.8 $\pm$ 1.1	6.0 $\pm$ 0.4	n.d.	0.524
75%	8.6 $\pm$ 0.2	6.2 $\pm$ 1.4	8.8 $\pm$ 0.2	0.092

n.d. not determined