Supplementary Materials: Transcriptome and Difference Analysis of Fenpropathrin Resistant Predatory Mite, *Neoseiulus barkeri* (Hughes)

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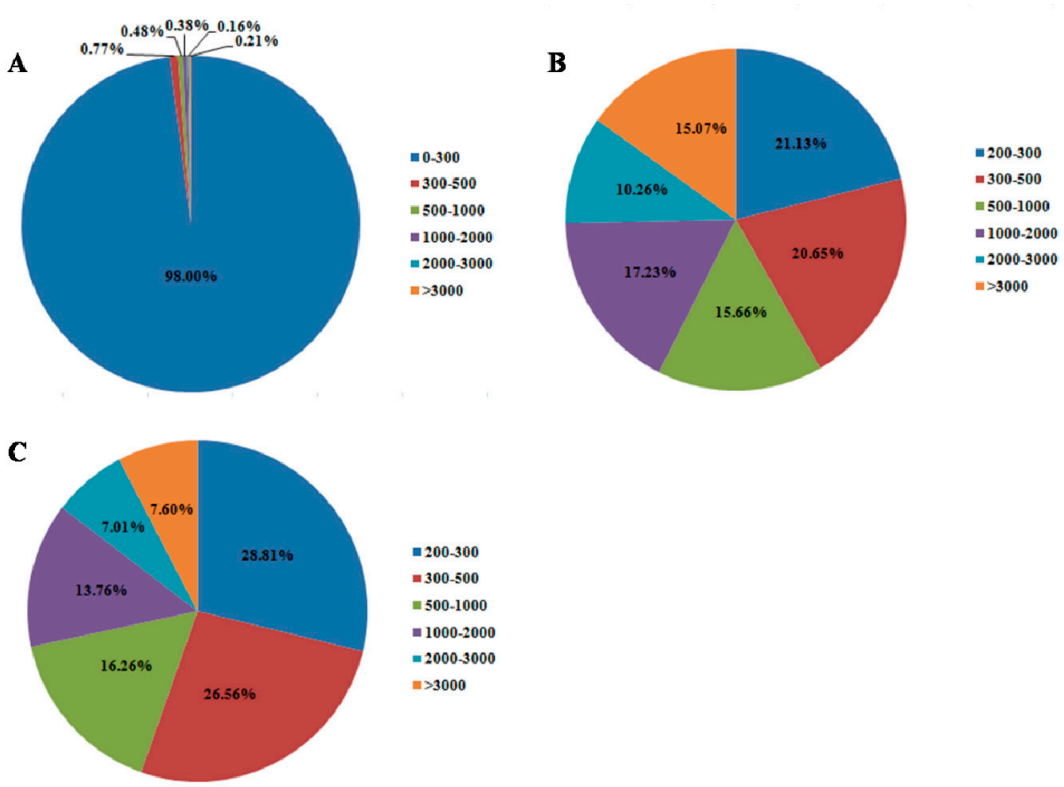

Figure S1. Length distributions of *N. barkeri* transcriptome data. (**A**) Length distribution of contig sequences; (**B**) length distribution of transcript sequences; (**C**) length distribution of unigene sequences.

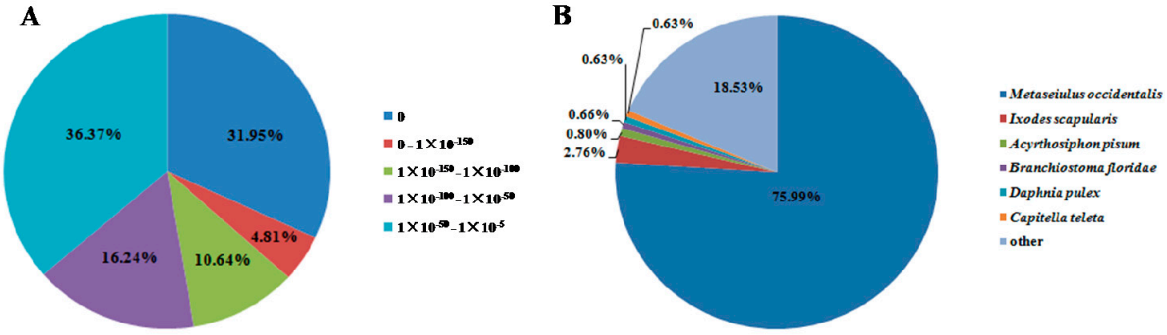

Figure S2. *E*-values and distributions of the *N. barkeri* unigenes. (**A**) E-value distribution of BLASTX hits in the non-redundant (nr) database for unigenes (cut-off $E < 10^{-5}$); (**B**) species distribution.

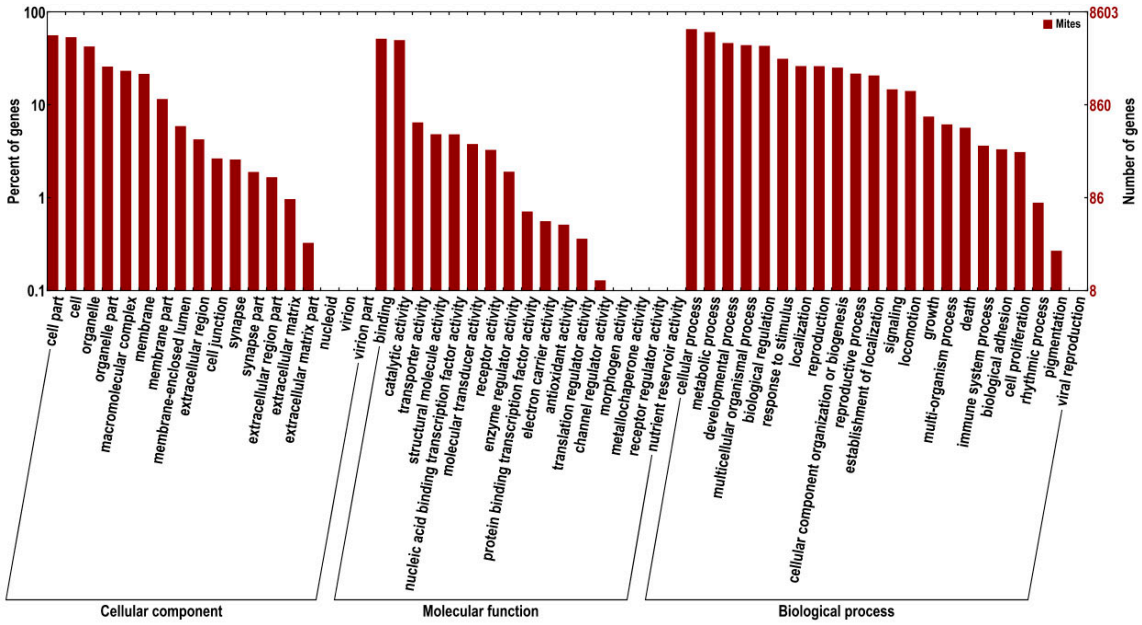

Figure S3. Gene Ontology (GO) analysis of the *N. barkeri* transcriptome.

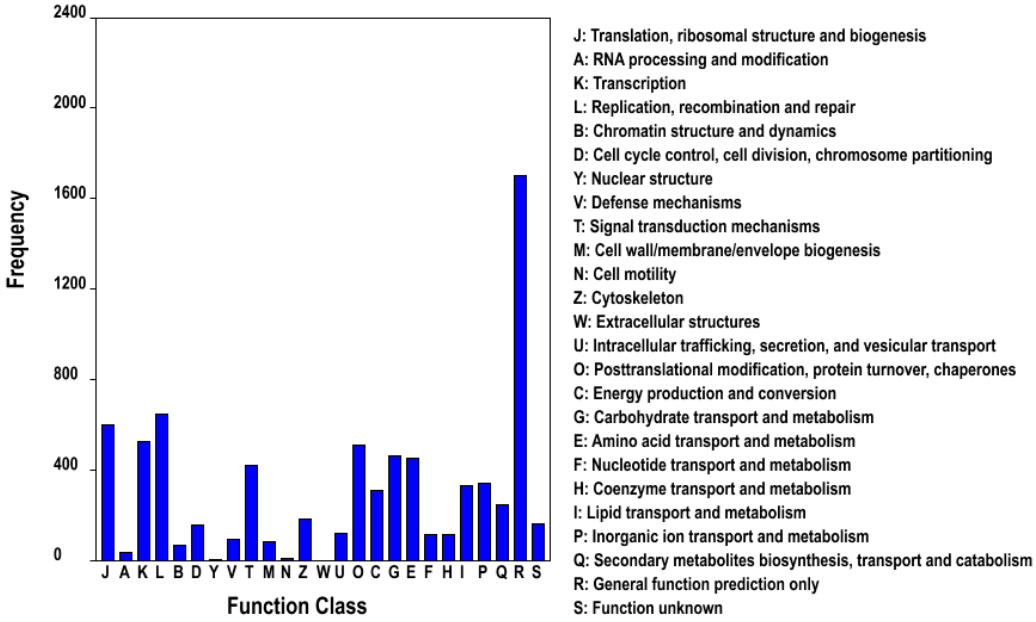

Figure S4. Classification of the Cluster of Orthologous Groups (COG) analysis of the *N. barkeri* transcriptome.

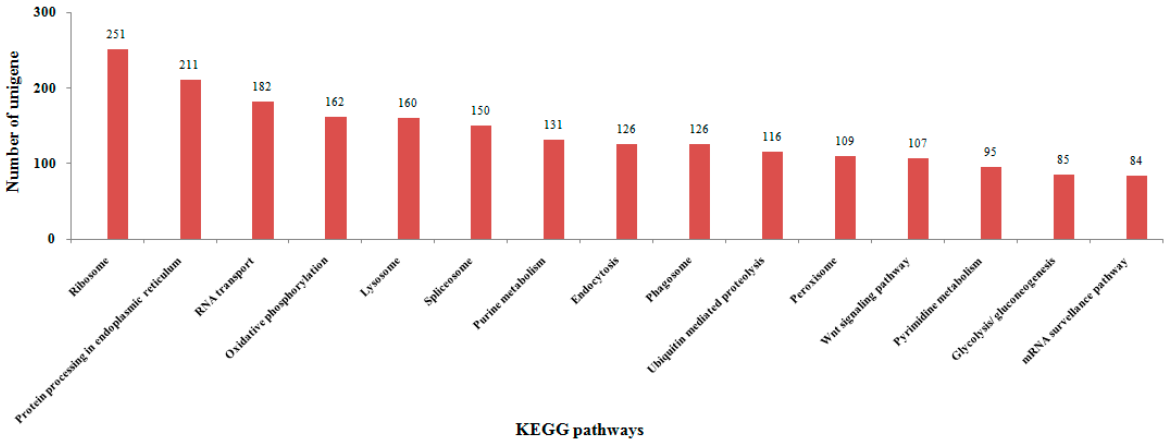

Figure S5. Kyoto Encyclopedia of Genes and Genomes (KEGG) annotation of the *N. barkeri* transcriptome. The top 15 pathways are shown.

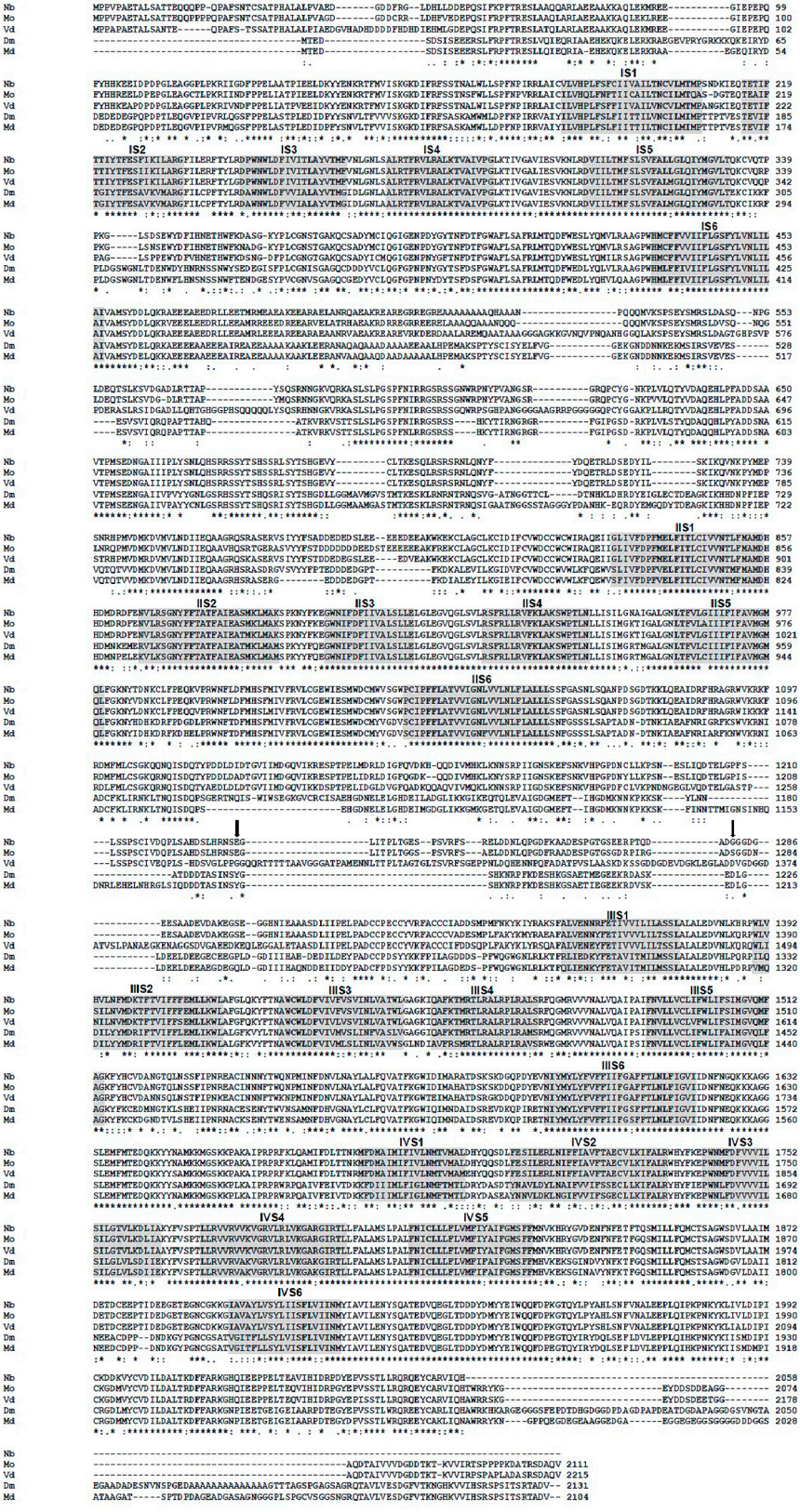

Figure S6. Alignment of deduced amino acid sequences of the sodium channels from *Neoseiulus barkeri* and other species using ClustalW2. Missing amino acids are indicated with dashed line. Asterisks, colons, and periods represent fully, strongly, and weakly conserved residues, respectively. The transmembrane regions (S1–S6) in the hydrophobic domains (I–IV) are shadowed. The locations of the mutations are indicated with "↓". Nb: *N. barkeri*; Mo: *M. occidentalis*; Vd: *V. destructor*; Dm: *D. melanogaster*; Md: *M. domestica*.

Table S1. Primers used to isolate the full-length *N. barkeri* sodium channel (*NbSc*) cDNA sequence and verify the *N. barkeri* mutations.

Primers	Primer Sequences (5′-3′)	Length of Fragments (bp)
NbSc-A-F	GCCGAGACTGCTTTGTCAGC	823
NbSc-A-R	GAAGCACACGGAATGTTCTA	
NbSc-B-F	TAGAACATTCCGTGTGCTTC	1180
NbSc-B-R	GTAAAGAGGAATAATGATGG	
NbSc-C-F	CCATCATTATTCCTCTTTAC	759
NbSc-C-R	GTAACGACAGTGCAACAATG	
NbSc-D-F	CATTGTTGCACTGTCGTTAC	808
NbSc-D-R	GCCAATGATAGGTCGGGAAT	
NbSc-E-F	ATTCCCGACCTATCATTGGC	930
NbSc-E-R	CGACCCTCATGCCTTGGAAG	
NbSc-F-F	CTTCCAAGGCATGAGGGTCG	546
NbSc-F-R	GATCCCATTTTCTTCATTGC	
NbSc-G-F	GCAATGAAGAAAATGGGATC	902
NbSc-G-R	CAGATCTCGTAGTACATATC	
NbSc-H-F	CTGGAACATGTTCGACTTCG	953
NbSc-H-R	TGTGCTGGATAACTCGGGCG	
NbSc-M-F	CCCAACACCCGAACTCAT	-
NbSc-M-R	AGCCGTCCAACGAAAGCC	

F: forward primer; R: reverse primer.

Table S2. Primers for *N. barkeri* P450s, GSTs and reference genes by *q*PCR.

Primers	Primer Sequences (5′-3′)
NbCYP4EZ1-Q-F	ACTACTCACCGATGGATATGCTT
NbCYP4EZ1-Q-R	TTCGCCACATTGACGTTGTCC
NbCYP4EV2-Q-F	ATTCTATCGGACACAACGAAC
NbCYP4EV2-Q-R	CCAGTCAAGAGACCGTTGCC
NbCYP3107E3-Q-F	CATAAAATATTGCCCCTTCGT
NbCYP3107E3-Q-R	AAGTTCTTTCGCTTCTCGTCT
NbCYP3110C1-Q-F	GATGTCATAGCGAACTCGAT
NbCYP3110C1-Q-R	TCAACTATTTCCTGCCGAAG
NbCYP3110B2-Q-F	ATGAACCTAAAATACTTGGACCG
NbCYP3110B2-Q-R	TCTCCTCGTTGTGAATCCTGT
NbCYP3011C2-Q-F	ATTCCAAAAGGCCAGGTTTGC
NbCYP3011C2-Q-R	CCATGCCATGATGTCAATGTTCG
NbCYP3011B8-Q-F	GGTGATATTCTCAAGACCGTTC
NbCYP3011B8-Q-R	TCACCTCTTTCCATCGCTTC
NbCYP3011B7-Q-F	ATCTCGTTTCCCGTATTGTGG
NbCYP3011B7-Q-R	ACAGGATTTGTTCCGTCGTTC
NbCYP3011B10-Q-F	AGATTTTCACAACTTTGCCGAT
NbCYP3011B10-Q-R	CAGCCTCTTTGATGTGAACGA
NbCYP3011B9-Q-F	GCGCTTCCTAATACAACGAT
NbCYP3011B9-Q-R	GGATCAATGACAGCCCGAAC
NbCYP3103A2-Q-F	TTCGATAACCCGTATGAGTTCCG
NbCYP3103A2-Q-R	TTGCCAATTGAGAAGGACCAC
NbCYP3103A3-Q-F	CTATACTTCGCAACGCTCCT

Table S2. *Cont.*

Primers	Primer Sequences (5′-3′)
NbCYP3103A3-Q-R	AGTTTCTGCGATAAGACTCC
NbGSTd01-Q-F	CTGTTTGAAAGCCGAGCCAT
NbGSTd01-Q-R	TCCACCTTTGCCCGAGCTTG
NbGSTd02-Q-F	AATCGAGAGCCATCATGTGC
NbGSTd02-Q-R	GCTCACAAGTAACGCGAACC
NbGSTd03-Q-F	AAAGTATTCCGCAAACGACT
NbGSTd03-Q-R	CCGTTGTATCCGAAATGTCC
NbGSTm03-Q-F	ATTGAGCTCGGCATAGCACT
NbGSTm03-Q-R	GACCGCTCCGTCTCTCGAAC
NbGSTo01-Q-F	CATCCGCCTTTATTGTCACC
NbGSTo01-Q-R	CCGGTTTATCTTTGACGTTG
NbGSTk02-Q-F	CCCTGAACACGTCGAAGCAA
NbGSTk02-Q-R	AGCAACTTCGGGTATGCATT
NbBactin-Q-F	TACGACCAGAAGCGTACAGC
NbBactin-Q-R	CCAACCGTGAAAAGATGACC

F: forward primer; R: reverse primer.