



Title	Transcriptome dynamics of blood-fed and starved poultry red mites, <i>Dermanyssus gallinae</i>
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Supplemental table 1. Numbers of reads obtained in each process

	Blood-fed	Starved
Raw data	168,996,962	165,252,914
Trimmed data	167,594,546	163,337,310
Trimmed data (host-removed)	167,508,352	-
No. of mapped reads (%)	154,386,218 (92.12)	143,329,002 (87.75)
No. of unmapped reads (%)	13,208,328 (7.88)	20,008,308 (12.25)

Supplemental table 2. Summary of the *de novo* assembly

No. of contigs	Total length (bp)	Average contig length (bp)	Largest contig length (bp)	N50 contig length (bp) ^a
162,263	164,301,068	1,013	17,417	1,888

^aThe minimum contig required to cover 50 % of the genomes.

Supplemental table 3. Summary of the expression analysis and functional annotation

Gene expression metrics	No. of contigs ($\log_2\text{CPM} \geq 0$)	40,642
	Genes expressed in blood-fed PRMs ($\log_2\text{CPM} \geq 0$, $\text{FPKM} > 0$)	37,900
	Genes expressed in starved PRMs ($\log_2\text{CPM} \geq 0$, $\text{FPKM} > 0$)	39,374
	Genes expressed both in blood-fed and starved PRMs ($\log_2\text{CPM} \geq 0$, both $\text{FPKM} > 0$)	36,632
Functional annotation metrics	Total No. of annotated contigs	36,785
	No. of annotated contigs ($\log_2\text{CPM} \geq 0$)	19,666
	No. of annotated contigs ($\log_2\text{CPM} \geq 0$, excluded virus-derived and ribosomal RNA genes)	19,114

Supplemental table 4. Motifs/domains predicted by the IPR IDs in the top 15 contigs that indicated high expression intensities and were associated with “Metabolic pathways” in table 7

Blood-fed mites				Starved mites				
IPR ID	Contig No.	FPKM (blood-fed)	Predicted motifs/domains	IPR ID	Contig No.	FPKM (starved)	Predicted motifs/domains	
1	IPR001564	TRINITY_DN450 47_c0_g1_i1	1591.02	Nucleoside diphosphate kinase	IPR008209	TRINITY_DN418 63_c2_g3_i3	558.95	Phosphoenolpyruvate carboxykinase, GTP-utilizing
2	IPR019344	TRINITY_DN414 65_c1_g1_i2	1121.97	Mitochondrial F1-F0 ATP synthase subunit F, predicted	IPR004046	TRINITY_DN392 00_c7_g1_i1	522.48	Glutathione S-transferase, C-terminal
3	IPR006808	TRINITY_DN420 35_c4_g2_i2	1051.95	ATP synthase, F0 complex, subunit G, mitochondrial	IPR006089	TRINITY_DN398 74_c1_g1_i1	280.24	Acyl-CoA dehydrogenase, conserved site
4	IPR024571	TRINITY_DN393 70_c0_g2_i4	719.13	ERAP1-like C-terminal domain	IPR000644	TRINITY_DN449 67_c0_g1_i3	251.53	CBS domain
5	IPR000194	TRINITY_DN394 38_c0_g1_i3	574.94	ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain	IPR024571	TRINITY_DN450 85_c3_g2_i1	223.29	ERAP1-like C-terminal domain
6	IPR008386	TRINITY_DN392 77_c7_g1_i4	560.47	ATP synthase, F0 complex, subunit E, mitochondrial	IPR002347	TRINITY_DN408 96_c4_g2_i1	182.58	Short-chain dehydrogenase/reductase SDR
7	IPR008387	TRINITY_DN430 86_c0_g2_i1	559.59	ATP synthase-coupling factor 6, mitochondrial	IPR000183	TRINITY_DN414 49_c4_g6_i2	145.65	Ornithine/DAP/Arg decarboxylase
8	IPR008181	TRINITY_DN427 66_c2_g2_i2	559.27	Deoxyuridine triphosphate nucleotidohydrolase	IPR004839	TRINITY_DN435 75_c2_g1_i2	137.06	Aminotransferase, class I/classII
9	IPR006721	TRINITY_DN450 25_c2_g3_i2	492.98	ATP synthase, F1 complex, epsilon subunit, mitochondrial	IPR000836	TRINITY_DN437 10_c2_g1_i6	113.69	Phosphoribosyltransferase domain
10	IPR004205	TRINITY_DN400 18_c2_g1_i1	427.30	Cytochrome b-c1 complex subunit 8	IPR033469	TRINITY_DN400 23_c4_g1_i1	107.19	CYTH-like domain superfamily
11	IPR000793	TRINITY_DN393 58_c10_g1_i6	324.92	ATP synthase, alpha subunit, C-terminal	IPR001805	TRINITY_DN398 18_c6_g1_i1	101.38	Adenosine kinase
12	IPR002347	TRINITY_DN395 65_c7_g1_i1	305.25	Short-chain dehydrogenase/reductase SDR	IPR003033	TRINITY_DN413 61_c4_g2_i11	98.18	SCP2 sterol-binding domain
13	IPR006424	TRINITY_DN421 58_c2_g1_i1	295.71	Glyceraldehyde-3-phosphate dehydrogenase, type I	IPR000573	TRINITY_DN372 12_c0_g1_i2	95.52	Aconitase A/isopropylmalate dehydratase small subunit, swivel domain
14	IPR029055	TRINITY_DN366 14_c0_g1_i2	258.72	Nucleophile aminohydrolases, N-terminal	IPR001085	TRINITY_DN404 54_c0_g1_i7	90.85	Serine hydroxymethyltransferase
15	IPR000711	TRINITY_DN447 10_c4_g1_i4	255.54	ATPase, OSCP/delta subunit	IPR015590	TRINITY_DN442 20_c3_g1_i1	90.71	Aldehyde dehydrogenase domain