

**Appendix A. Supplemental Tables:**  
**Sequence reads and expression.**

**Supplemental Table A1: Summary of the library preparation, sequencing and quality filtering of the sequence data of *R. appendiculatus*.**

Dataset	Library preparation (concentration of starting total RNA)	Library preparation (RNA fragmentation time)	Library preparation (number of amplification cycles)	Library preparation (size selection by excision from agarose gel)	Illumina instrument used for sequencing	Sequence read length	Number of raw sequence reads (read 1/ read 2)	Size of raw sequence reads (bp)	Number of quality filtered sequence reads (read 1/ read 2)	Average size of quality filtered sequence reads (bp)	Percentage of reads discarded (read 1/ read 2)
<b>HiSeq 2000 generated sequence reads</b>											
HiSeq	4 ug	8 min	15	±300 bp	HiSeq 2000	100 x 100	413 323 262/ 413 323 262	100	366 810 605/ 338 340 792	20-100	11.3/ 18.1
<b>MiSeq generated sequence reads</b>											
MiSeq SE*	4 ug	8 min	15	±300 bp	MiSeq	240 (SE)	3 855 867	240	2 961 283	20-240	23.2
MiSeq PE*	3.1 ug	3 min	12	±600 - 1200 bp	MiSeq	250 x 250	13 216 382/ 13 216 382	250	8 781 175/ 6 297 010	20-250	33.6/ 52.4
<b>Total MiSeq data</b>											
<b>Total generated sequence reads</b>											
Total sequence data (HiSeq and MiSeq)							430 395 511/ 426 539 644	100-250	379 375 881/ 343 814 984	20-250	11.9/19.4

\* SE = single end sequencing; PE = paired end sequencing

**Supplemental Table A2: Top expressing transcripts in the *R. appendiculatus* transcriptome.**

Expression rank *	Transcript ID	ORF ID	Annotation	TPM value	Percentage of transcriptome
1	c33374_g1_i1	Rapp_Mc2208	Glycine rich superfamily: RIM36	43 988	4.40
2	c53945_g1_i1	No ORF predicted	16S ribosomal RNA	40 496	4.05
3	c43993_g1_i2	Rapp_Mc13679	Glycine rich superfamily	33 290	3.33
4	c15622_g1_i1	Rapp_Mc13680	Unknown function	28 031	2.81
5	c22478_g1_i1	Rapp_Mc950	Glycine rich superfamily	25 459	2.55
6	c53938_g1_i1	Rapp_Mc8886	Lipocalin family: Male-specific histamine-binding salivary protein	21 780	2.18
7	c46457_g2_i1	Rapp_Mc13681	Glycine rich superfamily	20 255	2.03
8	c37026_g1_i1	Rapp_Mc13629	Glycine rich superfamily	16 012	1.60
9	c43993_g1_i1	Rapp_Mc13812	Glycine rich superfamily	15 173	1.52
10	c41649_g1_i1	Rapp_Mc12875	Unknown function	13 758	1.38
11	c41162_g1_i1	Rapp_Mc4548	Lipocalin family: Female-specific histamine-binding protein 1	13 316	1.33
12	c41649_g1_i2	Rapp_Mc12173	Unknown function	13 177	1.32
13	c43993_g1_i3	Rapp_Mc10553	Glycine rich superfamily	13 151	1.32
14	c48158_g1_i1	Rapp_Mc8700	No hit	12 495	1.25
15	c36384_g1_i1	Rapp_Mc13682	Glycine rich superfamily	12 489	1.25
16	c17798_g1_i1	Rapp_Mc774	ML domain: Immunoglobulin G binding protein C	11 353	1.14
17	c39014_g2_i1	Rapp_Mc9768	Glycine rich superfamily	10 864	1.09
18	c36396_g1_i1	Rapp_Mc9443	No hit	9 103	0.91
19	c50957_g1_i1	Rapp_Mc13626	Unknown function	8 589	0.86
20	c1612_g1_i1	Rapp_Mc13700	Energy metabolism: Cytochrome c oxidase subunit 1	8 340	0.83

\* Transcripts ranked based on TPM (transcripts per million) value

**Supplemental Table A3: Characterisation of the tick secretory protein family expression in the *R. appendiculatus* transcriptome.**

Secretory protein family	Number of family members	Proportion of the total number of secretory proteins represented by this family (%)	Protein family average TPM value	Proportion of the secretory protein class expression represented by this family (%)	ORF ID of the top expressing member in the family	TPM value of the top expressing member in the family	Proportion of the protein family represented by the top expressing member (%)
Lipocalin	516	24.18	133.12	12.47	Rapp_Mc8886	21 779.87	31.71
Bovine pancreatic trypsin inhibitor	236	11.06	58.43	2.50	Rapp_Mc8896	2447.72	17.75
Reprolysin	133	6.23	34.93	0.84	Rapp_Mc5881	628.36	13.52
Glycine rich superfamily	119	5.58	3072.04	66.34	Rapp_Mc2208	43 988.23	11.55
TIL domain	108	5.06	164.00	3.21	Rapp_Mc1646	2898.99	16.37
8.9 kDa family	102	4.78	84.00	1.55	Rapp_Mc13118	1185.58	13.84
Basic tail secreted protein	90	4.22	75.77	1.24	Rapp_Mc4488	879.84	12.90
Evasin	68	3.19	55.54	0.69	Rapp_Mc9039	619.77	16.41
Ixodegrin B	57	2.67	30.13	0.31	Rapp_Mc823	450.18	26.21
Gluzincin	52	2.44	7.63	0.07	Rapp_Mc4972	115.13	29.02
Mucin	52	2.44	44.87	0.42	Rapp_Mc417	876.51	37.57
Digestive system (including Serine proteases)	50	2.34	25.01	0.23	Rapp_Mc1191	137.69	11.01
Cystatin	47	2.20	54.35	0.46	Rapp_Mc13730	776.50	30.40
Folding, sorting and degradation (including Cathepsins)	40	1.87	96.78	0.70	Rapp_Mc945	1498.52	38.71
28 kDa Metastriate family	31	1.45	50.68	0.29	Rapp_Mc2646	557.06	35.46
Chitin-binding proteins	30	1.41	23.00	0.13	Rapp_Mc9698	223.55	32.39
Serpin	27	1.27	8.98	0.04	Rapp_Mc5185	74.71	30.81

DA-P36 family	25	1.17	23.86	0.11	Rapp_Mc8808	340.81	57.13
Transport and catabolism	25	1.17	36.14	0.16	Rapp_Mc2177	535.87	59.31
One of each family	23	1.08	9.44	0.04	Rapp_Mc3057	42.46	19.57
Lipid metabolism	22	1.03	4.28	0.02	Rapp_Mc1456	12.14	12.89
Carboxypeptidase inhibitor	22	1.03	42.89	0.17	Rapp_Mc10222	388.49	41.17
5'-Nucleotidase	16	0.75	14.33	0.04	Rapp_Mc6697	47.63	20.77
Microplusin	16	0.75	65.37	0.19	Rapp_Mc1964	434.68	41.56
ML domain	16	0.75	1111.82	3.23	Rapp_Mc774	11 353.27	63.82
Antigen 5 family	13	0.61	188.87	0.45	Rapp_Mc1903	1014.98	41.34
Signaling molecules and interaction	13	0.61	1.56	0.00	Rapp_Mc8916	2.75	13.60
Translation	13	0.61	10.99	0.03	Rapp_Mc13622	43.10	30.17
24 kDa family	12	0.56	24.22	0.05	Rapp_Mc9762	91.56	31.50
Defensin	12	0.56	464.44	1.01	Rapp_Mc8698	1899.98	34.09
8 kDa Amblyomma family	11	0.52	28.78	0.06	Rapp_Mc13004	154.27	48.73
Glycan biosynthesis and metabolism	11	0.52	14.00	0.03	Rapp_Mc6227	80.50	52.27
Sphingomyelinase	9	0.42	10.67	0.02	Rapp_Mc837	22.89	23.84
Signal transduction	8	0.37	7.80	0.01	Rapp_Mc1131	14.98	24.01
Transcription	8	0.37	4.42	0.01	Rapp_Mc1617	9.48	26.79
Carbohydrate metabolism	7	0.33	4.31	0.01	Rapp_Mc5896	7.62	25.24
Fibrinogen-related domain	7	0.33	52.55	0.07	Rapp_Mc9028	248.58	67.58
Secretory - unknown function	7	0.33	12.81	0.01	Rapp_Mc9124	51.43	65.04
Immunoglobulin G binding protein A	6	0.28	2051.82	2.23	Rapp_Mc1190	4721.78	38.35
Metabolism of other amino acids	6	0.28	29.87	0.03	Rapp_Mc5888	67.37	37.59
Phospholipase A2	6	0.28	22.53	0.02	Rapp_Mc8892	44.33	32.79
Replication and repair	6	0.28	5.26	0.01	Rapp_Mc2861	9.23	29.23
7DB family	5	0.23	26.52	0.02	Rapp_Mc5571	66.08	49.84
Metalloprotease	5	0.23	12.08	0.01	Rapp_Mc12946	38.89	64.40

SALP15	4	0.19	10.25	0.01	Rapp_Mc1541	28.69	69.99
Astacin	3	0.14	1.77	0.00	Rapp_Mc7012	3.39	63.84
Cell growth and death	3	0.14	6.83	0.00	Rapp_Mc3897	17.39	84.91
Dermacentor 9 kDa expansion	3	0.14	14.72	0.01	Rapp_Mc1065	26.04	58.95
Histidine rich	3	0.14	2.87	0.00	Rapp_Mc450	3.95	45.82
14 kDa family	3	0.14	25.10	0.01	Rapp_Mc8740	54.41	72.25
Kazal domain	3	0.14	21.10	0.01	Rapp_Mc421	59.70	94.33
Kazal/vWF domain	3	0.14	18.64	0.01	Rapp_Mc2515	35.48	63.46
TELEM	3	0.14	1.99	0.00	Rapp_Mc5946	2.32	38.93
Thyropin	3	0.14	67.58	0.04	Rapp_Mc1844	99.53	49.09
Cysteine rich	2	0.09	1.03	0.00	Rapp_Mc1691	1.10	53.66
Energy metabolism	2	0.09	15.83	0.01	Rapp_Mc6151	25.10	79.28
Hirudin	2	0.09	310.16	0.11	Rapp_Mc11642	418.25	67.42
Bovine pancreatic trypsin inhibitor - Lipocalin	1	0.05	3.56	0.00	Rapp_Mc3211	3.56	100.00
Chitin deacetylase activity	1	0.05	1.17	0.00	Rapp_Mc2536	1.17	100.00
Cell motility	1	0.05	3.36	0.00	Rapp_Mc4124	3.36	100.00
Cysteine rich hydrophobic domain 2	1	0.05	13.39	0.00	Rapp_Mc7198	13.39	100.00
Fatty acid-binding protein	1	0.05	40.42	0.01	Rapp_Mc2582	40.42	100.00
Histamine release factor	1	0.05	1211.56	0.22	Rapp_Mc12631	1211.56	100.00
Immune system	1	0.05	24.15	0.00	Rapp_Mc8912	24.15	100.00
26 kDa family	1	0.05	7.18	0.00	Rapp_Mc5668	7.18	100.00
Kazal/SPARC domain	1	0.05	64.96	0.01	Rapp_Mc1895	64.96	100.00

**Supplemental Table A4: Differential expression between female and male ticks in the salivary transcriptome of *R. appendiculatus*.**

Protein families	Female up regulated *	Male up regulated *
Secretory protein families	570	553
24 kDa family	3	4
28 kDa Metastriate family	18	4
5'-Nucleotidase	3	2
7DB family	0	1
8 kDa Amblyomma family	2	6
8.9 kDa family	45	28
Antigen 5 family	1	2
Astacin	0	2
Basic tail secreted protein	36	21
Bovine pancreatic trypsin inhibitor	61	71
Carbohydrate metabolism	2	0
Carboxypeptidase inhibitor	6	5
Cell motility	0	1
Chitin-binding proteins	0	5
Cystatin	19	15
Cysteine rich	1	1
DA-P36 family	15	2
Defensin	2	5
Dermacentor 9 kDa expansion	0	3
Digestive system (including Serine proteases)	3	25
Evasin	36	16
Fibrinogen-related domain	2	0
Folding, sorting and degradation (including Cathepsins)	1	8
Gluzincin	2	33
Glycan biosynthesis and metabolism	2	0
Glycine rich superfamily	14	31
Hirudin	2	0
Histidine rich	3	0
Immunoglobulin G binding protein A	0	6
Ixodegrin B	36	7
Kazal domain	2	1
Kazal/vWf domain	1	1
Lipid metabolism	7	5
Lipocalin	157	154
Microplusin	3	5
ML domain	1	8
Mucin	11	3
No hit	0	1
One of each family	17	1
Phospholipase A2	0	2
Reprolysin	27	15

SALP15	0	1
Secretory - unknown function	0	2
Serpin	3	5
Signal transduction	1	0
Signaling molecules and interaction	3	0
Sphingomyelinase	0	5
TIL domain	20	34
Transport and catabolism	2	6
Housekeeping protein class	220	413
Unknown function protein class	130	288
No hit protein class	111	172
Transcripts without predicted ORFs	727	920
<b>Total</b>	<b>1758</b>	<b>2346</b>

\* Transcripts estimated as up regulated (fold change > 2) by the edgeR (Empirical analysis of digital gene expression data in R) software package.