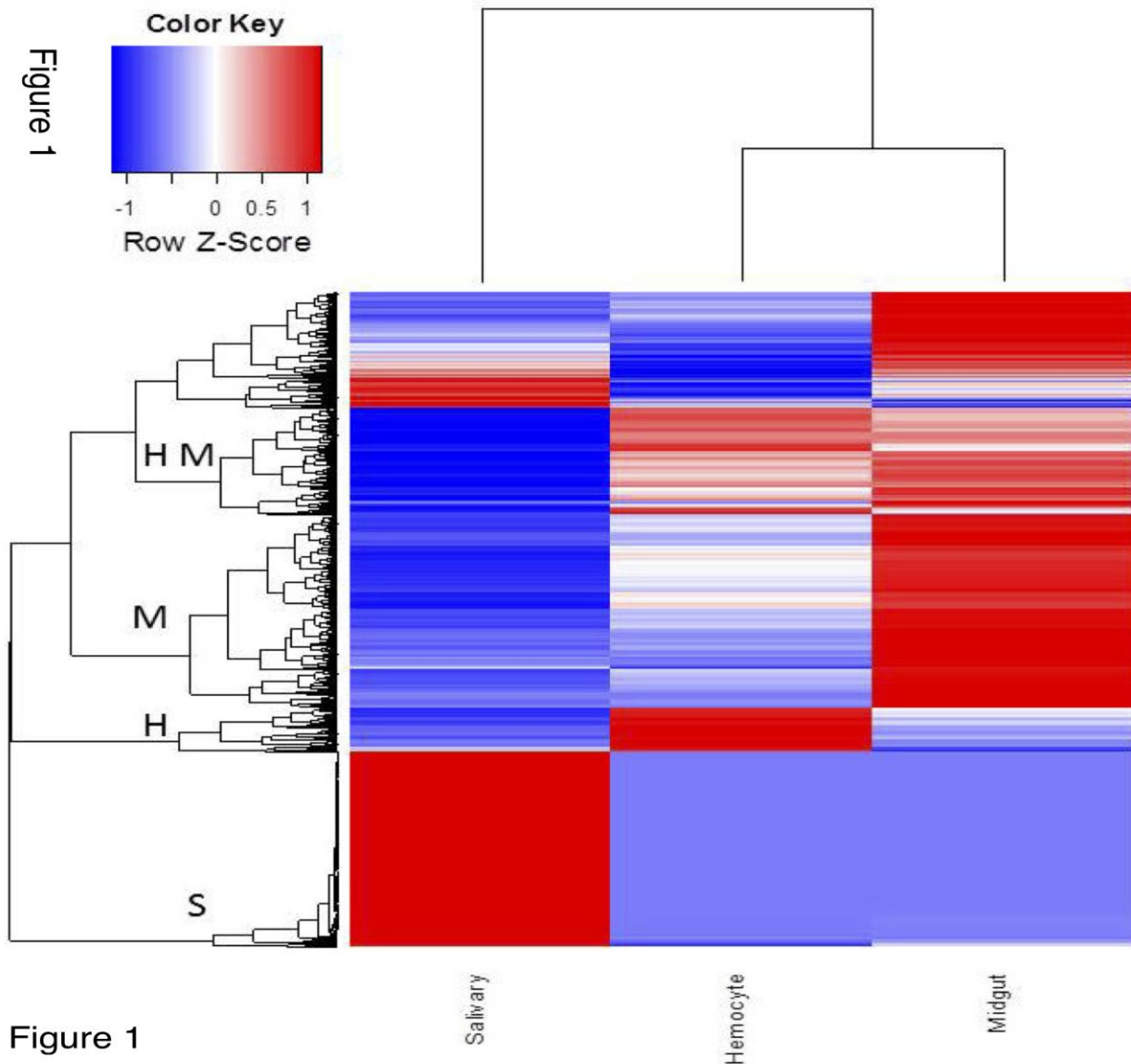
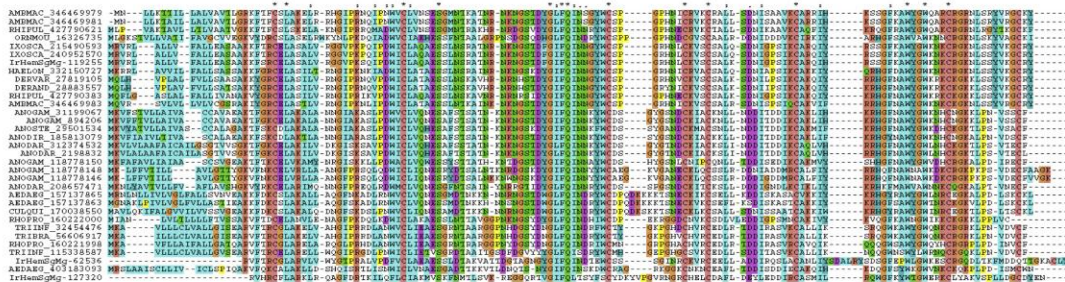


Supplemental Figures



Supplemental Figure A. 3,915 CDS have a RPKM value of 50 or more in at least one of the three tick tissues. The heat map was constructed from the RPKM data for these 3,915 coding sequences according to their tissue of origin. The Z-score represents the deviation from the mean by standard deviation units of the normalised row data. The letters H, M, and S at the row cladogram nodes indicate clades that are enriched in Haemocyte, Midgut, or Salivary gland tissues, respectively.

A



B

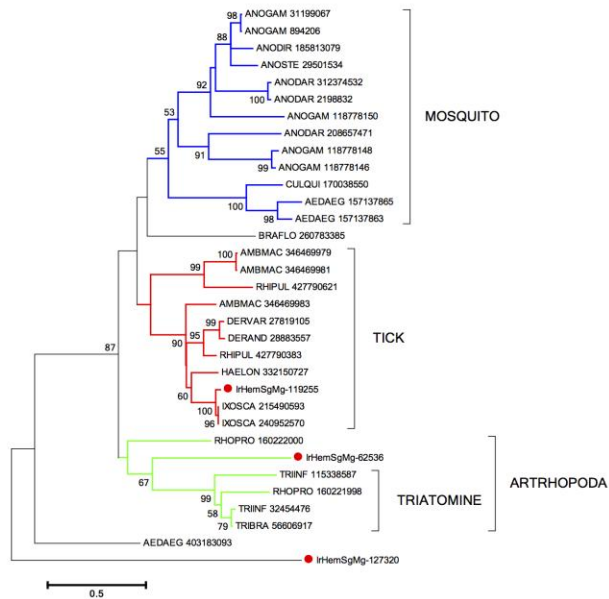


Figure 2

Supplemental Figure B. Arthropod lysozymes. A) ClustalW alignment. The symbols at the top of the figure represent (*) identity and (.) lesser similarity. B) The neighbour-joining phylogenetic tree from the alignment in (A) following 1,000 bootstraps. Sequence names are represented by the first three letters of the genus name, followed by the first three letters of the species name, followed by their GenBank gene identifier (gi) accession number. Sequences from this work start with IrHem or IrSgp and include IrHemSgMg-127320, which is expressed in haemocytes. The *Ixodes ricinus* sequences are identified with a red symbol. The bar at the bottom represents 50% amino acid diversity. The numbers at the nodes represent the per cent bootstrap support. Values below 50 are not shown.

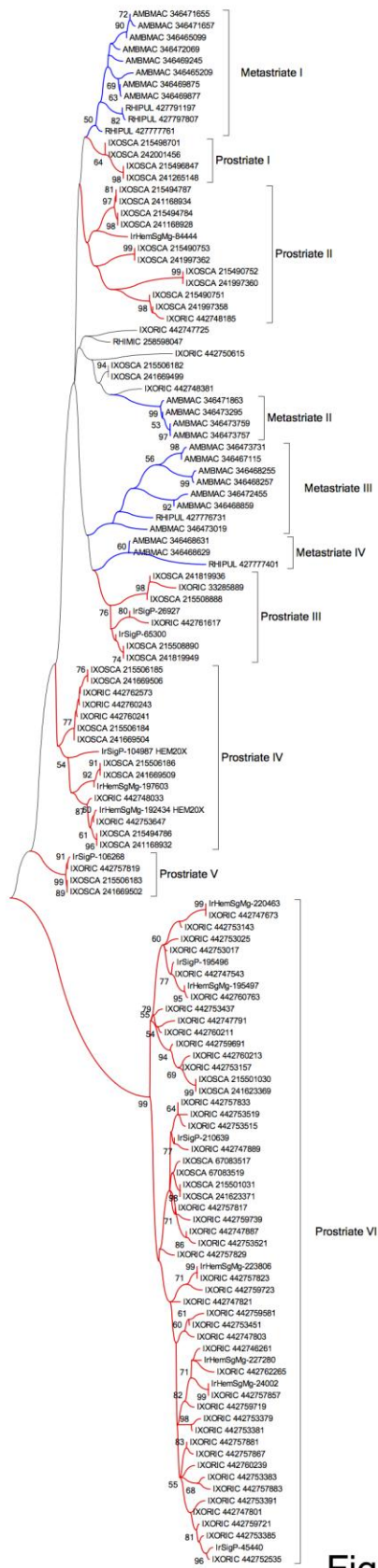


Figure 3

Supplemental Figure C. The TIL domain peptide family of ticks. The neighbour-joining phylogenetic tree following 1,000 bootstraps. Sequence names are represented by the first three letters of the genus name, followed by the first three letters of the species name, followed by their GenBank gene identifier (gi) accession number. Sequences from this work start with IrHem or IrSigg and include IrSigP-201840, which is 20-fold overexpressed in haemocytes. Metastriate and prostriate clades are indicated. The bar at the bottom represents 20% amino acid diversity. The numbers at the nodes indicate the percentage bootstrap support.

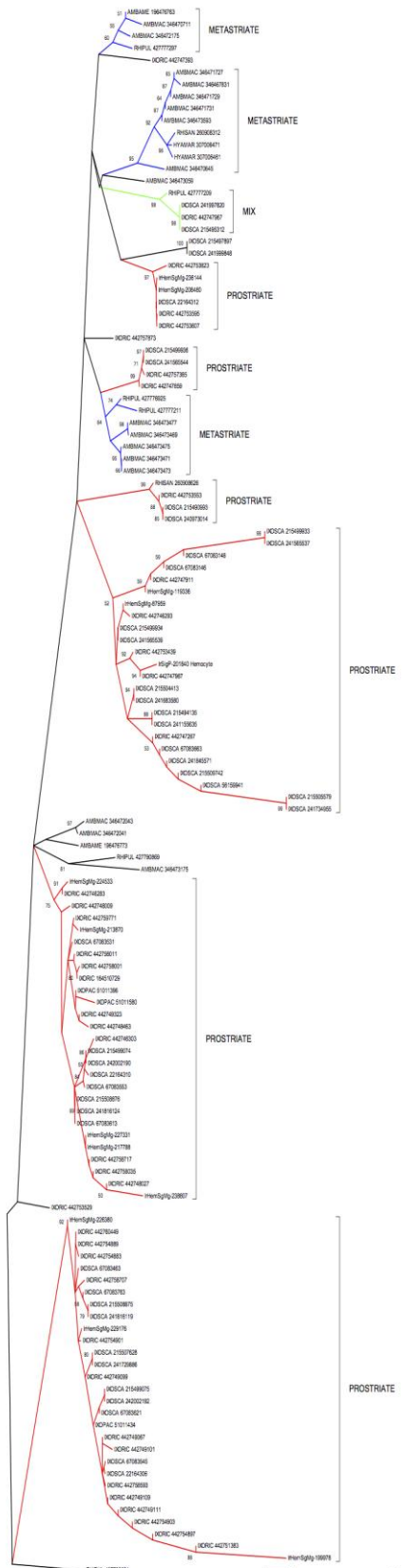


Figure 4

Supplemental Figure D. The 8.9 kDa family of ticks. The neighbour-joining phylogenetic tree following 1,000 bootstraps. Sequence names are represented by the first three letters of the genus name, followed by the first three letters of the species name, followed by their GenBank gene identifier (gi) accession number. Sequences from this work start with IrHem or IrSigp and include IrSigP-201840, which is 20 fold overexpressed in haemocytes. Metastriate only, prostriate only, and mixed clades are indicated. The bar at the bottom represents 100% amino acid diversity. The numbers at the nodes indicate the percentage bootstrap support.

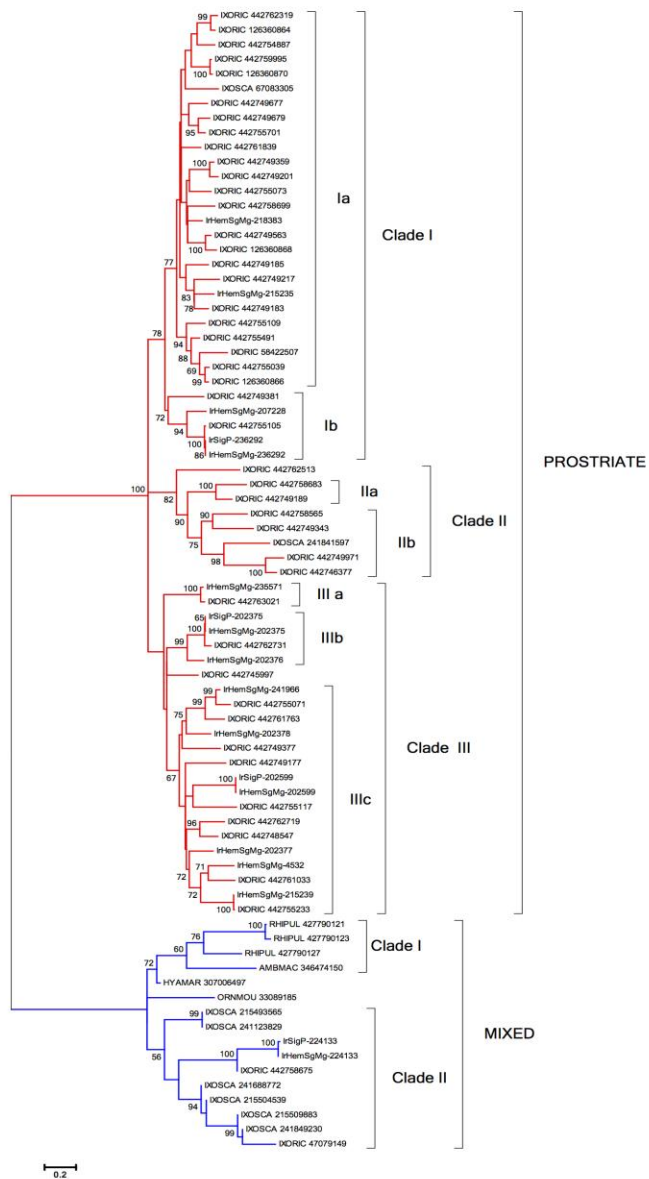


Figure 5

Supplemental Figure E. The Ixoderin family of ticks. The neighbour-joining phylogenetic tree following 1,000 bootstraps is shown. Sequence names are represented by the first three letters of the genus name, followed by the first three letters of the species name, followed by their GenBank gene identifier (gi) accession number. Sequences from this work start with IrHem or IrSigp. Clades and subclades with strong bootstrap support are indicated. The bar at the bottom represents 20% amino acid diversity. The numbers at the nodes indicate the percentage bootstrap support.

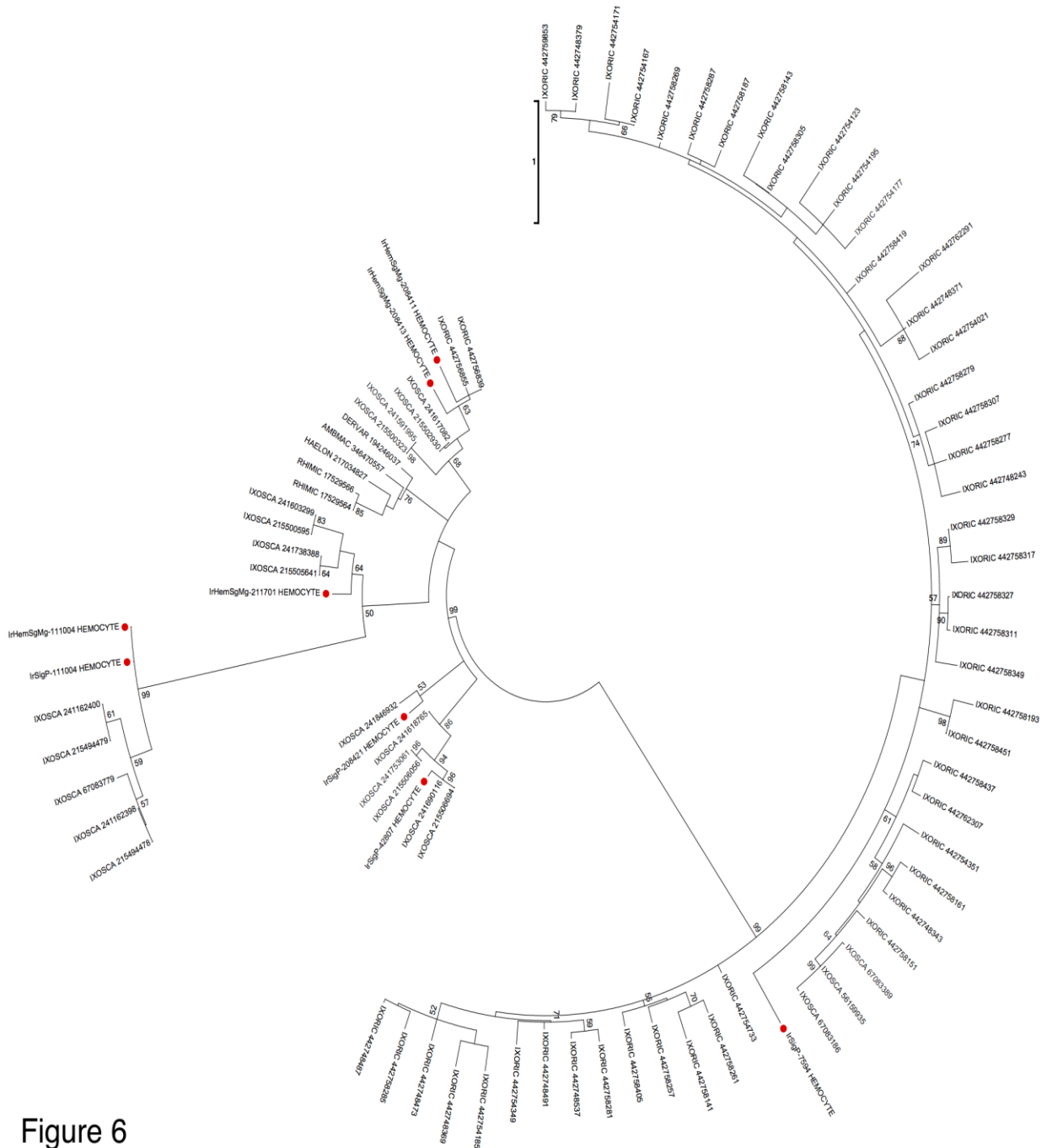


Figure 6

Supplemental Figure F. The immune Kunitz domain peptide family of *Ixodes ricinus* compared to other tick proteins. The neighbour-joining phylogenetic tree following 1,000 bootstraps is shown. Sequence names are represented by the first three letters of the genus name, followed by the first three letters of the species name, followed by their GenBank gene identifier (gi) accession number. Sequences from this work start with IrHem or IrSigp and include peptide sequences highly expressed in haemocytes, identified by a red symbol. The bar at the top indicates 100% amino acid diversity. The numbers at the nodes indicate the percentage bootstrap support.