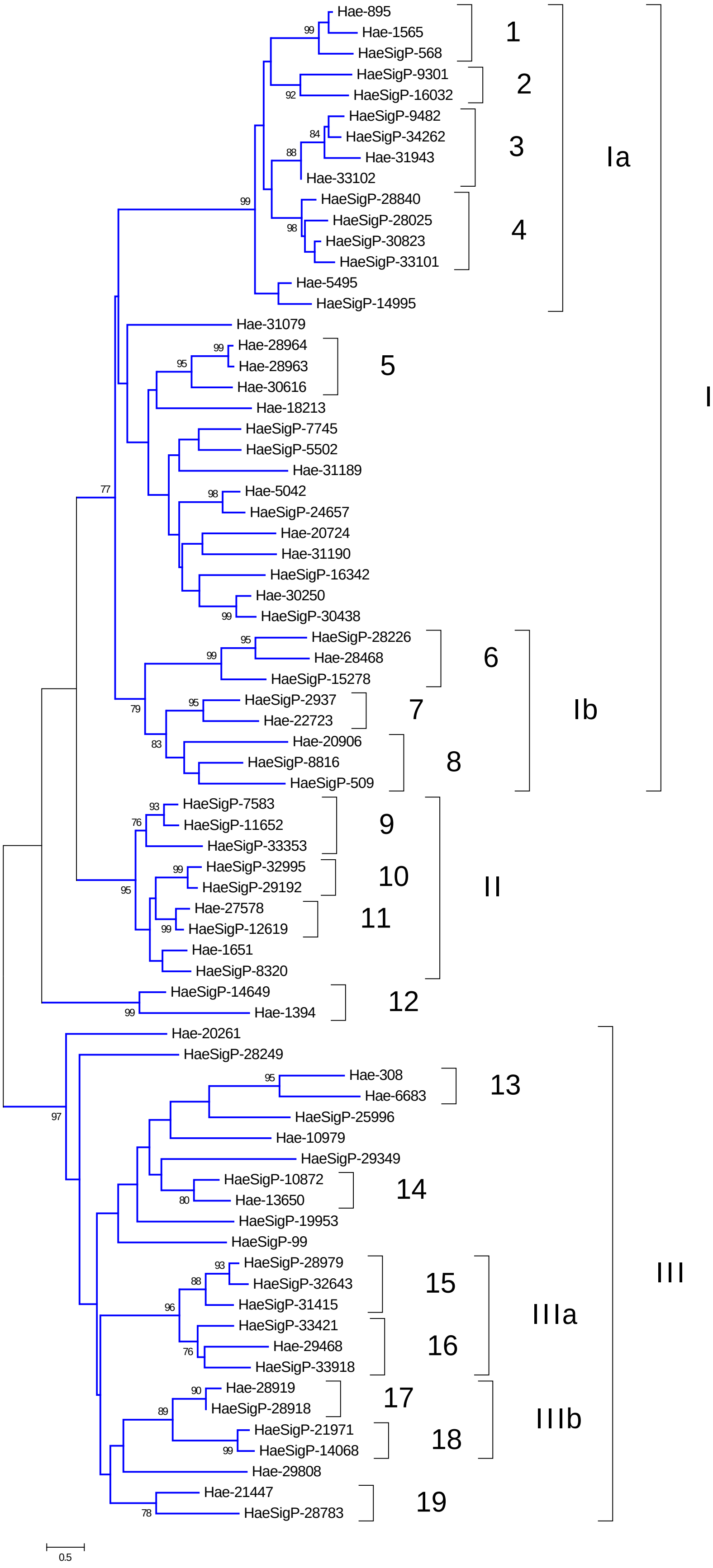
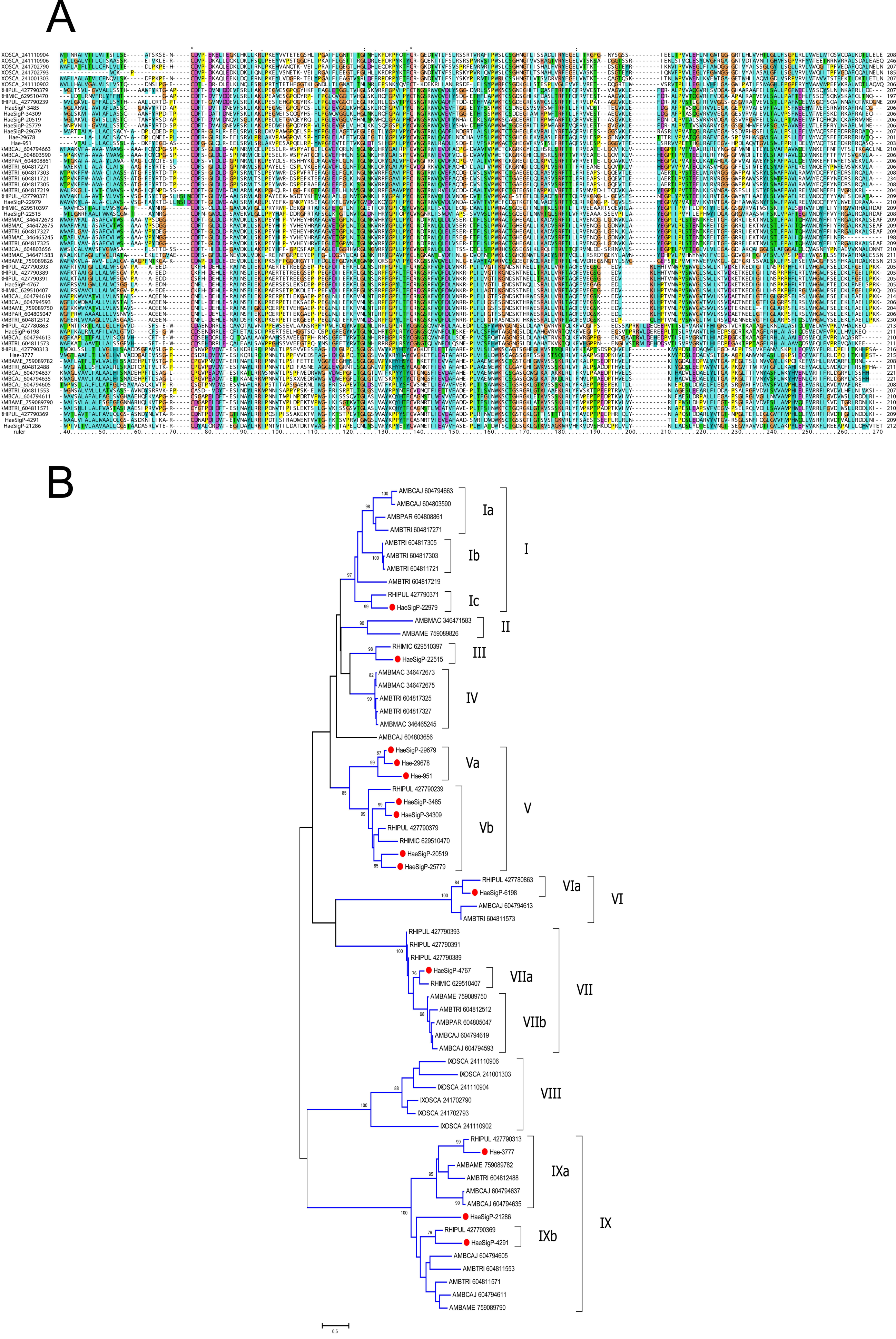
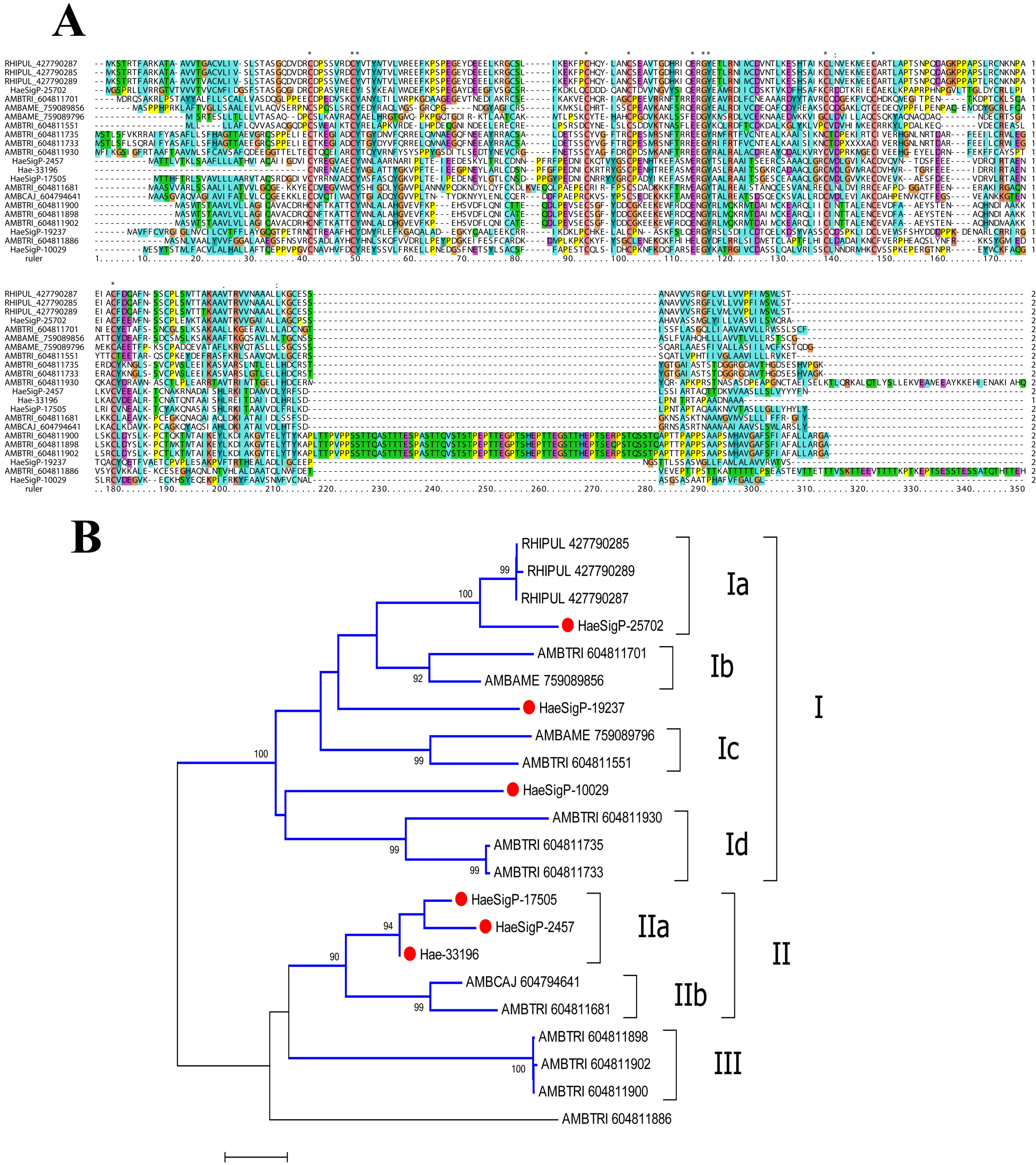
Supplemental figure 1. Evolutionary relationships of tick metalloproteases of the reprolysin family. The evolutionary history was inferred using the Neighbor-Joining method [1]. The optimal tree with the sum of branch length = 114.06814666 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method [3] and are in the units of the number of amino acid substitutions per site. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). The analysis involved 316 amino acid sequences. All ambiguous positions were removed for each sequence pair. There were a total of 1623 positions in the final dataset. Evolutionary analyses and part of this legend writing were conducted in MEGA6 [4]. The *Hyalomma excavatum* sequences are recognized by a red symbol. Other sequences are represented by the three first letters of the genus name followed by the first three letters of the species name followed by their NCBI gi| accession number.



Supplemental figure 2. Evolutionary relationships of Group I lipocalins of *Hyalomma excavatum.*
The evolutionary history was inferred using the Neighbor-Joining method [1]. The optimal tree with the sum of branch length = 69.61982398 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method [3] and are in the units of the number of amino acid substitutions per site. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). The analysis involved 73 amino acid sequences. All ambiguous positions were removed for each sequence pair. There were a total of 433 positions in the final dataset. Evolutionary analyses and this legend writing were conducted in MEGA6 [4].



Supplemental figure S3. Evolutionary relationships of the "One-of-each" family of tick proteins. A) Clustal alignment. B) Phylogram of the alignment in A. The evolutionary history was inferred using the Neighbor-Joining method [1]. The optimal tree with the sum of branch length = 33.21015025 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [2]. Values smaller than 75% are not shown. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method [3] and are in the units of the number of amino acid substitutions per site. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). The analysis involved 64 amino acid sequences. All ambiguous positions were removed for each sequence pair. There were a total of 299 positions in the final dataset. Evolutionary analyses and part of this legend were conducted in MEGA6 [4]. The Hyalomma excavatum sequences are recognized by a red symbol. Other sequences are represented by the three first letters of the genus name followed by the first three letters of the species name followed by their NCBI gi| accession number.



Supplemental figure S4. Evolutionary relationships of the novel 22 kDa protein family of metastriate ticks.
A) Clustal alignment. B) Phylogram of the alignment in A.The evolutionary history was inferred using the Neighbor-Joining method [1]. The optimal tree with the sum of branch length = 21.84913049 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method [3] and are in the units of the number of amino acid substitutions per site. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). The analysis involved 22 amino acid sequences. All ambiguous positions were removed for each sequence pair. There were a total of 389 positions in the final dataset. Evolutionary analyses and part of this legend were conducted in MEGA6 [4]. The *Hyalomma excavatum* sequences are recognized by a red symbol. Other sequences are represented by the three first letters of the genus name followed by the first three letters of the species name followed by their NCBI gi| accession number.