sample correlation matrix
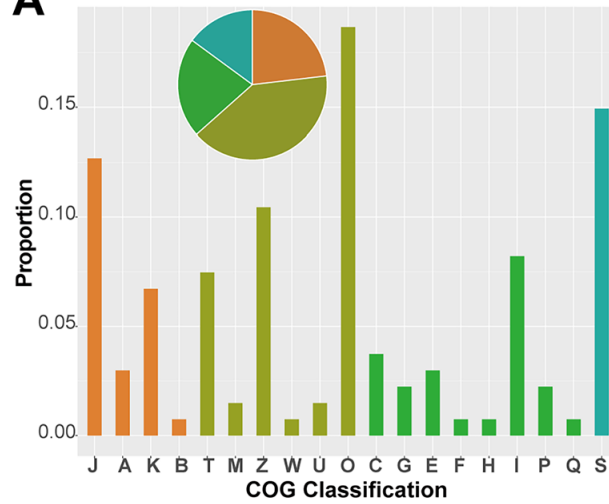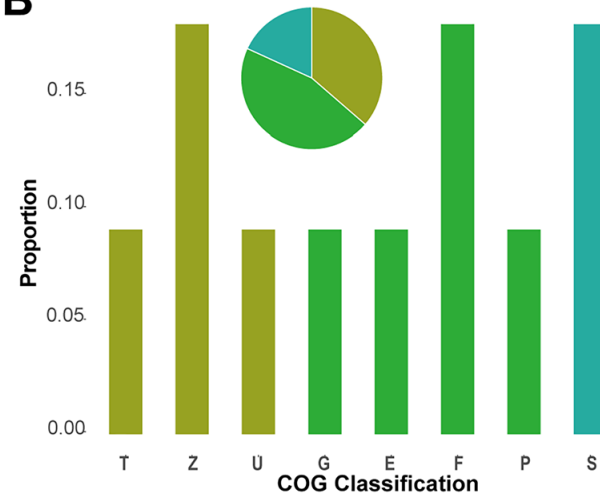diffExpr.P5e−2_C1.5.matrix.log2.centered

Figure S1. RNAseq analysis of tick gene transcripts detected in pools of flat and fully-fed *Ixodes persulcatus* ticks removed from human patients at Mudanjiang Forestry Central Hospital in Heilongjiang Province, China. Heatmap with clusters showing the Pearson correlation matrix for pairwise sample comparisons of differentially-expressed genes in flat (pools TG1, TG2, and TG13) and fully-fed (pools TG5, TG6, and TG15) ticks.

A

B

CELLULAR PROCESSES AND SIGNALING
[T] Signal transduction mechanisms
[M] Cell wall/membrane/envelope biogenesis
[Z] Cytoskeleton
[W] Extracellular structures
[U] Intracellular trafficking, secretion, and
vesicular transport
[O] Posttranslational modification, protein
turnover, chaperones

INFORMATION STORAGE AND PROCESSING
[J] Translation, ribosomal structure and biogenesis
[A] RNA processing and modification
[K] Transcription
[B] Chromatin structure and dynamics

POORLY CHARACTERIZED
[S] Function unknown

METABOLISM
[C] Energy production and conversion
[G] Carbohydrate transport and metabolism
[E] Amino acid transport and metabolism
[F] Nucleotide transport and metabolism
[H] Coenzyme transport and metabolism
[I] Lipid transport and metabolism
[P] Inorganic ion transport and metabolism
[Q] Secondary metabolites biosynthesis,
transport and catabolism

Figure S2. RNAseq comparison of tick gene transcripts detected in pools of flat and fully-fed *Ixodes persulcatus* ticks removed from human patients at Mudanjiang Forestry Central Hospital in Heilongjiang Province, China. Taxonomic classification of differentially-expressed genes with similar expression patterns based on the Clusters of Orthologous Groups (COG) database (A) COG classification of genes up-regulated in fed versus unfed ticks; (B) COG classification of genes down-regulated in fed versus unfed ticks.