Supplementary Materials:

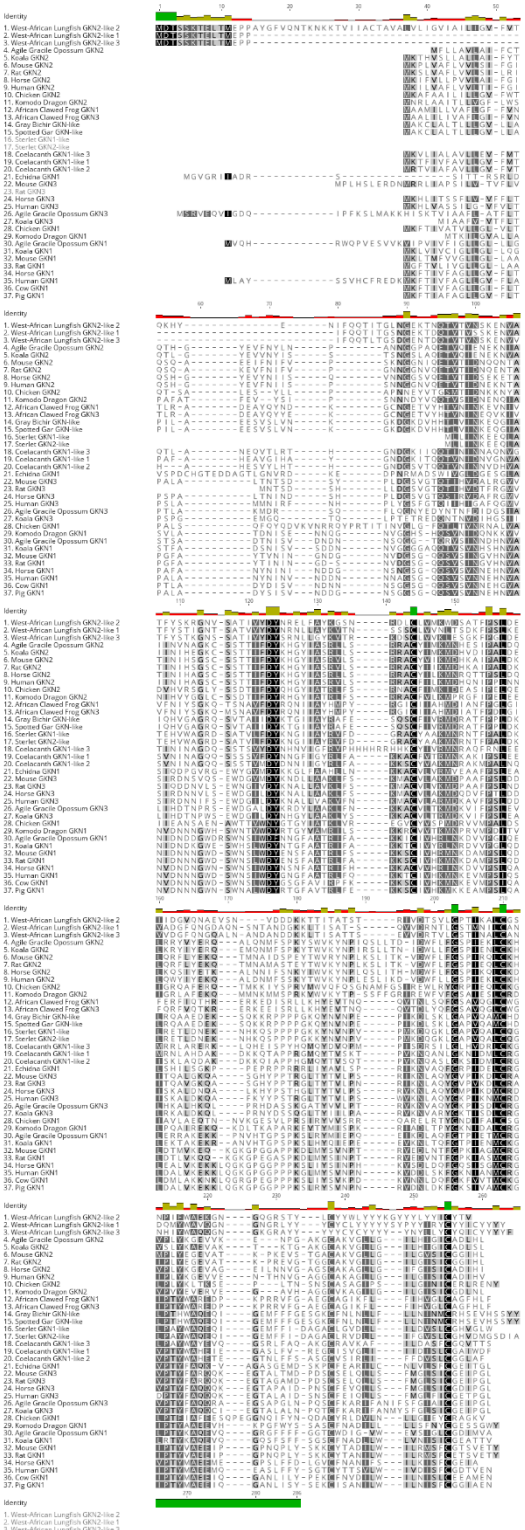

Figure S1: Clustal Omega amino acid alignment of vertebrate gastrokine sequences (GKN1, GKN2, GKN3, GKN-like) with sequence consensus metrics. Dark-shaded boxes indicate 100% sequence identity, whereas lighter-shaded gray boxes indicate lower sequence identity metrics.

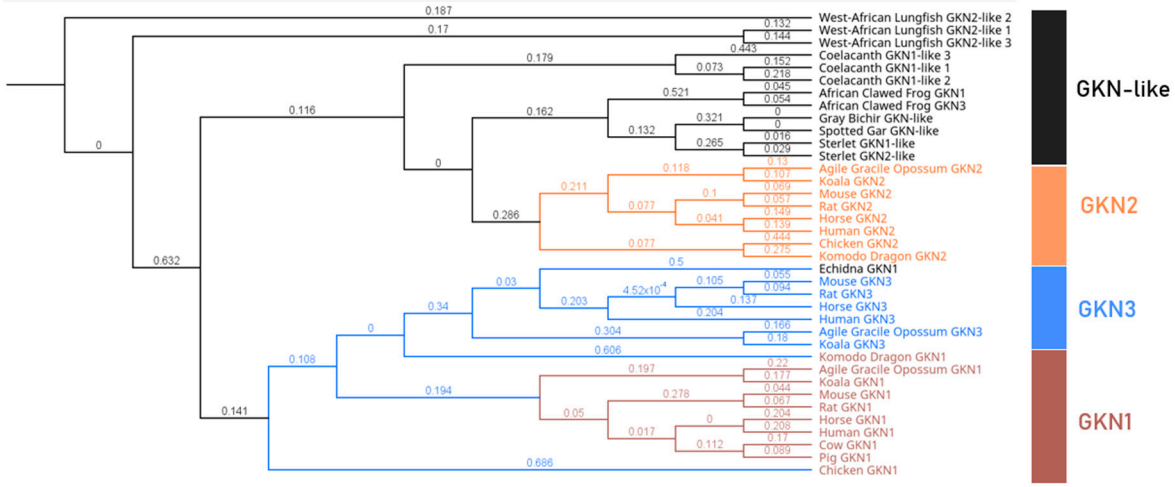

Figure S2: Maximum-likelihood phylogeny of vertebrate gastrokine-like amino acid sequences constructed by the IQ-Tree web server using the JTT + G4 substitution model and 1000 bootstrap replicates. Branch values indicate bootstrap percentage, the scale represents substitutes per site and groupings of gastrokine-like sequences are superimposed on the right.