

Supplementary Material

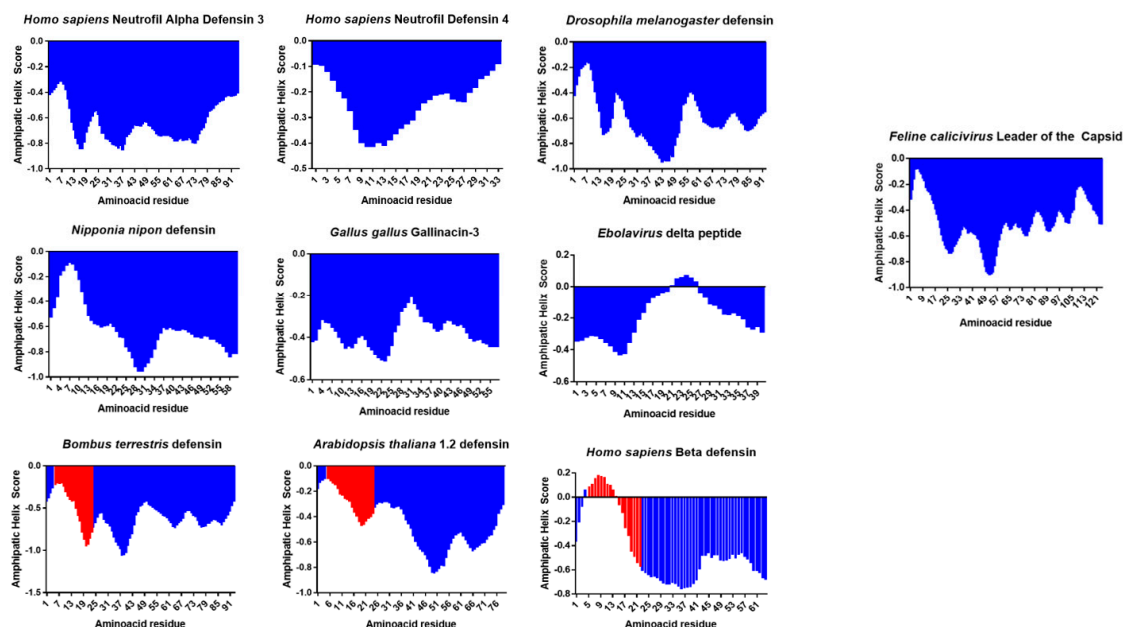


Figure S1. Bioinformatical analysis of different defensins. Protein sequence of diverse defensins retrieved from the NCBI database and the protein sequence of the WT-LC protein were analyzed with TMHMM 2.0 and AmphipaSeek servers to predict TMDs or amphipathic helices. Amino acid residues of predicted TMDs were plotted in red and the threshold for amphipathic helix (0 value) is indicated in the “y” axis.

Table S1. Transmembrane domains and alpha helices of diverse defensines.

| Protein | Species | Transmembrane Domain Prediction | Amphipathic Helix Prediction |
|--------------------------------------|--------------------------------|---------------------------------|------------------------------|
| Defensin alpha 3 neutrophil specific | <i>Homo sapiens</i> | No | No |
| Neutrofil Defensin 4 | <i>Homo sapiens</i> | No | No |
| Defensin | <i>Drosophila melanogaster</i> | No | No |
| Defensin | <i>Nipponia nipon</i> | No | No |
| Gallinacin 3 | <i>Gallus gallus</i> | No | No |
| Delta peptide | <i>Ebolavirus</i> | No | Yes |
| Defensin | <i>Bombus terrestris</i> | Yes | No |
| Defensin | <i>Arabidopsis thaliana</i> | Yes | No |
| Beta Defensin 106 | <i>Homo sapiens</i> | Yes | Yes |
| Leader of the Capsid | <i>Feline calicivirus</i> | No | No |