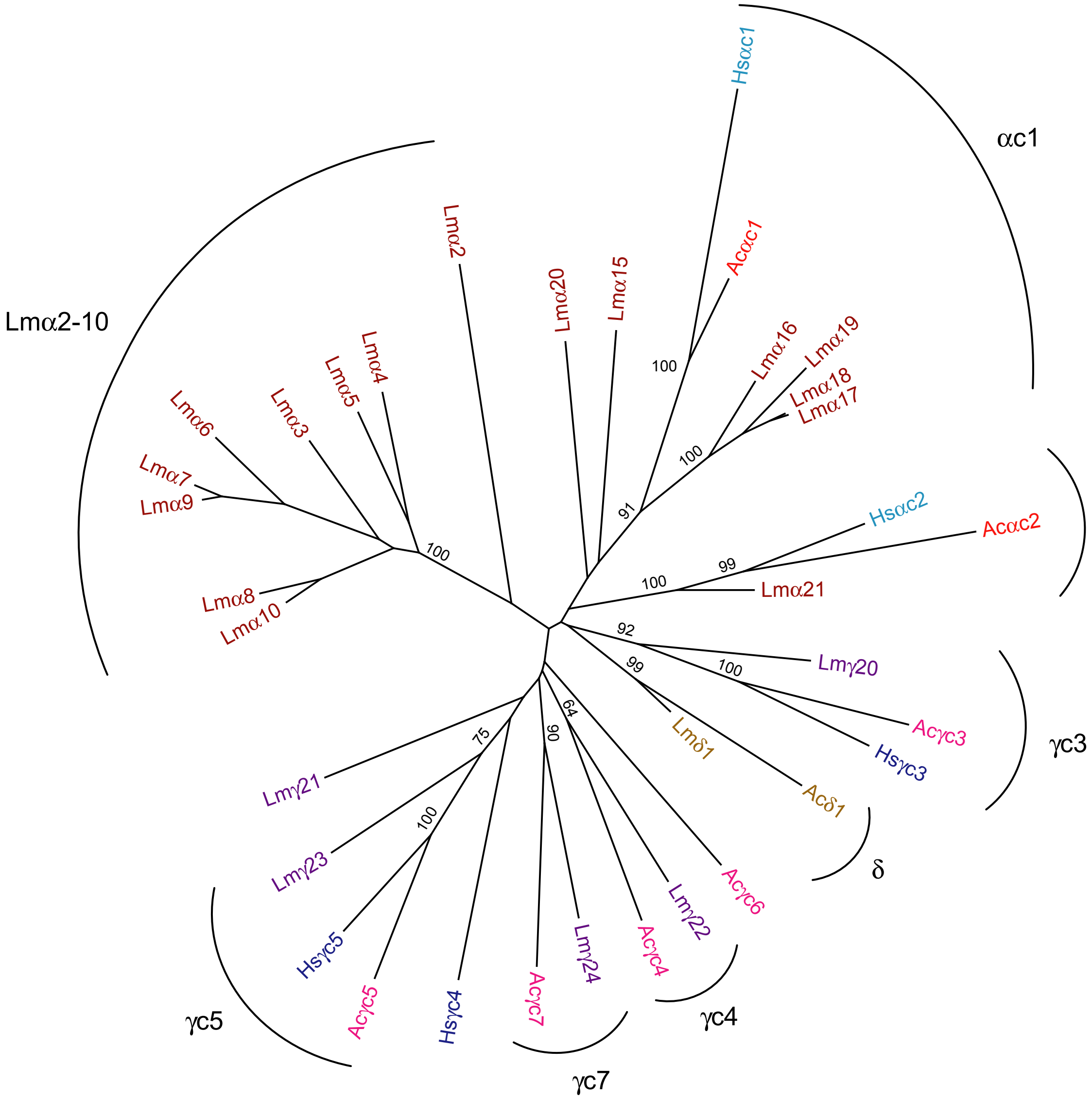

Figure S1. Phylogenetic analysis of c-type protocadherin and the protocadherin δ subcluster genes.

Amino acid sequences for the EC1-EC3 ectodomain region of anole, human and coelacanth protocadherin variable exons were aligned by ClustalW. The phylogenetic tree was constructed by the maximum-likelihood method. Genes in different protocadherin subclusters are indicated by color. Numbers at the nodes are the percentage of bootstrap values of 100 replicates. The tree is unrooted.