Supplementary figure 4- Phylogenetic network of shared gene clusters based upon individual gene tree topologies.
The gene trees of 91 family-wide shared gene clusters were input to SplitsTree4 to construct an unrooted phylogenetic network that best represented all the individual relationships. Most gene trees were found to disagree, resulting in a star-like topology. Branch coloring is based upon listed habitat (yellow = oral; red = sediment; green = rumen; blue = human GI tract).