Principal Coordinate Analysis of Kendall-Colijn Distance Showing Ordination of Rooted Topologies under Different Approaches. Six approaches were tested: V1 - iteration before Treeshrink (standard); V2 - iteration after TreeShrink; V3 - as (V2), but excluding genes with less than a quarter of the all samples; V4 - as (V3) with p-values of 0.0001; V5 - as (V3) p-values of 0.001; V6 - as (V3) p-values of 0.05.

Distribution of Tree topologies
(Kendall-Colijn distance)