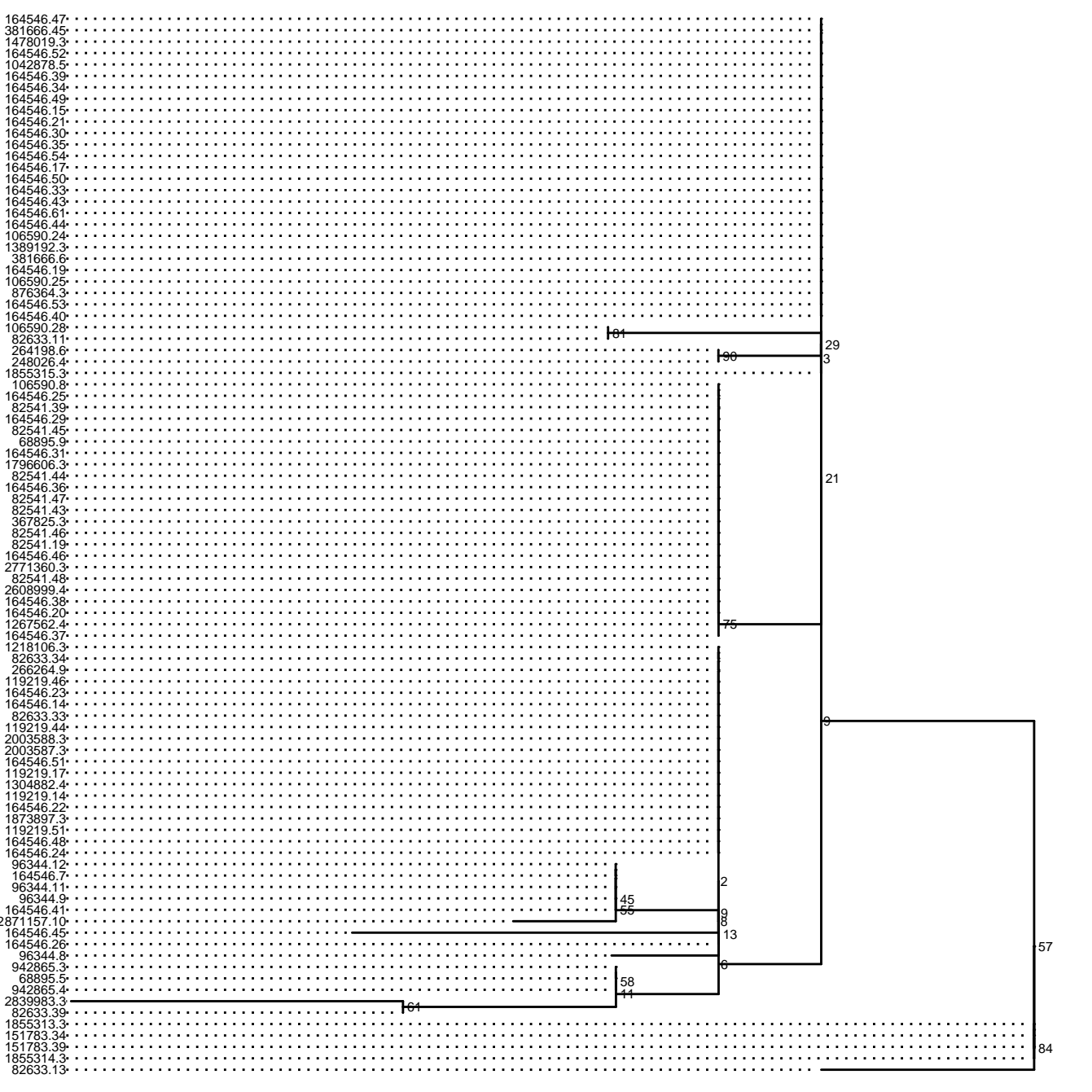
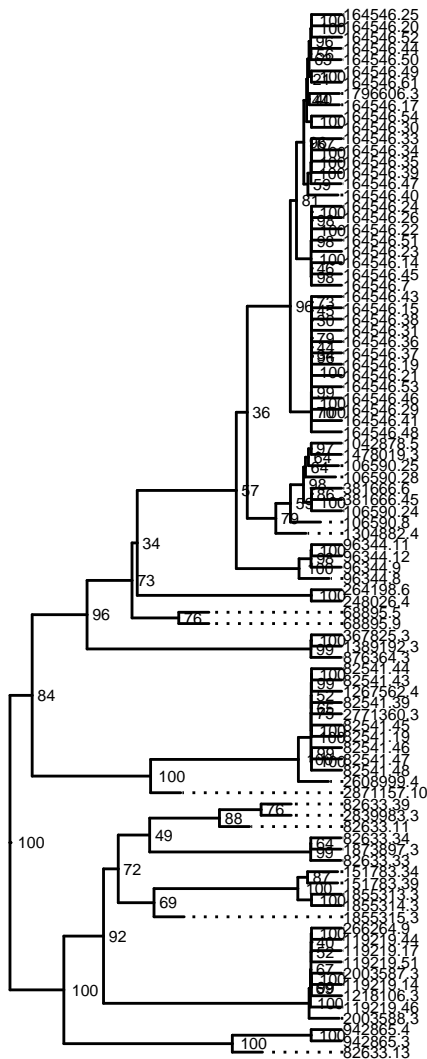


A phylogenetic tree with 100 numbered taxa (1-100) at the tips. The tree is rooted on the left and branches to the right. Bootstrap values are indicated at the nodes. The tree shows a complex branching pattern with several well-supported clades. For example, a large clade containing taxa 1-100 is supported by a bootstrap value of 96 at its base. Other notable bootstrap values include 99, 98, 97, 96, 95, 94, 93, 92, 91, 90, 89, 88, 87, 86, 85, 84, 83, 82, 81, 80, 79, 78, 77, 76, 75, 74, 73, 72, 71, 70, 69, 68, 67, 66, 65, 64, 63, 62, 61, 60, 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1.

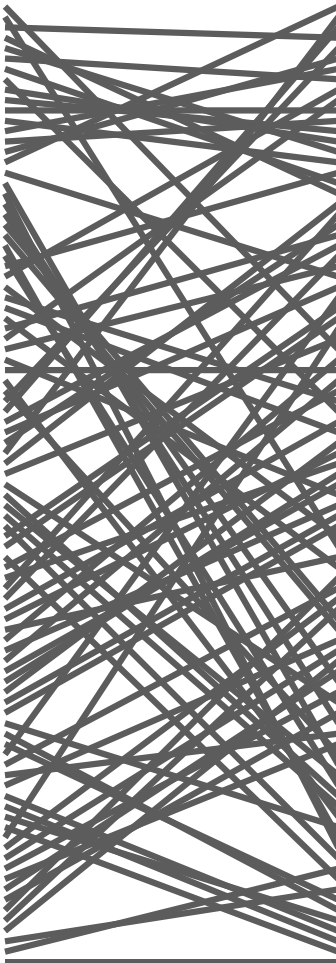
A phylogenetic tree diagram showing the relationships between 1000 simulated sequences. The tree is rooted at the bottom and branches upwards. The sequences are labeled with numbers from 1 to 1000 along the left side. The tree structure is highly complex, with many internal nodes and branches. The labels on the left are arranged in a way that suggests a specific order or grouping of the sequences. The tree shows a clear pattern of branching, with some sequences forming distinct clusters and others branching off more frequently. The overall structure is a dense, interconnected web of lines representing the evolutionary relationships between the sequences.



ANI dendrogram



JRF = 0.704 MCI = 0.214



V6-V8 region tree

