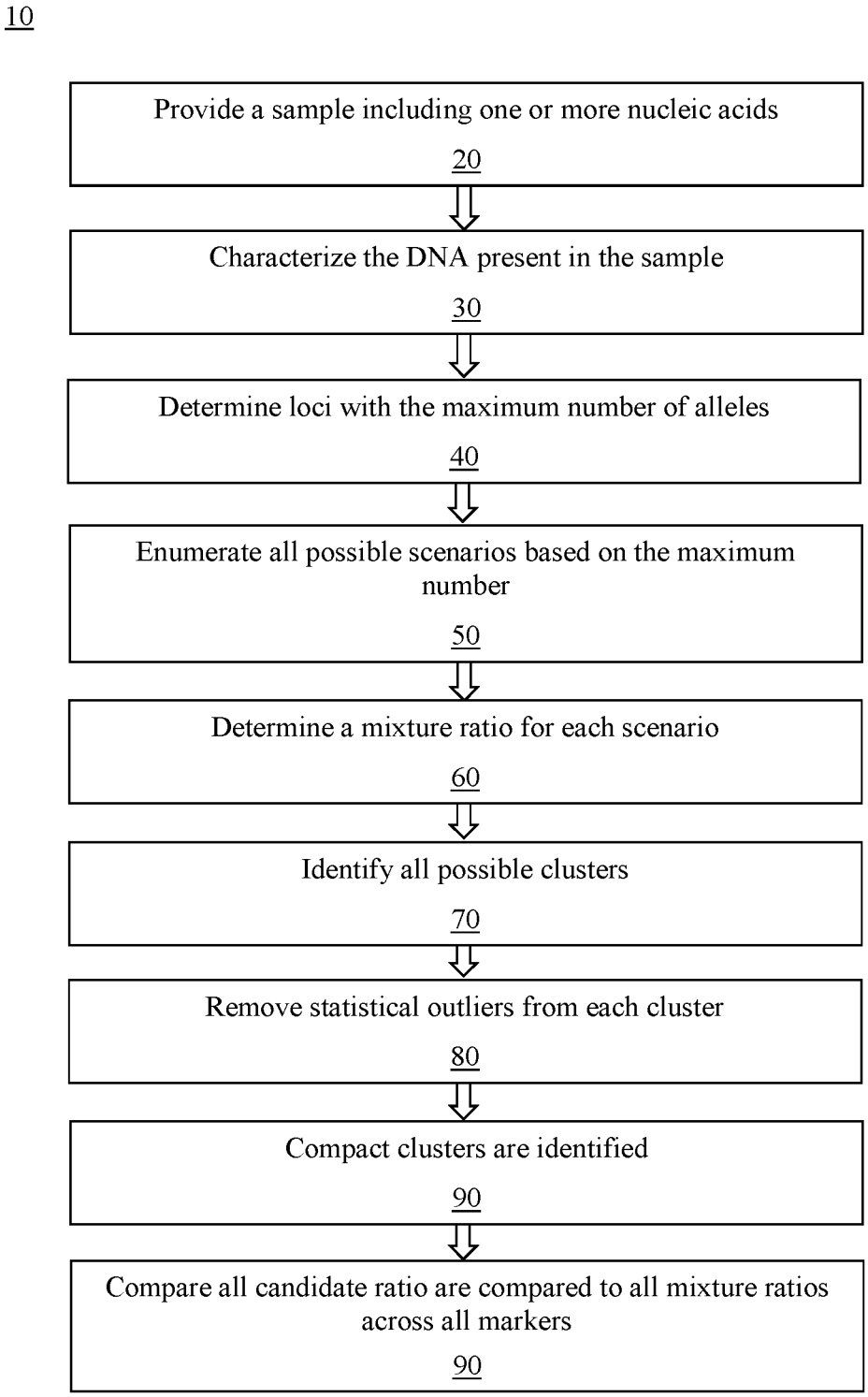
10
Provide a sample including one or more nucleic acids
20
Characterize the DNA present in the sample
30
Determine loci with the maximum number of alleles
40
Enumerate all possible scenarios based on the maximum number
50
Determine a mixture ratio for each scenario
60
Identify all possible clusters
70
Remove statistical outliers from each cluster
80
Compact clusters are identified
90
Compare all candidate ratio are compared to all mixture ratios across all markers
90

FIG. 1