

Figure S1: Examples of 10 selected pictures of each class for the experimental dataset.

Figure S2: Setup of the five-fold experiments;

Figure S3: Structure of the convolutional neural network model.

Figure S4: Optimized population structure patterns were assigned into three clusters ($K = 3$), based on Evanno's ΔK .

Figure S5: Phylogenetic relationship between all individual Asian elephants (*Elephas maximus*, Linnaeus, 1758) and the GenBank accession numbers: AY589513, AY589516, AY589515, AY365432, AY365433, AY245823, AY589514, AY589512, AY365433, AY365432, AY245823, AY245826, AY245825, AY245824, AY245822, AY245822, AY245821, AY245820, AY245819, AY245818, AY245817, AY245816, AY245815, AY2458214, AY245813, AY245812, AY245811, AY245810, AY245809, AY245808, AY245807, AY245806, AY245805, AY245804, AY245803, AY245802, and AY245827, constructed with the help of the Bayesian inference (BI) analysis using the mt D-loop sequencing. Support values at each node are bootstrap values of the Bayesian posterior probability.

Figure S6: Mismatch distributions analysis (a) the National Elephant Institute of Thailand (NEI, Lampang), (b) Maetaeng Elephant Park (MEP, Chiang Mai), (c) Baan Chang Elephant Park (BCEP, Chiang Mai). The x-axis represents the number of pairwise differences (mismatches), while the y-axis represents the frequency of these differences. The observed mismatch distribution (blue line) is compared to the expected distribution (purple line) for a stable population.

Figure S7: Example of the top-3 rank prediction results.