To assess the validity of the 500 SNPs in calling haplogroups with Haplogrep3, over 17K whole mtDNA sequences were downloaded from NCBI in fasta format and haplogroups were called using Haplogerep3. Of these 17K, 190 samples (10 each from haplogroup "H","M","L3","L2","L0","L1","U","D","R","L4","T","F","A","C","J","N","G","E","W") were used as spike-ins. Each of the 190 samples had the 500 SNPs extracted into VCF format and were ran through Haplogrep3 for haplogroup calling. For each spike-in, the Haplogrep3 calls from the 500 SNPs were compared to the whole mtDNA call. All 19 haplogroups had 8 or more samples agree with the exception of haplogroup M, in which 4 were miss classified as H.