







**Figure S2.** Possible errors in mitochondrial consensus sequence calling for analyzed samples as indicated during haplogroup prediction, presented by base quality filter, by two alternative tools and pipelines (ANGSD *vs* schmutzi). Dark grey bars indicate that there was a wrong haplogroup perdition, thus the number of missed expected polymorphisms and possible incorrect base calls is not applicable. These haplotypes should be assumed to have the maximum number of errors in both parameters. Samples for which a bar is missing, indicates that the approach did not result in a consensus mitogenome sequence, particularly after filtering: (a) sample ZBC [29]; (b) sample ZHAG [29]; (c) sample ZMOJ [29]; (d) sample ZKO [29]; (e) sample ZHJ [29]; (f) sample ZHAJ [29]; (g) sample KFH2 [29]; (h) sample BAJ001 [29]; (i) sample CBT018 [30]; (j) sample MTT001 [30]; (k) sample POT002 [30]; (l) sample KRD001 [30]; (m) sample KRD002 [30]; (n) sample KRD003 [30]; (o) sample KRD004 [30]; (p) sample KRD005 [30];. (q) sample KRD006 [30].