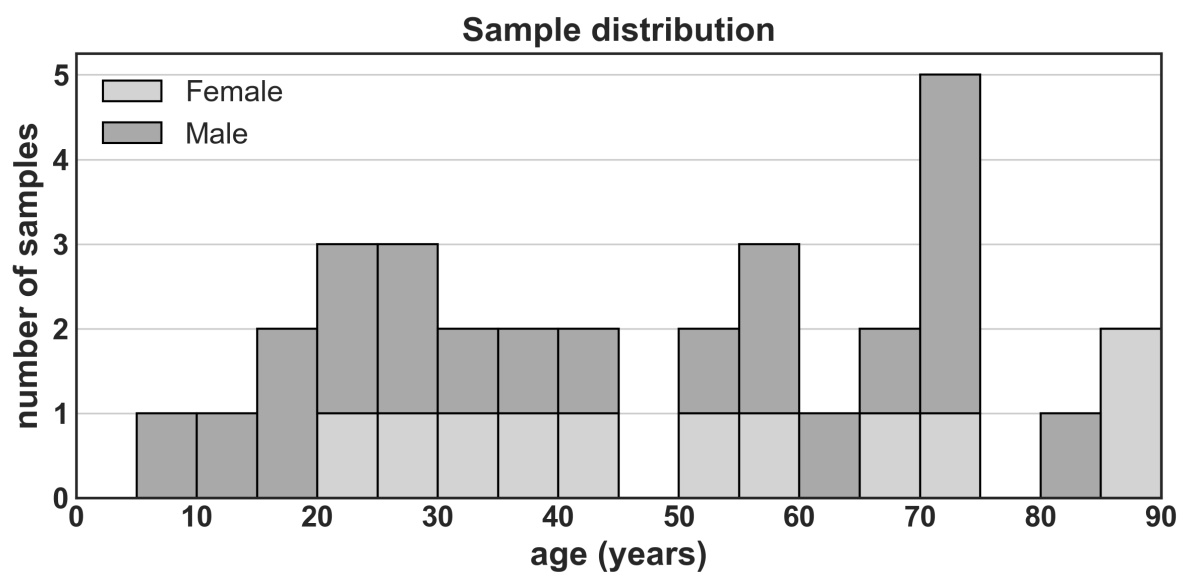


**Supplementary Material to:**

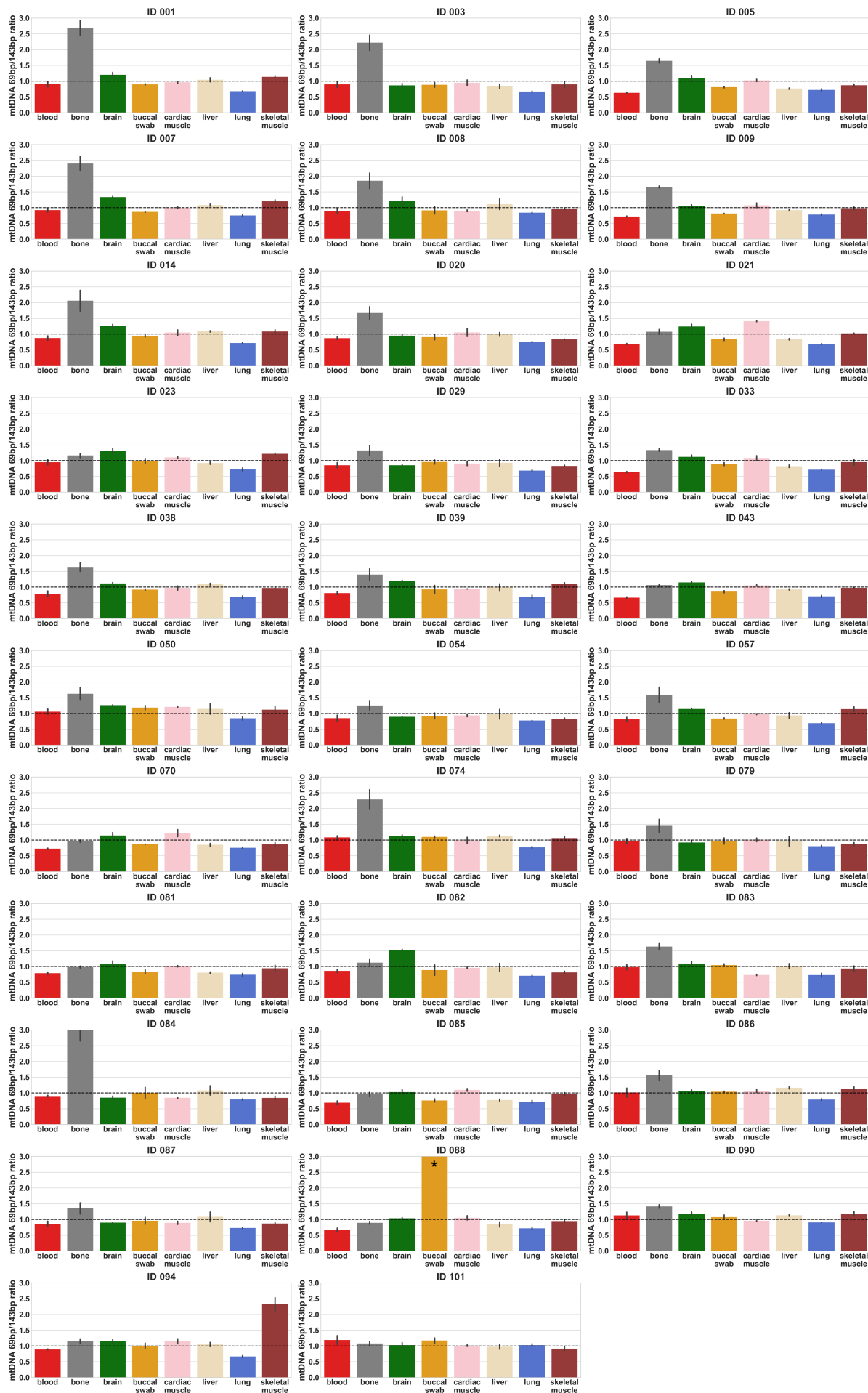
**Assessment of mitochondrial DNA copy number variation relative to nuclear DNA quantity between different tissues**

Jana Naue, Catarina Xavier, Steffen Hörer, Walther Parson, Sabine Lutz-Bonengel

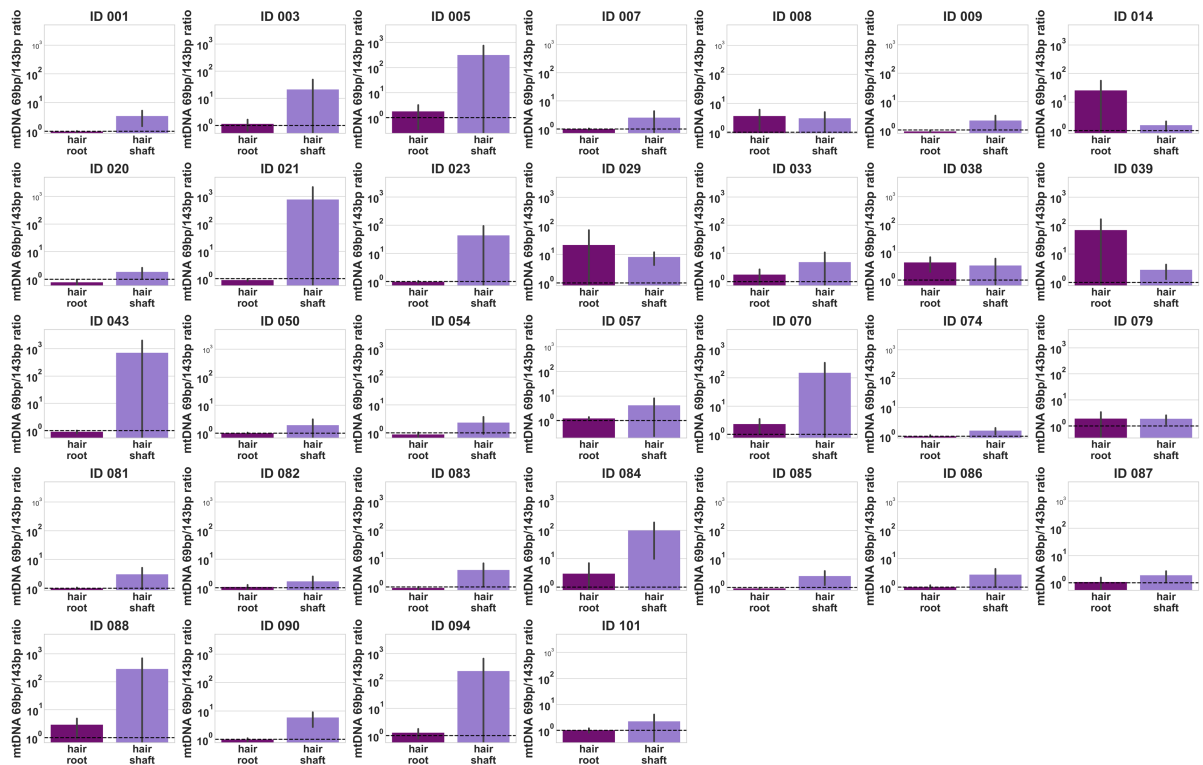


**Supplementary Figure S1: Age and gender distribution of deceased individuals.** A dataset containing individuals covering a large age range and containing both sexes was anticipated.

**A**

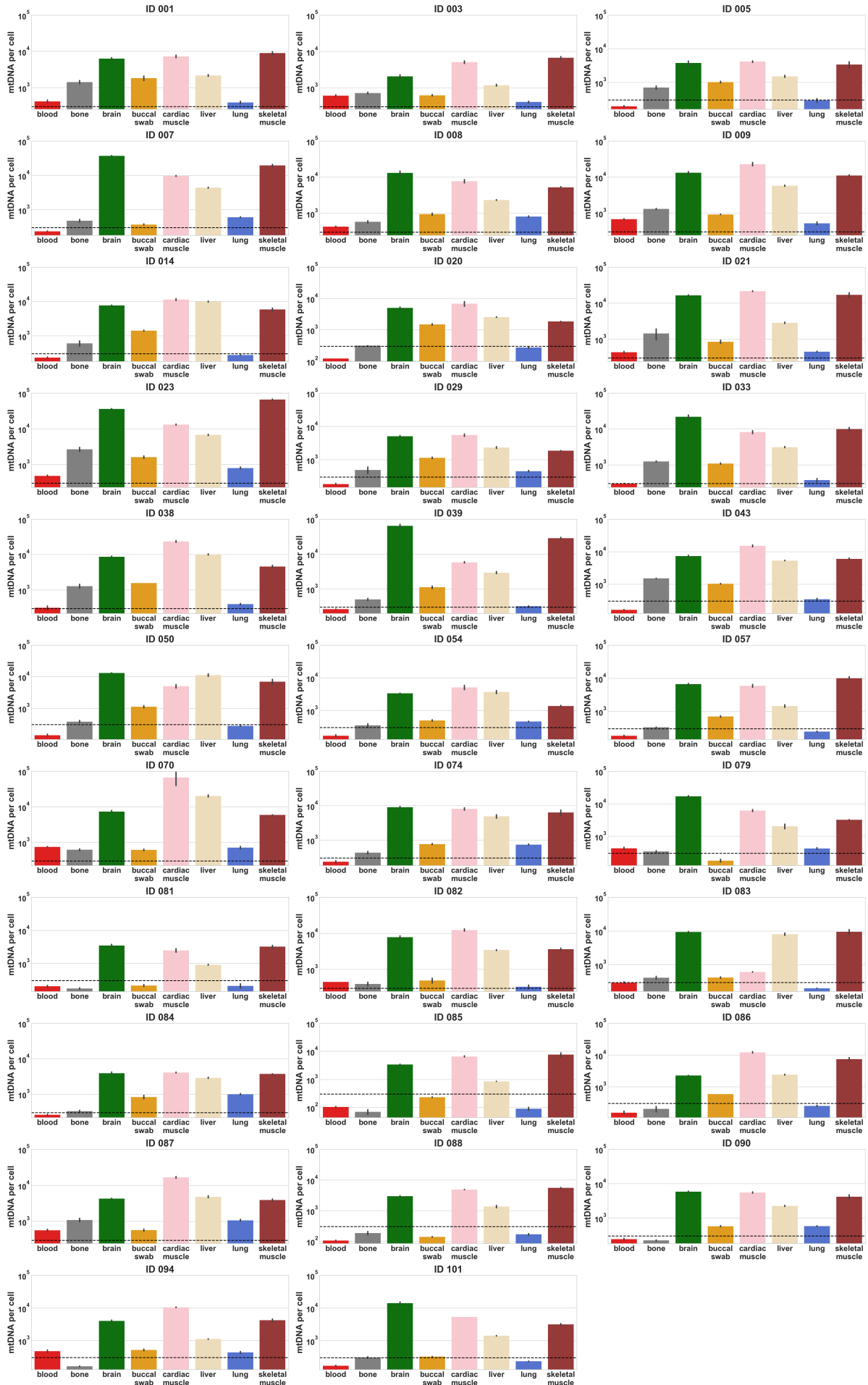


**B**

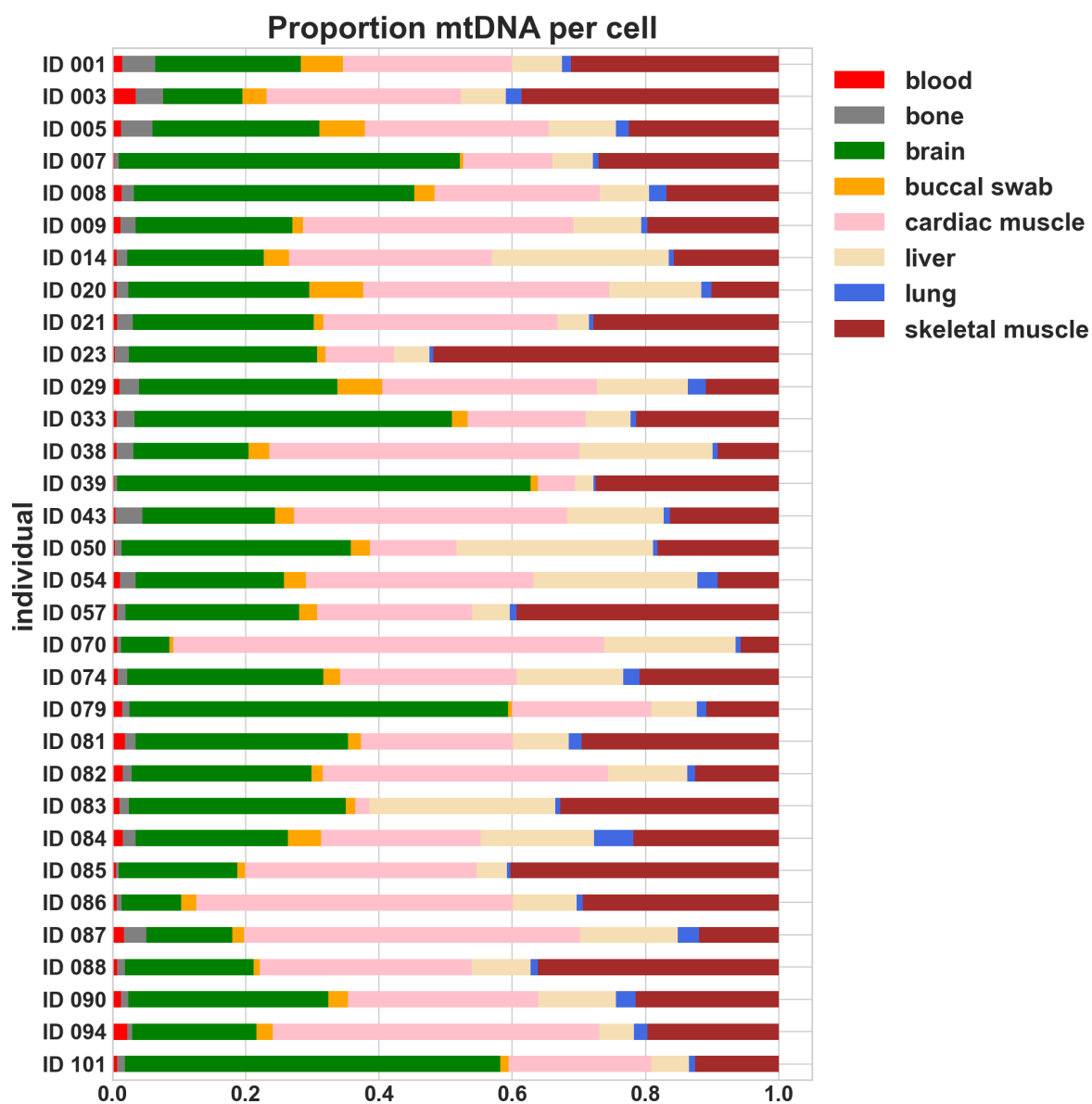


**Supplementary Figure S2: MtDNA degradation per individual.** The degradation index was calculated by dividing the shorter (69 bp) by the longer (143 bp) fragment. A: Tissue samples. B: Hair samples with log<sub>10</sub>-scale. \*outlier value of 255.6 (scale not adapted for better visualization)

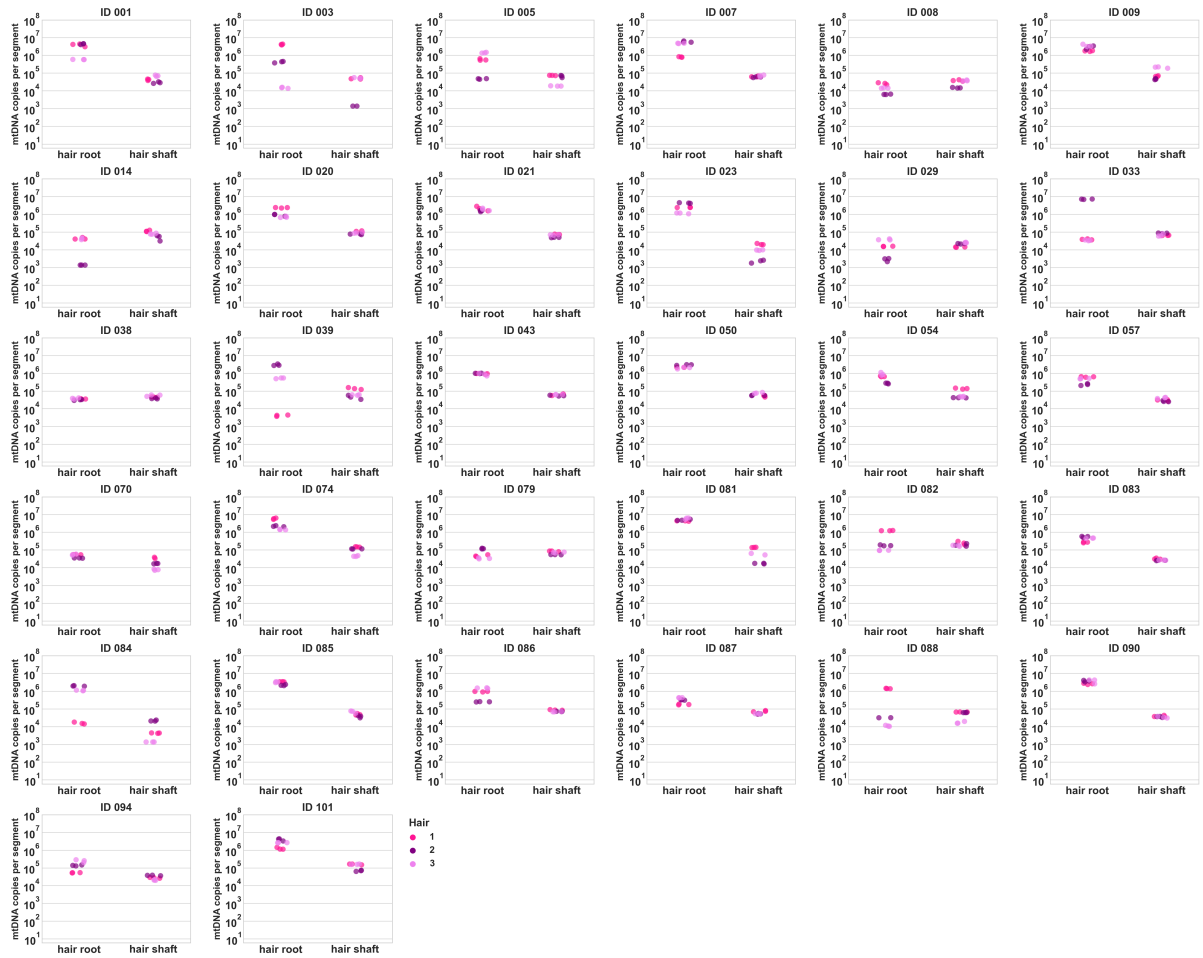
A



B



**Supplementary Figure S3: MtDNA content per individual.** The mtDNA content was calculated using the 69 bp mtDNA fragment. A: mtDNA content per tissue and individual. Dashed line: 300 mtDNA copies B: Relative mtDNA content within the different tissues (except for hair) per individual.



**Supplementary Figure S4: MtDNA content in hair per individual.** The mtDNA content per 1 cm hair segment was calculated using the 69 bp mtDNA fragment. Technical and biological replicates are presented as single dots to show the variation between hairs as well as technical fluctuations.