

Supplementary Figures Legends

Supplementary Figure S1. Two techniques of quantification of nucleic acid concentration – fluorometric based using Qubit and spectrophotometric using NanoDrop – give similar results for both RNA and DNA irrespective of extraction method. **(A)** Concentration of RNA, extracted with *Protocol_O*. **(B)** Concentration of RNA, extracted with *Protocol_P*. **(C)** Concentration of DNA, extracted with *Protocol_O*. **(D)** Concentration of DNA, extracted with *Protocol_P*.

Supplementary Figure S2. 260/230 ratio does not differ significantly between samples isolated with protocols *O* and *P*, and is positively correlated with amounts of purified nucleic acids. **(A)**. Comparison between 260/230 ratios for RNA, isolated with *Protocol_O* versus *Protocol_P*. Pooled data from all samples, irrespective of the organ of origin. Statistic comparison was performed only if samples isolated with both protocols were available ($n = 20/28$; paired t-test, $p = 0.215$) **(B)**. Comparison between 260/230 ratios for DNA, isolated with *Protocol_O* versus *Protocol_P*. Pooled data from all samples, irrespective of the organ of origin. Statistic comparison was performed only if samples isolated with either protocol were available ($n = 28/28$; paired t-test, $p = 0.497$). **(C)**. Linear correlation between 230/260 ratios and RNA concentration, irrespective of the purification protocol used and organ of origin. **(D)**. Linear correlation between 230/260 ratios and RNA concentration, irrespective of the purification protocol used and organ of origin.

Supplementary Figure S3. Suitability of samples extracted with *Protocol_P* for RT-qPCR. Comparison of expression of *ACTB* using RNA extracted with **(A)** *Protocol_PC+O* versus *Protocol_P* (phenol-chloroform extraction) and **(B)** *Protocol_O* versus *Protocol_P*. **(C)** Linear correlation between the percentage share of 5S peak and the difference between RT-qPCR outcome (Ct) between samples isolated with *Protocol_O* versus *Protocol_P*.

Supplementary Figure S4. Analysis of levels of low-abundant transcripts, using RNA extracted with *Protocol_O* versus *Protocol_P*. Samples where no transcript was detected were given a Ct = 41 for illustrative purposes. Horizontal line on the graph refers to the last amplification cycle, Ct = 40. **(A)** *CDKN1A*, **(B)** *Gli1*, **(C)** – *IL-8*, **(D)** – *Hes5*, **(E)** – *Rad51*, **(F)** – *MYC*, **(G)** – *TP53*, **(H)** – *USP2* (All gene expression assays are from Applied Biosystems; a detailed list can be found in supplementary table S3).