## Supplementary Material



Figure S1: Results of stability analysis of blood plasma samples using the DBS method. Mass-to-charge values (m/z) selected to characterize changes in the content of DBS samples are indicated on the right axis; p-values for between-samples comparison are indicated in square brackets. Data are represented for pretreatment protocols.

## Supplementary Material

Analysis of DBS (dried blood spots) plasma-derived proteins composition has been performed according to the Protocol #1 and Protocol #2 (see details in the main text) after storage at different temperature conditions (-20°C, +4°C and +25°C) during 7, 14, 21 and 30 days after deposing the sample. The stability assay was conducted using MALDI-TOF mass spectrometry (see subsection 2.5 MALDI-TOF-MS Analysis in the main text). Samples stability was evaluated using ten selected m/z-signatures utilized in both Protocols of samples preparation and indicating alterations in the sample under the certain storage condition to select the most proper Protocol of samples storage. Figures S1 and S2 demonstrate typical spectra of the plasma-derived proteins extracted according the Protocol #1 and Protocol #2.

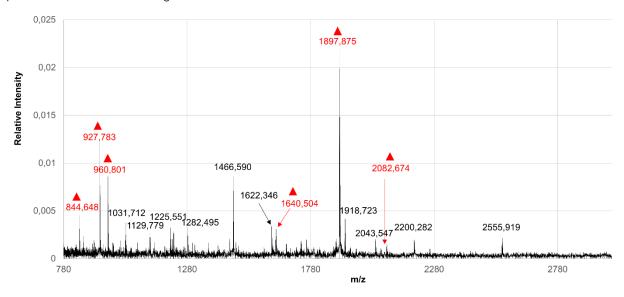


Figure S2: MALDI-TOF mass spectra obtained from the proteins extracted by the Protocol #1. The sample was stored at the temperature t= - 20°C for 35 days. Spectra was acquired using Autoflex III time-of-flight mass-spectrometer (Bruker, Germany) after accumulation of 50,000 laser shots (see details in the main text). Picked peaks are characterized by signal-to-noise ration of SNR >5. The spectrum data are represented after smoothing and normalization as described in the subsection 2.6 Statistical Analysis. Red arrows indicate m/z-signatures used for the sample stability evaluation.

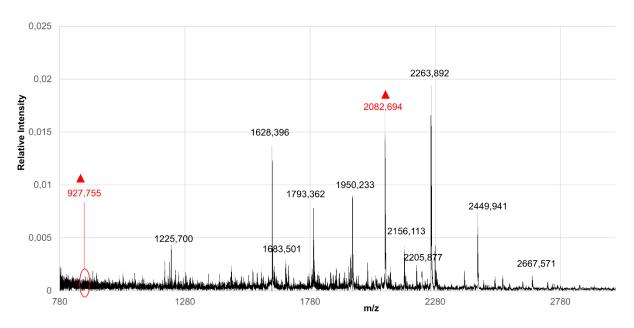


Figure S3: MALDI-TOF mass spectra obtained from the proteins extracted by the Protocol #2. The sample was stored at the temperature t= + 4°C for 1day after sample deposition. Spectra was acquired using Autoflex III time-of-flight mass-spectrometer (Bruker, Germany) after accumulation of 50,000 laser shots (see details in the main text). Picked peaks are characterized by signal-to-noise ration of SNR >5. The spectrum data are represented after smoothing and normalization as described in the subsection 2.6 Statistical Analysis. Red arrows indicate m/z-signatures used for the sample stability evaluation.

Table 1. The p-value for the comparison groups of biosamples for the selected 10 mass-charge characteristics (m/z). 0 day of storage versus day 7 (column 7th day), 0 day versus day 14 of storage (column 14th day), 0 day versus 35-20 days of storage (column 35th day) for different temperature conditions. The background indicates the comparison groups for which p <0.05

	PROTOCOL 1				PROTOCOL 2		
-20°C, p-value							
m/z	7 <sup>th</sup> day	14th day	35th day	7th day	14th day	35th day	
780.834	0.014	0.24	0.0034	0.48	0.64	0.55	
808.848	0.0036	0.24	0.00084	0.35	0.43	0.55	
844.621	0.057	0.44	0.55	0.48	0.43	0.17	
927.760	0.0036	0.0036	0.0059	0.76	0.64	0.55	
949.726	0.0036	0.039	0.0034	0.61	0.43	0.71	
960.794	0.0036	0.0036	0.1	0.91	0.64	0.9	
1018.72	0.0036	0.0036	0.00084	0.48	0.86	0.26	
1640.49	0.0036	0.025	0.7	0.26	0.071	0.0095	
1897.50	0.014	0.44	0.0034	0.26	0.29	0.095	
2082.66	0.057	0.15	0.032	0.067	0.071	0.38	
+4°C, p-value							
780.834	0.17	0.036	0.47	0.82	0.48	0.82	
808.848	0.038	0.015	0.18	0.82	0.26	0.82	
844.621	0.93	0.56	0.000074	0.82	0.35	0.59	
927.760	0.019	0.12	0.029	0.82	0.48	0.59	
949.726	0.019	0.036	0.11	0.94	0.48	0.94	
960.794	0.3	0.036	0.017	0.94	0.48	0.7	
1018.72	0.11	0.69	0.0032	0.18	0.17	0.39	
1640.49	1	0.38	0.0014	0.94	0.48	0.13	
1897.50	0.019	0.021	0.036	0.396	1	0.026	
2082.66	0.038	0.6	0.52	0.39	0.26	0.071	
+25°C, p-value							
780.834	0.039	0.019	0.01	0.48	1	0.76	
808.848	0.0036	0.019	0.00084	0.48	0.29	1	
844.621	0.3	0.019	0.16	0.019	0.071	0.0095	
927.760	0.0036	0.0036	0.0059	0.11	0.64	0.16	
949.726	0.0036	0.0019	0.00084	0.61	0.64	0.76	
960.794	0.0036	0.019	0.00084	0.91	0.64	0.61	
1018.72	0.082	0.019	0.00048	0.26	0.64	0.35	
1640.49	0.61	0.019	0.045	0.038	0.071	0.0095	
1897.50	0.24	0.019	0.2	0.61	0.071	0.0095	
2082.66	0.8	0.8	0.7	0.019	0.071	0.019	