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**SUPPLEMENTARY MATERIALS**

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**IDENTIFICATION OF HUMAN BLOOD PLASMA PROTEINS USING SPIKE-IN PEPTIDES IN SHOTGUN PROTEOMICS**

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**Figure1.** Results of co-alignment in Progenesis software of LC-MS runs of a mixtures samples of proteolytic peptides of human blood plasma (SamplePP) and samples of the same mixtures with added spike-in stable isotope-labeled synthetic peptides (SampleSP). The ion intensity map regions of all aligned runs shown here have matching RTs and m/z. Ion maps: ‘magenta’ – alignment target; ‘green’ – the run being aligned.

**Figure2.** SRM identification of the peptides of human blood plasma accepted in the course of quality control. Shown chromatograms of native and stable isotope-labeled synthetic (heavy) peptide (see Manuscript, Table 1) from the Skyline software.