Supplementary file for Blood targeted proteomics:

Centrifugal filter sample preparation vs dilute-and-shoot

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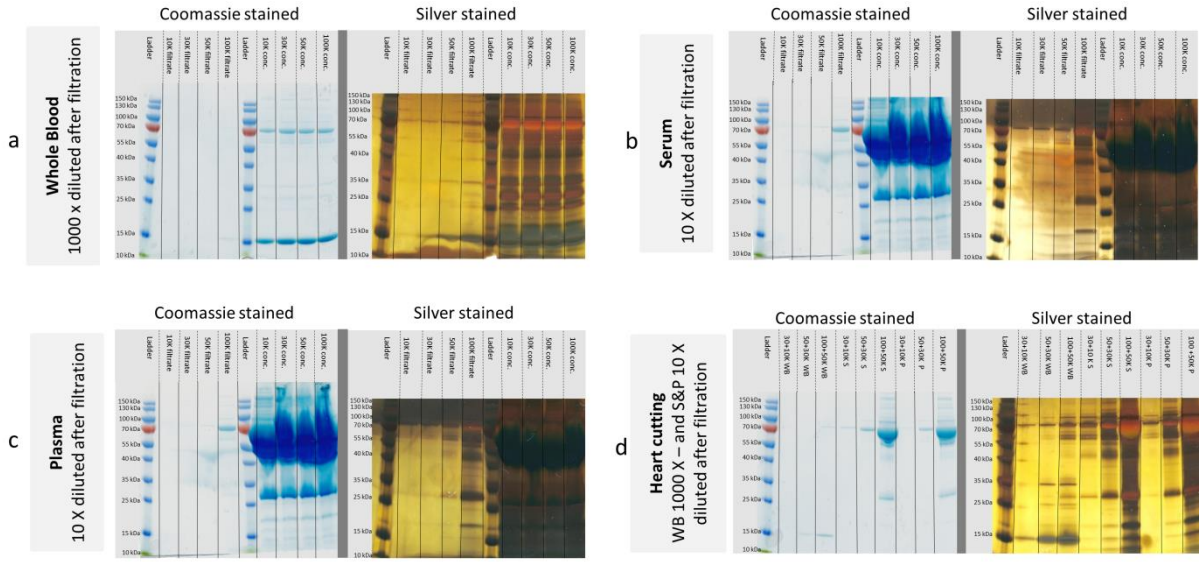
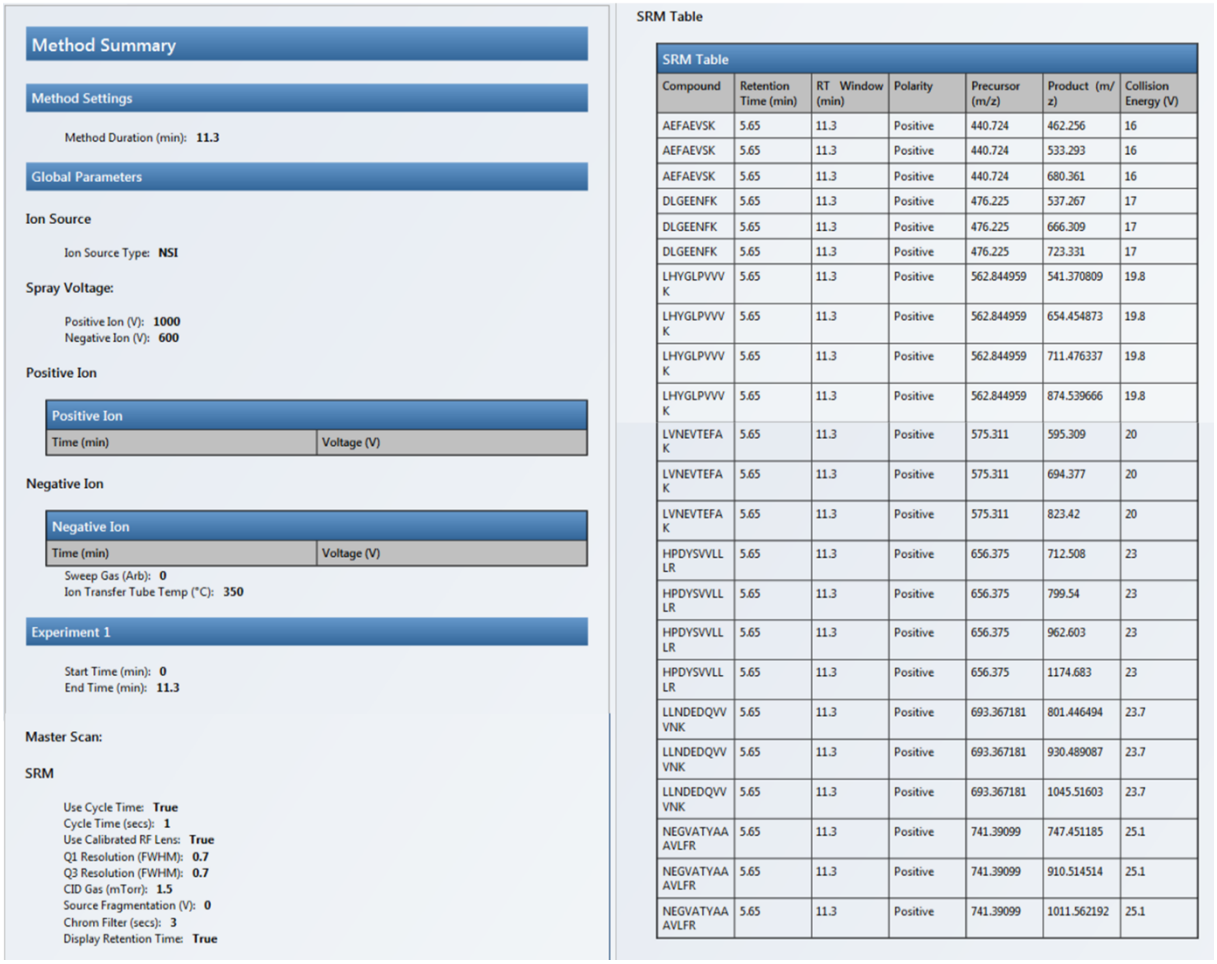


Figure S1: Coomassie and silver stained GE results for filtrates and concentrated samples from whole blood (a), serum (b), plasma (c) and whole blood, serum and plasma with the filter combinations (d). The whole blood filter samples were diluted 1000 times before GE so that the gel was not overloaded, while serum and plasma was 10 times diluted before GE.



Method Summary

Method Settings

Method Duration (min): **11.3**

Global Parameters

Ion Source

Ion Source Type: **NSI**

Spray Voltage:

Positive Ion (V): **1000**
Negative Ion (V): **600**

Positive Ion

Positive Ion	
Time (min)	Voltage (V)

Negative Ion

Negative Ion	
Time (min)	Voltage (V)

Sweep Gas (Arb): **0**
Ion Transfer Tube Temp (°C): **350**

Experiment 1

Start Time (min): **0**
End Time (min): **11.3**

Master Scan:

SRM

Use Cycle Time: **True**
Cycle Time (secs): **1**
Use Calibrated RF Lens: **True**
Q1 Resolution (FWHM): **0.7**
Q3 Resolution (FWHM): **0.7**
CID Gas (mTorr): **1.5**
Source Fragmentation (V): **0**
Chrom Filter (secs): **3**
Display Retention Time: **True**

SRM Table

SRM Table

Compound	Retention Time (min)	RT Window (min)	Polarity	Precursor (m/z)	Product (m/z)	Collision Energy (V)
AEFAEVSK	5.65	11.3	Positive	440.724	462.256	16
AEFAEVSK	5.65	11.3	Positive	440.724	533.293	16
AEFAEVSK	5.65	11.3	Positive	440.724	680.361	16
DLGEENFK	5.65	11.3	Positive	476.225	537.267	17
DLGEENFK	5.65	11.3	Positive	476.225	666.309	17
DLGEENFK	5.65	11.3	Positive	476.225	723.331	17
LHYGLPVVVK	5.65	11.3	Positive	562.844959	541.370809	19.8
LHYGLPVVVK	5.65	11.3	Positive	562.844959	654.454873	19.8
LHYGLPVVVK	5.65	11.3	Positive	562.844959	711.476337	19.8
LHYGLPVVVK	5.65	11.3	Positive	562.844959	874.539666	19.8
LVNEVTEFAK	5.65	11.3	Positive	575.311	595.309	20
LVNEVTEFAK	5.65	11.3	Positive	575.311	694.377	20
LVNEVTEFAK	5.65	11.3	Positive	575.311	823.42	20
HPDYSVVLLLR	5.65	11.3	Positive	656.375	712.508	23
HPDYSVVLLLR	5.65	11.3	Positive	656.375	799.54	23
HPDYSVVLLLR	5.65	11.3	Positive	656.375	962.603	23
HPDYSVVLLLR	5.65	11.3	Positive	656.375	1174.683	23
LLNDEDQVVVNK	5.65	11.3	Positive	693.367181	801.446494	23.7
LLNDEDQVVVNK	5.65	11.3	Positive	693.367181	930.489087	23.7
LLNDEDQVVVNK	5.65	11.3	Positive	693.367181	1045.51603	23.7
NEGVATYAAAVLFR	5.65	11.3	Positive	741.39099	747.451185	25.1
NEGVATYAAAVLFR	5.65	11.3	Positive	741.39099	910.514514	25.1
NEGVATYAAAVLFR	5.65	11.3	Positive	741.39099	1011.562192	25.1

Figure S2: Summary of SRM MS-method for in-solution digested beta-catenin and HSA.SRM table includes precursor ions (*m/z*) and its product ions (*m/z*) for beta-catenin and HSA peptides. The precursor and product ions were generated by Skyline software.

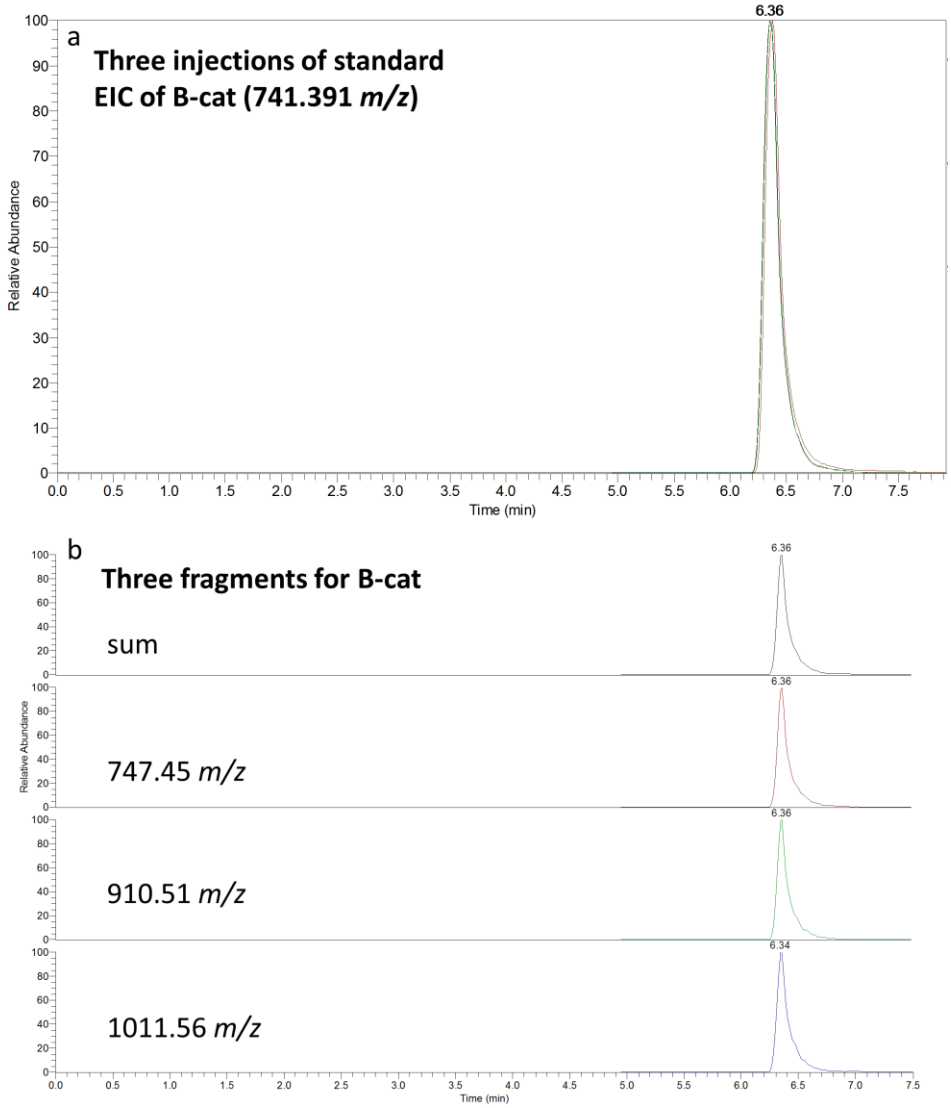


Figure S3: (a) Three injections of in-solution digested beta-catenin peptide NEGVATYAAAVLFR (741.391 *m/z*) to illustrate the repeatability of the LC-MS system. (b) Three fragments (747.45, 910.51 and 1011.56 *m/z*) confirming the beta-catenin peptide NEGVATYAAAVLFR.