

SUPPLEMENTAL FIGURE LEGENDS

Fig s1. Examples of automated fits obtained with the Nonprofit software. A fit to a small section of the average spectrum is shown together with the corresponding fits associated with two individual samples from patients with (lane 27 of Fig 1) and without (lane 10 of Fig 1) bone metastases.

Fig s2. Identification of proteins at 11.7 kDa using preparative 2D gels, PMF and MS/MS. **A**, a sample from a patient without bone metastasis (WO) and with bone metastasis (BM) group were separated on 2D gels optimized for the mass range of interest where 4 unique spots were observed in the BM sample. WO and BM correspond to lanes 8 and 37 respectively of Fig. 1. **B**, amino acid sequence of unprocessed SAA with the first 16 amino acids being the signal peptide [1,16] MKLLTGLVFCSLVLGV. Boxed amino acids are variable in different variants of SAA. Barred sequences were identified by PMF shown in C. **C**, representative MALDI-TOF spectra of spot 4 in-gel tryptic digestion with the 8 most prominent peaks labelled. Peptide mass fingerprinting using Mascot was conducted and spot 4 was putatively identified as serum amyloid A1 with a score of 80 and expect value of 0.014 (searched against MSDB, with 1 missed tryptic cleavage allowed). Peaks labelled with an (*) were involved in the Mascot hit. **D**, Representative MS/MS spectra of the 2178.0 Da (M+H)⁺ ion. Identity of the 2178.0 Da (M+H)⁺ peptide was confirmed as FFGHGAEDSLADQAANEWGR from serum amyloid A with a Mascot ion score of 131 and expect value of 3.6×10^{-11} . Observed b- and y-ion species involved in the Mascot identification are labeled and underlined in the peptide sequence.