



Figure S1: ITIH5^{681aa} purified from HEK supernatant and analyzed by 2D-SDS-Page analyses. **(A)** Scheme of the truncated ITIH5 protein including the VIT and vWA domains. SP: signal peptide; VIT: Vault Inter-Trypsin domain; vWA: von Willebrand factor type-A domain according to EMBOSS 6.3.1:sigcleave, Ensembl.org, and PFAM.sanger.ac.uk. **(B)** Coomassie-stained 2D gel (upper image) of the supernatant of cultured human HEK cells after transfection with cloned pMS-L-A-IV vectors. Lower image shows the corresponding anti-(His)tag western blot analysis in a pH range of 3-11 and a mass range of 40-120 kDa. **(C)** Confirming the ITIH5^{681aa} by mass spectrometric PMF assays (MALDI-TOF). Shown gel highlights regions included in the PMF analysis (white bordered). The following data are based on the spot marked with an asterisk. **(D)** Exemplary PMF spectrum of a trypsin-digested spot. The signals (here: shown for the highest signal values #1-#10) could be assigned to the mass of corresponding peptide sequences **(E)** of the ITIH5^{681aa} fragment with a score of 157. Used PMF parameters were selected as follows: *Organism*: Homo sapiens; *Enzyme*: Trypsin; variable modification: oxidation (M); mass value: monoisotopic; protein mass: Unrestricted; Peptide mass tolerance limit: ± 0.8 Da; Number of mass value searches: 13.