Supplementary File 1 Summary of mass spectrometry results for the three types of samples

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|  | **Samples** |  | **Peptides** |  | **PSM** |  | **Proteins** |  | **MeOx** |  | **NQ** |  | **Data depiction**  |
| **Citrate plasma** | 3 |  | 770 |  | 2827 |  | 65 |  | 126(4.5%) |  | 87(3.1%) |  | F3 SD1 |
| **Acute wound fluids** | 5 |  | 7809 |  | 47228 |  | 373 |  | 10243(21.7%) |  | 3009(6.4%) |  | F1-4 SF2, SD2 |
| **Dressing extracts** | 6 |  | 10789 |  | 52091 |  | 418 |  | 5059(9.7%) |  | 1774(3.4%) |  | F5-8, F5FS1SF3, SD3  |
|  |  |  |  |  |  |  |  |  |  |  |  |  | **Proteins** |

Total numbers of unique samples, identified unique peptides, peptide spectrum matches (PSM), and unique proteins. Furthermore, total numbers and percentages of peptides with post translational modifications (MeOx: methionine oxidation; NQ: deamidation) are indicated. Finally, it is indicated in which figures (F), figure supplements (FS), supplementary files (SF), and supplementary datasets (SD) the results of the sample analyses are shown.