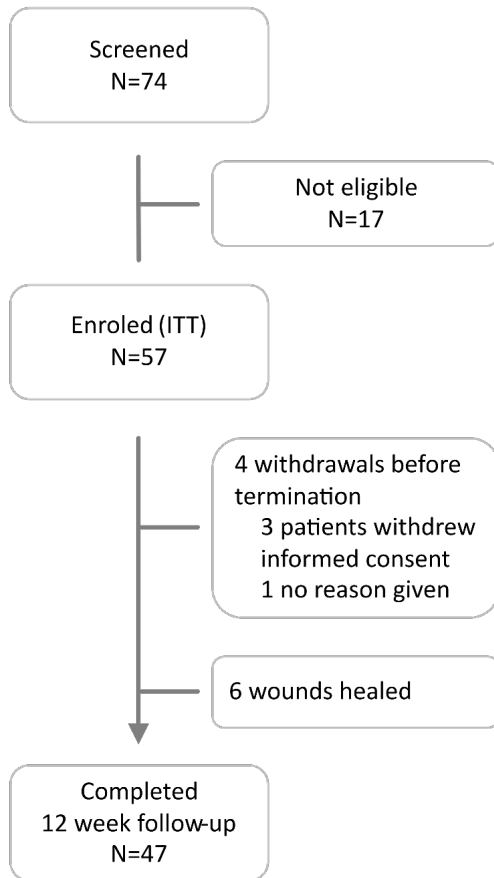


Fig. S1. Patient flow of the ITT study population.

A



B

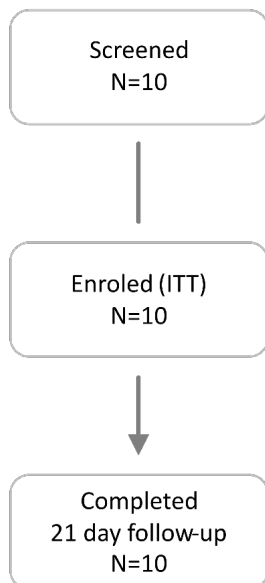


Fig. S2. Comparative proteome analysis of wound exudates extracted from Medicomp® (MEC) and HydroClean® (HYC) wound dressing. A Venn diagram of all proteins identified in either MEC or HYC exudates (supplementary Tables S9 and S10, respectively) using unique gene names (PG.Genes) as identifiers. B Venn diagram of the top 100 most abundant (PG.Label-Free Quant) proteins extracted from each dataset. C Comparison of protein abundances determined by label-free quantification (LFQ) for proteins identified in both proteomes, indicating no systematic shift between exudates from either dressing type.

