**Table S1. Tryptic peptides identified from healthy and infected mouse proteomes**

1Monoisotopic mass, [M+H+]+1

2Except for *m/z* 1819.88, all peptides were identified after LIFT sequencing directly from tissue. The fragmentation spectra are given in Supplementary Fig. S5B. For *m/z* 1819.88, MS/MS spectrum from on-tissue sequencing was not informative. The peptide was sequenced after LIFT fragmentation from a lesion-enriched tissue extract, which was submitted to in-solution digestion using standard protocols, followed by spotting onto MALDI plate and data acquisition.

3Proteins identified in the course of the analysis, with NCBI access numbers given in parentheses. The identification parameters are given in Figure S5.

4Spectral abundance of the individual peptides was determined in the course of ROC curve analysis with ClinProTools 2.2 software (Bruker), according to manufacturer’s recommendations. Increased abundance was defined when AUC≥0.85 in multiple pair-wise comparisons (2 vs. 2 biological replicates, and 3 vs. 3 biological replicates).