Figure 1S. Network representation of the interconnected elements in the proteome data from STAT1/STAT2. a: components of the antiviral response, b: components of the MHC and proteasome. Color intensities represent protein changes in treated samples compared to cell control, as indicated in the bar intensity color according to Student's T-test Difference LFQ intensity HF_LFQ intensity CC (log2 (Fold change)) from Table 2S. Bisogenet (v.3.0.0) plugin was used on the Cytoscape framework (v.3.8.2). HF: HeberFERON; CC: cell control.