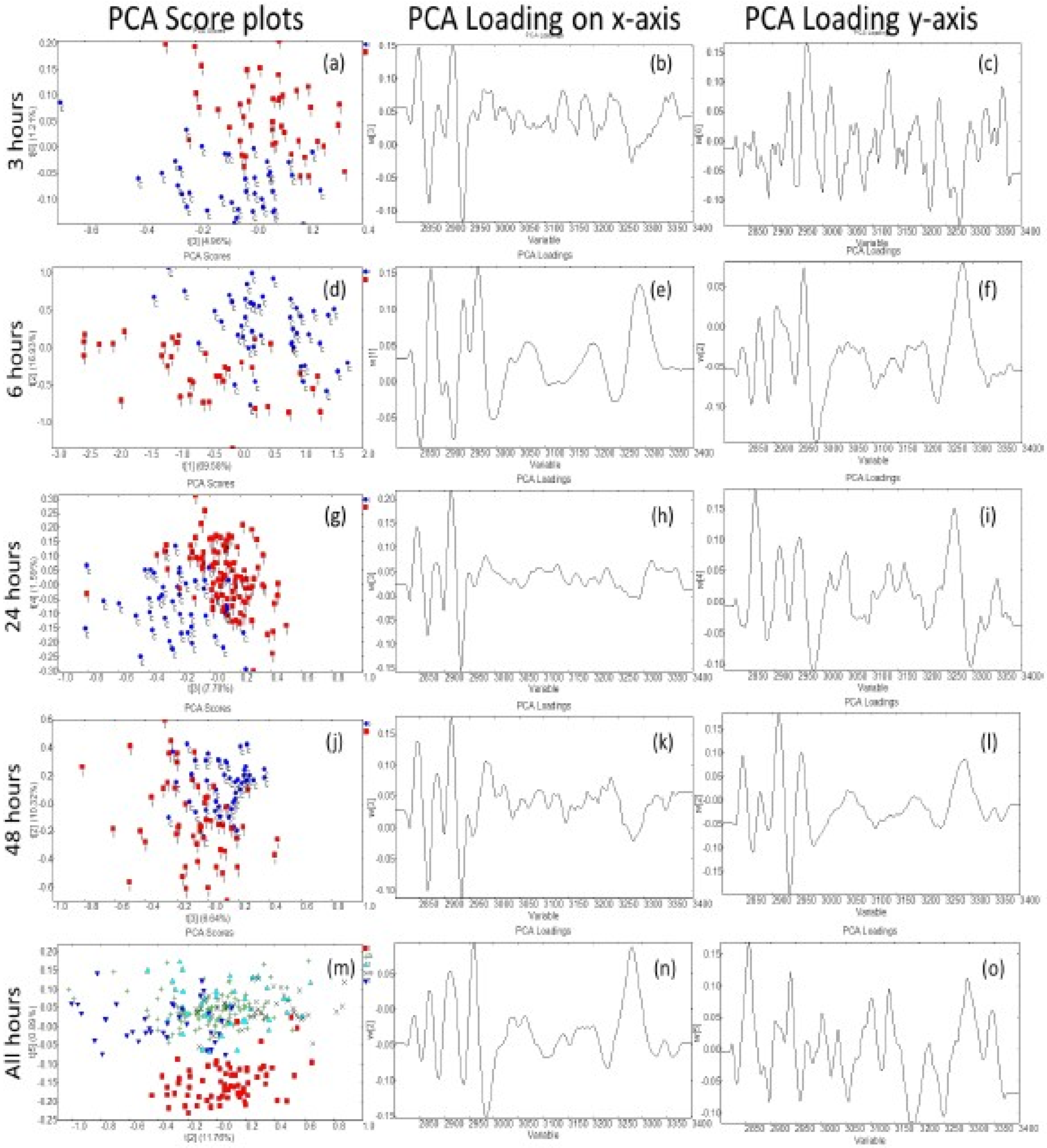

Fig. S1 The score and loading plots of the PCA of infected (red◷) and control (blue•) hBMECs at various hours after infection in the 3400–2800 cm^{-1} region. The bottom row is the PCA of the spectral data from all hours where 0, 3, 6, 24 and 48 hours are respectively denoted by red ◷, turquoise ☐, blue ❑, green + and black + symbols.

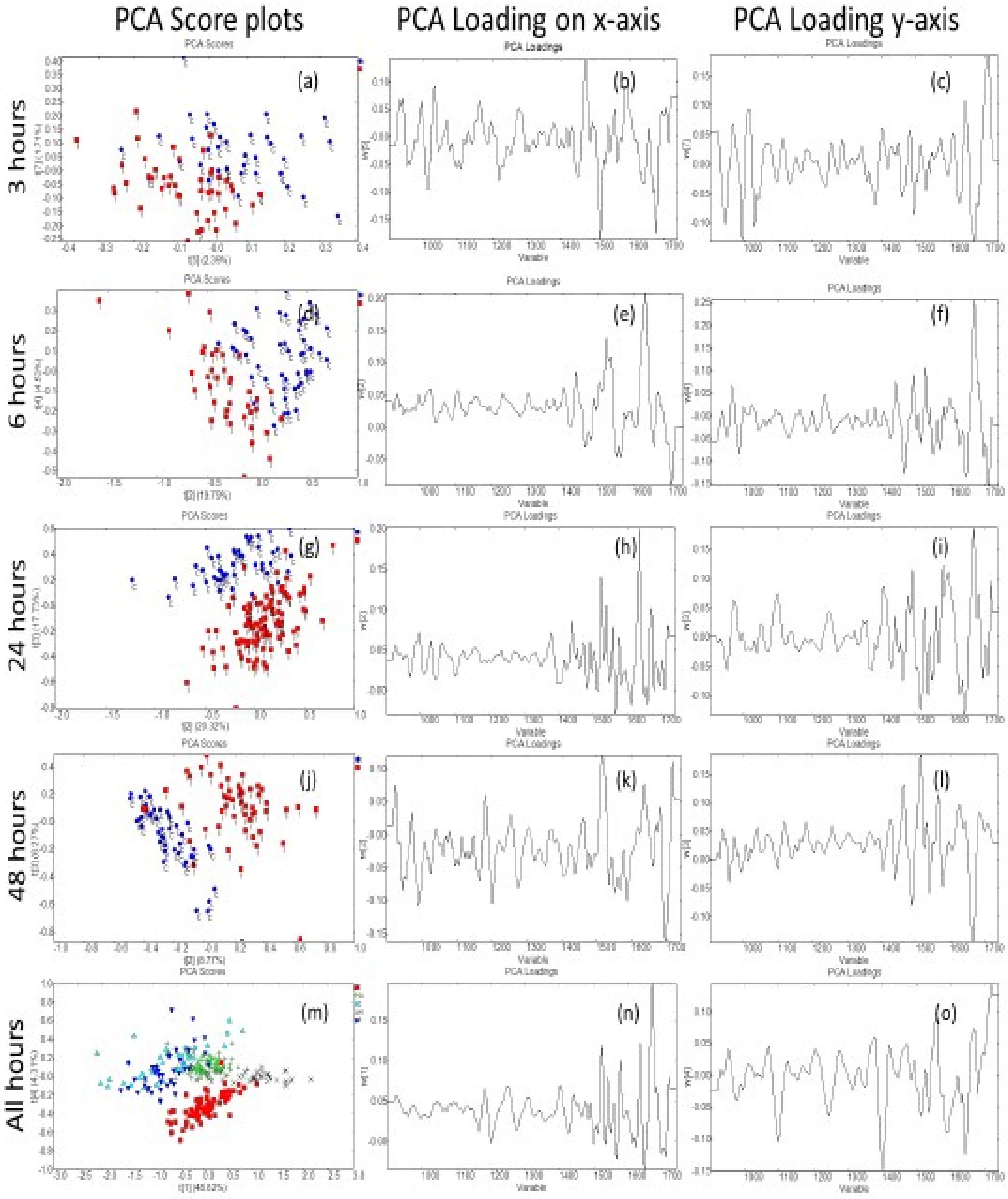

Fig. S2 The score and loading plots of the PCA of infected (red🕘) and control (blue•) hBMECs at various hours postinfection in the 1740–900 cm^{-1} region. The bottom row is the PCA of the spectral data from all hours where 0, 3, 6, 24 and 48 hours are respectively represented by red 🕘, turquoise ◻, blue ◻, green + and black + symbols.

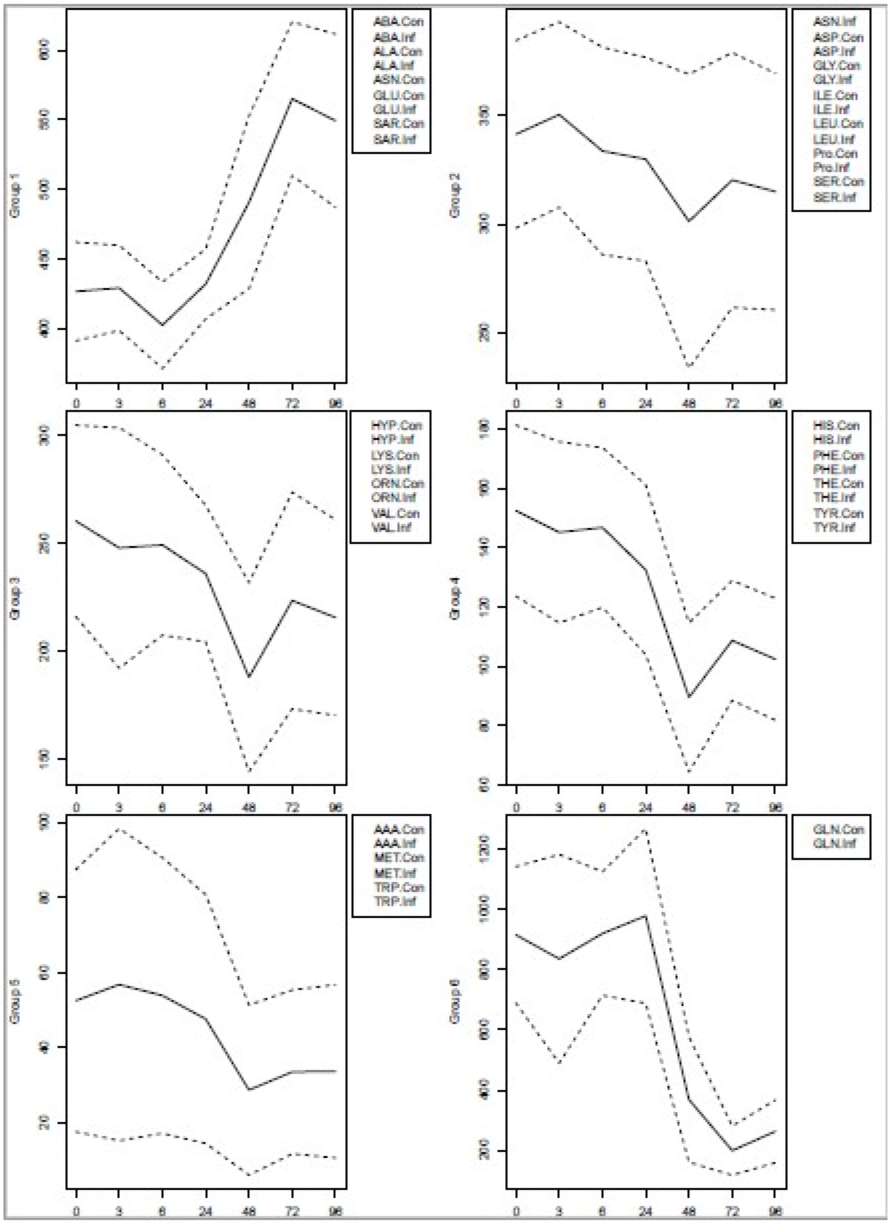

Fig. S3 The dendrogram in Figure 8 was cut to create seven groups of amino acids. The mean was calculated across the individual replicates, which constitute the amino acids in each group. Kinetic shape templates (+/- 1 s.d.) of the similar dynamic patterns of amino acids within each group are plotted. Some of the groups had similar shaped responses, but on different scales (e.g. groups 2 and 4), whereas some groups had different shaped responses (e.g. amino acids in group 1 increase concentration over time and amino acids in group 5 decrease concentration over time).

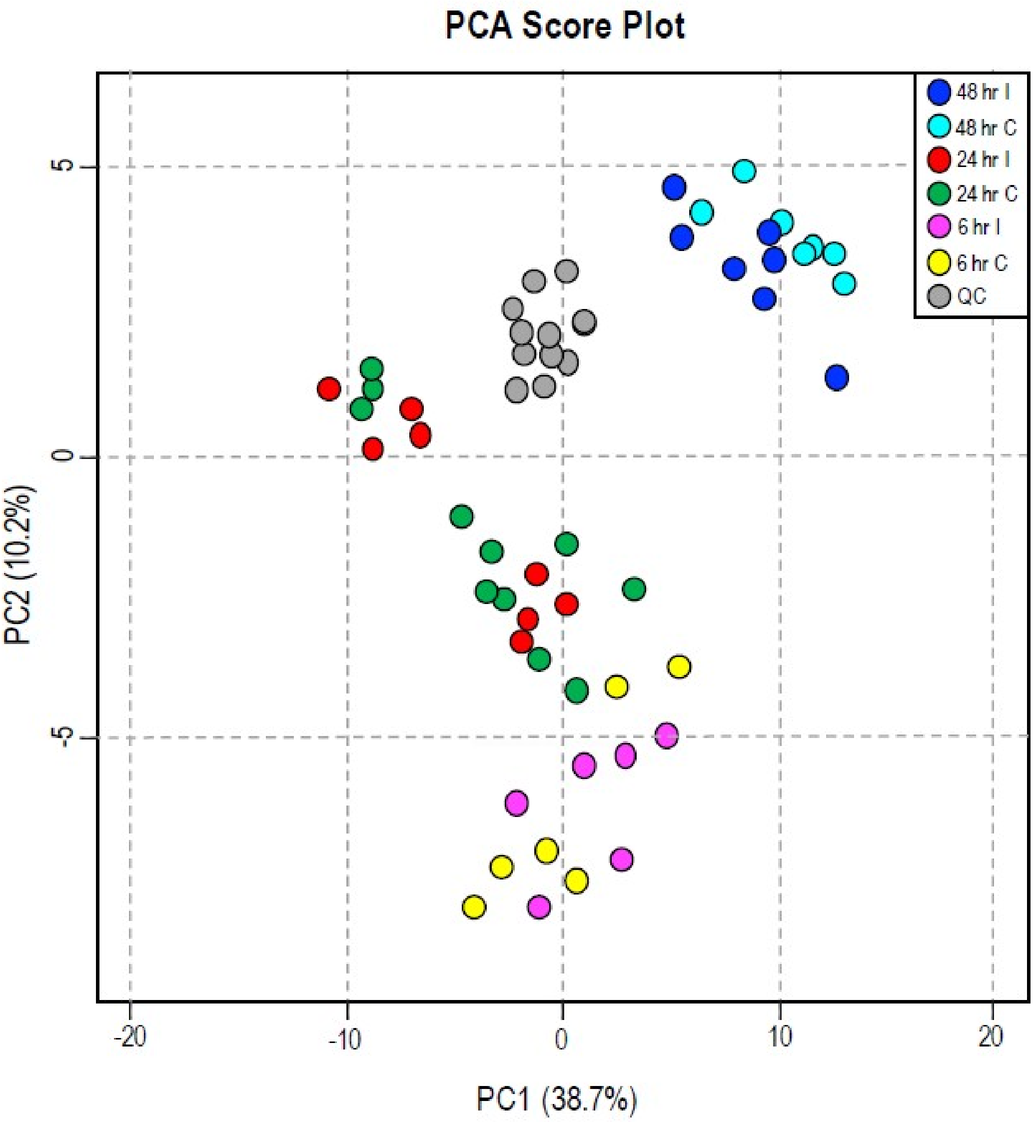

Fig. S4 PCA score plot generated from all metabolites of different samples. The metabolic profiling of infected and uninfected hBMECs at 6, 24 and 48 hours after infection was investigated using an untargeted GC-MS-based metabolomics analysis.

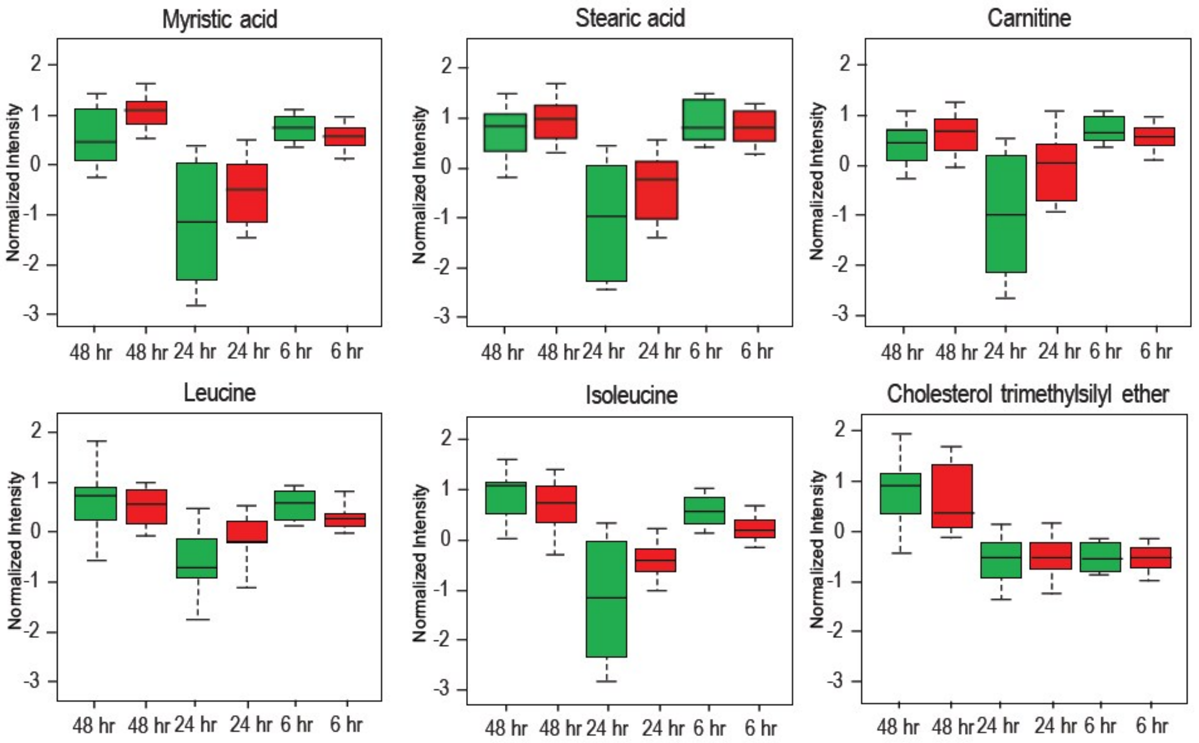

Fig. S5 Boxplot-visualization of the relative abundance of metabolites in infected and uninfected hBMECs at the indicated time points. The metabolites in infected and uninfected cells are show in red and green, respectively.