Supplementary Figure 1 - Hierarchical clustering analyses of metabolomics data of rat plasma samples in responses to hemorrhage and hemorrhagic shock

Heat map of clustered (1-Pearson correlation) of metabolic changes in rat plasma upon exposure to gradual hemorrhage (H1 to H5), prolonged hemorrhage (S10, S20) and hemorrhagic shock (Shock) in comparison to the baseline. Each square is representative of the levels of that metabolite (names and hierarchical clustering are indicated in the right handy axis of the map). Row values are Z-score normalized for each metabolite across all biological replicates per each time point, while quantitative changes are color-coded from blue (low) to red (high). Pathways assignment is provided in the right y axis of the map.
Suppl. Fig. 2 - Line plots panels showing time course metabolite trends in each rat plasma sample
Supplementary Figure 3 - Metabolite measurements in Sham rat plasma samples
Supporting Figure 4 - Amino acid data elaboration. Amino acid fold-change enrichment in Shock samples vs baseline, in comparison to their observed frequency in vertebrates, as roughly estimated from the codon frequency in the known vertebrate genomes.