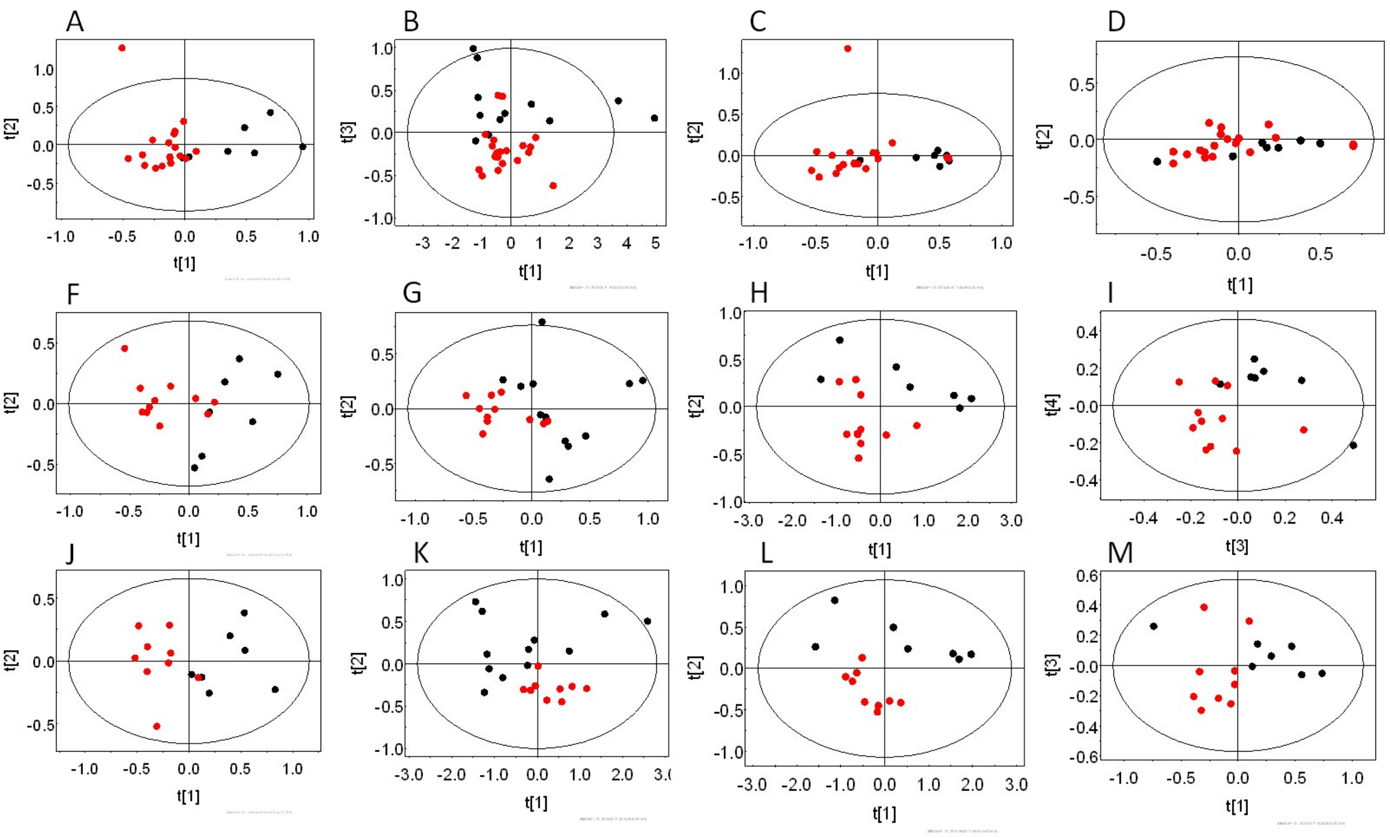
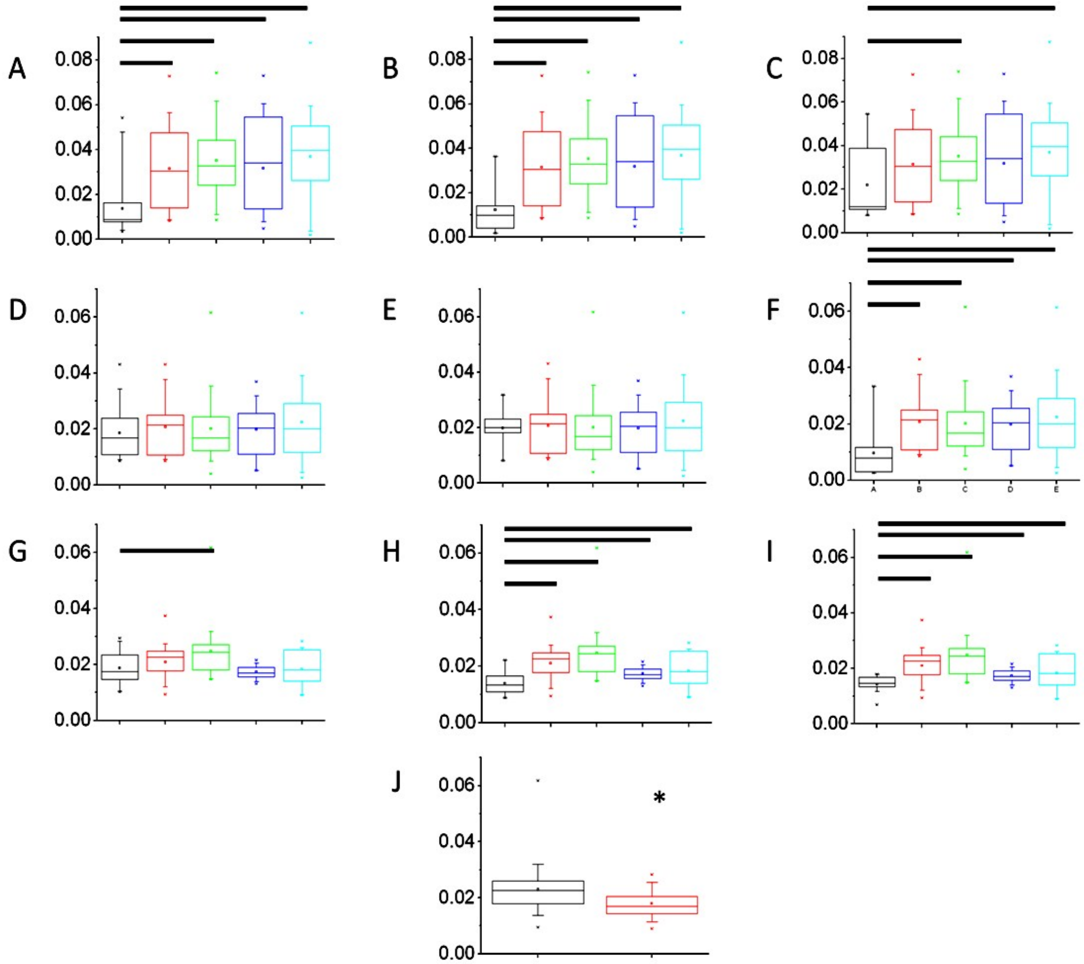
Supplementary information

Supplementary information S1



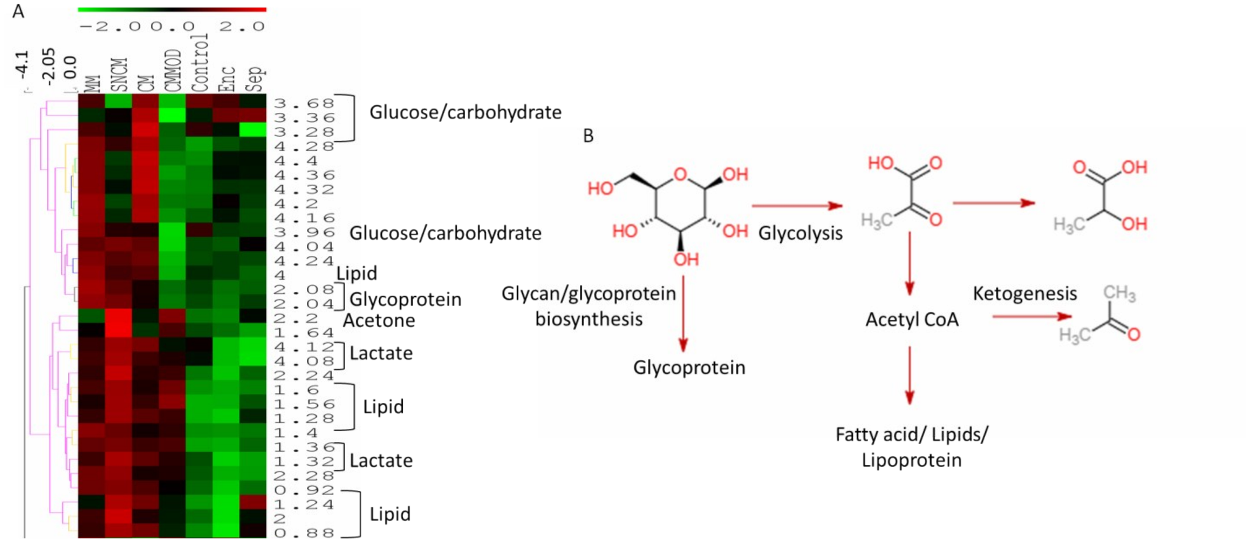
The PCA scores plots of the serum NMR profiles of the different malaria infected subtypes with different control population. A – D: malaria infected subtypes compared with uninfected controls, F – I: malaria infected subtypes compared with sepsis patients and J – M: malaria infected subtypes compared with encephalitis patients. A/F/J: MM, B/G/K: SNCM, C/H/L: CM and D/I/M: CMMOD. Black – malaria subtype and red – relevant control population.

Supplementary information S2



The relative levels of the metabolites in the test and validation sample set compared with specific controls (A-I) and compared within cerebral and non-cerebral subtypes. A-C: comparison of lipoprotein levels of all the malarial subtypes with uninfected control (A), encephalitis (B) and sepsis(C). D-F: comparison of lactate levels of all the malarial subtypes with uninfected control (D), encephalitis (E) and sepsis (F). G-I: comparison of glycoprotein levels of all the malarial subtypes with uninfected control (G), encephalitis (H) and sepsis (I). In each panel, box color representations are as follows: red - MM, green - SNCM, blue - CM, cyan - CMMOD, black - uninfected control (A/D/G), encephalitis (B/E/H) and sepsis (C/F/I). In each panel the black bar denotes the two pairs among which $p < 0.05$. J- comparison of glycoprotein levels in the cerebral (red) and non-cerebral (black) subtypes. *$p < 0.05$.

Supplementary information S3



A. Portion of Support tree cluster and heat-map constructed from the signal rich aliphatic region of NMR data. The mean of each spectral variable was used for each group of individuals. A bootstrap resampling method was employed (n=100). The metabolites corresponding to the spectral variables are shown. B. The pathway analysis from the Support tree data.