Dengue, due to its global burden, is the most important arthropod-born flavivirus disease. Brazil is one of the most affected countries in Latin America and until the present date, 229 deaths were registered, corresponding to a 45% increase when compared to the same period of 2014. There is no specific treatment for dengue disease and early detection lowers fatality rates to below 1%. Since the metabolic resources crucial for viral replication are provided by host cells, detecting changes in the metabolic profile associated with the pathological condition could help identifying markers of prognostic and diagnostic importance. We applied $^1$H NMR exploratory metabolomics to study overall longitudinal changes in plasma metabolites in a cohort in Recife, Brazil. To gain statistical power, we used innovative statistics of paired multivariate data to discriminate individuals with dengue fever (DF; mild) and dengue hemorrhagic fever (DHF; severe) presenting primary and secondary infection and subjects with non-specific infection (ND). Multivariate statistics discriminated DF and DHF plasma metabolome from ND subjects. Variables that contributed to discrimination of groups were VLDL and LDL lipoproteins, valine, lactate, glutamine, citrate, glicerophosphocholine, tyrosine and betaine. A decrease in plasma glutamine and lipoproteins was a characteristic of DHF with primary and secondary infections when compared to DF and NS subjects. Additionally, an increase in plasma acetate in DHF was observed when compared to NS subjects. Longitudinal increase in plasma valine was characteristic of DF secondary and ND subjects. Histidine also increase in ND subject over the course of infection. We hypothesize that these changes in plasma metabolome are characteristic of liver dysfunction and could provide insights into the underlying molecular mechanisms of dengue pathogenesis. Moreover, following plasma metabolome during the course of dengue infection could help discriminating individuals at risk to develop severe infection and to predict disease outcome.