Supplementary data:

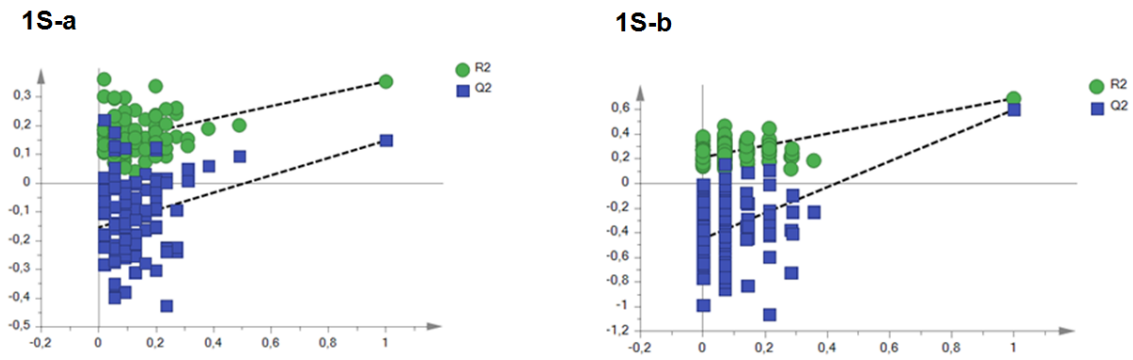

Figure 1S:

Permutation analysis of OPLS-DA model derived (a) D7 versus M3 and (b) D7 versus M12 for 1H NMR data. Statistical validation of the OPLS-DA model by permutation analysis using 100 different model permutations. The goodness of fit (R2) and predictive capability (Q2) of the original model are indicated on the far right. The blue regression line of the Q2-points intersects the vertical axis (on the left) below zero. The intercept value= (0.0, -0.161) for figure 1S-a and the intercept value= (0.0, -0.43) for figure 1S-b.

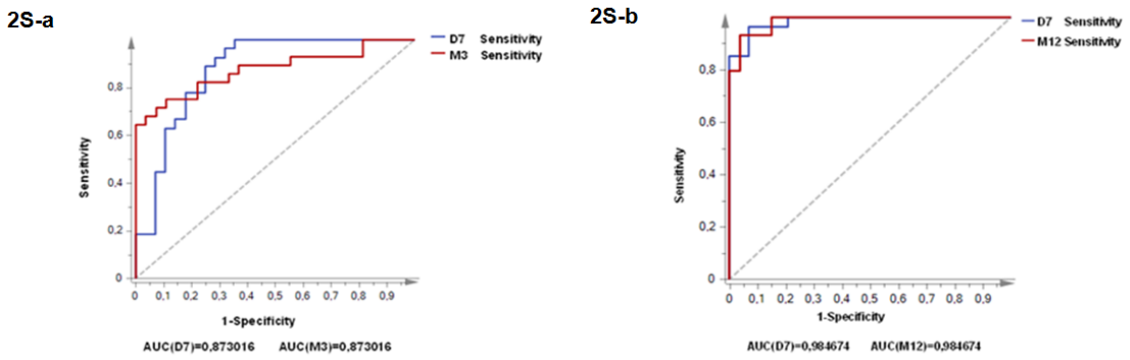

Figure 2S: The ROC plot of 1H NMR data depicts OPLS-DA model performance(a)for the D7 compared with M3,and (b) for the D7 compared with M12.

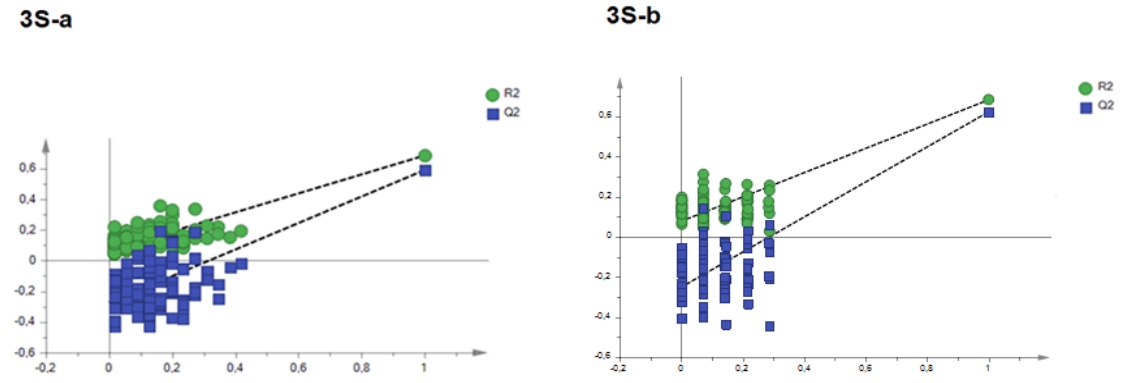

Figure 3S:

Permutation analysis of OPLS-DA model derived (a) D7 versus M3 and (b) D7 versus M12 for GC-MS data. Statistical validation of the OPLS-DA model by permutation analysis using 100 different model permutations. The goodness of fit (R2) and predictive capability (Q2) of the original model are indicated on the far right. The blue regression line of the Q2-points intersects the vertical axis (on the left) below zero. The intercept value= (0.0, -0.291) for figure 3S-a and the intercept value= (0.0, -0.249) for figure 3S-b.

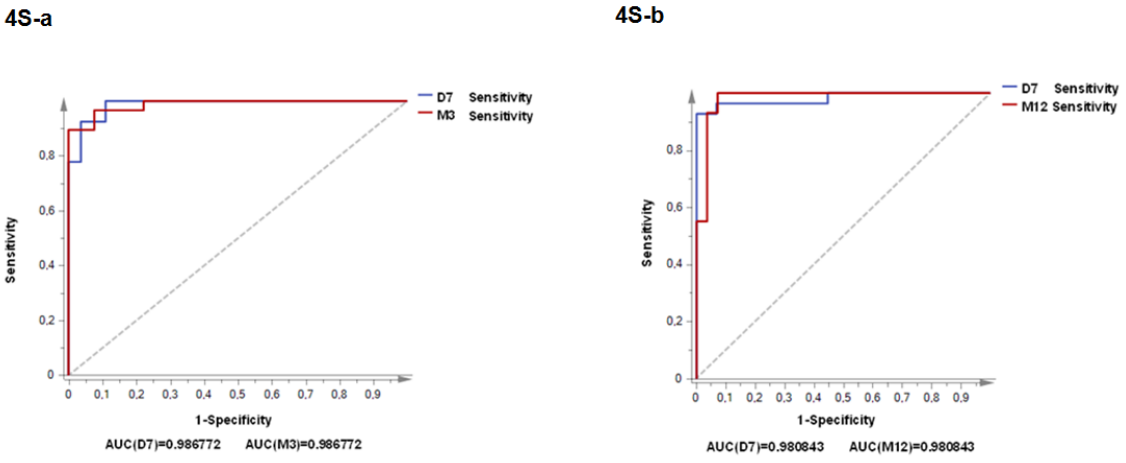

Figure 4S: The ROC plot of GC-MS data depicts OPLS-DA model performance (a) for the D7 compared with M3, and (b) for the D7 compared with M12.

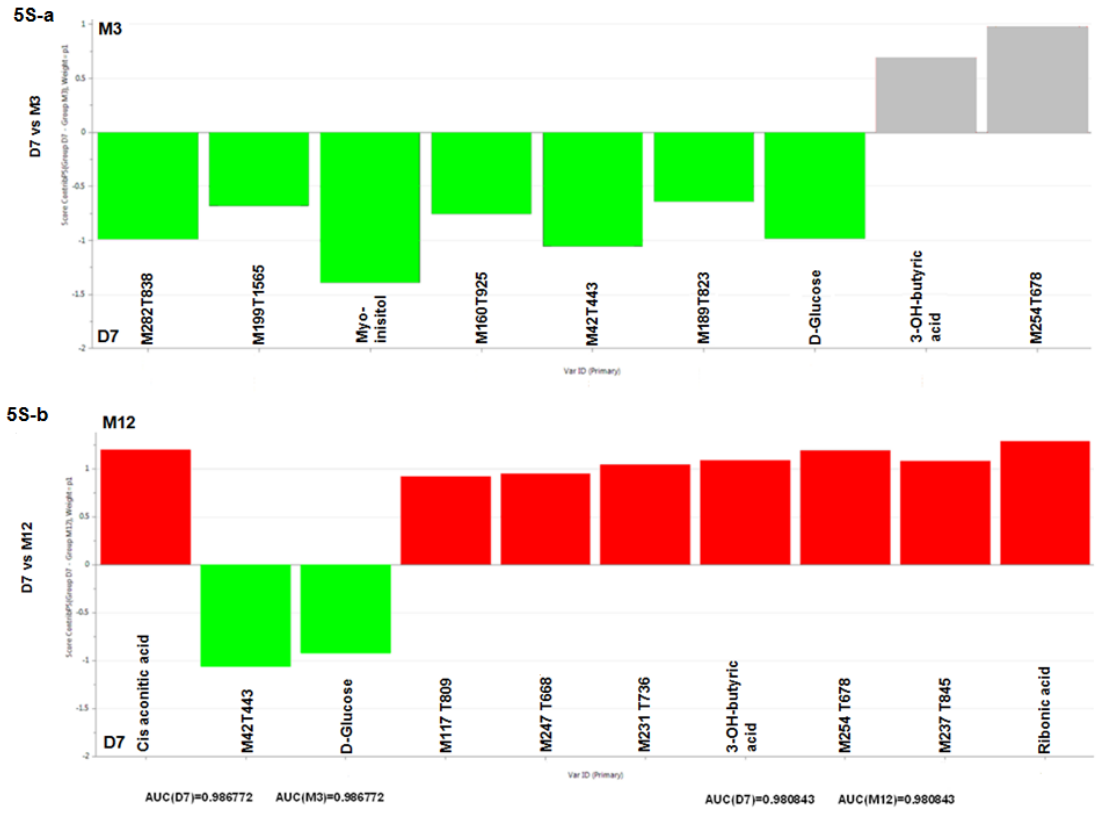

Figure 5S: Contribution plots of GC-MS data showing the major metabolites accounting for the separation between (a) urine at D7 (green) and at M3 (gray) and between (b) urine at D7 (green) and at M12 (red); positive values show the metabolites that are highly abundant at M3 (5a) and at M12 (5b), whereas negative values show those that are highly abundant at D7 (5a and 5b).

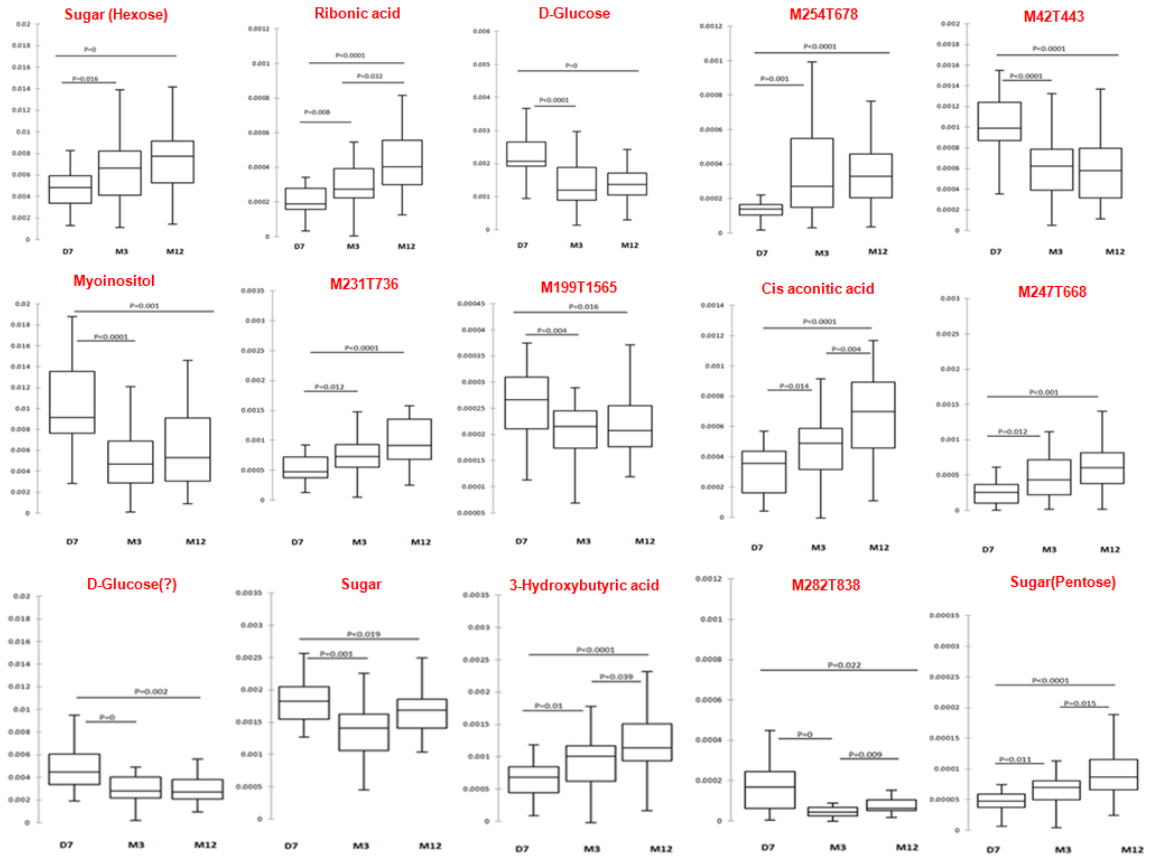

Figure 6S: Univariate analysis comparing metabolite concentrations (GC-MS data normalized to total area) at the three time points (D7, M3 and M12).