Figure 1: Scatter plots comparing random-fed to fasted lipid quantitations per mice. Each lipid value was log2 transformed, then averaged across 3 weeks for each rat. The averaged lipid values were collapsed into one point by taking the median. Each value is plotted against one of 5 phenotype observations per animal, and each animal is colored by glucose tolerance.

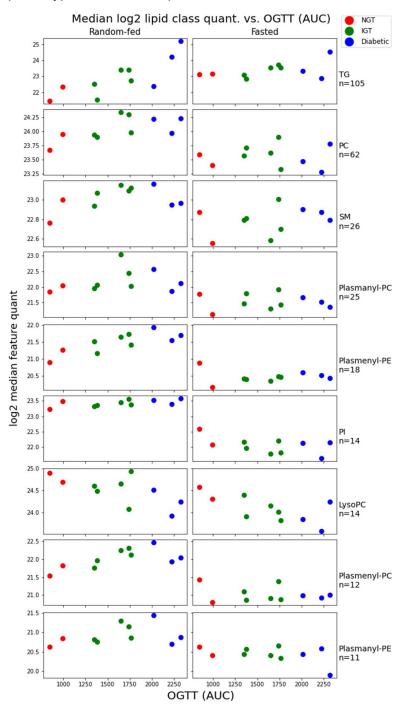


Figure 1a: OGTT

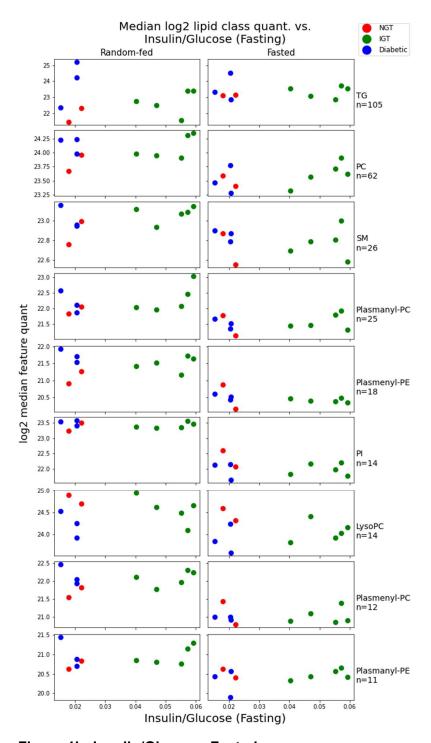


Figure 1b: Insulin/Glucose, Fasted

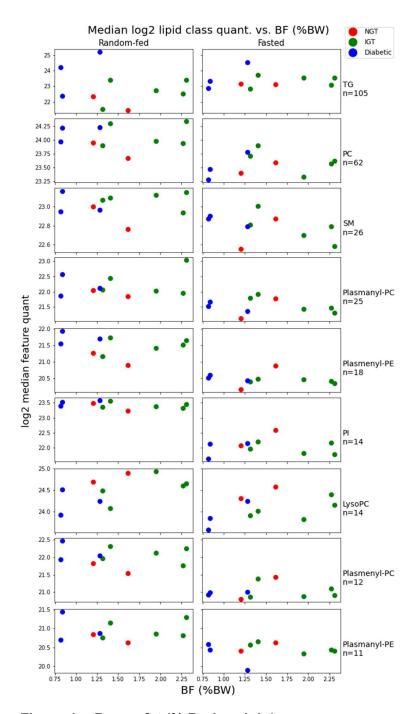


Figure 1c: Brown fat (% Bodyweight)

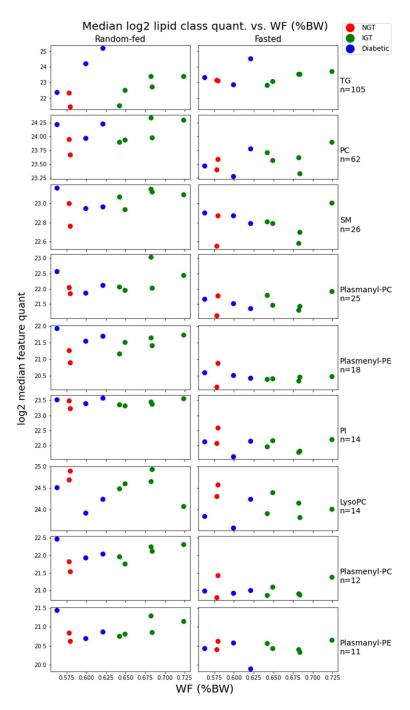


Figure 1d: White fat (% Bodyweight)

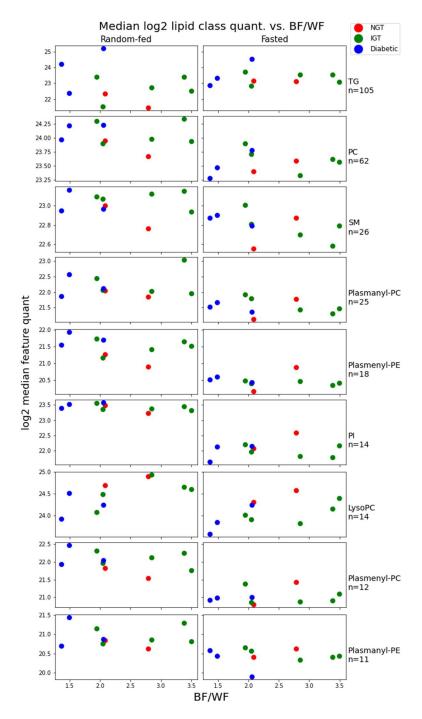


Figure 1e: Brown fat to White Fat

Figure 2: Heatmaps with hierarchical clustering comparing the correlation of each phenotype observation (rows) to identified lipid. Lipids are colored by lipid superclass. Each lipid was filtered based on significance value of the Pearson correlation >0.63 or <-0.63, corresponding to p <0.05.

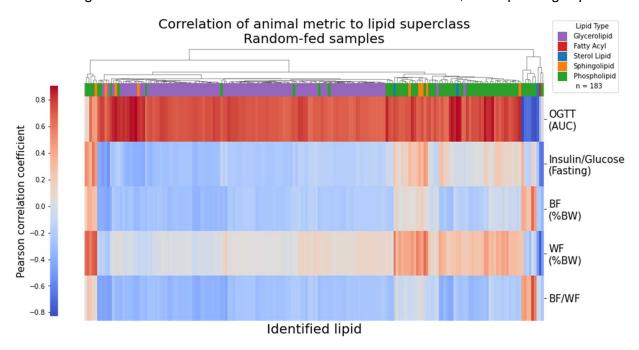


Figure 2a: Random-fed correlations

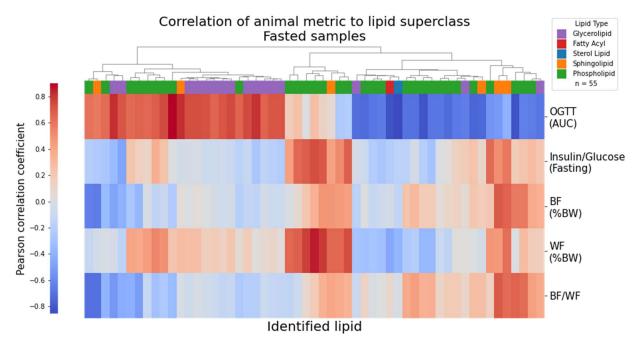


Figure 2b: Fasted correlations