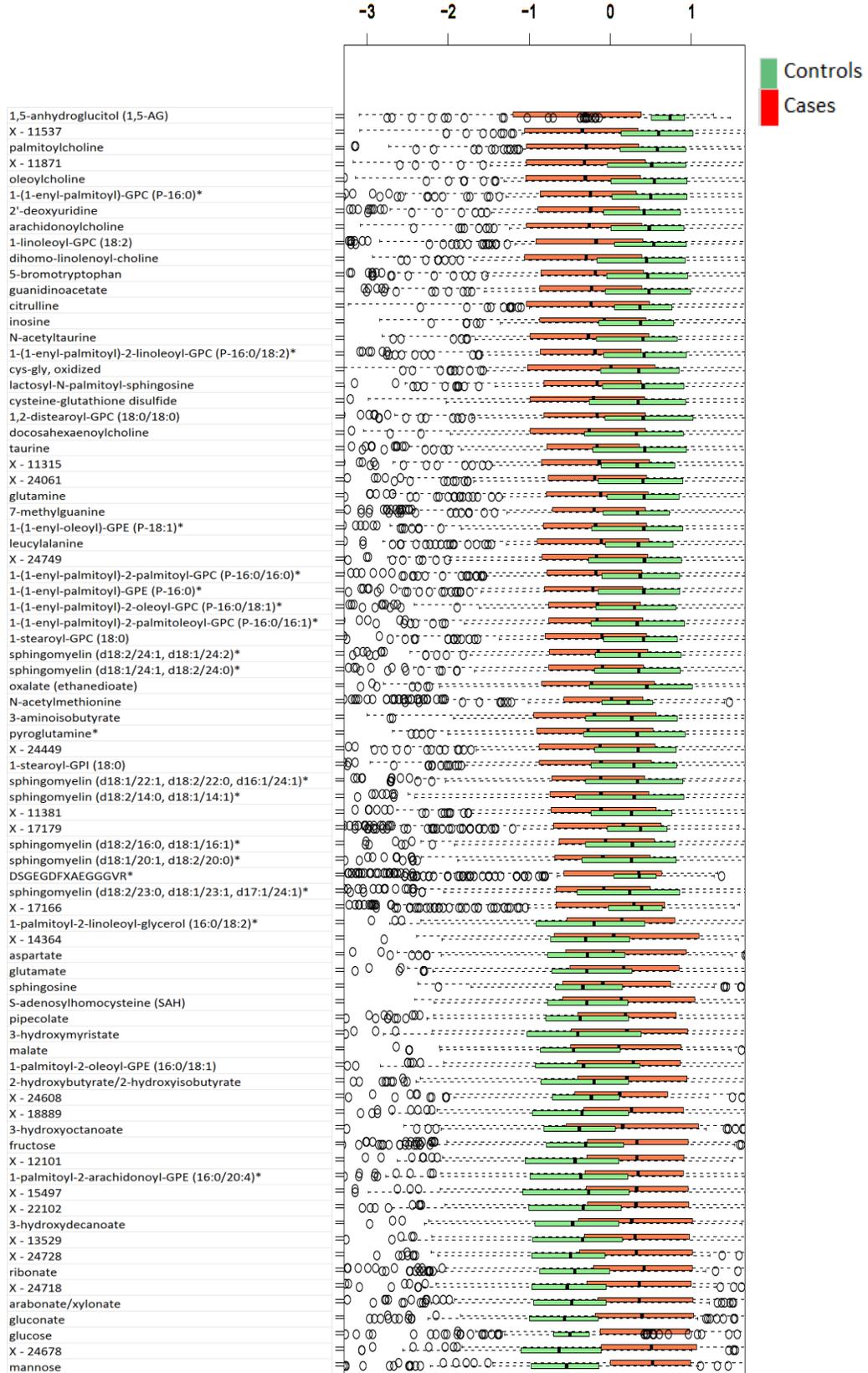


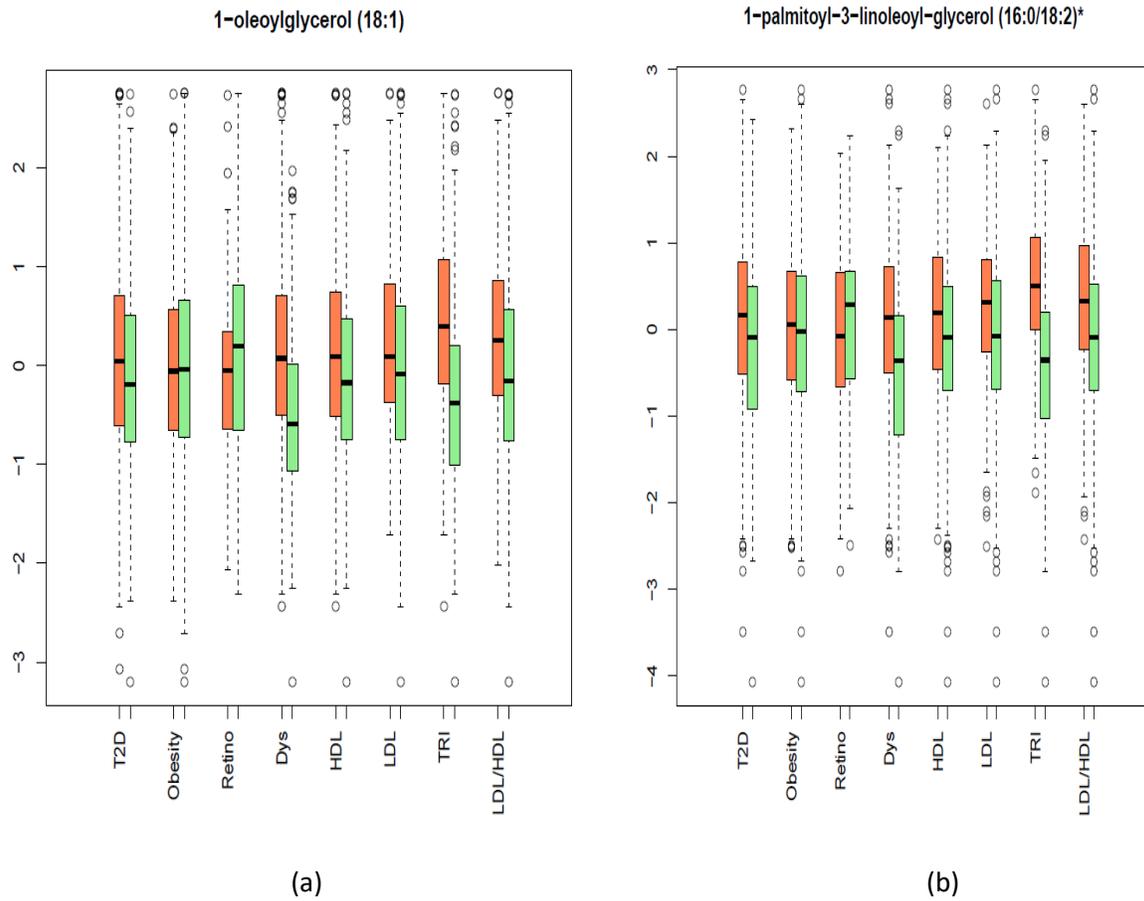
Supplementary Figure 1: OPLS-DA classification results. Score plot for 996 samples of T2D using metabolomics data to classify T2D patients from controls. “Yes” indicates T2D patients and “No” indicates controls.



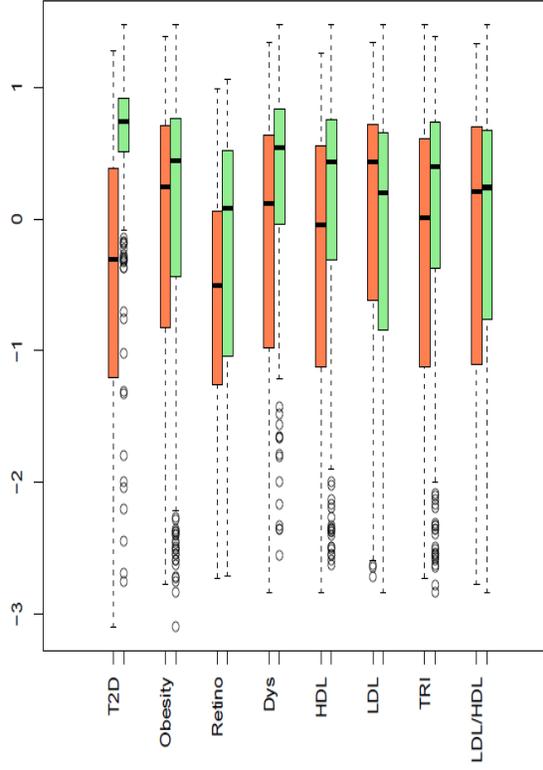
Supplementary Figure 2: Boxplots of the 80 most significant metabolites associated with T2D sorted on their beta values of regression. The y-axis is the metabolite name, and the x-axis is the metabolite value. Black circles are outliers.

	BMI	Retinopathy	LDL/HDL	HDL	LDL	TRI	Dyslipidemia
T2D	0.176005	-0.12613	0.082466	-0.38771	-0.21402	0.294968	0.344756
BMI		-0.20787	0.147036	-0.33574	-0.05467	0.208565	0.291359
Retinopathy			-0.24464	0.06353	-0.158	-0.17971	-0.14818
LDL/HDL				-0.38981	0.71815	0.570698	0.50559
HDL					0.258981	-0.67185	-0.79574
LDL						0.058548	-0.03268
TRI							0.882566

Supplementary Figure 3. Pairwise correlations of clinical variables based on their associations with metabolites.

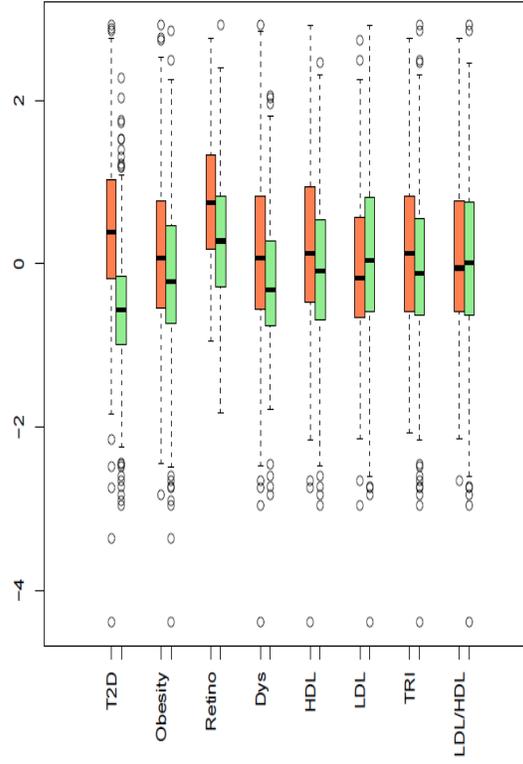


1,5-anhydroglucitol (1,5-AG)



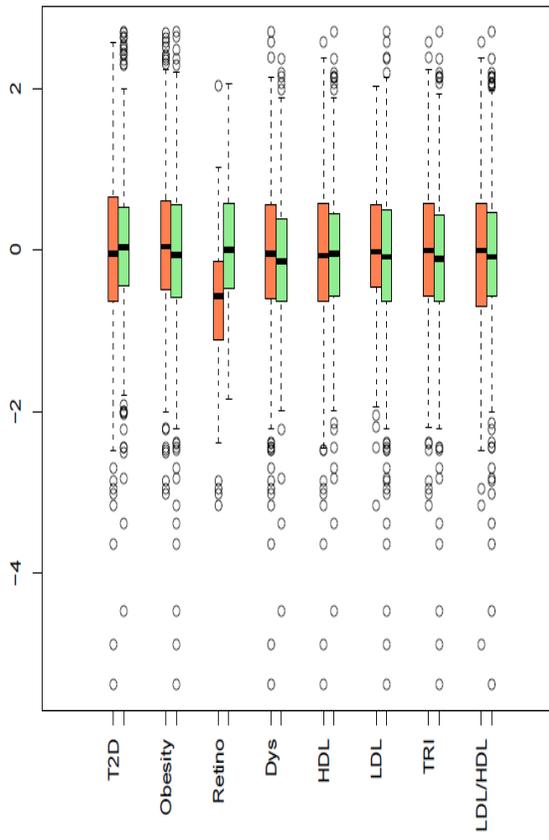
(c)

gluconate



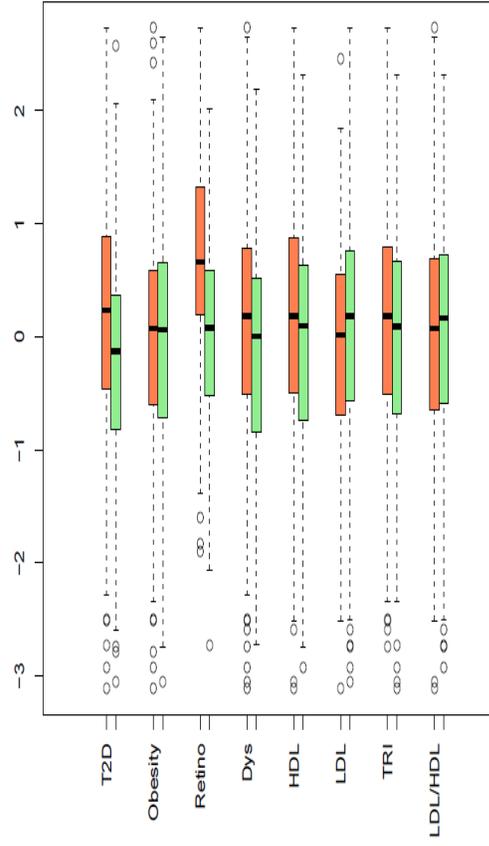
(d)

xanthine

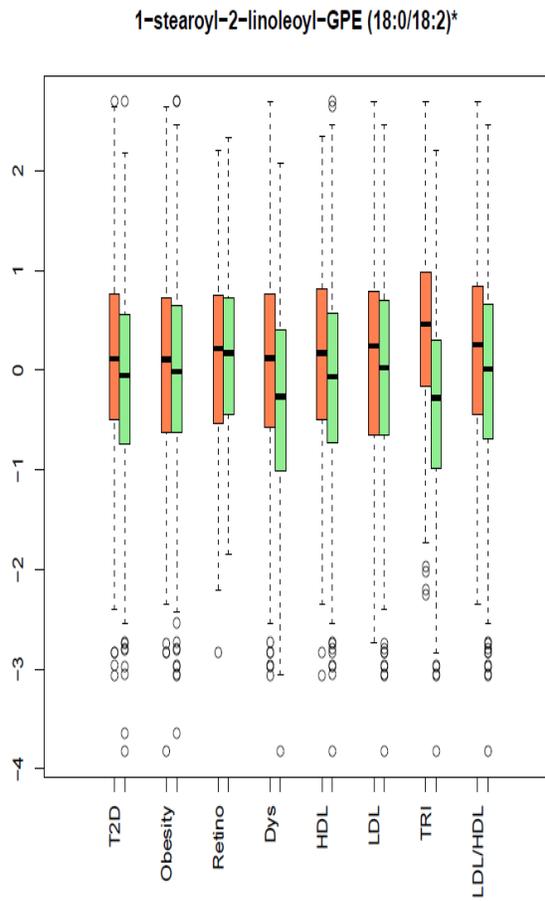


(e)

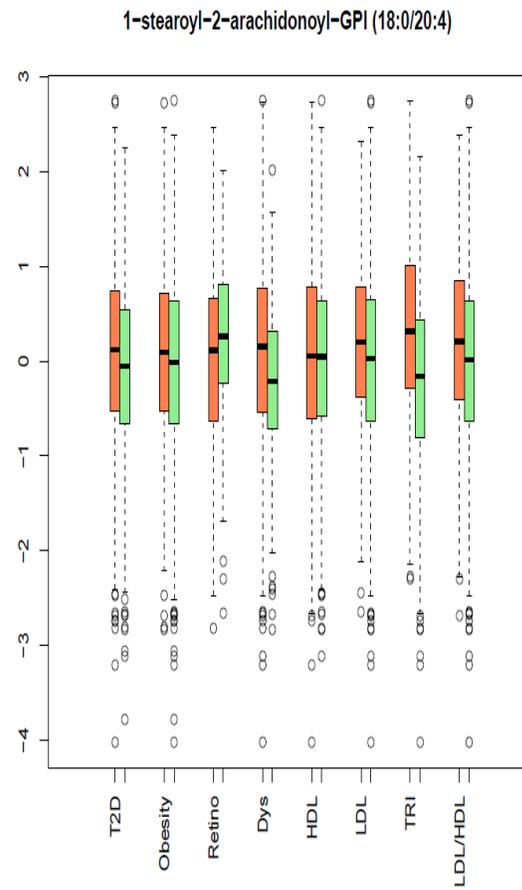
phenylacetylglutamine



(f)

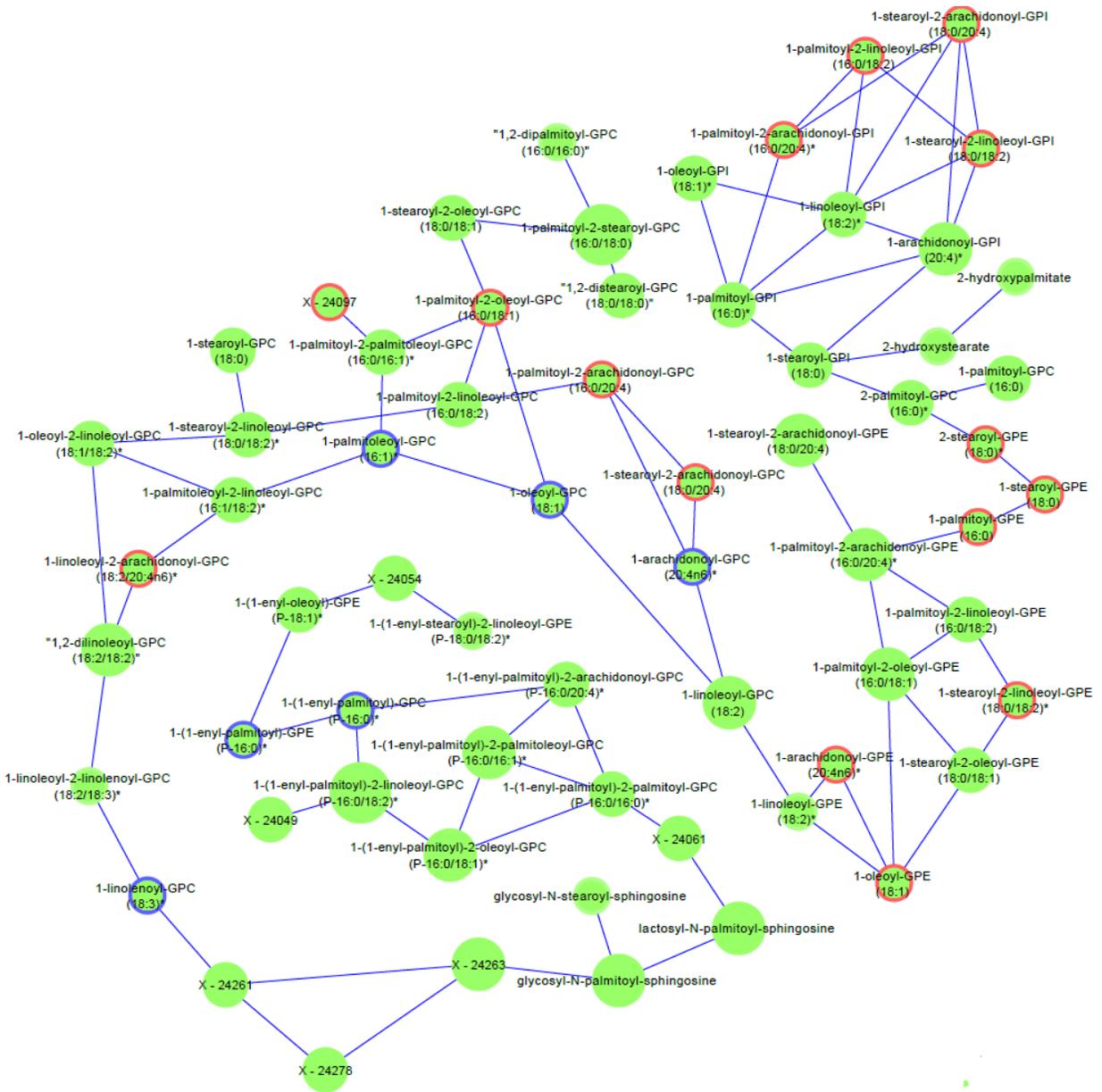


(g)

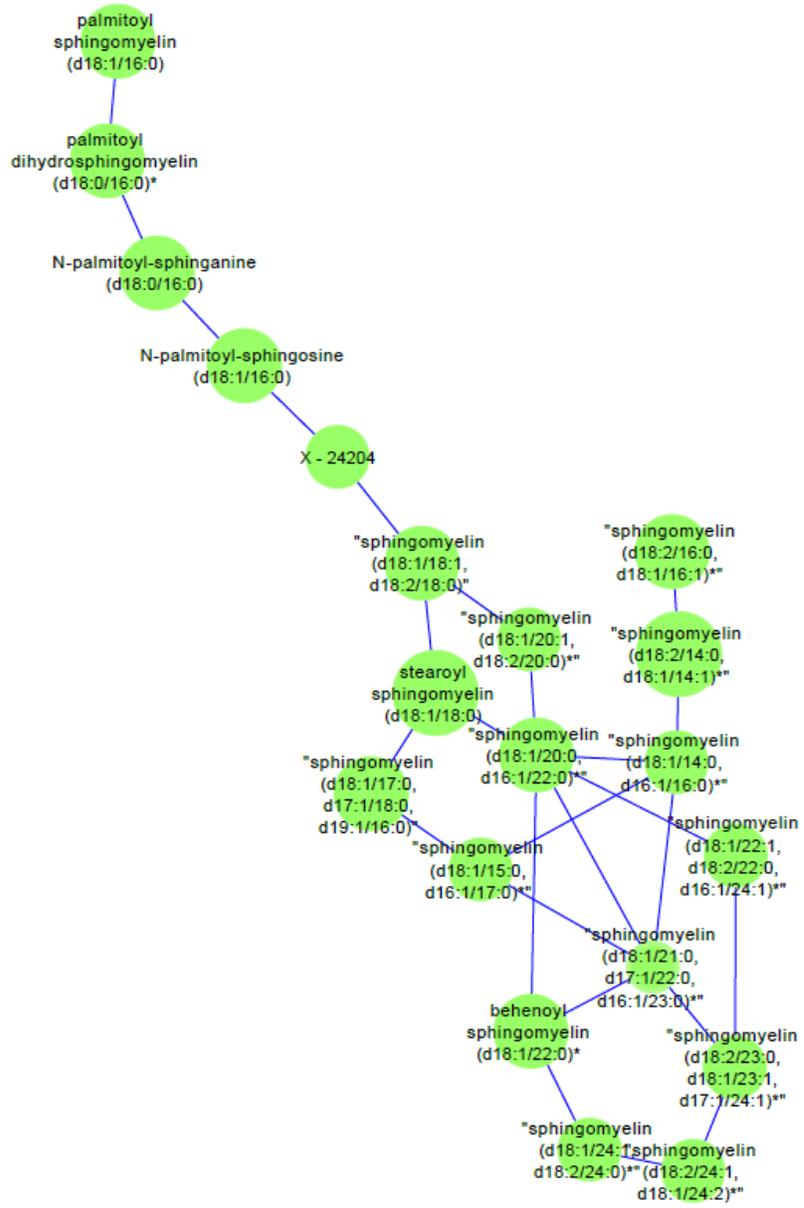


(h)

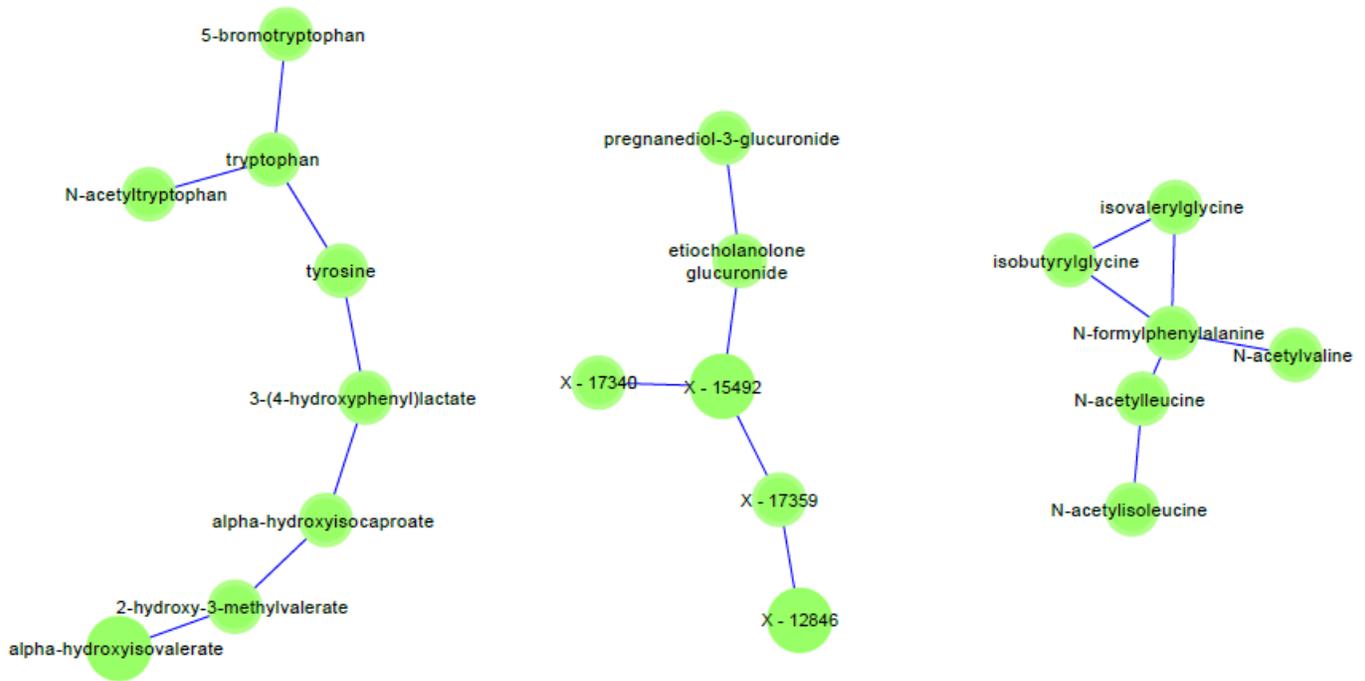
Supplementary Figure 4: Boxplots of metabolites associated with five or more variables (a, b) or associated only with T2D (c, d), retinopathy (e, f), or TRI (g, h). Red represents the case (T2D, obesity, retinopathy, dyslipidemia [Dys], and levels above/below threshold for quantitative variables), and green represents the controls. Y-axes are levels of the metabolites.



(a)



(b)

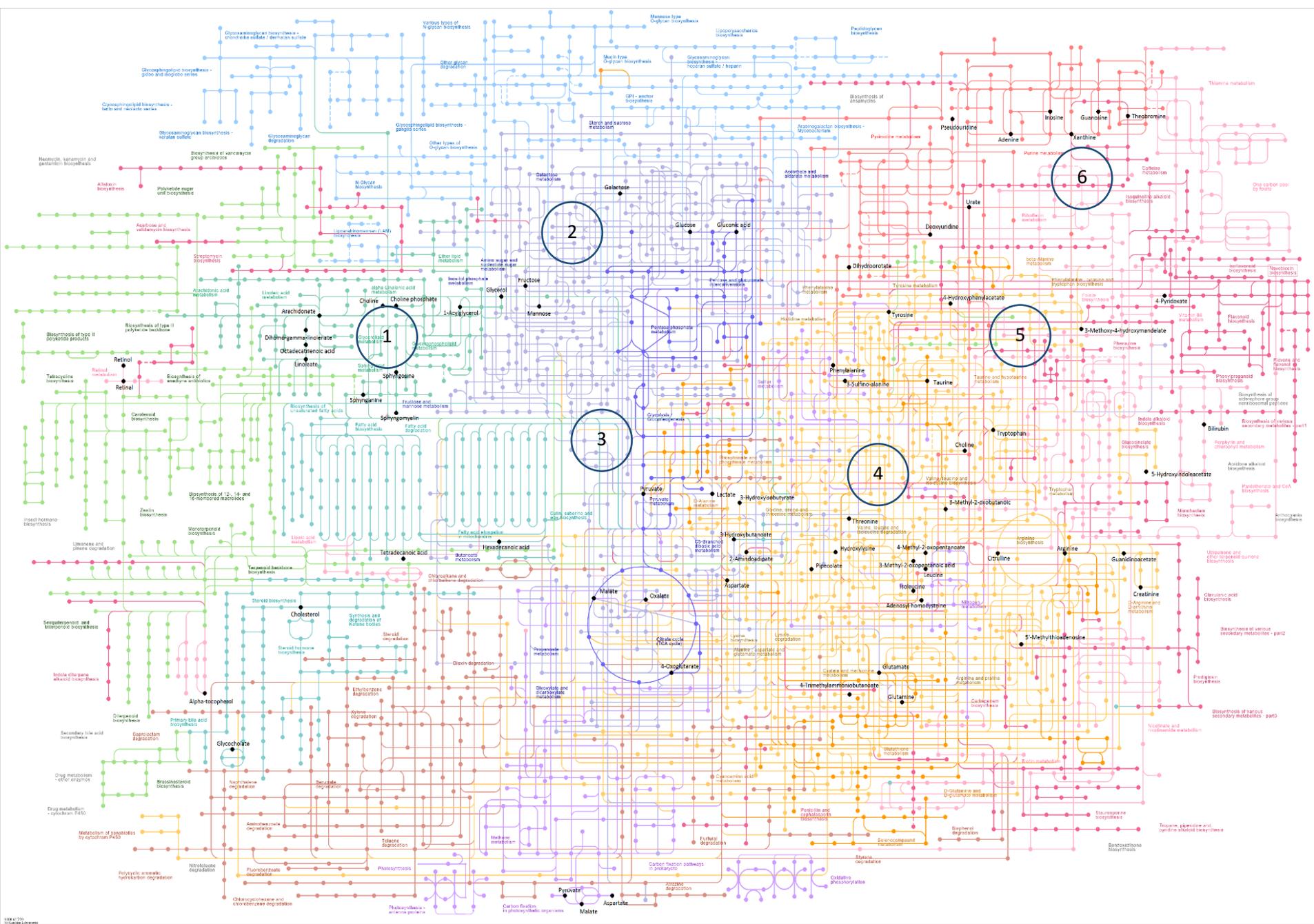


(c)

(d)

(e)

Supplementary Figure 5: Additional GGM subnetworks from the 11 largest subnetworks presented in Figure 3. The larger the node, the more phenotypes are associated with the metabolite (up to six phenotypes can be associated with metabolites). If four or more metabolites are associated only with a single clinical variable, the border of the node is colored: a red border indicates association with TRI only, and a blue border indicates association with T2D only. (a) Lipid subnetwork (palmitoyls/stearoyl/arachidonoyl/oleoyl/linoleoyl- GPC/GPE/GPI) with 65 metabolites; (b) sphingomyelin subnetwork (20 metabolites); (c,e) branched chain Amino Acids (BCAAs)/phenylalanine and tyrosine; (d) glucuronides/unknowns subnetworks.



Supplementary Figure 6: KEGG pathways with metabolites mapped from 373 metabolites are labelled with black dots. 1-(linoleic acid metabolism, arachidonic acid metabolism, sphingolipid metabolism, alpha-linolenic, glycerophospholipid). 2-(amino sugar and nucleotide sugar, starch and sucrose metabolism, and galactose metabolism). 3-(pantose phosphate metabolism, glycolysis, and TCA cycle). 4-(arginine, aspartate and glutamate metabolism, serine, glycine and threonine metabolism, leucine-valine-isoleucine [BCAA] metabolism). 5-(taurine and hypotaurine metabolism, phenylalanine-tyrosine-tryptophan metabolism). 6-(pyrimidine, purine and caffeine metabolism).