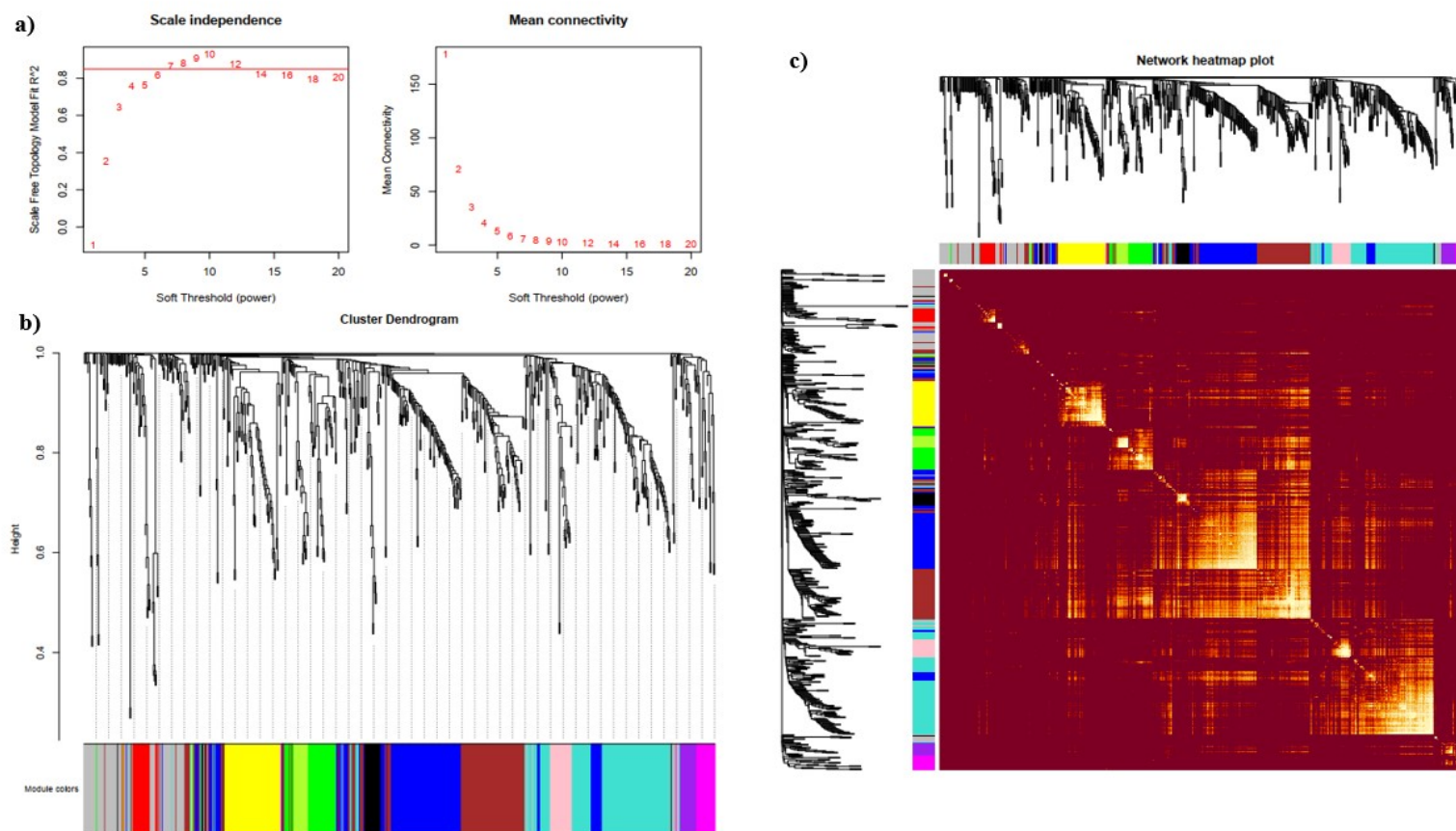
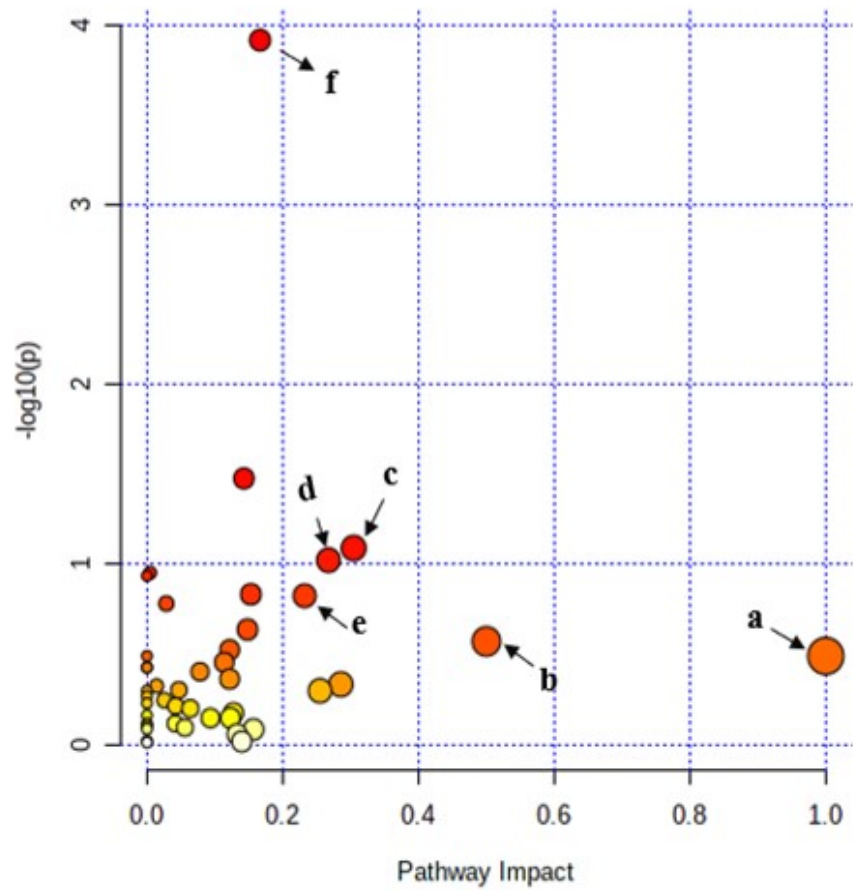


Suppl Fig.1. Weighted Gene Co-expression Network Analysis (WGCNA). a) Scale free topology criteria. Influence of different powers on the scale independence (left) and on the mean connectivity (right). The horizontal red line indicates the selected soft threshold power $\beta=5$ and $R^2>0.8$ used for merging the modules. b) Cluster dendrogram of all the metabolites classified into different modules. The color bars at the bottom of the module indicate the division of modules. c) Network heatmap plot. Indicates the adjacencies of the network, each row and column in the heatmap belong to be a single metabolite. Dark brown indicates low adjacencies and progressive yellow indicates higher adjacencies among metabolites in the module.



Suppl Fig.2. Summary of pathway analysis. Where, (a) Linoleic acid metabolism, (b) Phenylalanine, tyrosine and tryptophan biosynthesis, (c) Arginine biosynthesis (d) Glycine, serine and threonine metabolism (e) Arginine and proline metabolism, (f) Aminoacyl-tRNA biosynthesis.



Suppl. Table S1: Clinical and biochemical characteristics of study groups

Variables	Control (CT) (n=22)	T2DM (n= 21)	CAD (n=21)	T2DM_CAD (n=39)
Age in years	45.2±9.6	44.9±9.3	47.7±7.8	51.9±7.8
Sex (Male/Female)	15/6	9/11	21/3	34/5
BMI	25.03±8.7	26.3± 5.3	23.7±3.4	25.2±3.9
FBS (mg/dl)	92.0(89.0±108.0)	192.0(140.8±269.8)*	98.0(77.0-112.0)	192.0(148.0±237.0)*
HbA1c (%)	5.5(5.05-6.1)	7.4(6.8-9.5)*	5.5(5.2-6.0)	8.4(7.0-9.4)*
SBP (mm/Hg)	130.6±11.7	128.2±13.4	134.9±15.5	131.8±21.7
DBP (mm/Hg)	80.1±10.8	79.1±9.5	81.2±10.6	85.1±10.0
LDL-C (mg/dl)	87.4 (73.0-115.8)	74.0(60.0-98.1)	69.8 (55.2-82.0)	66.8(55.6-78.4)
HDL-C (mg/dl)	33.9±6.8	36.6±6.4	31.9±8.9	27.9±8.2
Total cholesterol (mg/dl)	157.9±22.7	152.6±28.6	141.9±37.4	152.9±26.8
Triglycerides (mg/dl)	149.0(89.7-236.0)	160.5(104.8-220.3)	141.0(101.0-205.0)	146.0 (110.0-242.0)
Creatinine (mg/dl)	0.8±0.19	0.8±0.2	1.0±0.6	1.0±0.4

Data are mean (SD) and median (Q1–Q3) for normally distributed and non-normally distributed variables respectively. *P<0.05.

Suppl. Table S2: Summary of module assignment

Module colour	Total metabolites assigned
Black	24
Blue	126
Brown	111
Green	42
Greenyellow	17
Grey	91
Magenta	22
Pink	24
Purple	18
Red	24
Turquosie	132
Yellow	63

Suppl.Table S3: Summary of pathway analysis

S.No	Pathway Name	Match Status	p	-log(p)	Holm p	FDR	Impact	Metabolites
1	Linoleic acid metabolism	1/5	0.32021	0.49457	1.0	1.0	1.0	Linoleic acid
2	Phenylalanine, tyrosine and tryptophan biosynthesis	1/4	0.26558	0.57581	1.0	1.0	0.5	L-Tyrosine
3	Arginine biosynthesis	3/14	0.079379	1.1003	1.0	1.0	0.30457	L-Citrulline, L-Arginine, L-Glutamine
4	Glycine, serine and threonine metabolism	5/33	0.091952	1.0364	1.0	1.0	0.26741	Guanidinoacetate, Creatinine, L- Serine, Glycerol L-Threonine
5	Arginine and proline metabolism	4/38	0.14944	0.82555	1.0	1.0	0.23223	L-Arginine, Guanidinoacetate, Creatine, L- Proline
6	Aminoacyl-tRNA biosynthesis	13/48	2.4399	4.6126	0.0020495	0.0020495	0.16667	L-Asparagine, L-Arginine, L-Glutamine, L-Serine, L-Methionine, L-Valine, L-Alanine, L-Lysine, L-Isoleucine, L-Threonine, L-Tryptophan, L-Tyrosine, L-Cysteine
7	Starch and sucrose metabolism	3/18	0.14659	0.83391	1.0	1.0	0.15312	Trehalose, D-Glucose 1-phosphate, D-Fructose 6-phosphate
8	Phenylalanine metabolism	3/10	0.033238	1.4784	1.0	0.93066	0.14286	Phenylacetaldehyde, L-Tyrosine, Hippurate