

Figure S1

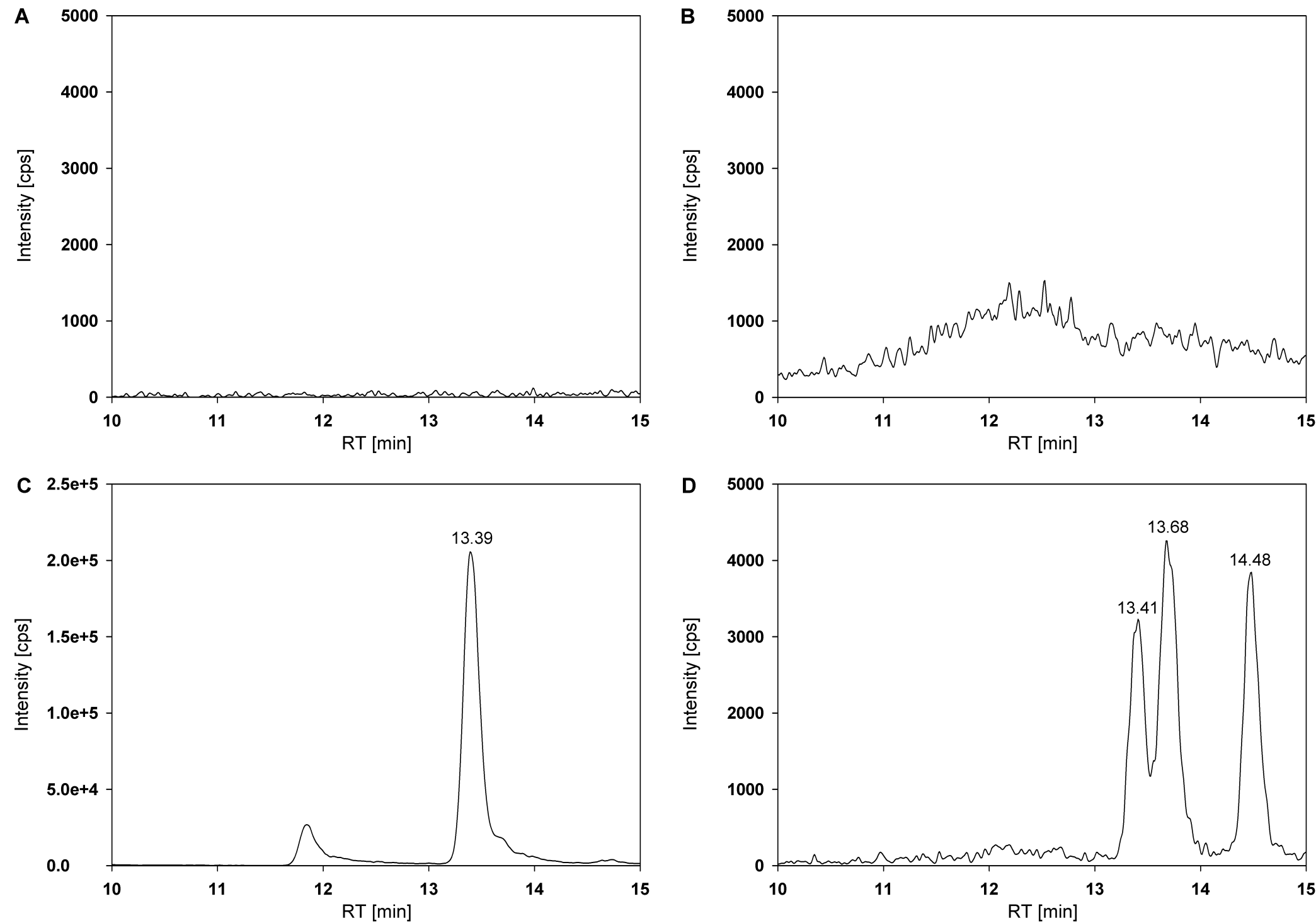


Figure S1: MRM-chromatograms for the detection of B[a]P-1,6-dione using LC-MS/MS.

Extraction of the B[a]P-dione specific MRM-transition m/z 283->226 in a retention time range of 10 – 15 min. Analyses were verified by a second MRM-transition (m/z 283->255; data not shown).

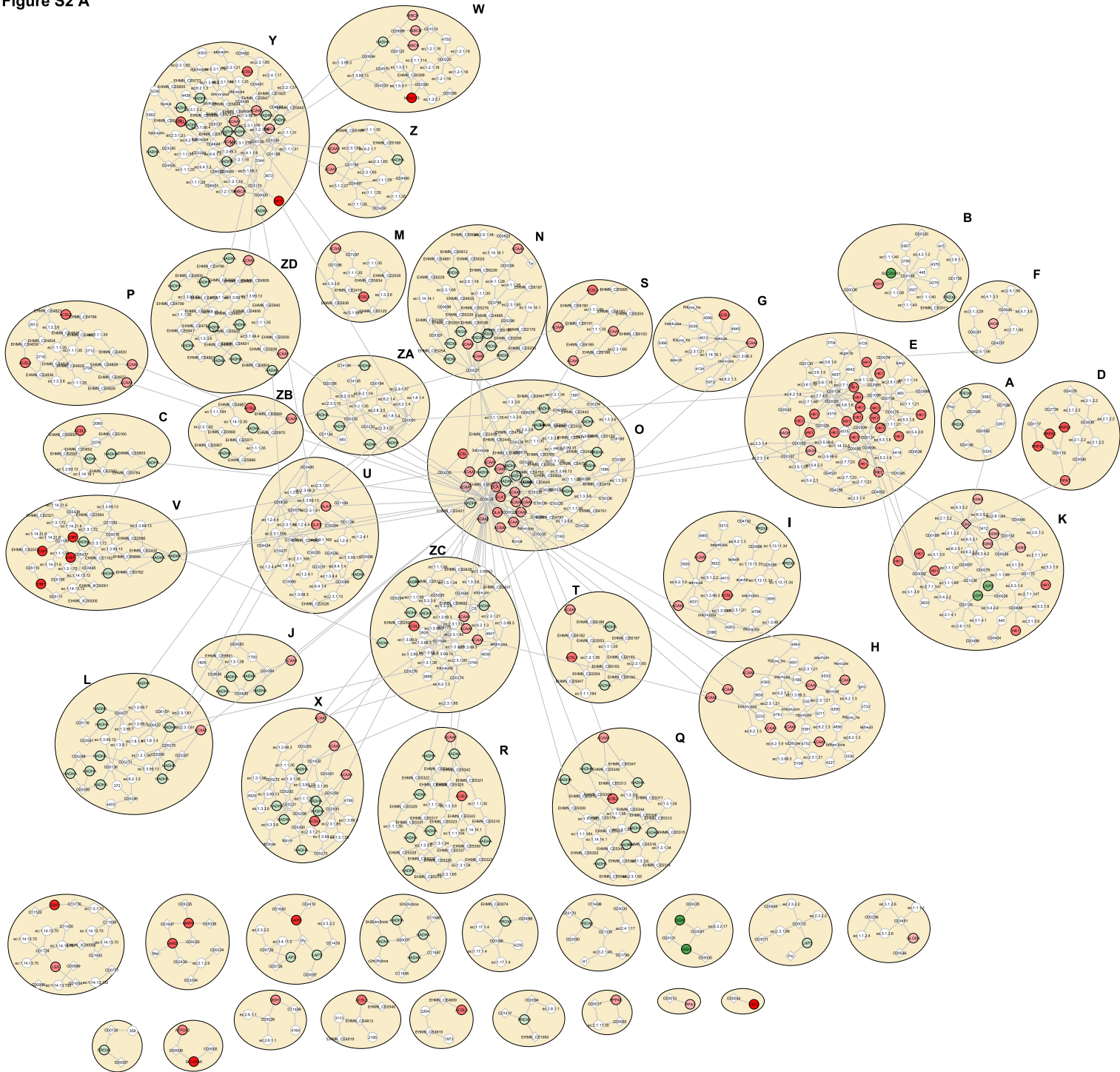
A: Blank sample of Methanol.

B: Extract of Jurkat T cells exposed to DMSO for 4h.

C: B[a]P-1,6-dione reference standard at 10 ng/ml.

D: Extract of Jurkat T cells exposed to 50 μ M B[a]P for 4h.

Figure S2 A



Module	Functional Assignment
A	Tyrosine metabolism
B	Citrate (TCA) cycle
C	Mono-unsaturated fatty acid beta-oxidation
D	Purine metabolism
E	Amino sugar metabolism
F	CMP-N-acetylneuraminate biosynthesis I
G	Omega-3 fatty acid metabolism
H	Omega-3 fatty acid metabolism
I	Arachidonic acid metabolism
J	Fatty acid elongation
K	Starch and sucrose metabolism
L	Saturated fatty acids beta-oxidation
M	Phytanic acid peroxisomal oxidation
N	Tyrosine metabolism
O	Di-unsaturated fatty acid beta-oxidation
P	Omega-3 fatty acid metabolism
Q	Leukotriene metabolism
R	Leukotriene metabolism
S	Omega-3 fatty acid metabolism
T	Leukotriene metabolism
U	Valine, leucine and isoleucine degradation
V	Mono-unsaturated fatty acid beta-oxidation
W	Oxidative phosphorylation
X	Saturated fatty acids beta-oxidation
Y	Pentose and glucuronate interconversions
Z	Leukotriene metabolism
ZA	Butanoate metabolism
ZB	Leukotriene metabolism
ZC	Di-unsaturated fatty acid beta-oxidation
ZD	Saturated fatty acids beta-oxidation

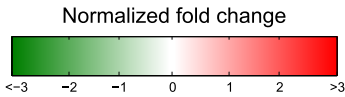
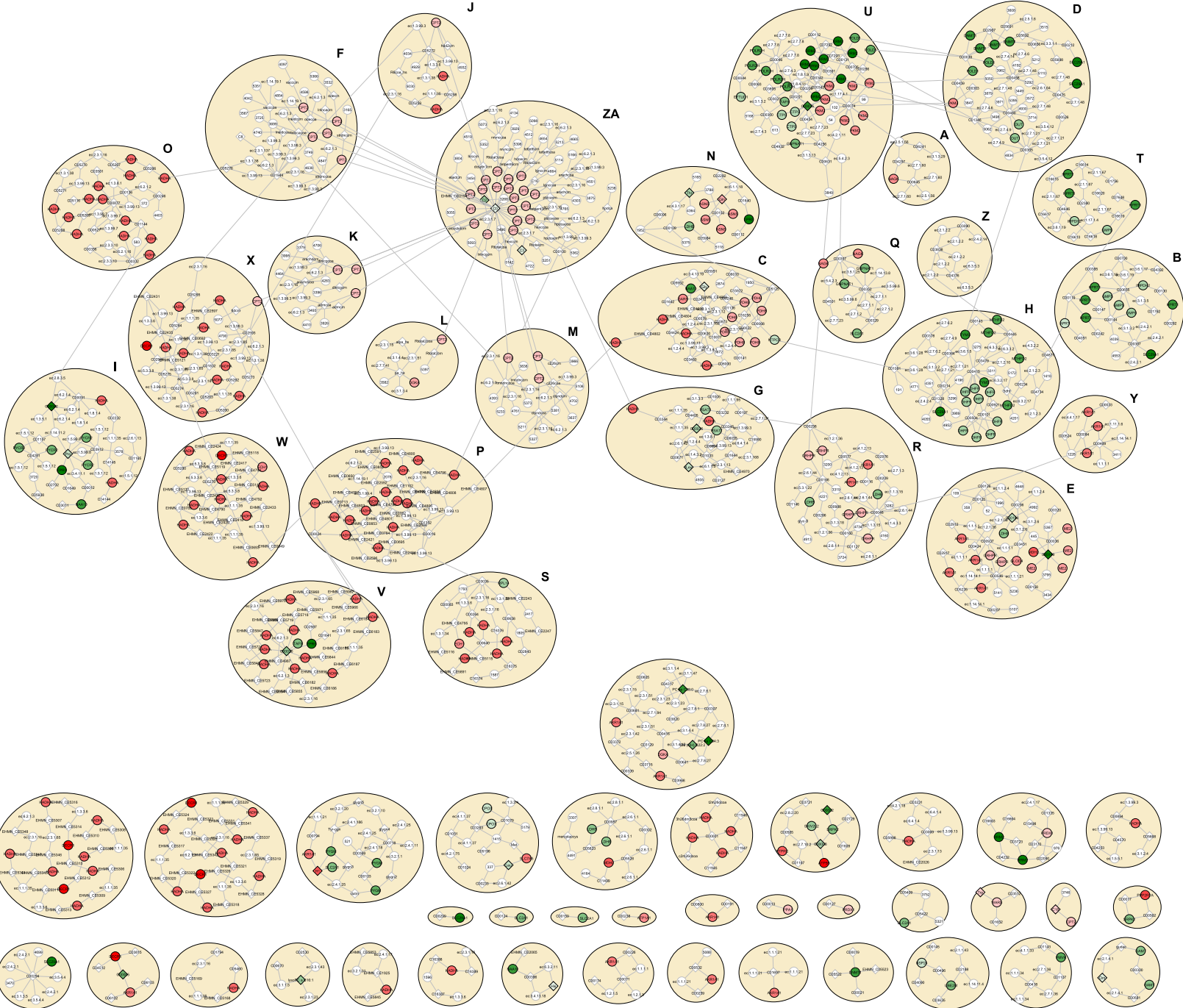


Figure S2 B



Module	Functional Assignment
A	CMP-N-acetylneuramate biosynthesis I
B	Purine metabolism
C	Valine, leucine and isoleucine degradation
D	Pyrimidine metabolism
E	Pyruvate metabolism
F	Fatty acid metabolism
G	Valine, leucine and isoleucine degradation
H	One carbon pool by folate
I	Citrate cycle (TCA cycle)
J	Saturated fatty acids
K	beta-oxidation
L	Fatty acid metabolism
M	Glycerophospholipid metabolism
N	Fatty acid metabolism
O	Aminoacyl-tRNA biosynthesis
P	Saturated fatty acids
Q	beta-oxidation
R	Mono-unsaturated fatty acid
S	Synthesis of UDP-N-acetyl-glucosamine
T	Glycolysis / Gluconeogenesis
U	Biosynthesis of unsaturated fatty acids
V	Drug metabolism - other enzymes
W	Pyrimidine metabolism
X	Leukotriene metabolism
Y	Di-unsaturated fatty acid
Z	beta-oxidation
ZA	Saturated fatty acids

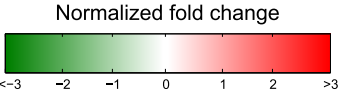
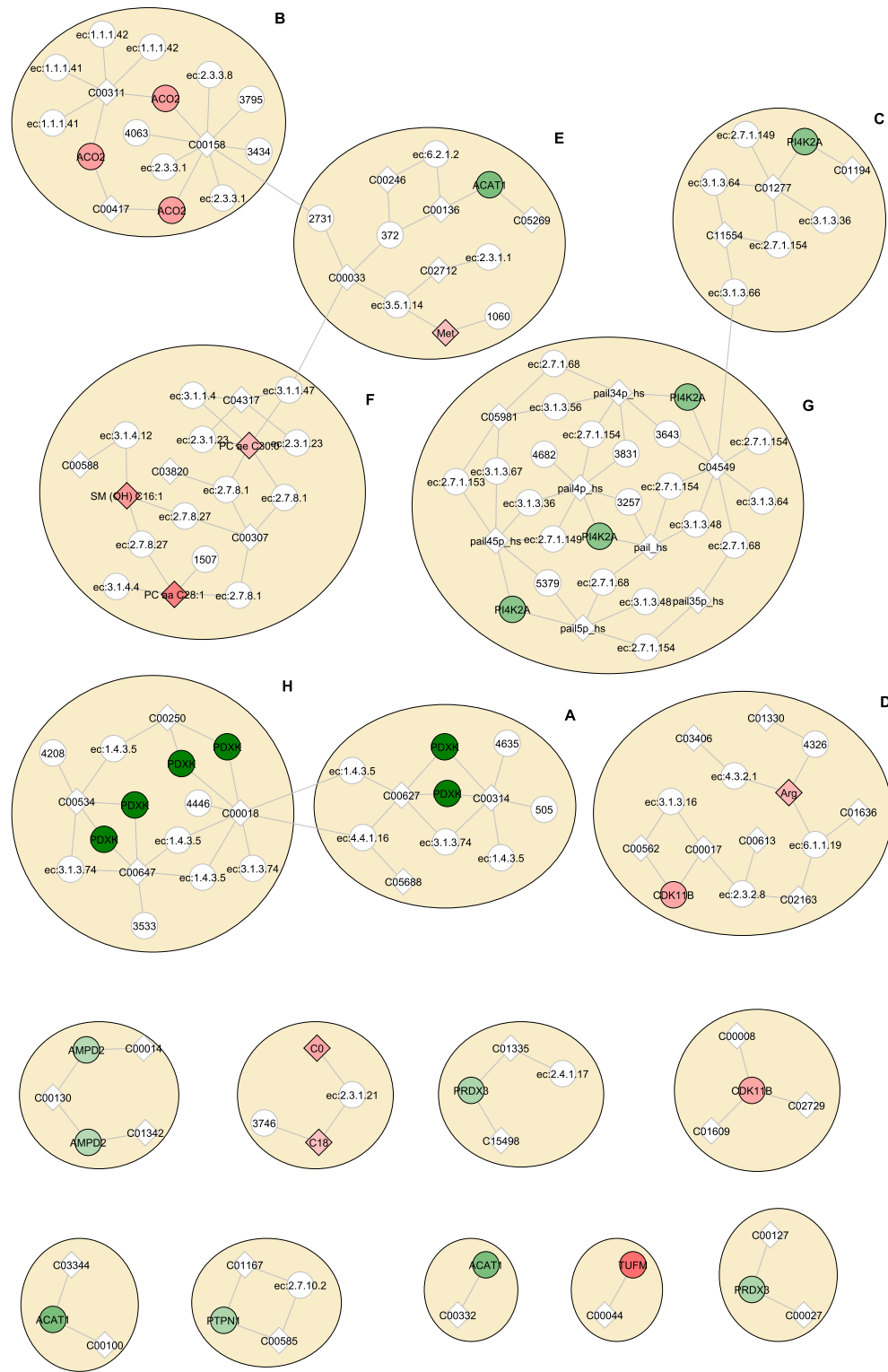


Figure S2 C



Module	Functional Assignment
A	Vitamin B6 metabolism
B	Citrate cycle (TCA cycle)
C	Inositol phosphate metabolism
D	IL-7 signaling
E	Butanoate metabolism
F	Glycerophospholipid metabolism
G	Phosphatidylinositol signaling system
H	Vitamin B6 metabolism

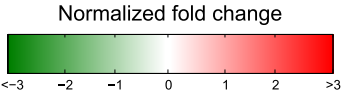


Figure S2 D

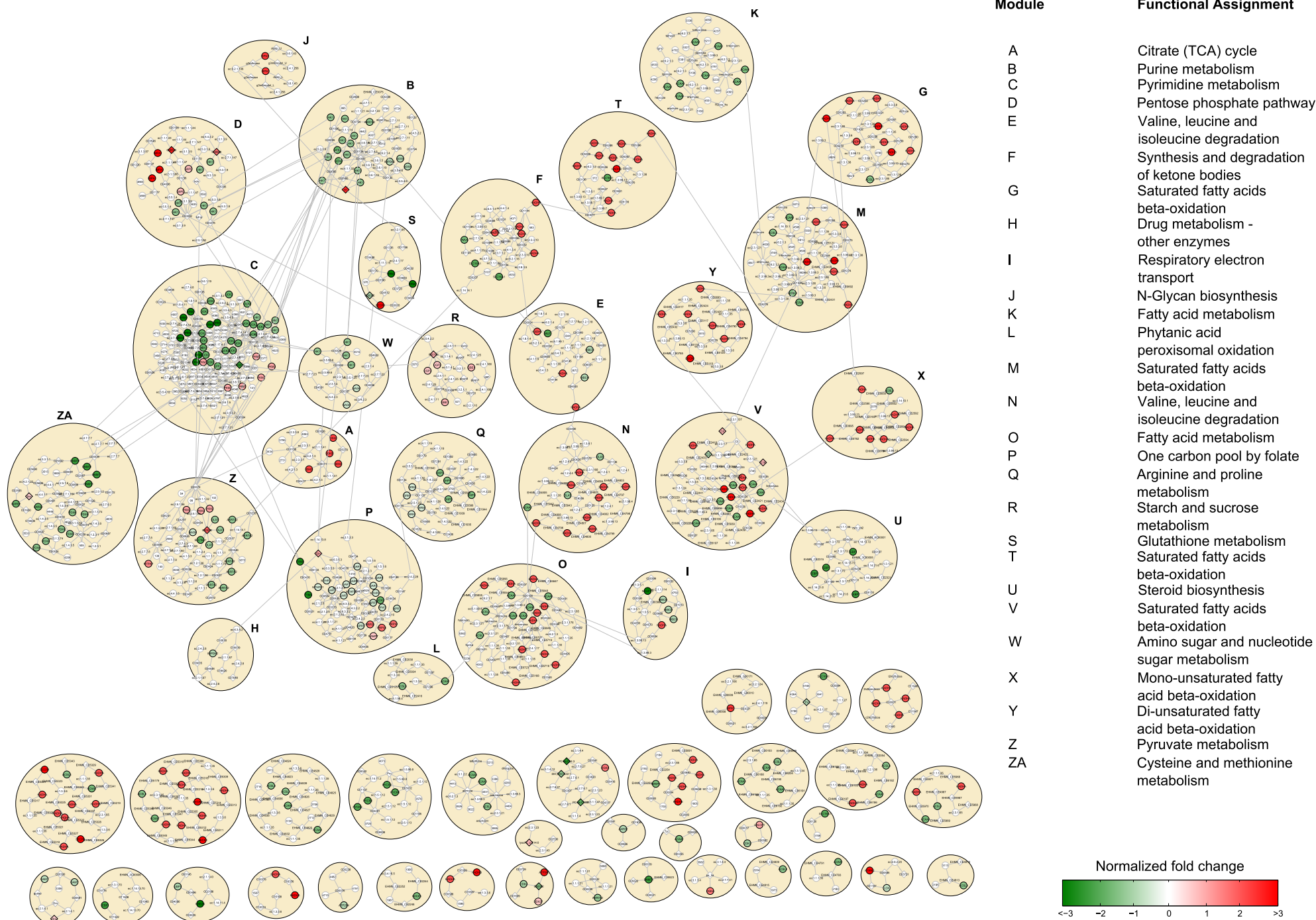


Figure S2:

Metabolic subnetworks inferred from significantly changed proteins and metabolites by the k-walks approach. Modules (highlighted ellipses) were calculated with the algorithm of Blondel et al. [1]. Functional assignment of the modules was performed by an overrepresentation analysis using the gene set and metabolite set analysis function of ConsensusPathDB [2]. Diamonds represent metabolites and circles depict reactions. In case of measured proteins catalyzing a reaction, the node is assigned to the respective encoding gene. Otherwise the nodes are labeled by the associated EC number. Measured metabolites are labeled by the respective name from the experimental platform, all others by an identifier of the database they originate from. Seed nodes are colored according to their fold-change normalized by the standard deviation. Nodes that are either not measured or not significantly changed are colored in white. A - B[a]P/control; B - activated/control; C - activated+B[a]P/activated; D - activated+B[a]P/B[a]P. Of note, the identified affected subnetworks and clusters are varying in size, indicating the assigned importance of the incorporated paths and pathways by the random walker.

1. Blondel VD, Guillaume J-L, Lambiotte R, Lefebvre E (2008) Fast unfolding of communities in large networks. *J Stat Mech Theory Exp* 2008: P10008. doi:10.1088/1742-5468/2008/10/P10008.
2. Kamburov A, Pentchev K, Galicka H, Wierling C, Lehrach H, et al. (2011) ConsensusPathDB: toward a more complete picture of cell biology. *Nucleic Acids Res* 39: D712–717. doi:10.1093/nar/gkq1156.