

Uncovering Metabolic Signatures in Cancer-Derived Exosomes: LC-MS/MS and NMR Profiling.

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Supplementary Figures:

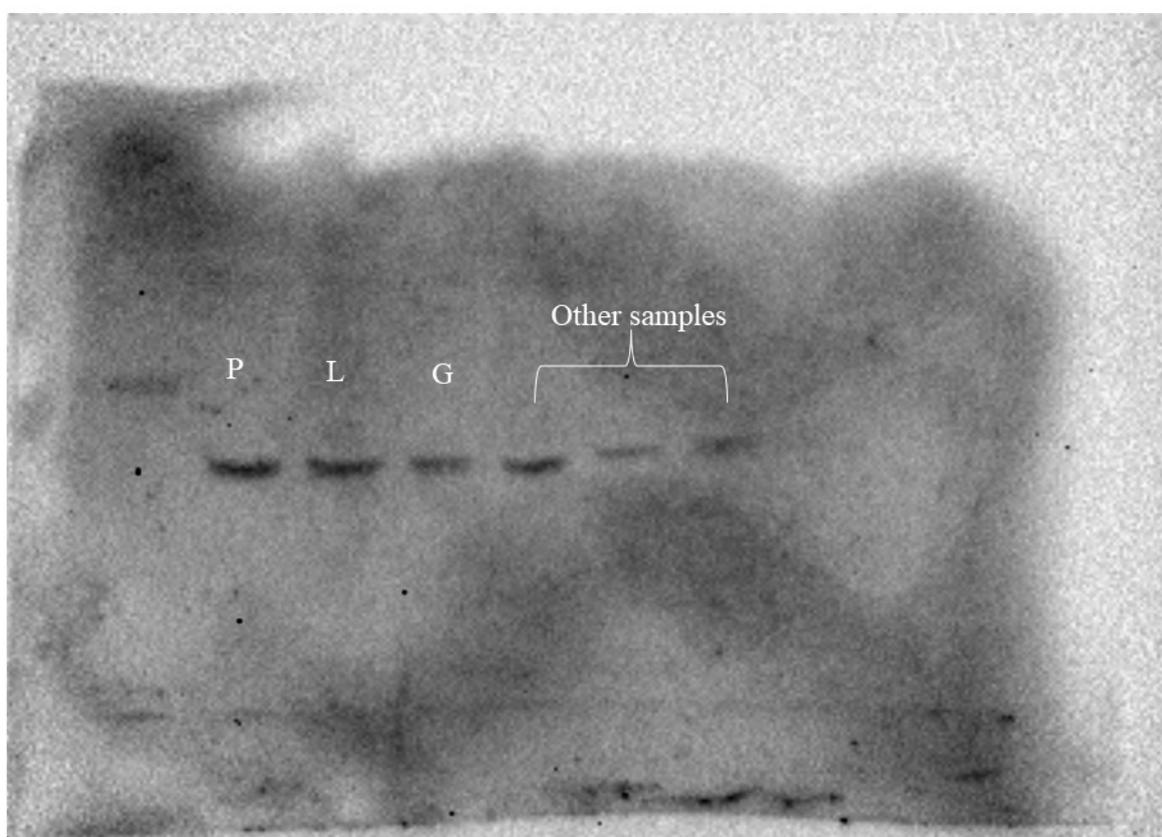


Fig S1: Full Western blot of common tetrapanin cell surface exosomal marker CD63 of exosomes derived Pancreatic (P), Lung (L) and Glioma (G).

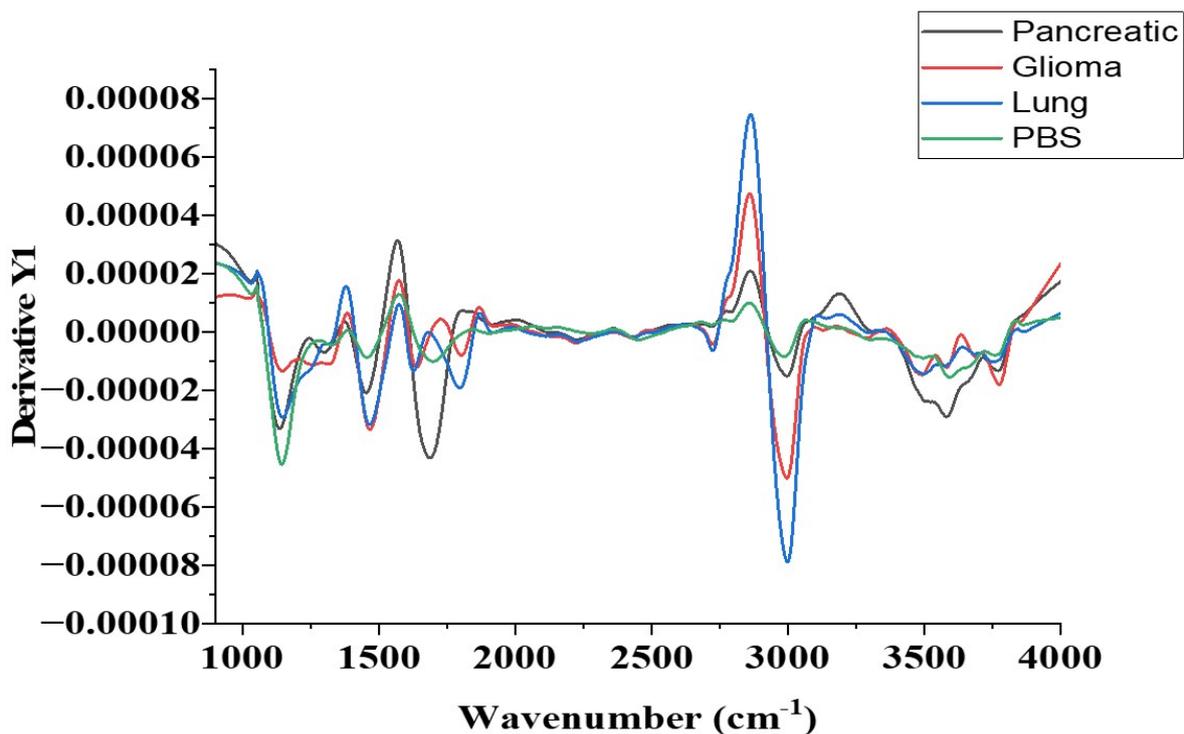


Fig S2: ATR-FTIR first derivative spectra of Exosomes derived from Pancreatic, Glioma and Lung cancer cells.

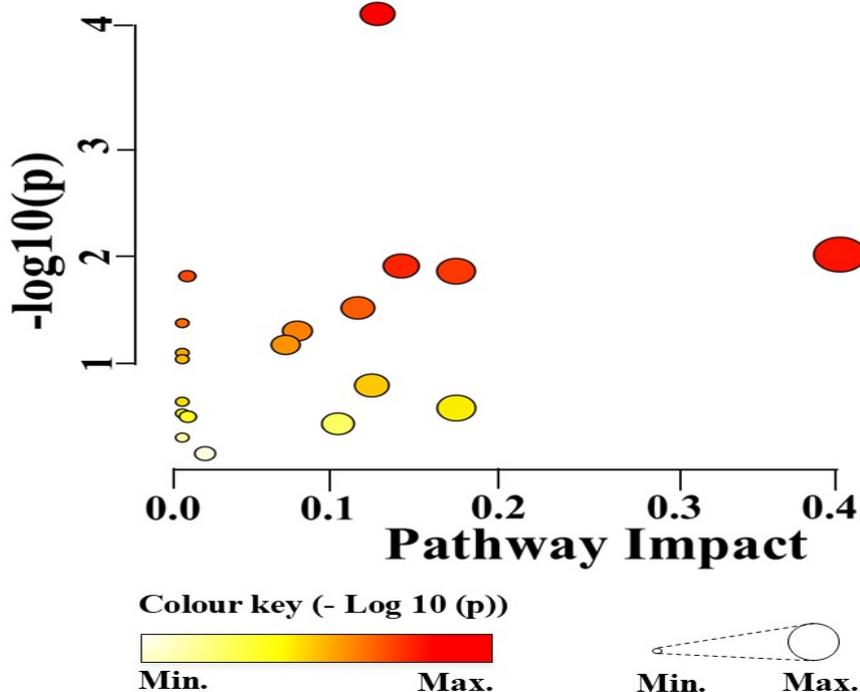


Fig S3: Pathway analysis of metabolites obtained from Pancreatic cancer cells via NMR using Metaboanalyst 6.0

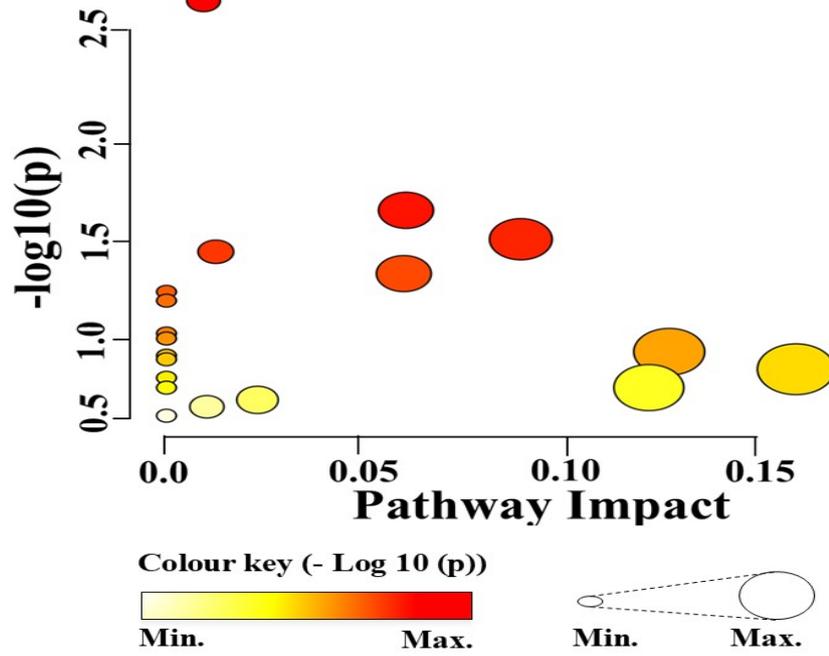


Fig S4: Pathway analysis of metabolites obtained from Lung cancer cells via NMR using Metaboanalyst 6.0

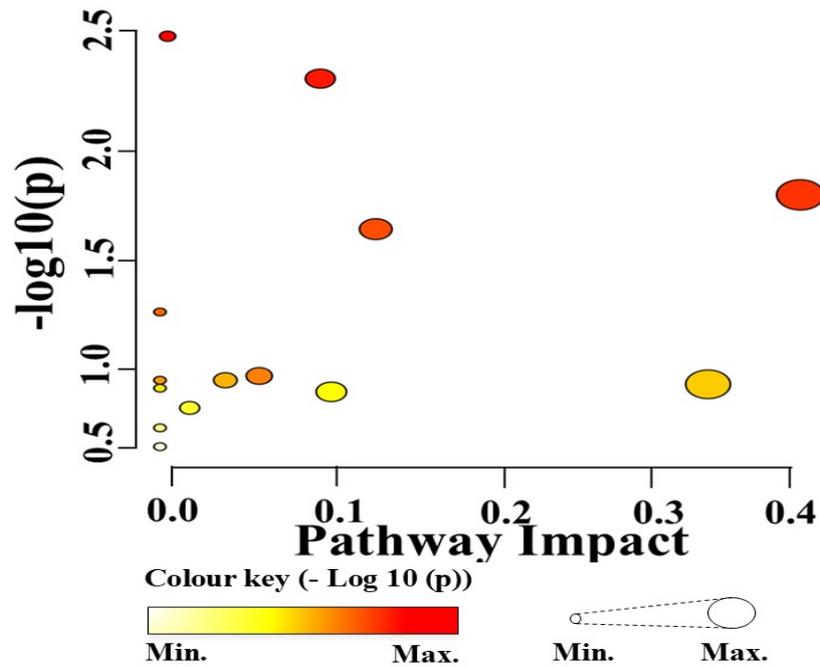


Fig S5: Pathway analysis of metabolites obtained from Glioma cancer cells via NMR using Metaboanalyst 6.0

Tables:**S1: Pancreatic cancer**

Pathway Name	-Log 10(p)	Impact	Hit/Total	-Log10 (FDR)
Galactose metabolism	4.2137	0.12027	4/27	0.0048907
Glycerolipid metabolism	2.086	0.40498	2/16	0.20364
Starch and Sucrose metabolism	1.9849	0.13486	2/18	0.20364
Pentose and glucuronate interconversions	1.9388	0.16867	2/19	0.20364
Fructose and Mannose Metabolism	1.8953	0.00311	2/20	0.20364
Alanine, Aspartate and Glutamate metabolism	1.6142	0.10817	2/28	0.32417
Glycine, Serine and Threonine metabolism	1.48	0.0	2/33	0.3784
Arginine and Proline metabolism	1.4099	0.07093	2/36	0.3891
Amino sugar and nucleotide sugar metabolism	1.2875	0.06367	2/42	0.45854
Thiamine metabolism	1.2168	0.0	1/7	0.4856
Taurine and hypotaurine metabolism	1.1606	0.0	1/8	0.50245
Arginine biosynthesis	0.92825	0.11675	1/14	0.78642
Pantothenate and CoA Biosynthesis	0.78397	0.0	1/20	1.0
Pentose Phosphate pathway	0.72856	0.16884	1/23	1.0
Glycolysis/Gluconeogenesis	0.68058	0.0	1/26	1.0
Glutathione metabolism	0.6519	0.00343	1/28	1.0
Cysteine and methionine metabolism	0.58927	0.09592	1/33	1.0
Primary Bile acid biosynthesis	0.4675	0.0	1/46	1.0
Purine metabolism	0.32581	0.01406	1/10	1.0

Table S2: Lung Cancer

Pathway Name	-Log 10(p)	Impact	Hit/Tota l	-Log10 (FDR)
Galactose metabolism	2.7487	0.00905	3/27	0.1427
Purine metabolism	1.5842	0.06425	3/70	0.88521
Glycine, Serine and Threonine metabolism	1.4236	0.09505	2/33	0.88521
Glycerophospholipid metabolism	1.354	0.01324	2/36	0.88521
Amino sugar and Nucleotide Metabolism	1.2326	0.06367	2/42	0.936555
Valine, Leucine and Isoleucine biosynthesis	1.1316	0.0	1/8	0.9454
Ascorbate and Aldarate metabolism	1.0824	0.0	1/9	0.9454
Arginine Biosynthesis	0.12587	0.0	1/14	1.0
Butanoate metabolism	0.87201	0.0	1/15	1.0
Starch and Sucrose metabolism	0.79854	0.13486	1/18	1.0
Pentose and glucuronate interconversions	0.77696	0.0	1/19	1.0
Fructose and Mannose metabolism	0.75658	0.0	1/20	1.0
Pentose Phosphate pathway	0.70156	0.16884	1/23	1.0
Glycolysis/Gluconeogenesis	0.65398	0.0	1/26	1.0

Lysine degradation	0.59935	0.0	1/30	1.0
Inositol Phosphate metabolism	0.59935	0.1293	1/30	1.0
Arginine and proline metabolism	0.53138	0.02442	1/36	1.0
Valine, Leucine and isoleucine degradation	0.49305	0.01064	1/40	1.0
Primary Bile acid biosynthesis	0.4434	0.0	1/46	1.0

Tabl1 S3: Glioma Cancer

Pathway Name	-Log 10(p)	Impact	Hit/Total	-Log10 (FDR)
Pyrimidine metabolism	2.4706	0.00555	3/39	0.21657
Arginine biosynthesis	2.2665	0.11675	2/14	0.21657
Galactose metabolism	1.7.65	0.46646	2/27	0.52415
Cysteine and Methionine metabolism	1.5413	0.15717	2/33	0.57505
Ascorbate and Aldarate metabolism	1.1423	0.0	1/9	1.0
Pentose and glucuronate interconversions	0.83422	0.07229	1/19	1.0
Fructose and Mannose metabolism	0.81358	0.0	1/20	1.0
Arginine Biosynthesis	0.12587	0.0	1/14	1.0
Pantothenate and CoA Biosynthesis	0.81358	0.04762	1/20	1.0
Beta-Alanine metabolism	0.79402	0.39925	1/21	1.0
Propanoate metabolism	0.77544	0.0	1/22	1.0
Pentose Phosphate pathway	0.75777	0.12481	1/23	1.0
Alanine, aspartate and glutamate metabolism	0.68046	0.02163	1/28	1.0
Arginine and proline metabolism	0.58422	0.00	1/36	1.0
Primary Bile acid biosynthesis	0.49377	0.0	1/46	1.0

