Supporting Duccoment

Supplementary Figures

Figure S1- A- Figure showing retention time of peptides of FASN and ACLY in control and CAC groups.
B. Figure showing average peak area intensity of peptides of FASN i.e. R. DNLEFFLAGIGR.L and R. LSIPTYGLQCTR.A in control and CAC groups; **C.** Abundance of the peptides of FASN in individual samples
D. Figure showing average peak area intensity of peptides of ACLY i.e. R. EAYPEEAYIADLDAK.S and K. DLVSSLTSGLLTIGDR.F in control and CAC groups; **E.** Abundance of the peptides of ACLY in individual samples

Figure S2-A- Multiscatter plot showing the correlation of *de novo* lipogenesis inhibited samples with controls with each other; **B**. Histogram showing sample distribution; **C.** Figure showing violin plot of some important proteins altered significantly as a result of inhibition of *de novo* lipogenesis

Figure S3- A. Heatmap showing alteration of metabolic pathway as a result of *de novo* lipogenesis inhibition; **B.** Protein-protein interaction network showing the significant metabolic pathways in *de novo* lipogenesis inhibited samples

Figure S4- Figure showing intensity and retention time comparison of GAPDH across the samples

Figure S5- Figure showing relative intensity of peptides of PSMC5 across the control and de novo lipogenesis inhibited samples and their peptide spectrum match with PROSIT library

Figure S6- Figure showing relative intensity of peptides of RPS27A across the control and de novo lipogenesis inhibited samples and their peptide spectrum match with PROSIT library

Figure S7- Figure showing relative intensity of peptides of ATMK across the control and de novo lipogenesis inhibited samples and their peptide spectrum match with PROSIT library

Supplementary Tables

Table S1- Sample Details

Tables S2- List of significantly differentially expressed proteins identified from iTRAQ analysis

Tables S3- Peak intensities of Lipogenic proteins and their respective peptides

Table S4- Cell cycle analysis & apoptosis assay result in HCT116 controls and *de novo* lipogenesis inhibited cells

Table S5- List of significant proteins identified from deep proteomics of *de novo* lipogenesis inhibition

Table S6- GSEA input file having log transformed peptide intensity

Table S7- Statistical analysis of significant proteins validated from *de novo* lipogenesis inhibition using PRM

Table S8- List of FDA approved drugs used in our study for *in-silico* molecular docking.

Table S9- Binding Affinity of top drugs identified in in-silico molecular docking with interacting residues.