Supplementary materials

Granulocyte Colony-Stimulating Factor Promotes an Aggressive Phenotype of Colon and Breast Cancer Cells with Biochemical Changes Investigated by Single-Cell Raman Microspectroscopy and Machine Learning Analysis

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Methods

TaqMan Gene Array

The TaqMan mouse gene array from ThermoFisher Scientific was customized to contain the following validated primers: 18S, Actb, Aldh1a1, Atm, Bad, Bcl2, Birc5, Casp8, Ccl2, Cdc25a, Cdh1, Cdk2, Cdk4, Csf3r, Ctnnb1, Cxcr4, Egfr, Fasl, Fgf1, Flt1, Fos, Gadph, Grb2, Hgf, Il-6, Jak1, Jak2, MapKap2, Met, Mmp2, Mmp9, Nanog, Pcna, Pdgfra, serpine1, Snail, Socs3, Sox2, Stat1, Stat3, Stat5a, Tnf, Trp53, Twist1, Vegfa, and Vim. Samples were run in triplicate and data presented as genes with significant changes.

Raman data pre-processing

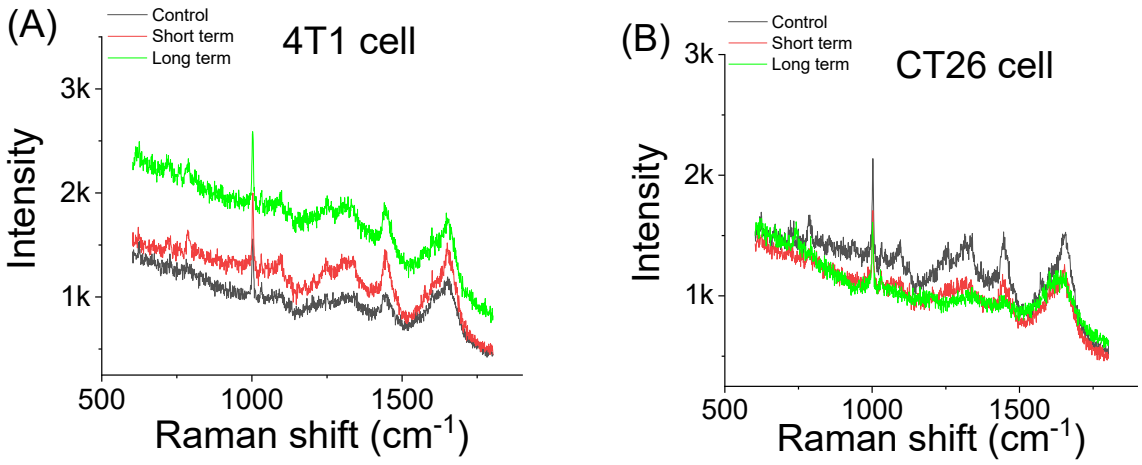

Figure S1. Raw averaged Raman spectra of 4T1 cell (A) and CT26 cell (B).

Table S1. Raman assignments

Raman shift (cm^{-1})	Assignment	Reference
720	Adenine	[1]
786	DNA: O-P-O, cytosine, uracil, thymine	[2]
802	Nucleic acids (C-O-P-O-C in RNA backbone)	[3]
1002	Symmetric ring breathing mode of phenylalanine	[4]
1095	DNA	[5]
1443	CH_2 bending mode of proteins and lipids	[6]
1608	Cytosine (NH_2)	[7]
1655	Amide I (C= O stretching mode of proteins, α-helix conformation)/ C= C lipid stretching	[4]

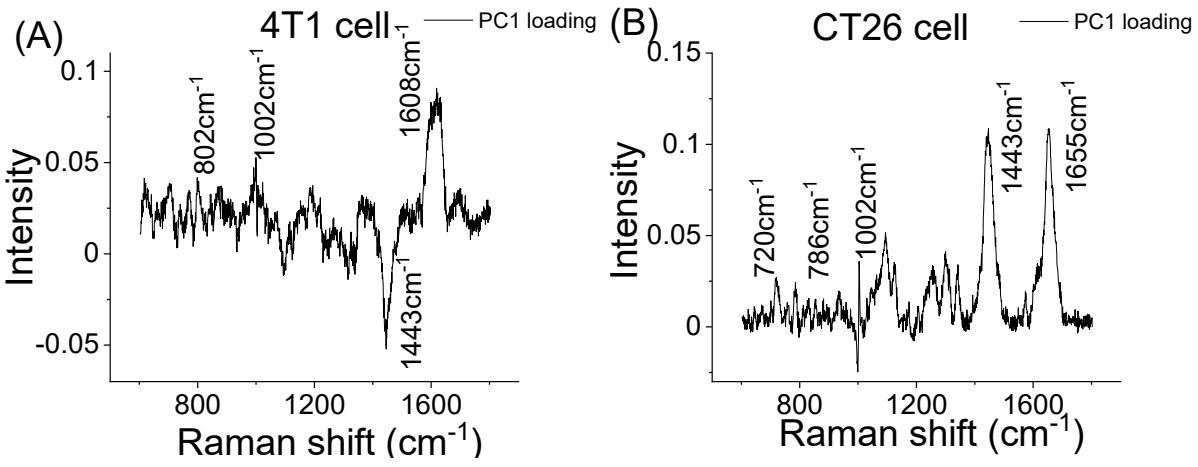

Figure S2. PCA loading in 4T1 cells (A) and CT26 cells (B)

Reference:

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