Analytical and Bioanalytical Chemistry

Electronic Supplementary Material

Monitoring of changes in lipid profiles during PLK1 knockdown in cancer cells using DESI MS

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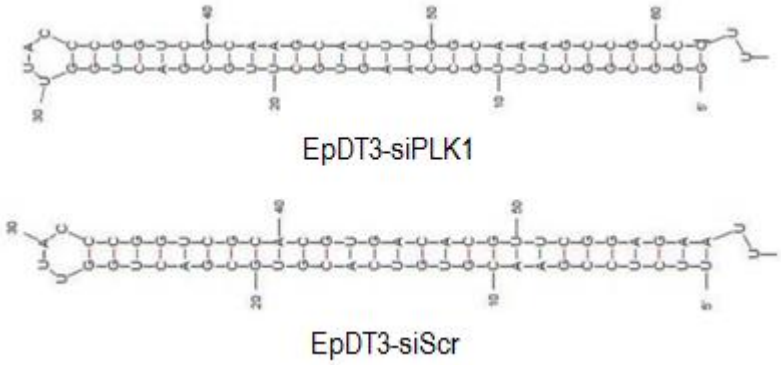

Fig. S1 Secondary structure of EpDT3-siPLK1 and EpDT3-siScr

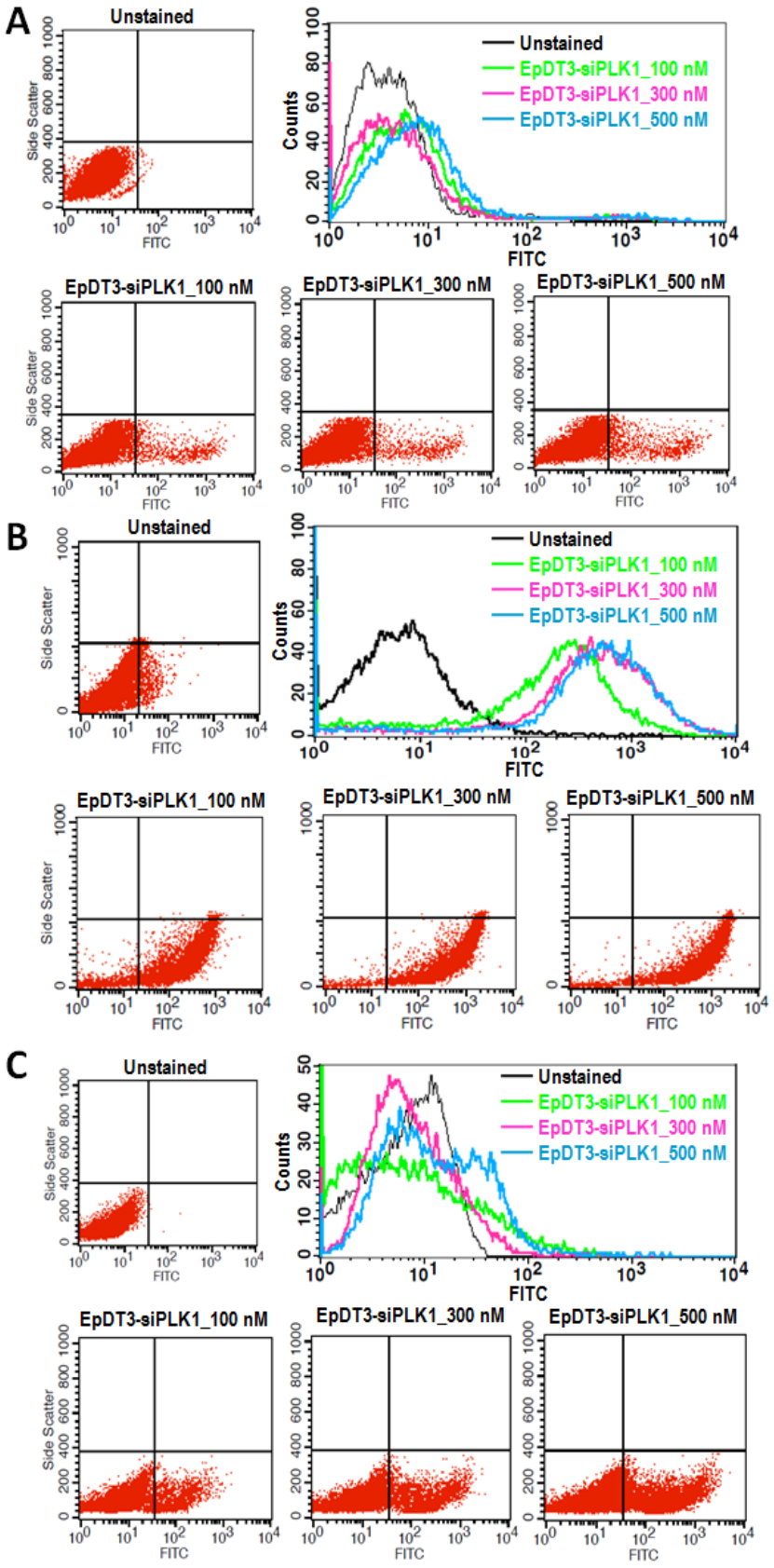

Fig. S2 Histogram overlay plots and side scatter plots of (A) MIO-M1, (B) MCF-7, and (C) WERI-RB1 cells in unstained conditions and after treating with different concentrations of EpDT3-siPLK1 chimera

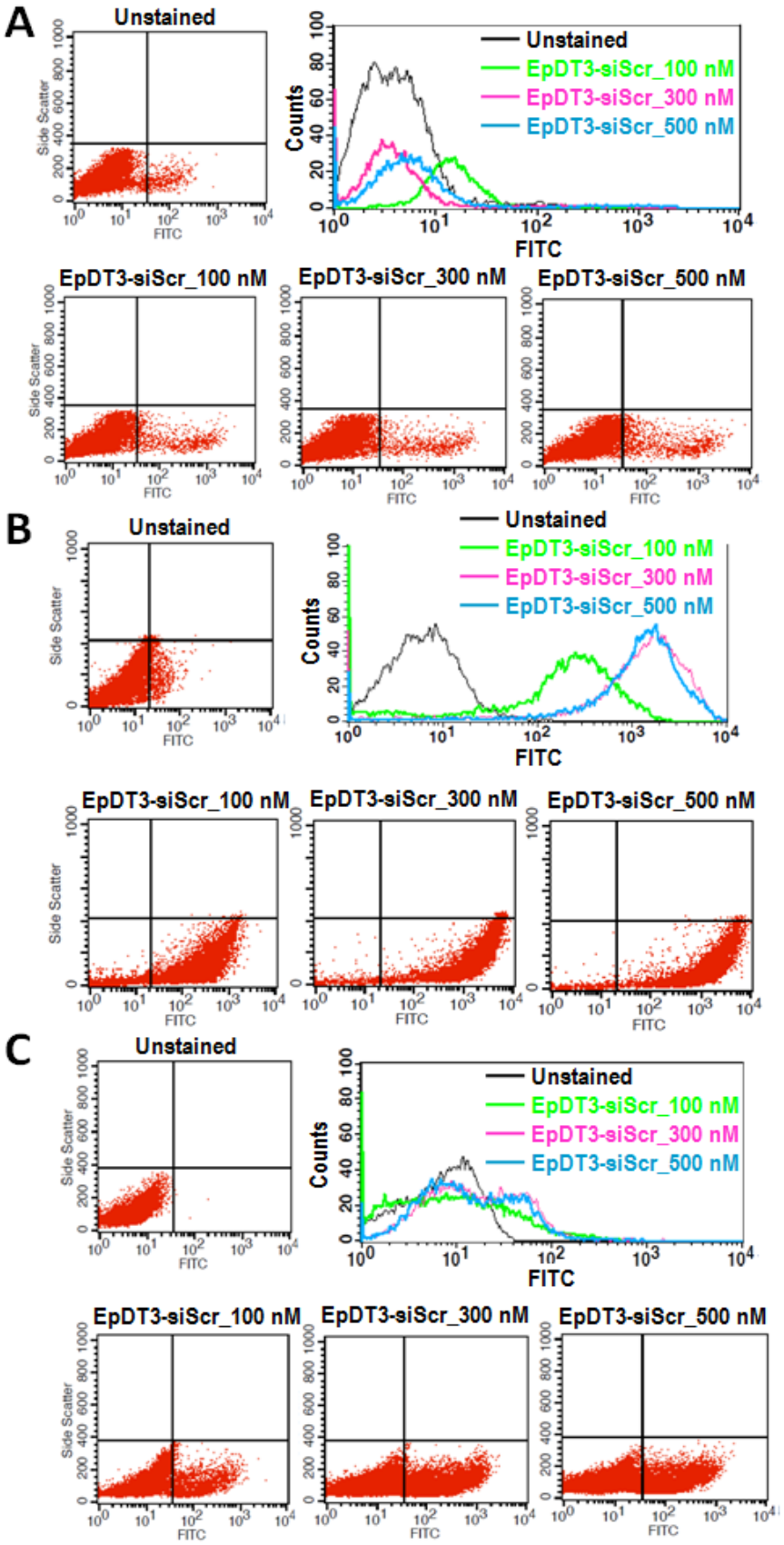

Fig. S3 Histogram overlay plots and side scatter plots of (A) MIO-M1, (B) MCF-7, and (C) WERI-RB1 cells in unstained conditions and after treating with different concentrations of EpDT3-siScr chimera

Fig. S4 PAGE data showing bands of siPLK1 and EpDT3

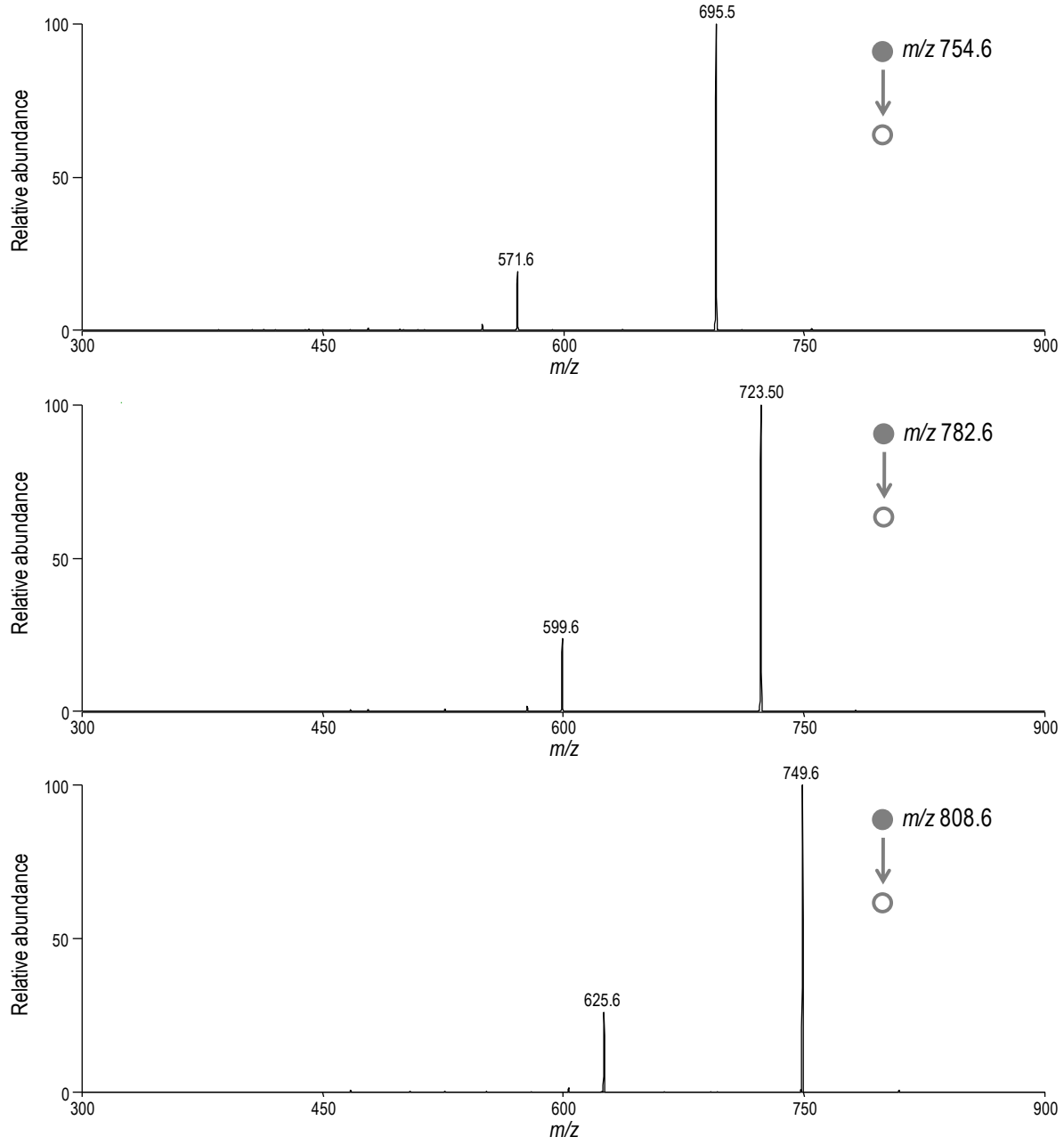

Fig. S5 Positive mode DESI MS/MS spectra of *m/z* 754.6, *m/z* 782.6, and *m/z* 808.6 from MCF-7 cells

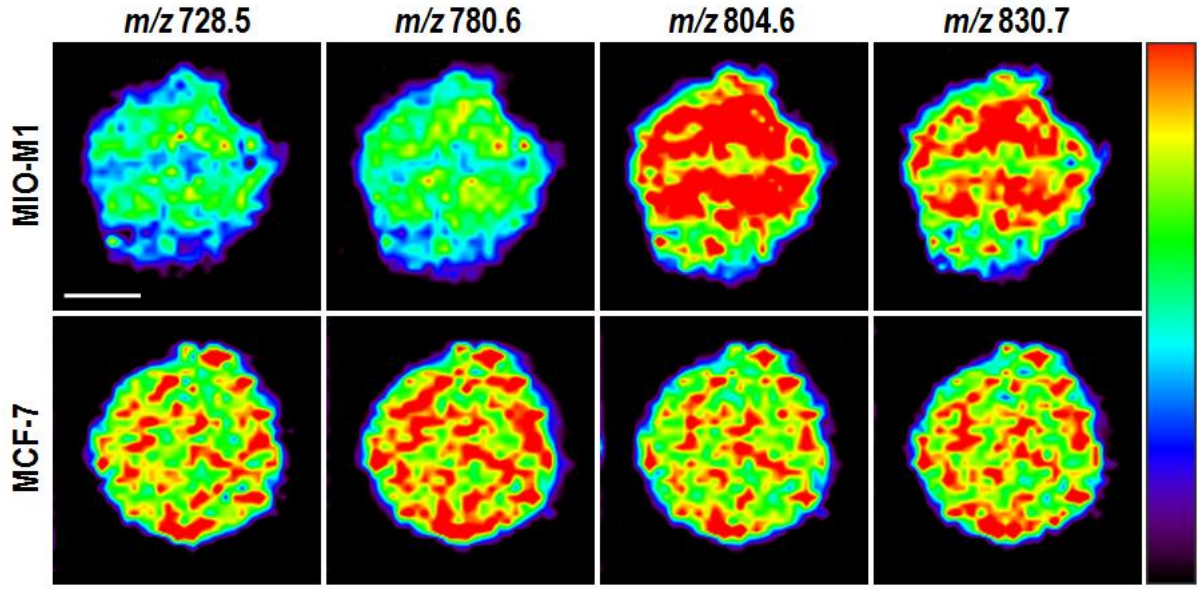

Fig. S6 DESI MS images of different lipids from MIO-M1 and MCF-7 cell lines. Scale bar of 2 mm applies to all the images. Intensity is color coded; from black (low) to red (high)

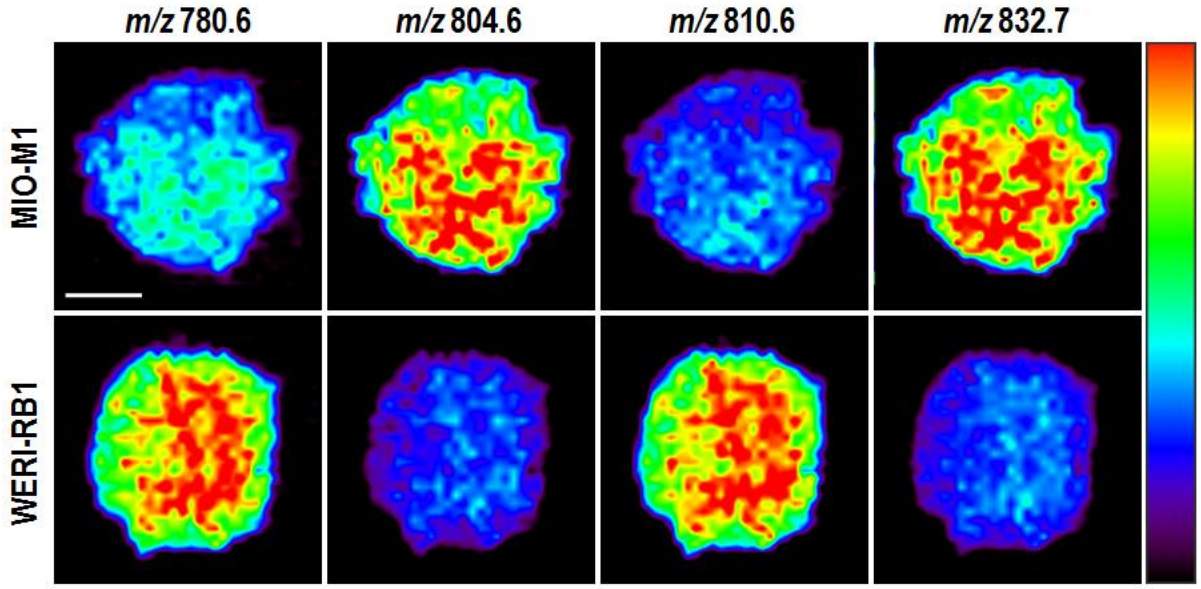

Fig. S7 DESI MS images of different lipids from MIO-M1 and WERI-RB1 cell lines. Scale bar of 2 mm applies to all the images. Intensity is color coded; from black (low) to red (high)

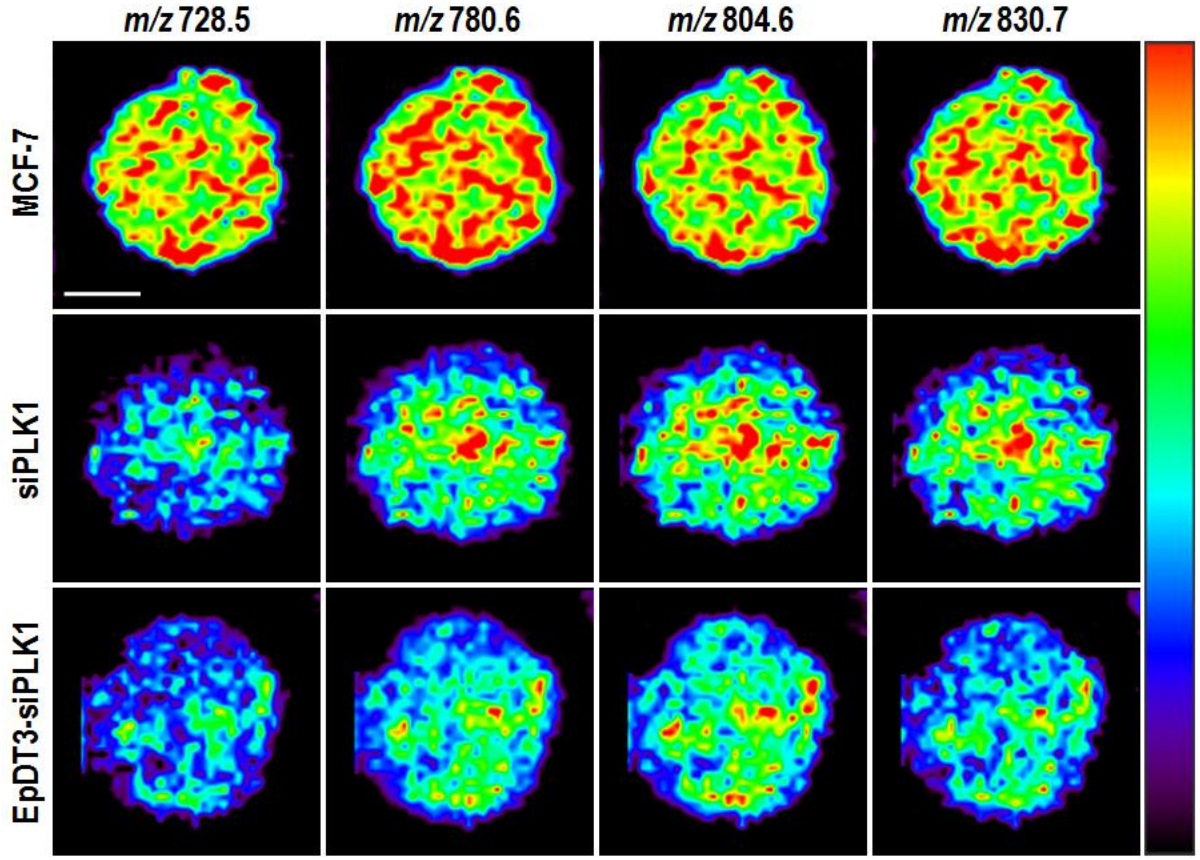

Fig. S8 DESI MS images of different lipids from MCF-7 cells with different treatment conditions. Scale bar of 2 mm applies to all the images. Intensity is color coded; from black (low) to red (high)

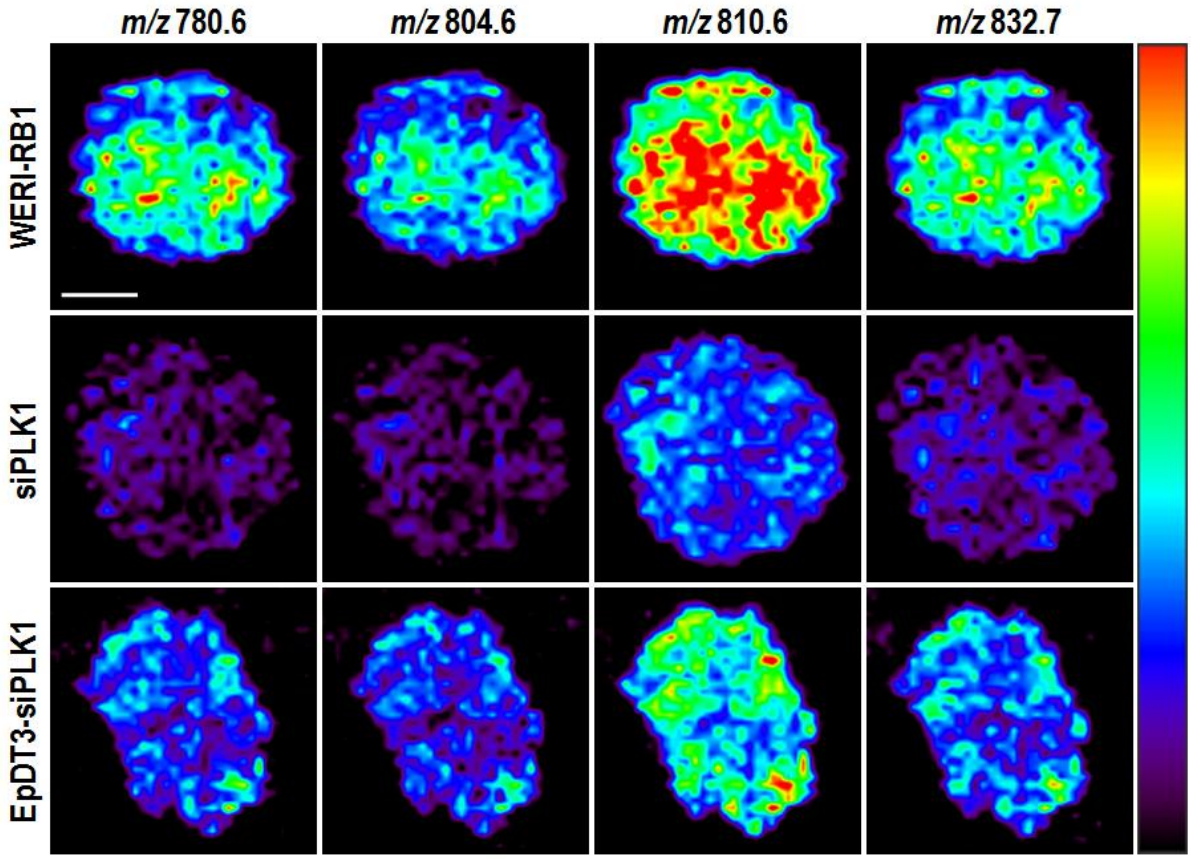

Fig. S9 DESI MS images of different lipids from WERI-RB1 cells with different treatment conditions. Scale bar of 2 mm applies to all the images. Intensity is color coded; from black (low) to red (high)

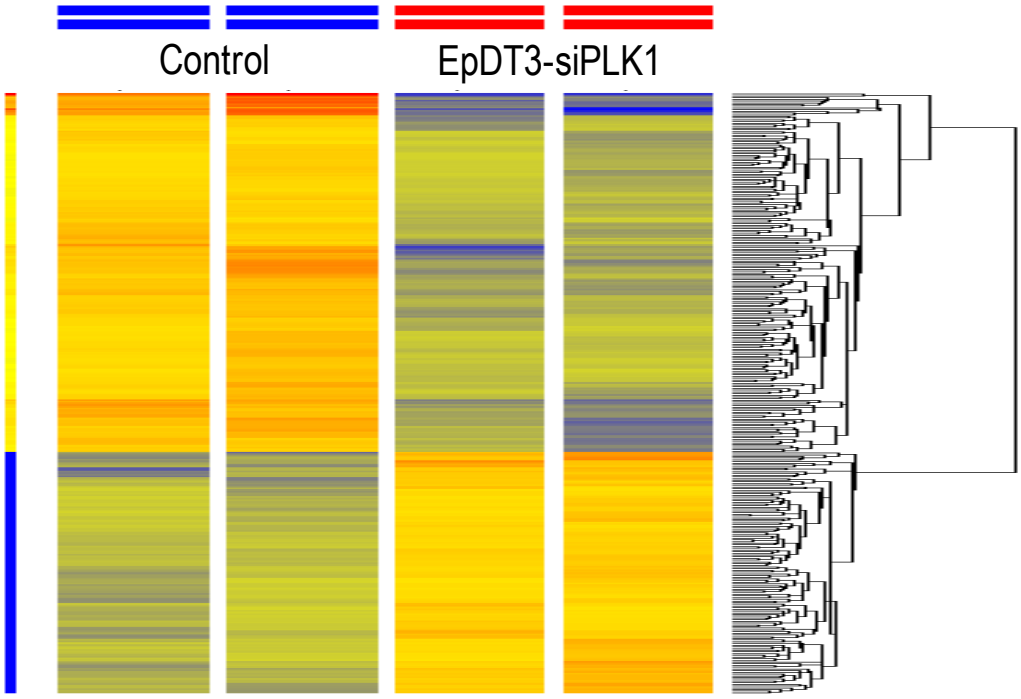

Fig. S10 Whole genome microarray analysis of MCF-7 cells. Hierarchical clustering reveals that control cells (N=2) are different from EpDT3-siPLK1 treated cells (N=2)

Sl. no.	Gene	Gene symbol	Type of change	Fold regulation
1	Dual specificity phosphatase 10	DUSP10	Up	2.5
2	Fatty acyl-CoA reductase 2	FAR2	Up	2.1
3	cAMP responsive element binding protein 3-like 2	CREB3L2	Up	2.0
4	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	NDUFS2	Up	2.0
5	Phospholipase A2, group IVC (cytosolic, calcium-independent)	PLA2G4C	Up	2.0
6	Protein kinase, AMP-activated, alpha 1 catalytic subunit	PRKAA1	Up	2.0
7	Kruppel-like factor 7 (ubiquitous)	KLF7	Down	18.6
8	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)	CDKN1A	Down	13.0
9	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	RAC1	Down	9.1
10	Fas associated factor family member 2	FAF2	Down	5.1
11	Polo-like kinase 1	PLK1	Down	4.2
12	Neuroblastoma RAS viral (V-ras) oncogene homolog	NRAS	Down	3.3

Table S1 Partial list of genes and gene expression changes dysregulated by EpDT3-siPLK1 treatment in MCF-7 cells

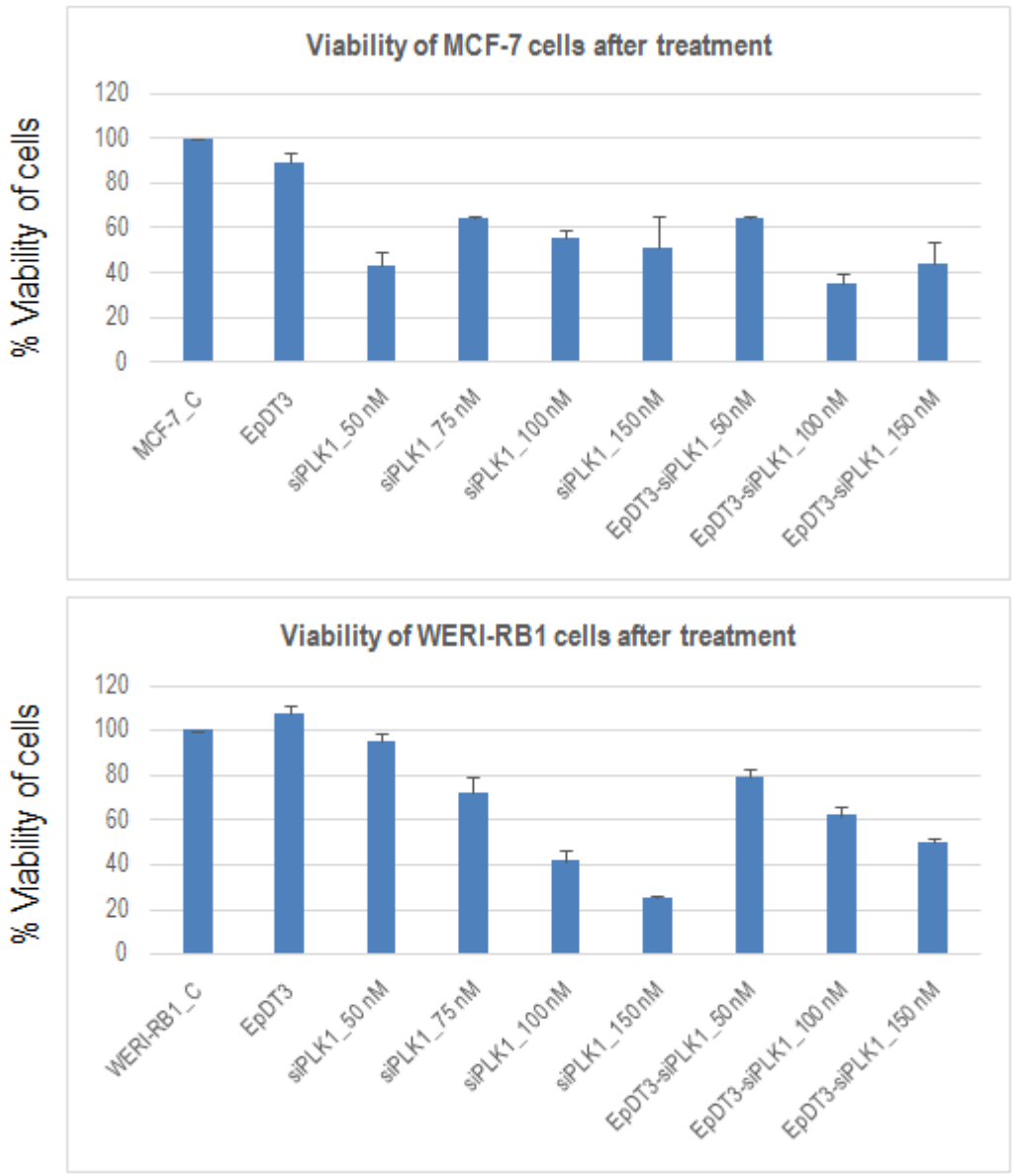

Fig. S11 Cell viability of MCF-7 (top) and WERI-RB1 (bottom) cells when they were treated with EpDT3, different concentrations of siPLK1, and EpDT3-siPLK1

GO process	P-value	No. of hits
Intracellular	1.81E-11	275
Cellular macromolecule metabolic process	1.44E-05	145
Positive regulation of cellular metabolic process	1.44E-05	63
Death	4.32E-06	44
Apoptotic process	4.04E-05	37
Regulation of cell cycle	4.47E-06	31
DNA conformation change	2.30E-08	20
Chromatin assembly	3.10E-11	19
Phosphatidylinositol mediated signalling	2.39E-12	17
Centromere complex assembly	9.19E-16	15
Cell cycle arrest	1.83E-04	10
Glycosylceramide catabolic process	2.74E-04	3
Sphingoid biosynthetic process	4.05E-04	3

Table S2 Gene Ontology processes regulated by PLK1 knockdown in MCF-7 cells