

Supplementary Materials: Cholesterol-Induced Metabolic Reprogramming in Breast Cancer Cells Is Mediated via the ERR α Pathway

Faegheh Ghanbari, Anne-Marie Fortier, Morag Park and Anie Philip

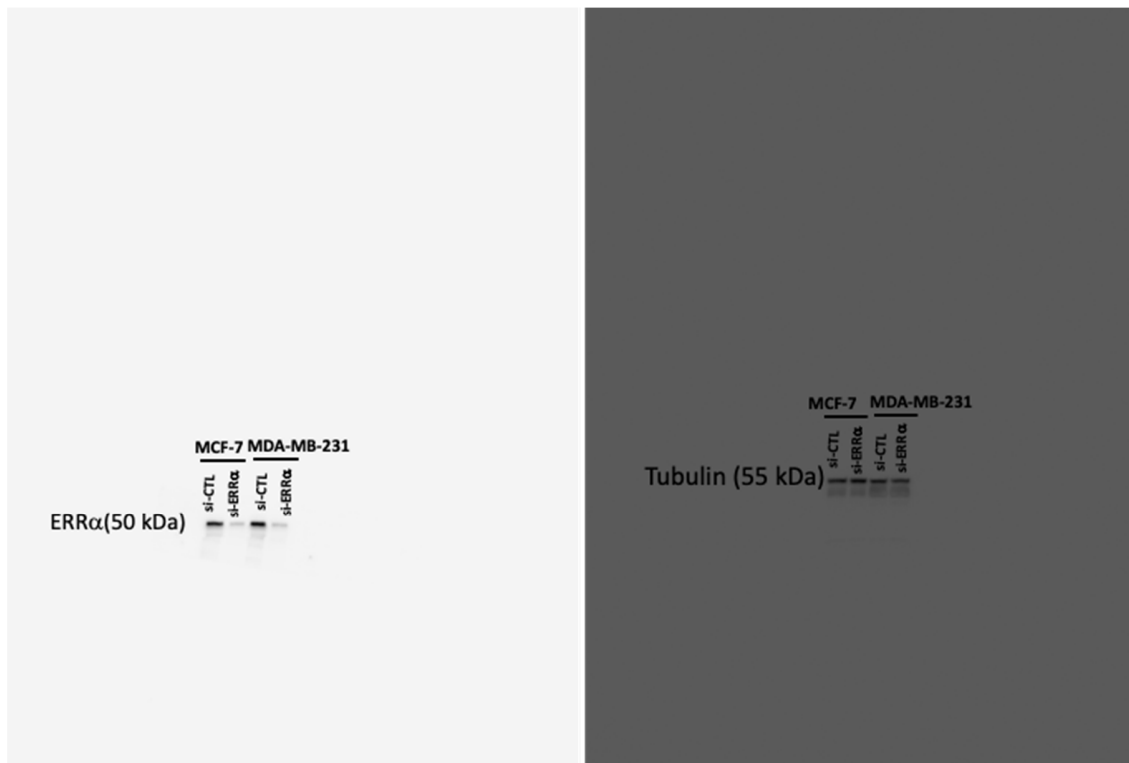


Figure S1. Uncorrupted western blot for Figures 1B & 1G.

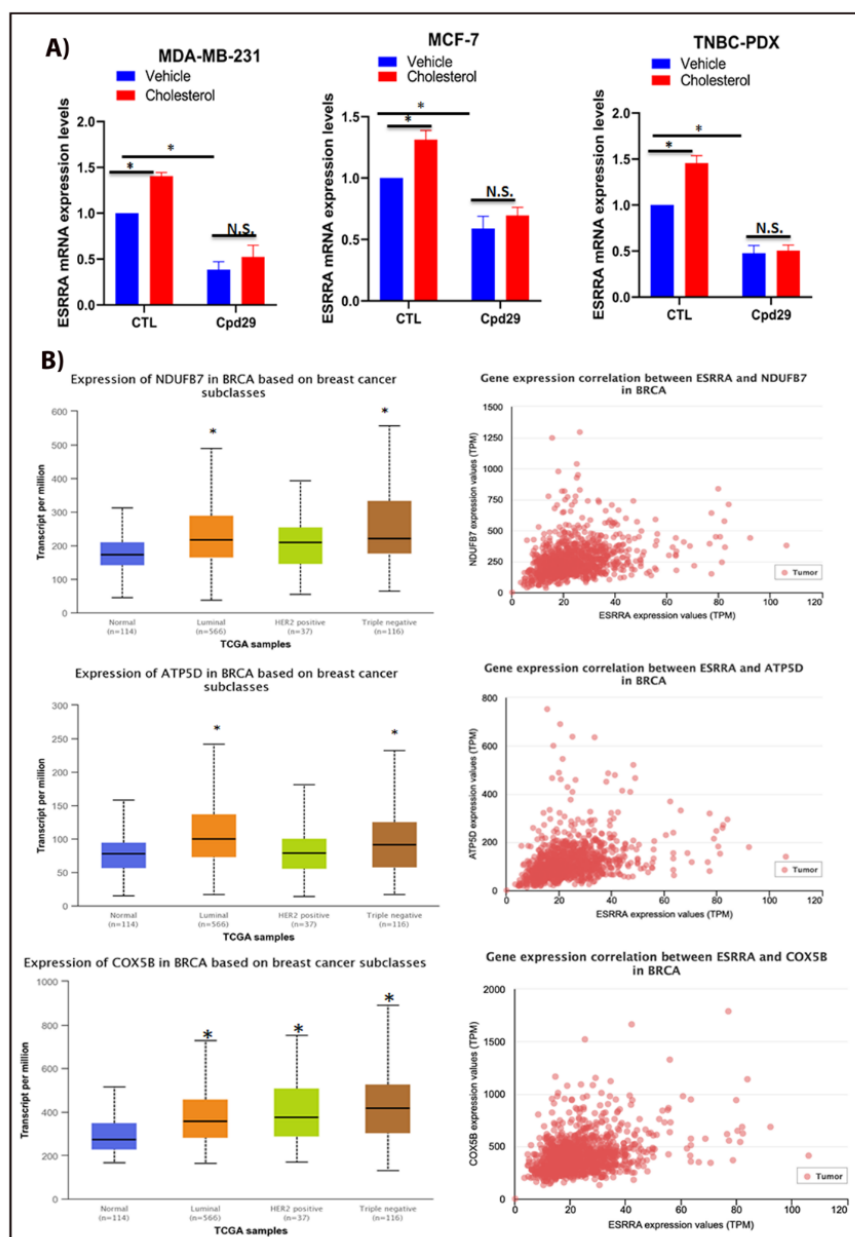


Figure S2. ERRα gene expression levels are positively correlated with the key enzymes involved in OXPHOS using TCGA databases. **(A)** The relative mRNA levels of ERRα in MDA-MB-231, MCF-7, and TNBC-PDX cells. Total RNA was extracted and analyzed using RT-qPCR. MDA-MB-231 cells were treated with vehicle (Veh), cholesterol (Chol, 5 μM) and/or cpd29 (5 μM) for 48 h. MCF-7 and TNBC-PDX cells were treated with vehicle (Veh), cholesterol (Chol, 10 μM) and/or cpd29 (10 μM) for 48 h. **(B)** The data represents the mRNA levels of the indicated genes in breast tumors and corresponding normal tissue obtained from the TCGA database. The graphs were visualized using the UALCAN web-portal. Expression of NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 (NDUFB7) and ATP synthase subunit delta, mitochondrial (ATP5D) and COX5B: Cytochrome c oxidase subunit 5B in different subtypes of breast cancer and their correlation to the ERRα gene expression in breast tumors. The significance (*) was defined by comparing each subtype to the normal tissue.

Table 1. The human primers used for qPCR.

Name	Oligo Name	Sequence (5' to 3')
Glyceraldehyde 3-phosphate dehydrogenase	GAPDH Forward(F)	GTCTCCTCTGACTTCAACAGCG
	GAPDH Reverse (R)	ACCACCCTGTTGCTGTAGCCAA
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	NDUFB7 F	CTGCTCAAGTGCAAGCGTGACA
	NDUFB7 R	CGCTCAAACCTCCTTCATGCGCA
Cytochrome <i>c</i> oxidase subunit 5B, mitochondrial	COX5B F	GGAGATCATGCTGGCTGCAAAG
	COX5B R	GCAGCCTACTATTCTCTTGTG
ATP synthase subunit <i>g</i> , mitochondrial	ATP5L F	CCTGCTGAGATCCCTAGAGCTA
	ATP5L R	CCGACATAAAACCATCAACACC
Methionine synthase	MTR F	CCAACCTGTCTTCTCCTTCCG
	MTR R	CATACACAGGGAGGTTTCCAGC
Trifunctional purine biosynthetic protein adenosine-3	GART F	GCACATCTCTGCCTGTTTGGCT
	GART R	CATGGAACACCTCCAGTCCTAG
Glucose-6-phosphate dehydrogenase	G6PD F	CTGTTCCGTGAGGACCAGATCT
	G6PD R	TGAAGGTGAGGATAACGCAGGC
6-Phosphogluconate dehydrogenase	6PGD F	GTTCCAAGACACCGATGGCAAAC
	6PGD R	CACCGAGCAAAGACAGCTTCTC
Estrogen-related receptor alpha	ESRRA F	CCACTATGGTGTGGCATCCTGT
	ESRRA R	GGTGATCTCACACTCGTTGGAG
Citrate synthetase	CS F	CACAGGGTATCAGCCGAACCAA
	CS R	CCAATACCGCTGCCTTCTCTGT
Fumarate hydratase	FH F	CCGCTGAAGTAAACCAGGATTATG
	FH R	ATCCAGTCTGCCATACCACGAG
Aconitase 2	ACO2 F	CAATCGTCACCTCCTACAACAGG
	ACO2 R	GTCTCTGGGTTGAACTTGAGGG

Table 2. Basal-like breast tumor patient identification obtained from GEO: GSE78958 study.

BMI status	Patient ID
BMI>25 N=16	GSM2082151
	GSM2082188
	GSM2082294
	GSM2082303
	GSM2082370
	GSM2082160
	GSM2082163
	GSM2082205
	GSM2082300

BMI ≤ 25 N=15	GSM2082310
	GSM2082440
	GSM2082325
	GSM2082454
	GSM2082382
	GSM2082340
	GSM2082298
	GSM2082095
	GSM2082109
	GSM2082169
	GSM2082177
	GSM2082274
	GSM2082352
	GSM2082384
	GSM2082400
	GSM2082385
	GSM2082297
	GSM2082234
	GSM2082341
	GSM2082379
	GSM2082270
	GSM2082423