





























Supplementary Table S3. Twenty-eight of the 364 deregulated genes ($FDR \geq 0.01$ and fold change ≥ 2) between CM untreated (control) and CM treated (CMT) MCF-7 BC cells.

	MetaCore net symbol	MetaCore Name	Localizations	Edges
1		AHRR	nucleus	1
2		Amphiregulin	extracellular region	0
3		Aquaporin 3	membrane	0
4		C/EBPbeta	nucleus	6
5		C5aR	membrane	0
6		Cacng6	membrane	0
7		CADPS	cytoplasm	0
8		Calmegin	cytoplasm	0
9		CEBPG	nucleus	0
10		CEP3	cytoplasm	0
11		Ceruloplasmin	extracellular region	1
12		Collagen II	extracellular region	1
13		CYP1A1	cytoplasm	2
14		CYP4F3	cytoplasm	0
15		ENPP2	extracellular region	0
16		EPAS1	nucleus	4
17		Epiregulin	extracellular region	1
18		GluR7	membrane	0
19		IBP5	extracellular region	1
20		IL-1RI	membrane	0
21		ITGB6	membrane	0
22		PDE11A	cytoplasm	0
23		PTG	cytoplasm	1
24		SLC3A2	membrane	1
25		SLC7A5	membrane	2
26		SOCS2	cytoplasm	0
27		VEGFR-2	membrane	1
28		WNT3A	extracellular region	0