

Table S2. Changes in Global Methylation Between 5-Aza-dC- and Control-Treated Cell Lines			
	Change in Methylation	Filter	No. of CpG Sites
TMX2-28-5-Aza-dC v. TMX2-28-Control	Hypermethylated	Fold change ≥ 1.8 in TMX2-28-Aza (TMX2-28-5-Aza-dC/TMX2-28-Control), β -value ≥ 0.1 in TMX2-28-5-Aza-dC, Detection p-value ≤ 0.01 for TMX2-28-5-Aza-dC and TMX2-28-Control	59 (0.01%)
	Hypomethylated	Fold change ≥ 1.8 in TMX2-28-Control (TMX2-28-Control/TMX2-28-5-Aza-dC), β -value ≥ 0.1 in TMX2-28-Control, Detection p-value ≤ 0.01 for TMX2-28-5-Aza-dC and TMX2-28-Control	6,637 (1%)
	No Change	Detection p-value ≤ 0.01 for TMX2-28-Control and TMX2-28-5-Aza-dC (484,841) minus No. of hypermethylated and hypomethylated CpG sites	478,145 (99%)
MCF-7-5-Aza-dC v. MCF-7-Control	Hypermethylated	Fold change ≥ 1.8 in MCF-7-5-Aza-dC (MCF-7-5-Aza-dC/MCF-7-Control), β -value ≥ 0.1 in MCF-7-5-Aza-dC, Detection p-value ≤ 0.01 for MCF-7-5-Aza-dC And MCF-7-Control	32 (0.01%)
	Hypomethylated	Fold change ≥ 1.8 in MCF-7-Control (MCF-7-Control/ MCF-7-5-Aza-dC), β -value ≥ 0.1 in MCF-7-Control, Detection p-value ≤ 0.01 for MCF-7-5-Aza-dC and MCF-7-Control	1,050 (0.2%)
	No Change	Detection p-value ≤ 0.01 for MCF-7-Control and MCF-7-5-Aza-dC (485,577) minus No. of hypermethylated and hypomethylated CpG sites	484,495 (99%)