

Supplementary Table 9B. Gene ontology enrichment analysis (GO protein function) of the 101 genes, for which the 255 probes belonging to Probe Cluster I and showing significant ($P < 0.05$) inverse correlation ($r < -0.2$) between DNA methylation levels and the mRNA expression levels in the endometrial cancer dataset deposited in The Cancer Genome Atlas database (<https://tcgadata.nci.nih.gov/tcga/>) were designed, using MetaCore software.

Protein class	r	n	R	N	Expected	Ratio	<i>P</i>
Transcription factors	10	96	1220	40065	2.92	3.42	<u>6.97×10^{-4}</u>
Ligands	3	96	536	40065	1.28	2.34	1.38×10^{-1}
Receptors	6	96	1701	40065	4.08	1.47	2.23×10^{-1}
Enzymes	11	96	2853	40065	6.84	1.61	7.94×10^{-2}
Kinases	1	96	680	40065	1.63	0.61	5.14×10^{-1}
Other	65	96	32295	40065	77.38	0.84	1.85×10^{-3}

r, number of objects from the present data set for a given protein class; n, total number of objects from the present data set; R, number of background objects from the database for a given class; N, total number of background objects from the database; Expected, mean value for hypergeometric distribution ($n \times R/38526$); Ratio, the ratio of actual/expected. If the ratio is more than 1, $P < 0.05$ means significant enrichment, and these are underlined.