

**Supplementary Table 9C.** Statistically significant GO molecular functions revealed by MetaCore software analysis using 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.

Molecular functions	<i>P</i> value
DNA binding	$5.91 \times 10^{-6}$
transcription regulator activity	$1.50 \times 10^{-5}$
DNA binding transcription factor activity	$2.95 \times 10^{-5}$
RNA polymerase II transcription factor activity, sequence-specific DNA binding	$5.58 \times 10^{-5}$
calcium ion binding	$6.12 \times 10^{-4}$
nucleic acid binding	$9.13 \times 10^{-4}$
cell adhesion molecule binding	$3.14 \times 10^{-3}$
structural molecule activity conferring elasticity	$3.23 \times 10^{-3}$
electron transfer activity	$4.33 \times 10^{-3}$
integrin binding	$4.33 \times 10^{-3}$
binding	$4.38 \times 10^{-3}$
cysteine dioxygenase activity	$4.48 \times 10^{-3}$
transcriptional repressor activity, RNA polymerase II transcription factor binding	$6.47 \times 10^{-3}$
glycolipid binding	$7.45 \times 10^{-3}$
metal ion binding	$8.21 \times 10^{-3}$
thymidine kinase activity	$8.94 \times 10^{-3}$
branched-chain-amino-acid transaminase activity	$8.94 \times 10^{-3}$
L-leucine transaminase activity	$8.94 \times 10^{-3}$
L-isoleucine transaminase activity	$8.94 \times 10^{-3}$
L-valine transaminase activity	$8.94 \times 10^{-3}$
integrin binding involved in cell-matrix adhesion	$8.94 \times 10^{-3}$
interleukin-1, Type I, activating receptor activity	$8.94 \times 10^{-3}$
deoxycytidine kinase activity	$8.94 \times 10^{-3}$
heme-copper terminal oxidase activity	$9.02 \times 10^{-3}$
cytochrome-c oxidase activity	$9.02 \times 10^{-3}$
oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor	$9.02 \times 10^{-3}$
oxidoreductase activity, acting on a heme group of donors	$9.57 \times 10^{-3}$
cation binding	0.012
endothelin receptor activity	0.013
type II activin receptor binding	0.013
natriuretic peptide receptor activity	0.013
ion binding	0.015
guanine/thymine mispair binding	0.018
ganglioside binding	0.018
deoxynucleoside kinase activity	0.018
leukotriene-C4 synthase activity	0.018

beta-1 adrenergic receptor binding	0.018
heterocyclic compound binding	0.021
IgG receptor activity	0.022
regulatory region RNA binding	0.022
receptor-receptor interaction	0.022
Roundabout binding	0.022
L-glutamine transmembrane transporter activity	0.027
organic cyclic compound binding	0.027
cell-matrix adhesion mediator activity	0.031
extracellular matrix constituent conferring elasticity	0.031
epoxide hydrolase activity	0.031
peptide receptor activity	0.033
protein heterodimerization activity	0.035
MutSalpha complex binding	0.035
interleukin-1 receptor activity	0.035
GPI anchor binding	0.040
ceramide binding	0.044
NAD binding	0.046
myosin binding	0.047
activin receptor binding	0.048
immunoglobulin receptor activity	0.048
mismatch repair complex binding	0.048
I-SMAD binding	0.048

---