

Supplementary Table S10. Genes for which DNA methylation levels were significantly correlated with lymphovascular invasion (LVSI) in tissue samples of early-onset endometrioid endometrial cancer (n=34).

Target ID ^a	Gene symbol ^b	DNA methylation levels in EE samples (mean ± SD)		<i>P</i> value	DNA methylation status in LVSI-positive cases ^c
		LVSI-positive (n=5)	LVSI-negative (n=29)		
cg22855255	<i>CA10</i>	0.639 ± 0.127	0.480 ± 0.182	7.22×10^{-3}	DNA hypermethylation
cg14231749	<i>CA10</i>	0.544 ± 0.108	0.374 ± 0.171	1.69×10^{-3}	DNA hypermethylation
cg21385821	<i>CA10</i>	0.534 ± 0.153	0.341 ± 0.161	2.97×10^{-3}	DNA hypermethylation
cg00701946	<i>GPR75</i>	0.695 ± 0.131	0.544 ± 0.173	9.88×10^{-3}	DNA hypermethylation
cg25390440	<i>GYPC</i>	0.660 ± 0.092	0.546 ± 0.132	8.23×10^{-3}	DNA hypermethylation
cg08129583	<i>GYPC</i>	0.677 ± 0.085	0.559 ± 0.112	2.45×10^{-3}	DNA hypermethylation
cg17105014	<i>GYPC</i>	0.646 ± 0.087	0.539 ± 0.109	5.50×10^{-3}	DNA hypermethylation
cg01285501	<i>HOXA9</i>	0.676 ± 0.101	0.537 ± 0.178	8.37×10^{-3}	DNA hypermethylation
cg20649017	<i>HOXD10</i>	0.648 ± 0.128	0.520 ± 0.144	5.93×10^{-3}	DNA hypermethylation
cg21591742	<i>HOXD10</i>	0.691 ± 0.086	0.520 ± 0.196	1.81×10^{-3}	DNA hypermethylation
cg00983904	<i>IFFO1</i>	0.764 ± 0.055	0.682 ± 0.108	8.00×10^{-3}	DNA hypermethylation
cg10689784	<i>NPR2</i>	0.554 ± 0.184	0.368 ± 0.144	9.16×10^{-3}	DNA hypermethylation
cg23002957	<i>ORAI3</i>	0.697 ± 0.063	0.560 ± 0.118	1.48×10^{-4}	DNA hypermethylation
cg22732749	<i>PCDHB15</i>	0.630 ± 0.130	0.454 ± 0.200	5.30×10^{-3}	DNA hypermethylation
cg17023770	<i>PCDHB15</i>	0.613 ± 0.107	0.453 ± 0.145	1.39×10^{-3}	DNA hypermethylation
cg09207053	<i>PCDHGA11</i>	0.680 ± 0.102	0.544 ± 0.141	4.07×10^{-3}	DNA hypermethylation
cg06157602	<i>PCDHGB6</i>	0.580 ± 0.147	0.416 ± 0.165	8.37×10^{-3}	DNA hypermethylation
cg01560972	<i>RIC3</i>	0.574 ± 0.068	0.459 ± 0.146	5.15×10^{-3}	DNA hypermethylation
cg16717065	<i>SOX11</i>	0.641 ± 0.130	0.420 ± 0.202	7.70×10^{-4}	DNA hypermethylation
cg06092815	<i>SPHKAP</i>	0.612 ± 0.104	0.477 ± 0.156	6.61×10^{-3}	DNA hypermethylation
cg21911021	<i>ZIK1</i>	0.595 ± 0.142	0.433 ± 0.150	6.15×10^{-3}	DNA hypermethylation
cg26465391	<i>ZNF154</i>	0.737 ± 0.084	0.602 ± 0.161	4.55×10^{-3}	DNA hypermethylation
cg13871633	<i>ZNF662</i>	0.671 ± 0.105	0.477 ± 0.138	1.25×10^{-4}	DNA hypermethylation
cg20765086	<i>ZSCAN12</i>	0.671 ± 0.080	0.540 ± 0.152	3.05×10^{-3}	DNA hypermethylation

^aProbe ID of the Infinium MethylationEPIC BeadChip. ^bNational Center for Biotechnology Information (NCBI) database (Genome Build 37). ^cCompared to DNA methylation status in LVSI-negative cases.