Supplementary Table 1. The 28 CpG probes with prognostic potential in 40 ESCC patients by univariate Cox regression analyses.

cg_number[a]	Gene symbol	Gene name	HR (95%CI)[b]
cg01521573	*ADCYAP1*	*Adenylate cyclase activating polypeptide precursor*	1.72 (1.11-2.65)
cg19520710	*DDIT3*	*Homo sapiens DNA-damage-inducible transcript 3*	1.60 (1.07-2.40)
cg20175079	*DLK1*	*Delta-like 1 homolog isoform 1*	1.76 (1.02-3.06)
cg10886497	*FES*	*Homo sapiens feline sarcoma oncogen*	1.95 (1.22-3.13)
cg23603794	*FLT3*	*Homo sapiens fms-related tyrosine kinase 3*	1.94 (1.17-3.22)
cg04775393	*HCK*	*Hemopoietic cell kinase isoform p61HCK*	1.84 (1.04-3.26)
cg26034501	*HTR1B(1)*	*5-hydroxytryptamine (serotonin) receptor 1B*	1.59 (0.94-2.66)
cg23424273	*HTR1B(2)*	*5-hydroxytryptamine (serotonin) receptor 1B*	1.65 (1.05-2.59)
cg21449657	*IFNGR2*	*Interferon-gamma receptor beta chain precursor*	1.60 (1.02-2.52)
cg05635754	*JAK3*	*Janus kinase 3*	1.65 (1.05-2.60)
cg01352108	*KCNK4*	*Potassium channel, subfamily K, member 4 isoform 1*	1.86 (1.14-3.04)
cg20325846	*MYOD1*	*Myogenic differentiation 1*	2.01 (1.09-3.70)
cg20666532	*NPY(1)*	*Neuropeptide Y*	1.74 (1.01-3.00)
cg25884711	*NPY(2)*	*Neuropeptide Y*	1.75 (1.05-2.91)
cg20961293	*NPY(3)*	*Neuropeptide Y*	1.79 (1.09-2.93)
cg00865584	*NTRK3*	*Homo sapiens neurotrophic tyrosine kinase, receptor, type 3, transcript variant 2*	1.79 (1.04-3.09)
cg26114392	*PLSCR3*	*Phospholipid scramblase 3*	1.63 (1.05-2.54)
cg15468095	*PYCARD*	*PYD and CARD domain containing isoform b*	1.82 (1.20-2.74)
cg01250674	*SEPT5*	*Homo sapiens septin 5, transcript variant 2*	1.60 (1.01-2.52)

| cg11617283	*SEPT9(1)*	*Homo sapiens septin 9*	1.80 (1.15-2.79)
cg05428394	*SEPT9(2)*	*Homo sapiens septin 9*	1.65 (1.02-2.66)
cg13433302	*SLC5A8(1)*	*Solute carrier family 5 (iodide transporter), member 8*	1.67 (0.96-2.92)
cg05722918	*SLC5A8(2)*	*Solute carrier family 5 (iodide transporter), member 8*	1.66 (1.07-2.57)
cg23071766	*SOX1*	*Homo sapiens SRY (sex determining region Y)-box 1*	1.50 (0.94-2.37)
cg19346665	*SOX17(1)*	*Homo sapiens SRY (sex determining region Y)-box 17*	1.86 (1.06-3.27)
cg09626193	*SOX17(2)*	*Homo sapiens SRY (sex determining region Y)-box 17*	2.30 (1.27-4.20)
cg03402455	*TBX1*	*T-box 1 isoform A*	1.56 (0.97-2.51)
cg09698887	*TMEFF2*	*Transmembrane protein with EGF-like and two follistatin-like domains 2*	1.61 (1.01-2.55)

[a] cg_number is the CpG number of designated probe used in Illumina's GoldenGate Genotyping Array.

[b] HR: hazard ratio; CI: confidence interval.

Supplementary Figures
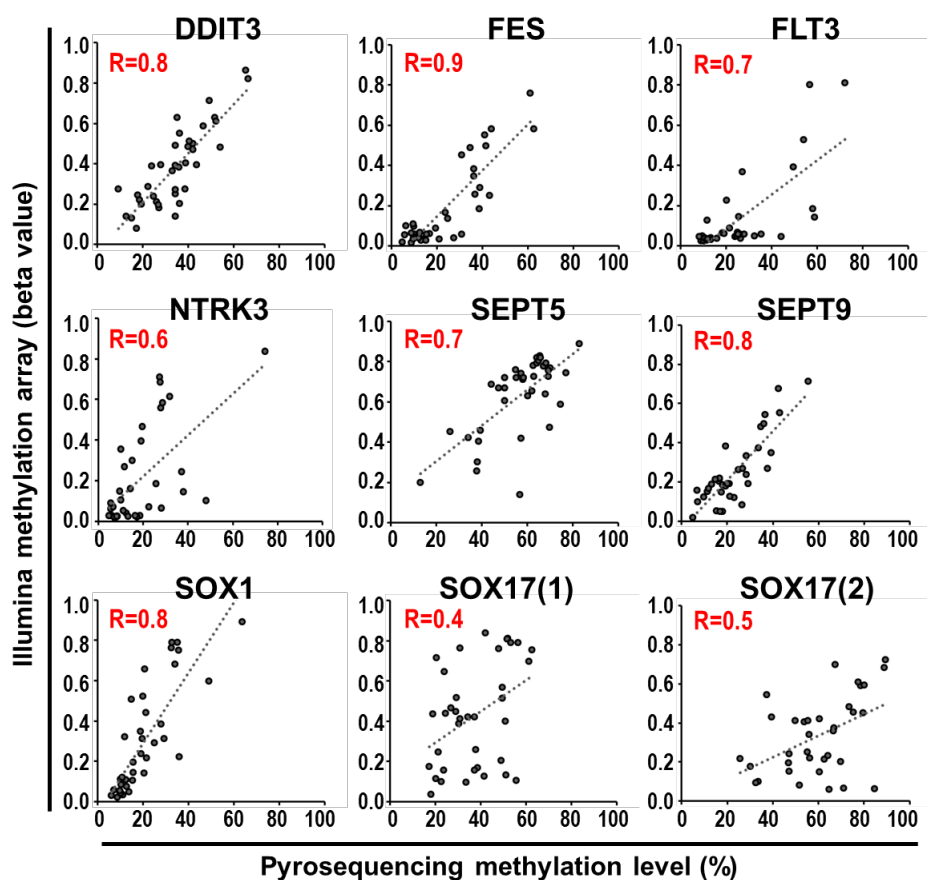
Supplementary Figure 1. Dot-plot analyses show a high concordance of methylation level between Illumina genome-wide methylation assay (Y-axis: β value) and pyrosequencing methylation validation (X-axis) of nine CpG probes. The correlation coefficient (R) value for each gene probe is shown.
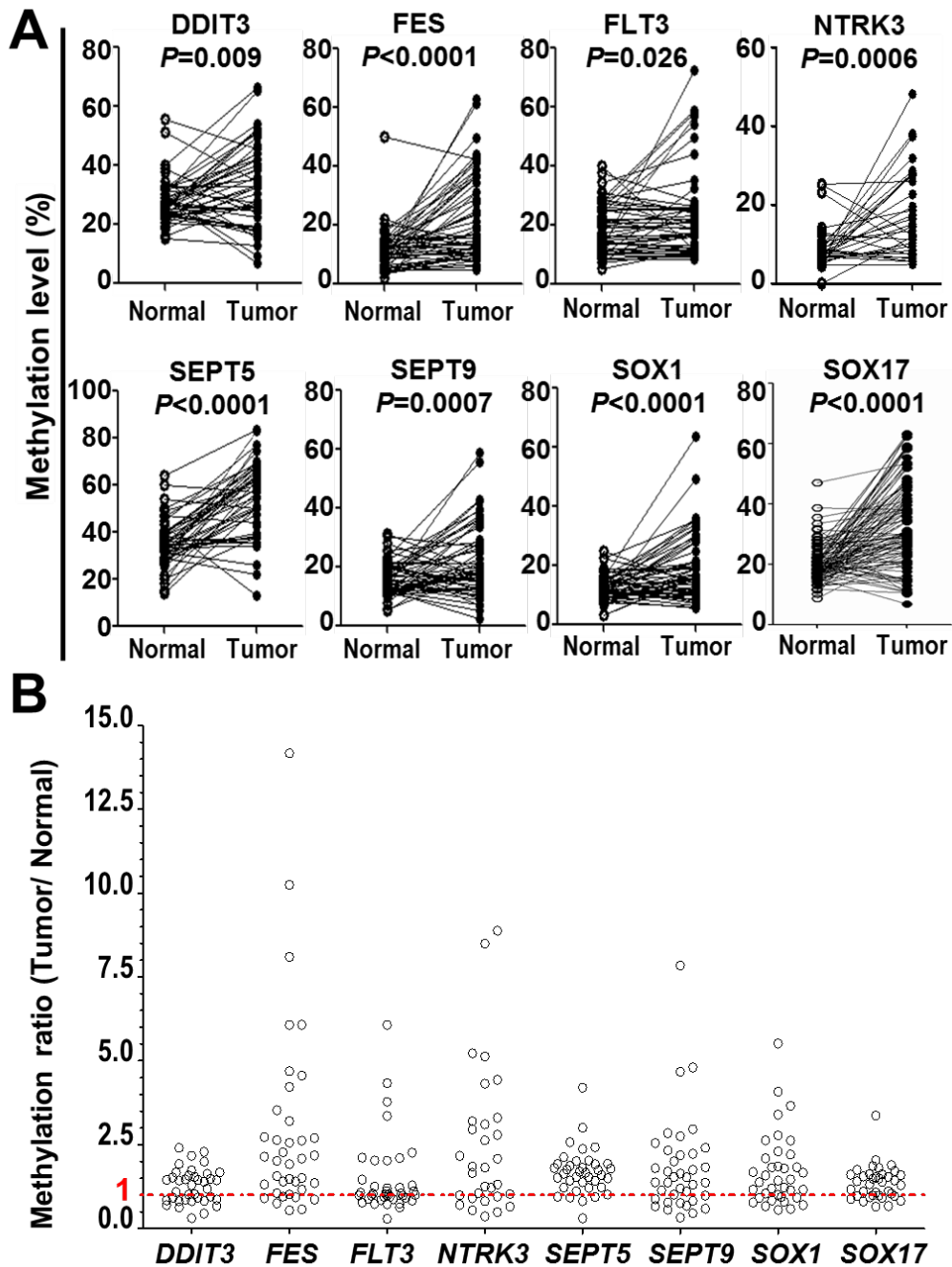
Supplementary Figure 2. Dot plot analyses of pyrosequencing results confirmed that methylation level of the eight selected genes was significantly higher in tumor tissues than in their corresponding normal tissues for the ESCC patients analyzed. (A) DNA methylation level is indicated on the Y-axis and X-axis represents the normal vs. tumor. P values were calculated by two-tailed paired t test and are shown as indicated. (B) DNA methylation ratio of tumor / normal is indicated in the Y-axis, whereas eight genes are shown on the X-axis. A ratio of >1 on the Y-axis indicated patients with tumor tissue showing higher gene methylation level than the corresponding normal tissue. The cut-off value is indicated with a red horizontal line.
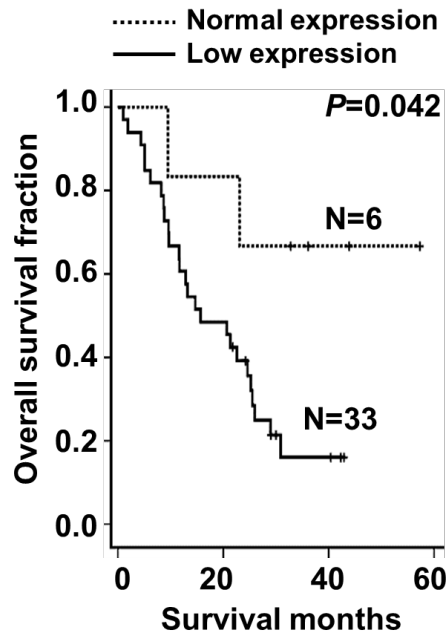
Supplementary Figure 3. Kaplan-Meier analysis of overall survival curves in the validation cohort of 39 ESCC patients from another hospital. The results showed that ESCC patients with low *SOX17* mRNA expression had significantly poorer overall survival than patients with normal *SOX17* mRNA expression. Patient with mRNA expression level was grouped by the mean of the mRNA expression ratio of tumor/normal. *P* value was calculated by log-rank test and is shown as indicated.