Supplementary Table 11. The 11 probes showing an area under the curve value of 1 in receiver operating characteristic curve analysis for discriminating 12 samples belonging to Cluster EB from 22 samples belonging to Cluster EA.

Target ID[a]	Chromosome	Position[b]	Gene symbol[c]	Gene region[d]	CpG type[e]
cg02320740	10	106,400,259	*SORCS3*	TSS1500	Island
cg06248767	8	56,852,290	*LYN*	Gene body/5'UTR/1st intron	Open sea
cg13539545	14	60,973,823	*N/A*		N Shore/Island
cg13997680	6	28,226,980	*ZKSCAN4*	Gene body/5'UTR/1st exon	Island
cg23049458	1	62,660,624	*L1TD1*	Gene body/5'UTR/1st intron	Island
cg24452128	6	10,390,919	*N/A*		S Shore/Island
cg12197571	21	31,972,506	*KRTAP22-1*	TSS1500	Open sea
cg14269191	11	5,346,249	*OR51B2*	TSS1500	Open sea
cg26980111	8	132,321,917	*N/A*		Open sea
cg02065293	2	1,928,480	*MYT1L*	Gene body	Open sea
cg05353872	1	248,366,399	*OR2M3*	GeneBody/1st exon	Open sea

[a]Probe ID of the Infinium MethylationEPIC BeadChip. [b]National Center for Biotechnology Information (NCBI) database (Genome Build 37). [c]N/A, not annotated (designed for the intergenic regions). [d]Probe CpG sites were were annotated as (a) from 200 bp upstream of the transcription start site (TSS) to 1500 bp upstream of it (TSS1500), (b) from TSS to 200 bp upstream of TSS (TSS200), (c) the 5' untranslated region (UTR), (d) the first exon, (e) the first intron, (f) the gene body (TSS to transcription termination site), (g) the 3' UTR and (h) the intergenic region based on the RefSeq database (http://www.ncbi.nlm.nih.gov/refseq/). [e]Probe CpG type were also categorized into CpG island, (j) N-Shelf (2000 bp region 5' adjacent to N-Shore), (k) N-Shore (2000 bp region 5' adjacent to CpG island), (l) S-Shore (2000 bp region 3' adjacent to CpG island), (m) S-Shelf (2000 bp region 3' adjacent to S-Shore) and (n) open sea based on the UCSC Genome Browser (https://genome.ucsc.edu/).