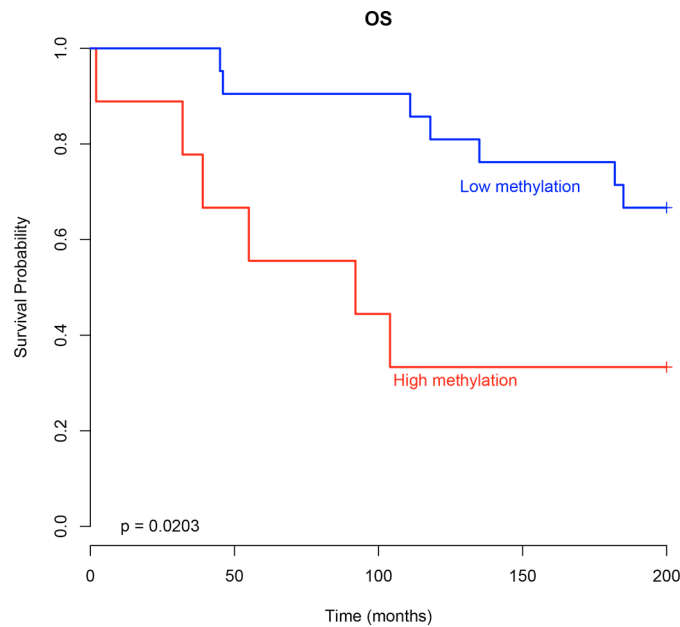
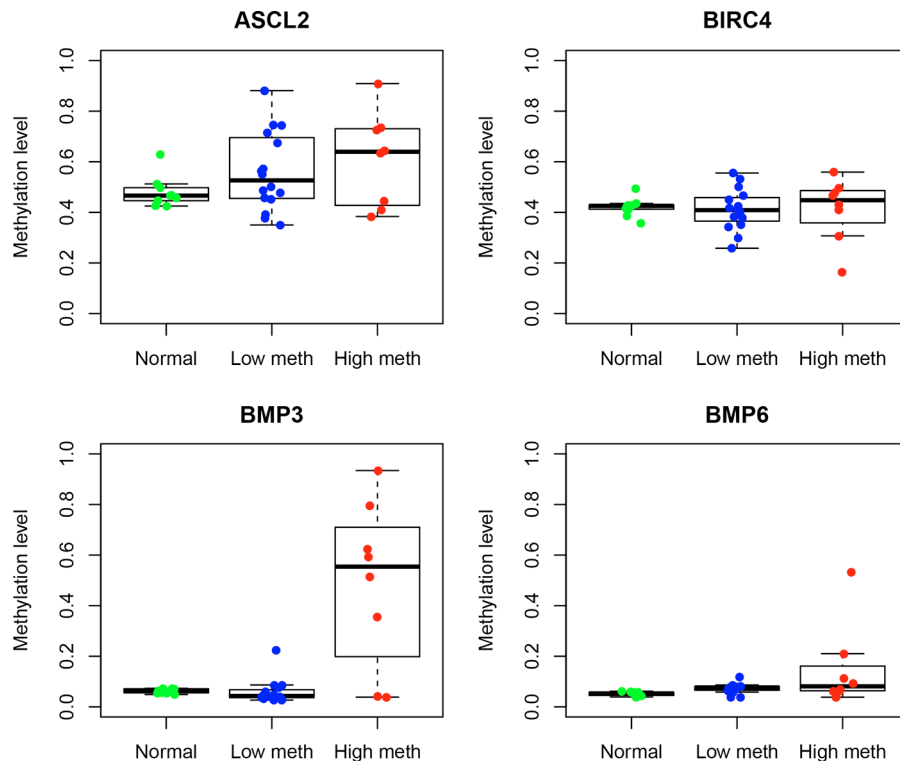


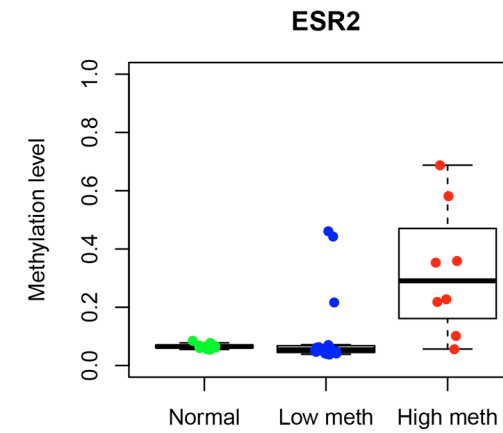
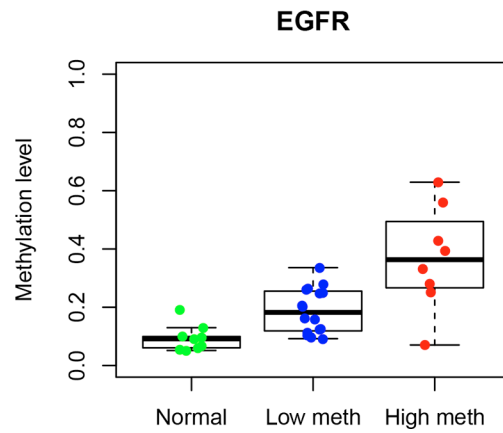
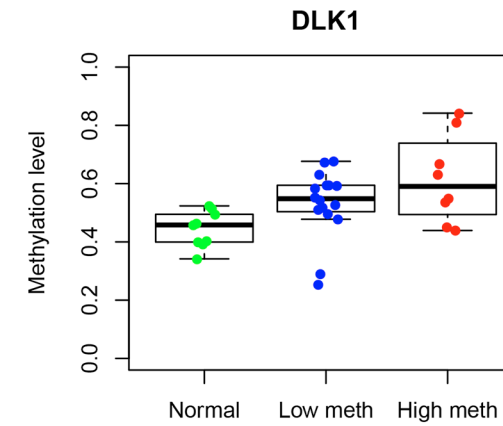
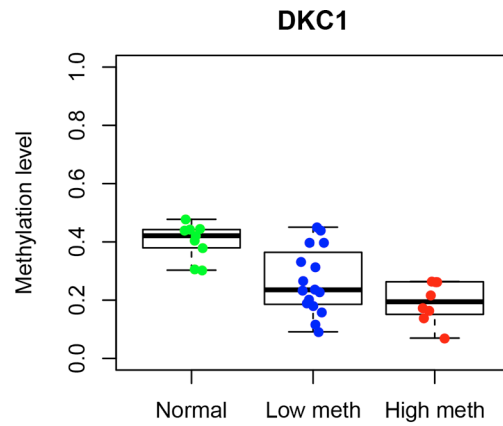
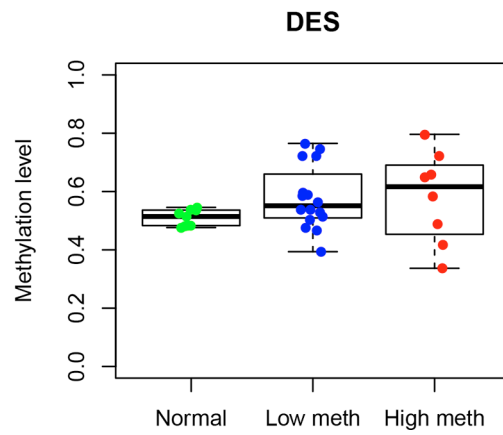
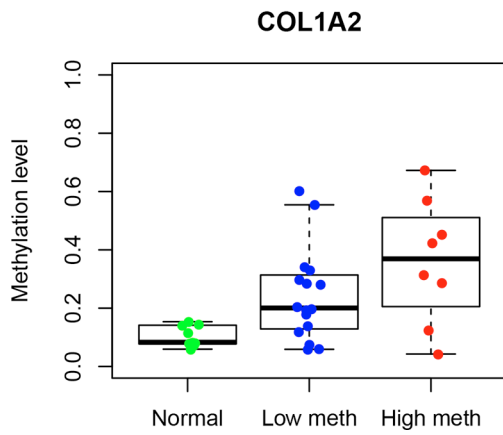
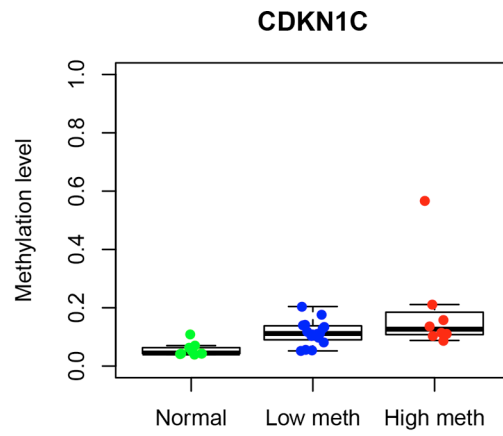
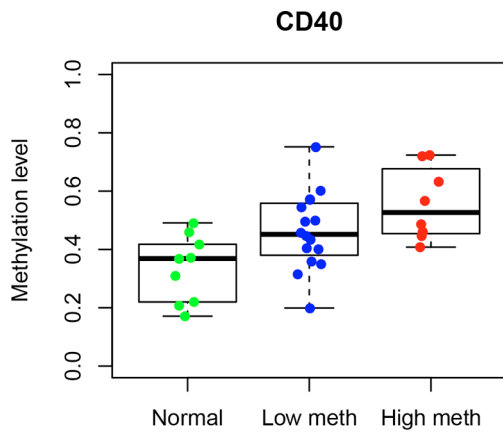
# DNA methylation signature (SAM40) identifies subgroups of the Luminal A breast cancer samples with distinct survival

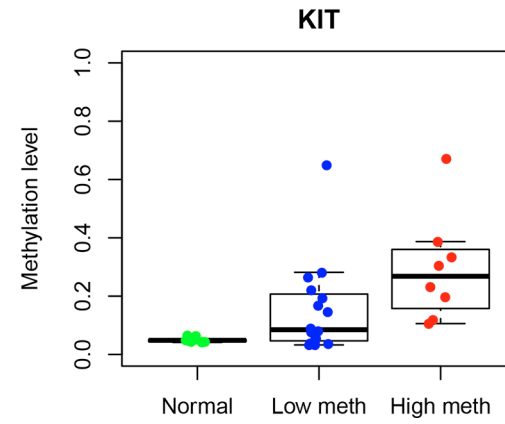
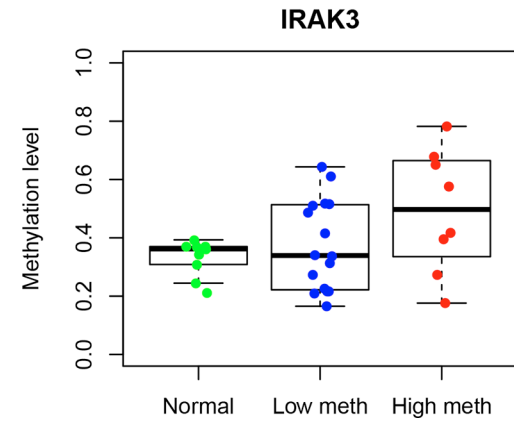
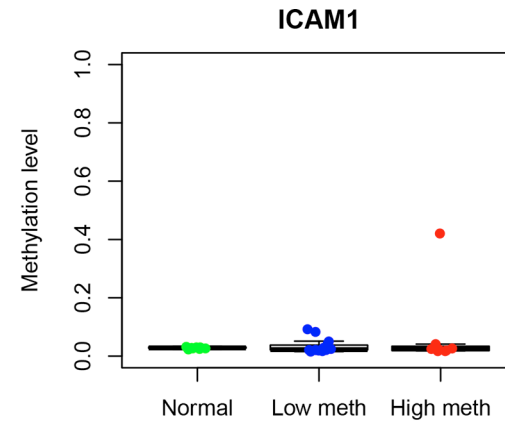
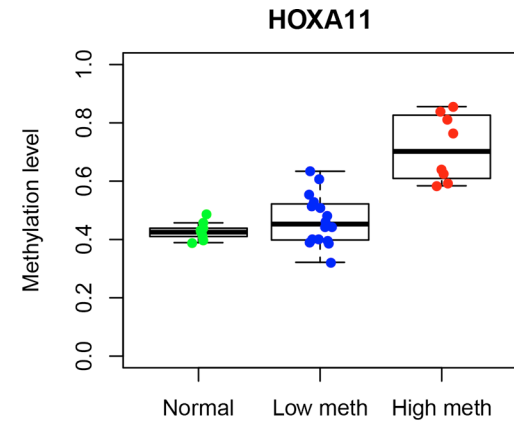
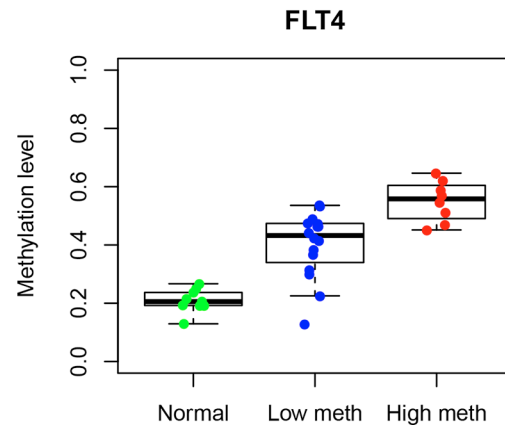
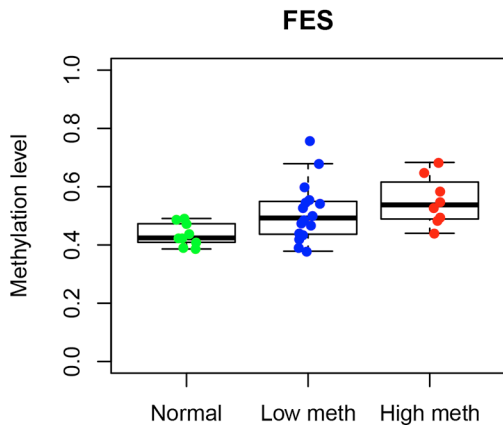
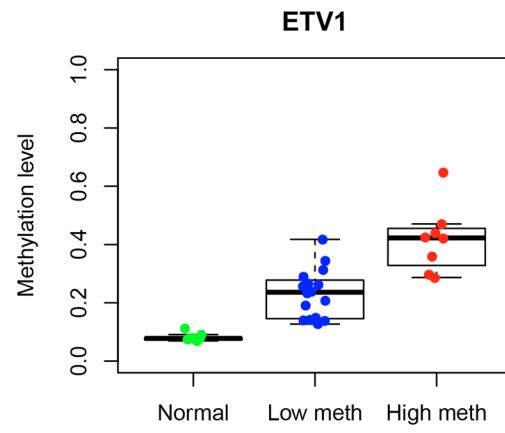
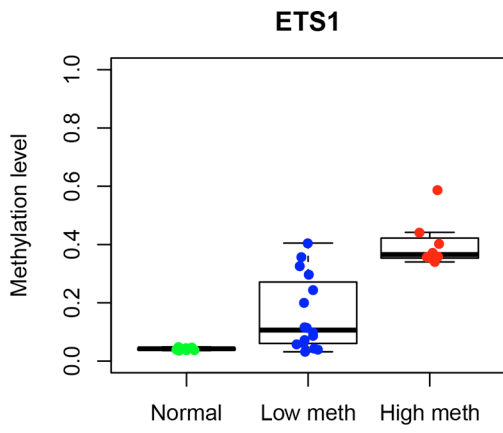
## Supplementary Materials

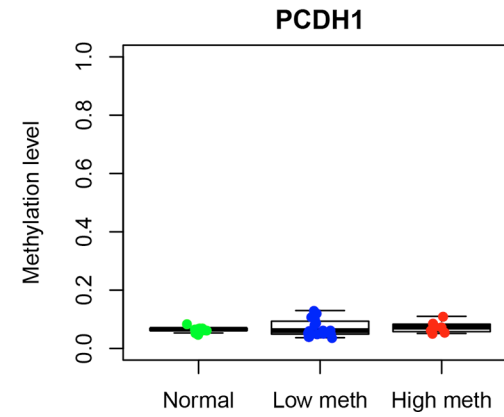
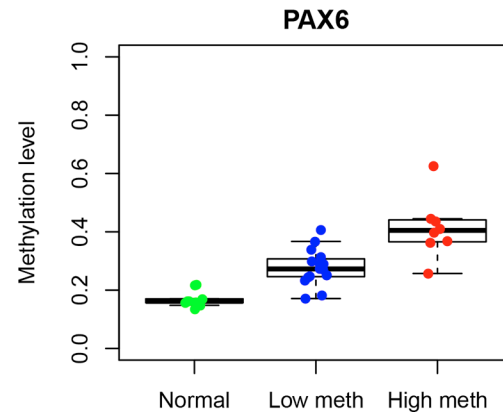
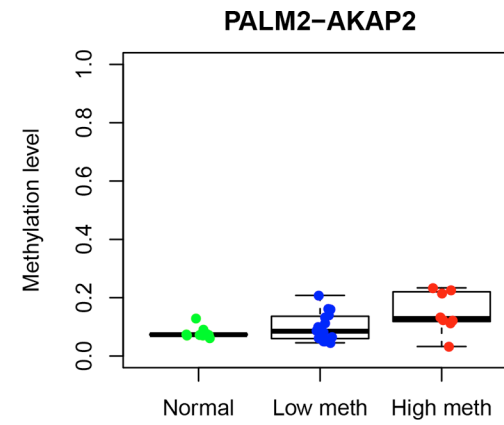
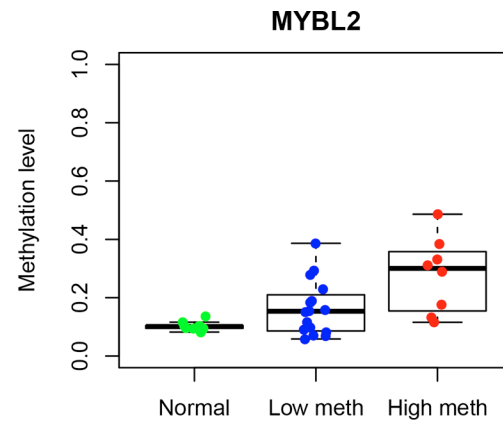
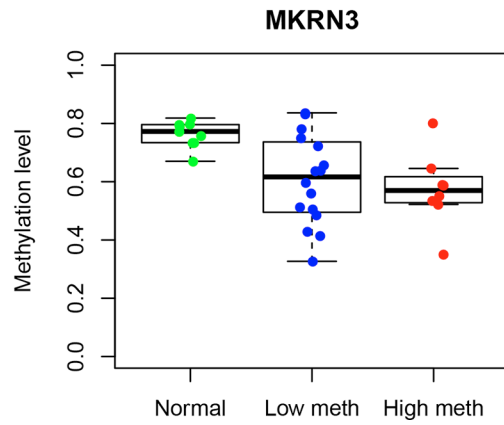
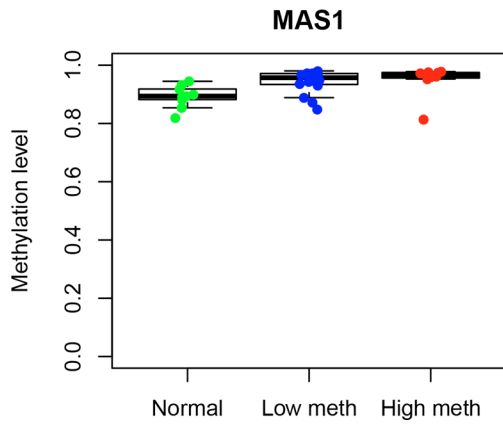
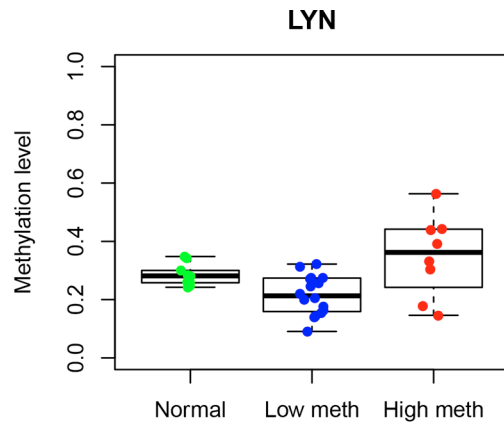
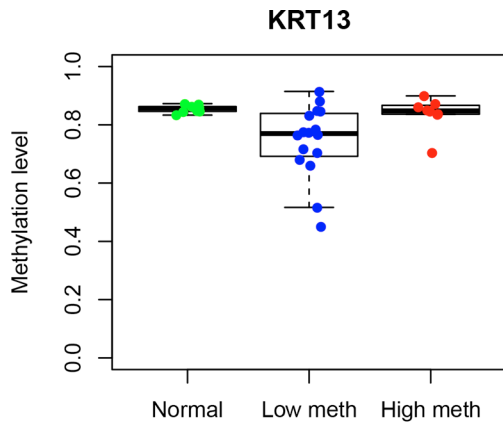


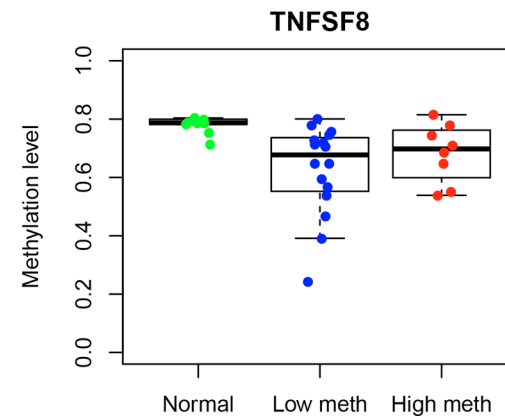
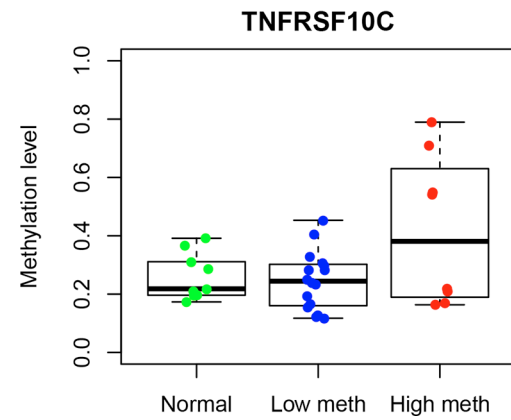
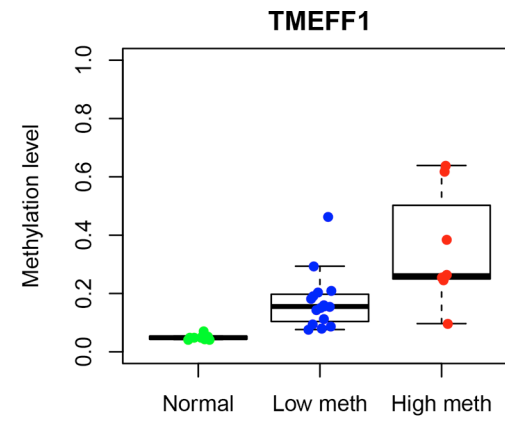
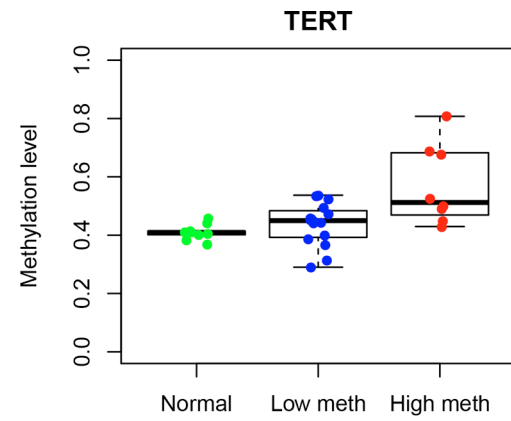
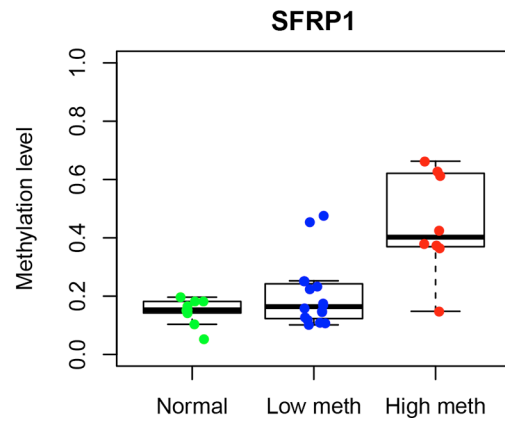
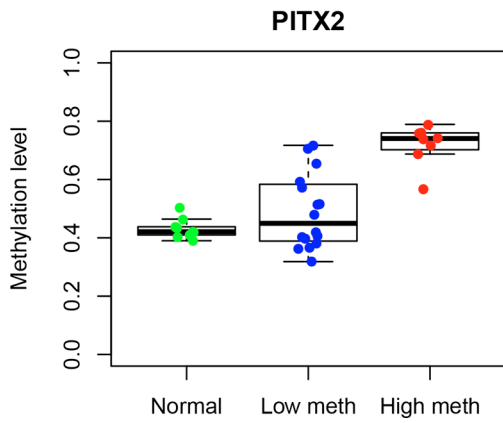
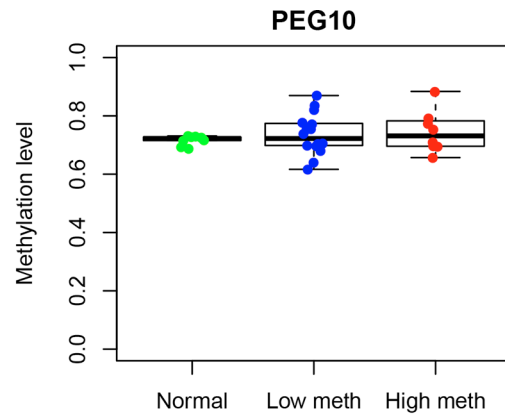
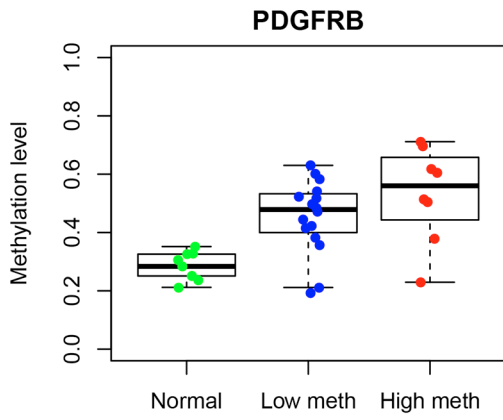
**Supplementary Figure S1: Overall survival analysis of the OsloVal study cohort.** The prognostic impact of classification using the SAM40 signature is statistically significant.

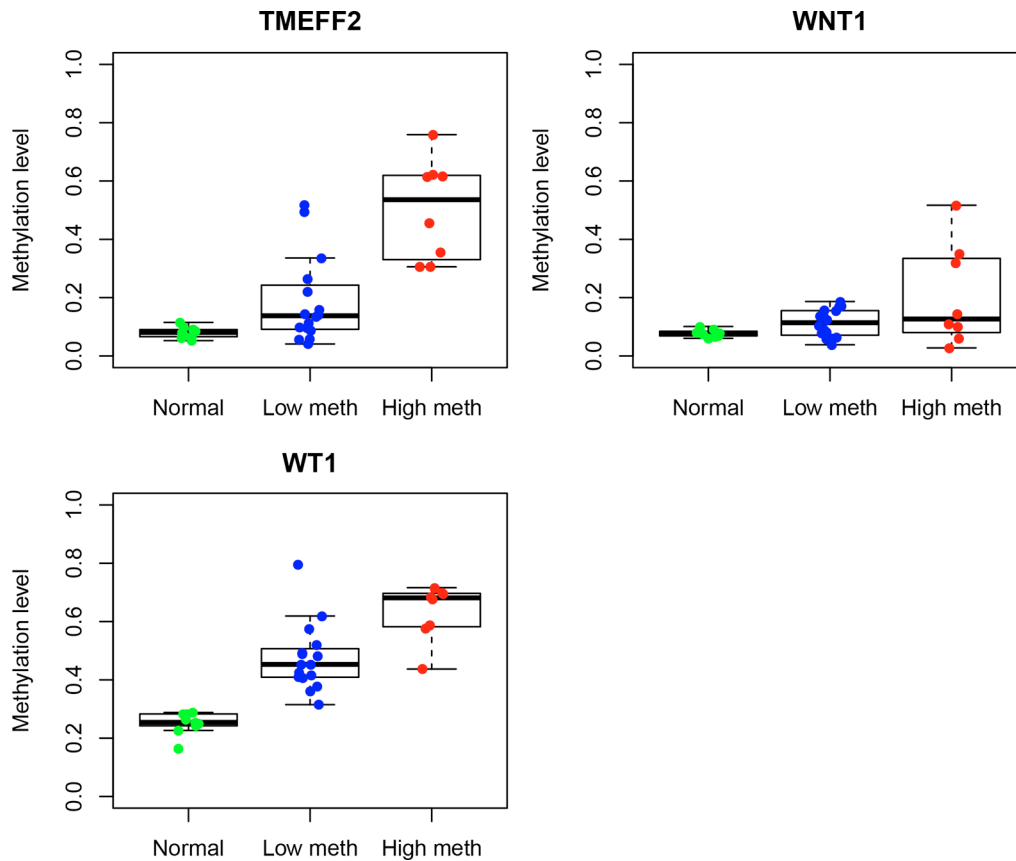












Supplementary Figure S2: Absolute methylation level for genes in the SAM40 signature.

Supplementary Table S1: Material overview

Study cohort	Main cohort	Number of patients	Reference	Ethical approval
Norway27K	MicMa	12	19	IRB approval no S-97103
	Ull	9	20	IRB approval no 285/05
	LB	3	21	IRB approval no 39/92-69.91
Norway450K	MicMa	16	19	IRB approval no S-97103
	FW06	5	22	IRB approval no Dnr 2005:118
OsloVal	MDG	11	23	IRB approval no S-02036
	OsloVal	30	24	IRB approval no 2010/498
TCGA	TCGA	108	13	Not relevant

**Supplementary Table S2: Patient characteristics for all four study cohorts**

	Norway27K <i>n</i> = 24	Norway450K <i>n</i> = 32	OsloVal <i>n</i> = 30	TCGA <i>n</i> = 108
Age (median)	59	71	60	58
Age (range)	43–90	36–82	33–85	27–83
Age unknown	3	11	0	0
ER negative	2	0	2	6
ER positive	21	32	26	102
ER unknown	1	0	2	0
Her2 negative	10	29	0	38
Her2 positive	2	1	0	2
Her2 unknown	12	2	30	68
Nstatus negative	10	7	9	47
Nstatus positive	13	7	0	58
Nstatus unknown	1	18	4	3
PAM50 Luminal A	24	32	30	108
PAM50 Luminal B	0	0	0	0
PAM50 Her2 enriched	0	0	0	0
PAM50 Basal-like	0	0	0	0
PAM50 Normal-like	0	0	0	0
PAM50 unknown	0	0	0	0
TP53 wild type	23	26	0	0
TP53 mutated	1	1	0	0
TP53 unknown	0	5	30	108
Tstatus 1	9	8	14	31
Tstatus 2	10	6	10	58
Tstatus 3	2	0	2	16
Tstatus 4	1	1	2	2
Tstatus unknown	2	17	2	1
Received adjuvant chemotherapy	8	2	6	30
No adjuvant chemotherapy	16	19	18	38
Unknown adjuvant chemotherapy	0	11	6	40
Received adjuvant hormone therapy	12	10	6	39
No adjuvant hormone therapy	12	11	18	29
Unknown adjuvant hormone therapy	0	11	6	40
Received neoadjuvant chemotherapy	3	0	0	0
No neoadjuvant chemotherapy	21	32	30	108
Unknown neoadjuvant chemotherapy	0	0	0	0

**Supplementary Table S3: Statistical comparisons of absolute methylation values for genes in the SAM40**

Gene	<i>p</i> -value		
	Hyper vs Hypo	Hypo vs Normal	Hyper vs Normal
ASCL2	6.5E-01	2.3E-01	3.2E-01
BIRC4	5.3E-01	5.2E-01	5.4E-01
BMP3	7.1E-03	7.4E-02	9.3E-02
BMP6	4.9E-01	2.2E-03	7.9E-03
CD40	1.4E-01	3.7E-02	3.7E-03
CDKN1C	2.1E-01	4.7E-04	3.3E-04
COL1A2	1.9E-01	1.7E-02	2.1E-02
DES	9.8E-01	8.4E-02	2.4E-01
DKC1	1.7E-01	5.3E-03	8.2E-05
DLK1	4.2E-01	8.0E-03	1.1E-02
EGFR	8.7E-03	1.4E-03	1.6E-03
ESR2	3.6E-03	1.5E-01	5.5E-03
ETS1	2.6E-04	1.1E-03	8.2E-05
ETV1	1.8E-04	9.8E-07	8.2E-05
FES	2.9E-01	4.3E-02	1.6E-03
FLT4	1.3E-03	2.6E-04	8.2E-05
HOXA11	5.2E-05	3.3E-01	8.2E-05
ICAM1	8.8E-01	2.5E-01	2.4E-01
IRAK3	1.5E-01	8.0E-01	5.9E-02
KIT	1.3E-02	7.4E-02	8.2E-05
KRT13	3.8E-02	5.3E-03	6.7E-01
LYN	1.6E-02	1.4E-02	2.0E-01
MAS1	3.5E-01	6.5E-03	7.9E-03
MKRN3	7.0E-01	9.6E-03	5.5E-03
MYBL2	3.8E-02	2.3E-01	5.8E-04
PALM2-AKAP2	1.1E-01	8.0E-01	2.1E-02
PAX6	9.4E-04	1.2E-05	8.2E-05
PCDH1	4.2E-01	7.2E-01	3.2E-01
PDGFRB	1.7E-01	1.4E-03	5.5E-03
PEG10	9.3E-01	6.0E-01	6.1E-01
PITX2	1.8E-04	7.2E-01	8.2E-05
SFRP1	3.6E-03	4.5E-01	2.5E-03
TERT	2.7E-02	1.5E-01	5.8E-04
TMEFF1	7.1E-03	9.8E-07	8.2E-05
TNFRSF10C	2.1E-01	6.4E-01	4.2E-01
TNFSF8	6.1E-01	6.3E-04	2.1E-02
TMEFF2	3.7E-04	2.7E-02	8.2E-05
WNT1	4.9E-01	9.5E-02	9.3E-02
WT1	3.6E-03	9.8E-07	8.2E-05
# <i>p</i> -values < 0.05	18	21	27