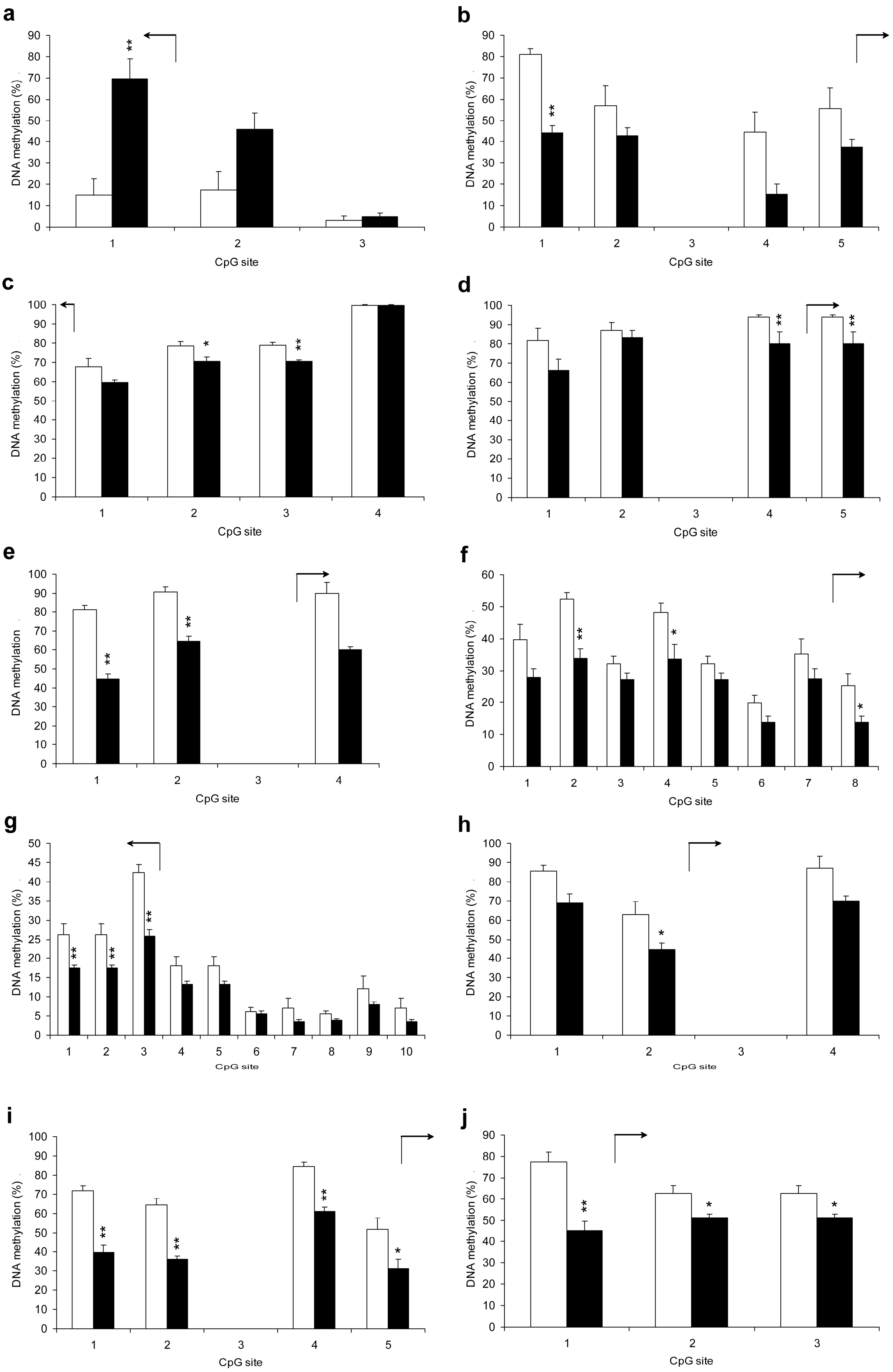
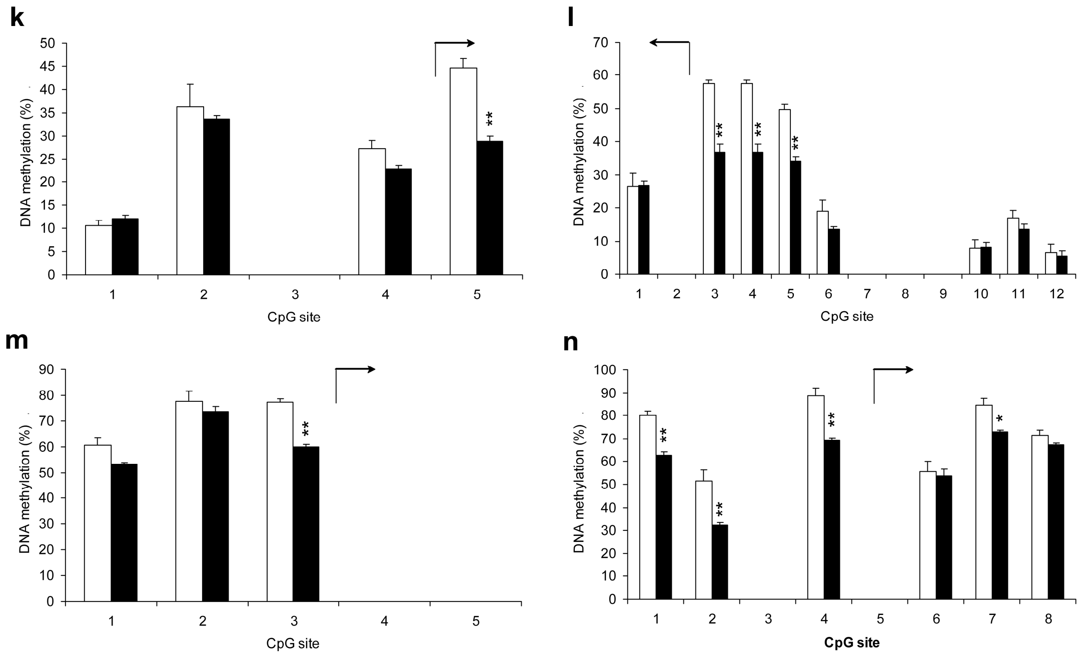

a
DNA methylation (%)
0 10 20 30 40 50 60 70 80 90
**
CpG site
1 2 3
b
DNA methylation (%)
0 10 20 30 40 50 60 70 80 90
**
CpG site
1 2 3 4 5
c
DNA methylation (%)
0 10 20 30 40 50 60 70 80 90 100
*
**
CpG site
1 2 3 4
d
DNA methylation (%)
0 10 20 30 40 50 60 70 80 90 100
**
**
CpG site
1 2 3 4 5
e
DNA methylation
0 10 20 30 40 50 60 70 80 90 100
**
**
CpG site
1 2 3 4
f
DNA methylation (%)
0 10 20 30 40 50 60
**
*
*
CpG site
1 2 3 4 5 6 7 8
g
DNA methylation (%)
0 5 10 15 20 25 30 35 40 45 50
**
**
**
CpG site
1 2 3 4 5 6 7 8 9 10
h
DNA methylation (%)
0 10 20 30 40 50 60 70 80 90 100
*
CpG site
1 2 3 4
i
DNA methylation (%)
0 10 20 30 40 50 60 70 80 90 100
**
**
**
*
CpG site
1 2 3 4 5
j
DNA methylation (%)
0 10 20 30 40 50 60 70 80 90
**
*
*
CpG site
1 2 3



ESM Fig. 2 Bisulfite MassArray analysis of DNA methylation at promoter regions of genes with an absolute difference in methylation above 5% that demonstrated inverse relationship with mRNA expression levels: *Gpr119* (**a**), *Fbp2* (**b**), *S100a4* (**c**), *Il33* (**d**), *Pah* (**e**), *Lgals1* (**f**), *Mgst1* (**g**), *Dpt* (**h**), *C4b* (**i**), *Col3a1* (**j**), *Prss35* (**k**), *Tf* (**l**), *Spp1* (**m**) and *Cxcl9* (**n**). Data is shown per individual CpG dinucleotide; missing columns depict CpG dinucleotides contained within fragments with masses outside the range of 1,500-7,000 Da that cannot be analyzed by Sequenom. For all panels, white bars correspond to three months old (3M) samples and black bars to fifteen months old (15M) samples. Data represent the mean of n=5-6 samples; error bars represent SEM; * p<0.05; ** p<0.01; *** p<0.001 by Mann-Whitney tests; arrows indicate transcription start sites.