

Fig. S1

Oslo2

TCGA

- miRNA expression - Agilent array designID 029297
- Unit: log2
- Illumina HumanMethylation450 array
- Unit: beta values

- miRNA expression - IlluminaHiSeq miRNASeq
- Unit: log2(RPM+1)
- Illumina HumanMethylation450 array
- Unit: beta values

- Samples with miRNA and methylation: n=297
- Filter out miRNAs expressed in $\leq 10\%$
 - Filter out CpGs with interquartile range (IQR) ≤ 0.1

- Samples with miRNA and methylation: n=439
- Filter out miRNAs expressed in $\leq 10\%$
 - Filter out CpGs with IQR ≤ 0.1

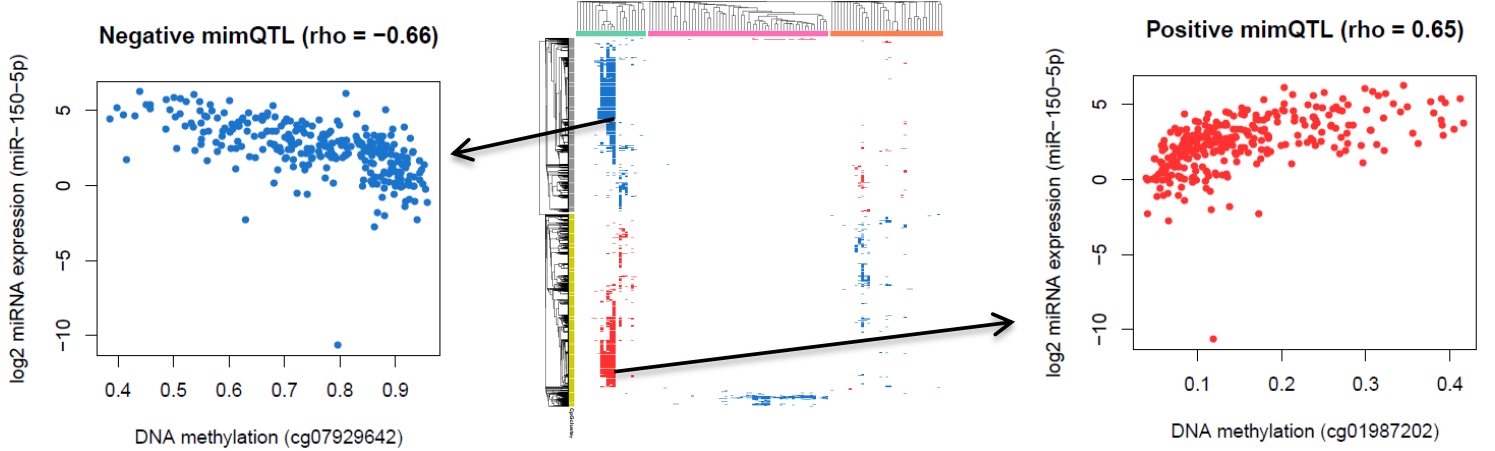
Only consider overlapping miRNAs and CpGs
 → 346 miRNAs
 → 142 804 CpGs

Spearman correlation: 346 miRNAs x 142 804 CpGs
 Bonferroni-corrected p-value < 0.05

Oslo2: 140 443 significant miRNA-CpG associations

TCGA: 1 351 887 significant miRNA-CpG associations

Overlap: 89 118 miRNA-CpG associations
 → miRNA-methylation Quantitative Trait Loci (mimQTL)



Definitions

- Cis association:** Any association between a CpG and a miRNA located on the *same* chromosome
- Trans association:** Any association between a CpG and a miRNA located on *different* chromosomes

Fig. S2

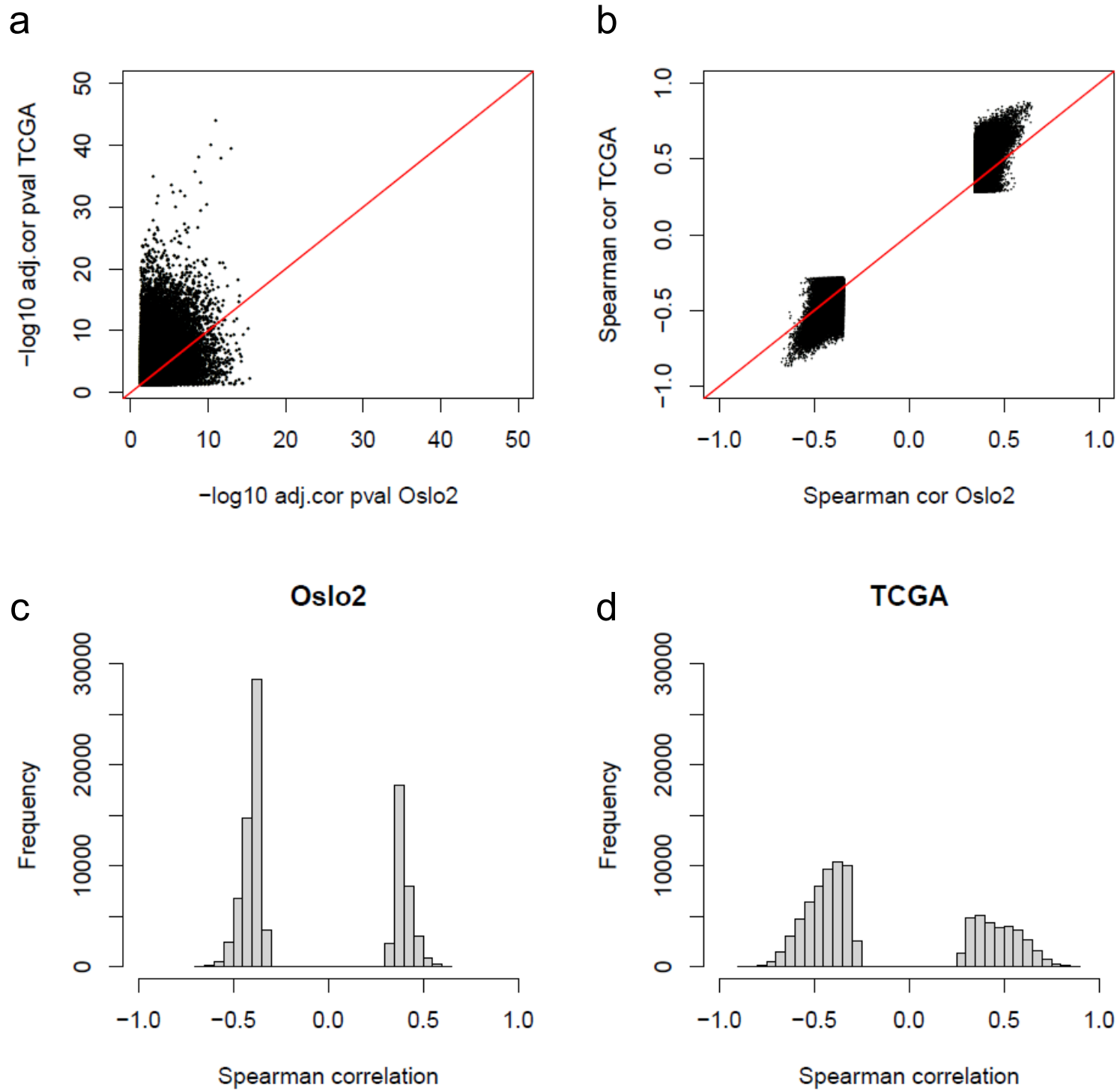


Fig. S3

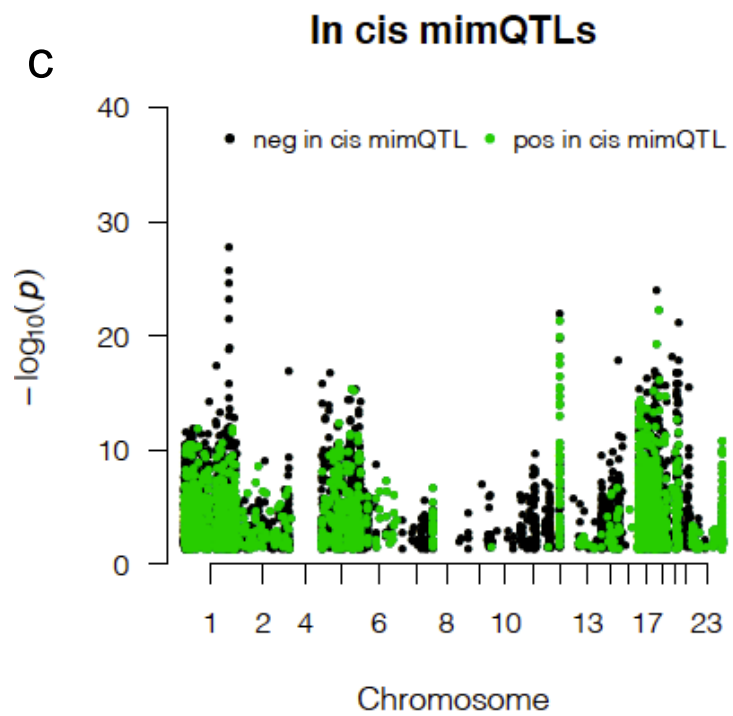
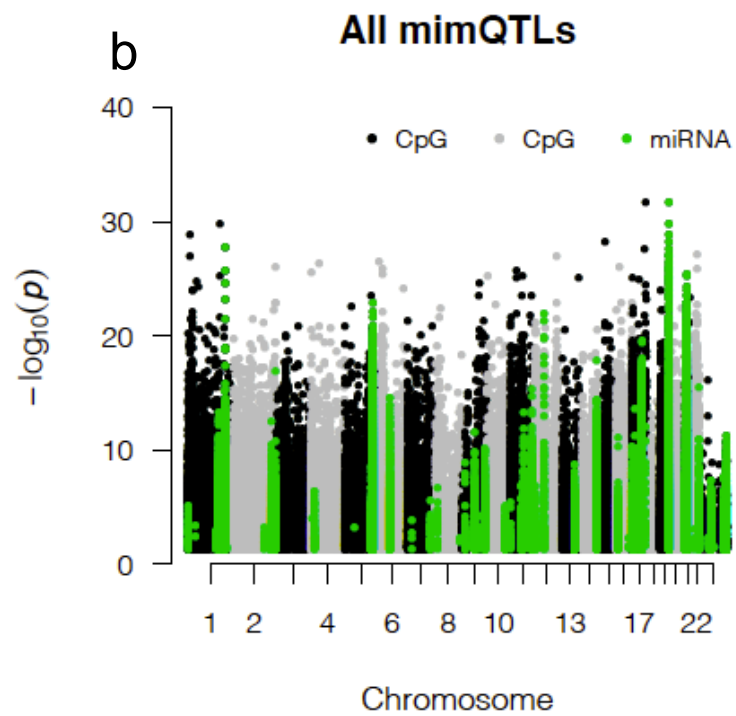
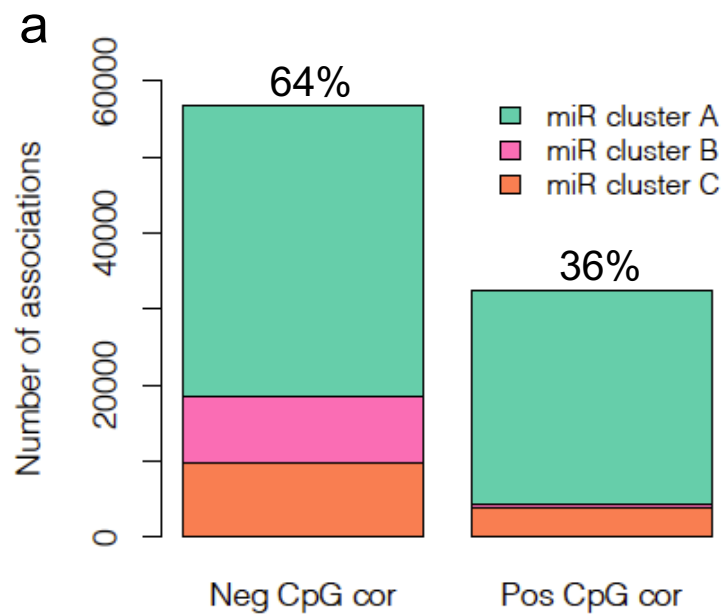


Fig. S4

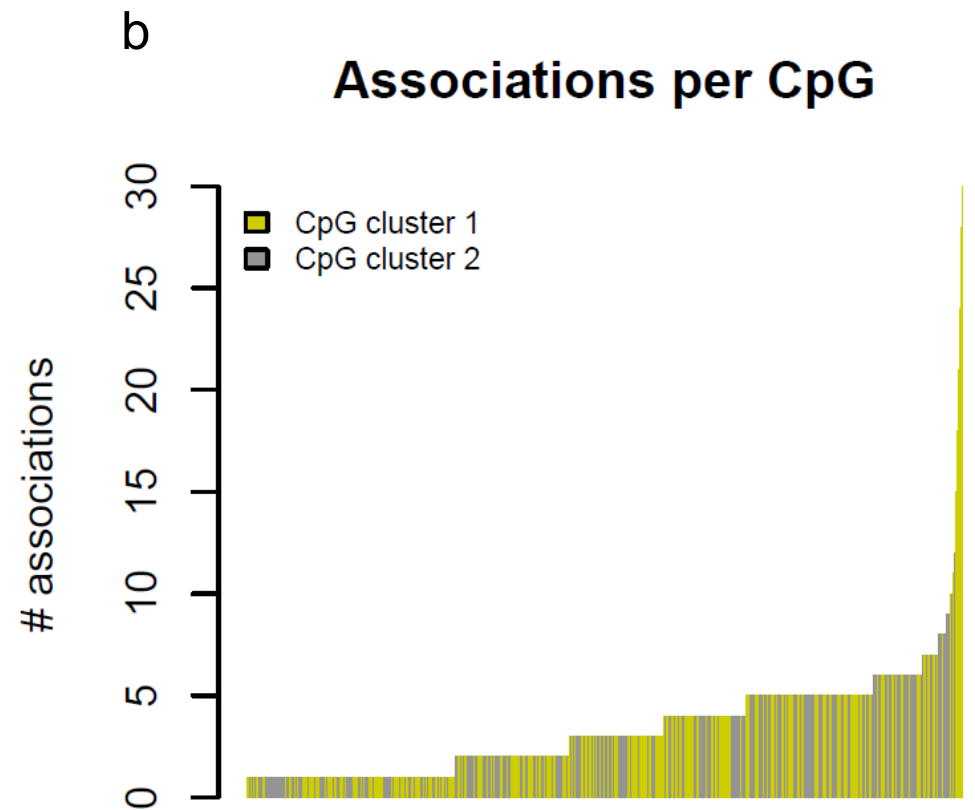
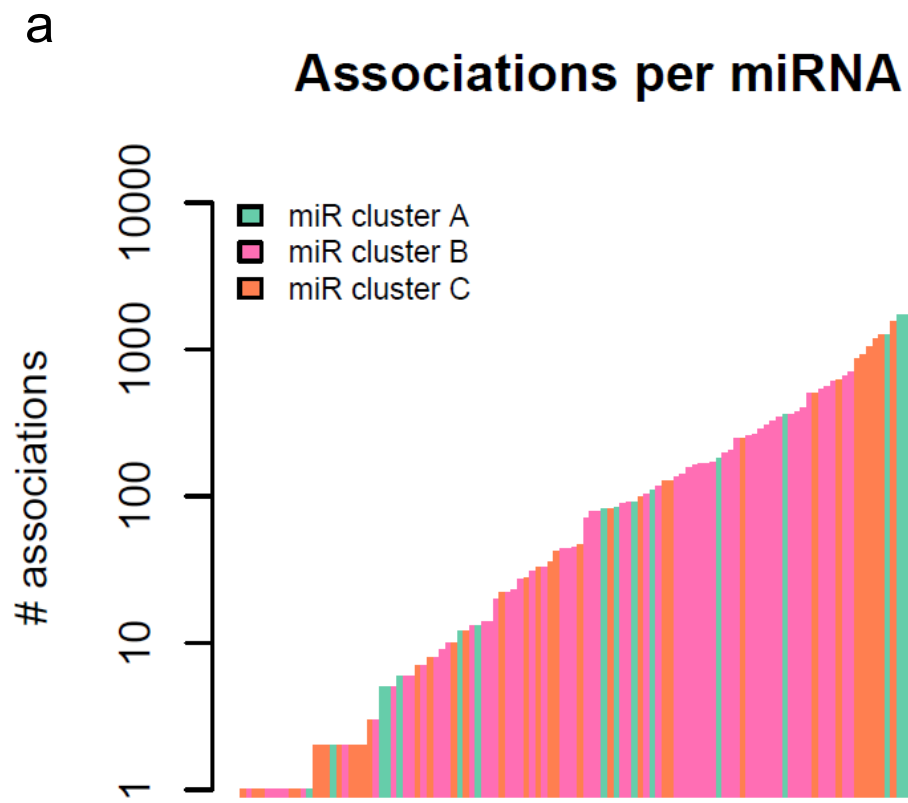
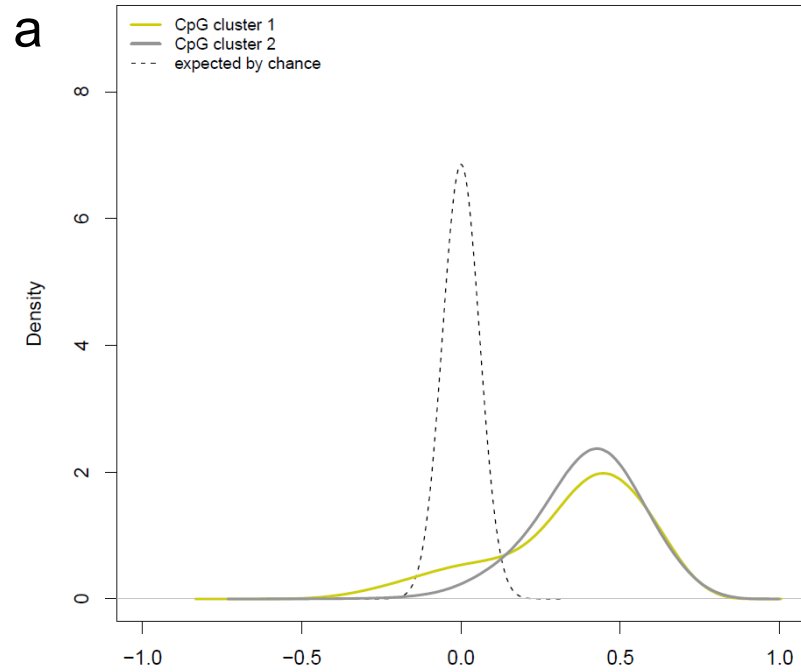


Fig. S5

Oslo2



TCGA

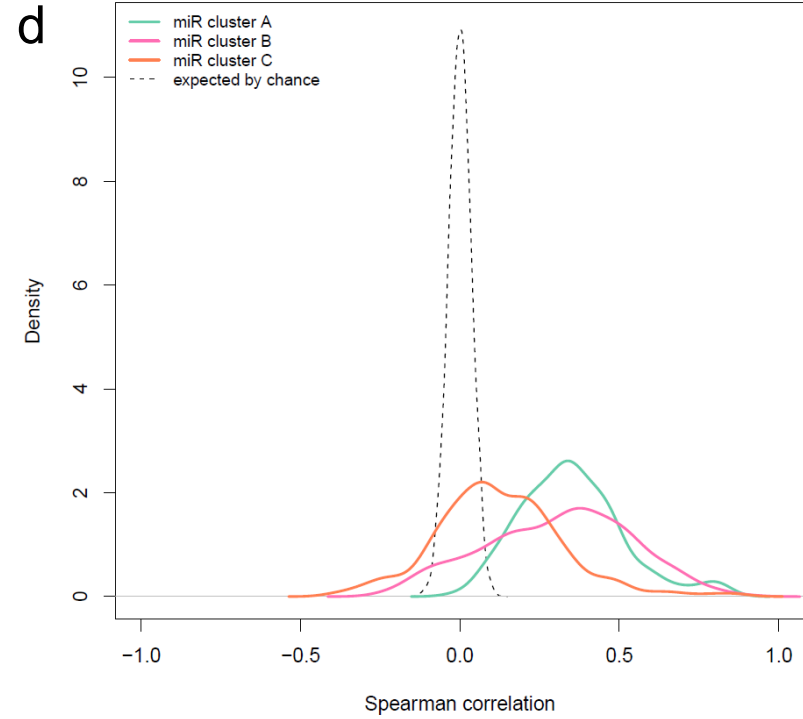
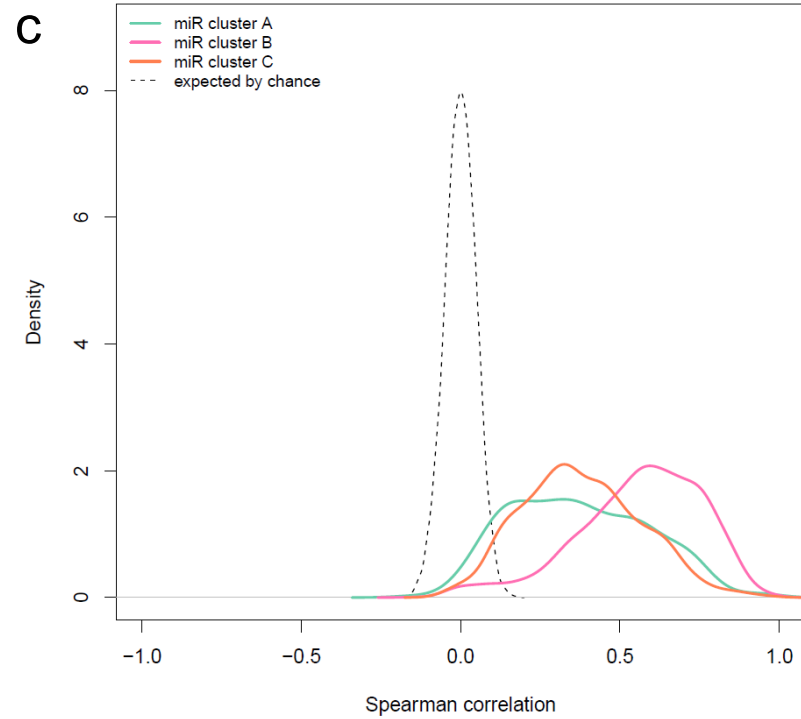
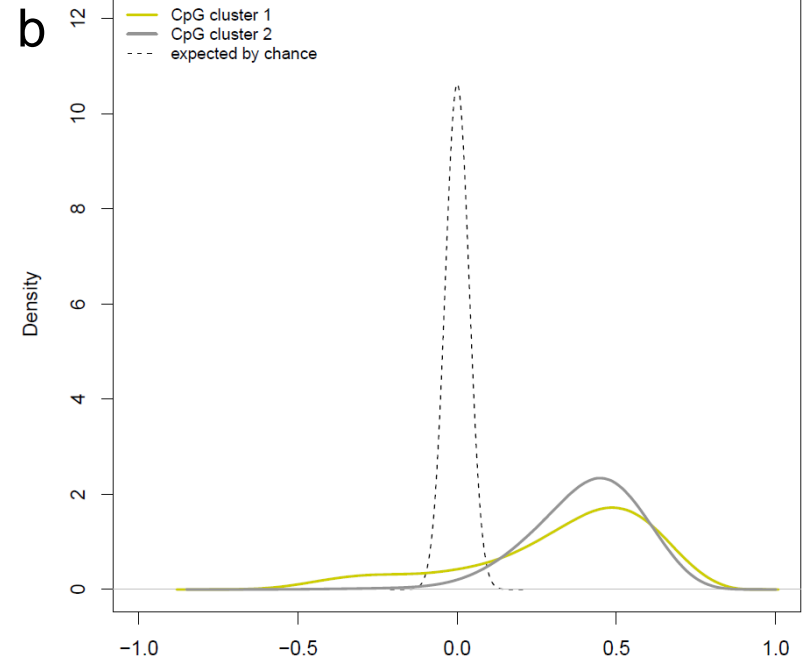


Fig. S6

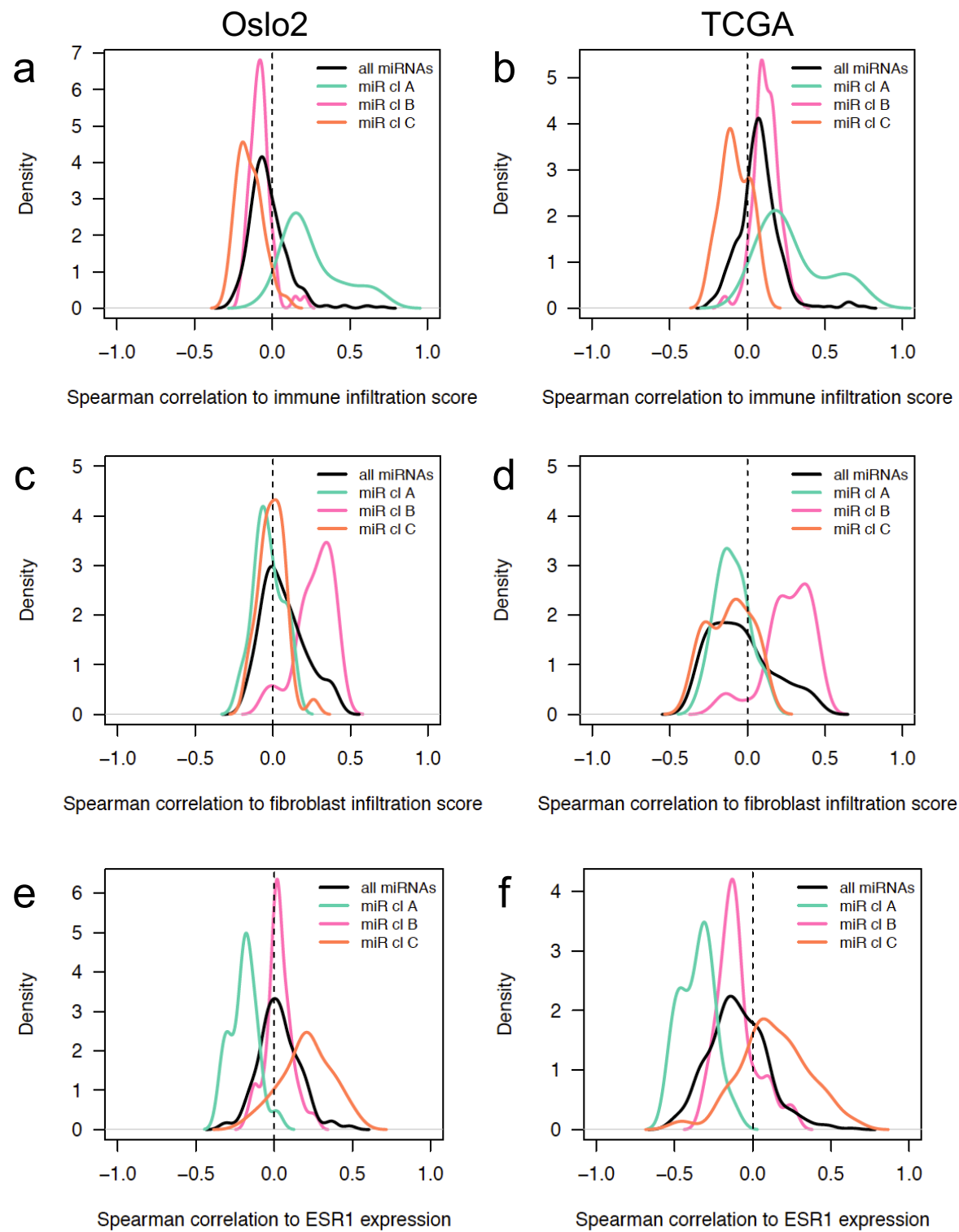


Fig. S7

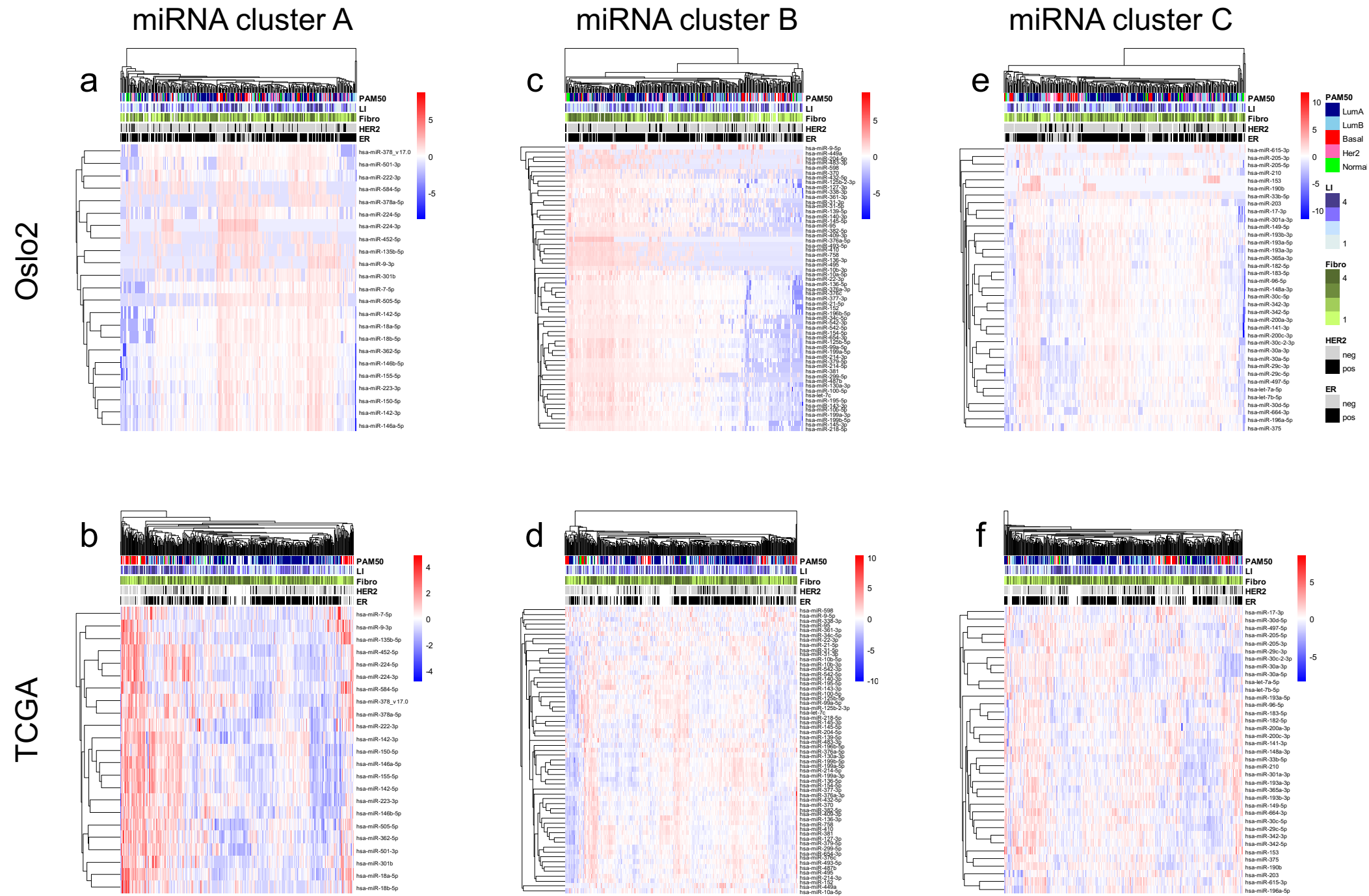
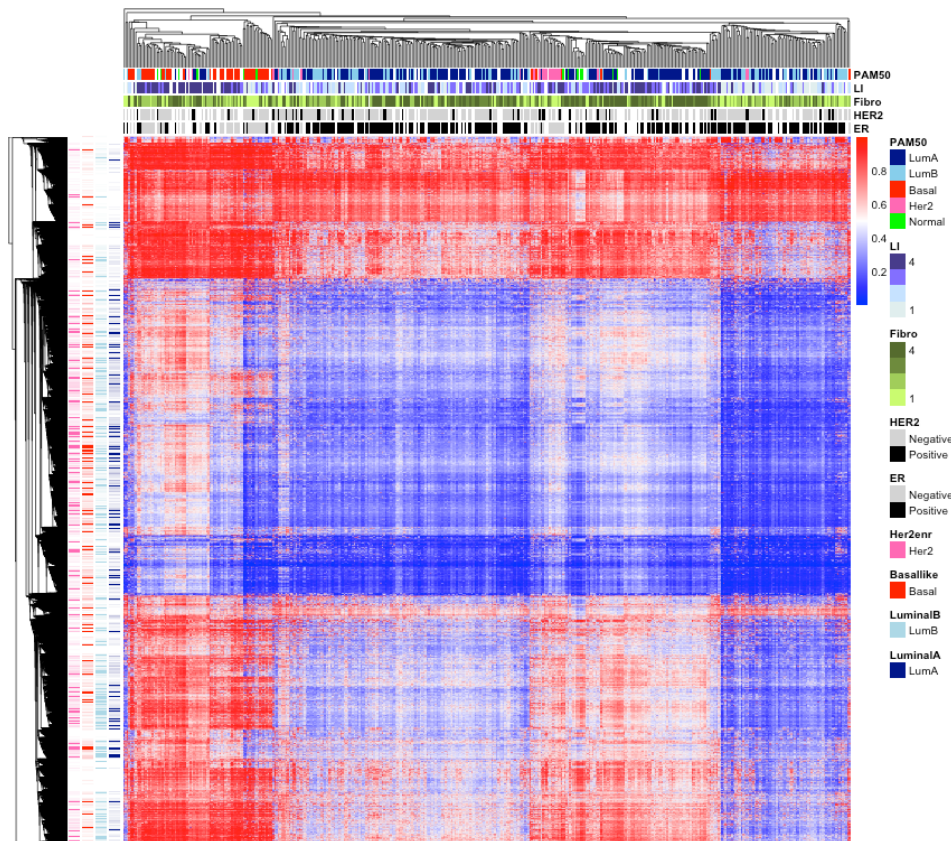


Fig. S8

CpG cluster 1
(TCGA)

a



CpG cluster 2
(TCGA)

b

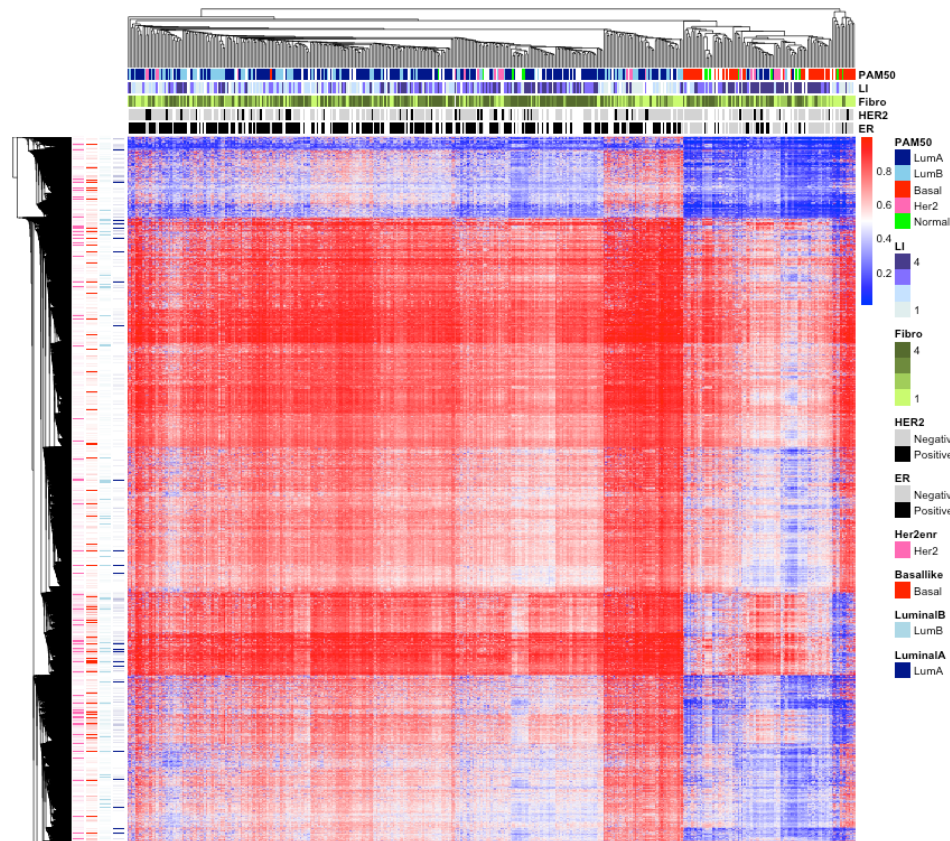
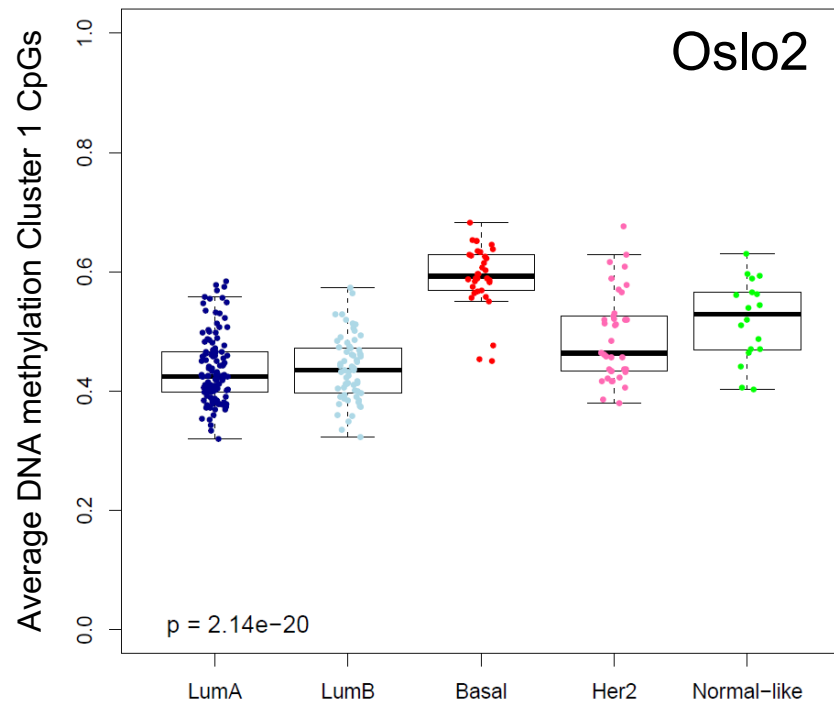
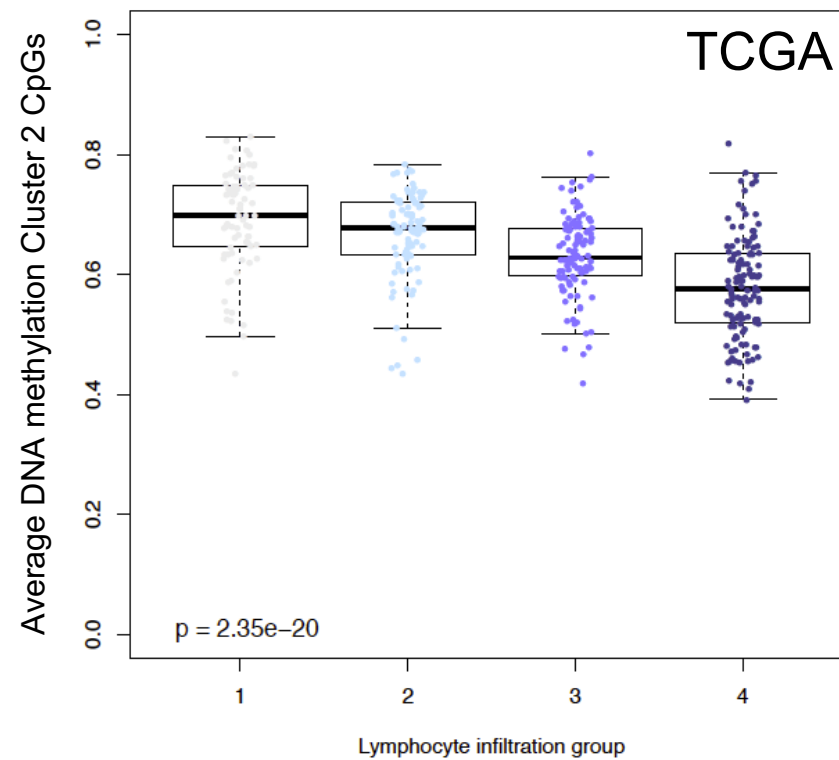


Fig. S9

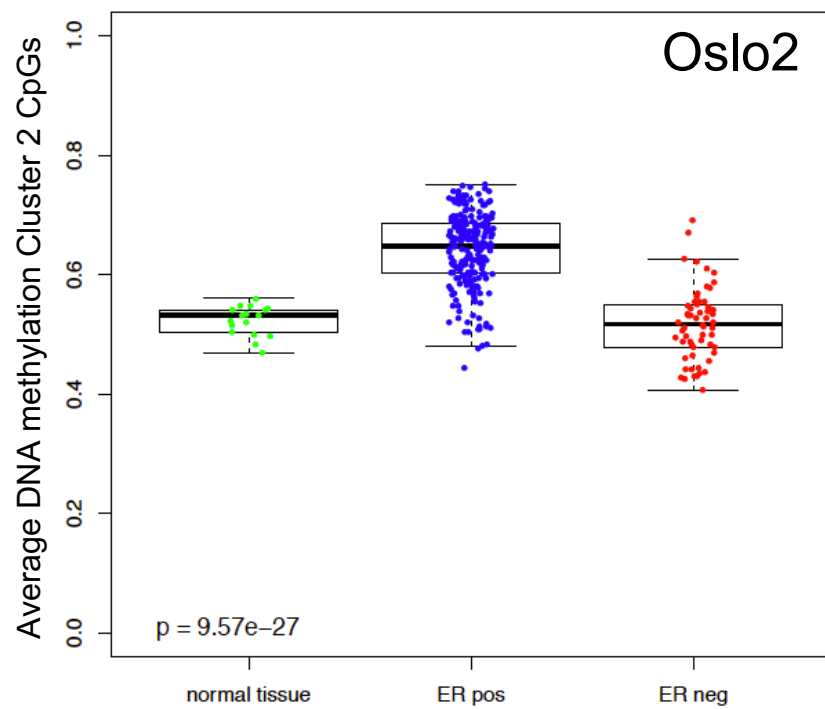
a



b



c



d

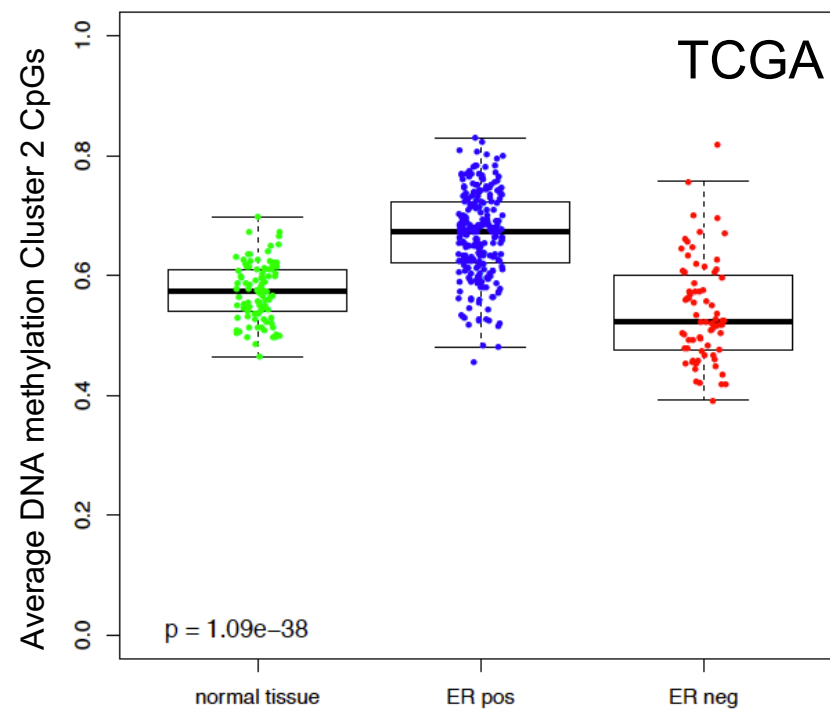


Fig. S10

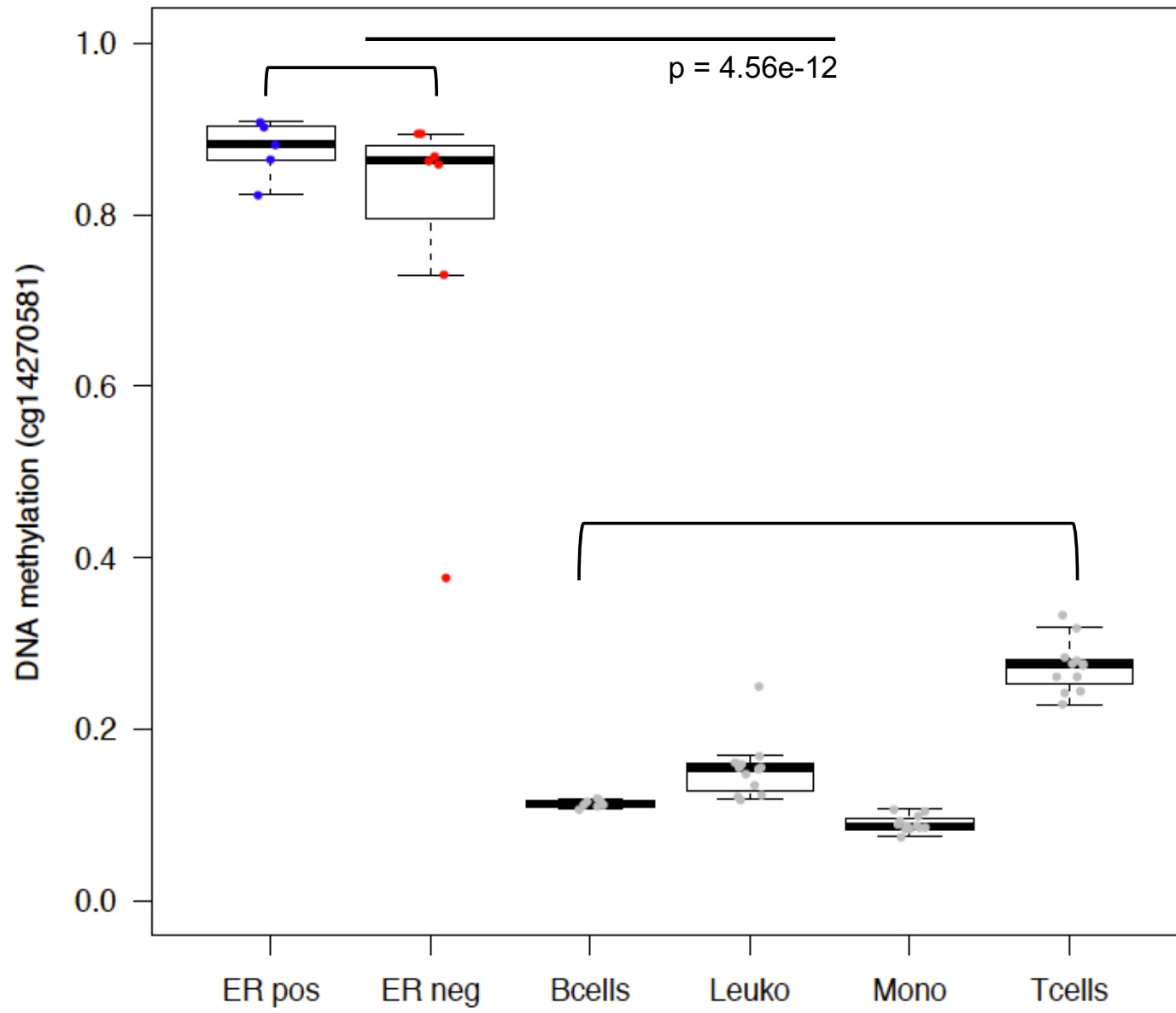


Fig. S11

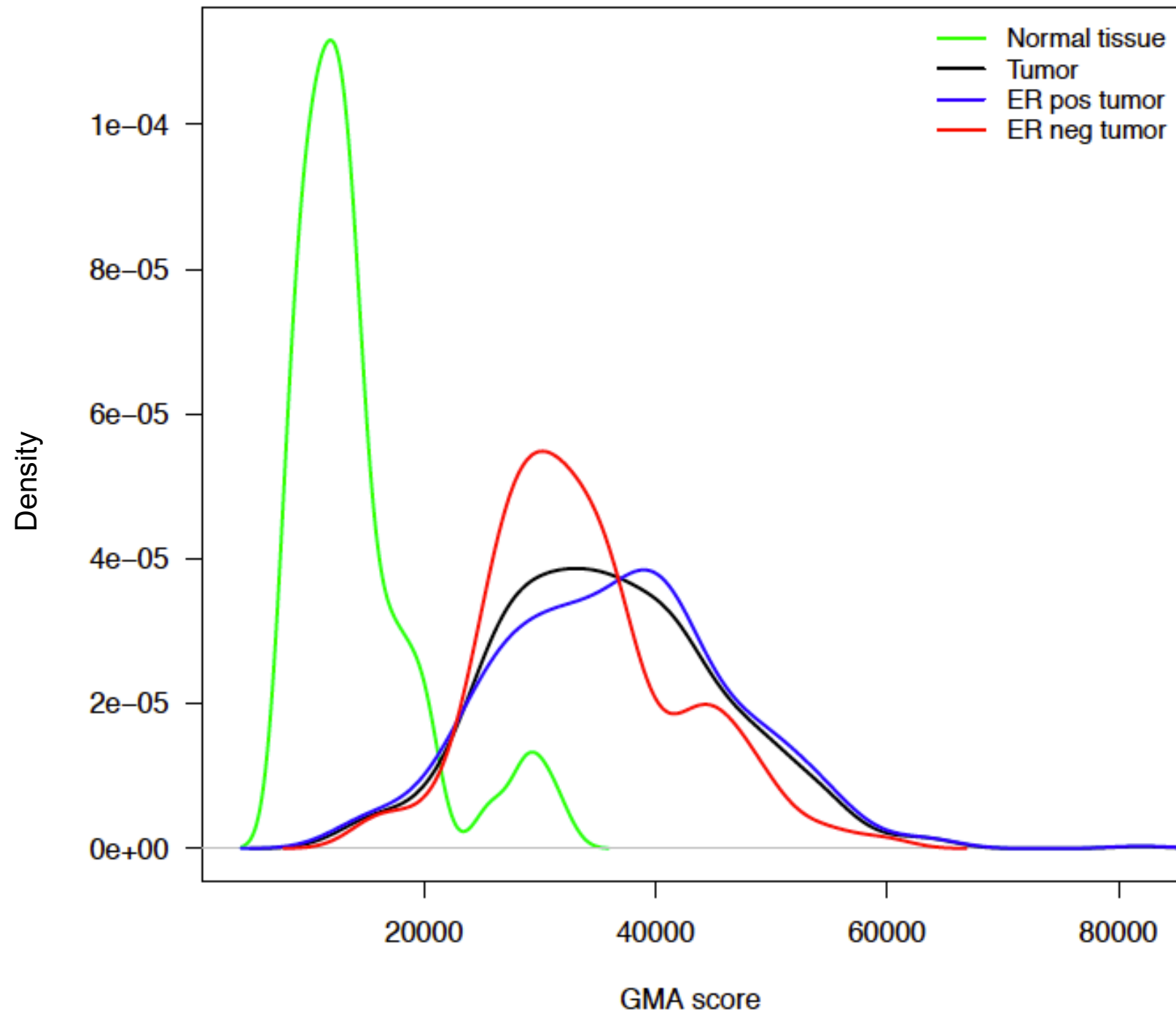


Fig. S12

