

Article

A Global Gene Body Methylation Measure Correlates Independently with Overall Survival in Solid Cancer Types - *Supplement*

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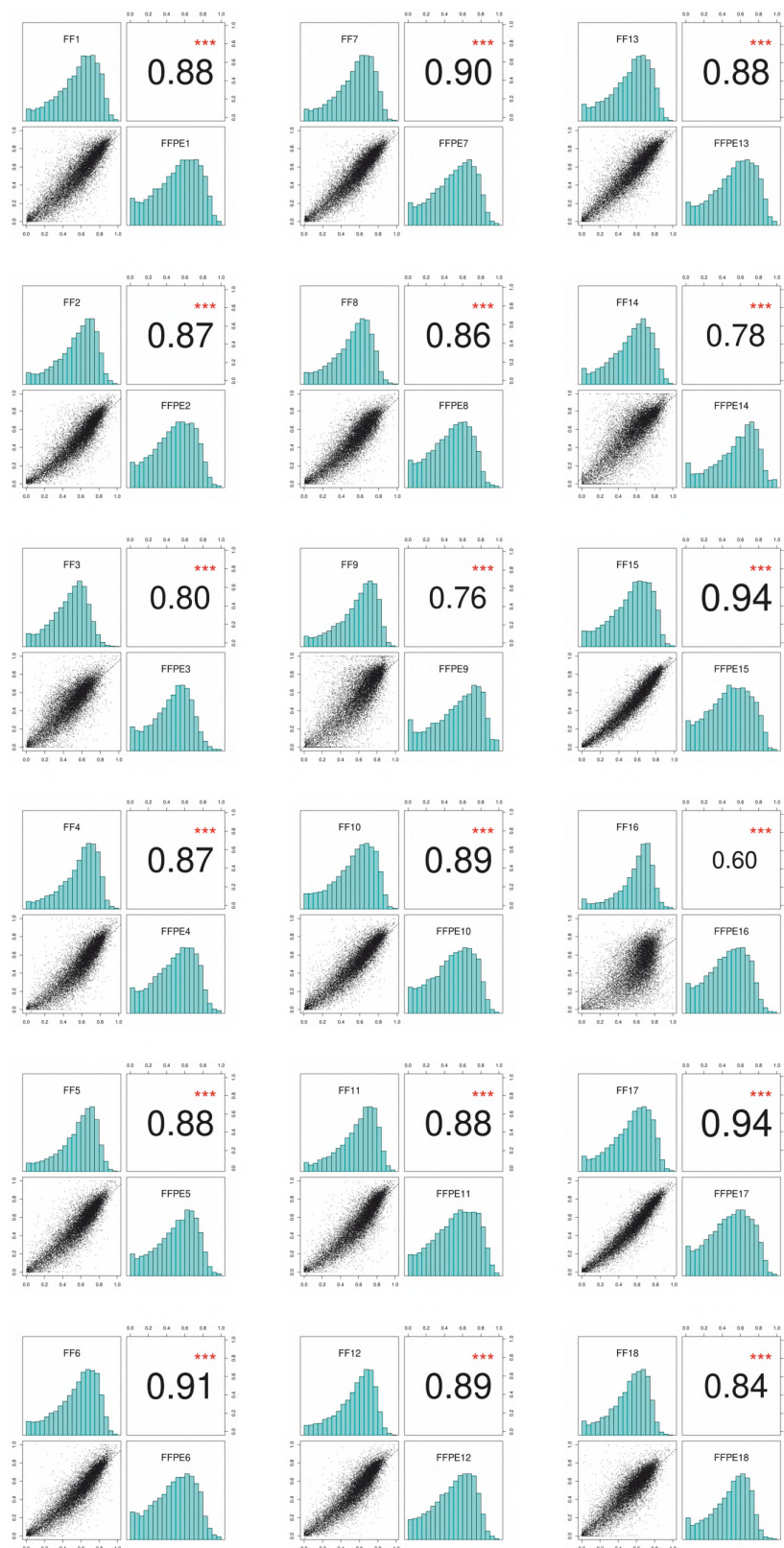


Figure S1. Correlation plots of averaged GB methylation values between DNA isolated from fresh frozen tumor tissues and macro/microdissected FFPE tumor tissues of the same patients.

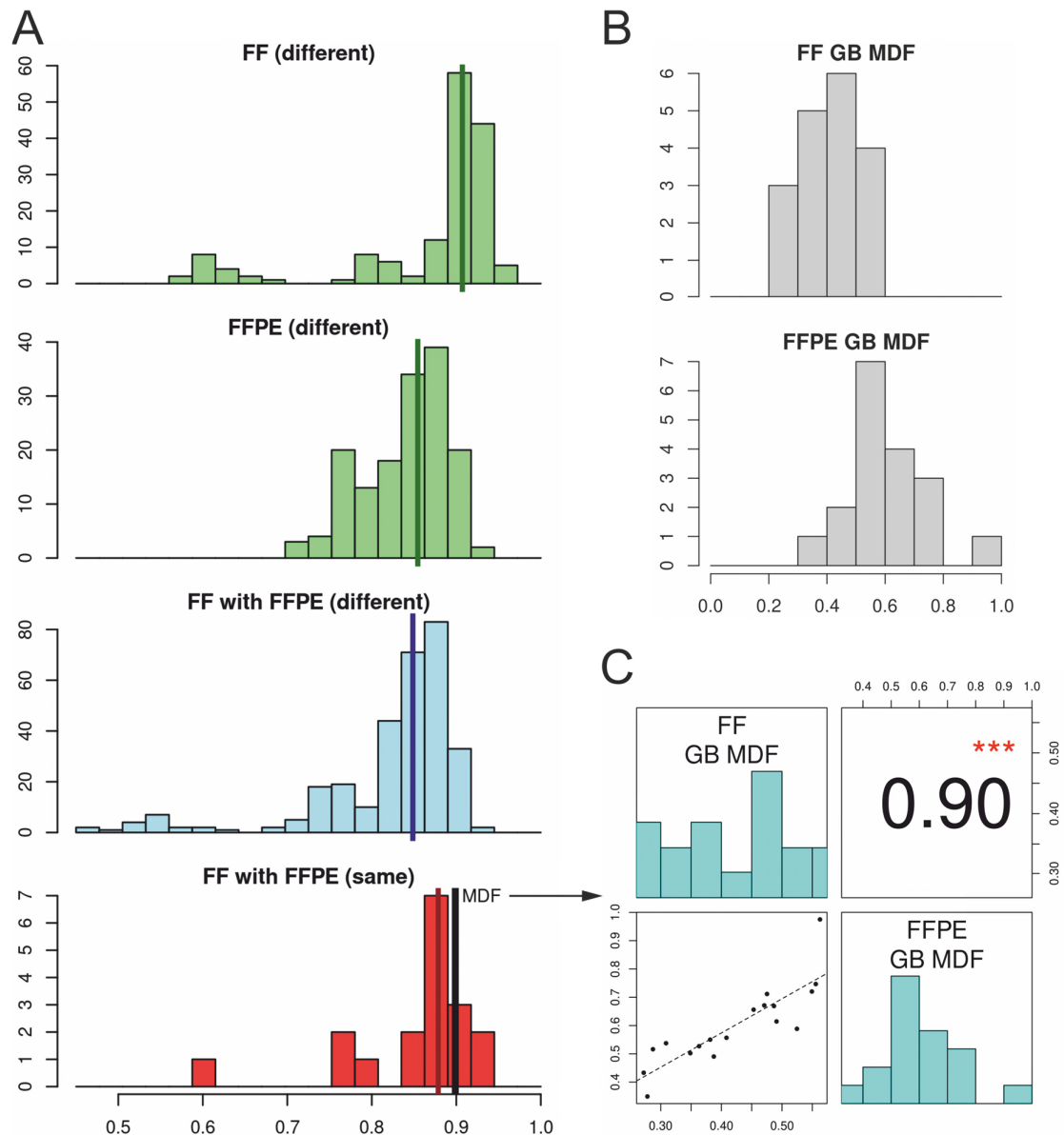


Figure S2. (A) Histograms of correlation coefficients of averaged GB methylation values between different samples within (fresh frozen) FF and (formalin fixed and paraffin embedded) FFPE tissues (green color), between different samples across FF and FFPE sample (blue color) and between the matched pairs of samples (from the same patients) from FF and FFPE tissues (red color). The black line indicates the correlation coefficient of the MDF values between matched pairs of FF and FFPE tissues (*cf.* C). (B) Histograms of the calculated "Methylation Definition Factor" (MDF) from FF and FFPE tissues from the same patients and (C) the correlation between these MDF values of the matched pairs of FF and FFPE tissues.

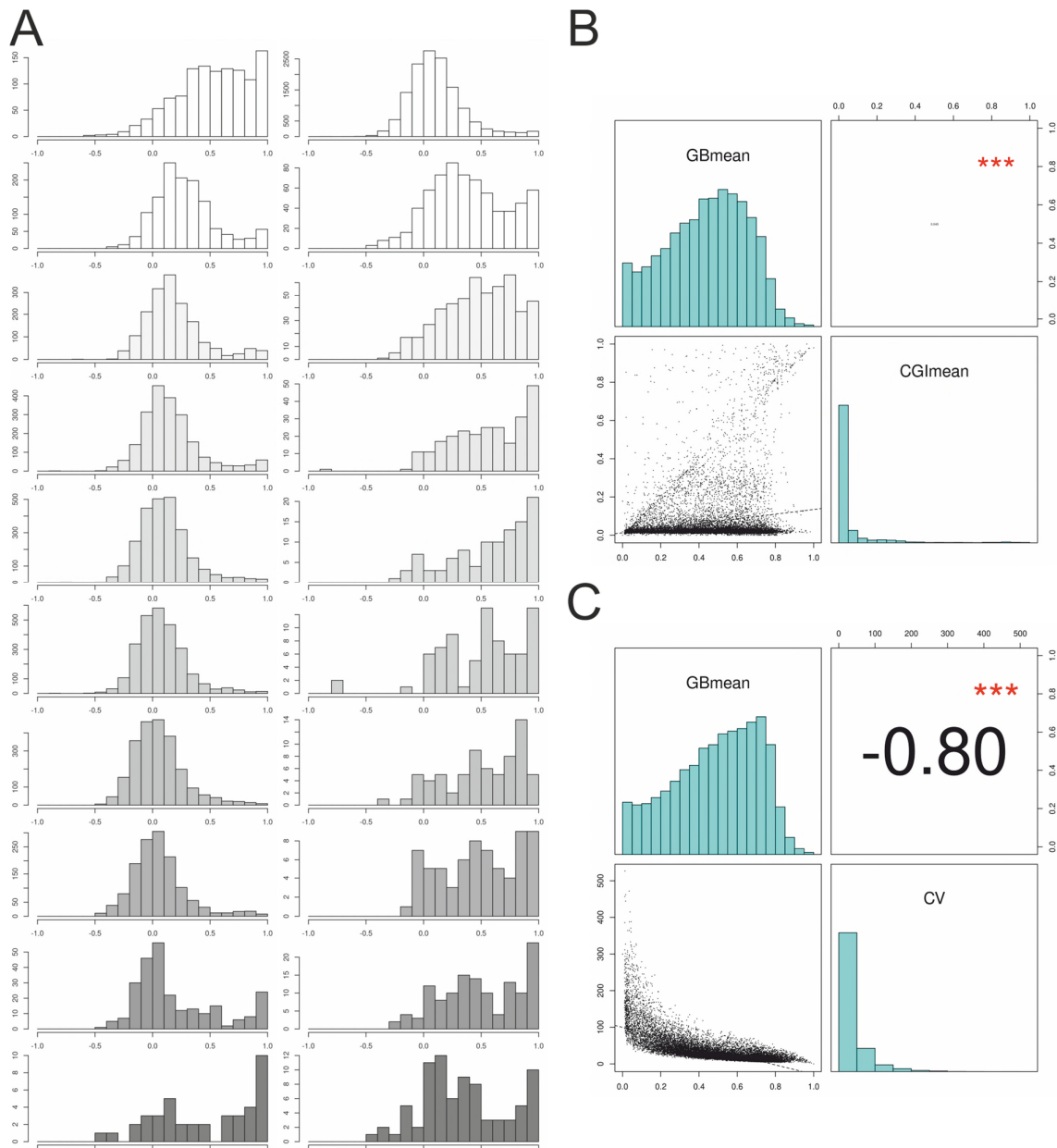


Figure S3. (A) Histograms of correlation coefficients of averaged GB methylation values with corresponding averaged CGI methylation values, split into slots of low to high mean methylation levels, *i.e.* 0%-10%, 10%-20%, ..., 90%-100% (colored white to dark grey). On the left side, split according to GB methylation levels and of the right side according to CGI methylation levels. (B) Overall correlation of corresponding averaged GB and CGI methylation levels. (C) Association of the coefficient of variation (CV) with the averaged GB methylation level.

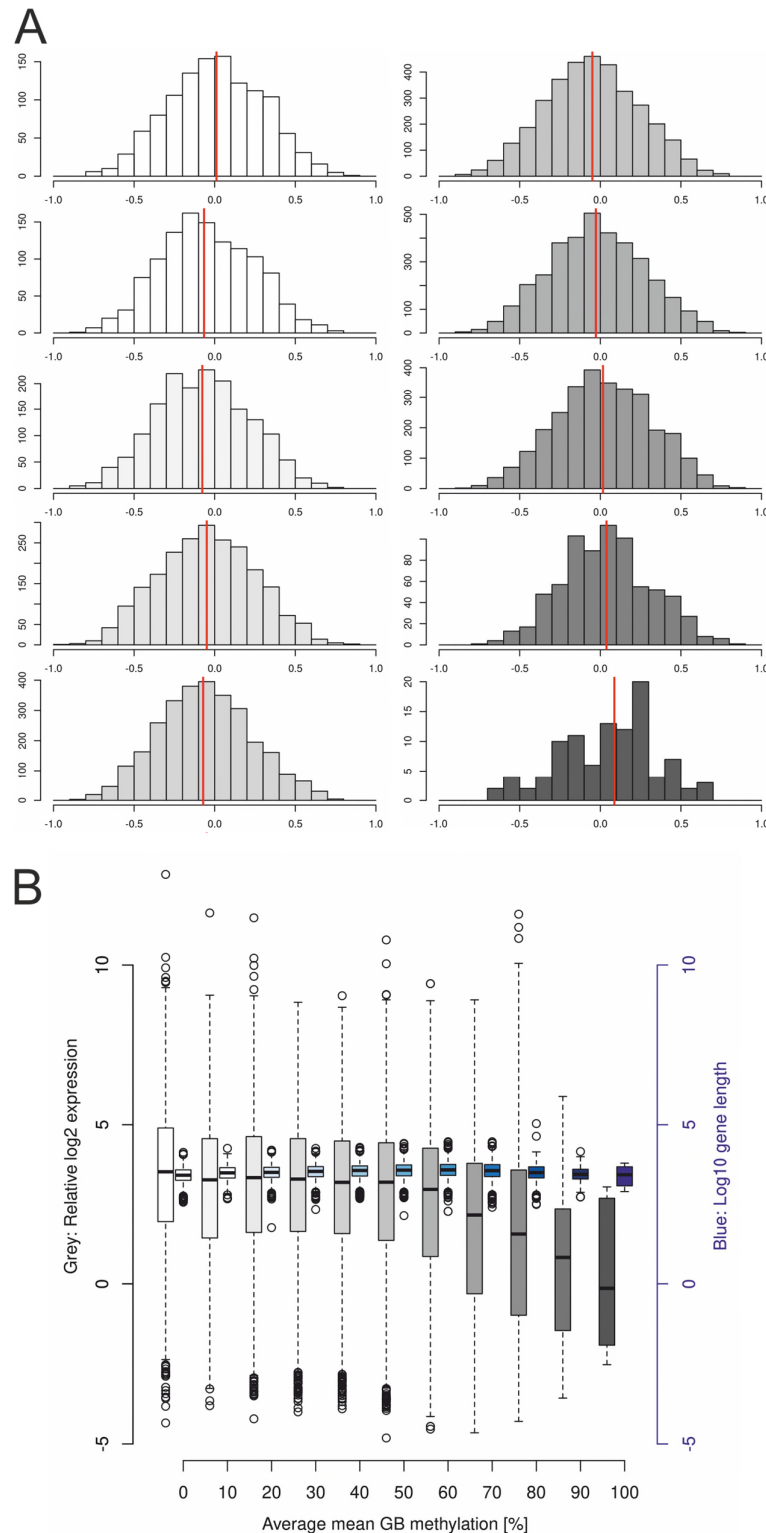
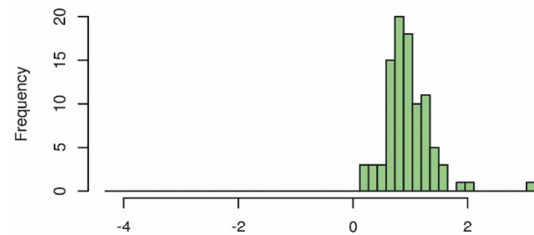
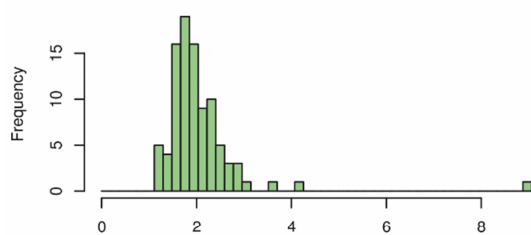
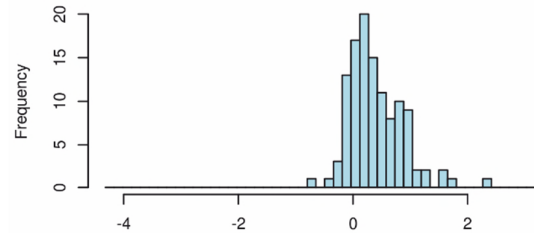
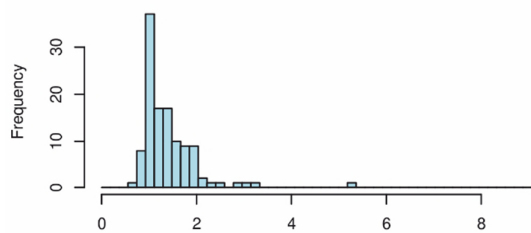


Figure S4. (A) Histograms of correlation coefficients between GB methylation values and corresponding gene expression values, split into slots of low to high mean GB methylation levels, *i.e.* 0%-10%, 10%-20%, ..., 90%-100% (colored white to dark grey). **(B)** Boxplots of \log_2 expression values of genes in slots of 0%-10%, 10%-20%, ..., 90%-100% methylated GBs (different grey colors, left y-axis) and corresponding \log_{10} gene length of genes in these slots (different blue colors, right y-axis).

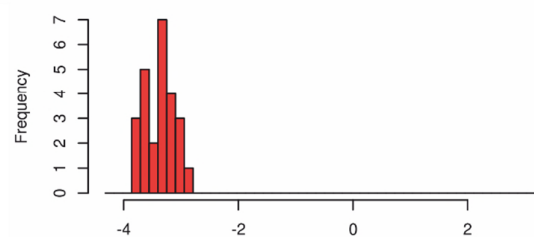
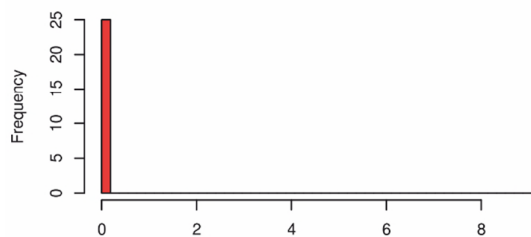
A) Normal human cells and tissues



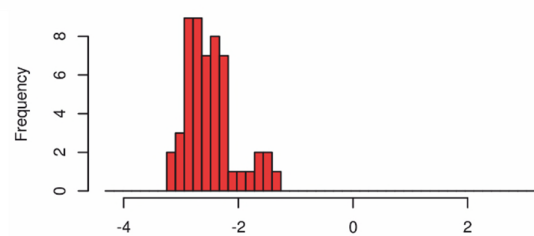
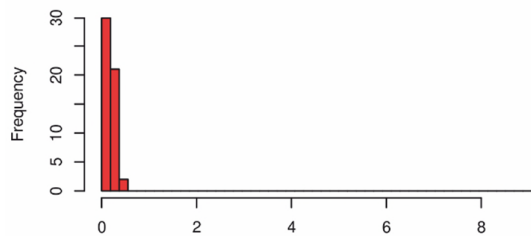
B) Cancer cell lines



C) Fresh frozen ovarian cancer tissues



D) FFPE ovarian cancer tissues

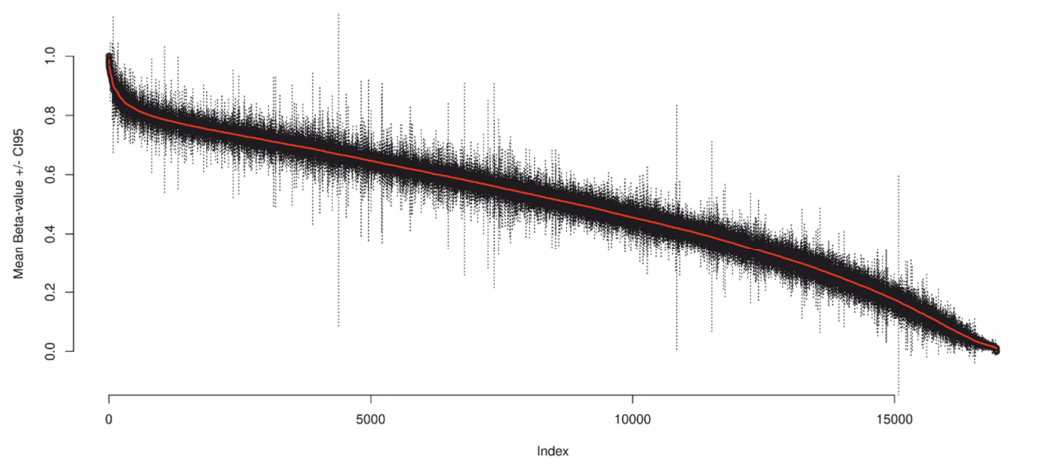


Linear

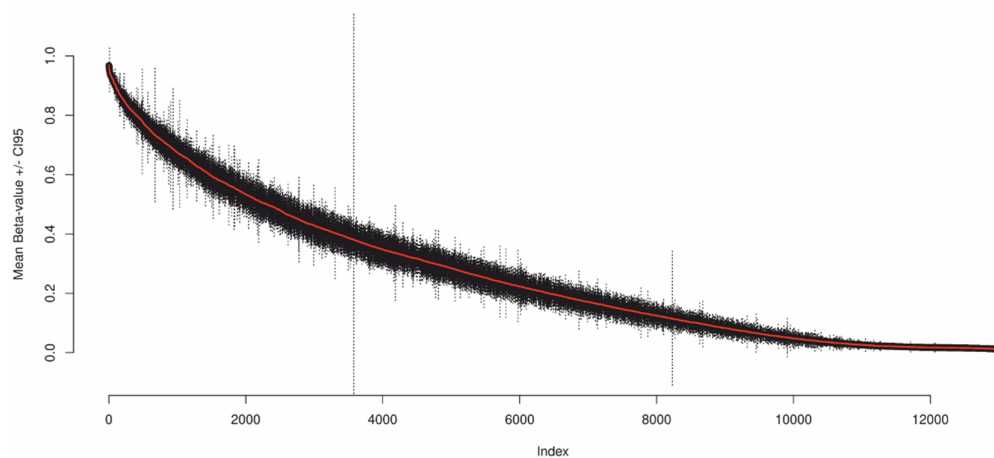
Log₂

Figure S5. Histograms of methylation definition factors (MDF, calculated as follows: (no average GB betas <0.1 + no average GB betas >0.9) / no average GB betas between 0.2 and 0.8) of **(A)** 41 normal human primary cells and tissues (astrocyte (primary cell), foreskin fibroblast (primary cell), islet of Langerhans (tissue), placenta (tissue), hepatocyte (primary cell), mononuclear cell (primary cell), testis (tissue), adrenal gland (tissue), zone of skin (tissue), mammary epithelial cell (primary cell), uterus (tissue), non-pigmented ciliary epithelial cell (primary cell), epithelial cell of alveolus of lung (primary cell), iris pigment epithelial cell (primary cell), epithelial cell of esophagus (primary cell), epithelial cell of proximal tubule (primary cell), pericardium (tissue), heart left ventricle (tissue), bronchial epithelial cell (primary cell), kidney epithelial cell (primary cell), lung (tissue), renal cortical epithelial cell (primary cell), epithelial cell of prostate (primary cell), kidney (tissue), cardiac fibroblast (primary cell), skeletal muscle cell (primary cell), stomach (tissue), epidermal melanocyte (primary cell), myoblast (primary cell), pancreas (tissue), skeletal muscle myoblast (primary cell), aortic smooth muscle cell (primary cell), osteoblast (primary cell), cardiac muscle cell (primary cell), brain (tissue), skeletal muscle tissue (tissue), choroid plexus epithelial cell (primary cell), liver (tissue), retinal pigment epithelial cell (primary cell), amniotic epithelial cell (primary cell), breast (tissue)); **(B)** 43 cancer cell lines (MCF, 10A, LNCaP, K562, IMR-90, MCF-7, HEK293, H1, HTR-8/SVneo, NB4, U-87, MG, BJ, HepG2, Caco-2, HeLa-S3, GM19240, HL-60, BE2C, T47D, CMK, Panc1, A549, GM19239, AG09319, NT2/D1, GM06990, HCT116, SK-N-SH, GM12891, SK-N-MC, AG04450, Ishikawa, AG10803, Jurkat, AG08470, AG09309, GM12878, UCH-1, PFSK-1, OVCAR3, HGPS, GM12892, AG04449, hTERT-HM); **(C)** fresh frozen ovarian cancer tumor tissues; and **(D)** formalin fixed paraffin embedded (FFPE) ovarian cancer tumor tissues.

A) Ovarian cancer tumor tissue



B) Cancer cell lines



C) Normal human primary cells or tissues

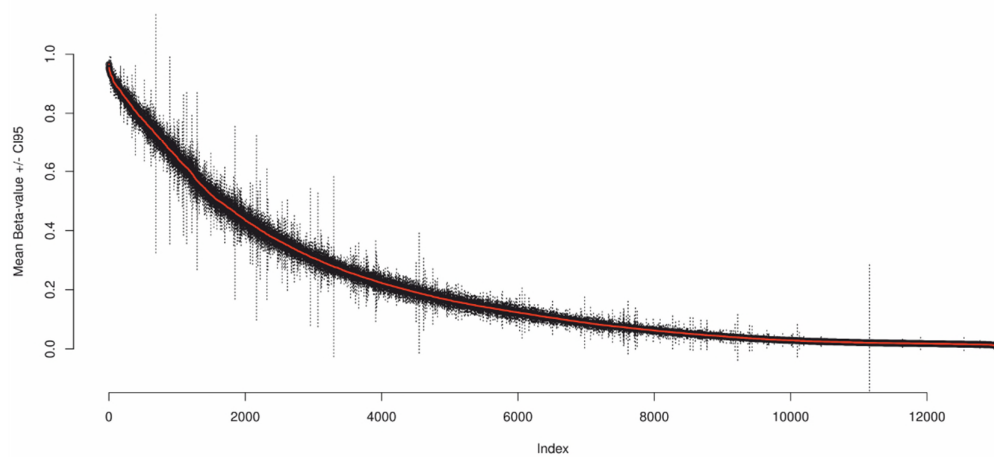


Figure S6. Distribution of average gene body methylation values (beta values \pm CI₉₅ over samples) of gene bodies of protein coding genes. **(A)** 45 ovarian cancer tumor tissues; **(B)** 43 cancer cell lines (MCF, 10A, LNCaP, K562, IMR-90, MCF-7, HEK293, H1, HTR-8/SVneo, NB4, U-87, MG, BJ, HepG2, Caco-2, HeLa-S3, GM19240, HL-60, BE2C, T47D, CMK, Panc1, A549, GM19239, AG09319, NT2/D1, GM06990, HCT116, SK-N-SH, GM12891, SK-N-MC, AG04450, Ishikawa, AG10803, Jurkat, AG08470, AG09309, GM12878, UCH-1, PFSK-1, OVCAR3, HGPS, GM12892, AG04449, hTERT-HM); **(C)** 41 normal human primary cells and tissues (astrocyte (primary cell), foreskin fibroblast (primary cell), islet of Langerhans (tissue), placenta (tissue), hepatocyte (primary cell), mononuclear cell (primary cell), testis (tissue), adrenal gland (tissue), zone of skin (tissue), mammary epithelial cell (primary cell), uterus (tissue), non-pigmented ciliary epithelial cell (primary cell), epithelial cell of alveolus of lung (primary cell), iris pigment epithelial cell (primary cell), epithelial cell of esophagus (primary cell), epithelial cell of proximal tubule (primary cell), pericardium (tissue), heart left ventricle (tissue), bronchial epithelial cell (primary cell), kidney epithelial cell (primary cell), lung (tissue), renal cortical epithelial cell (primary cell), epithelial cell of prostate (primary cell), kidney (tissue), cardiac fibroblast (primary cell), skeletal muscle cell (primary cell), stomach (tissue), epidermal melanocyte (primary cell), myoblast (primary cell), pancreas (tissue), skeletal muscle myoblast (primary cell), aortic smooth muscle cell (primary cell), osteoblast (primary cell), cardiac muscle cell (primary cell), brain (tissue), skeletal muscle tissue (tissue), choroid plexus epithelial cell (primary cell), liver (tissue), retinal pigment epithelial cell (primary cell), amniotic epithelial cell (primary cell), breast (tissue)).

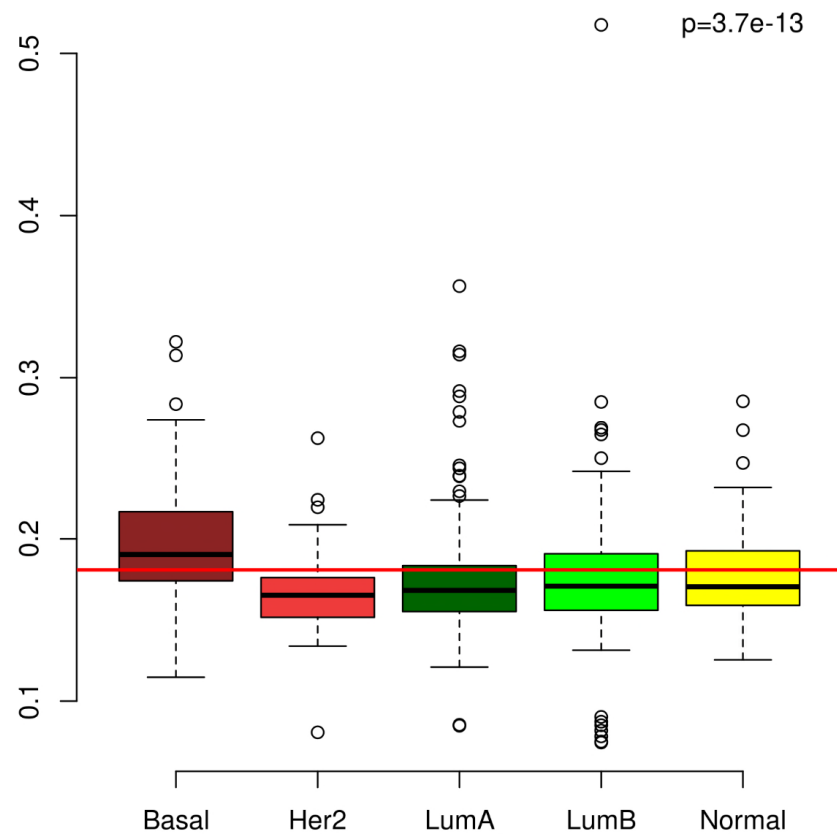


Figure S7. Correlation of the methylation definition factor (MDF), Y-axis, with the breast cancer subtypes, determined with the PAM50 gene signature. Red line, cutoff for the optimal dichotomization of the MDF as obtained from multiple Cox regression models.

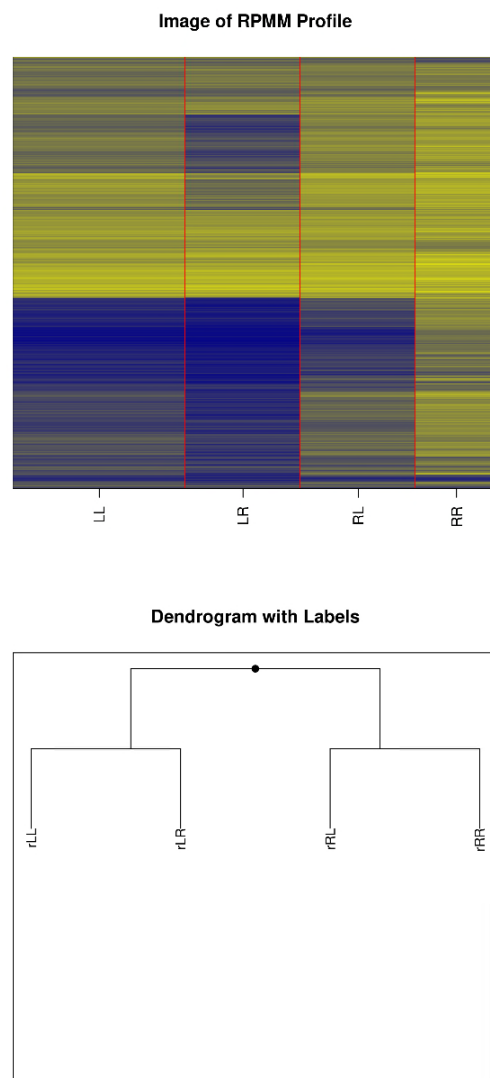


Figure S8. The CpG island methylator phenotype (CIMP) status determined from TCGA colorectal cancer samples according to Hinoue *et al.* [1]. rRR, CIMP-H; rRL, CIMP-L; rLL, type 3; rLR, type 4.

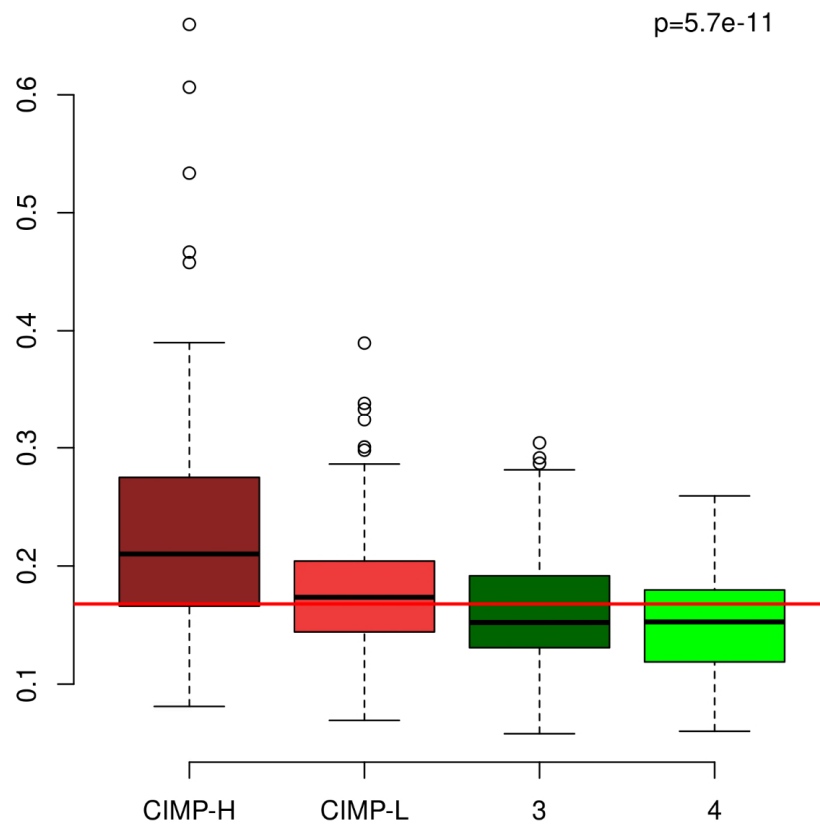


Figure S9. Correlation of the methylation definition factor (MDF), Y-axis, with the CpG Island Methylator Phenotypes determined with the function `bclTree` of R-package `RPM` 1.25. Red line, cutoff for the optimal dichotomization of the MDF as obtained from multiple Cox regression models.

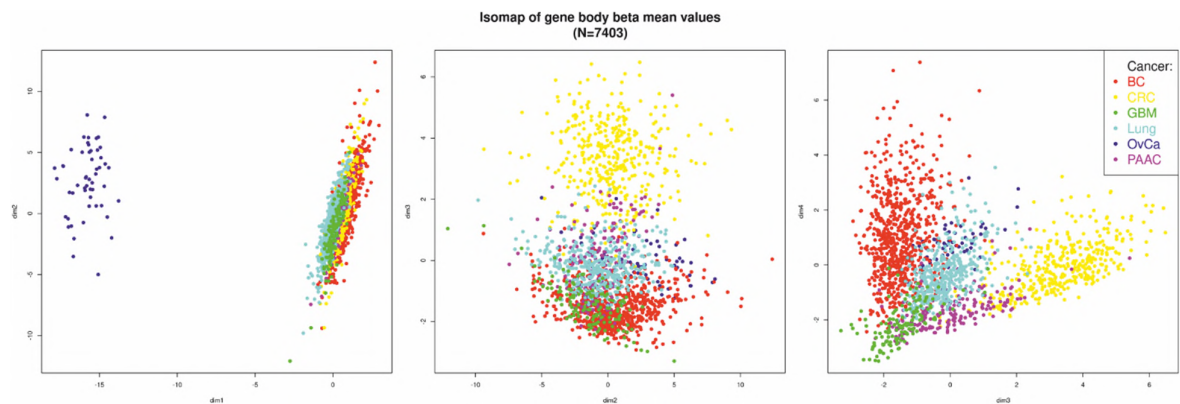


Figure S10. Isomap representation of all samples from all cancer entities using the averaged gene body beta values (if present and without missing data in all samples, N=7,403).

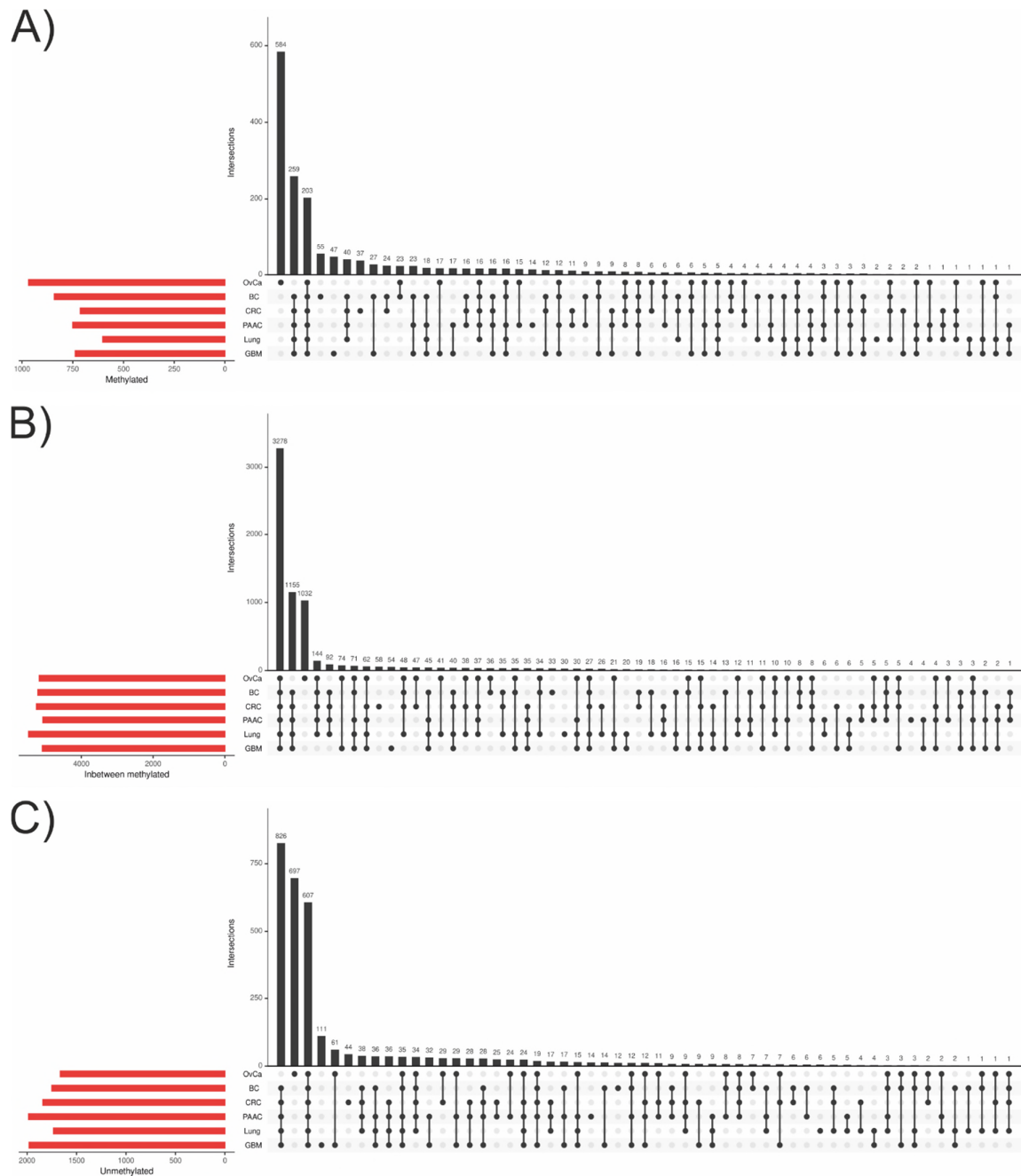


Figure S11. Overlap of **(A)** genes with methylated gene bodies (mean averaged beta values >0.7), **(B)** with intermediate methylated gene bodies (mean averaged beta values <0.7 and >0.3), and **(C)** unmethylated (mean averaged beta value <0.3) over all indicated cancer types. Only gene bodies with available averaged beta values present in all cancer entities were considered; $N=7,801$.

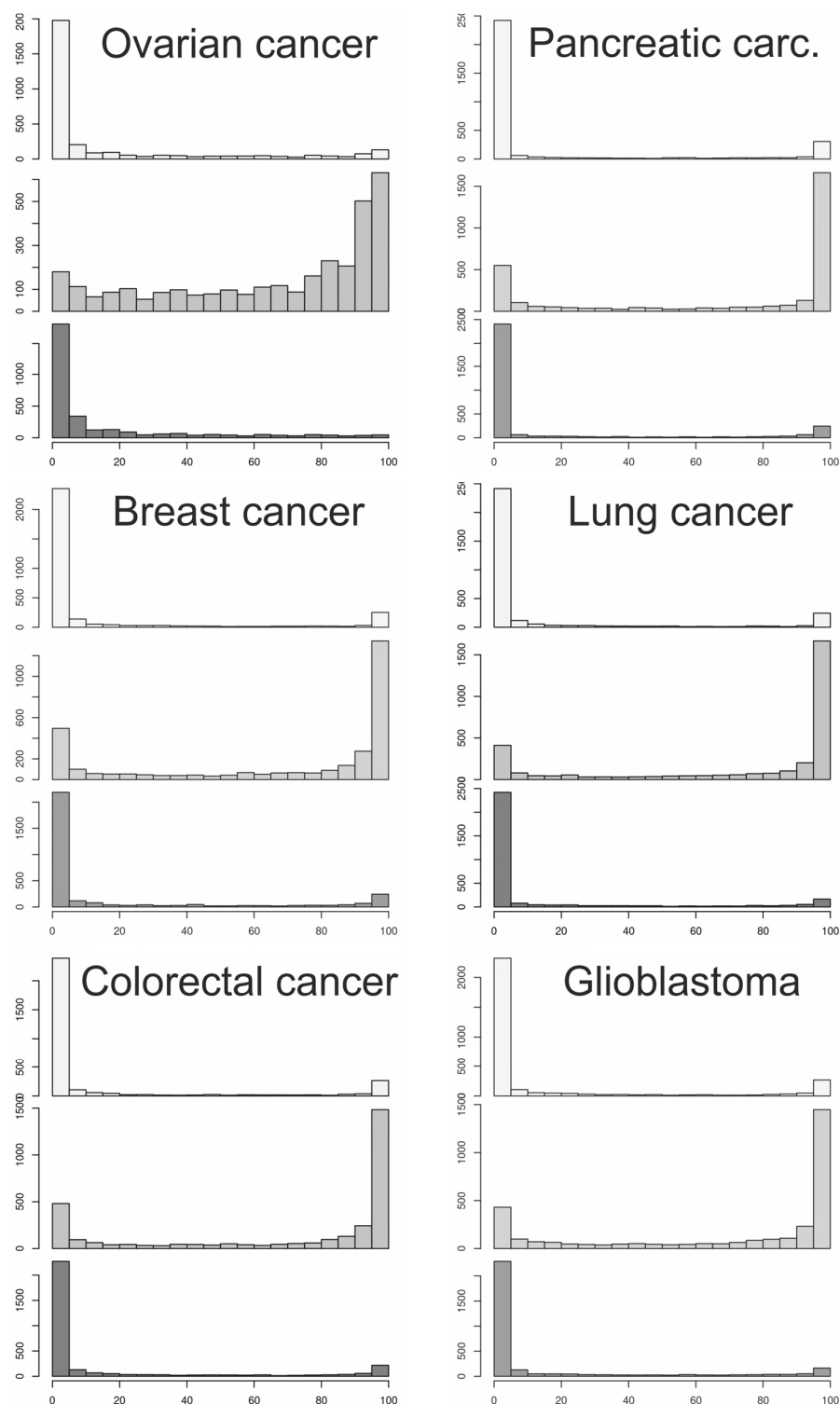


Figure S12. Histograms showing the percentages of genes which are consistently annotated to a specific GB methylation slot, divided into three mean GB methylation slots, low methylation (<0.3; light grey), intermediate methylation (≥ 0.3 and ≤ 0.7 ; grey), and high methylation (>0.7; dark grey).

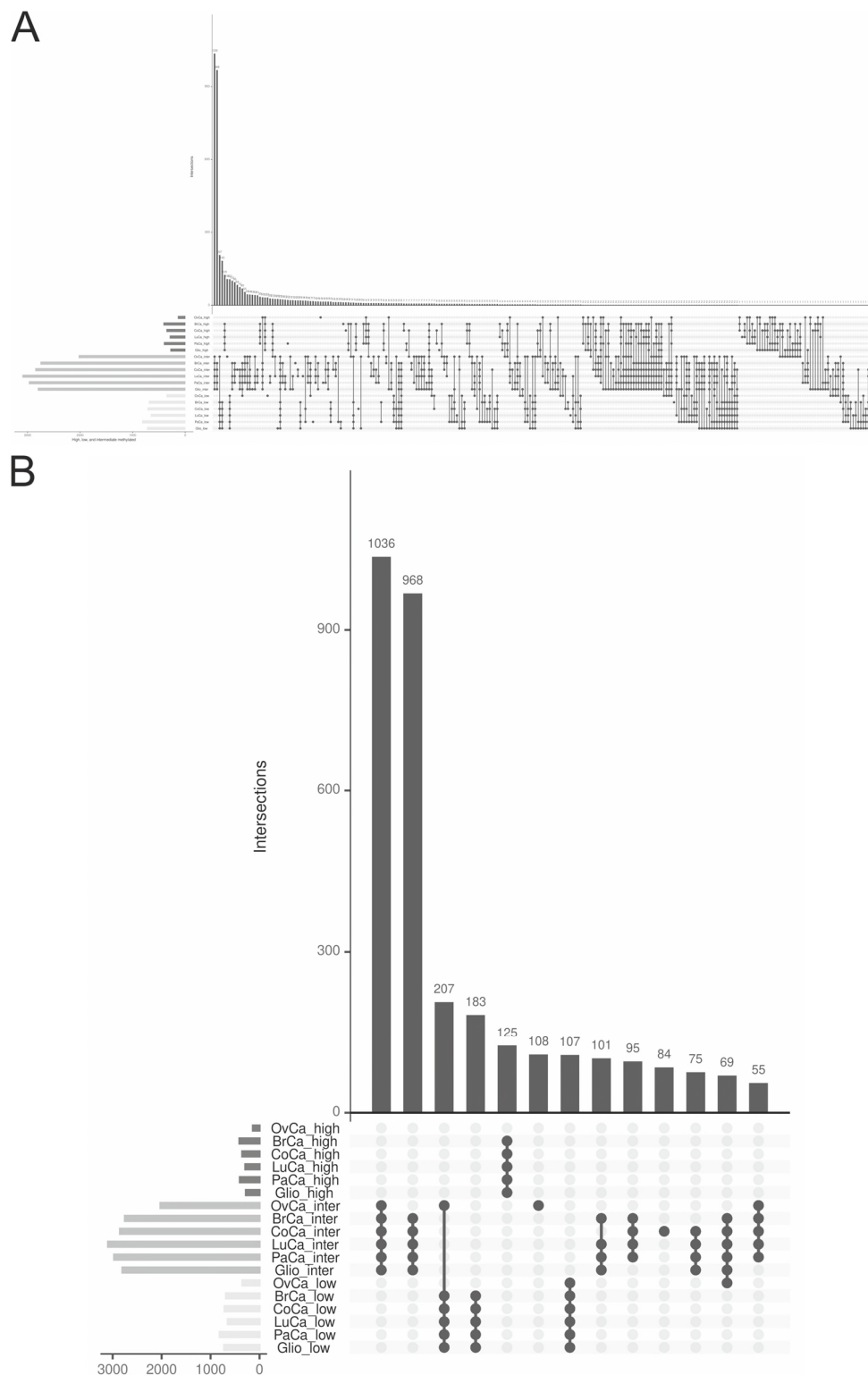


Figure S13. (A) Overlap of gene lists consistently categorized (*i.e.* in >90% of samples) to one of the GB methylation slots (high, >0.7; intermediate; and low, <0.3) from different cancer entities, derived from data shown in Figure S12. **(B)** Subset of the first 13 gene overlaps from A).

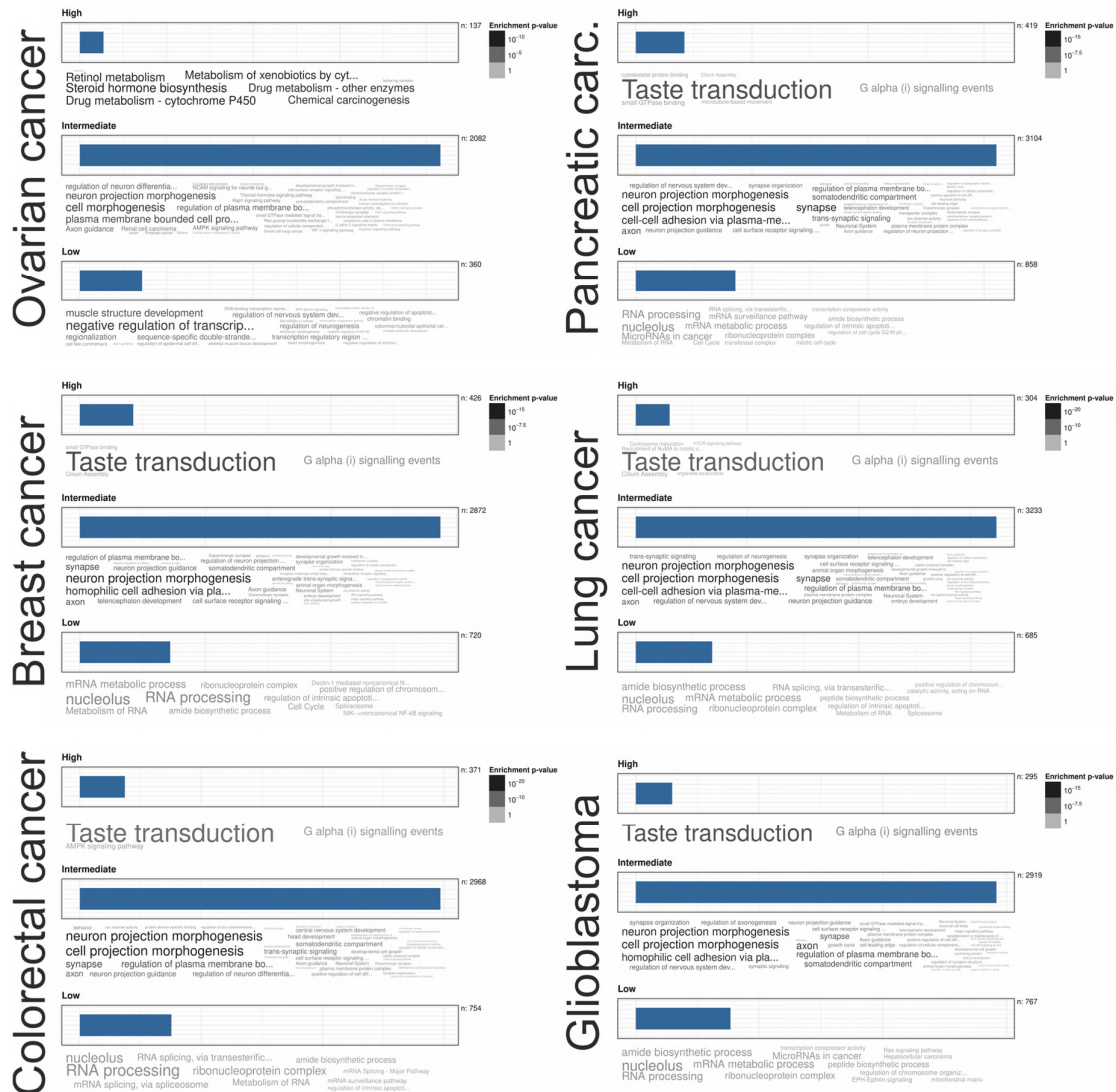
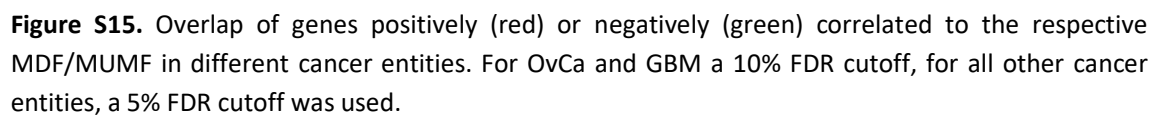
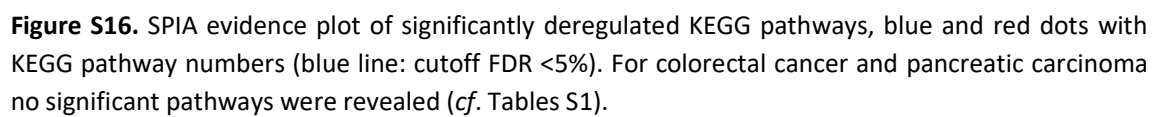
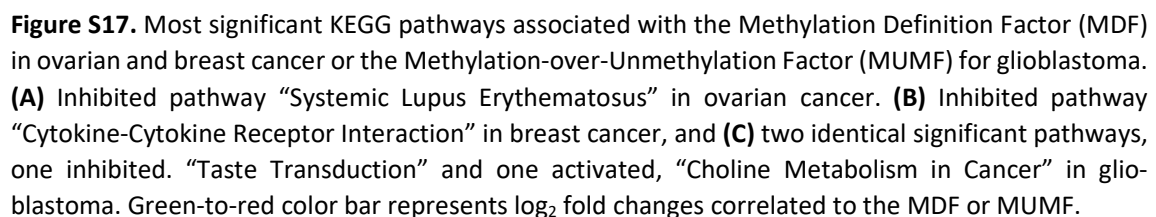


Figure S14. Enrichment plots of gene ontology terms and pathways of lists of consistently as high, intermediate, or low methylated categorized genes. Enrichments are indicated in word clouds by size and color (p-values). Overlap of gene lists across cancer entities is shown in Figure S13.







1. Hinoue, T.; Weisenberger, D.J.; Lange, C.P.; Shen, H.; Byun, H.M.; Van Den Berg, D.; Malik, S.; Pan, F.; Noushmehr, H.; van Dijk, C.M., et al. Genome-scale analysis of aberrant DNA methylation in colorectal cancer. *Genome Res* **2012**, *22*, 271-282, doi:10.1101/gr.117523.110.



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