

Supplementary Material

Survival analysis of multi-omics data identifies potential prognostic markers of pancreatic ductal adenocarcinoma

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1 Supplementary Data

Supplementary tables are available on FigShare.

Table S2: <https://figshare.com/s/2f2359bf82e3a8db118f>

Table S3: <https://figshare.com/s/90c7a4decd480006ab9f>

Table S4: <https://figshare.com/s/6033221610cca1fe4fb8>

Table S5: <https://figshare.com/s/e183e0a487f87bebc3a8>

Table S6: <https://figshare.com/s/205a5f6ecd86a81314d7>

Table S7: <https://figshare.com/s/083f83bb641bd4901ec1>

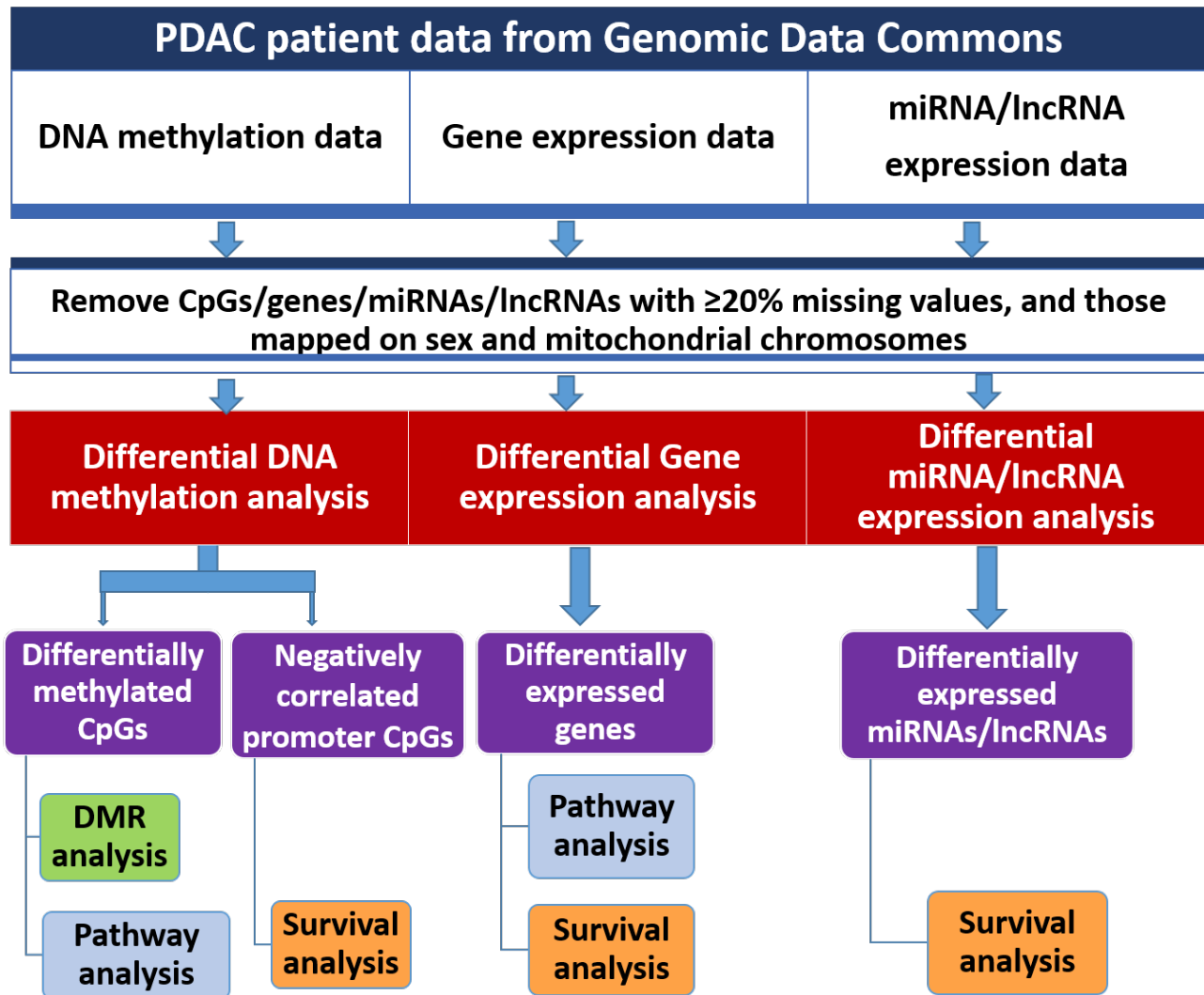
2 Supplementary Tables and Figures

2.1 Supplementary Tables

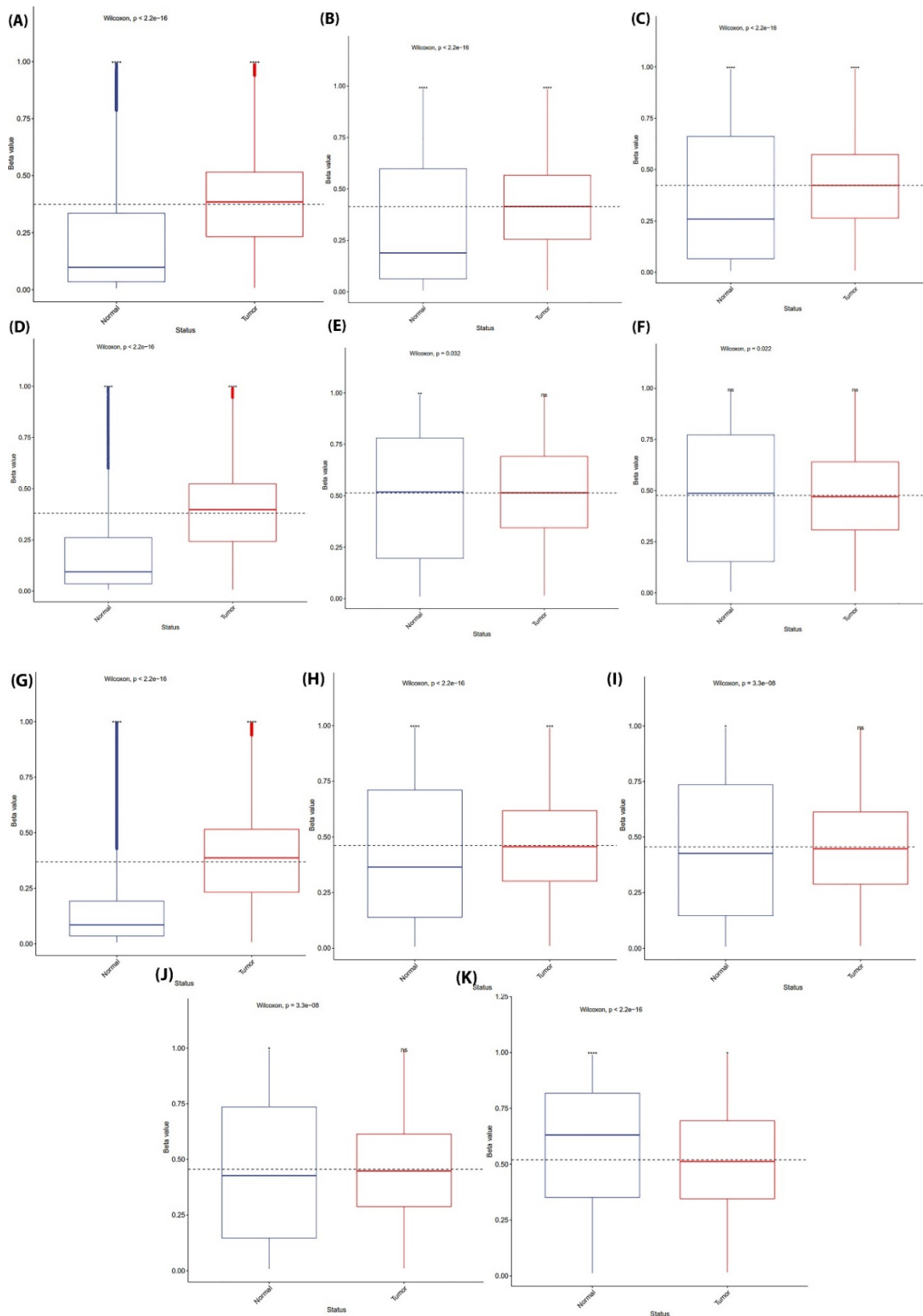
Table S1: List of R/Bioconductor tools and database used in pancreatic ductal cancer data analysis.

Resource	Source	Identifier
Software and algorithms		
R	R core team	https://www.r-project.org/
Bioconductor	Bioconductor	https://www.bioconductor.org/
TCGAbiolinks	Bioconductor	https://github.com/BioinformaticsFMRP/TCGAbiolinks
BMIQ	R program	https://sourceforge.net/projects/bmiq/
Limma	Bioconductor	https://bioconductor.org/packages/release/bioc/html/limma.html
ROCR	R package	https://rocr.bioinf.mpi-sb.mpg.de/
Gtrelis	Bioconductor	https://github.com/jokergoo/gtrelis
DMRcate	Bioconductor	https://www.bioconductor.org/packages/release/bioc/html/DMRcate.html
DESeq2	Bioconductor	https://www.bioconductor.org/packages/release/bioc/html/DESeq2.html
clusterProfiler	Bioconductor	https://github.com/GuangchuangYu/clusterProfiler
missMethyl	Bioconductor	https://bioconductor.org/packages/release/bioc/html/missMethyl.html
Survival	R package	https://cran.r-project.org/web/packages/survival/index.html
survMiner	R package	https://cran.r-project.org/web/packages/survminer/index.html
Impute	R package	https://bioconductor.org/packages/release/bioc/html/impute.html
Gviz	Bioconductor	https://bioconductor.org/packages/release/bioc/html/Gviz.html
Data		
GDC	NCI	https://portal.gdc.cancer.gov/
cBioPortal	Memorial Sloan	http://www.cbioportal.org/
FireHose	Broad Institute	https://gdac.broadinstitute.org/
Illumina 450k Methylation Annotation	Van Andel Institute	http://zwdzwd.github.io/InfiniumAnnotation

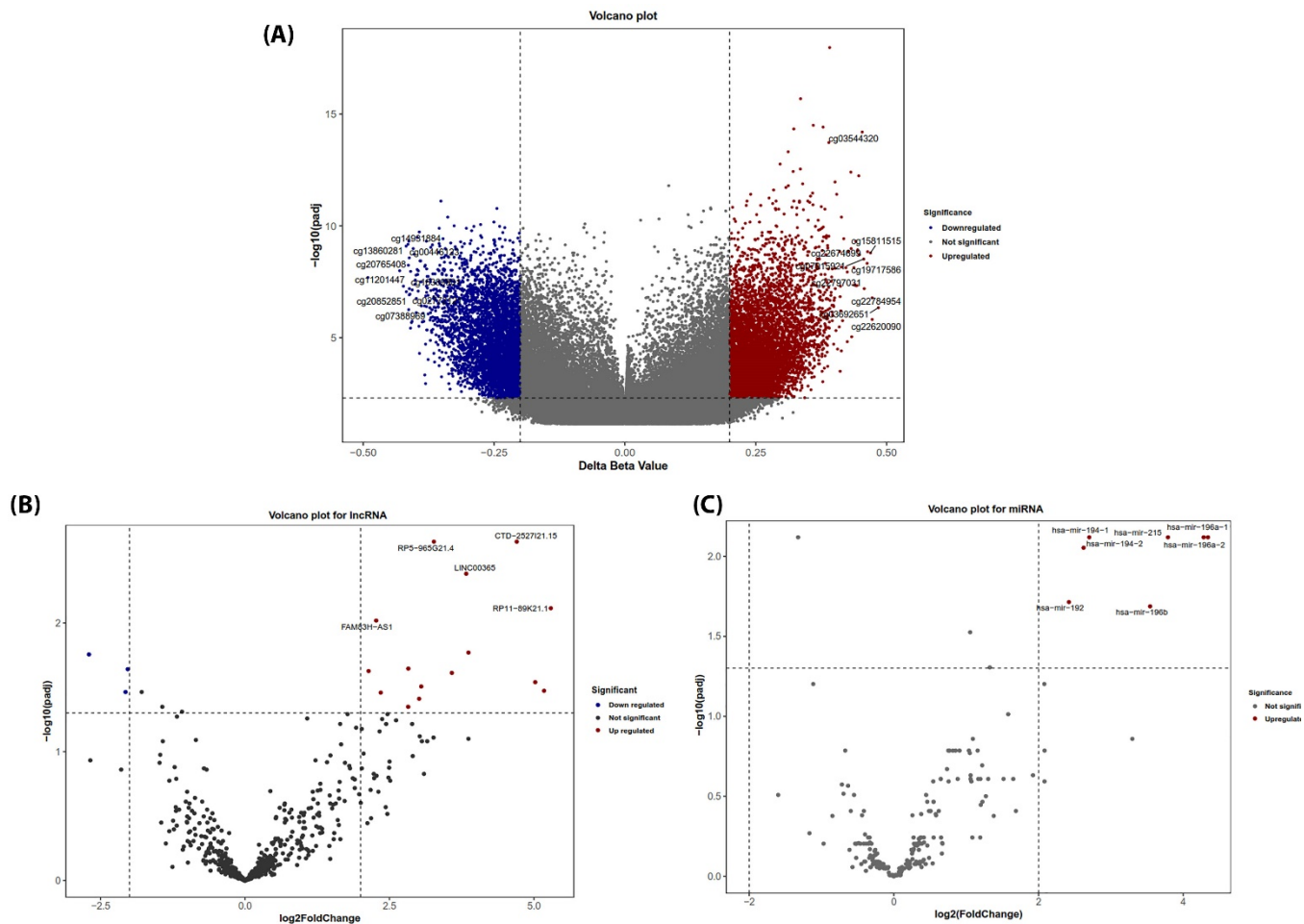
2.2 Supplementary Figures



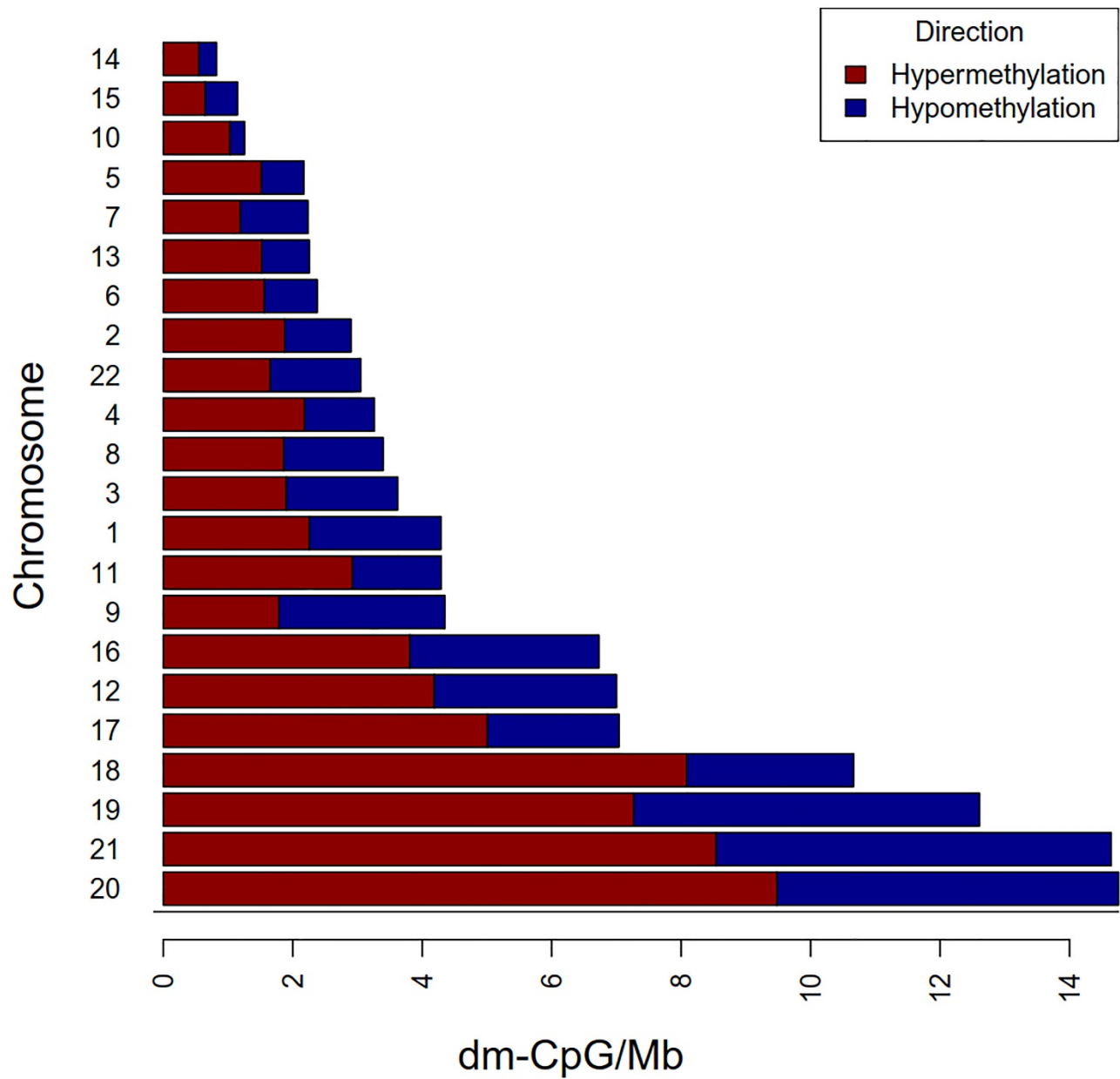
Supplementary Figure 1. Flowchart for the proposed methodology for TCGA pancreatic ductal adenocarcinoma data analysis.



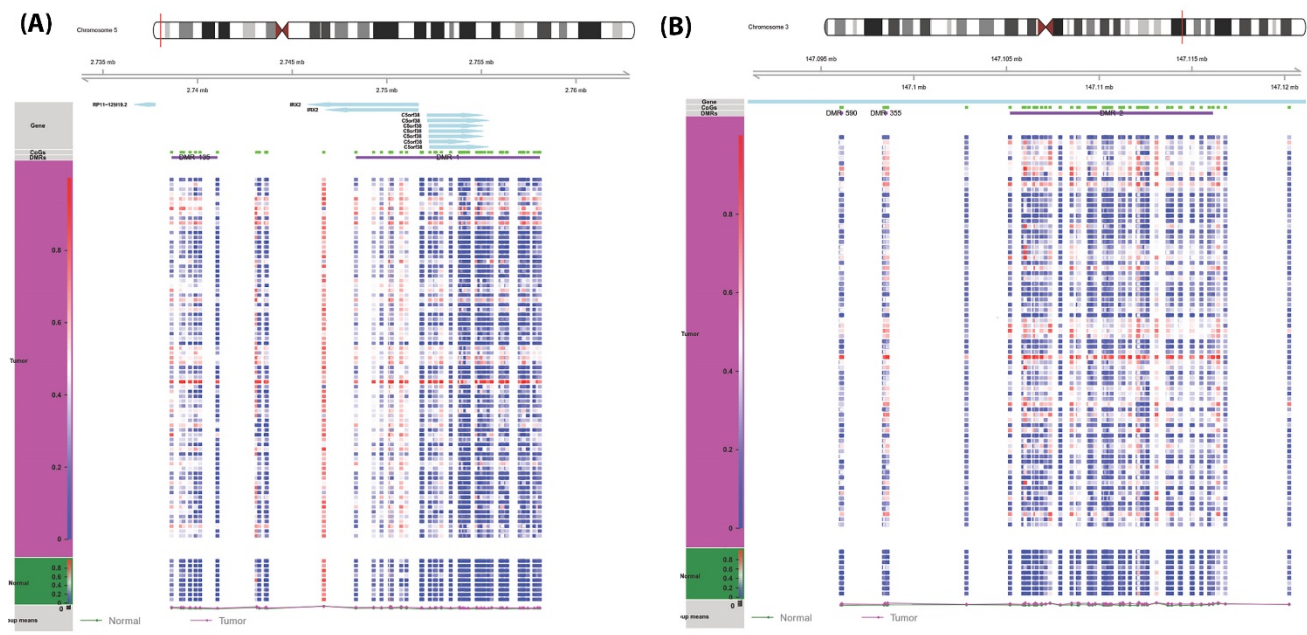
Supplementary Figure 2. DNA methylation distribution of tumor and normal samples in all genomic regions. Boxplot for- (A) TSS200 (B) TSS1500 (C) 5'UTR (D) 1ST Exon (E) Gene body (F) 3'UTR (G) CpG island (H) n-shore (I) s-shore (J) n-shelf (K) s-shelf



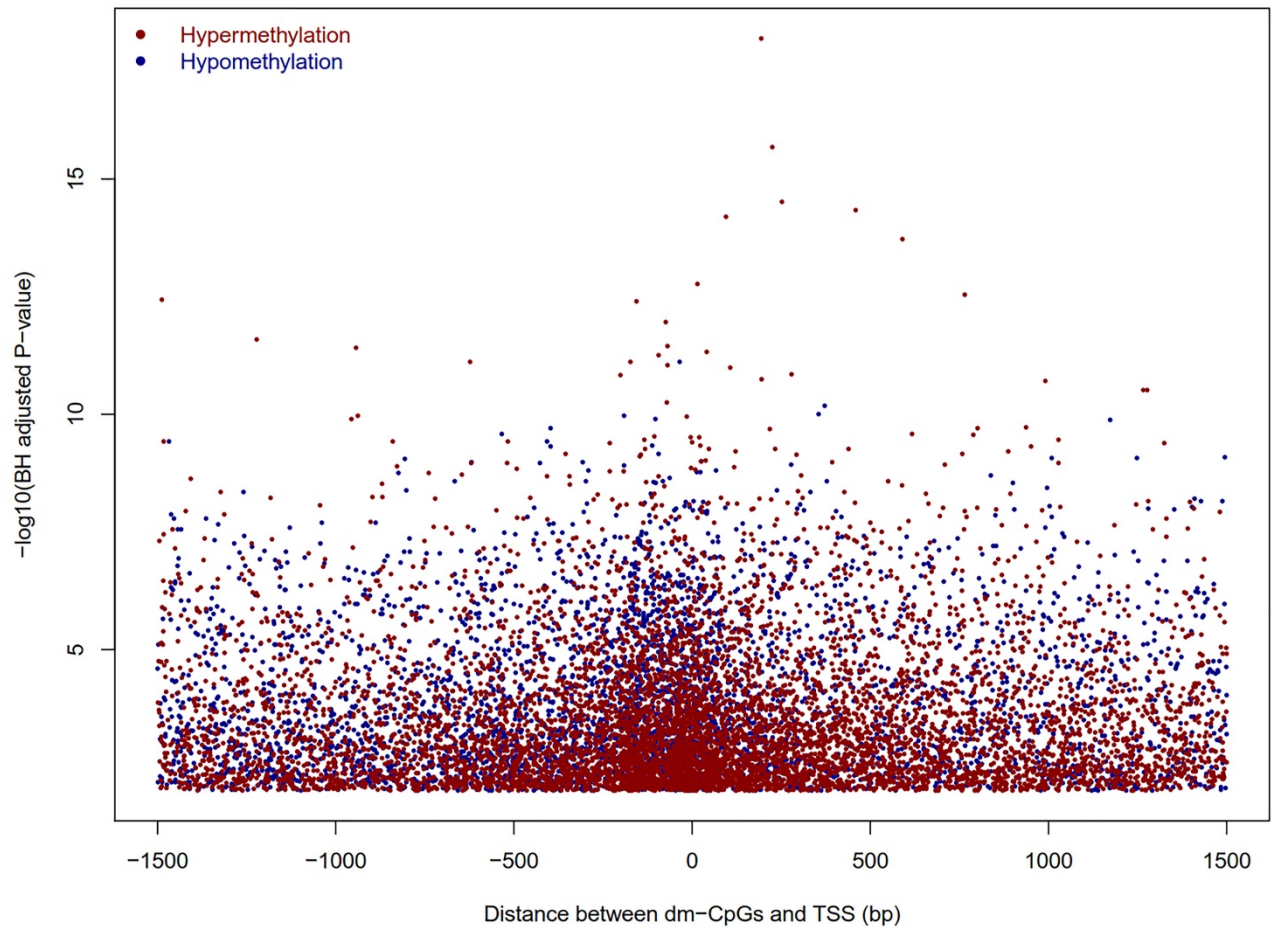
Supplementary Figure 3. Volcano plot for the differentially methylated CpGs, and differentially expressed lncRNA and miRNA. Genes/CpG which are in red and blue colors are highly upregulated and downregulated, respectively in PDAC. Vertical and horizontal dot line represents a cutoff point for log-fold-change p-value respectively



Supplementary Figure 4. Stacked barplot for differential hyper and hypomethylation frequencies for each chromosome. Chromosomes are sorted based on total differential methylation in per megabase pair length of the chromosomes.



Supplementary Figure 5. *DMRcate* differentially methylated regions (DMRs). (A) DMR1 (B) DMR2



Supplementary Figure 6. CpG sites whose DNA methylation levels were significantly correlated with gene expression with Bonferroni corrected P-value < 0.005