# Brief outline

- Using R packages TCGAbiolinks to download methylation data for pancreatic cancers (code: PAAD).

- Filter to focus on autosomal Chr, remove SNPs and rare alleles

- Use the normal tissue (NT) vs Tumor Pancreas (TP) annotations from the associated clinical data annotations for differential methylation analysis. Use head of pancreas tissue to narrow analysis down as it has the most paired NT ant TP tissues.

- Undertake differential methylation analysis using linear model and bayes statistics to determine statistically significant differentially methylated regions.

- Plot top 10 differentially methylated CG regions (Fig1)

- Use Ddmrcate package to annotate differentially methylated sites.

-  Create chromosome specific visualization map showing differentially methylated CG sites and regions mapped onto chromosome (Fig2)

- Save differentially methylated regions into csv.
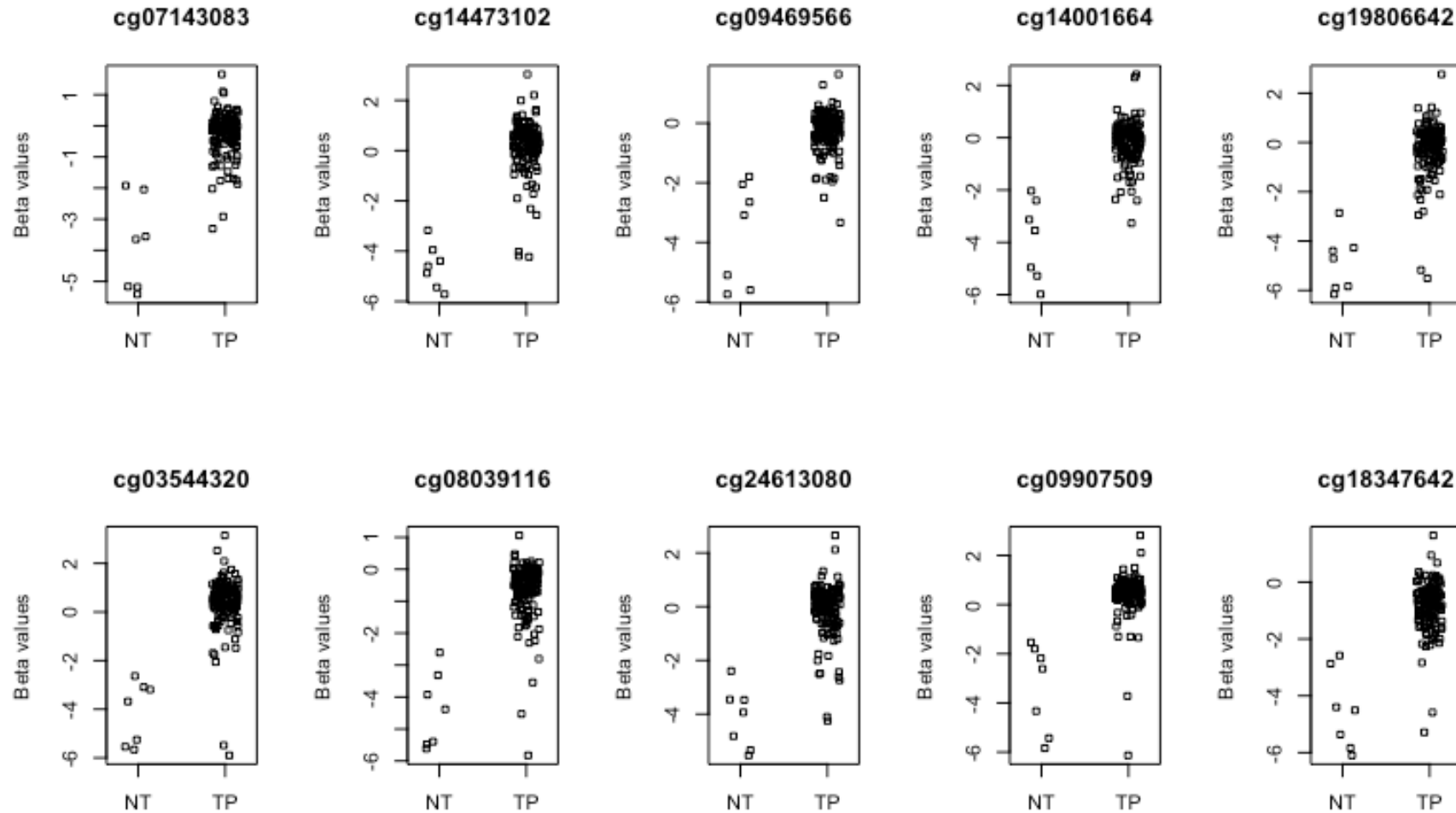
# Fig 1: Top 10 differentially methylated CG sites

# Fig 2: Mapping the CG sites and DMR onto chromosomes 7 for pancreatic cancer.