CNTNAP2 hypermethylation in colorectal adenocarcinoma

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EpiGenPlot
Compare methylation of healthy and tumor tissues
www.epigenplot.com

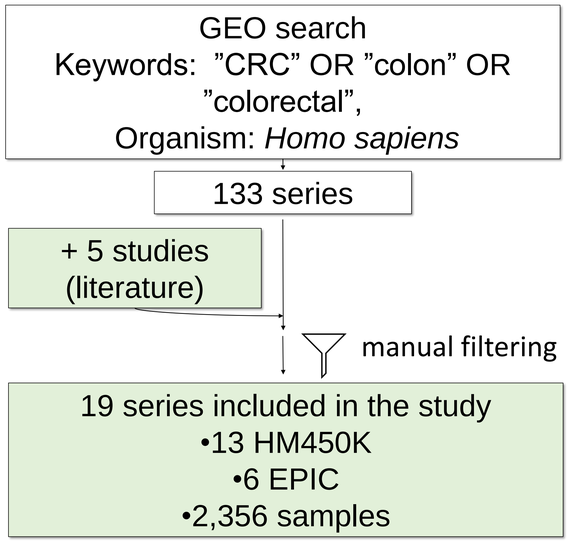
Background.

- methylation changes represent the most researched layer of epigenetic gene regulation
- genome-wide methylation analysis of large cohorts facilitates the identification of novel biomarkers and a better understanding of cancer biology

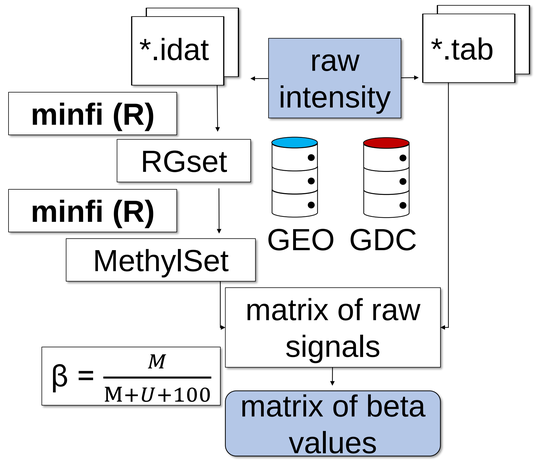
Aims.

to evaluate the methylation changes of *CNTNAP2* through tumor progression in colorectal cancer using methylation microarray data.

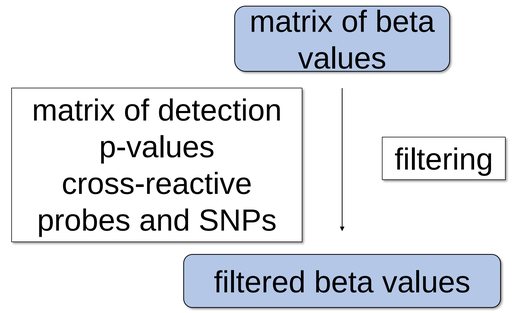
I. Methods: Data collection



Methods II: Processing raw Illumina array data



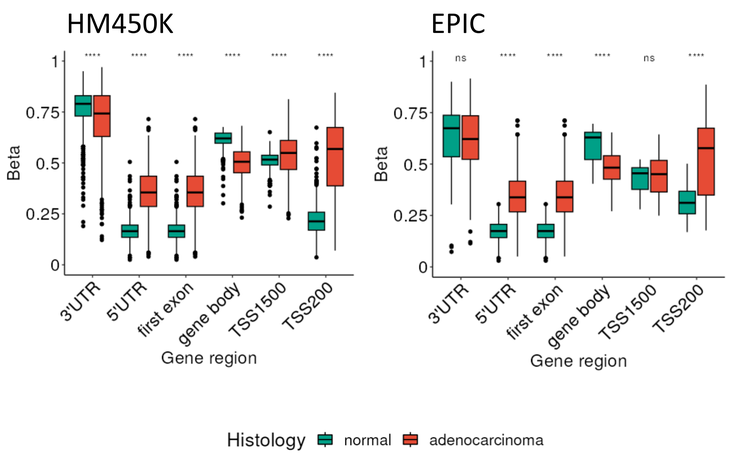
Methods III: Quality control and integration



Methods IV. EpigenPlot web platform for automated analysis

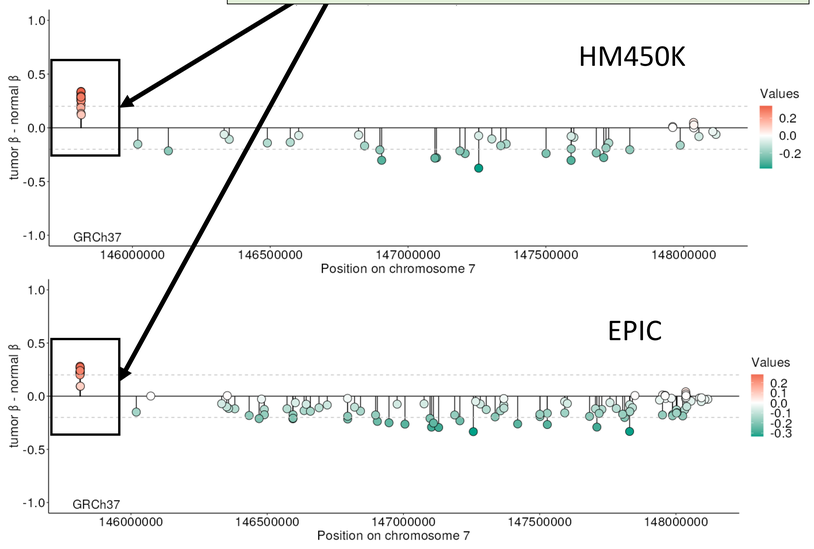
Results I: Methylation by regions

- The **TSS200 region** had the most prominent **hypermethylation** (HM450K Δβ =0.29, AUC 0.85; EPIC Δβ = 0.2, AUC 0.78, p<0.0001)



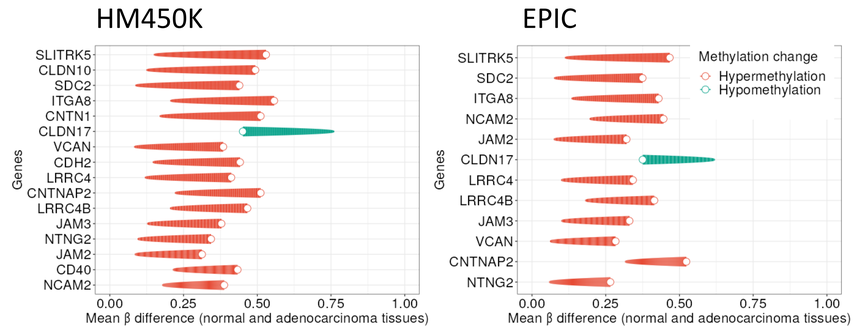
Results II: Methylation by nucleotides

- 59 of the HM450K and 119 of the EPIC array probes were assigned to the *CNTNAP2* gene
- probes hypermethylated in adenocarcinoma tissues belonged to the **CpG island chr7:145813030-145814084**



Results III: Methylation by KEGG pathway

- 14 genes associated to cell adhesion were similarly hypermethylated in the TSS200 region (Δβ >= 0.2)
- hypermethylation of *LRRC4, SDC2* and *CNTNAP2* paralogue *CNTNAP5*



Scan the code to save the web address

Conclusions.

Hypermethylation of the *CNTNAP2* gene previously associated with glioma and myeloma, could be a potential prognostic biomarker candidate in colorectal adenocarcinoma.