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ATAC-seq allows for the investigation of chromatin accessibility, a feature which can have important

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implications for gene regulation. Here the authors present ATAC-array to assess accessibility ...

Pancreatic cancer prognosis is predicted by an ATAC-array ...

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H3K9me3 is an epigenetic modification to the DNA packaging protein Histone H3. It is a mark that indicates the tri-methylation at the 9th lysine residue of the histone H3 protein and is

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often associated with
heterochromatin

H3K9me3 - Wikipedia

Epigenomix: A Bioconductor
(R) package that lets you
integrate your RNA-seq or
microarray data with your

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ChIP-seq data. It lets you preprocess and create differential gene lists for both data sets. HMCAN: a tool to call peaks in ChIP-seq/ATAC-seq data generated from cancer cells. It corrects for GC-content bias

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and DNA copy number
aberrations.

Epigenetic Tools and Databases for Bioinformatic Analyses

H3K36me3 is an epigenetic
modification to the DNA

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packaging protein Histone H3. It is a mark that indicates the trimethylation at the 36th lysine residue of the histone H3 protein and often associated with gene bodies. There are diverse

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modifications at H3K36 and have many important biological processes. H3K36 has different acetylation and methylation states with no similarity to each other.

H3K36me3 - Wikipedia

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