EPIGENOMICS: DECIPHERING THE OTHER GENETIC CODE

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Genomics
EPIGENOME ANALYSIS

PROJECTS

The Roadmap Epigenomic Project

ENCODE Project

Genome-scale DNA methylation maps of pluripotent and differentiated cells. Nature (2008);454:766-771
LINEAGE-SPECIFIC GENE EXPRESSION

- PROMOTERS
- INSULATORS
- ENHANCERS
- Cys-REC ELEMENTS

- H3K4me1
- H3K4me3
LINEAGE-SPECIFIC GENE EXPRESSION

Histone modifications at human enhancers reflect global cell type-specific patterns of lineage-specific expression. 

Figure a: Distribution of enhancers to TSS (kb) with number of enhancers and random distribution.

Figure b: Venn diagram showing the overlap of HeLa and K562 enhancers.

Figure c: Venn diagram showing the overlap of HeLa and K562 expressed genes.

Figure d: Enrichment ratio for HeLa and K562 enhancers.

Figure e: Differential gene expression, HeLa versus K562 (log).

Figure f: Heatmap representation of H3K4me1 and H3K4me3 modifications at human enhancers.
DISEASE ASSOCIATION
CONCLUSIONS

DNA methylation and histone modification are essential for normal development and has been implicated in many pathologies.

Enhancer associated marks have the greatest ability to distinguish tissue-specific enrichments for regulatory regions.

Epigenomic modifications may have an important roll in diseases development.
REFERENCES


THANK YOU