TITLE

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Abstract

1 Words

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1 Introduction

1.1 FOXA1 Expression and ER+ Breast Cancer

1.2 tRNAs and Gene Expression

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2 Materials & Methods

2.1 MCF7L ChIP-seq Data from NCBI

ChIP-seq was performed on MCF7L cells expressing Dox-inducible FOXA1[1]. Datasets were deposited into the National Centre for Biotechnology Information (NCBI) Sequence Read Archive (SRA) under accession no. PRJNA512997[2] (Table 1). SRAs were downloaded by Galaxy (v23.0.rc1)[3] and converted to FastQ files and then into BAM files using "Genetic Manipulation Tools".

Table 1. Publicly available ChIP-seq SRA files aquired from the NCBI SRA database (accession no. PRJNA512997).

Experiment	SRA	Factor	Tissue	Assembly
PRJNA512997	SRR8393424	FOXA1	MCF-7LP	GRCh37 Hg19
	SRR8393425			
	SRR8393426			
	SRR8393427	H3K27ac		
	SRR8393428			
	SRR8393431	None (input)		
	SRR8393432			

2.2 EaSeq for the Quantification of FOXA1 and H3K27ac at tRNA genes

EaSeq (v1.111)[4].

2.3 Motif Analysis

2.4 Statistics

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3 Results

3.1 Localisation of FOXA1 at tRNA genes in MCF-7 cells

3.2 Co-localisation of FOXA1 with enhancer marks at tRNA genes

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4 Discussion

112 Words

References

1 Fu X, Pereira R, De Angelis C, Veeraraghavan J, Nanda S, Qin L *et al.* FOXA1 upregulation promotes enhancer and transcriptional reprogramming in endocrine-resistant breast cancer. *Proceedings of the National Academy of Sciences* 2019; **116**: 26823–26834.

2 Leinonen R, Sugawara H, Shumway M. The Sequence Read Archive. *Nucleic Acids Research* 2010; **39**: D19–D21.

3 Afgan E, Nekrutenko A, Grüning BA, Blankenberg D, Goecks J, Schatz MC *et al.* The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2022 update. *Nucleic Acids Research* 2022; **50**: W345–W351.

4 Lerdrup M, Johansen JV, Agrawal-Singh S, Hansen K. An interactive environment for agile analysis and visualization of ChIP-sequencing data. *Nature Structural & Molecular Biology* 2016; **23**: 349–357.