

TITLE

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TITLE

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Abstract

1 Words

Introduction

FOXA1 Expression and ER α Breast Cancer

tRNAs and Gene Expression

Materials & Methods

Acquisition of Public ChIP-seq Datasets

ChIP-seq was performed on genetically modified MCF7L cells (*insertion, using a lentiviral cDNA delivery system to express Dox-inducible FOXA1*)^[1]. Datasets were deposited into the National Centre for Biotechnology Information (NCBI) Sequence Read Archive (SRA)^[2] under accession no. PRJNA512997 (Table 1). Using “Genetic Manipulation Tools” within the Galaxy^[3] environment (v 23.0.rc1), SRAs were converted to FastQ files. FastQ files were then aligned to the human genome assembly GRCh37 (hg19) using Bowtie2 (v 2.5.0)^[4] to output BAM files.

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

Experiment	SRA	Factor	Tissue	Assembly
PRJNA512997	SRR8393424 SRR8393425	FOXA1	MCF-7LP	GRCh37 (Hg19)

Experiment	SRA	Factor	Tissue	Assembly
	SRR8393426			
	SRR8393427	H3K27ac		
	SRR8393428			
	SRR8393431	None (input)		
	SRR8393432			

EaSeq for Chip-seq Peak Quantification

BAM files were uploaded into EaSeq (v1.111) as “Datasets” using the standard settings for Chip-seq data. GRCh37 (hg19) tRNA sequences (n = 606) were downloaded as a “Geneset” from the UCSC Table Browser^[5], (available at <https://genome.ucsc.edu>). High-confidence tRNAs (n = 416) identified in the GtRNAdb^[6] were extracted as a “Regionset”.

Signal peak intensities surrounding tRNAs were quantified using the EaSeq “quantify” tool. Here the default settings “Normalize to reads per million” and “Normalize counts to DNA-fragments” were left checked. The default setting “Normalise to a signal of 1000 bp” was unchecked. The window size was offset ± 500 bp from the start of each tRNA gene. Outputs are referred to as “Q-values”.

To quantify upstream and downstream signals, the “quantify” tool was used with adjusted window sizes. The upstream region was defined as 500 bp preceding and the first nucleotide of tRNA loci. Thus, the start position was offset to 0 bp, and the end position was offset to -500 bp. The downstream region constitutes the 500 bp region beginning with the first nucleotide of tRNA gene body. The start position was offset to 1 bp, and the end position was offset to 500 bp.

Following quantification, tRNA binding events were arranged in ascending order -DOX Q-value and visualised as heatmaps. Data was also visualised with “average”, and “overlay” EaSeq tools.

EaSeq^[7] is available at <http://easeq.net>.

Motif Analysis

Multiple EM for Motif Elicitation CHIP (MEME) Suite

Statistics

Statistical tests and graphs were generated with R^[8] (v 4.2.3), R Studio^[9] (v 2023.03.0.386) and the tidyverse^[10] package.

Results

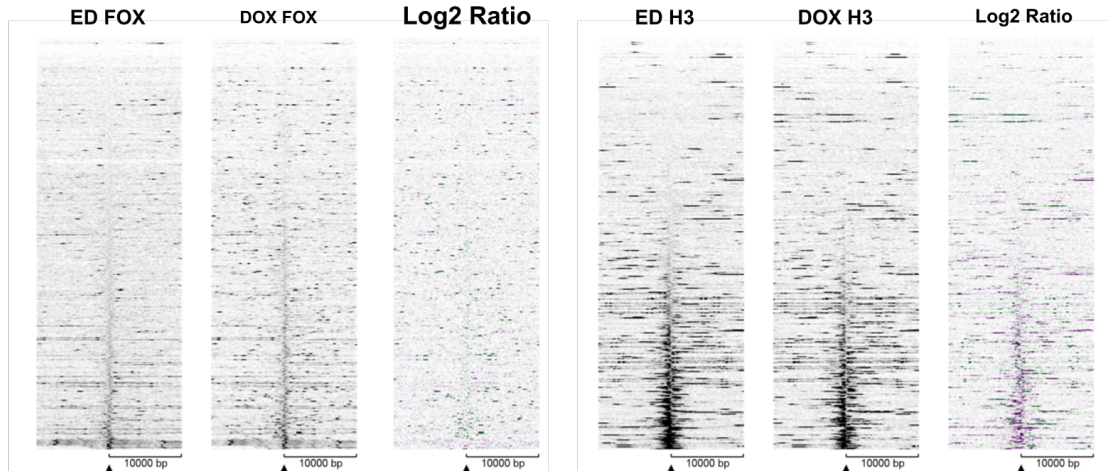
Binding of FOXA1 and H3k27ac to tRNA Genes

To investigate the impact of FOXA1 on tRNA enhancers in ER+ MCF-7 cells, public ChIP-Seq datasets from Fu et al. (2019)^[1] were interrogated. In this paper, a doxycycline (Dox) inducible OE system was used to achieve FOXA1 OE akin to tamoxifen-resistant (TamR) MCF-7 cells^[1]. Quantification of 416 high-confidence tRNAs revealed that FOXA1 interacts with 100% of tRNAs and H3k27ac with 99.5%. of tRNA genes, relative to ± 500 bp flanking regions (Figure 1A). Whereas input reads generated minimal peak enrichment (Supplementary Figure X). The number of genes bound was unchanged by OE of FOXA1.

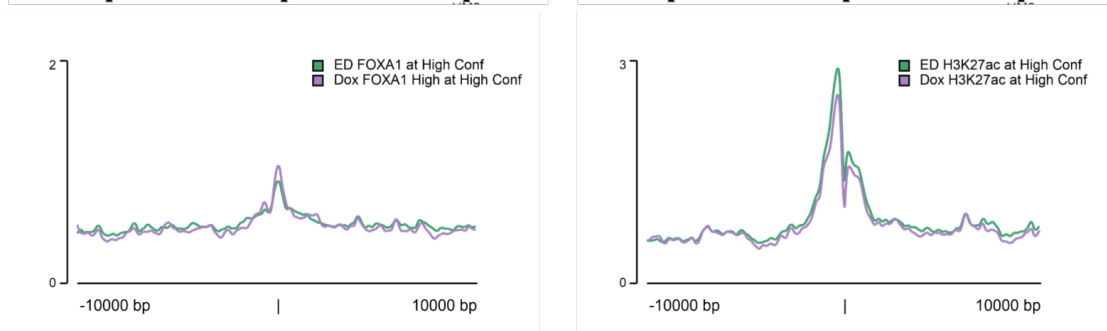
Mapped reads of FOXA1 and H3K27ac binding were visualised as heatmaps and ordered by increasing -DOX Q-value. This revealed a concentration of FOXA1 and H3k27ac at approximately half of tRNAs, relative to ± 10 kb flanking regions. Upon FOXA1 OE, FOXA1 binding increased at a small proportion of tRNAs genes and H3K27ac binding decreases at approximately half of tRNA genes (Figure 1A). This was confirmed by average signal intensity plots of FOXA1 and H3K27ac binding (Figure 1B).

Upon FOXA1 OE, the mean Q-values for FOXA1 binding significantly decreased 0.16-fold and insignificantly decrease by 0.62 for H3K27ac (Mann-Whitney: $p < 0.005$) (Supplementary Figures X). However, there is a significant difference in binding between -DOX and +DOX tRNAs for both FOXA1 and H3K27ac (Wilcoxon Signed Rank Test : $p < 0.0001$) (Figure 1C). Changes in FOXA1 and H3K27ac binding has been visualised as a parameter heatmap in Figure 1D. Together, these results suggest that FOXA1 overexpression alters the binding landscape of FOXA1 and H3K27ac at tRNAs.

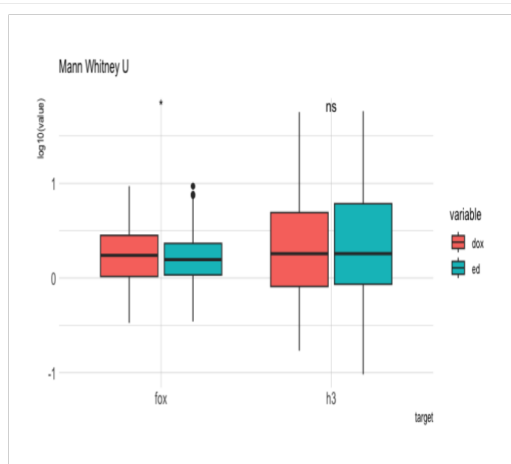
A



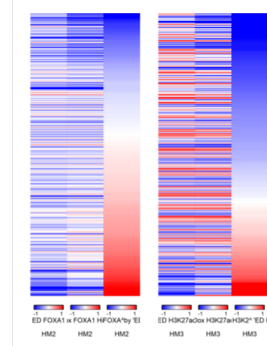
B



C



D Wilcoxon signed rank
Q Values Heatmap



D

Fill Tracks?

Figure 1. (B) Ratiometric heatmaps of the log2 ratio between the binding of FOXA1 or H3k27ac with endogenous FOXA1 expression vs. the binding of FOXA1 or H3k27ac with FOXA1 OE.

Boxplots

Why?

FOX OE alters binding at tRNAs (fig1).

What?

Using Q-values, tRNAs that are differently enriched upon FOXA1 OE were categorised as 'GAIN' or 'LOSS'. This discovered substantially more tRNAs with increased (GAIN) than decreased (LOSS) FOXA1 (96 vs. 23) (Figure 2A). However, for H3K27ac, the number of tRNAs with an increase (GAIN) was comparable to those with a decrease (LOSS) (54 vs. 52)(Figure 2B).

Of the tRNAs which gained FOXA1, 14% also gained H3K27ac. and 13.5% lost H3K27ac. These subsets represent approximately 25% of all tRNAs with GAIN H3K27ac or LOSS H3K27ac, respectively (Figure 2C).

Examples of these tRNAs are shown in Figure 2D.

Suggests

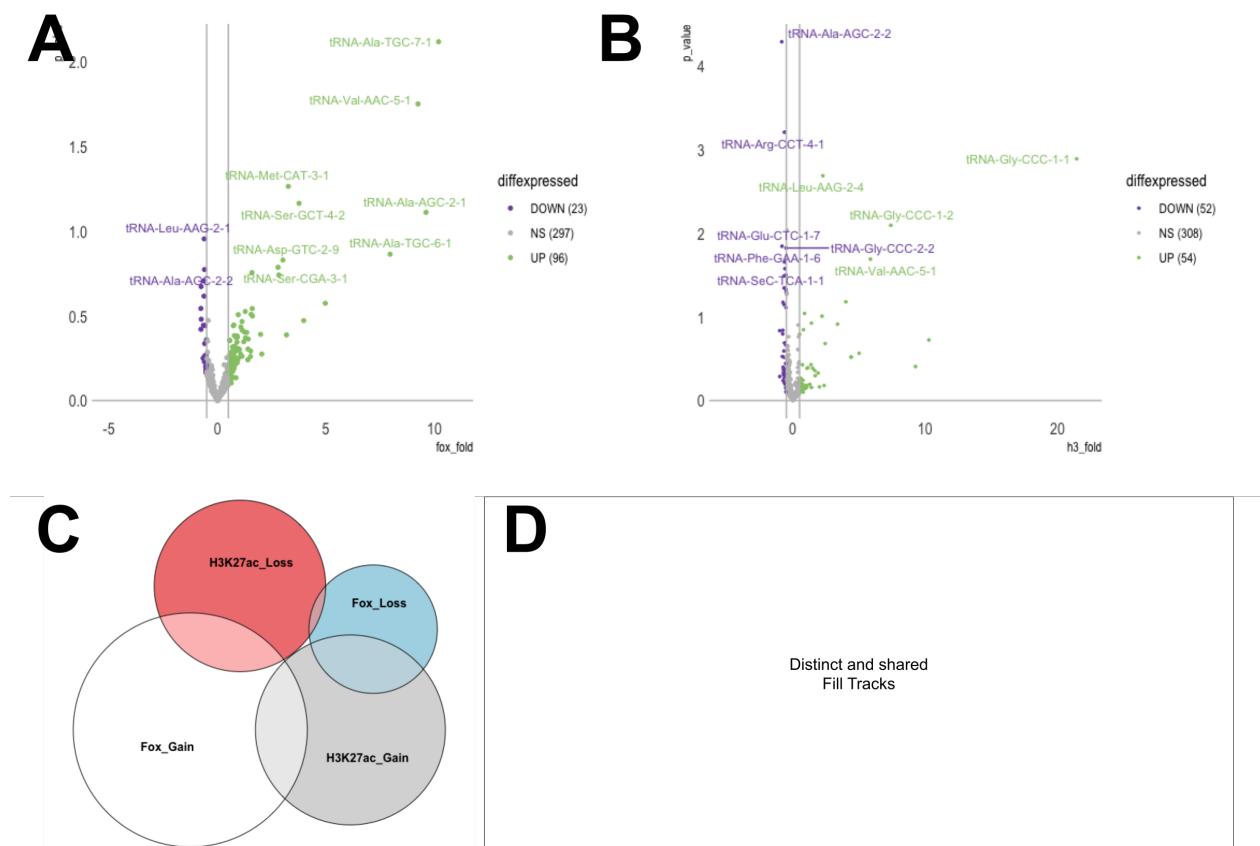


Figure 2. (B) Ratiometric heatmaps of the log2 ratio between the binding of FOXA1 or H3k27ac with endogenous FOXA1 expression vs. the binding of FOXA1 or H3k27ac with FOXA1 OE.

Figure 3

Why?

What?

Suggests?

A

Active tRNA genes
-dox +dox

B

Heatmap
Fox
binding in
in tRNAs
that
become
active

C

Venn diagram
Gain h3
Gain fox
Lose h3
Lose fox

Figure 3. .

Figure 4

Why?

What?

Suggests?

Venn of Motif
inputs

De novo
Identified
Motifs

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

Why?

What?

Suggests?

Table 2. .

Group	Function
ALOXE	Insulator Function ^[11,12]
Ebersole	Insulator Function ^[12,13]
HES7	
Per1	
TMEM107	Insulator Function ^[11,12]
Arg-CCG	Implicated in Cancer Progression ^[14]
Glu-TTC	Implicated in Cancer Progression ^[14]
iMET	Proliferation of Breast Cancer
Met	iMet Control
SeC	Involved in REDOX ^[15]

Discussion

- not compared mcf-7 to treatment responsive cells

Future

- FOXA1 alone not efficient to increase activity
 - p300
- FOXA1 moves nucleosomes to make other TF accessible
- Loses fox = weak binding?
- Dynamic and stable marks
- perturbations

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