Intro :

Results

\*elincRNAs enriched at TAD boundaries

\*[more to come]

methods :

\*TAD boundaries definition

\*enrichment test

\*conservation

\*tissue specificity

\*expression levels

Tools :

- GAT 1.2

- BEDtools 2.26

- R

Introduction :

Genomic DNA is folded onto itself, forming compact structures that affect gene expression. On a large scale, regions presenting a high degree of compaction are classified as heterochromatin while uncondensed regions are classified as euchromatin. These are respectively associated with lower and higher expression levels. On a smaller scale, areas where DNA-DNA interactions are especially frequent are called topologically associated domains (TADs). Those domains are conserved across cell lines and contain smaller loop structures that allow different genetic elements such as enhancers and promoters to contact each other. The boundaries of TADs act as insulators, preventing DNA-DNA interactions across them. They are also gene-dense and enriched in highly transcribed genes (Ong et Corces, 2014).

Long intergenic non-coding RNAs (lincRNAs) might play a role in the control of nuclear architecture as they have been shown to mediate promoter-enhancer interactions and are enriched in TAD-boundaries (Chen et al 2016). LincRNAs promoters are also enriched in enhancer marks (Popadin et al, 2013), which suggest a role in transcriptional regulation. LincRNAs whose promoter region is associated with enhancers (elincRNAs) are good candidates for studying their involvement in the regulation DNA-DNA contacts.

[...]

In this work, we study the role of elincRNAs in the organization of TADs using bioinformatics tools and publicly available data from the ENCODE project. ~~The study of elincRNAs is of particular interest as they have been linked to various disease phenotypes (SOURCE)~~