Report 1D: Expression level, subcellular localization and tissue-specificity of lincRNAs and pegenes categorized by overlaps with promoters and enhancers.

Cyril Matthey-Doret November 18, 2016

Introduction

Here, lincRNAs and protein-coding genes were split into categories for each combination of overlap/absence of overlap with promoters and enhancers.

Data

lincRNAs

promoter	enhancer	number of genes
yes	yes	38
yes	no	480
no	yes	236
no	no	1756
both	yes	274
both	no	2236

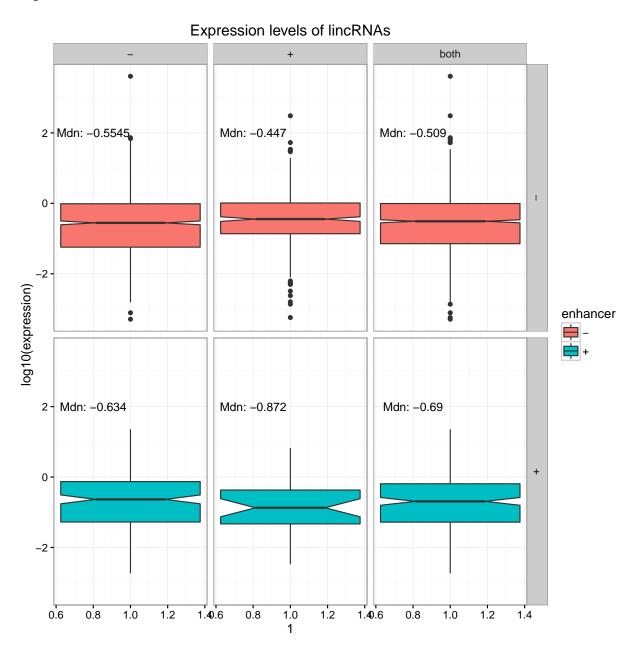
protein-coding genes

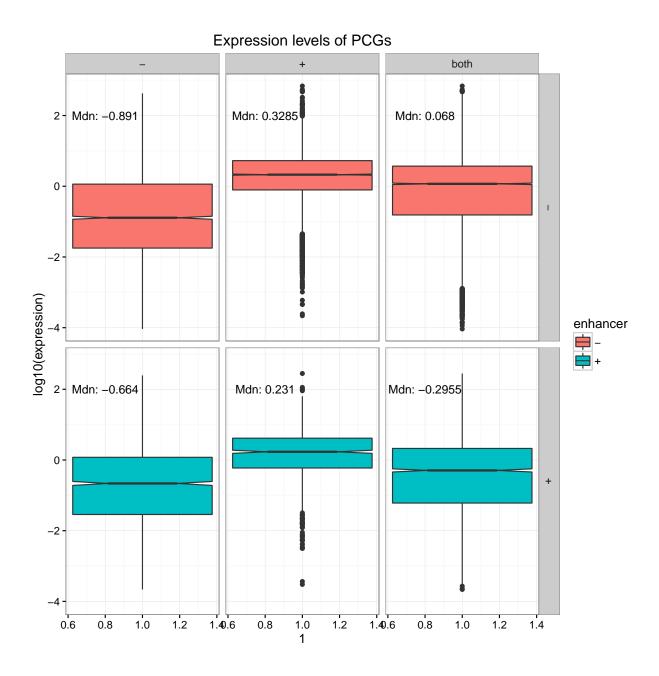
promoter	enhancer	number of genes
yes	yes	914
yes	no	7074
no	yes	2105
no	no	4753
both	yes	3019
both	no	11827

Results

All p-values displayed on plots were obtained by performing Mann-Whitney tests.

Expression levels

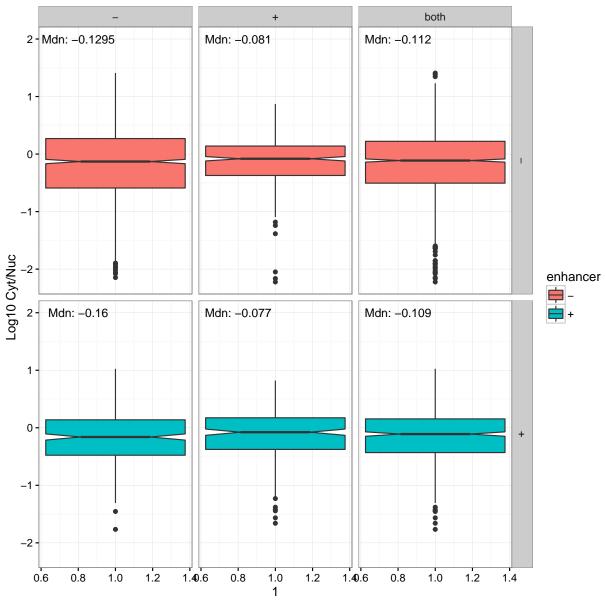




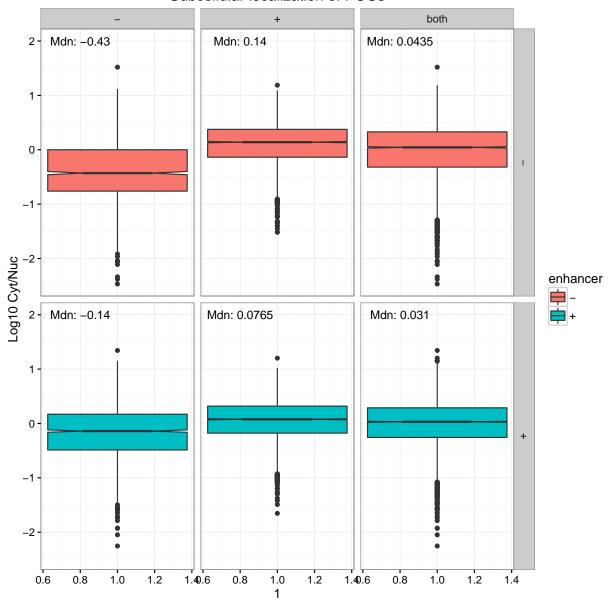
Subcellular localization

The ratios depicted below represent the abundance of RNA in the cytoplasm relative to the nucleus. There is no significant difference between the localization of TAD-bound and non-TAD-bound lincRNAs, while the TAD-bound protein-coding genes are more abundant in the cytoplasm than in the nucleus.

Subcellular localization of lincRNAs



Subcellular localization of PCGs



Tissue specificity

 τ was calculated from a set of tissue-wise expression level for all transcripts. Again, there seem to be no difference in tissue specificity between TAD-bound and nonTAD-bound lincRNAs or protein coding genes. Overall the lincRNAs are more tissue specific than protein coding genes.

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