

Investigation of TGF β 1-induced Long Non-Coding RNAs in Endothelial Cells

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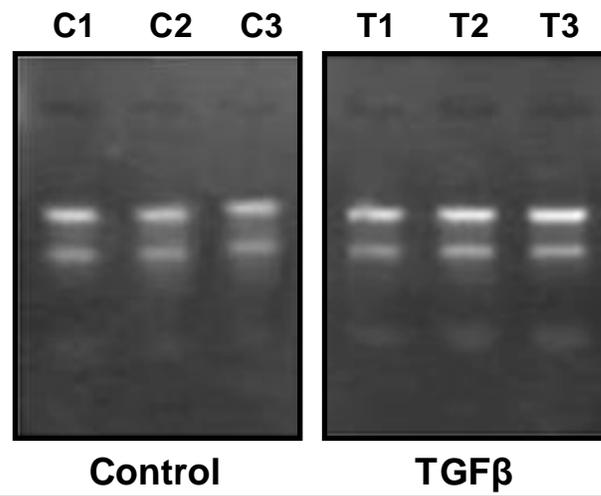
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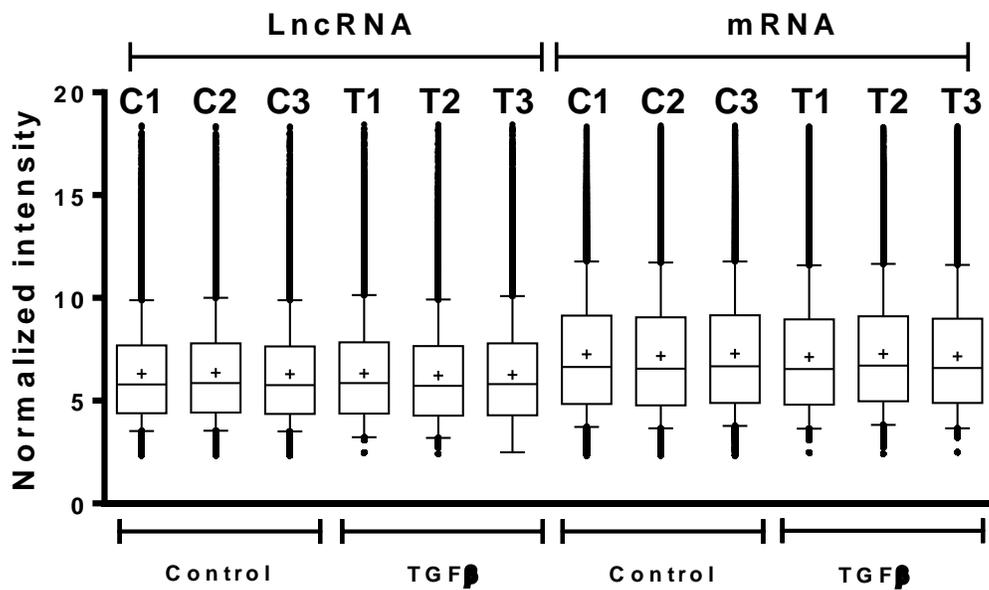
Supplementary Figure 1

A



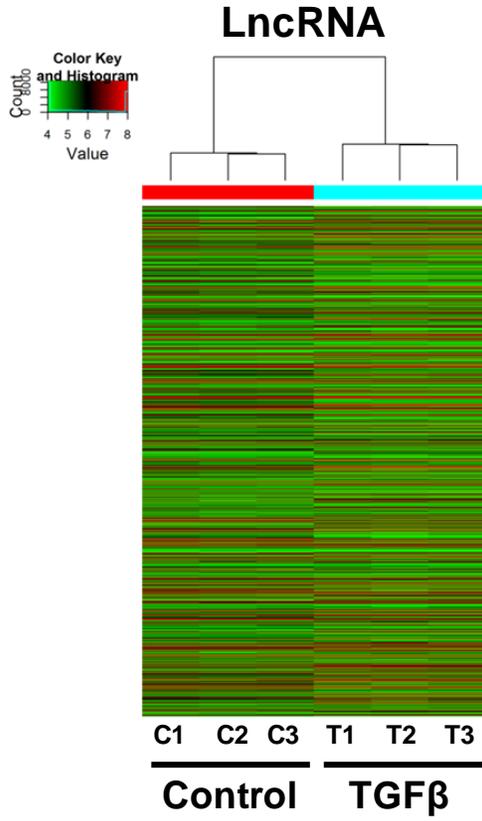
Sample	OD260/280 Ratio	OD60/230 Ratio	Concentration (ng/μl)	Volume (μl)	Quantity (ng)
C1	2.03	1.99	177.66	30	5329.8
C2	2.02	2.03	152.35	30	4570.5
C3	2.06	2.05	185.49	30	5564.7
T1	1.98	2.00	242.89	30	7286.7
T2	2.04	2.09	209.66	30	6289.8
T3	2.03	2.07	223.61	30	6708.3

B

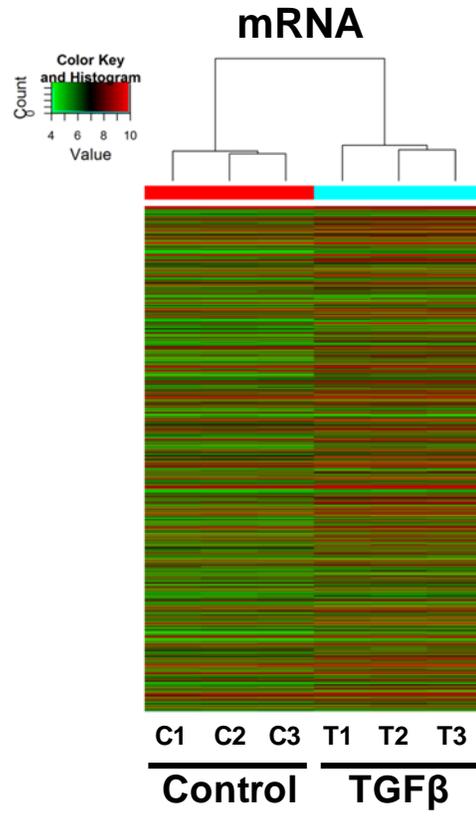


Supplementary Figure 2

A



B



Supplementary Figure 1. Quality assessment of RNAs, lncRNAs and mRNAs Data. A.

Image of denaturing agarose gel (1%) used to assess RNA integrity and genomic DNA contamination. The 28s and 18s rRNA bands were clear and intact. The larger rRNA (28s) bands were more intense in comparison to the corresponding lower rRNA (18s) bands. The table shows the absorbance ratio for wavelengths 260nm/280nm and 260nm/230nm, concentration and the quantity of RNA used for array. **B.** Box-and-Whisker plots (10th, 90th percentile) showing normalized intensity for the 6 study samples to quickly visualize the distribution of our dataset. Mean intensity is denoted with a “+” sign. C1, C2 and C3 represent the control group, and T1, T2 and T3 represent the TGFβ1 (10 ng/mL)-treated group.

Supplementary Figure 2. Heat map and hierarchical clustering of differences in lncRNA and mRNA expression from HUVECs exposed to TGFβ1 (10 ng/mL) vs. Control. A & B.

The dendrogram shows the relationships among the expression levels of samples. Hierarchical clustering that was performed based on ‘differentially expressed lncRNAs and mRNAs’, shows a distinguishable lncRNA and mRNA expression profiling among samples.