

# Total Functional Score of Enhancer Elements Identifies Lineage-Specific Enhancers that Drive Differentiation of Pancreatic Cells

This manuscript ([permalink](#)) was automatically generated from [vsmalladi/tfsee-manuscript@334f52b](#) on April 28, 2018.

## Authors

---

- **Venkat S. Malladi**

 0000-0002-0144-0564 ·  [vsmalladi](#) ·  [katatonikkat](#)

The Laboratory of Signaling and Gene Regulation, Cecil H. and Ida Green Center for Reproductive Biology Sciences and Division of Basic Reproductive Biology Research, Department of Obstetrics and Gynecology, University of Texas Southwestern Medical Center; Department of Bioinformatics, University of Texas Southwestern Medical Center"

- **Anusha Nagari**

The Laboratory of Signaling and Gene Regulation, Cecil H. and Ida Green Center for Reproductive Biology Sciences and Division of Basic Reproductive Biology Research, Department of Obstetrics and Gynecology, University of Texas Southwestern Medical Center

- **Hector L. Franco**

The Laboratory of Signaling and Gene Regulation, Cecil H. and Ida Green Center for Reproductive Biology Sciences and Division of Basic Reproductive Biology Research, Department of Obstetrics and Gynecology, University of Texas Southwestern Medical Center; Department of Genetics and Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill"

- **W. Lee Kraus**

The Laboratory of Signaling and Gene Regulation, Cecil H. and Ida Green Center for Reproductive Biology Sciences and Division of Basic Reproductive Biology Research, Department of Obstetrics and Gynecology, University of Texas Southwestern Medical Center

# Abstract

---

The ability to integrate different genome data sets to systematically identify active enhancers together with their cognate transcription factors (TF) remains a difficult and somewhat arbitrary process. We have developed a computational framework that systematically identifies active enhancers in any cell or tissue type together with the TFs bound at the enhancers by integrating multiple genomic assays that probe the transcriptional (GRO-seq and RNA-seq) and epigenetic (ChIP-seq) states of the cells. Our method, called Total Functional Score of Enhancer Elements (TFSEE), integrates the magnitude of enhancer transcription as a measure of enhancer activity, enrichment of histone modifications typically associated with enhancers (H3K4me1 and H3K27ac), TF expression levels, and TF motif p-values to compute a probability score of TF binding events at active enhancers across the genome. This method has allowed us to define the enhancer landscape during differentiation of embryonic stem cells into pancreatic lineages and in breast cancer cells to define the regulatory pathways of the distinct molecular subtypes of breast cancer. Using TFSEE, we have identified key breast cancer subtype-specific transcription factors that are bound at active enhancers and dictate gene expression patterns determining growth outcomes. To demonstrate the broader utility of our approach, we have used this algorithm to identify transcription factors during the differentiation of embryonic stem cells into pancreatic cells. The analysis has revealed transcription factors maintaining the multipotency of endoderm stem cells and promoting differentiation into pancreatic progenitor cells. Taken together our results show that TFSEE can be used to perform multilayer genomic data integration to uncover novel cell type-specific transcription factors that control lineage-specific enhancers.

# Background

---

Enhancers and the transcription factors (TFs) regulating their formation have been shown to play an important role in cell type-specific activation of gene expression [1,2]. Although thousands of potential enhancers have been identified in cell lines and tissues, identification of the enhancers that are active versus not active or poised remains a major challenge [3]. In addition, the ability to identify the TFs acting at the numerous enhancers in each cell type is technically challenging [4,5].

Active enhancers have been shown to share several common features; such as increased chromatin accessibility (as measured by DNase-seq or ATAC-seq) [6,7,8] and enrichment of post-translational modification of histone tails (as assessed by ChIP-seq), including H3K4me1 and H3K27ac [10,11,9]. While these epigenetic features can successfully identify the location of many enhancers across the genome, they cannot readily differentiate between active and non-active enhancers [12,13]. However, recent genomic assays have shown that enhancers tend to be bound by RNA polymerase II (Pol II) and transcribed, producing non-coding RNAs known as enhancer RNAs ('eRNAs') [14,15,16]. While the functions of the enhancer RNA transcripts are unknown, we and others have shown that enhancer transcription (as measured by total RNA-seq, GRO-seq or PRO-seq) can be used in the absence of any other genomic information to as a predictor of enhancer activity [15,16,17,18,19,2,20,21,22,23].

In recent years, advances in technology have facilitated the large scale functional characterization of enhancer activity [24,25,26,27] and annotation of genome-wide binding sites of TFs in various cell types and tissues [28,4]. However, due to countless cell types, experimental conditions and the large number of TFs [29], integration of these independent data sets to achieve a comprehensive analysis of gene expression and actionable predictions of TFs driving cell type-specific gene expression can be very challenging. Furthermore, analyses that predict TF binding sites (TFBSs), which are usually 4-12 nucleotides in length [30], using TF binding profile databases [31,32,33], fail to consider that such sequences occur frequently by chance throughout the genome and that TF binding is cell type specific [34]. To overcome these limitations, we established a novel method called Total Functional Score of Enhancer Elements (TFSEE), which can be used to identify location and activity of enhancers in any cell or tissue type together with their cognate TFs.

In TFSEE, we integrate enhancer location and activity, TF motif prediction for each enhancer and the level of TF expression (Figure 2). We have previously demonstrated TFSEE in the identification of key breast cancer subtype-specific transcription factors determining growth outcomes [35]. In the studies presented herein, we demonstrate the broader use of TFSEE to identify enhancers and TFs during the differentiation of embryonic stem cells into pancreatic progenitor cells. Taken together our results show that TFSEE can be used to perform multilayer genomic data integration to uncover novel cell type-specific transcription factors that control lineage-specific enhancers (Figure 3A).

# Results

---

## The TFSEE model

The TFSEE model integrates multiple genomics assays, GRO-seq, RNA-seq, and ChIP-seq, data with TF motif information to predict TFs driving the formation of active enhancers and the locations of their cognate enhancers. The TFSEE model consists of five key data processing steps (Figure 1) followed by a data integration stage (Figure 2). In step 1 of TFSEE, a universe of active enhancers across the different constituent cell types are identified. The enhancers can be identified either by enhancer transcription (GRO-seq or total RNA-seq) (Figure S1A) or enrichment of epigenomic marks (H3K4me1 and H3K27ac) (Figure S1B). In step 2 of TFSEE, genome-wide enhancer activity levels are assessed by calculating the enrichment (H3K4me1 and H3K27ac) and eRNA transcription (GRO-seq or total RNA-seq) profiles under the universe of enhancers per cell type. TFSEE was designed to detect enhancer activity changes and TF:enhancer links for each cell type. All TF to enhancer links are determined by a de novo motif search and summarizing the probability of that TF using the tools in steps 3-4 of TFSEE, which creates a table annotating enhancer to TF for each cell type. For all TFs identified TFSEE calculates the expression profile using (GRO-seq or RNA-seq) across every cell type in step 5.

The final stage integrates all the data in steps 1-5 (Figure 2) to determine TFSEE score matrix and heatmap. First, we generate an enhancer activity matrix  $A_{C \times E}$  for all cell types  $C$  for the universe active of  $E$  enhancers, as determined from step 2. We assume that the enhancer activity of each cell type is linearly correlated to the amount enhancer transcription (GRO-seq or total RNA-seq,  $G$ ), and to the epigenomic marks (H3K4me1,  $M$  and H3K27ac,  $H$ ). To reduce bias each individual enhancer enrichment is scaled between 0 and 1. Enhancer activity can be expressed as the following formula:

$$A = G + M + H$$

Next, the enhancer activity matrix  $A_{C \times E}$ , is combined with motif prediction matrix  $T_{E \times F}$ , represent scaled motif prediction p-values,  $T$ , for each enhancer  $E$ , to form an intermediate matrix product. This matrix product is entrywise combined with TF expression matrix  $R$ , from step 5, the expression of each TF  $F$  for each cell type  $C$ , into a resulting matrix  $Z$  composed of  $C$  cell types and  $F$  TFs. TFSEE can be expressed as the following formula:

$$Z = (A \times T) \circ R$$

## Choice of biological model system and data

To better understand the TF-driven transcriptional programs using TFSEE, we used previously published transcriptional and epigenomic data from time course differentiation of human embryonic

stem cells (hESC) towards pancreatic cell type [36,37] (Figure 3A). For these analyses, we used GRO-seq and RNA-seq, as well as ChIP-seq for 3 different histone modifications at five defined stages of differentiation: hESCs, definitive endoderm (DE), primitive gut tube (GT), posterior foregut (FG), and pancreatic endoderm (PE) (Figure 3A, Table S1). This embryonic development model allows us to explore the spatiotemporal gene regulation during development, by enhancers and TFs.

## Unbiased Identification of Enhancers during Pancreatic Differentiation

We and other have shown that enhancers can be identified using enrichment of histone modifications (e.g. H3K4me1 and H3K27ac) [10,11,9] or by enhancer transcription [16]. We used a computational pipeline to identify a universe of eRNA transcripts from GRO-seq (Figure S1A) or enrichment of epigenomic marks (H3K4me1 or H3K27ac) (Figure S1B) for the cell lines in the pancreatic differentiation time course model. All potential enhancers were filtered to be  $> 3$  kb away from known transcription start sites (TSSs) of protein-coding genes from Gencode version 19 annotations [38], and active promoters, as identified by H3K4me3 [39] (Figure S2A) to avoid complications in the analysis associated with overlapping promoter transcription.

Using enrichment of H3K4me1 and H3K27ac, RPKM cutoff of  $\geq 1$  (Figure S2B and C) in at least one cell line, we determined there to be set of 182,335 candidate enhancers across all stages of pancreatic differentiation (Figure 3B). We categorized these candidate enhancers for each cell line and found that  $\leq 20\%$  of the enhancers, as determined by presences of H3K4me1 and H3K27ac, are active in each cell line and the majority are marked by only H3K4me1 (Figure 3B). These results confirm the enhancer landscape across pancreatic differentiation reported by Wang *et al.* We then identified a set of 4,974 candidate enhancers (Figure 3B) by GRO-seq as described previously [19], using RPKM  $\geq 0.5$  or  $\geq 1$  (Figure S2D and E) in at least one cell line. Compared to active enhancer by histone modifications, we found that the number of active enhancers in each cell line ranged from 77-25% of all candidate enhancers.

We compared the overlap from histone enhancer prediction methods (H3K4me1 or H3K27ac) to output from an enhancer transcription based approach (GRO-seq). We found that 12% of enhancers called based on enhancer transcription using GRO-seq data are identified by all the of the other methods (enrichment of H3K4me1 and H3K27ac) (Figure 3C, S3A). In contrast, greater than 75% of the enhancers were solely identified by enhancer transcription (Figure 3C and D, S3B). Although H3K27ac and H3K4me1 might be two histone modifications commonly associated with enhancers, these are not the only chromatin mark involved and other modifications may be present that were not assayed for [40]. Additionally, less than 1% of enhancers called based on enrichment of H3K4me1 or H3K27ac are identified by the other methods (Figure 3C). This may be due, in part, to the fact that enhancer calling based on H3K4me1 or H3K27ac enrichment, yields much larger numbers of putative enhancers (Figure 3D), many of which may be false positives or inactive as the true regulatory elements (Figure S3C and D). Nonetheless, as we show below,

incorporating enhancer transcription into an TFSEE pipeline that includes information about H3K4me1 and H3K27ac enrichment, improves the identification cell type-specific enhancers.

## **TFSEE identifies cell type-specific enhancers and their cognate TFs**

We used the enhancer calls by Figure 3B, to identify cell type-specific enhancers and their cognate TFs, using TFSEE, either by enhancer transcription or enrichment of epigenomic marks. We visualized the results from TFSEE using unsupervised hierarchical clustering, which grouped the cell types into two major clades: (1) FG, and PE (2) hESC, DE, and GT (Figure 4A, S4A). To better understand the TF:enhancer dynamics across all differentiation stages we clustered the TSEE score across all differentiation stages, revealing four major categories using enhancer transcription (Figure 4B). We examined the enrichment of putative enhancers and their associated TFs across stages by quantifying their normalized TFSEE score. This analysis revealed four major clusters: 1. driving early (hESC, DE) and late pancreatic differentiation (FG and PE), 2. enriched in GT, 3. driving pre-pancreatic lineage (hESC, DE and GT), and 4. driving late-pancreatic differentiation (FG and PE) (Figure 4D). In contrast, using only histone enrichment to identify enhancers, we retrieve only three clusters (Figure S4B). These results highlight TF:enhancers driving pre-pancreatic lineage (hESC, DE and GT), and late-pancreatic differentiation (FG and PE), but fails to highlight any other stage specific drivers (Figure S4C). We were particularly interested in TFs and enhancers that provided a clear demarcation of enrichment between pre- and late- pancreatic differentiation.

To investigate the the distinct roles of lineage specific enhancers and their cognate TFs, we first examined the mRNA levels of the corresponding predicted TFs of each cluster in each of the stages. Our analysis revealed that TFs identified in pre-pancreatic lineage show equal expression across stages, while late-pancreatic TFs are highly expressed in FG and PE (Figure 5A, S5A) coinciding with pancreatic induction at the FG stage (Figure 3A). Conversely, we didn't see an enrichment of TFs in a stage specific manner for either TFs enriched early (hESC, DE) and late pancreatic differentiation (FG and PE) or those maintaining GT pluripotency (Figure S6A).

Next, we determined if enhancer transcription corresponding to the enriched TFs, using TFSEE score, and the regulation of their nearby genes might regulate differentiation biology. To do so, we identified the enhancers corresponding to the predicted TFs using enriched binding motif prediction, and then determined the level of transcription for each enhancer, using GRO-seq or H3K27ac ChIP-seq, (Figure 5B, S5B, S6B) and the nearest neighboring gene (upstream or downstream), using RNA-seq (Figure 5C, S5C, S6C). Interestingly, transcribed enhancers exhibited stage specific enrichment, which doesn't correspond to the patterns found from TFSEE enrichment (Figure 5B, S5B, S6B). This result reflects that 48% - 99% of the enhancers are shared between clusters and the variation between clusters is due to differences in TF expression.

## **Discussion**

---

## **Acknowledgments**

---

# Material and Methods

## Genomic Data Curation

We used previously published GRO-seq, ChIP-seq and RNA-seq data from [36,37] time course differentiation of human embryonic stem cells (hESC) to pancreatic endoderm (PE). All data sets are available from NCBI’s Gene Expression Omnibus [41] or EMBL-EBI’s ArrayExpress [42] repositories using the accession numbers listed in Table S1.

Table S1: **Description and accession numbers of GRO-seq, ChIP-seq and RNA-seq datasets.**

Assay	Accessions
GRO-seq	GSM1316306, GSM1316313, GSM1316320, GSM1316327, GSM1316334
H3K4me3 ChIP-seq	ERR208008, ERR208014, ERR207998, ERR20798, ERR207999
H3K4me1 ChIP-seq	GSM1316302, GSM1316303, GSM1316309, GSM1316316, GSM1316317, GSM1316310, GSM1316323, GSM1316324, GSM1316330, GSM1316331
H3K27ac ChIP-seq	GSM1316300, GSM1316301, GSM1316307, GSM1316308, GSM1316314, GSM1316315, GSM1316321, GSM1316322, GSM1316328, GSM1316329
Input ChIP-seq	ERR208001, ERR208012, ERR207984, ERR208011, ERR207986, GSM1316304, GSM1316305, GSM1316311, GSM1316312, GSM1316318, GSM1316319, GSM1316325, GSM1316326, GSM1316332, GSM1316333
RNA-seq	ERR266333, ERR266335, ERR266337, ERR266338, ERR266341, ERR266342, ERR266344, ERR266346, ERR266349, ERR266351

## Analysis of ChIP-seq Data Sets

The raw reads were aligned to the human reference genome (GRCh37/hg19) using default parameters in Bowtie version 1.0.0 [43]. The aligned reads were subsequently filtered for quality and uniquely mappable reads were retained for further analysis using Samtools version 0.1.19 [44] and Picard version 1.127 [45]. Library complexity was measured using BEDTools version 2.17.0 [46] and meets ENCODE data quality standards [47]. Relaxed peaks were called using MACS



version 2.1.0 [48] with a p-value of  $1 \times 10^{-2}$  for each replicate, pooled replicates' reads and pseudoreplicates. Peak calls from the pooled replicates that are either observed in both replicates, or in both pseudoreplicates were used for subsequent analysis.

## Analysis of RNA-seq Data Sets

The raw reads were aligned to the human reference genome (GRCh37/hg19) using default parameters in STAR version 2.4.2a [49]. Quantification of genes against Gencode version 19 [38] annotations was done using default parameters in RSEM version 1.2.31 [50].

## Analysis of GRO-seq Data

The GRO-seq reads were trimmed to the first 36 bases to trim adapter and low quality sequence, using default parameters of fastx\_trimmer in fastx-toolkit version 0.0.13.2 [51]. The trimmed reads were aligned to the human reference genome (GRCh37/hg19) using default parameters in BWA version 0.7.12 [52].

## Kernel Density

Kernel density plot representations were used to express the univariate distribution of ChIP-seq reads under peaks, RNA-seq reads for protein-coding genes and GRO-seq reads for short paired and short unpaired eRNAs. The kernel density plots were calculated in Python (ver. 2.7.11) using the kdeplot function from [seaborn](#) version 0.7.1 [53] with default parameters.

## Defining Transcription Start Sites and Promoters

We made distinct transcription start sites (TSS) for protein-coding genes from Gencode version 19 [38] annotations using MakeGencodeTSS [54]. We identified active promoters, as identified by H3K4me3 [39]. A RPKM cutoff of  $\geq 1$  for H3K4me3 in at least one cell line was used to identify a peak as an active enhancer (Figure S2A).

## Enhancer calling by ChIP-seq

### *Calling Active Enhancers.*

We built a universe of peak calls by merging the peaks from individual cell lines for histone modifications (H3K4me1 and H3K27ac) and stratifying the boundaries to remove overlaps/redundancies occurring from the union of all peaks. Potential enhancers were defined as peaks that were  $> 3\text{kb}$  from known TSS, protein coding genes from Gencode version 19 annotations [38], and H3K4me3 peaks. A RPKM cutoff of  $\geq 1$  for H3K4me1 and H3K27ac (Figure S2B and C) in at least one cell line was used to identify a peak as an active enhancer. The universe of active enhancers was assembled using the cutoffs noted above for each cell line and was used for further analyses.

### ***Motif Analyses.***

De novo motif analyses were performed on a 1 kb region ( $\pm$  500 bp) surrounding the peak summit for the top 10000 enhancers, using the command-line version of MEME-ChIP from MEME Suite version 4.11.1 [55,56]. The following parameters were used for motif prediction: (1) zero or one occurrence per sequence (-mod zoops); (2) number of motifs (-nmotifs 15); (3) minimum, maximum width of the motif (-minw 8, -maxw 15). All the other parameters were set at the default. The predicted motifs from MEME were matched to known motifs in the JASPAR database (JASPAR\_CORE\_2016\_vertbrates.meme) [32] using TOMTOM [33].

## **Enhancer calling by GRO-seq**

### ***Transcript calling.***

Transcript calling was performed using a two-state hidden Markov model using the groHMM data analysis package version 3.4 [16,21,57] on each individual cell lines. The negative log transition probability of the switch between transcribed state to non-transcribed state and the variance in read counts in the non-transcribed state that are used to predict the transcription units for the cell lines in this study are listed Table S2.

Table S2: **groHMM tuning parameters.**

Cell Line	-Log Transition Probability	Variance in read counts
hES	50	45
DE	50	35
GT	50	50
FG	50	35
PE	50	35

We then built a universe of transcripts by merging the groHMM-called transcripts from individual cell lines and stratifying the boundaries to remove overlaps/redundancies occurring from the union of all transcripts.

### ***Calling Enhancer Transcripts.***

We filtered and collected a subset of short intergenic transcripts  $< 9$  kb in length and  $> 3$  kb away from known transcription start sites (TSSs) of protein-coding genes from Gencode version 19 annotations [38], and H3K4me3 peaks. These were further classified into (1) short paired eRNAs and (2) short unpaired eRNAs as described previously [19]. For the short paired eRNAs, the sum

of the GRO-seq RPKM values for both strands of DNA was used to determine if an enhancer transcript pair is expressed using a cutoff of  $\text{RPKM} \geq 0.5$  (Figure S2D). An RPKM cutoff of  $\geq 1$  was used to determine the universe expressed short unpaired eRNAs (Figure S2E). The comprehensive of expressed eRNAs (short paired and short unpaired) was assembled using the cutoffs noted above for each cell line was used for further analyses.

### ***Motif Analyses.***

De novo motif analyses was performed on a 1 kb region ( $\pm 500$  bp) surrounding the overlap center or the transcription start site for short paired and short unpaired eRNAs, respectively, using the command-line version of MEME from MEME Suite version 4.11.1 [55]. The following parameters were used for motif prediction: (1) zero or one occurrence per sequence (-mod zoops); (2) number of motifs (-nmotifs 15); (3) minimum, maximum width of the motif (-minw 8, -maxw 15); and (4) search for motif in given strand and reverse complement strand (-revcomp). The predicted motifs from MEME were matched to known motifs in the JASPAR database (JASPAR\_CORE\_2016\_vertebrates.meme) [32] using TOMTOM [33].

### **Generating Heatmaps and Clusters**

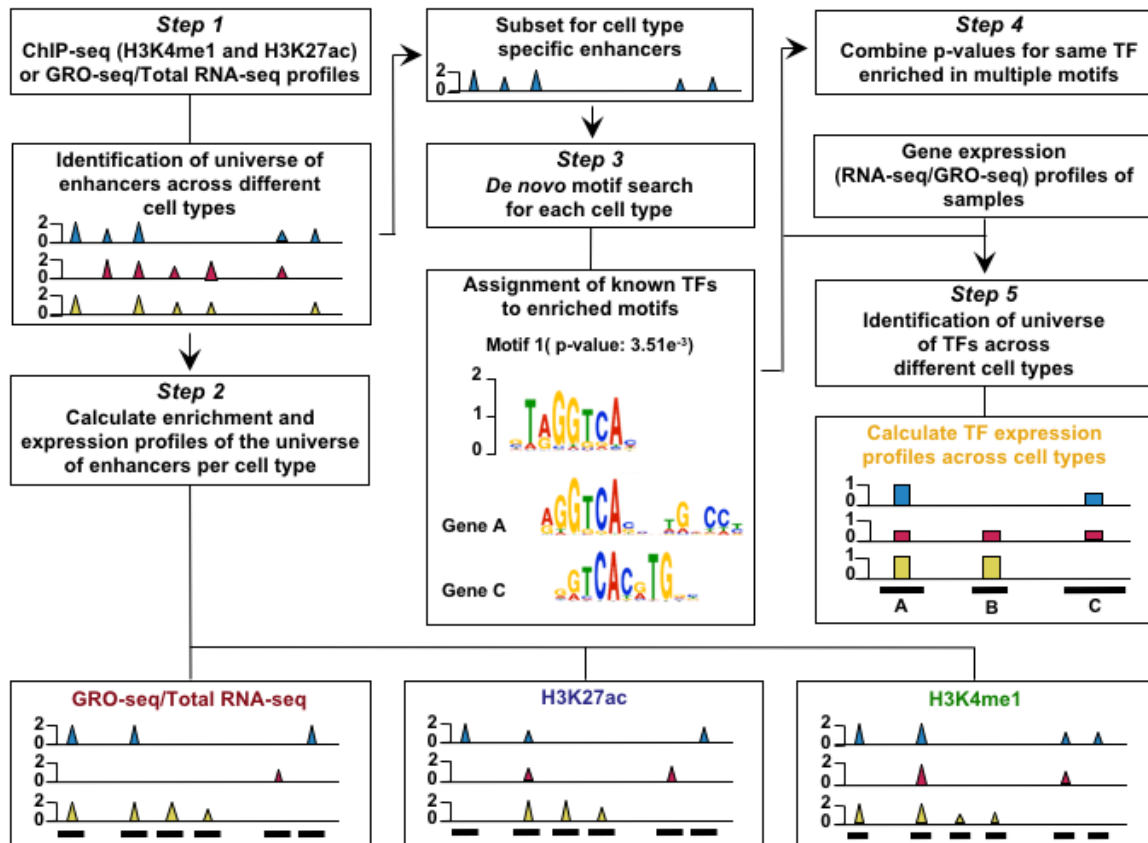
For each cell line, the functional scores were Z-score normalized. To identify cognate transcription factors by cell type, we performed hierarchical clustering by calculating the Euclidean distance using clustermap from [seaborn](#) version 0.7.1 [53]. For visualization of the multidimensional TFSEE scores, we performed t-distributed stochastic neighbor embedding analysis (t-SNE) [58] using the TSNE function and labeled the clusters by calculating K-means clustering using the KMeans function with the expectation-maximization algorithm in [scikit-learn](#) version 0.17.1 [59,60,61].

### **Nearest Neighboring Gene Analyses and Box Plots**

The universe of expressed genes in each cell line was determined from the RNA-seq data using a FPKM cutoff of  $> 0.4$  (Figure S2F). The set of nearest neighboring expressed genes for each enhancer defined by an expressed eRNA or the enrichment of active histone marks was determined for each cell line. Box plot representations were used to express the levels of transcription or enrichment for each called enhancer and transcription of their nearest neighboring expressed genes. The read distribution (RPKM) for each enhancer or (FPKM) gene was calculated and plotted using the boxplot function from [matplotlib](#) version 2.0.2 [62,63]. Wilcoxon rank sum tests were performed to determine the statistical significance of all comparisons.

## Figures and Figure Legends

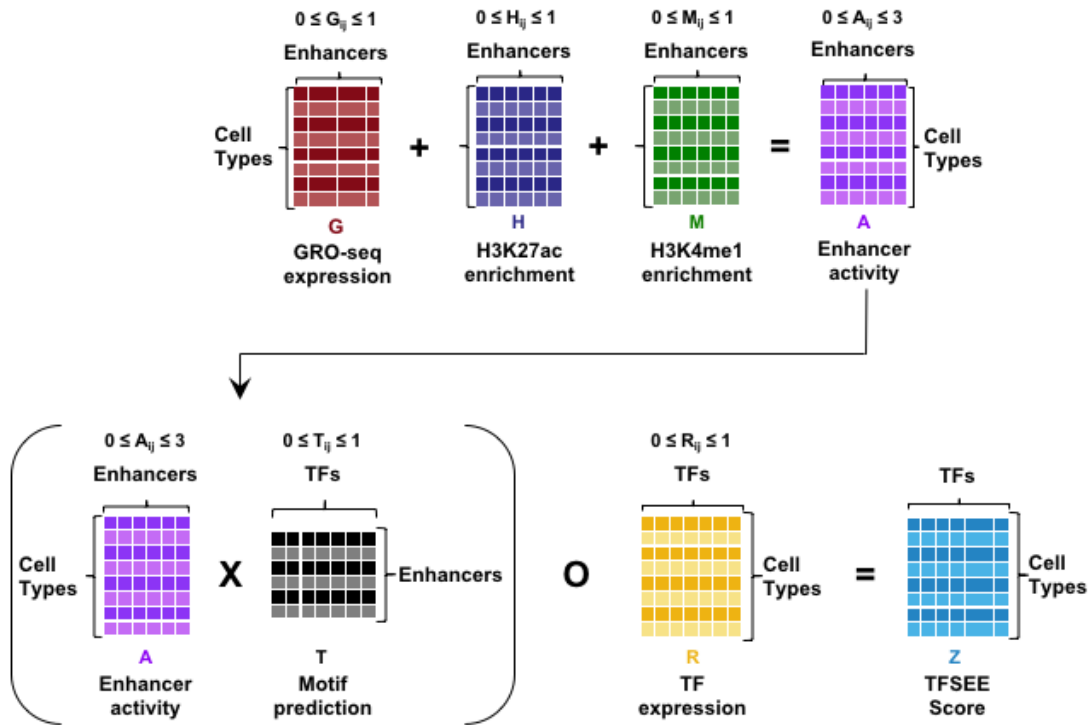
---



**Figure 1 – Malladi et al. (2018)**

**Figure 1: Data Processing for Total Functional Score of Enhancer Elements (TFSEE) Method.** The TFSEE method has five data processing steps that are used to identify enhancer location and activity and their cognate transcription factors (TFs). In step 1, epigenomic (ChIP-seq) or the transcriptional (GRO-seq or total RNA-seq) profiles are used to generate a universe of active

enhancers across the different constituent cell types. In step 2, TFSEE calculates the enrichment (H3K4me1 and H3K27ac) and eRNA transcription (GRO-seq and total RNA-seq) profiles under all identified active enhancers per cell type. Cell type-specific enhancers are used as input for step 3, where a de novo motif search is performed to identify potential TFs at each enhancer. If a motif is represented multiple times for a given enhancer location, TFSEE combines the probability of that motif into a single p-value in step 4. Step 5 integrates the amount of eRNA transcription (GRO-seq or total RNA-seq) and the expression of the TFs whose motifs were predicted in step 3 and 4 for all cell types, to provide an output of TF expression profiles across every cell type.

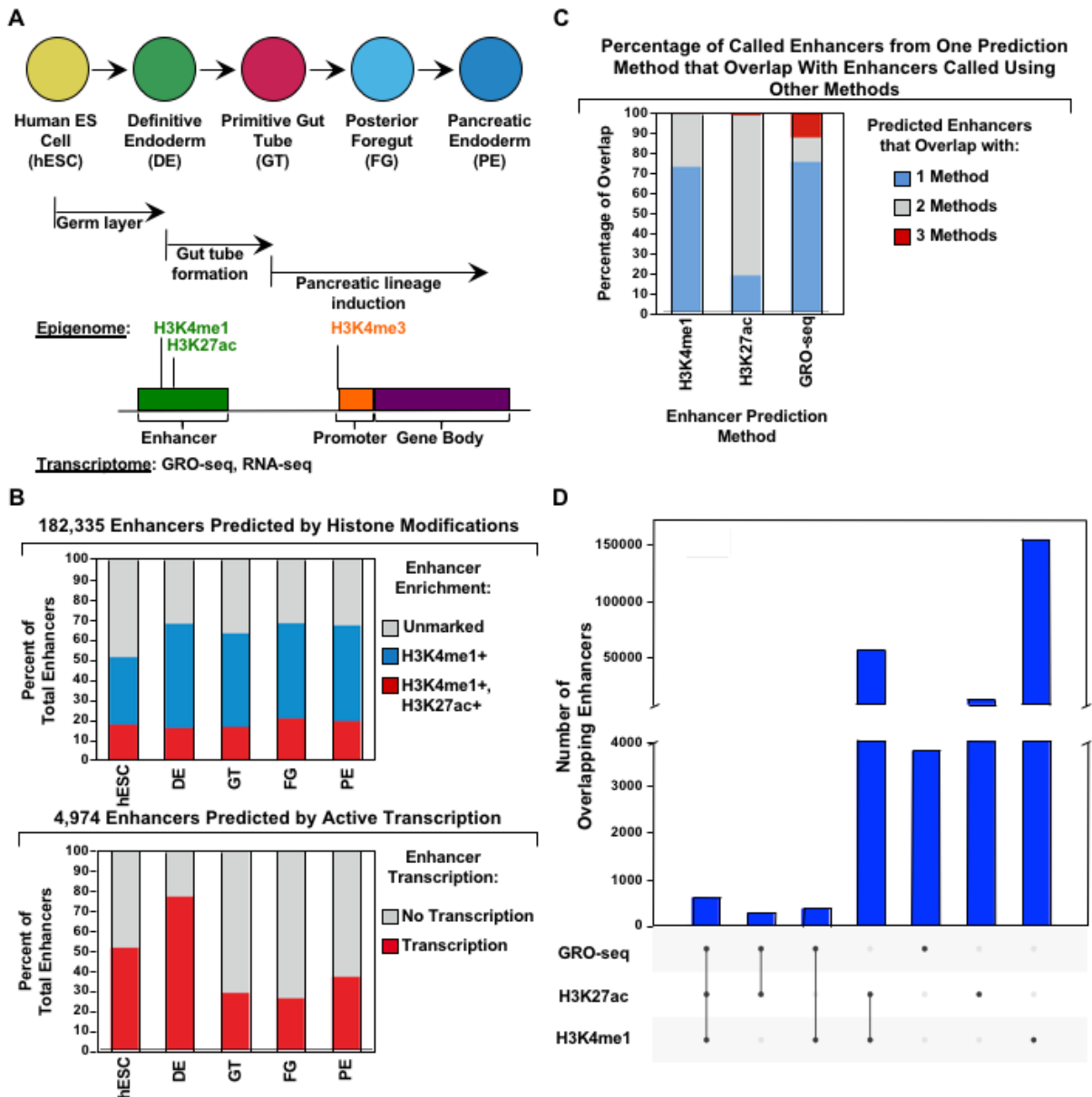


**Figure 2 – Malladi et al. (2018)**

Figure 2: **Overview of Total Functional Score of Enhancer Elements (TFSEE) Method.** TFSEE combines diverse data sets to identify enhancer location and activity and their cognate transcription factors (TFs). An illustration of TFSEE data integration stage, taking the outputs generated in panel A, to identify the location, activity level, and predicted TFs at each enhancer

across all cell types. (Top) All matrices represent scaled enhancer activity for each cell type in each enhancer prediction method (G, H, and M). All matrices are linearly combined into a resulting matrix A, to provide a total enhancer activity score. (Bottom) Enhancer activity matrix A, is combined with motif prediction matrix T, represent scaled motif prediction p-values for each enhancer, to form an intermediate matrix product. This matrix product is entrywise combined with TF expression matrix R (scaled TF expression for each cell type), into a resulting matrix Z, on which TFSEE clustering is performed.

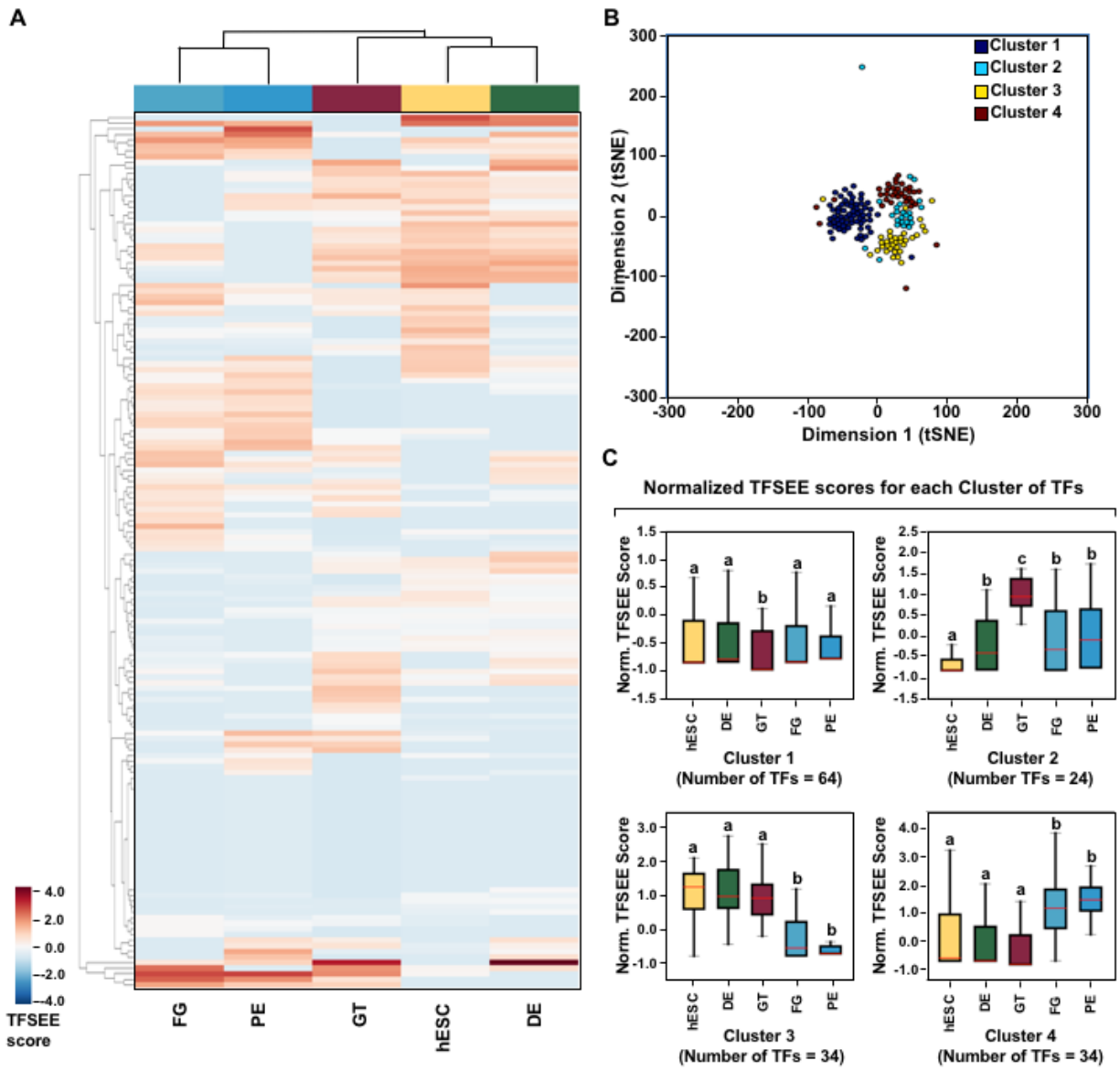




**Figure 3 – Malladi et al. (2018)**

Figure 3: **Comparison of genome-wide prediction of enhancers during pancreatic differentiation.** (A) (Top) Schematic of pancreatic differentiation starting from Human embryonic stem cells (hESCs) to pancreatic endoderm (PE). (Bottom) Depiction of epigenomic (ChIP-seq) and transcriptional (GRO-seq and RNA-seq) profiles for each cell line used for analysis. (B)

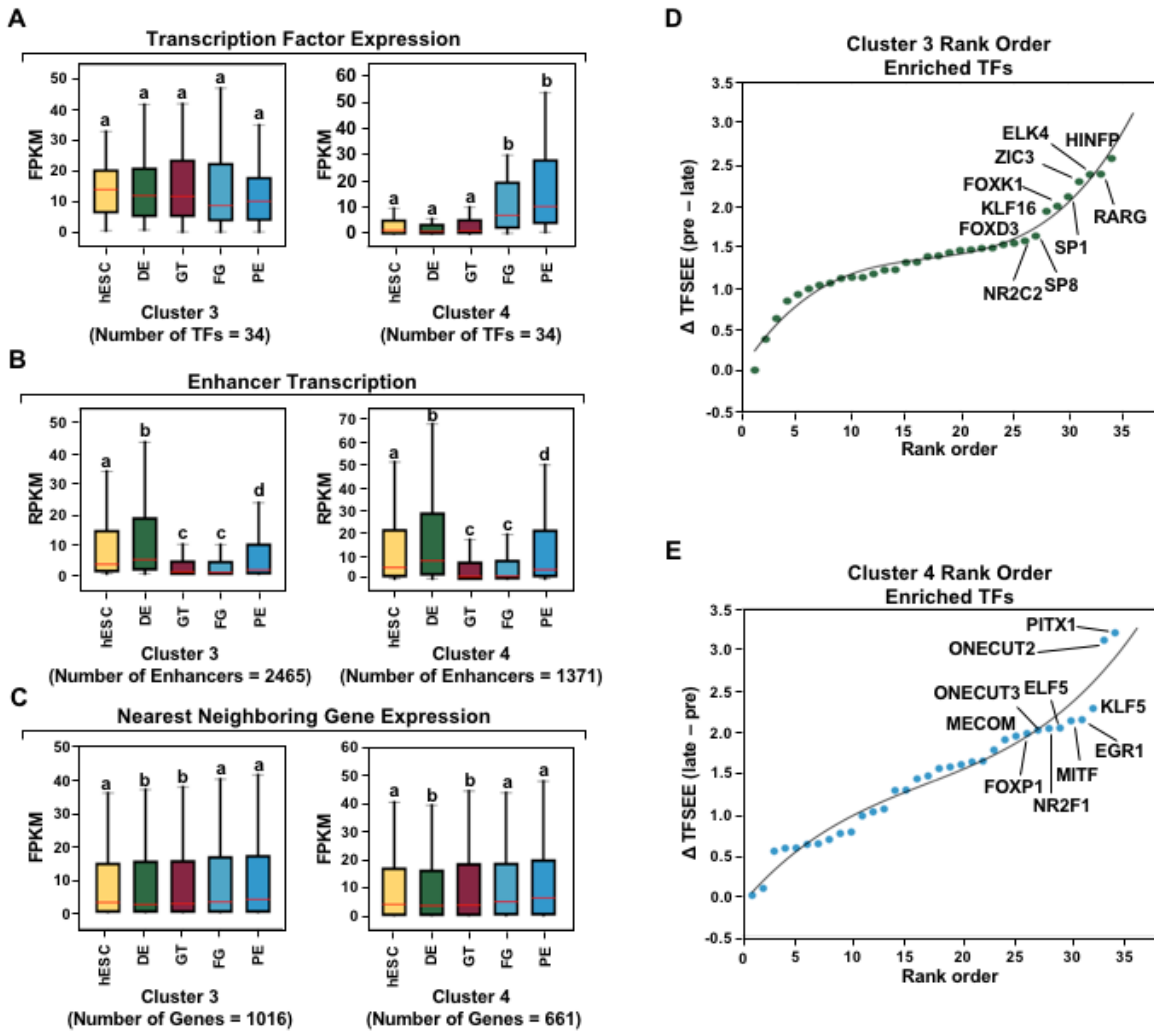
Stacked bar chart comparing expression of candidate enhancers categorized by (*Top*) H3K4me1 and H3K27ac enrichment, or (*Bottom*) enhancer transcription (GRO-seq). **(C)** Stacked bar chart comparing enhancer prediction methods in pancreatic differentiation. Enhancers were called using enhancer transcription (GRO-seq) or by using H3K4me1 enrichment, or H3K27ac enrichment. The percentage of called enhancers from one prediction method that overlap with enhancers called using other methods is shown. **(D)** UpSet plot showing the set intersection of enhancer identification methods shown in panel C.



**Figure 4 – Malladi et al. (2018)**

Figure 4: **TFSEE identifies cell type-specific enhancers and their cognate TFs that drive gene expression during pancreatic differentiation.** (A) Unsupervised hierarchical clustering of cell type-normalized TFSEE scores shown in a heatmap representation. hESC (human embryonic stem cell); DE (definitive endoderm); GT (primitive gut tube); FG (posterior foregut); PE (pancreatic

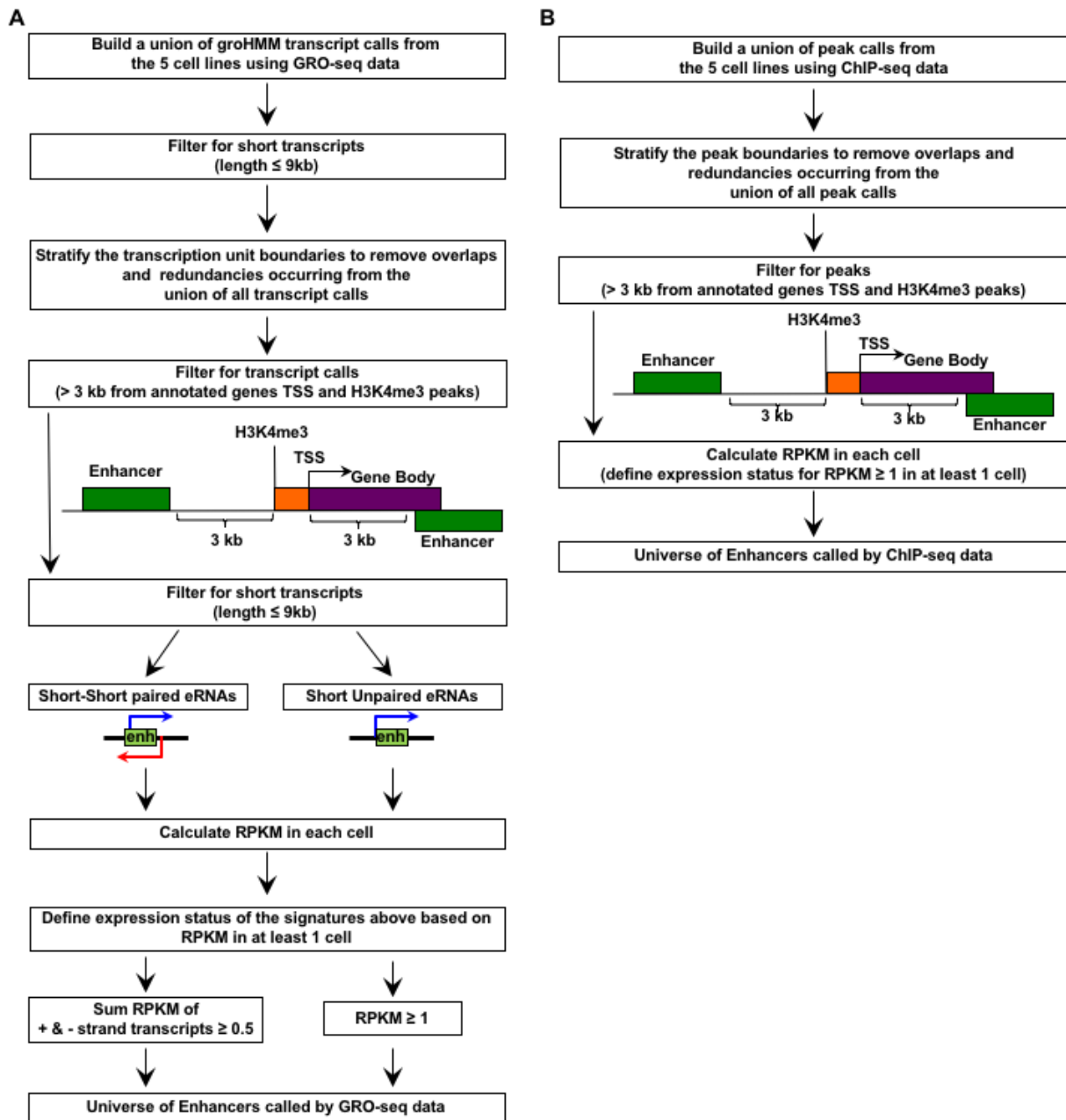
endoderm). **(B)** Biaxial t-SNE clustering plot of cell type-normalized TFSEE scores showing evidence of four distinct clusters, each point represents an individual TF. **(C)** Box plots of normalized TFSEE score for clusters identified in pancreatic differentiation (panel B), number of TFs are indicated in each cluster. Bars marked with different letters are significantly different (Wilcoxon rank sum test,  $p < 1 \times 10^{-4}$ ). Cluster 1, TFs associated with early (hESC, DE) and late pancreatic differentiation (FG and PE). Cluster 2, TFs associated with GT pluripotency. Cluster 3, TFs associated with pre-pancreatic lineage induction (hESC, DE and GT). Cluster 4, TFs associated with late-pancreatic differentiation (FG and PE).



**Figure 5 – Malladi et al. (2018)**

Figure 5: TFSEE-Predicted TFs are enriched in pre- and late- pancreatic differentiation. (A-C) Box plots of normalized TF expression (panel A), enhancer transcription (panel B), and gene expression for the nearest neighboring genes to active enhancers (panel C) in pre- (cluster 3) and late-pancreatic (cluster 4) differentiation across the different cell types. Bars marked with different

letters are significantly different from each other (Wilcoxon rank sum test). hESC (human embryonic stem cell); DE (definitive endoderm); GT (primitive gut tube); FG (posterior foregut); PE (pancreatic endoderm). **(A)** TFs identified in cluster 3 by TFSEE show equal expression across differentiation. While, cluster 4 highlights TFs highly expressed in FG and PE. TF expression as measured by RNA-seq. Number of TFs in each cluster are in parenthesis. ( $p1 \times 10^{-4}$ ) **(B)** Enhancer transcription as measured by GRO-seq. Number of enhancers in each cluster are in parenthesis. ( $p1 \times 10^{-4}$ ). **(C)** Gene expression as measured by RNA-seq. Number of genes in each cluster are in parenthesis. ( $p0.05$ ) **(D and E)** Rank order of TFs enriched in the Cluster 3 and the Cluster 4 identified using TFSEE. The top ten TFs in each Cluster are noted.

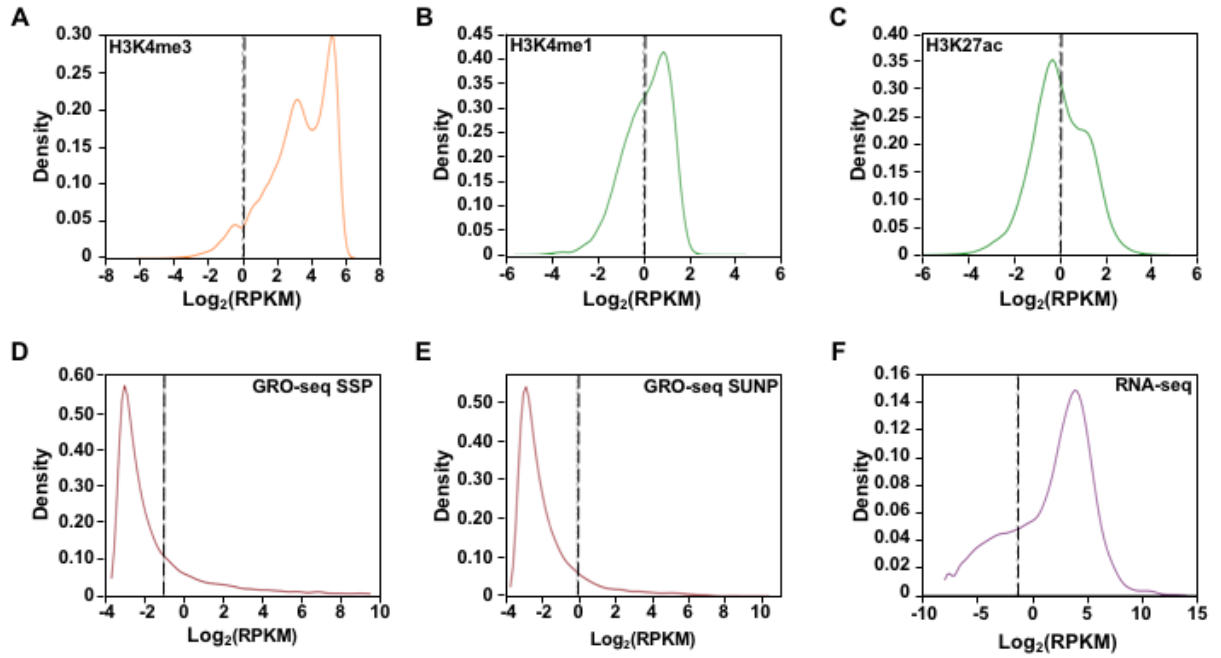


**Supp. Figure 1 – Malladi et al. (2018)**

Figure S1: **Unbiased, genome-wide prediction of active enhancers.** **(A)** Overview of the computational pipeline used for the genome-wide annotation of enhancer transcripts (eRNAs) and prediction of active enhancers using GRO-seq data. **(B)** Overview of the computational pipeline

used for the genome-wide annotation of and prediction of active enhancers using ChIP-seq (H3K4me1 and H3K27ac) data.

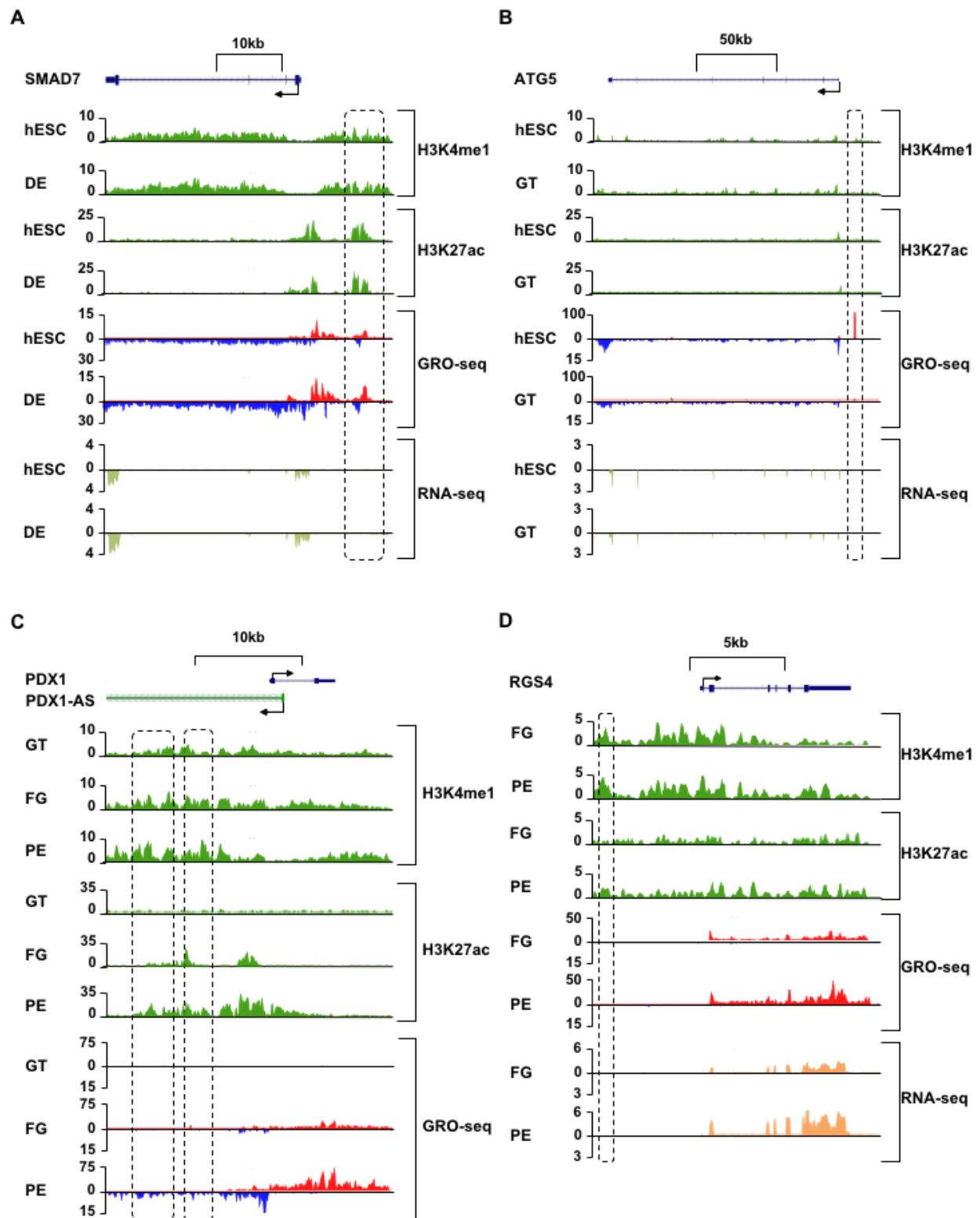




**Supp. Figure 2 – Malladi et al. (2018)**

Figure S2: **Density plots of enhancer and gene expression levels across all cell types.** Kernel density plots of log-transformed RPKM and FPKM values for determining active enhancers and genes. The dashed grey line represents the minimum expression cutoff. **(A)** Density plot of H3K4me3 (promoter mark) cutoff  $\text{RPKM} \geq 1$ . **(B)** Density plot of H3K4me1 (enhancer mark) cutoff

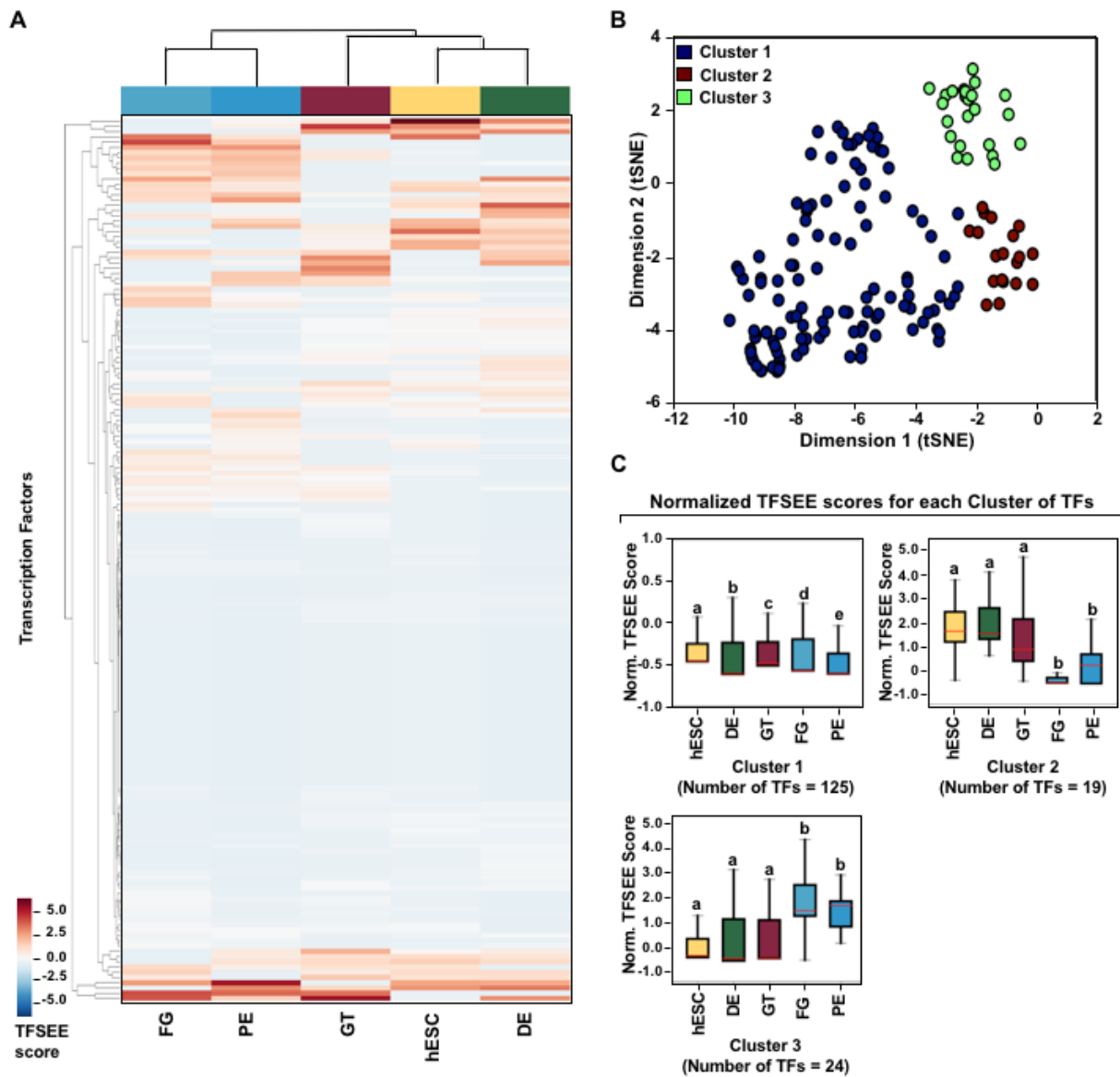
RPKM  $\geq 1$ . **(C)** Density plot of H3K27ac (enhancer mark) cutoff RPKM  $\geq 1$ . **(D)** Density plot of short-short paired GRO-seq transcription (SSP) (enhancer mark) cutoff RPKM  $\geq 1$ . **(E)** Density plot of short-unpaired GRO-seq transcription (SUNP) (enhancer mark) cutoff RPKM  $\geq 0.5$ . **(F)** Density plot of RNA-seq (gene expression) cutoff FPKM  $\geq 0.4$



Supp. Figure 3 – Malladi et al. (2018)

**Figure S3: Enhancer transcription is a better predictor of enhancer activity and target gene expression than other features of active chromatin. (A-D)** UCSC Genome browser views of GRO-seq, histone modification ChIP-seq and RNA-seq data showing a transcribed enhancer (*black box with dashed line*) and its nearest neighboring gene. hESC (human embryonic stem cell);

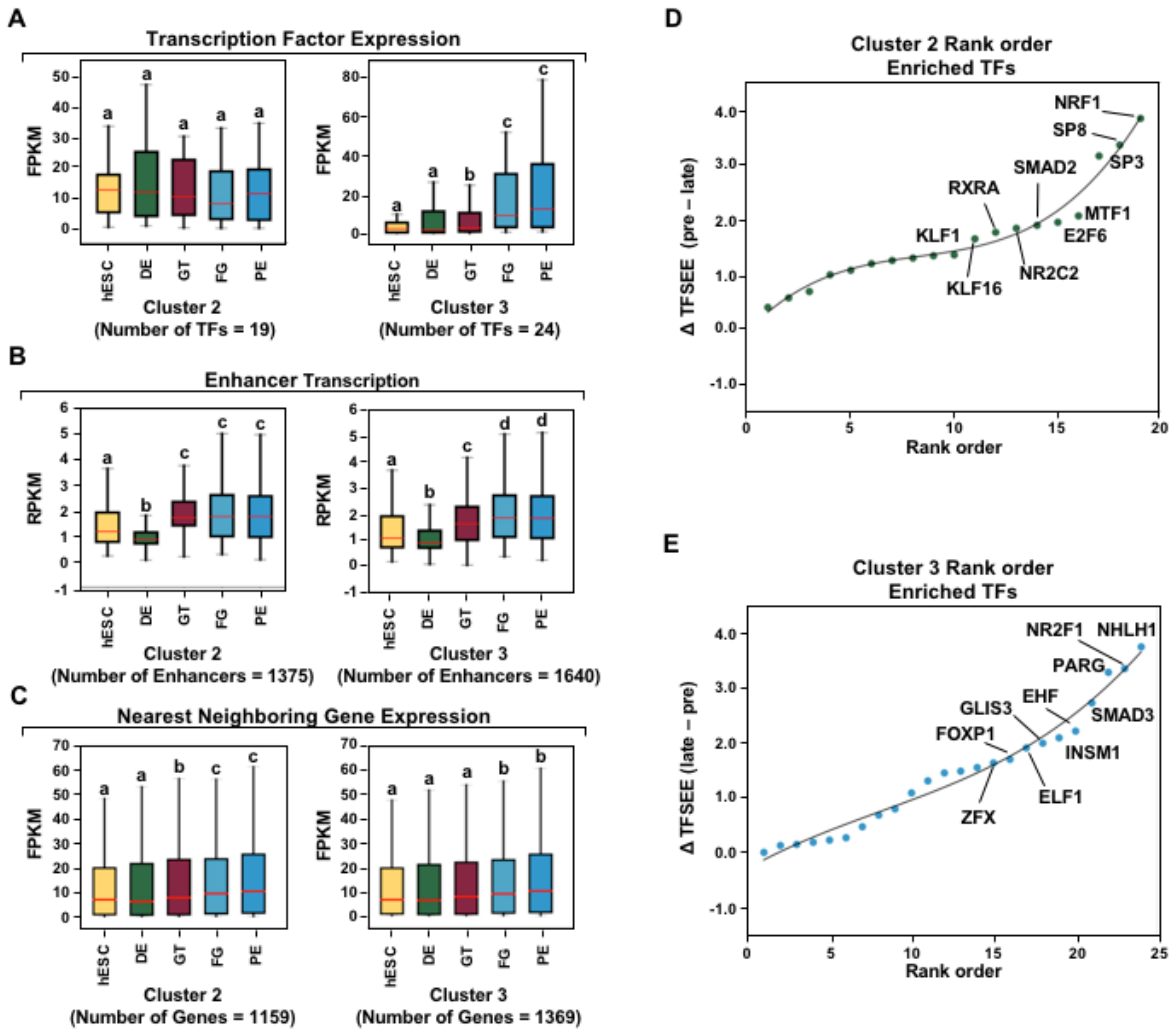
DE (definitive endoderm); GT (primitive gut tube); FG (posterior foregut); PE (pancreatic endoderm). **(A)** Browser view showing a transcribed enhancer and its nearest neighboring gene (SMAD7). The data highlights histone modifications typically enriched at enhancers (*green*), however the increased transcription determined by GRO-seq (*red/blue*) for DE correlates to expression of nearest genes determined by RNA-seq (*orange/light green*). **(B)** Browser view showing a transcribed enhancer and its nearest neighboring gene (ATG5). The data highlights an enhancer identified by GRO-seq (*red/blue*), however lacks typical histone modifications enriched at enhancers (*green*). The increased transcription determined by GRO-seq for hESC correlates to expression of nearest genes determined by RNA-seq (*orange/light green*). **(C)** Browser view showing a transcribed enhancer and its nearest neighboring gene (PDX1). The data highlights an enhancer identified by histone modifications enriched at enhancers (*green*), however increased transcription determined by GRO-seq (*red/blue*) correlates with antisense gene (AS-PDX1). **(D)** Browser view showing a transcribed enhancer and its nearest neighboring gene (RGS4). The data highlights an enhancer identified by histone modifications enriched at enhancers (*green*), however lacks enhancer transcription identified by GRO-seq (*red/blue*). The increased enhancer signal determined by histone modifications for PE shows correlates to expression of nearest genes determined by RNA-seq (*orange/light green*) and GRO-seq (*red/blue*).



Supp. Figure 4 – Malladi et al. (2018)

Figure S4: TFSEE defined by histone modifications identifies cell type-specific enhancers and their cognate TFs that drive gene expression in pancreatic differentiation. (A) Unsupervised hierarchical clustering of cell line normalized TFSEE scores shown in a heatmap representation.

**(B)** Biaxial t-SNE clustering plot of cell type-normalized TFSEE scores showing evidence of three distinct clusters, each point represents an individual TF. **(C)** Boxplots of normalized TFSEE score for clusters identified in pancreatic differentiation. Bars marked with different letters are significantly different from each other (Wilcoxon rank sum test,  $p < 10^{-2}$ ). Number of TFs in each cluster are in parenthesis. Cluster 1, TFs associated across pancreatic lineage Cluster 2, TFs associated with pre-pancreatic lineage induction (hESC, DE and GT). Cluster 3, TFs associated with late-pancreatic differentiation (FG and PE).

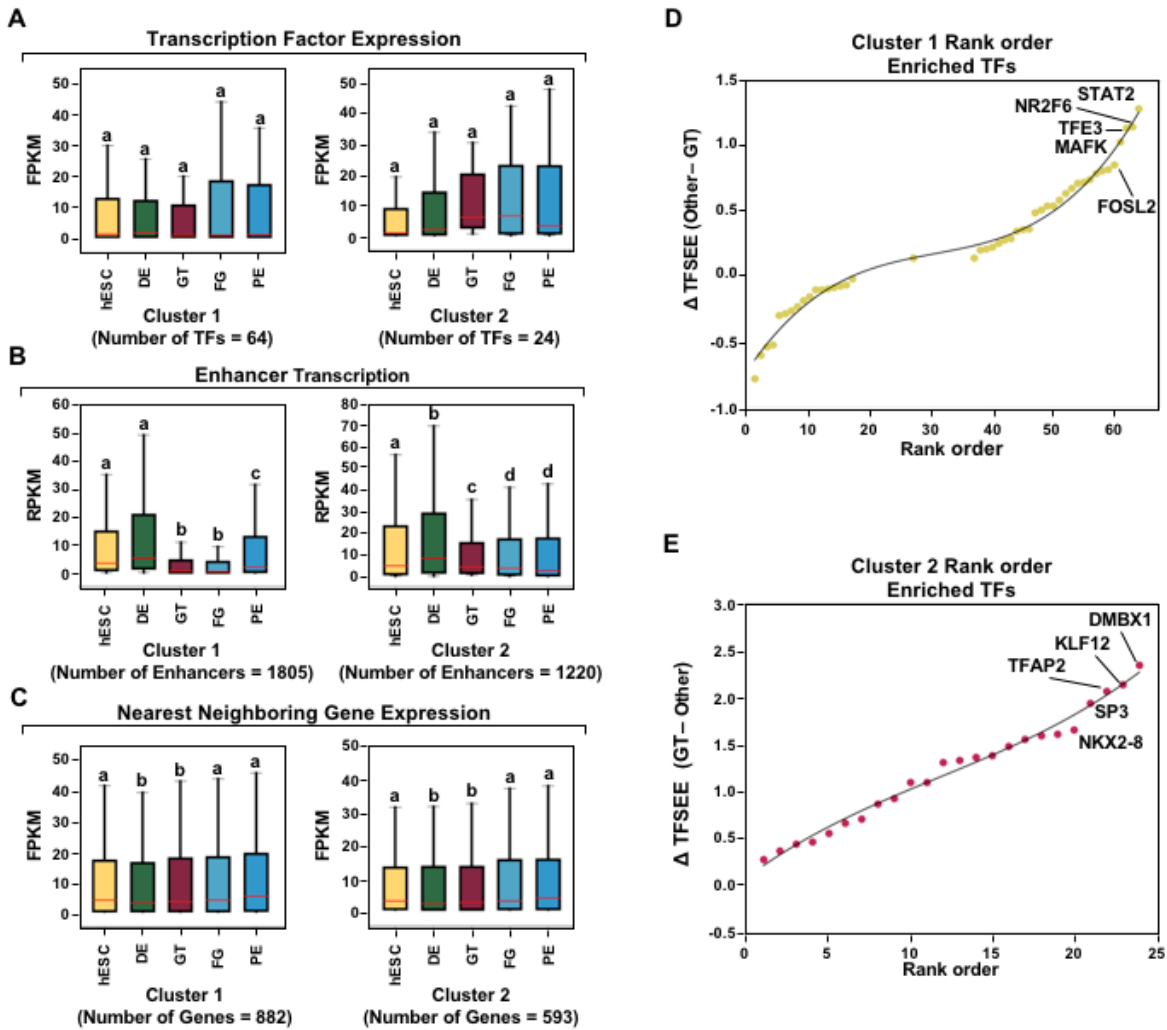


Supp. Figure 5 – Malladi et al. (2018)

Figure S5: TFSEE-Predicted TFs, by histone modifications, are enriched in pre- and late-pancreatic differentiation. (A-C) Box plots of normalized TF expression (panel A), enhancer transcription (panel B), and gene expression for the nearest neighboring genes to active enhancers (panel C) in pre- (cluster 2) and late-pancreatic (cluster 3) differentiation across the different cell

types. Bars marked with different letters are significantly different from each other (Wilcoxon rank sum test). hESC (human embryonic stem cell); DE (definitive endoderm); GT (primitive gut tube); FG (posterior foregut); PE (pancreatic endoderm). **(A)** TFs identified in cluster 2 by TFSEE show equal expression across differentiation. While, cluster 3 highlights TFs highly expressed in FG and PE. TF expression as measured by RNA-seq. Number of TFs in each cluster are in parenthesis. ( $p1 \times 10^{-4}$ ) **(B)** Enhancer transcription as measured by ChIP-seq (H3K27ac enrichment). Number of enhancers in each cluster are in parenthesis. ( $p1 \times 10^{-4}$ ). **(C)** Gene expression as measured by RNA-seq. Number of genes in each cluster are in parenthesis. ( $p0.05$ ). **(D and E)** Rank order of TFs enriched in the Cluster 2 and the Cluster 3 identified using TFSEE. The top ten TFs in each Cluster are noted.





Supp. Figure 6 – Malladi et al. (2018)

Figure S6: TFSEE-Predicted TFs are enriched and depleted in Primitive Gut Tube during pancreatic differentiation. (A-C) Box plots of normalized TF expression (panel A), enhancer transcription (panel B), and gene expression for the nearest neighboring genes to active enhancers (panel C) in depleted (cluster 1) and enriched (cluster 2) in primitive gut tube during pancreatic

differentiation across different cell types. Bars marked with different letters are significantly different from each other (Wilcoxon rank sum test). hESC (human embryonic stem cell); DE (definitive endoderm); GT (primitive gut tube); FG (posterior foregut); PE (pancreatic endoderm). **(A)** TF expression as measured by RNA-seq. Number of TFs in each cluster are in parenthesis. ( $p1 \times 10^{-2}$ ) **(B)** Enhancer transcription as measured by GRO-seq. Number of enhancers in each cluster are in parenthesis. ( $p1 \times 10^{-4}$ ). **(C)** Gene expression as measured by RNA-seq. Number of genes in each cluster are in parenthesis. ( $p0.05$ ). **(D and E)** Rank order of TFs enriched in the Cluster 1 and the Cluster 2 identified using TFSEE. The top five TFs in each Cluster are noted.

# References

---

**1. Transcriptional enhancers: from properties to genome-wide predictions**

Daria Shlyueva, Gerald Stampfel, Alexander Stark

*Nature Reviews Genetics* (2014-03-11) <https://doi.org/10.1038/nrg3682>

**2. The selection and function of cell type-specific enhancers**

Sven Heinz, Casey E. Romanoski, Christopher Benner, Christopher K. Glass

*Nature Reviews Molecular Cell Biology* (2015-02-04) <https://doi.org/10.1038/nrm3949>

**3. Progress and challenges in bioinformatics approaches for enhancer identification**

Dimitrios Kleftogiannis, Panos Kalnis, Vladimir B. Bajic

*Briefings in Bioinformatics* (2015-12-03) <https://doi.org/10.1093/bib/bbv101>

**4. An integrated encyclopedia of DNA elements in the human genome**

*Nature* (2012-09) <https://doi.org/10.1038/nature11247>

**5. Integrative analysis of 111 reference human epigenomes**

Anshul Kundaje, Wouter Meuleman, Jason Ernst, Misha Bilenky, Angela Yen, Alireza Heravi-Moussavi, Pouya Kheradpour, Zhizhuo Zhang, Jianrong Wang, Michael J. Ziller, ... Manolis Kellis  
*Nature* (2015-02-18) <https://doi.org/10.1038/nature14248>

**6. Genome-wide mapping of DNase hypersensitive sites using massively parallel signature sequencing (MPSS)**

G. E. Crawford

*Genome Research* (2005-12-12) <https://doi.org/10.1101/gr.4074106>

**7. Patterns of regulatory activity across diverse human cell types predict tissue identity, transcription factor binding, and long-range interactions**

N. C. Sheffield, R. E. Thurman, L. Song, A. Safi, J. A. Stamatoyannopoulos, B. Lenhard, G. E. Crawford, T. S. Furey

*Genome Research* (2013-03-12) <https://doi.org/10.1101/gr.152140.112>

**8. Discovery of Transcription Factors and Regulatory Regions Driving In Vivo Tumor Development by ATAC-seq and FAIRE-seq Open Chromatin Profiling**

Kristofer Davie, Jelle Jacobs, Mardelle Atkins, Delphine Potier, Valerie Christiaens, Georg Halder, Stein Aerts

*PLOS Genetics* (2015-02-13) <https://doi.org/10.1371/journal.pgen.1004994>

**9. Distinct and predictive chromatin signatures of transcriptional promoters and enhancers in the human genome**

Nathaniel D Heintzman, Rhona K Stuart, Gary Hon, Yutao Fu, Christina W Ching, R David

Hawkins, Leah O Barrera, Sara Van Calcar, Chunxu Qu, Keith A Ching, ... Bing Ren  
*Nature Genetics* (2007-02-04) <https://doi.org/10.1038/ng1966>

**10. Histone modifications at human enhancers reflect global cell-type-specific gene expression**

Nathaniel D. Heintzman, Gary C. Hon, R. David Hawkins, Pouya Kheradpour, Alexander Stark, Lindsey F. Harp, Zhen Ye, Leonard K. Lee, Rhona K. Stuart, Christina W. Ching, ... Bing Ren  
*Nature* (2009-03-18) <https://doi.org/10.1038/nature07829>

**11. Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies**

Nisha Rajagopal, Jason Ernst, Pradipta Ray, Jie Wu, Michael Zhang, Manolis Kellis, Bing Ren  
*G3&#58; Genes|Genomes|Genetics* (2014-08-12) <https://doi.org/10.1534/g3.114.013565>

**12. Effects on the transcriptome upon deletion of a distal element cannot be predicted by the size of the H3K27Ac peak in human cells**

Yu Gyoung Tak, Yuli Hung, Lijing Yao, Matthew R. Grimmer, Albert Do, Mital S. Bhakta, Henriette O'Geen, David J. Segal, Peggy J. Farnham  
*Nucleic Acids Research* (2016-01-06) <https://doi.org/10.1093/nar/gkv1530>

**13. Occupancy by key transcription factors is a more accurate predictor of enhancer activity than histone modifications or chromatin accessibility**

Nergiz Dogan, Weisheng Wu, Christopher S Morrissey, Kuan-Bei Chen, Aaron Stonestrom, Maria Long, Cheryl A Keller, Yong Cheng, Deepti Jain, Axel Visel, ... Ross C Hardison  
*Epigenetics & Chromatin* (2015-04-23) <https://doi.org/10.1186/s13072-015-0009-5>

**14. A Large Fraction of Extragenic RNA Pol II Transcription Sites Overlap Enhancers**

Francesca De Santa, Iros Barozzi, Flore Mietton, Serena Ghisletti, Sara Polletti, Betsabeh Khoramian Tusi, Heiko Muller, Jiannis Ragoussis, Chia-Lin Wei, Gioacchino Natoli  
*PLoS Biology* (2010-05-11) <https://doi.org/10.1371/journal.pbio.1000384>

**15. Architectural and Functional Commonalities between Enhancers and Promoters**

Tae-Kyung Kim, Ramin Shiekhataar  
*Cell* (2015-08) <https://doi.org/10.1016/j.cell.2015.08.008>

**16. A Rapid, Extensive, and Transient Transcriptional Response to Estrogen Signaling in Breast Cancer Cells**

Nasun Hah, Charles G. Danko, Leighton Core, Joshua J. Waterfall, Adam Siepel, John T. Lis, W. Lee Kraus  
*Cell* (2011-05) <https://doi.org/10.1016/j.cell.2011.03.042>

**17. Tissue-Specific RNA Expression Marks Distant-Acting Developmental Enhancers**

Han Wu, Alex S. Nord, Jennifer A. Akiyama, Malak Shoukry, Veena Afzal, Edward M. Rubin, Len A.

Pennacchio, Axel Visel

*PLoS Genetics* (2014-09-04) <https://doi.org/10.1371/journal.pgen.1004610>

**18. Reprogramming transcription by distinct classes of enhancers functionally defined by eRNA**

Dong Wang, Ivan Garcia-Bassets, Chris Benner, Wenbo Li, Xue Su, Yiming Zhou, Jinsong Qiu, Wen Liu, Minna U. Kaikkonen, Kenneth A. Ohgi, ... Xiang-Dong Fu

*Nature* (2011-05-15) <https://doi.org/10.1038/nature10006>

**19. Enhancer transcripts mark active estrogen receptor binding sites**

N. Hah, S. Murakami, A. Nagari, C. G. Danko, W. L. Kraus

*Genome Research* (2013-05-01) <https://doi.org/10.1101/gr.152306.112>

**20. Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers**

Leighton J Core, André L Martins, Charles G Danko, Colin T Waters, Adam Siepel, John T Lis

*Nature Genetics* (2014-11-10) <https://doi.org/10.1038/ng.3142>

**21. groHMM: a computational tool for identifying unannotated and cell type-specific transcription units from global run-on sequencing data**

Minho Chae, Charles G. Danko, W. Lee Kraus

*BMC Bioinformatics* (2015-07-16) <https://doi.org/10.1186/s12859-015-0656-3>

**22. Functional roles of enhancer RNAs for oestrogen-dependent transcriptional activation**

Wenbo Li, Dimple Notani, Qi Ma, Bogdan Tanasa, Esperanza Nunez, Aaron Yun Chen, Daria Merkurjev, Jie Zhang, Kenneth Ohgi, Xiaoyuan Song, ... Michael G. Rosenfeld

*Nature* (2013-06) <https://doi.org/10.1038/nature12210>

**23. TNF $\alpha$  Signaling Exposes Latent Estrogen Receptor Binding Sites to Alter the Breast Cancer Cell Transcriptome**

Hector L. Franco, Anusha Nagari, W. Lee Kraus

*Molecular Cell* (2015-04) <https://doi.org/10.1016/j.molcel.2015.02.001>

**24. VISTA Enhancer Browser—a database of tissue-specific human enhancers**

A. Visel, S. Minovitsky, I. Dubchak, L. A. Pennacchio

*Nucleic Acids Research* (2007-01-03) <https://doi.org/10.1093/nar/gkl822>

**25. Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay**

P. Kheradpour, J. Ernst, A. Melnikov, P. Rogov, L. Wang, X. Zhang, J. Alston, T. S. Mikkelsen, M. Kellis

*Genome Research* (2013-03-19) <https://doi.org/10.1101/gr.144899.112>

26. **Genome-Wide Quantitative Enhancer Activity Maps Identified by STARR-seq**  
C. D. Arnold, D. Gerlach, C. Stelzer, L. M. Boryn, M. Rath, A. Stark  
*Science* (2013-01-17) <https://doi.org/10.1126/science.1232542>
27. **High-throughput functional testing of ENCODE segmentation predictions**  
Jamie C. Kwasnieski, Christopher Fiore, Hemangi G. Chaudhari, Barak A. Cohen  
*Genome Research* (2014-07-17) <https://doi.org/10.1101/gr.173518.114>
28. **Architecture of the human regulatory network derived from ENCODE data**  
Mark B. Gerstein, Anshul Kundaje, Manoj Hariharan, Stephen G. Landt, Koon-Kiu Yan, Chao Cheng, Xinmeng Jasmine Mu, Ekta Khurana, Joel Rozowsky, Roger Alexander, ... Michael Snyder  
*Nature* (2012-09) <https://doi.org/10.1038/nature11245>
29. **A census of human transcription factors: function, expression and evolution**  
Juan M. Vaquerizas, Sarah K. Kummerfeld, Sarah A. Teichmann, Nicholas M. Luscombe  
*Nature Reviews Genetics* (2009-04) <https://doi.org/10.1038/nrg2538>
30. **DNA-dependent formation of transcription factor pairs alters their binding specificity**  
Arttu Jolma, Yimeng Yin, Kazuhiro R. Nitta, Kashyap Dave, Alexander Popov, Minna Taipale, Martin Enge, Teemu Kivioja, Ekaterina Morgunova, Jussi Taipale  
*Nature* (2015-11-09) <https://doi.org/10.1038/nature15518>
31. **DNA-Binding Specificities of Human Transcription Factors**  
Arttu Jolma, Jian Yan, Thomas Whittington, Jarkko Toivonen, Kazuhiro R. Nitta, Pasi Rastas, Ekaterina Morgunova, Martin Enge, Mikko Taipale, Gonghong Wei, ... Jussi Taipale  
*Cell* (2013-01) <https://doi.org/10.1016/j.cell.2012.12.009>
32. **JASPAR 2016: a major expansion and update of the open-access database of transcription factor binding profiles**  
Anthony Mathelier, Oriol Fornes, David J. Arenillas, Chih-yu Chen, Grégoire Denay, Jessica Lee, Wenqiang Shi, Casper Shyr, Ge Tan, Rebecca Worsley-Hunt, ... Wyeth W. Wasserman  
*Nucleic Acids Research* (2015-11-03) <https://doi.org/10.1093/nar/gkv1176>
33. **Quantifying similarity between motifs**  
Shobhit Gupta, John A Stamatoyannopoulos, Timothy L Bailey, William Noble  
*Genome Biology* (2007) <https://doi.org/10.1186/gb-2007-8-2-r24>
34. **Functional analysis of transcription factor binding sites in human promoters**  
Troy W Whitfield, Jie Wang, Patrick J Collins, E Christopher Partridge, Shelley Aldred, Nathan D Trinklein, Richard M Myers, Zhiping Weng  
*Genome Biology* (2012) <https://doi.org/10.1186/gb-2012-13-9-r50>

**35. Enhancer transcription reveals subtype-specific gene expression programs controlling breast cancer pathogenesis**

Hector L. Franco, Anusha Nagari, Venkat S. Malladi, Wenqian Li, Yuanxin Xi, Dana Richardson, Kendra L. Allton, Kaori Tanaka, Jing Li, Shino Murakami, ... W. Lee Kraus

*Genome Research* (2017-12-22) <https://doi.org/10.1101/gr.226019.117>

**36. Dynamic Chromatin Remodeling Mediated by Polycomb Proteins Orchestrates Pancreatic Differentiation of Human Embryonic Stem Cells**

Ruiyu Xie, Logan J. Everett, Hee-Woong Lim, Nisha A. Patel, Jonathan Schug, Evert Kroon, Olivia G. Kelly, Allen Wang, Kevin A. D'Amour, Allan J. Robins, ... Maïke Sander

*Cell Stem Cell* (2013-02) <https://doi.org/10.1016/j.stem.2012.11.023>

**37. Epigenetic Priming of Enhancers Predicts Developmental Competence of hESC-Derived Endodermal Lineage Intermediates**

Allen Wang, Feng Yue, Yan Li, Ruiyu Xie, Thomas Harper, Nisha A. Patel, Kayla Muth, Jeffrey Palmer, Yunjiang Qiu, Jinzhao Wang, ... Maïke Sander

*Cell Stem Cell* (2015-04) <https://doi.org/10.1016/j.stem.2015.02.013>

**38. GENCODE: The reference human genome annotation for The ENCODE Project**

J. Harrow, A. Frankish, J. M. Gonzalez, E. Tapanari, M. Diekhans, F. Kokocinski, B. L. Aken, D. Barrell, A. Zadissa, S. Searle, ... T. J. Hubbard

*Genome Research* (2012-09-01) <https://doi.org/10.1101/gr.135350.111>

**39. A Chromatin Landmark and Transcription Initiation at Most Promoters in Human Cells**

Matthew G. Guenther, Stuart S. Levine, Laurie A. Boyer, Rudolf Jaenisch, Richard A. Young

*Cell* (2007-07) <https://doi.org/10.1016/j.cell.2007.05.042>

**40. Predicting enhancer transcription and activity from chromatin modifications**

Yun Zhu, Lin Sun, Zhao Chen, John W. Whitaker, Tao Wang, Wei Wang

*Nucleic Acids Research* (2013-09-12) <https://doi.org/10.1093/nar/gkt826>

**41. GEO**

Gene Expression Omnibus

<https://www.ncbi.nlm.nih.gov/geo/>

**42. ArrayExpress**

ArrayExpress – functional genomics data

<http://www.ebi.ac.uk/arrayexpress/>

**43. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome**

Ben Langmead, Cole Trapnell, Mihai Pop, Steven L Salzberg

*Genome Biology* (2009) <https://doi.org/10.1186/gb-2009-10-3-r25>

**44. The Sequence Alignment/Map format and SAMtools**

H. Li, B. Handsaker, A. Wysoker, T. Fennell, J. Ruan, N. Homer, G. Marth, G. Abecasis, R. Durbin,  
*Bioinformatics* (2009-06-08) <https://doi.org/10.1093/bioinformatics/btp352>

**45. Picard**

Broad Institute

*GitHub* <http://broadinstitute.github.io/picard/>

**46. BEDTools: a flexible suite of utilities for comparing genomic features**

Aaron R. Quinlan, Ira M. Hall

*Bioinformatics* (2010-01-28) <https://doi.org/10.1093/bioinformatics/btq033>

**47. ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia**

S. G. Landt, G. K. Marinov, A. Kundaje, P. Kheradpour, F. Pauli, S. Batzoglou, B. E. Bernstein, P. Bickel, J. B. Brown, P. Cayting, ... M. Snyder

*Genome Research* (2012-09-01) <https://doi.org/10.1101/gr.136184.111>

**48. Identifying ChIP-seq enrichment using MACS**

Jianxing Feng, Tao Liu, Bo Qin, Yong Zhang, Xiaole Shirley Liu

*Nature Protocols* (2012-08-30) <https://doi.org/10.1038/nprot.2012.101>

**49. STAR: ultrafast universal RNA-seq aligner**

Alexander Dobin, Carrie A. Davis, Felix Schlesinger, Jorg Drenkow, Chris Zaleski, Sonali Jha, Philippe Batut, Mark Chaisson, Thomas R. Gingeras

*Bioinformatics* (2012-10-25) <https://doi.org/10.1093/bioinformatics/bts635>

**50. RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome**

Bo Li, Colin N Dewey

*BMC Bioinformatics* (2011) <https://doi.org/10.1186/1471-2105-12-323>

**51. FASTX-Toolkit**

Hannon Lab

[http://hannonlab.cshl.edu/fastx\\_toolkit/](http://hannonlab.cshl.edu/fastx_toolkit/)

**52. Fast and accurate short read alignment with Burrows-Wheeler transform**

H. Li, R. Durbin

*Bioinformatics* (2009-05-18) <https://doi.org/10.1093/bioinformatics/btp324>

**53. Seaborn: V0.7.1 (June 2016)**

Michael Waskom, Olga Botvinnik, Drewokane, Paul Hobson, David, Yaroslav Halchenko, Saulius Lukauskas, John B. Cole, Jordi Warmenhoven, Julian De Ruiter, ... Antony Lee

*Zenodo* (2016-06-05) <https://doi.org/10.5281/zenodo.54844>



**54. MakeGenecodeTSS**

Sarah Djebali

GitHub <https://github.com/sdjebali/MakeGencodeTSS>

**55. MEME SUITE: tools for motif discovery and searching**

T. L. Bailey, M. Boden, F. A. Buske, M. Frith, C. E. Grant, L. Clementi, J. Ren, W. W. Li, W. S. Noble  
*Nucleic Acids Research* (2009-05-20) <https://doi.org/10.1093/nar/gkp335>

**56. MEME-ChIP: motif analysis of large DNA datasets**

Philip Machanick, Timothy L. Bailey

*Bioinformatics* (2011-04-12) <https://doi.org/10.1093/bioinformatics/btr189>

**57. groHMM**

Minho Chae Charles G. Danko

*Bioconductor* (2017) <https://doi.org/10.18129/b9.bioc.grohmm>

**58. Visualizing data using t-SNE**

Laurens van der Maaten, Geoffrey Hinton

*Journal of Machine Learning Research* 9 (2008-11)

**59. Scikit-learn: Machine Learning in Python**

Fabian Pedregosa, Gaël Varoquaux, Alexandre Gramfort, Vincent Michel, Bertrand Thirion, Olivier Grisel, Mathieu Blondel, Gilles Louppe, Peter Prettenhofer, Ron Weiss, ... Édouard Duchesnay  
*arXiv* (2012-01-02) <https://arxiv.org/abs/1201.0490v3>

**60. Visualizing Large-scale and High-dimensional Data**

Jian Tang, Jingzhou Liu, Ming Zhang, Qiaozhu Mei

*Proceedings of the 25th International Conference on World Wide Web - WWW '16* (2016) <https://doi.org/10.1145/2872427.2883041>

**61. Scikit-Learn: 0.17.1 Release Tag For Doi**

Olivier Grisel, Andreas Mueller, Fabian Pedregosa, Lars, Alexandre Gramfort, Gilles Louppe, Peter Prettenhofer, Mathieu Blondel, Vlad Niculae, Arnaud Joly, ... Maheshakya Wijewardena  
*Zenodo* (2016-04-17) <https://doi.org/10.5281/zenodo.49911>

**62. Matplotlib: A 2D Graphics Environment**

John D. Hunter

*Computing in Science & Engineering* (2007) <https://doi.org/10.1109/mcse.2007.55>

**63. Matplotlib/Matplotlib V2.0.2**

Michael Droettboom, Thomas A Caswell, John Hunter, Eric Firing, Jens Hedegaard Nielsen, Nelle Varoquaux, Benjamin Root, Phil Elson, Darren Dale, Jae-Joon Lee, ... Nikita Kniazev  
*Zenodo* (2017-05-10) <https://doi.org/10.5281/zenodo.573577>