

GTEx data – Transition analysis

Evaluating “transitions” from cell lines to tissue:

- 2 separate comparisons:

- 1.) “cells_ebv-transformed_lymphocytes” vs “whole_blood”

n1=132 n2=445

- 2.) “cells_transformed_fibroblasts” vs “skin”

n1=306 n2=663

- 29,000 genes, filtered to 19,000 by variance
- 625 Transcription factors
- Ran pandaM, 200 null permutations per analysis

Need to map TFs back to proper identifier

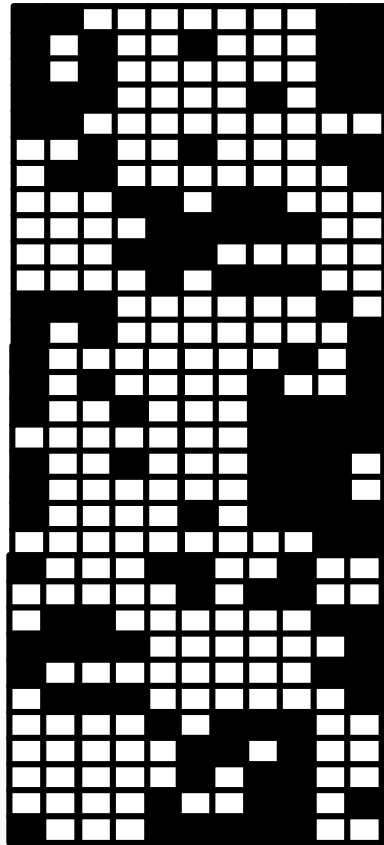
Interesting results summary:

Highly significant results... many differentially involved TFs characterize transition from cell line to tissue.

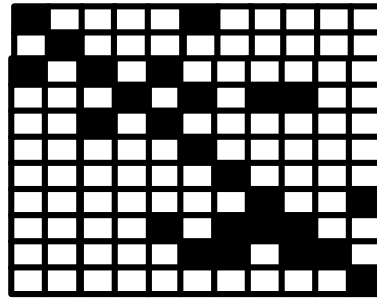
Low concordance between tissue types... the TFs defining cell line to tissue transition for skin compared to blood have little agreement.

Recall: Transition Matrix Approach

Cell line



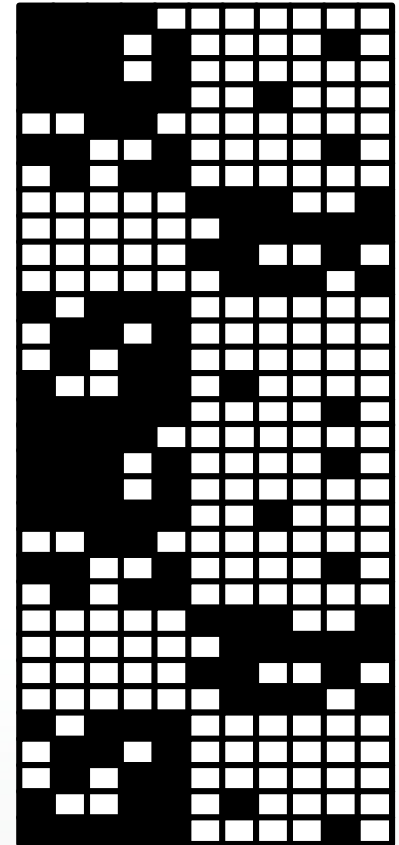
Tau



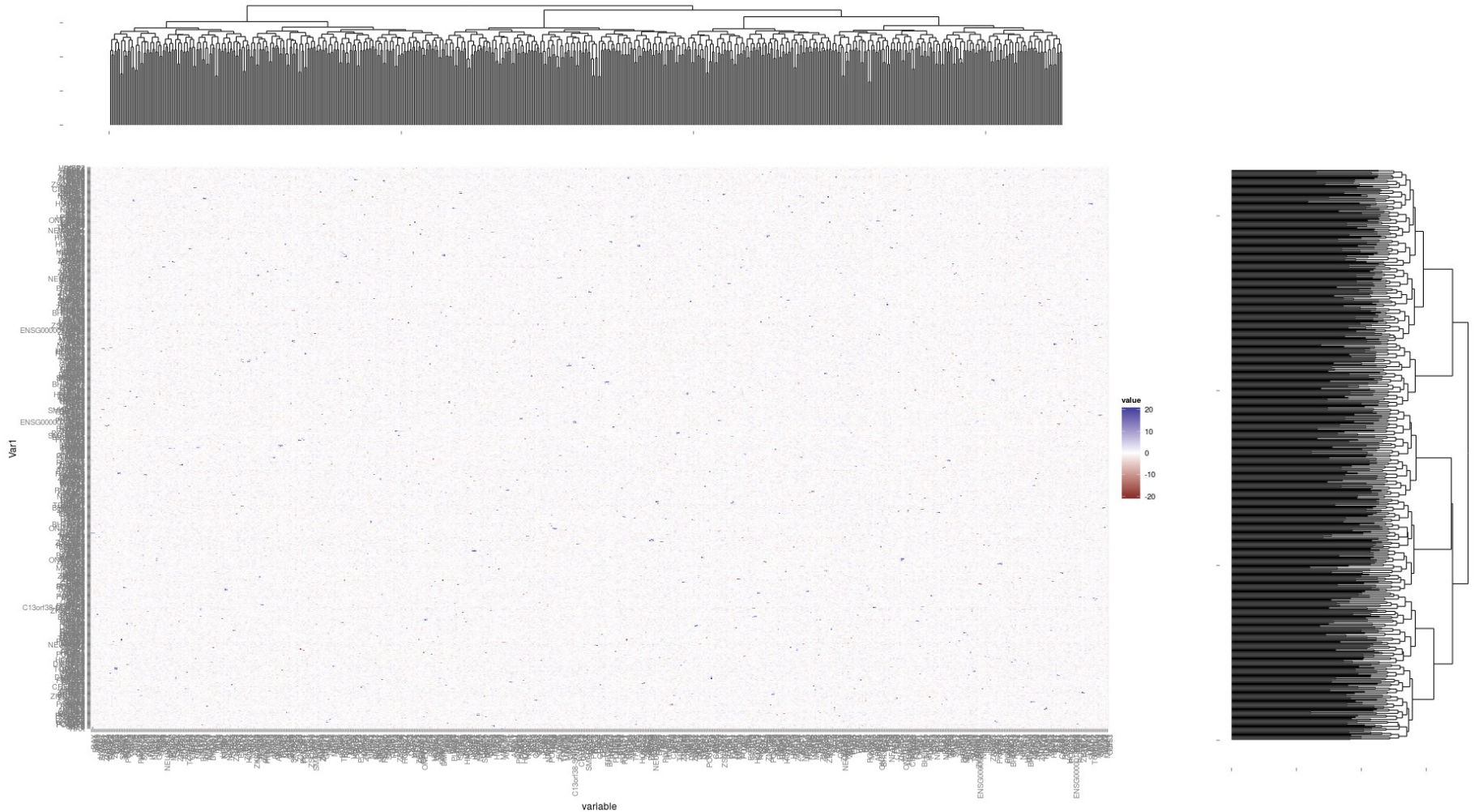
X

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Tissue

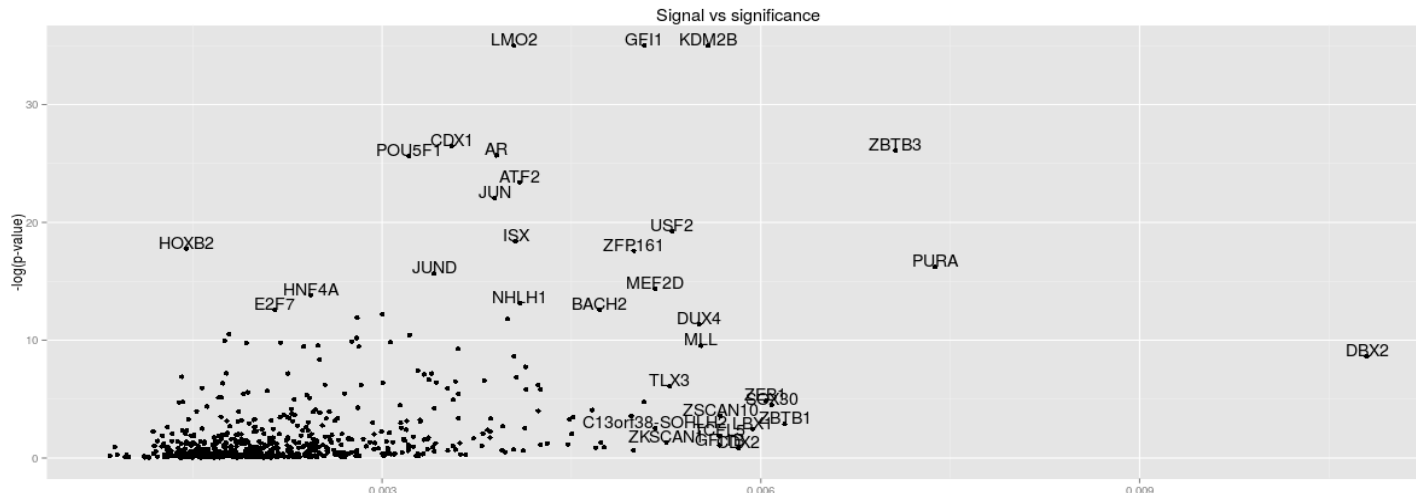


Transition matrix - Cell line to Tissue (Blood)

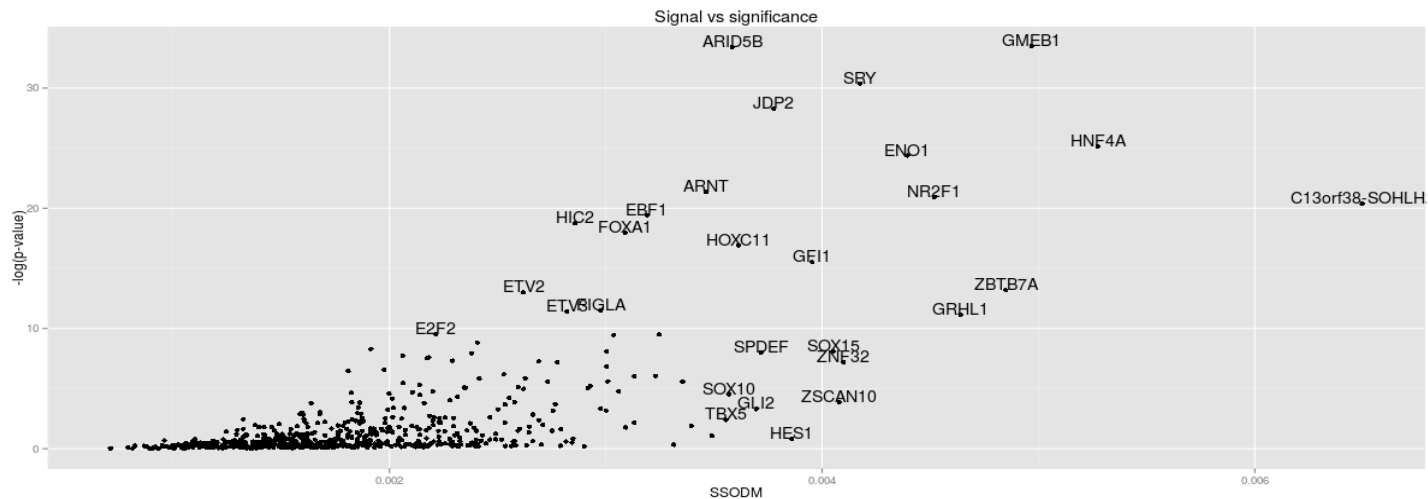


GTEx data

Highly significant results for both comparisons

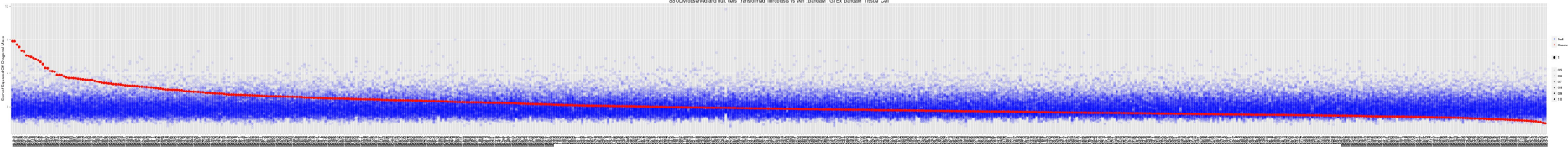


Blood



Skin

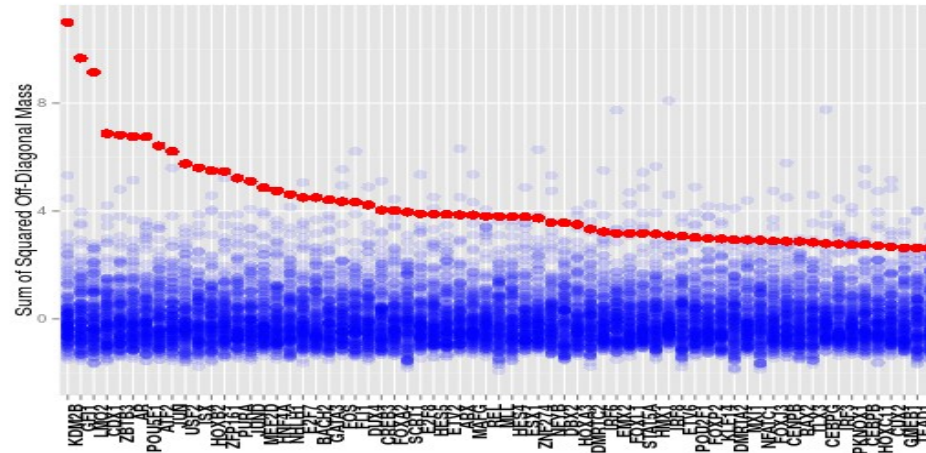
GTEx data



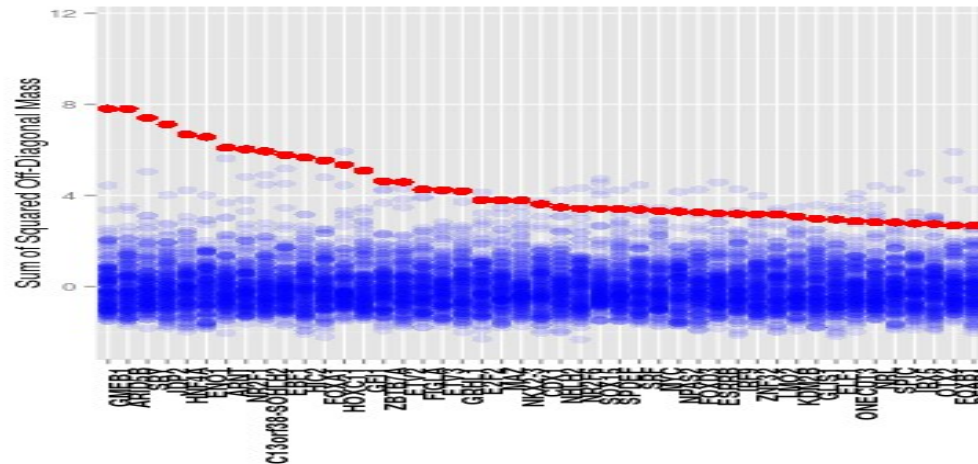
Effectively independent set
of driver TFs for blood
compared to skin.

Each analysis had >10
TFs found at $FDR < .01$

What are these TFs?



Blood



Skin

Top differentially involved TFs

Cell line to Tissue

Blood

Rank	TF	Magnitude
1	KDM2B	0.0056
2	GFI1	0.0051
3	LMO2	0.0040
4	CDX1	0.0036
5	ZBTB3	0.0071
6	AR	0.0039
7	POU5F1	0.0032
8	ATF2	0.0041
9	JUN	0.0039
10	USF2	0.0053
11	ISX	0.0041
12	HOXB2	0.0015
13	ZFP161	0.0050
14	PURA	0.0074
15	JUND	0.0034

Skin

	Magnitude
GMEB1	0.004967972
ARID5B	0.0035837379
SRY	0.0041735983
JDP2	0.0037764129
HNF4A	0.0052749029
ENO1	0.0043939602
ARNT	0.0034624085
NR2F1	0.0045191668
C13orf38-SOHLH2	0.0064960371
EBF1	0.0031899499
HIC2	0.0028565361
FOXA1	0.0030886264
HOXC11	0.0036117532
GFI1	0.0039538974
ZBTB7A	0.0048494209

Pearson correlation (all TFs) = 0.0485 (p=0.2164)

Top 15 results all significant at FDR<.01

Differential involvement, Cell line to Tissue - Skin vs Blood

