

PARALLEL SINGLE-CELL SEQUENCING LINKS TRANSCRIPTIONAL AND EPIGENETIC HETEROGENEITY

Angermueller et al., Nature Methods, January 11, 2016.
[doi:10.1038/nmeth.3728](https://doi.org/10.1038/nmeth.3728).

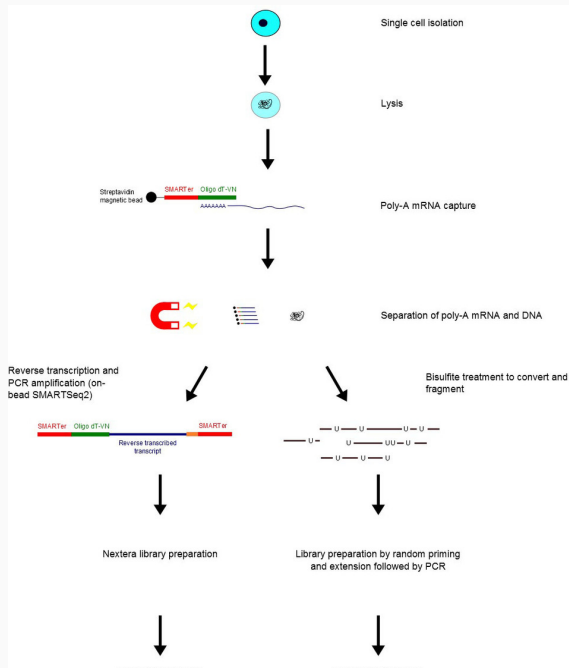
Saket Choudhary

February 11, 2016

BISC 542

scM&T-seq: Parallel single-cell genome-wide
methylation & transcriptome seq
⇒ Coupled/Uncoupled?

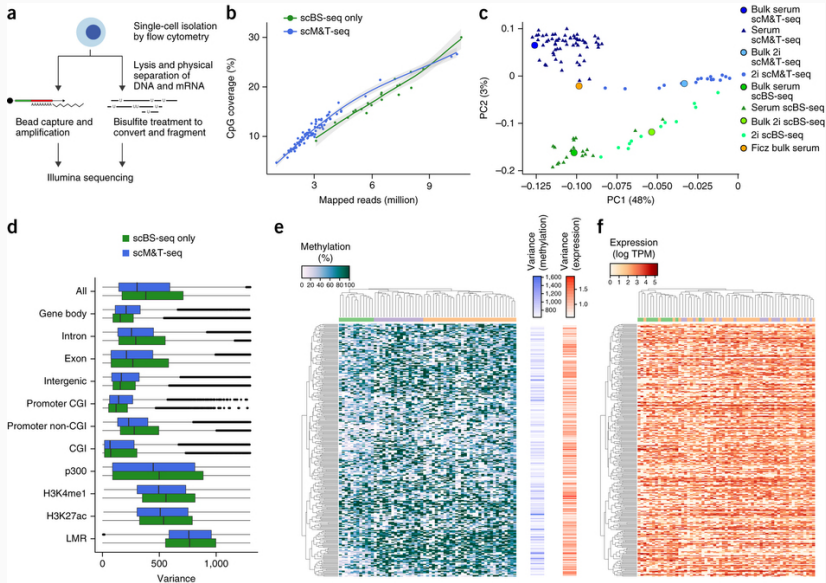
Protocol



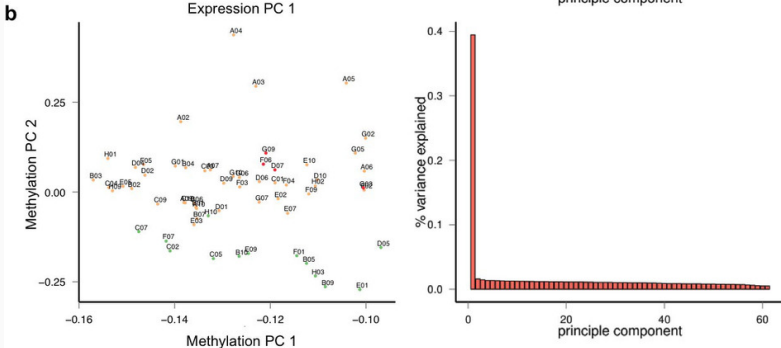
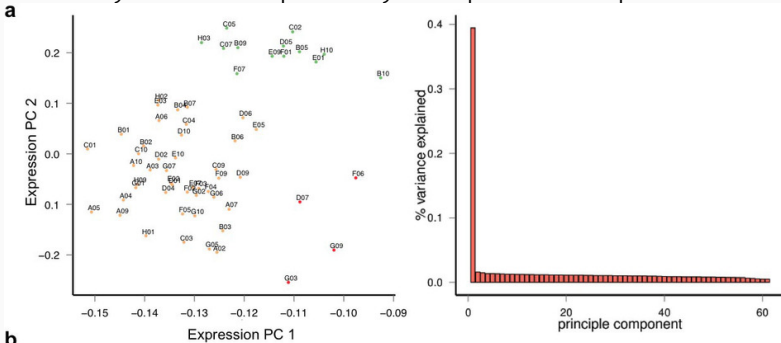
Data:

76 individual serum ESC + 16 ESCc in '2i'[induces hypomethylation]

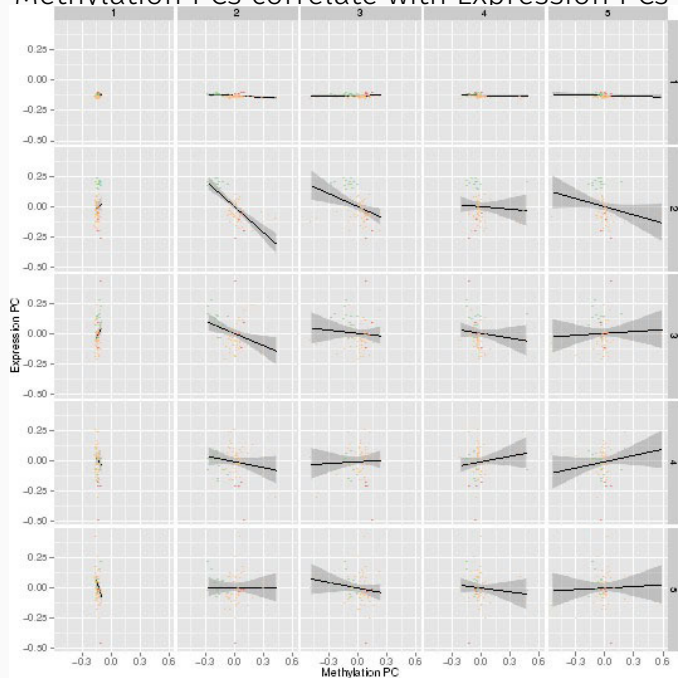
Variation in methylation levels are explained by cell type



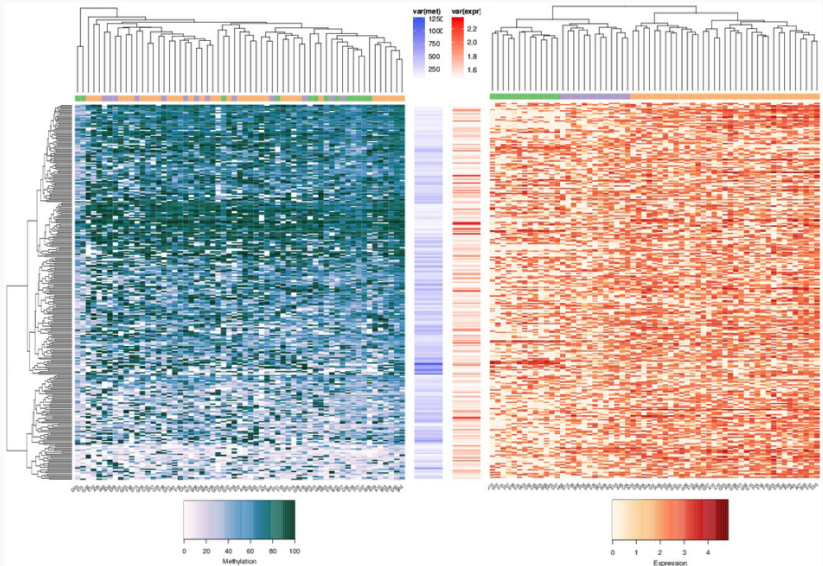
Methylation PCs partially recapitulate expression



Methylation PCs correlate with Expression PCs

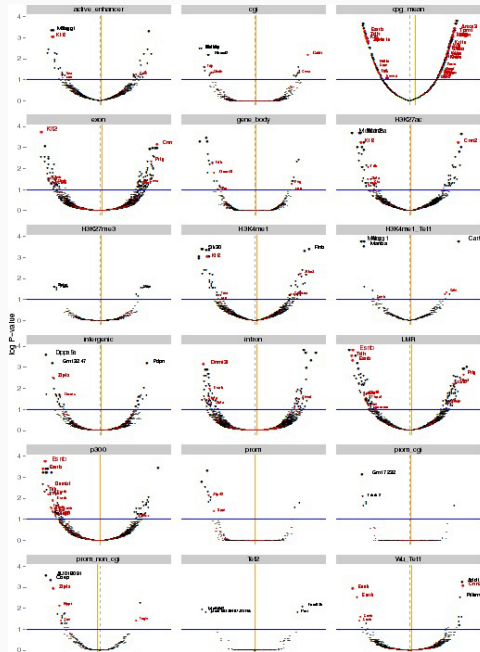


Global methylome and transcriptome profiles are complementary

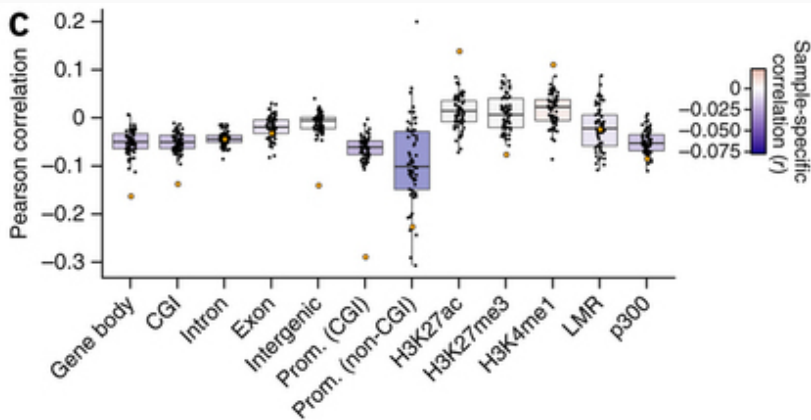


Association between expression
levels and methylation : BOTH
negative and positive \Rightarrow
Interactions are Complex!

Correlation coefficients in alternative genomic context:



Validates with bulk RNA-seq and
BS-seq[Oranges]



Insights

Transcriptome and Methylome can be
uncoupled

Insights

Association with transcription:

- v/s methylation at non-CpG island promoters :
negative (known)
- v/s methylation at distal regulatory elements :
both

Summary

- Parallel methylome & transcriptome profiling: feasible
- Associations can be quantified at single-cell level
- Fluctuating pluripotency in serum ESC \cong Epigenetic heterogeneity

References

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