Lineage-specific dynamic and pre-established enhancerpromoter contacts cooperate in terminal differentiation

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• Biological systems

epidermal differentiation in vitro (D0;D3;D6)

undifferentiated progenitor-containing cell populations (day 0)

early (day 3) late (day 6)

Data set

Hi-C (1.36 billion reads)

Promoter capture Hi-C (1.09 billion reads)

ATAC-seq

RNA-seq

ChIP-seq: KLF4 ZNF750 EHF H3K27ac

UMI-4C

model



Domain boundary contacts



		Dynamic boundary domains			
	All	Decreasing		Increasing	
	Domains	D3 vs. D0	D6 vs. D0	D3 vs. D0	D6 vs. D0
# of domains	4309	49	162	55	166
# induced genes	729 (100%)	12 (1.6%)	20 (2.7%)	15 (2.1%)	28 (3.8%)
# repressed genes	436(100%)	4(0.9%)	16 (3.7%)	5 (1.1%)	19 (4.4%)

Domain boundary contacts were stable during differentiation Regulatory dynamics occur via intra-domain contacts

E-P contacts reside in TADs



CHi-C identified 207,663 enhancer–promoter contacts and 89,752 promoter–promoter contacts

Both P-P and E-P contacts were largely restricted to single domains

Contact changes



3,575 increased E-P contacts (>2-fold: 1,975) 3,207 decreased E-P contacts (>2-fold: 1,481)



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Contact changes and expression

		Intacts			
	All	Decreasing		Increasing	
	Contacts	D3 vs. D0	D6 vs. D0	D3 vs. D0	D6 vs. D0
# of contacts	89711	905	2686	1107	2856
# induced genes	898 (100%)	40 (4.5%)	94(10.5%)	77 (8.6%)	205 (22.8%)
# repressed genes	605 (100%)	47 (7.8%)	95 (15.7%)	24 (4.0%)	75 (12.4%)

Contact enrichment based on promoter expression status



global bias

increased contacts - differentiation-induced genes, reduced contacts - differentiation-repressed genes



epidermal differentiation terms

Gene set: Lost EP contact, Repressed expression



progenitor state, such as proliferation

Induced genes engage in stable E-P contacts



tissue-invariant structural contacts form a universal architecture that guides tissue-specific enhancer–promoter interactions ??



differentiation genes within each category of E-P contacts had similar GO terms



GS or G genes exhibited more lineagespecific expression than S-only genes

enhancer chromatin state; E-P contact; gene expression



Number of dynamic H3K27ac enhancers

gene induction ~ number of H3K27ac-gained enhancers

multiple classes of enhancers with distinct H3K27ac dynamics interact with a gene, not only to provide regulatory robustness but also to increase the magnitude of gene induction.



Lineage specificity of induced gene-linked enhancers

log2 FC

(n=1623)



stable enhancers and H3K27ac-gained enhancers were specifically marked by H3K27ac in keratinocytes

Some somatic E–P contacts is established after pluripotency but before induction of terminal differentiation genes



both gained and pre-established enhancer–promoter contacts associated with differentiation genes showed significant reduction in signal in hESCs relative to kerationcytes, unlike the tissue-invariant contacts described in the mouse Hox loci.

chromatin state activation and contact dynamics



gain of H3K27ac at an enhancer or promoter was associated with significant increases in contact strength



chromatin state activation and contact dynamics



Pre-established E-P contacts are associated with premarked H3K27ac and constitutive cohesin binding at enhancers

E–P contacts acquired in differentiation are associated with enhancers that gain H3K27ac and lack cohesin.

Gained enhancers and TFs





KLF4 binding was enriched at enhancers that acquired H3K27ac and depleted at enhancers that lost H3K27ac



frequently overlapped super-enhancers

TF motif enrichment in gained enhancers

KLF4/ZNF750 contribute to enhancer activation and expression



Depletion of either factor impaired acquisition of H3K27ac at regions bound by these factors

transcription factor depletion altered epidermal differentiation but did not alter epidermal identity

KLF4/ZNF750 influence E-P contacts



Depleting KLF4 or ZNF750 decreased contact strength. ft

function at a subset of enhancers targeting induced genes

Stable enhancers and TFs



Motif family	% sites	P value	Motif
ETS	26.96	1×10^{-243}	202TT202
MYB	35.59	1 × 10 ⁻⁷⁶	G&C&GTT&
E2F	21.87	1×10^{-68}	SCCCCCCAAAA
PRDM1	11.76	1 × 10 ⁻⁵⁰	ACTITCACITAS

Why not these fators





EHF expression was largely stable during differentiation

The EHF ETS-family transcription factor showed the most lineage-specific expression in stratified epithelia

EHFi





Gene

desert 1

ECM1

D0 lgG

D0 EHF

D3 lgG

D3 EHF

Gene

desert 2

EHF is required both for induction of differentiation-related genes and for repression of ectopic gene expression.

EHF-bound, H3K27ac-premarked enhancers generally engaged in stable contacts with differentiation-associated genes

EHF ChIP-qPCR

EHFi



EHF regulates gene expression in a manner distinct from KLF4 and ZNF750

Summary

		WT	EHFi
	regulator	EHF (stable expressed)	
	contact	stable	not affected
stable E-P	H3K27ac	stable	not affected
	differentiation-induced genes	induced	reduced
	cohesin colocalized	Yes	
		WT	KLF4i;ZNF750i
	regulator	KLF4;ZNF750 (induced)	
	contact	gained	reduced
gained E-P	H3K27ac	gained	reduced
	differentiation-induced genes	induced	reduced
	cohesin colocalized	Yes	



Progenitor cells partially pre-establish a regulatory apparatus that is fully engaged in terminal differentiation.

comments

- the differentiation-repressed genes ? (contact loss)
- CTCF-mediated loop changes, relation with gene expression? relation with TF-mediated E-P interaction?
- Casual relation of looping and expression changes? (editing some enhancer region)

THANK YOU