

Overview of the Registry of cREs & SCREEN

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Creating the Registry of cREs

1. Defining representative DNase hypersensitivity sites (rDHSs)



Mouse:

For this analysis, we adapted the DNase master peak script by Bob Thurman in John Stam's lab

Creating the Registry of cREs

- Defining representative DNase 1. hypersensitivity sites (rDHSs)
- 2. Filter & classify rDHSs using DNase, H3K4me3, H3K27ac, and CTCF signals



204,749

Genomic Coverage of cREs



Cell Type Specific Classification: Two Models

9 States



- For each cell type, we classify cREs with DNase Z-score < 1.64 as inactive (if DNase is available)
- The remaining cREs fall into 8 states based on if the Z-scores for H3K4me3, H3K27ac, or CTCF are > 1.64
- For example, a cRE with the grey-yellow-grey-green combination of colors would have H3K27ac & DNase Z-scores > 1.64 and H3K4me3 & CTCF Z-scores ≤ 1.64



Cell Type Specific Classification: Relating Models



Cell Type Specific Classification: Visualization

9 States





5 Groups

Additional Analysis Using cREs (From Manuscript)

- Enrichment of cREs in complementary data (i.e. cREs with promoter-like signatures are enriched in POL2 signal)
- Cell type clustering
- Use Cases:
 - Correlation of expression & cRE activity in Limb at Ogn locus during development
 - Fine mapping multiple sclerosis variant and identifying a new potential target gene
 - Fine mapping schizophrenia variants using orthologous human and mouse cREs

SCREEN overview (recap): three perspectives cRE / locus-centric Search View

1) enter search keywords (genes, coordinates, SNPs...)

rs3			
rs305668	80		
rs306178	25		
rs314719	51		
rs324126	63		
rs326812	67		
rs367896	724		
rs369606	208		
rs372841	554		
rc27/020	747		

2) use facets to filter search results; click result for details

Cell types 🕄				Chromosom	A				
cell type	Search: Hel	.a tissue ↓1		chr13				\otimes	
HeLa-S3		cervix		Coordinates	: chr13:3	2444841-3244	8842 🕄		
HeLa-S3 G11	o phase	cervix		3	2444841	-	32448842		
accession € ↓↑	H3 K562 3	K4me3 H Z ↓↑	H3K27ac Z ↓↑	CTCF Z	chr↓î	start ↓î	length 1	near protein	est genes: -coding / all
EH37E1091086 ★P		3.65	0.36	0.08	chr11	13,298,849	607	pc: ARN all: ARNTL	TL, BTBD10, PTH , RN7SKP151, CTC 497E21.5
EH37E1090291 ★P		5.84	4.24	1.32	chr11	6,502,226	750	pc: ARFIP2, all: ARFIP2,	TIMM10B, TIMM10 TIMM10B, TIMM10
Senes within TAD	0				Ж. г	500 bases		hg19	
symbol						5,391,000 gene	neral cREs (9 state ral cREs (9 state)	5,391,500 e) CTCF H3K27ac	
AC025300.1 TFs	that bind this	s cRE 📵				gene cREs in	ral cREs (9 state) K562 by high DNas	H3K4me3 e (9 state)	
AC084859.1 facto	or ↓↑	# of experin binding	nents that s	upport TF		CRES in CRES in CRES in	K562 by high H3K4a K562 by high H3k27 h <mark>K562 by high CTC</mark>	e3 (9 state) Mac (9 state) F (9 state)	
RNTL	P2A	36				ENC	F686NUN Signal DN	ase K562	
3TBD10 EZH	2	12				ENCFF	-689ТМV Signal H3K-	4me3 K562	
SP1		7			Γ	ENCFY	"000BWY Signal H3k	27ac x562	
FOS	i	7				ENC	PP BUBYRH Signal CT	CPI K562	

SCREEN overview (recap): three perspectives Gene-centric View

Choose sort order: by value

1) RNA-seq: human and mouse gene expression app, cRE details



2) RAMPAGE: human only *cRE details*

Transcript: ENST00000298386.2 V + UCSC chr13:32313679-32313679 (+) protein coding



3) Differential Expression: mouse only *self-contained app*



SCREEN overview (recap): three perspectives SNP-centric GWAS View

1) select study

Search: inflammatory		
👫 Author 👫 Pub	med 🌡	
ory bowel disease Jostins 2312	23128233	
bry bowel disease Liu 2619	26192919	
ory skin disease Baurecht 255	74825	
# of LD blocks overlapping cREs # of overlapp	ing cREs	
# of LD blocks overlapping cREs # of overlapping cREs 106 (97%) 1205	pp	

 browse cREs intersecting LD blocks from study by cell type

	Ce	II Туре	17	p ↓	FDR	11	
	T-o ye	cell male adult (3 ⁻ ars)	7	3.1e-17	4.2e-1	5	
	C	04-positive helper	r T cell	2.2e-16	1.5e-14	4	
	C	04-positive helper	r T cell	2.7e-15	1.2e-13	3	
	pe mo	ripheral blood ononuclear cell		5.2e-15	1.8e-13	3	
accessio	n 💷	T-cell male adult (37 years)	H3K4me3 Z ↓	H3K27ac	DNase Z	SNPs	↓t gene ↓t
EH37E108	9569		6.81	3.62	1.934	rs11041476	LSP1
EH37E125	0115		6.22	4.54	3.772	rs2617434	LNPEP
EH37E108	1006		6.15	4.37	3.401	rs306587	MAP3K8
EH37E125	0117		5.98	3.41	2.545	rs3842058	CTD- 2260A17.2

New since last update: UCSC browser configuration



click and drag selected cell types with handles to change order of tracks in the browser

New since last update: UCSC buttons for transcripts

RNA-seq

OR51B6 UCSC **OR51B6** ENSG00000176239.7 ENSG00000176239.7 (18,402 bases from cRE) This plot is displaying cell-wide expression of OR51B6. To view expression in d Transcript: ENST00000380219.1 ▼ ↑↓ UCSC Choose sort order: by expression (TPM) Data: TPI chr11:5372738-5372738 (+) protein coding . **Tissue of origin Tissue of origin** brain blood connective tissue heart 0.33 cardiac muscle cell skin extraembryonic structure 0.15 umbilical cord esophagus 0.0144 esophagus squamous epithelium (-) strand ESC blood 0.09 K562 0 H7-hESC (+) strand ESC 0 H7-hESC (-) strand brain 0.05 bipolar spindle neuron adinaga liver 0.04 liver blood 0.03 GM12878 eve 0.03 camera-type eye fat 0.02 omental fat pad 0.02 cardiac muscle cell heart liver 0.02 HepG2 blood 0.01 K562 bronchus 0 bronchial smooth muscle cell

RAMPAGE

Choos

0.0346

0.0256 HT1080 (-) strand

0.0226 SK-MEL-5 (-) strand

New since last update: summary symbols

Available data types by cell type

A172	brain	
A549	lung	
A549 treated with dexamethasone	lung	
A549 treated with ethanol	lung	
A673	muscle	
ACC112	salivary glands	

search results table: P/D (proximal/distal), concordant support star, Z-scores by data type



key below search results table

New since last update: new tutorials on homepage



cRE details

OREEN NUEP						Seith 1	* Bi			
Accession	and Search Results	(PE Details								
Ready Ready # EndTaintian	EH37E1090	EH37E1090139 west5.585.09.585.585.99 + • •								
California ()	Nearby Genes	Nearby Genes 0 Nearby cR			try cREs O Newby Sh			* 0		
Containt to	CEV Sead					494	Seeth			
Seath	symbol	T. monte		IT distance	- B.	-	I deserve	B.		
and type II. Broken II.	160			419		+++2723 better	11	were .		
a Aura bran	E 1400	4.000		1,470		10003709	110	14.94		
				1411						
- A549	Addres .	8,205	for demodal.			101010-0480	345	ALC: NO		

- six tutorials
 - main search
 - results table, cart, browser
 - cRE details
 - gene expression
 - differential expression
 - GWAS
- hosted on SCREEN YouTube channel
 - <u>https://www.youtube.com/channel/</u> <u>UCFX89WFjvf-1NCj_4mVObRg</u>