Encyclopedia Update

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Part I – Visualizer 4 Alpha

Alpha release

Try it out!

http://zlab-annotations-v4.umassmed.edu/

- Please send comment/problems/suggestions to purcaro@gmail.com
 - Need more visualization ideas!
- Alpha version
 - Has rankings for 3 cell types (HeLa-S3, GM12878, K562)
 - UCSC Genome Browser visualization
 - Has heatmaps for ranks and gene expression
 - Venn diagrams to compare rank similarity between cell types
 - Shopping cart to group and visualize subsets of results

Visualizer 4 Alpha: Results Page

Candidate RE Viz (alpha version) hg19	HeLa-S3 chr14:	35792756-35	319812				Search	e encode
Assembly	Candidate R	E Search	Nearby Gene E	xpression	Comparison			
hg19 🛞		• entries	o to rt	and				
Cell types	accession EE4140684	-log(p) chr 324.0 chr	start 14 35,799,625	end 35,799,775	nearest gene	nearest protein-coding gene		genome browsers
HeLa-S3	EE4140004	524.0 CIII	14 35,799,025	55,799,775	FSIMAU	FSIMAU	je je	UCSC WashU Ensembl
Chromosome	EE0172427	324.0 chr	14 35,800,980	35,801,130	PSMA6	PSMA6	Ê	UCSC WashU Ensembl
chr14 🛞	EE2849498	324.0 chr	14 35,801,420	35,801,570	PSMA6	PSMA6	Æ₽	UCSC WashU Ensembl
Coordinates	EE4140654	324.0 chr	14 35,802,300	35,802,450	PSMA6	PSMA6	Ê	UCSC WashU Ensembl
coordinates: 35792756 - 35819812	EE1256909	324.0 chr	14 35,803,160	35,803,310	PSMA6	PSMA6	Ê	UCSC WashU Ensembl
	EE3523940	324.0 chr	14 35,803,625	35,803,775	PSMA6	PSMA6	Ê	UCSC WashU Ensembl
TF peak intersection	EE3523944	324.0 chr	14 35,804,640	35,804,790	PSMA6	PSMA6	Ê	UCSC WashU Ensembl
Enter TF:	EE1257002	324.0 chr	14 35,804,800	35,804,950	PSMA6	PSMA6	Ê	UCSC WashU Ensembl
Distance to Genes	EE4111457	324.0 chr	14 35,805,005	35,805,155	PSMA6	PSMA6	Ê	UCSC WashU Ensembl
Facets for:		0 cł	Results t	able:			Ê	UCSC WashU Ensembl
Genome)9 entr			ndidate RI	Es in region		
Cell types			• Ge		rowser lin	ks	7 Next	
Genomic position			0	UCS	-			
Candidate RE	root acr					J + Ensembl		
 Distance to nea Ranks 	irest gene			eresting	cart links t results	o group		4

Visualizer 4 Alpha: Candidate RE Details

Candidate RE Viz (alpha version)	hg19 H	g19 HeLa-S3 chr14:35792756-35819812							Æ	ENCODE
Assembly		Candidate RE Search	RE Details	Nearby	Gene Expr	ession	Comparison			
hg19	\otimes	EE41406	84							
Cell types										
HeLa-S3	\otimes	Top-ranked cell type	es		Nearest	genes		Nearest	SNPs	
Chromosome		promoter-like: K562 enhancer-like: K562 DNase: GM128 CTCF: K562	GM12878 HeL GM12878 HeL 78 K562 HeL GM12878 HeL	<mark>a-S3</mark> a-S3	symbol RALGAP/ IGBP1P1 EAPP	A1	distance (bp) 207,933 390,082 790,859	symbol rs5679132		distance (bp) 3
chr14 Coordinates	\otimes	CTCF. 1302	GM12070 HEL	a-33	PTCSC3 MBIP		805,689 968,145			
coordinates: 35792756 - 35819812	- ib-41	Nearest candidate F			Intersec	• •		Intersect	ting histor	
		EE1595817 37	stance (bp) 2,535		K562	KAT2B, 1	1 CHD7, 1 WHSC1, 1 NCOR1, 1 ZBTB33, 1	HepG2	H3K4me1,	ne1, 1 H3K4me2, 1 , 1 H2AFZ, 1 H3K27me3
TF peak intersection			381,145 383,185		H1-bESC	1 HDAC2	SETDB1, 1 CREBBP , 1 SIRT6, 1 CHD7, 1	A549		2, 1 H3K4me1, 1 1 H2AFZ, 1 H3K36me3
Enter TF:			923,875 933,745		osteoblas	HDAC6, 1	I SUZ12, 1 EP300	keratinocy K562	H3K36me 1 H4K20m	ne1, 1 H3K9me3
Distance to Genes								GM12878	1 H4K20m	ne1, 1 H3K9ac
Ranks										

Candidate RE shopping cart

Candidate RE Viz (alpha version)

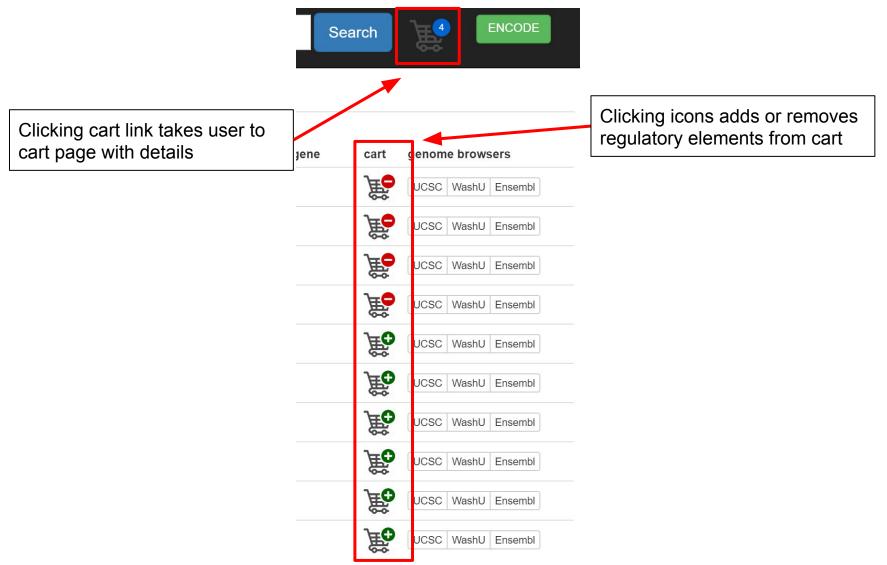
hg19 HeLa-S3 chr14:35792756-35819812





Assembly	Candidate RE Search			learby Gene E	xpression	Comparison		
hg19 🛞	Show 10	• entrie	S					\land
Cell types	accession	-log(p)	chr	start	end	nearest gene	nearest protein-coding gene	cart genome browsers
HeLa-S3	EE4140684	324.0	chr14	35,799,625	35,799,775	PSMA6	PSMA6	UCSC WashU Ensembl
	EE0172427	324.0	chr14	35,800,980	35,801,130	PSMA6	PSMA6	UCSC WashU Ensembl
Chromosome	EE2849498	324.0	chr14	35,801,420	35,801,570	PSMA6	PSMA6	
Coordinates	EE4140654	324.0	chr14	35,802,300	35,802,450	PSMA6	PSMA6	
coordinates: 35792756 - 35819812	EE1256909	324.0	chr14	35,803,160	35,803,310	PSMA6	PSMA6	UCSC WashU Ensembl
	EE3523940	324.0	chr14	35,803,625	35,803,775	PSMA6	PSMA6	UCSC WashU Ensembl
TF peak intersection	EE3523944	324.0	chr14	35,804,640	35,804,790	PSMA6	PSMA6	CSC WashU Ensembl
Enter TF:	EE1257002	324.0	chr14	35,804,800	35,804,950	PSMA6	PSMA6	CSC WashU Ensembl
Distance to Genes	EE4111457	324.0	chr14	35,805,005	35,805,155	PSMA6	PSMA6	UCSC WashU Ensembl
Ranks	EE0385318	324.0	chr14	35,805,740	35,805,890	PSMA6	PSMA6	

Candidate RE shopping cart



Candidate RE shopping cart: details page

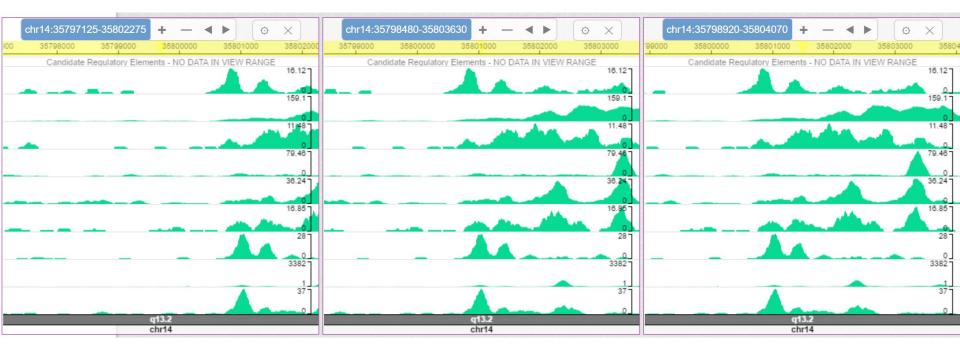
Candidate RE V	Search ENCODE						
Summary							
Compare in Was	shU			alize in Wasl browsers to			
accession	-log(p)	chr	start	end	nearest gene	nearest protein-coding gene	genome browsers
EE2849498	324.0	chr14	35,801,420	35,801,570	PSMA6	PSMA6	UCSC WashU Ensembl
EE4140654	324.0	chr14	35,802,300	35,802,450	PSMA6	PSMA6	UCSC WashU Ensembl
EE0172427	324.0	chr14	35,800,980	35,801,130	PSMA6	PSMA6	UCSC WashU Ensembl
EE4140684	324.0	chr14	35,799,625	35,799,775	PSMA6	PSMA6	UCSC WashU Ensembl

Showing 1 to 4 of 4 entries



Data table shows summary details displayed on search results page

WashU browser visualization



TODOs

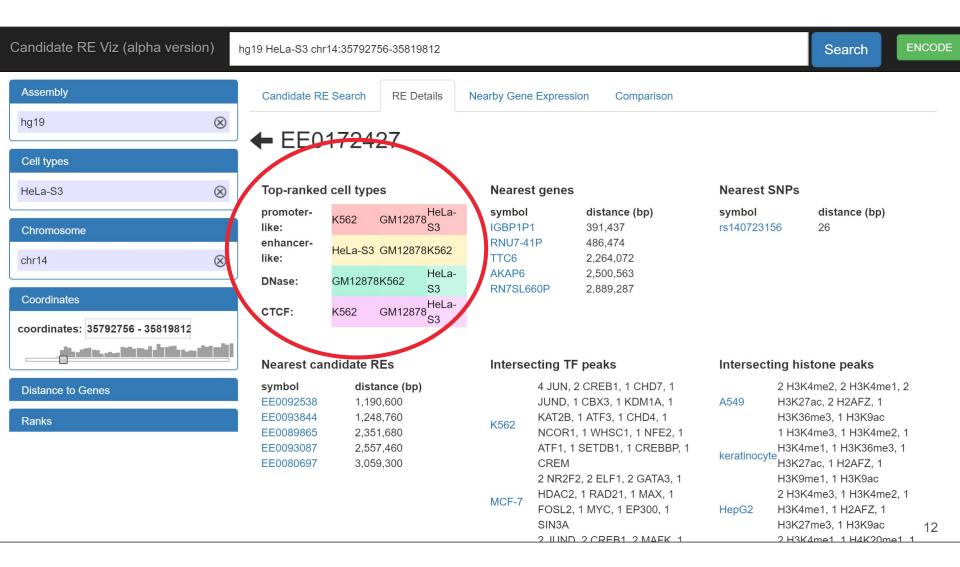
- Add more cell types
- Incorporate TF data
- More visualizations!
 - Self-organizing maps? (Sheffield, et., Genome Res 2012)

Candidate RE Viz (alpha version)	hg19	HeLa-S3 chr14:	35792756-	-358198	12				Search	ENCODE
Assembly		Candidate F	RE Search	Nea	arby Gene Exp	ression Co	mparison			
hg19	\otimes	Show 10	• entries							
Cell types		accession	-log(p)	chr	start	end	nearest gene	nearest protein-coding g		genome browsers
HeLa-S3	\otimes	EE4140684	324.0	chr14	35,799,625	35,799,775	PSMA6	PSMA6	Ê	UCSC WashU Ensemb
Chromosome		EE0172427	324.0	chr14	35,800,980	35,801,130	PSMA6	PSMA6	ĴÊ c	UCSC WashU Ensemb
chr14	\otimes	EE2849498	324.0	chr14	35,801,420	35,801,570	PSMA6	PSMA6)É c	UCSC WashU Ensemb
Coordinates		EE4140654	324.0	chr14	35,802,300	35,802,450	PSMA6	PSMA6	Ê	UCSC WashU Ensemb
coordinates: 35792756 - 35819812		EE1256909	324.0	chr14	35,803,160	35,803,310	PSMA6	PSMA6	ĴÊ ĉ	UCSC WashU Ensemi
		EE3523940	324.0	chr14	35,803,625	35,803,775	PSMA6	PSMA6	ĴÊ ĉ	UCSC WashU Ensemi
TF peak intersection		EE3523944	324.0	chr14	35,804,640	35,804,790	PSMA6	PSMA6	ĴÊ ĉ	UCSC WashU Ensemi
Enter TF:		EE1257002	324.0	chr14	35,804,800	35,804,950	PSMA6	PSMA6	ĴÊ ĉ	UCSC WashU Ensemi
✓ ctcf		EE4111457	324.0	chr14	35,805,005	35,805,155	PSMA6	PSMA6	ĴÊ ĉ	UCSC WashU Ensemb
Distance to Genes Ranks		EE0385318	324.0	chr14	35,805,740	35,805,890	PSMA6	PSMA6	Ê	UCSC WashU Ensemt
- Hallio		Showing 1 to 1	0 of 69 en	tries			Dest			

Previous **1** 2 3 4 5 6 7 Next

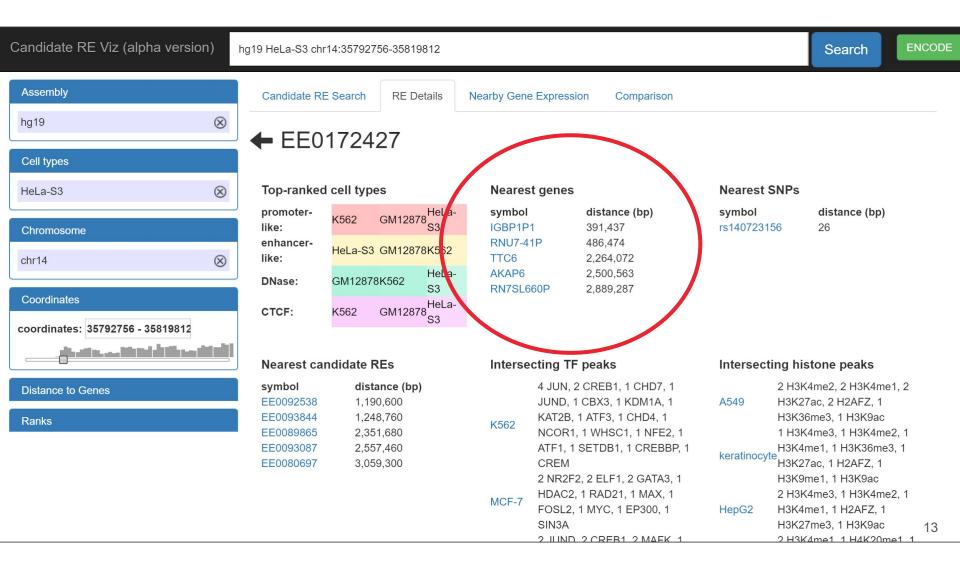
TODO (After discussions w/ Ross Hardison, Barbara Wold, and Ben Hitz)

• Convert rank table to heatmap across all cell types (or tissues...)



TODO (After discussions w/ Ross Hardison, Barbara Wold, and Ben Hitz)

• Use consensus TAD calls to filter nearest genes?



TODO (After discussions w/ Ross Hardison, Barbara Wold, and Ben Hitz)

• Gene expression should use hierarchical clustering

Candidate RE Viz (alpha version)	hg19	HeLa-S3 chr14:35819812-3	Search	Æ0	ENCODE		
Assembly		Candidate RE Search	Nearby Gene Expression	Comparison			
hg19	\otimes						
Cell types				ع∓مەم±¢	9600		
HeLa-S3	\otimes			0006704 010072 148384.	148404. 148672. 148942. 149571. 110429. 110429.		
Chromosome					(600001488 (6000001488 (6000001488 (6000001108 (6000001108		
chr14	\otimes		aortio	دیمن ۵۵ می یک ۲۵ می smooth muscle cell (ENCSR000AAA, rep1) cular endothelial cell (ENCSR000AAB, rep1)			
Coordinates			smooth m bro bronchia	uscle cell of bladder (ENCSR000AAC, rep1) prchial epithelial cell (ENCSR000AAD, rep1) I smooth muscle cell (ENCSR000AAE, rep1)	11		
coordinates: 35819812 - 35819812		nasal cavity resp	endothelial c smooth muscle cell o regu dermis blood v dermis lymphatic v dermis microvascular lymphatic v iratorv eoithelial cell of vi	ell of coronary artery (ENCSR000AAF, rep1) f the coronary artery (ENCSR000AAG, rep1) ular cardiac myocyte (ENCSR000AAH, rep1) ressel endothelial cell (ENCSR000AAI, rep1) essel endothelial cell (ENCSR000AAJ, rep1) scerocranial mucosa (ENCSR000AAL, rep1) tery endothelial cell (ENCSR000AAM, rep1)	ł.		
TF peak intersection Enter TF:			lung microvas renal c tr smooth m	cular endothelial cell (ENCSR000AAP, rep1) cortical epithelial cell (ENCSR000AAQ, rep1) acheal epithelial cell (ENCSR000AAQ, rep1) uscle cell of trachea (ENCSR000AAS, rep1)	н.		
Distance to Genes Ranks			epithelial c smooth muscle cell o uterine	ell of umbilical artery (ENCSR000AAT, rep1) f the umbilical artery (ENCSR000AAU, rep1) e smooth muscle cell (ENCSR000AEC, rep1) GM12878 (ENCSR000AEC, rep1) GM12878 (ENCSR000AEE, rep1) GM12878 (ENCSR000AEE, rep1) GM12878 (ENCSR000AEF, rep1) GM12878 (ENCSR000AEF, rep1)	11		

Part II – Linking Candidate REs with Genes

Discussion at ENCODE Meeting

What Genes Might Be Regulated by This Element?

Physical connectivity between elements and genes should be presented as part of the third layer (?)

The question of regulatory implications of a physical connection is key for our users, but not yet easy for us to arbitrate. How to handle? Call them EL0000n (Encode Link) or El0000n (Encode Interaction)?

We therefore aim to provide all evidence for a given regulatory element (and vice versa for a gene) along with its statistical significance. How much of this is ready to go into version 1 of encyclopedia?

Explicitly state the type of evidence per element: chromatin interactions, eQTLs, or functional assays (knock-out)

Creating Gene Links: Proposed Plan



Evidence supporting link:

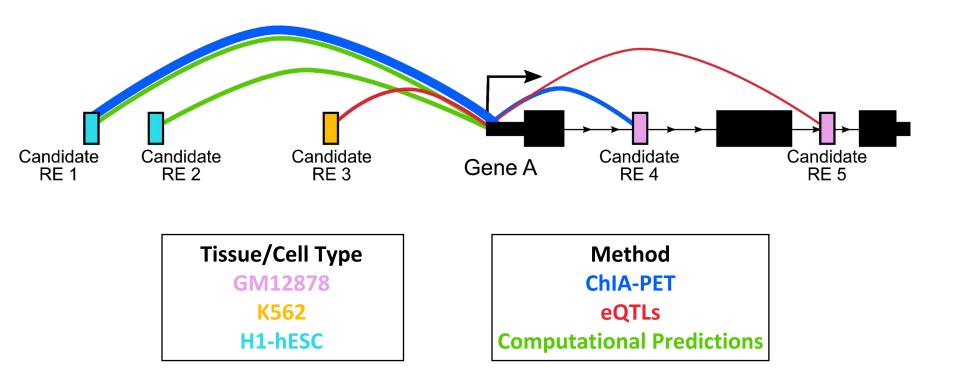
Method	Tissue/Cell Type	Confidence Score
CTCF ChIA-PET	GM12878	56.8
eQTLs	Whole blood	4.5
Computational Prediction	GM12878	10.3

Creating Gene Links: Proposed Plan

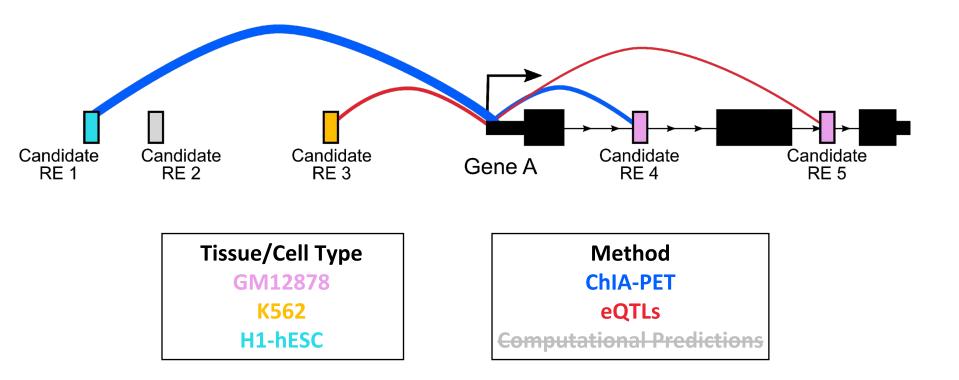
- Users can search for links using candidate RE or gene
- Users will be able to select facets to filter their results. Such facets will include:
 - Cell type
 - Linking method (ChIA-PET, eQTLs, computation predictions etc.)
 - Confidence of link

Visualization Ideas

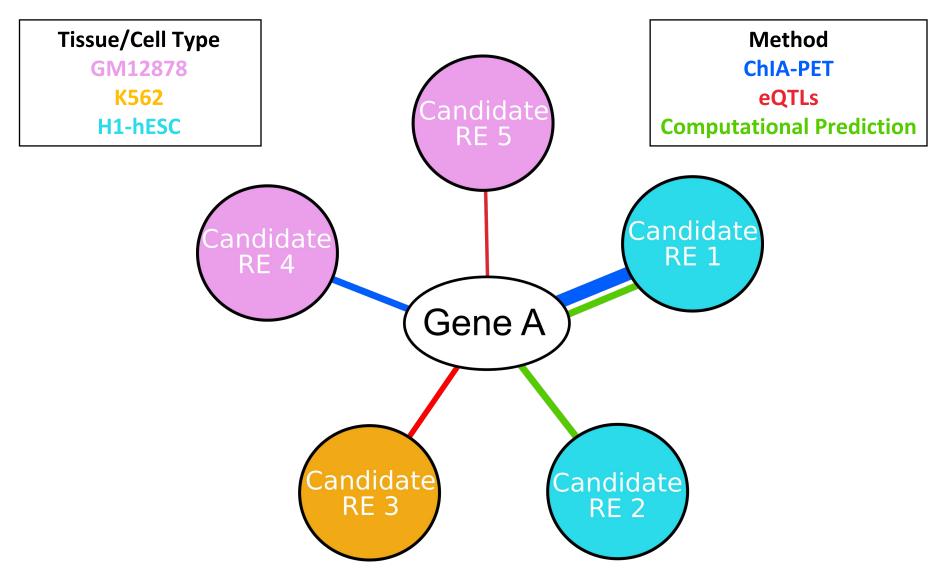
Genome Browser-like View



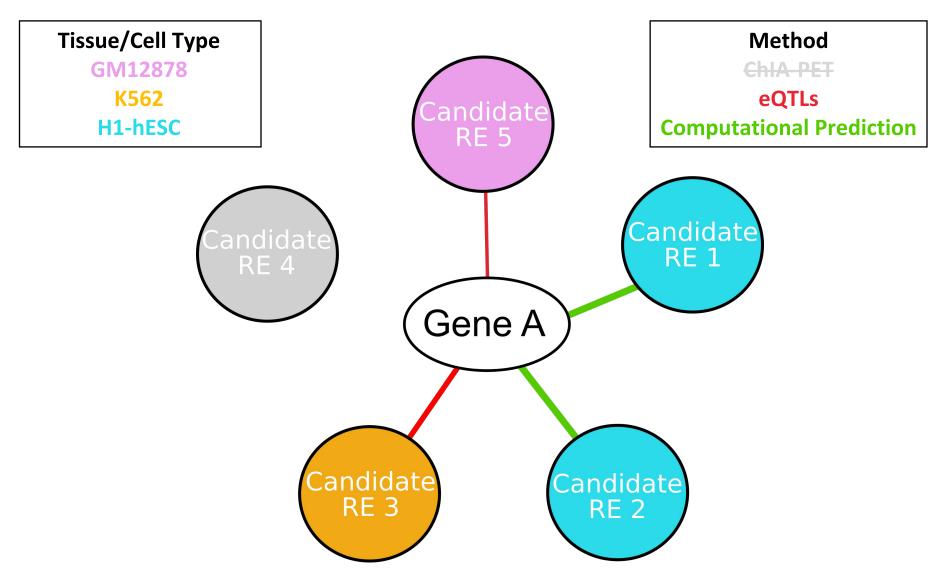
User Selects Facets to Filter Results



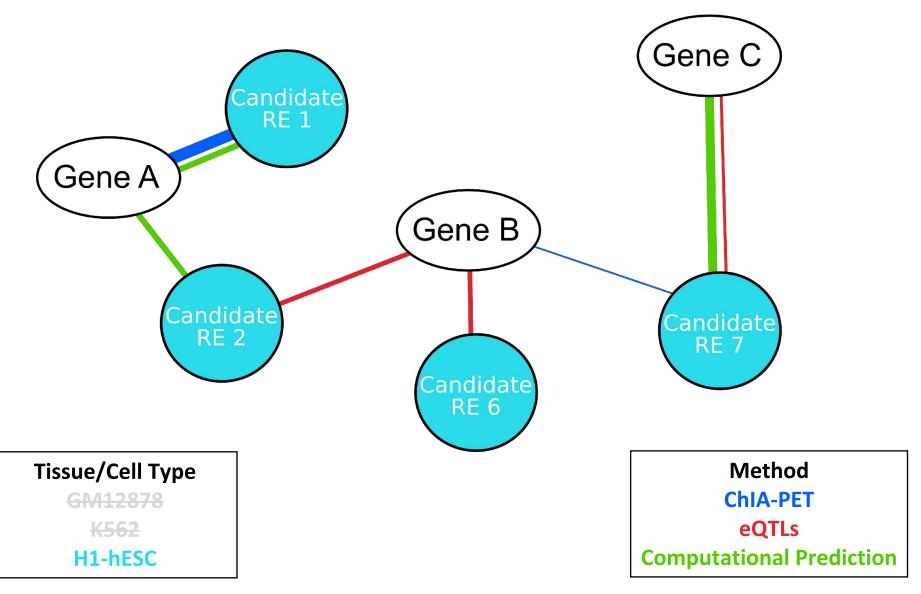
Network View



User Selects Facets to Filter Results



User Can Explore Network of Links Using Facets



Moving Forward...

- 1. Assemble links for ChIA-PET and eQTL data
- 2. Continue developing Random Forest method:
 - Create new training/testing/validation sets for V4 Encyclopedia
 - Test method across cell-types

Optional open discussion on V4 alpha

http://zlab-annotations-v4.umassmed.edu/