	Browse	Browse enhancers by cell line		
H A C E R		SNP: Search a GWAS risk SNP or eQTL variant to find cell-type-specific enhancers harboring the SNP/variant, and show TF-enhancer-gene interactions.		
		Gene: Search a gene to find cell-type-specific enhancers targeting this gene.		
	Query	Coordinate : Search a genomic region to find cell-type-specific enhancers overlapping this region.		
		Batch : Search a set of genomic regions to obtain an annotation summary on cell-type-specific enhancers, TF-enhancer-target interactions and associated GWAS phenotypes, and to prioritize them based on their annotations.		
	Download	Download enhancers by cell line		
	Contact	Report new dataset		
	Contact	Submit feed back		

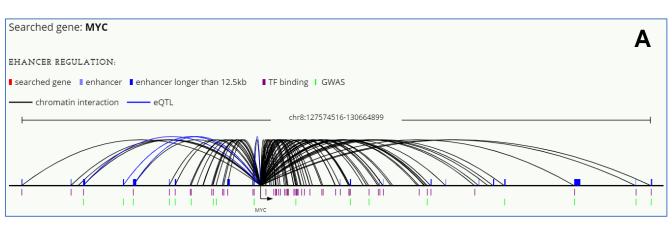
Supplementary Figure S1. Functionality of HACER. Functionality of HACER includes browse, query, download and contact. The query function provides four ways: SNP-centric, gene-centric, coordinate-centric, and batch query.

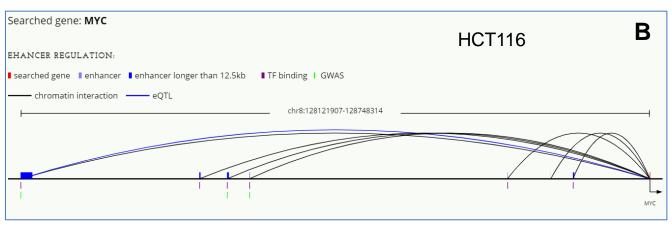
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Supplementary Figure S2. Screenshot of browsing HACER. (A) Select the cell type for browsing. (B) List of enhancers in the cell type. (C-G) Detailed information of a selected enhancer, including basic information (C), TF binding (D), target genes (E), NHGRI-EBI GWAS SNP hits (F), and GTEx eQTL traits (G).

SNP Gene Coord	linate Batch	I					
414							
Interpret GWAS risk SN	Ps or eQTL var	iants by exp	loring enhance	er function:			
SNP (rsID): rs614367	e.g.: rs614367	Type:	All	-			
Active in Cell: MCF7	• e	.g.: MCF7	Chromatin	nteraction in Cell/Ti		• e.	a · MCE
	•	.g WICF/	Chroniathri		MCF7	• e.	.g.: MCF7
Go Clear							
Searched SNP: rs614367							
EHANCER REGULATION:							
enhancer gene TF bindi	-						
	eQTL		chr11:68451982-6945	5872			
					E2F1/GAT	A3/MYC/TCF7L2/ZNF21	17
GAL				MYEOV		1	CCND1
EHANCERS WITH THE S	SEARCHED GWAS	S SNP AND/OI	R EQTL VARIAN	Γ:			
Show 10 • entries					Search:		
Enhancer_ID	^ Chr	Start	End	Technique	CellType	Genome	¢
AE_hg19_MCF7_82564	chr11	69327651	69331536	GRO-seq	MCF7	hg19	
AE_hg19_MCF7_85455	chr11	69316698	69335855	GRO-seq	MCF7	hg19	
AE_hg19_MCF7_92292	chr11	69327651	69331539	GRO-seq	MCF7	hg19	
AE_hg19_MCF7_97091	chr11	69327904	69334044	GRO-seq	MCF7	hg19	
Showing 1 to 4 of 4 entries						Previous 1	Next

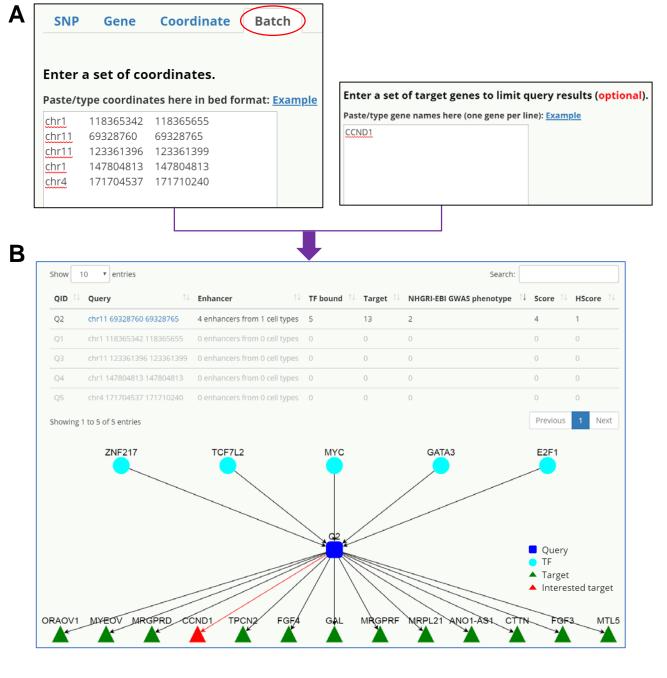
Supplementary Figure S3. An example of interpreting the association of SNP rs614367 with breast cancer risk. (A) Query HACER by SNP rs614367 in MCF7 cell line. (B) Enhancer-mediated regulatory network, which shows enhancers (blue) harbouring the SNP (lime), their upstream TF binding (purple) and downstream targeted genes (teal). Enhancer-gene interactions are denoted by black lines if experimentally validated or blue lines if predicted from eQTL analysis.





Searched gene: MYC		C
	K562	U
EHANCER REGULATION:		
searched gene enhancer enhancer longer than 12.5kb TF binding I GWAS		
chr8:128748314-130693253		
		I.
MYC		

Supplementary Figure S4. An example of exploring tumor-specific enhancers targeting MYC. Query HACER by MYC gene in all cells (A), only in HCT116 cell (B) or in K562 cell (C). Enhancers (light blue or blue boxes) targeting MYC, along with their upstream TF binding (purple) and GWAS risk SNP (lime) are shown. Enhancer-MYC interactions are denoted by black lines if experimentally validated or blue lines if predicted from eQTL analysis.



Supplementary Figure S5. An example for prioritizing/annotating non-coding variants/enhancers. (A) Query HACER by a set of coordinates (locations of enhancer or non-coding variants) and a set of target genes. (B) Queries can be ranked by the number of available functional evidence (Score) or by the number of target genes of interest (HScore) (top panel). A network is provided to show upstream TFs (cyan circle) and downstream targets (green triangle) of queries (blue rectangle) with interactions and genes of interest highlighted in red.(bottom panel).