

A

A. Human heart CAGE TSS view

Please select cell type of interest in "F5 cell ontology" window to see or download subset of related peaks in "heart CAGE peaks" table.

The table includes pval of DPI specificity (from FANTOM5), name of associated gene, location link for navigation in the browser, cumulative expression level (TPM), differential expression analysis results (logFoldChange and FDR) for comparisons: cambers - atrium vs ventricle, side - left vs right, and gender - female vs male.

You can select columns of interest or download sub table to view all columns.

Alternative TSS table contains numbers of DPVTSS/ATG(peaks before start codon) per gene. Remaining columns define numbers of specific clusters according to differential expression (logFC>1, FDR<0.05). Double-click on "location" for navigation. Select a row to see or download analysis results for gene from "heart CAGE peaks" window.

Check also: B [heart CAGE enhancers view](#); C [heart GWAS SNPs view](#)

B

F5 cell ontology

term	name
CL.0000522	adipar.cell
CL.0002823	adipar.cell.of.subcutan.olanc
CL.0002140	adipar.cell.of.subcutan.olanc
CL.0002817	adipocyte.of.breast
CL.0002819	adipocyte.of.american.liver
CL.0002819	adult.endothelial.progenitor.cell
CL.0000789	alpha.beta.T.cell
CL.0002537	amniotic.mesenchymal.stem.cell
CL.0002536	angioblastic.endothelial.cell
CL.0000511	antipogen.binding.protein.secreting.cell
CL.0002802	anulus.rubrosus.cell
CL.0000940	anulus.secreting.cell
CL.0002544	aortic.endothelial.cell
CL.0002539	aortic.smooth.muscle.cell

382 features

heart CAGE peaks : cardiocyte

term	pval	location	TSS_class	cumulative_tpm	GeneName	logFC_chamber	FDR_chamber
CL.0002494	4.520e-7	location	TRUE	1047	VCAN	-1.771	2.171e-12
CL.0002494	2.110e-7	location	TRUE	783.0	VCAN	-1.716	1.717e-13
CL.0002494	7.220e-7	location	NOT	22.91	UBTD1	0.1581	0.9603
CL.0002494	6.980e-7	location	TRUE	20.94	TWIST2	-0.9190	0.4944
CL.0002494	5.990e-7	location	NOT	421.7	TNSI	-1.432	3.243e-8
CL.0002494	1.410e-7	location	NOT	9.049	THFAIPBL3	-0.4448	0.9076
CL.0002494	2.200e-7	location	NOT	40.29	THFAIPBL3	-0.8928	0.6499
CL.0002494	1.520e-7	location	NOT	201.8	THFAIP5	-0.9611	0.1983
CL.0002494	1.140e-8	location	NOT	20.30	TMEM87B	0.64512	1
CL.0002494	4.830e-7	location	NOT	25.93	TMEM445A	-1.178	0.3071
CL.0002494	1.870e-8	location	NOT	1261	TIMP1	-1.462	0.0001313
CL.0002494	1.870e-10	location	NOT	35.81	TIMP1	-0.7065	0.7286
CL.0002494	3.680e-9	location	NOT	12.37	TIMP1	-0.7913	0.6439
CL.0002494	2.250e-9	location	NOT	16.48	TIMP1	-0.9255	0.6098
CL.0002494	8.110e-9	location	NOT	24.62	TIMP1	-1.515	0.2952
CL.0002494	3.330e-4	location	NOT	730.4	THBS2	-1.039	0.007168
CL.0002494	4.820e-9	location	TRUE	39.21	TFPI2	-1.233	0.3487

349 edges

D

Alternative TSS

location	name	DPI	TSS	ATG	Atrium_DPI	Ventricle_DPI
location	MRL1	18	0	5	17	0
location	MTR6	18	0	4	14	0
location	MIB208A	14	0	0	13	0
location	PAM	16	1	3	12	0
location	KCNJ3	11	2	0	11	0
location	CH23	15	0	5	9	0
location	CHL1	10	4	9	9	0
location	LOC105371648	9	0	0	9	0
location	NTN1	9	4	7	8	0
location	FRS3	13	5	13	8	0
location	SFRP5	9	2	7	8	0
location	AMOTL1	13	7	6	8	1
location	TAGLN	11	0	0	8	0
location	ZNF358	10	4	2	8	0

13850 features

heart CAGE peaks : PAM

location	TSS_class	cumulative_tpm	GeneName	logFC_chamber	FDR_chamber	WGCRNA_set1	WGCRNA_set2
location	NOT	1.388e+4	PAM	-1.783	1.314e-14	green	lightcyan
location	NOT	8721	PAM	-2.143	7.308e-12	green	darkgreen
location	NOT	7562	PAM	-1.885	1.088e-12	green	greenyellow
location	TRUE	3008	PAM	-1.318	2.726e-16	red	darkorange
location	NOT	120.5	PAM	-1.747	0.00006834	turquoise	royalblue
location	NOT	84.30	PAM	-1.346	0.001627	cyan	grey
location	NOT	82.58	PAM	-1.846	0.001222	darkgreen	turquoise
location	NOT	37.31	PAM	-3.342	0.00001213	pink	grey
location	NOT	33.69	PAM	-1.813	0.009176	midnightblue	grey
location	NOT	31.88	PAM	-1.582	0.03650	NA	black
location	NOT	31.88	PAM	-1.582	0.005243	midnightblue	purple
location	NOT	29.83	PAM	-1.588	0.05109	magenta	grey
location	NOT	28.90	PAM	-0.8772	0.8280	black	grey
location	NOT	24.06	PAM	-1.515	0.1349	red	grey
location	NOT	21.27	PAM	-1.716	0.08406	lightyellow	turquoise

16 edges

Human heart CAGE TSS view on Zenbu reports page. A - brief description and links to other Heart library pages. B - FANTOM5 cell ontology table based on CAGE peaks overlap between FANTOM5 and heart CAGE. Select cell type of interest to see related heart CAGE peaks in table C. C - heart CAGE peaks annotation table. Includes differential expression, co-expression, gene name data. You can add or remove columns, sort by value, and select location of the feature for navigation in the browser (tough click). D - Gene annotation table by heart CAGE clusters. You can search genes of interest or order by columns (additional columns are available). This table helps to find cases of alternative TSS usage in heart. By clicking on the row of interest you can get information about CAGE clusters related to the gene in table E. You can also download these tables.

https://fantom.gsc.riken.jp/zenbu/reports/#Human_Heart_CAGE_A

A**B. Human heart CAGE enhancers view**

The first table includes all predicted heart enhancers. Click to see associated genes in "connections" table.

The second table contains information about gene-enhancer connections, TSS location link, and TSS related data.

Select a row to see more details in "connections" table. Genes and its TSS were linked to enhancers if CAGE data correlation > 0.5 and p-val<0.05
Double-click on location for navigation in browser (tough click might be required).

Use category filter to subset enhancers by localization.

Check also:

A. [heart CAGE TSS view](#); C. [heart GWAS SNPs view](#)

B

All heart CAGE enhancers table					
name	location	connections	genes	tagcount	localization
chr1:158043048-158044041	location	1	0	577	intron
chr12:902920335-90292997	location	9	2	421	intergenic
chr12:46742675-46743142	location	6	1	282	intron
chr11:130499945-130450484	location	2	0	223	intron
chr9:70419482-70420525	location	1	1	211	intergenic
chr2:231004480-231005249	location	0	0	144	intergenic
chr13:50124382-50124882	location	0	0	138	intron
chr10:29292793-29293523	location	0	0	134	intron
chr21:21503789-21504500	location	0	0	131	intergenic
chr1:2199173-2199274	location	0	0	121	exon
chr10:807209-808032	location	0	0	113	intergenic
chr12:67650025-67650092	location	3	1	109	intron
chr19:38091905-38092347	location	2	1	102	intron
chr5:79097210-79097759	location	4	1	101	intron

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C

Gene to enhancer table					
GeneName	location	TSS	TSS_class	logFC_chamber	FDR_chamber
TBX5	location	114400808	NOT	2.160	6.12E-11
TBX5	location	114400829	NOT	0.6615	0.03915
TBX5	location	114400829	NOT	0.6615	0.03915
LMNB2	location	2450931	TRUE	-0.1083	0.9961
TBX5	location	114400829	NOT	0.6615	0.03915
TBX5	location	114400017	NOT	0.3828	0.7310
TBX5	location	114400017	NOT	0.3828	0.7310
TBX5	location	114400017	NOT	0.3828	0.7310
TBX5	location	114400004	NOT	-0.8129	0.03053
TBX5	location	114400004	NOT	-0.8129	0.03053
TBX5	location	114400004	NOT	-0.8129	0.03053
TBX5	location	114400006	TRUE	-1.881	0.01215
TBX5	location	114400006	TRUE	-1.881	0.01215
TBX5	location	114400006	TRUE	-1.881	0.01215

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D

Connections table						
location	connections	genes	TSS	cor	p_val	GeneName name
location	2	114404226	0.5976	0.00003702	TBX5	chr12:114404462-114404810
location	2	114400054	0.7144	1.500e-7	TBX5	chr12:114404462-114404810
location	2	114400006	0.6624	0.000002382	TBX5	chr12:114404462-114404810

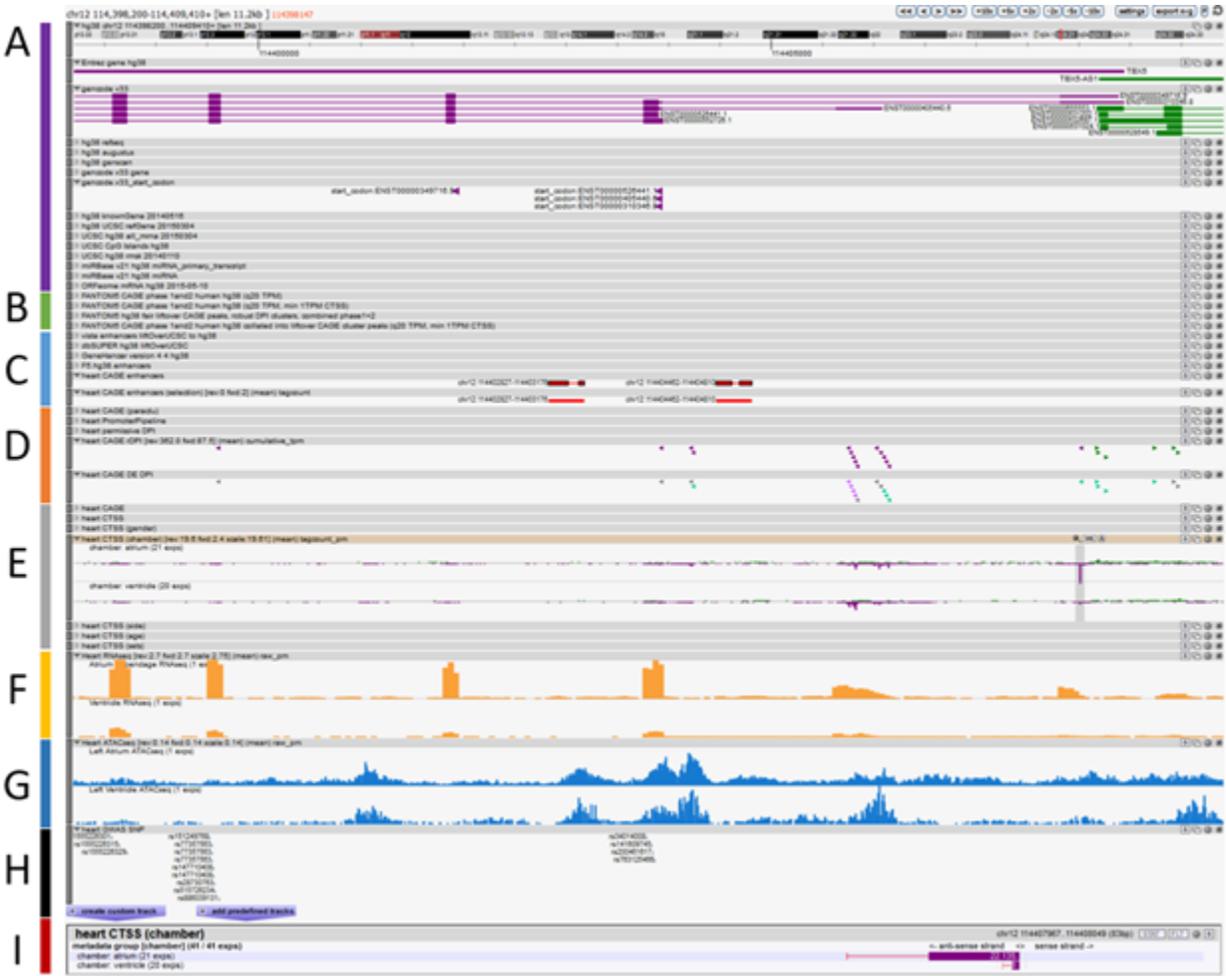
edges

E

localization		
<input checked="" type="checkbox"/> intron		3999
<input checked="" type="checkbox"/> intergenic		1666
<input type="checkbox"/> exon		310
<input type="checkbox"/> CDS		47

Human heart CAGE enhancer view on Zenbu reports page. A - brief description and links to other Heart library pages. B - heart CAGE enhancer table, includes all predicted regions, numbers of mapped CAGE tag counts, numbers of enhancer-to-DPI, and enhancer-to-gene connections based on expression correlation and distance, location link to enhancer (tough click). C - Gene annotation table by heart CAGE enhancers. If the gene was connected to the heart CAGE enhancer it will be available in this table. Location link to connected DPI. E - category filter for enhancer localization for table C. For example, keep genes annotated by only intronic and intergenic enhancers. Select a row of interest in table B or C to see correlation test results in table D (location link for enhancer).

https://fantom.gsc.riken.jp/zenbu/reports/#Human_Heart_CAGE_B



Zenbu browser view on Heart CAGE library of promoters and enhancers. A - genome and gene model tracks. B - FANTOM5 CAGE data tracks and DPI peaks. C - enhancer annotation tracks from multiple sources, including heart CAGE, 'selection' track will highlight selected enhancer on the enhancer view page. D - heart CAGE peaks called by DPI, Promoter Pipeline, paraclu algorithms. Heart CAGE rDPI track will highlight selected robust DPI clusters on the TSS view page. Heart CAGE DE DPI track use grey, green, and purple color for stable, atrium and ventricle specific robust DPI ($|\log_{2}FC| > 1$, $FDR < 0.05$), respectively. E - grouped heart CAGE experiments by chamber (ventricle and atrium), by side (left, right), by age, by gender, by experimental set. Heart CAGE track allows quality filtration of mapped reads. F - RNAseq experiments for atrial appendage and ventricle from GEO GSE128188 and GSE116250 (non-failing), CPM normalized. G - ATACseq tracks from Broad Institute's Cardiovascular Disease Knowledge Portal liftovered on hg38. H - heart GWAS SNP track. Selected SNP will be highlighted on the SNP view page. I - expression barplot for the selected track (for example, heart CAGE for chambers in E).

<https://fantom.gsc.riken.jp/zenbu/gLyphs/#config=mRP7PqjCNhKi9gn0ajOwwC>