

DGE-Vis

Visualisation of RNA-seq data for
Differential Gene Expression analysis

<http://www.vicbioinformatics.com/dge-vis/>

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RNA-seq Differential Expression

- Sequence mRNA & align
- Count number of reads per gene, as a measure of “gene expression”



- Typically interested in comparing expression between conditions.
- “Fold-change” is the relative change in expression between conditions
- Produce a “p-value” as a measure of significance

Results?

	A	B	C	D	E	F	G	H
1	Feature	log2 average	log2 Mut1	log2 Mut2	p	adj.P.Val	ID	Name
2	ENSMUSG00	4.23062319	-2.6396155	-3.0044038	8.57E-52	1.87E-47	ENSMUSG00	Zfp362
3	ENSMUSG00	3.46279016	1.01936738	6.43928734	5.95E-26	6.50E-22	ENSMUSG00	Gm6588
4	ENSMUSG00	2.5090724	-2.0805272	-2.5170288	3.00E-24	2.18E-20	ENSMUSG00	Gm17292
5	ENSMUSG00	0.98084448	-2.5629303	-3.0268283	5.14E-23	2.81E-19	ENSMUSG00	4930558J18F
6	ENSMUSG00	1.92909084	0.54216445	3.80281647	2.81E-16	1.23E-12	ENSMUSG00	Glt1d1
7	ENSMUSG00	3.18601511	-0.0541189	2.77095027	2.13E-12	7.75E-09	ENSMUSG00	Rltpr
8	ENSMUSG00	1.84933015	0.79851214	3.06591248	4.50E-11	1.40E-07	ENSMUSG00	Tex14
9	ENSMUSG00	2.9935711	-2.8853003	-3.912567	1.01E-10	2.76E-07	ENSMUSG00	Gm13886
10	ENSMUSG00	1.80979173	0.25261012	2.31910518	1.37E-10	3.33E-07	ENSMUSG00	Xcr1
11	ENSMUSG00	3.70018874	3.77432743	0.44091057	2.03E-09	4.44E-06	ENSMUSG00	Slc17a8
12	ENSMUSG00	0.70875935	2.366711	2.36280907	3.14E-09	6.24E-06	ENSMUSG00	Chrm5
13	ENSMUSG00	-0.460869	-2.5316145	-1.9556674	8.33E-09	1.52E-05	ENSMUSG00	Nxn12
14	ENSMUSG00	-0.487262	-2.4182556	-2.1096005	3.24E-08	5.45E-05	ENSMUSG00	Gm13599
15	ENSMUSG00	1.61161444	3.1378618	1.07556075	6.47E-08	0.00010088	ENSMUSG00	Arhgap33
16	ENSMUSG00	4.5886935	1.01521713	1.01860937	7.68E-08	0.00011178	ENSMUSG00	AC124613.1
17	ENSMUSG00	5.77875727	1.57883347	0.92821764	8.65E-08	0.0001181	ENSMUSG00	AC087117.4
18	ENSMUSG00	4.30735746	-0.9673369	0.26821664	1.52E-07	0.00019586	ENSMUSG00	Rnd1
19	ENSMUSG00	-1.8046834	99999983.3	99999986.7	1.62E-07	0.00019641	ENSMUSG00	Gm10974
20	ENSMUSG00	4.87213122	1.34702031	1.14012893	1.95E-07	0.00022456	ENSMUSG00	AL807811.1
21	ENSMUSG00	1.2635756	-1.2251005	-2.3291224	3.11E-07	0.00033983	ENSMUSG00	Gzmf
22	ENSMUSG00	3.87973205	0.99784304	1.24765719	3.76E-07	0.00039087	ENSMUSG00	Snap25
23	ENSMUSG00	2.97237649	1.00030983	1.11561456	6.18E-07	0.00059759	ENSMUSG00	SNORA48
24	ENSMUSG00	3.90682004	1.0648741	0.95437005	6.30E-07	0.00059759	ENSMUSG00	Plxna3
25	ENSMUSG00	8.40462095	1.10844944	1.02438989	6.60E-07	0.00059759	ENSMUSG00	SNORD73
26	ENSMUSG00	-0.0606829	1.36794196	2.38688153	6.84E-07	0.00059759	ENSMUSG00	U1
27	ENSMUSG00	7.68258968	1.20566372	0.93203706	8.56E-07	0.00071686	ENSMUSG00	Snord1b
28	ENSMUSG00	4.56035914	1.01325334	0.88117128	1.03E-06	0.00077308	ENSMUSG00	SNORD121A
29	ENSMUSG00	6.60419127	0.8553127	0.88348791	1.22E-06	0.00088884	ENSMUSG00	Snord1a

Bioinformatician



Biologist



Comparing Gene Lists

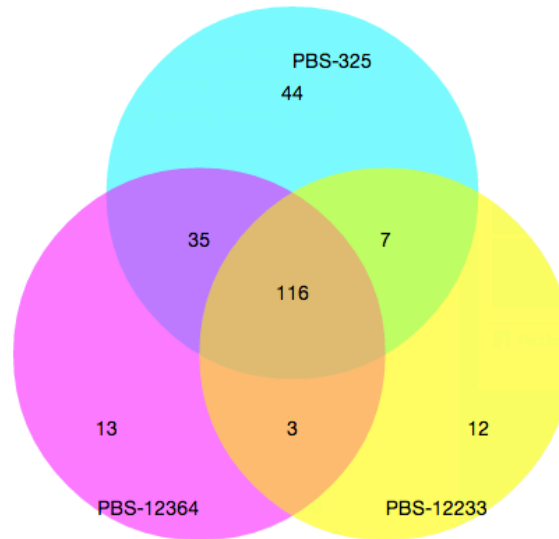
DGE lists

PBS-12233
 PBS-12364
 PBS-325

138	133↑	5↓
167	163↑	4↓
202	187↑	15↓

FDR cut-off

Venn
 Table



Genes

- ✓PBS-12233
- ✓PBS-12364
- ✓PBS-325

Search:

Feature	product	logFC - PBS-12233	logFC - PBS-12364	logFC - PBS-325
ENSMUSG00000000204	Slfn4	3.229	3.178	3.12
ENSMUSG00000000555	Itga5	2.218	2.341	2.193
ENSMUSG00000000982	Ccl3	5.406	5.66	5.747
ENSMUSG00000001156	Mxd1	1.84	2.023	2.472
ENSMUSG000000003153	Slc2a3	1.869	1.9	2.203
ENSMUSG000000003484	Cyp4f18	2.834	2.811	3.142

A Better Solution?

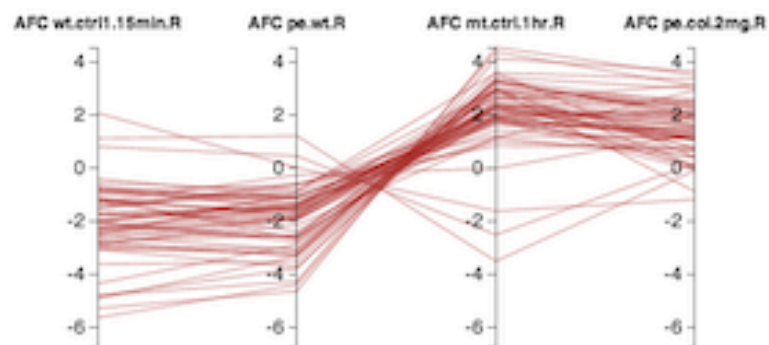


Think Again!

Conditions

pe-col-2mg:R
pe-wt:R *pr*
pe-col-dori:R
pe-dori:R
wt-ctrl1-15min:R *pr*
wt-dori-0.25-15min:R
wt-col-2mg-15min:R
wt-ctrl-1hr:R
wt-col-0.2-1hr:R
wt-col-2mg-1hr:R
mt-ctrl-1hr:R *pr*
mt-col-2mg-1hr:R

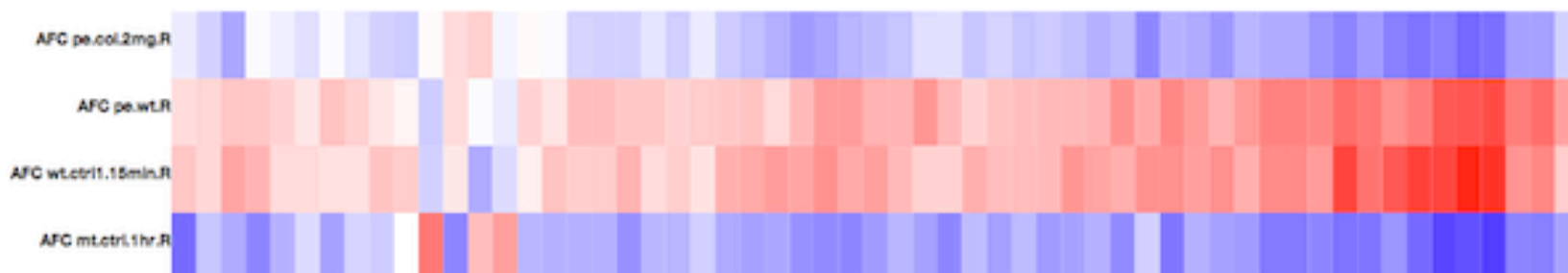
Expression



Options

FDR cut-off 1e-5
abs log FC 0
FC from Avg
Show Counts
Annot. genes
p-val colour

Kegg Pathway



Genes

Showing 0..12 of 57

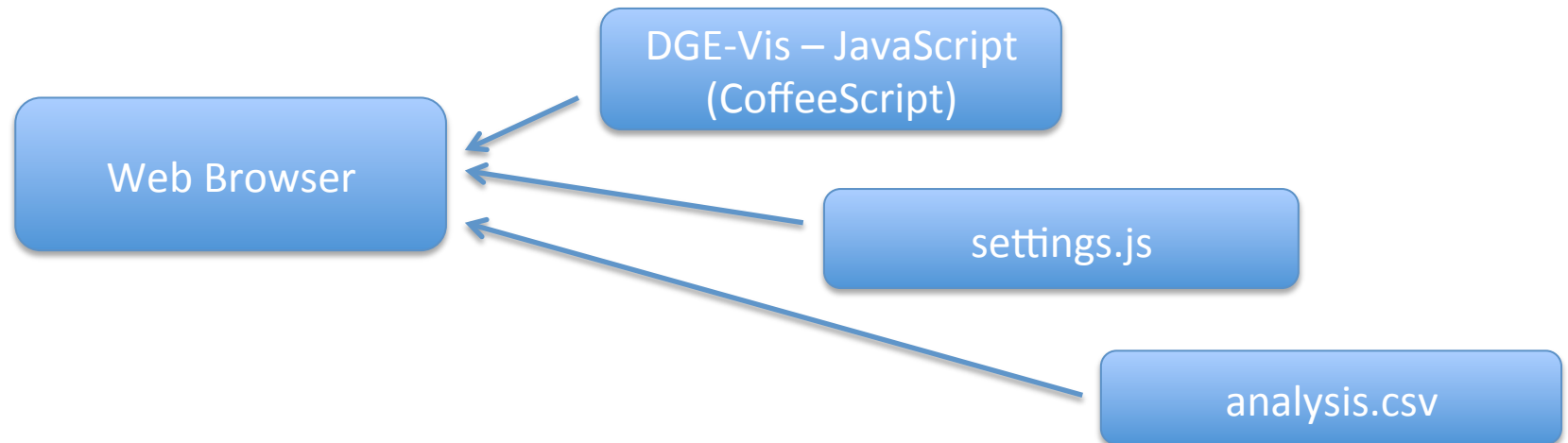
[Download CSV](#)

Search:

Feature	product	gene	adj.P.Val \downarrow	AFC pe.col.2mg.R	AFC pe.wt.R	AFC wt.ctrl1.15...	AFC mt.ctrl.1hr.R
HMPREF0010_01714	RND efflux transporter		3.66e-8	1.87	-3.06	-2.90	3.31
HMPREF0010_03357	amino-acid N-acetyltr...		4.29e-8	1.14	-1.33	-1.97	2.65
HMPREF0010_00184	luciferase family mono...		1.44e-7	1.25	-1.34	-2.02	2.10
HMPREF0010_03655	conserved hypothetica...		1.44e-7	2.22	-2.51	-2.78	2.87
HMPREF0010_02579	tolA		1.44e-7	2.31	-3.73	-3.07	3.16
HMPREF0010_03296	conserved hypothetica...		1.44e-7	2.43	-1.75	-2.29	2.67
HMPREF0010_00180	xylanase/chitin deacet...		2.03e-7	1.60	-1.96	-2.44	2.38
HMPREF0010_01333	outer membrane lipop...		2.03e-7	1.84	-2.55	-2.21	2.93
HMPREF0010_01713	macrolide transporter		2.03e-7	2.05	-3.23	-3.03	3.25
HMPREF0010_01851	ribosomal protein L31		2.37e-7	0.41	-0.86	-1.45	3.58
HMPREF0010_02025	rossmann fold nucleot...		2.37e-7	1.46	-1.95	-1.74	1.80

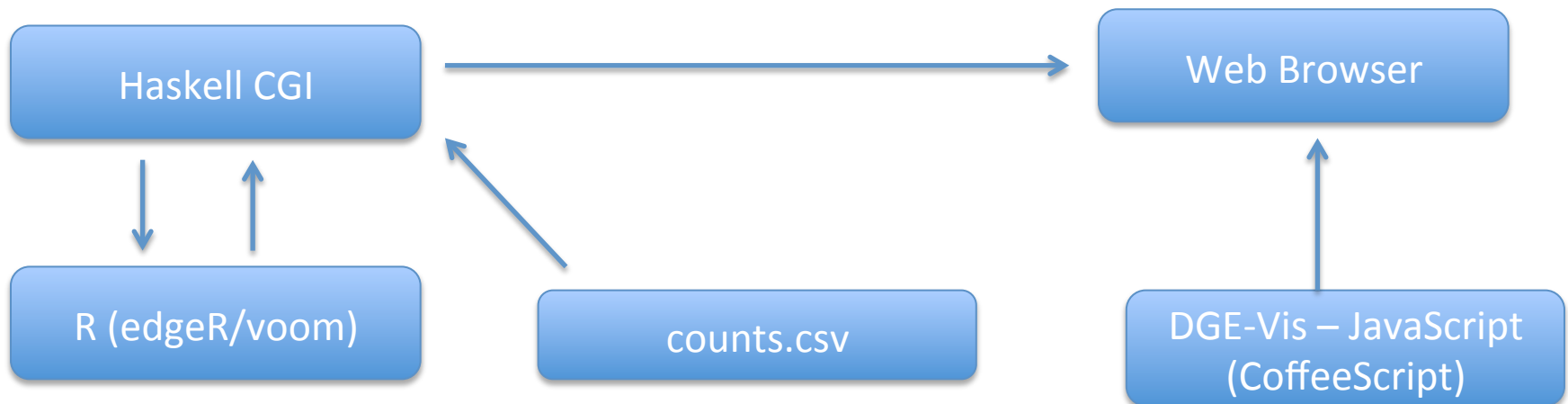
Deployment : Frontend only

- Do your own DGE analysis, use DGE-Vis to visualise and explore
 - Only JavaScript required
 - Create a CSV file of your analysis
 - Configure settings.js



Deployment : Server

- Install requirements
 - Haskell & Libraries
 - R & Libraries
- Compile haskell backend & install



Technology bingo

- Haskell backend
 - Hamlet templates
- R for analysis
 - Voom, Limma & edgeR
- CoffeeScript compiling to JavaScript
- JavaScript libraries
 - D3, jQuery, Bootstrap, SlickGrid

Parallel Coordinates

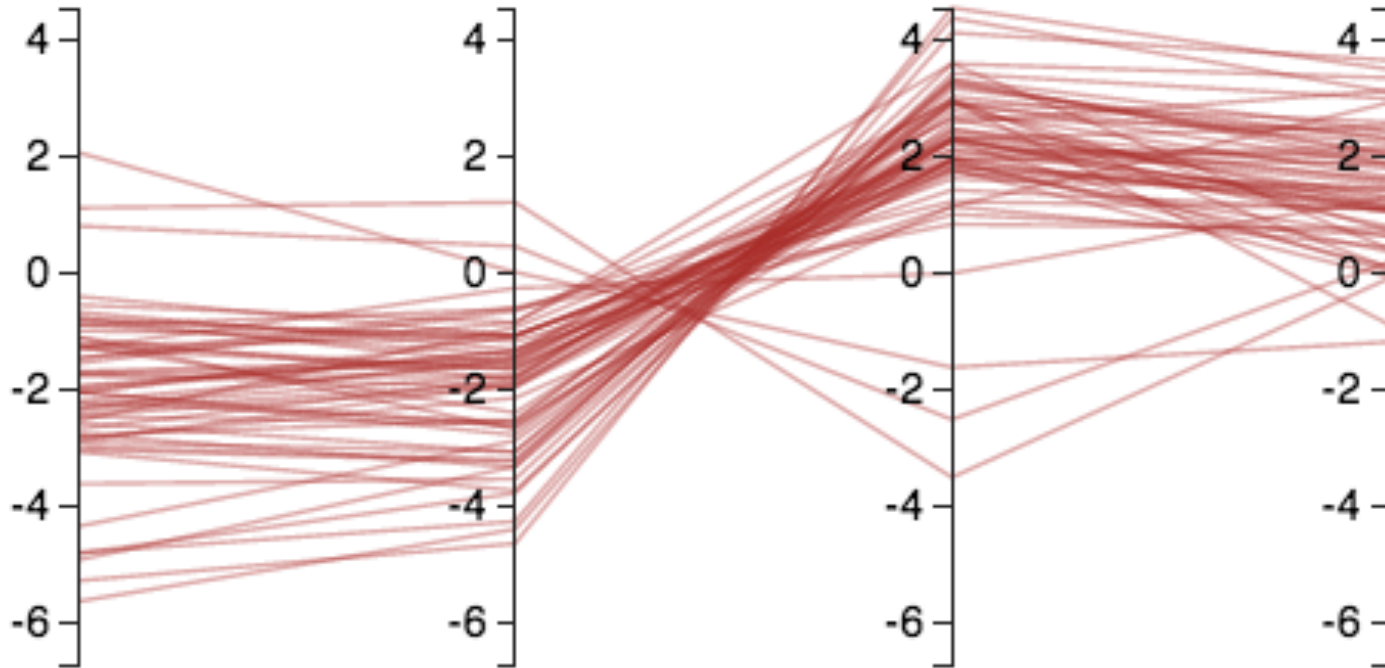
Expression

AFC wt.ctrl1.15min.R

AFC pe.wt.R

AFC mt.ctrl.1hr.R

AFC pe.col.2mg.R



Dynamic Filter Controls

Options

FDR cut-off

abs log FC

FC from Avg

Show Counts

Annot. genes

p-val colour

Kegg Pathway

--- No pathway selected ---

Configuration

Settings

Name

Format type Comma separated (CSV) TAB separated (TSV)

ID column

Info columns

EC Number column

Hide columns

Condition name Replicates

Pre-selected

Pre-selected

Pre-selected

Pre-selected

Number of columns = 17

Feature	cdhR-rep1	cdhR-rep2	GppX-re...	GppX-re...	luxS-rep1	luxS-rep2	luxS-rep3	wt-rep1	wt-rep2	wt-rep3	Length	gene	product	On same...	Ambiguo...	EC Numb...
PG_0001	491	258	198	442	480	737	651	336	633	286	1422	dnaA	chromoso...	53xPG_0...		
PG_0002	69	54	45	86	84	72	119	92	94	63	573		hexapept...	53xPG_0...		
PG_0003	107	45	54	62	47	93	76	72	86	26	1020		membran...	37xPG_0...		
PG_0004	145	70	100	45	141	170	85	99	232	95	705		transcrip...			3.5.1-
PG_0005	276	172	104	233	189	475	277	181	269	115	1155		conserve...			
PG_0006	140	92	84	118	85	186	169	89	161	47	1329		MATE efl...			
PG_0007	10	0	5	0	4	2	0	7	1	0	159		hypothet...			
PG_0008	0	0	0	0	0	0	0	0	0	0	939		ISPg5 tra...			

Gene Table

- Drill down to detailed information
- Search for specific gene
- Download CSV of the filtered genes

Genes

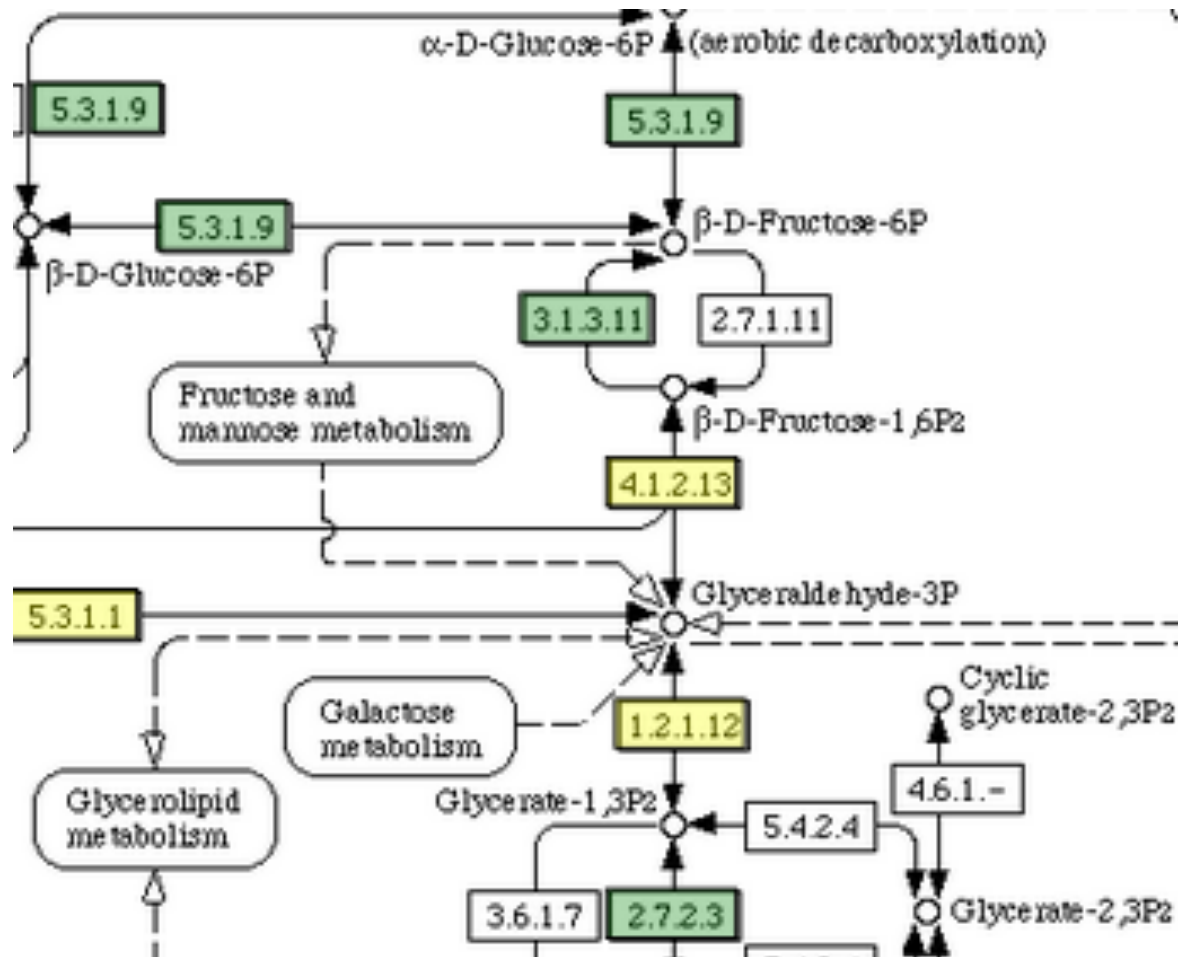
Showing 9..21 of 3799

[Download CSV](#)

Search:

Feature	product	adj.P.Val ▲	AFC pe.col.2mg.R	AFC pe.wt.R
HMPREF0010_03182	conserved hypothetical protein	9.35e-6	1.65 (1441,3240)	-2.77 (170,125)
HMPREF0010_00180	xylanase/chitin deacetylase	2.09e-5	1.60 (769,1362)	-1.96 (58,236)
HMPREF0010_03355	conserved hypothetical protein	2.09e-5	2.58 (4157,9785)	-3.07 (192,173)
HMPREF0010_03357	amino-acid N-acetyltransferase	2.09e-5	1.14 (753,1009)	-1.33 (156,324)
HMPREF0010_01712	membrane-fusion protein	2.56e-5	2.01 (4127,4680)	-3.20 (115,247)
HMPREF0010_00593	membrane-fusion protein	3.46e-5	1.31 (772,714)	-0.95 (199,254)
HMPREF0010_00184	luciferase family monooxygenase	3.50e-5	1.25 (434,640)	-1.34 (86,174)
HMPREF0010_02124	lipoprotein releasing system, transme...	4.12e-5	1.11 (2952,3629)	-2.39 (499,327)
HMPREF0010_00179	biofilm synthesis protein	4.18e-5	1.52 (1092,2015)	-1.81 (125,348)
HMPREF0010_02888	outer membrane lipoprotein carrier p...	4.41e-5	2.30 (8231,10709)	-3.33 (393,185)
HMPREF0010_00614	coenzyme PQQ biosynthesis protein C	5.69e-5	0.65 (275,374)	-1.17 (127,136)

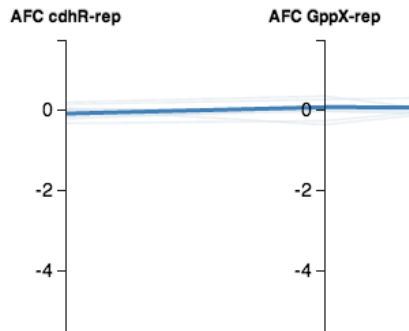
Incorporate a Kegg Pathway



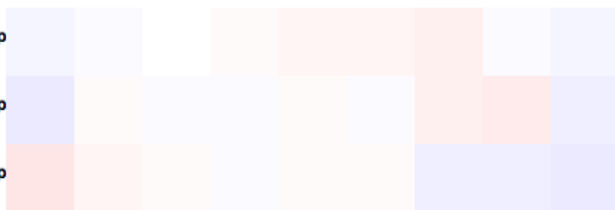
Conditions

cdhR-rep	
GppX-rep	pri
luxS-rep	
wt-rep	pri

Expression



AFC cdhR-rep
AFC GppX-rep
AFC wt-rep

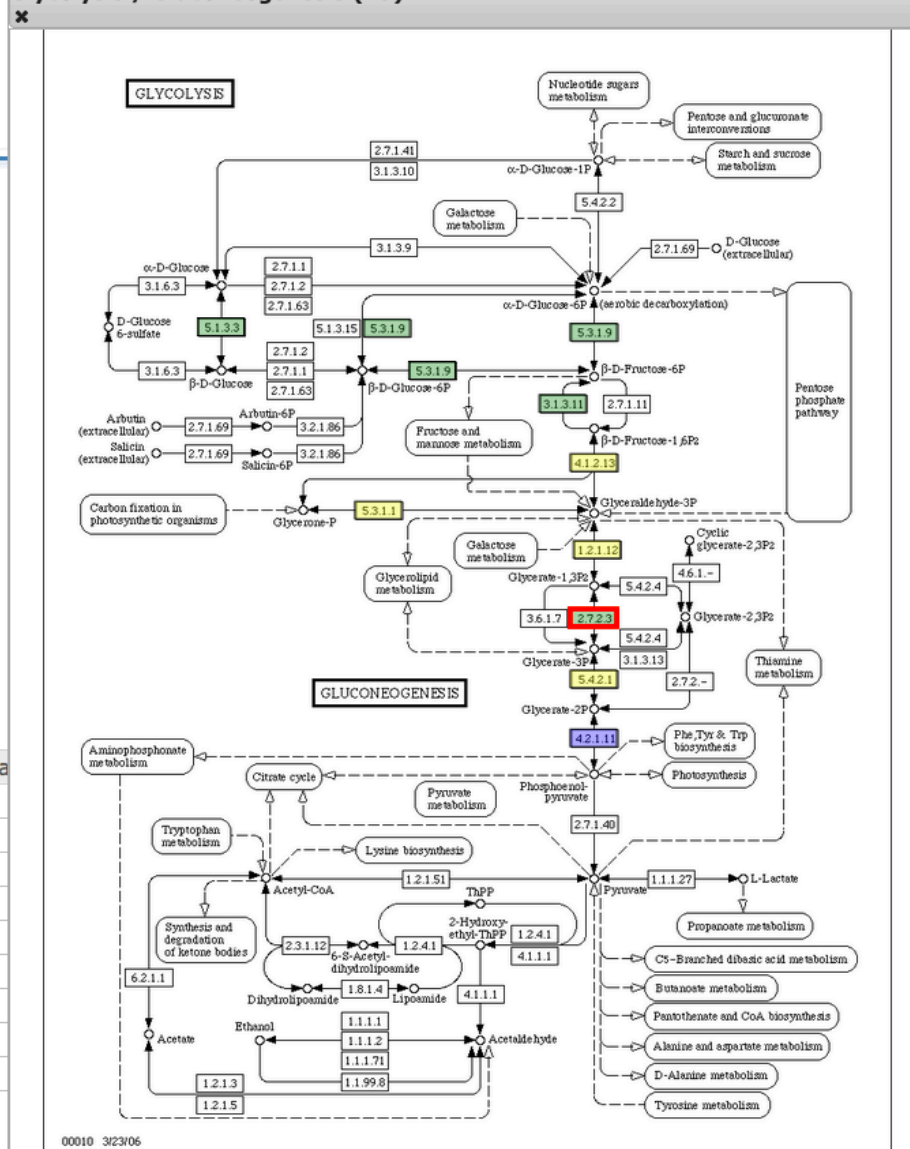


Genes

Showing 0..9 of 9

Feature	gene	product	adj.P.Val
PG_0130	gpm	phosphoglycerate mutase	1.00
PG_0623	tpiA	triosephosphate isomerase	1.00
PG_0793	fbp	fructose-1,6-bisphosphata...	1.00
PG_1368	pgi	glucose-6-phosphate isom...	1.00
PG_1632	galM	aldose 1-epimerase	1.00
PG_1677	pgk	phosphoglycerate kinase	1.00
PG_1755	fbaB	fructose-bisphosphate ald...	1.00
PG_1824	eno	enolase	1.00
PG_2124	gapA	glyceraldehyde 3-phospha...	1.00

Glycolysis / Gluconeogenesis (23)



Contact

DGE-Vis: <http://www.vicbioinformatics.com/dge-vis/>

Source: [on GitHub](#)

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