BV-BRC Test Report

A21. Service – Expression Import - Bacteria

Item to test	Expression Import Service using bacterial gene expression dataset
URL	https://www.bv-brc.org/app/Expression
Prerequisites	Bacterial gene expression dataset in tsv format
References	https://www.bv- brc.org/docs/quick references/services/expression data import service.html https://www.bv-brc.org/docs/tutorial/expression import/expression import.html
Tester(s)	Rebecca Wattam, Maulik Shukla
Test date	10-May-2022 (follow-up from original test)
Test result	Passed

Overview

- Test the Expression Import Service using exemplar bacterial gene expression datasets.
- For each job submitted, verify successful completion of the job and presence of output files.
- Review the dataset using interactive gene list. Test filters to identify differentially expressed genes.
- Test interactive heatmap viewer and clustering tool to identify genes with similar expression patterns across one or more samples.

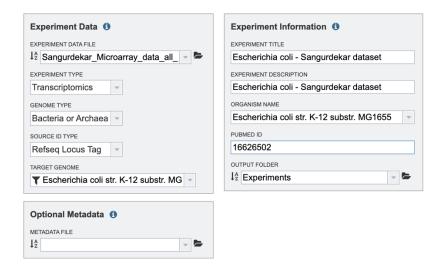
Test Data

Dataset	Rational	Input Format	Input
Escherichia coli – Sangurdekar	Workshop	Gene Matrix in excel format	sangurdekar_Microarray_data_all_c
dataset	example		onditions.xlsx

 All test datasets and corresponding job results are available in the following public workspace: https://www.bv-brc.org/workspace/BVBRC@patricbrc.org/BVBRC%20Tests/Expression%20Import

Test Results

- All jobs completed successfully, without any errors.
- All jobs resulted in expected output files in corresponding job output directory.
- •
- All test datasets and corresponding job results are available in the following public workspace: <u>https://www.bv-brc.org/workspace/BVBRC@patricbrc.org/BVBRC%20Tests/Expression%20Import</u>
- Below are a series of screenshots showing successful completion of the jobs, availability of the result files in the workspace, excerpts of the bacterial and viral binning reports.



Reset Submit

Status	ID	Service	Output Name	Submit •	Start	Completed
completed	7748536	Expression Import	Escherichia coli - Sangurdekar Expression Dataset	5/10/22, 3:24 PM	5/10/22, 3:25 PM	5/10/22, 3:26 PM

	Name	•	Size	Owner	Members	Created	0
t	Parent folder				-		
	experiment.json		358 B	me	2 members	5/10/22, 3:25 PM	
	expression.json		226.0 MB	me	2 members	5/10/22, 3:25 PM	
	mapping.json		331.1 kB	me	2 members	5/10/22, 3:26 PM	
	sample.json		70.6 kB	me	2 members	5/10/22, 3:26 PM	

BVBRC / home / Experiments / Escherichia coli - Sangurdekar Expression Dataset

Platform Organism: Escherichia coli str. K-12 substr. MG1655 Pubmed ID: Undefined Genes Mapped/Genes Total: 3406/3607 Samples: 240

Title	Genes	Significar Genes (Log Ratio)	n Significan Genes (Z Score)	Strain	Gene Modification	Experiment Condition	Time Point C
5min .02M SodiumAzide	3607	837	222				
15min .02M SodiumAzide	3607	588	227				
300min .02M SodiumAzide	3607	789	209				
600min .02M SodiumAzide	3607	690	212				
C410+0Ecb0+0IPTG0(toxic) v s.0C430mutant+0Ecb0+0IPTG	3607	401	207				
10' trp starvation vs.00', W31100trpA33	3607	401	194				
25' trp starvation vs.00', W31100trpA33	3607	328	199				
50' trp starvation vs.00', W31100trpA33	3607	482	200				
lexA05' after UV v s.00', MG1655	3607	58	231				
lexA010' after UV v s.00', MG1655	3607	28	205				
lexA020' after UV v s.00', MG1655	3607	27	203				
lexA040' after UV v s.00', MG1655	3607	43	196				
lexA060' after UV v s.00', MG1655	3607	63	190				
2min Nor(50ug/ml)_beforeTreatment	3607	79	160				
5min Nor(50ug/ml)_beforeTreatment	3607	55	164				
10min Nor(50ug/ml)_beforeTreatment	3607	216	189				
20min Nor(50ug/ml)_beforeTreatment	3607	258	190				
30min Nor(50ug/ml)_beforeTreatment	3607	217	197				
5ug/ml Novobiocin 5min v s.0untreated, LE2340acrD-, LB, axon5	3607	60	199				
20ug/ml Novobiocin 5min v s.0untreated, LE2340acrD-, LB, axon5	3607	166	203				
50ug/ml Novobiocin 5min v s.0untreated, LE2340acrD-, LB, axon5	3607	327	223				

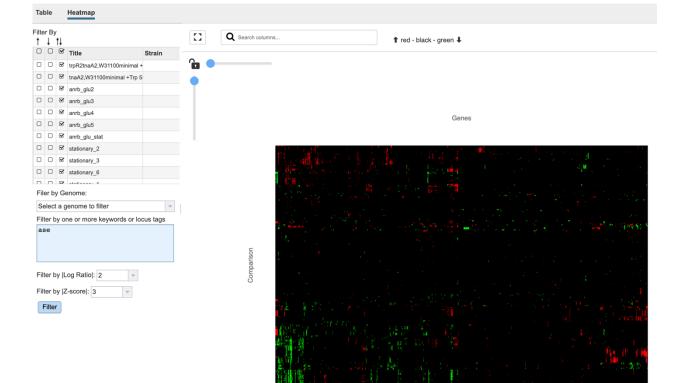
EXPRMNT

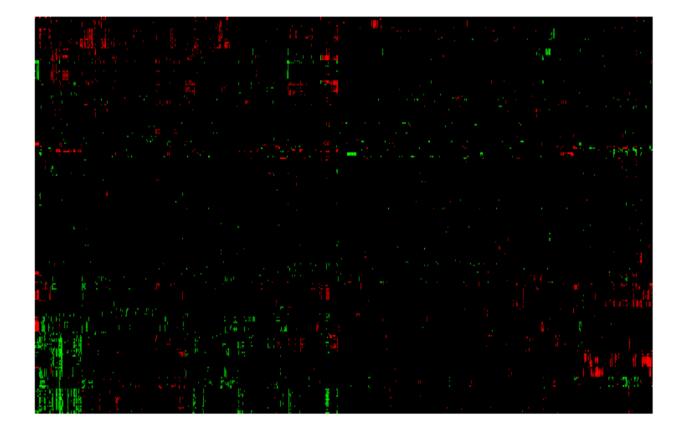
O VIEW

100	Transcriptomics	Genes

lter By I ↓ 1↓									Dov
	Title	Strain	BRC ID	RefSeq Locus	Gene Symbol	Product	Comparisons	Up	Down
	5min .02M SodiumAzide			Tag					
	15min .02M SodiumAzide		fig 511145.12.peg.	65 b0628	lipA	Lipoyl synthase (EC 2.8.1.8)	237	119	118
	300min .02M SodiumAzide		fig 511145.12.peg.	93 b0901	ycaK	putative NAD(P)H dehydrogenase	230	93	137
	600min .02M SodiumAzide		fig 511145.12.peg.	86 b0082	mraW	16S rRNA (cytosine(1402)-N(4))-methyltransferase (E	237	164	73
	C410+0Ecb0+0IPTG0(toxic)	v	fig 511145.12.peg.	16 b1627	rsxA	Electron transport complex protein RnfA	235	134	101
	10' trp starvation vs.00', W31	1	fig 511145.12.peg.	19 b1862	yebB	Uncharacterized protein YebB	222	113	109
	25' trp starvation vs.00', W31	1	fig 511145.12.peg.	26 b2522	sseB	Protein SseB	233	94	139
	50' trp starvation vs.00', W31	1	fig 511145.12.peg.	74 b0713	ybgL	Lactam utilization protein LamB	215	93	122
	lexA05' after UV v s.00', MG1	14 I	fig 511145.12.peg.	19 b1880	flhB	Flagellar biosynthesis protein FlhB	238	72	166
	lexA010' after UV v s.00', MG		fig 511145.12.peg.	33 b3212	gltB	Glutamate synthase [NADPH] large chain (EC 1.4.1.1	120	49	71
n n 🕫			fig 511145.12.peg.	46 b0447	ybaO	DNA-binding transcriptional activator DecR, AsnC fam	226	118	108
iler by G	Senome:		fig 511145.12.peg.	43 b4175	hflC	HfIC protein	240	131	109
Select a	genome to filter	*	fig 511145.12.peg.	11 b1094	acpP	Acyl carrier protein	232	127	105
ilter by c	one or more keywords or lo	cus tags	fig 511145.12.peg.	31 b3053	gInE	Glutamine synthetase adenylyl-L-tyrosine phosphoryl	218	97	121
			fig 511145.12.peg.	33 b3251	mreB	Rod shape-determining protein MreB	239	143	96
			fig 511145.12.peg.	18 b1822	rimA	23S rRNA (guanine(745)-N(1))-methyltransferase (EC	239	111	128
			fig 511145.12.peg.	40 b3965	trmA	tRNA (uracil(54)-C5)-methyltransferase (EC 2.1.1.35)	238	122	116
			fig 511145.12.peg.	36 b3508	yhiD	Putative magnesium transporter YhiD	234	129	105
ilter by	Log Ratio : 0		fig 511145.12.peg.	26 b0264	insB	IS1 protein InsB	240	129	111
ilter by 2	Z-score : 0		fig 511145.12.peg.	38 b3755	yieP	Uncharacterized transcriptional regulator YieP, GntR f	238	102	136
Filter			fig 511145.12.peg.	16 b1604	ydgH	Protein YdgH	238	139	99
1 mor			fig 511145.12.peg.	22 b2142	yohK	Inner membrane protein YohK	123	52	71
			fig 511145.12.peg.	11 b1088	yceD	FIG01269488: protein, clustered with ribosomal prote	232	116	116
			fig 511145.12.peg.	25 b2420	yfeS	Molybdate metabolism regulator	222	85	137
		1	fig 511145.12.peg.	57 b0554	essD	Phage holin/antiholin component S	232	86	146
			fig 511145.12.peg.	19 b1867	yecD	Isochorismatase family protein YecD	237	141	96
			fig 511145.12.peg.	33 b3247	rng	Ribonuclease G	240	132	108

Ε, Τ	rans	criptomics Genes									
Table	н	leatmap									
ilter By ↑ ↓ ↑↓											
		Fitle 5min .02M SodiumAzide	Strain		BRC ID	RefSeq Locus Tag	Gene Symbol	Product	Comparisons	Up	Down
	-	15min .02M SodiumAzide			fig 511145.12.peg.65		lipA	Lipoyl synthase (EC 2.8.1.8)	240	19	9
		300min .02M SodiumAzide		n	fig 511145.12.peg.93			putative NAD(P)H dehydrogenase	240	2	4
		500min .02M SodiumAzide			fig 511145.12.peg.86	b0082	mraW	16S rRNA (cytosine(1402)-N(4))-methyltransferase (E	240	13	8
		C410+0Ecb0+0IPTG0(toxic) v		$\overline{\Box}$	fig 511145.12.peg.16		rsxA	Electron transport complex protein RnfA	240	14	3
		10' trp starvation vs.00', W311			fig 511145.12.peg.19	b1862	yebB	Uncharacterized protein YebB	240	5	7
		25' trp starvation vs.00', W311			fig 511145.12.peg.19	b1880	flhB	Flagellar biosynthesis protein FlhB	240	8	29
	₹ 5	50' trp starvation vs.00', W311	1		fig 511145.12.peg.33	b3212	gltB	Glutamate synthase [NADPH] large chain (EC 1.4.1.1	240	19	44
	☑ 1€	exA05' after UV v s.00', MG1			fig 511145.12.peg.46	b0447	ybaO	DNA-binding transcriptional activator DecR, AsnC fam	240	5	4
	3 16	exA010' after UV v s.00', MG			fig 511145.12.peg.43	b4175	hflC	HflC protein	240	10	11
	.				fig 511145.12.peg.11	b1094	acpP	Acyl carrier protein	240	23	15
Filer by (Gen	nome:			fig 511145.12.peg.31	b3053	gInE	Glutamine synthetase adenylyl-L-tyrosine phosphoryla	240	5	11
Select a	a gei	nome to filter	-		fig 511145.12.peg.33	b3251	mreB	Rod shape-determining protein MreB	240	24	14
Filter by	one	e or more keywords or loo	cus tags		fig 511145.12.peg.18	b1822	rimA	23S rRNA (guanine(745)-N(1))-methyltransferase (EC	240	12	2
					fig 511145.12.peg.40	b3965	trmA	tRNA (uracil(54)-C5)-methyltransferase (EC 2.1.1.35)	240	24	7
					fig 511145.12.peg.36	b3508	yhiD	Putative magnesium transporter YhiD	240	18	5
					fig 511145.12.peg.26	b0264	insB	IS1 protein InsB	240	21	6
					fig 511145.12.peg.38	b3755	yieP	Uncharacterized transcriptional regulator YieP, GntR f	240	6	7
Filter by	Log	g Ratio : 1			fig 511145.12.peg.16	b1604	ydgH	Protein YdgH	240	14	18
Filter by	Z-s	score : 2 -			fig 511145.12.peg.22	b2142	yohK	Inner membrane protein YohK	240	4	3
Filter	i.				fig 511145.12.peg.11	b1088	yceD	FIG01269488: protein, clustered with ribosomal prote	240	25	5
Filter	J				fig 511145.12.peg.57	b0554	essD	Phage holin/antiholin component S	240	1	2
					fig 511145.12.peg.19	b1867	yecD	Isochorismatase family protein YecD	240	14	3
					fig 511145.12.peg.21	b2081	yegQ	Uncharacterized protease YegQ	240	37	12
					fig 511145.12.peg.96	b0932	pepN	Membrane alanine aminopeptidase N (EC 3.4.11.2)	240	26	16
					fig 511145.12.peg.24	b2381	ypdB	Two-component transcriptional response regulator Yp	240	2	6
					fig 511145.12.peg.36	b3532	bcsB	Cyclic di-GMP-binding protein BcsB	240	6	14
				1 - 2	200 of 2928 res	ults					(1 2 3 15





References

- Expression Import Quick Reference Guide
- Expression Import Tutorial