Interactive Toxicogenomics: Gene Set Discovery, Clustering and Analysis in Toxygates

Nyström-Persson, J., Natsume-Kitatani, Y., Igarashi, Y., Satoh, D., and Mizuguchi, K.

## Supplementary Methods

This supplementary document includes the details of the analytical flow in our case study in which the new analytical functions in Toxygates were utilized. For the figures of heatmap and the interpretation of the obtained results, please refer to the main manuscript. For the general tutorial for Toxygates, please refer to the user guide (http://toxygates.nibiohn.go.jp/toxygates/toxygatesManual.pdf)



Toxygates is an integrated platform for toxicogenomics data analysis. For more information, please see our *BioInformatics* paper, or use the help menu.

#### 2016-10-20 ("v2.0")

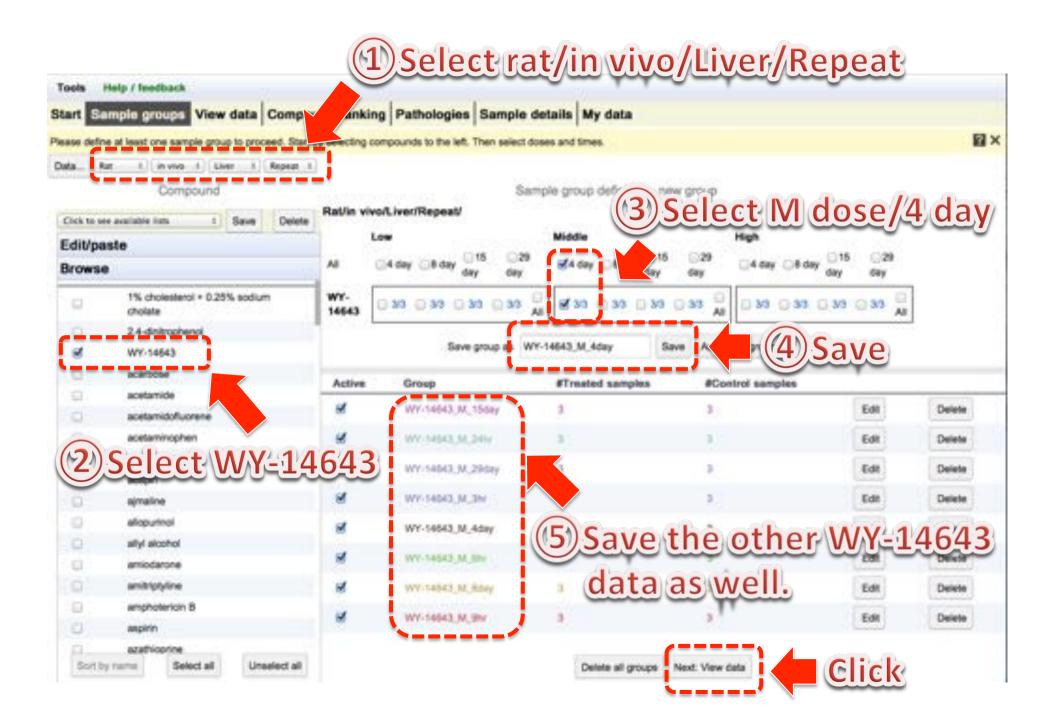
Several major new features have now been released.

- · A clustering and heat-map visualisation feature has been added.
- Users may now upload their own data and analyse it alongside existing data in Toxygates.
- KEGG pathways and GO terms are now updated automatically on a weekly basis.

With the addition of user data uploads and clustering/visualisation, Toxygates is now a much more powerful analysis environment than previously, and we urge users to try these functions for themselves.

For more information, please see the user guide, or use the help menu.

#### Click here to begin.



## **Observed pathologies as starting point**

	at least one sample group to proceed. Start b	by selecting o	propounds to the left. Then select	doses and times.			10 s
16a	a E an avec E Liver E Repeat E						
	Compound			Click	new group		
Click to see	evalable lats + Save Delete	Rat/in viv	a/Liver/Repeat/	CIICK			
Edit/par	sie		ow Contraction of the second s	Middle	High		
Browse		AI	(]4 day (]8 day ()15 ()26	M 4 CBY I D CBY	4 day 5 c	tay 015 029	
1000140			any any	day			
9	1% cholesterol + 0.25% sodium cholate	WY- 14643	320 0 20 0 20 0 20	M 8 30 0 30 0 3	0 0 30 M	E 30 E 30 M	
0	2,4-dinitrophenol	10000	23 <b>r</b>		and here and	(and a second se	
	WY-14643		Save group as	WY-14643_M_4(bity	Save Automatic groups		
17	acarbose	Active	Group	#Treated samples	#Control samples		
0	acetamide	(>				(mar)	(marging)
9	acetamidofluorene		WY-14043_M_15day	3	5	Edit	Delete
0	acetaminophen		WV-14963;M_242e	1	3	Edit	Delete
0	acetazolamide		WY-14043_M_29day	3	3	Edit	Delete
12	adapin		and the second second		8.		- Denie
0	spraine	9	WY-14643_M_3ht	3	3	Edit	Delete
13	allopurinol		WY-14643_M_4day	3	3	Edit	Delete
	willy! alcohol		<ul> <li>Contract (Contract (Con</li></ul>	10	10 X	0000	( and the second
0	amiodarone	9	WY-14543_M_BW	3	2	Edit	Delete
0		ef.	WY-14643_M_6day	3	2	Edit	Delete
	ambriptyline						
0	ambriptyline amphotencin B		WV-14643.M.0W	2	3	Edit	Delete

1 Select repeat dose data

his is the list of pathologi	ies in the sample groups you have defined.	Click on	an icon to see detailed sample information	()			<b>a</b> >
WY-14643_M_16day 3W	Y-14643/Middlw15 day WY-14643_M_29c	ay :WY-5	4543Mittide(29 day WY-14643_M_4day 3	WY-14643/MiddleH day W	Y-14643_XL, 8589-9	W-MARANACONT IN	v
Group	Sample		Finding Topography Grade Spontaneous				
WY-14643_M_15day	WY-14543/Modie/15 daylunderined	a,	Degeneration, granular, eosinophilic	Hepatocyte	Severe (+++)	faise	Viewer
WY-14643_M_15day	WY-54643/Middle/15 daylundefined	Q.	Degeneration, granular, eosinophilic	Hepatocyte	Severe (+++)	false	Viewer
WY-14643_M_15day	WY-14643/Middle/15 daylundefined	9	Degeneration, granular, eosinophilic	Hepatocyte	Severe (+++)	false	Vewer
WY-14643_M_15day	WY-14643/Middle/15 day/undefined	٩	Necrosis	Hepatocyte	Minimal (±)	faise	Viewer
WY-14643_M_15day	WY-14643/Middle/15 daylundefined	9,	Hypertrophy	Bile duct, interlobular	Slight (+)	false	Varwar
WY-14643_M_8day	WY-14643/Middle/8 daylundefined	a,	Single cell neorosis	Hepatocyle.	Minimal (2)	false	Viewer
WY-14643_M_8day	WY-14643/Middle/8 daylundefined	Q.	Degeneration, granular, eosinophilic	Hepatocyte	Severa (+++)	Taise	Viewer
WY-14643_M_8day	WY-14643/Middle/8 daylundefined	Q.	Degeneration, granular, eosinophilic	Hepatocyte	Severe (+++)	Talso	Viewer
WY-14643_M_8day	WY-14643/Middle/8 daylundefined	a,	Degeneration, granular, eosinophilic	Hepatocyte	Severe (+++)	false	Viewer
WY-14643_M_8day	WY-14643/Middle/8 daylundefined	a,	Hypertrophy	Bile duct, interlobular	Slight (+)	faiter	Vewer
WY-14643_M_15day	WY-14643/Middlei15 daylundefined	Q,	Hypertrophy	Bile duct, interlobular	Minimal (x)	faise	Vewer
WY-14643_M_15day	WY-14543/Middler15 daylunderined	Q.	Hypertrophy	Bile duct, interlobular	Minimal (2)	faine	Viewer
WY-14643_M_290ay	WY-14643/Middle/29 daylundefined	a,	Necrosis	Hepatocyte	Slight (+)	faite	Viewer
WY-14643_M_4day	WY-14643/MiddleH daytundefined	Q.	Increased mitosis	Hepatocyte	Slight (+)	faise	Viewer
WY-14643_M_4day	WY-14643/Middle/4 day/undefined	9	increased mitosis	Hepatocyte	Slight (+)	false	Viewer
WY-14643_M_29day	WY-14643Middle/29 daylundefined	Q.	Hypertrophy	Bile duct, interlobular	Minimal (±)	false	Vewer
WY-14643_M_29day	WY-14643/Middle/29 daylundefined	a,	Degeneration, granular, eosinophilic	Hepatocyte	Severa (+++)	taise	Viewer
WY-14643_M_29day	WY-14643/Middle/29 daylundefined	a,	Hypertrophy	Bile duct, interlobular	Slight (+)	false	Viewer
WY-14643_M_29day	WY-14643/Middle/29 daylundefined	Q,	Degeneration, granular, eosinophilic	Hepatocyte	Severa (+++)	faise	Viewer
WY-14643_M_29day	WY-54643/Middle/29 daylundefined	Q.	Hypertrophy	Bile duct, interiobular	Slight (+)	faise	Viewer
WY-14643_M_29day	WY-14643/Middle/29 daylundefined	a,	Degeneration, granular, eosinophilic	Hepatocyte	Severe (+++)	faine	Vewer
		0					1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.

Supplementary Table 1: summary of this table

## **<u>Cluster analysis</u>**

a M	E E H VIVE E EVER E Repeat E	1					
	Compound	12/12/07/2		mple group definition - new	v group		
ick to see	evaluble lists I Save Delete	Rat/in vivo	/Liver/Repeat/				
dit/pas	ite	L	**	Middle	High		
owse		Al (	4 day 0 th day 0 15 0 29	₩4 day 08 day 015 day	⊡29 ⊡4 day ⊡8 day day	⊡15 ⊡29 day day	
0	1% cholesterol + 0.25% sodium cholate	WY- 14643	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	G g aa D aa D aa	0 30 0 10 0 10 0 10 0 10 0 10 0 10 0 10	30 0 30 0	
9	2,4-dintrophenol	· · · · · · · · · · · · · · · · · · ·		102			
8	WY-14643		Save group as	Y-14643_M_4day Sa	e Automatic groups		
1	acarbose	Active	Group	#Treated samples	#Control samples		
	acetamide	( w	WY-14643_M_15day	3	3	Edit	Delete
3	acetamidofluorene		minimus_m_room	*	4.5	EVA	Canada
3	acetaminophen	8	WW-14043_30_24hr	3	1	Edt	Delete
			INTERNATION OF STREET	a (	37	an inc	Delete
	acetazolamide	8	WY-14643_M_29day			E dit	COMPANY
2	adapin						
2	adapin ajmaline	8	WY-14643_M_3hr	3	3	Edt	Delete
a 2-	adapin ajmaline allopurinol						
	adapin ajmaline allopurinol allyt atcohol	8	WY-14643_M_3hr	3	3	Edt	Delete
	adapin ajmaine aligurinoi aliyi alcohol amiodarone	<b>R R</b>	WY-14643_M_3hr WY-14643_M_4day WY-14643_M_6hy	3 3 3	3 3 3	Edt Edt Edt	Delete Delete Delete
	adapin ajmaline allopurinol allyt atcohol	8 8	WY-14643_M_3hr WY-14643_M_4day	3	3	Edt Edt	Delete Delete

		n case of M						× 19
Y-14	543_M_4day /WY-14	643Midde/4 day Show all	Bhow More	Le columna Al Probes		lick this		
	Gene Symbol	Probe Title	Probe	* WY-14643_M?	WY-14643_M ?	WY-14643_M 🖗	₩Y-14643_M 🗑	WY-14643
鱼	Acot1	acyl-CoA thioesterase 1	1398250,at	10.307	11.123	15,505	4.068	10.941
th.	Agp3	aquaporin 3	1387100_st	8.368	jibeerd	6.004	(street)	7.499
da.	LOC100911217	adipogenin-like	1376296_at	6.15	(iddeerd)	6.052	(absent)	5.391
the state			1384474_at	7.818	6.072	6.932	(steeds)	6.184
di.	Ctvna2	cholinergic receptor - nicolinic - alpha 2 (neuronal)	1387574_at	7.573	2.529	6.721	(absent)	3.367
曲	Hdo	histidine decarboxylase	1370491_a_at	7,257	6.121	7.585	(ebsect)	7.247
<u>sh.</u>	Fabp3	fatty acid binding protein 3 - muscle and heart	1367660,at	6.833	1.307	6.71	(absent)	6.627
曲	RGD1305929	hypothetical LOC300207	1380536_at	6.615	3.226	6.8	(atomic)	5.616
<u>sh</u>	Acot1 Acot2	acyl-CoA thioesterase 1	1388211_s_M	0.489	5.652	6.167	2.2	6.76
<u>\$</u>	Fbp2	fructose-1 -6-bisphosphatase 2	1368622_at	0.078	5.001	5.799	(absent)	4.471
sh.	Abhd3	abhydrolase domain containing 3	1382137_at	5.922	1,200	4.042	(steen)	5.105
曲			1383757_at	5.757	(steerd)	5.309	(atment)	(absent)
sh.	Cpt1b	camitine palmitoyitransferase 1b - muscle	1367742_st	5.648	1.953	5414	(sbeen0	5.372
th.	App7	aquaporin 7	1368317_at	.5.838	3.84	4.867	(streets)	4.852
sh	Spink3	serine peptidase inhibitor - Kazal type 3	1388447_x_st	5.097	1.807	4.123	0.076	1.297
de	LOC100912489	acyl-CoA desaturase 2-like	1367666_a_at	4.505	0.008	6,296	-0.322	0.636

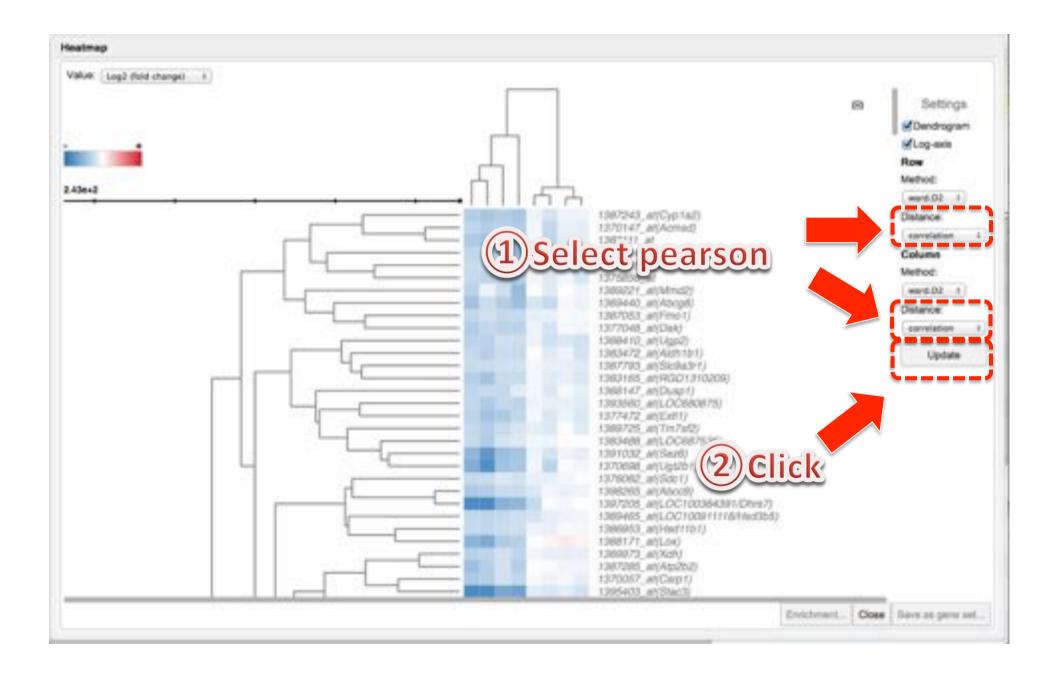
		sion values for the sample groups you h				IV WY-SHEED, M., BH: WY-S	404346adw3 hr	
	543_M_4day WY-14 dold change()	(1) New po	pp-up	11	And I see			
d.	Gene Symbol	Probe Title		* WY-14643_M 7	WY-14643_M 7	WY-14643_M ?	WY-14643_M ?	WY-14843
111 11	Acot1	acyl-CoA thioesterase 1		10.307	11,423			10.941
-	Aqp3	aquaporin 3	1387100 at	8.500		(2)Inpu	t 1.5	7.499
出	LOC100911217	adpogenin-like	1276 Edit filb	er .		6.932		5.391
1. 1.	Chma2	cholinergic receptor - nicotinic - alpha 2 (neuronal)	1867 Please	thoose a bound for WY-5		6.721	(absent)	6.184
the	Hdc	histicine decarboxylase	107C	2.5 1.5		7.385	(sbaeet)	7.247
<u>th</u>	Fabp3	faity acid binding protein 3 - muscle and heart	1367	OK Clear filter		6.71	(sbeent)	6.627
曲	RGD1305926	hypothetical LOC300207	13005.00.81	17		6.9	(staard)	5.616
th	Acot1 Acot2	acyl-CoA thioesterase 1	1300211_8_0		A.812	6.157	22	6.76
sh.	Fbp2	huctose-1 -6-bisphosphatase 2	*568622_st	LOTO	1.007	5.790	(abaent)	4.471
<u>th.</u>	Abhd3	abhydrolase domain containing 3	2)Clic	(A22)	1.208	4.042	(ubserf)	5.105
њ.		(	CONTRACT OF	10/67	(down)	5.389	(abaani)	(absent)
sh.	Carto	camitine palmitoyitransferase 15 - muscle	1367742_at	5.648	2,653	5,454	(ebsect)	5.372
曲	Aup?	aquaporin 7	1368317_at	5.638	1.84	4.867	(absen0	4.852
<u>ıh.</u>	Spink3	serine peptidase inhibitor - Kazal type 3	1368447_x_at	5.097	1.007	4.123	0.076	1.297
曲	LOC100912469 Sod	acyl-CoA desaturase 2-like	1367668_#_#L	4.986	0.038	6.290	-0.322	0.636

File         Gene Sets         View         Tools         Help / feedback           Start         Sample groups         View data         Compound ranking         Pathologies         Sample details         My data								
tere yo	ou can inspect expres	sion values for the sample groups you h	ave defined. Click o	n column headers to sort di	rta.	12-		
al animation in	and the second	1643/Middler15 day WY-14643_M_34tr	WY-1464335356	24 to WY-14643_M_29day	WY-14543/Middle/29 day	WY-14643_M_3hr 3WY-	14643/Midde/3 hy	
VY-14	643_M_6day :WY-14	M3Middel4 day Show all						
Log2	fold change)	* 1 1-25 of 420 🖡 🖷 🕷 Sh	ow More Opvalue	columns All Probes Ne	w Bdt			
	Gene Symbol	Probe Title	Probe	* WY-14643_M T	WY-14643_M V	WY-14643_M 7	WY-14643_M 7	WY-1464
<u>th.</u>	Acot1	acyl-CoA thioesteras	NICAS M	10.307	11.125	10.505	4.068	10.941
止	Aqp3	aquaporin 3	1)420	probes	areext	racted	(absent)	7.499
the state	LDC100911217	adipogenin-like	1376296_at	Juli		8.052	(advennt)	5.391
曲			1384474_ <i>M</i>	7.818	4.972	6.932	(absent)	6.184
sh	Chma2	cholinergic receptor - nicotinic - alpha 2 (neuronal)	1387574_at	7.573	2.529	6.721	(abserd)	3.357
th	Hdc	histicine decarboxylase	1370491_a_at	7.257	3.121	7.365	(absord)	7.247
th	Fabp3	fatty acid binding protein 3 - muscle and heart	1367660_at	6.633	2.362	6.71	(street)	6.627
sh	RGD1305928	hypothetical LDC300207	1380536_at	8.815	8,228	6.9	(absent)	5.616
曲	Acot1 Acot2	acyl-CoA thioesterase 1	1388211_i_i_at	6.489	5.953	6.967	2.2	6.76
曲	Fbp2	fructose-1 -6-bisphosphatase 2	1369622_at	6.076	2,901	5.799	(absent)	4.471
da.	Abhd3	abhydrolase domain containing 3	1382137_at	5.922	1.208	4.042	(absent)	5.105
曲			1383757_at	6.757	(phase)	5.369	(absent)	(absent)
<u>d1</u>	Cprtib	camiline palmitoythansferase 15 - muscle	1367742_M	5.648	2.855	5.414	(obsent)	6.372
止	Aqp7	aquaporin 7	1368317_at	6.638	1.84	4.887	(absent)	4.852
th.	Spink3	serine peptidase inhibitor - Kazal type 3	1368447_X,M	5.097	1.887	4.123	0.070	1.297
the	LOC100912489 Sod	acyl-CoA desaturate 2-like	1367668_a_at	4.995	0.0061	6.296	-0.322	0.636

ene yo	Sample group	Compare two sample groups	defined. Click o	pies Sample deta	1.1		(artananta)	₽×
Y-14	POSS A PROPERTY AND A PROPERTY AND A	443/Middle/4 diry Show at	_	CK 14643 M				
	Gene Symbol	Probe Title		CK 14643_M_	WY-14643_M 7	WY-14643_M 7	WY-14643_M 7	WY-14643
th.	Acot1	acyl-CoA thioesterase 1	1398250_at	10.307	11.123	50.605	4.058	10.941
ŝ.	Aqp3	aquaporin 3	1387100_mt	8.500	(advante)	8.004	(abaant)	7.499
삺	LOC100911217	adipogenin-like	1376296_at	8.15	(utraint)	6.052	(abaset)	6.391
<u>th</u>			1384474_at	7.818	4,972	6.832	(abaard)	6.184
<u>th</u>	Chma2	cholinergic receptor - nicotinic - alpha 2 (neuronal)	1387574_at	7.573	2.529	6.721	(abaset)	3.367
曲	Hdc	Netidine decarboxylase	1370491_a_at	7.257	16.121	7.385	(pheeds)	7.247
<u>th</u>	Fabp3	fatty acid binding protein 3 - muscle and heart	1367660_at	8.833	2.542	6.71	(steent)	6.627
ь	RGD1306928	hypothetical LOC300207	1380536_at	6.015	3.226	8.8	[abased]	5.616
<u>th</u>	Acot1 Acot2	acyl-CoA thioesterase 1	1388211_A_M	6.489	6.952	6.187	2.2	6.76
曲	Pbp2	fructose-1 -8-bisphosphatase 2	1368622_at	6.076	3.001	5.790	(about)	4.471
胁	Abhd3	abhydrolase domain containing 3	1382137_at	5.922	1.204	4.042	(preedic)	5.105
th.			1383757_at	5.757	(phane)	5.300	(about)	(absent)
th	Cpt1b	camitine palmitoyltransferase 1b - muscle	1367742_at	5.648	2.953	5.414	(abased)	5.372
th.	Aqp7	aquaporin 7	1366317_at	5.638	1.04	4.867	(abeant)	4.852
ŝ	Spink3	serine peptidase inhibitor - Kazal type 3	1368447_x.at	5.097	1.887	4.123	0.076	1.297
曲	LOC100912489 Sod	acyl-CoA desaturase 2-like	1367668_a_at	4.996	0.034	8,296	4.322	0.638

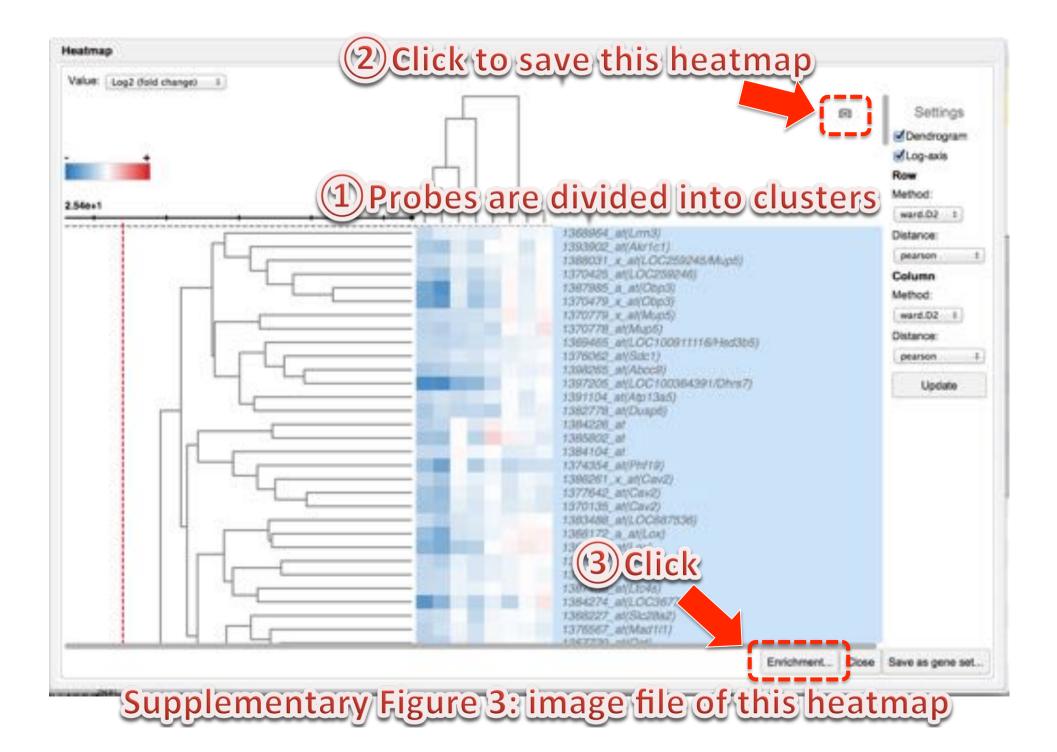
# **1** New pop-up window appears

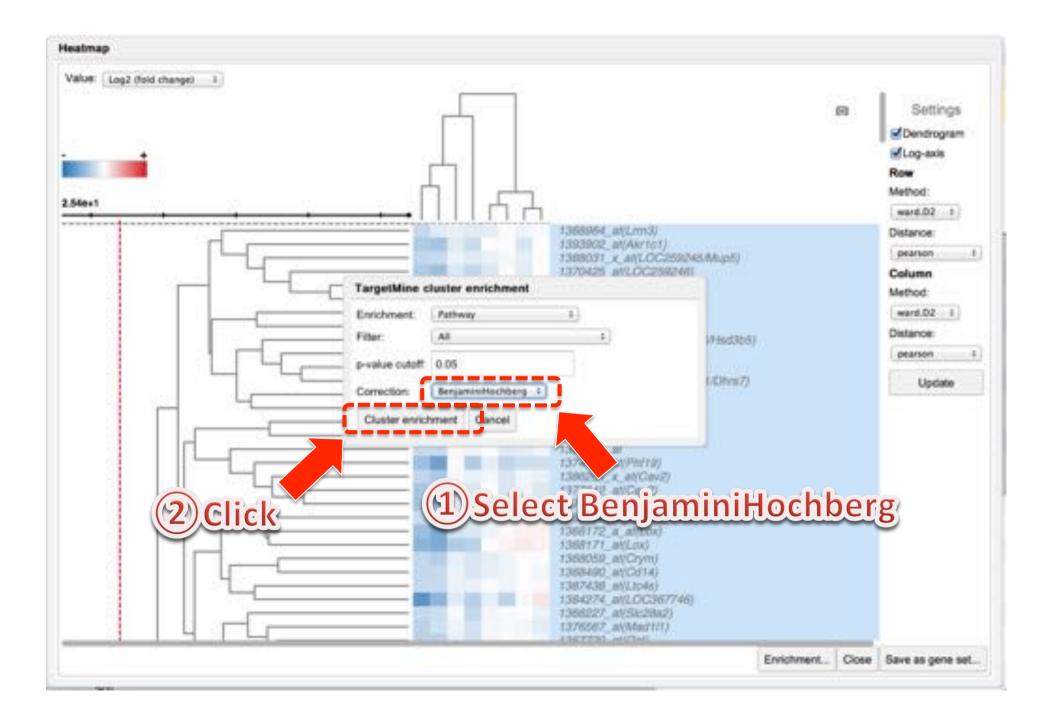


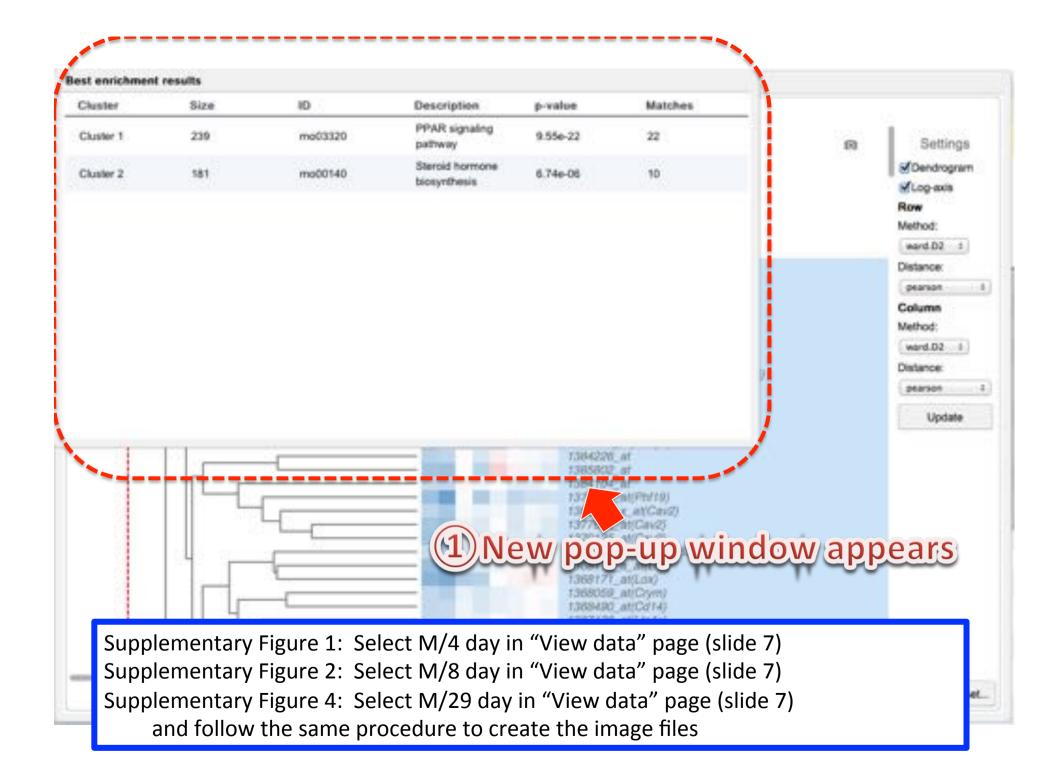


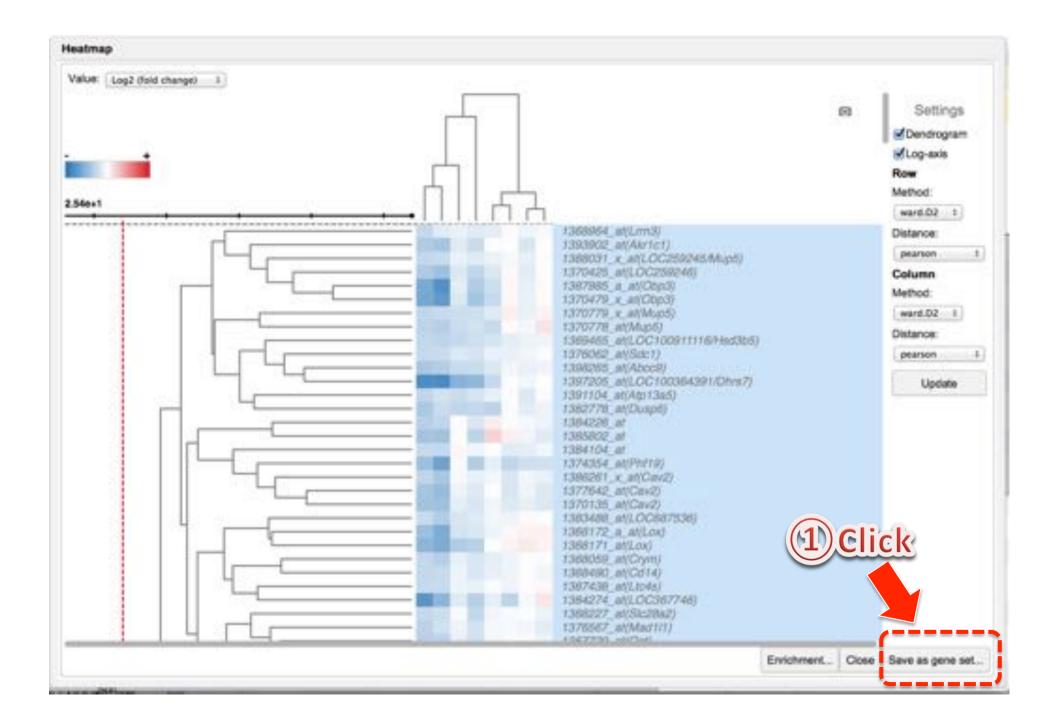
# 1 Heatmap is updated

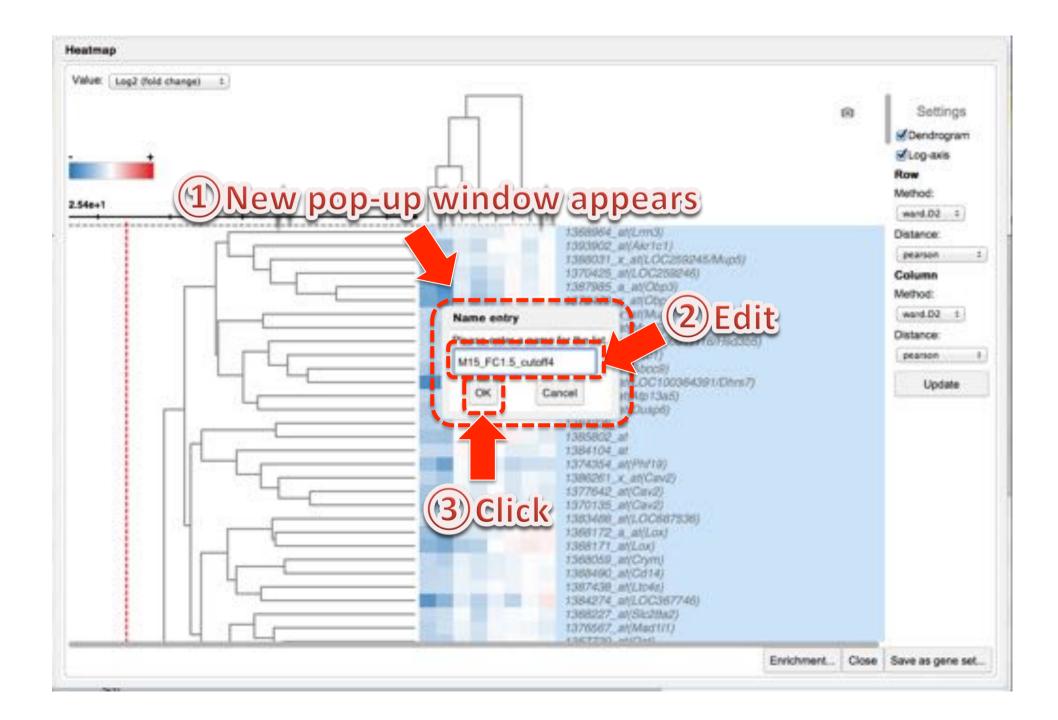
Value: Log2 (fold change) 1 Settings 63 Dendrogram 2) Select cut-off=4 by pointing and click Log-axis Row Method: 2.560+1 ward.02 il 1368964 at/Lmn31 Distance: 1393902 at/Akr1c11 268/501 . . 1388031 x at/LOC259245/Mup5) T370425 at/LOC250248) Column 1387985 a at(Obc3) Method: 1370479 x at(Obp3) 1370779 x at/Mub5) ward.02 1 1370778 at(Mup3) Distance: 1369465\_at(LOC100911116/96d3b5) 1376062 at(Sdc1) pearson. -1398265 at(Abec0) 1397205\_atlLOC100384397/Dhrs7) Update 1391104\_al(Ato13a5) 1382778 at(Dusp6) 1384228 at 1385802 at 1384104 at 1374354\_at(Ph/19) 1386261\_x\_at/Cav23 1377642 at/Cav2) 1370135 at/Cav2) 1383488\_at(LOC887536) 1368172 a at(Los) 1368171 at(Lox) 1368059\_at(Crym) 1368490\_#ECd142 1387438\_at(Lto4s) 1384274 at(LOC367746) 1368227 at(Sic28a2) 1376587 at(Mad1/IT) 62677300\_+KOT+K Close Save as gene set. Enrichment.

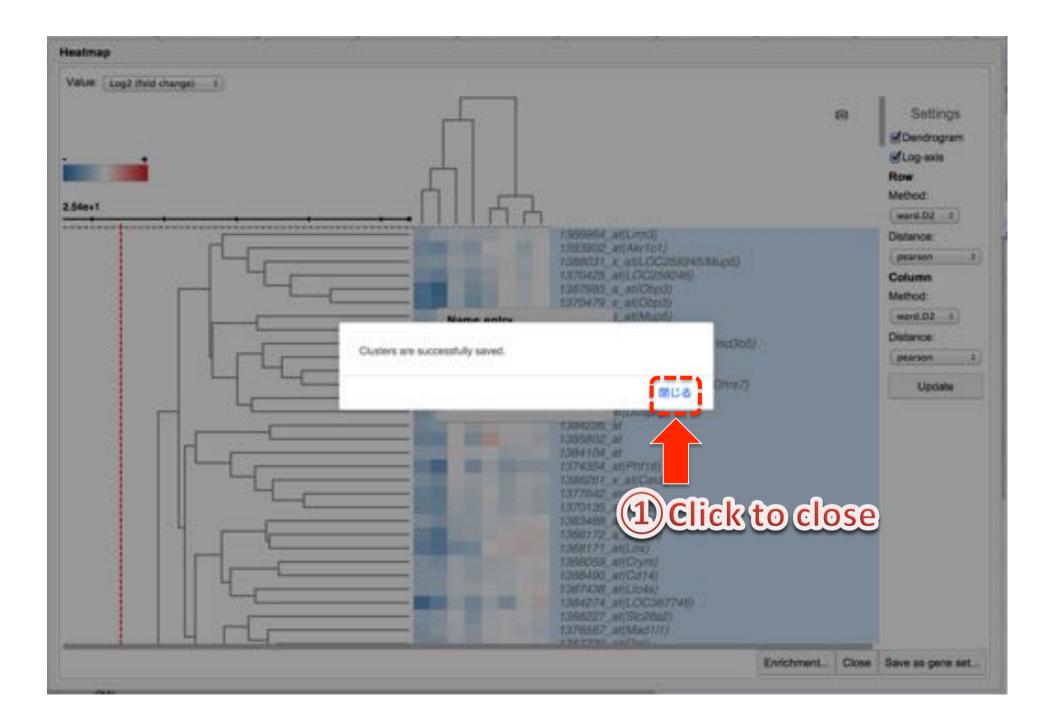














#### Start Sample groups View data Compound ranking Pathologies Sample details My data

Here you can inspect expression values for the sample groups you have defined. Click on column headers to sort data.

1)Click

Incident

WY-14543\_M\_15day\_WY-14643/Mode/15 day\_WY-14643\_M\_3 Http://WY-14643/Mode/24.1v\_WY-14643\_M\_29day\_WY-14643/Mode/29 day\_WY-14643\_M\_3tv\_WY-14643/Mode/3.1v

WY-14643 M\_4day WY-14643/Midde/4 day Show all

File

Gene Sets

View Tools

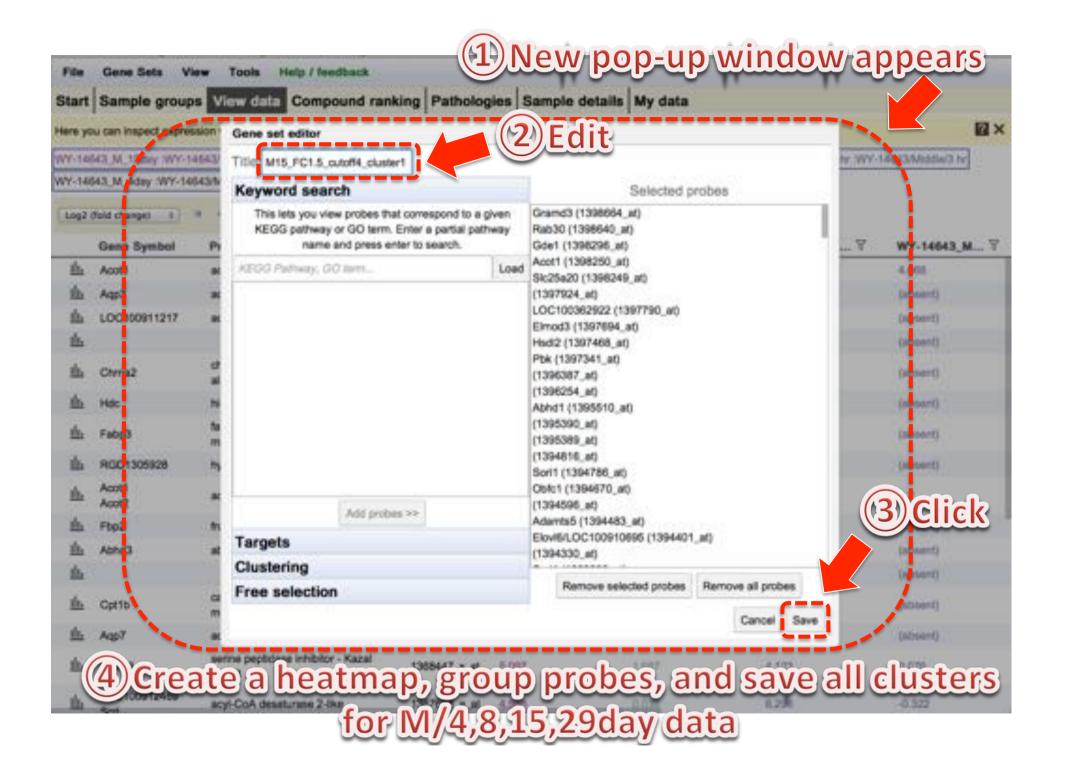
Log2 (fold change) | # 4 1-25 of 420 🕨 # 🕷 Show More Opvisive columns All Probes New 1012

	Gene Symbol	Probe Title	Probe	* WY-14643_M T	WY-14643_M 7	WY-14643_M 7	WY-14643_M T	WY-14643
止	Acot1	acyl-CoA thioesterase 1	1398250_itt	10.307	11.123	10.505	4.058	10.941
止	Aqp3	aquaporin 3	1387100_at	8.000	(abound)	6.004	(absent)	7.499
the state	LDC100911217	adipogenin-lika	1376296_at	8.15	(analy)	8.052	(absent)	5.391
曲			1384474_at	7.818	4.972	6.932	(absent)	6.184
sh	Ctena2	cholinergic receptor - nicotinic - alpha 2 (neuronal)	1387574_at	7.573	2.529	6.721	(absent)	3.357
dh.	Hdc	histicine decarboxylase	1370491_a_at	7.257	3.121	7.365	(staard)	7.247
th	Fabp3	fatty acid binding protein 3 - muscle and heart	1367660_at	6.633	2.367	6.71	(stasse)	6.627
th,	RGD1305928	hypothetical LOC300207	1380536_at	8.815	8.726	6.9	(atoent)	5.616
山	Acot1 Acot2	acyl-CoA thioesterase 1	1388211_4_at	6.439	5.952	6.167	2.2	6.76
th.	Fbp2	fructose-1 -6-bisphosphatase 2	1366622_at	6.078	2,001	5.790	(abserd)	4.471
ds.	Abhd3	abhydrolase domain containing 3	1382137_at	5.922	1,200	4.042	(abanet)	5.105
<u>th</u>			1383757_at	6.757	(Meent)	5.369	(absent)	(abeent)
di.	Cpt1b	camiline palmitoyitransferase 15 - muscle	1367742_M	5.648	2.855	5,414	(obsent)	6.372
曲	Ap7	aquaporin 7	1368317_ml	5.638	1084	4.867	(absent)	4.852
sh.	Spink3	serine peptidase inhibitor - Kazal type 3	1368447_X,M	5.097	1.887	4.123	0.070	1.297
dh.	LOC100912469 Sod	scyl-CoA desaturase 2-like	1367668_R_st	4.995	0.006	6.296	-0.302	0.636

2 ×

File	Gene Sets Vi	ew Tools Help / leedback	and the second second		1		
Start	Show all	data Compound ran	nking Patholog	pies Sample details	My data		
tere yo	NewGeneSet	s for the sample groups you?	have defined. Click o	n column headers to sort d	ata.		2
VY-146	Add new	w/15 day WY-14043_M_24h	r :WY-14643/Micrie/	24.1+ WY-14643_M_29day	www.14643/Middle/29 da	WY-14843_M_3hr /WY-1	14643/Middle/3 hr
VY-148	Chamings (1997)	v4 day Show all		1)Click			and the second states of
1092 (	M15_FC1.5_outof4		DW P P-Wate	Tonoma Al Probes Ne	w Edit		
some a	Add new	M15_FC1.5_cutoff4 1					120001000000000000000000000000000000000
	Gene Sympor	PT00 W15 FG15 Octor4 2	Probe	* WY-14643_M T	WY-14643_M Ÿ	WY-14643_M 🕅	WY-14643_M %
曲	Acot1	acyl-C Delete	1396250_wt	10.307	11.123	10.505	4.068
曲	Aqp3	aquaporin 3	1387100_et	8.366	(ubased)	8.064	(Insede)
the	LOC100911217	adipogenin-like	1376296_at	6.15	(obsect)	6.052	(Interda)
the			1384474_at	7.818	4.972	8.932	(sheent)
<u>th.</u>	Chma2	cholinergic receptor - nicotinic - alpha 2 (neuronal)	1367574_at	7.573	2,579	6.721	(sbeent)
<u>th.</u>	Hide	histidine decarboxylase.	1370491_a_at	7.257	5.121	7.385	(absent)
th	Fabp3	fatty acid binding protein 3 - muscle and heart	1367660_at	6.633	2.312	8.71	(absent)
the	RGD1305928	hypothetical LOC300207	1380536_at	6.615	3.226	6.9	(phoent)
th	Acot1 Acot2	acyl-CoA thicesterase 1	1388211_s_at	6.489	5.952	6.167	2.2
the	Fbp2	fructose-1 -5-bisphosphatase 2	1368622_at	6.078	3.001	5.799	(absent)
the	Abhd3	abhydrolase domain containing 3	1382137_at	5.922	1.205	4.042	(steent)
th.			1383757_at	6.757	(sbeer)	5.399	(sbeen!)
ш	Cpt1b	camitine paimitoyitransferase 1b - muscle	1367742_at	5.648	2.053	5.454	(absent)
曲	Agp7	aquaporin 7	1368317_at	0.636	5.04	4.057	(stoent)
<u>th</u>	Spink3	serine peptidase inhibitor - Kazal type 3	1368447_x_at	5.097	1.667	4.123	0.076
ılı.	LOC100912469	acyl-CoA desaturase 2-like	1367668 a at	4.985	0.036	8,296	-0.322

iere yt	ou can inspect expres	ision values for the sample groups you h					
		4643Middle/15 day WY 19943 1/ 34hr	1)230	nrohes	in clust	er 1 are	shown
Y-14	643_M_4day :WY-14	643Midde/4 day Show	<u> </u>	PIONES	meruse		
Log2	(fold change)	1 1-25 of 239 💌 🖷 🕷 Sh	ow More Cip-value	columns M15_FC1.5_cu	doff4 / M15_FC1.5_cutoff4	1 New Edit	
	Gene Symbol	Probe Title	Probe	¥ WY-14643_M ₹	WY-14643_M ∀	₩ 14643_M Ÿ	WY-14643_M 7
<u>\$</u>	Acot1	acyl-CoA thioesterase 1	1398250_at	10.307	11.120	5	4.068
th,	Aqp3	aquaporin 3	1387100_ml	6.305	(staart)		(absent)
<u>h</u>	LOC100911217	adipogenin-like	1376296_at	8.15	(absent)	Click	(absent)
ń.			1384474_at	7.818	8.872	2)Click	(atment)
ŝ	Chma2	cholinergic receptor - nicotinic - alpha 2 (neuronal)	1387574_at	7.573	2.529	8.721	(abient)
ħ.	Hdc	histicine decarboxylase	1370491_a_at	7.257	5.121	7.385	(absent)
<u>1</u>	Fabp3	fatty acid binding protein 3 - muscle and heart	1367660_at	6.833	2.382	8.71	(sbeent)
ń.	RGD1305928	hypothetical LOC300207	1380536_at	6.615	3.226	8.8	(absent)
th.	Acot1 Acot2	acyl-CoA thioesterase 1	1388211_s_at	6.489	5.952	8.167	2.2
ŝ	Fbp2	fructose-1 -6-bisphosphatase 2	1368622_at	6.078	3.901	5.799	(absent)
ŝ.	Abhd3	abhydrolase domain containing 3	1382137_at	6.922	1.200	4.042	(absent)
<u>\$</u>			1383757_at	6.757	(investia)	5.389	(streets)
ŝ	Cpt1b	camitine painitoy/transferase 1b - muscle	1367742_M	5.648	2.953	5.414	(absort)
鱼	Aqp7	aquaporin 7	1308317_at	5.638	5.84	4.607	(streent)
<u>h</u>	Spink3	serine peptidase inhibitor - Kazal type 3	1366447_x_at	6.097	1.687	4.123	0.076
4	LOC100912469	acyl-CoA desaturase 2-like	1367668_a_at	4.986	0.038	8.298	-0.322



Start Sample groups View data Compound ranking Pathologies Sample details My data

Here you can inspect expression values for the sample groups you have defined. Click on column headers to sort data.

WY-14643\_M\_15day\_WY-14643Middle/15 day\_WY-14643\_M\_34hr\_WY-14643Middle/34 hr\_WY-14643\_M\_29day\_WY-14643Middle/29 day\_WY-14643\_M\_3hr\_WY-14643Middle/3 hr

WY-14643\_M\_4day :WY-14643/Middle/4 day Show all

Gene Sets View Tools

File

Log2 (fold change) | H + 1-25 of 239 🕑 III B Show More \_p-value columns M15\_FC1.5\_cutoff4 / M15\_FC1.5\_cutoff4 1 New Edit

(1)Click

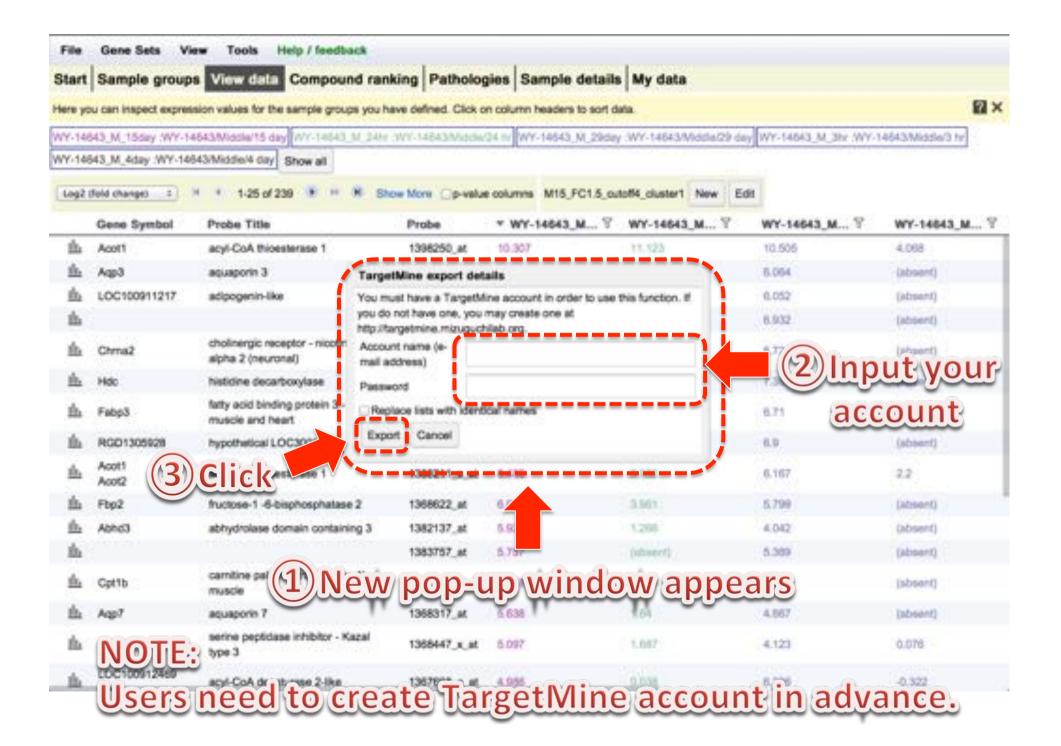
	Gene Symbol	Probe Title	Probe	¥ WY-14643_M ₹	WY-14643_M Ÿ	WY-14643_M Ÿ	WY-14643_M 7
<u>\$</u>	Acot1	acyl-CoA thioesterase 1	1396250_at	10.307	11.123	10.505	4.068
th.	Aqp3	aquaporin 3	1387100_mt	6.305	(stass)	6.064	(atment)
血	LOC100911217	adipogenin-like	1376296_at	8.15	(absent)	6.052	(absent)
血			1384474_at	7.818	4.872	8.937	(absent)
ŝ	Ctrna2	cholinergic receptor - nicotinic - alpha 2 (neuronal)	1387574_at	7.573	2.529	6.721	(absent)
ħ.	Hdc	histicine decarboxylase	1370491_a_m	7.257	5.121	7.385	(absent)
<u>\$</u>	Fabp3	fatty acid binding protein 3 - muscle and heart	1367660_at	6.833	2.382	8.71	(abuent)
ŝ.	RGD1305928	hypothetical LOC300207	1380536_at	6.615	3.226	0.9	(absent)
ħ	Acot1 Acot2	acyl-CoA thioesterase 1	1388211_s_at	6.489	5.962	8.167	2.2
曲	Fbp2	fructose-1 -6-bisphosphatase 2	1368622_at	6.078	3.901	5.799	(sboard)
ŝ.	Abhd3	abhydrolase domain containing 3	1382137_at	6.922	1.205	4.042	(adment)
血			1383757_at	6.757	(inventa)	6.389	(streeds)
ŝ	Cpt1b	camitine painitoy/transferase 1b - muscle	1367742_M	5.648	2.953	5.414	(absort)
鱼	Aqp7	aquaporin 7	1308317_at	5.638	1.04	4.667	(streent)
<u>ŝ</u>	Spink3	serine peptidase inhibitor - Kazal type 3	1368447_x_at	6.097	1.667	4.123	0.076
<u>h.</u>	LOC100912469	acyl-CoA desaturase 2-like	1367668_a_at	4.985	0.034	8.298	-0.322

X

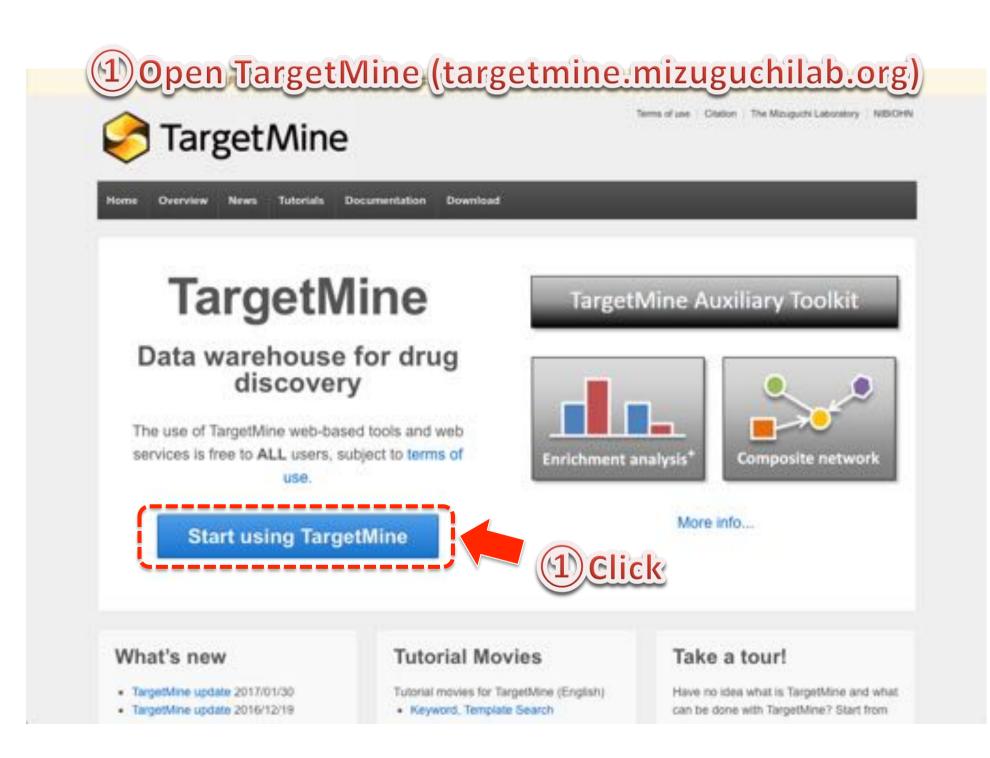
Start Sample groups	TargetMine data	• Imposi panasala kanuTarpat/kan	(1) Click	
and the second se	Compare two sample groups	Export gene sets to TargetMine		2 ×
Here you can inspect expression	Enrichment	ENOMAL.		-
WY-14643_M_15day_WY-14643/	Show heat map	Go to TargetMine	:WY-14643/Middie/29 day WY-14643 M 3hr WY-14643/Middie/3 hr	

### Leg2 fold charget = + + 1-25 of 239 + + K Show More \_p-value columns M15\_FC1.5\_cutoff4\_cluster1 New Edit

	Gene Symbol	Probe Title	Probe	▼ WY-14643_M Ÿ	WY-14643_M Y	WY-14643_M?	WY-14643_M 7
<u>th</u>	Acot1	acyl-CoA thioesterase 1	1396250_wt	10.307	11,123	10.505	4.068
曲	Aqp3	aquaporin 3	1387100_at	8.366	[sbeen]]	6.064	(absent)
<u>th</u>	LOC100911217	adipogenin-like	1376296_at	6.15	(sbeed)	6.052	(streets)
曲			1384474_M	7.818	4372	6.932	(absent)
<u>th</u>	Chma2	cholinergic receptor - nicotinic - sipha 2 (neuronal)	1387574_at	7.573	2.529	8.721	(absent)
<u>th.</u>	Hido	histidine decarboxylase	1370491_a_at	7.257	5.121	7.385	(absent)
曲	Fabp3	fatty acid binding protein 3 - muscle and heart	1367660_wt	6.833	2.562	6.71	(absent)
<u>th.</u>	RGD1305928	hypothetical LOC300207	1380536_at	6.615	3.725	8.9	(absent)
<u>th.</u>	Acot1 Acot2	acyl-CoA thioesterase 1	1388211_s_at	6.489	5.357	6.167	2.2
<u>th.</u>	Fbp2	fructose-1 -6-bisphosphatase 2	1368622_at	6.078	3.001	5.799	(Advand)
<u>th.</u>	Abhd3	abhydrolase domain containing 3	1382137_at	6.922	1.266	4.042	(Insede)
<u>th.</u>			1383757_at	6.757	(absect)	5.389	(atsent)
ш	Cpt1b	carritine palmitoyitransferase 1b - muscle	1367742_at	5.648	2.953	5.414	(absent)
山	App7	aquaporin 7	1368317_at	5.638	3.84	4.667	(absort)
th.	Spink3	serine peptidase inhibitor - Kazal type 3	1368447_x_st	5.097	5.647	4.123	0.076
th.	LOC100912469	acyl-CoA desaturase 2-like	1367668_a_at	4.905	0.000	6.295	-0.322



¥-14		and the second se	And the second sec	n column headars to sort d			12
-		4643Modw15 day WY-14043 M 3	es www.sadatamices	24.50 WY-54643_M_2956	y WY-14643/Middle/29 day	WY-14643 M 3hr WY-1	4643/06356/3 51
1014	643_M_40iy :WY-14	643/Middle/4 day Show all					
Log2	thold changet E	• • 1-25 of 239 • • • •	Show More p-value	columne M15_FC1.5_cu	tof4_cluster1 New Edit		
	Gene Symbol	Probe Title	Probe	* WY-14043_M ?	WY-14043_M_ ?	WY-14043_M 7	WY-14643_M
th.	Appt1	acyl-CoA thiosterase 1	1398250_m	10.307	11-121	10.505	4.068
<u>ш</u>	Aqp3	squeporin 3	1387100_at	8.360		5.054	(absent)
止	LOC100911217	adpogenin-like	1376296_at	6.15		8.052	(streets)
the		_	1101111	****	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	8.952	(starri)
<u>u.</u>	Chma2	cholinergic receptor - nicott Th slpha 2 (neuronal)	e lists were successfully	exported.		8.721	(Manerit)
<u>11.</u>	Hac	histidine decarboxylase			MILE	7.385	Esternity .
th.	Pebp3	faily acid binding protein 3 muscle and heart	1367660_st	4.833		8.71	(sharri)
<u>u</u>	RGD1305928	hypothetical LOC300207	1380536_at	6.615		1.0	(sizert)
ш	Acot1 Acot2	acyl-CoA thioesterase 1	1388211_s_at	6.480	1107	6.167	2.2
14	Fbp2	fructose-1 -6-bisphosphatase 2	1368622_st		lick to cl	ase	(athearth)
曲	Abhd3	abhydrolase domain containing 3	1382137_st	5.522			(addressed)
山			1383757_at	6.767		8.300	(sbaern)
th.	Cpt1b	camitine painstoytransferase 1b - muscle	1367742_st	5.648		5.414	(strante)
ile.	App7	aquaporin 7	1368317_m	5,636		8.007	(adverti)
di.	Spink3	serine peptidase inhibitor - Kazal type 3	1368447_x_ot	5.097		4.123	0.07%
ň.	LOC100912469	acyl-CoA desaturase 2-like	1367668_a_at	4.500		8.296	





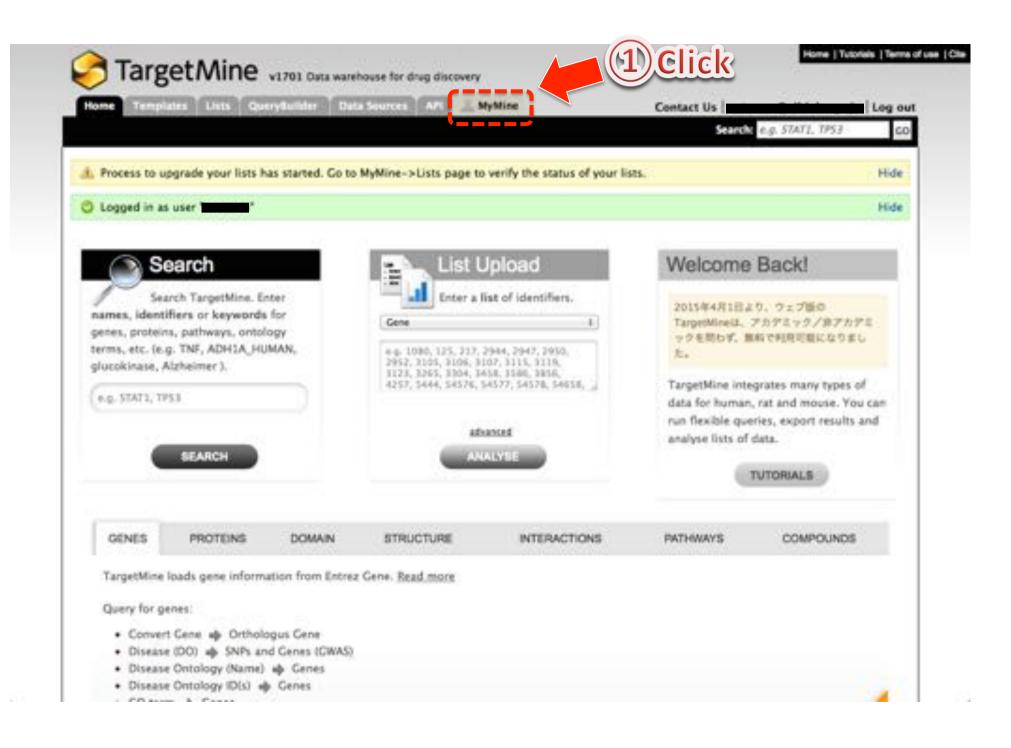
TargetMine v1701 Data warehouse for drug discovery	Home   Tutorials   Terms of use   Cite
Home Templates Lists QueryBuilder Data Sources (API 2. MyMine	Contact Us   Log in
Mulata   History   SQuerres   Account Details	Search: e.g. 51471, 7P53 60
Account	







11



TargetMine v1701 Data warehouse for drug discovery	Home    Tutoriais   Terms of use   Cite
Harre Templates Lists QueryBallder Data Sources API MyMine	Contact Us   Log out
Salists   History   SQueries   STemplates   Password   Account Details	Search: e.g. STAT2, TPS3 GD

### **Your Lists**

1

Ø	O LIST NAME	E DESCRIPTION	TYPE	I NUMBER OF OBJECTS	T PATE CREATED
0					
Ģ	MIS /CT S. could a counter D ST	Click Created with Java Wabservice Client	Gene	180 values	
0					
0					
ø					
Ø					

6	Targe	etMine v1701 0	lata warehouse for drug disc	overy	Home (Tutori	als ( Terris of us
	Home Templa		Tota Sources Art	MyMine	Contact Us	Log out
U	Ipload   View				Stranda e.g. STATI, TP53	GO
₿ <u>a</u> L	ist Analy:	sis for M15_FC1	.5_cutoff4_cluste	er1 (180 Genes	)	
🗇 Manag	e Columns				Convert to a different type	
T Manage	e Filters		Generate Python code	- 🗊 Export	Protein 185	
< Manage	e Relationships			A Save as List +	Orthologues H. sapiens (144) M. muscalus (149)	
howing ro	ws 1 to 25 of 18	0				
≎ x → T Lat Gene DB identifier	≎ x → T Lat Gene Symbol	¢ x — T iai Gene Name		C x - T Lat Gene Organism . Name		
100360507	LOC100360507	Inducible carbonyl reductase	- Ra	Pattus norvegicus	<b>1</b> Scroll dov	Nn
100362922	LOC100362922	r0G41077-like		Rattus norvegicus		
100365047	LOC100365047	scaveriger receptor class B.	member 2-like	Pattus norvegicus		
100910040	LOC100910040	Iver carboxylesterase-like		Rathus controlicute		

## NOTE: Since TargetMine updates monthly, the result can be slightly different from that in Suupelemnatry Table 2

Click to select widgets you would like to display.

Pathway Enrichment III Integrated Pathway Cluster Enrichment III Cene Ontology Enrichment III COSIIn Enrichment III Disease Enrichment
 Disease Ontology Enrichment III InterPro domain Enrichment III CATH classification Enrichment III Compound Enrichment III Tissue Enrichment

	hway Enrichme vays enriched for gen	ent es in this list - data from	n KEGG, Reactor	me and NCI		-	vay Cluster Enrich ters(PCs) enriched for ge		
Numl	per of Genes in this la	It not analysed in this w	idget: 61		Num	ber of Genes in this	list not analysed in this w	idget: 61	
Test	Correction 1	Max p-value	DataSet		Test	Correction	Max p-value	Background p	opulation
Ber	jamini Hochber 🛊	0.05 ¢	Al		Be	njamini Hochbei 😫	0.05 \$	Default Chang	<b>a</b>
1925	ground population					w Download IPCs		p-Value 🚺	Matche
Vav	Download				G	Metabolism of lipids	and Ipoproteins (9005)	8.689558e-33	58
Ð	Pathways		p-Value	Matches	Q	Glycerophospholipi	d metabolism(Arachidonic	1.120517#-8	18
0	PPAR signaling pathw	ay (mo03320)	9.552407e-22	22		acid metabolism (R	praj		
Q	Metabolism of lipids a 556833]	nd lipoproteins [R-RNO-	2.645616e-16	36	Q	Biological exidation (POOE)	siChemical carcinogenesis	5.939390e-6	18
0	Fatty acid degradation	[r10000r1]	3.654209e-14	14	G	Carbon metabolism	(R00)	0.004272	10
Ø	Biosynthesis of unsats [mo01040]	urated fallby acids	4.743065e-14	12					
0	Fatty acid metabolism	[ma01212]	1.950668e-13	34					
0	Supp	lement	ary T	able	2:				
0			_			M/4.8	8,15,29 d	dav da	ata

## **Compound ranking**

	at [ in vivo 1 [ Liver 1 ] Repeat 1	3						
	Compound			ampie group definition - ne	w group			
ick to se	e evalable lists + Save Delete		Rat/in vivo/Liver/Repeat/					
dit/pa	ste	U	0w	Middle	High			
owse	Ê	Al	All _4 day _8 day					
e.	1% cholesterol + 0.25% sodium cholate	WY- 14643	3 30 D 30 D 30 D 30	A 8 30 0 30 0 30	0 30 G A	E 30 G 33 G		
0	2,4-dinitrophenol	• •	25					
e .	WY-14643		Save group as	WY-14643_M_45ay 5	ave Automatic groups			
	acarbose	Active	Group	#Treated samples	#Control samples			
9	acetamide	( The second sec	WY-14043_M_15day	3	3	Edit	Delete	
3	acetamidofluorene				#.C.			
	acetaminophen	9	WV-14943_M_249#	3	3.5	Edit	Delete	
3	acetazolamide		WY-14043_M_29day	3	3	Edit	Delete	
2	adapin	0	WY-14643_M_3hr	3	3	Edit	Delete	
3	ajmaline allopurinol		an internet of the	1. A.		0.000		
	ally! alcohol	.8	WY-14643_M_4day	3	3	Edit	Delete	
0	amiodarone	0	WY-14643_M_8W	3	3.5	Edit	Delete	
2	amitriptyline		WY-14643.M. 6day	2	3	Edit	Delete	
	amphotericin 8					00000		
			WV-14643_M_0tw	3	3	Edit	Delete	

-----

tere yo	M15_FC1.5_cutofH NewGeneSet	Lickaster1	mper groups you	0.000 500 / 2001-000	have defined. Click on column headers to sort data.						
Log2 (	Add new Claimings (seet)		,042 🕨 🗰 🕷	Show More Cop-w	slue columns All Probes	New					
	M15_FC1.5_outoff4	•		Probe	* WY-14643_M Ÿ	WY-14643_M ∀	WY-14643_M 🕅	WY-14643_M Ÿ			
曲	Add new		borase 1	1398250_at	10.307	10.505	10.941	0.335			
曲	Agp3	adnabouu 3		1387100_at	8.366	6.064	7.499	7.185			
山	LOC100911217	adipogenin-like	•	1376296_at	8.15	6.062	5.391	5.681			
<u>ш</u>				1384474_at	7.618	6.932	6.184	8,679			
曲	Chma2	100 00100	cholinergic receptor - nicotinic - alpha 2 (neuronal)		7.573	6.721	3.367	4.603			
<u>th</u>	Hdc	histidine decar	boxylase	1370491_a_at	7.257	7.305	7.247	7.373			
<u>th.</u>	Fabp3	fatty acid bindi muscle and he		1367660_at	6.833	6.71	6.627	6.918			
曲	RGD1305928	hypothetical L/	DC300207	1380536_at	6.615	6.9	5.618	5.754			
<u>th</u> ,	Acot1 Acot2	acyl-CoA thice	isterace 1	1388211_x_at	6.489	6.167	6.76	8.733			
<u>th.</u>	Fbp2	fructose-1 -6-b	isphosphatase 2	1368622_at	6.078	5.799	4.471	8.139			
<u>th</u>	Abhd3	abhydrolase d	omain containing 3	1382137_at	5.922	4.042	5.105	1.753			
血				1383757_at	5.757	5.389	(absent)	5.54			
<u>u.</u>	Cpt1b	camitine paim muscle	camitine paimitoy/transferase 1b - muscle		5.648	5.414	5.372	5.450			
止	Aqp7	aquaporin 7		1368317_at	5.638	4.667	4.652	4.205			
щı	Spink3	serine peptide type 3	se inhibitor - Kazal	1368447_x_at	5.097	4.123	1.297	2.602			
曲	LOC100912469 Sod	acyl-CoA desa	durase 2-like	1367668_#_#t	4.988	6.296	0.636	2.691			
	0001100011	similar to Glute	aminyi-peplida								

0.20		ision values for the sample groups you h	12.242.2642.572		<u> 2602266</u> 7		1 III 1
	fold changes 2	4643/Middle/15 day WY-14643_M_29d	THE REAL PROPERTY.	alue columns All P	ALC: Discontinues	144 day (111-14643_M_Boay 111-	-186431Middle/6.day
	Gene Symbol	Probe Title	Probe	* WY-14643_8	WY-14643_M.	¥ WY-14643_M. ¥	WY-14643_M 9
ա	Acot1	acyl-CoA thioesterase 1	1398250_at	10.307	10.505	10.041	9.335
<u>u.</u>	Aqp3	aquaporin 3	1387100_at	6.366	8.064	7.499	7,105
ıh.	LOC100911217	adipogenin-like	1376296_at	8.15	6.052	5.391	5.881
th,			Edit filter			6.184	5.979
4	1) Char	fatty acid binding protein 3 - muscle and heart		xamples: 2.1, 1E-3		2) Input -1	
<u>th.</u>	RGD1305928	hypothetical LOC300207				all filter	5 6.754
<u>th</u>	Acot1 Acot2	acyl-CoA thioesterase 1	1388211_s_at	6.489	8.167	6.76	6.733
dh.	Fbp2	fructose-1 -6-bisphosphatase 2	1368622_at	6.078	5.790	4,471	8.139
ш.	Abhd3	abhydrolase domain containing 3	1382137_at	5.922	4.042	5.105	1.755
<u>h.</u>			1383757_at	5.757	5.389	(absent)	5.84
<u>du</u>	Cpt1b	camitine palmitoytransferase 1b - muscle	1367742_at	5.648	5.414	5.372	5.456
<u>h.</u>	Aqp7	aquaporin 7	1368317_at	5.638	4.667	4.852	4.205
<u>lı.</u>	Spink3	serine peptidase inhibitor - Kazal type 3	1368447_x_at	5.097	4.123	1.297	2.882
<u>di.</u>	LOC100912469 Sod	acyl-CoA desaturase 2-like	1367668_a_at	4.995	6.290	0.636	2.891
	La seconda de	similar to Glutaminyl-peptide					

sere yo	ou can inspect expres	sion values for the sample groups you h	ave defined. Click o	n column headers to sort d	lata.	22	
WY-14	1643_M_15day :WY-1	4643/Widdler15.day WY-14643_M_29d	ry WY-14643/Midd	ie/29 day WY-14643_M_4	day WY-14643/Middle/4 d	wy WY-14643_M_Bday W	V-14643/M6cdie/8 day
Log2	fold change)	H H 1-25 of 73 ▶ H K Sho	w More Op-value	columns All Probes Ne	(2)	Click	
	Gene Symbol	Probe Title	Probe	* WY-14643_M T	WY-14643_M	WY-14643_M T	WY-14643_M 1
the	LOC100362769 Mt1a Thr	hypothetical protein LOC100362769	73 pro	obes are	extracte	ed 72	-2.655
ш	Stigainec3	ST6 (alpha-N-acetyl-neuraminyl-2 -3-beta-galactosyl-1 -3)-N- acetylgalactosaminide alpha-2 -6- sialyltransferase 3	1368882_at	-1.303	-2.41	-1.582	-1.101
<u>th</u>	C8	complement component 6	1384580_at	-1.163	-1.617	-1.121	-1.527
<u>th</u>	Cyp2d4	cytochrome P450 - family 2 - subfamily d - polypeptide 4	1367913_at	-1.568	-1.623	-1.735	-1.045
th	Wipi1	WD repeat domain - phosphoinositide interacting 1	1373270_st	-1.233	-1.265	-1.364	-1.37
th	Sipi	secretory leukocyte peptidase inhibitor	1367998_at	-1.258	-1.503	-2.14	-1.332
<u>th</u>	Ass1	argininosuccinate synthase 1	1370964_at	-1,264	-1.226	-1.188	-1.500
the			1392713_s_st	-1.275	-1,208	-1.056	-1.533
曲	Ednna	endothelin receptor type A	1383641_at	-1.301	-1.958	-1.622	-1.847
<u>th</u>	LOC100362572	Mpv17 transgene - kidney disease mutant-like (predicted)-like	1377051_at	-1.331	-1.900	-1.121	-1.579
th	Lrp3	low density lipoprotein receptor- related protein 3	1368239_at	-1.344	-1.151	-1.179	-1.295
th	Plpf	protein tyrosine phosphatase - receptor type - F	1368036_at	-1.39	-1.423	-1.22	-1.422
th	Pde45	phosphodiesterase 4B - cAMP specific	1374157_at	-1.429	-1.914	-1.04	-1.674

			ies for the sample groups you f								
VY754	643_M_15day WV-5	4645WF	Gene set editor	WV.TARENTICS	aren PCa	NV-14543 M 4/	W-984-145438	toretaile reservoirsamen an	Hoay WY-	14643/Model® day	1
Logi	(fold change) 0	4.4	Title downregulated_WY		(1)	Edit					
	Gene Symbol	Pro	Keyword search				Selected p	robes		WY-14643_M	_ <b>T</b>
<u>ш.</u>	LOC100362769 Mt1a Tr	tur	This lets you view probes KEGG pathway or GO ter		-	LOC100362769 St6galnac3 (136 C6 (1364580, at	Mt1a/Ttr (13712 8882_wl)	Contraction of the second s		-2.005	
the	585painec3	311 -3-1 -809 -810	KEGG Pathway, GO term		Load	d Cyp2d4 (1387913_at) Wipi1 (1373270_at) Sipi (1367996_at) Ass1 (1370964_at)				-6.589	
the	CR	con				Ass1 (1370964_ (1392713_a_at)	#Q			-1.827	
ıh,	Cyp2d4	cyk sub	Ednra (1383641_at) LOC100362572 (1377 Lrp3 (1368239_at)				(1377051_at)			+0.040	
<u>11</u>	Wpi1	WD pho				Ptprf (1368036_) Pde4b (1374157	#() _#()			-1.37	
曲	Spi	and inte				Cyp2t1 (136826 Ptprf (1368035_				-1.332	
th.	Asa1	arg				Aboc9 (1374171 Bmf (1389902, a				-1.556	
<u>h</u>						Abcc8 (1369632	08.80			-1.333	
ш,	Ednna	enc	Add pr	obes >>		Sic22a8 (13850) Sic9a3r1 (13877				-1.047	
the	LOC100362572	Mp	Targets			Nat8 (1387336)	#0			-1.478	
di.	The second second	low	Clustering			Cyp2e11/LOC10	0911826 (13872	(28_e0)		1.000	
m	L/p3	rela	Free selection			Remove s	elected probes	Remove all probes		(4.296	
th.	Ppr	nero bua						Cancel Save		<b>(2)</b> Cli	icl
di.	Pde4b	speci	Active and the second second	1374157_M	-1.429		-1.914	-1.04		-1.874	
<u>sh</u>	Cyp2t1		strome P450 - family 2 - amily t - polypeptide 1	1366265_at	-1.471		-1.663	-1.127		4.77	
曲	Plof	prote	in tyrosine phosphatase -	1368035_a_at	-1.502		-1.407	-1.037		-1.529	

## File Gene Sets View Tools Help / feedback

## Start Sample groups View data Compound ranking

Here you can inspect expression values for the sample groups you have defined. Click on column headers to sort data.

WY-14643\_M\_16day\_WY-14643Middle/16 day\_WY-14643\_M\_20day\_WY-14643Middle/29 day\_WY-14643\_M\_4day\_WY-14643Middle/4 day\_WY-14643\_M\_0day\_WY-14643Middle/4 day

Gick My data

Log2 flold change) 1 H 4 1-25 of 73 🕨 H 🕷 Show More \_p-value columns downregulated\_WY New Edit

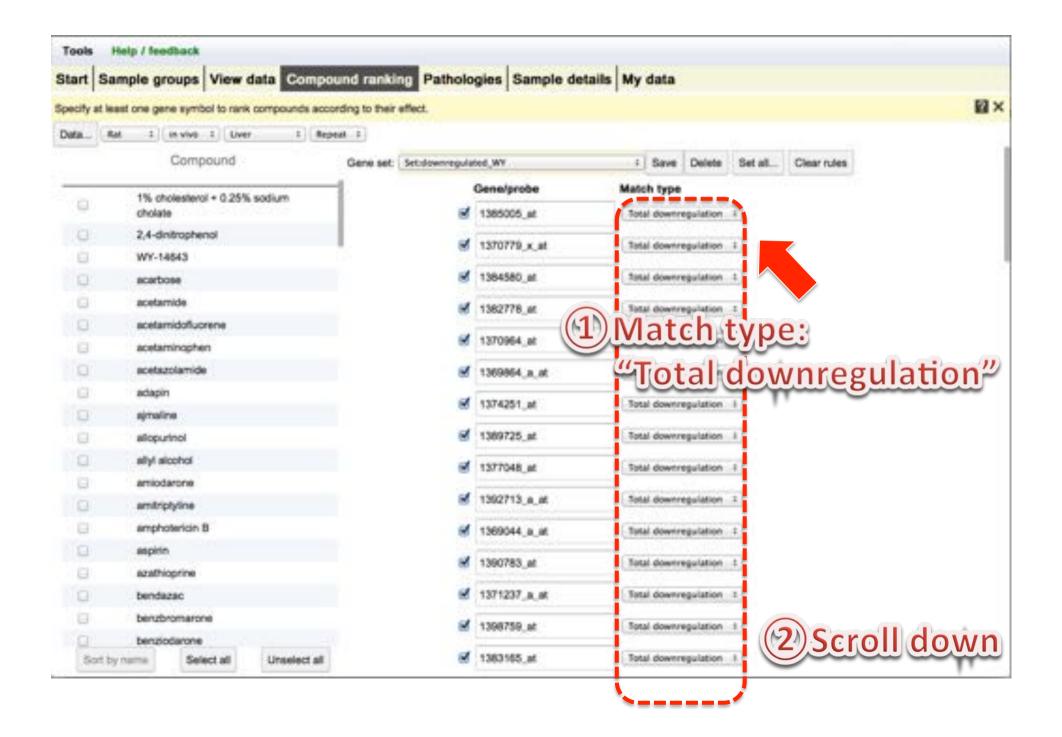
	Gene Symbol	Probe Title	Probe	* WY-14643_M ?	WY-14643_M ?	WY-14643_M ?	WY-14643_M 7
ш,	LOC100362769 Mt1a Tir	transtityretin	1371237_a_at	-1.068	-2.126	-2.372	-2.855
dı.	Stégainac3	ST8 (alpha-N-acetyl-neuraminyl-2 -3-beta galactosyl-1 -3)-N- acetylgalactosaminide alpha-2 -6- sialyttransferase 3	1368682, at	-1.503	-2.41	-1.582	-1.181
<u>14.</u>	C6	complement component 6	1384580_at	-1.163	-1.817	-1.121	1.527
<u>h</u>	Cyp2d4	cytochrome P450 - family 2 - subfamily d - polypeptide 4	1387913_at	-1.568	-1.623	-1.735	-1,845
dı.	Wpi1	WD repeat domain - phosphoinositide interacting 1	1373270_at	-1.233	-1.268	-1.364	-1.37
ш	Sipi	secretory leukocyte peptidase inhibitor	1367998_at	-1,258	-1.503	-2.14	-1.332
ш	Asst	argininosuccinate synthase 1	1370964_at	-1.284	-1.228	-1.188	1.506
dh.			1392713_a_at	-1.275	-1.208	-1.058	-1.000
<u>11.</u>	Ednra	endothelin receptor type A	1383641_at	-1.301	-1.959	-1.522	-1.842
<u>h</u> .	LOC100362572	Mpv17 transgene - kidney disease mutant-like (predicted)-like	1377051_at	-1.301	-1,108	-1.121	-1.579
ılı.	երմ	low density lipoprotein receptor- related protein 3	1368239_at	-1.344	-1.151	-1.179	+1.295
ф	Plant	protein tyrosine phosphatase - receptor type - F	1368036_at	-1.39	-1.423	-1.22	-1.422
da.	Pde4b	phosphodiesterase 48 - cAMP specific	1374157_at	-1.429	-1,914	-1.04	+1.074

**N**×

	Help / feedback	Tranking Pathologies Sample details My data
	ast one gene symbol to rank compounds	
da		
	Compound	Gene set Cick to see available lists i Save Delete Set al Clear rules
0	2,4-dinitrophenol	Gene/probe Match type
0	2-nitrofluorene	Upregulation . 1
0	3-methylcholanthrene	Bank
0	LPS	
12	N-methyl-N-nitrosourea	2 Select "Set:downregulated_WY"
0	N-nitrosomorpholine	
	TNFelpha	
0	WY-14643	
12	acarbose	
0	acetamidofluorene	
0	acetaminophen	
G.:	acetazolamide	
0	adapin	
0.	aflatoxin B1	
0	ajmaline	
0	allopurinol	
8	ally/ alcohol	
0	amiodarone	
8	amitriptyline	
0	amphotericin B	

	sast one gene symbol to rank compounds ac	cording to their effect.			
18	lat I invivo I Liver I a	epeat #			
	Compound	Gene set: Set.downregula	ced_WY	i Save Delete Set al.	Clear rules
-	1% cholesterol + 0.25% sodium	-1	Gene/probe	Match type	
9	cholate	8	1385005_at	Total upregulation 1	
8	2,4-dinitrophenol		1370779_x_at	Total upregulation #	
G	WY-14643		13/07/9,8,8		
0	acarbose	8	1384580_at	Total upregulation 1	
G	acetamide	(	1) Solo	total dou	vnregulation
0	acetamidofluorene				vincgulation
G	acetaminophen		1370964_at	Total upregulation 1	
0	acetazolamide	8	1309864_a_at	Total upregulation 7	
3	adapin	4	1374251_at	(Total upregulation 1)	
	ajmaline		1014601,001	( the spope of the	
8	allopurinol	S.	1389725_at	Total upregulation 2	
D.	allyl alcohol	8	1377048_at	Total upregulation 1	
3	amiodarone				
9	amitriptyline		1392713_a_at	Total upregulation 1	
0	amphotenicin B	st.	1309044_a_at	Total upregulation 2	
9	aspirin	2	1390783.at	(Total upregulation 1)	
3	azathioprine				
9	bendazad	9	1371237_a_at	Total upregulation 1	
9	benzbromarone	8	1398759_at	Total upregulation	
0	benziodarone				

ity at lea	at one gene symbol to rank compounds as	coording to their effect.							12
8_ (R.	( 1) ( 14 viug 1) ( Uver 1) ( 1	apeat 2							
	Compound	Gene set. Setutes	nitgila	ted_WV	: Save	Delete	Set al.	Clear rules	
_	1% cholesterol + 0.25% sodium	-		Gene/probe	Match type				
	cholate			1385005_M	Total downe	rgulation	±		
	2,4-dintrophenol			1370775 x.ml	Tatal Levep	Aution	1	_	
	WY-14643		100						
	acertose		1	1384580,at	Total uprep	alation .		1) Click	
	acetamide	-		1382778 at	Tatal uprep	- control			
	acetamidofluorene								
	acetaminophen	Overwrite all ruk	e param	eters by copying the first	1207		<u> </u>		
	acetazolamide				*+>**	1	1		
	adapin	-	1	1374251_#	Table sprep		-		
	ajmaine								
	aloputrol		s	1389725_st	Tatal uprep	utation	<u>#</u>		
	ally! alcohol		đ	1377048_M	Total serve	alation	¥)		
	amiodarorw			1302713 A.M	Total server	and the second	÷1		
	ambiptyline					anta_			
	amphotericin B		-	1369044_a_at	Batat Levrep	Autient	*		
	aspinn			1390783.at	Total upreg	elabora .	4		
	azathloprine			per contraction of the second s					
	bendazec			1371237_R_st	Tatal upreg	allings -	쾨		
	benzbromarone		1	1398759_at	Tatal uprep	ulation	10		



ipecify at le	east one gene symbol to rank comp	ounds according to their effect.			2 × 12
Deta_	Aut 1 (in vive 1) Liver	I Repeat I	*		
	Compound		1390873_at	Total downregulation 2	
	1% cholesterol + 0.25% sodiu		1369491_at	Total downregulation 1	
0	cholate	S 8	1385001_at	Total downvegulation ( 1	
0	2,4-dinitrophenol		√ 1369632 a_at	Total downregulation 1	
0	WY-14643		5 1009608_8_8_8	(	
0	acarbose		2 1309440_at	Total downregulation I	
0	acetamide		Z 1300953_at	Total downrogulation 8	
0	acetamidofluorene		₹ 1383111_at	Total downrogulation - I	
0	acetaminophen		e 1303111,38	tota operreguation 1	
0	acetazolamide		₫ 1377472_at	Total downregulation 4	
0	adapin		1383641_at	Total downregulation ==	
0	ajmaline		√ 1368239_at	(*************************************	
0	aliopurinol aliopholi		₫ 1368239_wt	Total downregulation 2	
12	amiodarone		1369973_at	Total dowrvegulation =	
Rai	amitriptyline		1387913_at	Total downregulation 1	
0	amphotericin B		✓ 1368543 at	Total downregulation 1	
10	aspirtin		s 1300043,at	( tota operation 1)	
0	azathioprine		2 1387063_at	Total downregulation 1	
0	bendazac		2 1307998_at	Total downvogulation 1	
0	benzbromarone		0	Total downrogulation I	
0	benziodarone		-	Conta doern egenander 1	

ty at	Rat 1 in vivo 1	0.000	1 Repeat		ick for r	next analysis	F
-	Compoun	d.		<u> </u>	Z 1390673_at	Total downregulation is	
		Score	1		1369491_at	Total downregulation 8	
a)	WY-14643	34.985 (1)	<u>#</u>		2 1385001_at	Total downregulation 8	
2	fenofibrate	25.208 (2)	the		l 1369632_a_at	Total downregulation 1	
5	methapyrliene	19.388 (3)	the		/ 1369440_at	Total downregulation 3	
5	nitrosodiethylamine	11.938	th		/ 1386053_at	Total downregulation 1	
si.	thioacetamide	9,803	th.		1383111_at	Total downregulation 1	
2	ethambutol	9.78	th		esult o	f compound ranking	5
	methylene dianiline	9.586	<u>th.</u>		1368239_at	Total downregulation (	
2	ethionamide	9.426	曲		/ 1369973_at	Total downregulation 8	
	acetamidofuorene	8.304	the		2 1387913_at	{ Total downregulation #	
2	meloxicam	5.085	曲		1368543_at	Total downregulation 1	
3	genfibrazi	5.072	the		1387053_at	Total downregulation 2	
	terbinafine	5.048	<u>th</u>		- 1.437 900 (at	Contraction of the second s	

## **Welch's t-test filtering**

	1 Click to	ve defined. Click of	dolumn headers to sort da	la.		2
	M_295e	/WY-14643/Middle	x29 day WY-14643_M_4d	iy WY-14643/Middle/4 d	WY-14643_M_85ey_WY	14643/Middle/Ti day
¢		More Opvalue o	olumns downregulated_W	Y New Edit		
]	:	Probe	▼ WY-14643_M 🗟	WY-14643_M 7	WY-14643_M Ÿ	WY-14643_M ∛
		1371237_a_at	-1.098	2.120	-2.372	-2.855
	194-2 2-6-	1368882_at	-1.103	-2.41	-1.582	-1.191
	i.	1384560_at	-1.163	-1.617	-1,121	-1.527
	:	1387913_at	-1.105	-1.623	-1.735	-1.645
	:	1373270_at	-1.233	-1.206	-1.364	-1.32
		1367998_at	-1.258	-1.503	-2.14	-1.332
	:	1370964_at	-1.204	-1.226	-1,188	-1.509
		1392713_#_#I	-1.275	-1.208	-1.058	-1.333
	•	1383641_at	-1.301	-1.959	-1.522	-1,847
	asse a	1377061_at	-1.331	-1.106	-1.121	-1.579
	* ×.	1368239_at	-1.344	-1.151	-1,179	-1.298
	2	1368036_at	-1.39	-1.423	-1.22	-1.422
	• •	1374157_at	-1.429	-1.914	-1.04	-1.874

File Gene Sets View	Tools K	Click		
Start Sample groups	Targettike det	Import pane sets from "vetMine	My data	
Here you can burned experience	Compare two sample groups		ct	<b>X</b>
Here you can inspect expression	Errichment	Em		
WY-14643_M_15day :WY-14643	Show heat map	Go to TargetVine	ay WY-14643/Middle/4 day WY-14643_M_Boxy (WY-14643/Middle/8 day	

Leg2 (fold changes 4 H 4 1-25 of 31,042 💌 🗰 🕷 Show More p-value columns All Probes New Edit

	Gene Symbol	Probe Title	Probe	* WY-14643_M ?	WY-14643_M ?	WY-14643_M 🕅	WY-14643_M 🖗
<u>th</u>	Acot1	acyl-CoA thioesterase 1	1398250_at	10.307	10.005	10.941	0.335
止	Aqp3	aquaporin 3	1387100_at	6.360	6.064	7.499	7.185
<u>th</u>	LOC100911217	adipogenin-like	1376296_at	8.15	6.052	5.391	5.681
曲			1384474_at	7.818	6.932	8.164	5.679
the	Chma2	cholinergic receptor - nicotinic - alpha 2 (neuronal)	1387574_at	7.573	6.721	3,357	4.693
止	Hido	histidne decarboxylase	1370491_a_at	7.257	7.385	7.247	7.573
th	Fabp3	fatty acid binding protein 3 - muscle and heart	1367660_at	6.833	6.71	6.627	6.918
曲	RGD1305928	hypothetical LOC300207	1380536_at	6.615	6.9	5.616	5754
th	Acot1 Acot2	acyl-CoA thioesterase 2	1388211_s_M	6.489	6.167	6.76	6.733
胁	Fbp2	fructose-1 -6-biaphosphatase 2	1368622_at	6.078	5.799	4.471	6.139
the	Abhd3	abhydrolese domain containing 3	1382137_at	5.922	4.042	5.105	1,753
曲			1383757_at	5.757	5.389	(absent)	5.54
曲	Cpt1b	camitine paimtoyltransferase 1b - muscle	1367742_at	5.648	5.414	5.372	5.455
肍	Aqp7	aquaporin 7	1368317_at	5.638	4.667	4.852	4.205
th	Spink3	serine peptidase inhibitor - Kazal type 3	1368447_x_st	5.097	4.123	1.297	2.692
<u>th</u>	LOC100912499 Sod	stearoyi-CoA desaturase (delta-9- desaturase)	1367868_a_al	4.986	6.296	0.636	2.891
d.		similar to Glutaminel-peotide	100000				

100	u can inspect express		The wards	column headers to so		NAME AND ADDRESS AND ADDRESS ADDRE	2
.693 ( W-14	fold change) t	* * 1-25 of 31.042 * # # * - 1-4643_M_4day 1 Add T-Teat A	dore _p-val	ue columns All Prob id-change difference	es New Edit Remove tests	WY-14643_M 7	WY-14643_M ₹
ıh.	Aced 1	anyl Cott Biosethrase 1	1396250_at	10.307	10.505	10.941	0.335
<u>th</u>	Aqp3	aquaporin 3	(13) C	lick	6.064	7,499	7,186
th.	LOC1009112*	adipogenin-like		IICK	0.052	5.391	5,801
<u>h.</u>			1384474_at	7.818	6.937	6.184	5.979
th <u></u>	Chma2	cholinergic receptor - nicotinic - alpha 2 (neuronal)	1387574_at	7,573	8.721	3-357	4.695
46	2) Sala	ct "WY=1464		4day"	7.385	7.247	7.373
1	2 JEIE			Huay	8.71	6.627	5.918
<u>th</u>	RSD and	"WY-14643	<u>M_8c</u>	lay"	6.9	5.618	5.754
<u>th</u>	Acot2	acyl-CoA thioestenase 2	1386211_s_at	8.488	6.167	6.76	E.733
th,	Fbp2	fructose-1 -6-bisphosphatase 2	1368622_at	6.078	5.799	4.471	10,150
di,	Abhd3	abhydrolase domain containing 3	1382137_at	5.922	4.042	5.105	1.763
di.			1383757_at	5.757	5.389	(absent)	5.54
th.	Cpt1b	camitine paimitoytransferase 1b - muscle	1367742_at	5.648	5.414	5.372	E-450
th.	Agp7	aquaporin 7	1368317_at	5.638	4.667	4.852	4.205
th.	Spink3	serine peptidase inhibitor - Kazal type 3	1368447_x_at	5.097	4.123	1.297	2,692
	LOC100912489	stearoyi-CoA desaturase (delta-9-	1367668 a at	1.001	8.106	0.636	1 891

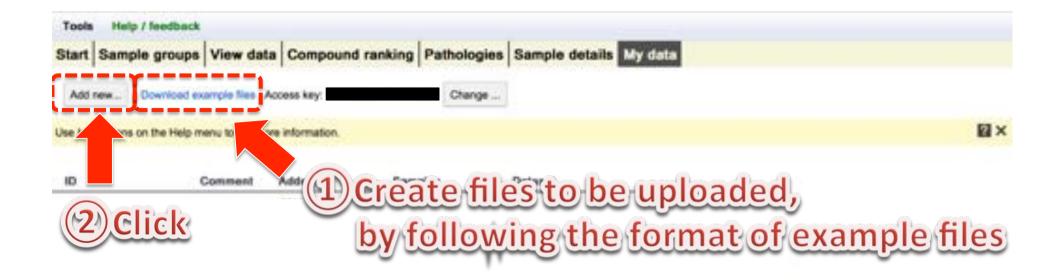
Sta	rt Sample groups View data	Compound r	anking Pathologie	Sample details		Vewlyap		
lene	you can inspect expression values for the	sample groups yo	u have defined. Click on a	column headers to sort dat			2)Clic	
NY	14643_M_15day /WY-14643/Middle/15 da	NY-14643_M_3	196ey WY-14643/Model	29 day WY-14643_M_4da	y :WY-14643/Middle/4 day	WY-14643_M		
Log2 (fold change) - 1 + 1-25 of 31,042 • • • Show More _p-value columns All Probes New Edit								
WY	-14643_M_4day1   WY-14643_M_8day	F Add T-Test	Add U-Test Add fok	5-change difference Re	move tests			
	Probe Title	Probe	* WY-14643_M Y	WY-14643_M Y	WY-14643_M_ 7	WY-14643_M Y	(T) p(WY-1 🗑	
	acyl-CoA thioesterase 1	1396250_at	10.307	10.505	10.941	0.335	0.001	
	aquaporin 3	1387100_st	8.300	6.004	7.499	7.165	0.997	
	adipogenin-like	1376296_at	8.15	6.052	5.391	5.881	0.434	
		1384474_at	7.818	6.932	6.184	5.979	0.703	
	cholinergic receptor - nicotinic - alpha 2 (neuronal)	1387574_at	7.573	6.721	3.357	4.603	0.027	
	histidine decarboxylase	1370491_a_at	7.257	7,385	7.247	7.373	0.693	
	fatty acid binding protein 3 - muscle and heart	1367660_at	6.833	6.71	6.627	6.918	0.37	
	hypothetical LOC300207	1380536_at	6.015	6.9	5.616	5.754	0.682	
	acyl-CoA thioesterase 2	1386211_s_at	6.439	6.167	6.76	6.733	0.879	
	fructose-1 -6-bisphosphatase 2	1366622_at	6.078	5.799	4.471	6.139	0.007	
	abhydrolase domain containing 3	1382137_at	5.922	4.042	6.105	1.753	0.069	
		1383757_at	5.757	5.389	(absent)	1.54	(absent)	
	camitine palmitoyitransferase 1b - muscle	1367742_at	5.648	5.414	5.372	8.458	0.755	
	aquaporin 7	1368317_at	5.638	4.667	4.852	4.205	0.134	
	serine peptidase inhibitor - Kazal type 3	1368447_x_st	5.097	4.123	1.297	2.692	0.07	
1	stearoyi-CoA desaturase (delta-8-			0.200	0.000	-	0.001	

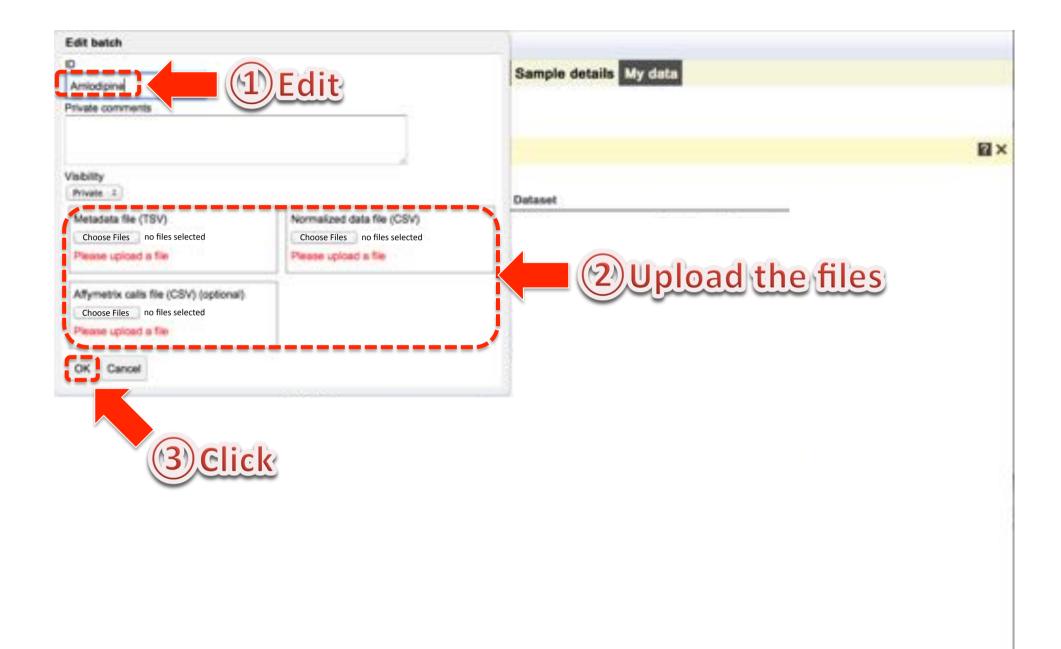
Hen	you can inspect expression values for t	the sample groups y	ou have defined. Click	on column headers to sort di	rta.		<b>國</b> ×
iNY	-14643_M_15day /WY-14643/Middle/15	day WY-14643_M	29day :WY-14643/Mid	Se/29 day WY-14643_M_4	Say :WY-14643/Middler4 day	WY-14643_M_Bday_WY-	146433Middlefti Gay
Lo	g2 (feld change) 1 H 4 1-25 d	(31,042 )	B Show More Op-	alue columns All Probes	New Edit		
-	-14643_M_4day =1 (1) NG		nnoarc	fold chance differences B	and the second second		
-	Probe Title	Probe	ppears	fold-change difference R	WY-14643_M 7	WY-14643_M 🗑	(T) p(WY-1 T
	acyl-CoA thioestenase 1	13962	10.307	10.505	10.941	8.335	0.001
	aquaporin 3	1387100	1			7.185	0.997
	adipogenin-lika	1376296	Edit filter			5.601	0.434
		1384474_at		choose a bound for '(T) p(W ay, WY-14643_M_8day)'. Ex		5.979	0.703
	cholinergic receptor - nicotinic - alpha 2 (neuronal)	1387574_at	57	2.1, 16-3		201	0.027
	histidine decarboxylase	1370491_a_at	25			2)Input	0.01
	fatty acid binding protein 3 - muscle and heart	1367660_at	83	OK Clear filter		8.918	0.37
	hypothetical LOC300207	1380536_at	8.635		5.616	5.754	0.682
	acyl-CoA thioesterase 2	1386211_s_at	6.489	167	6.76	8.738	0.879
	fructose-1 -6-bisphosphatase 2	1368622_at	8.078	E 799	4,471	8.139	0.007
	abhydrolase domain containing 3	1382137_st	5.922 ((13)	Click	5.105	1.753	0.069
		1383757_at	5.757	5.309	(absent)	5.54	(absent)
	camitine palmitoyltransferase 1b - muscle	1367742,at	5.648	5.414	5.372	ñ 456	0.755
	aquaporin 7	1366317_at	5.638	4.867	4.852	4.205	0.134
	serine peptidase inhibitor - Kazal type 3	1366447_x_at	5.097	4.123	1.297	2.692	0.07
	stearoyl-CoA desaturase (delta-9-	1367055 a at		6.295	0.436	1000	0.001

lene yo	u can inspect expres	ssion v. Or the sample groups you h	ave defined. Click o	n column headers to sort	Seta.		8
VY-14	643_M_15day WY-1	14543/www.15 day_WY-14643_M_296	iy /WY-14643/Midd	le/29 day WY-14643_M_4	kday :WY-14643/Middler4	day WY-14643_M_85ay WY	14543/Widdle/Tidey
Log2 (	(fold change) t	1 1-25 of 618 🕑 🖶 🕷 Sh	ow More Dp-value	e columns All Probes N	ew Edit		
WY-14	4643_M_4day 1	WY-14643_M_Bday 1 Add T-Test /	Add U-Test Add	fold-change difference	Remo		
	Gene Symbol	Probe Title	Probe	* WY-14643_M_ ?	WY-140	WY-14643_M Ÿ	WY-14643_M Ÿ
此	Acot1	acyl-CoA thioestarase 1	1398250_at	(D) Carro	thoram	to hac ac	9.335
曲	Fbp2	fructose-1 -6-bisphosphatase 2	1368622_at	<b>Z</b> Save	<u>unese p</u>	robes as	6.139
the	LOC100912469 Sod	stearoyl-CoA desaturase (delta-9- desaturase)	1367668_a_at	4565 "M4	vsM8 p	0.01"	2,891
th	Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)	1387631_m	4.595	3.303	1.831	4.195
止	Asns	asparagine synthetase (glutamine- hydrolyzing)	1387925_at	4.090	4.058	1.995	3.204
曲	Aldh1a1	aldehyde dehydrogenase 1 family - member A1	1387022_st	3.688	3.437	3.251	3.654
止	Ech1	encyl CoA hydratase 1 - peroxisomal	1386885_at	3.364	3.451	3.212	3.611
th	Ehhadh	encyl-CoA - hydratase/3- hydroxyacyl CoA dehydrogenase	1368283_at	3.044	3.139	3.129	3.557
曲	Acaa1a Acaa1b	acetyl-Coenzyme A acyltransfenase 1B	1387783_a_at	2.744	3.016	2.894	3.253
<u>th.</u>	Sort1	sortilin-related receptor - LDLR class A repeats-containing	1394786_at	2.499	2.036	1.326	1,744
the	Ten1	TEN1 telomerase capping complex subunit	1383230_at	2.458	3.131	0.812	1.949
曲	Max	myo-inositol oxygenase	1367937_at	2.306	2.581	2.701	2.02
<u>th</u>	Lanc2	taminin - gamma 2	1379340_at	1.689	(absent)	1.031	2.957
- alar	boot.	imports 5	1306742 #	1411	1.268	0.889	100

## **Uploading user data to aid the investigation**

1		ession values for the sample groups you h 14643/Middle/16 day WY-14643_M_290				WV-14643_M_Bday_WV	-14643/Modie/8 day
Log2	(fold change) 1	🖂 4 1-25 of 618 💌 🗰 🕷 S	how More  _p-value	e columns M4vsM8_p0.01	New Edit	(1)Click	49
w-14	4643_M_4day 4	wy-14643_M_8day I Add T-Test	Add U-Test Add	bld-change difference	ternove teeta		
	Gene Symbol	Probe Title	Probe	* WY-14643_M 🕅	WY-14643_M 🕅	WY-14643_M ∀	WY-14643_M ?
sh.	Acot1	acyl-CoA thioesterase 1	1398250_at	10.307	10.505	10.941	0.535
<u>6</u> .	Fbp2	fructose-1 -6-bisphosphatase 2	1308622_at	8.078	5.799	4.471	0.139
<u>1</u>	LOC100912469 Sod	stearoyl-CoA desaturase (delta-9- desaturase)	1367668_a_at	4.995	6.296	0.636	2,891
ń.	Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)	1387631_M	4.595	3.303	1.831	4.105
<u>h</u>	Asns	asparagine synthetase (glutamine- hydrolyzing)	1387925_at	4.098	4.068	1.996	3.204
sh.	Aldh1a1	aldehyde dehydrogenase 1 family - member A1	1387022_at	1.688	3.437	3.251	3.654
sh.	Ech1	encyl CoA hydratase 1 - peroxisomal	1386885_at	3.364	3.451	3.212	3.611
da,	Ehhadh	encyl-CoA - hydratase/3- hydroxyacyl CoA dehydrogenase	1368283_at	3.044	3.139	3.129	3.557
th.	Acasta Acastb	acetyl-Coenzyme A acytransferase 1B	1387783_a_at	2,744	3.016	2.894	3.253
ŝ.	Sort1	sortilin-related receptor - LDLR class A repeats-containing	1394786_at	2.499	2.036	1.326	1.764
ŝ.	Tent	TEN1 telomerase capping complex subunit	1383230_at	2.450	3.131	0.812	1.049
ŝ.	Mick	myo-inositol oxygenase	1367937_at	2.300	2.581	2.701	2.00
<u>\$</u>	Lamo2	taminin - gamma 2	1379340_at	1,889	(abeent)	1.031	2.962
6.	inni	importin 5	1308242 at	1411	1 268	0.660	1 401

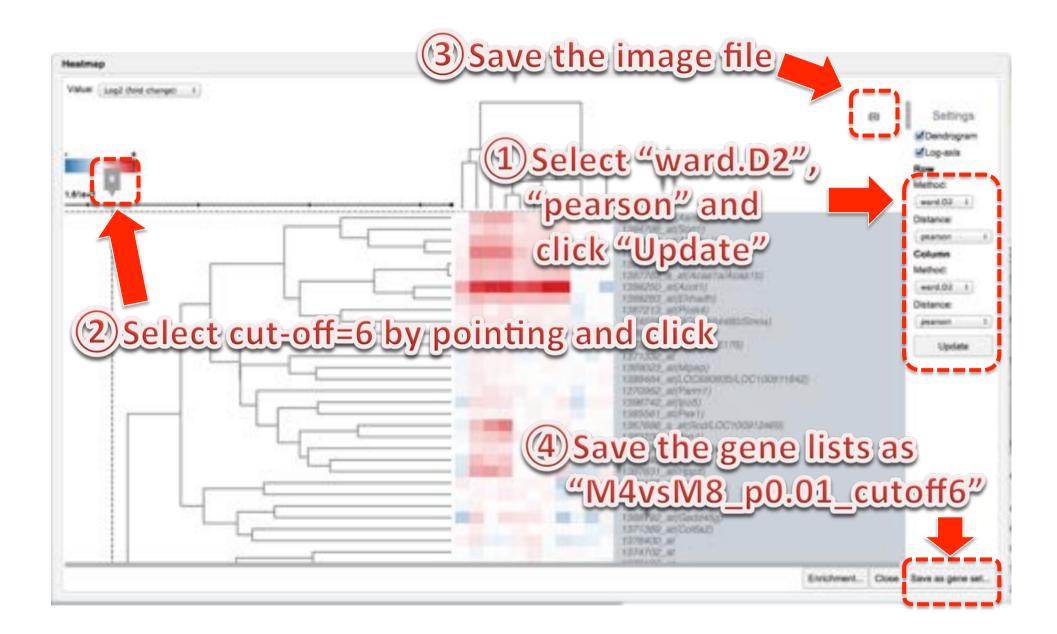




84	z 1 in vivo 1 Liver, 1 Repeat 1						
.,	Compound	8	Sa	mple group definition - ner	w group		
D	Newly appear	clin	"Samplo o	rounc <sup>20</sup> n	200		
Upa		200	Jampie	Joupstop			
wse		0					
		(2)	Save WY-1	4643 sing	gle dose d	data	and
ł,	cholesterol + 0.25% sodium						
1	2,4-dinitrophenol	ŀ	Amlodipin	e data as	introduc	ed a	bov
							~~~~
1	Am/odipine (user)						
	Amlodipine (user) GW3965 (user)	Active	Group	#Treated samples	#Control samples		
		Active	Group Ansodgen, L., 26hr	#Treated samples	#Control samples	Edit	Delete
	GW3965 (user)	Active	Aniodipin_1_29hr	#Treated samples	14		C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.
	GW3965 (user) PF-04923503 WY-14643 acarbose			a a	14 20	Edit	C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.
2	GW3965 (user) PF-04923503 WY-14643 acarbose acetamide	Active S S	Aniodipin_1_29hr	#Treated samples	14		Delete
	GW3965 [user] PF-04923503 WY-14643 acarbose acetamide acetamide		Antodipin_L_26hr Amtodipin_L_5hr	a a	14 20	Edit	Delete Delete Delete
2	GW3965 (user) PF-04923503 WY-14643 acatbose acetamide acetamidofluorene acetaminophen		Antiodipin_L_2ktr Amlodipin_L_Shr Amlodipin_M_3day WY-14643_M_15day	a a a	14 20 12	Edt Edt Edt	Delete
2	GW3965 (user) PF-04923503 WY-14643 acarbose acetamide acetamidofluorene acetaminophen acetazolamide	8 8 8 8	Antodipin_L_2Khr Antodipin_L_Shr Antodipin_M_3day WY-14643_M_15day WY-14643_M_24hr	a a a a	14 20 12	Edit Edit Edit Edit	Delete Delete Delete Delete
2	GW3965 (user) PF-04923503 WY-14643 acarbose acetamide acetamidefluorene acetaminophen acetazolamide adapin		Antiodipin_L_2ktr Amlodipin_L_Shr Amlodipin_M_3day WY-14643_M_15day	a a a	14 20 12	Edt Edt Edt	Delete Delete Delete Delete
2	GW3965 (user) PF-04923503 WY-14643 acarbose acetamide acetamidofluorene acetaminophen acetazolamide	8 8 8 8	Antodipin_L_2Khr Antodipin_L_Shr Antodipin_M_3day WY-14643_M_15day WY-14643_M_24hr	a a a a	14 20 12	Edit Edit Edit Edit	Delete Delete Delete
	GW3965 (user) PF-04923503 WYY-14643 acarbose acetamide acetamidofluorene acetaminophen acetaminophen acetazolamide adapin ajmaline	8 8 8 8 8 8 8	Antodipin_L_2khr Antodipin_L_Shr Antodipin_M_3day WY-14643_M_15day WY-14643_M_24hv WY-14643_M_24kv	3 3 3 3 3	14 20 12	Edit Edit Edit Edit Edit	Delete Delete Delete Delete

-

Start	Sample group			ts from TargetMine ts to TargetMine	My data		
niod	ou can inspect expres pin_L_240vr Amlodipi pin_L_340vr Amlodipi	Show heat map	Enter net.		ta Ct dipine (user)/Middle	/3 day WY-14643_M_16da	y :WY-14643/Middle/15 day
	(fold change) = 1			e columns M4vsM8_p0.0	New Edit		
	Gene Symbol	Probe Title	Probe	▼ Amlodipin ₹	Amlodipin V	Aniodipin Y	WY-14643_M_, 7
the	Ottnbp2	cortactin binding protein 2	1382913_at	0.906	0,528	0.233	-0.416
血		_	1382236_at	0.797	D.446	-0.119	0.084
th	9(11) If	M4vsM8_p0	011n	-618) ic	not dicr	havel	-2.618
曲	G		.OT(II		lingans	Jiayeu,	0.678
the	KINS CLI	ck "Gene Set	ts" an	d select	MAvsM	8 n0 01	0.235
曲	CII	un dene be		M JUILUL			
			1395373_st		Dillion in the second		0411
th	Aldh1a1	aldehyde dehydrogenase 1 family - member A1	1395373_at	0.042	0.223	-0.073	
th th	Aldh1a1 Adh7		1385373_87 1387022_at 1389072_at	- 6 (dati	- Billing	~	0.411
фь фь фь		- member A1 alcohol dehydrogenase 7 (class	-	0.043	0.223	-0.073	2.688
-	Adh7	- member A1 alcohol dehydrogenase 7 (class IV) - mu or sigma polypeptide	1369072_at	0.042	0.223	-0.073 -0.544	0.411
<u>њ</u>	Adh7 Sv2b	- member A1     alcohol dehydrogenase 7 (class     IV) - mu or sigma polypeptide     synaptic vesicle glycoprotein 20     pleckstrin homology domain     containing - family B (evectins)	1369072_at 1369628_at	0.042 0.03 0.672	0.225 0.011 0.444	-0.073 -0.544 -0.164	0.411 2.688 0.98 0.221
出	Adh7 Sv2b Plekhb2	- member A1 alcohol dehydrogenase 7 (class IV) - mu or sigma polypeptide synaptic vesicle glycoprotein 2b pleckstrin homology domain containing - family B (evectins) member 2	1369072_at 1369628_at 1376137_at	0.04J 0.03 0.672 0.048	0.223 0.011 0.444 -0.902	-0.073 -0.544 -0.164 0.318	0.411 1.688 0.98 0.221 0.56
出出出	Adh7 Sv2b Plekhb2	- member A1 alcohol dehydrogenase 7 (class IV) - mu or sigma polypeptide synaptic vesicle glycoprotein 2b pleckstrin homology domain containing - family B (evectins) member 2	1369072_at 1369628_at 1376137_at 1396742_at	0.042 0.63 0.672 0.948 0.516	0.223 0.011 0.444 0.902 0.664	-0.073 -0.544 -0.164 0.318 0.567	0.411 3.088 0.98 0.221 0.56 1.411
	Adh7 Sv2b Plekhb2	- member A1 alcohol dehydrogenase 7 (class IV) - mu or sigma polypeptide synaptic vesicle glycoprotein 2b pleckstrin homology domain containing - family B (evectins) member 2	1369072_at 1369628_at 1376137_at 1396742_at 1370544_at	0.042 0.042 0.0572 0.048 0.0516	0.223 0.011 0.444 -0.902 -0.664 0.547	-0.073 -0.544 -0.164 0.318 0.567 -0.162	0.411 2.086 0.98 0.221 0.56 1.411 0.154



		vereate a n	eatmap	as intr	oduced	above
(Hersel )	H + 1-25 of 268	→Fig.2A	WAB_DD 21_0.4085/144+eM8	plist, out #1 New 1	Con .	
Fig 2R.	Select M/ws	V18 p0.01 cutoff6 2	and create	a heatman		
•		<pre>//8_p0.01_cutoff6 3</pre>		•		
01181	- member A1	SHOUL M LINE	0.025	40.67.8	7.500	11.00
10	alcohol dehydrogenase 7 (c) fv) - mu or sigma poly	1300072_41	RATS	0.544	0.00	0.076
NN62	pleckatrin homology	export gen	e lists t	o Targe	etMine	1.04
6	importin 5	asintrodu	ced abo	Ve	5411	10.500
		1379544 H		-0.1HZ	0.154	-0.154
	esparagine synthetase (glut hydrolyzing)	\$387925,at 0.496	0.837	-0.423	4.096	0.421