Creating a gene list using the Venn Diagram

The List Manager can be used to generate lists of genes by applying criteria such as fold change and false discovery rate (FDR) adjusted p-value thresholds.

- Select the Analysis tab
- Select ANOVAResults in the spreadsheet tree
- Select Create Gene List from the Analysis section of the Gene Expression workflow (Figure 1)

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1-removeresult (batch-remove)		Column #	Probeset ID	Entrez Gene	Gene Symbol	Gene Inte	Transcript ID	ent)	me)	View Sample Information		
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	1.	4490	33799_at	6478	SIAH2	siah E3	NM_005067	1.59274e-07	0.243475	✓ QA/QC		
	2.	2489	31798_at	7031	TFF1	trefoil factor 1	NM_003225	3.43187e-07	0.0096470	PCA Scatter Plot		
	3.	1141	1237_at	8870	IER3	immediate early	NM_003897 ///	5.46804e-07	0.112467	Sample Box & Whiskers Chart		
	4.	4994	34303_at	219654	ZCCHC24	zinc finger,	NM_153367 ///	5.50565e-07	4.33981e-	Samela Histogram		
	5.	1836	1933 <u>g</u> at	10057	ABCC5	ATP binding	NM_001023587	1.36059e-06	0.0028372			
	6.	10472	39781_at	3487	IGFBP4	insulin like	NM_001552	1.42754e-06	0.275441			
	7.	7717	37026_at	1316	KLF6	Kruppel-like	NM_001008490	1.73458e-06	6.14322e-	Detect Differentially Expressed Genes		
	8.	6979	36288_at	3887	KRT81	keratin 81,	NM_002281 ///	2.05143e-06	1.84419e-	View Sources of Variation		
	9.	274	368_at	7162	TPBG	trophoblast	NM_001166392	3.07097e-06	0.0164127	Create Gene List		
	10.	11950	41259_at	51491 NOP16 NOP16	NOP16	NM_001256539	3.57845e-06 4.66809	4.66809e-	Visualization			
	11.	4062	33371_s_at	11031	RAB31	RAB31,	NM_006868	3.85637e-06	0.608732	Biological Interpretation		
	12.	9420	38729_at	2288	FKBP4	FK506 binding	NM_002014 ///	4.30285e-06	0.113071			
	13.	9003	38312_at	169611	OLFML2A	olfactomedin	NM_001282715	5.05105e-06	0.252829			
	14.	11681	40990_at	10098	TSPAN5	tetraspanin 5	NM_005723 ///	5.80858e-06	0.110513			
	15.	10333	39642_at	54898	ELOVL2	ELOVL fatty	NM_017770 ///	6.11469e-06	0.0229098			
	16.	1835	1932_at	10057	ABCC5	ATP binding	NM_001023587	7.66495e-06	0.862655			
	17.	7481	36790_at	7168	TPM1	tropomyosin 1	NM_000366 ///	8.15471e-06	0.188266			
	18.	12283	41592_at	8651	SOCS1	suppressor of	NM_003745	8.6549e-06	0.334994			
	19.	9330	38639_at	10608	MXD4	MAX	NM_006454 ///	9.51684e-06	0.0834692			
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Figure 4. Selecting Create Gene List from the Gene Expression workflow

- Select E2 vs. Control from the Contrast panel of the ANOVA Streamlined tab in the List Manager dialog
- Deselect the *Include size of the change* option
- Set *p-value with FDR* < to **0.1** (Figure 2)

🤣 List Manager							×					
List Spreadsheet Name	^	List Info Venn Diagram	ANOVA Streamlined	Advanced								
A 1 (Breast_Cancer.txt)		Single factor: find genes that vary across all samples upon single factor										
B 1-removeresult (batcl	h-rer	Name		Setting		# Pass						
C 1-removeresult/ANO	VA-3	 Treatment 										
D I/ANOVA-3way (ANO	JVA	⊖ Time										
		Interaction: find genes that vary across all samples upon interaction 🕡										
		Name		Setting		# Pass						
		O Treatment * Time										
		Contrast: find genes that	change between two o	ategories								
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		Ez vs. Control		have Any change		704	^					
		 E2+ICI vs. Control 										
		O E2+Ral vs. Control										
		O E2+TOT vs. Control					*					
		Configuration for "E2 vs.	Control"			# Pass: 584						
		Include size of the c	hange									
		Include significance	of the change p	-value with FDR V	2							
		584 genes passed the spe You are about to create a Have Any Chan	ecified criteria. list of genes that ge in E2 relative to Con	trol with fdr (step up) < 0.1			*					
<	>	Save list as: E2 vs.	Control	Browse Create		Configure	÷					
						Close						

Figure 5. Configuring the List Manager using the ANOVA Streamlined filtering options

There should be ~545 probe(sets)/genes that meet this threshold.

• Select Create

A new spreadsheet, E2 vs. Control, will be added as a child spreadsheet of Breast_Cancer.txt.

• Repeat the steps listed above to create lists for *E2+/Cl vs. Control* (~24 genes), *E2+Ral vs. Control* (~22 genes), and *E2+TOT vs. Control* (~177 genes) with the same threashold

Now we can use the Venn Diagram to create a list of genes that are differentially regulated in all treatment groups.

• Select the Venn Diagram tab in the List Manager dialog

The Venn Diagram shows overlap between selected gene lists.

• Select the four created lists (E-H) in the spreadsheet list in the List Manager dialog by selecting each while holding the Ctrl key on your keyboard

The Venn Diagram will display the number of overlapping and distinct genes from the four lists (Figure 3).



Figure 6. Viewing the Venn Diagram with intersections of four lists of significant genes

The intersection of the four ellipses shows that 14 differentially regulated genes are in common between the four threatment schemes.

- Select the region intersecting all four ellipses
- Right-click the intersected region
- Select Create List From Highlighted Regions
- Select Close to exit the *List Manager* dialog

The new list will appear in the spreadsheet tree with a temporary file name (ptpm).

- · Select the temporary list in the spreadsheet tree
- Select (1) from the command bar
- Save the list as *fourtreatments*

« Removing batch effects Hierarchical clustering using a gene list »

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

