

# META-ANALYSIS

**STEP 4)** In addition to investigating the results of individual studies, a set of related studies can be selected for **Meta-Analysis**.

Select studies for Meta-Analysis using the check boxes to the left of analyses of interest, and then click the **Advanced Analysis** button (see page 1).

- D** On the **Meta-Analysis page** select whether to view over- or under-expressed genes, and whether to apply **filters**.
- E** Once Expression and Filter selections have been made, select **Draw Metamap** or **View Gene List**:

In a **Meta-Map** each column is a study and each row is a gene. A pull-down menu at the top of the page allows the user to determine whether to utilize the default "leave-one-out" strategy or select a different number of studies for a new calculation. Genes at the top are most significantly over- or under-expressed across all selected studies.

Alternatively, the **Gene List** view shows more genes per page, and provides statistical values for each individual study.

# ONCOMINE™ QUICKSTART GUIDE TO profile search

Use Profile Search to identify differential analyses ("profiles") of interest in the OncoMine database. Profiles can be analyzed individually using Heat Maps, Gene Lists, Advanced Analysis techniques, or analyzed jointly using Meta-Analysis.

## SEARCH & SELECT

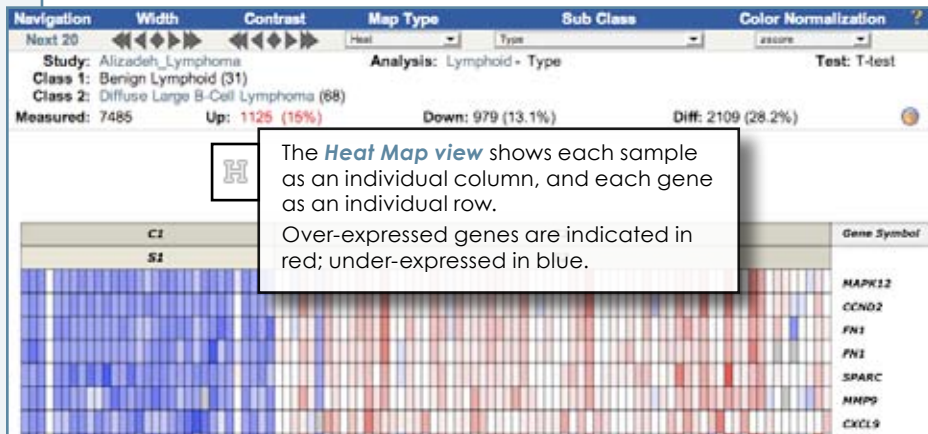
**STEP 1)** Enter a profile search term in the **Profile Search** box and click Search.

**STEP 2)** From resulting profiles, select from one of the following:

- A** Use **filters** to narrow results to a specific area of interest
- B** For any individual profile, select the **Heat Map**, **Gene List**, or **Advanced Analysis** icon to view gene expression results or access other options
- C** For any set of profiles, conduct **Meta-Analysis** by selecting check boxes to the left of the appropriate profiles, and then **Advanced Analysis** button (see page 4).

# ANALYZE

**STEP 3)** To investigate the results of an *individual analysis*, use the icons within the profile box.



The **Heat Map view** shows each sample as an individual column, and each gene as an individual row. Over-expressed genes are indicated in red; under-expressed in blue.

The **Gene List view** provides the same list of genes with more statistical information, and more genes per page.

Rank	Gene Symbol	Reporter ID	Count 1	Count 2	Mean 1	Mean 2	T-test	P-Value	Q Value	Box Plot
1	S5BP2	203787_at	249	54	-.132	1.0276	-21.754	5E-51	1.4E-47	View
2	EST	218218_s_at	249	54	-.1782	.8592	-23.121	9.6E-49	1.3E-45	View
3	TMEM48	234672_s_at	249	54	.6482	1.2734	-23.371	5.9E-48	5.4E-45	View
4	VRK1	203856_at	249	54	.5914	1.1071	-20.791	6.7E-48	4.6E-45	View
5	SAC3D1	205449_at	249	54	.316	1.0518	-23.743	2.7E-45	1.5E-42	View
6	RFC3	204127_at	249	54	.8205	1.4342	-20.545	1.4E-44	6.4E-42	View
7	SPBC24	235572_at	249	54	-.2166	.4079	-18.78	1.1E-43	4.2E-41	View
8	BUB1B	203755_at	249	54	.7873	1.3288	-18.849	2.4E-43	8.4E-41	View
9	BYSL	203612_at	249	54	-.1194	.7619	-19.509	9.1E-43	2.6E-40	View
10	MME	203434_s_at	249	54	-.7675	.5814	-16.491	8.8E-42	1.9E-39	View
11	HIP1R	38340_at	249	54	4.281	1.0941	-17.705	5.7E-41	1.4E-38	View
12	STRBP	223522_at	249	54	-.0773	.7143	-23.148	6.1E-40	1.4E-37	View
13	CD320	218529_at	249	54	-.3784	4.171	-16.91	1.4E-39	2.9E-37	View

The **Gene List view** provides the same list of genes with more statistical information, and more genes per page.

Selecting the **Advanced Analysis icon** generates a whole new series of analysis options organized in tabs.

**Profile Summary Report**

**Cancer Gene Census**  
15 of 71 measured genes from the Cancer Gene Census are in the selected profile ( $p < 0.01$ )

1) Gene: WAS	P-Value: 2E-20	☒
2) Gene: HMGA1	P-Value: 3E-8	☒
3) Gene: MYC	P-Value: 4.5E-6	☒
4) Gene: SS18	P-Value: 8.2E-5	☒
5) Gene: SDHB	P-Value: 2.5E-4	☒

**Therapeutic Target Database**  
18 of 74 measured genes from the Therapeutic Target Database are in the selected profile ( $p < 0.01$ )

Use the **Filter tab** to view only the genes in the analysis that meet specific, filterable criteria.

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Use the **Enrichment tab** to discover links between differentially expressed genes in the selected profile and other biological processes.

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Use the **Interactome tab** to look at the expression of known interacting pairs of genes in the profile of interest.

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Use the **Outlier tab** to discover which genes in the selected profile are highly expressed, but only in a subset of samples in the study.

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