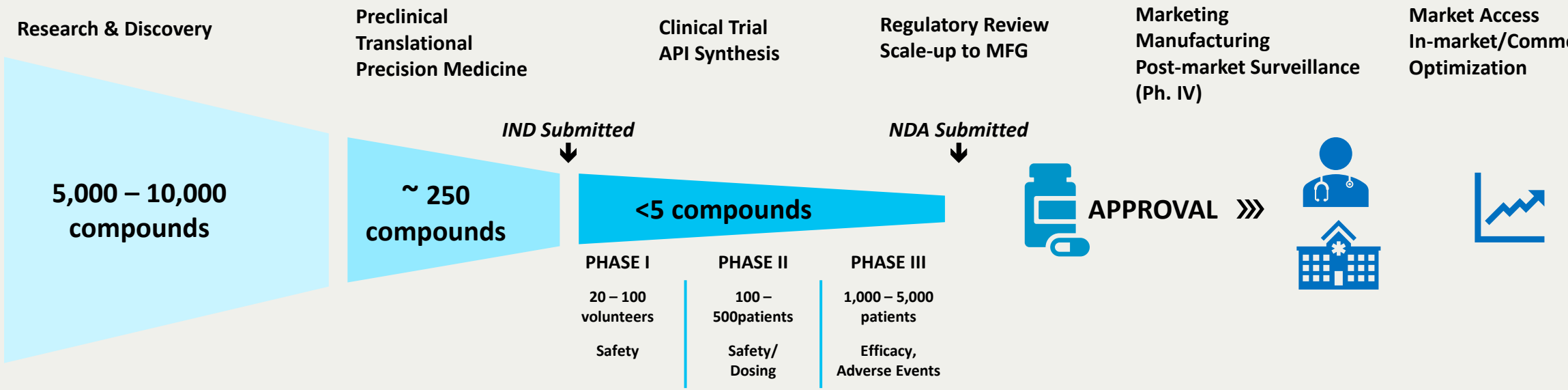
Clarivate Cortellis™

MetaCore
Accelerating the pace of innovation with trusted content, analytics, and technology

Kinsi Oberoi, Solution Scientist

04/06/2021

Our premier suite of solutions uniquely spans the entire innovation & product lifecycle

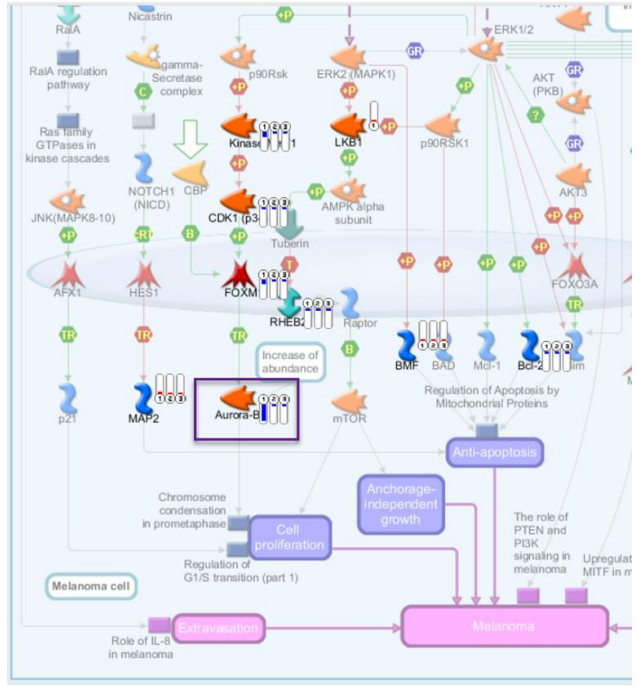


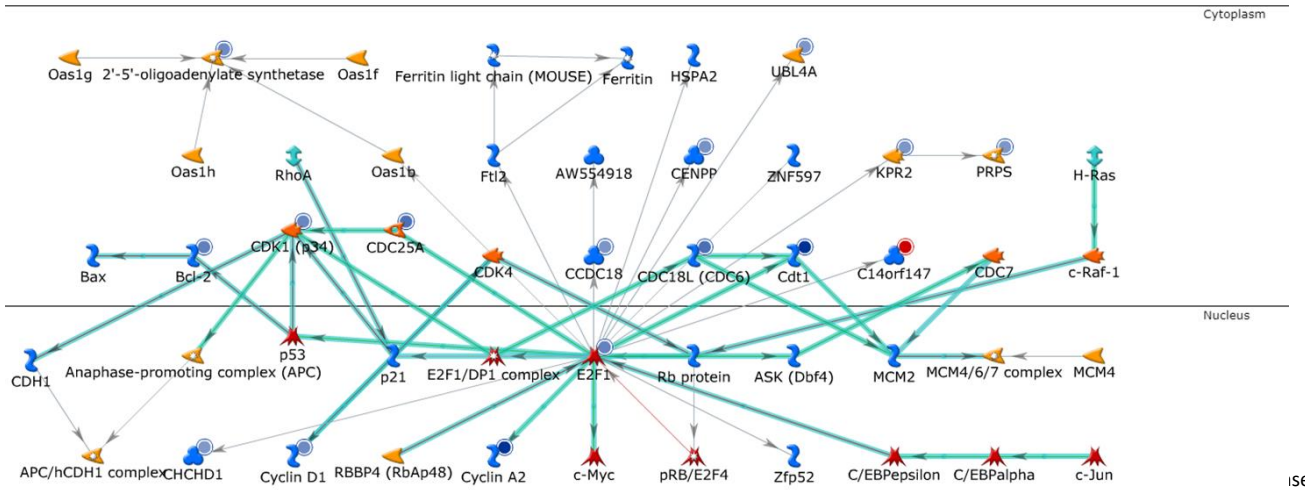
Web of Science	Cortellis							Decision Resources Group		
Web of Science	MetaCore	Drug Discovery (formerly Integrity)	Clinical Trials	CI & Deals, Timeline & Success Rates	Regulatory, CMC, PV, CIRS	Digital Health	Generics (formerly Newport)	Market Access	Multi-Channel Engagement	*Software Solutions*
Bioinformatics Knowledge Mgmt	Drug Repurposing	Clinical Benchmarking	Asset Evaluation	Reg Strategy & Process	Predictive Data Sciences	HEOR & Access Strategy	Real-World Evidence	*Consulting*		
Data as a Service, APIs, Custom Data		MDM, Ontologies, Data Lakes		Content as a Service				*Data*		

Agenda

Metacore Training

- Metacore Overview with live demo session showing how to:
  - Knowledge Mining
  - Upload data
  - Pathway Map Enrichment
  - Network Building
  - Metadrug
  - Q&A



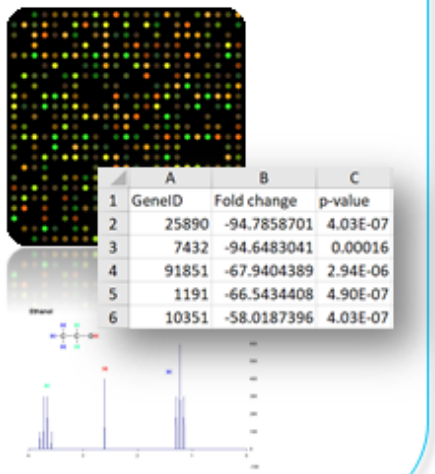


MetaCore: Your GPS in Pathway Analysis

INPUT

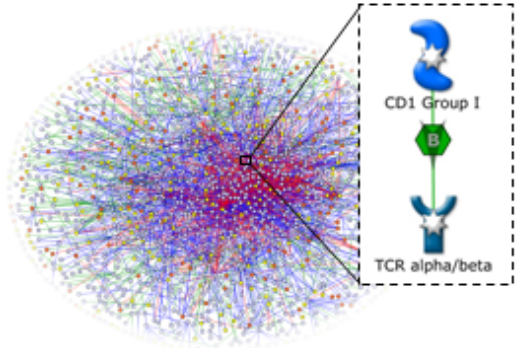
Data mining
Content Browsing

OMICs analysis



	A	B	C
1	GeneID	Fold change	p-value
2	25890	-94.7858701	4.03E-07
3	7432	-94.6483041	0.00016
4	91851	-67.9404389	2.94E-06
5	1191	-66.5434408	4.90E-07
6	10351	-58.0187396	4.03E-07

METABASE



> 2,315,000 molecular interactions

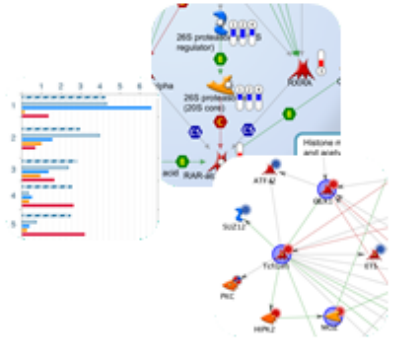
From Human, mouse and rat

Manually curated by editorial team

(>50 PhD, MD)

3,701 journals

METACORE



1,567 Pathway Maps

- **Understand your data in the context of validated biological pathways.**
- **Generate and confirm hypotheses for novel biomarkers, targets, mechanisms of action.**

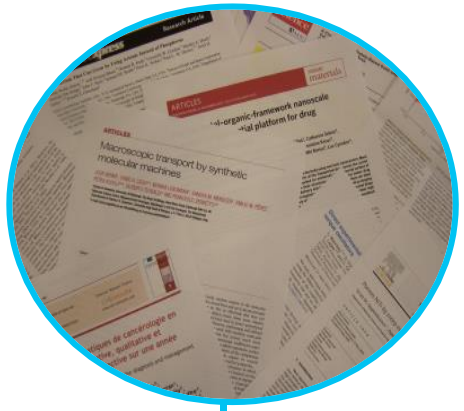
- Analyze molecular pathways and accelerate discovery research

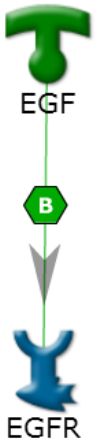
MetaBase/ MetaCore Content Overview

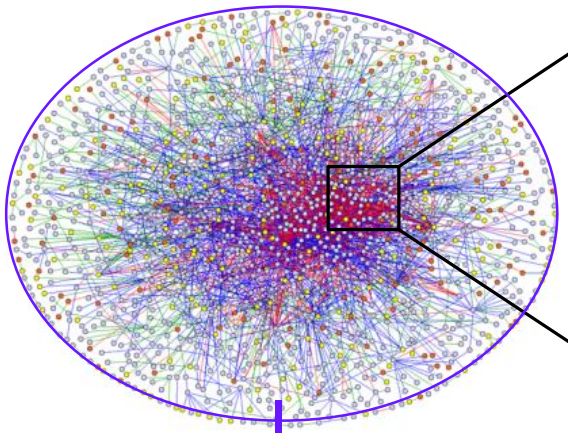
MetaBase	number
Human Genes	61167
Human SwissProt proteins	20430
Mouse genes	72698
Mouse SwissProt proteins	17019
Rat genes	47891
Rat SwissProt proteins	8071
Compounds	891976
Compounds with structure	875221
Endogenous compounds	5448
Nutritional compounds	126
Metabolites of xenobiotic	32389
Drugs	9118
- Biologics	1362
- Small Molecules	7756
- Approved drugs	2290
- Withdrawn drugs	261
- Clinical trial drugs	4993
- Discontinued drugs	1187
- Preclinical drugs	251
- Unknown	136
- Drug combination regimens	8445

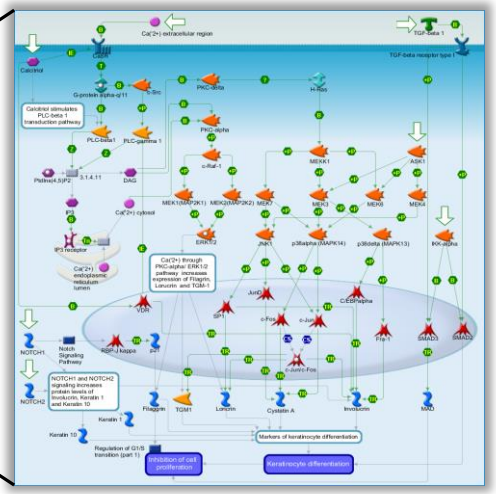
MetaCore	number
Human genes in network	25210
Mouse genes in network	22189
Rat genes in network	18780
Chemical compounds	435319
Drugs	4786
Endogenous compounds	3583
Metabolic reactions	40550
Transport reactions	3717
Processing Reactions	4410
Pubmed journals	3717
Pubmed records	2683859
Pubmed articles (unique)	294571
Total amount of interactions	2397073
- Protein – Protein	967668
- Compound – Protein	830890
- Compound – Compound	11699
- Metabolic enzyme -Reaction	51020
- Transporter – Reaction	4787
- Substrate, Product – Reaction	110739
- RNA – Protein	420278
Pathway maps	1578
- Human genes in maps	7750
- Mouse genes in maps	7042
- Rat genes in maps	6930
- Interactions in maps	33153

From Peer-Reviewed Publications to Signaling Pathways









Publications → **Molecular Interaction** → **Global Network**

207 publications cited for EGF-EGFR interaction	2,355,252 molecular interactions

1,545

CANONICAL AND DISEASE SIGNALING PATHWAYS

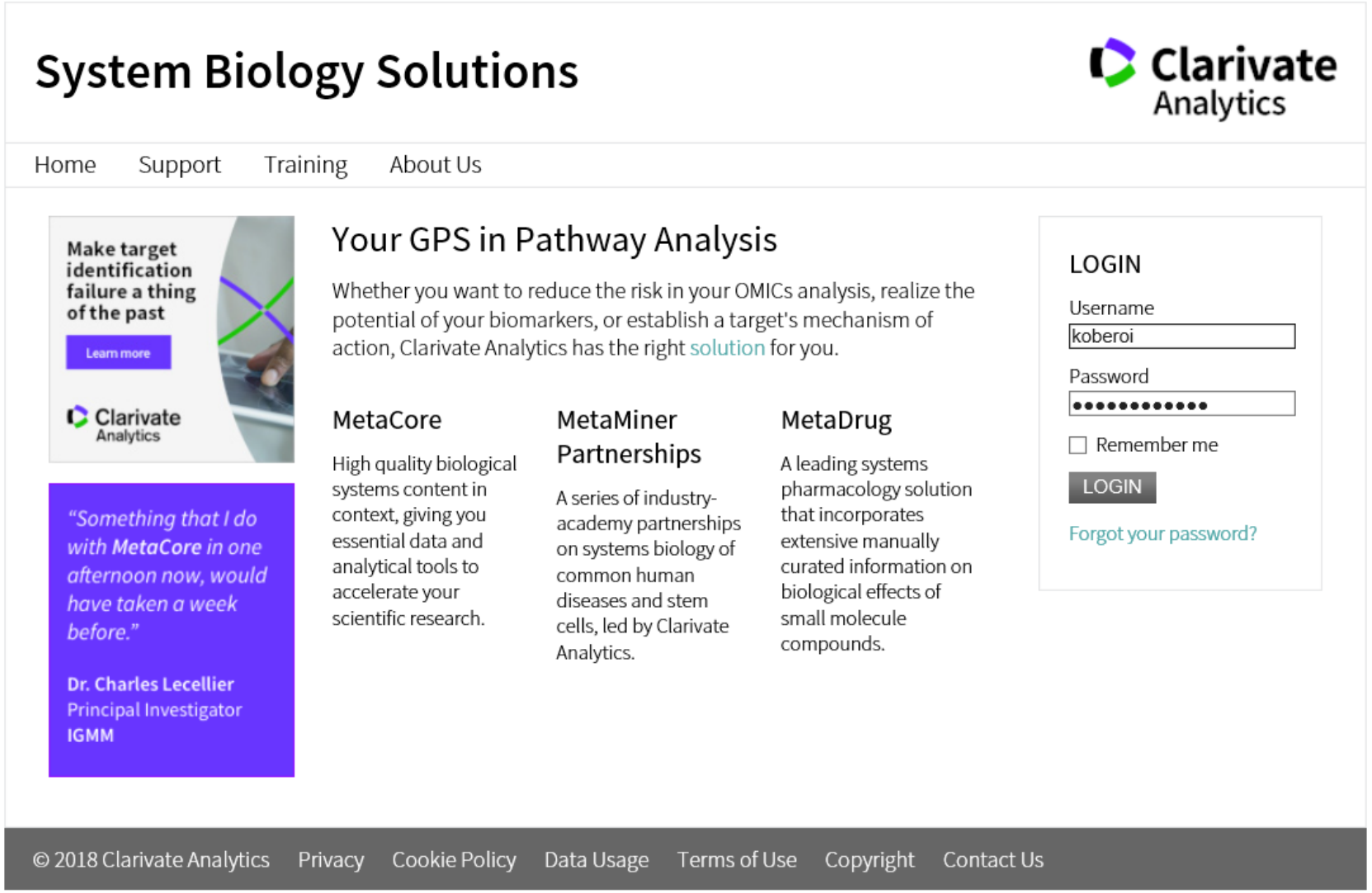
Manual annotation from 3,712 peer-reviewed journals (updated quarterly)

- 290,790 published articles cited with strong experimental evidence
- Team of PhDs & MDs curating for more than 10 years
- Every interaction has directionality, effect, mechanism, and source

Cortellis™

Metacore Login Page

https://portal.genego.com/



Training Dataset

GSE95153- Combining BET and MEK inhibitors synergistically targets NRAS mutant Melanoma

- Platform :Illumina NextSeq 500 (Homo sapiens)
- P value - 0.05, Threshold - 1
- Comparison: untreated
  DMSO-treated
  JQ1-treated (BET inhibitor)
  PD901-treated (MEK inhibitor)
  JQ1+PD901-combination treated

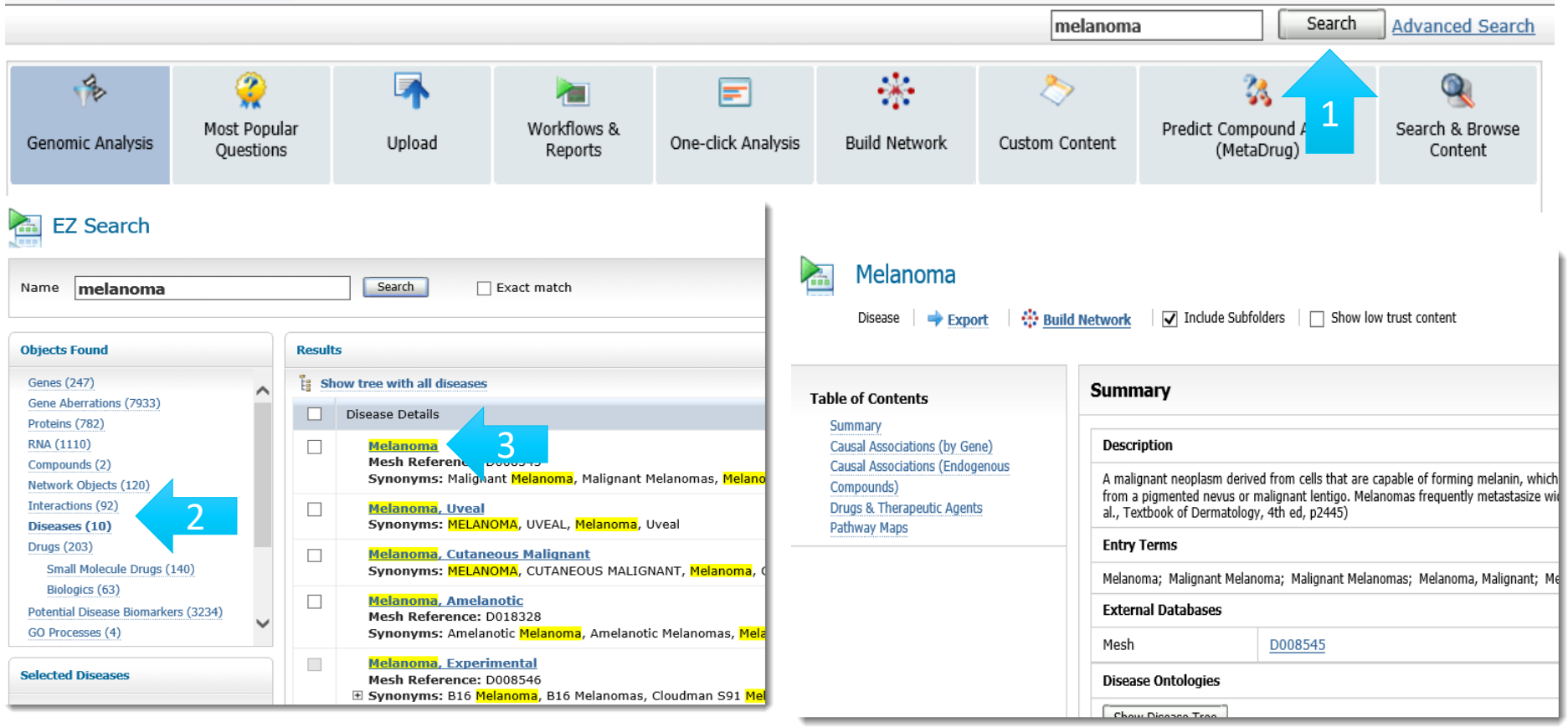
Question?

1.The impact of MEK inhibition of Signaling pathways in Melanoma?

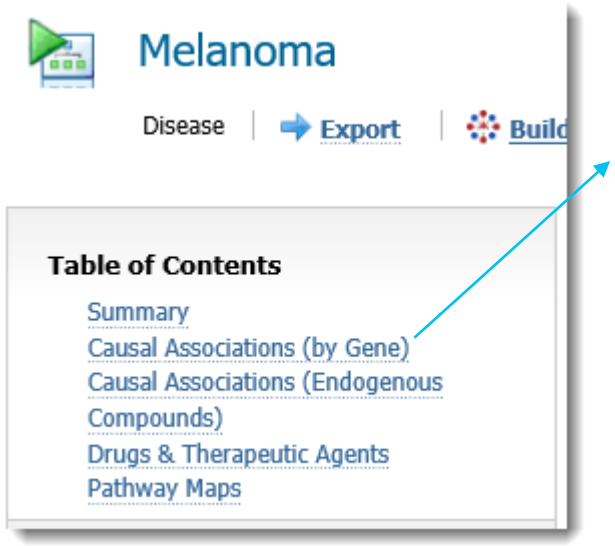
2. Hypothesizing the relationship between the JQ/D and PD/D single treatments with the combo/D treatments?

Knowledge Mining

Do Ez search to find information related to Melanoma



What can I learn about genes being overly expressed in Melanoma?



Causal Associations (by Gene)

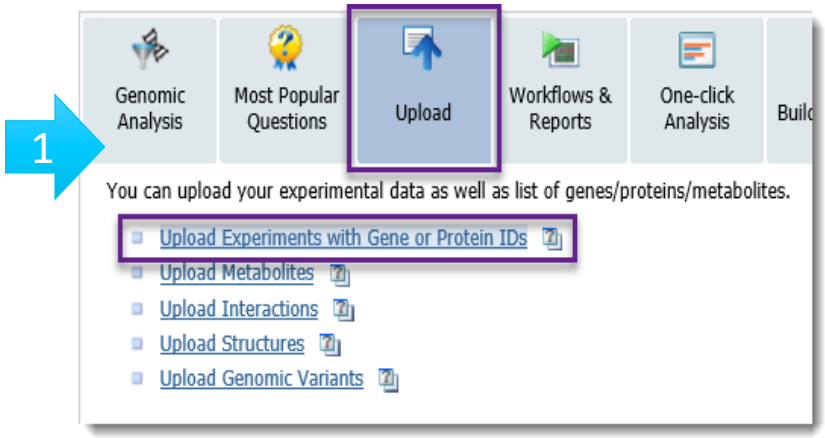
highlight text... 0/0

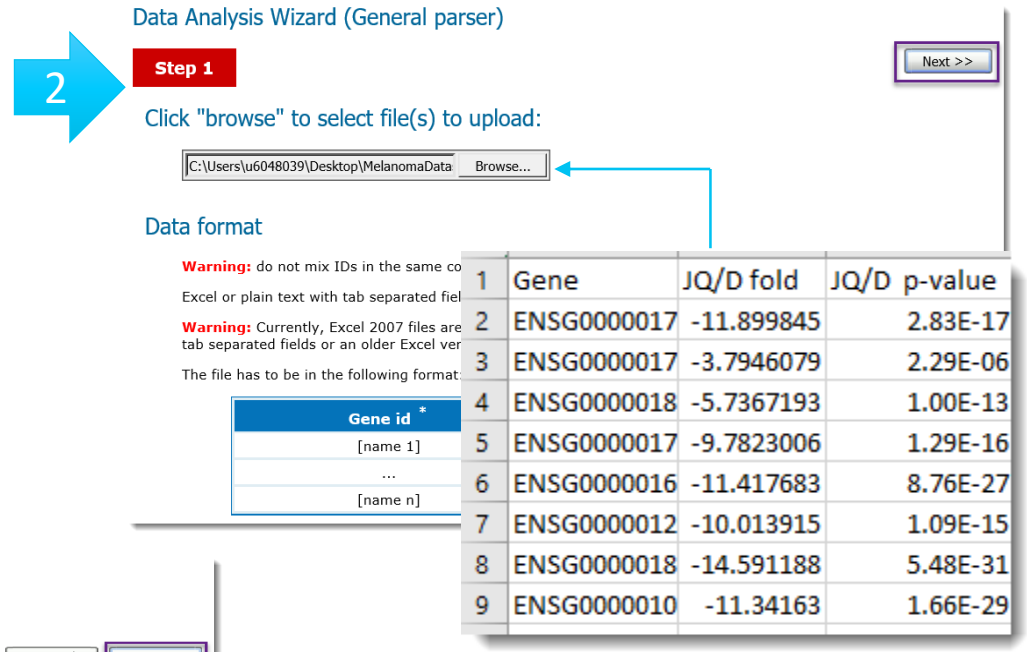
Result pages: 1 2 3 • 171 (Showing results 1 to 20 of 3419)

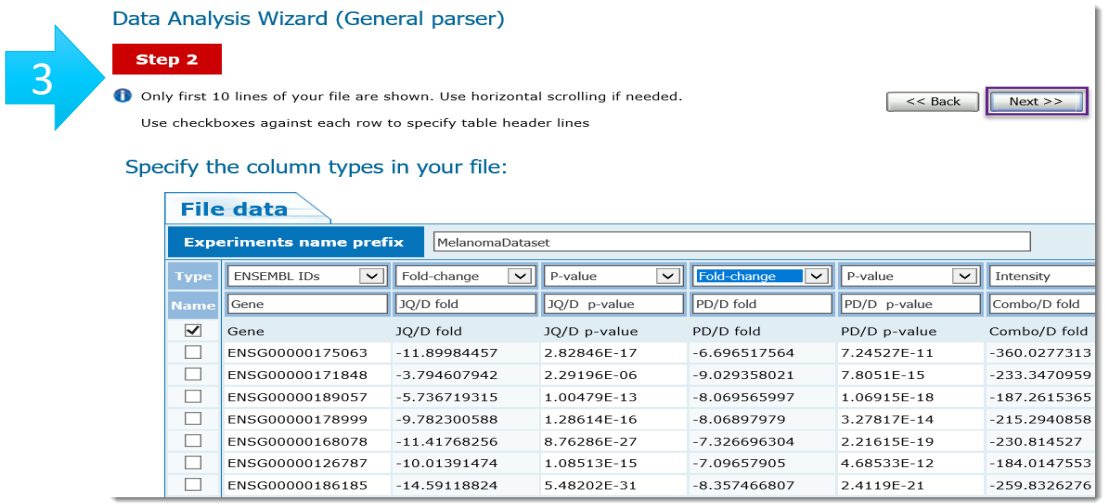
#	Gene	Alteration Level	Alteration Type	Alteration Subtype	Details	Abundance	Activity/Gain/Loss of Function	Normal/Pathology Concentration	Subcellular Localization Change	Organ/Tissue Distribution	Disease	Info
11	TGFI	DNA level	Gene rearrangements	STR/VNRT	TGFI_HUMAN_c.?(CA)19		down			Blood	Melanoma, Cutaneous Malignant	
12	TP53	DNA level	Haplotype/SNP		TP53_HUMAN_c.860A>G(G)					Melanocytes	Melanoma, Cutaneous Malignant	
13	BPIFA3	DNA level	Haplotype/SNP		BPIFA3_HUMAN_rs17305657(T)					Blood	Melanoma, Cutaneous Malignant	
14	TGFA	DNA level	Locus change		TGFA_HUMAN_locus_change_2p13					Melanocytes	Melanoma	
15	KIT	DNA level	Haplotype/SNP		KIT_HUMAN_c.1673A>G(G)					Melanocytes, Skin	Melanoma	
16	MMP28	DNA level	Haplotype/SNP		MMP28_HUMAN_c.728G>C(C)					Melanocytes	Melanoma	
17	HLA-DRB3, HLA-DRB1	DNA level	Haplotype/SNP		HLA-DRB1_HUMAN_DRB1*1103					Leukocytes	Melanoma	
18	BRAF	DNA level	Haplotype/SNP		BRAF_HUMAN_rs121913227(GT) / BRAF_HUMAN_rs121913227((A)2)					Melanocytes	Melanoma	
19	RASEF	DNA level	Epigenetics	Methylation	RASEF_HUMAN_Methylation	up				Uvea	Melanoma, Uveal	
20	KIT	DNA level	Haplotype/SNP		KIT_HUMAN_c.1672A>G(G)					Melanocytes	Melanoma	

Upload data

Upload data into Metacore







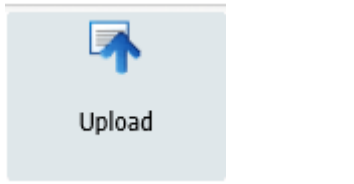
Pathway Map Enrichment

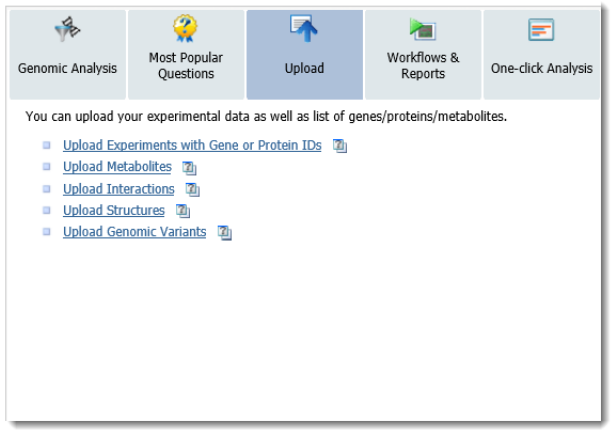
Which maps are significantly enriched

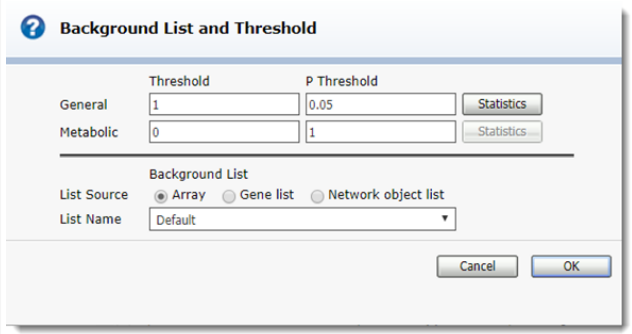
Upload dataset into Metacore

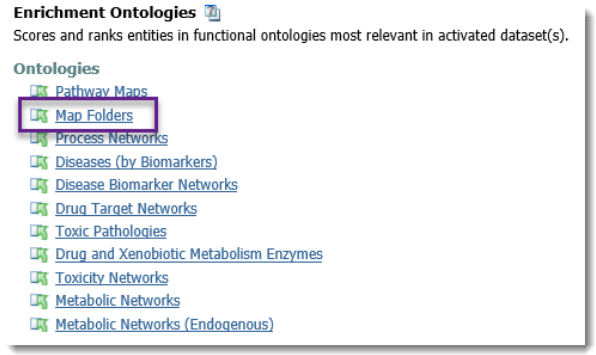
Set Background and Threshold

Analyze Map Folders









What overall process is impacted when comparing single treatment vs. combo treatment ?

Ratio of differentially expressed genes from dataset (**GREEN**) over all network objects in folder (**RED**)

Graphical representation of –log(pValue)

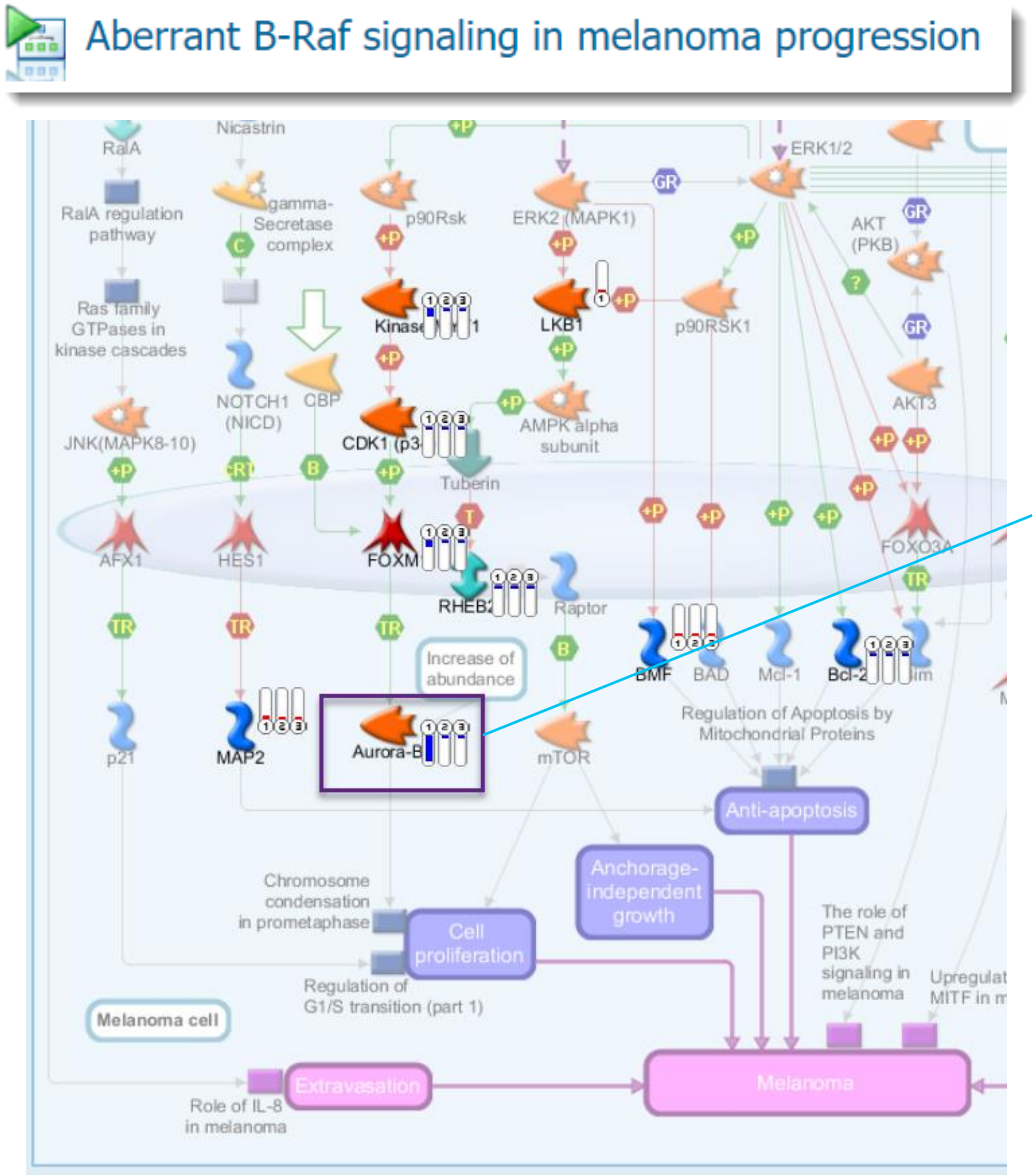
#	Map folders	0 5 10 15 20 25 -log(pValue)	pValue	min(pValue)	FDR	Ratio
1	Cell cycle and its regulation		1.291e-29 1.014e-33 2.336e-28	1.014e-33	8.648e-28 6.792e-32 1.565e-26	107/991 105/991 123/991
2	Colorectal Neoplasms		8.797e-20 3.864e-22 6.222e-27	6.222e-27	1.965e-18 8.629e-21 2.084e-25	124/1660 118/1660 164/1660
3	Lung cancer		1.661e-20 3.838e-22 1.824e-26	1.824e-26	5.565e-19 8.629e-21 4.074e-25	150/2213 140/2213 195/2213
4	Melanoma		8.908e-17 2.183e-17 4.263e-23	4.263e-23	1.194e-15 2.089e-16 7.141e-22	119/1691 110/1691 158/1691

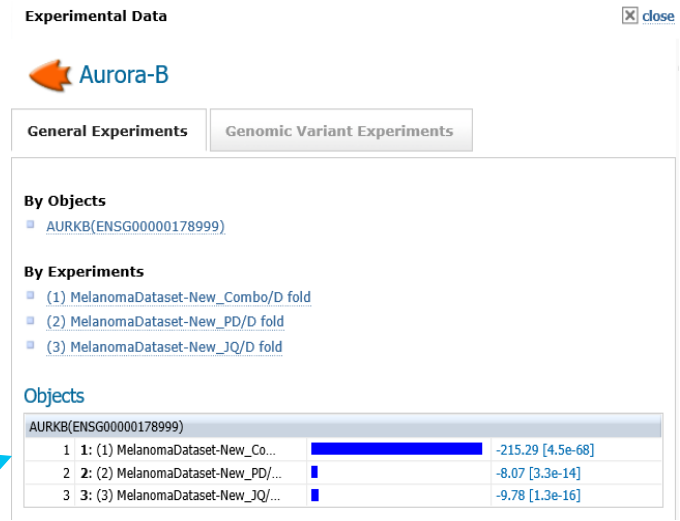
Map folder name

Significance of overlap of differentially expressed genes in the folder

Marked difference in the presence of differentially expressed genes between single treatment and combo treatment in Melanoma Map folder

What pathways are disrupted by the differentially expressed genes?





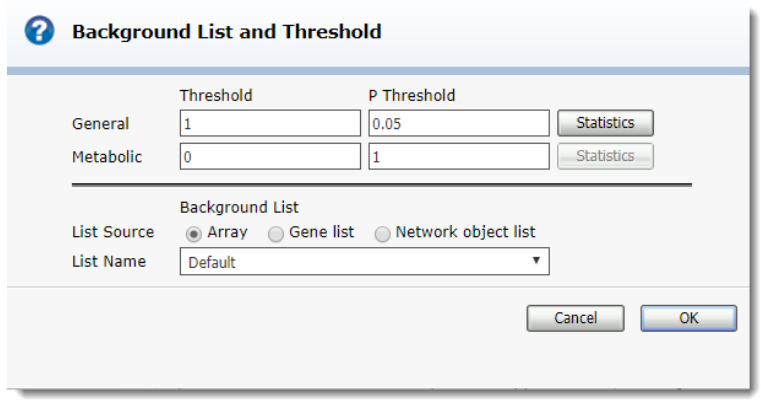
Kinase such as Aurora-B are significantly down regulated in Combo/D treatment compared to JQ /D and PD/D single group in Melanoma progression pathway map

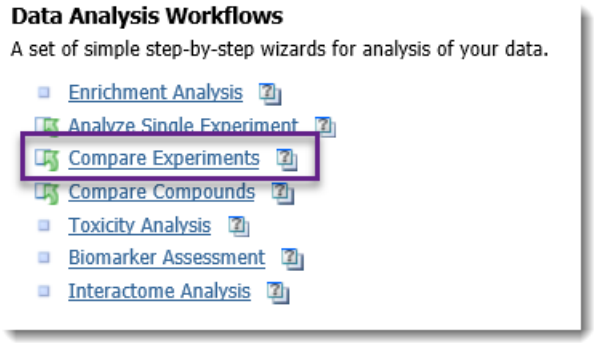
Compare Experiment

Compare experiment workflow

Set Background and Threshold

Compare Experiments





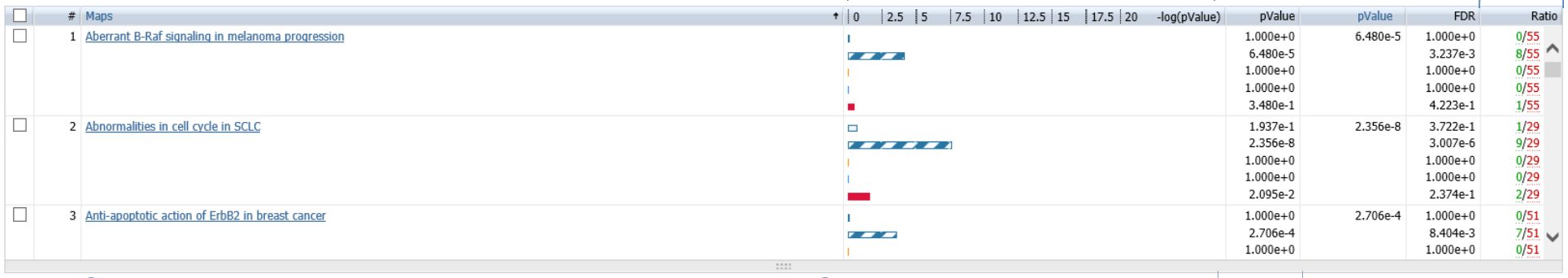
Question:
What process is impacted when comparing patient groups?

What process is impacted when comparing patient groups ?

Experiment name	Species	Network Objects
MelanomaDataset_JQ/D fold	Homo sapiens	889
MelanomaDataset_PD/D fold	Homo sapiens	777
MelanomaDataset_Combo/D fold	Homo sapiens	1200

Ratio of differentially expressed genes from dataset **(GREEN) over all network objects in** folder (**RED**)

Graphical representation of –log(pValue)



Map name

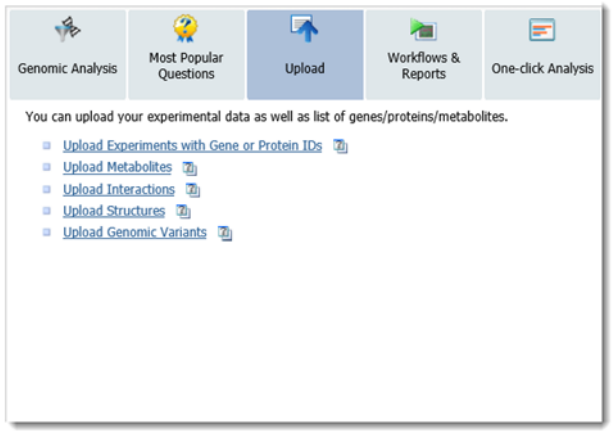
Significance of overlap of differentially expressed genes in the Map

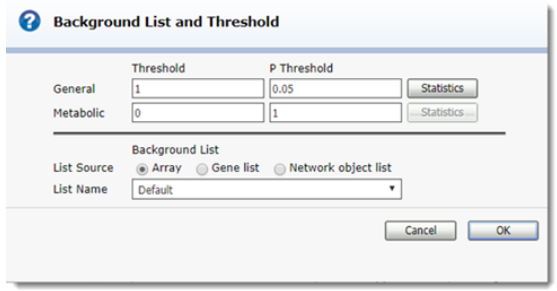
Build Network for your Experimental Data

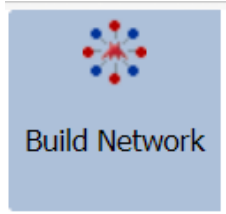
Upload dataset into Metacore

Set Background and Threshold

Build Network

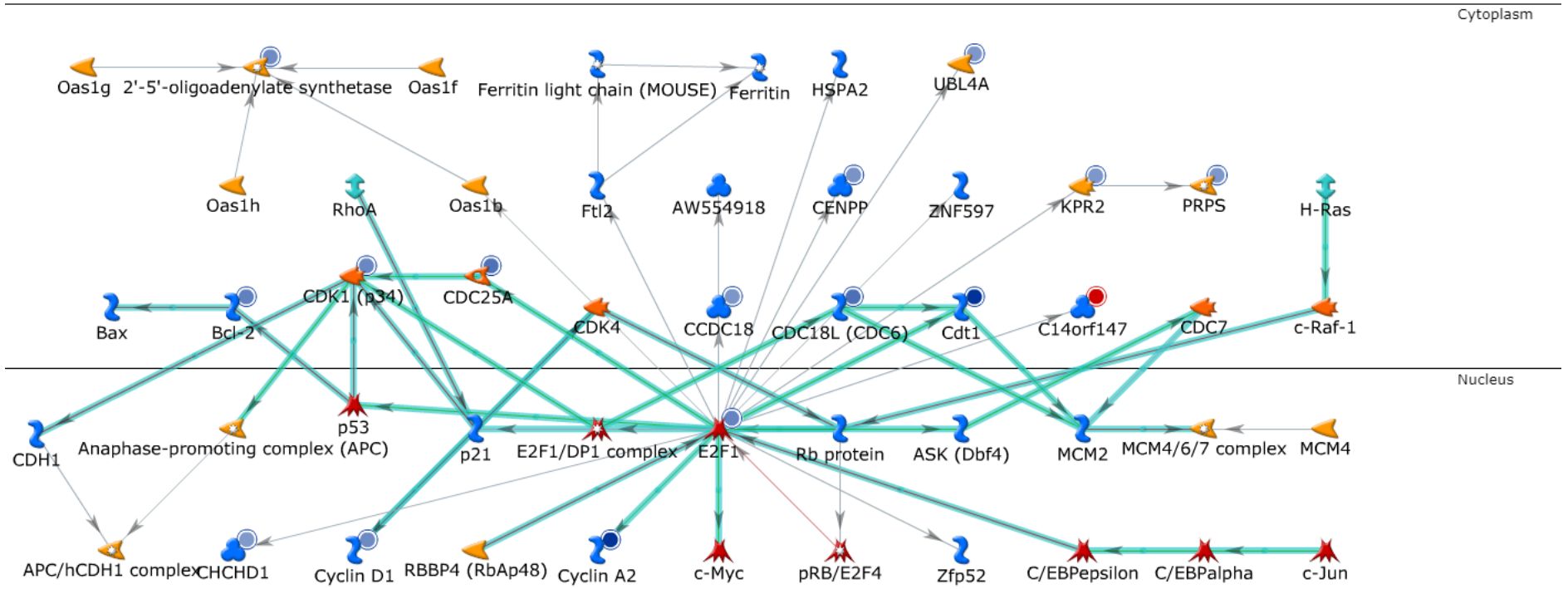






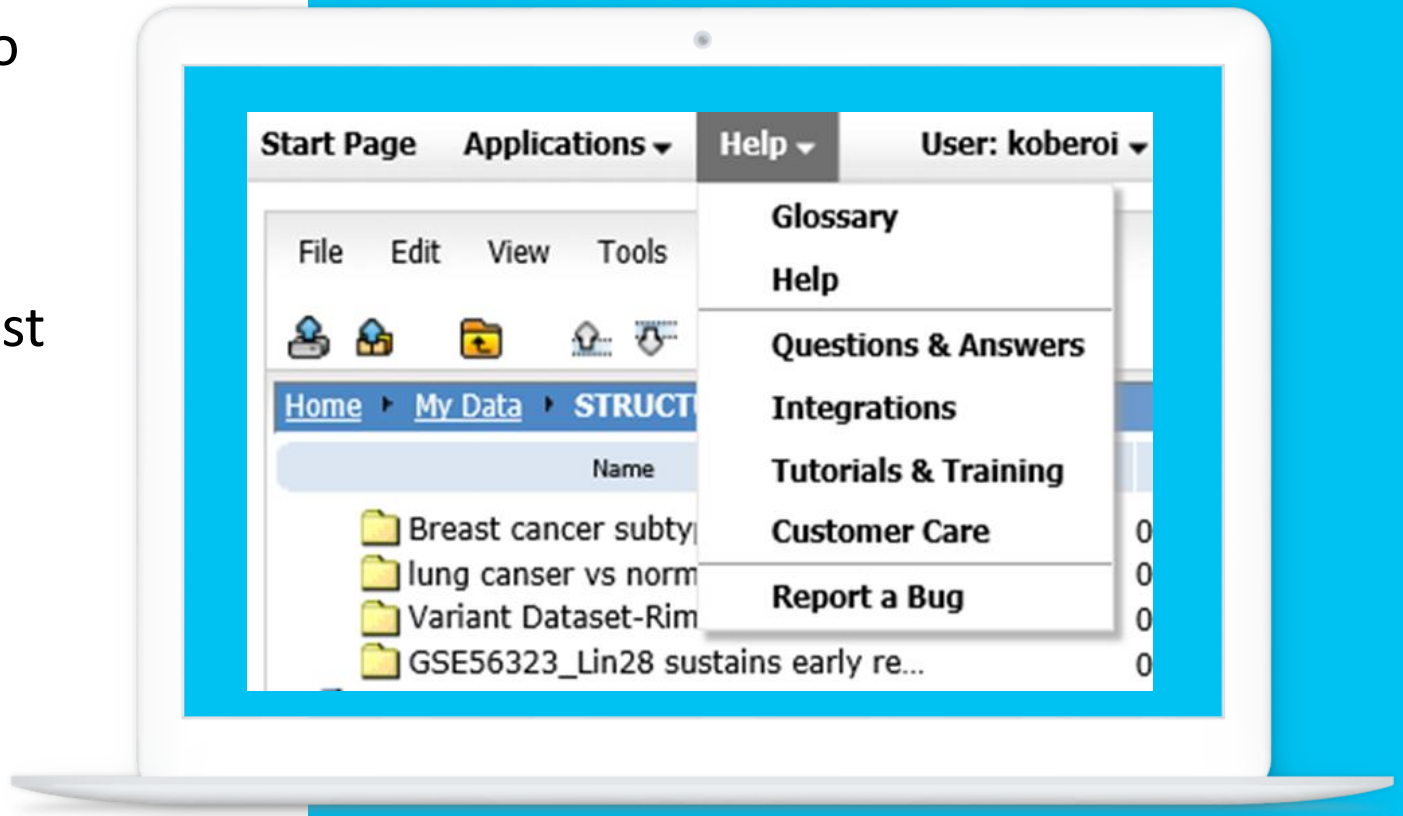
Network Building

Hypothesizing mechanisms of action behind MEK inhibitors by building network



Learn More

- You can learn more about upcoming webinars by going on to Help tab, Tutorials&Training, on MetaCore's start page
- Look for Pendo on left corner of landing page introduced earlier last month to help deliver a great product experience

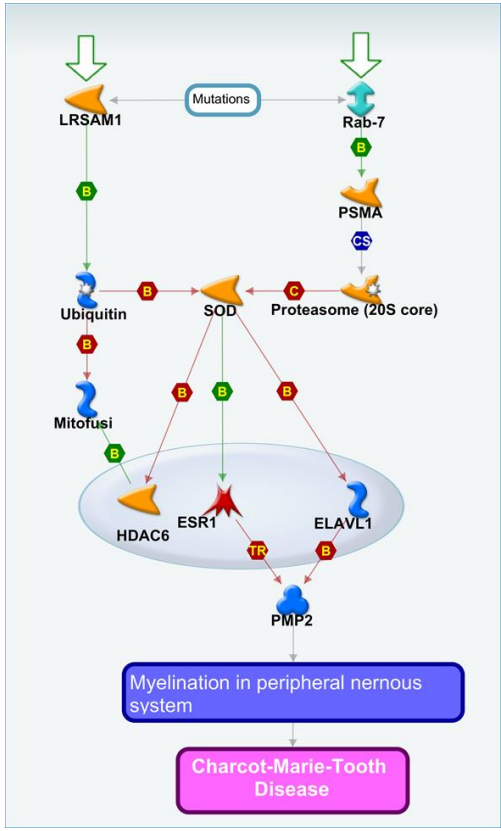


Screen caption

What would be covered in advanced training session

Pick topic for next session

1. Find Key Hubs using Over-Connectivity Analysis
2. Network building
3. Using Microarray repository for gene comparisons against public data
4. Constructing your own pathway maps
5. Analyzing multi-omics data (RNA-seq, proteomics, metabolomics, etc)



You've invited! MetaCore Advanced training

Training session details:

Please join us in this hands-on training session to learn further insights about the Clarivate MetaCore resource.

- Date: Tue April 13, 2021
- Time: 12pm – 1.30pm

Sign up

Based on your feedback during the first introductory MetaCore session on April 6th, we have designed a tailored training to cover your main areas of interest.

Come to this **hands-on Advanced session** to learn:

- How to work with multi-omics data.
- How to upload metabolite data.
- How to run enrichment analysis.

Don't forget to bring your questions with you!

Host:
Kinsi Oberoi
Solution Scientist
Clarivate

Cortellis™

A Clarivate Analytics solution

Thank you

Kinsi Oberoi
Kinsi.oberoi@Clarivate.com