OmicsNet Tutorial: Build network from a SNPs list

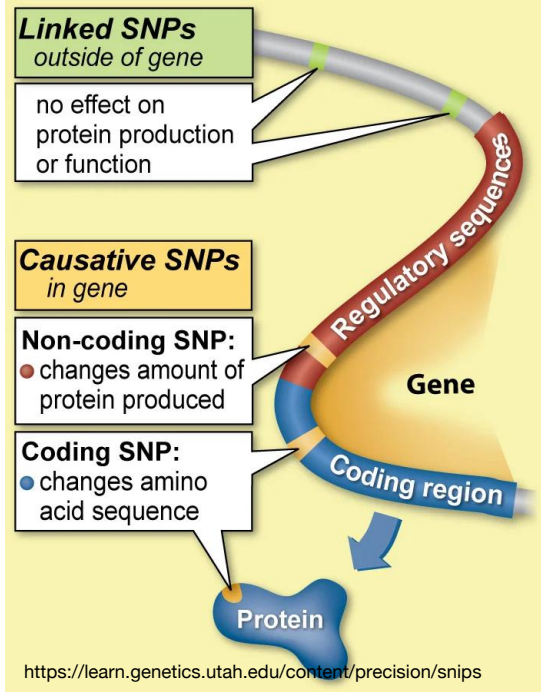
Computer Requirement

- Modern browser supporting WebGL
- Chrome 50+, Firefox 47+, Safari 10.1+ and Edge 12+
- Please make sure WebGL is enabled in your browser
  - Please consult this web page to verify: https://get.webgl.org/
- If not enabled, please consult our FAQ page for instructions
- For best performance and visualization, use:
- Latest version of Google Chrome
- A modern computer with at least 4GB of physical RAM
- A 15-inch screen or bigger (larger is better)
- Retina Display is supported

Motivation

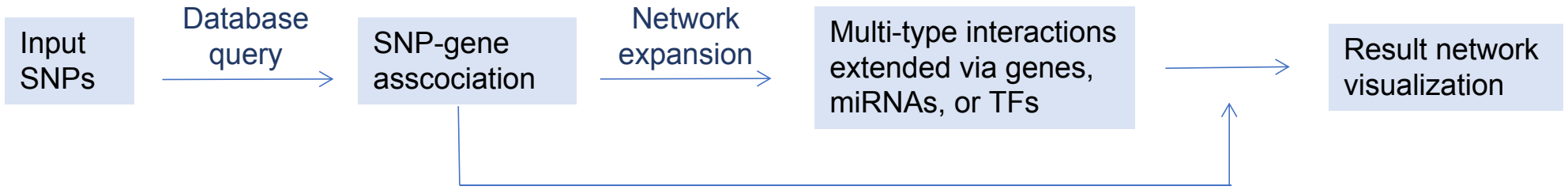
- **Background**: Single nucleotide polymorphism (SNP), the simplest form of DNA variation among individuals, was known to be responsible for interindividual differences in varies pehnotypes including disease states, cellular processing and drug response. Identify and annotate the numerous variations in genes can serve as a stepping stone for better understanding of their impact on gene fucntions and for further faciliting treatment options and future drug discovery.

- **Bottleneck**: Despite our accumulating knowledge to the human genome landscape and documentation of sequence variations among individuals due to the advances in genome sequencing during the past two decades, the functional interpretation of the SNPs is still at the starting point.



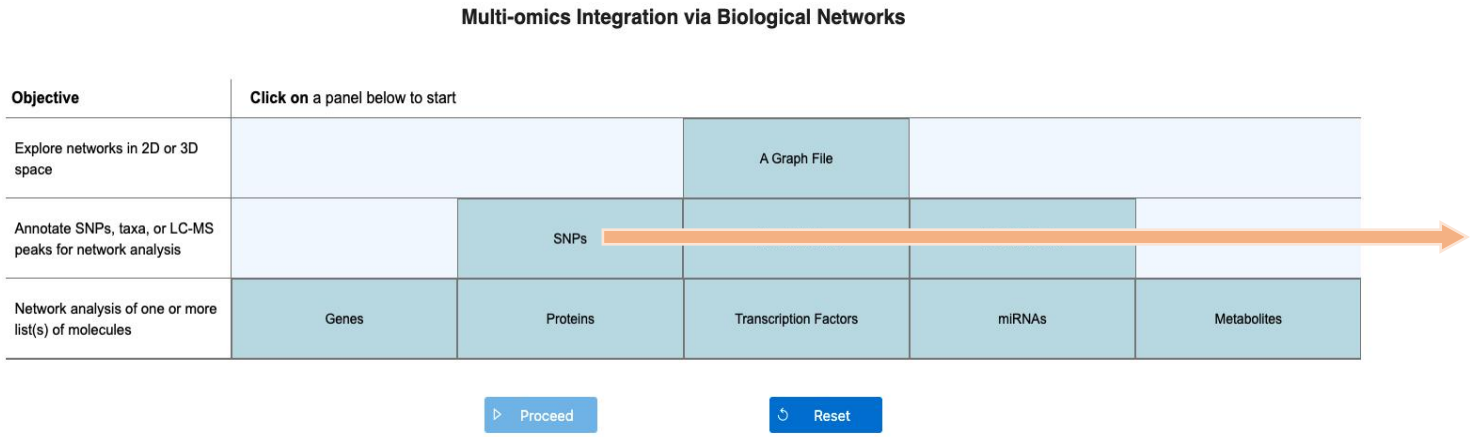
Overview

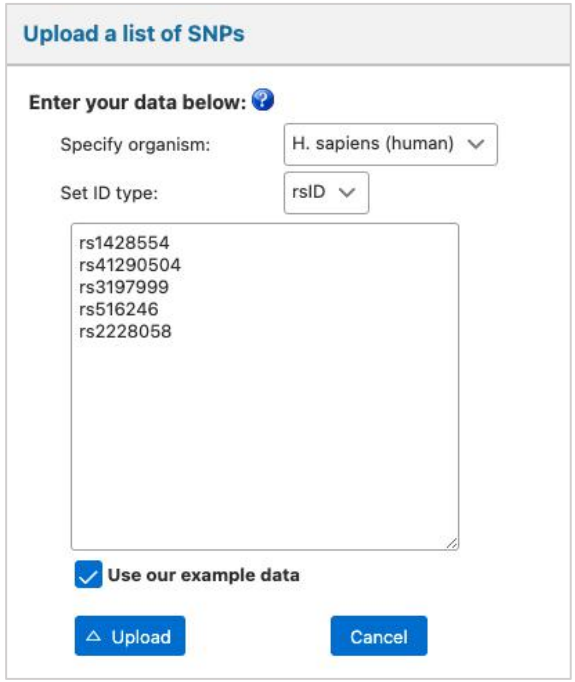
- **Aim:** To facilitate the understanding of the potential function of the user interested SNPs.
- **Procedure:**



- **SNP Annotation Database:** Ensembl Variant Effect Predictor (VEP) toolset and PhenoScanner$_{V2}$ are leveraged to query the general SNP-gene asscociation for the input SNPs. User can choose either the positional mapping or to use the the expression quantitative trait loci (eQTL) analysis. ADmiRE and SNP2TFBS are dedicated specifically for mapping SNPs to miRNAs and transcription factor binding sites.
- **Network expansion:** The SNP-gene interaction can be extended via genes, miRNAs, or TFs (e.g. by adding PPI)
- **Network analysis and visualization:** Approches such as Steiner forest can be used to pruning the network for better understanding the potential functional pathway in downstream. The final relsult will be present as an interactive multi-layers network.

Data Upload

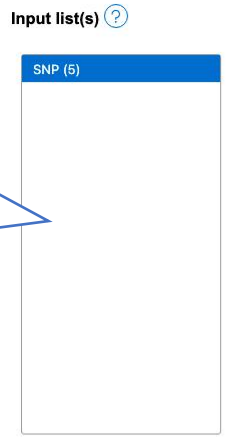




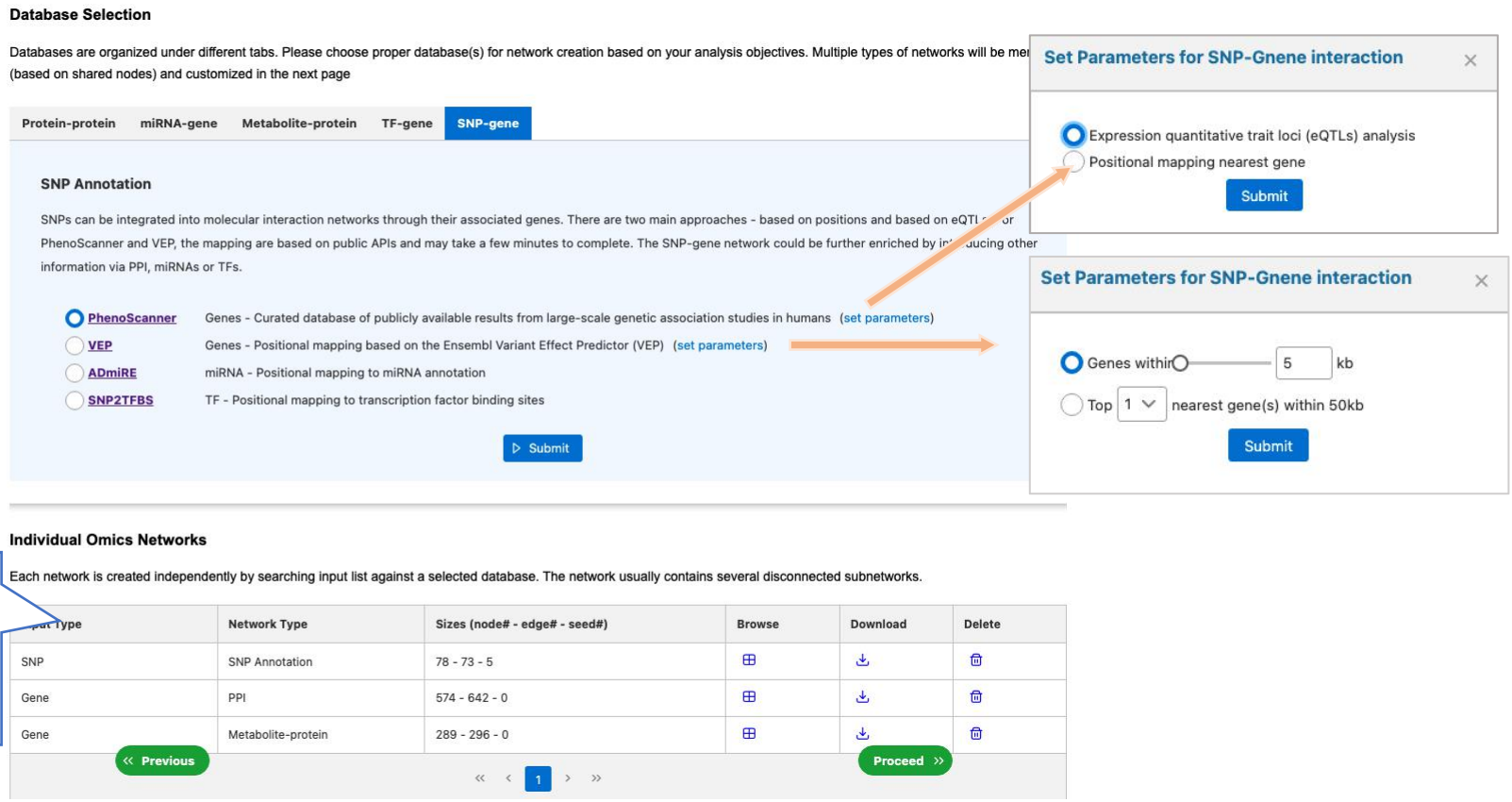
Users can upload a **SNP list** using **rsID** to start the analysis.
We support only for **human** study currently.

Database Selection

Records of type and numer of the input list



Records of the generated network that users can browse, download or deleted accordingly



Users need to select the database and related parameter to perform the SNP-gene asscociation:

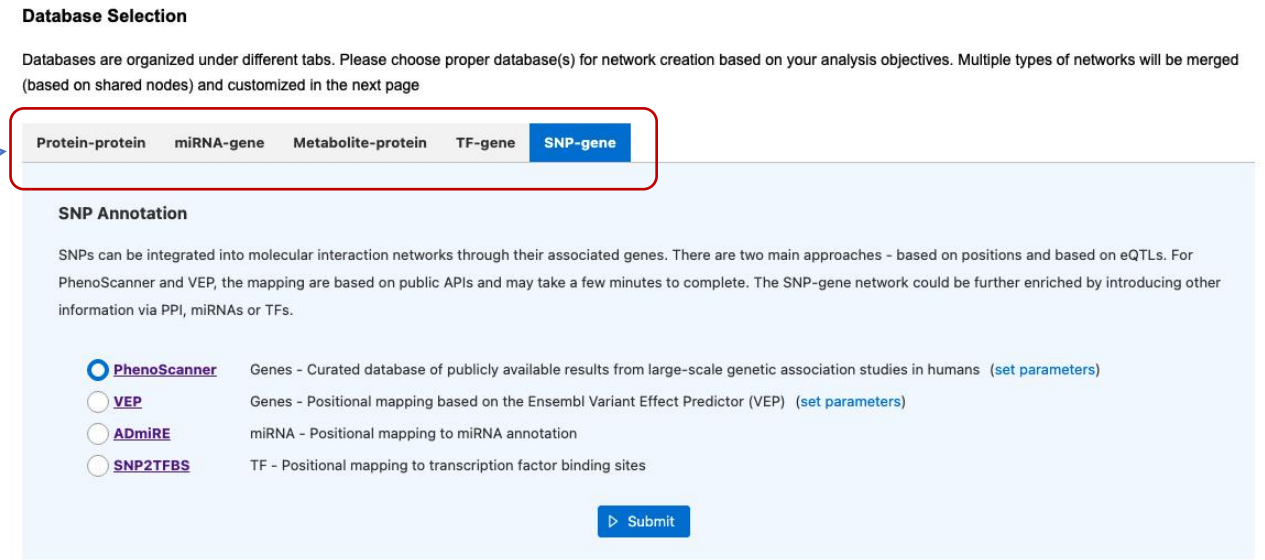
- PhenoScanner: positional mapping merely provide the nearest gene associated with the input SNPs; eQTIs analysis provide all the related genes within 500 Kb with P value < 10-5.
- VEP: user need to select either the distance (5kb~50kb) or a top rank to perform the positional mapping.

Details for the database please refer to FAQ #8

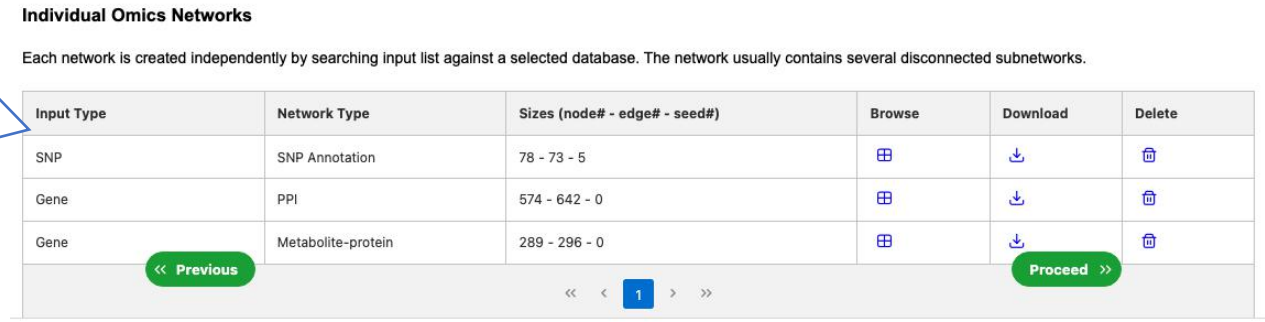
Network expansion

In the **database selection page**, users can also expand their SNP-gene network:

The SNP-gene network can be extended to include Protein-protein, miRNA-gene, or TF-gene interactions by querying the related databases.



Users can trace the networks built in different types individually:



Network interaction table

For each indvidual network, an interaction table is provided for users to dig into the details of their query results in :

Individual Omics Networks

Each network is created independently by searching input list against a selected database. The network usually contains several disconnected subnetworks.

Input Type	Network Type	Sizes (node# - edge# - seed#)	Browse	Download	Delete
SNP	SNP Annotation	78 - 73 - 5			
Gene	PPI	574 - 642 - 0			
Gene	Metabolite-protein	289 - 296 - 0			

Individual Network Interaction Table

You can browse, search or manual delete an interaction (edge), or use the **Advanced Filter** to exclude a node (and its all associated edges). Advanced Filter

Id1 ↑↓ Query ID	Id2 ↑↓ Result ID	Name1 ↑↓ Query Name	Name2 ↑↓ Result Name	Action
rs1428554	134466	rs1428554	ZNF300P1	Delete
rs1428554	345611	rs1428554	IRGM	Delete
rs1428554	91975	rs1428554	ZNF300	Delete
rs1428554	2878	rs1428554	GPX3	Delete
rs1428554	55696	rs1428554	RBM22	Delete
rs1428554	10318	rs1428554	TNIP1	Delete
rs41290504	RP11-129J12.2	rs41290504	RP11-129J12.2	Delete
rs41290504	159296	rs41290504	NKX2-3	Delete
rs41290504	7484	rs41290504	WNT9B	Delete
rs41290504	55280	rs41290504	CWF19L1	Delete
rs3197999	327	rs3197999	APEH	Delete
rs3197999	7318	rs3197999	UBA7	Delete
rs3197999	100847079	rs3197999	MIR5193	Delete
rs3197999	4485	rs3197999	MST1	Delete
rs3197999	8927	rs3197999	BSN	Delete

« Previous (1 of 5) 1 2 3 4 5 15 Proceed »

Note: Query ID list is the input SNPs for the first network and result genes can be used as quries in the following networks, and so forth.

Users can tailor their network by deleting the reults they are not interested in

Network Building

After generating the network individually, users will be lead to the summary of the integrated network:

Methods for pruning and tailoring the network for better visualization and enhanced functional interpretation

Multi-omics Network Building

If more than one network was generated in the previous page, they are merged together to form multi-omics network through shared nodes. In some cases, the result will contain a larger subnetwork containing most of queries, and several smaller subnetworks containing one or a few queries. These subnetworks will be available for visual analysis in the next page.

If the network is too large, it is recommended to trim the network to a smaller size that is suitable for visual analytics (less than 2000 nodes), you can use network tools located on the left hand side for trimming and filtering.

Networks	Sizes (node# - edge# - seed#)	Topology	Download (edge list)
subnetwork1	168 - 230 - 3	Details	Download
subnetwork2	5 - 4 - 1	Details	Download
subnetwork3	4 - 3 - 1	Details	Download

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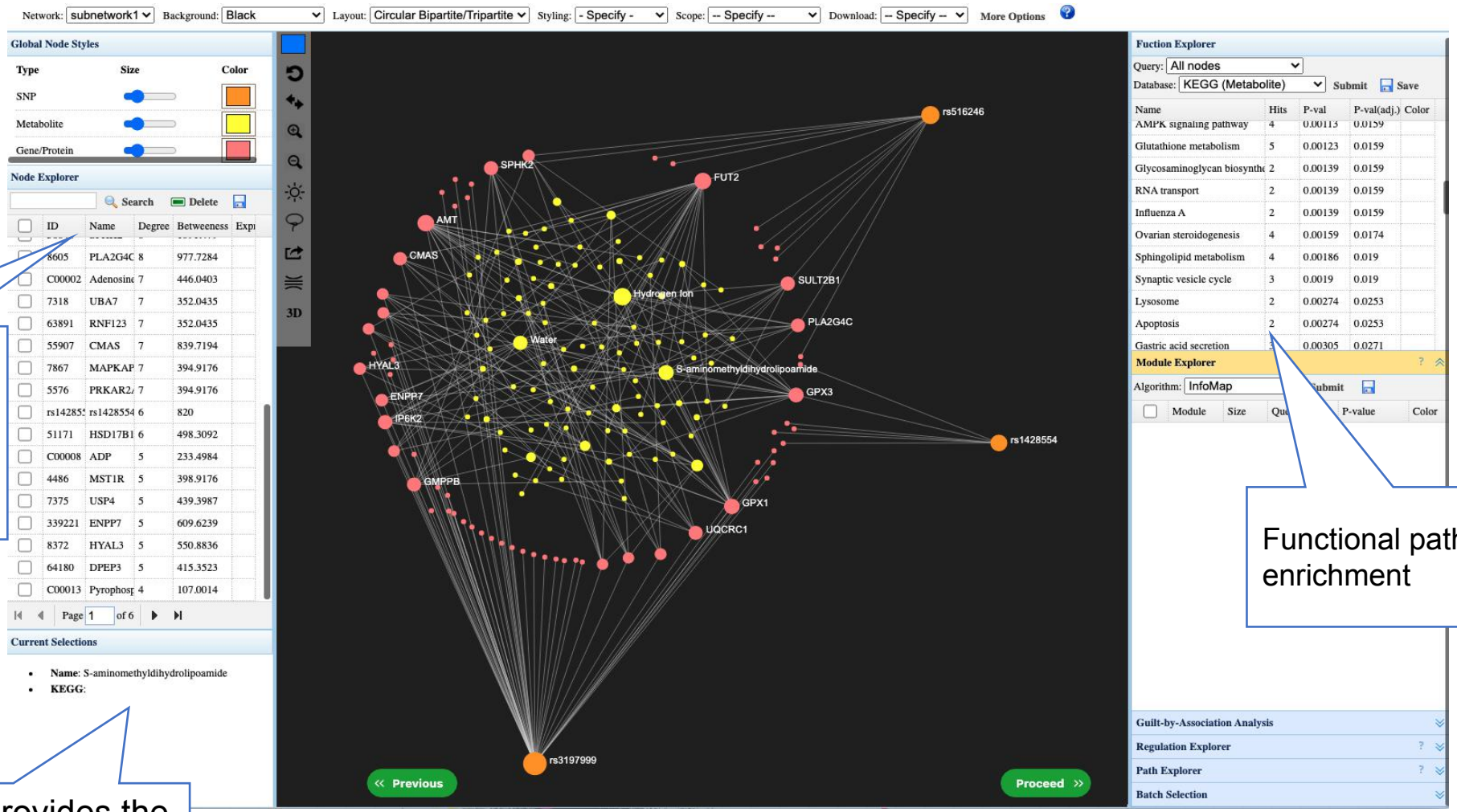
Detail topology information of the final integrated network.

Proceed for visualization

Network Visualization



Result list of the SNPs and their associated genes or other features quried

Functional pathway enrichment

Result panel provides the detail information of the highlight nodes

The End