Supporting Online Materials

Enrichr-KG: Bridging Enrichment Analysis across Multiple Libraries

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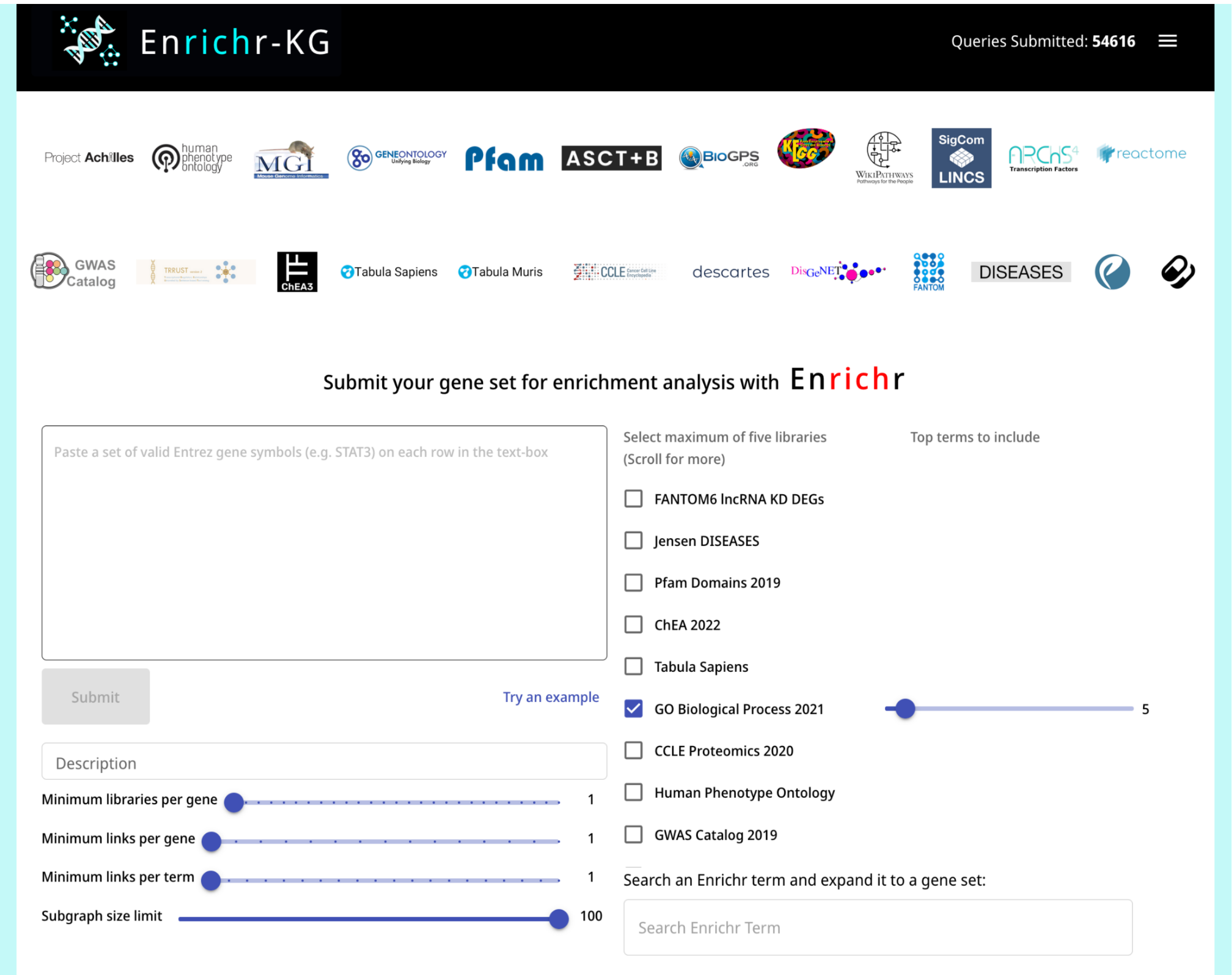
Supporting Figures



Submit your gene set for enrichment analysis with Enrichr

Paste a set of valid Entrez gene symbols (e.g. STAT3) on each row in the text-box

Description

Minimum libraries per gene 1

Minimum links per gene 1

Minimum links per term 1

Subgraph size limit 100

Select maximum of five libraries (Scroll for more)

Top terms to include

☐ FANTOM6 lncRNA KD DEGs
☐ Jensen DISEASES
☐ Pfam Domains 2019
☐ ChEA 2022
☐ Tabula Sapiens
☑ GO Biological Process 2021 5
☐ CCLE Proteomics 2020
☐ Human Phenotype Ontology
☐ GWAS Catalog 2019

Search an Enrichr term and expand it to a gene set:

Search Enrichr Term

Fig. S1 The Enrichr-KG gene set enrichment analysis input form. Gene IDs are automatically validated. Users can change the minimum libraries per gene, the minimum links per gene, the minimum links per term, and set the subgraph maximum size. In addition, users can select up to five gene set libraries to include in their analysis.

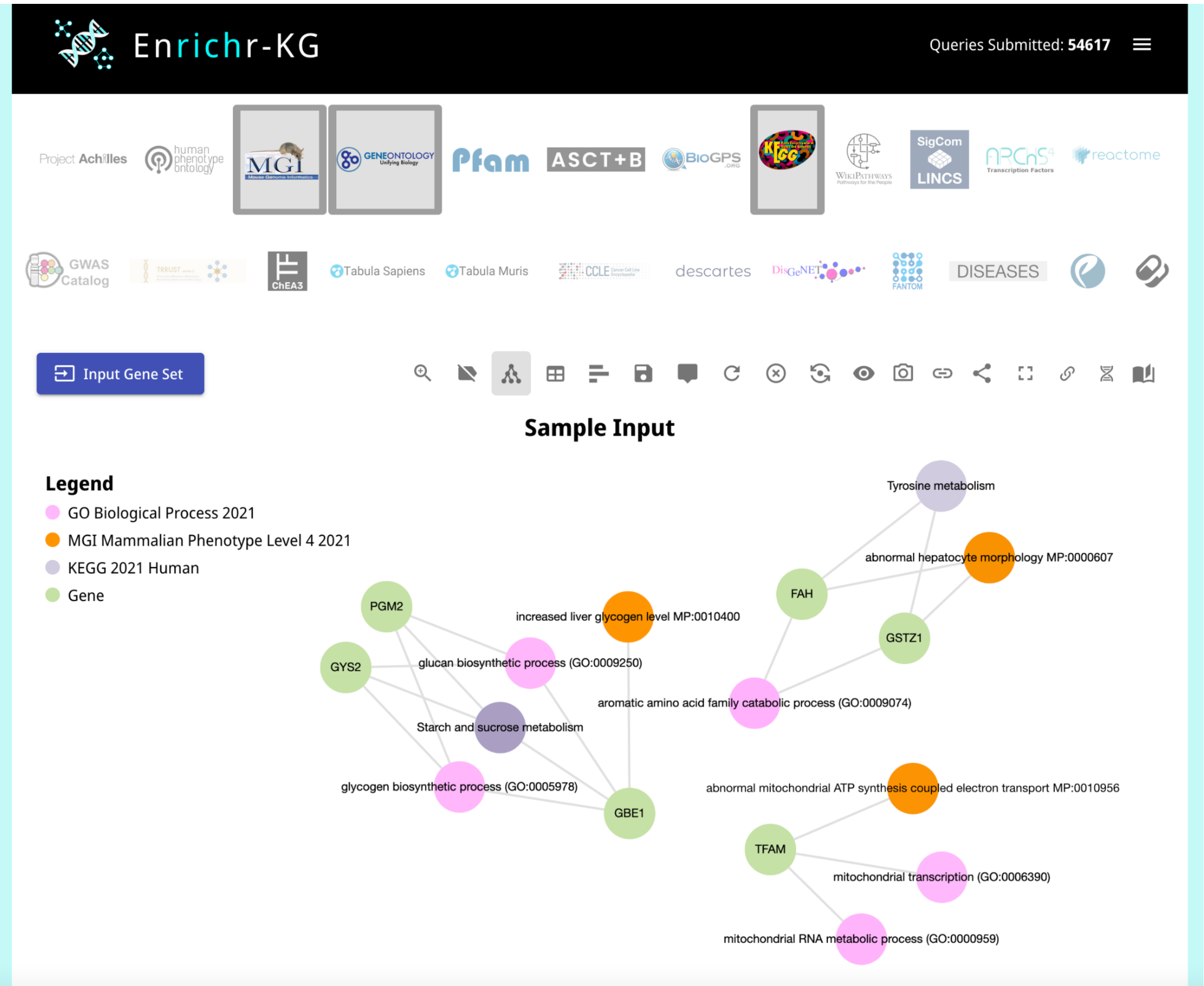


Fig. S2 The Enrichr-KG gene set enrichment analysis subnetwork display. Results from enrichment analysis queries are first returned as subnetworks that connect genes (green) to enriched terms (red - GO biological processes; blue - MGI phenotypes; orange - KEGG pathways).

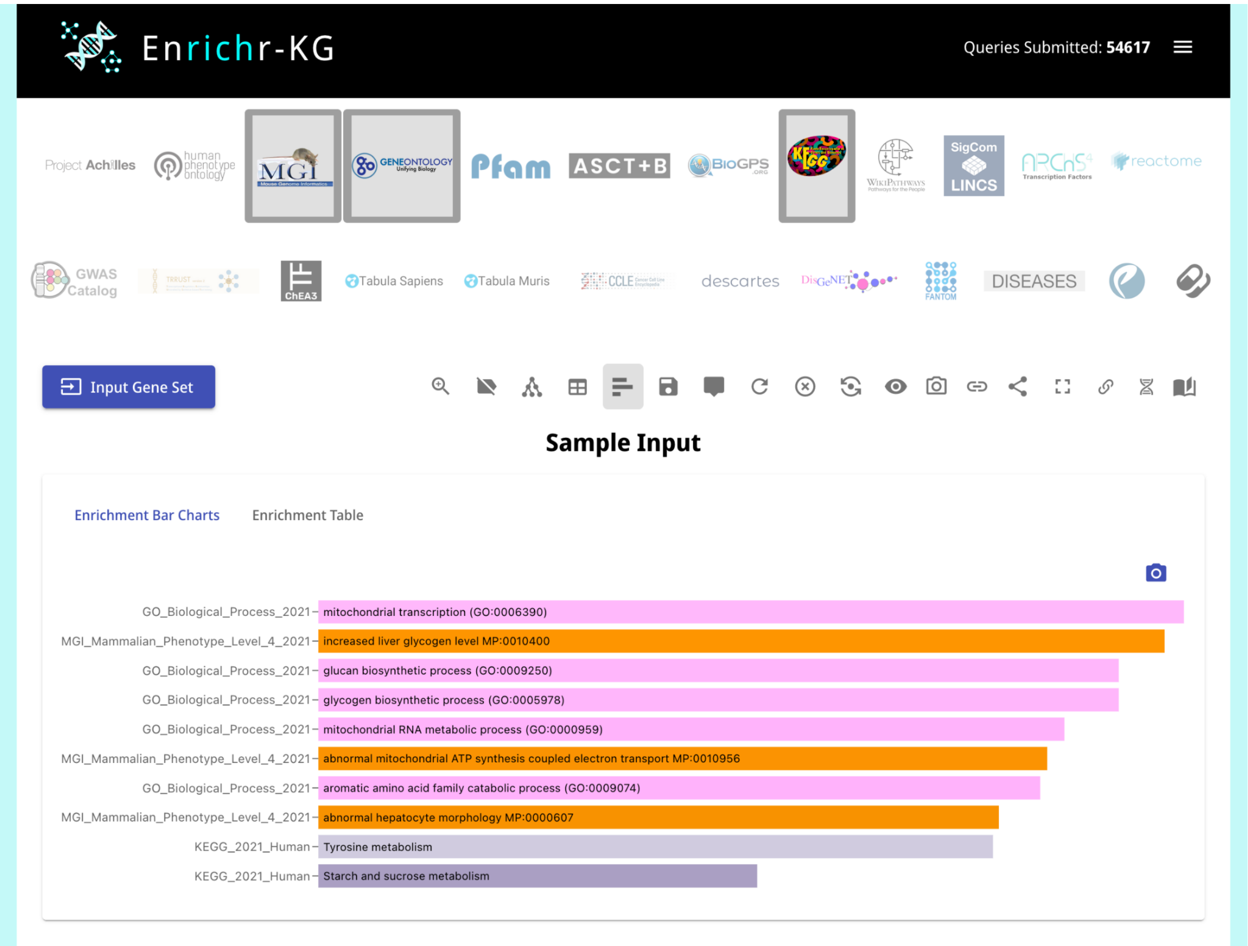
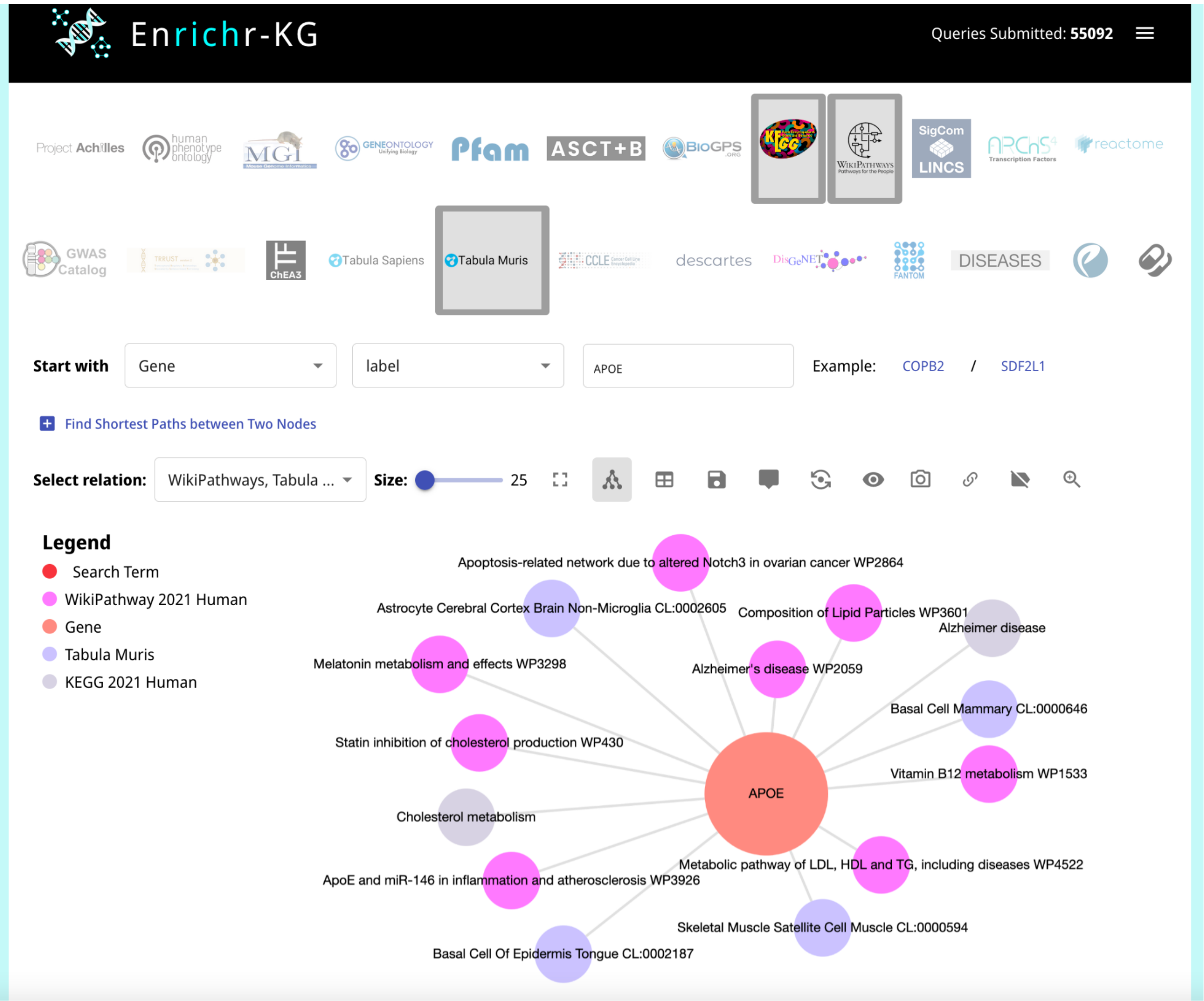


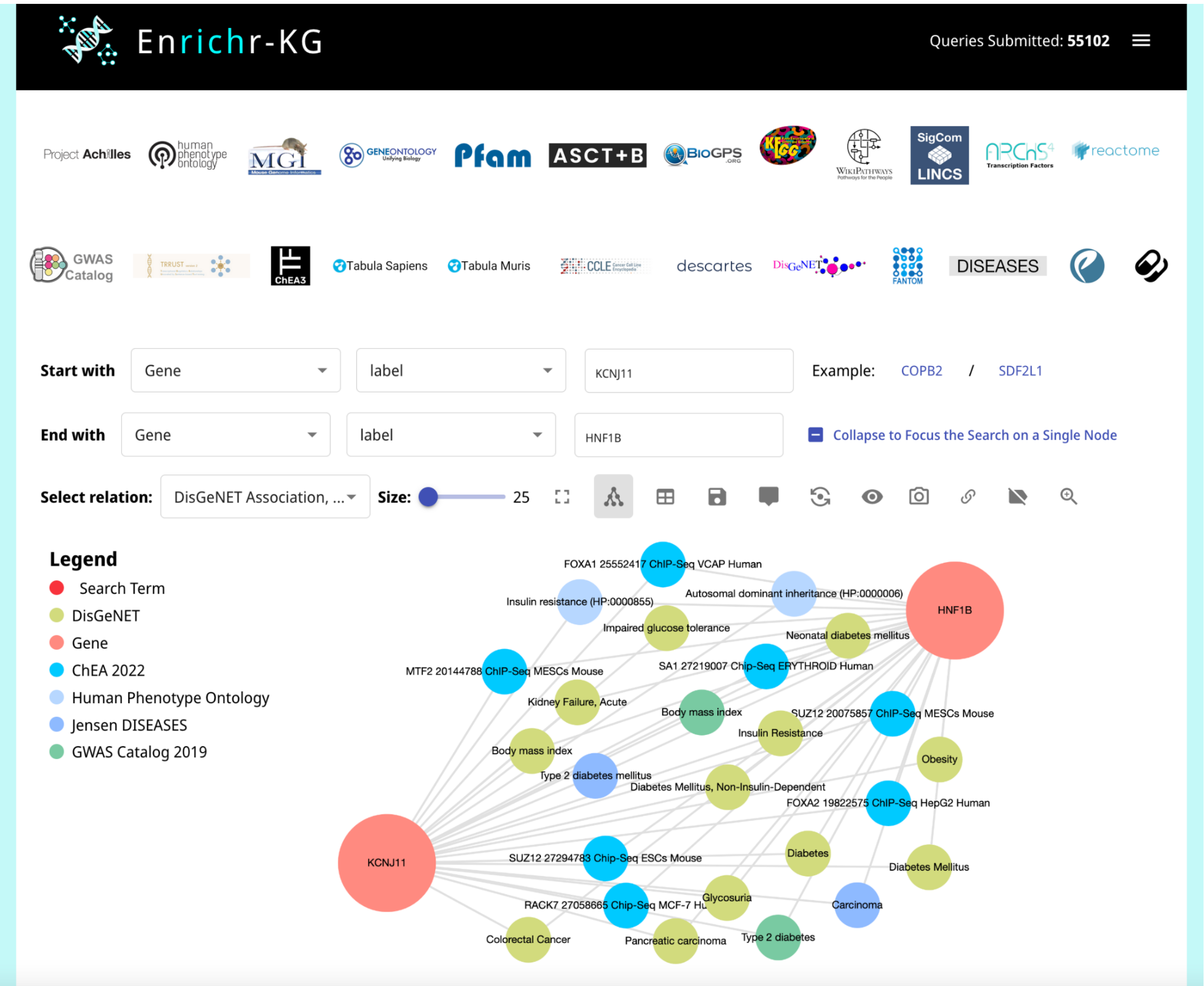
Fig. S3 The Enrichr-KG gene set enrichment analysis bar chart visualization. The enrichment results are visualized as a bar chart where the colors of the bars denote the source library. In this example, red bars represent GO biological processes; blue - MGI phenotypes; and orange - KEGG pathways. The size of the bars is proportional to the -log(p-value) of the enrichment score computed by the Fisher exact test.



Start with: Gene | label | APOE

Select relation: WikiPathways, Tabula ...

Fig. S4 The Enrichr-KG visualization centered around a specific gene or a specific term. The example shows associations for the gene APOE in the KEGG, WikiPathways and Tabula Muris gene set libraries.



Enrichr-KG

Queries Submitted: **55102**

Start with Gene · label · KCNJ11

Example: COPB2 / SDF2L1

End with Gene · label · HNF1B

Collapse to Focus the Search on a Single Node

Select relation: DisGeNET Association, ...

Size: 25

Legend
- ● Search Term
- ● DisGeNET
- ● Gene
- ● ChEA 2022
- ● Human Phenotype Ontology
- ● Jensen DISEASES
- ● GWAS Catalog 2019

Fig. S5 The Enrichr-KG visualization of a search between two terms. The example shows the shortest paths between the genes KCNJ11 and HNF1B (larger red nodes).