

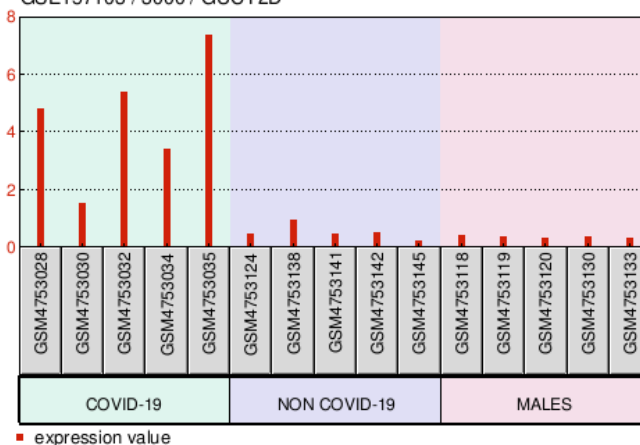
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Most services will be unavailable for 24+ hours starting 9 PM EDT. [Learn more about the maintenance.](#)

Use GEO2R to compare two or more groups of Samples in order to identify genes that are differentially expressed across experimental conditions. Results are presented as a table of genes ordered by significance. [Full instructions](#) [YouTube](#)

GEO accession [Large-scale Multi-omic Analysis of COVID-19 Severity](#)RNA-seq Series analysis ▸ **Samples**▸ [Define groups](#)Selected **15** out of **126** samples[GEO2R](#)[Options](#)**[Profile graph](#)**[R script](#)Enter gene symbol or ID: [Download gene annotation](#)

GSE157103 / 3000 / GUCY2D

[Sample values](#)

This tab allows you to view a specific gene expression profile graph by entering a gene symbol or the corresponding identifier from the GeneID column of the [Human_GRCh38.p13.annot.tsv.gz](#) annotation file. This feature does not perform any calculations; it merely displays the [TPM normalized](#) expression values of the gene across Samples. Sample groups may or may not be defined for this feature to work.

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