

# GSEA Report for Dataset MesenvsImmuno\_RNASeq\_ranks

## Enrichment in phenotype: **na**

- 3296 / 5931 gene sets are upregulated in phenotype **na\_pos**
- 1500 gene sets are significant at FDR < 25%
- 862 gene sets are significantly enriched at nominal pvalue < 1%
- 1204 gene sets are significantly enriched at nominal pvalue < 5%
- [Snapshot](#) of enrichment results
- Detailed [enrichment results in html](#) format
- Detailed [enrichment results in TSV](#) format (tab delimited text)
- [Guide to](#) interpret results

## Enrichment in phenotype: **na**

- 2635 / 5931 gene sets are upregulated in phenotype **na\_neg**
- 1475 gene sets are significant at FDR < 25%
- 811 gene sets are significantly enriched at nominal pvalue < 1%
- 1173 gene sets are significantly enriched at nominal pvalue < 5%
- [Snapshot](#) of enrichment results
- Detailed [enrichment results in html](#) format
- Detailed [enrichment results in TSV](#) format (tab delimited text)
- [Guide to](#) interpret results

## Dataset details

- The dataset has 15194 native features
- After collapsing features into gene symbols, there are: 15128 genes

## Gene set details

- Gene set size filters (min=15, max=200) resulted in filtering out 13630 / 19561 gene sets
- The remaining 5931 gene sets were used in the analysis
- List of [gene sets used and their sizes](#) (restricted to features in the specified dataset)

## Gene markers for the **na\_pos** *versus* **na\_neg** comparison

- The dataset has 15128 features (genes)
- Detailed [rank ordered gene list](#) for all features in the dataset

## Global statistics and plots

- Plot of [p-values vs. NES](#)
- [Global ES](#) histogram

## Other

- [Parameters](#) used for this analysis

## Comments

- Timestamp used as the random seed: 1710955387202

## Warnings

- There were duplicate row identifiers in the specified ranked list. One id was arbitrarily chosen. Details are below. Generally this is OK but if you want to avoid this, edit your ranked list so that all row ids are unique

# of row ids in original dataset: 15195

# of row UNIQUE ids in original dataset: 15194

The duplicates were

SLC35E2

- Mixed MSigDB versions detected. The selected CHIP does not match the version of the MSigDB collection selected. Some gene identifiers may not be mapped.

## Citing GSEA and MSigDB

To cite your use of the GSEA software please reference the following:

- [Subramanian, A., Tamayo, P., et al. \(2005, PNAS\).](#)
- [Mootha, V. K., Lindgren, C. M., et al. \(2003, Nature Genetics\).](#)

For use of the Molecular Signatures Database (MSigDB), to cite please reference one or more of the following as appropriate, along with the source for the gene set as listed on the gene set page:

- [Liberzon A, et al. \(Bioinformatics, 2011\).](#)
- [Liberzon A, et al. \(Cell Systems 2015\).](#)

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xtools.gsea.GseaPreranked [Wed., Mar. 20, '24 1 p.m. 23] Report: gsea\_analysis.GseaPreranked.1710955387202.rpt by user: annat  
Website: [www.gsea-msigdb.org/gsea](http://www.gsea-msigdb.org/gsea) Questions & Suggestions: [Contact page](#)