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Seminar

Lichuang Huang

Wie-Biotech

2023-10-12

Last Month

Order 1: WES (mutation detection)

- QC
- Detect variants
- filter variants
- Annotation

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Order 2: Multi-Omics

- Network pharm.
- Omics: Microbiota (16s RNA)
- Omics: Metabolites
- Microbiota ⇒ Metabolites:
  gutMDisorder
- Omics: RNA
- drug Binding: Molecular docking

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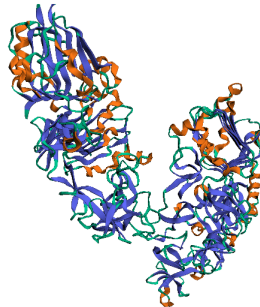**Issues**
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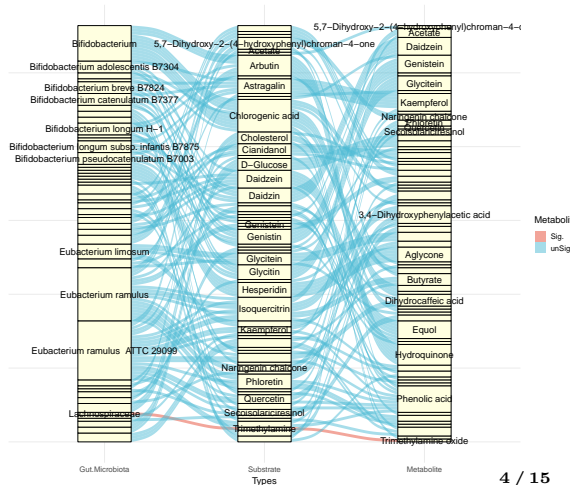
Order 3: Package touchPDB

- Protein basic Information
- Active sites
- Binding sites
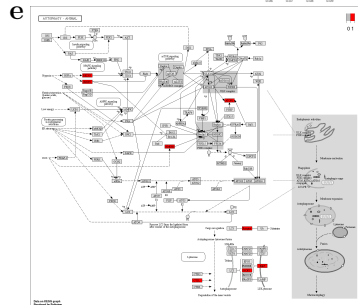- Visualization
- . . .
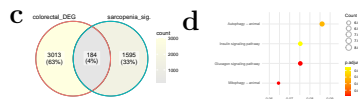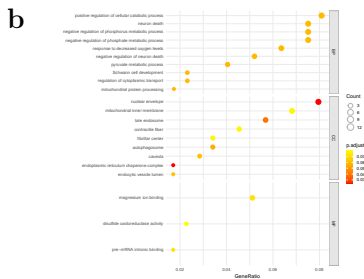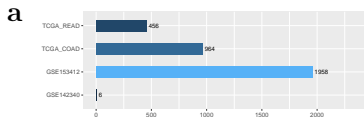

1.4   Structure View
PDB ID: 2AHX

Order 4: dual disease and pathway selection

- Multi datasets
  - TCGA
  - GEO
- WGCNA
- Enrichment

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Article

Article

A molecular cell atlas of the human lung from single-cell RNA sequencing

Kyle J. Travaglini[1,2,16], Ahmad N. Nabhan[1,2,12,16], Lolita Penland[3,13], Rahul Sinha[4,5], Astrid Gillich[1,2], Rene V. Sit[3], Stephen Chang[1,2], Stephanie D. Conley[4,5], Yasuo Mori[4,5,14], Jun Seita[4,5,15], Gerald J. Berry[5], Joseph B. Shrager[6], Ross J. Metzger[2,7], Christin S. Kuo[8], Norma Neff[3], Irving L. Weissman[4,5,9,10], Stephen R. Quake[3,11✉] & Mark A. Krasnow[1,2✉]

Travaglini KJ, et al. (2020). *Nature.*

A molecular cell atlas of the human lung

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Marker identification

a Lymphocytes / Granulocytes / Platelets / Myeloid cell tree with abundance bar chart showing Blood and Lung fractions for cell types 34–58.

b DC subtypes — dot plot of HLA-DPB1, GPR183, LAMP3, CLEC9A, CD1C, PLD4, GPR34, IGSF21, EREG, CLEC5A, TREM2, CHI3L1 across mDC1, mDC2, IGSF21+, EREG+, TREM2+.

c General (CREM, RGS2, SLA, NFE2L2), Lymphocyte (CD69, RGS1, LMNA, RGCC, DUSP6, SOCS1), Myeloid (AREG, THBD, MPHOSPH6, PLAUR, HBEGF, MERTNL, GNAI3, IL1B, BRE-AS1) signature scores across cell types.

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Usefull and available data

Supplementary Table

Supplementary Table 2. Human lung cell cluster identities, abundances, and locations. Cell numbers are stratified by type, subject, and sequencing technology. Cell abbreviations indicated are used throughout.

Supplementary Table

Supplementary Table 3. Surface markers used to isolate canonical immune cell types in bulk mRNA sequencing. See Methods for details on antibodies.

Supplementary Table

Supplementary Table 4. Enriched markers found in each cluster, with transcription factors, receptors/ligands, and disease associated genes annotated. Includes all enriched genes for each type (p-val > 0.05, MAST, downsampled cells per group to 100 for SS2 clusters or 500 for 10x clusters). Abbreviations: avg_logFC, the natural log of the average fold change between the cell type and other cell types in its tissue compartment; pct_in_cluster, percentage of cells within the cluster that express the gene; pct_out_cluster, percentage of cells outside cluster that express the gene; p_val_adj, p-value with Bonferroni correction applied; TF, transcription factor; OMIM, Online Mendelian Inheritance in Man; GWAS, genome wide association study.

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1. No public available data
2. No correlation between multi-omics
3. Computation is time-consumed

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Projects

- Gene selection: XiaGuoLian
- Spatial transcriptome: CaoZhuo
- . . .
- Dual disease correlation: KIRC and CKD
- Image repeat detection