

Last Month
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Article Sharing
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Issues
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Schedule
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Seminar

Lichuang Huang

Wie-Biotech

2023-11-10

Last Month
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Article Sharing
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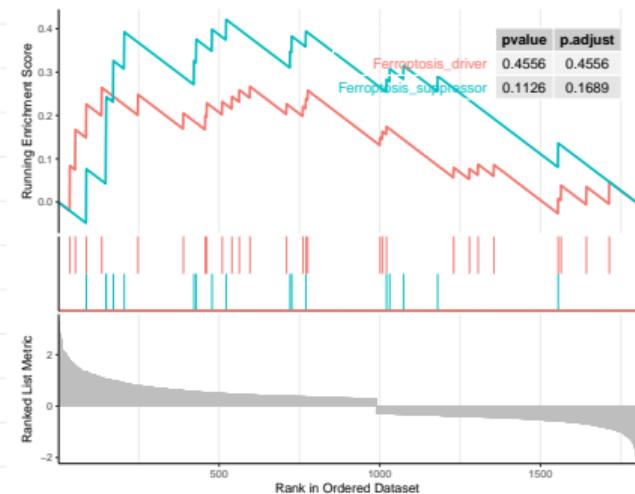
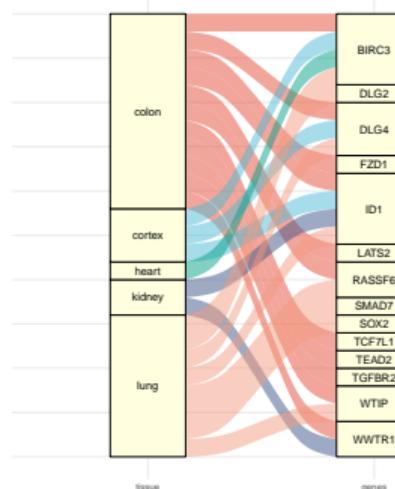
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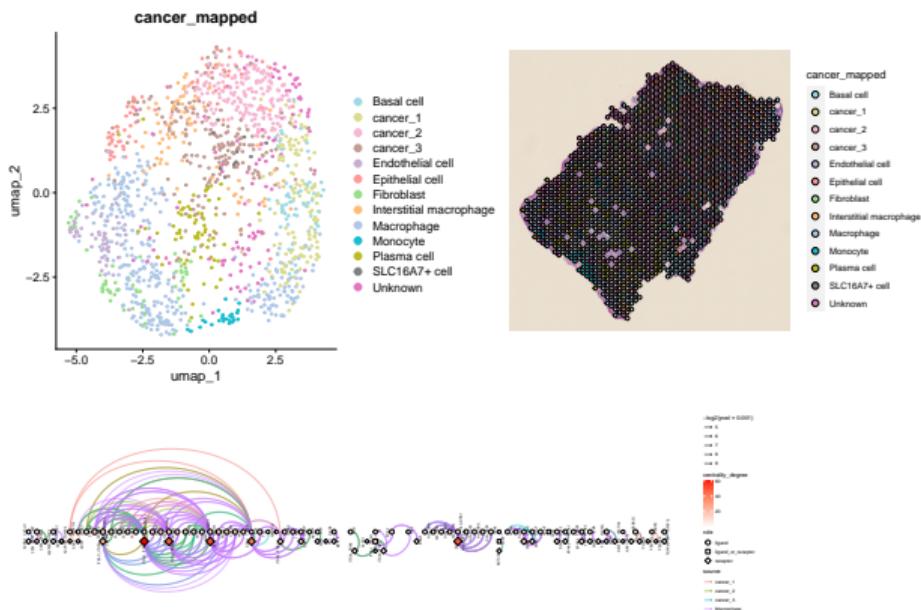
Order 1: TNA and Sepsis

- Screen DEGs
- Microbiota
- Ferroptosis



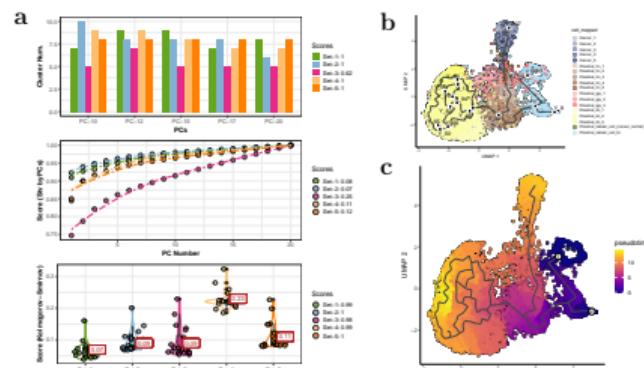
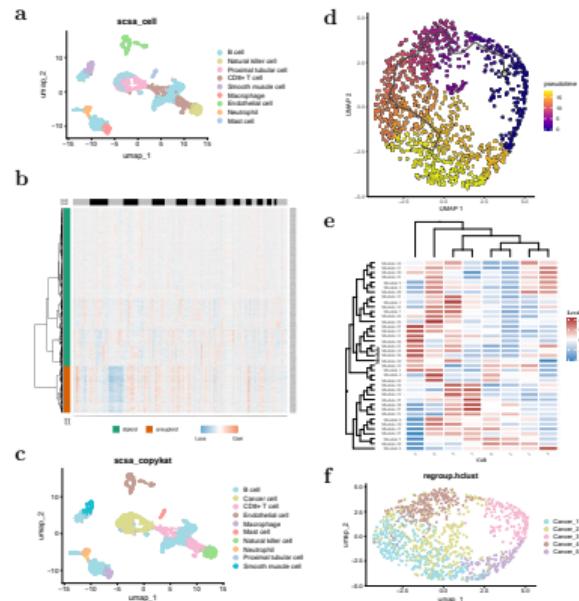
Order 2: Spatial scRNA

- Cell annotation
- Cancer cell prediction
- Cancer cell subtype
- Cell communication
- ...



Order 3: CKD and Renal Cancer

- RCC
- CKD
- HN
- IgA
- IMN



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Article Sharing

Article

Article

RNA editing underlies genetic risk of common inflammatory diseases

<https://doi.org/10.1038/s41586-022-05052-x>

Received: 24 March 2021

Accepted: 29 June 2022

Published online: 3 August 2022

 Check for updates

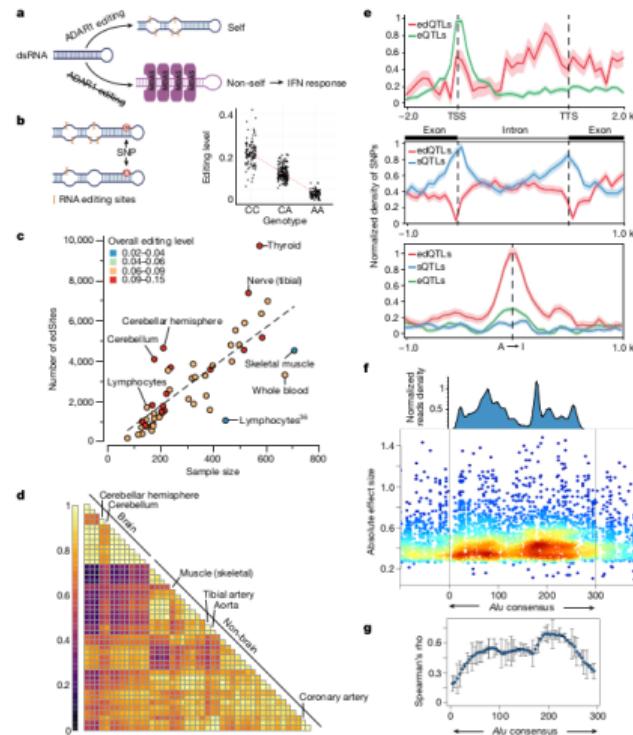
Qin Li¹, Michael J. Gloudemans^{2,3}, Jonathan M. Geisinger¹, Boming Fan⁴, François Aguet⁵, Tao Sun¹, Gokul Ramaswami¹, Yang I. Li^{1,6}, Jin-Biao Ma⁶, Jonathan K. Pritchard^{1,7}, Stephen B. Montgomery^{1,2,8} & Jin Billy Li^{1,8}✉

A major challenge in human genetics is to identify the molecular mechanisms of trait-associated and disease-associated variants. To achieve this, quantitative trait locus (QTL) mapping of genetic variants with intermediate molecular phenotypes such as gene expression and splicing have been widely adopted^{1,2}. However, despite successes, the molecular basis for a considerable fraction of trait-associated and disease-associated variants remains unclear^{3,4}. Here we show that ADAR-mediated adenosine-to-inosine RNA editing, a post-transcriptional event vital for suppressing cellular double-stranded RNA (dsRNA)-mediated innate immune interferon responses^{5–11}, is an important potential mechanism underlying genetic variants

Li Q, et al. (2022). *Nature*.

A molecular cell atlas of the human lung

- RNA editing
 - A-to-I editing (mostly)
 - C-to-U editing
- eQTLs
- edQTLs
- sQTLs
- ...



edQTLs data in GTEx database

Single Tissue cis-RNA Editing QTL Data

cis-RNA editing QTLs (cis-edQTLs) mapped in GTEx subjects in each of the 49 tissues. The level of RNA editing for 14,993–60,581 sites per tissue is quantified and used as the phenotype for FastQTL mapping. Please see:
<https://www.nature.com/articles/s41586-022-05052-x>

Name	Description	Size	Download
GTEx_Analysis_v8_edQTL README.txt	README file describing edQTL data.	4.5 kB	
GTEx_Analysis_v8_edQTL.tar	edSite and significant variant-site associations based on permutations. The archive contains a *.edsite.txt.gz and *.signif_variant_site_pairs.txt.gz file for each tissue.	625.9 MB	
GTEx_Analysis_v8_edQTL_phenotype_matrices.tar	Fully processed RNA editing level matrices for each tissue, which were used as input into FastQTL for edQTL mapping. Sites with ≥20 reads coverage in ≥60 samples per tissue are used for edQTL mapping. The archive contains a *.20cov.60samples.txt.gz file for each tissue.	724 MB	
GTEx_Analysis_v8_edQTL_covariates.tar.gz	Covariates used in edQTL analysis. Includes genotyping principal components and PEER factors. The archive contains a *.combined_covariates.txt file for each tissue.	2.1 MB	

editing QTL All Associations

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Issues

Issues

- 1 Meta-analysis: Literatures

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Projects

- RNA-seq and GPBAR/TGR5
- RNA-editing and inflammation
- ...