

# Single-Cell RNA-Seq

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## Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells

Alex K. Shalek, Rahul Satija, Xian Adiconis, Rona S. Gertner, Jellert T. Gaublomme, Raktima Raychowdhury, Schragi Schwartz, Nir Yosef, Christine Malboeuf, Diana Lu, John T. Trombetta, Dave Gennert, Andreas Gnirke, Alon Goren, Nir Hacohen, Joshua Z. Levin, Hongkun Park & Aviv Regev

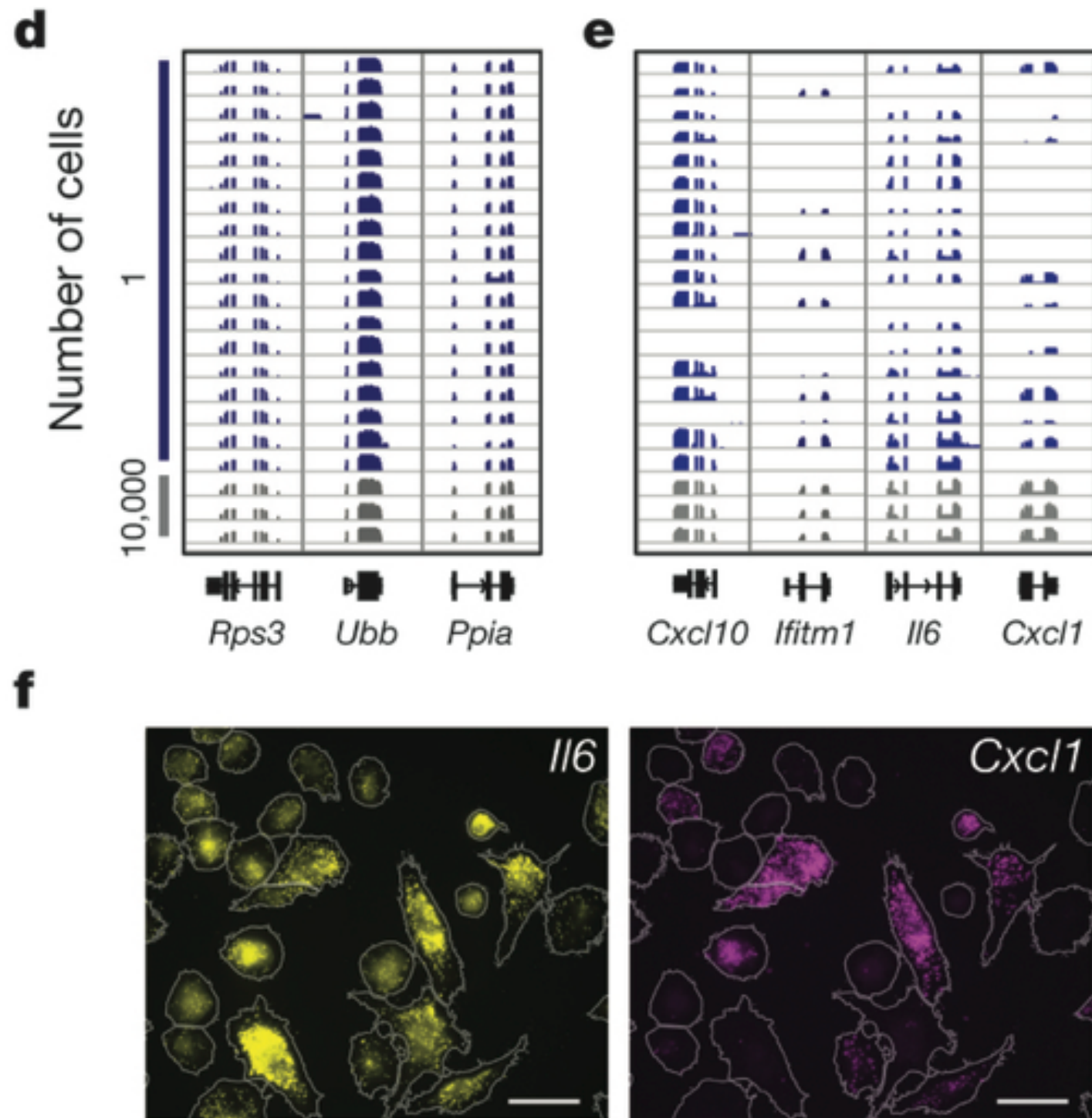
[Affiliations](#) | [Contributions](#) | [Corresponding authors](#)

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- At the cell community level, expression and splicing is bimodal across cells!

# Single-Cell RNA-Seq



# Transcriptional variation across human populations

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## Transcriptome and genome sequencing uncovers functional variation in humans

Tuuli Lappalainen, Michael Sammeth, Marc R. Friedländer, Peter A. C. 't Hoen, Jean Monlong, Manuel A. Rivas, Mar González-Porta, Natalja Kurbatova, Thasso Griebel, Pedro G. Ferreira, Matthias Barann, Thomas Wieland, Liliana Greger, Maarten van Iterson, Jonas Almlöf, Paola Ribeca, Irina Pulyakhina, Daniela Esser, Thomas Giger, Andrew Tikhonov, Marc Sultan, Gabrielle Bertier, Daniel G. MacArthur, Monkol Lek, Esther Lizano  *et al.*

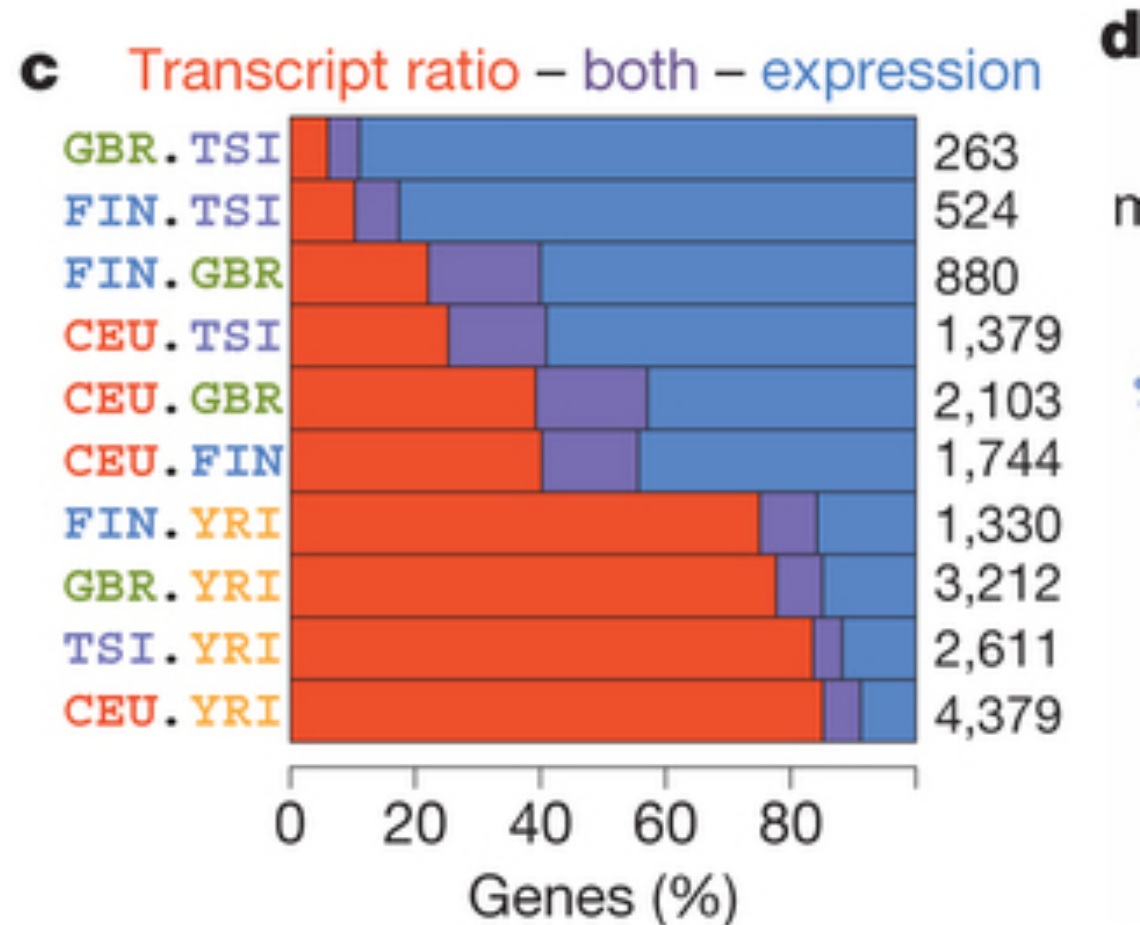
[Affiliations](#) | [Contributions](#) | [Corresponding authors](#)

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- Variation in transcript usage is greater than expression variation in distant populations

# Transcriptional variation across human populations



Of genes that show differences, the % that show difference in transcript usage, expression level, or both (CEU: Central European European, YRI: African)

# Gene fusions in cancer

Research article

Highly accessed

Open Access

## Identification of gene fusion transcripts by transcriptome sequencing in *BRCA1*-mutated breast cancers and cell lines

Kevin CH Ha<sup>1,2</sup>, Emilie Lalonde<sup>1,2</sup>, Lili Li<sup>1,3,4</sup>, Luca Cavallone<sup>3,4</sup>, Rachael Natrajan<sup>5</sup>, Maryou B Lambros<sup>5</sup>, Costas Mitsopoulos<sup>5</sup>, Jarle Hakas<sup>5</sup>, Iwanka Kozarewa<sup>5</sup>, Kerry Fenwick<sup>5</sup>, Chris J Lord<sup>5</sup>, Alan Ashworth<sup>5</sup>, Anne Vincent-Salomon<sup>6</sup>, Mark Basik<sup>4,7,8</sup>, Jorge S Reis-Filho<sup>5</sup>, Jacek Majewski<sup>1,2</sup> and William D Foulkes<sup>1,3,4,7</sup>\*

\* Corresponding author: William D Foulkes [william.foulkes@mcgill.ca](mailto:william.foulkes@mcgill.ca)

▼ Author Affiliations

1 Department of Human Genetics, McGill University, Room N5-13, Stewart Biology Building, 1205 Dr. Penfield Ave, Montreal, Quebec, H3A 1B1, Canada

2 McGill University and Genome Quebec Innovation Centre, 740 Dr. Penfield Ave, Montreal, Quebec, H3A 1A4, Canada

3 Program in Cancer Genetics, McGill University, 546 Pine Ave, Montreal, Quebec, H2W 1S6, Canada

4 Segal Cancer Centre, Lady Davis Institute, Jewish General Hospital, 3755 Côte-Ste-Catherine Road, Montreal, Quebec, H3T 1E2, Canada

5 The Breakthrough Breast Cancer Research Centre, The Institute of Cancer Research, 237 Fulham Road, London, SW3 6JB, UK

6 Institut Curie, 26 Rue d'Ulm, 75248, Paris, France

7 Department of Oncology, Lady Davis Institute, Jewish General Hospital, McGill University, 3755 Côte-Ste-Catherine Road, Montreal, H3T 1E2, Canada

8 Department of Surgery, Lady Davis Institute, Jewish General Hospital, McGill University, 3755 Côte-Ste-Catherine Road, Montreal, Quebec, H3T 1E2, Canada

For all author emails, please [log on](#).

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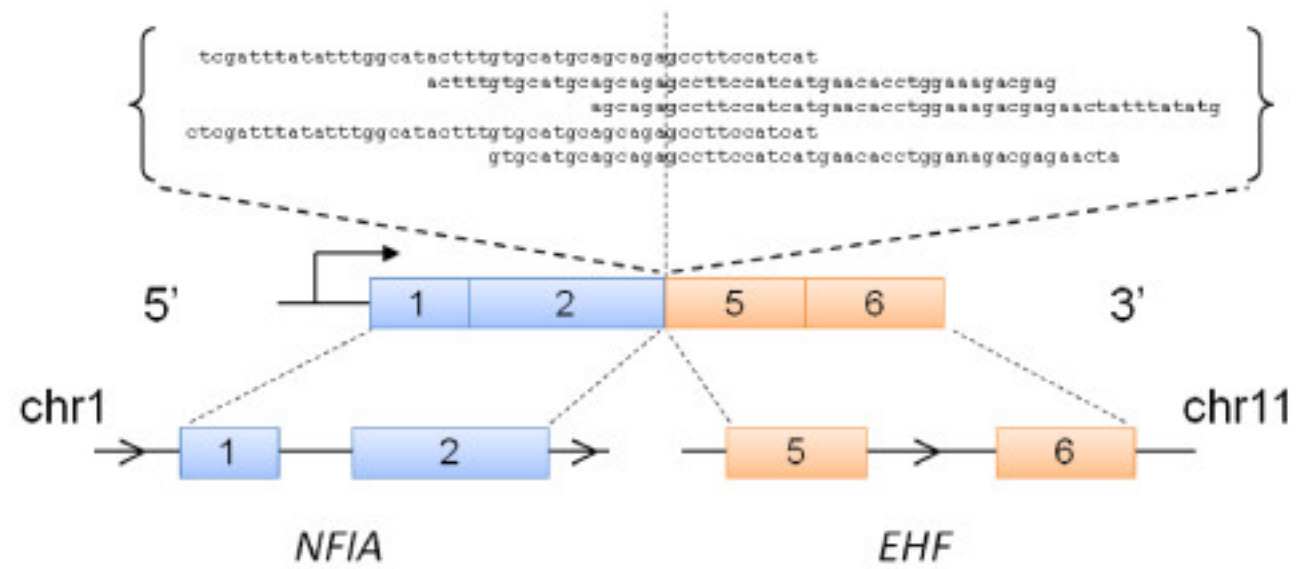
doi:10.1186/1755-8794-4-75



# Gene fusions in cancer

**Figure 1.**

**A**



**B**

