

Bioinformatics



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Presented by Theo N.

Foundation

Variability

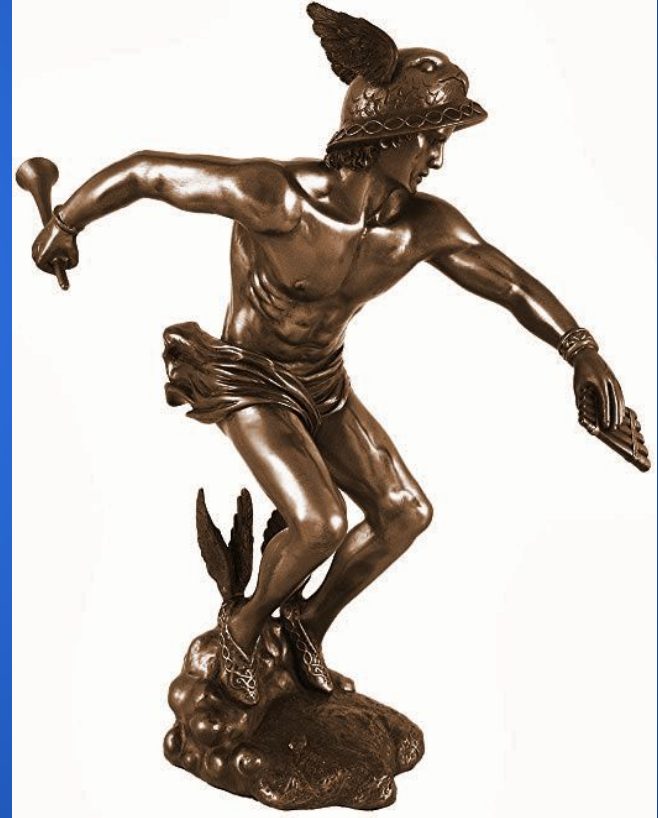
DNA

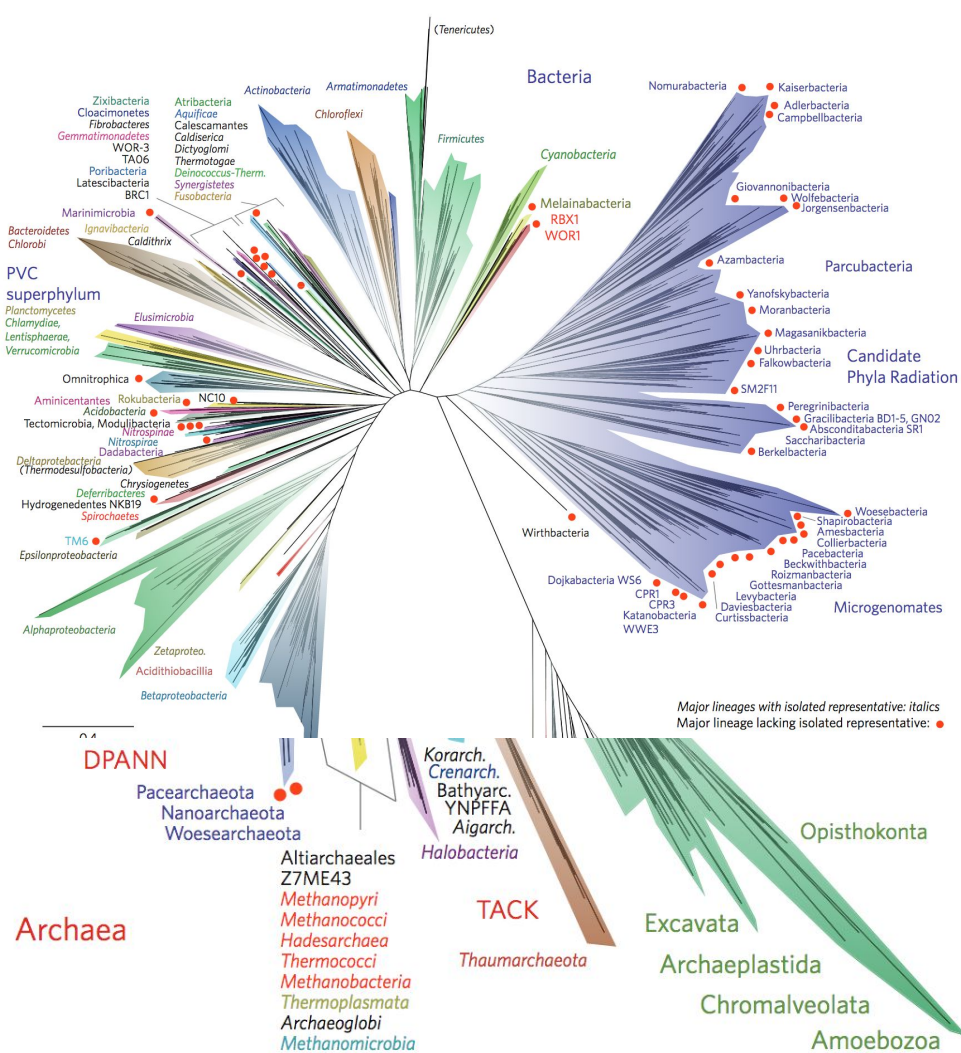
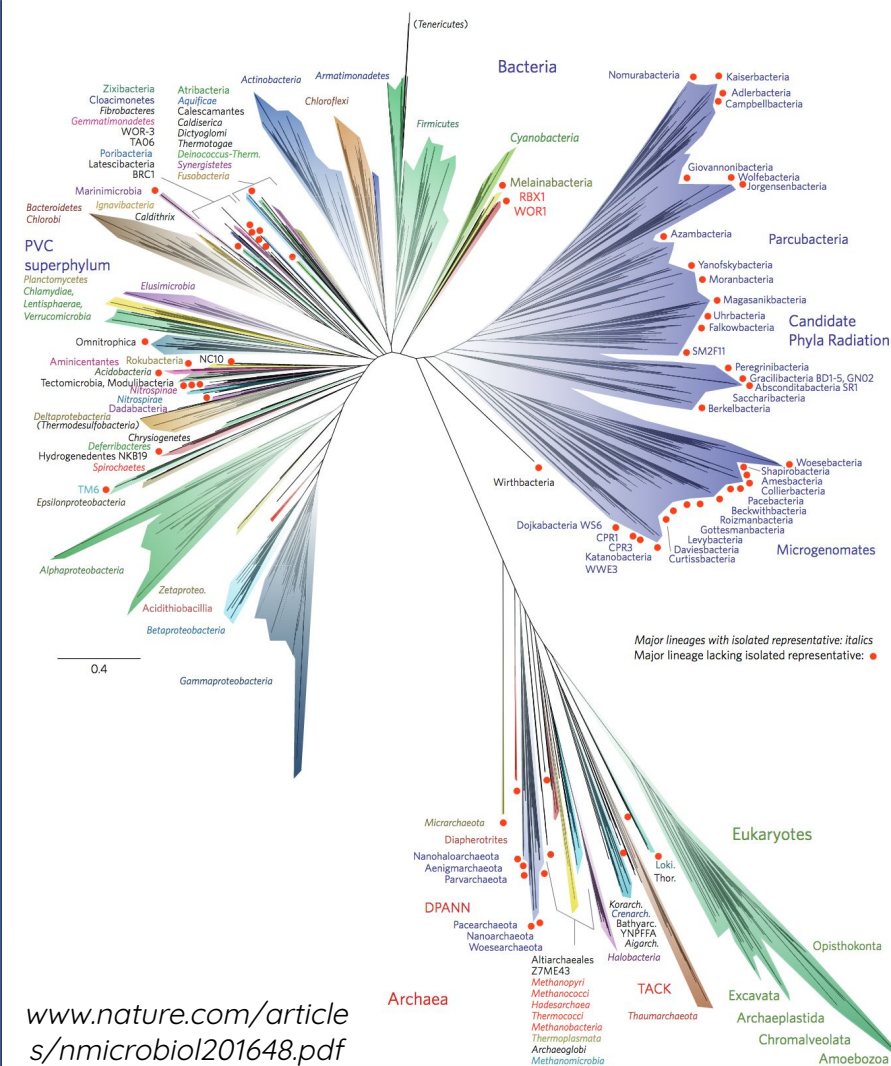


RNA



Protein



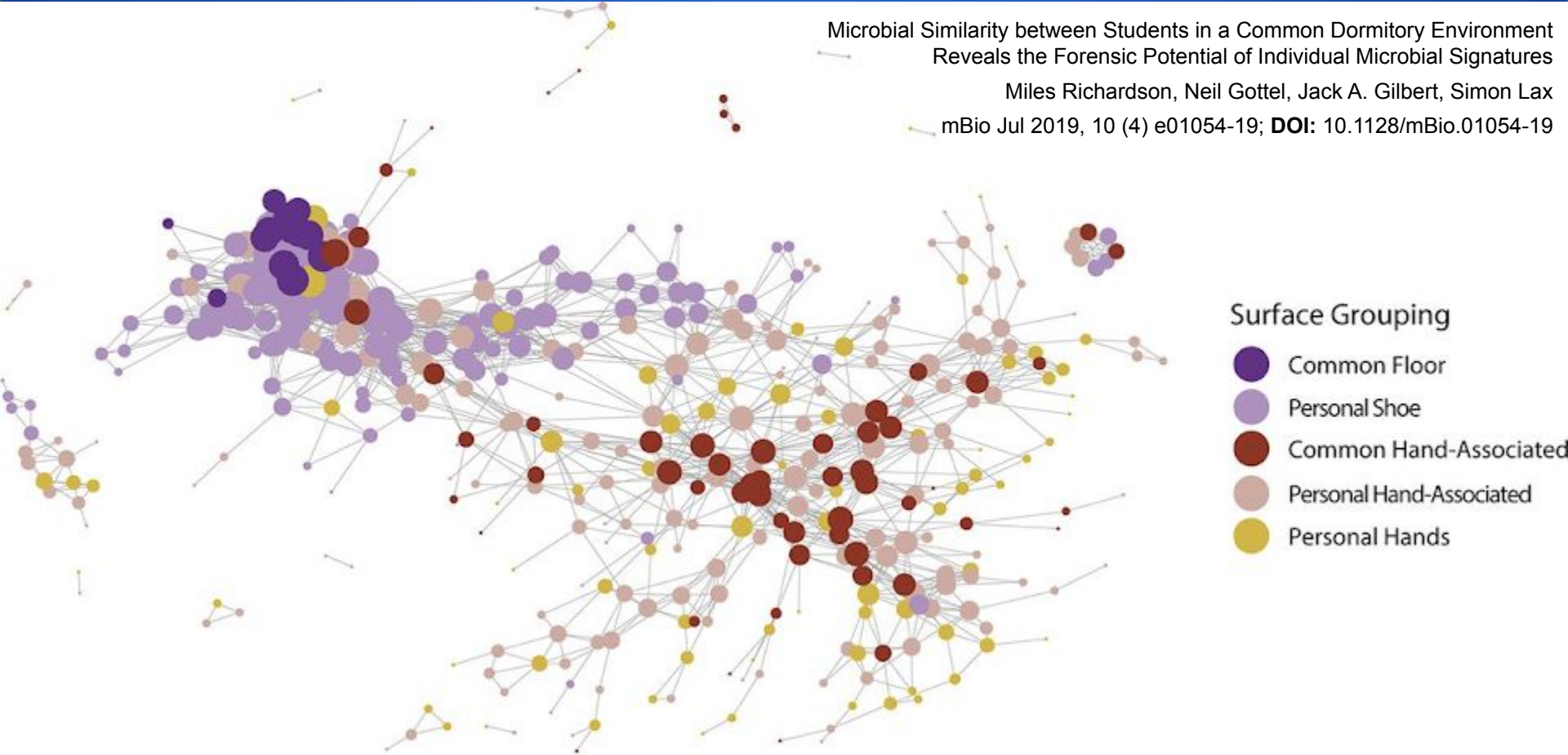


Significance - College Dorms

Microbial Similarity between Students in a Common Dormitory Environment
Reveals the Forensic Potential of Individual Microbial Signatures

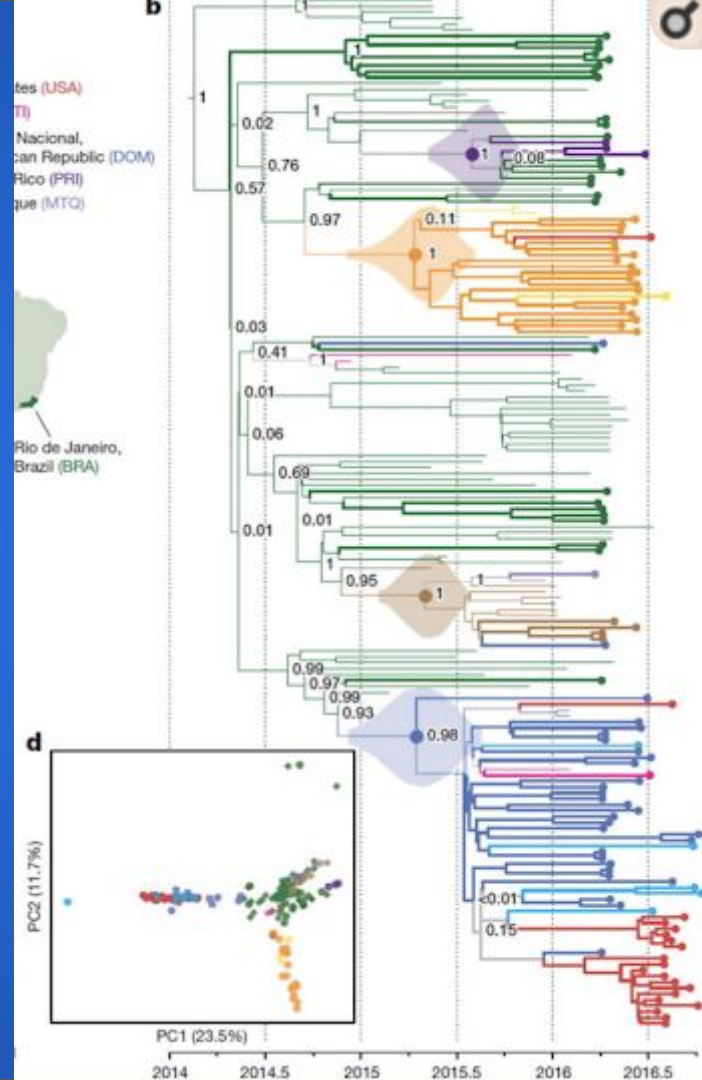
Miles Richardson, Neil Gottel, Jack A. Gilbert, Simon Lax

mBio Jul 2019, 10 (4) e01054-19; DOI: 10.1128/mBio.01054-19



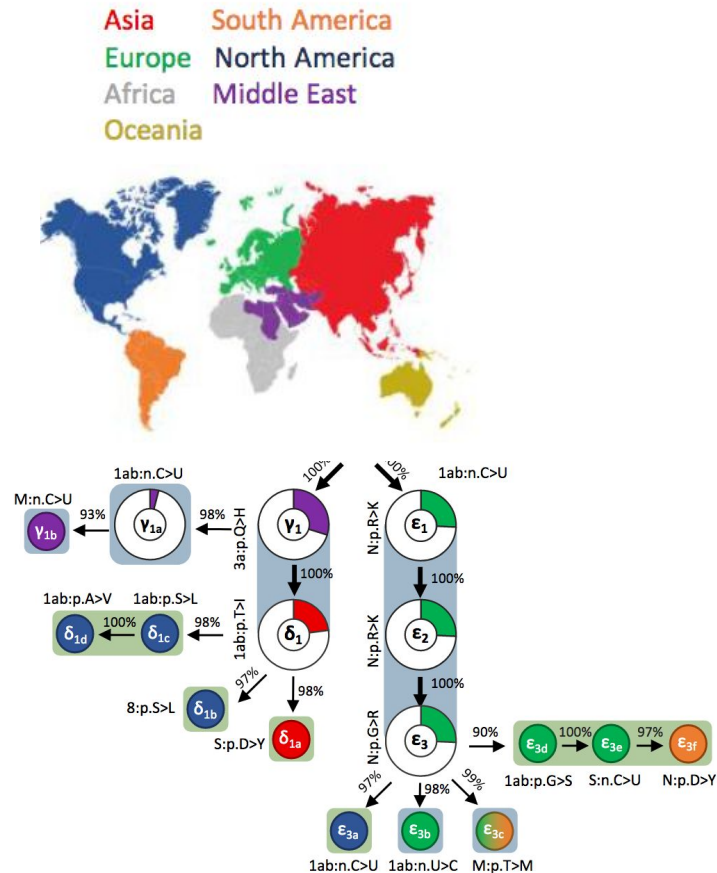
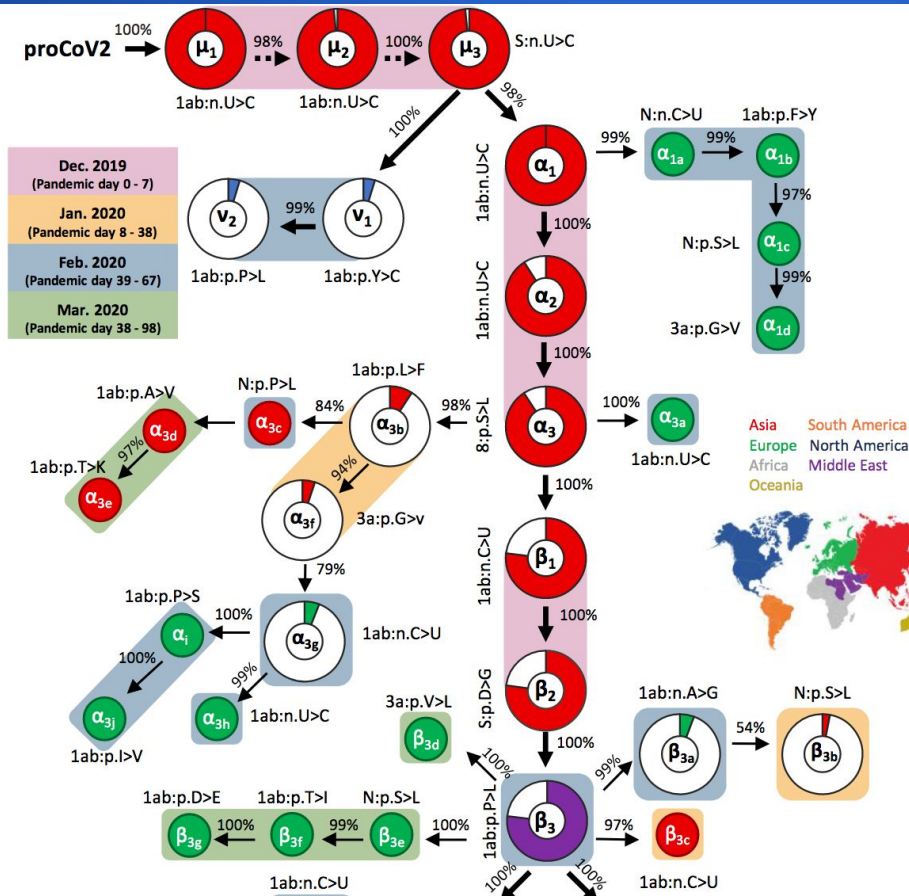
Significance - ZIKA

Metsky HC, Matranga CB, Wohl S, et al. Zika virus evolution and spread in the Americas. *Nature*. 2017;546(7658):411–415. doi:10.1038/nature22402



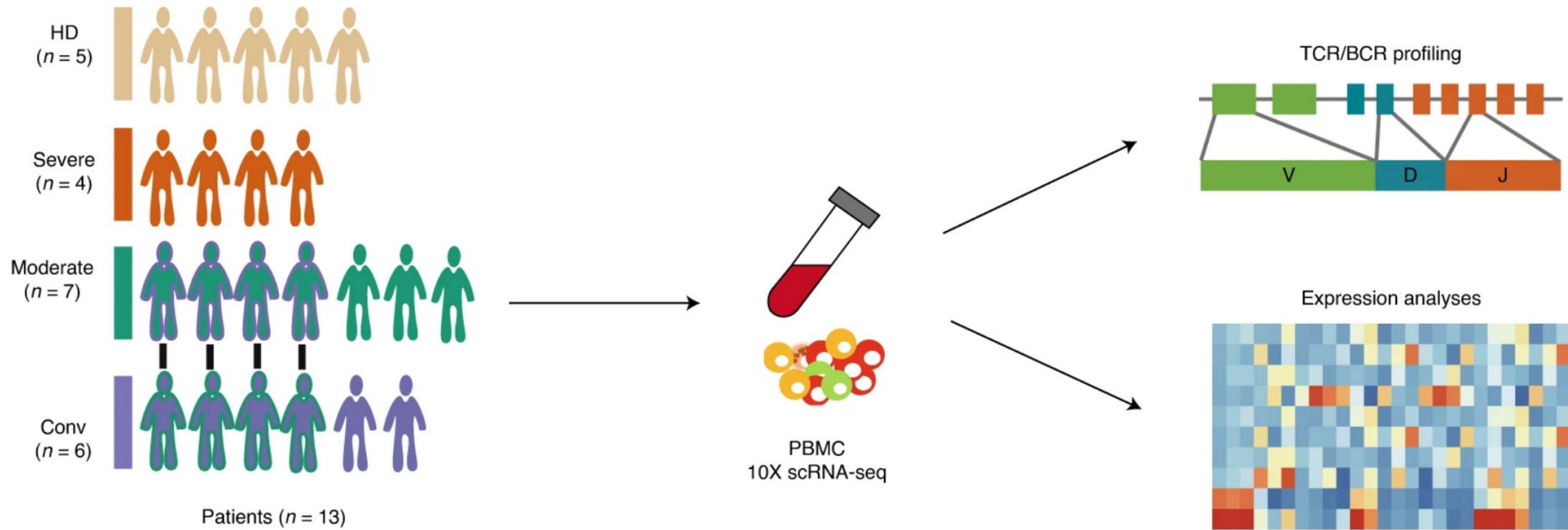
Significance –

An evolutionary portrait of the progenitor SARS-CoV-2 and its dominant offshoots in COVID-19 pandemic
 Sudhir Kumar, Qiqing Tao, Steven Weaver, Maxwell Sanderford, Marcos A. Caraballo-Ortiz, Sudip Sharma, Sergei L. K. Pond, Sayaka Miura
 bioRxiv 2020.09.24.311845; doi: <https://doi.org/10.1101/2020.09.24.311845>



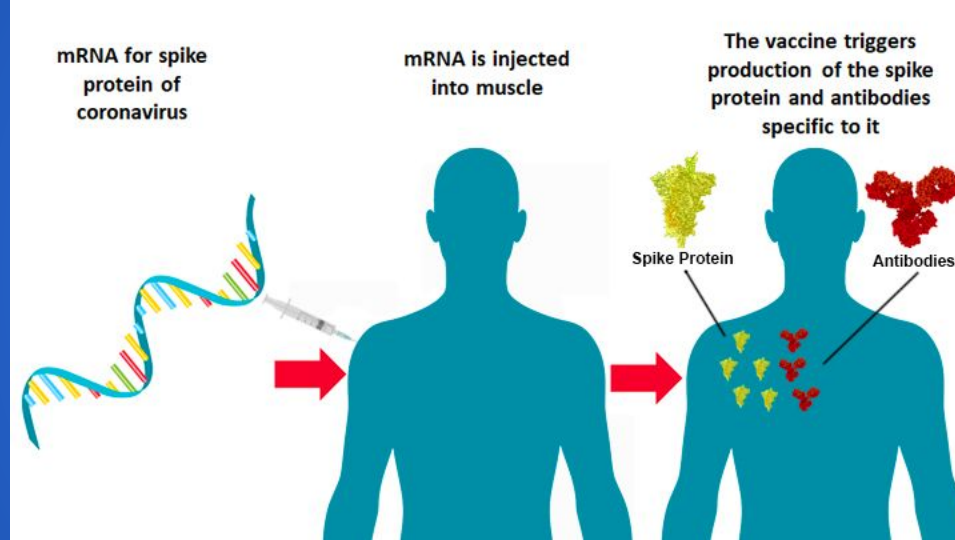
Significance – COVID19

a



Zhang, JY., Wang, XM., Xing, X. et al. Single-cell landscape of immunological responses in patients with COVID-19. Nat Immunol 21, 1107–1118 (2020).
<https://doi.org/10.1038/s41590-020-0762-x>

Significance – COVID19



<https://directorsblog.nih.gov/2020/07/16/researchers-publish-encouraging-early-data-on-covid-19-vaccine/>

Monocytes

Kupffer



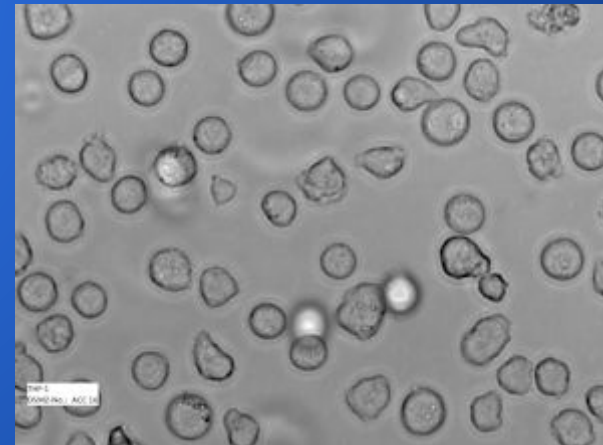
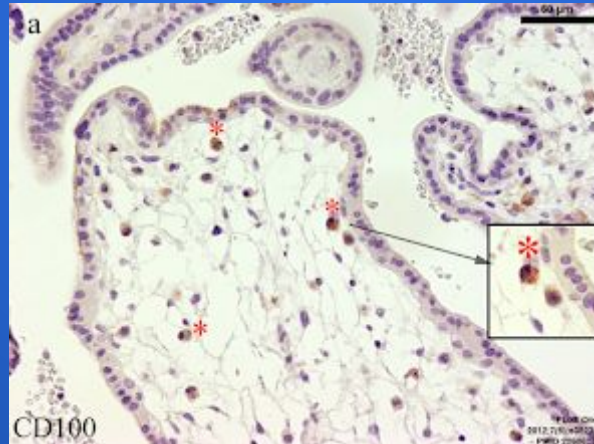
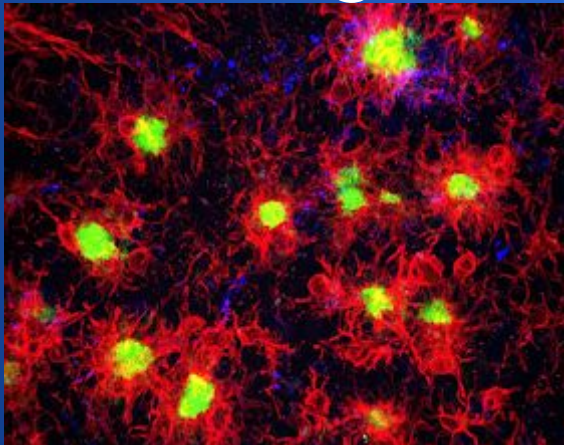
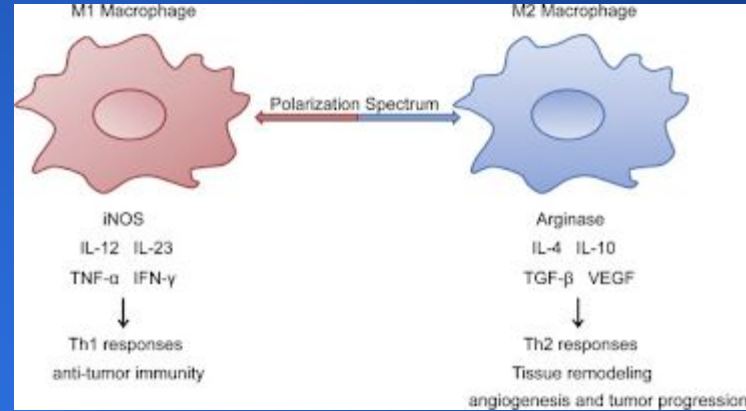
Decidual



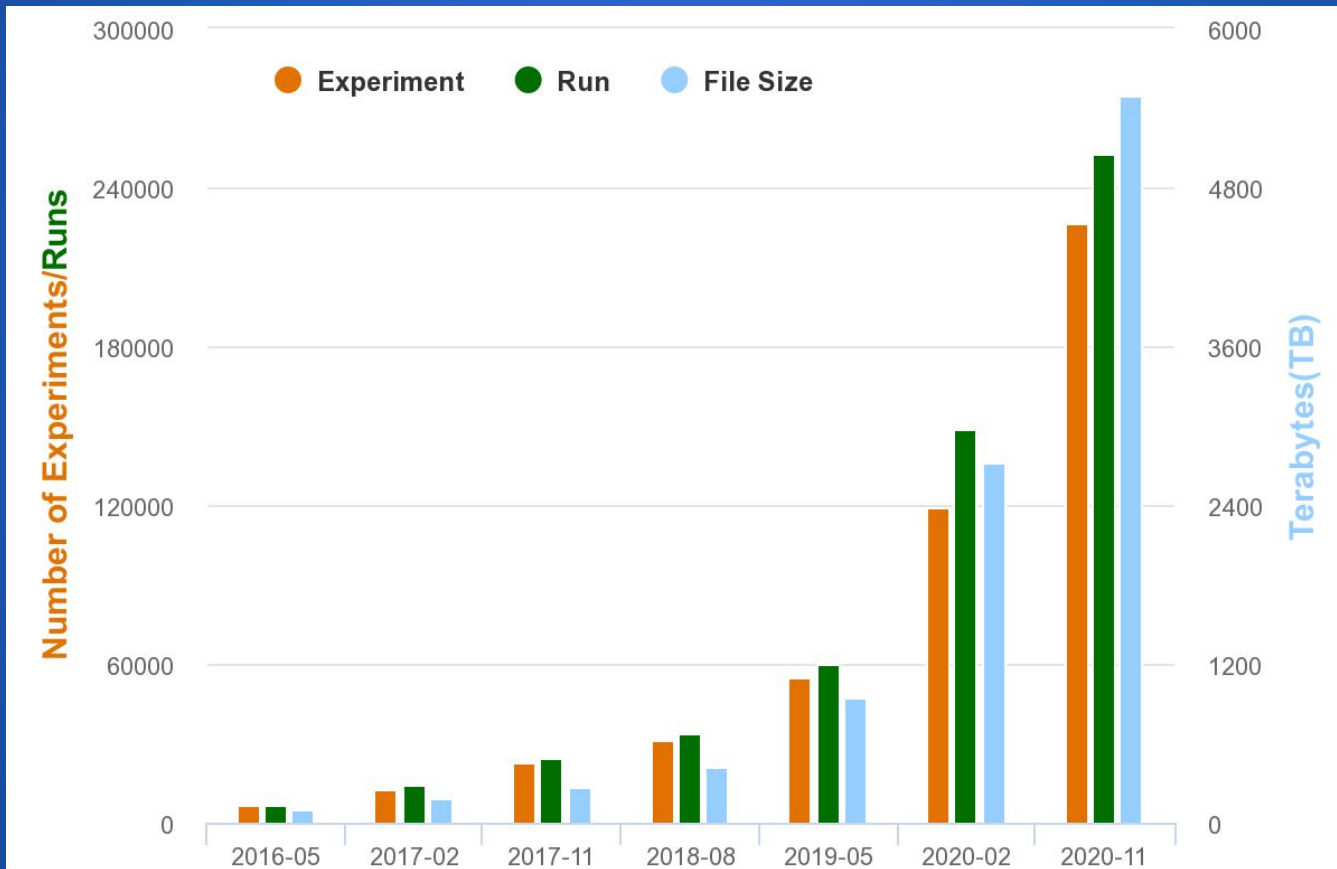
Microglia

HBC

THP1



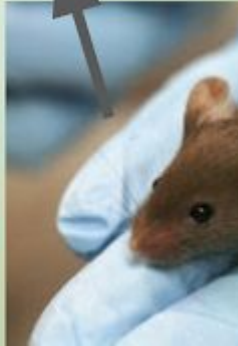
Exponential Data Increase



Computational Biology vs. Bioinformatics



Programming of
Commensal Bacteria
Bacteroides theta
to Sense and Respond
in the Murine Gut



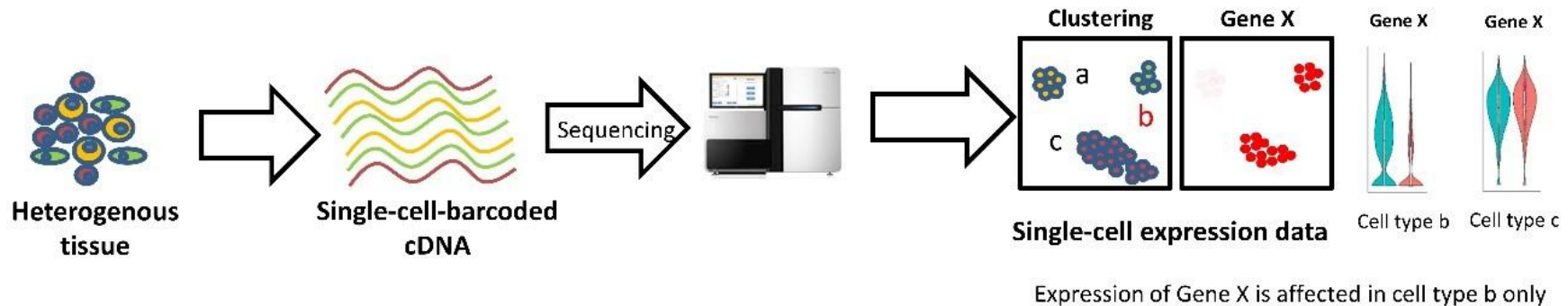
Presented by Theo Nelson

Bulk vs. sc RNAseq

Bulk RNA sequencing

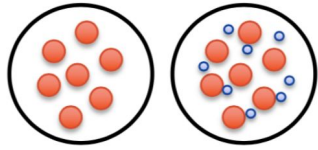


Single-cell RNA sequencing



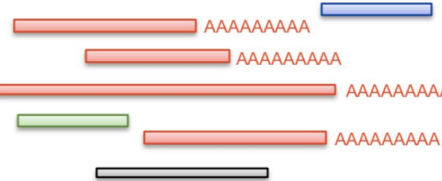
Experimental Design

Experimental design

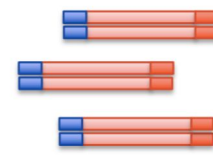


untreated treated

Isolate RNA



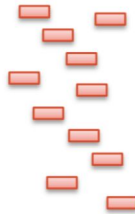
Prepare library



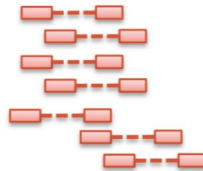
Sequence



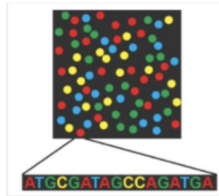
Single reads



Paired end reads



FASTQ files



Data Collection Techniques

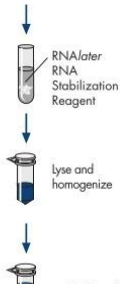
RNeasy Mini Procedure

Cells



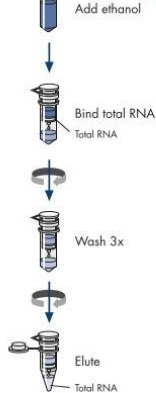
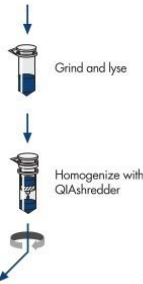
RNeasy Protect Mini Procedure

Animal tissue



RNeasy Plant Mini Procedure

Plant or fungal material



Library preparation

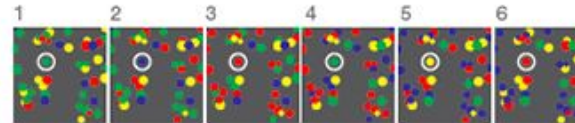
Cluster growth

Sequencing

DNA ($< 1 \mu\text{g}$)

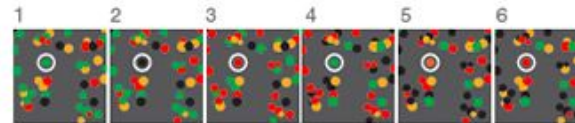
Imaging

4-channel

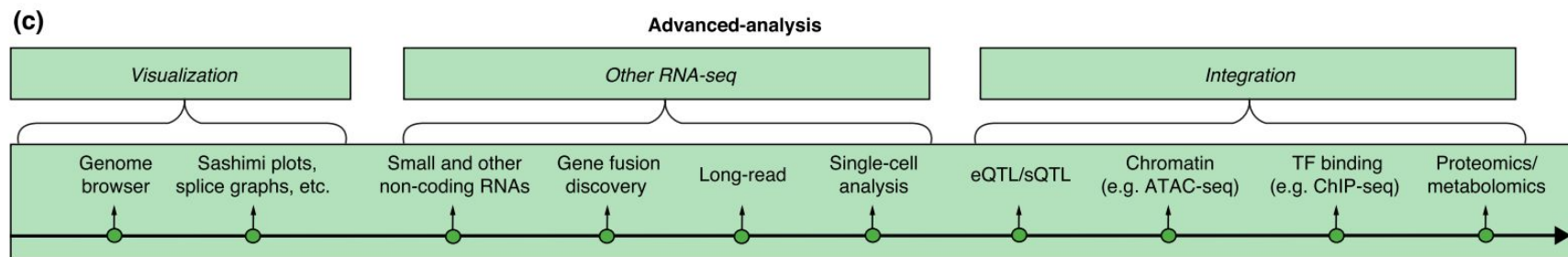
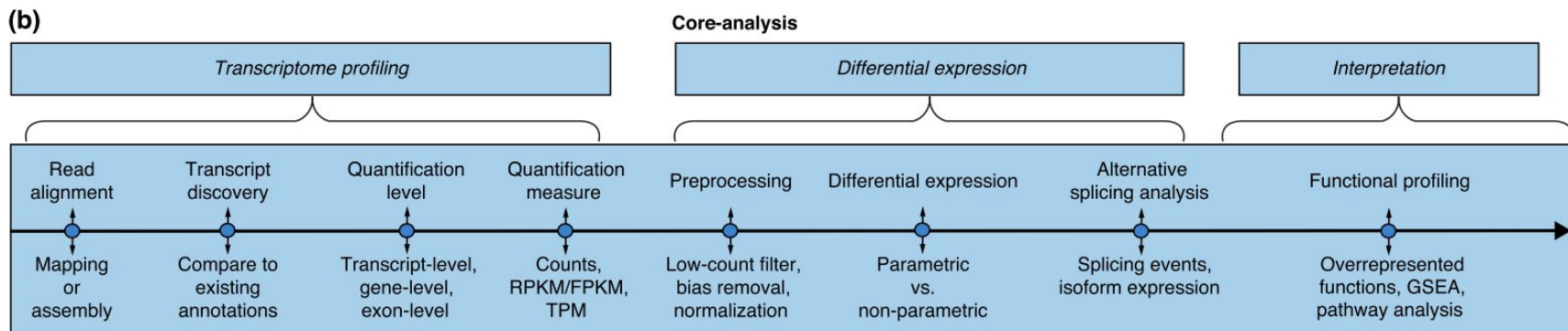
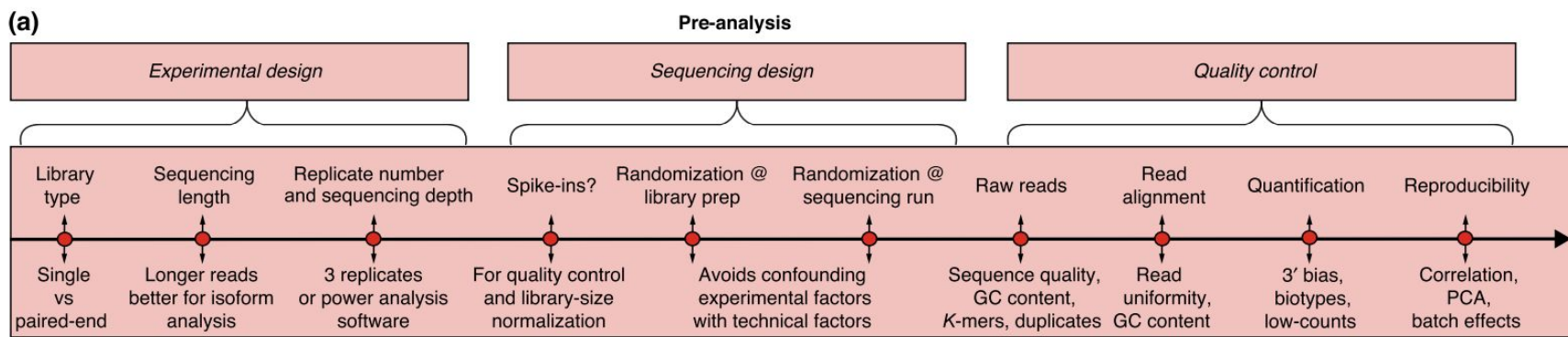


→ TGCTAC
Base calling

2-channel



→ TGCTAC
Base calling



Partek®
Flow®



colab



Questions?

tmn2126@columbia.edu

Status	Public on Apr 16, 2011
Title	RNA sequencing reveals two major classes of gene expression levels in metazoan cells
Organism	Mus musculus
Experiment type	Expression profiling by high throughput sequencing
Summary	<p>The expression level of a gene is often used as a proxy for determining whether the protein or RNA product is functional in a cell or tissue. Therefore, it is of fundamental importance to understand the global distribution of gene expression levels, and to be able to interpret it mechanistically and functionally. Here we use RNA sequencing of mouse Th2 cells, coupled with a range of other techniques, to show that all genes can be separated, based on their expression abundance, into two distinct groups: one group comprising of lowly expressed and putatively non-functional mRNAs, and the other of highly expressed mRNAs with active chromatin marks at their promoters. Similar observations are made in other data sets, including sources such as <i>Drosophila</i>.</p>
Overall design	RNA-seq data of two biological replicates of murine Th2 cells.
Contributor(s)	Hebenstreit D , Fang M , Gu M , Charoensawan V , van Oudenaarden A , Teichmann SA
Citation(s)	<p>Hebenstreit D, Fang M, Gu M, Charoensawan V et al. RNA sequencing reveals two major classes of gene expression levels in metazoan cells. <i>Mol Syst Biol</i> 2011 Jun 7;7:497. PMID: 21654674</p> <p>Mahata B, Zhang X, Kolodziejczyk AA, Proserpio V et al. Single-cell RNA sequencing reveals T helper cells synthesizing steroids de novo to contribute to immune homeostasis. <i>Cell Rep</i> 2014 May 22;7(4):1130-42. PMID: 24813893</p>