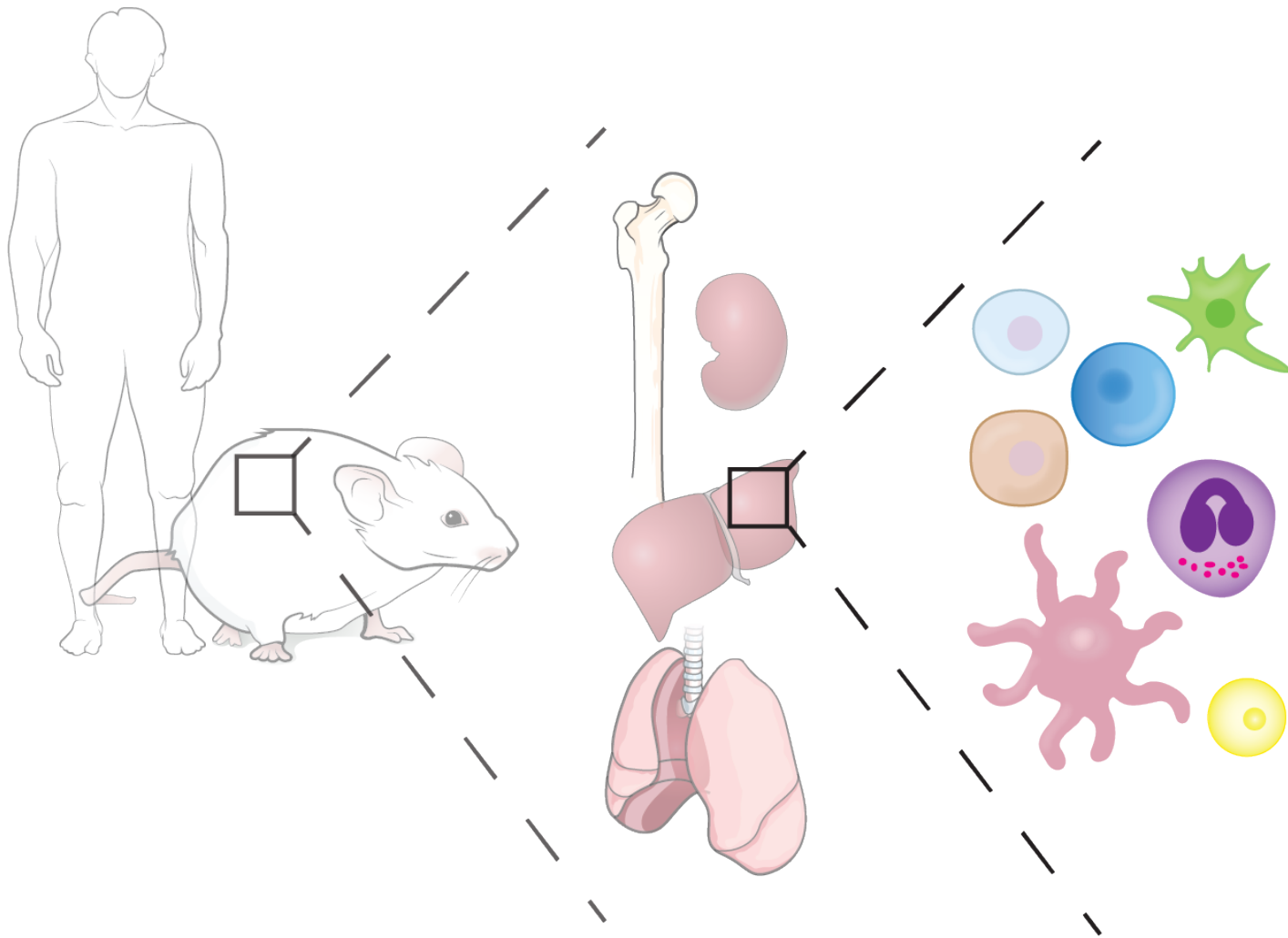


Systems Immunology

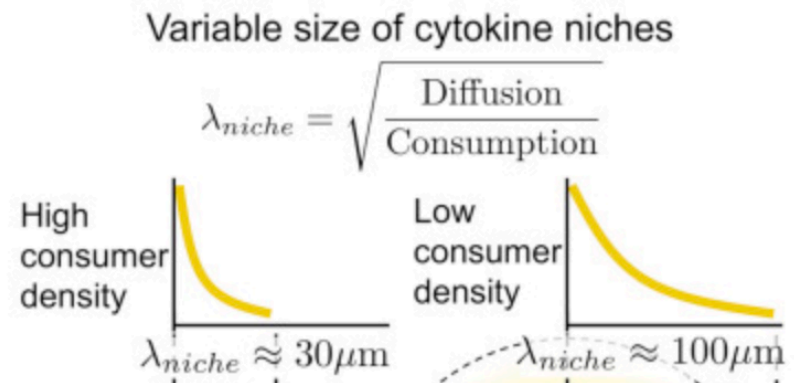
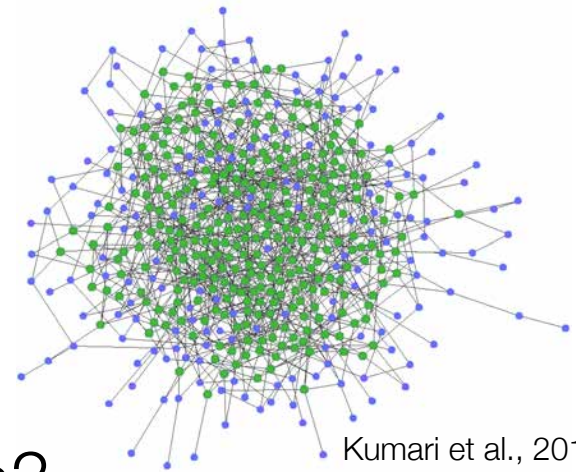


Matt Spitzer

Micro 204
Nov 26, 2018

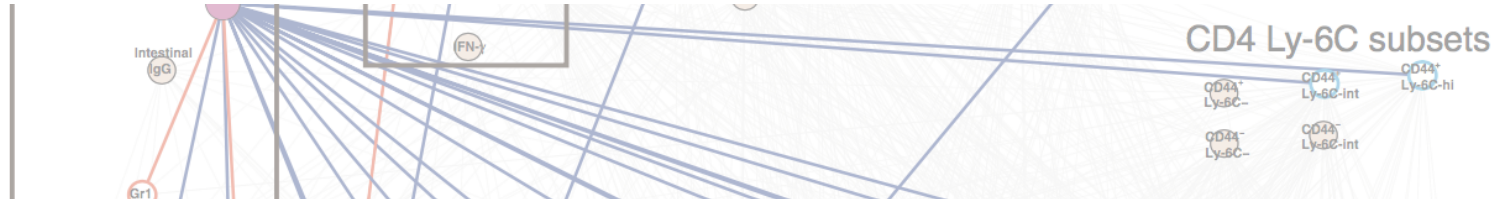
What is “Systems Immunology”?

- Big data?
- “-omics”?
- Computation? Informatics?
- High throughput/content screens?
- Mechanistic modeling?



Oyler-Yaniv et al., 2017

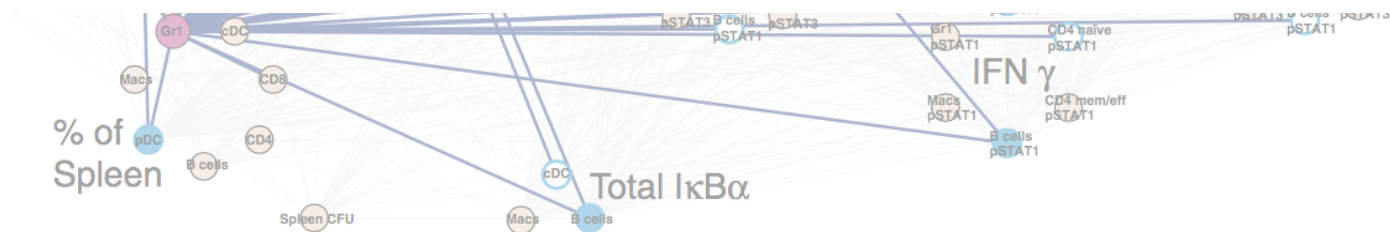
What is “Systems Immunology”?



- A mindset rather than any single approach:

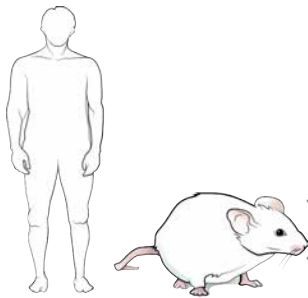
- Embracing complexity to learn how components interact/coordinate/regulate to drive emergent properties.

- Data-driven rather than reductionist in nature



Systems Immunology Across Scales:

Organismal Level



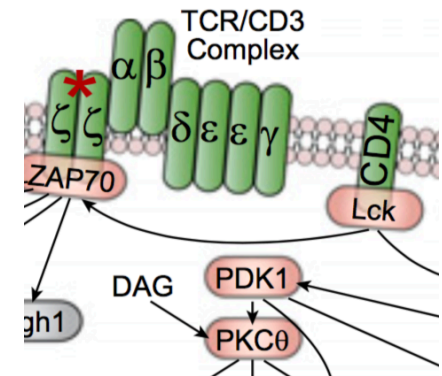
Tissue Level



Cellular Level



Sub-cellular Level



Gene expression

Single-cell analysis

Phenotype data

Shotgun proteomics

Phospho-flow

Clinical data

Metabolomics

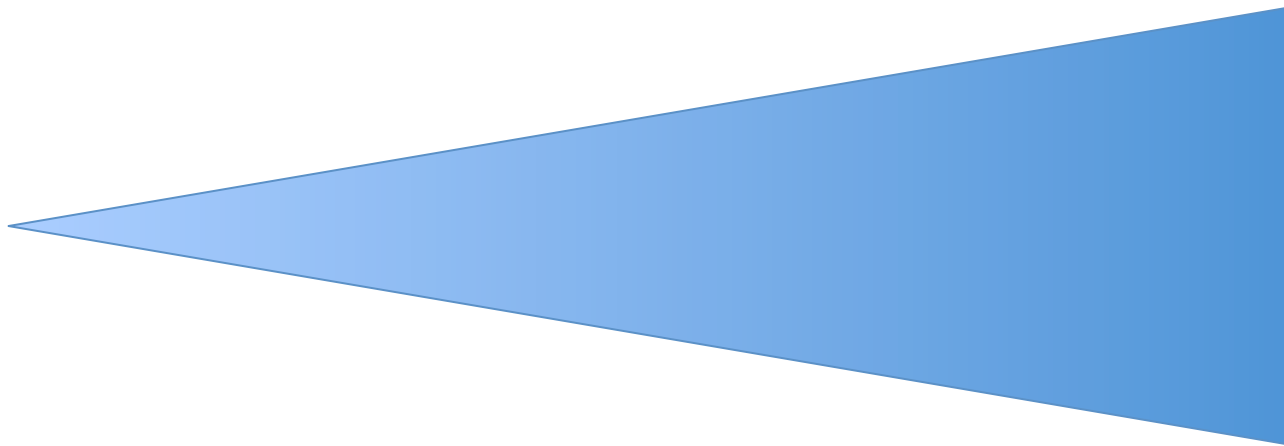
High-content microscopy

Cytokine quantification

Projects vary widely in scope:

Mechanistic Modeling

Data Mining



Goal: mathematically formalize
understanding of a simple system

Goal: extract information
from large data sets

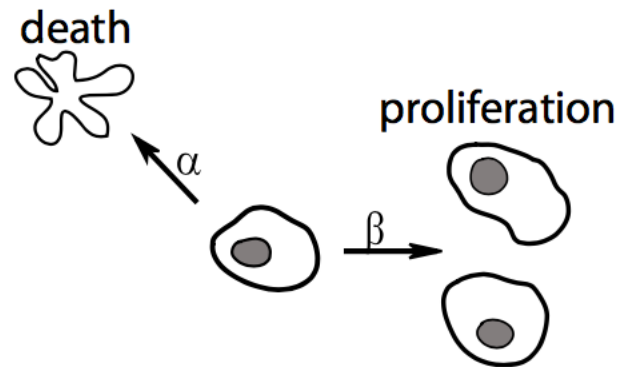
Paradoxical Signaling by a Secreted Molecule Leads to Homeostasis of Cell Levels

Yuval Hart,^{1,3} Shlomit Reich-Zeliger,^{2,3} Yaron E. Antebi,^{2,3} Irina Zaretsky,² Avraham E. Mayo,¹ Uri Alon,¹
and Nir Friedman^{2,*}

Cell 158, 1022–1032, August 28, 2014

- What parameters govern the frequency of a cell population?
 - How do T cells reach a homeostatic number without reaching their carrying capacity?
- Why does this paradoxical effect of IL-2 (and many other signaling ligands) exist?

Simple, first-order kinetics of cell population size are unstable



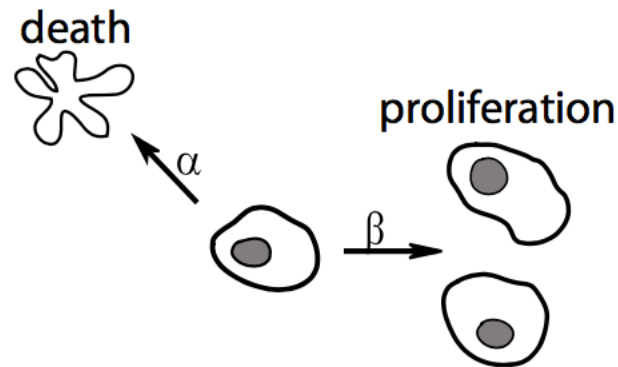
$$\frac{dX}{dt} = (\beta - \alpha)X$$

X = cell number

α = cell death rate

β = cell proliferation rate

Simple, first-order kinetics of cell population size are unstable



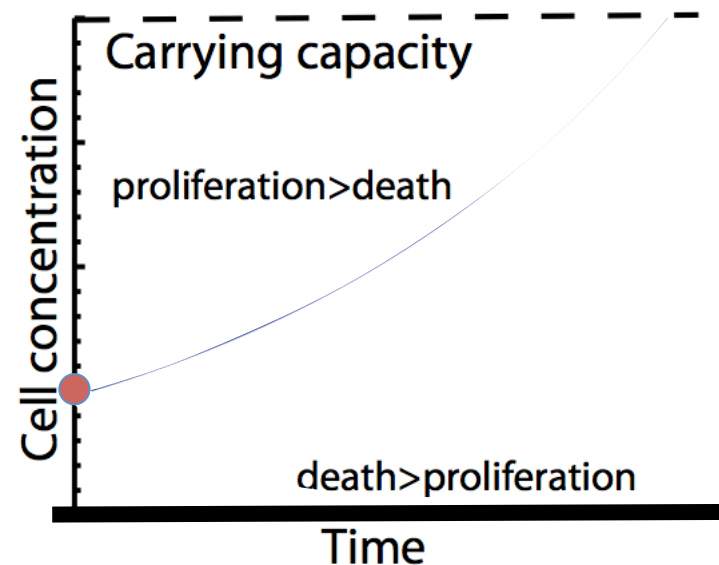
$$\frac{dX}{dt} = (\beta - \alpha)X$$

X = cell number

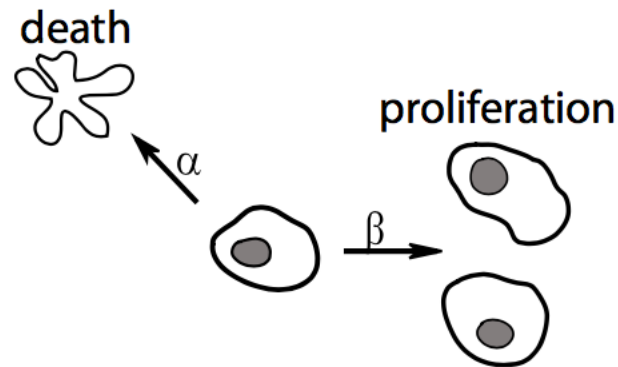
α = cell death rate

β = cell proliferation rate

Cellular first-order kinetics are unstable



Simple, first-order kinetics of cell population size are unstable



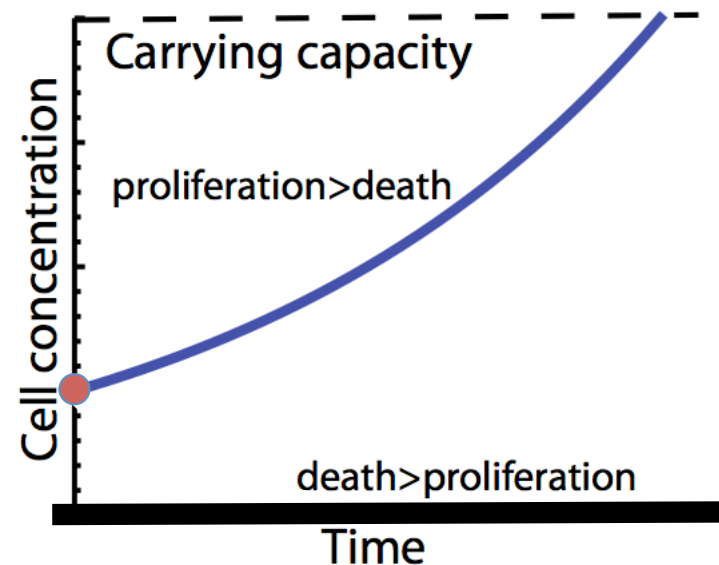
$$\frac{dX}{dt} = (\beta - \alpha)X$$

X = cell number

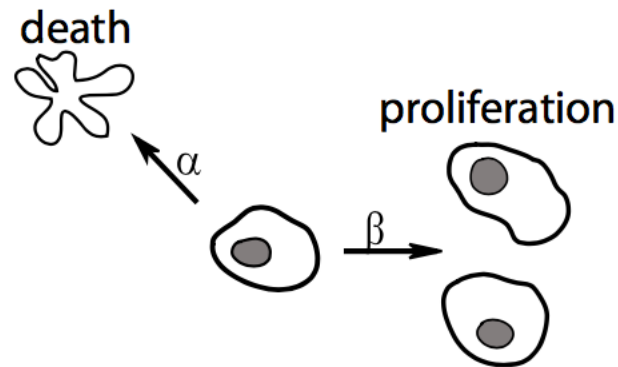
α = cell death rate

β = cell proliferation rate

Cellular first-order kinetics are unstable



Simple, first-order kinetics of cell population size are unstable



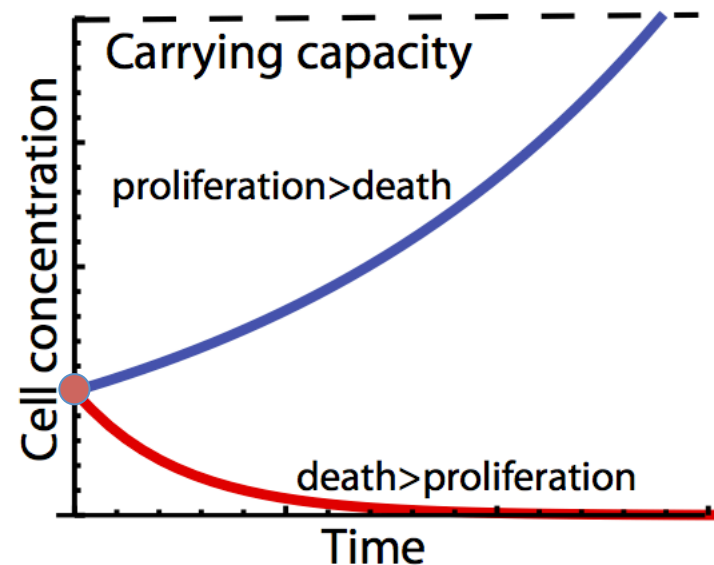
$$\frac{dX}{dt} = (\beta - \alpha)X$$

X = cell number

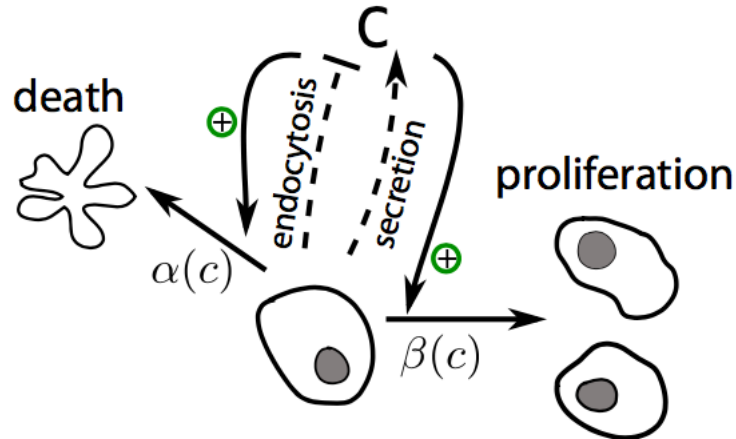
α = cell death rate

β = cell proliferation rate

Cellular first-order kinetics are unstable



Adding in the effect of a secreted regulator:



$$\frac{dX}{dt} = (\beta(c) - \alpha(c))X$$
$$\frac{dc}{dt} = I_0 + (\beta_1 - f(c))X - \gamma c$$

X = cell number

α = cell death rate

β = cell proliferation rate

c = concentration of cytokine

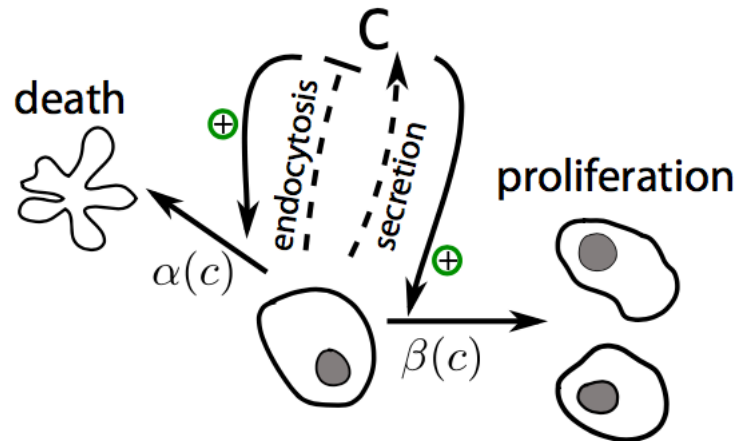
I_0 = external cytokine supply

β_1 = cytokine production rate by cells

$f(c)$ = cytokine consumption rate by cells

γ = rate of cytokine decay

Adding in the effect of a secreted regulator:



$$\frac{dX}{dt} = (\beta(c) - \alpha(c))X$$

$$\frac{dc}{dt} = I_0 + (\beta_1 - f(c))X - \gamma c$$

X = cell number

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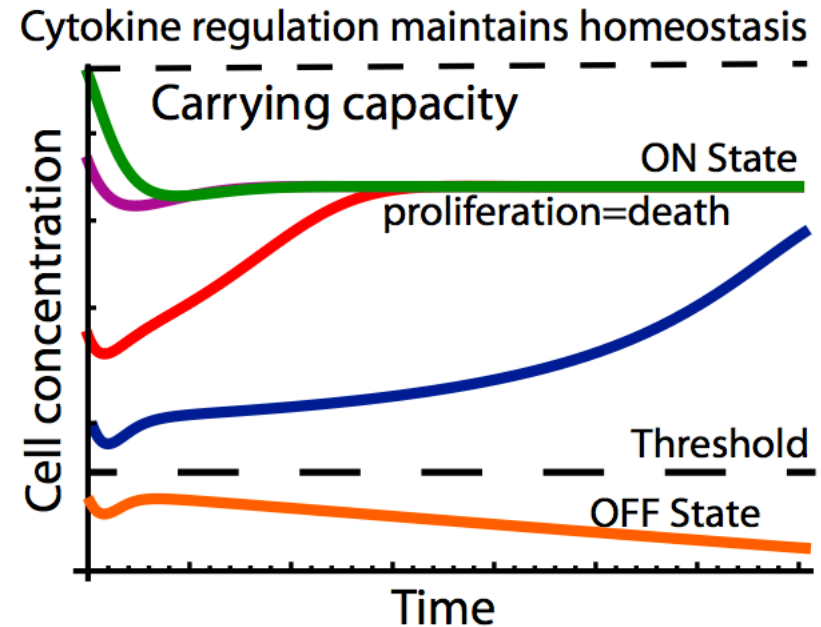
c = concentration of cytokine

I_0 = external cytokine supply

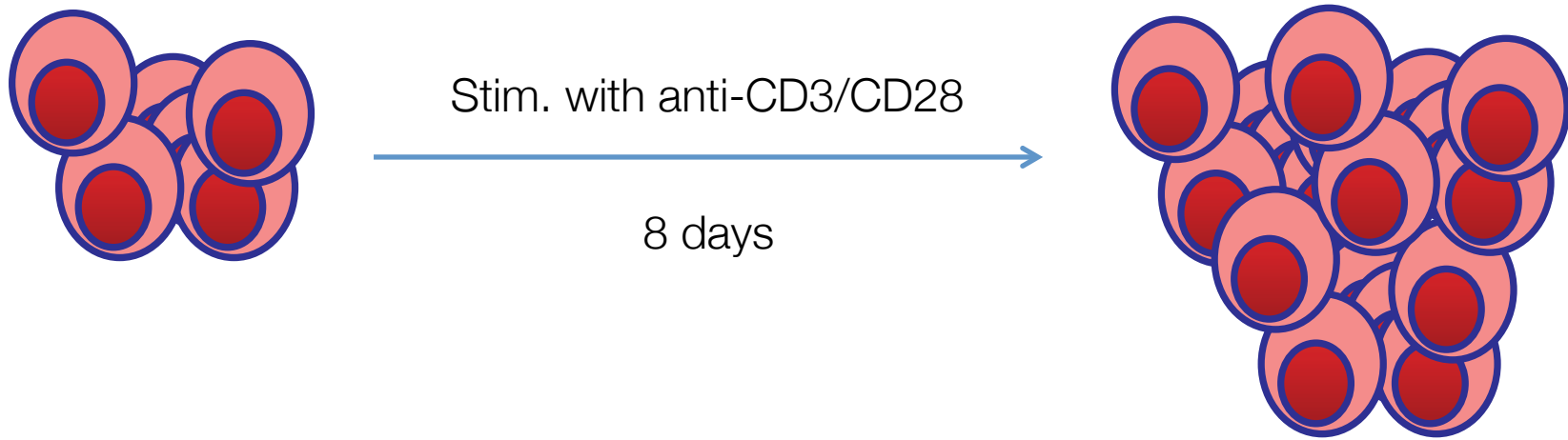
β_1 = cytokine production rate by cells

$f(c)$ = cytokine consumption rate by cells

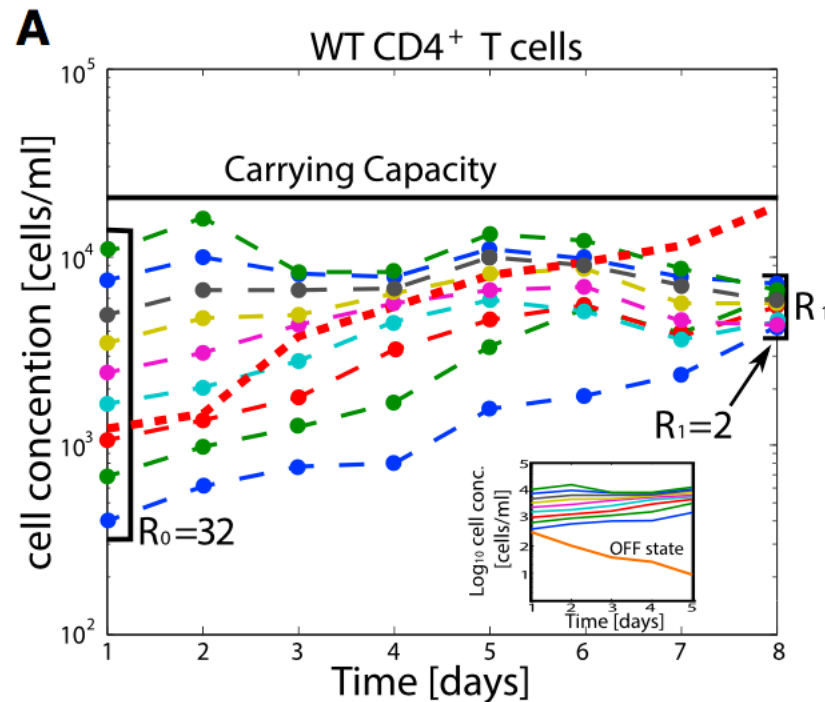
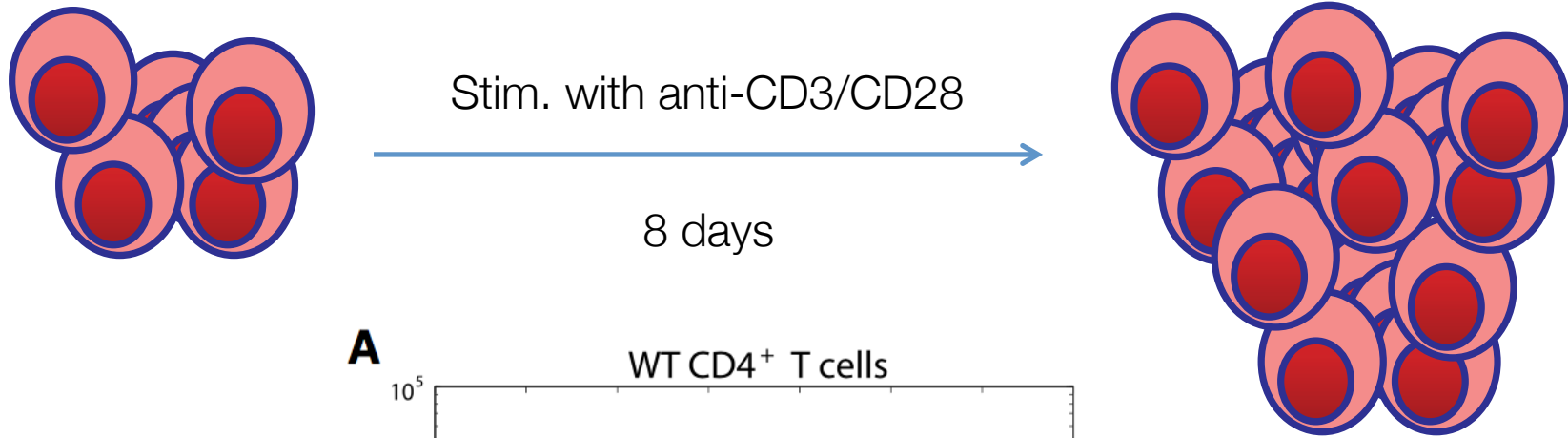
γ = rate of cytokine decay



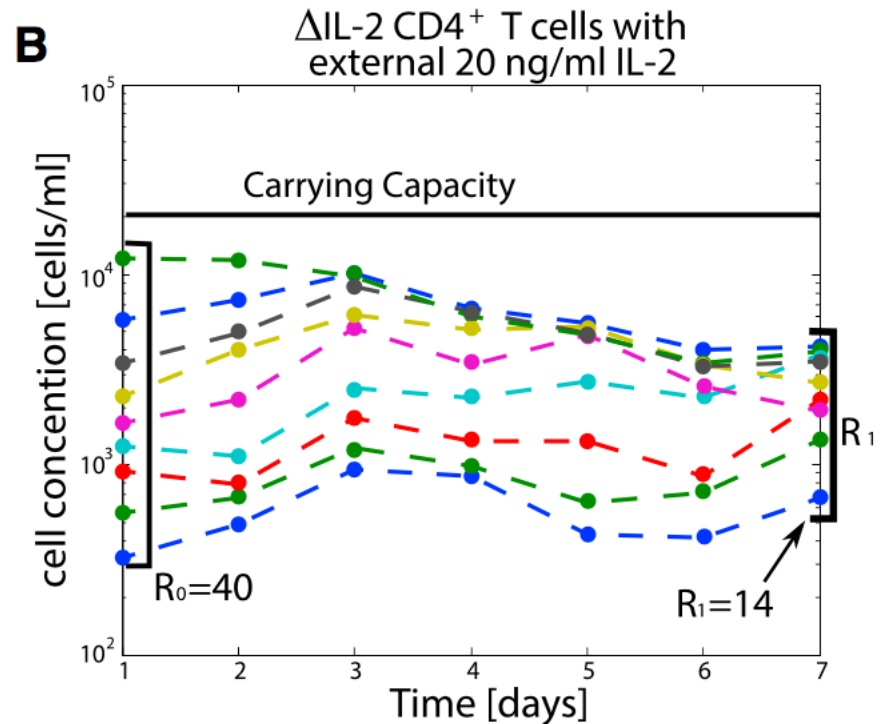
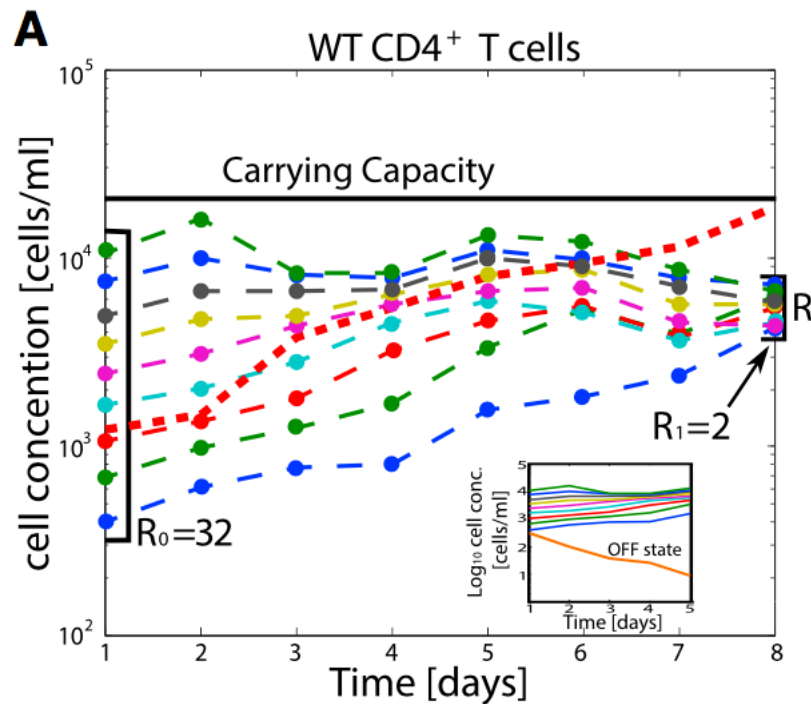
Testing the model: In vitro activation of CD4 T cells



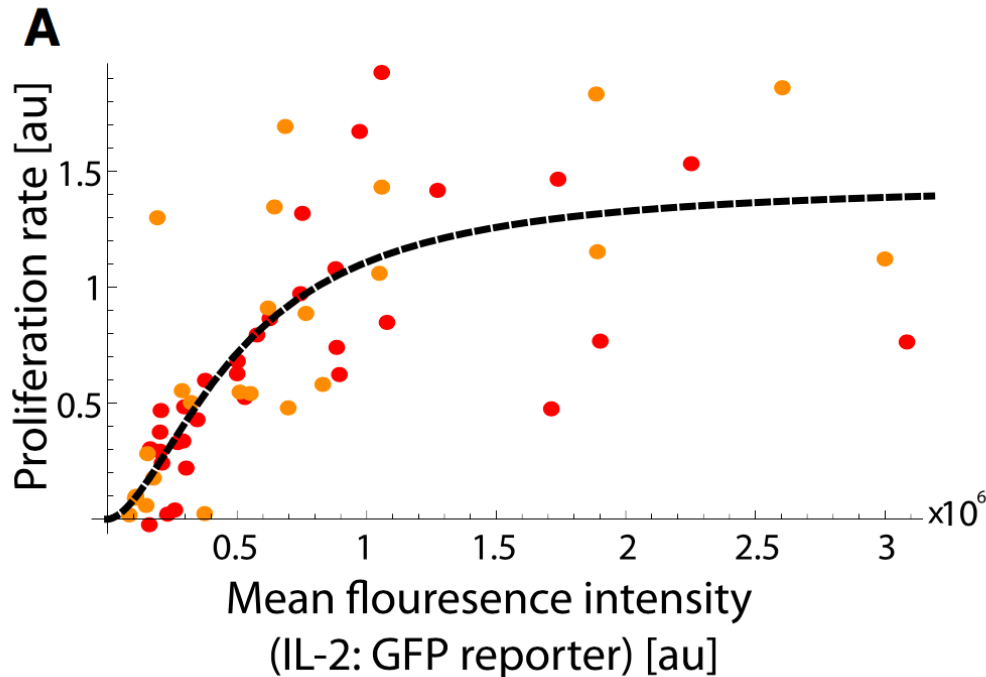
Testing the model: In vitro activation of CD4 T cells



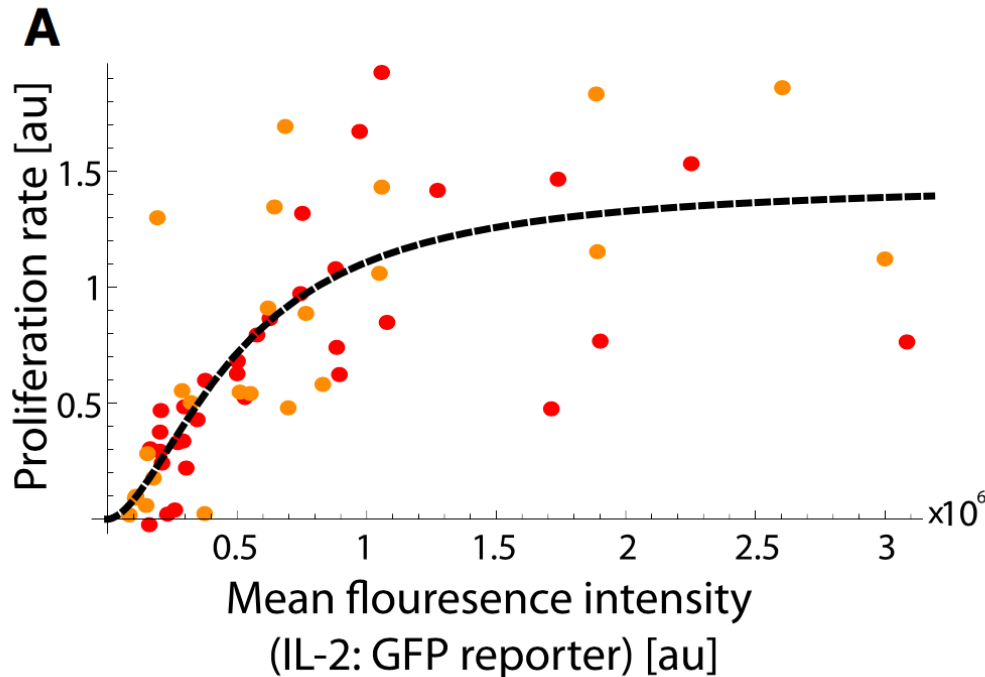
Autocrine production of IL-2 is required for “homeostatic” behavior



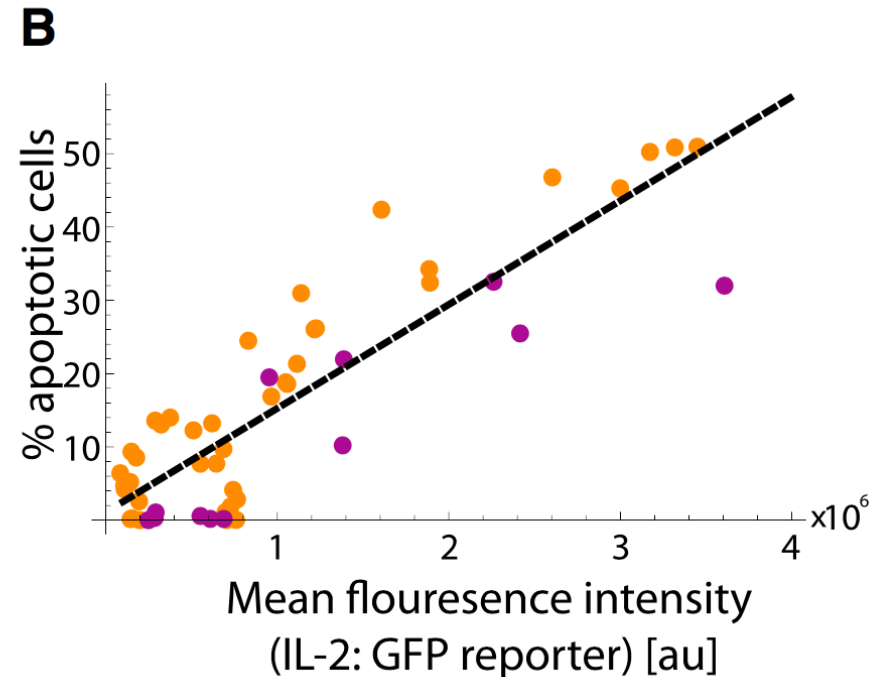
IL-2 regulates T cell proliferation and death in fundamentally different ways



IL-2 regulates T cell proliferation and death in fundamentally different ways

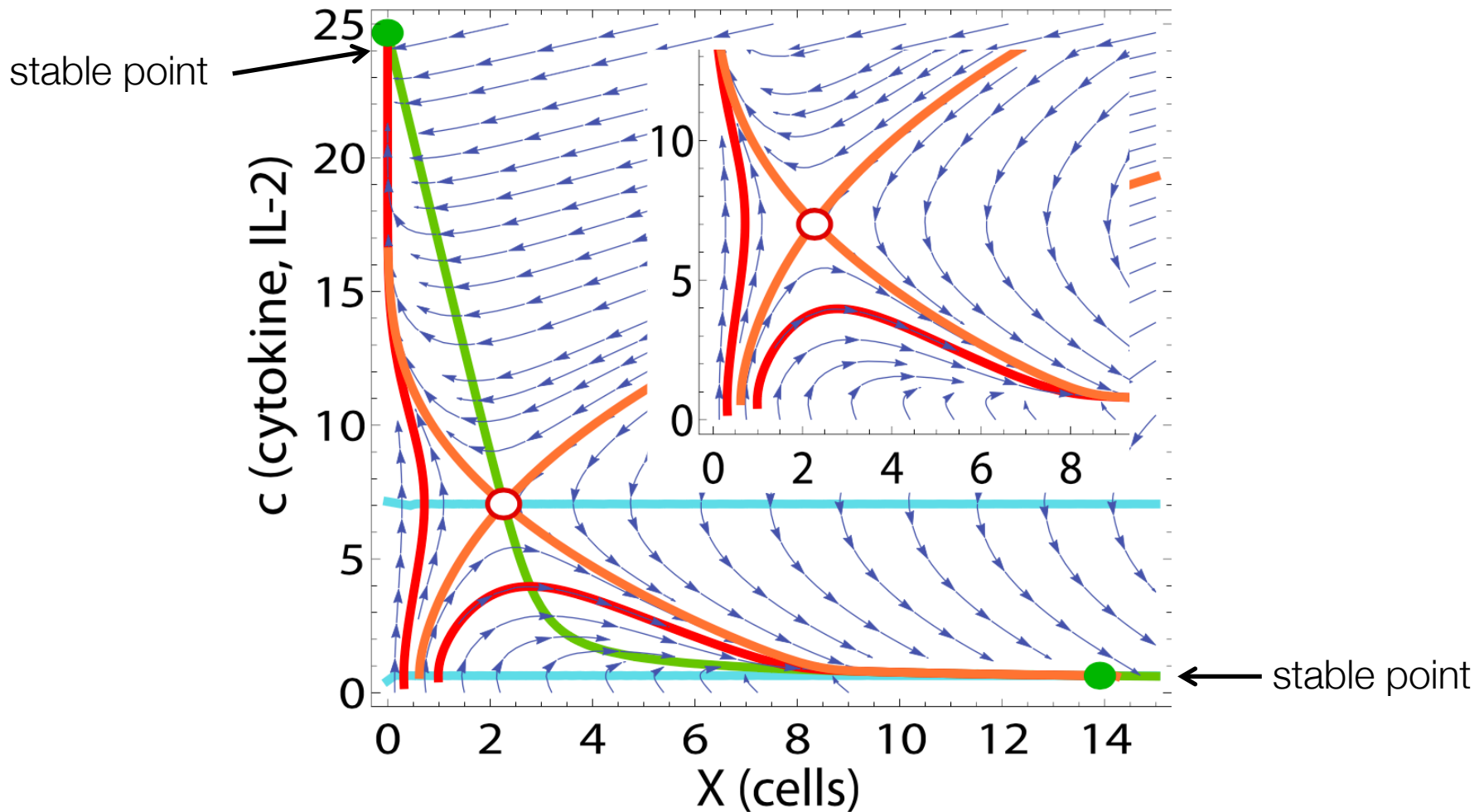


Cooperative, or “ultrasensitive”
Hill coefficient = 1.7



Linear
Hill coefficient = 1

These model parameters can create
a “bistable” system

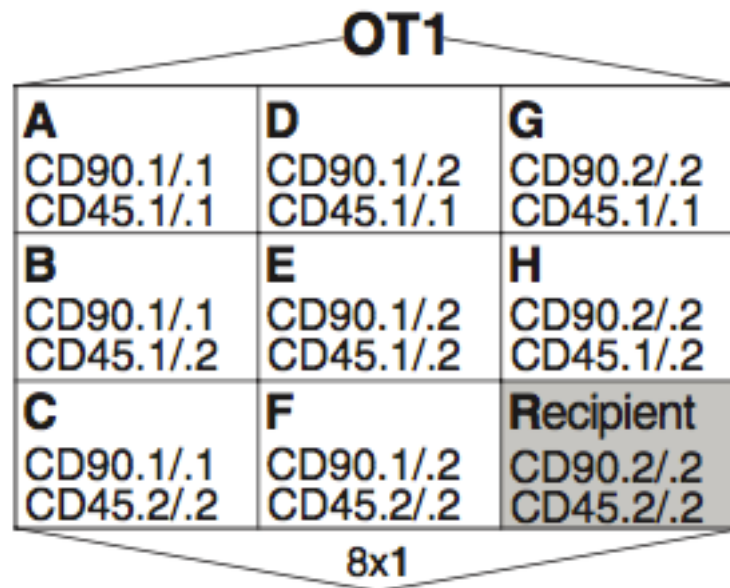


Disparate Individual Fates Compose Robust CD8⁺ T Cell Immunity

Veit R. Buchholz,^{1*} Michael Flossdorf,^{2,3*} Inge Hensel,¹ Lorenz Kretschmer,¹ Bianca Weissbrich,¹ Patricia Gräf,¹ Admar Verschoor,¹ Matthias Schiemann,^{1,4} Thomas Höfer,^{2,3†} Dirk H. Busch^{1,4,5,6†}

3 MAY 2013 VOL 340 SCIENCE

- What is the differentiation pattern of CD8 T cells during an immune response?

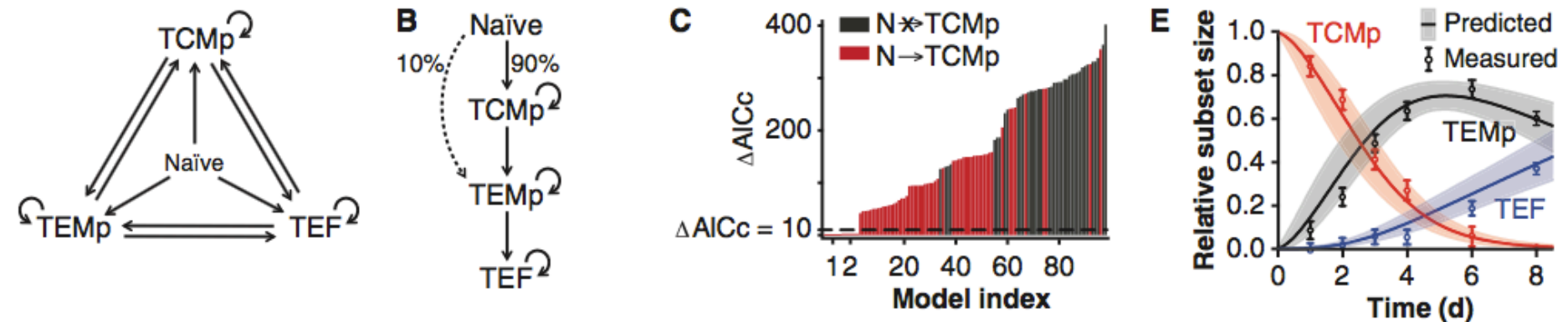


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3 MAY 2013 VOL 340 SCIENCE

- What is the differentiation pattern of CD8 T cells during an immune response?



Conditional density-based analysis of T cell signaling in single-cell data

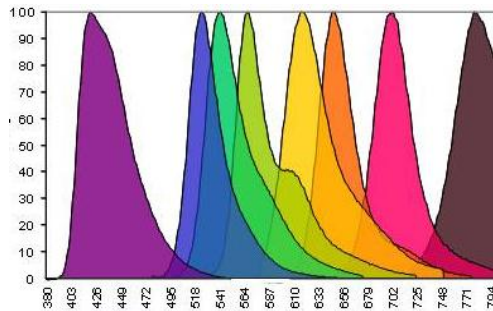
Smita Krishnaswamy, Matthew H. Spitzer, Michael Mingueneau, Sean C. Bendall, Oren Litvin, Erica Stone, Dana Pe'er,*† Garry P. Nolan†

28 NOVEMBER 2014 • VOL 346 ISSUE 6213 **1079**

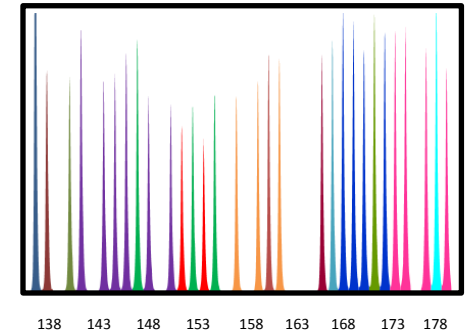
- Signaling through the T cell receptor triggers a well-defined phosphorylation cascade.
- Can we model signal transduction using single cell data?
- Is TCR signaling impacted by the state/context of the T cell?

The diversity of immune cells has prompted development of single-cell technologies

Flow
Cytometry



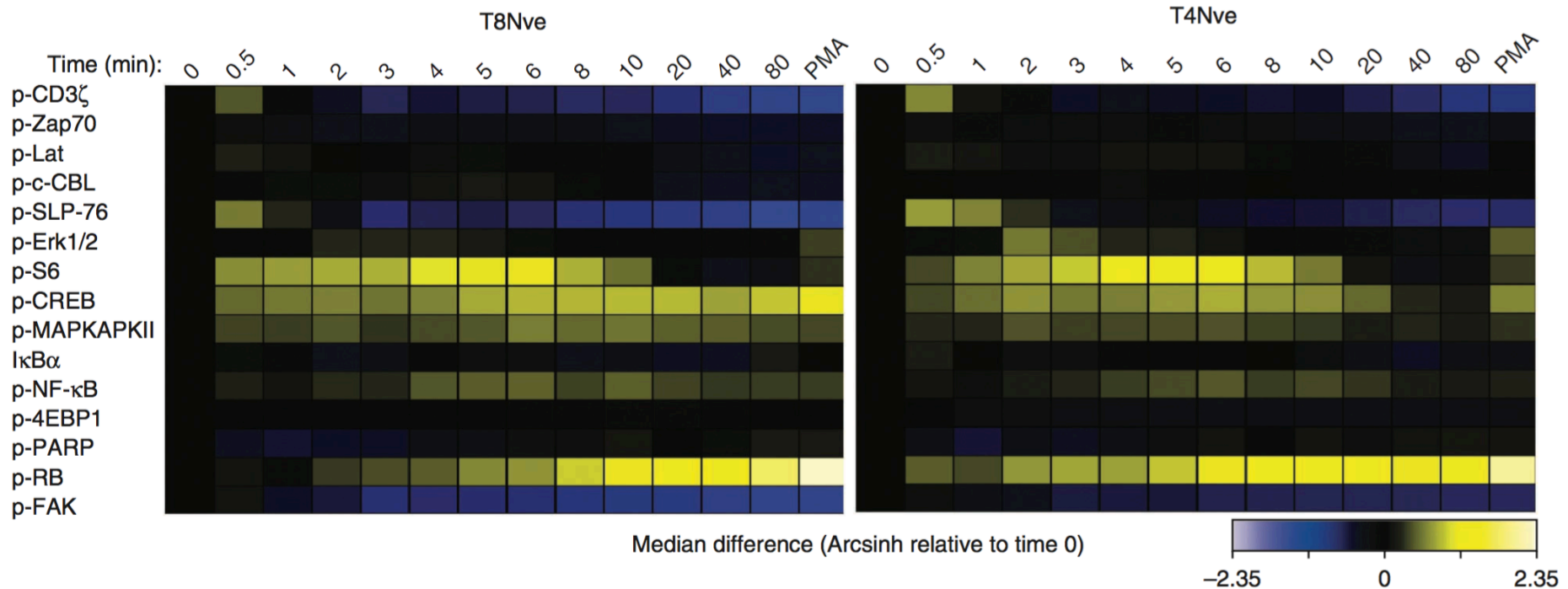
Mass
Cytometry



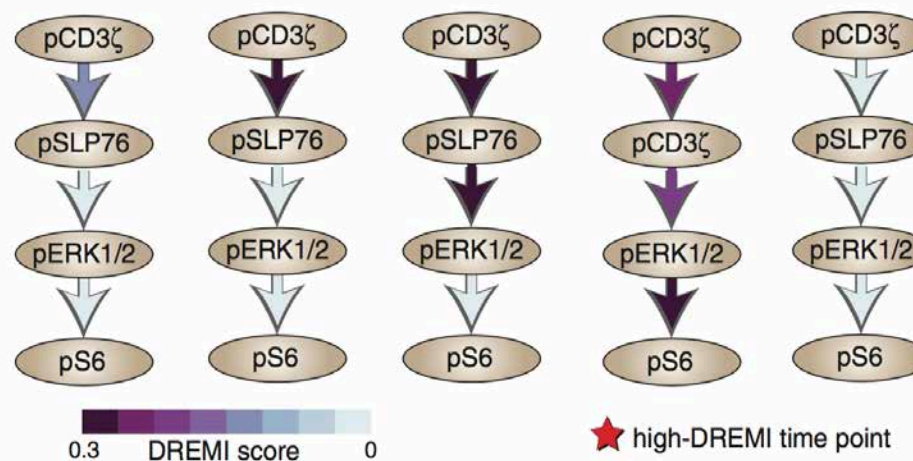
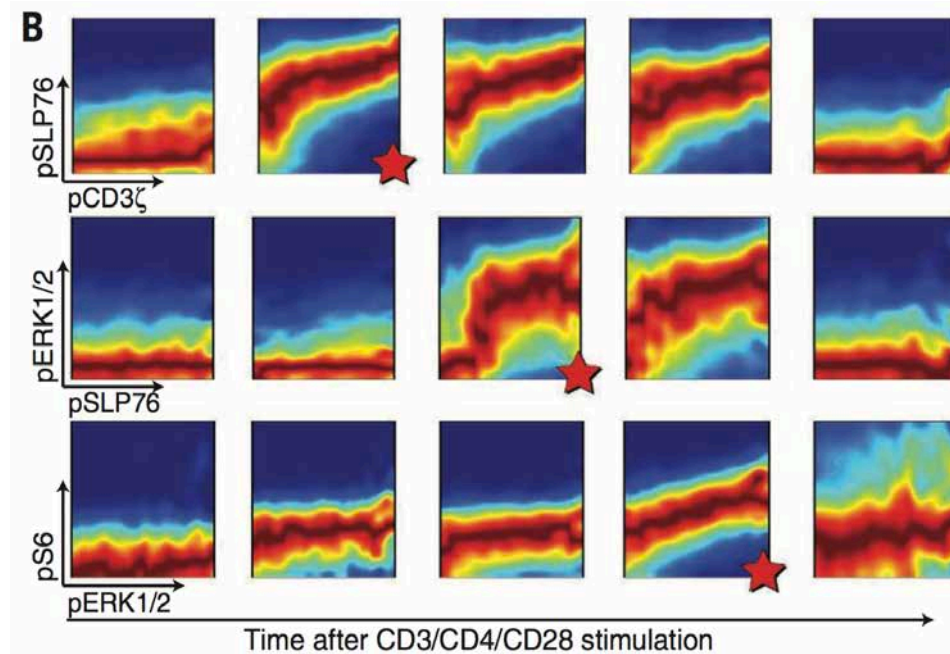
Replacing light with mass enables significantly more multiplexing.

A new powerful experimental tool for “systems immunology”
at multiple levels of molecular and cellular function.

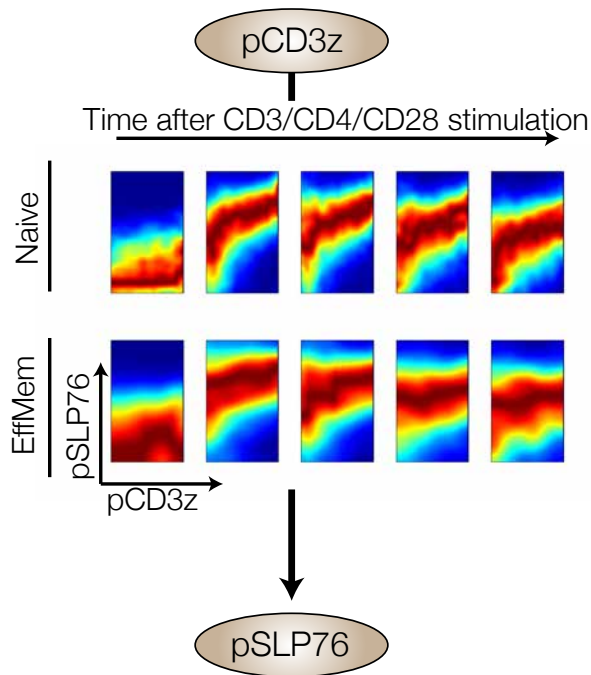
The primary data at the population level



Conditional density analysis reveals information transfer through signal transduction



Requirement for information transfer softens through CD4 T cell differentiation

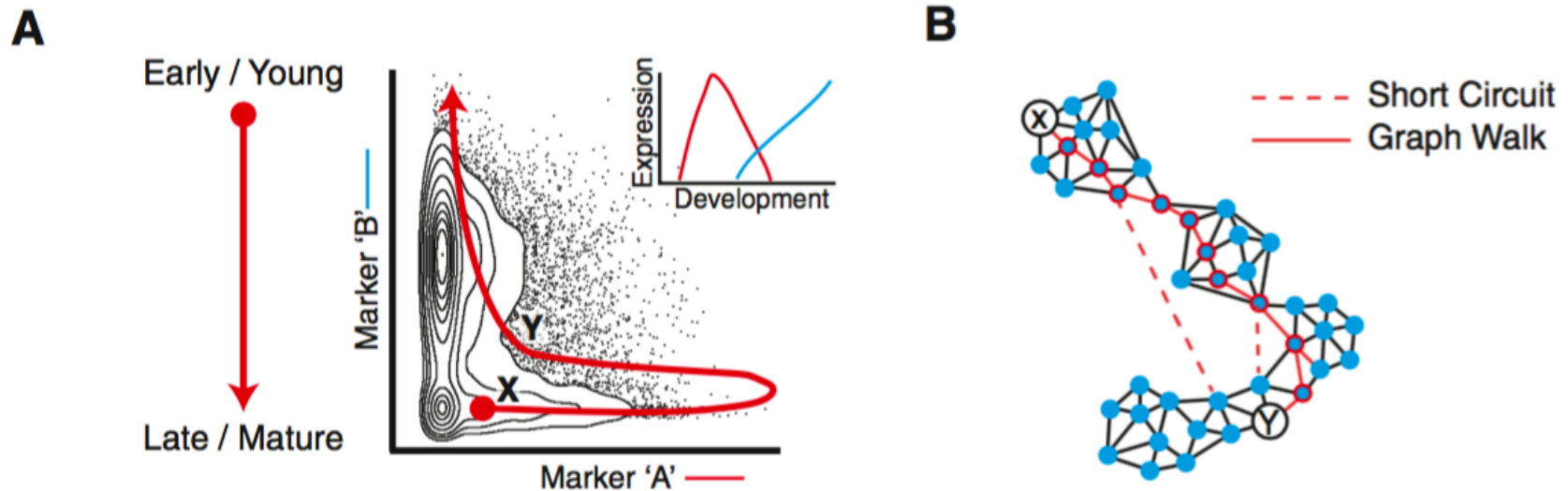


Single-Cell Trajectory Detection Uncovers Progression and Regulatory Coordination in Human B Cell Development

Sean C. Bendall,^{1,2,7} Kara L. Davis,^{1,3,7} El-ad David Amir,^{4,7} Michelle D. Tadmor,⁴ Erin F. Simonds,¹ Tiffany J. Chen,^{1,5,6} Daniel K. Shenfeld,⁴ Garry P. Nolan,^{1,8,*} and Dana Pe'er^{4,8,*}

- Healthy human bone marrow contains individual cells at all stages of B cell development in a “snapshot.”
 - Can single-cell data help clarify this trajectory?

Organizing individual cells according to their developmental time



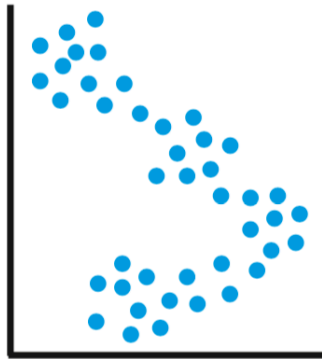
Developmental trajectories are often non-linear.

Organizing individual cells according to their developmental time: The Wanderlust algorithm

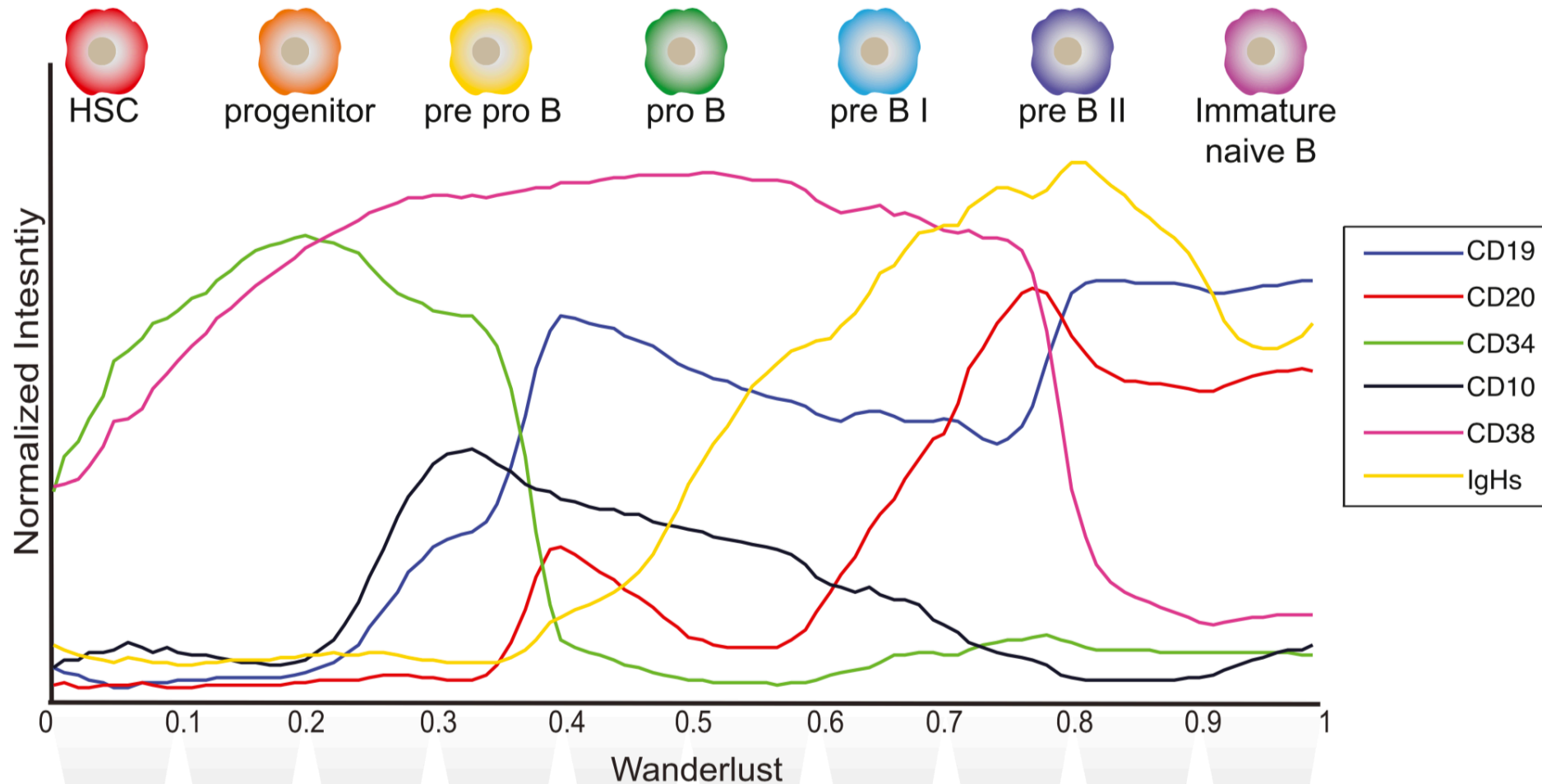
- Cells
- User Defined Start cell
- Random Waypoint cells

Wanderlust Analysis

n-dimensional plot

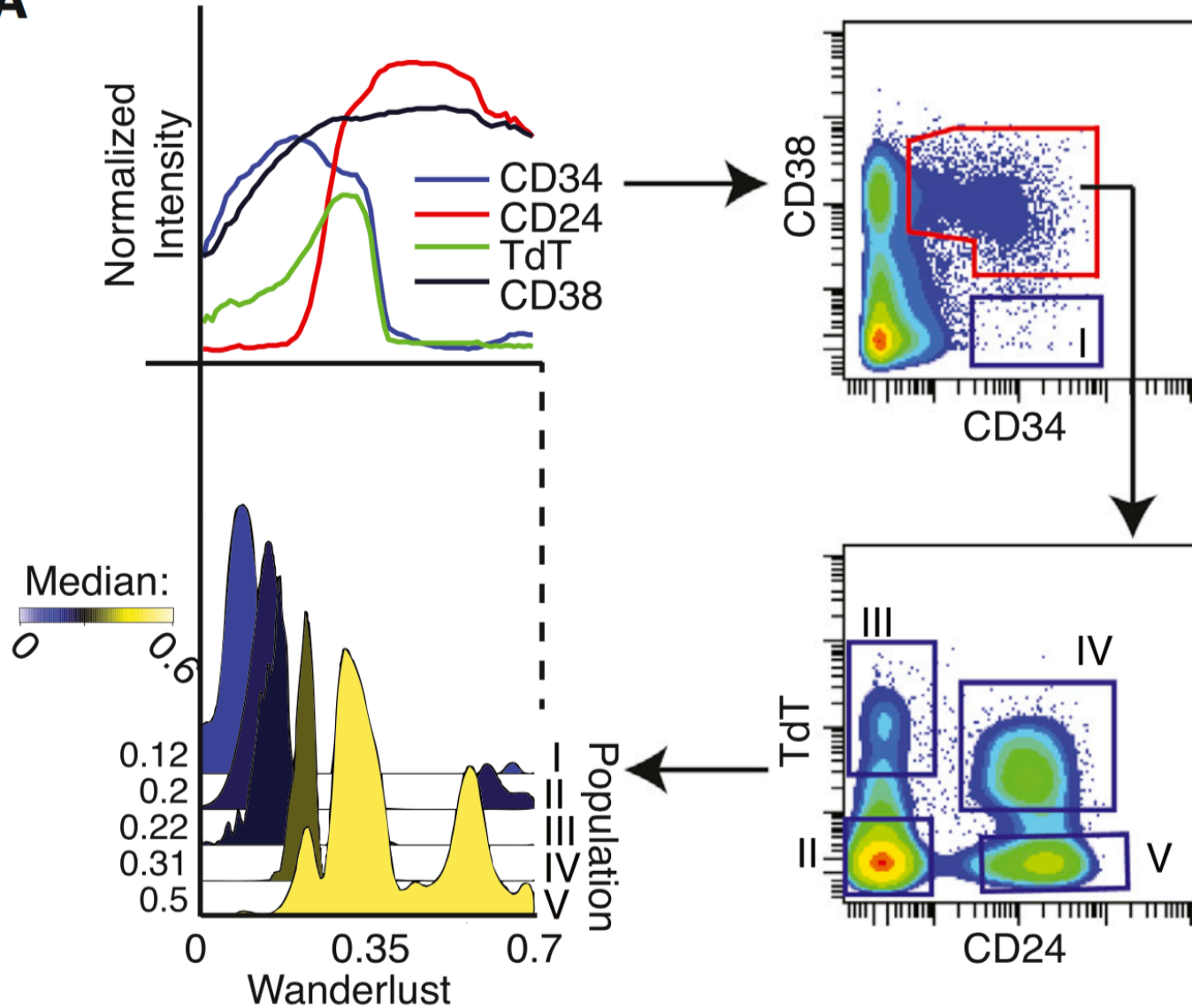


Applying the method to human bone marrow B cells

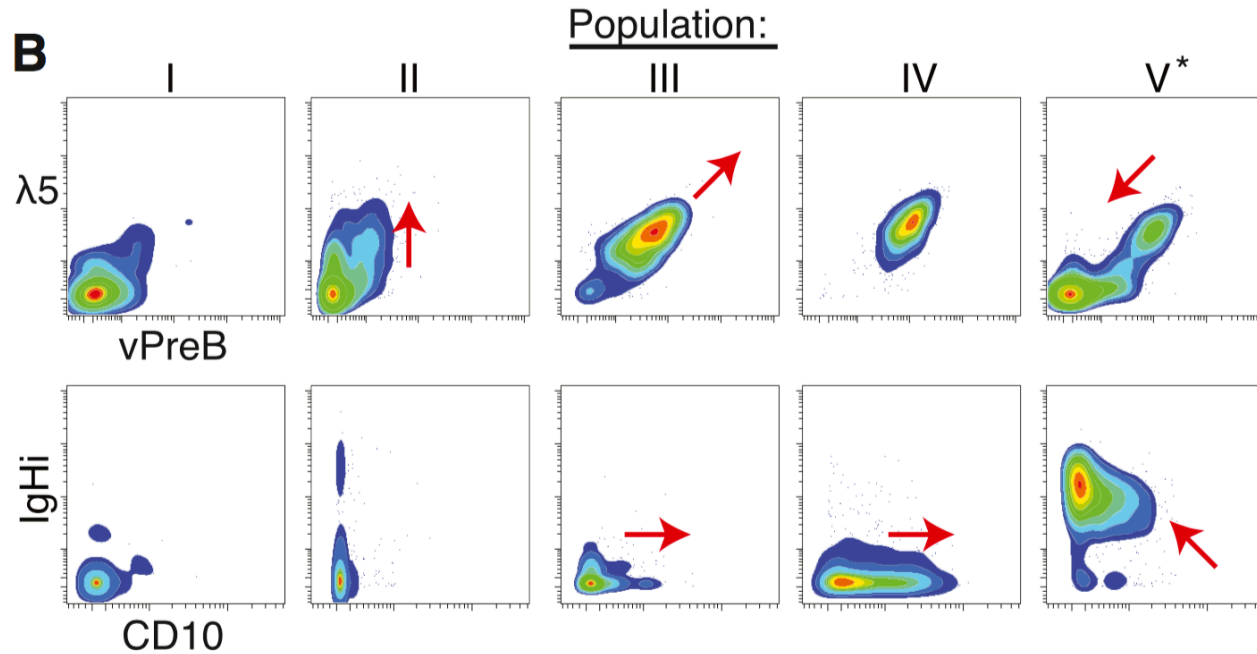


Identification of early B cell progenitor subsets

A



Identification of early B cell progenitor subsets



IL-7 requirement in mice vs. humans

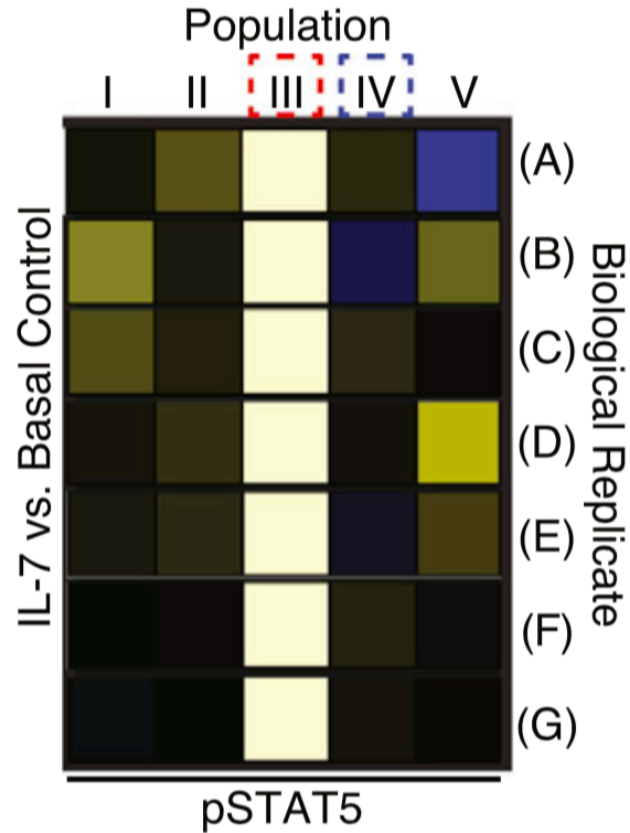
J. Exp. Med. (1980)

Early Lymphocyte Expansion Is Severely Impaired in Interleukin 7 Receptor-deficient Mice

Imm. Rev. (2005)

T ⁻ B ⁺ SCID	Gene defective	Defective pathway	Circulating lymphocytes		
			T	B	NK
X-linked SCID	IL2RG	Multiple cytokine mediated signaling	↓↓	Normal	↓↓
Jak3 deficiency	Jak3	Multiple cytokine mediated signaling	↓↓	Normal	↓↓
IL-7R deficiency	IL7RA	IL-7-mediated signaling	↓↓	Normal	Normal

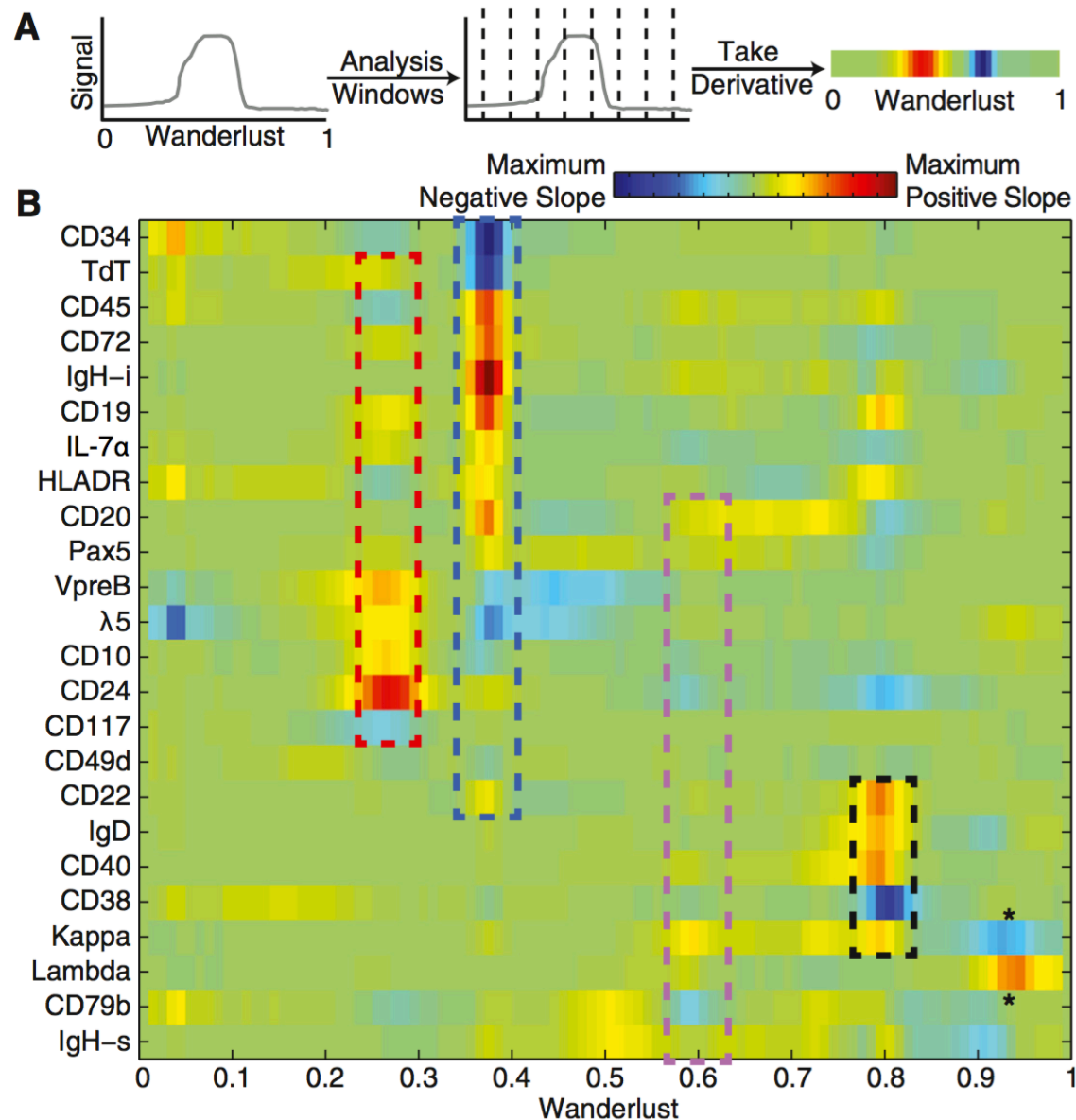
Which B cell subset responds to IL-7?



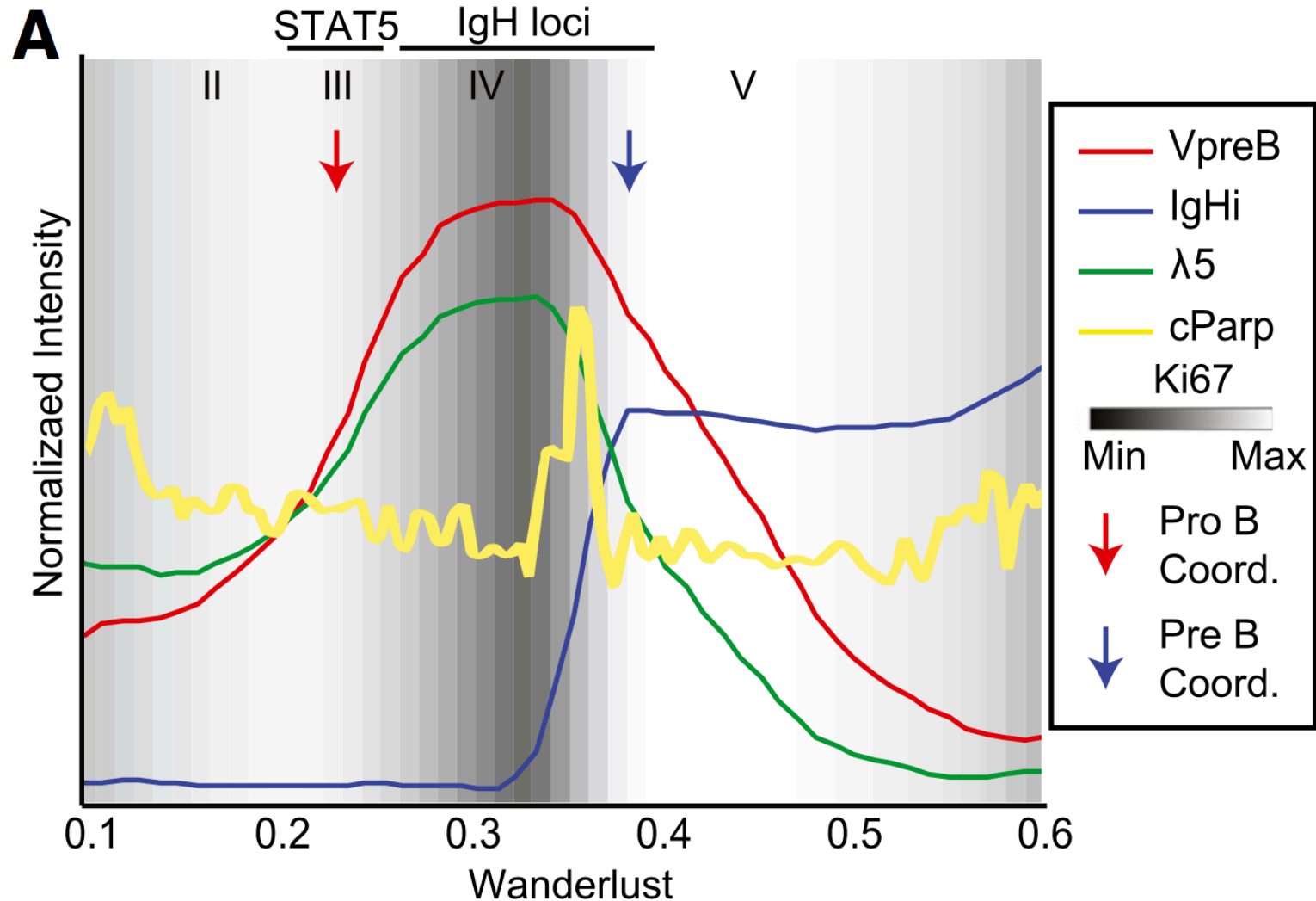
Phosphorylation
Induction vs. Basal

Max(-) 0 Max(+)

Derivative analysis reveals B cell checkpoints



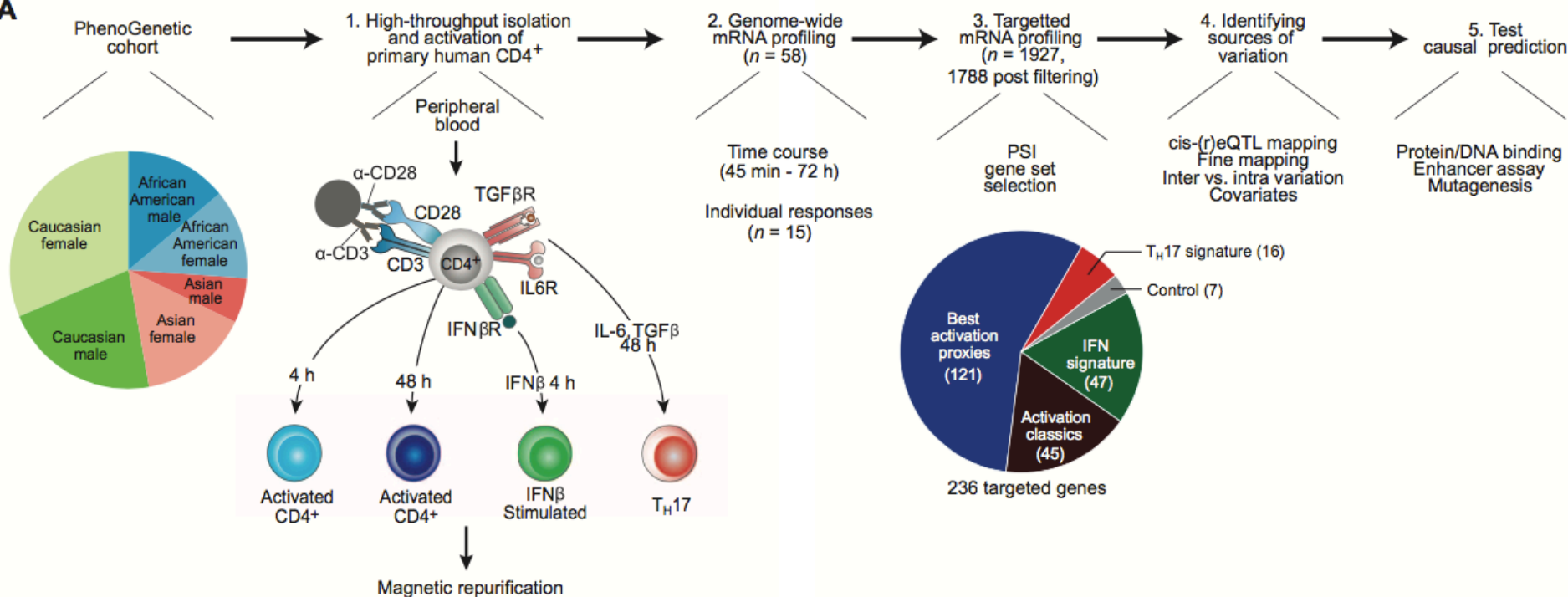
Derivative coordination points represent
pro- and pre-B cell transition points



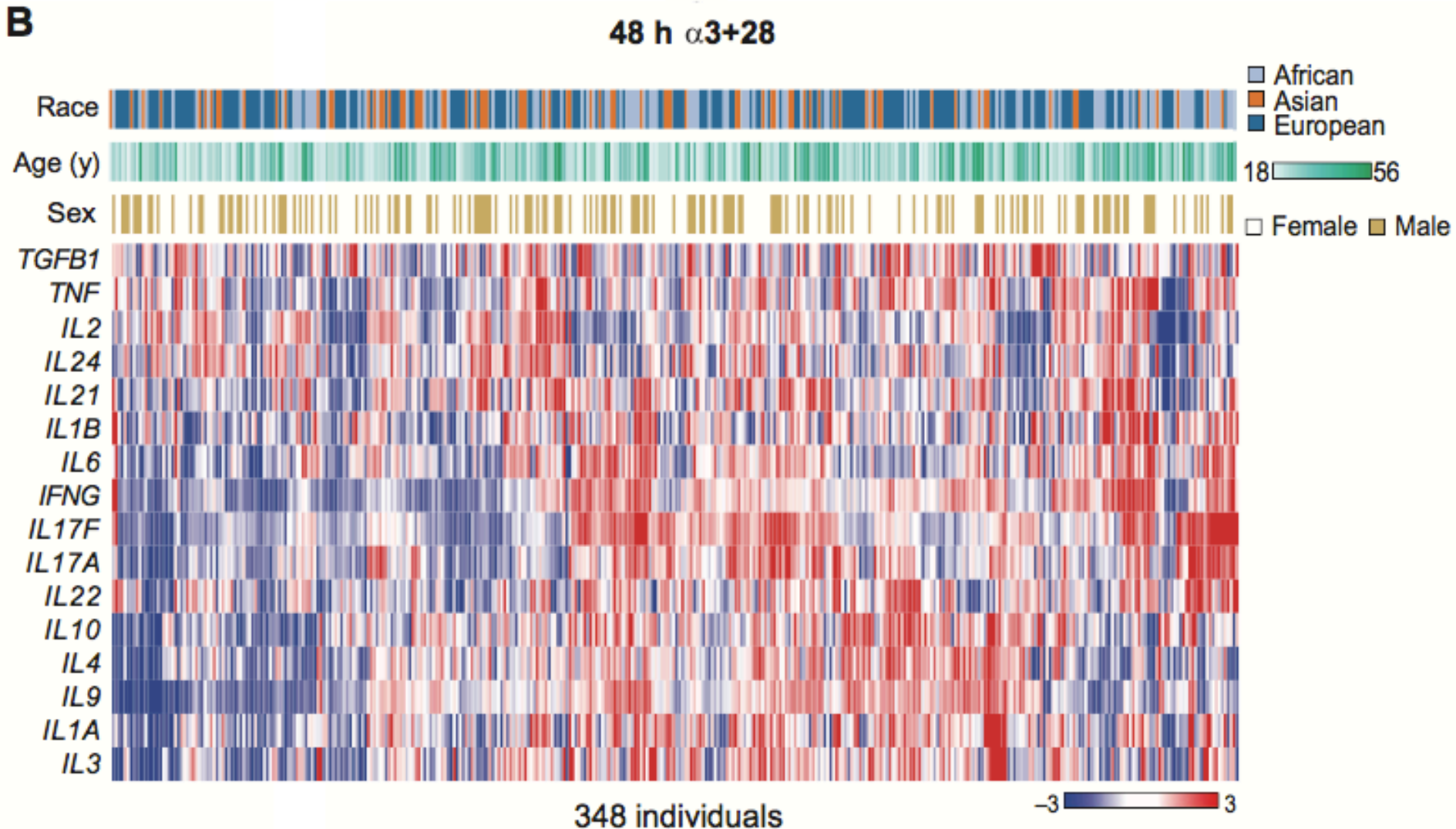
Intersection of population variation and autoimmunity genetics in human T cell activation

Chun Jimmie Ye,¹ Ting Feng,² Ho-Keun Kwon,² Towfique Raj,^{1,3} Michael T. Wilson,² Natasha Asinovski,² Cristin McCabe,^{1,3} Michelle H. Lee,³ Irene Frohlich,³ Hyun-il Paik,² Noah Zaitlen,⁴ Nir Hacohen,² Barbara Stranger,⁵ Philip De Jager,^{1,3} Diane Mathis,^{1,2} Aviv Regev,^{1,6*} Christophe Benoist^{1,2*}

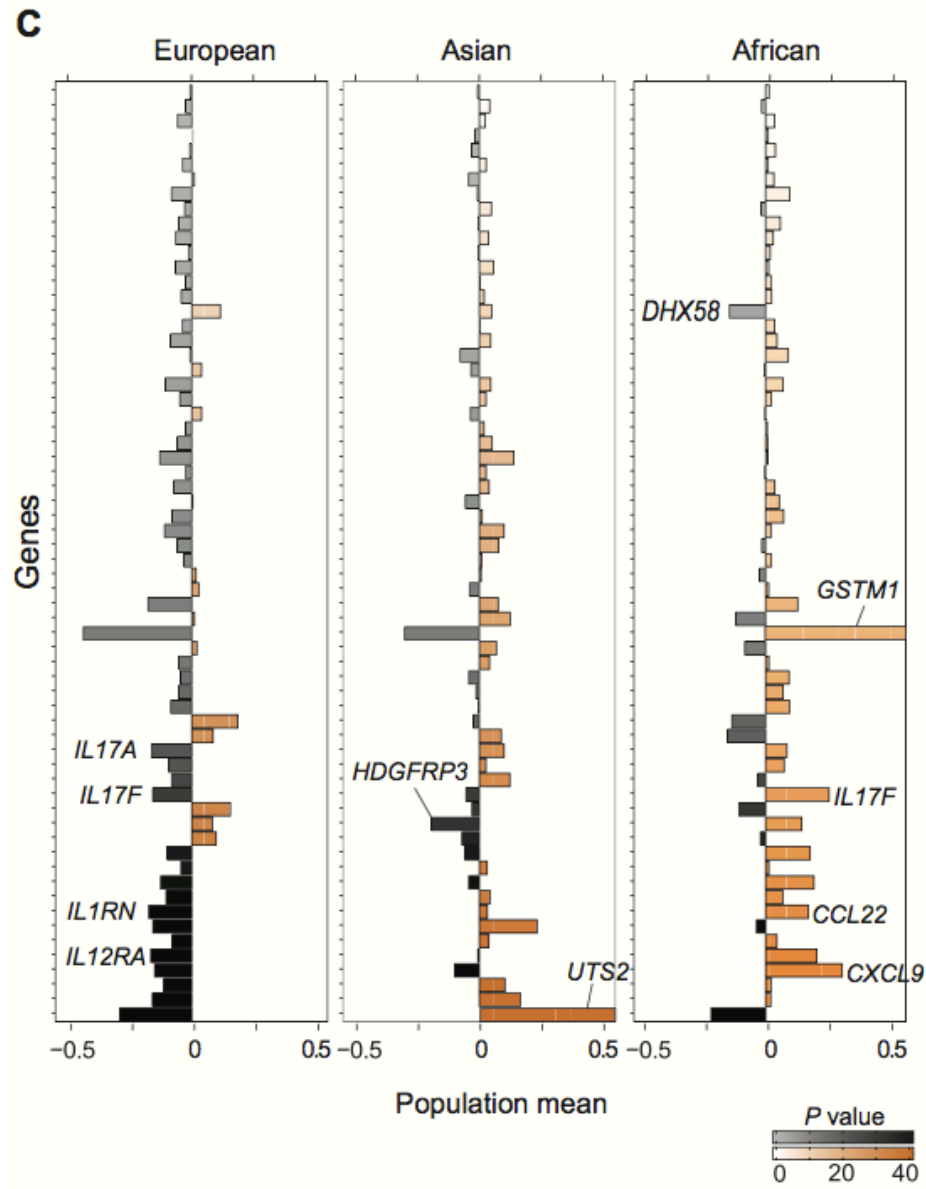
A



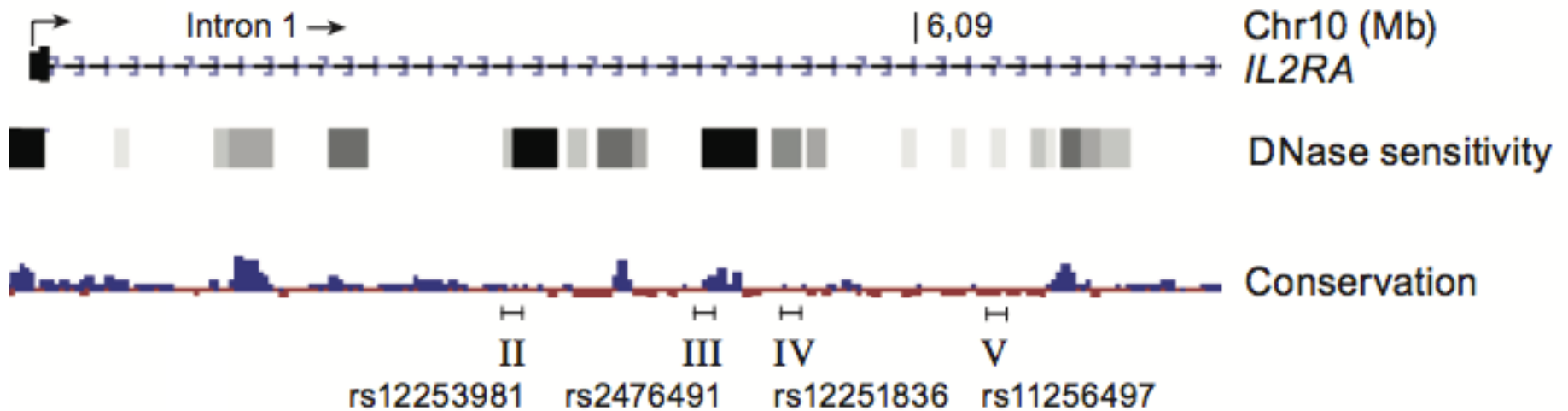
Significant variability across individuals in cytokine gene transcript levels



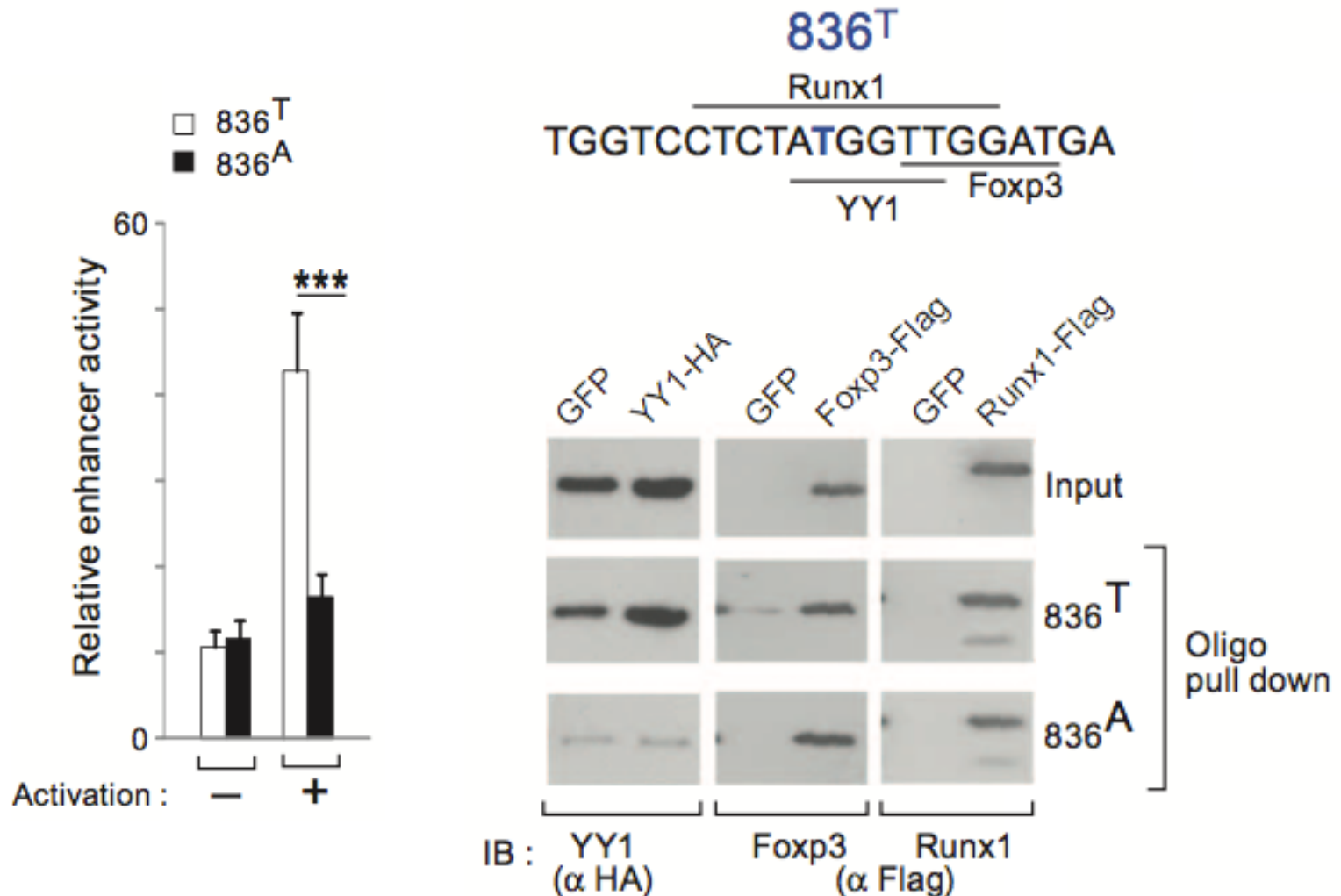
Specific gene expression patterns correlated with ethnicity



Identifying a SNP in an enhancer of IL-2 that regulates expression upon TCR stimulation



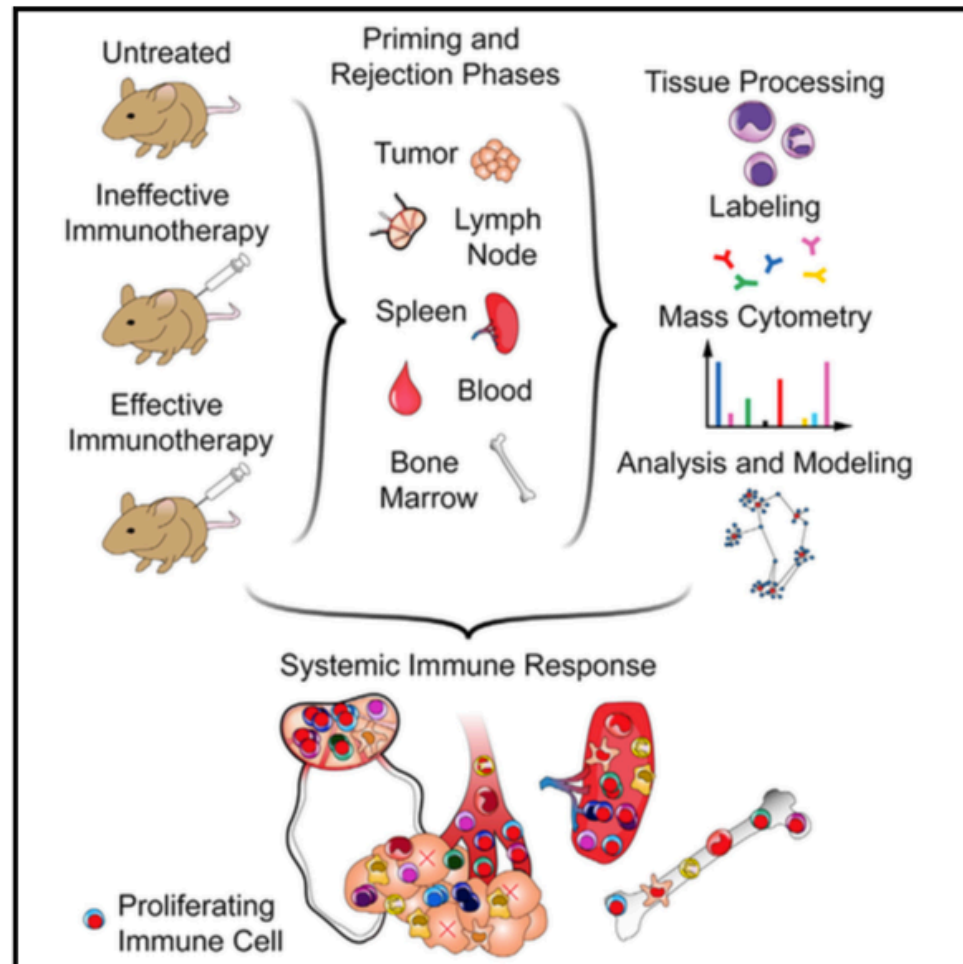
Identifying a SNP in an enhancer of IL-2 that regulates expression upon TCR stimulation



Systemic Immunity Is Required for Effective Cancer Immunotherapy

Matthew H. Spitzer,^{1,2,3,4,6,8,9,*} Yaron Carmi,^{1,7,8} Nathan E. Reticker-Flynn,^{1,8} Serena S. Kwek,⁵ Deepthi Madhiredy,² Maria M. Martins,¹ Pier Federico Gherardini,² Tyler R. Prestwood,¹ Jonathan Chabon,¹ Sean C. Bendall,¹ Lawrence Fong,^{5,6} Garry P. Nolan,^{2,3,*} and Edgar G. Engleman^{1,3,*}

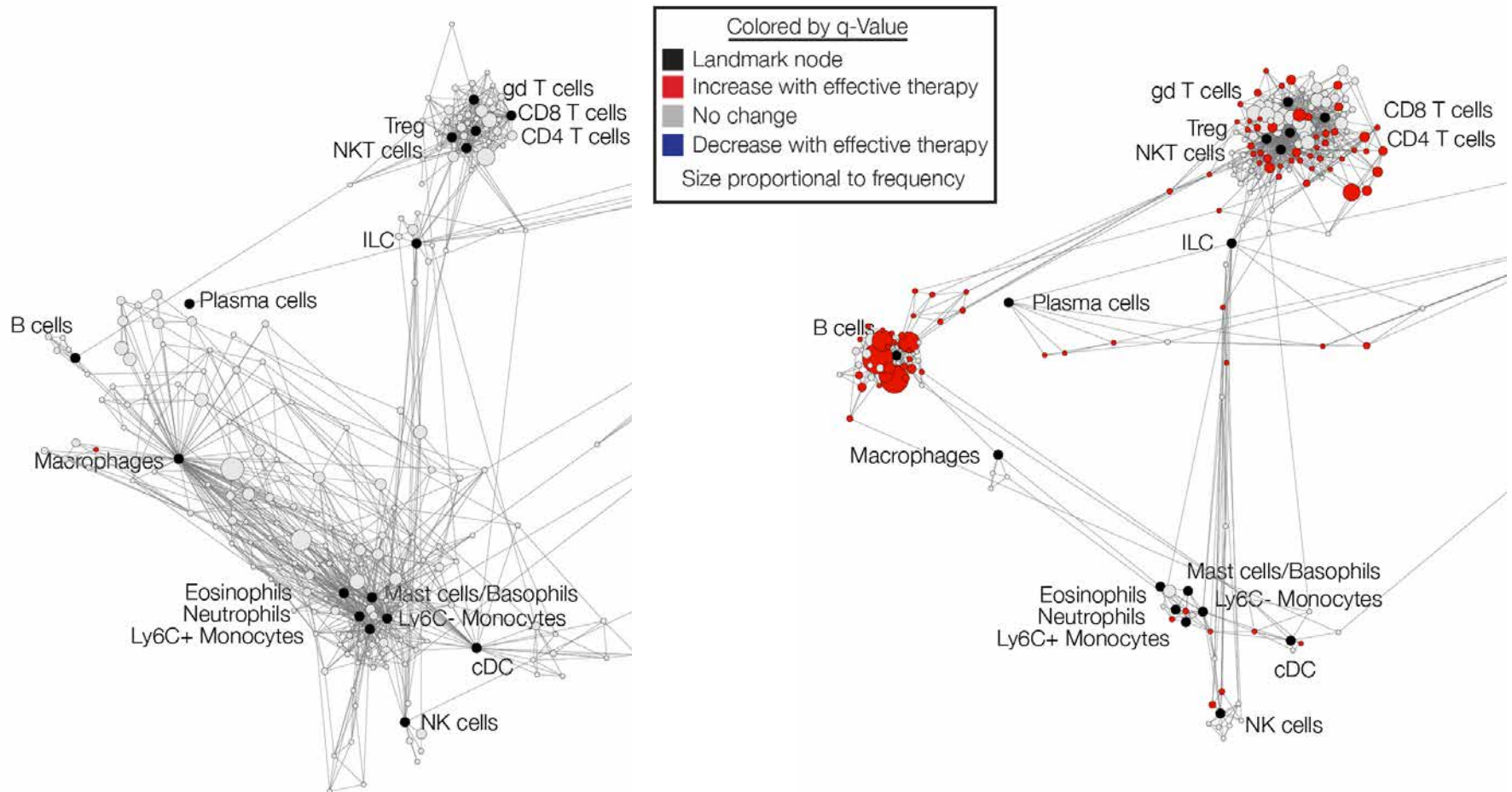
Cell 168, 487–502, January 26, 2017 © 2016



Immune cell proliferation is sustained from outside the tumor during effective immunotherapy

Tumor Microenvironment

Draining Lymph Node

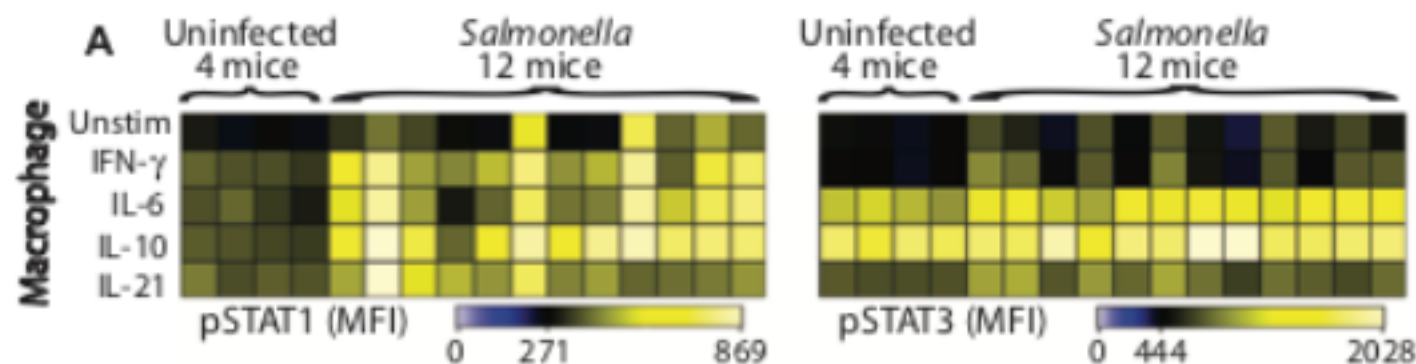


Red nodes are subsets with increased proliferation after therapy.

SYSTEMS IMMUNOLOGY

Coordinate actions of innate immune responses oppose those of the adaptive immune system during *Salmonella* infection of mice

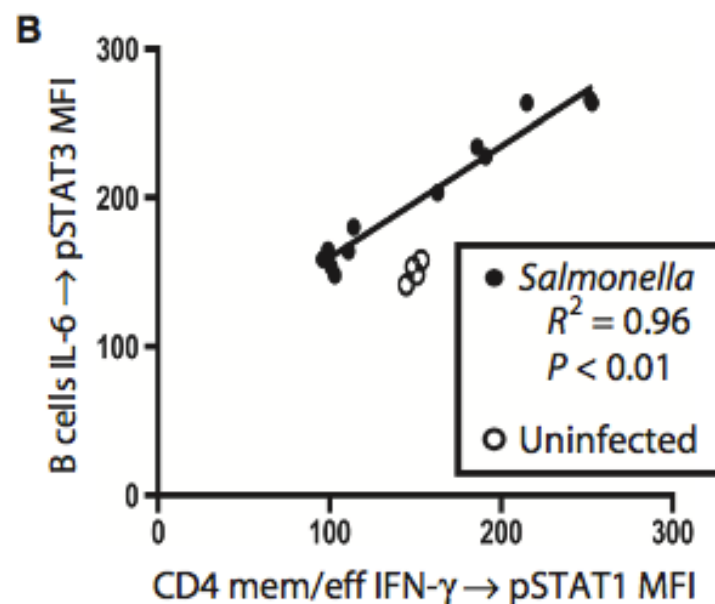
Andrew N. Hotson,^{1,2*} Smita Gopinath,^{2*} Monica Nicolau,¹ Anna Khasanova,¹ Rachel Finck,^{1,2} Denise Monack,² Garry P. Nolan^{1,2†}



SYSTEMS IMMUNOLOGY

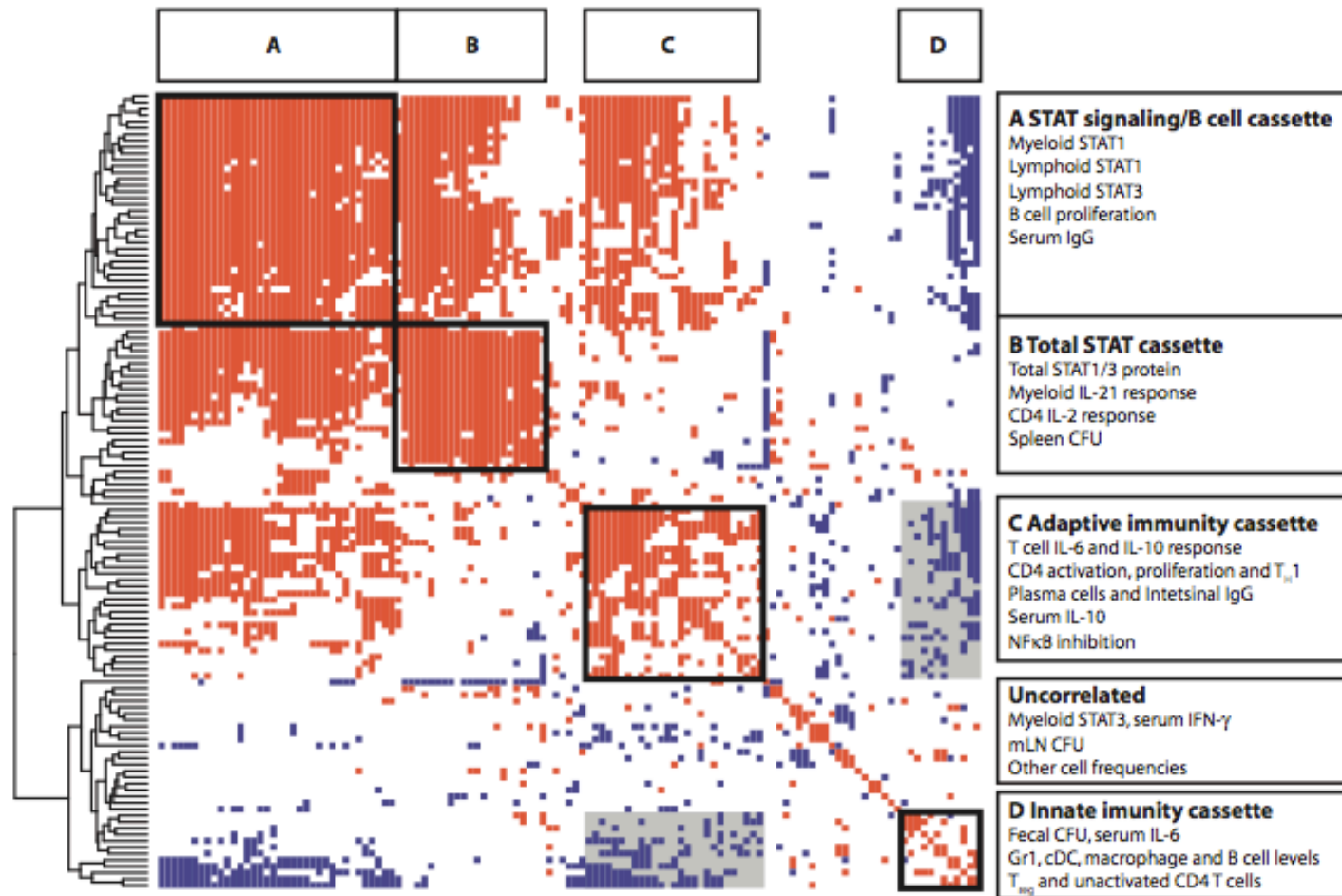
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Rachel Finck,^{1,2} Denise Monack,² Garry P. Nolan^{1,2†}



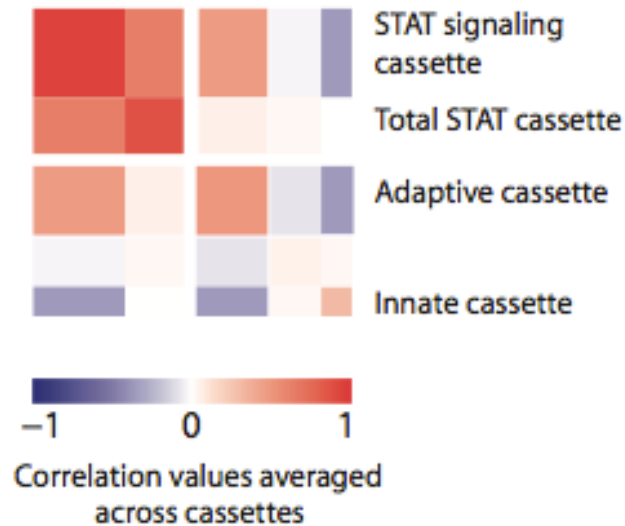
Immune cell signaling is highly correlated across animals after infection

A Infected correlation matrix clustered using Ward algorithm

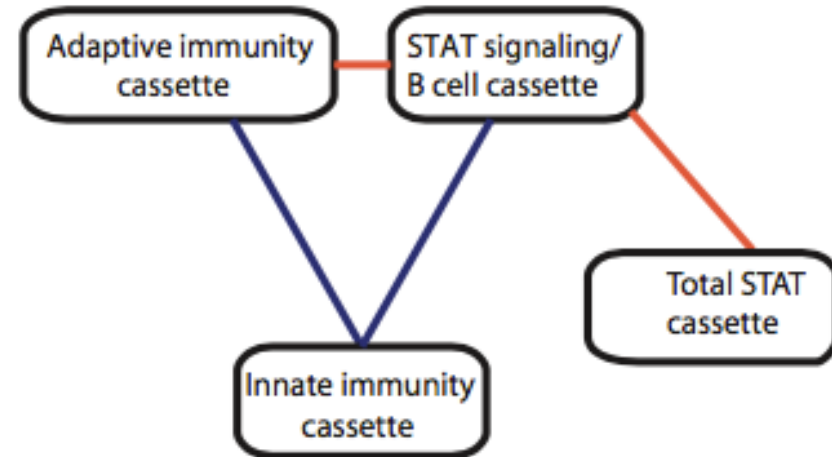


These relationships can be simplified into a model that changes during infection

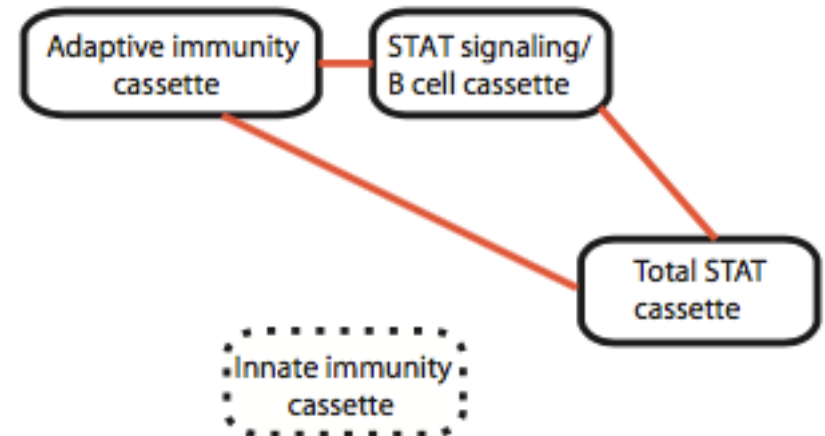
B Correlations averaged



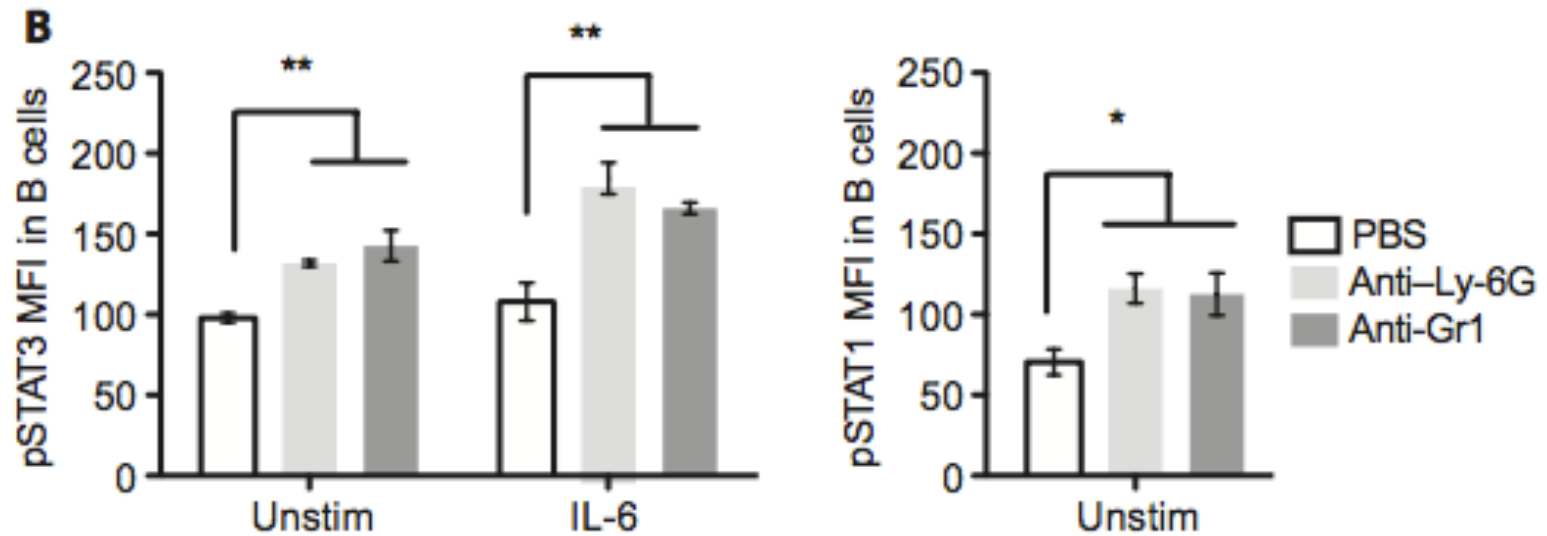
C Infected immune network



Uninfected immune network



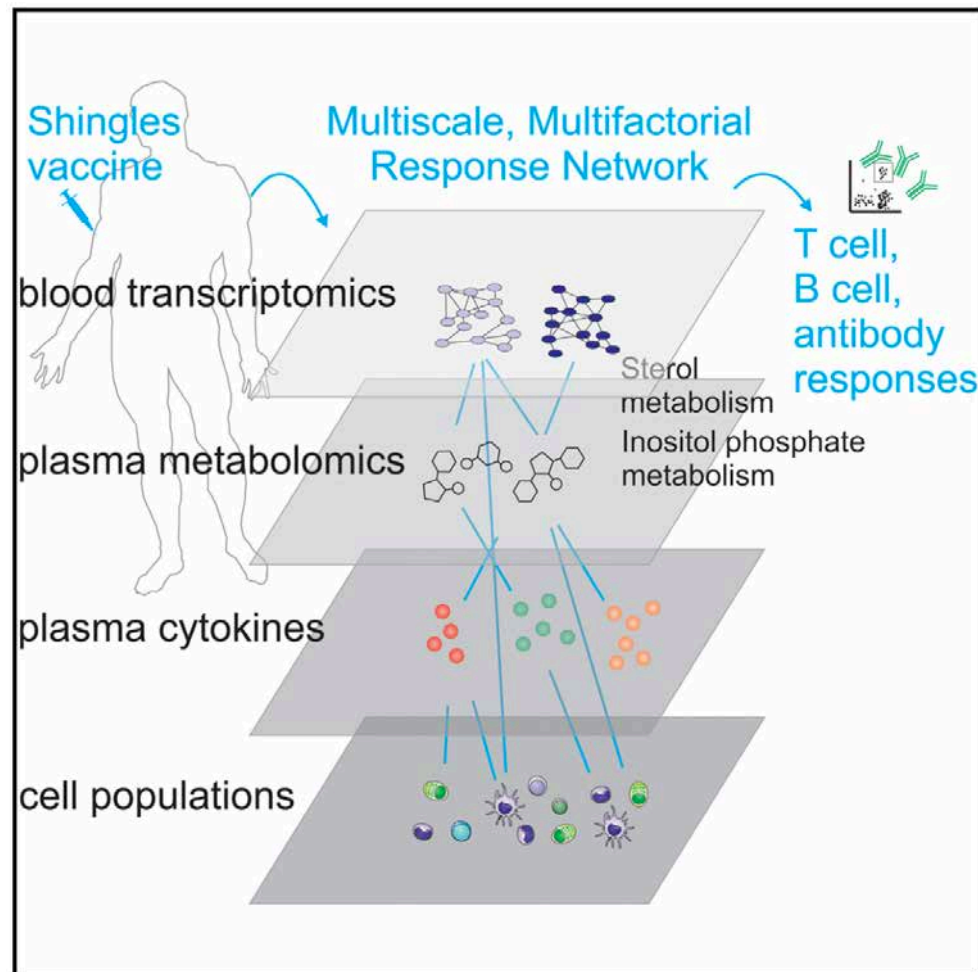
Depleting neutrophils augments B cell signaling during *Salmonella* infection



Metabolic Phenotypes of Response to Vaccination in Humans

Cell 169, 862–877, May 18, 2017

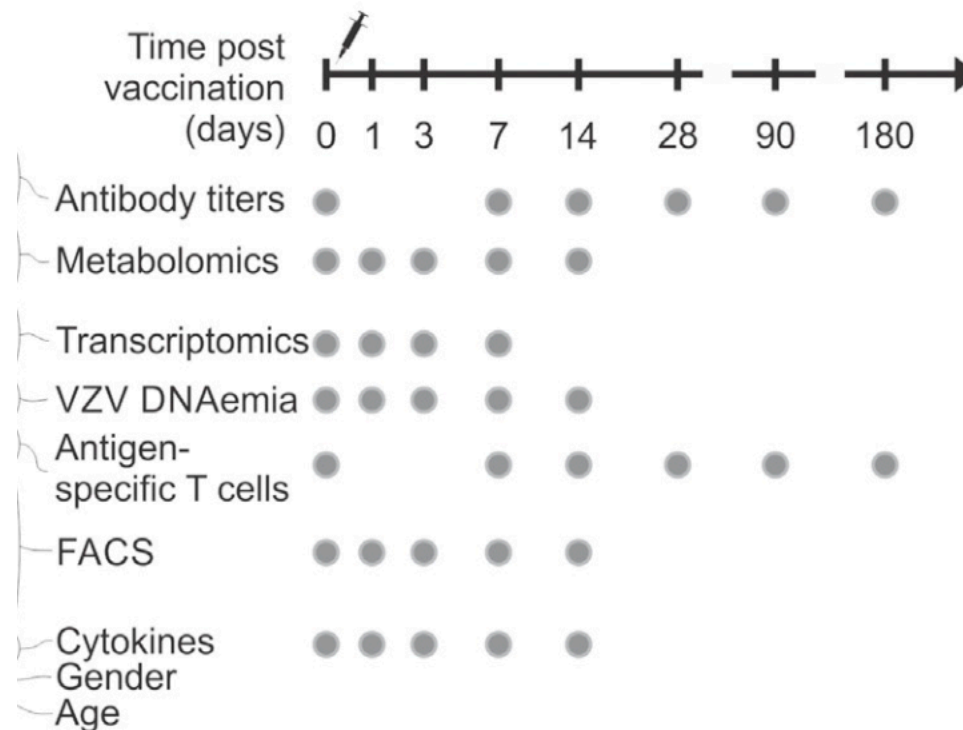
Shuzhao Li,^{1,12} Nicole L. Sullivan,^{2,12,14} Nadine Rouphael,^{1,3} Tianwei Yu,⁴ Sophia Banton,¹ Mohan S. Maddur,² Megan McCausland,² Christopher Chiu,² Jennifer Canniff,⁵ Sheri Dubey,⁶ Ken Liu,¹ ViLinh Tran,¹ Thomas Hagan,² Sai Duraisingham,² Andreas Wieland,² Aneesh K. Mehta,¹ Jennifer A. Whitaker,^{1,13} Shankar Subramaniam,⁷ Dean P. Jones,¹ Alessandro Sette,⁸ Kalpit Vora,⁶ Adriana Weinberg,⁵ Mark J. Mulligan,^{1,3} Helder I. Nakaya,^{9,10} Myron Levin,⁵ Rafi Ahmed,^{2,11} and Bali Pulendran^{2,10,15,*}



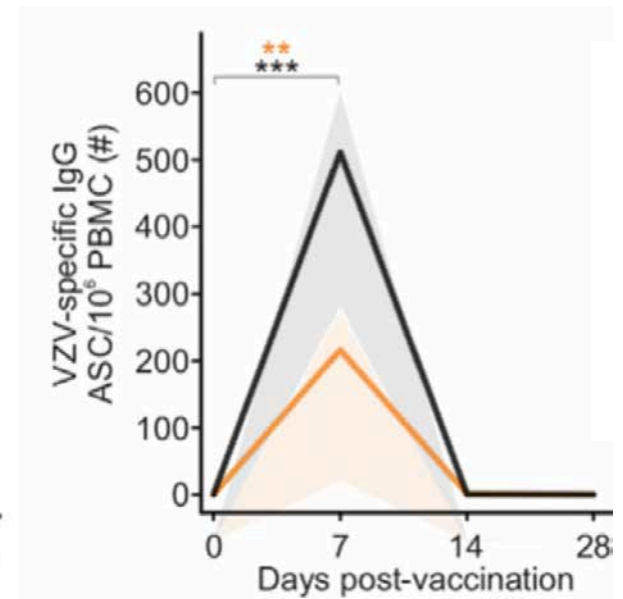
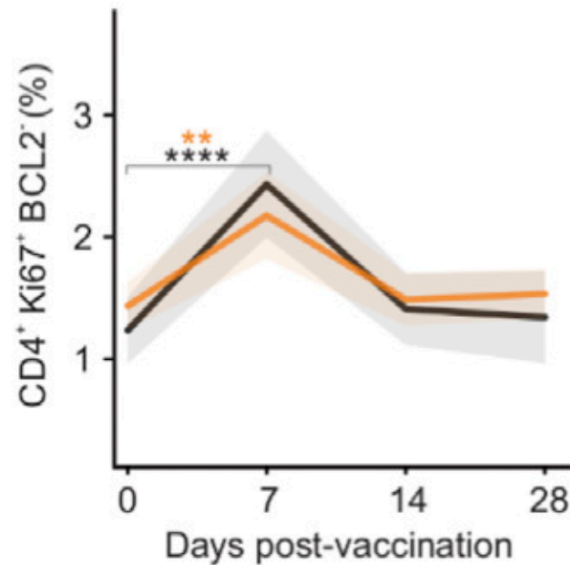
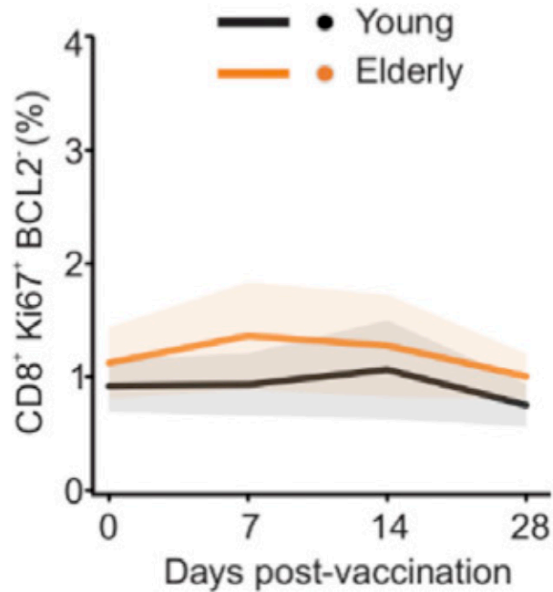
Metabolic Phenotypes of Response to Vaccination in Humans

Cell 169, 862–877, May 18, 2017

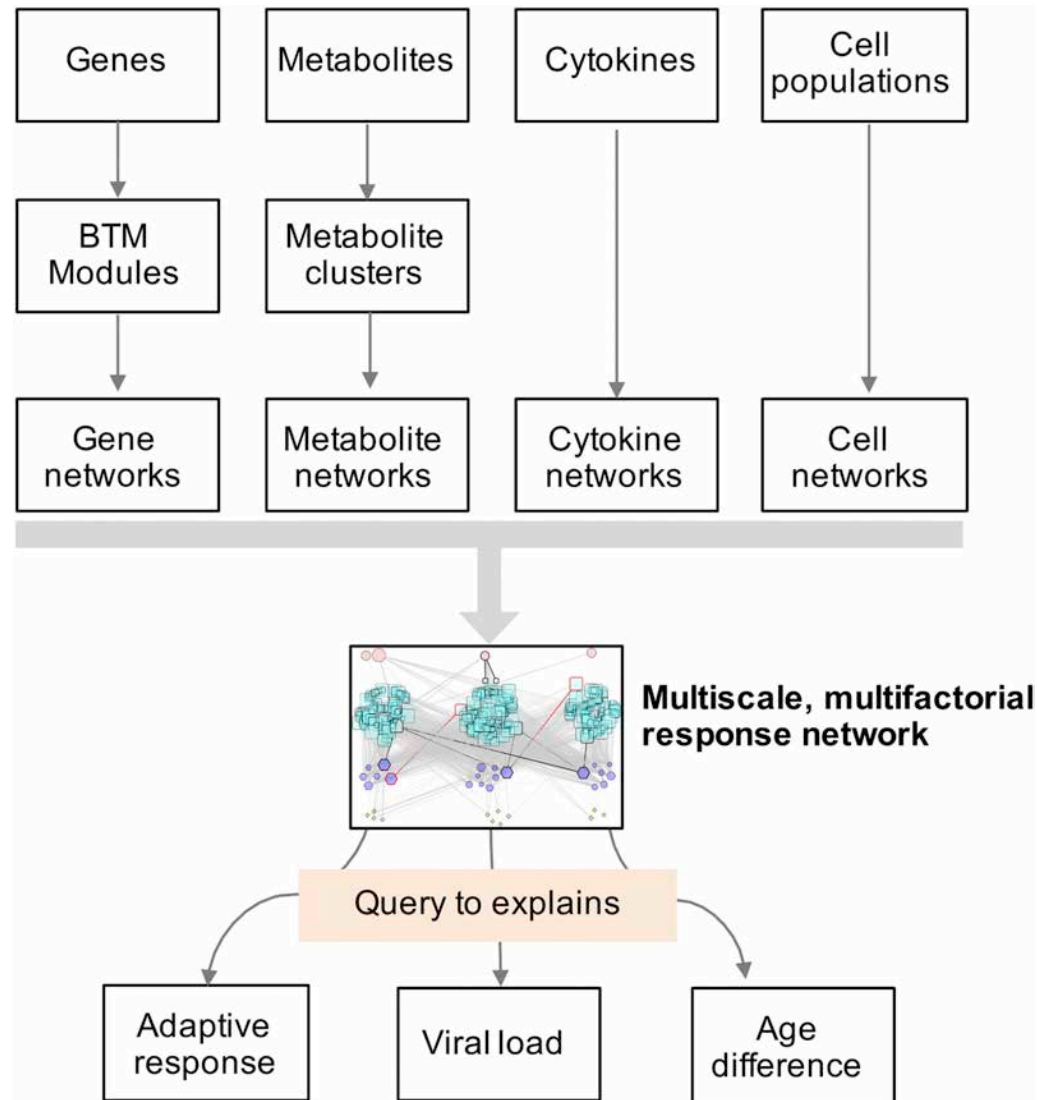
Shuzhao Li,^{1,12} Nicole L. Sullivan,^{2,12,14} Nadine Rouphael,^{1,3} Tianwei Yu,⁴ Sophia Banton,¹ Mohan S. Maddur,² Megan McCausland,² Christopher Chiu,² Jennifer Canniff,⁵ Sheri Dubey,⁶ Ken Liu,¹ ViLinh Tran,¹ Thomas Hagan,² Sai Duraisingham,² Andreas Wieland,² Aneesh K. Mehta,¹ Jennifer A. Whitaker,^{1,13} Shankar Subramaniam,⁷ Dean P. Jones,¹ Alessandro Sette,⁸ Kalpit Vora,⁶ Adriana Weinberg,⁵ Mark J. Mulligan,^{1,3} Helder I. Nakaya,^{9,10} Myron Levin,⁵ Rafi Ahmed,^{2,11} and Bali Pulendran^{2,10,15,*}



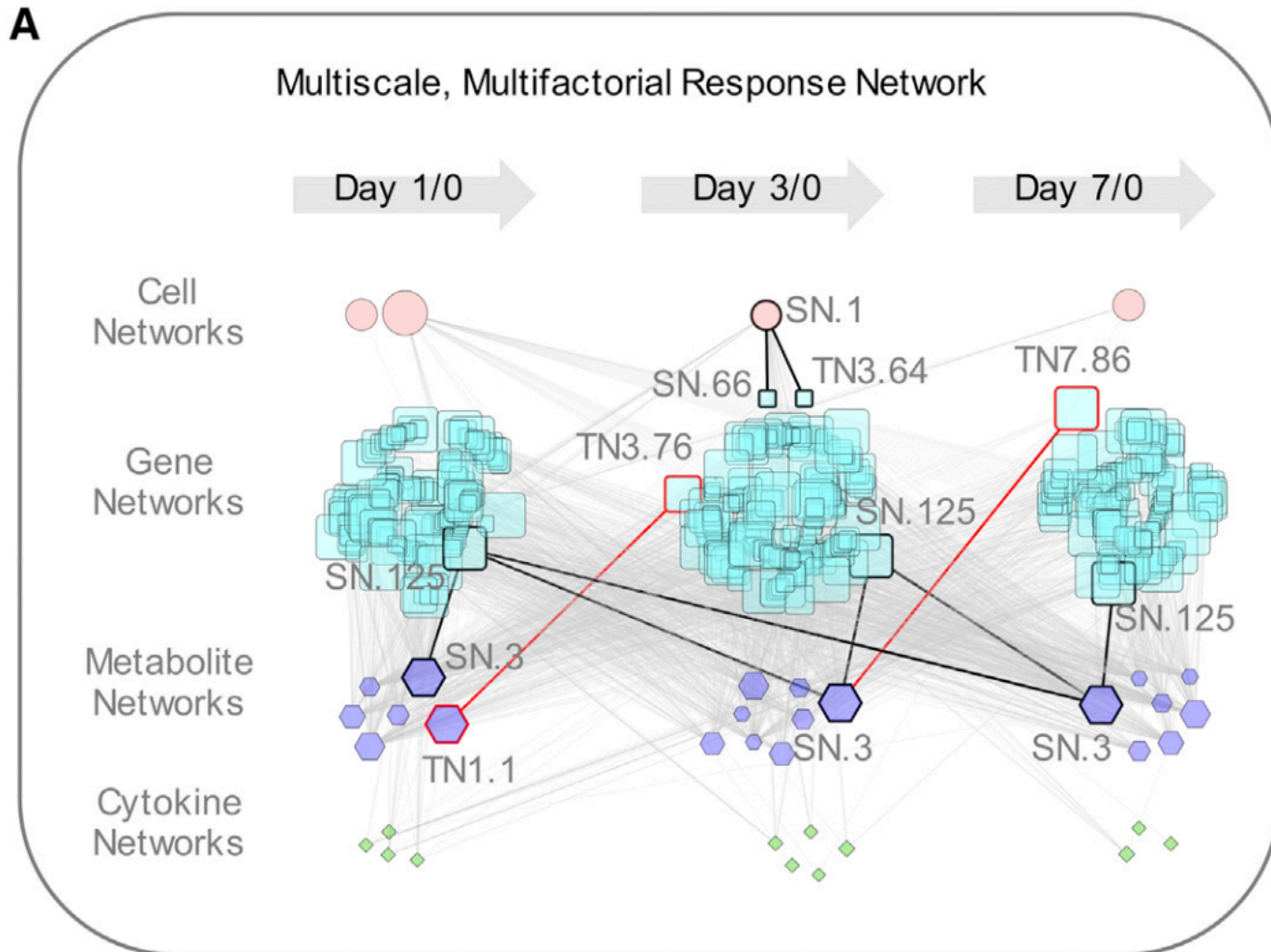
T cells and B cells become activated after vaccination



Development of a multiscale model incorporating different data types

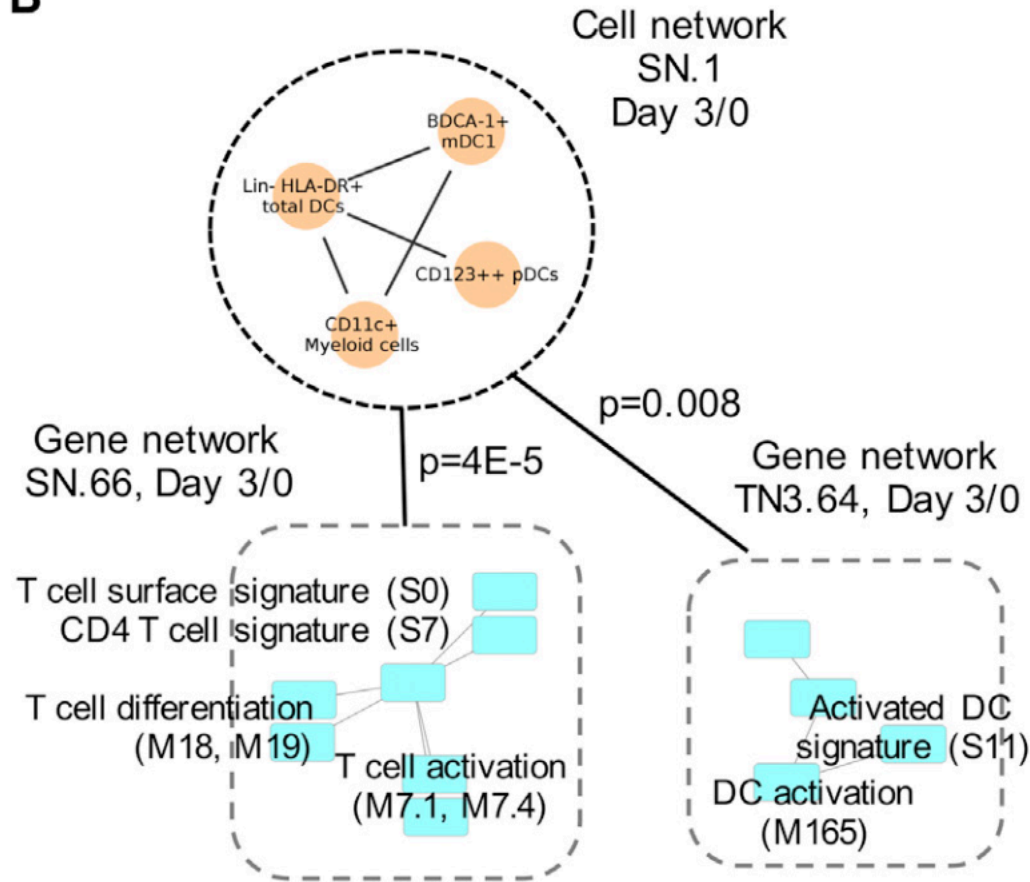


Development of a multiscale model incorporating different data types

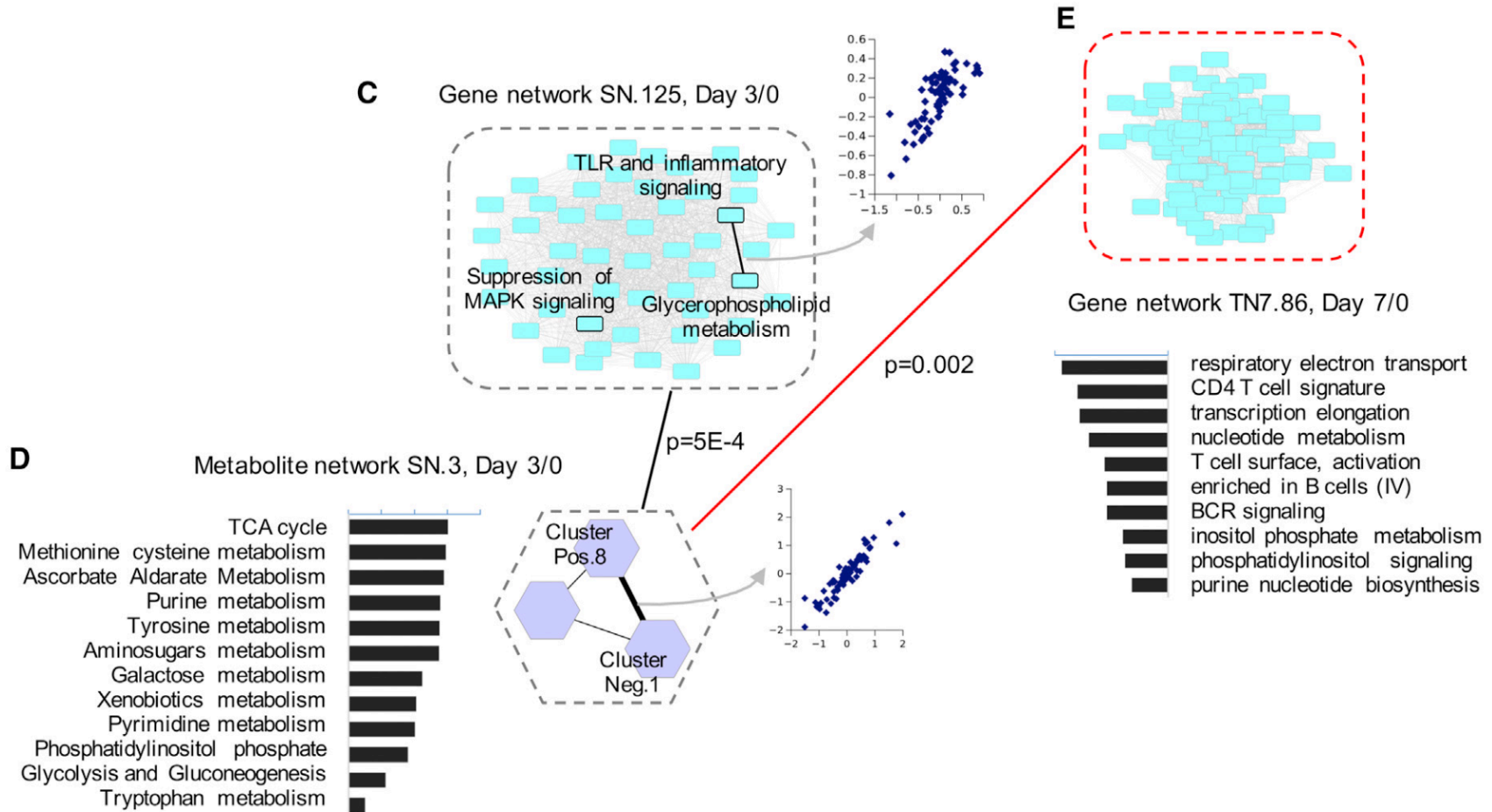


A DC activation network associates with a T cell activation network

B

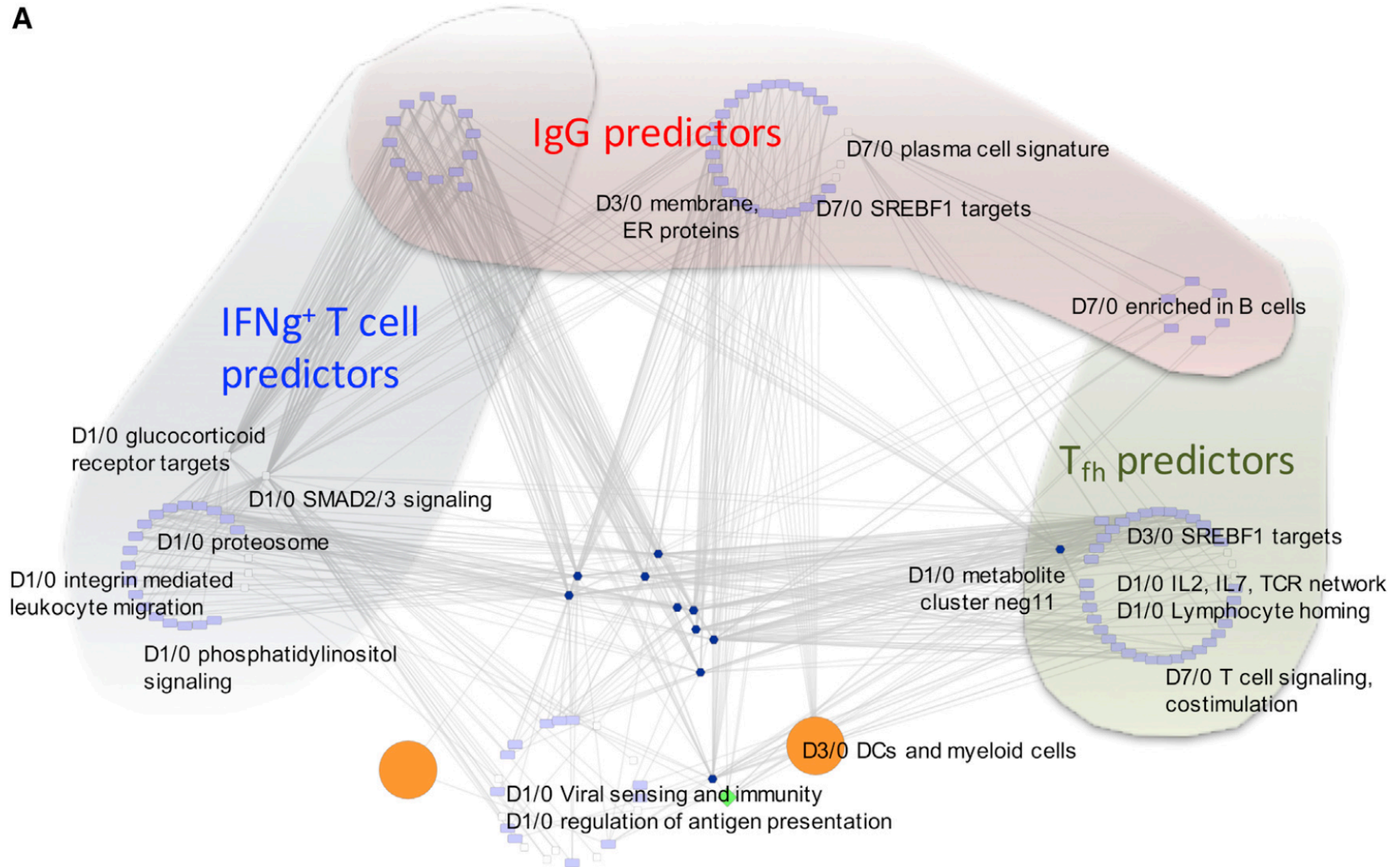


Associations of TCA, nucleotide and phosphatidylinositol metabolism across data types

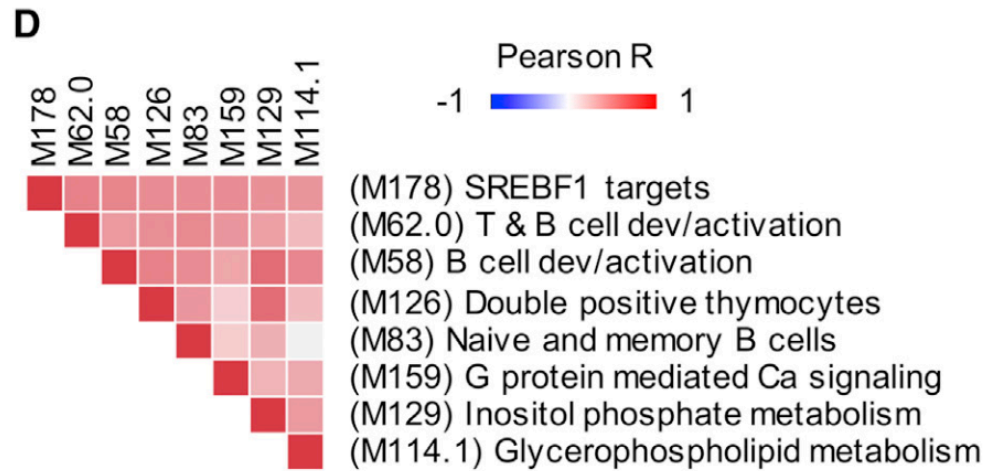
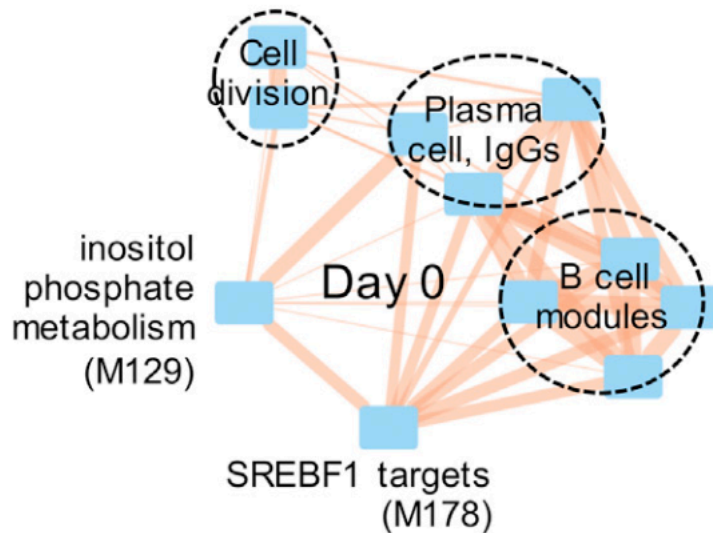


Predictors of adaptive immune response strength

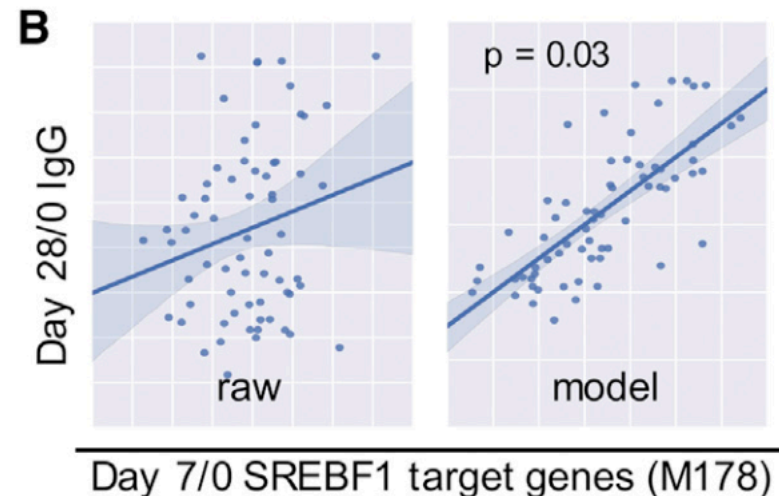
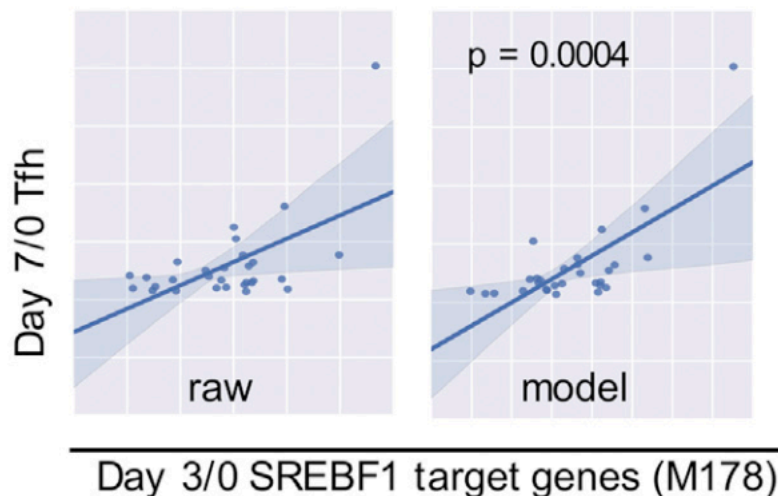
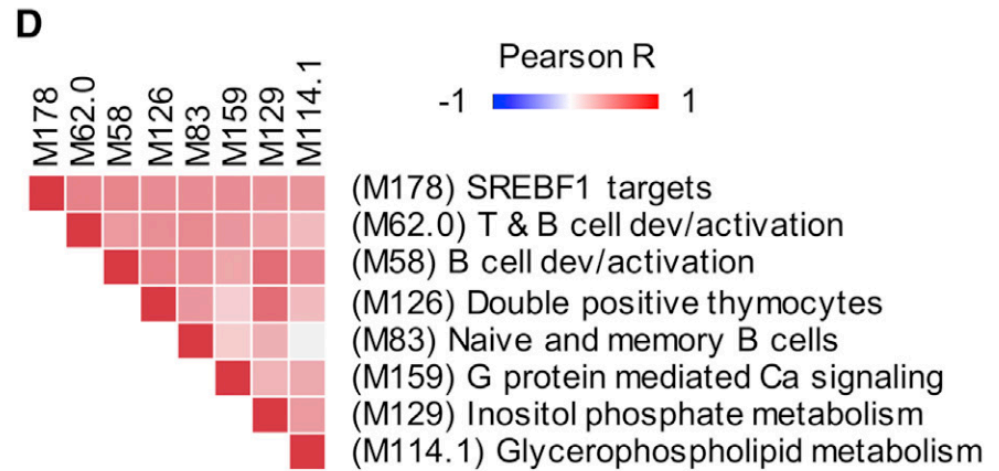
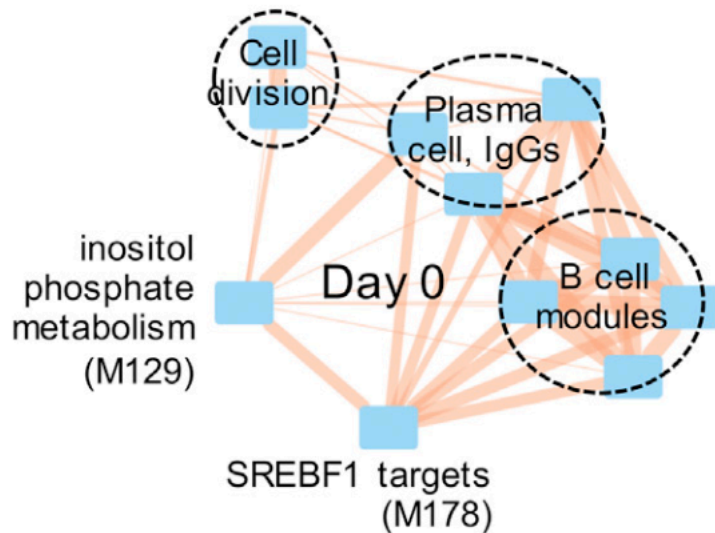
A



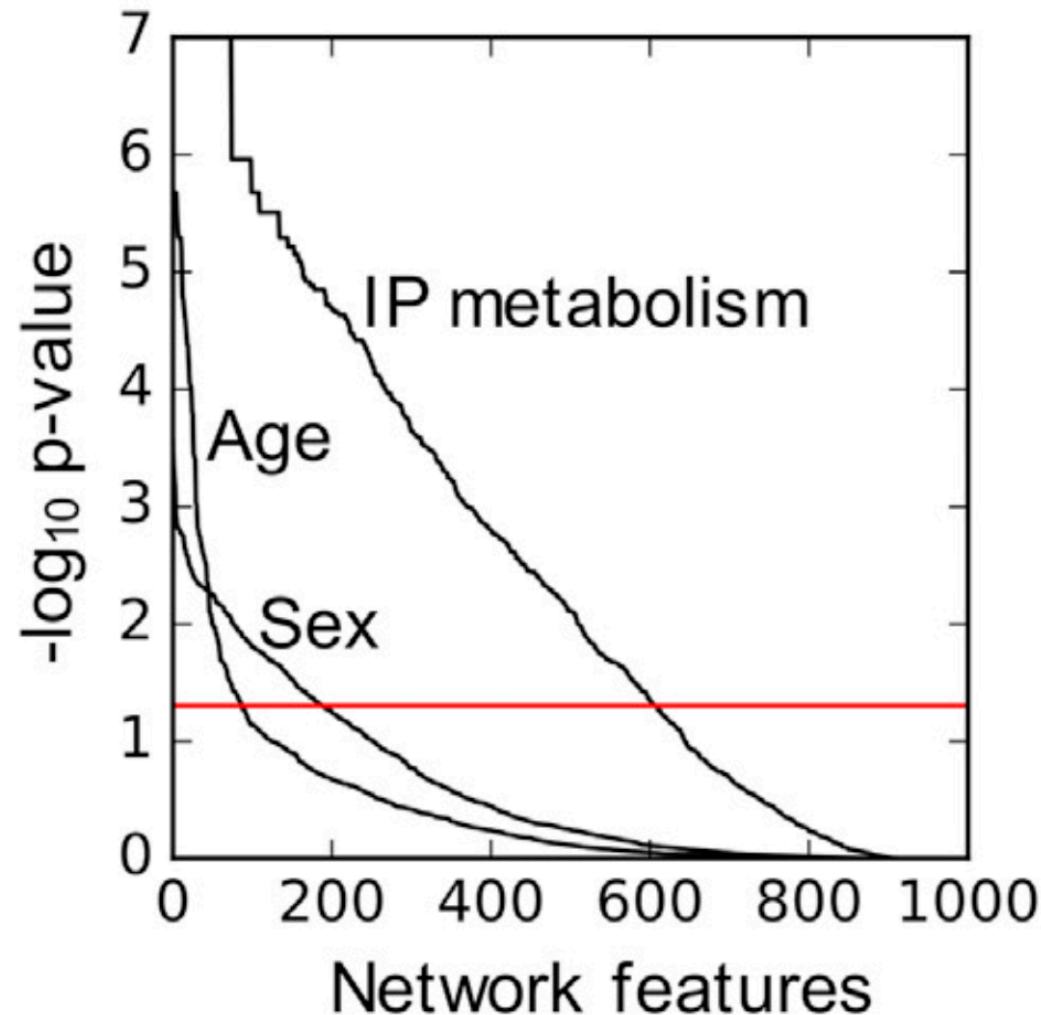
Sterol metabolism as a central hub of immune coordination



Sterol metabolism as a central hub of immune coordination



Inositol phosphate metabolism is highly associated with numerous aspects of the immune response



Systems biology approach predicts immunogenicity of the yellow fever vaccine in humans

Troy D Querec^{1,8}, Rama S Akondy^{1,8}, Eva K Lee², Weiping Cao¹, Helder I Nakaya¹, Dirk Teuwen³, Ali Pirani⁴, Kim Gernert⁴, Jiusheng Deng¹, Bruz Marzolf⁵, Kathleen Kennedy⁵, Haiyan Wu⁵, Soumaya Bennouna¹, Herold Oluoch¹, Joseph Miller¹, Ricardo Z Vencio⁵, Mark Mulligan^{1,6}, Alan Aderem⁵, Rafi Ahmed¹ & Bali Pulendran^{1,7}

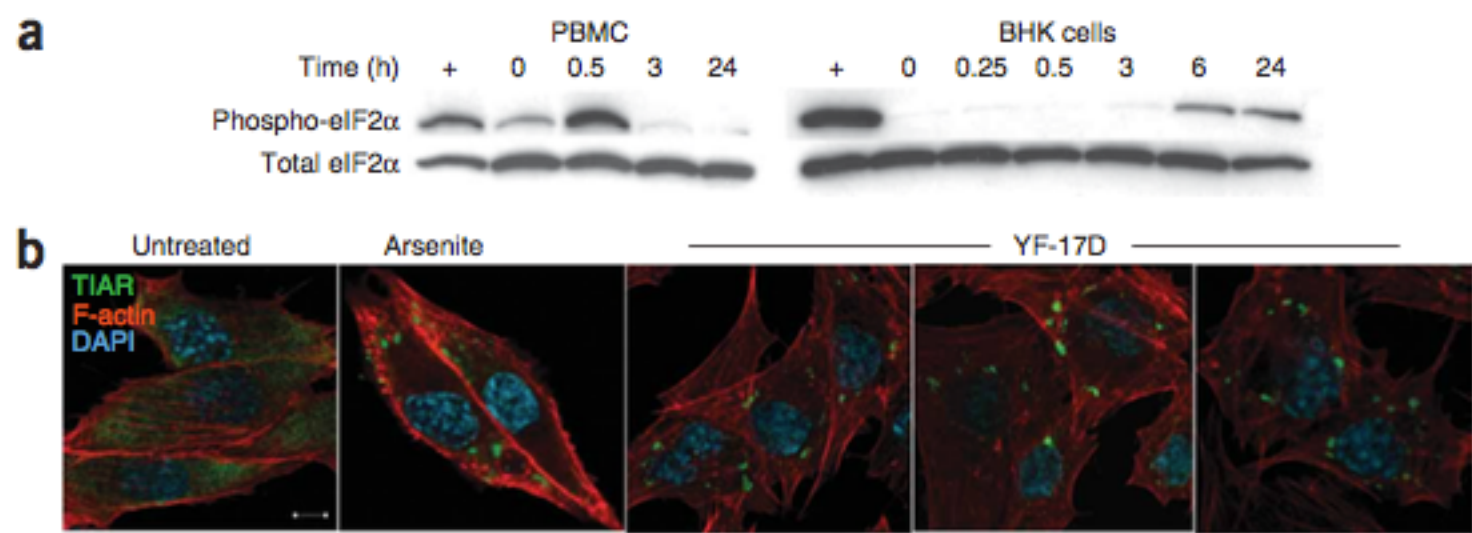
25 healthy humans vaccinated with yellow fever vaccine

Luminex, flow cytometry and gene expression longitudinally

EIF2AK4 (GCN1), regulator of the integrated stress response, is a strong predictor of CD8 T cell responses

Table 2 Genomic signatures that predict the magnitude of the CD8⁺ T cell responses using the DAMIP model

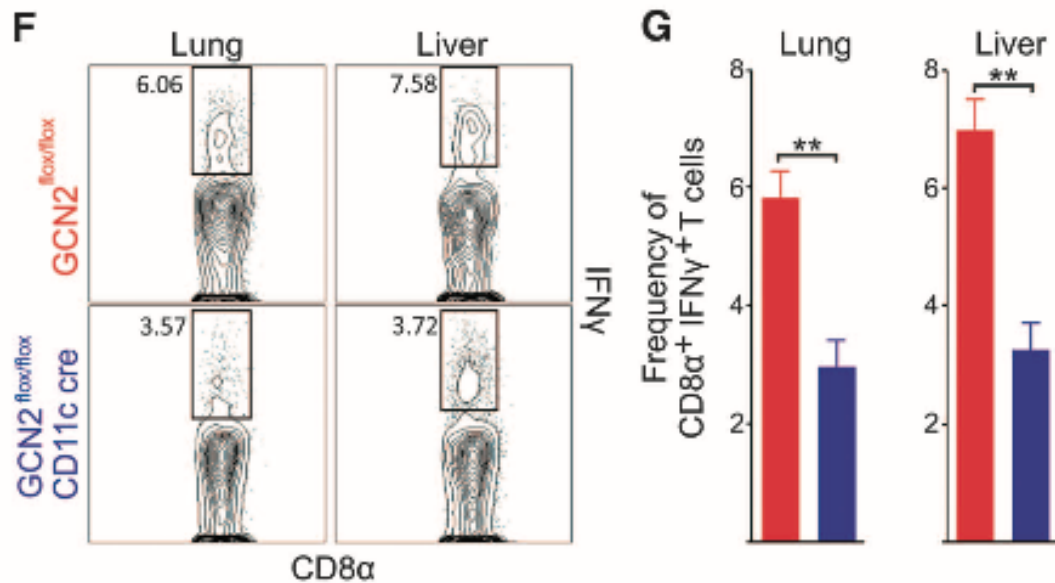
Gene name	Gene symbol	Gene ID	DAMIP model predictive signatures													
			Train on trial 1, test on trial 2								Train on trial 2, test on trial 1					
			1	2	3	4	5	6	7	8	1	2	3	4	5	6
Solute carrier family 2 (facilitated glucose transporter), member 6	<i>SLC2A6</i>	Hs.244378	Day 7	X		X	X	X	X	X	X	X	X		X	
Eukaryotic translation initiation factor 2 alpha kinase 4	<i>EIF2AK4</i>	Hs.412102	Day 7	X	X	X		X		X	X				X	



Vaccine Activation of the Nutrient Sensor GCN2 in Dendritic Cells Enhances Antigen Presentation

Rajesh Ravindran,^{1*} Nooruddin Khan,^{1,2*} Helder I. Nakaya,^{1,3} Shuzhao Li,¹ Jens Loebbermann,¹ Mohan S. Maddur,¹ Youngja Park,⁴ Dean P. Jones,⁵ Pascal Chappert,^{6,7} Jean Davoust,^{6,7} David S. Weiss,⁸ Herbert W. Virgin,⁹ David Ron,¹⁰ Bali Pulendran^{1,3†}

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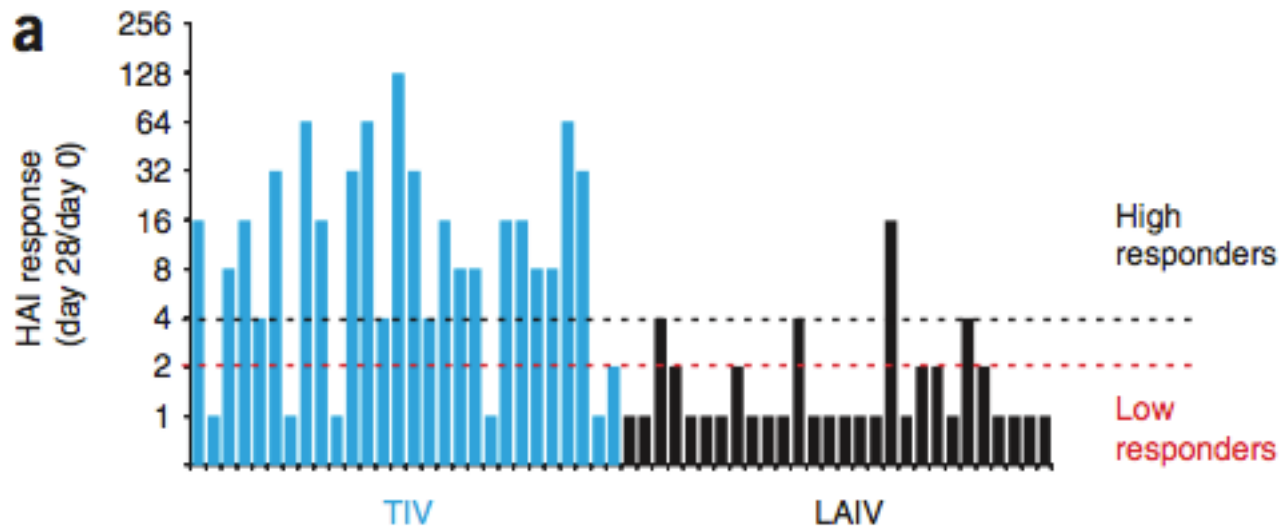


GCN2 regulates autophagy in DC, which promotes cross-presentation to CD8 T cells.

Systems biology of vaccination for seasonal influenza in humans

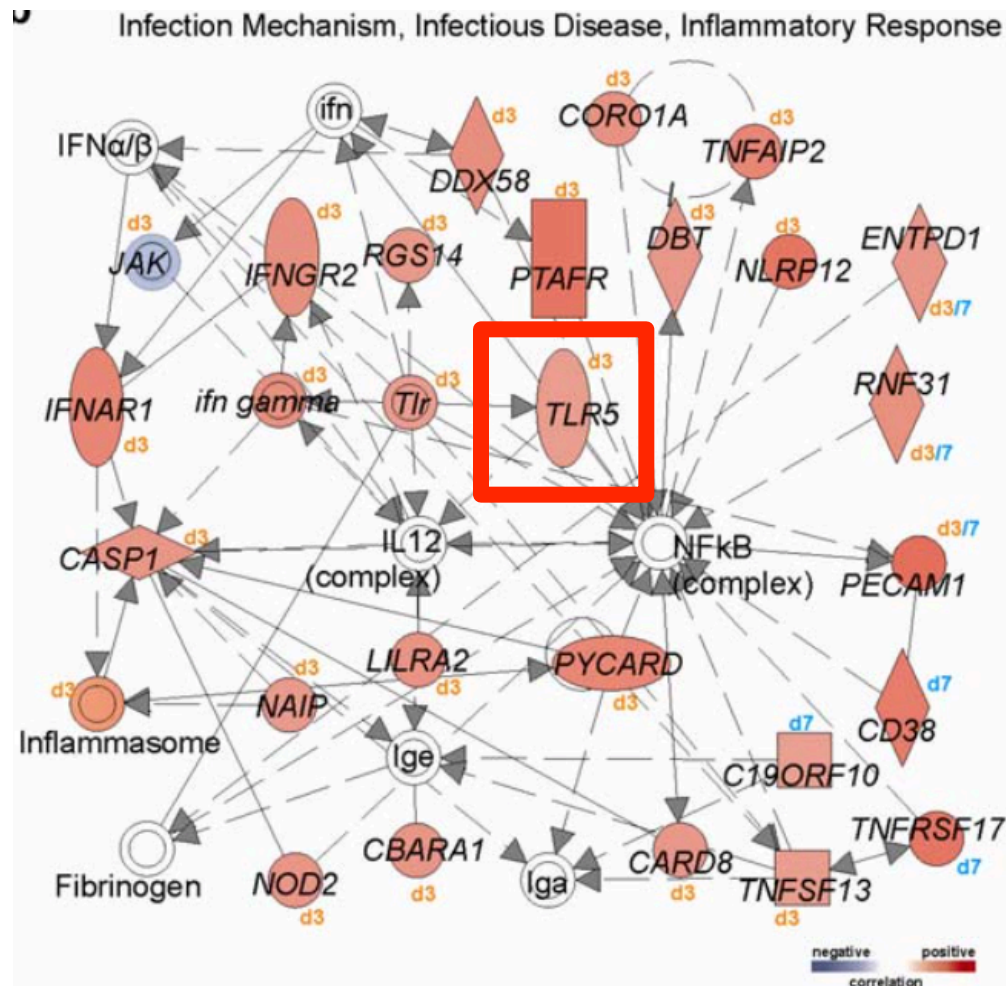
Helder I Nakaya^{1,2}, Jens Wrammert^{1,3}, Eva K Lee⁴, Luigi Racioppi^{5,6}, Stephanie Marie-Kunze^{1,2}, W Nicholas Haining⁷, Anthony R Means⁶, Sudhir P Kasturi^{1,2}, Nooruddin Khan^{1,2}, Gui-Mei Li^{1,3}, Megan McCausland^{1,3}, Vibhu Kanchan^{1,3}, Kenneth E Kokko⁸, Shuzhao Li^{1,2}, Rivka Elbein⁹, Aneesh K Mehta⁹, Alan Aderem¹⁰, Kanta Subbarao¹¹, Rafi Ahmed^{1,3} & Bali Pulendran^{1,2,12}

VOLUME 12 NUMBER 8 AUGUST 2011 NATURE IMMUNOLOGY



Healthy individuals vaccinated with trivalent inactivated or live-attenuated influenza vaccine

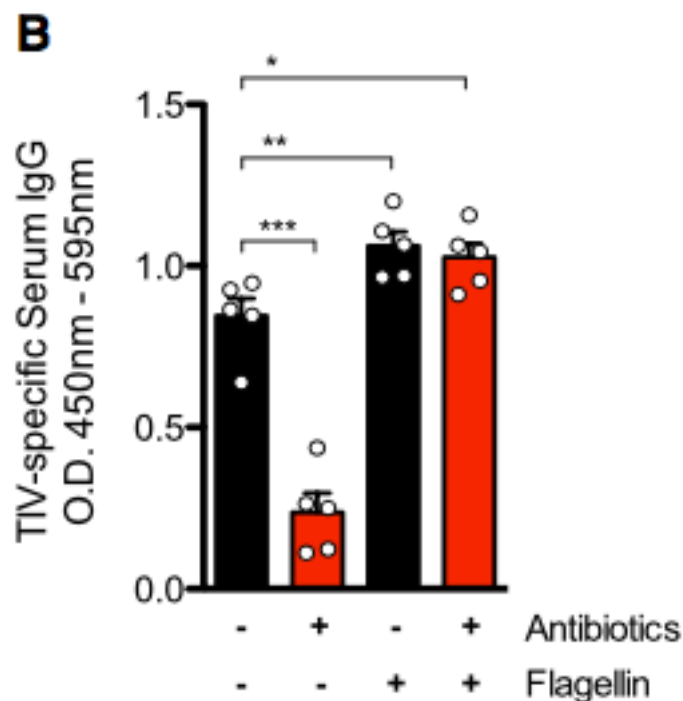
TLR5 induction is correlate with strong responses to the vaccine



Immunity 41, 478–492, September 18, 2014 ©2014

TLR5-Mediated Sensing of Gut Microbiota Is Necessary for Antibody Responses to Seasonal Influenza Vaccination

Jason Z. Oh,^{1,2} Rajesh Ravindran,^{1,2} Benoit Chassaing,⁴ Frederic A. Carvalho,^{4,5} Mohan S. Maddur,^{1,2} Maureen Bower,⁶ Paul Hakimpour,² Kiran P. Gill,^{1,2} Helder I. Nakaya,^{3,7} Felix Yarovsky,⁸ R. Balfour Sartor,⁶ Andrew T. Gewirtz,⁴ and Bali Pulendran^{1,2,3,*}



Immunity 41, 478–492, September 18, 2014 ©2014

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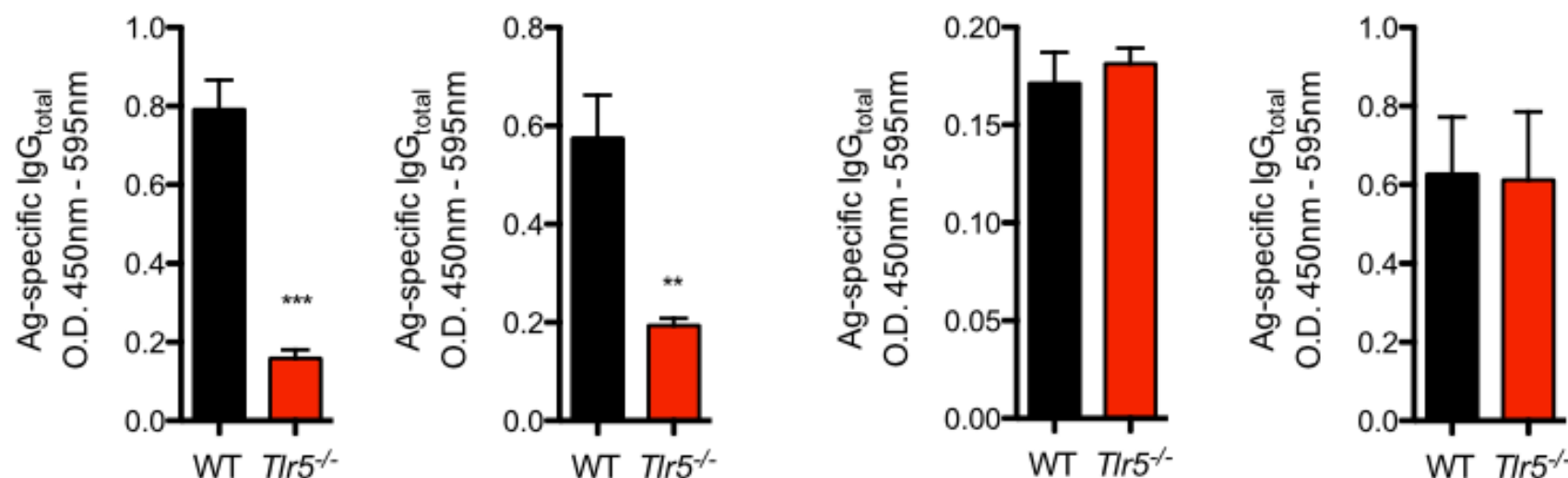
Not AdjuvantedAdjuvanted

TIV

IPOL

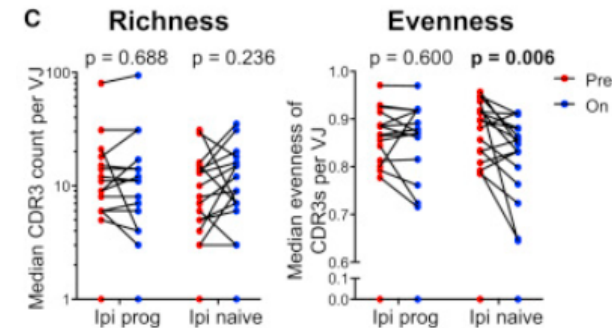
Recombivax HB (+Alum)

YF-17D

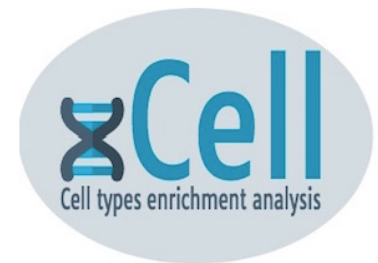


Additional Topics of Current Interest

- Single-cell genomics
- T and B cell repertoire analysis
- MHC (neo)epitope prediction
- Deconvolution of gene expression data
- Mining public datasets



Riaz et al., *Cell*, 2017



Challenges with Systems Immunology

- Large data sets require (a) simplification or (b) lots of time
- Integrative models of immune function don't exist (yet...)
- Complexity is exciting but intellectually daunting
- Some observations are difficult to study mechanistically
- New technologies may not have a “gold standard” for comparison or analysis
- New experimental designs or data combinations often require new analytical strategies

Questions?



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