

Milieu Interieur: 15 years of studying immune variability

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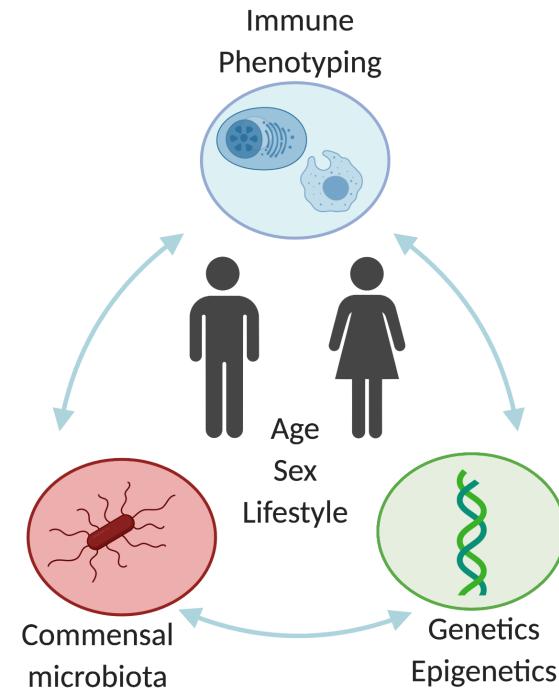


Milieu Interieur: concept and objectives

- ✓ Immune responses are highly variable
- ✓ We can dissect what causes this variance in healthy state
- **Hypothesis: A better understanding of this variability can identify new strategies for managing disease & health**



Claude Bernard 1813-1878



“La fixité du milieu intérieur est la condition de la vie libre et indépendante”



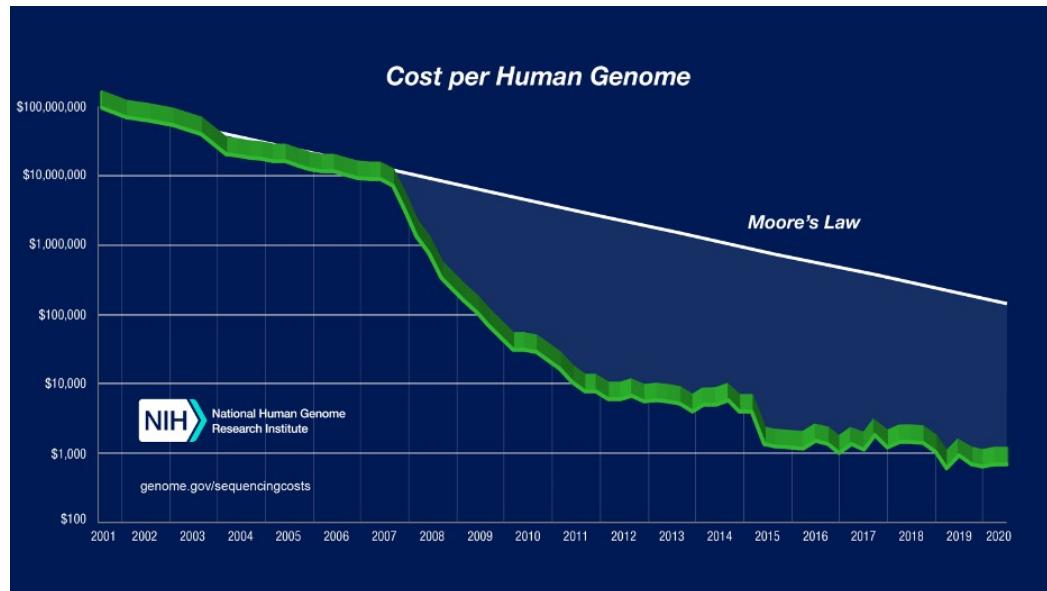
Matthew
Albert



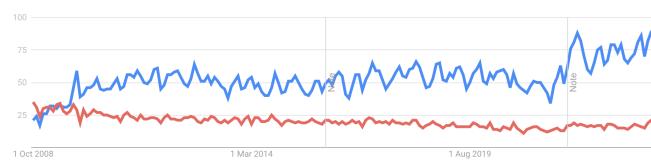
Lluis
Quintana-Murci

- ✓ Vaccine response
- ✓ Outcome to infection
- ✓ Cancer immunotherapy
- ✓ Autoimmunity / Allergy
- ✓ Neurologic disease and degenerations

Revolution in genomics has not lead to revolution in genetic clinical testing...



Google search trends since 2008



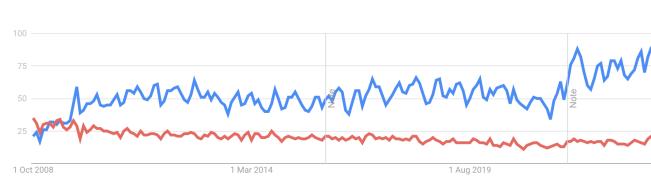
GWAS
Clinical
Genetics

Revolution in genomics has not lead to revolution in genetic clinical testing...

39 FDA approved pharmacogenomic Biomarkers



Google search trends since 2008



GWAS
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Genetics

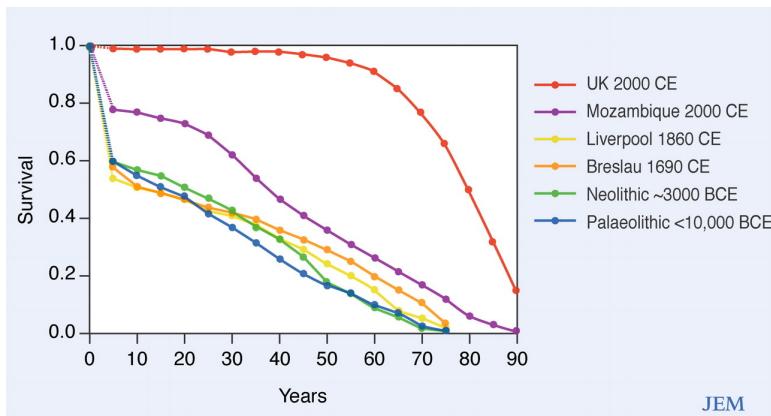
Biomarker	Disease Area
ALK	Oncology
Antithrombin III deficiency	Hematology
APOE2	Metabolic, Endocrinology
BRAF	Oncology
C-Kit	Oncology
CCR5	Antivirals
CD20 antigen	Oncology
CD25	Oncology
CD30	Oncology
CFTR (G551D)	Pulmonary
Chromosome 5q	Hematology
CYP1A2	Gastroenterology
CYP2C19	Multiple
CYP2C9	Analgesics, Hematology
CYP2D6	Multiple
DPD	Oncology
EGFR	Oncology
ER	Oncology
ER &/ PGR	Oncology
ERBB2 (HER2)	Oncology
Factor V Leiden (FV)	Oncology
FIP1L1-PDGFR α	Oncology
G6PD	Antiinfectives
HGPRT	Transplantation
HLA-B*1502	Neurology
HLA-B*5701	Antivirals
IL28B	Antivirals
KRAS	Oncology
LDL receptor	Metabolic & Endocrinology
NAT1; NAT2	Cardiovascular
NAT1; NAT2	Antiinfectives
PDGFR	Oncology
Ph Chromosome	Oncology
PML/RAR α	Oncology
Prothrombin mutations (F2)	Oncology
TPMT	Rheumatology
UCD	Gastroenterology
UGT1A1	Oncology
VKORC1	Hematology

Only 5 for infectious disease

Biomarker	Disease Area	Drug
CCR5	HIV	Maraviroc
G6PD	Malaria	Chloroquine
HLA-B*5701	HIV	Abacavir
IL28B	HCV	Peginterferon alfa-2b, Boceprevir, Telaprevir
NAT1; NAT2	TB	Rifampin, Isoniazid, and Pyrazinamide

Genetics reflects our evolutionary history & environment our modern present

Life expectancy ~25 years
(pre-industrial revolution)

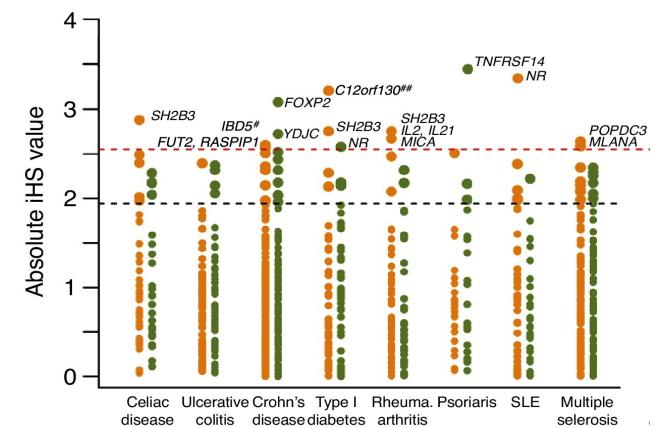


Clean water &
Environments
Antibiotics
Vaccines

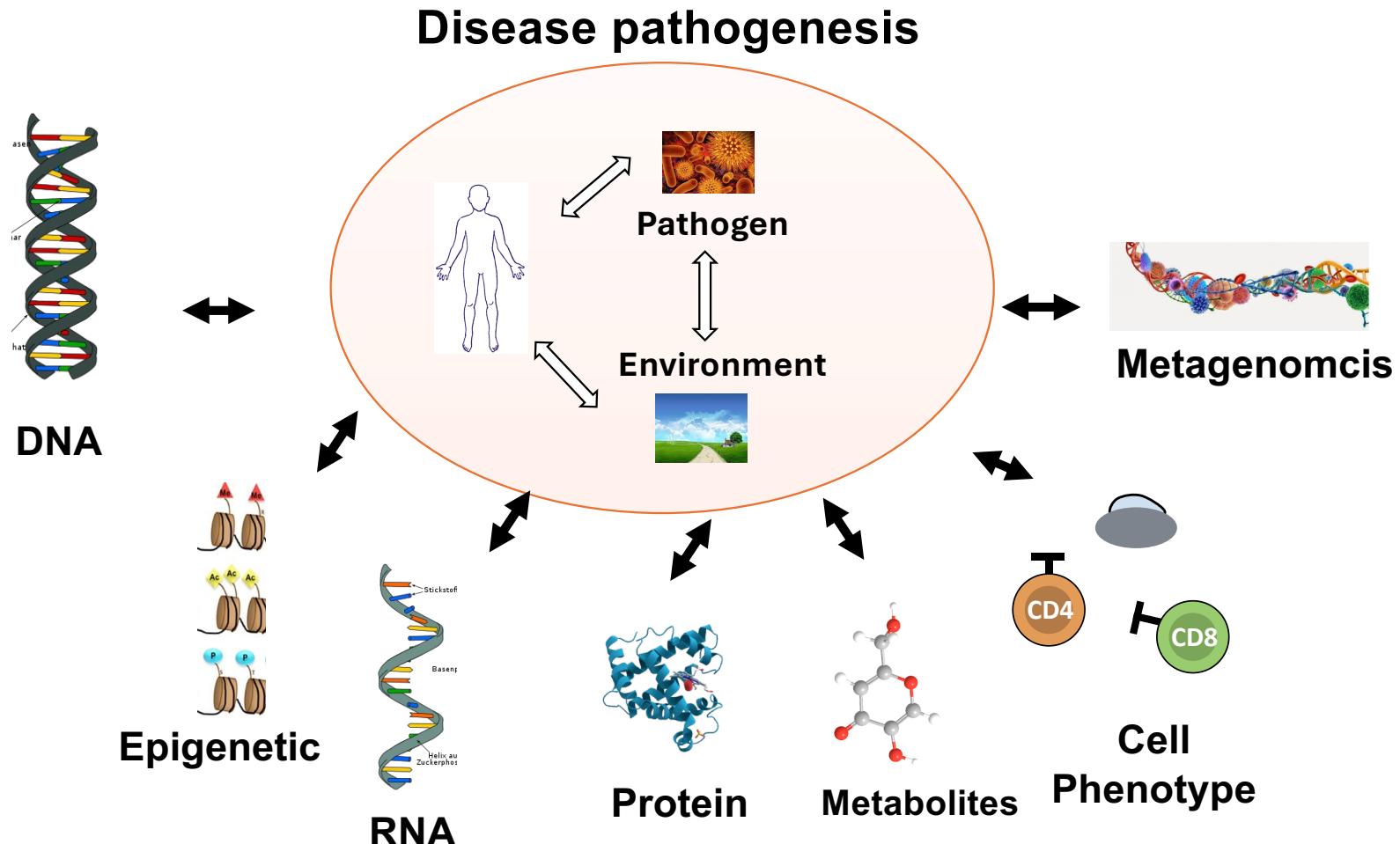


Rich diets
Alcohol & smoking
Sedentary lifestyles
Pollution

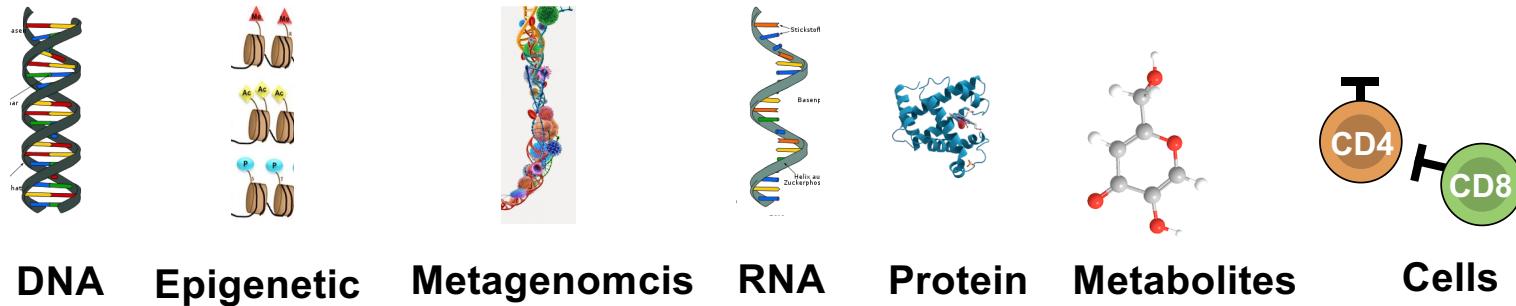
Genes with recent evolutionary selection
→ autoimmune/inflammatory diseases



Binary approach to identify correlates to treatment response

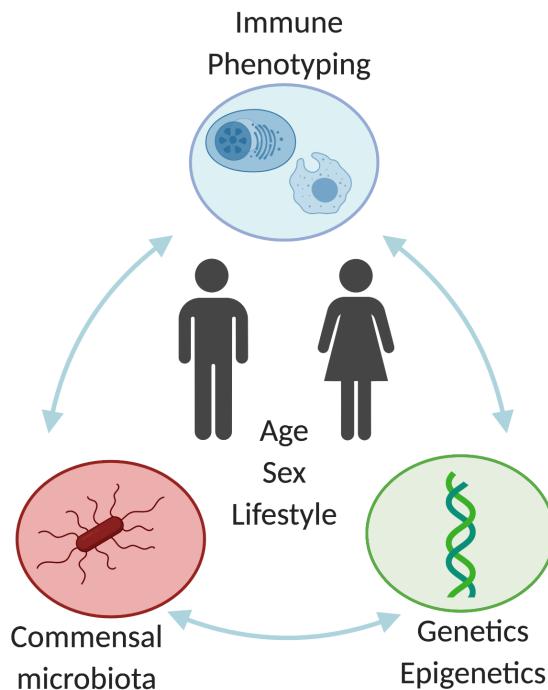


Milieu Interieur: integrated systems biology approach



1. Define the “normal boundaries” of a functional healthy immune response & identify outliers
2. Associate natural immune variance with physiological, environmental, & genetic factors
3. Comparison studies in disease populations

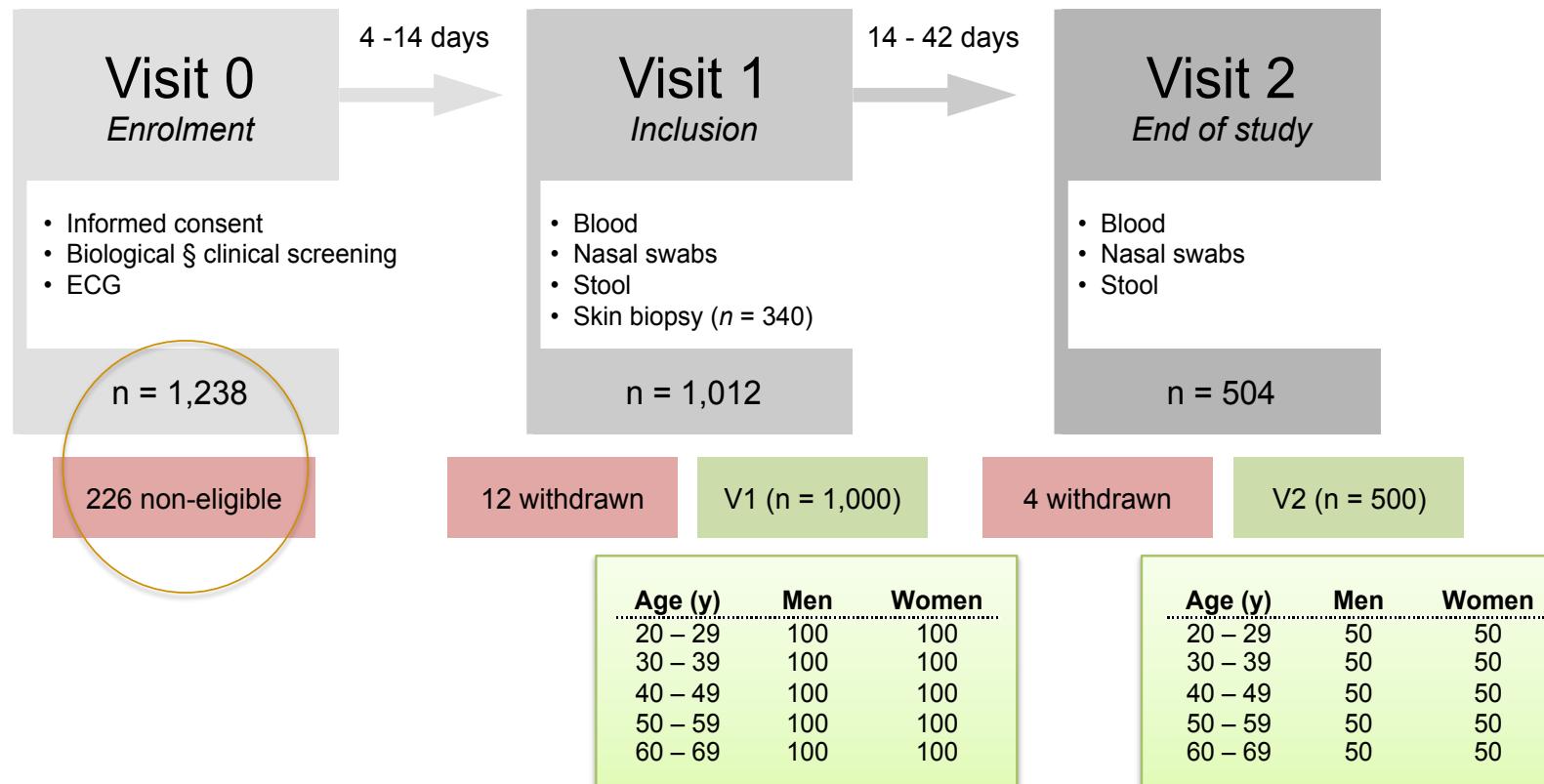
How to define “healthy” ?



Inclusion Criteria	Exclusion criteria (for complete list see Supplementary Text)
<ul style="list-style-type: none"> Subjects considered as healthy by the investigator based on medical history, clinical examination, laboratory results and ECG[§] Availability for all scheduled visits at the investigational site. Healthy male or female aged between 20 and 69 (included) years Metropolitan French origin for 3 generations $18.5 \leq \text{BMI} \leq 32 \text{ kg/m}^2$ Ability to give their informed consent in writing Must understand spoken and written French Affiliated to the French social security or assimilated regimens Registered on the French “Fichier des Volontaires se prêtant à la Recherche Biomédicale (VRB)”** 	<ul style="list-style-type: none"> Relatedness to previously recruited individuals in the study cohort Travel in (sub-)tropical countries within the last 3 months For women: pregnant or breastfeeding or intending to become pregnant or perimenopausal Any physical exercise within the last 8 hours before inclusion (V1) and before (V2) Subjects following a special diet for medical reasons Alcohol abuse Illicit drug use or substance abuse within 3 months prior to inclusion Presence of evidence of neurological or psychiatric diagnoses Severe/chronic/recurrent pathological conditions Chronic administration of immunosuppressants or other immune-modifying drugs within the 6 months prior to the inclusion Receipt of any vaccination 3 months before the inclusion Receipt of blood products or immunoglobulins within 3 months prior the inclusion Hemoglobin measurement less than 10.0 g/dL for women and less than 11.5 g/dL for men Platelet count less than 120.000/mm³ ALT and/or AST > 3 times the upper limit of the norm[†] Allergy to lidocaine

Recruitment of 1000 healthy donors

- Donors recruited at one site in Rennes (Biotrial) from September 2012 – July 2013



Establishing a rich healthy donor biobank and data warehouse



1,000 Healthy donors
Well-defined healthy state
500 men/women
20-69 yrs

Clinical data



Serology



Whole blood



Whole blood
stimulations



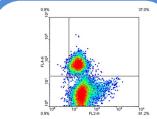
Stool



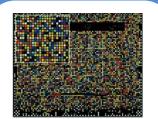
Nasal Swabs



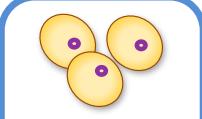
eCRF



Cytometry
Panels



Genotypes
+methylation



TREC: Thymic
Function



Plasma
proteins



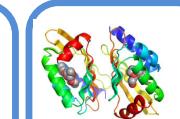
Supernatant:
Protein



Cell Pellet:
Transcriptome



Enterotypes



Cytokines



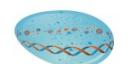
Antibodies



Virus &
Microbiome
16S

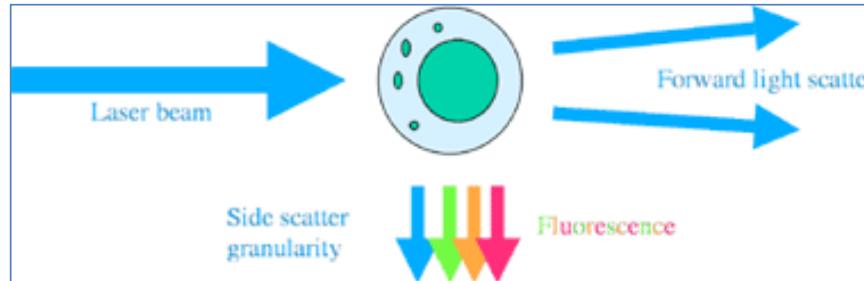
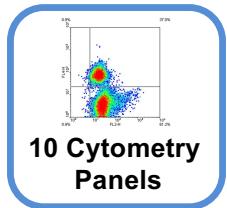


Centre for
Immunology & Infection
免疫與感染研究中心



Milieu Intérieur
Vers une médecine personnalisée

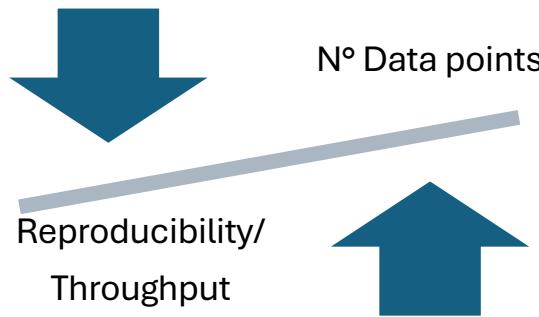
Flow cytometry – characterising multi-parameter cellular populations



Standard Flow (8-12 colours)



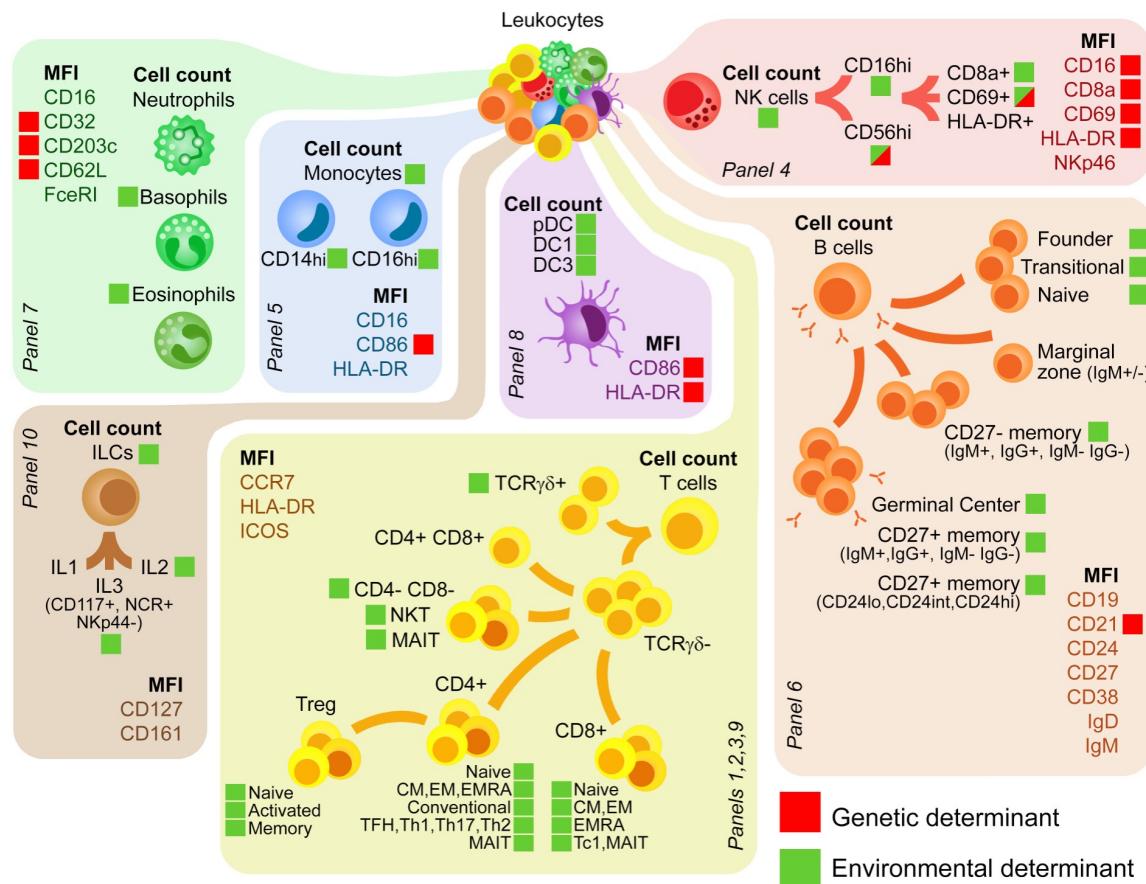
CyTOF – Mass Spec based (>50)



Genetic and environmental determinants of circulating immune cells

x10 panels 8 colour flow cytometry

- 74 subpopulations quantified
- 89 cell surface marker expression



Patin E, Hasan M, Bergstedt J, Rouilly V et al (Nat Imm 2018)



Milena Hasan



Etienne Patin



Jacob Bergstedt



Vincent Rouilly

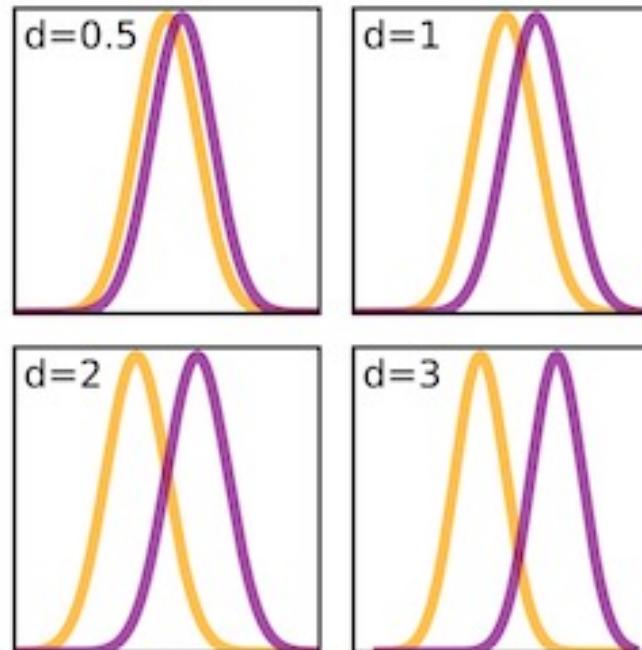
What does an effect size measure ?

Significance: tells how likely it is that a result is due to chance

Effect size: tells you how important the result is

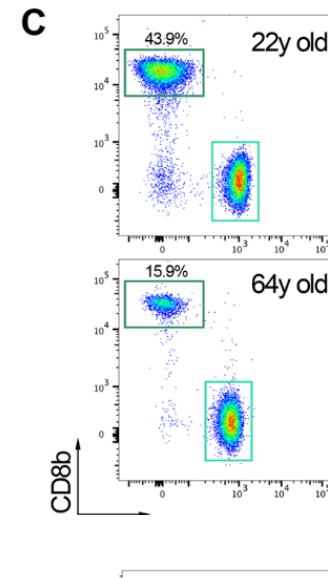
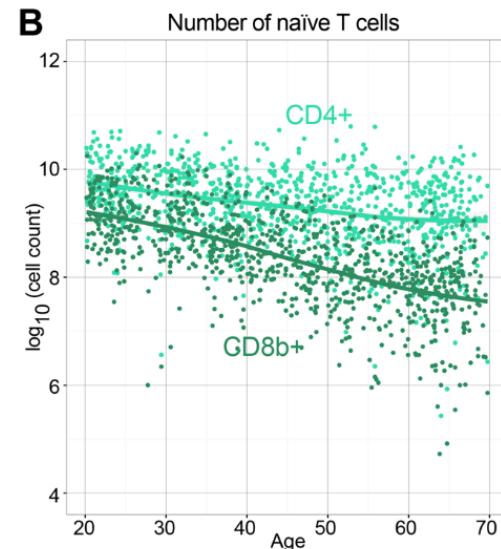
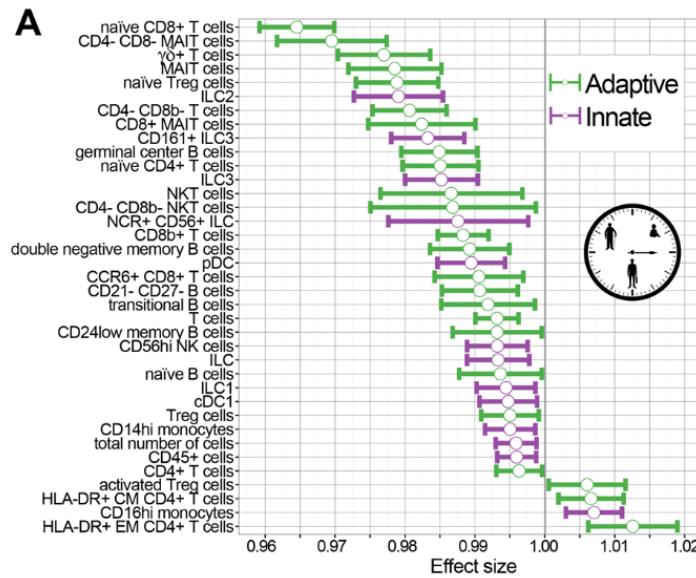
$$\text{Cohen's } d = (x_1 - x_2) / s$$

x_1 and x_2 are the sample means of group 1 and group 2,
 s is the standard deviation of the population from which the two groups were taken



Dissecting environmental determinants of Immune cells - Age

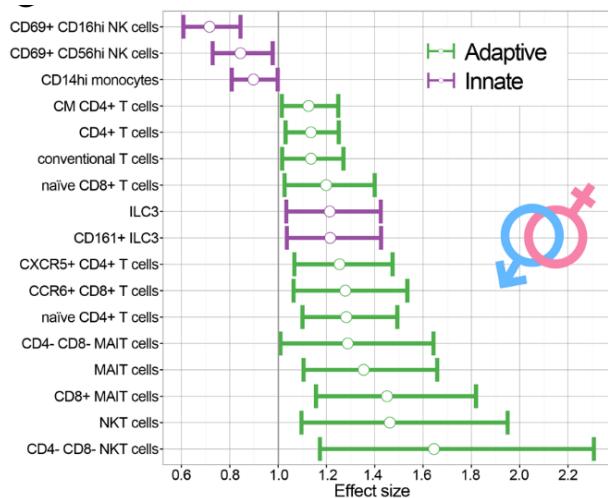
42/74 subsets affected by age



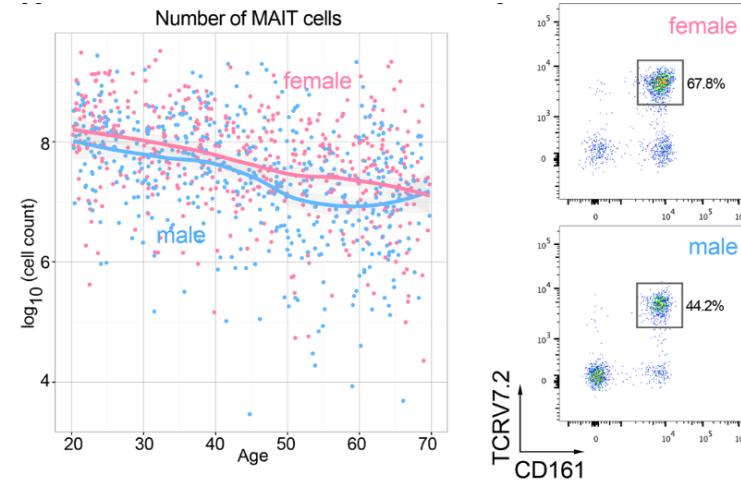
- No increase with age of memory T cells
- Stronger decline with age of naïve CD8+ T cells, with respect to CD4+ (3.5% and 1.5% per year, respectively)
- CD8+ T cells are more susceptible to homeostatic cytokines and/or the production of CD4+ T cells is preferentially enhanced in the human thymus?

Dissecting environmental determinants of Immune cells - Sex

17/74 subsets different between sexes

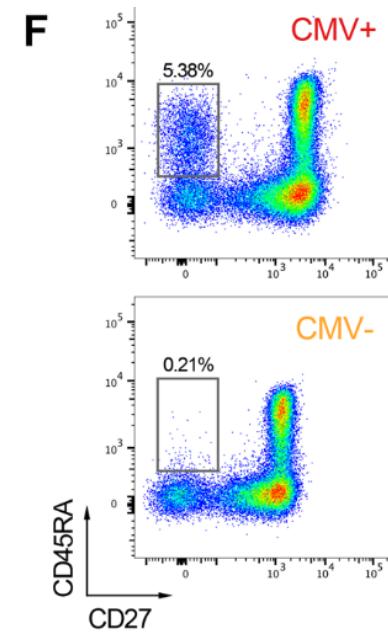
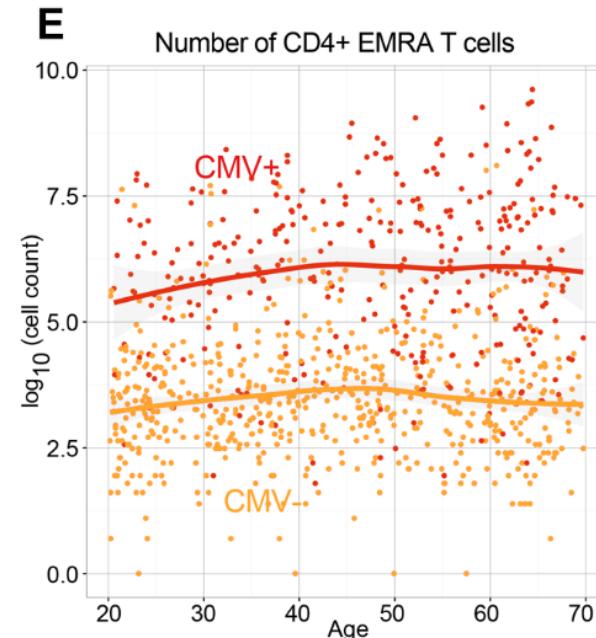
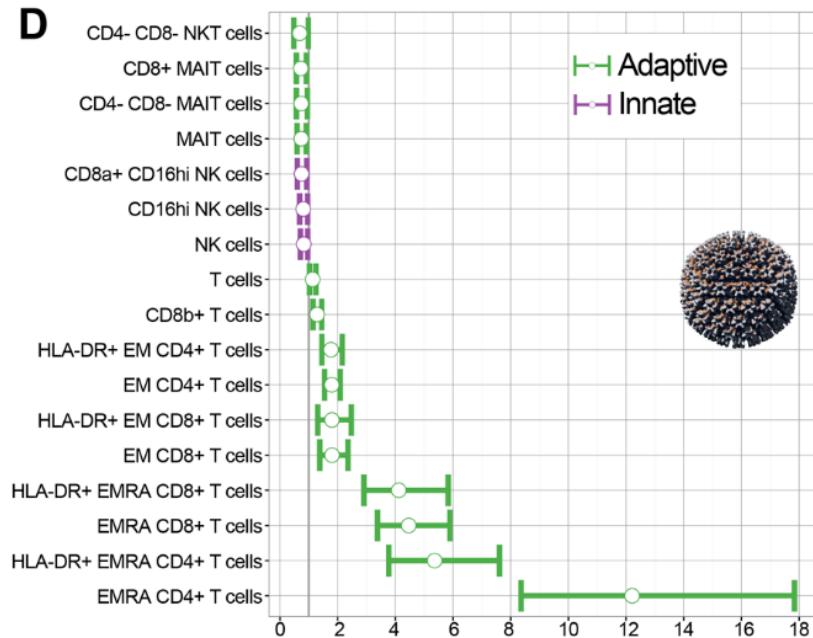


MAIT cells
Sex effect 1.39/Age effect 0.97



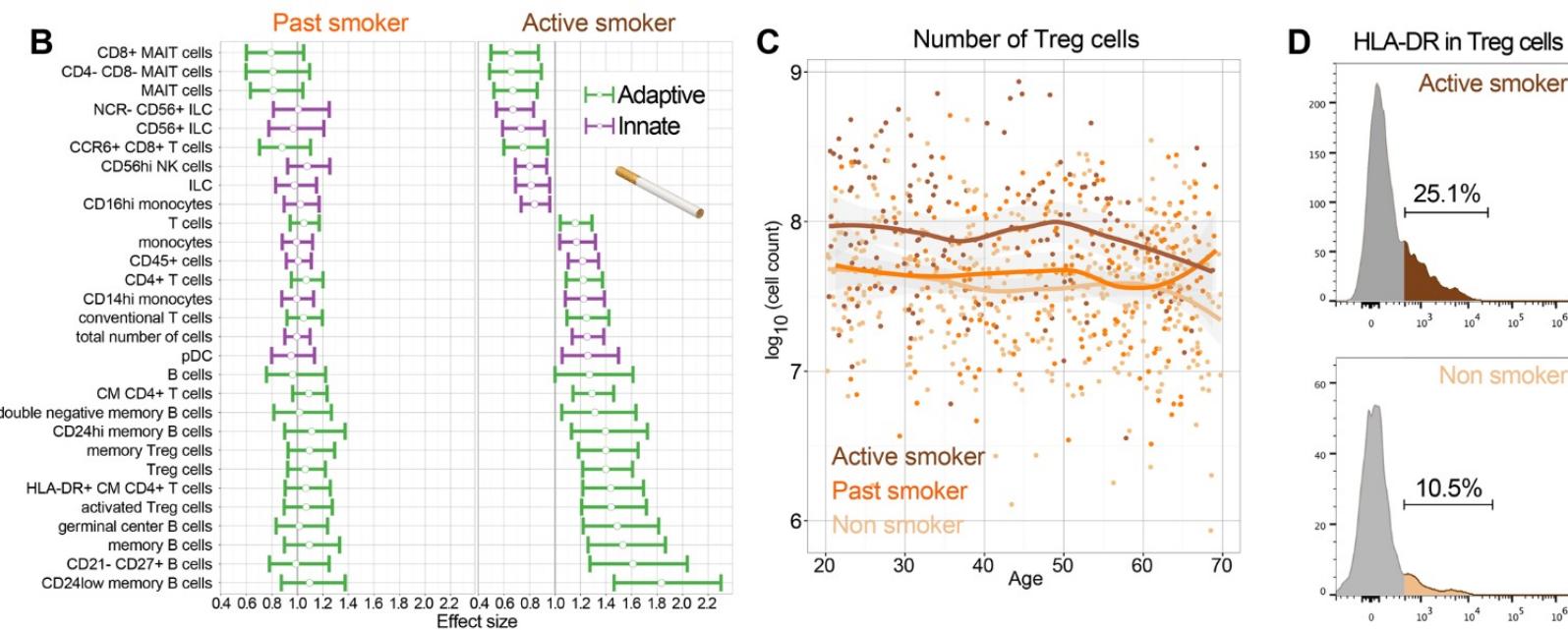
- Women have greater numbers of MAIT cells, NK T cells, naive CD4+ T cells, ILC3
- Men have greater numbers of CD14^{hi} monocytes, NK cell subsets

Dissecting environmental determinants of Immune cells - CMV



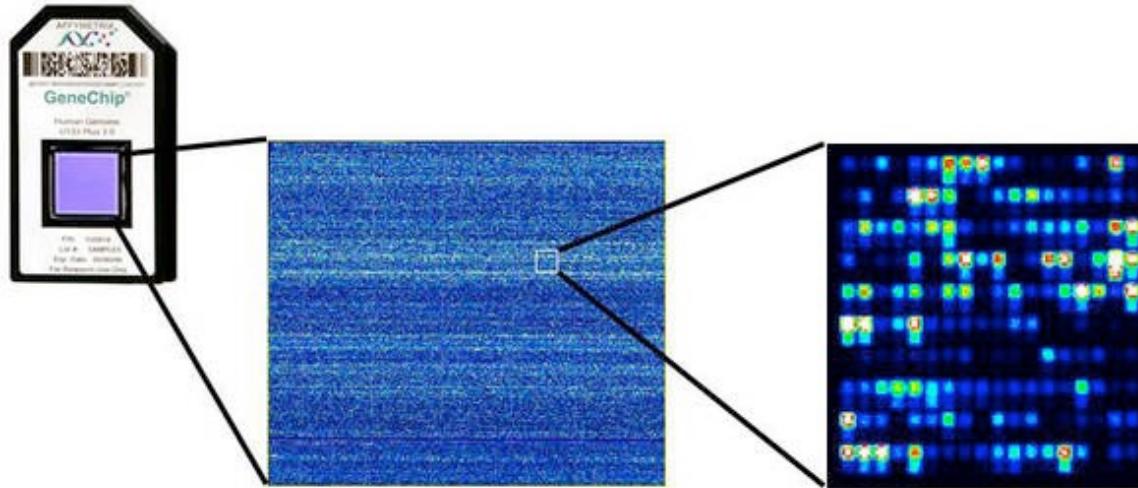
→ CMV seropositivity associates with the presence CD4+ and CD8+ T_{EM} and T_{EMRA} compartments, but not naïve T cells and T_{CM} compartments, suggesting independent regulation of the naïve and EM/EMRA T cell pools

Dissecting environmental determinants of Immune cells - Smoking

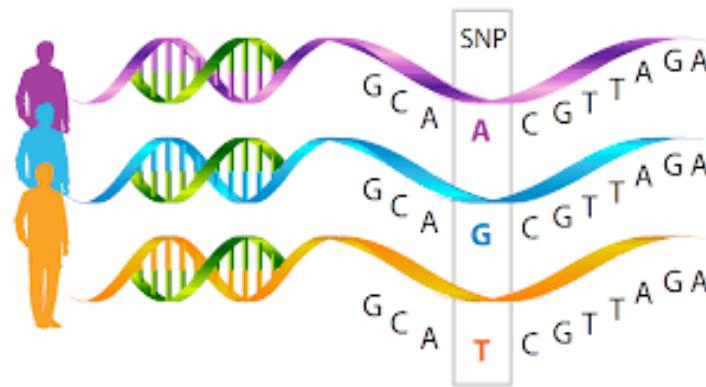


→ The increase in Treg cells may contribute to the diminished Th1 immunity observed in smokers, and the increased susceptibility to bacterial infection

Genome wide association studies -GWAS

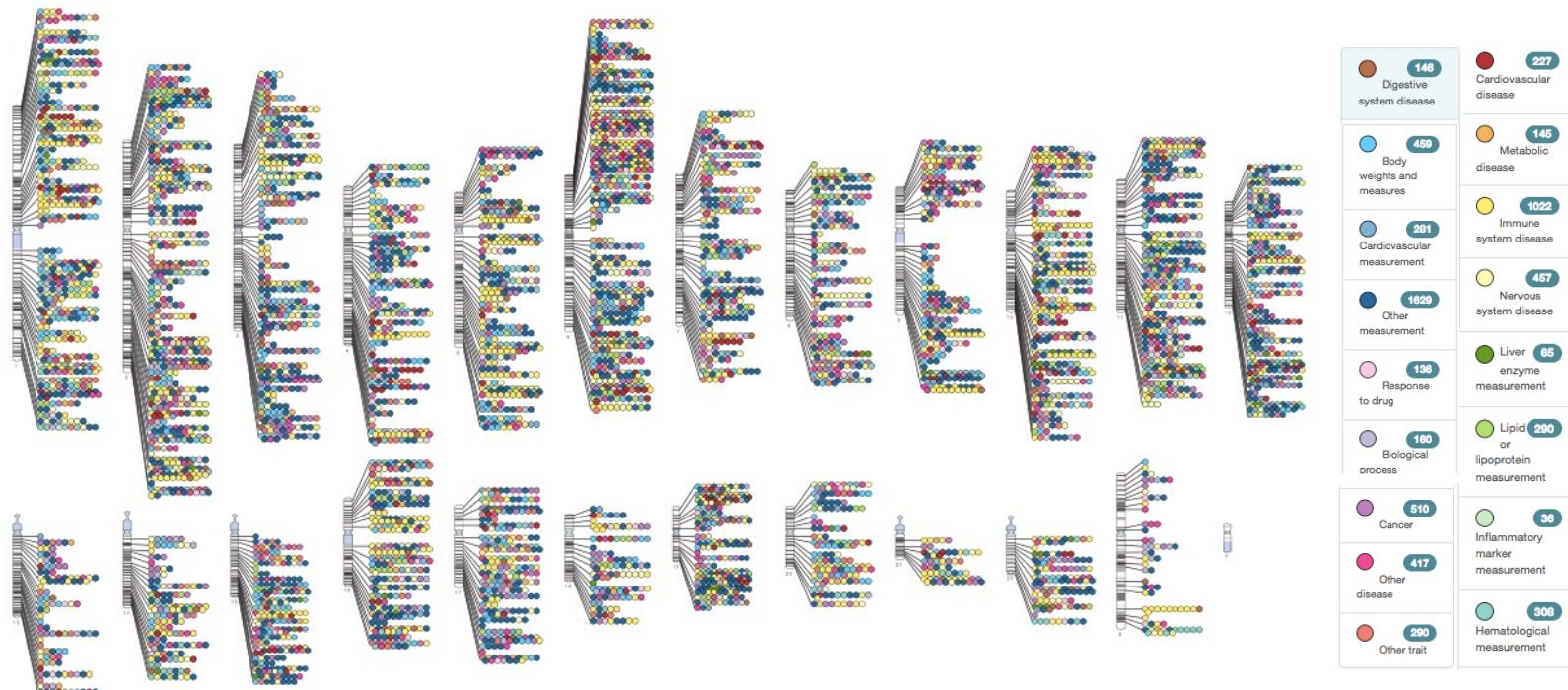


SNP: Single Nucleotide Polymorphisms: 10^6 differences within 10^9 nucleotides estimated to account for 90% genetic variability in humans

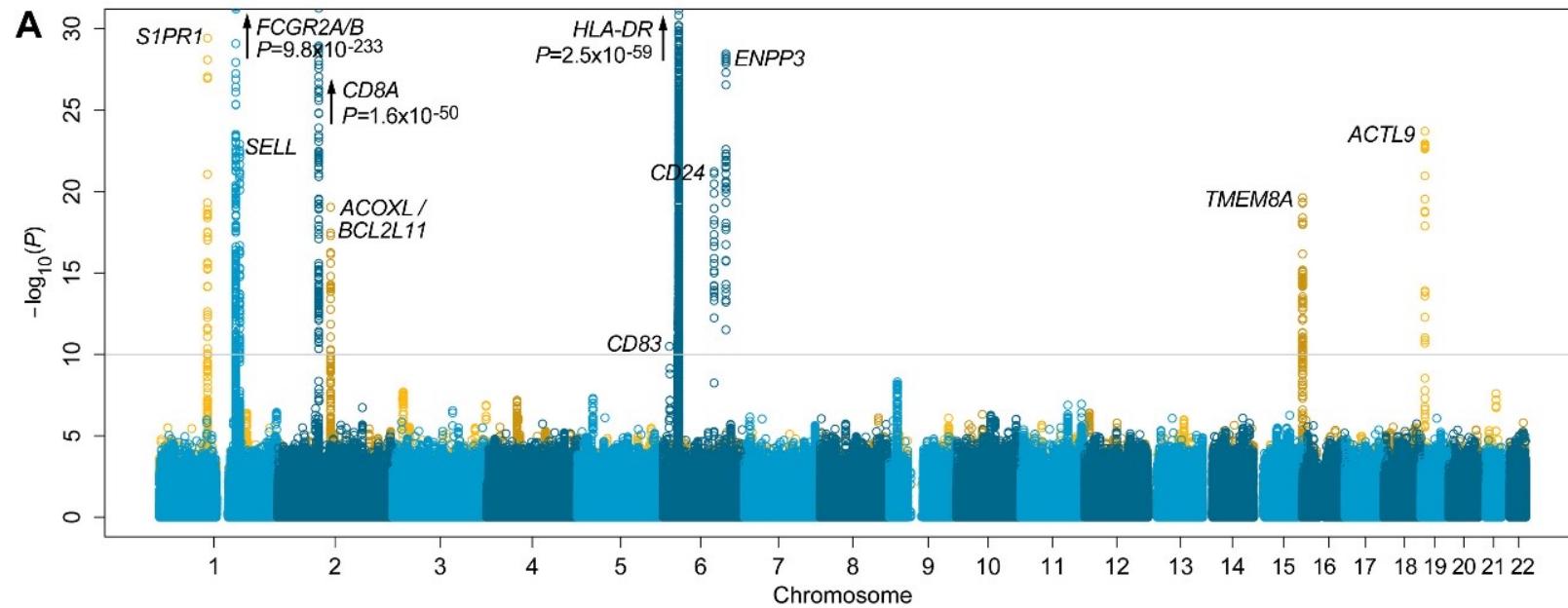


Genome wide association studies -GWAS

GWAS Catalog: a quality controlled, manually curated, literature-derived collection of all published genome-wide association studies with at least 100,000 SNPs and all SNP-trait associations with p -values $< 1.0 \times 10^{-5}$



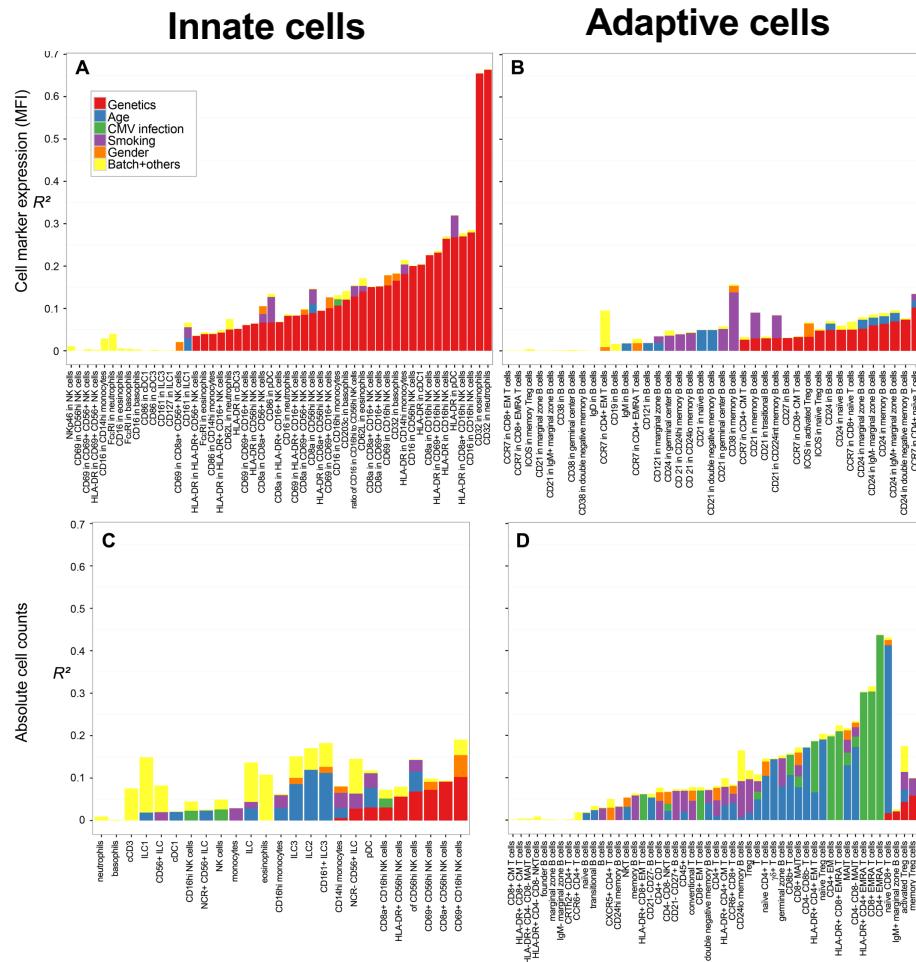
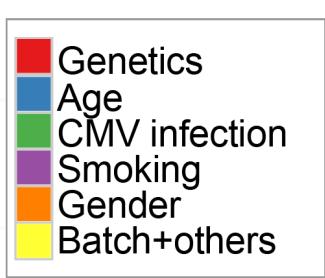
Dissecting genetic determinants of Immune cells



- 14 independent loci are genome-wide significant ($P < 10^{-10}$), of which 11 are novel
- 10 are local pQTLs of cell-surface expression of immune cell markers (CD32a/b, CD62L, CD24, CD8a, HLA-DR, CD203c)
- 4 are *trans*-acting QTLs associated with either cell counts and MFIs (*S1PR1*, *BCL2L11*, *TMEM8A*, *ACTL9*)

Variation in innate immune cells is driven by genetic factors

Linear mixed models applied to each Immune cell phenotype



Patin E, Hasan M, Bergstedt J, Rouilly V et al (Nat Imm 2018)

Can we identify the same genetic and environmental associations for induced immune responses?

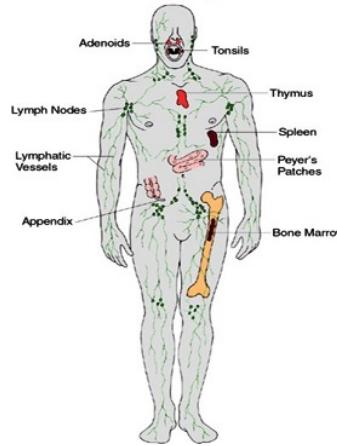
Standardized profiling of induced immune responses

How is your immune system feeling today ?



Robust Diagnostics for Cardiology

- ✓ Blood pressure
- ✓ Electrocardiogram
- ✓ Cholesterol testing



Assessing the Health of your Immune System

???



TruCulture: standardized immunomonitoring

Standardization of immunophenotyping

- Recent progress in standardizing immunophenotyping readouts



- Sample source and preparation equally important to reduce technical variability
→ Particularly for studying **induced immune responses**

Current “bronze standard” based on PBMC stimulation

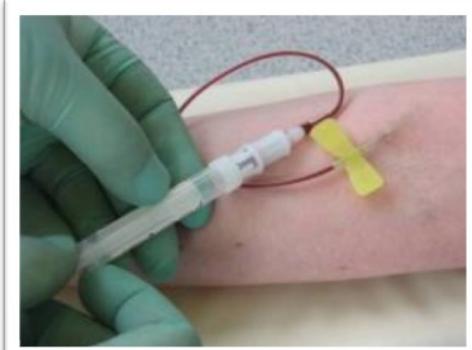
→ source of huge variability through

- Transport of blood (eg time, temperature)
- Ficoll separation of leukocytes
- Freeze/Thaw of cells
- Removal of granulocytes, platelets, plasma



Setting up a TruCulture

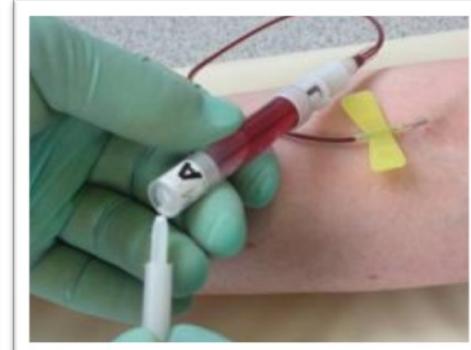
TruCulture: syringe based device for whole blood collection and incubation



A) Pre-fill tubing with blood



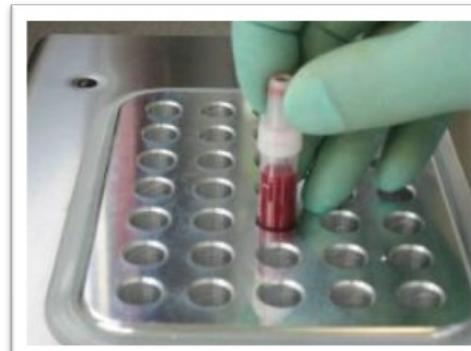
B) Pull, until it “clicks”



C) Break away plunger



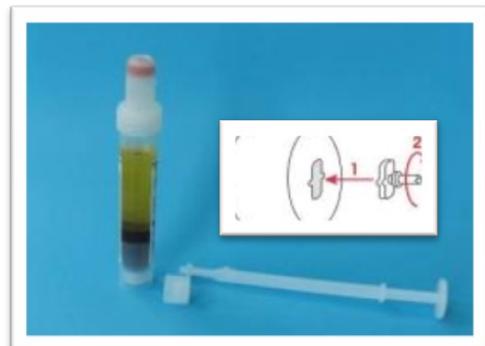
D) Mix gently 3x (end-over-end)



E) Incubate for defined time (1-48hrs)

Harvesting a TruCulture

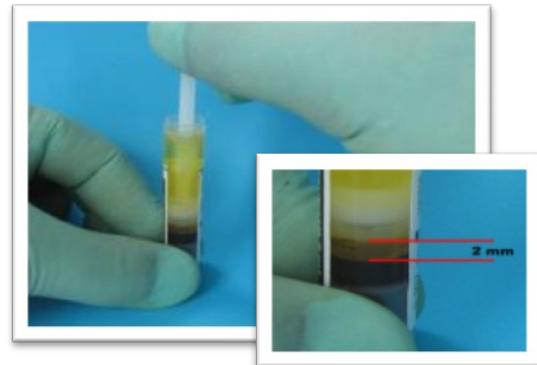
TruCulture: syringe based device for whole blood collection and incubation



1) Assemble valve separator



2) Insert valve separator

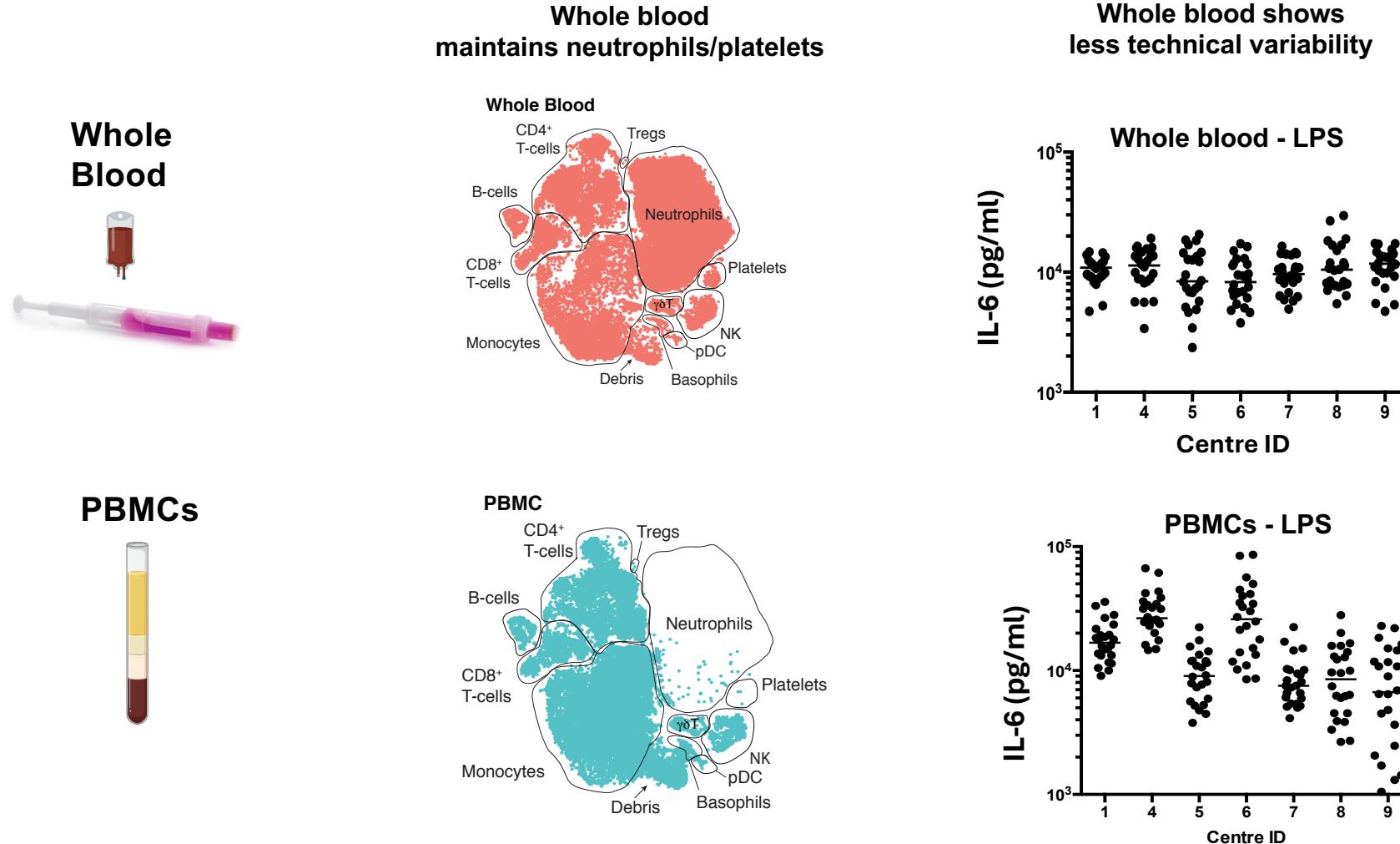


3) Push down, leave 1-2 mm between
septum and cells

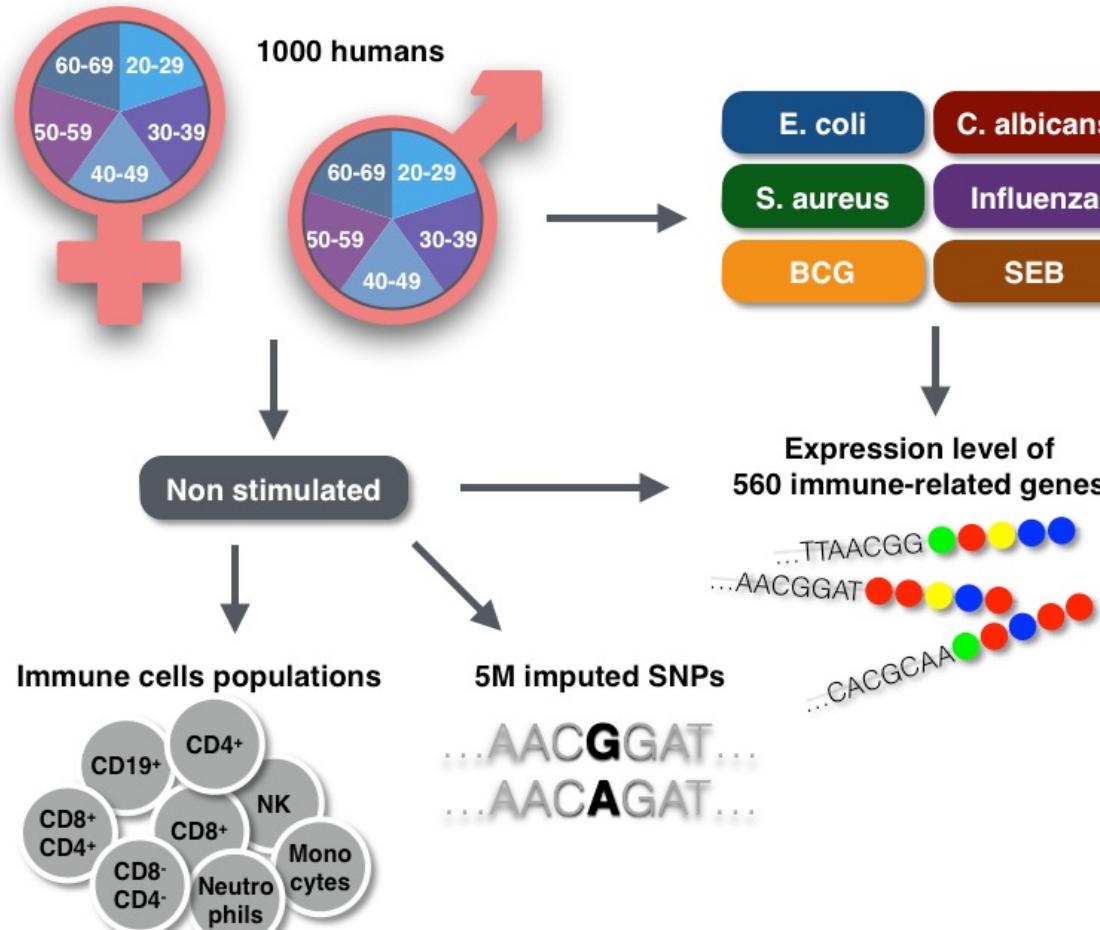


4) Remove rod and discard;
close tube and freeze at -20°C
(or aliquot supernatant for stabilizing RNA)

Whole blood maintains granulocytes, platelets & plasma matrix



Studying variability in induced transcriptomic responses to microbial stimuli



Alejandra Urrutia



Bruno Charbit



Celine Posseme

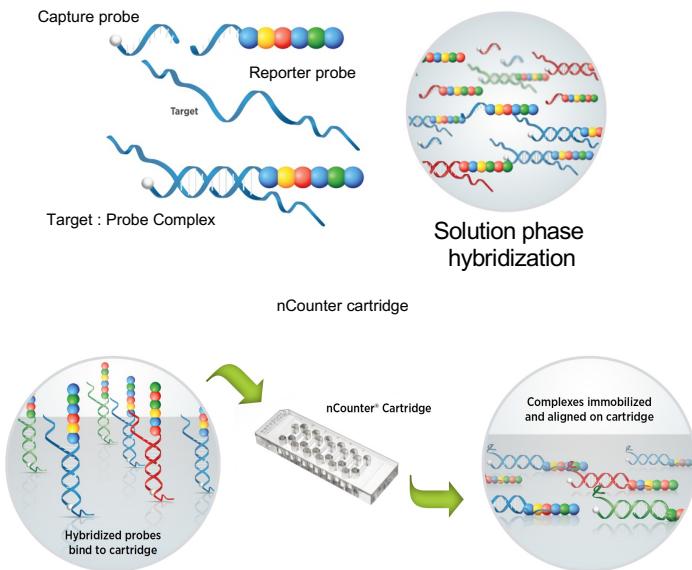


Barbara Piasecka

Standardization of mRNA signatures

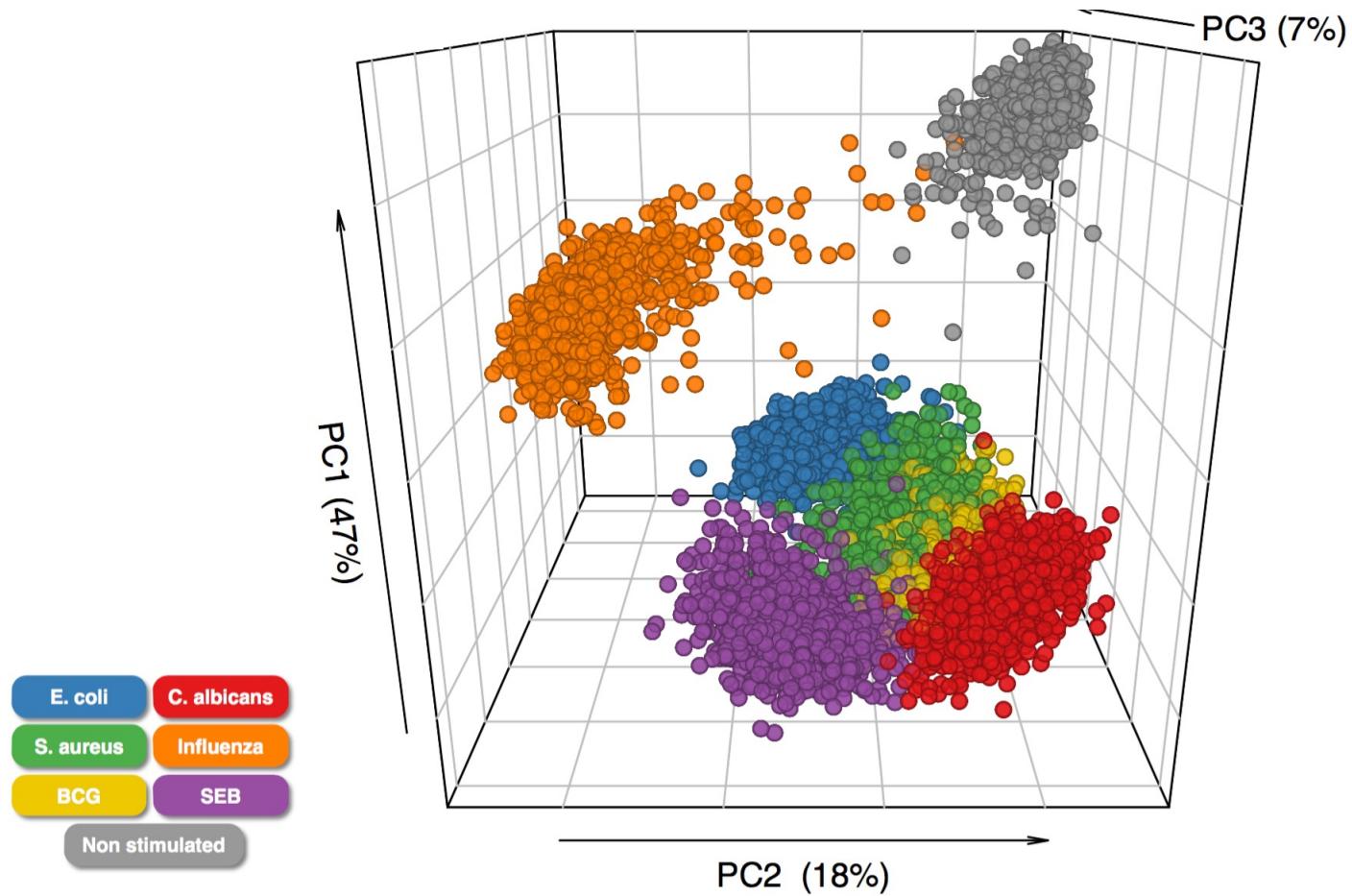
Hybridisation Arrays

No amplification step

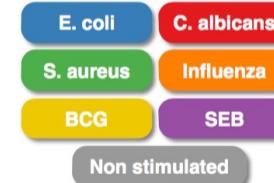
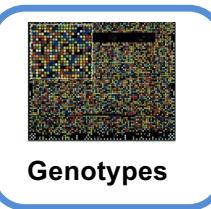
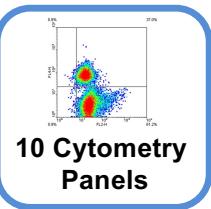
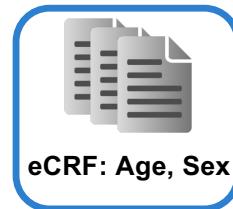


Technology	Method	Gene set	Adaptable for use with whole blood
Fluidigm Biomark	Microfluidic-based PCR	80 genes	<ul style="list-style-type: none"> • cDNA preparation required = pre-analytical bias • PCR reaction inhibited by presence of heparin
Nanostring nCounter	RNA Hybridization	780 genes	<ul style="list-style-type: none"> • Absolute counts • suitable for partially extracted RNA
Affymetrix	cDNA Hybridization	Whole genome	<ul style="list-style-type: none"> • requirement for high quality RNA • cDNA preparation required = pre-analytical bias
Ion Torrent	NGS	Whole genome	<ul style="list-style-type: none"> • requirement for high quality RNA • globin RNA dominate read count (90% of total RNA)

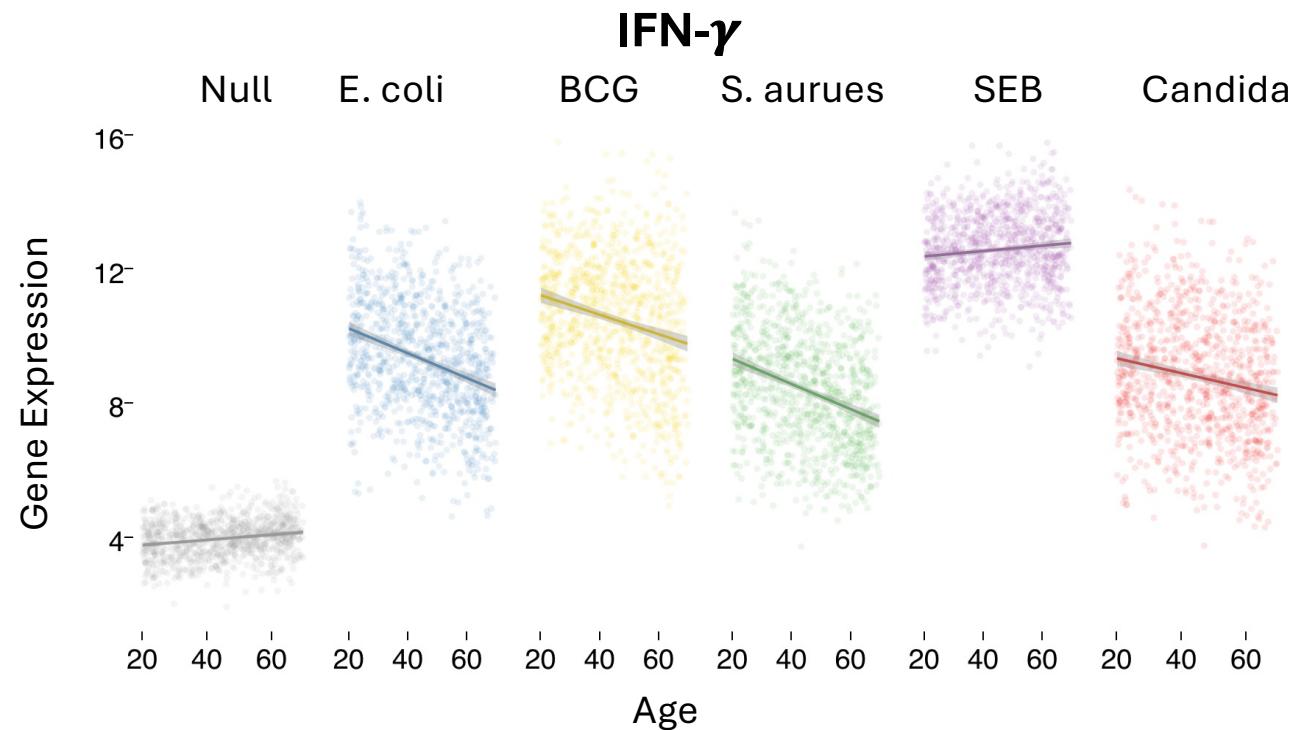
Differential changes in expression induced by stimulations



Age associated changes in induced gene expression in healthy donors

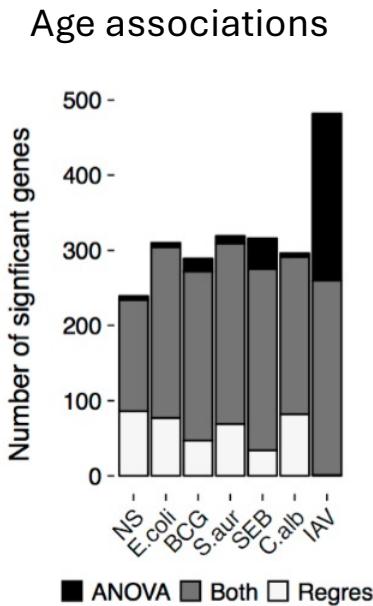


473/560 genes show a significant age associated effect (FDR<0.01, n=1,000)



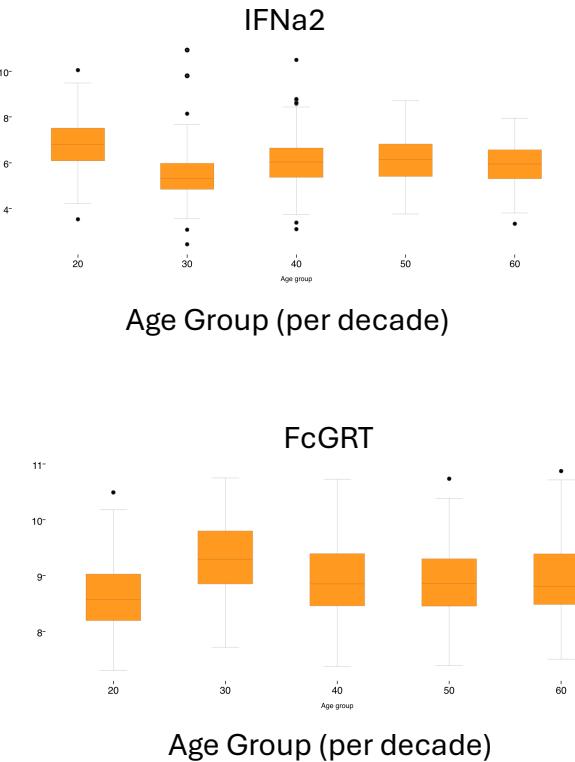
Piasecka B, Duffy D et al (PNAS 2017)

Age associated changes in influenza induced gene expression



87 genes
20-29yr > 30-39yr
Tukey HSD test; $p < 0.05$
Enriched in innate response genes
($p = 6.5 \times 10^{-3}$ InnateDB)

119 genes
20-29yr > 30-39yr
Tukey HSD test; $p < 0.05$



H1N1 (A/PR/8/34 strain)

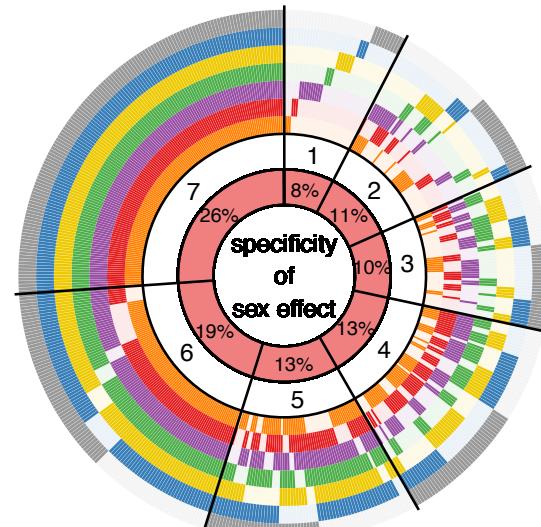
Hypothesis: Reflects pre-existing serological immunity in 30yr+ donors (Nat Imm Sobolev 2015)
and a H1N1 antigenic shift around 1983

Or

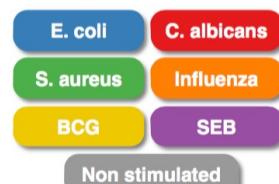
Reflects real age related differences in response to influenza (Sci Imm HIPC-CHI 2017)

Integration of clinical, flow cytometry, genetics & transcriptomic responses

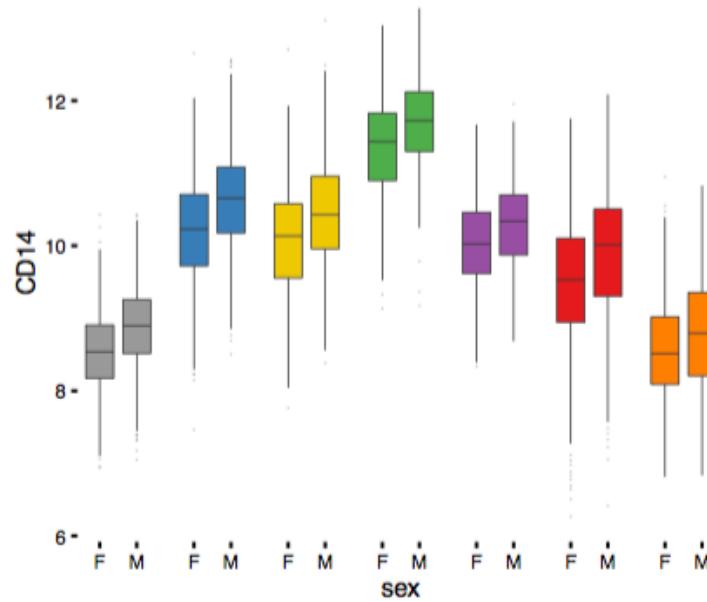
Sex effects are more common across stimuli – 48% shared across 5 stimuli



509/560 genes: (FDR<0.01)



Common sex association (CD14)

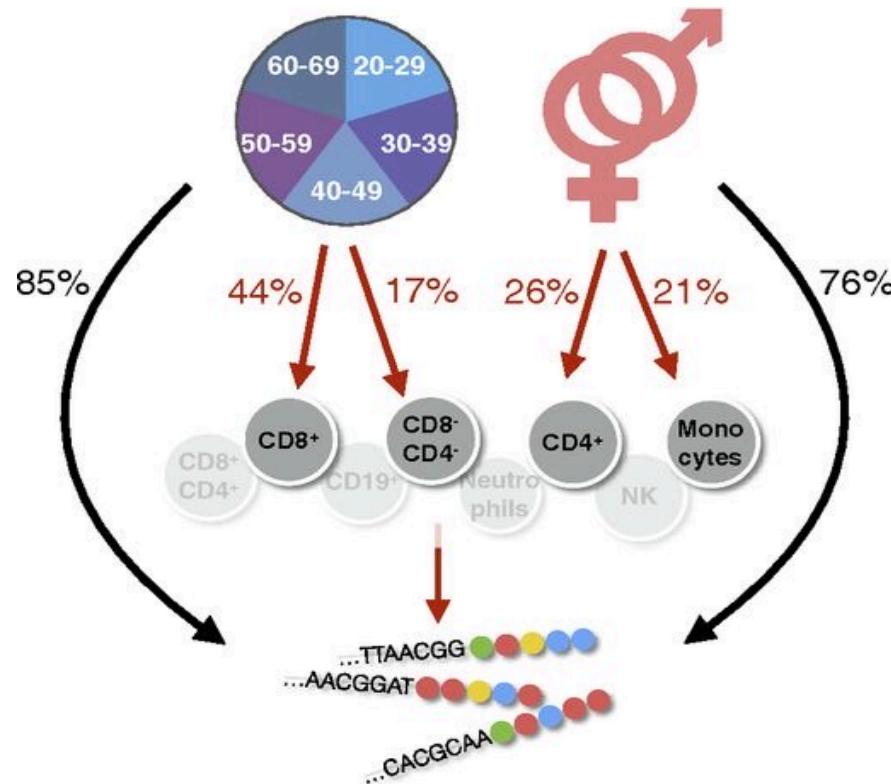


Testing direct versus indirect effects of age and sex on immune responses

Are age and sex directly affecting gene expression changes or are these changes mediated through cellular changes ?

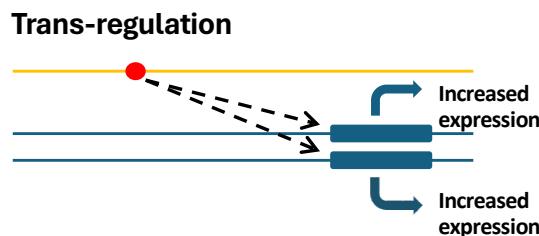
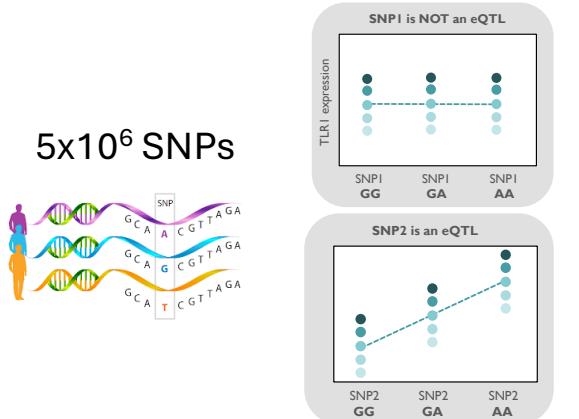
Structural equation modelling

Each age/sex associated gene: model with 8 indirect effects (each cell type) & one direct effect

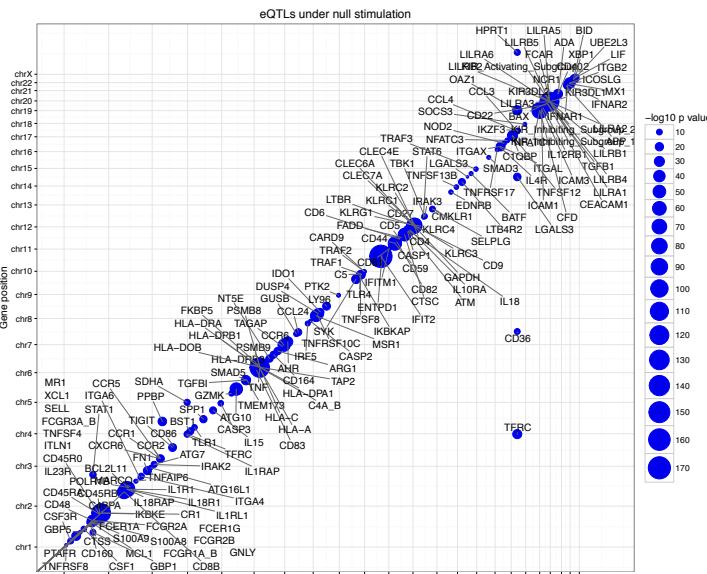


How to identify genetic associations with immune responses ?

Quantitative Trait Loci mapping (QTL)

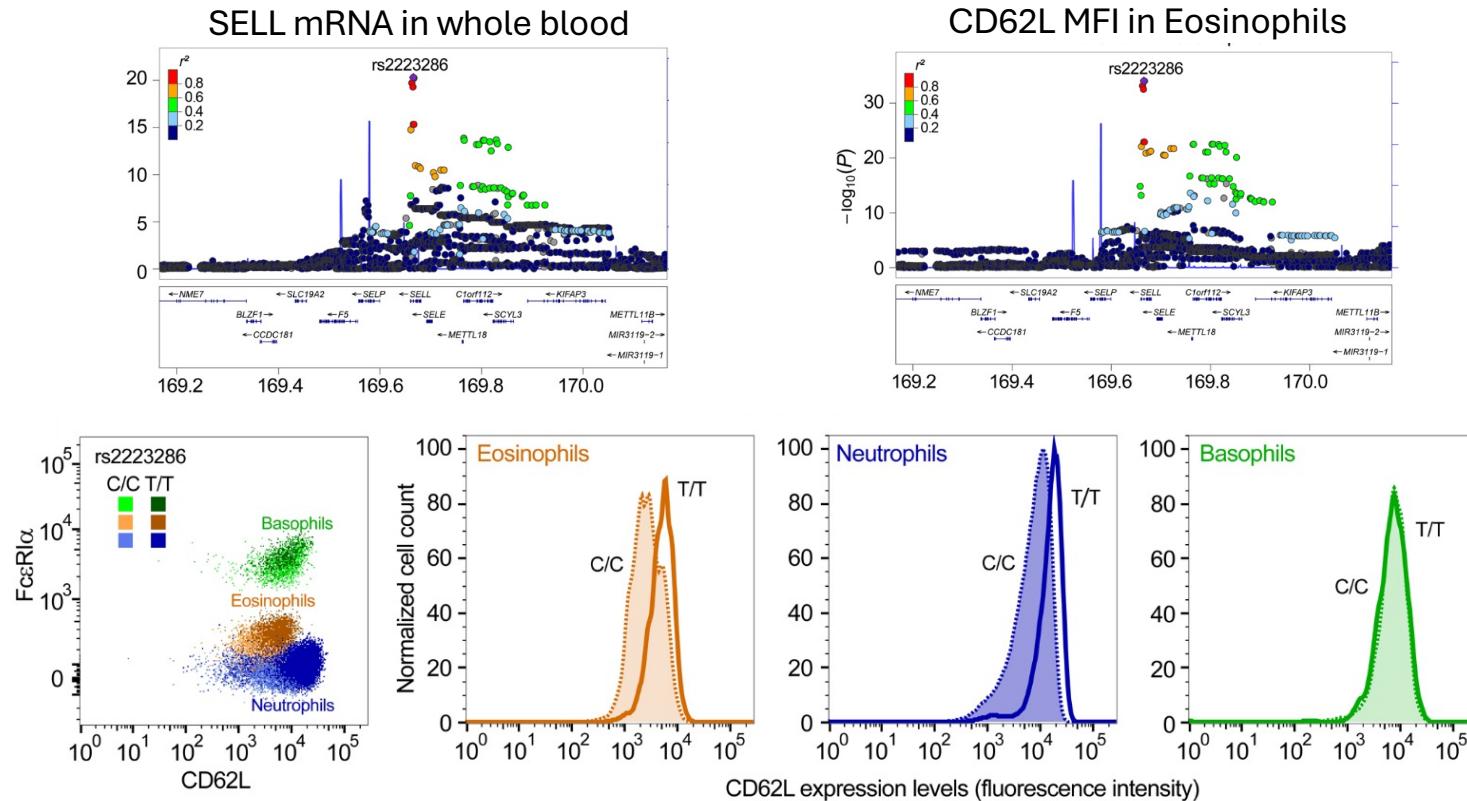


Null control



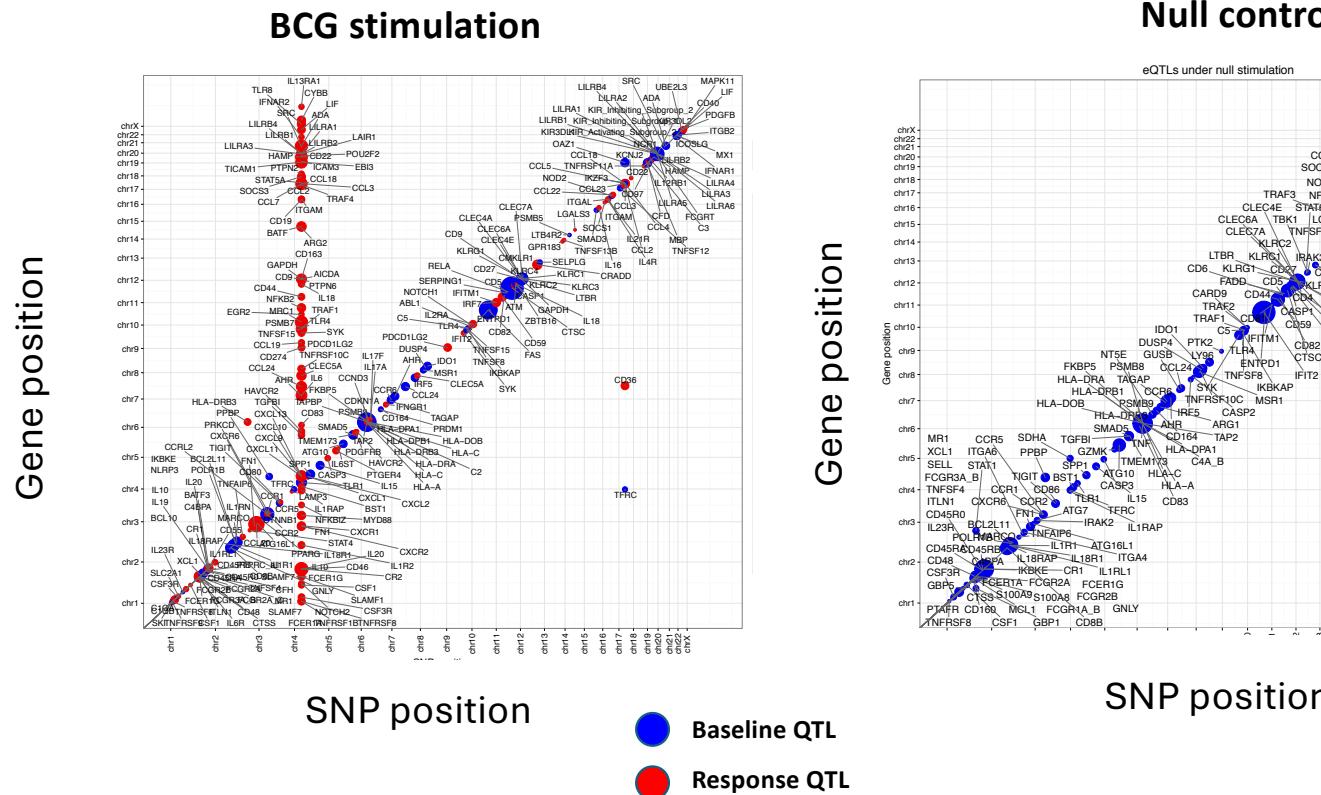
SNP position

Integrating transcriptional & flow cytometry data sets to identify cellular determinants of genetics



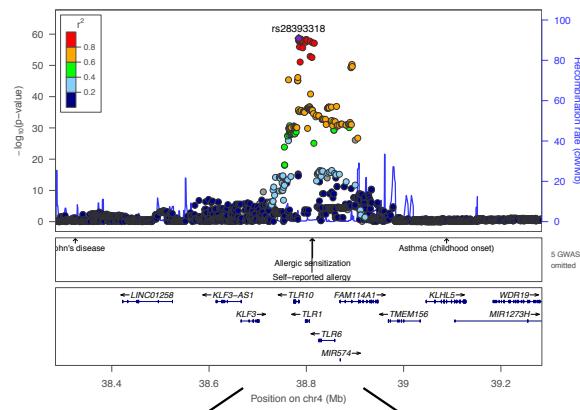
→ Cell specific pQTLs: MFI in eosinophils ($P = 9.2 \times 10^{-35}$) and neutrophils (4.6×10^{-14}) but not in basophils
 TT allele: higher expression in monocytes/lower in B cells (Fairfax Nat Gen 2012)

Mapping Quantitative Trait Loci (eQTL) identifies novel genetic associations

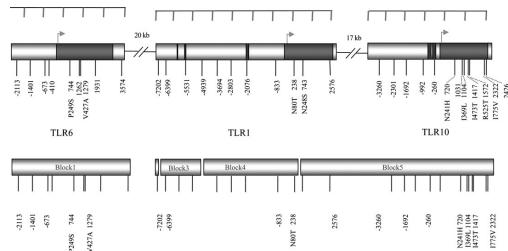


TLR 10/1/6: master regulator of bacterial induced expression

Genetic variability in Europeans



TLR 10 / 1 / 6 genetic locus



(Quach *et al* Cell 2016)

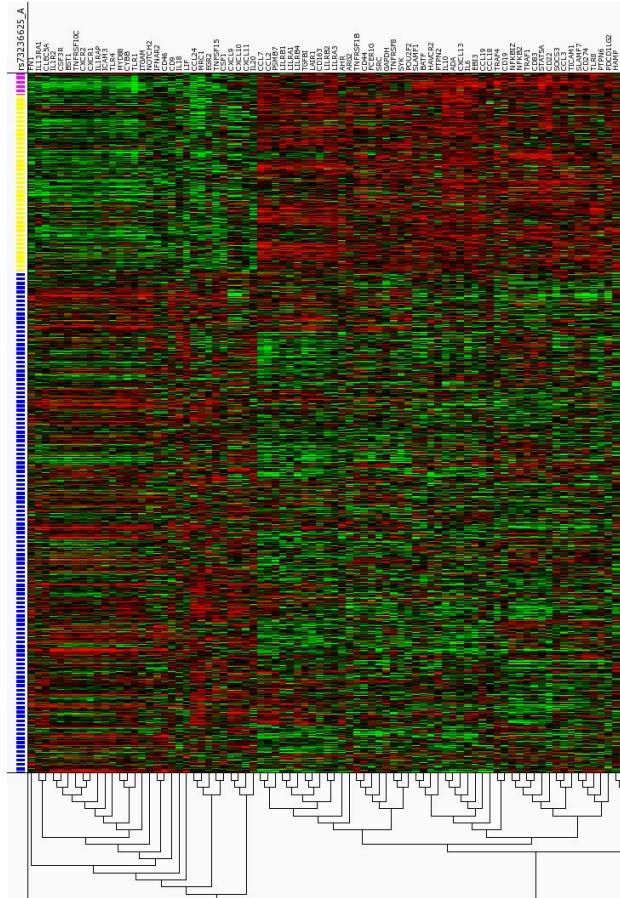
Pro-inflammatory Anti-inflammatory

(e.g, IL18, TLRs,)

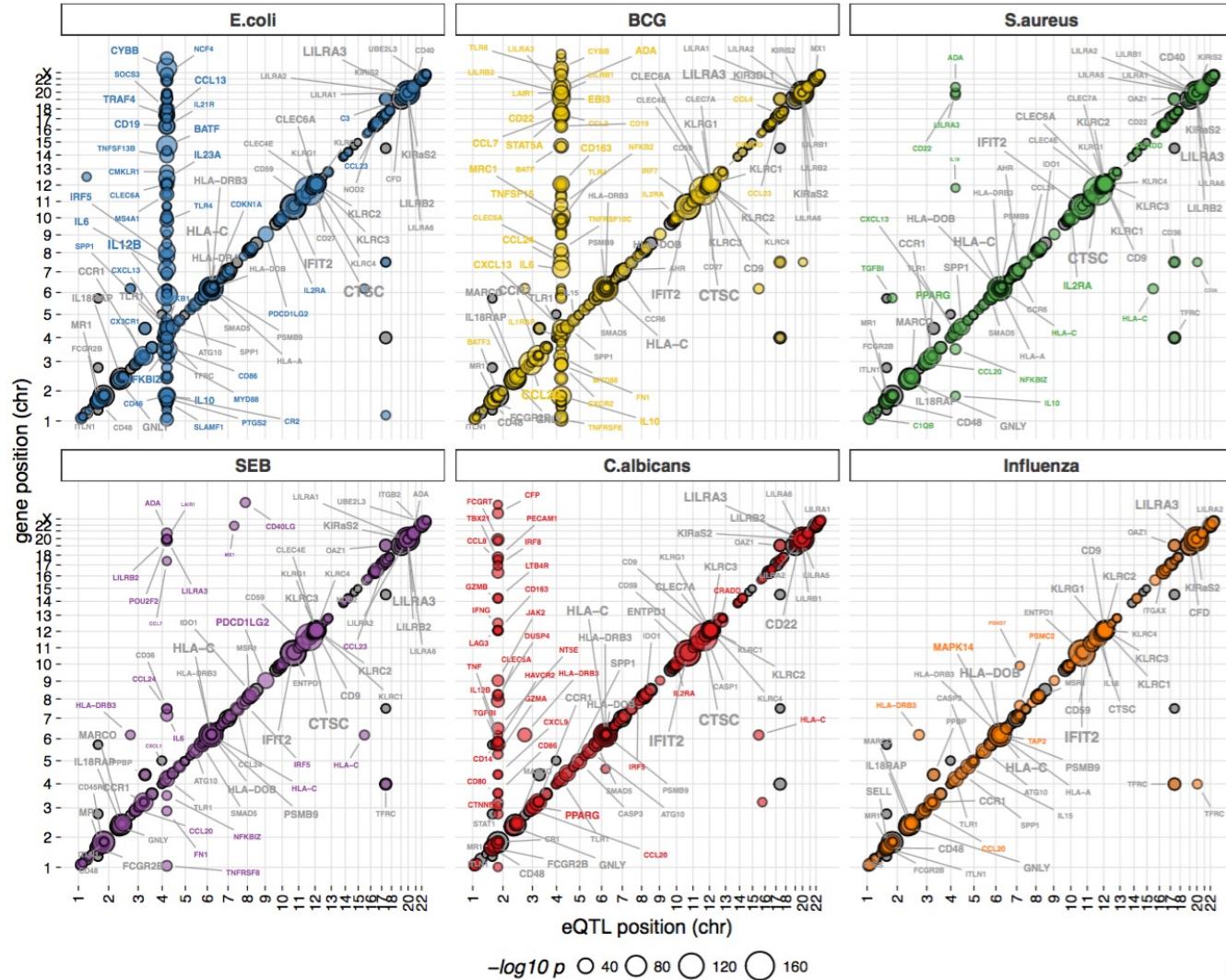
(e.g., IL-10, IL10, LILR)

Heterozygous

Homozygous major

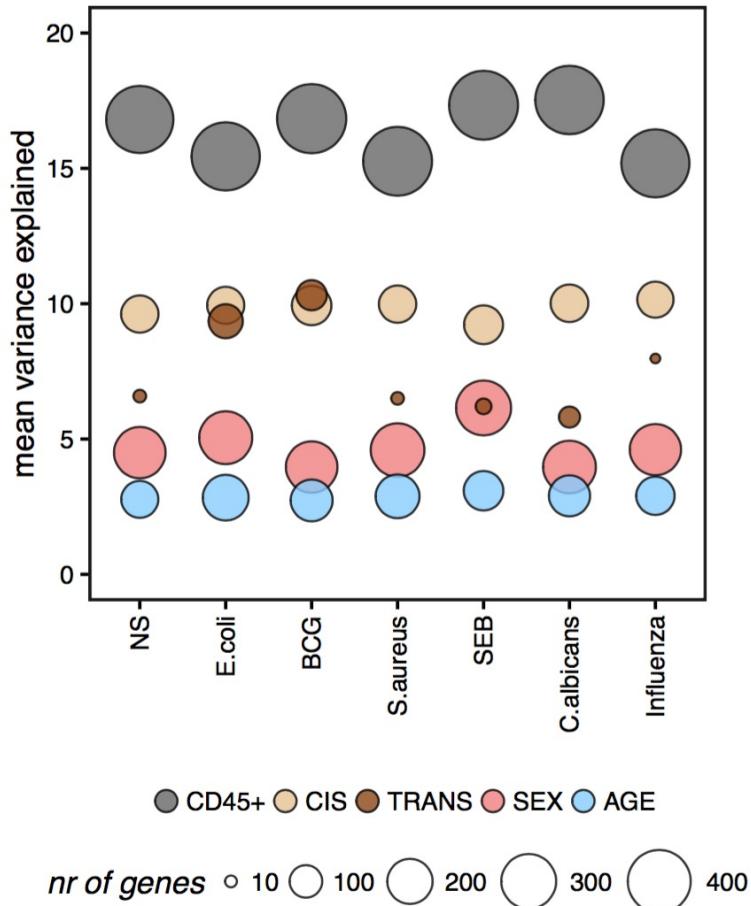


Mapping stimuli specific Quantitative Trait Loci (eQTL)



Dissecting factors responsible for gene expression variance

- Cellular composition accounts for largest proportion of gene expression variance in whole blood
- Genetics affects high percentage of genes with Medium-strong effect
- Age & sex affect numerous genes but to lower degree



Identification of novel environmental – immune response associations



Whole blood stimulation

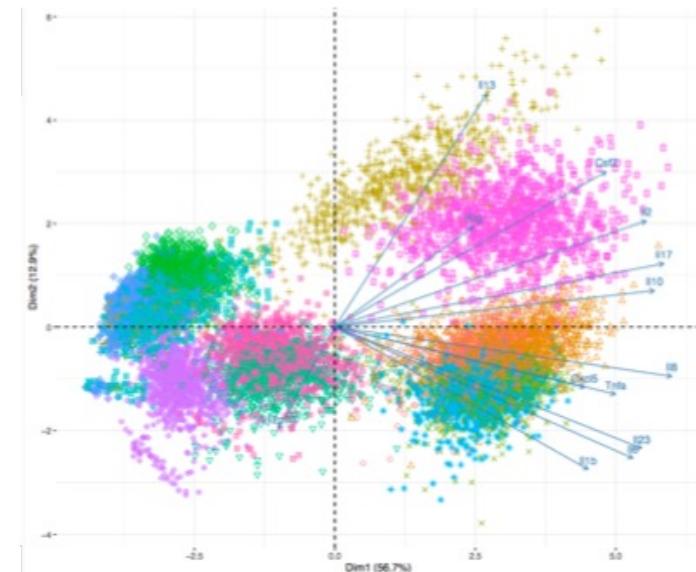


1,000 Healthy donors

12 stimuli

- Cytokines
 - IFNg
 - TNF
 - IL1b
 - SEB
 - CD3+CD28
- T-cell
- Viral
 - PolyIC
 - Influenza
- Microbial
 - *E.coli*
 - LPS
 - BCG
 - *C.albicans*
 - Control

13 cytokines by Luminex



Identification of novel environmental – immune response associations

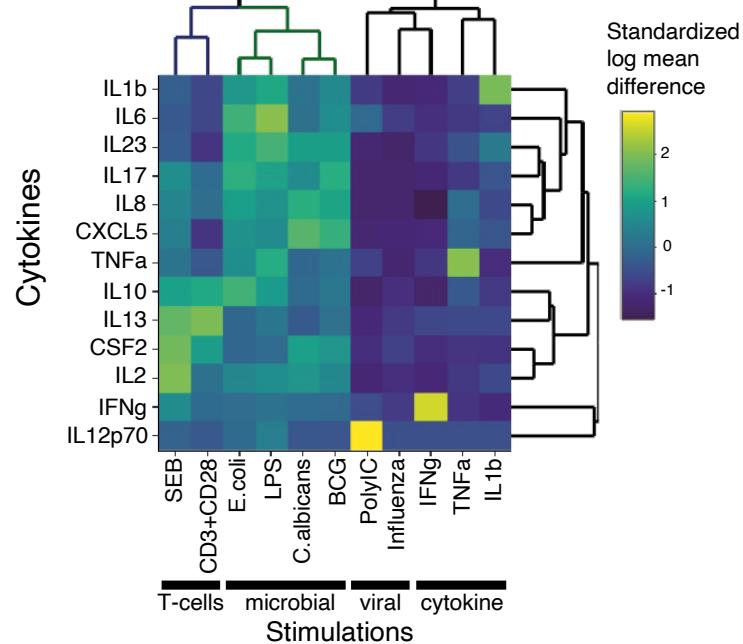


Whole blood stimulation



1,000 Healthy donors

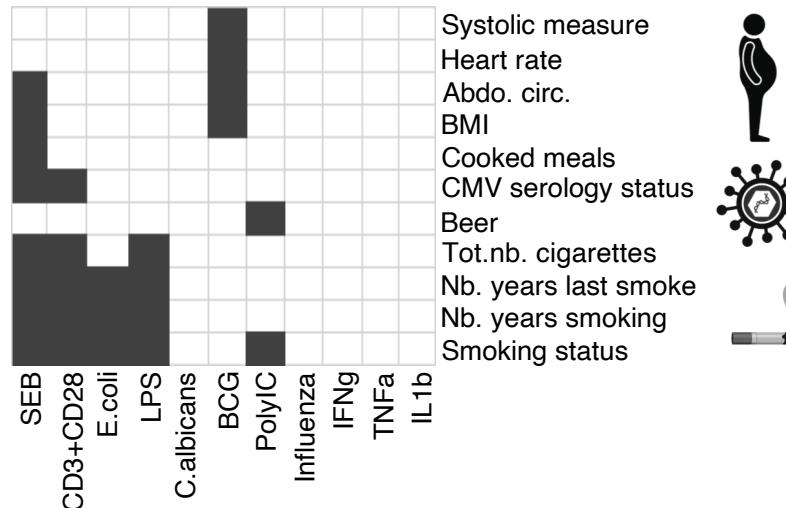
12 stimuli



Associate with 140 environmental factors (CRF)

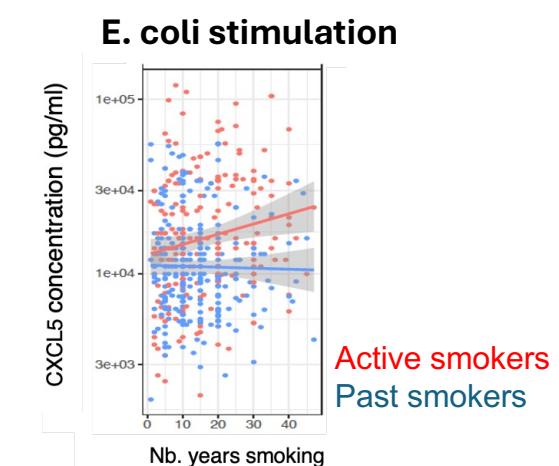
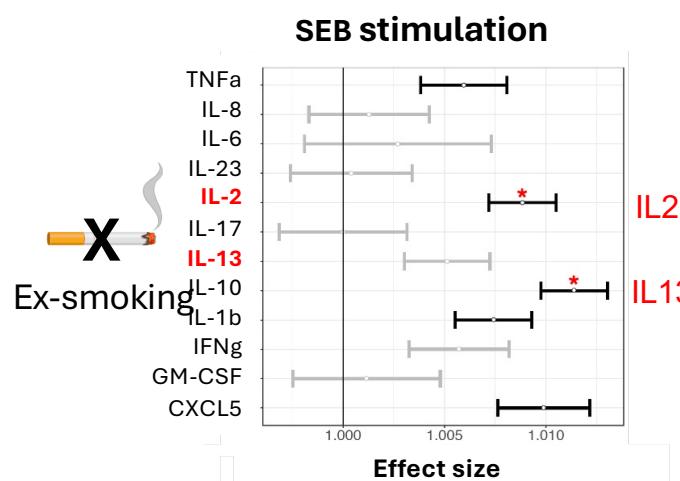
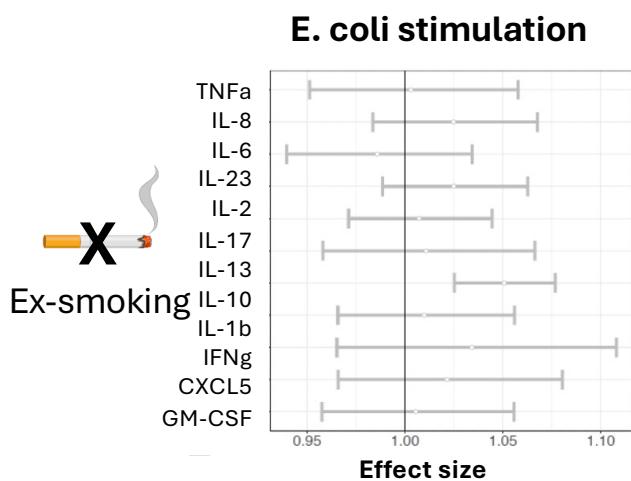
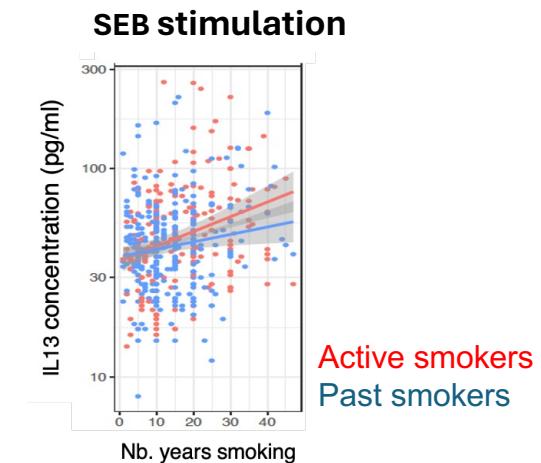
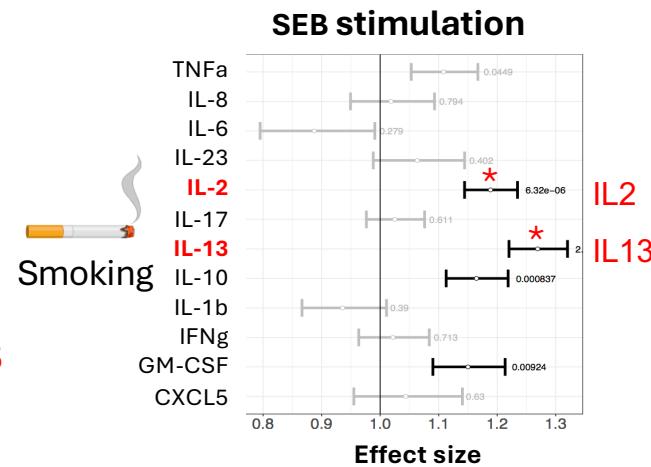
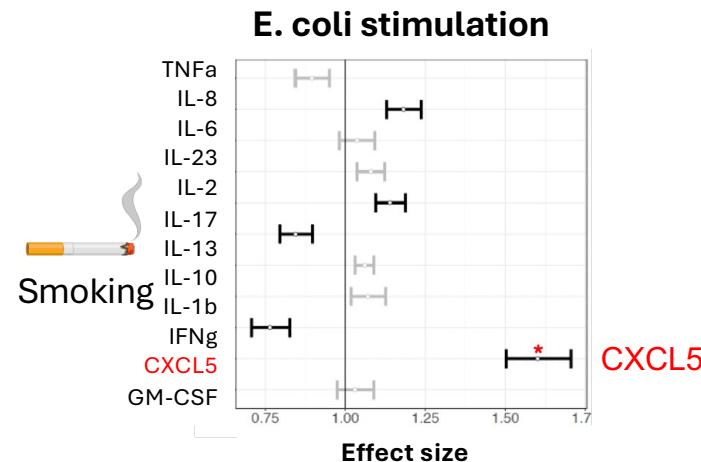
(Age and Sex corrected)

→ 11 factors significantly associated
(adj-P val LRT < 0.01)



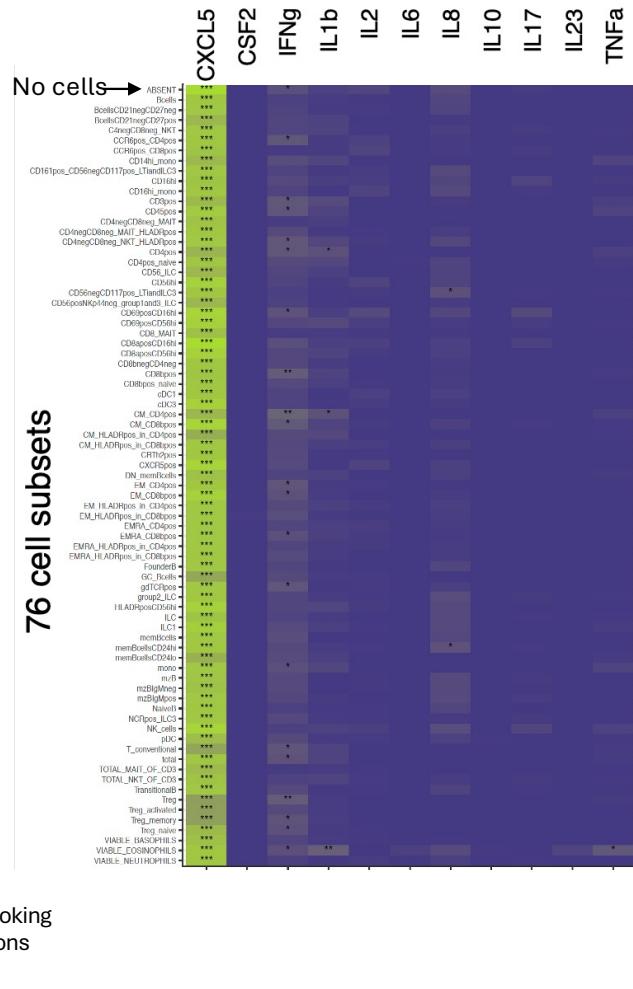
Violaine
Saint-André

Smoking differentially affects innate and adaptive immune responses

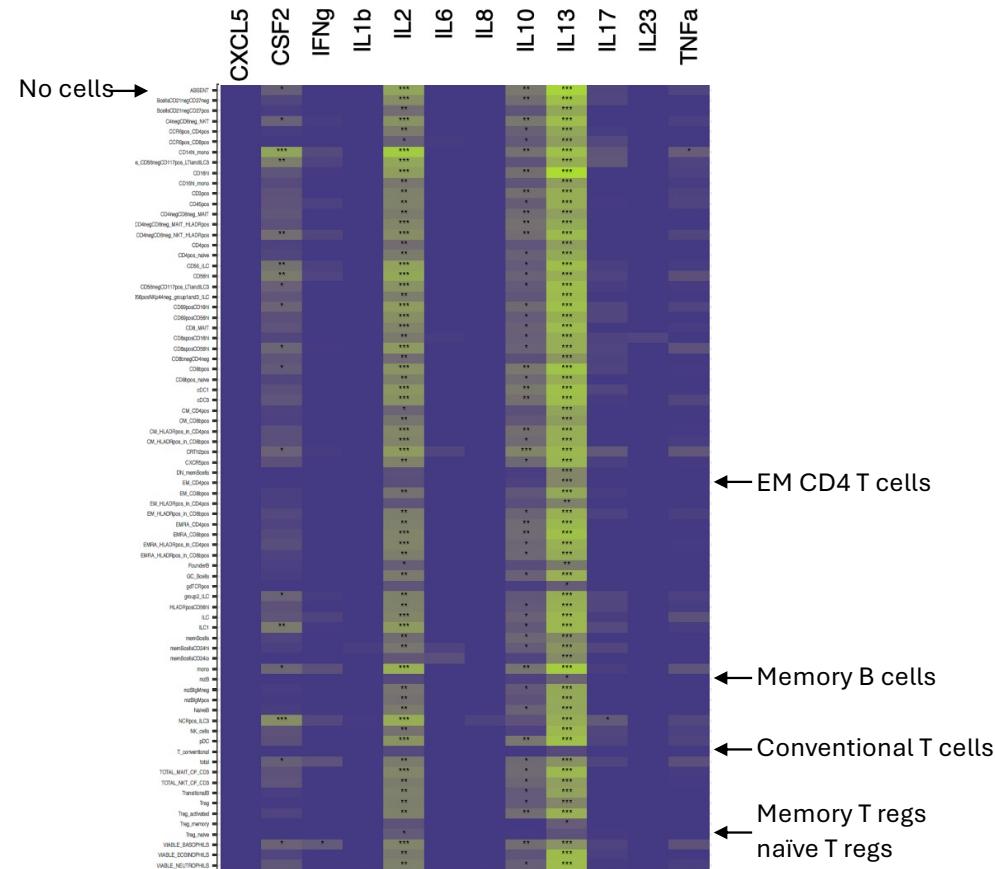


Identification of cellular mediators of smoking effects on cytokines

***E. Coli* stimulation- smoking associations**



SEB stimulation – smoking associations



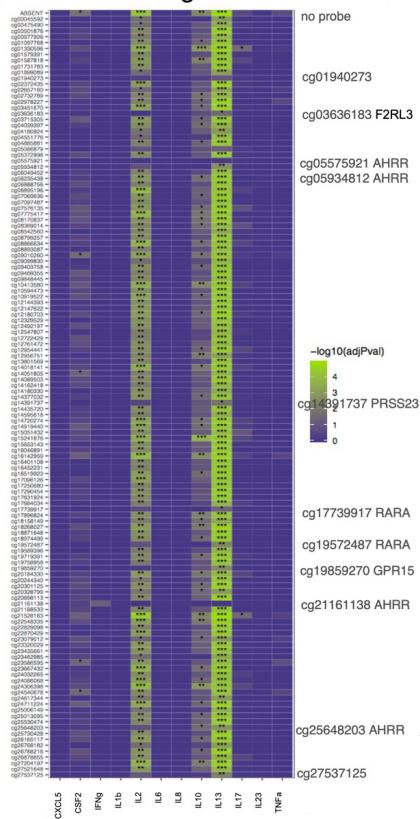
Epigenetic mediation of past smoking effect

Hypothesis: The past effect of smoking acting through long lived B & T cells is epigenetically mediated

Blood methylome 850k CpG sites – **2416 directly** (not through cellular associations) associated with **smoking** (Bergstedt et al, Nat Com 2022)

→ 129 significantly associated with IL2 in SEB stimulation (BY adj-pval of LRT < 0.001)

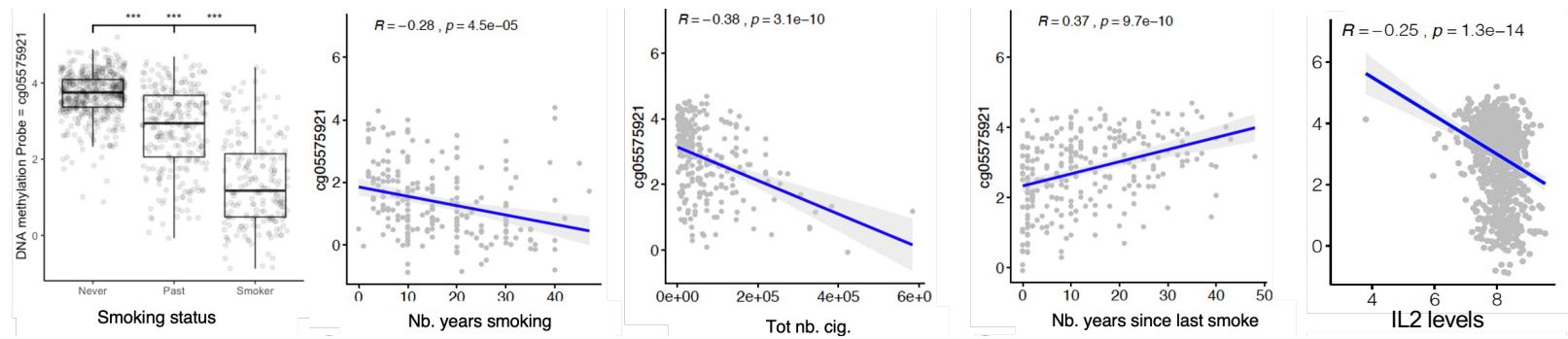
SEB – smoking associations



→ 11 probes removed association of IL2/IL13 and smoking:

AHRR (Aryl Hydrocarbon Receptor Repressor)
F2RL3 & *GPR15* (G protein-coupled receptors)
RARA (Retinoic acid receptor)
PRSS23 (serine protease)

AHRR DNA methylation



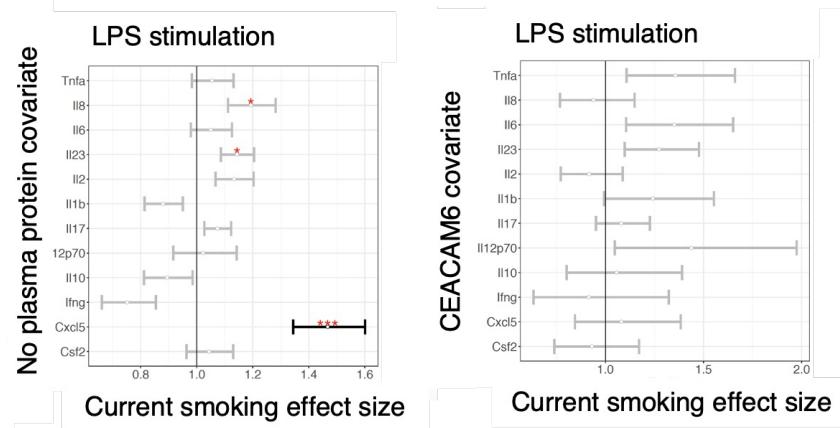
Saint-Andre, et al (Nature 2024)

Non cellular mediators of active smoking on inflammatory responses

Hypothesis: If no cellular mediator of active smoking effect on CXCL5 can we identify a soluble factor

326 plasma proteins measured by Luminex in subset of 400 donors (Caron *et al*, Genome Med 2022)

→ CEACAM6 protein removed active smoking effect on CXCL5 in LPS/E. coli stimulation



CEACAM6

- Glycosylphosphatidylinositol (GPI)-linked cell surface protein
- Expressed by neutrophils, macrophages, & lung/intestinal epithelial cells
- Elevated in multiple cancers

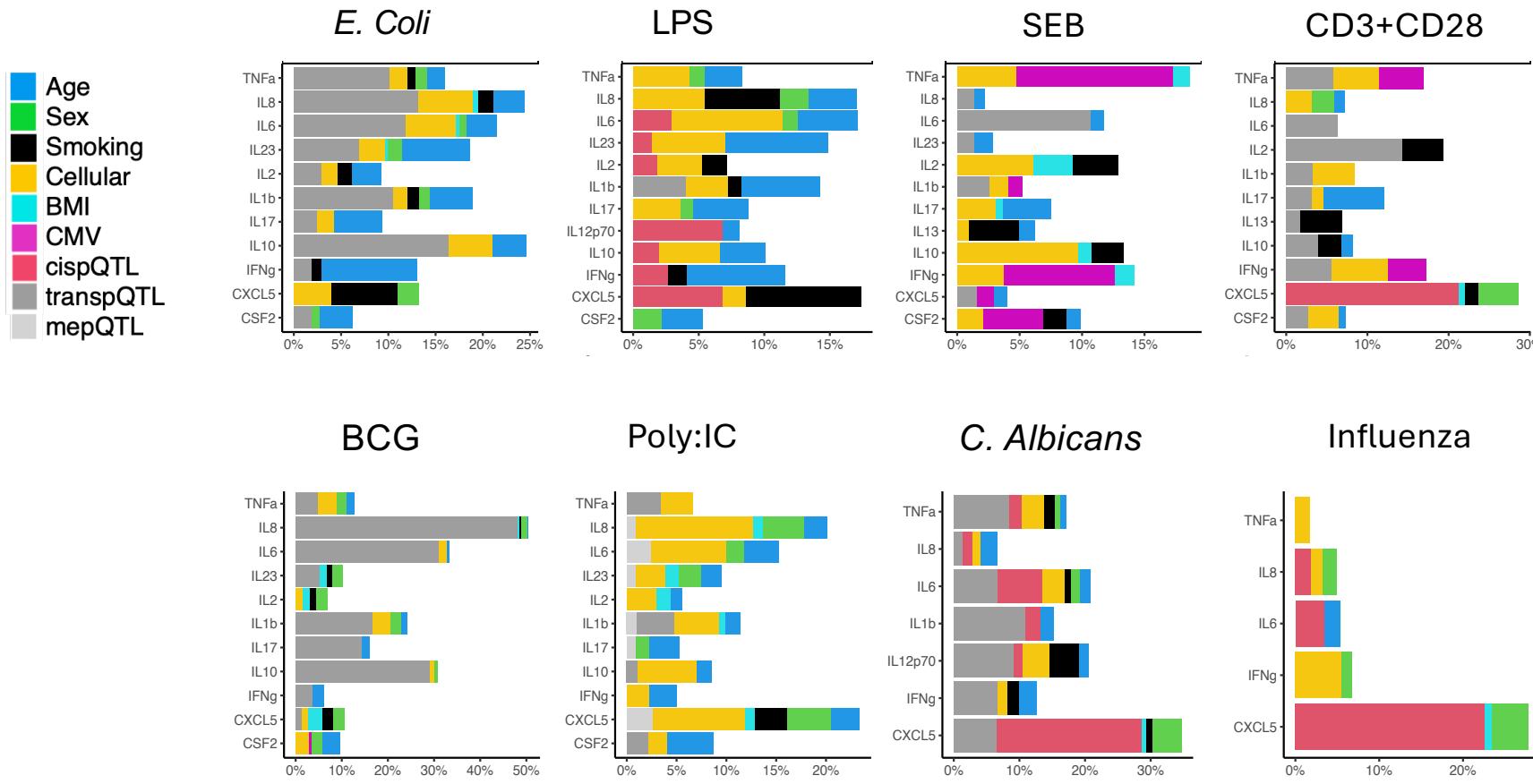
Hypothesis

- Smoking leads to elevated CEACAM6 in the blood
→ increases inflammatory response of neutrophils

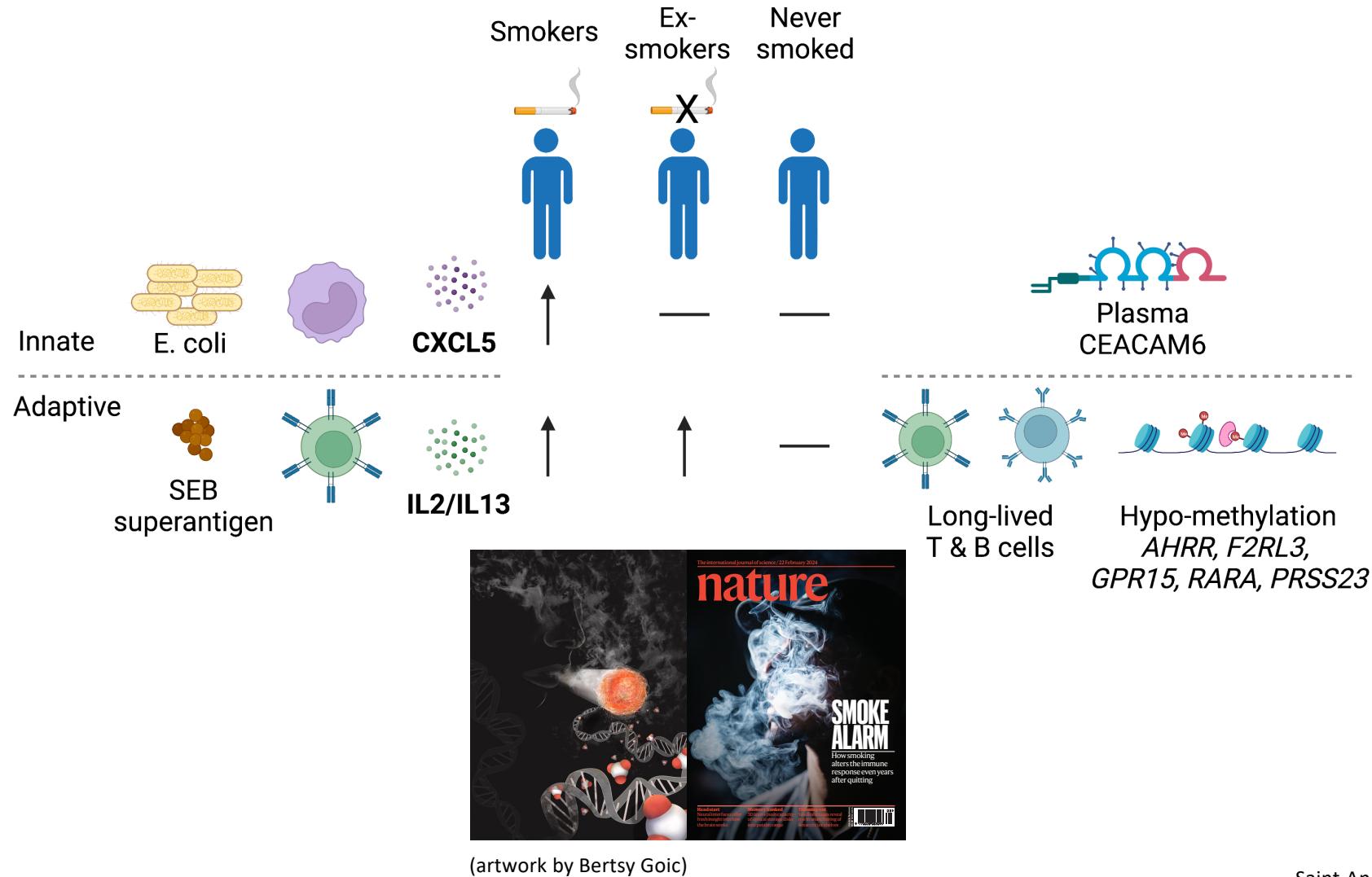
May explain the contradictory findings of smoking and COVID-19 ?

Summary of environmental and genetic effects on cytokine responses

Linear regression models including all identified significant effects on cytokine responses



Summary of smoking findings



Saint-Andre, et al (Nature 2024)

Ongoing impact of Milieu Interieur - media

Widespread international press coverage from Nature paper on smoking-immune effects (Saint-Andre et al)

Le Monde

RECHERCHE MÉDICALE

Le tabagisme nuit à l'immunité sur le long terme, selon une étude de l'Institut Pasteur

Par La rédaction numérique de France Inter

Le tabac affaiblit la réponse immunitaire, même dix ou quinze ans après son arrêt

Chez les anciens fumeurs, l'immunité apparaît lagrégée, même des années après l'arrêt du tabac, établissant une étude de l'Institut Pasteur, publiée dans le journal Nature.

Liberation

Accueil Société Santé

Santé

Cigarette : de nouvelles études éclairent les effets du tabac sur l'espérance de vie et les défenses immunitaires

D'après deux récentes publications scientifiques, l'espérance de vie diminue presque au niveau des non-fumeurs après dix ans d'abstinence. Des perturbations du système immunitaire peuvent toutefois persister plusieurs années après l'arrêt.

Le Parisien

Accueil Politique de France Santé

Le tabagisme détériore la santé et l'immunité pour des années après l'arrêt, selon des études

Selon les scientifiques, l'immunité adaptative, constituée au fur et à mesure des infections, reste lésée pendant des années après avoir arrêté de fumer.

Le Point

Politique Internationaux Débats Sciences Culture Sport Santé

Tabac et immunité : des effets néfastes 10 à 15 ans après l'arrêt de la cigarette

Selon une étude de l'Institut Pasteur, pour ce mercredi, le tabac pourrait avoir autant d'influence sur certaines réponses immunitaires que l'âge, le sexe ou les variables génétiques.

inter

Grille des programmes Podcasts Info Culture Humour

RECHERCHE MÉDICALE

Tabac : l'immunité des anciens fumeurs reste altérée longtemps après l'arrêt

Publié le jeudi 16 février 2023 à 06h30 | 2 min | PARTAGER

HUFFPOST

Comment le tabac perturbe le système immunitaire sur le long terme

Par Marie-Pierre le 14.03.2023 à 17h30

LEXPRESS

Le tabagisme : après l'arrêt de la cigarette, le système immunitaire reste affecté plusieurs années

Par LEONIE DROOGERS le 17.02.2023 à 17h30

Le Quotidien du Médecin

Le système immunitaire

Le tabac a des effets à long terme sur le système immunitaire

Le tabac a des effets à long terme sur le système immunitaire

Le tabac a des effets à long terme sur le système immunitaire

Les Echos

Tabagisme : après l'arrêt de la cigarette, le système immunitaire reste affecté plusieurs années

Le tabagisme altère le système immunitaire long terme

santé magazine

immunitaire, même des années après avoir arrêté de fumer

Selon une étude, le tabac altère l'immunité jusqu'à 15 ans après l'arrêt de la cigarette

nature

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ARTICLE | 14 February 2024

Smoking scars the immune system for years after quitting

A cigarette habit and previous infection with a common virus both have important effects on the immune system.

By Hélène Létard

ARTICLE

EL PAIS

Clencia / Materia

ASTROFÍSICA - MEDIO AMBIENTE - INVESTIGACIÓN MÉDICA - M

Курение необратимо разрушает иммунную систему

Le tabac es el factor que más altera las defensas, incluso años después de dejarlo

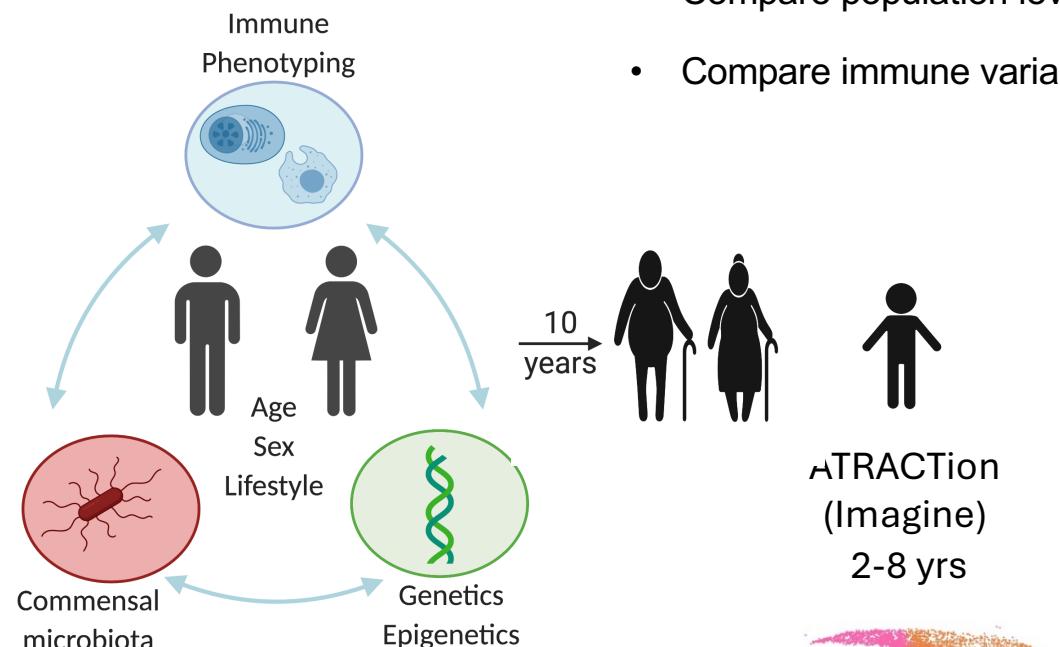
Un ingenioso experimento, con 1.000 personas de una misma ciudad analizadas a fondo, revela los desconocidos efectos persistentes del tabaquismo

le Scienze

<p

The ongoing evolution of Milieu Interieur

Extending the MI approach to more integration, deeper phenotyping, other ages & populations



- Compare population level aging effects with individual level variation
- Compare immune variability with and within other populations



ATRACTION
(Imagine)
2-8 yrs



TILDA
(Trinity)
>75 yrs



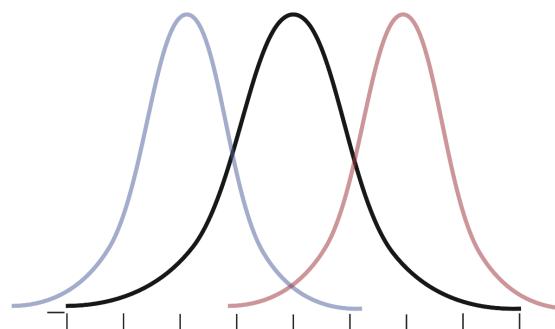
University
of Tartu

Healthy Human Global Project (HHGP)
Institut Pasteur Senegal
Institut Pasteur Hong Kong



How does immune variability impact disease risk, drug or vaccine response

Normal distribution of immune responses



Tuberculosis **Urinary Tract Infection**
(Tom Scriba) (Molly Ingersoll)

Viral resistance
(Jamie Sugrue/Cliona O'Farrelly) **Type I diabetes**
(Kristin Tarbell)

COVID-19
(Trinity College Dublin/Hopital Cochin)

Pertusis
(Julie Toubiana)

Multiple Sclerosis
(Frederique Michel)

Spondyloarthritis
(Lars Rogge)

Vaccine responsiveness
COVID-19 – C2i/HK
Influenza – H2020 Incentive

Sarcoidosis
(Karim Sacre)

Juvenile Dermatomytis
(Mathieu Rodero/Cyril Gitaux) **Cancer immunotherapy**
(Nader Yatim/Celeste Lebbe)

ITP
(Richard Lee/Charlotte Bradbury) **Lupus**
(JP Herbeuvel/Anne-Sophie Korganow)

Duffy et al, Clin Inf Dis 2018

Rodrigues et al, Diabetologia 2020

Menegatti et al, Ann Rheum Dis 2021

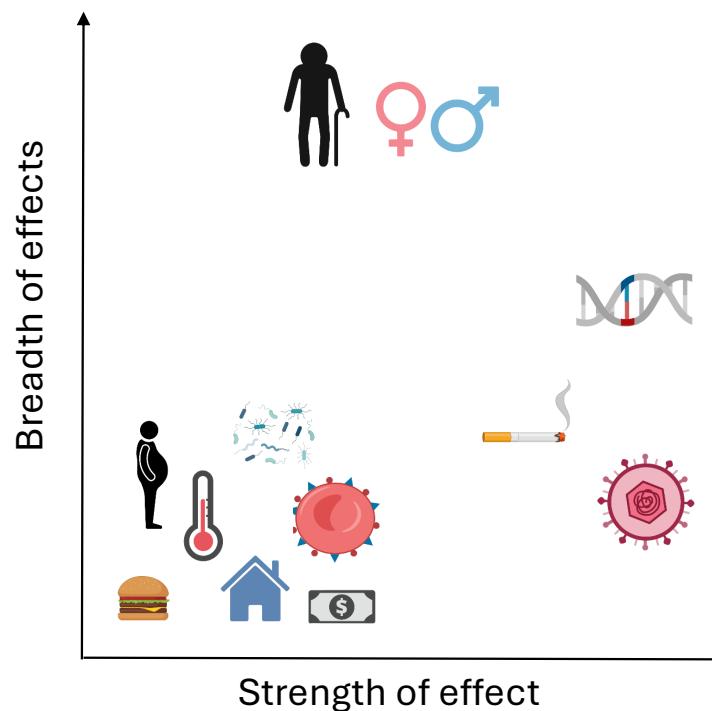
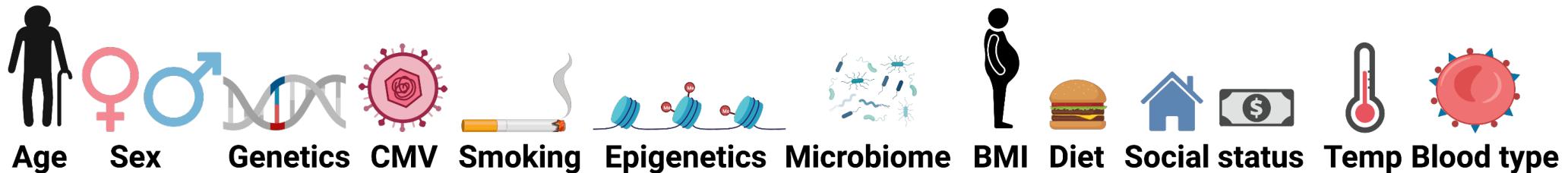
Devi-Marulkar et al, Frontiers Imm 2021

Llibre et al, Frontiers 2022

Sugrue et al, Cell Reports 2022

Smith et al, Nat Comms 2022

Conclusion - why are immune responses different between individuals



- Immune responses are highly diverse & variable
- Widespread effects of age, sex & host genetics
- Specific & strong effects of smoking & CMV infection
- Many other specific environmental factors important
- Results can be context specific

Ongoing work

- Need to include other ages & diverse populations
- Need to assess age*sex*genetic*environment interactions
- Longitudinal assessment required
- Comparison with patient populations

“Art is I, Science is We” Claude Bernard 1865



Translational Immunology



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Marie Robert

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Alexandra Serris
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Violaine Saint-Andre
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Mucosal Inflammation & Immunity

Léa Deltourbe
Molly Ingersoll

Human Evolutionary Genetics

Auerlie Bisiaux
Anthony Jaquaniello
Etienne Patin
Maxime Rotival
Marwan Sharawy
Lluis Quintana-Murci

Innate Immunity

James Di Santo
Jean Marc Doisne
Eva Eleftheri
Toshiki Eri
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Infectious Disease Epidemiology & Analytics

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Thanks for your attention !

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Smoking changes adaptive immunity with persistent effects. Saint-André V, Charbit B, Biton A, Rouilly V, Possémé C, Bertrand A, Rotival M, Bergstedt J, Patin E, Albert ML, Quintana-Murci L, Duffy D; Milieu Intérieur Consortium. *Nature*. 2024 Feb;626(8000):827-835. doi: 10.1038/s41586-023-06968-8

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Piasecka B*, Duffy D*, Urrutia A, Quach H, Patin E, Posseme C, Bergstedt J, Charbit B, Rouilly V, MacPherson C R, Hasan M, Albaud B, Gentien D, Fellay J, Albert M L*, Quintana-Murci L*, Milieu Intérieur Consortium.

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Standardized whole blood stimulation improves immunomonitoring of induced immune responses in multi-center study.

Duffy D, Rouilly V, Braudeau C, Corbière V, Djebali R, Ungeheuer M N, Josien R, LaBrie S, Lantz O, Louis D, Martinez-Caceres E, Mascart F, Ruiz de Morales J G, Ottone C, Redjah L, Salabert-Le Guen N, Savenay A, Schmolz M, Toubert A, Albert M L, for the Multinational FOCIS Centers of Excellence.

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Standardized whole-blood transcriptional profiling enables the deconvolution of complex induced immune responses.

Urrutia A*, Duffy D*, Rouilly V, Posseme C, Djebali R, Illanes G, Libri V, Albaud B, Gentien D, Piasecka B, Hasan M, Fontes M, Quintana-Murci L*, Albert ML* for The Milieu Intérieur Consortium.

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Functional analysis using standardized whole blood stimulation systems defines the boundaries of a healthy immune response to complex stimuli.

Duffy D*, Rouilly V*, Libri V*, Hasan M, Beitz B, David M, Urrutia A, Bisiaux A, La Brie S, Dubois A, Delval C, Thomas S, Rogge L, Schmolz M, Quintana-Murci L, Albert M* for The Milieu Intérieur Consortium.

Immunity 2014 March 20 40(3):436-50