





#### The Canadian Partnership for

# Tomorrow Project

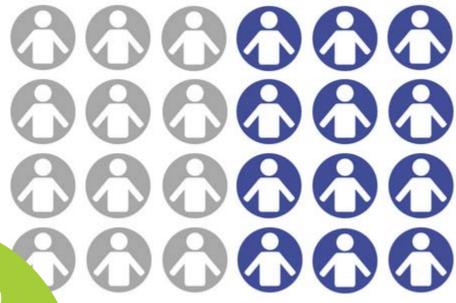
**Philip Awadalla**, PhD National Scientific Director, CPTP

Ontario Institute for Cancer Research Canadian Data Integration Centre University of Toronto





Understanding disease risk factors is challenging

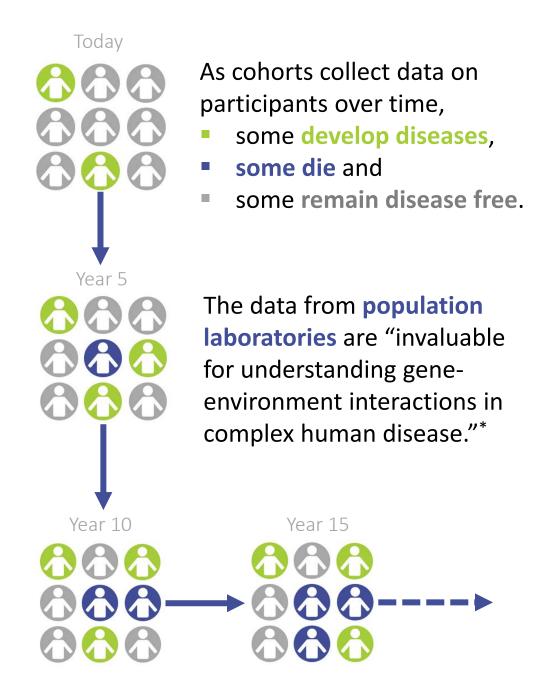


## 1 in 2

Canadians will die from cancer or a chronic disease\*

- 1 in 2 Canadians will be diagnosed with cancer
- 1 in 12 Canadians live with diagnosed heart disease
- 1 in 10 Canadians live with asthma or COPD

Large-scale population health laboratories help assess disease risks



<sup>\*</sup>Genes, environment and the value of prospective cohort studies, Manolio TA, 2006



Large-scale cohort studies drive the discovery of personalized diagnostics and treatment

#### **OPINION**

## As world embraces precision medicine, Canada falls behind



ANDRÉ PICARD >
PUBLISHED OCTOBER 4, 2016

The United States is going to analyze the genetic information of more than one million Americans. The United Kingdom has a 100,000 Genomes Project and Australia is following suit with its own plan to decode 100,000 genomes.

Yet, as the world embraces precision medicine and funds ambitious cohort studies, Canada remains largely on the sidelines. It's a shame.

# The Canadian Partnership for Tomorrow Project (CPTP) is a Pan-Canadian platform for research on chronic disease



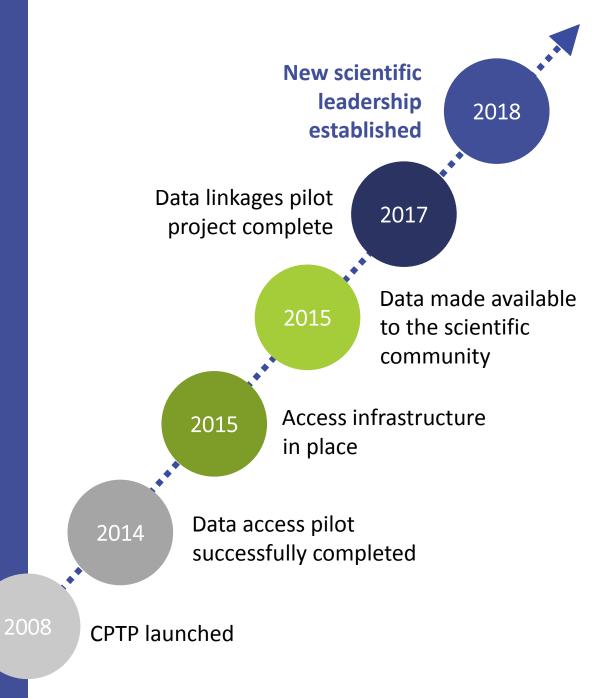
CPTP is a **population-health research platform** for assessing the effect of genetics, behaviour, family health history and environment on chronic diseases.







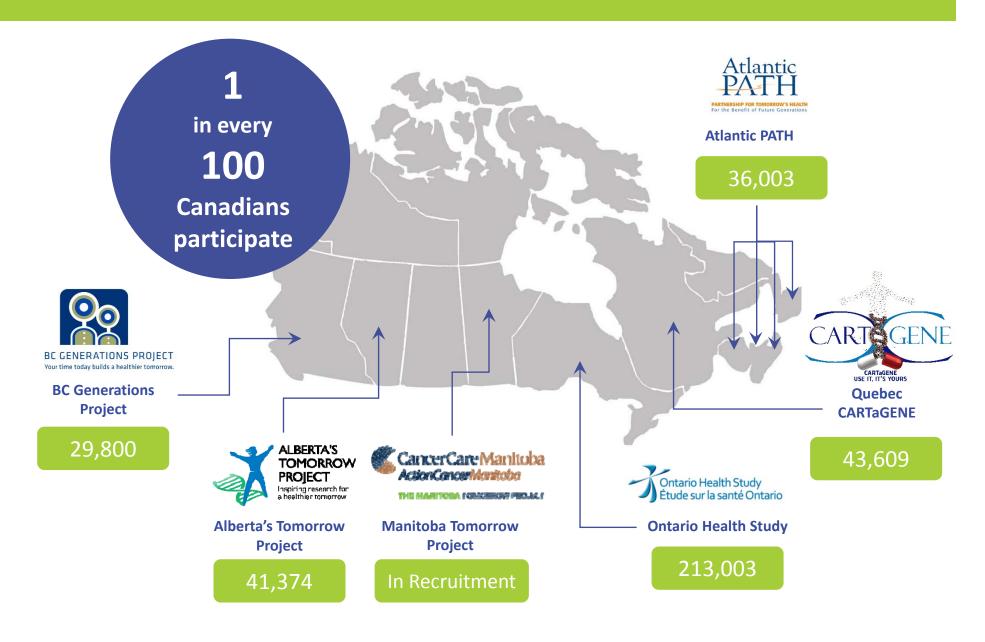
# Entering a new era of scientific leadership



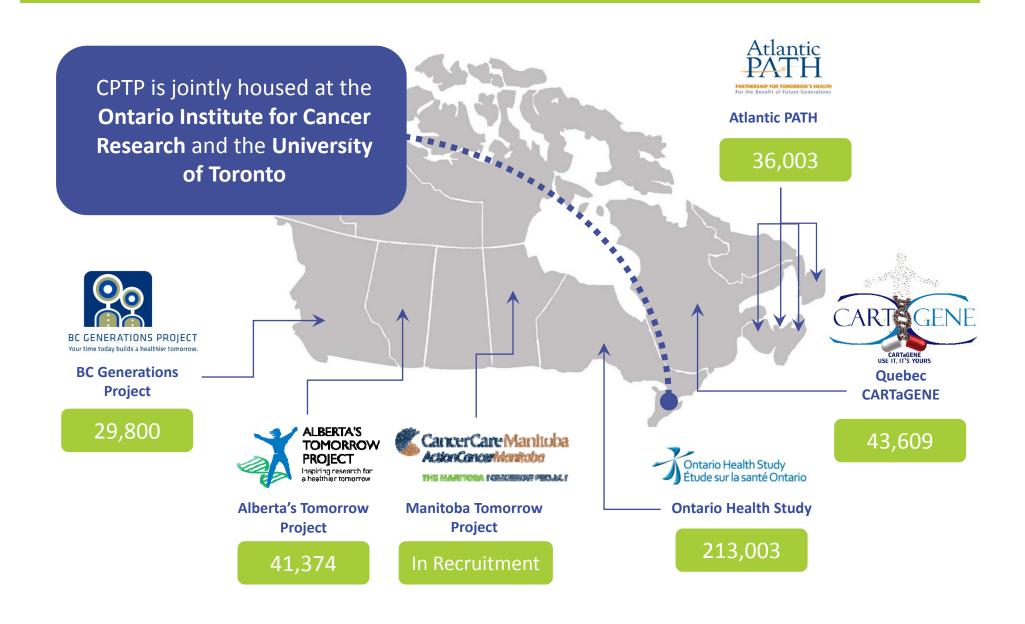
### Canada's largest population health research platform



### Recruited more than 320,000 participants



## Confederation of 6 regional cohorts



#### Canadian Partnership for Tomorrow Project (CPTP)

Quebec

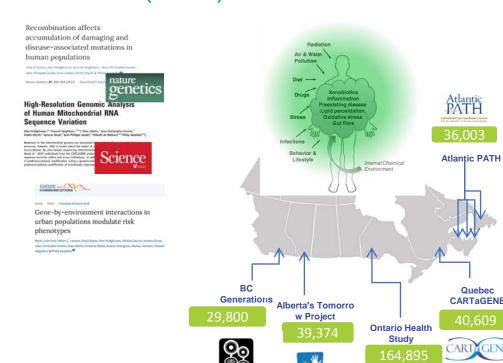
**CARTAGENE** 

40.609

Ontario Health Study

Étude sur la santé Ontario

countmein



#### ~310,000 participants aged 30-74

No selection criteria 1 in 60 Canadians aged 30-74 have taken part (based on 2016 Census)

Questionnaire data Lifestyle, health Physical measures blood pressure, complete blood count, biochem, MRIs etc.

Biological samples - blood, plasma, serum, DNA, RNA, genotypes, exomes, RNASeq,

Longitudinal cohort - Canadawide recontact and linkage to administrative data

single-cell, inflammatory markers...

#### **Retrospective and Prospective**

Data including Drugs and Treatments, Outcomes, Genetic Testing Data etc.

> The Canadian Partnership for Tomorrow Project: a pan-Canadian platform for research on chronic disease prevention

> Trevor J.B. Dummer PhD, Philip Awadalla PhD, Catherine Boileau PhD, Camille Craig MSc, Isabel Fortier PhD, Vivek Goel MD, Jason M.T. Hicks MSc, Sébastien Jacquemont MD, Bartha Maria Knoppers PhD, Nhu Le PhD, Treena McDonald MSc, John McLaughlin PhD, Anne-Marie Mes-Masson PhD, Anne-Monique Nuyt MD, Lyle J. Palmer PhD, Louise Parker PhD, Mark Purdue PhD, Paula J. Robson PhD, John J. Spinelli PhD, David Thompson MSc, Jennifer Vena PhD, Ma'n Zawati LLM; with the CPTP Regional Cohort Consortium

■ Cite as: CMA/2018 June 11:190:E710-7. doi: 10.1503/cmai.170292

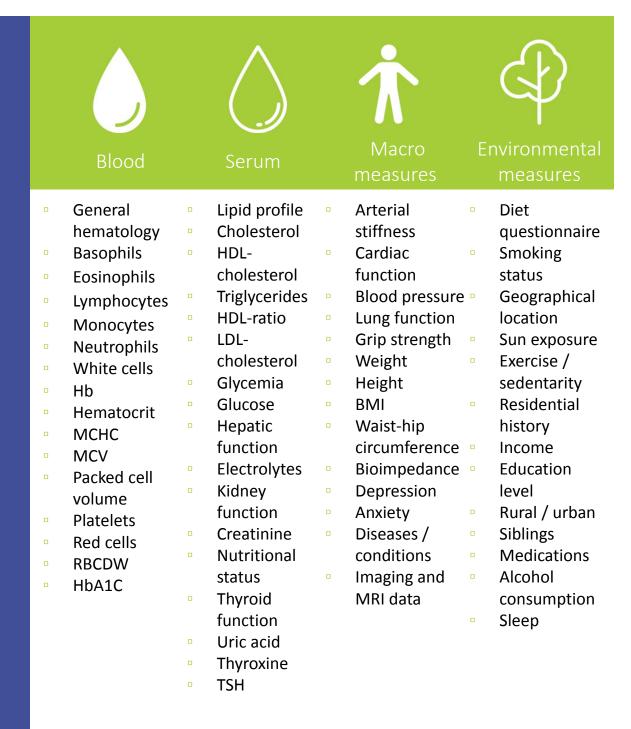
Enabling healthrelated research for scientists today and for those in years to come

- Following participants over 25 years
- Linking 6 cohorts over 9 provinces
- Recruited more than 320,000 actively engaged participants
- Supported more than 80 projects to date





# Capturing comprehensive health and lifestyle data



# Capturing comprehensive physical measures data



Cognitive test Reaction time, memory, executive function

Anthropometric Height, sitting height, waist and hip

measures circumference, weight

Bioimpedance BMI, impedance, % body fat, fat mass, fat free

Mass, total body water, basal metabolic rate

**Grip strength** Right and/or left hands

**Bone density** Heel of non-dominant leg: Stiffness index, %

young adult, T score, % age matched, Z-score,

**BUA** and SOS values

**Lung function** Timed peak and forced inspiratory and expiratory

flow, vital capacity: FVC, FEV1, FEV1/FVC, FEF25,

FEF50, FEF75, FEF25-75, FET, FEV3,

FEV3/FVC, FEV6, PEF, EVol, FIVC, FIV1, PIF, ELA.

MVV.

**Blood pressure** Systolic and diastolic blood pressure, heart rate

Arterial stiffness Heart rate, Aortic Systolic and diastolic pressures,

Aortic augmentation, Aortic augmentation index,

Ejection duration, and Buckberg ratio

Partial resting Leads: I,II, III, aVR, aVL et aVF. Heart rate, PQ

electrocardiogram Interval, QRS duration, QT, QTC, P-R-T axis, P

duration, RR and PP Intervals.

MRI (n=10,000 Full body, n=10,000 participants, Combination of

participants) hospital centres and mobile units.

# Longitudinal sampling of biological data







Biological Samples

Venous Blood (145,760) Saliva (18,799)

Urine (99,500)



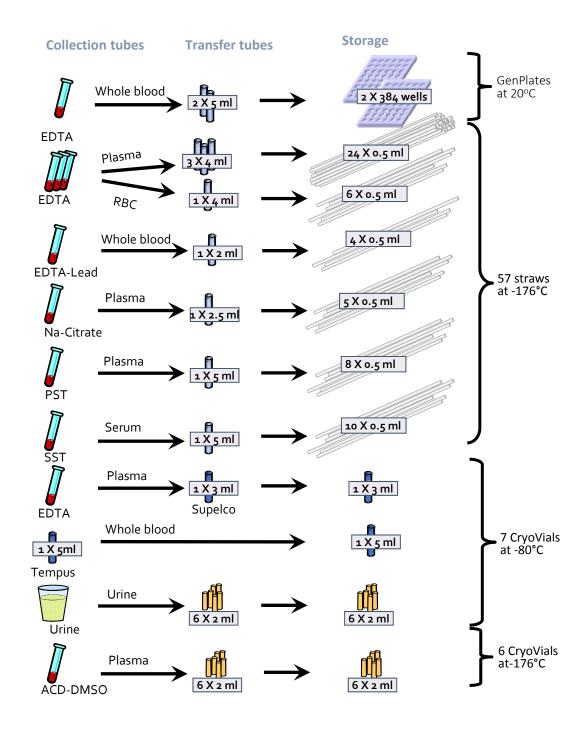
Blood Spots (10,642)

DNA Source Material (159,266)

# Comprehensive data capture

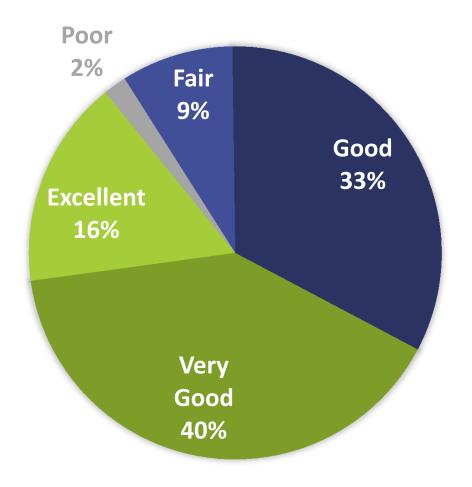
Total blood volume collected: 160.5 mL





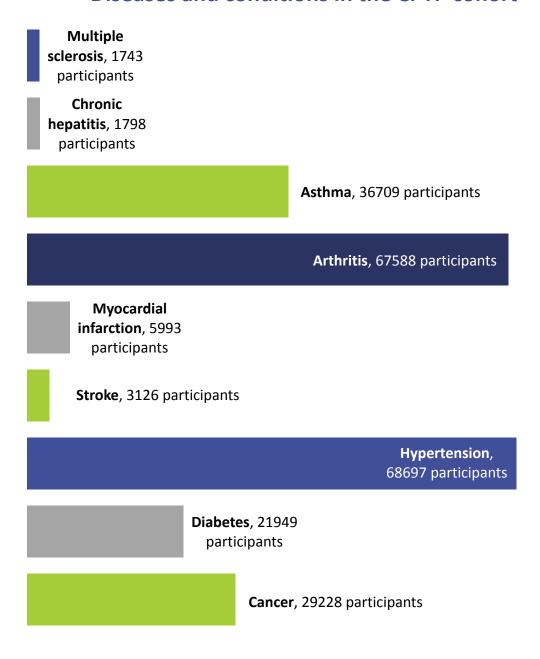
Following both healthy and affected participants over time

## Overall perception of health status in the CPTP cohort



Including participants with various chronic diseases and conditions

#### Diseases and conditions in the CPTP cohort



Working with a network of internationally recognized large-scale initiatives

- 1) The International Hundred Thousand Cohort Consortium (IHCC)
- 2) International Common Disease Alliance

**Biobank Japan** China Kadoorie Biobank **Canadian Partnership for Tomorrow Project (CPTP)** Kaiser Permanente Research Program LifeGene Million Veteran Program Million Women Study Multiethnic Cohort Study MyCode Community Health Initiative Nurses' Health Study (NHS/NHSII) US Precision Medicine Initiative/ All of Us Tohoku Medical Megabank Project

23andMe

**UKBioBan** 

CPTP is
Canada's
largest
population
health cohort



### International 100K Cohort Consortium (IHCC)

Linking cohorts, understanding biology, improving health

#### National Medical Genome Projects and Cohorts



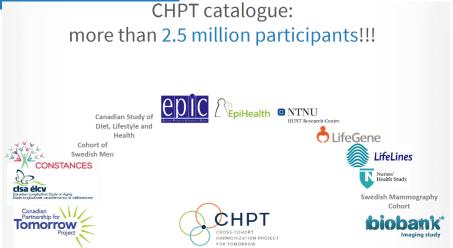
Over 20 million participants will be linked and harmonized through this consoritum







Leverage the use of existing North American and European cohort studies focused on better understanding of the risk factors that contribute to cancer and other major chronic diseases





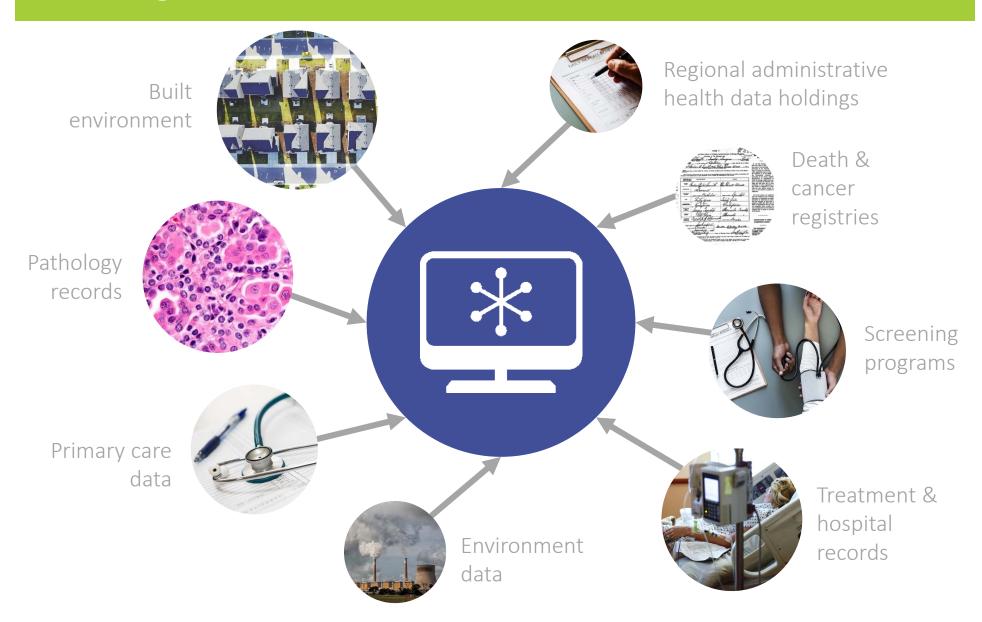


"I am interested in pooling data across cohort studies to explore the effect of physical activity and social participation on quality of life in older adults, adjusting for SES"

#### Displays only studies collecting all variables of interest for the research project

į		Socio-demographic and economic characteristics x			Lifestyle and health behaviours ×	Health status and functional limitations $\mathbf x$	Social environment x
•	Study	Education ×	Labour force and retirement ×	Income, possessions, and benefits x	Physical activity	Quality of life	Social participation
)	ALSA	18	28	198	75	63	<b>177</b>
)	CaPS	18	37	0	<b>1</b>	0	13
)	CSHA	23	174	10	48	10	30
3	ELSA	491	3.325	37,630	295	134	261
)	FRèLE	12	27	42	120	138	123
)	NuAge	0	6	11	430	256	03
0	OATS	34	43	•	121	40	50
)	PATH	158	228	7	150	281	•
)	TILDA	16	60	374	21	28	46
1	VETSA	21	28	0	24)	54	0
	All	789	3,994	38,371	1,355	984	856

### Linking data to better understand disease risk



Enabling healthrelated research for scientists today and for those in years to come



CPTP serves both **retrospective and prospective** research studies.



# Linking cancer data: a pilot project

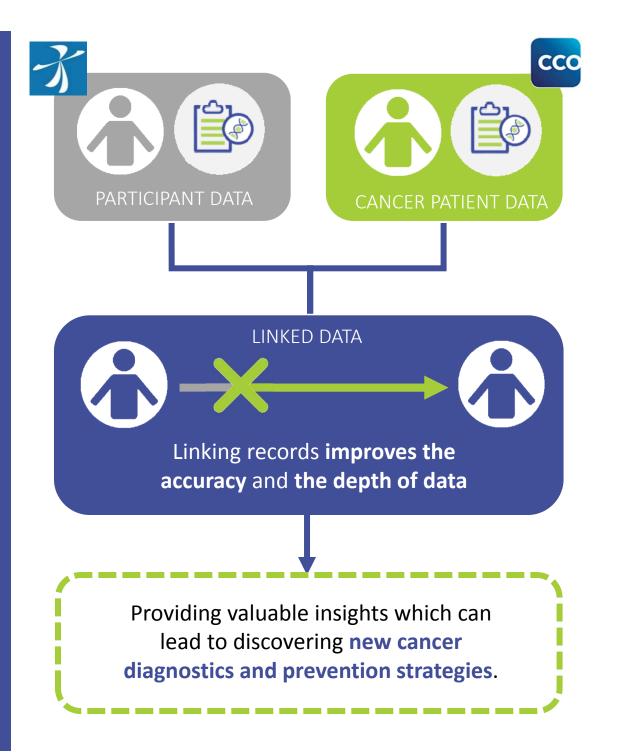
Awadalla Lab Pilot Project, 2018

The Awadalla Lab's pilot project successfully linked Ontario Health Study data with Cancer Care Ontario data, to analyze the effects of health, environment and lifestyle factors on early cancer development.



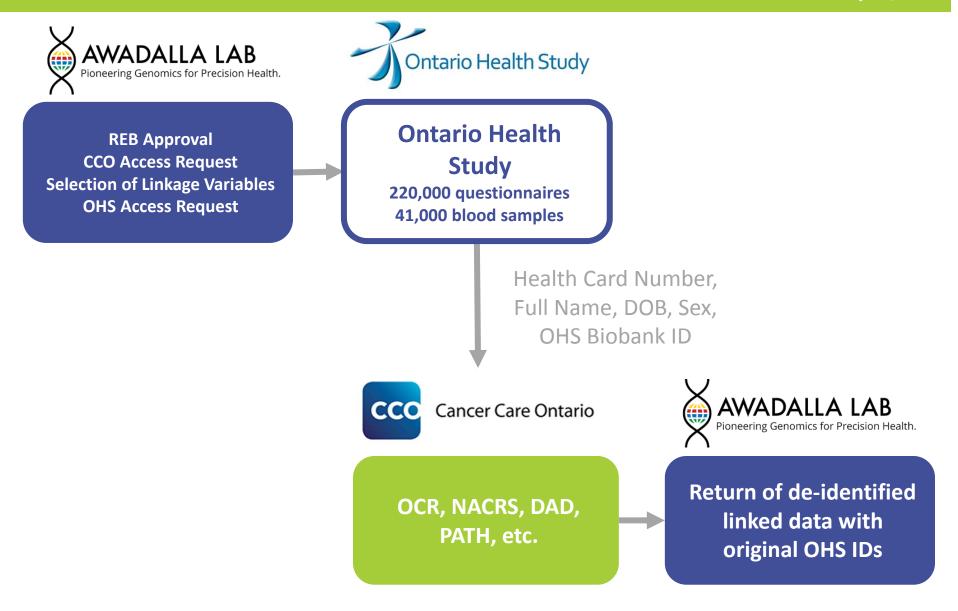
# Linking cancer data: the concept

Awadalla Lab Pilot Project, 2018



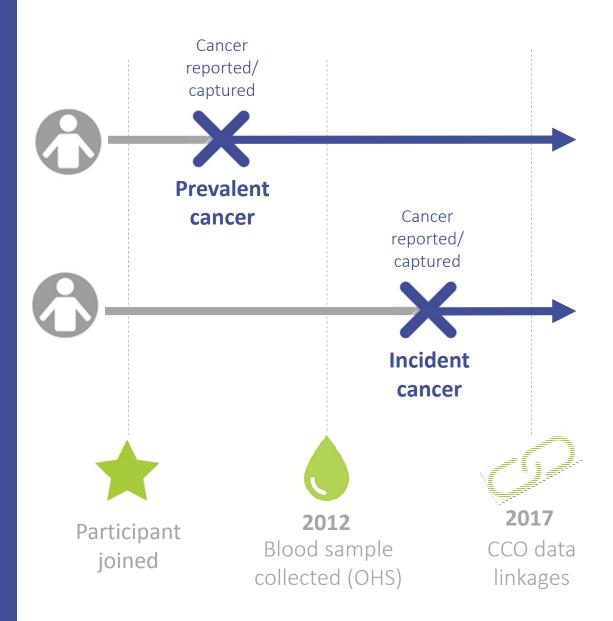
### Linking cancer data: the process

Awadalla Lab Pilot Project, 2018



# Capturing both incident and prevalent cancers

Awadalla Lab Pilot Project, 2018



Leveraging cohort data to find leukemia years before it surfaces

case study

Acute myeloid leukemia (AML) progresses quickly and requires treatment soon after diagnosis. Early indicators of AML were thought to be indistinguishable from healthy aging.



We investigated cohort study data (EPIC and OHS) to find traces of AML in patients samples that were collected before the disease developed

We found traces of the disease up to 10 years before the patients were diagnosed with AML.

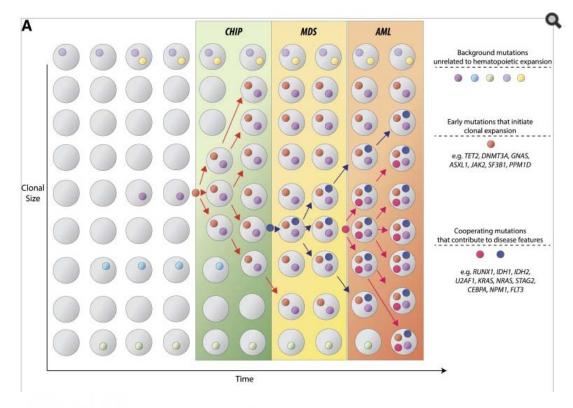


"This could in future enable **earlier detection** and monitoring, and may help to inform intervention."\*

\*Prediction of acute myeloid leukaemia risk in healthy individuals, Abelson et al., 2018 Using EPIC and OHS data to evaluate clonal hematopoiesis and AML risk

case study

Supported by \$10 million from OICR, Dr.
John Dick and collaborators (including
Awadalla) are investigating clonal
hematopoiesis and acute myeloid leukemia
(AML) risk





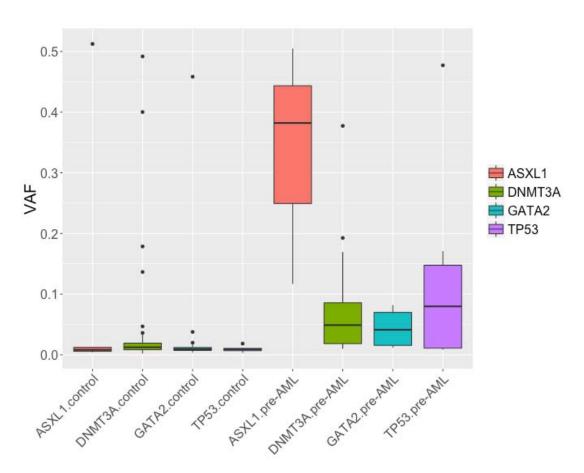




Using EPIC and OHS data to evaluate clonal hematopoiesis and AML risk

case study

Pre-AML cases have higher variant allele frequency in recurrently mutated AML related genes



(derived from preliminary analysis of EPIC cohort)

# Using EPIC and OHS data to evaluate clonal hematopoiesis and AML risk

case study



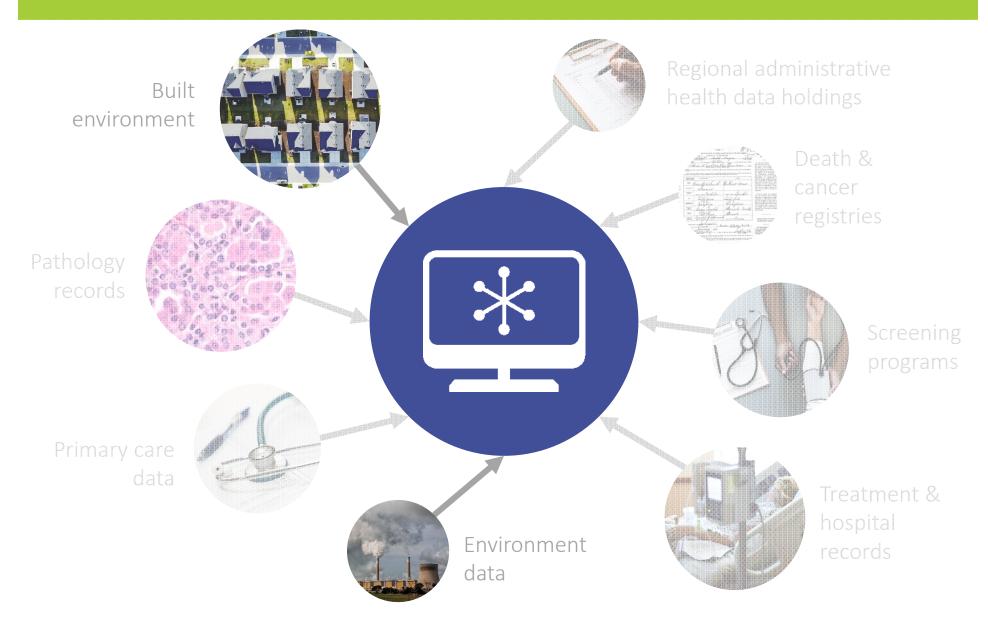
Letter | Published: 09 July 2018

## Prediction of acute myeloid leukaemia risk in healthy individuals

Sagi Abelson, Grace Collord, [...] Liran I. Shlush ■

- Found how to distinguish between individuals who are at high risk of developing AML and those who are not
- Made possible by long-term health research cohorts
- "This could in future enable earlier detection and monitoring, and may help to inform intervention."

### Linking key environment data to health data





## Linking environmental and health research

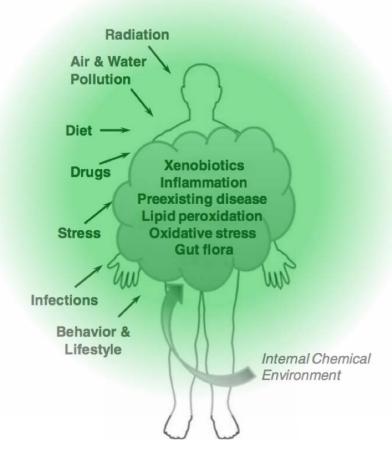
case study

 CIHR awarded \$4.2 million to Dr. Jeffrey Brook and Dr. Philip Awadalla to lead CANUE (2016 – 2021), a national platform for big environmental data



Exploiting the cohort to study gene-by-environment interactions

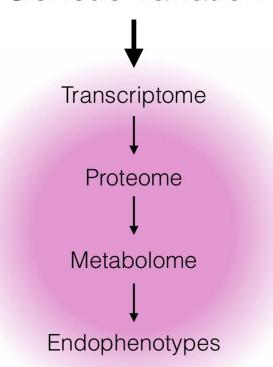
case study



Exploiting the cohort to study gene-by-environment interactions

case study

### Genetic variation





## Phenotypic variation

Synergistic participation of genotype and environment on the phenotype

Exploiting the cohort to study gene-by-environment interactions

case study

## Recombination affects accumulation of damaging and disease-associated mutations in human populations

Julie G Hussin, Alan Hodgkinson, Youssef Idaghd Jean-Philippe Goulet, Elias Gbeha, Elodie Hip-Ki

Nature Genetics **47**, 400–404 (2015) | Download



# High-Resolution Genomic Analysis of Human Mitochondrial RNA Sequence Variation

Alan Hodgkinson, 1x Youssef Idaghdour, 1,2x† Elias Gbeha, 1 Jean-Christophe Grenier, 1 Elodie Hip-Ki, 1 Vanessa Bruat, 1 Jean-Philippe Goulet, 2 Thibault de Malliard, 1,2 Philip Awadalla 1,2‡

Mutations in the mitochondrial genome are associated w processes; however, little is known about the extent of s transcriptome. By ultra-deeply sequencing mitochondrial blood of ~1000 individuals from the CARTaGENE project sequence variation within and across individuals, as well of posttranscriptional modification. Using a genome-wid posttranscriptional modification of functionally importan

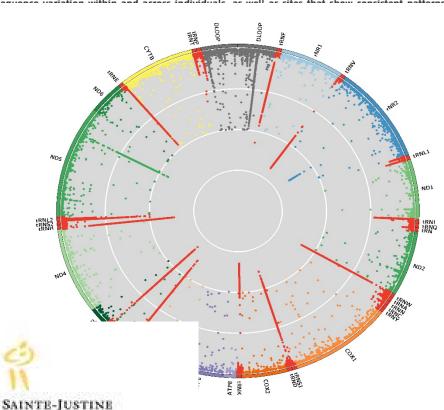


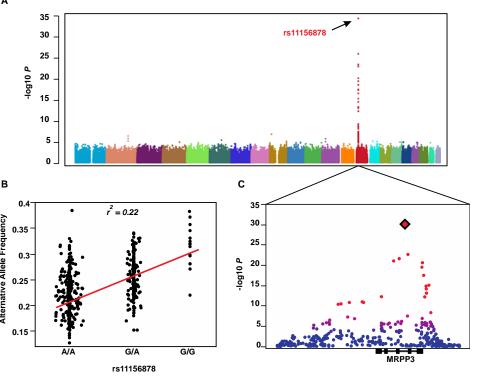
# High-Resolution Genomic Analysis of Human Mitochondrial RNA Science Sequence Variation



Alan Hodgkinson, <sup>1\*</sup> Youssef Idaghdour, <sup>1,2\*</sup>† Elias Gbeha, <sup>1</sup> Jean-Christophe Grenier, <sup>1</sup> Elodie Hip-Ki, <sup>1</sup> Vanessa Bruat, <sup>1</sup> Jean-Philippe Goulet, <sup>2</sup> Thibault de Malliard, <sup>1,2</sup> Philip Awadalla <sup>1,2</sup>‡

Mutations in the mitochondrial genome are associated with multiple diseases and biological processes; however, little is known about the extent of sequence variation in the mitochondrial transcriptome. By ultra-deeply sequencing mitochondrial RNA (>6000×) from the whole blood of  $\sim$ 1000 individuals from the CARTaGENE project, we identified remarkable levels of





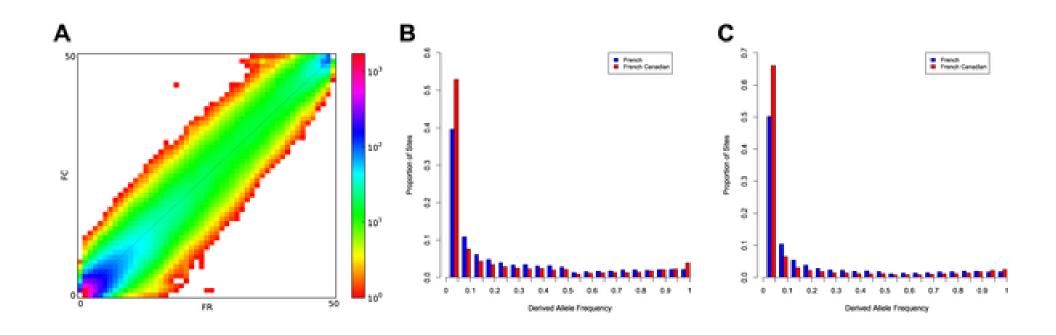
FOUNDATION

For the love of children

HOSPITAL.

## Site frequency spectrum of genetic variation in the French and French-Canadian populations

Unique demographic history: original bottleneck less than 20 generations ago followed by a demographic explosion and genetic isolation











Large population cohort

Founder population in Quebec

#### Environment







Transcriptome clinical traits

#### Genome



Ancestry: Continental and regional

#### Gene-by-environment interactions in urban populations modulate risk phenotypes

Marie-Julie Favé, Fabien C. Lamaze, David Soave, Alan Hodgkinson, Héloïse Gauvin, Vanessa Bruat, Jean-Christophe Grenier, Elias Gbeha, Kimberly Skead, Audrey Smargiassi, Markey Johnson, Youssef Idaghdour & Philip Awadalla

Nature Communications 9, Article number: 827 (2018) | Download Citation ±

#### Allele-specific expression reveals interactions between genetic variation and environment

David A Knowles, Joe R Davis, Hilary Edgington, Anil Raj, Marie-Julie Favé, Xiaowei Zhu, James B Potash, Myrna M Weissman, Jianxin Shi, Douglas F Levinson, Philip Awadalla, Sara Mostafavi, Stephen B Montgomery <sup>™</sup> & Alexis Battle <sup>™</sup>

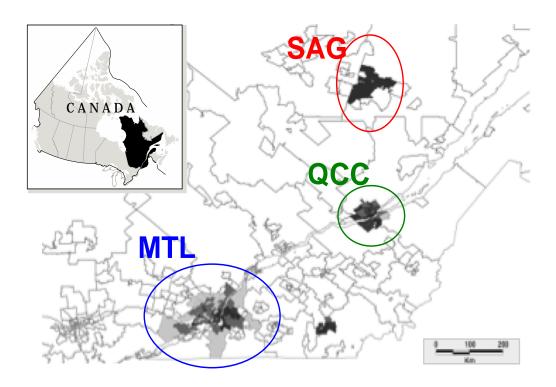
Nature Methods 14, 699-702 (2017) Download Citation ±



Unraveling the polygenic architecture of complex traits using blood eQTL meta-analysis

## French Canadian Genetics

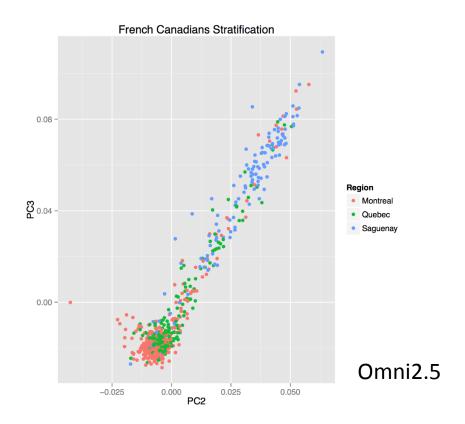
case study

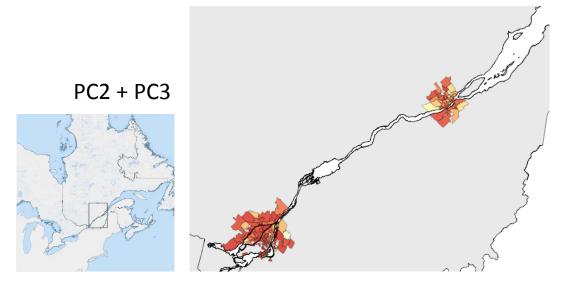


- The French Canadian (FC) gene pool is spatially structured with genetic diversity following a West-East gradient of similarity
- Regional founder effect in the Saguenay region

# Genotype structure follows a geographic cline

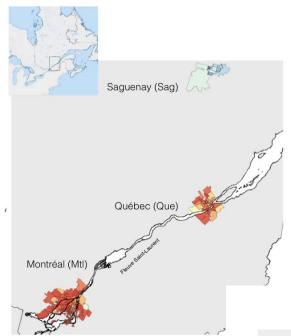
case study



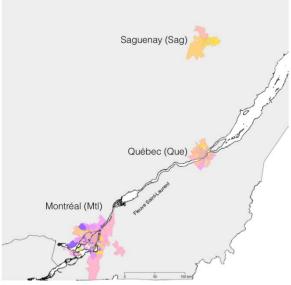


## Transcriptomic variation

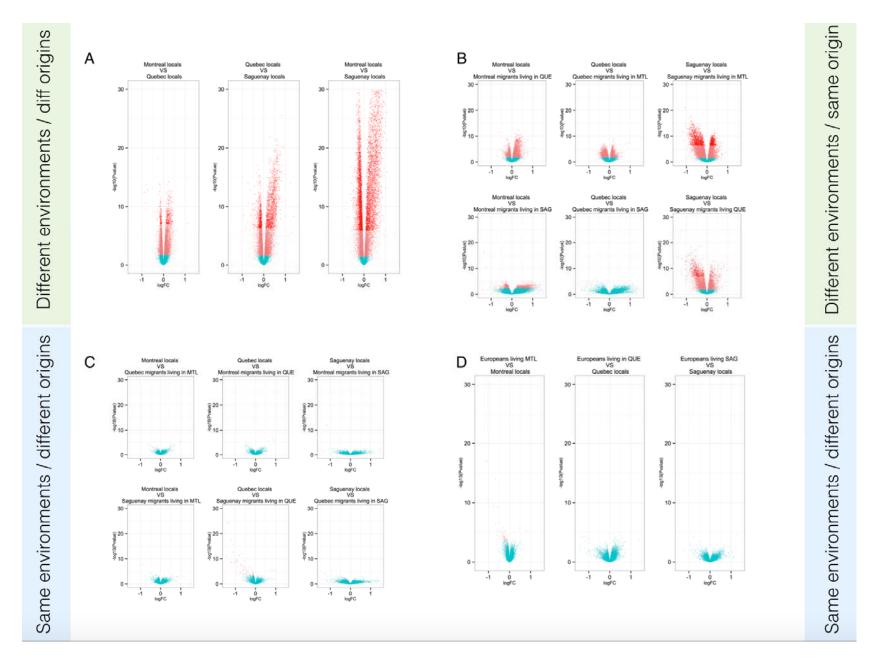
case study



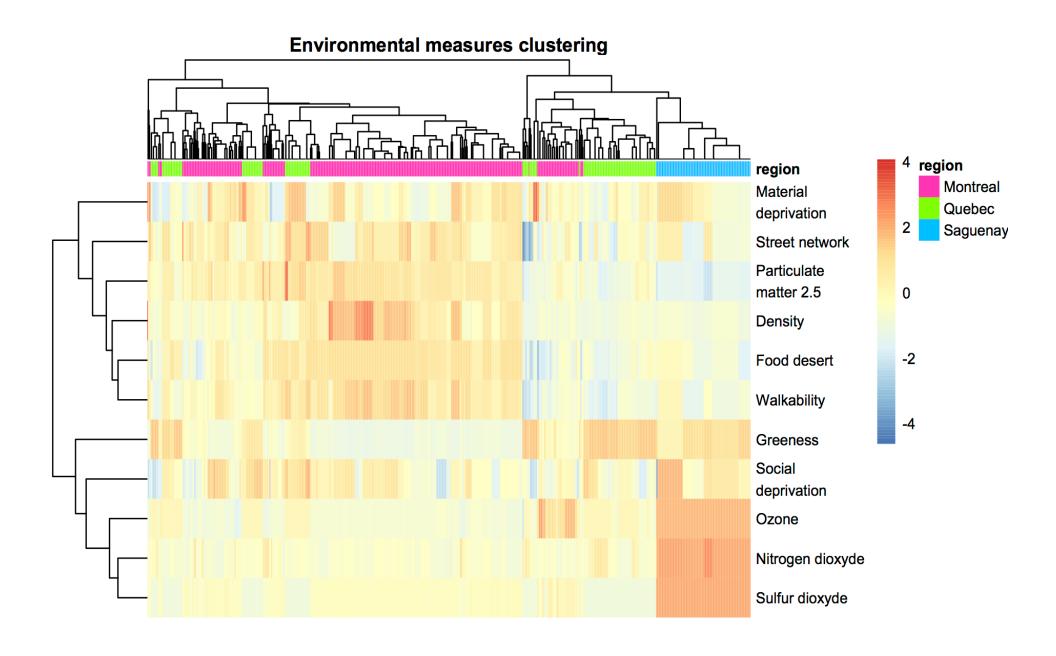
Genotypic cline



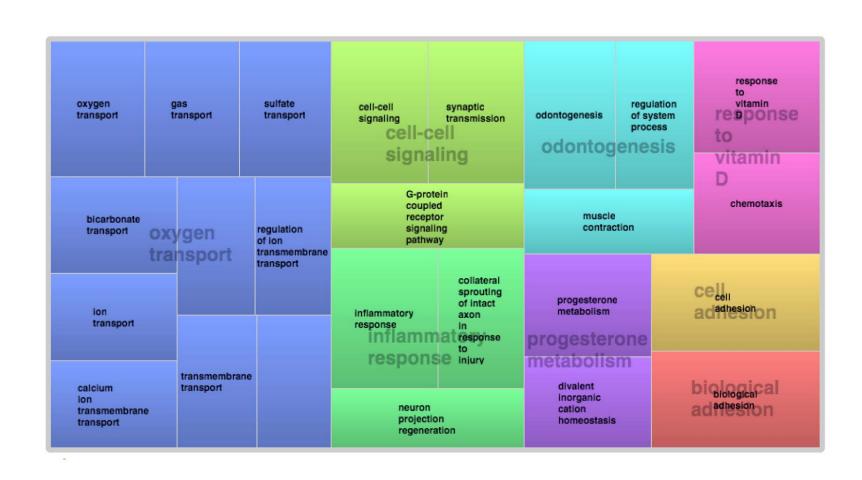
Transcriptomic cline DGE after SVA removals of SVs



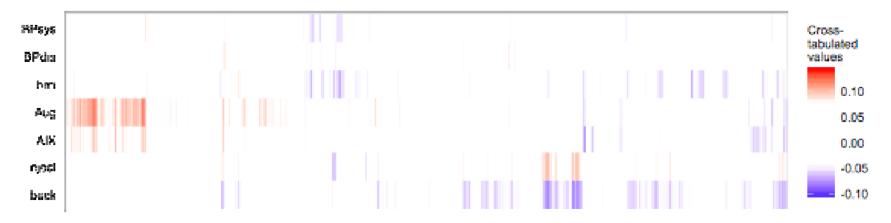
Marie-Julie Fave



## Gene enrichment - top 500 DE genes



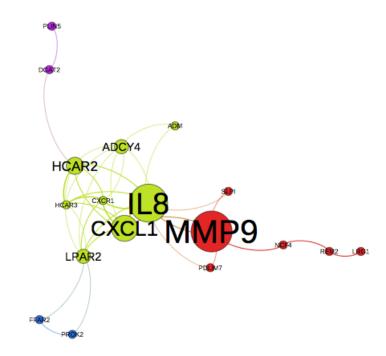
## Rare variant eQTLs interact with environment and are associated with arterial stiffness



Matrix 1: DEG between Mtl and Sag

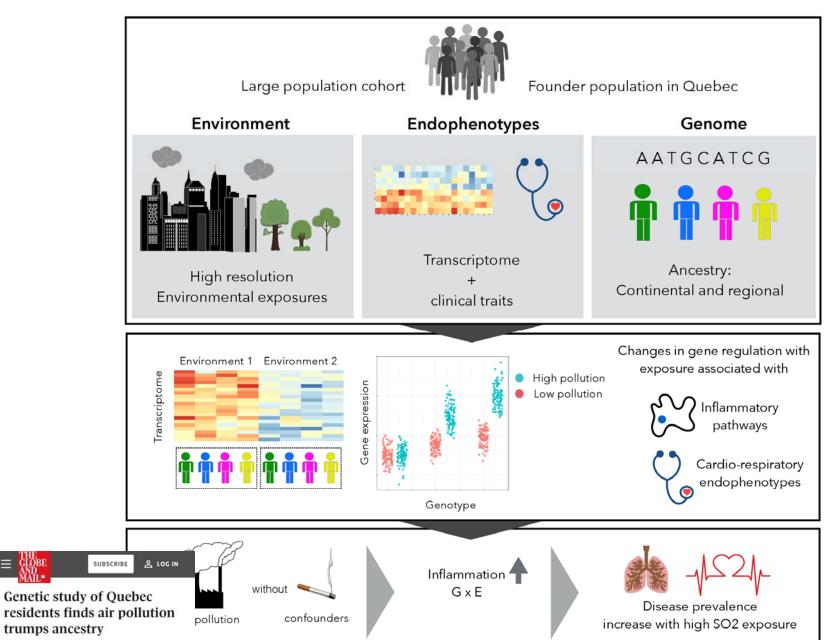
Matrix 2: Phenotypes

Association with AIX: among the genes that show the strongest association, we find 12 out of 18 genes from our MMP9 network (which was identified as associated with the pollution gradient).



Marie-Julie Fave, Nature communications

## Summary



trumps ancestry

## Ongoing and future enrichment

### Strategic Priorities (2017-2021)



- 1 Enrichment of the cohort with biomarkers
- 2 Linkages to environmental data
- Collection of residential and occupational histories
- 4 Regular follow-up questionnaires
- <sup>5</sup> Linkage of participants to their health-related records
- <sup>6</sup> Continued development of key strategic partnerships

## Accessing the CPTP Data

### portal.partnershipfortomorrow.ca



OME COHORT DATASETS BIOSAMPLES ACCESS -

The Canadian Partnership for Tomorrow Project (CPTP) Portal provides the research community with the necessary resources to identify epidemiological and biological data available from five participating cohorts to answer innovative research questions. A request for access to CPTP data is initiated directly through the CPTP Portal.

#### **Cohort design**



Find out more about the five regional cohorts of the CPTP.

Read more

#### **Datasets**



Find out more about the CPTP datasets and data harmonization approach.

Read more

## Biological samples



Find out more about CPTP's biological-sample collection and its upcoming availability.

Read more

#### Access



Find out more about CPTP Access Policy, the access process, and approved research projects.

Read more

Welcome to the CPTP Portal! The Portal includes comprehensive information on cohort design, the data harmonized across five regional cohorts, the biological samples collected, and CPTP's Access Policy and access process.

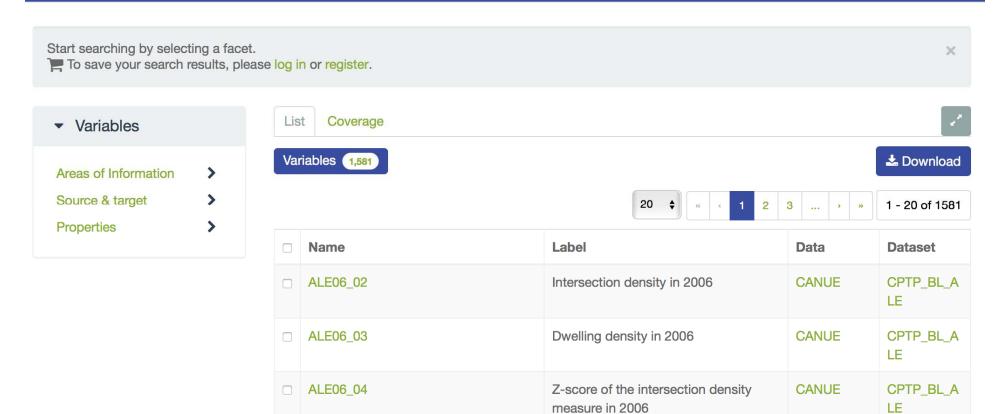
#### Data available

CPTP harmonized datasets are available to researchers through an access request and include:



HOME COHORT DATA BIOSAMPLES ACCESS → SEARCH SUPPORT →

## Search



52

## Accessing the CPTP Data



HOME

COHORT

DATASETS

BIOSAMPLES

ACCESS -

### **Access Process**

Requests for access, as well as requests for further information on the CPTP datasets, are received by the CPTP Access Office. Prior to submitting an Access Application Form, we strongly recommend that you consult the CPTP Policy documents, which will provide you with detailed information about the process and CPTP's access, publications and intellectual property policies. For inquiries about the access process, please contact our Access Office at access@partnershipfortomorrow.ca.

#### **CPTP Access Application Process**

#### STEP 1.

#### Create an account

Before initiating a request for access, all researchers must create a CPTP Portal User account.

#### STEP 2.

#### Complete and submit your request

Researchers are encouraged to contact the Access Office to understand the requirements involved before submitting an application.

When researchers are ready to complete and submit an access request, they must fill and submit an application form online and attach all of the required CPTP access documentation by logging into their CPTP Portal User account, and going to New Access Request.

#### STEP 3.

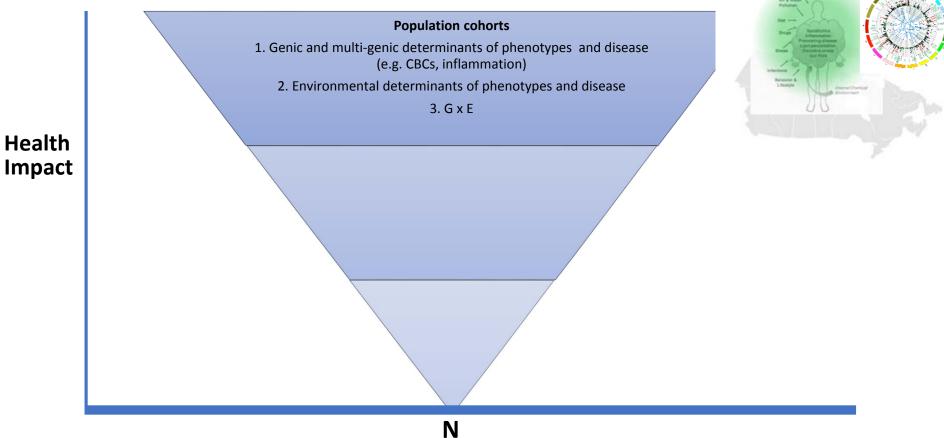
#### Track your request

Researchers will be able to track the progress and history of their access request online, by logging into their CPTP Portal User account, and going to My Access Requests.

### Accessing the **Applicant from approved** institution **CPTP** Data **CPTP Access Committee CPTP Access Office** Independent committee that **Access Officer** reviews and advises access **National Access Coordinator,** 3 **National Biosamples Coordinator** applications **CPTP Access Approved** Registry Research Public registry of **Project CPTP** approved

projects

Health Impact



## **Population cohorts** 1. Genic and multi-genic determinants of phenotypes and disease (e.g. CBCs, inflammation) 2. Environmental determinants of phenotypes and disease 3. G x E Health **Impact Disease Cohorts** 1. Genomic determinants (mutational and epigenomic) 2. Evolutionary dynamics of blood aging and malignancies.

#### **Population cohorts**

- 1. Genic and multi-genic determinants of phenotypes and disease (e.g. CBCs, inflammation)
  - 2. Environmental determinants of phenotypes and disease

3. G x E

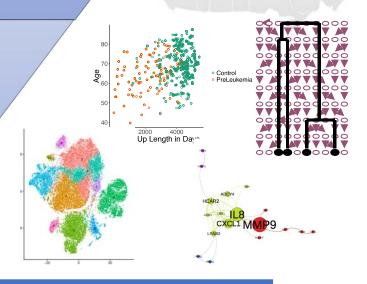
### Health Impact

#### **Disease Cohorts**

- 1. Genomic determinants (mutational and epigenomic)
- 2. Evolutionary dynamics of blood aging and malignancies.

#### **Individual Cellular populations**

- 1. Functional impact of aging on hematologic cellular populations
  - 2. Gene expression and phenotype or disease







Thank you to the Tomorrow Project participants across the 6 regional cohorts who generously donate their time, information and biological samples. The CPTP is a success because of the participants' ongoing commitment.





# Thank you to our sponsors and partners



































