



BQC19 – We made it ... and we want to continue, together

Vincent Mooser MD

Former Director BQC19 – Canada Excellence Research Chair CERC in Genomic Medicine

2nd Forum des Utilisateurs, CHUV / Virtual – November 29th, 2022

**Fonds de recherche
Santé**

Québec 



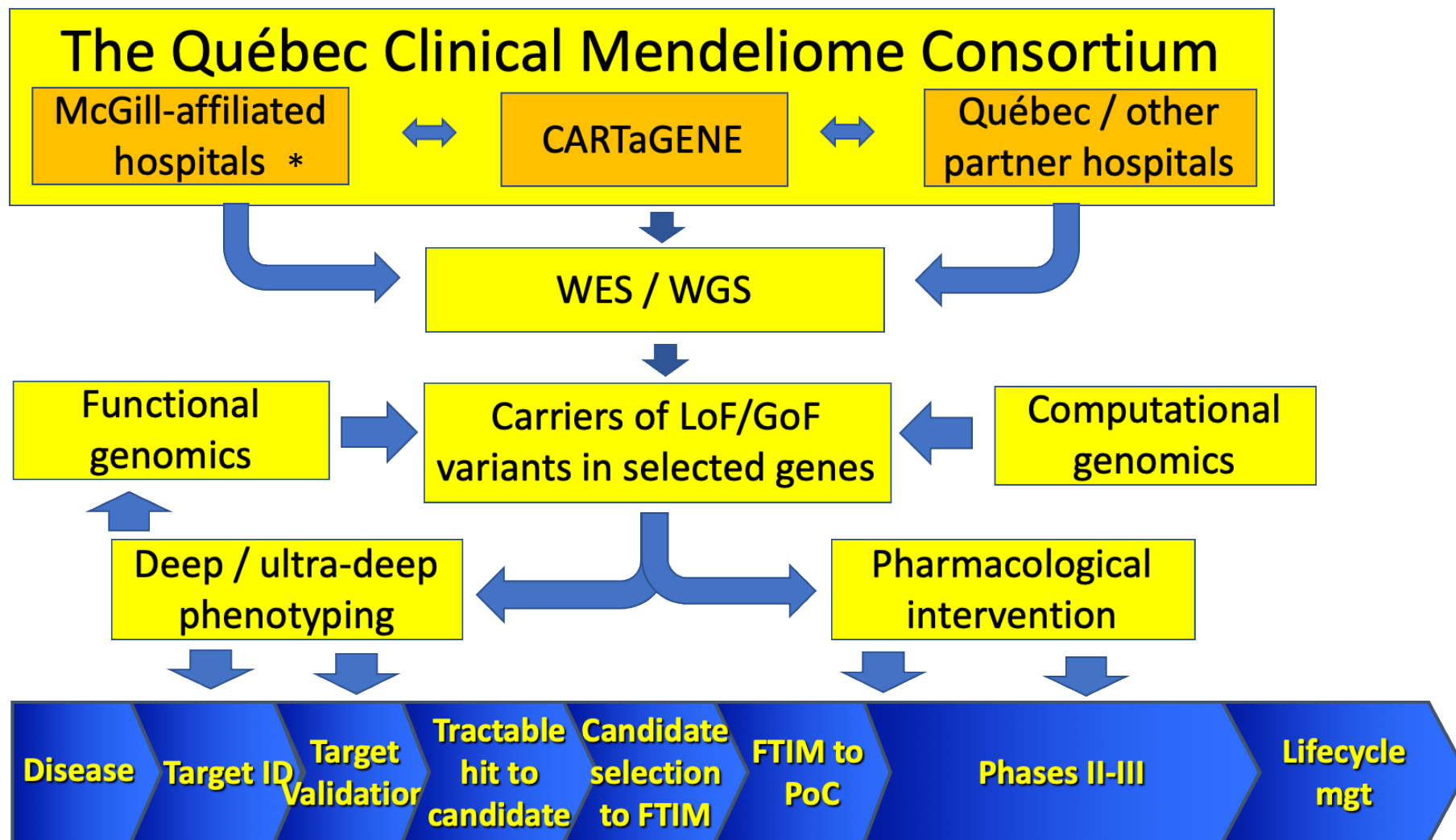
GenomeQuébec



Agence de la santé
publique du Canada

Public Health
Agency of Canada

CERC Overall Strategy



WES/WGS : whole exome/genome sequencing. LoF/GoF : Loss/Gain of function

*

How it all started...

Attendee Meeting **Format Text**

 **Delete**  **Appointment**  **Scheduling**  **Join Online**  **Accept**  **Tentative**  **Decline**  **Propose New Time**  **Reply**  **Reply All**  **Forward**  **Flag**

Subject: Rencontre Québec clinical mendeliome

Location: ZOOM

Organizer: Carole.Jabet@frq.gouv.qc.ca <Carole.Jabet@frq.gouv.qc.ca>

Duration: ☒ 1 Hour ☐ All day event

Starts: 2020-03-19  2:30 PM

Ends: 2020-03-19  3:30 PM

 This appointment occurs in the past.

 Accepted on 2020-03-16, 11:04 AM.

<https://zoom.us/j/140654766?pwd=WEtsQWxuT3FhdmczUDd3MHNqUjZtdz09>

All Attendees	
	Carole.Jabet@f...
	Quirion, Rémi
	dcoderre@geno...
	paul.larchevequ...
	Vincent Mooser,...
	smarchand@ge...
	flefebvre@geno...
	asmaa.kaima@...

Mandate given to BQC19

Support research to identify clinical and molecular determinants of COVID-19 susceptibility, severity and outcome

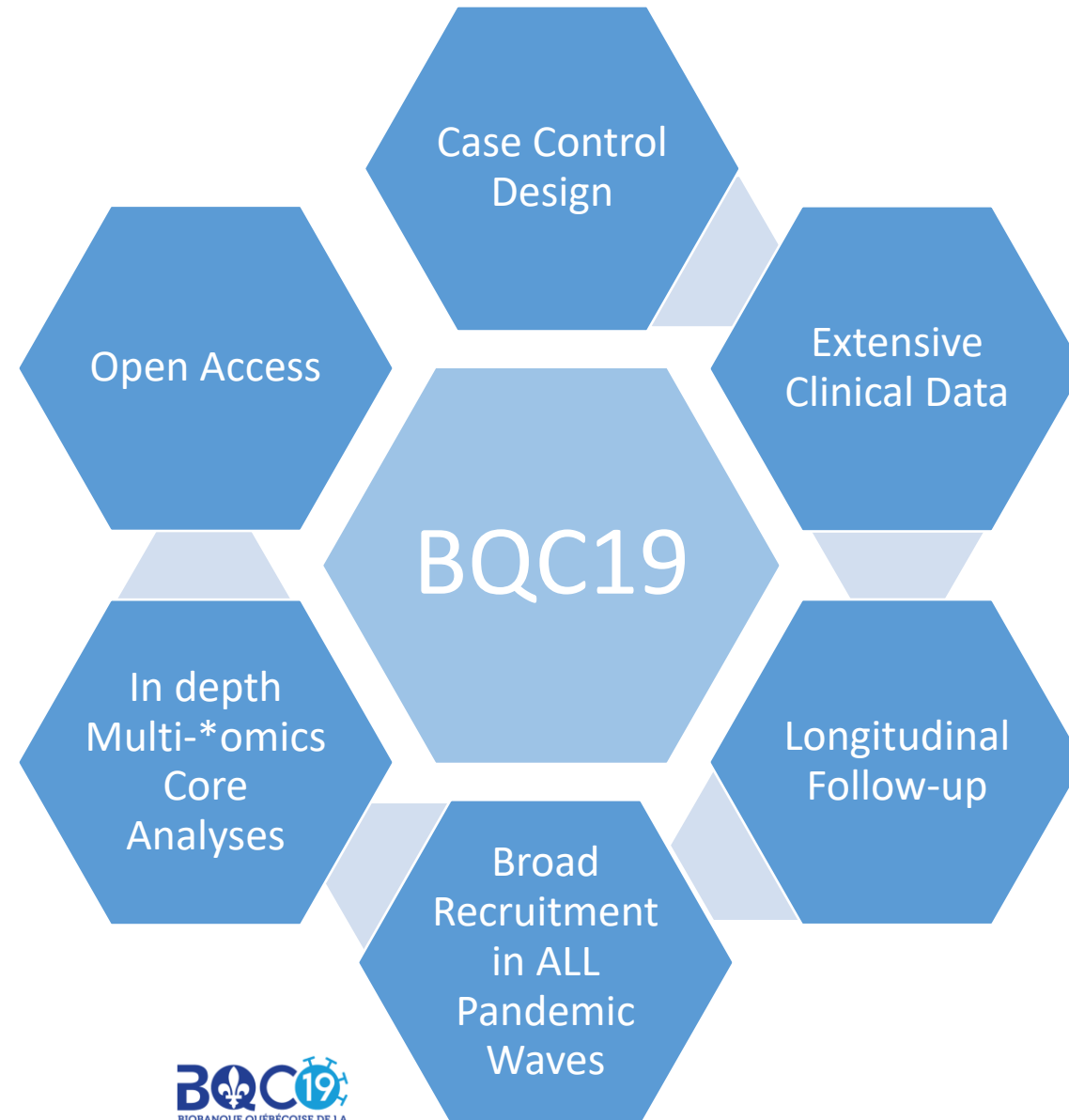
The BQC19 Task Force (Mar 22nd → Apr 21st 2020)

→ The BQC19 Executive Committee

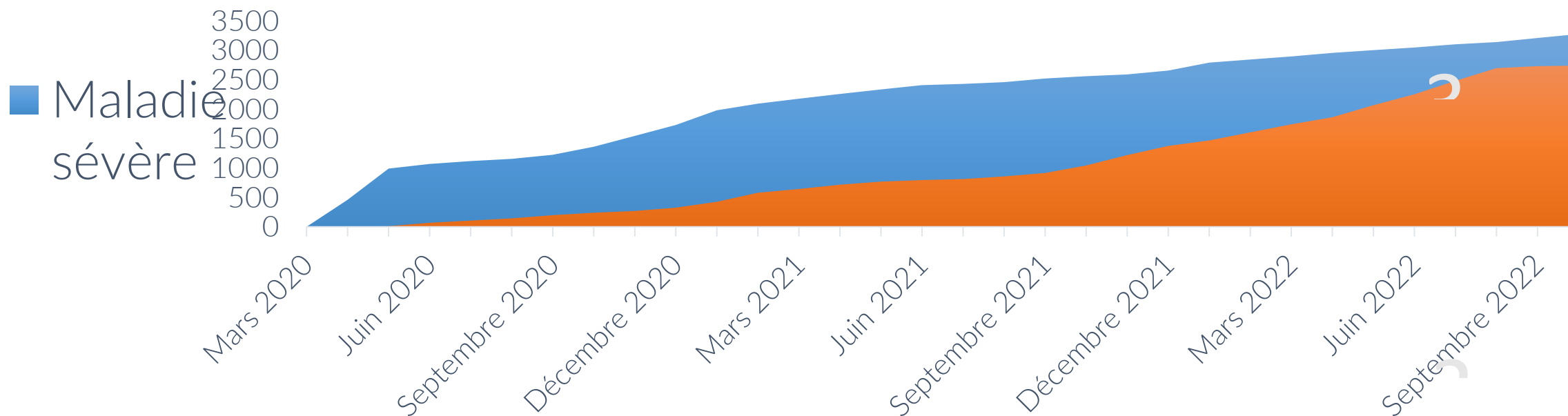
• Chair	Vincent Mooser MD	McGill / CERC
• *FRQS representative	Carole Jabet PhD	FRQS
• GQ representative	Alexandre Montpetit PhD	GQ
• IT	Michael Chassé MD PhD	UdeM / CHUM
• Science	Daniel Kaufmann MD	UdeM / CHUM
• Collaborations	Brent Richards MD PhD	McGill / JGH
• Network	Simon Rousseau PhD	McGill / MUHC
• Operations	Dan Auld PhD	McGill / Genome Center
• Communication	Karine Tremblay PhD	UQAC
• Populations	François Gros-Louis PhD	U Laval
• Ethics – law	Ma'n Zawati PhD	McGill/Centre of Genomics & Policy
• Pediatrics	Sze Man Tse MD PhD	UdeM / CHUSJ

* On the Task Force only

Uniqueness of BQC19



Recrutement participants (11 novembre 2022)



Participants

* Financement 2020-2022

4 035

Participants 5e vague

* Recrutés entre 26 déc 2021 et 31 mars 2022

605

Participants

* Financement 2022-23

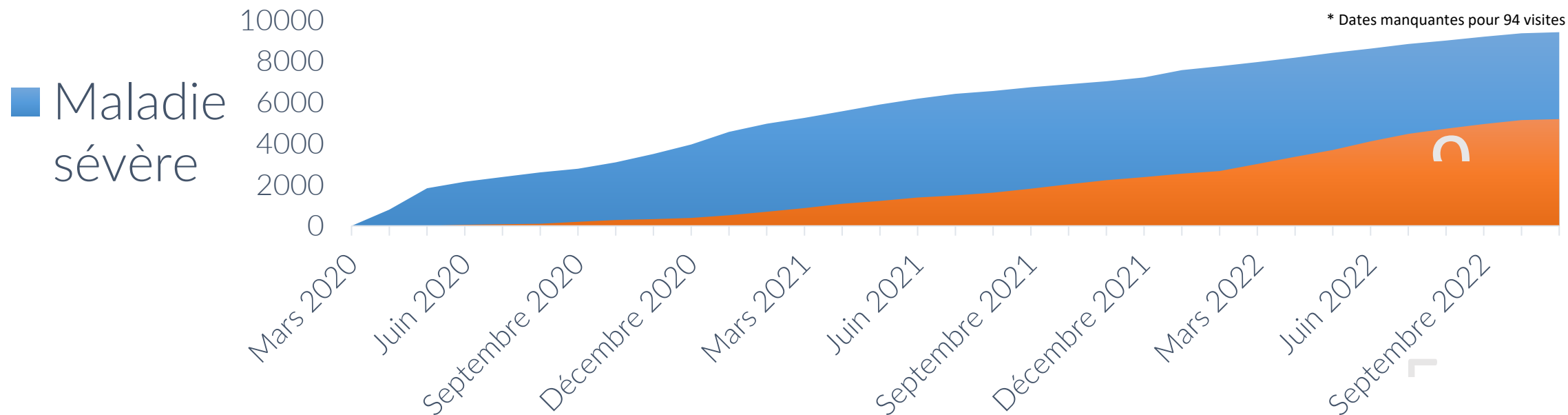
1 411

Participants réinfectés

25

7

Visites effectuées (11 novembre 2022)



Visites

* Financement 2020-2022

11 634

Visites 5e vague

* Recrutés entre 26 déc 2021 et 31 mars 2022

1 398

Visites

* Financement 2022-23

1 680

Visites réinfection

25

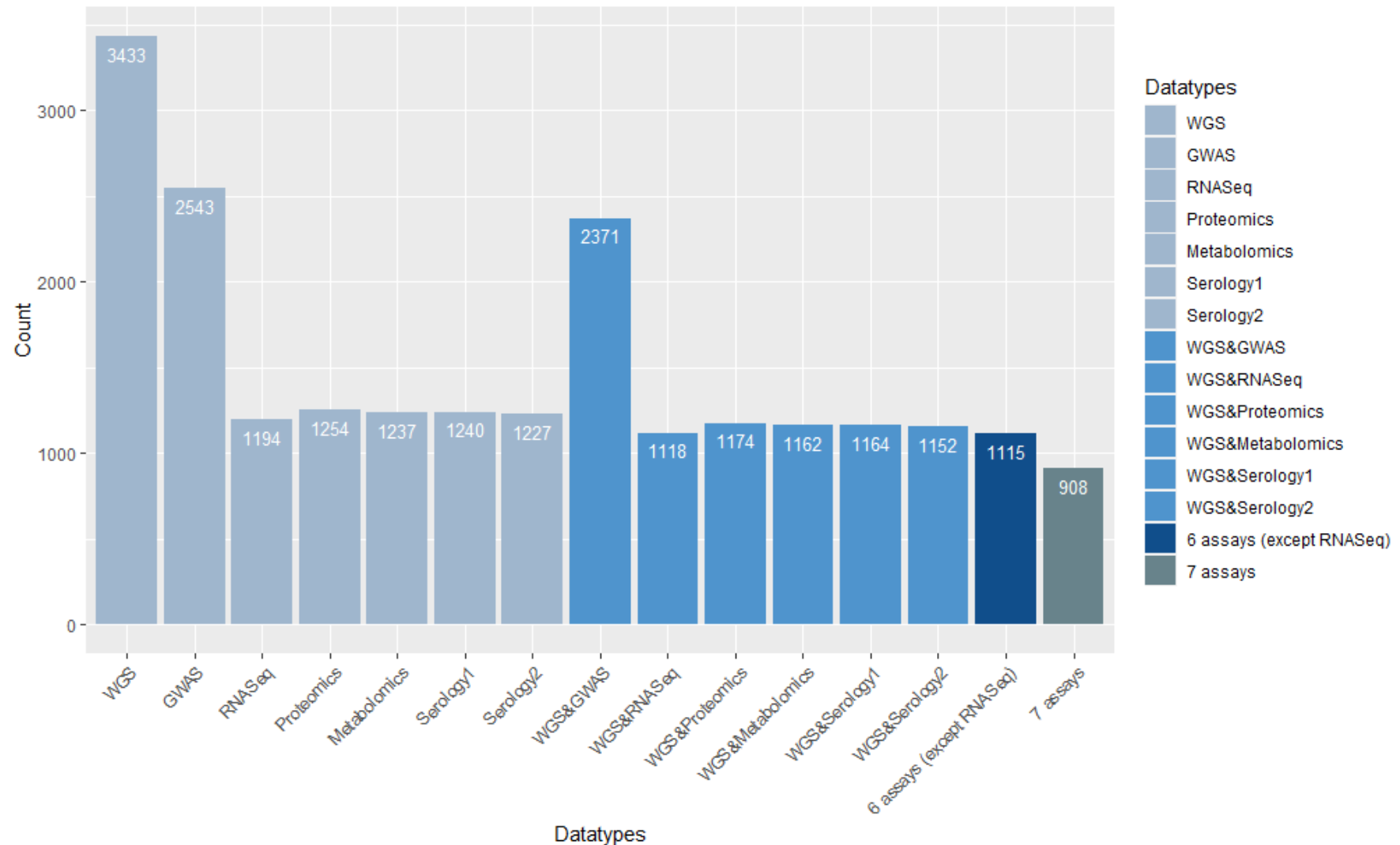
2

Mise à disposition des données

		Nombre total de participants Partage #8	Nombre d'ensemble de données Partage #8	Nombre total de participants Partage #9	Nombre d'ensemble de données Partage #9	Nombre total de participants Disponible	Nombre d'ensemble de données Disponible
Cliniques / Phénotypiques	ENRICHI	5143	30,243 (row)	6017	34,036 (row)	6017	34,036 (row)
RNA-seq	ENRICHI	938	1545	1279	1926	1279	1926
WGS GWAS <i>Axiom array genotype</i>	ENRICHI	3,290	3,290 2,543 2,441	3,487	3,487 2,543 2,441	3,487	3,487 2,543 2,441
Immuno-sérologie #1	COMPLET	-	-	-	-	1240	1969
Immuno-sérologie #2		1228	1911	1228	1,911	1228	1,911
Métabolomique	COMPLET	-	-	-	-	1,238	1,966
Protéomique #1 - Somalogic	COMPLET	-	-	-	-	1,254	1,957

Mise à disposition des données

Ensemble de données disponibles par patient



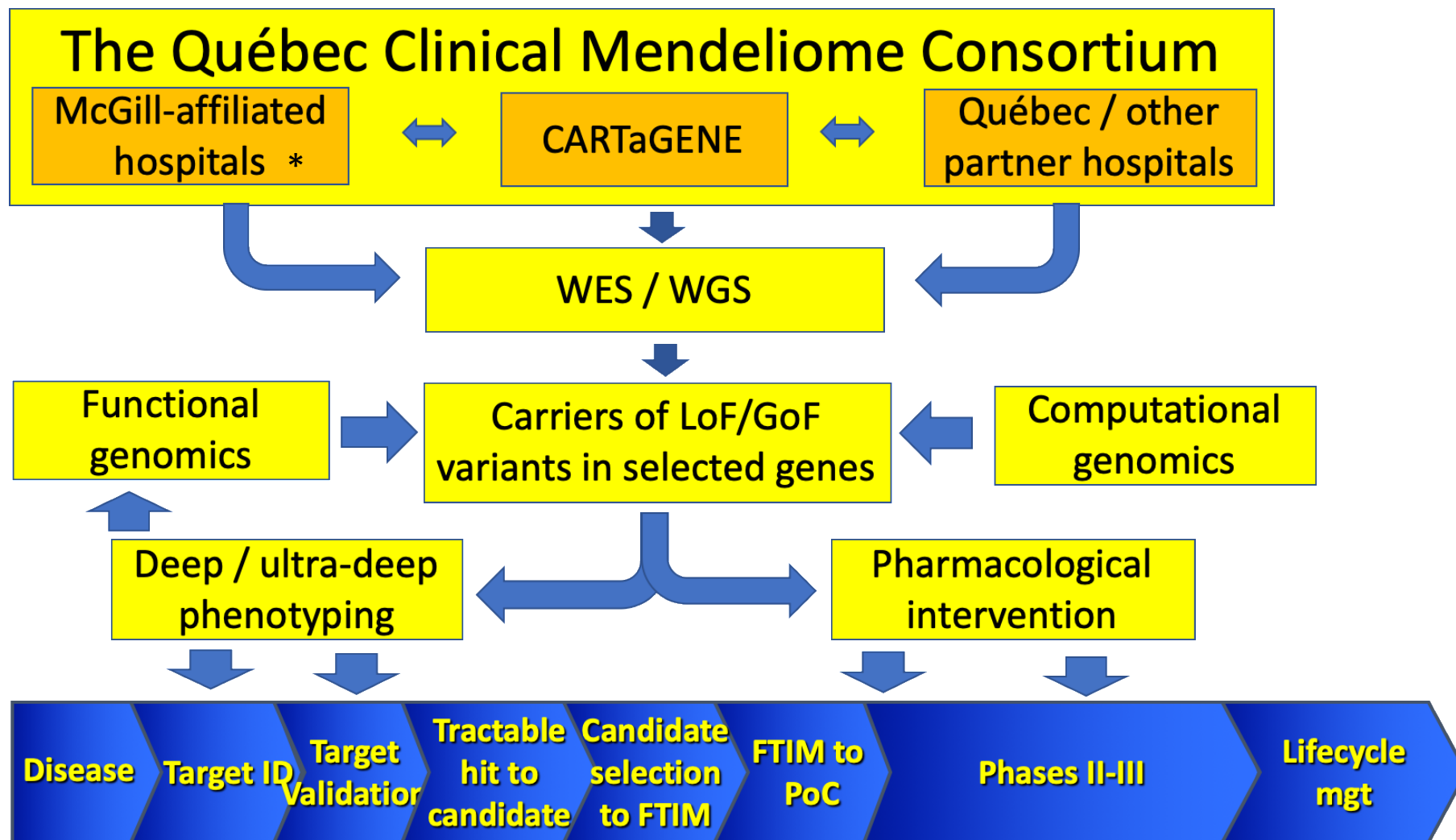
Publications

1. Knoppers, B.M., et al., *Modeling consent in the time of COVID-19*. J Law Biosci, 2020. **7**(1): p. Isaa020.
2. Butler-Laporte, G., et al., *The effect of angiotensin-converting enzyme levels on COVID-19 susceptibility and severity: a Mendelian randomization study*. Int J Epidemiol, 2021. **50**(1): p. 75-86.
3. Zhou, S., et al., *A Neanderthal OAS1 isoform protects individuals of European ancestry against COVID-19 susceptibility and severity*. Nat Med, 2021. **27**(4): p. 659-667.
4. Rebillard, R.M., et al., *Identification of SARS-CoV-2-specific immune alterations in acutely ill patients*. J Clin Invest, 2021. **131**(8).
5. Tremblay, K., et al., *The Biobanque quebecoise de la COVID-19 (BQC19)-A cohort to prospectively study the clinical and biological determinants of COVID-19 clinical trajectories*. PLoS One, 2021. **16**(5): p. e0245031.
6. Butler-Laporte, G., et al., *Vitamin D and COVID-19 susceptibility and severity in the COVID-19 Host Genetics Initiative: A Mendelian randomization study*. PLoS Med, 2021. **18**(6): p. e1003605.
7. Initiative, C.-H.G., *Mapping the human genetic architecture of COVID-19*. Nature, 2021. **600**(7889): p. 472-477.
8. Kosmicki, J.A., et al., *Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals*. Am J Hum Genet, 2021. **108**(7): p. 1350-1355.
9. Povysil, G., et al., *Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19*. J Clin Invest, 2021. **131**(14).
10. Brunet-Ratnasingham, E., et al., *Integrated immunovirological profiling validates plasma SARS-CoV-2 RNA as an early predictor of COVID-19 mortality*. Sci Adv, 2021. **7**(48): p. eabj5629.
11. Nakanishi, T., et al., *Age-dependent impact of the major common genetic risk factor for COVID-19 on severity and mortality*. J Clin Invest, 2021. **131**(23).
12. Fallarini, C., et al., *Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity*. Hum Genet, 2022. **141**(1): p. 147-173.
13. Huffman, J.E., et al., *Multi-ancestry fine mapping implicates OAS1 splicing in risk of severe COVID-19*. Nat Genet, 2022. **54**(2): p. 125-127.
14. Kousathanas, A., et al., *Whole-genome sequencing reveals host factors underlying critical COVID-19*. Nature, 2022. **607**(7917): p. 97-103.
15. Initiative, C.-H.G., *A first update on mapping the human genetic architecture of COVID-19*. Nature, 2022. **608**(7921): p. E1-E10.
16. Butler-Laporte, G., et al., *The dynamic changes and sex differences of 147 immune-related proteins during acute COVID-19 in 580 individuals*. Clin Proteomics, 2022. **19**(1): p. 34.
17. Butler-Laporte, G., et al., *Exome-wide association study to identify rare variants influencing COVID-19 outcomes: Results from the Host Genetics Initiative*. PLoS Genet, 2022. **18**(11): p. e1010367.

In press/under peer review

18. *SARS-CoV-2 infection outcomes associated with the Delta variant: A prospective cohort study*. (A. Piché) JAMMI Doi :10.3138/jammi-2022-0022 Octobre 2022
19. *Prevalence of persistent symptoms at least one month after SARS-CoV-2 Omicron in adults*. (A. Piché) JAMMI Doi:10.3138/jammi-2022-0026 Octobre 2022
20. Ma, W., et al., *Circulating proteome of hospitalized patients uncovers six endophenotypes of COVID-19 and points to FGFR and SHC4-signaling in acute respiratory distress syndrome* medRxiv : <https://doi.org/10.1101/2022.11.02.22281834>, submitted to Immunity, novembre 2022

CERC Overall Strategy



* McGill Clinical Genomics (MCG) Program. WES/WGS : whole exome/genome sequencing. LoF/GoF : Loss/Gain of function

