Cohort

Sample ID	long-COVID	Sex	Severity	Age
AD-021	No	Female	Cohort A = Community based	47
AD-090	No	Female	Cohort A = Community based	24
AD-080	No	Female	Cohort A = Community based	39
AD-301	No	Female	Cohort A = Community based	55
AD-317	No	Female	Cohort A = Community based	58
AD-018	No	Male	Cohort A = Community based	43
AD-048	No	Male	Cohort A = Community based	59
AD-062	No	Male	Cohort A = Community based	37
AD-074	No	Male	Cohort A = Community based	55
AD-020	No	Male	Cohort B = Inpatient	63
AD-022	Yes	Female	Cohort A = Community based	57
AD-313	Yes	Female	Cohort A = Community based	57
AD-315	Yes	Female	Cohort A = Community based	39
AD-322	Yes	Female	Cohort A = Community based	40
AD-320	Yes	Male	Cohort A = Community based	36
AD-323	Yes	Male	Cohort A = Community based	40
AD-303	Yes	Female	Cohort B = Inpatient	48
AD-007	Yes	Male	Cohort B = Inpatient	63
AD-011	Yes	Male	Cohort B = Inpatient	59
AD-016	Yes	Male	Cohort B = Inpatient	57

Blood samples were collected from 10 patients in the ADAPT study that had long-COVID symptoms two years after their original infection with SARS-COV2.*

An additional 10 blood samples were collected from patients that were also infected but had fully recovered.

In each of these groups, we have 5 females and 5 males, age matched. The severity of the original illness was classified based on hospital admission.

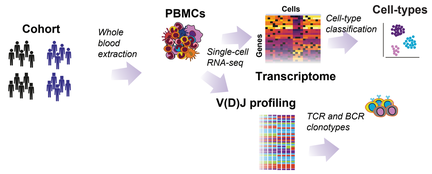
**Darley et al. (2021) Persistent symptoms up to four months after community and hospital-managed SARS-CoV-2 infection. The Medical Journal of Australia.*

github

Immune profiling of peripheral blood mononuclear cells (PBMCs)

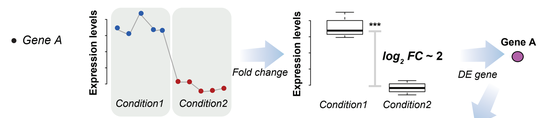
Samples are currently being sequenced on the 10X genomics platform. We are using the 5' gene expression and V(D)J profiling of B-cell and T-cell receptors.

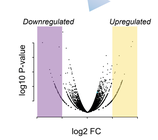
This will provide transcriptional profiles for each cell, and the antigen receptor profiles for B and T lymphocytes. T cells and B cells express receptors that recognize antigens and receptor repertoire analysis is useful for evaluating the diversity of an immune system.



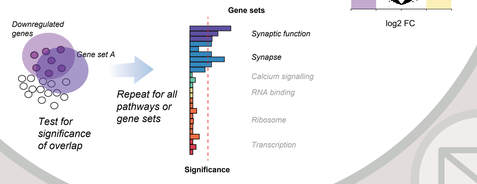
Expression analysis

Differential expression



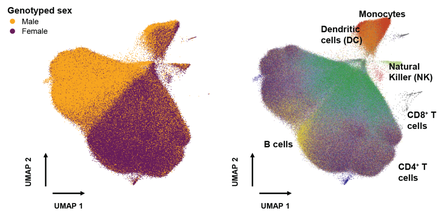


Pathway enrichment analysis



Exploring sex differences of long-COVID-19 at single-cell resolution

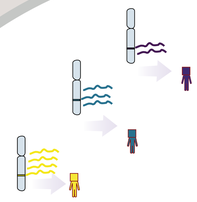
Single-cell UMAP of 1.2M PBMCs from the OneK1K* cohort



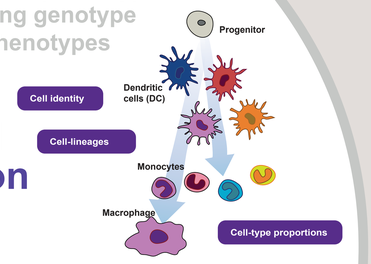
**Yazar et al. (2022). Single-cell eQTL mapping identifies cell type–specific genetic control of autoimmune disease. Science.*

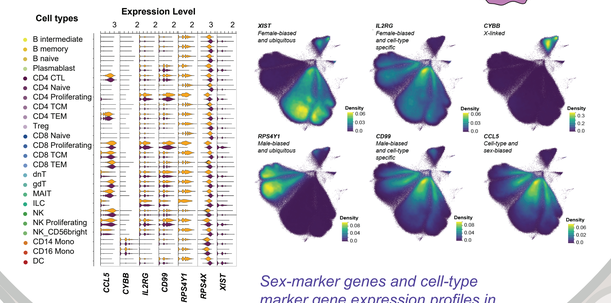
website

Single-cell RNA-seq for cellular resolution of gene expression



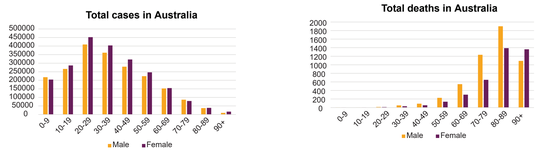
Transcriptome is an endophenotype linking genotype to phenotypes





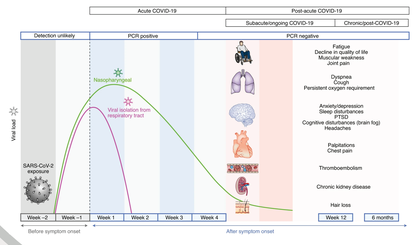
Sex-marker genes and cell-type marker gene expression profiles in the OneK1K cohort.

Death rates are different across sex and age



https://www.health.gov.au/health-alerts/covid-19/case-numbers-and-statistics#cases-and-deaths-by-age-and-sex

More males die from COVID-19 complications while females suffer more from long-COVID



Nalbandian et al. (2021). Post-acute COVID-19 syndrome. Nature Medicine.

Long-COVID refers to persistent symptoms beyond 3 months of infection

Interested? Reach out!

Sara Ballouz, PhD
email: s.ballouz@garvan.org.au
Group leader
Garvan-Weizmann Centre for Cellular Genomics

Conjoint Lecturer,
School of Medical Sciences,
UNSW Medicine

Questions to explore:

What genes and pathways are differentially expressed in long-COVID?

Interferons
Inflammatory cytokines
Lymphocte activation and dysregulation
Chronic myeloid cell activation

Are these the same when we look at sex-specific differential expression?

Autoimmunity

Viral reservoirs or viral remnants

Are there cell-type differences between cases and those who recover?

Long-COVID hypotheses

Dysbiosis

Tissue damage

Merad et al. The immunology and immunopathology of COVID-19. Science. (2022).

What other cellular or gene profiles are associated with long-COVID symptoms?

Garvan Institute of Medical Research

GARVAN–WEIZMANN CENTRE FOR CELLULAR GENOMICS