Ramaciotti Centre for Genomics

Annual Report 2022/2023

UNSW SYDNEY

Next generation science.
Working for you.

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Acknowledgement of Traditional Owners
We would like to acknowledge the Bedegal people that are the Traditional Custodians of the land on which the Ramaciotti Centre for Genomics is located. We pay our respects to the elders, past, present, and future, and recognise their continuing connection and contribution to this land.

Disclaimer
The information contained in this publication is correct at the time of printing but may be subject to change without notice. Please check the Centre's website for the latest information. UNSW assumes no responsibility for the accuracy of information provided by third parties.

Design
Slingshot Design

About Us

The Ramaciotti Centre for Genomics is Australia's leading genomics research and resource centre with the capabilities to deliver data, analysis, guidance and advice of the highest quality. It is a national infrastructure facility and a focus for the development and application of genomics in Australia. It was established in 1999 and is the largest genomics facility at any Australian University. It is comprehensively equipped with the latest next-generation sequencing technology, expression analysis and high throughput microarray systems.

Our Mission
Is to deliver internationally competitive genomic services of the highest quality using leading edge technology.

Our Objectives
- To provide our users with access to enabling technology and services, facilitating internationally competitive research.
- To provide genomics and related services of the highest possible quality.
- To provide support for bespoke and niche projects.
- To provide services at competitive rates.
- To build the genomics community in the state of NSW and beyond.

Our Values
- Excellence
- Collaboration
- Innovation
- Diversity
- Respect

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Acting Director's Report

Helena Mangs, Nov 2022-Dec 2023

The Ramaciotti Centre for Genomics has continued to excel in delivering genomic services to our client base. I am pleased to report that the Centre was successful in acquiring infrastructure support under a 5-year NCRIS grant, distributed via Bioplatforms Australia for 2023-2028. We are utterly grateful for the support from Bioplatforms Australia, which ensures that the Centre can continue to grow operations and support cutting-edge genomics research in NSW and beyond.

In 2023, the Centre processed a staggering 130,213 samples, up from 90,004 the year before. These were distributed over approximately 1,000 projects per year, so there was never a dull moment. We completed a large project for Sydney Water, producing 27,000 amplicons from freshwater and estuarine locations around Sydney. In addition, we processed samples from a variety of species: plants, bacteria, fungi, insects, trees, birds, fish, mammals—you name it, we have likely sequenced or genotyped it over 2022 and 2023!

We continued our collaboration with Prof. Vanessa Hayes, sequencing human whole genome prostate cancer patient samples and investigating health disparities between the South African population and Western society. The collaboration was highlighted in a video produced by the vendor Illumina, as it coincided with the acquisition of the high-throughput sequencer, the NovaSeq X Plus. The Centre was one of the first facilities to receive a NovaSeq X Plus in Australia, showing how the Centre keeps up with the newest technology to support researchers' needs.

In addition to the NovaSeq X Plus purchase, the Centre also acquired a NextSeq 1000 and an iScan/Infinium RoMa system. The latter supports genotyping and methylation arrays, complementing our Thermo Fisher Axiom genotyping system. Of the 220,217 samples processed over 2022-2023, 129,899 were processed by next-generation sequencing, 44,623 by microarray, 44,435 by Sanger sequencing, and 1,260 by NanoString technology.

The Centre continued to use robotics to assist in processing, but despite this, the enormous workload on our laboratory scientist staff must be acknowledged. I am eternally grateful for their commitment and hard work, and I am in awe of how they were able to handle the large, ongoing "never-ending" influx of samples. I must send a special shoutout to our next-generation sequencing and data team, who had to implement updated pipelines for our new sequencers and deal with teething issues that occurred during the first few months after installation. They, together with the Illumina Service Managers, navigated the rocky transition, and their expertise is truly remarkable.

Outreach and teaching future genomic scientists is key at UNSW. Our highly trained staff, many with research backgrounds, enjoyed showcasing our facility during 2022-2023 tours. On top of this, we passed our second surveillance audit by NATA, held nine successful internal audits, and worked on adding the PCR-free sample prep pipeline to our existing ISO17025 scope. This was truly a group effort, so I thank the full team, both laboratory, administration, and project management staff for this.

I would also like to thank our management team and steering committee for their commitment to the Centre. The Service Managers team and our Quality Manager excelled in service provision and assisted the hundreds of researchers that depend on our services. Their expertise, project management skills, and team leadership strongly contributed to our Centre's ongoing success. Our steering committee, made up of members from the NSW leadership and research community, provided excellent advice on our direction and strategy. I thank them for their contributions during 2022 and 2023.

Starting January 2024, we are thrilled to start a new era with the arrival of Dr. Martin Smith as our new Director. Dr. Smith, a seasoned computational biologist with a wealth of experience in genomics, will be a valuable addition to our team. We are excited to welcome him on board! Lastly, but not least, I must thank Professor Marc Wilkins, our former Director. Marc took up the Directorship role in 2011 and provided enormous leadership and strategic direction until he resigned in late 2022 to pursue a Deputy Dean of Research and Enterprise role at the Faculty of Science. The Centre team and I cannot thank him enough for his wisdom, enthusiasm, leadership, and strategic knowledge. We are pleased to still see him around in the Biosciences building. To all our collaborators, partners, clients, funding bodies, and other stakeholders, we look forward to continuing to support the national and international genomics community in the years to come.

Former Director's Report

Marc Wilkins, 2011 – 2022

I stepped down from the role of Director of the Ramaciotti Centre for Genomics in late 2022, to join the Faculty Executive team as Deputy Dean (Research and Enterprise). I was sad to be leaving the wonderful team that is the Centre, yet at the same time was proud to have witnessed its successes over an extended time. It remains the largest genomics facility at any Australian university and that which has supported the work of thousands of researchers in NSW and beyond.

When I joined the Centre as Director in 2011, after serving as Deputy, the genomics revolution was just beginning. The Centre had taken delivery of a Roche 454 sequencer, an Illumina GA II genome analyser and was running a suite of Affymetrix microarray stations. It had just retired its custom microarray robot. Any week where we managed a complete run on a next-generation sequencer was a victory; the technology worked but instruments were temperamental. The situation was not helped by our air conditioning, which was something between evil and vindictive. And since a paired-end run on the GA II took 9 long days, there were moments of utter misery when the instrument or the air conditioner or both conked out on day 8. We then had to start again. All of that effort for just 150 million reads per run. We were nevertheless delighted to have analysed about 500 samples in our first year of next-generation sequencing. It was a major achievement at that time.

In 2022, and now 2023, much has changed. The capacity of the Centre and the scale at which it operates is exceptional. As noted in the Helena's Acting Director's report, the Centre analysed a total of 130,000 samples in 2022-2023 by next-generation sequencing and a further 90,000 by genotyping or Sanger sequencing. The Centre's Illumina NovaSeq X Plus instrument can generate up to 52 billion reads per run and do that in about 2 days. One hundred and twenty-eight human genomes can be sequenced in one go. The march of genomic technology has been relentless, and the Centre has played an important role in the NSW biomedical community by keeping at the very cutting edge. It has helped researchers from all facets of the life and medical sciences stay internationally competitive in their fields.

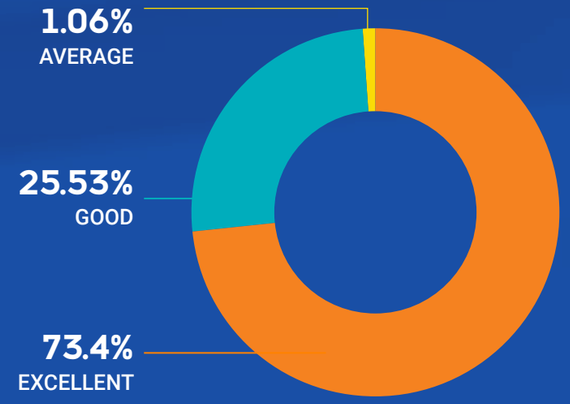
> The march of genomic technology has been relentless, and the Centre has played an important role in the NSW biomedical community by keeping at the very cutting edge.

There's been too many firsts and milestones to remember but some to mention are the sequencing of our first human genomes on the HiSeq 2000, revolutionary work to facilitate microbiome analysis via 16S amplicon analysis, the long-read sequencing and assembly of the koala genome, our first 10,000 sample genotyping project and our one-millionth sample analysed for one lucky researcher. You know who you are!

All of the above has only been possible through work of extraordinary individuals in the Centre, working as an extraordinary team. I thank them all for making my time as a Director an absolute privilege and pleasure. Very special acknowledgements and thanks go to Helen Speirs, Helena Mangs, Jason Koval and to Tonia Russel, with whom I had the chance to work closely for so long. For Helena, extra special thanks for taking on the responsibility of the Directorship. Thanks must also go to Bioplatforms Australia, for their continuous encouragement and support, to the Australian Research Council for considerable LIEF grant support, and to the University of New South Wales for recognising and supporting the Centre's ambitions. Final thanks must go to Ian Dawes, who gave me the opportunity to lead such an exceptional Centre, and for establishing the Centre's culture of excellence and collaboration. I look forward to seeing the Centre's continued growth and success; while no longer in the team I will continue to barrack from the sidelines.

Highlights from 2022 and 2023

Outreach activities



2023 client satisfaction survey

Operational output

220,217 samples processed

We processed 220,217 samples over 2022 and 2023, of these 129,899 were for next-generation sequencing and 44,623 for genotyping by array.

Video collaboration

The Centre collaborated with the vendor Illumina to produce a video, highlighting the use of genomics: https://youtu.be/OBpyqKLv5VM

12 official tours

Staff held 12 official tours of the laboratory showcasing equipment and staff.

2053 ongoing projects

We provided data for 991 and 1,062 ongoing projects, respectively, in 2022 and 2023.

282 acknowledgements

We were acknowledged in 137 and 145 publications, in 2022 and 2023, respectively.

10 seminars

Staff hosted or presented at 10 educational and research-focussed seminars.

14 national conferences

Staff exhibited at 14 national conferences and 2 symposiums.

Student research

The Centre supported the Genetics Society of AustralAsia (GSA) **Student Research Grant Scheme** in 2022 and 2023, in conjunction with the vendor Illumina. The award highlights how next generation sequencing can be utilised to advance innovative research projects and is aimed at Australian postgraduate students.

15 flowcells per week

On average 15 next gen sequencing machine runs or flowcells were done per week.

4000 submissions

We received close to 4,000 submissions over 2022-2023.

Capability increases

New machines

The Centre acquired three new high throughput machines, the NovaSeq X Plus, the NextSeq 1000 and the iScan/Infinium RoMa.

Staff growth

Staffing levels grew from 24 to 26, including QMS and IT support.

Steering Committee

The Ramaciotti Centre for Genomics is affiliated with other universities and medical research centres in the Sydney region and representative from each sit on the Centre's steering committee. The committee members provide input on the Centre's strategic direction and objectives.
We gratefully acknowledge their contribution during 2022 and 2023.

At the close of 2023 the committee consisted of:

Professor Marc Wilkins
(Chair, Deputy Dean of Research and Enterprise); UNSW Sydney

Dr Helena Mangs
(Deputy Director)
UNSW Sydney

A/Professor Mark Cowley
Children's Cancer Institute Sydney

Professor Garry Myers
University of Technology

A/Professor Sarah Kummerfeld
Garvan Institute of Medical Research

Professor Brett Neilan
University of Newcastle

Professor Carolyn Hogg
University of Sydney

A/Professor Amy Cain
Macquarie University

Alternates:
Professor Steven Djordevic
University of Technology, Sydney

Professor Ian Paulsen
Macquarie University

Professor Katherine Belov
University of Sydney

We warmly thank **Emeritus Professor Ian Dawes** (UNSW Sydney) for his many years as the committee chair. Ian established the Ramaciotti Centre in 1999, served as the Centre Director from 1999 until 2010, and continued to serve on the steering committee until 2023. Without Ian, there would not have been a Centre, so we are eternally grateful. **Professor Paul Munroe** (Deputy Dean, Faculty of Science, UNSW Sydney) also stepped down from the committee in 2023. We thank him for his contributions and service to the committee.

Our people

Our staff come from diverse backgrounds and bring a wealth of experience from various disciplines, including biomedical, environmental, conservation biology, and biotechnology. The team works closely together to deliver data for the thousands of projects we support each year. In 2022-2023, we saw changes in staffing in some teams, with staff leaving for maternity leave, career changes, or personal reasons.

In 2022, we bid farewell to Caitriona Murray and Chathurika Daulagala. We were pleased to welcome back Zena Kassir, who had worked at the Centre from 2016 to 2018 and returned after a few years in the industry. Jackie Chan and Jane Phan-Au went on maternity leave, with Matthew Wong and Nour Hawchar appointed to their roles. In 2022, two new roles were created: a Production Bioinformatician and a Service Manager for our genotyping service. Aravind Manda was recruited for the former role, leading and overseeing our bioinformatics pipelines and data production. Firoozeh Salehzadeh was appointed as the genotyping service lead, to develop and expand our Axiom and Infinium services. In 2022, we also saw our Director, Prof. Marc Wilkins, resign to take up a Deputy Dean role within the Science Faculty. Marc had been an integral part of the Centre's strategy and direction since 2011, and he is sorely missed.

In 2023, we welcomed four new members to the Illumina-seq prep team: Joshua Crowe, Aurelie Moya, Phanna Thianchetthakul and Ceavina Wu. We also farewelled Ani Lack, Angela Chilton, Jackie Chan and Aurelie Moya later this year. Crystal Cui took maternity leave from mid-2023. Matthew Wong was successful in the Service Manager role for amplicon-seq, which was merged with the Sanger-seq role. Antonika Nguyen joined in late 2023 to provide maternity cover for the Administration Officer role, with Abigail Teo taking maternity leave from early 2024.

As of the close of 2023 our team included:

Deputy Director & COO (Acting Director)
Dr Helena Mangs

Quality Manager
Keren Natalia, Natalia Consulting (SmartQMS)

Production Bioinformatician
Aravind Manda

Research Manager
Jason Koval

Senior Research Officers
Dr Jess Gurr
Dr Matthew Wong
Dr Firoozeh Salehzadeh
Tonia Russell

Research Officers
Dr Darshi Ramesh
Dr Erika Becker
Dr Christie Foster
Dr Kerry Nutt
Scott Genner
Rhys Stark
Crystal Cui (maternity leave)

Research Assistants
Jane-Phan Au
Steven Chan
Zena Kassir
Joshua Crowe
Phanna Thianchetthakul
Ceavina Wu
Nour Hawchar

Administrative Officers
Abigail Teo
(maternity leave 2024 onwards)
Antonika Nguyen

Partnership and collaboration highlights

Health disparities in prostate cancer

Prostate cancer is one of the most common cancers affecting men worldwide, with significant variation in incidence and mortality rates among different ethnic groups. Men of African descent are disproportionately affected, exhibiting higher rates of prostate cancer incidence and mortality compared to other groups. This disparity has been a central focus of Professor Vanessa Hayes' research. Professor Hayes, Petre Chair of Prostate Cancer Research and Head of the Ancestry and Health Genomics Laboratory located within the Charles Perkins Centre at the University of Sydney, aims to uncover how genetic diversity and ancestry influence the risk and development of prostate cancer with a particular focus on men of African ancestry. By examining the genomes of African men, Professor Hayes has identified specific genetic variations that may predispose individuals to prostate cancer.

Her research suggests that certain genetic markers are more prevalent in African populations, which may contribute to the increased susceptibility to prostate cancer observed in these groups.

The Centre has a long-standing partnership with Professor Hayes and partnering with the Centre for ongoing submission of human whole genome samples was a natural choice. Professor Hayes states: "We seek more than just a provider of genomic services; we value a partnership over a mere transactional relationship. Our samples are invaluable, and we expect anyone handling them to treat them with the utmost care. This is what we have with our long-standing relationship with the Ramaciotti Centre - we are partners, not just a client." Samples submitted in 2022 and 2023 were sequenced to either 30 or 60X coverage using the PCR-free prep and the NovaSeq 6000 or the NovaSeq X Plus, complemented by EPIC methylation arrays.

In addition to genetic factors, Professor Hayes' research acknowledges the role of environmental and lifestyle factors in prostate cancer risk. She has investigated how factors such as diet, lifestyle, and access to healthcare interact with genetic predispositions to influence prostate cancer outcomes. Her work emphasizes the importance of a holistic approach to understanding cancer risk, considering both genetic and non-genetic factors. "Using a combination of technologies, we can unravel the genetic and non-genetic factors that contribute to prostate cancer in the African population. My team uses cutting-edge computational data science to allow for pattern recognition to reveal the genetic background linked to different disease outcomes". Through recruiting 1,000 prostate cancer patients in a unique all African study (Africa1K) Professor Hayes' team will generate the largest precision health resource of its kind. Including clinical and lifestyle data, with multi-platformed genomic data, the team merges genomic data with environmental exposure data using a new wave of large-scale screening.

By identifying genetic markers and molecular pathways associated with prostate cancer, Professor Hayes' research holds promise for improving early detection, prevention, and treatment strategies, ultimately reducing the burden of prostate cancer and addressing health disparities. Her contributions continue to shape the field of cancer genetics and personalized medicine, paving the way for more inclusive and effective healthcare solutions.

Microbiota in health and disease

The gut microbiome, consisting of trillions of microorganisms, play a massive role in pregnancy health. Professor Emad El-Omar and his team at the Microbiome Research Centre (MRC) at UNSW have been exploring how to harness the maternal gut microbiome to give the baby the best start in life. A healthy gut microbiome aids in digesting food and regulating the immune system, but when dysfunctional, it can lead to chronic conditions like asthma and obesity. This impacts not just the mother but also the developing child, with microbial populations shifting between trimesters to extract more nutrition from food.

Professor Emad El-Omar finds the connection between pregnancy and the microbiome fascinating. MRC, a UNSW research centre set up in 2017, is running several research studies and amongst them a groundbreaking study called MothersBabies, which recruits 2000 women planning pregnancy. The study analyzes microbial species, their gene expression, and metabolites from self-collected swabs and stool samples before conception, during pregnancy, at delivery, and after delivery. MothersBabies aims to identify unique microbiome 'fingerprints' linked to pregnancy-related conditions like pre-eclampsia and gestational diabetes. The study will also track the microbiome and health of the newborns up to 12 months, with hopes of following them for 10 to 15 years. Fathers' microbiomes will also be analyzed for potential impacts on sperm and semen quality.

The goal is that microbiome tests will become as routine as fetal ultrasounds and maternal blood tests, allowing for pre-emptive diagnosis and prevention of conditions. Phase 2 of the study involves a clinical trial with at least 1000 women, where half will receive a cocktail of pro- and prebiotics and the other half a placebo. Tracking these babies into childhood could provide insights into conditions driven by the microbiome, such as autism, asthma, and allergies.

Professor El-Omar and his team have formed a close partnership with the Ramaciotti Centre over the years. The Centre has received ongoing submissions of samples for metagenome, amplicon and RNA-seq projects and values the partnership. The MRC team also looks at what a healthy microbiome looks like, by studying participants from diverse groups; teenagers, professional athletes, senior adults with dementia and non-active adults. Data from metagenome and amplicon-seq studies is compared to a range of metadata, such as height, weight, blood pressure, diet and lifestyle factors. Through the so-called "Healthy Optimal Australian Microbiome" (HOAM) study, researchers at the MRC hope to define what the ultimate healthy and normal microbiome looks like.

Wet Weather Overflow Monitoring Program (WWOMP) for environmental managing of water systems

Sydney Water, a NSW government-owned corporation, provides drinking water, wastewater services and some stormwater drainage in the Greater Sydney area. In 2022, the Centre produced a dataset of over 27,000 amplicons for Sydney Water, supporting the environmental management of wastewater systems. Within the urban area of the Sydney metropolitan area, sewer pipes are separate from the stormwater system. During heavy rainfall, urban stormwater can enter the wastewater system through incorrect stormwater connections and ingress and inflow through cracks or faults in sewer pipes, which can exceed the hydraulic capacity of the wastewater system. Emergency relief structures (designed overflow points) are situated throughout the wastewater system to allow this excess water to discharge into receiving waters and to protect homes and businesses from flooding. Without overflow points, wastewater could come up through toilets and floor waste drains in homes and businesses or gully traps in backyards.

The project was aimed at producing an extensive eDNA data set from freshwater and estuarine locations receiving waters across in Sydney and it was designed to provide a quantitative estimate of sewage impact wet weather overflow influence on the environment. The project highlights the integration of genomic data in Sydney Water's efforts for environmental protection. Extracted DNA was amplified for six loci/genes to capture a range of biota, which together with an extensive set of positive and negative control samples, were processed using the EpMotion robot. The Centre implemented increased multiplexing capacity, to be able to process samples on

> "I know from my experience working as a staff member that the work done by the Centre is high quality, backed by a can-do attitude and exceptional attention to detail."
>
> Dr Kylie Cairns, Conservation biologist

the NovaSeq 6000 rather than the MiSeq sequencer. The Centre and its staff value the collaboration with Sydney Water and hope to be able to contribute to future eDNA projects with the organization and other stakeholders requiring high-throughput data set for environmental management.

Diet-microbiome-immunotherapy link

Professor Georgina Long and team at the Melanoma Institute, University of Sydney, have made a significant connection between a patient's diet, the composition of their gut microbiome, and how they respond to immunotherapy treatment. Published in Nature Medicine, the study involved patients with high-risk metastatic melanoma from Australia, the Netherlands, and the United States. Results showed that patients with microbiomes indicating high fiber consumption had better responses to immunotherapy administered before surgery to remove tumors.

The study, involving 16S and metagenomic next-generation sequencing performed at the Centre, sheds light on the crucial role of the gut microbiome in influencing responses to immunotherapy. The findings revealed distinct patterns among Australian patients, with those consuming diets low in fiber and omega-3 fatty acids exhibiting poorer responses to immunotherapy. By prospectively analyzing the gut microbiota and dietary habits of 103 Australian and Dutch patients, alongside data from 115 US patients, the researchers identified microbiome signatures associated with treatment response. Microbiomes dominated by Ruminococcaceae, indicative of higher fiber intake, correlated with better responses, while those dominated by Bacteroidaceae showed lower response rates and increased inflammation. Professor Long, senior study author, stressed the importance of further investigations into the diet-microbiome-immunotherapy link. She highlighted the potential for dietary interventions at diagnosis to enhance patients' chances of responding to and overcoming resistance to immunotherapy, a critical advancement in treating advanced melanoma. The Centre is proud to have contributed to this study.

Dingo genetics

The dingo (Canis dingo) is Australia's only native canid, brought in from Southeast Asia around 4,000 years ago. It has long been assumed that dingoes crossbreed with dogs and that pure dingoes may in fact be on the path to extinction. Conservation biologist Dr Kylie Cairns has been studying dingo populations since 2010 and argues that the term "wild dogs", defined as "any dog living in the wild, including feral dogs, dingoes and their hybrids", should be removed from public language and legislation. The animals should be referred to as dingo and feral dogs instead.

Dr Cairns' research used Ramaciotti Centre services to genotype samples amongst a 391 captive and wild animal population, using an Axiom Canine array with 195,000 markers. Results showed that in Victoria, 87% of dingoes had pure dingo lineages, while in NSW and Queensland, more than half of those sampled had at least 99% dingo ancestry. In SA and WA, over 80% of wild dingoes were genetically pure. It should be noted that of the small proportion of wild dingoes with dog ancestry, there were no 50/50 hybrids or feral dogs in the wild-caught samples, that is, the ancestry dated further back than this. With the genetic data, Dr Cairns identified four distinct wild dingo populations in Australia. Prior to this study, using technology with only 23 markers, it was assumed that all dingoes across the country were the same, and that any differences were due to the dingo being a hybrid.

Dr Cairns worked as a technician in the Centre on a large-scale genotyping project (ASPREE) in 2019 and developed the idea to use Axiom genotyping for her research project through this. She says: "I chose to work with the Ramaciotti Centre because of their efficiency, competitive cost and the expert advice provided by Ramaciotti staff. I know from my experience working as a staff member that the work done by the Centre is high quality, backed by a can-do attitude and exceptional attention to detail." The Axiom genotyping assays builds advanced knowledge about the ancestry of dingoes across Australia and directly informs discussions about the conservation of this top predator.

National Framework Dataset Programs

The Centre supports and contributes to several Bioplatforms Australia-funded framework datasets. Projects we were involved in during 2022-2023 included:

- **Threatened Species Initiative (TSI)**
  Australia has the highest mammalian extinction rate globally. The Threatened Species Initiative (TSI), involving partners from universities, government organizations, and wildlife and zoo associations, supports the conservation of Australia's threatened biodiversity. The project aims to develop genomic resources, analytical pipelines, and reporting methods to aid conservation efforts. This project unites experts in genomics, population biology, bioinformatics, and zoology with conservation agencies to manage and boost genetic diversity in threatened species. The goal is to develop an online tool to help conservation managers use genomics to guide breeding programs. During 2023, the Centre sequenced transcriptomic samples for the initiative.
- **Genomics for Australian Plants (GAP)**
  Australian native plants are vital to agriculture, forestry, fisheries, aquaculture, tourism, and Indigenous communities, providing cultural and economic support. Since European settlement, these plants have faced significant disturbances. Genomic characterization can improve conservation and management, unlocking valuable evolutionary and conservation data from plant genomes. Genomic insights could aid in biofuel, drug, and crop breeding developments. The GAP Framework Data Initiative aims to sequence plant genomes, build genomic capacity in botanic gardens and herbaria, and provide tools to improve biodiversity conservation and decision-making. The Centre has performed sequencing for this initiative using both long-read and short-read technologies.
- **Amphibian and Reptile Genome Initiative (AusARG)**
  The Amphibian and Reptile Genome Initiative (AusARG) focuses on reptile and amphibian genomics, including de novo genome assembly, phylogenomics, and conservation genomics. The goals are to accelerate fundamental research in these areas, meet conservation needs, and enhance genome science capabilities across museum, university, and agency partnerships. The initiative aims to build a genomic data foundation for understanding and conserving Australia's unique reptiles and amphibians. The program raises awareness about how genomics can aid in conservation and management efforts. The Centre has contributed to this program with genomic and transcriptomic data over 2022 and 2023.
- **Australian Microbiome (AM)**
  Microbes are crucial for ecosystem health and processes, from global biogeochemical cycles to disease management. The Australian Microbiome (AM) project aims to create a comprehensive, publicly accessible database of microbial diversity across Australia's terrestrial and aquatic ecosystems. This database will offer searchable information on the occurrence and distribution of microbial resources, aiding research in microbial ecology. By providing access to extensive environmental microbiological data, the AM project will support large-scale studies on ecosystem function, biogeochemistry, and bio-discovery. The initiative aims to enhance microbial genomics for management, monitoring, and research, fostering collaboration and innovation. The Centre contributed to this project with extensive amplicon (16S, 18S and ITS) and metagenome sequencing datasets.

Operational update

iScan/Infinium RoMa system install 2022

The microarray service at the Centre has been running since 2000, processing samples for expression analysis and genotyping. The expression array service was discontinued prior to 2022, but genotyping using the Axiom workflow and the GeneTitan (Thermo Fisher Inc.) has seen increased usage over 2022 and 2023, processing an average of 22,300 samples per year. In 2022, the Centre decided to complement the Axiom service with the implementation of the Infinium iScan system. The iScan and associated Tecan high-throughput robot Infinium RoMa were purchased through CapEx funds from Bioplatforms Australia (BPA). The iScan can process genotyping arrays as well as methylation (EPIC) arrays.

The Centre has offered methylation analysis through sequencing-based pipelines for several years, with frequent requests for a methylation-based array service. The EPIC methylation arrays cover CpG islands, miRNA promoter regions, and other areas of importance in epigenetic regulation. Studies on the Infinium system have covered sample types such as humans, fruit, and animals. Since the acquisition, the Centre can process Biobank, precision medicine and screening arrays, as well as a range of custom arrays using either the Axiom system or the iScan system, depending on the needs of the researcher. Both systems are suitable for low as well as high throughput studies.

NextSeq1000 & NovaSeq X Plus install, 2022 and 2023

Genomics technology has a defined lifespan, with advances occurring at an unprecedented rate. The Centre has been running several Illumina sequencers over the years: a couple of HiSeq 2000/2500s, three MiSeqs, one iSeq100, one NextSeq500, and two NovaSeq 6000 systems. We ensure that we keep up with changes to provide our client base with the most efficient and cost-effective methods to generate genomic data. In 2023, we acquired a NextSeq1000 and a NovaSeq X Plus to complement our sequencing suite.

The NextSeq1000 is a mid-size benchtop sequencing machine with run lengths from 1x50bp to 2x300bp, making it useful for a range of applications. The longer read lengths are especially beneficial for amplicon-seq projects, as it's not only faster than the MiSeq but also offers remarkable cost savings. For example, a client with samples sequenced over three MiSeq 2x300bp runs can now transfer them to one NextSeq1000 run at a significantly reduced overall cost. Data shows that Q30 at 2x300bp is significantly higher for the NextSeq1000 than the MiSeq, meaning there is no reduction in quality. Additionally, the plastic cassettes are made of recyclable plastic, aligning with the Centre's commitment to a greener environment. The NextSeq1000 was purchased through a successful Research Infrastructure (RIS) grant offered at UNSW.

In mid-2023, we acquired Illumina's latest sequencer, released only a few months earlier. The NovaSeq X Plus is a high-throughput production-scale sequencer capable of generating up to 16Tb of data at 2x150bp over the dual flow cells. The machine is powered by XLEAP-SBS chemistry, a faster, higher quality, and more robust version of Illumina's sequencing by synthesis (SBS) chemistry. This chemistry will be available on the NextSeq1000 in mid to early 2024. Kits made with XLEAP-SBS chemistry have increased stability and can be shipped at room temperature, with reduced packaging and size. The Centre welcomed this change, as prior kits shipped on dry ice required considerable resources for waste handling and packaging.

The NovaSeq X Plus was purchased through a collaborative scheme, highlighting the partnership that the Centre has with various researchers and stakeholders. The Centre gratefully acknowledges Bioplatforms Australia (BPA), the Australian Cancer Research Foundation (ACRF, grant through the Children's Cancer Institute), the UNSW RNA Institute, the UNSW Microbiome Research Centre (MRC), and co-contributions from UNSW. Acquisitions of the NextSeq1000 and the NovaSeq X Plus mean that the Centre can continue to cater to small and large projects with increased speed and lower cost. We envisage that the NovaSeq X Plus will be essential in delivering, among other things, human whole genomes below $600 per genome, an important step towards the "$100 genome" publicly advertised a few years ago.

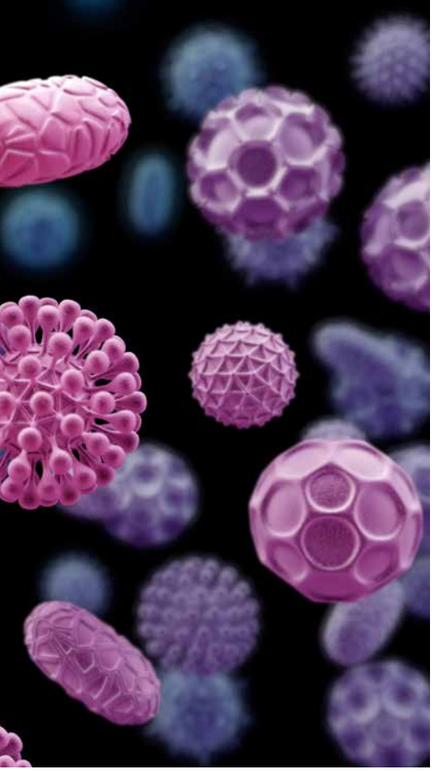
Quality system

The Centre acquired National Association of Testing Authorities (NATA) accreditation in early 2019. Since the first official surveillance audit in August of 2020, the Centre has undergone two additional official assessments and audits: a reassessment in March of 2022 and a surveillance audit in November of 2023. In addition, nine internal audits were performed over 2022 and 2023 to ensure continuous improvements to services and systems. Accredited workflows are next generation sequencing of client prepared libraries (CPL) and genotyping by microarray, but all other services offered by the Centre are run under the same quality management system in the accredited laboratories. In late 2023, the Centre applied to include the Illumina PCR-free sample preparation pipeline to the scope, allowing the Centre to offer accredited human whole genome data from early 2024.

The Centre continued to implement and streamline use of the cloud-based quality management system software, Ideagen Management System (IQMS, formerly Qualtrax). IQMS is a quality management system software solution from Ideagen, built for regulated and high-compliance industries.

By implementing the eQMS software, the Centre has successfully transitioned several processes to more automated workflows, including Change Control, Document Review and Approval, Non-Conformance Handling, and Personnel Training. This shift has significantly reduced administrative bottlenecks and improved the efficiency of record completion.

right from top to bottom
The NovaSeq X Plus,
The iScan/Infinium RoMa system, The NextSeq 1000



In late 2023, a new role was established to manage the CPL sequencing service and assist with quality management duties. This Service Manager/Quality Officer position is crucial for ensuring the streamlined management of the Centre's accredited services. We received 717 CPL samples for sequencing in 2022 and 2023, with expectations for increased submissions in the coming years.

The Centre has also completed Internal Proficiency Testing for all its accredited services with outstanding results and has enrolled in a third-party proficiency testing program for the Illumina PCR-free pipeline.

As the Service Manager/Quality Officer takes over the day-to-day management of quality operations in 2024, Keren Natalia, our current Quality Manager—who is also an independent contractor and director of SmartQMS, a quality consulting firm—will transition to an advisory and training role. She will focus on strategic improvement, process optimisation, and quality system training.

Technology and services

The Centre has an extensive suite of genomics technology, supporting a range of services.

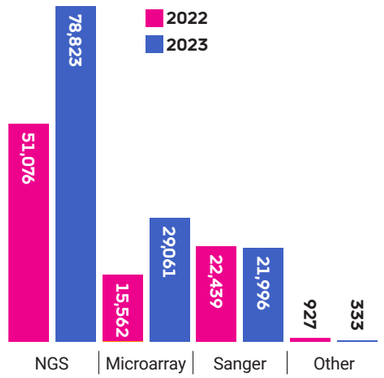
Short Read Next Generation Sequencing Applications
Whole Genome, Exome & Targeted Panels, methylation analysis, RNA (Total RNA, mRNA, miRNA), Microbiome, Amplicon, Metagenome, and Single cell sequencing (through UNSW Cellular Genomics Futures Institute).
Using
- Illumina NovaSeq X Plus
- Illumina NovaSeq 6000
- Illumina NextSeq 1000
- Illumina NextSeq 500
- Illumina MiSeq
- Illumina iSeq 100

Long Read Next Generation Sequencing Applications
Genome, Epigenome, RNA (direct RNA and cDNA), Cas9, Adaptive (targeted) sequencing.
Using
- Oxford Nanopore Technology GridION
- Oxford Nanopore Technology PromethION (collaboration with the Garvan genomics team)

Sanger Sequencing
Core and user prep, Fragment analysis, Custom design & validation
Using
- AB3730xl

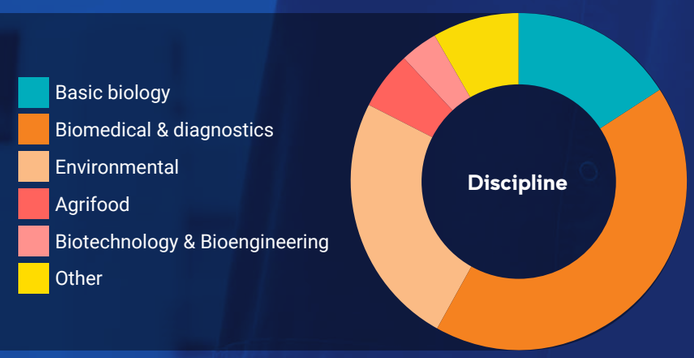
Gene Expression & Genotyping applications
DNA, RNA, methylation analysis
Using
- Thermo Fisher Scientific GeneTitan
- Illumina iScan/Infinium RoMa
- NanoString nCounter
- Fluidigm BioMark

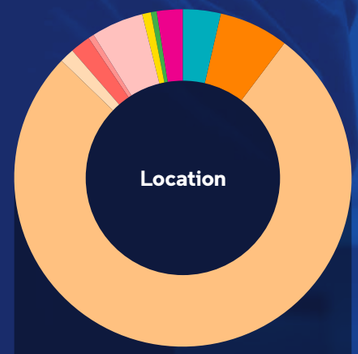
Support equipment: Liquid handlers
- Sciclone G3 NGSx iQ
- epMotion 5075
- Zephyr iQ
- Janus NGS
- Viaflo
- Myra



Client profile

The Centre has a customer base of over 500 research groups from academia and industry. We serve all the leading universities and research institutes in Australia and support a wide range of research covering many disciplines





Victoria
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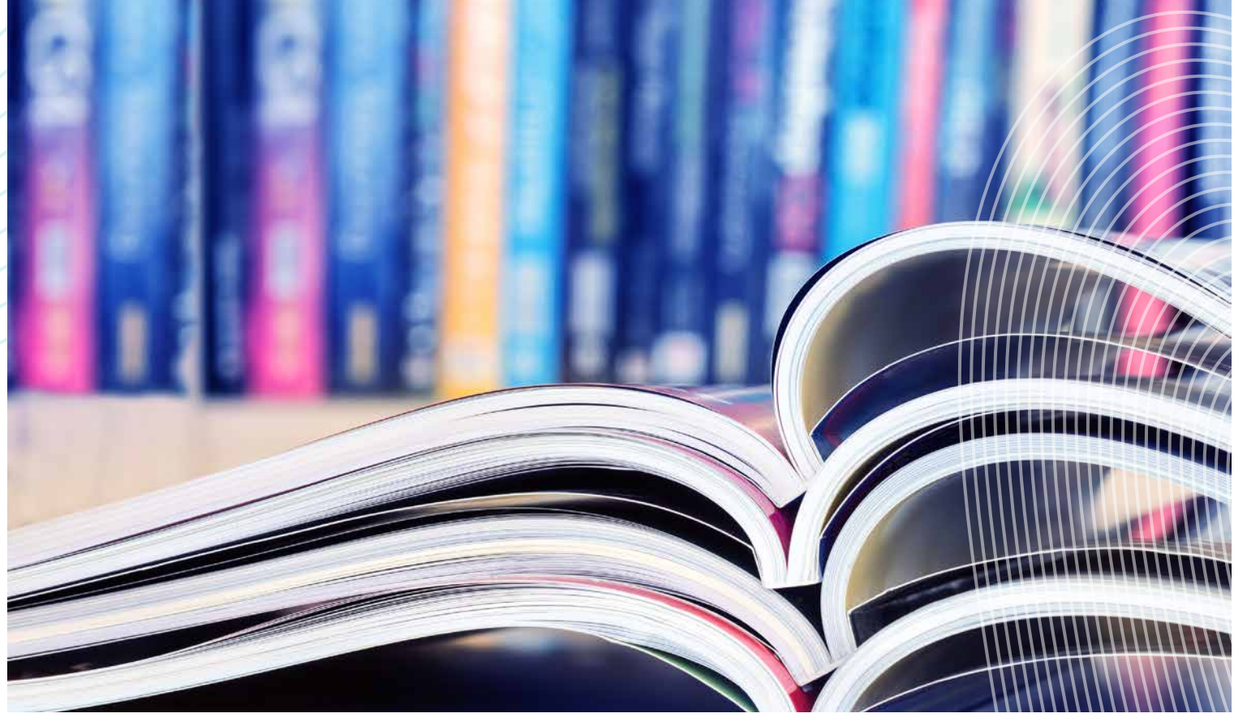
Western Australia
Northern Territory
Overseas

Publication highlights



The Centre was acknowledged as a service provider in 282 publications over 2022-2023. We thank the authors for acknowledging the Centre's contribution to their research output. Below is a snapshot of publications from 2022-2023.

Ji, E., Boerrigter, D., Cai, H. Q., Lloyd, D., Bruggemann, J., O'Donnell, M., … & Weickert, C. S. (2022). Peripheral complement is increased in schizophrenia and inversely related to cortical thickness. *Brain, Behavior, and Immunity, 101*, 423-434.

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The acquisition of the high-throughput genomic sequencer, the NovaSeq X Plus, was made possible through contributions from a range of stakeholders, listed to the right. We are deeply grateful for our network and collaborations that made this possible.

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