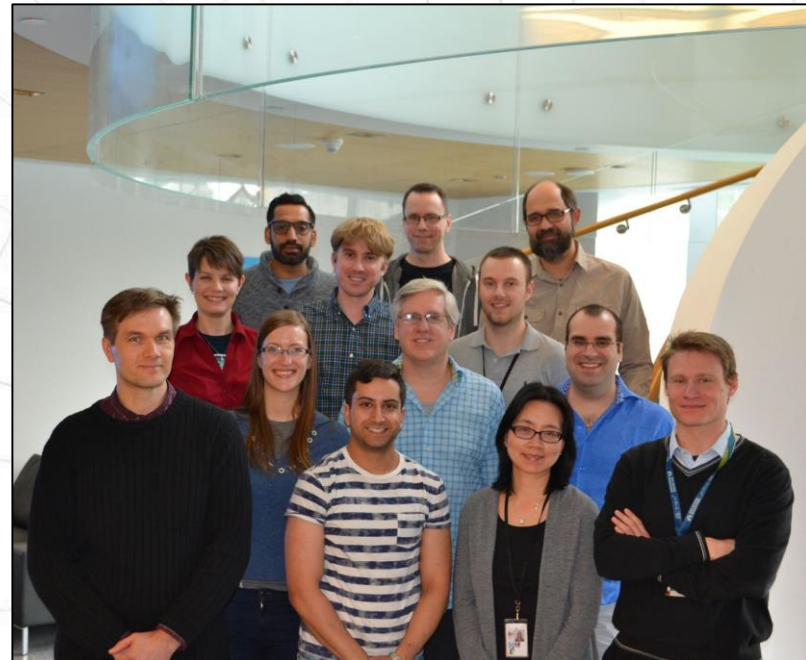




OICR Bioinformatics (GSI)

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- ▶ Difficult sample analysis (Low cellularity, degraded samples & FFPE)
- ▶ SNVs, copy number & structural variant analysis
- ▶ Pathway & other functional analyses
- ▶ Single cell methods
- ▶ Integration of public data sets
- ▶ Depositing generated results



IT Resources

- ▶ 8,000 cores, an aggregate of 30+TB of memory
- ▶ 6PB of network-attached storage
- ▶ Cloud Computing environments (OpenStack)



Dockstore
Create, Share, Use

Example Projects



ARTICLE

Received 16 Jun 2015 | Accepted 23 Oct 2015 | Published 9 Dec 2015

DOI: 10.1038/ncomms10001

OPEN

A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing

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LETTER

doi:10.1038/nature22993

Tracing the origins of relapse in acute myeloid leukaemia to stem cells

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ARTICLE

doi:10.1038/nature20788

Genomic hallmarks of localized, non-indolent prostate cancer

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ARTICLE

Received 26 Jul 2016 | Accepted 20 Oct 2016 | Published 9 Jan 2017

DOI: 10.1038/ncomms13671

OPEN

Germline *BRCA2* mutations drive prostate cancers with distinct evolutionary trajectories

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AML

1. First pass standard pipeline
2. Followed by more in-depth analysis
3. Helped with manuscript preparation
4. Deposition of data for publication in public archive (EGA)



Funding for the Ontario Institute for Cancer Research
is provided by the Government of Ontario

