

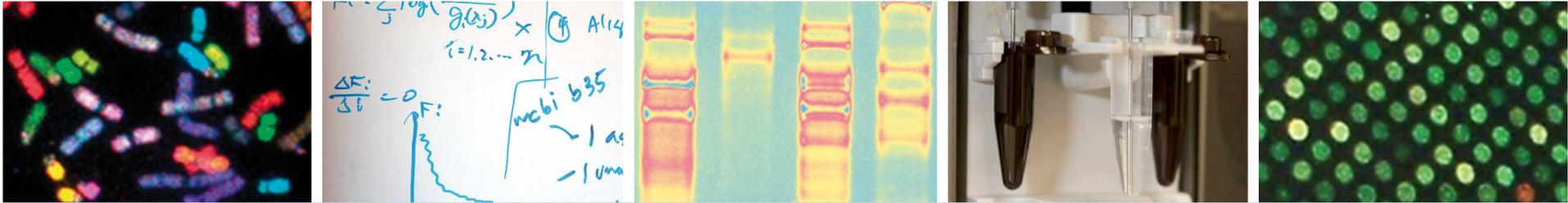
# The Centre for Applied Genomics

# The Centre for Applied Genomics (TCAG)

FGED Toronto  
 October 22, 2012



[www.tcag.ca](http://www.tcag.ca)



# The Centre for Applied Genomics

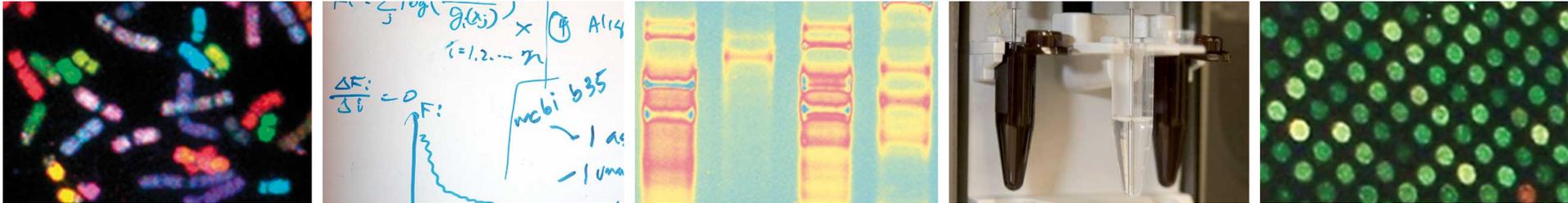
## TCAG – Mandate and Philosophy

Provide world-leading infrastructure support and services for innovative genomics research, including characterization of genes and genomes of medical, therapeutic, and biological interest.

- Open facility – anyone can use the services
- Never turn down a client (no matter how small or large the project)
- Provide services on cost-recovery basis
- Technology, services and large projects drive innovation
- Build a facility where capacity never becomes a rate-limiting factor

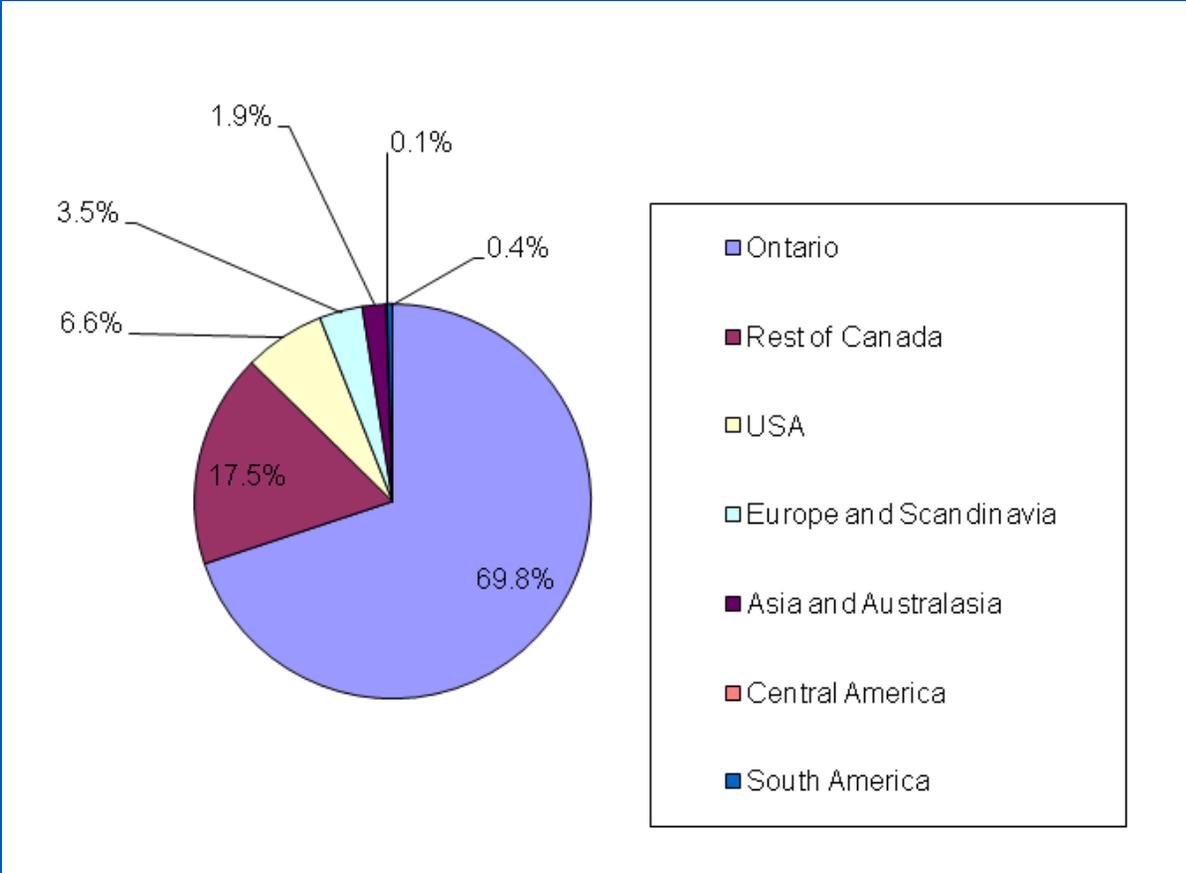


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# The Centre for Applied Genomics

## TCAG Users – Geographic Distribution



**>1,300 different PI labs worldwide (2006 – present)**

**~700 PI users / year**

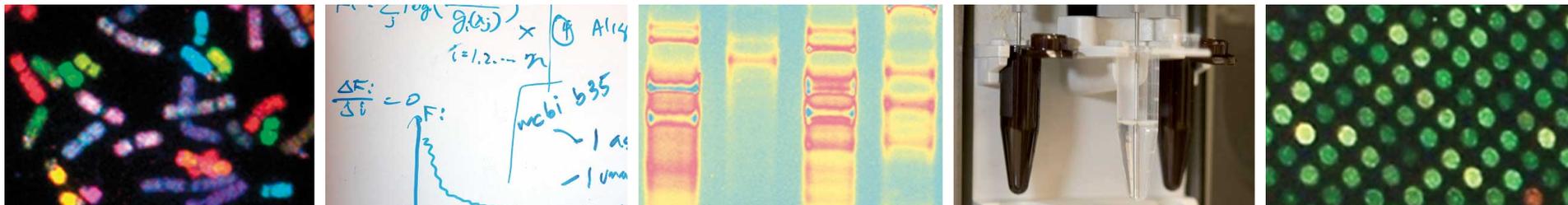
**~50 new PI users / quarter**

**33 countries**

**academic 92%  
private sector 5%  
government 3%**



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## The Centre for Applied Genomics

### Core Facilities

#### 1. Sequencing

- capillary sequencing, high-throughput sequencing
- oligo synthesis (in house, IDT portal)

#### 2. Microarrays

- microarrays for GWAS, CNV, gene expression, methylation, etc.

#### 3. Cytogenomics & Genome Resources

- karyotyping, FISH, spectral karyotyping, etc.
- FISH probes, genomic clones

#### 4. Informatics & Statistical Analysis

- data analysis, databases, scripting, coding, algorithm development
- project design, statistical power, data analysis

#### 5. Biobanking

- preparation of permanent cell stocks and DNA from blood or skin
- >50,000 cell lines banked



## Sequencing Instruments

8 x Life Technologies SOLiD 5500x/

1 x Illumina HiSeq 2000 (soon to be upgraded to 2500)

1 x Illumina HiScan SQ (not used much)

1 x Roche GS-FLX

2 x Ion Torrent PGM (in SickKids Mol. Diagnostics lab)\

2 x capillary (AB 3730xl)

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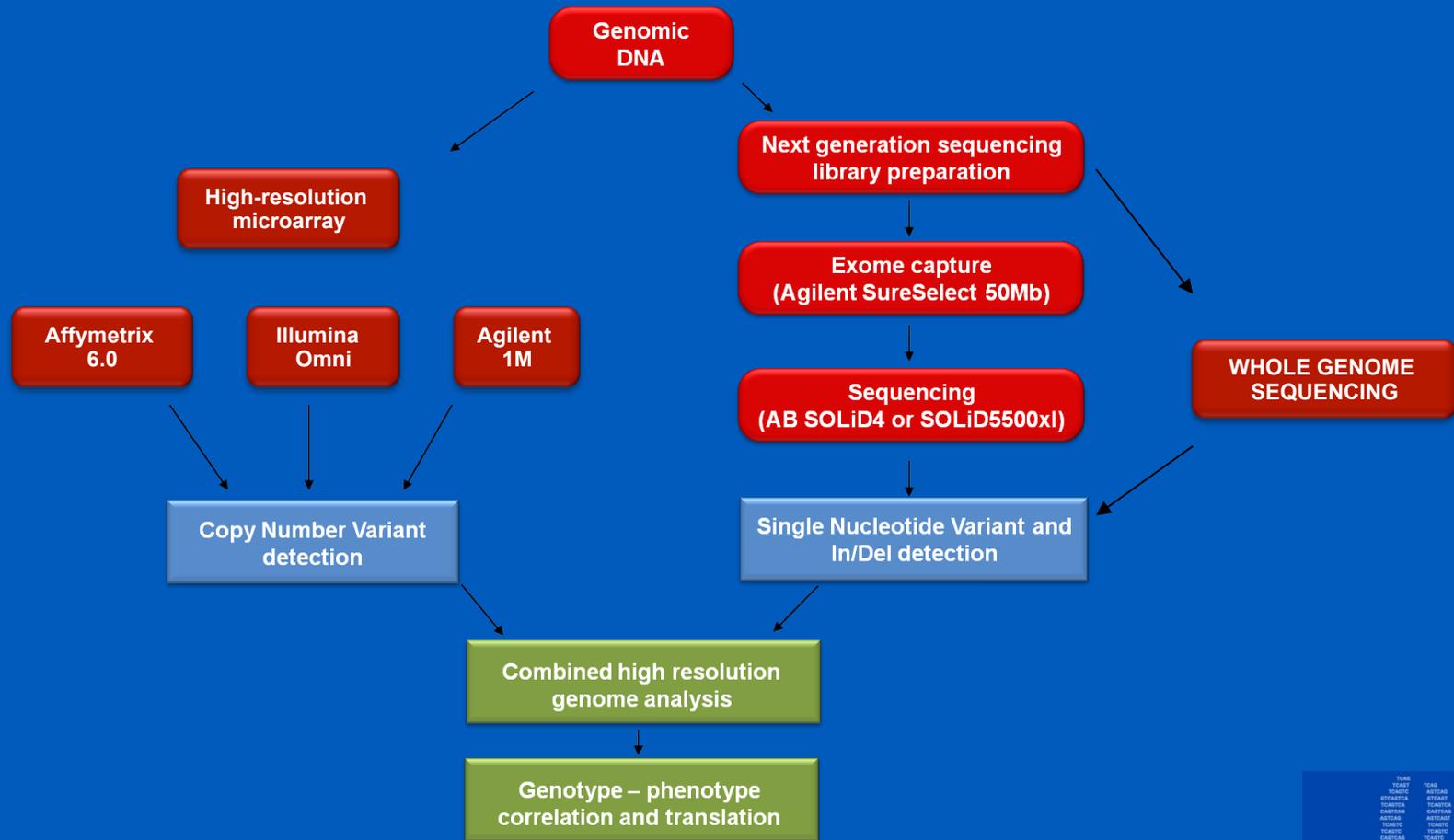
4 x Ion Proton (delivered; installation pending)

1 x Illumina HiSeq 2500

others?



# Current state of high-resolution genome analysis

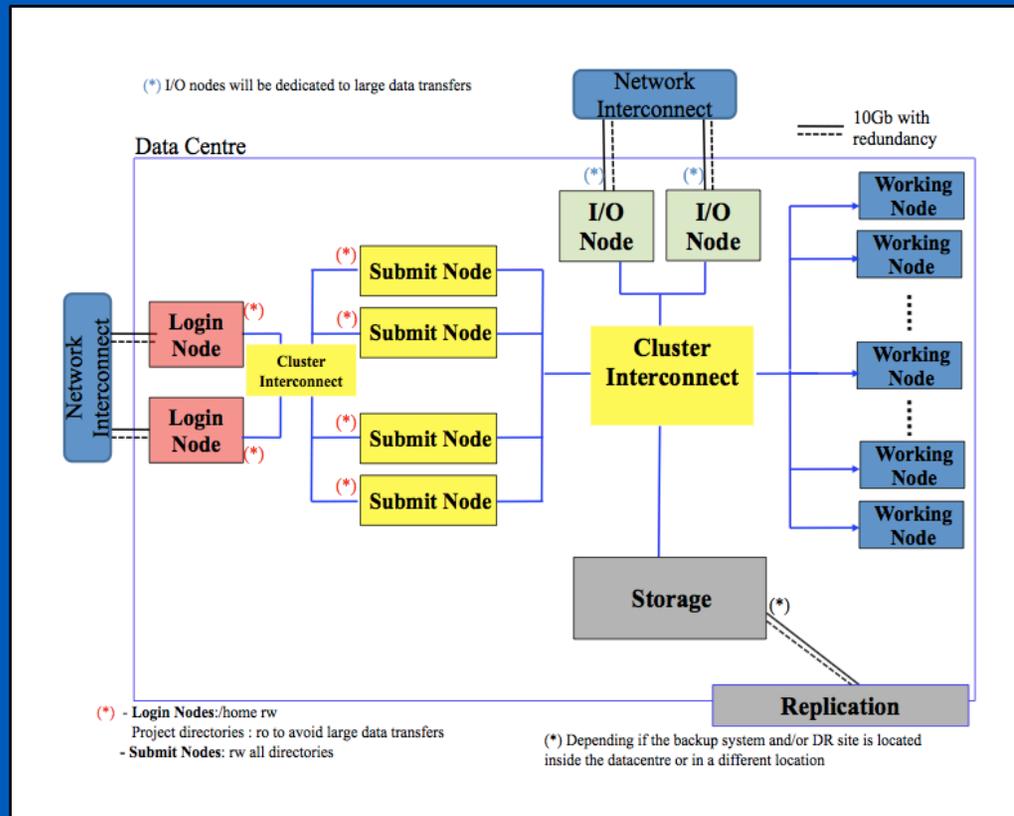


Captures CNVs (>10kb) across genome and SNVs/very small indels at exons





# Computing Resources

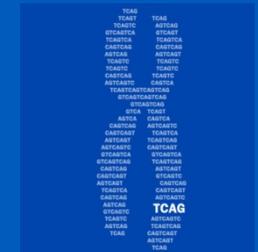


Data stores (inside firewall)

outside inside

## High Performance Computing Cluster (CCM)

- Linux-based parallel architecture; OUTSIDE hospital firewall
- storage is INSIDE the firewall
- need for privacy (personal health information – PHI)
- NO possibility for cloud-based resources (at present)



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# Challenges

LIMS (scalability, integration)

*Database of Genomic Variants* (ongoing scalability and interoperability with dbVar, DGVa)

Cloud (particularly in light of PHI)

Third- (and beyond) generation sequencing (particularly in light of cloud question)

