Belgian Medical Genomics Initiative

# *Country update* : BELGIUM , Belgian Medical Genomics Initiative

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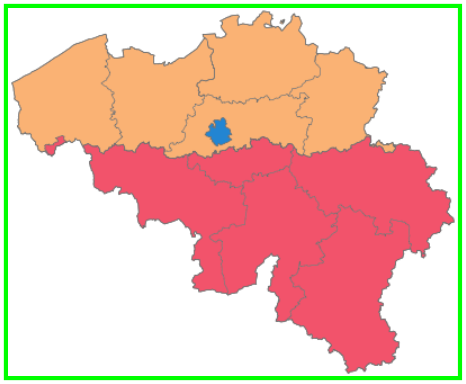
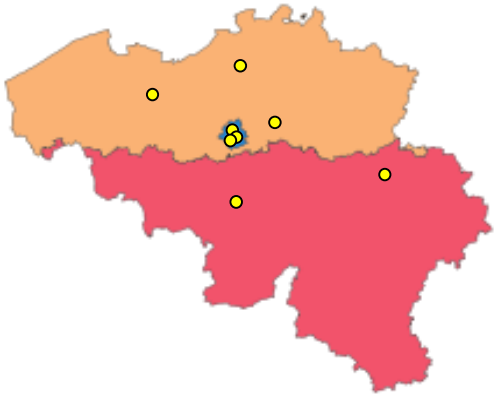
On behalf of BeMGI
www.BeMGI.be

# BELGIUM : Population 11M
# 1 federal state, 2 communities, 3 regions



Belgian Medical Genomics Initiative

- National Health Care System budget for clinical genetics:
  44 M€/year = 4€ (5$) / person/year
- Clinical genetics:
  organized in 8 Centers of Human Genetics
  in 7 universities (4+4 ; 3 in Brussels)



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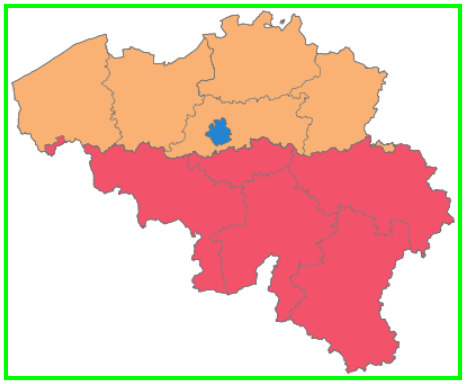

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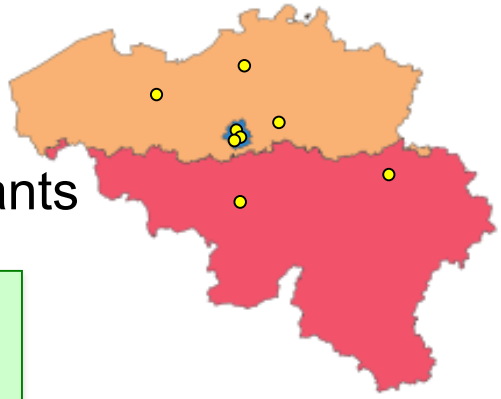

- Standard karyotype; aCGH
- Gene analysis / Gene panel analysis
- NOT mendeliome, exome, genome
- Clinical diagnosis / Genetic couneling

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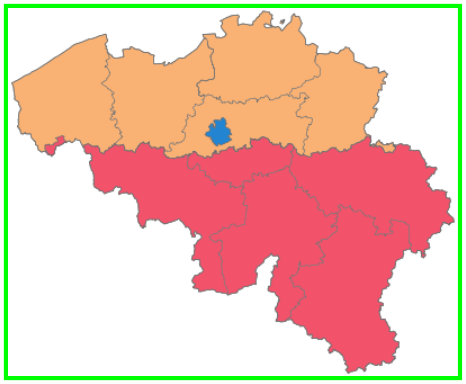

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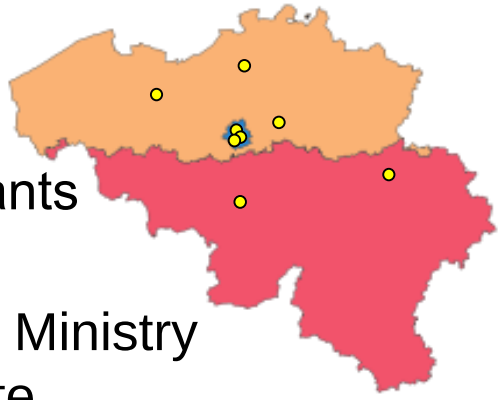
- Belgian Medical Genomics Initiative (BeMGI) :
  scientific, inter-university network, funded by federal Ministry in charge of Scientific Research. 8 centers participate.



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# An exemplary system?

- All genetic centres combine clinical and laboratory activities
- Accreditated diagnostic labs are closely associated with the academic research centres

- Parsimonious use of the national ‘envelope’ for testing
- Stratified reimbursement system allows flexibility
- Development of national guidelines
- But still no reimbursement of clinical exomes (genomes)

- System challenged by commercial companies
  - Disconnected from the needs (patient and population)
  - No genetic counselling

# Primary activities undertaken/completed 2014-2015

- **Streamline diagnostic NGS-based tests in the 8 genetics centres** (gene panels, mendeliomes and exomes).
  - Evaluation of the VCF files, comparing exome pipelines :
    8 centers together used: 2 aligners/3 versions of GATK /2 variant callers
  - Common Informed Consent

- Launch early discussions about the (2018 ? ) **introduction of whole genome sequencing** for clinical use, and the ways to fund and implement it at the national level.

- **Supercomputers** (Flanders ; Brussels and Wallonia pending)
- **ELIXIR** voting participant
  = European life-sciences Infrastructure for biological Information
- **HPO** recording of phenotypes

# Key accomplishments / Challenges 2014-15

- **National consensus for prenatal array testing**
  - indication for testing, array design, interpretation of CNVs (panel discussion, constant re-evaluation). All invasive samples have array CGH
  - Beyond pre-defined set of CNVs
  - how to deal with VUS and incidental findings prenatally

- **NGS gene panels / Mendeliome, with specific Core Genes**
  - National list of 800 genes / panels available for testing, with gov't € updated 2 x / yr
  - Some redundancy between the 8 Centres

- **NIPT for fetal trisomies** performed in 4 of the 8 Centers, 390€ (430 $) - - > CNVs
- **National Guidelines for clinical testing**
  CFTR, Hereditary cancers, …

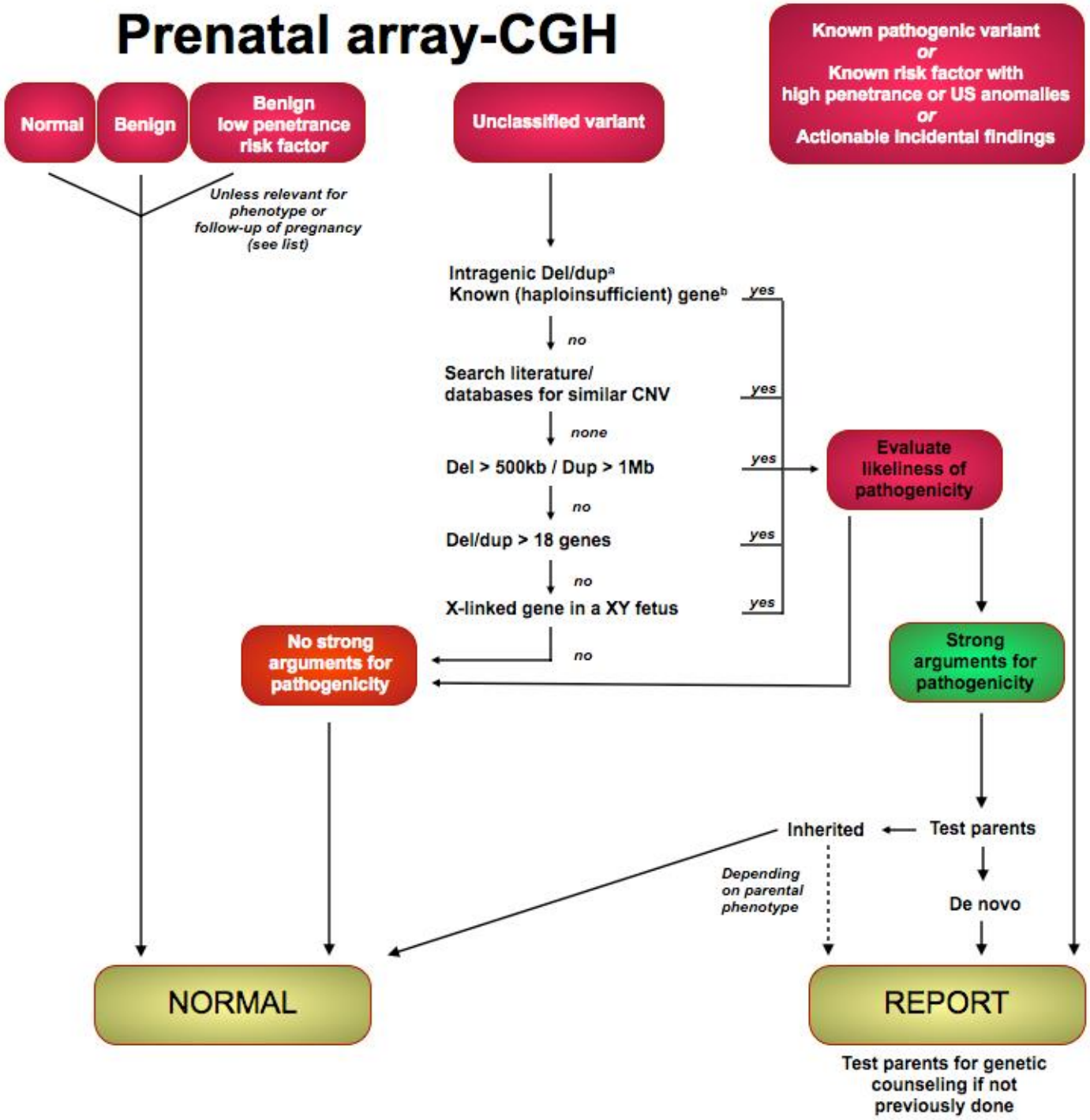
# Key accomplishments / **Challenges** 2014-15

- ISO 15189 **certification** (≈ CLIA)… and maintenance
- Guidelines, QC and reimbursement for **agnostic testing** exomes
- **Informatics for WGS**
- **Bioinformatics for WGS** (beyond mere tech transfer)
- **Confidentiality** (Phenotypes !)
- **Sharing information** on
  - Normal alleles
  - Disease-causing alleles
- **Counseling patients**
  - Train and tranfer activity to non-geneticists: oncologists, neurologists, …

# Opportunities for collaboration with G2MC

- Sharing data
  - International (clinical) variant databases
  - Including clinical information (preferably HPO)
- Build common resource for actionable variants
- Standardized informed consent for whole genome studies

# Prenatal array-CGH



# BRiDGE IRIS NGS PIPELINES COMPARISON

(workpackage 2 task 4)

| | UCL | UCL2 | UZ | IS | IS2 | ULB |
|---|---|---|---|---|---|---|
| Alignment | Bwa aln | Bwa aln | Bwa mem | Bwa aln | Bwa mem | Bwa aln |
| GATK version | 1.6 | 2.8 | 2.7 | 2.8 | 2.8 | 2.3 |
| Variant caller | UG* | HC* | UG | UG | HC | UG |
| Calling | Single sample | Single sample | Multi sample | Multi sample | Single sample | Multi sample |

* Unified Genotyper
* Haplotype Caller

6 exomes used for comparison (1 trio)

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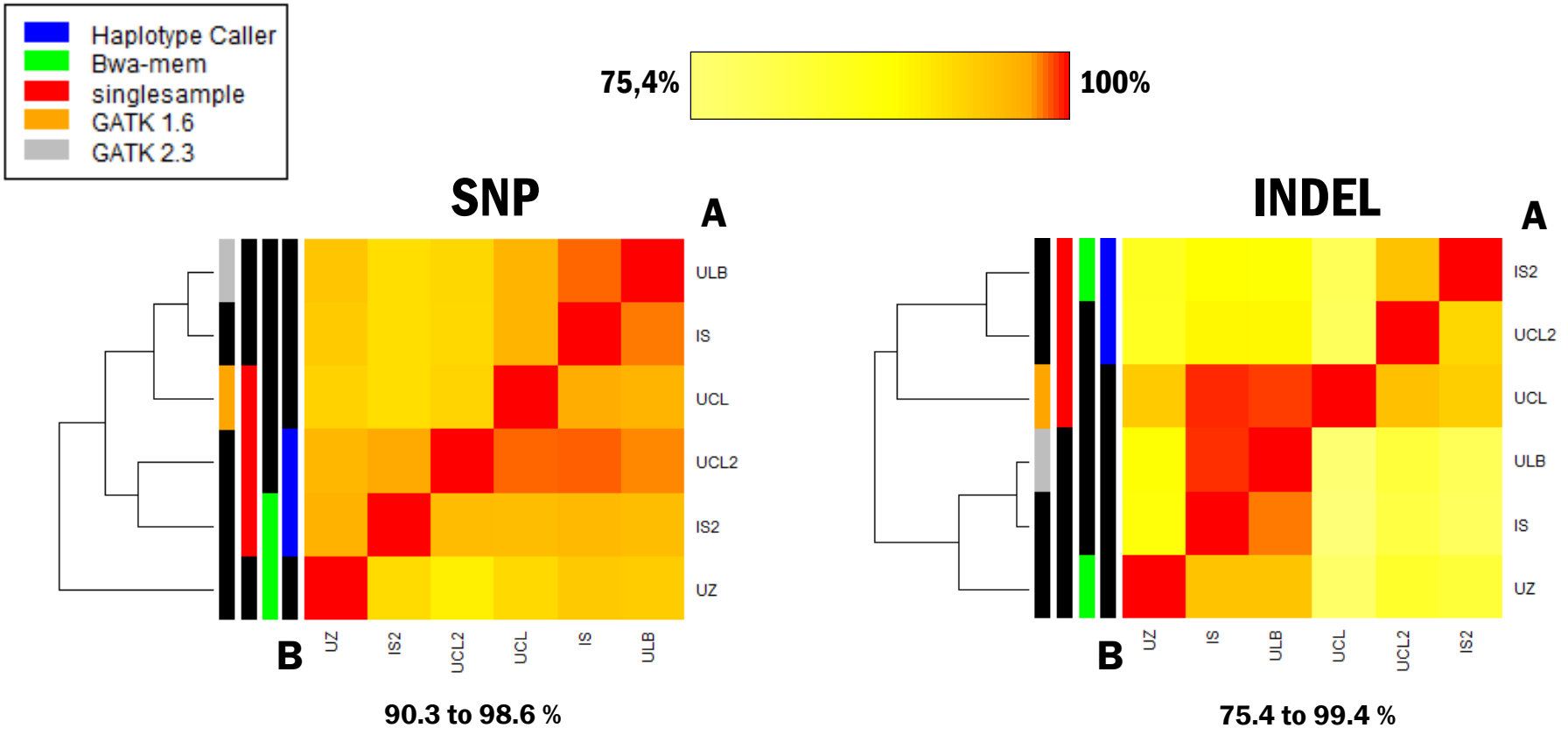
# BRiDGE IRIS OVERLAPPING VARIANTS

**Fraction of variants called by pipeline A also called by pipeline B**

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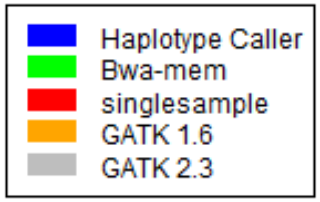
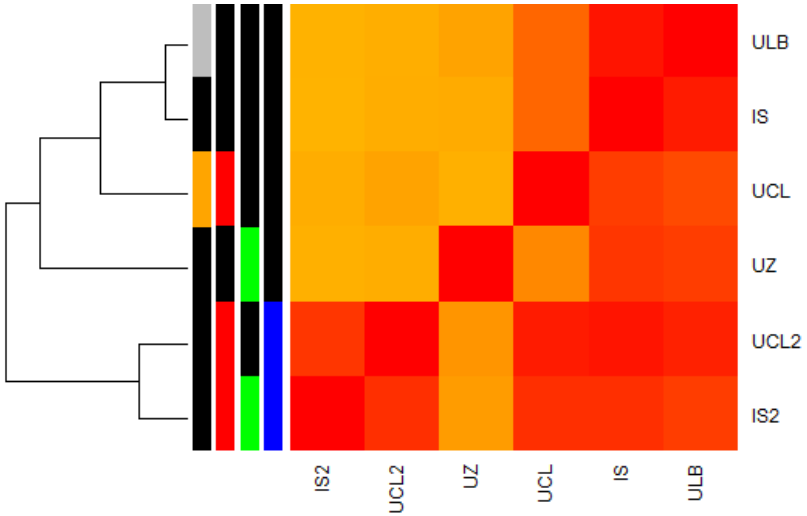
# BRiDGE$^{IRIS}$ dbSNP129 vs NOVEL

## dbSNP129 = pre-NGS variants



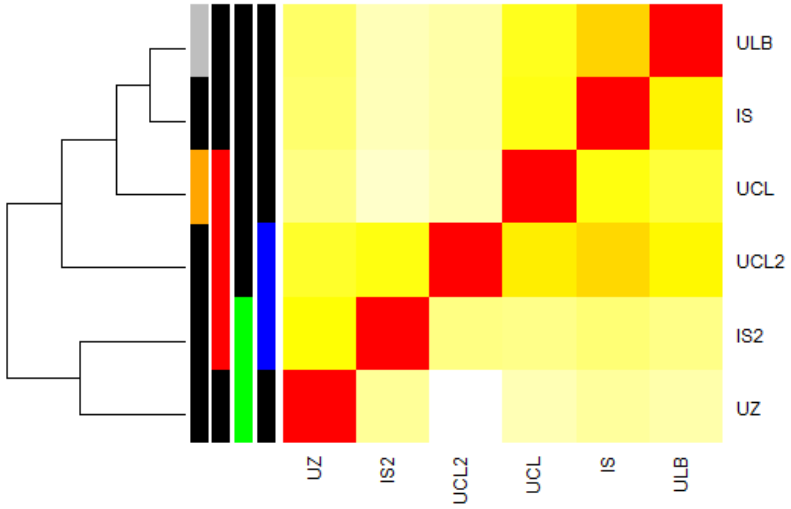


### SNP dbSNP129




96.5 to 99.7 %

### SNP NOVEL




57.5 to 93.2 %

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1. What are the primary activities related to genomic medicine that your group has undertaken or completed in the past two years?
2. What would you identify as your group's key accomplishments and challenges related to genomic medicine in the past two years?
3. What opportunities do you see for collaboration with G2MC or among the attendees?