EQA rondzending *KRAS*

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Some slides obtained from
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Role of Scheme organizers*

- Inventarisation of adequat FFPE material:
  - Type of mutation (similar among schemes)
  - Sufficient material
  - ≥ 30% tumor cells after microdissection
  - Quality control of samples in reference lab

- Preparation and distribution of slides:
  - 3 slides consecutive unstained slides/lab
  - Highest and lowest slide should be comparable
  - One or two spare sets
  - Last set of three slides > reference lab

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Role of Coordination centre Leuven

- Coordination role between all scheme organizers and participants
- Responsible for the harmonization of the samples
- Responsible for all communications
- Responsible for the website and electronic submission form
- Data collection of the results, draft first report and overview of results
- Logintudional research on performance

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Information submitted by the laboratory to the European QA coordinator

Tabular reporting form (electronic data submission)
- which mutations were tested
- which method was used
- % tumor cells and genotype results
- general information of the lab

Raw data of the lab results and the reports sent to treating physian of the first 3 samples

Data-analysis

- **Results have to be submitted within 10 workdays**
  - Mutation analysis of the samples
  - Analysis of tumor percentage
  - Written reports of the first 3 samples
  - Raw data
  - List with general questions
  - Minimal requirement 2014:
    KRAS & *NRAS* codons 12,13, 59, 61, 117, 146

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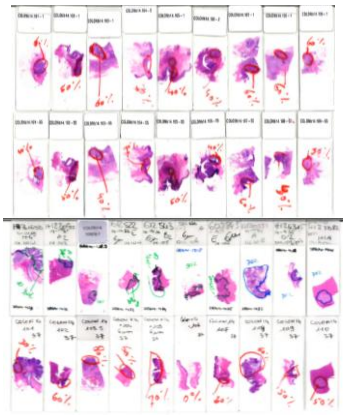


B

D

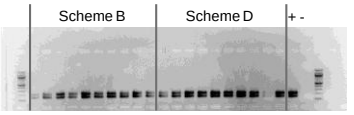
Genotypes of Scheme 2014-2015

Sample number	Genotype
COLONx14.101	*KRAS* c.38G>A; p.Gly13Asp
COLONx14.102	wild-type *KRAS*/*NRAS*/*BRAF*
COLONx14.103	subscheme A,B, D-I: *NRAS* c.182A>G; p.Gln61Arg subscheme C: *NRAS* c.181C>A; p.Gln61Lys
COLONx14.104	wild-type *KRAS*/*NRAS*/*BRAF*
COLONx14.105	subscheme A, B, C, E: *KRAS* c.183A>C; p.Gln61His subscheme G, H, I: *KRAS* c.183A>T; p.Gln61His subscheme D, E: *KRAS* c.182A>T; p.Gln61Leu
COLONx14.106	wild-type *KRAS*/*NRAS*/*BRAF* subscheme D: insufficient neoplastic cells (expected result: sample not contributive)
COLONx14.107	*KRAS* c.35G>A; p.Gly12Asp
COLONx14.108	*BRAF* c.1799T>A; p.Val600Glu
COLONx14.109	*KRAS* c.436G>A; p.Ala146Thr
COLONx14.110	wild-type *KRAS*/*NRAS*/*BRAF*

Dutch labs in schemes
B n= 15
D n= 7

Some labs just tested normal tissue

DNA quality of schemes B and D

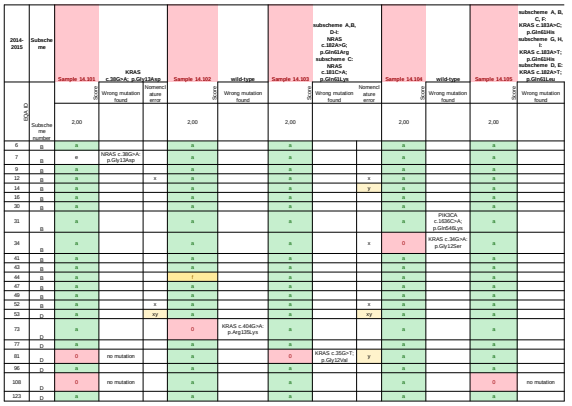


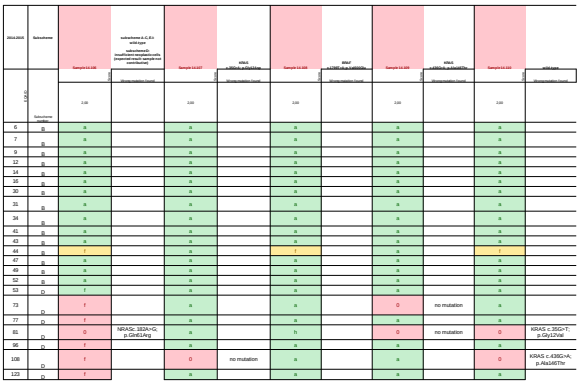
Size ladder with amplicons of 119 bp and 216 bp

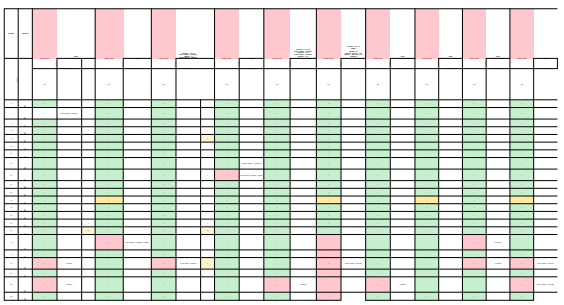
All samples performed well in AmpliSeq panel analyzed on PGM

Techniques in Dutch labs

- Sanger seq 9
- NGS 7x (PGM & Roche Junior)
- Therascreen 2
- Sequenom 1
- HRM 1
- Pyrosequencing 1
- Taqman 1







Total scores Dutch labs

labs without major phenotype error and >18 will be mentioned on the website

2014	
20,00	B
19,00	B
20,00	B
20,00	B
19,50	B
20,00	B
20,00	B
20,00	B
18,00	B
20,00	B
20,00	B
14,00	B
20,00	B
20,00	B
20,00	B
19,50	D
14,00	D
18,00	D
9,50	D
18,00	D
10,00	D
18,00	D

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Conclusion

- The ESP RAS EQA schemes **highlight the need for continuing EQA** in this field
- Still some labs do not test all required RAS codons
- EQA scheme assesses not only the laboratory's **ability to obtain accurate, reliable results**, but also **the ability to safely interpret the results** and ensure that the referring clinician has the correct information.
- The **quality of the reports improved**

Acknowledgement

Scheme co-ordinator and assistants co-ordinator
E Dequeker,L Tembuyser
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Medical and technical expert
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Scheme organisers

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The participating laboratories