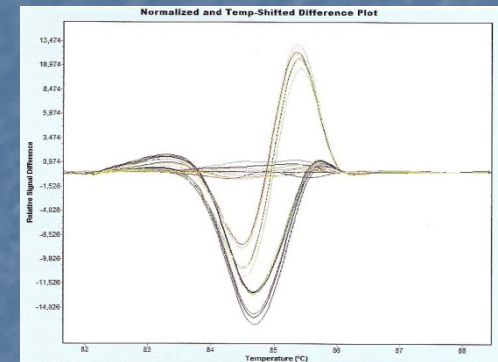


# BRCA screening by HRM on the LightCycler<sup>®</sup> 480



*Tom Janssens*



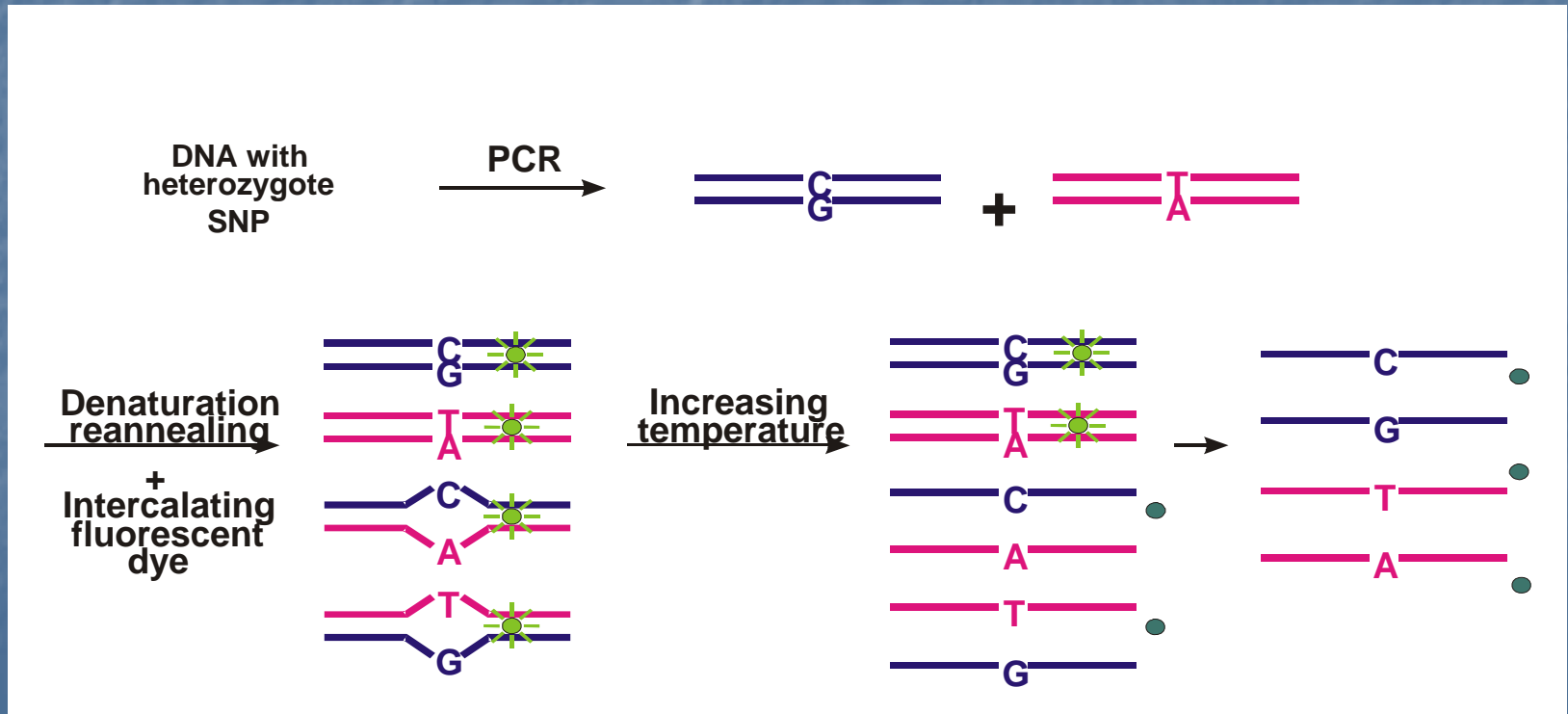
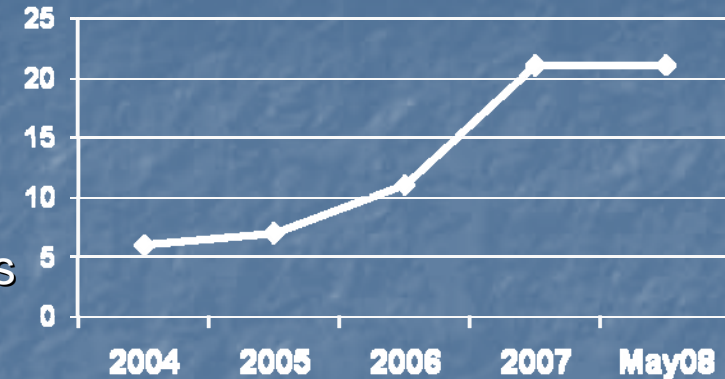
Center for Human Genetics  
Laboratory for Molecular Diagnostics  
University Hospital Leuven, Belgium

# HRM

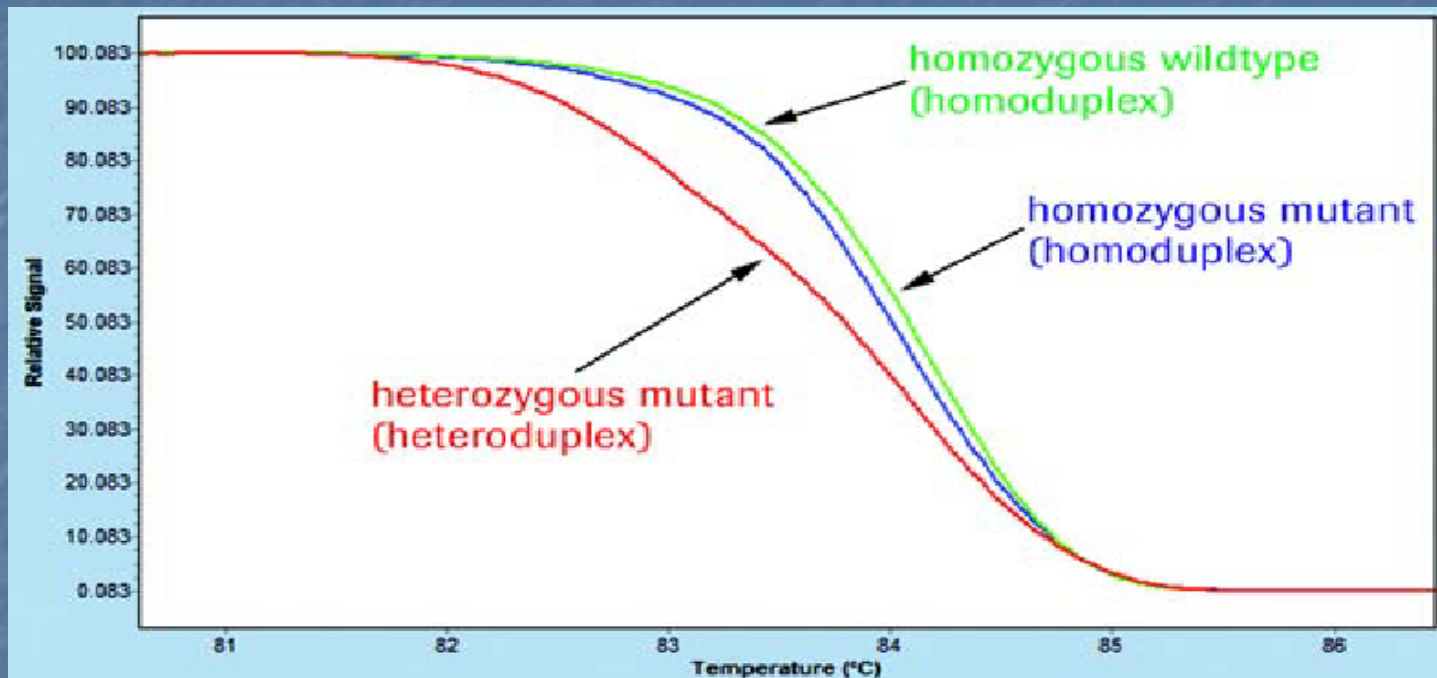
## ■ What is HRM?

- High resolution melting
- Mutation scanning
- Based on difference in melting patterns between homo- and heteroduplexes

## HRM papers on PubMed



# HRM



## ■ Applications

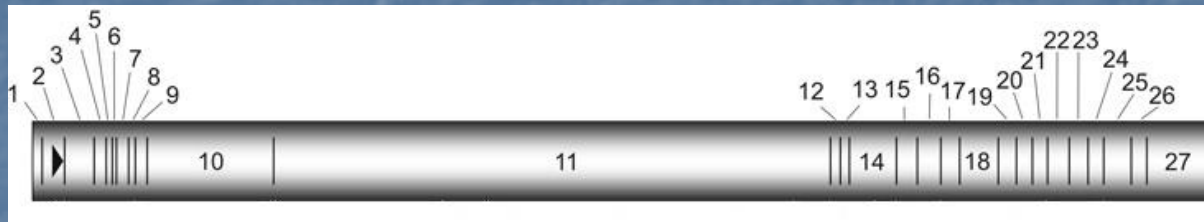
- Mutation scanning (screening for unknown sequence variations)
- Genotyping (detection of known SNPs using unlabeled probes)
- Mutation scanning + genotyping (combination)
- Methylation analysis

# BRCA1 and BRCA2 screening

- Very challenging genes
  - BRCA1: 22 coding exons



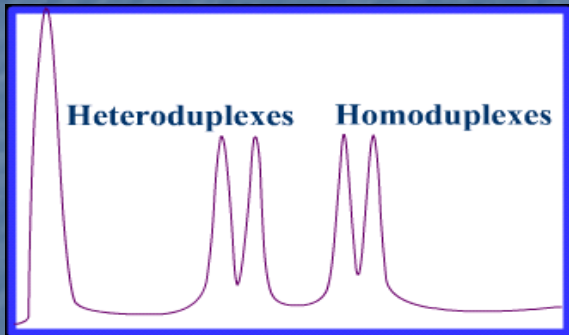
- BRCA2: 26 coding exons



- Lower than average GC content
- No mutation hot spots (insertions, deletions, duplications)
- Increasing number of clinical samples

➔ 2 strategies: **direct sequencing** or **2-tier strategy**

# DHPLC vs HRM



- **Good performance ...**
  - high sensitivity (>95%)
  - high specificity (>98%)

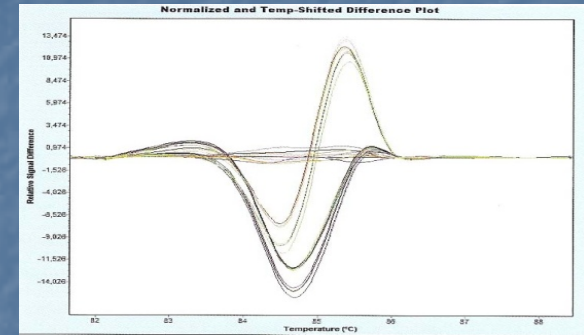
## ▪ ... but some limitations

### Throughput

- Serial system
- Separation of duplexes
- multiple  $T_m$

### Maintenance

- Daily
- Weekly
- Monthly



- Cheaper system
- No expensive consumables
- “maintenance-free”
- Closed-tube system
- No separation of duplexes
- 10-15min melt

**Much faster !!!**

# LC480 validation study: Setup

- **Extensive EuroGenetest validation**
  - Collaboration (Leuven, Leiden, Geneva)
  - Many samples – different types of sequence variations
  - Inter-laboratory parameters
  
- **3 phases**
  - PCR optimization
  - Mutation detection optimization
  - Blind study
  
- **Aim**
  - A complete primer set for BRCA1 and BRCA2 screening
  - Power to determine a sensitivity of at least 99%
  - Easy implementation in a diagnostic setting

# PCR optimization

## ■ Primers:

- Based on existing primer sets for dHPLC or sequencing
- SNPcheck (NGRL Manchester)
- Fragment length (~ 200 – 400bp)
- M13 tags → universal primers → streamlined sequencing

BRCA1: 42 amplicons

BRCA2: 61 amplicons

## ■ PCR

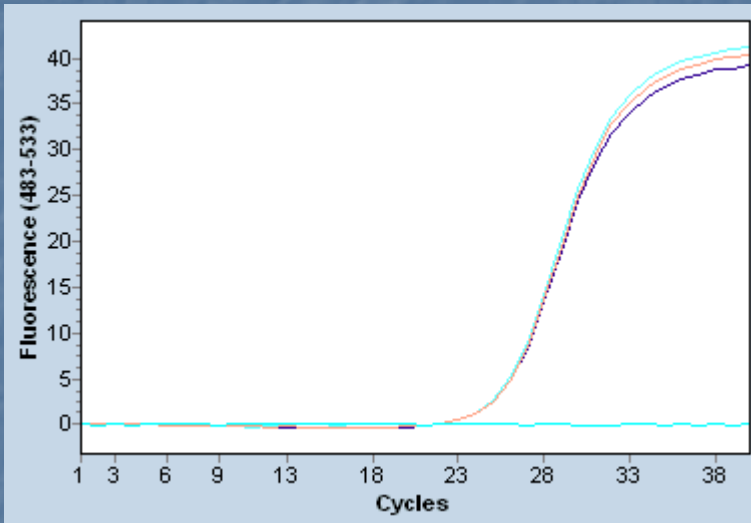
### Criteria

- sigmoid shape of real-time curve
- $C_p < 28$
- specific bands on 2% agarose
- < 3 melting domains

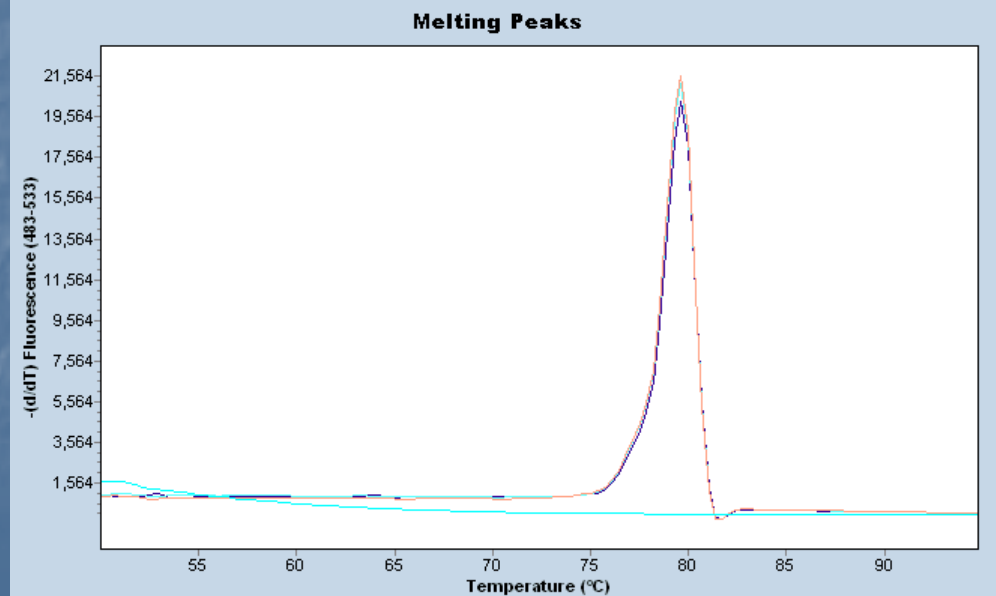
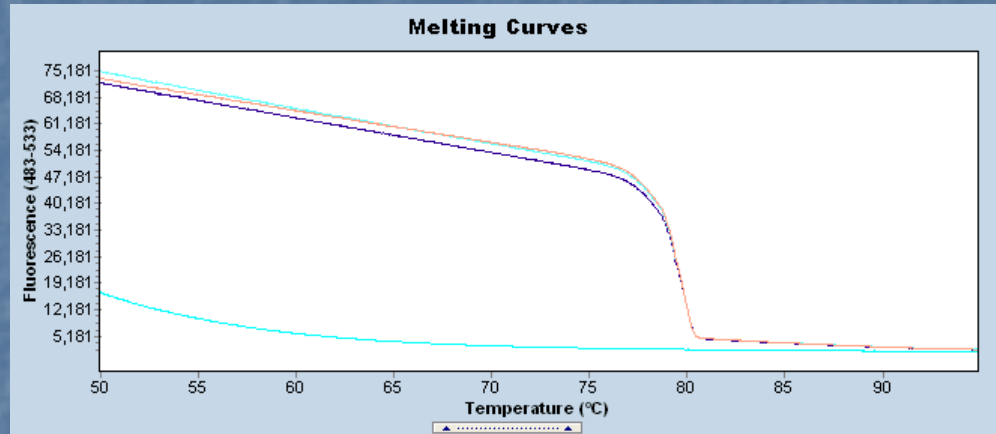
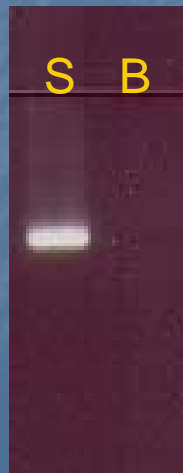
### Starting conditions

- 10  $\mu$ l reactions
- 1x HRM master (Roche Applied Science)
- 2 or 3 mM magnesium
- 250 nM primers
- 20 ng template DNA
- same annealing temperature if possible
- 40 cycles

# PCR optimization: starting conditions

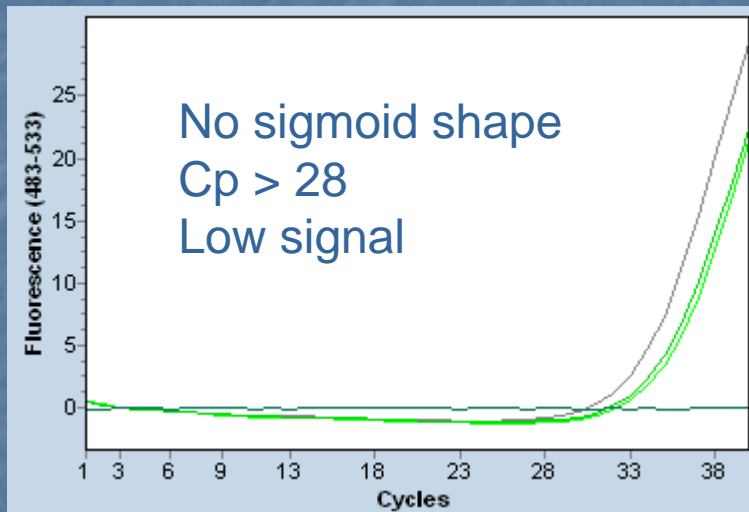


BRCA2 exon 2  
Ta: 60°C  
2mM Mg

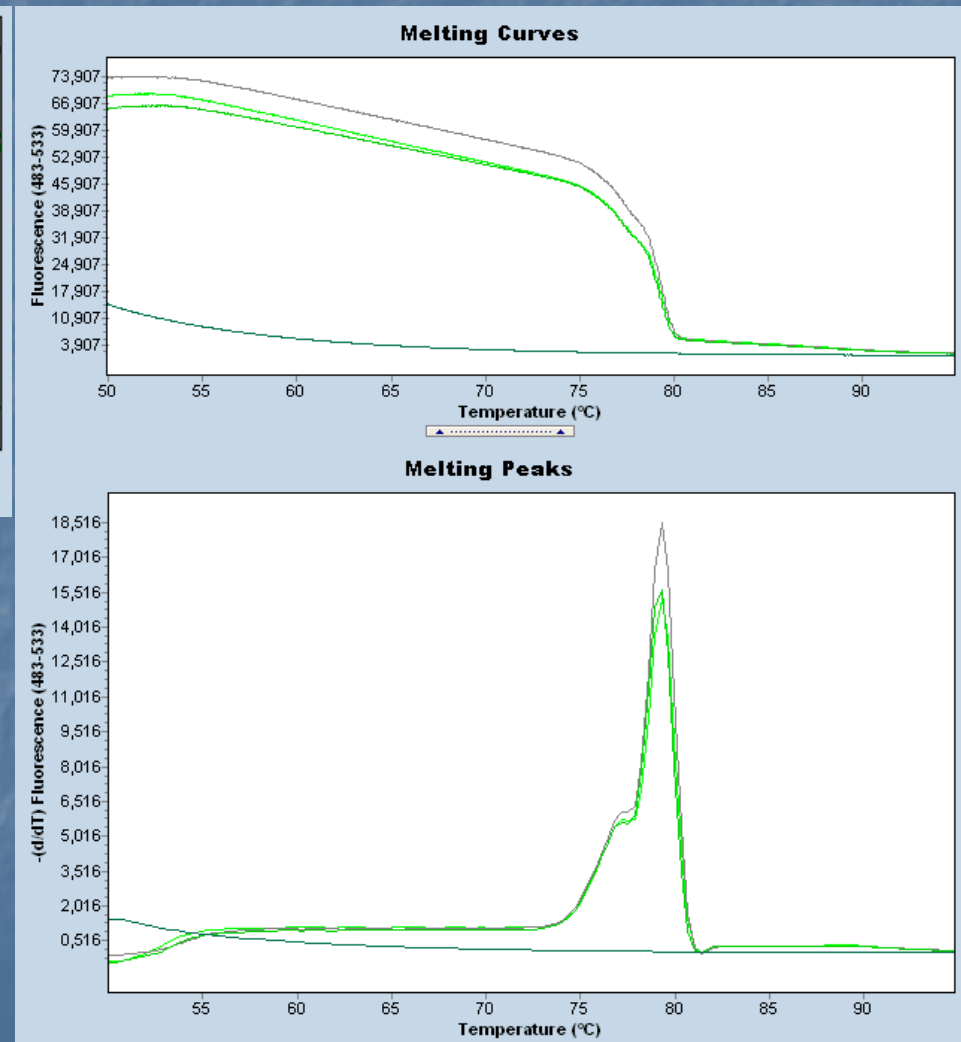
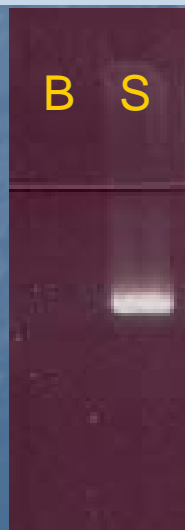




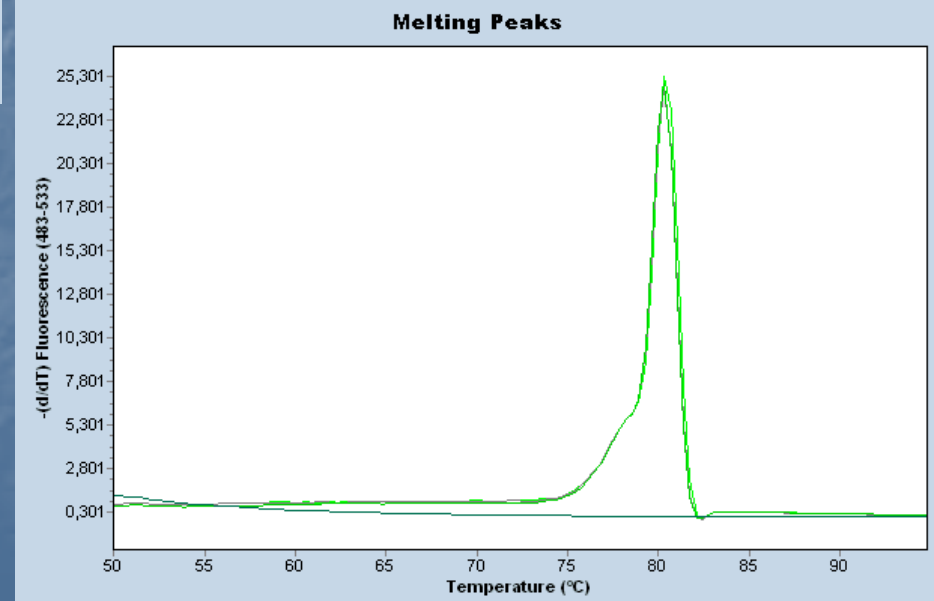
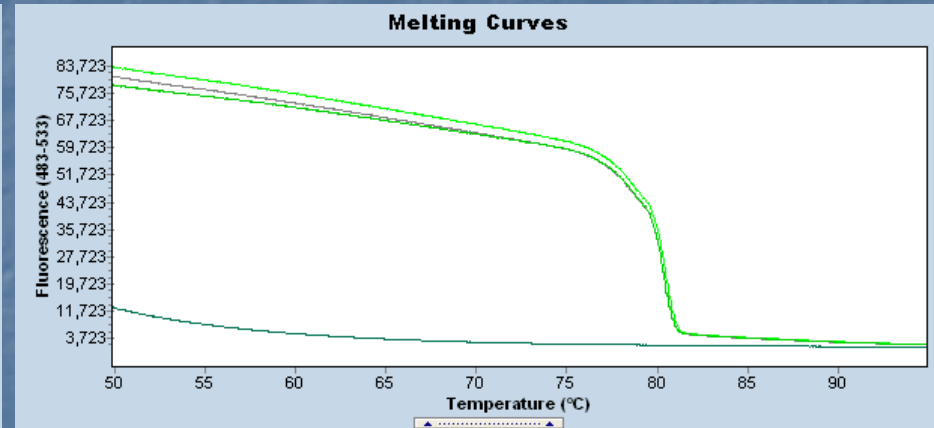
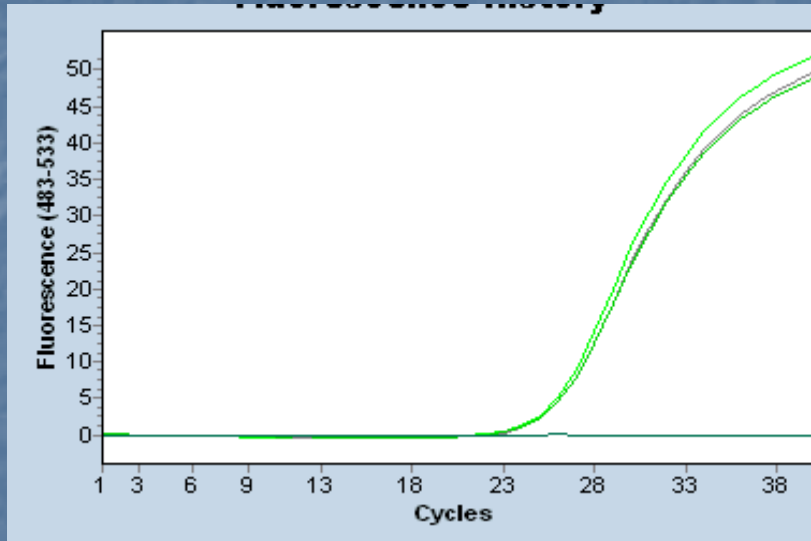
# PCR optimization: starting conditions



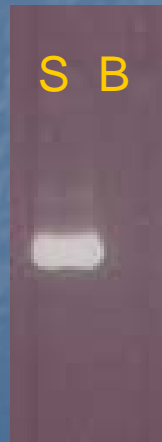
BRCA2 exon 3  
Ta: 60°C  
2mM Mg



# PCR optimization: fine-tuning



BRCA2 exon 3  
Ta: 57°C  
3mM Mg

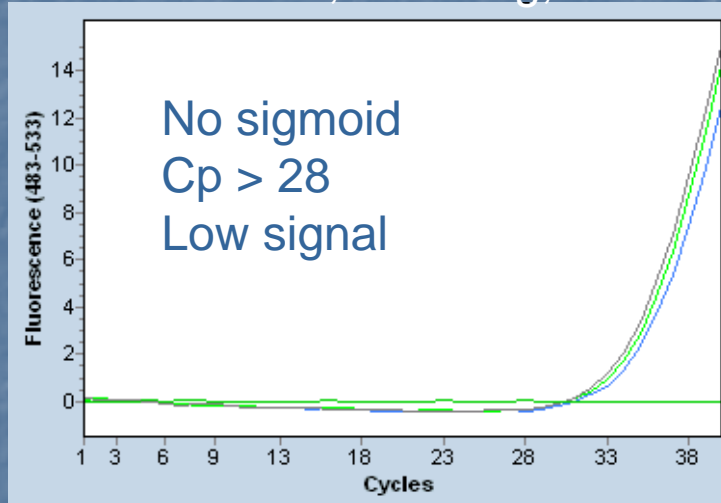


↳ Critical parameters

Annealing temperature      Magnesium concentration

# PCR optimization: redesign amplicon

BRCA2 exon 7, 3mM Mg, 60°C annealing



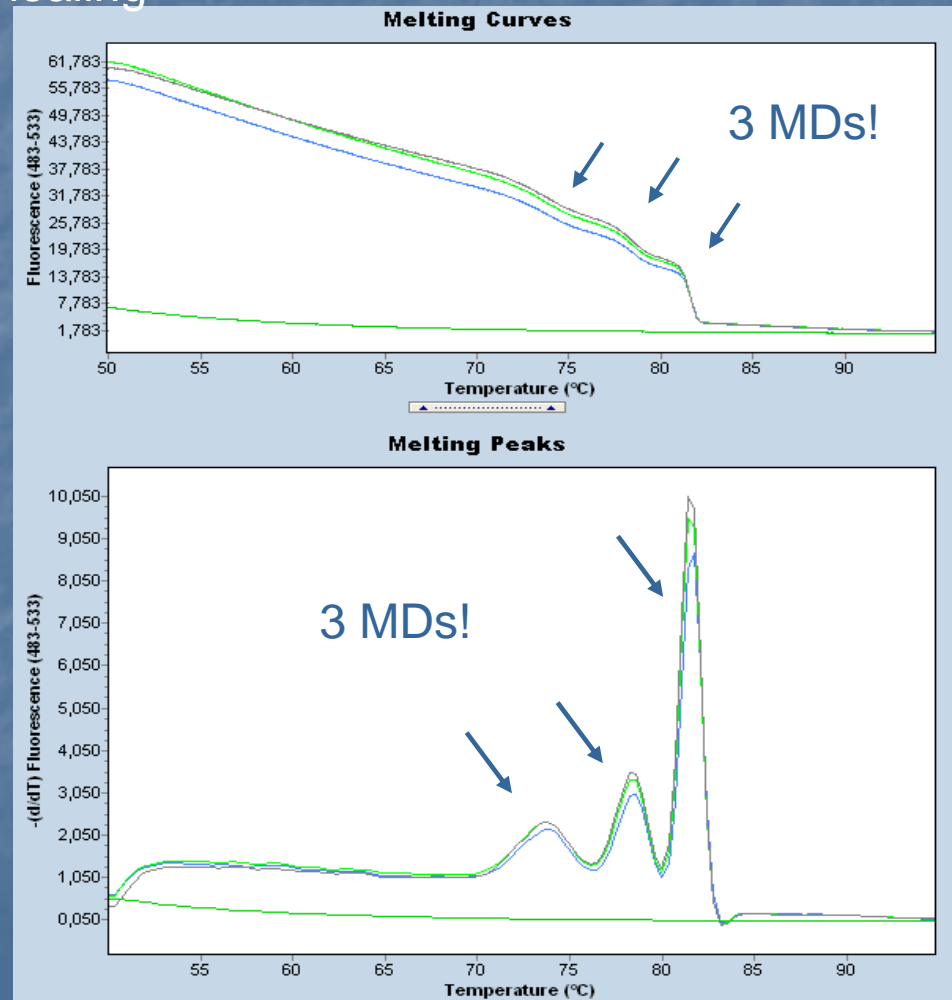
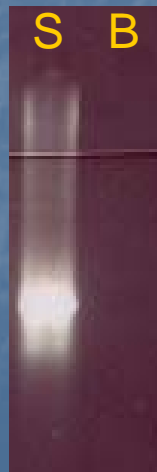
BRCA2 exon 7

Ta: 60°C

3mM Mg

Smear  
sample

Redesign primer!

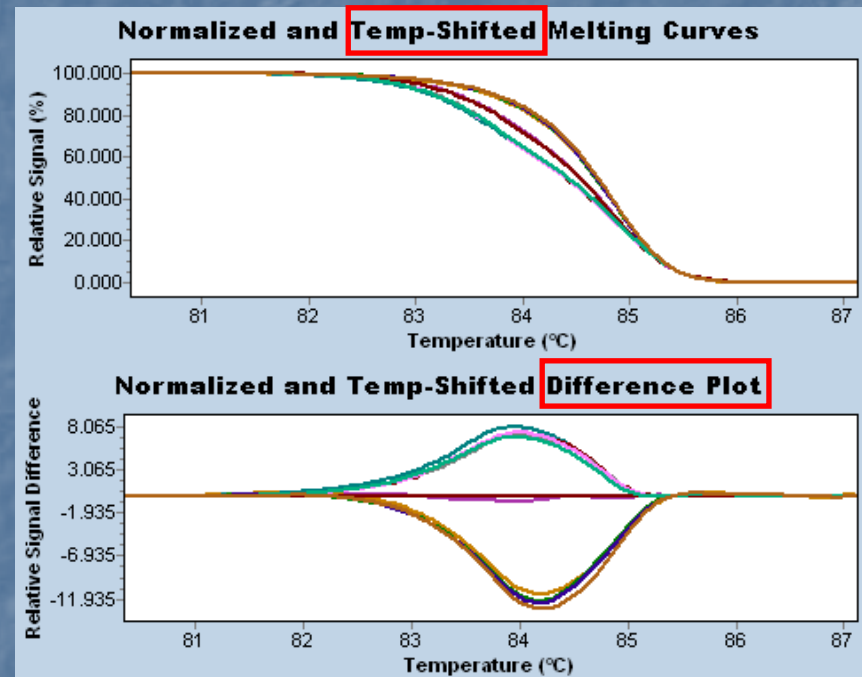
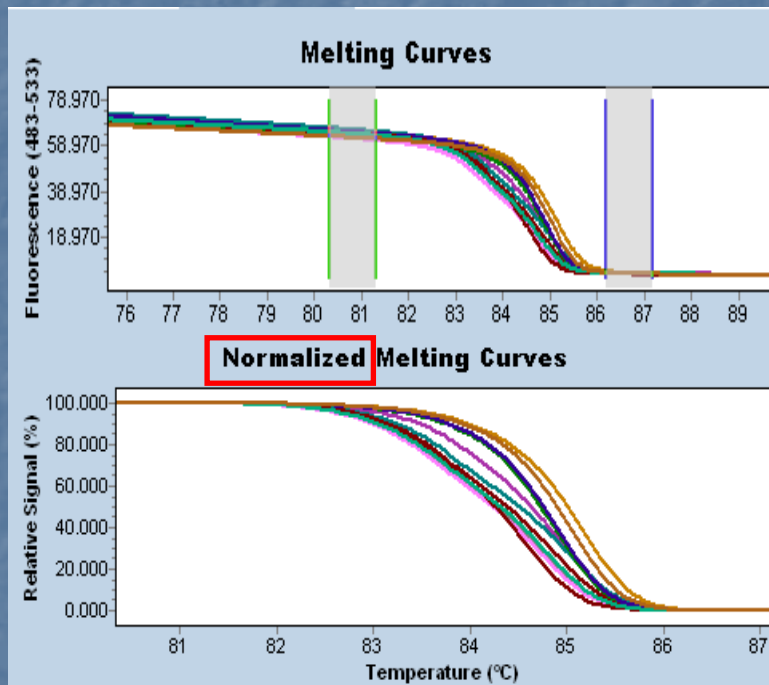


# PCR optimization: Summary

- 103 amplicons
  - BRCA1: 42
  - BRCA2: 61
  
- fixed annealing temperatures
  - BRCA1: 4 blocks of at least 6 amplicons (59°C, 62°C, 63°C, 65°C)
  - BRCA2: all at 57°C
  
- all amplicons met required criteria

# Mutation detection optimization

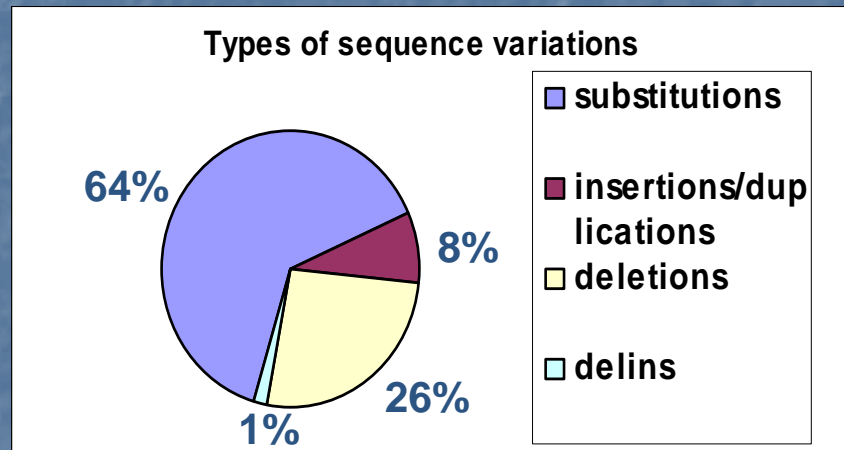
- Gene scanning software (v1.3 → v1.5)



- Critical parameters for mutation detection
  - Pre- and post normalization interval settings
  - Sensitivity setting

# Mutation detection optimization

- Setup
  - Set of ~ 300 DNA samples with known sequence variations



- Determine optimal settings for each amplicon
  - Normalization strategy: 1°C intervals right before and after melt region
  - Sensitivity: range without false negatives (and false positives)

# Mutation detection optimization: Example

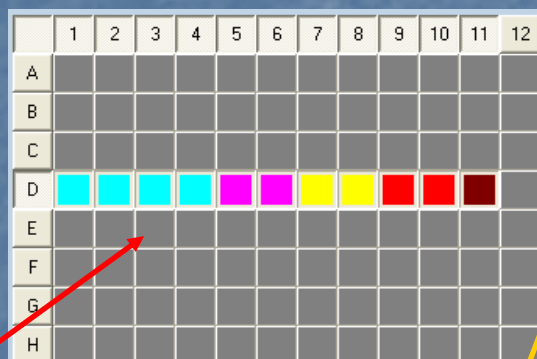
BRCA2 exon 9

Sensitivity range = 0.63 – 1.00

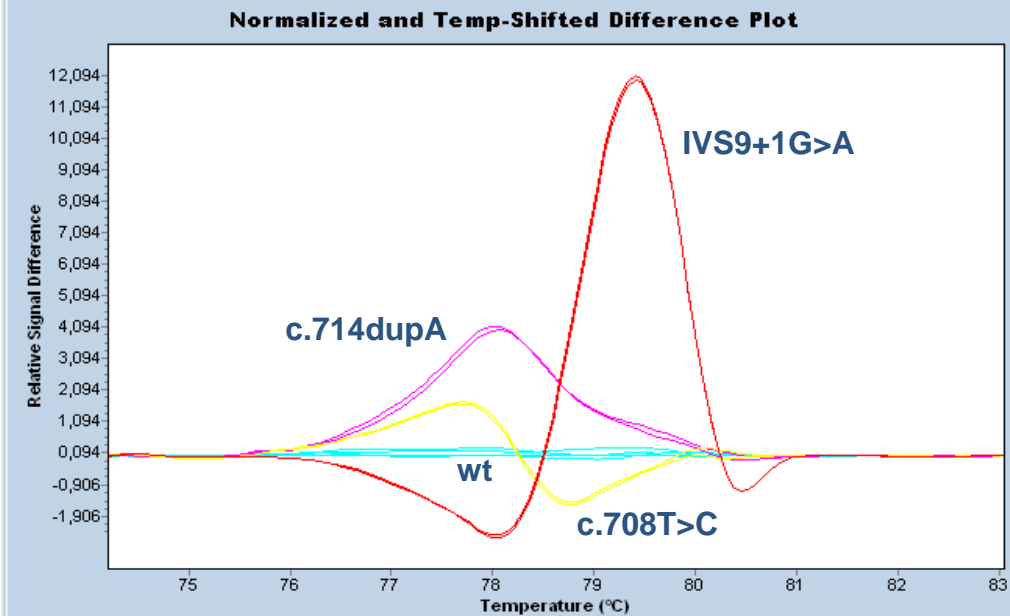
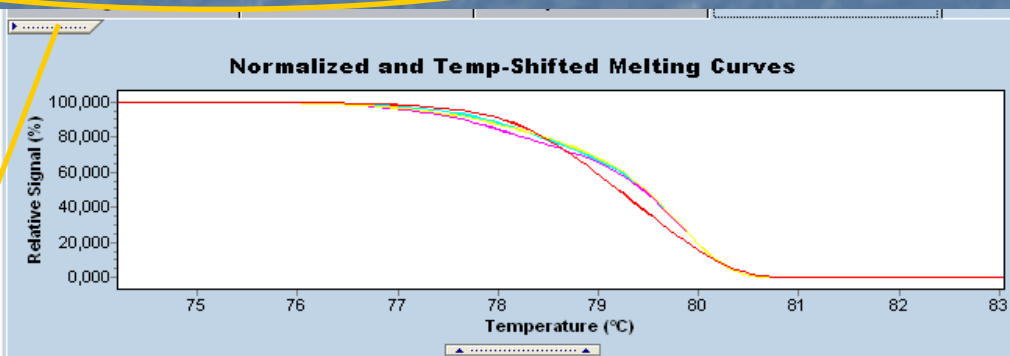
OK

Automatic grouping function

Sample ID



Results			Groups	Sensitivity
Include	Color	Pos. Name	Results	Group
<input checked="" type="checkbox"/>	Cyan	D1 Repl. of wt1	1	
<input checked="" type="checkbox"/>	Cyan	D2 Repl. of wt1	1	
<input checked="" type="checkbox"/>	Cyan	D3 Repl. of wt2	1	
<input checked="" type="checkbox"/>	Cyan	D4 Repl. of wt2	1	
<input checked="" type="checkbox"/>	Magenta	D5 GEN-BC2-06	4	
<input checked="" type="checkbox"/>	Magenta	D6 Repl. of GEN-BC2-C	4	
<input checked="" type="checkbox"/>	Yellow	D7 LEI-BC2-12	3	
<input checked="" type="checkbox"/>	Yellow	D8 Repl. of LEI-BC2-1	3	
<input checked="" type="checkbox"/>	Red	D9 LEI-BC2-13	2	
<input checked="" type="checkbox"/>	Red	D10 Repl. of LEI-BC2-1	2	
<input checked="" type="checkbox"/>	Magenta	D11 Repl. of NTC	*Negative	



# Mutation detection optimization: Summary

- All analyses performed on software v1.3
- Detection rates:
  - BRCA1: 94%
  - BRCA2: 97%
- Fixed normalization intervals
- Variable sensitivity ranges



# Blind study

## ■ Aim

- determine sensitivity and specificity of HRM
- ~ 300 positive control samples (~ 150 per gene)
- Power to reach a sensitivity of at least 99% (CI: 95%)
- At least as many wild type samples to have equal power for specificity

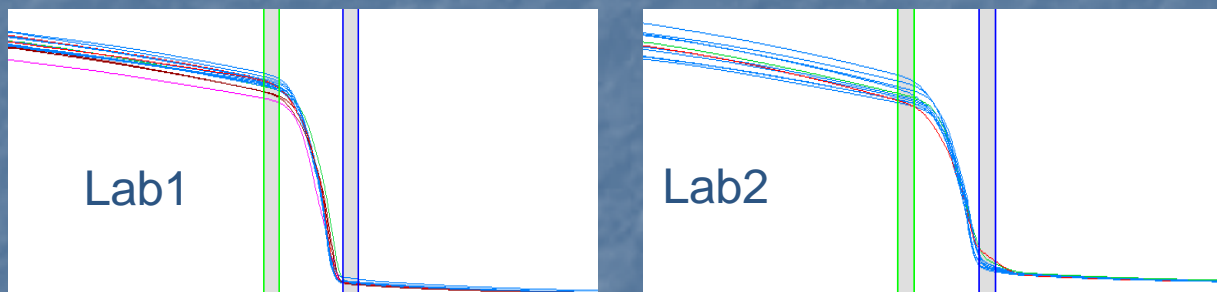
## ■ Setup

- Random distribution of samples (11 per amplicon + 1 ntc)
- Random distribution of amplicons over 3 labs → inter-lab variability
- Blind and automatic analysis
- Pre-defined and optimized normalization and sensitivity settings
- Upgrade from Software 1.3 to 1.5

# Blind study: Results

## ■ Normalization settings

- Poor reproducibility between laboratories
- Shift in normalization intervals



## ■ Sensitivity settings

- Fixed at 0.60 for most amplicons with software v1.5
- some amplicons higher sensitivity setting

## ■ Preliminary sensitivity

- BRCA1: > 97% (96% with v1.3)
- BRCA2: > 99% (96% with v1.3)

## ■ Preliminary specificity

- BRCA1: > 92% (88% with v1.3)
- BRCA2: > 77% (82% with v1.3)

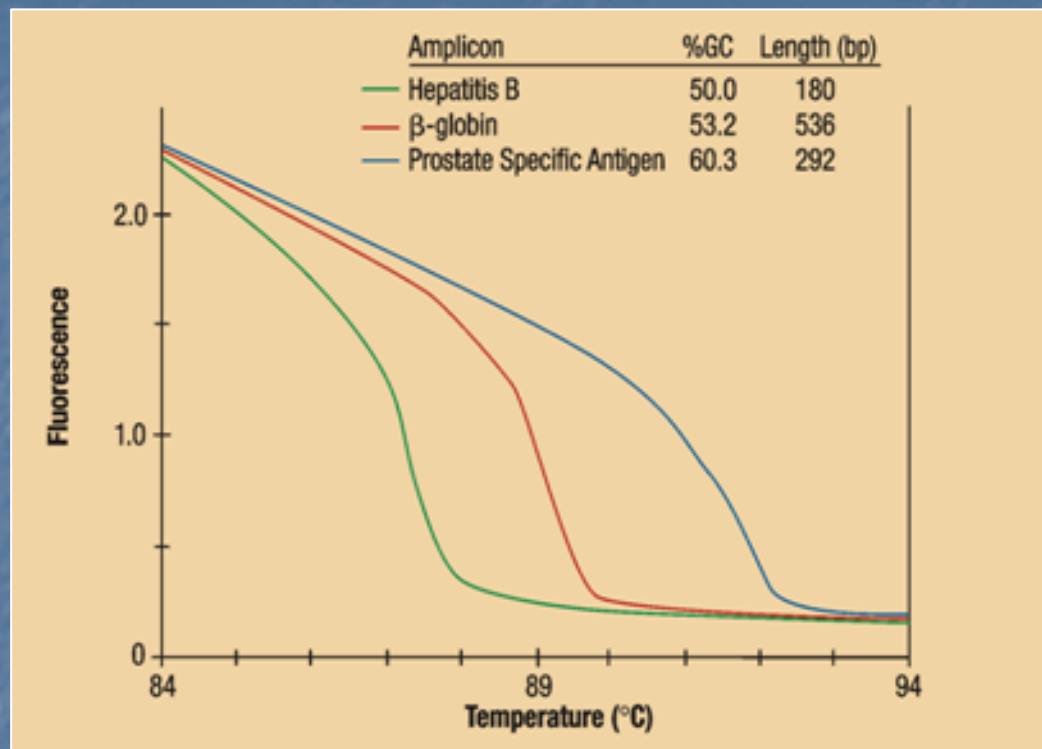
# Back to theory ...

T<sub>m</sub> varies by:

- GC-content
- amplicon length

T<sub>m</sub> is influenced by:

- Salt concentration
- MgCl<sub>2</sub> concentration
- dye concentration



**Highest Stability**

G:C > A:T > G:G > G:T = G:A > T:T = A:A > T:C > A:C > C:C

**Lowest Stability**



**BRCA genes are very challenging because of size and GC content!**

# Conclusions

- New software package v1.5:
  - Better performance
  - More user-friendly
- Normalization settings are not reproducible between labs
  - Use automatic software settings
- Specificity needs improvement → adjust sensitivity setting
- High sensitivity close to 99%...
- ... however still 4 false negatives out of 296 tested samples
  - Current primer set not finalized yet for diagnostic purpose

# Future work / actions

- Tackle false negative issues
  - Primer design
  - Secondary structures
  - GC content
  - Literature: touchdown PCR → increased specificity?
  
- Validation report
- Standard Operating Procedure (SOP) for practical use in diagnostic laboratories
  
- Poster at ESHG: P08.39
  - “Interlaboratory validation of High Resolution Melting (HRM) for BRCA1 and BRCA2 on the LightCycler<sup>®</sup> 480”

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