

# Monitoring CML patients by RQ-PCR

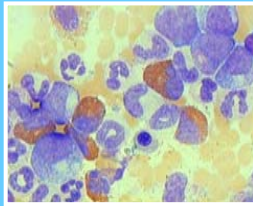
Andreas Hochhaus

Medizinische Fakultät Mannheim  
Ruprecht-Karls-Universität Heidelberg  
Mannheim, Germany

# Goals of CML Therapy

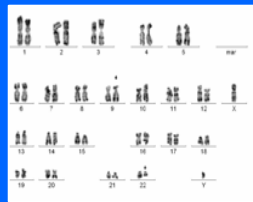
Leukemia cells

$>10^{12}$



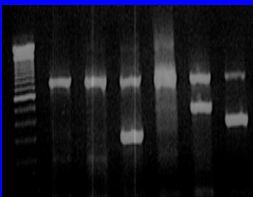
CHR

$10^{10}$



CCyR

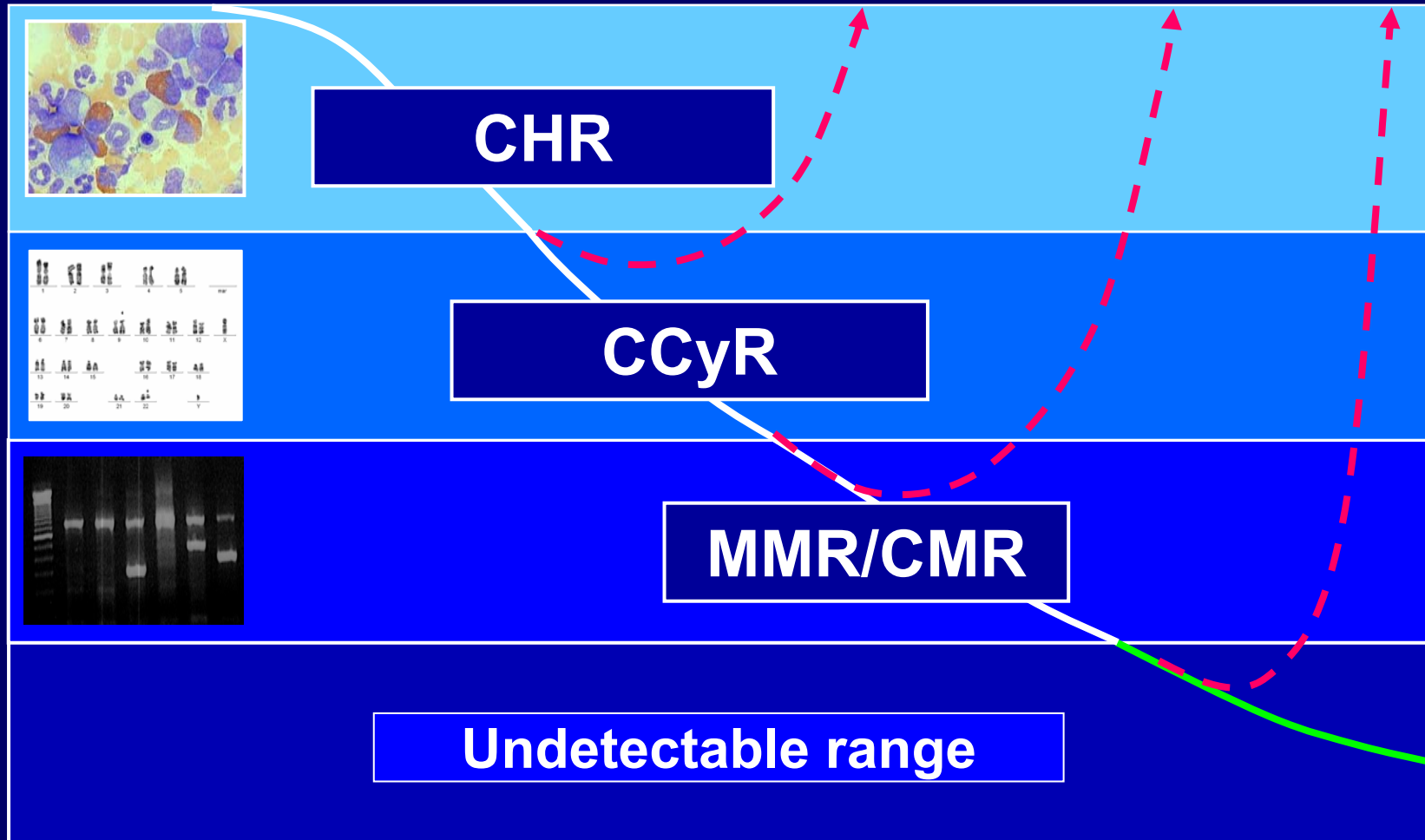
$10^8$



MMR/CMR

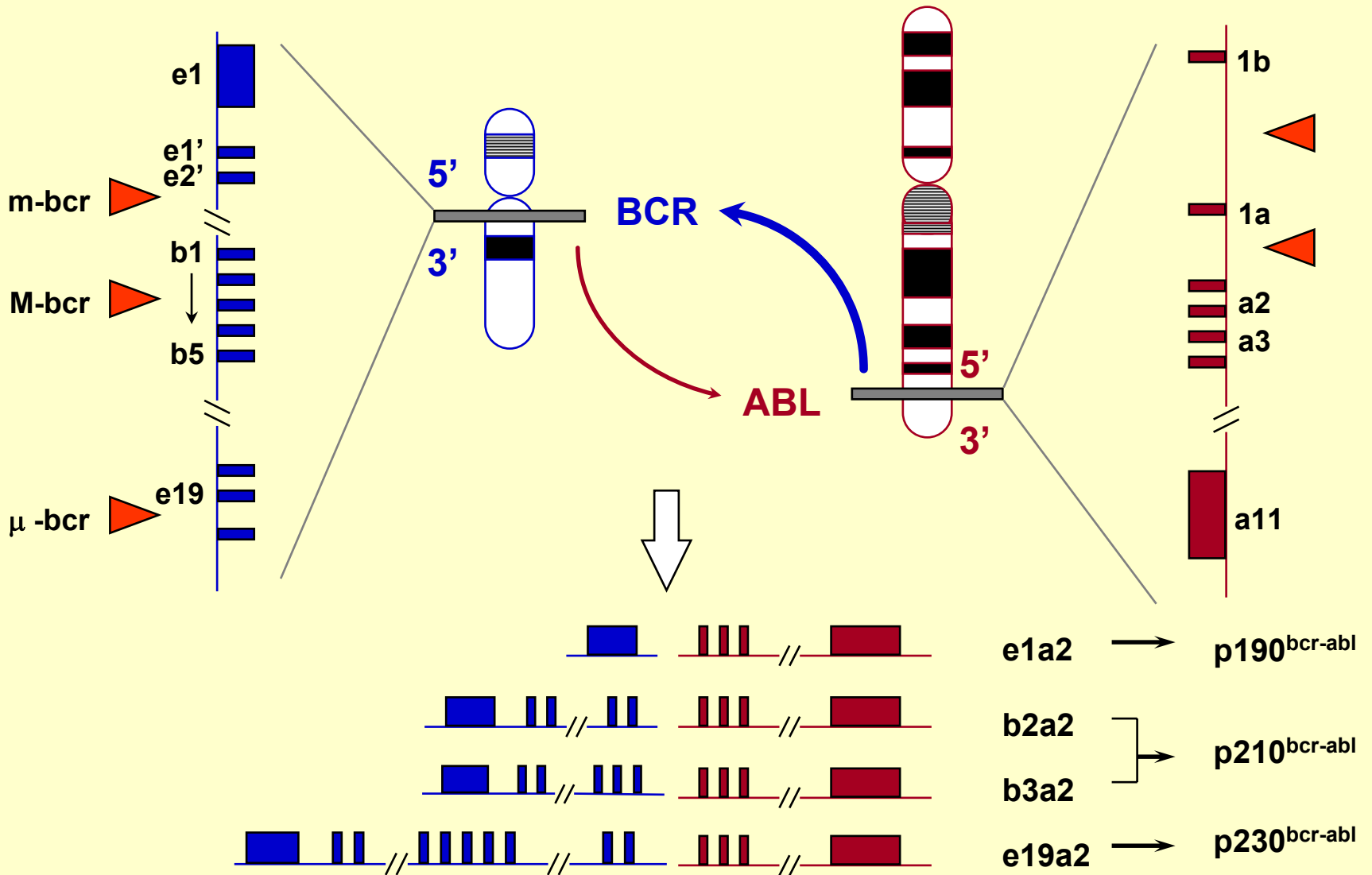
$10^6$

Undetectable range



# Chromosome 22

# Chromosome 9

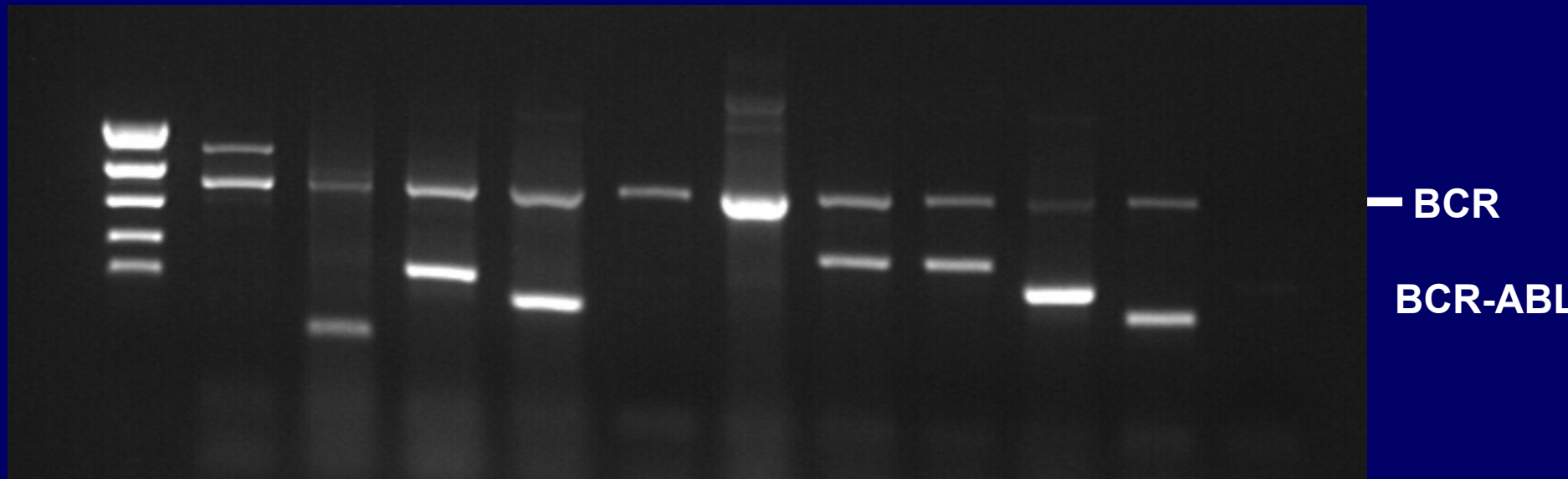


The PCR technique, although considered a valid clinical testing procedure, should be used cautiously as a laboratory test until sufficient data are available to show that it meets acceptable criteria of sensitivity, specificity, and positive and negative predictive values. How new PCR technologies such as "real-time" PCR quantification will solve these concerns and become a reliable tool for the clinician merits further investigation. **Until then, clinicians should exercise caution in basing clinical decision making on such studies, given the significant morbidity and mortality associated with aggressive therapeutic interventions aimed at molecular disease eradication in patients who might just do as well without.**

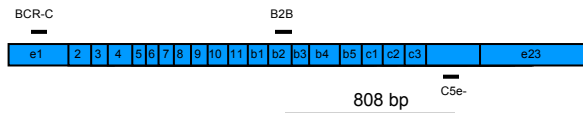
Stefan Faderl et al. (MDACC Houston), Blood 1999

# Multiplex-PCR for BCR-ABL transcripts

M	e6a2 CML	b3a3 CML	b3a2 CML	b2a2 CML	Ph- CML	normal control	e1a2 CML	SD1 Cell lines	K562	BV173	Neg.- control
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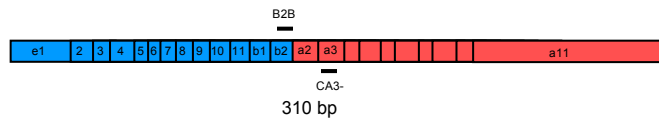
**BCR**



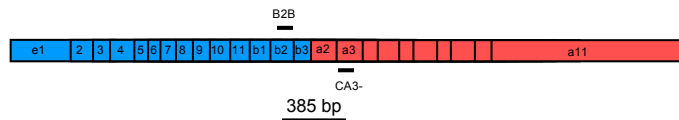
**ABL**



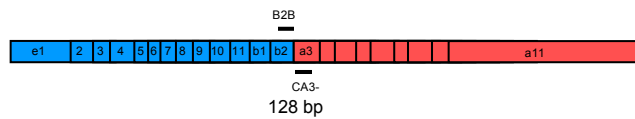
**b2a2**



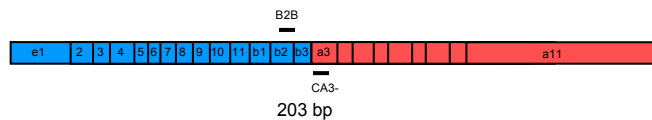
**b3a2**



**b2a3**

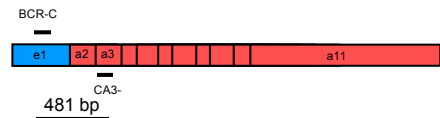


**b3a3**



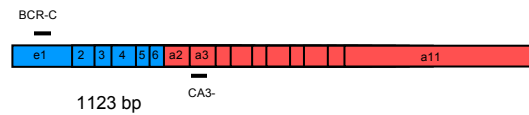
**p210  
BCR-ABL**

**e1a2**



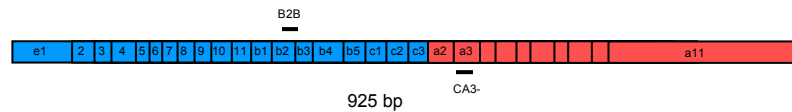
**p190  
BCR-ABL**

**e6a2**



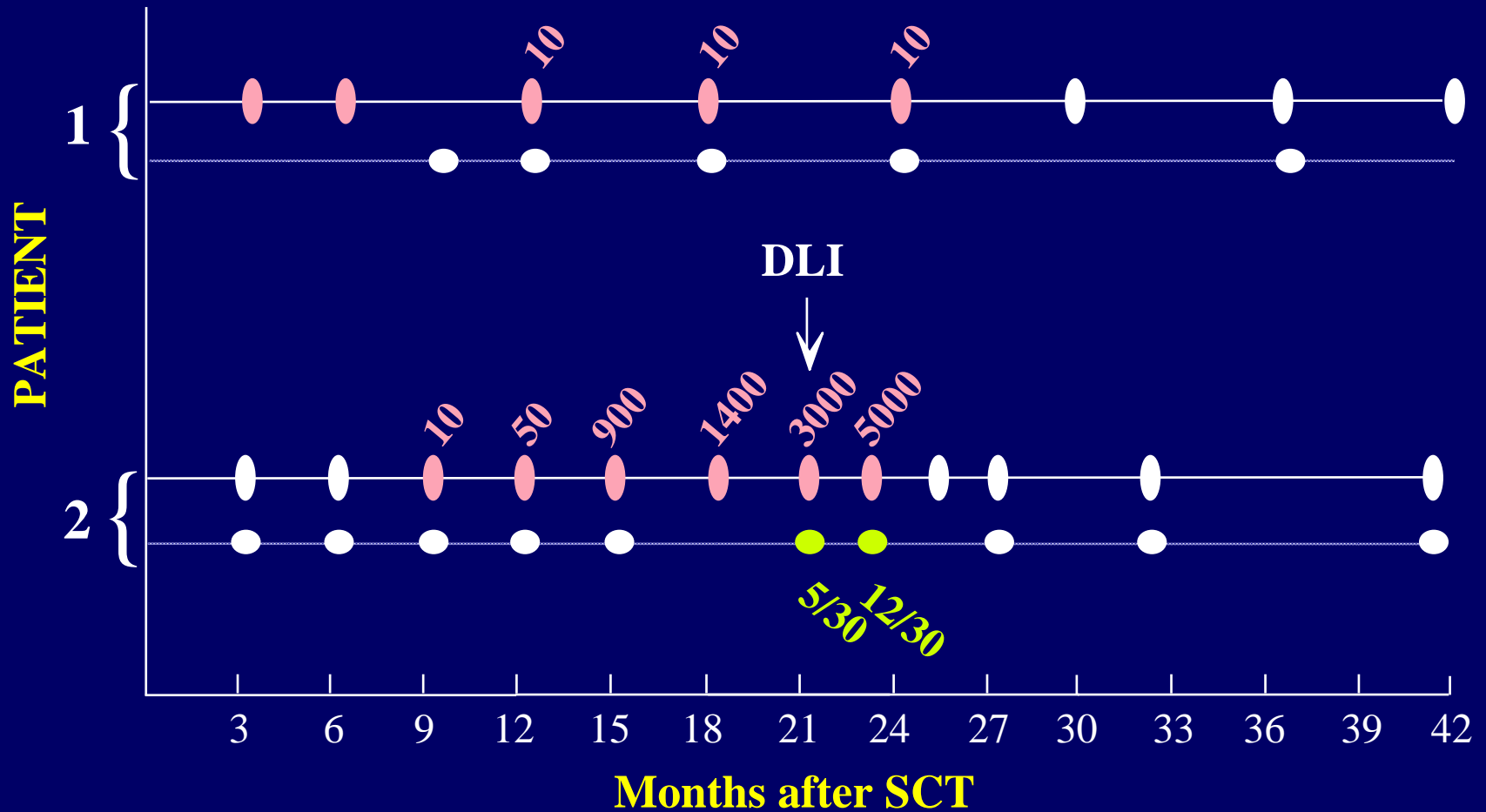
**p200  
BCR-ABL**

**c3a2**



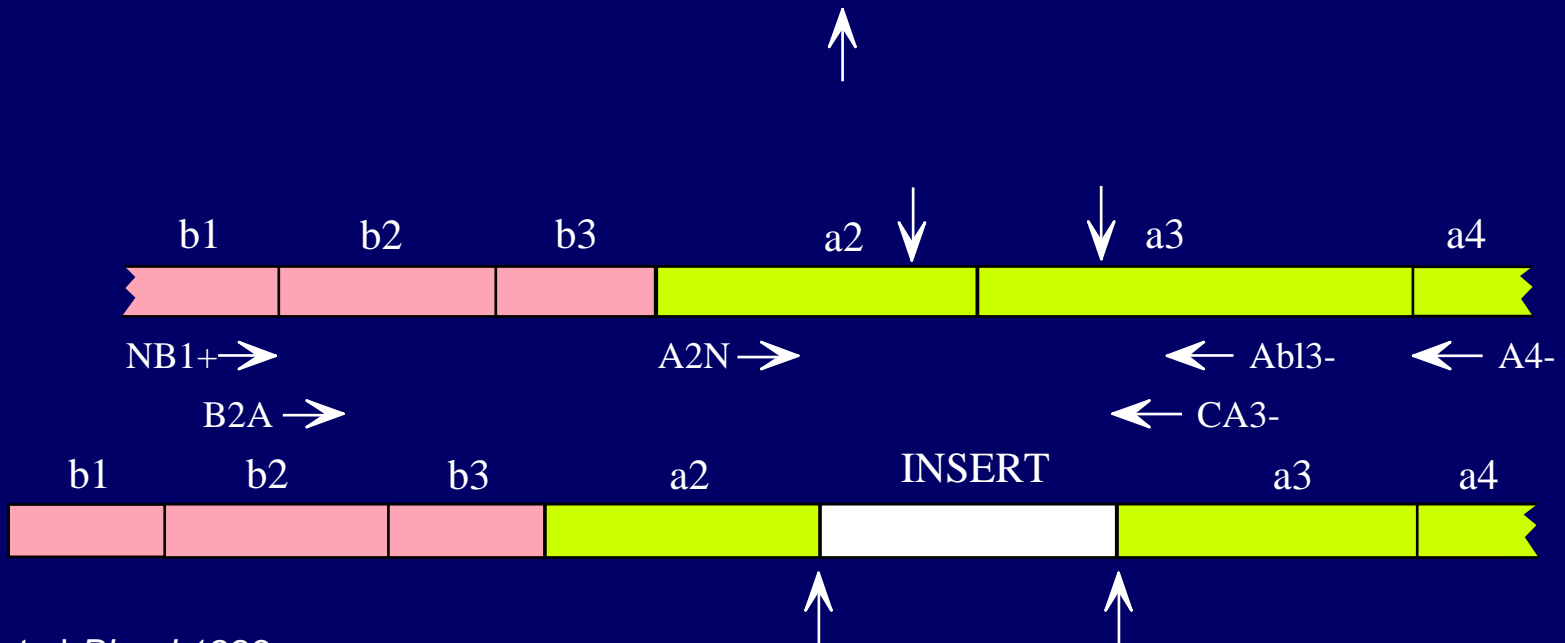
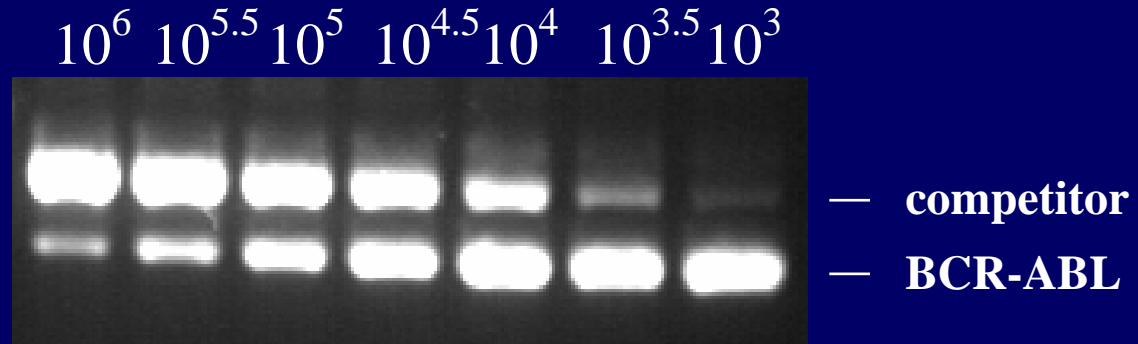
**p230  
BCR-ABL**

# Early detection of relapse after SCT



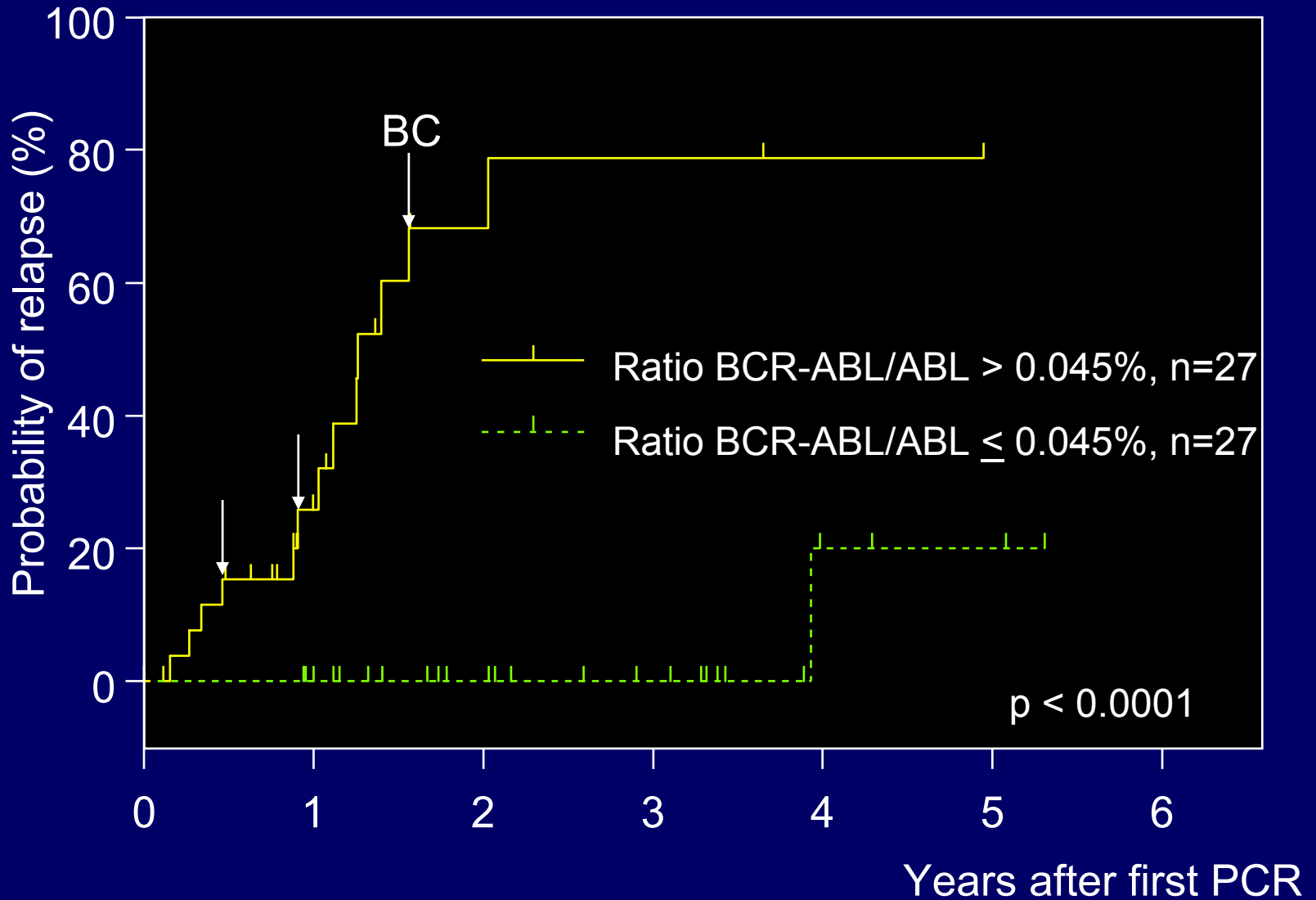
○ PCR neg    ● PCR pos    ○ Ph neg    ● Ph pos

# 1993: Competitive RT-PCR





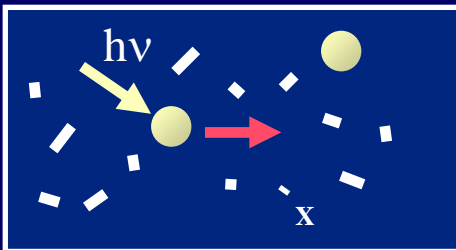
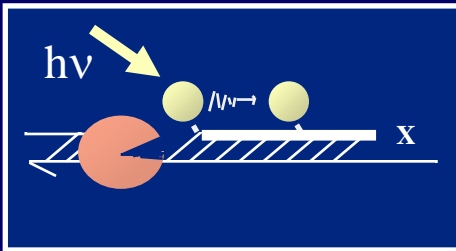
# Relapse free survival in complete cytogenetic responders after IFN therapy according to residual BCR-ABL transcript levels



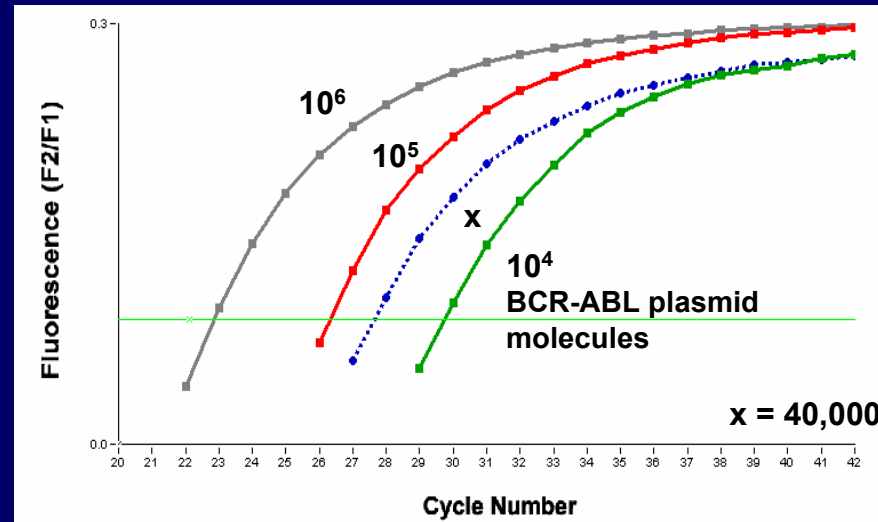
# Real time quantitative RT-PCR

## I. Hydrolysis Probes

Release from quenching by hydrolysis

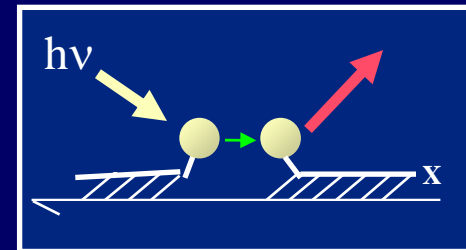
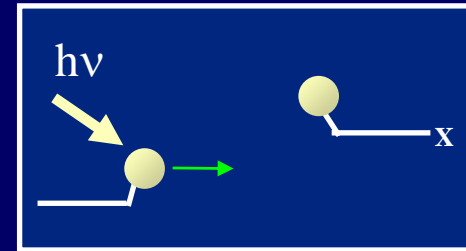


TaqMan™



## II. Hybridization Probes

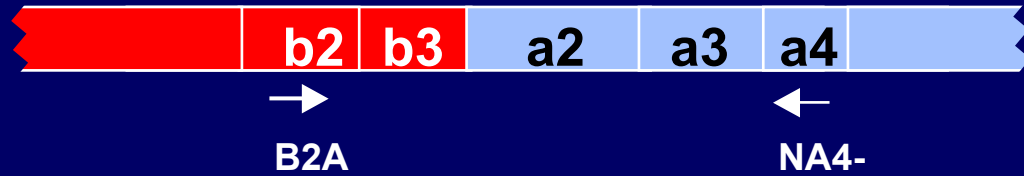
Increased resonance energy transfer by hybridization



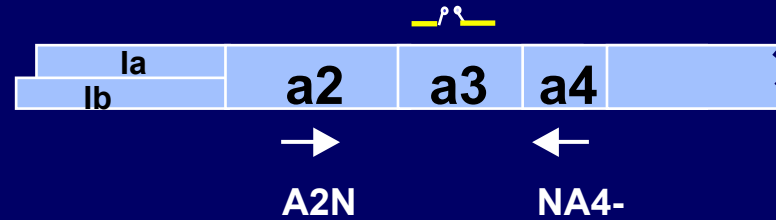
LightCycler™

# LightCycler

**BCR-ABL**



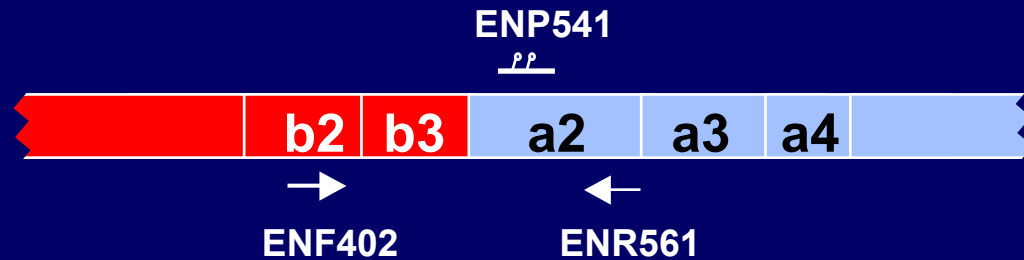
**ABL**



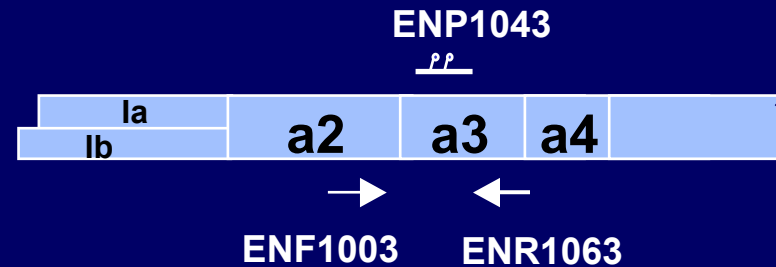
Emig et al. *Leukemia*. 1999.

# TaqMan

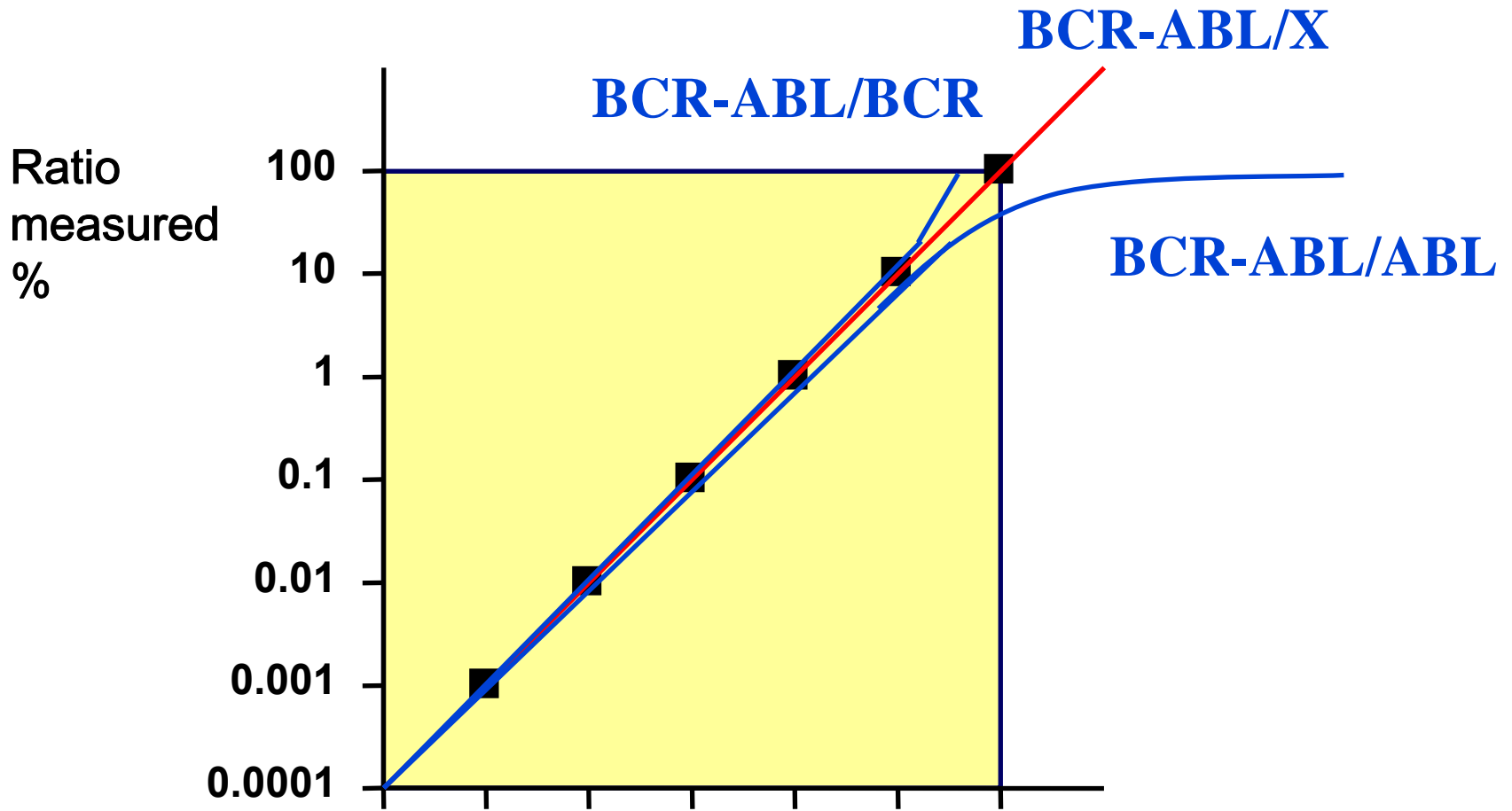
**BCR-ABL**



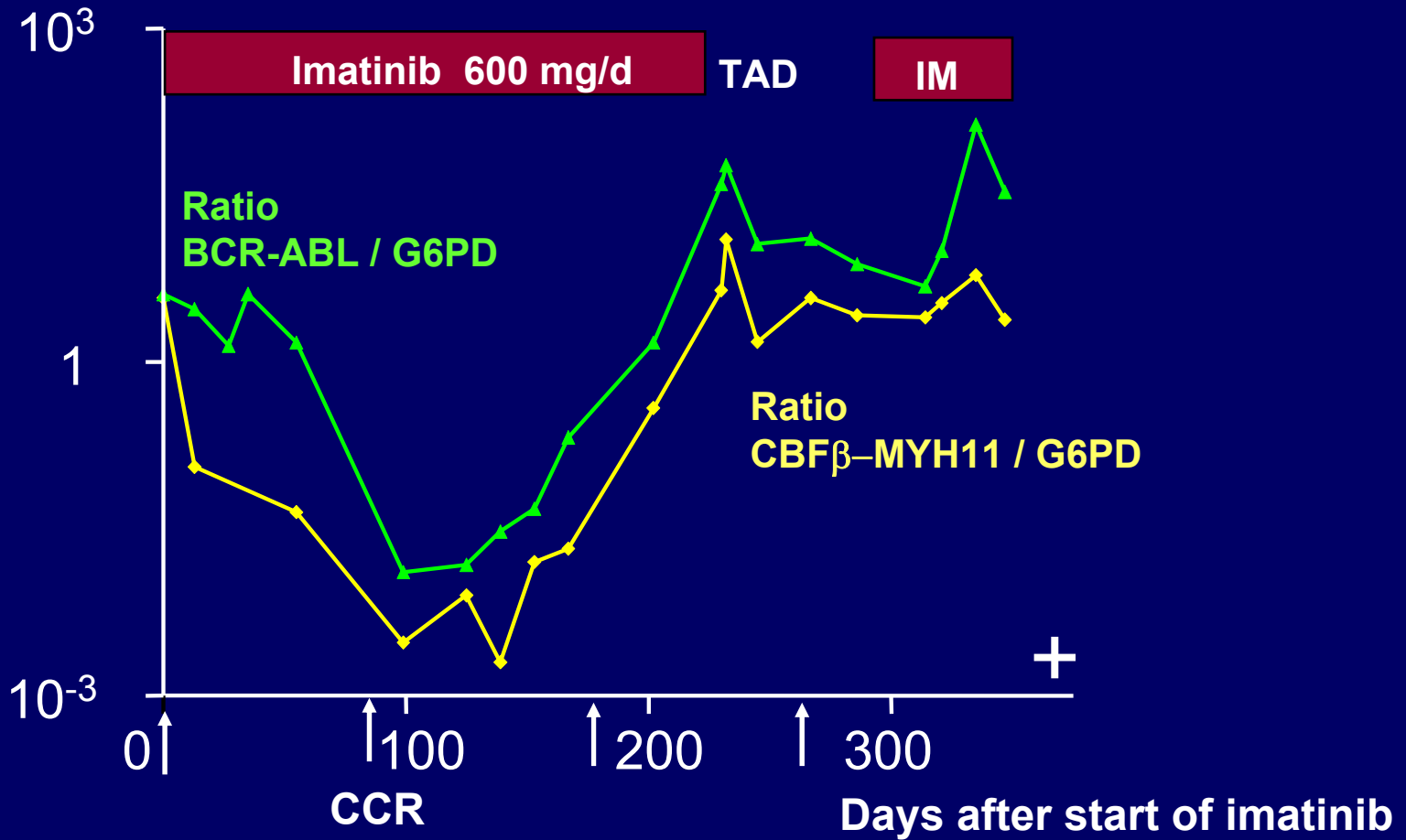
**ABL**



Gabert et al. *Leukemia*. 2003.



# Relapse of myeloid blast crisis after CCR

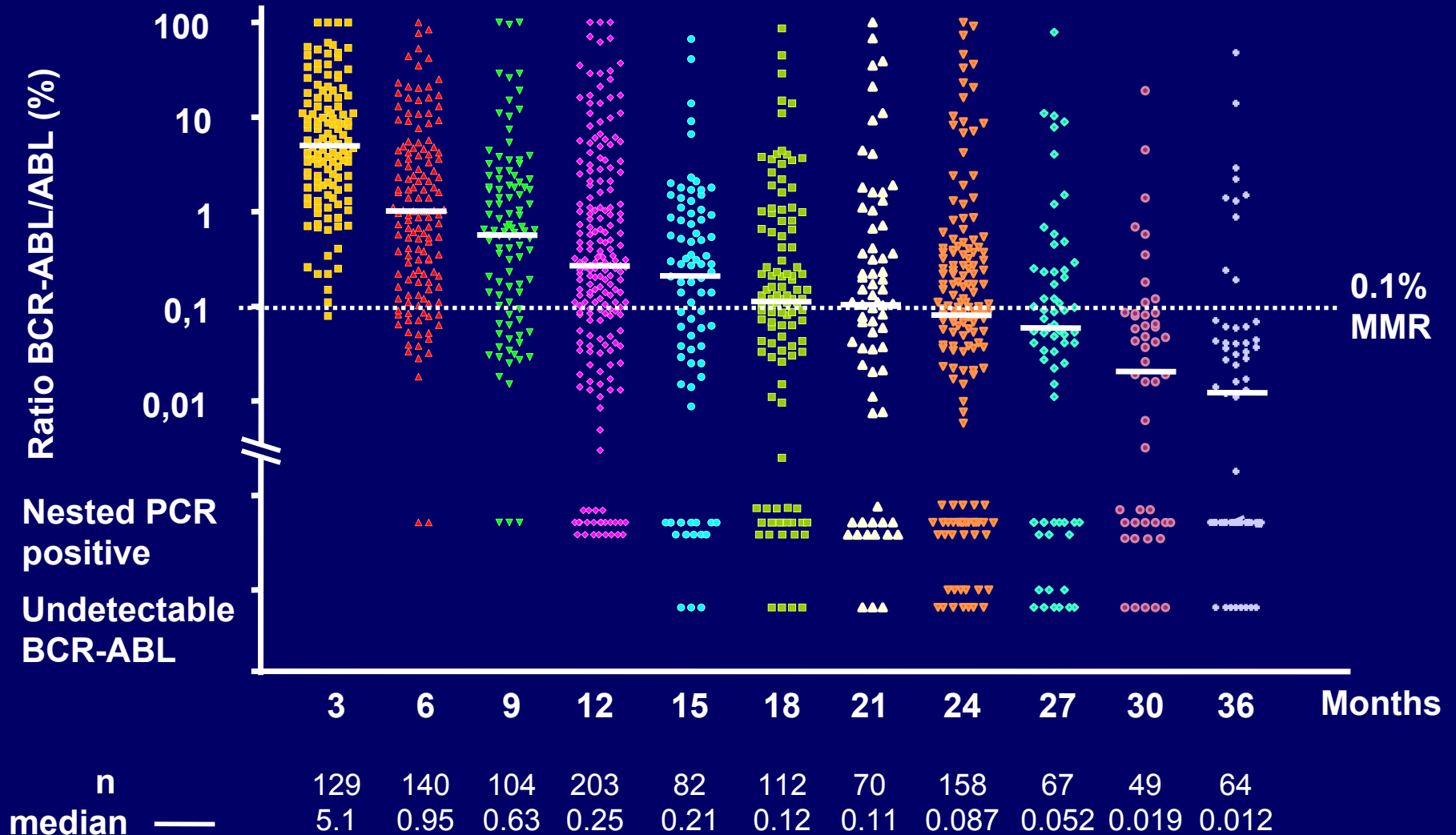


46, XY, Ph	[18]	[6]	[13]
46, XY, Ph, inv(16)	[7]	[2]	[7]
46, XY	[25]	[8]	[5]

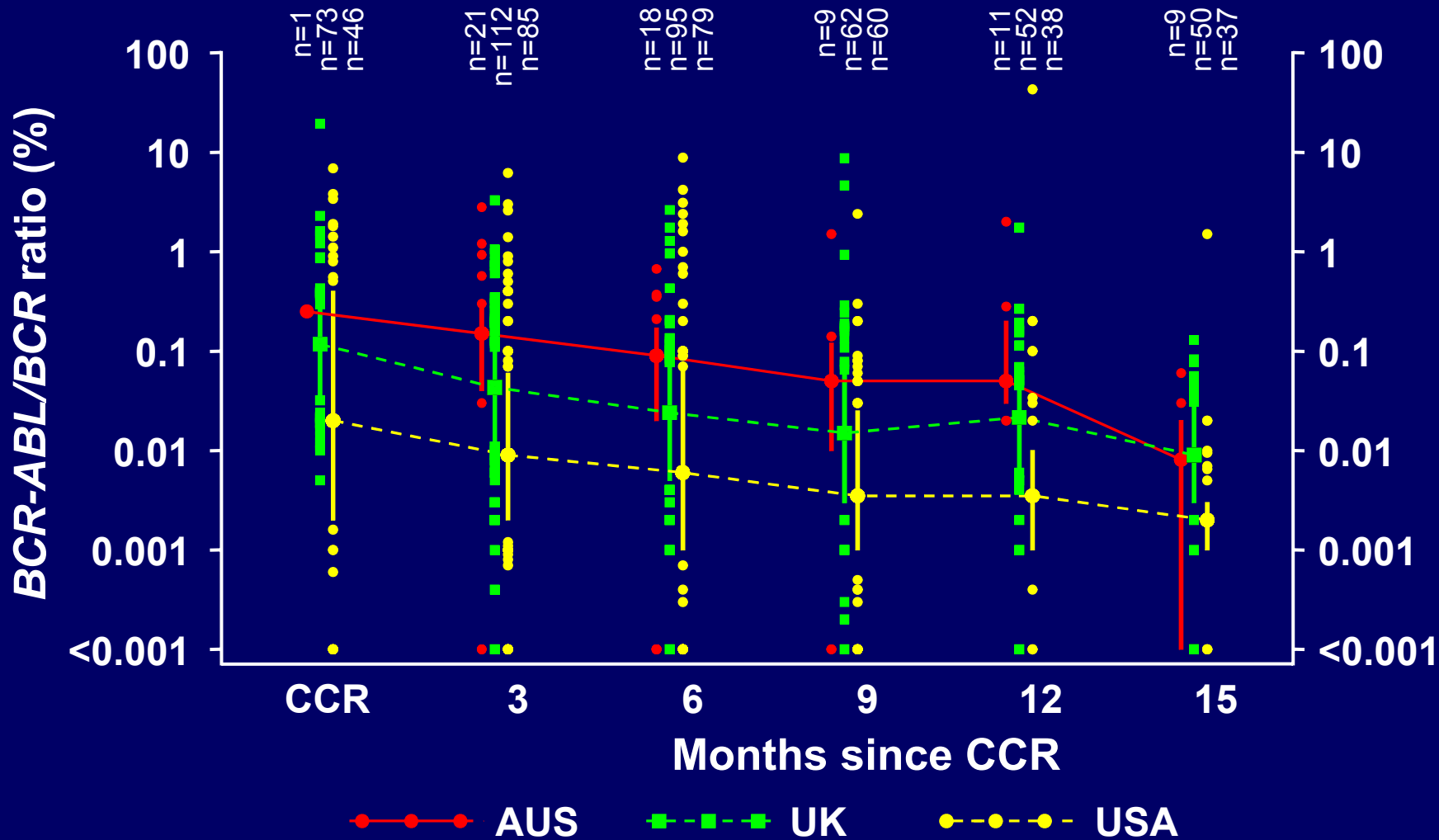
# *Molecular response precedes cytogenetic remission in CP patients*

Cytogenetic response at month 6	CR	PR	MR	NR	
n	16	18	12	14	
Ratio BCR-ABL / ABL (%): Month 1	29.0	49.0	50.0	52.0	n.s.
Month 2	<b>4.7</b>	31.0	40.0	74.0	p = 0.027
Month 3	<b>2.5</b>	18.0	40.0	38.0	p < 0.0001

# Molecular Monitoring, German CML Study IV

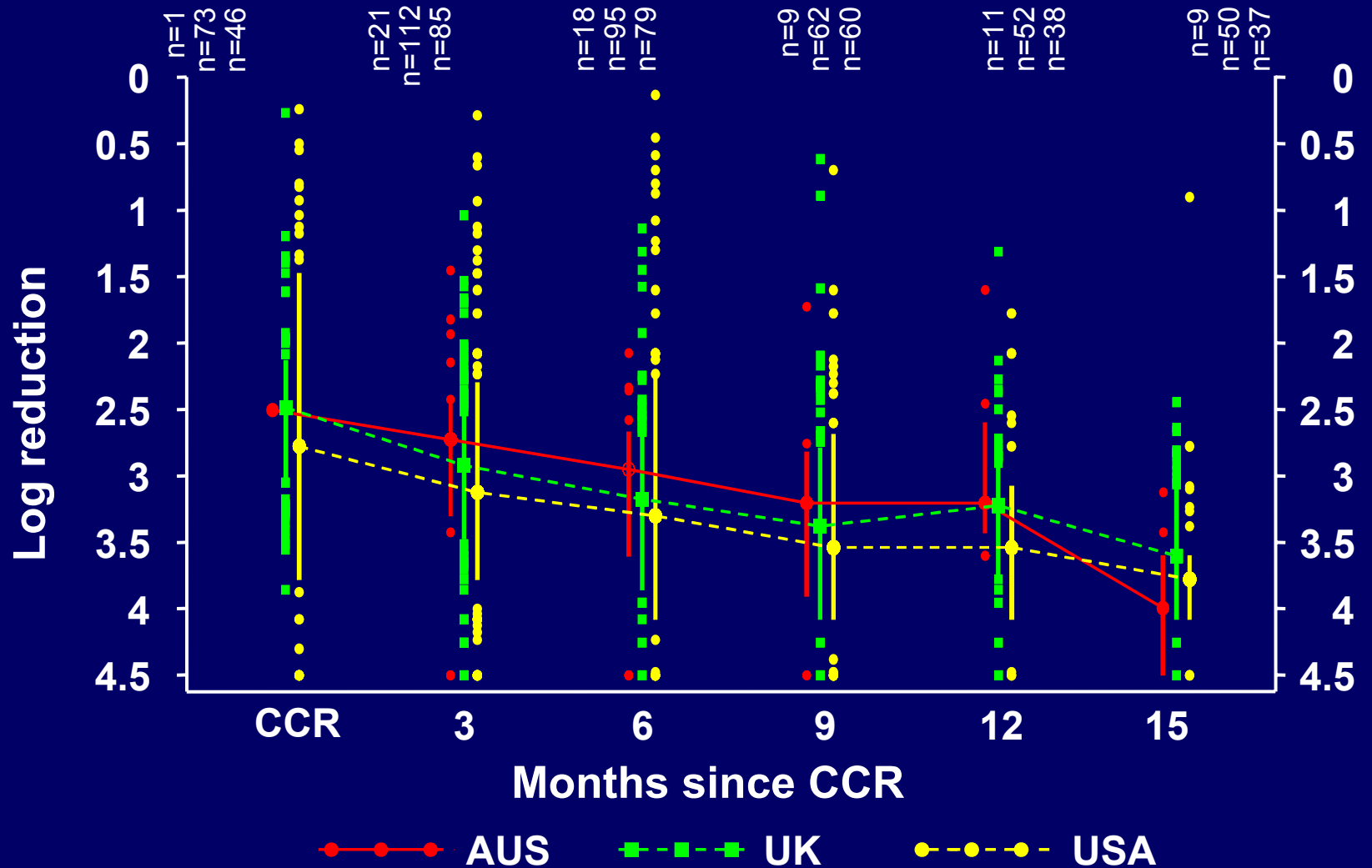


# IRIS Study: Ratio BCR-ABL/BCR - by Laboratory

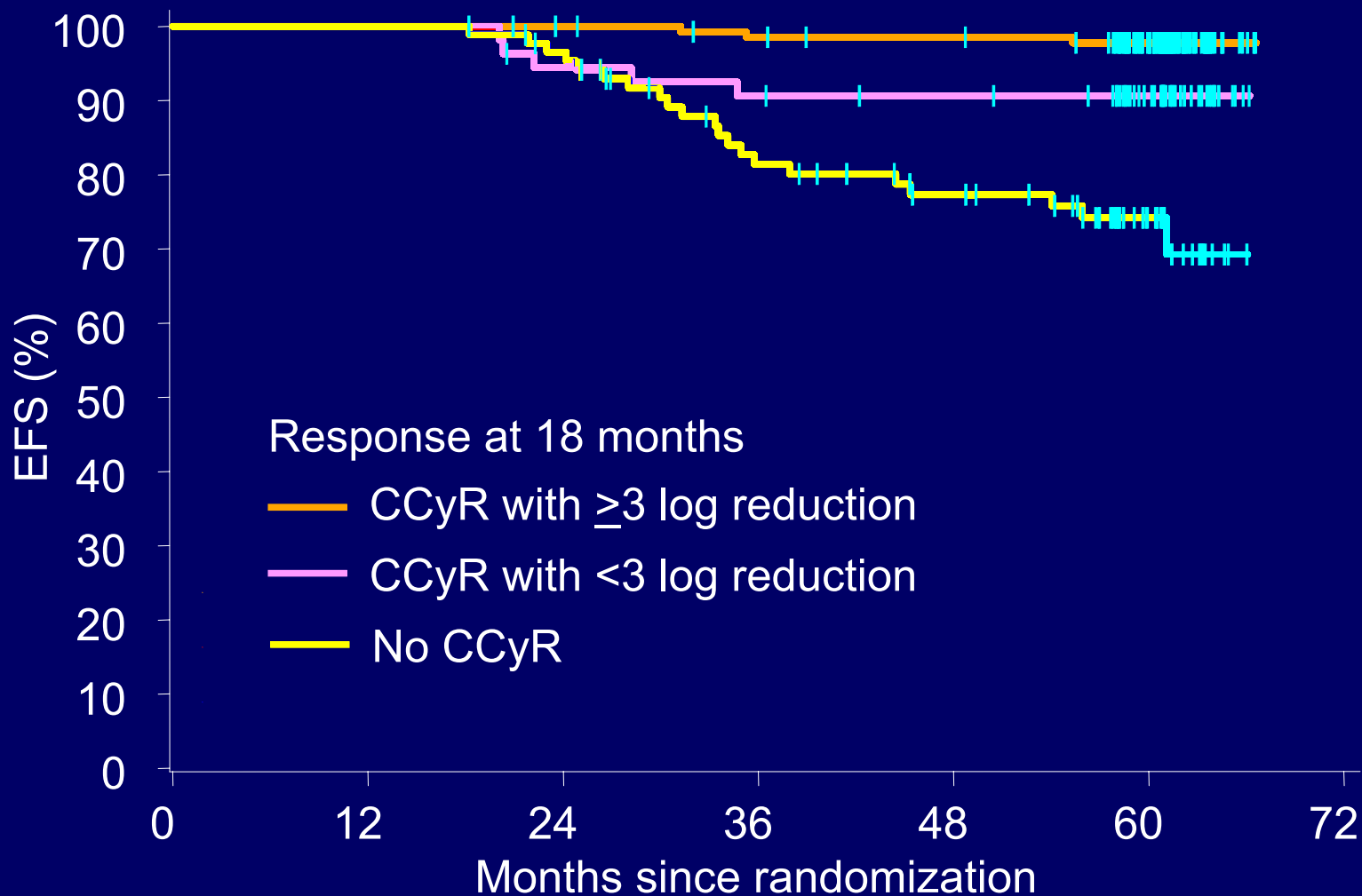




# Standardized Log Reduction - by Laboratory



# IRIS Study: Event-Free Survival by Molecular Response at 18 Months





# The UnOfficial Gleevec (STI571) Site



Yvonne Heimann here, today I received my 7/9/02 test results. 20 normal cells, Fish NEGATIVE PCR .6

Sounds like Gleevec did it again. Not sure if this qualifies me for the Zero club but pretty close.

Hi,

I don't think I'm on your list and would like to join the others.

My name is E.F. I was a member of the phase 1 group at UCLA. I was diagnosed 3/98 in Chronic Phase. I began Gleevec (300mg) 1/99 (The first person to take 300mg).

Reached CCR 6/99. Still not sure if I'm in MR.

UCLA **kept changing PCR tests** so my results were never very reliable although others like L.B. have been neg on all the different tests. Last year was neg on 2 successive highly sensitive quantitative tests but relapsed (?) in June...

E.F.

Hi George,

Molecular remission is when they look at a large number of cells in your blood, eg. 1 million. If no bcr/abl is found in 1 million cells, then you are in molecular remission. This can be done only through quantitative pcr testing. 0.08% means you are getting there but still not there. **Different institutions have different ways of pcr testing.** Some look at 10,000 cells, some look at 1 million. The bigger the sample size, more sensitive is the test. **There is no universal standard.** The trick is to go on testing at one particular machine and achieve their zero and maintain it. You must ask your doctor what number they consider pcr negative.

Rgds, Anjana

# Methods of Expression of Molecular Response

- **Ratios target/standard gene**

After standardization of methods and rigorous control rounds, eg, ratio BCR-ABL/ABL (%)

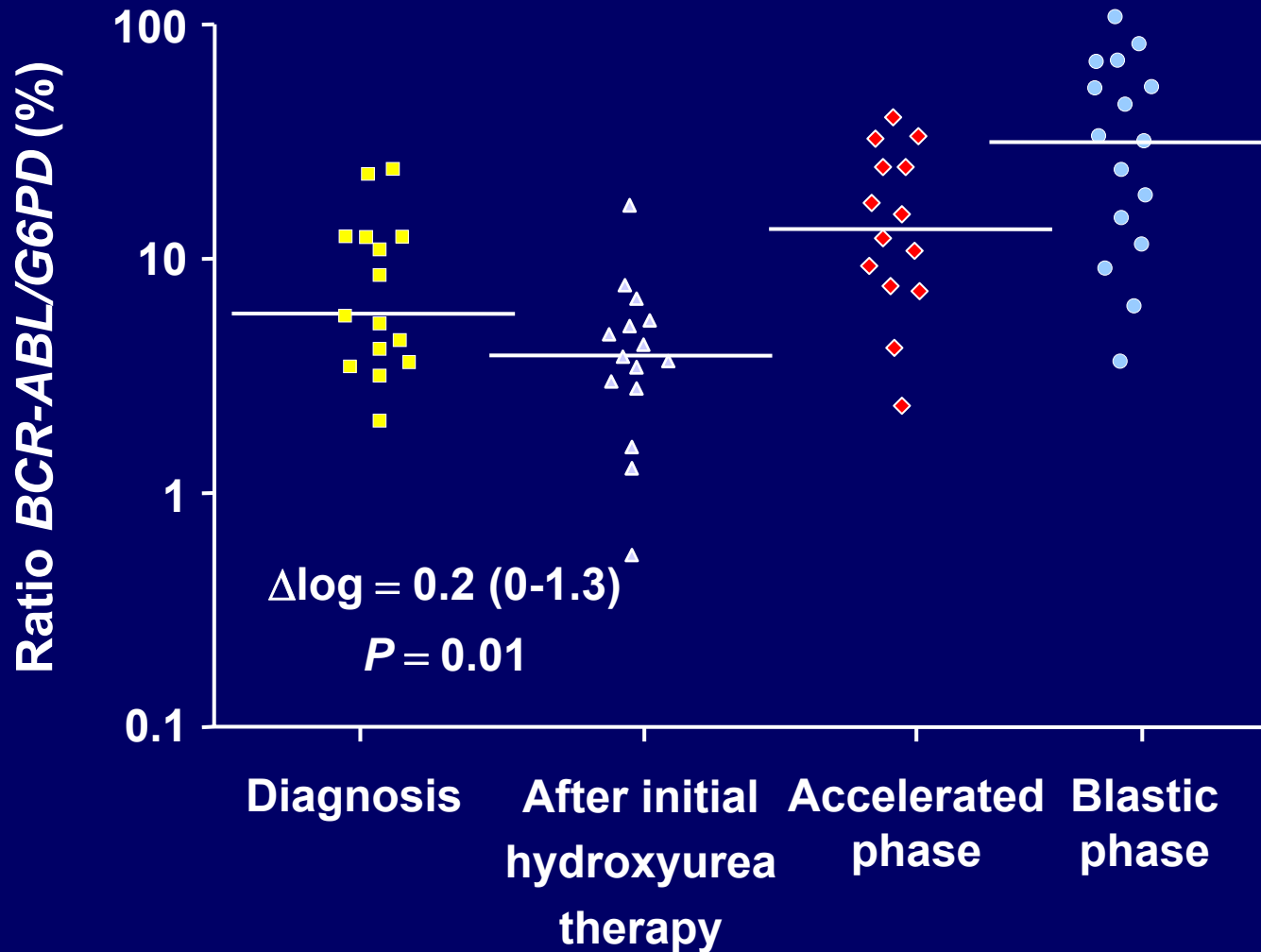
- **Lab-specific reference point:**

Pooled diagnostic samples,  
eg,  $\Delta \log$  ratio BCR-ABL/BCR (%)

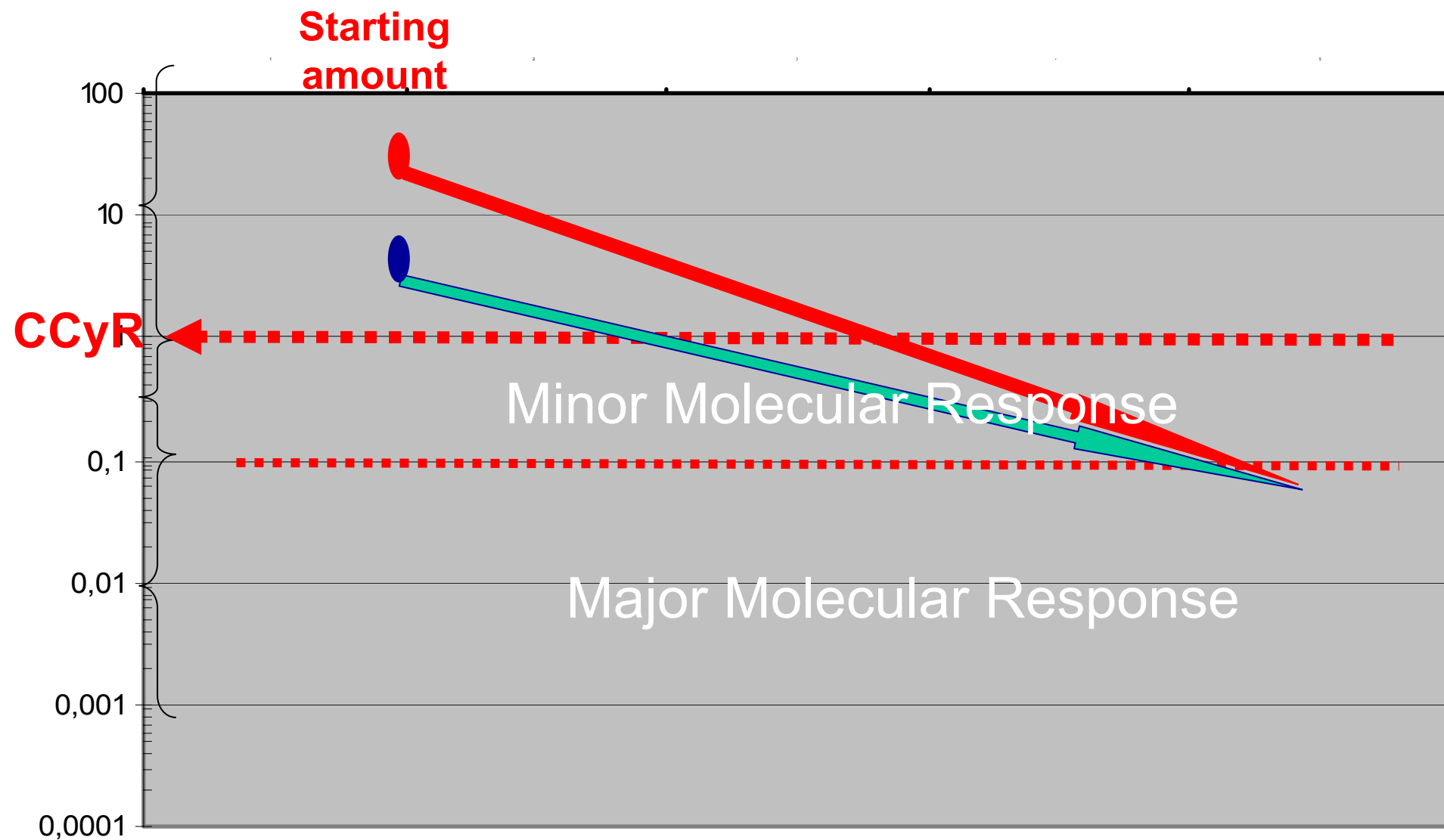
- **Individual calculation of relative molecular response:**

MRD level after therapy/pretherapeutic level,  
eg, individual  $\Delta \log$  ratio BCR-ABL/GUS (%)

# Variability of the Individual “Pretherapeutic *BCR-ABL* Level”



The evidence obtained with the IRIS study is that the absolute and not the relative amount is important!



Use of 10 mL peripheral blood ( $\sim 5 \times 10^7$  WBC)  
processed within 36 hours

Bedside RNA stabilization for multicenter trials

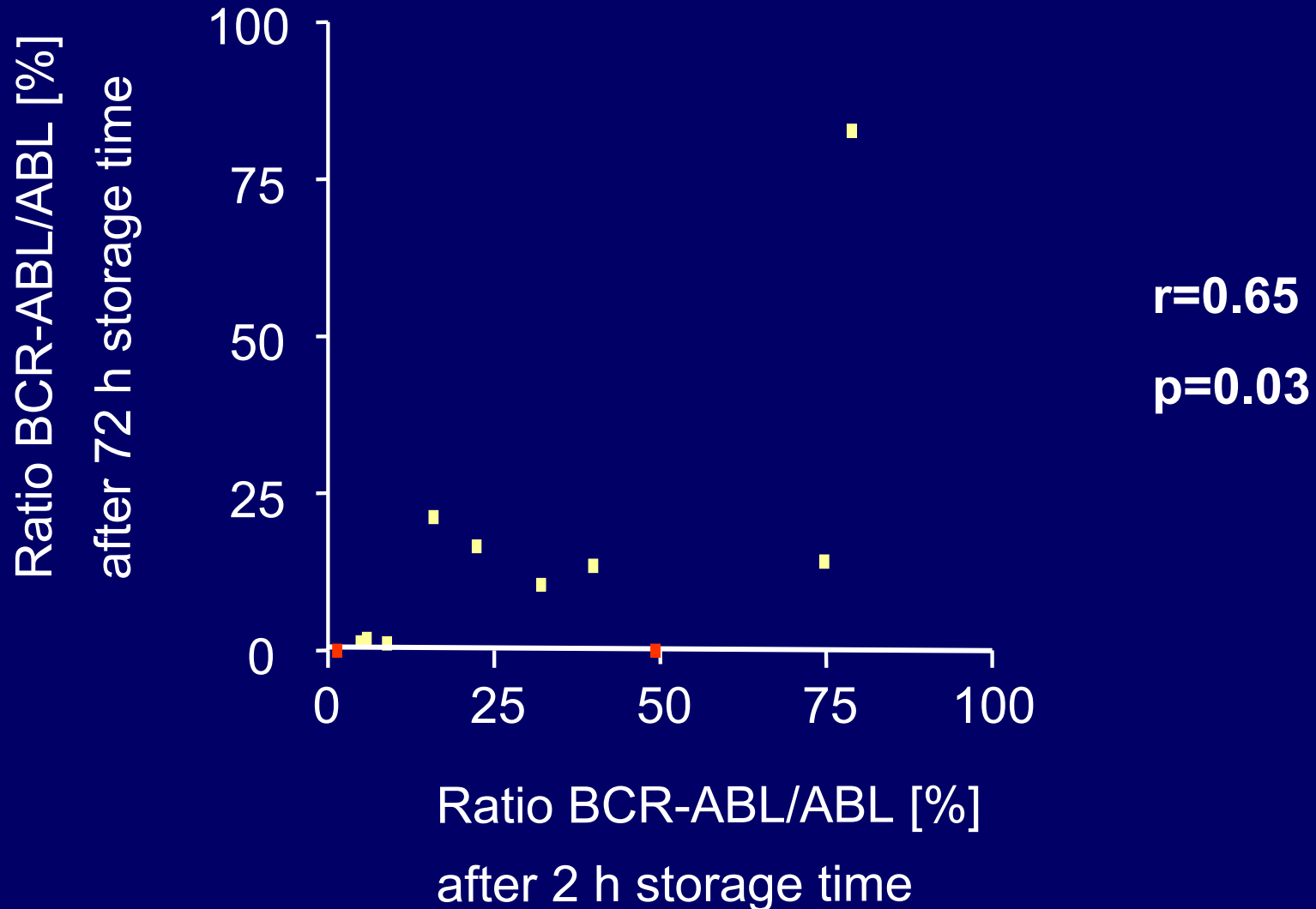
Standardized EAC (TaqMan) and LightCycler PCR  
protocols

Single plasmid dilution series for target and  
housekeeping genes

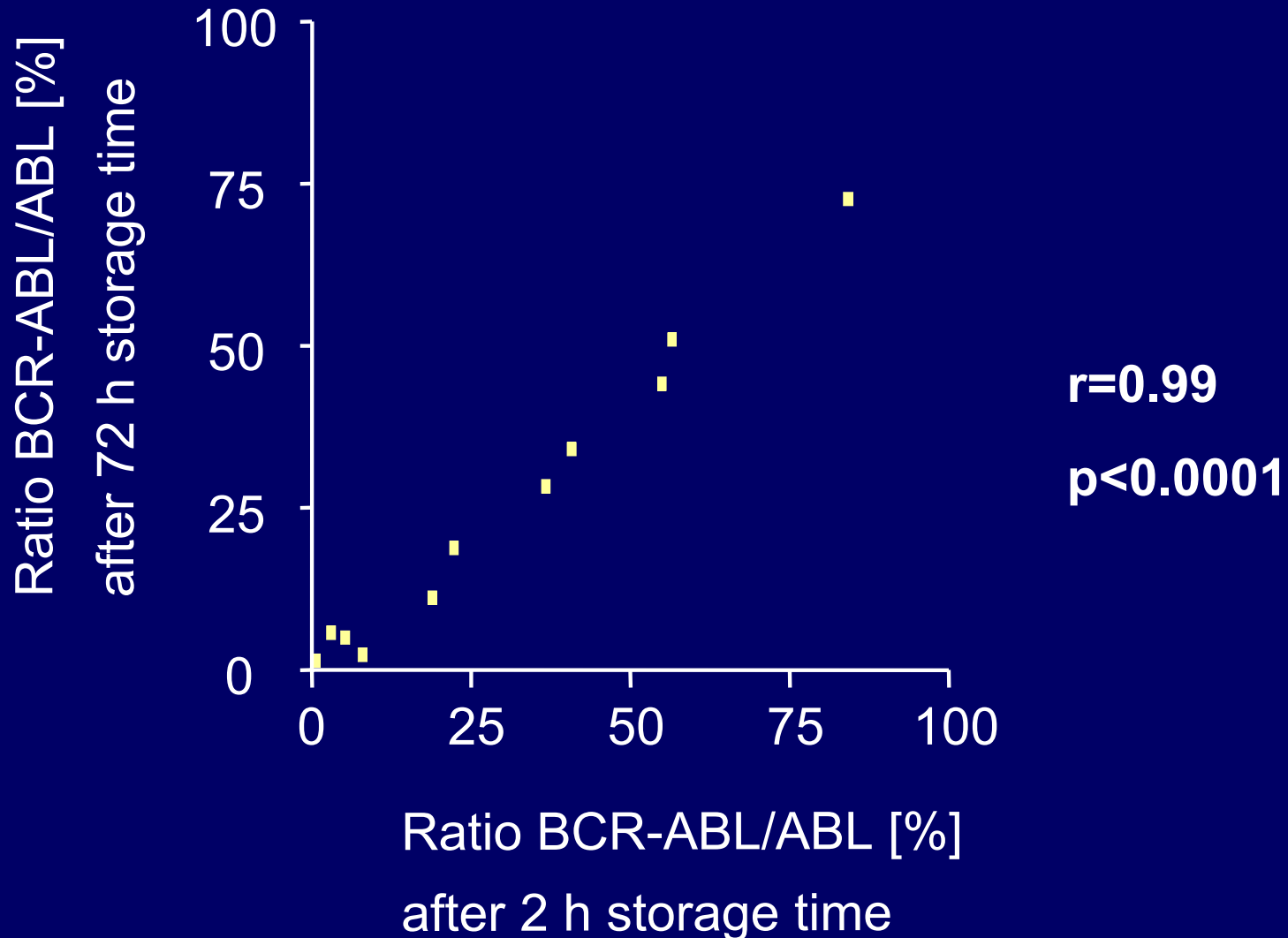
Housekeeping gene(s) for routine use:  
total *ABL*, *BCR* or *beta-GUS*



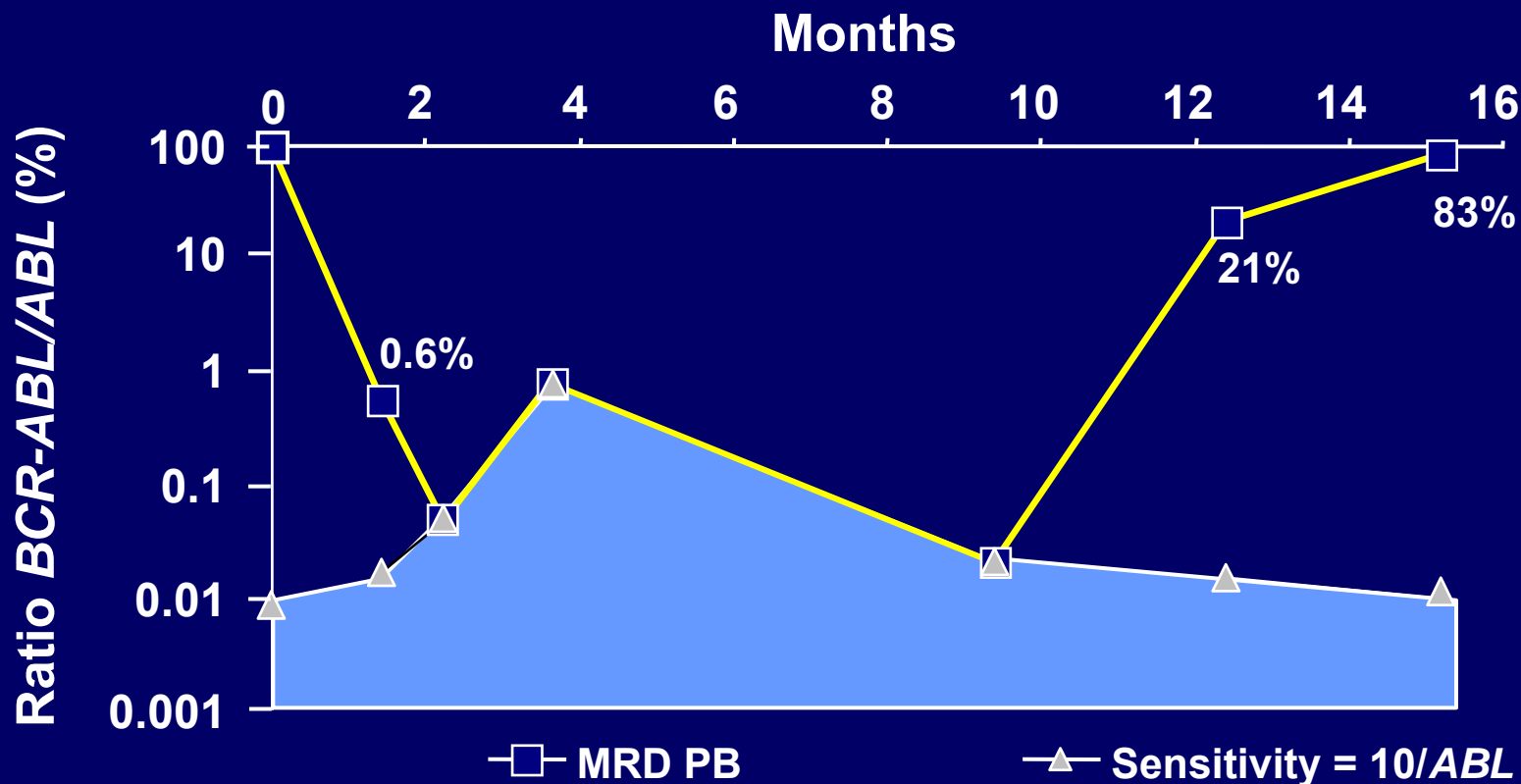
# Unstabilized PB after 2 hrs vs. 72 hrs



# PAXgene Stabilized PB after 2 hrs vs. 72 hrs



# Sensitivity Depends on the Quality of the Individual Sample



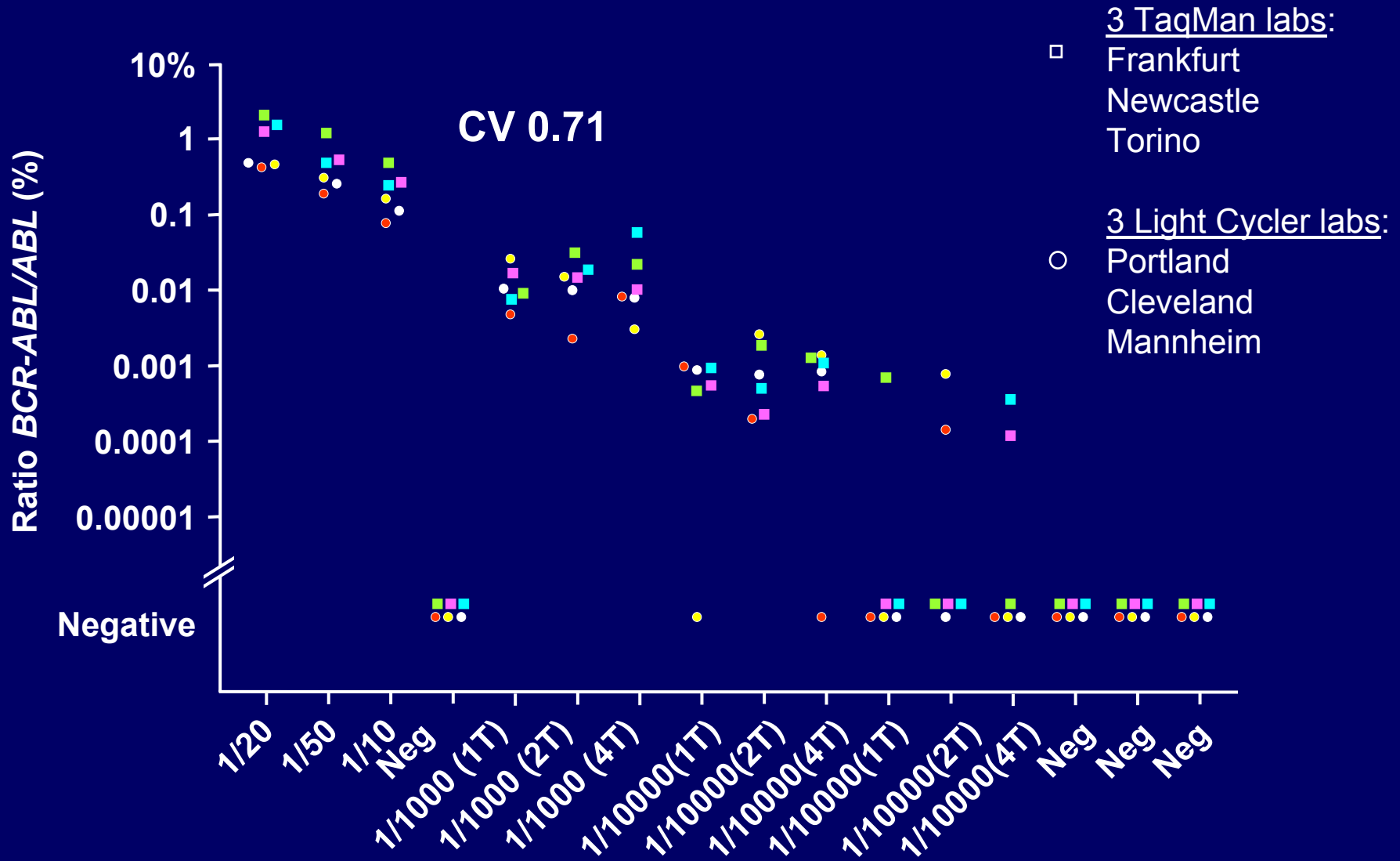
Disease detectable:

$BCR-ABL/ABL$  (%)

Disease undetectable:

Negative / [no. of ABL transcripts]

# International Control Round (n=6)



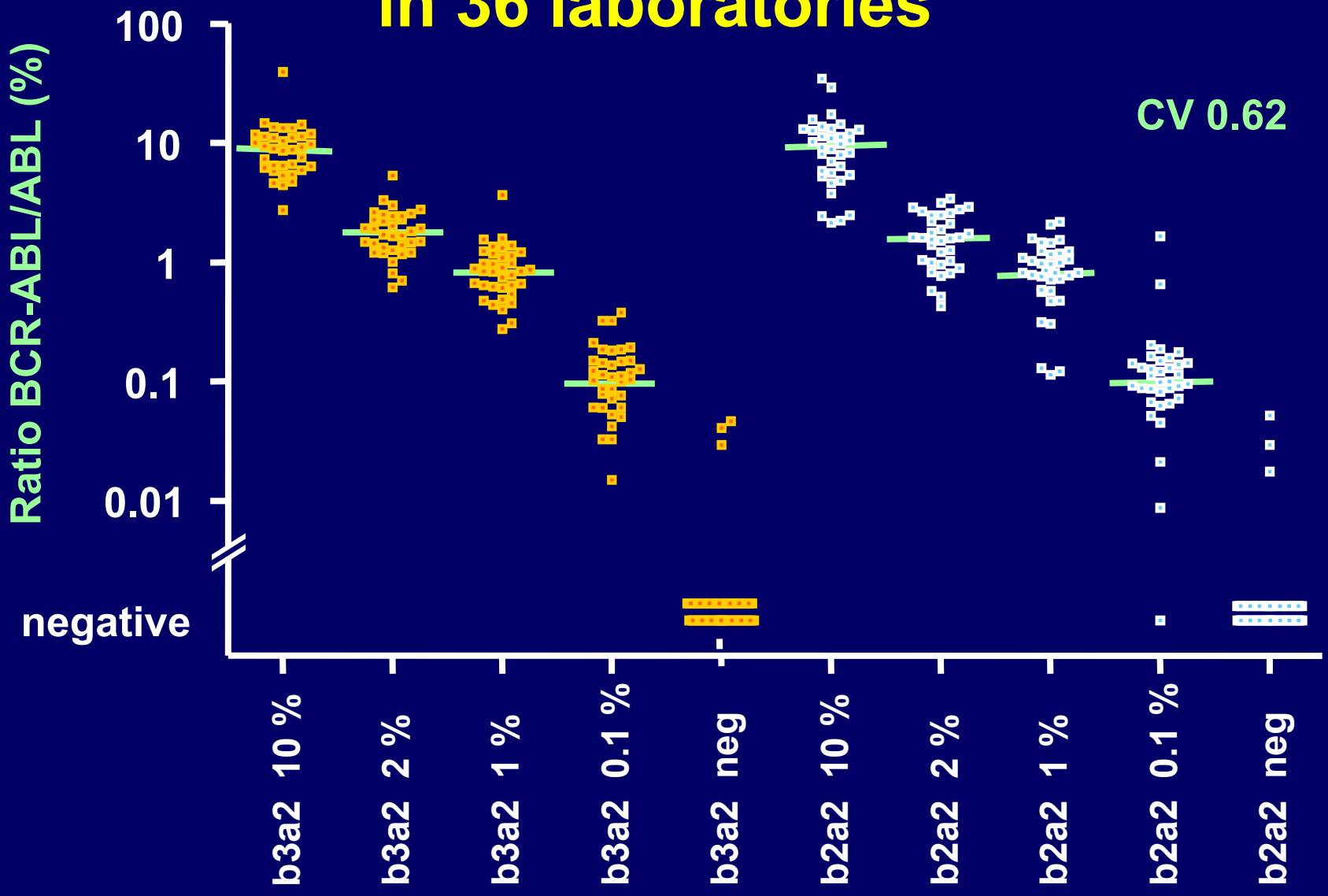
# European study to harmonize methodologies to quantify BCR-ABL mRNA transcripts



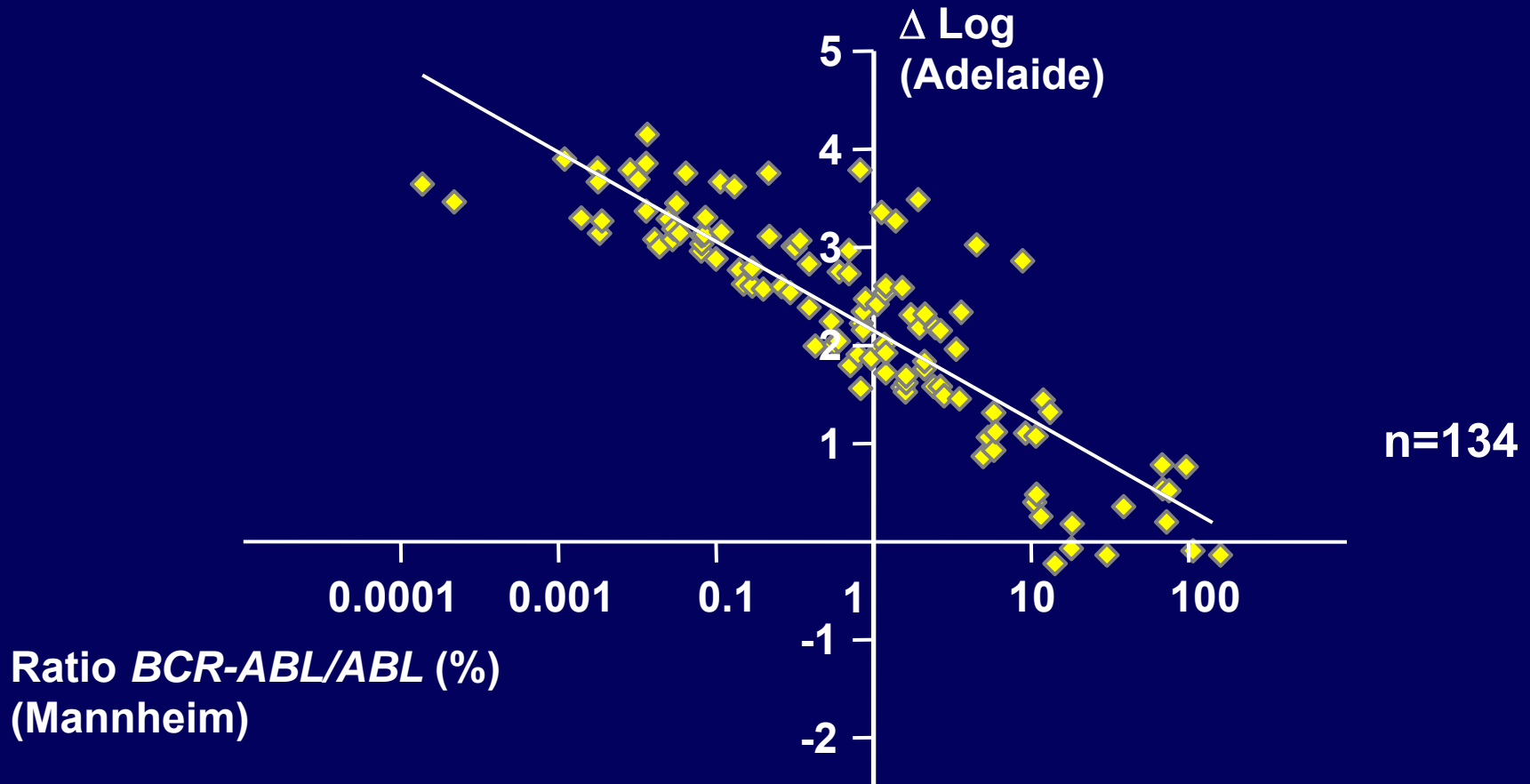
Exon 12  
 AGAAACGTTCTGGTCTGCCGTGAACAGTCCAGGAGGCACTTGTTCTGCTGCTGTGGAAGTCGCC  
 CTGACTCGGGGAGGAAGGGACACGCAGGTGGTATCAGTCTTGCTCAAGTAAACAGGCTGTTTTC  
 CAAACATTGTGACTTGGCTACTGAGTGGGGATACCTGGTTTTTCATTGGCAATCTTCCAGTATCTC  
 TCTCGCAAAGGAACGCTGCACTTTTTTGGTTGTCTCTG **CCGAGTGAAGATCCCCTTTT** ATTCC  
 CCAGCACTCTCGTCCGGT **ACTGTT** CAGTCATGAAATCGGCAAATTC **CA** **AATGAGCTCTCCAAC**  
 Exon 11  
**CACGTATTTT** CTGCGTTTTT **GATCCAGACCCAGATGGTACTGCTCTAGCAGACTTTTCTGGTAC**  
 TCTTCAGTGAACATCAGAGGTGGATCTG **GTGAAACCCTGCAATCGTTTCT** GCTCCATACTCGC  
 Exon 10  
 TCTGAATAATGGGCTTCTGATACTTCTTATAACCAGTTCT

	<b>ENR1162</b>	<b>ENF1102</b>	
<b>TaqMan</b>	<b>CCGAGTGAAGATCCCCTTTT</b>	<b>AATGAGCTCTCCAACCACGTATTTT</b>	<b>101 bp</b>
	<b>ENR1162</b>	<b>GUS10-LC</b>	
<b>Lightcycler</b>	<b>CCGAGTGAAGATCCCCTTTT</b>	<b>GTGAAACCCTGCAATCGTTTCT</b>	<b>205 bp</b>

# Variability of Ratios BCR-ABL/ABL (%) in 36 laboratories



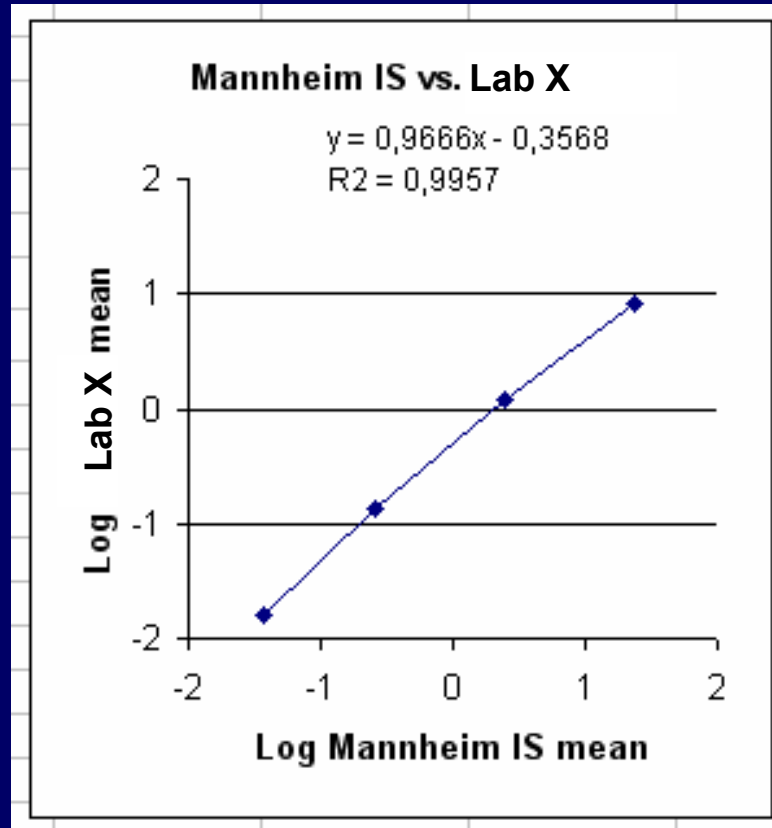
# Log Reduction (IRIS Method) vs Ratio *BCR-ABL/ABL*



$$\text{Log reduction} = -0.91 [\log (\text{BCR-ABL/ABL} (\%))] + 2.15$$

3 log = 0.12%

# „Good“ example



**Formula:**  $\text{Log } y = (\text{slope} \times (\text{log MMR}^{\text{IS}})) + \text{intercept}$

$\text{CF} = \text{MMR}^{\text{IS}} / \text{antilog } y$

**Example:**  $\text{Log } y = (0.9666 \times (-1)) - 0.3568$

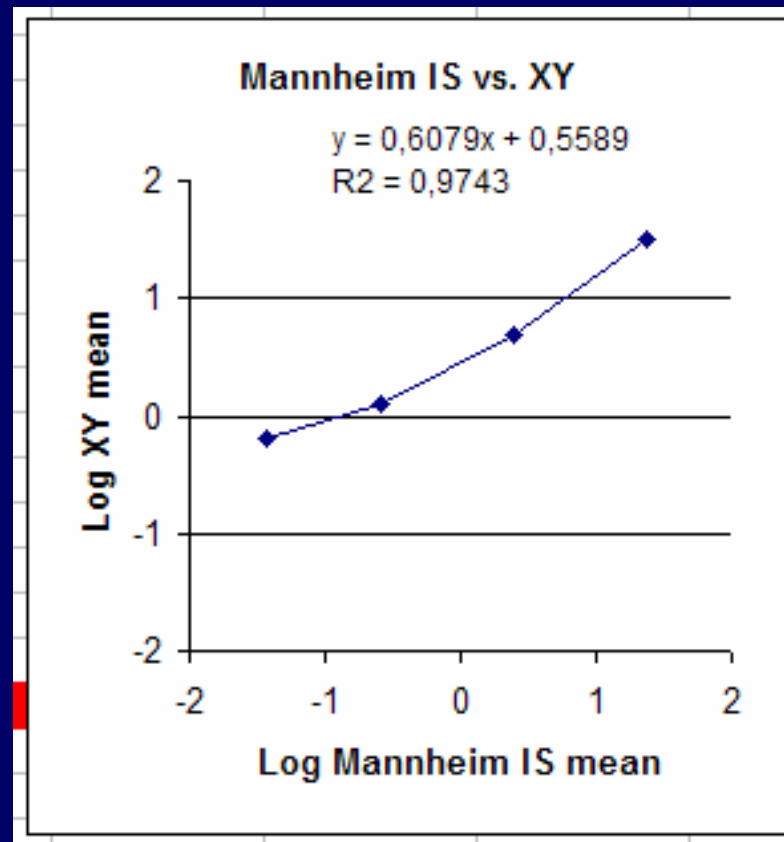
$\text{CF} = 0.1 / 0.04749 = \mathbf{2.1057}$



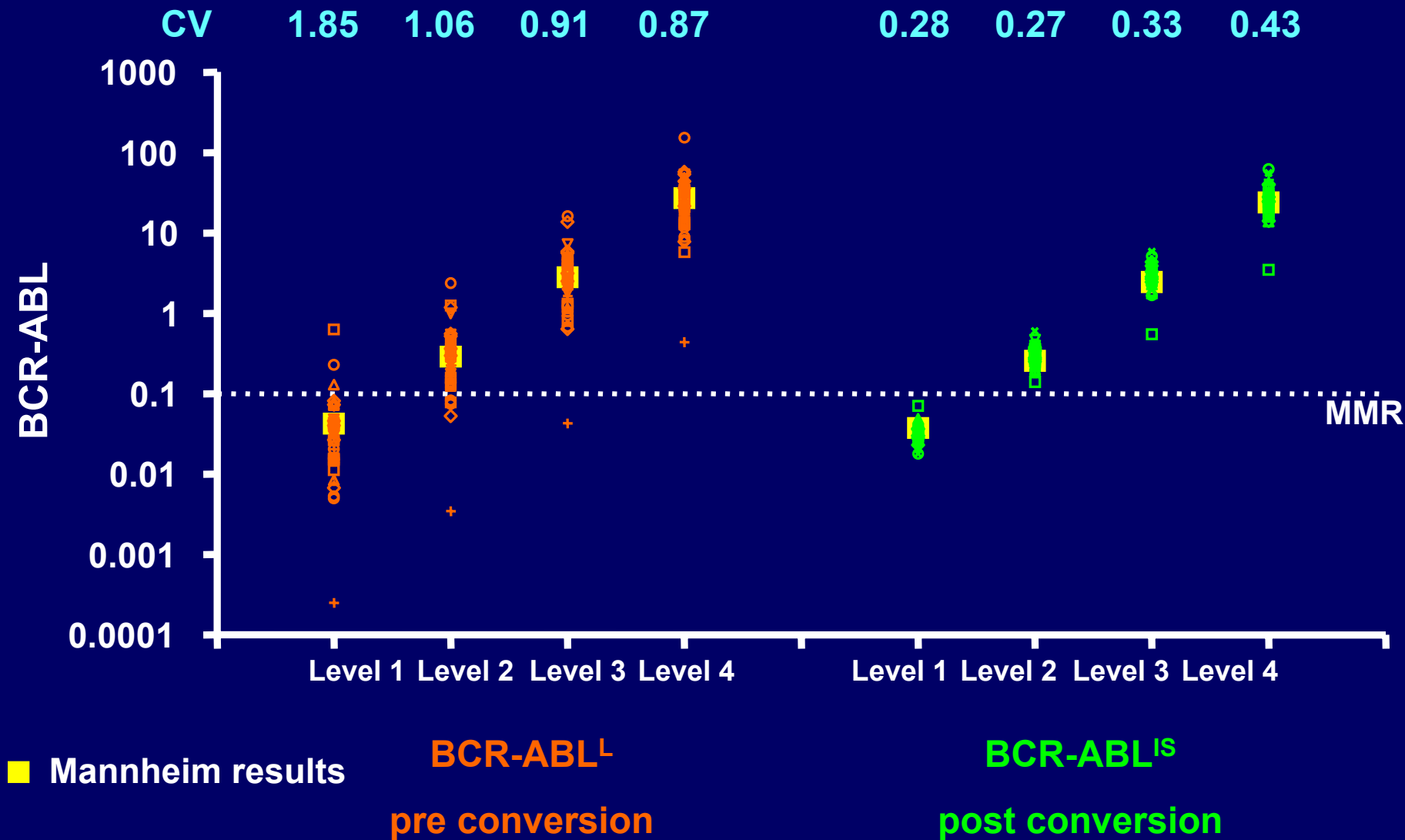
Mean values after conversion to the international scale (IS)			
	<b>CF 0.878</b>	<b>CF 2.1057</b>	
	Mannheim mean	Lab X mean	
Level 1	0,037	0,033	
Level 2	0,26	0,29	
Level 3	2,45	2,58	
Level 4	23,81	17,13	

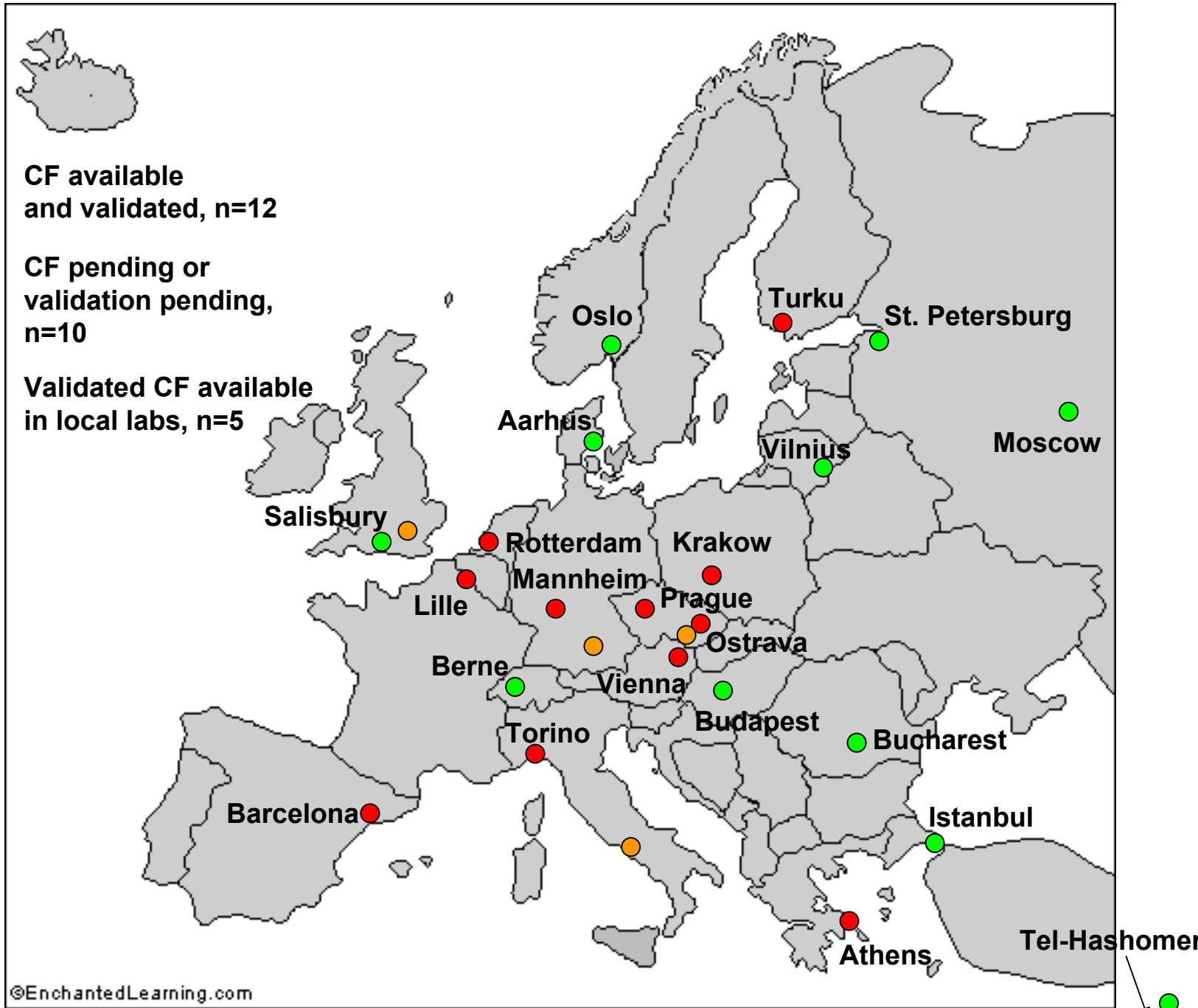
# „Bad“ example

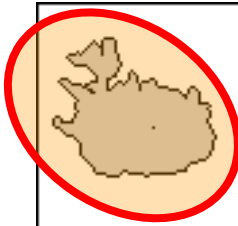
One of 4 labs with linearity problem



# BCR-ABL levels in 37 labs pre and post conversion



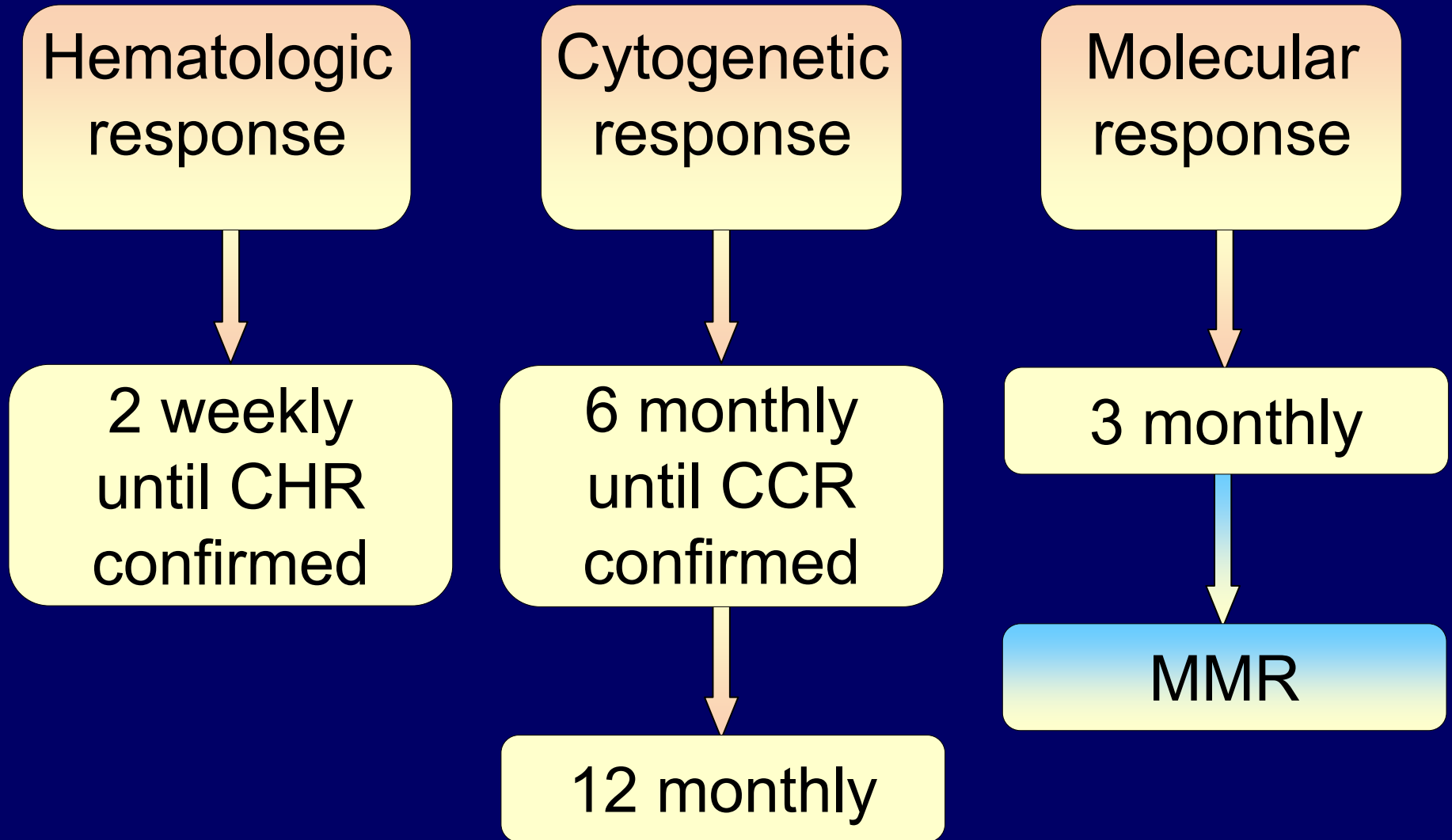




**Local standardization  
achieved or ongoing**



# Recommendations by an Expert Panel



# Value of Q-PCR as a Screen for Mutations

*214 patients with serial Q-PCR tests*

	<b>&gt;2-Fold Rise in <i>BCR-ABL</i></b>	
	<b>YES</b>	<b>NO</b>
	<b>56 (26%)</b>	<b>158 (74%)</b>
<b><i>BCR-ABL</i> mutations</b>	34/56 (61%)	1/158 (0.6%)
<b>Acquired resistance</b>		
<b>Mutations</b>	31/34 (91%)	1/1
<b>No mutations</b>	13/22 (59%)	1/158 (0.6%)

God Bless



America

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[Italiano](#)

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# BMS-354825 Discussion

**Caution** All Gleevec Patients , **Please Read This!**

**Click Here** for new Physician Interviews about CML and Gleevec (STI571)  
**Check Back Often...New Physician Interviews Are Added Regularly**

You Can Help Win The "

 PCR  
[by Sharon T](#)

three months i had my first PCR quantative test and the results were 0.001%. Today it was 0.027% My Dr. says it is a very sensitive test and that I should not be worried. I will have another in three months. Is 0.027% a bad number?

Help?  
Sharon T

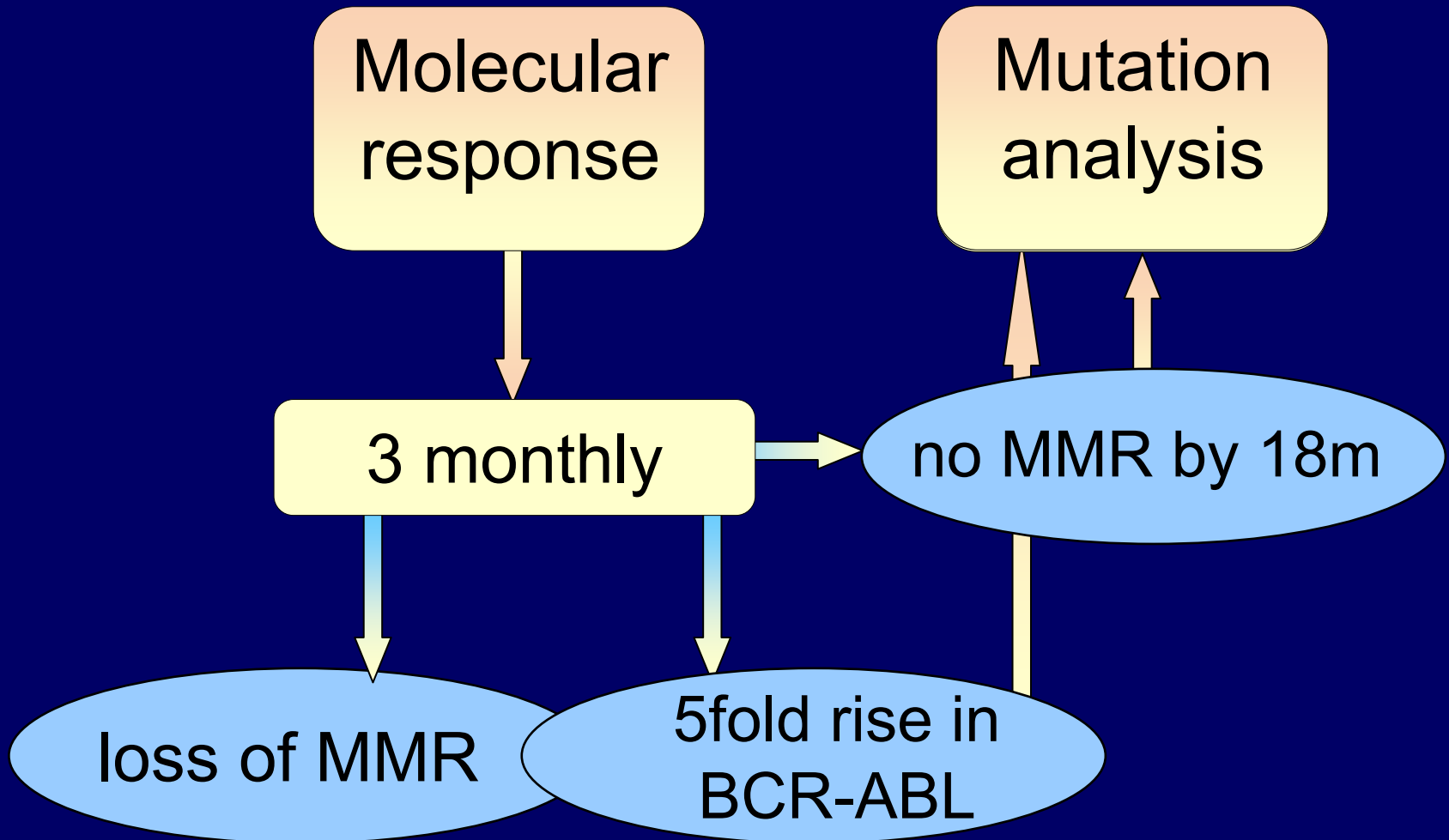
Name:

Email:

- [Home](#)
- [Jerry's Diary](#)
- [AMN Discussion](#)
- [BMS Discussion](#)
- [CML Discussion](#)
- [Childhood CML](#)
- [GIST Discussion](#)
- [Gleevec FAQ](#)
- [Gleevec History](#)
- [Thanks Dr. "D"](#)



# Recommendations by an Expert Panel





**Mutation testing:  
The impact of 2<sup>nd</sup> generation TK inhibitors**

Andreas Hochhaus

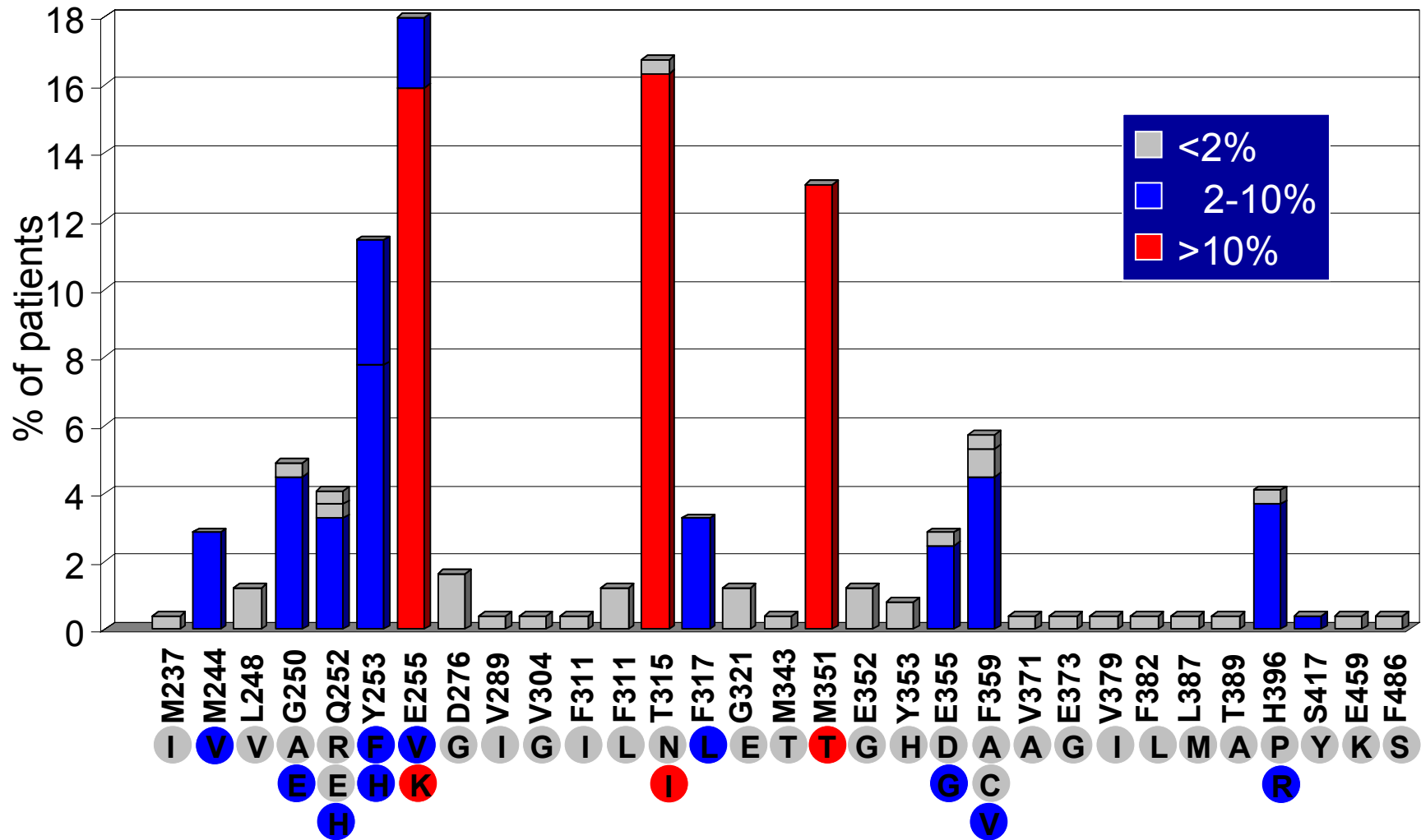
Medizinische Fakultät Mannheim  
Ruprecht-Karls-Universität Heidelberg  
Mannheim, Germany

# Molecular - Cytogenetic Causes of Resistance

Patients With Hematologic Resistance/Relapse	Chronic phase (n=35)	Accelerated phase (n=33)	Blastic phase (n=66)	All (n=134)
<b><i>BCR-ABL</i> mutations (%)</b>	10/20 (50)	13/21 (62)	10/33 (30)	<b>33/74 (45)</b>
<b>Clonal evolution (%)</b>	15/29 (52)	8/16 (50)	16/22 (73)	<b>39/67 (58)</b>
<b>Combination (%)</b>	5/17 (29)	2/9 (22)	4/17 (24)	<b>11/43 (26)</b>

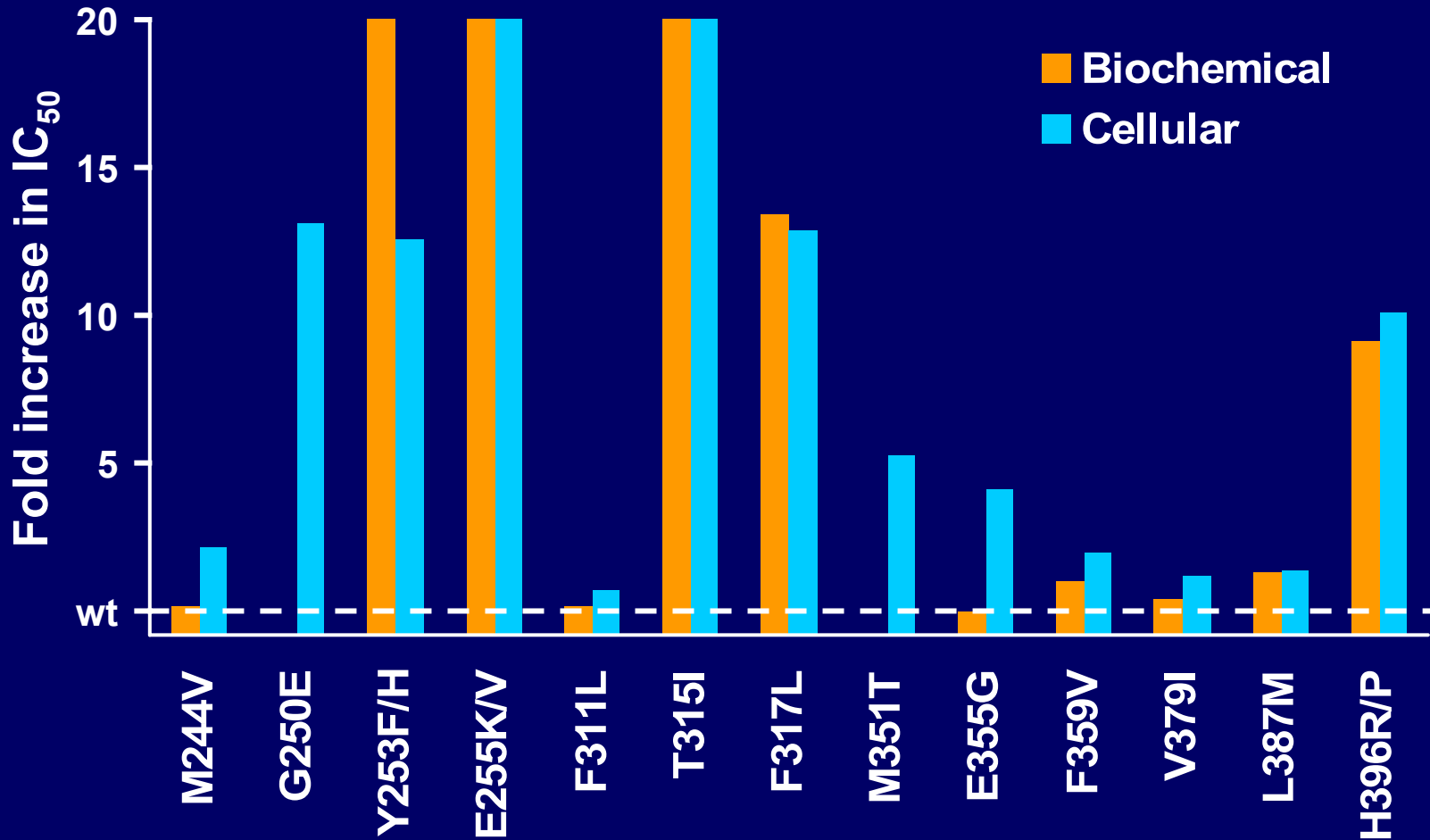
# Detection of BCR-ABL mutations

Kinase domain mutations associated with imatinib resistance



Amino acid (ABL-B)

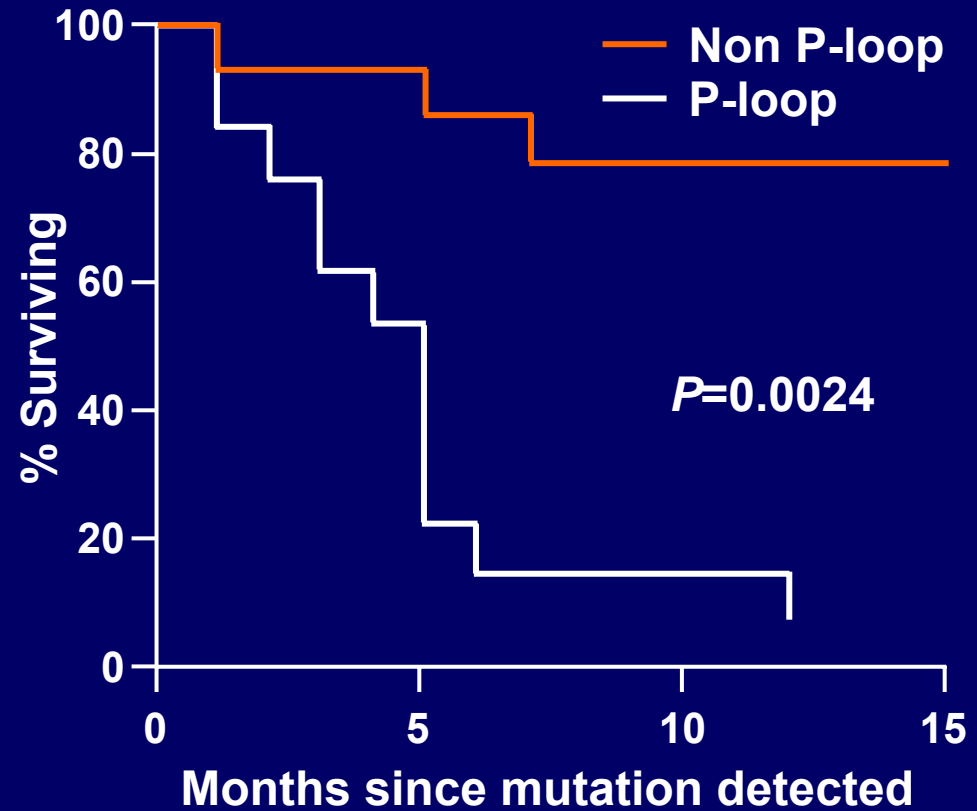
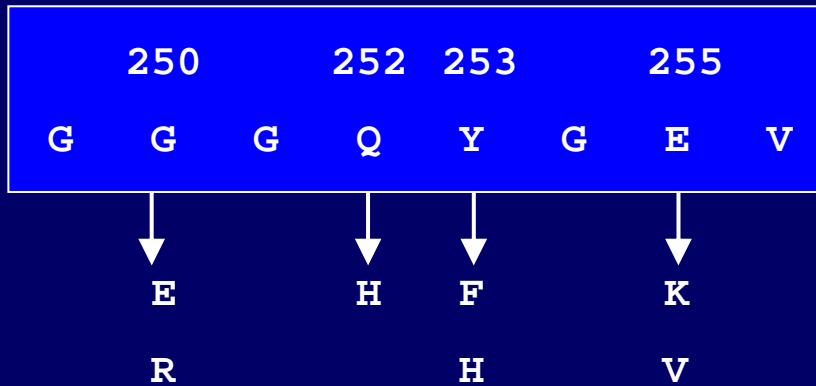
# Mutant *BCR-ABL* Have Increased $IC_{50}$ Values for Imatinib Mesylate



# Survival After Imatinib Resistance

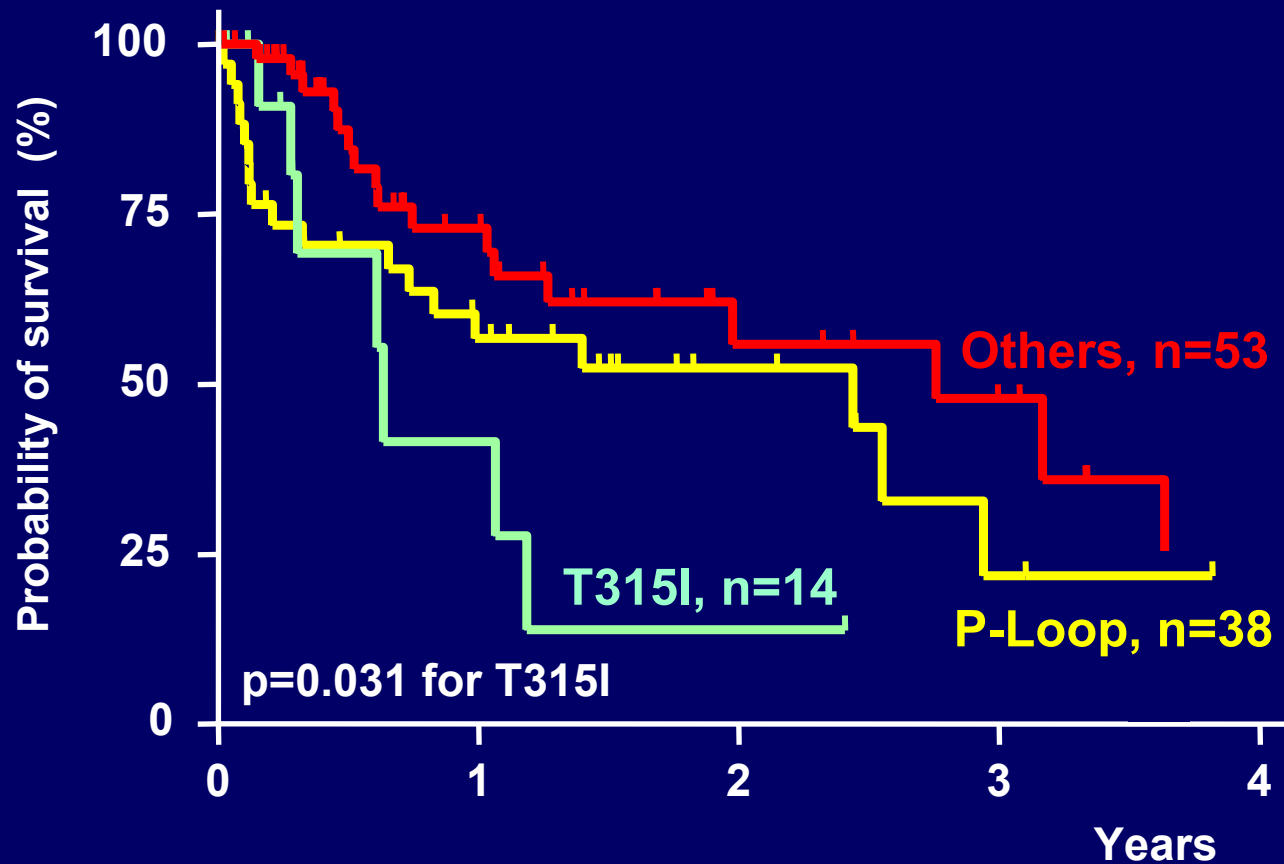
## Initial Australian experience, n=27

P-Loop: Highly conserved area



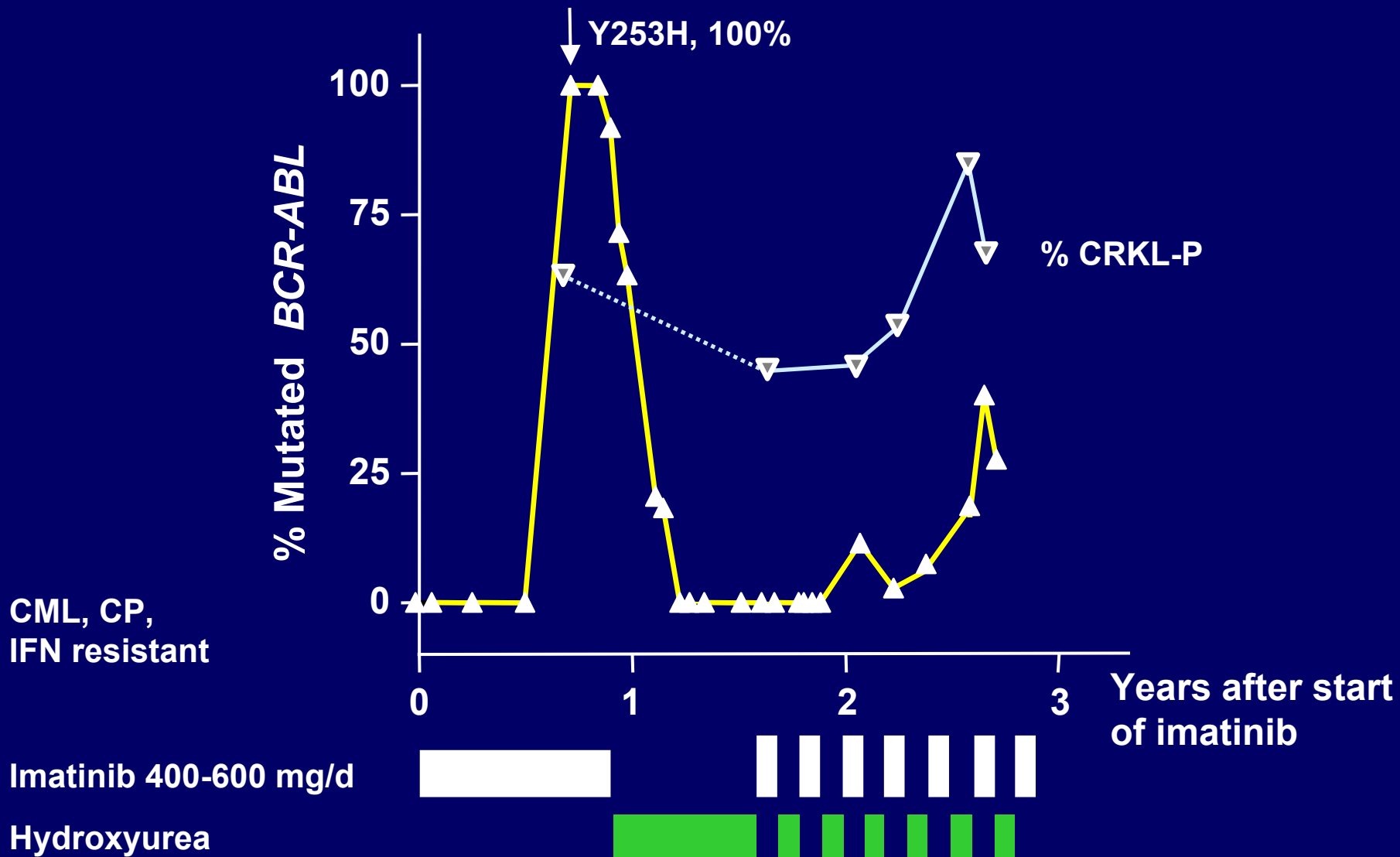
# Survival After Imatinib Failure

## Current Experience, n=105

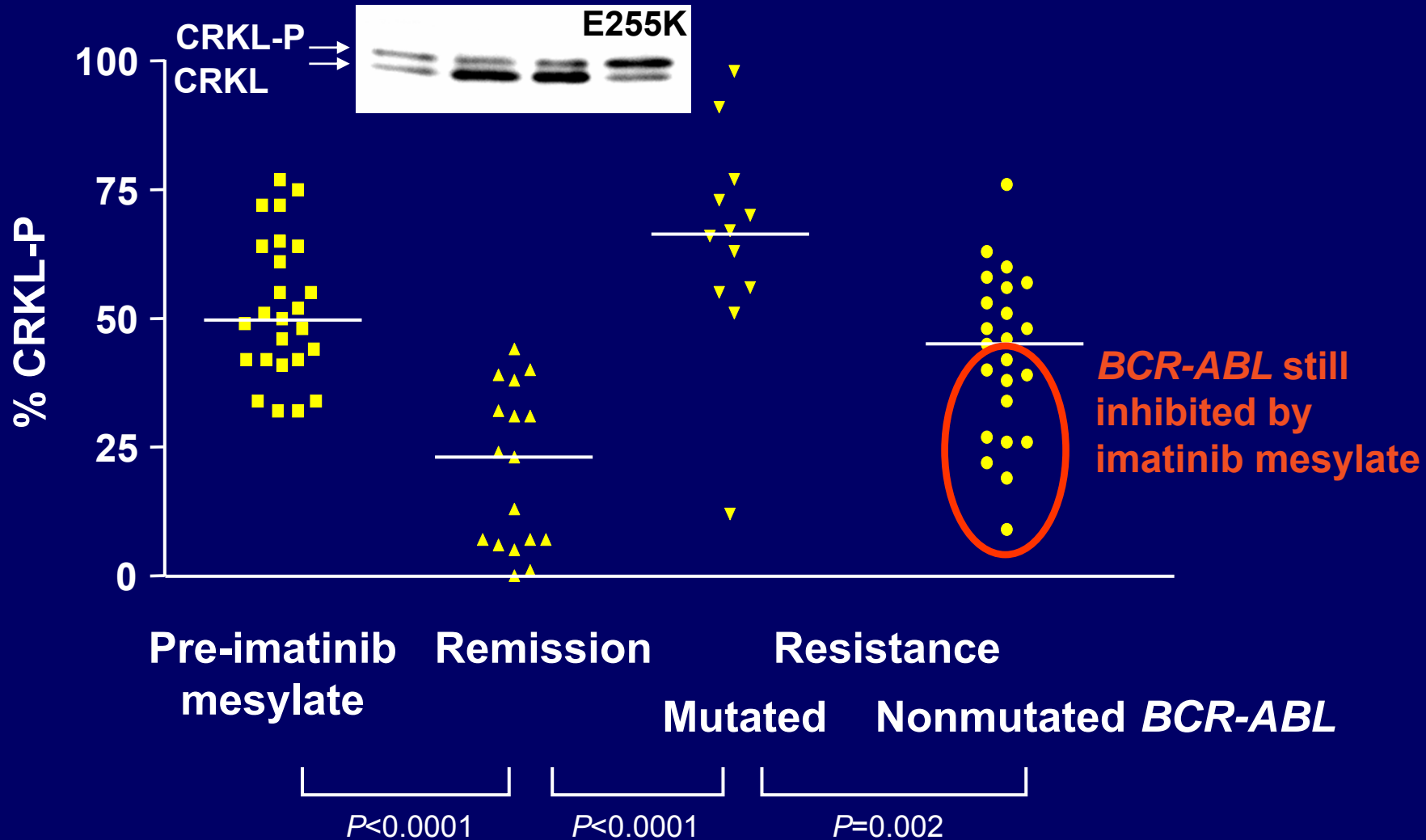




# Dynamics of resistance clones



# CRKL-P in Resistant Patients

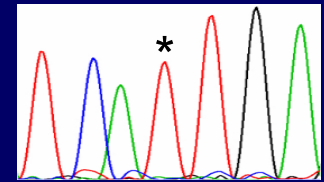
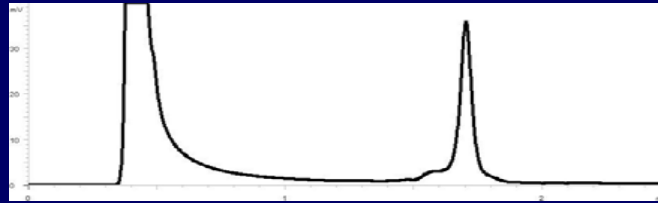


# Methods to detect and quantify BCR-ABL mutations

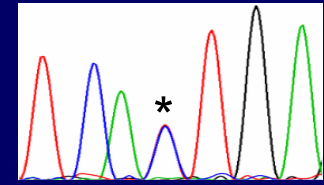
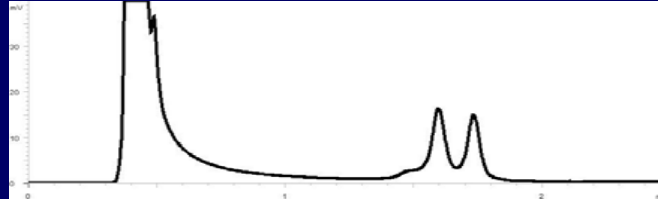
	Specificity	Sensitivity
Sequencing	non specific	~10%
Restriction digest analysis	specific	~2-5%
D-HPLC	non specific	0.1-1%
Allele specific PCR	specific	0.01%
Sequencing of clones	non specific	1-5%

**mutant BaF3<sup>T315I</sup>**

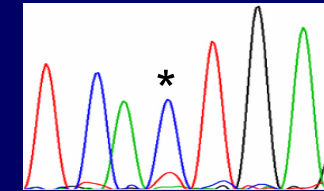
**100%**



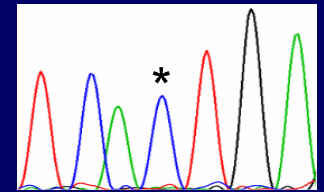
**50%**



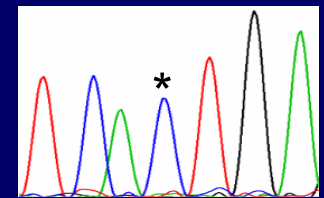
**10%**



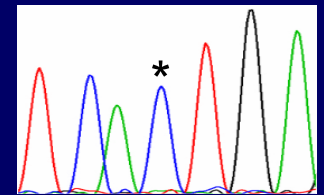
**1%**



**0.1%**



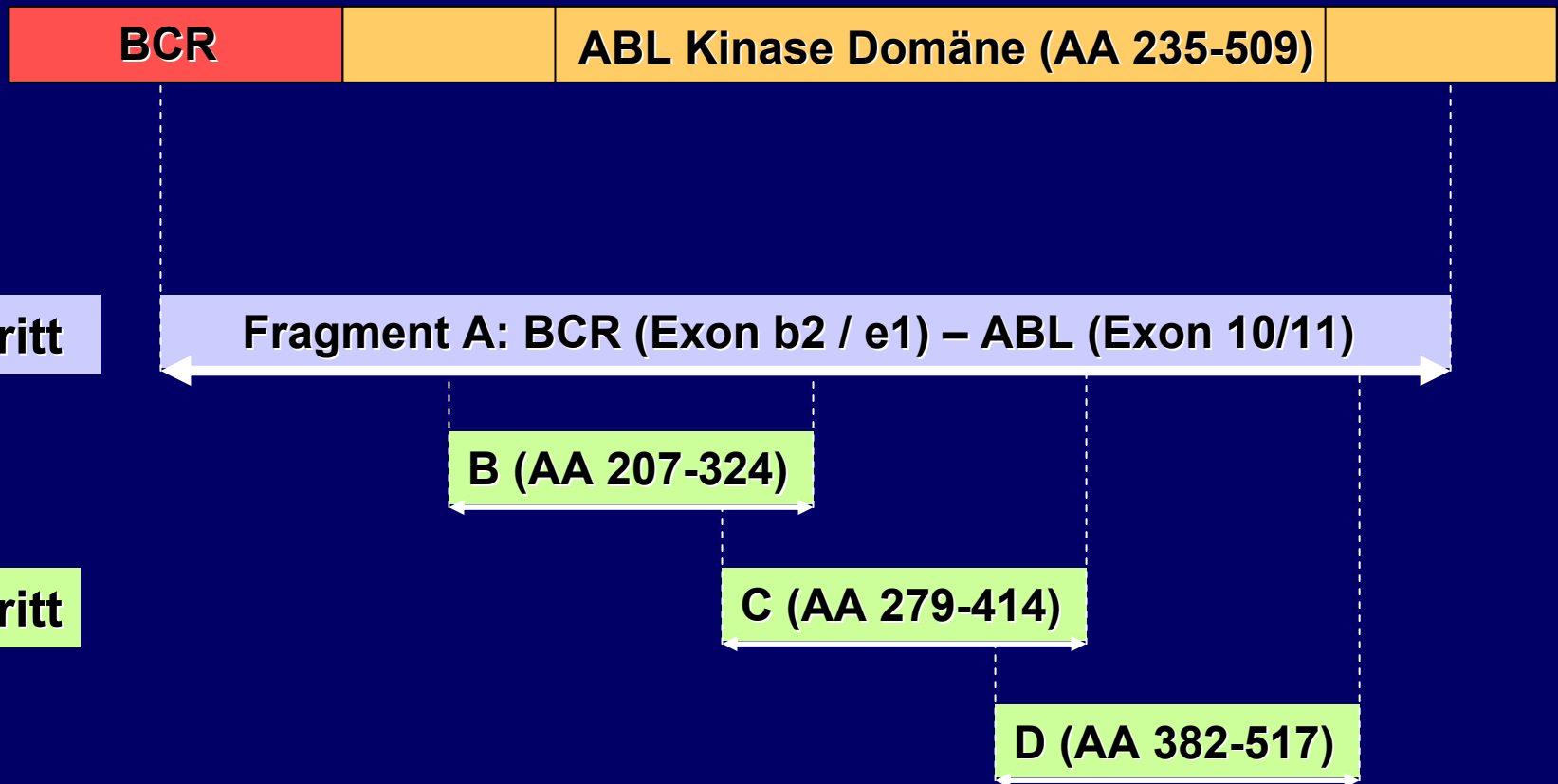
**normal BaF3<sup>BCR-ABL</sup>**



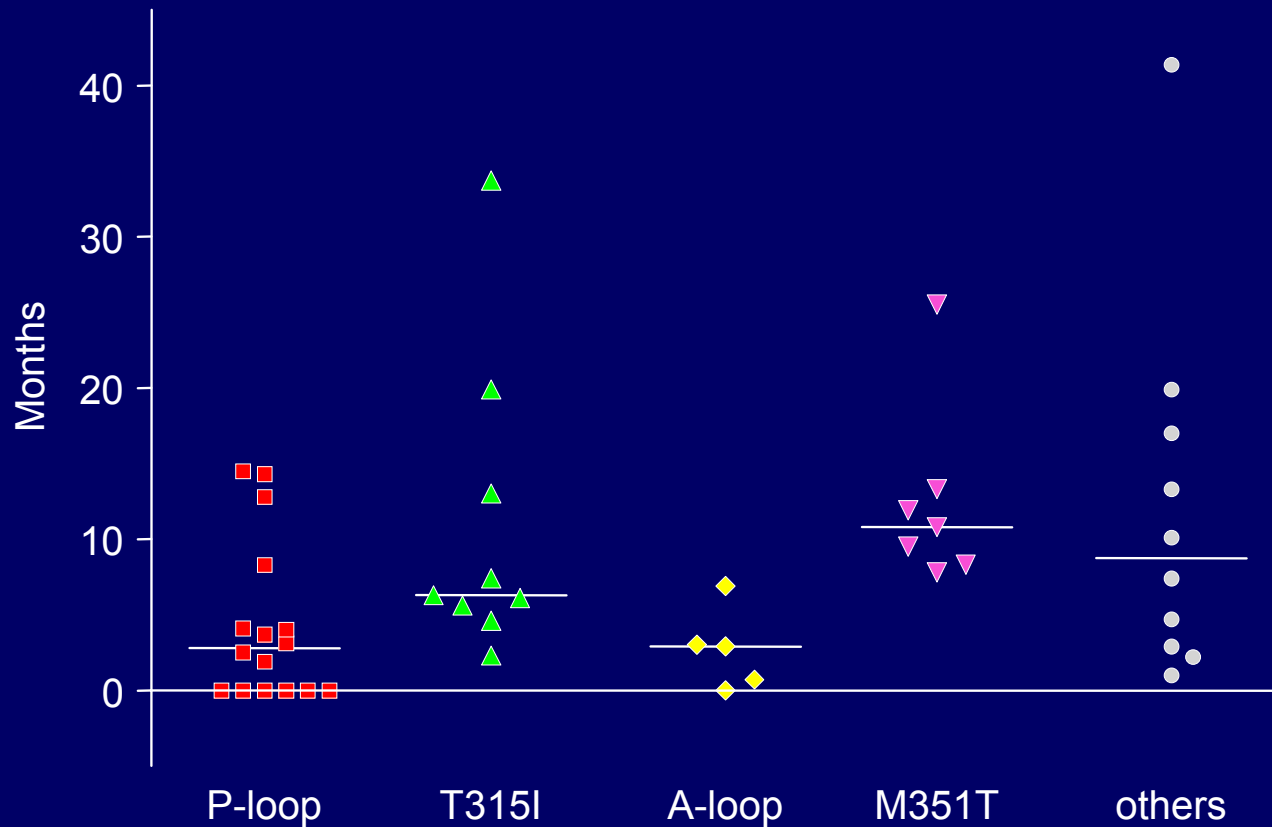
**Sensitivity of  
D-HPLC**

**0.1-1%**

# D-HPLC: Nested-PCR

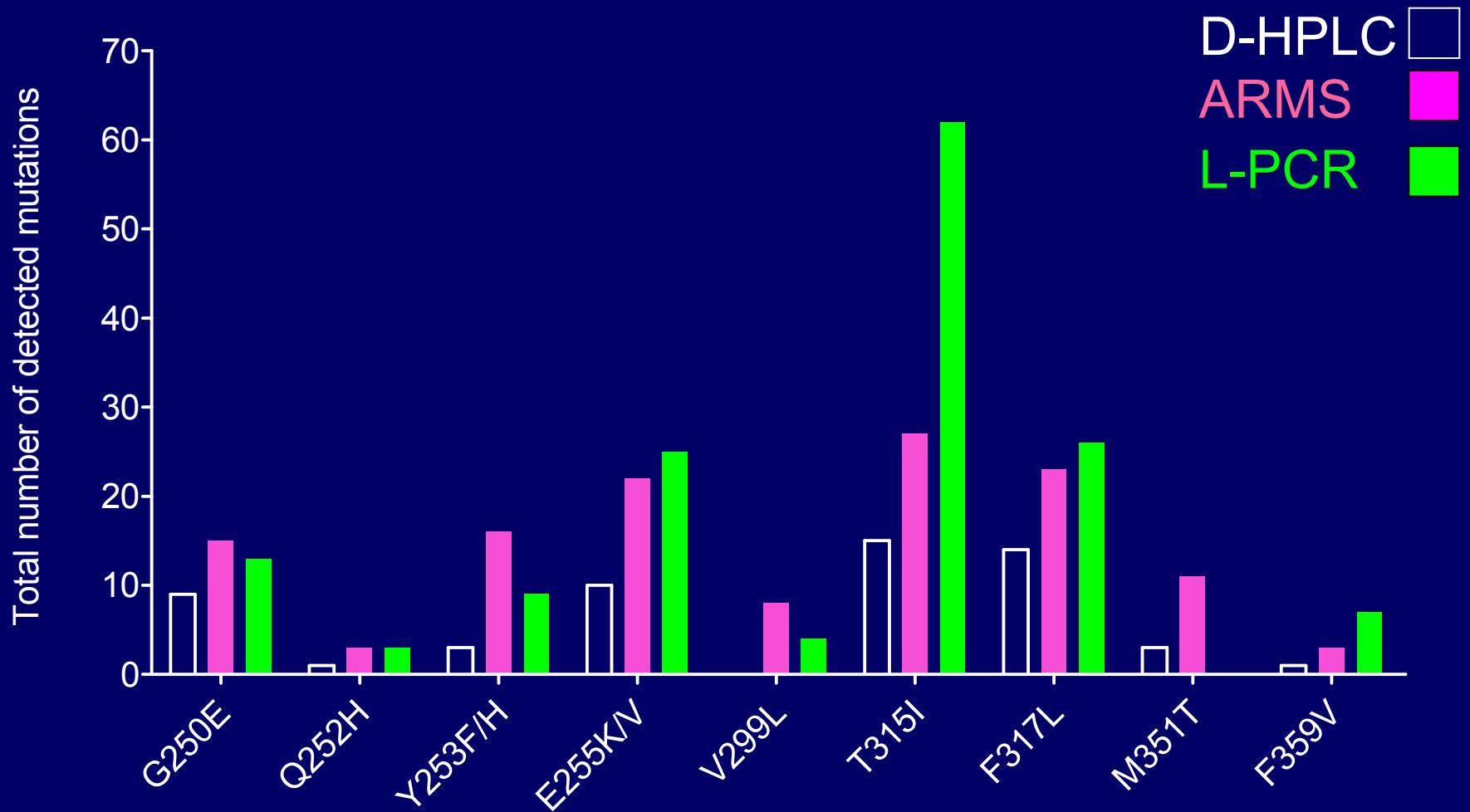


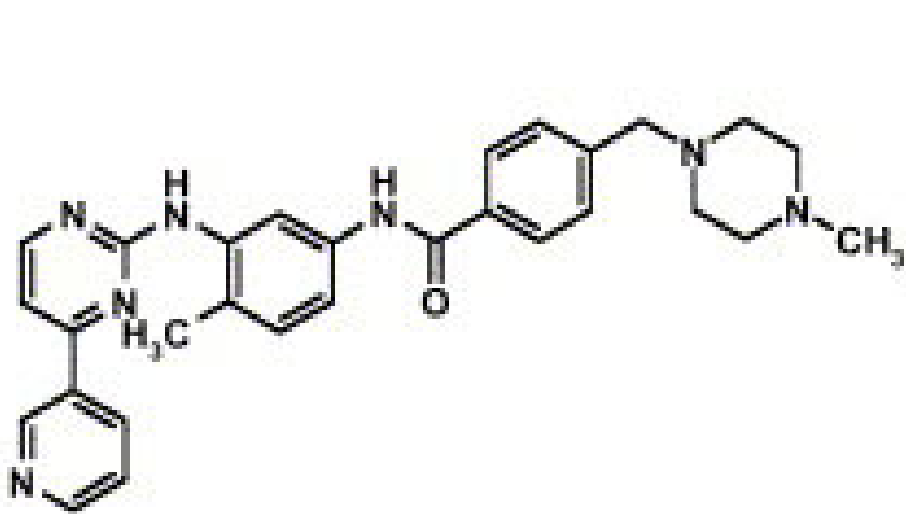
# Interval of D-HPLC positivity to hematological relapse



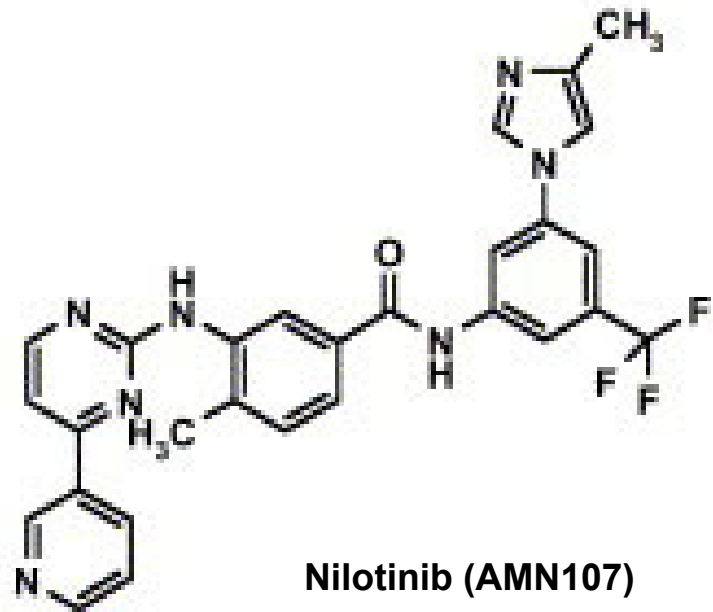
**Median (months)**      **2.8**      **6.3**      **2.9**      **10.8**      **8.7**

# Comparison of D-HPLC vs. allele-specific PCRs for 11 key mutations

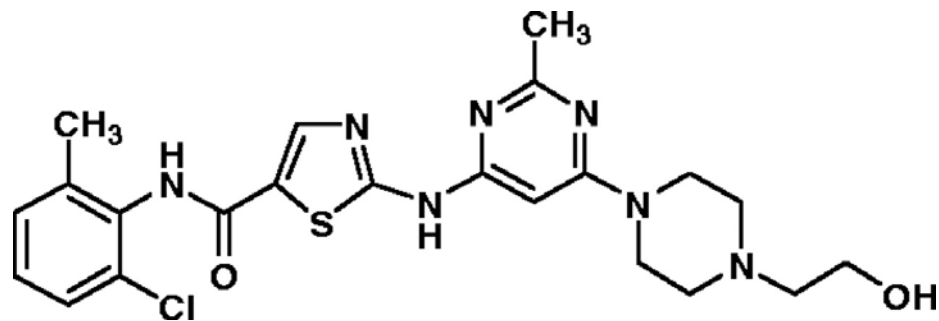




**Imatinib (STI-571)**



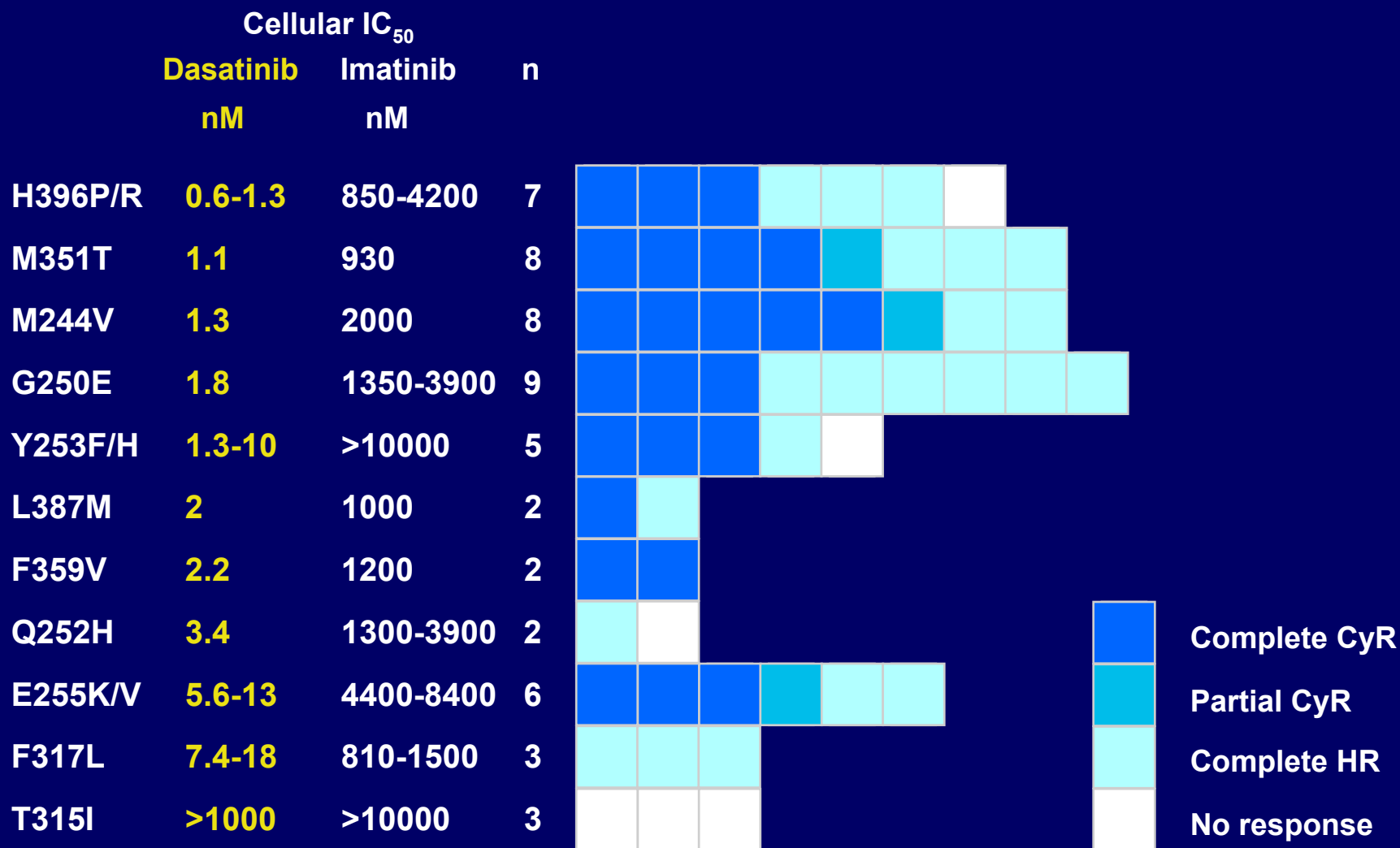
**Nilotinib (AMN107)**



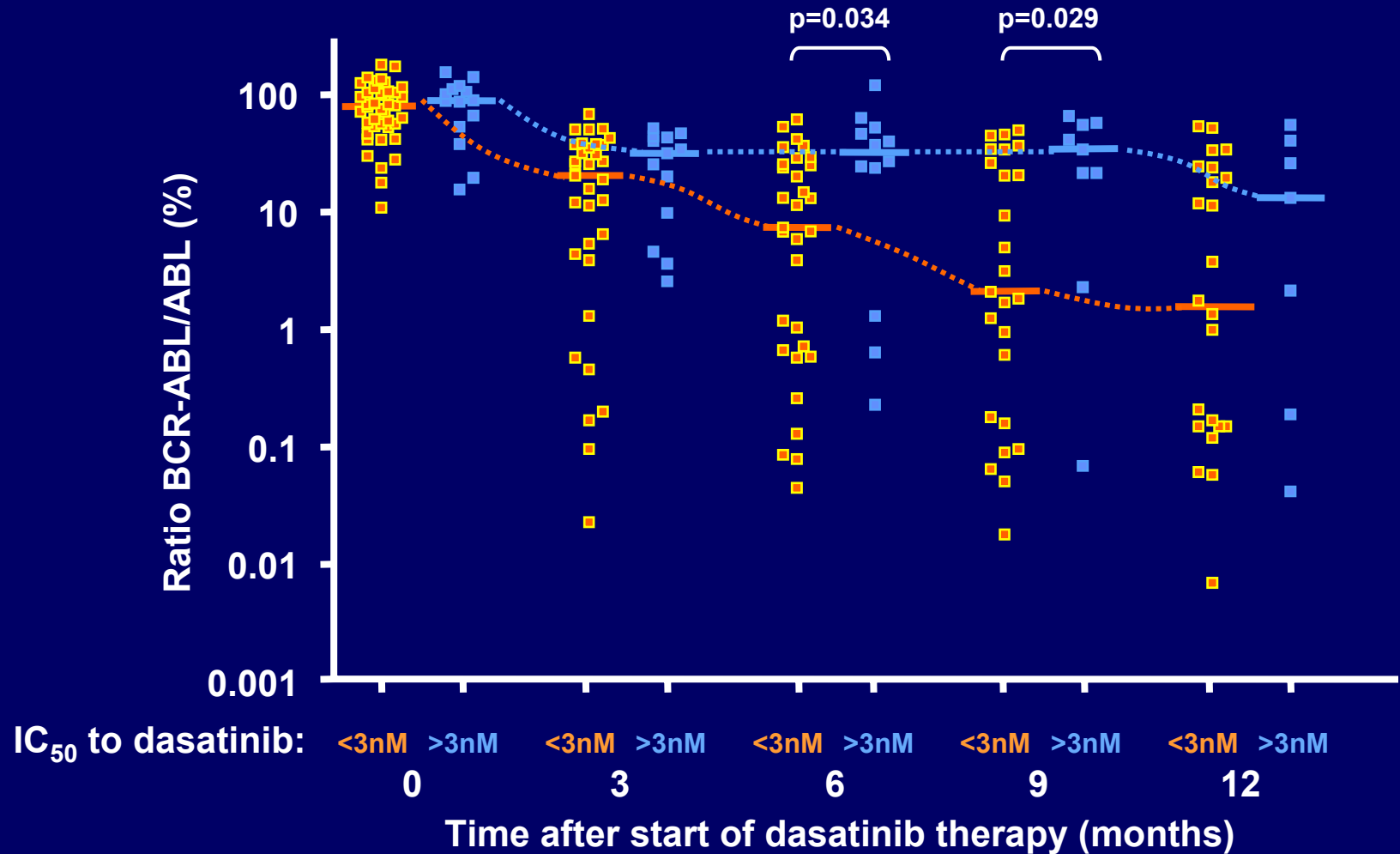
**Dasatinib (BMS-354825)**



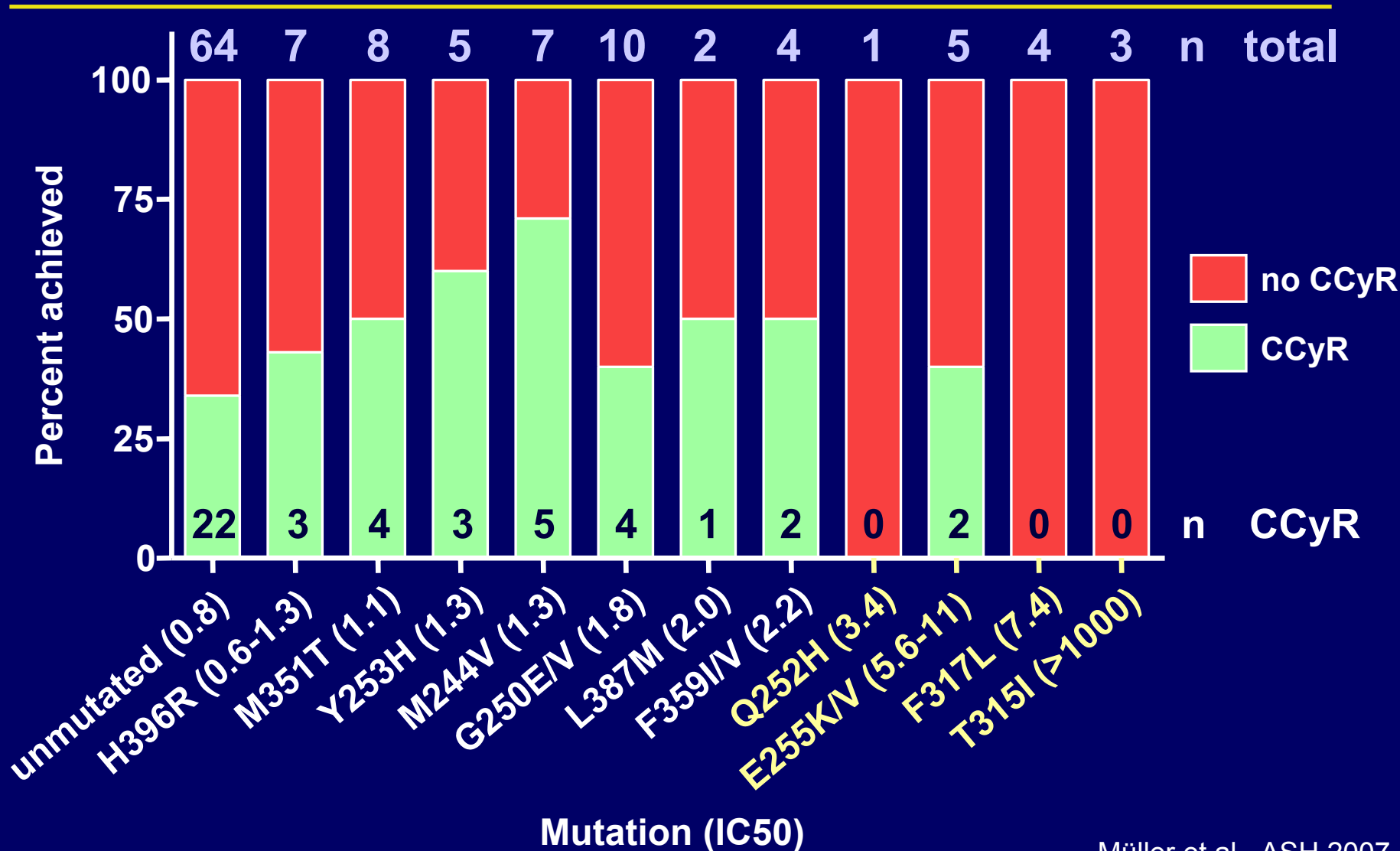
# Response to dasatinib is associated with cellular IC<sub>50</sub> of post-imatinib mutation (CP-CML)



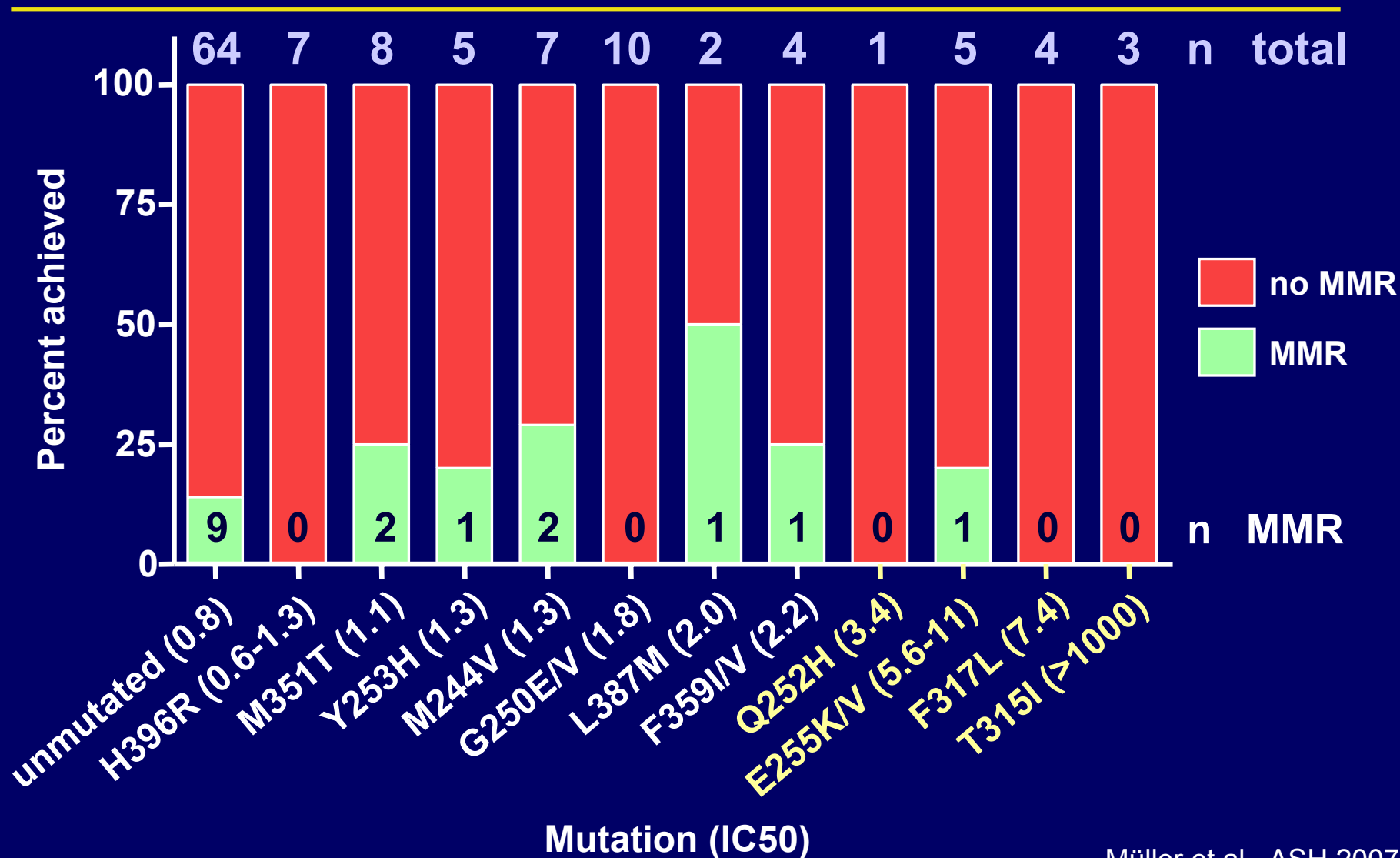
# Differential kinetics of response to dasatinib depending on cellular IC<sub>50</sub> of pretreatment mutation



# Achievement of CCyR by dasatinib according to baseline mutations



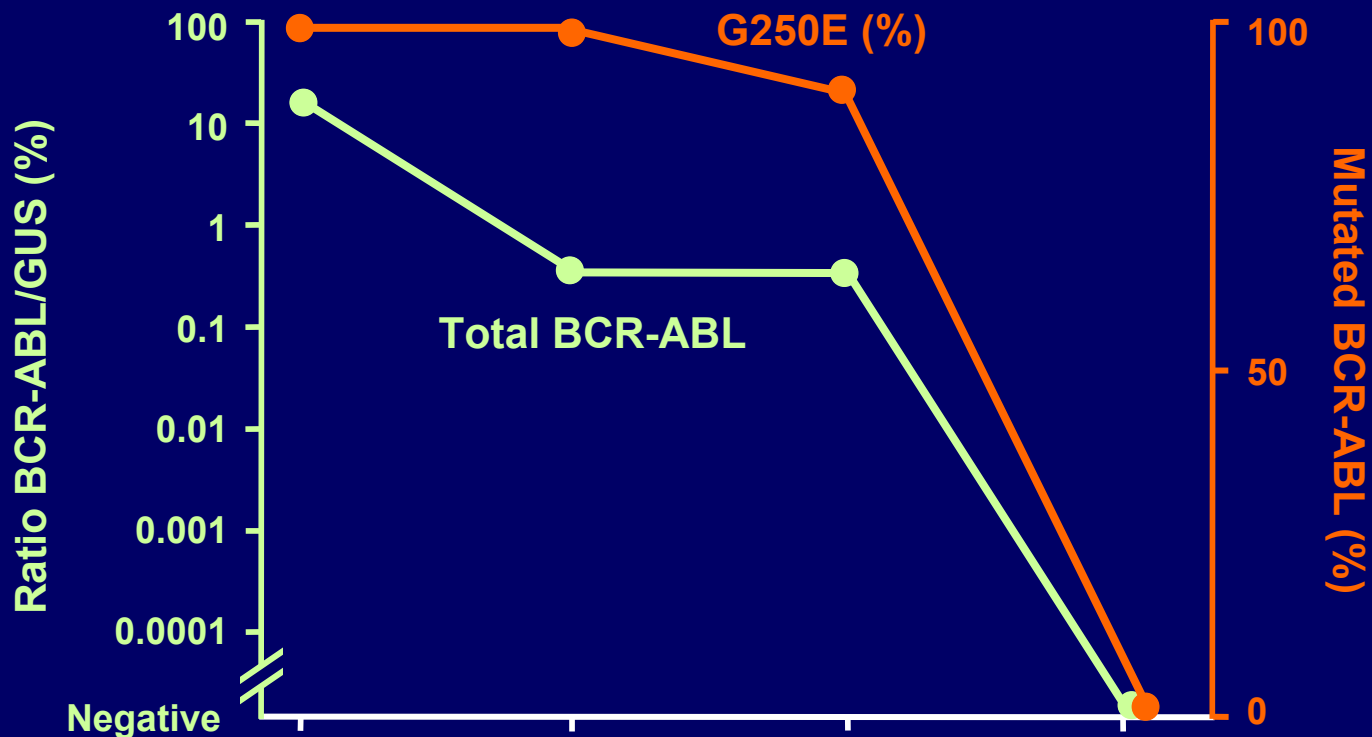
# Achievement of MMR (<0.1% BCR-ABL<sup>IS</sup>) after 24 months by dasatinib according to baseline mutations



# Course of mutated and unmutated BCR-ABL – 3 patterns –

- Pattern 1: n=30

⇒ Baseline mutation disappeared **AND** BCR-ABL decreased



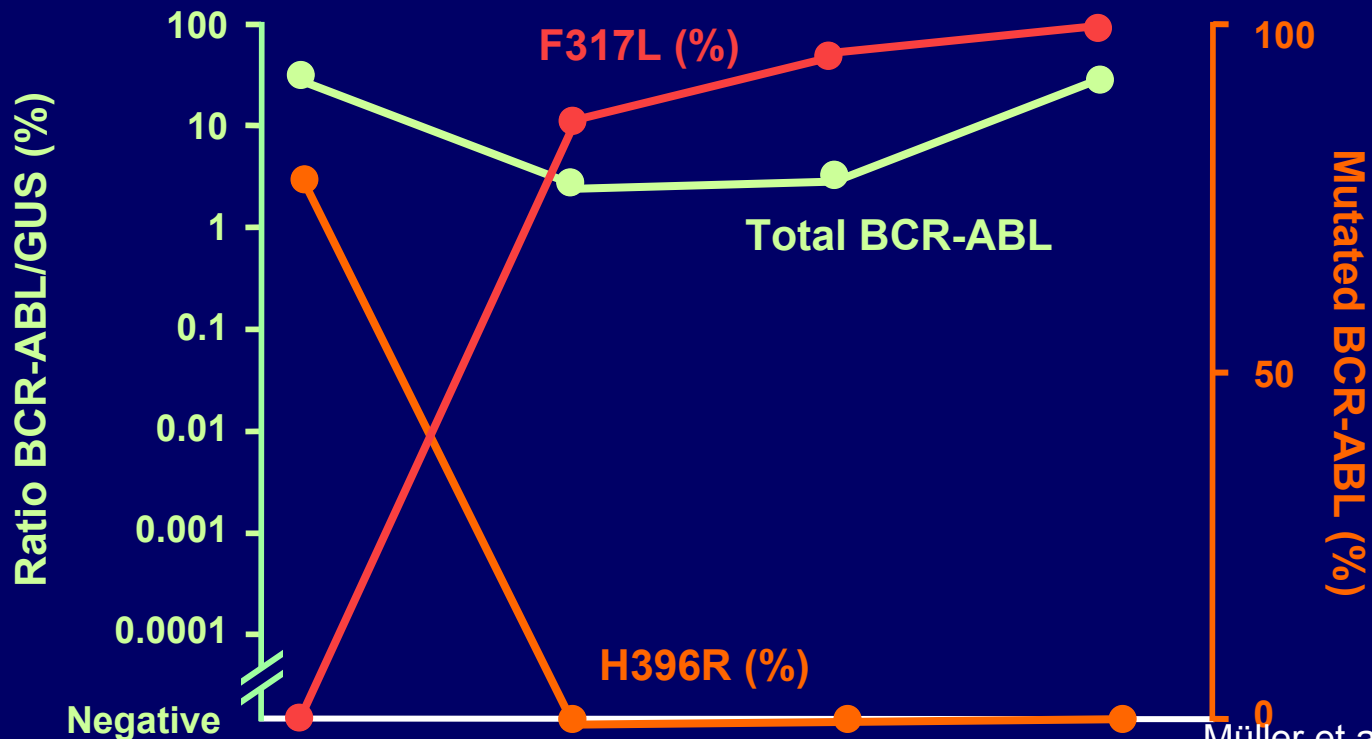
# Course of mutated and unmutated BCR-ABL – 3 patterns –

- **Pattern 2: n=23**

⇒ Baseline mutation disappeared **AND** BCR-ABL persisted

– new mutations evolved in **n=12** patients

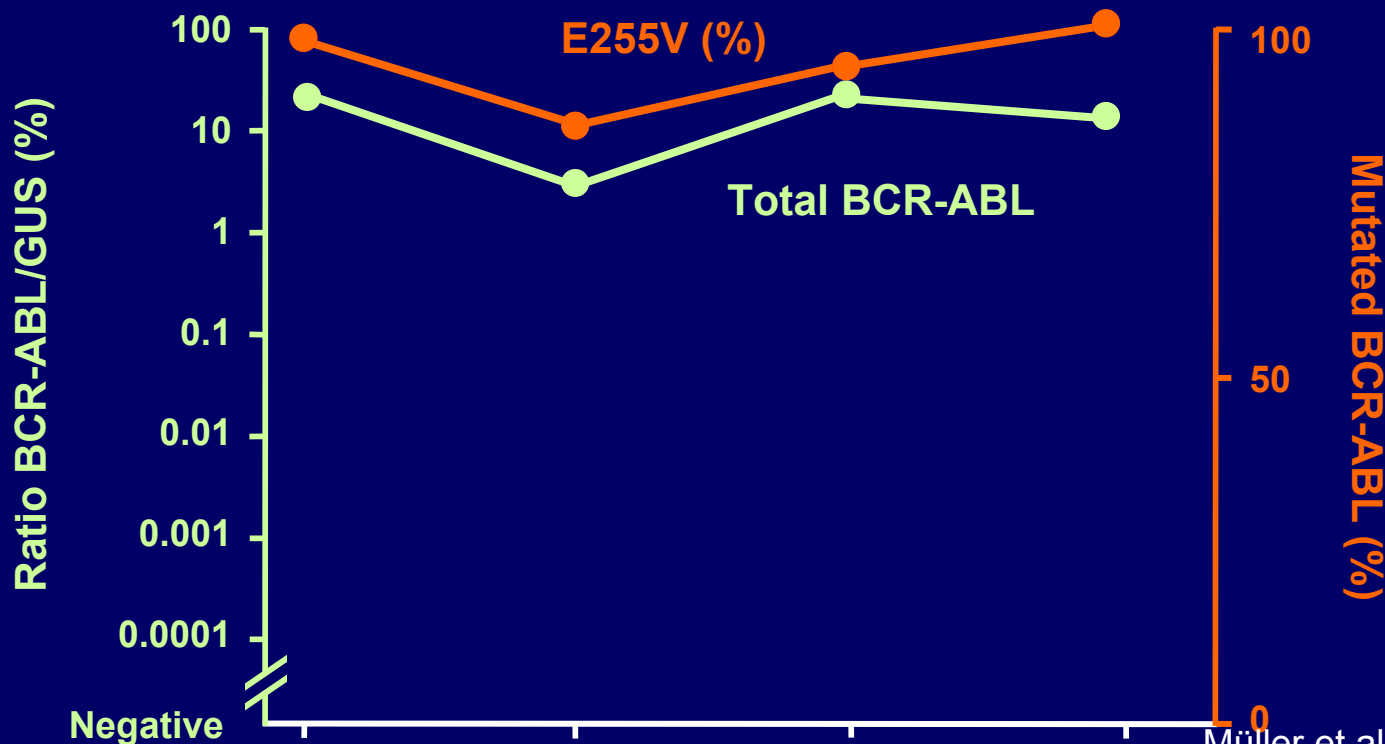
(T315I n=3; F317L n=7; M351T n=2; Y320C n=1)



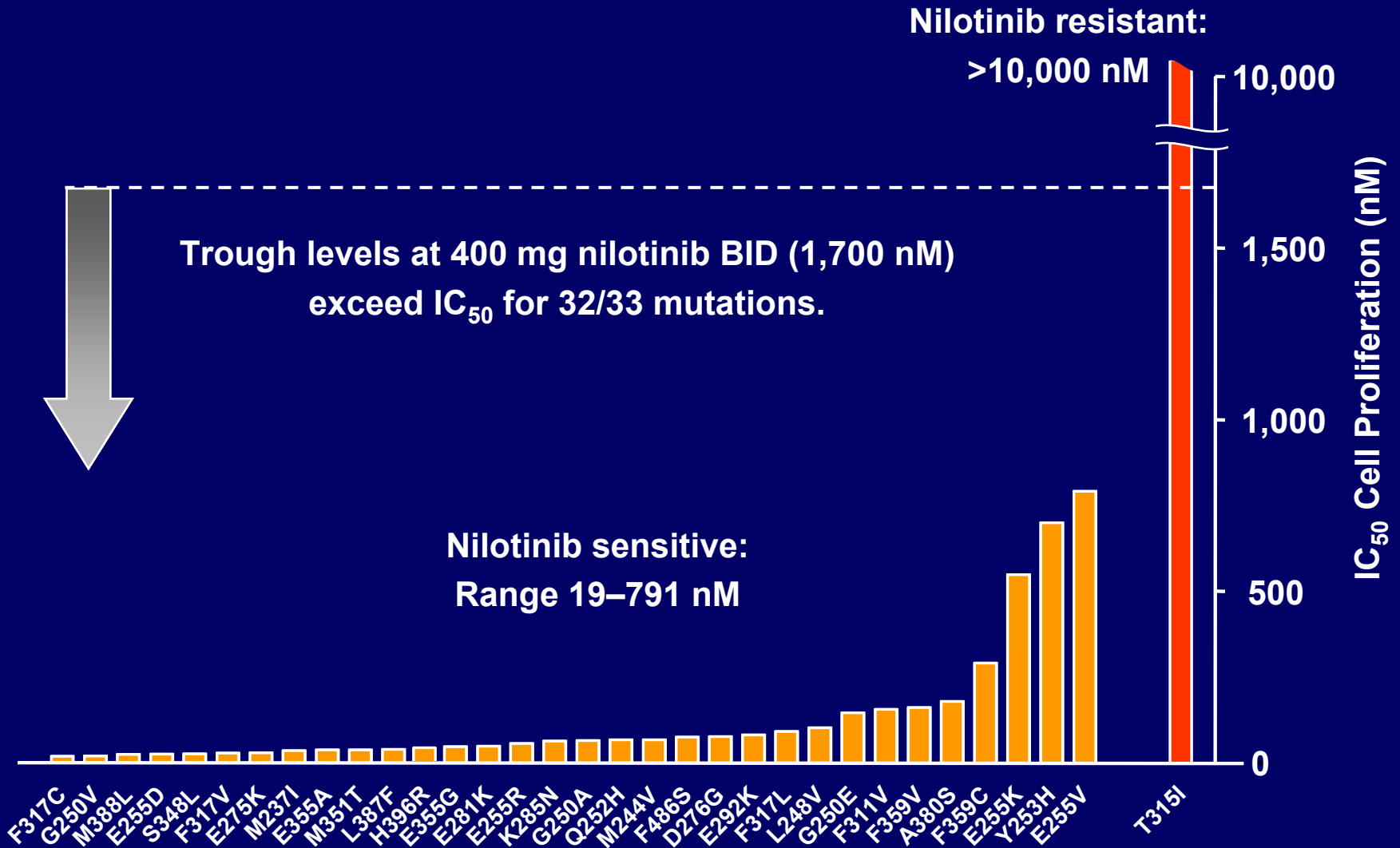
# Course of mutated and unmutated BCR-ABL – 3 patterns –

- **Pattern 3: n=18**

- ⇒ Baseline mutation persisted **AND** BCR-ABL persisted
  - additional mutations evolved in **n=3** patients  
(T315A n=1; V299L n=2)

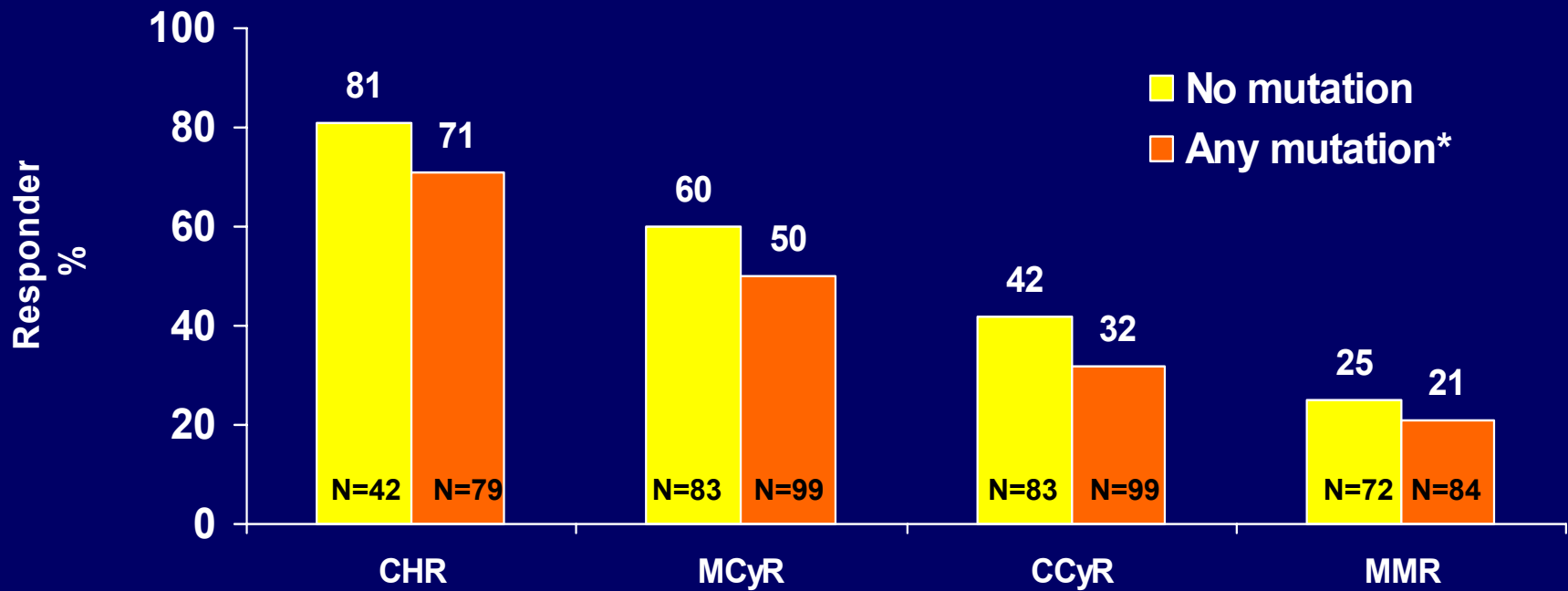


# Nilotinib sensitivity of cells expressing imatinib-resistant BCR-ABL with point mutations





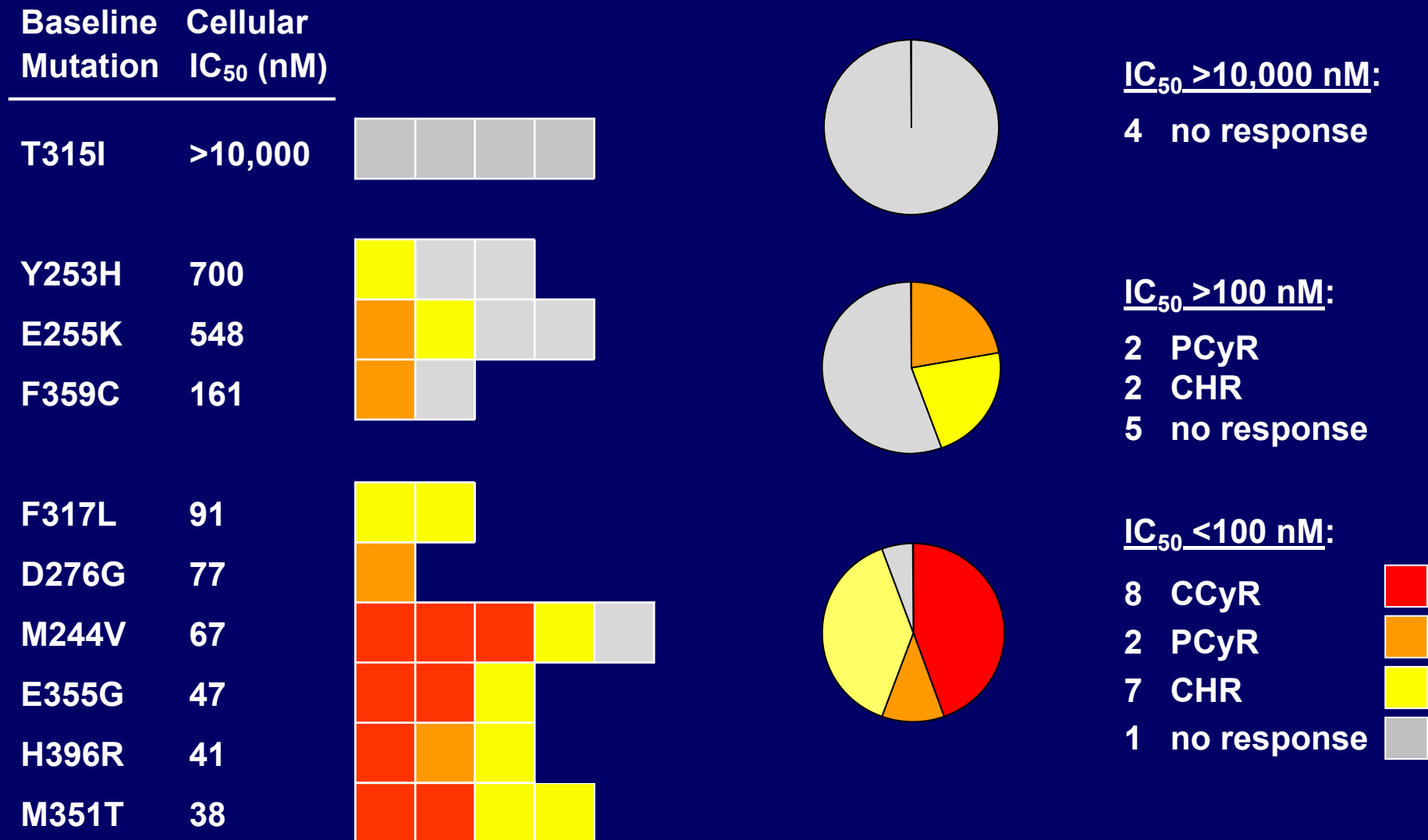
# Best Responses to Nilotinib in Imatinib-Resistant Patients with and without Baseline Mutations by 12 Months



\* patients with T315I were excluded

- Clinical efficacy of nilotinib demonstrated in both mutant and non-mutant group

# CML-CP: Best response within 6 months by cellular IC<sub>50</sub> to nilotinib



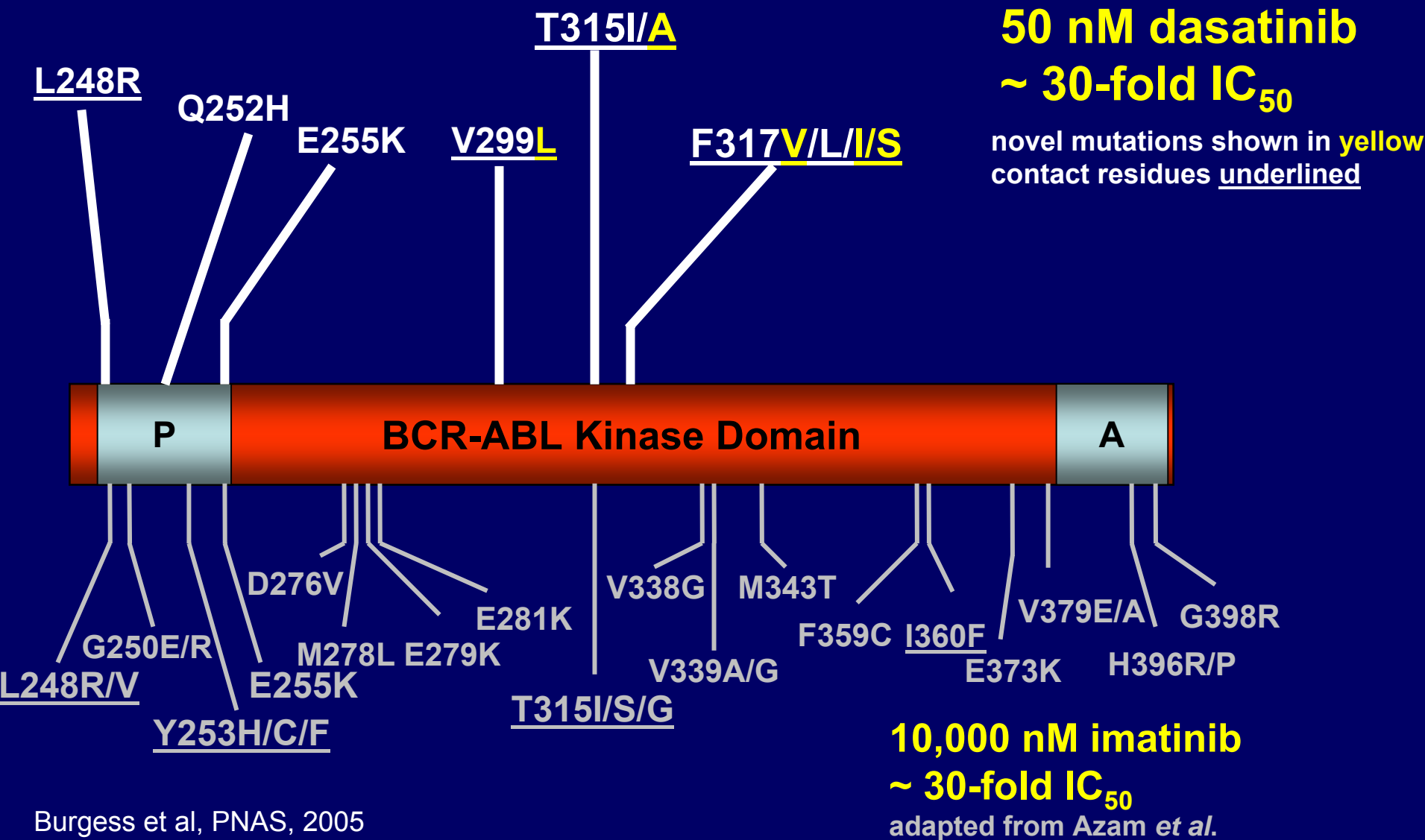
# Best Responses to Nilotinib by 12 Months in Imatinib-Resistant Patients with Different Mutant Types

Mutation	IC <sub>50</sub> (nM)	CHR	MCyR	CCyR	MMR
		n/N (%)	n/N (%)	n/N (%)	n/N (%)
No Mutation		34/42 (81)	50/83 (60)	35/83 (42)	18/72 (25)
IC <sub>50</sub> ≤150 nM		31/38 (82)	28/49 (57)	18/49 (37)	12/44 (27)
IC <sub>50</sub> >150 nM					
Y253H	700	0/6 (0)	1/8 (13)	0/8 (0)	0/7 (0)
E255K/V	548/791	5/8 (63)	3/8 (38)	0/8 (0)	1/7 (14)
F359C/V	258/161	2/9 (22)	1/10 (10)	0/10 (0)	0/9 (0)
Others		14/17 (82)	19/38 (50)	14/38 (37)	5/28 (18)

\* patients with T315I were excluded

- Patients with mutations of IC<sub>50</sub> ≤150 nM achieved comparable responses to the non-mutant group
- Less favorable responses seen in patients with Y253H, E255K/V, and F359C/V.

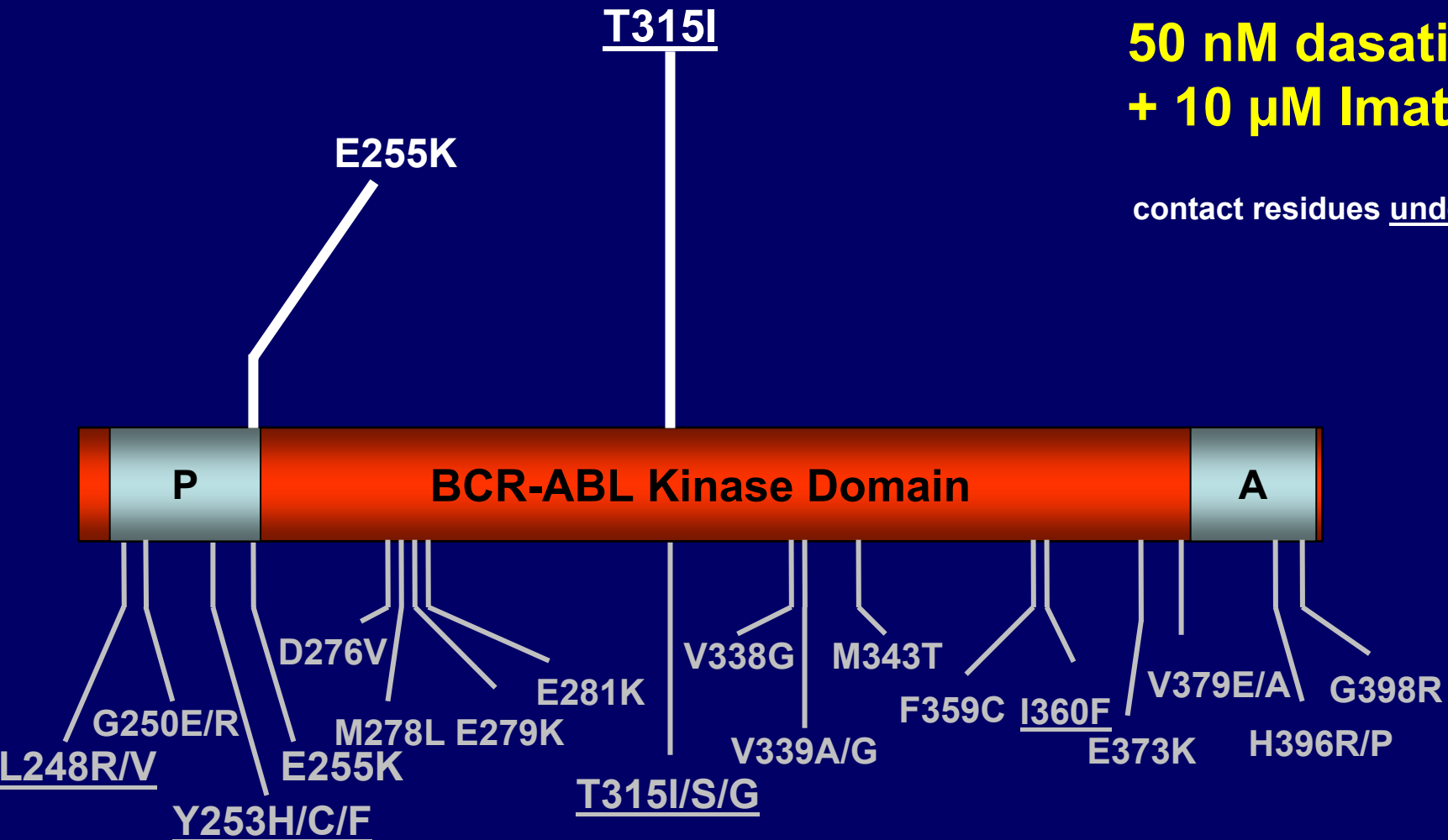
# Resistance to dasatinib *in vitro* is primarily caused by BCR-ABL mutations at contact residues



# Distinct mechanisms of resistance to imatinib and dasatinib

BaF3 Clone	IC <sub>50</sub> for growth (nM)	
	Imatinib	Dasatinib
Unmut. BCR-ABL	<1000	<5
T315I	>10000	>500
T315A	1000	100
F317L	2000	10
F317V	<1000	60
V299L	1000	20
L248R	>10000	20

# Combination of imatinib and dasatinib further reduces the range of resistant clones



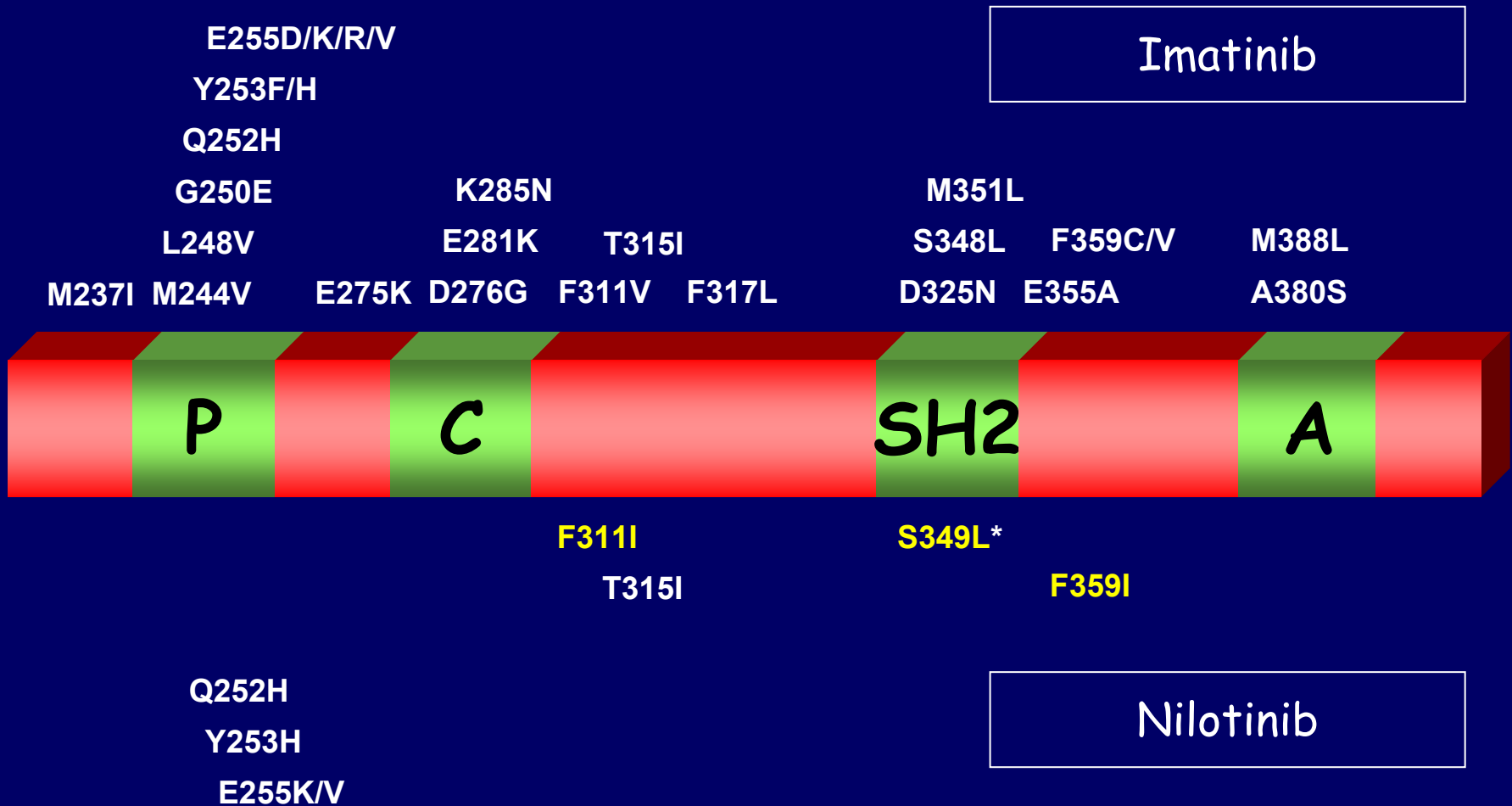
**50 nM dasatinib  
+ 10  $\mu$ M Imatinib**

contact residues underlined

**10,000 nM imatinib  
~ 30-fold IC<sub>50</sub>**

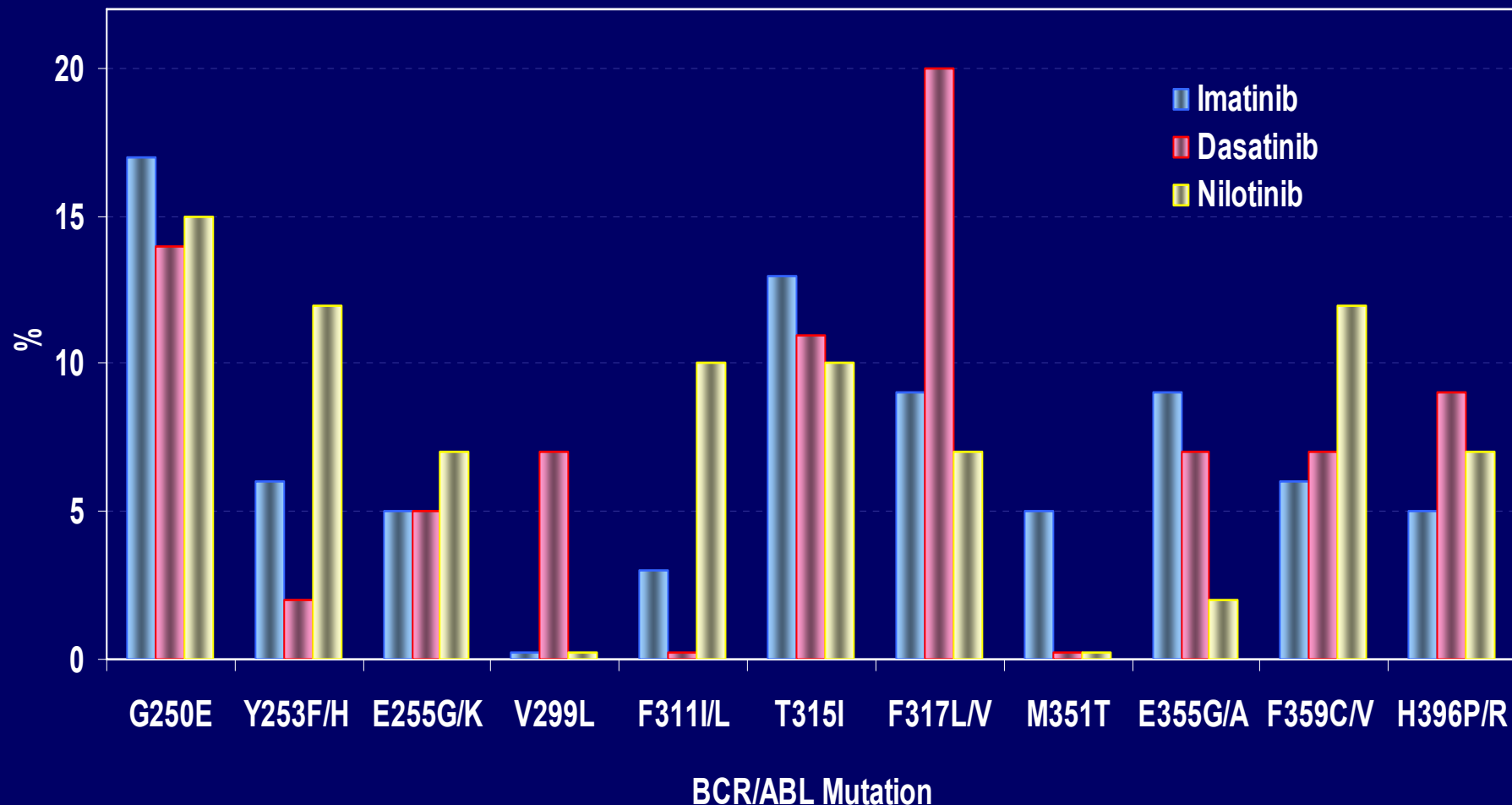
adapted from Azam *et al.*, Cell 112:831-843

# Nilotinib produces a limited number of resistance mutations



\* Q252H/S349L Double mutant

# Spectrum and frequency of BCR-ABL KD mutations recovered after TKI therapy



- T315I and F359V recovered after treatment with Bosutinib



# Emerging BCR-ABL mutations on Dasatinib

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- **New mutations: n=22**
  - F317L n=7; T315I n=3; V299L n=2; T315A n=1; M351T n=2; Y320C n=1; L248V n=1; G250E n=1; Y232H n=1; K271R n=1; A344V n=1; E507G n=1
  - **Incidence:** 22 cases in 288 yrs pt. exposure in 201 pts  
⇒ 7.6%/patient-year
  - **Time to detection:** 11 months (median, range 3–23)
  - **Baseline mutation:** in 17 of 22 (77%) patients
  - **Post CCyR:** 8/22 pts ⇒ risk to develop new mutations after achievement of CCyR  $8/55 = 14.5\%$
  - **Post MMR:** 4/22 pts ⇒ risk to develop new mutations after achievement of MMR  $4/30 = 13.3\%$

# Newly Detectable Mutations During Nilotinib Therapy

	All		Resistant		Intolerant	
	n/N	(%)	n/N	(%)	n/N	(%)
All Emerging Mutations	43/275	(16)	40/187	(21)	3/88	(3)
<b>With Baseline Mutations</b>	30/113	(27)	29/104	(28)	1/9	(11)
<b>Without Baseline Mutations</b>	13/162	(8)	11/83	(13)	2/79	(3)

- Patients with baseline mutation had higher incidence of emerging mutation compared to patients without baseline mutation
- Of 187 resistant patients, E255K/V was newly detected in 10 (5%) patients; T315I in 9 (5%); G250E in 7 (4%), and Y253H in 5 (3%) patients
- 57% of resistant patients with newly detectable mutation progressed

mutation  
analysis of  
BCR-ABL KD

3m - no CHR  
6m - no MCR  
12m - no CCR  
18m - no MMR

loss of CHR  
loss of CCR  
loss of MMR  
ACA in Ph+  
cells

progression  
AP  
BC

rise in  
BCR-ABL



**ELN** LeukemiaNet<sup>®</sup>  
European

**133 centers  
in 24  
countries**

