

Challenges in Personalized Cancer Medicine

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Personalized Cancer Medicine

Expectations and Reality

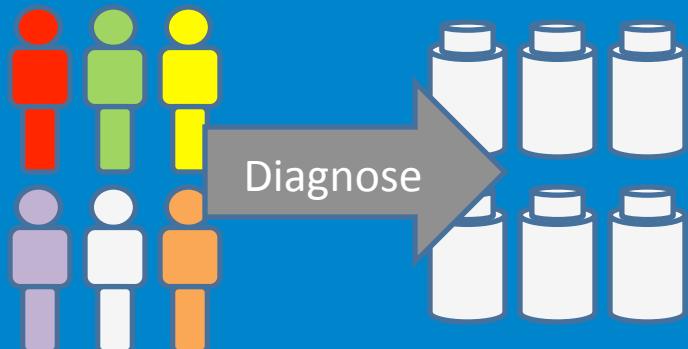
- **Expectations and Marketing**
 - Highly effective cancer therapy
 - Neglectable side effects
 - Higher cost effectiveness
 - Reduced attrition rate in clinical development
- **Reality**
 - Molecular or immunological targeted therapy is feasible (= personalized medicine?)
 - At least in some tumor entities or tumor subpopulations
 - Side effects changed in quality but are still an issue
 - Complexity of cancer genetics and other “-omics”
 - New challenges in translation and clinical development
 - Moderate improvement in cancer therapy associated with massively increasing costs

Zukunftsmarkt

Personalisierte und zielgerichtete Medizin

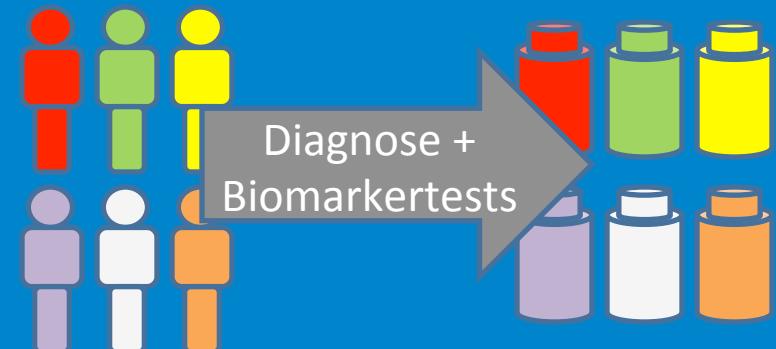
Symptombasierte Medizin

- „one fits all“/Blockbuster-Ansatz,
- geringe Wirksamkeit (nur 40-60%)
- hohe Nebenwirkungsraten
- hohe „Attrition Rates“
- lange Entwicklungszeiten
- hohe Kosten der Medikamentenentwicklung



Personalisierte Medizin

- auf Patientengruppen zugeschnittene Medizin
- effektivere Medikamente
- sicherere Medikamente
- niedrigere Ausfallraten
- bis zu 10 mal kleinere klinische Studien
- geringere Kosten für klinische Studien



Personalized Cancer Medicine

Expectations and Reality

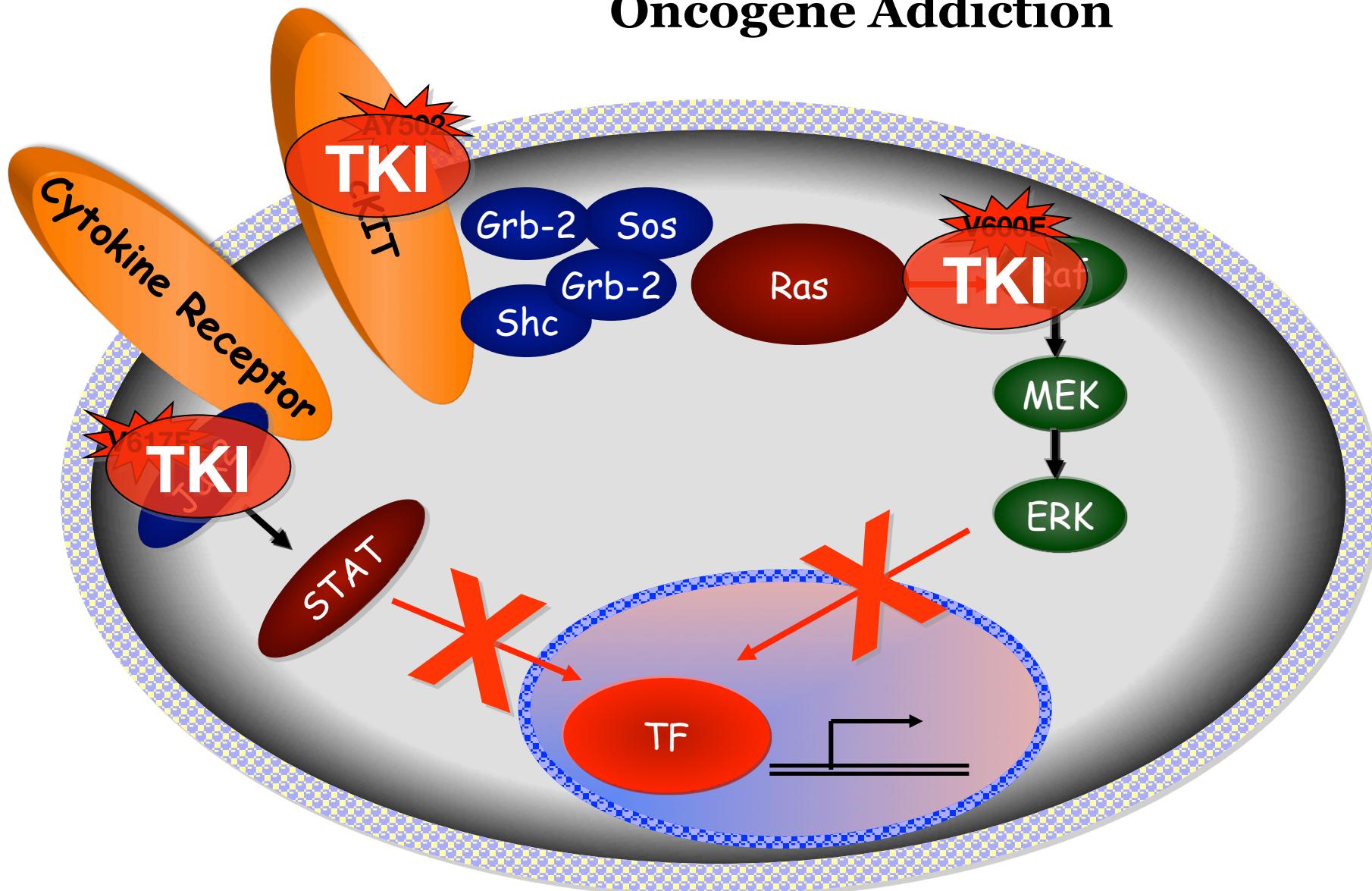
- **Expectations and Marketing**
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Definition and Rationale

(Tran et al JCO 2012)

- The US National Cancer Institute defines personalized medicine as „a form of medicine that uses information about a person's genes, proteins, and environment to prevent, diagnose, and treat disease”.
 - Genetic aberrations exist in human malignancies
 - A subset of these aberrations drives oncogenesis and tumor biology
 - These aberrations are actionable
 - Highly specific anticancer agents are available that effectively modulate these targets (druggable)
- Mission and Goals to facilitate PCM
 - Enhance the understanding of the molecular mechanisms of cancer
 - Accelerate genomic science and technology development
 - Translate genomic data to improve cancer prevention, early detection, diagnosis and treatment

Activating Mutations: Constitutive (Oncogenic) Signal Transduction = Oncogene Addiction



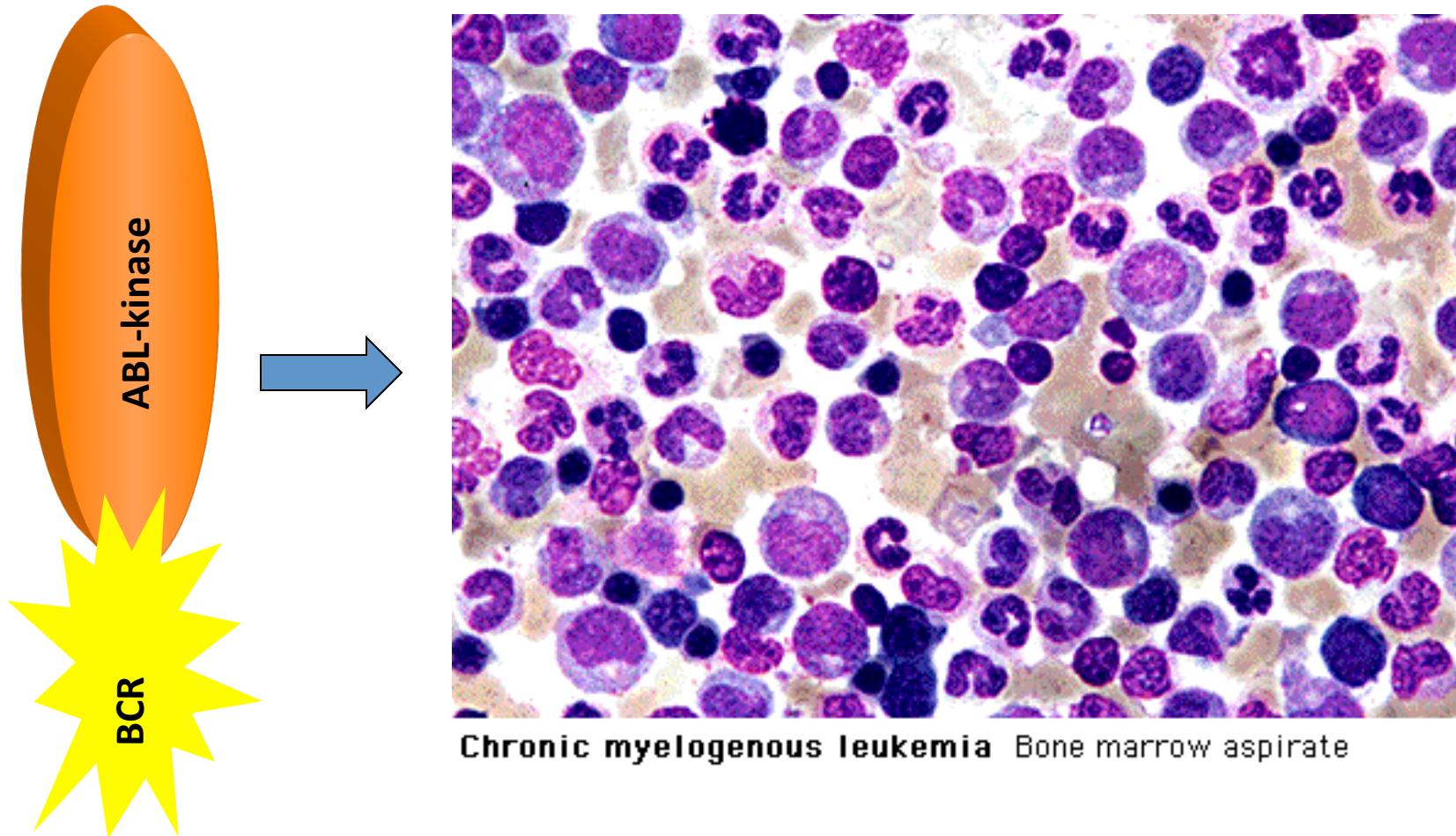
Kinase Inhibitors in Clinical Use

AML	<u>FLT3/ITD</u>	→ AC220, PKC412, MLN518, CEP-701, su5416, Sorafenib, Sunitinib
CEL	<u>FIP-PDGFRα</u>	→ Imatinib , Nilotinib, Dasatinib, Sorafenib
CML	<u>Bcr-Abl</u>	→ Imatinib, Dasatinib, Nilotinib , Bosutinib
GIST	<u>cKit, PDGFRA</u>	→ Imatinib, Sunitinib , Nilotinib, Dasatinib
IMF/PV/ET	<u>JAK1/2</u>	→ Ruxolitinib , Pacritinib, CYT387, TG101
Liver	<u>VEGFR</u>	→ Sorafenib
Lung	<u>EGFR</u>	→ Erlotinib, Gefitinib
	<u>ALK</u>	→ Crizotinib
Mamma	<u>HER-2</u>	→ Lapatinib
Melanoma	<u>B-RAF</u>	→ Vemurafenib
Kidney	<u>VEGFR</u>	→ Sunitinib, Sorafenib, Pazopanib
	<u>mTOR</u>	→ Tensirolimus, Everolimus
Pancreas	<u>EGFR</u>	→ Erlotinib
PNET	<u>mTOR</u>	→ Tensirolimus
Thyroid	<u>VEGFR, EGFR,</u>	→ Vandetanib
	<u>RET</u>	

green = licensed

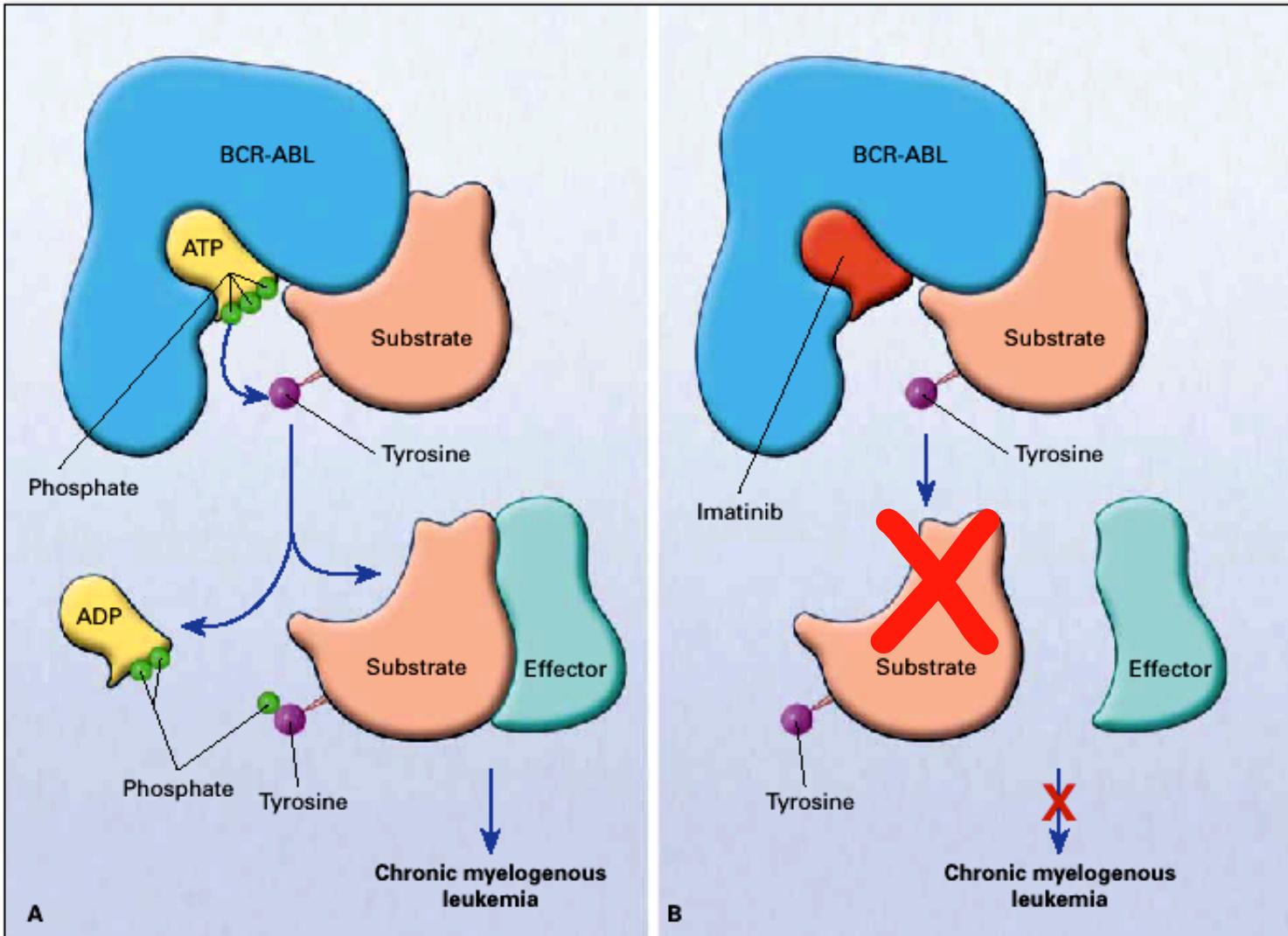
Chronic Myeloid Leukemia (CML)

Bcr-Abl = constitutively activated signal transduction

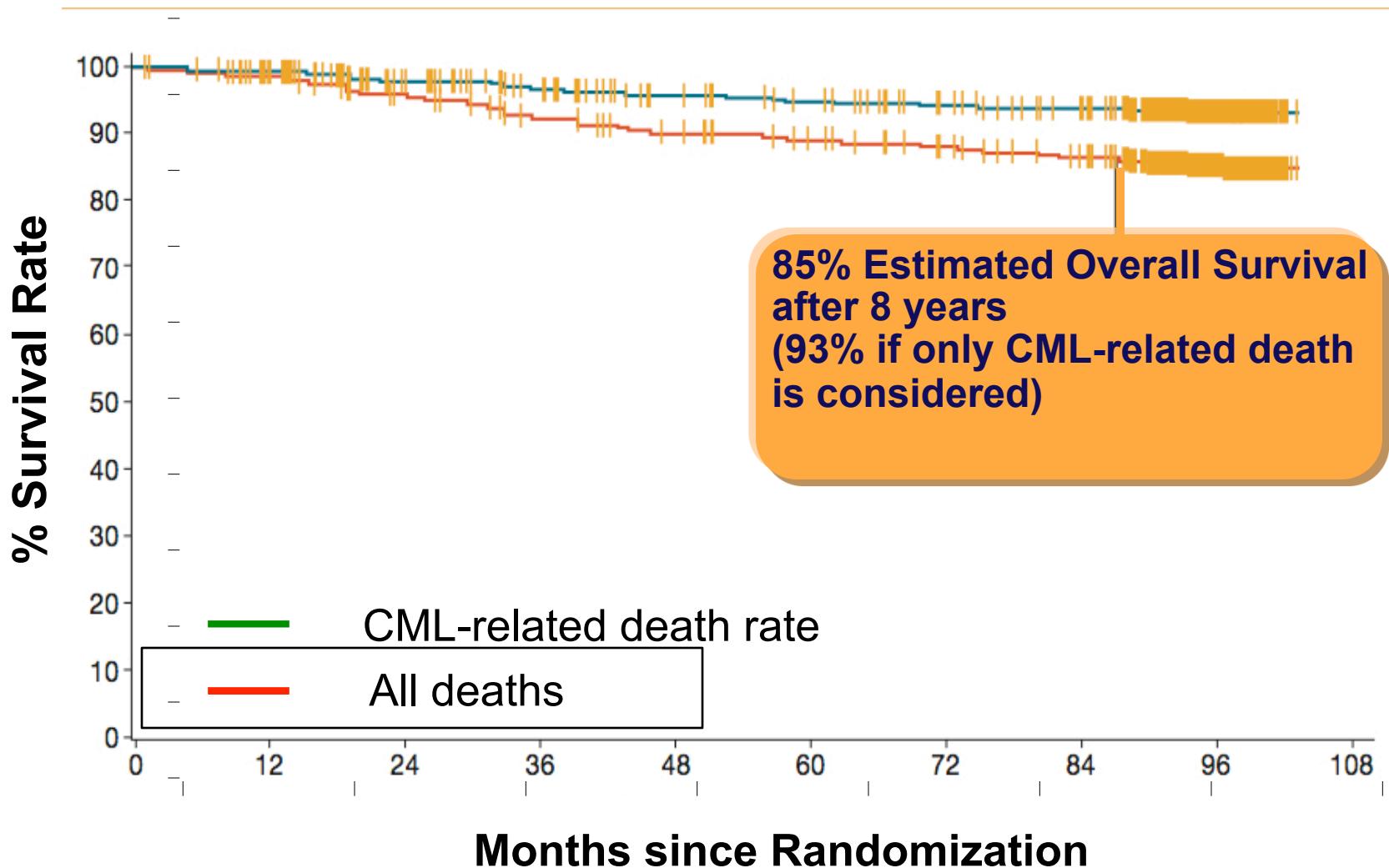


Bcr-Abl sufficient for induction of leukemia:
„single hit oncogene“

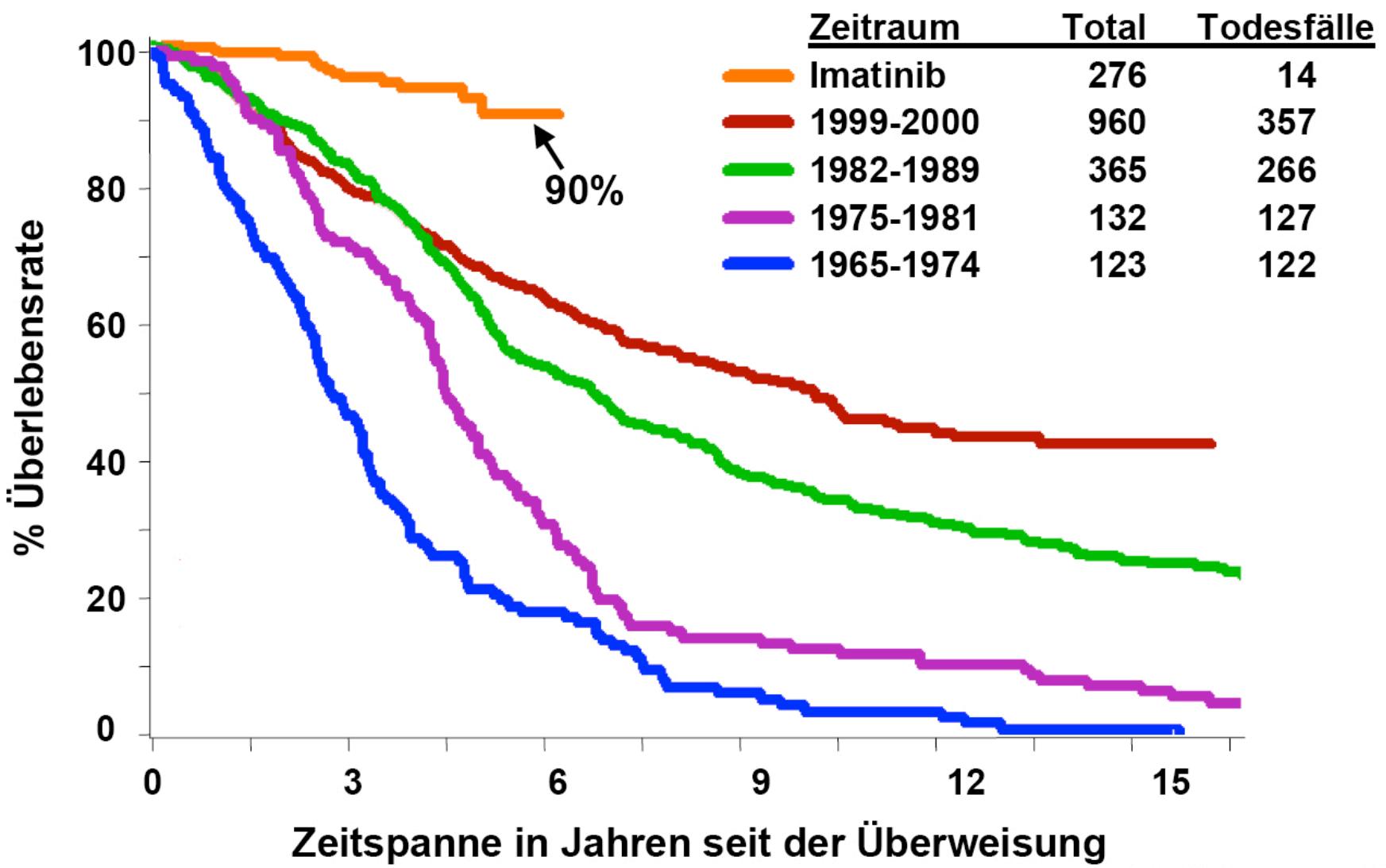
Imatinib (Glivec): ATP-competitor, disables kinase activity



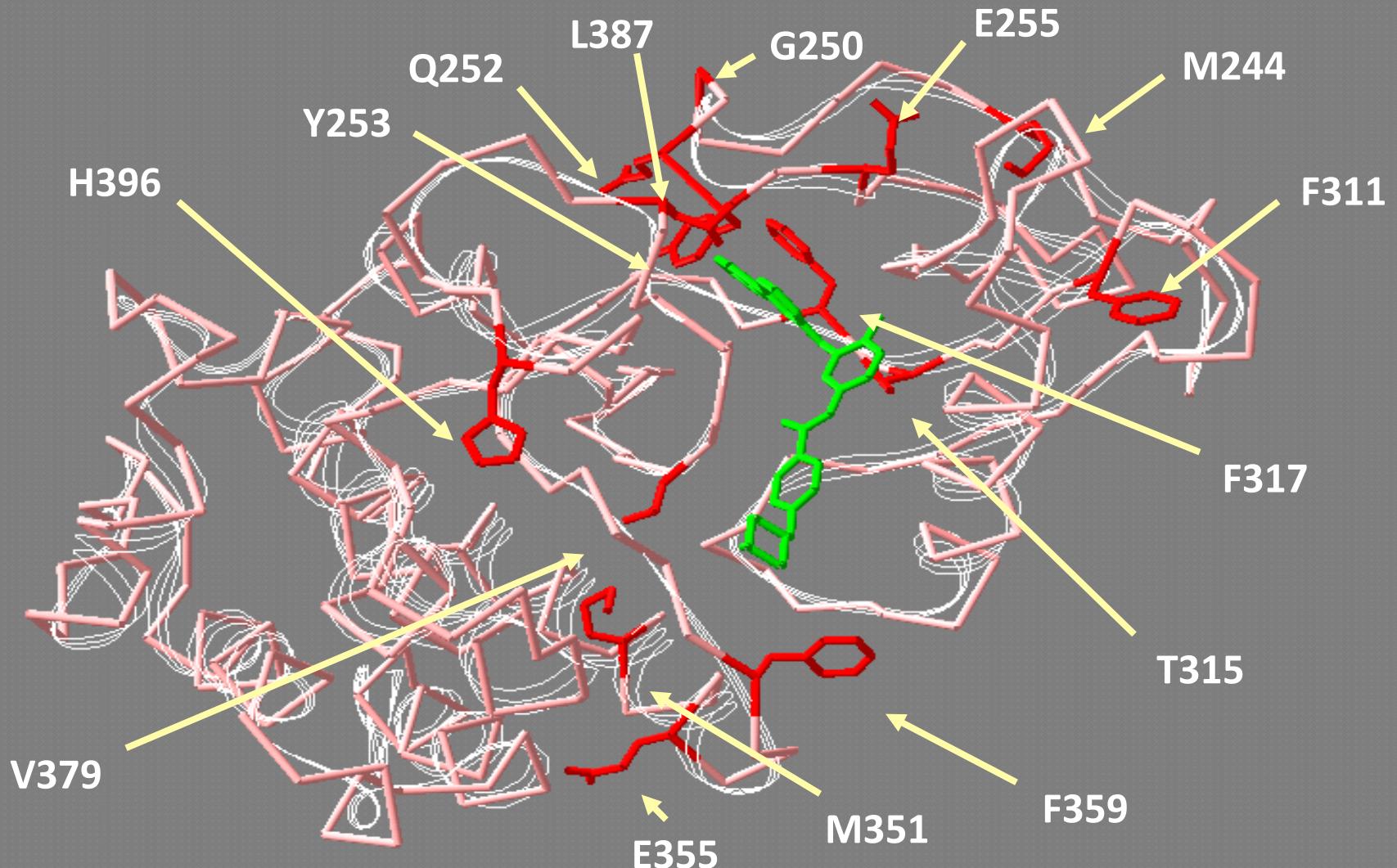
IRIS 8 Years Update: Overall Survival Rate (ITT)



Improved prognosis of CML



Bcr-Abl Punktmutationen: Hauptmechanismus der Imatinib-Resistenz



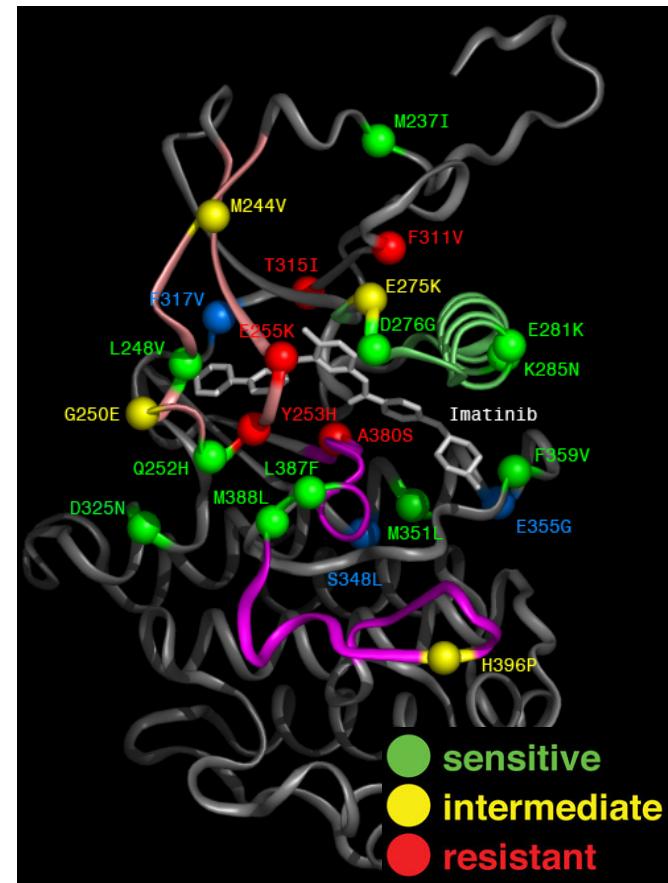
Gorre et al. 2001; von Bubnoff et al. 2002; Branford et al. 2002; Hochhaus et al. 2002; Hofmann et al. 2002; Roche-Lestienne et al. 2002; Shah et al. 2002

Novel BCR-ABL kinase inhibitors suppress all known imatinib resistant mutants

Mutation	Imatinib	Sprycel Dasatinib	Tasigna Nilotinib	SKI-606	INNO-406 NS-187	MK-0457 VX-680
G250E	✗	✓	✓	✓	✓	?
Y253F	✗	✓	✓	✓	✓	✓
Y253H	✗	✓	✓	✓	✗	?
E255K	✗	✓	✓	✓	✓	✓
E255V	✗	✓	✓	✓	✓	?
T315I	✗	✗	✗	✗	✗	✓
H396P	✗	✓	✓	✓	✓	✓

Gorre et al. Science 2001; von Bubnoff et al. Lancet 2002; Weisberg et al. Cancer Cell 2005; Shah et al. Science 2004; Golas et al. Cancer Research 2003; Soverini et al. EHA 2006; Kimura et al. Blood 2005; Tao et al. ASH 2006 #2179; Carter et al. PNAS 2005

Prediction of Resistance Pattern in Advance of Clinical Application?



imatinib



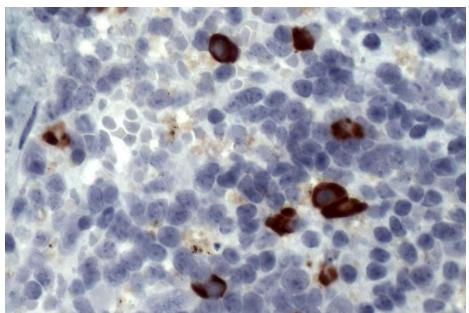
compound I



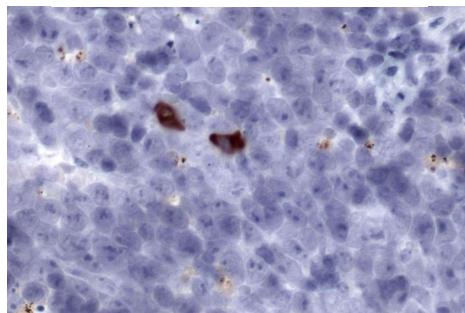
compound II

Persistence of CML Progenitors (LSC?) in CML Mouse Model

untreated



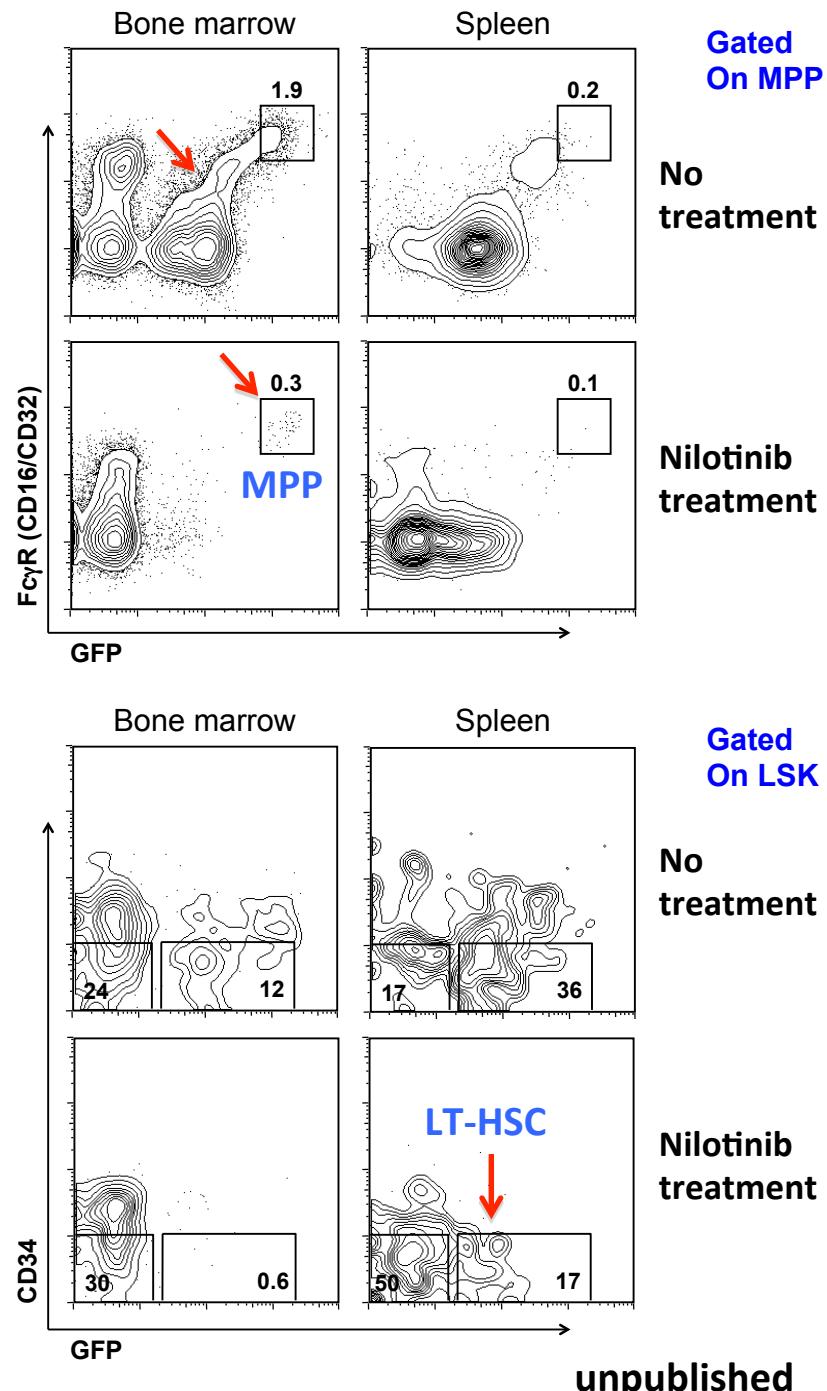
treated



Milz

A high-magnification micrograph of a tissue sample. The field is densely packed with small lymphoid cells, characterized by their dark, granular nuclei. Interspersed among these are several larger, more prominent cells, which are identified as Reed-Sternberg cells. These larger cells have large, pale, non-granular cytoplasmic areas and distinct, dark, nucleoli. The overall pattern is diagnostic of Hodgkin's lymphoma.

GFP-IHC

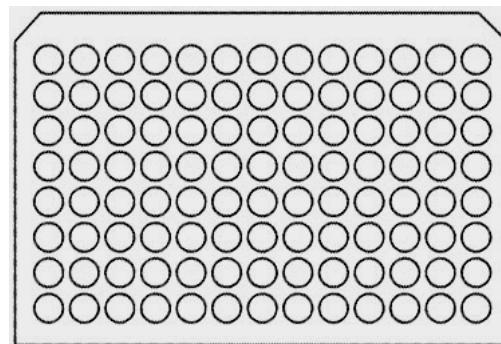


Zelllinien-basierte Methode zur Vorhersage von Resistenzmutationen gegenüber therapeutisch eingesetzten Kinaseinhibitoren

Ba/F3
Bcr-Abl

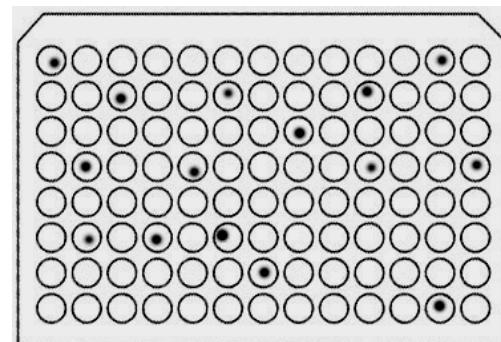
↓
Flüssigkultur
96-Lochplatte

Zugabe von
Inhibitor

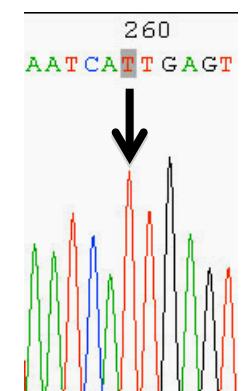
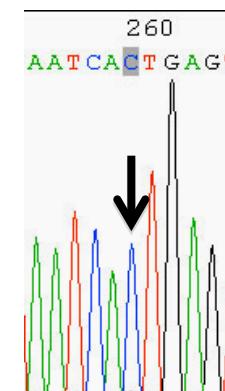


8-42 Tage
↓

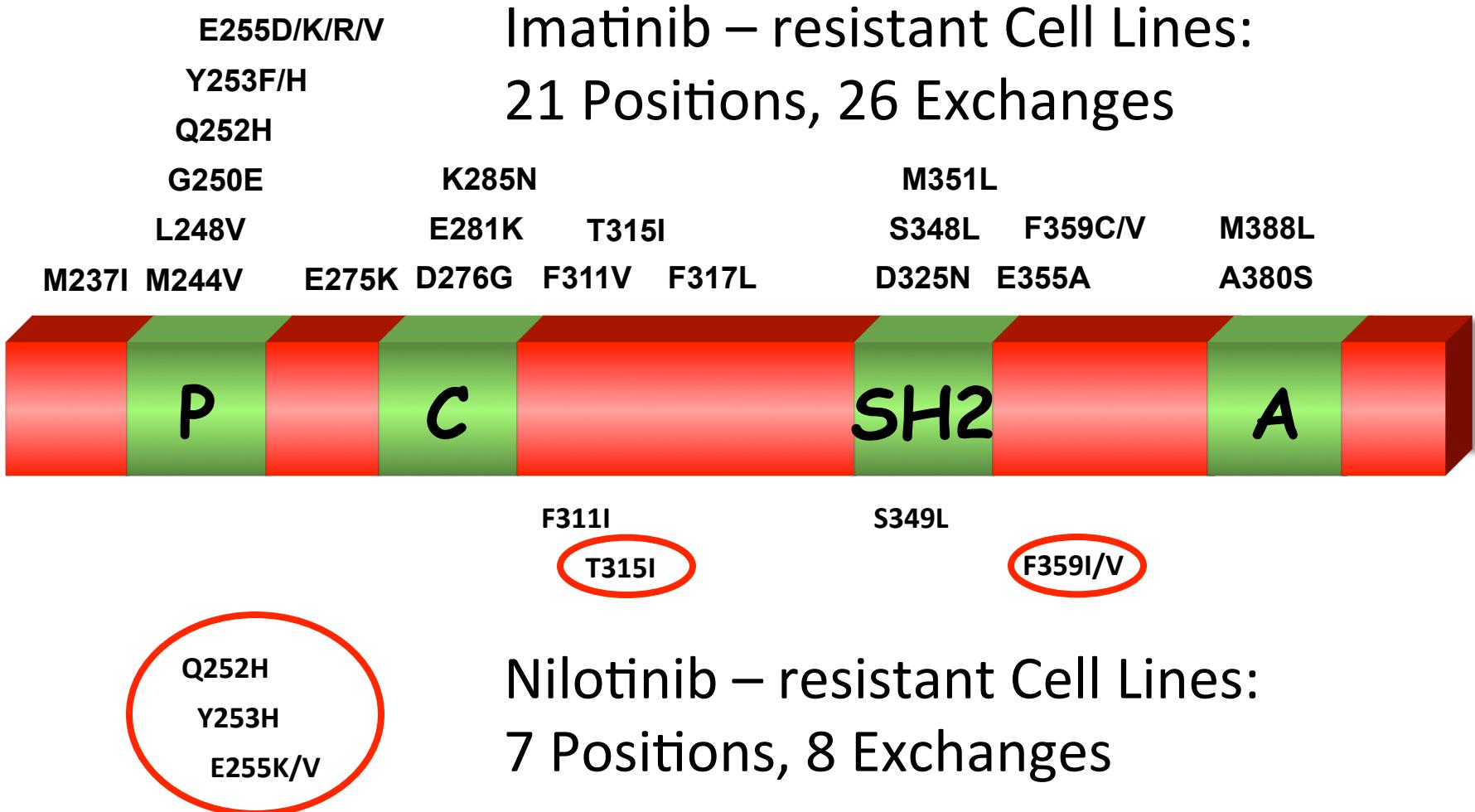
Resistente
Klone



Sequenzieren
Abl Kinasedomäne



CML: Bcr-Abl Resistance Spectrum



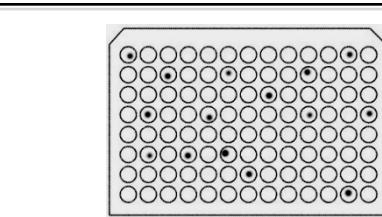
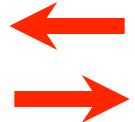
Nilotinib Efficacy According to Baseline BCR-ABL Mutations in CML-CP

Type of Newly Detectable Mutation During Nilotinib Therapy	
Imatinib-Resistant Patients	N = 202 n (%)
E255K/V	13 (6)
T315I	13 (6)
F359C/V	9 (4)
G250E	7 (3)
Y253H	7 (3)

* Patients with multiple mutations are counted in each category

Mechanismen der Behandlungsresistenz und Transformation bei malignen Erkrankungen

Klinische
Phase I/II
Studie



in vitro

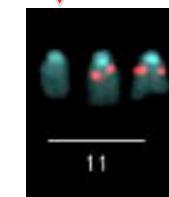
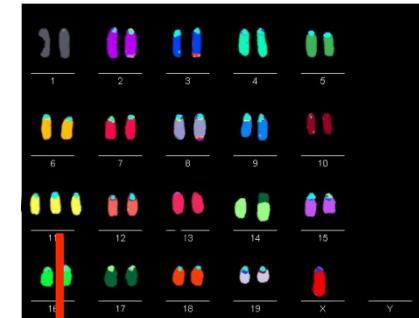
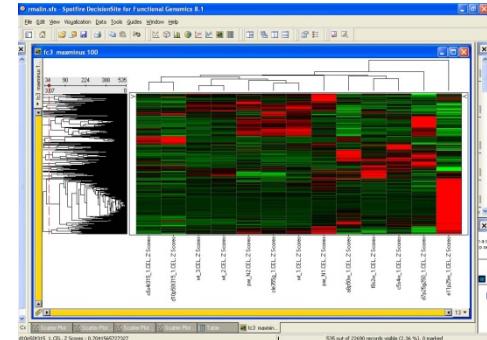
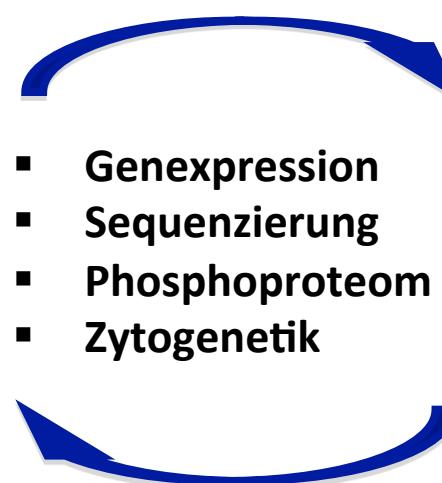


Maus-
modell

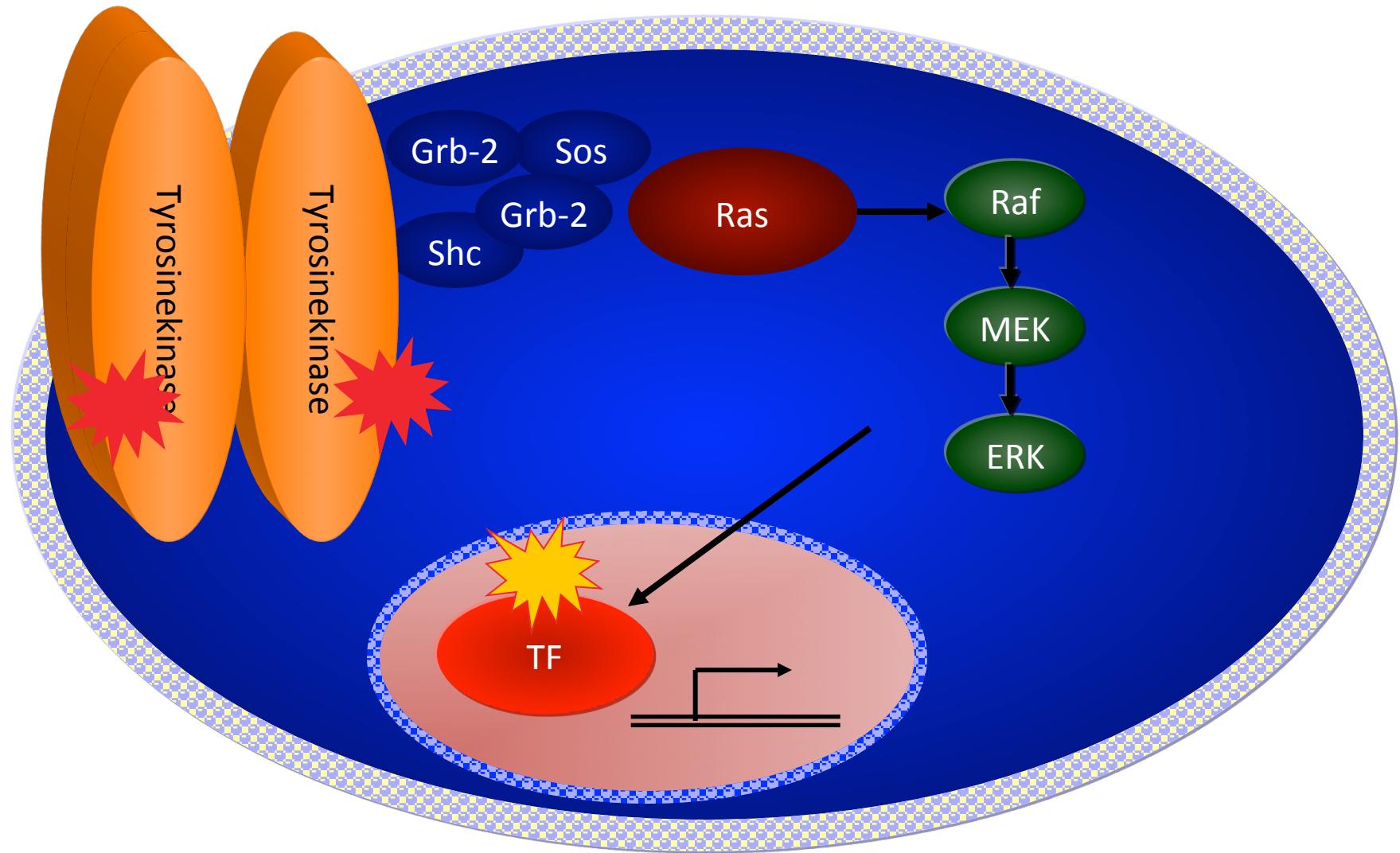


Klinische
Samples

- Genexpression
- Sequenzierung
- Phosphoproteom
- Zytogenetik

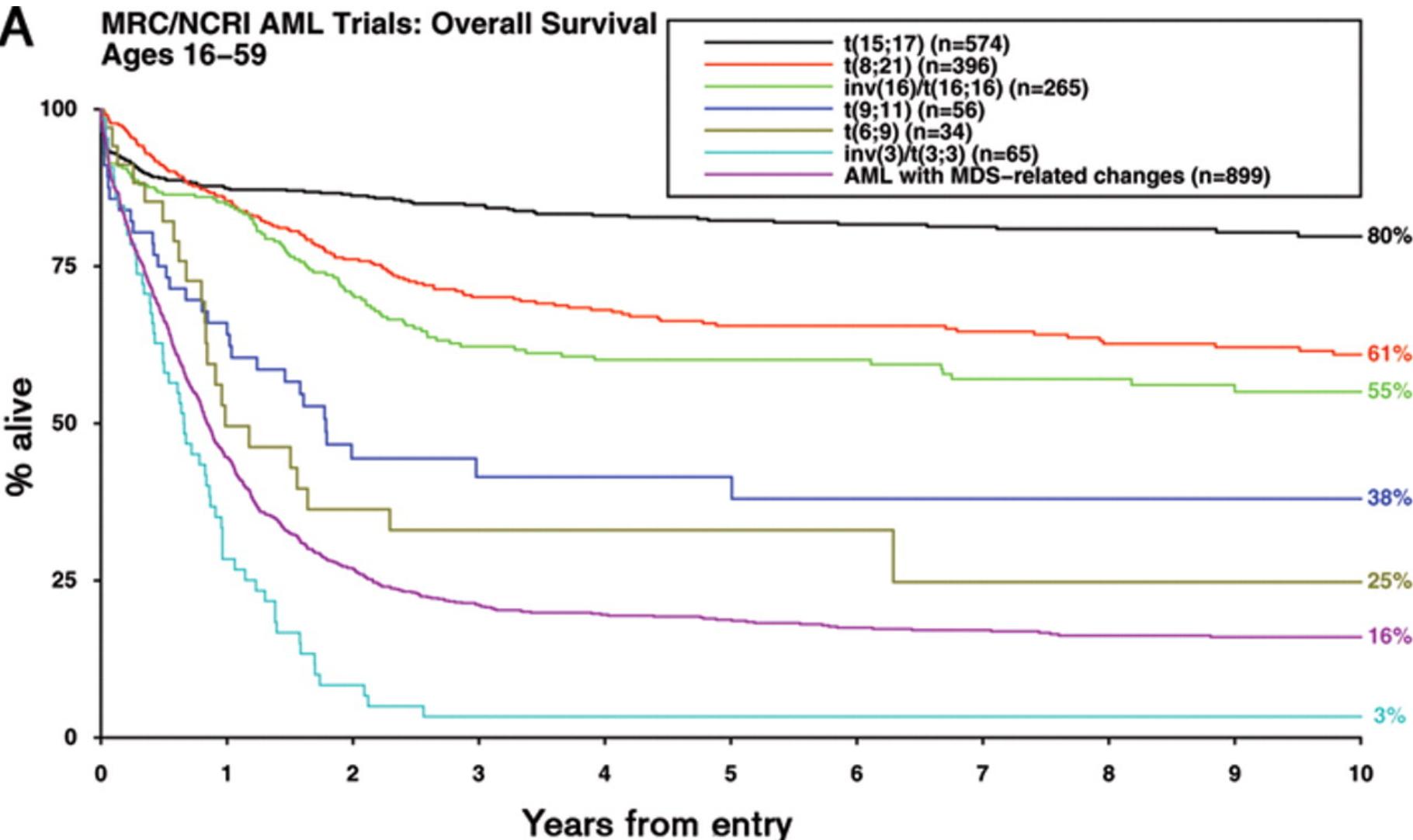


Oncogenic Mechanisms in Acute Myeloid Leukemia

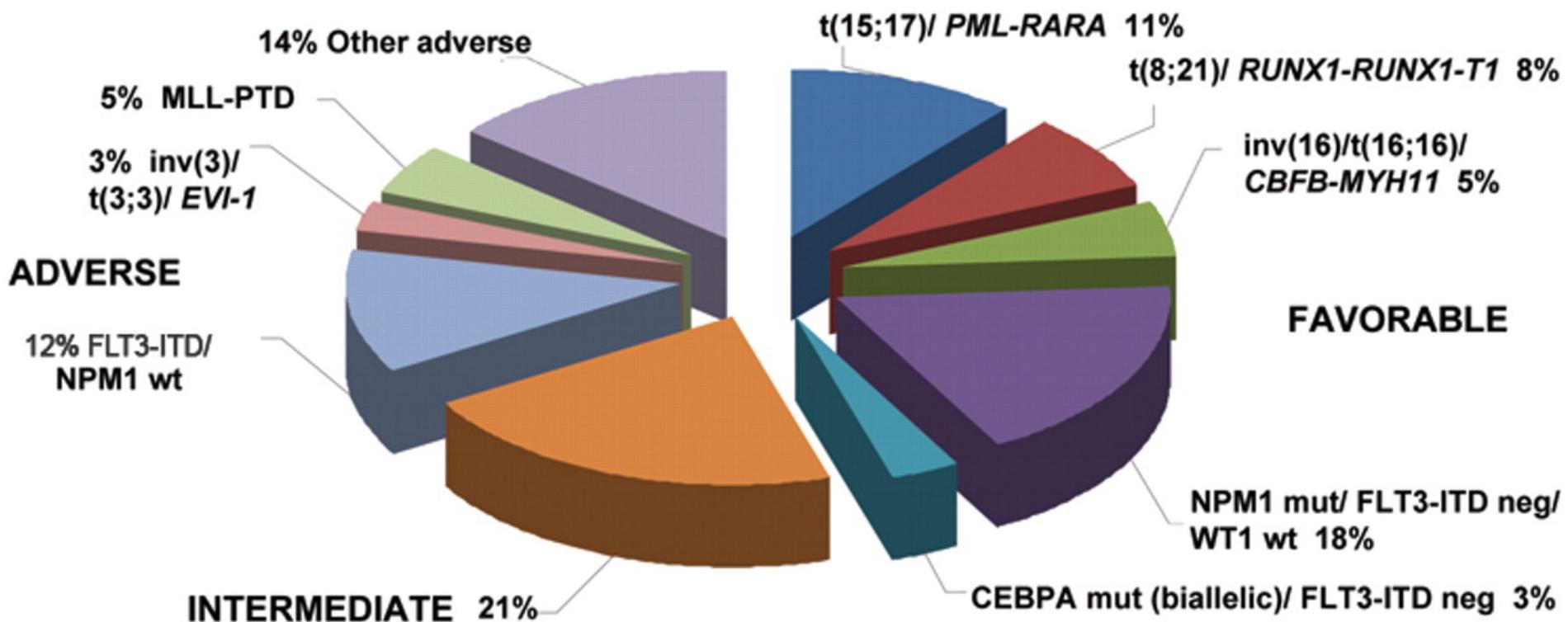


Impact of karyotype on outcome in younger adults with AML

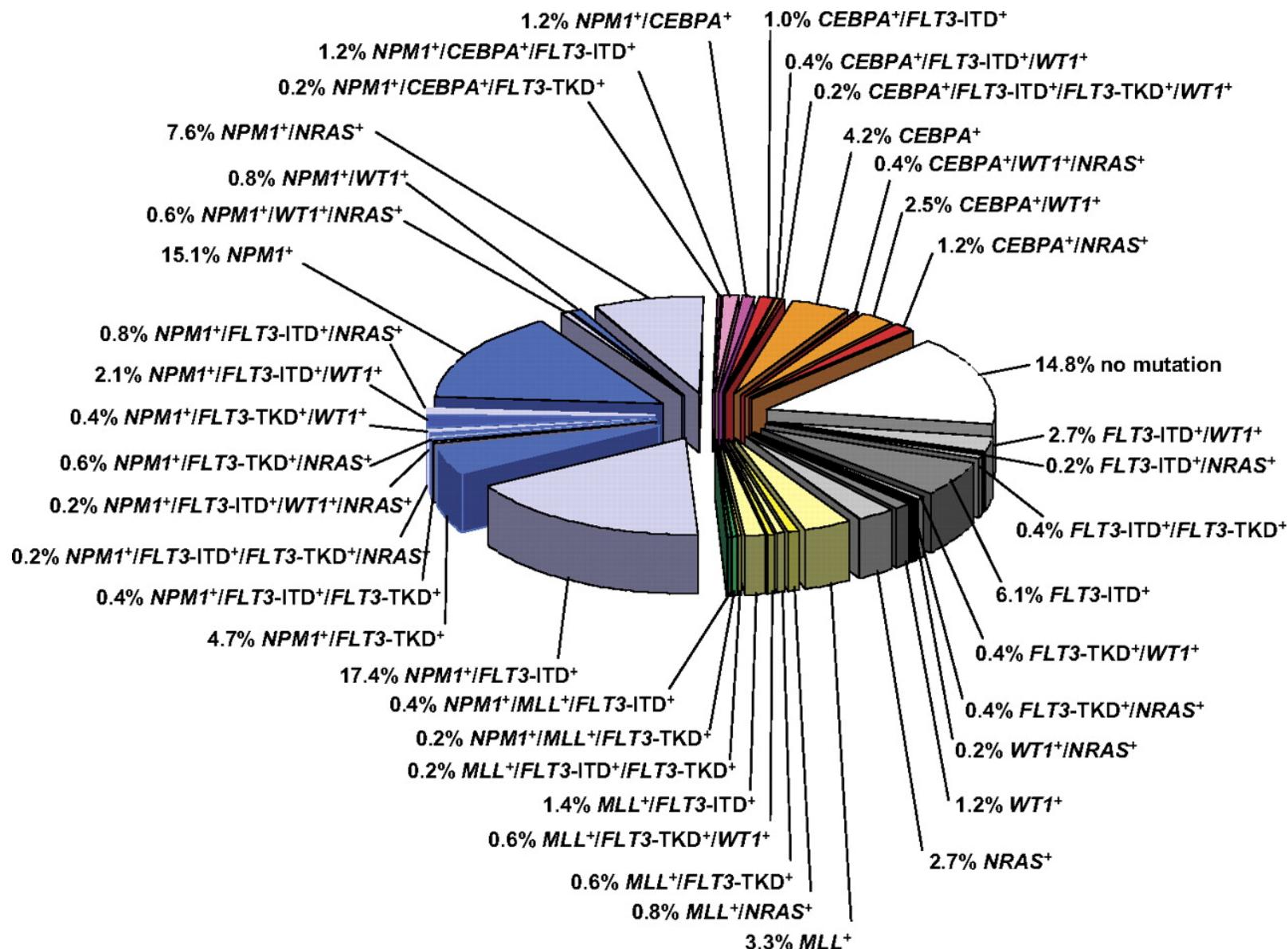
A



Frequency of prognostically relevant molecular and cytogenetic subgroups of AML arising in younger adults

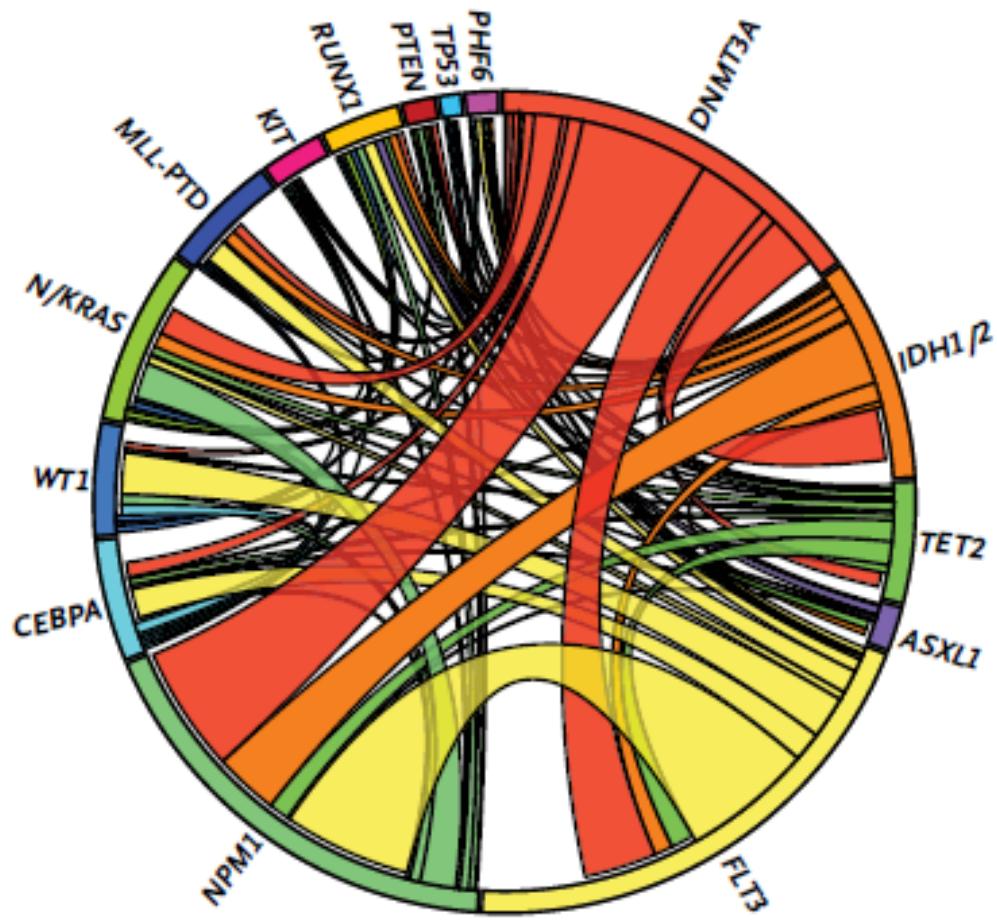


Pie chart illustrating the molecular heterogeneity of cytogenetically normal AML based on mutations in the NPM1, CEBPA, MLL, FLT3 (ITD and TKD mutations at codons D835 and I836), NRAS, and WT1 genes



Mutational Complexity of Acute Myeloid Leukemia (AML)

A Total Cohort



Gene	Overall Frequency (%)
FLT3 (ITD, TKD)	37 (30, 7)
NPM1	29
DNMT3A	23
NRAS	10
CEBPA	9
TET2	8
WT1	8
IDH2	8
IDH1	7
KIT	6
RUNX1	5
MLL-PTD	5
ASXL1	3
PHF6	3
KRAS	2
PTEN	2
TP53	2
HRAS	0
EZH2	0

Mutational Complexity of AML

- Molecular profiling of AML led to significant advances in pathobiology
- Definition of prognostically relevant subgroups of AML patients
- Current therapeutic strategy still based on conventional chemotherapy and stem cell transplantation in high risk patients
- Multiple potentially druggable targets in small subpopulations
- Disappointing results of early clinical trials using single targeting agents
- Clinical trials with optimized compounds and in combination are in progress

Targeted Anticancer Therapies (Solid Tumors)

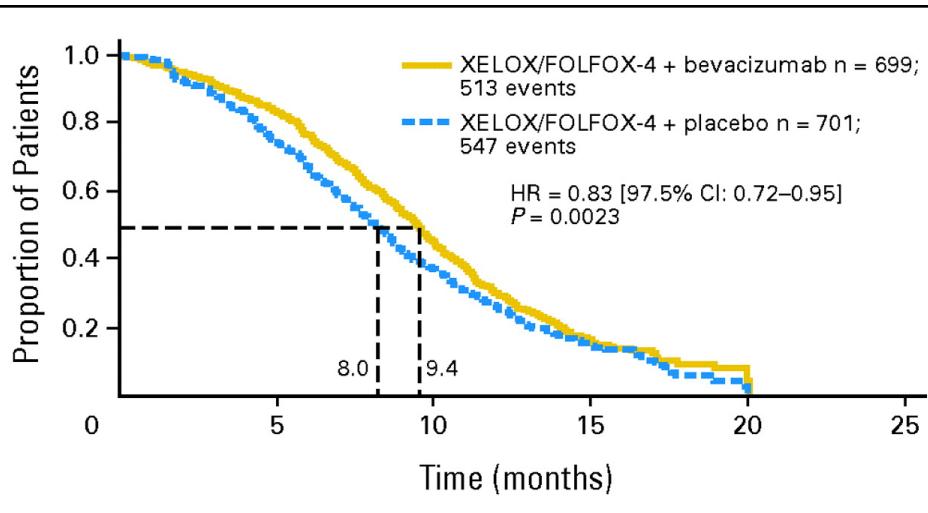
- Molecular defined subpopulations:
 - HER2: Trastuzumab, Lapatinib and breast cancer, gastric cancer
 - EGFR: Erlotinib, Gefitinib in non-small cell lung cancer (activating EGFR-mutations)
 - Crizotinib and NSCLC (alk-translocation)
 - Vemurafenib and melanoma (b-raf mutation)
 - PARP inhibitors and BRCA mutations
- Targeting more common oncogenic mechanisms:
 - Cetuximab and CRC, SCCHN, NSCLC
 - Bevacizumab mCRC, ovarian cancer
 - Ipilimumab and melanoma
 - PI3K and mTOR inhibitors

Well established targeted therapies and associated costs

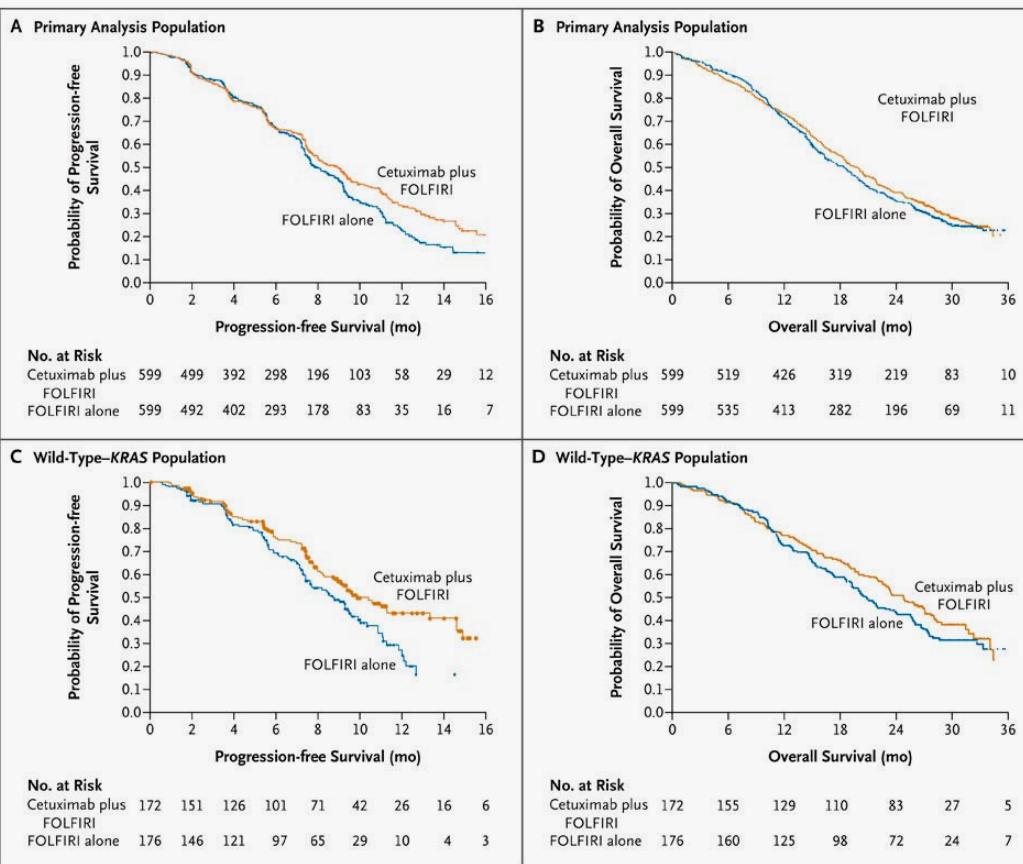
Drug	Approximate cost per QALY
Trastuzumab	\$ 50,000 – 70,000 in metastatic breast cancer
Bevacizumab	\$ 100,000 in mCRC; 50,000 in NSCLC
Erlotinib	\$ 37,000 in NSCLC
Sunitinib	\$ 50,000 in mRCC
Rituximab	\$ 50,000 in NHL
Imatinib	\$ 45,000 in CML

Predictive Biomarkers

- **Prognostication of therapeutic success**
- **Negative predictive markers**
 - Primary resistance
- **Mechanisms of secondary resistance**
 - Inhibition of drug binding/ interaction
 - Activation of alternative signaling pathways



Targeted Therapy (a-VEGF, a-EGFR) in Colorectal Carcinoma

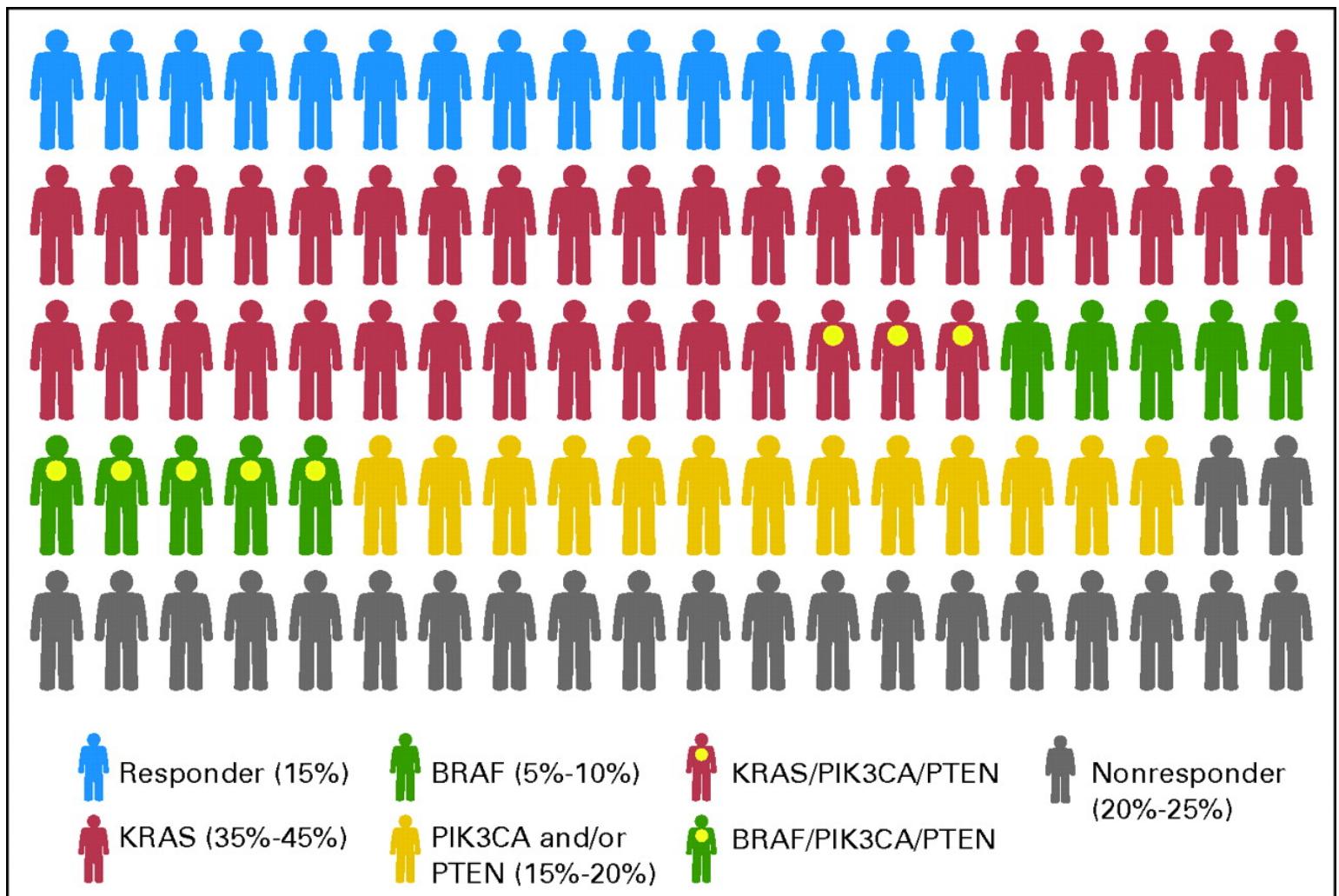


Predictive biomarkers:

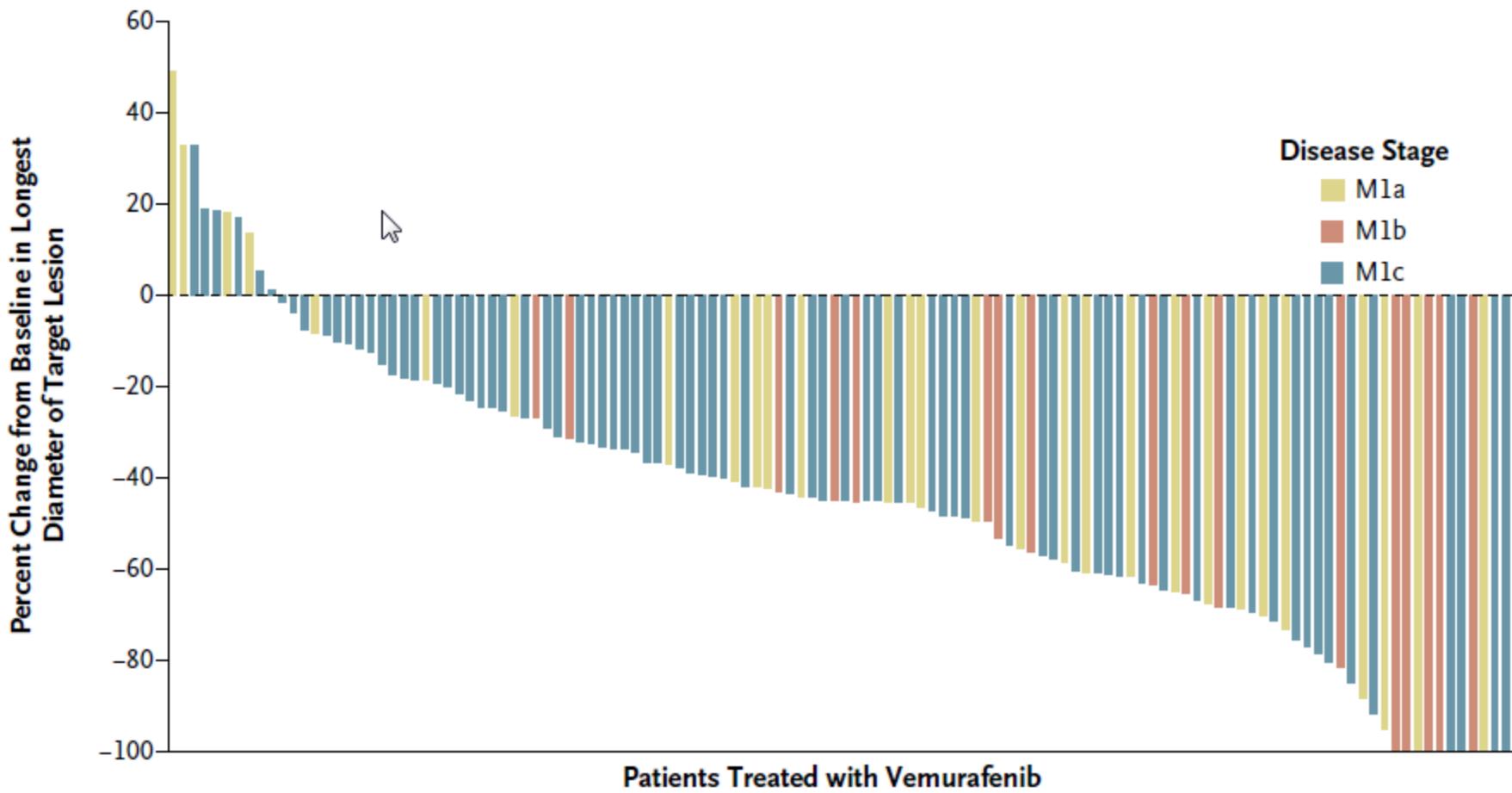
For antiangiogenetic therapy not available

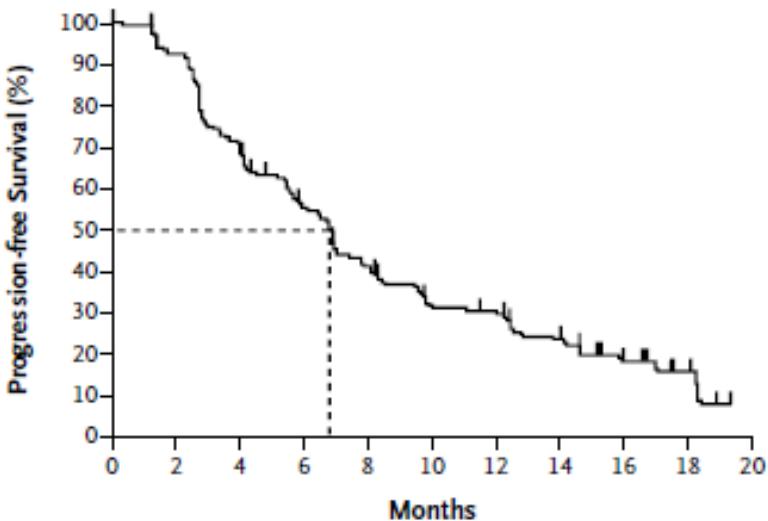
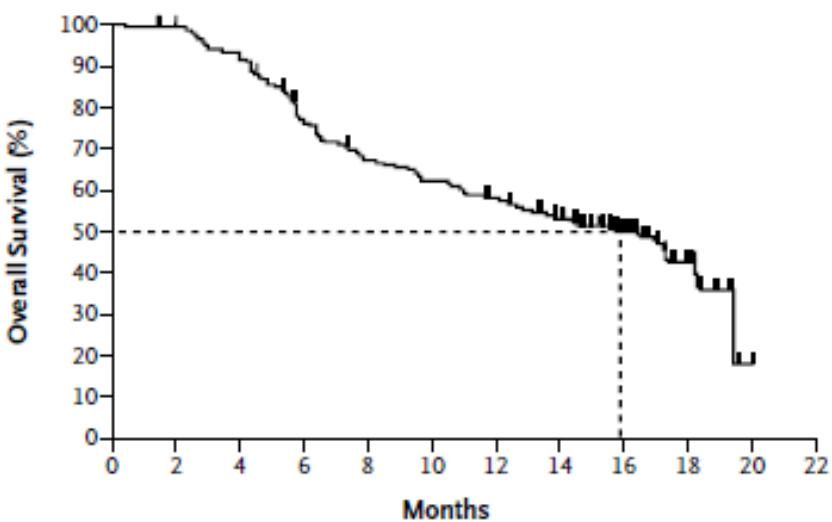
For anti-EGFR therapy only negative prediction for k-ras mutation

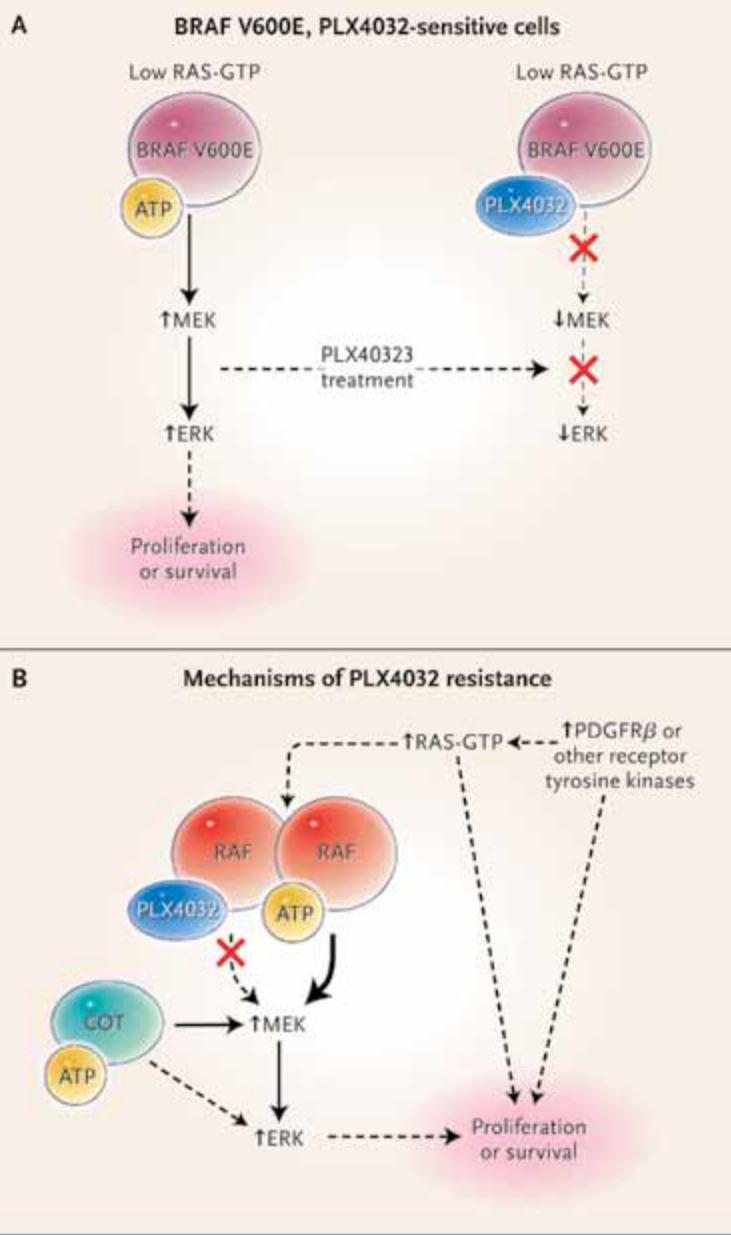
Graphic representation of a cohort of 100 patients with colorectal cancer treated with cetuximab or panitumumab



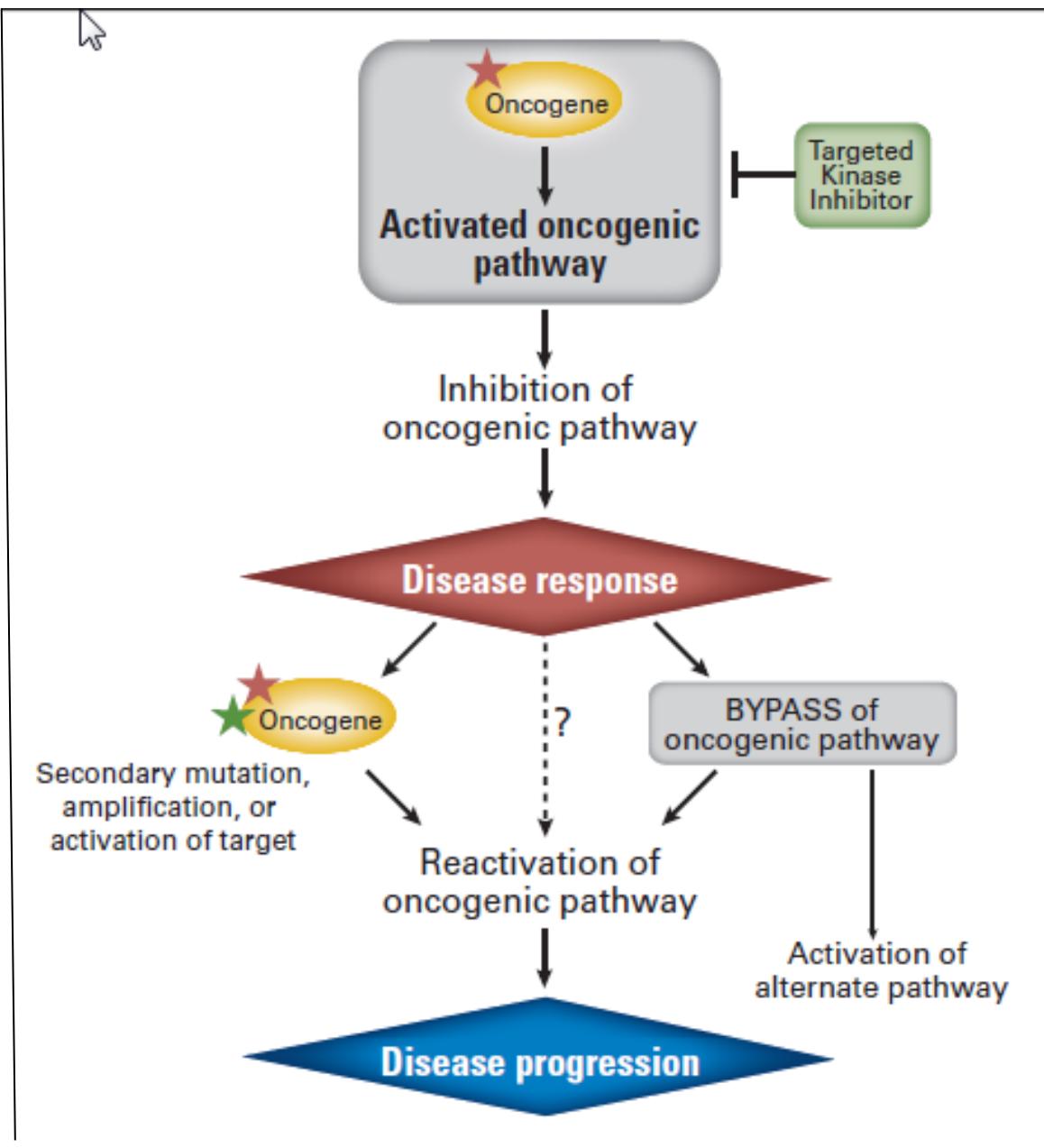
Targeted Therapy (Vemurafenib) in Malignant Melanoma (B-RAF Mutated)



A**B**



Novel Mechanism of Resistance against Vemurafenib in braf mutated malignant melanoma



Cancer Genomics – Promises and Limitations

Technology

- **Whole Genome Sequencing**
 - First generation (Sanger) sequencing
 - Read lengths of up to 1,000 base pairs
 - Resulted in completion of the Human Genome Project (\$ 2billion, took a decade to complete)
 - Limitations: High cost and low throughput
 - Next generation sequencing
 - Improved cost and throughput
 - Short read length
 - Significant data storage and interpretation requirements
 - Third generation sequencing technologies
 - High accuracy, run time is short, potentially allowing for real time clinical application
 - \$1000 genome sequencing within reach

Cancer Genomics – Promises and Limitations

Technology

- Targeted genome sequencing
 - Whole exome sequencing
 - Cancer genome (genes potentially involved in tumor biology)
 - Increased coverage of areas of interest
- Cancer genotyping
 - Mutation genotyping (recurrent mutations involved in certain cancer types)
 - SNP genotyping
 - High-throughput genotyping platforms, consisting of multiplexed assays and microarrays
 - Limited to known genetic alterations
- Bioinformatics

Cancer Genomics – Promises and Limitations

Discovery

- Sequenced cancer genomes
 - Discovery of new, clinically relevant mutations
- Epigenetic aberration in cancer
- Gene expression signatures, microRNA profiling
- Only minority of point mutations in exomes (0.6 %)
- Driver versus passenger mutations
- Identification of rare mutations requires hundreds of samples to be sequenced
- Functional validation in tissue cultures or model organisms

Cancer Genomics – Promises and Limitations

Translation/ Molecular Profiling

- Ultimate goal of personalized cancer medicine: Real-time MP of individual tumor samples enables matching of the identified mutational profile with targeted therapy
- Von Hoff et al: modest increase of PFS (1.3 times greater)
- Validation of potential predictors of efficacy
- Focus on oncogenes, tumor suppressor genes and genomic stability genes
- Should include drug metabolism (pharmacogenomics)
- Profiling archival versus current tumor samples (longitudinal changes of MP)
- Separation of tumor versus tumor stroma
- Heterogeneity of tumor genome in individual patients (primary tissue versus metastases, intratumor heterogeneity)

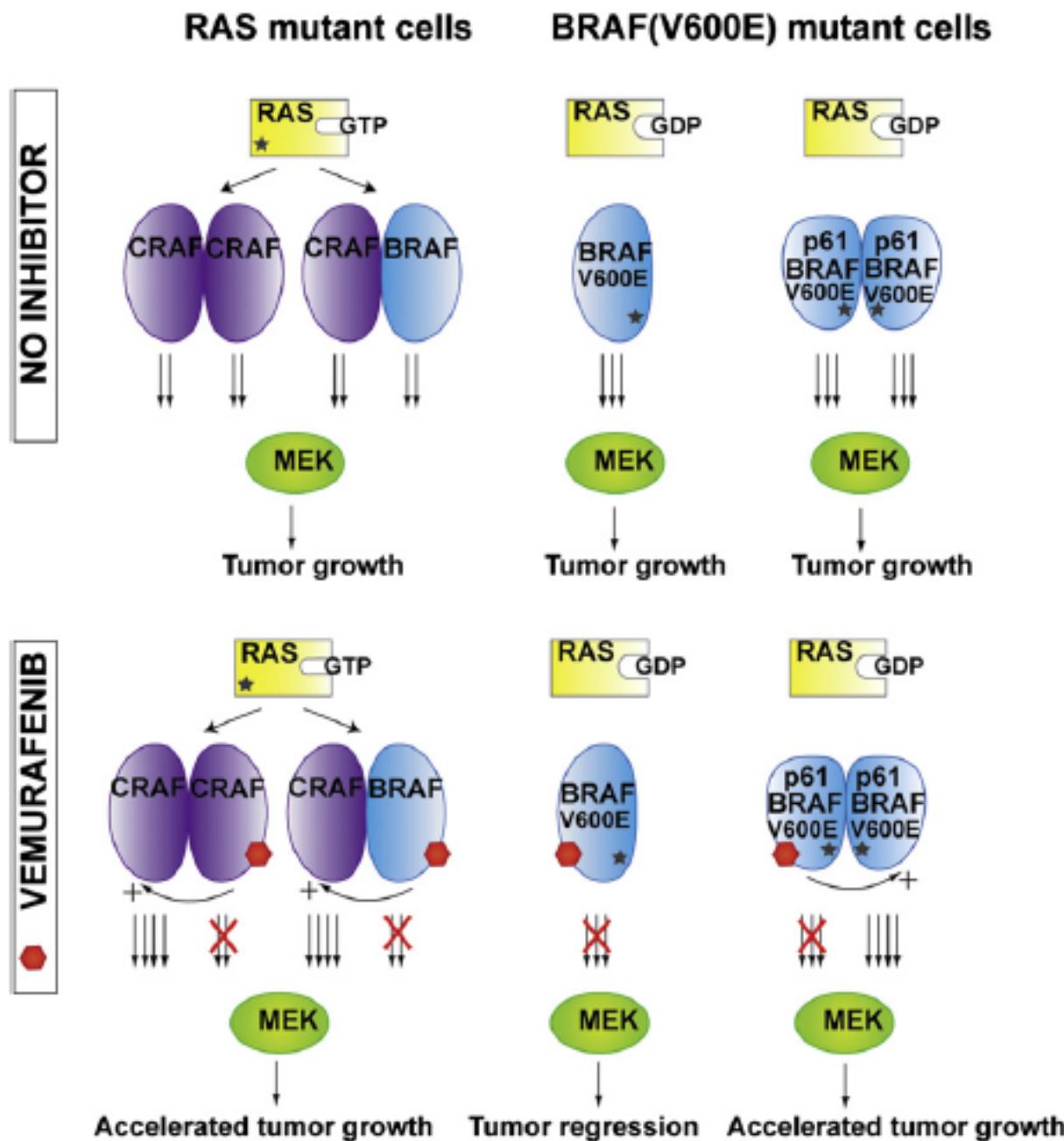
Conclusion

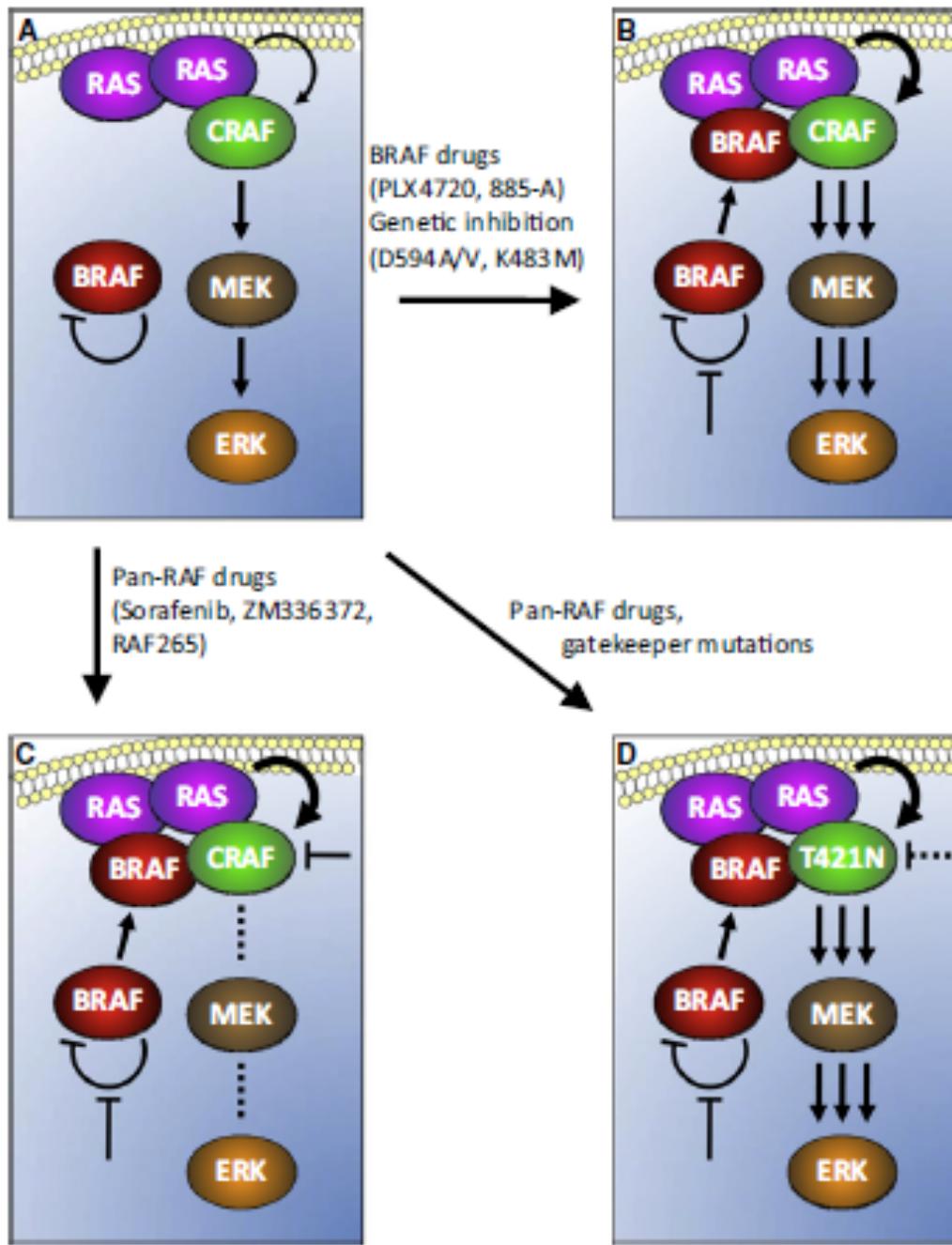
- Potential impact of cancer genomics is enormous
- Technology advances and cost reduction make personalized cancer medicine potentially feasible
- Bioinformatics, data integration and quality control essential
- Challenges must be recognized and addressed
- Benefit of PCM versus current standard approach of cancer therapy must be validated in clinical trials
- Improvement of quality of life and cost effectiveness must be considered

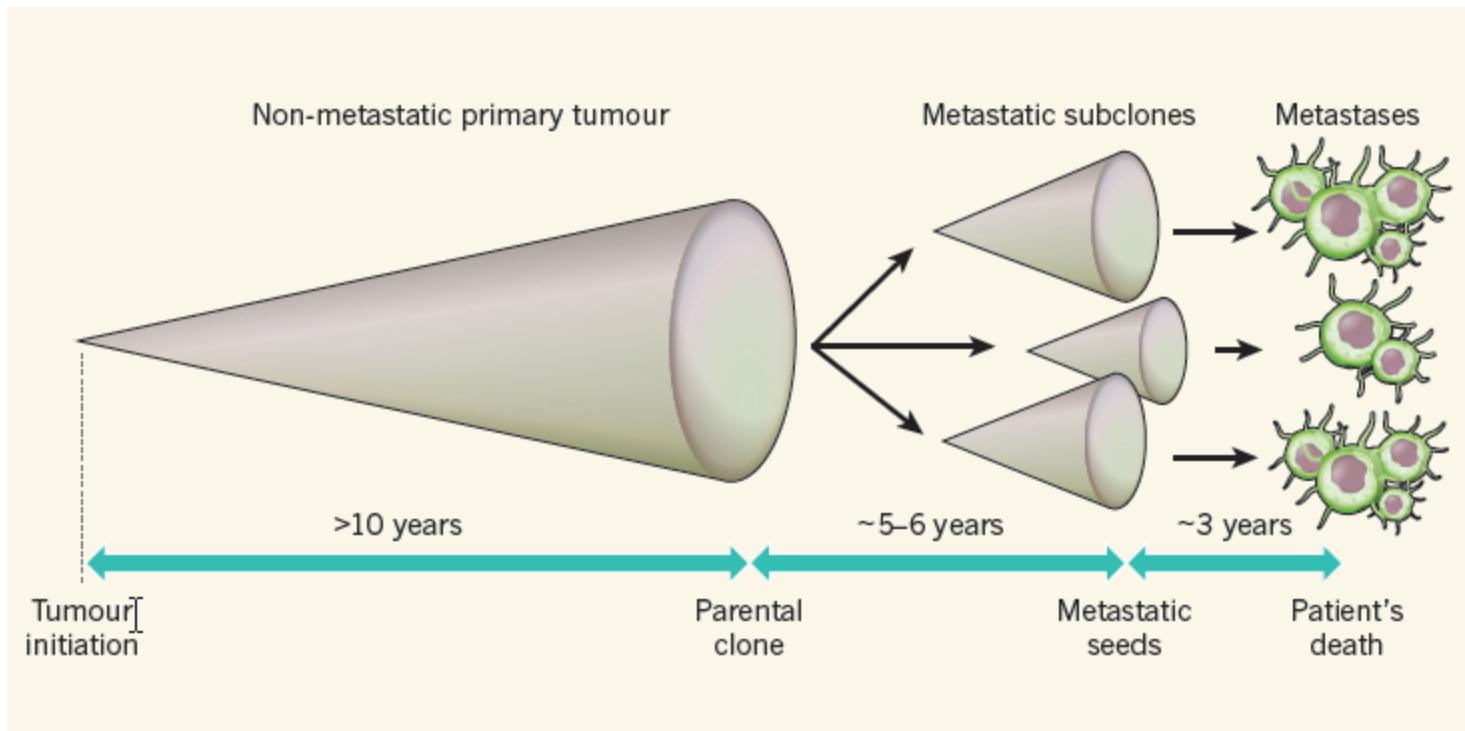
Thank you for your attention!

Table 2. Exemplary Mechanisms of Acquired Resistance to Kinase Inhibitors

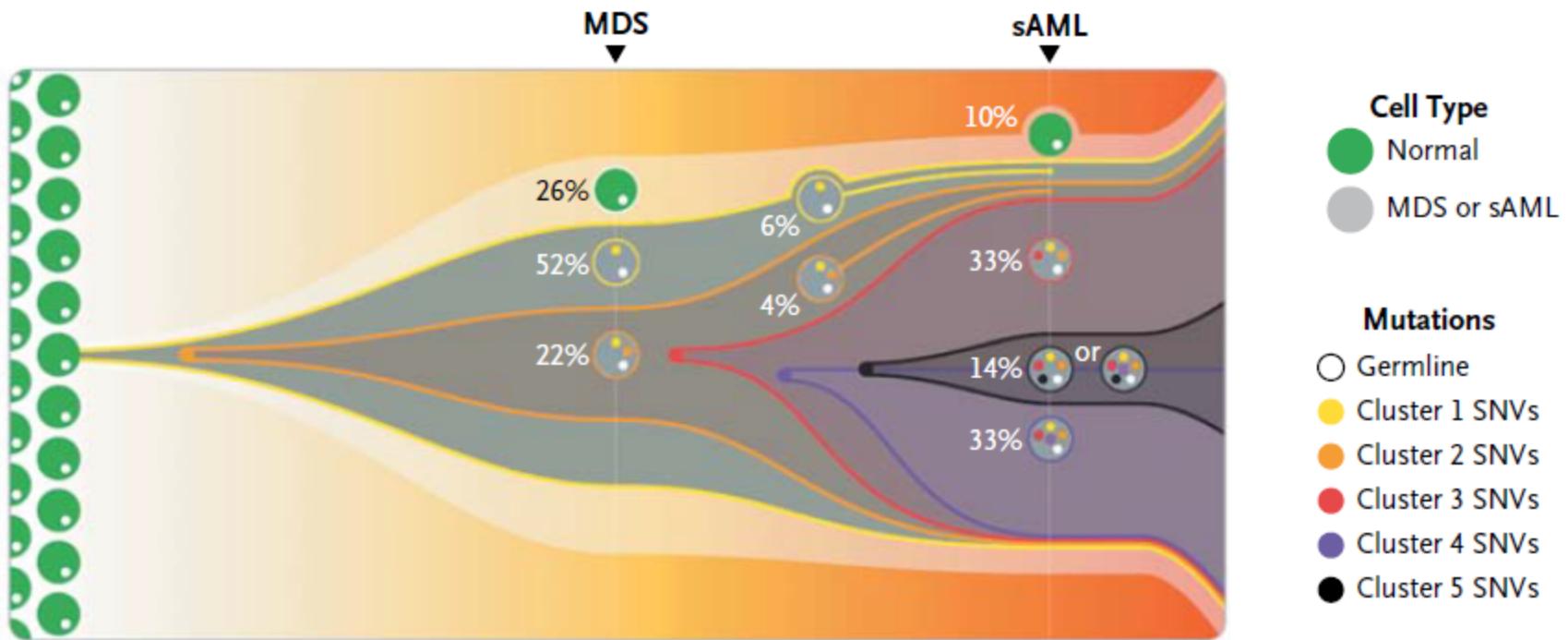
Targeted Agent	Target Gene	Acquired Resistance via Secondary Mutation, Amplification, or Activation of Target	Acquired Resistance via Bypass	Acquired Resistance via Downstream Mutation
Imatinib	<i>ABL</i>	T315I	<i>IGF1R</i> amplification	
		Y253F/H	AXL overexpression*†	
		E255K/V		
		<i>ABL</i> amplification		
Gefitinib or erlotinib	<i>EGFR</i>	T670I		
		V654A		
		D816A/G/H/W		
		D820A/E/G/Y		
Trastuzumab	<i>KIT</i>	Y823D		
		<i>KIT</i> amplification		
		T674I		
Lapatinib	<i>HER2</i>	T790M	<i>MET</i> amplification	
		D761Y	HGF overexpression*†	
		L747S	IGFBP3 loss*†	
		T854A		
PKC412	<i>EGFR</i>	<i>EGFR</i> amplification*		
AZD6044	<i>FLT3</i>	N676K		
PLX4032	<i>FGFR</i>			
Crizotinib	<i>MEK1</i>	MEK1 P124L		
		<i>BRAF</i> amplification*		
		NRAS Q61K	COT overexpression†	
			PDGFR β overexpression†	MEK1 C121S
	<i>BRAF</i>		CRAF overexpression†	
			AXL overexpression†	
			HER2 overexpression*†	
	<i>ALK/MET</i>	L1196M		
		C1156Y		
		F1174L		





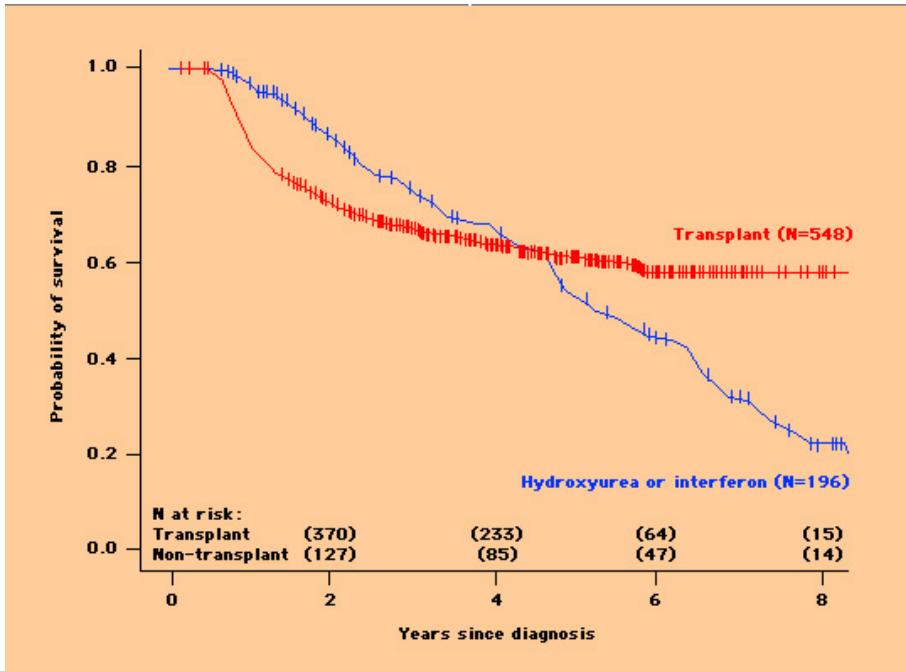


A Clonal Evolution from MDS to sAML

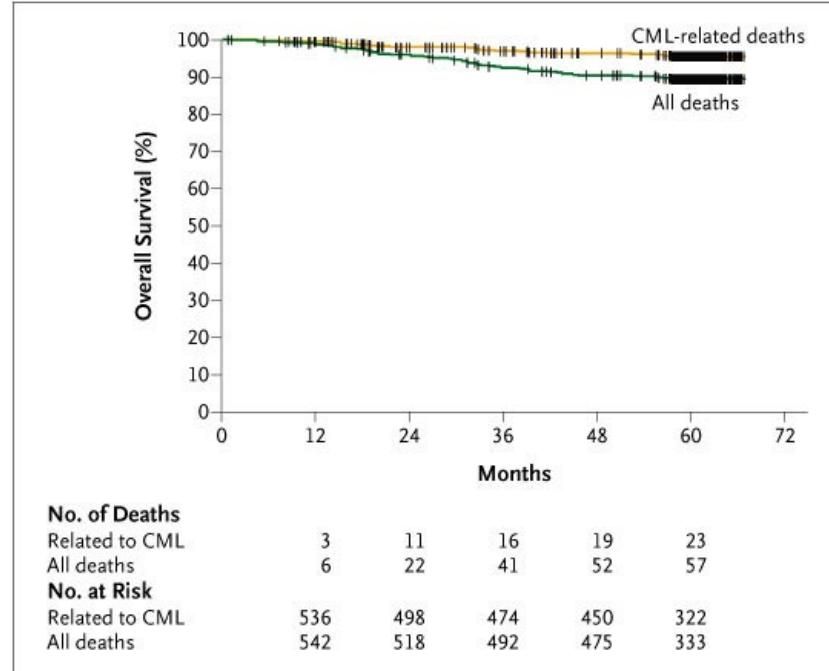


Chronisch myeloische Leukämie Modellerkrankung für „targeted therapy“

Gale et al, 1998



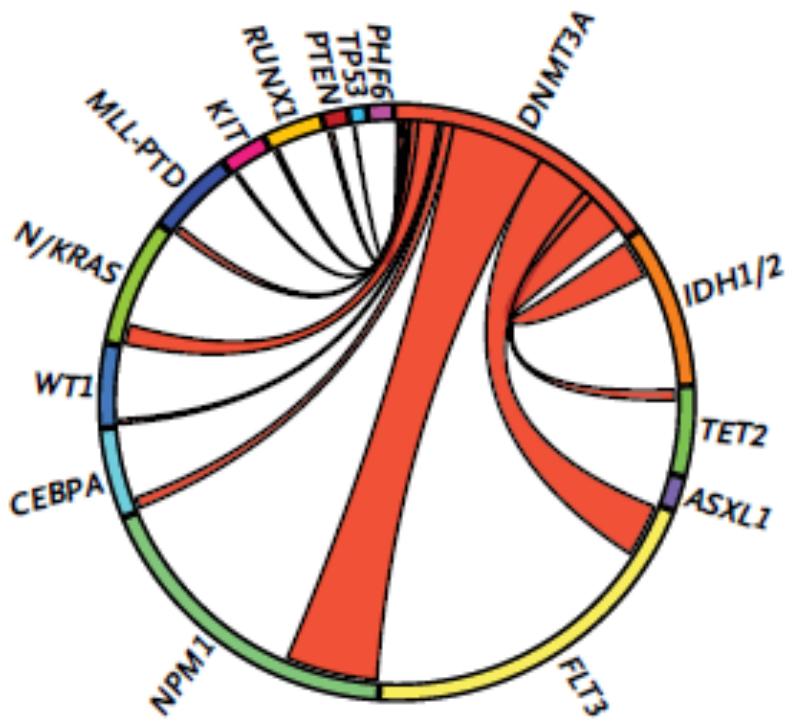
Druker et al, 2006



Molekulare Pathophysiologie:
Monogenetisch t(9;22)
BCR-ABL konstitutiv aktiverter
Signalweg
Ideales Mausmodell

Therapeutische Konsequenz:
TKI als Prototyp der targeted therapy
Biomarker (quant. bcr-abl)
Resistenzmutationen

B Patients with Mutant *DNMT3A*



C Patients with Mutant *FLT3*

