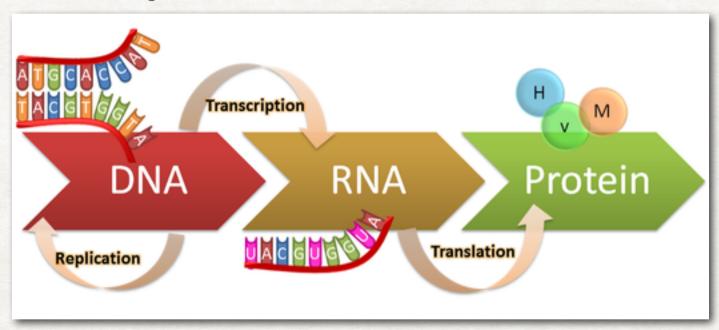
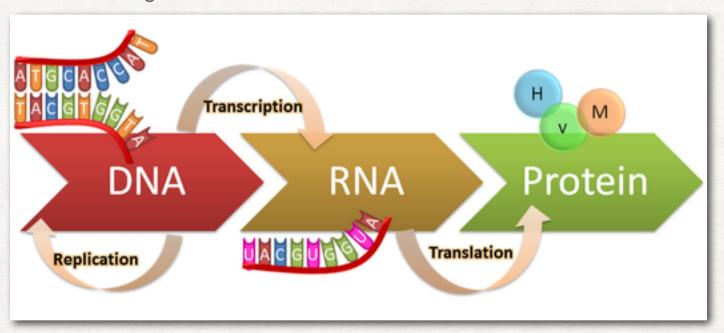
#### The central dogma

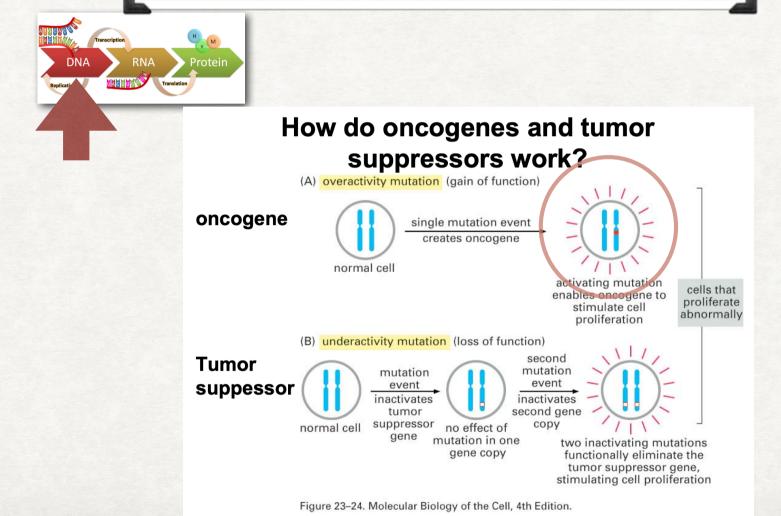


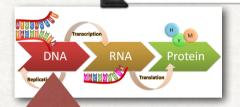
#### The central dogma

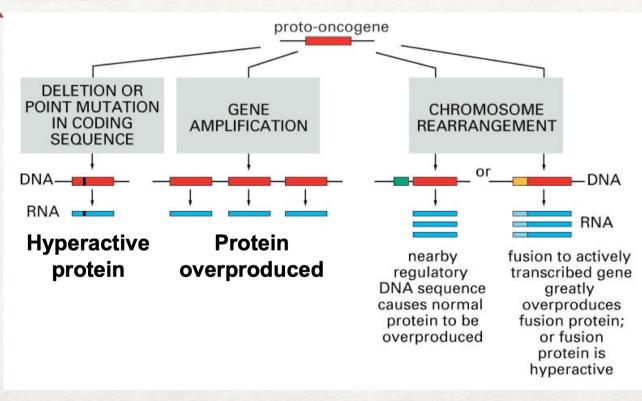


In-situ hybridization
Molecular methods (PCR, SEQ)

Immunohistochemistry







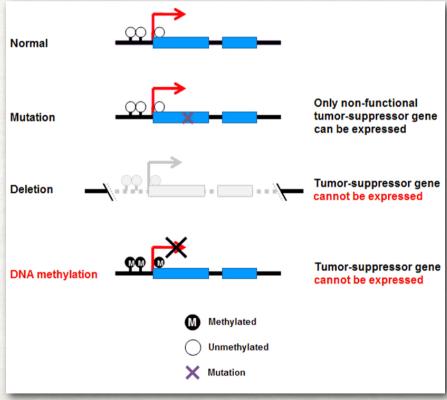


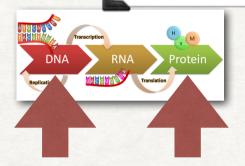
# How do oncogenes and tumor suppressors work?

(A) overactivity mutation (gain of function) oncogene single mutation event creates oncogene normal cell activating mutation cells that enables oncogene to proliferate stimulate cell abnormally proliferation (B) underactivity mutation (loss of function) second **Tumor** mutation mutation event suppessor event inactivates inactivates tumor second gene normal cell suppressor copy no effect of mutation in one two mactivating mutations gene copy functionally eliminate the tumor suppressor gene, stimulating cell proliferation

Figure 23-24. Molecular Biology of the Cell, 4th Edition.







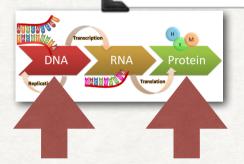
Mutation Changed protein

Translocation Absence of protein

Deletion Abnormal localisation

Amplification Over expression

Methylation Fussion protein



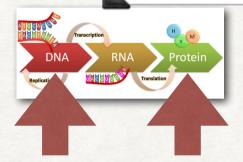
Mutation — Changed protein

Translocation Absence of protein

Deletion Abnormal localisation

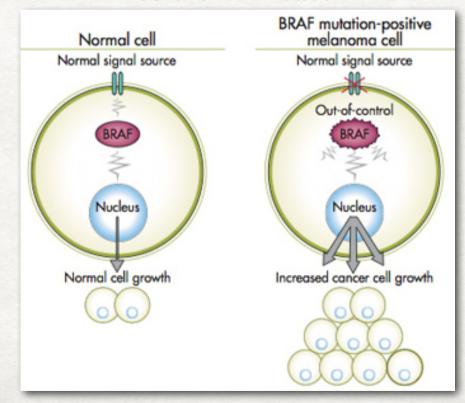
Amplification Over expression

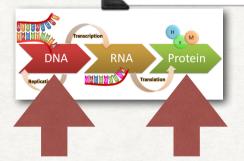
Methylation Fussion protein



Mutated protein (auto activated)

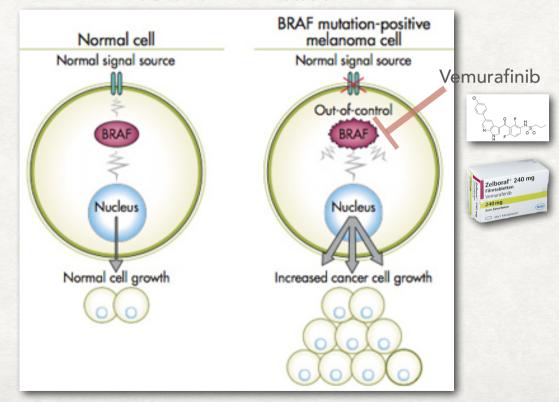
#### Melanoma BRAF mutation

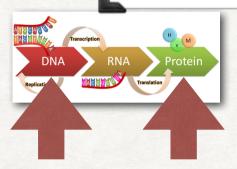




Mutated protein (auto activated)

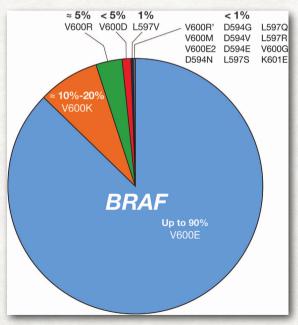
#### Melanoma BRAF mutation





Mutated protein (auto activated)

Melanoma BRAF mutation

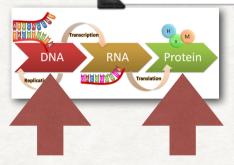


WT: GTG (valin)

V600E: GAG (glutamat)

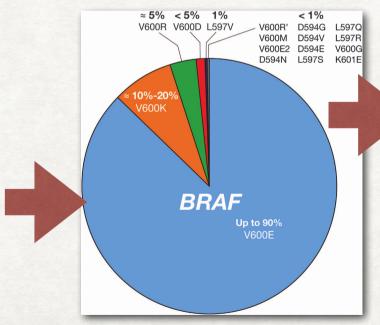
V600K: AAG (lysin)

V600R: AGG (Arginin)



Mutated protein (auto activated)

Melanoma BRAF mutation

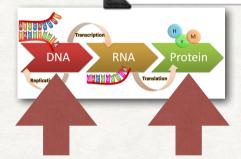


WT: GTG (valin)

V600E: GAG (glutamat)

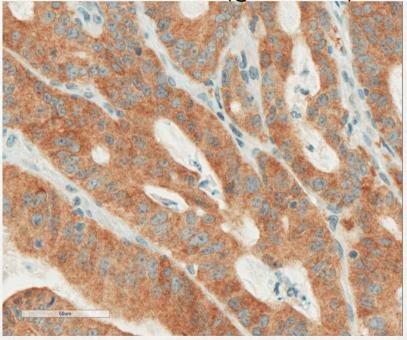
V600K: AAG (lysin)

V600R: AGG (Arginin)



Mutated protein (auto activated)

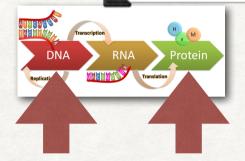
V600E: GAG (glutamat)



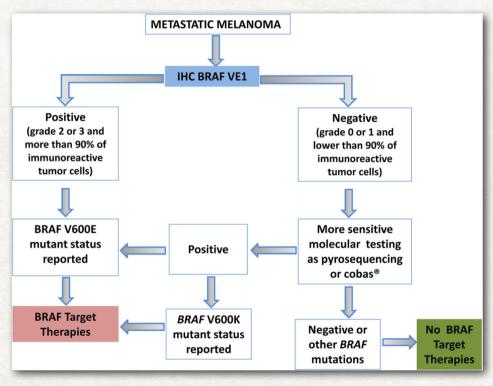
BRAF V600E (VE1)
Mouse Monoclonal Primary Antibode



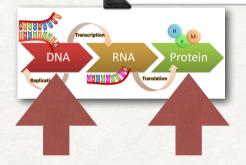




Mutated protein (auto activated)



Schirosi et al. BMC Cancer (2016) 16:905 DOI 10.1186/s12885-016-2951-4



Mutated protein (auto activated)



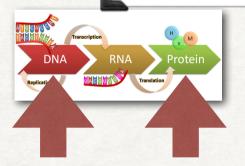
Immunohistochemistry BRAF V600E







Mutation analysis of BRAF gene



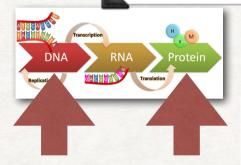
Mutation Changed protein

Translocation Absence of protein

Deletion Abnormal localisation

Amplification Over expression

Methylation Fussion protein

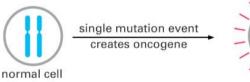


Often combination of Deletion Mutation Methylation

#### How do oncogenes and tumor suppressors work?

(A) overactivity mutation (gain of function)

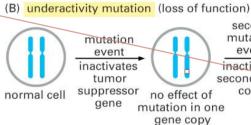
oncogene



activating mutation enables oncogene to stimulate cell proliferation

cells that proliferate abnormally

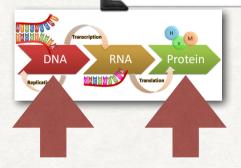
**Tumor** suppessor



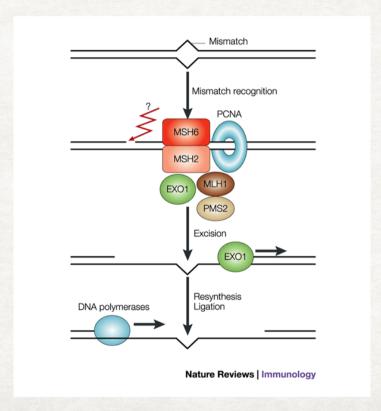
second mutation event inactivates second gene

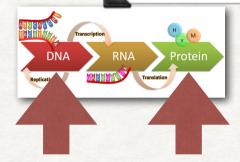
two inactivating mutations functionally eliminate the tumor suppressor gene, stimulating cell proliferation

Figure 23-24. Molecular Biology of the Cell, 4th Edition.



#### Absence of protein



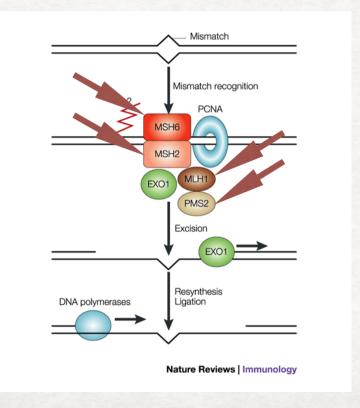


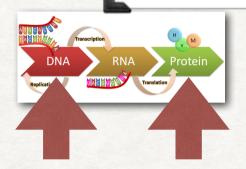
Absence of protein



Mutation (Methylation)

Mismatch Repair deficiency Microsatelite instability

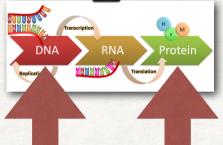




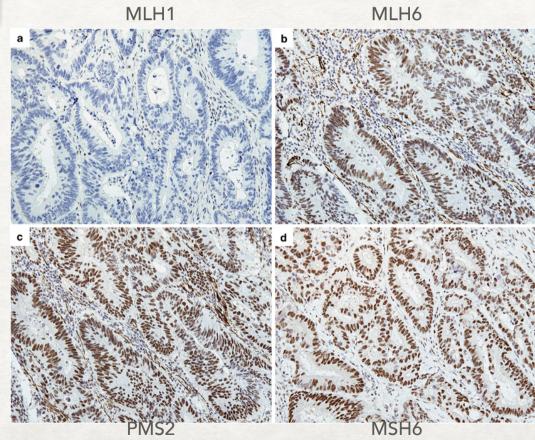
Absence of protein

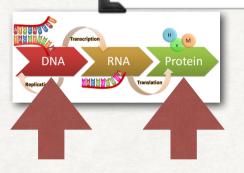
Identify colon cancer patients with inherited colon cancer (Lynch syndrome)

Identify patients with sporadic MSI colon cancers

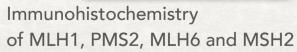


#### Absence of protein





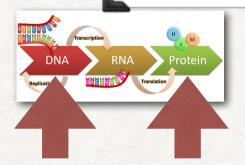








Mutation of MLH1, PMS2, MLH6 and MSH2 genes Measurement of length of Microsatilites



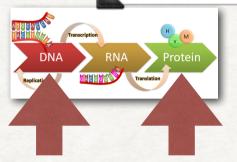
Mutation Changed protein

Translocation Absence of protein

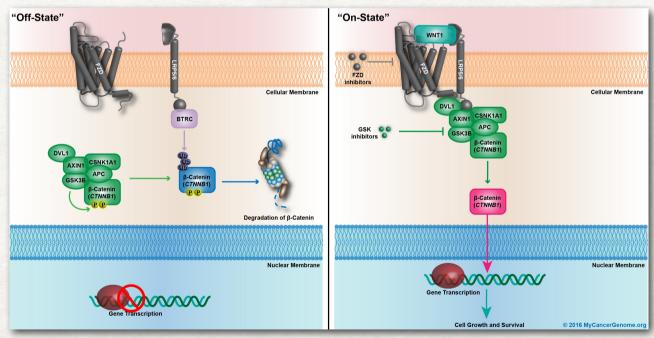
Deletion Abnormal localisation

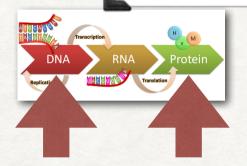
Amplification Over expression

Methylation Fussion protein



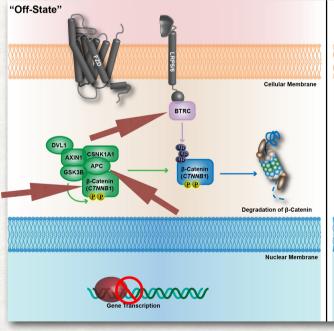
#### Abnormal localisation

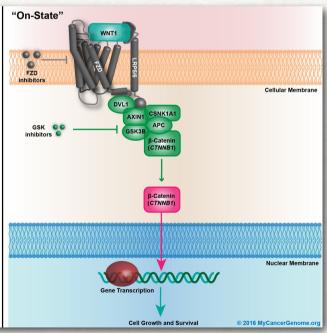


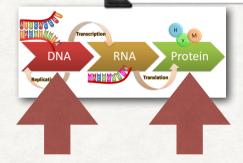


#### Abnormal localisation

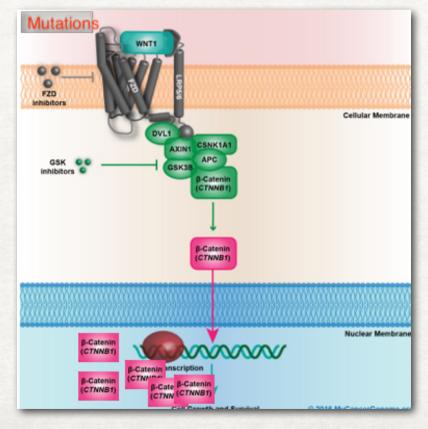






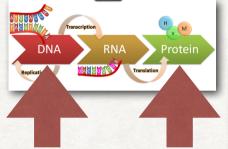


#### Abnormal localisation

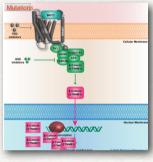




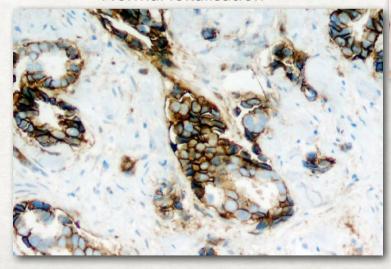
Mutations

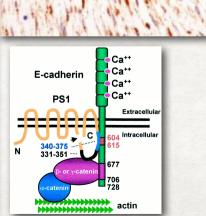


#### Abnormal localisation



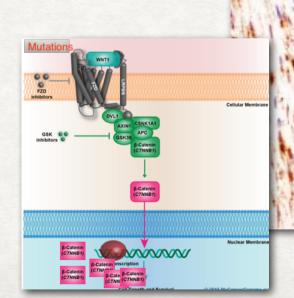
Normal lokalisation



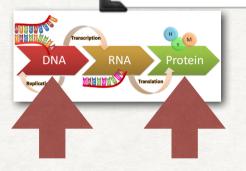




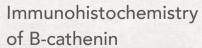
Abnormal localisation



Agressive fibromatosis



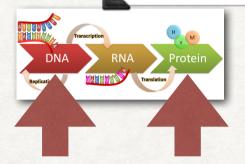








Mutations of B-cathenin, APC og BTRC



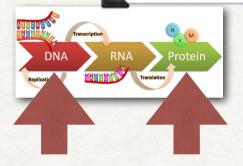
Mutation Changed protein

Translocation Absence of protein

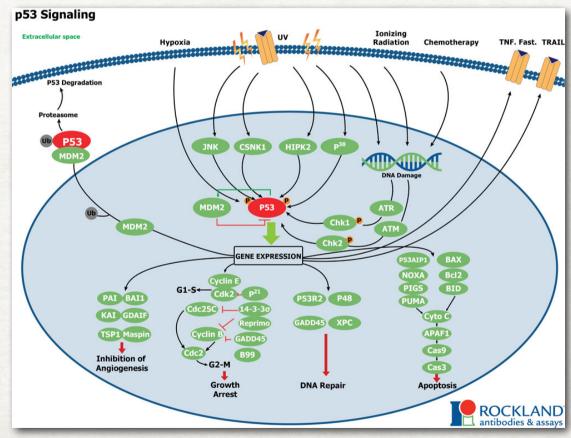
Deletion Abnormal localisation

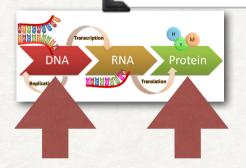
Amplification Over expression

Methylation Fussion protein



#### Over ekspression



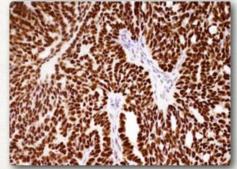


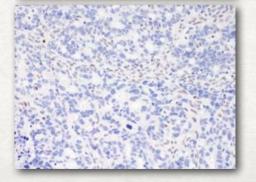
Normal expression

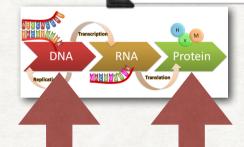
Some mutations cause (besides inactivation) that the P53 protein does not degrade and accumulates in the nucleus

Large deletions cause lack of protein expression









**Journal of Pathology** 

J Pathol 2010; 222: 191–198 Published online 13 July 2010 in Wiley Online Library (wileyonlinelibrary.com) DOI: 10.1002/path.2744 **ORIGINAL PAPER** 

# The biological and clinical value of p53 expression in pelvic high-grade serous carcinomas

Martin Köbel, Alexander Reuss, Andreas du Bois, Stefan Kommoss, Friedrich Kommoss, Dongxia Gao, Steve E Kalloger, David G Huntsman and C Blake Gilks

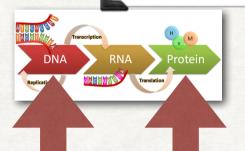
Department of Pathology and Laboratory Medicine, Calgary Laboratory Services/Alberta Health Services and University of Calgary, Canada

<sup>2</sup> Coordinating Centre for Clinical Trials (KKS), University Marburg (AGO-OVAR Statistical Centre), Germany

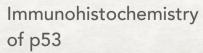
<sup>3</sup> Arbeitsgemeinschaft Gynaekologische Onkologie Studiengruppe (AGO-OVAR), Germany

<sup>4</sup> Genetic Pathology Evaluation Centre of the Prostate Research Centre, Department of Pathology, Vancouver General Hospital and British Columbia Cancer Agency, Vancouver, BC, Canada

stage, residual tumour, and stratification by cohort. The association of complete absence of p53 expression with unfavourable outcome suggests functional differences of *TP53* mutations underlying overexpression, compared to those underlying complete absence of expression.

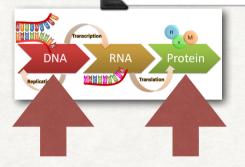








NGS of the p53 gene



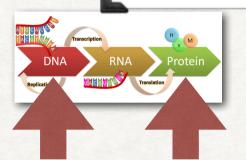
Mutation Changed protein

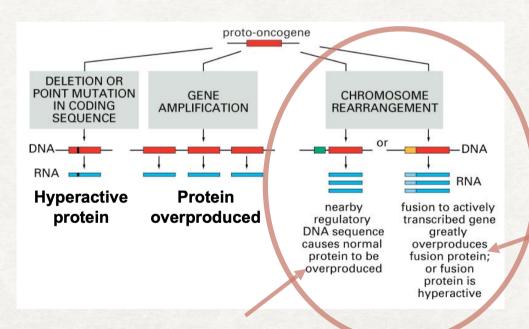
Translocation Absence of protein

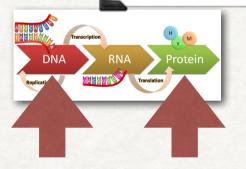
Deletion Abnormal localisation

Amplification Over expression

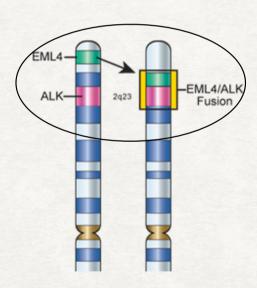
Methylation Fussion protein

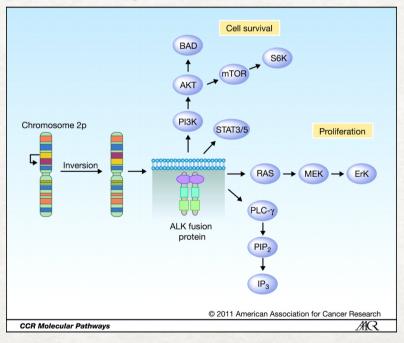


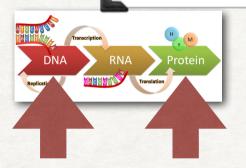




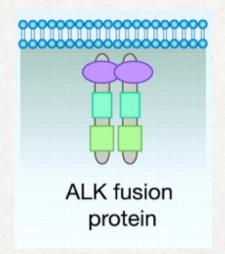
#### Lunge adenocarcinomer



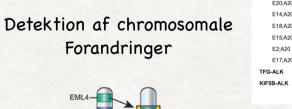


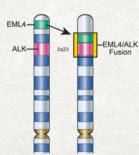


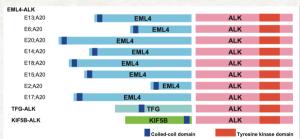
#### Detektion af fusion protein

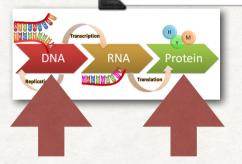


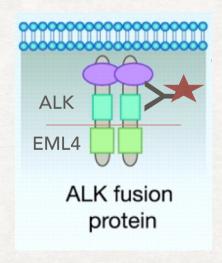
#### Detektion af fusions RNA

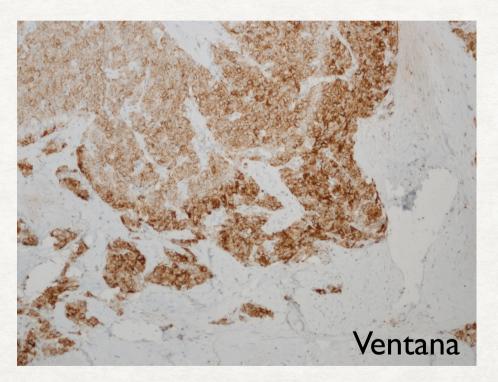




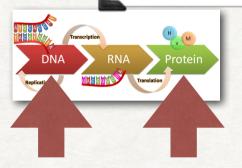








Detects ALK independent of fusion partner



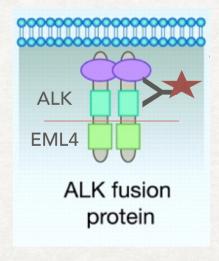
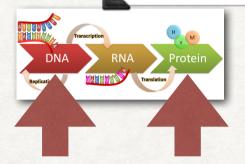
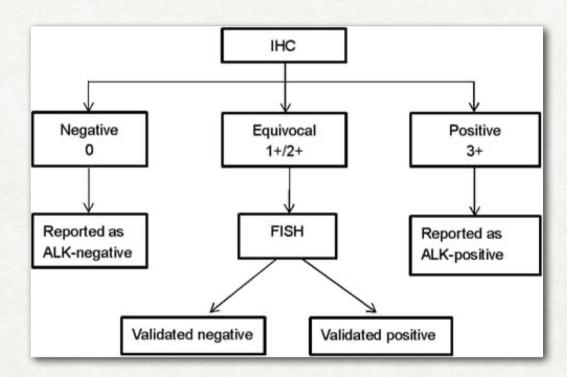


Table 1	Antihodies	and	assessment	marke	for	III-ALK	run 51	
Table 1.	Antiboules	anu	assessment	marks	101	IU-ALK,	Lau 2T	

Concentrated antibodies	n	Vendor	Optimal	Good	Borderline	Poor	Suff. <sup>1</sup>	Suff. OPS <sup>2</sup>
mAb clone <b>5A4</b>	43 1 1 1 1	Leica/Novocastra Abcam Biocare Monosan ThermoFisher	1	15	24	7	34%	22%
mAb clone <b>ALK1</b>	2	Dako Cell Marque	0	0	0	3	-	
rmAb clone <b>D5F3</b>	23	Cell Signaling	6	12	3	2	78%	94%
mAb clone OTI1A4	13	ORIGENE	10	3	0	0	100%	100%
Ready-To-Use antibodies								
mAb clone <b>5A4</b> <b>PA0306</b>	6	Leica/Novocatra	0	0	6	0		-
mAb clone <b>5A4</b> <b>MAB-0281</b>	1	Maixin	0	0	1	0	-	
mAb <b>5A4</b> <b>MAD-001720QD</b>	1	Master Diagnostica	0	0	1	0	-	
mAb clone <b>5A4</b> <b>MS-1104-R7</b>	1	ThermoFisher	0	1	0	0	-	- 25
mAb ALK1 IR641	9	Dako	0	0	1	8	-	
mAb clone ALK1 GA641	4	Dako	0	0	0	4	-(=	Di Company
mAb clone <b>ALK1</b> <b>790/800-2918</b>	7	Ventana	0	0	2	5	-	
rmAb clone SP8 AN770	1	BioGenex	0	0	0	1	-	
rmAb clone <b>D5F3</b> <b>790-4796</b>	70	Ventana	53	12	4	1	93%	100%
rmAb clone <b>D5F3</b> <b>790-4796</b> <sup>3</sup>	2	Ventana	1	0	1	0	-	( ) ( )
mAb clone <b>OTI1A4</b> <b>8344-C010</b>	1	Sakura Finetek	1	0	0	0	-	
Total	189		72	43	43	31	-	
Proportion			38%	23%	23%	16%	61%	

Proportion of sufficient stains (optimal or good).
 Proportion of sufficient stains with optimal protocol settings only, see below. . 3) RTU system developed for the Ventana BenchMark systems (Ultra/XT) but used by laboratories on different platforms (e.g Dako Autostainer)

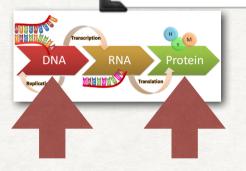




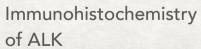
Improving Selection Criteria for ALK Inhibitor Therapy in Non–Small Cell Lung Cancer

A Pooled-Data Analysis on Diagnostic Operating Characteristics of Immunohistochemistry

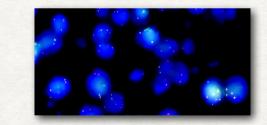
Long Jiang, MD, PhD,\*† Haihong Yang, MD, PhD,‡ Ping He, MD, PhD,\$ Wenhua Liang, MD, PhD,‡ Jianrong Zhang, MD,\*† Jingpei Li, MD,\*† Yang Liu, MD,\*† and Jianxing He, MD, PhD, FACS\*†



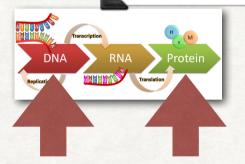








Fusions RNA analysis (PCR), NGS or FISH



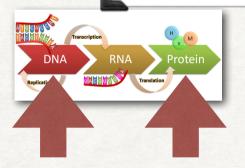
Mutation Changed protein

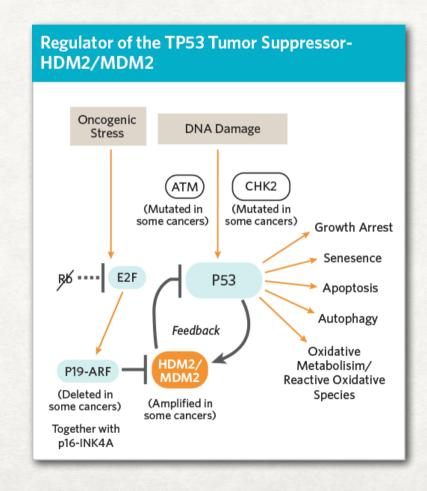
Translocation Absence of protein

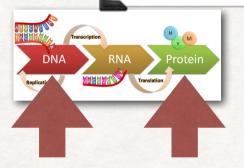
Deletion Abnormal localisation

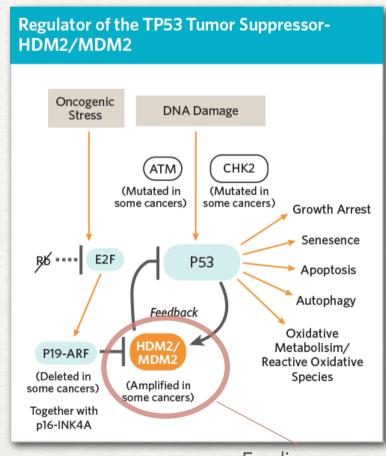
Amplification — Over expression

Methylation Fussion protein

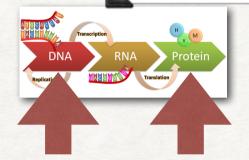




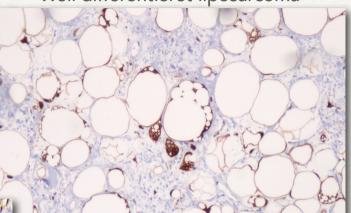




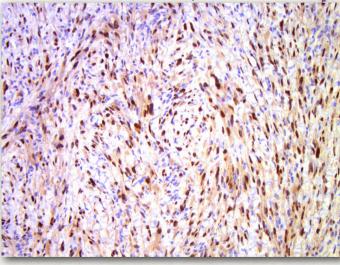
E.g. liposarcoma

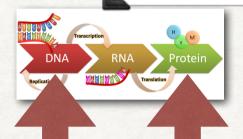


Well differentieret liposarcoma

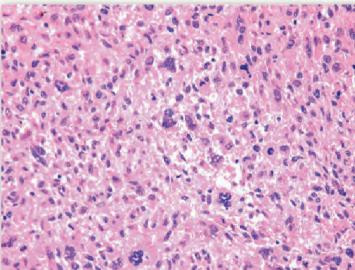


Dedifferentiated liposarcoma

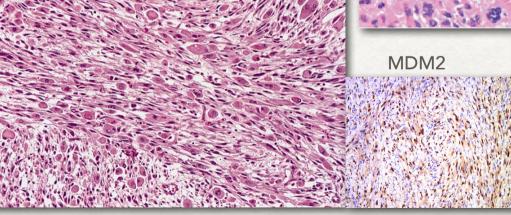


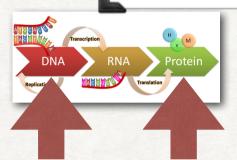


#### Pleomorph undifferentiated sarcoma

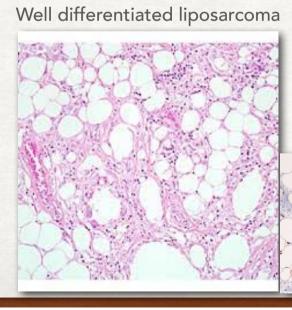


#### Dedifferentieret liposarcoma

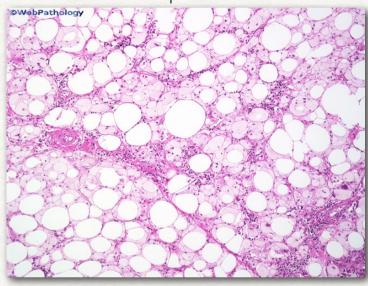




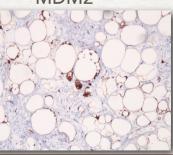


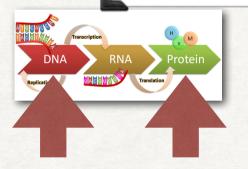


Lipoma

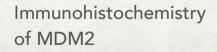


#### MDM2

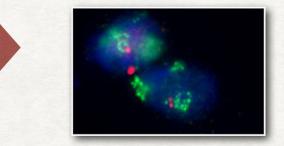












NGS or FISH analysis of amplification of MDM2 gene.