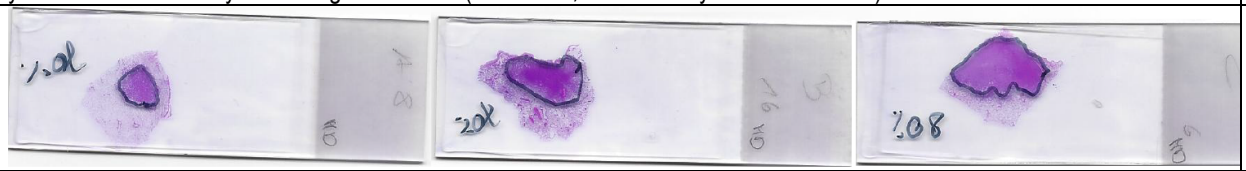
EGFR ring trial III October 2013- results

	Case A	Case B	Case C	Comments		Comments by distributor
definition	lobectomy, 2 condensed areas , 8 mm each, adenocarcinoma, dominant acinar and lepidic EGFR mutated	tumor, 2,4 cm peripheral, subpleural adenocarcinoma dominant acinar, papillary EGFR WT	subpleural tumor , 2,5 cm adenocarcinoma dominant papillary, lepidic, micorpapillary EGFR mutated			digital slides can be viewed www.iapaustria.com user: agpulmo PW: EGFR (case sensitive)
dates				reception	report	
ID01				09/10/2013	15.10.2103	
ID02				-	-	
ID04				16.10.13	18.10.13	
ID05				14.10.13	22.10.13	
ID06				-	-	
ID07				2013.10.14	2013.10.22 .	
ID08				14.10.2013	25.10.2013	
ID09				2013-10-11	2013-10-18	
ID10				08.10.2013	16.10.2013	
ID11				10.10.2013	14.10.2013	
ID12				09.10.2013 12.00	15.10.2013 10.00	
ID13				09.10.2103	15.10.2013	
ID14				09.10.13	11.10.13	
ID16				09.10.2013	17.10.2013	
ID17				09.10.2013	18.10.2013	
ID 18				11.10.2013	19.102103	
ID19				10.10.2013	17.10.2013	
ID20				15.10.2013	23.102013	
ID21				15 October 2013	24 October 2103	
percentage of tumor cells within section (as in regular report)						
ID01	80%	80%	80%			
ID02	30%	15%	70%			

ID04	20%	10%	15%		
ID05	50%	30%	50%		
ID06	25%	30%	50%		
ID07	30%	50%	70%		
ID08	20%	20%	20%		
ID09	50	35	70		
ID10	70% tumor cells in marked area	70% tumor cells in marked area	80% tumor cells in marked area		
ID11	40%	30%	60%		
ID12	75%	75%	75%		
ID13	Das analysierte Gewebe zeigte 40% Tumorzellen	Das analysierte Gewebe zeigte 20% Tumorzellen	Das analysierte Gewebe zeigte 40% Tumorzellen		
ID14	30% in marked area	20% in marked area	50% in marked area		
ID16	50%	40%	70%		
ID17	markierte Region = 80%	markierte Region = 70%	markierte Region = 80%		
ID18	40%	25-30%	40%		
ID19	30%	30%	50%		
ID20	40% of tumor cells content (TCC)	40% of tumor cells content (TCC)	50% of tumor cells content (TCC)		
ID21	25%	30%	70%		
how was percentage calculated ?					
ID01	area				
ID02	histomorpology				
ID04	Percentage of Tumor cells from total cell number in the selected area				
ID05	manual counting				
ID06	-				
ID07	histologic evaluation				
ID08	estimated by pathologist				
ID09	carcinoma cells in relation to normal cels, two pathologists				
ID10	Percentage of tumor cells in marked area in relation to normal (stroma) cells				
ID11	estimated				
ID 12	ratio of estimated number of tumor cells vs. normal cells				
ID13	amount of tumor cells in marked area				
ID14	estimated				
ID16	percentage of atypical epithelial cells in tumor area				
ID17	Klakulation durch den Pathologen				
ID18	semiquantitatively ba agreement of both evaluating pathologists				

ID19	histological evaluation				
ID20	Microscopic visual examination by pathologist and subjective estimation of tumor cells content (TCC) as % ratio of number of tumor to normal nucleated cells.				
ID21	counting on HE stained slides on approx 1000 cells				
Tumor cell enrichment – yes/no : method of enrichment (e.g. macrodissection by needle)					
ID01	macrodissection by scratching	macrodissection by scratching	macrodissection by scratching		
ID02	yes, macrodissection				
ID04	CaseA macrodissection and scrathcing, Case B and C entire section was used				
ID05	macrodissection by needle				
ID06	no				
ID07	macrodissection by needle				
ID08	macrodissection by scratching				
ID09	yes	no	no		
ID10	yes Macrodissection by scratching with needle (in Case A, B and C only the marked area)				
ID10					good and practicable documentation of slide jpg
ID11	macrodissection by needle	macrodissection ba needle	macrodissection by needle		
ID 12	macrodissection by scratching				
ID13	yes, tissue scratching of marked tumor area				
ID14	macrodissection, macrodissection;				
ID16	yes, scratching				
ID17	Anreicherung: ja; Makrodissektion; Für die Makrodissektion wurden die zwei verbliebenen Slides verwendet. Dabei wurde das vom Pathologen markierte Areal mit einem Skalpell abgekratzt				
ID18	no				
ID19	Not done				
ID20	Tumor cells enrichment was not performed; dissection was not necessary due to sensitivity of method used in our laboratory for EGFR mutations diagnostics				
ID21	Yes: macro dissection by scratching the marked tumor area				
method of DNA extraction					
ID01	Maxwell v. Promega				
ID02	Roche MagNA Pure Compact				
ID04	COBAS DNA Sample preparation kit (Roche)				
ID05	Cobas kit				

ID06	Roche High Pure PCR template Kit		
ID07	Quickgene DNA Tissue Kit		
ID08	High Pure PCR Template Preparation kit Roche		
ID09	DNA FFPE MiniKit (Quiagen)		
ID10	MAXWELL 16 Instrument , Fa.Promega		
ID11	Cobas DNA sample preparation kit		
ID12	EZ 1 AdvancedLS Automat Fa. Qiagen		
ID13	QIAmp DNA FFPE tissue kit Fa Qiagen		
ID14	fullautomatic/ Biorobot EZ1 QUIAGEN investigator kit		
ID16	Roche, DNA-Extraktionskit		
ID17	QIAamp DNA FFPE Tissue Kit von Qiagen. Die DNA wurde in 60 µL eluiert.		
ID18	cobas DNA Sample Preparation Kit Roche)		
ID19	DNA Sample preparation kit Roche		
ID20	Isolation of DNA with manual Cobas DNA Sample Preparation Kit (Roche)		
ID21	Extraction performed using the kit NucleoSpin FFPE DNA, manufacturer Macherey-Nagel		
method of measurement of DNA			
ID01	Qubit Fluoreszenzmessung (invitrogen)		
ID02	Bio spec nano		
ID04	Bio spec nano		
ID05	-		
ID06	Nanodrop Spectrophotometer		
ID07	GeneQuant Pro Photometer		
ID08	Nanodrop 1000		
ID09	NanoDrop Peqlab		
ID10	spectralphotometer Nanodrop		
ID 11	Biospec Nano		
ID 12	Nanodrop ND 1000 Fa Peqlab		
ID13	Quant-iT ds DNA BR Assay Kit, Fa Invitrogen(Qubit)		
ID14	photometric Gene Quant 1300		
ID16	Bio Spec Nano-DNA Messung		
ID1	NanoDrop Peqlab		
ID18	Qubit® dsDNA BR Assay Kit and Qubit® 2.0 Fluorometer, Invitrogen (LifeTechnologies)		
ID19	Quan iT ds DNA HS Assay Kit (Invitrogen)		
ID20	Spectrometric measurement of absorbance at 260 nm wavelength by NanoVue Spectrometer(GE Healthcare)		
ID21	UV spectrophotometer evaluation on a Eppendorf BiophotometerPlus and a Hellma TrayCell - Light path 1mm Second measure by fluorimetric method on a Qubit® 2.0 Fluorometer with the Qubit® dsDNA HS Assay Kit		
scratched from 1 or 2 slides/volume of elaute (µl)			

ID01	2 slides/ 100 µl	2 slides/ 100 µl	2 slides/ 100 µl		
ID02	2 slides/ 100µl	2 slides/ 100µl	2 slides/ 100µl		
ID04	-	-	-		
ID05	1 slide	1 slide	1 slide		
ID06	-	-	-		
ID07	scratched from 1 slide/ volume of eluate 100µl	scratched from 1 slide/ volume of eluate 100µl	scratched from 1 slide/ volume of eluate 100µl		
ID08					regret to have sent the wrong form
ID09	1	1	1		
ID10	from 2 slides/50µl Eluat	from 2 slides/50µl Eluat	from 2 slides/50µl Eluat		
ID11	1	1	1		
ID12	2 slides scratched/eluate 100µl	2 slides scratched/eluate 100µl	2 slides scratched/eluate 100µl		
ID13	2/ 30 µl ca 40 mm² Fläche x2	2/ 30 µl ca 100mm² Fläche x2	2/ 30 µl ca 100mm² Fläche x2		
ID14	2 slides / 50 µl	2 slides / 50 µl	2 slides / 50 µl		
ID16	2/100µl	2/100µl	2/100µl		
ID17					regret to have sent the wrong form.s.a
ID18	1	1	1		
ID19	scratched from 1 slide, 100 µl of eluate	scratched from 1 slide, 100 µl of eluate	scratched from 1 slide, 100 µl of eluate		
ID20	1 unstained slide	1 unstained slide	1 unstained slide		
ID21					regret to have sent the wrong form
Amount of DNA extracted (as in regular report)					
ID01	11,25 µg/ml	17,40 µg/ml	31 µg/ml		
ID02	8,12 µg/nl	3,35 ng/µL	5,08 ng/µL		
ID04	14,13 ng/µl	19,25 ng/µl	30,16 ng/µl		
ID05	16,2 ng/µl	19,4 ng/µl	33,8 ng/µl		
ID06	14,03 ng/µl	12,57 ng/µl	54,91 ng/µl		
ID07	10 ng/Ml	5 ng/µl	5 ng/µl		
ID08	41,94 ng/µl	65,88 ng/µl	42,4 ng/µl		
ID09	11,2 ng/µl	20,6 ng/µl	151,6 ng/µl		
ID10	23 ng/µl	41 ng/µl	63 ng/µl		
ID11	29,85 ng/µl	30,83 ng/µl	53,01 ng/µl		

ID 12	5,7 ng/µl	5,6 ng/µl	15,6 ng/µl		
ID13	3,6 µg/ml	15,6µg/ml	6,04 µg/ml	The amount is documented in a lab-report, not in the patients report	
ID14	1,2 ng/µl	10 ng/µl	20 ng/µl		
ID16	19,29 ng/µl	17,77 ng/µl	20,39 ng/µl		
ID17	13,2 ng/µL	24,0 ng/µL	29,3 ng/µL		
ID18	3,72 ng/µl	9,36 ng/µl	12,9 ng/µl		
ID19	14,9 ng/ml	30,8 ng/ml	29,5 ng/ml		
ID20	12,5 ng/ul (in 100 ul of elution buffer)	21,8 ng/ul (in 100 ul of elution buffer)	20,3 ng/ul (in 100 ul of elution buffer)		
ID21	12 ng/µl	18 ng/µl	44 ng/µl		
qualitiy of DNA					
ID01	-	-	-		
ID02	good	good	good		
ID04	1,64	1,40	1,76		
ID05	acceptable	acceptable	gacceptable		
ID06	good	good	good		
ID07	1,7	1,7	1,7		
ID08	good	good	good		
ID09	2,0	2,0	1,85		
ID10	1,96	1,86	1,88		
ID11	ok	ok	ok		
ID 12	260/280, 1,8	260/280, 1,9	260/280, 1,8		
ID13	good	good	good		
ID14	ratio 4,0	ratio 10	ratio 2,5		
ID16	1,35	1,06	1,36		
ID17	2,11	2,12	1,99		
ID18	optimal	optimal	optimal		
ID19	not done	not done	not done		
ID20	A260/280 = 1,78	A260/280 = 1,79	A260/280 = 1,79		
ID21	A_{260}/A_{280} = 1,31	A_{260}/A_{280} = 1,69	A_{260}/A_{280} = 1,64		
evaluation of DNA qualitiy					
ID01	-				
ID02	internal control of COBAS EGFR mutation test				
ID04	OD 260/280				

ID05	PAGE		
ID06	OD 260/280, 260/230		
ID07	-		
ID08	Nanodrop 1000 (260/280)		
ID09	control PCR		
ID10	ratio 260/280 (pure DNA 1,7 – 1,8):		
ID11	-		
ID12	Nanodrop ND 10000 Fa Peqlab		
ID13	Estimation in relation to peak height of the program and in relation to the control DNA		
ID14	(exon2) control mix (kit) assay + inhibitor control		
ID16	OD 260/280		
ID17	-		
ID18	convenient		
ID19	not done		
ID20	Measurement of absorbance at 260nm and 280nm wavelength for calculation of A260/A280 ratio		
ID21	A260/A280		
Method of sequencing (as in regular report)			
ID01	cobas 4800 EGFR mutation test		
ID02	-		
ID04	COBAS 4800 Roche		
ID05	Cobas and Sanger		
ID06	Quiagen pyrosequencing		
ID07	-		
ID08	next generation sequencing		
ID09	allele specific PCR		
ID10	Therascreen EGFR Pyro Kit Ref. 971480, Fa. QIAGEN		
ID11	COBAS EGFR Mutationsanalyse (Cobas 4800 System)		
ID 12	Sanger Sequencing ABI 3500xL Dx		
ID13	Pyrosequencing; Therascreen EGFR Pyro Kit, Fa. Qiagen „Verwendete Methode: DNA-Extraktion mit Qiagen QIAmp® DNamp FFPE Kit, Sequenzierung mit Therascreen® EGFR Pyro Kit (Quiagen, Hilden, Deutschland).“		
ID14	(real time PCR) Thera screen EGFR RGQ PCR kit Quiagen		
ID16	Cobas 4800 EGFR Mutation Test, Roche, Realtime-PCR		
ID1	Sangersequenzierung		
ID18	cobas® EGFR Mutation Test and cobas z 480 analyser for real-time PCR (Roche)		
ID19	Real Time PCR – Cobas EGFR Mutation Test		

ID20	Allele-specific real-time PCR method – Cobas EGFR Mutation Test (Cobas 4800 System)		
ID21	Mutant specific amplification by qPCR with a CE/IVD approved kit (supplier EntroGen- EGFR Mutation Analysis Kit for Real-Time PCR) run on a Applied Biosystems 7500 Real-Time PCR System		
What types of mutations can be detected by your method? Sensitivity of your method, if known?			
ID01	T790M, del, L858R, L861Q, G719Xm, S768I, Ins.		
ID02	siehe COBAS EGFRmutation test		
ID04	41 different mutations in Exon 18,19,20,21 (5% of mutated tumor cells in wildtyp background)		
ID05	exons: 18-21, sensitivity 5% (Cobas) , 15% Sanger		
ID06	point mutation, deletion		
ID07	exon, 19, exon 21		
ID08	EGFR 18 – 21 exon sensitivity (1-)5%		
ID09	41 mutations detected by the cobas® EGFR Mutation Kit. Sensitivity according to the manufacturer: 1%		
ID10	Exon 18: Mutations on Codon 719: G719X (X=S, C, A, D) Exon 19: all Deletions within Codon 746-750 Exon 20: Mutation Codon 768 (S768I), Insertion Codon 770, 771, 774; Mutation Codon 790 (T790M) Exon 21: Mutation Codon 858 and 861 (L858R, L861Q) 5% tumor cells should be tested in minimum to get reliable results		
ID11	Exon 18: Punktmutationen im Codon 719 Exon 19: sämtliche derzeit in Version 1.0/ Oktober 2011 beschriebene Deletionen Exon 20: Punktmutationen Codon 790 (T790M) und 768 (S768I) Insertionen Exon 21: Mutationen Codon 858 (L858R)		
Id 12	all types (del, ins, sub, dup)		
ID13	Point mutations codons 719, 768, 790, 858-861; Deletions Exon 19, Sensitivity 5-10% mt in wildtype		
ID14	19 deletions in exon 19, T790M,L858R. L861Q, G719X, S763I, 3 insertions in exon 20; sensitivity 1-10% mutated DNA		
ID16	T790M, Deletionen Exon 19, S768i, L858R, G719X, Insertionen Exon 20		
ID17	Alle Mutationen in Exon18, Exon 19, Exon 20 und Exon21		
ID18	41 specific mutations in exons 18, 19, 20 and 21 of the EGFR gene, e.g. deletions (e.g. exon 19 del), insertions (e.g. exon 20 ins) or point mutations (e.g. S768I, L858R, T790M or G719X) can be detected. Sensitivity: >5% mutant copies of FFPE DNA in a background of wild type DNA		
ID19	by our method 3 point mutations can be detected in exon 18 (G719A, G719C, G719S), 29 deletions and complex mutations in exon 19, 2 point mutations (S768I, T790M) and 5 insertions in exon 20 and L858R in exon 21. overall 41 mutations		
ID20	Cobas EGFR Mutation Test detects 41specific mutations (substitutions, insertions, deletions) in exons 18-21 of the EGFR gene. Test sensitivity, according to the manufacturer: 5% of mutant allele content in the wild-type background		
ID21	– T790M – Exon 19 Deletions - detects 19 deletions, but does not distinguish between them – L858R		

	– L861Q – S768I – G719X - detects G719A, G719S and G719C, but does not distinguish between them – Exon 20 Insertions - detects 2319-2320 insCAC and 2310-2311 insGGT, but does not distinguish between them – Exon 20 Insertion - detects 2307-2308 insGCCAGCGTG (ins9) The limit of detection varies, according to the manufacturer between 0,1-1% diluted in the wild-type genomic DNA. The exact sensitivity has not been locally validated in order to establish the minimum proportion and number of cancer cells needed for mutation detection as recommended by ACP/IASLC/AMP guidelines.				
result as in regular report					
ID01	L858R	neg	L858R		
ID02	Mutation exon 21 (L858R)	wildtype	Mutation exon 21 (L858R)		
ID04	Exon 21 (L858R)	mutation not detected	Exon 21 (L858R)		
ID05	L858R	wt	L858R		
ID06	exon 21 mutation L858R aminoacid change 15,2%	mutant	exon 21 mutation L858R aminoacid change 23,3%		
ID07	21 L858R, 20%	wild type	21, L858R, 30%		
ID08	L858R mutation (16%)	G719S mutation (26%)	L858R mutation (31%)		
ID09	detectable mutation: c.2573T>G (p.L858R)	wildtype	detectable mutation: c.2573T>G (p.L858R)		
ID10	using pyrosequencing technology the mutation p.L858R, c.2573T>G (19%) in Exon 21 detectable	using pyrosequencing technology a normal peak pattern is detected. This covers the mentioned DNA segments	using pyrosequencing technology the mutation p.L858R, c.2573T>G (36%) in Exon 21 detectable		
ID11	Mutation detected in Exon 21 L858R	Mutation onot detected	Mutation detected in Exon 21 L858R		
ID12	EGFR Exon 18, Exon 19 und Exon 20: keine Mutation EGFR Exon 21: somatische Mutation c.2573T>G, p.L858R	EGFR Exon 19, Exon 20 und Exon 21: keine Mutation]	EGFR Exon 18, Exon 19 und Exon 20: keine Mutation EGFR Exon 21: somatische Mutation c.2573T>G, p.L858R	Auf die Angabe von stillen Mutationen und Varianten wurde verzichtet.	
ID13	Molekulargenetische Analyse für EGFR: Mutation p.L858R	Molekulargenetische Analyse für EGFR: keine Mutation	Molekulargenetische Analyse für EGFR: Mutation p.L858R		
ID14	L858R	no mutation detected	L858R		
ID16	L858R	-mutation not detected	L858R		
ID17	p.L858R	Keine Mutation (Wildtyp)	p.L858R	In allen Fällen (Case 1-3) konnte folgende stille Mutation detektiert werden: p.Q787Q (silent mutation)	
ID18	EGFR mutation detected:	without EGFR mutations	EGFR mutation detected:		

	exon 21 L858R		exon 21 L858R		
ID19	activating mutation have been detected in sample Econ21 L858R	no mutation detected	activating mutation have been detected in sample Econ21 L858R		
ID20	L858R in EGFR exon 21	Mutation not detected	L858R in EGFR exon 21		
ID21	positive for the EGFR d 2573T>G (p.L858R) mutation in the exon 21	negative for the EGFR mutations on exon 18, 19, 20,& 21	positive for the EGFR d 2573T>G (p.L858R) mutation in the exon 21		
interpretation of result as in regular report					
ID01	-	-	-		
ID02	Im vorliegenden Untersuchungsmaterial ist eine aktivierende mutation des EGFR Gens NACHWEISBAR	Im vorliegenden Untersuchungsmaterial eine aktivierende Mutation des EGFR-Gen NICHT nachweisbar.	Im vorliegenden Untersuchungsmaterial ist eine aktivierende mutation des EGFR Gens NACHWEISBAR		
ID04	Im vorliegenden Untersuchungsmaterial findet sich eine aktivierende Mutation des EGFR Gens (Punktmutation Exon 21 L858R)	Im vorliegenden Untersuchungs-material ist eine aktivierende Mutation des EGFR Gens niicht nachweisbar	Im vorliegenden Untersuchungsmaterial findet sich eine aktivierende Mutation des EGFR Gens (Punktmutation Exon 21 L858R)		
ID05	classic activating exon 21 EGFR mutation	wild type EGFR	classic activating exon 21 EGFR mutation		
ID06	The mutatuion results in sensitivity for tyrosin kines inhibitor treatment, on the basis of tumor percent and percent of mutated DNA, the tumor comprised of mutant cells.	No activation mutation could be detected. The tumor would not respond for tyrosine kinase treatment	The mutatuion results in sensitivity for tyrosin kines inhibitor treatment, on the basis of tumor percent and percent of mutated DNA, the tumor comprised of mutant cells.		
ID07	activating EGFR mutation detected (L858R) 20%	activating EGFR mutation of codon 19 and 21 not detected	activating EGFR mutation detected (L858R), 30%		
ID08	activating mutation in exon 21	no mutatio found in exon 18 - 21	activating mutation in exon 21		
ID09	sensitivity to EGFR TKI possible	sensitivity to EGFR TKIs unlikely	sensitivity to EGFR TKI possible		
ID10	activating mutation	-	activating mutation		
ID11	Im vorliegenden Untersuchungsmaterial zeigt sich eine aktivierende Mutation im Exon 21, L858R	keine Mutation vorhanden	Im vorliegenden Untersuchungsmaterial zeigt sich eine aktivierende Mutation im Exon 21, L858R		
ID 12	-	-	-		
ID13	substitution missens Exon 21	Molekulargenetische Analyse für EGFR: Keine Mutation bzw. Deleti-on im EGFR-Gen	substitution missens Exon 21		
ID14	-"-"	"-"	-"-"		

ID16	-	-	-		
ID17	Die p.L858R-Mutation ist assoziiert mit einer erhöhten Sensitivität auf EGFR TKI's	-	Die p.L858R-Mutation ist assoziiert mit einer erhöhten Sensitivität auf EGFR TKI's		
ID18	This mutation is considered to represent an activating EGFR mutation sensitive to TKIs	Negative result – without the mutation (WT/WT) in the examined exons 18, 19, 20 and 21	This mutation is considered to represent an activating EGFR mutation sensitive to TKIs		
ID19	EGFR positive result confers TKI sensitivity	EGFR negative, no benefit with TKI treatment	EGFR positive result confers TKI sensitivity		
ID20	The sample tested exhibits the mutation sensitizing to EGFR tyrosine kinase inhibitors (EGFR-TKI).	The sample tested does not exhibit the mutation sensitizing to EGFR tyrosine kinase inhibitors (EGFR-TKI).	The sample tested exhibits the mutation sensitizing to EGFR tyrosine kinase inhibitors (EGFR-TKI).		
ID21	Presence of the L858R mutation of the EGFR gene confers sensitivity to the EGFR tyrosine-kinase inhibitors	-	Presence of the L858R mutation of the EGFR gene confers sensitivity to the EGFR tyrosine-kinase inhibitors		
Additional comments to oncology department or recommendations					
ID01	-				
ID02	In diesem Fall ist ein Ansprechen auf eine Therapie mit einem Tyrosin-Kinase-Inhibitor zu erwarten.		In diesem Fall ist ein Ansprechen auf eine Therapie mit einem Tyrosin-Kinase-Inhibitor zu erwarten.		
ID04	-	-	-		
ID05	sensitive to all type of EGFR TKI inhibitor	in case of KRAS wt status the tumor may be moderately sensitive to Tarceva	sensitive to all type of EGFR TKI inhibitor		
ID06	-	-	-		
ID07	exons required for drug prescription tested	exons required for drug prescription tested	exons required for drug prescription tested		
ID08	tumor sample shows *sensitivity* to anti EGFR therapy	tumor sample shows *resistance* to anti EGFR therapy	tumor sample shows *sensitivity* to anti EGFR therapy		
ID09	ALK rearrangement unlikely	KRAS mutation detected – c.34G>T (p.G12C) ALK rearrangement unlikely	ALK rearrangement unlikely		
ID10	-	-	-		
ID11	aktivierende Mutation, TKI-Therapie sinnvoll	-	aktivierende Mutation, TKI-Therapie sinnvoll		

ID 12	Datenlage **unterstützt** den Einsatz von IRESSA	Datenlage unterstützt **NICHT** den Einsatz von IRESSA	Datenlage **unterstützt** den Einsatz von IRESSA		
ID13	partial response	-	partial response		
ID14	-	-	-		
ID16	-	-	-		
Id17	Rücksprache mit dem Onkologen		Rückspraceh mit dem Onkologen		
ID18	Analyses of other genes genes (e.g. ALK, etc.) seem to be unnecessary	Adneocarcinoma, EGFR negative – al nalyses of other genes (e.g. ALK etc) seem to be recommended	Analyses of other genes genes (e.g. ALK, etc.) seem to be unnecessary		
ID19	-	-	-		
ID20	EGFR TKI therapy is **recommended**	EGFR TKI therapy is **not** recommended	EGFR TKI therapy is **recommended**		
ID21	Presence of the L858R mutation of the EGFR gene confers sensitivity to the EGFR tyrosine-kinase inhibitors	-	Presence of the L858R mutation of the EGFR gene confers sensitivity to the EGFR tyrosine-kinase inhibitors		
Diagnosis of case as done in regular reports					
ID01	azinärtes Adenocarcinom G2/3	azinäres Adenocarcinom G2	azinäres Adenocarcinom G2 + in situ		
ID02	NSCLC	NSCLC	NSCLC		
ID04	adenocarcinoma, lepidic	adenocacrcinoma (70% lepidic, 30% acinar)	adenocarcinoma (10% solid, 40% acinar, 40% papillär, 10% lepidic)		
ID05	EGFR mutant adenocarcinoma of lepidic variant	EGFR wt mixed adenocarcinoma (micropapillary and lepidic)	EGFR mutant adenocarcinoma of lepidic variant		
ID06	well differentiated acinar adenocarcinoma	fetal adenocarcinoma	adenocarcinoma micropapillare		
ID07	-	-	-		
ID08	adenocarcinoma with dominant lepidic pattern 90%	adenocarcinoma with dominant lepidic pattern 70%	adenocarcinoma with dominant lepidic pattern 80%		
ID09	Moderately differentiated predominant lepidic carcinoma of the lung	Moderately differentiated invasive adenocarcinoma of the lung with lepidic growth	Poorly differentiated invasive adenocarcinoma of the lung, micropapillary predominant		
ID10	moderately differentiated tubule papillary adenocarcinoma with 70% tumorcells in the marked area Using pyrosequencing technology the mutation	Moderately differentiated tubulo-papillary adenocarcinoma with 70% tumor cells in the marked area The most common mutations of	Moderately differentiated tubulo-papillary adenocarcinoma with 80% tumor cells in the marked area Using pyrosequencing technology the mutation		

	p.L858R, c.2573T>G (19%) in Exon 21 is detectable. The mutation L858R is described to be an activating mutation	the EGFR gene are not present.	**p.L858R, c.2573T>G (36%) in Exon 21** is detectable. The mutation L858R is described to be an activating mutation.		
ID11	Adenokarzinom, tw. lepidisches Wachstum, G1	Adenokarzinom mixed typ, tw. lepidisch, G1	Adenokarzinom, mixed typ, G2		
ID 12	-	-	-		
ID13	minimal invasives Adenocarcinom G1	Adenocarcinom G1 mixed acinar /lepidic	Adenocarcinom acinär G2/G3		
ID14	invasives Adenocarcnom, GII, glandular+ Adenocarcinoma in situ 10%	invasives Adenocarcnom GII glandular + Adenocarcinoma in situ 5 %	invasives Adenocarcinom GIII, glandulär		
ID16	Adenoca. well diff. präd. acinär	Adenoca. well diff. präd. acinär	Adenoca. mod. diff. präd. papillary (+acinär)		
ID17	Nicht muzinöses, Bronchioloalveoläres Karzinom	Bronchogenes Adenokarzinom (Grad 2)	Bronchogenes Adenokarzinom (Grad 3)		
ID18	(Micro-?)invasive predominantly lepidic (90%) adenocarcinoma, with septal fibrosis, solid-acinary component (5%) , papillary projections (5%) and isolated intraepithelial solidization, without detected necrosis, without detectable vascular or pleural invasion	Invasive predominantly lepidic adenocarcinoma with atypical transient (lepidic-tubuloalveolar, macro- and micropapillary) structure) associated with septal fibrosis and with invasion of lymphatic vessels, G2	Invasive adenocarcinoma, structurally not classifiable with a lepidic component (approx. 30%) and a complex of different structural components (acinary, macro-/micropapillary, solid, with giant cells - together 70%), G3 (due to a focal giant cell dedifferentiation)	Using available HE we have classified the case C only acc. to the WHO classification 2004 as “adenocarcinoma with mixed types”	
ID19	Adenocarcinoma, predominant lepidic pattern (lepidic 60%, papillary 20%, acinar 20%)	Adenocarcinoma, predominant acinar pattern (acinar 50%, lepidic 30%, papillary 10%, solid 5%, micropapillary 5%)	Adenocarcinoma, predominant lepidic pattern (lepidic 50%, acinar 40%, papillary 10%), focally mucinous		
ID20	Adenocarcinoma predominantly papillary (70%), lepidic (30%)	Adenocarcinoma predominantly acinosum (70%), lepidic(30%)	Adenocarcinoma predominantly papillary (60%), lepidic (20%9 , acinous (20%)		
ID21	lung adenocarcinoma acinar pattern	lung adenocarcinoma acinar pattern	lunge adenocarcinoma acinar pattern		