1. Fast Track Analysis

The fast track analysis includes immunohistochemistry for PD-L1, *ALK* and *ROS* (not reported here in this manuscript) and was completed by the analysis of *KRAS* exon 2 and *EGFR* exons 19 and 21. If DNA samples have a concentration of less than 5 ng/µL, fast track is omitted and only parallel sequencing is performed. High resolution melting was done for *KRAS* exon 2 and *EGFR* exon 21 with the high-resolution melting master mix according to the manufacturers protocol on a LightCycler 480® (Roche, Basel, Switzerland). Fragment length analysis was carried out for *EGFR* exon 19 due to the frequently occurring deletions. After the polymerase chain reaction (PCR) for *EGFR* exon 19 with one fluorescence labeled primer, 1µL of the PCR product, 12 µL formamide (Applied Biosystems, Darmstadt, Germany) and 1 µL of a standard marker (Gene scan™ 500 LIZ Size Standard, Applied Biosystems, Darmstadt) were analysed on the capillary electrophoresis ABI 3100 Genetic Analyzer (Applied Biosystems, Darmstadt). All primers were in-house designed.

Table S1. Primer fast track analysis for *KRAS* exon 2 and *EGFR* exons 19 and 21.

Primer High Resolution Melting	
KRAS exon 2 forward primer	CCTGCTGAAAATGACTGAATATAAACTT
KRAS exon 2 reverse primer	GCATATTAAAACAAGATTTACCTCTATTGT
EGFR exon 21 forward primer	AGGAACGTACTGGTGAAAACAC
EGFR exon 21 reverse primer	CCTCCTTCTGCATGGTATTCTTTC
Fragment Length Analysis	
EGFR exon 19 forward primer	ACAGGCTATTGTCCAAGAAGGTGT
EGFR exon 19 reverse primer	TGGTATCGATGCTGCTGTTGA

2. Next Generation Sequencing (NGS)

NGS was performed on all DNA extracts with validated gene panels using either AmpliSeq gene panels for poor DNA quality samples (Thermo Fisher Scientific, Waltham, MA; LUN3, 14 genes) or GeneRead gene panels for good DNA quality samples (Qiagen, Hilden, Germany; LUN5 panel, 19 genes; Supplementary Table S1) as described previously [19]. Genomic variants were called using a bioinformatic in-house algorithm and up to a minimum allelic frequency of 0.5% is shown in the variant table [20]. A coverage of 200, a minimum allelic fraction of 5%, location of the mutation on two different amplicons and a balanced base exchange in the reads are the quality criteria under which a variation is reported. Each variant is manually checked for all quality criteria.

Table S2. Parallel sequencing panel design.

Panel LUN3		**Panel LUN5**	
Gene	Exon	Gene	Exon
AKT1	4	*ALK*	22–25
ALK	21–25	*BRAF*	11,15
BRAF	1115	*CTNNB1*	3
CTNNB1	3	*EGFR*	18–21
DDR2	3–18	*ERBB2*	8,19,20
EGFR	18–21	*FGFR1*	4–7,10,12–15
ERBB2	19,20	*FGFR2*	6–15,18
KRAS	2,3	*FGFR3*	3,7,9,10,12 (codon 512–529),14,16,18 (codon 769–807)
MAP2K1	2	*FGFR4*	3,6,9,12,13, (codon 556–607),15,16
MET	14	*IDH1*	4
NRAS	2,3	*IDH2*	4
PIK3CA	10,21	*KRAS*	2–4

PTEN	1-8	*MAP2K1*	2,3
TP53	5-8	*MET*	14,16–19
		NRAS	2–4
		PIK3CA	10,21
		PTEN	1–8
		ROS1	34–41
		TP53	4 (codon 97–125),5–8

Table S3. Primer for parallel sequencing of lung cancer (LUN3 and LUN5).

Lung Cancer Panel LUN3

Chromosome	Start	Stop	f-primer	r-primer	Gene
chr1	115256352	115256453	AAAAGCTCTATCTTCCCTAG-TGTGGTA	GCTTCCTCTGTGTATTT-GCCATCAATAA	*NRAS Exon3*
chr1	115256453	115256550	AGGTTAATATCCGCAAATGACTT-GCTA	GTTATAGATGGTGAAACCTGTTT-GTTGG	*NRAS Exon3*
chr1	115256550	115256672	TCTTGTCCAGCTGTATCCAGTATGT	AGATGCTTATTTAACCTTGGCAA-TAGCA	*NRAS Exon3*
chr1	115258676	115258798	CCACTGGGCCTCACCTCTAT	ACCCTGATTACTGGTTTCCAACAG	*NRAS Exon2*
chr1	162688829	162688951	GCATTATTGGTTGGTGGCAGACT	TGCTGGTCTTCTAGCATA-TAGCTGA	*DDR2 Exon3*
chr1	162722872	162722995	CCATGTCCTCTCTTTTCTCTTT-GGTTT	GAACATGGGCTTTCTT-GATGTAACC	*DDR2 Exon4*
chr1	162724359	162724466	TGCTTGCCTGTGAACCAGTAA	GCAGAAACTCCTTCAGGTCATCAG	*DDR2 Exon5*
chr1	162724466	162724586	GCCCTGAGATTCCAGTGGAAC	GTGCCATCCCGACTGTAATTGA	*DDR2 Exon5*
chr1	162724586	162724687	GAGTTTGCCCCCATGTACAAGA	CCTTCTTCTCCTAGCCTAAGTCAA AAT	*DDR2 Exon5*
chr1	162724850	162724967	GTAGATGCATTCTGCTCCTCGAA	TCCAAGTCCTTTAG-GAAAATGTCATAGG	*DDR2 Exon6*
chr1	162724967	162725094	AGGTGCTGGATGGAAATAGTAACC	GCTTCCTGGGCTAGTGACCTA	*DDR2 Exon6*
chr1	162725447	162725572	ACTCACTTGGCTGTGTTTCCT	AGTGGCCAATTTCCCATTCTAA-TAAAGTT	*DDR2 Exon7*
chr1	162729566	162729694	TCAGATTTCTCTCTCCTTTTCCTCCT	CCATTGGTGGCACTCTCGTT	*DDR2 Exon8*
chr1	162729681	162729782	TGTGGCCCGGCTATGACT	TCCTTAAAGAAGTTCCACCACACC	*DDR2 Exon8*
chr1	162730973	162731107	ACCTTAGCAGGGCCAACCTA	TTGACGTCATCCAGGACAAGG	*DDR2 Exon9*
chr1	162731107	162731197	GAACCTAATGCCATTTCCTTCCC	TGAACATCATCCAGGTATCTG-CAAAA	*DDR2 Exon9*
chr1	162731197	162731276	AGTGCCATCAAGTGTCAATACCA	CATTCCTCCTTCATCACCTTGCT	*DDR2 Exon9*
chr1	162735765	162735879	TGTCTGTCTTCTCCCTGGCT	CCCCCAG-TAAGTCCCTTCAAATTAA	*DDR2 Exon10*
chr1	162736904	162737029	TAAGCAGAAGTATTAAGGTGG-CATCT	CGAGTGTTGCTGTCATCAACTTT	*DDR2 Exon11*
chr1	162737029	162737154	CCTGGTCACAGATCCAATGCTT	TTCTTATATCATGACCATTCTG-CACCTC	*DDR2 Exon11*
chr1	162740090	162740201	CTTTCTCCTTGCTCTTCTCTTCCA	GGAAAGATGCGATCG-TAAGTCGAG	*DDR2 Exon12*
chr1	162740201	162740327	CACCTAGTGAACAAGGGTCCAA	TTGCTGAGGTTTCTCCCTTGAC	*DDR2 Exon12*
chr1	162741756	162741887	CCTCCTCTCAGAGTTCCTTCCT	CTGTCACTCCTTGGAGGTTCAC	*DDR2 Exon13*
chr1	162741887	162742002	CCACTATGCAGAGGCTGACATA	TCCTTCTCCCAGCTTCTCTTTGA	*DDR2 Exon13*
chr1	162742002	162742088	AGTTCCCCAGGAAACTCCTAACTT	GAAGGGACTCTTTGTTC-TACTGATCATT	*DDR2 Exon13*
chr1	162743204	162743301	CAGGAAATGCCCAGCAAGAGTA	GCACTGACATCTAGGG-CAAAATCTT	*DDR2 Exon14*
chr1	162743301	162743421	TGGAGGGAATGGAAAAATTCAAA GACA	AGGAGTATTCCTGGTCCTAAA-GATGAAA	*DDR2 Exon14*

chr1	162745384	162745513	GCCTTGGTGTGCATTCTTCTC	CAGAGAGGGTCATCAGTGATA-CAC	*DDR2 Exon15*
chr1	162745513	162745634	CCCAAACATCATCCATCTATTAGCT GT	GAGAAGGAAGACCTGGCTTGTTTA	*DDR2 Exon15*
chr1	162745915	162746038	AGGCTACCTTCTGTCTTCTTGTCT	CCAAAGTCAGCTATCTTGATTGTG-TAGT	*DDR2 Exon16*
chr1	162746038	162746162	CACACGAAACTGTTTAGTGGG-TAAGA	CAGGGCTTTAAAATGCTGA-GAACTT	*DDR2 Exon16*
chr1	162748317	162748432	AGCTGCAGAT-TATGAAATTTAACAGGGT	GGGAATAGGGCTGTTCTT-GACAAAA	*DDR2 Exon17*
chr1	162748432	162748519	GGTTACTTTGTGGGAGACTTTCACC	ATCCATTCATCCCCAACAG-TTCTTAC	*DDR2 Exon17*
chr1	162749866	162749977	CCCCGTCTTTGTAA-TATTCTCTCTCTCT	CTTGGAATGAGGGACGGTTCT	*DDR2 Exon18*
chr1	162749977	162750066	AGCTGCTGGAGAAGAGATACGA	GGTCTTGTAGGGAGGACCTGAG	*DDR2 Exon18*
chr2	29432650	29432776	GGGTGAGGCAGTCTTTACTCA	CGTTGTACAC-TCATCTTCCTAGGGAT	*ALK Exon25*
chr2	29436843	29436974	ACAGGAAGAGCACAGTCACTTTG	CTCACTGACAAGCTCCTCGT	*ALK Exon24*
chr2	29443565	29443688	ACTGCAGCAAAGACTGGTTCTC	GCTCTGCAGCAAATTCAACCAC	*ALK Exon23*
chr2	29443688	29443772	CCAATGCAGCGAACAATGTTCTG	AGCTGCTGAAAATGTAACTTT-GTATCCT	*ALK Exon23*
chr2	29445200	29445332	GGGTGAGGGTGTCTCTCTG	TTGGCTTGCGGACTCTGTAG	*ALK Exon22*
chr2	29445369	29445489	AAGGGCAGGCTCAAGAGTG	CTGTTTGACTCTGTCTCCTCTTGT	*ALK Exon21*
chr3	41266072	41266193	AGACAGAAAAGCGGCTGTTAGT	GAGAAAATCCCTGTTCCCACTCAT	*CTNNB1 Exon3*
chr3	178935940	178936023	ATGTATTTGCTTTTTCTG-TAAATCATCTGTGAA	GAGCTGTTCTTT-GTCATTTTCCCTTAAT	*PIK3CA Exon10*
chr3	178936023	178936105	CAGAGTAACAGACTAGCTAGAGA-CAATGA	GCACTTACCTGTGACTCCA-TAGAAA	*PIK3CA Exon10*
chr3	178936092	178936180	CGAGATCCTCTCTCTGAAATCAC-TGA	ACATGCTGAGATCAGCCAAATT	*PIK3CA Exon10*
chr3	178951824	178951942	TCTAATTTTGTGACATTTGAG-CAAAGAC	GAGCCAAGCATCATTGAGAAAA-GATT	*PIK3CA Exon21*
chr3	178951942	178952063	CGACAGCATGCCAATCTCTTCATA	CCATGATGTGCATCATTCATTT-GTTTCA	*PIK3CA Exon21*
chr3	178952063	178952155	AGCAAGAGGCTTTGGAGTATTTCA	AGAGTGAGCTTTCATTTTCTCAG-TTATC	*PIK3CA Exon21*
chr7	55241596	55241679	TGAGGTGACCCTTGTCTCTGT	CCAGCACTTTGATCTTTTT-GAATTCAGT	*EGFR Exon18*
chr7	55241679	55241800	AGCTCTCTTGAGGATCTT-GAAGGAA	AAATATACAGCTT-GCAAGGACTCTG	*EGFR Exon18*
chr7	55242411	55242539	ACGTCTTCCTTCTCTCTCTGTCA	CTGAGGTTCAGAGCCATGGAC	*EGFR Exon19*
chr7	55248984	55249117	GCCTCTCCCTCCCTCCA	GGTACTGGGAGCCAA-TATTGTCTTT	*EGFR Exon20*
chr7	55249117	55249200	CTGGACTATGTCCGGGAACAC	TGAGGATCCTGGCTCCTTATCTC	*EGFR Exon20*
chr7	55259367	55259486	TGAATTCGGATGCAGAGCTTCTT	CCAAAATCTGTGATCTT-GACATGCTG	*EGFR Exon21*
chr7	55259484	55259567	CAGGAACGTACTGGTGAAAACAC	CTGACCTAAAGCCACCTCCTTAC	*EGFR Exon21*
chr7	116411701	116411801	CTGTGGCTGAAAAAGAGAAA-GCAA	CAGAACTCATGGGTTTTATGGAC-TACAT	*cMET Intron13/14*
chr7	116411801	116411909	CGTCGATTCTTGTGTGCTGTCTTAT	GCATCGTAGCGAACTAATTCACTG	*cMET Exon14,cMET Intron13/14*
chr7	116411894	116411998	CGTCTTTAACAA-GCTCTTTCTTTCTCTCT	CGGTAGTCTACAGATTCATTT-GAAACCA	*cMET Intron13/14,cMET Exon14*
chr7	116411998	116412072	CGAAGTGTAAGCCCAAC-TACAGAAA	ACAACCCAC-TGAGGTATATGTATAGGT	*cMET Exon14*

chr7	140453023	140453099	CCTTCAATGACTTTCTAG-TAACTCAGCA	GTGGGTCCCATCAGTTTGAACA	*BRAF Exon15*
chr7	140453099	140453224	CATCCACAAAATGGATCCAGA-CAAC	GCTTGCTCTGATAGGAAAATGA-GAT	*BRAF Exon15*
chr7	140481297	140481387	GATGCGAACAGTGAA-TATTTCCTTTGA	TGGATCATTTGGAACAGTC-TACAAGG	*BRAF Exon11*
chr7	140481387	140481511	CACATTACATACTTACCATGCCAC-TTTC	TCTGTTTGGCTTGACTTGACTTT	*BRAF Exon11*
chr10	89624207	89624322	GCCATCTCTCTCCTCCTTTTTCTT	GTGACAGAAAGGTAAAGAG-GAGCA	*PTEN Exon1*
chr10	89653745	89653817	TCCAAACATTATTGCTATGGGAT-TTCCT	ATCTTTTTCTGTGGCTTA-GAAATCTTTTC	*PTEN Exon2*
chr10	89653816	89653930	TCCAAACATTATTGCTATGGGAT-TTCCT	ATCTTTTTCTGTGGCTTA-GAAATCTTTTC	*PTEN Exon2*
chr10	89685258	89685374	TGTTAATGGTGGCTTTTTGTTT-GTTTGT	TCTACCTCACTCTAACAAGCAGA-TAACT	*PTEN Exon3*
chr10	89690819	89690917	AACTTTTCTTTTAGTT-GTGCTGAAAGACATT	TCACTCGATAATCTG-GATGACTCATT	*PTEN Exon4*
chr10	89692713	89692819	TGCAACATTTCTAAAGTTAC-CTACTTGT	TGGTCAA-GATCTTCACAAAAGGGTTT	*PTEN Exon5*
chr10	89692819	89692920	TAACCCACCACAGCTA-GAACTTATC	TGCCCCGATGTAATAAA-TATGCACAT	*PTEN Exon5*
chr10	89692920	89693032	GAAAGGGACGAACTGGTG-TAATGAT	TCTCAGATCCAGGAAGAGGAAAG	*PTEN Exon5*
chr10	89711802	89711928	TGGCTACGACCCAGTTACCAT	CCACTGGTCTATAATCCAGATGAT-TCTT	*PTEN Exon6*
chr10	89711917	89712018	CAGTCAGAGGCGCTATGTG-TATTATTATA	TGGAAGGATGAGAATTTCAA-GCACTT	*PTEN Exon6*
chr10	89717580	89717695	CGACGGGAAGACAAGTTCATGTA	TCTGTCCTTATTTTGGA-TATTTCTCCCAATG	*PTEN Exon7*
chr10	89717694	89717792	CGACGGGAAGACAAGTTCATGTA	TCTGTCCTTATTTTGGA-TATTTCTCCCAATG	*PTEN Exon7*
chr10	89720692	89720768	TCACTTTTGGG-TAAATACATTCTTCATACCA	TTCCTTGTCATTATCTGCACGCT	*PTEN Exon8*
chr10	89720769	89720842	AAGAAATCGATAGCATTTGCAG-TATAGA	TGGAGAAAAGTATCGGTTGGCTTT	*PTEN Exon8*
chr10	89724948	89725061	TTACAGTGCTTAAAAATTAA-TATGTTCATCTGC	ATTTGACGGCTCCTCTACTGTTTT	*PTEN Exon9*
chr10	89725058	89725147	ATTTTCTTTCTCTAGGTGAAGCTG-TACTTC	ATCAGAGTCAGTGGTGTCAGAA-TATCTA	*PTEN Exon9*
chr10	89725207	89725320	AGAATGAACCTTTTGATGAA-GATCAGCA	TGTTCCTATAACTGG-TAATCTGACACA	*PTEN Exon9*
chr12	25380167	25380240	AATGTCAGCTTATTA-TATTCAATTTAAACCCAC	GCAATGAGGGACCAGTACATGA	*KRAS Exon3B,KRAS Exon3*
chr12	25380240	25380357	GAAAGCCCTCCCCAGTCC	GCACTGTAA-TAATCCAGACTGTGTTTC	*KRAS Exon3B,KRAS Exon3*
chr12	25398183	25398304	AAAGAATGGTCCTGCACCAGTAA	AGGCCTGCTGAAAATGACTGAA-TATAA	*KRAS Exon2*
chr12	25398304	25398379	CCAGCTCCAACTACCACAAGT	CTGGTGGAGTATTTGATAGTG-TATTAACCTT	*KRAS Exon2*
chr14	105246406	105246502	CCCCAAATCTGAATCCCGAGA	CGCTACTTCCTCCTCAA-GAATGATG	*AKT1 Exon4*
chr14	105246500	105246583	GCTCCTTGTAGCCAATGAAGGT	GGGTCTGACGGGTAGAGTGT	*AKT1 Exon4*
chr15	66727356	66727487	GTATTGACTTGTGCTCCCCACTT	CCCAGCTCACTGATCTTCTCA	*MAP2K1 Exon2*

chr15	66727487	66727602	GGAGAACTGAAGGATGACGACTT	GCTTCTAAGTACCCTGAGAAA-TAATCCA	*MAP2K1 Exon2*
chr17	7577017	7577142	CGCTTCTTGTCCTGCTTGCTTA	TCCTATCCTGAGTAGTGG-TAATCTACTG	*TP53 Exon8*
chr17	7577140	7577233	GCACCTCAAAGCTGTTCCGT	CAAGGGTGGTTGGGAGTAGATG	*TP53 Exon8*
chr17	7577392	7577509	GGGATGTGATGAGAGGTGGAT	CCATCCTCACCATCATCACACTG	*TP53 Exon7*
chr17	7577508	7577611	GGCTCCTGACCTGGAGTCTT	CATCTTGGGCCTGTGTTATCTCC	*TP53 Exon7*
chr17	7578141	7578234	GCCACTGACAACCACCCTTAA	GGAAGGAAATTTGCGTGTG-GAGTA	*TP53 Exon6*
chr17	7578234	7578362	GTCGAAAAGTGTTTCTGTCATCCAAA	TCAGATAGCGATGGTGAGCAG	*TP53 Exon6*
chr17	7578310	7578425	GACCTAAGAGCAATCAGTGAGGAA	CATCTACAAGCAGTCACAGCAC	*TP53 Exon5*
chr17	7578425	7578555	CGCCTCACAACCTCCGTCAT	CTCTGTCTCCTTCCTCTTCCTACA	*TP53 Exon5*
chr17	7579278	7579385	GGATACGGCCAGGCATTGAAG	TCATCTTCTGTCCCTTCCCAGA	*TP53 Exon4*
chr17	7579385	7579502	CGTAGCTGCCCTGGTAGGTTT	CTGAAGACCCAGGTCCAGATG	*TP53 Exon4*
chr17	7579502	7579590	CTCTGGCATTCTGGGAGCTT	ACTGCTCTTTTCACCCATCTACAG	*TP53 Exon4*
chr17	37880155	37880283	GCTCTTCTCACTCATATCCTCCTCTT	TCCTTCCTGTCCTCCTAGCAG	*HER2 Exon19*
chr17	37880960	37881074	GTGGTCTCCCATACCCTCTCA	GTCTAAGAGGCAGCCATAGGG	*HER2 Exon20*
chr17	37881074	37881206	CAGCTGGTGACACAGCTTATG	CCTAGCCCCTTGTGGACATAG	*HER2 Exon20*

Lung Cancer Panel LUN5

Chromo-som	**Start**	**Stop**	**f-primer**	**r-primer**	***Gene***
chr1	115252163	115252266	GTTAATCAACTGATGCAAACTCTTG	TGTGATTTGCCAACAAGGACA	*NRAS Exon4*
chr1	115252231	115252334	GTTTCAATGAATGGAATCCCGTA	CGTTTTTAGGGAGCAGATTAAGC	*NRAS Exon4*
chr1	115252279	115252382	TTTTGTATCAACTGTCCTTGTTGG	TGTACCCAGCCTAATCTTGTTT	*NRAS Exon4*
chr1	115256403	115256505	ACACAAAGATCATCCTTTCAGA-GAA	GAAGAGTACAGTGCCATGAGA	*NRAS Exon3*
chr1	115256473	115256565	GCTATTATTGATGGCAAATACACA	CAGAAAACAAGTGGTTATA-GATGGT	*NRAS Exon 3*
chr1	115256545	115256632	TTCTTGTCCAGCTGTATCCAG	GTGGTTTTTAATAAAAATT-GAACTTCCC	*NRAS Exon 3*
chr1	115258629	115258716	GGGTAAAGATGATCCGACAAGT	GAAAAGCGCACTGACAATCC	*NRAS Exon 2*
chr1	115258692	115258790	CCTCTATGGTGGGATCATATTCA	CTGGTTTCCAACAGGTTCTTG	*NRAS Exon 2*
chr2	29432600	29432708	GCCACACCCCATTCTTGAG	AAACTGCCTCTTGACCTGTC	*ALK Exon 25*
chr2	29432657	29432758	GGCAGTCTTTACTCACCTGTAG	CCTAGGGATAAAATTAG-GAAATGCAT	*ALK Exon 25*
chr2	29436828	29436911	GCGACAGGATGACAGGAAG	GCCATGCTGGACCTTCT	*ALK Exon 24*
chr2	29436880	29436984	TGAAGTGGTTTTCCTCCAAATACT	GATTTCCCTCCTCTCACTGAC	*ALK Exon 24*
chr2	29443562	29443666	ACTGCAGCAAAGACTGGTT	CAGAACATTGTTCGCTGCATT	*ALK Exon 23*
chr2	29443607	29443710	TCTCGGAGGAAGGACTTGAG	CAGTTAATTTT-GGTTACATCCCTCTC	*ALK Exon 23*
chr2	29445156	29445246	CGATCTGTTAGAAACCTCTCCAG	CCTGAAGTGTGCTCTGAACAG	*ALK Exon 22*
chr2	29445209	29445317	GGTGTCTCTCTGTGGCTTTAC	CTGTAGGCTGCAGTTCTCAG	*ALK Exon 22*
chr2	209113079	209113161	AAAAACATGCAAAATCACATTATTGC	CAGAGAAGCCATTATCTGCAA	*IDH1 Exon 4*
chr2	209113149	209113255	GTTTTACCCATCCACTCACAAG	CTCCTGATGAGAAGAGGGTTG	*IDH1 Exon 4*
chr2	209113211	209113305	GTGCCACCCAGAATATTTCGTA	CTGCAGAAGCTATAAAGAAGCA	*IDH1 Exon 4*
chr2	209113279	209113381	ACCCTCTTCTCATCAGGAGTG	TGCTTCTAATTTTTCTCTTTCAA-GCT	*IDH1 Exon 4*
chr2	209113372	209113459	GGTGGCATCACGATTCTCTATG	CGCTTTCTGCATAATGAGCTCTA	*IDH1 Exon 4*
chr3	41266002	41266080	ACATTTCCAATCTACTAATGCTAA-TACTG	CAGAGTCCAGGTAAGACTGTTG	*CTNNB1 Exon 3*
chr3	41266076	41266184	AAAAGCGGCTGTTAGTCACT	TGTTCCCACTCATACAGGACT	*CTNNB1 Exon 3*
chr3	41266173	41266265	CAATCCTGAGGAAGAGGATGT	CTGCATTCTGACTTTCAGTAAGG	*CTNNB1 Exon 3*

chr3	178936003	178936086	AGCTATATAAGA-TATTATTTTATTTTACAGAGTAAC	GAAAATCTTTCTCCTGCTCAGT	*PIK3CA Exon 10*
chr3	178936031	178936127	ACTAGCTAGAGA-CAATGAATTAAGGG	AAGAAACAGA-GAATCTCCATTTTAGC	*PIK3CA Exon 10*
chr3	178936071	178936173	CTCAAAGCAATTTCTACACGAGA	CTGAGATCAGCCAAATTCAGTTA	*PIK3CA Exon 10*
chr3	178951871	178951970	CCAAACTGACCAAACTGTTCTTA	ATCAAAAGATTGTAGTTCTGG-CATT	*PIK3CA Exon 21*
chr3	178951941	178952041	ACAGCATGCCAATCTCTTCAT	TCATGAAATACTCCAAAGCCTCTT	*PIK3CA Exon 21*
chr3	178952037	178952131	GAAAGACCCTAGCCTTAGA-TAAAAC	TTTCAGTTCAATGCATGCTGTT	*PIK3CA Exon 21*
chr3	178952116	178952199	CTGGACAACAAAAATGGATTGG	CTTTGCCTGCTGAGAGTTATTAAC	*PIK3CA Exon 21*
chr4	1800931	1801082	CACTGCTGTGTCTGTAAACG	CATCCTTGACCCAGACAGTG	*FGFR3 Exon 3*
chr4	1801025	1801159	CAGGAGCAGTTGGTCTTCG	CTCGTGGGAGGCATTCA	*FGFR3 Exon 3*
chr4	1801102	1801218	CCACTGTCTGGGTCAAGGAT	CACTGAAGTGGCACAGTAC	*FGFR3 Exon 3*
chr4	1801165	1801270	GGCTGCAGGTGCTGAAT	CTCGGCTCCTTTCTGTAGC	*FGFR3 Exon 6*
chr4	1803266	1803427	CATTGGAGGCATCAAGGTG	CCGGATGCTGCCAAACT	*FGFR3 Exon 6*
chr4	1803552	1803671	CCCCTGAGCGTCATCTG	GCTTGAGCCACTGGATGT	*FGFR3 Exon 7*
chr4	1803652	1803737	TGGAGTTCCACTGCAAGGT	CCACCTTGAGCACGGTAA	*FGFR3 Exon 7*
chr4	1803703	1803830	CAAGCACGTGGAGGTGAA	CCCTAGACCCAAATCCTCAC	*FGFR3 Exon 7*
chr4	1805950	1806092	GCGTGCTGAGGTTCTGA	GAGGATGCCTGCATACACA	*FGFR3 Exon 9*
chr4	1806052	1806135	CCTCAACGCCCATGTCTTT	GCCACCACCAGGATGAA	*FGFR3 Exon 9*
chr4	1806102	1806216	GCGGGCAGTGTGTATGC	CGGGAAGCGGGAGATCTT	*FGFR3 Exon 9*
chr4	1806147	1806258	CTTCTTCCTGTTCATCCTGGT	CAGCTCAGAACCTGGTATCT	*FGFR3 Exon 9*
chr4	1806459	1806573	ATGCTGGTGGAAGTCAGAAC	GTGGTGTGTTGGAGCTCAT	*FGFR3 Exon 10*
chr4	1806587	1806673	CGTCCATGAGCTCCAACA	CCCGAGACAGCTCCCATT	*FGFR3 Exon 10*
chr4	1806648	1806745	ACGCTGGCCAATGTCTC	TGACTGGTGGCTGTTTCAC	*FGFR3 Exon 10*
chr4	1807209	1807334	TGAAGATGCTGAAAGGTGAGG	TGTGTTTCCCGATCATCTTCAT	*FGFR3 Exon 12*
chr4	1807330	1807481	GACCTGGTGTCTGAGATGG	TACTCCACCAGCACGTACA	*FGFR3 Exon 12*
chr4	1807752	1807866	GAGAGGTGGAGAGGCTTCA	TTCTTGTAGTAGTCGAGGTTGTG	*FGFR3 Exon 14*
chr4	1807833	1807930	TGACCGAGGACAACGTGAT	GCGTCCTACTGGCATGAC	*FGFR3 Exon 14*
chr4	1808249	1808351	CCTGGGAGTCTCAGGACAG	CCTCCTTCAGCAGCTTGA	*FGFR3 Exon 16*
chr4	1808282	1808392	CCTGCAGCTGGTCCTTT	CAGGTCGTGTGTGCAGTT	*FGFR3 Exon 16*
chr4	1808356	1808497	CCTGTGGAGGAGCTCTTCAA	CCGCCTTATTCGGGAACAG	*FGFR3 Exon 16*
chr4	1808877	1809002	GCGCCTTTCGAGCAGTA	GGACCCCTCACATTGTTGG	*FGFR3 Exon 18*
chr5	176517268	176517427	GTGTGGGTGTCAAGGAGTG	CAAGGGCTACTGTCAGCTC	*FGFR4 Exon 3*
chr5	176517446	176517556	GGAGCTGACAGTAGCCCTT	GGTAGGAAGCTGGCAATCTC	*FGFR4 Exon 3*
chr5	176517505	176517615	TGGCCACTGGTACAAGGA	AGATTCTGCAGGACGATCATG	*FGFR4 Exon 3*
chr5	176517564	176517663	GGGCCGCCTAGAGATTG	TCCCTTCACTCCCTGCTAG	*FGFR4 Exon 3*
chr5	176518651	176518787	CCCCCTTGGTGGACATG	CAGCACATCTAGCAGGTAGT	*FGFR4 Exon 6*
chr5	176518719	176518842	CTGGAGTCTCGTGATGGAGA	CACAACTGAGCCCAAAATGG	*FGFR4 Exon 6*
chr5	176520107	176520188	TCTCACCACTGACCAGTTTG	CCGACGCGTACAGGATGA	*FGFR4 Exon 9*
chr5	176520183	176520290	GCCCGAGGCCAGGTATA	GAGAGCTTCTGCACAGTGG	*FGFR4 Exon 9*
chr5	176520311	176520394	CACTGTGCAGAAGCTCTCC	AGGGAGAACTGCAAAGTGG	*FGFR4 Exon 9*
chr5	176522257	176522368	GGTCCAGTGCTGCTTGT	TCAGCTTCATCACCTCCATCT	*FGFR4 Exon 12*
chr5	176522335	176522473	TGCTGCCCTTACAGACAAC	CTTTGGCTCTGCACCCTAA	*FGFR4 Exon 12*
chr5	176522549	176522697	GGGCCCCTGTACGTGAT	GGACTCCAGATACTGCATGC	*FGFR4 Exon 13*
chr5	176522709	176522847	CCCGAGGCATGCAGTAT	AATGCAGGAAAGCGTGAATG	*GFR4 Exon 13*
chr5	176523269	176523388	GTGGGACTCTGCACTGAG	GTGCCTTGCCCTTTTTGTG	*FGFR4 Exon 15*
chr5	176523535	176523654	GTGGTGGGTCATGTCTGTG	ACCGGGATGCCAGGATAC	*FGFR4 Exon 16*
chr5	176523641	176523767	CTGCTATGGGAGATCTTCACC	AGGAGGAGGACTGGAAAGTG	*FGFR4 Exon 16*
chr6	117629921	117630024	AAGATTGTATGTGCACATGTTTTTG	GCCTTATCCAGCTCATTCCAA	*ROS1 Exon 41*
chr6	117629975	117630068	AACTTACAGATCATCAG-GACAATTTC	AGGTCTTTTGGAATTCTGATTTGG	*ROS1 Exon 41*
chr6	117630032	117630131	ATAGTTTAACACATCAAGGTT-GGAAT	AGAAACTACTGTAAACCTGGTGTT	*ROS1 Exon 41*
chr6	117631231	117631325	TGTCAGCATTACTCTGTGTCC	CAGAGACATCTATAAAAATGAT-TACTATAGAAAG	*ROS1 Exon 40*

chr6	117631297	117631402	CATCAAACTTTCTGGAGCCATC	GCCTTGTTTCCGTGAAAGACT	*ROS1 Exon 40*
chr6	117631389	117631490	TCCAAAGTCTCCAATCTTCACTAT	GGCTACTTCTTTGATTTCTGGAAC	*ROS1 Exon 40*
chr6	117632173	117632259	CGTAATAACCCTGTATCCAGAAGA	TTACAG-TTTTATGGTCCTTTACTCAC	*ROS1 Exon 39*
chr6	117632201	117632301	GTACCTGTGAATGAAATGCATCC	TCATGCAAACTAGATAACTAC-CTGTA	*ROS1 Exon 39*
chr6	117638283	117638383	GGCATTTGCATTATGAAACCAAT	GCTTGGAGTTTGTCTGCTGAA	*ROS1 Exon 38*
chr6	117638336	117638431	CGGGCTTTACGCAAATAAGTA	TGTCTTTCCACCTTTCAGCAA	*ROS1 Exon 38*
chr6	117638399	117638492	GGTTCATTCAGCAGACAAACT	GAATTGCTGTACTCCATAAAGACC	*ROS1 Exon 38*
chr6	117639334	117639431	CTTCTTACCCATACCAGGAGAAA	GTCTGCTATACTGATTCCTGACTT	*ROS1 Exon 37*
chr6	117640996	117641090	AGGTCAATCTTTGTAGA-TATGGTGAT	TGGAGCCTTTGGAGAAGTGTA	*ROS1 Exon 36*
chr6	117641085	117641183	CCTAAGATGTCCACTGCTGTT	ATGTTGCTATTTTACAG-TACTCTTCC	*ROS1 Exon 36*
chr6	117641168	117641251	AGGGAAGGCAGGAAGATTTTC	CAAACACAAATACCAATAC-CAACAC	*ROS1 Exon 36*
chr6	117642406	117642481	GCCTAGGTGCTCCATAATGATG	GTGCTTATAAACGAAGACAAA-GAGT	*ROS1 Exon 35*
chr6	117642444	117642544	GTATTGCATAGCAGGCATTAGC	TTTTTCCTTTATAGTCTGGCATA-GAA	*ROS1 Exon 35*
chr6	117642509	117642607	TCTTTGTCTTCGTTTATAAGCACTG	GCACTGTTAACATTTCCTAAAGGA	*ROS1 Exon 35*
chr6	117645470	117645556	TATGATTAAGTAAACAGTTTGTT-GCCTA	ATTTATATTATTAGATGATTTTT-GGATACCAGAAA	*ROS1 Exon 34*
chr6	117645510	117645608	CTTACCAAAGGTCAGTGGGAT	GGGCAACTTAGCTTTTATCTATGA	*ROS1 Exon 34*
chr7	55241596	55241689	AGGTGACCCTTGTCTCTGT	AGCCCAGCACTTTGATCTTT	*EGFR Exon 18*
chr7	55241631	55241731	GCTTGTGGAGCCTCTTACA	TGCCAGGGACCTTACCTTA	*EGFR Exon 18*
chr7	55241674	55241776	AAGCTCTCTTGAGGATCTTGA	CCCCACCAGACCATGAGAG	*EGFR Exon 18*
chr7	55242402	55242508	GCCAGTTAACGTCTTCCTTCTC	GCAAAGCAGAAACTCACATCG	*EGFR Exon 19*
chr7	55242461	55242562	GAAAGTTAAAATTCCCGTCGCTAT	TGCCAGACATGAGAAAAGGTG	*EGFR Exon 19*
chr7	55248999	55249101	TCCAGGAAGCCTACGTGAT	GTCTTTGTGTTCCCGGACATA	*EGFR Exon 20*
chr7	55249104	55249198	GGCTGCCTCCTGGACTA	GATCCTGGCTCCTTATCTCC	*EGFR Exon 20*
chr7	55259390	55259495	CATGATGATCTGTCCCTCACA	CCAGCCCAAAATCTGTGATCT	*EGFR Exon 21*
chr7	55259432	55259537	GGCATGAACTACTTGGAGGAC	TCCTTCTGCATGGTATTCTTTCT	*EGFR Exon 21*
chr7	55259482	55259580	CAGGAACGTACTGGTGAAAAC	GGAAAATGCTGGCTGACCTAA	*EGFR Exon 21*
chr7	116411694	116411786	TTTTTCCTGTGGCTGAAAAAGAG	TGGACTACATATAAGACAG-CACAC	*MET Intron13_14*
chr7	116411759	116411853	TAGAAGTTACCTTAAGAACACAG-TCA	TGTTAAAGACGGCTATCATGGG	*MET Intron13_14*
chr7	116411825	116411924	ATGTAGTCCATAAAACCCATGAGT	AGTGTGTACTCTTGCATCGTA	*MET Exon 14*
chr7	116411915	116412020	TGTTTTAAGATCTGGGCAGTGA	CTTCTGGAAAAGTAGCTCGGTA	*MET Exon 14*
chr7	116412002	116412099	AAGCCCAACTACAGAAATGGT	GCAAAACCAAAAA-TAAACAACAATGT	*MET Exon 14*
chr7	116412053	116412151	GCTACTTTTCCAGAAGGTATATTTCA	CTTACTTGGCAGAGGTAAA-TACTTC	*MET Intron 14_15*
chr7	116412098	116412192	CCTATACATATACCTCAGTGGGTTG	GGTTCTTTTAAAATTAA-GAGCCATGT	*MET Intron 14_15*
chr7	116417432	116417522	GCAGTGCTAACCAAGTTCTTTC	CCATGGTTAAATAAAATGCCAC-TTAC	*MET Exon 16*
chr7	116417511	116417611	CAAGAAAATTCACTGTGCTGTGA	GTAGCTGATTTTTCCACAAGGG	*MET Exon 16*
chr7	116418794	116418890	TTTGACAAAAGTATTCAC-TGTTCCAT	CGAGAGGACATTGGGATGACT	*MET Exon 17*
chr7	116418876	116418971	CAATTTCTGACCGAGGGAATC	GAATGAAATTTCGAA-GATCTCCATG	*MET Exon 17*
chr7	116418911	116419015	TTTAGTCATCCCAATGTCCTCTC	AGTTAGTAAGCTTGGCAGTCAA	*MET Exon 17*
chr7	116418976	116419060	TGGTCCTACCATACATGAAACATG	GCAGGCCTATTTTGAAGGGAT	*MET Exon 17*
chr7	116422007	116422092	GGTCAAAATTAGAACAG-TAGATGCT	AAACTTTTTGCTTGCAAGA-TATTTCA	*MET Exon 18*

chr7	116422039	116422150	GCTTTTCTAACTCTCTTTGACTGC	TGGCACAGAGATTCTGATACTTAC	*MET Exon 18*
chr7	116422116	116422199	CATGAAATATCTTGCAA-GCAAAAAG	CATTGAACAGTGGGAAACAGATT	*MET Exon 18*
chr7	116423336	116423438	TTATTCTATTTCAGCCACGGGTAA	CAGCTTTGCACCTGTTTTGTT	*MET Exon 19*
chr7	116423423	116423520	TGCCAGAGACATGTATGATAAAGA	ACTCAGAGATAAC-CAATACATTACCA	*MET Exon 19*
chr7	116423515	116423611	AACTCAAAAGTTTACCACCAAGT	CTGGAATTGGTGGTGTTGAATT	*MET Exon 19*
chr7	140453056	140453155	GGCCAAAAATTTAATCAGTGGAAA	CATGAAGACCTCACAGTAAAAA-TAGG	*BRAF Exon 15*
chr7	140453105	140453202	AATGGATCCAGACAACTGTTCA	AATGA-GATCTACTGTTTTCCTTTACTTAC	*BRAF Exon 15*
chr7	140481364	140481452	ACTTGTCACAATGTCACCACAT	ACTCGAGTGATGATTGGGAGA	*BRAF Exon 11*
chr7	140481429	140481511	AATGATCCAGATCCAATTCTTTGTC	TCTGTTTGGCTTGACTTGACTT	*BRAF Exon 11*
chr8	38272035	38272123	GACTCTACAGTGCTAGAAGCTC	GACTGCCTGTGAAGTGGAT	*FGFR1 Exon 15*
chr8	38272114	38272239	GTGTAGATCCGGTCAAATAATGC	TTCATCTGAGAAGCAAGGAGTG	*FGFR1 Exon 15*
chr8	38272270	38272362	GCTTCTCAGATGAAACCACCAG	GGTGACAGAGGACAATGTGAT	*FGFR1 Exon 14*
chr8	38272307	38272412	GCACTCACGTTGGTTGTCT	TCCTCCTTCCTCAGTGCATA	*FGFR1 Exon 14*
chr8	38272381	38272488	TCTTCATCACATTGTCCTCTGTC	AAGTCGGCTAGTTGCATGG	*FGFR1 Exon 14*
chr8	38273361	38273481	TGTTCCCACCCTGGCATTA	GGCTGGAATACTGCTACAACC	*FGFR1 Exon 13*
chr8	38273408	38273559	CTTCTTGGAGGCCAGATACTC	CAGGTCCCTTGTATGTCATCG	*FGFR1 Exon 13*
chr8	38273555	38273690	GTTGCCCTTGGAGGCATA	CCAGGTCCCCTAAGAGGAG	*FGFR1 Exon 13*
chr8	38274785	38274877	TACCCCAGCTCAGATCTTCTC	TCTCAGAAATGGAGATGATGAAG	*FGFR1 Exon 12*
chr8	38274862	38274946	CCCAGCAGGTTGATGATATTCT	CTTCCCAAGTAAATGAGTCTCAAC	*FGFR1 Exon 12*
chr8	38275736	38275857	CCTTCAAAAAGTTGGGAGTCAAAG	CCAGTGCATCCATGAACTCT	*FGFR1 Exon 10*
chr8	38275798	38275907	GGGAAGCTCATACTCAGAGAC	CTCCTTGCTCTAGGGTGAC	*FGFR1 Exon 10*
chr8	38281997	38282087	TGGTCTCCTTCCCAGTAGAC	CACATCCAGTGGCTAAAGC	*FGFR1 Exon 7*
chr8	38282027	38282129	AAGACTGGTGCCATGATTACC	GCAACGTGGAGTTCATGTGTA	*FGFR1 Exon 7*
chr8	38282106	38282215	GTGCTTTAGCCACTGGATGT	CCTCTCCCATCTTCCACAGA	*FGFR1 Exon 7*
chr8	38282150	38282258	CTTACACATGAACTCCACGTTG	CACCCCTCTTTAGCCATGG	*FGFR1 Exon 7*
chr8	38283611	38283700	CTGGCTCTTCCCACTAAACTC	CCTCTGACAAGGGCAACTA	*FGFR1 Exon 6*
chr8	38283670	38283771	CAGCTGGTATGTGTGGTTGAT	CTCAATGTATCCCTTTGGCATT	*FGFR1 Exon 6*
chr8	38283741	38283849	GCACCACAGAGTCCATTATGA	CCACCAGGCTCTGATATGGA	*FGFR1 Exon 6*
chr8	38285427	38285528	CATTACTCTAACTTTCGCATGCA	TGCCAAGACAGTGAAGTTCAA	*FGFR1 Exon 5*
chr8	38285490	38285592	GTTTGAATTCTTTGCCATTTTTCAAC	GCCGTAGCTCCATATTGGA	*FGFR1 Exon 5*
chr8	38285588	38285738	GCAATTTCTTTTCCATCTTTTCTGG	GGTGCCTGTTCTGCTAAGTG	*FGFR1 Exon 5*
chr8	38285854	38285949	AAAGGGCAGTAAGATAGGAAACA	CCCCTTCTTCTTCCCATAGATG	*FGFR1 Exon 4*
chr8	38285890	38285993	CGGTTTGGTTTGGTGTTATCTG	CTAGCCTTGGTGAAATCTAGGG	*FGFR1 Exon 4*
chr10	89624163	89624266	CATTTCCATCCTGCAGAAGAAG	TCGAATCCATCCTCTTGATATCTC	*PTEN Exon 1*
chr10	89624241	89624331	CCAGACATGACAGCCATCATC	GTTCTAAGAGAG-TGACAGAAAGGTA	*PTEN Exon 1*
chr10	89653754	89653850	TAGTTTGATTGCTG-CATATTTCAGAT	AGCATTCTTACCTTACTA-CATCATCA	*PTEN Exon 2*
chr10	89653838	89653932	GCAGAAAGACTTGAAGGCGTAT	ATCTTTTTCTGTGGCTTA-GAAATCTT	*PTEN Exon 2*
chr10	89685247	89685336	CTCATTTTTGTTAATGGTGGCTTTT	GTTGTTTTAGAAGATATTTGCAA-GCA	*PTEN Exon 3*
chr10	89690791	89690860	GTGCAAAAGATAACTTTATATCAC-TTTTAAAC	CGGGTTTAAGTTATA-CAACATAGTACAG	*PTEN Exon 4*
chr10	89692710	89692805	GTATGCAACATTTCTAAAGTTAC-CTACT	ACAAAAGGGTTTGA-TAAGTTCTAGC	*PTEN Exon 5*
chr10	89692777	89692878	TTATCTTTTTACCACAGTTGCACAA	CCCTTTCCAGCTTTACAGTGAAT	*PTEN Exon 5*
chr10	89692871	89692974	GGCTAAGTGAAGATGACAATCATG	TGGTCCTTACTTCCCCATAGAA	*PTEN Exon 5*
chr10	89692964	89693044	GGGCAAATTTTTAAAGGCACAAG	TCTGTTTTCCAA-TAAATTCTCAGATCC	*PTEN Exon 5*
chr10	89711816	89711916	CCAGTTACCATAGCAATTTAG-TGAA	CCAGATGATTCTTTAACAGGTAGC	*PTEN Exon 6*
chr10	89711888	89711984	CCACCAGGGAGTAACTATTCC	CGCCACTGAACATTGGAATAGT	*PTEN Exon 6*

chr10	89711943	89712025	GCTACCTGTTAAAGAATCATCTG-GAT	CAATACATGGAAGGATGA-GAATTTC	*PTEN Exon 6*
chr10	89717595	89717682	TTTCCTGTGAAATAATACTGG-TATGT	AG-GGAACTCAAAGTACATGAACTT	*PTEN Exon 7*
chr10	89717646	89717748	CTGCCAGCTAAAGGTGAAGAT	TTTTTAGCATCTTGTTCTGTTTGTG	*PTEN Exon 7*
chr10	89717688	89717789	CACGACGGGAAGACAAGTT	CCTTATTTTGGA-TATTTCTCCCAATGAA	*PTEN Exon 7*
chr10	89720575	89720719	AATGTTTAACATAGGTGACAGAT-TTTCT	TTTCTTGATCACATA-GACTTCCATTTT	*PTEN Exon 8*
chr10	89720755	89720850	GTCTATGTGATCAAGAAATCGA-TAGC	GACCTTAAAATTTGGA-GAAAAGTATCG	*PTEN Exon 8*
chr10	89720786	89720892	ATAGAGCGTGCAGATAATGACA	AAGTCAACAACCCCCACAAA	*PTEN Exon 8*
chr10	123239322	123239413	GGTCTCCCTGCTCAGTGTA	CCCATGCCTTACGAACCAT	*FGFR2 Exon 18*
chr10	123239392	123239495	TTCATGTTTTAACACTGCCGTTT	CCAACCTCTCGAACAGTATTCA	*FGFR2 Exon 18*
chr10	123239466	123239545	AAAAACAGAATCATCTCCTGAAGA	CAAGATGAAATAAAAC-GTCTCTCTTC	*FGFR2 Exon 18*
chr10	123246845	123246940	CTCAAGCCCAGGAAAAAGC	AGTTTTTGCATTTTCCTC-TACATTTG	*FGFR2 Exon 15*
chr10	123246908	123246981	TGTATACTCTATCAAACAGGGCTTC	CCTATTGAGCCTGCTAAGA-TAAATT	*FGFR2 Exon 15*
chr10	123247460	123247557	CTTTCTTCCTGGAACATTCTGAG	AAAACAATGTGATGAAAA-TAGCAGAC	*FGFR2 Exon 15*
chr10	123247529	123247625	CATTGGTGGTCTTTTTGTAATAGTCT	CTCTTGCTTCTTTCTTGATTTCAGT	*FGFR2 Exon 14*
chr10	123247620	123247722	TTTCTGGCTGCTAAATCTCGAT	GCAACTGGTTTTTAACATCAGC-TAT	*FGFR2 Exon 14*
chr10	123256036	123256128	CCCAGCCAAGTAGAATGTGA	ACTCCTATGACATTAACCGTGTT	*FGFR2 Exon 14*
chr10	123256117	123256218	CACCAAGTCCTTGAAGGTCAT	AACAGGGCCTCTCTATGTCATA	*FGFR2 Exon 13*
chr10	123256191	123256283	CGGGCTCGGAGGTATTCTC	TTTTGCTGAATTGCCCAAGG	*FGFR2 Exon 13*
chr10	123257995	123258094	GTATTTGGGCGAATGCAGTTTT	ATGCCACAGAGAAAGACCTTT	*FGFR2 Exon 12*
chr10	123258064	123258142	TGATATTCTTGTGTTTCCCAATCATC	CATGAGTTAGAG-GAAATGAACTGATT	*FGFR2 Exon 12*
chr10	123260302	123260385	GGAACTTTCTTGATAAGACTCTCCA	GGAAGCAGTGGGAATTGACAA	*FGFR2 Exon 11*
chr10	123260353	123260454	CGCTCACCTTTCAACATCTTC	CCCTATTTACACATTTAGGCTGAC	*FGFR2 Exon 11*
chr10	123260401	123260505	CTTGTCTTTGTCAATTCCCACT	TTCTGGAATTTCCCTCACTACAC	*FGFR2 Exon 11*
chr10	123263278	123263381	ATTTATAGCTGAGTCTCCATCCTG	AACAACACGCCTCTCTTCAA	*FGFR2 Exon 10*
chr10	123263355	123263457	TCTGGAAGTTCATACTCGGAGA	CATCTGTGTCTTTGCATTTTGTATC	*FGFR2 Exon 10*
chr10	123263438	123263528	GTGTTGGAGTTCATGGAGGAG	TCCTTTCTAAGATTCGATACTCTGG	*FGFR2 Exon 10*
chr10	123274571	123274690	CATCAAAGCAGAGGACAAGATC	CGACCAAGAAGCCAGACTT	*FGFR2 Exon 10*
chr10	123274671	123274776	GGATACGTTTGGTCAGCTTGT	AGACTACCTGGAGATAGCCATT	*FGFR2 Exon 9*
chr10	123274747	123274835	CAGGATGACTGTTACCACCAT	CTCCTCCTGTGATCTGCAATC	*FGFR2 Exon 9*
chr10	123274770	123274876	AGGCGATTAAGAAGACCCCTA	GTCAGTCTGGTGTGCTAACTC	*FGFR2 Exon 9*
chr10	123276787	123276869	AAGCTGTGTTAATTTTATAGCAG-TCA	CTTGGCGGGTAATTCTATTGG	*FGFR2 Exon 8*
chr10	123276843	123276947	GAACAGTATATACCTGGCAGAACT	TGTTAACACCACGGACAAAGA	*FGFR2 Exon 8*
chr10	123276891	123276996	CCAATAGAATTACCCGCCAAG	CTGTGTCGTCTAGCCTTTTCTT	*FGFR2 Exon 8*
chr10	123278161	123278241	TTCAGCTTCTATATCCAGCTTTCT	GGAATATATATGTAAGGTCTCCAA TTATATAGG	*FGFR2_NM_022970 Exon8*
chr10	123278193	123278295	AAAAAGACAAAAATGAAAGCATT-GTT	GAAGTGCTGGCTCTGTTCAA	*FGFR2_NM_022970 Exon8*
chr10	123278254	123278352	GTTGGCCTGCCCTATATAATTG	GCCGTTATATTGTTCTCCTGTG	*FGFR2_NM_022970 Exon8*
chr10	123279434	123279539	AACAGGAAATCAAAGAACCTGTG	ATCAAGCACGTGGAAAAGAAC	*FGFR2 Exon 7*
chr10	123279496	123279600	TAGATTCAGAAAGTCCTCACCTTG	CGGAGGAGACGTAGAGTTTGT	*FGFR2 Exon 7*
chr10	123279596	123279714	CTGGGCATCACTGTAAACCT	TTATTGGTCTCTCATTCTCCCATC	*FGFR2 Exon 7*
chr10	123298066	123298168	CAAACGAGTCAAGCAAGAATGG	GTCCCATCTGACAAGGGAAAT	*FGFR2 Exon 6*
chr10	123298136	123298238	CAGGTGGTACGTGTGATTGAT	GTTAAATAACCGCCTTTGCTTTG	*FGFR2 Exon 6*

chr12	25378528	25378623	TGATTTTGCAGAAAACAGATCTG-TAT	TAAATGTGATTTGCCTTCTA-GAACAG	*KRAS Exon 4*
chr12	25378580	25378667	GTCTTTGCTGATGTTTCAA-TAAAAGG	AGTTAAGGACTCTGAAGATGTACC	*KRAS Exon 4*
chr12	25378620	25378719	AGTCCTGAGCCTGTTTTGTG	TGTTACTAATGACTGTGC-TATAACTTTT	*KRAS Exon 4*
chr12	25380109	25380204	CATGGCATTAGCAAAGACTCAA	GGCTTTCTTTGTGTATTTGCCATA	*KRAS Exon 3*
chr12	25380199	25380295	CTATAATGGTGAA-TATCTTCAAATGATTTAGT	TGGAGAAACCTGTCTCTTGGA	*KRAS Exon 3*
chr12	25380259	25380354	CCTCATGTACTGGTCCCTCAT	CTGTAA-TAATCCAGACTGTGTTTCTC	*KRAS Exon 3*
chr12	25380295	25380397	GACCTGCTGTGTCGAGAAT	TGTTGTTGAGTTGTATATAACAC-CTTTT	*KRAS Exon 3*
chr12	25398188	25398288	GGTCCTGCACCAGTAATATGC	ACTGAATATAAACTTGTGGTAG-TTGG	*KRAS Exon 2*
chr12	25398258	25398351	CACAAAATGATTCTGAATTAGCTG-TAT	TTATGTGTGACATGTTCTAA-TATAGTCAC	*KRAS Exon 2*
chr15	66727346	66727442	TGGTGACAGTATTGACTTGTG	CACCTTCTGCTTCTGGGTAAG	*MAP2K1 Exon 2*
chr15	66727391	66727521	GGAGGCCTTGCAGAAGAA	GGAGACCTTGAACACCACAC	*MAP2K1 Exon 2*
chr15	66727476	66727579	CAGAAGGTGGGAGAACTGAAG	CCAATTAC-CTGTTAATCAAGGCAAA	*MAP2K1 Exon 2*
chr15	66727541	66727639	GGTGTGGTGTTCAAGGTCTC	AGTAAAATCAGTCTTCCTTC-TACCC	*MAP2K1 Exon 2*
chr15	66729065	66729163	CCTCTTTCTTTCATAAAACCTCTCTT	ACCATAGAAGCCCACGATGTA	*MAP2K1 Exon 3*
chr15	66729128	66729226	GCAATCCGGAACCAGATCATA	TGAGAGGGTGTCACATACCAT	*MAP2K1 Exon 3*
chr15	66729183	66729280	CGTACATCGTGGGCTTCTATG	CAGACCAAAGATTAGGCCAGAG	*MAP2K1 Exon 3*
chr15	90631798	90631891	TGCCCAGGTCAGTGGATC	CCGGGAGCCCATCATCT	*IDH2 Exon 4*
chr15	90631887	90631985	GGACTAGGCGTGGGATGTT	GTGGGACCACTATTATCTCTGTC	*IDH2 Exon 4*
chr15	90631975	90632080	TTTTCCACATCTTCTTCAGCTTG	ACTCTACTGCCTTCCTCATGA	*IDH2 Exon 4*
chr17	7576976	7577069	ATAAAAGTGAATCTGAGGCATAACTG	CGCACAGAGGAAGAGAATCTC	*TP53 Exon 8*
chr17	7577017	7577123	GCTTCTTGTCCTGCTTGCTTA	GGGACGGAACAGCTTTGAG	*TP53 Exon 8*
chr17	7577079	7577178	CCCTTTCTTGCGGAGATTCTC	CTGATTTCCTTACTGCCTCTTG	*TP53 Exon 8*
chr17	7577425	7577548	TGGAAGAAATCGGTAAGAGGTG	TGTAACAGTTCCTGCATGGG	*TP53 Exon 7*
chr17	7577520	7577626	GGAGTCTTCCAGTGTGATGA	CGCACTGGCCTCATCTTG	*TP53 Exon 7*
chr17	7578142	7578243	CCACTGACAACCACCCTTAAC	CCGAGTGGAAGGAAATTTGC	*TP53 Exon 6*
chr17	7578222	7578298	CCACACTATGTCGAAAAGTGTTT	GGCCTCTGATTCCTCACTGA	*TP53 Exon 6*
chr17	7578317	7578422	GCAATCAGTGAGGAATCAGAGG	ACAAGCAGTCACAGCACAT	*TP53 Exon 5*
chr17	7578382	7578482	CTGCTCACCATCGCTATCTG	TGCAGCTGTGGGTTGATTC	*TP53 Exon 5*
chr17	7578427	7578529	CTCACAACCTCCGTCATGT	CCCTGCCCTCAACAAGATG	*TP53 Exon 5*
chr17	7578523	7578604	GCAGGTCTTGGCCAGTT	GCCGTCTTCCAGTTGCTTTAT	*TP53 Exon 5*
chr17	7579290	7579377	GCATTGAAGTCTCATGGAAGC	TGTCCCTTCCCAGAAAACCTA	*TP53 Exon 4*
chr17	37868129	37868236	CACGGTAATGCTGCTCATG	TCCTCTGCTGTCACCTCTT	*ERBB2 Exon 8*
chr17	37868191	37868299	CTGATCTCCTTAGACAACTACCTT	GGGCAGTGAGTGGGTAC	*ERBB2 Exon 8*
chr17	37868262	37868370	GTGACAGCAGAGGATGGAAC	TCTGAGGAAGGATAGGACAGG	*ERBB2 Exon 8*
chr17	37880155	37880236	TCTTCTCACTCATATCCTCCTCTT	TCTAAGATTTCTTTGTTGGCTTTGG	*ERBB2 Exon 19*
chr17	37880219	37880328	CCAGTGGCCATCAAAGTGT	AAACCCCAATGAAGAGAGACC	*ERBB2 Exon 19*
chr17	37880952	37881061	GGGTGTGTGGTCTCCCATA	CCATAGGGCATAAGCTGTGT	*ERBB2 Exon 20*
chr17	37881019	37881130	GGGCTCCCCATATGTCTC	ATACACCAGTTCAGCAGGTC	*ERBB2 Exon 20*
chr17	37881095	37881204	CCTATGGCTGCCTCTTAGAC	TAGCCCCTTGTGGACATAGG	*ERBB2 Exon 20*

3. Fluorescence in situ Hybridization (FISH)

FISH assays were carried out to determine rearrangements and/or amplifications. Analyses of *MET* amplification, *RET-*, *ROS1-* and *ALK*-rearrangements were performed as described previously [21–24] Regarding to *MET* amplification it was differentiated

between low-, intermediate- and high-level amplification according to the criteria described by Schildhaus et al [25].

Table S4. FISH probes for *ALK*, *MET*, *RET* and *ROS1.*

Name	Company	Order Number
ZytoLight SPEC ALK/EML4 TriCheck Probe	Zytomed, Germany	Z-2117-200
ZytoLight SPEC MET/CEN7 Dual Color Probe	Zytomed, Germany	Z-2087-200
ZytoLight SPEC RET Dual Color Break Apart Probe	Zytomed, Germany	Z-2148-200
ZytoLight SPEC ROS1 Dual Color Break Apart Probe	Zytomed, Germany	Z-2144-200

Supplementary Material References

19 Michels, S.; Heydt, C.; van Veggel, B.M; Deschler-Baier, B.; Pardo, N.; Monkhorst, K.; Rüsseler, V.; Stratmann, J.; Griesinger, J.; Steinhauser, S.; et al. Genomic Profiling Identifies Outcome-Relevant Mechanisms of Innate and Acquired Resistance to Third-Generation Epidermal Growth Factor Receptor Tyrosine Kinase Inhibitor Therapy in Lung Cancer. *JCO Precis. Oncol.*, **2019**.

20 Peifer, M.; Fernández-Cuesta, L.; Sos, M.L.; George, J.; Seidel, D.;Kasper, L.H.;Plenker, D.; Leenders, F.; Sun, R.; Zander, T.; et al., Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. *Nat. Genet.*, **2012**, *44*, 1104–10.

21 Heydt, C.; Kostenko, A.; Merkelbach-Bruse, S.; Wolf, J.; Büttner, R. ALK evaluation in the world of multiplex testing: Network Genomic Medicine (NGM): the Cologne model for implementing personalised oncology. *Ann. Oncol.*, **2016**. 27 *Suppl 3*, iii25–iii34.

22 Michels, S., Scheel, A.H.; Scheffler, M.; Schultheis. A.M.; Gautschi, O.; Aebersold. F.; Diebold, J.; Pall. G.; Rothschild, S.; Bubendorf. L.; et al., Clinicopathological Characteristics of RET Rearranged Lung Cancer in European Patients. *J. Thorac. Oncol.*, **2016**, *11*, 122

23 Scheffler, M., Schultheis, A.; Teixido, C.; Michels, S.; Morales-Espinosa. D.; Viteri. S.; Hartmann, W.; Merkelbach-Bruse. S.; Fischer. R.; Schildhaus, H.-S.; et al., ROS1 rearrangements in lung adenocarcinoma: prognostic impact, therapeutic options and genetic variability. Oncotarget, **2015**, *6*, 10577–10585.

24 Wolff, A.C., Hammond, M.E.H.; Hicks, D.G.; Dowsett, M.; McShane, L.M.; Allison, K.H.; Allred, D.C.; Bartlett, J.M.S.; Bilous, M.; Fitzgibbons, P.; et al., Recommendations for Human Epidermal Growth Factor Receptor 2 Testing in Breast Cancer American Society of Clinical Oncology/College of American Pathologists Clinical Practice Guideline Update. *Arch. Pathol. Lab. Med.*, **2014**, *138*, 241–256.

25 Schildhaus, H.U., Schultheis. A.M.; Rüschoff. J.;Binot. E.; Merkelbach-Bruse, S.; Fassunke, J.; Schulte. W.; Ko, Y.-D.;Schlesinger. A.; Bos, M.; et al., MET amplification status in therapy-naive adeno- and squamous cell carcinomas of the lung. *Clin. Cancer Res.*, **2015**, 21, 907–15.