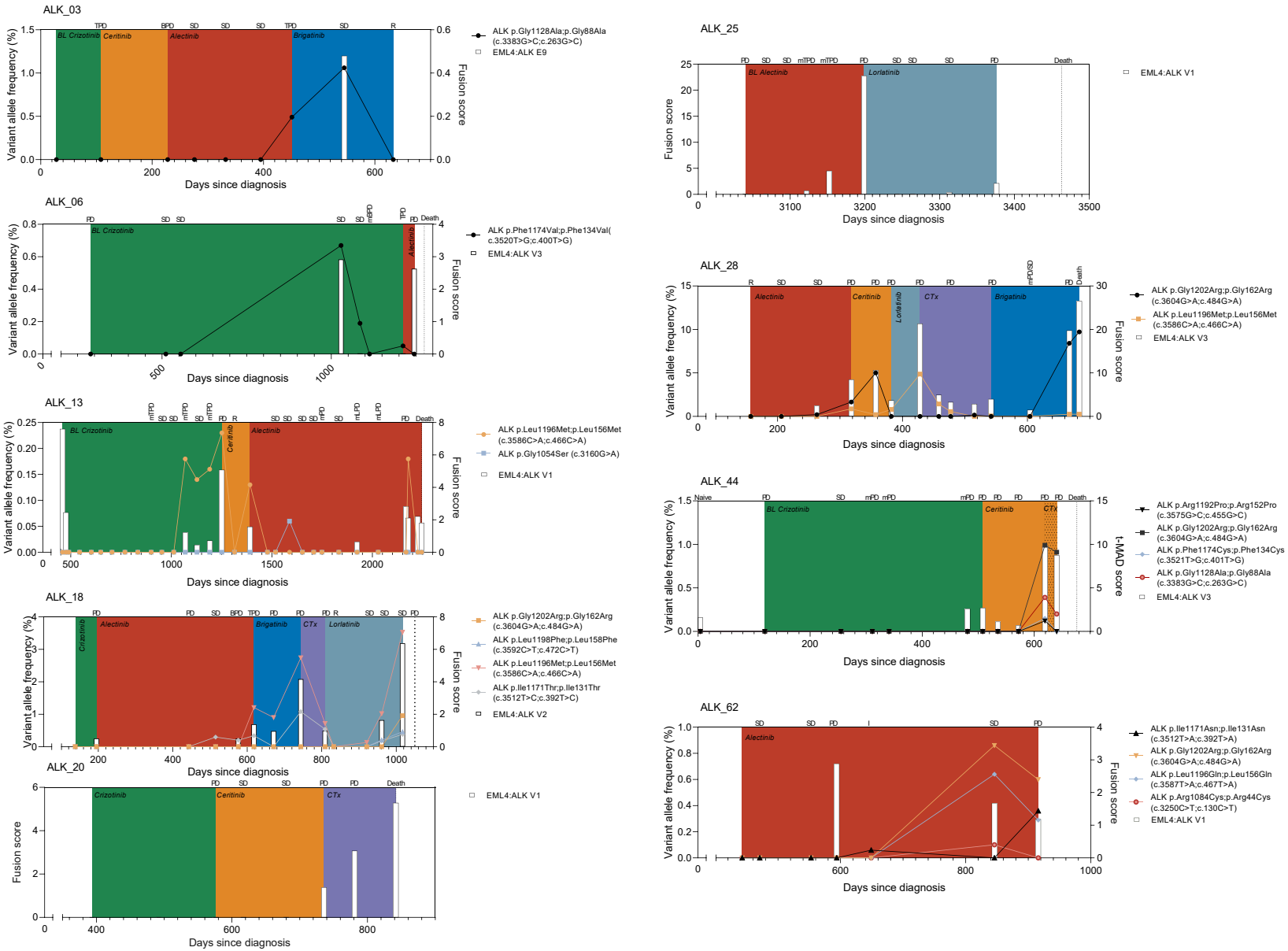
Early identification of disease progression in *ALK*-rearranged lung cancer using circulating tumor DNA analysis

Supplementary Information



Supplementary figure 1. ctDNA kinetics of representative patients showing the concordance of *ALK* alterations with clinical course across therapy lines. Only *ALK* alterations are shown here for clarity. PD: progressive disease. SD: stable disease. BPD: brain PD. mBPD: mild BPD. TPD: thoracic PD. mTPD: mild TPD. R: response. I: improvement. CTx: chemotherapy.

Supplementary Table 1. *ALK* mutations and rearrangements determined from targeted NGS of ctDNA.

Patient	Fusion detected	Mutations detected			
		Nomenclature		Clinical relevance	Reference (DOI)
ALK_03	EML4;ALK	p.Gly1128Ala;p.Gly88Ala	ALK c.3383G>C;c.263G>C	known resistance mutation	10.1016/j.lungcan.2018.07.004
ALK_04	ND	p.Ser631Ile	ALK c.1892G>T	predicted pathogenic (probable resistance mutation)	10.1093/nar/gky1015
ALK_05	EML4;ALK	ND	ND		
ALK_06	EML4;ALK	p.Phe1174Val;p.Phe134Val	ALK c.3520T>G;c.400T>G	known resistance mutation	10.1097/JTO.0000000000000094
ALK_08	EML4;ALK	ND	ND		
ALK_12	ND	p.Gly1269Ala;p.Gly229Ala	ALK c.3806G>C;c.686G>C	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_12		p.Phe1174Leu;p.Phe134Leu	ALK c.3522C>G;c.402C>G	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_12		p.Phe1174Leu;p.Phe134Leu	ALK c.3522C>A;c.402C>A	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_12		p.Phe1174Cys;p.Phe134Cys	ALK c.3521T>G;c.401T>G	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_12		p.Phe1174Val;p.Phe134Val	ALK c.3520T>G;c.400T>G	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_12		p.Phe1174Leu;p.Phe134Leu	ALK c.3520T>C;c.400T>C	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_12		p.Ile1171Thr;p.Ile131Thr	ALK c.3512T>C;c.392T>C	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_12		p.Leu1204Leu;p.Leu164Leu	ALK c.3612C>G;c.492C>G	silent mutation	
ALK_12		p.Arg1192Pro;p.Arg152Pro	ALK c.3575G>C;c.455G>C	known resistance mutation	10.18632/oncotarget.8173
ALK_12		p.Gly1269Ala;p.Gly229Ala	ALK c.3806G>C;c.686G>C	known resistance mutation	10.1111/1759-7714.13299
ALK_13	EML4;ALK	p.Leu1196Met;p.Leu156Met	ALK c.3586C>A;c.466C>A	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_13		p.Gly1054Ser	ALK c.3160G>A	predicted pathogenic (probable resistance mutation)	10.1093/nar/gky1015
ALK_16	EML4;ALK	ND	ND		
ALK_18	EML4;ALK	p.Gly1202Arg;p.Gly162Arg	ALK c.3604G>A;c.484G>A	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_18		p.Leu1198Phe;p.Leu158Phe	ALK c.3592C>T;c.472C>T	known resistance mutation	10.1056/NEJMoa1508887
ALK_18		p.Leu1196Met;p.Leu156Met	ALK c.3586C>A;c.466C>A	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_18		p.Ile1171Thr;p.Ile131Thr	ALK c.3512T>C;c.392T>C	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_20	EML4;ALK	ND	ND		
ALK_21	ND	p.Leu1044Leu	ALK c.3132C>T	silent mutation	
ALK_21		p.Gly1269Ala;p.Gly229Ala	ALK c.3806G>C;c.686G>C	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_25	EML4;ALK	ND	ND		
ALK_28	EML4;ALK	p.Gly1202Arg;p.Gly162Arg	ALK c.3604G>A;c.484G>A	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_28		p.Leu1196Met;p.Leu156Met	ALK c.3586C>A;c.466C>A	known resistance mutation	10.1158/2159-8290.CD-16-0596

ALK_30	ND	p.Gly1202Arg;p.Gly162Arg	ALK c.3604G>A;c.484G>A	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_32	EML4;ALK	ND	ND		
ALK_40	EML4;ALK RAD51AP2;ALK	ND	ND		
ALK_44	EML4;ALK	p.Gly1202Arg;p.Gly162Arg	ALK c.3604G>A;c.484G>A	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_44		p.Arg1192Pro;p.Arg152Pro	ALK c.3575G>C;c.455G>C	known resistance mutation	10.18632/oncotarget.8173
ALK_44		p.Phe1174Cys;p.Phe134Cys	ALK c.3521T>G;c.401T>G	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_44		p.Gly1128Ala;p.Gly88Ala	ALK c.3383G>C;c.263G>C	known resistance mutation	10.1016/j.lungcan.2018.07.004
ALK_101	ND	p.Gly1269Ala;p.Gly229Ala	ALK c.3806G>C;c.686G>C	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_101		p.Gly1202Arg;p.Gly162Arg	ALK c.3604G>A;c.484G>A	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_48	EML4;ALK	ND	ND		
ALK_56	EML4;ALK	p.Leu1196Met;p.Leu156Met	ALK c.3586C>A;c.466C>A	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_62	EML4;ALK	p.Ile1171Asn;p.Ile131Asn	ALK c.3512T>A;c.392T>A	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_62		p.Gly1202Arg;p.Gly162Arg	ALK c.3604G>A;c.484G>A	known resistance mutation	10.1158/2159-8290.CD-16-0596
ALK_62		p.Leu1196Gln;p.Leu156Gln	ALK c.3587T>A;c.467T>A	known resistance mutation	10.1158/1541-7786.MCR-12-0569
ALK_62		p.Arg1084Cys;p.Arg44Cys	ALK c.3250C>T;c.130C>T	predicted pathogenic (probable resistance mutation)	doi.org/10.1093/nar/gky1015
ALK_104	ND	p.Gly893Arg	ALK c.2677G>A	predicted pathogenic (probable resistance mutation)	doi.org/10.1093/nar/gky1015

ND: not detectable

Supplementary table 2. Genetic alterations emergent* at disease progression.

Alteration	Patient	VAF at PD†	Therapy line	Protein change	Short-hand
ALK c.1892G>T	ALK_04	0.11%	Ceritinib	p.Ser631Ile	S631I
ALK c.3250C>T;c.130C>T	ALK_62	0.10%	Alectinib	p.Arg1084Cys;p.Arg44Cys	R1084C
ALK c.3383G>C;c.263G>C	ALK_03	0.49%	Alectinib	p.Gly1128Ala;p.Gly88Ala	G1128A
ALK c.3383G>C;c.263G>C	ALK_44	0.39%	Ceritinib	p.Gly1128Ala;p.Gly88Ala	G1128A
ALK c.3512T>A;c.392T>A	ALK_62	0.36%	Alectinib	p.Ile1171Asn;p.Ile131Asn	I1171N
ALK c.3512T>C;c.392T>C	ALK_12	0.03%	Crizotinib	p.Ile1171Thr;p.Ile131Thr	I1171T
ALK c.3520T>C;c.400T>C	ALK_12	0.05%	Crizotinib	p.Phe1174Leu;p.Phe134Leu	F1174L
ALK c.3520T>G;c.400T>G	ALK_12	0.02%	Crizotinib	p.Phe1174Val;p.Phe134Val	F1174V
ALK c.3521T>G;c.401T>G	ALK_12	0.08%	Crizotinib	p.Phe1174Cys;p.Phe134Cys	F1174C
ALK c.3521T>G;c.401T>G	ALK_44	0.15%	Ceritinib	p.Phe1174Cys;p.Phe134Cys	F1174C
ALK c.3522C>A;c.402C>A	ALK_12	0.24%	Crizotinib	p.Phe1174Leu;p.Phe134Leu	F1174L
ALK c.3522C>G;c.402C>G	ALK_12	0.88%	Crizotinib	p.Phe1174Leu;p.Phe134Leu	F1174L
ALK c.3575G>C;c.455G>C	ALK_12	0.03%	Crizotinib	p.Arg1192Pro;p.Arg152Pro	R1192P
ALK c.3575G>C;c.455G>C	ALK_44	0.12%	Ceritinib	p.Arg1192Pro;p.Arg152Pro	R1192P
ALK c.3586C>A;c.466C>A	ALK_13	0.18%	Crizotinib	p.Leu1196Met;p.Leu156Met	L1196M
ALK c.3586C>A;c.466C>A	ALK_13	0.18%	Alectinib	p.Leu1196Met;p.Leu156Met	L1196M
ALK c.3586C>A;c.466C>A	ALK_18	1.21%	Alectinib	p.Leu1196Met;p.Leu156Met	L1196M
ALK c.3586C>A;c.466C>A	ALK_28	0.87%	Alectinib	p.Leu1196Met;p.Leu156Met	L1196M
ALK c.3586C>A;c.466C>A	ALK_13	0.13%	Ceritinib	p.Leu1196Met;p.Leu156Met	L1196M
ALK c.3604G>A;c.484G>A	ALK_28	8.41%	Alectinib	p.Gly1202Arg;p.Gly162Arg	G1202R
ALK c.3604G>A;c.484G>A	ALK_44	0.99%	Ceritinib	p.Gly1202Arg;p.Gly162Arg	G1202R
ALK c.3604G>A;c.484G>A	ALK_28	8.41%	Brigatinib	p.Gly1202Arg;p.Gly162Arg	G1202R
ALK c.3612C>G;c.492C>G	ALK_12	0.06%	Crizotinib	p.Leu1204Leu;p.Leu164Leu	L1204L
ALK c.3806G>C;c.686G>C	ALK_12	0.43%	Crizotinib	p.Gly1269Ala;p.Gly229Ala	G1269A
ALK;EML4 fusion	ALK_18	0.50752688	Crizotinib		
ALK;EML4 fusion	ALK_44	2.44638927	Crizotinib		

ALK;EML4 fusion	ALK_13	2.23385	Alectinib		
ALK;EML4 fusion	ALK_18	0.50770308	Alectinib		
ALK;EML4 fusion	ALK_25	0.7276359	Alectinib		
ALK;EML4 fusion	ALK_62	2.88461539	Alectinib		
ALK;EML4 fusion	ALK_13	1.57927	Ceritinib		
ALK;EML4 fusion	ALK_20	1.38	Ceritinib		
ALK;EML4 fusion	ALK_06	2.632088	Alectinib		
BRAF c.1405G>C	ALK_44	0.11%	Ceritinib	p.Gly469Arg	G469R
EGFR CNV	ALK_05	8.83	Crizotinib		
EGFR CNV	ALK_13	4.544	Crizotinib		
EGFR CNV	ALK_44	3.39224386	Crizotinib		
EGFR CNV	ALK_13	3.03324366	Alectinib		
EGFR CNV	ALK_25	3.85624385	Alectinib		
EGFR CNV	ALK_62	6.879243851; 0.541243732	Alectinib		
EGFR CNV	ALK_28	8.15124	Brigatinib		
EGFR CNV	ALK_30	4.30911446	Brigatinib		
EGFR CNV	ALK_28	0.96424	Lorlatinib		
ERBB2 c.1218C>T;c.1173C>T	ALK_13	0.20%	Alectinib	p.Ile406Ile;p.Ile406Ile;p.Ile391Ile	I406=
ERBB2 c.1976T>A;c.1976T>A;c.1931T>A	ALK_27	0.61%	Alectinib	p.Val659Asp;p.Val659Asp;p.Val644Asp	V659D
ERBB2 c.2313_2324dupATACGTGATGGC; c.2268_2279dupATACGTGATGGC	ALK_13	1.20%	Crizotinib	p.Ala775_Gly776insTyrValMetAla; p.Ala775_Gly776insTyrValMetAla; p.Ala760_Gly761insTyrValMetAla	
KRAS c.436G>A	ALK_12	0.16%	Crizotinib	p.Ala146Thr;p.Ala146Thr	A146T
KRAS c.436G>C	ALK_10	0.07%	Crizotinib	p.Ala146Pro;p.Ala146Pro	A146P
MET c.1690G>A	ALK_21	0.28%	Alectinib	p.Ala564Thr;p.Ala564Thr;p.Ala564Thr	A564T
MET c.1690G>A	ALK_05	0.09%	Crizotinib	p.Ala564Thr;p.Ala564Thr;p.Ala564Thr	A564T

MET c.3743A>G;c.3689A>G	ALK_05	0.02%	Crizotinib	p.Tyr1248Cys;p.Tyr1230Cys	Y1248C
MET CNV	ALK_05	7.78	Crizotinib		
MET CNV	ALK_13	4.796	Crizotinib		
MET CNV	ALK_18	0.29224363	Crizotinib		
MET CNV	ALK_13	1.97511435	Alectinib		
MET CNV	ALK_25	2.7981143	Alectinib		
MET CNV	ALK_28	14.1251	Brigatinib		
MET CNV	ALK_30	11.5672436	Brigatinib		
NRAS c.34G>T	ALK_44	0.03%	Ceritinib	p.Gly12Cys	G12C
NRAS c.38G>T	ALK_20	0.03%	CTx	p.Gly13Val	G13V
RET c.1907C>T;c.1907C>T	ALK_35	0.12%	Crizotinib	p.Thr636Met;p.Thr636Met	T636M
TP53 c.374C>G	ALK_20	1%	Ceritinib	p.Thr125Arg;p.Thr125Arg;p.Thr125Arg;p.Thr125Arg	T125R
TP53 c.581T>C;c.548T>C	ALK_05	0.18%	Crizotinib	p.Leu194Pro;p.Leu194Pro;p.Leu194Pro;p.Leu194Pro;p.Leu183Pro	L194P
TP53 c.586C>T;c.553C>T	ALK_13	2.02%	Alectinib	p.Arg196*;p.Arg196*;p.Arg196*;p.Arg196*;p.Arg185*	R196*
TP53 c.641A>G;c.608A>G	ALK_13	0.07%	Ceritinib	p.His214Arg;p.His214Arg;p.His214Arg;p.His214Arg;p.His203Arg	H214R
TP53 c.659A>G;c.626A>G	ALK_56	1.92%	Alectinib	p.Tyr220Cys;p.Tyr220Cys;p.Tyr220Cys;p.Tyr220Cys;p.Tyr209Cys	Y220C
TP53 c.715A>G;c.682A>G	ALK_20	0.12%	Crizotinib	p.Asn239Asp;p.Asn239Asp;p.Asn239Asp;p.Asn239Asp;p.Asn228Asp	N239D
TP53 c.722C>G;c.689C>G	ALK_03	0.17%	Alectinib	p.Ser241Cys;p.Ser241Cys;p.Ser241Cys;p.Ser241Cys;p.Ser230Cys	S241C
TP53 c.730G>T;c.697G>T	ALK_03	0.10%	Crizotinib	p.Gly244Cys;p.Gly244Cys;p.Gly244Cys;p.Gly244Cys;p.Gly233Cys	G244C
TP53 c.818G>T;c.785G>T	ALK_56	0.19%	Alectinib	p.Arg273Leu;p.Arg273Leu;p.Arg273Leu;p.Arg262Leu	R273L
TP53 c.920-2A>G;c.887-2A>G	ALK_28	5.19%	Alectinib	N/A	
TP53 c.994-2A>G;c.*101-2A>G; c.*13-2A>G;c.961-2A>G	ALK_20	0.30%	CTx	N/A	

*Genetic alterations detected in samples collected at clinical progression points which were not detected in previous sampling points within the course of a therapy line.

†Fusion score was quantified as the number of paired reads spanning the fusion breakpoint divided by the median sequencing depth. The CNV score reported here is the output from the Avenio analysis pipeline, which is defined as a statistical summary of a called amplification accounting the log2ratio to normal copy number.

Supplementary table 3. Genes included in the targeted sequencing panels.

Gene	Exon	SNV	Indel	Fusion	CNV
ALK	4, 12, 15, 20, 21, 22, 23, 24, 25, 28	x	x	x	
APC	6, 7, 9, 12, 14, 16	x	x		
BRAF	11, 15	x	x		
BRCA1	all	x			
BRCA2	all	x			
DPYD	all	x			
EGFR	all	x	x		x
ERBB2	all	x	x		x
KIT	8, 9, 11, 13, 14, 17	x	x		
KRAS	all	x			
MET	all	x	x		x
NRAS	2, 3	x			
PDGFRA	11, 12, 14, 15, 16, 18	x			
RET	11, 16	x		x	
ROS1	38	x		x	
TP53	all	x	x		

Supplementary table 4. %Δt-MAD used for ROC analyses.

ALK_ID	%Δt-MAD	Clinical status
ALK_03	25%	PDTC
ALK_03	157%	PDTC
ALK_03	-62%	SD
ALK_03	-1%	SD
ALK_03	-15%	SD
ALK_03	197%	PDTC
ALK_03	-26%	SD
ALK_03	-34%	SD
ALK_04	-29%	SD
ALK_04	32%	PDTC
ALK_05	-8%	SD
ALK_05	-43%	SD
ALK_05	129%	SD
ALK_05	-45%	SD
ALK_06	77%	SD
ALK_06	20%	SD
ALK_06	58%	SD
ALK_06	-79%	SD
ALK_06	12%	PDTC
ALK_07	-15%	SD
ALK_07	810%	PDTC
ALK_07	-84%	SD
ALK_07	-13%	SD
ALK_08	42%	SD
ALK_08	-28%	SD
ALK_08	-18%	SD
ALK_10	-31%	SD
ALK_10	-19%	SD
ALK_12	12%	SD
ALK_12	-21%	SD
ALK_12	8%	SD
ALK_12	197%	PDTC
ALK_12	-76%	SD
ALK_12	24%	SD
ALK_12	78%	SD
ALK_12	24%	SD
ALK_12	-14%	SD
ALK_12	26%	SD
ALK_13	-67%	SD
ALK_13	157%	SD
ALK_13	9%	SD
ALK_13	-27%	SD
ALK_13	-3%	SD
ALK_13	21%	SD

ALK_13	93%	SD
ALK_13	-8%	SD
ALK_13	-21%	SD
ALK_13	51%	PDTC
ALK_13	-64%	SD
ALK_13	115%	SD
ALK_13	16%	SD
ALK_13	2%	SD
ALK_13	39%	SD
ALK_13	-50%	SD
ALK_13	2%	SD
ALK_15	13%	SD
ALK_15	64%	SD
ALK_15	8%	PDTC
ALK_15	-26%	SD
ALK_15	135%	SD
ALK_15	-18%	SD
ALK_15	-17%	SD
ALK_16	45%	PDTC
ALK_16	-22%	SD
ALK_18	155%	PDTC
ALK_18	0%	SD
ALK_18	257%	PDTC
ALK_18	145%	PDTC
ALK_18	-61%	SD
ALK_18	25%	SD
ALK_18	13%	SD
ALK_18	791%	SD
ALK_20	3%	PDTC
ALK_20	-25%	SD
ALK_20	49%	SD
ALK_21	9%	SD
ALK_21	57%	PDTC
ALK_21	24%	PDTC
ALK_22	44%	SD
ALK_22	0%	SD
ALK_23	45%	SD
ALK_23	1%	SD
ALK_23	19%	SD
ALK_23	-21%	SD
ALK_23	50%	SD
ALK_23	-23%	SD
ALK_24	-15%	SD
ALK_24	15%	SD
ALK_24	64%	SD
ALK_24	-16%	SD
ALK_24	28%	SD

ALK_24	-5%	SD
ALK_24	-3%	SD
ALK_24	-8%	SD
ALK_25	39%	SD
ALK_25	-19%	SD
ALK_25	99%	PDTC
ALK_25	-51%	SD
ALK_25	34%	SD
ALK_25	-29%	SD
ALK_26	40%	SD
ALK_26	98%	SD
ALK_26	-54%	SD
ALK_26	77%	SD
ALK_26	-29%	SD
ALK_27	37%	PDTC
ALK_27	-44%	SD
ALK_27	-29%	SD
ALK_27	-25%	SD
ALK_27	13%	SD
ALK_28	-22%	SD
ALK_28	13%	SD
ALK_28	436%	PDTC
ALK_28	609%	PDTC
ALK_28	11%	PDTC
ALK_28	17%	PDTC
ALK_29	-9%	SD
ALK_29	34%	SD
ALK_30	23%	SD
ALK_30	300%	SD
ALK_30	-89%	SD
ALK_30	514%	PDTC
ALK_30	-29%	SD
ALK_30	-18%	SD
ALK_30	33%	SD
ALK_30	19%	SD
ALK_30	12%	PDTC
ALK_30	764%	PDTC
ALK_30	2%	PDTC
ALK_31	28%	SD
ALK_32	-51%	SD
ALK_32	8%	PDTC
ALK_32	21%	SD
ALK_32	-61%	SD
ALK_34	19%	SD
ALK_34	-12%	SD
ALK_34	131%	SD
ALK_34	-3%	SD

ALK_35	-8%	SD
ALK_35	67%	PDTC
ALK_35	-30%	SD
ALK_37	46%	SD
ALK_37	2%	PDTC
ALK_37	69%	SD
ALK_39	-3%	SD
ALK_39	18%	SD
ALK_39	-9%	SD
ALK_40	-19%	SD
ALK_40	-44%	SD
ALK_40	19%	SD
ALK_43	2%	SD
ALK_43	61%	PDTC
ALK_43	-55%	SD
ALK_43	109%	SD
ALK_43	34%	SD
ALK_44	11%	SD
ALK_44	1%	PDTC
ALK_44	267%	PDTC
ALK_48	36%	SD
ALK_48	41%	SD
ALK_56	89%	SD
ALK_56	91%	PDTC
ALK_56	-67%	SD
ALK_56	-64%	SD
ALK_57	-40%	SD
ALK_59	9%	SD
ALK_60	-35%	SD
ALK_62	23%	SD
ALK_62	-45%	SD
ALK_62	-85%	SD
ALK_62	131%	SD
ALK_66	34%	SD
ALK_66	-44%	SD
ALK_66	58%	SD
ALK_101	34%	PDTC
ALK_101	144%	SD
ALK_101	-47%	SD
ALK_102	-18%	SD
ALK_104	92%	SD
ALK_104	-20%	SD
ALK_104	-19%	SD
ALK_105	27%	SD
ALK_105	40%	PDTC
ALK_105	5%	SD

SD: stable disease; PD: progressive disease; PDTC: progressive disease with therapy change

Supplementary table 5. ΔVAF_{mean} used for ROC analyses.

ALK_ID	ΔVAFmean	Clinical status
ALK_03	0.10%	PDTC
ALK_03	-0.10%	PDTC
ALK_03	0.00%	SD
ALK_03	0.00%	SD
ALK_03	0.22%	SD
ALK_03	0.11%	PDTC
ALK_03	0.06%	SD
ALK_03	-0.39%	SD
ALK_04	0.14%	SD
ALK_04	0.05%	PDTC
ALK_05	-0.05%	SD
ALK_06	0.00%	SD
ALK_06	0.00%	SD
ALK_06	0.34%	SD
ALK_06	-0.15%	SD
ALK_06	-0.08%	PDTC
ALK_07	0.54%	SD
ALK_07	-0.15%	PDTC
ALK_07	0.30%	SD
ALK_07	-0.13%	SD
ALK_08	0.21%	SD
ALK_08	-0.21%	SD
ALK_08	0.00%	SD
ALK_10	0.00%	SD
ALK_10	-0.07%	SD
ALK_12	-0.03%	SD
ALK_12	0.02%	SD
ALK_12	0.04%	SD
ALK_12	-0.10%	PDTC
ALK_12	0.21%	SD
ALK_12	-0.13%	SD
ALK_13	0.00%	SD
ALK_13	0.00%	SD
ALK_13	0.00%	SD
ALK_13	0.00%	SD
ALK_13	0.00%	SD
ALK_13	0.00%	SD
ALK_13	0.00%	SD
ALK_13	0.00%	SD
ALK_13	-0.73%	SD
ALK_13	2.38%	PDTC

ALK_13	-2.91%	SD
ALK_13	0.59%	SD
ALK_13	0.18%	SD
ALK_13	-0.10%	SD
ALK_13	-0.08%	SD
ALK_13	0.00%	SD
ALK_13	0.26%	SD
ALK_15	0.00%	SD
ALK_15	0.00%	SD
ALK_15	0.17%	PDTC
ALK_15	-0.17%	SD
ALK_15	0.00%	SD
ALK_15	0.00%	SD
ALK_15	0.00%	SD
ALK_16	0.00%	PDTC
ALK_16	0.00%	SD
ALK_18	0.51%	PDTC
ALK_18	0.00%	SD
ALK_18	0.79%	PDTC
ALK_18	2.52%	PDTC
ALK_18	-0.85%	SD
ALK_18	0.13%	SD
ALK_18	1.87%	SD
ALK_20	-0.14%	PDTC
ALK_20	0.29%	SD
ALK_20	-0.45%	SD
ALK_21	0.00%	SD
ALK_21	0.11%	PDTC
ALK_21	0.17%	SD
ALK_21	0.26%	PDTC
ALK_23	0.00%	SD
ALK_23	0.00%	SD
ALK_23	0.00%	SD
ALK_23	0.14%	SD
ALK_23	-0.14%	SD
ALK_23	0.00%	SD
ALK_24	0.00%	SD
ALK_24	0.04%	SD
ALK_24	-0.04%	SD
ALK_24	0.00%	SD
ALK_24	0.05%	SD
ALK_24	-0.05%	SD
ALK_24	0.00%	SD
ALK_24	0.00%	SD

ALK_25	-0.26%	SD
ALK_25	0.52%	SD
ALK_25	-0.04%	PDTC
ALK_25	0.57%	SD
ALK_25	0.11%	SD
ALK_26	0.00%	SD
ALK_26	0.02%	SD
ALK_26	0.10%	SD
ALK_26	-0.12%	SD
ALK_26	0.13%	SD
ALK_27	0.61%	PDTC
ALK_27	-0.55%	SD
ALK_27	-0.06%	SD
ALK_27	0.00%	SD
ALK_27	0.00%	SD
ALK_28	0.00%	SD
ALK_28	0.11%	SD
ALK_28	1.83%	PDTC
ALK_28	2.63%	PDTC
ALK_28	-0.67%	PDTC
ALK_28	0.18%	PDTC
ALK_29	0.00%	SD
ALK_29	0.00%	SD
ALK_30	0.00%	SD
ALK_30	0.00%	SD
ALK_30	0.11%	SD
ALK_30	-0.11%	PDTC
ALK_30	0.00%	SD
ALK_30	0.00%	SD
ALK_30	0.00%	SD
ALK_30	0.16%	SD
ALK_30	0.28%	PDTC
ALK_30	4.77%	PDTC
ALK_30	0.69%	PDTC
ALK_31	-0.16%	SD
ALK_32	0.00%	SD
ALK_32	0.00%	PDTC
ALK_32	0.04%	SD
ALK_32	-0.04%	SD
ALK_34	-0.19%	SD
ALK_34	0.43%	SD
ALK_34	-0.21%	SD
ALK_34	-0.22%	SD
ALK_35	0.00%	SD

ALK_35	0.00%	PDTC
ALK_35	0.00%	SD
ALK_39	0.00%	SD
ALK_39	0.00%	SD
ALK_39	0.08%	SD
ALK_40	0.05%	SD
ALK_40	0.21%	SD
ALK_40	0.28%	SD
ALK_43	0.00%	SD
ALK_43	0.00%	PDTC
ALK_43	0.00%	SD
ALK_43	0.20%	SD
ALK_43	0.00%	SD
ALK_44	0.00%	SD
ALK_44	0.09%	PDTC
ALK_44	0.27%	PDTC
ALK_48	0.00%	SD
ALK_48	0.00%	SD
ALK_56	0.13%	SD
ALK_56	2.61%	PDTC
ALK_56	-2.74%	SD
ALK_56	0.10%	SD
ALK_62	0.03%	SD
ALK_62	-0.03%	SD
ALK_62	-2.40%	SD
ALK_101	-0.14%	PDTC
ALK_101	2.60%	SD
ALK_101	-2.11%	SD
ALK_102	0.00%	SD
ALK_104	-0.11%	SD
ALK_104	0.36%	SD
ALK_104	-0.29%	SD
ALK_104	0.00%	SD

SD: stable disease; PD: progressive disease; PDTC: progressive disease with therapy change