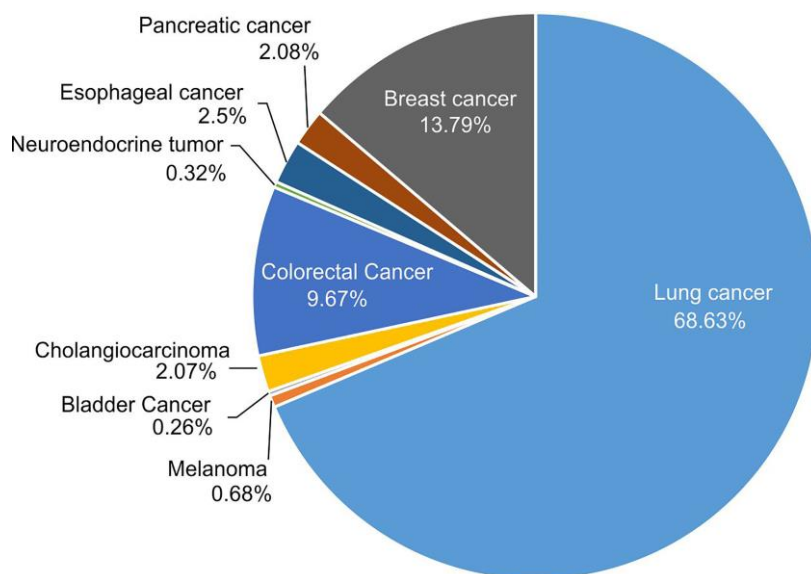


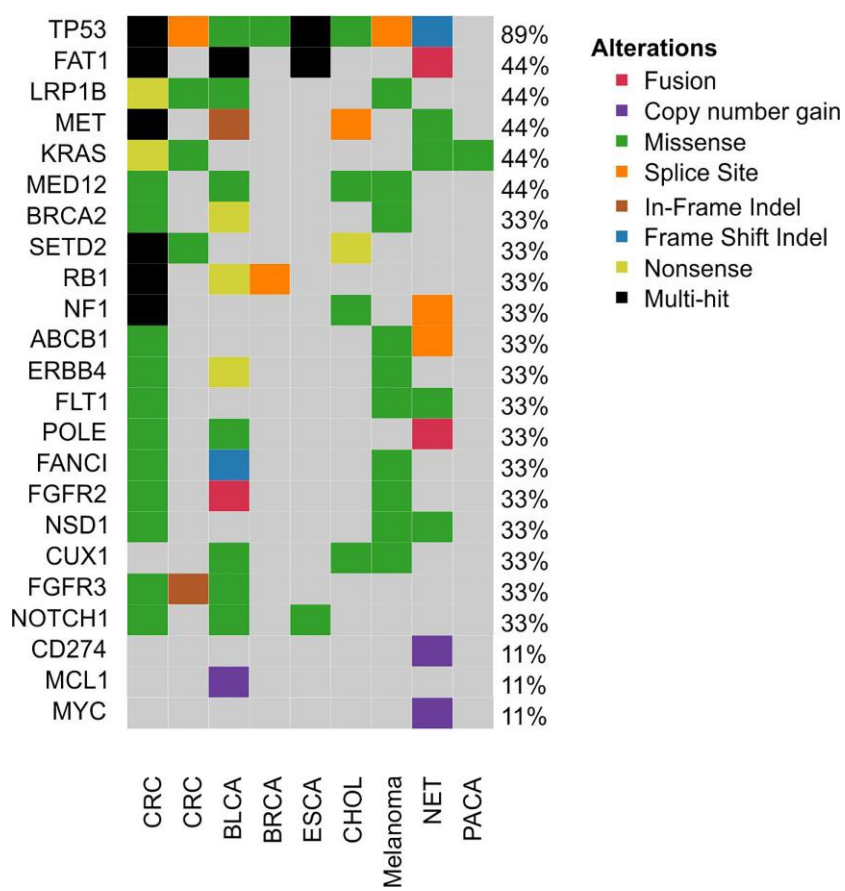
## **Supplementary Information**



**Supplementary Figure 1. Cancer type distribution of 26,391 screened cancer patients (A) and the mutation spectrum of nine non-lung cancer patients (B).**



**Supplementary Figure 2. Co-mutational plot of 175 lung cancer patients using the shared genes between 139- and 425-gene panels. All mutations in driver genes are plotted, and for non-drivers, only gene alterations with a frequency of greater than 2% are displayed.**



Supplementary Figure 3. Co-mutational plot of 9 non-lung cancer patients

Supplementary Table 1.

Gene	Exon/Intron Num.	Alterations	Chromosome Start Point	Chromosome End Point	Reference Sequence	Alternation Sequence
MET	exon14	c.2887+91_3028+3del	chr7:116411799	chr7:116412046	TATATGTAGTCCATAAAACCCATGAGTTCTGGGCACTGGGTCAAA GTCTCCTGGGGCCCATGATAGCCGTCTTTAACAAGCTCTTTCTTT CTCTCTGTTTTAAGATCTGGGCAGTGAATTAGTTTCGCTACGATGC AAGAGTACACACTCCTCATTGGATAGGCTTGTAAGTGCCCGAA GTGTAAGCCCAACTACAGAAATGGTTTCAAATGAATCTGTAGAC TACCGAGCTACTTTTCCAGAAGGTA	-
MET	exon14	c.2888-90_2899del	chr7:116411813	chr7:116411914	AAAACCCATGAGTTCTGGGCACTGGGTCAAAGTCTCCTGGGGC CCATGATAGCCGTCTTTAACAAGCTCTTTCTTTCTCTCTGTTTTA AGATCTGGGCAGTG	-
MET	exon14	c.2888-69_2889del	chr7:116411834	chr7:116411904	CTGGGTCAAAGTCTCCTGGGGCCCATGATAGCCGTCTTTAACAA GCTCTTTCTTTCTCTCTGTTTTAAGAT	-
MET	exon14	c.2888-55_2928 del&insA	chr7:116411848	chr7:116411943	CCTGGGGCCCATGATAGCCGTCTTTAACAAGCTCTTTCTTTCTCT CTGTTTTAAGATCTGGGCAGTGAATTAGTTTCGCTACGATGCAAG AGTACAC	-
MET	intron13	c.2888-47_2888- 26del&insGGT	chr7:116411856	chr7:116411877	CCATGATAGCCGTCTTTAACAA	GGT
MET	intron13	c.2888-46_2888-15del	chr7:116411857	chr7:116411888	CATGATAGCCGTCTTTAACAAGCTCTTTCTTT	-
MET	intron13	c.2888-41_2888-21del	chr7:116411862	chr7:116411882	TAGCCGTCTTTAACAAGCTCT	-
MET	intron13	c.2888-37_2888-20del	chr7:116411866	chr7:116411883	CGTCTTTAACAAGCTCTT	-
MET	intron13	c.2888-36_2888-12del	chr7:116411866	chr7:116411890	CGTCTTTAACAAGCTCTTCTTTCT	-
MET	intron13	c.2888-36_2888-29del	chr7:116411867	chr7:116411874	GTCTTTAA	-
MET	intron13	c.2888-36_2888-21del	chr7:116411867	chr7:116411882	GTCTTTAACAAGCTCT	-
MET	intron13	c.2888-36_2888-2del	chr7:116411867	chr7:116411901	GTCTTTAACAAGCTCTTCTTTCTCTCTGTTTTAA	-
MET	intron13	c.2888-35_2888-27del	chr7:116411868	chr7:116411876	TCTTTAACA	-
MET	intron13	c.2888-35_2888-20del	chr7:116411868	chr7:116411883	TCTTTAACAAGCTCTT	-
MET	exon14	c.2888-35_2888del	chr7:116411868	chr7:116411903	TCTTTAACAAGCTCTTTCTTTCTCTCTGTTTTAAGA	-
MET	intron13	c.2888-28_2888-2del	chr7:116411870	chr7:116411896	TTAACAAGCTCTTTCTTTCTCTCTGT	-
MET	intron13	c.2888-31_2888-13del	chr7:116411871	chr7:116411889	TTAACAAGCTCTTTCTTTCT	-
MET	intron13	c.2887-32_2967del	chr7:116411871	chr7:116411982	TTAACAAGCTCTTTCTTTCTCTCTGTTTTAAGATCTGGGCAGTGA ATTAGTTTCGCTACGATGCAAGAGTACACACTCCTCATTGGATAG GCTTGTAAGTGCCCGAAGTGA	-

MET	intron13	c.2888-31_2888-15del&insA	chr7:116411872	chr7:116411888	TAACAAGCTCTTTCTTT	A
MET	intron13	c.2888-31_2888-10del&insGTT	chr7:116411872	chr7:116411893	TAACAAGCTCTTTCTTTCTCTC	GTT
MET	intron13	c.2888-30_2888-3del	chr7:116411873	chr7:116411900	AACAAGCTCTTTCTTTCTCTCTGTTTAA	-
MET	intron13	c.2888-29_2888-10del	chr7:116411874	chr7:116411893	ACAAGCTCTTTCTTTCTCTC	-
MET	intron13	c.2888-27_2888-14del	chr7:116411875	chr7:116411888	CAAGCTCTTTCTTT	-
MET	intron13	c.2888-28_2888-14del&insA	chr7:116411875	chr7:116411889	CAAGCTCTTTCTTTCT	A
MET	intron13	c.2888-28_2888-5del	chr7:116411875	chr7:116411898	CAAGCTCTTTCTTTCTCTCTGTTT	-
MET	intron13	c.2888-27_2888-16del	chr7:116411876	chr7:116411887	AAGCTCTTTCTTT	-
MET	intron13	c.2888-27_2888-10del&insT	chr7:116411876	chr7:116411893	AAGCTCTTTCTTTCTCTC	T
MET	intron13	c.2888-24_2888-1del	chr7:116411876	chr7:116411899	AAGCTCTTTCTTTCTCTCTGTTTT	-
MET	exon14	c.2888-25_2893del	chr7:116411878	chr7:116411908	GCTCTTTCTTTCTCTCTGTTTTAAGATCTGG	-
MET	exon14	c.2888-23_2918del	chr7:116411878	chr7:116411931	GCTCTTTCTTTCTCTCTGTTTTAAGATCTGGGCAGTGAATTAGTT CGCTACGAT	-
MET	intron13	c.2888-24_2888-15del	chr7:116411879	chr7:116411888	CTCTTTCTTT	-
MET	intron13	c.2888-24_2888-13del	chr7:116411879	chr7:116411890	CTCTTTCTTTCT	-
MET	intron13	c.2888-22_2888-12del	chr7:116411881	chr7:116411891	CTTTCTTTCTC	-
MET	intron13	c.2888-22_2888-8del	chr7:116411881	chr7:116411895	CTTTCTTTCTCTCTG	-
MET	intron13	c.2888-21_2888-9del	chr7:116411882	chr7:116411894	TTTCTTTCTCTCT	-
MET	intron13	c.2888-18_2888-5del	chr7:116411882	chr7:116411895	TTTCTTTCTCTCTG	-
MET	intron13	c.2888-21_2888-7del	chr7:116411882	chr7:116411896	TTTCTTTCTCTCTGT	-
MET	intron13	c.2888-21_2888-6del	chr7:116411882	chr7:116411897	TTTCTTTCTCTCTGTT	-
MET	intron13	c.2888-20_2888-4del	chr7:116411882	chr7:116411898	TTTCTTTCTCTCTGTTT	-
MET	intron13	c.2888-21_2888-2del	chr7:116411882	chr7:116411901	TTTCTTTCTCTCTGTTTTAA	-
MET	intron13	c.2888-19_2888-9del	chr7:116411883	chr7:116411893	TTCTTTCTCTC	-
MET	exon14	c.2888-20_2888del	chr7:116411883	chr7:116411903	TTCTTTCTCTCTGTTTTAAGA	-
MET	exon14	c.2888-20_2913del	chr7:116411883	chr7:116411928	TTCTTTCTCTCTGTTTTAAGATCTGGGCAGTGAATTAGTTTCGCTA C	-
MET	intron13	c.2888-19_2888-10del	chr7:116411884	chr7:116411893	TCTTTCTCTC	-
MET	exon14	c.2888-19_2921del	chr7:116411884	chr7:116411936	TCTTTCTCTCTGTTTTAAGATCTGGGCAGTGAATTAGTTTCGCTAC GATGCAAG	-

MET	intron13	c.2888-18_2888-17insAGA	chr7:116411885	chr7:116411886	CT	AGA
MET	intron13	c.2888-17_2888-8del	chr7:116411886	chr7:116411895	TTTCTCTCTG	-
MET	intron13	c.2888-17_2888-7del	chr7:116411886	chr7:116411896	TTTCTCTCTGT	-
MET	intron13	c.2888-15_2888-4del	chr7:116411886	chr7:116411897	TTTCTCTCTGTT	-
MET	intron13	c.2888-16_2888-4del	chr7:116411886	chr7:116411898	TTTCTCTCTGTTT	-
MET	intron13	c.2888-16_2888-4del&insC	chr7:116411887	chr7:116411899	TTCTCTCTGTTTT	C
MET	exon14	c.2888-15_2893del	chr7:116411888	chr7:116411908	TCTCTCTGTTTTAAGATCTGG	-
MET	exon14	c.2888-8_2924del&insTAAA	chr7:116411895	chr7:116411939	GTTTTAAGATCTGGGCAGTGAATTAGTTCGCTACGATGCAAGAGT	-
MET	exon14	c.2888-4_2910del	chr7:116411899	chr7:116411925	TAAGATCTGGGCAGTGAATTAGTTCGC	-
MET	intron13	c.G2888-1T	chr7:116411902	chr7:116411902	G	T
MET	exon14	c.2930_2932delCTC	chr7:116411945	chr7:116411947	CTC	-
MET	exon14	c.2995_3024del	chr7:116412010	chr7:116412039	GAATCTGTAGACTACCGAGCTACTTTTCCA	-
MET	exon14	c.2998_3028+6del	chr7:116412013	chr7:116412049	TCTGTAGACTACCGAGCTACTTTTCCAGAAGGTATAT	-
MET	exon14	c.3004_3028+17del	chr7:116412019	chr7:116412060	GACTACCGAGCTACTTTTCCAGAAGGTATATTTTCAGTTTATT	-
MET	exon14	c.3005_3007del	chr7:116412020	chr7:116412022	ACT	-
MET	exon14	c.3007_3028+13del	chr7:116412022	chr7:116412056	TACCGAGCTACTTTTCCAGAAGGTATATTTTCAGTT	-
MET	exon14	c.3012_3023del	chr7:116412027	chr7:116412038	AGCTACTTTTCC	-
MET	exon14	c.3012_3028+4del	chr7:116412027	chr7:116412047	AGCTACTTTTCCAGAAGGTAT	-
MET	exon14	c.3015_3028+3del	chr7:116412030	chr7:116412046	TACTTTTCCAGAAGGTA	-
MET	exon14	c.3018_3028+5del	chr7:116412033	chr7:116412048	TTTCCAGAAGGTATA	-
MET	exon14	c.3019_3028+3del	chr7:116412034	chr7:116412046	TTTCCAGAAGGTA	-
MET	exon14	c.3019_3028+5del	chr7:116412034	chr7:116412048	TTTCCAGAAGGTATA	-
MET	exon14	c.3023_3028+13del	chr7:116412038	chr7:116412056	CAGAAGGTATATTTTCAGTT	-
MET	exon14	c.3024_3028+14del	chr7:116412039	chr7:116412057	AGAAGGTATATTTTCAGTTT	-
MET	exon14	c.3025_3028+2del	chr7:116412040	chr7:116412045	GAAGGT	-
MET	exon14	c.3028G>C(p.D1010H)	chr7:116412043	chr7:116412043	G	C
MET	intron14	c.G3028+1A	chr7:116412044	chr7:116412044	G	A
MET	intron14	c.3028+1_3028+4del	chr7:116412044	chr7:116412047	GTAT	-
MET	intron14	c.T3028+2C	chr7:116412045	chr7:116412045	T	C
MET	intron14	c.A3028+3T	chr7:116412046	chr7:116412046	A	T

MET	exon14	c.2887+95_3028+53del	chr7:116411803	chr7:116412096	TGTAGTCCATAAAAACCATGAGTTCTGGGCACTGGGTCAAAGTC TCCTGGGGCCCATGATAGCCGTCTTAAACAAGCTCTTCTTTCTC TCTGTTTTAAGATCTGGGCAGTGAATTAGTTCGCTACGATGCAA GAGTACACACTCCTCATTGGATAGGCTTGTAAGTGCCCGAAGT GTAAGCCCAACTACAGAAATGGTTTCAAATGAATCTGTAGACTAC CGAGCTACTTTTCCAGAAGGTATATTTTCAGTTTATTGTTCTGAGA AATACCTATACATATACCTCAGTGGGT	-
MET	exon14	c.2888- 20_3028+1133del	chr7:116411876	chr7:116413169	AAGCTCTTTCTTTCTCTGTTTTAAAGATCTGGGCAGTGAATTAG TTCGCTACGATGCAAGAGTACACACTCCTCATTGGATAGGCTT GTAAGTGCCCGAAGTGTAAAGCCCAACTACAGAAATGGTTTCAA TGAATCTGTAGACTACCGAGCTACTTTTCCAGAAGGTATATTTCA GTTTATTGTTCTGAGAAAATACCTATACATATACCTCAGTGGGTTG TGACATTGTTGTTTATTTTTGGTTTTGCATTATATTTTTATAAAA ACCTAAAGGAAGTATTTACCTCTGCCAAGTAAGTATTTGACACAA AATTACATGGCTCTTAATTTAAAAGAACCCTATGATATATACAT TATGATTTTAGAGTCCATAAGCTCTCATTTCACAAAAAGGTTAAT TTGAGCAAAAGTAATTTGTTTATCATCTAAGTGCAATAGTAAGAA ATTGCGAAGCTCTCTTTTACAATCCAGGAAGAGTTAAGTTACAAA ATATACTTATTTAAATGTAAGTTGGAAGTCTACATTTTTTACCTG TTGAAGCCCAACATTGAAATTATACTGTTAGTAATCTTTCGAAG TGTTTTCAATGAACTGTTAGTACACAGCCTTTTTCCACCATATT CTAGGACTTGAATGTATTTTGAGACTTAGCCAAGGAAAACCTTC AATTATGCCATGAAAAAAGGAGGGTCAATATCATCAGCTTTGT AAAACACTATGCCTAGTAATGTTTCAGGTTAATCAGAGTTTTCATG TTGTTTTATTTAAATCTCCTGGTAAAAGCAAAGGTCTGTATTGT ATCAGCTCCATTATCTTTAGAAGTTACAGGATGTGAGTCAAGTAC AAGCATTTCCTTGGTTGAATATTTACCATTGGACAAAATAAAATGA GTCACAGATCATTGAGGATACTGGAAAAGTTAGAAGTTGCTCAT CCAAACAAGTTCAAGAGCAATGAAGCACTTAACATTTTAACATTT TCAACACTTACTACCTCTTATGTTTTGAAGTTTATGTTATTTCTAT GGAGATACACATAGTAAACATTGTCTTTGCCCTGATTCCATTAC CTTAAAAATCCATTTCGTTTAAACCGTGTGGAAAAATCAAACCCTAG TTTATTGTTTTGAAATTTAGATCTATTTAGTATTTTATGTGCACATT TAGTGCATCTATTTAGTATTTTATATGCACATTTTCATAGTTCTAATC TGAGATCATTAATAATTTACAAATTTTCTTTGAAAAAAAACCTTAC CTAATCTTCTTTGAACCTCCTTACTCACCA	-
MET	exon14	c.3010_3028+1318del	chr7:116412025	chr7:116413361	CGAGCTACTTTTCCAGAAGGTATATTTTCAGTTTATTGTTCTGAGA AATACCTATACATATACCTCAGTGGGTGTGACATTGTTGTTTATT TTTGGTTTTGCATTATATTTTTATAAAAACCTAAAGGAAGTATT	-



				<p>ACCTCTGCCAAGTAAGTATTTGACACAAAATTACATGGCTCTTAA  TTTTAAAAGAACCCATGTATATATTACATTATGATTTTAGAGTCCA  TAAGCTCTCATTTCACAAAAAGGTTAATTTGAGCAAAAGTAATTT  GTTTATCATCTAAGTGCAATAGTAAGAAATTGCCAAGCTCTCTTT  TACAATCCAGGAAGAGTTAAGTTACAAAATATACTTATTTAAATGT  AAGTTGGAAGTCTACATTTTTTACCTGTTGAAGCCCAAACATTG  AAATTATACTGTTAGTAATTCCTCGAAGTGTTCATGAAGTGT  TAGTACACAGCCTTTTTCCCACCATATTCTAGGACTTGAATGTAT  TTTGAGACTTAGCCAAGGAAAACCTTCAATTATGCCATGAAAA  AAGGAGGGGTCAATATCATCAGCTTTGTAAAACACTATGCCTAGT  AATGTTGAGGTTAATCAGAGTTTTCATGTTGTTTTATTAAATCTC  CTGGTAAAAGCAAAAGGTCTGTATTGTATCAGCTCCATTATCTTT  AGAAGTTACAGGATGTGAGTCAAGTACAAGCATTTCCTTGGTTG  AATATTTACCATTGGACAAAATAAAATGAGTCACAGATCATTGAGG  ATACTGGAAAAGTTAGAAAGTTGCTCATCCAAACAAGTTCAAGAG  CAATGAAGCACTAACATTTTAAACATTTTCAACACTTACTACCTC  TTATGTTTTGAAGTTTATGTTATTTCTATGGAGATACACATAGTAA  ACATTGTCTTTGCCCTGATTCCATTCACCTTTAAAAATCCATTG  TTAACCCTGTGGAAAATCAAACCTAGTTTATTGTTTTGAAATT  TAGATCTATTTAGTATTTTATGTGCACATTTAGTGCATCTATTTAG  TATTTATATGCACATTTTATAGTTCTAATCTGAGATCATTAAAAAT  TTACAAATTTCTTTGAAAAAAAAAATTACCTAATCTTCTTTGAA  CCTCCTTACTACCAAAAGCTCTGTATCATTGCTAAGAAGGTTGA  GTTTCACACTCTTTTCTCATTGAGCCTGCTCCTTGGAGACATG  AAAAGAAAACAGGTAAGAGAGGGTCAATTTAGAGAGAATGAGAAA  ATAGGTGCACAGCCAAAACCTAATGAAGAGGCAACTGCAGAGCT  TTCCTCTCTACATCTGGTGGGGACAGCATT</p>	
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**Supplementary Table 2.** Patients harbored two different *MET*ex14 alteration types.

<b>Num.</b>	<b>Gene</b>	<b>Alteration</b>	<b>Sample type</b>	<b>MAF</b>
<b>1</b>	<i><b>MET</b></i>	c.3012_3023del (p.1022_1026del)	Tissue	0.82
		c.G3028+1T		0.82
<b>2</b>	<i><b>MET</b></i>	c.2995_3024del (p.1017_1026del)	Tissue	0.2886
		c.A3028+3G		0.2886
<b>3</b>	<i><b>MET</b></i>	c.2888-20_2888-4del	Tissue	0.0123
		c.3028+2T>C		0.2022

**Supplementary Table 3.** The mutations identified in pre- and post-treatment samples from three patients treated by crizotinib.

Patient ID	Gene	Alteration	Pre-treatment		Post-treatment	
			Sample type	MAF/CN ratio	Sample type	MAF/CN ratio
P5	<i>MET</i>	c.3028+1G>C	Plasma	0.701	Metastatic site (Adrenal gland)	0.5967
	<i>ATR</i>	c.695T>G (p.I232R)		0.0888		--
	<i>GNAQ</i>	c.303C>A (p.Y101*)		0.0575		--
	<i>TYMS</i>	c.2T>C (p.M1?)		0.0191		--
	<i>CYLD</i>	c.2173G>T (p.V725F)		0.0175		--
	<i>APC</i>	c.2534G>A (p.R845H)		0.0112		--
	<i>EPAS1</i>	c.95A>G (p.E32G)		0.0066		--
	<i>EPAS1</i>	c.96G>T (p.E32D)		0.006		--
	<i>FANCE</i>	c.274_364dup (p.Q122Pfs*37)		0.0138		--
	<i>TET2</i>	c.4222G>A (p.G1408R)		--		0.125
	<i>BRAF</i>	c.1801A>G (p.K601E)		--		0.0108
	<i>EGFR</i>	CNV		--		3.05
	<i>MET</i>	CNV		1.85		--
	<i>MDM2</i>	CNV		7.81		5.07
	<i>TERT</i>	CNV		5.76		2.56
	<i>FLT4</i>	CNV		2.23		--
	<i>KIT</i>	CNV		1.9		--
<i>FGFR4</i>	CNV	1.88	--			
<i>PDGFRA</i>	CNV	1.8	--			
<i>MYC</i>	CNV	1.77	--			
P12	<i>TP53</i>	c.476C>T (p.A159V)	Tissue	0.1771	Plasma	0.1283
	<i>MET</i>	c.2888-88_2901del		0.2517		0.3568
	<i>MET</i>	c.3688T>A (p.Y1230N)		--		0.1861
P14	<i>MET</i>	c.2888-22_2888-8delCTTTCTTCTCTCTG	Tissue	0.0433	Plasma	0.002
	<i>MET</i>	c.3682G>A (p.D1228N)		--		0.001

--: not detected. Mutation was shown as mutant allele frequency. Gene copy number gain was shown as relative fold change to normal control sample.