

Table S2. Distribution of genetic alterations in each gene

Gene Name <sup>a</sup>	Genetic alterations identified	n	(%)
<i>EGFR</i> (8, 6.2%)	ex19del	3	
	L858R	4	
	L858R + T790M		
	ex20ins		
	ex19del + T790M		
	ex19del + L858R		
	G719S		
	G719A	1	
	L861Q	2	
	ex19del + L858R + T790M	1	
	G719S + L861Q + T790M	1	
	Gene copy number gain	6	
<i>KRAS</i> (5, 3.9%)	G12C	2	
	G12D		
	G12A		
	G12V	1	
	Q61H	1	
	G12S	1	
	G12F		
	Gene copy number gain	19	
<i>PIK3CA</i> (17, 13.2%)	E545K	11	
	H1047R	3	
	E545Q	1	
	E542K	2	
	Gene copy number gain	19	
<i>NRAS</i> (1, 0.8%)	Q61R	1	
	Q61K		
<i>AKT1</i> (1, 0.8%)	E17K	1	
<i>FGFR1</i> (6, 4.7%)	Gene copy number gain	6	
<i>RET</i> (1/66, 1.5 %)	<i>KIF5B-RET</i> variant 2	1	

<sup>a</sup>Numbers in parentheses next to gene names indicate the number and frequency of patients who harbor genetic alterations in each gene.