

Tables

Table 1 Mutation hot spots investigated by the MINtS

Gene	Location of amplicon	Mutation hot spot
<i>EGFR</i>		
	Exon 18	G719S, G719C, G719A
	Exon 19	Exon 19 deletions*
	Exon 20	T790M, S768I
	Exon 21	L858R, L861Q
<i>KRAS</i>		
	Exon 2	G12S, G12R, G12C, G12D, G12A, G12V G13S, G13R, G13C, G13D, G13A, G13V
	Exon 3	G61K, Q61E, Q61R, Q61P, G61L, G61H
<i>BRAF</i>		
	Exon 11	G466V, G469A, G469E, G469V
	Exon 15	D594G, D594V, G596R, V600E

* A total of 55 different types of deletions were investigated (see **Supplemental Digital Content 1**, which demonstrates sequences of amplicons).

Table 2 Frequency of mutant reads identified by the MINtS in normal DNA samples

Amplicon	Read (Frequency) ^a	Reference frequency of the mutant reads	Allowable false-positive rate	Allowable false-negative rate
<i>EGFR</i> exon 18				
Normal	1703979			
G719S	134 (0.000079)	0.00019	0.00033	0.005
G719C	23 (0.000013)	0.000061	0.0001	0.005
G719A	18 (0.000011)	0.000054	0.00009	0.005
<i>EGFR</i> exon 19				
Normal	3413407			
Deletions ^b	59 (0.000017)	0.000173	0.0003	0.005
<i>EGFR</i> exon 20				
Normal	987236 ^c			
T790M	170 (0.000172)	0.000452	0.00078	0.005
<i>EGFR</i> exon 20				
Normal	1003479 ^c			
S768I	15 (0.000015)	0.000087	0.00015	0.005
<i>EGFR</i> exon 21				
Normal	1670410			
L858R	16 (0.00001)	0.00001	0.00002	0.005
L861Q	50 (0.00003)	0.000125	0.00022	0.005
<i>KRAS</i> exon 2				
Normal	413068			
G12S	53 (0.000128)	0.000555	0.00096	0.005
G12R	5 (0.000012)	0.000178	0.00031	0.005

G12C	4 (0.00001)	0.000144	0.00025	0.005
G12D	26 (0.000063)	0.000253	0.00044	0.005
G12A	2 (0.000005)	0.000075	0.00013	0.005
G12V	5 (0.000012)	0.000096	0.00017	0.005
G13S	44 (0.000107)	0.000391	0.00067	0.005
G13R	5 (0.000012)	0.000093	0.00016	0.005
G13C	4 (0.00001)	0.000139	0.00024	0.005
G13D	33 (0.00008)	0.000385	0.00066	0.005
G13A	4 (0.00001)	0.00014	0.00024	0.005
G13V	5 (0.000012)	0.000161	0.00028	0.005

KRAS exon 3

Normal	2027528			
Q61K	55 (0.000027)	0.00033	0.00057	0.005
Q61E	39 (0.000019)	0.000077	0.00013	0.005
Q61R	379 (0.000187)	0.000355	0.00061	0.005
Q61P	20 (0.00001)	0.000061	0.0001	0.005
G61L	71 (0.000035)	0.000103	0.00018	0.005
Q61H(183A >C)	16 (0.000008)	0.000045	0.00008	0.005
Q61H(183A >T)	118 (0.000058)	0.000226	0.00039	0.005

BRAF exon 11

Normal	4790654			
G466V	102 (0.000021)	0.000146	0.00025	0.005
G469A	84 (0.000018)	0.000052	0.00009	0.005
G469E	277 (0.000054)	0.000135	0.00023	0.005
G469V	65 (0.000014)	0.000047	0.00008	0.005

BRAF exon 15

Normal	2403031			
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D594G	176 (0.000073)	0.00014	0.00024	0.005
D594V	86 (0.000036)	0.000078	0.00013	0.005
G596R	25 (0.00001)	0.000066	0.00011	0.005
V600E	256 (0.000107)	0.000187	0.00032	0.005

^a Total number of reads obtained from 34 normal DNA samples.

^b Results of a total of 55 different exon 19 deletions were combined (see **Supplemental Digital Content 1**, which demonstrates sequences of amplicons).

^c Although the *EGFR* T790M hot spot and the *EGFR* S768I hot spots were amplified in one amplicon, they are 66-bp apart and thus have different numbers of informative reads.

Table 3 Mutation testing using admixture samples^a

Admixture	Calculated cancer-cell content (%) ^b				
<i>EGFR</i> G719S	2.1	2.9	2.5	2.1	2.3
<i>EGFR</i> E746-A750del type1	1.0	1.0	2.4	2.1	1.6
<i>EGFR</i> T790M	1.1	1.0	1.2	1.1	2.0
<i>EGFR</i> L858R	0.5	1.2	0.8	0.7	1.1
<i>KRAS</i> G12S	0.7	1.0	1.0	0.7	0.7
<i>KRAS</i> Q61K	0.6	1.6	0.8	1.4	1.2
<i>BRAF</i> G469A	1.3	1.0	1.1	1.2	0.7
<i>BRAF</i> V600E	0.9	2.4	2.5	0.9	0.7

^a For each mutation, 5 admixture samples were investigated. Additionally, 45 normal DNA samples were investigated. Only the results for the admixture samples are shown, because all normal DNA samples were negative for mutation.

^b Variations in the values were considered to be due to variations in the sampling procedure.

Table 4 Mutation testing in clinical specimens^a

No.	Mutation	Sample source	Calculated cancer-cell content (%)
1	<i>EGFR</i> E746-A750del Type1 ^b	Pleural effusion	100.0
2	<i>EGFR</i> E746-A750del Type1	Lung Cancer Tissue	100.0
3	<i>EGFR</i> E746-A750del Type1	Not described	100.0
4	<i>EGFR</i> E746-A750del Type1	Bronchial brushing	99.6
5	<i>EGFR</i> E746-A750del Type1	Lung Cancer Tissue	48.0
6	<i>EGFR</i> E746-A750del Type1	Bronchial brushing	10.5
7	<i>EGFR</i> E746-A750del Type1	Bronchial brushing	8.6
8	<i>EGFR</i> E746-A750del Type1	Bronchial brushing	6.1
9	<i>EGFR</i> E746-A750del Type2 ^b	Lung Cancer Tissue	34.2
10	<i>EGFR</i> E746-A750del Type2 + <i>EGFR</i> T790M	Pleural effusion	5.7 + 1.5
11	<i>EGFR</i> E746-A750del Type1 + <i>EGFR</i> T790M	Pleural effusion	78.6 + 20.9
12	<i>EGFR</i> L858R	Lung Cancer Tissue	100.0
13	<i>EGFR</i> L858R	Bronchial brushing	100.0
14	<i>EGFR</i> L858R	Lung Cancer Tissue	73.6
15	<i>EGFR</i> L858R	Bronchial brushing	60.0
16	<i>EGFR</i> L858R	Lung Cancer Tissue	45.1
17	<i>EGFR</i> L858R	Pleural effusion	36.0
18	<i>EGFR</i> L858R	Not described	35.4
19	<i>EGFR</i> L858R	Lung Cancer Tissue	34.9
20	<i>EGFR</i> L858R	Lung Cancer Tissue	33.7
21	<i>EGFR</i> L858R	Bronchial brushing	25.1
22	<i>EGFR</i> L858R	Not described	8.1
23	<i>EGFR</i> L858R	Bronchial brushing	7.7
24	<i>EGFR</i> L858R	Bronchial brushing	7.2
25	<i>EGFR</i> L858R	Pleural effusion	3.3

26	<i>EGFR</i> L858R	Bronchial brushing	1.2
27	<i>EGFR</i> L858R ^d	Lung Cancer Tissue	0.8
28	<i>KRAS</i> G12V	Not described	100.0
29	<i>KRAS</i> G12V	Bronchial brushing	93.9
30	<i>KRAS</i> G12V	Lung Cancer Tissue	24.3
31	<i>KRAS</i> G12V	Bronchial brushing	7.5
32	<i>KRAS</i> G12V	Lung Cancer Tissue	3.6
33	<i>KRAS</i> G12V	Bronchial brushing	1.4
34	<i>KRAS</i> G12S	Bronchial brushing	10.0
35	<i>KRAS</i> G12R	Not described	52.1
36	<i>KRAS</i> G12D	Lung Cancer Tissue	78.0
37	<i>KRAS</i> G12D	Bronchial brushing	59.3
38	<i>KRAS</i> G12D	Bronchial brushing	7.0
39	<i>KRAS</i> G12D	Bronchial brushing	1.8
40	<i>KRAS</i> G12A	Lung Cancer Tissue	81.0
41	<i>KRAS</i> G12A	Bronchial brushing	12.2
42	<i>KRAS</i> G12A + <i>KRAS</i> G12C	Lung Cancer Tissue	46.7 + 2.1
43	<i>KRAS</i> G12C	Lung Cancer Tissue	16.8
44	<i>KRAS</i> G13D	Bronchial brushing	100.0
45	<i>KRAS</i> Q61H 1	Pleural effusion	2.1
46	<i>BRAF</i> G469A	Lung Cancer Tissue	32.5
47	<i>BRAF</i> G466V	Pleural effusion	1.4
48	Negative	Bronchial brushing	
49	Negative	Bronchial brushing	
50	Negative	Not described	
51	Negative	Not described	
52	Negative	Lung Cancer Tissue	
53	Negative	Bronchial brushing	
54	Negative	Lung Cancer Tissue	
55	Negative	Lung Cancer Tissue	

56	Negative	Bronchial brushing
57	Negative	Bronchial brushing
58	Negative	Lung Cancer Tissue
59	Negative	Not described
60	Negative	Lung Cancer Tissue
61	Negative	Lung Cancer Tissue
62	Negative	Lung Cancer Tissue
63	Negative	Lung Cancer Tissue
64	Negative	Lung Cancer Tissue
65	Negative	Lung Cancer Tissue
66	Negative	Lung Cancer Tissue
67	Negative	Pleural effusion
68	Negative	Bronchial brushing
69	Negative	Bronchial brushing
70	Negative	Lung Cancer Tissue
71	Negative	Bronchial brushing
72	Negative	Lung Cancer Tissue
73	Negative	Not described
74	Negative	Lung Cancer Tissue
75	Negative	Lung Cancer Tissue
76	Negative	Lung Cancer Tissue
77	Negative	Lung Cancer Tissue
78	Negative	Lung Cancer Tissue
79	Negative	Not described
80	Negative	Not described
81	Negative	Lung Cancer Tissue
82	Negative	Lung Cancer Tissue
83	Negative	Pleural effusion
84	Negative	Bronchial brushing
85	Negative	Bronchial brushing
86	Negative	Bronchial brushing

87	Negative	Bronchial brushing
88	Negative	Bronchial brushing
89	Negative	Bronchial brushing
90	Negative	Bronchial brushing
91	Negative	Lung Cancer Tissue
92	Negative	Not described
93	Negative	Bronchial brushing
94	Negative	Bronchial brushing
95	Negative	Bronchial brushing
96	Not determined	Lung Cancer Tissue

^a The result was sorted first by the type of mutation and then the calculated cancer-cell content.

^b *EGFR* E746-A750del Type1 indicates *EGFR* 2235_2249delGGAATTAAGAGAAGC.

^c *EGFR* E746-A750del Type2 indicates *EGFR* 2236_2250delGAATTAAGAGAAGCA.

^d Negative for mutation when tested by the PNA-LNA PCR clamp method.

Figure 1

Step 1

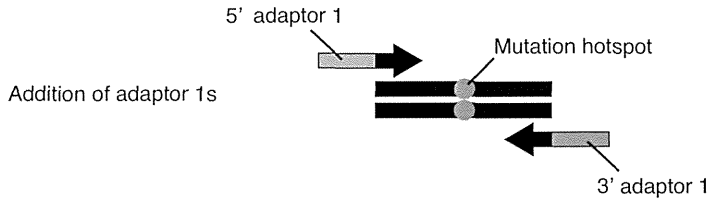
Multiplex amplification of the targets



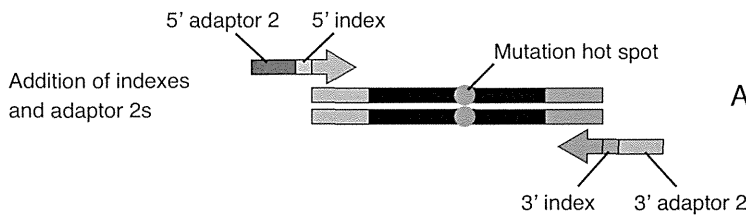
Multiplex PCR (28 cycles)

Step 2

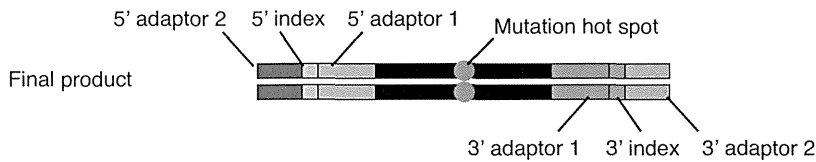
Addition of adaptors and indexes



Add-adaptor PCR (6 cycles)



Add-index-adaptor PCR (6 cycles)



Step 3

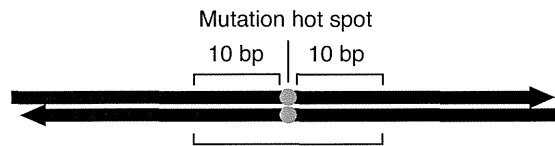
Sequencing in both strands of mutation hotspot



Pair-end read on MiSeq

Step 4

Selection of the informative reads



All nucleotides match and have a Phred score >30

Step 5

Statistical analysis using the informative reads

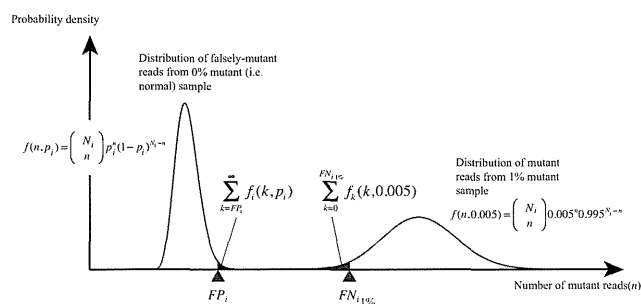


Table S1

Sequence information of the amplicons

Sequences of the amplicons investigated

Sequences indicated by a blue highlight are the 10-bp sequences that flank the mutation hot spot (see **Fig. 1** in the main text)

EGFR_ex18

CCAACCAAGCTCTCTTGAGGATCTTGAAGGAACTGAATTCAAAAAGATCAAAGTCTCTGGCTCCGGTCCGTTTCGGCA
CGGTGTATAAGGTAAGGTCCCTGGCACAGRCCTCTGGGCTGGGCCGCAGGG

EGFR_G719S

CCAACCAAGCTCTCTTGAGGATCTTGAAGGAACTGAATTCAAAAAGATCAAAGTCTCTGAGCTCCGGTCCGTTTCGGCA
CGGTGTATAAGGTAAGGTCCCTGGCACAGRCCTCTGGGCTGGGCCGCAGGG

EGFR_G719C

CCAACCAAGCTCTCTTGAGGATCTTGAAGGAACTGAATTCAAAAAGATCAAAGTCTCTGCTCCGGTCCGTTTCGGCA
CGGTGTATAAGGTAAGGTCCCTGGCACAGRCCTCTGGGCTGGGCCGCAGGG

EGFR_G719A

CCAACCAAGCTCTCTTGAGGATCTTGAAGGAACTGAATTCAAAAAGATCAAAGTCTCTGGCTCCGGTCCGTTTCGGCA
CGGTGTATAAGGTAAGGTCCCTGGCACAGRCCTCTGGGCTGGGCCGCAGGG

EGFR_ex19

AATTGCCAGTTAACGTCTTCCTTCTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTC
TCGCTATCAAAGGAATTAAGAGAAGCAACATCTCCGAAAGCCAACAAGGAAATCTCCGATGTGAGTTTCTGCTTTGCTG
TGTGGGG

EGFR_A750_K754del(2248_2262delGCAACATCTCCGAAA)

AATTGCCAGTTAACGTCTTCCTTCTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTC
TCGCTATCAAAGGAATTAAGAGAAGCCAACAAGGAAATCTCCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_A750del_insKP(2236_2248delGAATTAAGAGAAG_insAAGC)

AATTGCCAGTTAACGTCTTCCTTCTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTC
TCGCTATCAAAGGACCAACATCTCCGAAAGCCAACAAGGAAATCTCCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_A750del_insRP(2236_2248delGAATTAAGAGAAG_insAGAC)

AATTGCCAGTTAACGTCTTCCTTCTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTC
TCGCTATCAAAGAGACCAACATCTCCGAAAGCCAACAAGGAAATCTCCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_A750del_T751A(2237_2251delAATTAAGAGAAGCAA)

AATTGCCAGTTAACGTCTTCCTTCTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTC
TCGCTATCAAAGGCATCTCCGAAAGCCAACAAGGAAATCTCCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_A750del_T751A(2237_2253delAATTAAGAGAAGCAACA_insCT)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCAGAAAGGTGAGAAAGTTAAATTC
TCGCTATCAAGGCTTCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_A750del_T751F(2236_2253delGAATTAAGAGAAGCAACA_insTTC)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCAGAAAGGTGAGAAAGTTAAATTC
TCGCTATCAAGTTTCTCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_A750del_T751I(2235_2252delGGAATTAAGAGAAGCAAC_insAAT)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCAGAAAGGTGAGAAAGTTAAATTC
TCGCTATCAAAATATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_A750del_T751I(2236_2252delGAATTAAGAGAAGCAAC_insAT)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCAGAAAGGTGAGAAAGTTAAATTC
TCGCTATCAAGATATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_A750del_T751L(2236_2253delGAATTAAGAGAAGCAACA_insCTT)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCAGAAAGGTGAGAAAGTTAAATTC
TCGCTATCAAGCTTTCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_A750del_T751V(2237_2251delAATTAAGAGAAGCAA_2252CT)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCAGAAAGGTGAGAAAGTTAAATTC
TCGCTATCAAGGTATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_A750del_type1(2235_2249delGGAATTAAGAGAAGC)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCAGAAAGGTGAGAAAGTTAAATTC
TCGCTATCAAAACATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_A750del_type2(2236_2250delGAATTAAGAGAAGCA)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCAGAAAGGTGAGAAAGTTAAATTC
TCGCTATCAAGACATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_E749del_insAP(2235_2251delGGAATTAAGAGAAGCAA_insAGCAC)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCAGAAAGGTGAGAAAGTTAAATTC
TCGCTATCAAAGCACCATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_P753del_insDQPL(2238_2259delATTAAGAGAAGCAACATCTCCG_insTCAACCTCTA)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCAGAAAGGTGAGAAAGTTAAATTC
TCGCTATCAAGGATCAACCTCTAAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_P753del_insLS(2236_2257delGAATTAAGAGAAGCAACATCTC_insCTCT)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCAGAAAGGTGAGAAAGTTAAATTC
TCGCTATCAAGCTCTCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_P753del_insNPVA(2235_2257delGGAATTAAGAGAAGCAACATCTC_insAATTCCCGTCG)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAAGTTAAAATTCCCG
TCCGCTATCAAAATTCCCGTCGCGAAAGCCAACAAGGAAATCCTCCGATCTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_P753del_insVS(2237_2257delAATTAAGAGAAGCAACATCTC_instCT)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAAGTTAAAATTCCCG
TCCGCTATCAAGGTCTCGAAAGCCAACAAGGAAATCCTCCGATCTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del_insIA(2236_2251delGAATTAAGAGAAGCAA_insATAG)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAAGTTAAAATTCCCG
TCCGCTATCAAGATAGCATCTCCGAAAGCCAACAAGGAAATCCTCCGATCTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del_insIP(2235_2251delGGAATTAAGAGAAGCAA_insAATTC)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAAGTTAAAATTCCCG
TCCGCTATCAAAATTCCATCTCCGAAAGCCAACAAGGAAATCCTCCGATCTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del_insLS(2236_2251delGAATTAAGAGAAGCAA_insCTTT)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAAGTTAAAATTCCCG
TCCGCTATCAAAGCTTTCATCTCCGAAAGCCAACAAGGAAATCCTCCGATCTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del_insVA(2237_2253delAATTAAGAGAAGCAACA_instTGCT)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAAGTTAAAATTCCCG
TCCGCTATCAAAGGTGCTTCTCCGAAAGCCAACAAGGAAATCCTCCGATCTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del_insVP(2237_2253delAATTAAGAGAAGCAACA_instTCCT)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAAGTTAAAATTCCCG
TCCGCTATCAAAGGTTCCTTCTCCGAAAGCCAACAAGGAAATCCTCCGATCTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del_S752A(2237_2254delAATTAAGAGAAGCAACAT)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAAGTTAAAATTCCCG
TCCGCTATCAAAGGCTCCGAAAGCCAACAAGGAAATCCTCCGATCTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del_S752D(2238_2255delAATTAAGAGAAGCAACATC)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAAGTTAAAATTCCCG
TCCGCTATCAAAGGATCCGAAAGCCAACAAGGAAATCCTCCGATCTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del_S752E(2239_2256delTTAAGAGAAGCAACATCT)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAAGTTAAAATTCCCG
TCCGCTATCAAAGGAACCGAAAGCCAACAAGGAAATCCTCCGATCTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del_S752V(2237_2254delAATTAAGAGAAGCAACAT_2255CT)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAAGTTAAAATTCCCG
TCCGCTATCAAAGGTTCGAAAGCCAACAAGGAAATCCTCCGATCTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del_S752V(2237_2256delAATTAAGAGAAGCAACATCT_insTC)
AATTGCCAGTTAACGTCTTCCCTTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCG
TCGCTATCAAAGGTCCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del(2235_2251delGGAATTAAGAGAAGCAA_2252TC)
AATTGCCAGTTAACGTCTTCCCTTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCG
TCGCTATCAAATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_E746_T751del(2236_2253delGAATTAAGAGAAGCAACA)
AATTGCCAGTTAACGTCTTCCCTTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCG
TCGCTATCAAAGTCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_L747_A750del_T751A(2239_2253delTTAAGAGAAGCAACA_insGCT)
AATTGCCAGTTAACGTCTTCCCTTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCG
TCGCTATCAAAGGAAGCTTCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_L747_A750del_T751P(2239_2250delTTAAGAGAAGCA_2251AC)
AATTGCCAGTTAACGTCTTCCCTTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCG
TCGCTATCAAAGGAACCATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_L747_A750del_T751P(2239_2253delTTAAGAGAAGCAACA_insCCT)
AATTGCCAGTTAACGTCTTCCCTTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCG
TCGCTATCAAAGGAACCTTCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_L747_A750del_T751Q(2238_2252delATTAAGAGAAGCAAC_insGCA)
AATTGCCAGTTAACGTCTTCCCTTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCG
TCGCTATCAAAGGAGCAATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_L747_A750del_T751S(2240_2251delTAAGAGAAGCAA)
AATTGCCAGTTAACGTCTTCCCTTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCG
TCGCTATCAAAGGAATCATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_L747_A755del_insSRD(2240_2264delTAAGAGAAGCAACATCTCCGAAAGC_insCGAGAGA)
AATTGCCAGTTAACGTCTTCCCTTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCG
TCGCTATCAAAGGAATCGAGAGACAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_L747_E749del_A750P(2238_2248delATTAAGAGAAG_insGC)
AATTGCCAGTTAACGTCTTCCCTTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCG
TCGCTATCAAAGGAGCCAACATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_L747_E749del_A750P(2239_2247delTTAAGAGAA_2248GC)
AATTGCCAGTTAACGTCTTCCCTTCTCTCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCG
TCGCTATCAAAGGAACCAACATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGG

EGFR_L747_E749del_A750P(2239_2250delTTAAGAGAAGCA_insCCT)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAAGGTGAGAAAGTTAAAATCCCCG
TCGCTATCAA GGAACCTACATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGA GTTCTGCTTTGCTGTGTGGGG

EGFR_L747_K754del_insATSPE(2239_2260delTTAAGAGAAGCAACATCTCCGA_insGCAACATCTCCGG
)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAAGGTGAGAAAGTTAAAATCCCCG
TCGCTATCAA GGAAGCAACATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGA GTTCTGCTTTGCTGTGTGGGG

EGFR_L747_K754del_insSRE(2240_2260delTTAAGAGAAGCAACATCTCCGA_insCAAGAG)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAAGGTGAGAAAGTTAAAATCCCCG
TCGCTATCAA GGAATCAAGAGAAGCCAACAAGGAAATCCTCGATGTGA GTTCTGCTTTGCTGTGTGGGG

EGFR_L747_N756del_insQKAD(2239_2266delTTAAGAGAAGCAACATCTCCGAAAGCCA_insCAGAAAGC
CG)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAAGGTGAGAAAGTTAAAATCCCCG
TCGCTATCAA GGAACAGAAAGCCGACAAGGAAATCCTCGATGTGA GTTCTGCTTTGCTGTGTGGGG

EGFR_L747_P753del_insQQ(2239_2258delTTAAGAGAAGCAACATCTCC_insCAACA)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAAGGTGAGAAAGTTAAAATCCCCG
TCGCTATCAA GGAACAACAGAAAGCCAACAAGGAAATCCTCGATGTGA GTTCTGCTTTGCTGTGTGGGG

EGFR_L747_P753del_K754G(2239_2261delTTAAGAGAAGCAACATCTCCGAA_insGG)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAAGGTGAGAAAGTTAAAATCCCCG
TCGCTATCAA GGAAGGAGCCAACAAGGAAATCCTCGATGTGA GTTCTGCTTTGCTGTGTGGGG

EGFR_L747_S752del_insPC(2239_2255delTTAAGAGAAGCAACATC_insCCATG)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAAGGTGAGAAAGTTAAAATCCCCG
TCGCTATCAA GGAACCATGTCCGAAAGCCAACAAGGAAATCCTCGATGTGA GTTCTGCTTTGCTGTGTGGGG

EGFR_L747_S752del_insQH(2238_2255delTTAAGAGAAGCAACATC_insGCAACA)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAAGGTGAGAAAGTTAAAATCCCCG
TCGCTATCAA GGAGCAACATCCGAAAGCCAACAAGGAAATCCTCGATGTGA GTTCTGCTTTGCTGTGTGGGG

EGFR_L747_S752del_insQH(2239_2255delTTAAGAGAAGCAACATC_insCAACA)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAAGGTGAGAAAGTTAAAATCCCCG
TCGCTATCAA GGAACAACATCCGAAAGCCAACAAGGAAATCCTCGATGTGA GTTCTGCTTTGCTGTGTGGGG

EGFR_L747_S752del_P753Q(2236_2258delTTAAGAGAAGCAACATCTCC_insCA)
AATTGCCAGTTAACGTCTTCCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAAGGTGAGAAAGTTAAAATCCCCG
TCGCTATCAA GGAACAGAAAGCCAACAAGGAAATCCTCGATGTGA GTTCTGCTTTGCTGTGTGGGG

EGFR_L747_S752del_P753S(2240_2257delTTAAGAGAAGCAACATCTC)

AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCGG
TCGCTATCAAGGAATCGAAAGCCAACAAGGAAATC**CTCGATGTGA**GTTTCTGCTTTGCTGTGTGGGG

EGFR_L747_T751del_S752Q(2238_2256delATTAAGAGAAGCAACATCT_insGCAA)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCGG
TCGCTATCAAGGAATCGAAAGCCAACAAGGAAATC**CTCGATGTGA**GTTTCTGCTTTGCTGTGTGGGG

EGFR_L747_T751del(2239_2253delTTAAGAGAAGCAACA)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCGG
TCGCTATCAAGGAATCTCGAAAGCCAACAAGGAAATC**CTCGATGTGA**GTTTCTGCTTTGCTGTGTGGGG

EGFR_S752_I759del(2253_2276delATCTCCGAAAGCCAACAAGGAAAT)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCGG
TCGCTATCAAGGAATTAAGAGAAGCAACC**CTCGATGTGA**GTTTCTGCTTTGCTGTGTGGGG

EGFR_S752_I759del(2254_2277delTCTCCGAAAGCCAACAAGGAAATC)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCGG
TCGCTATCAAGGAATTAAGAGAAGCAACA**CTCGATGTGA**GTTTCTGCTTTGCTGTGTGGGG

EGFR_T751_E758del_I759N(2252_2275delCATCTCCGAAAGCCAACAAGGAAA_2276TA)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCGG
TCGCTATCAAGGAATTAAGAGAAGCAAAC**CTCGATGTGA**GTTTCTGCTTTGCTGTGTGGGG

EGFR_T751_E758del_I759S(2252_2266delACATCTCCGAAAGCCAACAAGGAAAT_insTC)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCGG
TCGCTATCAAGGAATTAAGAGAAGCATCC**CTCGATGTGA**GTTTCTGCTTTGCTGTGTGGGG

EGFR_T751_E758del_I759S(2252_2275delCATCTCCGAAAGCCAACAAGGAAA_2276TG)
AATTGCCAGTTAACGTCTTCTTCTCTCTGTGCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCGG
TCGCTATCAAGGAATTAAGAGAAGCAAGC**CTCGATGTGA**GTTTCTGCTTTGCTGTGTGGGG

EGFR_T790M_Area
GGTCCAYGTGCCCTCCTTCTGGCCACCATGCGAAGCCACACTGACGTGCCTCTCCCTCCCTCCAGGAAGCSTACGTG
ATGGCCAGCGTGGACAACCCACCGTGTGCCGCTGCTGGGCATCTGCCTCACCTCCACCGTG**CARCTCATCAT****GCAG**
CTCATGCCCTTCGGCTGCCTCCTGGACTATGTCCGGGAACACAAAGACAATATTGGCTCC

EGFR_T790M
GGTCCAYGTGCCCTCCTTCTGGCCACCATGCGAAGCCACACTGACGTGCCTCTCCCTCCCTCCAGGAAGCSTACGTG
ATGGCCAGCGTGGACAACCCACCGTGTGCCGCTGCTGGGCATCTGCCTCACCTCCACCGTG**CARCTCATCAT****GCAG**
CTCATGCCCTTCGGCTGCCTCCTGGACTATGTCCGGGAACACAAAGACAATATTGGCTCC

EGFR_S768I_Area
GGTCCAYGTGCCCTCCTTCTGGCCACCATGCGAAGCCACACTGACGTGCCTCTCCCTCCCTCCAGGAAGCSTAC**GTG**
ATGGCCA**CGGTGGACAAC**CCCCACCGTGTGCCGCTGCTGGGCATCTGCCTCACCTCCACCGTGCARCTCATCACGCAG

CTCATGCCCTTCGGCTGCCTCCTGGACTATGTCCGGGAACACAAAGACAATATTGGCTCC

EGFR_S768I

GGTCCAYGTGCCCTCCTTCTGGCCACCATGCGAAGCCACACTGACGTGCCTCTCCCTCCCTCCAGGAAGCSTAC**CTG**
ATGGCCATCGTGGACAACCCCACGTGTGCCGCTGCTGGGCATCTGCCTCACCTCCACCGTGCARCTCATCACGCAG
CTCATGCCCTTCGGCTGCCTCCTGGACTATGTCCGGGAACACAAAGACAATATTGGCTCC

EGFR_ex21

GCAGAGCTTCTTCCCATGATGATCTGTCCCTCACAGCAGGGTCTTCTCTGTTTCAGGGCATGAACTACTTGGAGGACC
GTCGCTTGGTGCACCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAAACCCGCAGCATGTCAAGATCAC**CAATTTTG**
GCCTGGCCAAACT**GCTGGGTCCG**GAAGAGAAAGAATACCATGCAGAAGGAGGCAAAGTAAGG

EGFR_L858R (2573TG)

GCAGAGCTTCTTCCCATGATGATCTGTCCCTCACAGCAGGGTCTTCTCTGTTTCAGGGCATGAACTACTTGGAGGACC
GTCGCTTGGTGCACCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAAACCCGCAGCATGTCAAGATCAC**CAATTTTG**
GCCGGGCCAAACT**GCTGGGTCCG**GAAGAGAAAGAATACCATGCAGAAGGAGGCAAAGTAAGG

EGFR_L858R (2573TG_2574GT)

GCAGAGCTTCTTCCCATGATGATCTGTCCCTCACAGCAGGGTCTTCTCTGTTTCAGGGCATGAACTACTTGGAGGACC
GTCGCTTGGTGCACCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAAACCCGCAGCATGTCAAGATCAC**CAATTTTG**
GCCGTGCCAAACT**GCTGGGTCCG**GAAGAGAAAGAATACCATGCAGAAGGAGGCAAAGTAAGG

EGFR_L861Q

GCAGAGCTTCTTCCCATGATGATCTGTCCCTCACAGCAGGGTCTTCTCTGTTTCAGGGCATGAACTACTTGGAGGACC
GTCGCTTGGTGCACCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAAACCCGCAGCATGTCAAGATCAC**CAATTTTG**
GCCTGGCCAAACA**GCTGGGTCCG**GAAGAGAAAGAATACCATGCAGAAGGAGGCAAAGTAAGG

KRAS_ex2

AATATAAACTTGTGGT**AGTTGGAGCT**GGTGG**CGTAGGCAAG**AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAAATATG

KRAS_G12S

AATATAAACTTGTGGT**AGTTGGAGCT**AGTGG**CGTAGGCAAG**AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAAATATG

KRAS_G12R

AATATAAACTTGTGGT**AGTTGGAGCT**CGTGG**CGTAGGCAAG**AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAAATATG

KRAS_G12C

AATATAAACTTGTGGT**AGTTGGAGCT**TGTGG**CGTAGGCAAG**AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAAATATG

KRAS_G12D

AATATAAACTTGTGGT **AGTTGGAGCT** GATGG **CCTAGGCAAG** AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAATATG

KRAS_G12A

AATATAAACTTGTGGT **AGTTGGAGCT** GCTGG **CCTAGGCAAG** AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAATATG

KRAS_G12V

AATATAAACTTGTGGT **AGTTGGAGCT** GTTGG **CCTAGGCAAG** AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAATATG

KRAS_G13S

AATATAAACTTGTGGT **AGTTGGAGCT** GGTAG **CCTAGGCAAG** AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAATATG

KRAS_G13R

AATATAAACTTGTGGT **AGTTGGAGCT** GGTGC **CCTAGGCAAG** AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAATATG

KRAS_G13C

AATATAAACTTGTGGT **AGTTGGAGCT** GGTTC **CCTAGGCAAG** AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAATATG

KRAS_G13D

AATATAAACTTGTGGT **AGTTGGAGCT** GGTGA **CCTAGGCAAG** AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAATATG

KRAS_G13V_1

AATATAAACTTGTGGT **AGTTGGAGCT** GGTGC **CCTAGGCAAG** AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAATATG

KRAS_G13V_2

AATATAAACTTGTGGT **AGTTGGAGCT** GGTGT **CCTAGGCAAG** AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
TGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTTAATATG

KRAS_ex3

TAATTGATGGAGAAACCTGTCTCTTGATATTCTCGA **CACAGCAGGT** CAA **GAGGAGTACA** GTGCAATGAGGGACCAGT
ACATGAGGACTGGG

KRAS_Q61K

TAATTGATGGAGAAACCTGTCTCTTGATATTCTCGA **CACAGCAGGT** AAA **GAGGAGTACA** GTGCAATGAGGGACCAGT
ACATGAGGACTGGG

KRAS_Q61E

TAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGA CACAGCAGCT GAA GAGGACTACA GTGCAATGAGGGACCAGT
ACATGAGGACTGGG

KRAS_Q61R

TAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGA CACAGCAGCT CGA GAGGACTACA GTGCAATGAGGGACCAGT
ACATGAGGACTGGG

KRAS_Q61P

TAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGA CACAGCAGCT CCA GAGGACTACA GTGCAATGAGGGACCAGT
ACATGAGGACTGGG

KRAS_Q61L

TAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGA CACAGCAGCT CTA GAGGACTACA GTGCAATGAGGGACCAGT
ACATGAGGACTGGG

KRAS_Q61H_1

TAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGA CACAGCAGCT CAC GAGGACTACA GTGCAATGAGGGACCAGT
ACATGAGGACTGGG

KRAS_Q61H_2

TAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGA CACAGCAGCT CAT GAGGACTACA GTGCAATGAGGGACCAGT
ACATGAGGACTGGG

BRAF_ex11

GAAAACACTTGGTAGACGGGACTCGAGTGTGATTGGGAGATTCCTGATGGGCAGATTACAGTGGGACAAAGA ATTGG
ATCTG GATCATTGG AACAGTCTAC AAGGGAAAGTGGCATGGTAAGTATGTAATGTGGTG

BRAF_G466V

GAAAACACTTGGTAGACGGGACTCGAGTGTGATTGGGAGATTCCTGATGGGCAGATTACAGTGGGACAAAGA ATTGG
ATCTG TATCATTGG AACAGTCTAC AAGGGAAAGTGGCATGGTAAGTATGTAATGTGGTG

BRAF_G469A

GAAAACACTTGGTAGACGGGACTCGAGTGTGATTGGGAGATTCCTGATGGGCAGATTACAGTGGGACAAAGA ATTGG
ATCTG GATCATTGG AACAGTCTAC AAGGGAAAGTGGCATGGTAAGTATGTAATGTGGTG

BRAF_G469E

GAAAACACTTGGTAGACGGGACTCGAGTGTGATTGGGAGATTCCTGATGGGCAGATTACAGTGGGACAAAGA ATTGG
ATCTG GATCATTGG AACAGTCTAC AAGGGAAAGTGGCATGGTAAGTATGTAATGTGGTG

BRAF_G469V

GAAAACACTTGGTAGACGGGACTCGAGTGTGATTGGGAGATTCCTGATGGGCAGATTACAGTGGGACAAAGA ATTGG
ATCTG GATCATTGG AACAGTCTAC AAGGGAAAGTGGCATGGTAAGTATGTAATGTGGTG

BRAF_ex15

CTTGCTCTGATAGGAAAATGAGATCTACTGTTTTCCCTTACTTACTACACCTCAGATATATTTCTTCATGAAGACCTC
ACAGTAAAAATAGGTCATTTTGGTCTAGCTACAGTGAATCTCGATGGAGTGGGTCCCATCAGTTGAACAGTTGTCT
GGATCCATTTTGTGGATGGTAAGAATTGAGGCTATTTTCCACTGATTAATTTTTGGCCCTGAGATGCTGCTGAGTT
ACTAG

BRAF_D594G

CTTGCTCTGATAGGAAAATGAGATCTACTGTTTTCCCTTACTTACTACACCTCAGATATATTTCTTCATGAAGACCTC
ACAGTAAAAATAGGTCGTTTTGGTCTAGCTACAGTGAATCTCGATGGAGTGGGTCCCATCAGTTGAACAGTTGTCT
GGATCCATTTTGTGGATGGTAAGAATTGAGGCTATTTTCCACTGATTAATTTTTGGCCCTGAGATGCTGCTGAGTT
ACTAG

BRAF_D594V

CTTGCTCTGATAGGAAAATGAGATCTACTGTTTTCCCTTACTTACTACACCTCAGATATATTTCTTCATGAAGACCTC
ACAGTAAAAATAGGTCGTTTTGGTCTAGCTACAGTGAATCTCGATGGAGTGGGTCCCATCAGTTGAACAGTTGTCT
GGATCCATTTTGTGGATGGTAAGAATTGAGGCTATTTTCCACTGATTAATTTTTGGCCCTGAGATGCTGCTGAGTT
ACTAG

BRAF_G596R

CTTGCTCTGATAGGAAAATGAGATCTACTGTTTTCCCTTACTTACTACACCTCAGATATATTTCTTCATGAAGACCTC
ACAGTAAAAATAGGTCATTTTCGTCTAGCTACAGTGAATCTCGATGGAGTGGGTCCCATCAGTTGAACAGTTGTCT
GGATCCATTTTGTGGATGGTAAGAATTGAGGCTATTTTCCACTGATTAATTTTTGGCCCTGAGATGCTGCTGAGTT
ACTAG

BRAF_V600E

CTTGCTCTGATAGGAAAATGAGATCTACTGTTTTCCCTTACTTACTACACCTCAGATATATTTCTTCATGAAGACCTC
ACAGTAAAAATAGGTCATTTTGGTCTAGCTACAGAGAAATCTCGATGGAGTGGGTCCCATCAGTTGAACAGTTGTCT
GGATCCATTTTGTGGATGGTAAGAATTGAGGCTATTTTCCACTGATTAATTTTTGGCCCTGAGATGCTGCTGAGTT
ACTAG