

Exon 21 sequence for your use (wild type):

ggcatgaactacttggaggaccgtcgcttgggtgcaccgacactggcagccaggaacgtactggtgaaaa  
caccgagcatgtcaagatcacagatTTTGGGCTGGCCAAACTGCTGGGTGCGGAAGAGAAAGAATACCA  
TGCAGAAGGAGGCAAA

Exon 21 sequence for your use (L858R point mutant):

ggcatgaactacttggaggaccgtcgcttgggtgcaccgacactggcagccaggaacgtactggtgaaaa  
caccgagcatgtcaagatcacagatTTTGGGCGGGCCAAACTGCTGGGTGCGGAAGAGAAAGAATACCA  
TGCAGAAGGAGGCAAA

### 5'3' Frame 1 Wild-type EGFR

```
ggcatgaactacttggaggaccgtcgcttgggtgcaccgacactggcagccaggaacgta
G M N Y L E D R R L V H R D L A A R N V
ctggtgaaaacaccgagcatgtcaagatcacagatTTTGGGCTGGCCAAACTGCTGGGT
L V K T P Q H V K I T D F G L A K L L G
gcggaagagaaagaataccatgcagaaggaggcaaa
A E E K E Y H A E G G K
```

### 5'3' Frame 1 L858R Mutant

```
ggcatgaactacttggaggaccgtcgcttgggtgcaccgacactggcagccaggaacgta
G M N Y L E D R R L V H R D L A A R N V
ctggtgaaaacaccgagcatgtcaagatcacagatTTTGGGCGGGCCAAACTGCTGGGT
L V K T P Q H V K I T D F G R A K L L G
gcggaagagaaagaataccatgcagaaggaggcaaa
A E E K E Y H A E G G K
```

Exon 19 for your use: (wild type)

ggactctggatcccagaaggtgagaaagttaaattcccgtcgctatcaaggaaatcaacatctccgaaagccaacaaggaat  
cctcgat

Exon 19 for your use: (deletion)

Ggactctggatcccagaaggtgagaaagttaaattcccgtcgctatcaaacatctccgaaagccaacaaggaatcctcgat

Wild-type

### 5'3' Frame 1

```
ggactctggatcccagaaggtgagaaagttaaattcccgtcgctatcaaggaattaaga
G L W I P E G E K V K I P V A I K E L R
gaagcaacatctccgaaagccaacaaggaaatcctcgat
E A T S P K A N K E I L D
```

Mutant:

### 5'3' Frame 1

```
ggactctggatcccagaaggtgagaaagttaaattcccgtcgctatcaaacatctccg
G L W I P E G E K V K I P V A I K T S P
aaagccaacaaggaaatcctcgat
K A N K E I L D
```

Negative control sequences for exon 21 (from MDA-MB231 cells):

>231\_exon21\_fp-exon21\_fp\_C12.ab1

NNNNNNNNNNNTNNTGNNGANNTNNTTGGTGCACCGGACCTGGCAGCCAGGAACGTAAGTGGTGAAAACACCCGCAGCA  
TGTC AAGATCACAGATTTTGGGCTGGCCAAACTGCTGGGTGCGGAAGANAAAGAATACCATGCAGAAGGAGGCAAAGTAA  
GGAGGTGNTNTAGGTGAGCCAAAANCTTACTTTGCCTCTTCTGCAGGTATTCTTTCTCTTCGCCGCAATTGGCGCCAAAAT  
CTGTGATCTNGACNTGCTGCGTGTTCNNTACTTCGGCGCGNTCCNNGCAGCANNNTCTCGTTAATTCAGCNGAAACAA  
AGAAAACCCNGCTTGAAGNAANNCATGAGCTCTATGGATCTATATAAAAANTGGAAAAATCCCCTAAAGTGAATGACGAT  
CTACTTAATTAATAAATAACTGGGANCGGCANGAATGGCGGAGCAGGTGTAAGTTCCTGCGCCAAACANNNTAATGA  
NNGANTCGAGNACAGCGGATANATAGAANGTTCNATTTGACAGGCAAGCATGTCTGCTATGTGGTGGATTGGNGANGANA  
TGNNNTGNANACAACAGNGTTCATGACCAANAATATANCGGTGANNGNCCGGNAANNTNNTNNGNNGNNCATCGAA  
CTCINNACTANTCCAGCCAGACGCTGTNNANCTAATNNANNTAANGANNNTTGCATGTTNNNCCNCGCTCANNANNATN  
ATNNNANGTTTCANCTNNTGANATTACGTTGAANGACTTGCCACTNTTCACTCGATACNTTANANCAGNGCAGACTC  
ATTC TAATANNNTGNTGTCNTCNTTTTTTTTGGANGATANGCATTGTCNNTGATANNTNNTAAATTTCCNNATNNGC  
ANGGATGAAGTCTAGTNNAATCNCNNAANAAGCGNTGTNTGNGTATATTANNTGATTCTNTANCANGAGNNTNAGGNN  
ACNNGNAGNNAATCNACTAGNNTNNGNAAATTTANNANGNTTACTNTTNNCNCNNTNNTNNTNNTAGGCTGGNNNN  
NGNCNTNNTTTTTNNNANNNNNTNNGACTNNGNNAANANCCNNGGNGTTACNCCAAGNTTAGTNCNCNTNGAANNNN  
NNNNNC

>231\_exon21\_rp-exon21\_rp\_D12.ab1

CNNNNNNNNCCNNNNNGNNGGATNNTNNTCNCNCGCACCCAGCAGTTTGGCCAGCCAAAATCTGTGATCTTGACAT  
GCTGCGGTGTTTTACCAGTACGTTCTGGCTGCCAGGTGCGGTCACCAAGCGACGGTCTCCAAGTAGTTCATGCCC  
TGAAACAGAGAAGACNTGCTGTGAGGAAANGTCAGGCTTGCCTGGGGGAGAAAGACTCTGCAGCGGGCCGGGACGTGC  
TAAGGCTTGATTCGCGCCGAGATGTAAGTCAATGGGAATGGAGGCTAACCCAGAGGGCCACCCTACCCTGACGT  
CATCACCTCACCTTGACCTGGTTGGAAGAATCATAGCGCACACGCTGGCAACTCTTATTCATCTTGTTCATCAACATCT  
TTCCGGTGCGGAAGTGAAGGTGCTGAGGTCCATGGATCCGCCAGGTAACGTGCCAGTTGTGGCTTGTGCGGAACTTC  
TTNNNTCAACATCTTTCCCGTGCNAANTGNGGGTGCAGGAGTCCGTGGATCCGCCAAGTCAAGTTGCAGTTGTGCAT  
TGGAGGAGAAATTGNTCAGAANCAANAGGNTCTCATGANGNANAATATCCTGTCCAGNGACCGTAAANNNGGCTTANNG  
NCTCATGTGTGTCATTGTTATCCNNTCANGNCTCCGTACAACTAAGAAACNGANGAATATNTTGTGANCCTGCGNGCCT  
ANCGANNNTGCTANCACGTNTNANTGNNCTGANATCACNGNCCNNGATCTGNTACTNTAACTGNNNTGTCANATGANT  
ACAAANNTCNCTCAANNNCNTGGNTGNNCNGNTTNGGTATTNGAGCNGCANNTTGCCTCGNTNNTGACACGTTGCGC  
TNTTTCGNCCNGNTGNNNNANAGTTAACTCCTCANNTCAGNGNTGNANTGNGNNTATCNGTATNCNNGGNGANGAGATN  
GANNNNNNTGGGANNAANGTCANCTANNCCAGAANTNAANAANNNTTATGNCTGCNTNNNACGNNGNNTNNTNNTNNT  
ACNNTTANNNNNNNGACTGNNNANN