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Thr Lys Leu Arg Tyr Met Asp Asn His Met Pro Ala Asp Ala Glu Arg
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Ala Gly Leu Phe Val Arg Thr Ser Ala Pro Cys Thr Ile Thr Gly Thr
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Val Gly Phe Thr Asp Ser Arg Lys Ile Ser His Ser Cys Thr His Pro
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Ala Ala Thr Thr Glu Glu Ile Lys Val His Met Pro Pro Asp Thr Pro
                165                 170                 175

Asp His Thr Leu Met Ser Gln Gln Ser Gly Asn Val Lys Ile Thr Val
            180                 185                 190

Asn Gly Gln Thr Val Arg Tyr Lys Cys Asn Cys Gly Gly Ser Asn Glu
        195                 200                 205

Gly Leu Thr Thr Thr Asp Lys Val Ile Asn Asn Cys Lys Val Asp Gln
    210                 215                 220

Cys His Ala Ala Val Thr Asn His Lys Lys Trp Gln Tyr Asn Ser Pro
225                 230                 235                 240

Leu Val Pro Arg Asn Ala Glu Leu Gly Asp Arg Lys Gly Lys Ile His
                245                 250                 255
```

```
Ile Pro Phe Pro Leu Ala Asn Val Thr Cys Arg Val Pro Lys Ala Arg
            260                 265                 270

Asn Pro Thr Val Thr Tyr Gly Lys Asn Gln Val Ile Met Leu Leu Tyr
        275                 280                 285

Pro Asp His Pro Thr Leu Leu Ser Tyr Arg Asn Met Gly Glu Glu Pro
    290                 295                 300

Asn Tyr Gln Glu Glu Trp Val Met His Lys Lys Glu Val Val Leu Thr
305                 310                 315                 320

Val Pro Thr Glu Gly Leu Glu Val Thr Trp Gly Asn Asn Glu Pro Tyr
                325                 330                 335

Lys Tyr Trp Pro Gln Leu Ser Thr Asn Gly Thr Ala His Gly His Pro
            340                 345                 350

His Glu Ile Ile Leu Tyr Tyr Tyr Glu Leu Tyr Pro Thr Met Thr Val
        355                 360                 365

Val Val Val Ser Val Ala Thr Phe Ile Leu Leu Ser Met Val Gly Met
    370                 375                 380

Ala Ala Gly Met Cys Met Cys Ala Arg Arg Arg Cys Ile Thr Pro Tyr
385                 390                 395                 400

Glu Leu Thr Pro Gly Ala Thr Val Pro Phe Leu Leu Ser Leu Ile Cys
                405                 410                 415

Cys Ile Arg Thr Ala Lys Ala
            420
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<210> 4
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> mutation arising from Vero passaging

<400> 4

Ser Thr Lys Asp Asn Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr Leu
1   5   10   15

Ala His Cys Pro Asp Cys Gly Glu Gly His Ser Cys His Ser Pro Val
            20   25   30

Ala Leu Glu Arg Ile Arg Asn Glu Ala Thr Asp Gly Thr Leu Lys Ile
        35   40   45

Gln Val Ser Leu Gln Ile Arg Ile Lys Thr Asp Asp Ser His Asp Trp
    50   55   60

Thr Lys Leu Arg Tyr Met Asp Asn His Met Pro Ala Asp Ala Glu Arg
65   70   75   80

Ala Gly Leu Phe Val Arg Thr Ser Ala Pro Cys Thr Ile Thr Gly Thr
                85   90   95

Met Gly His Phe Ile Leu Ala Arg Cys Pro Lys Gly Glu Thr Leu Thr
            100   105   110

Val Gly Phe Thr Asp Ser Arg Lys Ile Ser His Ser Cys Thr His Pro
        115   120   125

Phe His His Asp Pro Pro Val Ile Gly Arg Glu Lys Phe His Ser Arg
    130   135   140

Pro Gln His Gly Lys Glu Leu Pro Cys Ser Thr Tyr Val Gln Ser Thr
145   150   155   160

Ala Ala Thr Thr Glu Glu Ile Glu Val His Met Pro Pro Asp Thr Pro
                165   170   175

Asp His Thr Leu Met Ser Gln Gln Ser Gly Asn Val Lys Ile Thr Val

```
            180                 185                 190

Asn Gly Gln Thr Val Arg Tyr Lys Cys Asn Cys Gly Gly Ser Asn Glu
        195                 200                 205

Gly Leu Thr Thr Thr Asp Lys Val Ile Asn Asn Cys Lys Val Asp Gln
    210                 215                 220

Cys His Ala Ala Val Thr Asn His Lys Lys Trp Gln Tyr Asn Ser Pro
225                 230                 235                 240

Leu Val Pro Arg Asn Ala Glu Leu Gly Asp Arg Lys Gly Lys Ile His
                245                 250                 255

Ile Pro Phe Pro Leu Ala Asn Val Thr Cys Arg Val Pro Lys Ala Arg
            260                 265                 270

Asn Pro Thr Val Thr Tyr Gly Lys Asn Gln Val Ile Met Leu Leu Tyr
        275                 280                 285

Pro Asp His Pro Thr Leu Leu Ser Tyr Arg Asn Met Gly Glu Glu Pro
    290                 295                 300

Asn Tyr Gln Glu Glu Trp Val Met His Lys Lys Glu Val Val Leu Thr
305                 310                 315                 320

Val Pro Thr Glu Gly Leu Glu Val Thr Trp Gly Asn Asn Glu Pro Tyr
                325                 330                 335

Lys Tyr Trp Pro Gln Leu Ser Thr Asn Gly Thr Ala His Gly His Pro
            340                 345                 350

His Glu Ile Ile Leu Tyr Tyr Tyr Glu Leu Tyr Pro Thr Met Thr Val
        355                 360                 365

Val Val Val Ser Val Ala Thr Phe Ile Leu Leu Ser Met Val Gly Met
    370                 375                 380
```

```
Ala Ala Gly Met Cys Met Cys Ala Arg Arg Arg Cys Ile Thr Pro Tyr
385                 390                 395                 400


Glu Leu Thr Pro Gly Ala Thr Val Pro Phe Leu Leu Ser Leu Ile Cys
                405                 410                 415


Cys Ile Arg Thr Ala Lys Ala
            420
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<210> 5
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> mutation arising from Vero passaging

<400> 5

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Ser Thr Lys Asp Asn Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr Leu
1               5                   10                  15


Ala His Cys Pro Asp Cys Gly Glu Gly His Ser Cys His Ser Pro Val
            20                  25                  30


Ala Leu Glu Arg Ile Arg Asn Glu Ala Thr Asp Gly Thr Leu Lys Ile
        35                  40                  45


Gln Val Ser Leu Gln Ile Gly Ile Lys Thr Asp Asp Ser His Asp Trp
    50                  55                  60


Thr Lys Leu Arg Tyr Met Asp Asn His Met Pro Ala Asp Ala Glu Arg
65                  70                  75                  80


Ala Gly Leu Phe Val Arg Thr Ser Ala Pro Cys Thr Ile Thr Gly Thr
                85                  90                  95


Met Gly His Phe Ile Leu Ala Arg Cys Pro Lys Gly Glu Thr Leu Thr
            100                 105                 110
```

```
Val Gly Phe Thr Asp Ser Arg Lys Ile Ser His Ser Cys Thr His Pro
        115                 120                 125

Phe His His Asp Pro Pro Val Ile Gly Arg Glu Lys Phe His Ser Arg
    130                 135                 140

Pro Gln His Gly Lys Glu Leu Pro Cys Ser Thr Tyr Val Gln Ser Thr
145                 150                 155                 160

Ala Ala Thr Thr Glu Glu Ile Glu Val His Met Pro Pro Asp Thr Pro
                165                 170                 175

Asp His Thr Leu Met Ser Gln Gln Ser Gly Asn Val Lys Ile Thr Val
            180                 185                 190

Asn Gly Gln Thr Val Arg Tyr Lys Cys Asn Cys Gly Gly Ser Asn Glu
        195                 200                 205

Gly Leu Thr Thr Thr Asp Lys Val Ile Asn Asn Cys Lys Val Asp Gln
    210                 215                 220

Cys His Ala Ala Val Thr Asn His Lys Lys Trp Gln Tyr Asn Ser Pro
225                 230                 235                 240

Leu Val Pro Arg Asn Ala Lys Leu Gly Asp Arg Lys Gly Lys Ile His
                245                 250                 255

Ile Pro Phe Pro Leu Ala Asn Val Thr Cys Arg Val Pro Lys Ala Arg
            260                 265                 270

Asn Pro Thr Val Thr Tyr Gly Lys Asn Gln Val Ile Met Leu Leu Tyr
        275                 280                 285

Pro Asp His Pro Thr Leu Leu Ser Tyr Arg Asn Met Gly Glu Glu Pro
    290                 295                 300

Asn Tyr Gln Glu Glu Trp Val Met His Lys Lys Glu Val Val Leu Thr
```

```
305                 310                 315                 320

Val Pro Thr Glu Gly Leu Glu Val Thr Trp Gly Asn Asn Glu Pro Tyr
                325                 330                 335

Lys Tyr Trp Pro Gln Leu Ser Thr Asn Gly Thr Ala His Gly His Pro
            340                 345                 350

His Glu Ile Ile Leu Tyr Tyr Tyr Glu Leu Tyr Pro Thr Met Thr Val
        355                 360                 365

Val Val Val Ser Val Ala Thr Phe Ile Leu Leu Ser Met Val Gly Met
    370                 375                 380

Ala Ala Gly Met Cys Met Cys Ala Arg Arg Arg Cys Ile Thr Pro Tyr
385                 390                 395                 400

Glu Leu Thr Pro Gly Ala Thr Val Pro Phe Leu Leu Ser Leu Ile Cys
                405                 410                 415

Cys Ile Arg Thr Ala Lys Ala
            420
```

<210> 6
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> mutation arising from Vero passaging

<400> 6

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Ser Thr Lys Asp Asn Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr Leu
1               5                   10                  15

Ala His Cys Pro Asp Cys Gly Glu Gly His Ser Cys His Ser Pro Val
            20                  25                  30

Ala Leu Glu Arg Ile Arg Asn Glu Ala Thr Asp Gly Thr Leu Lys Ile
```

```
        35                  40                  45

Gln Val Ser Leu Gln Ile Gly Ile Lys Thr Asp Asp Ser His Asp Trp
    50                  55                  60

Thr Lys Leu Arg Tyr Met Asp Asn His Met Pro Ala Asp Ala Glu Arg
65                  70                  75                  80

Ala Arg Leu Phe Val Arg Thr Ser Ala Pro Cys Thr Ile Thr Gly Thr
                85                  90                  95

Met Gly His Phe Ile Leu Ala Arg Cys Pro Lys Gly Glu Thr Leu Thr
            100                 105                 110

Val Gly Phe Thr Asp Ser Arg Lys Ile Ser His Ser Cys Thr His Pro
        115                 120                 125

Phe His His Asp Pro Pro Val Ile Gly Arg Glu Lys Phe His Ser Arg
    130                 135                 140

Pro Gln His Gly Lys Glu Leu Pro Cys Ser Thr Tyr Val Gln Ser Thr
145                 150                 155                 160

Ala Ala Thr Thr Glu Glu Ile Glu Val His Met Pro Pro Asp Thr Pro
                165                 170                 175

Asp His Thr Leu Met Ser Gln Gln Ser Gly Asn Val Lys Ile Thr Val
            180                 185                 190

Asn Gly Gln Thr Val Arg Tyr Lys Cys Asn Cys Gly Gly Ser Asn Glu
        195                 200                 205

Gly Leu Thr Thr Thr Asp Lys Val Ile Asn Asn Cys Lys Val Asp Gln
    210                 215                 220

Cys His Ala Ala Val Thr Asn His Lys Lys Trp Gln Tyr Asn Ser Pro
225                 230                 235                 240
```

```
Leu Val Pro Arg Asn Ala Glu Leu Gly Asp Arg Lys Gly Lys Ile His
                245                 250                 255

Ile Pro Phe Pro Leu Ala Asn Val Thr Cys Arg Val Pro Lys Ala Arg
            260                 265                 270

Asn Pro Thr Val Thr Tyr Gly Lys Asn Gln Val Ile Met Leu Leu Tyr
        275                 280                 285

Pro Asp His Pro Thr Leu Leu Ser Tyr Arg Asn Met Gly Glu Glu Pro
    290                 295                 300

Asn Tyr Gln Glu Glu Trp Val Met His Lys Lys Glu Val Val Leu Thr
305                 310                 315                 320

Val Pro Thr Glu Gly Leu Glu Val Thr Trp Gly Asn Asn Glu Pro Tyr
                325                 330                 335

Lys Tyr Trp Pro Gln Leu Ser Thr Asn Gly Thr Ala His Gly His Pro
            340                 345                 350

His Glu Ile Ile Leu Tyr Tyr Tyr Glu Leu Tyr Pro Thr Met Thr Val
        355                 360                 365

Val Val Val Ser Val Ala Thr Phe Ile Leu Leu Ser Met Val Gly Met
    370                 375                 380

Ala Ala Gly Met Cys Met Cys Ala Arg Arg Arg Cys Ile Thr Pro Tyr
385                 390                 395                 400

Glu Leu Thr Pro Gly Ala Thr Val Pro Phe Leu Leu Ser Leu Ile Cys
                405                 410                 415

Cys Ile Arg Thr Ala Lys Ala
            420
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<210> 7

<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> mutation arising from Vero passaging

<400> 7

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Ser Thr Lys Asp Asn Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr Leu
1               5                   10                  15


Ala His Cys Pro Asp Cys Gly Glu Gly His Ser Cys His Ser Pro Val
            20                  25                  30


Ala Leu Glu Arg Ile Arg Asn Glu Ala Thr Asp Gly Thr Leu Lys Ile
        35                  40                  45


Gln Val Ser Leu Gln Ile Gly Ile Lys Thr Asp Asp Ser His Asp Trp
    50                  55                  60


Thr Lys Leu Arg Tyr Met Asp Asn His Met Pro Ala Asp Ala Glu Arg
65                  70                  75                  80


Ala Gly Leu Phe Val Arg Thr Ser Ala Pro Cys Thr Ile Thr Gly Thr
                85                  90                  95


Met Gly His Phe Ile Leu Ala Arg Cys Pro Lys Gly Glu Thr Leu Thr
            100                 105                 110


Val Gly Phe Thr Asp Ser Arg Lys Ile Ser His Ser Cys Thr His Pro
        115                 120                 125


Phe His His Asp Pro Pro Val Ile Gly Arg Glu Lys Phe His Ser Arg
    130                 135                 140


Pro Gln His Gly Lys Glu Leu Pro Cys Ser Thr Tyr Val Gln Ser Thr
145                 150                 155                 160


Ala Ala Thr Thr Glu Glu Ile Glu Val His Met Pro Pro Asp Thr Pro
```

```
                165                 170                 175

Asp His Thr Leu Met Ser Gln Gln Ser Gly Asn Val Lys Ile Thr Val
            180                 185                 190

Asn Gly Gln Thr Val Arg Tyr Lys Cys Asn Cys Gly Gly Ser Asn Glu
        195                 200                 205

Gly Leu Thr Thr Thr Asp Lys Val Ile Asn Asn Cys Lys Val Asp Gln
    210                 215                 220

Cys His Ala Ala Val Thr Asn Tyr Lys Lys Trp Gln Tyr Asn Ser Pro
225                 230                 235                 240

Leu Val Pro Arg Asn Ala Glu Leu Gly Asp Arg Lys Gly Lys Ile His
                245                 250                 255

Ile Pro Phe Pro Leu Ala Asn Val Thr Cys Arg Val Pro Lys Ala Arg
            260                 265                 270

Asn Pro Thr Val Thr Tyr Gly Lys Asn Gln Val Ile Met Leu Leu Tyr
        275                 280                 285

Pro Asp His Pro Thr Leu Leu Ser Tyr Arg Asn Met Gly Glu Glu Pro
    290                 295                 300

Asn Tyr Gln Glu Glu Trp Val Met His Lys Lys Glu Val Val Leu Thr
305                 310                 315                 320

Val Pro Thr Glu Gly Leu Glu Val Thr Trp Gly Asn Asn Glu Pro Tyr
                325                 330                 335

Lys Tyr Trp Pro Gln Leu Ser Thr Asn Gly Thr Ala His Gly His Pro
            340                 345                 350

His Glu Ile Ile Leu Tyr Tyr Tyr Glu Leu Tyr Pro Thr Met Thr Val
        355                 360                 365
```

Val Val Val Ser Val Ala Thr Phe Ile Leu Leu Ser Met Val Gly Met
370 375 380

Ala Ala Gly Met Cys Met Cys Ala Arg Arg Arg Cys Ile Thr Pro Tyr
385 390 395 400

Glu Leu Thr Pro Gly Ala Thr Val Pro Phe Leu Leu Ser Leu Ile Cys
405 410 415

Cys Ile Arg Thr Ala Lys Ala
420

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ttaggatccg atggctgcgt gagacac 27

<210> 9
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<400> 9
taactcgagc cgtcaggtct gttgaacat 29

<210> 10
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<400> 10

ttaggatcct accaccaggc gattaaag 28

<210> 11
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<400> 11
taactcgagc tttgcccact tactgaagg 29

<210> 12
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<400> 12
ttaggatcct gctacagaag tcacgcc 27

<210> 13
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<400> 13
taactcgagg ccaaagcgtg aatcag 26

<210> 14
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<400> 14
ttaggatcca acagcttgag gacagagcg 29

<210> 15
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<220>
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<400> 15
taactcgagc tctgtctcat cacgtcgg 28

<210> 16
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<212> DNA
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<400> 16
ttaggatcca aattgcagtc ataggagtct tc 32

<210> 17
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<400> 17
taactcgaga gtacgttgac gtgctctga 29

<210> 18
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<400> 18
ttaggatccg tgggttaaac aactgcaaa 29

<210> 19

<211> 33
<212> DNA
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<400> 19
taactcgagg gttaaagtct tctatcctcc tgg 33

<210> 20
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ttaggatccg gataaccact gggataatag g 31

<210> 21
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<223> primer

<400> 21
taactcgaga gttgtgaaat tccttctgcc 30

<210> 22
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<220>
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<400> 22
ttaggatccc gcagatagaa ccagtgaac 29

<210> 23
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<400> 23
taactcgagc agcagctcta cttgggtc 28

<210> 24
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<220>
<223> primer

<400> 24
ttaggatcca ggagggaaag acaggct 27

<210> 25
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<400> 25
taactcgagc cctcgccttc ttctg 25

<210> 26
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<400> 26
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taactcgagc ctggagtttc ttaagtaata gttgc 35

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ttaggatccc aacgaacagg gctaattg 28

<210> 35
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<400> 35

taactcgagg accgcttaaa ggccag 26

<210> 36
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taactcgagt ggtcttgtgg ctttatagac a 31

<210> 38
<211> 27
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<400> 38
ttaggatcca accggaggaa accctac 27

<210> 39
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taactcgagg taccgcaccg tctgg 25

<210> 40
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<400> 40
ttaggatcca gctaccttgc agcacgt 27

<210> 41
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<400> 41
taactcgagc ccaccatcga cagg 24

<210> 42
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<400> 42
ttaggatccc gagccgtata agtattggc 29

<210> 43
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<220>
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<400> 43
taactcgagc gccggtgaag accttac 27

<210> 44

<211> 32
<212> DNA
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<220>
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<400> 44
ttaggatcca ctactgtcag tcactttgga gc 32

<210> 45
<211> 29
<212> DNA
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<223> primer

<400> 45
taactcgagt accgggtttg ttgctattt 29

<210> 46
<211> 30
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<400> 46
ttaggatccc acaactggta ctgcagagac 30

<210> 47
<211> 30
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<400> 47
taactcgagg cgtagccctt tgatctatag 30

<210> 48
<211> 26
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<400> 48
ttaggatccg gtgctatgcg tgtcgt 26

<210> 49
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