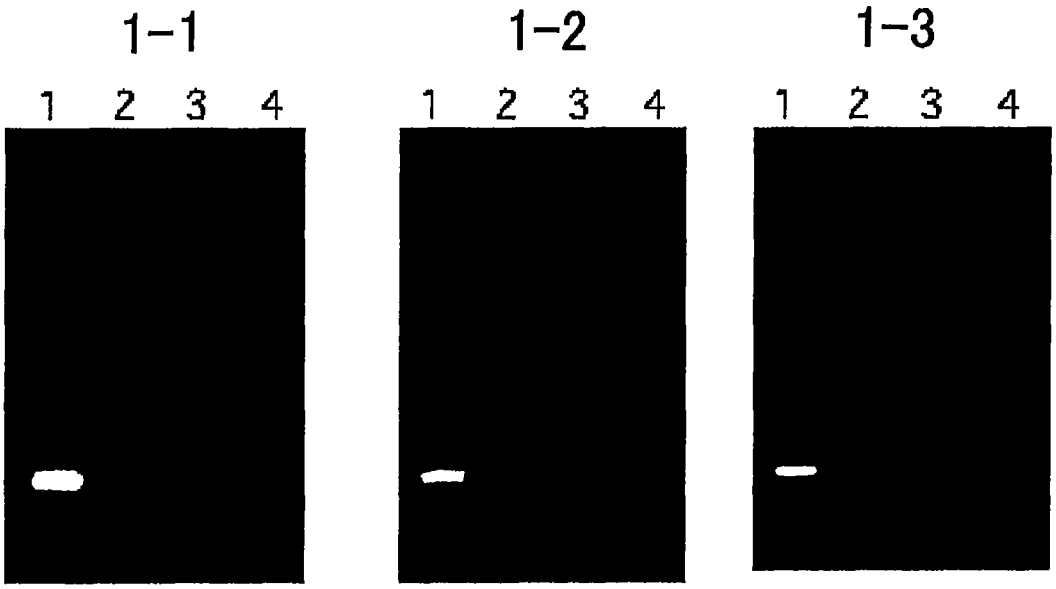
Fig. 1



G00002

163163

Fig. 2

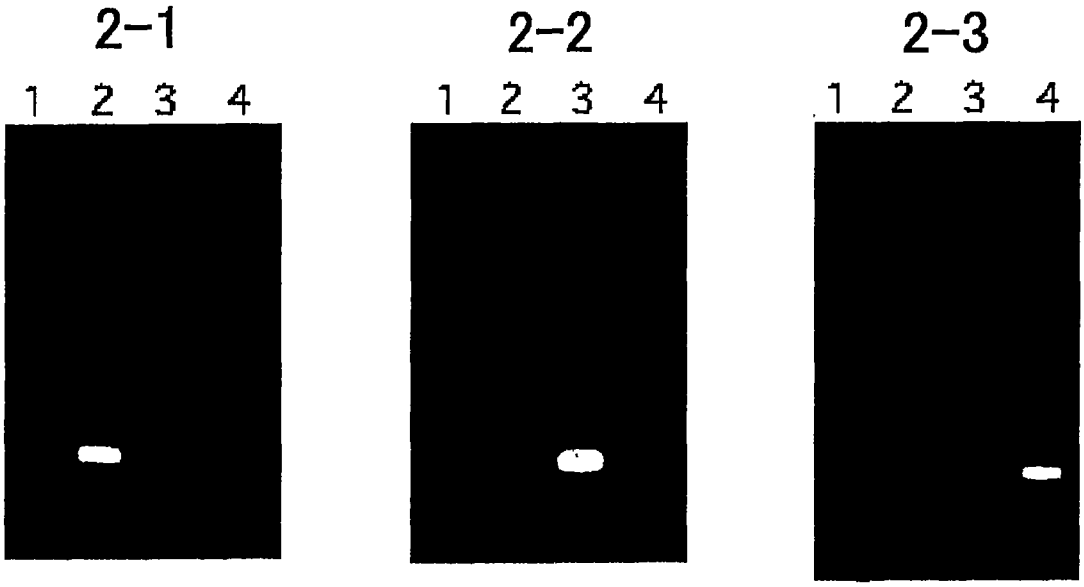


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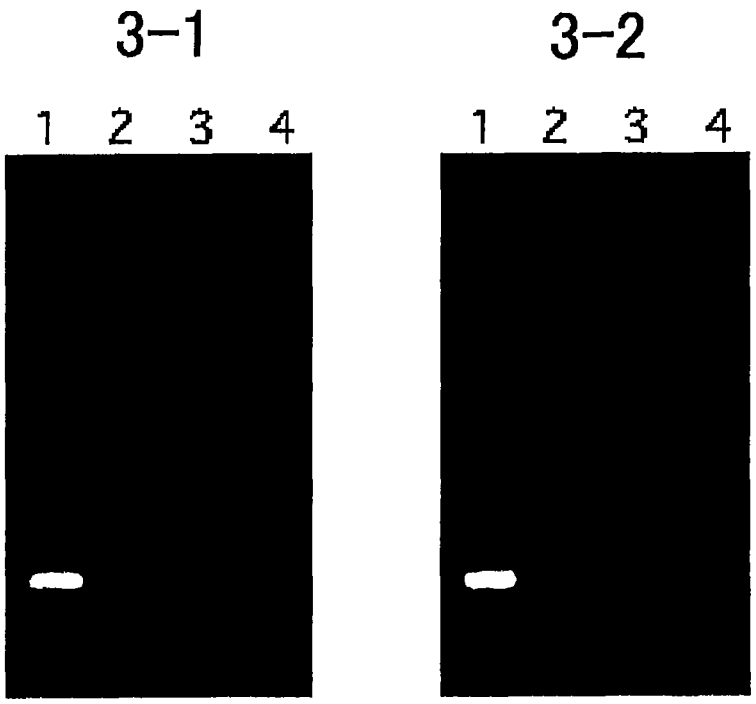


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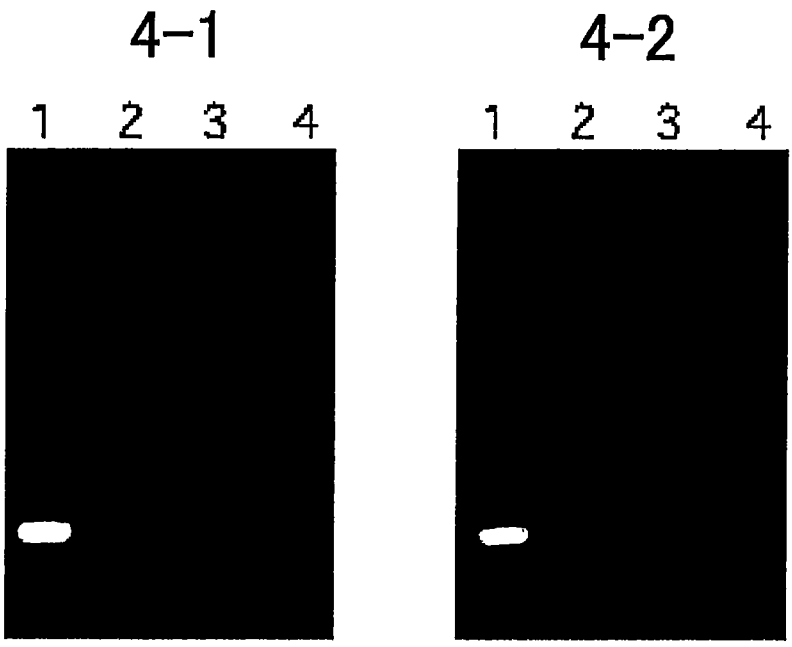


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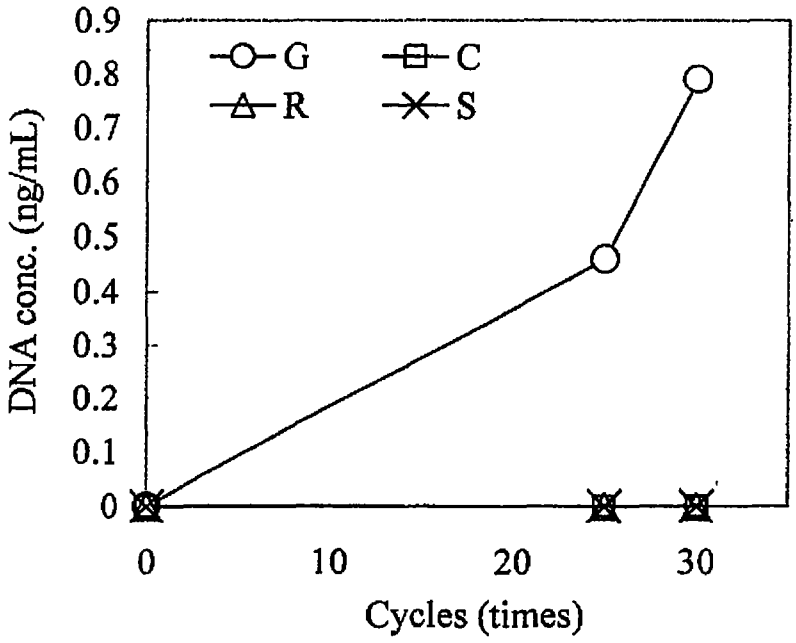

0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
DNA conc. (ng/mL)
G
C
R
S
0
10
20
30
Cycles (times)

Fig. 6

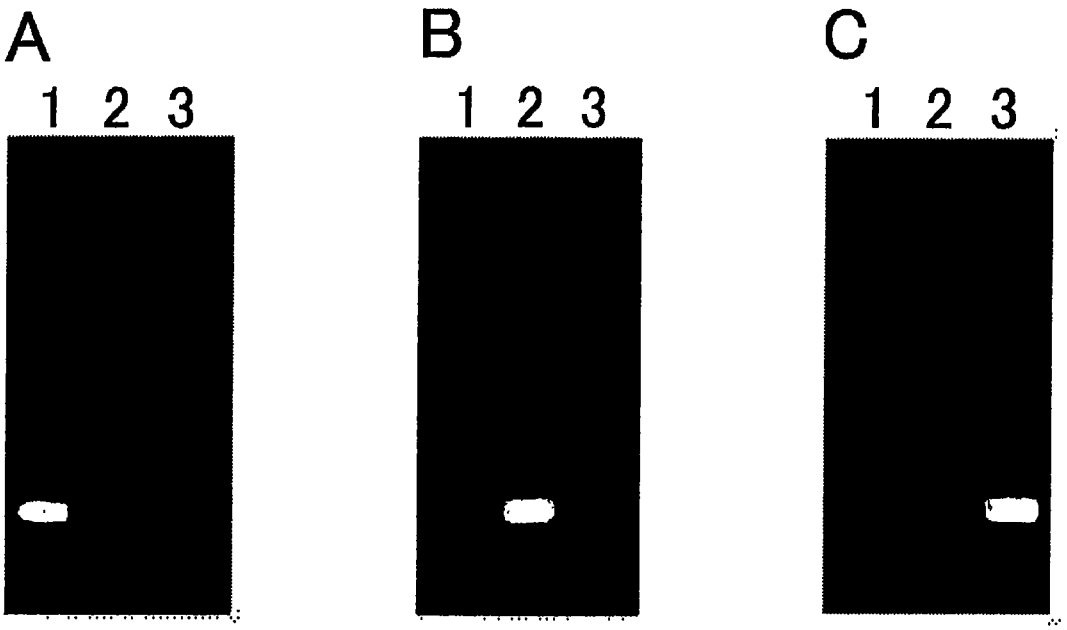


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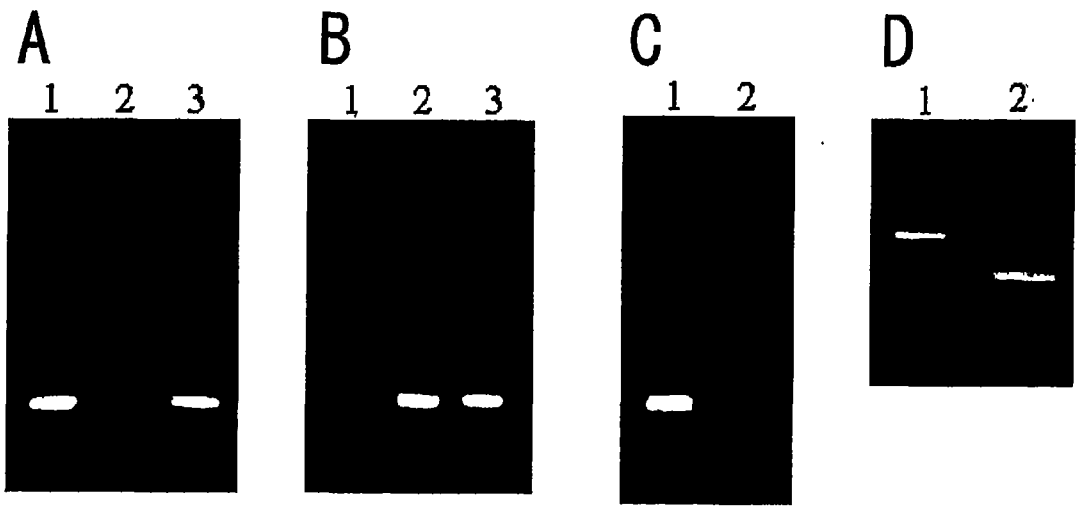
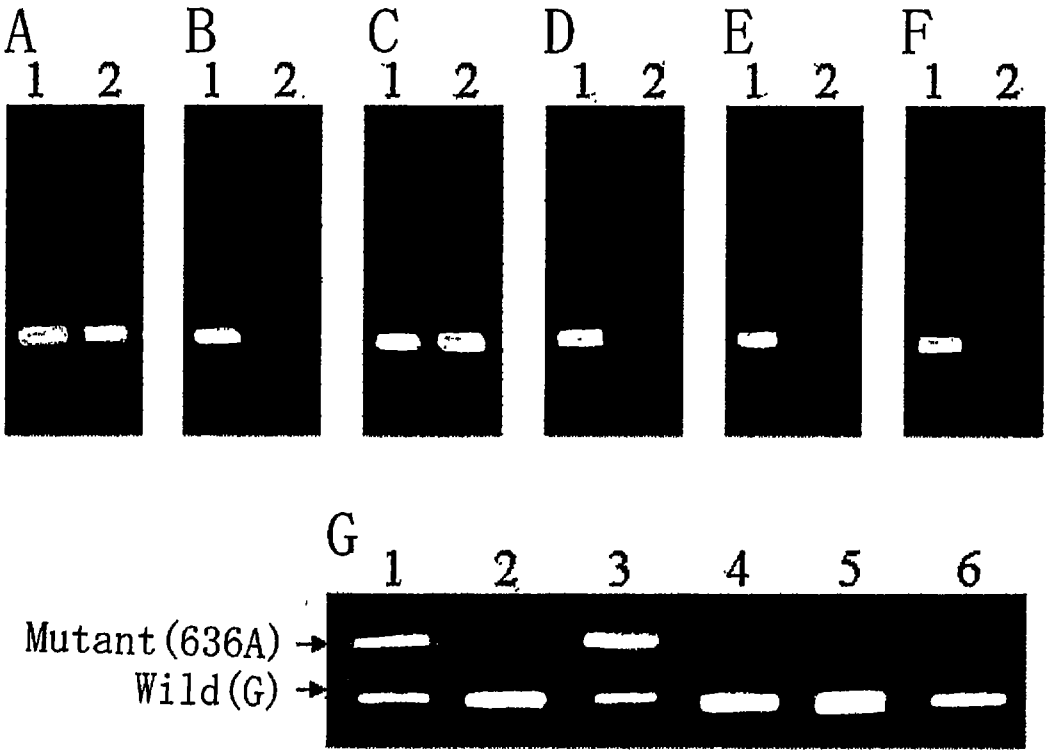


Fig. 8



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<213> Pyrococcus horikoshii

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tccaaacaat taactcctgg gcaacgtgaa aaactattta gcaaattaat agatatccta 180

gacgattatt atgttcttct cgttaccccc aaggaaatag atgagaggca tcattctatg 240

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caaaagtatg gggaatttgg ttctggctat ccgagtgatc cgagaactaa ggagtggctt 540

gaagaatatt acaaacaata tggtgacttt cctccaatag ttaggagaac ttgggaaacc 600

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<210> 2

<211> 33

<212> DNA

<213> Artificial Sequence

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<400> 2

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<210> 3

<211> 33

<212> DNA

<213> Artificial Sequence

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<400> 3

gaaggttgtg gatccacttt ctaaggtttc tta 33

<210> 4

<211> 672

<212> DNA

<213> Pyrococcus furiosus

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tccaaacaac taacacccca tgaaaggaag aatttatttt cccagataac ctcaatagcg 180

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agactcaatt ataaggcgaa gattattgcc gaacacaagg ccgatgcaaa gtatccagta 420

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aagcaatatg gagactttgg ctctgggtat ccaagtgatc caaaaaccaa gaaatggctt 540

gaagagtact acaaaaaaca caactctttc cctccaatag tcagacgaac ctgggaaact 600

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<211> 224

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Glu Lys Leu Arg Asn Ile Gly Val Lys Asp Ser Lys Gln Leu Thr
35 40 45

Pro His Glu Arg Lys Asn Leu Phe Ser Gln Ile Thr Ser Ile Ala
50 55 60

Asp Asp Tyr Lys Ile Val Ile Val Ser Pro Glu Glu Ile Asp Asn
65 70 75

Arg Ser Gly Thr Met Asn Glu Leu Glu Val Glu Lys Phe Ala Leu
80 85 90

Ala Leu Asn Ser Leu Gln Ile Lys Pro Ala Leu Ile Tyr Ala Asp
95 100 105

Ala Ala Asp Val Asp Ala Asn Arg Phe Ala Ser Leu Ile Glu Arg
110 115 120

Arg Leu Asn Tyr Lys Ala Lys Ile Ile Ala Glu His Lys Ala Asp

125 130 135

Ala Lys Tyr Pro Val Val Ser Ala Ala Ser Ile Leu Ala Lys Val

140 145 150

Val Arg Asp Glu Glu Ile Glu Lys Leu Lys Lys Gln Tyr Gly Asp

155 160 165

Phe Gly Ser Gly Tyr Pro Ser Asp Pro Lys Thr Lys Lys Trp Leu

170 175 180

Glu Glu Tyr Tyr Lys Lys His Asn Ser Phe Pro Pro Ile Val Arg

185 190 195

Arg Thr Trp Glu Thr Val Arg Lys Ile Glu Glu Ser Ile Lys Ala

200 205 210

Lys Lys Ser Gln Leu Thr Leu Asp Lys Phe Phe Lys Lys Pro

215 220

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

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<211> 18

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<213> Artificial Sequence

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<400> 7

tggtagttgg agcuggtg 18

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

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<400> 8

tggtagttgg agcuggng 18

<210> 9

<211> 18

<212> DNA

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<400> 9

tggtagttgg agcuggtg 18

<210> 10

<211> 18

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<400> 10

tggtagttgg agcuugtg 18

<210> 11

<211> 18

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<400> 11

tggtagttgg agcucgtg 18

<210> 12

<211> 18

<212> DNA

<213> Artificial Sequence

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<400> 12

tggtagttgg agcuagng 18

<210> 13

<211> 626

<212> DNA

<213> Archaeoglobus fulgidus

<400> 13

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ctaagtcagg ggaggagaga ggaactagcc gaggaaataa ggaaaatctg cagaacggag 180
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<210> 14
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<212> DNA
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<210> 15
<211> 30

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<400> 15

tggtaataac ggatccgttt agaaatcgtc 30

<210> 16

<211> 638

<212> DNA

<213> Archaeoglobus fulgidus

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aagctaagtc aggggaggag agaggaacta gccgaggaaa taaggaaaat ctgcagaacg 180

gaggttttga aagtttctcc cgaaaatctc gacgaaagga tggctgctaa aaccataaac 240

gagattttga aggagtgcta cgctgaaata attctcaggc tgaagccgga aattgcttat 300

gttgacagtc ctgatgtgat tcccgagaga ctttcgaggg agcttgagga gattacgggg 360

ttgagagttg tggccgagca caaggcggac gagaagtatc ccctggtagc tgcggcttca 420

atcatcgcaa aggtggaaag ggagcgggag attgagaggc tgaaagaaaa attcggggat 480

ttcggcagcg gctatgcgag cgatccgagg acaagagaag tgctgaagga gtggatagct 540

tcaggcagaa ttccgagctg cgtgagaatg cgctggaaga cggtgtcaaa tctgaggcag 600

aagacgcttg acgatttcta aacggatccc cgggtacc 638

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<211> 205

<212> PRT

<213> Archaeoglobus fulgidus

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Pro Leu Val Val Ala Gly Val Ala Cys Ser Asp Glu Asp Arg Leu
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Arg Lys Leu Gly Val Lys Asp Ser Lys Lys Leu Ser Gln Gly Arg
35 40 45
Arg Glu Glu Leu Ala Glu Glu Ile Arg Lys Ile Cys Arg Thr Glu
50 55 60
Val Leu Lys Val Ser Pro Glu Asn Leu Asp Glu Arg Met Ala Ala
65 70 75
Lys Thr Ile Asn Glu Ile Leu Lys Glu Cys Tyr Ala Glu Ile Ile
80 85 90
Leu Arg Leu Lys Pro Glu Ile Ala Tyr Val Asp Ser Pro Asp Val
95 100 105
Ile Pro Glu Arg Leu Ser Arg Glu Leu Glu Glu Ile Thr Gly Leu
110 115 120
Arg Val Val Ala Glu HisLys Ala Asp Glu Lys Tyr Pro Leu Val
125 130 135
Ala Ala Ala Ser Ile Ile Ala Lys Val Glu Arg Glu Arg Glu Ile
140 145 150
Glu Arg Leu Lys Glu Lys Phe Gly Asp Phe Gly Ser Gly Tyr Ala
155 160 165
Ser Asp Pro Arg Thr Arg Glu Val Leu Lys Glu Trp Ile Ala Ser
170 175 180

Gly Arg Ile Pro Ser Cys Val Arg Met Arg Trp Lys Thr Val Ser
185 190 195

Asn Leu Arg Gln Lys Thr Leu Asp Asp Phe
200 205

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

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<400> 18

ctattgttgg atcatattcg 20

<210> 19

<211> 19

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<400> 19

ttcctacgga agcaagtag 19

<210> 20

<211> 20

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<210> 21

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<400> 21

tcgacacagc aggucaag 18

<210> 22

<211> 18

<212> DNA

<213> Artificial Sequence

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<400> 22

tcgacacagc agguaaag 18

<210> 23

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<212> DNA

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<400> 23

tcgacacagc aggugaag 18

<210> 24

<211> 19

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<400> 24

acaaagaaag ccctcccca 19

<210> 25

<211> 21

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<211> 22

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<223> Designed PCR primer to amplify a portion of human CYP2C19 gene

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<211> 20

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<210> 29

<211> 18

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<400> 29

gtaagcaccc ccugaatc 18

<210> 30

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

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