

SEQUENCE LISTING

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<120> Predetermined nucleotide substitutions

<130> P4010PC00

<160> 26

<170> PatentIn version 3.5

<210> 1

<211> 1089

<212> DNA

<213> Hordeum vulgare

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cccggaacccg tggacgacct cagcaagctt ccaaagtgga atttcgacgg ctccagcacc	180
ggccaagcca cgggcgacga cagcgaagtc atcctccgac cccaagccat cttcagggac	240
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gcgggtgcgg agaaatctta cgggcgcgac atcgtcgacg ccactacaa ggcctgcctc	540
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caagtccggc cttccgtcgg yatctccgcc ggcgacgagc tctgggcggc tcgctacatt	660
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<212> PRT
<213> Hordeum vulgare

<400> 2

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20 25 30

Val Arg Ser Lys Ala Arg Thr Leu Pro Gly Pro Val Asp Asp Pro Ser
35 40 45

Lys Leu Pro Lys Trp Asn Phe Asp Gly Ser Ser Thr Gly Gln Ala Thr
50 55 60

Gly Asp Asp Ser Glu Val Ile Leu Arg Pro Gln Ala Ile Phe Arg Asp
65 70 75 80

Pro Phe Arg Lys Gly Asn Asn Ile Leu Val Ile Cys Asp Cys Tyr Ala
85 90 95

Pro Thr Gly Glu Pro Ile Pro Ser Asn Lys Arg Tyr Asn Ala Ala Arg
100 105 110

Ile Phe Gly His Pro Asp Val Lys Ser Glu Glu Pro Trp Tyr Gly Ile
115 120 125

Glu Gln Glu Tyr Thr Leu Leu Gln Lys Asp Thr Asn Trp Pro Ile Gly
130 135 140

Trp Pro Leu Gly Gly Tyr Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Ala
145 150 155 160

Ala Gly Ala Glu Lys Ser Tyr Gly Arg Asp Ile Val Asp Ala His Tyr
165 170 175

Lys Ala Cys Leu Tyr Ala Gly Ile Asn Ile Gly Gly Ile Asn Ala Glu
180 185 190

Val Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ser Val Gly Ile
195 200 205

Ser Ala Gly Asp Glu Leu Trp Ala Ala Arg Tyr Ile Leu Glu Arg Ile
210 215 220

Thr Glu Ile Ala Gly Val Val Val Ser Phe Asp Pro Lys Pro Ile Pro
225 230 235 240

Gly Glu Trp Asn Gly Ala Gly Ala His Thr Asn Tyr Ser Thr Lys Ser
245 250 255

Met Arg Ser Glu Gly Gly Tyr Glu Val Ile Lys Arg Ala Ile Lys Lys
260 265 270

Leu Glu Ala Arg His Thr Glu His Ile Ala Ala Tyr Gly Glu Gly Asn
275 280 285

Glu Arg Arg Leu Thr Gly Arg His Glu Thr Ala Asp Ile Asn Thr Phe
290 295 300

Val Trp Gly Val Ala Asn Arg Gly Ala Ser Val Arg Val Gly Arg Asp
305 310 315 320

Thr Glu Lys Glu Gly Arg Gly Tyr Phe Glu Asp Arg Arg Pro Ala Ser
325 330 335

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340 345 350

Leu Trp Lys Ala Gly Leu Ser Asn Gly Lys
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<223> Primer

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<210> 4

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<212> DNA

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<223> Primer

<400> 4

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<211> 14

<212> DNA

<213> Artificial sequence

<220>

<223> Probe

<400> 5

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14

<210> 6

<211> 14

<212> DNA

<213> Artificial sequence

<220>

<223> Probe

<400> 6

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14

<210> 7

<211> 503

<212> PRT

<213> Saccharomyces cerevisiae

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10

15

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20

25

30

Asn Leu Glu Val Gly Ala Ile Met Arg Lys Ala Tyr Glu Ser His Leu
 35 40 45

Pro Ala Pro Leu Phe Lys Asn Leu Lys Gly Ala Ser Lys Asp Leu Phe
 50 55 60

Ser Ile Leu Gly Cys Pro Ala Gly Leu Arg Ser Lys Glu Lys Gly Asp
 65 70 75 80

His Gly Arg Ile Ala His His Leu Gly Leu Asp Pro Lys Thr Thr Ile
 85 90 95

Lys Glu Ile Ile Asp Tyr Leu Leu Glu Cys Lys Glu Lys Glu Pro Leu
 100 105 110

Pro Pro Ile Thr Val Pro Val Ser Ser Ala Pro Cys Lys Thr His Ile
 115 120 125

Leu Ser Glu Glu Lys Ile His Leu Gln Ser Leu Pro Thr Pro Tyr Leu
 130 135 140

His Val Ser Asp Gly Gly Lys Tyr Leu Gln Thr Tyr Gly Met Trp Ile
 145 150 155 160

Leu Gln Thr Pro Asp Lys Lys Trp Thr Asn Trp Ser Ile Ala Arg Gly
 165 170 175

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

His Ile Arg Gln Ile Ala Asp Ser Trp Ala Ala Ile Gly Lys Ala Asn
 195 200 205

Glu Ile Pro Phe Ala Leu Cys Phe Gly Val Pro Pro Ala Ala Ile Leu
 210 215 220

Val Ser Ser Met Pro Ile Pro Glu Gly Val Ser Glu Ser Asp Tyr Val
 225 230 235 240

Gly Ala Ile Leu Gly Glu Ser Val Pro Val Val Lys Cys Glu Thr Asn
245 250 255

Asp Leu Met Val Pro Ala Thr Ser Glu Met Val Phe Glu Gly Thr Leu
260 265 270

Ser Leu Thr Asp Thr His Leu Glu Gly Pro Phe Gly Glu Met His Gly
275 280 285

Tyr Val Phe Lys Ser Gln Gly His Pro Cys Pro Leu Tyr Thr Val Lys
290 295 300

Ala Met Ser Tyr Arg Asp Asn Ala Ile Leu Pro Val Ser Asn Pro Gly
305 310 315 320

Leu Cys Thr Asp Glu Thr His Thr Leu Ile Gly Ser Leu Val Ala Thr
325 330 335

Glu Ala Lys Glu Leu Ala Ile Glu Ser Gly Leu Pro Ile Leu Asp Ala
340 345 350

Phe Met Pro Tyr Glu Ala Gln Ala Leu Trp Leu Ile Leu Lys Val Asp
355 360 365

Leu Lys Gly Leu Gln Ala Leu Lys Thr Thr Pro Glu Glu Phe Cys Lys
370 375 380

Lys Val Gly Asp Ile Tyr Phe Arg Thr Lys Val Gly Phe Ile Val His
385 390 395 400

Glu Ile Ile Leu Val Ala Asp Asp Ile Asp Ile Phe Asn Phe Lys Glu
405 410 415

Val Ile Trp Ala Tyr Val Thr Arg His Thr Pro Val Ala Asp Gln Met
420 425 430

Ala Phe Asp Asp Val Thr Ser Phe Pro Leu Ala Pro Phe Val Ser Gln
435 440 445

Ser Ser Arg Ser Lys Thr Met Lys Gly Gly Lys Cys Val Thr Asn Cys

450

455

460

Ile Phe Arg Gln Gln Tyr Glu Arg Ser Phe Asp Tyr Ile Thr Cys Asn
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Trp Lys Arg Tyr Gly Tyr Lys
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<211> 101

<212> PRT

<213> Triticum aestivum

<400> 8

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Gly Gly Gly Gly Asn Leu Lys Pro Trp Glu Cys Ser Ser Lys Cys Ser
 35 40 45

Ser Arg Cys Ser Gly Thr Gln Tyr Lys Lys Ala Cys Leu Thr Tyr Cys
 50 55 60

Asn Lys Cys Cys Ala Thr Cys Leu Cys Val Pro Pro Gly Thr Tyr Gly
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Asn Lys Gly Ala Cys Pro Cys Tyr Asn Asn Trp Lys Thr Lys Glu Gly
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Gly Pro Lys Cys Pro
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<211> 15

<212> DNA

<213> Artificial sequence

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	ctgggtggagt cgatgcacat cttccgggtcc ggcgccgacg cggcccccg cgtgatccgc	180
	gaggcgctgg gcaaggcgct ggccttcttc taccgcgtgg cggggcgcat cgtggagcag	240
	ccggagaagg ggtgccccgc catccgctgc accgccgacg gcgtctactt cgcggaggcc	300

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 <212> DNA
 <213> Artificial sequence

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 <223> Mutant cDNA

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<210> 19
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 <212> PRT
 <213> Hordeum vulgare

<400> 19

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Asp	Arg	Tyr	Pro	Thr	His	Arg	Gly	Leu	Val	Glu	Ser	Met	His	Ile	Phe
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Arg	Ser	Gly	Ala	Asp	Ala	Ala	Pro	Gly	Val	Ile	Arg	Glu	Ala	Leu	Gly
	50					55					60				

Lys Ala Leu Ala Phe Phe Tyr Pro Leu Ala Gly Arg Ile Val Glu Gln
65 70 75 80

Pro Glu Lys Gly Cys Pro Ala Ile Arg Cys Thr Ala Asp Gly Val Tyr
85 90 95

Phe Ala Glu Ala Val Ala Glu Cys Ser Leu Glu Asp Val Arg Phe Leu
100 105 110

Glu Arg Pro Leu Leu Leu Pro Lys Glu Asp Leu Val Pro Tyr Pro Ala
115 120 125

Ala Asp Leu Trp Ala Val Glu Pro His Asn Thr Ile Met Met Met Gln
130 135 140

Ile Thr Lys Phe Thr Cys Gly Gly Phe Val Met Gly Leu Arg Phe Asn
145 150 155 160

His Ala Ser Ala Asp Gly Met Gly Ala Ala Gln Phe Ile Lys Ala Val
165 170 175

Gly Asp Met Ala Arg Gly Leu Pro Glu Pro Thr Val Lys Pro Val Trp
180 185 190

Asp Arg Glu Lys Phe Pro Asn Pro Ser Ile Lys Pro Gly Pro Leu Pro
195 200 205

Glu Leu Pro Val Leu Ala Leu Asp Tyr Ile Val Leu Asp Phe Pro Thr
210 215 220

Gly Tyr Ile Asp Gly Leu Lys Thr Gln Tyr Lys Ala His Ser Gly Lys
225 230 235 240

Phe Cys Ser Gly Phe Asp Val Leu Thr Ala Lys Leu Trp Gln Cys Arg
245 250 255

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

Phe Ala Ser Val Arg His Leu Leu Lys Leu Asp Ala Gly Tyr Tyr Gly
275 280 285

Asn Ser Ile Phe Pro Val Lys Met Ser Gly Thr Ser Lys Lys Val Leu
 290 295 300

Glu Ser Ser Val Met Glu Val Ile Asp Met Ile Arg Glu Ala Lys Gln
 305 310 315 320

Arg Met Ala Val Glu Phe Phe Gln Phe Ala Lys Glu Glu Thr Arg Gln
 325 330 335

Asp Pro Phe Gln Met Thr Phe Asp Tyr Glu Ser Ile Tyr Val Ser Asp
 340 345 350

Trp Ser Lys Leu Gly Phe Ser Asp Val Asp Tyr Gly Phe Gly Pro Pro
 355 360 365

Met Phe Ala Gly Pro Leu Val Asn Asn Asp Phe Ile Ala Ser Val Val
 370 375 380

Ile Leu Lys Ala Pro Leu Pro Leu Asp Gly Thr Arg Met Leu Ala Ser
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Cys Val Thr Lys Glu His Ser Gln Glu Phe Ala Arg Gly Met Lys Glu
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Asp Leu Pro

<210> 20
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<220>
 <223> Primer

<400> 20
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<210> 21
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