

<110> CJ CheilJedang Corporation

<120> NOVEL PROMOTER AND METHOD OF PRODUCING GLUTATHIONE USING THE
SAME

<130> OPA21012

<150> KR 10-2020-0041184

<151> 2020-04-03

<160> 41

<170> KoPatentIn 3.0

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<213> Unknown

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<223> Saccharomyces cerevisiae CJ-5

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<223> S. cerevisiae CEN.PK-1D promoter-mutation-102 103

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atacatatag aagaataaa 499

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<211> 499

<212> DNA

<213> Artificial Sequence

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<223> S. cerevisiae CEN.PK-1D promoter-mutation-92 102

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tgaatcgttg tgctggagta gttggatctt tccacgtggc ctcgagtcac ttgtagaagc 420

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atacatatag aagaataaa 499

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<211> 499

<212> DNA

<213> Artificial Sequence

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<223> S. cerevisiae CEN.PK-1D promoter-mutation-92 103

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tcagtgagcc gactctacta caatgcttt tcattttca ctcagaaaaa cctgcaatt 240

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gcggcttacc aaaagttgaa gcttgtctt gcctctatg agtggagcaa tcgattatat 360

tgaatcgtt tgctggagta gttggatct tccacgtgg ctcgagtcac ttgtagaagc 420

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atacatatag aagaataaa 499

<210> 9

<211> 499

<212> DNA

<213> Artificial Sequence

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<223> S. cerevisiae CEN.PK-1D promoter-mutation-94 102

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tgaatcgttg tgctggagta gttggatctt tccacgtggt ctgagtcac tttagaagc 420

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atacatatag aagaataaa 499

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<223> S. cerevisiae CEN.PK-1D promoter-mutation-94 103

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tcagtgagcc gactctacta caatgcttt tcattttca ctcagaaaaa cctgcaatt 240

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gcggcttacc aaaagttgaa gcttgttctt gcctcttatg agtggagcaa tcgattatat 360

tgaatcgttg tgctggagta gttggatctt tccacgtggt ctcgagtcac ttgtagaagc 420

tgaaaattga gcagatttag tatagggcta cattgtaggg tggtttagag tatcgaaaat 480

atacatatag aagaataaa 499

<210> 11

<211> 499

<212> DNA

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<223> S. cerevisiae CEN.PK-1D promoter-mutation-92 94

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tcagtgagcc gactctacta caatgctttt tcattttca ctcagaaaaa cctgcaattt 240

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gctggctacc aaaagttgaa gcttgttctt gcctcttatg agtggagcaa tcgattatat 360

tgaatcgttg tgctggagta gttggatctt tccacgtggt ctcgagtcac ttgtagaagc 420

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atacatatag aagaataaa 499

<210> 12

<211> 499

<212> DNA

<213> Artificial Sequence

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<223> S. cerevisiae CEN.PK-1D promoter-mutation-249

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gcggcttacc aaaagttgaa gctgttctt gcctctatg agtggagcaa tcgattatat 360

tgaatcgtg tgctggagta gttgatctt tccacgtgg ctcgagtcac ttgtagaagc 420

tgaaaattga gcagatttag tatagggcta catttagggg tggtttagag tatcgaaaat 480

atacatatag aagaataaa 499

<210> 13

<211> 499

<212> DNA

<213> Artificial Sequence

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<223> S. cerevisiae CEN.PK-1D promoter-mutation-251

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tgaaaattga gcagatttag tatagggcta cattgtaggg tggtttagag tatcgaaaat 480

atacatatag aagaataaa 499

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<211> 499

<212> DNA

<213> Artificial Sequence

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<223> S. cerevisiae CEN.PK-1D promoter-mutation-92

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gcggcttacc aaaagttgaa gcttgttctt gcctcttatg agtggagcaa tcgattatat 360

tgaatcgttg tgctggagta gttggatctt tccacgtggc ctcgagtcac ttgtagaagc 420

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atacatatag aagaataaa 499

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<211> 499

<212> DNA

<213> Artificial Sequence

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<223> S. cerevisiae CEN.PK-1D promoter-mutation-94

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gcggcttacc aaaagttgaa gcttgttctt gcctcttatg agtggagcaa tcgattatat 360

tgaatcgttg tgctggagta gttggatctt tccacgtggt ctcgagtcac tttagaagc 420

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atacatatag aagaataaa 499

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<211> 499

<212> DNA

<213> Artificial Sequence

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<223> S. cerevisiae CEN.PK-1D promoter-mutation-102

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gcggcttacc aaaagttgaa gcttgttctt gcctcttatg agtggagcaa tcgattatat 360

tgaatcgttg tgctggagta gttggatctt tccacgtggt ctcgagtcac tttagaagc 420

tgaaaattga gcagatttag tatagggcta cattgtaggg tggtttagag tatcgaaaat 480

atacatatag aagaataaa 499

<210> 17
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 <212> DNA
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 <223> S. cerevisiae CEN.PK-1D promoter-mutation-103

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<223> S. cerevisiae CJ-5 promoter-mutation-92 94 102 103 249 251

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<223> S. cerevisiae CJ-5 promoter-mutation-249 251

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gcggcttacc aaaagttgaa gctgttctt gcttctatg agtggagcaa tcgattatat	360
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<210> 21

<211> 500

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<223> S. cerevisiae CJ-5 promoter-mutation-102 103

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<210> 24

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<220>

<223> S. cerevisiae CJ-5 promoter-mutation-94 102

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cagcatggcg cgcacgtgac tacaactgtg gctggaaacc tttcgtcct ccccggtttt	180
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tcagtgagcc gactctacta caatgctttt tcatttttca ctcaaaaaa cctgcaattt	240
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tccaaattgg ccatgctctg tgctccctt gacaaaggac atcttccctg ttataaacg	300
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tgaatcgttg tgctggagta gttggatctt tccacgtggt ctcgagtcac ttgtagaagc	420
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<210> 25

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<223> S. cerevisiae CJ-5 promoter-mutation-94 103

<400> 25

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cagcatggcg cgcacgtgac tacaactgtg gctggaaacc tttcgtcct ccccggttt	180
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tcagtgagcc gactctacta caatgctttt tcattttca ctcagaaaaa cctgcaattt	240
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tccaaattgg ccatgctctg tgcctccctt gacaaaggac atcttcctg ttataaacg	300
gcggttacc aaaagttgaa gctgttctt gcttctatg agtggagcaa tcgattatat	360
tgaatcgttg tgctggagta gttggatctt tccacgtggt ctcgagtcac tttagaagc	420
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<210> 26

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<223> S. cerevisiae CJ-5 promoter-mutation-92 94

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cagcatggcg cgcacgtgac tacaactgtg gctggaaacc tttcgtcct ccccggttt	180
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tcagttagcc gactctacta caatgctttt tcattttca ctcagaaaaa cctgcaattt	240
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tccaaattgg ccatgctctg tgcctccctt gacaaaggac atcttcctg ttataaacg	300
gcggcttacc aaaagttgaa gcttgttctt gcttctatg agtggagcaa tcgattatat	360
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<210> 27

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<223> S. cerevisiae CJ-5 promoter-mutation-249

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cagcatggcg cgcacgtgac tacaactgtg gctggaaacc tttcgtcct ccccggttt	180
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gcggcttacc aaaagtgaa gcttgttctt gcttctatg agtggagcaa tcgattatat	360
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<212> DNA

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cagcatggcg cgcacgtgac tacaactgtg gctggaaacc tttcgtcct ccccggtttt	180
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cagcatggcg cgcacgtgac tacaactgtg gctggaaacc tttcgtcct ccccggttt	180
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gcggttacc aaaagttgaa gcttgttctt gcttctatg agtggagcaa tcgattatat	360
tgaatcgtg tgctggagta gttgatctt tccacgtgt ctcgagtcac tttagaagc	420
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<210> 30

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<212> DNA

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<223> S. cerevisiae CJ-5 promoter-mutation-94

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gcggttacc aaaagttgaa gcttgttctt gcttcttatg agtggagcaa tcgattatat	360
tgaatcgttg tgctggagta gttggatctt tccacgtggt ctcgagtcac ttgtagaagc	420
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<223> S. cerevisiae CJ-5 promoter-mutation-102

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cagcatggcg cgcacgtgac tacaactgtg gctggaaacc tttcgtcct ccccggttt	180
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gcggttacc aaaagttgaa gctgttctt gcttctatg agtggagcaa tcgattatat	360
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<210> 32

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<212> DNA

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<223> S. cerevisiae CJ-5 promoter-mutation-103

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cagcatggcg cgcacgtgac tacaactgtg gctggaaacc tttcgtcct ccccggttt	180
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gcggttacc aaaagttgaa gctgttctt gcttctatg agtggagcaa tcgattatat	360
tgaatcgttg tgctggagta gttgatctt tccacgtgg ctcgagtcac tttagaagc	420
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<210> 33

<211> 678

<212> PRT

<213> Saccharomyces cerevisiae

<400> 33

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

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

Gly Glu Lys Val Cys Met Asn Val Pro Met Tyr Lys Asp Ile Ala Thr

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu

225

230

235

240

Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp

245

250

255

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln

260

265

270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn

275

280

285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys

290

295

300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala

305

310

315

320

Val Asp Asp Arg Thr Pro Lys Glu Arg Gly Val Ala Pro Leu Leu Pro
325 330 335

Lys Tyr Asn Lys Asn Gly Phe Gly Gly Ile Ala Lys Asp Val Gln Asp
340 345 350

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe
355 360 365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val
370 375 380

Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala
385 390 395 400

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg
405 410 415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr
420 425 430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu
435 440 445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser
450 455 460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465 470 475 480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485 490 495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500 505 510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515 520 525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530 535 540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly

545 550 555 560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val

565 570 575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu

580 585 590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro

595 600 605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr

610 615 620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
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<223> F_BamHI_GSH1

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<210> 35

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<211> 33

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<223> R_NcoI_GSH1_DW

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<211> 27

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<213> Artificial Sequence

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<223> R_AL killer

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<210> 41

<211> 24

<212> DNA

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<223> F_BR killer

<400> 41

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24