

15477SG41_Sequence Listing
SEQUENCE LISTING

<110> Heartseed Inc.
 <120> Method for Producing High-quality iPSCs
 <130> 2016C9493
 <150> JP 2015-138645
 <151> 2015-07-10
 <160> 60
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 <221> misc_feature
 <223> Inventor:YUASA, Shinsuke; FUKUDA, Keiichi; KUNITOMI, Akira

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15477SG41_Sequence Listing

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 Pro Lys Pro Gly Ala Ala Thr Glu Lys Ala Arg Lys Gln Gly Gly Ala
 50 55 60
 Ala Lys Asp Thr Arg Ala Gln Ser Gly Glu Ala Arg Lys Val Pro Pro
 65 70 75 80
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 85 90 95
 Arg Lys Ala Lys Ala Lys Gly Ser Arg Ser Ser Gln Gly Asp Ala Glu
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 Ala Tyr Arg Lys Thr Lys Ala Glu Ser Lys Ser Ser Lys Pro Thr Ala
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 Ser Lys Val Lys Asn Gly Ala Ala Ser Pro Thr Lys Lys Lys Val Val
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15477SG41_Sequence Listing

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15477SG41_Sequence Listing

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Thr Ala Asn Gly Gly Gln Lys Val Lys Arg Ser Gly Ser Arg Gln Glu
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15477SG41_Sequence Listing

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15477SG41_Sequence Listing

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15477SG41_Sequence Listing

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15477SG41_Sequence Listing

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15477SG41_Sequence Listing

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15477SG41_Sequence Listing

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15477SG41_Sequence Listing

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15477SG41_Sequence Listing

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15477SG41_Sequence Listing

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 35 40 45

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Gly Val Gly Leu Val Pro Gln Gly Gly Leu Glu Thr Ser Gln Pro Glu
 85 90 95

Gly Glu Ala Gly Val Gly Val Glu Ser Asn Ser Asp Gly Ala Ser Pro
 100 105 110

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Leu Glu Gln Asn Pro Glu Glu Ser Gln Asp Ile Lys Ala Leu Gln Lys

15477SG41_Sequence Listing

130

135

140

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Lys Val Phe Ser Gln Thr Thr Ile Cys Arg Phe Glu Ala Leu Gln Leu
180 185 190

Ser Phe Lys Asn Met Cys Lys Leu Arg Pro Leu Leu Gln Lys Trp Val
195 200 205

Glu Glu Ala Asp Asn Asn Glu Asn Leu Gln Glu Ile Cys Lys Ala Glu
210 215 220

Thr Leu Val Gln Ala Arg Lys Arg Lys Arg Thr Ser Ile Glu Asn Arg
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Val Arg Gly Asn Leu Glu Asn Leu Phe Leu Gln Cys Pro Lys Pro Thr
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260 265 270

Val Val Arg Val Trp Phe Cys Asn Arg Arg Gln Lys Gly Lys Arg Ser
275 280 285

Ser Ser Asp Tyr Ala Gln Arg Glu Asp Phe Glu Ala Ala Gly Ser Pro
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Phe Ser Gly Gly Pro Val Ser Phe Pro Leu Ala Pro Gly Pro His Phe
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Gly Thr Pro Gly Tyr Gly Ser Pro His Phe Thr Ala Leu Tyr Ser Ser
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15477SG41_Sequence Listing

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Lys Met His Asn Ser Glu Ile Ser Lys Arg Leu Gly Ala Glu Trp Lys
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Leu Leu Ser Glu Thr Glu Lys Arg Pro Phe Ile Asp Glu Ala Lys Arg
Page 15

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15477SG41_Sequence Listing

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90

95

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Gln Met Gln Pro Met His Arg Tyr Asp Val Ser Ala Leu Gln Tyr Asn
195 200 205

Ser Met Thr Ser Ser Gln Thr Tyr Met Asn Gly Ser Pro Thr Tyr Ser
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Met Ser Tyr Ser Gln Gln Gly Thr Pro Gly Met Ala Leu Gly Ser Met
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Gly Ser Val Val Lys Ser Glu Ala Ser Ser Ser Pro Pro Val Val Thr
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Ser Ser Ser His Ser Arg Ala Pro Cys Gln Ala Gly Asp Leu Arg Asp
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Met Ile Ser Met Tyr Leu Pro Gly Ala Glu Val Pro Glu Pro Ala Ala
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15477SG41_Sequence Listing

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cgcccctatg acctggcggc ggcgaccgtg gccacagacc tggagagcgg cggagccggt 240
gcggcttgcg gcggtagcaa cctggcgccc ctacctgga gagagaccga ggagttcaac 300
gatctcctgg acctggactt tattctctcc aattcgctga cccatcctcc ggagtcagtg 360
gccgccaccg tgcctcgtc agcgtcagcc tcctcttcgt cgtcgccgtc gagcagcggc 420
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ccgacggctc cttcaacct ggcgacatc aacgacgtga gcccctcggg cggcttcgtg 600
gccgagctcc tgcggccaga attggaccgg gtgtacattc cgccgcagca gccgcagccg 660
ccagggtggc ggctgatggg caagtctgtg ctgaaggcgt cgctgagcgc ccctggcagc 720
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gatgaactga ccaggcacta ccgtaaacac acggggcacc gccggtcca gtgcaaaaaa 1380
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```

```

<210> 52
<211> 479
<212> PRT
<213> Homo sapiens

```

<400> 52

```

Met Arg Gln Pro Pro Gly Glu Ser Asp Met Ala Val Ser Asp Ala Leu
1          5          10          15

```

```

Leu Pro Ser Phe Ser Thr Phe Ala Ser Gly Pro Ala Gly Arg Glu Lys

```

15477SG41_Sequence Listing

20

25

30

Thr Leu Arg Gln Ala Gly Ala Pro Asn Asn Arg Trp Arg Glu Glu Leu
 35 40 45
 Ser His Met Lys Arg Leu Pro Pro Val Leu Pro Gly Arg Pro Tyr Asp
 50 55 60
 Leu Ala Ala Ala Thr Val Ala Thr Asp Leu Glu Ser Gly Gly Ala Gly
 65 70 75 80
 Ala Ala Cys Gly Gly Ser Asn Leu Ala Pro Leu Pro Arg Arg Glu Thr
 85 90 95
 Glu Glu Phe Asn Asp Leu Leu Asp Leu Asp Phe Ile Leu Ser Asn Ser
 100 105 110
 Leu Thr His Pro Pro Glu Ser Val Ala Ala Thr Val Ser Ser Ser Ala
 115 120 125
 Ser Ala Ser Ser Ser Ser Ser Pro Ser Ser Ser Gly Pro Ala Ser Ala
 130 135 140
 Pro Ser Thr Cys Ser Phe Thr Tyr Pro Ile Arg Ala Gly Asn Asp Pro
 145 150 155 160
 Gly Val Ala Pro Gly Gly Thr Gly Gly Gly Leu Leu Tyr Gly Arg Glu
 165 170 175
 Ser Ala Pro Pro Pro Thr Ala Pro Phe Asn Leu Ala Asp Ile Asn Asp
 180 185 190
 Val Ser Pro Ser Gly Gly Phe Val Ala Glu Leu Leu Arg Pro Glu Leu
 195 200 205
 Asp Pro Val Tyr Ile Pro Pro Gln Gln Pro Gln Pro Pro Gly Gly Gly
 210 215 220
 Leu Met Gly Lys Phe Val Leu Lys Ala Ser Leu Ser Ala Pro Gly Ser
 225 230 235 240
 Glu Tyr Gly Ser Pro Ser Val Ile Ser Val Ser Lys Gly Ser Pro Asp
 245 250 255
 Gly Ser His Pro Val Val Val Ala Pro Tyr Asn Gly Gly Pro Pro Arg
 260 265 270

15477SG41_Sequence Listing

Thr Cys Pro Lys Ile Lys Gln Glu Ala Val Ser Ser Cys Thr His Leu
275 280 285

Gly Ala Gly Pro Pro Leu Ser Asn Gly His Arg Pro Ala Ala His Asp
290 295 300

Phe Pro Leu Gly Arg Gln Leu Pro Ser Arg Thr Thr Pro Thr Leu Gly
305 310 315 320

Leu Glu Glu Val Leu Ser Ser Arg Asp Cys His Pro Ala Leu Pro Leu
325 330 335

Pro Pro Gly Phe His Pro His Pro Gly Pro Asn Tyr Pro Ser Phe Leu
340 345 350

Pro Asp Gln Met Gln Pro Gln Val Pro Pro Leu His Tyr Gln Glu Leu
355 360 365

Met Pro Pro Gly Ser Cys Met Pro Glu Glu Pro Lys Pro Lys Arg Gly
370 375 380

Arg Arg Ser Trp Pro Arg Lys Arg Thr Ala Thr His Thr Cys Asp Tyr
385 390 395 400

Ala Gly Cys Gly Lys Thr Tyr Thr Lys Ser Ser His Leu Lys Ala His
405 410 415

Leu Arg Thr His Thr Gly Glu Lys Pro Tyr His Cys Asp Trp Asp Gly
420 425 430

Cys Gly Trp Lys Phe Ala Arg Ser Asp Glu Leu Thr Arg His Tyr Arg
435 440 445

Lys His Thr Gly His Arg Pro Phe Gln Cys Gln Lys Cys Asp Arg Ala
450 455 460

Phe Ser Arg Ser Asp His Leu Ala Leu His Met Lys Arg His Phe
465 470 475

<210> 53
<211> 1095
<212> DNA
<213> Homo sapiens

<400> 53
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cgctccacgg cgcccagcga ggacatctgg aagaaattcg agctggtgcc atcgcccccc 120
acgtcggccgc cctggggcctt ggggtcccggc gcagggggacc cggcccccg gattggtccc 180

15477SG41_Sequence Listing

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ccggagccgt ggcccggagg gtgcaccgga gacgaagcgg aatcccgggg ccactcgaaa 240
ggctgggggca ggaactacgc ctccatcata cgccgtgact gcatgtggag cggcttctcg 300
gcccgggaac ggctggagag agctgtgagc gaccggctcg ctctggcgc gcccggggg 360
aaccgcca aggcgtccgc cgcccggac tgcactcca gcctcgaagc cggcaaccg 420
gcgcccgcg cccctgtcc gctgggcgaa cccaagaccc aggctgctc cgggtccgag 480
agcccaagcg actcggagaa tgaagaaatt gatgttgta cagtagagaa gaggcagtct 540
ctgggtattc ggaagccgt caccatcacg gtgcgagcag accccctgga tccctgcatg 600
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gatgctgcag gggaaaagga agatgaggag gatgaagaga ttgtgagtcc cccacctgta 780
gaaagtgagg ctgcccagtc ctgccacccc aaacctgtca gttctgatac tgaggatgtg 840
accaagagga agaatacaca cttcctggag cgcaagaggc ggaatgacct gcgttcgcga 900
ttcttggcgc tgagggacca ggtgccacc ctggccagct gctccaaggc ccccaaagta 960
gtgatcctaa gcaaggcctt ggaatacttg caagccctgg tgggggctga gaagaggatg 1020
gctacagaga aaagacagct ccgatgccgg cagcagcagt tgcagaaaag aattgcatac 1080
ctcactggct actaa 1095

```

```

<210> 54
<211> 364
<212> PRT
<213> Homo sapiens

```

<400> 54

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Met Asp Tyr Asp Ser Tyr Gln His Tyr Phe Tyr Asp Tyr Asp Cys Gly
1      5      10      15

```

```

Glu Asp Phe Tyr Arg Ser Thr Ala Pro Ser Glu Asp Ile Trp Lys Lys
20      25      30

```

```

Phe Glu Leu Val Pro Ser Pro Pro Thr Ser Pro Pro Trp Gly Leu Gly
35      40      45

```

```

Pro Gly Ala Gly Asp Pro Ala Pro Gly Ile Gly Pro Pro Glu Pro Trp
50      55      60

```

```

Pro Gly Gly Cys Thr Gly Asp Glu Ala Glu Ser Arg Gly His Ser Lys
65      70      75      80

```

```

Gly Trp Gly Arg Asn Tyr Ala Ser Ile Ile Arg Arg Asp Cys Met Trp
85      90      95

```

15477SG41_Sequence Listing

Ser Gly Phe Ser Ala Arg Glu Arg Leu Glu Arg Ala Val Ser Asp Arg
 100 105 110
 Leu Ala Pro Gly Ala Pro Arg Gly Asn Pro Pro Lys Ala Ser Ala Ala
 115 120 125
 Pro Asp Cys Thr Pro Ser Leu Glu Ala Gly Asn Pro Ala Pro Ala Ala
 130 135 140
 Pro Cys Pro Leu Gly Glu Pro Lys Thr Gln Ala Cys Ser Gly Ser Glu
 145 150 155 160
 Ser Pro Ser Asp Ser Glu Asn Glu Glu Ile Asp Val Val Thr Val Glu
 165 170 175
 Lys Arg Gln Ser Leu Gly Ile Arg Lys Pro Val Thr Ile Thr Val Arg
 180 185 190
 Ala Asp Pro Leu Asp Pro Cys Met Lys His Phe His Ile Ser Ile His
 195 200 205
 Gln Gln Gln His Asn Tyr Ala Ala Arg Phe Pro Pro Glu Ser Cys Ser
 210 215 220
 Gln Glu Glu Ala Ser Glu Arg Gly Pro Gln Glu Glu Val Leu Glu Arg
 225 230 235 240
 Asp Ala Ala Gly Glu Lys Glu Asp Glu Glu Asp Glu Glu Ile Val Ser
 245 250 255
 Pro Pro Pro Val Glu Ser Glu Ala Ala Gln Ser Cys His Pro Lys Pro
 260 265 270
 Val Ser Ser Asp Thr Glu Asp Val Thr Lys Arg Lys Asn His Asn Phe
 275 280 285
 Leu Glu Arg Lys Arg Arg Asn Asp Leu Arg Ser Arg Phe Leu Ala Leu
 290 295 300
 Arg Asp Gln Val Pro Thr Leu Ala Ser Cys Ser Lys Ala Pro Lys Val
 305 310 315 320
 Val Ile Leu Ser Lys Ala Leu Glu Tyr Leu Gln Ala Leu Val Gly Ala
 325 330 335
 Glu Lys Arg Met Ala Thr Glu Lys Arg Gln Leu Arg Cys Arg Gln Gln

Gln Leu Gln Lys Arg Ile Ala Tyr Leu Thr Gly Tyr
355 360

<210> 55
<211> 20
<212> DNA
<213> Artificial

<220>
<223> SRF-F

<400> 55
accataagc cccagctatc 20

<210> 56
<211> 20
<212> DNA
<213> Artificial

<220>
<223> SRF-R

<400> 56
ggtgccaaga tggaagtcac 20

<210> 57
<211> 20
<212> DNA
<213> Artificial

<220>
<223> ACTG2-F

<400> 57
cggtggtctc ctcttcacac 20

<210> 58
<211> 22
<212> DNA
<213> Artificial

<220>
<223> ACTG2-R

<400> 58
cactgggaga agaacctctc at 22

<210> 59
<211> 1041
<212> DNA
<213> Homo sapiens

<400> 59
atggctcctg ggagcgtcac cagcgacatc tcacctcct cgacttcac agcaggatca 60

15477SG41_Sequence Listing

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ccgagccaca gcagcctccc ggtgggacgc cgccaccccc cggtgctacg catggtgctg	180
gaggcgctgc aggctgggga gcagcgccgg ggcacgtcgg tggcagctat caagctctac	240
atcctgcaca agtacccaac agtggacgtc ctccgcttca agtacctgct gaagcaggcg	300
ctggccactg gcatgcgccg tggcctcctc gccaggcccc tcaactccaa agccaggggg	360
gccactggca gcttcaaatt agttcccaag cacaagaaga aaatccagcc caggaagatg	420
gccccgcga cggtccccag gagagcgggt gaggccaagg ggaagggccc caagaaacca	480
agtgaggcca aggaggaccc tcccaacgtg ggcaagggtga aaaaggcagc caagaggcca	540
gcaaagggtc agaagcctcc tcccaagcca ggcgcagcca cagagaaggc tcgcaagcaa	600
ggcggcgcg gccaaggacac cagggcacag tcgggagagg ctaggaagggt gccccccaag	660
ccagacaagg ccatgcgggc accttccagt gctggtgggc tcagcaggaa ggcaaaggcc	720
aaaggcagca ggagcagcca aggagatgct gaggcttaca ggaaaaccaa agctgagagt	780
aagagttcaa aaccacggc cagcaagggtc aagaatggtg ctgcttcccc gacaaaaaag	840
aagggtggtg ccaaggccaa ggcccctaaa gctgggcagg ggccaaacac caaggctgct	900
gctctgcta agggcagtgg gtccaagggtg gtacctgcac atttgtccag gaagacagag	960
gcccccaagg gccctagaaa ggctgggctg cccatcaagg cctcatcatc caaagtgtcc	1020
agccagaggg ctgaagctta g	1041

<210> 60
 <211> 346
 <212> PRT
 <213> Homo sapiens
 <400> 60

Met Ala Pro Gly Ser Val Thr Ser Asp Ile Ser Pro Ser Ser Thr Ser
 1 5 10 15

Thr Ala Gly Ser Ser Arg Ser Pro Glu Ser Glu Lys Pro Gly Pro Ser
 20 25 30

His Gly Gly Val Pro Pro Gly Gly Pro Ser His Ser Ser Leu Pro Val
 35 40 45

Gly Arg Arg His Pro Pro Val Leu Arg Met Val Leu Glu Ala Leu Gln
 50 55 60

Ala Gly Glu Gln Arg Arg Gly Thr Ser Val Ala Ala Ile Lys Leu Tyr
 65 70 75 80

Ile Leu His Lys Tyr Pro Thr Val Asp Val Leu Arg Phe Lys Tyr Leu
 Page 23

15477SG41_Sequence Listing

85

90

95

Leu Lys Gln Ala Leu Ala Thr Gly Met Arg Arg Gly Leu Leu Ala Arg
 100 105 110
 Pro Leu Asn Ser Lys Ala Arg Gly Ala Thr Gly Ser Phe Lys Leu Val
 115 120 125
 Pro Lys His Lys Lys Lys Ile Gln Pro Arg Lys Met Ala Pro Ala Thr
 130 135 140
 Ala Pro Arg Arg Ala Gly Glu Ala Lys Gly Lys Gly Pro Lys Lys Pro
 145 150 155 160
 Ser Glu Ala Lys Glu Asp Pro Pro Asn Val Gly Lys Val Lys Lys Ala
 165 170 175
 Ala Lys Arg Pro Ala Lys Val Gln Lys Pro Pro Pro Lys Pro Gly Ala
 180 185 190
 Ala Thr Glu Lys Ala Arg Lys Gln Gly Gly Ala Ala Lys Asp Thr Arg
 195 200 205
 Ala Gln Ser Gly Glu Ala Arg Lys Val Pro Pro Lys Pro Asp Lys Ala
 210 215 220
 Met Arg Ala Pro Ser Ser Ala Gly Gly Leu Ser Arg Lys Ala Lys Ala
 225 230 235 240
 Lys Gly Ser Arg Ser Ser Gln Gly Asp Ala Glu Ala Tyr Arg Lys Thr
 245 250 255
 Lys Ala Glu Ser Lys Ser Ser Lys Pro Thr Ala Ser Lys Val Lys Asn
 260 265 270
 Gly Ala Ala Ser Pro Thr Lys Lys Lys Val Val Ala Lys Ala Lys Ala
 275 280 285
 Pro Lys Ala Gly Gln Gly Pro Asn Thr Lys Ala Ala Ala Pro Ala Lys
 290 295 300
 Gly Ser Gly Ser Lys Val Val Pro Ala His Leu Ser Arg Lys Thr Glu
 305 310 315 320
 Ala Pro Lys Gly Pro Arg Lys Ala Gly Leu Pro Ile Lys Ala Ser Ser
 325 330 335

15477SG41 Sequence Listing

Ser	Lys	Val	Ser	Ser	Gln	Arg	Ala	Glu	Ala
			340					345	