SEQUENCE LISTING

<110> LI, LINHONG
PESHWA, MADHUSUDAN

<120> METHODS AND COMPOSITIONS FOR MODIFYING GENOMIC DNA

<130> MAXC.P0040WO

<140> UNKNOWN
<141> 2015-03-04

<150> 61/979,178
<151> 2014-04-14

<150> 62/078,706
<151> 2014-11-12

<160> 43

<170> PatentIn version 3.5

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Met Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp
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Gly Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu
20 25 30

Leu Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp
35 40 45

Leu Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His
50 55 60

Gly Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp
65 70 75 80

Asn Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys
85 90 95

Leu His Val Asp Pro Glu Asn Phe Arg Leu Leu Gly Asn Val Leu Val
100 105 110

Cys Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln
115 120 125

Ala Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His
130 135 140

Lys Tyr His
145

<210> 20
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<212> PRT
<213> Homo sapiens

<400> 20

Met Gly Asn Trp Ala Val Asn Glu Gly Leu Ser Ile Phe Val Ile Leu
1 5 10 15

Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Trp Tyr Tyr Arg Val
20 25 30

Tyr Asp Ile Pro Pro Lys Phe Phe Tyr Thr Arg Lys Leu Leu Gly Ser
35 40 45

Ala Leu Ala Leu Ala Arg Ala Pro Ala Ala Cys Leu Asn Phe Asn Cys
50 55 60

Met Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg
65 70 75 80

Gly Ser Ser Ala Cys Cys Ser Thr Arg Val Arg Arg Gln Leu Asp Arg
85 90 95

Asn Leu Thr Phe His Lys Met Val Ala Trp Met Ile Ala Leu His Ser
100 105 110

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Ala Ile His Thr Ile Ala His Leu Phe Asn Val Glu Trp Cys Val Asn
        115                 120                 125

Ala Arg Val Asn Asn Ser Asp Pro Tyr Ser Val Ala Leu Ser Glu Leu
    130                 135                 140

Gly Asp Arg Gln Asn Glu Ser Tyr Leu Asn Phe Ala Arg Lys Arg Ile
145                 150                 155                 160

Lys Asn Pro Glu Gly Gly Leu Tyr Leu Ala Val Thr Leu Leu Ala Gly
                165                 170                 175

Ile Thr Gly Val Val Ile Thr Leu Cys Leu Ile Leu Ile Ile Thr Ser
            180                 185                 190

Ser Thr Lys Thr Ile Arg Arg Ser Tyr Phe Glu Val Phe Trp Tyr Thr
        195                 200                 205

His His Leu Phe Val Ile Phe Phe Ile Gly Leu Ala Ile His Gly Ala
    210                 215                 220

Glu Arg Ile Val Arg Gly Gln Thr Ala Glu Ser Leu Ala Val His Asn
225                 230                 235                 240

Ile Thr Val Cys Glu Gln Lys Ile Ser Glu Trp Gly Lys Ile Lys Glu
                245                 250                 255

Cys Pro Ile Pro Gln Phe Ala Gly Asn Pro Pro Met Thr Trp Lys Trp
            260                 265                 270

Ile Val Gly Pro Met Phe Leu Tyr Leu Cys Glu Arg Leu Val Arg Phe
        275                 280                 285

Trp Arg Ser Gln Gln Lys Val Val Ile Thr Lys Val Val Thr His Pro
    290                 295                 300

Phe Lys Thr Ile Glu Leu Gln Met Lys Lys Lys Gly Phe Lys Met Glu
305                 310                 315                 320

Val Gly Gln Tyr Ile Phe Val Lys Cys Pro Lys Val Ser Lys Leu Glu
                325                 330                 335
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Trp His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Asp Phe Phe Ser
            340                 345                 350

Ile His Ile Arg Ile Val Gly Asp Trp Thr Glu Gly Leu Phe Asn Ala
        355                 360                 365

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

Ile Ala Val Asp Gly Pro Phe Gly Thr Ala Ser Glu Asp Val Phe Ser
385                 390                 395                 400

Tyr Glu Val Val Met Leu Val Gly Ala Gly Ile Gly Val Thr Pro Phe
                405                 410                 415

Ala Ser Ile Leu Lys Ser Val Trp Tyr Lys Tyr Cys Asn Asn Ala Thr
            420                 425                 430

Asn Leu Lys Leu Lys Lys Ile Tyr Phe Tyr Trp Leu Cys Arg Asp Thr
        435                 440                 445

His Ala Phe Glu Trp Phe Ala Asp Leu Leu Gln Leu Leu Glu Ser Gln
    450                 455                 460

Met Gln Glu Arg Asn Asn Ala Gly Phe Leu Ser Tyr Asn Ile Tyr Leu
465                 470                 475                 480

Thr Gly Trp Asp Glu Ser Gln Ala Asn His Phe Ala Val His His Asp
                485                 490                 495

Glu Glu Lys Asp Val Ile Thr Gly Leu Lys Gln Lys Thr Leu Tyr Gly
            500                 505                 510

Arg Pro Asn Trp Asp Asn Glu Phe Lys Thr Ile Ala Ser Gln His Pro
        515                 520                 525

Asn Thr Arg Ile Gly Val Phe Leu Cys Gly Pro Glu Ala Leu Ala Glu
    530                 535                 540

Thr Leu Ser Lys Gln Ser Ile Ser Asn Ser Glu Ser Gly Pro Arg Gly
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Val His Phe Ile Phe Asn Lys Glu Asn Phe
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23

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gacagaaaag ccccatcctt aggcctcctc cttcctagtc tcc
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tccttaggcc
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<210> 27
<211> 26
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<400> 27
ctagggacag aagcttgatt ggtgac
26

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agtctgccgt tactgccctg tgg
23

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60

gcttggagaa gtctgccgtt actgccctgt ggggcaaggt gaacgtggat gaagttggtg
120

gtgaggccct gggcaggttg gtatca
146

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gcagagagtt tggctgtgca taatataaca gtttgtgaa
99

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ctcttcagac ggcaatga
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ctcttcagac ggcaatga
78