SEQUENCE LISTING

<110> TAIGA BIOTECHNOLOGIES, INC.
TURNER, Brian C.
REFAELI, Yosef
BIRD, Gregory A.

<120> ENHANCED RECONSTITUTION AND
AUTORECONSTITUTION OF THE HEMATOPOIETIC COMPARTMENT

<130> 691772000840

<140> Not Yet Assigned
<141> Concurrently Herewith

<150> US 61/785,691
<151> 2013-03-14

<150> US 61/674,224
<151> 2012-07-20

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 1
Met Arg Lys Lys Arg Arg Gln Arg Arg Arg Met Pro Leu Asn Val Ser
1 5 10 15
Phe Thr Asn Arg Asn Tyr Asp Leu Asp Tyr Asp Ser Val Gln Pro Tyr
20 25 30
Phe Tyr Cys Asp Glu Glu Glu Asn Phe Tyr Gln Gln Gln Gln Gln Ser
35 40 45
Glu Leu Gln Pro Pro Ala Pro Ser Glu Asp Ile Trp Lys Lys Phe Glu
50 55 60
Leu Leu Pro Thr Pro Pro Leu Ser Pro Ser Arg Arg Ser Gly Leu Cys
65 70 75 80
Ser Pro Ser Tyr Val Ala Val Thr Pro Phe Ser Leu Arg Gly Asp Asn
85 90 95
Asp Gly Gly Gly Gly Ser Phe Ser Thr Ala Asp Gln Leu Glu Met Val
100 105 110
Thr Glu Leu Leu Gly Gly Asp Met Val Asn Gln Ser Phe Ile Cys Asp
115 120 125
Pro Asp Asp Glu Thr Phe Ile Lys Asn Ile Ile Ile Gln Asp Cys Met
130 135 140
Trp Ser Gly Phe Ser Ala Ala Ala Lys Leu Val Ser Glu Lys Leu Ala
145 150 155 160
Ser Tyr Gln Ala Ala Arg Lys Asp Ser Gly Ser Pro Asn Pro Ala Arg
165 170 175
Gly His Ser Val Cys Ser Thr Ser Ser Leu Tyr Leu Gln Asp Leu Ser
180 185 190
Ala Ala Ala Ser Glu Cys Ile Asp Pro Ser Val Val Phe Pro Tyr Pro
195 200 205
Leu Asn Asp Ser Ser Ser Pro Lys Ser Cys Ala Ser Gln Asp Ser Ser
210 215 220
Ala Phe Ser Pro Ser Ser Asp Ser Leu Leu Ser Ser Thr Glu Ser Ser
225 230 235 240
Pro Gln Gly Ser Pro Glu Pro Leu Val Leu His Glu Glu Thr Pro Pro

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                245                 250                 255
Thr Thr Ser Ser Asp Ser Glu Glu Glu Gln Glu Asp Glu Glu Glu Ile
            260                 265                 270
Asp Val Val Ser Val Glu Lys Arg Gln Ala Pro Gly Lys Arg Ser Glu
        275                 280                 285
Ser Gly Ser Pro Ser Ala Gly Gly His Ser Lys Pro Pro His Ser Pro
    290                 295                 300
Leu Val Leu Lys Arg Cys His Val Ser Thr His Gln His Asn Tyr Ala
305                 310                 315                 320
Ala Pro Pro Ser Thr Arg Lys Asp Tyr Pro Ala Ala Lys Arg Val Lys
                325                 330                 335
Leu Asp Ser Val Arg Val Leu Arg Gln Ile Ser Asn Asn Arg Lys Cys
            340                 345                 350
Thr Ser Pro Arg Ser Ser Asp Thr Glu Glu Asn Val Lys Arg Arg Thr
        355                 360                 365
His Asn Val Leu Glu Arg Gln Arg Arg Asn Glu Leu Lys Arg Ser Phe
    370                 375                 380
Phe Ala Leu Arg Asp Gln Ile Pro Glu Leu Glu Asn Asn Glu Lys Ala
385                 390                 395                 400
Pro Lys Val Val Ile Leu Lys Lys Ala Thr Ala Tyr Ile Leu Ser Val
                405                 410                 415
Gln Ala Glu Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Leu Arg Lys
            420                 425                 430
Arg Arg Glu Gln Leu Lys His Lys Leu Glu Gln Leu Arg Lys Gly Glu
        435                 440                 445
Leu Asn Ser Lys Leu Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly
    450                 455                 460
Leu Asp Ser Thr Arg Thr Gly His His His His His His
465                 470                 475
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<210> 2
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

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ttctaccagc agcagcagca gagcgagctg cagcccccgg cgcccagcga ggatatctgg 180
aagaaattcg agctgctgcc caccccgccc ctgtccccta gccgccgctc cgggctctgc 240
tcgccctcct acgttgcggt cacacccttc tcccttcggg gagacaacga cggcggtggc 300
gggagcttct ccacggccga ccagctggag atggtgaccg agctgctggg aggagacatg 360
gtgaaccaga gtttcatctg cgacccggac gacgagacct tcatcaaaaa catcatcatc 420
caggactgta tgtggagcgg cttctcggcc gccgccaagc tcgtctcaga gaagctggcc 480
tcctaccagg ctgcgcgcaa agacagcggc agcccgaacc ccgcccgcgg ccacagcgtc 540
tgctccacct ccagcttgta cctgcaggat ctgagcgccg ccgcctcaga gtgcatcgac 600
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caagactcca gcgccttctc tccgtcctcg gattctctgc tctcctcgac ggagtcctcc 720
ccgcagggca gccccgagcc cctggtgctc catgaggaga caccgcccac caccagcagc 780
gactctgagg aggaacaaga agatgaggaa gaaatcgatg ttgtttctgt ggaaaagagg 840
caggctcctg gcaaaaggtc agagtctgga tcaccttctg ctggaggcca cagcaaacct 900
cctcacagcc cactggtcct caagaggtgc cacgtctcca cacatcagca caactacgca 960
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gaggagaatg tcaagaggcg aacacacaac gtcttggagc gccagaggag gaacgagcta 1140
aaacggagct tttttgccct gcgtgaccag atcccggagt tggaaaacaa tgaaaaggcc 1200
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<210> 3
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 3
Met Arg Lys Lys Arg Arg Gln Arg Arg Arg Met Ala His Ala Gly Arg
 1   5   10   15
Ser Gly Tyr Asp Asn Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys
            20   25   30
Leu Ser Gln Arg Ala Thr Ser Gly Ile Ser Ile Glu Ala Ala Gly Pro
        35   40   45
Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr Leu Arg Gln Ala
    50   55   60
Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met Ser
65   70   75   80
Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly Cys Phe Ala Thr
                85   90   95
Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val
            100   105   110
Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn Arg
        115   120   125
Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu Tyr
    130   135   140
Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp Asp
145   150   155   160
Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro Leu Phe Asp Phe
                165   170   175
Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly Ala
            180   185   190
Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys Lys Gly Glu Leu Asn
        195   200   205
Ser Lys Leu Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp
    210   215   220
Ser Thr Arg Thr Gly His His His His His His
225   230   235

<210> 4
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4
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atctcgatcg aggccgcggg gcctgcgctc agcccggtgc cacctgtggt ccacctgacc 180
ctccgccagg ccggcgacga cttctcccgc cgctaccgcc gcgacttcgc cgagatgtcc 240
agccagctgc acctgacgcc cttcaccgcg cggggatgct ttgccacggt ggtggaggag 300
ctcttcaggg acggggtgaa ctgggggagg attgtggcct tctttgagtt cggtggggtc 360
atgtgtgtgg agagcgtcaa ccgggagatg tcgcccctgg tggacaacat cgccctgtgg 420
atgactgagt acctgaaccg gcacctgcac acctggatcc aggataacgg aggctgggat 480
gcctttgtgg aactgtacgg ccccagcatg cggcctctgt ttgatttctc ctggctgtct 540
ctgaagactc tgctcagttt ggccctggtg ggagcttgca tcaccctggg tgcctatctg 600
agccacaaga agggcgagct caattcgaag cttgaaggta agcctatccc taaccctctc 660
ctcggtctcg attctacgcg taccggtcat catcaccatc accattga   708

<210> 5
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 5
Arg Lys Lys Arg Arg Gln Arg Arg Arg

1 5