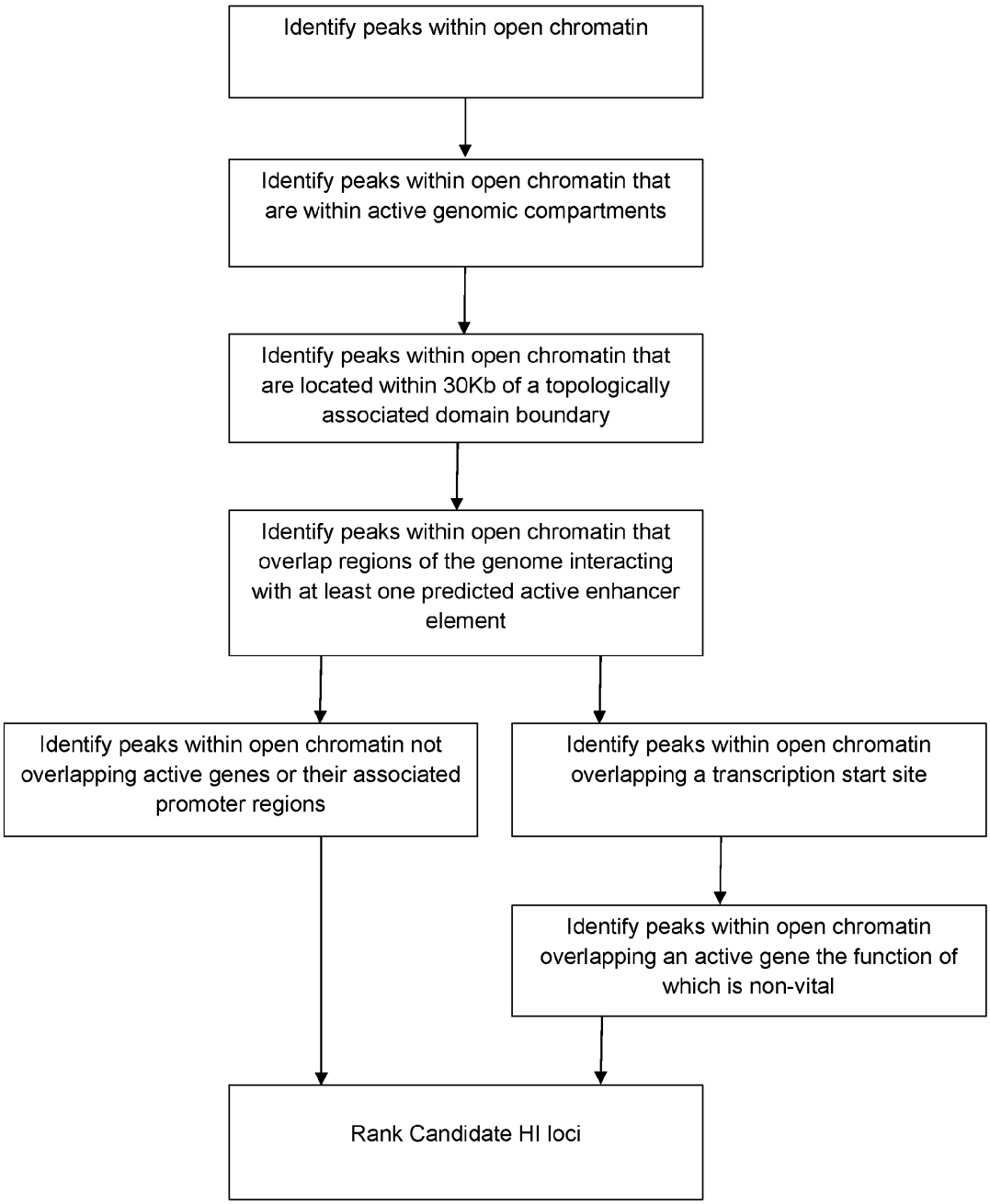

Identify peaks within open chromatin
Identify peaks within open chromatin that are within active genomic compartments
Identify peaks within open chromatin that are located within 30Kb of a topologically associated domain boundary
Identify peaks within open chromatin that overlap regions of the genome interacting with at least one predicted active enhancer element
Identify peaks within open chromatin not overlapping active genes or their associated promoter regions
Identify peaks within open chromatin overlapping a transcription start site
Identify peaks within open chromatin overlapping an active gene the function of which is non-vital
Rank Candidate HI loci

FIG. 1

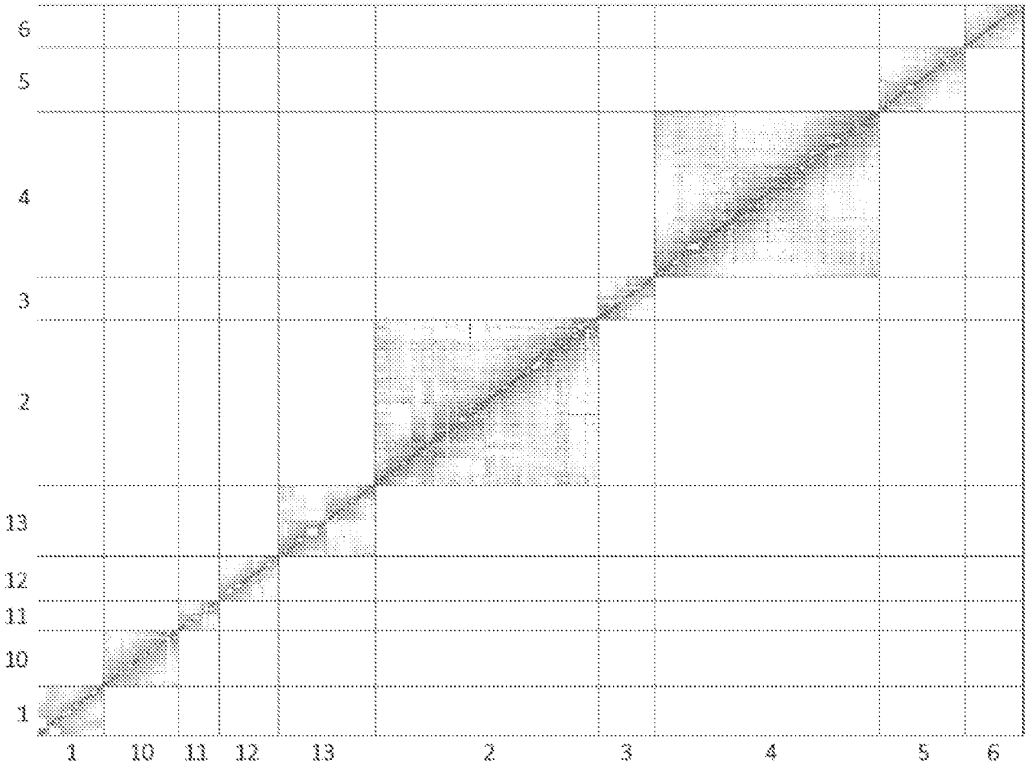


FIG. 2A

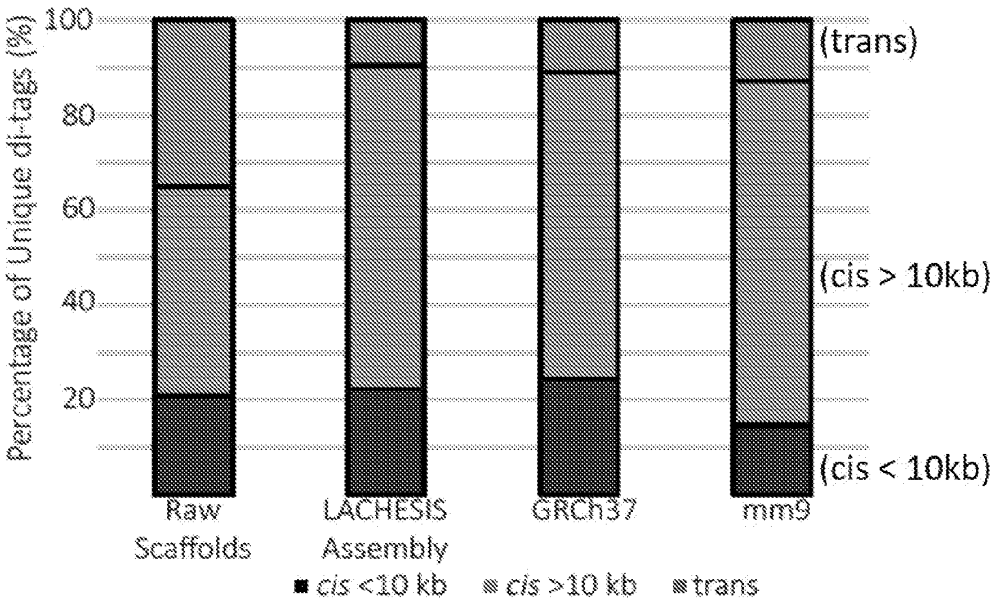

Percentage of Unique di-tags (%)
100
80
60
40
20
(trans)
(cis > 10kb)
(cis < 10kb)
Raw Scaffolds
LACHESIS Assembly
GRCh37
mm9
cis <10 kb
cis >10 kb
trans

FIG. 2B

FIG. 3A

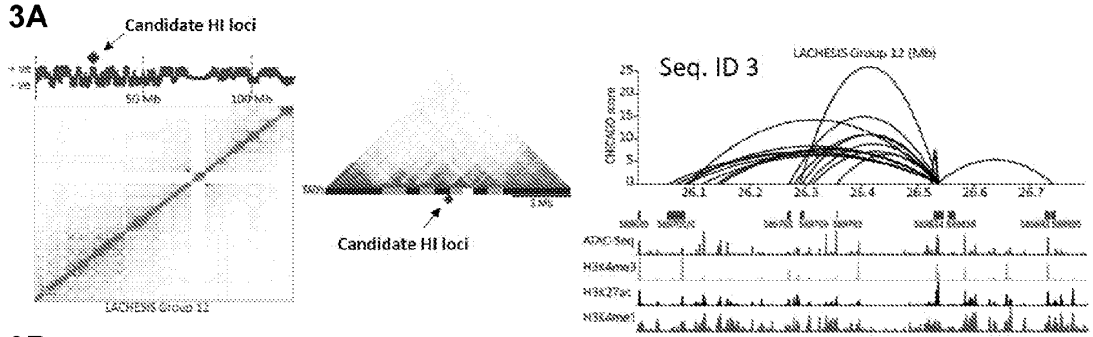


FIG. 3B

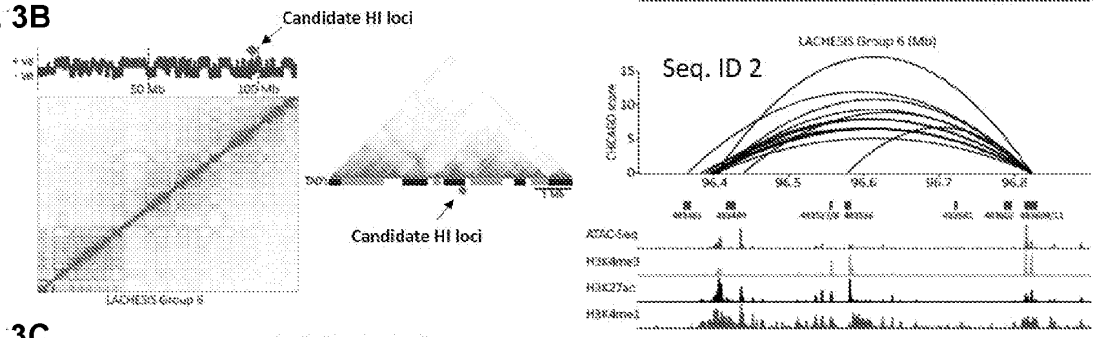
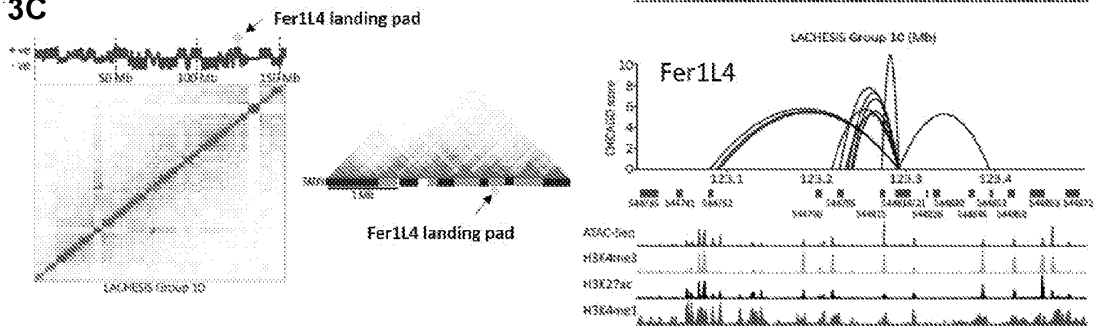


FIG. 3C



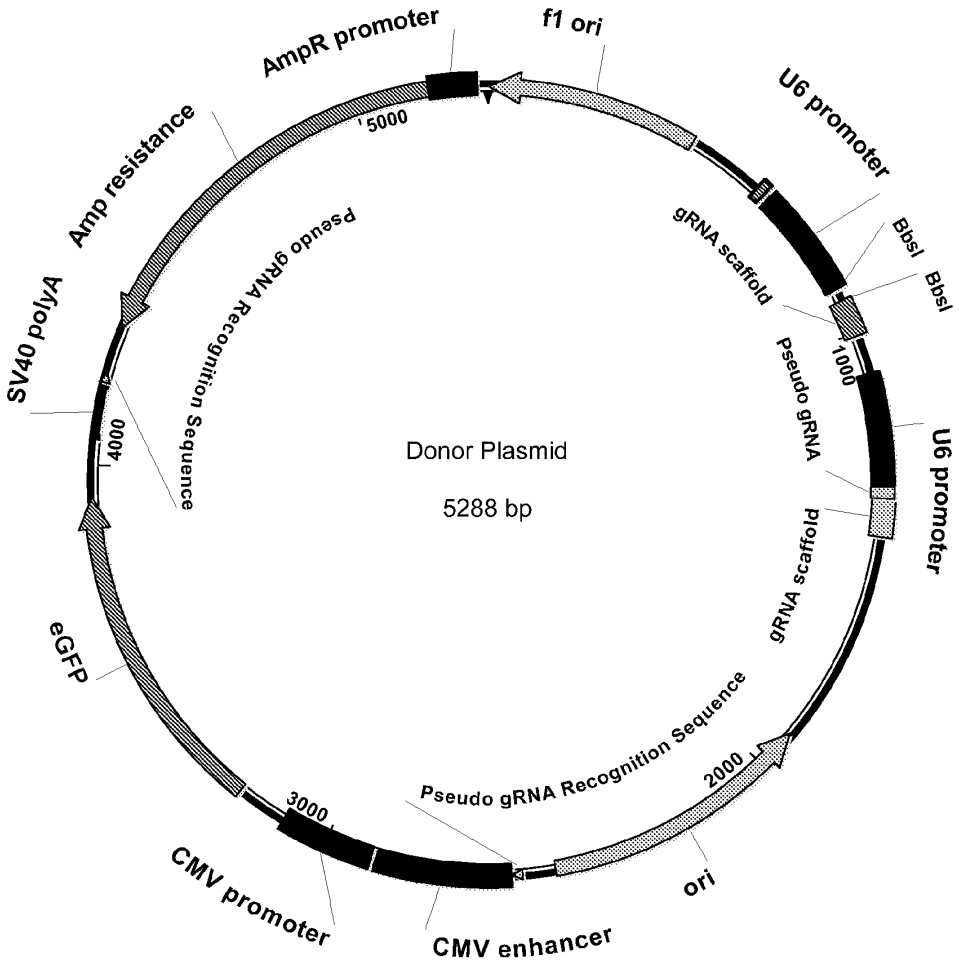

AmpR promoter
f1 ori
U6 promoter
Bbsl
Bbsl
U6 promoter
gRNA scaffold
Pseudo gRNA
gRNA scaffold
Pseudo gRNA Recognition Sequence
Pseudo gRNA Recognition Sequence
Donor Plasmid
5288 bp
5000
1000
2000
3000
4000
Amp resistance
SV40 polyA
eGFP
CMV promoter
CMV enhancer
ori

FIG. 4A

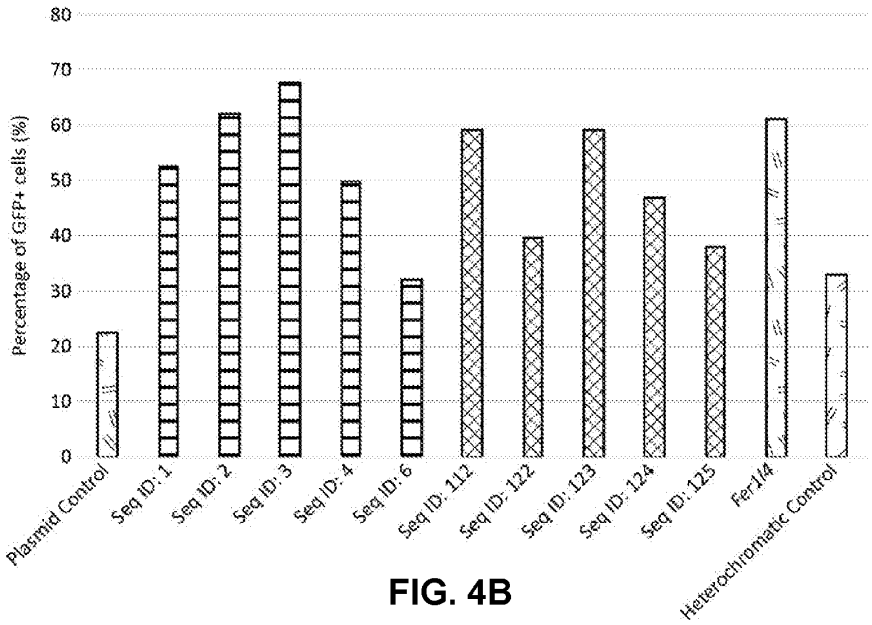

Percentage of GFP+ cells (%)
80
70
60
50
40
30
20
10
0
Plasmid Control
Seq ID: 1
Seq ID: 2
Seq ID: 3
Seq ID: 4
Seq ID: 6
Seq ID: 112
Seq ID: 122
Seq ID: 123
Seq ID: 124
Seq ID: 125
Fer1l4
Heterochromatic Control

FIG. 4B

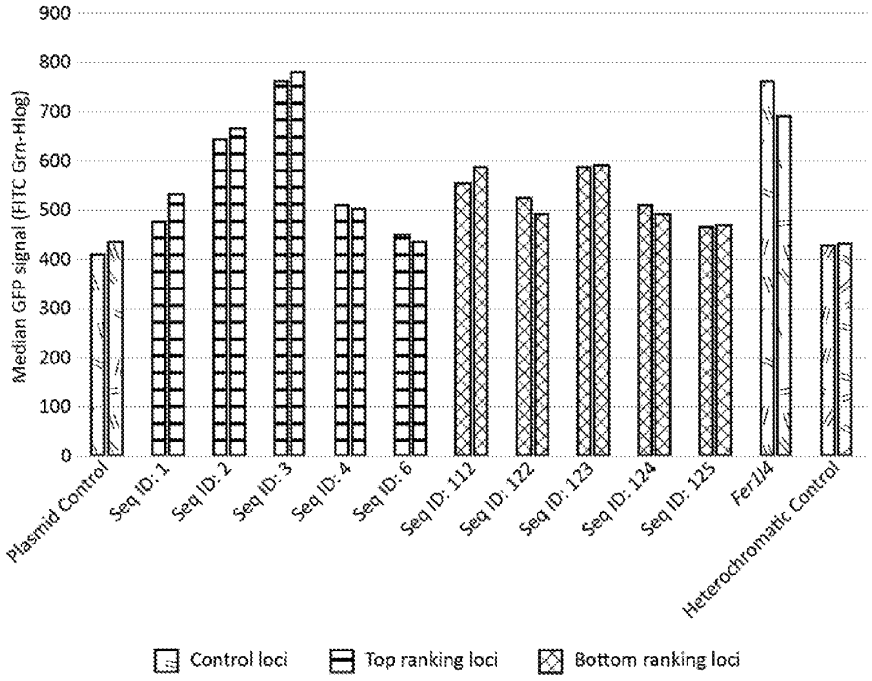

Median GFP signal (FITC Grn-Hlog)
900
800
700
600
500
400
300
200
100
0
Plasmid Control
Seq ID: 1
Seq ID: 2
Seq ID: 3
Seq ID: 4
Seq ID: 6
Seq ID: 112
Seq ID: 122
Seq ID: 123
Seq ID: 124
Seq ID: 125
Fer1l4
Heterochromatic Control
Control loci
Top ranking loci
Bottom ranking loci

FIG. 4C

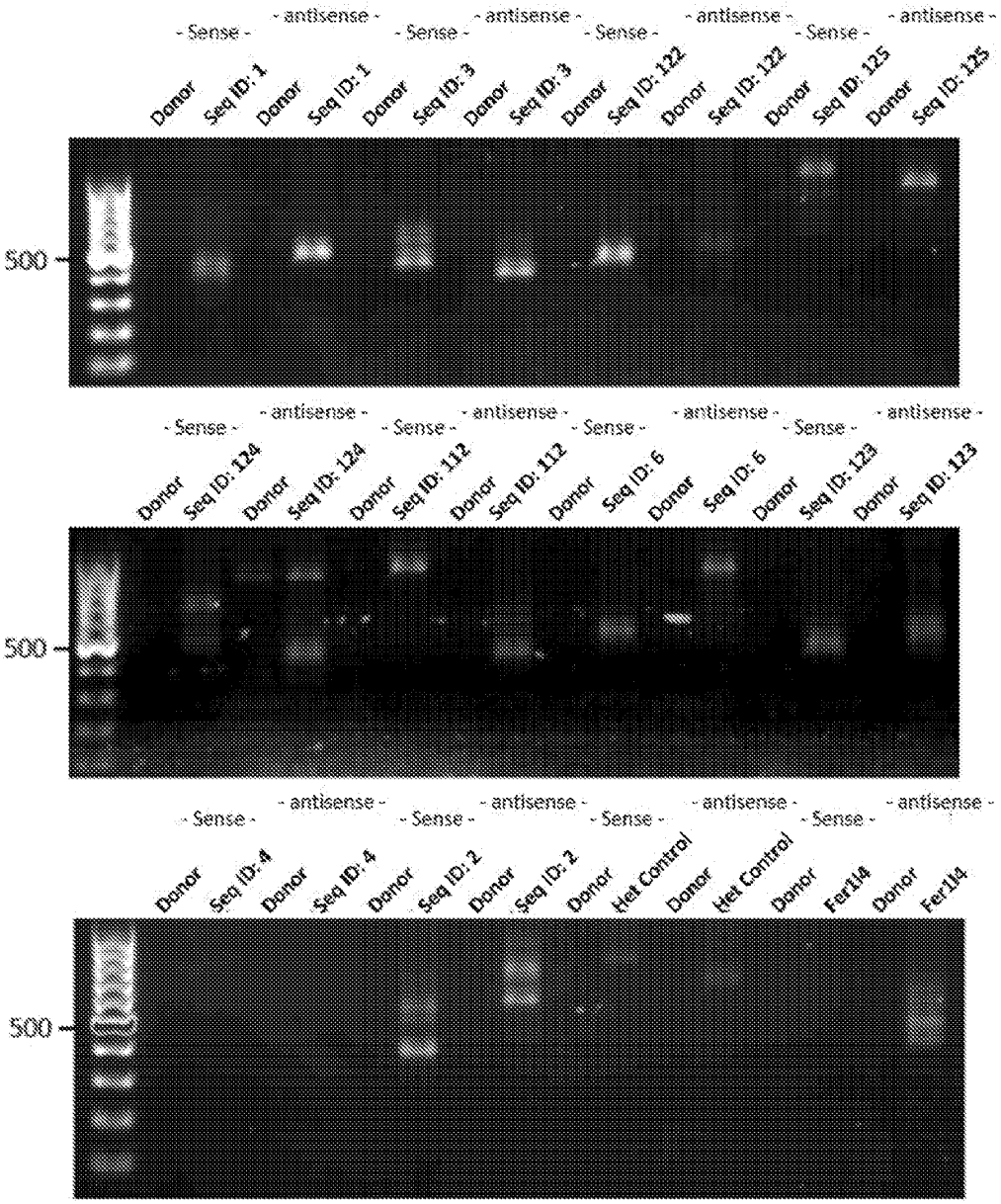

- Sense -
- antisense -
Donor
Seq ID: 1
Seq ID: 3
Seq ID: 122
Seq ID: 125
500
Seq ID: 124
Seq ID: 112
Seq ID: 6
Seq ID: 123
Seq ID: 4
Seq ID: 2
Het Control
Fer1l4

FIG. 4D