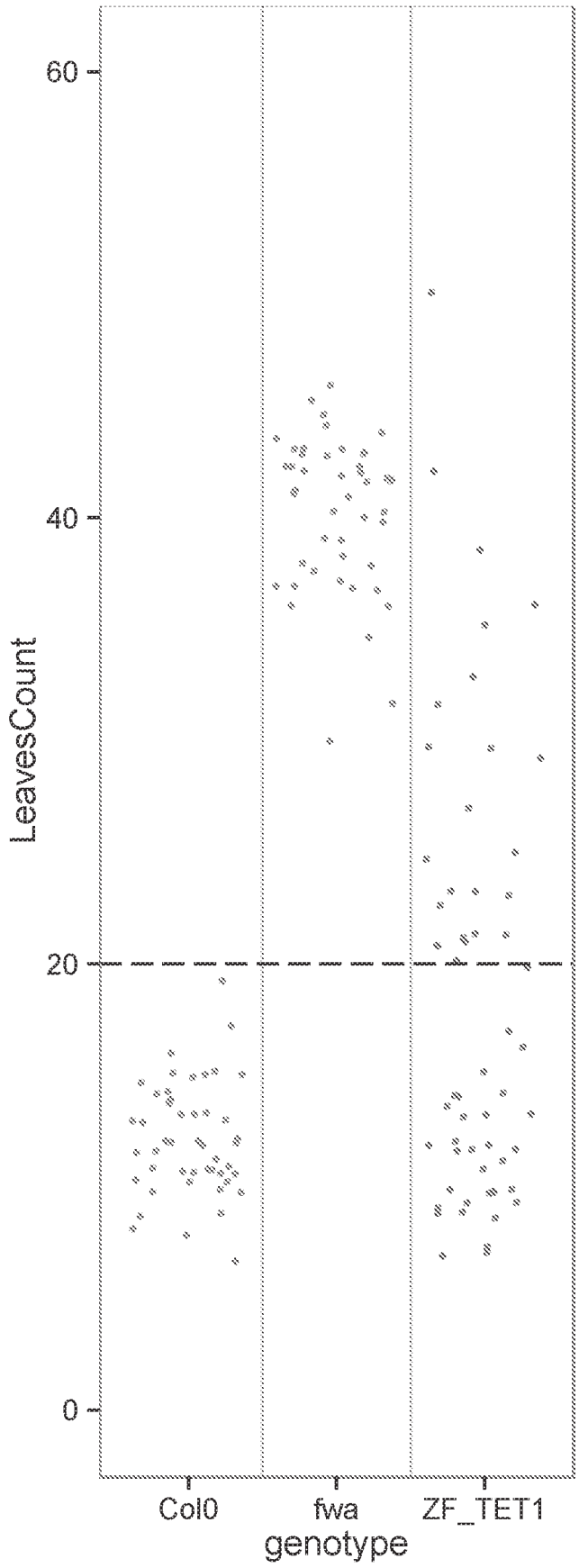


FIG. 1

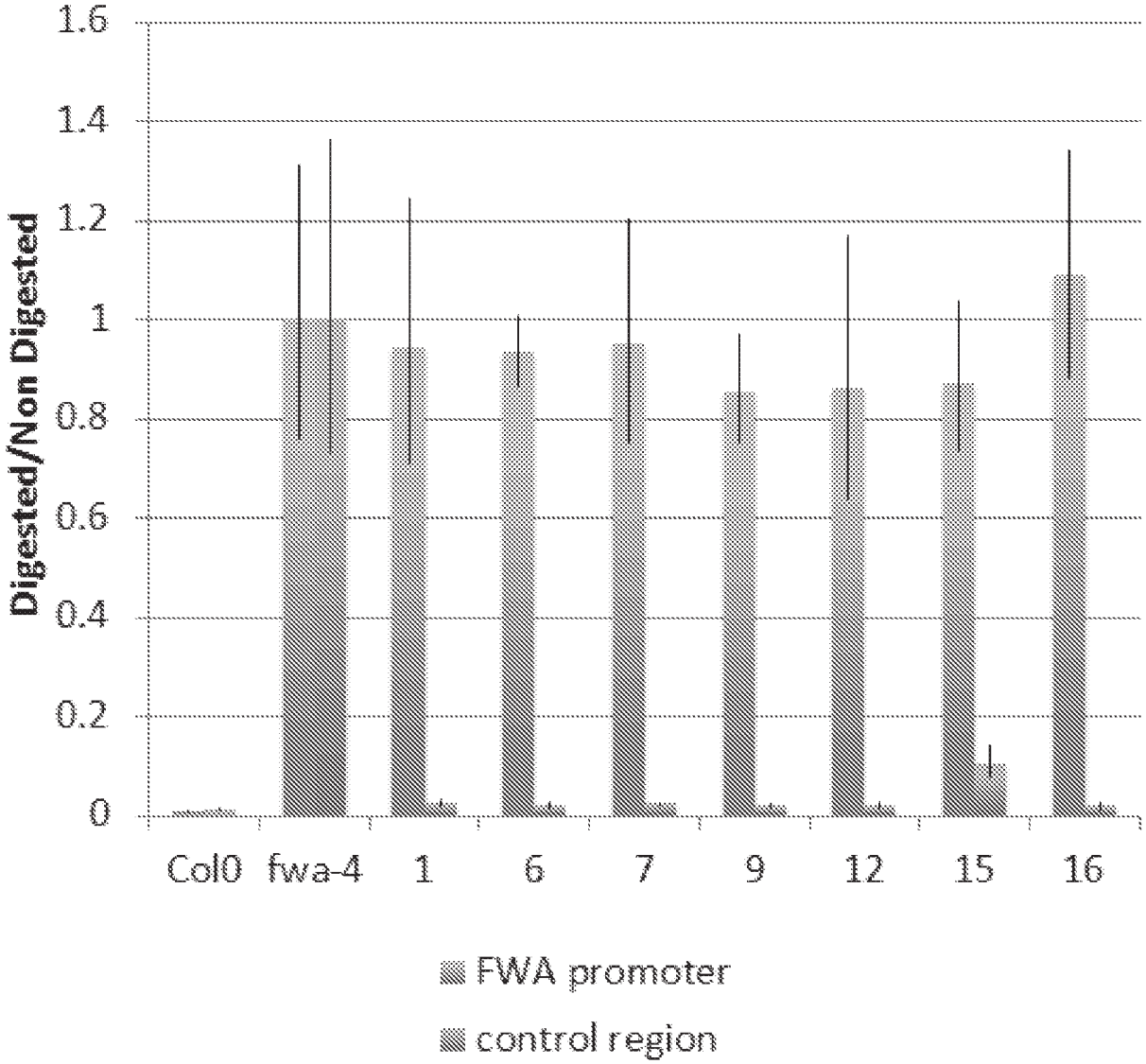

1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Digested/Non Digested
Col0
fwa-4
1
6
7
9
12
15
16
FWA promoter
control region

FIG. 2

FIG. 3

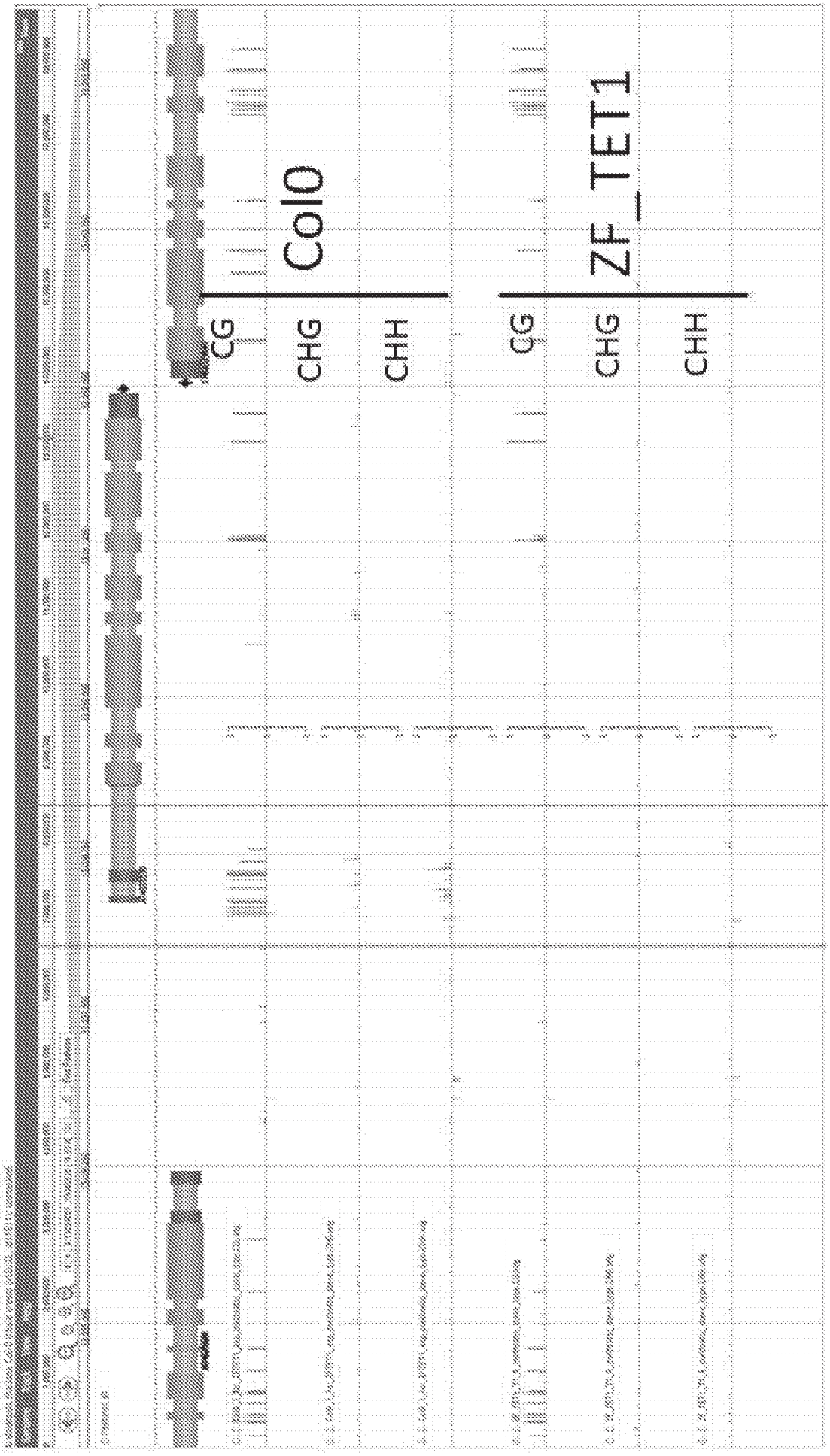
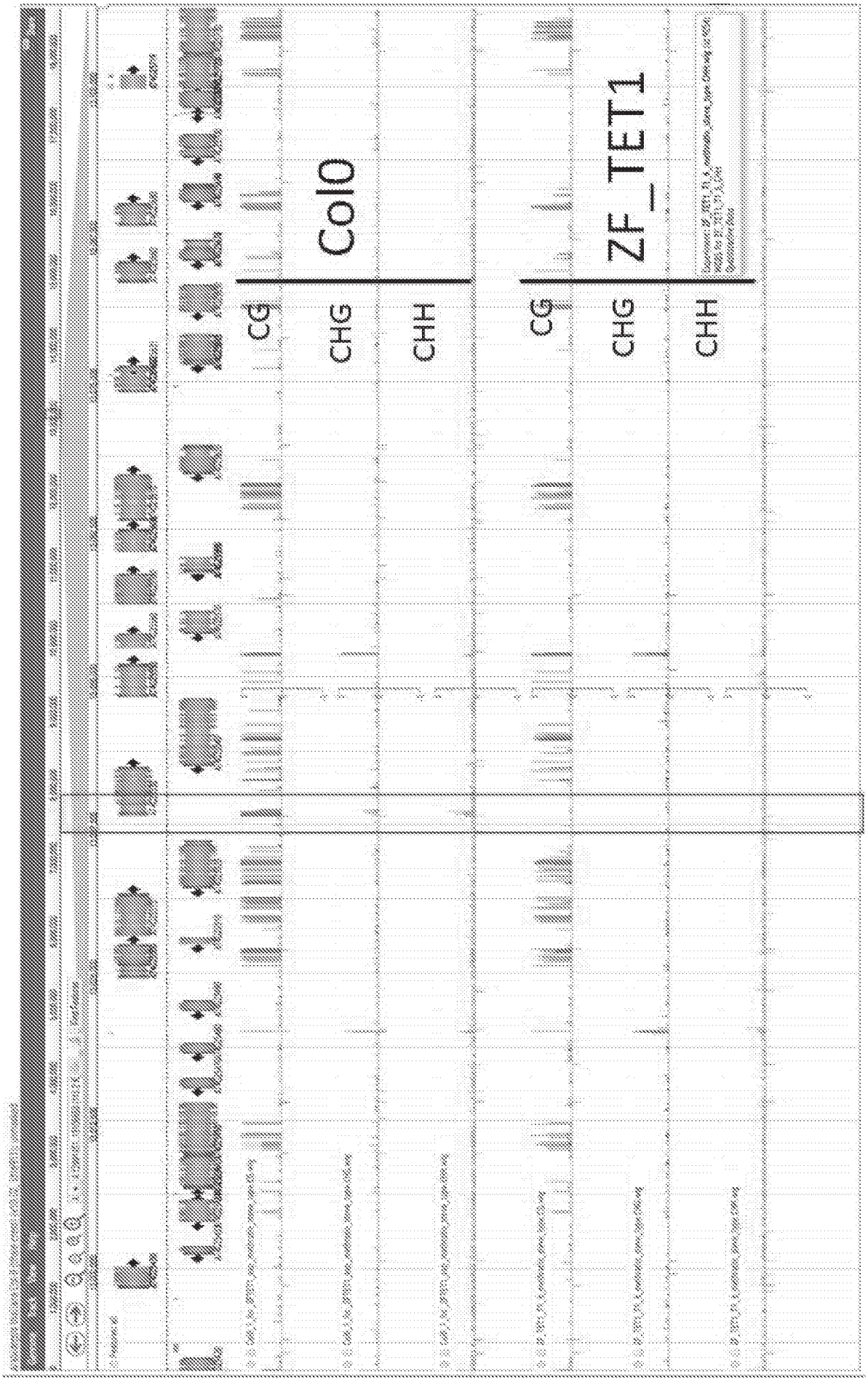


FIG. 4



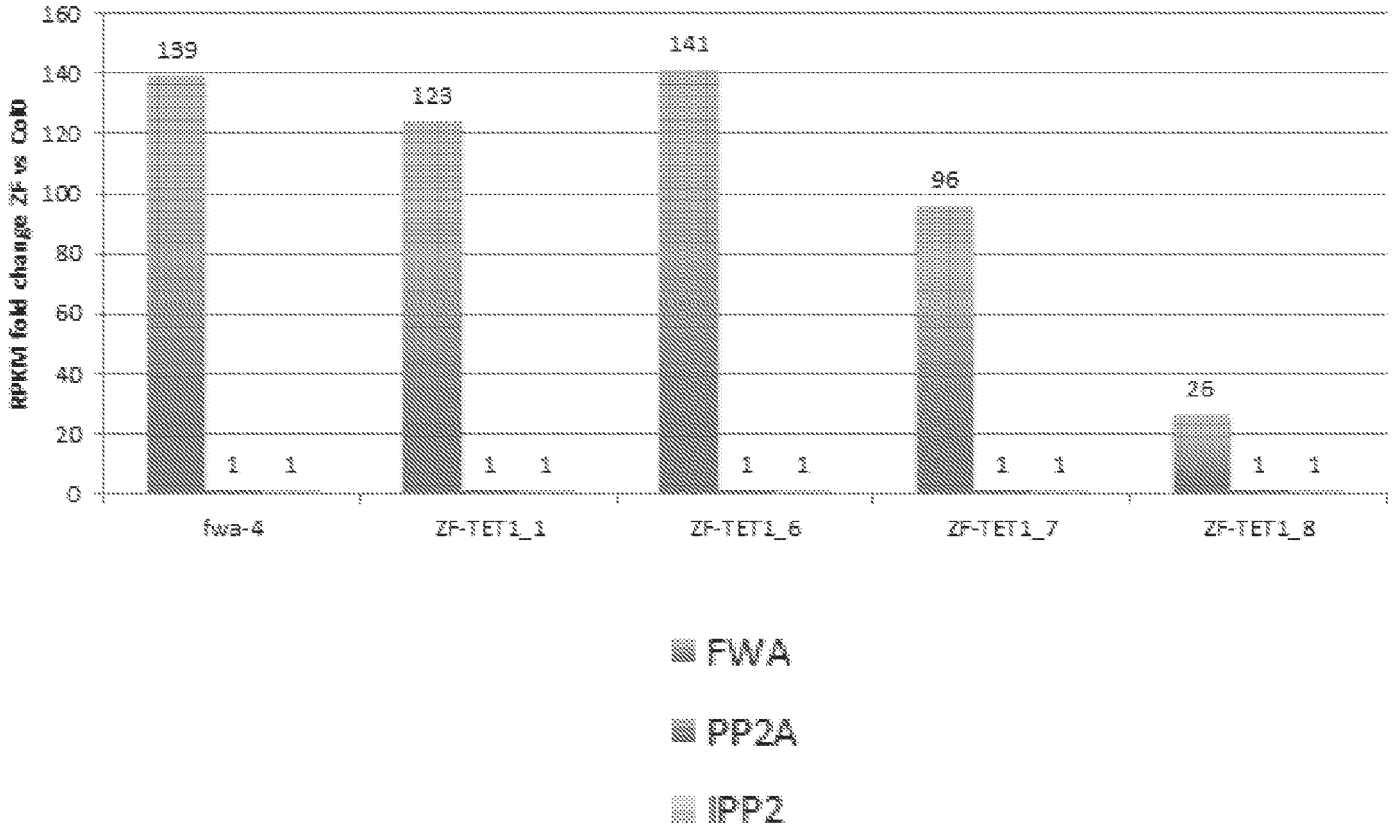

RPKM fold change ZF vs Col0
160
140
120
100
80
60
40
20
0
139
1
1
123
1
1
141
1
1
96
1
1
26
1
1
fwa-4
ZF-TET1_1
ZF-TET1_6
ZF-TET1_7
ZF-TET1_8
FWA
PP2A
IPP2

FIG. 5

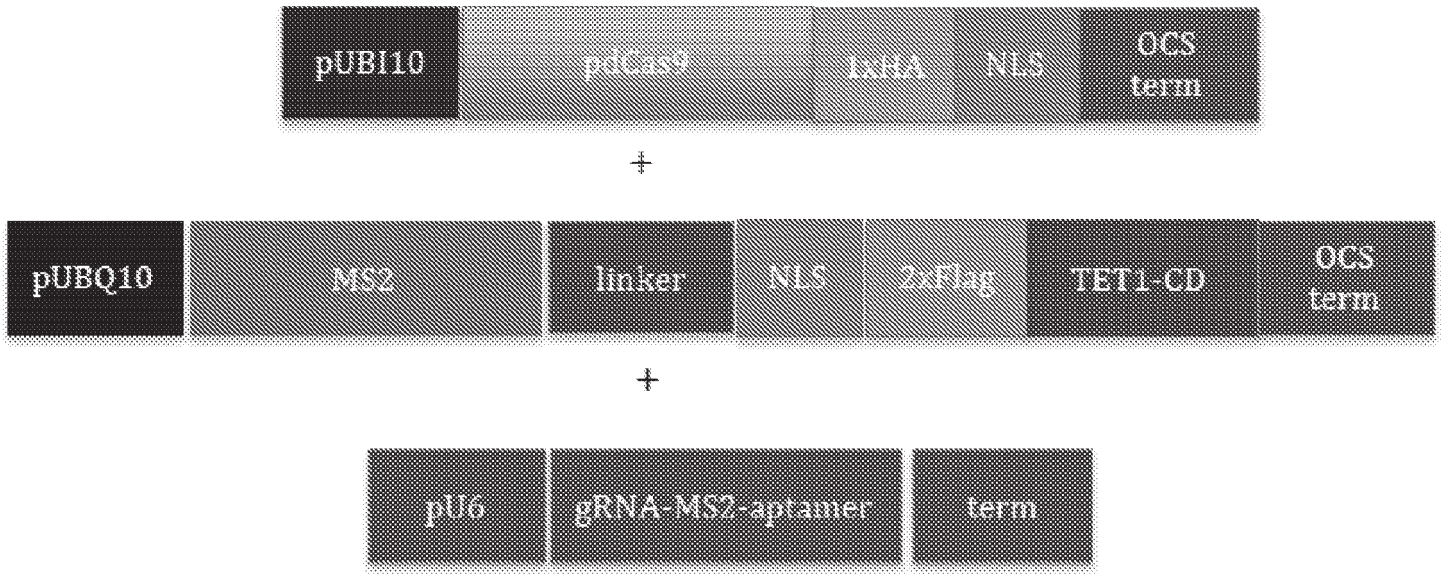
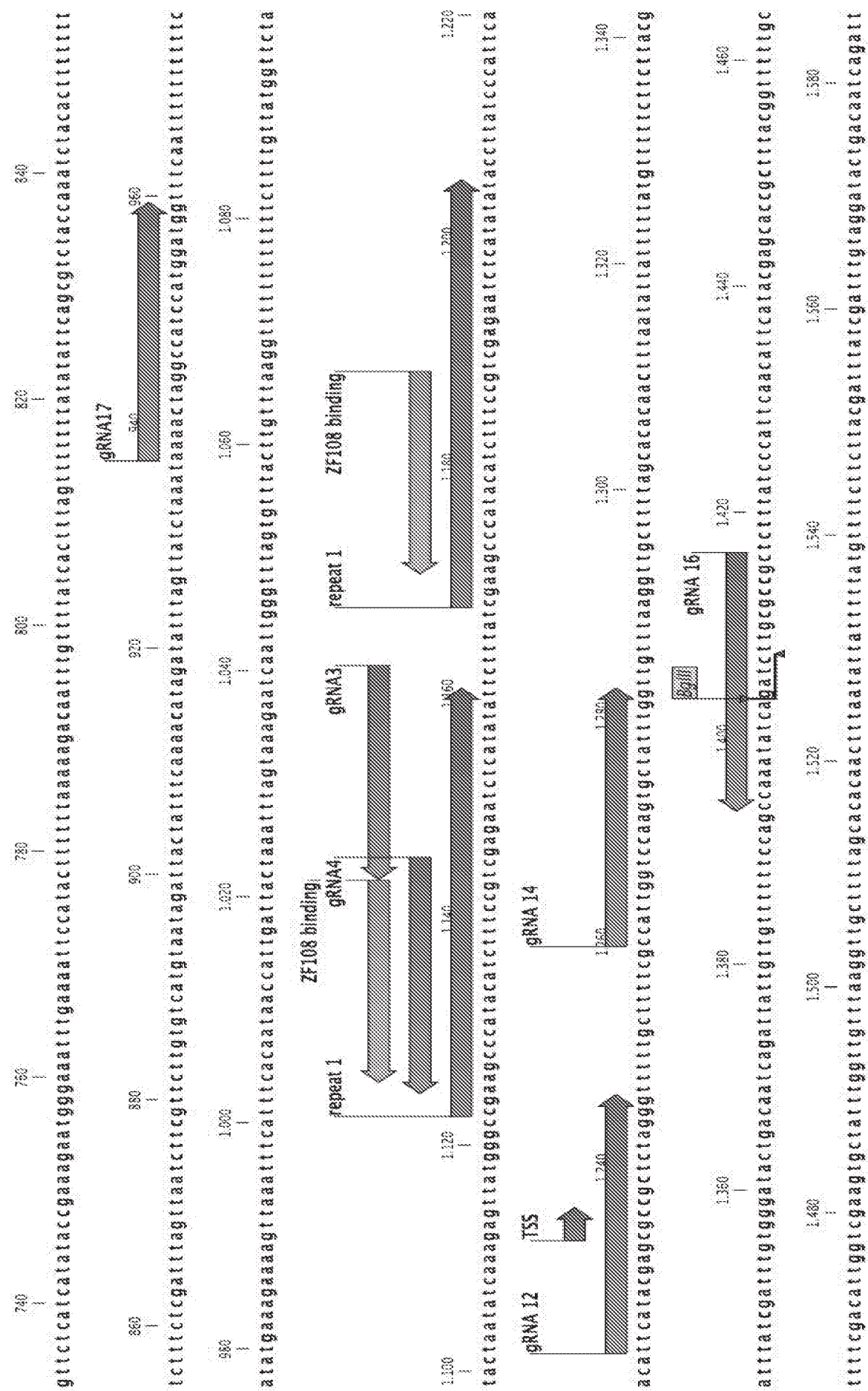

pUBI10
pdCas9
1xHA
NLS
OCS term
+
pUBQ10
MS2
linker
NLS
2xFlag
TET1-CD
OCS term
+
pU6
gRNA-MS2-aptamer
term

FIG. 6

FIG. 7


gRNA17
ZF108 binding
repeat 1
gRNA4
gRNA3
ZF108 binding
repeat 1
gRNA 14
gRNA 12
TSS
gRNA 16
PAM

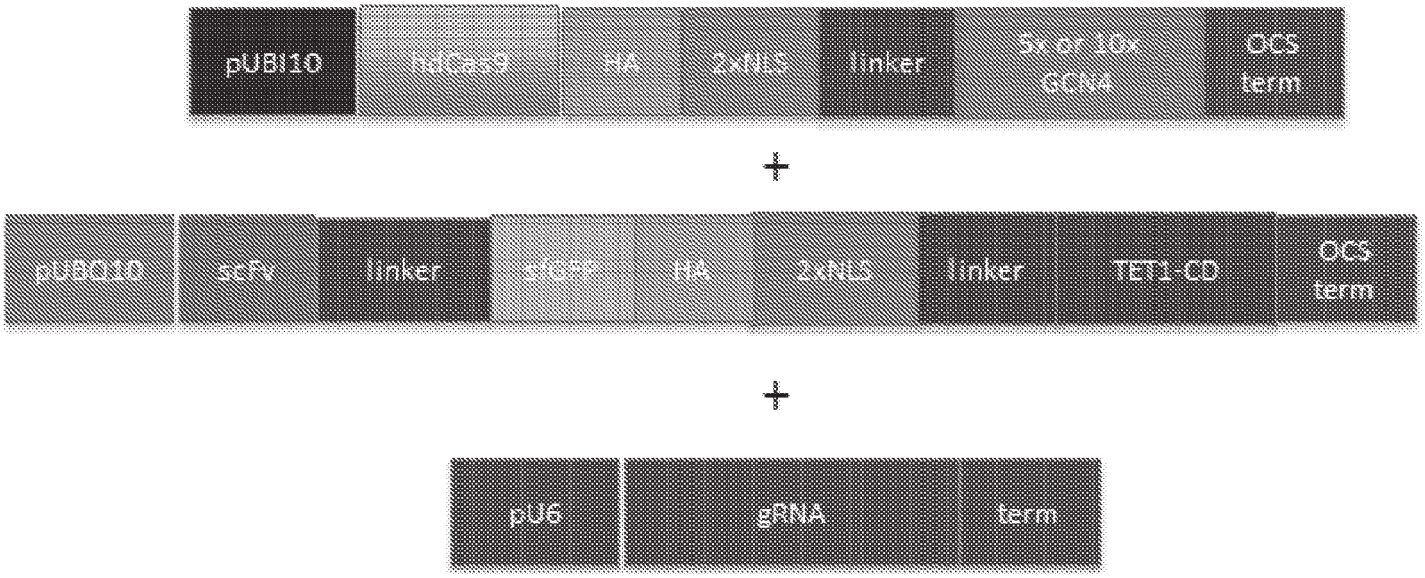

pUBI10
nlsCas9
HA
2xNLS
linker
5x or 10x GCN4
OCS term
+
pUBQ10
scFv
linker
sfGFP
HA
2xNLS
linker
TET1-CD
OCS term
+
pU6
gRNA
term

FIG. 8

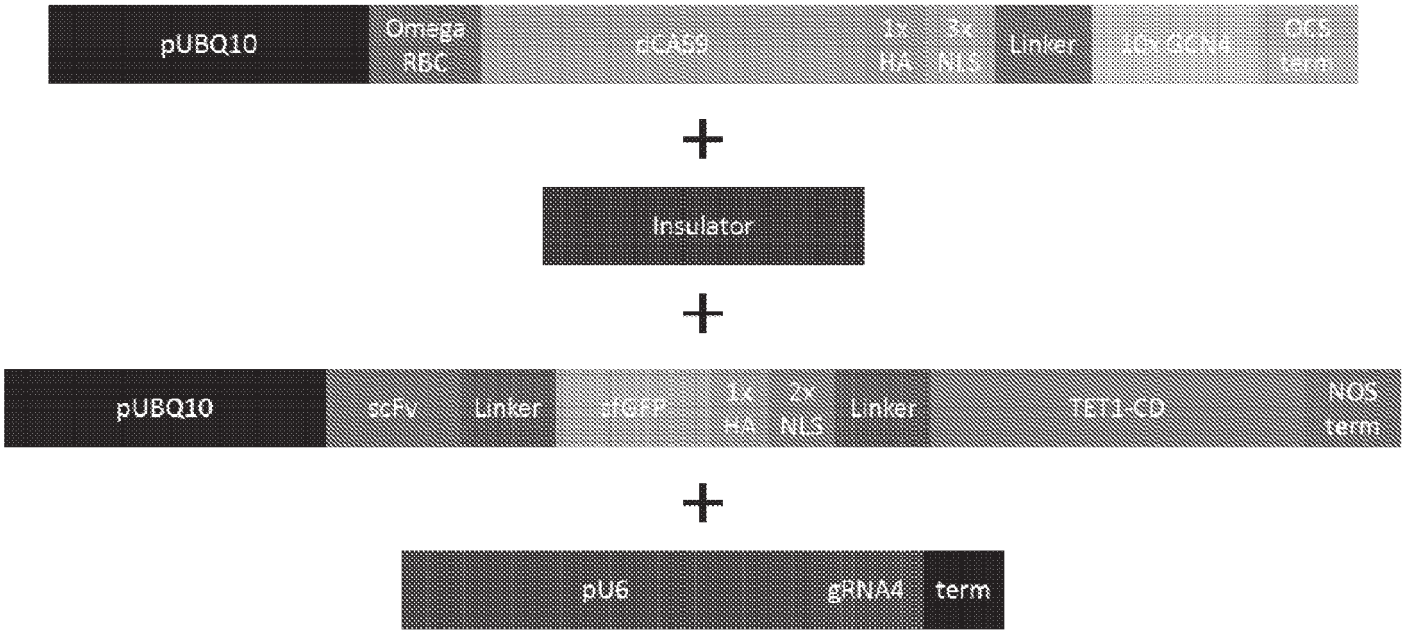

pUBQ10
Omega RBC
sfCAS9
1x HA
3x NLS
Linker
TET1-CD
OCS term
+
Insulator
+
pUBQ10
scFv
Linker
sfGFP
1x HA
2x NLS
Linker
TET1-CD
NOS term
+
pU6
gRNA4
term

FIG. 9

FIG. 10

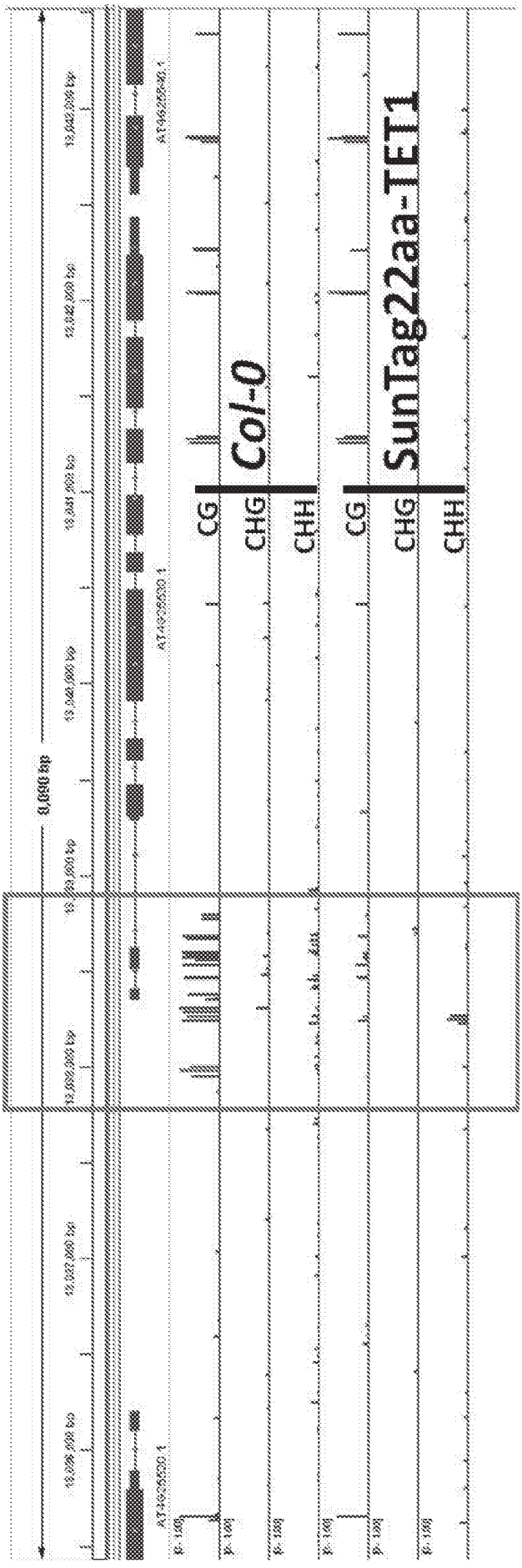


FIG. 11

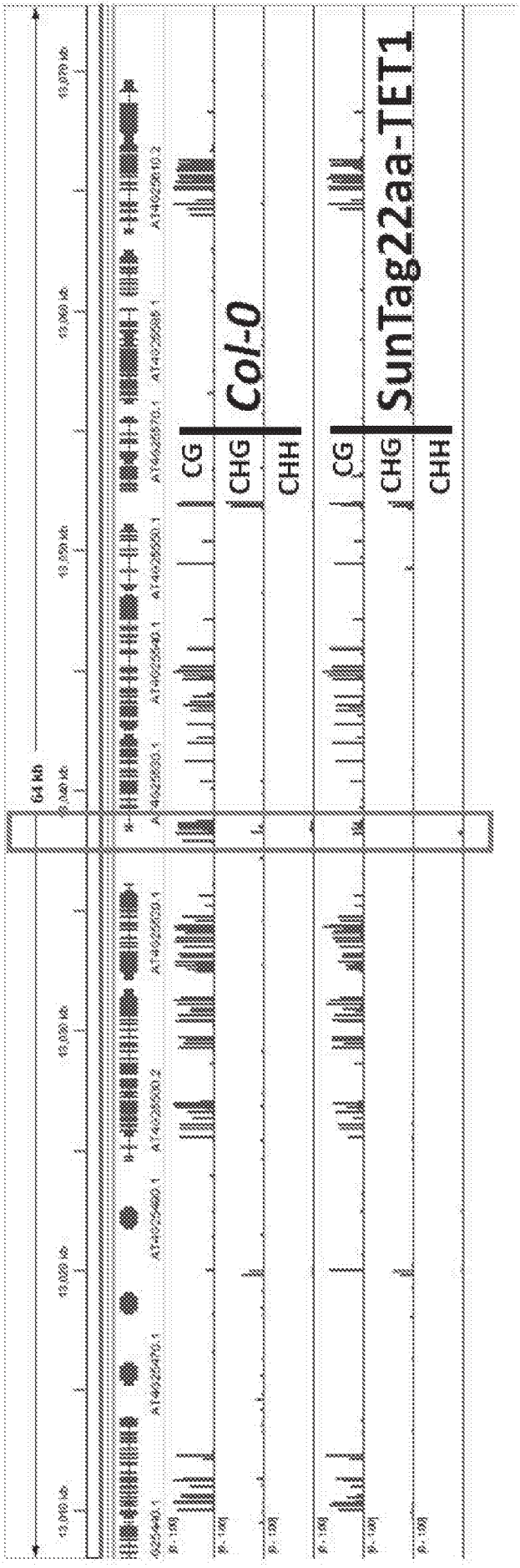


FIG. 12

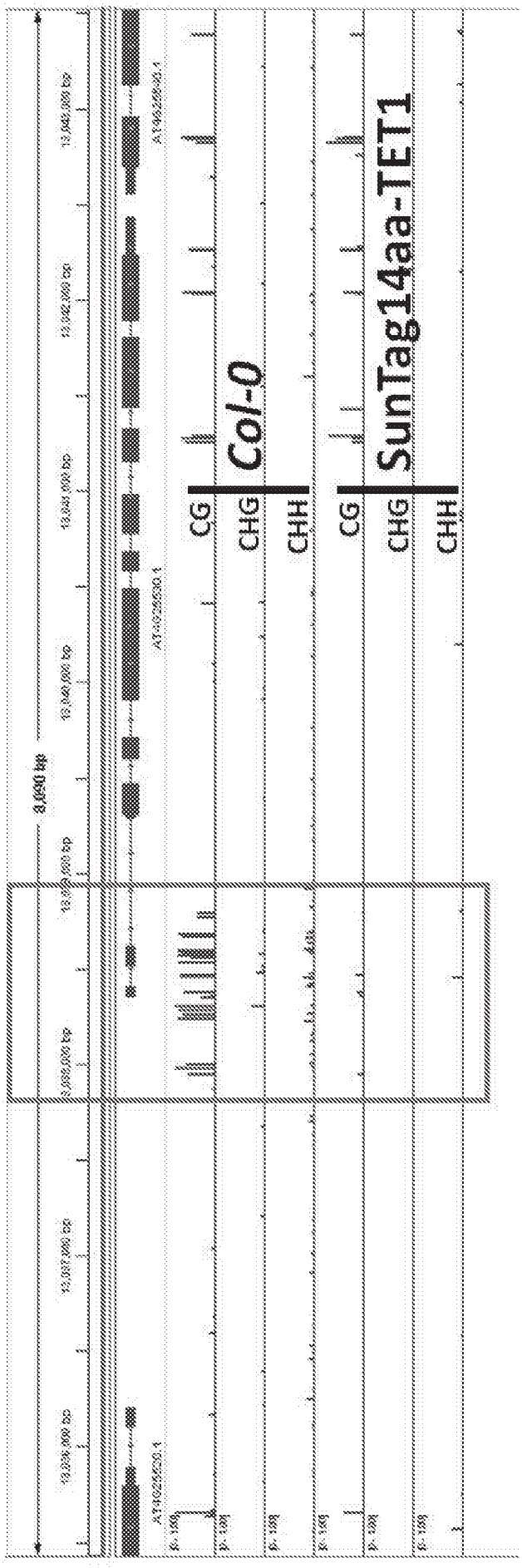
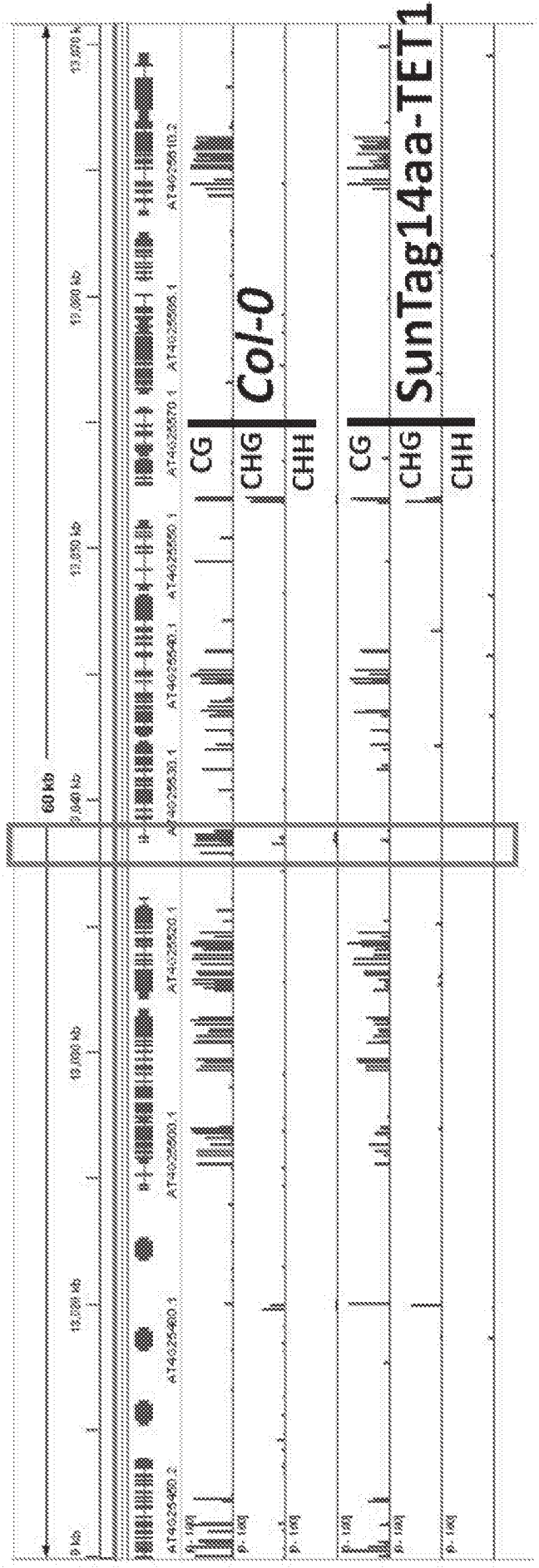


FIG. 13



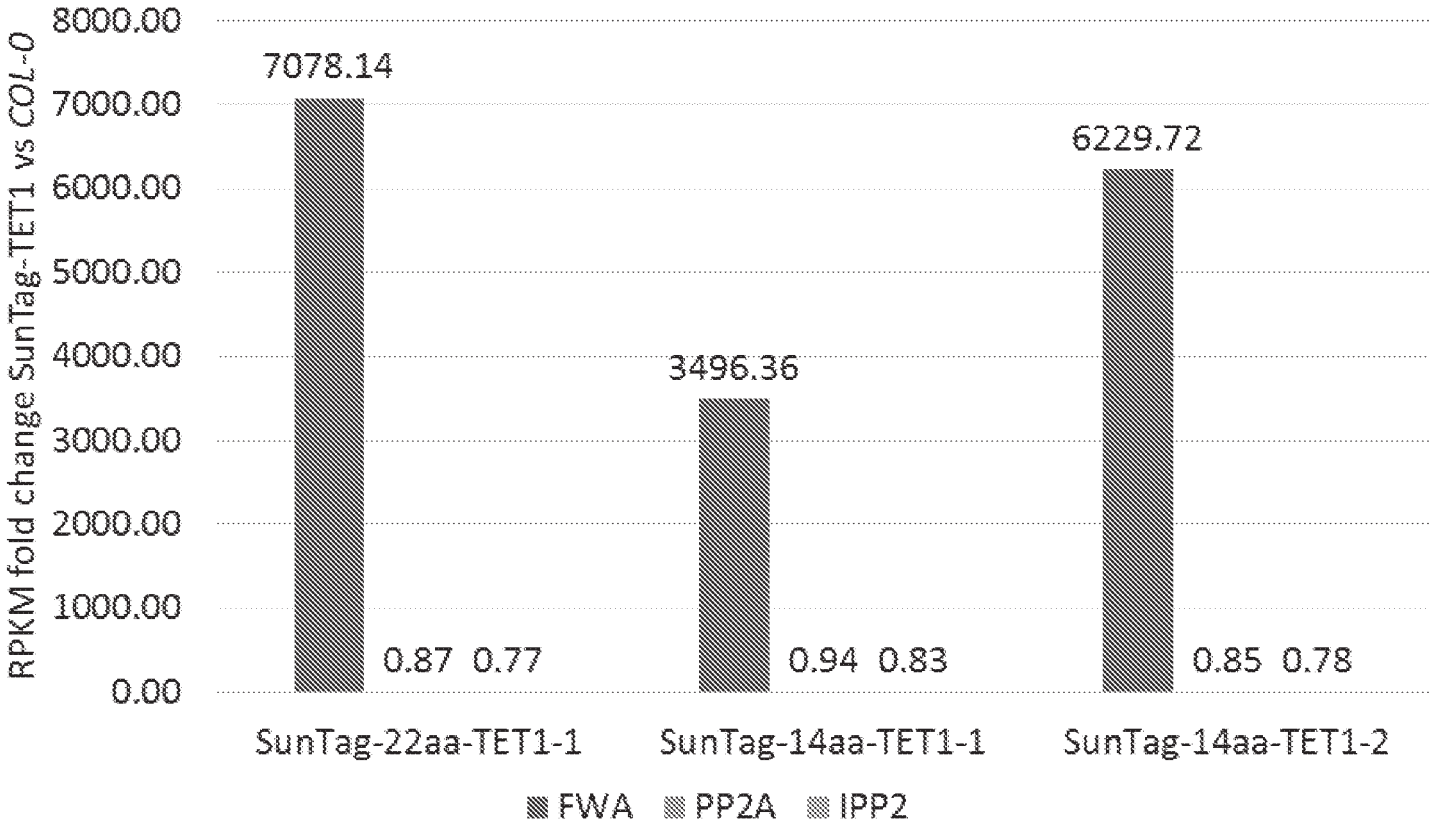
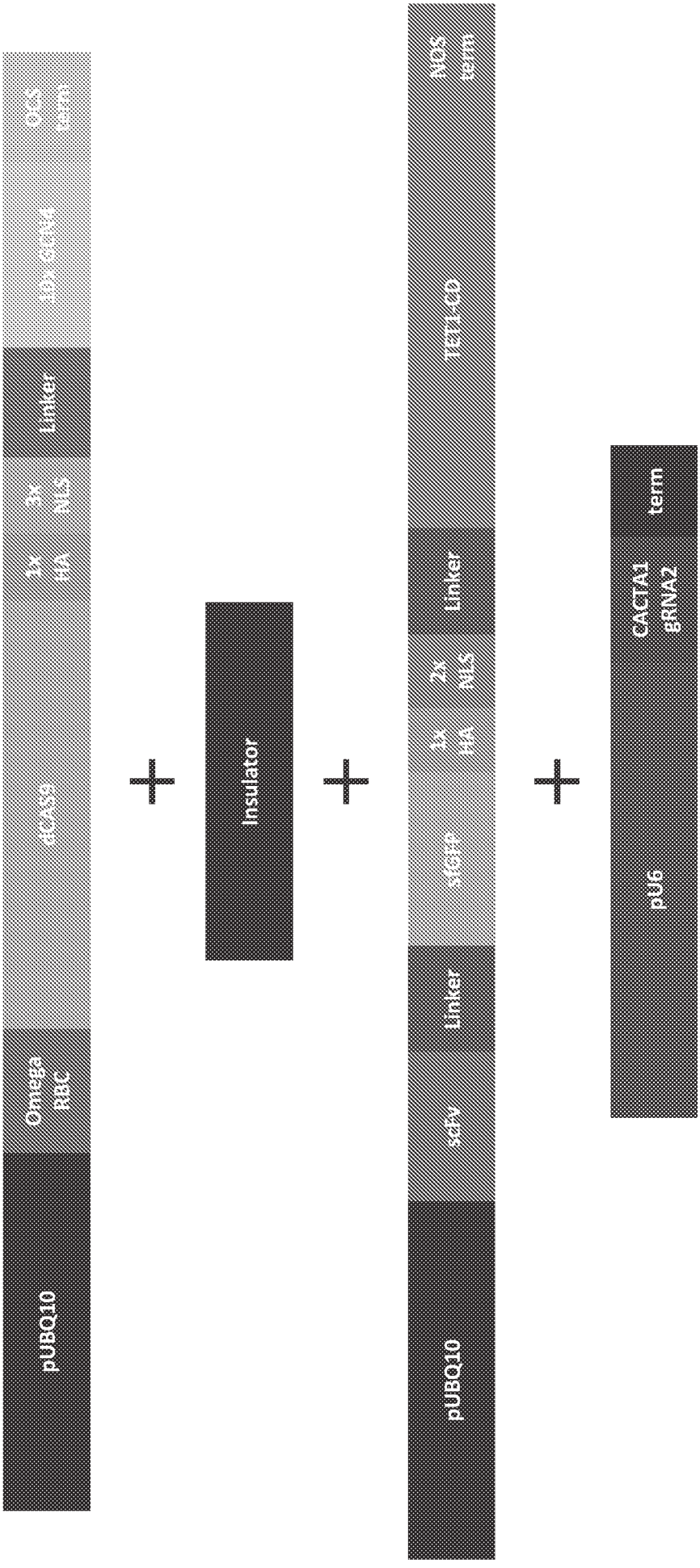

RPKM fold change SunTag-TET1 vs COL-0
8000.00
7000.00
6000.00
5000.00
4000.00
3000.00
2000.00
1000.00
0.00
7078.14
0.87
0.77
3496.36
0.94
0.83
6229.72
0.85
0.78
SunTag-22aa-TET1-1
SunTag-14aa-TET1-1
SunTag-14aa-TET1-2
FWA
PP2A
IPP2

FIG. 14

FIG. 15


pUBQ10
Omega RBC
dCAS9
3x HA
3x NLS
Linker
NOS term
+
Insulator
+
pUBQ10
sgRV
Linker
sgRNA
3x HA
3x NLs
Linker
U6-1-1-10
NOS term
+
pU6
CACTA1 tRNA2
term

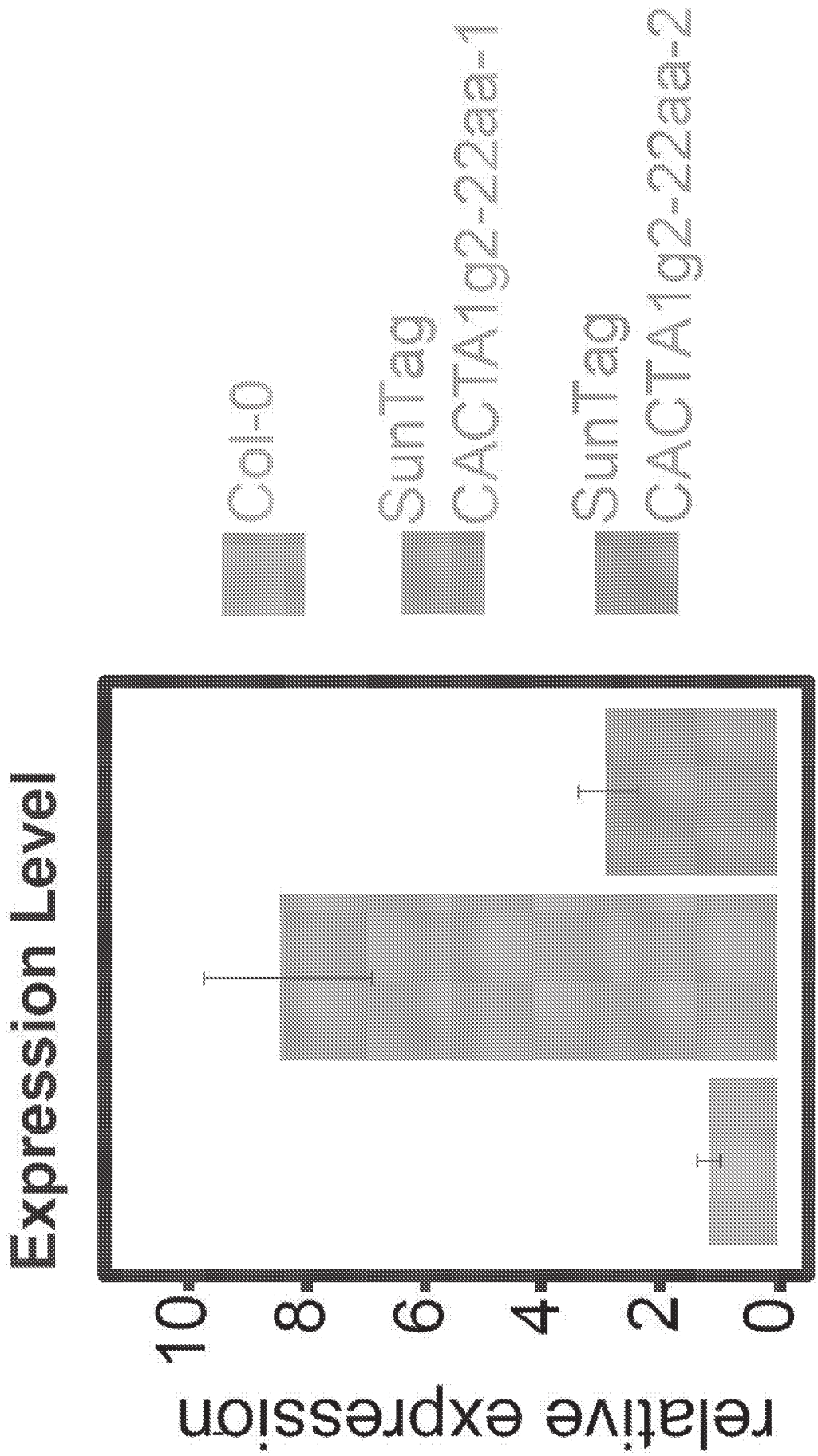

Expression Level
relative expression
0
2
4
6
8
10
Col-0
SunTag CACTA1g2-22aa-1
SunTag CACTA1g2-22aa-2

FIG. 16

FIG. 17

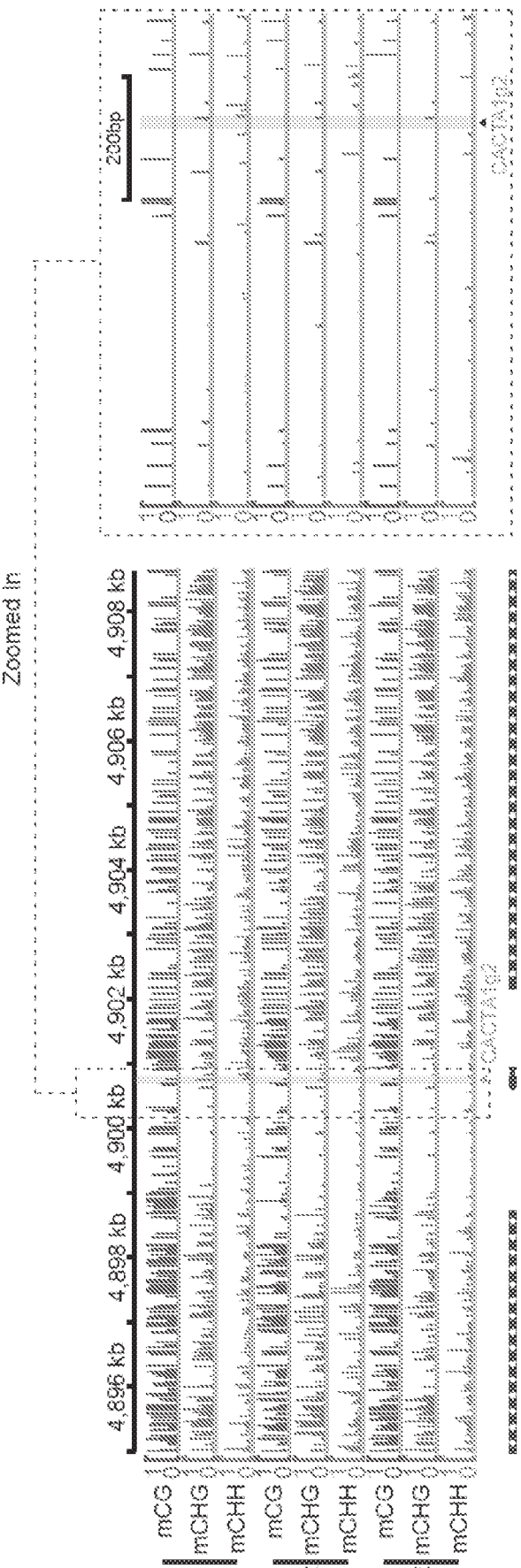

Zoomed in
4,896 kb
4,898 kb
4,900 kb
4,902 kb
4,904 kb
4,906 kb
4,908 kb
200bp
mCG
mCHG
mCHH
Col-0
SunTag CACTA1g2 22aa-1
SunTag CACTA1g2 22aa-2
AT2G12195
AT2G12200
AT2G12210 (CACTA1)
CACTA1g2

FIG. 18

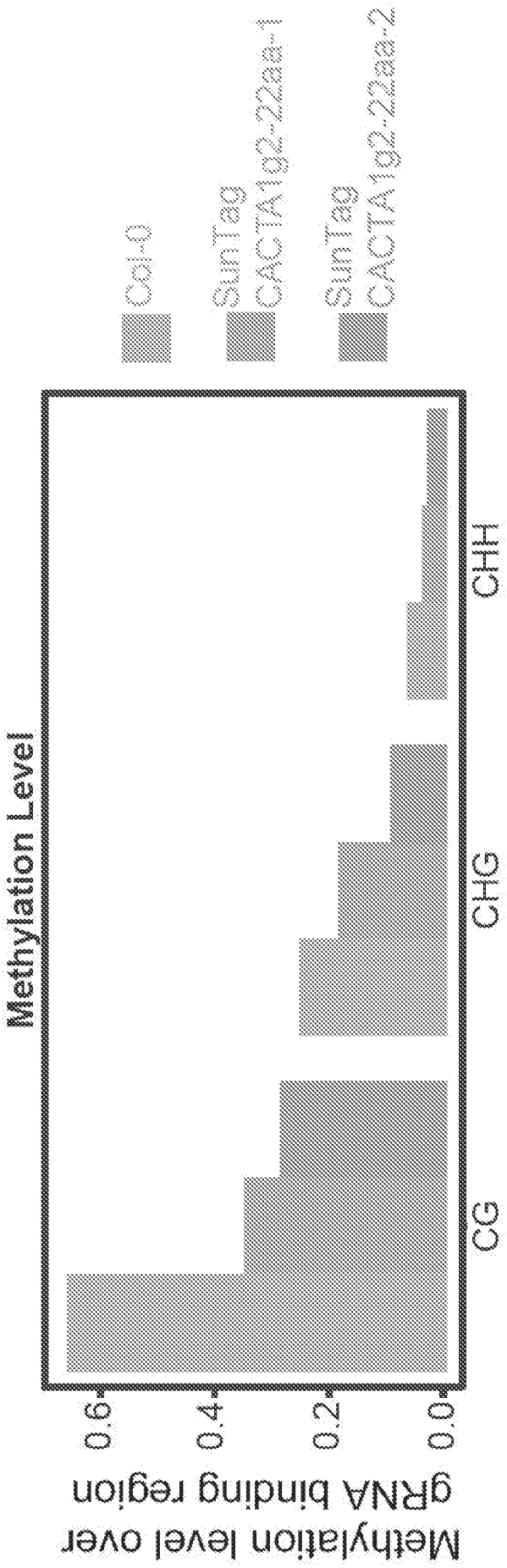

Col-0
SunTag CACTA1g2-22aa-1
SunTag CACTA1g2-22aa-2
Methylation Level
0.6
0.4
0.2
0.0
CG
CHG
CHH
Methylation level over gRNA binding region

FIG. 19

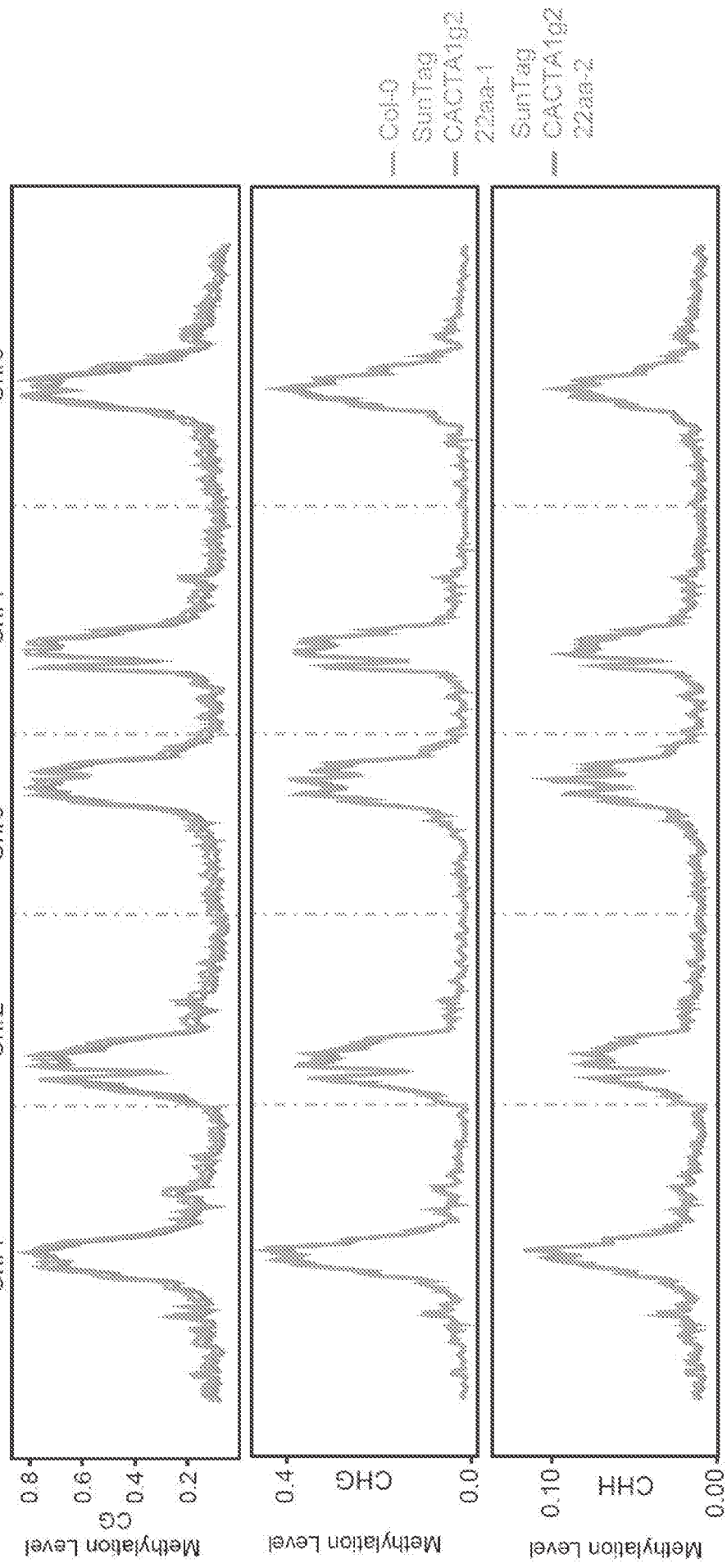
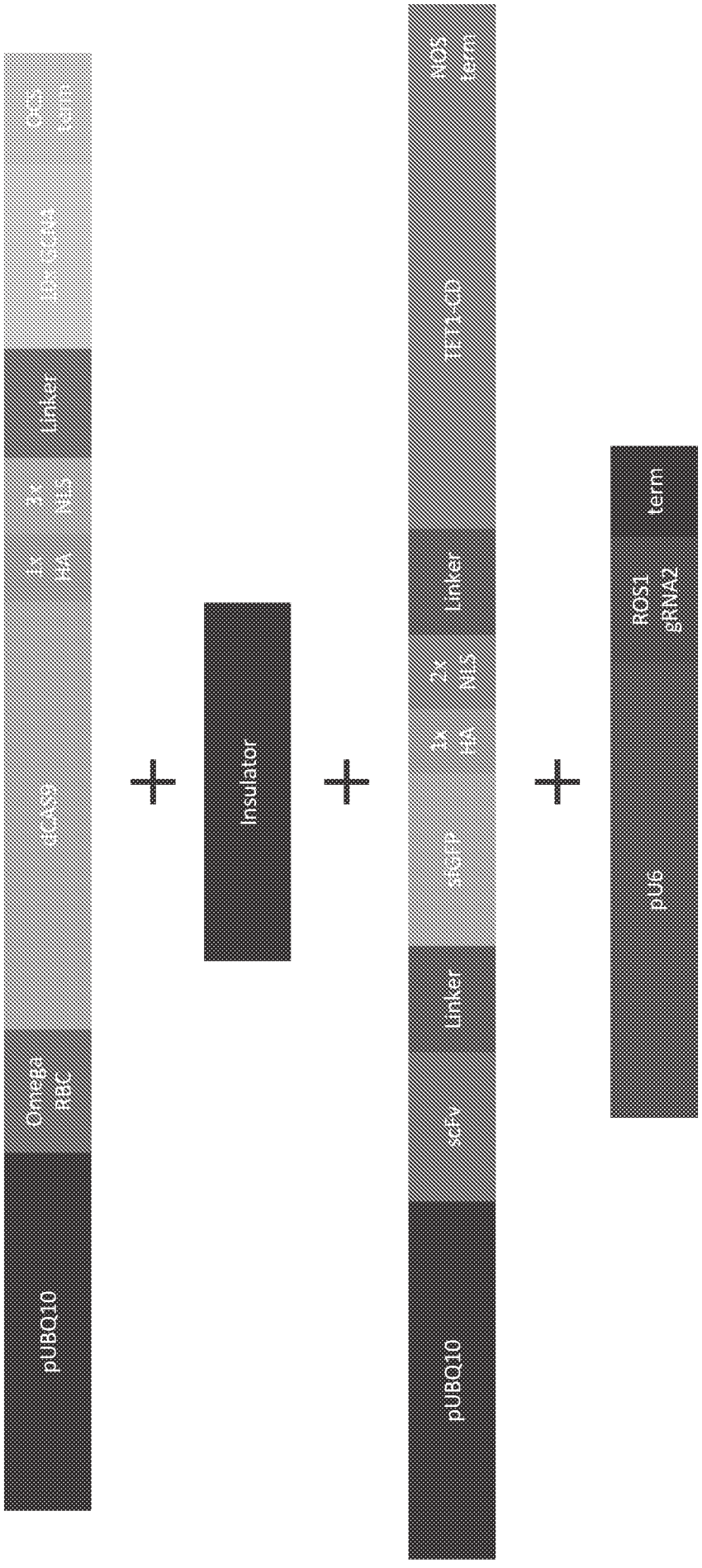

Col-0
SunTag
CACTA1g2 22as-1
SunTag
CACTA1g2 22as-2
Chr1
Chr2
Chr3
Chr4
Chr5
CG
CHG
CHH
Methylation Level
0.8
0.6
0.4
0.2
0.4
0.0
0.10
0.00

FIG. 20


pUBQ10
Omega
hSAS9
1x HA
3x NLS
linker
OsU3 terminator
+
Insulator
+
pUBQ10
SgRV
linker
sfGFP
3x HA
2x NLS
linker
TT11420
MOS term
+
pU6
ROS1 gRNA2
term

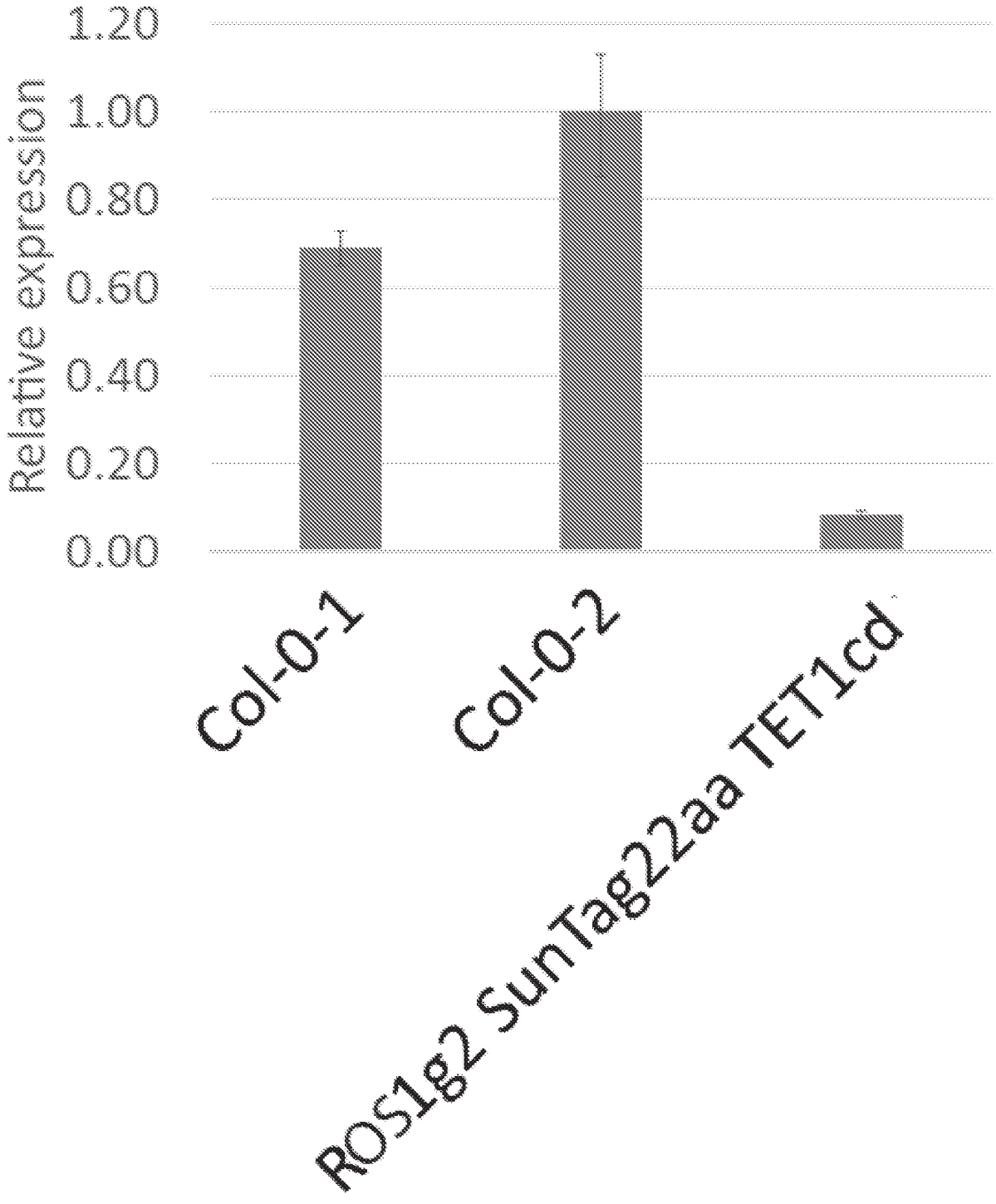

Relative expression
1.20
1.00
0.80
0.60
0.40
0.20
0.00
Col-0-1
Col-0-2
ROS1g2 SunTag22aa TET1cd

FIG. 21

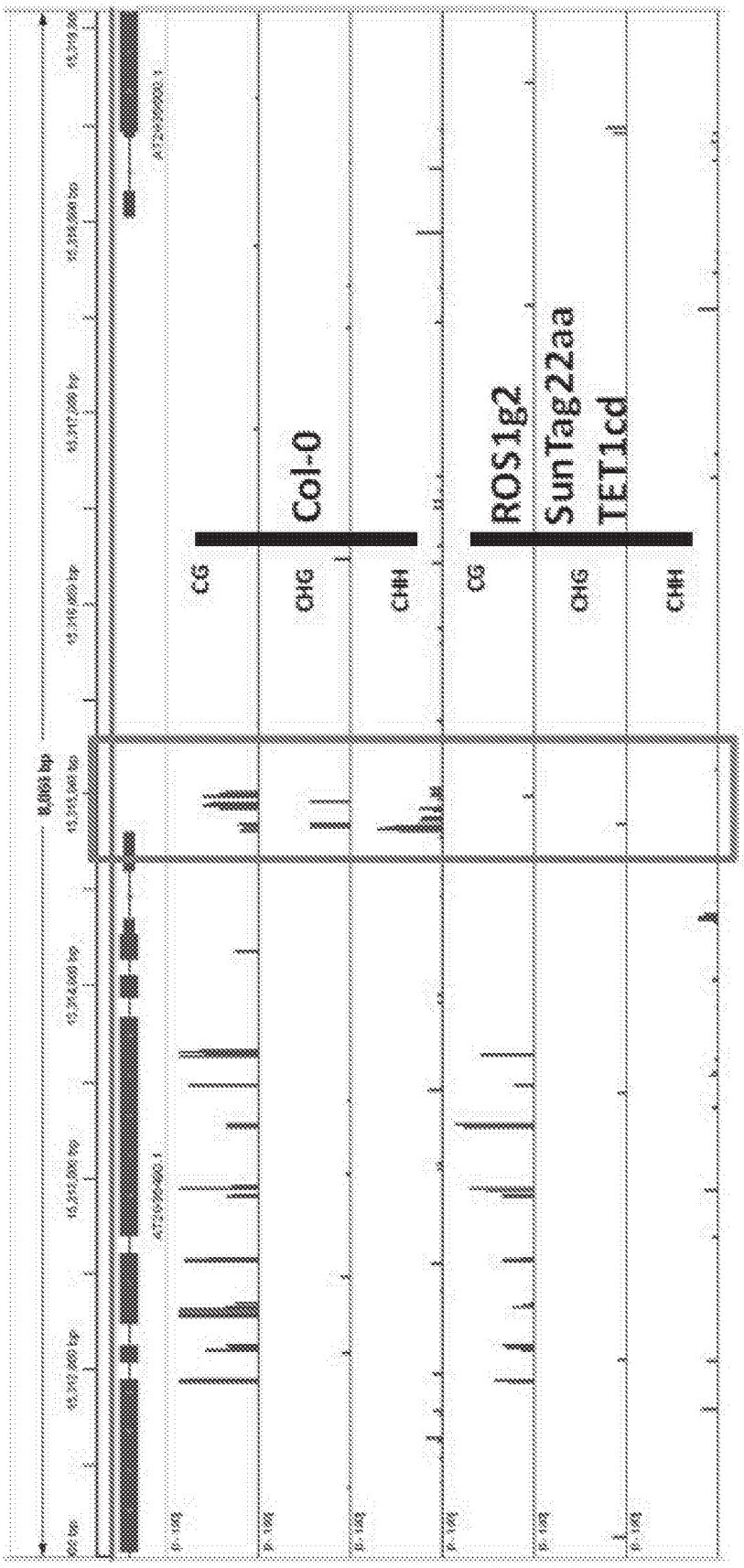


FIG. 22

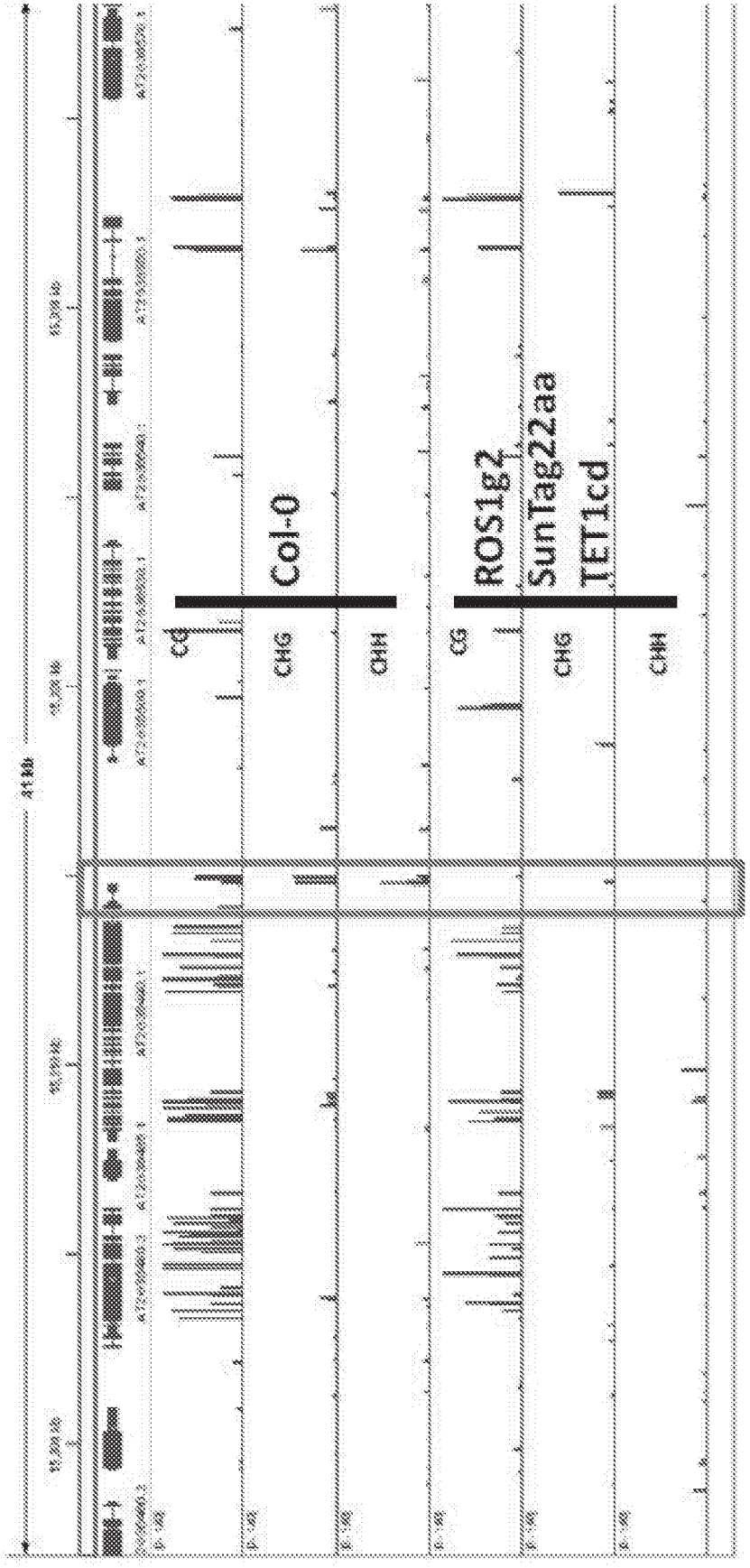


FIG. 23

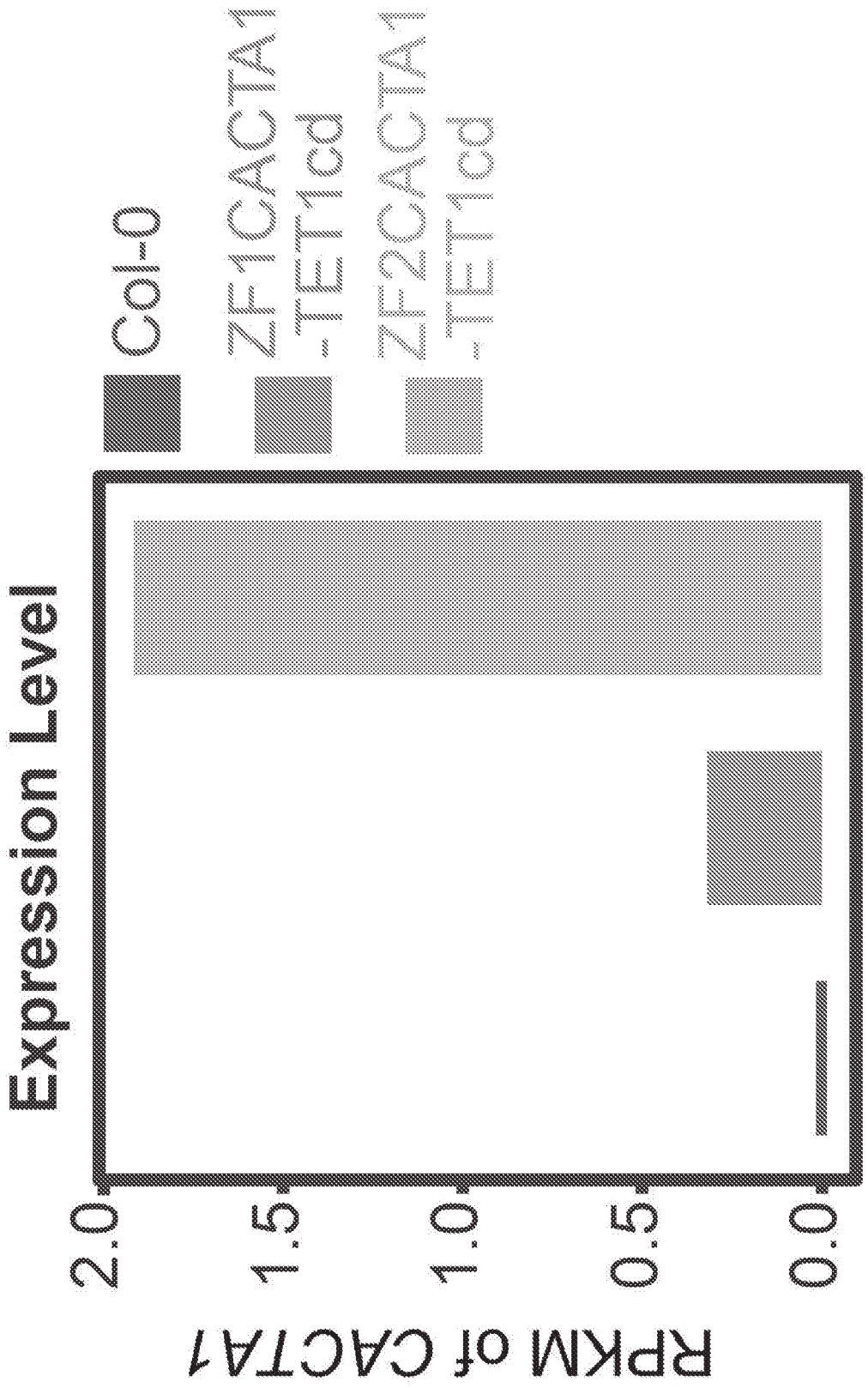

Col-0
ZF1CACTA1 -TET1cd
ZF2CACTA1 -TET1cd
Expression Level
RPKM of CACTA1
2.0
1.5
1.0
0.5
0.0

FIG. 24

FIG. 25

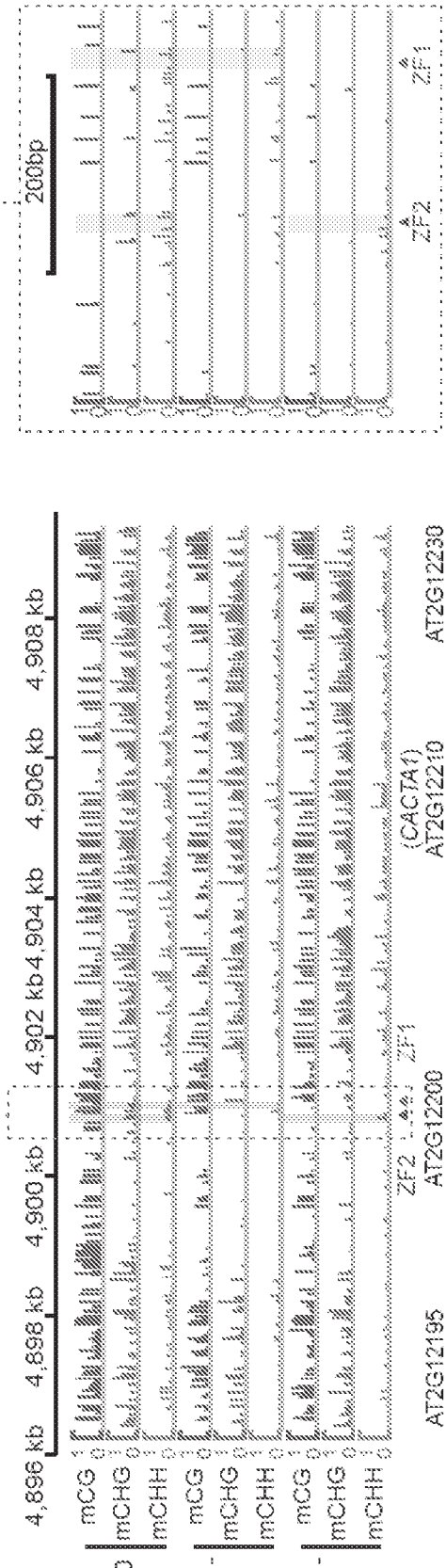

Zoomed In
200bp
4,896 kb
4,898 kb
4,900 kb
4,902 kb
4,904 kb
4,906 kb
4,908 kb
mCG
mCHG
mCHH
Col-0
ZF1CACTA1-TET1cd
ZF2CACTA1-TET1cd
ZF2
ZF1
AT2G12195
AT2G12200
(CACTA1)
AT2G12210
AT2G12230

FIG. 26

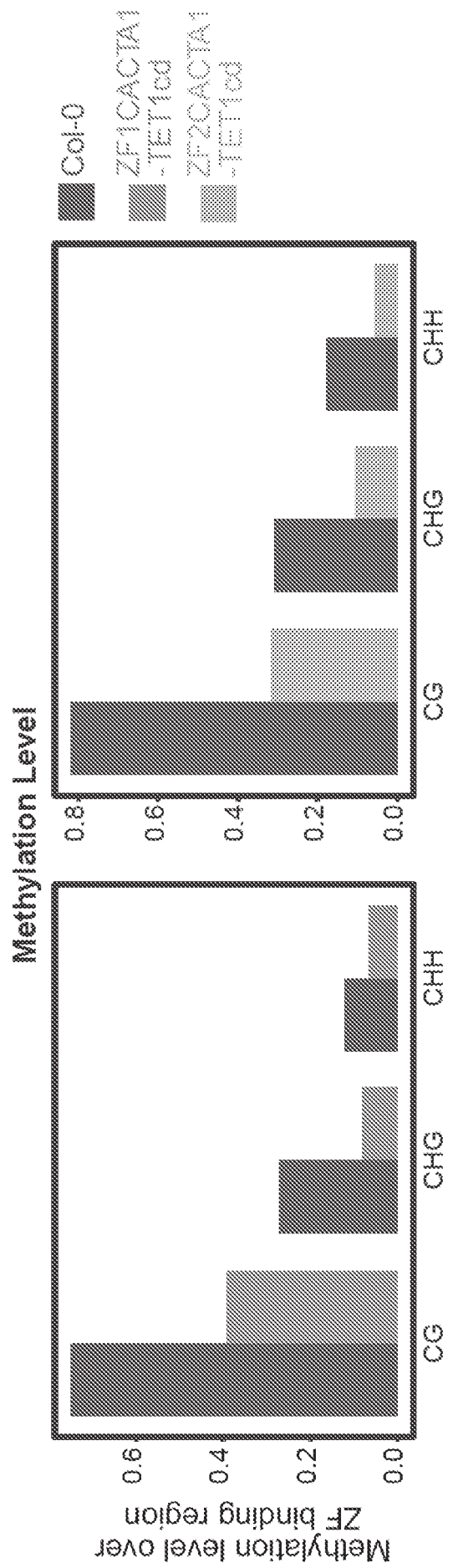
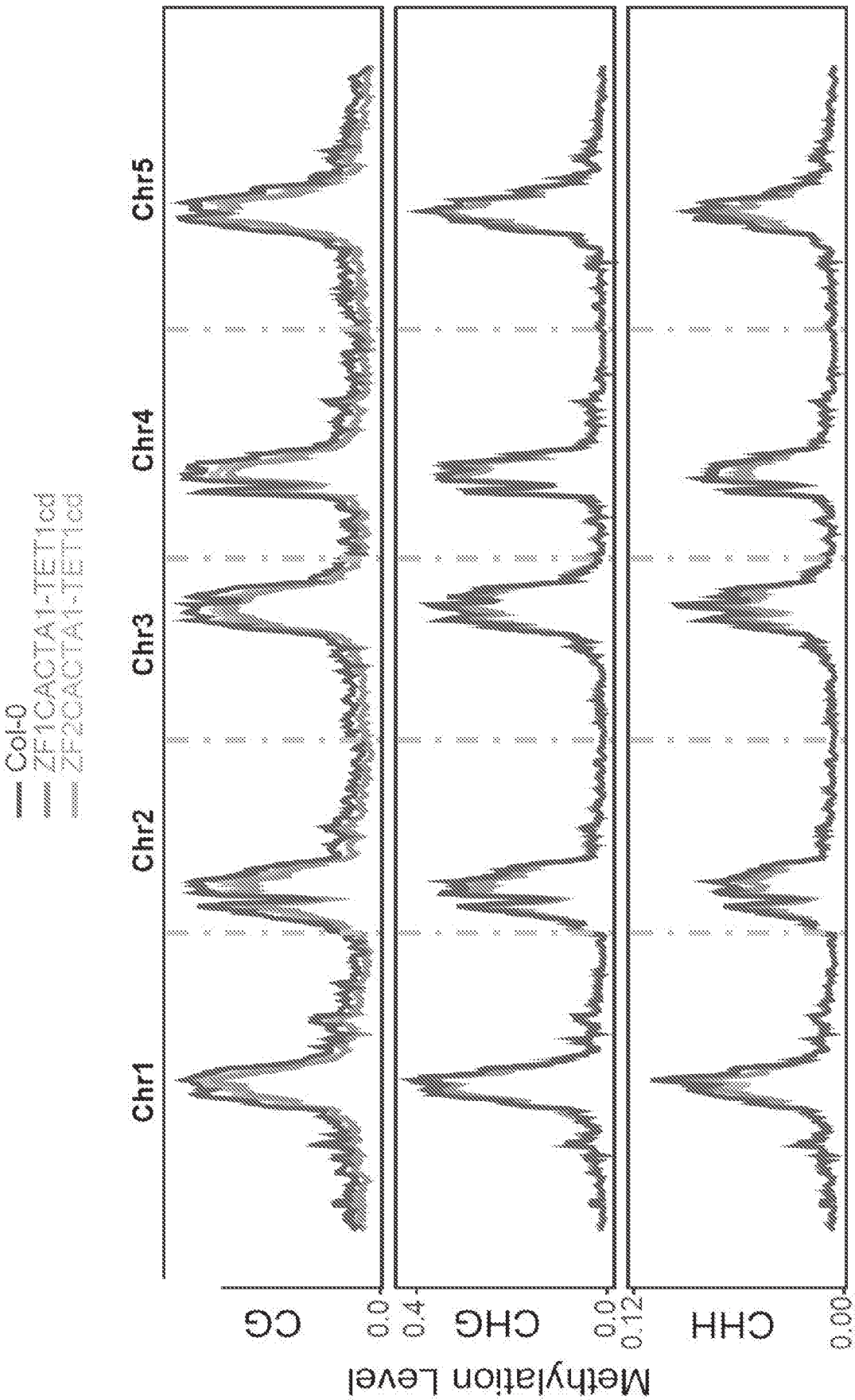

Col-0
ZF1CACTA1 -TET1cd
ZF2CACTA1 -TET1cd
Methylation Level
0.0
0.2
0.4
0.6
0.8
CG
CHG
CHH
Methylation level over ZF binding region
0.0
0.2
0.4
0.6
CG
CHG
CHH

FIG. 27


Col-0
ZF1CACTA1-TET1cd
ZF2CACTA1-TET1cd
Chr1
Chr2
Chr3
Chr4
Chr5
CG
CHG
CHH
0.0
0.4
0.0
0.12
0.00
Methylation Level

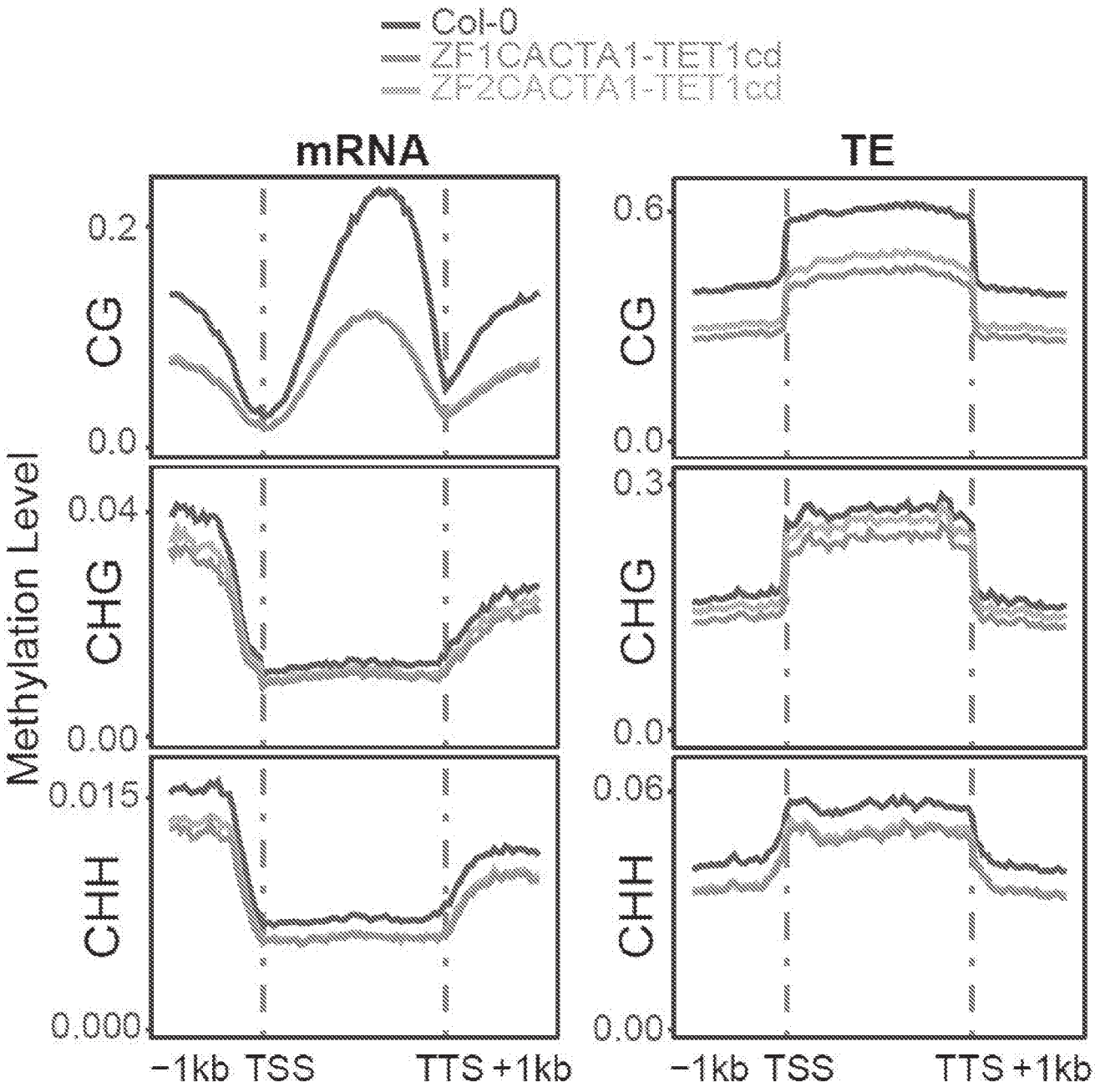

Col-0
ZF1CACTA1-TET1cd
ZF2CACTA1-TET1cd
mRNA
TE
Methylation Level
CG
CHG
CHH
0.2
0.0
0.04
0.00
0.015
0.000
0.6
0.3
0.06
−1kb TSS
TTS +1kb

FIG. 28

FIG. 29

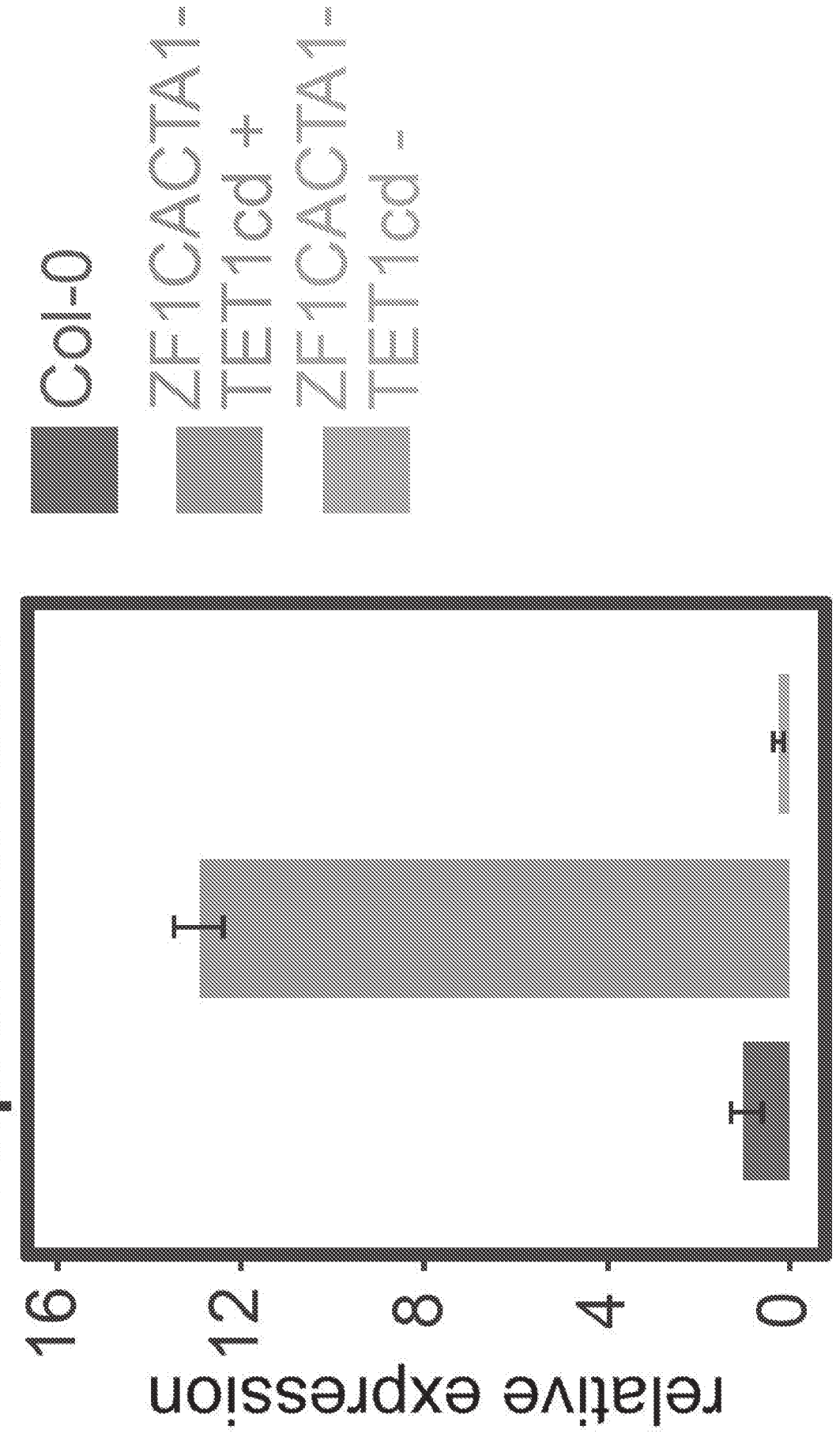

Expression Level
relative expression
16
12
8
4
0
Col-0
ZF1CACTA1-TET1cd+
ZF1CACTA1-TET1cd-

FIG. 30

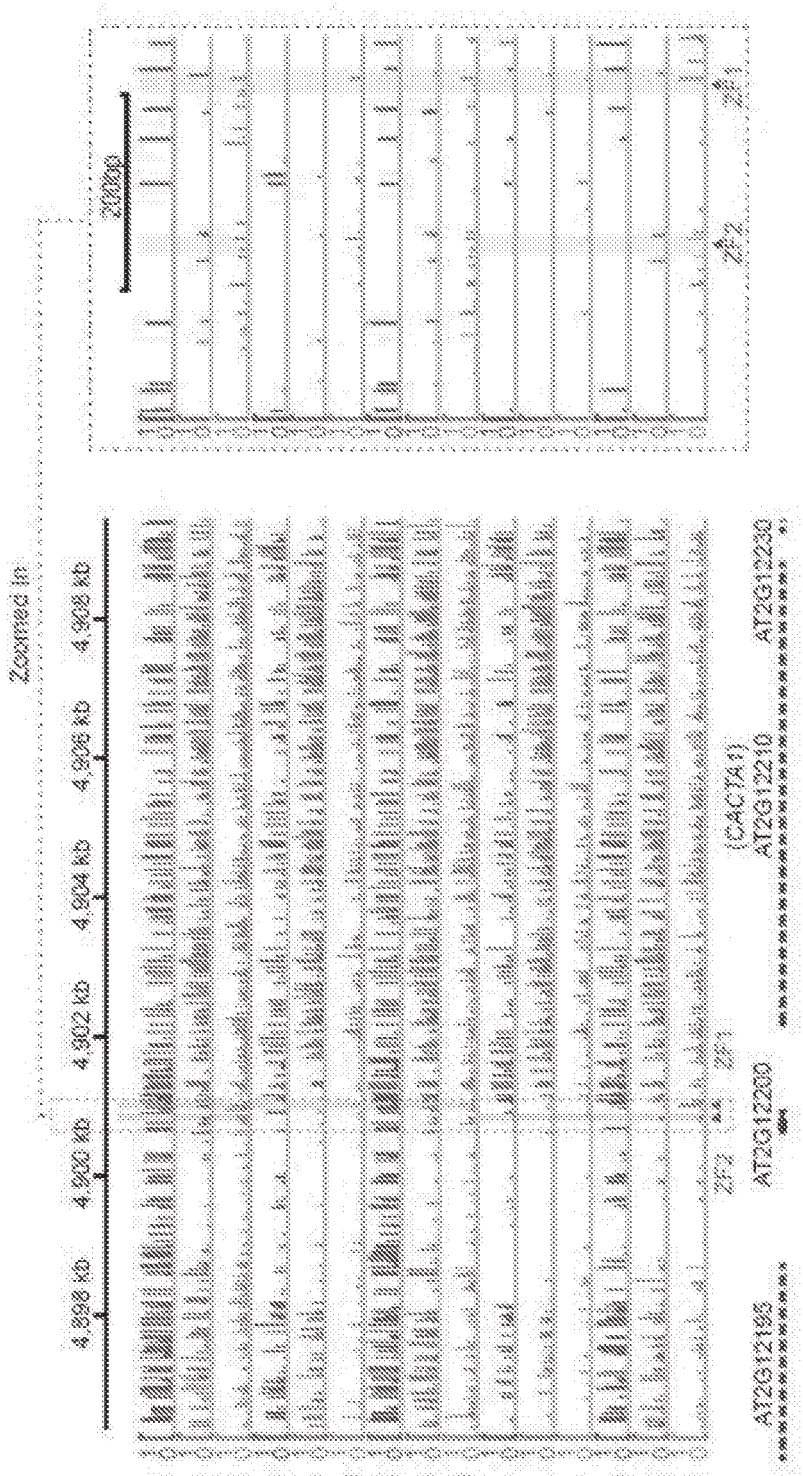

Zoomed in
4,898 kb
4,900 kb
4,902 kb
4,904 kb
4,906 kb
4,908 kb
200bp
ZF2
ZF1
AT2G12195
AT2G12200
AT2G12210
AT2G12230
(CACTA1)
Col-0
ZF1CACTA1-TET1cd +
ZF1CACTA1-TET1cd -
ZF2CACTA1-TET1cd +
ZF2CACTA1-TET1cd -
mCG
mCHG
mCHH

FIG. 31

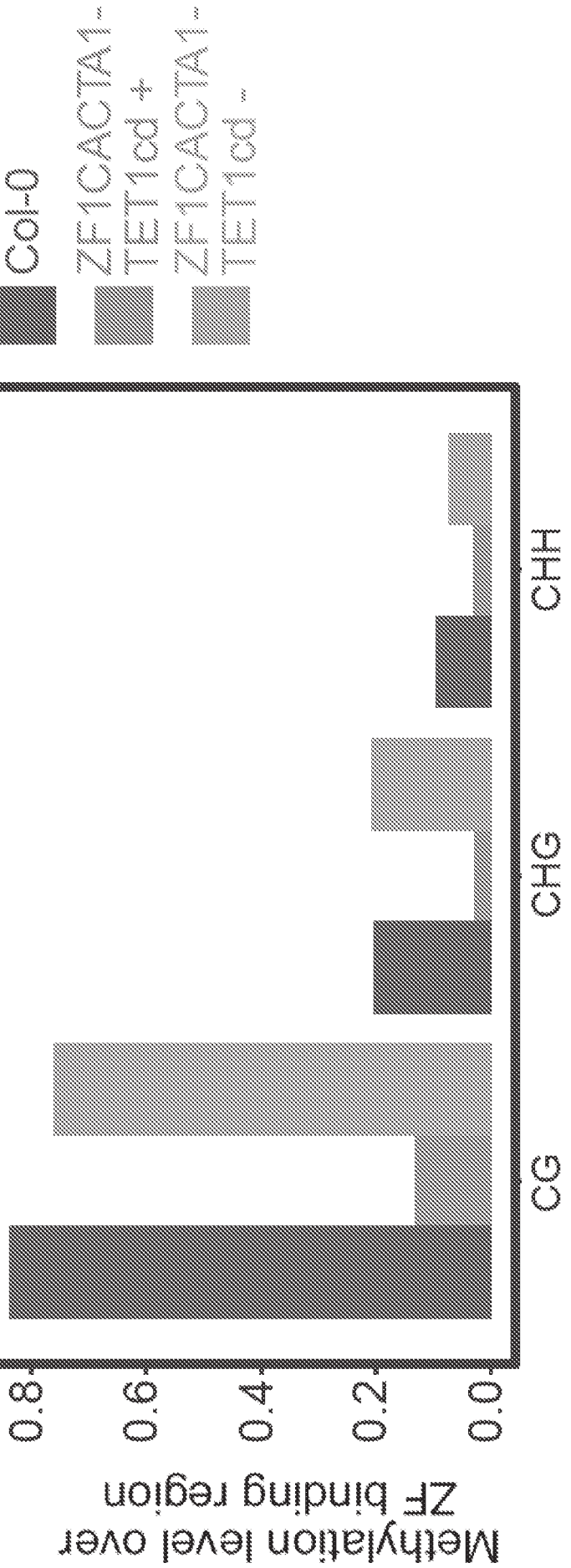
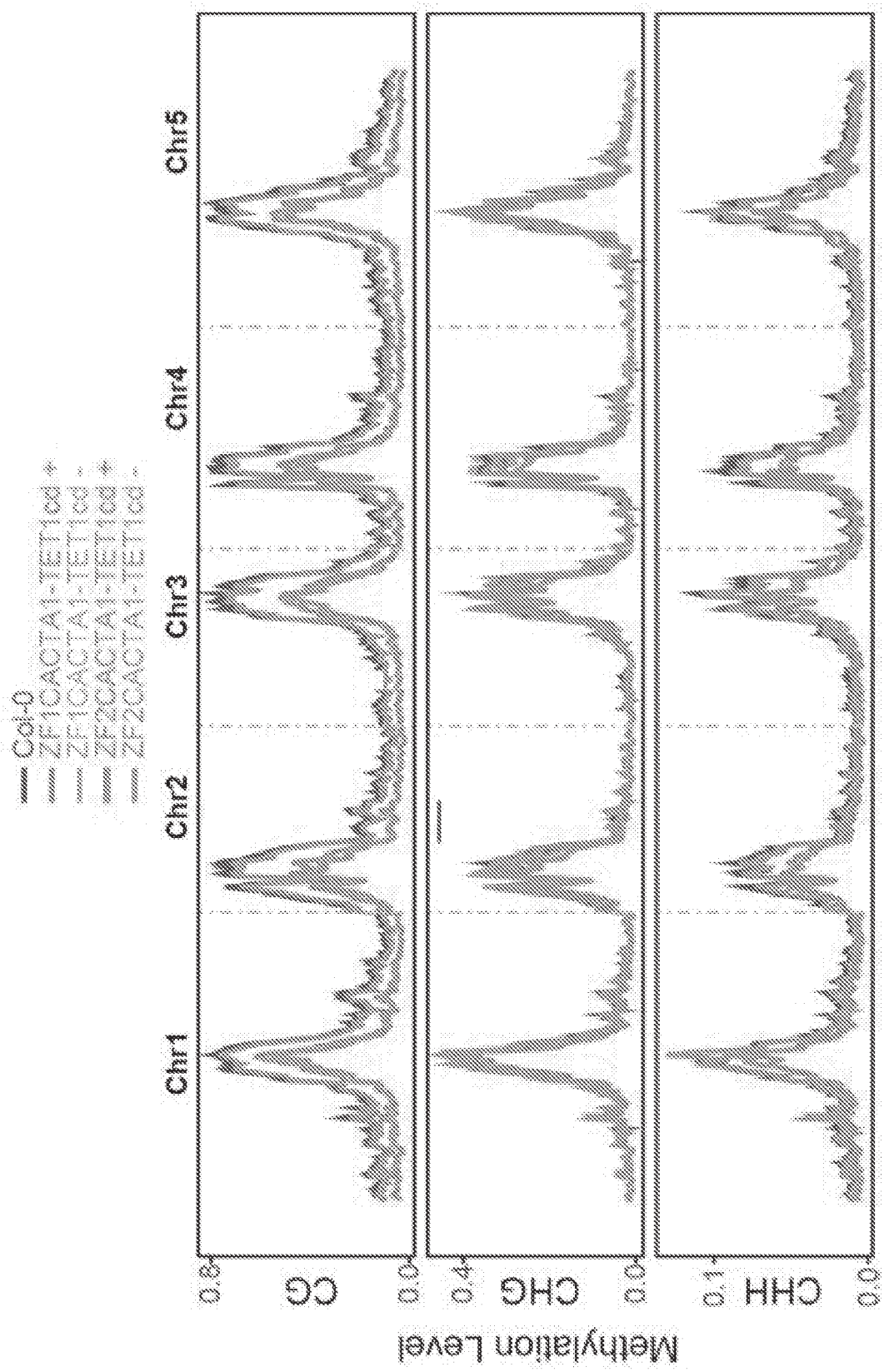

Methylation level over
ZF binding region
Methylation Level
0.0
0.2
0.4
0.6
0.8
CG
CHG
CHH
Col-0
ZF1CACTA1-
TET1cd +
ZF1CACTA1-
TET1cd -

FIG. 32


Col-0
ZF1CACTA1-TET1cd +
ZF1CACTA1-TET1cd -
ZF2CACTA1-TET1cd +
ZF2CACTA1-TET1cd -
Chr1
Chr2
Chr3
Chr4
Chr5
CG
CHG
CHH
0.6
0.0
0.4
0.0
0.1
0.0
Methylation Level

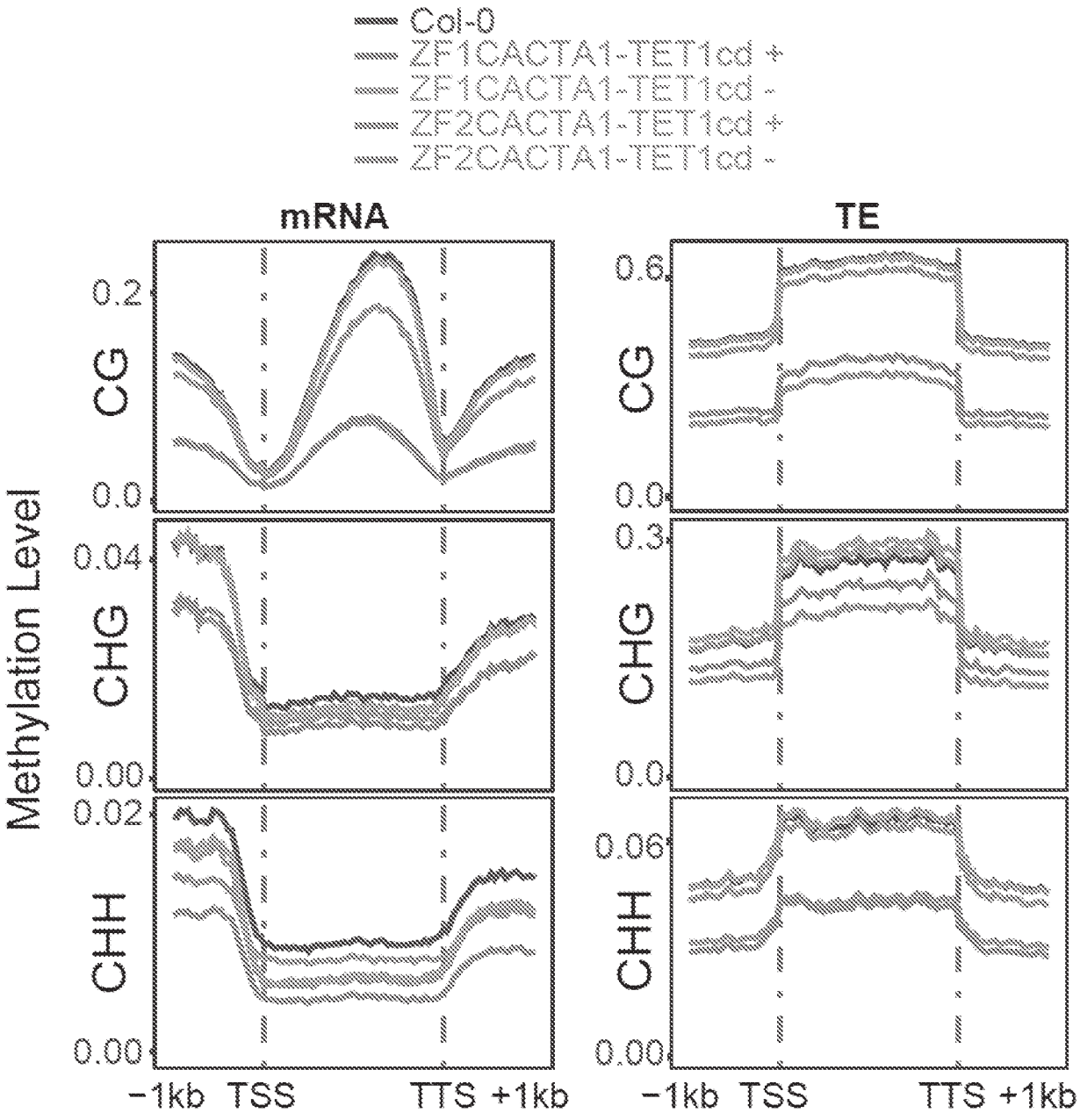

Col-0
ZF1CACTA1-TET1cd +
ZF1CACTA1-TET1cd -
ZF2CACTA1-TET1cd +
ZF2CACTA1-TET1cd -
mRNA
TE
Methylation Level
CG
CHG
CHH
0.2
0.0
0.04
0.00
0.02
0.00
0.6
0.0
0.3
0.0
0.06
0.00
−1kb TSS
TTS +1kb
−1kb TSS
TTS +1kb

FIG. 33

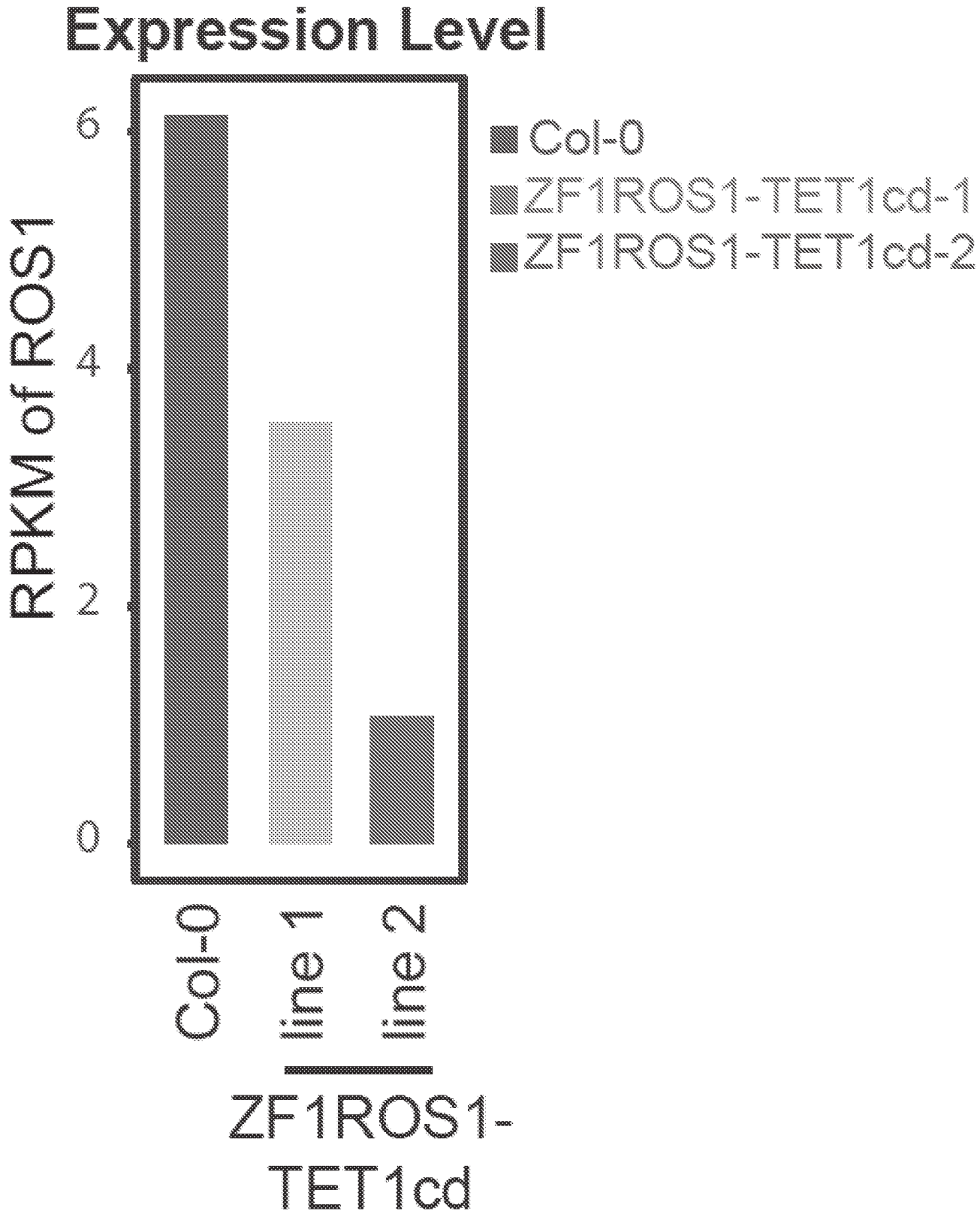

Expression Level
RPKM of ROS1
6
4
2
0
Col-0
ZF1ROS1-TET1cd-1
ZF1ROS1-TET1cd-2
Col-0
line 1
line 2
ZF1ROS1-TET1cd

FIG. 34

FIG. 35

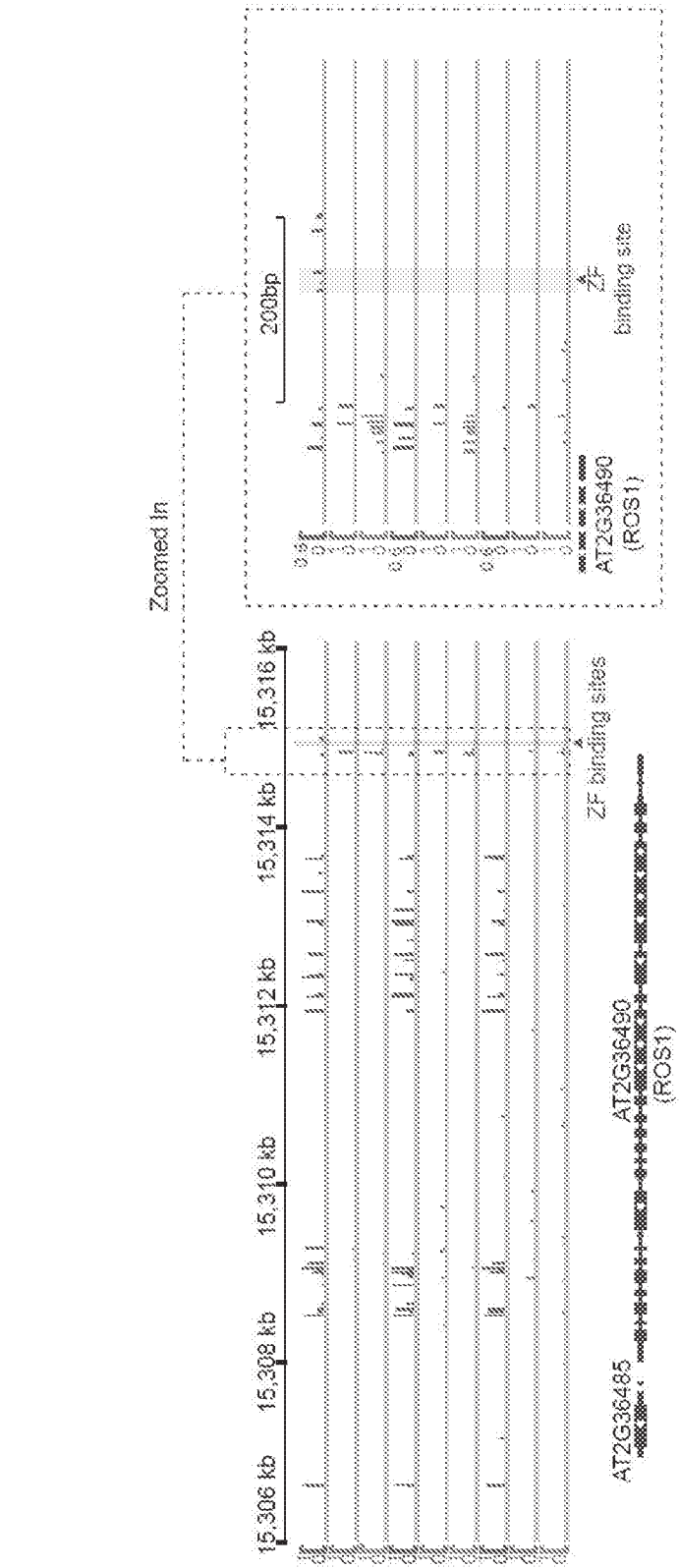

WGBS
Col-0
ZF1ROS1-TET1cd-1
ZF1ROS1-TET1cd-2
mCG
mCHG
mCHH
15,306 kb
15,308 kb
15,310 kb
15,312 kb
15,314 kb
15,316 kb
AT2G36485
AT2G36490
(ROS1)
ZF binding sites
Zoomed In
200bp
ZF
binding site
AT2G36490
(ROS1)

FIG. 36

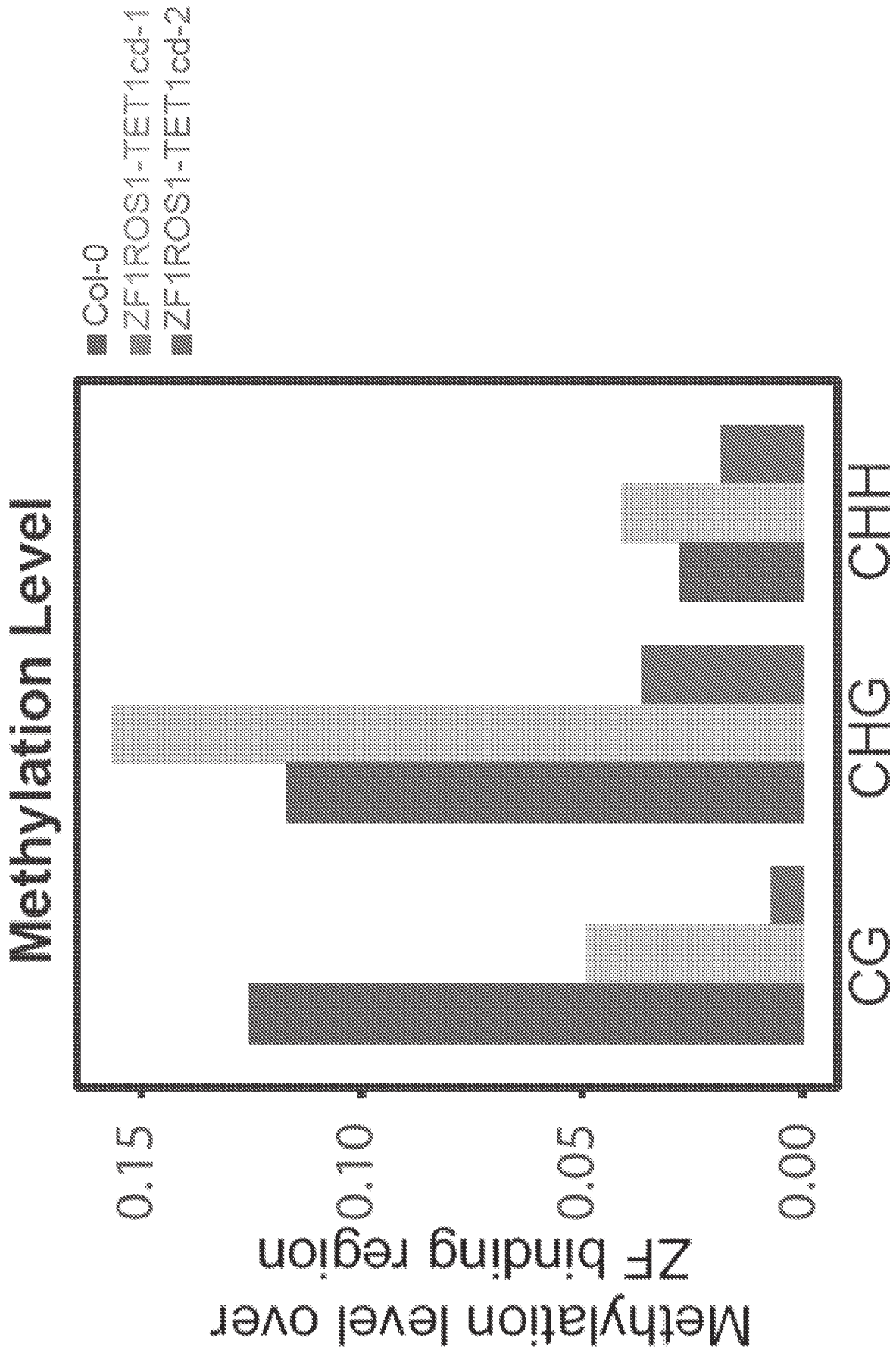
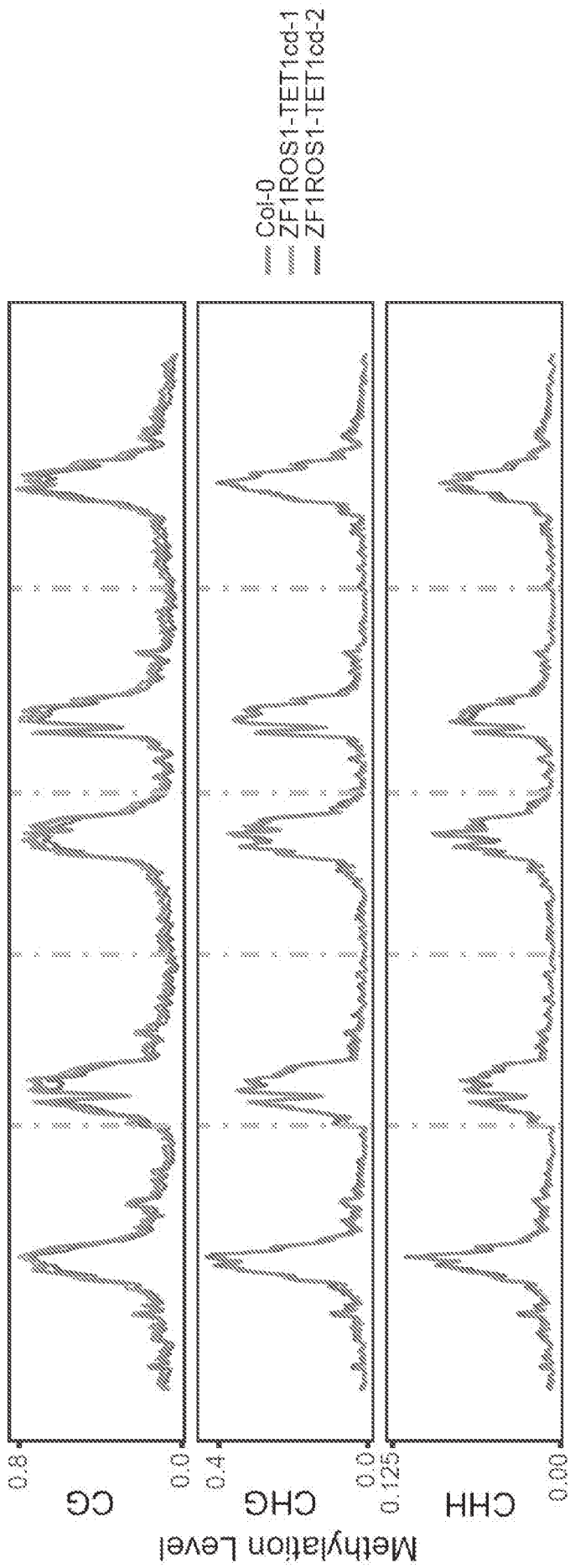

Methylation Level over ZF binding region
Methylation Level
Col-0
ZF1ROS1-TET1cd-1
ZF1ROS1-TET1cd-2
0.15
0.10
0.05
0.00
CG
CHG
CHH

FIG. 37


Col-0
ZF1ROS1-TET1cd-1
ZF1ROS1-TET1cd-2
Chr1
Chr2
Chr3
Chr4
Chr5
CG
CHG
CHH
0.8
0.0
0.4
0.0
0.125
0.00
Methylation Level

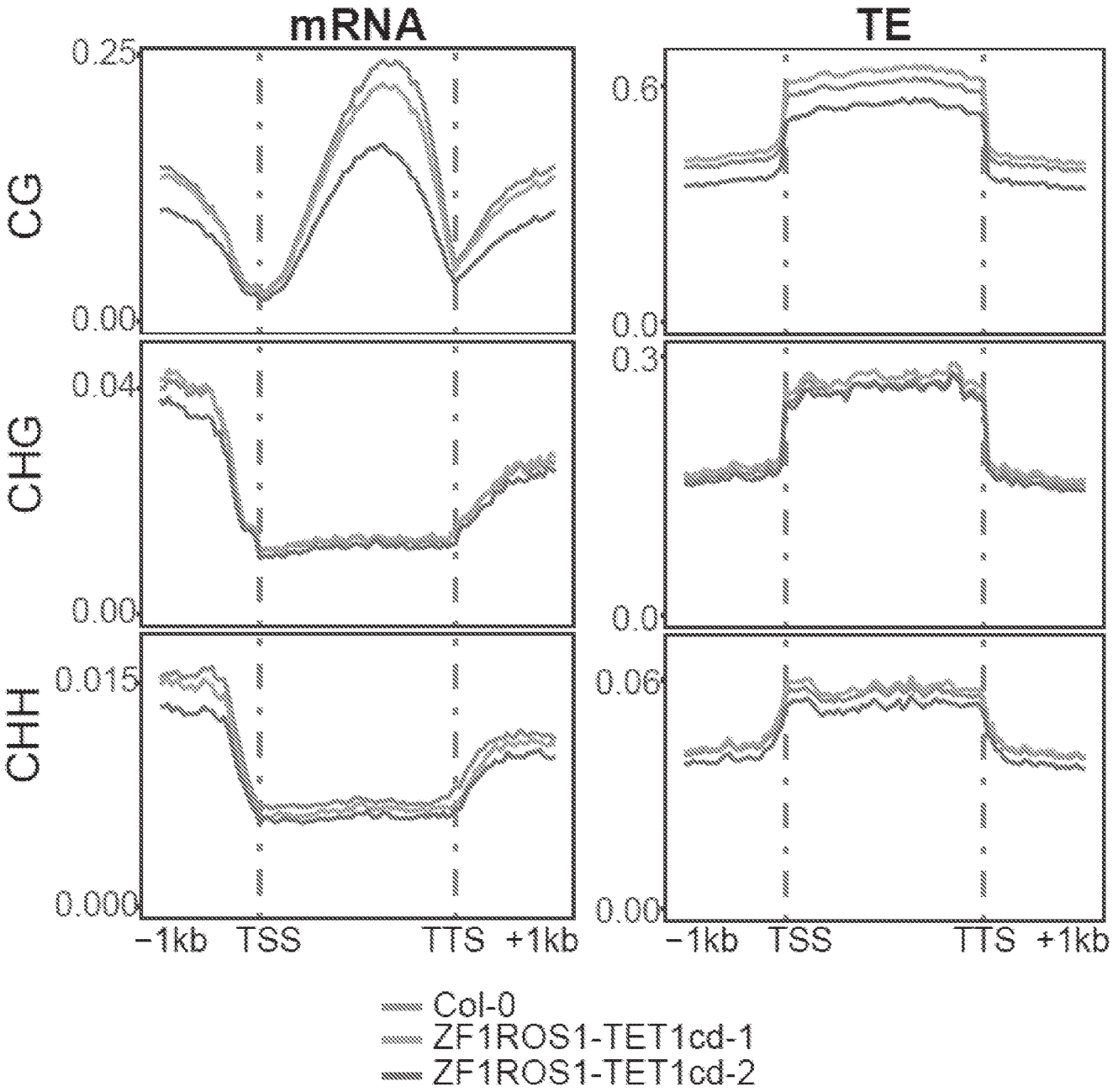

mRNA
TE
CG
CHG
CHH
0.25
0.00
0.6
0.0
0.04
0.00
0.3
0.0
0.015
0.000
0.06
0.00
−1kb TSS TTS +1kb
−1kb TSS TTS +1kb
Col-0
ZF1ROS1-TET1cd-1
ZF1ROS1-TET1cd-2

FIG. 38

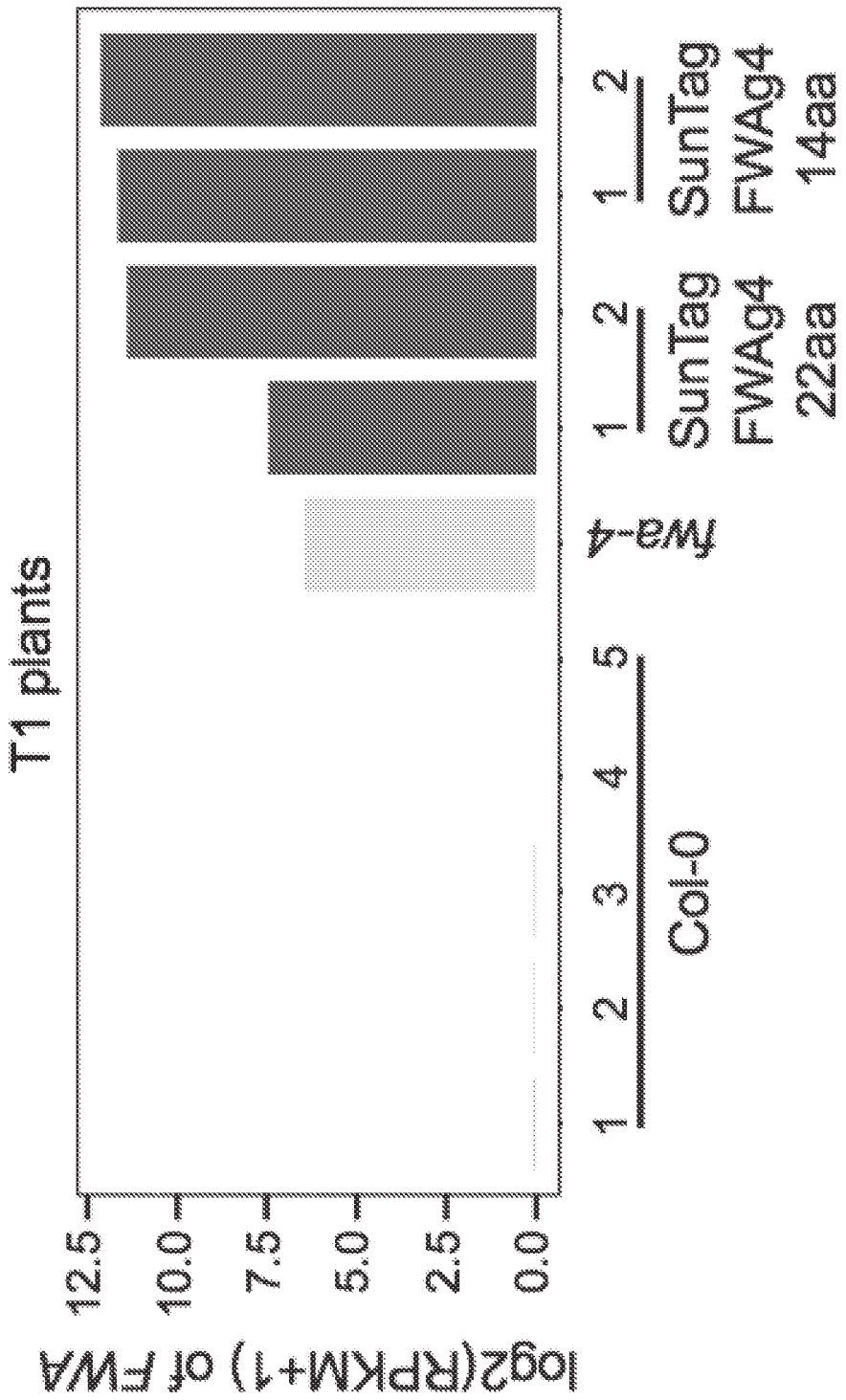

log2(RPKM+1) of FWA
12.5
10.0
7.5
5.0
2.5
0.0
T1 plants
Col-0
1 2 3 4 5
fwa-4
1 2 SunTag FWAg4 22aa
1 2 SunTag FWAg4 14aa

FIG. 39

FIG. 40

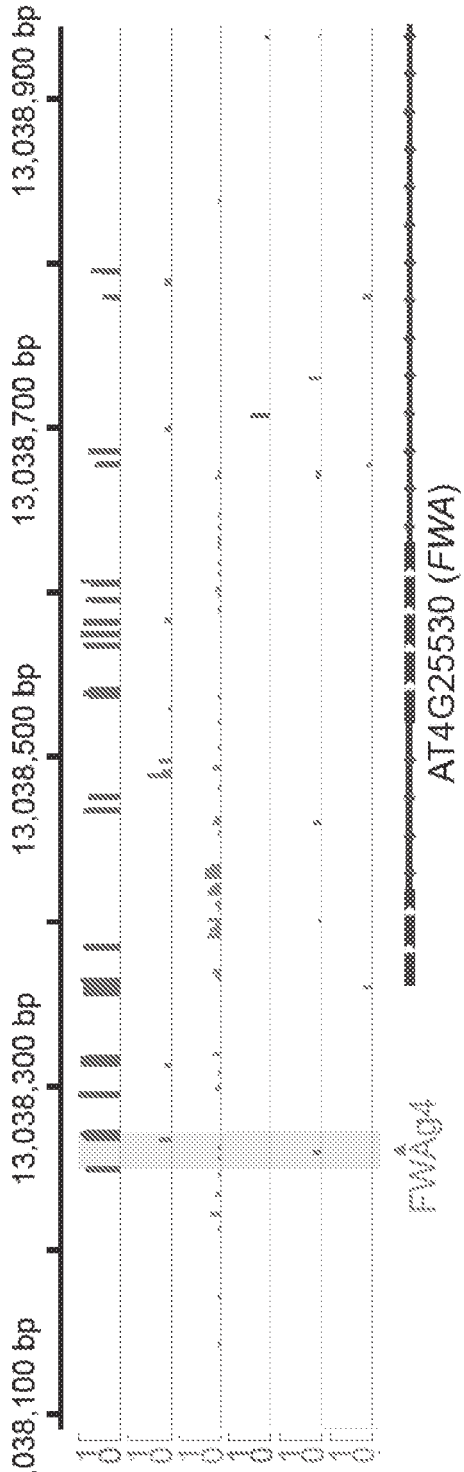
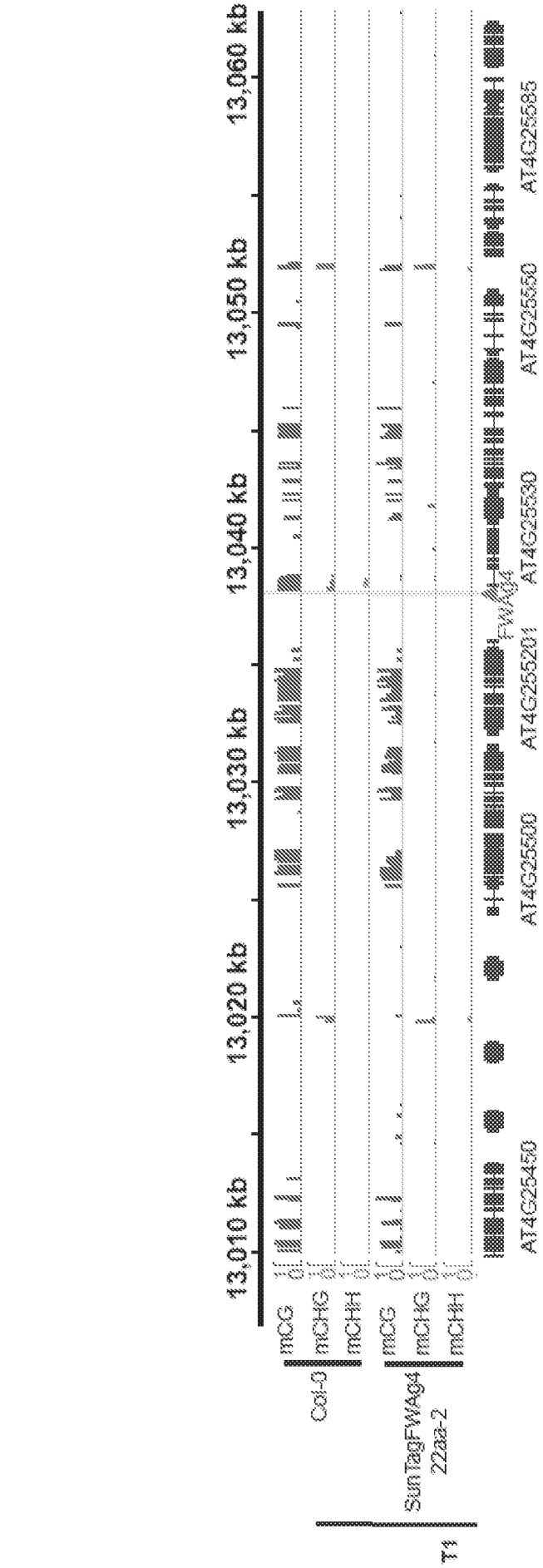

13,038,100 bp
13,038,300 bp
13,038,500 bp
13,038,700 bp
13,038,900 bp
T1
Col-0
SunTag FWAg4 22aa-2
mCG
mCHG
mCHH
mCG
mCHG
mCHH
1
0
FWAg4
AT4G25530 (FWA)

FIG. 41


13,010 kb
13,020 kb
13,030 kb
13,040 kb
13,050 kb
13,060 kb
T1
SunTagFWAg4 22aa-2
Col-0
mCG
mCHG
mCHH
AT4G25450
AT4G25500
AT4G25520
FWAg4
AT4G25530
AT4G25550
AT4G25585

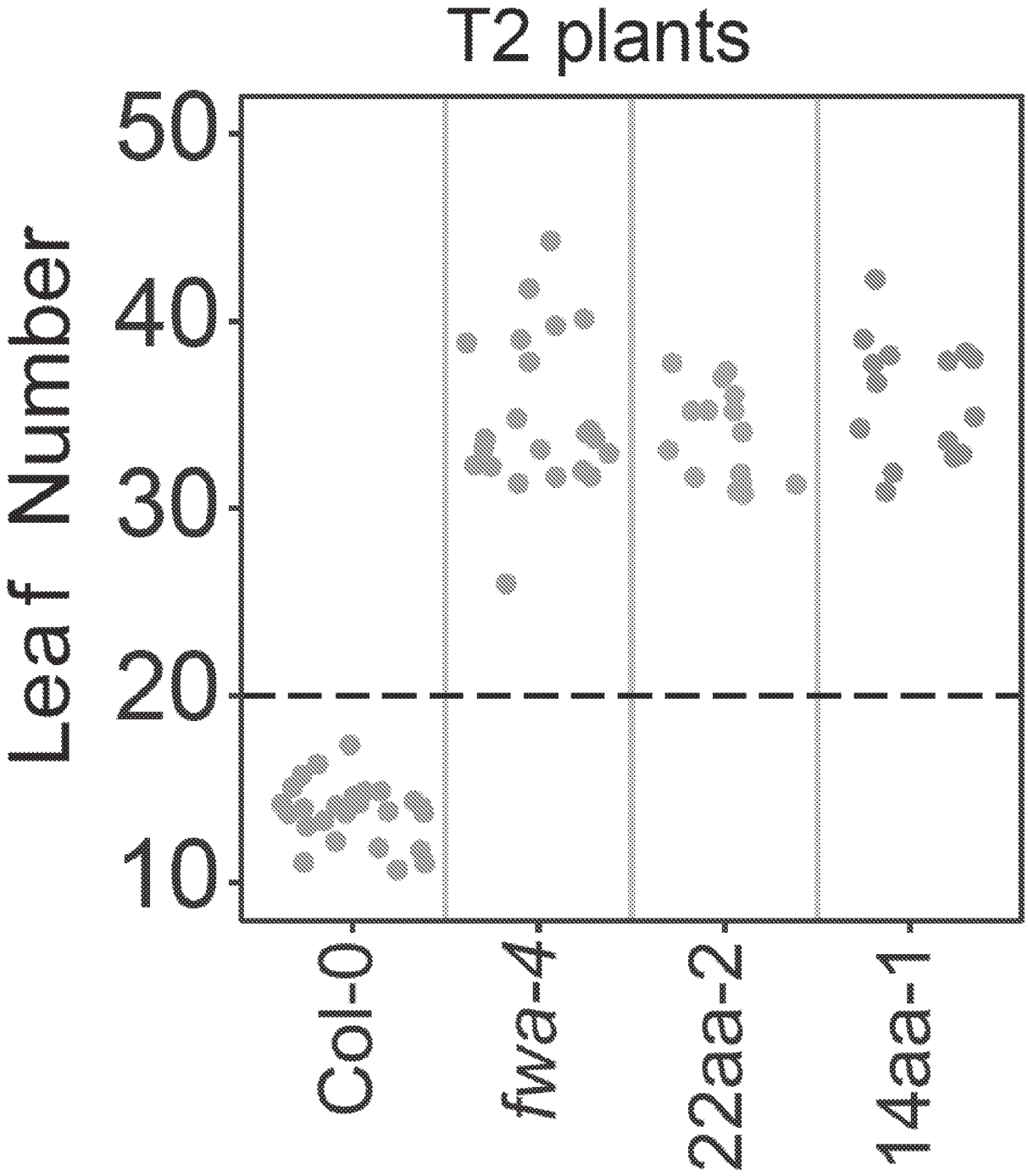


FIG. 42

FIG. 43

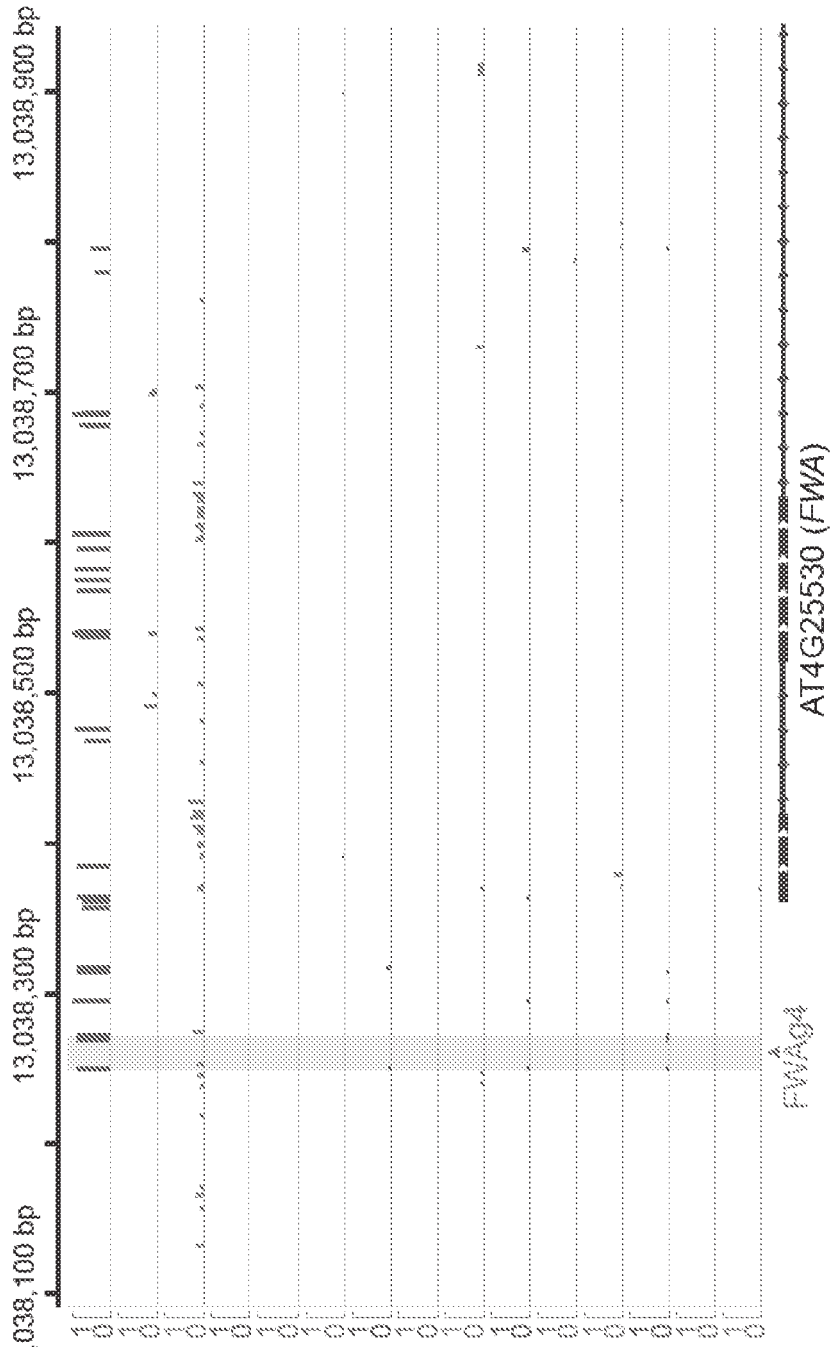

T2
Col-0
SunTag FWAg4 22aa-2 +
SunTag FWAg4 22aa-2 -
SunTag FWAg4 14aa-1 +
SunTag FWAg4 14aa-1 -
mCG
mCHG
mCHH
1
0
13,038,100 bp
13,038,300 bp
13,038,500 bp
13,038,700 bp
13,038,900 bp
FWAg4
AT4G25530 (FWA)

FIG. 44

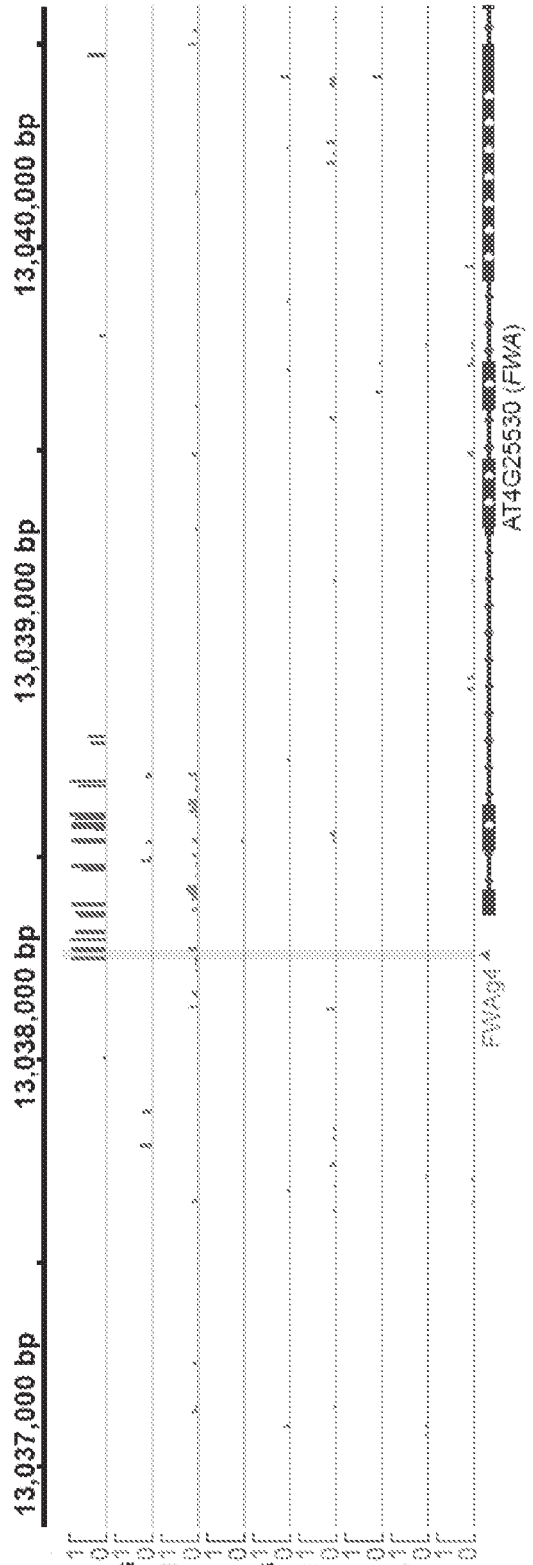

13,037,000 bp
13,038,000 bp
13,039,000 bp
13,040,000 bp
T2
Col-0
SunTag FWAg4 22aa-1 +
SunTag FWAg4 22aa-1 -
mCG
mCHG
mCHH
FWAg4
AT4G25530 (FWA)

FIG. 45

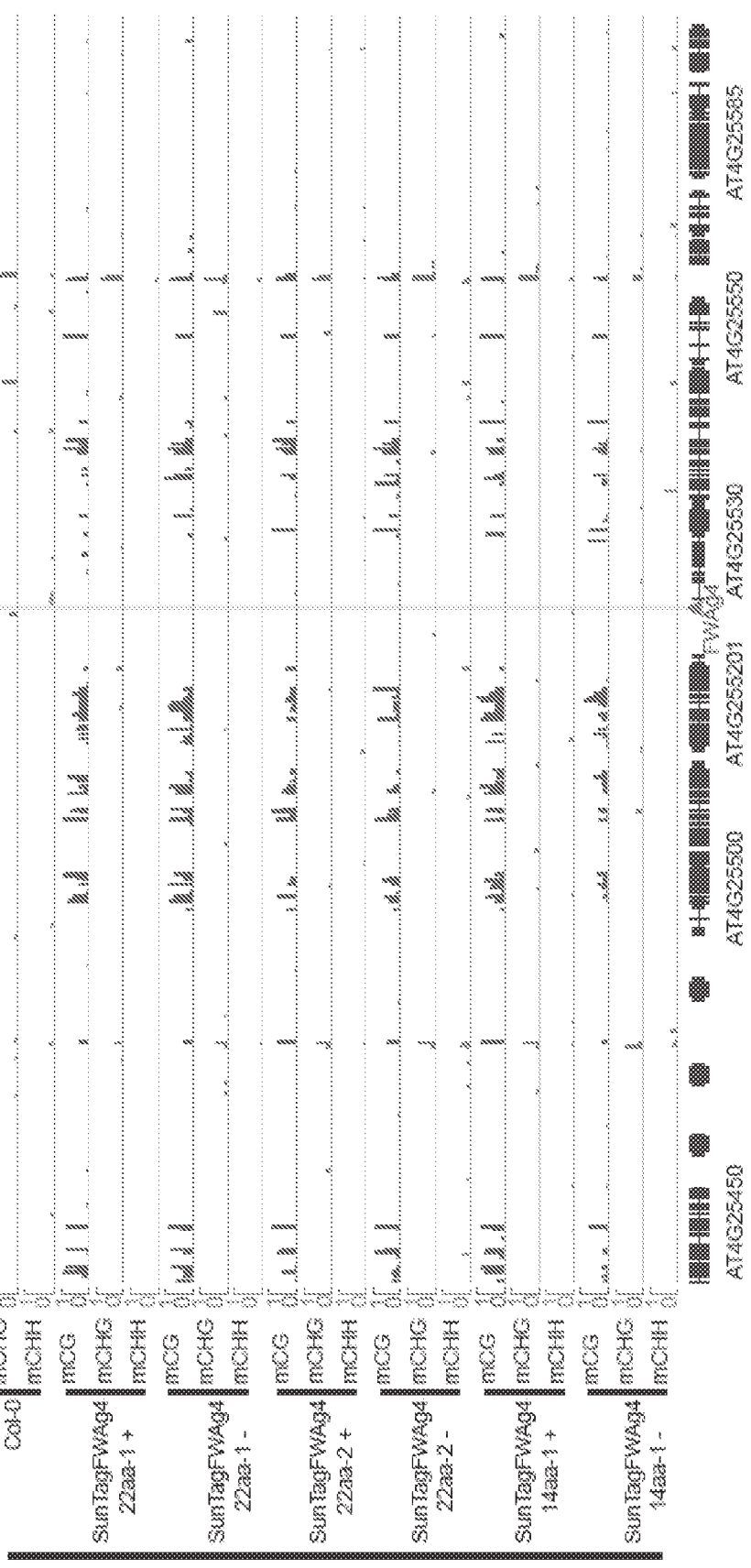

13,010 kb
13,020 kb
13,030 kb
13,040 kb
13,050 kb
13,060 kb
T2
Col-0
SunTagFWAg4 22aa-1 +
SunTagFWAg4 22aa-1 -
SunTagFWAg4 22aa-2 +
SunTagFWAg4 22aa-2 -
SunTagFWAg4 14aa-1 +
SunTagFWAg4 14aa-1 -
mCG
mCHG
mCHH
AT4G25450
AT4G25500
AT4G25201
FWA
AT4G25530
AT4G25550
AT4G25585

FIG. 46

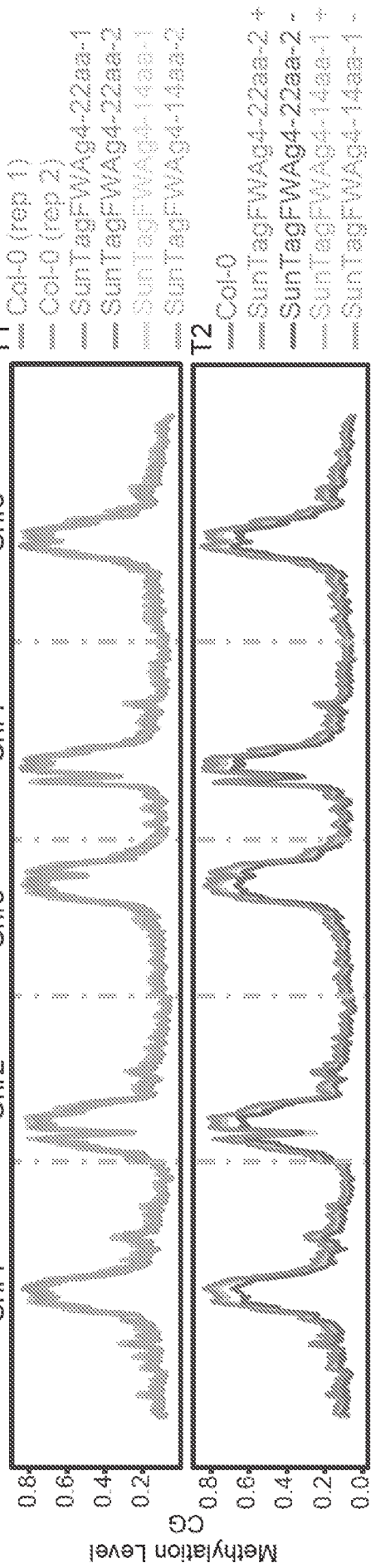

T1
Col-0 (rep 1)
Col-0 (rep 2)
SunTagFWAg4-22aa-1
SunTagFWAg4-22aa-2
SunTagFWAg4-14aa-1
SunTagFWAg4-14aa-2
T2
Col-0
SunTagFWAg4-22aa-2 +
SunTagFWAg4-22aa-2 -
SunTagFWAg4-14aa-1 +
SunTagFWAg4-14aa-1 -
Chr1
Chr2
Chr3
Chr4
Chr5
0.8
0.6
0.4
0.2
0.0
CG
Methylation Level

FIG. 47

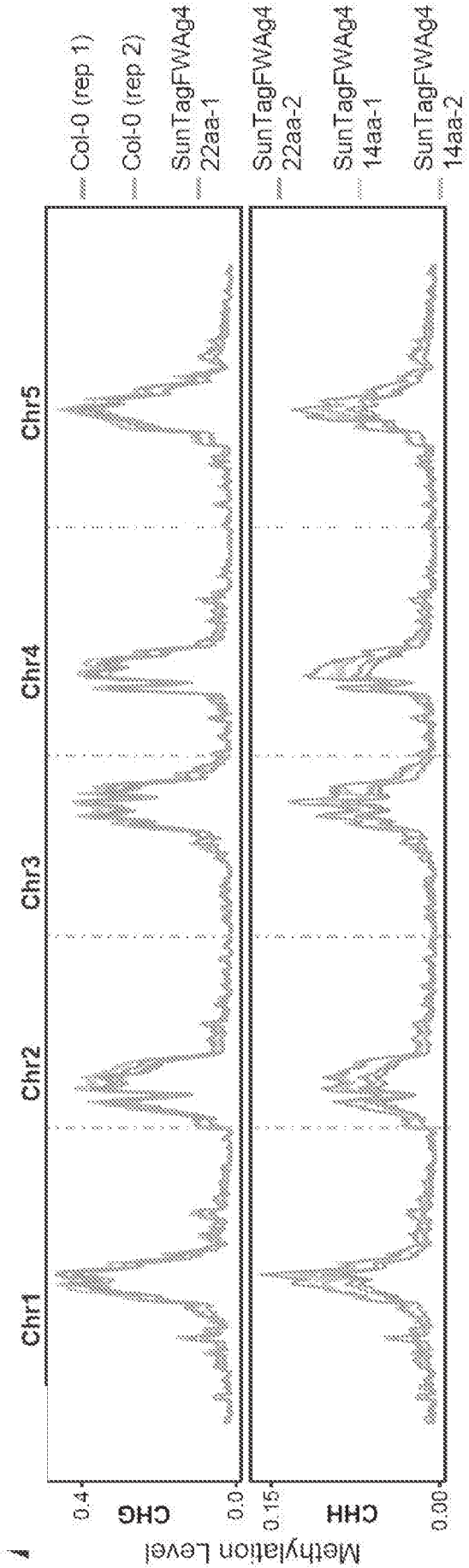

Chr1
Chr2
Chr3
Chr4
Chr5
Col-0 (rep 1)
Col-0 (rep 2)
SunTagFWAg4 22aa-1
SunTagFWAg4 22aa-2
SunTagFWAg4 14aa-1
SunTagFWAg4 14aa-2
CHG
CHH
0.4
0.0
0.15
0.00
Methylation Level

FIG. 48

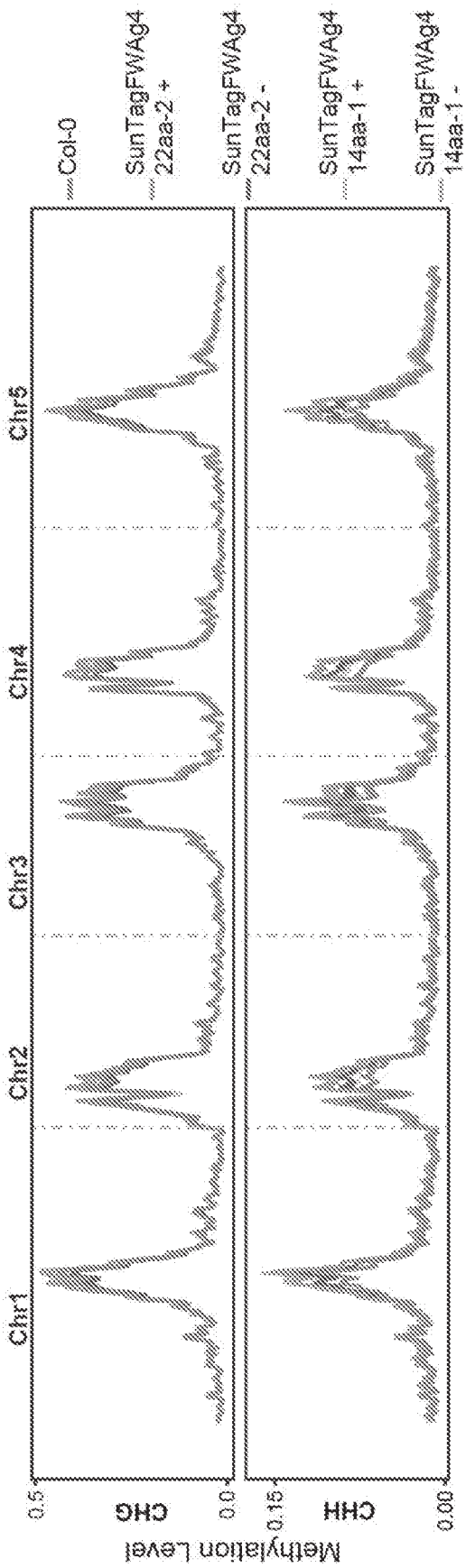

Col-0
SunTagFWAg4 22aa-2 +
SunTagFWAg4 22aa-2 -
SunTagFWAg4 14aa-1 +
SunTagFWAg4 14aa-1 -
Chr1
Chr2
Chr3
Chr4
Chr5
CHG
CHH
0.5
0.0
0.15
0.00
Methylation Level

FIG. 49

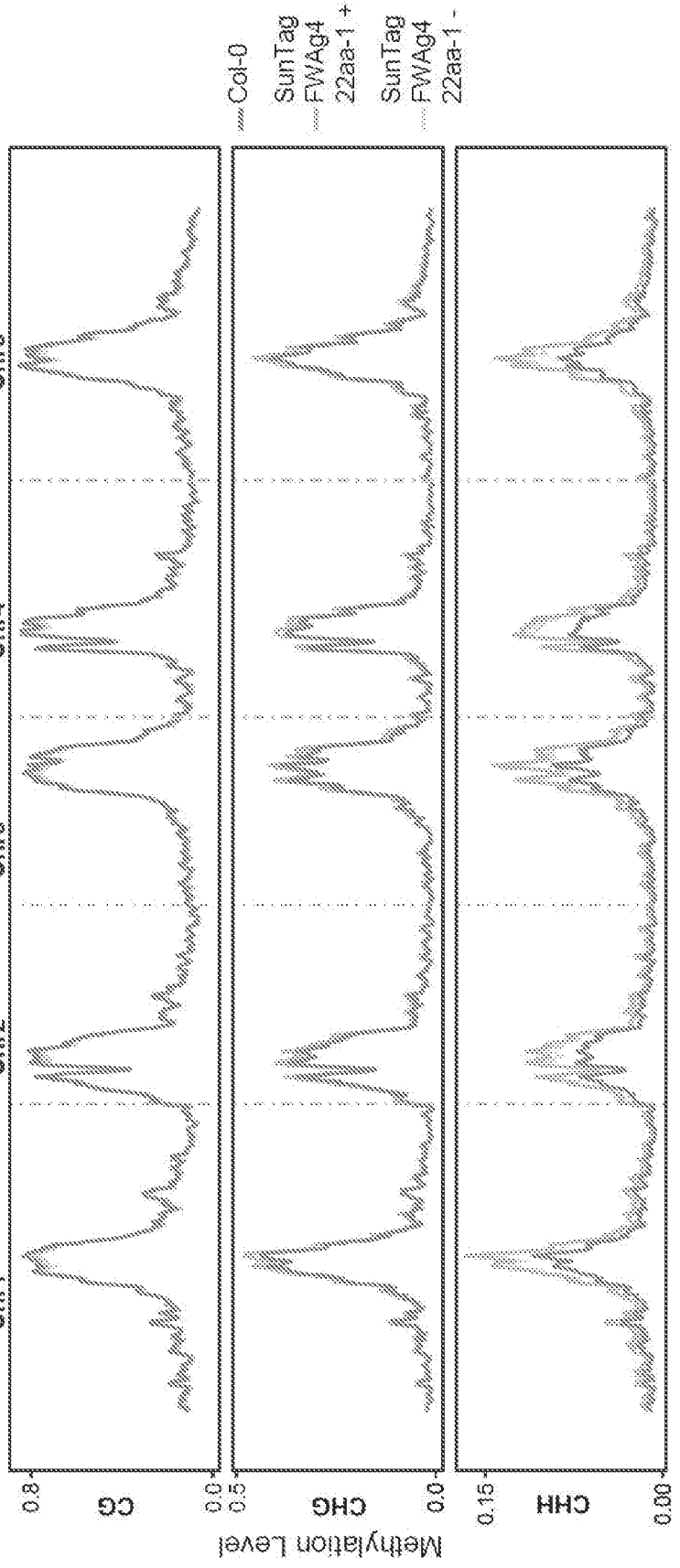
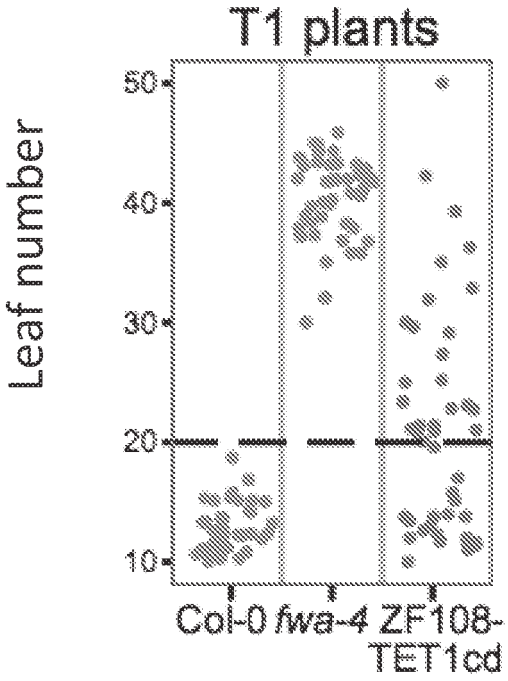

Chr1
Chr2
Chr3
Chr4
Chr5
CG
CHG
CHH
0.8
0.0
0.5
0.0
0.15
0.00
Methylation Level
Col-0
SunTag
FWAg4
22aa-1 +
SunTag
FWAg4
22aa-1 -

FIG. 50A



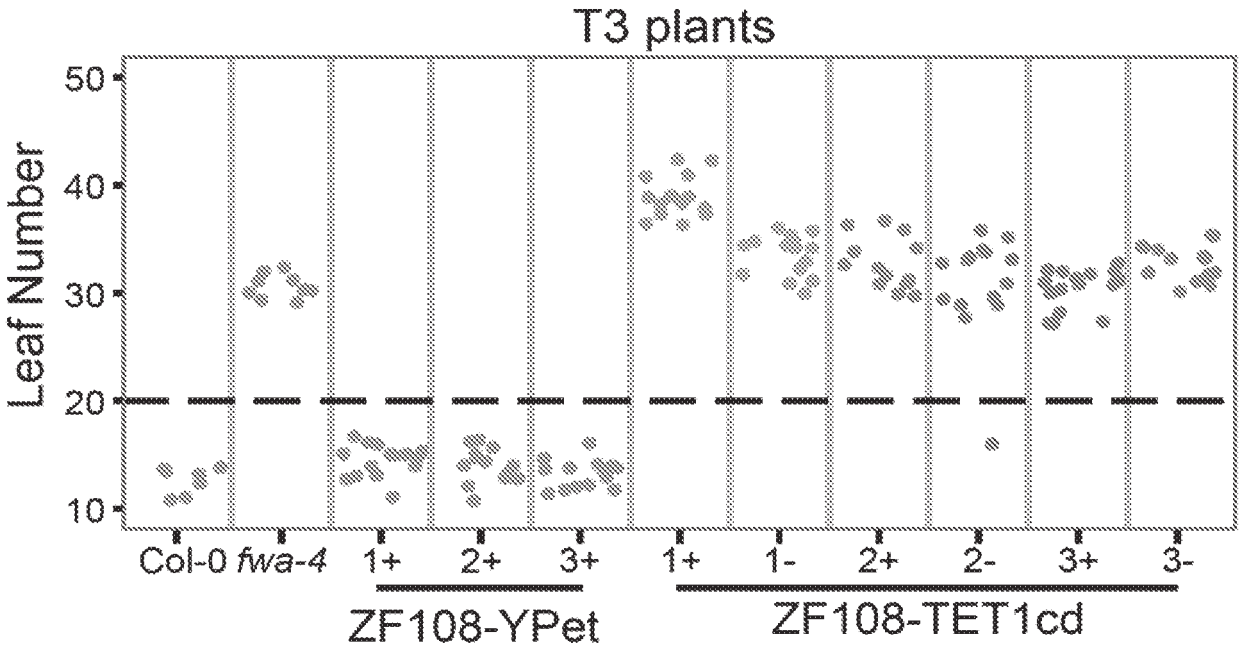
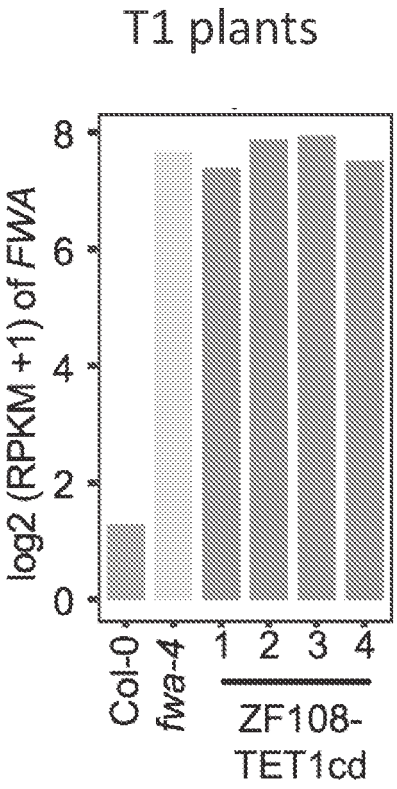


FIG. 50B

FIG. 51A



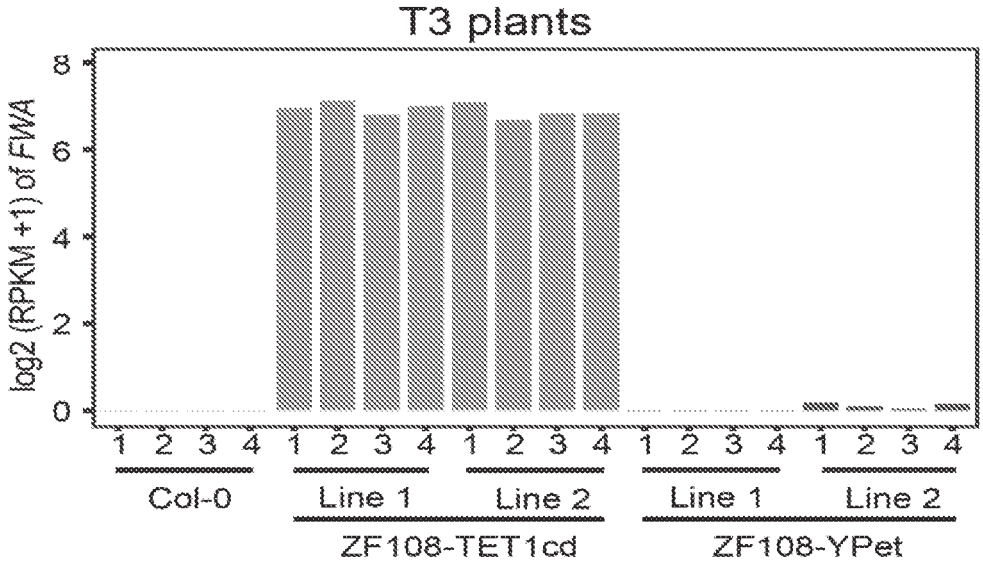


FIG. 51B

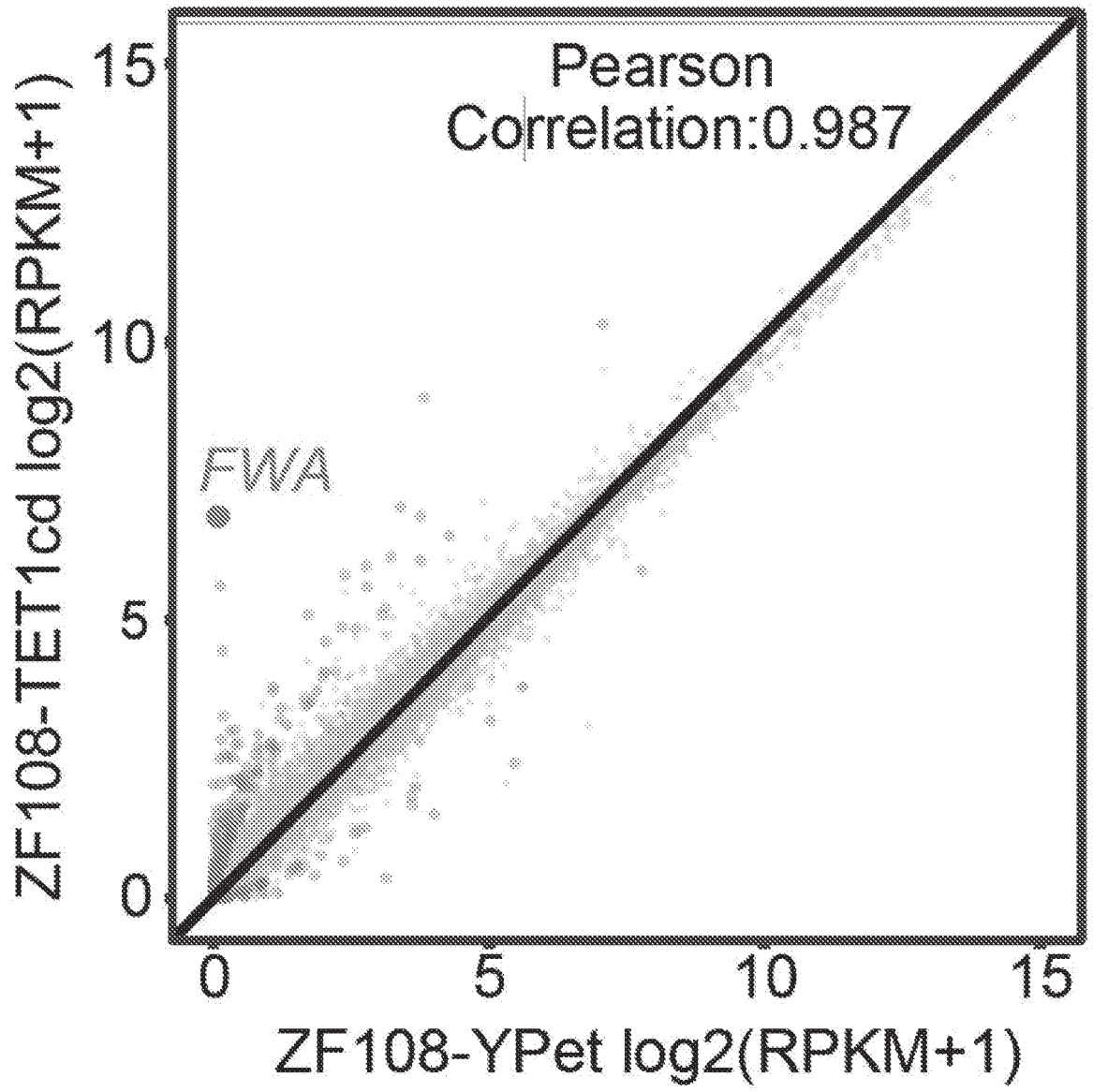

Pearson
Correlation:0.987
FWA
ZF108-TET1cd log2(RPKM+1)
ZF108-YPet log2(RPKM+1)
0
5
10
15

FIG. 52

FIG. 53

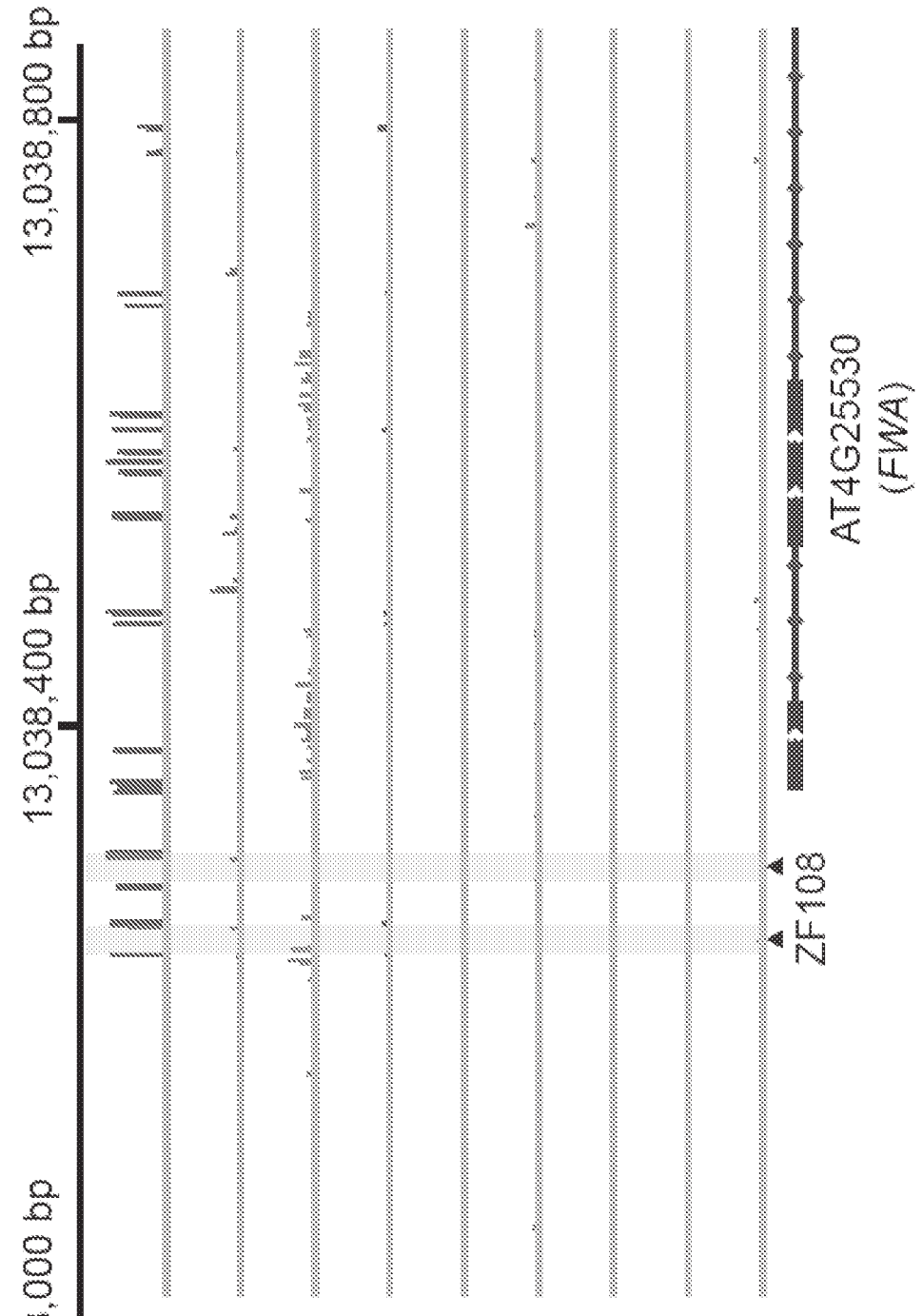

13,038,000 bp
13,038,400 bp
13,038,800 bp
T3
Col-0
ZF108-TET1cd-1
+
-
mCG
mCHG
mCHH
1
0
ZF108
AT4G25530
(FWA)

FIG. 54

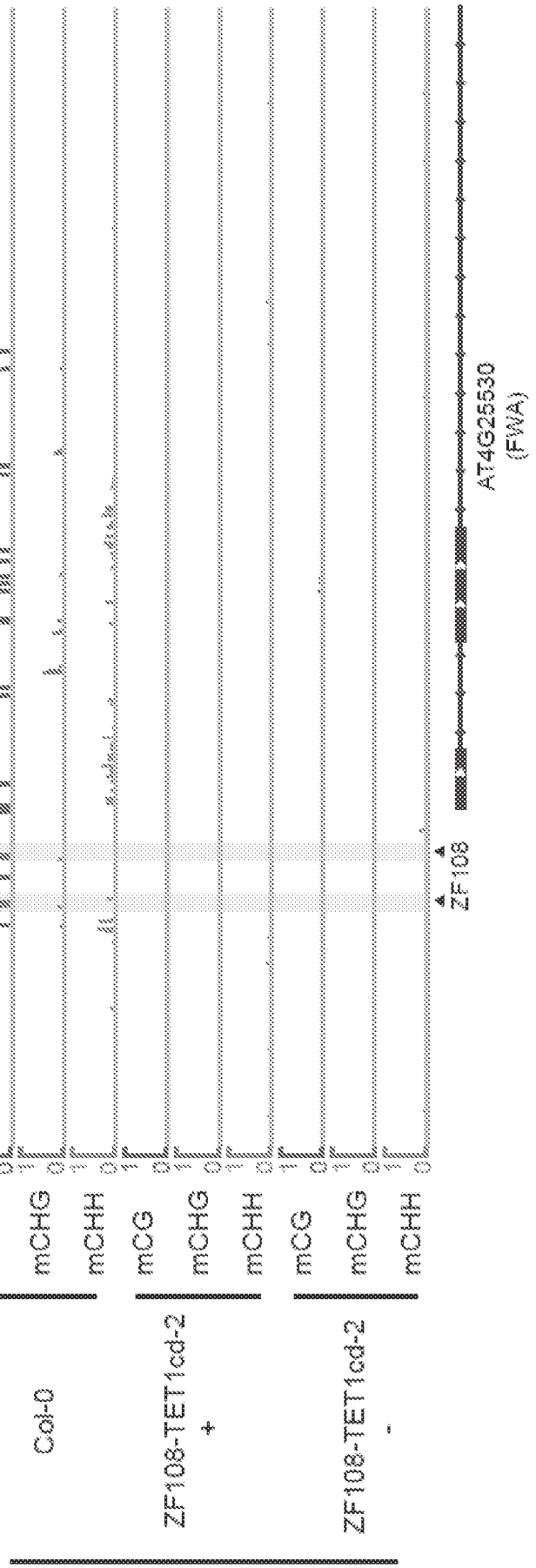

T3
Col-0
ZF108-TET1cd-2
+
ZF108-TET1cd-2
-
mCG
mCHG
mCHH
13,038,200 bp
13,038,400 bp
13,038,600 bp
13,038,800 bp
13,039,000 bp
ZF108
AT4G25530
(FWA)

FIG. 55

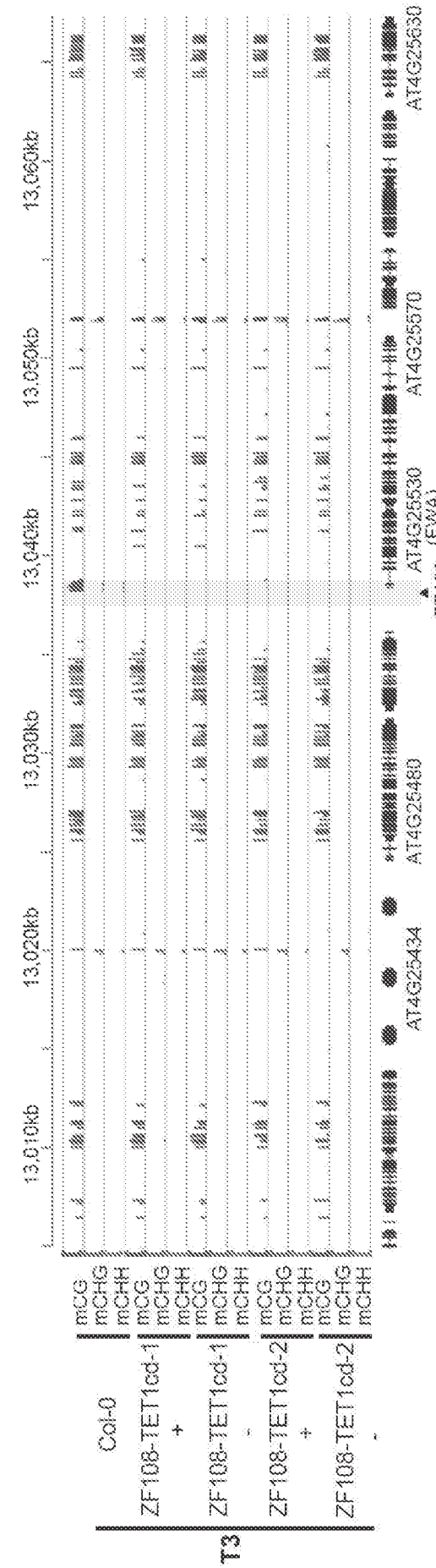

T3
Col-0
ZF108-TET1cd-1
+
-
ZF108-TET1cd-1
-
ZF108-TET1cd-2
+
ZF108-TET1cd-2
-
mCG
mCHG
mCHH
13,010kb
13,020kb
13,030kb
13,040kb
13,050kb
13,060kb
AT4G25434
AT4G25480
AT4G25530
AT4G25570
AT4G25630
ZF108 (FWA)

FIG. 56

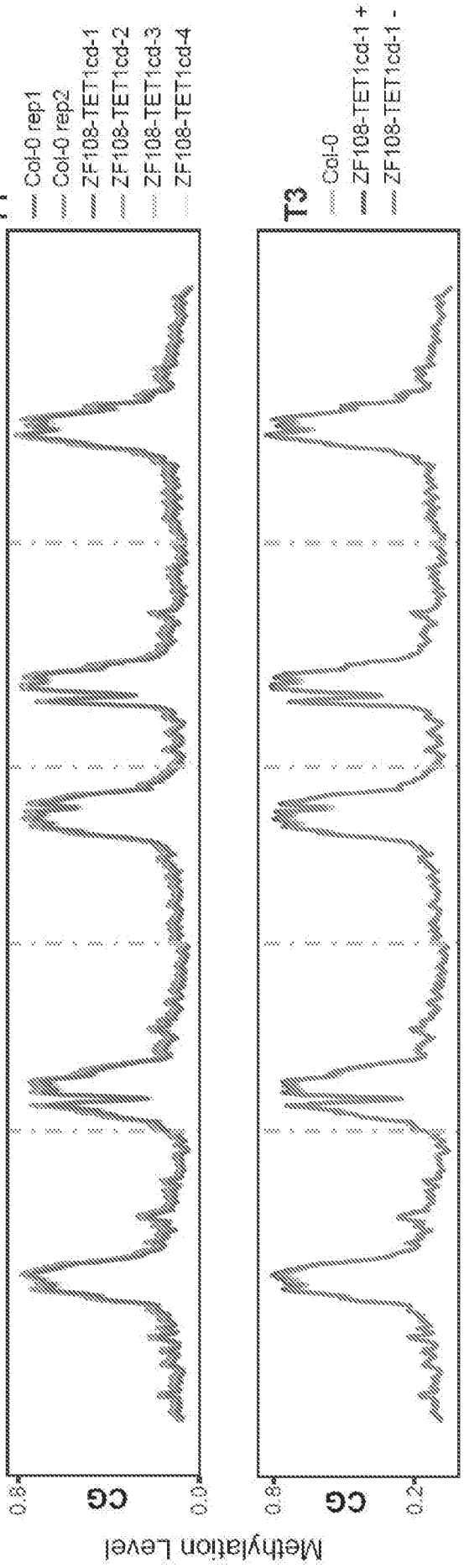

T1
Col-0 rep1
Col-0 rep2
ZF108-TET1cd-1
ZF108-TET1cd-2
ZF108-TET1cd-3
ZF108-TET1cd-4
Chr1
Chr2
Chr3
Chr4
Chr5
CG
0.8
0.0
T3
Col-0
ZF108-TET1cd-1 +
ZF108-TET1cd-1 -
CG
0.8
0.2
Methylation Level

FIG. 57

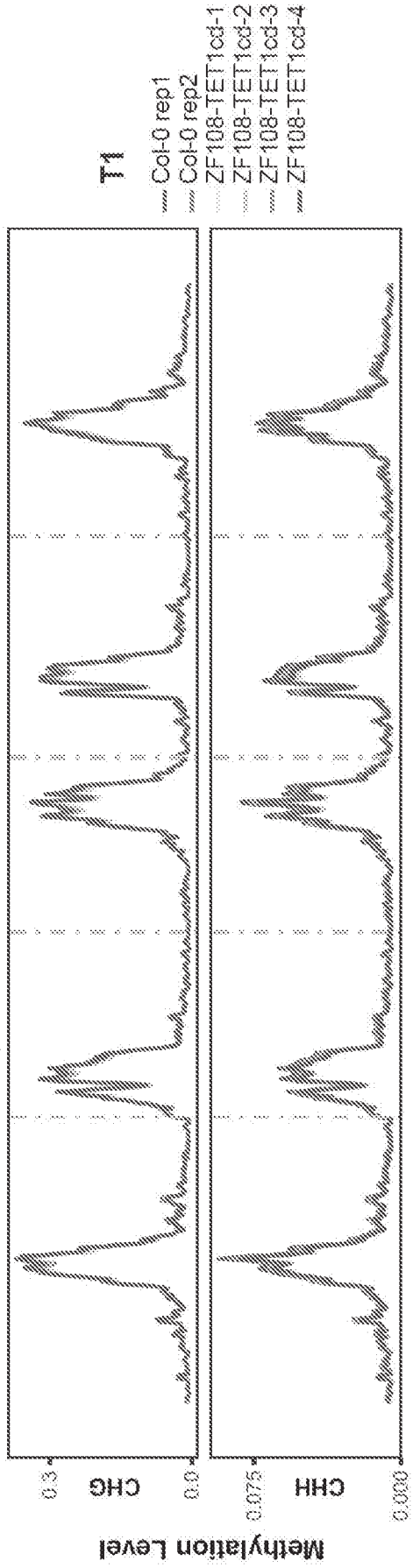

T1
Col-0 rep1
Col-0 rep2
ZF108-TET1cd-1
ZF108-TET1cd-2
ZF108-TET1cd-3
ZF108-TET1cd-4
Chr1
Chr2
Chr3
Chr4
Chr5
CHG
CHH
0.3
0.0
0.075
0.000
Methylation Level

FIG. 58

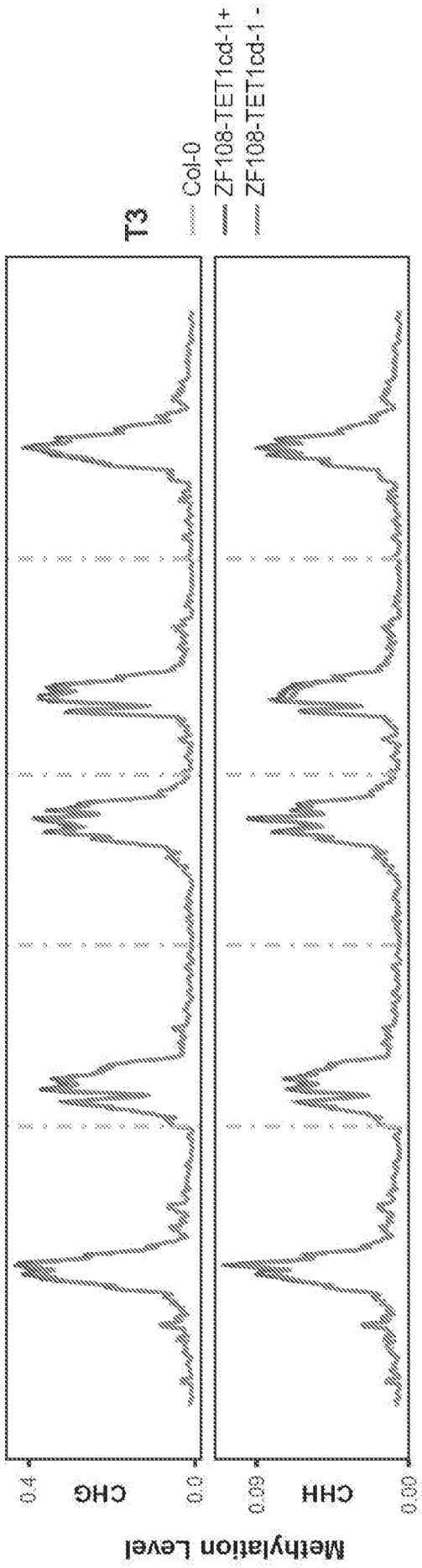
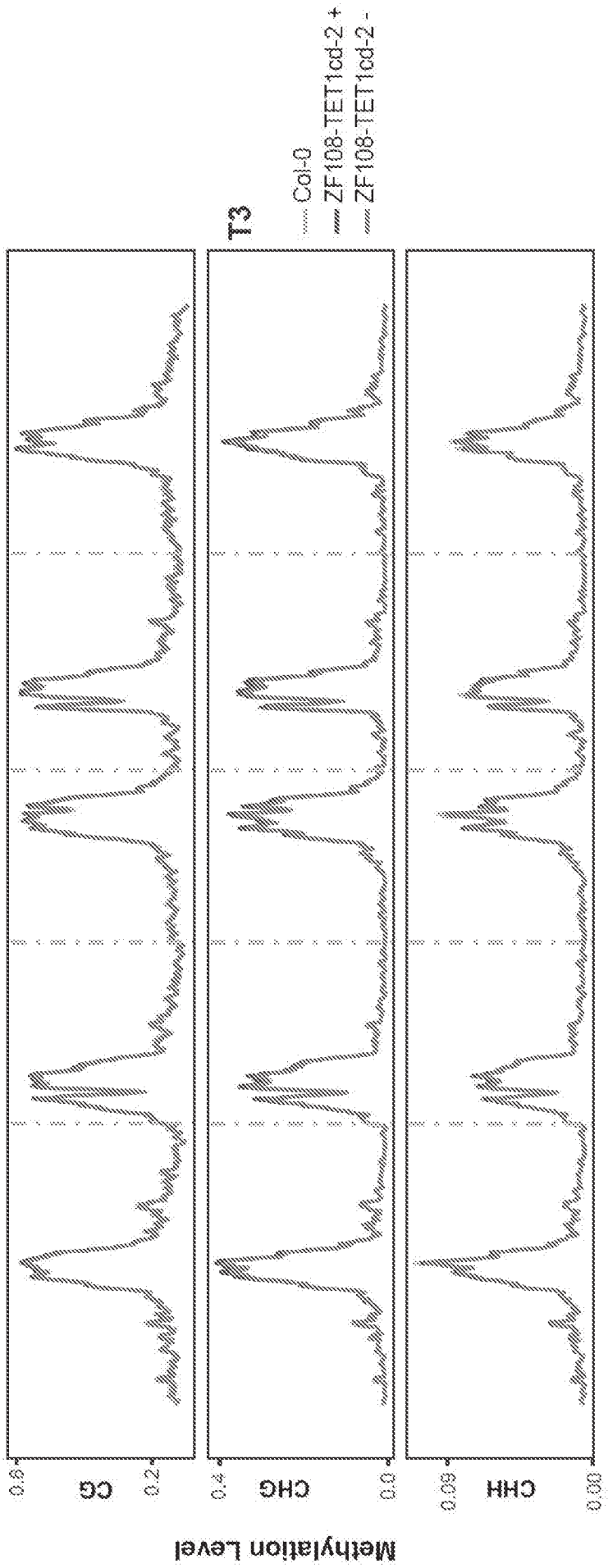

T3
Col-0
ZF108-TET1cd-1+
ZF108-TET1cd-1 -
Chr1
Chr2
Chr3
Chr4
Chr5
CHG
CHH
0.4
0.0
0.03
0.00
Methylation Level

FIG. 59


T3
Col-0
ZF108-TET1cd-2 +
ZF108-TET1cd-2 -
Chr1
Chr2
Chr3
Chr4
Chr5
CG
CHG
CHH
0.6
0.2
0.4
0.0
0.03
0.00
Methylation Level

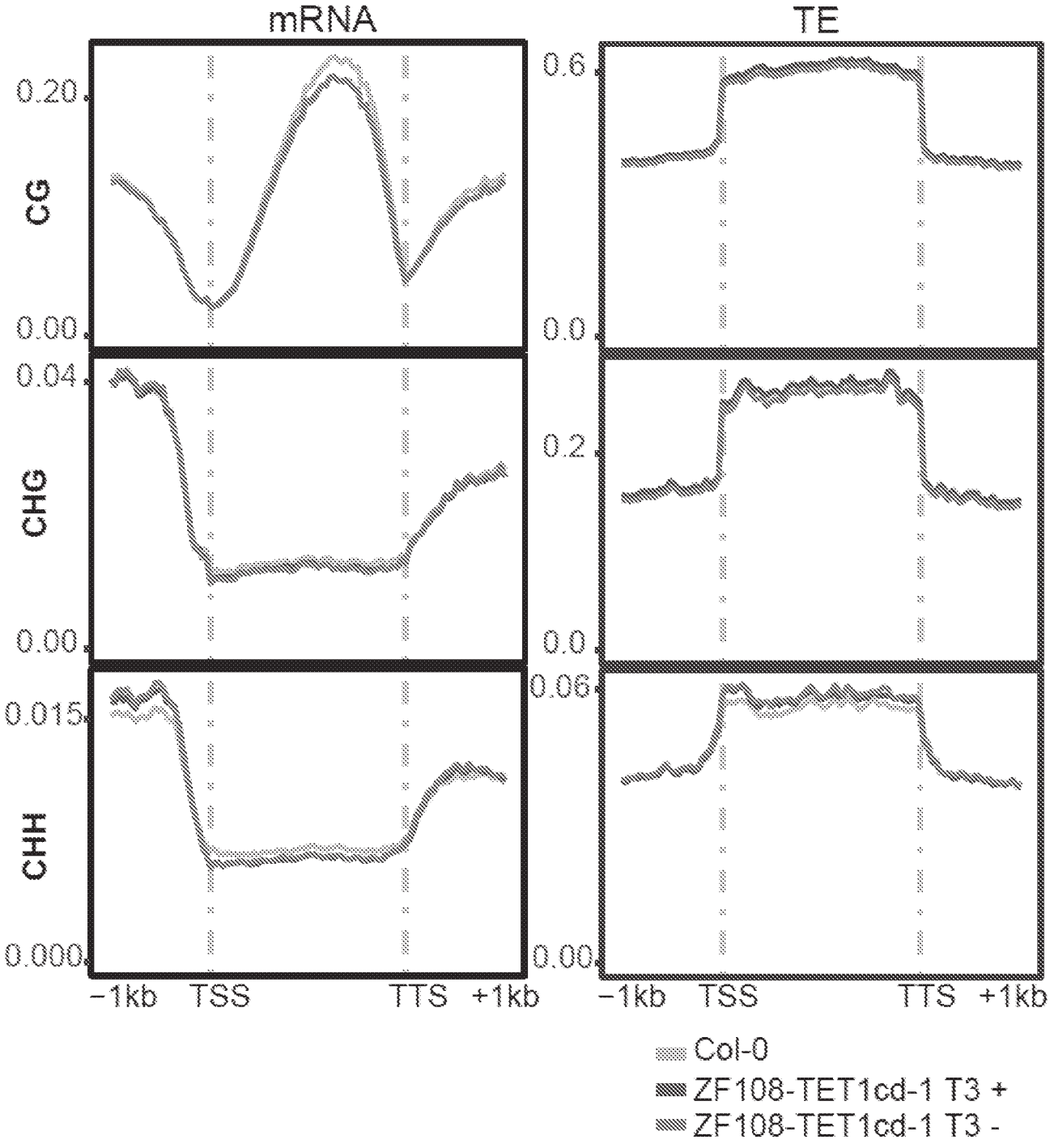
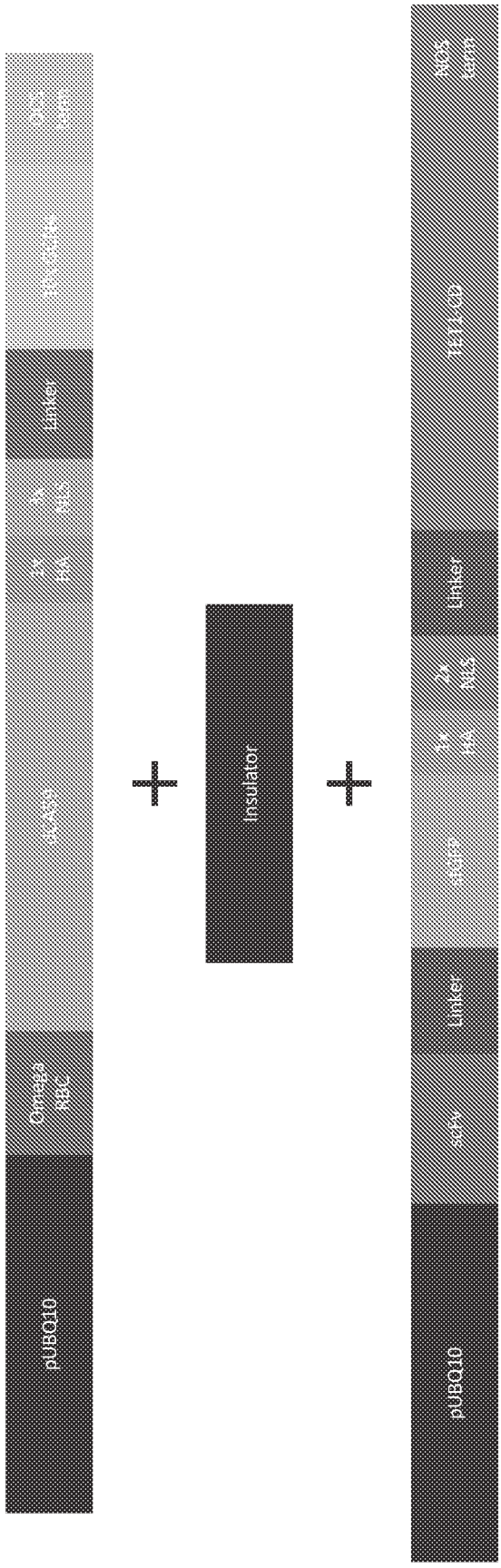

mRNA
TE
CG
CHG
CHH
0.20
0.00
0.04
0.00
0.015
0.000
0.6
0.0
0.2
0.0
0.06
0.00
−1kb
TSS
TTS
+1kb
−1kb
TSS
TTS
+1kb
Col-0
ZF108-TET1cd-1 T3 +
ZF108-TET1cd-1 T3 -

FIG. 60

FIG. 61


pUBQ10
Omega RBC
35S-Ω5'
Linker
35S-Ω5'-HA
35S 3'
Insulator
pUBQ10
35SV
Linker
Hygro
5' HA
NOS
Linker
TT1-109
NOS term

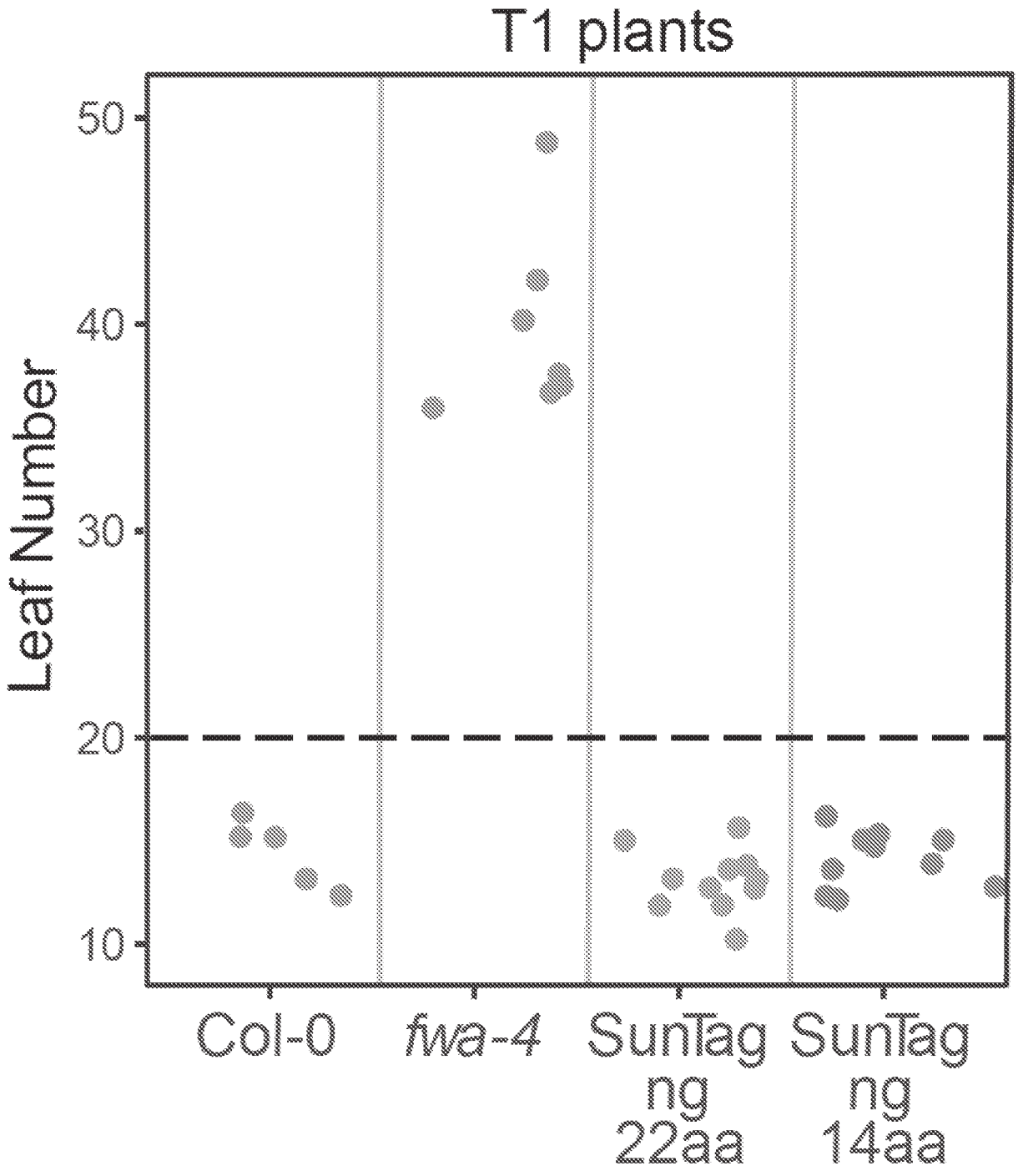

T1 plants
Leaf Number
50
40
30
20
10
Col-0
fwa-4
SunTag ng 22aa
SunTag ng 14aa

FIG. 62

FIG. 63

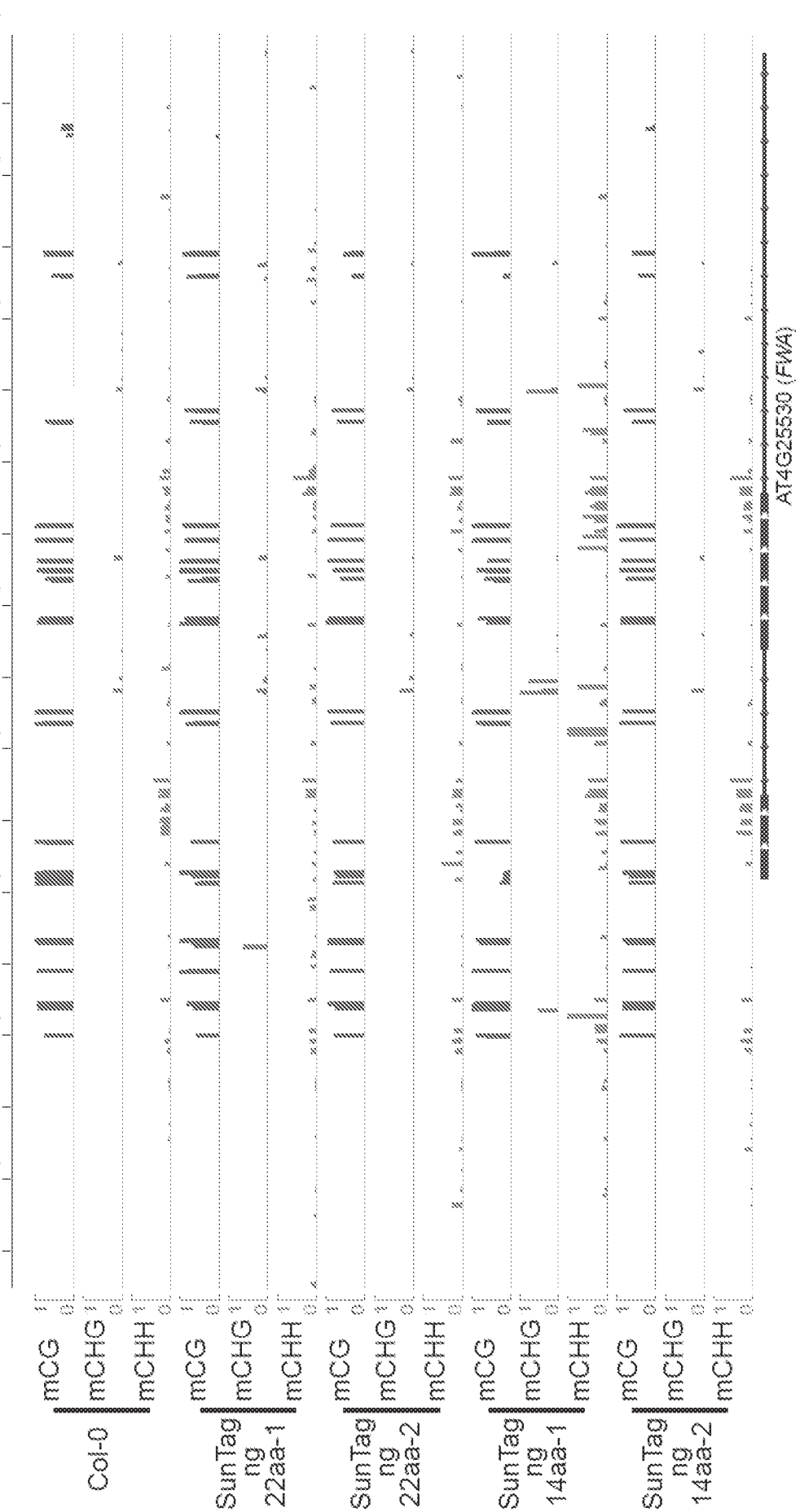

13,038,100 bp
13,038,200 bp
13,038,300 bp
13,038,400 bp
13,038,500 bp
13,038,600 bp
13,038,700 bp
13,038,800 bp
13,038,900 bp
mCG
mCHG
mCHH
Col-0
SunTag ng 22aa-1
SunTag ng 22aa-2
SunTag ng 14aa-1
SunTag ng 14aa-2
AT4G25530 (FWA)

FIG. 64

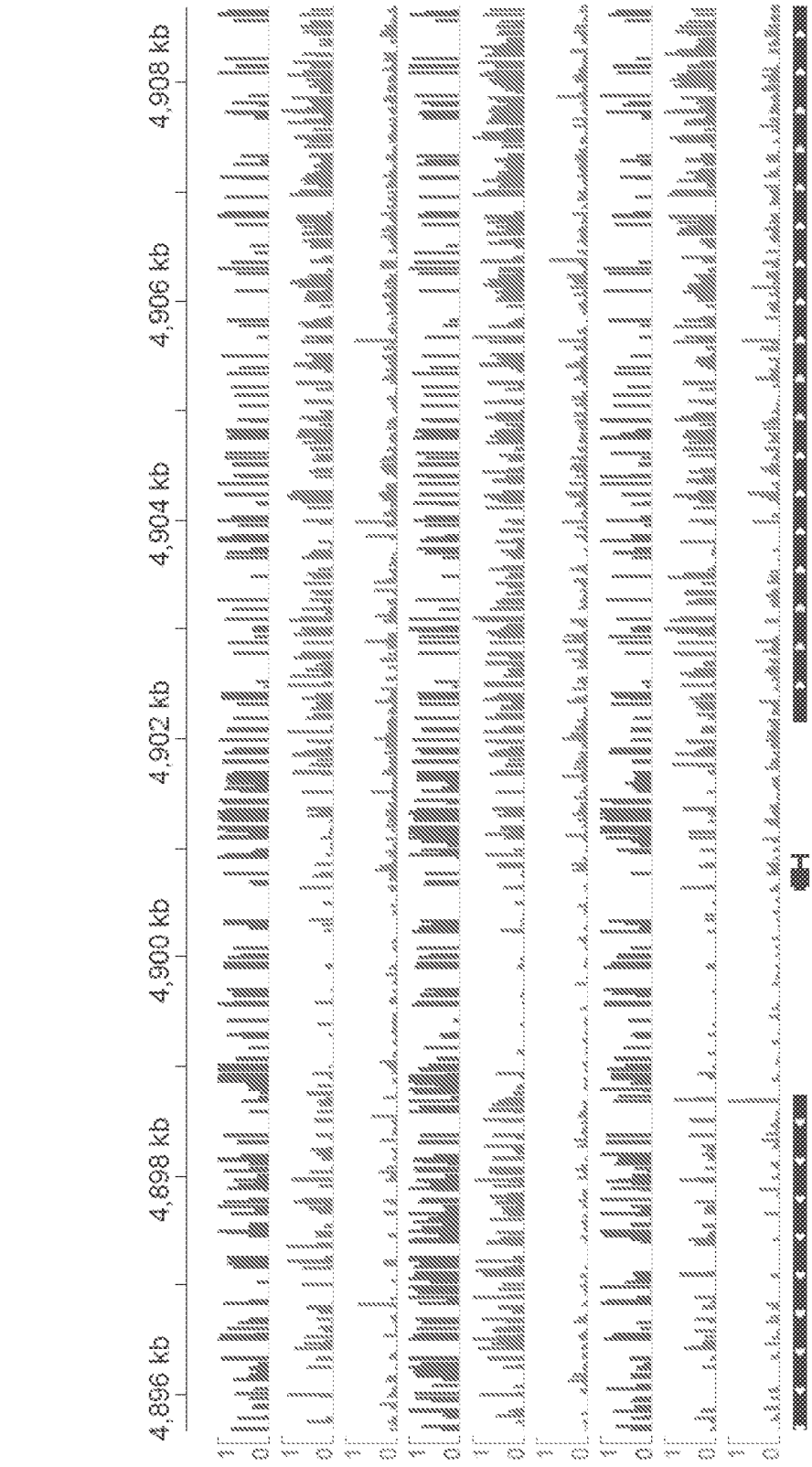
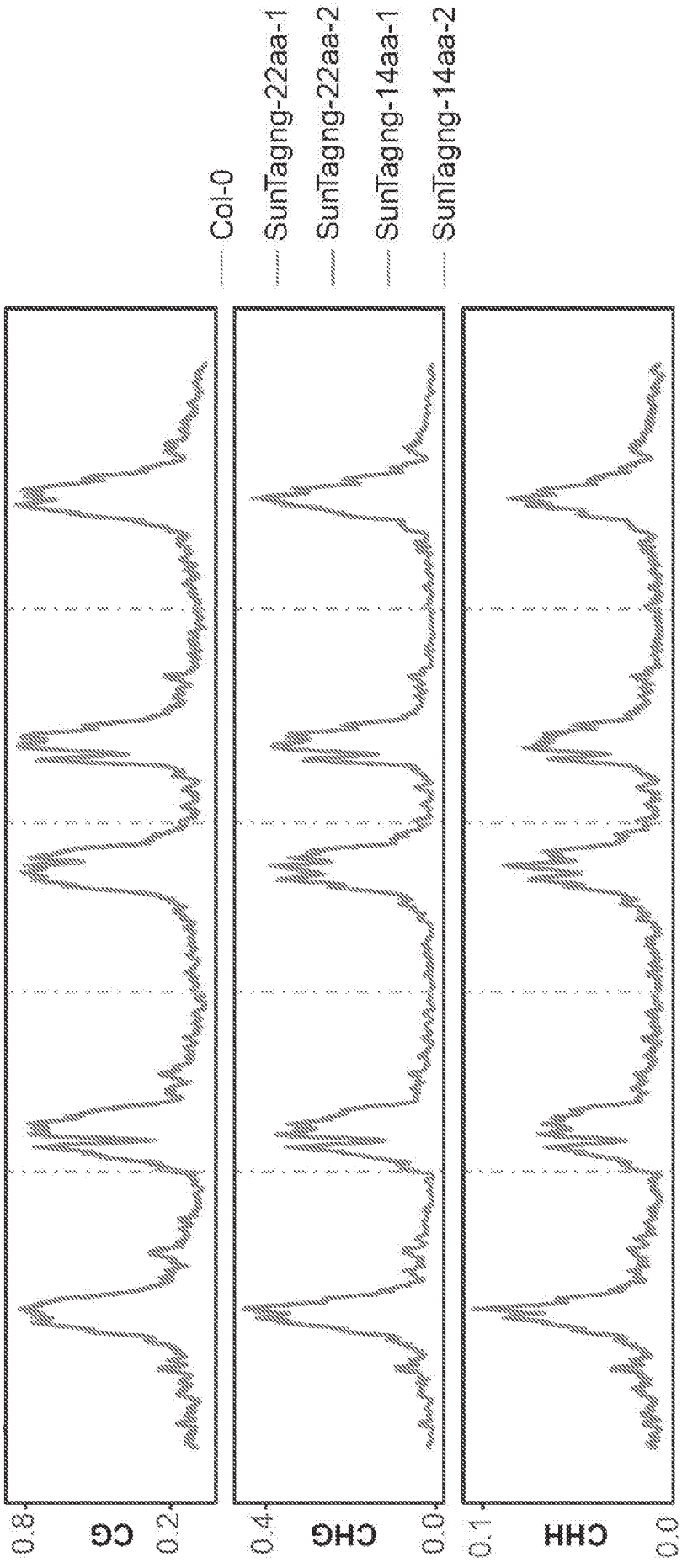

4,896 kb
4,898 kb
4,900 kb
4,902 kb
4,904 kb
4,906 kb
4,908 kb
Col-0
SunTag ng 22aa-1
SunTag ng 22aa-2
mCG
mCHG
mCHH
1
0
AT2G12195
AT2G12200
AT2G12210 (CACTA1)

FIG. 65


Col-0
SunTagng-22aa-1
SunTagng-22aa-2
SunTagng-14aa-1
SunTagng-14aa-2
Chr1
Chr2
Chr3
Chr4
Chr5
CG
CHG
CHH
0.8
0.2
0.4
0.0
0.1
0.0

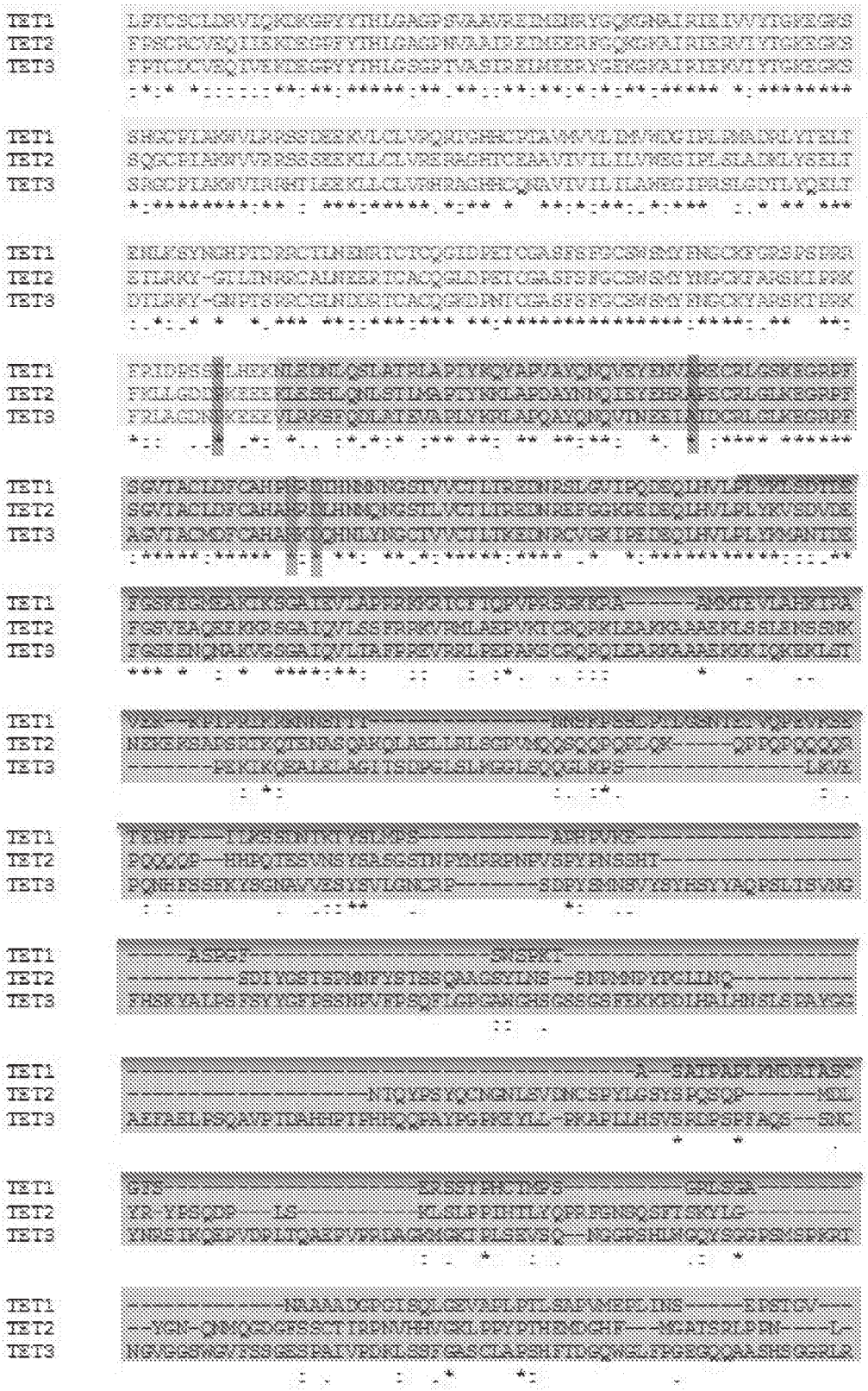


FIG. 66A

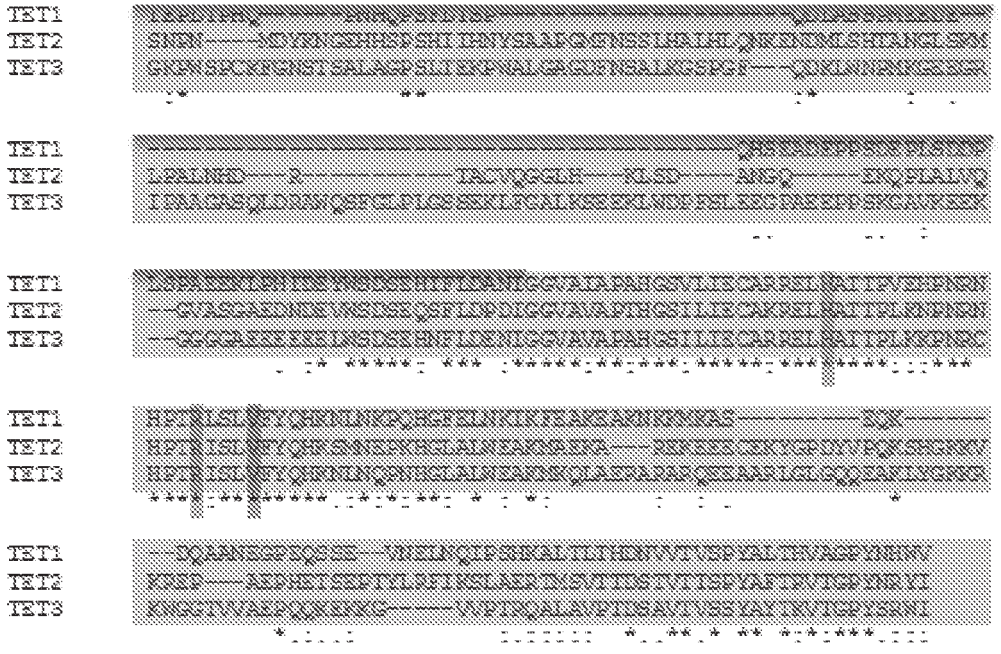


FIG. 66B

```
TET1      ELPTCSCLDRVIQKDKGPYYTHLGAGPSVAAVREIMENRYGQKGNAIRIEIVVYTGKEGK
TET2      DFPSCRCVEQIIEKDEGPFYTHLGAGPNVAAIREIMEERFGQKGKAIRIERVIYTGKEGK
TET3      EFPTCDCVEQIVEKDEGPYYTHLGSGPTVASIRELMEERYGEKGKAIRIEKVIYTGKEGK
          ::*:* *:::::::**:**:*****:**.**::**:**:*:*:**:***** *:*******

TET1      SSHGCPIAKWVLRRSSDEEKVLCLVRQRTGHHCPTAVMVVLIMVWDGIPLPMADRLYTEL
TET2      SSQGCPIAKWVVRRSSSEEKLLCLVREPAGHTCEAAVIVILILVWEGIPLSLADKLYSEL
TET3      SSRGCPIAKWVIRRHTLEEKLLCLVRHRAGHHCQNAVIVILILAWEGIPRSLGDTLYQEL
          **:*********:** : ***:*****.*:** *  **:*:**:.*:***  :.* ** **

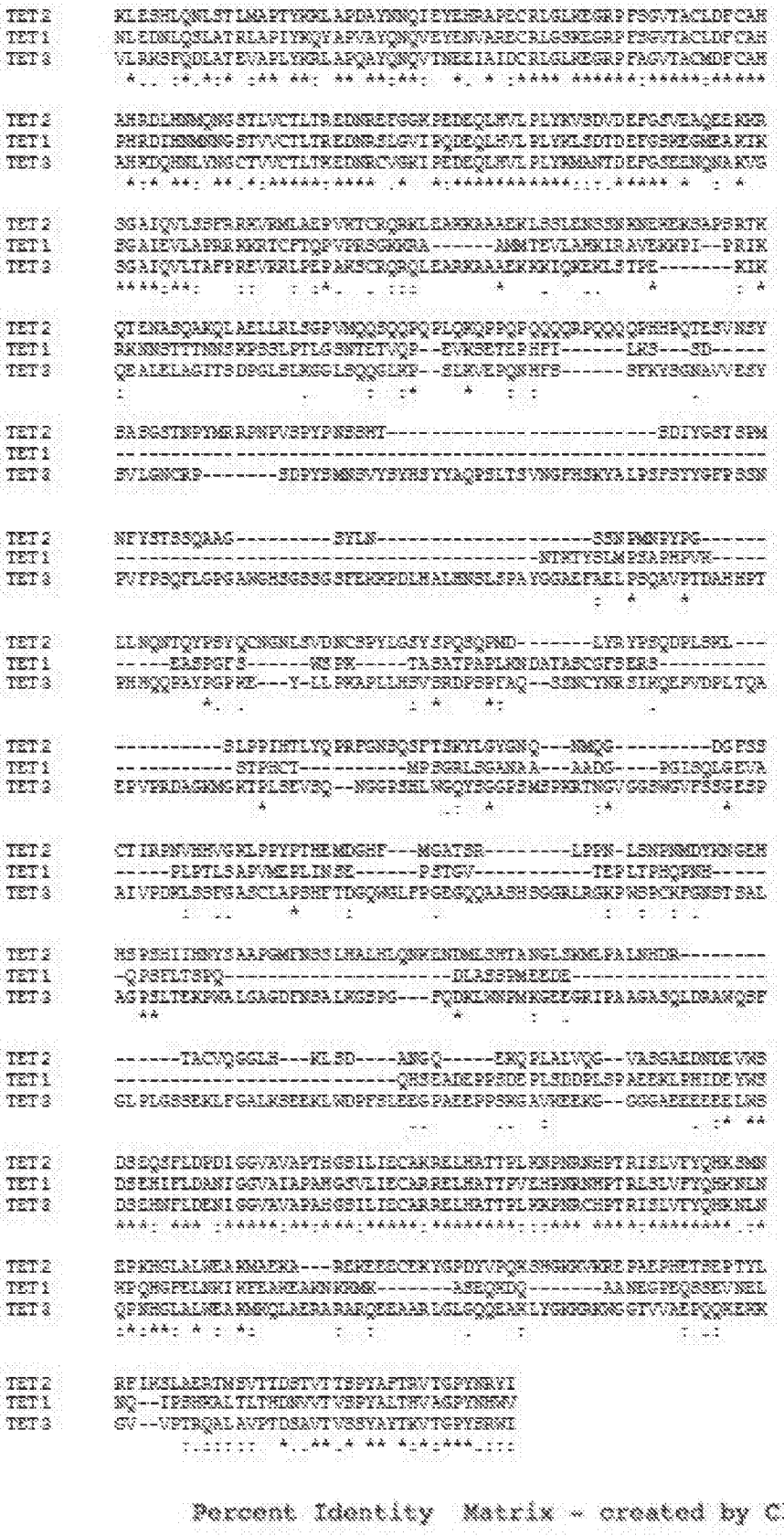
TET1      TENLKSYNGHPTDRRCTLNENRTCTCQGIDPETCGASFSFGCSWSMYFNGCKFGRSPSPR
TET2      TETLRKY-GTLTNRRCALNEERTCACQGLDPETCGASFSFGCSWSMYYNGCKFARSKIPR
TET3      TDTLRKY-GNPTSRRCGLNDDRTCACQGKDPNTCGASFSFGCSWSMYFNGCKYARSKTPR
          *:.*:.* *  *.*** **::***:*** **:****************:****:.**  **

TET1      RFRIDPSSPLHEK
TET2      KFKLLGDDPKEEE
TET3      KFRLAGDNPKEEE
          :*::  ..* .*:
```

Percent Identity Matrix - created by Clustal2.1

1: TET1	100.00	69.27	66.15
2: TET2	69.27	100.00	78.65
3: TET3	66.15	78.65	100.00

FIG. 67



Percent Identity Matrix - created by Clustal2.1

1: TET2	100.00	40.64	42.22
2: TET1	40.64	100.00	41.59
3: TET3	42.22	41.59	100.00

FIG. 68