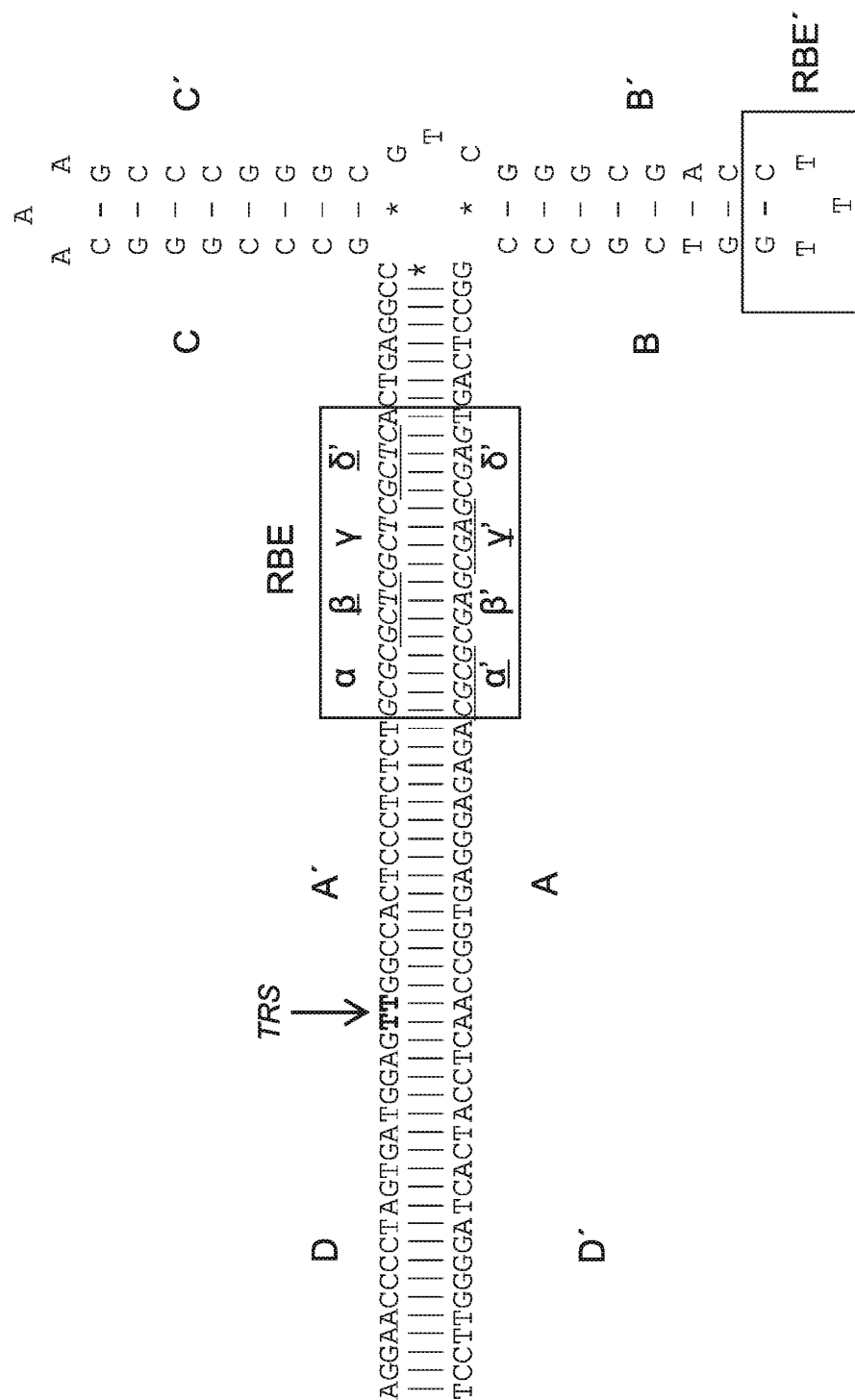
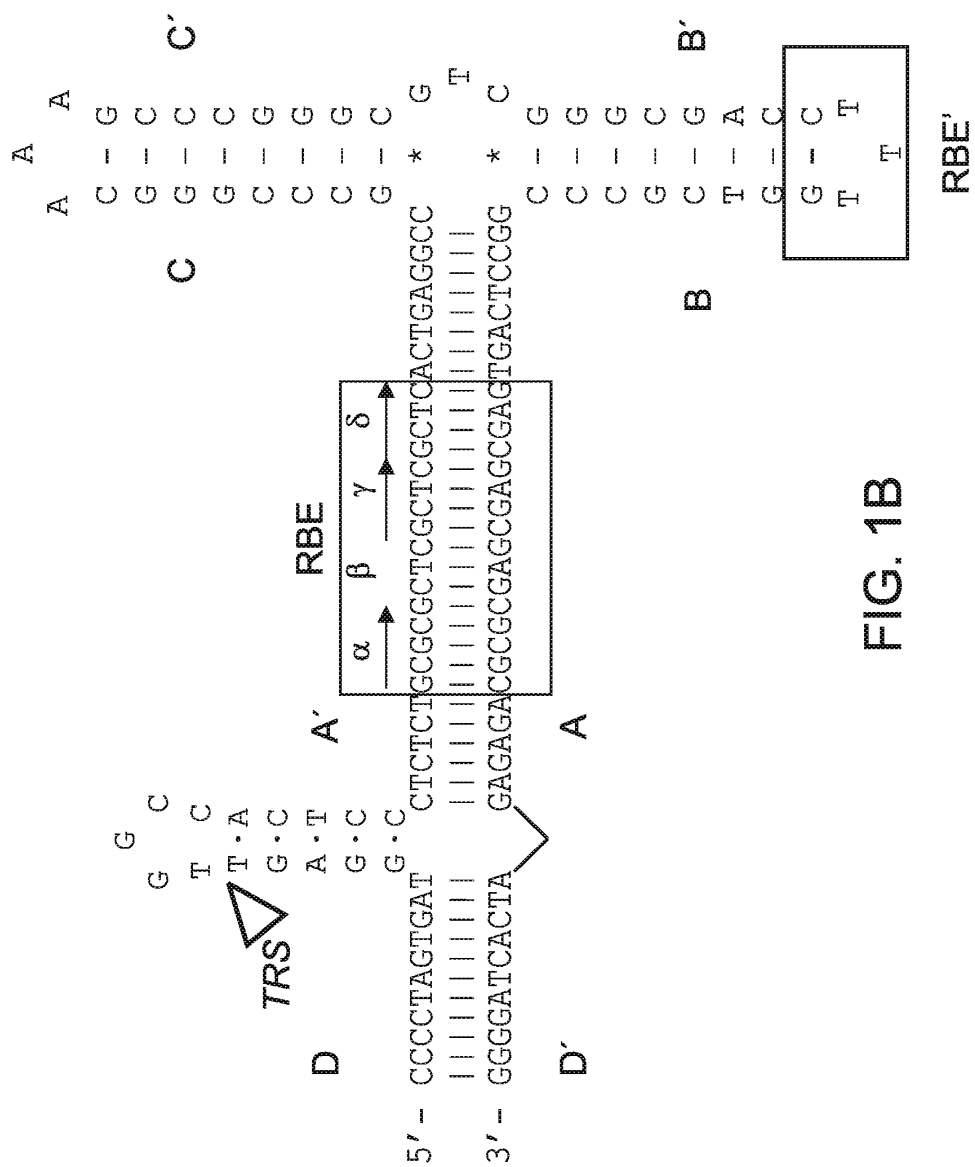
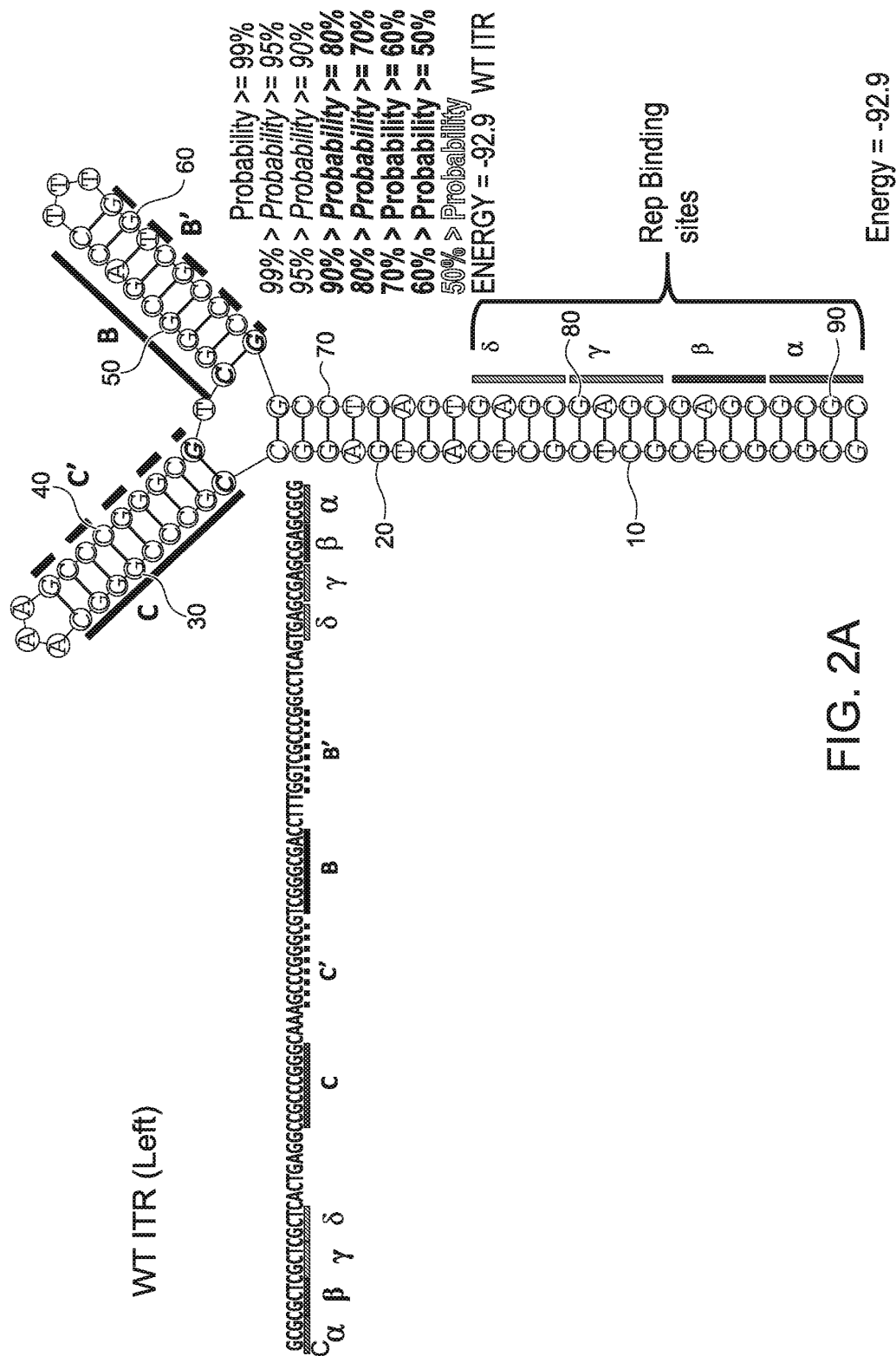




1A
G^x
E





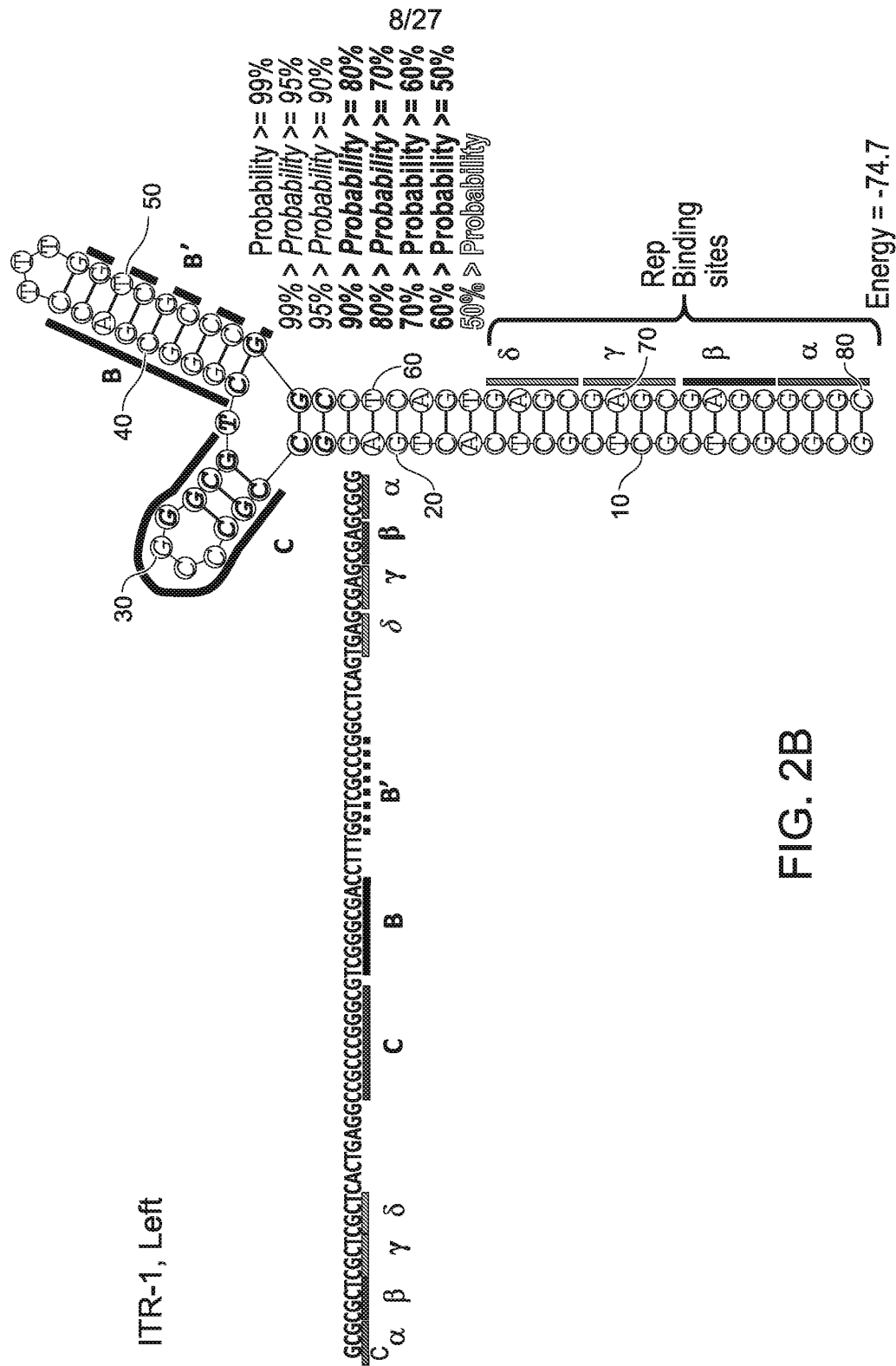


FIG. 2B

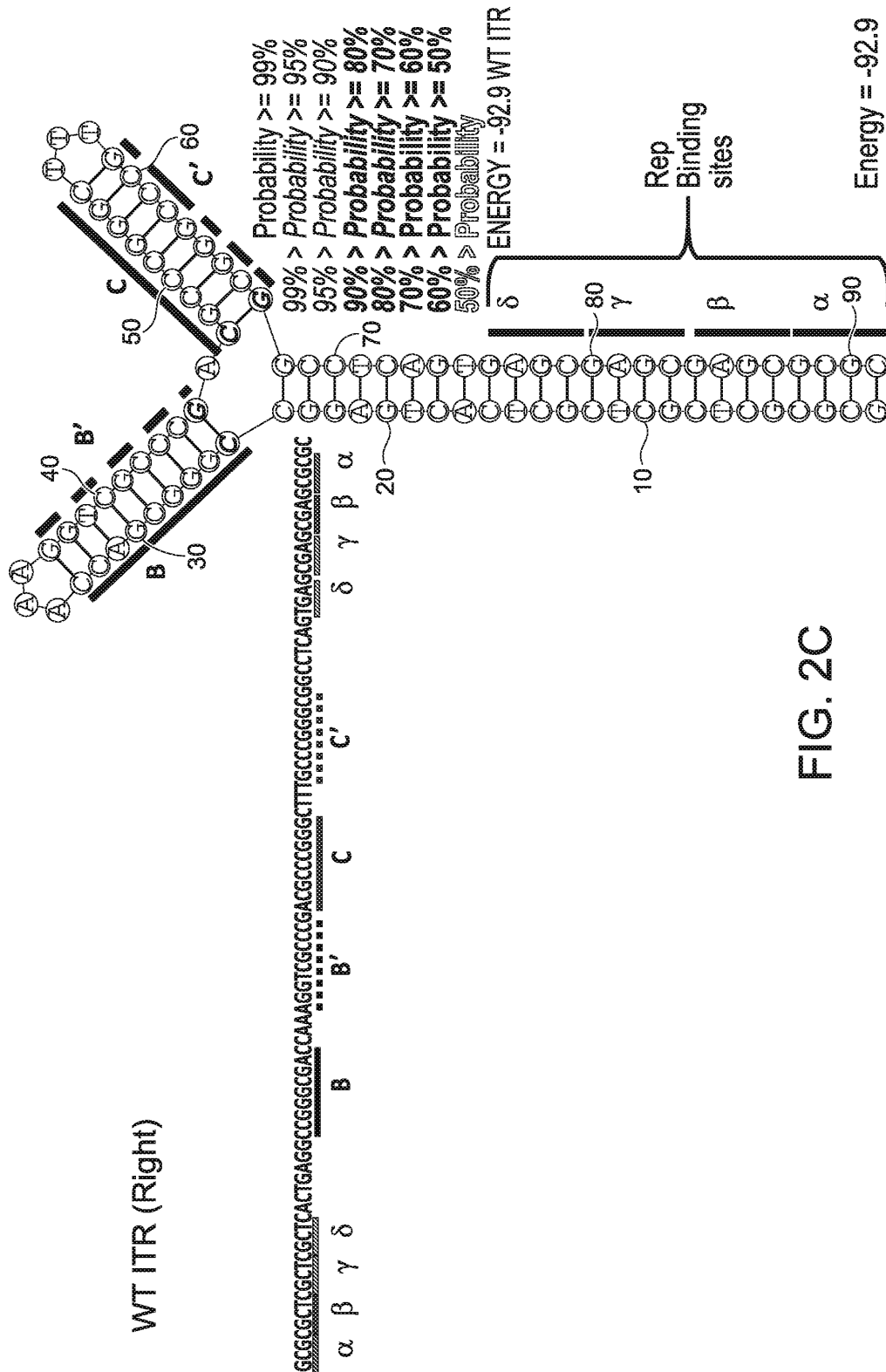


FIG. 2C

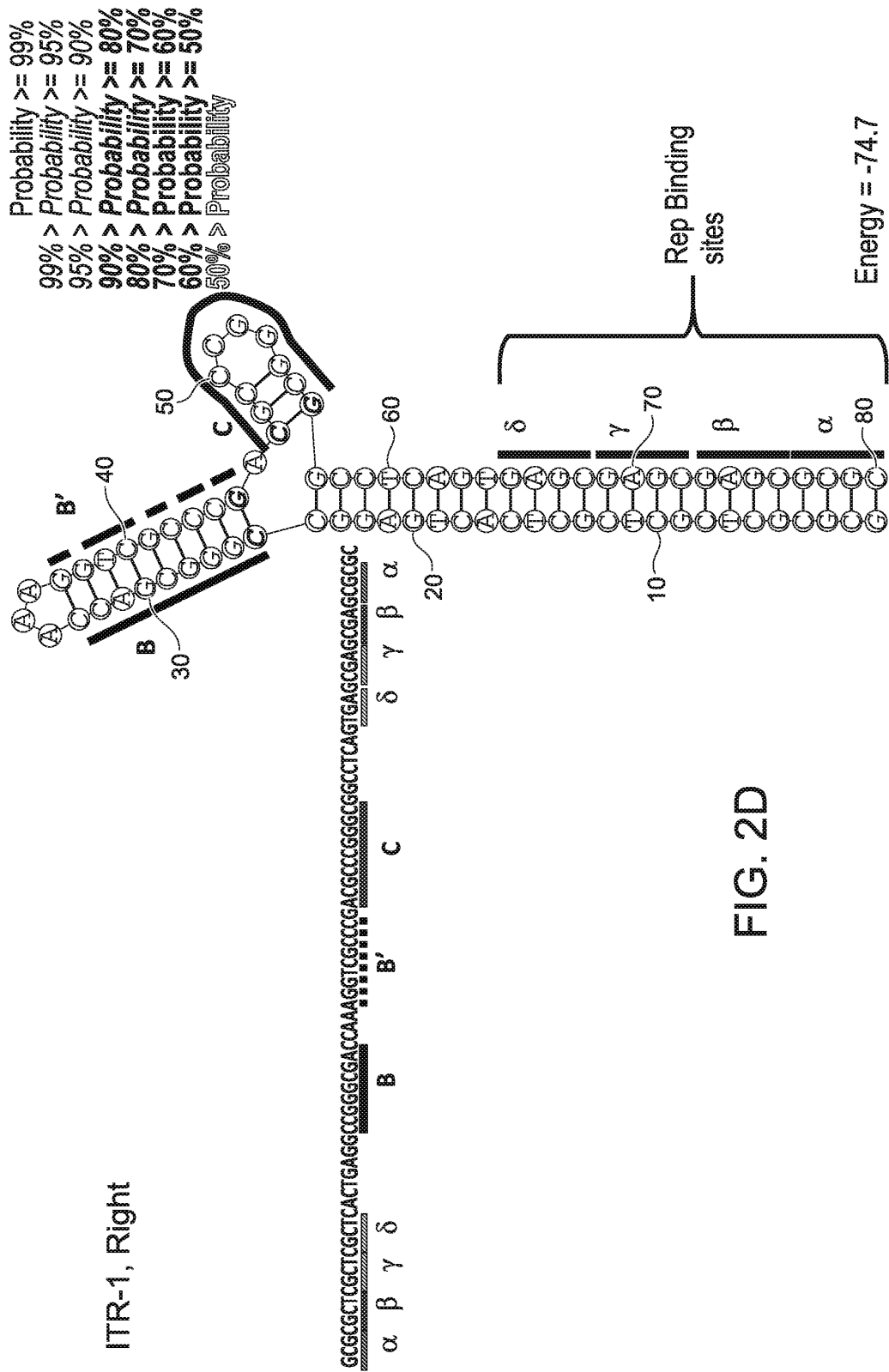


FIG. 2D

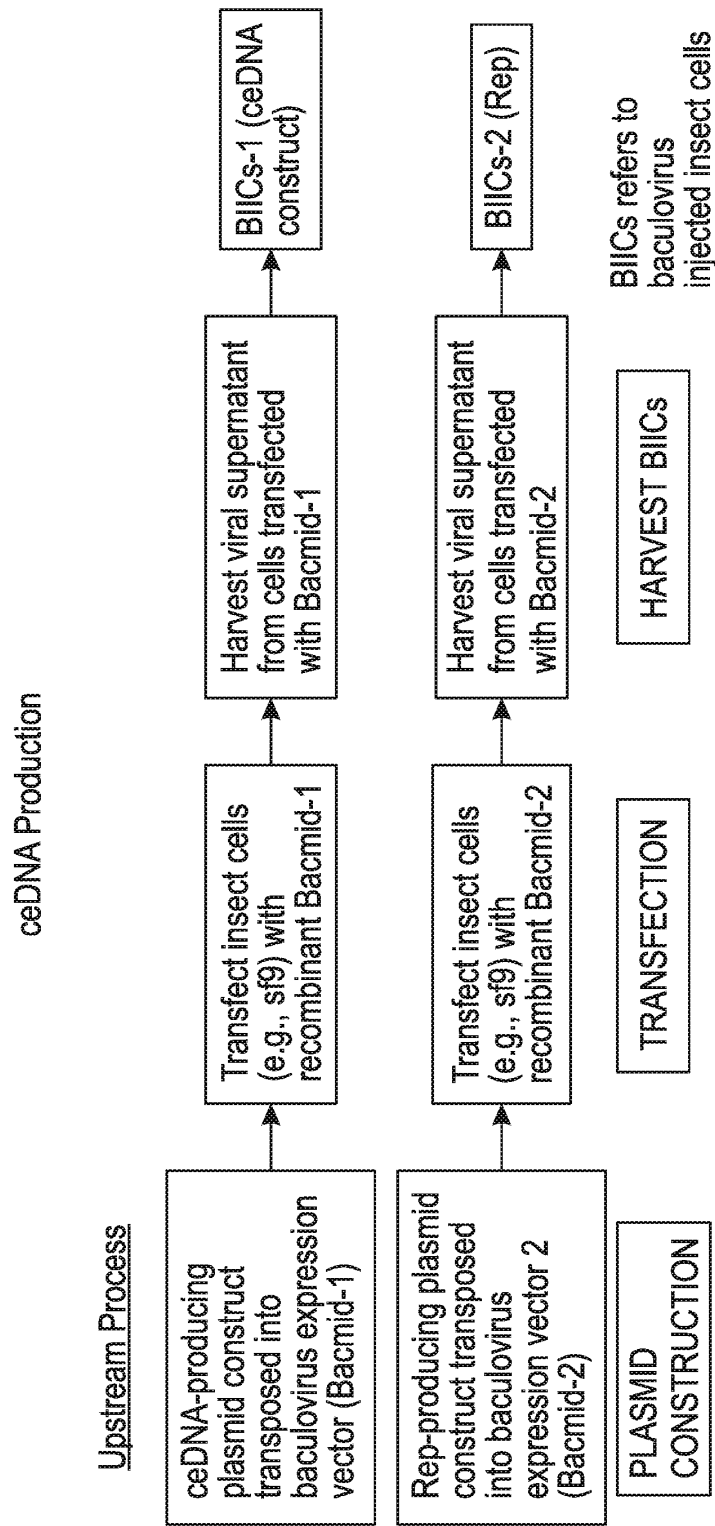


FIG. 3A

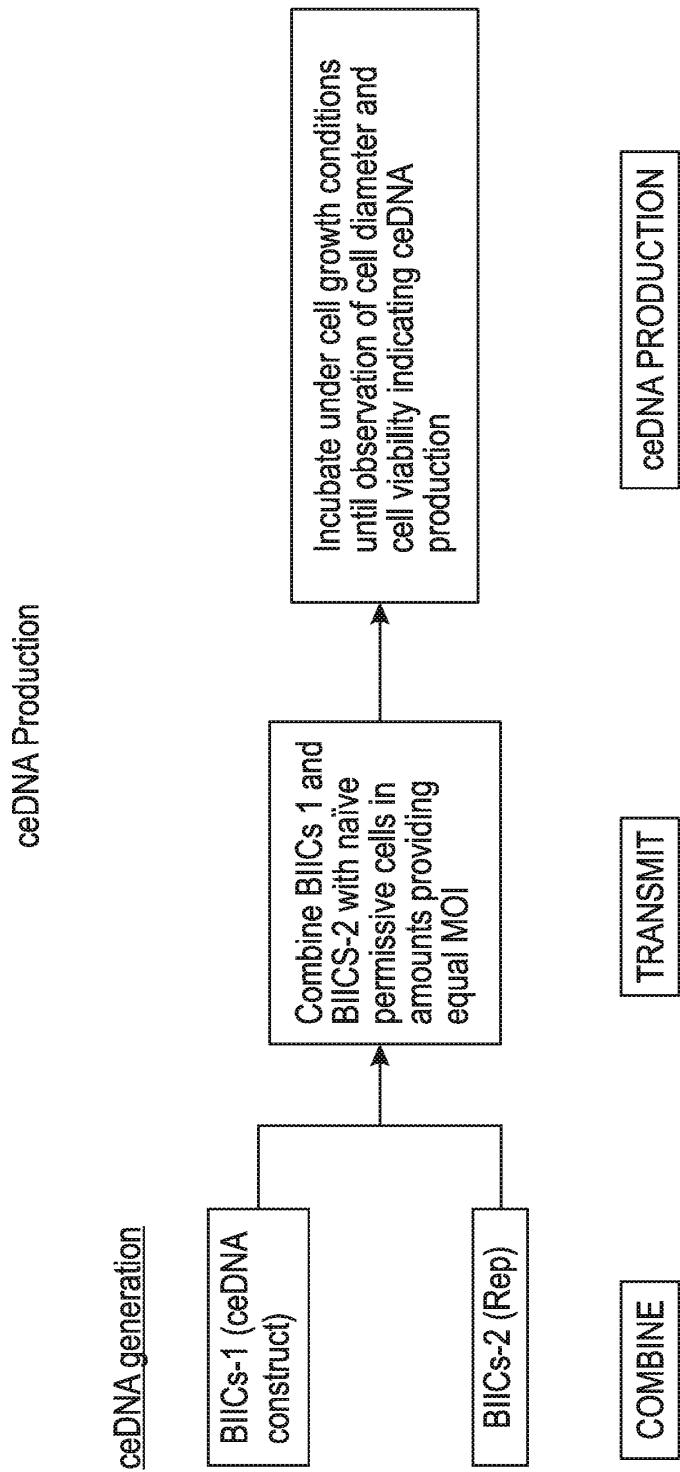


FIG. 3B

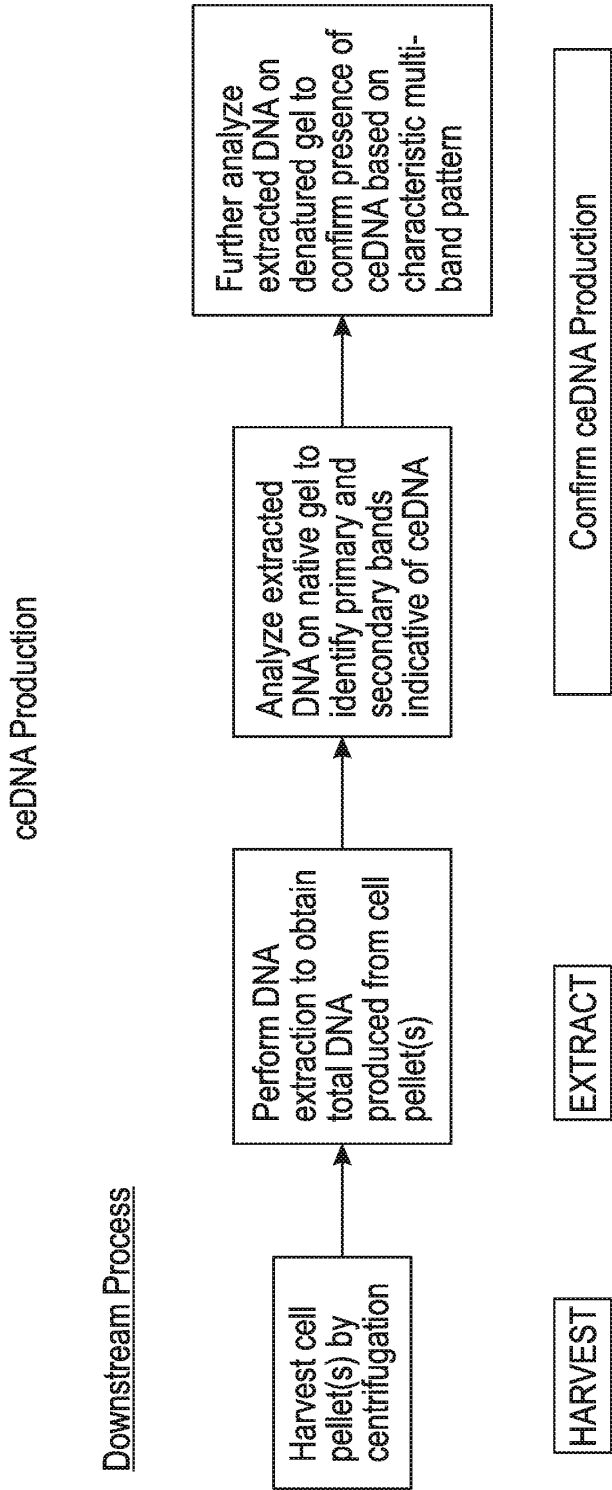


FIG. 3C

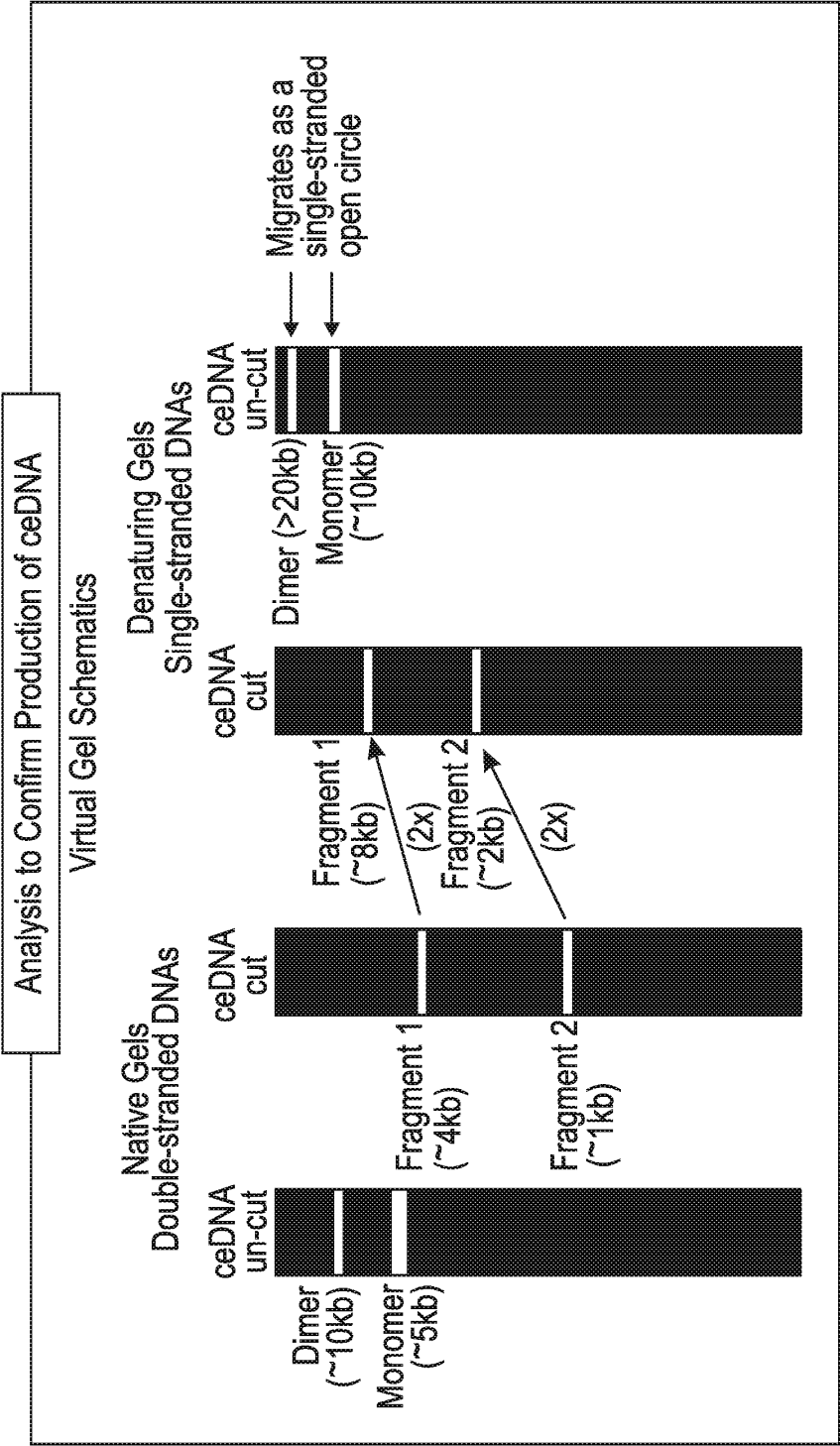


FIG. 3D

FIG. 3E

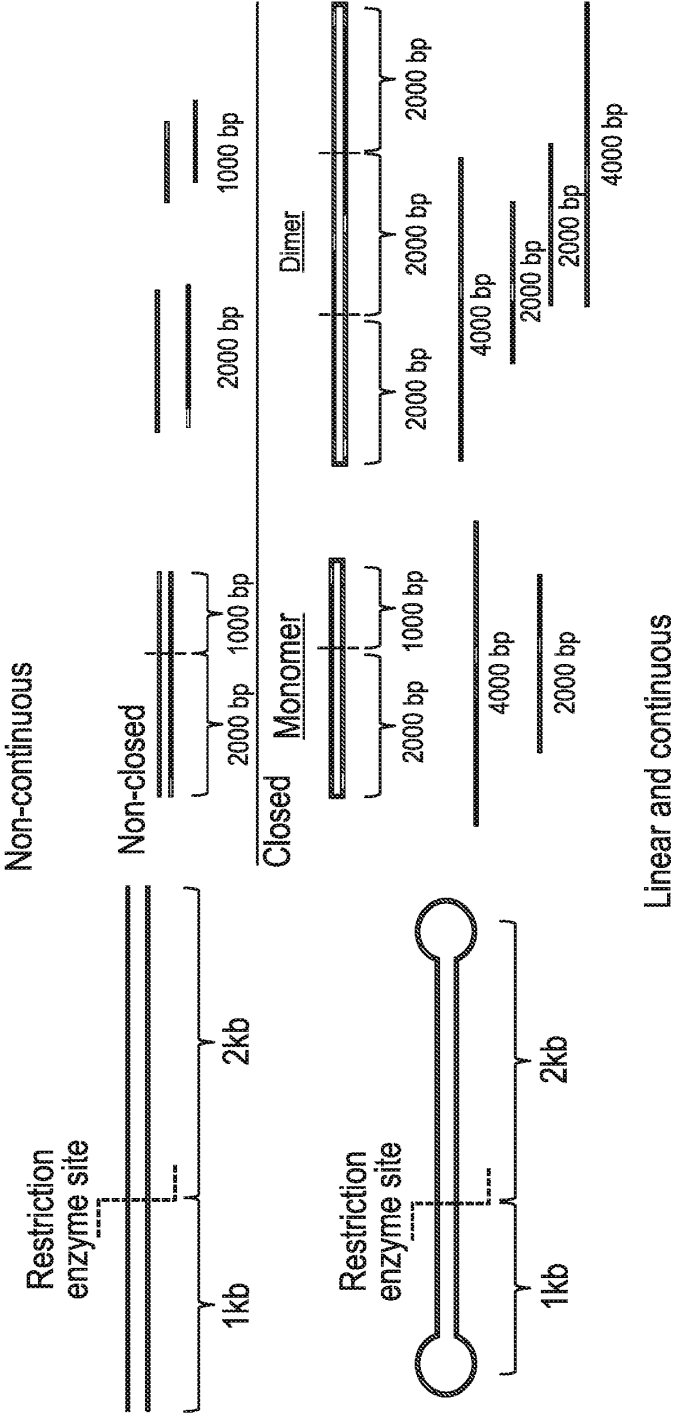


FIG. 4

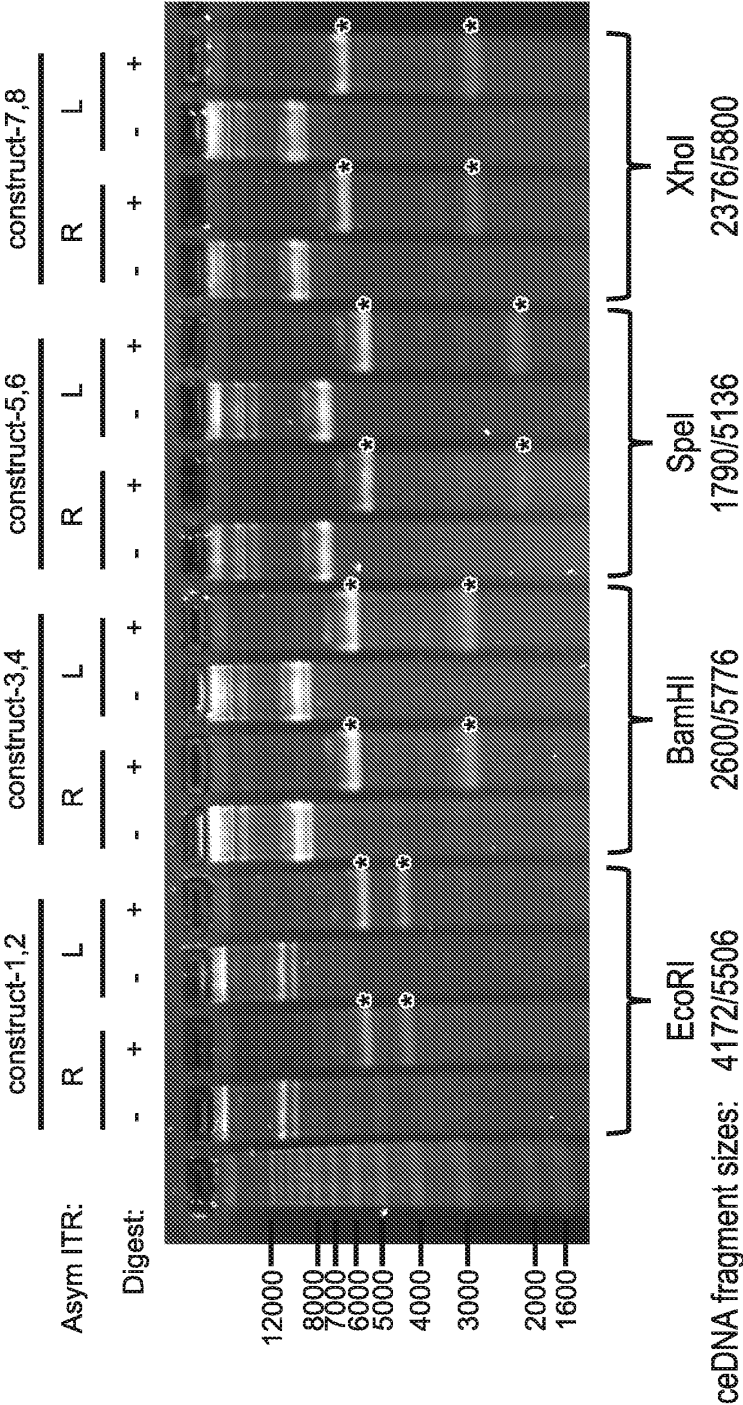
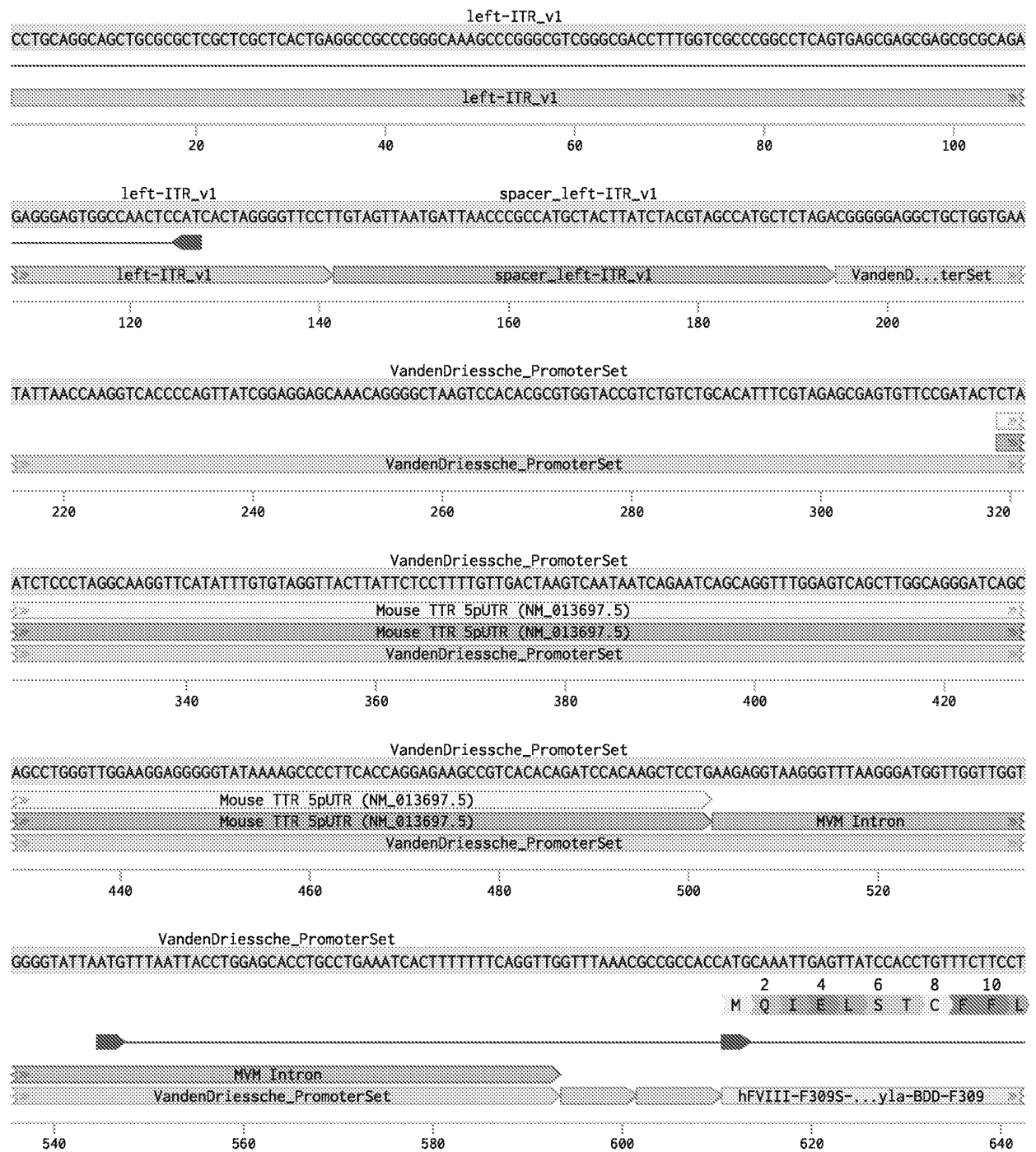
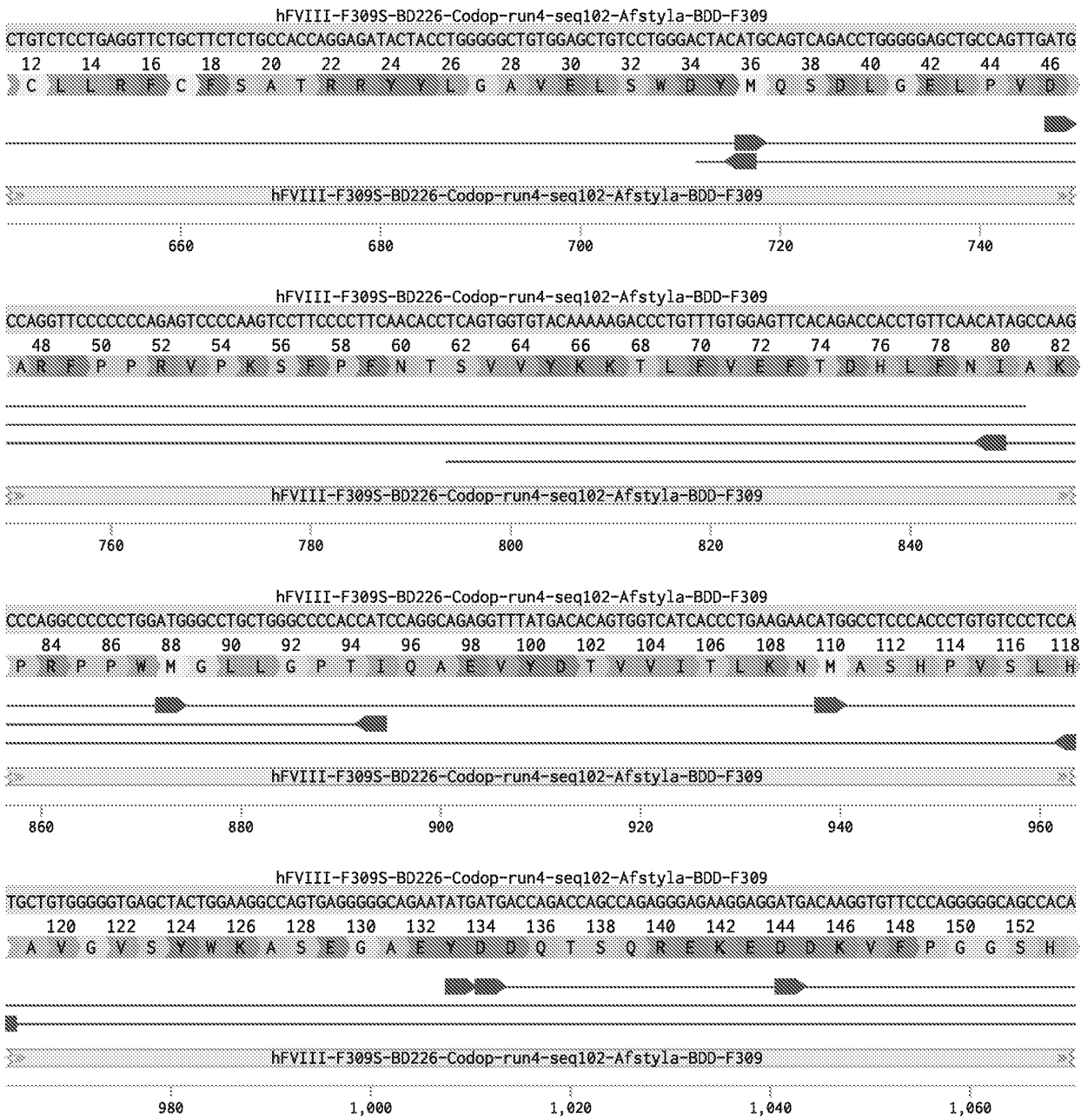


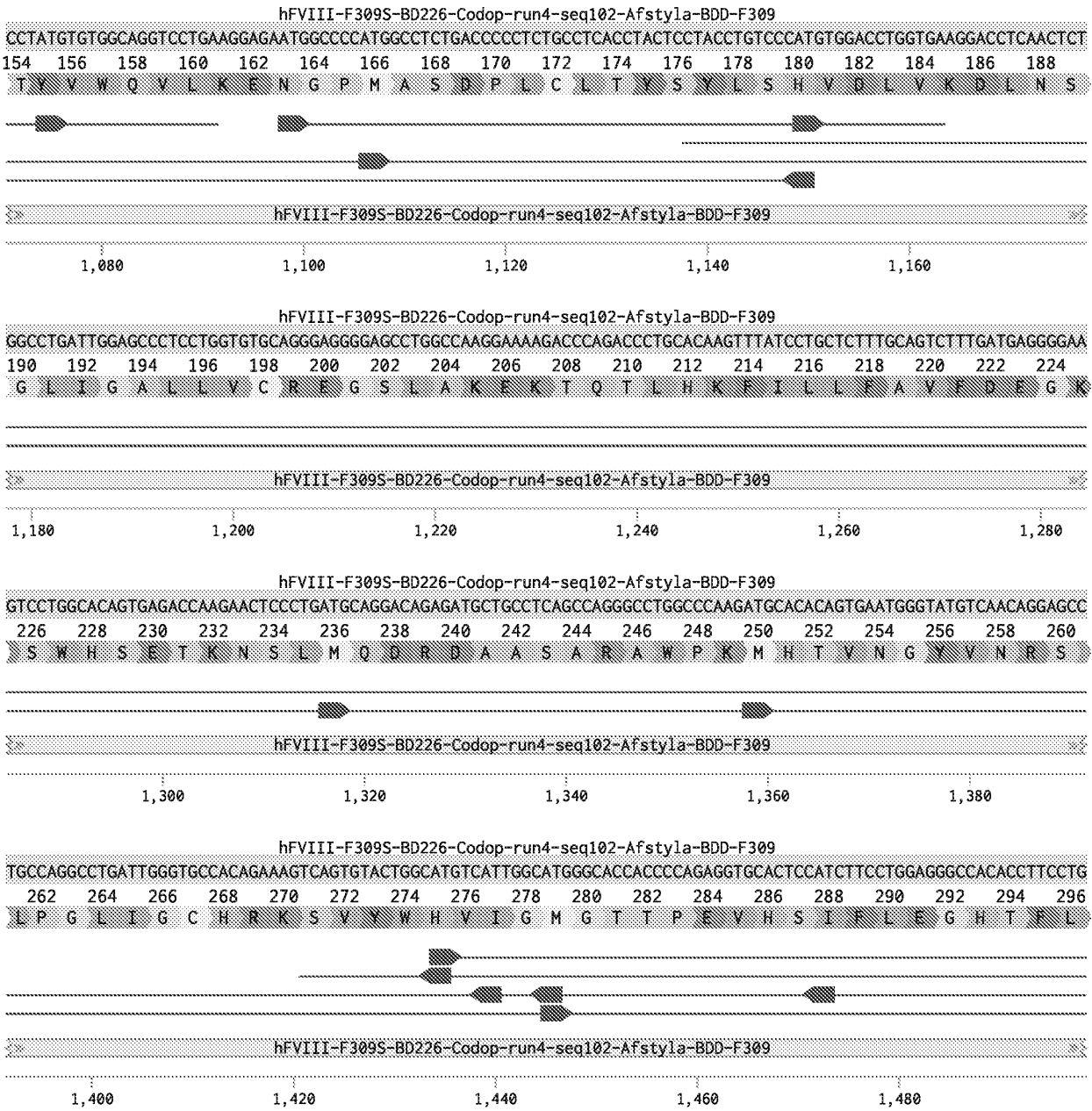
FIG. 5
ceDNA1368 (6007 bp)
(from 1-642 bp)



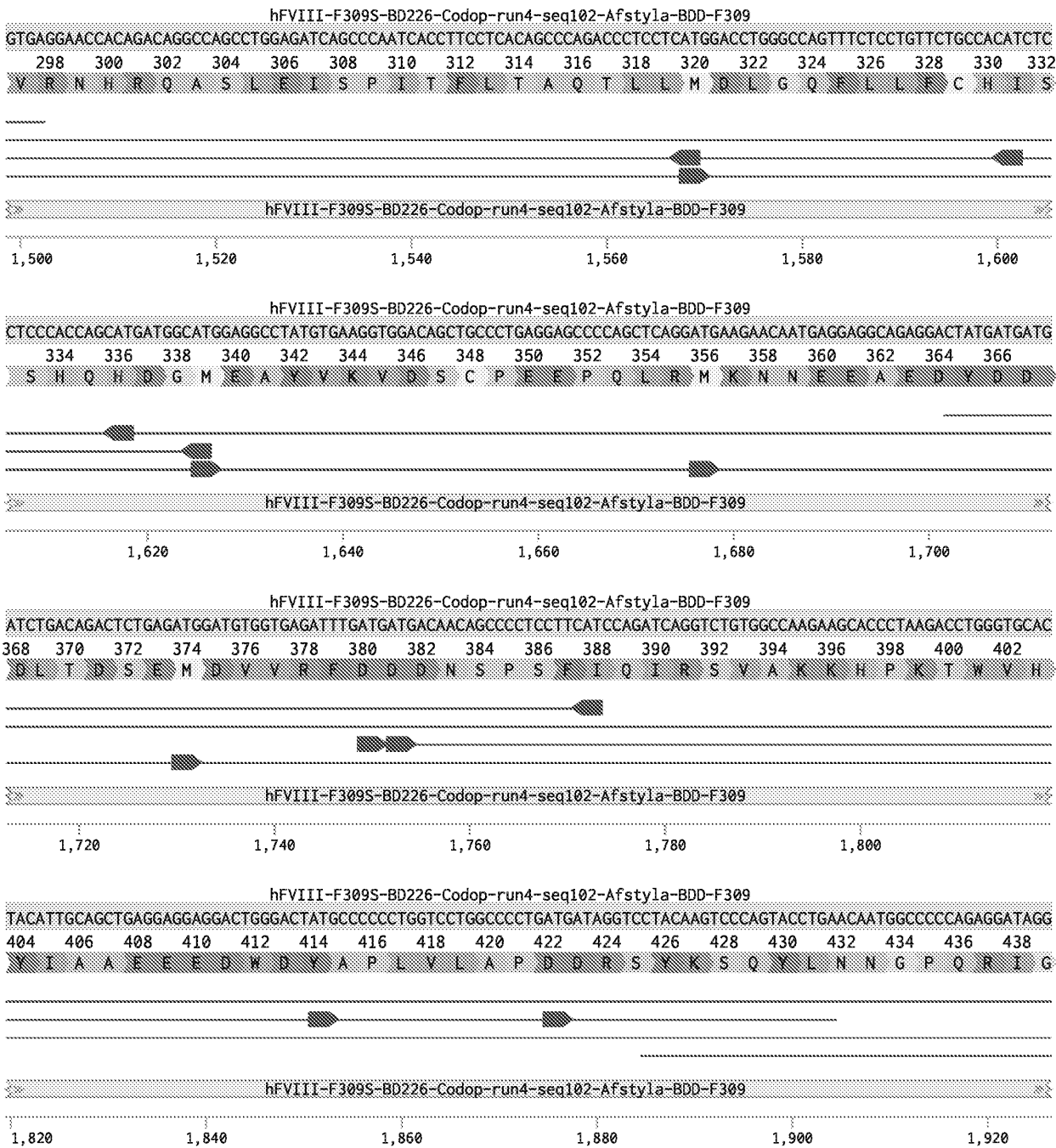
ceDNA1368 (6007 bp) (from 643-1070 bp)



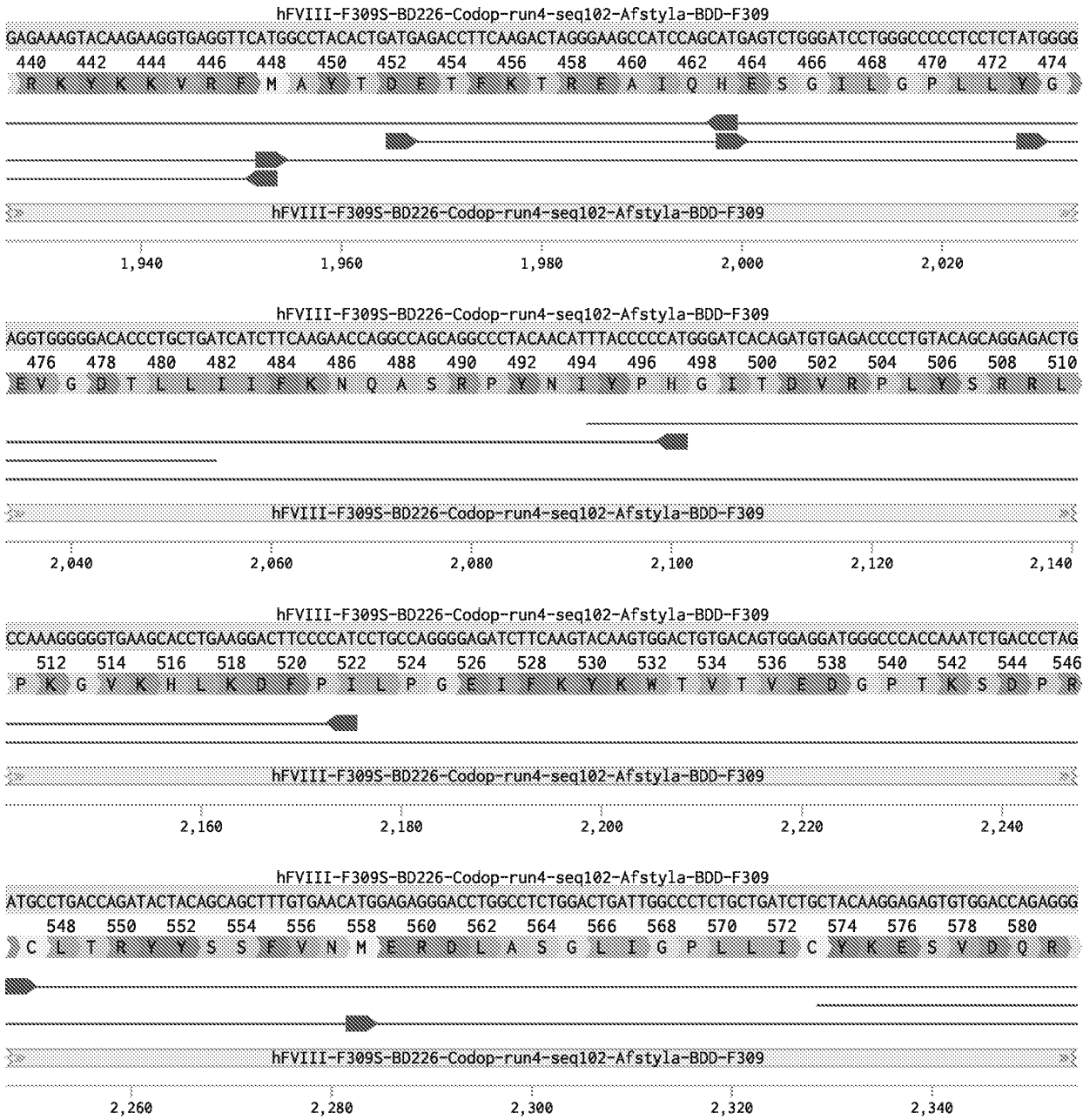
ceDNA1368 (6007 bp) (from 1071-1498 bp)



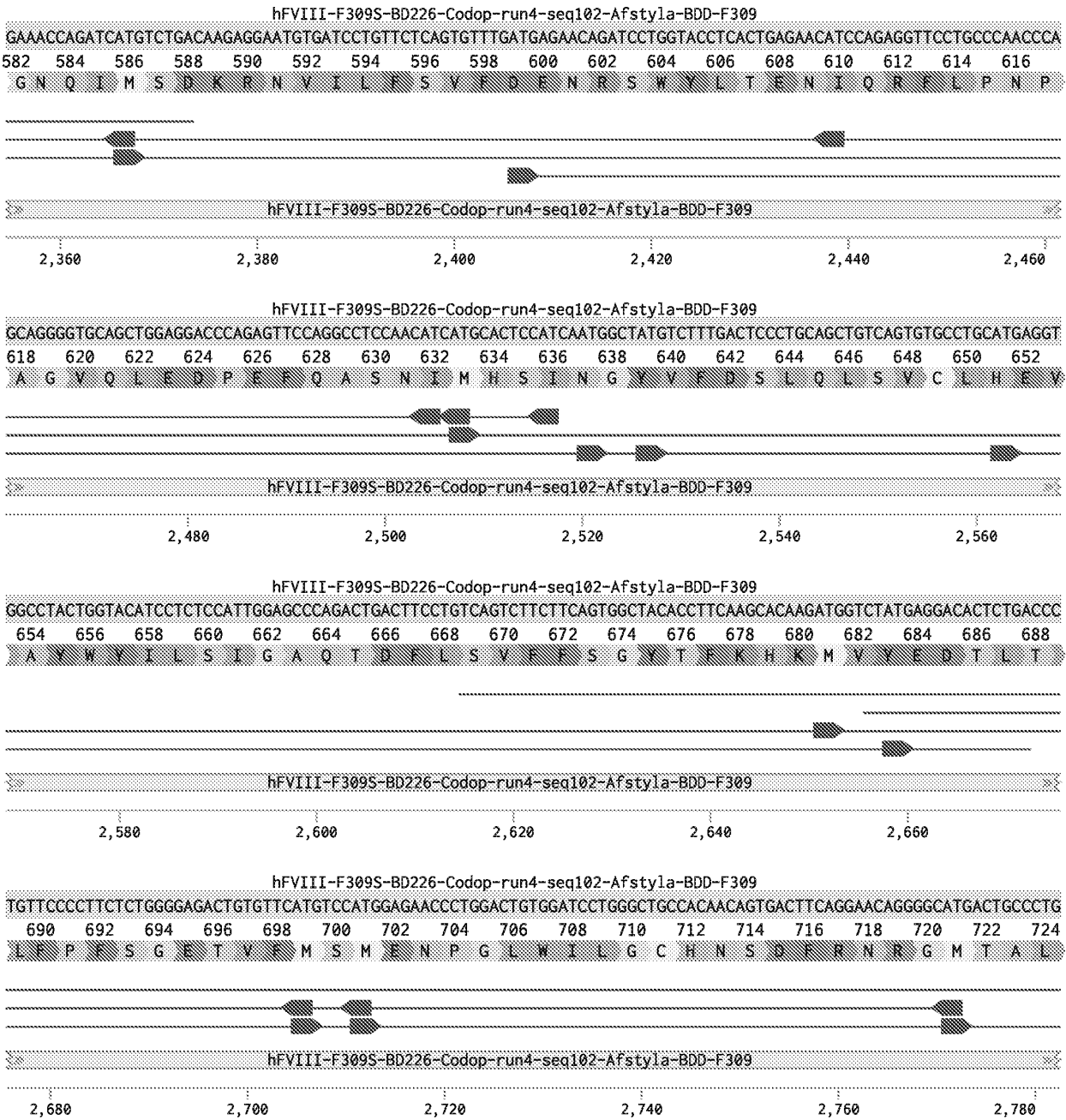
ceDNA1368 (6007 bp) (from 1499-1926 bp)



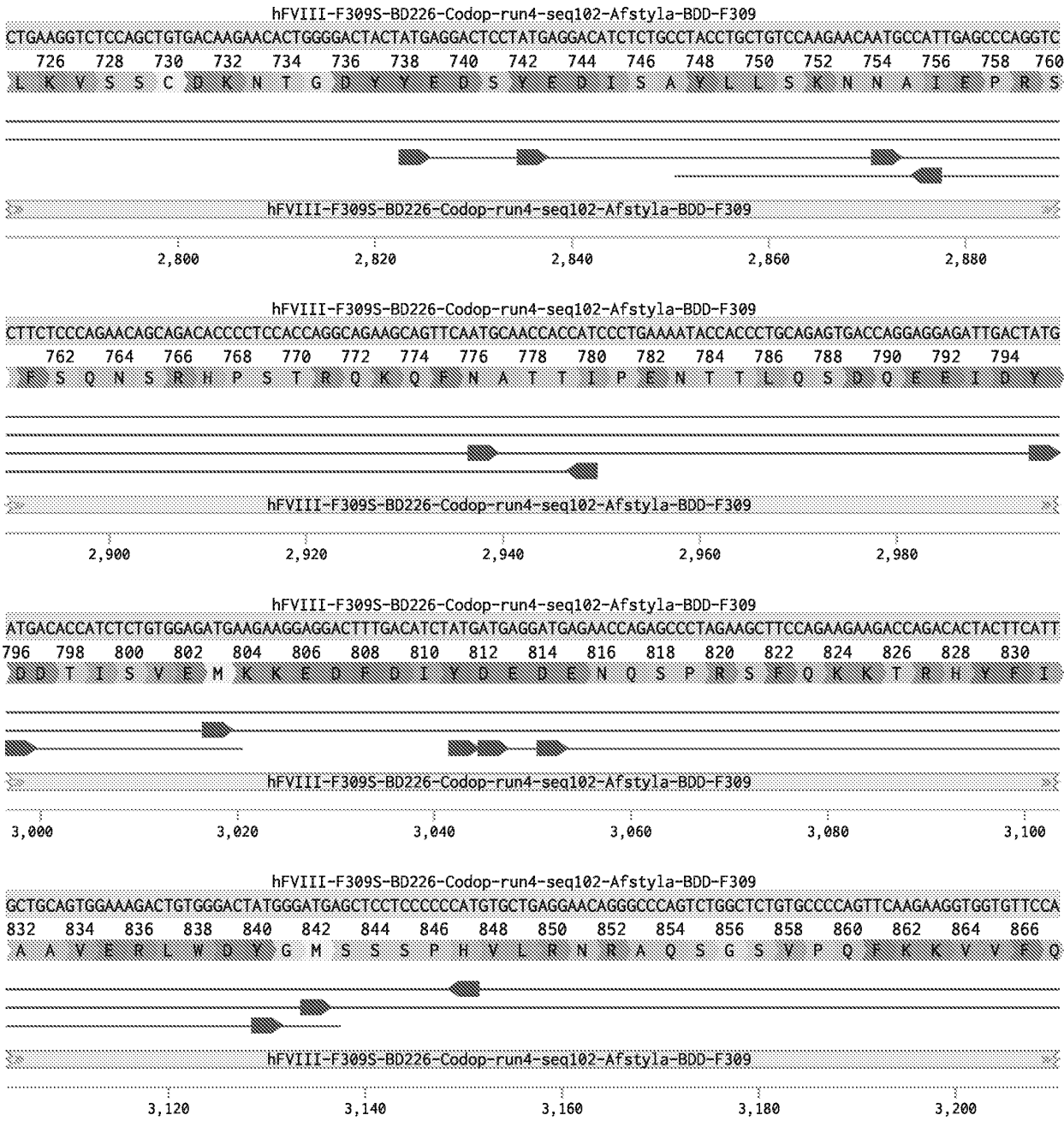
ceDNA1368 (6007 bp) (from 1927-2354 bp)



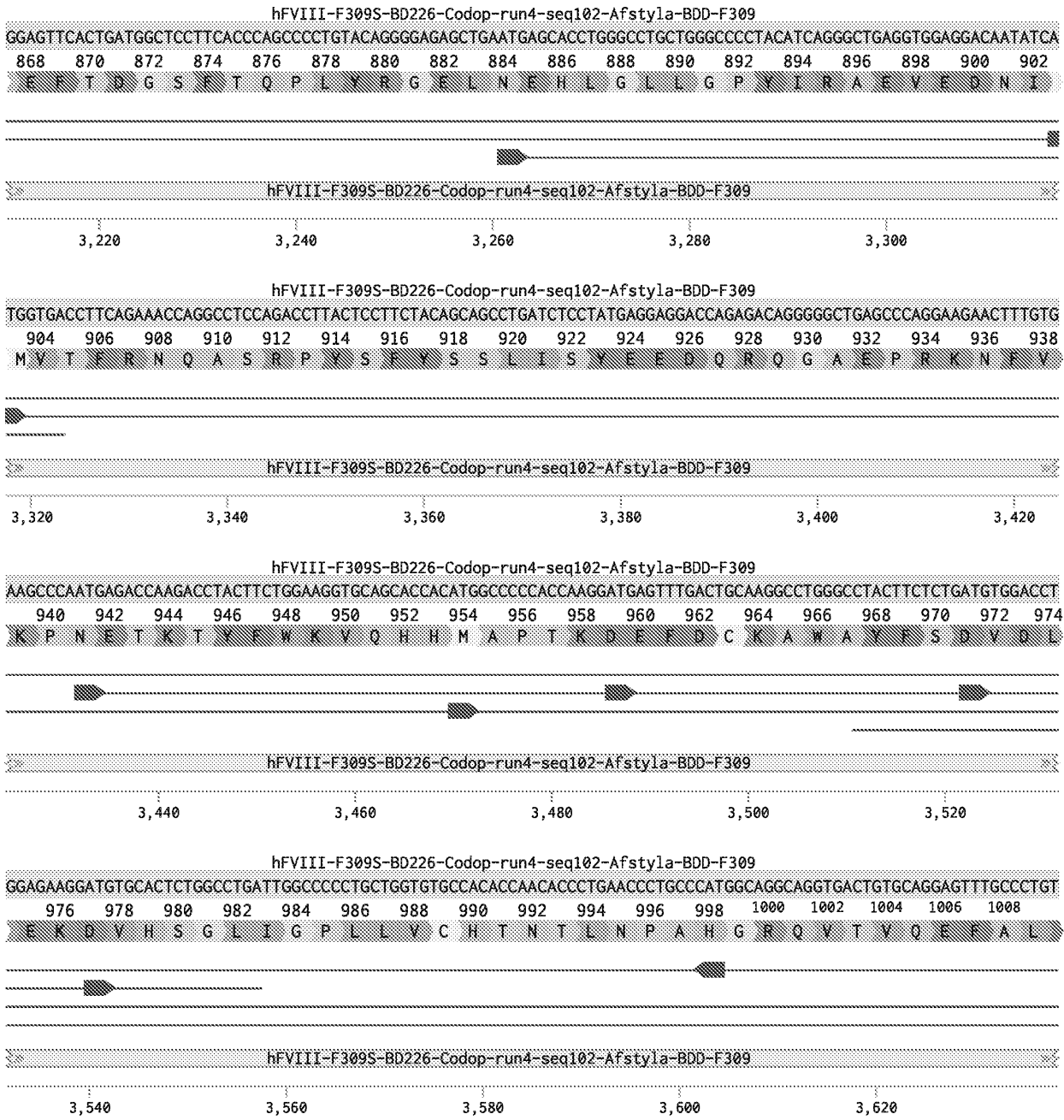
ceDNA1368 (6007 bp) (from 2355-2782 bp)



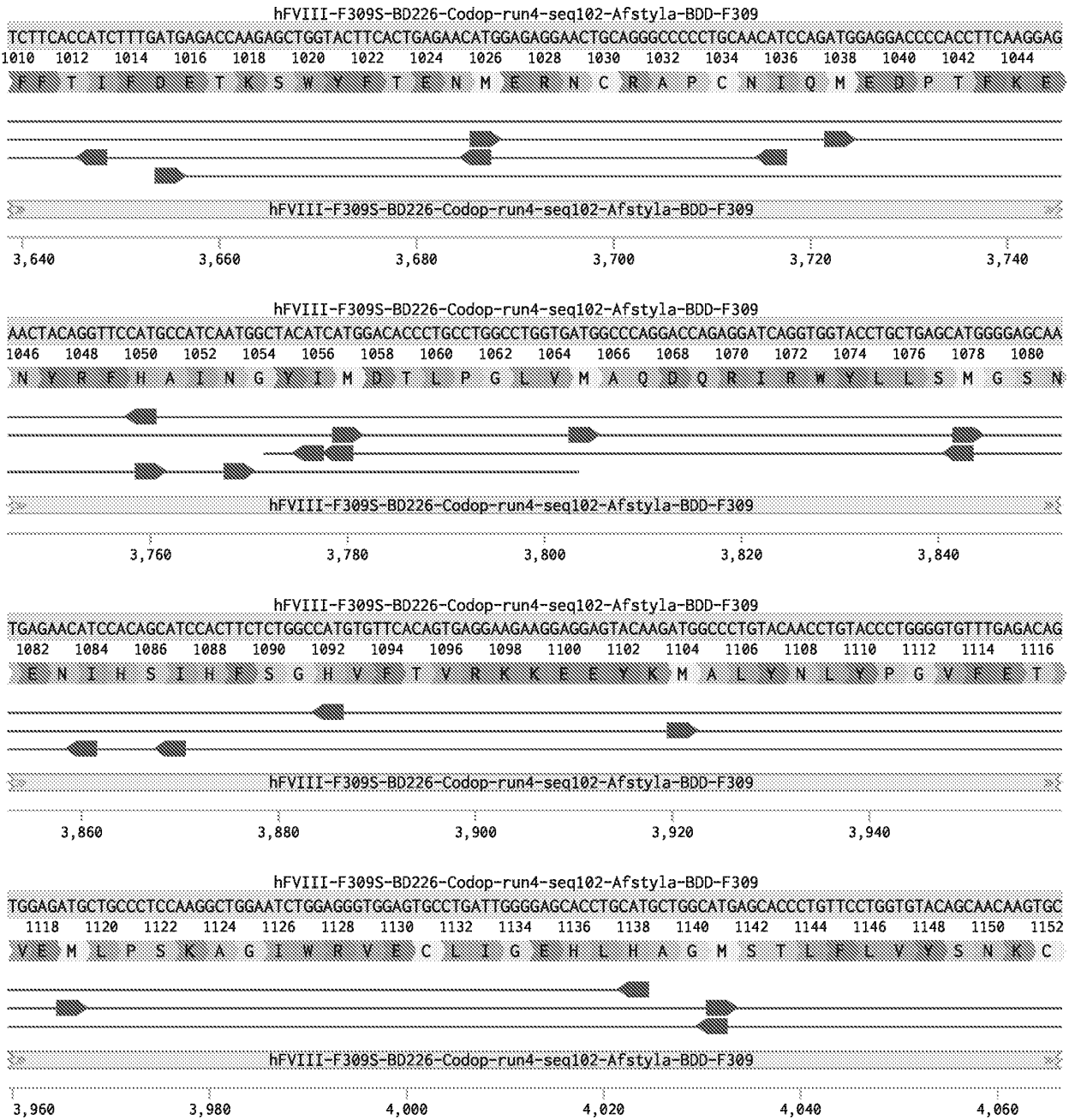
ceDNA1368 (6007 bp) (from 2783-3210 bp)



ceDNA1368 (6007 bp) (from 3211-3638 bp)



ceDNA1368 (6007 bp) (from 3639-4066 bp)



hFVIII-F309S-BD226-Codop-run4-seq102-Afstyla-BDD-F309

CAGACCCCCCTGGGCATGGCCTCTGGCCACATCAGAGACTTCCAGATCACAGCCTCAGGCCAGTATGGCCAGTGGGCCCCCAAGCTGGCCAGGCTGCACTACTCTGG
1154 1156 1158 1160 1162 1164 1166 1168 1170 1172 1174 1176 1178 1180 1182 1184 1186 1188
Q T P L G M A S G H I R D F Q I T A S G Q Y G Q W A P K L A R L H Y S G

hFVIII-F309S-BD226-Codop-run4-seq102-Afstyla-BDD-F309

hFVIII-F309S-BD226-Codop-run4-seq102-Afstyla-BDD-F309

CAGCATCAATGCCTGGTCCACCAAGGAGCCCTTCAGCTGGATCAAGGTGGACCTCCTGGCCCCCATGATCATCCATGGCATCAAGACCCAGGGGGCCAGGCAGAGAAT
1190 1192 1194 1196 1198 1200 1202 1204 1206 1208 1210 1212 1214 1216 1218 1220 1222
S I N A W S T K E P F S W I K V D L L A P M I I H G I K T Q G A R Q K

hFVIII-F309S-BD226-Codop-run4-seq102-Afstyla-BDD-F309

hFVIII-F309S-BD226-Codop-run4-seq102-Afstyla-BDD-F309

TCAGTCCCTGTACATCTCCAGTTTCATCATGTACTCCCTGGATGGCAAGAAGTGGCAGACCTACAGAGGCAACAGCACAGGCACCCTGATGGTGTTCTTTGGC
1224 1226 1228 1230 1232 1234 1236 1238 1240 1242 1244 1246 1248 1250 1252 1254 1256 1258
P S S L Y I S Q F I I M Y S L D G K K W Q T Y R G N S T G T L M V F F G

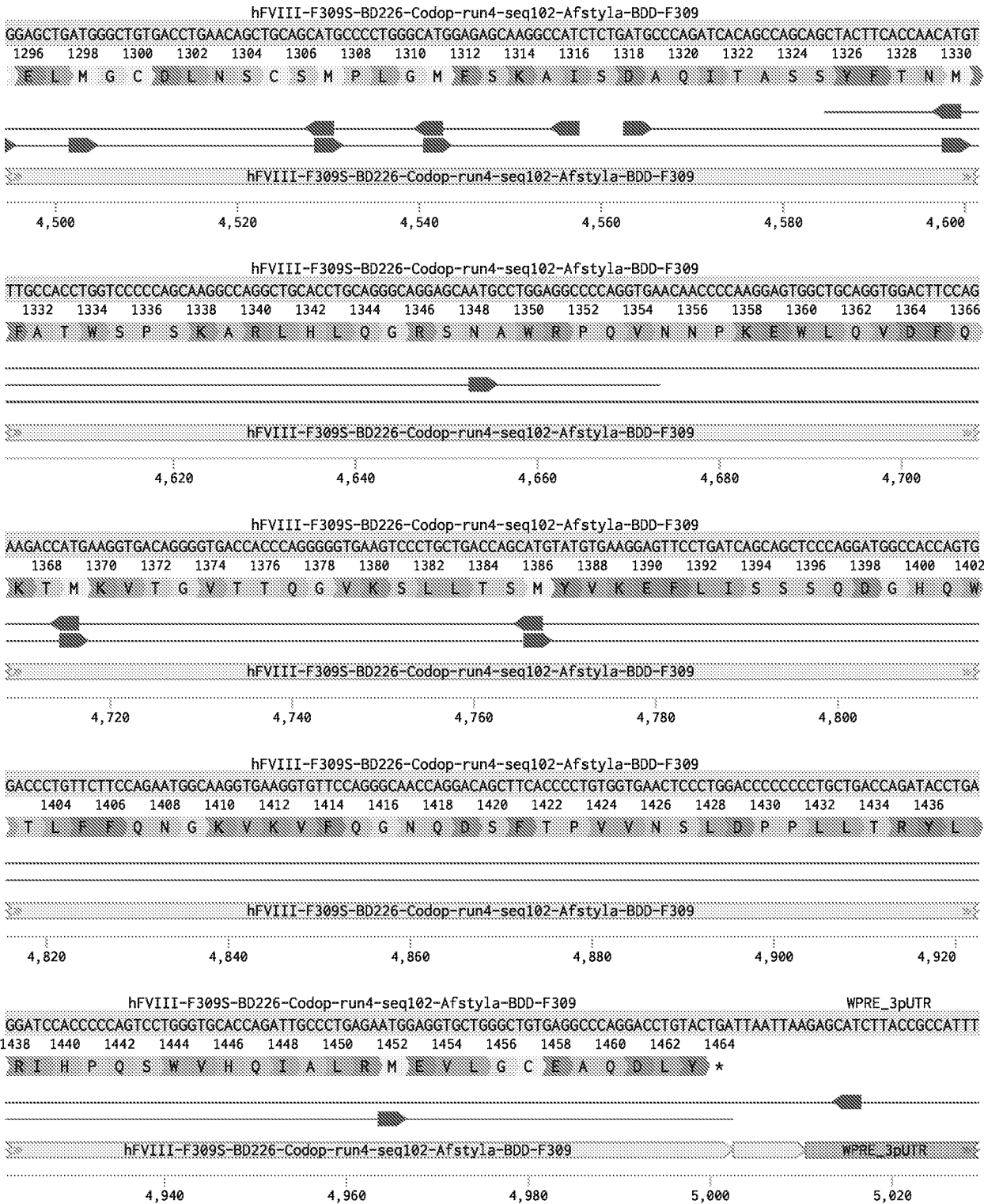
hFVIII-F309S-BD226-Codop-run4-seq102-Afstyla-BDD-F309

hFVIII-F309S-BD226-Codop-run4-seq102-Afstyla-BDD-F309

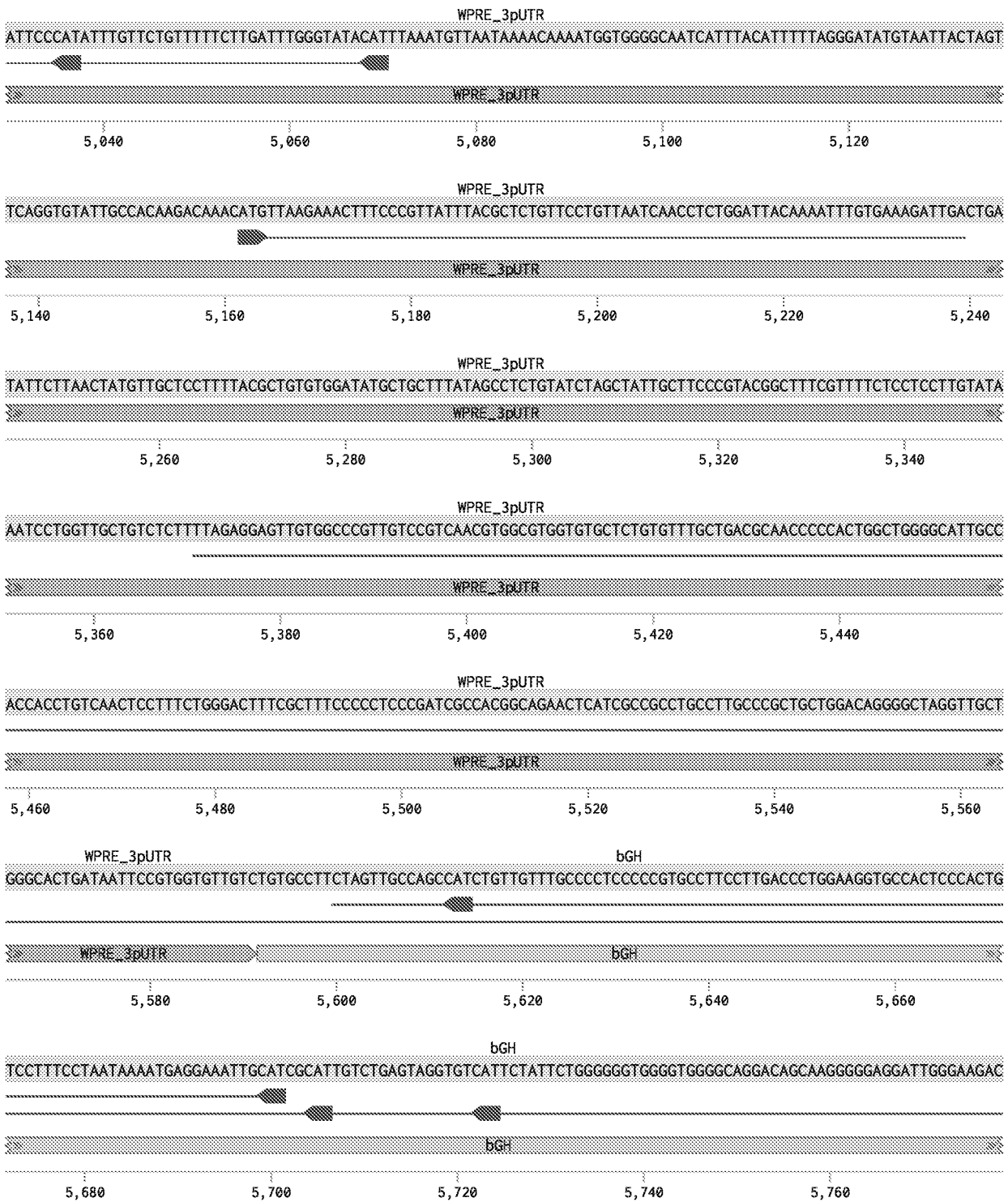
AATGTGGACAGCTCTGGGATCAAGCACAACATCTTCAACCCCCCATCATTGCCAGGTACATCAGACTGCACCCCACTACTCCATCAGGTCCACCCTGAGAAT
1260 1262 1264 1266 1268 1270 1272 1274 1276 1278 1280 1282 1284 1286 1288 1290 1292 1294
N V D S S G I K H N I F N P P I I A R Y I R L H P T H Y S I R S T L R M

hFVIII-F309S-BD226-Codop-run4-seq102-Afstyla-BDD-F309

ceDNA1368 (6007 bp) (from 4495-5029 bp)



ceDNA1368 (6007 bp) (from 5030-5778 bp)

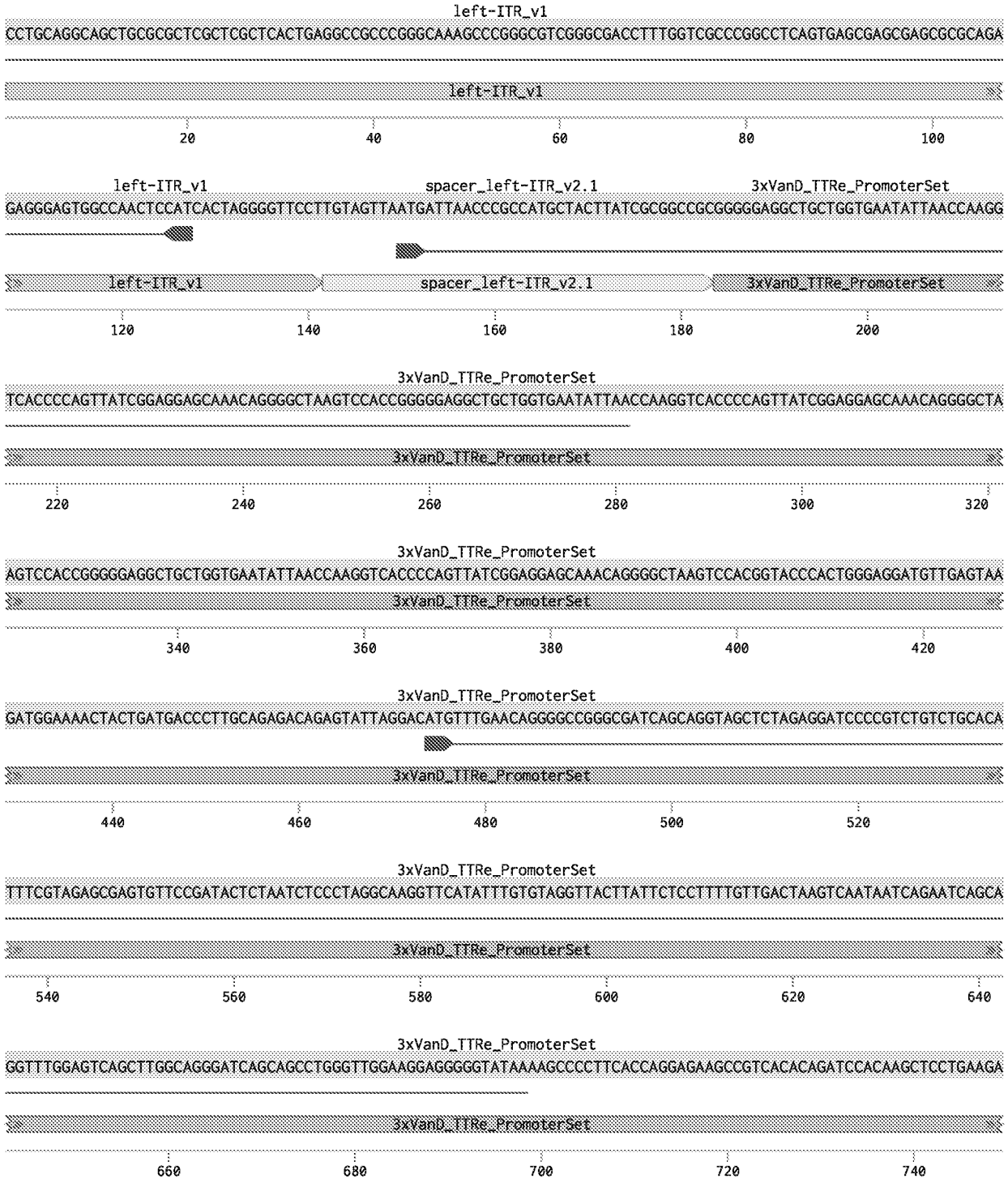


Genomic map of the right-ITR_v1 region. The map shows a DNA sequence with various features labeled. The top track shows the sequence AATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTCTAGAGCATGGCTACGTAGATAAGTAGCATGGCGGGTTAATCATTAACCTACACCTGCAGGAGGAACCC. Below this, a feature labeled 'bGH' is shown as a grey arrow pointing right, starting at position 5,780 and ending at 5,820. Another feature labeled 'spacer_right-ITR_v1' is shown as a grey arrow pointing right, starting at position 5,820 and ending at 5,880. The bottom track shows the sequence CTAGTGATGGAGTTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGGACCAAAGGTCGCCCCGACGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGC. Below this, a feature labeled 'right-ITR_v1' is shown as a grey arrow pointing right, starting at position 5,900 and ending at 5,980. The map includes a scale bar at the bottom with positions 5,780, 5,800, 5,820, 5,840, 5,860, 5,880, 5,900, 5,920, 5,940, 5,960, 5,980, and 6,000.

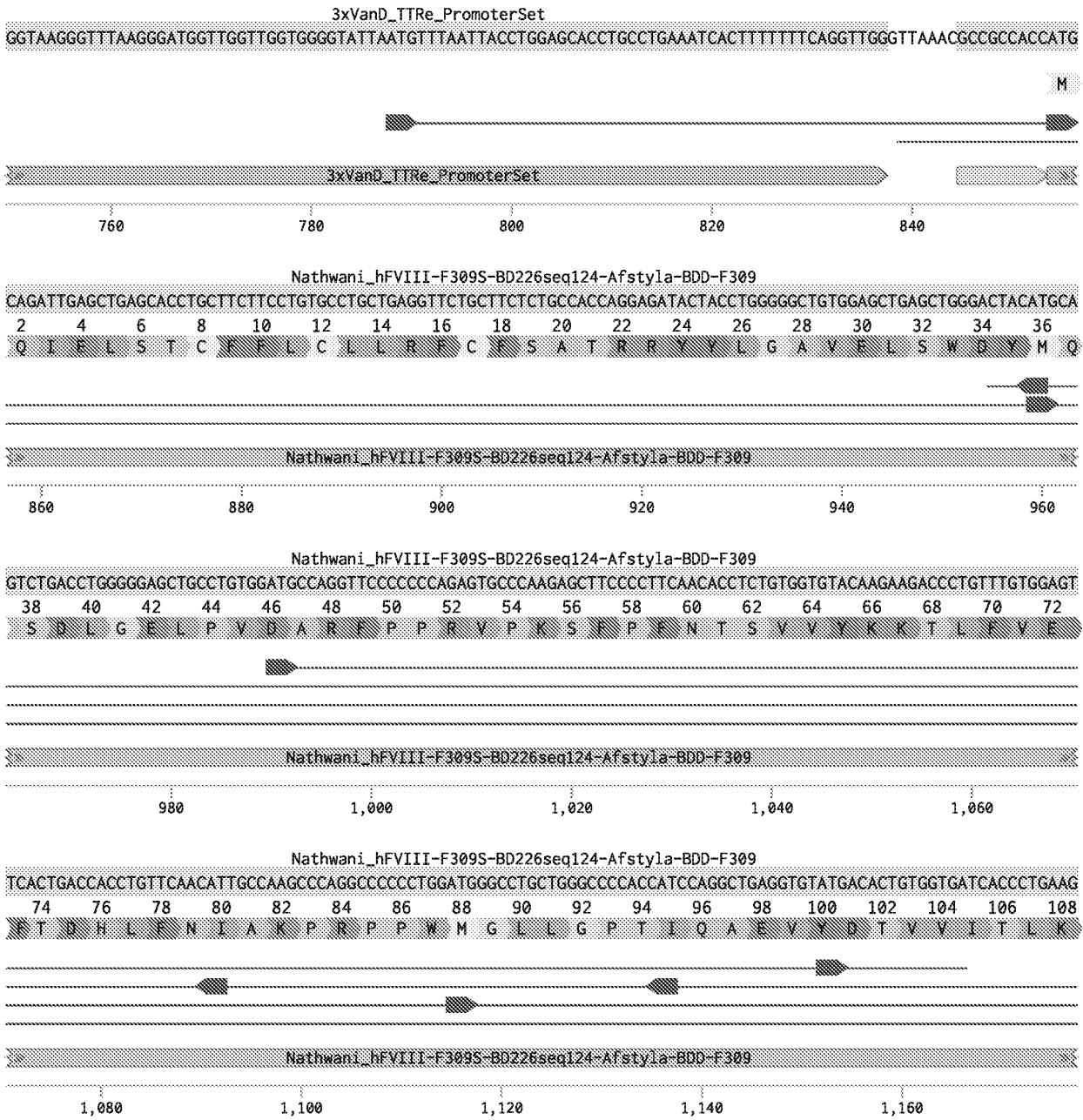
FIG. 6

ceDNA1652 (6250 bp)

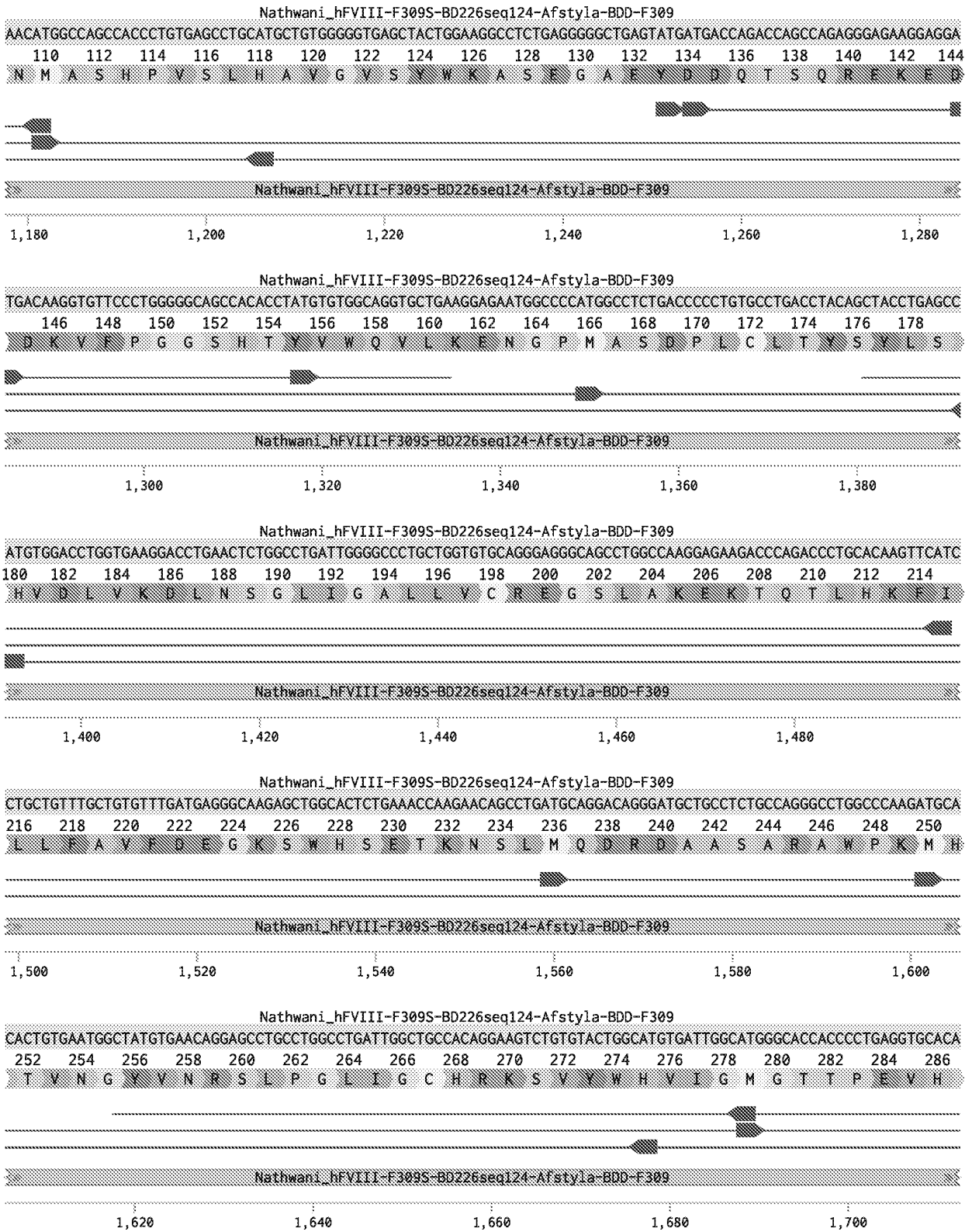
(from 1-749 bp)



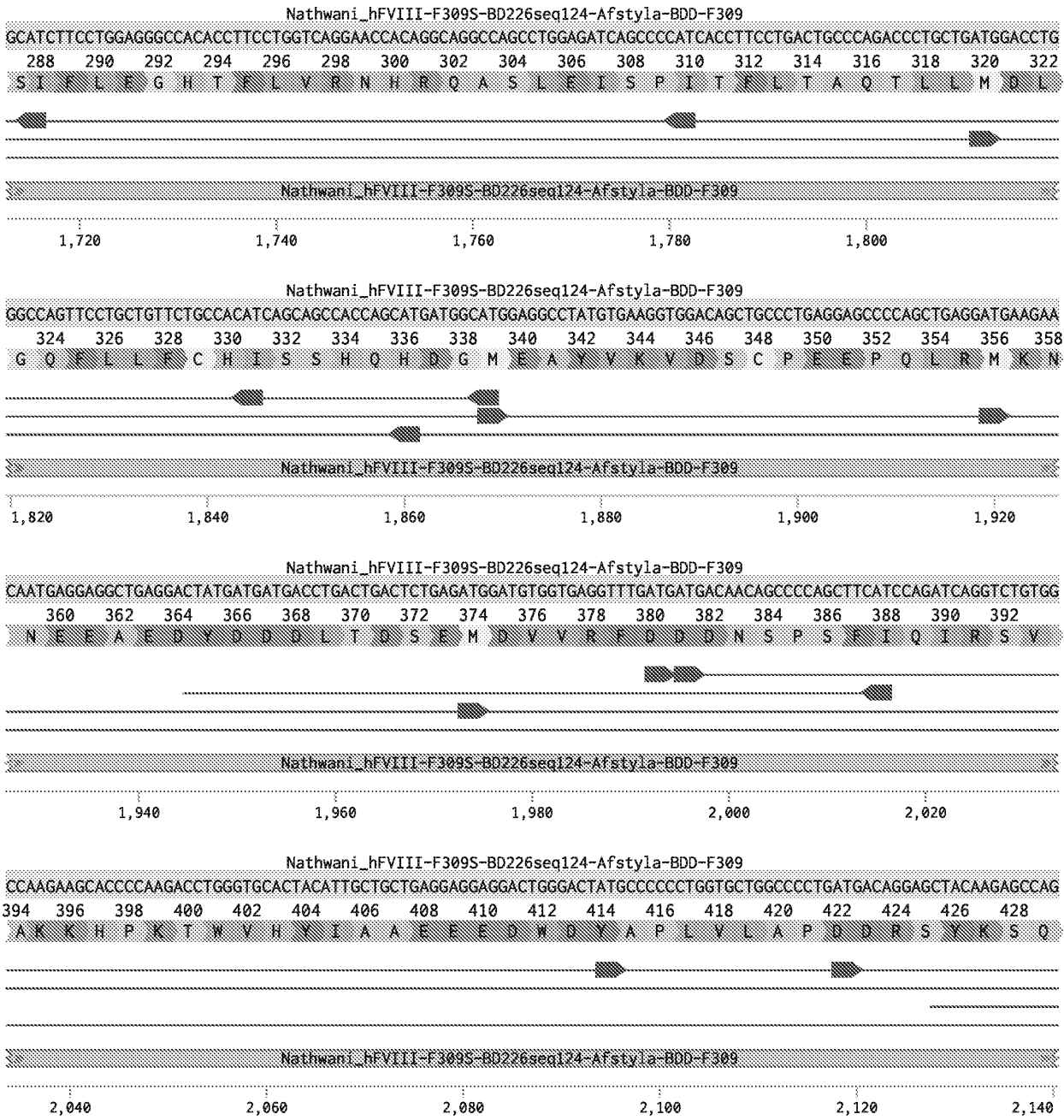
ceDNA1652 (6250 bp) (from 750-1177 bp)



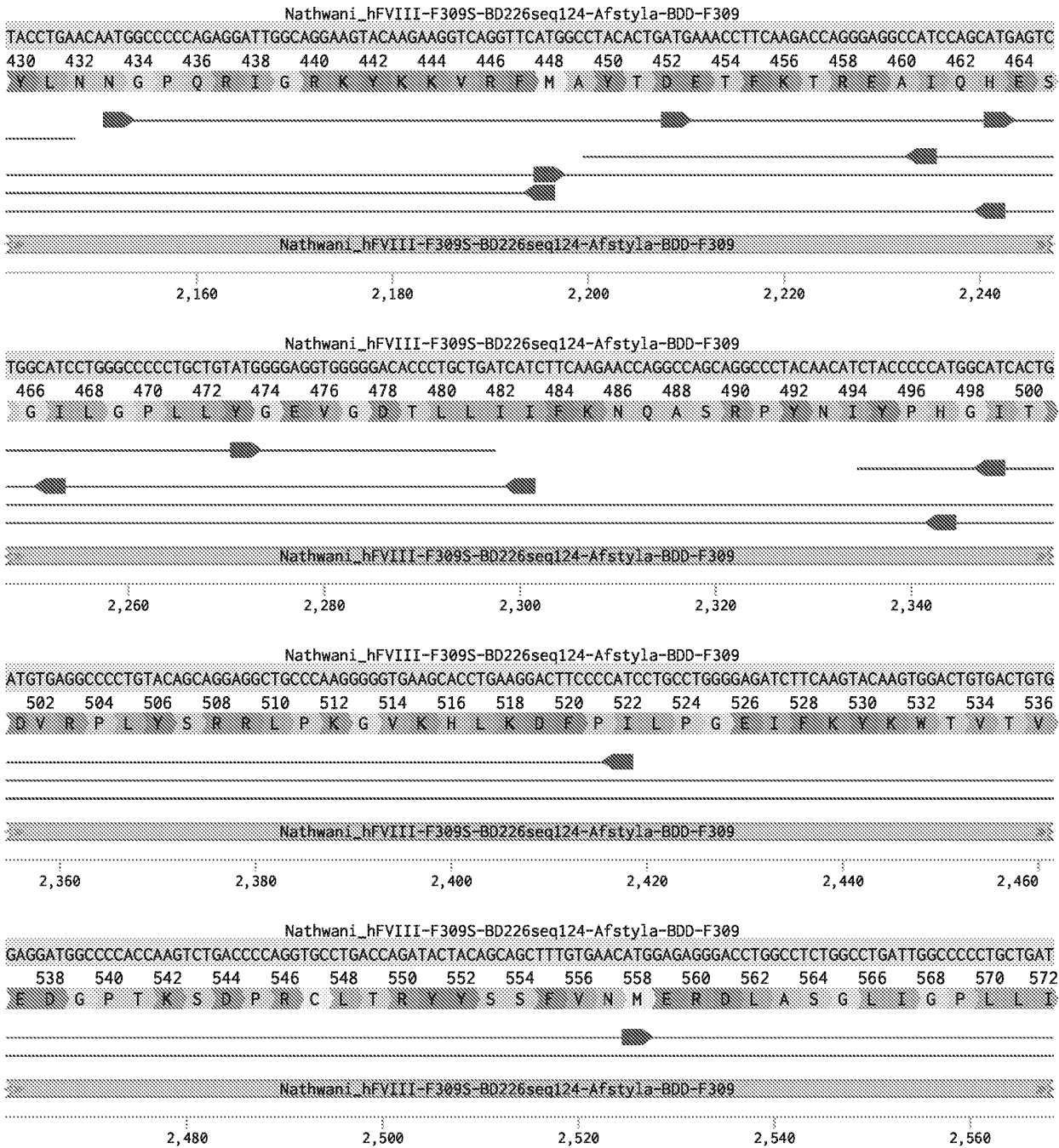
ceDNA1652 (6250 bp) (from 1178-1712 bp)



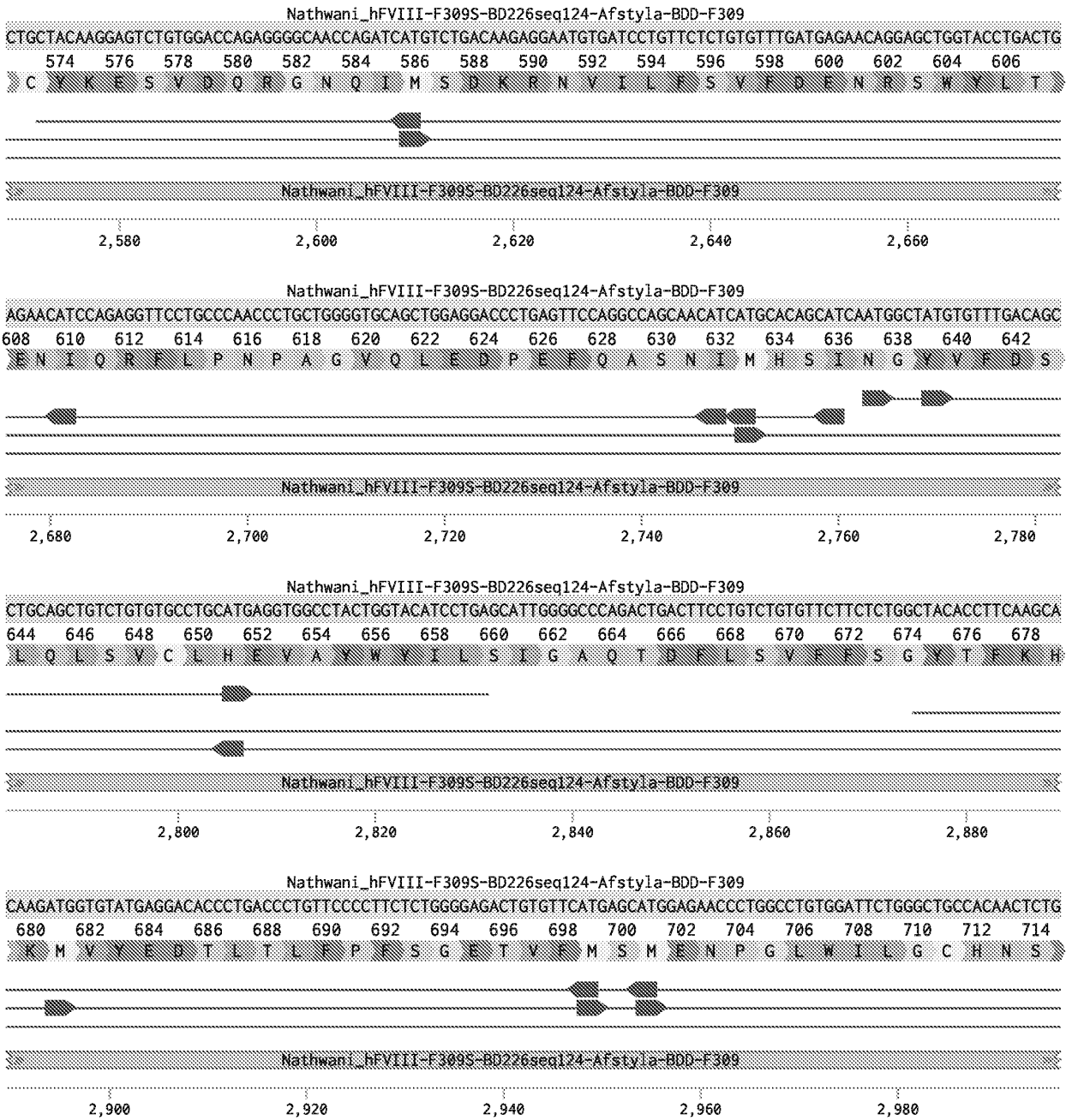
ceDNA1652 (6250 bp) (from 1713-2140 bp)



ceDNA1652 (6250 bp) (from 2141-2568 bp)

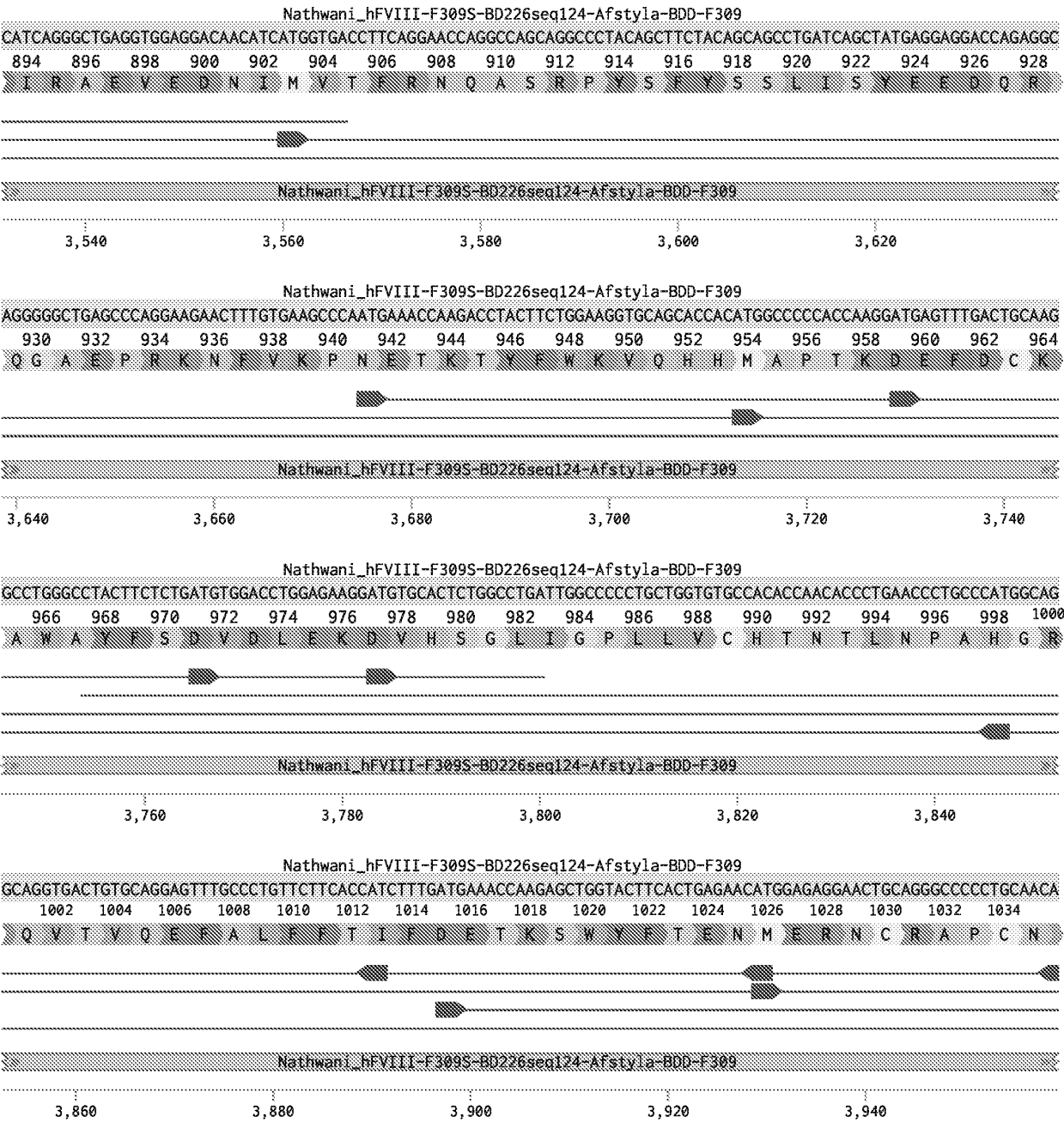


ceDNA1652 (6250 bp) (from 2569-2996 bp)

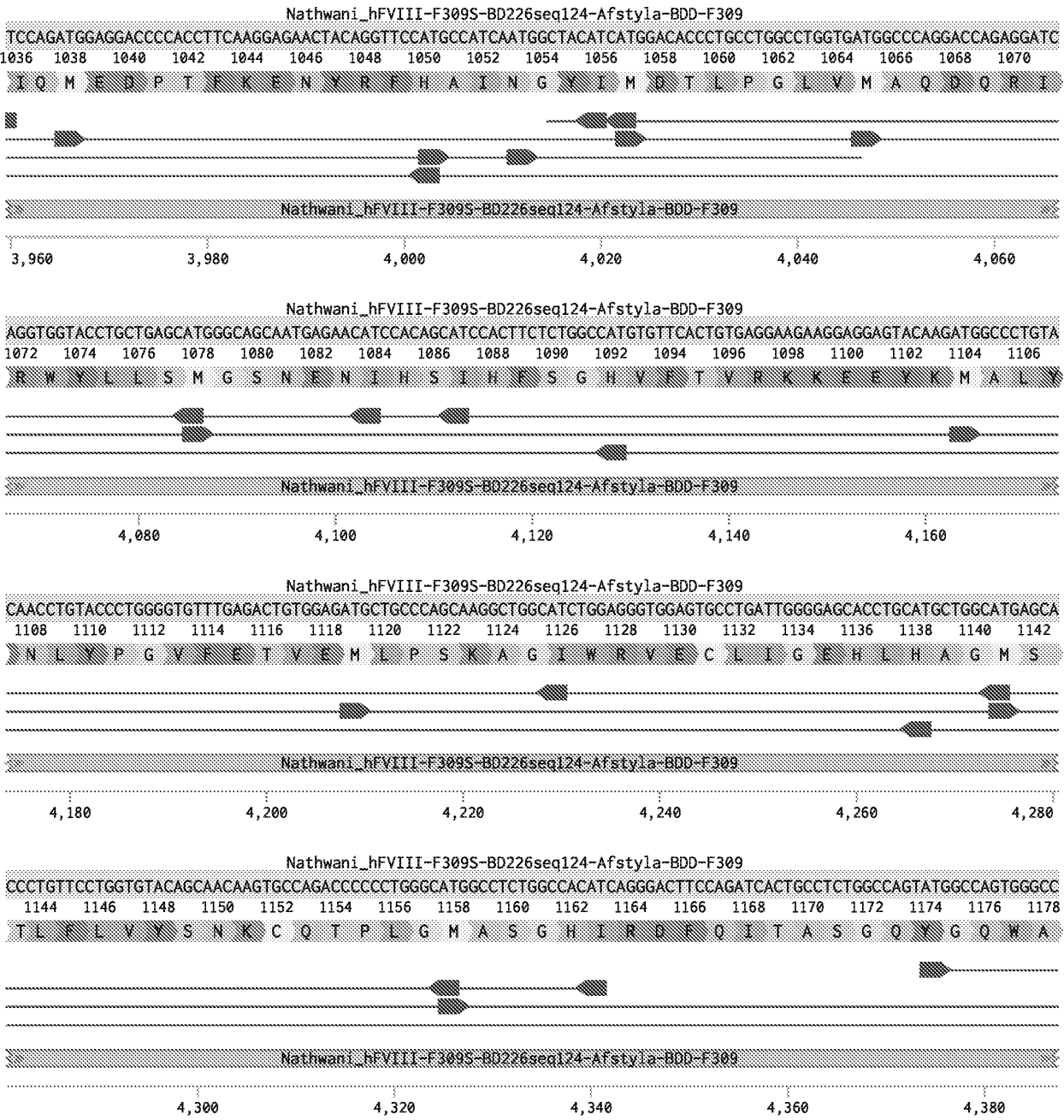


ACTTCAGGAACAGGGGCATGACTGCCCTGCTGAAAGTCTCCAGCTGTGACAAGAACTGGGGACTACTATGAGGACAGCTATGAGGACATCTCTGCCTACCTGCTG
 716 718 720 722 724 726 728 730 732 734 736 738 740 742 744 746 748 750
 D F R N R G M T A L L K V S S C D K N T G D Y Y E D S Y F D I S A Y L L
 Nathwani_hFVIII-F309S-BD226seq124-Afstyla-BDD-F309
 3,000 3,020 3,040 3,060 3,080 3,100
 Nathwani_hFVIII-F309S-BD226seq124-Afstyla-BDD-F309
 AGCAAGAACAATGCCATTGAGCCCAGGAGCTTCAGCCAGAATAGCAGGCACCCAGCAGGAGGAGAGCAGTTCATGCCACCACCATCCCAGAGAATACCACCCT
 752 754 756 758 760 762 764 766 768 770 772 774 776 778 780 782 784 786
 S K N N A I E P R S F S Q N S R H P S T R O K Q F N A T T I P E N T T L
 Nathwani_hFVIII-F309S-BD226seq124-Afstyla-BDD-F309
 3,120 3,140 3,160 3,180 3,200
 Nathwani_hFVIII-F309S-BD226seq124-Afstyla-BDD-F309
 GCAGTCTGACCAGGAGGAGATTGACTATGATGACACCATCTCTGTGGAGATGAAGAAGGAGGACTTTGACATCTACGACGAGGACGAGAACCAGAGCCCCAGGAGCT
 788 790 792 794 796 798 800 802 804 806 808 810 812 814 816 818 820
 Q S D Q E E I D Y D D T I S V E M K K E D F D I Y D E D E N Q S P R S
 Nathwani_hFVIII-F309S-BD226seq124-Afstyla-BDD-F309
 3,220 3,240 3,260 3,280 3,300
 Nathwani_hFVIII-F309S-BD226seq124-Afstyla-BDD-F309
 TCCAGAAGAAGACCAGGCACTACTTCATTGCTGCTGTGGAGAGGCTGTGGGACTATGGCATGAGCAGCAGCCCCATGTGCTGAGGAACAGGGCCAGTCTGGCTCT
 822 824 826 828 830 832 834 836 838 840 842 844 846 848 850 852 854 856
 F Q K K T R H Y F I A A V E R L W D Y G M S S S P H V L R N R A Q S G S
 Nathwani_hFVIII-F309S-BD226seq124-Afstyla-BDD-F309
 3,320 3,340 3,360 3,380 3,400 3,420
 Nathwani_hFVIII-F309S-BD226seq124-Afstyla-BDD-F309
 GTGCCCCAGTTCAAGAAGTGGTGTTCAGGAGTTCACTGATGGCAGCTTCACCACGCCCTGTACAGAGGGAGCTGAATGAGCACCTGGGCCTGCTGGGCCCTA
 858 860 862 864 866 868 870 872 874 876 878 880 882 884 886 888 890 892
 V P Q F K K V V F Q E F T D G S F T Q P L Y R G E L N E H L G L L G P Y
 Nathwani_hFVIII-F309S-BD226seq124-Afstyla-BDD-F309
 3,440 3,460 3,480 3,500 3,520

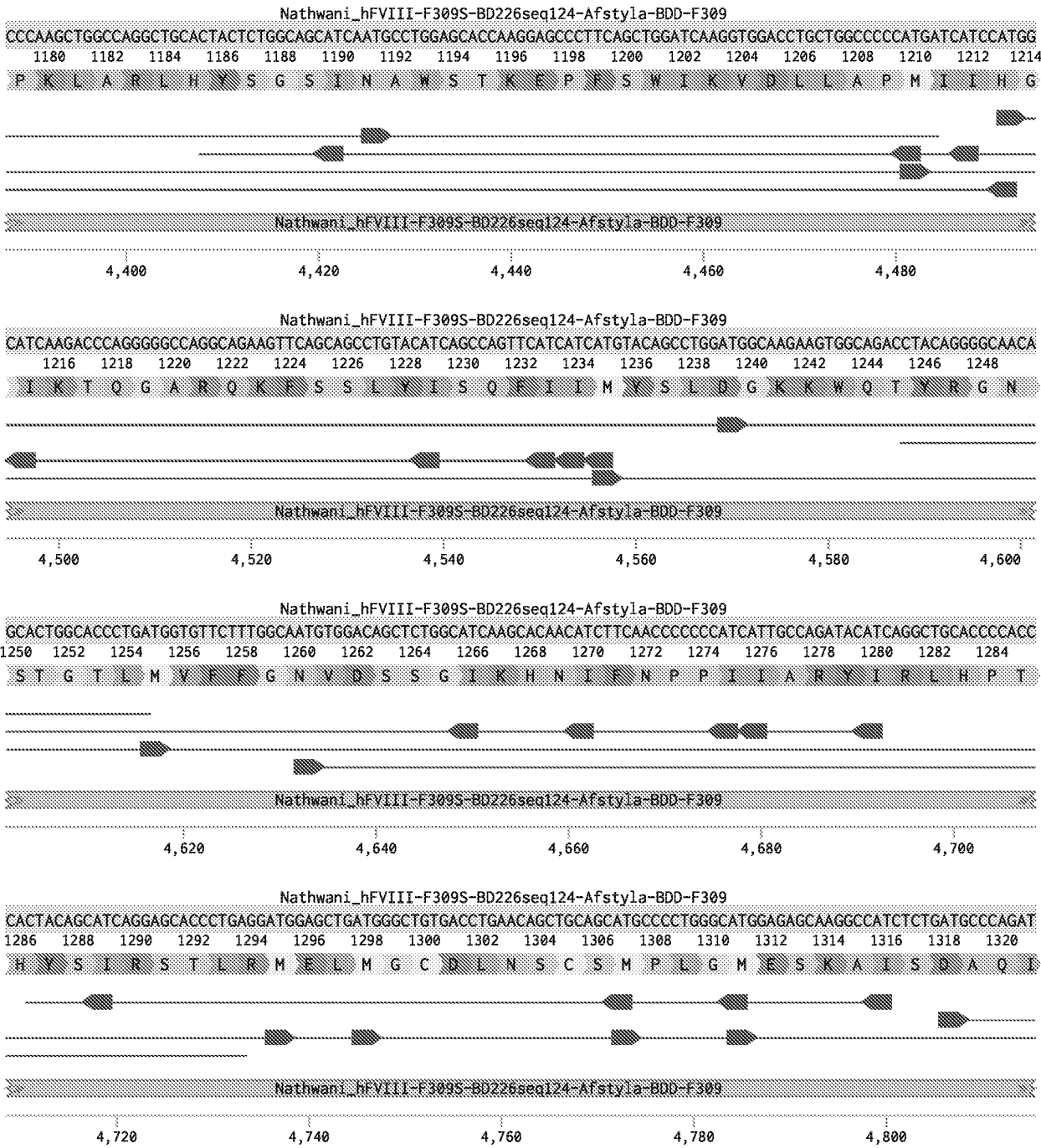
ceDNA1652 (6250 bp) (from 3532-3959 bp)



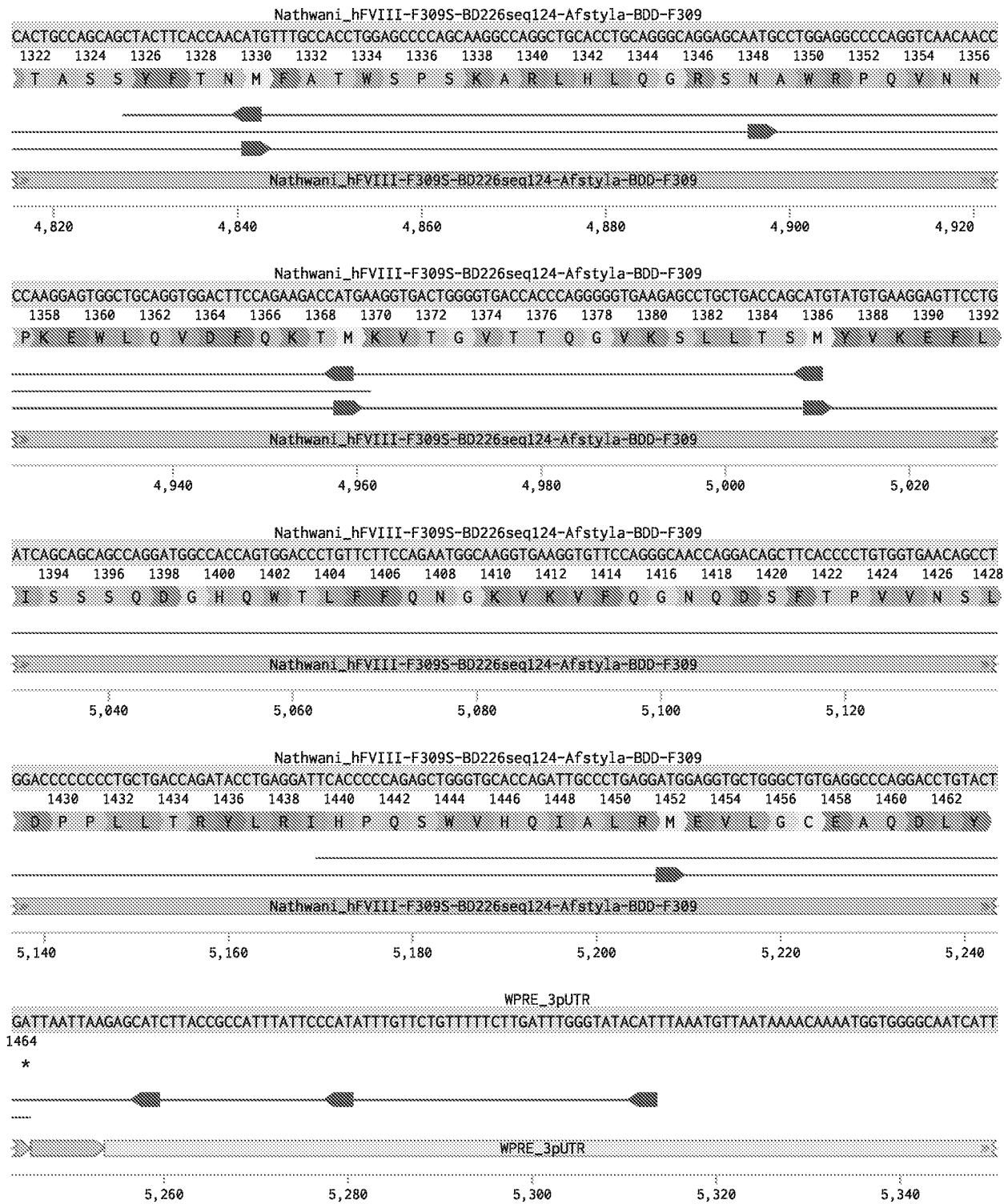
ceDNA1652 (6250 bp) (from 3960-4387 bp)



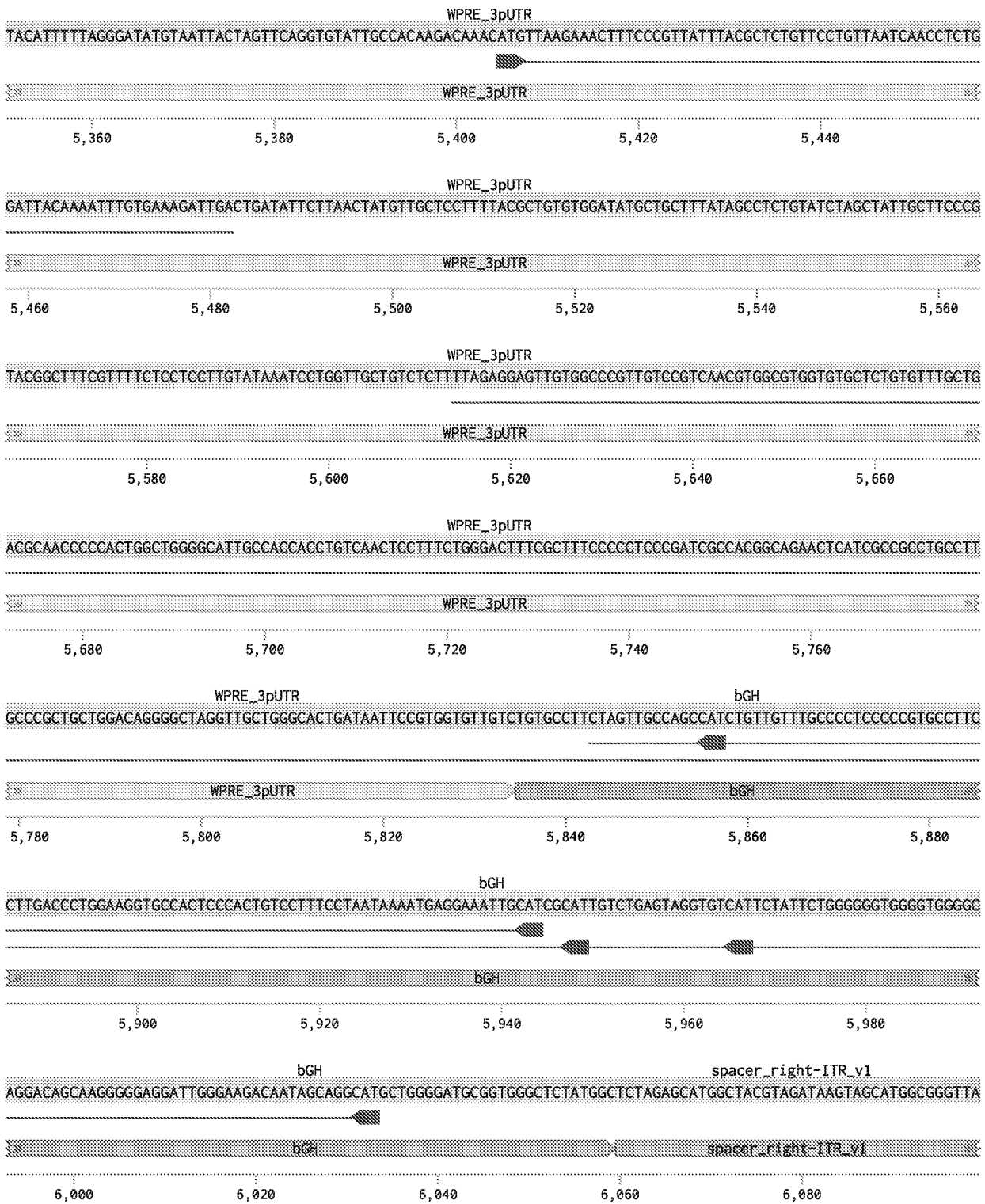
ceDNA1652 (6250 bp) (from 4388-4815 bp)



ceDNA1652 (6250 bp) (from 4816-5350 bp)



ceDNA1652 (6250 bp) (from 5351-6099 bp)



ceDNA1652 (6250 bp) (from 6100-6250 bp)

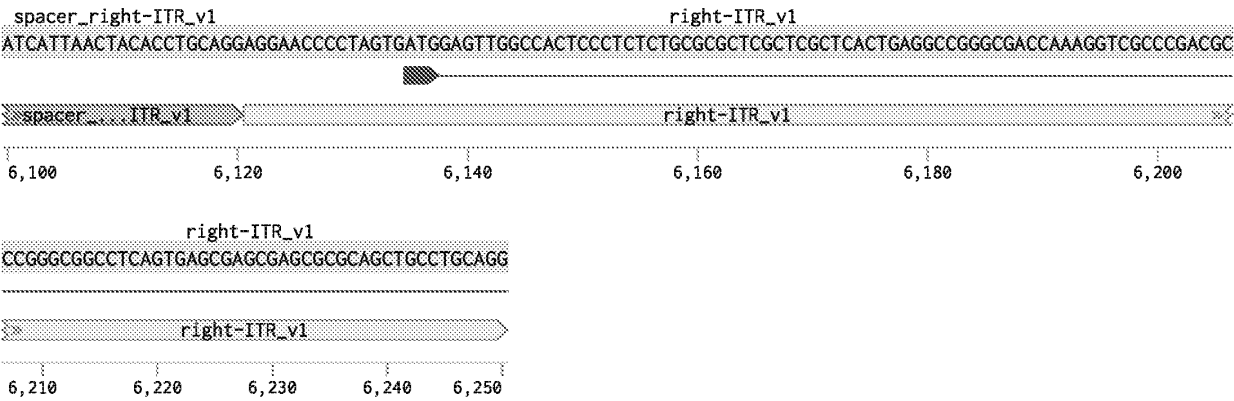
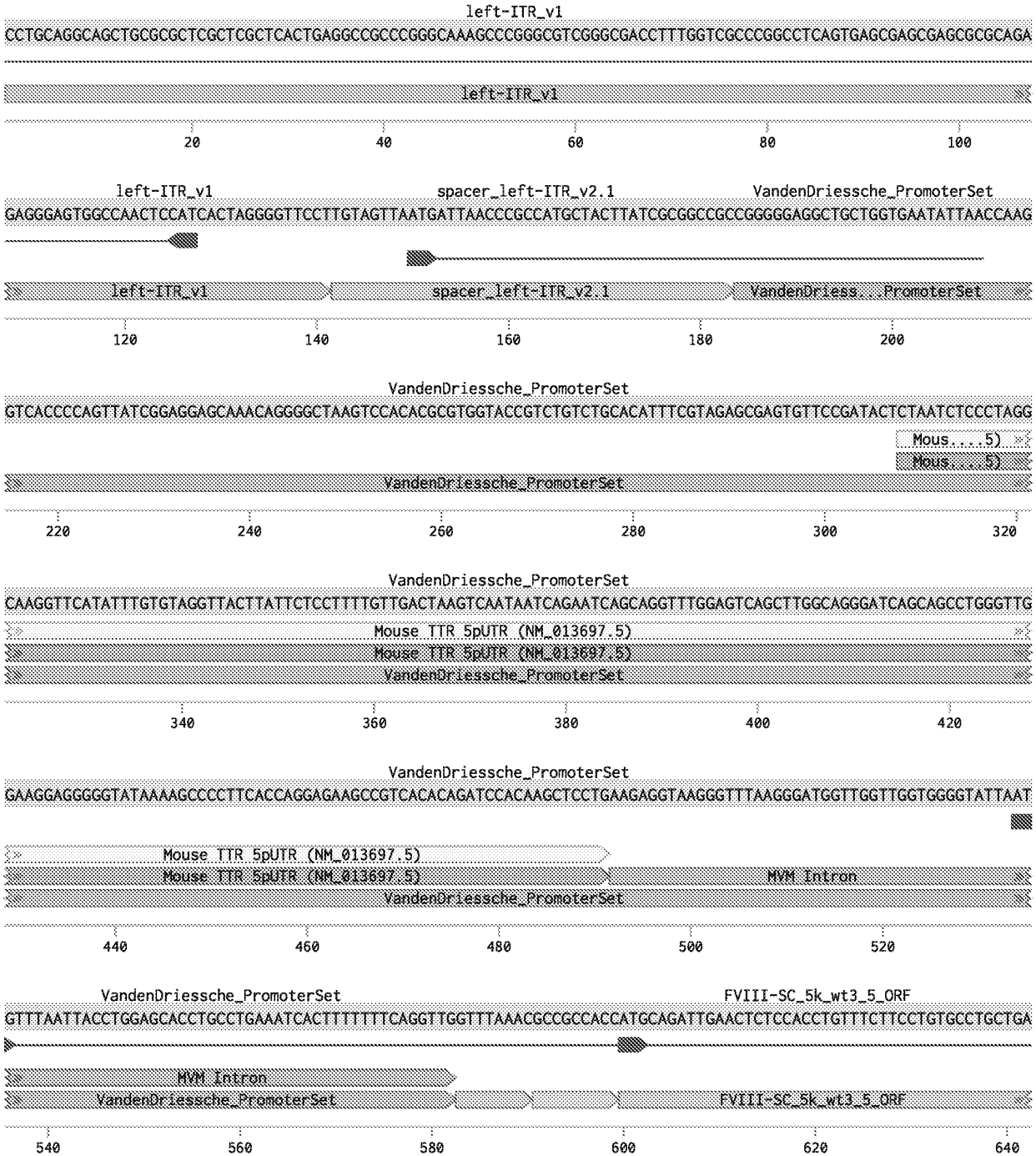
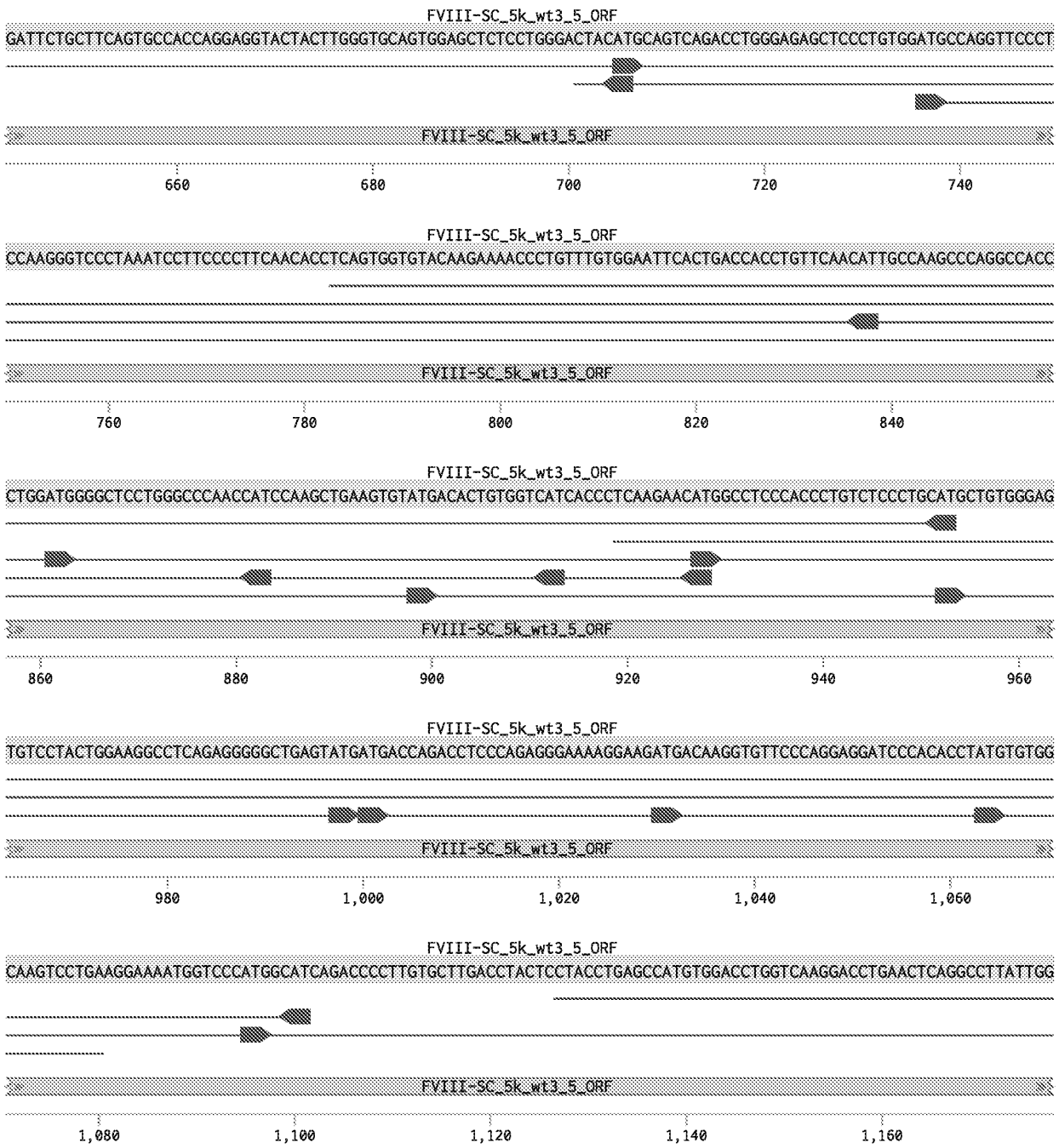


FIG. 7

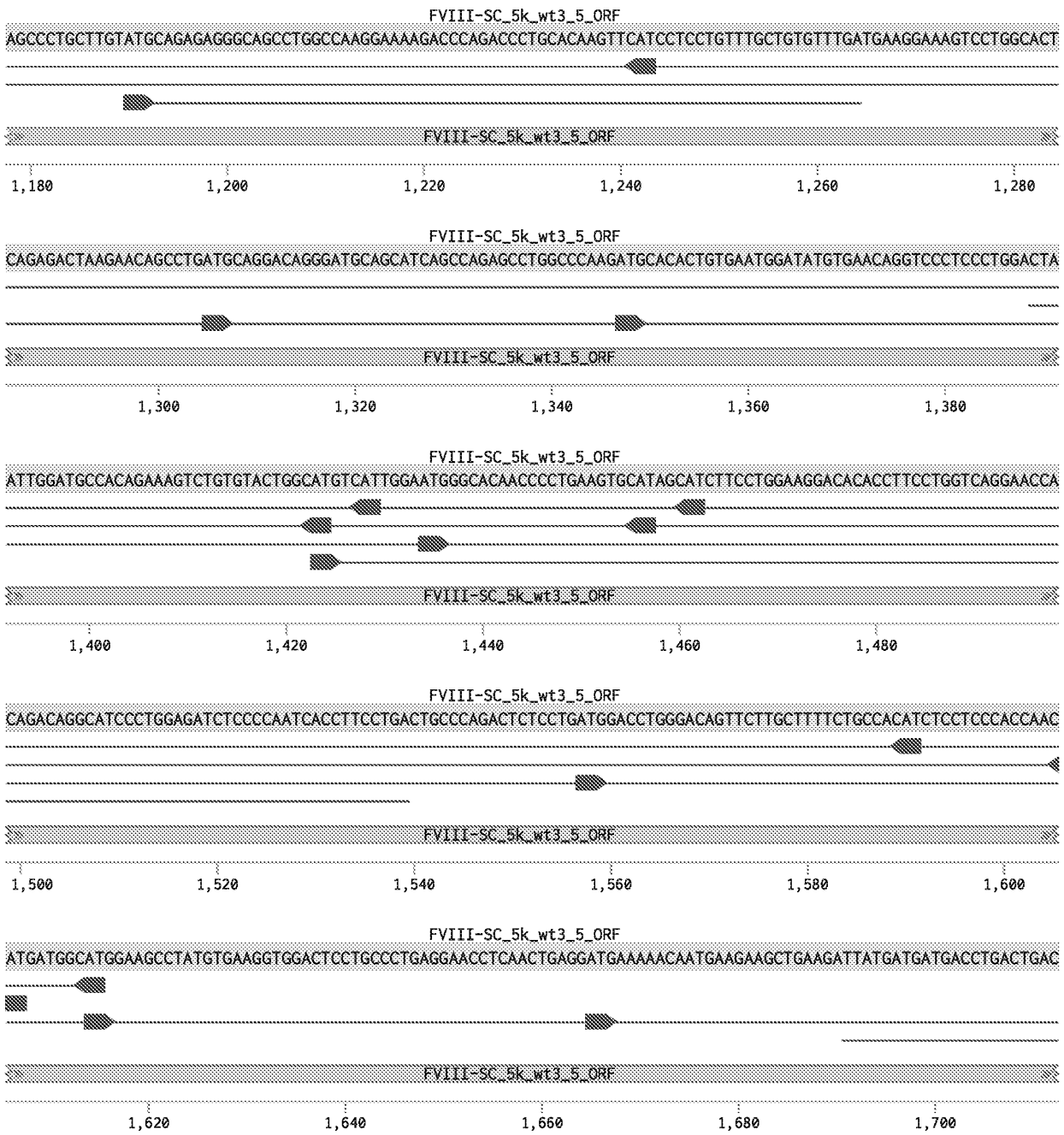
ceDNA1923 (5996 bp)
(from 1-642 bp)



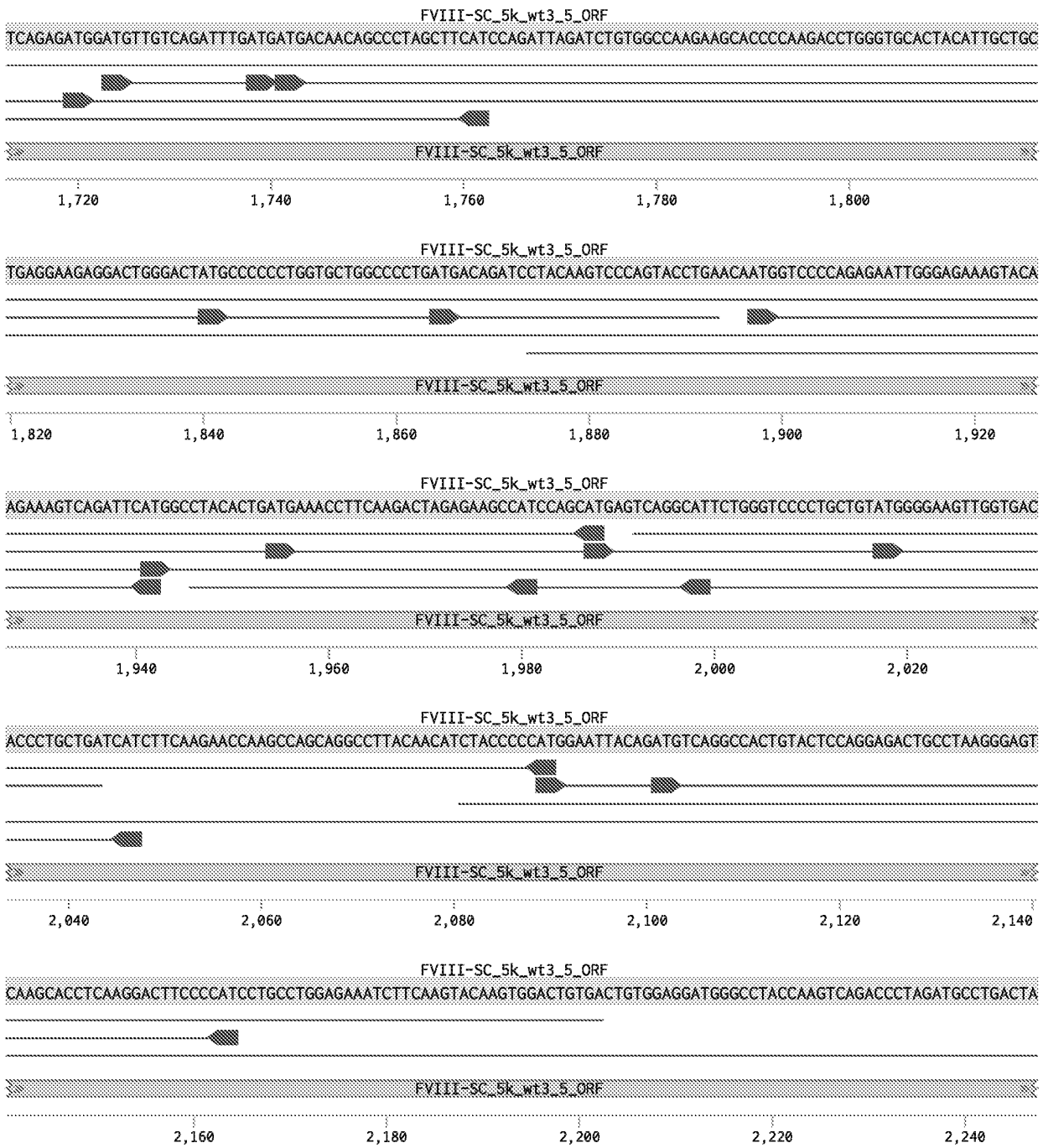
ceDNA1923 (5996 bp) (from 643-1177 bp)



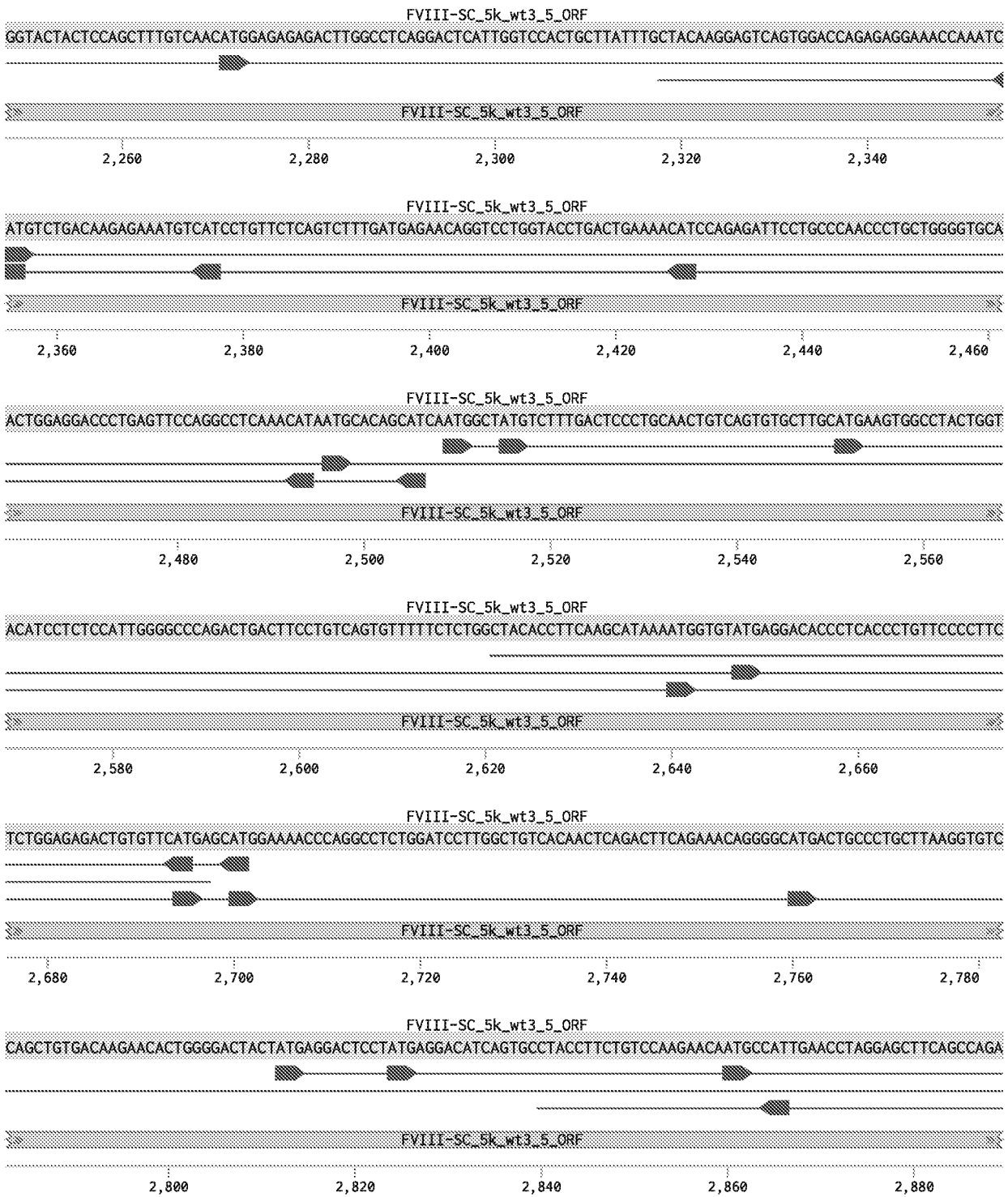
ceDNA1923 (5996 bp) (from 1178-1712 bp)



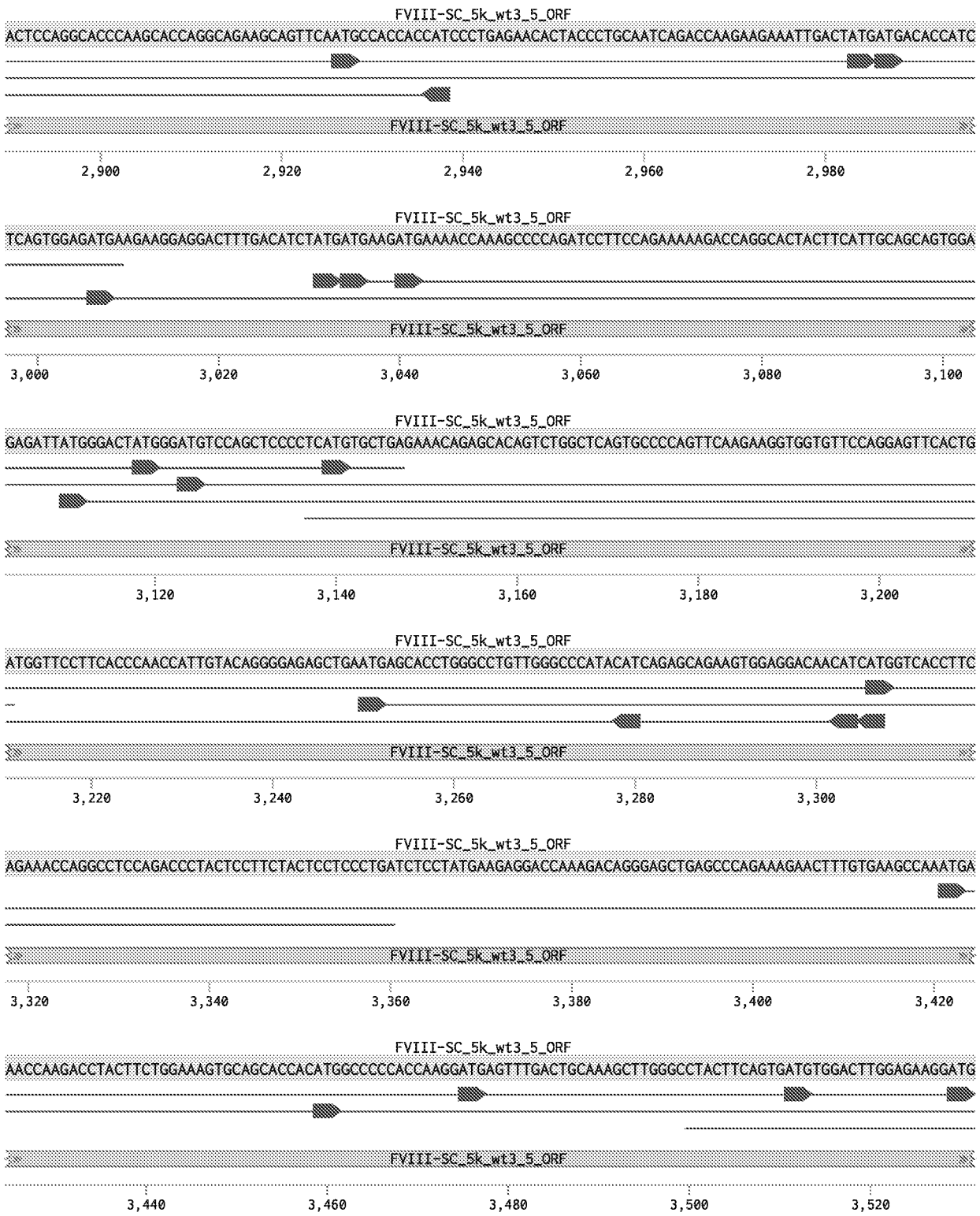
ceDNA1923 (5996 bp) (from 1713-2247 bp)



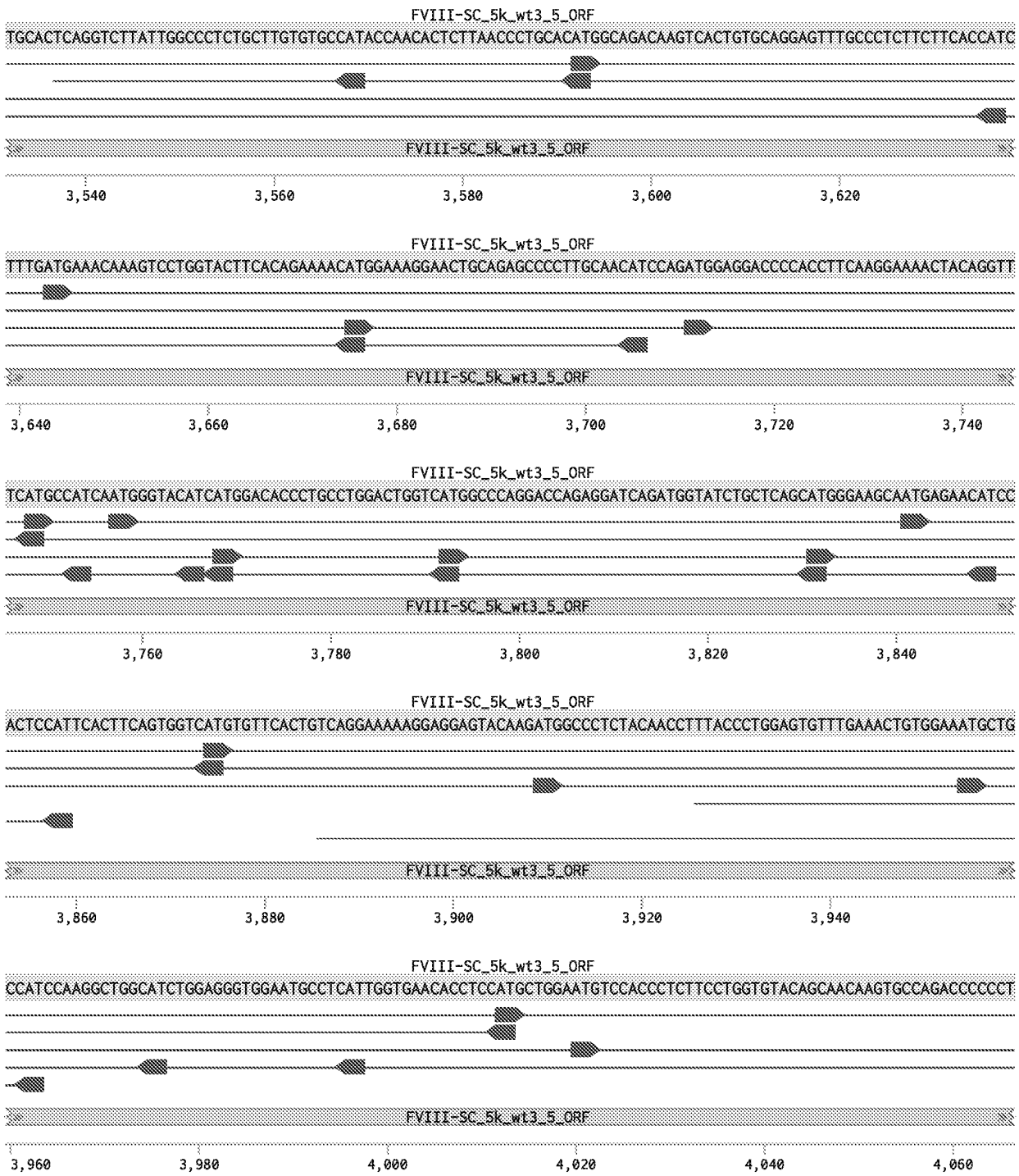
ceDNA1923 (5996 bp) (from 2248-2889 bp)



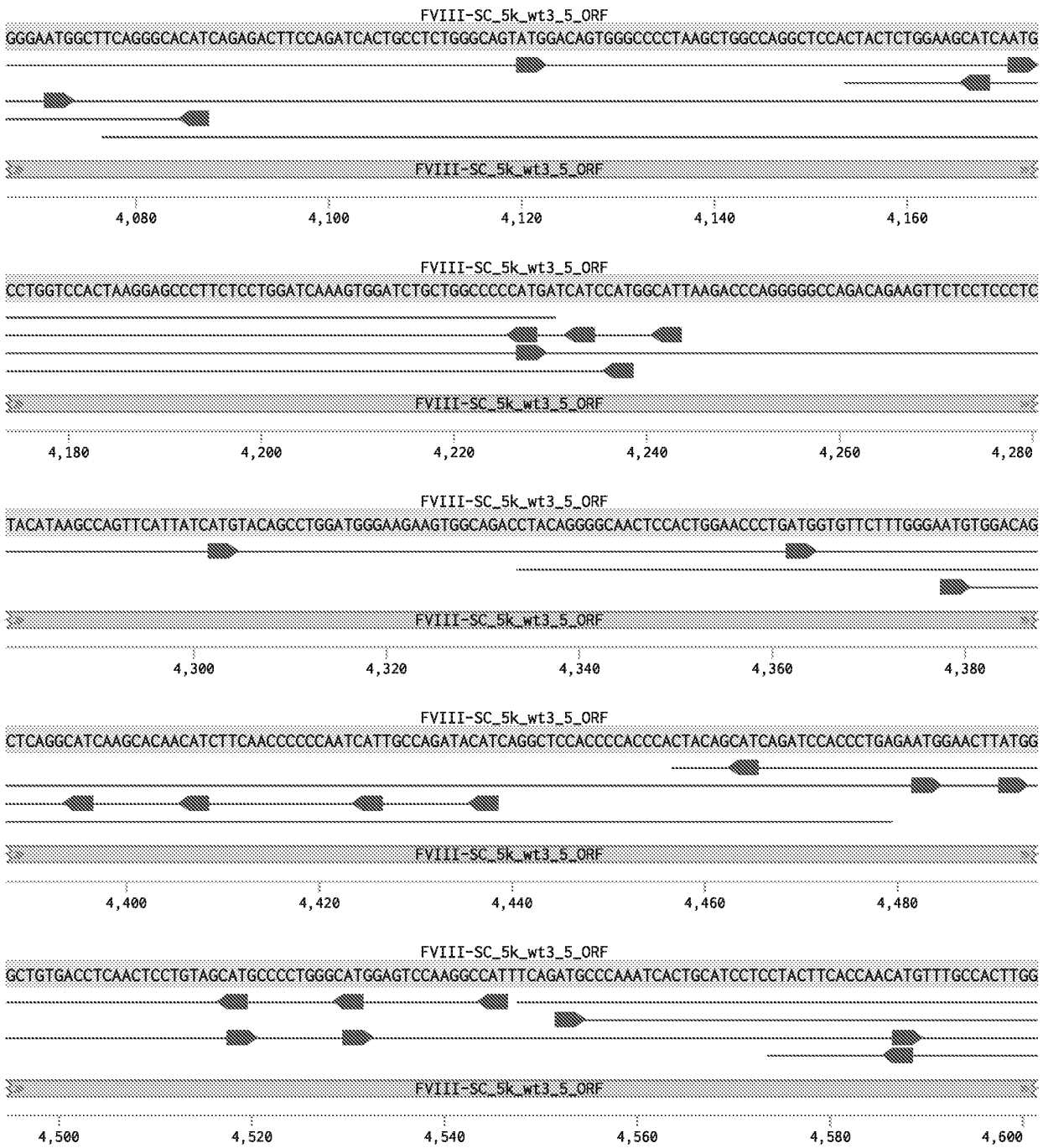
ceDNA1923 (5996 bp) (from 2890-3531 bp)



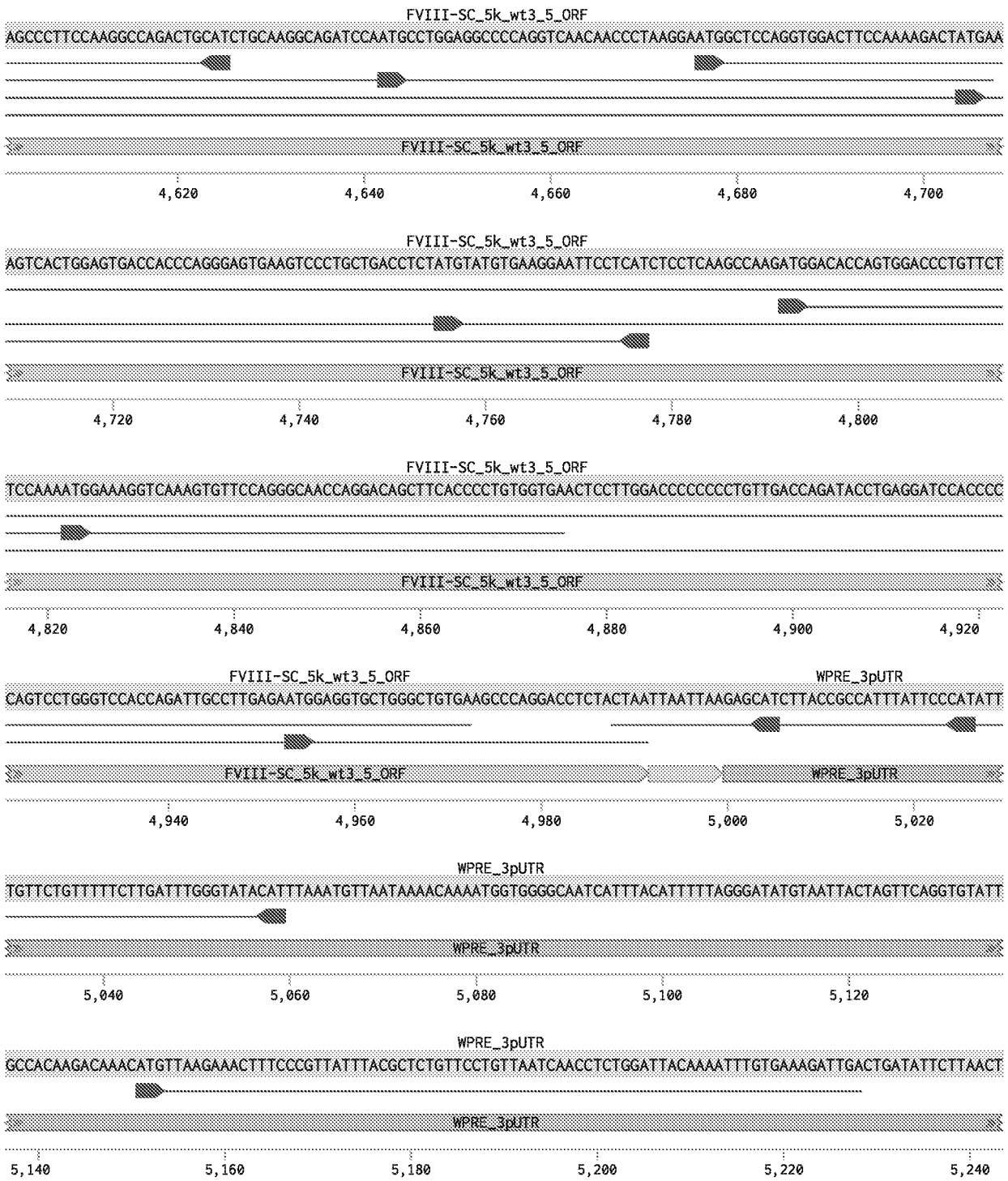
ceDNA1923 (5996 bp) (from 3532-4066 bp)



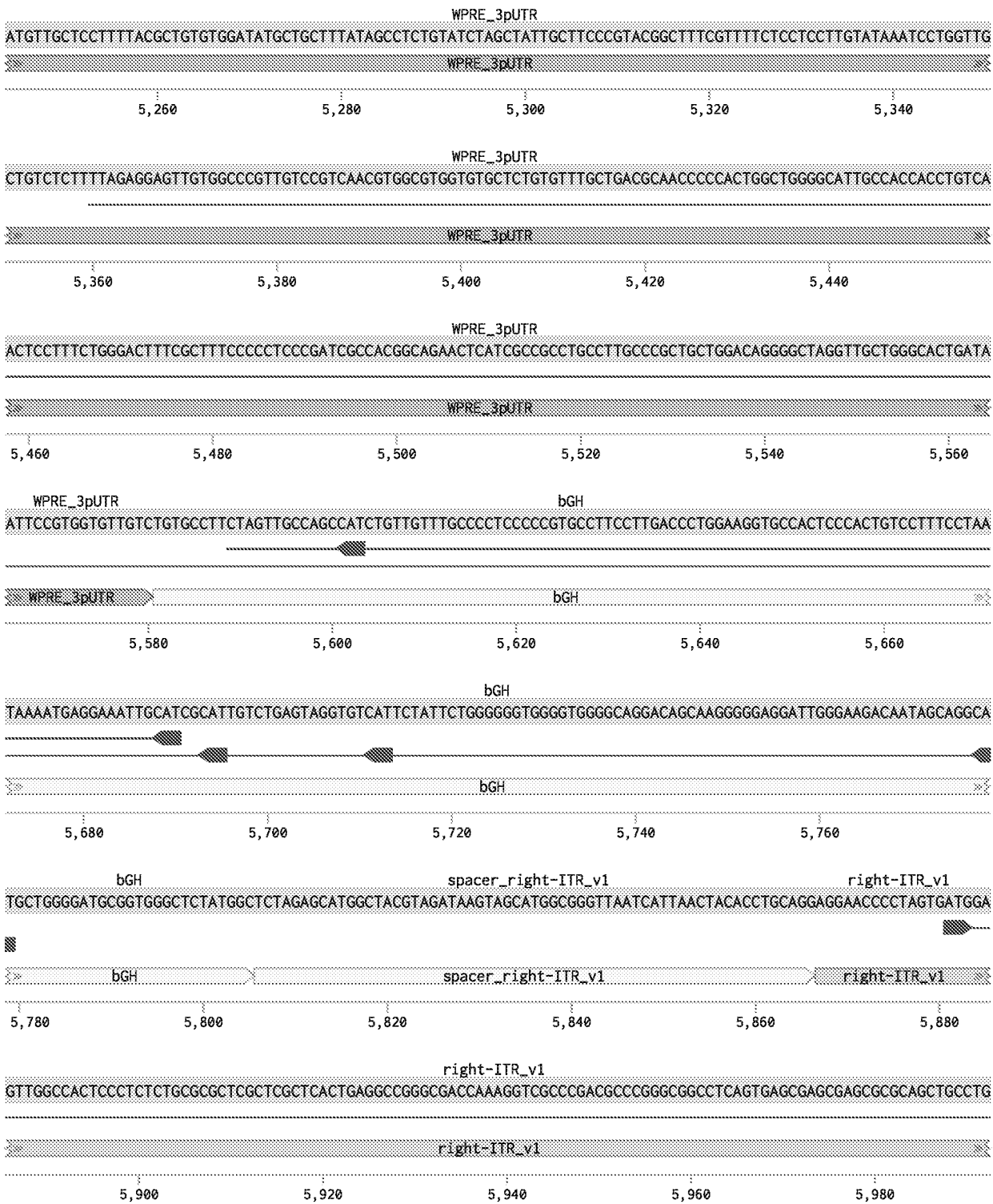
ceDNA1923 (5996 bp) (from 4067-4601 bp)



ceDNA1923 (5996 bp) (from 4602-5243 bp)



ceDNA1923 (5996 bp) (from 5244-5992 bp)

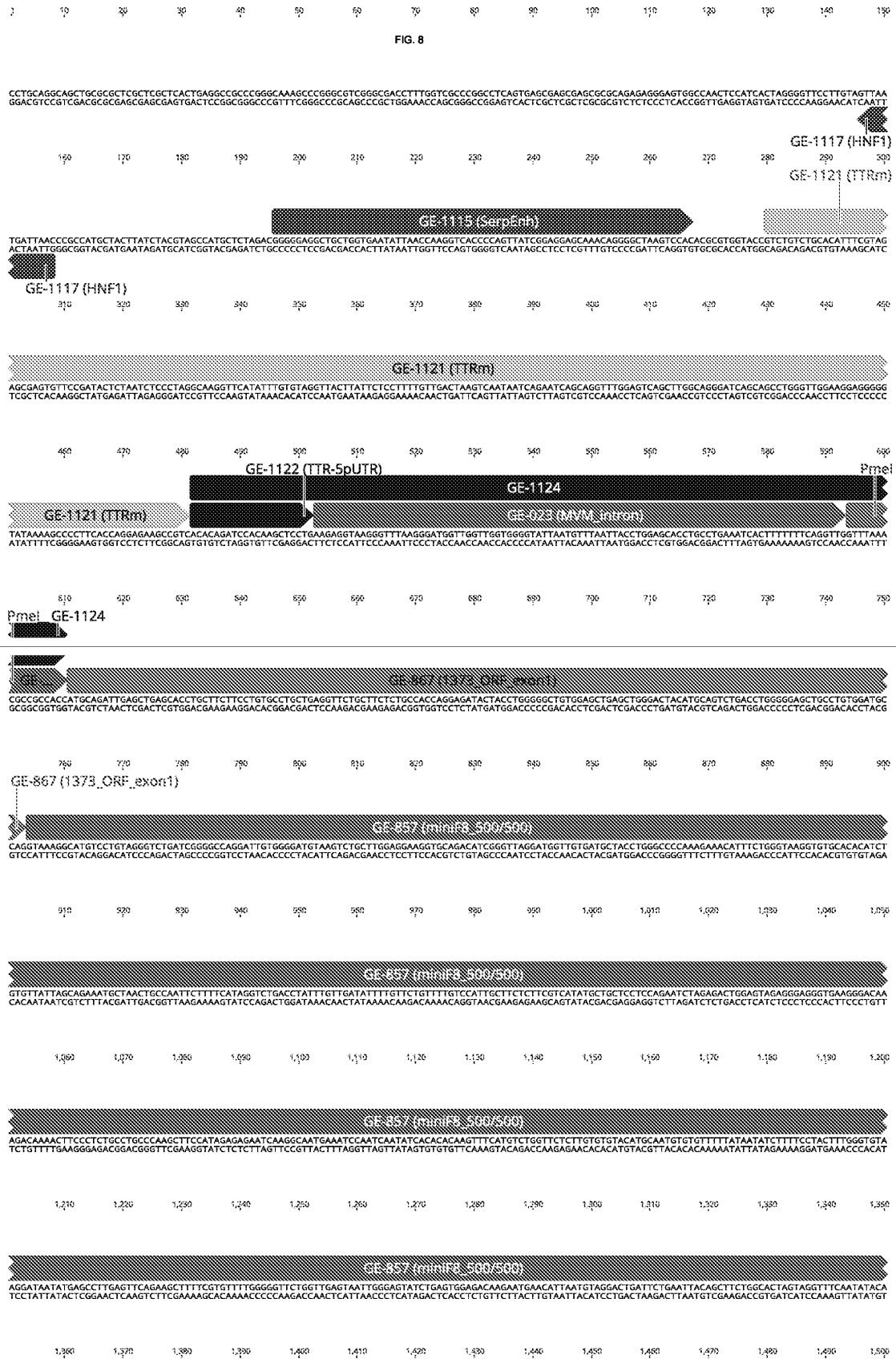


ceDNA1923 (5996 bp) (from 5993-5996 bp)

CAGG



5,995



TAGTCTGCTGAAAGGTAATTTCTCTGTGATATTCCTGGTATCCCTAAGGAGGGAAGTATAATTTAGGTACATACTGACAAAATTGAACACAAAGGTAAGTATAGTCTGTTTATAGAGATGAAATTGAAGGATGCAGTAATCAGACGACTTCCATTAAAGAGACACTATAAGGACCATAGGGATTCCTCCCTTCATTAAAAATCATGTATGACTGTTTTAAACTGTGTCCATGAATCTACTTTCAATATCAGACAAAATCTCTACTTTAACTTCTACGTCAT

1,510	1,520	1,530	1,540	1,550	1,560	1,570	1,580	1,590	1,600	1,610	1,620	1,630	1,640	1,650
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

GCCTATGCTTTGGCAAGGATTTTGGCTGATCAGTGTATGGTTATTGATTTTATGATTCCTATCATATGGCACTTAATGTATCAGTTGAGTTGTGAAAAACAGTGTTCGCGTTTAAATGGATGTTAGGGATTATATACAACCTCAAATTCGATAACGAAACCGTTTCTAAAAACCGACTACGTCACATACCAATAACTAAAATACTAAGAATAGTATACCGTGGATTACATAGTCAACTCAACACTTTTGTCAAAAGCCAAATTACCTACAATCCCTAAATATATGTTGAAGTTTAA

1,660	1,670	1,680	1,690	1,700	1,710	1,720	1,730	1,740	1,750	1,760	1,770	1,780	1,790	1,800
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

GE-858 (1373_ORF_exon2-26)

TGCCCTCCTTGCTAATAGTAGAAAAGAGTAGTATGGAAGCATTACTTCCAGCTGCTTTTGAAGTGTCCACCAAAATGAACGACTTTTTCCTTTCTTCACGCAGGTTCCCCCAGAGTGCCCAAGAGCTTCCCTTCAACACCTCTGTGG
 ACGGAGGAACGATTATCATCTTTTCTCATACCTTCTGAATGAAGGTCTGACGAAAACTTCACAGGTGGTTTACTTGTCTGAAAAAGGAAAGAGTGGCTCAAGGGGGGGTCTCACGGGTTCTCGAAGGGGAAGTTGTGGAGACAC

1,810	1,820	1,830	1,840	1,850	1,860	1,870	1,880	1,890	1,900	1,910	1,920	1,930	1,940	1,950
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

TGACAAAGACCTGTTTGTGGAGTCACTGACCCTGTTCAACATTGCCAAGCCAGGCCCTCTGGATGGGCTCTGGGCCCCACCATTCAGGCTGAGGTGTATGACACTGTGGTGATACCTGAAGAACATGCCAGCCACC
 ACATGTTCTTCTGGGACAAACACCTCAAGTGACTGGTGGACAAGTTGTAACGGTTCGGGTCCGGGGGAGCTACCCGACGACCCGGGTGGTAGGTCCGACTCCACATACTGTGACACCACTAGTGGGACTTCTTGTACCGGTCGGTGG

	1,970	1,975	1,980	1,990	2,000	2,010	2,020	2,030	2,040	2,050	2,060	2,070	2,080	2,090	2,100
--	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

CTGTGAGCCTGCATGCTGTGGGGGTGAGCTACTGGAAGGCCTCTGAGGGGGCTGAGTATGATGACCAGACCAGCCAGAGGGAGAGGAGGATGACAAGGTGTTCCTGGGGGACGCCACACCTATGTGTGGCAGGTGCTGAAGGAGAA
GACACTGGAGCTACGACACCCCACTCGATGACCTCCGGAGACTCCCCGACTCATACTACTGGTCTGGTGGTCTCCCTCTTCTCTCTACTGTTCCACAAGGGAACCCCGTGGGTGGATACACACCTCCACGACTTCTCTTAC

2,110	2,120	2,130	2,140	2,150	2,160	2,170	2,180	2,190	2,200	2,210	2,220	2,230	2,240	2,250
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

CCCCATGGCCTCTGACCCCTGTGCTGACCTACAGCTACTGAGCCATGTGGACCTGGTGAAGGACCTGAACCTCTGGCCTGATTGGGGCCTGCTGGTGTGACGGGAGGGCAGCTGTGCCAAGGAGAAGACCCAGACCTTGCACAACT
CGGGGTACCGGAGACTGGGGACACGGACTGGATGTGATGGACTCGGTACACCTGGACCCTTCTCGGACTTGAGACCGGACTAACCCGGGACGACCACAGTCTCTCCCTCGGACCGGTCTCTCTGGGTCTGGGACGTGTTC

2,260 2,270 2,280 2,290 2,300 2,310 2,320 2,330 2,340 2,350 2,360 2,370 2,380 2,390 2,400

TCATCTGCTGTTTGCTGTTTATGAGGGCAAGAGCTGGCACTCTGAACCAAGAACAGCCTGATGCAGGACAGGGATGCTGCCTCTGCCAGGGCTTGGCCCAAGATGCACACTGTGAATGGCTATGTGAACAGGAGCCTGCCTGGCCAGTAGGACGACAAACGACACAACTACTCCCGTTCTCGACCGTGAGACTTTGGTTCTTGTCGGACTACGTCCTGTCCCTACGACGGAGACGGTCCCGGACCGGGTTCTACGTGTGACACTTACCGATACACTTGTCTCTGGACGGACCG

2,470	2,480	2,490	2,500	2,510	2,520	2,530	2,540	2,550
-------	-------	-------	-------	-------	-------	-------	-------	-------

TGATTGGCTGCGACAGGAAGTCTGTGACTGGCATGTGATTGGCATGGGCACCAACCTGAGGTGCACAGCATCTTCTGGAAGGGCCACACTTCCTGTGTCAGGAACACAGGCAGGCCAGCCTGGAGATCAGCCCATACCTTCCTGA
 ACTAACCACGCGTCTTCTCAGACACATGACCGTACACTAACCCTACCGTGGTGGGGAETCCACGTGTCGTAGAAGGACCTCCCGGTGCGAAGGACCACTCCTGTGTGTCGTCCGTCGGTCCGACCTCTAGTCGGGGTAGTGAAGGACT

2,560 2,570 2,580 2,590 2,600 2,610 2,620 2,630 2,640 2,650 2,660 2,670 2,680 2,690 2,700

CTGCCAGACCCCTGCTGATGGACCTGGGCGAATTCTGCTGAGCTGCCACATACGACGCCACCAGCATGATGGCATGGAGGCCATATGTGAAGGTGGACAGCTGCCCTGAGGAGCCCCAGCTGAGGATGAAGAACAATGAGGAGGCTGAGG
GACGGGCTGGGACGACTACCTGGACCCGGTCAAGGACGACTGCACGGTGTAGTCTGCTGGTGGTCTGACTACCGTACCTCCGGATACACTCCACCTGTGACGGGACTCCTCGGGGTCGACTCCTACTTCTGTGTACTCTCCGACTCC

2,710 2,720 2,730 2,740 2,750 2,760 2,770 2,780 2,790 2,800 2,810 2,820 2,830 2,840 2,850

ACTATGATGATGACCTGACTGACTCTGAGATGGATGTGGTGAGGTTTATGATGATGACAAACAGCCCCAGCTTCATCCAGATCAGGTCCTGTGGCCAAAGAAGCACCCCAAGACCTGGGTGCACTACATTGCTGCTGAGGAGGAGGACTGGGACT
TGATACTACTACTGGACTGACTGAGACTCTACCTACACCACTCCAACTACTACTGTTGTGCGGGTCTGAAGTAGGTCATGTCAGACACCGGTTCTTCTGTTGGGTTCTGGACCCACGTGATGAACGACGACTCCTCCTGACCTGTA

4,210	4,220	4,230	4,240	4,250	4,260	4,270	4,280	4,290	4,300	4,310	4,320	4,330	4,340	4,350
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

GF-868 (1373, ORF, exon2-26)

TGGTGTTCAGGAGTTCACTGATGGCAGCTTCAACCAGCCCTGTACAGAGGGAGCTGAATGAGCACTGGGCTGTGGGCCCTTACATCAGGGCTGAGGTGGAGGCAACATCATGGTACCTTCAGGAACCAAGCCAGCAGGCCCT
ACCACAAGGTCTCAAGTGACTACGTGCAAGTGGGTCGGGACATGTCTCCCTCBACTTACTGTGGACCCGGACGACCCGGGATGTAGTCCCGACTCCACTCTCTGTGTAGTACCACTGGAAGTCTTGGTCCGGTCGTCGGGGA

4,360 4,370 4,380 4,390 4,400 4,410 4,420 4,430 4,440 4,450 4,460 4,470 4,480 4,490 4,500

GF-868 (1373, ORF, exon2-26)

ACACCTTCTACAGCAGCTGATCAGCTATGAGGAGGACAGAGGCGGGGCTGAGCCAGGAAGAACTTTGTGAAGCCCAATGAACCAAGACTACTTCTGGAAGGTGACAGCACATGGCCCCCACCAGGATGAGTTTGACTGCA
TGTGGAAGATGTCTCGGACTATGTCGATACTCTCTCCGTCTCCGTCCCCGACTCGGGTCTTCTTGAACACTCTGGGTACTTGGTTCTGGATGAAGACCTTCCACGTCTGGTGTACCGGGGTGGTCTTACTCAAACTGACGT

4,510 4,520 4,530 4,540 4,550 4,560 4,570 4,580 4,590 4,600 4,610 4,620 4,630 4,640 4,650

GF-868 (1373, ORF, exon2-26)

AGGCTTGGGCTACTTCTCTGATGTGGACCTGGAGAAGGATGTGCACTCTGACCTGATTGGCCCCCTGTGGTGTGGCCACCAACACCTGAACCTGCCATGGCAGGCAAGGTGACTGTGCAAGGATTTGCCCTGTCTTCAACATCT
TCCGGACCGGATGAAGAGACTACACTGGACTCTTCTTACAGTGAAGCCGACTAACCGGGGACGACACACGGTGTGGTTGTGGGACTTGGGACGGTACCCTCCCTCCACTGACACGTCTCAACGGGCAAGAGTGGTGA

4,660 4,670 4,680 4,690 4,700 4,710 4,720 4,730 4,740 4,750 4,760 4,770 4,780 4,790 4,800

GF-868 (1373, ORF, exon2-26)

TTGATGAACCAAGAGCTGGTACTTCACTGAGAATCGAGAGGAAGTGCAGGGCCCCCTGCAACATCCAGATGGAGGACCCCACTTCAAGGAGAACTACAGGTTCCATGCCATCAATGGCTACATCATGGACACCTGCTTGGCTCG
AACTACTTTGGTTCTCGACCATGAAGTGAATCTTGTACCTCTCTTGAAGTCCCGGGGACGTTGTAGGTCTACTCTCTGGGTGGAAGTTCTCTTGTATGCCAAGGTACGGTGTACCGATGTAGTACCTGTGGGACGGACGGAC

4,810 4,820 4,830 4,840 4,850 4,860 4,870 4,880 4,890 4,900 4,910 4,920 4,930 4,940 4,950

GF-868 (1373, ORF, exon2-26)

TGATGCCCCAGGACCAAGGATCAGGTGGTACTGCTGAGCATGGGAGCAATGAGAATCCACAGCATCACTTCTTGGCCATGTGTTCACTGTGAGGAAGAGGAGGATACAAGATGGCCCTGTACAACCTGTACCTGGGGGT
ACTACCGGGTCTGGTCTCTAGTCCACATGGACGACTGTAACCGTCTGTTACTTGTAGTGTCTGTAGGTGAAGACCGGTACACAAGTGAACACTCTTCTTCTCTCATGTCTTACCGGAGATGTGTGACATGGGACCCCA

4,960 4,970 4,980 4,990 5,000 5,010 5,020 5,030 5,040 5,050 5,060 5,070 5,080 5,090 5,100

GF-868 (1373, ORF, exon2-26)

TTGAGACTGTGGAGATGCTGCCAGCAAGCTGGCACTTGGAGGGTGGAGTGGCTGATTGGGAGGACCTGCATGCTGGCATGAGCACTTGTCTTGGTGTACAGCAACAGTGCAGACCCCTCTGGGATGGCTCTGGCCACATCA
AACTCTGACACCTCTACGACGGGTCTTCCGACCGTAGACTCCCACTCACGACTAACCCCTGTGGAGTACGACCTGACTCTGTGGGACAAGGACACATGTCGTTGTTACAGCTGTGGGGGACCCGTACCGGAGACCGGTGTAGT

5,110 5,120 5,130 5,140 5,150 5,160 5,170 5,180 5,190 5,200 5,210 5,220 5,230 5,240 5,250

GF-868 (1373, ORF, exon2-26)

GGGACTTCCAGATCACTGCTCTGCCCCAGTATGCCCCAGCTGGCCAGGCTGCACACTCTGGCAGCATCAATGCTGGAGCAACCAAGGAGCCCTTCACTGCTGGATCAAGGTGGACCTGCTGGCCCCATGATCATCCATG
CCCTGAAGGTCTAGTGACGGAGACCGGTATACCGGTACCCGGGGGTTGACCGGTCCGACGTGATGAGACCGTCTGAGTTACGGACCTGTGGTTCTCGGGAAAGTGCACCTAGTTCCACTGGAGACCGGGGGTACTAGTAGGTAC

5,260 5,270 5,280 5,290 5,300 5,310 5,320 5,330 5,340 5,350 5,360 5,370 5,380 5,390 5,400

GF-868 (1373, ORF, exon2-26)

GCATCAAGACCCAGGGGCAAGGAACTTCAGCAGCTGTATCATGACCAATTATCATCATGTACAGCTGGATGGCAAGAGTGGCAGACCTACAGGGGCAACAGCACTGGCACCTGATGGTGTCTTTGGCAATGTGACAGCT
CGTAGTCTGGGTCCCCCGTCCGTCTTCAAGTCGTGGACATGTAGTCGTCAGTAGTAGTACATGTGGACCTACCGTCTTCTCACCTGCTGGATGTCCTCCGTGTGCTGACCTGGGACTACCAAGAAGACGTTACACCTGTGCA

5,410 5,420 5,430 5,440 5,450 5,460 5,470 5,480 5,490 5,500 5,510 5,520 5,530 5,540 5,550

GF-868 (1373, ORF, exon2-26)

CTGGCATCAAGCACAACATCTTCAACCCCCCCATCATTGCCAGATACATCAGGCTGCACCCCACTACAGCATCAGGAGCACTTGAAGATGGAGCTGATGGGCTGTGACCTGAACAGCTGCAGCATGCCCTGGGCAAGGAGCA
GACCGTAGTGTGTGTGTAGAGATTGGGGGGGTAGTAACGGTCTATGATGTCGAGCTGGGGTGGGTGATGTCTGAGTCTCTGGGACTCTACTCTGACTACCCGACACTGGACTTGTGAGCTGTGACGGGACCGGTACTCTCTGT

5,560 5,570 5,580 5,590 5,600 5,610 5,620 5,630 5,640 5,650 5,660 5,670 5,680 5,690 5,700

GF-868 (1373, ORF, exon2-26)

AGGCCATCTCTGATGCCAGATCACTGCCAGCACTTCAACCAATGTTTGCACCTGGAGCCCCAGGCAAGGCAAGCTGCACCTGCAAGGCAAGCAATGCTGGAGGCCCAAGGTCAACAACCCCAAGGAGTGGCTGACAGTGG
TCCGGTAGAGACTACGGGTCTAGTGACGGTCTGATGAAGTGGTTGTACAAAGGCGGACTCGGGGCTTCCGGTCCGACGTGGAGCTCCGTCCTGTTACGGACCTCCGGGGTCAAGTTGTTGGGTTCTCACCGACGTCCACC

5,710 5,720 5,730 5,740 5,750 5,760 5,770 5,780 5,790 5,800 5,810 5,820 5,830 5,840 5,850

GE-868 (1373_ORF_exon2-26)

ACTTCCAGAAAGACCATGAAGTCACTGGGTGACCAACCCAGGGGTGAAGAGCTGCTGACCAAGATGTATGTGAAGAGTTCTCTGATCAGCAGCACCAGGATGGCCACCACTGGACCTGTCTTCCAGAAATGGCAAGGTGAAGTGTGAAGGTCTTCTGCTACTTCCACTGACCCACTGGTGGTCCCTCACTCTCGGACGACTGGTGTACATACACTCTCTCAAGGACTAGTCTGCTCGCTCTACCCTGGTGGTCACTGGGACAAAGAGTCTTACCGTTCACCTCCACA

5,860 5,870 5,880 5,890 5,900 5,910 5,920 5,930 5,940 5,950 5,960 5,970 5,980 5,990 6,000

GE-868 (1373_ORF_exon2-26)

TCCAGGGCAACAGGACAGCTTCACTCCCTGTGGTGAACAGCTGGACCCCTCTGCTGACCAAGATCTGAGGATTCACCCCAAGACTGGGTGCACAGATTGCCCTGAGGATGGAGGTGCTGGCTGTGAGGCCAGGACCTGTACTAGTCCCGTGTGGTCTGCTGAAGTGGGACACCACTTGTCTGGACCTGGGGGGGACCACTGGTCTATGAGACTCTTAAGTGGGGTCTCGACCCACTGGTCTAACGGGACTCTTACTTCAACGCCGACACTCCGGCTCTGGACATGA

6,010 6,020 6,030 6,040 6,050 6,060 6,070 6,080 6,090 6,100 6,110 6,120 6,130 6,140 6,150

GE-868 (1373_ORF_exon2-26)

GE-007 (WPRE_3pUTR)

GATTAATTAAGAGCATCTTACGCCATTTATCCCATATTTGTTCTGTTTCTTCTGATTGGGTATACATTTAAATGTTAATAAAACAAATGTTGGGCAATCATTTACATTTTGGGATATGTAATTACTAGTCAAGTGTATTGCCCTAATTAATTTCTGTAAGTGGCGTAAATAAGGTATAAACAAGACAAAAGAACTAAACCATATGTAAATTTACAACTTATTTTGTATACCACCCGTTAGTAAATGTAAAAATCCCTATACATTAATGATCAAGTCCACATTAACGG

6,160 6,170 6,180 6,190 6,200 6,210 6,220 6,230 6,240 6,250 6,260 6,270 6,280 6,290 6,300

GE-007 (WPRE_3pUTR)

ACAAGACAAACATGTTAAGAACTTTCCGTTATTTACGCTCTGTTCTGTTAATCAACCTCTGGATTACAAAATTTGTAAGGATTGACTGATATTTAACTATGTTGCTCTTTTACGCTGTGTGGATATGCTGCTTTATAGCCTCTGTTCTGTTTGTACAATTTCTTGAAGGGCAATAAATGCGAGACAGGACAATTAAGTTGGAGACCTAATGTTTAAACACTTCTTAACCTGACTATAAGAATTGATACACGAGGAAATGCGACACACCTATACGACGAAATATCGGAGA

6,310 6,320 6,330 6,340 6,350 6,360 6,370 6,380 6,390 6,400 6,410 6,420 6,430 6,440 6,450

GE-007 (WPRE_3pUTR)

GTATCTAGCTATTGCTTCCGCTACGGCTTTCGTTTCTCTCTCTTGTATAAATCTGTTGCTGCTCTTTTAGAGGAGTTGTCGCCCTGTTGCTCGTCAACGTGGCTGGTGTGCTCTGTTTGTGCTGACGCAACCCCACTGGCTGGGGCATAGATCGATAACGAAGGGCATGCCGAAGCAAAAGAGGAGGAGACATATTAGGACCAACGACAGAGAAATCTCTCAACACCGGGCAACAGGCACTGCAACCGCACACAGAGACAAACGACTGCTTGGGGGTGACCGACCC

6,460 6,470 6,480 6,490 6,500 6,510 6,520 6,530 6,540 6,550 6,560 6,570 6,580 6,590 6,600

GE-001 (bGH)

GE-007 (WPRE_3pUTR)

CATTGCCACCACTGTCACTCTTTCTGGGACTTTCGCTTCCCCCTCCGATCGCCACGGCAGAACTCATCGCCGCTGCTTGGCCCTGCTGGACAGGGGCTAGGTTGCTGGGCACTGATAATCCGTGGTGTGCTGTGCTGCTGCTGTAACGGTGGGACGTTGAGGAAGACCTTGAAGCAAGGCTGAAAGCGAAGGGGGGAGGGCTAGCGGTGCCGCTCTTGAATAGCGGGCGACGGAAGGGGCGACGACTGTCCCGATCCAACGACCCGTGACTATTAAAGGACCAACAGACACGGGAAG

6,610 6,620 6,630 6,640 6,650 6,660 6,670 6,680 6,690 6,700 6,710 6,720 6,730 6,740 6,750

GE-001 (bGH)

TAGTTGACCACTCTGTTGTTTGGCCCTCCCGGTGCTTCTTGACCTTGAAGGTGCCACTCCCACTGCTCTTCTTAATAAATGAGGAAATGCATCGATTGCTGAGTAGGTGCTATTCTATTCTGGGGGGTGGGGTGGGGCAATCAACGGTCGGTAGACAACAAACGGGAGGGGGCACGGAAGAACTGGGACCTTCCAGGTGAGGGTGACAGGAAAGGATTTTACTCTTTAACGTAGCGTAACAGACTCATCCAGTAAGATAAGACCCCAACCCCACTCCCTG

6,760 6,770 6,780 6,790 6,800 6,810 6,820 6,830 6,840 6,850 6,860 6,870 6,880 6,890 6,900

GE-001 (bGH)

GE-1117 (HNF1)

GGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGCATGCTGGGGATGCGGTGGGCTCTATGGCTCTAGAGCATGGCTACGTAGATAAGTAGCATGGCGGTTAATCATTAACACACCTGCAGGAGGAACCCCTAGTGTGAGGTTGGCTGTGCTTCCCTCTCAACCTTCTGTTATGCTGCTAGACCCCTACGCCACCGAGATACCGGAGATCTGCTACCGATGATCTATTCTATGCTACCGCCCAATTAGTAATTGATGTGGAGTCTCTCTTGGGGGACTACCTCACTCAAC

6,910 6,920 6,930 6,940 6,950 6,960 6,970 6,980 6,990 7,000 7,007

GCCACTCCCTCTCTGCGCTCTGCTCACTGAGGCCGGGCGACCAAGGTCGCCGACGCCGGGCGGCTCAGTGAGCGAGCGAGCGCGAGCTGCTGCAAGCGGTGAGGGAGAGACGCGCGAGCGAGCGAGTCACTCCGGCCGCTGGTTTCCAGCGGGCTGCGGGCCCGGAGTCACTCGCTCGCTCGCGCTGCAAGGAGTCC

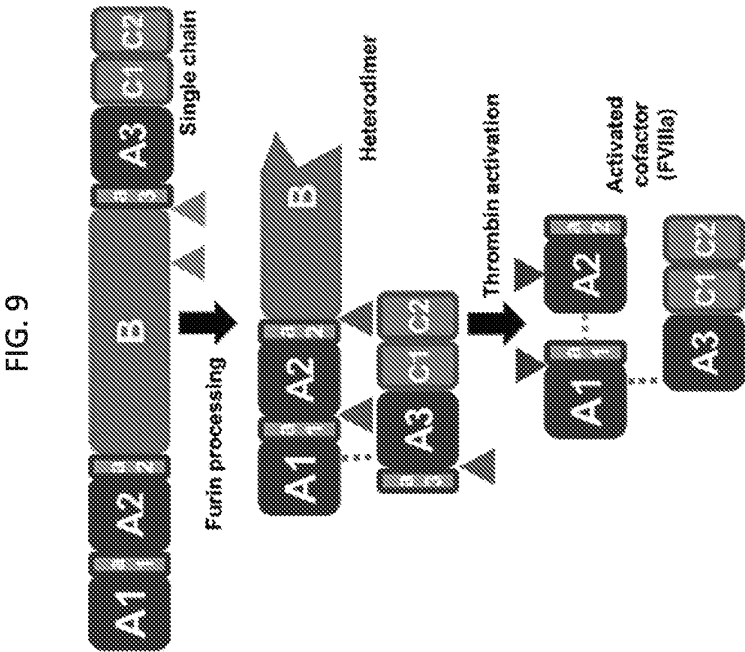


FIG. 10

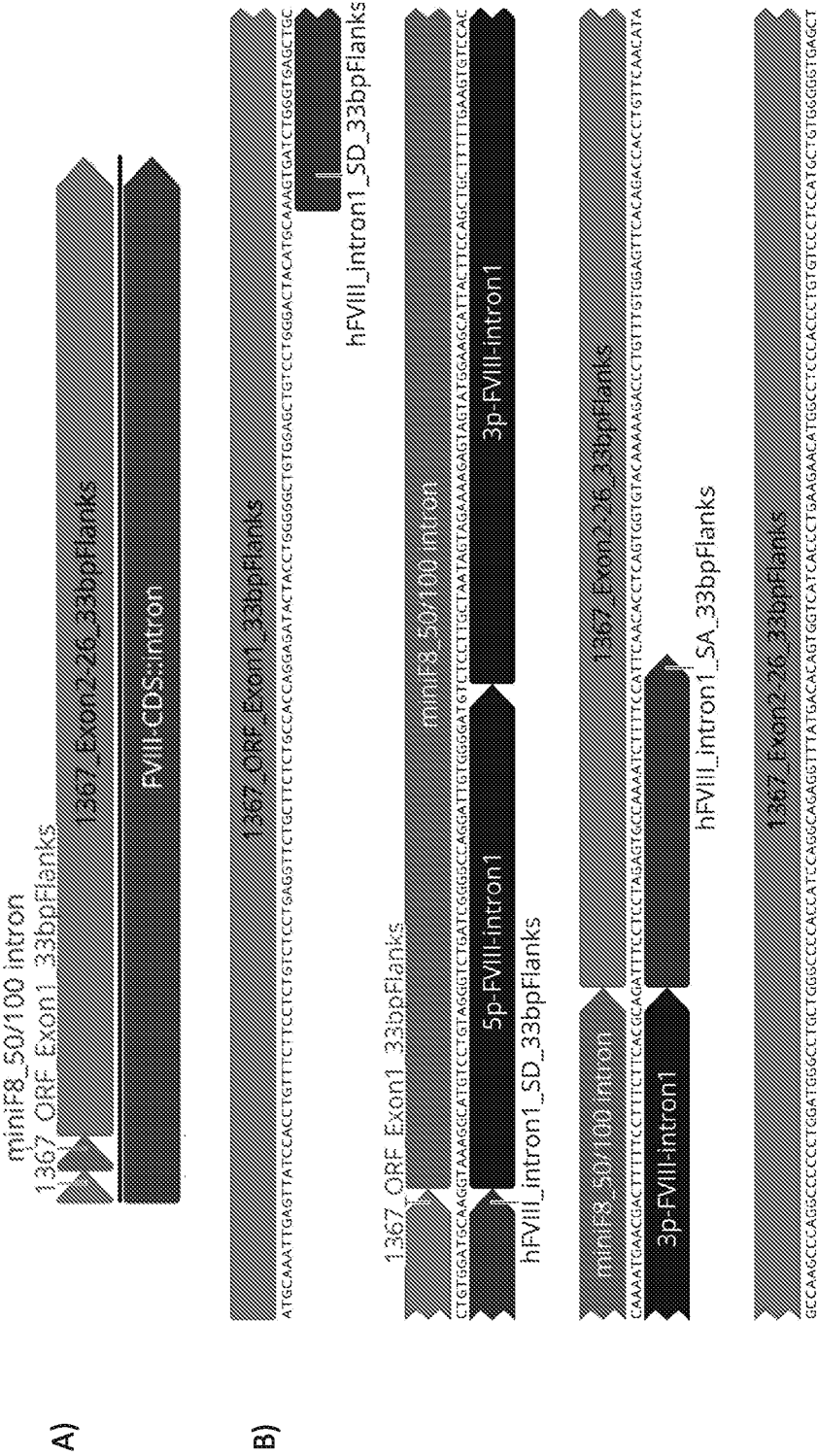


FIG. 12

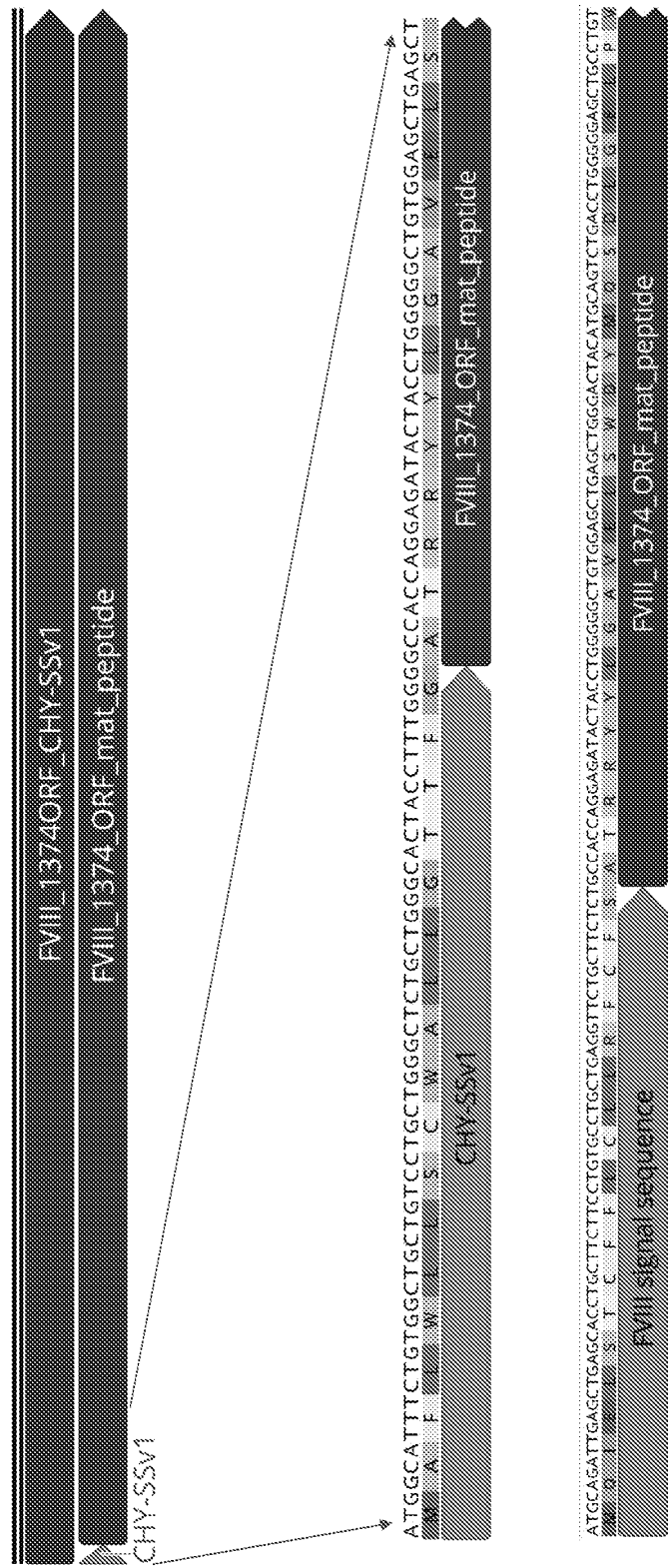


FIG. 13

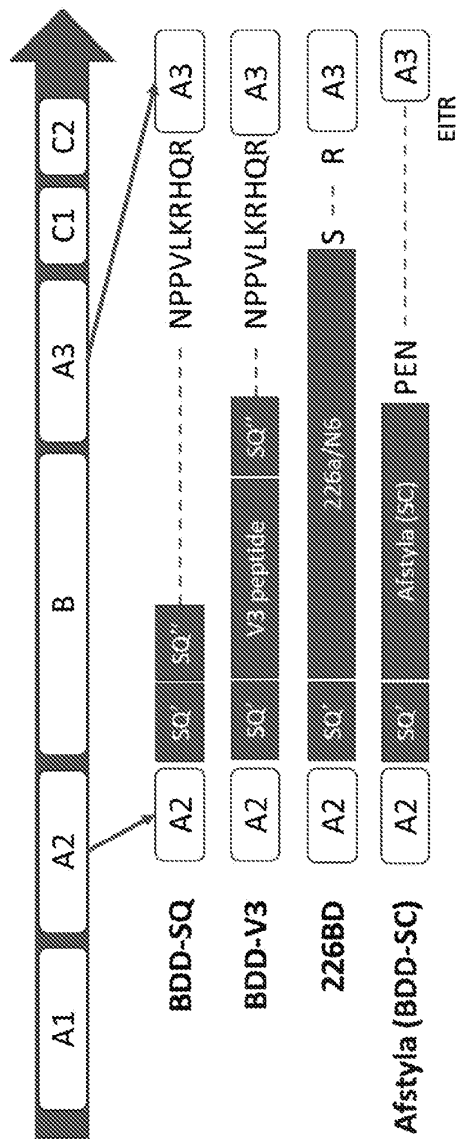


FIG. 14

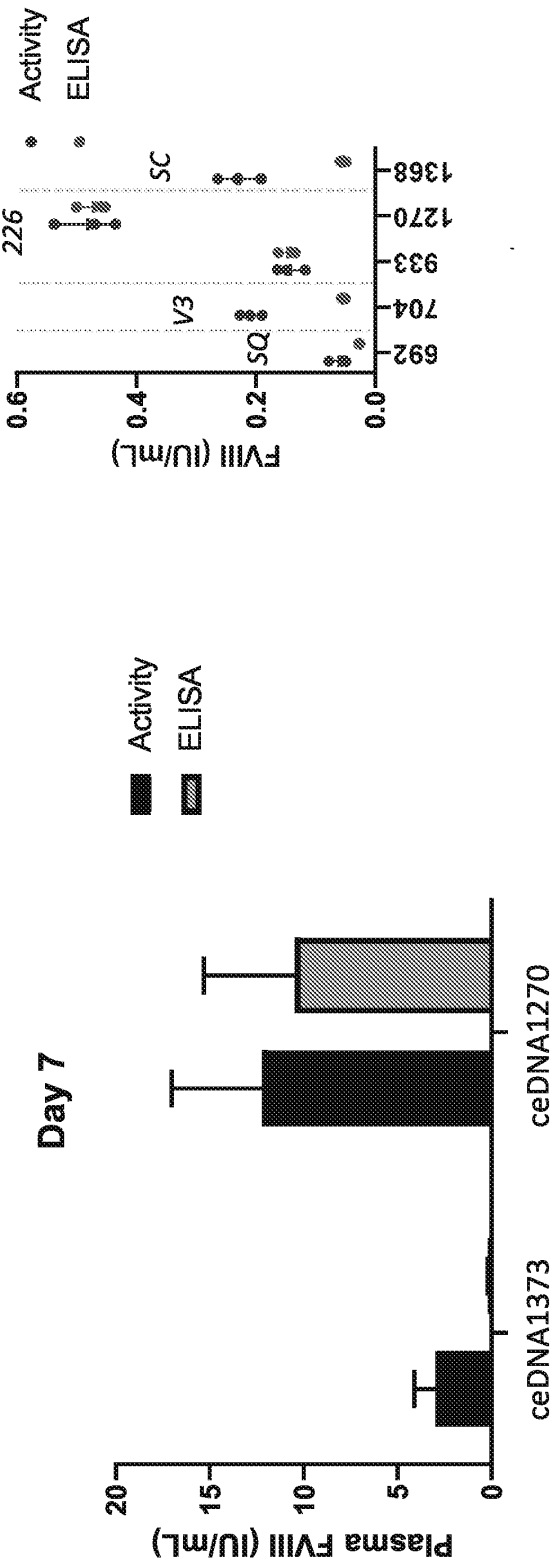


FIG. 15

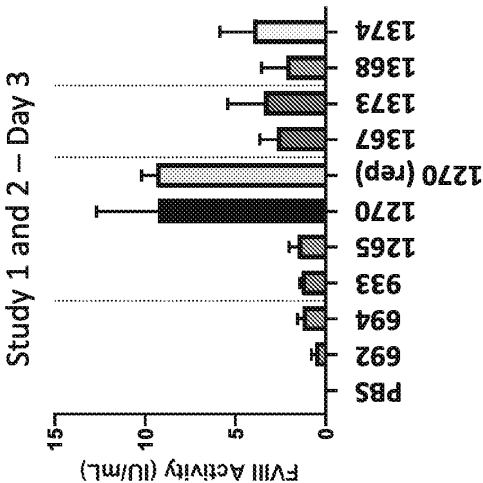
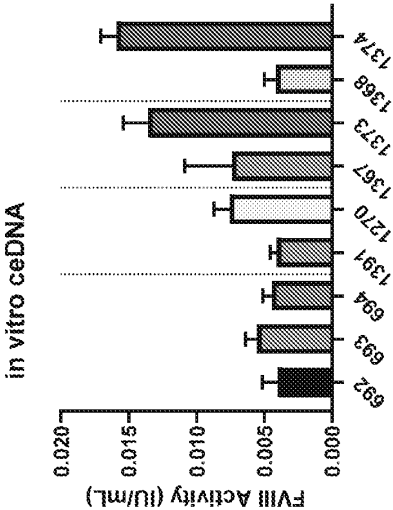
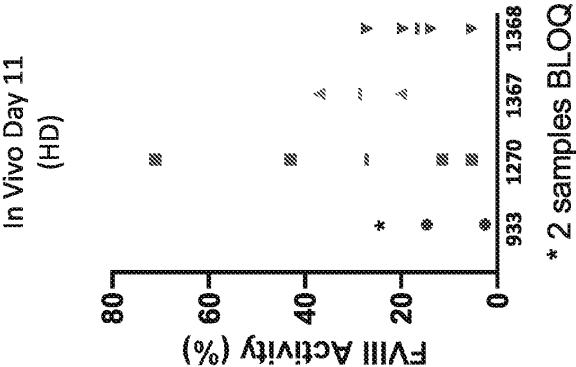


FIG. 16



Strain	Group	Treatment	Condition B. (mL/kg)	Secretion: Mutant (500µg/l)	Initiator: Regimen	Dose Vol (mL/kg)	Dose (mg/kg)	Treatment Regimen: IV
FVIII KO (B6;129S-F8<tm1Kaz>/J)	5	LNP 0933	226/N6	Yes	300 mg/kg, 10 ml/kg, Day 0 30 min. pre-dose & 5 hr post-dose	5	2.0	Once on Day 0 by IV
	6	LNP 1270	226/N6	Yes				
	7	LNP 1367	SC	Yes				
	8	LNP 1368	SC	No				

FIG. 17

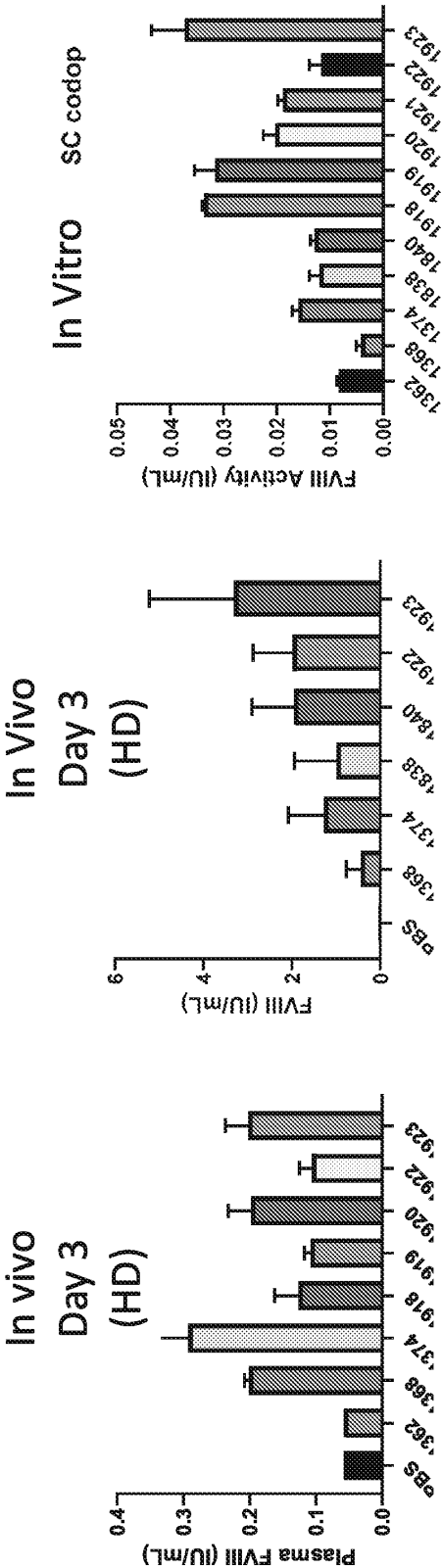


FIG. 18

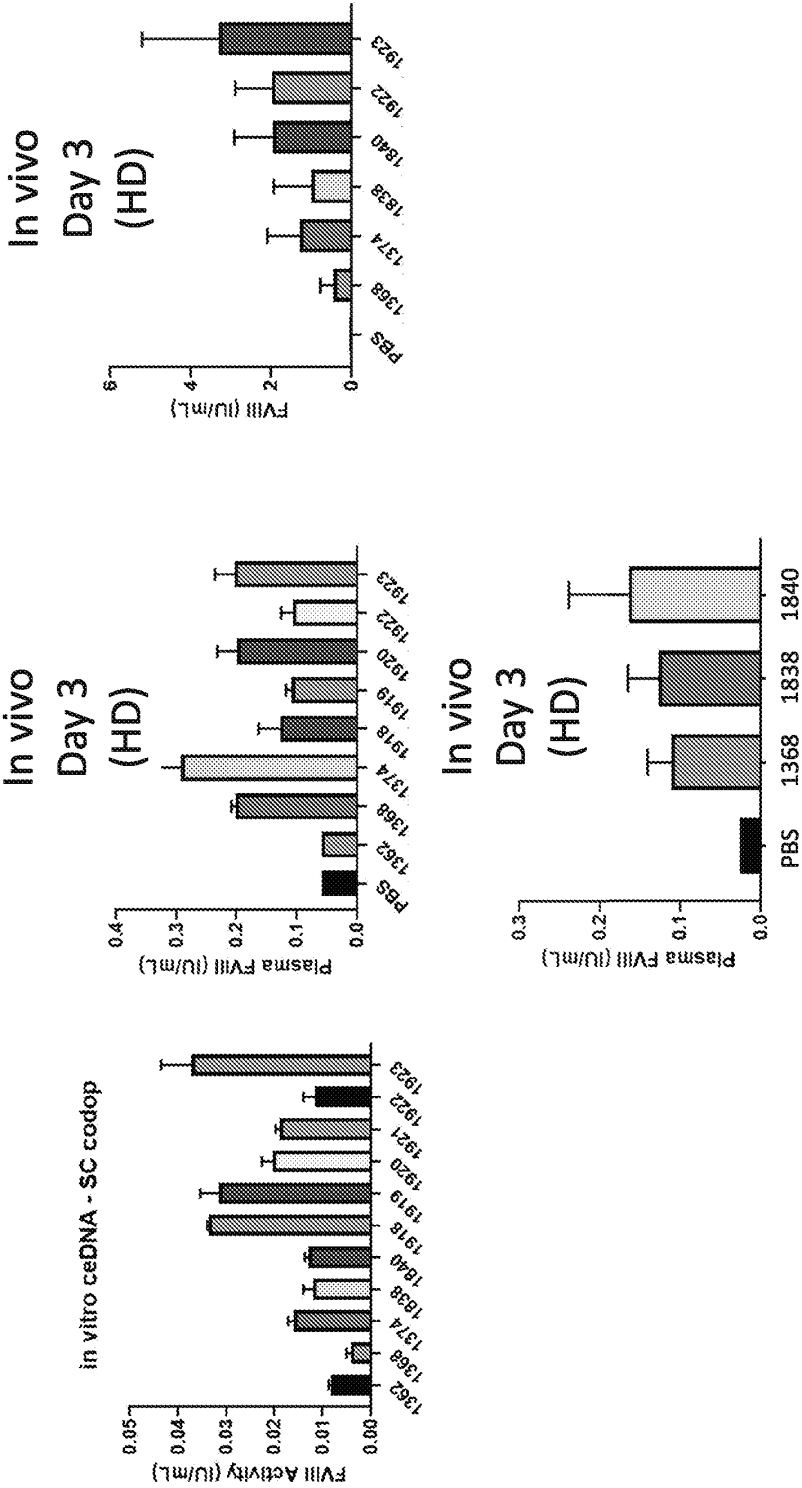


FIG. 19

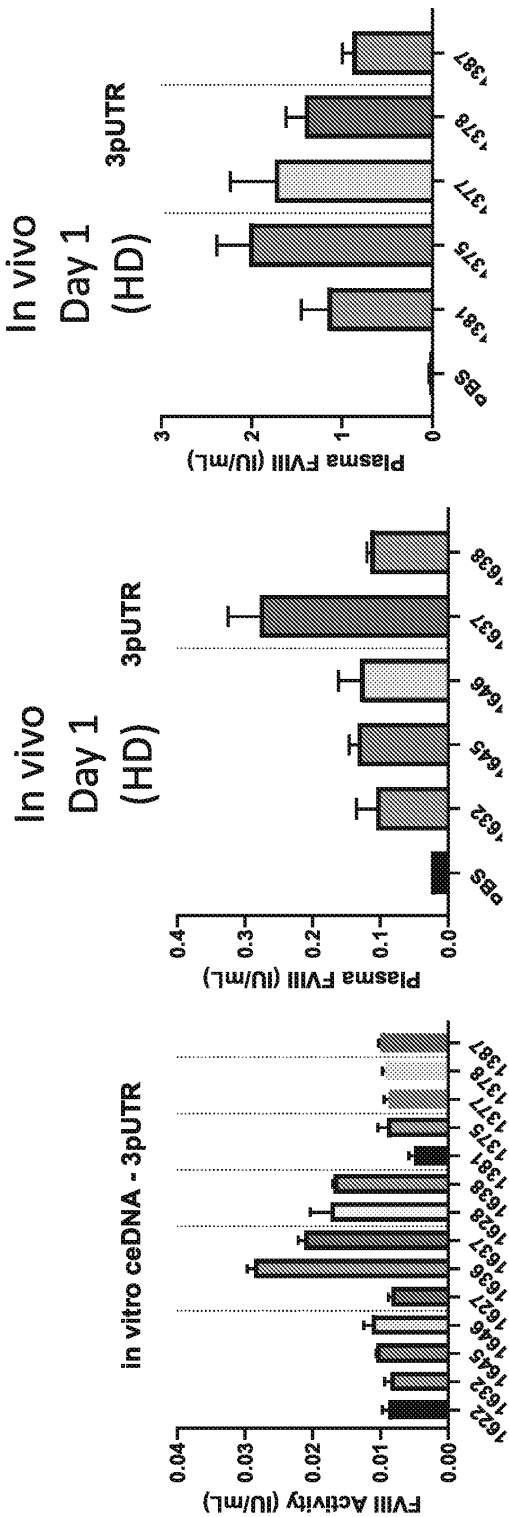


FIG. 20

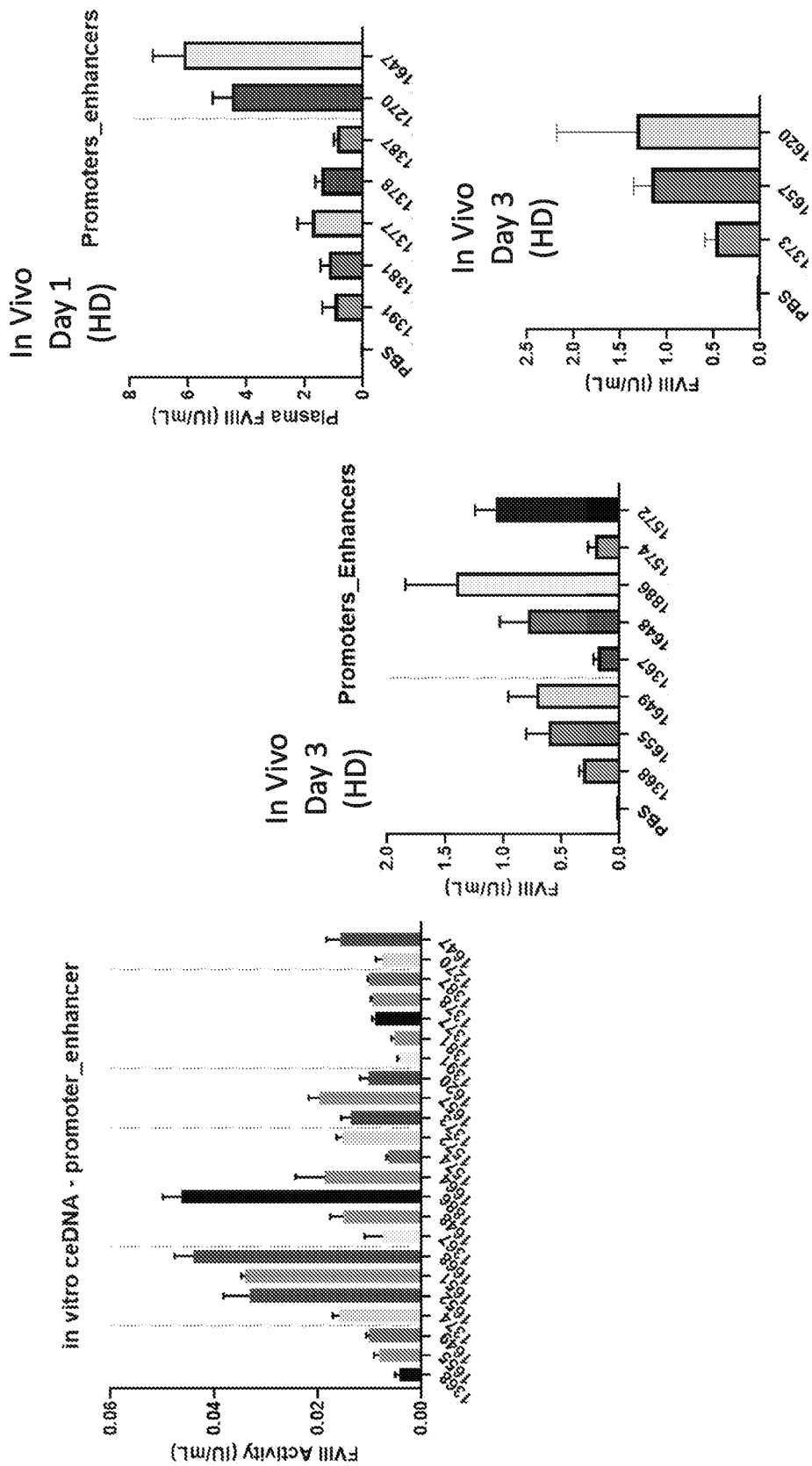


FIG. 21

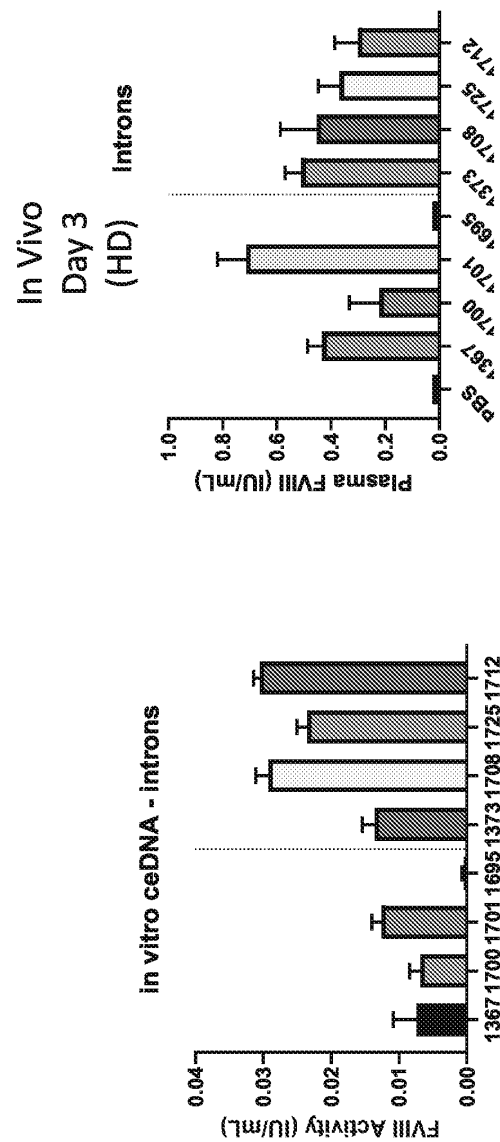


FIG. 22

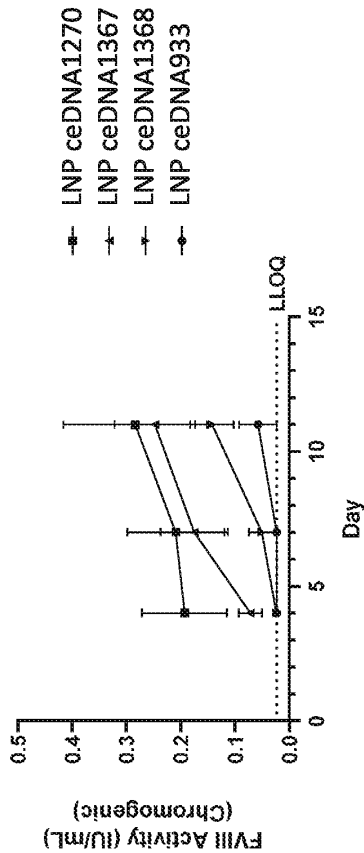


FIG. 23

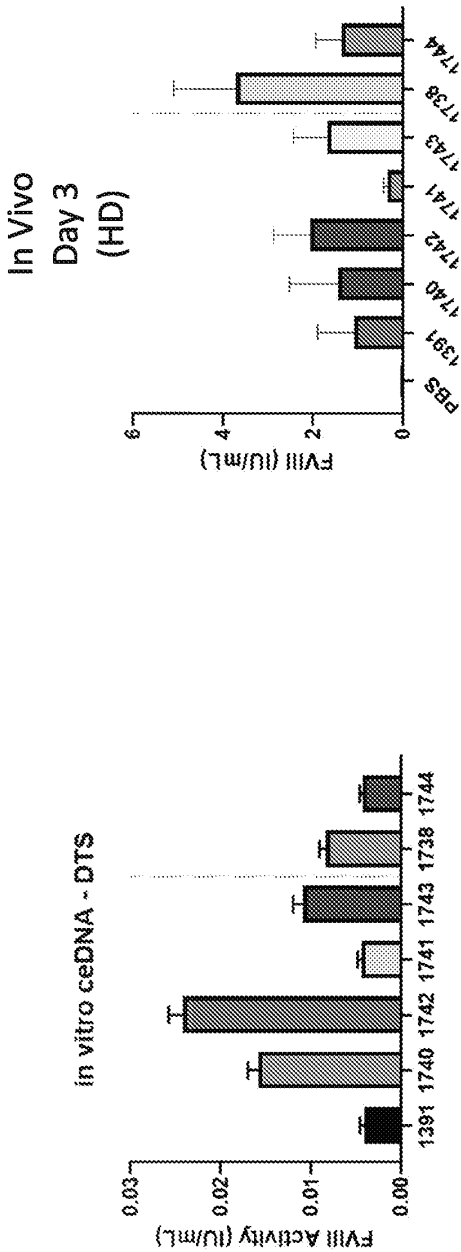


FIG. 24

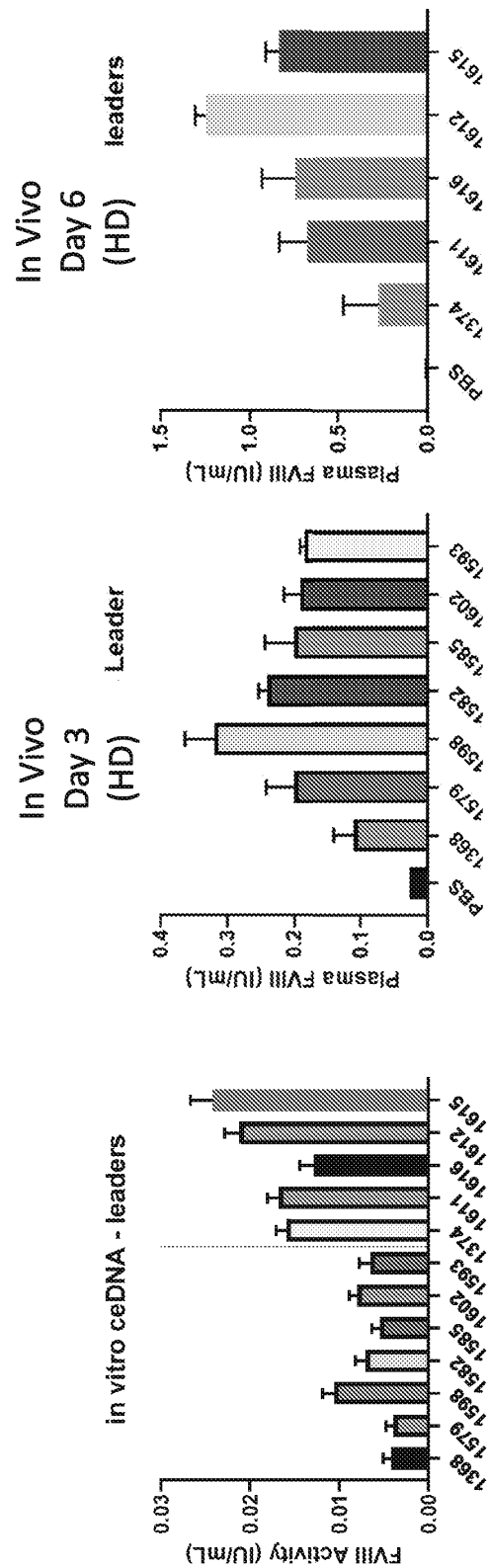


FIG. 25

