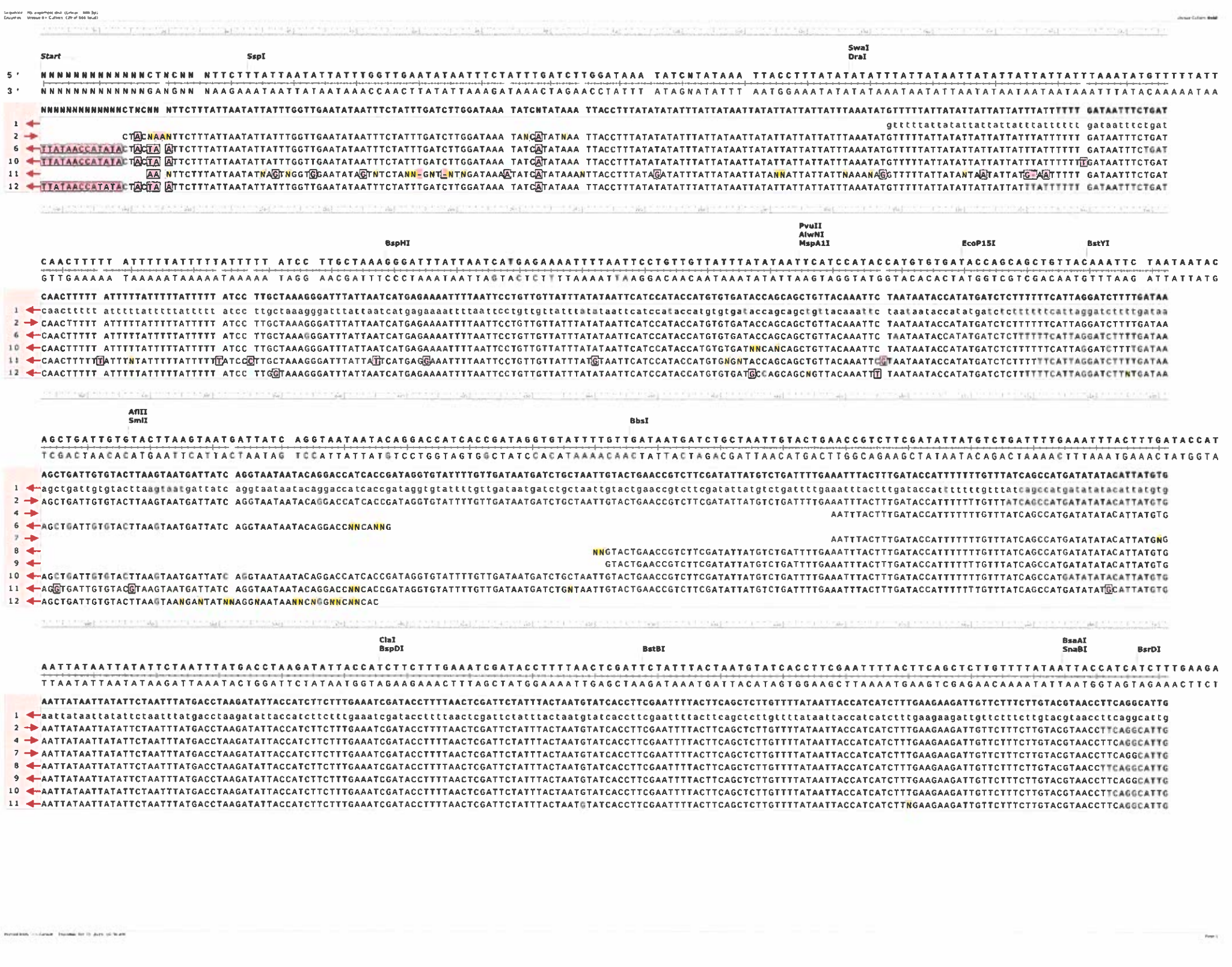
Start
SspI
SwaI
DraI
BspHI
PvuII
AlwNI
MspA1I
EcoP15I
BstYI
AflII
SmlI
BbsI
ClaI
BspDI
BstBI
BsaAI
SnaBI
BsrDI

Original Sequence: HS alignment.dna

1: Template DNA_COX1 GFPm
1093 bases
325 .. 1066 (1 mismatch)

2: 3-F
886 bases
15 .. 883 (12 mismatches, 2 gaps)

3: 1-15
464 bases
24 .. 55 (1 mismatch)

4: 1-12
829 bases
22 .. 418 (1 mismatch)

5: 2-15
467 bases
20 .. 59 (7 mismatches)

6: 3-14
453 bases
18 .. 424 (22 mismatches)

7: 2-12
831 bases
24 .. 420 (2 mismatches)

8: 1-C
834 bases
386 .. 820 (3 mismatches)

9: 2-C
832 bases
385 .. 817 (1 mismatch)

10: 4-11
887 bases
30 .. 857 (26 mismatches, 2 gaps)

11: 3-11
897 bases
47 .. 845 (47 mismatches, 10 gaps)

12: 4-14
455 bases
23 .. 428 (34 mismatches, 1 gap)