GENETICS

Supporting Information
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Tissue Culture-Induced Novel Epialleles of a *Myb* Transcription Factor Encoded by *pericarp color1* in Maize

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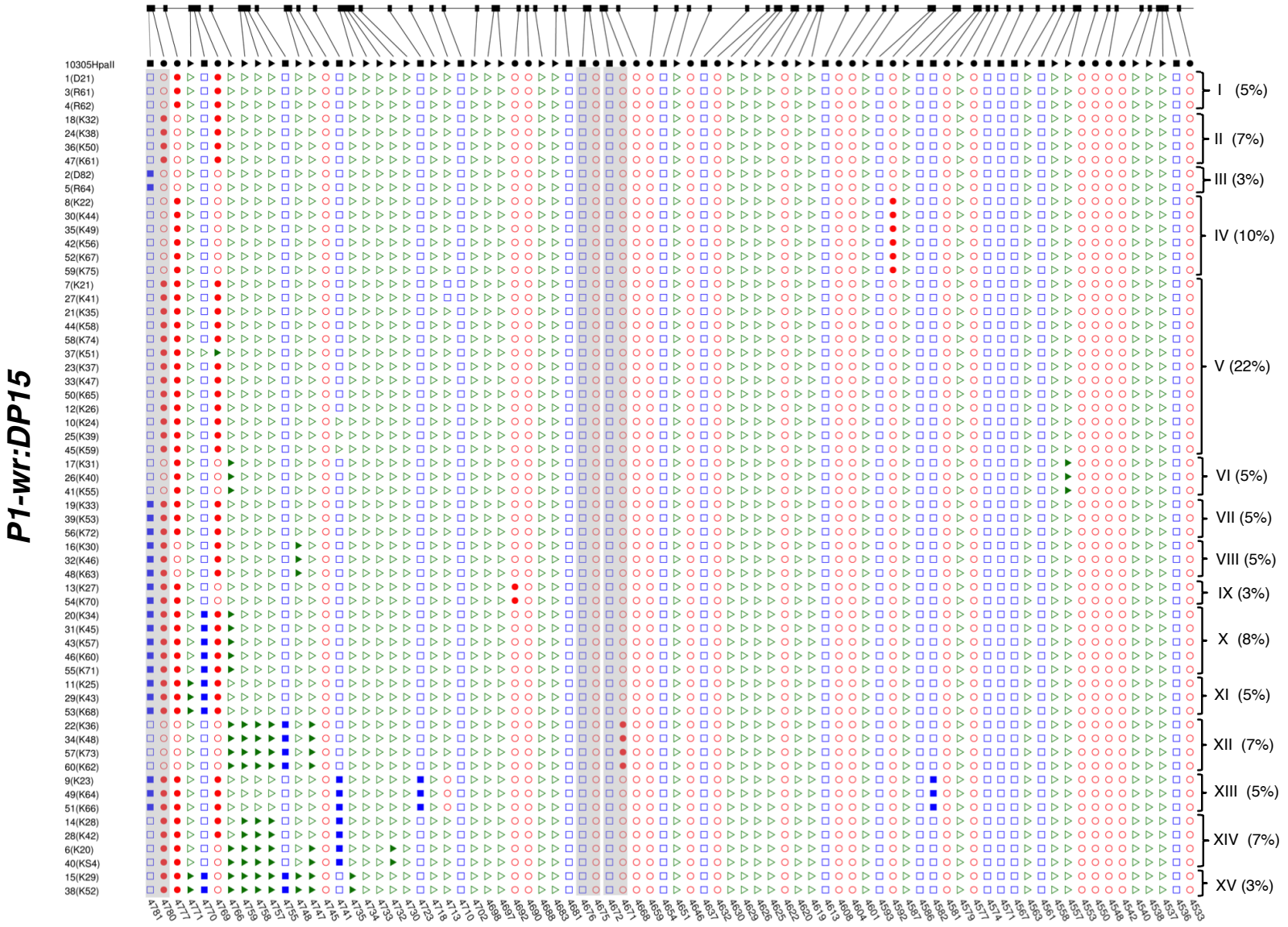
A.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4(R62)
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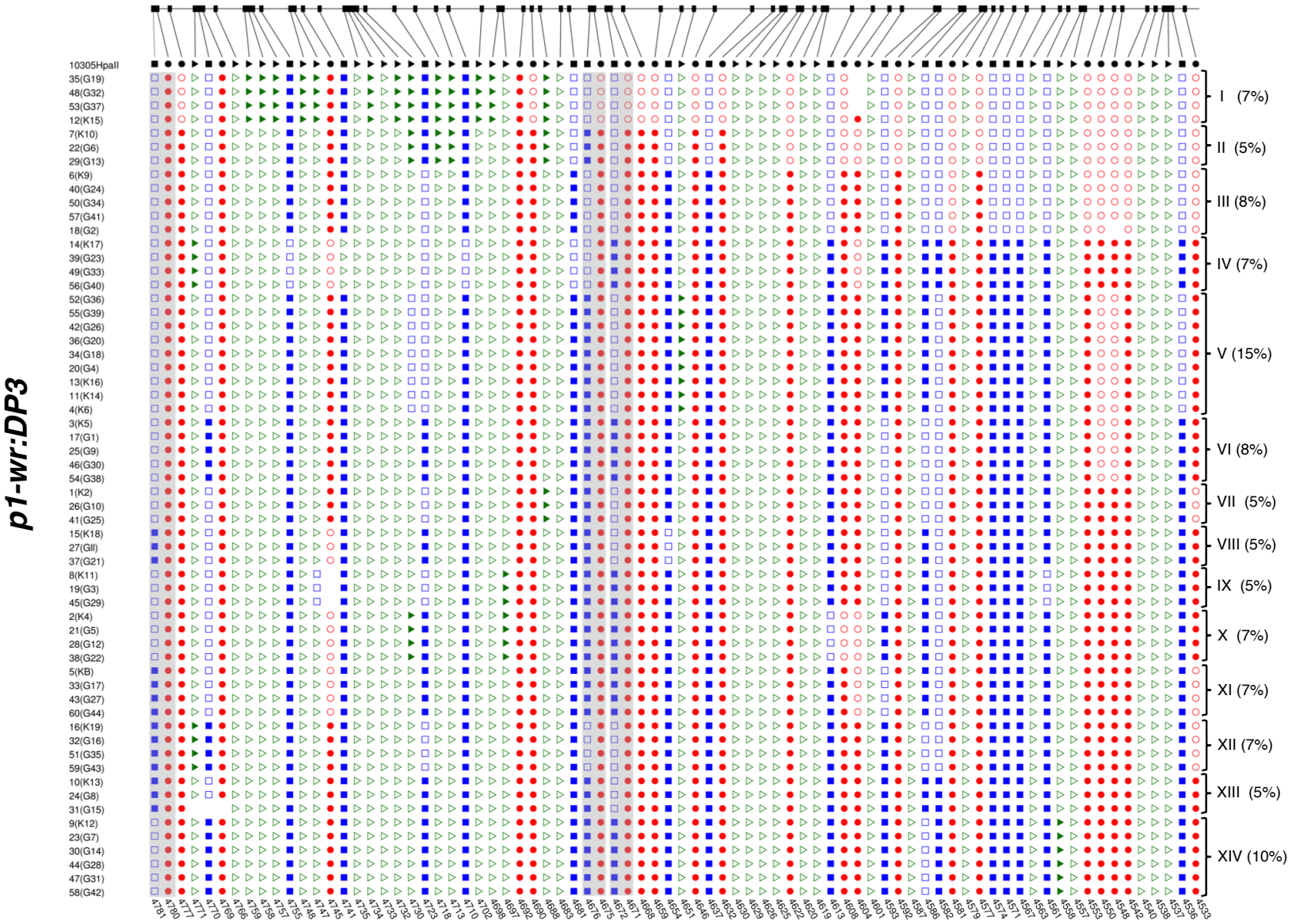
24(K38)
36(K50)
47(K61)
2(D82)
5(R64)
8(K22)
30(K44)
35(K49)
42(K56)
52(K67)
59(K75)
7(K21)
27(K41)
21(K35)
44(K58)
58(K74)
37(K51)
23(K37)
33(K47)
50(K65)
12(K26)
10(K24)
25(K39)
45(K59)
17(K31)
26(K40)
41(K55)
19(K33)
39(K53)
56(K72)
16(K30)
32(K46)
48(K63)
13(K27)
54(K70)
20(K34)
31(K45)
43(K57)
46(K60)
55(K71)
11(K25)
29(K43)
53(K68)
22(K36)
34(K48)
57(K73)
60(K62)
9(K23)
49(K64)
51(K66)
14(K28)
28(K42)
6(K20)
40(KS4)
15(K29)
38(K52)
I (5%)
II (7%)
III (3%)
IV (10%)
V (22%)
VI (5%)
VII (5%)
VIII (5%)
IX (3%)
X (8%)
XI (5%)
XII (7%)
XIII (5%)
XIV (7%)
XV (3%)

B.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7(K10)
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29(G13)
6(K9)
40(G24)
50(G34)
57(G41)
18(G2)
14(K17)
39(G23)
49(G33)
56(G40)
52(G36)
55(G39)
42(G26)
36(G20)
34(G18)
20(G4)
13(K16)
11(K14)
4(K6)
3(K5)
17(G1)
25(G9)
46(G30)
54(G38)
1(K2)
26(G10)
41(G25)
15(K18)
27(GII)
37(G21)
8(K11)
19(G3)
45(G29)
2(K4)
21(G5)
28(G12)
38(G22)
5(KB)
33(G17)
43(G27)
60(G44)
16(K19)
32(G16)
51(G35)
59(G43)
10(K13)
24(G8)
31(G15)
9(K12)
23(G7)
30(G14)
44(G28)
47(G31)
58(G42)
I (7%)
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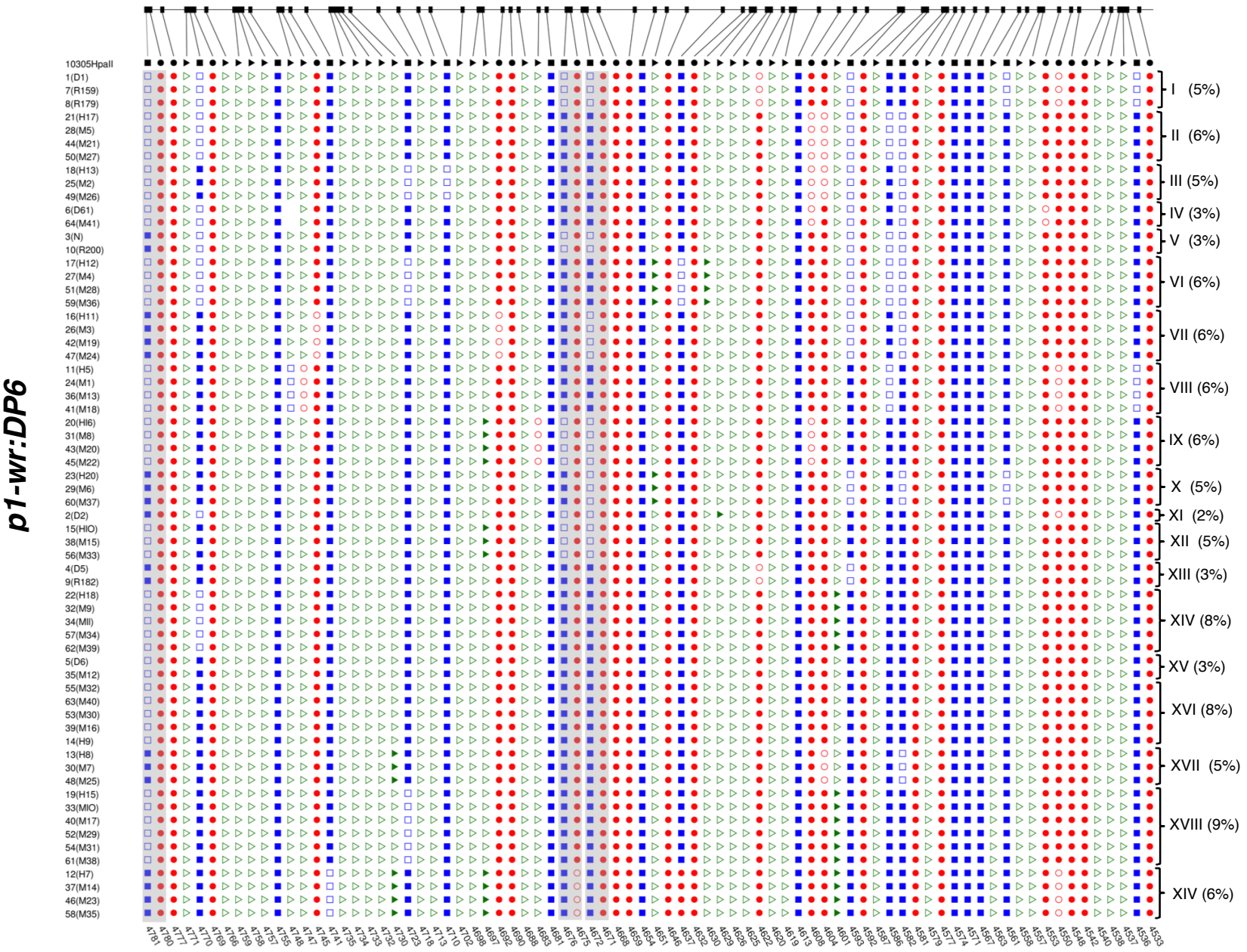
III (8%)
IV (7%)
V (15%)
VI (8%)
VII (5%)
VIII (5%)
IX (5%)
X (7%)
XI (7%)
XII (7%)
XIII (5%)
XIV (10%)
4781 4780 4777 4771 4770 4769 4766 4759 4758 4757 4755 4748 4747 4745 4741 4735 4734 4733 4730 4723 4718 4713 4710 4702 4698 4697 4692 4690 4688 4683 4681 4676 4675 4672 4671 4668 4659 4654 4651 4646 4637 4632 4630 4629 4626 4625 4622 4620 4619 4613 4608 4604 4601 4593 4592 4587 4586 4582 4581 4579 4577 4574 4571 4567 4563 4561 4558 4557 4553 4550 4548 4542 4540 4538 4537 4536 4533

C.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50(M27)
18(H13)
25(M2)
49(M26)
6(D61)
64(M41)
3(N)
10(R200)
17(H12)
27(M4)
51(M28)
59(M36)
16(H11)
26(M3)
42(M19)
47(M24)
11(H5)
24(M1)
36(M13)
41(M18)
20(HI6)
31(M8)
43(M20)
45(M22)
23(H20)
29(M6)
60(M37)
2(D2)
15(HIO)
38(M15)
56(M33)
4(D5)
9(R182)
22(H18)
32(M9)
34(MII)
57(M34)
62(M39)
5(D6)
35(M12)
55(M32)
63(M40)
53(M30)
39(M16)
14(H9)
13(H8)
30(M7)
48(M25)
19(H15)
33(MIO)
40(M17)
52(M29)
54(M31)
61(M38)
12(H7)
37(M14)
46(M23)
58(M35)
I (5%)
II (6%)
III (5%)
IV (3%)
V (3%)
VI (6%)
VII (6%)
VIII (6%)
IX (6%)
X (5%)
XI (2%)
XII (5%)
XIII (3%)
XIV (8%)
XV (3%)
XVI (8%)
XVII (5%)
XVIII (9%)
XIV (6%)

FIGURE S1.—Methylation profile of individual clones in the the wild type (*P1-wr:DP15*), leaky (*p1-ww:DP3*), and silent (*p1-ww:DP6*) alleles in the R-III region of second intron. Shown here are the methylation patterns of cytosine residues in all the clones sequenced after bisulfite treatment. Location of individual CG (ovals), CNG (squares), and CHH (triangles) sites in R-III in the reference *P1-wr* sequence is shown at the top. In sequenced clones, open and filled shapes represent non-methylated and methylated sites, respectively. Some discrepancies between certain sites in the reference sequence and the corresponding sites in the cloned sequences indicate sequence polymorphisms. Coordinates of individual cytosine residues are shown at the bottom. For each genotypes, the clones were divided into groups based on their methylation profile and/or sequence polymorphisms. The groups are indicated on right and percentage of these clones is shown in parentheses. Grey shaded boxes mark the three *Hpa*II sites that are covered in R-III; two adjacent sites that were partially methylated in *p1-ww:DP3* in DNA gel blot analysis are at nt positions 4671 and 4675 (on the anti-sense strand) in the middle of the region.

TABLE S1

Details of three regions analyzed through genomic bisulfite sequencing

Region	Coordinates (Size)	Target strand	Primers used for amplification
R-I	-169 to 157 (326-bp)	Sense	Forward-Prom: 5'-AGTAAAGGGTTTAAAATTGT-3' Reverse-Prom: 5'-AAATCACACTACTACTTA-3'
R-II	4093 to 3800 (294-bp)	Antisense	Forward-SalI: 5'-AGATGGTAGAAATAAAGTTTGAGT-3' Reverse-SalI: 5'-CATAACCTTACTTTACCCACATTA-3'
R-III	4781 to 4532 (250-bp)	Antisense	Forward-Hpa: 5'-GGGAAATTATTAGGGAGGG-3' Reverse-Hpa: 5'-CTCTTCATTCAAACTAACTAA-3'