

Table S1: TFsitedscan transcription factor binding sites prediction results

	Site (Length)	PositionScore (Gaps)	Occurrence	EA Probability
EKLF_CS' (9)	26	7 (0)	0	2.87e-01
c-Myb-pseudorabies				
SREBP-1_CS' (9)	54	7 (0)	0	1.44e-01
C/EBP-beta_CS' (9)	88	7 (0)	0	2.87e-01
PAUSE-1_CS2 (15)	137	10 (0)	0	1.00e00
CNTF_response_eleme				
JCV-B-1' (11)	159	10 (0)	0	1.00e00
MAZ-PTHR (9)	163	9 (0)	0	4.49e-03
MAZ_CS2 (8)	164	7 (0)	0	7.18e-02
Sp1-alp-inhibitor_(5' (11)	164	10 (0)	0	1.00e00
MAZ_CS2' (8)	168	7 (0)	0	7.18e-02
MAZ_CS2 (8)	168	7 (0)	0	7.18e-02
CTF/NF1-CF1-2 (11)	183	10 (0)	0	1.00e00
Yi-consensus' (10)	188	7 (0)	0	2.87e-01
apoE-PET' (12)	188	12 (0)	0	7.02e-05
APOE-PET (10)	190	10 (0)	0	1.12e-03
apoE-B1-II' (9)	190	9 (0)	0	4.49e-03
ApoE_B1' (9)	190	8 (0)	0	8.98e-03
APRT-human_US' (8)	192	8 (0)	0	1.80e-02
APRT-CHO_US' (8)	192	8 (0)	0	1.80e-02
ZFX-HLA-A11-1' (9)	194	9 (0)	0	4.49e-03
Yi-consensus' (10)	215	7 (0)	0	2.87e-01
AP-2_beta_CS' (9)	216	6 (0)	0	5.75e-01
AP1-ET-I (8)	228	8 (0)	0	1.80e-02
AP-1_CS1 (8)	228	7 (0)	0	7.18e-02
claudin-CdxB' (11)	285	10 (0)	0	1.00e00
Rev-erb-alpha-CS (12)	291	10 (0)	0	1.12e-03
ROR-alpha-2_CS (12)	291	10 (0)	0	1.00e00
Rev-ErbAalpha_CS (11)	292	9 (0)	0	1.00e00
E2_RS1' (12)	316	8 (0)	0	2.87e-01
E2_RS1 (12)	316	8 (0)	0	2.87e-01
BPV-E2_CS2' (12)	316	8 (0)	0	2.87e-01
BPV-E2_CS2 (12)	316	8 (0)	0	2.87e-01
TFII-I-fos-SRE (11)	347	10 (0)	0	1.00e00
ANF-SRE/406' (12)	348	11 (0)	0	2.94e-01
PAI-2-TRM' (11)	356	10 (0)	0	1.00e00

AP-2_beta_CS (9)	363	6 (0)	0	5.75e-01
ssT1_CS (12)	376	8 (0)	0	1.44e-01
proximal_region/_A (8)	394	8 (0)	0	1.80e-02
AP1-TGF-beta1.2' (8)	412	8 (0)	0	1.80e-02
TEF1-GTI* (9)	425	9 (0)	0	4.49e-03
SiX5_CS (9)	458	7 (0)	0	7.18e-02
CP2-consensus (11)	530	8 (0)	0	7.18e-02
PuF_site (8)	540	8 (0)	0	1.80e-02
IgHC.8' (8)	630	8 (0)	0	1.80e-02
CuE3.1' (8)	630	8 (0)	0	1.80e-02
GBP/GAS-pIRE' (11)	654	10 (0)	0	1.00e00
Oct-X_CS (9)	669	7 (0)	0	7.18e-02
OTF-2A_RS (9)	669	9 (0)	0	4.49e-03
OTF-1_RS (9)	669	9 (0)	0	4.49e-03
Ig-dc.2' (10)	670	9 (0)	0	4.49e-03
Ig-kappa.2' (8)	670	8 (0)	0	1.80e-02
dc_element_CS' (10)	670	9 (0)	0	4.49e-03
cd_element_CS (10)	670	9 (0)	0	4.49e-03
Octa-U2snRNA (8)	670	8 (0)	0	1.80e-02
NF-A2-IgkLc' (8)	670	8 (0)	0	1.80e-02
NF-A1-IgkLc' (8)	670	8 (0)	0	1.80e-02
IgNF-A-Igk' (8)	670	8 (0)	0	1.80e-02
IgHC.16' (8)	670	8 (0)	0	1.80e-02
IgNF-A-IgH_(1)' (8)	670	8 (0)	0	1.80e-02
IgHC.15' (8)	670	8 (0)	0	1.80e-02
IgHC.14' (8)	670	8 (0)	0	1.80e-02
IgNF-A-IgH_(2) (8)	670	8 (0)	0	1.80e-02
IgHC.2' (8)	670	8 (0)	0	1.80e-02
NF-A2-IgHC' (8)	670	8 (0)	0	1.80e-02
NF-A1-IgHC' (8)	670	8 (0)	0	1.80e-02
IgHC.1' (8)	670	8 (0)	0	1.80e-02
histone-H2B-US' (8)	670	8 (0)	0	1.80e-02
dc_box.2' (10)	670	9 (0)	0	4.49e-03
OCTA3 (8)	670	8 (0)	0	1.80e-02
OCTA1.1' (8)	670	8 (0)	0	1.80e-02
Ig_cd (10)	670	9 (0)	0	4.49e-03
dc_box' (10)	670	9 (0)	0	2.24e-03
HIF-1-guanylin' (11)	683	10 (0)	0	1.00e00

NF-E2-consensus_(1)' (8)	686	8 (0)	0	1. 80e-02
AP1-TRE-4/C (9)	686	9 (0)	0	4. 49e-03
NF-E2_CS2 (9)	687	8 (0)	0	1. 80e-02
AP-1_CS2 (8)	687	8 (0)	0	1. 80e-02
AP-2_beta_CS' (9)	694	6 (0)	0	5. 75e-01
IL2-TCep (10)	700	10 (0)	0	1. 12e-03
Six5_CS (9)	714	7 (0)	0	7. 18e-02
Sp1-GPC_(2)' (11)	731	10 (0)	0	1. 00e00
Sp1-KDR/flk-1-IV (11)	732	10 (0)	0	1. 00e00
Sp1-alpha-actin_(4)' (11)	732	10 (0)	0	1. 00e00
KLF15-CS' (9)	733	7 (0)	0	7. 18e-02
EKLF_CS' (9)	733	7 (0)	0	2. 87e-01
KKLF_CS (9)	733	7 (0)	0	7. 18e-02
MAZ_CS2' (8)	734	7 (0)	0	7. 18e-02
MAZ_CS2 (8)	734	7 (0)	0	7. 18e-02
AP-2_beta_CS' (9)	762	6 (0)	0	5. 75e-01
AP-2_beta_CS (9)	762	6 (0)	0	5. 75e-01
AP-2_site' (9)	762	7 (0)	0	2. 87e-01
AP-2_site (9)	762	7 (0)	0	2. 87e-01
Olf-1-consensus (11)	781	10 (0)	0	2. 24e-03
AP-2-p62_(2) (8)	790	8 (0)	0	1. 80e-02
Ad5_EIA_element_I' (11)	799	10 (0)	0	1. 00e00
E1A_element_I. 2' (11)	799	10 (0)	0	1. 00e00
MyoD-PRR-M-CAT (8)	822	8 (0)	0	1. 80e-02
KLF15-CS (9)	841	7 (0)	0	7. 18e-02
MAZ_CS2' (8)	841	7 (0)	0	7. 18e-02
KKLF_CS' (9)	841	7 (0)	0	7. 18e-02
IRF-1/pIRE' (11)	911	10 (0)	0	1. 00e00
TTF-TP0-2' (8)	936	8 (0)	0	1. 80e-02
T3R_TRE1_CS (8)	1064	7 (0)	0	7. 18e-02
EKLF_CS' (9)	1072	7 (0)	0	2. 87e-01
hIGFBP-1-HRE-2' (8)	1081	8 (0)	0	1. 80e-02
CP1-gamma-globin_(3) (8)	1092	8 (0)	0	1. 80e-02
PEA-3-TBXAS1 (8)	1119	8 (0)	0	1. 80e-02
MDR1-HT-p53-site-1' (11)	1209	10 (0)	0	1. 00e00
MyoD_CS2' (9)	1233	7 (0)	0	1. 44e-01
YY1_CS' (9)	1250	7 (0)	0	1. 44e-01
ESE-3_CS (9)	1286	8 (0)	0	1. 80e-02

Ets1-Fgf8 (8)	1312	8 (0)	0	1.80e-02
c-Ets-2_CS' (8)	1312	7 (0)	0	7.18e-02
AP-2_beta_CS' (9)	1341	6 (0)	0	5.75e-01
AP-2_beta_CS (9)	1341	6 (0)	0	5.75e-01
AP-1_CS1 (8)	1341	7 (0)	0	2.87e-01
ApoB-site_g (8)	1358	8 (0)	0	1.80e-02
PEA3_site_CS (8)	1360	7 (0)	0	3.59e-02
TCF-2-alpha_CS (8)	1360	7 (0)	0	7.18e-02
GABP_CS (8)	1361	7 (0)	0	3.59e-02
Ad5_EIA_element_I (11)	1361	10 (0)	0	1.00e00
E1A_element_I.2 (11)	1361	10 (0)	0	1.00e00
AP2-FGFR4' (11)	1417	10 (0)	0	6.23e-01
AluA' (13)	1483	13 (0)	0	1.75e-05
delta-rpL7' (8)	1488	8 (0)	0	1.80e-02
AT-Alu (16)	1501	14 (0)	0	1.22e-03
Gfi-1-P21' (27)	1510	26 (0)	0	1.45e-10
HiNF-A_RS (12)	1538	9 (0)	0	1.80e-02
YY1_CS' (9)	1558	7 (0)	0	1.44e-01
YY1_CS4 (11)	1559	9 (0)	0	1.00e00
PAI-2-CRE-element (8)	1560	8 (0)	0	1.80e-02
TSE/TRE/DR4_(1)' (16)	1560	12 (0)	0	1.56e-01
ESE-3_CS (9)	1587	8 (0)	0	1.80e-02
Ets1-Fgf8 (8)	1587	8 (0)	0	1.80e-02
c-Ets-2_CS' (8)	1587	7 (0)	0	7.18e-02
SREBP-1_CS (9)	1594	7 (0)	0	1.44e-01
AP-2-p62_(1)' (8)	1614	8 (0)	0	1.80e-02
Gfi-1-AZU-1 (30)	1617	29 (0)	0	2.27e-12
Gfi-1-ACT' (30)	1618	28 (0)	0	2.51e-09
LUN_RS' (16)	1618	16 (0)	0	2.74e-07
PLOD1-Bic-NKE' (15)	1622	14 (0)	0	2.43e-03
HIOMT-A-E4 (18)	1625	17 (0)	0	3.80e-05
bicoid-CAMLG (8)	1631	8 (0)	0	1.80e-02
C/EBP-TTRS3' (8)	1643	8 (0)	0	1.80e-02
C/EBP_CS2' (8)	1643	7 (0)	0	7.18e-02
TTF-1-SP-D (11)	1642	10 (0)	0	6.23e-01
E47-MyoD_CS' (8)	1646	7 (0)	0	5.39e-02
MT-IG-MRE-b' (13)	1651	12 (0)	0	3.90e-02
GABP-Slp_site' (8)	1659	8 (0)	0	1.80e-02

Elk-1_CS (8)	1661	7 (0)	0	7.18e-02
IL2R-Ets (8)	1661	8 (0)	0	1.80e-02
Initiator_CS' (8)	1677	7 (0)	0	7.18e-02
Initiator_CS' (8)	1717	7 (0)	0	7.18e-02
crystallin-DE1A' (11)	1728	10 (0)	0	6.23e-01
dc_box.2 (10)	1745	9 (0)	0	4.49e-03
Ig_cd' (10)	1745	9 (0)	0	4.49e-03
dc_box (10)	1745	9 (0)	0	4.49e-03
Ig-dc.2 (10)	1745	9 (0)	0	2.24e-03
dc_element_CS (10)	1745	9 (0)	0	4.49e-03
cd_element_CS' (10)	1745	9 (0)	0	4.49e-03
Oct-X_CS' (9)	1747	7 (0)	0	4.49e-03
OTF-2A_RS' (9)	1747	9 (0)	0	4.49e-03
OTF-1_RS' (9)	1747	9 (0)	0	4.49e-03
Ig-kappa.2 (8)	1747	8 (0)	0	1.80e-02
Octa-U2snRNA' (8)	1747	8 (0)	0	1.80e-02
NF-A2-IgkLc (8)	1747	8 (0)	0	1.80e-02
NF-A1-IgkLc (8)	1747	8 (0)	0	1.80e-02
IgNF-A-Igk (8)	1747	8 (0)	0	1.80e-02
IgHC.16 (8)	1747	8 (0)	0	1.80e-02
IgHC.15 (8)	1747	8 (0)	0	1.80e-02
IgHC.14 (8)	1747	8 (0)	0	1.80e-02
IgNF-A-IgH_(2)' (8)	1747	8 (0)	0	1.80e-02
IgHC.2 (8)	1747	8 (0)	0	1.80e-02
NF-A2-IgHC (8)	1747	8 (0)	0	1.80e-02
NF-A1-IgHC (8)	1747	8 (0)	0	1.80e-02
IgHC.1 (8)	1747	8 (0)	0	1.80e-02
IgNF-A-IgH_(1) (8)	1747	8 (0)	0	1.80e-02
histone-H2B-US (8)	1747	8 (0)	0	1.80e-02
OCTA3' (8)	1747	8 (0)	0	1.80e-02
OCTA1.1 (8)	1747	8 (0)	0	1.80e-02
IRF-2_RS' (8)	1758	6 (0)	0	2.87e-01
STE6.2 (8)	1762	8 (0)	0	1.80e-02
CK-8-mer (8)	1770	7 (0)	0	7.18e-02
RIPE3b' (8)	1782	8 (0)	0	1.80e-02
Ets1-erk1' (8)	1812	8 (0)	0	1.80e-02
TCF-1alpha-ADA (11)	1866	10 (0)	0	6.23e-01
AP-2-cyclinD2_(1) (8)	1866	8 (0)	0	1.80e-02

AP-2-erk1 (9)	1889	9 (0)	0	4. 49e-03
C/EBP-beta_CS (9)	1917	7 (0)	0	2. 87e-01
Math3-E-box (8)	1942	8 (0)	0	1. 80e-02
CP2-consensus' (11)	1965	8 (0)	0	7. 18e-02
CK-8-mer (8)	1972	7 (0)	0	7. 18e-02
keratinocyte_CS (8)	1972	7 (0)	0	3. 59e-02
MEIS1_CS' (8)	1979	7 (0)	0	1. 44e-01
Oct-1-IE-3_ (3) (9)	2075	9 (0)	0	4. 49e-03
AP-2-TBXAS1 (8)	2110	8 (0)	0	1. 80e-02

Table S2. List of oligo primers used in this study

Primer name	Sequence (5'→3')	Used in plasmid construction
hE-1p-2.1F	TTCTCTATCGATAACGCGTTTGCTCCTGACCTAAAATTCCATTAATGGG	pE2.1p
hE-1p-2.1R	CGAGCCCGGGCTAGCAAGCTTGGTGCCAGTTGGAGGCCAAAAAGG	pE2.1p
F1	GCAGTGAGCCGAGATTGCCCTAGGCTTGTCCTTCT	pE2.1p-d1350/1250
R1	ATCTCGAGTTTTCTGCCCATGCGCCAGGT	pE2.1p-d1350/1250
F2	AAGGTACCGGAGTCATCCTTAAGTGTCTTCCCAGC	pE2.1p-d1350/1250
R2	GACAAGCCTAGGGCAATCTCGGCTCACTGCAACCT	pE2.1p-d1350/1250
F3	AAGGTACCGGAGTCATCCTTAAGTGTCT	pE2.1p-d1485/1350
R3	GGCTGGATGCAGCAGTGTGACCTGATCTCAAAGTCTTGA	pE2.1p-d1485/1350
F4	TCAAGAGTTTGAGATCAGGTCACACTGCTGCACTCCAGCC	pE2.1p-d1485/1350
R4	AAAGGCCTCTTAAAGGCAGCCGAAGGC	pE2.1p-d1485/1350
F5	AAGGTACCGGAGTCATCCTTAAGTGTCT	pE2.1p-d1649/1486
R5	CCAATGGCTGCTTCATTTGCAT	pE2.1p-d1649/1486
F6	TCAGAGACACGTTTATTCTGCTCTTACTCA	pE2.1p-d1749/1650
R6	ATCTCGAGTTTTCTGCCCATGC	pE2.1p-d1749/1650
F7	AAGGTACCGGAGTCATCCTTAAGTGTCTTCC	pE2.1p-d1749/1650
R7	TGAGTAAGAGCAGAATAAACGTGTCTCTGACTCCT	pE2.1p-d1749/1650
F8	GCACTTGGAAGGGATGTGGTGCCAACCCAGGGAG	pE2.1p-d1850/1750
R8	ATCTCGAGTTTTCTGCCCATGCGCCAGGTTGAACAGTTGCTGGTGGGTTA	pE2.1p-d1850/1750
F9	GGAACCGGAGTCATCCTTAAGTGTCTTCC	pE2.1p-d1850/1750
R9	TGGGTTGGCACCACATCCCTTCCAAGTGTCAGCT	pE2.1p-d1850/1750

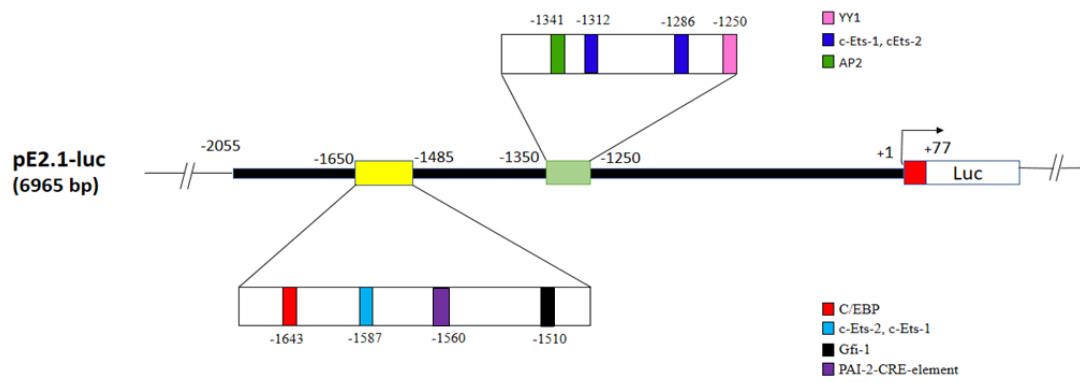
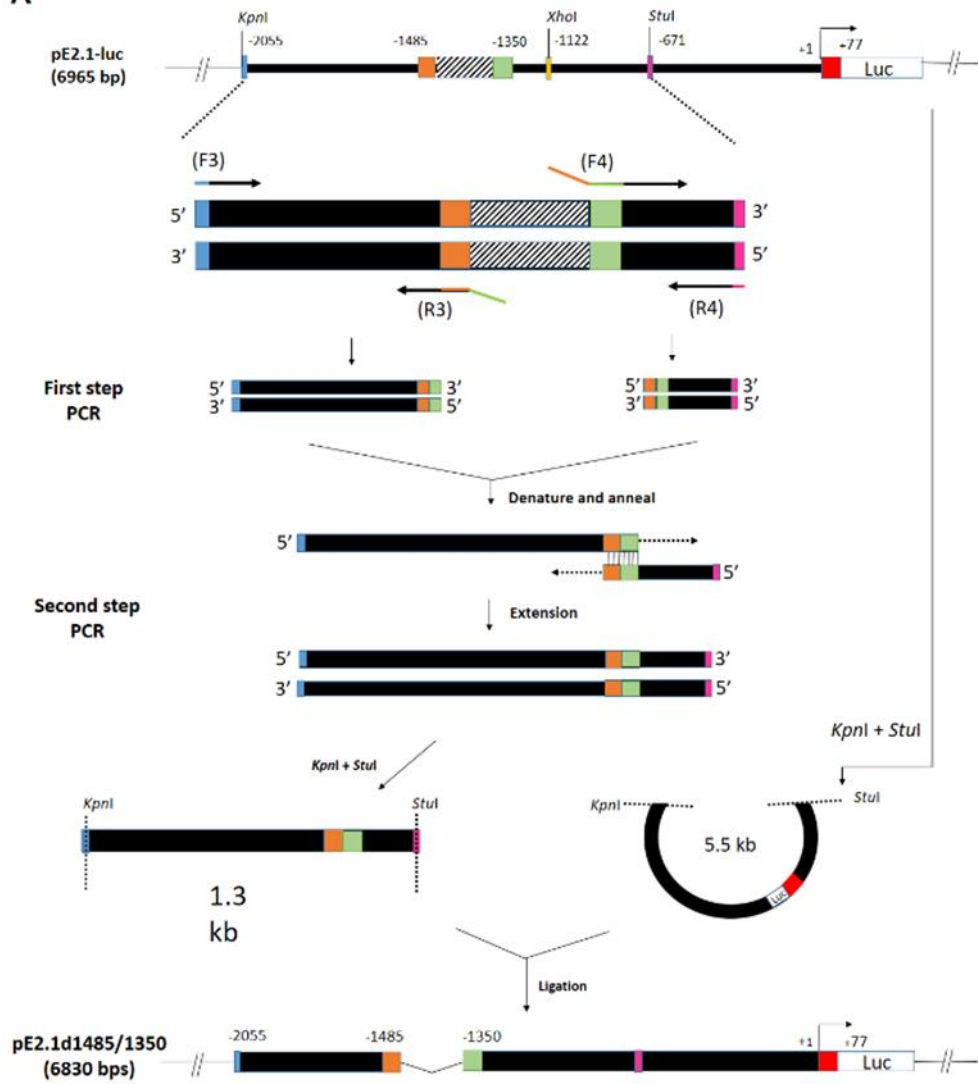


Figure S1. TFBSs within the -1650~-1485 and -1350~-1250 segments of human *ENDOU-1* gene, as predicted using TFsitiescan.

A



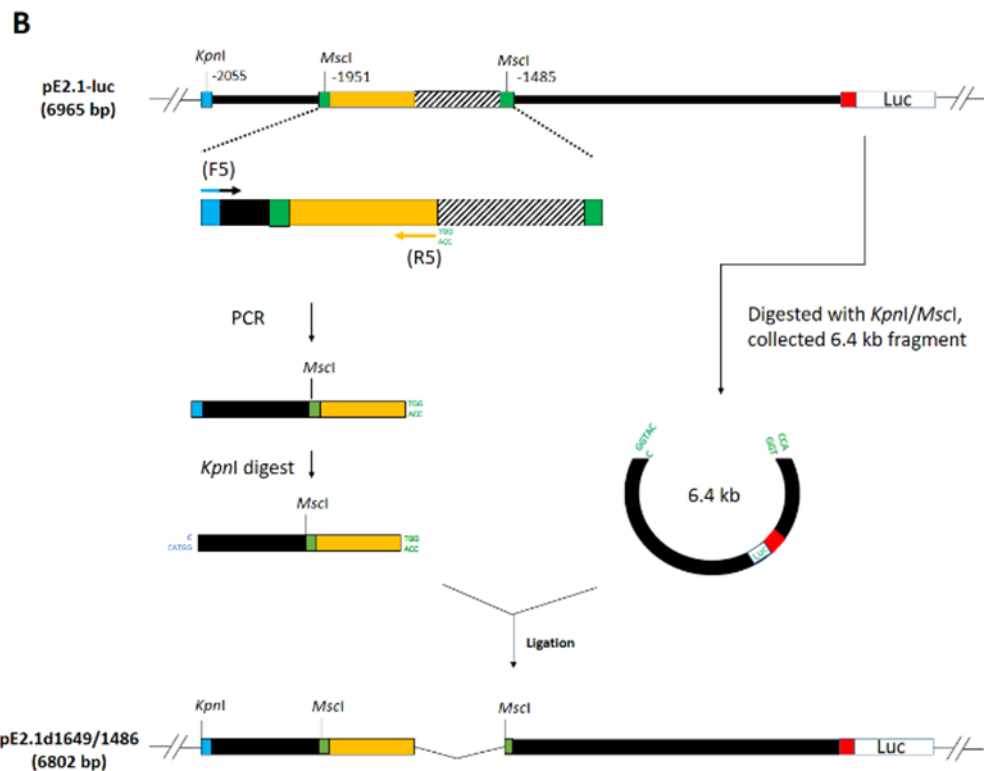


Figure S2. Scheme of plasmid construction. (A) Two-step PCR strategy to generate plasmids harboring various internal deletions within the pE2.1p construct. For example, pE2.1p lacking -1485~-1350 (pE2.1p-d1485/1350). Plasmids pE2.1p-d1850/1750 and pE2.1p-d1749/1650 were generated using the same strategy except of using restriction enzymes KpnI and XhoI and corresponding primers (Table 1). Similarly, pE2.1p-d1350/1250 was generated using XhoI and StuI and corresponding primers. (B) Restriction and ligation strategy to generate plasmid pE2.1p-d1649/1486. A 0.5 kb PCR product containing an internal MscI cutting site was amplified using primers F5 and R5, followed by insertion into KpnI and MscI-digested plasmid pE2.1p.