Supplementary Information

Supplementary Figure Legends

Figure S1. Promoter activities of the single-base substitutions in a BPs lysogen of *M. smegmatis* mc^{2}155. (A) The fluorescence of P_R-mCherry transcriptional fusions with single base substitutions in the extended -10 and -10 motifs (as shown in Fig. 2A) in a BPs lysogen. (B) The fluorescence of P_R-mCherry transcriptional fusions with single base substitutions in the -35 hexamer (as shown in Fig. 2B) in a BPs lysogen. The wild-type P_R sequence and most active substitution are included below. N= any base; H= A, C, or T; M= A or C; R= A or G; S= G or C; V= A,C or G

Figure S2. Effect of single base pair substitutions in the spacer region on promoter activity and derepression of P_R in a BPs lysogen. (A) The fluorescence of P_R-mCherry transcriptional fusions in *M. smegmatis* mc^{2}155 and *M. smegmatis* mc^{2}155(BPs) containing single base substitutions in the spacer region from -26 to -15. This region is the operator O_R (coordinates 29484 to 29495), which is the binding site of the BPs repressor, gp33. The bases of O_R that overlap with the extended -10 motif (E) are noted. (B) The amount of derepression caused by the substitutions from (A) was calculated by taking the reciprocal of the ratio of activity in mc^{2}155 to mc^{2}155(BPs). The bases from O_R that overlap with the extended -10 motif are noted (E). ND= not determined

Figure S3. Comparative expression of combinatorial mutants in *E. coli.* A subset of the P_R promoter mutants were assayed for promoter activity in *E. coli*, including a promoterless vector (pLO73), the hsp60 promoter (pLO74), the wild-type P_R promoter (pLO75) and a number of the combinatorial mutants. The strengths of the combinatorial mutations in mycobacteria are reported in Figures 4, 5 and 6, except for pLO160 (C-16T, C-14G, G-10A, T-9C, C-34A).

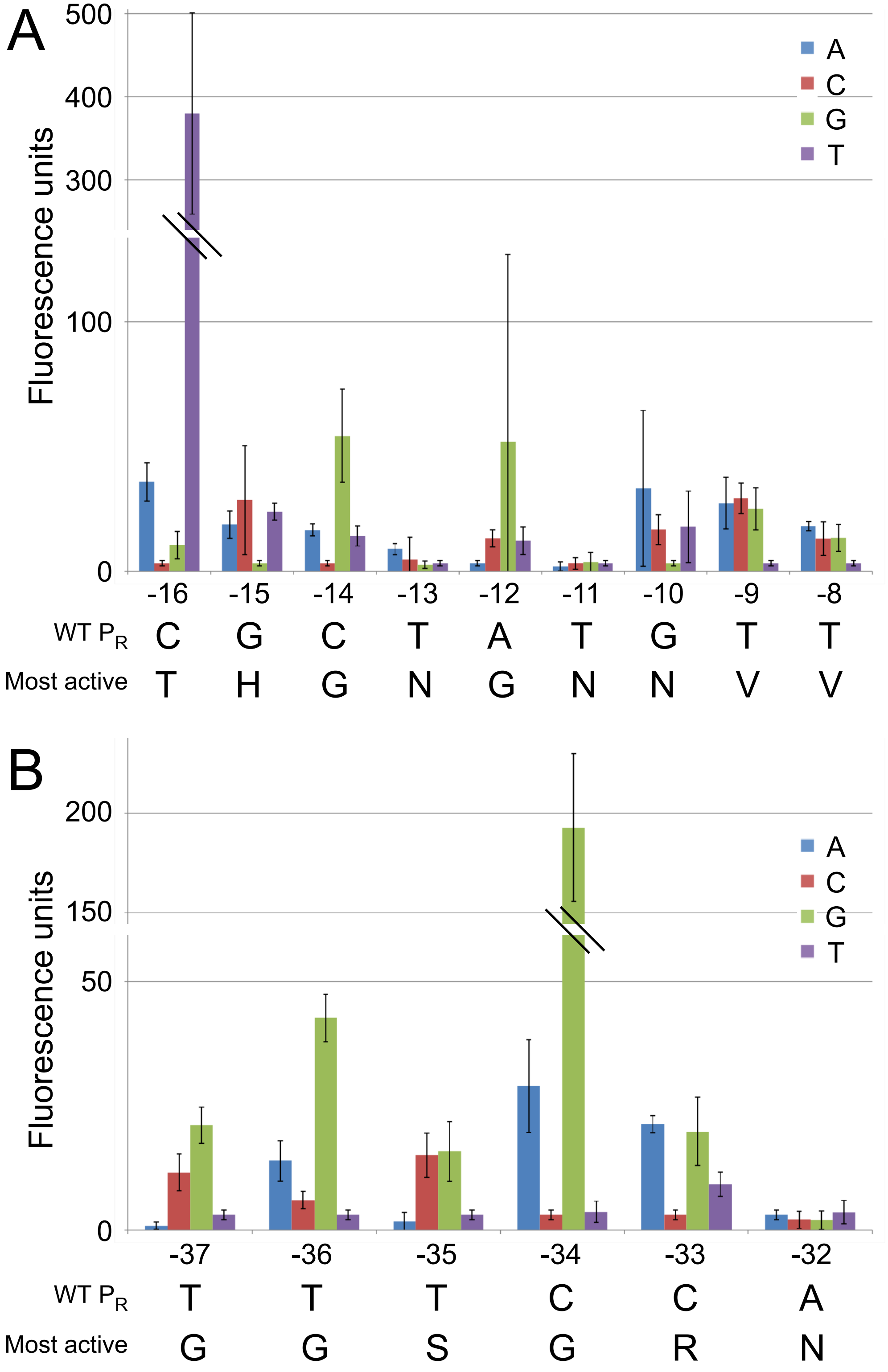
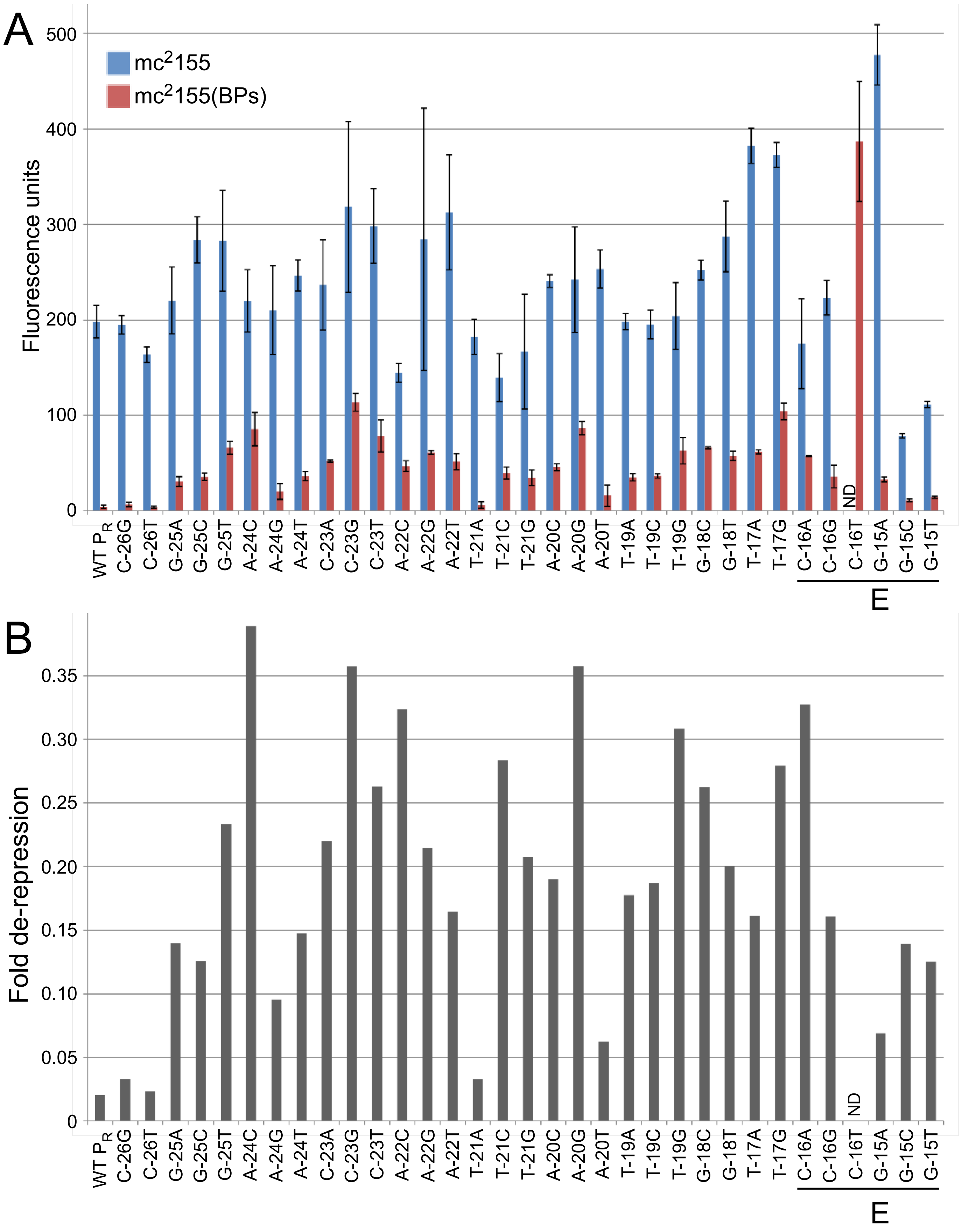

A
Fluorescence units
500
400
300
100
0
A
C
G
T
-16
-15
-14
-13
-12
-11
-10
-9
-8
WT P_R C G C T A T G T T
Most active T H G N G N N V V
B
Fluorescence units
200
150
50
0
A
C
G
T
-37
-36
-35
-34
-33
-32
WT P_R T T T C C A
Most active G G S G R N

Figure S1



A
mc²155
mc²155(BPs)
Fluorescence units
0
100
200
300
400
500
ND
B
Fold de-repression
0
0.05
0.10
0.15
0.20
0.25
0.30
0.35
ND
WT P_R
C-26G
C-26T
G-25A
G-25C
G-25T
A-24C
A-24G
A-24T
C-23A
C-23G
C-23T
A-22C
A-22G
A-22T
T-21A
T-21C
T-21G
A-20C
A-20G
A-20T
T-19A
T-19C
T-19G
G-18C
G-18T
T-17A
T-17G
C-16A
C-16G
C-16T
G-15A
G-15C
G-15T
E

Figure S2

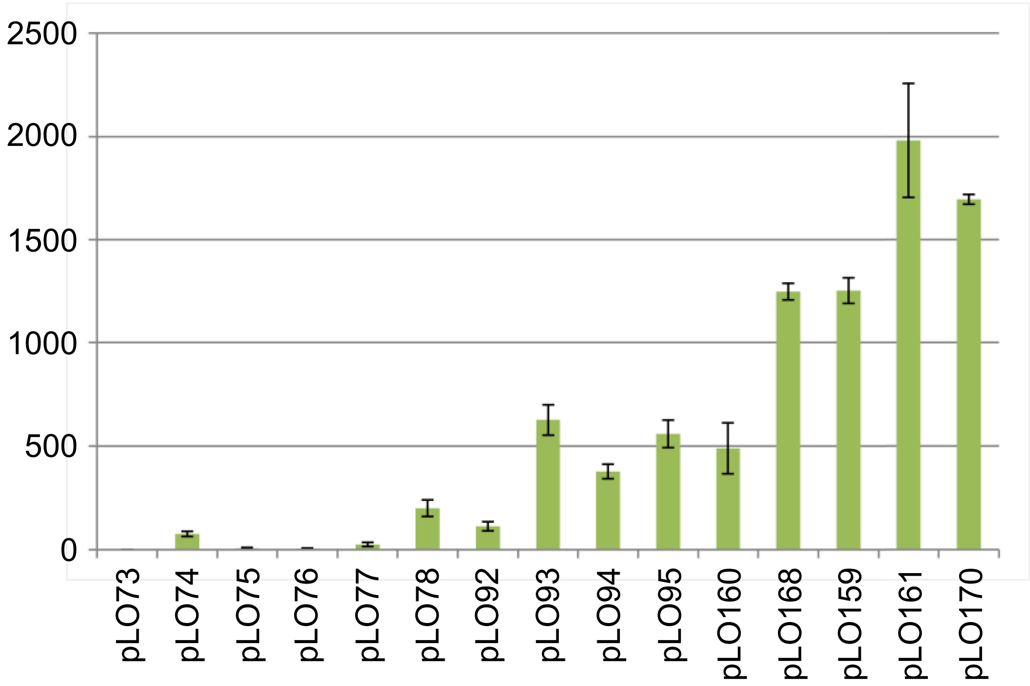

2500
2000
1500
1000
500
0
pLO73
pLO74
pLO75
pLO76
pLO77
pLO78
pLO92
pLO93
pLO94
pLO95
pLO160
pLO168
pLO159
pLO161
pLO170

Figure S3

Table S1. Plasmids used in this study.

Plasmid	Promoter mutations	BPs coordinates	Description	Reference
pLO86	NA	NA	Replicative parental vector with no promoter driving mCherry expression	Broussard et al. 2013
pLO87	NA	NA	Replicative parental vector with the hsp60 promoter driving mCherry expression	Broussard et al. 2013
pLO07	none	29224-29598	Replicative vector with P_R (genes *33-34* intergenic region, coordinates 29224-29598) driving mCherry expression	Broussard et al. 2013
pLO224	T-37A	T29473A	pLO07 site directed mutant with point mutation T>A at P_R -37 (BPs coordinate 29473)	this study
pLO225	T-37C	T29473C	pLO07 site directed mutant with point mutation T>C at P_R -37 (BPs coordinate 29473)	this study
pLO226	T-37G	T29473G	pLO07 site directed mutant with point mutation T>G at P_R -37 (BPs coordinate 29473)	this study
pLO227	T-36A	T29474A	pLO07 site directed mutant with point mutation T>A at P_R -36 (BPs coordinate 29474)	this study
pLO228	T-36C	T29474C	pLO07 site directed mutant with point mutation T>C at P_R -36 (BPs coordinate 29474)	this study
pLO229	T-36G	T29474G	pLO07 site directed mutant with point mutation T>G at P_R -36 (BPs coordinate 29474)	this study
pLO230	T-35A	T29475A	pLO07 site directed mutant with point mutation T>A at P_R -35 (BPs coordinate 29475)	this study
pLO231	T-35C	T29475C	pLO07 site directed mutant with point mutation T>C at P_R -35 (BPs coordinate 29475)	this study
pLO232	T-35G	T29475G	pLO07 site directed mutant with point mutation T>G at P_R -35 (BPs coordinate 29475)	this study
pLO233	C-34A	C29476A	pLO07 site directed mutant with point mutation C>A at P_R -34 (BPs coordinate 29476)	this study
pLO234	C-34G	C29476G	pLO07 site directed mutant with point mutation C>G at P_R -34 (BPs coordinate 29476)	this study
pLO235	C-34T	C29476T	pLO07 site directed mutant with point mutation C>T at P_R -34 (BPs coordinate 29476)	this study
pLO236	C-33A	C29477A	pLO07 site directed mutant with point mutation C>A at P_R -33 (BPs coordinate 29477)	this study
pLO237	C-33G	C29477G	pLO07 site directed mutant with point mutation C>G at P_R -33 (BPs coordinate 29477)	this study

pLO238	C-33T	C29477T	pLO07 site directed mutant with point mutation C>T at P_R -33 (BPs coordinate 29477)	this study
pLO239	A-32C	A29478C	pLO07 site directed mutant with point mutation A>C at P_R -32 (BPs coordinate 29478)	this study
pLO240	A-32G	A29478G	pLO07 site directed mutant with point mutation A>G at P_R -32 (BPs coordinate 29478)	this study
pLO241	A-32T	A29478T	pLO07 site directed mutant with point mutation A>T at P_R -32 (BPs coordinate 29478)	this study
pLO242	C-16A	C29494A	pLO07 site directed mutant with point mutation C>A at P_R -16 (BPs coordinate 29494)	this study
pLO243	C-16G	C29494G	pLO07 site directed mutant with point mutation C>G at P_R -16 (BPs coordinate 29494)	this study
pLO244	C-16T	C29494T	pLO07 site directed mutant with point mutation C>T at P_R -16 (BPs coordinate 29494)	this study
pLO245	G-15A	G29495A	pLO07 site directed mutant with point mutation G>A at P_R -15 (BPs coordinate 29495)	this study
pLO246	G-15C	G29495C	pLO07 site directed mutant with point mutation G>C at P_R -15 (BPs coordinate 29495)	this study
pLO247	G-15T	G29495T	pLO07 site directed mutant with point mutation G>T at P_R -15 (BPs coordinate 29495)	this study
pLO248	C-14A	C29496A	pLO07 site directed mutant with point mutation C>A at P_R -14 (BPs coordinate 29496)	this study
pLO249	C-14G	C29496G	pLO07 site directed mutant with point mutation C>G at P_R -14 (BPs coordinate 29496)	this study
pLO250	C-14T	C29496T	pLO07 site directed mutant with point mutation C>T at P_R -14 (BPs coordinate 29496)	this study
pLO251	T-13A	T29497A	pLO07 site directed mutant with point mutation T>A at P_R -13 (BPs coordinate 29497)	this study
pLO252	T-13C	T29497C	pLO07 site directed mutant with point mutation T>C at P_R -13 (BPs coordinate 29497)	this study
pLO253	T-13G	T29497G	pLO07 site directed mutant with point mutation T>G at P_R -13 (BPs coordinate 29497)	this study
pLO254	A-12C	A29498C	pLO07 site directed mutant with point mutation A>C at P_R -12 (BPs coordinate 29498)	this study
pLO255	A-12G	A29498G	pLO07 site directed mutant with point mutation A>G at P_R -12 (BPs coordinate 29498)	this study

pLO256	A-12T	A29498T	pLO07 site directed mutant with point mutation A>T at P_R -12 (BPs coordinate 29498)	this study
pLO257	T-11A	T29499A	pLO07 site directed mutant with point mutation T>A at P_R -11 (BPs coordinate 29499)	this study
pLO258	T-11C	T29499C	pLO07 site directed mutant with point mutation T>C at P_R -11 (BPs coordinate 29499)	this study
pLO259	T-11G	T29499G	pLO07 site directed mutant with point mutation T>G at P_R -11 (BPs coordinate 29499)	this study
pLO260	G-10A	G29500A	pLO07 site directed mutant with point mutation G>A at P_R -10 (BPs coordinate 29500)	this study
pLO261	G-10C	G29500C	pLO07 site directed mutant with point mutation G>C at P_R -10 (BPs coordinate 29500)	this study
pLO262	G-10T	G29500T	pLO07 site directed mutant with point mutation G>T at P_R -10 (BPs coordinate 29500)	this study
pLO263	T-9A	T29501A	pLO07 site directed mutant with point mutation T>A at P_R -9 (BPs coordinate 29501)	this study
pLO264	T-9C	T29501C	pLO07 site directed mutant with point mutation T>C at P_R -9 (BPs coordinate 29501)	this study
pLO265	T-9G	T29501G	pLO07 site directed mutant with point mutation T>G at P_R -9 (BPs coordinate 29501)	this study
pLO266	T-8A	T29502A	pLO07 site directed mutant with point mutation T>A at P_R -8 (BPs coordinate 29502)	this study
pLO267	T-8C	T29502C	pLO07 site directed mutant with point mutation T>C at P_R -8 (BPs coordinate 29502)	this study
pLO268	T-8G	T29502G	pLO07 site directed mutant with point mutation T>G at P_R -8 (BPs coordinate 29502)	this study
pLO156	ΔA-29	ΔA29481	pLO07 site directed mutant with deletion of 1 bp from the P_R spacer region (BPs coordinate 29481)	this study
pLO157	ΔA-29 ΔG-28	ΔA29481 ΔG29482	pLO07 site directed mutant with deletion of 2 bp from the P_R spacer region (BPs coordinate 29481-29482)	this study
pLO158	T at G-28 and A-27	ins29482-29483T	pLO07 site directed mutant with insertion of T in the P_R spacer region (BPs coordinates 29482 and 29483)	this study
pTTB1b	NA	NA	Tweety integrative parental vector	Pham et al. 2007
pLO73	NA	NA	pTTP1b with promoterless mCherry	this study
pLO74	NA	NA	pTTP1b with hsp60 promoter-mCherry	this study
pLO75	none	29224-29598	pTTP1b with P_R-mCherry	this study

pLO76	C-16T	C29494T	pTTP1b with P_R C-16T-mCherry	this study
pLO77	C-16T T-9C	C29494T T29501C	pLO76 site directed mutant with 2 point mutations: C-16T in extended -10 and T-9C in -10	this study
pLO78	C-16T T-9C G-10A	C29494T T29501C G29500A	pLO77 site directed mutant with 2 point mutations: C-16T in extended -10 and T-9C, G-10A in -10	this study
pLO80	T-35G C-16T	T29475G C29494T	pLO76 site directed mutant with 2 point mutations: C-16T in extended -10 and T-35G in -35	this study
pLO81	T-35G C-34G C-16T	T29475G C29476G C29494T	pLO76 site directed mutant with 3 point mutations: C-16T in extended -10 and T-35G, C-34G in -35	this study
pLO82	T-37C T-35G C-34G C-16T	T29473C T29475G C29476G C29494T	pLO76 site directed mutant with 4 point mutations: C-16T in extended -10 and T-35G, C-34G, T-37C in -35	this study
pLO83	T-35G C-16T T-9C	T29475G C29494T T29501C	pLO77 site directed mutant with 3 point mutations: C-16T in extended -10, T-9C in -10, and T-35G in -35	this study
pLO84	T-35G C-34G C-16T T-9C	T29475G C29476G C29494T T29501C	pLO77 site directed mutant with 4 point mutations: C-16T in extended -10, T-9C in -10, and T-35G, C-34G in -35	this study
pLO85	T-37C T-35G C-34G C-16T T-9C	T29473C T29475G C29476G C29494T T29501C	pLO77 site directed mutant with 4 point mutations: C-16T in extended -10, T-9C in -10, and T-35G, C-34G, T-37C in -35	this study
pLO92	C-16T C-14G T-9C G-10A	C29494T C29496G T29501C G29500A	pLO78 site directed mutant with 3 point mutations: C-16T, C-14G in extended -10 and T-9C, G-10A in -10	this study
pLO93	T-35G C-16T C-14G T-9C G-10A	T29475G C29494T C29496G T29501C G29500A	pLO83 site directed mutant with 4 point mutations: C-16T, C-14G in extended -10 and T-9C, G-10A in -10 and T-35G in -35	this study
pLO94	T-35G C-34G C-16T C-14G T-9C G-10A	T29475G C29476G C29494T C29496G T29501C G29500A	pLO84 site directed mutant with 4 point mutations: C-16T, C-14G in extended -10 and T-9C, G-10A in -10 and T-35G, C-34G in -35	this study

pLO95	T-37C T-35G C-34G C-16T C-14G T-9C G-10A	T29473C T29475G C29476G C29494T C29496G T29501C G29500A	pLO85 site directed mutant with 4 point mutations: C-16T, C-14G in extended -10 and T-9C, G-10A in -10 and T-35G, C-34G, T-37C in -35	this study
pLO159	T-35G C-16T C-14G T-9C G-10A ΔG-28	T29475G C29494T C29496G T29501C G29500A ΔG29482	pLO93 site directed mutant with 4 point mutations: C-16T, C-14G in extended -10 and T-9C, G-10A in -10 and T-35G in -35, and single base deletion in spacer	this study
pLO160	C-34A C-16T C-14G T-9C G-10A	C29476A C29494T C29496G T29501C G29500A	pLO83 site directed mutant with 4 point mutations: C-16T, C-14G in extended -10 and T-9C, G-10A in -10 and C-34A in -35	this study
pLO161	T-35G C-34A C-16T C-14G T-9C G-10A	T29475G C29476A C29494T C29496G T29501C G29500A	pLO83 site directed mutant with 4 point mutations: C-16T, C-14G in extended -10 and T-9C, G-10A in -10 and T-35G, C-34A in -35	this study
pLO162	T-37C T-36G T-35G C-34A C-16T C-14G T-9C G-10A	T29473C T29474G T29475G C29476A C29494T C29496G T29501C G29500A	pLO83 site directed mutant with 4 point mutations: C-16T, C-14G in extended -10 and T-9C, G-10A in -10 and T-37C, T-36G, T-35G, C-34A in -35	this study
pLO168	T-35G C-16T C-14G T-9C G-10A ΔA-29	T29475G C29494T C29496G T29501C G29500A ΔA29481	pLO93 site directed mutant with 4 point mutations: C-16T, C-14G in extended -10 and T-9C, G-10A in -10 and T-35G in -35, and single base deletion in spacer	this study
pLO170	T-35G C-34A C-16T C-14G T-9C G-10A ΔA-29	T29475G C29476G C29494T C29496G T29501C G29500A ΔA29481	pLO161 site directed mutant with 7 point mutations: C-16T, C-14G in extended -10 and T-9C, G-10A in -10 and T-35G, C-34G in -35, and single base deletion in spacer	this study
pLO185	T-35G C-16T T-9C G-10A	T29475G C29494T T29501C G29500A	pLO78 site directed mutant with 4 point mutations: C-16T in extended -10 and T-9C, G-10A in -10 and T-35G in -35	this study

pLO186	T-35G C-34G C-16T T-9C G-10A	T29475G C29476G C29494T T29501C G29500A	pLO78 site directed mutant with 5 point mutations: C-16T in extended -10 and T-9C, G-10A in -10 and T-35G, C-34G in -35	this study
pLO187	T-35G C-34G T-37C C-16T T-9C G-10A	T29473C C29475G T29476G C29494T T29501C G29500A	pLO78 site directed mutant with 6 point mutations: C-16T in extended -10 and T-9C, G-10A in -10 and T-35G, C-34G, T-37G in -35	this study
pLO269	C-26G	C29484G	pLO07 site directed mutant with point mutation C>G at O_R -26 (BPs coordinate 29484)	this study
pLO270	C-26T	C29484T	pLO07 site directed mutant with point mutation C>T at O_R -26 (BPs coordinate 29484)	this study
pLO271	G-25A	G29485A	pLO07 site directed mutant with point mutation G>A at O_R -25 (BPs coordinate 29485)	this study
pLO272	G-25C	G29485C	pLO07 site directed mutant with point mutation G>C at O_R -25 (BPs coordinate 29485)	this study
pLO273	G-25T	G29485T	pLO07 site directed mutant with point mutation G>T at O_R -25 (BPs coordinate 29485)	this study
pLO274	A-24C	A29486C	pLO07 site directed mutant with point mutation A>C at O_R -24 (BPs coordinate 29486)	this study
pLO275	A-24G	A29486G	pLO07 site directed mutant with point mutation A>G at O_R -24 (BPs coordinate 29486)	this study
pLO276	A-24T	A29486T	pLO07 site directed mutant with point mutation A>T at O_R -24 (BPs coordinate 29486)	this study
pLO277	C-23A	C29487A	pLO07 site directed mutant with point mutation C>A at O_R -23 (BPs coordinate 29487)	this study
pLO278	C-23G	C29487G	pLO07 site directed mutant with point mutation C>G at O_R -23 (BPs coordinate 29487)	this study
pLO279	C-23T	C29487T	pLO07 site directed mutant with point mutation C>T at O_R -23 (BPs coordinate 29487)	this study
pLO280	A-22C	A29488C	pLO07 site directed mutant with point mutation A>C at O_R -22 (BPs coordinate 29488)	this study
pLO281	A-22G	A29488G	pLO07 site directed mutant with point mutation A>G at O_R -22 (BPs coordinate 29488)	this study
pLO282	A-22T	A29488T	pLO07 site directed mutant with point mutation A>T at O_R -22 (BPs coordinate 29488)	this study

pLO283	T-21A	T29489A	pLO07 site directed mutant with point mutation T>A at O_R -21 (BPs coordinate 29489)	this study
pLO284	T-21C	T29489C	pLO07 site directed mutant with point mutation T>C at O_R -21 (BPs coordinate 29489)	this study
pLO285	T-21G	T29489G	pLO07 site directed mutant with point mutation T>G at O_R -21 (BPs coordinate 29489)	this study
pLO286	A-20C	A29490C	pLO07 site directed mutant with point mutation A>C at O_R -20 (BPs coordinate 29490)	this study
pLO287	A-20G	A29490G	pLO07 site directed mutant with point mutation A>G at O_R -20 (BPs coordinate 29490)	this study
pLO289	A-20T	A29490T	pLO07 site directed mutant with point mutation A>T at O_R -20 (BPs coordinate 29490)	this study
pLO290	T-19A	T29491A	pLO07 site directed mutant with point mutation T>A at O_R -19 (BPs coordinate 29491)	this study
pLO291	T-19C	T29491C	pLO07 site directed mutant with point mutation T>C at O_R -19 (BPs coordinate 29491)	this study
pLO291	T-19G	T29491G	pLO07 site directed mutant with point mutation T>G at O_R -19 (BPs coordinate 29491)	this study
pLO292	G-18C	G29492C	pLO07 site directed mutant with point mutation G>C at O_R -18 (BPs coordinate 29492)	this study
pLO293	G-18T	G29492T	pLO07 site directed mutant with point mutation G>T at O_R -18 (BPs coordinate 29492)	this study
pLO294	T-17A	T29493A	pLO07 site directed mutant with point mutation T>A at O_R -18 (BPs coordinate 29493)	this study
pLO295	T-17G	T29493A	pLO07 site directed mutant with point mutation T>G at O_R -18 (BPs coordinate 29493)	this study

Table S2. Primers used in this study.

Primer	Sequence	Description
LMO51	GCCATGCCTGTCTCGTTGCGTG	F for sequencing of pLO86 and pLO07 derivatives
LMO52	GGAAGCTCAGCTTCAGGTAGTCG	R for sequencing of pLO86 and pLO07 derivatives
LMO92	GCATTTTCCAATAGACGACACATGTCGCTATGTTGGTGCAC	SDM for O_R spacer T-21C (T29489C)
LMO94	GCATTTTCCAATAGACGACAVATGTCGCTATGTTGGTGCAC	SDM for O_R spacer T-21V (T29489V)
LMO96	GGCGCATTTTCCAATAGACGBCATATGTCGCTATGTTGGTG	SDM for O_R spacer A-24B (A29486B)
LMO100	GTGGCGCATTTTCCAATAGADGACATATGTCGCTATGTTG	SDM for O_R spacer C-26D (C29484D)
LMO102	GGCGCATTTTCCAATAGACHACATATGTCGCTATGTTGGT	SDM for O_R spacer G-25H (G29485H)
LMO104	CGCATTTTCCAATAGACGADATATGTCGCTATGTTGGTGC	SDM for O_R spacer C-23D (C29487D)
LMO106	CGCATTTTCCAATAGACGACBTATGTCGCTATGTTGGTGC	SDM for O_R spacer A-22B (A29488B)
LMO108	CATTTTCCAATAGACGACATBTGTCGCTATGTTGGTGCAC	SDM for O_R spacer A-20B (A29490B)
LMO110	ATTTTCCAATAGACGACATAVGTCGCTATGTTGGTGCACA	SDM for O_R spacer T-19V (T29491V)
LMO112	TTTCCAATAGACGACATATHTCGCTATGTTGGTGCACATG	SDM for O_R spacer G-18H (G29492H)
LMO114	TTTCCAATAGACGACATATGVCGCTATGTTGGTGCACATG	SDM for O_R spacer T-17V (T29493V)
LMO116	TCCAATAGACGACATATGTDGCTATGTTGGTGCACATGAC	SDM for P_R extended -10 promoter C-16D (C29494D)
LMO118	CCAATAGACGACATATGTCHCTATGTTGGTGCACATGACC	SDM for P_R extended -10 promoter G-15H (G29495H)
LMO126	CAATAGACGACATATGTCGDTATGTTGGTGCACATGACCC	SDM for P_R extended -10 promoter C-14D (C29496D)
LMO128	CCAATAGACGACATATGTCGCVATGTTGGTGCACATGACC	SDM for P_R -10 promoter T-13V (T29497V)
LMO130	CAATAGACGACATATGTCGCTBTGTTGGTGCACATGACC	SDM for P_R -10 promoter A-12B (A29498B)
LMO132	CCAATAGACGACATATGTCGCTAVGTTGGTGCACATGACC	SDM for P_R -10 promoter T-11V (T29499V)
LMO134	GACGACATATGTCGCTATHTTGGTGCACATGACCCCAAC	SDM for P_R -10 promoter G-10H (G29500H)
LMO136	GACGACATATGTCGCTATGVTGGTGCACATGACCCCAAC	SDM for P_R -10 promoter T-9V (T29501V)
LMO138	ACGACATATGTCGCTATGTVGGTGCACATGACCCCAAC	SDM for P_R -10 promoter T-8V (T29502V)
LMO142	CAATAGACGACATATGTCGGTATGTTGGTGCACATGACCC	SDM for P_R extended -10 promoter C-14G (C29496G)
LMO144	CCAATAGACGACATATGTCGCCATGTTGGTGCACATGACC	SDM for P_R -10 promoter T-13C (T29497C)
LMO146	CAATAGACGACATATGTCGCTGTGTTGGTGCACATGACC	SDM for P_R -10 promoter A-12G (A29498G)
LMO148	GACGACATATGTCGCTATATTGGTGCACATGACCCCAAC	SDM for P_R -10 promoter G-10A (G29500A)
LMO150	GACGACATATGTCGCTATGCTGGTGCACATGACCCCAAC	SDM for P_R -10 promoter T-9C (T29501C)
LMO152	ACGACATATGTCGCTATGTCGGTGCACATGACCCCAAC	SDM for P_R -10 promoter T-8C (T29502C)
LMO174	CGGGCGTGGCGCATVTTCCAATAGACGAC	SDM for P_R -35 promoter T-37V (T29473V)
LMO175	CGGGCGTGGCGCATTVTCCAATAGACGAC	SDM for P_R -35 promoter T-36V (T29474V)
LMO176	CGGGCGTGGCGCATTTVCCAATA	SDM for P_R -35 promoter T-35V (T29475V)

	GACGAC	
LMO177	CGGGCGTGGCGCATTTTDCAATAGACGACATATG	SDM for P_R -35 promoter C-34D (C29476D)
LMO178	CGGGCGTGGCGCATTTTCDAATAGACGACATATG	SDM for P_R -35 promoter C-33D (C29477D)
LMO179	CGGGCGTGGCGCATTTTCCBATAGACGACATATG	SDM for P_R -35 promoter A-32B (A29478B)
LMO187	CGGGCGTGGCGCATATTCCAATAGACGAC	SDM for P_R -35 promoter T-37A (T29473A)
LMO340	CGGGCGTGGCGCATTTCCCAATAGACGAC	SDM for P_R -35 promoter T-35C (T29475C)
LMO350	TTTTTTCTAGAGCTTGTGGTGGCATCCGTGG	F to amplify promoter-mCherry and add XbaI sites
LMO351	TTTTTTCTAGACGTCAGGTGGCTAGCTGATCAC	R to amplify promoter-mCherry and add XbaI sites
LMO354	GCTATTACGCCAGCTGGCGAAAG	F for sequencing of pTTP1b derivatives
LMO355	GCGAGTGTGGATGCGCAGCG	R for sequencing of pTTP1b derivatives
LMO358	GACGACATATGTTGCTATGCTGGTGCACATGACCCCAAC	SDM for P_R -10 combination of C-16T and T-9C
LMO359	GACGACATATGTTGCTATACTGGTGCACATGACCCCAAC	SDM for P_R -10 combination of C-16T, T-9C and G-10A
LMO360	CGGGCGTGGCGCATTTGCCAATAGACGAC	SDM for P_R -35 T-35G
LMO361	CGGGCGTGGCGCATTTGGCAATAGACGACATATG	SDM for P_R -35 combination T-35G and C-34G
LMO362	CGGGCGTGGCGCATCTGGCAATAGACGAC	SDM for P_R -35 combination T-35G, C-34G and T-37C
LMO369	GACGACATATGTTGGTATACTGGTGCACATGACCCCAAC	SDM for P_R -10 combination of C-16T, T-9C, G-10A, and C-14G
LMO449	TGGCGCATTTTCCAATGACGACATATGTCGCTA	SDM for 1bp spacer deletion in P_R ΔA-29 with wild-type P_R -35
LMO450	TGGCGCATTTTCCAATACGACATATGTCGCTA	SDM for 2bp spacer deletion in P_R ΔA-29 and ΔG-28 with wild-type P_R -35
LMO451	TGGCGCATTTTCCAATAGTACGACATATGTCGCTA	SDM for 1bp spacer insertion of T in P_R between G-28 and A-27 with wild-type P_R -35
LMO452	TGGCGCATTTGCCAATAACGACATATGTTGGTA	SDM for 1bp spacer deletion in P_R ΔG-28
LMO454	CGGGCGTGGCGCATTTGACAATAGACGACATATG	SDM for P_R -35 combination T-35G and C-34A
LMO455	CGGGCGTGGCGCATGGGACAATAGACGACATATG	SDM for P_R -35 combination T-37C, T-36G, T-35G and C-34A
LMO464	TGGCGCATTTGCCAATGACGACATATGTTGGTA	SDM for 1bp spacer deletion in P_R ΔA-29 with T-35G P_R -35
LMO466	TGGCGCATTTGACAATGACGACATATGTTGGTA	SDM for 1bp spacer deletion in P_R ΔA-29 with T-35G, C-34A P_R -35