Supplementary Table 1 Primers for site-directed mutagenesis in this study

Primers	Sequence 5'-3'	Substitution	Codon change
E2A_F	CCTGCAGCCATGGCATTCCGGCAGC	Glu2Ala	GAA → GCA
E2A_Rev	None		
R4A_F	CTGCAGCCATGGAATTCGCGCAGCTCAAG	Arg4Ala	CGG → GCG
R4A_Rev	None		
K7A_F	CCGGCAGCTCGCGTATTTCATCGC	Lys7Ala	AAG → GCG
K7A_Rev	GCGATGAAATACGCGAGCTGCCGG		
N17A_F	CGGAAGCAGGGGCGATGGCTGCAGC	Asn17Ala	AAC → GCG
N17A_Rev	GCTGCAGCCATCGCCCCTGCTTCCG		
K23A_F	CTGCAGCAGCCGCGCGCCTGCACG	Lys23Ala	AAG → GCG
K23A_Rev	GACGTGCAGGCGCGCGGCTGCTGCAGC		
K23G_F	GCTGCAGCAGCCGGGCGCCTGCACG	Lys23Gly	AAG → GGG
K23G_Rev	CGTGCAGGCGCCCGGCTGCTGCAGC		
K23Q_F	GCTGCAGCAGCCCAGCGCCTGCACG	Lys23Gln	AAG → CAG
K23Q_Rev	CGTGCAGGCGCTGGGCTGCTGCAGC		
K23R_F	GCTGCAGCAGCCAGGCGCCTGCACG	Lys23Arg	AAG → AGG
K23R_Rev	CGTGCAGGCGCCTGGCTGCTGCAGC		
K23V_F	GCTGCAGCAGCCGTGCGCCTGCACG	Lys23Val	AAG → GTG
K23V_Rev	CGTGCAGGCGCACGGCTGCTGCAGC		
H26A_F	GCCAAGCGCCTGGCCGTCTCACAGCCC	His26Ala	CAC → GCC
H26A_Rev	GGGCTGTGAGACGGCCAGGCGCTTGGC		
V27A_F	AGCGCCTGCACGCCTCACAGCCCCC	Val27Ala	GTC → GCC
V27A_Rev	GGGGGCTGTGAGGCGTGCAGGCGCT		
S28A_F	CTGCACGTCGCACAGCCCCCCATC	Ser28Ala	TCA → GCA
S28A_Rev	ATGGGGGGCTGTGCGACGTGCAGGCG		
Q29A_F	ACGTCTCAGCGCCCCCCATCACG	Gln29Ala	CAG → GCG
Q29A_Rev	GATGGGGGGCGCTGAGACGTGC		
Q29C_F	TGCACGTCTCATGTCCCCCCATCAC	Gln29Cys	CAG → TGT
Q29C_Rev	GTGATGGGGGGACATGAGACGTGCA		
Q29D_F	TGCACGTCTCAGACCCCCCCATCAC	Gln29Asp	CAG → GAC
Q29D_Rev	GTGATGGGGGGGTCTGAGACGTGCA		
Q29E_F	GCACGTCTCAGAGCCCCCCATCACG	Gln29Glu	CAG → GAG
Q29E_Rev	CGTGATGGGGGGCTCTGAGACGTGC		
Q29F_F	GCACGTCTCATTTCCCCCCATCACG	Gln29Phe	CAG → TTT
Q29F_Rev	CGTGATGGGGGGAAATGAGACGTGC		
Q29G_F	TGCACGTCTCAGGACCCCCCATCAC	Gln29Gly	CAG → GGA
Q29G_Rev	GTGATGGGGGGTCCTGAGACGTGCA		
Q29H_F	GCACGTCTCACACCCCCCCATCACG	Gln29His	CAG → CAC
Q29H_Rev	CGCGTGATGGGGGGGTGTGAGACGTGC		
Q29I_F	TGCACGTCTCAATACCCCCCATCAC	Gln29Ile	CAG → ATA
Q29I_Rev	GTGATGGGGGGTATTGAGACGTGCA		

Primers	Sequence 5'-3'	Substitution	Codon change
Q29K_F	GCACGTCTCAAAGCCCCCCATCACGCG	Gln29Lys	CAG → AAG
Q29K_Rev	CGCGTGATGGGGGGCTTTGAGACGTGC		
Q29L_F	GCACGTCTCACTGCCCCCCATCACGCG	Gln29Leu	CAG → CTG
Q29L_Rev	CGCGTGATGGGGGGCAGTGAGACGTGC		
Q29M_F	TGCACGTCTCAATGCCCCCCATCAC	Gln29Met	CAG → ATG
Q29M_Rev	GTGATGGGGGGCATTGAGACGTGCA		
Q29N_F	GCACGTCTCAAACCCCCCATCACG	Gln29Asn	CAG → AAC
Q29N_Rev	CGTGATGGGGGGGTTTGAGACGTGC		
Q29P_F	GCACGTCTCACCGCCCCCCATCACGCG	Gln29Pro	CAG → CCG
Q29P_Rev	CGCGTGATGGGGGGCGGTGAGACGTGC		
Q29R_F	TGCACGTCTCACGACCCCCCATCAC	Gln29Arg	CAG → CGA
Q29R_Rev	GTGATGGGGGGTCGTGAGACGTGCA		
Q29S_F	GCACGTCTCATCGCCCCCCATCACG	Gln29Ser	CAG → TCG
Q29S_Rev	CGTGATGGGGGGCGATGAGACGTGC		
Q29T_F	TGCACGTCTCAACGCCCCCCATCAC	Gln29Thr	CAG → ACG
Q29T_Rev	GTGATGGGGGGCGTTGAGACGTGCA		
Q29V_F	TGCACGTCTCAGTGCCCCCCATCAC	Gln29Val	CAG → GTG
Q29V_Rev	GTGATGGGGGGCACTGAGACGTGCA		
Q29W_F	TGCACGTCTCATGGCCCCCCATCAC	Gln29Trp	CAG → TGG
Q29W_Rev	GTGATGGGGGGCCATGAGACGTGCA		
Q29Y_F	TGCACGTCTCATACCCCCCATCAC	Gln29Tyr	CAG → TAC
Q29Y_Rev	GTGATGGGGGGGTATGAGACGTGCA		
P30A_F	CGTCTCACAGGCCCCCATCACGC	Pro30Ala	CCC → GCC
P30A_Rev	GCGTGATGGGGGCCTGTGAGACG		
T33A_F	AGCCCCCCATCGCGCGGCAGATGC	Thr33Ala	ACG → GCG
T33A_Rev	GCATCTGCCGCGCGATGGGGGGC		
R34A_F	CCATCACGGCGCAGATGCAAGCC	Arg34Ala	CGG → GCG
R34A_Rev	GCTTGCATCTGCGCCGTGATGGG		
Q37A_F	GCGGCAGATGGCAGCCCTGGAAGC	Gln37Ala	CAA → GCA
Q37A_Rev	GCTTCCAGGGCTGCCATCTGCCGC		
E40A_F	GCAAGCCCTGGCAGCGGACTTGG	Glu40Ala	GAA → GCA
E40A_Rev	CCAAGTCCGCTGCCAGGGCTTGC		
D42A_F	CCTGGAAGCGGCCTTGGGCGTCG	Asp42Ala	GAC → GCC
D42A_Rev	CGACGCCCAAGGCCGCTTCCAGG		
R50A_F	GCTTCTGGAGGCAAGCCACCGCG	Arg50Ala	CGA → GCA
R50A_Rev	CGCGGTGGCTTGCCTCCAGAAGC		
H52A_F	GGAGCGAAGCGCCCGCGGGATCG	His52Ala	CAC → GCC
H52A_Rev	CGATCCCGCGGGCGCTTCGCTCC		
F98A_F	AGCGTGGCGTATGCCGGAACGCCCATC	Phe98Ala	TTC → GCC
F98A_Rev	GATGGGCGTTCCGGCATACGCCACGCT		

Primers	Sequence 5'-3'	Substitution	Codon change
T100A_F	GCGTATTTCGGAGCGCCCATCTACCGC	Thr100Ala	ACG → GCG
T100A_Rev	GCGGTAGATGGGCGCTCCGAAATACGC		
K129A_F	ACGCACATGACCGCGGACGAGCAGGTG	Lys129Ala	AAG → GCG
K129A_Rev	CACCTGCTCGTCCGCGGTCATGTGCGT		
R147A_F	GTGGGCTTCAGCGCCTTCTTTCCCCGG	Arg147Ala	CGC → GCC
R147A_Rev	CCGGGGAAAGAAGGCGCTGAAGCCCAC		
R199A_F	CCGCGCGGCGGCGCGCCGAGCTTCGCC	Arg199Ala	CGG → GCG
R199A_Rev	GGCGAAGCTCGGCGCGCCGCCGCGCGG		
F202A_F	GGCCGGCCGAGCGCCGCCGATGAGGTG	Phe202Ala	TTC → GCC
F202A_Rev	CACCTCATCGGCGGCGCTCGGCCGGCC		
V246A_F	GTCCCTGCGTCTGCCGCAGCGATCCGT	Val246Ala	GTC → GCC
V246A_Rev	ACGGATCGCTGCGGCAGACGCAGGGAC		
P267A_F	CGGGTCAAGGTGGCCATCAGCTGCATC	Pro267Ala	CCC → GCC
P267A_Rev	GATGCAGCTGATGGCCACCTTGACCCG		

Notes: The replaced codon was underlined.

Supplementary Table 2 Binding ratios of wild-type CbnR and Gln29 mutants to the *cbnA* promoter

Substitution	Concentration of CbnR protein (nM)				
	0	39.0	97.5	195	390
Wild type	0	0	4.77 ± 1.9	34.2 ± 6.9	100
Gln29Ala	0	20.5 ± 7.2	59.2 ± 2.4	100	100
Gln29Gly	0	14.0 ± 1.7	38.6 ± 6.7	100	100
Gln29Ser	0	6.37 ± 2.4	26.1 ± 2.4	80.8 ± 5.6	100
Gln29Thr	0	8.20 ± 1.3	24.4 ± 3.5	87.7 ± 11.1	100

Notes: See Materials and Methods for details.