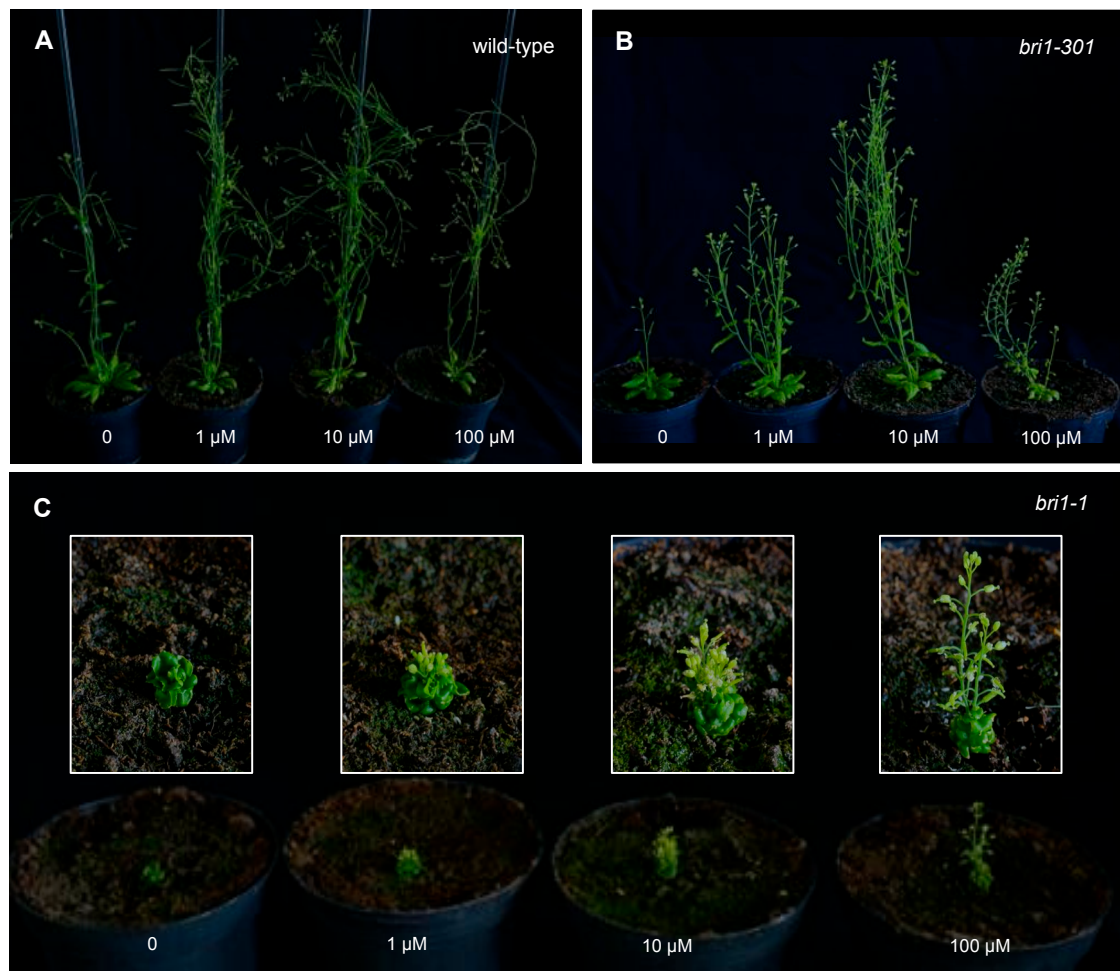
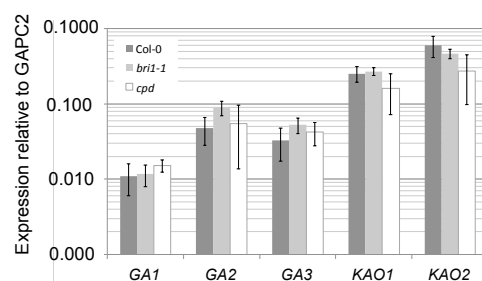




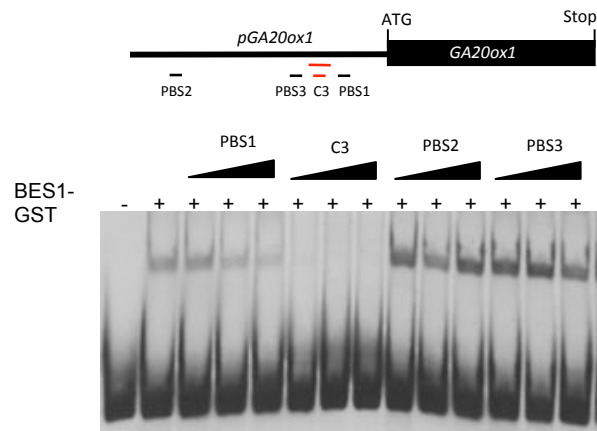
Supplemental Figure 1. GA Application Rescues Growth Defects of adult BR Mutant Plants. The pictures show a representative four-week-old plant out of 20 plants per line of wild-type (A), *bri1-301* (B) and *bri1-1* (C) plants that were sprayed 3x a week with 1 μM GA₄₊₇, 10 μM GA₄₊₇, 100 μM GA₄₊₇ or with water as a control.



Supplemental Figure 2. Expression of Upstream GA Biosynthesis Genes in BR Mutants. qPCR analysis of the expression of GA biosynthesis genes in the lines shown, grown for 10 days in standard conditions. The mean and SDs are shown and were calculated from 3 biological repeats, each measured in 4 technical replicates.

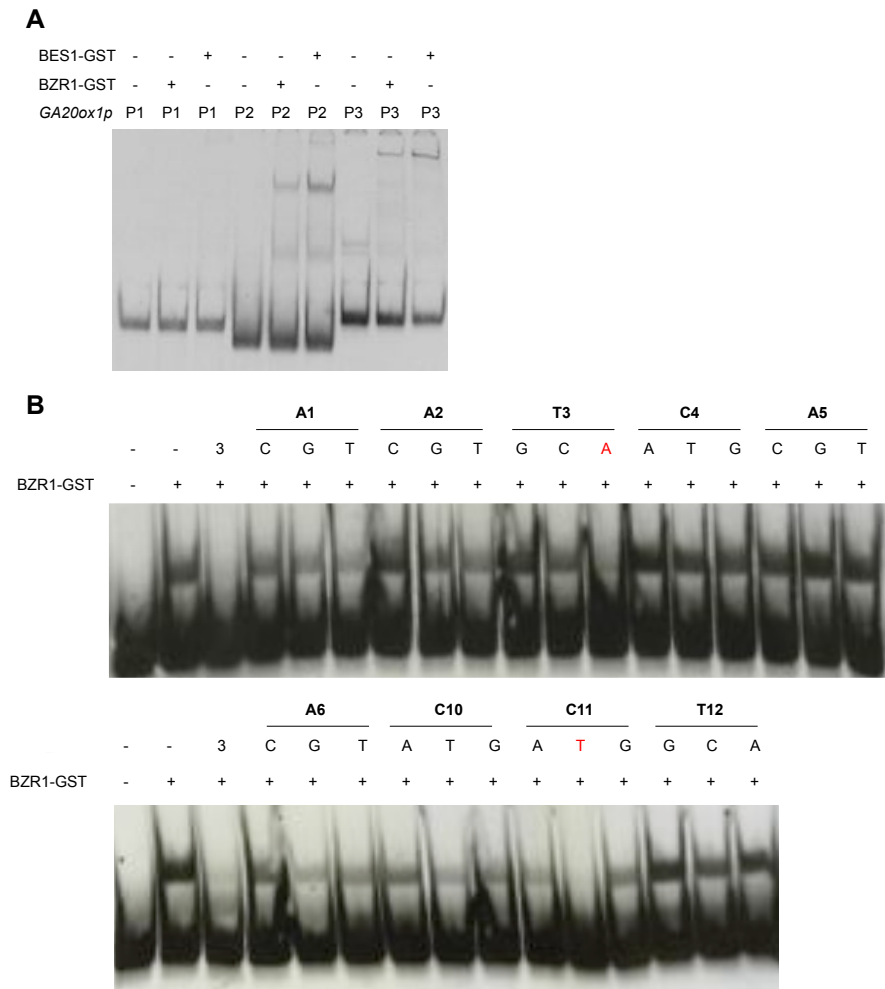


Supplemental Figure 3. *GA20ox1* Expression Restores *bri1-301* Leaf Phenotypes. Leaves of one representative 4-week-old plant of each of the indicated lines grown in LD conditions.

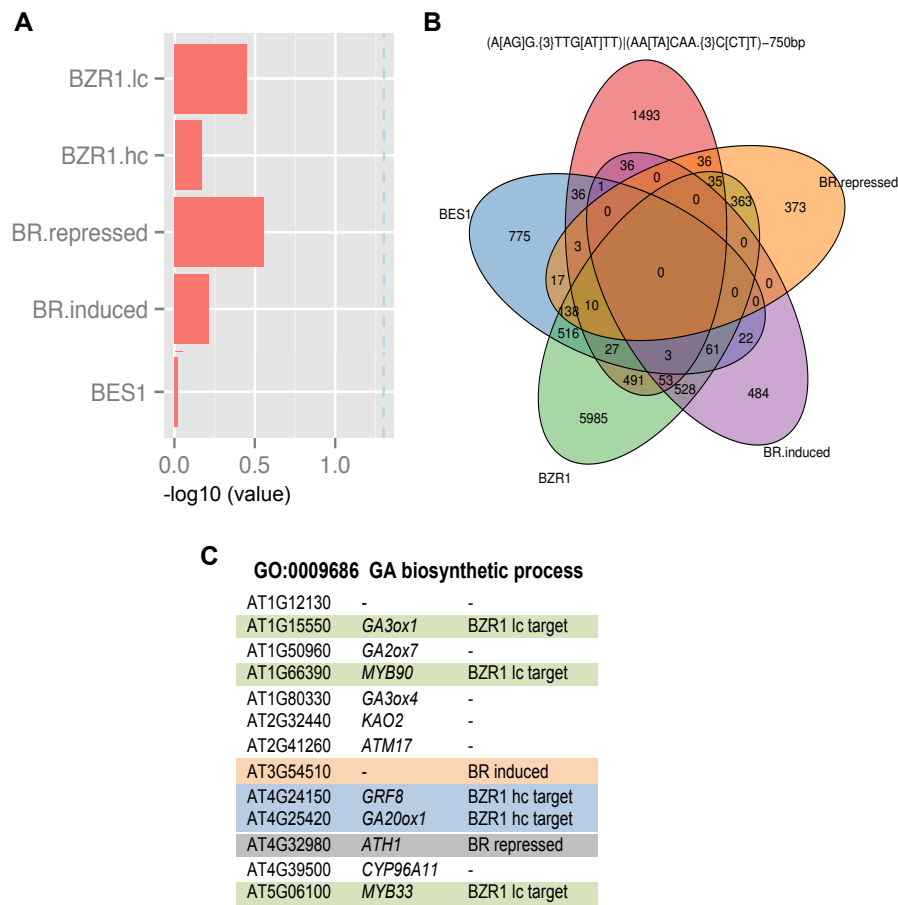


Supplemental Figure 4. BES1-GST Binds Specifically to the -552 to -517 Region (from the ATG) in the *GA20ox1* Promoter.

EMSA with recombinant BES1-GST using probe P3f (as in Figure 5C) as a template and 10x, 100x or 1000x molar excess of competitor DNA fragments, which are located in different regions of the *GA20ox1* promoter and contain the core AATCAA sequence of the non E-box motif. Putative Binding Site 1 (PBS1, -341 to -329): 5'-AATCAAnnGTT-3'; PBS2 (-1774 to 1762): 5'-AATCAAnnGAA-3'; PBS3: (-722 to -710): 5'-AATCAAnnAAT-3'.



Supplemental Figure 5. BES1 and BZR1 Bind to the Same Motif *In Vitro*.
(A) EMSA to analyse BES1-GST and BZR1-GST binding to three overlapping radiolabelled 250 bp DNA fragments P1 (-188 to +102), P2 (-165 to -426) and P3 (-393 to -692).
(B) EMSA to investigate BZR1-GST binding to probe P3f in the presence of 10x molar excess of competitor oligonucleotides in which the indicated base of the binding motif was mutated to all other possible bases.



Supplemental Figure 6. Enrichment of the Identified Non E-Box Motif in ChIP-Chip and Microarray Data.

(A) Motif occurrence test of the non-E-Box motif in BZR1 high confident (hc) and low confident (lc) target genes identified in ChIP-Chip by Sun, et al (2010) and in BES1 target identified in ChIP-Chip as well as genes BR induced or repressed are from Yu, et al (2011).

(B) Venn-diagram of genes with the non E-Box motif in their promoter (-750 bp upstream of the transcriptional start site) with the same data as in **(A)**.

Table **(C)** show genes from the GO Gibberellin biosynthetic process which carry the non E-Box motif. Genes found in the Venn-diagram are highlighted.

References

Sun Y., Fan X. Y., Cao D. M., Tang W., He K., Zhu J. Y., He J. X., Bai M. Y., Zhu S., Oh E., Patil S., Kim T. W., Ji H., Wong W. H., Rhee S. Y., Wang Z. Y. 2010. Integration of brassinosteroid signal transduction with the transcription network for plant growth regulation in Arabidopsis. Dev Cell 19: 765-777.

Yu X., Li L., Zola J., Aluru M., Ye H., Foudree A., Guo H., Anderson S., Aluru S., Liu P., Rodermel S., Yin Y. 2011. A brassinosteroid transcriptional network revealed by genome-wide identification of BES1 target genes in Arabidopsis thaliana. Plant J 65: 634-646.

Supplemental Table 1. GO Enrichment of the Identified Non-E-Box Motif in Arabidopsis

GOID	Pvalue	GO enrichment results			Revigo results			
		Count	Universe	Term	frequency	log10 p-value	uniqueness	dispensability
GO:0009686	0,000867416	12	54	gibberellin biosynthetic process	0.001 %	-3,0618	0,8	0
				negative regulation of chromosome				
GO:2001251	0,00185787	3	4	organization	0.003 %	-2,731	0,66	0,01
GO:0010089	0,002270535	15	84	xylem development	0.001 %	-2,6439	0,87	0
GO:0016101	0,003989067	12	64	diterpenoid metabolic process	0.003 %	-2,3991	0,79	0,53
GO:0051570	0,004370762	3	5	regulation of histone H3-K9 methylation	0.001 %	-2,3594	0,55	0,77
GO:0042128	0,00555124	4	10	nitrate assimilation	0.066 %	-2,2556	0,86	0,23
GO:2001057	0,00555124	4	10	reactive nitrogen species metabolic process	0.121 %	-2,2556	0,94	0
				positive regulation of histone H3-K9				
GO:1900111	0,006249593	2	2	dimethylation	0.000 %	-2,2041	0,56	0,8
GO:0070482	0,007543372	16	104	response to oxygen levels	0.020 %	-2,1224	0,79	0,67
GO:0031062	0,008228191	3	6	positive regulation of histone methylation	0.002 %	-2,0847	0,53	0,93
GO:0042744	0,010421643	12	72	hydrogen peroxide catabolic process	0.049 %	-1,9821	0,7	0,06
GO:0006468	0,01087055	117	1202	protein phosphorylation	1.206 %	-1,9637	0,73	0,04
GO:0001666	0,01188902	15	100	response to hypoxia	0.019 %	-1,9249	0,78	0,38
GO:0016114	0,012405102	28	227	terpenoid biosynthetic process	0.275 %	-1,9064	0,76	0,72
GO:0018027	0,01776137	2	3	peptidyl-lysine dimethylation	0.001 %	-1,7505	0,73	0,42
GO:0032196	0,01776137	2	3	transposition	0.610 %	-1,7505	0,88	0,08
GO:0035067	0,01776137	2	3	negative regulation of histone acetylation	0.001 %	-1,7505	0,52	0,82
GO:1901984	0,01776137	2	3	negative regulation of protein acetylation	0.001 %	-1,7505	0,64	0,91
				positive regulation of protein metabolic				
GO:0051247	0,018038737	7	35	process	0.111 %	-1,7438	0,67	0,33
GO:0015914	0,020505015	4	14	phospholipid transport	0.019 %	-1,6881	0,92	0,03
GO:0019375	0,023706732	14	99	galactolipid biosynthetic process	0.002 %	-1,6251	0,81	0,7
GO:0032204	0,024713973	9	54	regulation of telomere maintenance	0.003 %	-1,6071	0,61	0,81
GO:2000028	0,026248176	4	15	regulation of photoperiodism, flowering	0.001 %	-1,5809	0,62	0,56
GO:0009740	0,027289355	12	82	gibberellic acid mediated signaling pathway	0.001 %	-1,564	0,66	0,64
GO:0032200	0,0279368	10	64	telomere organization	0.021 %	-1,5538	0,77	0,61
GO:0010555	0,028867734	3	9	response to mannitol	0.000 %	-1,5396	0,81	0,54
GO:0010014	0,029206453	21	171	meristem initiation	0.003 %	-1,5345	0,81	0,6
GO:0034614	0,030569018	15	112	cellular response to reactive oxygen species	0.185 %	-1,5147	0,72	0,9
GO:0060249	0,030760619	10	65	anatomical structure homeostasis	0.034 %	-1,512	0,82	0,18

GO:0006995	0,031149301	5	23	cellular response to nitrogen starvation	0.001 %	-1,5066	0,79	0,37
GO:0009559	0,031149301	5	23	embryo sac central cell differentiation	0.000 %	-1,5066	0,8	0,36
GO:0046467	0,031161144	20	162	membrane lipid biosynthetic process	0.262 %	-1,5064	0,78	0,42
GO:0006915	0,03366487	2	4	apoptotic process	0.247 %	-1,4728	0,88	0,09
GO:0032922	0,03366487	2	4	circadian regulation of gene expression	0.003 %	-1,4728	0,73	0,42
GO:2000756	0,03366487	2	4	regulation of peptidyl-lysine acetylation	0.003 %	-1,4728	0,62	0,96
GO:0071370	0,034939364	12	85	cellular response to gibberellin stimulus	0.001 %	-1,4567	0,75	0,98
GO:0090305	0,035401073	16	124	nucleic acid phosphodiester bond hydrolysis	2.508 %	-1,451	0,85	0,18
GO:0008356	0,036863685	5	24	asymmetric cell division	0.002 %	-1,4334	0,9	0,04
GO:0018205	0,036863685	5	24	peptidyl-lysine modification	0.061 %	-1,4334	0,74	0,58
				positive regulation of protein modification				
GO:0031401	0,038860517	3	10	process	0.048 %	-1,4105	0,62	0,8
GO:0048575	0,038860517	3	10	short-day photoperiodism, flowering	0.000 %	-1,4105	0,7	0,81
GO:0080092	0,040355691	4	17	regulation of pollen tube growth	0.000 %	-1,3941	0,66	0,7
GO:0016106	0,044881079	7	42	sesquiterpenoid biosynthetic process	0.002 %	-1,3479	0,8	0,55
GO:0009827	0,046633184	25	222	plant-type cell wall modification	0.002 %	-1,3313	0,85	0,28
GO:0009585	0,048738548	4	18	red, far-red light phototransduction	0.002 %	-1,3121	0,67	0,62
GO:0010315	0,048738548	4	18	auxin efflux	0.000 %	-1,3121	0,67	0,51

Supplemental Table 2. Primers Used in This Study

Name of primer	Sequence (5'-3')
Primers for cloning	
Ga20ox1 fwd	TACTATAATCTCTCAACATGTATGGCCGT
Ga20ox1 rev	AACCCATCAGCGGCCGCTAAGAAATAAAT
bri1 _{pro} fwd	ACATATCTCGAGTTTAATTGAAAAGTTT
bri1 _{pro} rev	GAATTCTCAAGAGTTTGTGAGAGAG
Primers for qPCRs	
Ga2_ox1 fwd	TGATGGCTCATGGATCTCTGTCC
Ga2_ox1 rev	CCTCCCATTTGTCATCACCTGGAG
Ga2_ox2 fwd	AGATGGAAGTTGGGTCGCTGTC
Ga2_ox2 rev	CCCGTTAGTCATAACCTGAAGAGC
Ga2_ox3 fwd	ACTCTTCAGGTGATGACAAACGG
Ga2_ox3 rev	AGGACCTGCGAAGTAGATCATCG
Ga2_ox4 fwd	TTCACACTAACGACCCTGCCTTTC
Ga2_ox4 rev	AACAATTCACTGCCGAGCTGAAG
Ga2_ox6 fwd	TGACTGCCTTCAGGCATTGACG
Ga2_ox6 rev	GTGGCTTCTTTGCTGTGTTTGC
Ga2_ox7 fwd	TGATGATCGCAACAACCTCAGAAC
Ga2_ox7 rev	TCATTTGTGCCACTCGAGCTATC
Ga2_ox8 fwd	TGGTGACTTATTTTCAGGCATGGAG
Ga2_ox8 rev	GGTTCGTCATCACACGGTGTTT
Ga3_ox1 fwd	CCCAACATCACCTCAACTACTGC
Ga3_ox1 rev	GCTAACCACATCAATTTTCGATGCC
Ga3_ox2 fwd	CCAGCCACCACCTCAAATACTGTG
Ga3_ox2 rev	ATGCGAACCACATCAACTTGGC
Ga3_ox3 fwd	TCATGCCGAGTTCTGCAATGTG
Ga3_ox3 rev	CCTAACGAGCCCATCAACATGC
Ga3_ox4 fwd	TCTTCCACGGTGACACCAAGTG
Ga3_ox4 rev	CCTCATGATCACACCAAGTACTGC
Ga20_ox1 fwd	AGATTACTTCTGCGATGCGTTGG
Ga20_ox1 rev	TCTTGATACACCTTCCCAAATGGC
Ga20_ox2 fwd	CAAGAGTTCGAGCAGTTTGGAAG
Ga20_ox2 rev	TCGGAATAGTCTCGGTTTACGC
Ga20_ox3 fwd	ACATAGGCGACACCTTCATGGC
Ga20_ox3 rev	TCCTTTCTCTCTCGCTGTTACC
Ga20_ox4 fwd	GAACATTGGCGACACTTTAATGGC
Ga20_ox4 rev	CAAGTGTCTTCCTTGTCTGCTCG
Ga20_ox5 fwd	AACGTTGGAGACACCTTCATGGC
Ga20_ox5 rev	ACTGCCCTGTGGTAACAACCTCC
KAO1 fwd	TGAGGTTCTACAAAGAGCAAAGGC
KAO1 rev	ACTCGAAGTGTCTCATCGACAACC
KAO2 fwd	AAGAGTGATGTCCAAATGGATGGC
KAO2 rev	GGTCCAAATGGACGTTCTTAAACC
GA1 fwd	TTGCATTCATGCAGACCCGAGAC
GA1 rev	CCACGGGAAAGACATTGGGAACCTC

Primers for qPCRs (continued)

GA2 fwd
GA2 rev
GA3 fwd
GA3 rev

Sequence (5'-3')

TGTCCAGCTGGGTTAAGACCTC
AAGCAAGAGCATCCTCGACCTC
TCGGTGTAGCATTGAAGCAAGC
TCGACAAAGTCACACCGAGTTC

Primers for ChIPs

pGa20ox1 ChIP fwd
pGa20ox1 ChIP rev
pGA3ox1 ChIP fwd
pGA3ox1 ChIP rev
pGA3ox4 ChIP fwd
pGA3ox4 ChIP rev
UBQ5 fwd
UBQ5 rev
5SrRNA fwd
5SrRNA rev

TTATGTATGGAGAAATAGAAGGGAGTA
GCAACATGCACAATTACCACTATTC
ACAAGTAGAATAACCAATAATATTG
GAGTTTTATTTATAGTGGTGGAG
TACATTCATAACATATGTGTGTAG
ACTTGTGAACTAATGAGAGAATG
ACCAAGCCGAAGAAGATCAA
ATGACTCGCCATGAAAGTCC
GGATGCGATCATACCAGCACT
GAGGGATGCAACACGAGGACT

Primers for EMSAs (300bp fragments)

P1 fwd
P1 rev
P2 fwd
P2 rev
P3 fwd
P3 rev

TAAGCATTGAAGGGTTGAAGAT
GTGGCAAAGTATTGATAACTCCAT
TGGAGTTATCAATACTTTTGCCAC
CAACATTTTCACCATTTTCAGTTAAA
ATTTTTTTTTTTAACTGAAATGGTG
GCAACTACGTAATTTTATTT

Primers for EMSAs (100bp fragments)

P3a fwd
P3a rev
P3b fwd
P3b rev
P3C fwd
P3c rev
P3d fwd
P3d rev
P3e fwd
P3e rev
P3f fwd
P3f rev
P3g fwd
P3g rev

TGGAGTTATCAATACTTTT
ACTTGTTTTAGCGAATTTA
ATTCAGTGAATGGAGTT
ATTAGATTTATAATATAAAAATTT
GGAATCATTCCTAAATTTT
TAGCTTTGCGTACAAAAA
CTTTTGTCTTTCTTTTTTTTT
AAACATGTAGGGAATCGA
TTGAAAAGTGTCTTTTATC
ACCTATGACTAGTAAGCT
TTCCACTAATAATGTATAG
TATAATCTTTAAGGTATCC
ATTTCTCCATACATAAGG
CAATTCAGAAATATTTTTATA

Competitors for EMSAs

C1 fwd
C1 rev
C2 fwd
C2 rev
C3 fwd
C3 rev
C4 fwd
C4 rev
C5 fwd

TATAATCTTTAAGGTATCCTTATGTATGGAGAAATA
TATTTCTCCATACATAAGGATACCTTAAAGATTATA
CTTATGTATGGAGAAATAGAAGGGAGTAAATTCAA
TTTGAATTTACTCCCTTCTATTTCTCCATACATAAG
GAAGGGAGTAAATTCAAATAAAATCAACCACCTATG
CATAGGTGGTTGATTTTATTTGAATTTACTCCCTTC
TAAATCAACCACCTATGACTAGTAAGCTATACATT
AATGTATAGCTTACTAGTCATAGGTGGTTGATTTTA
CCACCTATGACTAGTAAGCTATACATTATTAGTGGA

Competitors for EMSAs (continued)

Sequence (5'-3')

C5 rev	TCCACTAATAATGTATAGCTTACTAGTCATAGGTGG
C*1 fwd	GAAGGGAGTAAATTCAAAGCCAATCAACCACCTATG
C*1 rev	CATAGGTGGTTGATTGGCTTTGAATTTACTCCCTTC
C*2 fwd	GAAGGGAGTAAATTCAAATAACCGCAACCACCTATG
C*2 rev	CATAGGTGGTTGCGGTTATTTGAATTTACTCCCTTC
C*3 fwd	GAAGGGAGTAAATTCAAATAAAATACCCACCTATG
C*3 rev	CATAGGTGGGTATTTTATTTGAATTTACTCCCTTC
C*4 fwd	GAAGGGAGTAAATTCAAATAAAATCAAAACCTATG
C*4 rev	CATAGGGTTTTGATTTTATTTGAATTTACTCCCTTC
C*5 fwd	GAAGGGAGTAAATTCAAATAAAATCAACCAAAGATG
C*5 rev	CATCTTTGGTTGATTTTATTTGAATTTACTCCCTTC
C*a1c fwd	GTAAATTCAAATAACATCAACCACCTATGACTAGTA
C*a1c rev	TACTAGTCATAGGTGGTTGATGTTATTTGAATTTAC
C*a1g fwd	GTAAATTCAAATAAGATCAACCACCTATGACTAGTA
C*a1g rev	TACTAGTCATAGGTGGTTGATCTTATTTGAATTTAC
C*a1t fwd	GTAAATTCAAATAATATCAACCACCTATGACTAGTA
C*a1t rev	TACTAGTCATAGGTGGTTGATATTATTTGAATTTAC
C*a2c fwd	GTAAATTCAAATAAACTCAACCACCTATGACTAGTA
C*a2c rev	TACTAGTCATAGGTGGTTGAGTTTATTTGAATTTAC
C*a2g fwd	GTAAATTCAAATAAAGTCAACCACCTATGACTAGTA
C*a2g rev	TACTAGTCATAGGTGGTTGACTTTATTTGAATTTAC
C*a2t fwd	GTAAATTCAAATAAATTCAACCACCTATGACTAGTA
C*a2t rev	TACTAGTCATAGGTGGTTGAATTTATTTGAATTTAC
C*t3g fwd	GTAAATTCAAATAAAAGCAACCACCTATGACTAGTA
C*t3g rev	TACTAGTCATAGGTGGTTGCTTTTATTTGAATTTAC
C*t3c fwd	GTAAATTCAAATAAAACCAACCACCTATGACTAGTA
C*t3c rev	TACTAGTCATAGGTGGTTGGTTTTATTTGAATTTAC
C*t3a fwd	GTAAATTCAAATAAAAACAACCACCTATGACTAGTA
C*t3a rev	TACTAGTCATAGGTGGTTGTTTTTATTTGAATTTAC
C*c4a fwd	GTAAATTCAAATAAAATAAACCACCTATGACTAGTA
C*c4a rev	TACTAGTCATAGGTGGTTTATTTTATTTGAATTTAC
C*c4t fwd	GTAAATTCAAATAAAATTAACCACCTATGACTAGTA
C*c4t rev	TACTAGTCATAGGTGGTTAATTTTATTTGAATTTAC
C*c4g fwd	GTAAATTCAAATAAAATGAACCACCTATGACTAGTA
C*c4g rev	TACTAGTCATAGGTGGTTCATTTTATTTGAATTTAC
C*a5c fwd	GTAAATTCAAATAAAATCCACCACCTATGACTAGTA
C*a5c rev	TACTAGTCATAGGTGGTGGATTTTATTTGAATTTAC
C*a5g fwd	GTAAATTCAAATAAAATCGACCACCTATGACTAGTA
C*a5g rev	TACTAGTCATAGGTGGTCGATTTTATTTGAATTTAC
C*a5t fwd	GTAAATTCAAATAAAATCTACCACCTATGACTAGTA
C*a5t rev	TACTAGTCATAGGTGGTAGATTTTATTTGAATTTAC
C*a6c fwd	GTAAATTCAAATAAAATCACCACCTATGACTAGTA
C*a6c rev	TACTAGTCATAGGTGGGTGATTTTATTTGAATTTAC
C*a6g fwd	GTAAATTCAAATAAAATCAGCCACCTATGACTAGTA
C*a6g rev	TACTAGTCATAGGTGGCTGATTTTATTTGAATTTAC
C*a6t fwd	GTAAATTCAAATAAAATCATCCACCTATGACTAGTA
C*a6t rev	TACTAGTCATAGGTGGATGATTTTATTTGAATTTAC
C*c10a fwd	GTAAATTCAAATAAAATCAACCACTATGACTAGTA

Competitors for EMSAs (continued)**Sequence (5'-3')**

C*c10a rev	TACTAGTCATAGTTGGTTGATTTTATTTGAATTTAC
C*c10t fwd	GTAAATTCAAATAAAATCAACCATCTATGACTAGTA
C*c10t rev	TACTAGTCATAGATGGTTGATTTTATTTGAATTTAC
C*c10g fwd	GTAAATTCAAATAAAATCAACCAGCTATGACTAGTA
C*c10g rev	TACTAGTCATAGCTGGTTGATTTTATTTGAATTTAC
C*c11a fwd	GTAAATTCAAATAAAATCAACCACATATGACTAGTA
C*c11a rev	TACTAGTCATATGTGGTTGATTTTATTTGAATTTAC
C*c11t fwd	GTAAATTCAAATAAAATCAACCACTTATGACTAGTA
C*c11t rev	TACTAGTCATAAGTGGTTGATTTTATTTGAATTTAC
C*c11g fwd	GTAAATTCAAATAAAATCAACCACGTATGACTAGTA
C*c11g rev	TACTAGTCATACGTGGTTGATTTTATTTGAATTTAC
C*t12g fwd	GTAAATTCAAATAAAATCAACCACCGATGACTAGTA
C*t12g rev	TACTAGTCATCGGTGGTTGATTTTATTTGAATTTAC
C*t12c fwd	GTAAATTCAAATAAAATCAACCACCCATGACTAGTA
C*t12c rev	TACTAGTCATGGGTGGTTGATTTTATTTGAATTTAC
C*t12a fwd	GTAAATTCAAATAAAATCAACCACCAATGACTAGTA
C*t12a rev	ACTAGTCATTGGTGGTTGATTTTATTTGAATTTAC
C cct-1 fwd	GTAAATTCAAATAAAATCAACACCTATGACTAGTAA
C cct-1 rev	TTACTAGTCATAGGTGTTGATTTTATTTGAATTTAC
C cct-2 fwd	GTAAATTCAAATAAAATCAACCCTATGACTAGTAAA
C cct-2 rev	TTTACTAGTCATAGGGTTGATTTTATTTGAATTTAC
C cct-3 fwd	GTAAATTCAAATAAAATCAACCTATGACTAGTAAA
C cct-3 rev	TTTTACTAGTCATAGGGTTGATTTTATTTGAATTTAC
C cct+2 fwd	GTAAATTCAAATAAAATCAACCAAACCTATGACTAG
C cct+2 rev	CTAGTCATAGGTTTGGTTGATTTTATTTGAATTTAC
C cct+4 fwd	GTAAATTCAAATAAAATCAACCAAAACCTATGACT
C cct+4 rev	AGTCATAGGTTTTTGGTTGATTTTATTTGAATTTAC
CpGA3ox1 fwd	AATAATATTGGACCAAAACAAGTGCTTTAACATATG
CpGA3ox1 rev	CATATGTTAAAGCACTTGTTTTGGTCCAATATTATT
CpGA3ox4 fwd	ATATATCCAAAGTAATTGTTTATGTGATGAGCATCC
CpGA3ox4 rev	GGATGCTCATCACATAAACAATTACTTTGGATATAT
CpGA20ox2 fwd	AAGATGTTGGCCAAAAAACAATTCATAATAAGTAA
CpGA20ox2 rev	GTGAAGACATTTGAAAATCACCCCACTGCAAACCTCC
PBS1 fwd	AAAAAAAAAAAAACTAATCAATATGTTAATTAGATT
PBS1 rev	AATCTAATTAACATATTGATTAGTTTTTTTTTTTTT
C3 fwd	AGTAAATTCAAATAAAATCAACCACCTATGACTAGT
C3 rev	ACTAGTCATAGGTGGTTGATTTTATTTGAATTTACT
PBS2 fwd	AACTGTAAGTGAACCAATCAAATTGAATTCAACCAA
PBS2 rev	TTGGTTGAATTCAATTTGATTGGTTCAGTTACAGTT
PBS3 fwd	TTAAATCATTTACATAATCAAAATAATTTAATTAAT
PBS3 rev	ATTAATTAAATTATTTTGATTATGTAAATGATTTAA
