

Supplemental Information:

“Selective activation of alternative *MYC* core promoters by Wnt-responsive enhancers”

Figure S1.- Effect of cell differentiation on total *MYC* expression.

Figure S2.- Effect of LiCl mediate Wnt activation on *MYC* mRNA in HCT-116 cells.

Figure S3.- Activity of *MYC*'s promoters by luciferase assay

Figure S4.- Enhancer deletions information and results of Sanger Sequencing

Figure S5.- Growth curves of single enhancer deleted clonal lines.

Figure S6.- Conservation of core promoter elements in *MYC* promoters

Figure S7.- Effect of core promoter mutants on P2 basal activity and fold activation

Figure S8.- Influence of INR and DPE on P1 promoter maximum promoter activity.

Table S1 Oligonucleotides used to generate promoter reporter assays and mutants

Table S2 Primers for RT-PCR

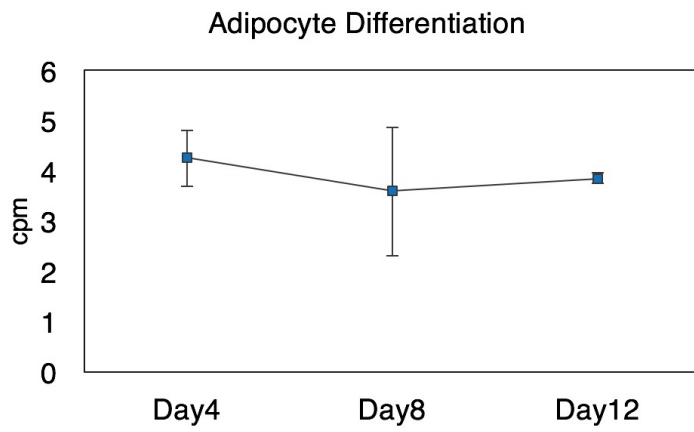
Table S3 Primers used to generate px330 plasmids

Annex S1 *MYC* reporter plasmids

Annex S2 Sequences of the promoter mutants

Supplementary References.

A



B

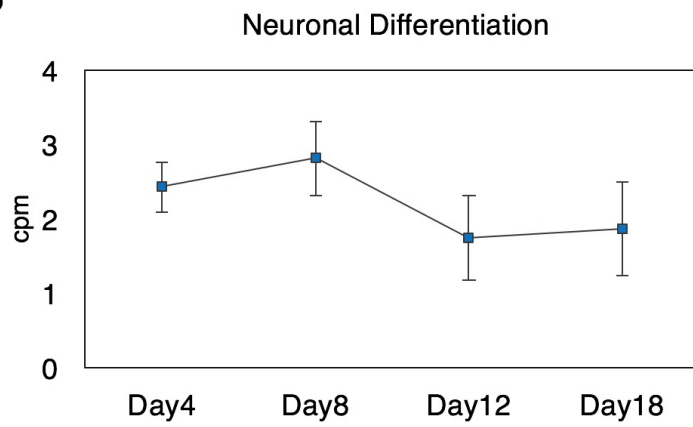


Figure S1.- Effect of cell differentiation on total *MYC* expression.
(A) Adipocyte differentiation leads to minor downregulation of *MYC* expression.
(B) Neuronal differentiation leads to downregulation of *MYC* expression.

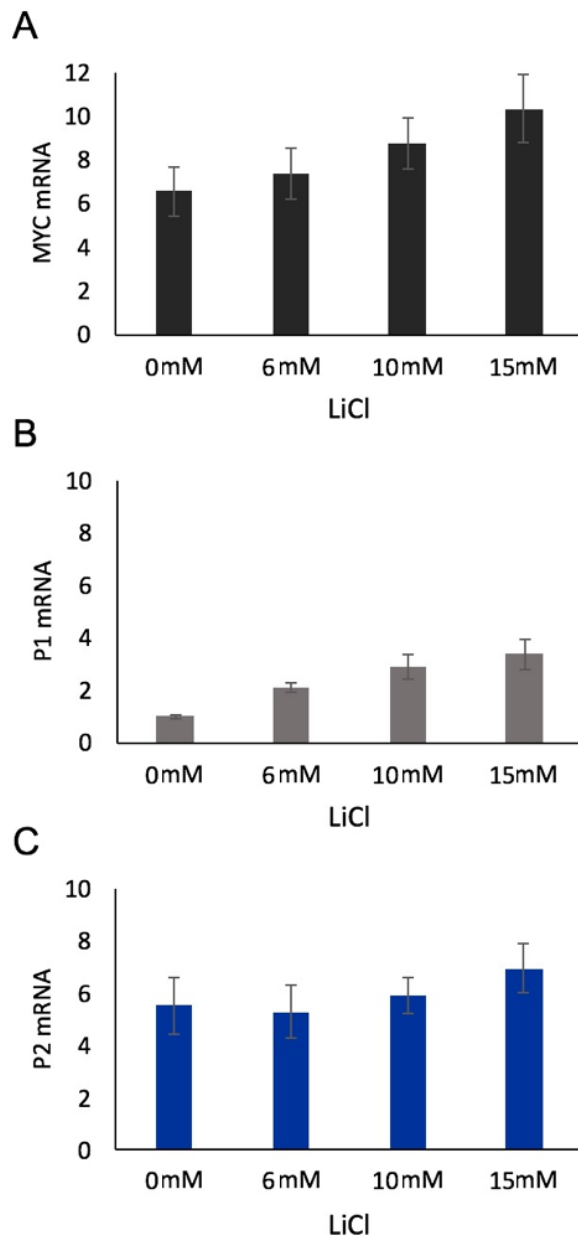


Figure S2.- Effect of Wnt activation on *MYC* mRNA in HCT-116 cells.

(A) Wnt induction upregulates total *MYC* transcription.

(B) Wnt induction upregulates transcriptional activity of the P1 promoter.

(C) Wnt induction does not upregulates transcriptional activity of the P2 promoter.

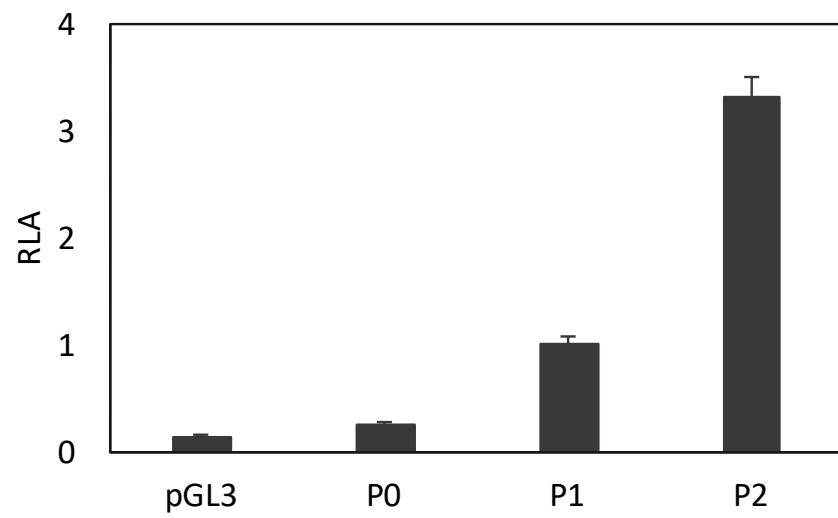


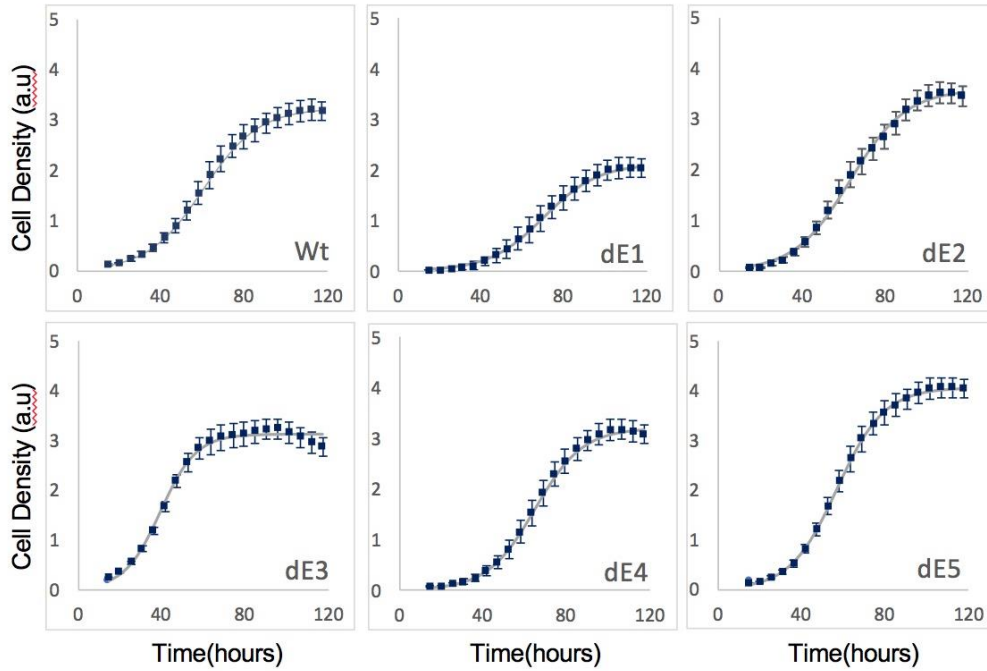
Figure S3.- Activity of MYC's promoters by luciferase assay.

The P0, P1 & P2 MYC promoters were cloned from the -100 to +50 with respect to the transcription start site into a pGL3 vector to assess promoter strength. As can be seen, transcription initiating from P0 is minimal in comparison to P1 or P2.

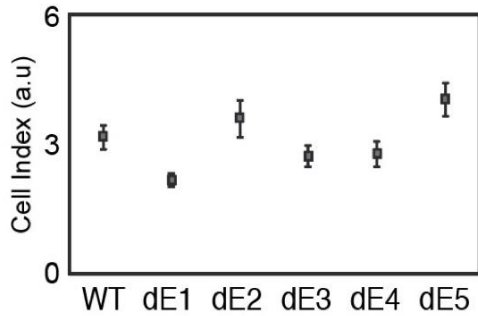
Enhancer Deletion Information	Sanger sequencing chromatogram	Ref.
Enhancer 1 Target Sequence: Left: CTCATCCTGAGTCCTTGAAA Right: TAATCAAGAATCGGACGTGA Genomic location: Left: 128754988 ^ Right: 128755777 Deletion size: 808bp		(1,2)
Enhancer 2 Target Sequence: Left: TGAAGTAGGAAATTAATGCC Right: CTGTGAGTATAAATCATCGC Genomic location: Left: 128746967 ^ Right: 128747978 Deletion size: 1016bp		(2-4)
Enhancer 3 Target Sequence: Left: GCAATTCGAGGTGATCAGG Right: ATATCCCCGGTTCATAGATA Genomic location: Left: 128412657 ^ Right: 128415055 Deletion size: 2403bp		(5-7)
Enhancer 4 Target Sequence: Left: GTGGACGGTGCTACAGACTC Right: GAGAATCCATGATTACTGCT Genomic location: Left: 128342323 ^ Right: 128343112 Deletion size: 775bp		(7)
Enhancer 5 Target Sequence: Left: AGGTGCATAACCCTTTAAAC Right: GATCTCATTAATTGACTGCG Genomic location: Left: 128227129 ^ Right: 128228107 Deletion size: 983bp		(7-9)

Figure S4.- Enhancer deletions information and results of Sanger Sequencing. This figure provides information about the sequences that were targeted by CRISPR/Cas9, the genomic coordinates, the respective sizes of the enhancer deletions, sample sanger sequencing results and relevant references.

A



B



C

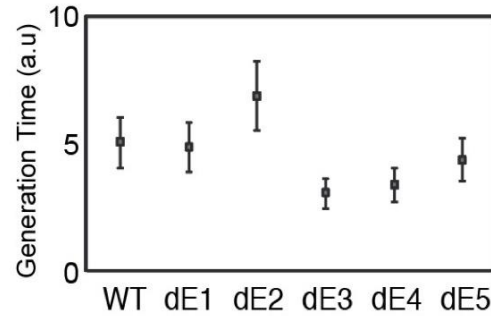


Figure S5.- Growth curves of single enhancer deleted clonal lines.

(A) Growth curves were performed in wild type HCT-116 cells as well as the five Wnt-responsive enhancer deleted single clonal lines.

(B) The cell index, a measurement of maximum cell density, was calculated. As can be observed, the cell index is significantly modified for some enhancer deletions.

(C) The generation time, a measurement of speed of cell division, was calculated. As can be observed, the generation time is significantly modified for some enhancer deletions.

A

P1 Promoter



B

P2 Promoter



Figure S6.- Conservation of core promoter elements in *MYC* promoters.

(A) Comparison of P1 promoter sequences across five different mammals with ~90 million years of evolutionary divergence. As can be seen, the TATA box and the BRE motifs are conserved.

(B) Comparison of P2 promoter sequences across five mammals with ~90 million years of evolutionary divergence. As can be seen, the TATA box, the INR and DPE motifs are highly conserved.

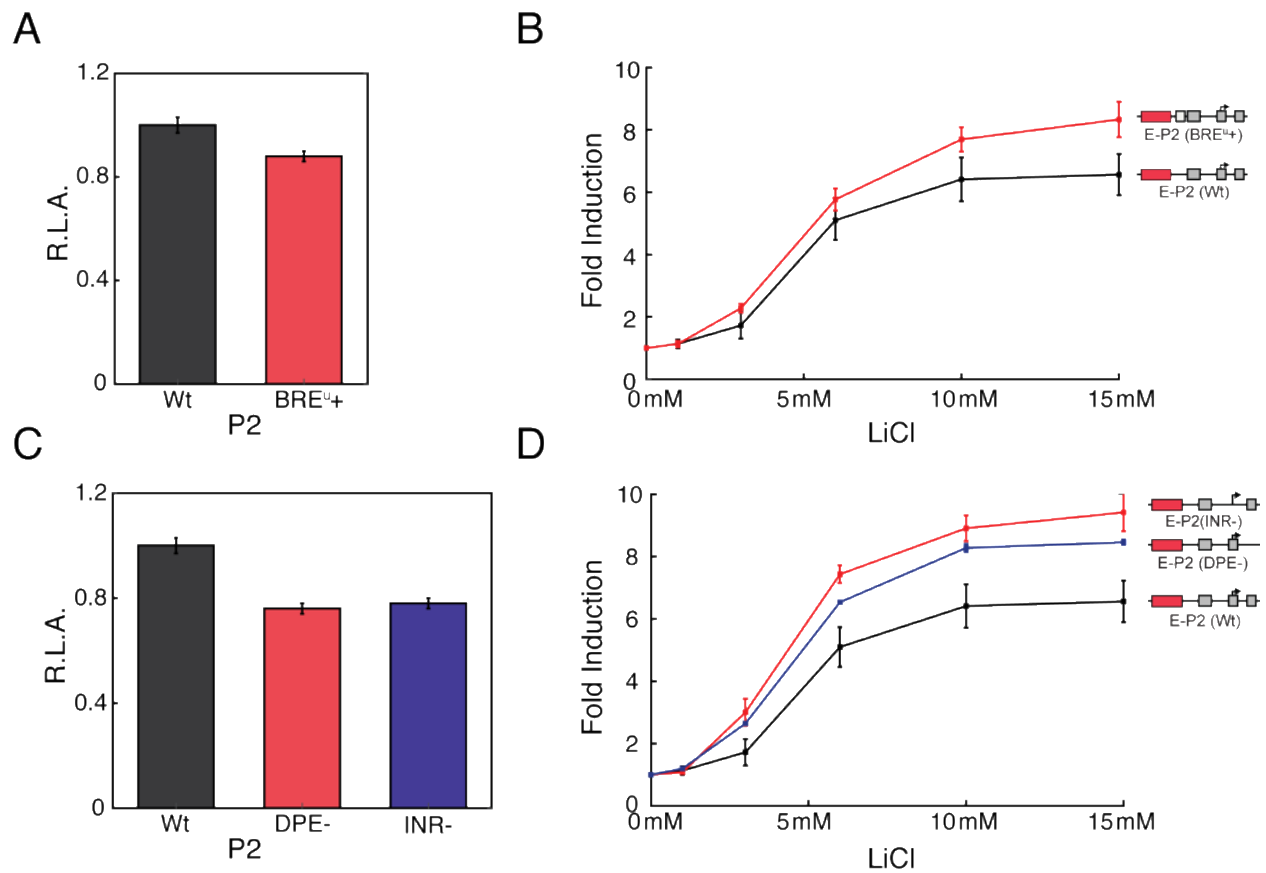


Figure S7.- Effect of core promoter mutants on P2 basal activity and fold activation.
 (A) P2 promoter with a BRE^u motif generates a slight decrease of the basal promoter activity.
 (B) P2 promoter with a BRE^u motif has a decreased fold activation.
 (C) P2 promoters lacking DPE or INR motif shown downregulation in the promoter basal activity.
 (D) P2 promoter lacking DPE or INR motif have a decreased fold activation.

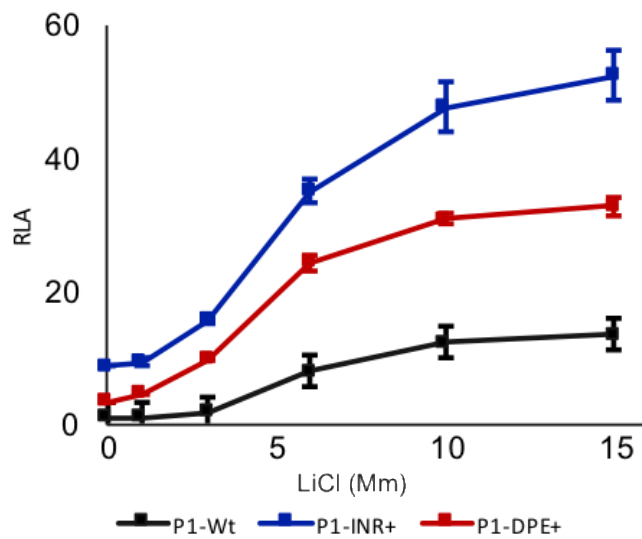


Figure S8.- Influence of INR and DPE on P1 promoter maximum promoter activity. Non normalized curves of LiCl activation on the P1 promoter mutants harboring INR or DPE motifs. As can be observed, under no LiCl induction the basal transcription levels for each of the promoter is drastically different.

Table S1 Oligonucleotides used to generate promoter reporter assays and mutants

Cloning P1 and P2 promoters	
atgcGGTCTCATCGACCGGGTCCCAAAGCAGAGG	Cloning Myc Promoter into pGL3
atgcAAGCTTGGAGCCAGGGACGGCCGG	Cloning Myc Promoter into pGL3
atgcGGTCTCATCGACTGCCTCGAGAAGGGCAGGG	Cloning Myc Promoter into pGL3
atgcAAGCTTGCTCTTCCACCCTAGCCG	Cloning Myc Promoter into pGL3
Luciferase Mutations P1 promoter	
ccagaccctcgattataaacgtgtgtggcgaggattagcgag	Mut BRE-P1
ctcgctaattctcgcccaacacgtttataatgcgagggctgg	Mut BRE-P1
ctcagccgtccagaccctcgagggcgccggcggtggcgaggattagc	Mut TATA-P1
gctaattctcgccaccggcccgccccctgcgagggctctggacggctgag	Mut TATA-P1
cagcacagctcggaactgatcagccgtccagaccctcgattat	Mut INR-P1
ataatgcgagggctctggacggctgatcagttccgagctgtgctg	Mut INR-P1
cggccggggcccgaggtctgcggccgcgagca	Mut DPE-P1
tgctcgcgccgcagacctcgggccccggcgcg	Mut DPE-P1
Luciferase Mutations P2 promoter	
ccgaaaaccggctttatagcgccccgatccctccctcggttct	Mut BRE-P2
agaacggaggaggagggatcgggcgccataaaagccggttttcgg	Mut BRE-P2
gaacggaggaggagggatcgcgctgaggcgcccccggttttcggggcttatctaac	Mut TATA-P2
gttagataaaagccccgaaaaccggcgggcgccctcagcgcatccctccctcgttc	Mut TATA-P2
tcgctggaattactacagcggtccgataaaagccccgaaaaccg	Mut INR-P2
cggttttcggggctttatcggaaccgctgtagtaattccagcga	Mut INR-P2
gcccggccggcctcgctcatgaggcctctcgctggaattac	Mut DPE-P2
gtaattccagcgagaggcctcatgagcgagcgggcgggccggc	Mut DPE-P2

Table S2 Primers for RT-PCR

qPCR Primers	
TCCCTGGAGAAGAGCTACGA	qPCR b-actin
AGCACTGTGTTGGCGTACAG	qPCR b-actin
AATCCCATCACCATCTTCCA	qPCR GAPDH
TGGACTCCACGACGTACTCA	qPCR GAPDH
CAGCTGCTTAGACGCTGGATT	qPCR Myc
GTAGAAATACGGCTGCACCGA	qPCR Myc
AGCGAATAGGGGGCTTCGC	qPCR P1+2 Fw
TCGTGGATGCGGCAAGGGTT	qPCR P1+2 Rv
CTTGGCGGGAAAAAGAACGG	qPCR P1 Fw
AGTTAGATAAAGCCCCGAAAACC	qPCR P1 Rv

Table S3 Primers used to generate px330 plasmids

px330 gRNA construction	
caccAGGTGCATAACCCTTTAAAC	px330-E5 Right fw
aaacGTTTAAAGGGTTATGCACCT	px330-E5 Right rv
caccGATCTCATTAAATTGACTGCG	px330-E5 Left fw
aaacCGCAGTCAATTAATGAGATC	px330-E5 Left rv
caccGTGGACGGTGCTACAGACTC	px330-E4 Right fw
aaacGAGTCTGTAGCACCGTCCAC	px330-E4 Right rv
caccGAGAATCCATGATTACTGCT	px330-E4 Left fw
aaacAGCAGTAATCATGGATTCTC	px330-E4 Left rv
caccGCAATTCCGAGGTGATCAGG	px330-E3 Right fw
aaacCCTGATCACCTCGGAATTGC	px330-E3 Right rv
caccATATCCCCGGTTCATAGATA	px330-E3 Left fw
aaacTATCTATGAACCGGGGATAT	px330-E3 Left rv
caccAGGCCTTTGCCGCAAACGCG	px330-E2 Right fw
aaacCGCGTTTGCGGCAAAGGCCT	px330-E2 Right rv
caccCTATTCAACCGCATAAGAGA	px330-E2 Left fw
aaacTCTCTTATGCGGTTGAATAG	px330-E2 Left rv
caccCTCATCCTGAGTCCTTGAAA	px330-E1 Right fw
aaacTTTCAAGGACTCAGGATGAG	px330-E1 Right rv
caccTAATCAAGAATCGGACGTGA	px330-E1 Left fw
aaacTCACGTCCGATTCTTGATTA	px330-E1 Left rv

Annex S1: MYC reporter plasmids

All the reporter plasmids were build using the the Pgl3-Basic reporter plasmid. The reporter plasmids sequences presented in the article were inserted in the Pgl3-Basic between KpnI and HindIII sites.

Promoter sequences are underline. enhancer sequences, when present, are double underline.

P1 Promoter:

GGTACCGAGCTCTTACGCGTGCTAGCCCGGGCTCGACCGGGTTCCCAAAGCAGAGGGCGTGGGGGAA
AAGAAAAAAGATCCTCTCTCGCTAATCTCCGCCCACCGGCCCTTTATAATGCGAGGGTCTGGACGGCT
GAGGACCCCCGAGCTGTGCTGCTCGCGGCCGCCACCGCCGGGCCCGGCCGTCCCTGGCTCCAAGCTT

P2 promoter:

GGTACCGAGCTCTTACGCGTGCTAGCCCGGGCTCGACTGCCTCGAGAAGGGCAGGGCTTCTCAGAGGC
TTGGCGGGAAAAAGAACGGAGGGAGGGATCGCGCTGAGTATAAAAGCCGGTTTTTCGGGGCTTTATCT
AACTCGCTGTAGTAATTCCAGCGAGAGGCAGAGGGAGCGAGCGGGCGGCCGGCTAGGGTGGAAGAG
CAAGCTT

Wnt-responsive enhancer + P1 promoter:

GGTACCGAGCTCTTACGCGAGATCAAAGGGGGTAAGATCAAAGGGGGTAAGATCAAAGGGGCGCGA
GATCAAAGGGGGTAAGATCAAAGGGGGTAAGATCAAAGGGGGTAAGATCAAAGGGGCGCGCCCCGCG
TGCTAGCCCGGGCTCGACCGGGTTCCCAAAGCAGAGGGCGTGGGGGAAAAAGAAAAAAGATCCTCTCT
CGCTAATCTCCGCCCACCGGCCCTTTATAATGCGAGGGTCTGGACGGCTGAGGACCCCCGAGCTGTGC
TGCTCGCGGCCGCCACCGCCGGGCCCGGCCGTCCCTGGCTCCAAGCTT

Wnt-mutated enhancer + P1 promoter:

GGTACCTTACGCGAGGCCAAAGGGGGTAAGGCCAAAGGGGGTAAGGCCAAAGGGGGTAAGGCCAA
GGCGCGAGGCCAAAGGGGGTAAGGCCAAAGGGGGTAAGGCCAAAGGGGGTAAGGCCAAAGGCCCG
GGCTCGAGCTAGCCCGGGCTCGACCGGGTTCCCAAAGCAGAGGGCGTGGGGGAAAAAGAAAAAAGAT
CCTCTCTCGCTAATCTCCGCCCACCGGCCCTTTATAATGCGAGGGTCTGGACGGCTGAGGACCCCCGA
GCTGTGCTGCTCGCGGCCGCCACCGCCGGGCCCGGCCGTCCCTGGCTCCAAGCT

Wnt-responsive enhancer + P2 promoter:

GGTACCGAGCTCTTACGCGAGATCAAAGGGGGTAAGATCAAAGGGGGTAAGATCAAAGGGGCGCGA
GATCAAAGGGGGTAAGATCAAAGGGGGTAAGATCAAAGGGGGTAAGATCAAAGGGGCGCGCCCCGCG
TGCTAGCCCGGGCTCGACTGCCTCGAGAAGGGCAGGGCTTCTCAGAGGCTTGCGGGGAAAAAGAACG
GAGGGAGGGATCGCGCTGAGTATAAAAGCCGGTTTTTCGGGGCTTTATCTAACTCGCTGTAGTAATTCC
ACGAGAGGCAGAGGGAGCGAGCGGGCGGCCGGCTAGGGTGGAAGAGCAAGCTT

Wnt-mutated enhancer + P2 promoter:

GGTACCTTACGCGAGGCCAAAGGGGGTAAGGCCAAAGGGGGTAAGGCCAAAGGGGGTAAGGCCAA
GGCGCGAGGCCAAAGGGGGTAAGGCCAAAGGGGGTAAGGCCAAAGGGGGTAAGGCCAAAGGCCCG
GGCTCGAGCTAGCCCGGGCTCGACTGCCTCGAGAAGGGCAGGGCTTCTCAGAGGCTTGCGGGGAAA
AGAACGGAGGGAGGGATCGCGCTGAGTATAAAAGCCGGTTTTTCGGGGCTTTATCTAACTCGCTGTAGT
AATTCCAGCGAGAGGCAGAGGGAGCGAGCGGGCGGCCGGCTAGGGTGGAAGAGCAAGCTT

Annex S2: Sequences of the promoter mutants

- P1 WT
GGTTCCCAAAGCAGAGGGCGTGGGGGAAAAGAAAAAAGATCCTCTCTCGCTAATCTCCGCCCACC
GGCCCTTTATAATGCGAGGGTCTGGACGGCTGAGGACCCCCGAGCTGTGCTGCTCGCGGCCGCCAC
CGCCGGGCCCCGGCCGTCC
- P1 BREm
GGTTCCCAAAGCAGAGGGCGTGGGGGAAAAGAAAAAAGATCCTCTCTCGCTAATCTCCGCCCACaa
cagTTTATAATGCGAGGGTCTGGACGGCTGAGGACCCCCGAGCTGTGCTGCTCGCGGCCGCCACCGC
CGGGCCCCGGCCGTCC
- P1 TATAm
GGTTCCCAAAGCAGAGGGCGTGGGGGAAAAGAAAAAAGATCCTCTCTCGCTAATCTCCGCCCACC
GGCCCGgccccTGCGAGGGTCTGGACGGCTGAGGACCCCCGAGCTGTGCTGCTCGCGGCCGCCACCG
CCGGGCCCCGGCCGTCC
- P1 INRm
GGTTCCCAAAGCAGAGGGCGTGGGGGAAAAGAAAAAAGATCCTCTCTCGCTAATCTCCGCCCACC
GGCCCTTTATAATGCGAGGGTCTGGACGGCTGAtcagttCCGAGCTGTGCTGCTCGCGGCCGCCACCGC
CGGGCCCCGGCCGTCC
- P1 DPE
GGTTCCCAAAGCAGAGGGCGTGGGGGAAAAGAAAAAAGATCCTCTCTCGCTAATCTCCGCCCACC
GGCCCTTTATAATGCGAGGGTCTGGACGGCTGAGGACCCCCGAGCTGTGCTGCTCGCGGCCGCagacc
tCGGGCCCCGGCCGTCC
- P2 WT
CTGCCTCGAGAAGGGCAGGGCTTCTCAGAGGCTTGGCGGGAAAAAGAACGGAGGGAGGGATCGCG
CTGAGTATAAAAGCCGTTTTCGGGGCTTTATCTAACTCGCTGTAGTAATTCCAGCGAGAGGCAGAG
GGAGCGAGCGGGCGGCC
- P2 BREm
CTGCCTCGAGAAGGGCAGGGCTTCTCAGAGGCTTGGCGGGAAAAAGAACGGAGGGAGGGATCGgg
gcccTATAAAAGCCGTTTTCGGGGCTTTATCTAACTCGCTGTAGTAATTCCAGCGAGAGGCAGAGG
GAGCGAGCGGGCGGCCG
- P2 TATAm
CTGCCTCGAGAAGGGCAGGGCTTCTCAGAGGCTTGGCGGGAAAAAGAACGGAGGGAGGGATCGCG
CTGAGgccccGCCGTTTTCGGGGCTTTATCTAACTCGCTGTAGTAATTCCAGCGAGAGGCAGAGG
AGCGAGCGGGCGGCCG
- P2 INRm
CTGCCTCGAGAAGGGCAGGGCTTCTCAGAGGCTTGGCGGGAAAAAGAACGGAGGGAGGGATCGCG
CTGAGTATAAAAGCCGTTTTCGGGGCTTTATCggaccCGCTGTAGTAATTCCAGCGAGAGGCAGAGG
GAGCGAGCGGGCGGCCG
- P2 DPE
CTGCCTCGAGAAGGGCAGGGCTTCTCAGAGGCTTGGCGGGAAAAAGAACGGAGGGAGGGATCGCG
CTGAGTATAAAAGCCGTTTTCGGGGCTTTATCTAACTCGCTGTAGTAATTCCAGCGAGAGGCctcatG
AGCGAGCGGGCGGCCG

Supplementary References:

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4. Yochum GS, McWeeney S, Rajaraman V, Cleland R, Peters S, Goodman RH. Serial analysis of chromatin occupancy identifies β -catenin target genes in colorectal carcinoma cells. *Proc Natl Acad Sci.* 2007 Feb 27;104(9):3324–9.
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