

SUPPLEMENTAL MATERIAL

Kodgire et al., <http://www.jem.org/cgi/content/full/jem.20121523/DC1>

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GGTTGGGATAAGGCTGGATTATCTGAGTCCAAGCTAGGCCCTTTGCTAATCATGTCATACCTCTTAICTCTCTCCCAAGCTCCTGGGCAACGTGCT 100
GGTCTGTGTGCTGGCCCATCCTTTGGCAAAGAATTCACCCACCAGTGCAGGCTGCCTATCAGAAAAGTGGTGGCTGGTGGCTAATGCCCTGGCCAC 200
AAGTATCACTAAGCTCGCTTTCTTGCTGTCCAATTTCTATTAAGGTTCCCTTTGTTCCCTAAGTCCAACCTAACTGGGGATATTTAAGGGCCTT 300
GAGCATCTGGATTCTGCCTAATAAAACATTTATTTTCATTGCAATGATGTATTTAAATTAATTTCTGAATATTTTACTAAAAAGGGAATGGGAGGTC 400
AGTGCATTTAAACATAAAGAATGAAGAGCTAGTTCAAACCTTGGGAAAAACACTATATCTTAACTCCATGAAAGAAGGTGAGGCTGCAACAGCTA 500
ATGCACATTTGGCAACAGCCCTGATGCATATGCCTTATTCATCCCTCAGAAAAGGATTTAGCATAGTGTTACCATCAACCACCTTAACCTCATTTCCTT 600
ATTCAATACCTAGGTAGGTAGATGCATAGATTCGGAAATAAATATAGTCTCAAGTGGTCCCTTGTCTCTCTCCAGTCAAATTTCTGAATCTAGTTGGC 700
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GAAATCAGACCCTTGTCTTACACCATAAACAAAATAAATTTGAATGGTTAAAGAATTAACCTAAGACCTAAACCCATAAAAAATTTTAAAGAAATCAA 900
AAGAAGAAAATTTCTAATATTCACGTTGCAGCCGTTTTTTGAATTTGATATGAGAAGCAAAGGCARCAAAAAGGAAAAATAAGAAGTGAGGCTACATCAA 1000
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GGCAGAAATTTGATGAACCTGGAGGATGTAATAACTAAGAAAAATAAGCCTGACACAAAAAGACAAATACACACACCTTGCTCATATGTGAAACATAAAAA 1300
AGTCACCTCATGGAAACAGACAGTAGAGGTATGGTTCCAGGGTTGGGGTGGGAGAATCA 1363
    
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Figure S1. Human β -globin transcription terminator sequence (1,363 bp). The splice acceptor site is shown in blue. The intronic region of the terminator is shown in italics. Three poly(A) sequences located at 320, 637, and 834 bp, respectively, from the start of the terminator sequence, are shown in red. The first AATAAA hexamer located at 320 bp is underlined and referred as the poly(A) site in this study.

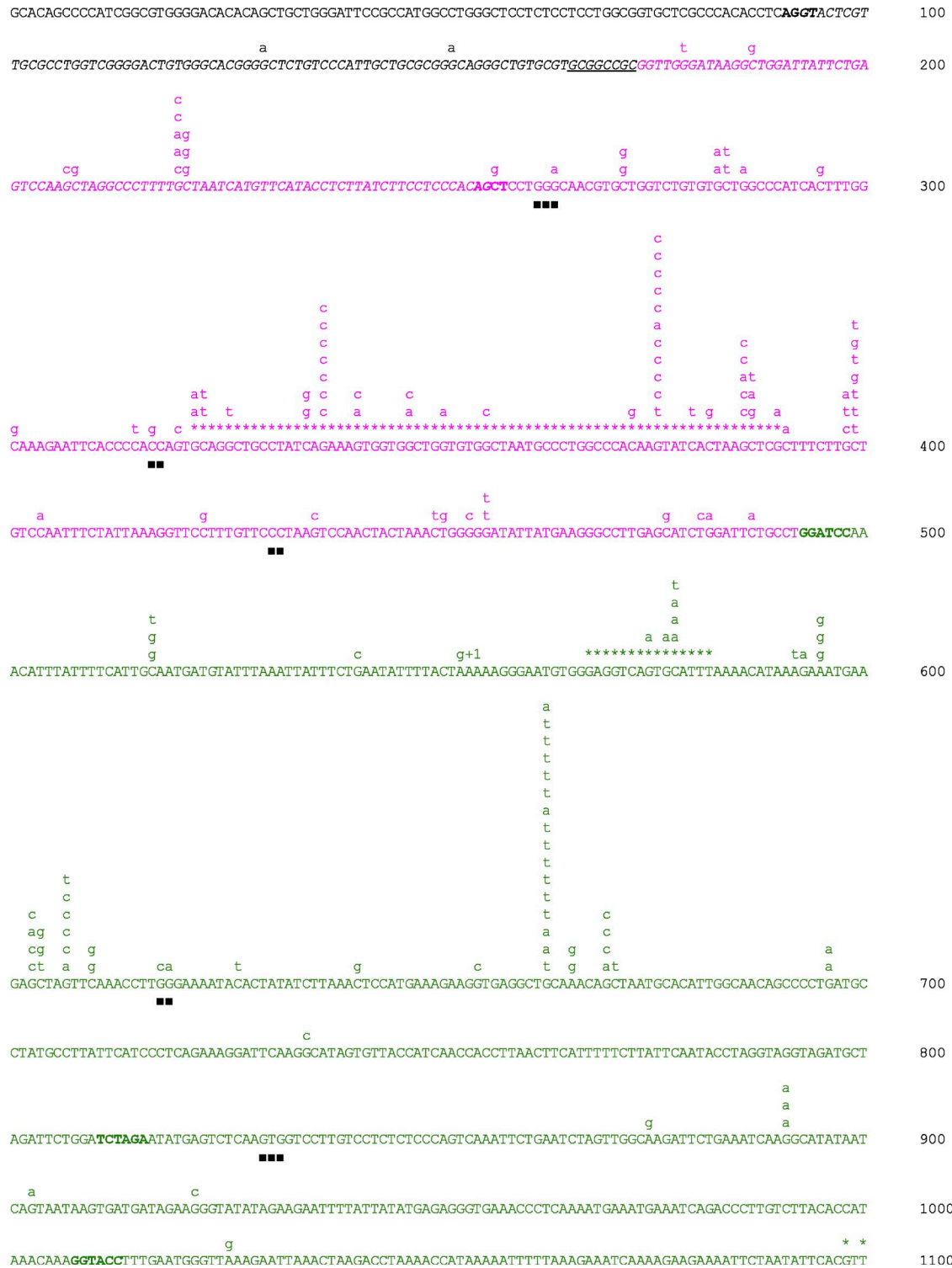


Figure S3. Mutations in the active and inactivated terminator knock-in clones. (+1 to +1,100 from the transcription start site), Ig gene sequence is highlighted in gray, NotI site used for cloning the β -globin terminator is shown by underlined nucleotides, poly(A) sequences (or mutations created to inactivate these) are marked in bold case, terminator sequence upstream of the first poly(A) site is in pink, terminator sequence downstream of poly(A) is in green, intron between IgL leader exon and terminator is shown in italics, splice donor site (AGGT) in the leader exon/intron border and acceptor site (AGCT) in the terminator region are shown in bold case, deletion mutations are indicated by *, and insertions are indicated by + followed by number of bp inserted. ssDNA patches in the terminator regions and location of C or G converted in the bisulfite analysis are shown as black bars

Table S1. Primers used in this study

Primer	Direction	Location ^a	Sequence (5' to 3') ^b
pk03	Rev	165	gcagcgccgcACGCACAGCCCTGCCCGCGCAGCAGTGGGA
pk07	For	166	gcatcgccgcGGTTGGGATAAGGCTGGATTATTCTG
pk10	Rev	947	gcatgacgtcCGGCTGCAACGTGAATATTAGAATTTTC
pk12	For	1,762	gcatatcgatGTGCAGGCAGCGCTGACTCAGCCGTCCTCGGTGTCAGCA
pk22	Rev	541	gaataaggCATATGCATCAGGGGCTGTTGCCAATGTGC
pk24	Rev	2,081	CTAGGACGGTCAGGGTTGTCCCGGCCCAAATATA
pk31	For	494	gcatggatccAAACATTTATTTTCATTGCAATGATG
pk33	Rev	810	gcattctagaTCCAGAATCTAGCATCTACCTACCTA
pk48	For	1,379	AAGCTTGCATGCCTGCAGGTCGACTCTAGA
pk50	Rev	1,688	gcatcgccgcGAATTCTGGTAGCACCTGGTCTGCAGTGTA
pk64	For	-48	GGGCGTGTGCGGAAGGACGCGGTATAAA
pk85	Rev	36	GGAACAAAGGAACCTTTAATAGAAATGGACAGC
pk87 ^c	For	269	GGGATCCGCCATGGCCTGGGCTCCTCTCC
pk93	For	948	gcagcatgcTTTTTGAATTTGATATGAGAAGCAAAGGC
pk94	Rev	1,378	gcagcatgcTGATTCTCCACCCCAACCCCTGG
pk95	For	-48	ccaaagcttGGGCGTGTGCGGAAGGACGCGGG
pk96	Rev	165	cctgatcatatgACGCACAGCCCTGCCCGCGCAGCA
pk99	For	166	ccaaagcttGTTGGGATAAGGCTGGATTATTCTG
pk100	Rev	493	cctgatcatatgAGGCAGAATCCAGATGCTCAAGGCC
pk103 ^c	For	494	ccaaagcttAAACATTTATTTTCATTGCAATGATG
pk104	Rev	810	cctgatcatatgTCCAGAATCTAGCATCTACCTACCTA
pk107 ^c	For	811	ccaaagcttATATGAGTCTCAAGTGGTCTTGTC
pk108	Rev	1,107	cctgatcatatgCGGCTGCAACGTGAATATTAGAATTTTC
pk111	Rev	1,571	cctgatcatatgGCATGCCTGCAGGTCGACTCTAGA
pk112	For	1,878	ccaaagcttCGGTGTGAAATACCGCACAGATGCGT
pk113	For	1,967	ccaaagcttGTGCAGGCAGCGCTGACTCAGCCGTCCTCG
pk114	Rev	2,285	cctgatcatatgCTAGGACGGTCAGGGTTGTCCCGGCCCAAATATA
pk117	For	4,023	ccaaagcttGCCTCTCTTGCAGGCCAGCCCAA
pk118	Rev	4,336	cctgatcatatgAGGGTCTCGTGATAGAGGTGCCGTTG
pk154	For	270	GCTGTCCAATTCTATTAAGGTTCTTTGTCCC
pk155	For	542	GCACATTGGCAACAGCCCTGATGCATATGCCTTATTC
pk174 ^c	For	4,178	CTCCACCCGCTCTGGCGAGACCA
pk182 ^c	Rev	493	TTTTTTTTTTTTTTTTTTTATTAGGCAGAATCCAG
pk183 ^c	Rev	810	TTTTTTTTTTTTTTTTTTTATTCCAGAATCTAGCATC
pk184 ^c	Rev	1,007	TTTTTTTTTTTTTTTTTTTATTTTGTATGGTGAAG
pk185 ^c	Rev	4,532	TTTTTTTTTTTTTTTTTTTATTAATGTGACACCTGG
pk186	For	174	GGTTGGGATAAGGCTGGATTATT
pk187	Rev	572	ACCTCCACATCCCTTTTAA
pk188	For	552	TAAAAAGGGAATGTGGGAGGT
pk189	Rev	1037	GTTTAATTCTTAAACCCATTGA
gg-actin1	For		CCCCAAGCTTACTCCACAGCCAGCCATGG
gg-actin2	Rev		GGCTCTAGATAGTCCGTCAGG

^aLocation of primers related to transcription start site.

^bComplementary region with genomic DNA is shown in capital case.

^cPrimers used in polyadenylated RNA assay.