SUPPLEMENTAL MATERIAL

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

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.

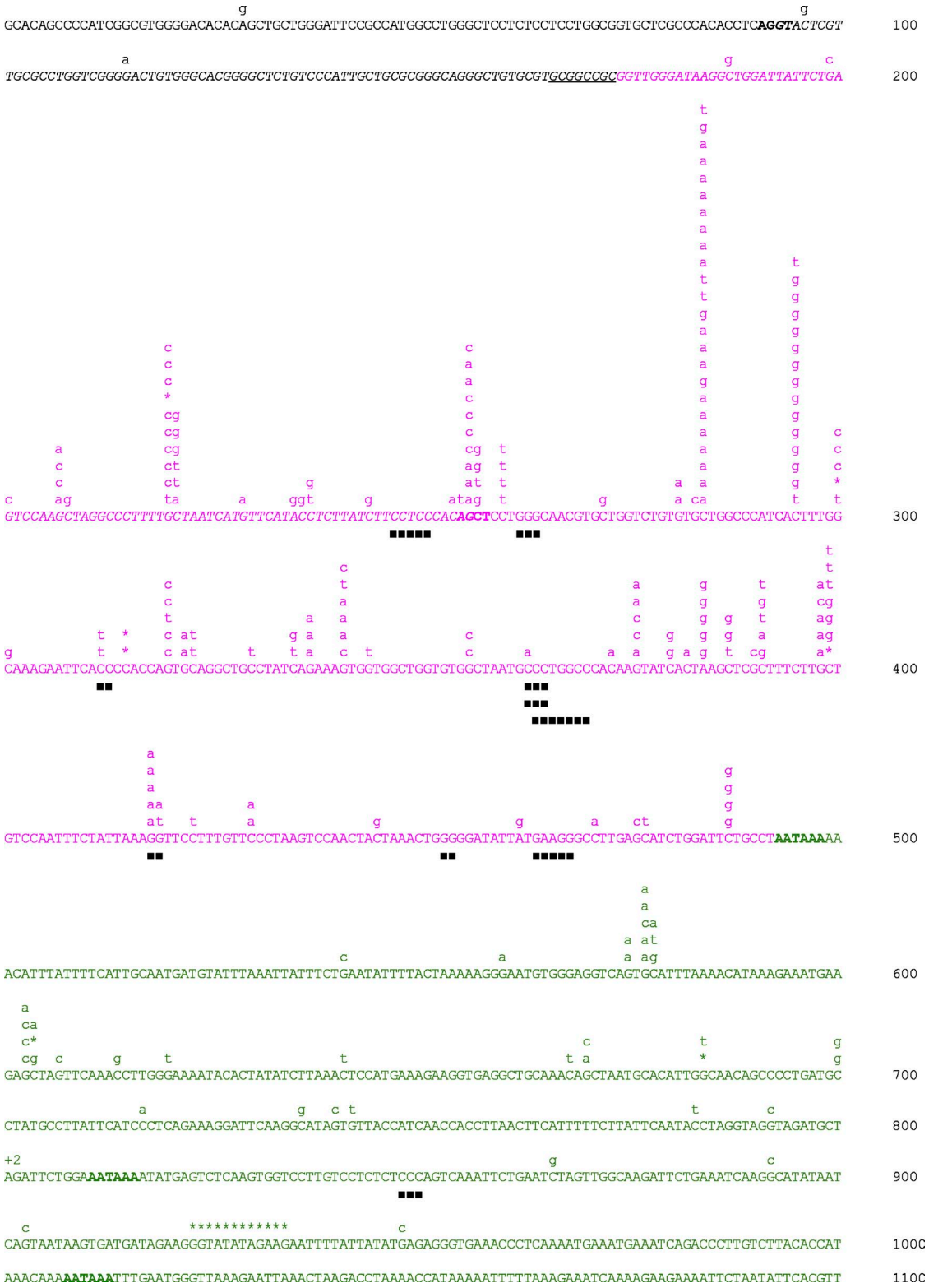

Figure S2. Mutations in the active and inactivated terminator knock-in clones. (+1 to +1,100 from the transcription start site), Ig gene sequence is highlighted in gray, NotI site used for cloning the β-globin terminator is shown by underlined nucleotides, poly(A) sequences (or mutations created to inactivate 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.

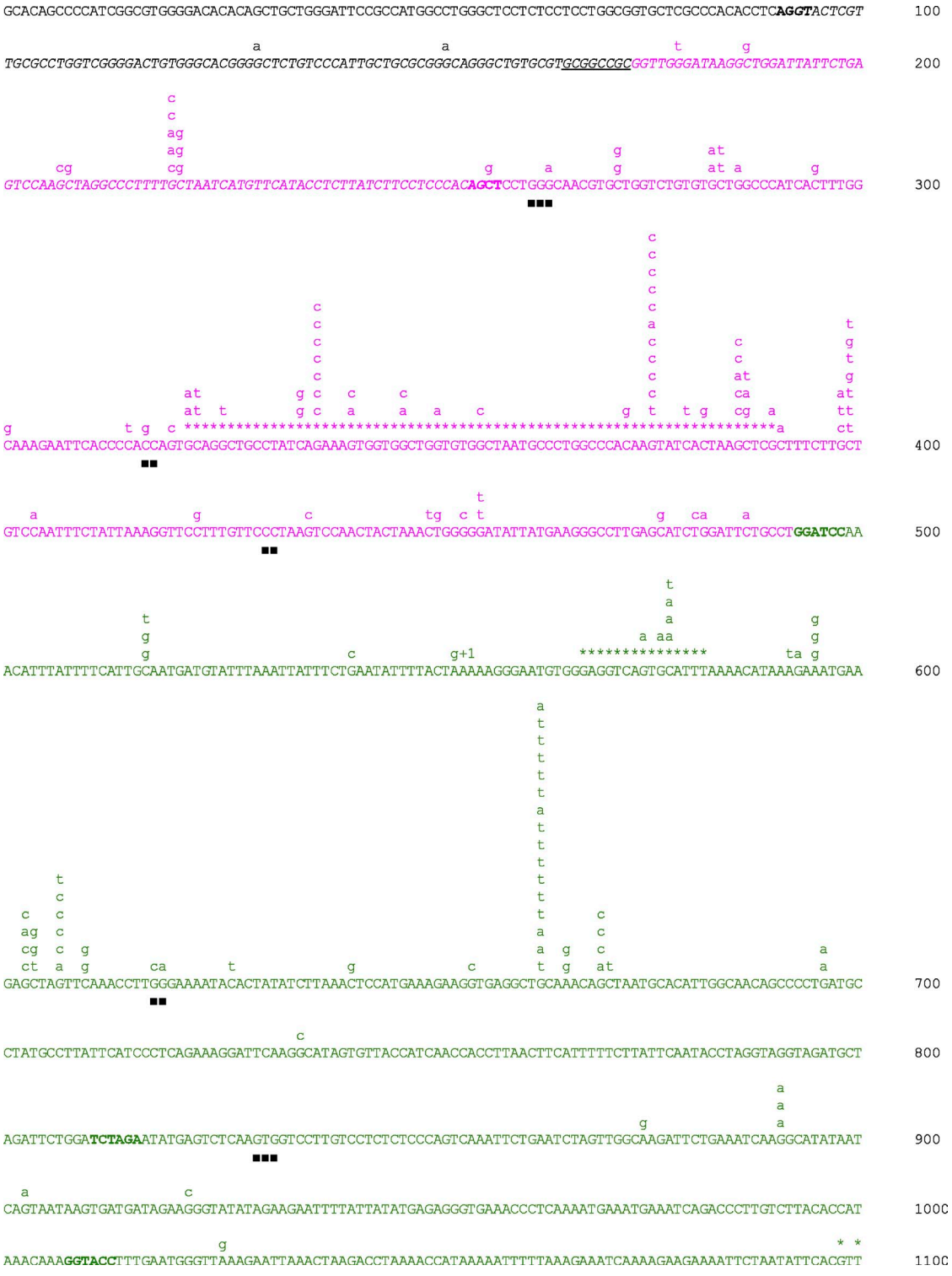

Figure S3. Mutations in the active and inactivated terminator knock-in clones. (+1 to +1,100 from the transcription start site), Ig gene sequence is highlighted in gray, NotI site used for cloning the β-globin terminator is shown by underlined nucleotides, poly(A) sequences (or mutations created to inactivate 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	gcagcggccgcACGCACAGCCCTGCCCGCGCAGCAGTGGGA
pk07	For	166	gcatgcggccgcGGTTGGGATAAGGCTGGATTATTCTG
pk10	Rev	947	gcatgacgtcCGGCTGCAACGTGAATATTAGAATTTTC
pk12	For	1,762	gcatatcgatGTGCAGGCAGCGCTGACTCAGCCGTCCTCGGTGTCAGCA
pk22	Rev	541	gaataaggCATATGCATCAGGGGCTGTTGCCAATGTGC
pk24	Rev	2,081	CTAGGACGGTCAGGGTTGTCCCGGCCCCAAATATA
pk31	For	494	gcatggatccAAACATTTATTTTCATTGCAATGATG
pk33	Rev	810	gcattctagaTCCAGAATCTAGCATCTACCTACCTA
pk48	For	1,379	AAGCTTGCATGCCTGCAGGTCGACTCTAGA
pk50	Rev	1,688	gcatgcggccgcGAATTCTGGTAGCACCTGGTCTGCAGTGTA
pk64	For	-48	GGGCGTGCTGCGGAAGGACGCGGGTATAAA
pk85	Rev	36	GGGAACAAAGGAACCTTTAATAGAAATTGGACAGC
pk87[c]	For	269	GGGATTCCGCCATGGCCTGGGCTCCTCTCC
pk93	For	948	gcagcatgcTTTTTTGAATTTGATATGAGAAGCAAAGGC
pk94	Rev	1,378	gcagcatgcTGATTCTCCCACCCCCAACCCCTGG
pk95	For	-48	ccaaagcttGGGCGTGCTGCGGAAGGACGCGGG
pk96	Rev	165	cctgatcatatgACGCACAGCCCTGCCCGCGCAGCA
pk99	For	166	ccaaagcttGGTTGGGATAAGGCTGGATTATTCTG
pk100	Rev	493	cctgatcatatgAGGCAGAATCCAGATGCTCAAGGCCC
pk103[c]	For	494	ccaaagcttAAACATTTATTTTCATTGCAATGATG
pk104	Rev	810	cctgatcatatgTCCAGAATCTAGCATCTACCTACCTA
pk107[c]	For	811	ccaaagcttATATGAGTCTCAAGTGGTCCTTGTCC
pk108	Rev	1,107	cctgatcatatgCGGCTGCAACGTGAATATTAGAATTTTC
pk111	Rev	1,571	cctgatcatatgGCATGCCTGCAGGTCGACTCTAGA
pk112	For	1,878	ccaaagcttCGGTGTGAAATACCGCACAGATGCGT
pk113	For	1,967	ccaaagcttGTGCAGGCAGCGCTGACTCAGCCGTCCTCG
pk114	Rev	2,285	cctgatcatatgCTAGGACGGTCAGGGTTGTCCCGGCCCCAAATATA
pk117	For	4,023	ccaaagctTGCCTCTCTCTTGCAGGCCAGCCCAA
pk118	Rev	4,336	cctgatcatatgAGGGTCTTCGTGATAGAGGTGCCGTTG
pk154	For	270	GCTGTCCAATTTCTATTAAAGGTTCCTTTGTTCCC
pk155	For	542	GCACATTGGCAACAGCCCCTGATGCATATGCCTTATTC
pk174[c]	For	4,178	CTCCACCCGCTCTGGCGAGACCA
pk182[c]	Rev	493	ttttttttttttttttttttTTTATTAGGCAGAATCCAG
pk183[c]	Rev	810	ttttttttttttttttttttTTTATTTCCAGAATCTAGCATC
pk184[c]	Rev	1,007	ttttttttttttttttttttTTTATTTTTGTTTATGGTGTAAG
pk185[c]	Rev	4,532	ttttttttttttttttttttTTTATTAATGTGACACCTGG
pk186	For	174	GGTTGGGATAAGGCTGGATTATT
pk187	Rev	572	ACCTCCCACATTCCCTTTTTA
pk188	For	552	TAAAAAGGGAATGTGGGAGGT
pk189	Rev	1037	GTTTAATTCTTTAACCCATTGA
gg-actin1	For		CCCCAAGCTTACTCCCACAGCCAGCCATGG
gg-actin2	Rev		GGCTCTAGATAGTCCGTCAGG

[a]Location of primers related to transcription start site.
[b]Complementary region with genomic DNA is shown in capital case.
[c]Primers used in polyadenylated RNA assay.