SUPPLEMENTAL TABLE 1. PCR primers for constructs in this study

Primer name	Sequence	For
Transgene construction		
C1-s	AAGCAGGCTTCACGCCTTTC	
C1-as(Ml1)	ACGCGTGTGAGATGCCTTACTGTGGC	
miniEpo frag.2 F(Nt1)	AACAAAAGCTGGAGCTGGCGGCCGCGGGAATTCGATACGC	
miniEpo frag.2 R	GAAGGGAAATGCAGCCCAGGCTAGTCTTGAAC	
miniEpo frag.3 F	GGCTGCATTTCCCTTCTCCAGCATTCTCATTT	*miniEpoHE-tdT* and *δF3miniEpoHE-tdT*
miniEpo frag.3 R	CATCCCAGCTTCCCTGGACTGTTGTCACCTCG	
miniEpo frag.4 F	CAGGGAAGCTGGGATGACTGGAGCACACTACC	
miniEpo frag.4 R	CCATGGTGGCGGGATCAAGCAGCAGGGTGGGACGTTCTGG	
HE_t_AS(Sal1)	GCCGTCGACCACTCAGCACTTGTCCTAGC	
Cla1_HE_h S	TGGATCGATGGCATCAGATCTGGGAAACC	
dF3 S	CTGGGATGACTGGAGCACACT	*δF3miniEpoHE-tdT*
dF3 AS	ATGCAGCCCAGGCTAGTCTTG	
-8kHRE F	GTATCGATAGAAGCTGAGCCCGTATGAAGCTC	
-8kHRE R	AGTCTAGAGGCTGGTCTGCCTTCAGTAGCATC	*sF2-mP-GFP*
Ms Epo pro F	GACCAGCCTCTAGACTCCAGCCTTAGTTGTTT	
Ms Epo pro R	CTCACCATCTCCGCGCCTAGCTGCCGGAGCTC	
-9arm S	CGAGAGGTAGAACTCAGTCC	
-8arm AS	TGAAACCCTGTCTCCAGAGG	Targeting vector for *δF2-60k-GFP*
-7arm S	CACGCGAGCACATGCTGTAG	
-7arm AS	AGAGCTGACAGTTCCTGAGG	
-18 s	AGGCAGTTGAGCCAACCTTC	
-17 as	TACTGAAGGCTGGAAAGGGA	Targeting vector for *δCURE-Epo/GFP*
-3.6 s	CAGGCTCAGGTTCATCTGAC	
-2.6 as	CTCCACGTGTGTGCCATGTA	
Luciferase reporter construction		
5'HRE S	AGAAGCTGAGCCCGTATGAA	sF2-mP-Luc
5'HRE AS	GGCTGGTCTGCCTTCAGTAG	
inv mu5'HRE S	TATGTGTTCTTGACTCTGCTCTCCTGGC	Mu-sF2-Luc
inv mu5'HRE AS	AAAGCAGGGAGACACAACTGCAGCTG	

SUPPLEMENTAL TABLE 2. PCR primers for genotyping in this study.

Primer name	Sequence	For
GFP s4	CTGAAGTTCATCTGCACCACC	*EGFP* gene
GFP as4	GAAGTTGTACTCCAGCTTGTGC	
int1 s	AGAAGTGGATGCCGGTCGCTTG	*tdTomato* at *Epo* gene locus
EpotdT AS2	TCACCATGGTGGCGGGATCAA	
dCURE S	GCTCGGAGTAAACTGAGGTC	Deleted CURE locus
dCURE AS	GTCAGATGAACCTGAGCCTG	
Epo-129sv/B6 S	TCTAAGGGTGTATTCTGGATGCCCC	B6 *Epo* gene (genome) and *δCURE-Epo* transgene
Epo-129sv AS	TCGTGCTGTCTGGGGAAGAATTC	*δCURE-Epo* transgene
Epo-B6 AS	TGGGGAAACCCCCATGAGATC	B6 *Epo* gene (genome)
-18.6k 40mer s	AGTCTTAAGGGGCTGGCAAGATGG ATCAGTGTGTGAGCTG	Long range PCR for checking transgene orientation of δCURE-GFP and δCURE-Epo
HE 40mer as	AATGGAGCCTGCTTATTGACTAGC GTGGGCAGGCATTGTG	

SUPPLEMENTAL TABLE 3. PCR primers for copy number detection in this study.

Primer name	Sequence	For
-50k s	GTGGCCTTGCTGGTGTTGTT	50-kb upstream region from *Epo* TSS
-50k as	CCTCCAAGGCATCAGATGTG	
-20k s	GTGTGCTGGCATTACAGGTG	20-kb upstream region
-20k as	ACACACACATCCCAATGAGC	from *Epo* TSS
-18k s	AGGCAGTTGAGCCAACCTTC	18-kb upstream region
-18.2k as	ACACCAAGCCATTGGAGAAAG	from *Epo* TSS
-14k s	GAATTACAAAGATCGCCCCA	14-kb upstream region
-14k as	CCAGAGTCGTCTGGAAAAGC	from *Epo* TSS
Cla1_HE_h S	TGGATCGATGGCATCAGATCTGGGAAACC	3'HRE enhancer
HE as	ATTGTGGCCTCAAGCCCAGA	region of *Epo* gene
Myb f	GGTTAGTGTTTCAGGAGGTTGG	Internal control (*Myb*)
Myb r	AAATGAGTTTTGACATGTGTGTGA	
GATA2 f	GCCCTGTACAACCCCATTCTC	Internal control
GATA2 r	TTGTTCCCGGCGAAGATAAT	(*Gata2*)

SUPPLEMENTAL TABLE 4. PCR primers for qRT-PCR analysis in this study.

Primer name	**Sequence**	**For**
mEpo-GFP qRT S	GAAGACTTGCAGCGTGGACA	*Epo-GFP*
mEpo-GFP qRT AS	GGTGGATCCTAAAGCAGCAG	
mEpo f	CATCTGCGACAGTCGAGTTCTG	*Epo*
mEpo r	CACAACCCATCGTGACATTTTC	
Gapdh f	GTCGTGGAGTCTACTGGTGTCTT	*Gapdh*
Gapdh r	GAGATGATGACCCTTTTGGC	
Hprt f	GTTGGATACAGGCCAGACTTTGT	*Hprt*
Hprt r	CCACAGGACTAGAACACCTGC	