Supplemental information

Super-enhancers include classical enhancers

and facilitators to fully activate gene expression

Joseph W. Blayney, Helena Francis, Alexandra Rampasekova, Brendan Camellato, Leslie Mitchell, Rosa Stolper, Lucy Cornell, Christian Babbs, Jef D. Boeke, Douglas R. Higgs, and Mira Kassouf

Stage	Hom	Het	WT
E9.5	1	5	2
E10.5	2	12	6
E12.5	5	7	5
E14.5	4	6	3
E17.5	3	7	6
Cumulative	15	37	22
Cumulative %	20	50	30

Table S1. Related to Figure 2A. Summary of genotypes from heterozygote crosses showing the observed Mendelian ratio at each gestational stage.

Application	Target	Vector	Guide RNA sequence
Allele deletion	Left breakpoint	pX458	ACAAGATGCTCTCCGCTGT
	Right breakpoint	pX458-Ruby	AGGACAAATCCCGAAGGTC
R1 deletion	Left breakpoint	pX458	GTGACCATAAGTTGATTAG
	Right breakpoint	pX458-Ruby	GTACATACGCCGGGCGTGG
R2 deletion	Left breakpoint	pX458-Ruby	TACCTCCAAGGTTTTGCTC
	Right breakpoint	pX458	GCCGTGACACTTCATGCTCA
R3 deletion	Left breakpoint	pX458	GGACTGAGGGAATTTTGTACA
	Right breakpoint	pX458-Ruby	GGACTGGCAGAAAGCTATGT
Rm deletion	Left breakpoint	pX458	GGACCAGCGTAGTCTAACTCC
	Right breakpoint	pX458-Ruby	GGACTCAACCACATGACTCA
R4 deletion	Left breakpoint	pX458-Ruby	GGTGCATCACCTCAACTCCCA
	Right breakpoint	pX458	GGCTAGCTGAATAATTTGCGG
R4 for reinsertion by HDR	Right breakpoint	pX458	GGATCCCAGGTTAGTTAGTCC

Table S2. Related to STAR Methods. Guide RNA sequences used in mESC CRISPR editing.