

WT <i>Sid1</i>	GATGACCTGGATGTGGTCCGGAGAGACCAGATCCCTGTCTTCTGAGCACCAGCATCACAGGGGAAGAC
ssDNA	GATGAttTGGAcGTcGTtaGacGcGAtCAGATCCCTGTCTTCTGAGCACCAGCATCACAGGGGcAAGAC
mice 1-32	GATGACCTGGATGTGGTCCGGAGAGACCAGATCCCTGTCTTCTGAGCACCAGCATCACAGGGGAAGAC
	96 nt Myc (3X)
	96 nt Myc (3X)

WT <i>Sid2</i>	CCTCCACCCACCCCTTAGGTTTTGCTGACGTTGGATGACGACTTGGACACAGTACAGCGGGACAAGATCTATGTCTTCTAGCA
ssDNA	CCTCCA ^g CCACCCCTTAGGTTTTGCTGACGTTGGATGACGA ^t cTcGAtACcGTtCAGCGcGACAAGATCTATGTCTTCTAGCA
mice 1,2,4, 10,13,17,22, 24,25,29,31	CCTCCA ^g CCACCCCTTAGGTTTTGCTGACGTTGGATGACGA ^t cTcGAtACcGTtCAGCGcGACAAGATCTATGTCTTCTAGCA
mouse 26	CCTCCACCCACCCCTTAGGTTTTGCTGACGTTGGATGACGA ^t cTcGAtACcGTtCAGCGcGACAAGATCTATGTCTTCTAGCA
	87nt HA (3X)
	87nt HA (3X)
	87nt HA (3X)

Figure S4. Sequence analysis of recovered *Sid1* alleles.

A) *Sid1* sequence of mouse om11 (Figure S3) produced with the commercial oligo shows that the sgRNA1 associated PAM mutation introduced by the ssDNA oligo was not incorporated into the knock-in locus, while the sgRNA2 associated PAM mutation was incorporated. B) *Sid1* sequence analysis of truncation allele from outcrossed F₂ progeny (T142, T165, and T166) derived from F₀ mouse 2 (Figure 3) shows that the truncation is associated with an 8-10bp inverted insertion (yellow highlighted region) and a 39 bp deletion. The expected location of the single-strand nicks is shown (V).