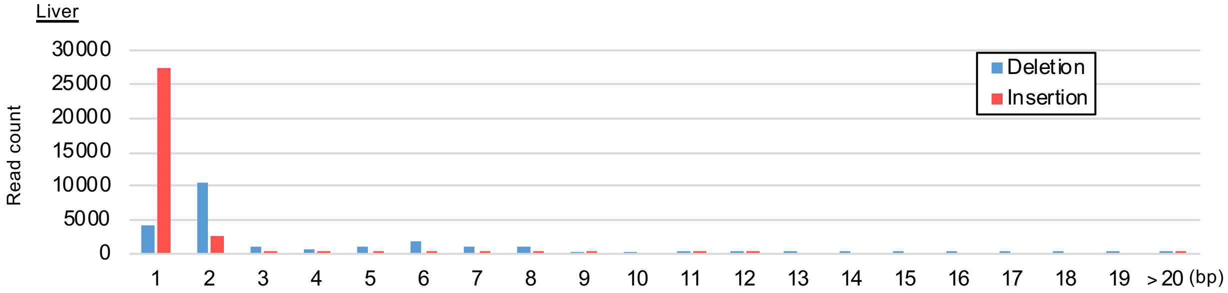
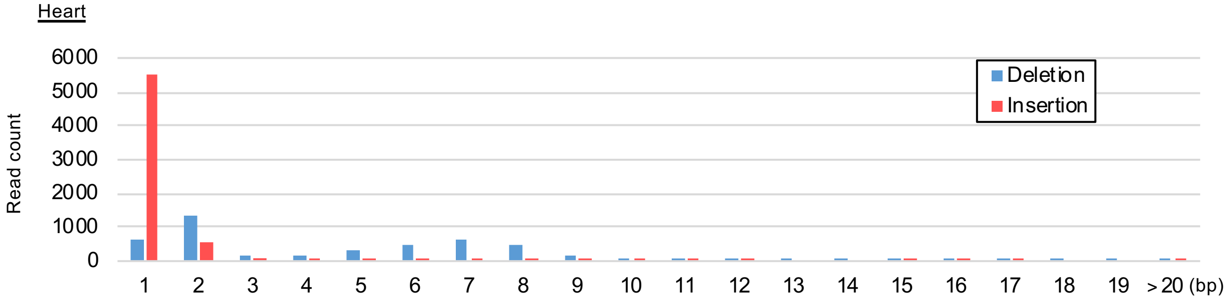
a

Analyzed organ	Total read (gRNA target)	Indels		HITI		Total read (c.1827 site)	Gene correction	
		Read	%	Read	%		Read	%
Liver	853230	54514	6.39	14888	1.74	886972	18256	2.06
Heart	877839	10905	1.24	1916	0.22	1346160	4523	0.34
Muscle	856777	3462	0.40	717	0.08	1543707	2141	0.14

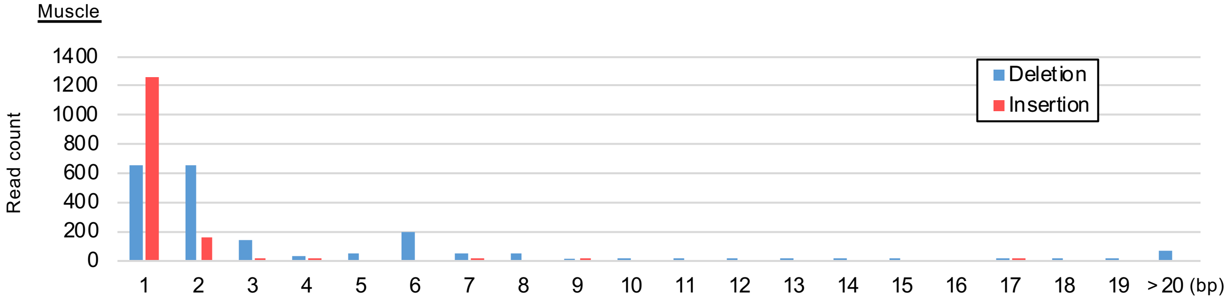
b



c



d



e

Target name	Sequence	Indel (%)
On	CCCATAAGTGTCTAAGATTCAGG	7.7
OTS1	GTCATAATTGTCTAAGATTATAG	0.0094
OTS2	GCCATAAAGTTCTAAGATTCAAG	0.0046
OTS3	GACATTTGTGTCTAAGATTCAAG	0.000035
OTS4	GCAATGAGGGTCTAAGATTCTAG	0.0038
OTS5	GAAATAGGTTTCTAAGATTCTGG	0.041
OTS6	GCCCCAGGTTTCTAAGATTCTAG	0.000087
OTS7	GTCATCAATTTCTAAGATTCCAG	0.051
OTS8	GCCACAAGTGACTAAGATTAAAG	0.00017
OTS9	GCCAGAAGTGGCTAAGATTATGG	0.00019
OTS10	TTAATAAGTGTGTAAGATTCAAG	0.000033

Supplementary Figure S11 | NGS analysis in SATI-treated mice. a Read count (Read) and genome editing (indels, HITI and correction) efficiency (%) by deep sequencing from the indicated organs. **b-d** Distribution of indel size in liver (**b**), heart (**c**), and muscle (**d**). Size of indel (bp) are indicated at bottom. **e** List of on-target site (On, *Lmna* intron 10) and off-target sites (OTS) that were used to determine the indel frequency of SATI mediated genome editing using genomic DNA isolated from the liver of progeria mouse at day 100. The nucleotide letters shown in red are the individual mismatches in predicted off-target sites.