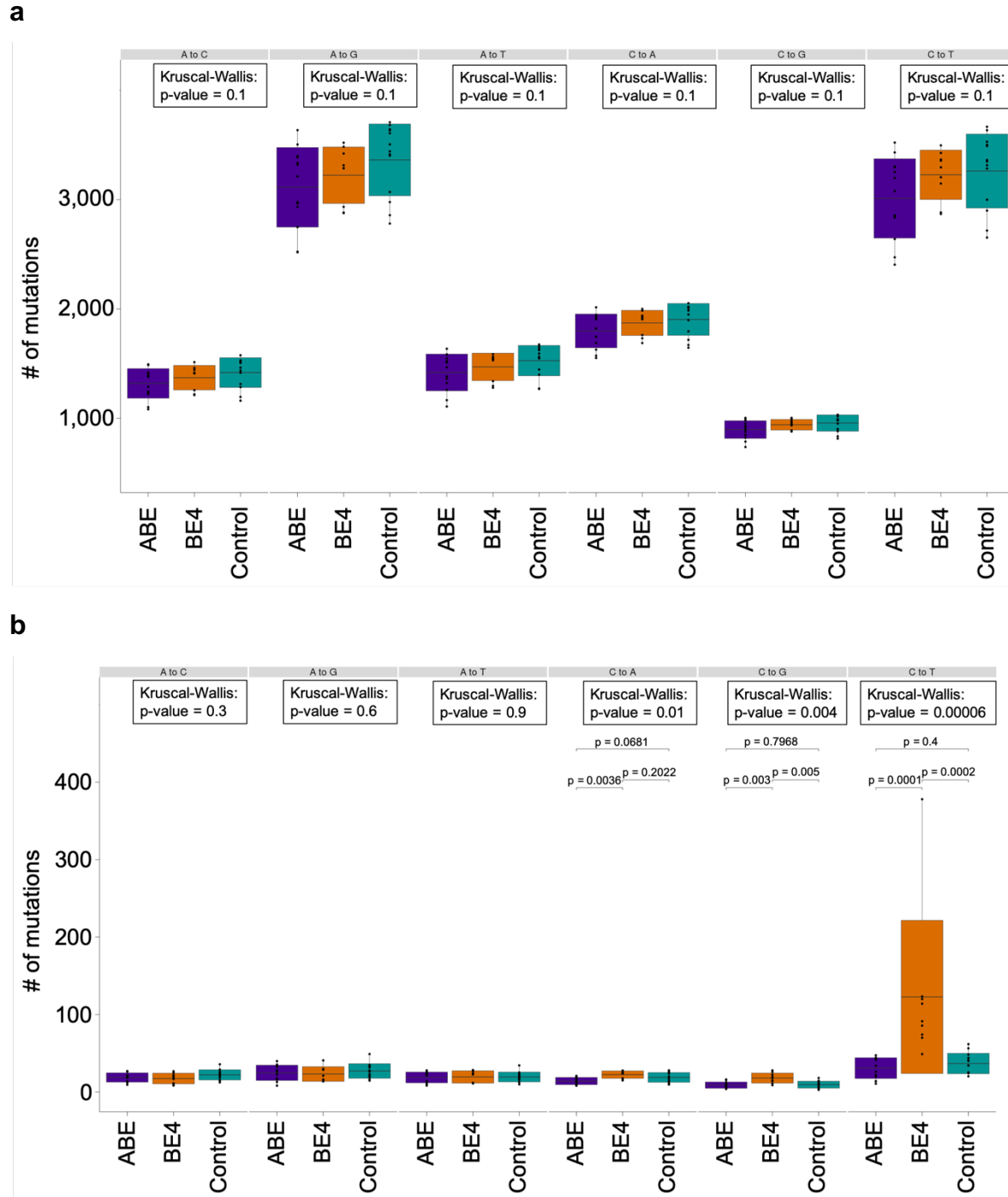


	-36	Frequency (%)
WT	CCCAGCAGGACATCTCTTCTGCCCCATGACACCCTTGGCACAGTATGGGCCCTTCTGGGAAGTG	
ABE 1G.G.....	49.5
G.G.G.....	30.5
G.G.....	15.3
ABE 2G.G.....	60.2
G.G.....	18.4
G.G.G.....	18.1
ABE 3G.G.G.....	69.8
G.G.....	27.0
ABE 4G.G.....	89.6
G.G.....	6.4
ABE 5G.G.G.....	57.6
G.G.....	39.2
ABE 6G.G.G.....	45.3
G.G.....	28.2
G.G.....	23.3
ABE 7G.G.....	36.8
G.G.G.....	34.2
G.G.....	24.8
	^GCAC	
ABE 8G.G.....	92.5
G.....	5.8
ABE 9G.G.G.....	45.9
G.G.....	39.0
G.G.....	11.3
ABE 10G.G.G.....	70.3
G.G.....	26.0
ABE 11G.G.....	50.0
G.G.....	45.3
ABE 12G.G.....	44.0
G.G.....	32.3
G.G.G.....	19.5
ABE 13G.G.....	50.2
G.G.G.....	37.8
G.G.....	6.1

	-36	Frequency (%)
WT	CCCAGCAGGACATCTCTTCTGCCCCATGACACCCTTGGCACAGTATGGGCCCTTCTGGGAAGTG	
BE4 1T.....	41.0
T.....	54.1
BE4 2	...T.T.....	37.8
G.....	37.5
A.....	12.2
BE4 3T.....	53.4
	...A.....T.....	46.6
BE4 4T.T.....	47.2
BE4 5T.....	62.9
	...T.T.....T.....	37.1
BE4 6	...T.....T.T.....	56.9
	...T.T.....T.....	38.8
BE4 7	...T.....T.T.....	42.8
T.....	6.3
BE4 8T.....	55.6
	...T.T.....	42.0
BE4 9G.....	100

Supplementary Fig. 1 Alignments of mutant sequences from founder mice carrying base-edited mutations. The sgRNA is underlined and the corresponding PAM sequence is shown in green. Within the editing window, the target nucleotides for base editing and nucleotides substituted by base editing are shown in bold black and blue, respectively. Bystanders are highlighted in red and deletions are indicated using a deletion symbol. WT, wild-type.



Supplementary Fig. 2 The frequencies of different types of total (a) and *de novo* SNVs (b) in individuals edited by the base editors and in the control group.