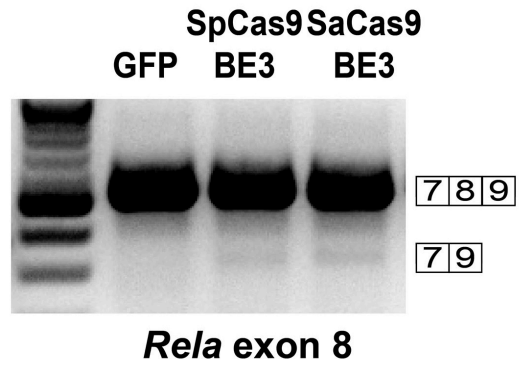


RELA EXON 7		INTRON 6																				SPICE ACCEPTOR			EXON 7					
		PAM			T	T	G	T	T	T	T	C	A	C	T	G	C	T	C	A	G	C	A	G	G	T	G	C	C	C
WT	A	0.03	0.04	0.16	0.03	0.01	0.10	0.02	0.08	0.03	0.09	0.05	99.41	0.02	0.05	0.14	0.03	0.11	0.08	0.02	99.62	0.11	0.12	0.03	0.19	0.05	0.16	0.10		
	C	99.84	99.87	99.77	0.27	0.22	0.01	0.32	0.38	0.45	0.29	99.88	0.10	99.88	0.30	0.02	99.85	99.79	0.41	99.88	0.08	0.03	0.04	0.31	0.05	99.79	99.85	99.87		
	G	0.02	0.01	0.01	0.05	0.03	99.77	0.09	0.04	0.02	0.08	0.01	0.35	0.01	0.06	99.73	0.01	0.01	0.04	0.02	0.28	99.73	99.82	0.08	99.71	0.02	0.05	0.07		
SP-BE3	A	0.02	0.09	0.25	0.04	0.04	0.20	0.02	0.08	0.04	0.16	0.06	99.13	0.02	0.05	0.39	0.05	0.13	0.11	0.03	99.59	6.26	0.65	0.06	0.18	0.05	0.35	0.22		
	C	99.81	99.77	99.86	0.28	0.29	0.03	0.33	0.38	0.38	0.37	99.84	0.16	99.87	0.32	0.03	99.83	99.75	0.35	99.87	0.07	0.59	0.07	0.26	0.08	99.71	99.41	99.48		
	G	0.04	0.03	0.03	0.08	0.04	99.58	0.10	0.07	0.06	0.14	0.03	0.49	0.02	0.11	99.43	0.02	0.02	0.08	0.02	0.30	93.00	99.23	0.06	99.70	0.05	0.10	0.11		
		0.13	0.11	0.07	99.80	99.64	0.18	99.54	99.52	99.52	99.33	0.07	0.22	0.09	99.53	0.16	0.11	0.10	99.46	0.08	0.04	0.24	0.05	99.62	0.08	0.20	0.14	0.18		

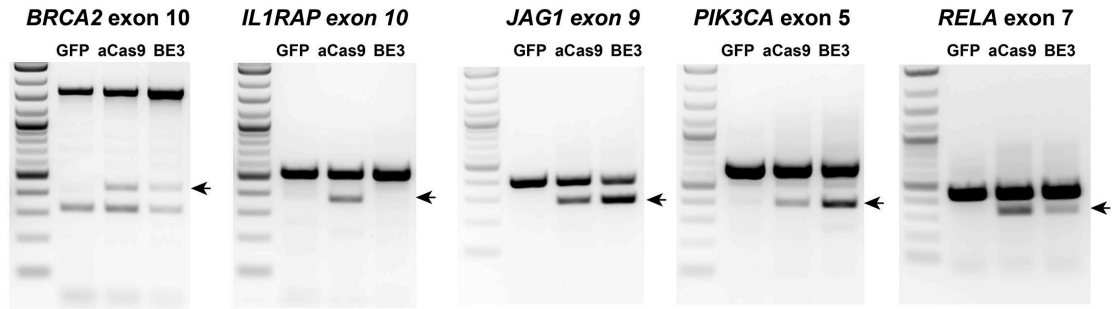
  

PIK3CA EXON 5		INTRON 4																		SPICE ACCEPTOR			EXON 5					
		PAM			C	C	T	T	A	A	T	C	T	C	T	A	A	T	A	C	A	G	T	A	T	A	T	A
WT	A	0.16	0.15	0.20	0.20	0.09	0.07	0.09	99.86	99.70	0.18	0.03	0.13	0.09	0.15	0.01	99.34	0.12	99.30	0.24	0.02	99.64	0.04	99.68	0.05	99.70	99.51	0.03
	C	99.53	99.66	99.57	99.64	99.83	0.30	0.19	0.03	0.03	0.42	99.92	0.35	99.88	0.38	0.18	0.08	99.77	0.07	0.05	0.19	0.06	0.16	0.04	0.20	0.07	0.09	0.01
	G	0.12	0.05	0.06	0.06	0.02	0.21	0.06	0.09	0.25	0.24	0.00	0.10	0.00	0.00	0.07	0.27	0.02	0.47	99.56	0.04	0.21	0.12	0.20	0.08	0.16	0.33	99.86
SP-BE3	A	0.12	0.07	0.31	0.43	0.06	0.08	0.04	99.45	99.70	0.10	0.06	0.06	0.04	0.11	0.01	99.39	0.08	99.39	26.38	0.03	99.61	0.02	99.68	0.12	99.65	99.49	10.34
	C	99.70	99.73	99.50	99.43	99.53	0.27	0.20	0.02	0.02	0.33	99.47	0.36	99.74	0.41	0.12	0.06	99.66	0.05	14.88	0.22	0.04	0.21	0.05	0.16	0.05	0.03	0.99
	G	0.05	0.08	0.05	0.05	0.01	0.15	0.05	0.48	0.25	0.19	0.42	0.05	0.08	0.08	0.13	0.39	96.38	0.16	0.25	0.08	0.21	0.04	0.18	0.27	87.92		
		0.12	0.13	0.14	0.09	0.40	99.49	99.71	0.06	0.03	99.37	0.05	99.52	0.15	99.41	99.76	0.19	0.12	0.16	2.58	99.59	0.11	99.69	0.06	99.67	0.12	0.22	0.75

**Figure S1.** Expanded view of NGS analysis shown in **Fig. 2D**. Orange box: PAM sequence. Light blue: Reference sequence shown in sense orientation for clarity. Gray box: sgRNA target sequence. Deep sequencing performed on biological duplicates and averaged.



**Figure S2.** Neuro2A cells were transfected with either SpCas9 or SaCas9-KKH C>T base editors targeting the splice acceptor of *Rela* exon 8. Analysis of exon skipping by RT-PCR demonstrated that both base editors effectively induced splicing.



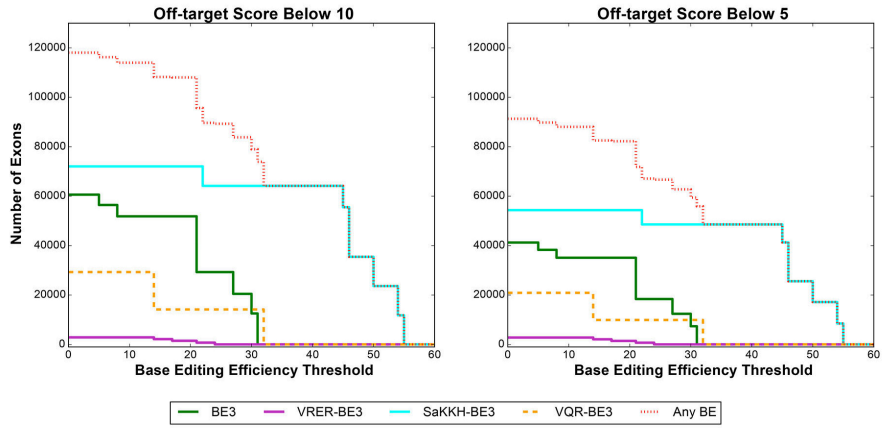
**Figure S3.** Comparison of CRISPR-SKIP and active SpCas9 using the same sgRNAs targeting the splice acceptor of *BRCA2* exon 10, *IL1RAP* exon 10, *JAG1* exon 9, *PIK3CA* exon 5 and *RELA* exon 7.

BRCA2		INTRON 25																				SPICE ACCEPTOR				EXON 26											
EXON 26		PAM			A	C	T	T	T	T	T	T	T	C	T	T	A	G	A	A	T	A	T	T	G	A	C	A									
WT	A	0.21	0.21	0.20	98.35	0.30	0.08	0.02	99.70	0.09	0.03	0.14	0.17	0.14	0.13	0.11	99.68	0.24	99.56	99.48	0.14	99.71	0.11	0.13	0.32	99.31	0.11	99.45									
	C	0.36	99.61	99.64	0.48	99.60	0.26	0.22	0.10	0.21	0.32	0.37	0.33	99.78	0.22	0.14	0.03	0.02	0.03	0.07	0.16	0.05	0.29	0.40	0.03	0.12	99.71	0.08									
	G	0.17	0.07	0.05	0.51	0.01	0.08	0.14	0.14	0.16	0.05	0.28	0.32	0.03	0.18	0.10	0.26	99.65	0.33	0.40	0.16	0.20	0.31	0.27	99.45	0.47	0.06	0.38									
SP-BE3	A	99.28	0.11	0.12	0.05	0.09	99.57	99.62	0.05	99.54	99.60	99.21	99.18	0.05	99.47	99.65	0.03	0.09	0.07	0.05	99.54	0.03	99.34	99.20	0.21	0.09	0.11	0.10									
	C	0.37	99.81	99.77	0.24	99.77	0.29	0.17	0.04	0.19	0.31	0.33	0.32	99.88	0.22	0.12	0.01	0.16	0.03	0.02	0.16	0.01	0.27	0.34	0.02	0.08	99.84	0.03									
	G	0.07	0.03	0.02	0.37	0.01	0.05	0.06	0.09	0.09	0.03	0.14	0.13	0.02	0.11	0.06	0.18	98.86	0.31	0.32	0.06	0.16	0.13	0.13	99.67	0.44	0.02	0.32									
VQR	A	0.10	0.10	0.13	99.11	0.16	0.05	0.02	99.83	0.04	0.02	0.06	0.08	0.07	0.08	0.05	99.77	98.35	99.63	99.63	0.05	99.80	0.06	0.07	0.23	99.41	0.07	99.61									
	C	0.37	99.81	99.77	0.24	99.77	0.29	0.17	0.04	0.19	0.31	0.33	0.32	99.88	0.22	0.12	0.01	0.16	0.03	0.02	0.16	0.01	0.27	0.34	0.02	0.08	99.84	0.03									
	G	0.07	0.03	0.02	0.37	0.01	0.05	0.06	0.09	0.09	0.03	0.14	0.13	0.02	0.11	0.06	0.18	98.86	0.31	0.32	0.06	0.16	0.13	0.13	99.67	0.44	0.02	0.32									
		s]			T	G	A	A	T	A	A	A	G	A	A	T	C	T	T	A	T	A	A	A	G	T	f]										

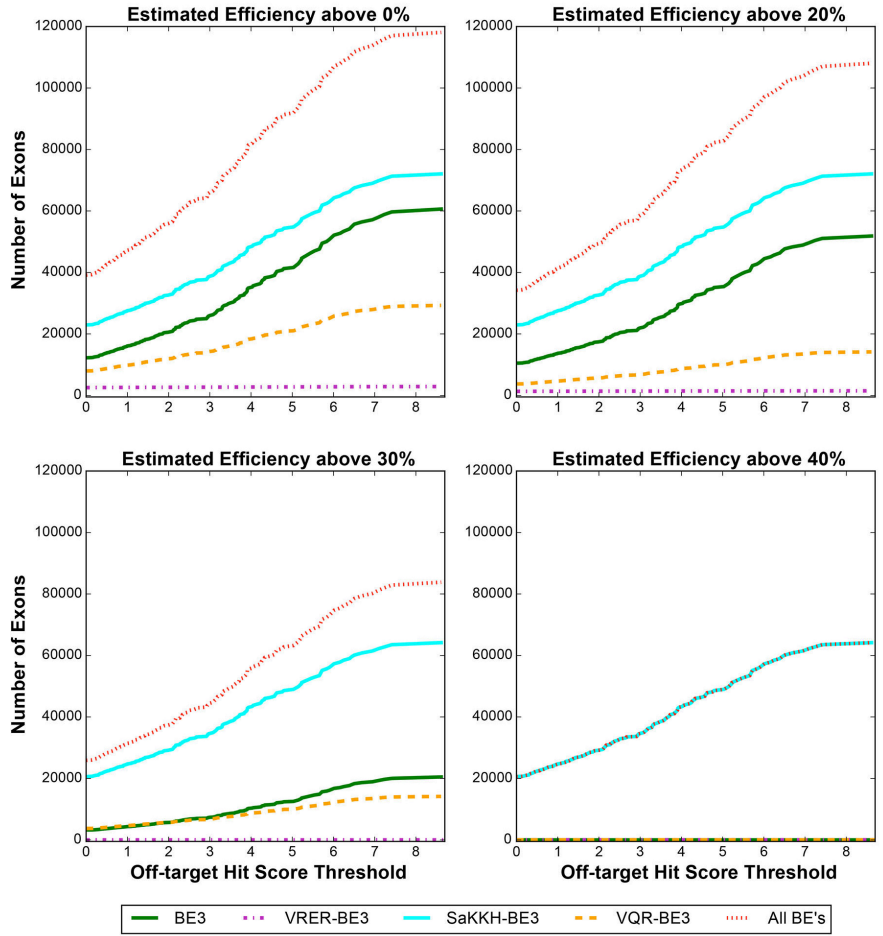
  

RELA		INTRON 9																				SPICE ACCEPTOR				EXON 10											
EXON 10		PAM			A	C	T	T	T	T	T	T	T	T	T	T	T	A	G	A	A	T	A	T	G	A	C	C	A	C							
WT	A	86.57	0.10	0.09	0.10	99.43	0.20	0.09	0.05	0.04	0.04	0.03	0.16	0.23	0.16	0.12	0.05	98.42	0.06	99.26	0.23	0.15	98.49	0.06	0.10	0.05	97.38	0.11									
	C	0.54	99.78	99.75	0.30	0.16	0.11	99.72	99.71	99.77	0.31	0.35	0.07	99.06	99.68	99.71	0.04	0.83	99.83	0.12	0.07	0.03	0.63	99.84	99.73	99.86	1.44	99.75									
	G	0.69	0.03	0.04	0.13	0.26	99.61	0.04	0.07	0.07	0.17	0.18	99.67	0.13	0.08	0.01	0.11	0.45	0.01	0.54	99.58	99.72	0.66	0.01	0.05	0.01	1.08	0.03									
SA-BE3	A	0.20	0.09	0.12	99.47	0.15	0.08	0.14	0.18	0.12	99.48	99.44	0.11	0.37	0.09	0.16	99.60	0.31	0.10	0.08	0.12	0.10	0.23	0.09	0.12	0.08	0.10	0.11									
	C	0.79	99.64	99.57	0.33	0.32	0.20	99.54	99.46	99.51	0.29	0.37	0.14	98.68	99.29	99.52	0.23	1.30	99.67	0.23	0.68	2.30	1.59	99.79	99.54	99.76	2.51	99.66									
	G	0.95	0.07	0.09	0.27	0.37	99.25	0.05	0.16	0.15	0.21	0.29	99.18	0.16	0.22	0.02	0.26	0.60	0.03	0.58	51.80	47.52	1.01	0.03	0.08	0.02	1.61	0.08									
KKH	A	97.59	0.23	0.18	0.17	99.06	0.37	0.19	0.07	0.14	0.03	0.07	0.46	0.42	0.40	0.19	0.12	97.64	0.20	99.07	46.61	46.95	96.83	0.08	0.22	0.12	95.64	0.14									
	C	0.95	0.07	0.09	0.27	0.37	99.25	0.05	0.16	0.15	0.21	0.29	99.18	0.16	0.22	0.02	0.26	0.60	0.03	0.58	51.80	47.52	1.01	0.03	0.08	0.02	1.61	0.08									
	T	0.37	0.09	0.16	99.23	0.25	0.18	0.23	0.31	0.20	99.47	99.27	0.23	0.73	0.09	0.27	99.39	0.46	0.10	0.11	0.91	1.23	0.99	0.10	0.15	0.10	0.23	0.12									
		s]			G	G	G	A	A	C	G	G	G	A	T	G	T	C	C	T	G	G	G	T	f]												

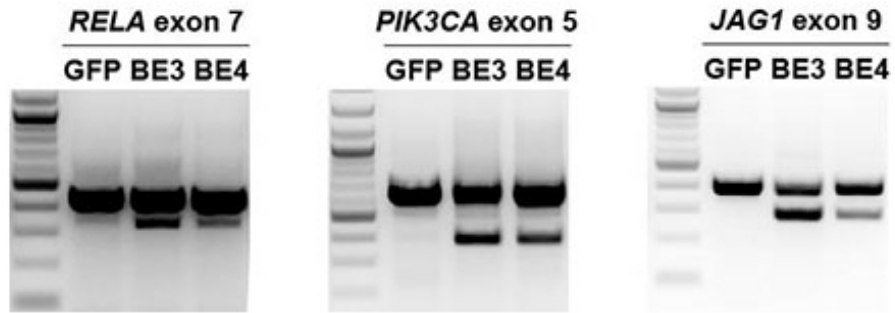
**Figure S4.** Expanded view of NGS analysis shown in **Fig. 5C** and **5D**. Orange box: PAM sequence. Light blue: Reference sequence shown in sense orientation for clarity. Gray box: sgRNA target sequence. Deep sequencing performed on biological duplicates and averaged.



**Figure S5.** Estimation of the number of exons that can be targeted by each base editor with subplots filtered by the maximum allowed off-target score. The y-axis denotes the number of exons that can be targeted with estimated efficiency of modifying intronic flanking G at or above the corresponding value on the x-axis.



**Figure S6.** Estimation of the number of exons that can be targeted by each base editor with subplots filtered by estimated efficiency of editing the flanking G nucleotide. The y-axis denotes the number of exons that can be targeted with maximum off-target score at or below the corresponding value on the x-axis.



**Figure S7.** Comparison of CRISPR-SKIP using the C>T base editors BE3 or BE4 for inducing skipping of *PIK3CA* exon 5, *RELA* exon 7, and *JAG1* exon 9 by RT-PCR analysis.