Supplementary Table S2. NGS targeted deep sequencing data of PCR amplicons from injected wild-type, heterozygous, and homozygous P23H retinas and uninjected heterozygous retinas

Cas9	*sgRNAs*	*Genotypes*	*Total pairs*	*wt pairs*	*wt allele (%)*	*P23H pairs*	*P23H allele (%)*	*Indel pairs*	*Indel frequency (%)*
SaCas9-KKH	sgRNA1	wt	173,761	107,771	62.0%	0	0.0%	65,758	37.8%
		het	175,385	71,517	40.8%	34,431	19.6%	69,225	39.5%
		hom	131,972	0	0.0%	87,061	66.0%	44,674	33.9%
—	—	het	93,145	46,889	50.3%	45,972	49.4%	0	0.0%
SpCas9-VQR	sgRNA2	wt	90,126	53,833	59.7%	0	0.0%	36,044	40.0%
		het	78,850	26,457	33.6%	11,063	14.0%	40,656	51.6%
		hom	104,079	0	0.0%	90,045	86.5%	13,605	13.1%
—	—	het	78,423	39,464	50.3%	38,767	49.4%	0	0.0%
SpCas9-VQR	tru-sgRNA2	wt	99,930	99,375	99.4%	0	0.0%	184	0.2%
		het	94,178	50,549	53.7%	31,265	33.2%	12,090	12.8%
		hom	97,624	0	0.0%	70,248	72.0%	27,139	27.8%
—	—	het	113,685	56,464	49.7%	57,012	50.1%	0	0.0%