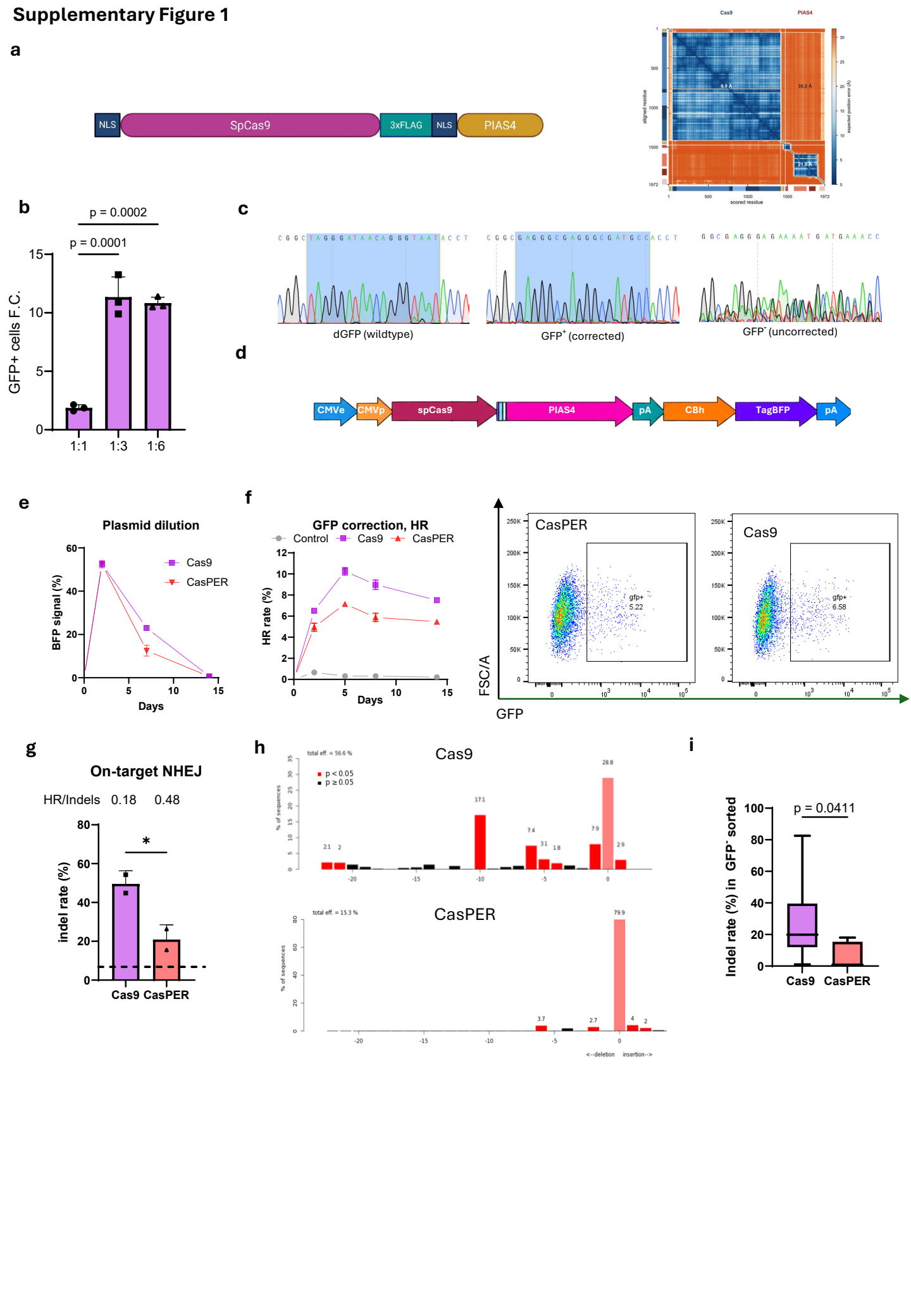
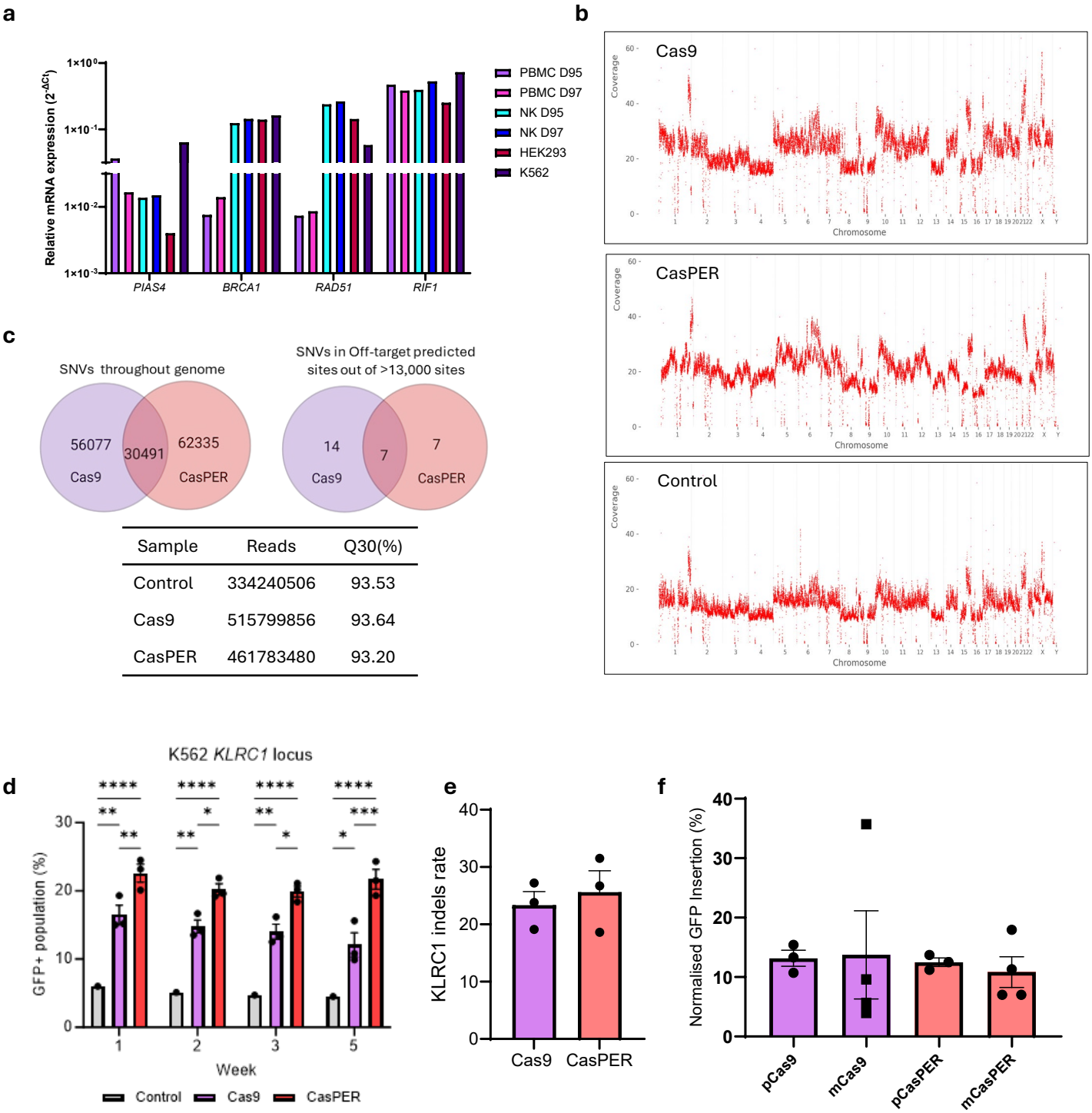
Supplementary Figure 1

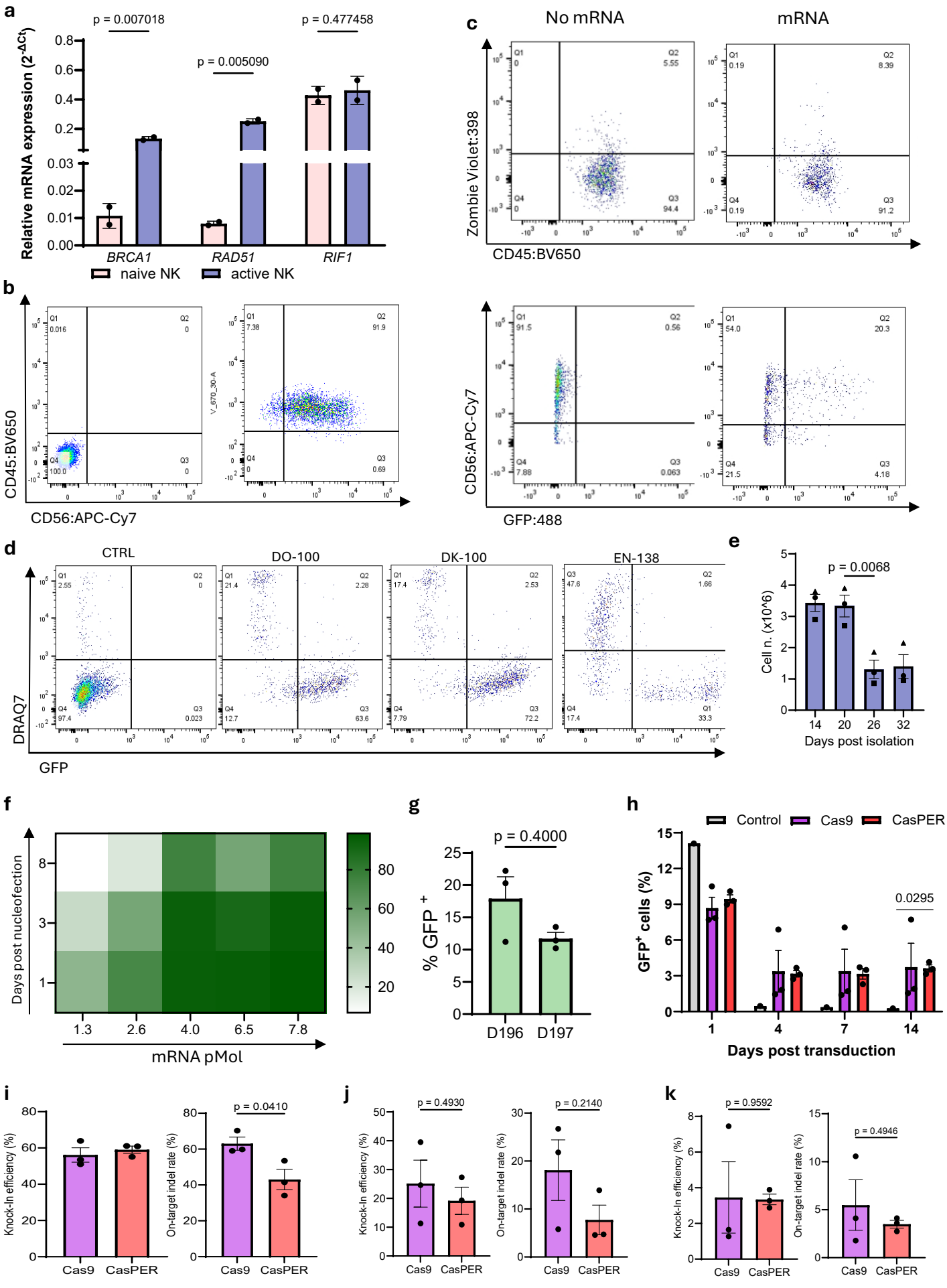


Supplementary Figure 2

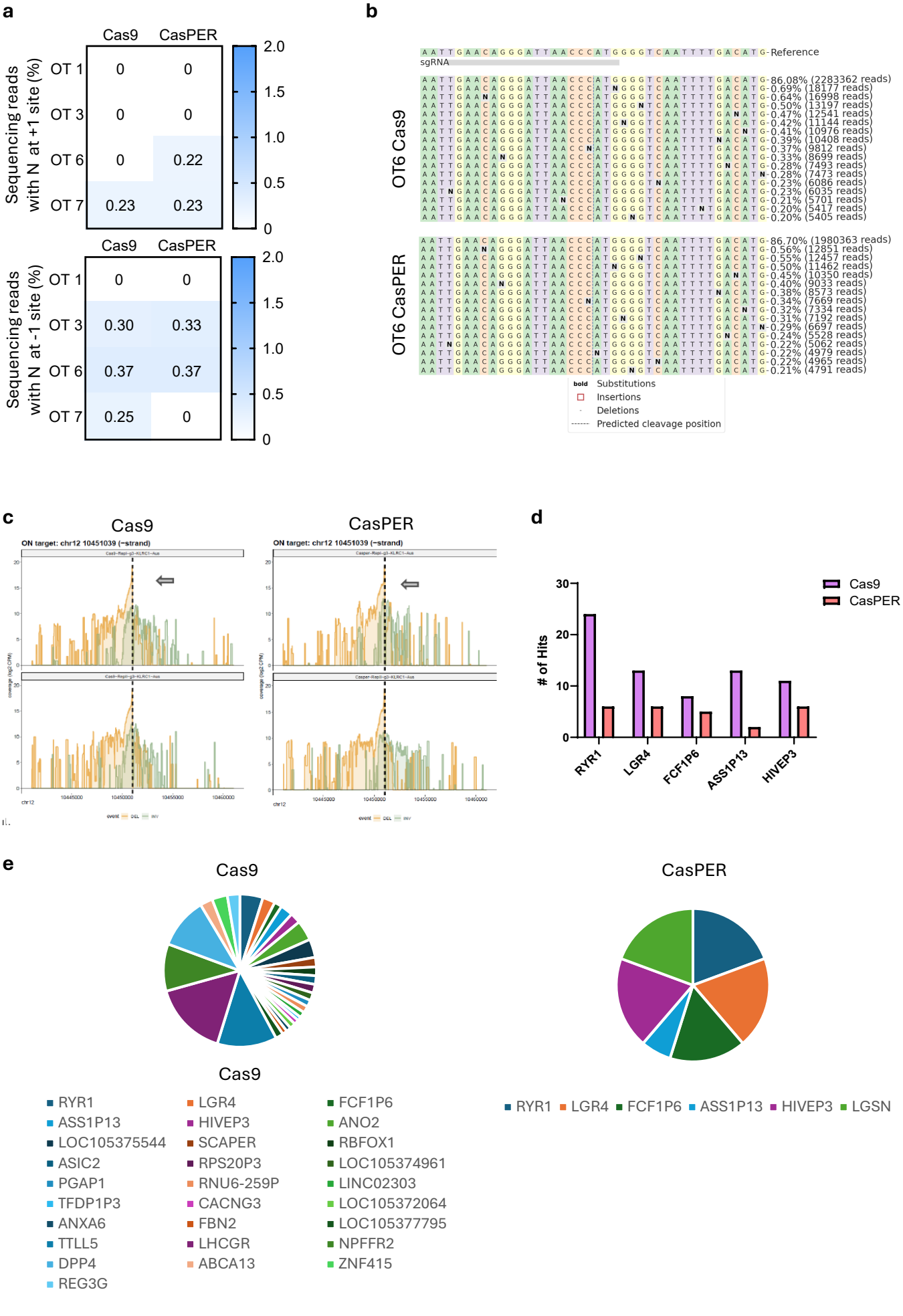


Sample	Reads	Q30(%)
Control	334240506	93.53
Cas9	515799856	93.64
CasPER	461783480	93.20

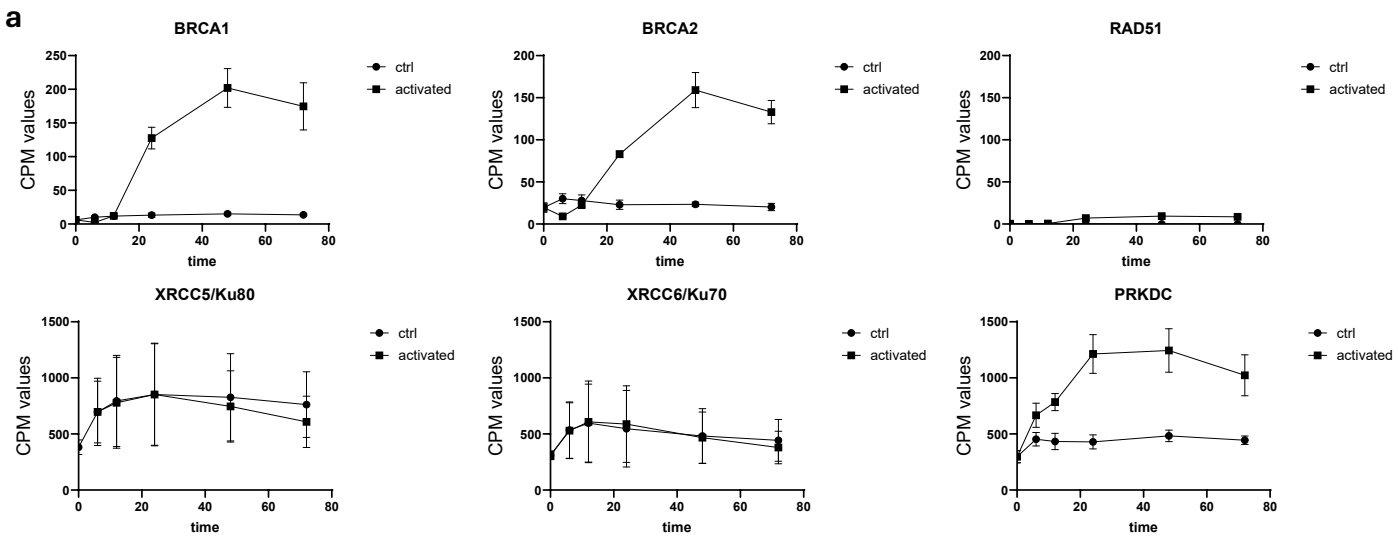
Supplementary Figure 3

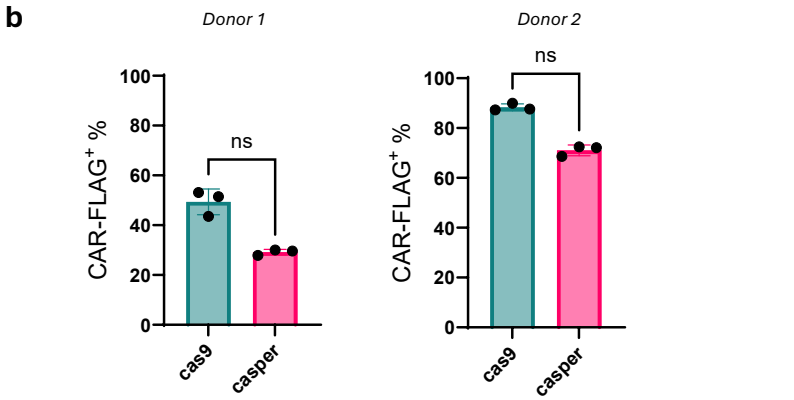


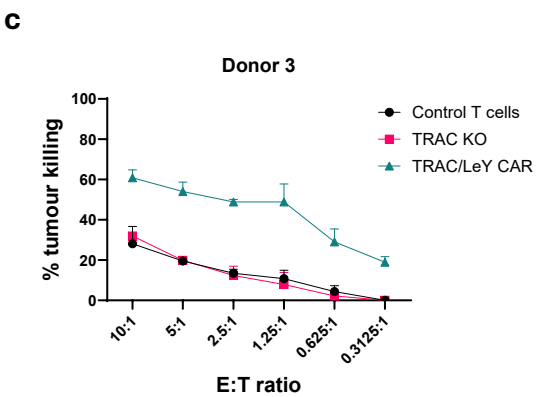
Supplementary Figure 4

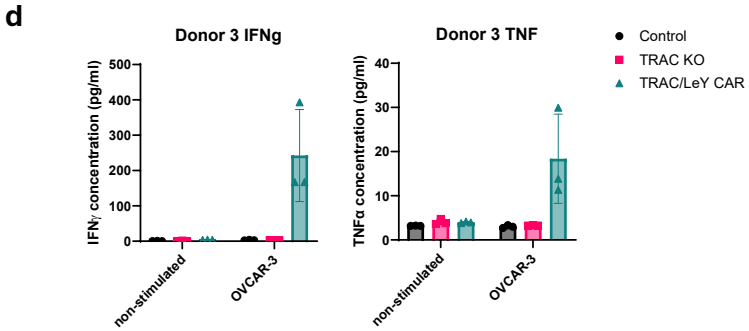


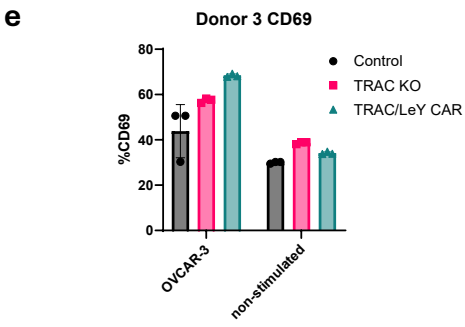
Supplementary Figure 5











Supplementary legends

Supplementary Fig. 1

a Predicted aligned error (PAE) plot for the top-ranked AlphaFold2 model of CasPER. Blue indicates low expected positional error and greater confidence in the relative placement of residue pairs, whereas red indicates high positional uncertainty. The high interdomain PAE indicates that the relative orientation of the Cas9 and PIAS4 domains is not confidently resolved. **b** Validation of the dGFP reporter line following Cas9-mediated editing. GFP restoration was quantified by flow cytometry 48 h after transfection (n = 3). **c** Sanger-sequencing chromatograms confirming correction of the 18-bp defective GFP sequence in GFP-positive cells and mutagenic editing outcomes in GFP-negative cells. **d** Schematic of the CasPER expression vector. CasPER expression is driven by the cytomegalovirus (CMV) promoter, whereas the blue fluorescent protein (BFP) selection marker is driven by the hybrid chicken β-actin (CBh) promoter. **e** BFP expression over time, showing progressive loss of the transiently delivered editor plasmid. **f** Time-course analysis of GFP restoration in reporter cells edited with Cas9 or CasPER over 14 days (n = 3). CasPER delivered without gRNA was used as the negative control. At 48 h, transfected BFP-positive cells and corrected GFP-positive cells were enriched by FACS to remove untransfected cells while retaining cells corrected during the initial 48-h period. **g** Quantification of on-target indel formation by T7 endonuclease I mismatch-cleavage assay and the corresponding ratio of HR-mediated correction to indel formation (n = 2). **h** Representative indel profiles showing deletions extending to approximately 20 bp in Cas9-edited cells, compared with approximately 5 bp in CasPER-edited cells. **i** On-target indel frequencies in the FACS-isolated GFP-negative populations shown in Fig. 1d. Data are presented as the mean ± SEM. Statistical significance was assessed by one-way ANOVA in **b** and t-test in **g**; $P < 0.02$ in **g**.

Supplementary Fig 2.

a Relative mRNA expression of PIAS4 and selected DNA-repair factors across human cell lines and primary cells. **b** Whole-genome sequencing coverage across chromosomes in unedited, Cas9-edited and CasPER-edited HEK293T cells targeted at the *AAVS1* locus. Mean sequencing depth was approximately 20×; one sample was analysed per condition. **c** Venn diagrams showing the overlap among conditions of all genomic sites containing single-nucleotide variants (SNVs) and the subset of SNV-positive sites overlapping Cas-OFFinder predictions. One sample was analysed per condition. **d** Time-course analysis of HDR-mediated GFP knock-in at the *KLRC1* locus in K562 cells over 5 weeks, quantified by flow cytometry. **e** On-target indel frequencies at the *KLRC1* locus determined by Sanger sequencing and TIDE analysis. **f** Comparison of GFP knock-in at the *AAVS1* locus in K562 cells following delivery of Cas9 or CasPER as mRNA together with a AAV6 donor.

Supplementary Fig. 3

a qPCR analysis of the HR-associated genes *BRCA1* and *RAD51* and the NHEJ-associated gene *RIF1* in resting and activated primary human NK cells. Expression was normalised to the housekeeping gene *HPRT*. NK cells were obtained from two independent donors and analysed using two technical replicates per donor. **b** Representative flow-cytometry analysis confirming CD45 and CD56 expression in expanded primary NK cells before editing. **c** Representative flow-cytometry plots showing NK-cell viability and retention of CD45 and CD56 expression following genetic manipulation. **d** Optimisation of mRNA nucleofection using three electroporation programmes. DRAQ7-positive cells indicate non-viable cells, whereas GFP-positive cells indicate successful mRNA delivery. **e** Viable-cell counts during feeder-cell-mediated expansion of NK cells from three independent donors (D189, D190 and D191). **f** Heatmap showing eGFP expression across three time points following titration of eGFP-encoding mRNA. **g** Quantification of eGFP expression following mRNA nucleofection of NK cells from two

independent donors. Three independent nucleofections were performed per donor; statistical significance was assessed using a two-tailed Mann–Whitney test. **h** Flow-cytometry analysis of GFP knock-in at the *KLRC1* locus in primary NK cells from donor D206 following nucleofection with Cas9 or CasPER mRNA and transduction with an AAV6 donor carrying the homologous repair template. Statistical significance was assessed using an unpaired two-tailed *t*-test; $P < 0.05$. **i–k** GFP knock-in efficiency and on-target indel frequency at the *KLRC1* locus in primary NK cells from donors D241 (**i**), D240 (**j**) and D206 (**k**). Knock-in was quantified as the percentage of GFP-positive cells, and indel frequencies were determined by Sanger sequencing followed by TIDE analysis.

Supplementary Fig.4

a Targeted next-generation sequencing of four computationally predicted *KLRC1* off-target sites analysed using CRISPResso2. Substitution frequencies at positions −1 and +1 relative to the predicted cleavage position are shown. **b** Representative CRISPResso2 allele-frequency outputs for the nominated off-target loci, showing the sequence, read count and relative frequency of each detected allele. **c** CAST-seq coverage at the on-target *KLRC1* locus in Cas9- and CasPER-edited samples. Upper and lower tracks represent independent technical replicates. **d** Number of rearrangement-associated CAST-seq events per gene at loci detected in both Cas9- and CasPER-edited samples. **e** Relative enrichment of CAST-seq signals at distal genomic loci reproducibly detected across technical replicates of Cas9- and CasPER-edited samples.

Supplementary Fig. 5

a Time-course analysis of *PIAS4* and selected DNA-repair gene expression in resting T cells and during the 72 h following activation. **b** Total frequency of CAR-expressing T cells generated using Cas9 or CasPER, quantified across two independent donors. **c** Specific lysis of ^51Cr-labelled LeY-positive OVCAR-3 tumour cells by unedited control T cells, *TRAC*-knockout T cells and *TRAC*-targeted LeY CAR-T cells derived from donor 3 at the indicated effector-to-target ratios. **d** IFNγ and TNFα concentrations in culture supernatants from donor 3-derived T cells cultured alone or exposed to LeY-positive OVCAR-3 tumour cells. **e** Percentage of CD69-positive donor 3-derived T cells following exposure to OVCAR-3 tumour cells, determined by flow cytometry.

LOCI detected as significant and confirmed in both technical replicates

CAS9

chr	start	end	Cas9.Repl g3.KLRC1 _Aus_read _unique	Cas9.Repl g3.KLRC 1.Aus_rea d_unique	Cas9.Repl g3.KLRC1 _Aus_read	Cas9.Repl g3.KLRC 1.Aus_rea d	Cas9.Repl g3.KLRC1 _Aus_read _ctl	Cas9.Repl g3.KLRC 1.Aus_rea d_ctl	Cas9.Repl g3.KLRC1 _Aus_hits	Cas9.Repl g3.KLRC 1.Aus_hits ctl	Cas9.Repl g3.KLRC1 _Aus_hits _ctl	Cas9.Repl g3.KLRC 1.Aus_hits ue	Cas9.Repl g3.KLRC1 _Aus_pval pvalue	Cas9.Repl g3.KLRC 1.Aus_pval lue	Cas9.Repl g3.KLRC1 _Aus_adj. _pvalue	Cas9.Repl g3.KLRC 1.Aus_adj que	reads_uni reads	hits	read/hit	NB_ OVL	NB_ SIGNIF	site	log10read _hits	BarcodeH opping	start.site	end.site	top_coord	start.bin	end.bin	aln_id	pattern_ gRNA3	subject_ gRNA3	aln_sum_ _gRNA3	aln_orient __gRNA3	NRG_gR _gRNA	score _gRNA	homology _gRNA3	nb_mism_ RNA3	nb_ins_g _RNA3	length_ins RNA3	nb_del_g RNA3	length_de l__gRNA3	aln_chr_ gRNA3	aln_abs_s tart_gRN A3	aln_rel_st art_gRN A3	kcss_fw_le ngth_ON ON1	kcss_rc_le ngth_ON ON1	group	ON	OMT	HMT	OMT_adj. OMT_pv_ _gRNA 3	HMT_pv_ _ON1	HMT_adj. pv__ON1	alignment _id	annotatio n	geneChr	geneStart	geneEnd	geneLengt h	geneStran d	geneId
chr12	104502036	104518044	10633	11211	2707628	4739516	26349	26326	6071	7165	60	61	0	0	0	0	23849	74381136	13251	561	2	2 site_1	2.749215 no		104104515	104518044	104504864	104514064 aln1		TGAATCAGTGAACAGGtgaaAggaacc		TRUE	20.5	91.3	2	0	0	0	0	TGAAC3tgc 104514064		50 GAAATTATG		500 GAGTTTGG	10 OMT	ON1	gRNA3	ON1	0	0	0	0.085	1	Promoter (	12	104427564	104548665	121021	2	1 KLRC1
chr19	38517749	38518549	16	12	83	49	1	1	14	10	1	1	2.12E-22	1.73E-20	2.06E-13	1.37E-11	28	132	24	6	2	2 site_2138	0.740363 no		38518145	38518549	38518149	38517749	38518549 aln1290		TGAATCAG TGAA-CAGtgaa+cagg arc		TRUE	11.5	74.07	3	3	4	0	0	TGAA+CAG	38518261	112 ACTGTACTA		9 TTGAGGAT	9 OMT		gRNA3		0	0	0.603	0.608599	aln_1290	Intron (NM	19	38433691	38587564	153874	1	1 RYR1
chr12	5639268	5640068	15	11	97	80	1	1	12	9	1	1	2.92E-26	3.01E-24	4.1E-22	5.34E-20	26	177	21	8	2	2 site_1548	0.925754 no		5639615	5639793	5639668	5639268	5640068 aln1000		TGAATGGGTGAACAGGtgaaTGggc+rc.		TRUE	10.5	70.83	6	1	1	0	0	TGAA??GG	5639331	-337 TTTAGGTT		10 TCTCTTTCC	10 OMT		gRNA3		0.002	0.239521	0.222	0.28623	aln_1000	Intron (NM	12	5562655	5946232	383578	2	2 ANO2
chr7	1.43E+08	1.43E+08	11	9	57	84	1	1	10	9	1	1	2.89E-15	1.26E-13	3.05E-23	4.07E-21	20	141	19	7	2	2 site_1988	0.870466 no		1.43E+08	1.43E+08	1.43E+08	1.43E+08	1.43E+08 aln1210		AGAACAT+TGAACAGG AgaacaT+aa+w.		TRUE	11.5	75	4	1	1	1	1	?GAACA?-I	1.43E+08	326 GGAATTCT		8 AGGTTATT	9 OMT		gRNA3		0	0	0.603	0.608599	aln_1210	Intron (XR_	7	1.43E+08	1.43E+08	11673	2	2 LOC105375544
chr11	27396935	27397735	11	2	128	45	1	1	11	2	1	1	7.74E-35	1.16E-32	2.68E-12	1.47E-10	13	173	13	13	2	2 site_1584	1.124103 no		27397336	27397340	27397335	27396935	27397735 aln1021		T-AACAGG-TGAACAGG t-aacaggaa+w.		TRUE	10.5	73.91	4	0	0	2	2	T-AACAGG-	27397615	280 TAAAAGGC		12 CTTTGCAAa	10 OMT		gRNA3		0.002	0.239521	0.025	0.148104	aln_1021	Intron (NM	11	27365961	27472790	106830	2	1 GRA4
chr11	1.07E+08	1.07E+08	12	1	83	9	11	1	12	1	1	1	1.19E-13	4.36E-12	0.013894	0.038572	13	92	13	7	2	2 site_3263	0.849844 no		1.07E+08	1.07E+08	1.07E+08	1.07E+08	1.07E+08 aln1903		TGAAGAG-TGAACAGG tgaaGag-aa+w.		TRUE	10.5	75	3	1	1	2	2	TGAA?AG-I	1.07E+08	-263 TGTACCCC		9 CTTTCCCCA	10 OMT		gRNA3		0.002	0.239521	0.222	0.28623	aln_1903	Distal Inter	11	1.07E+08	1.07E+08	1555	1	1 ASS1P13
chr1	41826904	41827704	7	4	49	16	1	1	7	4	1	1	4.38E-13	1.47E-11	0.000221	0.001218	11	65	11	6	2	2 site_5067	0.771521 no		41827304	41827304	41827304	41826904	41827704 aln3005		TGAACAGG TGAACAGGtgaacaggatCtw.		TRUE	10.5	70.83	6	1	1	0	0	TGAACAGG	41827068	-236 TTGCTGCC		11 TTTAGGTT	10 OMT		gRNA3		0.002	0.239521	0.066	0.163934	aln_3005	Intron (NM	1	41506365	42035934	529570	2	2 HIVEP3
chr15	76868021	76868821	7	3	35	14	2	2	7	3	1	1	2.44E-08	3.74E-07	0.003073	0.011345	10	49	10	5	2	2 site_7154	0.690196 no		76868421	76868421	76868021	76868021	76868821 aln4449		TGAACAAG TGAACAGG tgaacaAgaa+w.		FALSE	10.5	69.57	7	0	0	0	0	TGAACA?G	76868111	-310 ATCTTTTA		8 CTTTAGGT	11 OMT		gRNA3		0.002	0.239521	0.066	0.163934	aln_4449	Intron (NM	15	76347904	76905340	557437	2	2 SCAPER
chr16	5945954	5946754	3	7	42	88	1	1	3	6	1	1	3.48E-11	8.74E-10	2.26E-24	3.12E-22	10	130	9	14	2	2 site_2197	1.159701 no		5946355	5946355	5946354	5945954	5946754 aln1320		TGAGCCTC TGAACAGC tgaGcCTCa+rc.		TRUE	10.5	70.83	6	1	1	0	0	TGA?C???	5946313	-41 TTGGGTTT		8 TCCCTTCTC	9 OMT		gRNA3		0.002	0.239521	0.603	0.608599	aln_1320	Intron (NM	16	5239721	7713340	2473620	2	1 RBFOX1
chr17	33559853	33560653	6	4	32	29	1	1	5	4	1	1	1.72E-08	2.63E-07	6.99E-08	1.44E-06	10	61	9	7	2	2 site_5484	0.831087 no		33560251	33560253	33560253	33559853	33560653 aln3288		TGAACAAG TGAACAGG tgaacaAgaa+w.		TRUE	12.5	73.91	6	0	0	0	0	TGAACA?G	33559861	-392 TGTGTGAT		10 AAATGGTT	10 OMT		gRNA3		0	0	0.222	0.28623	aln_3288	Intron (XR_	17	33013087	34156768	1143682	2	2 ASIC2
chr5	1.09E+08	1.09E+08	4	6	24	50	1	1	4	5	1	1	2.3E-06	2.1E-05	1.08E-13	7.58E-12	10	74	9	8	2	2 site_4282	0.914989 no		1.09E+08	1.09E+08	1.09E+08	1.09E+08	1.09E+08 aln2512		TGAACAGG TGAACAGC tgaacaggGi+rc.		FALSE	11	78.26	1	0	0	2	4	TGAACAGG	1.09E+08	195 CTTTGCAA		10 TTGAAAAT	12 OMT		gRNA3		0.002	0.239521	0.025	0.148104	aln_2512	Distal Inter	5	1.09E+08	1.09E+08	520	1	1 RP5-20P3
chr6	19304817	19305617	7	3	51	25	1	1	5	3	1	1	1.25E-13	4.45E-12	8.59E-07	1.23E-05	10	76	8	10	2	2 site_4151	0.977724 no		19305218	19305218	19305217	19304817	19305617 aln2433		TGGAAAAC TGAACAGC tgGaAaAgaAw.		TRUE	10.5	69.57	7	0	0	0	0	TG?A?A?G	19305192	-25 GTTTTTATT		10 GTCTTCATA	9 OMT		gRNA3		0.002	0.239521	0.222	0.28623	aln_2433	Distal Inter	6	19317052	19322285	5234	2	1 LOC105374961
chr1	50405521	50406321	6	2	55	19	1	1	6	2	1	1	1.02E-14	4.11E-13	3.54E-05	0.000155	8	74	8	9	2	2 site_4294	0.966142 no		50405922	50405922	50405921	50405521	50406321 aln2519		TGCACACC TGAACAGC tgCacaCCa+rc.		TRUE	10.5	69.57	7	0	0	0	0	TG?ACA??	50405622	-299 TTTAGGTT		10 GAATTCTG	9 OMT		gRNA3		0.002	0.239521	0.222	0.28623	aln_2519	Promoter (	1	50405040	50406062	1023	2	2 FCF1P6
chr2	1.97E+08	1.97E+08	7	1	61	8	1	1	6	1	1	1	2.33E-16	1.13E-14	0.024492	0.061622	8	69	7	10	2	2 site_4721	0.993751 no		1.97E+08	1.97E+08	1.97E+08	1.97E+08	1.97E+08 aln2776		GGAACATC TGAACAGC tGgaacaTga+w.		TRUE	10.5	69.57	7	0	0	0	0	?GAACA?G	1.97E+08	174 AGTTGCTA		9 CTTGAAAA	9 OMT		gRNA3		0.002	0.239521	0.603	0.608599	aln_2776	Distal Inter	2	1.97E+08	1.97E+08	93704	2	2 PGAP1
chr2	1.25E+08	1.25E+08	3	4	19	41	1	1	3	4	1	1	4.7E-05	0.000284	3.45E-11	1.57E-09	7	60	7	9	2	2 site_5623	0.933053 no		1.25E+08	1.25E+08	1.25E+08	1.25E+08	1.25E+08 aln3388		TGGGCAGC TGAACAGC tgGGCagaGi+rc.		TRUE	10.5	70.83	6	1	1	0	0	TG??CAGG	1.25E+08	-39 GAAGTTAA		11 AATTAAAA	8 OMT		gRNA3		0.002	0.239521	0.066	0.163934	aln_3388	Distal Inter	2	1.25E+08	1.25E+08	107	1	1 RNU6-259P
chr14	45721853	45722653	2	4	21	33	1	1	2	4	1	1	1.42E-05	0.000102	5.59E-09	1.54E-07	6	54	6	9	2	2 site_6423	0.954243 no		45722251	45722253	45722253	45721853	45722653 aln3939		GGGACAGT TGAACAGC tGgGacag+gFw.		FALSE	11	75	4	1	1	1	1	?G?ACAG+	45722304	51 TTGCAGTG		9 TAGGTTAT	11 OMT		gRNA3		0.002	0.239521	0.066	0.163934	aln_3939	Distal Inter	14	45706258	45715602	9345	2	1 LINC02303
chr15	79549903	79550703	4	2	18	36	1	1	2	2	1	1	8.55E-05	0.00047	8.34E-10	2.83E-08	6	54	6	14	2	2 site_6422	1.130334 no		79550302	79550303	79550303	79549903	79550703 aln3974		TGAATGAG TGAAC-AGt tgaaT+aggatc.		TRUE	10.5	73.08	3	2	3	1	1	TGAA?+AG	79550615	312 ATGGAGTT		9 TCTTTGCA	8 OMT		gRNA3		0.002	0.239521	0.603	0.608599	aln_3974	Distal Inter	15	79556565	79560666	4102	2	1 TFDP1P3
chr16	24292549	24293349	3	3	24	26	1	1	3	2	1	1	2.3E-06	2.1E-05	4.6E-07	7.28E-06	6	50	5	10	2	2 site_7109	1 no		24292948	24292949	24292949	24292549	24293349 aln4422		GGAACAGC TGAACAGC tGgaacaggaa+w.		TRUE	10.5	69.57	7	0	0	0	0	TGAACA6G	24292884	-65 CTTCTCTTT		9 TTTCCTGTT	10 OMT		gRNA3		0.002	0.239521	0.222	0.28623	aln_4422	Intron (NM	16	24256335	24362412	106078	1	1 CACNG3
chr18	35759970	35760770	5	1	39	16	1	1	5	1	1	1	8.21E-16	3.78E-14	0.000221	0.001218	6	75	6	13	2	2 site_4245	1.09691 no		35760261	35761300	35760370	35759970	35760770 aln2493		TGAA-AG TGAACAGG tgaa-agAaa+w.		FALSE	10.5	73.91	4	0	0	2	2	TGAA-AG?	35760090	-280 TATATTGA		8 CTTTGGGT	10 OMT		gRNA3		0.002	0.239521	0.222	0.28623	aln_2493	Distal Inter	18	35690076	35730856	40781	2	2 LOC105372064
chr5	1.51E+08	1.51E+08	4	2	29	36	1	1	4	1	1	1	1.09E-07	1.4E-06	8.34E-10	2.83E-08	6	65	5	13	2	2 site_5139	1.113943 no		1.51E+08	1.51E+08	1.51E+08	1.51E+08	1.51E+08 aln3051		TAAACAGG TGAACAGC tAaacagGaa+w.		FALSE	12.5	78.26	4	0	0	1	1	?TAACAGG	1.51E+08	-29 CTCTTTGG		8 TTATTTCCT	12 OMT		gRNA3		0	0	0.025	0.148104	aln_3051	Exon (NM_	5	1.51E+08	1.51E+08	57074	2	2 ANXA6
chr5	1.28E+08	1.28E+08	4	2	35	13	1	1	3	2	1	1	2.69E-09	4.86E-08	0.004368	0.0147	6	46	5	9	2	2 site_7871	0.963788 no		1.28E+08	1.28E+08	1.28E+08	1.28E+08	1.28E+08 aln4954		TGTCACTC TGAACAGC tgTacaCTaTa+c.		TRUE	10.5	70.83	6	1	1	0	0	TG?ACA??	1.28E+08	-8 CCTTTAGG		11 AGGTTATT	9 OMT		gRNA3		0.003	0.239521	0.066	0.163934	aln_4954	Intron (NM	5	1.28E+08	1.29E+08	280337	2	1 FBN2
chr8	5999708	6000508	4	1	52	19	1	1	4	1	1	1	6.69E-14	2.45E-12	3.54E-05	0.000265	5	71	5	14	2	2 site_4571	1.152288 no		6000108	6000108	6000108	5999708	6000508 aln2688		TGAGACAA TGA-ACAGt tgaAcaAgaFw.		TRUE	10.5	72	5	2	2	0	0	TGA+ACA?	6000085	-23 TGGGTTTG		8 GTTAATAA	9 OMT		gRNA3		0.002	0.239521	0.603	0.608599	aln_2688	Intron (XR_	8	5858276	6004226	145951	2	2 LOC105377795
chr14	75724744	75725544	92	41	1147	305	777	777	31	31	11	11	1.3E-10	3E-09	1	1	133	1452	62	23	2	1 site_301	1.369575 no		75725145	75725145	75725144	75724744	75725544 aln291		TTAA-AGG/TGAACAGC tTaa-aggaa rc.		FALSE	10.5	73.91	5	0	0	1	1	T?AA-AGG/	75725454	310 GGTTATTTt		11 TTTACATTC	9 OMT		gRNA3		0.002	0.239521	0.066	0.163934	aln_291	Intron (NM	14	75661246	75955079	293834	1	1 TTLL5
chr2	48701119	48701919	75	40	669	239	465	465	51	27	16	16	4.99E-06	4.22E-05	1	1	115	908	78	12	2	1 site_405	1.065991 no		48701520	48701524	48701519	48701119	48701919 aln373		TGAATAAG TGAACAGC tgaaTaAg+rc.		TRUE	10.5	70.83	6	1	1	0	0	TGAA?A?G	48701692	173 CTTTGGGT		10 ACAATGAG	8 OMT		gRNA3		0.002	0.239521	0.222	0.28623	aln_373	Intron (NM	2	48686774	48755724	68951	2	1 LHCGR
chr4	71945857	71946657	86	23	845	210	425	425	33	16	6	6	1.51E-24	1.42E-22	1	1	109	1055	49	22	2	1 site_360	1.333056 no		71946258	71946262	71946257	71945857	71946657 aln342		TGAATGTG TGAACAGC tgaaTGTgac+rc.		TRUE	11.5	73.91	5	0	0	1	1	?GAA??TG	71946473	216 TGCCTTTAC		15 TGAAGGTT	9 OMT		gRNA3		0	0	0.001	0.058824	aln_342	Distal Inter	4	72032000	72148305	116306	1	1 NPFFR2
chr2	1.62E+08	1.62E+08	62	21	582	121	402	402	35	18	10	10	1.3E-05	0.000101	1	1	83	703	53	13	2	1 site_467	1.122679 no		1.62E+08	1.62E+08	1.62E+08	1.62E+08	1.62E+08 aln419		TGAAGAGC TGAACAGC tgaaGaggaTw.		TRUE	11.5	73.91	5	0	0	1	1	T GAA?AGG	1.62E+08	156 TTTTAAATC		9 CCTTTAGG	9 OMT		gRNA3		0	0	0.603	0.608599	aln_419	Intron (NM	2	1.62E+08	1.62E+08	81971	2	2 DPP4
chr7	48437542	48438342	14	3	103	17	37	37	11	2	2	2	2.39E-07	2.89E-06	0.999111	1	17	120	13	9	2	1 site_2396	0.965238 no		48437338	48438010	48437942	48437542	48438342 aln1423		TGCCCAGA TGAACAGG tgCCcaGa+rc.		TRUE	11.5	73.91	5	0	0	1	1	?GCCAGA	48437829	-113 TTTGCAAA		9 ACATTGAA	10 OMT		gRNA3		0	0	0.222	0.28623	aln_1423	Intron (XM	7	48171458	48647497	476040	1	1 ABCA13
chr19	53115329	53116129	12	4	72	32	37	37	12	4	1	1	0.002725	0.008738	0.838662	1	16	104	16	7	2	1 site_2818	0.812913 no		53115730	53115730	53115729	53115329	53116129 aln1669		TGACCAGA TGAACAG+tgACcagTtc.		TRUE	10.5	70.83	6	1	1	0	0	TGA?CAG+	53115817	88 ATGAGCAC		9 AAAAGGG1	9 OMT		gRNA3		0.002	0.239521	0.603	0.608599	aln_1669	5' UTR	19	53107879	53132910	25032	2	1 ZNF415
chr2	78991775	78992575	11	5	102	61	67	67	8	5	1	1	0.023034	0.051864	0.836888	1	16	163	13	13	2	1 site_1687	1.098244 no		78992176	78992176	78992175	78991775	78992575 aln1070		TTAAGAGG TGAACAGC tTaaGagg+rc.		TRUE	10.5	70.83	6	1	1	0	0	T?AAAGG	78992559	384 CAGTCTTC		11 ATACAGGA	8 OMT		gRNA3		0.002	0.239521	0.066	0.163934	aln_1070	Distal Inter	2	79025702	79028501	2800	1	1 REG3G
TOTAL HITS																			488																																	

CasPER

chr.	start	end	Casper.Re pl.g3.KLR C1.Aus_re ad_uniqu e	Casper.Re pll.g3.KLR C1.Aus_re ad_uniqu e	Casper.Re pl.g3.KLR C1.Aus_re ad	Casper.Re pll.g3.KLR C1.Aus_re ad	Casper.Re pl.g3.KLR C1.Aus_re ad_ctl	Casper.Re pll.g3.KLR C1.Aus_re ad_ctl	Casper.Re pl.g3.KLR C1.Aus_hi ts	Casper.Re pll.g3.KLR C1.Aus_hi ts	Casper.Re pl.g3.KLR C1.Aus_hi ts_ctl	Casper.Re pll.g3.KLR C1.Aus_hi ts_ctl	Casper.Re pl.g3.KLR C1.Aus_p value	Casper.Re pll.g3.KLR C1.Aus_p value	Casper.Re pl.g3.KLR C1.Aus_a dj.pvalue	Casper.Re pll.g3.KLR C1.Aus_a dj.pvalue	Casper.Re pl.g3.KLR reads_ unique	Casper.Re pll.g3.KLR reads_ unique	reads	hits	read/hit	NB_OVL	NB_SIGNI F	site	log10read hits	BarcodeH opping	top_coor start.site	d end.site	start.bin	end.bin	aln_id	pattern_ gRNA3	subject_ gRNA3	aln_sum_ _gRNA3	aln_orien t_gRNA3	NRG_gR NA3	score_ gRNA	homology _gRNA3	nb_mism _gRNA3	nb_ins_ gRNA3	length_in s_gRNA3	nb_del_ gRNA3	length_de l_gRNA3	aln_abs_s tart_gR NA3	aln_rel_st art_gRN A3	lcss_fw_l ength_O N1	lcss_rc_le ngth_O N1	OMT_adj OMT_pv_ _gRNA3	OMT_adj _pv_gR NA3	HMT_adj HMT_pv_ _ON1	HMT_adj _pv_ON 1	alignment _id	annotatio n	geneChr	geneStart	geneEnd	geneLeng th	geneStra nd	geneId
chr12	10450208	10451808	10636	12245	3737446	3680460	25039	25063	5955	6415	41	39	0	0	0	0	22881	7417906	12370	600	1	F	site_1	2.777912	no	10438623	10468967	10451008	10450608	10451408	aln1	TGAACAGCTGAACAGCtgaacaggaa rc.	TRUE	20.5	91.3	2	0	0	0	0 TGAACAGC	10451054	46 CAAACTTC	500 GGGTTTGC	10 OMT	ON1	gRNA3	ON1	0	0	0.603	0.610942	aln_498	Intron (NM	19	38433691	38587564	153874	1	RYR1
chr6	63460955	63461755	3	3	11	14	2	2	3	3	1	1	0.012724	0.19715	0.004092	0.03913	6	25	6	4	2	2	site_3129	0.619789	no	63461356	63461356	63461355	63460955	63461755	aln1375	TTCACAGGTGAACAGCtTCacaggaa rc.	TRUE	10.5	69.23	5	1	3	0	0 TTPACAGG	63461543	188 GTTATTTCI	12 AGCATATC	10 OMT	gRNA3	0.002	0.236686	0.025	0.188356	aln_1375	Intron (XM	6	63275951	63673607	297657	2	LGSN
chr11	27396935	27397735	3	3	7	15	1	1	3	3	1	1	0.038213	0.320511	0.000564	0.009371	6	22	6	4	2	2	site_3701	0.564271	no	27397336	27397336	27397335	27396935	27397735	aln1686	T-AACAGG.TGAACAGCt-aacaggaa fw.	TRUE	10.5	73.91	4	0	0	2	2 T-AACAGG	27397615	280 TAAAAGGC	12 CTTTGCAA	10 OMT	gRNA3	0.002	0.236686	0.025	0.188356	aln_1686	Intron (NM	11	27365961	27472790	106830	2	LGR4
chr1	50405521	50406321	2	3	7	11	1	1	2	3	1	1	0.038213	0.320511	0.005545	0.043657	5	18	5	4	2	2	site_4794	0.556303	no	50405922	50405922	50405921	50405521	50406321	aln2352	TGCACACCTGAACAGCtgCacaCCa rc.	TRUE	10.5	69.57	7	0	0	0	0 TGACACA??	50405622	-299 TTTAGGTT	10 GAATTCTG	9 OMT	gRNA3	0.002	0.236686	0.222	0.304945	aln_2352	Promoter (	1	50405040	50406062	1023	2	FCF1P6
chr11	1.07E+08	1.07E+08	1	1	9	7	1	1	1	1	1	1	0.011987	0.186108	0.049455	0.181964	2	16	2	8	2	2	site_6109	0.90309	no	1.07E+08	1.07E+08	1.07E+08	1.07E+08	1.07E+08	aln3202	TGAAGAG-TGAACAGCtgaaGag-ai fw.	TRUE	10.5	75	3	1	1	2	2 TGAA?AG-	1.07E+08	-263 TGTACCCC	9 CTTTCCCCI	10 OMT	gRNA3	0.002	0.236686	0.222	0.304945	aln_3202	Distal Inter	11	1.07E+08	1.07E+08	1555	1	AS51P13
chr1	41826904	41827704	4	2	9	7	1	1	4	2	1	1	0.011987	0.186108	0.049455	0.181964	6	16	6	3	2	2	site_5672	0.425969	no	41827304	41827304	41827304	41826904	41827704	aln2932	TGAACAGCTGAACAGCtgaacaggaat fw.	TRUE	10.5	70.83	6	1	1	0	0 TGAACAGC	41827068	-236 TTGCTGCC	11 TTTAGGTT	10 OMT	gRNA3	0.002	0.236686	0.066	0.188356	aln_2932	Intron (NM	1	41506365	42035934	529570	2	HIVEP3
TOTAL HITS																					39																																				
chr2	2.36E+08	2.36E+08	0	16	0	9021	0	1	0	5	0	1	1	1	0	0	16	9021	5	1804	1	1	site_70	3.256285	no	2.36E+08	2.36E+08	2.36E+08	2.36E+08	2.36E+08	aln70	CGAACAGCTGAACAGCCgaacagga rc.	FALSE	10.5	70.83	6	1	1	0	0 ?GAACAGC	2.36E+08	-148 TTTCCTGT	10 AGGTTTTC	9 OMT	gRNA3	0.002	0.236686	0.222	0.304945	aln_70	Exon (XR_C	2	2.35E+08	2.36E+08	637751	1	AGAP1
chr7	1.3E+08	1.3E+08	10	0	8530	0	1	0	5	0	1	0	0	0	1	1	10	8530	5	1706	1	1	site_78	3.231979	no	1.3E+08	1.3E+08	1.3E+08	1.3E+08	1.3E+08	aln78	TGAACAGTTGAACAGCtgaacagTaC fw.	TRUE	10.5	69.57	7	0	0	0	0 TGAACAG?	1.3E+08	-196 AAAATCCT	10 TACTCTAT	8 OMT	gRNA3	0.002	0.236686	0.222	0.304945	aln_78	Intron (XM	7	1.3E+08	1.3E+08	122229	2	UBE2H
chr1	2.14E+08	2.14E+08	0	10	0	6787	0	1	0	4	0	1	1	1	0	0	10	6787	4	1697	1	1	site_98	3.229618	no	2.14E+08	2.14E+08	2.14E+08	2.14E+08	2.14E+08	aln98	TGATCACT.TGAACAGCtgaTcaCTa rc.	TRUE	10.5	69.57	7	0	0	0	0 TGA?CA??	2.14E+08	237 AAGATATA	10 CACATTCC	12 OMT	gRNA3	0.002	0.236686	0.025	0.188356	aln_98	Intron (XM	1	2.14E+08	2.14E+08	58360	1	PROX1
chr6	507840	508640	0	11	0	6264	0	1	0	6	0	1	1	1	0	0	11	6264	6	1044	1	1	site_108	3.0187	no	508239	508249	508240	507840	508640	aln108	TGTAACAGTG-AACAG tg+aacaggc rc.	TRUE	10.5	75	3	1	1	2	2 TG+AACAG	508514	274 TTAAATGC	9 ATCTCTGC	9 OMT	gRNA3	0.002	0.236686	0.603	0.610942	aln_108	3' UTR	6	485154	693139	207986	2	EXOC2