
Supplementary information

Programmable deletion, replacement, integration and inversion of large DNA sequences with twin prime editing

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Supplementary Information

Programmable deletion, replacement, integration, and inversion of large DNA sequences with twin prime editing

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Supplementary Table 1: Sequences of pegRNAs and sgRNAs used in mammalian cell experiments

All sequences are shown in 5' to 3' orientation. pegRNAs are a concatenation of the spacer sequence, the sgRNA scaffold, and the 3' extension (contains PBS and RT template, and a 3' motif in the case of epegRNAs).

sgRNA scaffold sequence (5' to 3')

gttttagagctagaaatagcaagttaaaataaggctagtcctgtatcaacttgaaaaagtggcaccgagtcggtgc

Figure 1c pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
HEK3_attB_A_38	ggcccagactgagcacgtga	atgatcctgacgacggagaccgcccgtcgtcgacaagcccgtgctcagttg	indicated on the x-axis indicated on the x-axis indicated on the x-axis indicated on the x-axis indicated on the x-axis indicated on the x-axis indicated on the x-axis indicated on the x-axis indicated on the x-axis indicated on the x-axis
HEK3_attB_A_34	ggcccagactgagcacgtga	tcctgacgacgagaccgcccgtcgtcgacaagcccgtgctcagttg	
HEK3_attB_A_30	ggcccagactgagcacgtga	gacgacgagacgacgcccgtcgtcgacaagcccgtgctcagttg	
HEK3_attB_B_38	gtcaaccagtatcccgggtgc	ggcttctgacgacgacgcccgtcgtcgacgagatcatccgggatactgg	
HEK3_attB_B_34	gtcaaccagtatcccgggtgc	tgctgacgacgacgcccgtcgtcgacgagatcatccgggatactgg	
HEK3_attB_B_30	gtcaaccagtatcccgggtgc	gacgacgacgcccgtcgtcgacgagatcatccgggatactgg	
HEK3_attP_A_43	ggcccagactgagcacgtga	taccgtacaccactgagaccgcccgtggtgacagacaaacctcgtgctcagttg	
HEK3_attP_A_39	ggcccagactgagcacgtga	gtacaccactgagaccgcccgtggtgacagacaaacctcgtgctcagttg	
HEK3_attP_A_35	ggcccagactgagcacgtga	accactgagaccgcccgtggtgacagacaaacctcgtgctcagttg	
HEK3_attP_B_44	gtcaaccagtatcccgggtgc	gtctggtcaaccaccgcccgtgctcagttggtgacggtacaaacctccgggatactgg	
HEK3_attP_B_40	gtcaaccagtatcccgggtgc	gggtcaaccaccgcccgtgctcagttggtgacggtacaaacctccgggatactgg	
HEK3_attP_B_36	gtcaaccagtatcccgggtgc	aaccaccgcccgtcagttggtgacggtacaaacctccgggatactgg	
Figure 2b pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
PE3_HEK3_FKBP_ins12 bp	ggcccagactgagcacgtga	tggaggaaagcagggtctcttctctgcatcacacctgcactcccgtgctcagttg	indicated on the x-axis
PE3_HEK3_FKBP_ins36 bp	ggcccagactgagcacgtga	tggaggaaagcagggtctcttctctgcatcacacctgcactcccgtggttcc	indicated on the x-axis
PE3_HEK3_FKBP_ins10 8bp	ggcccagactgagcacgtga	tggaggaaagcagggtctcttctctgcatcaaaaatttcttccatttcaagcatccc	indicated on the x-axis
twiPE_HEK3_FKBP_in s108bp_A	ggcccagactgagcacgtga	gggtgtagtgcaccacgcaggtctggccgcgcttggggaaggtgcccgtctctg	indicated on the x-axis
twiPE_HEK3_FKBP_in s108bp_B	gtcaaccagtatcccgggtgc	ggagatggtttccacctgcactcccgtgctcagttg	
sgRNA	spacer sequence	3' extension	indicated on the x-axis
HEK3_3b_+90_nicking	gtcaaccagtatcccgggtgc	accacgcaggtctgcccgcgttggggaaggtgcgcccgtctctggtggagatggtt	
		tcacacctgcactcccgtgctcagttg	indicated on the x-axis
		accttcccaagcgcggcagacgtcgtggtgcactacaccgggatgcttgaagat	
		ggaaagaatttccgggatactgg	
Figure 2c pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
PAH_E4.2_45	gcccagaaccattcaagagc	gttcggtctccgtaggacaagattgattagcgaacctatcaagttctgaatggttc	exon 4 24-bp overlap (64 bp recoded)
PAH_E4.4_43	gtacgggcatggactcaca	aaatctgtctctacggagccgaactgacgctgatcatcctgtgagtcattggcc	exon 4 24-bp overlap (64 bp recoded)
PAH_E4.2_45_EvoPreQ1	gcccagaaccattcaagagc	gttcggtctccgtaggacaagattgattagcgaacctatcaagttctgaatggttctct	exon 4 24-bp overlap epegRNA (64 bp recoded)
PAH_E4.4_43_EvoPreQ1	gtacgggcatggactcaca	aaatctgtctctacggagccgaactgacgctgatcatcctgtgagtcattggcctctct	exon 4 24-bp overlap epegRNA (64 bp recoded)
PAH_E4.2_50	gcccagaaccattcaagagc	gtcaagttcggtctccgtaggacaagattgattagcgaacctatcaagttctgaatggtt	exon 4 36-bp overlap (64 bp recoded)
PAH_E4.4_50	gtacgggcatggactcaca	gtcaatcaaatctgtctctacggagccgaactgacgctgatcatcctgtgagtcattgg	exon 4 36-bp overlap (64 bp recoded)
PAH_E4.2_50_EvoPreQ1	gcccagaaccattcaagagc	gtcaagttcggtctccgtaggacaagattgattagcgaacctatcaagttctgaatggtt	exon 4 36-bp overlap epegRNA (64 bp recoded)
PAH_E4.4_50_EvoPreQ1	gtacgggcatggactcaca	gtcaatcaaatctgtctctacggagccgaactgacgctgatcatcctgtgagtcattgg	exon 4 36-bp overlap epegRNA (64 bp recoded)
PAH_E4.2_62	gcccagaaccattcaagagc	aggatgatcagcgctcaagttcggctccgtaggacaagattgattagcgaacctatcaa	exon 4 59-bp overlap (64 bp recoded)
PAH_E4.4_61	gtacgggcatggactcaca	gttctggaatgggttc	exon 4 59-bp overlap (64 bp recoded)
PAH_E4.2_62_EvoPreQ1	gcccagaaccattcaagagc	aggatgatcagcgctcaagttcggctccgtaggacaagattgattagcgaacctatcaa	exon 4 59-bp overlap epegRNA (64 bp recoded)
PAH_E4.4_61_EvoPreQ1	gtacgggcatggactcaca	gttctggaatgggttc	exon 4 59-bp overlap epegRNA (64 bp recoded)

PAH_E7.2_34	gtggtttccgcctccgacctg	agaagaagtctctactgctcaagagcccgcaacgggtcggaggcg	exon 7 22-bp overlap (46 bp recoded)
PAH_E7.5_34	gagtggaagactcgggaaggcc	tcttgagcagtagagactttctgggggtctcgccttccgagttcttc	exon 7 22-bp overlap (46 bp recoded)
PAH_E7.2_34_EvoPreQ1	gtggtttccgcctccgacctg	agaagaagtctctactgctcaagagcccgcaacgggtcggaggcgtctctcttgcagc	exon 7 22-bp overlap epegRNA (46 bp recoded)
PAH_E7.5_34_EvoPreQ1	gagtggaagactcgggaaggcc	cggttctatctagttacgcgttaaaccaactagaaa	exon 7 22-bp overlap epegRNA (46 bp recoded)
PAH_E7.2_44	gtggtttccgcctccgacctg	tcttgagcagtagagactttctgggggtctcgccttccgagttctctcttgcagc	exon 7 42-bp overlap (46 bp recoded), exon 7 24-bp overlap (64 bp recoded)
		cggttctatctagttacgcgttaaaccaactagaaa	exon 7 42-bp overlap (46 bp recoded)
		gagacccccagaaagtctctactgctcaagagcccgcaacgggtcggaggcg	exon 7 42-bp overlap (46 bp recoded)
PAH_E7.5_44	gagtggaagactcgggaaggcc	gtgcccgggctcttgagcagtagagactttctgggggtctcgccttccgagttcttc	exon 7 42-bp overlap (46 bp recoded)
PAH_E7.2_44_EvoPreQ1	gtggtttccgcctccgacctg	gagacccccagaaagtctctactgctcaagagcccgcaacgggtcggaggcgtct	exon 7 42-bp overlap epegRNA (46 bp recoded), exon 7 24-bp overlap epegRNA (64 bp recoded)
		ctctcttgacgcgggtctatctagttacgcgttaaaccaactagaaa	exon 7 42-bp overlap epegRNA (46 bp recoded)
PAH_E7.5_44_EvoPreQ1	gagtggaagactcgggaaggcc	gtgcccgggctcttgagcagtagagactttctgggggtctcgccttccgagttctctct	exon 7 42-bp overlap epegRNA (46 bp recoded)
PAH_E7.6_44	gtctgatgtactgtgtgcag	ctctcttgacgcgggtctatctagttacgcgttaaaccaactagaaa	exon 7 24-bp overlap (64 bp recoded)
		agttagagactttctgggggtctcgcattccgcgtgtttcattgcacacagtaca	exon 7 24-bp overlap epegRNA (64 bp recoded)
PAH_E7.6_44_EvoPreQ1	gtctgatgtactgtgtgcag	agttagagactttctgggggtctcgcattccgcgtgtttcattgcacacagtacatctctc	exon 7 47-bp overlap (64 bp recoded)
PAH_E7.2_55	gtggtttccgcctccgacctg	tcttgacgcgggtctatctagttacgcgttaaaccaactagaaa	exon 7 47-bp overlap (64 bp recoded)
PAH_E7.6_56	gtctgatgtactgtgtgcag	acgcgggaatgcgagacccccagaaagtctctactgctcaagagcccgcaacggg	exon 7 47-bp overlap (64 bp recoded)
		tcggaggcg	exon 7 47-bp overlap (64 bp recoded)
PAH_E7.2_55_EvoPreQ1	gtggtttccgcctccgacctg	gggctcttgagcagtagagactttctgggggtctcgcattccgcgtgtttcattgcaca	exon 7 47-bp overlap epegRNA (64 bp recoded)
PAH_E7.6_56_EvoPreQ1	gtctgatgtactgtgtgcag	cagtaca	exon 7 47-bp overlap epegRNA (64 bp recoded)
		acgcgggaatgcgagacccccagaaagtctctactgctcaagagcccgcaacggg	
		tcggaggcgctctctcttgacgcgggtctatctagttacgcgttaaaccaactagaaa	
		gggctcttgagcagtagagactttctgggggtctcgcattccgcgtgtttcattgcaca	
		cagtacatctctctcttgacgcgggtctatctagttacgcgttaaaccaactagaaa	

Figure 2e
pegRNA

	spacer sequence	3' extension	Edits made by the specified pegRNA
HEK3_DF_A_SA_del77nt	ggcccagactgagcacgtga	tcctctgccatcacgtgctcagttctg	SA (Δ 77nt)
HEK3_DF_B_SA_del77nt	gtcaaccagtatcccggtgc	tgatggcagaggaccgggatactgg	SA (Δ 77nt)
HEK3_DF_A_SA_del56nt	ggcccagactgagcacgtga	tggagggaagcagggtctcttctctgccatcacgtgctcagttctg	SA (Δ 56nt)
HEK3_DF_B_SA_del56nt	gtcaaccagtatcccggtgc	tgatggcagaggaaagggaagccctgcttctccaccgggatactgg	SA (Δ 56nt)
HEK3_DF_A_HA_del64nt	ggcccagactgagcacgtga	tgcaggagctgcatcctctgccatcacgtgctcagttctg	HA (Δ 64nt)
HEK3_DF_B_HA_del64nt	gtcaaccagtatcccggtgc	tgatggcagaggatgcagctcctgcaccgggatactgg	HA (Δ 64nt)
HEK3_DF_A_PD_del90nt	ggcccagactgagcacgtga	gcccagccaaactgtcaaccagtatcccggtgctcagttctg	PD (Δ 90nt)
HEK3_DF_B_PD_del90nt	gtcaaccagtatcccggtgc	gggtcaatccttggggcccagactgagcacccgggatactgg	PD (Δ 90nt)
HEK3_DF_A_SA_del77nt_EvoPreQ1	ggcccagactgagcacgtga	tcctctgccatcacgtgctcagttctgtaataacgcgttctatctagttacgcgttaaac	SA-EvoPreQ1 (Δ 77nt)
HEK3_DF_B_SA_del77nt_EvoPreQ1	gtcaaccagtatcccggtgc	tgatggcagaggaccgggatactggaaataacgcgttctatctagttacgcgttaa	SA-EvoPreQ1 (Δ 77nt)
HEK3_DF_A_SA_del56nt_EvoPreQ1	ggcccagactgagcacgtga	accactagaaa	SA-EvoPreQ1 (Δ 56nt)
HEK3_DF_B_SA_del56nt_EvoPreQ1	gtcaaccagtatcccggtgc	tggagggaagcagggtctcttctctgccatcacgtgctcagttctgtaataatcgcgg	SA-EvoPreQ1 (Δ 56nt)
HEK3_DF_A_HA_del64nt_EvoPreQ1	ggcccagactgagcacgtga	ttctatctagttacgcgttaaaccaactagaaa	SA-EvoPreQ1 (Δ 64nt)
HEK3_DF_B_HA_del64nt_EvoPreQ1	gtcaaccagtatcccggtgc	tgatggcagaggaaagggaagccctgcttctccaccgggatactggaaaaaaacgc	SA-EvoPreQ1 (Δ 64nt)
HEK3_DF_A_PD_del90nt_EvoPreQ1	ggcccagactgagcacgtga	ggttctatctagttacgcgttaaaccaactagaaa	SA-EvoPreQ1 (Δ 90nt)
HEK3_DF_B_PD_del90nt_EvoPreQ1	gtcaaccagtatcccggtgc	tgcaggagctgcatcctctgccatcacgtgctcagttctgataataacgcggttctatc	SA-EvoPreQ1 (Δ 90nt)
		agttacgcgttaaaccaactagaaa	
		tgatggcagaggatgcagctcctgcaccgggatactggaaaaaggcgcggttctat	
		ctagttacgcgttaaaccaactagaaa	
		gcccagccaaactgtcaaccagtatcccggtgctcagttctgtaataacgcggtt	
		ctatctagttacgcgttaaaccaactagaaa	
		gggtcaatccttggggcccagactgagcacccgggatactggaaataatcgcggt	
		tctatctagttacgcgttaaaccaactagaaa	

Figure 2f
pegRNA

	spacer sequence	3' extension	Edits made by the specified pegRNA
DMD-Exon51-A1_a_SA	gattggctttgatttccta	ttgaataggaagtaaattaattgaagctggaccctagggaatacaa	SA-1 (Δ 780nt)
DMD-Exon51-B1_A1_b_SA	gcagttgcctaagaactggt	taggggtccagcttcaaaftaatttacttctattcaaaagtcttaggc	SA-1 (Δ 780nt)
DMD-Exon51-a3-b1_a_PD	gtatatgattgttactgaga	tgctgagagagaacagttgcctaagaactcagtaacaat	PD-1 (Δ 627nt); PD-2 (Δ 627nt)

DMD-Exon51-b1-a3_a- PD	gcagttgcctaagaactggt	accacttcccaaatgtatatgattgttactgagttcttagg	PD-1 (Δ 627nt)
DMD-Exon51-b1-a3_b- PD	gcagttgcctaagaactggt	accacttcccaaatgtatatgattgttactgagttcttaggca	PD-2 (Δ 627nt)
DMD-Exon51-A3_b_attB	gtatatgattgttactgaga	atgatcctgacgacggagaccgctgctgcagaagcccagtaacaatc	tPE-1 attB (Δ 589nt); tPE-2 attB (Δ 589nt); tPE-1 attB (Δ 558nt); tPE-2 attB (Δ 558nt)
DMD-Exon51-A3_c_attB	gtatatgattgttactgaga	atgatcctgacgacggagaccgctgctgcagaagcccagtaacaatcata	tPE-3 attB (Δ 589nt); tPE-4 attB (Δ 589nt); tPE-3 attB (Δ 558nt); tPE-4 attB (Δ 558nt)
DMD-Exon51-B1_b_attB	gcagttgcctaagaactggt	ggcttgtcgacgacggcggtctccgtcgtcaggatcatagttcttaggc	tPE-1 attB (Δ 589nt); tPE-3 attB (Δ 589nt)
DMD-Exon51-B1_c_attB	gcagttgcctaagaactggt	ggcttgtcgacgacggcggtctccgtcgtcaggatcatagttcttaggcaac	tPE-2 attB (Δ 589nt); tPE-4 attB (Δ 589nt)
DMD-Exon51-B2_b_attB	gaggagagtaaaagtattgg	ggcttgtcgacgacggcggtctccgtcgtcaggatcatatcatttactc	tPE-1 attB (Δ 558nt); tPE-3 attB (Δ 558nt)
DMD-Exon51-B2_c_attB	gaggagagtaaaagtattgg	ggcttgtcgacgacggcggtctccgtcgtcaggatcatatcatttactctcc	tPE-2 attB (Δ 558nt); tPE-4 attB (Δ 558nt)
sgRNA	spacer sequence		Edits made by the paired sgRNA
DMD-Exon51-A1	gattggctttgatttcccta		Cas9 (Δ 818nt)
DMD-Exon51-A3	gtatatgattgttactgaga		Cas9 (Δ 627nt)
DMD-Exon51-B1	gcagttgcctaagaactggt		Cas9 (Δ 818nt); Cas9 (Δ 627nt)

Figure 3b
pegRNA

	spacer sequence	3' extension	Edits made by the specified pegRNA
CCR5_A223c	gtcatcctgataaactgcaaa	atgatcctgacgacggagaccgctgctgcagaagccgagtttaccagg	indicated on the x-axis
CCR5_B272a	gaaggaaaaacaggtcagaga	ggcttgtcgacgacggcggtctccgtcgtcaggatcatctgacctg	indicated on the x-axis
CCR5_B291b	gcccgaaaggggacagtaaga	ggcttgtcgacgacggcggtctccgtcgtcaggatcattactgtccct	indicated on the x-axis
CCR5_B305a	ggcagcatagttagcccgaga	ggcttgtcgacgacggcggtctccgtcgtcaggatcatgggtcact	indicated on the x-axis
CCR5_B326b	gatttccaaagtcctcactggg	ggcttgtcgacgacggcggtctccgtcgtcaggatcatagtgggacttfg	indicated on the x-axis
CCR5_B330b	gttgtatttccaaagtccac	ggcttgtcgacgacggcggtctccgtcgtcaggatcatggacttfgaa	indicated on the x-axis
CCR5_A260c	gtgacatctacctgctcaacc	atgatcctgacgacggagaccgctgctgcagaagcctgagcaggtagat	indicated on the x-axis
CCR5_B305c	ggcagcatagttagcccgaga	ggcttgtcgacgacggcggtctccgtcgtcaggatcatgggtcactatgc	indicated on the x-axis
CCR5_B330c	gttgtatttccaaagtccac	ggcttgtcgacgacggcggtctccgtcgtcaggatcatggacttfgaaat	indicated on the x-axis
CCR5_A325b	gtcactatgtctgcccccag	atgatcctgacgacggagaccgctgctgcagaagccgcgccgagcat	indicated on the x-axis
CCR5_B414a	ggtacatctgattgtcagg	ggcttgtcgacgacggcggtctccgtcgtcaggatcatgacaatcga	indicated on the x-axis
CCR5_A360b	gacaagtgtgcaactcttgac	atgatcctgacgacggagaccgctgctgcagaagcccaaggttgacac	indicated on the x-axis
CCR5_A506c	gacaagtgtgacacttggg	atgatcctgacgacggagaccgctgctgcagaagcccaaggtgacactt	indicated on the x-axis
CCR5_B584a	gtatgaaaaatgagagctgc	ggcttgtcgacgacggcggtctccgtcgtcaggatcatgctctcatt	indicated on the x-axis
CCR5_A509a	gaagtgtgacacttgggtgg	atgatcctgacgacggagaccgctgctgcagaagccccaagtgga	indicated on the x-axis
CCR5_B535c	gacttgtaaaagtattcc	ggcttgtcgacgacggcggtctccgtcgtcaggatcatatctttaccag	indicated on the x-axis
CCR5_A531c	gtctgttttgcgtctctccc	atgatcctgacgacggagaccgctgctgcagaagccagagacgcaaaa	indicated on the x-axis
CCR5_B584b	gtatgaaaaatgagagctgc	ggcttgtcgacgacggcggtctccgtcgtcaggatcatgctctcatttc	indicated on the x-axis

Figure 3c
pegRNA

	spacer sequence	3' extension	Edits made by the specified pegRNA
AAVS1_A1077b	gcagagccaggaaacccctgt	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctggggtctctgg	indicated on the x-axis
AAVS1_B1154b	gtccttggcgaagcccaggag	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctctgggtgcc	indicated on the x-axis
AAVS1_A1098b	gggaaggggcagagagagcca	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctctctctgcc	indicated on the x-axis
AAVS1_B1154a	gtccttggcgaagcccaggag	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctctgggttg	indicated on the x-axis
AAVS1_A1246c	gaatatgtcccagatagcac	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctctatctgggacat	indicated on the x-axis
AAVS1_B1314b	gtgcgtcctaggtgttcacc	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctgaacacctagg	indicated on the x-axis
AAVS1_B1376a	gtccttggcaggggtgtgtgtg	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctcacagccct	indicated on the x-axis
AAVS1_A1267c	ggggactctttaagaaaaga	taccgtacaccactgagaccgcggtgtgtgaccagacaaaccttctctaaagagt	indicated on the x-axis
AAVS1_A1293a	gagaaagagaaagggagtag	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctctcccttc	indicated on the x-axis
AAVS1_A1307b	gagtagagcgccacgacc	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctctggtgccct	indicated on the x-axis
AAVS1_B1314a	gtgcgtcctaggtgttcacc	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctgaacacct	indicated on the x-axis
AAVS1_A1582c	gatcagtgaacgcaccaga	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctggtgctttcact	indicated on the x-axis
AAVS1_B1640a	gtgacctgtcccgttctcag	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctagaaccggg	indicated on the x-axis
AAVS1_B1676a	gagcttggcagggggtggga	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctacccctgc	indicated on the x-axis
AAVS1_B1701a	gagccagagagatcctggg	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctagatctc	indicated on the x-axis
AAVS1_B1705b	gatggagccagagagatcc	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctctctctggc	indicated on the x-axis
AAVS1_A1615b	gcagctcaggttctgggaga	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctcccgaacctg	indicated on the x-axis
AAVS1_B1640a	gtgacctgtcccgttctcag	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctagaaccggg	indicated on the x-axis
AAVS1_A1615a	gcagctcaggttctgggaga	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctcccgaacc	indicated on the x-axis
AAVS1_B1676a	gagcttggcagggggtggga	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctacccctgc	indicated on the x-axis
AAVS1_A1647b	gtggccactgagaaccgggc	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctggttctcag	indicated on the x-axis
AAVS1_B1676b	gagcttggcagggggtggga	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctacccctgc	indicated on the x-axis
AAVS1_B1701a	gagccagagagatcctggg	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctagatctc	indicated on the x-axis
AAVS1_B1705a	gatggagccagagagatcc	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctctctctgc	indicated on the x-axis
AAVS1_A1810b	gaatctgcctaacaggaggt	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctctgttaggc	indicated on the x-axis
AAVS1_B1883b	ggggccactagggacaggat	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctgtgctcag	indicated on the x-axis

AAVS1_B1902a	gtccctccacccacagtg	gtctggtcaaccaccgcggtctcagtggtgtacggtacaacctgtggggtg	indicated on the x-axis
AAVS1_A1890b	gtcaccaatctgtccctag	taccgtacaccctagagaccgcggtggttgaccagacaacctgggacaggatt	indicated on the x-axis
AAVS1_A1890c	gtcaccaatctgtccctag	taccgtacaccctagagaccgcggtggttgaccagacaacctgggacaggattgg	indicated on the x-axis
AAVS1_B1962c	gggacacacctatattccca	tctgtgtcaaccaccgcggtctcagtggtgtacgttacaacctgaatataaagtggtg	indicated on the x-axis
AAVS1_A3786c	gtctgccccccacgccccca	taccgtacaccctagagaccgcggtggttgaccagacaacctgtgcggtggggggc	indicated on the x-axis
AAVS1_B3839c	gacctgccacgacacctgt	tctgtgtcaaccaccgcggtctcagtggtgtacggtacaacctgtgtgtctgggca	indicated on the x-axis
AAVS1_A3786a	gtctgccccccacgccccca	taccgtacaccctagagaccgcggtggttgaccagacaacctgtgcggtgggg	indicated on the x-axis
AAVS1_B3903b	gcgactctcggaagtggccca	gtctgtgtcaaccaccgcggtctcagtggtgtacgttacaacctccacttcagg	indicated on the x-axis
AAVS1_B3930a	ggactctccagtggtcatcg	gtctgtgtcaaccaccgcggtctcagtggtgtacggtacaacctgtcacactg	indicated on the x-axis
AAVS1_A3835b	gacgtcacggcgtgcccaca	taccgtacaccctagagaccgcggtggttgaccagacaacctgcgagccgcgt	indicated on the x-axis
AAVS1_B3930b	ggactctccagtggtcatcg	gtctgtgtcaaccaccgcggtctcagtggtgtacggtacaacctgtgcacactgg	indicated on the x-axis
AAVS1_A3856a	gtgtgtctgtggcagtgccgc	taccgtacaccctagagaccgcggtggttgaccagacaacctgacctgcc	indicated on the x-axis

Figure 3d
pegRNA

Accession	Sequence	Accession	Sequence	Accession	Sequence	Accession	Sequence
CCR5_A325a	gctcatctatgctgccgccag	atgatcctgacgacggagaccgccgtctgcgacaaagccggcgacgc	325/414	CCR5_B414b	ggtagctatcgaattctcagg	ggctgtgacgacgacggcggtctccgtctcaggatcatgacaatcgata	325/414
CCR5_A506c	gacaagtgatgactactggg	atgatcctgacgacggagaccgccgtctgcgacaaagccaagtgtacacactt	506/584	CCR5_A509b	gaagtgatgactactgggtgg	atgatcctgacgacggagaccgccgtctgcgacaaagccccaagtgatc	509/584
CCR5_A531b	gctgtgttgcgtctctccc	atgatcctgacgacggagaccgccgtctgcgacaaagccgacgacgacaa	531/584	CCR5_B584b	gtatggaaaatgagagctgc	ggctgtgacgacgacggcggtctccgtctcaggatcatgctctctatttc	506/584, 509/584, 531/584
AAVS1_A1077c	gcagagccaggaaacccctgt	taccgtacaccactgagaccgcgggtgttgaccagcaaaacctggggttcctggct	1077/1154	AAVS1_B1154c	gtccttggaagcccaggag	tctggtcaaacaccgcgggtctcagtggtgtacgggtacaacacctctgggtgcgaa	1077/1154
AAVS1_A3786c	gctgccccccaccgcgccca	taccgtacaccactgagaccgcgggtgttgaccagcaaaacctctggcgtggggggc	3786/3903, 3786/3930	AAVS1_B3903c	gcgactctctggaagtcggcca	tctggtcaaacaccgcgggtctcagtggtgtacgggtacaacacctccactccagag	3786/3903
AAVS1_B3930c	gtactcccaatgtgcatcgc	tctggtcaaacaccgcgggtctcagtggtgtacgggtacaacacctccacactggaa	3786/3930				

Figure 3e
pegRNA

		specific pBgtA
CCR5_A531b	gctgtgtttgcgtctctccc	atgatcctgacgacggagaccgccgtctgcagaagccagagacgcaa
CCR5_B584b	gtatggaataatgagagctgc	ggctgtgtcgcagcagggcggtctccgtctcaggatcatgtctctatttc
CCR5_A7_attB_30	gctgtgtttgcgtctctccc	tcttgacgacggagaccgccgtctgcagaagccagagacgacaaa
CCR5_B8_attB_30	gtatggaataatgagagctgc	tgtcgcagcagcggctctccgtctcaggtatcatgtctctatttc
CCR5_A7_attB_20	gctgtgtttgcgtctctccc	acgacggagaccgccgtctgcgacaagccagagacgacaaa
CCR5_B8_attB_20	gtatggaataatgagagctgc	acgacggcggtctccgtctgcaggtatcatgtctctatttc
CCR5_A7_attB_GA_38	gctgtgtttgcgtctctccc	atgatcctgacgacggagtcgccgtctgcagaagccagagacgacaaa
CCR5_B8_attB_GA_38	gtatggaataatgagagctgc	ggctgtgtcgcagcagggcgactccgtctgcaggtatcatgtctctatttc
CCR5_A7_attB_GA_30	gctgtgtttgcgtctctccc	tcttgacgacggagtcgccgtctgcagaagccagagacgacaaa
CCR5_B8_attB_GA_30	gtatggaataatgagagctgc	tgtcgcagcagcggcgactccgtctgcaggtatcatgtctctatttc
CCR5_A7_attB_GA_20	gctgtgtttgcgtctctccc	acgacggagtcgccgtctgcagaagccagagacgacaaa
CCR5_B8_attB_GA_20	gtatggaataatgagagctgc	acgacggcggtactccgtctgcaggtatcatgtctctatttc
CCR5_A7_attP_50	gctgtgtttgcgtctctccc	gggtttgtaccgtacaccactgagaccgccgtgtgttgaccagacaaccaagagacg
CCR5_B8_attP_50	gtatggaataatgagagctgc	tgggtttgtctgtcaaccaccgccgtctcagttggtgtacggtacaaaaccgctctcatttc
CCR5_A7_attP_40	gctgtgtttgcgtctctccc	c
CCR5_B8_attP_40	gtatggaataatgagagctgc	tgtaccgtacaccactgagaccgccgtgtgttgaccagacaaccaagagacgacaaa
CCR5_A7_attP_30	gctgtgtttgcgtctctccc	tgtctgtgtcaaccaccgccgtctcagttggtgtacggtacaaaaccgctctcatttc
CCR5_B8_attP_30	gtatggaataatgagagctgc	cgtacaccactgagaccgccgtgtgttgaccagacaaccaagagacgacaaa
CCR5_A7_attP_GA_50	gctgtgtttgcgtctctccc	ggtaaccaccgccgtctcagttggtgtacgggtacaaaaccgctctcatttc
CCR5_B8_attP_GA_50	gtatggaataatgagagctgc	gggtttgtaccgtacaccactgagtcgccgtgtgtgtgaccagacaaccaagagacg
CCR5_A7_attP_GA_40	gctgtgtttgcgtctctccc	caaa
CCR5_B8_attP_GA_40	gtatggaataatgagagctgc	tgtgtttgtctgtcaaccaccgccgactcagttggtgtacggtacaaaaccgctctcatttc
CCR5_A7_attP_GA_30	gctgtgtttgcgtctctccc	tg
CCR5_B8_attP_GA_30	gtatggaataatgagagctgc	tgtaccgtacaccactgagtcgccgtgtgttgaccagacaaccaagagacgacaaa
CCR5_A7_attP_GA_20	gctgtgtttgcgtctctccc	tgtctgtgtcaaccaccgccgactcagttggtgtacggtacaaaaccgctctcatttc
CCR5_B8_attP_GA_20	gtatggaataatgagagctgc	cgtacaccactgagtcgccgtgtgttgaccagacaaccaagagacgacaaa
CCR5_A7_attP_GA_10	gctgtgtttgcgtctctccc	ggtaaccaccgccgactcagttggtgtacggtacaaaaccgctctcatttc
CCR5_B8_attP_GA_10	gtatggaataatgagagctgc	gggtttgtaccgtacaccactgagtcgccgtgtgtgtgaccagacaaccaagagacg

Figure 3f
pegRNA

	gactgaaacttcacagaata	aacttcacagaggctgtcgcacgacggcggtctccgtcgtcaggatcat	indicated on the x-axis
CCR5_A277b	gactgaaacttcacagaata	gaaacttcacagaggctgtcgcacgacggcggtctccgtcgtcaggatcat	indicated on the x-axis
CCR5_A277c	gatttatgagatcaacagcac	ggctgtctgcacgacggcggtctccgtcgtcaggatcatctgttgatctc	indicated on the x-axis
CCR5_B358b	gatttatgagatcaacagcac	ggctgtctgcacgacggcggtctccgtcgtcaggatcatctgttgatctc	indicated on the x-axis
CCR5_B358c	gatttatgagatcaacagcac	ggctgtctgcacgacggcggtctccgtcgtcaggatcatctgttgatctc	indicated on the x-axis

Figure 3g
pegRNA

Accession	Sequence	Species
CCR5_A7_attB_20	gctgtgtttgcgtctctccc	CCR5 attB (HEK293T and Huh7)
CCR5_B8_attB_20	gtatggaaaatgagagctgc	CCR5 attB (HEK293T and Huh7)
CCR5_A277c	gactgaaacttcacagaata	ALB attB (HEK293T and Huh7)

CCR5_B358c	gatttatgagatcaacagcac	ggcttgtcgacgacggcggtctccgtcgtcaggatcatctgttgatctcat	ALB attB (HEK293T and Huh7)
Figure 4b pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
IDS2_DF_A1_a_attP_rev	gacacaaaaactgccacagg	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctgtggcagtta	A1B2 (attP rev)
IDS2_DF_A1_a_attP_fwd	gacacaaaaactgccacagg	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctgtggcagtta	A1B2 (attP fwd)
IDS2_DF_A1_c_attP_rev	gacacaaaaactgccacagg	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctgtggcagtttta	A1B3 (attP rev); A1B4 (attP rev)
IDS2_DF_A1_c_attP_fwd	gacacaaaaactgccacagg	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctgtggcagtttta	A1B3 (attP fwd); A1B4 (attP fwd)
IDS2_DF_A4_b_attP_rev	gcactcatttctccaagctc	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctcttgaggaaa	A4B7 (attP rev)
IDS2_DF_A4_b_attP_fwd	gcactcatttctccaagctc	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctcttgaggaaa	A4B7 (attP fwd)
IDS2_DF_B2_a_attP_rev	gtaggtacaggacagggcag	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctccctgtcc	A1B2 (attP rev)
IDS2_DF_B2_a_attP_fwd	gtaggtacaggacagggcag	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctccctgtcc	A1B2 (attP fwd)
IDS2_DF_B3_a_attP_rev	gagataggttaggtacaggaca	tctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctctgtacct	A1B3 (attP rev)
IDS2_DF_B3_a_attP_fwd	gagataggttaggtacaggaca	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctctgtacct	A1B3 (attP fwd)
IDS2_DF_B4_b_attP_rev	gtgaaaagataggttaggtac	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctctacatctcta	A1B4 (attP rev)
IDS2_DF_B4_b_attP_fwd	gtgaaaagataggttaggtac	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctctacatctcta	A1B4 (attP fwd)
IDS2_DF_B7_b_attP_rev	gttatggtttactccatcta	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctatggagtaaacct	A4B7 (attP rev)
IDS2_DF_B7_b_attP_fwd	gttatggtttactccatcta	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctatggagtaaacct	A4B7 (attP fwd)
IDS_DF_C2_c_attB_rev	gttttggtttaccctatcta	atgatcctgacgacggagaccgccgtcgtcgacaagccatagggtaaacca	C2D2 (attB rev); C2D2 (attB rev)
IDS_DF_C2_c_attB_fwd	gttttggtttaccctatcta	ggcttgtcgacgacggcggtctccgtcgtcaggatcatatagggtaaacca	C2D1 (attB fwd); C2D2 (attB fwd)
IDS_DF_D1_b_attB_rev	gctgtggaactgcaacacact	ggcttgtcgacgacggcggtctccgtcgtcaggatcatgtgttcagtg	C2D1 (attB rev)
IDS_DF_D1_b_attB_fwd	gctgtggaactgcaacacact	atgatcctgacgacggagaccgccgtcgtcgacaagccgtgttcagtg	C2D1 (attB fwd)
IDS_DF_D2_c_attB_rev	gtgccacctaacagtgagctg	ggcttgtcgacgacggcggtctccgtcgtcaggatcatctcactgttaggt	C2D2 (attB rev)
IDS_DF_D2_c_attB_fwd	gtgccacctaacagtgagctg	atgatcctgacgacggagaccgccgtcgtcgacaagccctcactgttaggt	C2D2 (attB fwd)
Figure 4c pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
IDS2_DF_A4_b_a_attP_rev	gcactcatttctccaagctc	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctcttgaggaaa	pegRNA set1 installing attP_rev in IDS2 and attB_fwd in IDS
IDS2_DF_B7_b_attP_rev	gttatggtttactccatcta	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctatggagtaaacct	pegRNA set1 installing attP_rev in IDS2 and attB_fwd in IDS
IDS_DF_C2_c_attB_fwd	gttttggtttaccctatcta	ggcttgtcgacgacggcggtctccgtcgtcaggatcatatagggtaaacca	pegRNA set1 installing attP_rev in IDS2 and attB_fwd in IDS
IDS_DF_D1_b_attB_fwd	gctgtggaactgcaacacact	atgatcctgacgacggagaccgccgtcgtcgacaagccgtgttcagtg	pegRNA set1 installing attP_rev in IDS2 and attB_fwd in IDS
IDS2_DF_A4_b_attP_fwd	gcactcatttctccaagctc	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctcttgaggaaa	pegRNA set2 installing attP_fwd in IDS2 and attB_rev in IDS
IDS2_DF_B7_b_attP_fwd	gttatggtttactccatcta	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctatggagtaaacct	pegRNA set2 installing attP_fwd in IDS2 and attB_rev in IDS
IDS_DF_C2_c_attB_rev	gttttggtttaccctatcta	atgatcctgacgacggagaccgccgtcgtcgacaagccatagggtaaacca	pegRNA set2 installing attP_fwd in IDS2 and attB_rev in IDS
IDS_DF_D1_b_attB_rev	gctgtggaactgcaacacact	ggcttgtcgacgacggcggtctccgtcgtcaggatcatgtgttcagtg	pegRNA set2 installing attP_fwd in IDS2 and attB_rev in IDS
Extended Data Figures			
ED Figure 1a - Comparison of twinPE- and PE3-mediated <i>FKBP</i> insertion at <i>CCR5</i> region 1			
pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
PE3_CCR5_1_F414a_34_FKBP108	ggtacatcatcgattgtcagg	tactgtccccctctgtgggtcactatgtgccgccaaatttttccatcttcaagcatcccg gtgtagtgcaccacgcaggtgtggccgcgttggggaaggtgcgcccgtctcctggg gagatggtttccacctgactccgacaatcga	indicated on the x-axis
PE3_CCR5_1_F414a_29_FKBP108	ggtacatcatcgattgtcagg	tcccccttctgggtcactatgtgccgccaaatttttccatcttcaagcatcccggtga gtgcaccacgcaggtctgtgccgcgttggggaaggtgcgcccgtctcctggggaga tggtttccacctgactccgacaatcga	indicated on the x-axis
PE3_CCR5_1_F414a_23_FKBP108	ggtacatcatcgattgtcagg	tctgggtcactatgtctgccgccaaatttttccatcttcaagcatcccggtgtagtgtca ccacgcaggtgtgccgcgcttggggaaggtgcgcccgtctcctggggagatggttt ccacctgactccgacaatcga	indicated on the x-axis

twinPE_CCR5_1_F414a_FKBP108	ggtacatcatcgattgtcagg	accttccccagcgccgacacgtgctggtgcactacaccgggatgcttgaagatggaagaatttgacaatcga	indicated on the x-axis
twinPE_CCR5_1_E325b_FKBP108	gtcactatgtctgccgccag	accacgcaggctctggccgcgttggggaagggtgcgccgtctcctgggagatggtt	indicated on the x-axis
sgRNA	spacer sequence		
PE3_CCR5_A1_sgRNA	gcattctgataaactgcaaa		
PE3_CCR5_A2_sgRNA	ggacatctacctgtcaacc		
PE3_CCR5_A4_sgRNA	gcaatgtgtcaactcttgac		

ED Figure 1b - Comparison of twinPE- and PE3-mediated *FKBP* insertion at *CCR5* region 2

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
PE3_CCR5_2_F2_34_FKBP108	gtgaaagacagcctggagtc	agattggagaacccttgaaagacatcaagcacaatttcttccatttcaagcatcccggtgtagtgcaccacgcaggctgtgccgccttggggaagggtgcgccgtctcctgggagatggtttccacctgcactcctccaggct	indicated on the x-axis
PE3_CCR5_2_F2_28_FKBP108	gtgaaagacagcctggagtc	gagaacccttgaaagacatcaagcacaatttcttccatttcaagcatcccggtgtagtgcaccacgcaggctgtgccgccttggggaagggtgcgccgtctcctgggagatggtttccacctgcactcctccaggct	indicated on the x-axis
PE3_CCR5_2_F2_23_FKBP108	gtgaaagacagcctggagtc	acccttgaaagacatcaagcacaatttcttccatttcaagcatcccggtgtagtgcaccacgcaggctgtgccgccttggggaagggtgcgccgtctcctgggagatggtttccacctgcactcctccaggct	indicated on the x-axis
twinPE_CCR5_2_F2a_FKBP108	gtgaaagacagcctggagtc	accttccccagcgccgacacgtgctggtgcactacaccgggatgcttgaagatggaagaattttccaggct	indicated on the x-axis
twinPE_CCR5_2_E2c_FKBP108nt	gaaaagacatcaagcacaga	accacgcaggctgtgccgccttggggaagggtgcgccgtctcctgggagatggtt	indicated on the x-axis
sgRNA	spacer sequence		
PE3_CCR5_C1_sgRNA	gatgcagagtcagagaact		
PE3_CCR5_C1.5_sgRNA	ggaagtgagggtcagagagg		
PE3_CCR5_C4_sgRNA	gatggattggtgtaaaggga		

ED Figure 1c - Long twinPE insertions at *CCR5*

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
CCR5_A7_attP_spacer27	gctgtgtttgcgtctctccc	ttcgtttatagccattcttcgcgaaagtgtgtaccgtacaccactgagaccgcggtgtgaccagacaaccagagacgcaaa	attB-spacer-attP
CCR5_B8_spacer_attB	gtatggaaaatgagagctgc	tttcgcgaagaaatggcgataacgaaggctgtgcgacgacggcggtctcctgcgtcagatcatgctctcattttc	attB-spacer-attP, attB-spacer-attB
CCR5_A7_attB_spacer27	gctgtgtttgcgtctctccc	ttcgtttatagccattcttcgcgaaagtgtgtaccgtacaccactgagaccgcggtgtcgaacccagagacgcaaa	attB-spacer-attB

ED Figure 2 - *PAH* exon recoding via twinPE

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
PAH_2.1.1	gtcacaataagcgcaatactt	tgatcttcagcctgaagggaagggtggcgccctggcgaaggattgctgctt	indicated on the x-axis
PAH_2.1.2	gtcacaataagcgcaatactt	tgatcttcagcctgaagggaagggtggcgccctggcgaaggattgctgcttatt	indicated on the x-axis
PAH_2.1.3	gtcacaataagcgcaatactt	tgatcttcagcctgaagggaagggtggcgccctggcgaaggattgctgcttatttg	indicated on the x-axis
PAH_2.2.1	gaagacaactgcaatcaaaa	tcttccttcagcctgaagatcagagagatagcgccgttctgattgcag	indicated on the x-axis
PAH_2.2.2	gaagacaactgcaatcaaaa	tcttccttcagcctgaagatcagagagatagcgccgttctgattgcagttg	indicated on the x-axis
PAH_2.2.3	gaagacaactgcaatcaaaa	tcttccttcagcctgaagatcagagagatagcgccgttctgattgcagttg	indicated on the x-axis
PAH_4.1.1	gttctctgtgtttcagtgccc	aagatttgattagcgaacctatcaagttcctgaattgtccgtggaaccacggcactgaaac	indicated on the x-axis
PAH_4.1.2	gttctctgtgtttcagtgccc	aagatttgattagcgaacctatcaagttcctgaattgtccgtggaaccacggcactgaaacac	indicated on the x-axis
PAH_4.1.3	gttctctgtgtttcagtgccc	aagatttgattagcgaacctatcaagttcctgaattgtccgtggaaccacggcactgaaacacag	indicated on the x-axis
PAH_4.1.4	gttctctgtgtttcagtgccc	gacaagatttgattagcgaacctatcaagttcctgaattgtccgtggaaccacggcactgaaac	indicated on the x-axis
PAH_4.1.5	gttctctgtgtttcagtgccc	gacaagatttgattagcgaacctatcaagttcctgaattgtccgtggaaccacggcactgaaacac	indicated on the x-axis
PAH_4.1.6	gttctctgtgtttcagtgccc	gacaagatttgattagcgaacctatcaagttcctgaattgtccgtggaaccacggcactgaaacacag	indicated on the x-axis
PAH_4.2.1	gccaagaaccattcaagagc	ggctccgtaggacaagatttgattagcgaacctatcaagttcttgaatgg	indicated on the x-axis
PAH_4.2.2	gccaagaaccattcaagagc	ggctccgtaggacaagatttgattagcgaacctatcaagttcttgaatgggttc	indicated on the x-axis
PAH_4.2.3	gccaagaaccattcaagagc	ggctccgtaggacaagatttgattagcgaacctatcaagttcttgaatgggttc	indicated on the x-axis
PAH_4.2.4	gccaagaaccattcaagagc	gttcggctccgtaggacaagatttgattagcgaacctatcaagttcttgaatgg	indicated on the x-axis
PAH_4.2.5	gccaagaaccattcaagagc	gttcggctccgtaggacaagatttgattagcgaacctatcaagttcttgaatgggttc	indicated on the x-axis
PAH_4.2.6	gccaagaaccattcaagagc	gttcggctccgtaggacaagatttgattagcgaacctatcaagttcttgaatgggttc	indicated on the x-axis
PAH_4.2.7	gccaagaaccattcaagagc	gatgatcagcgctcaagttcggctccgtaggacaagatttgattagcgaacctatcaagttcttgaatgg	indicated on the x-axis
PAH_4.2.8	gccaagaaccattcaagagc	gatgatcagcgctcaagttcggctccgtaggacaagatttgattagcgaacctatcaagttcttgaatgggttc	indicated on the x-axis
PAH_4.2.9	gccaagaaccattcaagagc	gatgatcagcgctcaagttcggctccgtaggacaagatttgattagcgaacctatcaagttcttgaatgggttc	indicated on the x-axis
PAH_4.3.1	gcgggccatggactcacaggg	ataggttcgctaataaattctgtctacggagccgaacttgacgctgatcatcctgtgagtc	indicated on the x-axis
PAH_4.3.2	gcgggccatggactcacaggg	ataggttcgctaataaattctgtctacggagccgaacttgacgctgatcatcctgtgagtc	indicated on the x-axis

PAH_7.6.6	gtctgatgtactgtgtgcag	agttagagactttctgggggtctgcattccgcgtgtttcattgcacacagtacatc	indicated on the x-axis
PAH_7.6.7	gtctgatgtactgtgtgcag	tgggggggtctgcattccgcgtgtttcattgcacacagta	indicated on the x-axis
PAH_7.6.8	gtctgatgtactgtgtgcag	tgggggggtctgcattccgcgtgtttcattgcacacagtata	indicated on the x-axis
PAH_7.6.9	gtctgatgtactgtgtgcag	tgggggggtctgcattccgcgtgtttcattgcacacagtacatc	indicated on the x-axis
PAH_7.7.1	gttcgggggtatacatgggct	gggtctcgcattccgcgtgtttcattgtaccagatattaggcatggttcaaaacccatg	indicated on the x-axis
PAH_7.7.2	gttcgggggtatacatgggct	tatacc	
PAH_7.7.3	gttcgggggtatacatgggct	gggtctcgcattccgcgtgtttcattgtaccagatattaggcatggttcaaaacccatg	indicated on the x-axis
PAH_7.7.4	gttcgggggtatacatgggct	tatacc	
PAH_7.7.5	gttcgggggtatacatgggct	attccgcgtgtttcattgtaccagatattaggcatggttcaaaacccatgtatac	indicated on the x-axis
PAH_7.7.6	gttcgggggtatacatgggct	attccgcgtgtttcattgtaccagatattaggcatggttcaaaacccatgtatacc	indicated on the x-axis
PAH_7.7.7	gttcgggggtatacatgggct	gtgtttcattgtaccagatattaggcatggttcaaaacccatgtatacc	indicated on the x-axis
PAH_7.7.8	gttcgggggtatacatgggct	gtgtttcattgtaccagatattaggcatggttcaaaacccatgtatacc	indicated on the x-axis
PAH_7.7.9	gttcgggggtatacatgggct	attccgcgtgtttcattgtaccagatattaggcatggttcaaaacccatgtatacc	indicated on the x-axis
PAH_7.8.1	ggacagtactcacggttcgg	gcgtgtttcattgtaccagatattaggcatggttcaaaacccatgtacacaccagaac	indicated on the x-axis
PAH_7.8.2	ggacagtactcacggttcgg	cgtaga	
PAH_7.8.3	ggacagtactcacggttcgg	gcgtgtttcattgtaccagatattaggcatggttcaaaacccatgtacacaccagaac	indicated on the x-axis
PAH_7.8.4	ggacagtactcacggttcgg	cgtagtac	
PAH_7.8.5	ggacagtactcacggttcgg	attgtaccagatattaggcatggttcaaaacccatgtacacaccagaacccgtga	indicated on the x-axis
PAH_7.8.6	ggacagtactcacggttcgg	attgtaccagatattaggcatggttcaaaacccatgtacacaccagaacccgtgagt	indicated on the x-axis
PAH_8.1.1	gtgacatctgccatgagctgt	c	
PAH_8.1.2	gtgacatctgccatgagctgt	gaaggacatctgcgtgaacagtggcacgtgaccgagaagctcatggc	indicated on the x-axis
PAH_8.1.3	gtgacatctgccatgagctgt	gaaggacatctgcgtgaacagtggcacgtgaccgagaagctcatggcag	indicated on the x-axis
PAH_8.2.1	gtaaaaatccattccttacc	gaaggacatctgcgtgaacagtggcacgtgaccgagaagctcatggcagat	indicated on the x-axis
PAH_8.2.2	gtaaaaatccattccttacc	actgttcacgcgataggctccttcgcacagttctctcaggtaaggaatgg	indicated on the x-axis
PAH_8.2.3	gtaaaaatccattccttacc	actgttcacgcgataggctccttcgcacagttctctcaggtaaggaatgga	indicated on the x-axis
PAH_9.1.1	gttccccaattacaggaaat	actgttcacgcgataggctccttcgcacagttctctcaggtaaggaatggatt	indicated on the x-axis
PAH_9.1.2	gttccccaattacaggaaat	tataatactcgtctgtgctccaggcttgcacagaccgatctcctgtaatt	indicated on the x-axis
PAH_9.1.3	gttccccaattacaggaaat	tataatactcgtctgtgctccaggcttgcacagaccgatctcctgtaattgg	indicated on the x-axis
PAH_9.1.4	gttccccaattacaggaaat	tataatactcgtctgtgctccaggcttgcacagaccgatctcctgtaattggg	indicated on the x-axis
PAH_9.1.5	gttccccaattacaggaaat	ttctctataatactcgtctgtgctccaggcttgcacagaccgatctcctgtaatt	indicated on the x-axis
PAH_9.1.6	gttccccaattacaggaaat	ttctctataatactcgtctgtgctccaggcttgcacagaccgatctcctgtaattgg	indicated on the x-axis
PAH_9.2.1	gggagagaagggacttactg	ttctctataatactcgtctgtgctccaggcttgcacagaccgatctcctgtaattggg	indicated on the x-axis
PAH_9.2.2	gggagagaagggacttactg	tgggagcaccagacgagtatatagagaaacttgcacagtaagtcctt	indicated on the x-axis
PAH_9.2.3	gggagagaagggacttactg	tgggagcaccagacgagtatatagagaaacttgcacagtaagtccttctc	indicated on the x-axis
PAH_9.3.1	gaccatccaccaggagagaga	tgggagcaccagacgagtatatagagaaacttgcacagtaagtccttctc	indicated on the x-axis
PAH_9.3.2	gaccatccaccaggagagaga	accagacgagtatatagagaaacttgcacagtaagtccttctcctcgggt	indicated on the x-axis
PAH_9.3.3	gaccatccaccaggagagaga	accagacgagtatatagagaaacttgcacagtaagtccttctcctcgggtgga	indicated on the x-axis
PAH_10.2.1_EvoPreQ1	gccagatttactggtttactg	gtaggctttaaagtctatcacctcgttacacaatccgaattcgacggtaaacagtaaat	indicated on the x-axis
PAH_10.2.2_EvoPreQ1	gccagatttactggtttactg	ctctctcttgacgcgggttctatctagtacgcgttaaaccaactagaaa	indicated on the x-axis
PAH_10.2.3_EvoPreQ1	gccagatttactggtttactg	ctctctcttgacgcgggttctatctagtacgcgttaaaccaactagaaa	indicated on the x-axis
PAH_10.3.1_EvoPreQ1	gtaattcaccaaaggatgac	gtaggctttaaagtctatcacctcgttacacaatccgaattcgacggtaaacagtaaat	indicated on the x-axis
PAH_10.3.2_EvoPreQ1	gtaattcaccaaaggatgac	ctgtctctcttgacgcgggttctatctagtacgcgttaaaccaactagaaa	indicated on the x-axis
PAH_10.3.3_EvoPreQ1	gtaattcaccaaaggatgac	taagcagggtgatagcattaaagcctacggagcaggtttgctctatctcttgggtctct	indicated on the x-axis
PAH_11.1.1_EvoPreQ1	gaagccaaagcttctcccc	ctcttgacgcgggttctatctagtacgcgttaaaccaactagaaa	indicated on the x-axis
PAH_11.1.2_EvoPreQ1	gaagccaaagcttctcccc	taagcagggtgatagcattaaagcctacggagcaggtttgctctatctcttgggtatc	indicated on the x-axis
PAH_11.1.3_EvoPreQ1	gaagccaaagcttctcccc	ctctcttgacgcgggttctatctagtacgcgttaaaccaactagaaa	indicated on the x-axis
PAH_11.2.1_EvoPreQ1	gaaagcttctccccctggagc	taagcagggtgatagcattaaagcctacggagcaggtttgctctatctcttgggtatc	indicated on the x-axis
PAH_11.2.2_EvoPreQ1	gaaagcttctccccctggagc	ctctcttgacgcgggttctatctagtacgcgttaaaccaactagaaa	indicated on the x-axis
PAH_11.2.3_EvoPreQ1	gaaagcttctccccctggagc	gtgactgtatagttcgaattgcagctcttttcgagttcgagtgaggagaagcttctctct	indicated on the x-axis
PAH_11.4.1_EvoPreQ1	gaactctctgccagtaatag	tgacgcgggttctatctagtacgcgttaaaccaactagaaa	indicated on the x-axis
PAH_11.4.2_EvoPreQ1	gaactctctgccagtaatag	gtgactgtatagttcgaattgcagctcttttcgagttcgagtgaggagaagcttggctct	indicated on the x-axis
PAH_11.4.3_EvoPreQ1	gaactctctgccagtaatag	ctcttgacgcgggttctatctagtacgcgttaaaccaactagaaa	indicated on the x-axis
PAH_12.2.1_EvoPreQ1	gaacttctctgccacaatacct	gtgactgtatagttcgaattgcagctcttttcgagttcgagtgaggagaagcttctctct	indicated on the x-axis
PAH_12.2.2_EvoPreQ1	gaacttctctgccacaatacct	tgacgcgggttctatctagtacgcgttaaaccaactagaaa	indicated on the x-axis

PAH_12.2.3_EvoPreQ1	gactttgtgccacaataacct	ttcgatgcgctgtgtataaaggatcatatctcagcgtaaatggcttggattgtggcagct	indicated on the x-axis
PAH_12.3.1_EvoPreQ1	gtctacgaccatacacccaa	ctctctcttgacgcgggtctatctagttacgcgttaaccaactagaaa	indicated on the x-axis
PAH_12.3.2_EvoPreQ1	gtctacgaccatacacccaa	gatctcaattgttgtagttatcgagcacttcgatgcgctgggtgatggctctctcttg	indicated on the x-axis
PAH_12.3.3_EvoPreQ1	gtctacgaccatacacccaa	acgcgggtctatctatgttacgcgttaaccaactagaaa	indicated on the x-axis
PAH_12.4.1_EvoPreQ1	gcagccaaaatcttaagctgc	gatctcaattgttgtagttatcgagcacttcgatgcgctgggtgatgggtctctctctt	indicated on the x-axis
PAH_12.4.2_EvoPreQ1	gcagccaaaatcttaagctgc	gacgcgggtctatctatgttacgcgttaaccaactagaaa	indicated on the x-axis
PAH_12.4.3_EvoPreQ1	gcagccaaaatcttaagctgc	gatctcaattgttgtagttatcgagcacttcgatgcgctgggtgatgggtctctctctt	indicated on the x-axis
PAH_12.5.1_EvoPreQ1	gtgtaaattacttactgttaa	ttgatcccttatacacagcgcgtcgaagtgcgtcgataacactcaacagcttaagatttctc	indicated on the x-axis
PAH_12.5.2_EvoPreQ1	gtgtaaattacttactgttaa	ctctctcttgacgcgggtctatctatgttacgcgttaaccaactagaaa	indicated on the x-axis
PAH_12.5.3_EvoPreQ1	gtgtaaattacttactgttaa	ttgatcccttatacacagcgcgtcgaagtgcgtcgataacactcaacagcttaagattttag	indicated on the x-axis

ED Figure 3- pegRNA screen in CCR5

3' extension	3' extension	3' extension	3' extension
CCR5_A223a	gtcatcctgataaactgc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagttatc	indicated on the x-axis
CCR5_A223b	gtcatcctgataaactgc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagttatcag	indicated on the x-axis
CCR5_A223c	gtcatcctgataaactgc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagttatcagg	indicated on the x-axis
CCR5_A260a	gtgacatctacctgctcaacc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagttatcagg	indicated on the x-axis
CCR5_A260b	gtgacatctacctgctcaacc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagttatcagg	indicated on the x-axis
CCR5_A260c	gtgacatctacctgctcaacc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagttatcagg	indicated on the x-axis
CCR5_A325a	gtcactatgctgcgccccag	atgatcctgacgacggagaccgcgctcgtcgacaagccgcgagcagc	indicated on the x-axis
CCR5_A325b	gtcactatgctgcgccccag	atgatcctgacgacggagaccgcgctcgtcgacaagccgcgagcagc	indicated on the x-axis
CCR5_A325c	gtcactatgctgcgccccag	atgatcctgacgacggagaccgcgctcgtcgacaagccgcgagcagc	indicated on the x-axis
CCR5_A360a	gacaatgtgtcaactcttgac	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_A360b	gacaatgtgtcaactcttgac	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_A360c	gacaatgtgtcaactcttgac	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_A506a	gacaagtgtgatcacttggg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_A506b	gacaagtgtgatcacttggg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_A506c	gacaagtgtgatcacttggg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_A509a	gaagtgtgatcacttgggtgg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_A509b	gaagtgtgatcacttgggtgg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_A509c	gaagtgtgatcacttgggtgg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_A531a	gctgtgtttgcgtctctccc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_A531b	gctgtgtttgcgtctctccc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_A531c	gctgtgtttgcgtctctccc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B272a	gaaggaaaaacaggtcagaga	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B272b	gaaggaaaaacaggtcagaga	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B272c	gaaggaaaaacaggtcagaga	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B291a	gccagaaaggggacagtaaga	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B291b	gccagaaaggggacagtaaga	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B291c	gccagaaaggggacagtaaga	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B305a	ggcagcatatgtgacccaga	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B305b	ggcagcatatgtgacccaga	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B305c	ggcagcatatgtgacccaga	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B326a	gatttccaaagtcccactggg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B326b	gatttccaaagtcccactggg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B326c	gatttccaaagtcccactggg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B330a	gttgtatttccaaagtcccac	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B330b	gttgtatttccaaagtcccac	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B330c	gttgtatttccaaagtcccac	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B414a	ggtacctatcgtattgtcagg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B414b	ggtacctatcgtattgtcagg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B414c	ggtacctatcgtattgtcagg	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B535a	gatctgtgtaaagatgattcc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B535b	gatctgtgtaaagatgattcc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B535c	gatctgtgtaaagatgattcc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B584a	gtatggaataatgagagctgc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B584b	gtatggaataatgagagctgc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B584c	gtatggaataatgagagctgc	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B601a	gcagaattgatactgactgta	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B601b	gcagaattgatactgactgta	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis
CCR5_B601c	gcagaattgatactgactgta	atgatcctgacgacggagaccgcgctcgtcgacaagccgcagagttgac	indicated on the x-axis

ED Figure 4 - pegRNA screen at AAVS1

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
AAVS1_A1077a	gcagagccaggaaacccctgt	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctggggttcct	indicated on the x-axis
AAVS1_A1077b	gcagagccaggaaacccctgt	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctggggttcctgg	indicated on the x-axis
AAVS1_A1077c	gcagagccaggaaacccctgt	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctggggttcctgct	indicated on the x-axis

AAVS1_A1098a	gggaaggggcaggagagcca
AAVS1_A1098b	gggaaggggcaggagagcca
AAVS1_A1098c	gggaaggggcaggagagcca
AAVS1_A1246a	gaatatgtcccatagcac
AAVS1_A1246b	gaatatgtcccatagcac
AAVS1_A1246c	gaatatgtcccatagcac
AAVS1_A1267a	ggggactctttaaggaaga
AAVS1_A1267b	ggggactctttaaggaaga
AAVS1_A1267c	ggggactctttaaggaaga
AAVS1_A1293a	gagaagaagaaagggagtag
AAVS1_A1293b	gagaagaagaaagggagtag
AAVS1_A1293c	gagaagaagaaagggagtag
AAVS1_A1307a	gagtagagggcgccacgacc
AAVS1_A1307b	gagtagagggcgccacgacc
AAVS1_A1307c	gagtagagggcgccacgacc
AAVS1_A1582a	gatcagtgaaacgcaccaga
AAVS1_A1582b	gatcagtgaaacgcaccaga
AAVS1_A1582c	gatcagtgaaacgcaccaga
AAVS1_A1615a	gcagctcaggttctgggaga
AAVS1_A1615b	gcagctcaggttctgggaga
AAVS1_A1615c	gcagctcaggttctgggaga
AAVS1_A1647a	gtggccactgagaacccgggc
AAVS1_A1647b	gtggccactgagaacccgggc
AAVS1_A1647c	gtggccactgagaacccgggc
AAVS1_A1810a	gaatctgcctaaccaggaggt
AAVS1_A1810b	gaatctgcctaaccaggaggt
AAVS1_A1810c	gaatctgcctaaccaggaggt
AAVS1_A1890a	gtcacaatcctgtccctag
AAVS1_A1890b	gtcacaatcctgtccctag
AAVS1_A1890c	gtcacaatcctgtccctag
AAVS1_A3786a	gctgccccccaccgcccca
AAVS1_A3786b	gctgccccccaccgcccca
AAVS1_A3786c	gctgccccccaccgcccca
AAVS1_A3835a	gacgtcacggcgctgcccca
AAVS1_A3835b	gacgtcacggcgctgcccca
AAVS1_A3835c	gacgtcacggcgctgcccca
AAVS1_A3856a	gggtgtctggggcaggctcgc
AAVS1_A3856b	gggtgtctggggcaggctcgc
AAVS1_A3856c	gggtgtctggggcaggctcgc
AAVS1_B1154a	gtccttggcaagcccaggag
AAVS1_B1154b	gtccttggcaagcccaggag
AAVS1_B1154c	gtccttggcaagcccaggag
AAVS1_B1314a	gtcgtctctagggtttcacc
AAVS1_B1314b	gtcgtctctagggtttcacc
AAVS1_B1314c	gtcgtctctagggtttcacc
AAVS1_B1376a	gtccttggcaggcgtgtgtgt
AAVS1_B1376b	gtccttggcaggcgtgtgtgt
AAVS1_B1376c	gtccttggcaggcgtgtgtgt
AAVS1_B1640a	gtgacctgccccgtttctag
AAVS1_B1640b	gtgacctgccccgtttctag
AAVS1_B1640c	gtgacctgccccgtttctag
AAVS1_B1676a	gagcttggcagggggtggga
AAVS1_B1676b	gagcttggcagggggtggga
AAVS1_B1676c	gagcttggcagggggtggga
AAVS1_B1701a	gagccagagaggatctctgg
AAVS1_B1701b	gagccagagaggatctctgg
AAVS1_B1701c	gagccagagaggatctctgg
AAVS1_B1705a	gatggagccagagaggatcc
AAVS1_B1705b	gatggagccagagaggatcc
AAVS1_B1705c	gatggagccagagaggatcc
AAVS1_B1883a	ggggccactaggacacggat
AAVS1_B1883b	ggggccactaggacacggat
AAVS1_B1883c	ggggccactaggacacggat
AAVS1_B1902a	gtccccctaccaccacagt
AAVS1_B1902b	gtccccctaccaccacagt
AAVS1_B1902c	gtccccctaccaccacagt
AAVS1_B1962a	gggaccaccttatattccca
AAVS1_B1962b	gggaccaccttatattccca
AAVS1_B1962c	gggaccaccttatattccca
AAVS1_B3839a	gaacctgcccgacacacctg
AAVS1_B3839b	gaacctgcccgacacacctg
AAVS1_B3839c	gaacctgcccgacacacctg
AAVS1_B3903a	gcgactctcggaagtggcca
AAVS1_B3903b	gcgactctcggaagtggcca
AAVS1_B3903c	gcgactctcggaagtggcca
AAVS1_B3930a	ggactctccagtggtcatcg
AAVS1_B3930b	ggactctccagtggtcatcg
AAVS1_B3930c	ggactctccagtggtcatcg

[illegible][illegible]

ED Figure 5a - Comparison of twinPE- and PE3-mediated attB insertion at CCR5 region 1

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
CCR5_A325b_attB	gtcactatgctgccgccag	atgatcctgacgacggagaccgctgctgacaagccggcgagcat	indicated on the x-axis
CCR5_B414a_attB	ggtacatcatgattgtcagg	ggctgtgacgacggcggtctccgtcgtcagatcatgacaatcga	indicated on the x-axis
CCR5_B414_23	ggtacatcatgattgtcagg	tctggctcactatgctgccgcccgttctgacgacggcggtctccgtcgtcaggatcatgacaatcga	indicated on the x-axis
CCR5_B414_29	ggtacatcatgattgtcagg	tccccttctgggtcactatgctgccgcccgttctgacgacggcggtctccgtcgtcaggatcatgacaatcga	indicated on the x-axis
CCR5_B414_34	ggtacatcatgattgtcagg	tactgtccccttctgggtcactatgctgccgcccgttctgacgacggcggtctccgtcgtcaggatcatgacaatcga	indicated on the x-axis
sgRNA	spacer sequence		
PE3_CCR5_A1_sgRNA	gcatcctgataaactgcaaa		
PE3_CCR5_A2_sgRNA	ggacatcatcctgtcaacc		
PE3_CCR5_A4_sgRNA	gcaatgtgtcaactcttgac		

ED Figure 5b - Comparison of twinPE- and PE3-mediated attB insertion at CCR5 region 2

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
CCR5_C2c_attB	gaaaagacatcaagcacaga	atgatcctgacgacggagaccgctgctgacaagccgtgcttgatgctt	indicated on the x-axis
CCR5_D2a_attB	gtgaaagacagcctggagtc	ggctgtgacgacggcggtctccgtcgtcagatcatccaggct	indicated on the x-axis
CCR5_D2_23	gtgaaagacagcctggagtc	acccttgaaaagacatcaagcagcggttctgacgacggcggtctccgtcgtcaggatcatccaggct	indicated on the x-axis
CCR5_D2_28	gtgaaagacagcctggagtc	gagaaaccttgaaaagacatcaagcagcggttctgacgacggcggtctccgtcgtcaggatcatccaggct	indicated on the x-axis
CCR5_D2_34	gtgaaagacagcctggagtc	agattggagaaccttgaaaagacatcaagcagcggttctgacgacggcggtctcctgctcaggatcatccaggct	indicated on the x-axis
sgRNA	spacer sequence		
PE3_CCR5_C1_sgRNA	gatgcagagtcagcagaact		
PE3_CCR5_C1.5_sgRNA	ggaagtggaggtcagagagg		
PE3_CCR5_C4_sgRNA	gatggattgggtgtaaaagga		

ED Figure 6b - HTS junction purity

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
CCR5_A325a	gtcactatgctgccgccag	atgatcctgacgacggagaccgctgctgacaagccggcgagcagc	325/414
CCR5_B414b	ggtacatcatgattgtcagg	ggctgtgacgacggcggtctccgtcgtcagatcatgacaatcga	325/414
CCR5_A506c	gacaagtgtgatacttggg	atgatcctgacgacggagaccgctgctgacaagcccaagtgtacacatt	506/584
CCR5_A509b	gaaagtgtgatacttgggtgg	atgatcctgacgacggagaccgctgctgacaagcccaagtgtac	509/584
CCR5_A531b	gctgtgtttgctctctccc	atgatcctgacgacggagaccgctgctgacaagccagagacgcaaa	531/584
CCR5_B584b	gtatggaaaatgagagctgc	ggctgtgacgacggcggtctccgtcgtcagatcatgctctcatttc	506/584, 509/584, 531/584
AAVS1_A1077c	gcagagccaggaaacctgt	taccgtacaccactgagaccgctggtgtgaccagacaaacctggggtctctggct	1077/1154
AAVS1_B1154c	gtccttgccaagcccaggag	tctggtcaaccaccgctgctcagtggtgtacggtacaaaccttgggtctgcca	1077/1154
AAVS1_A3786c	gctggccccccaccgcccca	taccgtacaccactgagaccgctggtgtgaccagacaaacctggcggtggggggc	3786/3903, 3786/3930
AAVS1_B3903c	gcgactcctggaaatggcca	tctggtcaaccaccgctgctcagtggtgtacggtacaaacctccacttccaggag	3786/3903
AAVS1_B3930c	ggacttcccagtgatcagc	tctggtcaaccaccgctgctcagtggtgtacggtacaaaccttgacactgggaa	3786/3930

ED Figure 6c - Multiplex single transfection knock-in

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
AAVS1_A1077c	gcagagccaggaaacctgt	taccgtacaccactgagaccgctggtgtgaccagacaaacctggggtctctggct	AAVS1 attP, all samples on x-axis
AAVS1_B1154c	gtccttgccaagcccaggag	tctggtcaaccaccgctgctcagtggtgtacggtacaaaccttgggtctgcca	AAVS1 attB, all samples on x-axis
CCR5_A7_attB_20	gctgtgtttgctctctccc	acgacggagaccgctgctgacaagccagagacgcaaa	CCR5 attB
CCR5_B8_attB_20	gtatggaaaatgagagctgc	acgacggcggtctccgtcgtcagatcatgctctcatttc	CCR5 attB
CCR5_A7_attB_GA_20	gctgtgtttgctctctccc	acgacggagtcgccgctgctgacaagccagagacgcaaa	CCR5 attB-GA
CCR5_B8_attB_GA_20	gtatggaaaatgagagctgc	acgacggcggaactccgtcgtcagatcatgctctcatttc	CCR5 attB-GA
CCR5_A7_attP_30	gctgtgtttgctctctccc	cgtacaccactgagaccgctggtgtgaccagacaaaccaagagacgcaaa	CCR5 attP
CCR5_B8_attP_30	gtatggaaaatgagagctgc	ggttaaccaccgctgctcagtggtgtacggtacaaacctgctctcatttc	CCR5 attP
CCR5_A7_attP_GA_30	gctgtgtttgctctctccc	cgtacaccactgagtcgccggtgtgtgaccagacaaaccaagagacgcaaa	CCR5 attP-GA
CCR5_B8_attP_GA_30	gtatggaaaatgagagctgc	ggttaaccaccgctggaactcagtggtgtacggtacaaacctgctctcatttc	CCR5 attP-GA

ED Figure 6d - Overlap reduction

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
CCR5_A531b	gctgtgtttgctctctccc	atgatcctgacgacggagaccgctgctgacaagccagagacgcaaa	attB 38
CCR5_B584b	gtatggaaaatgagagctgc	ggctgtgacgacggcggtctccgtcgtcagatcatgctctcatttc	attB 38
CCR5_A7_attB_30	gctgtgtttgctctctccc	tctgacgacggagaccgctgctgacaagccagagacgcaaa	attB 30
CCR5_B8_attB_30	gtatggaaaatgagagctgc	gtgacgacggcggtctccgtcgtcagatcatgctctcatttc	attB 30
CCR5_A7_attB_20	gctgtgtttgctctctccc	acgacggagaccgctgctgacaagccagagacgcaaa	attB 20
CCR5_B8_attB_20	gtatggaaaatgagagctgc	acgacggcggtctccgtcgtcagatcatgctctcatttc	attB 20

ED figure 7 - Factor 9 knock-in

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
CCR5_A7_attB_20	gctgtgtttgcgtctctccc	acgacggagacggccggtcgtcgacaagccagagacgcaaa	CCR5 attB
CCR5_B8_attB_20	gtagtgaataatgagagctgc	acgacggcggtctccgtcgtcaggtatcatctctcattttc	CCR5 attB
CCR5_A277c	gactgaaacttcacagaata	gaaacttcacagagcgtgtcgcagacggcggtctccgtcgtcaggtatcat	ALB attB
CCR5_B358c	gatttatgagatcaacagcac	ggctgtgtcgcagacggcggtctccgtcgtcaggtatcatctgtgtatctcat	ALB attB

ED figure 8 - TwinPE+Bxb1 mediated inversion in the GFP reporter cells

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
AAVS1_A1077b_attB_rev	gcagagccagggaacccctgt	ggctgtgtcgcagacggcggtctccgtcgtcaggtatcatggggttctctgg	twinPE-mediated insertion of attB_rev in AAVS1 upstream of H2B_EGFP sequences
AAVS1_B1154b_attB_fwd	gtccttggcgaagcccaggag	atgatcctgacgacggagacggccgtcgtcgacaagccctggggttggc	twinPE-mediated insertion of attB_rev in AAVS1 upstream of H2B_EGFP sequences
AAVS1_A3835b	gacgtcacggcgctgccccca	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctggcagcgccgt	twinPE-mediated insertion of attP_fwd in AAVS1 downstream of H2B_EGFP sequences
AAVS1_B3903b	gcgactcctggaagtggcca	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctccacttccagg	twinPE-mediated insertion of attP_fwd in AAVS1 downstream of H2B_EGFP sequences

ED Figure 9c - IDS and IDS2 pegRNA screen

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
IDS2_A1_a_attP_rev	gacacaaaaaactgccacagg	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctgtggcagttta	A1B2 (attP rev)
IDS2_A1_a_attP_fwd	gacacaaaaaactgccacagg	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctgtggcagttta	A1B2 (attP fwd)
IDS2_A1_c_attP_rev	gacacaaaaaactgccacagg	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctgtggcagtttta	A1B3 (attP rev); A1B4 (attP rev)
IDS2_A1_c_attP_fwd	gacacaaaaaactgccacagg	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctgtggcagtttta	A1B3 (attP fwd); A1B4 (attP fwd)
IDS2_A4_b_attP_rev	gcactcatttctccaagctc	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctcttgaggagaaa	A4B7 (attP rev)
IDS2_A4_b_attP_fwd	gcactcatttctccaagctc	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctcttgaggagaaa	A4B7 (attP fwd)
IDS2_B2_a_attP_rev	gtaggtacagggacagggcag	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctccctgtcc	A1B2 (attP rev)
IDS2_B2_a_attP_fwd	gtaggtacagggacagggcag	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctccctgtcc	A1B2 (attP fwd)
IDS2_B3_a_attP_rev	gagataggttaggtacaggaca	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctctgtacct	A1B3 (attP rev)
IDS2_B3_a_attP_fwd	gagataggttaggtacaggaca	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctctgtacct	A1B3 (attP fwd)
IDS2_B4_b_attP_rev	gtgaaaagataggttaggtac	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctctctacctata	A1B4 (attP rev)
IDS2_B4_b_attP_fwd	gtgaaaagataggttaggtac	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctctctacctata	A1B4 (attP fwd)
IDS2_B7_b_attP_rev	gttatgttttactccatcta	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctatggagtaaacct	A4B7 (attP rev)
IDS2_B7_b_attP_fwd	gttatgttttactccatcta	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctatggagtaaacct	A4B7 (attP fwd)
IDS_C2_c_attB_rev	gttttggtttacctatcta	atgatcctgacgacggagacggccgtcgtcgacaagccatagggttaaacca	C2D2 (attB rev); C2D2 (attB fwd)
IDS_C2_c_attB_fwd	gttttggtttacctatcta	ggctgtgtcgcagacggcggtctccgtcgtcaggtatcatatagggttaaacca	C2D1 (attB fwd); C2D2 (attB fwd)
IDS_D1_b_attB_rev	gctgtggaactgcaacacact	ggctgtgtcgcagacggcggtctccgtcgtcaggtatcatgtgttcaggt	C2D1 (attB rev)
IDS_D1_b_attB_fwd	gctgtggaactgcaacacact	atgatcctgacgacggagacggccgtcgtcgacaagccgtgtgttcaggt	C2D1 (attB fwd)
IDS_D2_c_attB_rev	gtgccacttaacagttagctg	ggctgtgtcgcagacggcggtctccgtcgtcaggtatcatctactgttaggt	C2D2 (attB rev)
IDS_D2_c_attB_fwd	gtgccacttaacagttagctg	atgatcctgacgacggagacggccgtcgtcgacaagccctactgttaggt	C2D2 (attB fwd)
IDS2_A1_a_attP_rev_Ev oPreQ1_motif	gacacaaaaaactgccacagg	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctgtggcagtttaaaatt	A1B2 (attP rev)
IDS2_A1_a_attP_fwd_Ev oPreQ1_motif	gacacaaaaaactgccacagg	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctgtggcagtttaaaatt	A1B2 (attP fwd)
IDS2_A1_c_attP_rev_Ev oPreQ1_motif	gacacaaaaaactgccacagg	atgcgcgggttctatctagttagtcggttaaaccaactagaa	A1B3 (attP rev); A1B4 (attP rev)
IDS2_A1_c_attP_fwd_Ev oPreQ1_motif	gacacaaaaaactgccacagg	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctgtggcagttttataca	A1B3 (attP fwd); A1B4 (attP fwd)
IDS2_A1_a_attP_rev_Ev oPreQ1_motif	gacacaaaaaactgccacagg	tacacgcgggttctatctagttagtcggttaaaccaactagaa	A1B3 (attP rev); A1B4 (attP rev)
IDS2_A1_c_attP_fwd_Ev oPreQ1_motif	gacacaaaaaactgccacagg	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctgtggcagttttataaa	A1B3 (attP fwd); A1B4 (attP fwd)
IDS2_A4_b_attP_rev_Ev oPreQ1_motif	gcactcatttctccaagctc	atfttcgcgggttctatctagttagtcggttaaaccaactagaa	A4B7 (attP rev)
IDS2_A4_b_attP_fwd_Ev oPreQ1_motif	gcactcatttctccaagctc	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctcttgaggagaaacata	A4B7 (attP fwd)
IDS2_B2_a_attP_rev_Ev oPreQ1_motif	gtaggtacagggacagggcag	ataacgcgggttctatctagttagtcggttaaaccaactagaa	A1B2 (attP rev)
IDS2_B2_a_attP_fwd_Ev oPreQ1_motif	gtaggtacagggacagggcag	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctctgtccctcatag	A1B2 (attP fwd)
IDS2_B3_a_attP_rev_Ev oPreQ1_motif	gagataggttaggtacaggaca	tcgcgggttctatctagttagtcggttaaaccaactagaa	A1B3 (attP rev)
IDS2_B3_a_attP_fwd_Ev oPreQ1_motif	gagataggttaggtacaggaca	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctctgtacacctgaaag	A1B3 (attP fwd)
IDS2_B4_b_attP_rev_Ev oPreQ1_motif	gtgaaaagataggttaggtac	aacgcgggttctatctagttagtcggttaaaccaactagaa	A1B4 (attP rev)
IDS2_B4_b_attP_fwd_Ev oPreQ1_motif	gtgaaaagataggttaggtac	gtctgtgtcaaccaccgcggtctcagtggtgtacgggtacaaacctctctacctataaata	A1B4 (attP rev)
IDS2_B4_b_attP_fwd_Ev oPreQ1_motif	gtgaaaagataggttaggtac	atccgcgggttctatctagttagtcggttaaaccaactagaa	

IDS2_B4_b_attP_fwd_Ev oPreQ1_motif	gtgaaaagataggtaggtac	taccgtacaccactgagaccgcggtgtgaccagacaaacctctactatctaataa	A1B4 (attP fwd)
IDS2_B7_b_attP_rev_Ev oPreQ1_motif	gttatggtttactccatcta	atgccgcggttctatctagttacgcgttaaccaactagaa	A4B7 (attP rev)
IDS2_B7_b_attP_fwd_Ev oPreQ1_motif	gttatggtttactccatcta	gtctgtcaaccaccgcggtctcagtggtgtacggtacaaacctatggagtaaacccc	A4B7 (attP fwd)
IDS_C2_c_attB_rev_Evo PreQ1_motif	gttttggtttaccctatcta	ctttgccgcggttctatctagttacgcgttaaccaactagaa	C2D2 (attB rev); C2D2 (attB rev)
IDS_C2_c_attB_fwd_Evo PreQ1_motif	gttttggtttaccctatcta	taccgtacaccactgagaccgcggtgtgaccagacaaacctatggagtaaacccc	C2D1 (attB fwd); C2D2 (attB fwd)
IDS_D1_b_attB_rev_Evo PreQ1_motif	gctgtggaactgcaacacact	ctttctgcggttctatctagttacgcgttaaccaactagaa	C2D1 (attB rev)
IDS_D1_b_attB_fwd_Ev oPreQ1_motif	gctgtggaactgcaacacact	atgatcctgacgacggagaccgcggtcgtcgacaagccgtgttcagtaattaatccg	C2D1 (attB fwd)
IDS_D2_c_attB_rev_Evo PreQ1_motif	gtgccacctaacagttagctg	cgggttctatctagttacgcgttaaccaactagaa	C2D2 (attB rev)
IDS_D2_c_attB_fwd_Ev oPreQ1_motif	gtgccacctaacagttagctg	ggctgtgacgacggcggtctccgtcgtcaggatcatatagggtaaacatttaaga	C2D2 (attB fwd)

ED Figure 10a - twinPE mediated attB insertion in CCR5 region 2

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
CCR5_2_C1c	gatgcagagtcagcagaact	atgatcctgacgacggagaccgcggtcgtcgacaagccctctgactctg	indicated on the x-axis
CCR5_2_D1c	gggtccttgatgtctttcaa	ggctgtgacgacggcggtctccgtcgtcaggatcataaaagacatcaage	indicated on the x-axis
CCR5_2_C2b	gaaaagacatcaagcacaga	atgatcctgacgacggagaccgcggtcgtcgacaagccgtgcttgatgtc	indicated on the x-axis
CCR5_2_D4c	gacccctcagttattcagct	ggctgtgacgacggcggtctccgtcgtcaggatcattgaataactgagg	indicated on the x-axis
CCR5_2_C2c	gaaaagacatcaagcacaga	atgatcctgacgacggagaccgcggtcgtcgacaagccgtgcttgatgtctt	indicated on the x-axis
CCR5_2_D2a	gtgaaagacagcctggagtc	ggctgtgacgacggcggtctccgtcgtcaggatcattccaggct	indicated on the x-axis
CCR5_2_C3b	ggttttaggtcaagaagaaga	atgatcctgacgacggagaccgcggtcgtcgacaagccctcttctgaccta	indicated on the x-axis
CCR5_2_D2b	gtgaaagacagcctggagtc	ggctgtgacgacggcggtctccgtcgtcaggatcattccaggctgt	indicated on the x-axis
CCR5_2_D4a	gacccctcagttattcagct	ggctgtgacgacggcggtctccgtcgtcaggatcattgaataactg	indicated on the x-axis
CCR5_2_C5c	cacagtctcaccagactcc	atgatcctgacgacggagaccgcggtcgtcgacaagccgtctgggtgagac	indicated on the x-axis
CCR5_2_D3b	gtatttcagctgggatggga	ggctgtgacgacggcggtctccgtcgtcaggatcatatcccagct	indicated on the x-axis
CCR5_2_D4b	gacccctcagttattcagct	ggctgtgacgacggcggtctccgtcgtcaggatcattgaataactgag	indicated on the x-axis
CCR5_2_C6c	gctagattatgaatacacg	atgatcctgacgacggagaccgcggtcgtcgacaagccgttattcataatct	indicated on the x-axis
CCR5_2_D5c	gaacccatgaatgactact	ggctgtgacgacggcggtctccgtcgtcaggatcatatgatttcatggg	indicated on the x-axis
CCR5_2_C7c	gcacacatgagatctaggtg	atgatcctgacgacggagaccgcggtcgtcgacaagccctatagatctatgt	indicated on the x-axis
CCR5_2_D6b	gatgtgctaaatgctgcctg	ggctgtgacgacggcggtctccgtcgtcaggatcatgcagcatttag	indicated on the x-axis

ED Figure 10b - twinPE in multiple human cells

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
IDS2_A4_b_attP_rev	gcactcatttctccaagctc	taccgtacaccactgagaccgcggtgtgaccagacaaacctcttgaggaaaa	IDS2 (attP rev)
IDS2_B7_b_attP_rev	gttatggtttactccatcta	gtctgtgacacaccgcggtctcagtggtgtacggtacaaacctatggagtaaacct	IDS2 (attP rev)
IDS_C2_c_attB_fwd	gttttggtttaccctatcta	ggctgtgacgacggcggtctccgtcgtcaggatcatatagggtaaacca	IDS (attB fwd)
IDS_D2_c_attB_fwd	gtgccacctaacagttagctg	atgatcctgacgacggagaccgcggtcgtcgacaagccctcactgttaggt	IDS (attB fwd)
MYC_pegRNA_F1_22nt-insert	gaggctattctgccatttg	aaatgatggtgatgattgtttatgggcaga	MYC (22-nt)
MYC_pegRNA_R1_22nt-insert	gctttaccgccatccagttc	aacaccatcatcaccatcatttctggtatcggtg	MYC (22-nt)
TIMM44_pegRNA_F1_22nt-insert	gctggccagcctttctccag	ttcagagaagagatggaagacagagaaaggctgg	TIMM44 (22-nt)
TIMM44_pegRNA_R1_22nt-insert	gtcctgtctctggggccatcg	tgcttccatctcttctgaatggccccag	TIMM44 (22-nt)
CCR5_2_C5c	cacagtctcaccagactcc	atgatcctgacgacggagaccgcggtcgtcgacaagccgtctgggtgagac	CCR5_a (attB fwd)
CCR5_2_D3b	gtatttcagctgggatggga	ggctgtgacgacggcggtctccgtcgtcaggatcatatcccagct	CCR5_a (attB fwd)
CCR5_2_C2c	gaaaagacatcaagcacaga	atgatcctgacgacggagaccgcggtcgtcgacaagccgtgcttgatgtctt	CCR5_b (attB fwd)
CCR5_2_D2a	gtgaaagacagcctggagtc	ggctgtgacgacggcggtctccgtcgtcaggatcattccaggct	CCR5_b (attB fwd)

ED figure 10c – Editing activity of Cas9 nickase, PE2-dead RT variant, and PE2

pegRNA	spacer sequence	3' extension	Edits made by the specified pegRNA
PAH_E7.2_55_EvoPreQ1	gtggtttccgctccgacctg	acgcggaatgcgagacccccagaaagtctctactgtcaagagcccggaacggg	Also used in Fig. 2c
PAH_E7.6_56_EvoPreQ1	gtctgatgtactgtgtgcag	tcgagggcggtctctcttgcagcggttctatctatgacggttaaccaactagaaa	Also used in Fig. 2c
AAVS1_A3835a	gacgtcacggcgctgccccca	gggtcttctgacgtagagactttctgggggtctcgcattccgctgttttattgcaca	Also used in ED Fig. 3
AAVS1_B3930a	ggacttccagtggtcatcg	cagtacatctcttcttgacgcggttctatctagttacgcgttaaccaactagaaa	Also used in ED Fig. 3
CCR5_2_C2_c_attP	gaaaagacatcaagcacaga	taccgtacaccactgagaccgcggtgtgaccagacaaacctggcagcgcc	
fwd_pegRNA1		gtctgtgacacaccgcggttctcagtggtgtacggtacaaacctgtcacactg	
CCR5_2_D2_a_attP	gtgaaagacagcctggagtc	agggtttgtaccgtacaccactgagaccgcggtgtgaccagacaaacctgtgcttgat	
rev_pegRNA2		gtctt	
PE3_CCR5_1_F414a_34_FKBP108	ggtacatctgattgtcagg	agggtttgtgtgtaaccaccgcggtctcagtggtgtacggtacaaaccttcaggct	
		tactgtcccttctgggtcactatctgtccgccaatttttccatcttcaagcatcccg	Also used in ED Fig. 1a
		gtgtagtgcaccacgcaggtctgtcccgcttggggaaggtgcgcccgtctcctggg	
		gagatggtttccactgcactccgacaatcga	

PE3_CCR5_1_F414a_29_FKBP108	ggtacatcatcattgtcagg	tcccccttgggctcactatgctgccccaatttcttccatcttcaagcatcccgggtgta gtgaccacgcaggtctggccgcgttggggaaggctgcgccgtctctctggggaga tggttccactgcactccgacaatcga	Also used in ED Fig. 1a
IDS2_DF_A4_b_attP_fw d	gcactcatttctccaagctc	gtctggtcaaccaccgcggtctcagtgggtgtacgggtacaaaccttggagggaaa	Also used in Fig. 4b
IDS2_DF_B7_b_attP_fw d	gttatggtttactccatcta	taccgtacaccactgagaccgcggtgtgtgaccagacaaacctatggagtaaacc	Also used in Fig. 4b

**Supplementary Note 1 - TwinPE PCR bias assessment
pegRNA**

	spacer sequence	3' extension	Edits made by the specified pegRNA
CCR5_A223c	gtcatctgataaactgcaaa	atgatcctgacgacggagaccgccgtcgtcgacaagccgcagtttatcagg	A223c+B272a; A223c+B291b; A223c+B305a; A223c+B326b; A223c+B330b
CCR5_B272a	gaaggaaaaacagggtcagaga	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatctgacctg	A223c+B272a
CCR5_B291b	gccagaaagggacagtaaga	ggcttgtcgcacgacggcggtctccgtcgtcaggatcattactgtccct	A223c+B291b
CCR5_B305a	ggcagcatatgtgagccaga	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatgggtcact	A223c+B305a
CCR5_B326b	gatttccaaatgccactggg	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatagtgggactttg	A223c+B326b; A260c+B326b
CCR5_B330b	gtgtatttccaaagtcccac	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatggactttggaa	A223c+B330b
CCR5_A260c	gtgacatctactcgtcaacc	atgatcctgacgacggagaccgccgtcgtcgacaagcctgagcaggtagat	A260c+B305c; A260c+B326b; A260c+B330c
CCR5_B305c	ggcagcatatgtgagccaga	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatgggtcactatgc	A260c+B305c
CCR5_B330c	gtgtatttccaaagtcccac	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatggactttggaaat	A260+B330c
CCR5_A325b	gtcactatgtgtgcccccag	atgatcctgacgacggagaccgccgtcgtcgacaagccggcgagcat	A325b+B414a
CCR5_B414a	ggtacatcatcattgtcagg	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatgacaatcga	A325b+B414a; A360b+B414a
CCR5_A360b	gacatgtgtcaactcttgac	atgatcctgacgacggagaccgccgtcgtcgacaagccaagagttgacac	A360b+B414a
CCR5_A506c	gacaagtgatcacttggg	atgatcctgacgacggagaccgccgtcgtcgacaagccaagtgatcacatt	A506c+B584a
CCR5_B584a	gtatggaaaatgagagctgc	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatgtctcatt	A506c+B584a
CCR5_A509a	gaagtgtgatcacttgggtgg	atgatcctgacgacggagaccgccgtcgtcgacaagccccaagtga	A509a+B535c; A509a+B584a
CCR5_B535c	gatctggtaaagatttcc	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatatcatctttaccag	A509_B535c
CCR5_A531c	gctgtgtttgcgtctctccc	atgatcctgacgacggagaccgccgtcgtcgacaagccagagacgcaaaaca	A531c+B584b
CCR5_B584b	gtatggaaaatgagagctgc	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatgtctcattttc	A531c+B584b
CCR5_2_C2b	gaaaagacatcaagcacaga	atgatcctgacgacggagaccgccgtcgtcgacaagccgtgcttgatgtc	C2b+D4c
CCR5_2_D4c	gaccctcagttattcagct	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatgaaatactgaggg	C2b+D4c
CCR5_2_C2c	gaaaagacatcaagcacaga	atgatcctgacgacggagaccgccgtcgtcgacaagccgtgcttgatgtctt	C2c+D2a
CCR5_2_D2a	gtgaaagacagcctggagtc	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatcaggct	C2c+D2a
CCR5_2_C3b	ggtttaggtcaagaagaaga	atgatcctgacgacggagaccgccgtcgtcgacaagccctcttcttgaccta	C3b+D2b; C3b+D4a
CCR5_2_D2b	gtgaaagacagcctggagtc	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatccaggctgt	C3b+D2b
CCR5_2_D4a	gaccctcagttattcagct	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatgaaatactg	C3b+D4a
CCR5_2_C4b	gatggattggtgtaaaagga	atgatcctgacgacggagaccgccgtcgtcgacaagccctttacaccaatc	C4b+D2a
CCR5_2_D2a	gtgaaagacagcctggagtc	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatcaggct	C4b+D2a
CCR5_2_C5c	cacagtctcaccagactcc	atgatcctgacgacggagaccgccgtcgtcgacaagccgtctgggtgagac	C5c+D3b; C5c+D4b
CCR5_2_D3b	gtatttcagctgggatggga	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatcatccagct	C5c+D3b
CCR5_2_D4b	gaccctcagttattcagct	ggcttgtcgcacgacggcggtctccgtcgtcaggatcatgaaatactgag	C5c+D4b
HEK3_DF_A_SA_ del77nt	ggcccagactgagcacgtga	tcctctgccatcacgtgtcagctg	SA (Δ 77nt)
HEK3_DF_B_SA_ del77nt	gtcaaccagtatcccgtgc	tgatggcagagagaccgggatactgg	SA (Δ 77nt)
HEK3_DF_A_SA_ del56nt	ggcccagactgagcacgtga	tggaggaagcagggcttctctctgccatcacgtgtcagctgtg	SA (Δ 56nt)
HEK3_DF_B_SA_ del56nt	gtcaaccagtatcccgtgc	tgatggcagagaaaggaagccctgcttccaccgggatactgg	SA (Δ 56nt)
HEK3_DF_A_HA_ del64nt	ggcccagactgagcacgtga	tgacaggagctgcatcctctgccatcacgtgtcagctgtg	HA (Δ 64nt)
HEK3_DF_B_HA_ del64nt	gtcaaccagtatcccgtgc	tgatggcagagatgacagctcctgcaccgggatactgg	HA (Δ 64nt)
HEK3_DF_A_PD_ del90nt	ggcccagactgagcacgtga	gcccagccaaactgtcaaccagtatcccggcgtgtcagctgtg	PD (Δ 90nt)
HEK3_DF_B_PD_ del90nt	gtcaaccagtatcccgtgc	gggtcaatccttggggcccagactgagcacggcgatactgg	PD (Δ 90nt)

Supplementary Table 2. Sequences of primers used for mammalian cell genomic DNA amplification and HTS

Primers (All sequences are shown in 5' to 3' orientation)

Figure 1

HEK3_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNATGTGGGCTGCCTAGAAAGG
HEK3_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCAGCCAACTTGCAACC

Figure 2

PAH_AVA1686	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCCATCACCATTGGCTGGGAT
PAH_AVA1687	TGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGAGGAGAGGCACTGAA
PAH_AVA1696	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNACCTAAAGGTCTCCTAGTGCCT
PAH_AVA1697	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCAGCAATGAACCCAAACCTC
HEK3_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNATGTGGGCTGCCTAGAAAGG
HEK3_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCAGCCAACTTGCAACC
DMD_UMI_fwd1	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNNNNNNNNNNTGCTGGCCAGTTTACTAACAAT
DMD_UMI_fwd2	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNNNNNNNNNNCAGAAAGAAGATCTTATCCCATC
	TTG
DMD_rev0	TGGAGTTCAGACGTGTGCTCTTCCGATCTGGCTACTTTTGTATTGTCATT

Figure 3

AAVS1_AVA1713	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCAGAGCAGGGTCCCGCTTC
AAVS1_AVA1717	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNACGGGGCTCAGTCTGAAGAG
AAVS1_AVA1651	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGCCAAGGACTCAAACCCAGA
AAVS1_AVA1652	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCCGTGCGTCAGTTTACCT
AAVS1_AVA1653	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNAACTGCTTCTCCTCTTGGGAA
AAVS1_AVA1715	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCCGATCTGCCAGAACCTCTAAGGT
AAVS1_AVA1655	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNATCCTCTCTGGCTCCATCGTA
AAVS1_AVA1656	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCCACTTCAGGACAGCATGTTT
AAVS1_AVA1707	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCGCCGGGAAGTCCCGCTGGC
AAVS1_AVA1710	TGGAGTTCAGACGTGTGCTCTTCCGATCTGAGGAGGCCCTCATCTGGCG
CCR5_AVA1678	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNAAATCAATGTGAAGCAAATCGCAGC
CCR5_AVA1679	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCGATTGTCAGGAGGATGATGAA
CCR5_AVA1680	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTCCTTCTTACTGTCCCTTCTGGGC
CCR5_AVA1681	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCAAAACACAGCATGGACGAC
CCR5_AVA1682	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNACAATCGATAGGTACCTGGCTGTC
CCR5_AVA1683	TGGAGTTCAGACGTGTGCTCTTCCGATCTACCAGCCCCAAGATGACTAT
ALB_AVA1760	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNTTGGCATTATTTCTAAAAATGGCATA
ALB_AVA1759	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCTATCAACAGCAACCAAGAAGACAGACT

Figure 4

IDS_AVA1763	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCTGAAAACCTGAGCTTGGAGG
IDS_AVA1764	TGGAGTTCAGACGTGTGCTCTTCCGATCTGTCTACTCCAGCTTAATGGAAGTGG
IDS_AVA1765	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGAGAAGATGTGGAAATGCCTCAC
IDS_AVA1766	TGGAGTTCAGACGTGTGCTCTTCCGATCTAATCAACATGAAGGGTTGTGTTGT
IDS_AVA1769	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGTTCACACATGCGTTCCCTC
IDS_AVA1770	TGGAGTTCAGACGTGTGCTCTTCCGATCTGGCATGAAGGGTTGTTTAAATTGA
IDS_UMI_junc1_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNNNNNNNNNCCCTGTCTGTACCTACCTAT
IDS_junc2_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNTTGACTCATGCCCTACGAGG
IDS_universal_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTCTCAAATTTACCCGTGGCAGC

ED Figure 1 - Long tPE insertions at CCR5

CCR5_AVA1682	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNACAATCGATAGGTACCTGGCTGTC
CCR5_AVA1683	TGGAGTTCAGACGTGTGCTCTTCCGATCTACCAGCCCCAAGATGACTAT

ED Figure 2 - pegRNAs screen at PAH

PAH_AVA1684	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNTGTCCATGGAGGTTTAACAGGA
PAH_AVA1685	TGGAGTTCAGACGTGTGCTCTTCCGATCTACATGGAAGTTTGCTACGACAT
PAH_AVA1686	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCCATCACCATTGGCTGGGAT
PAH_AVA1687	TGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGAGGAGAGGCACTGAA
PAH_AVA1689	TGGAGTTCAGACGTGTGCTCTTCCGATCTGGTAAGAGGAAGGAGGGGA
PAH_AVA1690	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGAGAGCCCCATTCAAAGCA
PAH_AVA1691	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCAGGACTCTTCATGCTGGT
PAH_AVA1696	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNACCTAAAGGTCTCCTAGTGCCT
PAH_AVA1697	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCAGCAATGAACCCAAACCTC
PAH_AVA1702	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGGCCAAGTACTAGGTTGGTTCT
PAH_AVA1703	TGGAGTTCAGACGTGTGCTCTTCCGATCTTAACCTGGCTTCCAGGGGAGT
PAH_exon10_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGACACACCCCAAAATAATGC
PAH_exon10_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTTTGAAAGCACAATAATGTTTTT
PAH_exon11_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCAGGGAATACTGATCCTGAT
PAH_exon11_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTCAACCAACCCACAGATGAGT
PAH_exon12_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGAGGTGTCCGTGTTCTAA
PAH_exon12_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTCGATGGTAGGGAAAGACAGT

ED Figure 3 - pegRNA screen at CCR5 region 1

CCR5_AVA1678	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNAAATCAATGTGAAGCAAATCGCAGC
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CCR5_AVA1679	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCGATTGTCAAGGAGGATGATGAA
CCR5_AVA1680	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTCCTTCTTACTGTCCCCTTCTGGGC
CCR5_AVA1681	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCAAAACACAGCATGGACGAC
CCR5_AVA1682	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNACAATCGATAGGTACCTGGCTGTC
CCR5_AVA1683	TGGAGTTCAGACGTGTGCTCTTCCGATCTACCAGCCCCAAGATGACTAT

ED Figure 4 - pegRNA screen at AAVS1

AAVS1_AVA1713	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCAGAGCAGGGTCCCGCTTC
AAVS1_AVA1717	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNACGGGGCTCAGTCTGAAGAG
AAVS1_AVA1651	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGCCAAGGACTCAAACCCAGA
AAVS1_AVA1652	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCCGTGCGTCAGTTTACCT
AAVS1_AVA1653	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNAACTGCTTCTCTCTTGGGAA
AAVS1_AVA1715	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCCCTTGCCAGAACCCTCTAAGGT
AAVS1_AVA1655	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNATCCTCTCTGGCTCCATCGTA
AAVS1_AVA1656	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCCACTTCAGGACAGCATGTTT
AAVS1_AVA1707	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCGCCGGGAAGTCCCGCTGGC
AAVS1_AVA1710	TGGAGTTCAGACGTGTGCTCTTCCGATCTGAGGAGGCCCTCATCTGGCG

ED Figure 5 - Comparison of twinPE- and PE3-mediated attB insertion at CCR5 region 1

CCR5_AVA1680	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTCCTTCTTACTGTCCCCTTCTGGGC
CCR5_AVA1681	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCAAAACACAGCATGGACGAC
CCR5-2_fwd2	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNAGAGGAGTCAAGAGAGAATCCC
CCR5-2_rev2	TGGAGTTCAGACGTGTGCTCTTCCGATCTTTCCTAGACCTCATACCTCGT

ED Figure 6b - HTS Junction Purity

CCR5_AVA1680	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTCCTTCTTACTGTCCCCTTCTGGGC
CCR5_AVA1682	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNACAATCGATAGGTACCTGGCTGTC
AAVS1_AVA1717	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNACGGGGCTCAGTCTGAAGAG
AAVS1_AVA1707	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCGCCGGGAAGTCCCGCTGGC
Donor_CJP140	TGGAGTTCAGACGTGTGCTCTTCCGATCTGAACCTCAGGGTCAGCTTGC

ED Figure 6c - HTS Junction Purity (the other donor-genome junction)

CCR5_AVA1681	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCAAAACACAGCATGGACGAC
CCR5_AVA1683	TGGAGTTCAGACGTGTGCTCTTCCGATCTACCAGCCCCAAGATGACTAT
AAVS1_AVA1713	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCAGAGCAGGGTCCCGCTTC
AAVS1_AVA1710	TGGAGTTCAGACGTGTGCTCTTCCGATCTGAGGAGGCCCTCATCTGGCG
Donor_other_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGCAAGCTTACATCGAGATCC

ED Figure 6e - Overlap reduction

CCR5_AVA1682	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNACAATCGATAGGTACCTGGCTGTC
CCR5_AVA1683	TGGAGTTCAGACGTGTGCTCTTCCGATCTACCAGCCCCAAGATGACTAT

ED Figure 7b

OT1_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGGAAATAAGTTATCACAATGGGAAAT
OT1_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTCGCGATTCTTAAAGGAGAGG
OT2_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCCATTTCATATTTTGAAACAAAAGG
OT2_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCATTGCACTCCTACATACAACA
OT3_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGCTGTGGTTATTCCCAGCTC
OT3_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTGGGAACACTGGACAAAATCC
OT4_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGGAAAGCTTTGACAAGTGGA
OT4_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCCTACTTGCCCTTCTTCT
OT5_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGCATTGCACTCCTACATACAACA
OT5_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCATTTCATATTTTGAAACAAAAGG

ED Figure 7c

Donor_CJP140 (with OT1_fwd or OT2_fwd)	TGGAGTTCAGACGTGTGCTCTTCCGATCTGAACCTCAGGGTCAGCTTGC
Donor_fwd_primer (with OT3_rev, or OT4_rev, or OT5_rev)	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGAACTTCAGGGTCAGCTTGC

ED Figure 9

IDS_AVA1763	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCTGAAAACCTGAGCTTGAGG
IDS_AVA1764	TGGAGTTCAGACGTGTGCTCTTCCGATCTGTCTACTCCAGCTTAATGGAAGTGG
IDS_AVA1765	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGAGAAGATGTGGAAATGCCTCAC
IDS_AVA1766	TGGAGTTCAGACGTGTGCTCTTCCGATCTAATCAACATGAAGGGTTGTGTTGT
IDS_AVA1769	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGTCCACACATGCGTTCTC
IDS_AVA1770	TGGAGTTCAGACGTGTGCTCTTCCGATCTGGCATGAAGGGTTGTTTAAATTGA

ED Figure 10

CCR5-2_Fwd1	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGGTATTCGTGCAGCATATGAG
CCR5-2_Rev1	TGGAGTTCAGACGTGTGCTCTTCCGATCTTATTTCAAGCTGGGATGGGAAGG
CCR5-2_fwd2	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNAGAGGAGTCAAGAGAGAATCCC
CCR5-2_rev2	TGGAGTTCAGACGTGTGCTCTTCCGATCTTTCCTAGACCTCATACCTCGT
CCR5-2_Fwd3	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCACTGAATGCTTCTGACTTCATAG
CCR5-2_Rev3	TGGAGTTCAGACGTGTGCTCTTCCGATCTTTTGTCTAATGCTTTGTCTCAGT
IDS_AVA1765	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNGAGAAGATGTGGAAATGCCTCAC
IDS_AVA1766	TGGAGTTCAGACGTGTGCTCTTCCGATCTAATCAACATGAAGGGTTGTGTTGT

IDS_AVA1769	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGTTCACACATGCGTTCCTC
IDS_AVA1770	TGGAGTTCAGACGTGTGCTCTTCCGATCTGGCATGAAGGGTTGTTTAAATTGA
CCR5-2_fwd2	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNAGAGGAGTCAGAGAGAATCCC
CCR5-2_rev2	TGGAGTTCAGACGTGTGCTCTTCCGATCTTTCCTAGACCTCATACCTCGT
MYC_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNTTGCACCTGGAACCTACAACAC
MYC_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTGGCAGAAATCTCGAAAGG
TIMM44_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNAGACCTGTACATTGCGGC
TIMM44_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTAAAAGCCCAGTGCTGCTC

Supplementary Table 5 - TwinPE-mediated off-target genome editing

HEK3_OT1_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNTCCCTGTGACCTGGAGAA
HEK3_OT1_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTCACTGTACTTGCCCTGACCA
HEK3_OT2_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNTTGGTGTGACAGGGAGCAA
HEK3_OT2_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTCTGAGATGTGGGCAGAAAGGG
HEK3_OT3_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNTGAGAGGGAACAGAAGGGCT
HEK3_OT3_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTGTCCAAAGGCCCAAGAACCT
HEK3_OT4_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNTCCTAGCACTTTGGAAGGTGCG
HEK3_OT4_rev	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCTCATCTTAATCTGCTCAGCC

Supplementary Note 1 - Analysis of editing quantification bias

UMI_HEK3_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNNNNNNNNNNNATGTGGGCTGCCTAGAAAGG
UMI_CCR5-2_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNNNNNNNNNNNAGAGGAGTCAGAGAGAATCCC
UMI_AVA1678_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNNNNNNNNNNAATCAATGTGAAGCAAATCGCAG C
UMI_AVA1680_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNNNNNNNNNNTCCTTCTTACTGTCCCCTTCTGGG C
UMI_AVA1682_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNNNNNNNNNNACAATCGATAGGTACCTGGCTGT C
5p constant primer	ACACTCTTTCCCTACACG

Supplementary Table 3. Sequences of primers and probes used for ddPCR assays

Fig 3d				
Assay	fwd	rev	Probe	Samples
CCR5_B6	catctctgacctgttttcc	tcctcgcccttctcac	/56-FAM/ACGACGGCG/ZEN/GTCTCAGTGGTG/3IABkFQ/	325/414
CCR5_B8_1	gccaggacgggtcacctt tg	tcctcgcccttctcac	/56-FAM/ACGACGGCG/ZEN/GTCTCAGTGGTG/3IABkFQ/	507/584, 510/584, 532/584
AAVS1_1077	ggaacggggctcagtct	tcctcgcccttctcac	/56-FAM/ACCACCGCG/ZEN/GTCTCCGTCGT/3IABkFQ/	1077/1154
AAVS1_3786	ggcaagcttacatcgag atcc	gaggaggccctcatctg gcg	/56-FAM/ACGACGGCG/ZEN/GTCTCAGTGGTG/3IABkFQ/	3786/3903, 3786/3930
ACTB	acactgtgcccatctac	aatgtcacgcacgatttc	/5HEX/CGGGACCTG/ZEN/ACTGACTACCTCAT/3IABkFQ/	all
Fig 3e				
Assay	fwd	rev	Probe	Samples
CCR5_B8_2	gccaggacgggtcacctt tg	tcctcgcccttctcac	/56-FAM/CTCAGTGGT/ZEN/GTACGGTACAAACCC/3IABkFQ/	all
ACTB	acactgtgcccatctac	aatgtcacgcacgatttc	/5HEX/CGGGACCTG/ZEN/ACTGACTACCTCAT/3IABkFQ/	all
Fig 3g				
Assay	fwd	rev	Probe	Samples
CCR5_B8_1	gccaggacgggtcacctt tg	tcctcgcccttctcac	/56-FAM/ACGACGGCG/ZEN/GTCTCAGTGGTG/3IABkFQ/	CCR5 samples
ALB	gtgactgtaattttctttg cg	tcctcgcccttctcac	/56-FAM/ACGACGGCG/ZEN/GTCTCAGTGGTG/3IABkFQ/	ALB samples
ACTB	acactgtgcccatctac	aatgtcacgcacgatttc	/5HEX/CGGGACCTG/ZEN/ACTGACTACCTCAT/3IABkFQ/	all
ED Fig 6a				
Assay	fwd	rev	Probe	Samples
CCR5_B8_2	gccaggacgggtcacctt tg	tcctcgcccttctcac	/56-FAM/CTCAGTGGT/ZEN/GTACGGTACAAACCC/3IABkFQ/	all
ACTB	acactgtgcccatctac	aatgtcacgcacgatttc	/5HEX/CGGGACCTG/ZEN/ACTGACTACCTCAT/3IABkFQ/	all
ED Fig 6c				
Assay	fwd	rev	Probe	Samples
AAVS1_1077	ggaacggggctcagtct	tcctcgcccttctcac	/56-FAM/ACCACCGCG/ZEN/GTCTCCGTCGT/3IABkFQ/	all
CCR5_B8_1	gccaggacgggtcacctt tg	tcctcgcccttctcac	/56-FAM/ACGACGGCG/ZEN/GTCTCAGTGGTG/3IABkFQ/	attB
CCR5_B8_2	gccaggacgggtcacctt tg	tcctcgcccttctcac	/56-FAM/CTCAGTGGT/ZEN/GTACGGTACAAACCC/3IABkFQ/	attB-GA
CCR5_B8_3	gccaggacgggtcacctt tg	tcctcgcccttctcac	/56-FAM/ACCACCGCG/ZEN/GTCTCCGTCGT/3IABkFQ/	attP
CCR5_B8_4	gccaggacgggtcacctt tg	tcctcgcccttctcac	/56-FAM/CTCCGTCGT/ZEN/CAGGATCATCCGT/3IABkFQ/	attP-GA
ACTB	acactgtgcccatctac	aatgtcacgcacgatttc	/5HEX/CGGGACCTG/ZEN/ACTGACTACCTCAT/3IABkFQ/	all

Supplementary Table 4. Sequence of recoded exonic *PAH* sequences

Nucleotides labeled in red indicate positions where silent mutations were introduced.

Spacer 1	Spacer 2	Recoded allele product
2.1	2.2	GAAGACAAC T GCAATCA G AACGGCGCTATCTCTCTGATCTTCAGCCTGAAGGAAGAGGTGGCGCCCTGGC GAA G GTATTGCGCTTATTTGAG
4.1	4.3	TTCTCTGTGTTTCAGTGCC G TGGTTTCCACGGACAA T TCAGGA A CTTGATAGGTT C GTAA T CAAA T CTTGT CCTACGGAGCCGA A CTTGACGCTGATCA T CCTGTGAGTCCATGGCCCG
4.1	4.4	TTCTCTGTGTTTCAGTGCC G TGGTTTCCACGGACAA T TCAGGA A CTTGATAGGTT C GTAA T CAAA T CTTGT CCTACGGAGCCGA A CTTGACGCTGATCA T CCTGTGAGTCCATGGCCCGTAG
4.2	4.3	CCCAAGAACCATTCAAGAA A CTTGATAGGTT C GTAA T CAAA T CTTGTCTACGGAGCCGA A CTTGACGCTG ATCA T CCTGTGAGTCCATGGCCCG
4.2	4.4	CCCAAGAACCATTCAAGAA A CTTGATAGGTT C GTAA T CAAA T CTTGTCTACGGAGCCGA A CTTGACGCTG ATCA T CCTGTGAGTCCATGGCCCGTAG
4.2	4.5	CCCAAGAACCATTCAAGAA A CTTGATAGGTT C GTAA T CAAA T CTTGTCTACGGAGCCGA A CTTGACGCTG ATCA T CCTGTGAGTCCATGGCCCGTAGGATGAGATT
5.1	5.2	CAGGTGCTCTTTTCTCTAGGGCTTCAAGGACCCCGTTATCGCGCCCGCCGTAAGCAATT C GC C GATATT GCATATA A TTATCGCCAGTAAGTCTGCCTTGCTT
7.1	7.5	CTTTTCATCCCAGCTTGTACTGGCTTTCGACTCCGCCCGTTGCCGGGCTCTTGAGCAGTAGAGACTTCTTG GGGGTCTCGCCTTCCGAGTCTTCCACT
7.1	7.6	CTTTTCATCCCAGCTTGTACTGGCTTTCGACTCCGCCCGTTGCCGGGCTCTTGAGCAGTAGAGACTTCTTG GGGGTCTCGCATTC C CGCTGTTTCATTGCACACAGTACATCAGAC
7.2	7.5	TGGTTTCCGCCTCCGACCCGT T GCCGGGCTCTTGAGCAGTAGAGACTTCTTGGGGGGTCTCGCCTCCGAGT CTTCCACT
7.2	7.6	TGGTTTCCGCCTCCGACCCGT T GCCGGGCTCTTGAGCAGTAGAGACTTCTTGGGGGGTCTCGCATTC C CGT GTTTCATTGCACACAGTACATCAGAC
7.2	7.7	TGGTTTCCGCCTCCGACCCGT T GCCGGGCTCTTGAGCAGTAGAGACTTCTTGGGGGGTCTCGCATTC C CGT GTTTCATTGT A CCAGTATATTAGGCATGGTTCAAAACCGATGTACACACCAGAA
7.3	7.6	GGCTGGCCTGCTTCTCTGTAGAGACTTCTTGGGGGGTCTCGCATTC C CGTGTTTCATTGTACCAGTATATT CAGAC
7.3	7.7	GGCTGGCCTGCTTCTCTGTAGAGACTTCTTGGGGGGTCTCGCATTC C CGTGTTTCATTGTACCAGTATATT AGGCATGGTTCAAAACCGATGTACACACCAGAACCGTGAGTACTGTCC
9.1	9.2	TTCCCCCAATTACAGGAGATCGGTCTGGCAAGCCTGGGAGCACCAGACGAGTATATAGAGAACTTGCTAC AGTAAGTCCCTTCTCTCC
9.1	9.3	TTCCCCCAATTACAGGAGATCGGTCTGGCAAGCCTGGGAGCACCAGACGAGTATATAGAGAACTTGCTAC AGTAAGTCCCTTCTCTCCCTGGGTGGATGGT
10.2	10.3	CCAGATTTACTGGTTTACCGTCGAATT C GGATTGTGTAA G CAGGGTGATAGCATTAA G CCTACGGAGCAG GTTTGCTCTCATCCTTGGTGAAATTAC
11.1	11.4	GAAGCCAAAGCTTCTCCC A CTCGA A CTCGAAAAGACTGCAATT C AGA A CTATACAGTGACAGAA T TTCAAC CA T TGTATTACGTGGCAGAGAGTT
11.2	11.4	AAAGCTTCTCCCCTGGA A CTCGAAAAGACTGCAATT C AGA A CTATACAGTGACAGAA T TTCAACCATTGT ATTACGTGGCAGAGAGTT
12.2	12.4	ACTTTGCTGCCACAATACCA A GAC A TTTAGCGTGAGATATGATCCTTATACACAGCGCATCGAAGTGCTC GATA A CACTCAACAGCTTAAGATTTTGGCTG
12.3	12.5	GCTACGACCCATACACCCA G CGCATCGAAGT G CTCGATA A CACTCA A CAATTGAAGATCCTCGCAGACAGT ATCAACAGTAAGTAATTTACAC

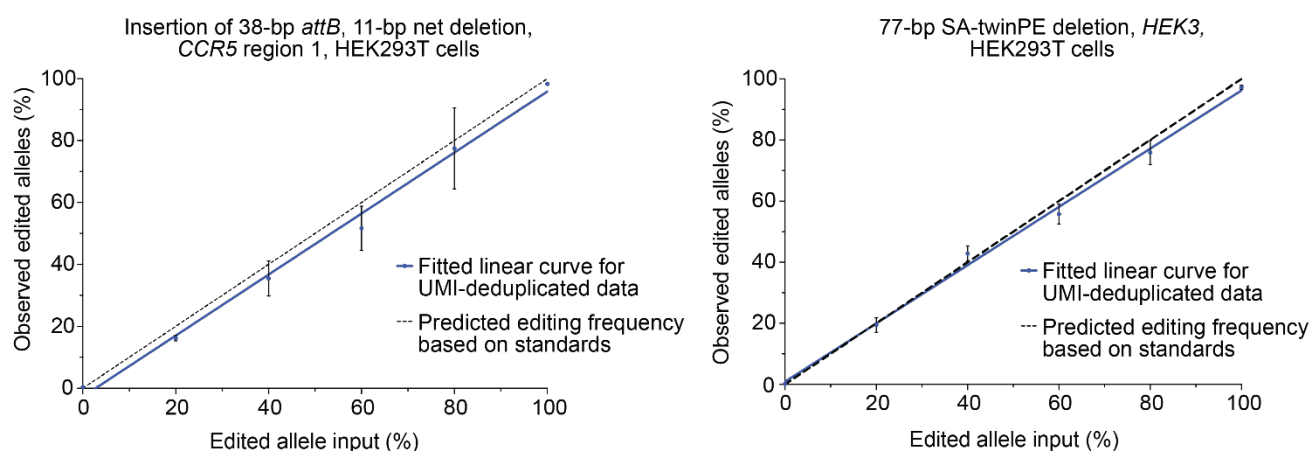
Supplementary Table 5. TwinPE-mediated off-target genome editing.

twinPE-mediated % editing at <i>HEK3</i> on-target site and off-target sites									
<i>HEK3</i>		standerd pegRNAs				enhanced pegRNAs			
	Untreated	SA ($\Delta 77$ nt)	SA ($\Delta 56$ nt)	HA ($\Delta 64$ nt)	PD ($\Delta 90$ nt)	SA ($\Delta 77$ nt)	SA ($\Delta 56$ nt)	HA ($\Delta 64$ nt)	PD ($\Delta 90$ nt)
on-target site	<0.1	14.8	18.8	11.7	40.4	29.6	28.5	29.5	59.5
off-target site 1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
off-target site 2	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
off-target site 3	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
off-target site 4	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1

Supplementary Note 1. Analysis of editing quantification

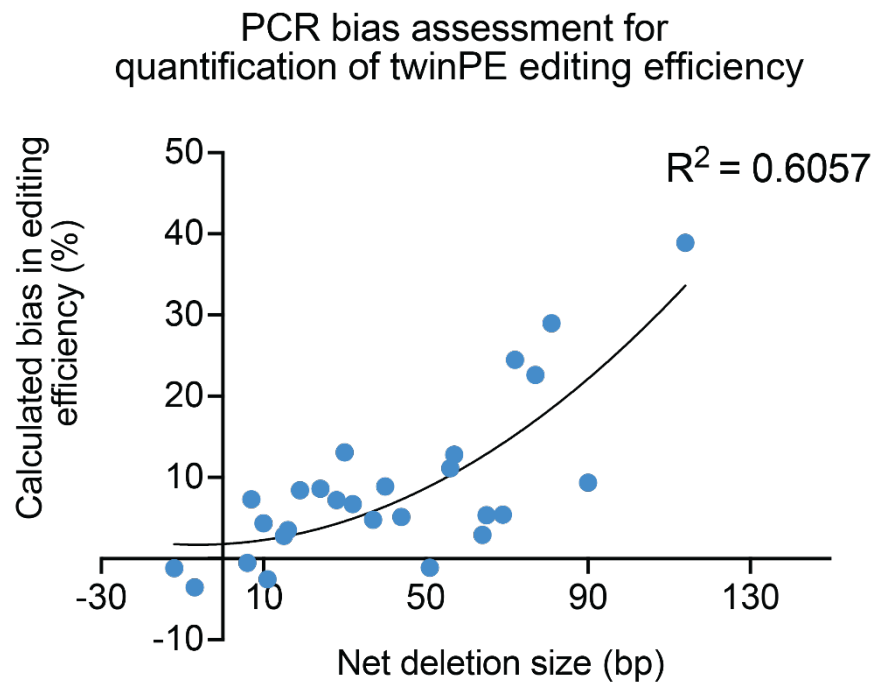
To assess quantification bias, we applied unique molecular identifiers (UMIs) to index individual allele copies using linear amplification followed by bead-based purification, PCR amplification, and Illumina MiSeq amplicon sequencing (see method section for details) similar to the method used by Choi, et al¹ and Bolukbasi, et al². Reads containing identical UMIs are first aligned and then collapsed (deduplicated) to a single consensus sequence. This workflow allows for quantification of allele frequencies based on UMI counts instead of total read counts, which may be subject to PCR amplification bias based on sequence composition or amplicon size differences between different allele products.

To ensure the UMI-sequencing protocol can faithfully quantify the editing efficiency, we mixed chemically synthesized gene fragments (IDT) replicating either an edited or wild-type allele for the given edits (insertion of *attB* at *CCR5* or 77-nt deletion at *HEK3*) to simulate 0%, 20%, 40%, 60%, 80%, and 100% editing efficiencies before diluting the mixed standards to 2000 genetic copies/ μ L, which is the estimated allele copy number amplified from our cell editing experiments. Diluted standards were then subjected to UMI barcoding, MiSeq analysis, and deduplication. We plotted the percentage of observed edited alleles from three independent biological replicates after sequencing and UMI deduplication against the expected edited allele percentage based on the input allele fraction.



Next, we prepared libraries of twinPE-edited samples from *CCR5* region 1 (15 samples), *CCR5* region 2 (7 samples), *HEK3* (4 samples), and *IDS* (1 sample). By comparing the editing efficiency calculated from total reads and the editing efficiency calculated from reads deduplicated based on UMIs, we estimated the bias in editing efficiency quantification

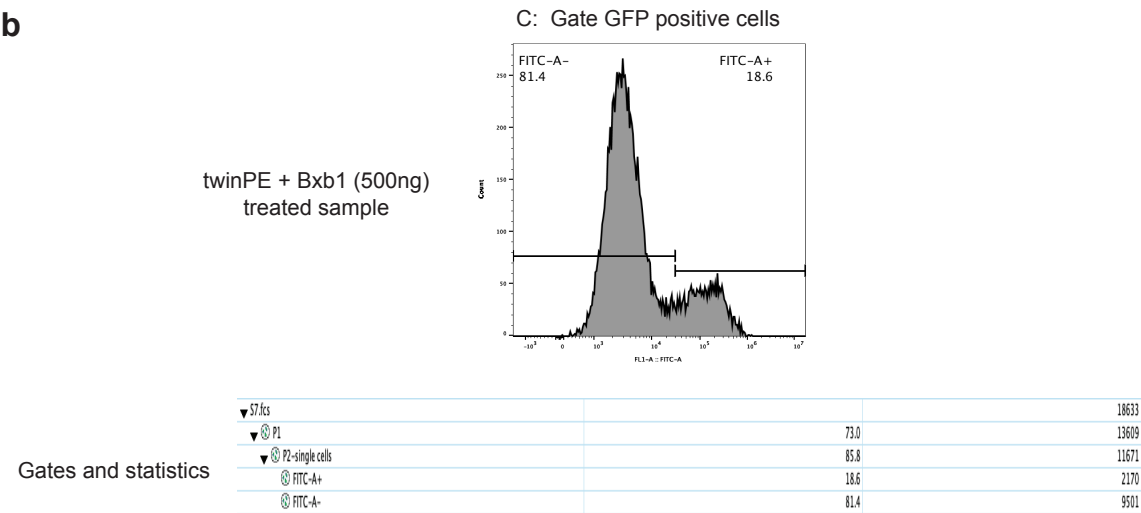
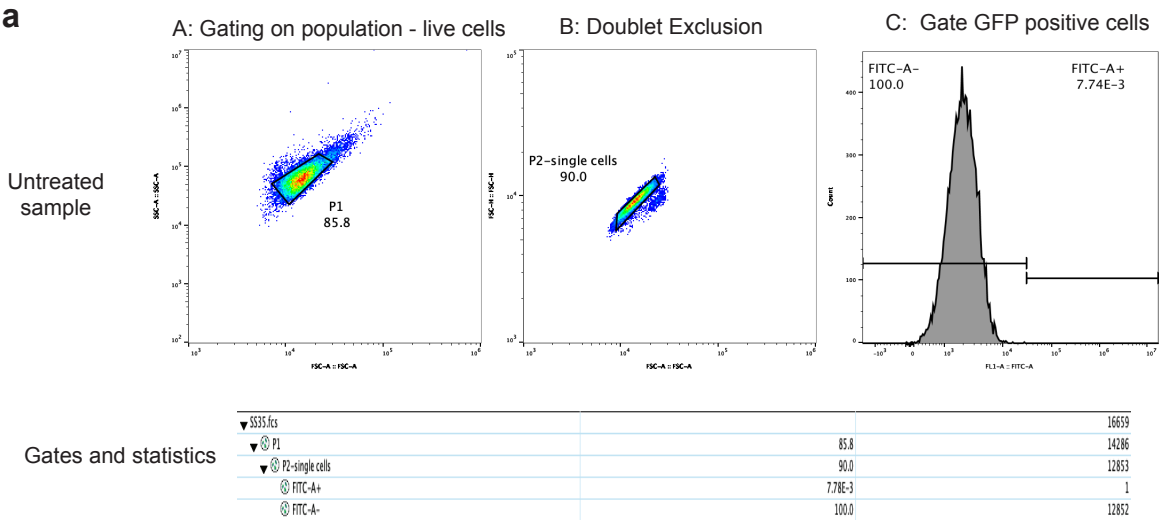
using the linear amplification with UMIs as the “true” editing efficiency. When plotting quantification bias vs. absolute size difference between the starting and edited alleles (net deletion size), we observed a positive correlation between bias and twinPE-induced deletion size. Although bias in this workflow could still exist at the linear amplification stage due to differences in sequence composition at the target DNA locus, this bias does not propagate over the course of repeated PCR cycles and should therefore more accurately represent the true editing efficiency in twinPE editing experiments analyzed by amplicon sequencing.



Each point in the above graph represents the mean value of bias calculated from three independent biological replicates. The percentage of bias in editing efficiency was defined by the following equation: $100 \times (A - B) \div B$, where “A” represents the editing efficiency calculated from total read counts without UMI-based deduplication, and “B” represents the editing efficiency calculated after UMI-based deduplication. For example, if the non-deduplicated editing efficiency is 60% and the deduplicated editing efficiency is 46%, the calculated bias is 30%, i.e., the deduplicated editing efficiency is 1.3-fold lower than the non-deduplicated editing efficiency. The bias in editing efficiency is plotted above as a function of the net deletion between the starting and edited alleles, which shows a positive correlation (a second-order polynomial trend line, $R^2 = 0.6057$).

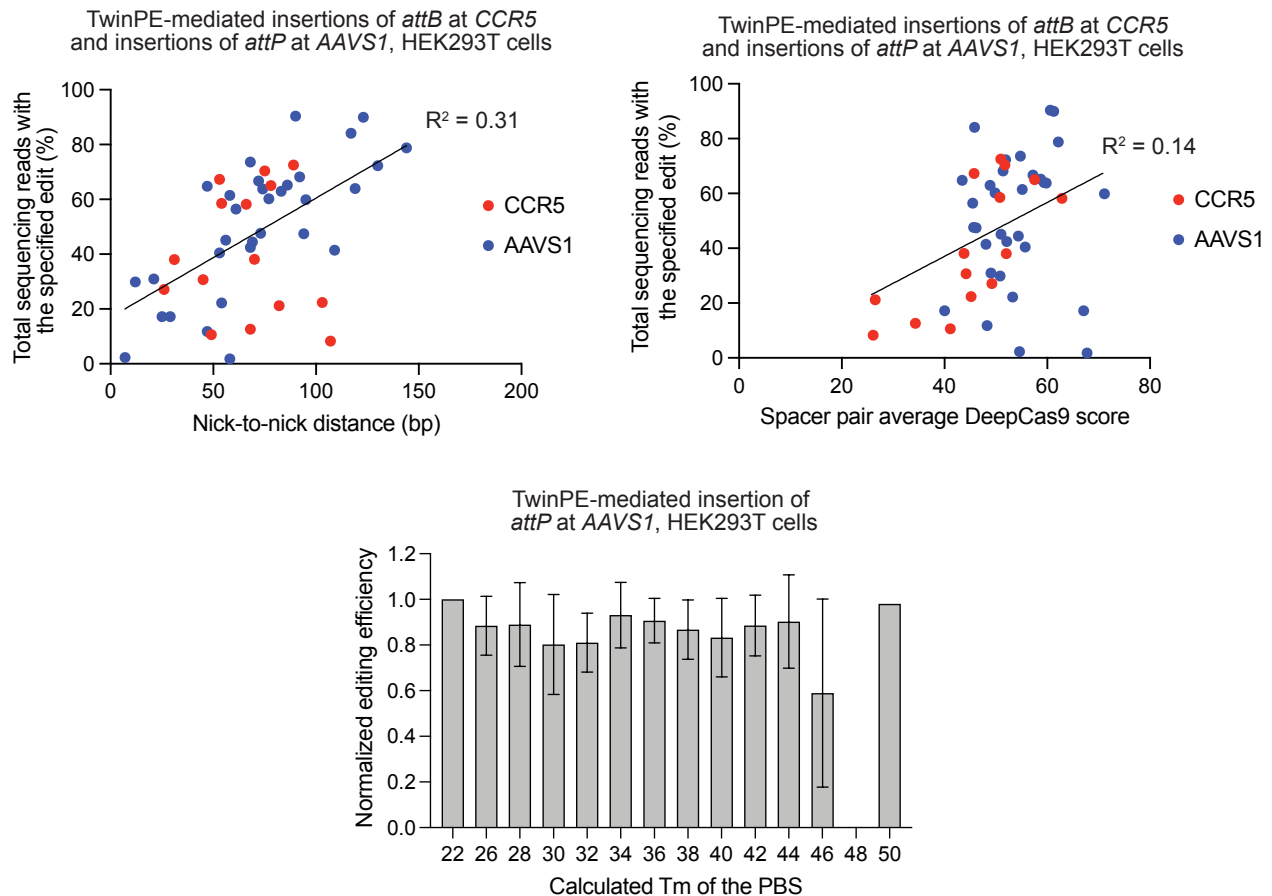
Supplementary Note 2. Representative plot of FACS gating for GFP reporter assay

25,000 HEK293T stable GFP reporter cells were seeded into 48-well poly-D-lysine coated plates (Corning). 16-24 h post-seeding, cells were transfected with 1uL of Lipofectamine 2000 (Thermo Fisher Scientific) using the protocol described in the methods section and 750 ng of PE2, 250 ng AAVS1 targeting pegRNAs (62.5 ng each), and Bxb1 plasmid DNA (100 ng, 200 ng, 500 ng, or 1000 ng). The untreated and twinPE+Bxb1 treated cells were cultured for 72 hours, and then collected for flow cytometry analysis. HEK293T stable GFP reporter cells were first gated (Gate A) based on forward (FSC-A) and side scattering (SSC-A) to remove dead cells and other debris. A second gate (Gate B) was used to select singlets based on FSC-H and FSC-A. Finally, GFP positive and GFP negative cells were gated (Gate C) and analyzed via FITC channel.



Supplementary Note 3. Analysis of twinPE design principles

To identify design principles that lead to efficient twinPE editing, we analyzed our dataset of *attP* insertions at *AAVS1* and *attB* insertions at *CCR5*. For each spacer pair, we calculated nick-to-nick distances between predicted pegRNA-induced nick sites, the DeepCas9 score³ for each spacer, and the predicted T_m of the pegRNA primer binding sequence (PBS) for *AAVS1*. For comparing nick-to-nick distances and DeepCas9 scores, the highest efficiency pegRNA pair for each spacer pair was chosen for analysis (*i.e.*, the optimal individual pegRNAs were used). For analyzing the influence of predicted spacer activities, the average of the individual DeepCas9 scores for each spacer was used. For comparing predicted T_m values for PBS variants, the editing efficiency of each pegRNA was normalized to the maximum editing achieved within the spacer pair group. The editing efficiency for a given PBS variant was then averaged across the three paired pegRNA editing efficiencies (each experiment with the paired spacer). T_m was calculated according to the following formula⁴: $T_m = 4N_{G-C} + 2N_{A-T}$.



Although efficient targeting of both DNA protospacers is likely necessary for achieving efficient twinPE, we observed only weak correlations between *in silico* predictions of Cas9 spacer activity and observed twinPE editing efficiencies (top right panel). This poor correlation could arise from other determinants of twinPE efficiency beyond the protospacer, including RT template and PBS choice. While PBS optimization was important for high editing efficiency at many sites, we did not observe an optimal PBS melting temperature across the pegRNA designs in this study (bottom panel). A correlation between prime editing efficiency and the distance between pegRNA-induced nicks was observed (top left panel), which may suggest an optimal spacing of 50 to 100 bp, although many exceptions exist.

Supplementary Note 4. Discussion of other targeted integration methods

TwinPE and Bxb1-mediated recombination offer advantages over other approaches. The serine integrase ϕ C31⁵ and fusions of zinc fingers, TALEs, or dCas9 to the catalytic domain of Gin recombinase⁶⁻⁹ have been used to integrate or excise DNA at endogenous pseudo-sites in the human genome, but the efficiency of these sequence manipulations has generally been low and, more importantly, the extensive sequence preferences inherent to these recombinases limit the number of targetable loci to a minute fraction of pseudo-sites in the genome. The programmable integration of attachment sites by twinPE overcomes this challenge by enabling insertion of cognate recombinase recognition sequences at any PE-targetable locus.

Compared to nuclease-based methods, the twinPE and recombinase approach avoids the generation of DSBs, which typically lead to uncontrolled mixtures of by products¹⁰, and can also lead to chromosomal rearrangements¹¹, chromothripsis¹², large deletions¹³⁻¹⁵, and p53 activation¹⁶⁻¹⁸. Integration orientation using twinPE and Bxb1 recombinase is strictly controlled by the directionality of the *attB* and *attP* sequences¹⁹, in contrast to uncontrolled integration orientation using homology-independent repair²⁰. Methods that use HDR also enable control of sequence orientation, and can achieve efficiencies on the order of 5-10% without drug selection or suppression of NHEJ²¹⁻²³, but HDR is less efficient than NHEJ in most cell types and typically requires DSBs^{24,25}. Methods have also been developed for making targeted gene-sized insertions through paired nicking of the genome and a donor cassette^{26,27}. These approaches do not require double strand breaks, but remain reliant on HDR and supportive cell types²⁷.

Supplementary Sequences 1. Sequences of plasmid donor DNA sequences harboring Bxb1 recombination sites

att site: highlighted in yellow

Promoter-less EGFP: highlighted in green

EF1a promoter: underlined

PuroR: highlighted in red

BFP: highlighted in blue

KanR: highlighted in grey

attB-Puro-GA donor DNA:

```
gatgccagctcattctcccactcatgatctatagatccccgggctgcaggaattctaccactctgtcgataccccaccgagacc
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attP Factor IX donor (the vector backbone is pMC.BESPX-MCS1 from System Biosciences)

attP: highlighted in yellow

Factor IX intron 1: highlighted in grey

Factor IX exons 2-8 CDS: highlighted in green

Factor IX exon 8 3'UTR: underlined

bGH poly(A) signal: highlighted in cyan

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Supplementary Sequence 2. Sequence of codon-optimized Bxb1 plasmid

CMV enhancer/promoter: highlighted in grey

SP6 promoter: underlined

Codon-optimized Bxb1: highlighted in green

SV40 poly(A): highlighted in cyan

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Supplementary Sequence 3. Sequence of the lentiviral GFP reporter vector (the vector bone is pLVX-EF1a-IRES-Puro from Takara Bio inc.).

LTR: in bold

EF1α promoter: underlined

AAVS1 target sequence: highlighted in yellow

Inverted H2B-EGFP coding sequence: highlighted in green

IRES: highlighted in grey

Puromycin resistance gene: highlighted in red

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