

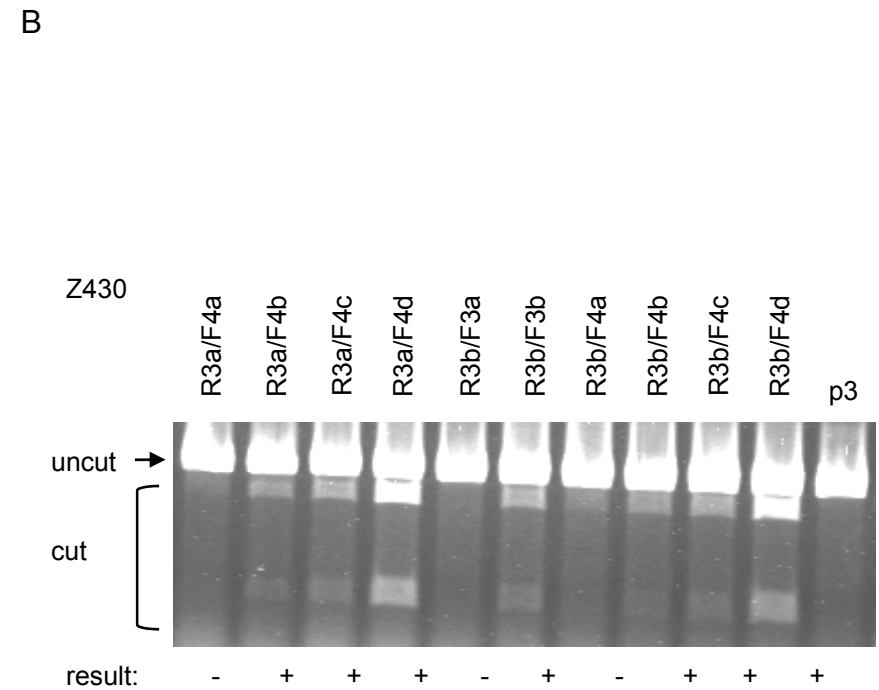
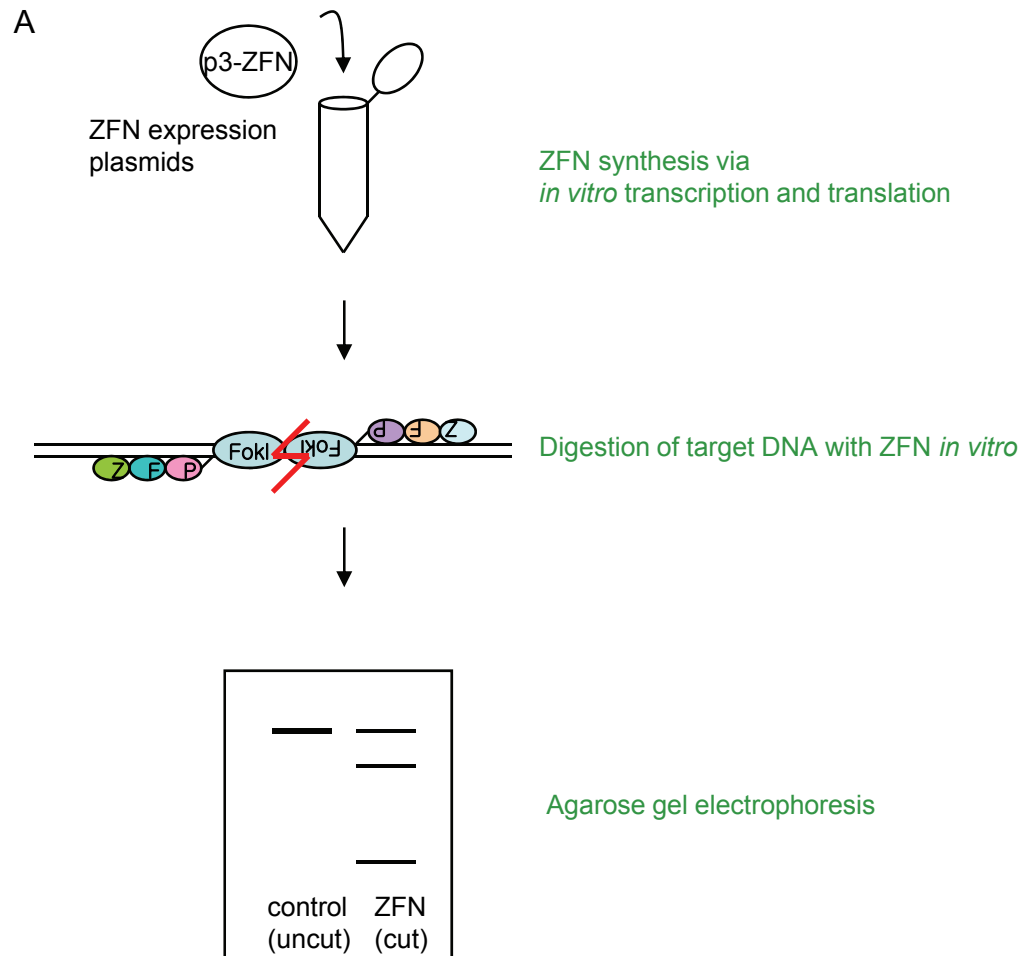
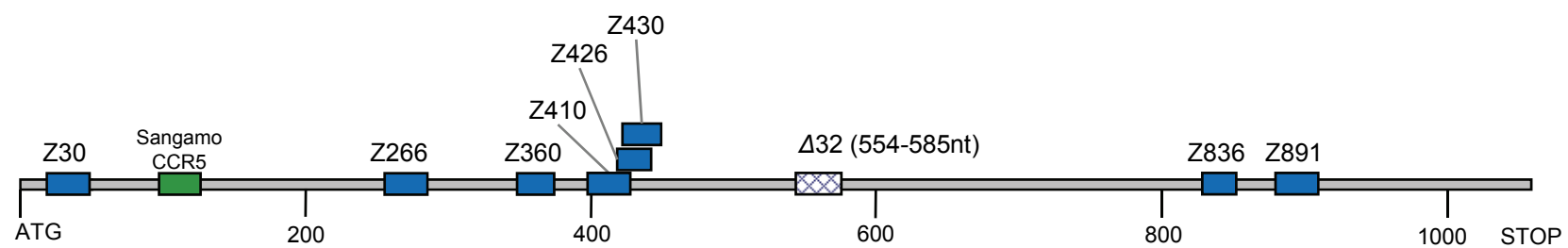


Figure S2



Z30

DELETIONS:

TCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCT (wt)
 TCAAGTGTCAAGTCCAATCTAT-ACATCAATTATTATACATCGGAGCCCT (2)

INSERTIONS:

TCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCT (wt)
 TCAAGTGTCAAGTCCAATCTATGACA**ca**TCAATTATTATACATCGGAGCC
 TCAAGTGTCAAGTCCAATCTATGACAT**acat**CAATTATTATACATCGGAG (6)
 TCAAGTGTCAAGTCCAATCTATGACAT**tgt--81nt--atca**ATTATTA

COMPLEX:

TCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCT (wt)
 TCAAGTGTCAAGTCCAATCTATG----**ta**ATTATTATACATCGGAGCCCT

Z266

INSERTIONS:

CTGTCCCCTTCTGGGCTCACTATGCTGCCGCGCCAGTGGGACTTTGGAAAT (wt)
 CTGTCCCCTTCTGGGCTCACTATGCTGC**tg**cCGCCAGTGGGACTTTGGA (3)
 CTGTCCCCTTCTGGGCTCACTATGCTG**gctg**CCGCCAGTGGGACTTTGG (5)

Z360

DELETIONS:

CTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTG (wt)
 CTCTGGAATCTTCTTCATCATCCTCC-----ACCTGGCTG
 CTCTGGAATCTTCTTCATCAT-----40nt-----
 CTCTGGAATCTTCTTCATCATCC-----56nt-----

INSERTION:

CTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTG (wt)
 CTCTGGAATCTTCTTCATCAT**aat--81nt--tcc**TGACAATCGATAGG

Z410

DELETIONS:

TCGTCCATGCTGTGTTTGCTTTAAAGCCAGGACGGTCACCTTTGGGGTG (wt)
 TCGTCCATGCTGTGTTTGCTTTAAA-GCCAGGACGGTCACCTTTGGGGTG (2)
 TCGTCCATGCTGTGTTTGCTTTA-----CTTTGGGGTG
 T-----AAAGCCAGGACGGTCACCTTTGGGGTG

INSERTIONS:

TCGTCCATGCTGTGTTTGCTTTAAAGCCAGGACGGTCACCTTTGGGGTG (wt)
 TCGTCCATGCTGTGTTTGCTTTAAAA**aa**GCCAGGACGGTCACCTTTGGGG (2)

Z426

INSERTIONS:

TGCTTTAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCA (wt)
 TGCTTTAAAGCCAGGACGGTCACCTT**cctt**TGGGGTGGTGACAAGTGTG (2)

COMPLEX:

TGCTTTAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCA (wt)
 TGCTTTAAAGCCAGGACGGT--**t**CCTTTGGGGTGGTGACAAGTGTGATCA

Z430

DELETION:

TTAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTG (wt)
 TTAAAGCCAGGACGGTC-----TGGGGTGGTGACAAGTGTGATCACTTG

INSERTIONS:

TTAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTG (wt)
 TTAAAGCCAGGACGGTCACCTTTGGGG**tgggg**TGGTGACAAGTGTGATC (2)

COMPLEX:

TTAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTG (wt)
 TTAAAGCCAGGACGGTC---**ccacctt**TGGTGACAAGTGTGATCACTTG

Z891

DELETIONS:

GCTGCATCAACCCCATCATCTATGCCTTTGTCGGGGAGAAAGTTCAGAACTACCTCTTAG (wt)
 GCTGCATCAACCCCATCATCTATGC-TTGTGCGGGAGAAAGTTCAGAACTACCTCTTAG
 GCTGCATCAACCCCATCATCTATGCCTT-GTCGGGGAGAAAGTTCAGAACTACCTCTTAG
 GCTGCATCAACCCCATCATCTATGCCTT-----GGAGAAAGTTCAGAACTACCTCTTAG (2)
 GCTGCATCAACCCCATCATCT-----CGGGGAGAAAGTTCAGAACTACCTCTTAG
 GCTGCATCAACCCCATCATCTAT-----CAGAACTACCTCTTAG

INSERTIONS:

GCTGCATCAACCCCATCATCTATGCCTT-----TGTGCGGGAGAAAGTTCAGAACTACCTC (wt)
 GCTGCATCAACCCCATCATCTATGCCTT**cctt**TGTGCGGGAGAAAGTTCAGAACTACCTC (3)

COMPLEX:

GCTGCATCAACCCCATCATCTATGCC--TTTGTGCGGGAGAAAGTTCAGAACTACCTCTT (wt)
 GCTGCATCAACCCCATCATCTATGC**gga**TTTGTGCGGGAGAAAGTTCAGAACTACCTCTT

Z891R4

HA tag *nuclear localization signal*

MVYPYDVPDYAELPPKKKRKVGIRIPGEKPYKCMCECGKAFN**RRSHLTRH**
 RIHTGEKPYRCKYCDRSFS**ISSNLQR**HVRNIHTGEKPYRCKYCDRSFS**IS**
SNLQRHVRNIHTGEKPYTCSYCGKSFT**QSNLTKQ**HTRIHTGEKQLVKSEL
 EEKKSELRHKLKYVPHEYIELIEIARNSTQDRILEMKVMEFFMKVYGYRG
 KHLGGSRKPDGAIYTVGSPIDYGVIVDTKAYSGGYNLPIGQADEMQRYVE
 ENQTRNKHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKAQLTRLNHITN
 CNGAVLSVEELLIGGEMIKAGTLTLEEVRKFNNGEINF

Z891F4

HA tag *nuclear localization signal*

MVYPYDVPDYAELPPKKKRKVGIRIPGEKPFACPECPKRFM**RSDNLTQ**HI
 KTHHTGEKPYKCHQCGKAFI**QSFNLRR**HERTHHTGEKPYKCMCECGKAFN**RRS**
HLTRHQRIHTGEKPYSCGICGKSFS**DSSAKRR**HCILHTGEKQLVKSELEE
 KKSELRHKLKYVPHEYIELIEIARNSTQDRILEMKVMEFFMKVYGYRGKH
 LGGSRKPDGAIYTVGSPIDYGVIVDTKAYSGGYNLPIGQADEMQRYVEEN
 QTRNKHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKAQLTRLNHITNCN
 GAVLSVEELLIGGEMIKAGTLTLEEVRKFNNGEINF

Supplemental Figure 1. *In vitro* DNA digestion assay. (a) Schematic illustration of the DNA digestion assay performed using ZFNs produced via an *in vitro* transcription and translation system. (b) Photographs of representative agarose gels.

Supplemental Figure 2. Schematic overview of ZFN target sites in the *CCR5* coding region. ZFN target sites are shown as boxes. The numbers indicate the positions of ZFN target sites relative to the start codon. The crosshatched box indicates the locus of the $\Delta 32$ mutation.

Supplemental Figure 3. DNA sequences of ZFN-targeted sites. ZFN recognition elements are underlined. Deletions are indicated with dashes, and inserted bases are shown in small letters. In cases where a mutation is detected more than once, the number of occurrences is shown in parentheses.

Supplemental Figure 4. The amino acid sequence of a ZFN pair.

Supplemental Table 1. Summary of ZFN analyses. The number of ZFN pairs or target sites that gave rise to positive results in each assay is shown.

	ZFN pairs (positive/total)	Target sites (positive/total)
In vitro DNA digestion assay	134/302 (44%)	20/33 (61%)
Cell-based SSA system	23/315 (7.3%)	8/33 (24%)
T7E1 mismatch detection assay	21/23 (91%)	8/8 (100%)

Supplemental Table 2. Success rates of different types of ZFNs. Successful ZFN pairs or target sites are defined as those that gave rise to positive results in the T7E1 mismatch detection assay.

	ZFN pairs (successful/total)	Target sites (successful/total)
3-finger ZFN/3-finger ZFN	4/138 (2.9%)	3/33 (9.1%)
4-finger ZFN/3-finger ZFN	8/125 (6.4%)	3/25 (12%)
4-finger ZFN/4-finger ZFN	9/52 (17%)	5/19 (26%)
Total	21/315 (6.7%)	8/33 (24%)

Supplemental Table 3. ZFNs used for module swap experiments.

ZFN name		F1	F2	F3	F4	Half-site sequence (from 5' to 3')
Z360	R4	QSNR1	QSNR1	ISNR	ISNR	GAT GAT GAA GAA
	BR4	ZF63	ZF63	ZF64	ZF64	GAT GAT GAA GAA
	SR4	ZF1	ZF18	ZF21	ZF39	GAT GAT GAA GAA
	F3	QSHV	VSNV	DSNR		GAC AAT CGA
Z426	R3	tnse	srtA	DSNR		GAC CGT CCT
	F3	RDER2	RDER1	RDHR1		GGG GTG GTG
	BF3	ZF66	ZF66	ZF58		GGG GTG GTG
	SF3	ZF15	ZF15	ZF51		GGG GTG GTG
Z430	R3	rdte	QSHV	RDKR		AGG TGA CCG
	F4	RDER2	QSNV2	QSHV	RDHT	TGG TGA CAA GTG
	BF4	ZF66	ZF89	ZF105	ZF106	TGG TGA CAA GTG
Z836	R3	RDHT	VSTR	QNTQ		ATA GCT TGG
	BR3	ZF106	ZF72	ZF86		ATA GCT TGG
	F3	CSNR1	QTHQ	DSNR		GAC AGA GAC
	BF3	ZF65	ZF82	ZF65		GAC AGA GAC
Z891	R4	RSHR	ISNR	ISNR	QNTQ	ATA GAT GAT GGG
	BR4	ZF58	ZF64	ZF64	ZF86	ATA GAT GAT GGG
Z891	F4	rdnq	QFNR	RSHR	DSAR2	GTC GGG GAG AAG

The ZFN monomers whose names start with “B” such as “BR4” are composed exclusively of Barbas modules, and those with “S”, such as “SR4”, are composed exclusively of Sangamo modules. The zinc fingers that compose these ZFNs are described in Supplemental Table 4.

Supplemental Table 4. Zinc finger modules.

(a) Zinc fingers used for construction of ZFNs

ZF No. ¹	ZF name	Source	Amino acid sequence	Target subsite	Activity score ²	Recommendation for future use
ZF107	CSNR1	ToolGen	YKCKQCGKAFGCPNLRHGRTH	GAC	19 (3/16)	O
N.A.	DSAR2	ToolGen	YSCGICGKSFSDSAKRRHCILH	GTC	36 (4/11)	O
ZF108	DSCR	ToolGen	YTCSDCGKAFRDKSCLNRHRRTH	GCC	14 (2/14)	O
N.A.	DSNR	ToolGen	YRCKYCDRSFSDSLNRHVRNIH	GAC	35 (6/17)	O
ZF110	HSNK	ToolGen	YKCKECGKAFNHSSNFNKHHRTH	GAC	0 (0/9)	
ZF111	HSSR	ToolGen	FKCPVCGKAFRHSSSLVRHQRTTH	GTT	0 (0/7)	
ZF112	ISNR	ToolGen	YRCKYCDRSFSISSNLQRHVRNIH	GAT	20 (7/35)	O
ZF113	KSNR	ToolGen	YGCHLCGKAFFSKSSNLRRHEMIH	GAG	20 (2/10)	O
ZF115	QFNR	ToolGen	YKCHQCGKAFIQSFNLRRHERTH	GAG	22 (2/9)	
N.A.	QNTQ	ToolGen	YTCSYCGKSFTQSNTLKQHTRTH	ATA	50 (3/6)	O
ZF117	QSHR2	ToolGen	YKCGQCGKFYSQVSHLTRHQKIH	GGA	25 (1/4)	O
ZF119	QSHT	ToolGen	YKCEECGKAFRQSSHLTTHKIIH	YGA	9 (3/33)	
ZF120	QSHV	ToolGen	YECDCGKSFSQSSHLNVHKRTH	YGA	23 (7/30)	O
ZF121	QSN1	ToolGen	YMCSECGRGFSQKSNLTIHQRTTH	AAA	5 (1/19)	O
ZF122	QSNK	ToolGen	YKCEECGKAFTQSSNLTKHKKIH	TAA	0 (0/15)	
ZF123	QSNR1	ToolGen	FECKDCGKAFFQKSNLIRHQRTTH	GAA	16 (3/19)	O
ZF125	QSNV2	ToolGen	YVCSKCGKAFTQSSNLTVHQKIH	CAA	5 (2/37)	O
ZF126	QSSR1	ToolGen	YKCPDCGKSFSQSSSLIRHQRTTH	GYA	4 (1/27)	O
ZF127	QSTR	ToolGen	YKCEECGKAFFNQSSLTTRHKIVH	GYA	0 (0/14)	
ZF128	QTHQ	ToolGen	YECDCGKSFRQSTHLTQHRRTH	AGA	6 (1/16)	O
ZF129	QTHR1	ToolGen	YECDCGKSFRQSTHLTRHRRTH	GGA	8 (1/13)	
ZF130	RDER1	ToolGen	YVCDVEGCTWKFARSDENLRHKKRH	GYG	13 (3/24)	O
N.A.	RDER2	ToolGen	YHCDWDGCGWKFARSDENLRHYRKH	GYG	16 (5/31)	O
ZF131	RDHR1	ToolGen	FLCQYCAQRFRGRDHLTRHMKKSH	GGG	22 (2/9)	O
ZF132	RDHT	ToolGen	FQCKTCQRKFSRSDHLKTHTRTH	YGG	19 (4/21)	O
ZF133	RDKR	ToolGen	YVCDVEGCTWKFARSDKLNLRHKKRH	AGG	10 (2/21)	O
ZF134	RSHR	ToolGen	YKCEECGKAFFNRSHLTRHQRIH	GGG	38 (5/13)	O
ZF135	RSNR	ToolGen	YICRKCGRGRFSRKSNIIRHQRTTH	GAG	0 (0/4)	
N.A.	VDYK	ToolGen	FHCGYCEKSFSVKDYLTKHIRTH	TAT	11 (2/19)	O

ZF137	VSNV	ToolGen	YECDHCGKAFSVSSNLNVHRRIH	AAT	25	(5/20)O
ZF138	VSSR	ToolGen	YTCKQCGKAFSVSSSLRRHETTH	GTT	0	(0/8)
ZF139	VSTR	ToolGen	YECNYCGKTFSSVSTLIRHQRIH	GCT	7	(1/14)O
ZF140	WSNR	ToolGen	YRCEECGKAFRWPSNLTRHKRIH	GGT	7	(1/14)O
ZF52	rdnq	Sangamo	FACPECPKRFMRSDNLTQHIKTH	AAG	12	(2/17)O
ZF61	dghr	Barbas	YKCPECGKSFSDPGHLVRHQRTTH	GGC	50	(1/2) O
ZF75	dgnv	Barbas	FQCRICMRNFSDSGNLRVHIRTH	AAC	20	(1/5) O
ZF78	sadr	Barbas	YKCPECGKSFSSPADLTRHQRTTH	ACA	100	(3/3) O
ZF81	tldr	Barbas	YKCPECGKSFSTHLDLIRHQRTTH	ACT	100	(1/1) O
ZF83	eshe	Barbas	YKCPECGKSFSESHLREHQRTTH	AGC	0	(0/1)
ZF85	httn	Barbas	YKCPECGKSFSSHRTTLTNHQRTTH	AGT	0	(0/2)
ZF87	rdev	Barbas	YKCPECGKSFSSRRDELNVHQRTTH	ATG	0	(0/2)
ZF90	skae	Barbas	YKCPECGKSFSSKKALTEHQRTTH	CAC	100	(1/1) O
ZF91	rdne	Barbas	YKCPECGKSFSSRADNLTEHQRTTH	CAG	16	(3/19)O
ZF92	tgne	Barbas	YKCPECGKSFSTSGNLTEHQRTTH	CAT	0	(0/2)
ZF93	thse	Barbas	YKCPECGKSFSTSHSLTEHQRTTH	CCA	8	(2/24)O
ZF94	skhe	Barbas	YKCPECGKSFSSKKHLAEHQRTTH	CCC	0	(0/11)
ZF95	rdte	Barbas	YKCPECGKSFSSRNDTLTEHQRTTH	CCG	33	(2/6) O
ZF96	tnse	Barbas	YKCPECGKSFSTKNSLTEHQRTTH	CCT	29	(2/7) O
ZF98	hghe	Barbas	YKCPECGKSFSSHTGHLLEHQRTTH	CGC	33	(2/6) O
ZF100	srta	Barbas	YKCPECGKSFSSRRTCRAHQRTTH	CGT	40	(2/5) O
ZF101	qste	Barbas	YKCPECGKSFSSQNSTLTEHQRTTH	CTA		(0/0)
ZF102	rdae	Barbas	YKCPECGKSFSSRNDALTEHQRTTH	CTG	0	(0/15)
ZF103	tgae	Barbas	YKCPECGKSFSTTGALTEHQRTTH	CTT	0	(0/1)
ZF104	rdnt	Barbas	YKCPECGKSFSSREDNLHTEHQRTTH	TAG	19	(3/16)O

¹ ZF No. is based on the numbering scheme of the Zinc Finger Consortium Modular Assembly Kit 1.0 available from Addgene.

² The activity score is calculated by dividing the number of occurrences of each zinc finger in the 23 ZFN pairs that scored positively in the SSA system with the number of occurrences of the module in all 215 ZFN monomers.

(b) Zinc fingers used for module swap experiments.

ZF No.	ZF name	Source	Amino acid sequences	Target subsite
ZF1	yqrl	Sangamo	HICHIQGCGKVYGQRSNLVRHLRWH	GAA
ZF15	yrsl	Sangamo	HICHIQGCGKVYGRSDALTRHLRWH	GTG
ZF18	rtqn	Sangamo	FMCTWSYCGKRFTQSGNLARHKRTH	GAA
ZF21	tsgv	Sangamo	MCTWSYCGKRFTTSGNLVRHKRTH	GAT
ZF39	tanr	Sangamo	FACPECPKRFMTSANLSRHIKTH	GAT
ZF51	rdhr	Sangamo	FACPECPKRFMRSDHLSRHIKTH	GGG
ZF58	rdkr	Barbas	YKCPECGKSFSRSDKLVRHQ RTH	GGG
ZF63	qsnr	Barbas	YKCPECGKSFSQSSNLVRHQ RTH	GAA
ZF64	tgnr	Barbas	YKCPECGKSFSSTSGNLVRHQ RTH	GAT
ZF65	dgnr	Barbas	YKCPECGKSFSDPGNLVRHQ RTH	GAC
ZF66	rder	Barbas	YKCPECGKSFSRSDLV RHQ RTH	GTG
ZF72	tger	Barbas	YKCPECGKSFSSTSGELVRHQ RTH	GCT
ZF82	qaha	Barbas	YKCPECGKSFSQLAHLRAHQ RTH	AGA
ZF86	qssa	Barbas	YKCPECGKSFSQKSSLIAHQ RTH	ATA
ZF89	qgne	Barbas	YKCPECGKSFSQSGNLTEHQ RTH	CAA
ZF105	qgha	Barbas	YKCPECGKSFSQAGHLASHQ RTH	TGA
ZF106	rdht	Barbas	YKCPECGKSFSRSDHLTTHQ RTH	TGG

Sander JD. *et al.* Zinc Finger Targeter (ZiFiT): an engineered zinc finger/target site design tool. *Nucleic Acids Res.* **35**, W599-605.

Wright, D. A. *et al.* Standardized reagents and protocols for engineering zinc finger nuclease by modular assembly. *Nature Protocol* **1**, 1637-1652 (2006)

Supplemental Table 5. List of ZFNs tested for editing the human *CCR5* gene.

ZFN	Site	Half-site sequence (5' to 3')	F1	F2	F3	F4
Z10R3	10R	GAT AAT CCA	thse	VSNV	ISNR	
Z17F3	17	CAA GTC CAA	QSNV2	DSAR2	QSNV2	
Z30R3	30R	ATA GAT TGG	RDHT	ISNR	QNTQ	
Z30R4	30R	ATA GAT TGG ACT	tldr	RDHT	ISNR	QNTQ
Z37F3	37	AAT TAT TAT	VDYK	VDYK	VSNV	
Z37F4	37	AAT TAT TAT ACA	sadr	VDYK	VDYK	VSNV
Z47R3a	47R	GTA TAA TAA	QSNK	QSNK	QSTR	
Z47R3b	47R	GTA TAA TAA	QSNK	QSNK	QSSR1	
Z54F3	54	GCC CTG CCA	thse	rdae	DSCR	
Z54F4	54	GCC CTG CCA AAA	QSNi	thse	rdae	DSCR
Z50R3a	50R	GAT GTA TAA	QSNK	QSTR	ISNR	
Z50R3b	50R	GAT GTA TAA	QSNK	QSSR1	ISNR	
Z50R4a	50R	GAT GTA TAA TAA	QSNK	QSNK	QSTR	ISNR
Z50R4b	50R	GAT GTA TAA TAA	QSNK	QSNK	QSSR1	ISNR
Z57F3	57	CTG CCA AAA	QSNi	thse	rdae	
Z57F4	57	CTG CCA AAA AAT	VSNV	QSNi	thse	rdae
Z156R3a	156R	GAT GAC CAG	rdne	DSNR	ISNR	
Z156R3b	156R	GAT GAC CAG	rdne	HSNK	ISNR	
Z156R3c	156R	GAT GAC CAG	rdne	CSNR1	ISNR	
Z156R4	156R	GAT GAC CAG CAT	tgne	rdne	CSNR1	ISNR
Z163F3	163	CTG ATA AAC	dgnv	QNTQ	rdae	
Z168R3	168R	TAT CAG GAT	ISNR	rdne	VDYK	
Z168R4a	168R	TAT CAG GAT GAG	KSNR	ISNR	rdne	VDYK
Z168R4b	168R	TAT CAG GAT GAG	QFNR	ISNR	rdne	VDYK
Z168R4c	168R	TAT CAG GAT GAG	RSNR	ISNR	rdne	VDYK
Z175F3	175	AAA AGG CTG	rdae	RDKR	QSNi	
Z175F4	175	AAA AGG CTG AAG	rdnq	rdae	RDKR	QSNi
Z171R3a	171R	GTT TAT CAG	rdne	VDYK	HSSR	
Z171R3b	171R	GTT TAT CAG	rdne	VDYK	VSSR	
Z171R4a	171R	GTT TAT CAG GAT	ISNR	rdne	VDYK	HSSR
Z171R4b	171R	GTT TAT CAG GAT	ISNR	rdne	VDYK	VSSR
Z178F3	178	AGG CTG AAG	rdnq	rdae	RDKR	

Z178F4	178	AGG CTG AAG AGC	eshe	rdnq	rdae	RDKR
Z174R3a	174R	GCA GTT TAT	VDYK	HSSR	QSTR	
Z174R3b	174R	GCA GTT TAT	VDYK	VSSR	QSTR	
Z174R3c	174R	GCA GTT TAT	VDYK	HSSR	QSSR1	
Z174R3d	174R	GCA GTT TAT	VDYK	VSSR	QSSR1	
Z174R4	174R	GCA GTT TAT CAG	rdne	VDYK	VSSR	QSTR
Z180F3a	180	GCT GAA GAG	KSNR	QSNR1	VSTR	
Z180F3b	180	GCT GAA GAG	QFNR	QSNR1	VSTR	
Z180F3c	180	GCT GAA GAG	RSNR	QSNR1	VSTR	
Z180F4	180	GCT GAA GAG CAT	tgne	KSNR	QSNR1	VSTR
Z204R3a	204R	GTA GAT GTC	DSAR2	ISNR	QSTR	
Z204R3b	204R	GTA GAT GTC	DSAR2	ISNR	QSSR1	
Z204R4	204R	GTA GAT GTC AGT	httn	DSAR2	ISNR	QSSR1
Z211F3	211	AAC CTG GCC	DSCR	rdae	dgnv	
Z258R3a	258R	CCA GAA GGG	RDHR1	QSNR1	thse	
Z258R3b	258R	CCA GAA GGG	RSHR	QSNR1	thse	
Z258R4a	258R	CCA GAA GGG GAC	DSNR	RDHR1	QSNR1	thse
Z258R4b	258R	CCA GAA GGG GAC	HSNK	RDHR1	QSNR1	thse
Z258R4c	258R	CCA GAA GGG GAC	CSNR1	RDHR1	QSNR1	thse
Z258R4d	258R	CCA GAA GGG GAC	DSNR	RSHR	QSNR1	thse
Z258R4e	258R	CCA GAA GGG GAC	HSNK	RSHR	QSNR1	thse
Z258R4f	258R	CCA GAA GGG GAC	CSNR1	RSHR	QSNR1	thse
Z265F3	265	TAT GCT GCC	DSCR	VSTR	VDYK	
Z265F4	265	TAT GCT GCC GCC	DSCR	DSCR	VSTR	VDYK
Z262R3a	262R	GAG CCC AGA	QTHQ	skhe	KSNR	
Z262R3b	262R	GAG CCC AGA	QTHQ	skhe	QFNR	
Z262R3c	262R	GAG CCC AGA	QTHQ	skhe	RSNR	
Z262R4a	262R	GAG CCC AGA AGG	RDKR	QTHQ	skhe	KSNR
Z262R4b	262R	GAG CCC AGA AGG	RDKR	QTHQ	skhe	QFNR
Z262R4c	262R	GAG CCC AGA AGG	RDKR	QTHQ	skhe	RSNR
Z269F3	269	CTG CCG CCC	skhe	rdte	rdae	
Z269F4	269	CTG CCG CCC AGT	httn	skhe	rdte	rdae
Z266R3a	266R	TAG TGA GCC	DSCR	QSHT	rdnt	
Z266R3b	266R	TAG TGA GCC	DSCR	QSHV	rdnt	
Z266R4a	266R	TAG TGA GCC CAG	rdne	DSCR	QSHT	rdnt
Z266R4b	266R	TAG TGA GCC CAG	rdne	DSCR	QSHV	rdnt

Z273F3a	273	CGC CCA GTG	RDER1	thse	hghe	
Z273F3b	273	CGC CCA GTG	RDER2	thse	hghe	
Z273F4a	273	CGC CCA GTG GGA	QTHR1	RDER1	thse	hghe
Z273F4b	273	CGC CCA GTG GGA	QSHR2	RDER1	thse	hghe
Z273F4c	273	CGC CCA GTG GGA	QTHR1	RDER2	thse	hghe
Z273F4d	273	CGC CCA GTG GGA	QSHR2	RDER2	thse	hghe
Z269R3a	269R	GCA TAG TGA	QSHT	rdnt	QSTR	
Z269R3b	269R	GCA TAG TGA	QSHV	rdnt	QSTR	
Z269R3c	269R	GCA TAG TGA	QSHT	rdnt	QSSR1	
Z269R3d	269R	GCA TAG TGA	QSHV	rdnt	QSSR1	
Z269R4a	269R	GCA TAG TGA GCC	DSCR	QSHT	rdnt	QSTR
Z269R4b	269R	GCA TAG TGA GCC	DSCR	QSHV	rdnt	QSTR
Z269R4c	269R	GCA TAG TGA GCC	DSCR	QSHT	rdnt	QSSR1
Z269R4d	269R	GCA TAG TGA GCC	DSCR	QSHV	rdnt	QSSR1
Z276F3a	276	CCA GTG GGA	QTHR1	RDER1	thse	
Z276F3b	276	CCA GTG GGA	QSHR2	RDER1	thse	
Z276F3c	276	CCA GTG GGA	QTHR1	RDER2	thse	
Z276F3d	276	CCA GTG GGA	QSHR2	RDER2	thse	
Z276F4	276	CCA GTG GGA CTT	tgae	QTHR1	RDER2	thse
Z360R3	360R	GAT GAT GAA	QSNR1	ISNR	ISNR	
Z360R4	360R	GAT GAT GAA GAA	QSNR1	QSNR1	ISNR	ISNR
Z366F3a	366	GAC AAT CGA	QSHT	VSNV	DSNR	
Z366F3b	366	GAC AAT CGA	QSHV	VSNV	DSNR	
Z366F3c	366	GAC AAT CGA	QSHT	VSNV	HSNK	
Z366F3d	366	GAC AAT CGA	QSHV	VSNV	HSNK	
Z366F3e	366	GAC AAT CGA	QSHT	VSNV	CSNR1	
Z366F3f	366	GAC AAT CGA	QSHV	VSNV	CSNR1	
Z366F4	366	GAC AAT CGA TAG	rdnt	QSHV	VSNV	DSNR
Z368R3	368R	GTC AGG AGG	RDKR	RDKR	DSAR2	
Z368R4	368R	GTC AGG AGG ATG	rdev	RDKR	RDKR	DSAR2
Z375F3a	375	TAG GTA CCT	tnse	QSTR	rdnt	
Z375F3b	375	TAG GTA CCT	tnse	QSSR1	rdnt	
Z375F4	375	TAG GTA CCT GGC	dghr	tnse	QSSR1	rdnt
Z410R3a	410R	AAA GCA AAC	dgnv	QSTR	QSN1	
Z410R3b	410R	AAA GCA AAC	dgnv	QSSR1	QSN1	
Z410R4	410R	AAA GCA AAC ACA	sadr	dgnv	QSSR1	QSN1

Z417F3a	417	CAG GAC GGT	WSNR	DSNR	rdne	
Z417F3b	417	CAG GAC GGT	WSNR	HSNK	rdne	
Z417F3c	417	CAG GAC GGT	WSNR	CSNR1	rdne	
Z417F4	417	CAG GAC GGT CAC	skae	WSNR	CSNR1	rdne
Z426R3a	426R	GAC CGT CCT	tnse	srtA	DSNR	
Z426R3b	426R	GAC CGT CCT	tnse	srtA	HSNK	
Z426R3c	426R	GAC CGT CCT	tnse	srtA	CSNR1	
Z426R4	426R	GAC CGT CCT GGC	dghr	tnse	srtA	DSNR
Z433F3a	433	GGG GTG GTG	RDER1	RDER1	RDHR1	
Z433F3b	433	GGG GTG GTG	RDER2	RDER1	RDHR1	
Z433F3c	433	GGG GTG GTG	RDER1	RDER2	RDHR1	
Z433F3d	433	GGG GTG GTG	RDER2	RDER2	RDHR1	
Z433F3e	433	GGG GTG GTG	RDER1	RDER1	RSHR	
Z433F3f	433	GGG GTG GTG	RDER2	RDER1	RSHR	
Z433F3g	433	GGG GTG GTG	RDER1	RDER2	RSHR	
Z433F3h	433	GGG GTG GTG	RDER2	RDER2	RSHR	
Z433F4	433	GGG GTG GTG ACA	sadr	RDER2	RDER1	RDHR1
Z430R3a	430R	AGG TGA CCG	rdte	QSHT	RDKR	
Z430R3b	430R	AGG TGA CCG	rdte	QSHV	RDKR	
Z437F3a	437	TGG TGA CAA	QSNV2	QSHT	RDHT	
Z437F3b	437	TGG TGA CAA	QSNV2	QSHV	RDHT	
Z437F4a	437	TGG TGA CAA GTG	RDER1	QSNV2	QSHT	RDHT
Z437F4b	437	TGG TGA CAA GTG	RDER2	QSNV2	QSHT	RDHT
Z437F4c	437	TGG TGA CAA GTG	RDER1	QSNV2	QSHV	RDHT
Z437F4d	437	TGG TGA CAA GTG	RDER2	QSNV2	QSHV	RDHT
Z432R3a	432R	AAA GGT GAC	DSNR	WSNR	QSN1	
Z432R3b	432R	AAA GGT GAC	HSNK	WSNR	QSN1	
Z432R3c	432R	AAA GGT GAC	CSNR1	WSNR	QSN1	
Z432R4	432R	AAA GGT GAC CGT	srtA	DSNR	WSNR	QSN1
Z438F3a	438	GGT GAC AAG	rdnq	DSNR	WSNR	
Z438F3b	438	GGT GAC AAG	rdnq	HSNK	WSNR	
Z438F3c	438	GGT GAC AAG	rdnq	CSNR1	WSNR	
Z433R3a	433R	CAA AGG TGA	QSHT	RDKR	QSNV2	
Z433R3b	433R	CAA AGG TGA	QSHV	RDKR	QSNV2	
Z433R4a	433R	CAA AGG TGA CCG	rdte	QSHT	RDKR	QSNV2
Z433R4b	433R	CAA AGG TGA CCG	rdte	QSHV	RDKR	QSNV2

Z440F3a	440	TGA CAA GTG	RDER1	QSNV2	QSHV	
Z440F3b	440	TGA CAA GTG	RDER2	QSNV2	QSHV	
Z440F3c	440	TGA CAA GTG	RDER1	QSNV2	QSHV	
Z440F3d	440	TGA CAA GTG	RDER2	QSNV2	QSHV	
Z440F4a	440	TGA CAA GTG TGA	QSHV	RDER1	QSNV2	QSHV
Z440F4b	440	TGA CAA GTG TGA	QSHV	RDER1	QSNV2	QSHV
Z440F4c	440	TGA CAA GTG TGA	QSHV	RDER2	QSNV2	QSHV
Z440F4d	440	TGA CAA GTG TGA	QSHV	RDER2	QSNV2	QSHV
Z440F4e	440	TGA CAA GTG TGA	QSHV	RDER1	QSNV2	QSHV
Z440F4f	440	TGA CAA GTG TGA	QSHV	RDER1	QSNV2	QSHV
Z440F4g	440	TGA CAA GTG TGA	QSHV	RDER2	QSNV2	QSHV
Z440F4h	440	TGA CAA GTG TGA	QSHV	RDER2	QSNV2	QSHV
Z436R3	436R	CCC CAA AGG	RDKR	QSNV2	skhe	
Z436R4a	436R	CCC CAA AGG TGA	QSHV	RDKR	QSNV2	skhe
Z436R4b	436R	CCC CAA AGG TGA	QSHV	RDKR	QSNV2	skhe
Z443F3a	443	CAA GTG TGA	QSHV	RDER1	QSNV2	
Z443F3b	443	CAA GTG TGA	QSHV	RDER1	QSNV2	
Z443F3c	443	CAA GTG TGA	QSHV	RDER2	QSNV2	
Z443F3d	443	CAA GTG TGA	QSHV	RDER2	QSNV2	
Z501R3	501R	GGT AAA GAT	ISNR	QSNV2	WSNR	
Z501R4	501R	GGT AAA GAT GAT	ISNR	ISNR	QSNV2	WSNR
Z508F3	508	CAA AAA GAA	QSNR1	QSNV2	QSNV2	
Z508F4	508	CAA AAA GAA GGT	WSNR	QSNR1	QSNV2	QSNV2
Z502R3	502R	TGG TAA AGA	QTHQ	QSNK	RDHT	
Z502R4a	502R	TGG TAA AGA TGA	QSHV	QTHQ	QSNK	RDHT
Z502R4b	502R	TGG TAA AGA TGA	QSHV	QTHQ	QSNK	RDHT
Z509F3	509	AAA AAG AAG	rdnq	rdnq	QSNV2	
Z509F4	509	AAA AAG AAG GTC	DSAR2	rdnq	rdnq	QSNV2
Z503R3a	503R	CTG GTA AAG	rdnq	QSTR	rdae	
Z503R3b	503R	CTG GTA AAG	rdnq	QSSR1	rdae	
Z503R4	503R	CTG GTA AAG ATG	rdev	rdnq	QSSR1	rdae
Z510F3	510	AAA AGA AGG	RDKR	QTHQ	QSNV2	
Z667R3a	667R	GAA GCA GAG	KSNR	QSSR1	QSNR1	
Z667R3b	667R	GAA GCA GAG	QFNR	QSSR1	QSNR1	
Z673F3a	673	CGA AAT GAG	KSNR	VSNV	QSHV	
Z673F3b	673	CGA AAT GAG	QFNR	VSNV	QSHV	

Z673F4a	673	CGA AAT GAG AAG	rdnq	KSNR	VSNV	QSHT
Z673F4b	673	CGA AAT GAG AAG	rdnq	QFNR	VSNV	QSHT
Z819R3a	819R	GTT AGA GCT	VSTR	QTHQ	HSSR	
Z819R3b	819R	GTT AGA GCT	VSTR	QTHQ	VSSR	
Z826F3a	826	GAC CAA GCT	VSTR	QSNV2	DSNR	
Z826F3b	826	GAC CAA GCT	VSTR	QSNV2	CSNR1	
Z836R3	836R	ATA GCT TGG	RDHT	VSTR	QNTQ	
Z843F3a	843	GAC AGA GAC	DSNR	QTHQ	DSNR	
Z843F3b	843	GAC AGA GAC	DSNR	QTHQ	CSNR1	
Z843F3c	843	GAC AGA GAC	CSNR1	QTHQ	DSNR	
Z843F3d	843	GAC AGA GAC	CSNR1	QTHQ	CSNR1	
Z891R3	891R	ATA GAT GAT	ISNR	ISNR	QNTQ	
Z891R4	891R	ATA GAT GAT GGG	RSHR	ISNR	ISNR	QNTQ
Z898F3a	898	GTC GGG GAG	KSNR	RSHR	DSAR2	
Z898F3b	898	GTC GGG GAG	QFNR	RSHR	DSAR2	
Z898F4a	898	GTC GGG GAG AAG	rdnq	KSNR	RSHR	DSAR2
Z898F4b	898	GTC GGG GAG AAG	rdnq	QFNR	RSHR	DSAR2
Z955R3a	955R	GTT TGG CAA	QSNV2	RDHT	HSSR	
Z955R3b	955R	GTT TGG CAA	QSNV2	RDHT	VSSR	
Z962F3	962	GCA AAT GCT	VSTR	VSNV	QSSR1	
Z962F4a	962	GCA AAT GCT GTT	HSSR	VSTR	VSNV	QSSR1
Z962F4b	962	GCA AAT GCT GTT	VSSR	VSTR	VSNV	QSSR1
Z1022R3	1022R	CGG GTG TAA	QSNK	RDER2	RDHT	
Z1029F3	1029	TGG GGA GCA	QSSR1	QTHR1	RDHT	
Z1029F4	1029	TGG GGA GCA GGA	QTHR1	QSSR1	QTHR1	RDHT
Z1025R3	1025R	GAT CGG GTG	RDER2	RDHT	ISNR	
Z1025R4	1025R	GAT CGG GTG TAA	QSNK	RDER2	RDHT	ISNR
Z1032F3	1032	GGA GCA GGA	QTHR1	QSSR1	QTHR1	
Z1032F4	1032	GGA GCA GGA AAT	VSNV	QTHR1	QSSR1	QTHR1
Z1028R3	1028R	GTG GAT CGG	RDHT	ISNR	RDER2	
Z1028R4	1028R	GTG GAT CGG GTG	RDER2	RDHT	ISNR	RDER2
Z1035F3	1035	GCA GGA AAT	VSNV	QTHR1	QSSR1	

Supplemental Table 6. Primer sequences

Primer number	Sequence (5' to 3')
1	CGCGGATCCTGAACTCCTCTGGATCTACTG
2	CCGCTCGAGTTACACGGCGATCTTTCCGCC
3	CTCGGCCTCTGAGCTATTCC
4	CGCGGATCCACAACCTTCGCTTCAAAAAAT
5	GATCATAGGGATAACAGGGTAATG
6	GATCCATTACCCTGTTATCCCTAT
7	GGGGATCCATGGATTATCAAGTGTC A
8	GGGGATCCTCACAAGCCCACAGATAT
9	CCGCTCGAGGAGCCAAGCTCTCCATCTAGT
10	TACGAATTCGATGGATTATCAAGTGTC AAG
11	CCCAAGCTTGTTCTGGGCTCACTATGCTGC
12	AGAGGATCCCCGTATGGAAAATGAGAGCTG
13	TACGAATTCGTTAAAGATAGTCATCTTGGG
14	TCACAAGCCCACAGATATTT