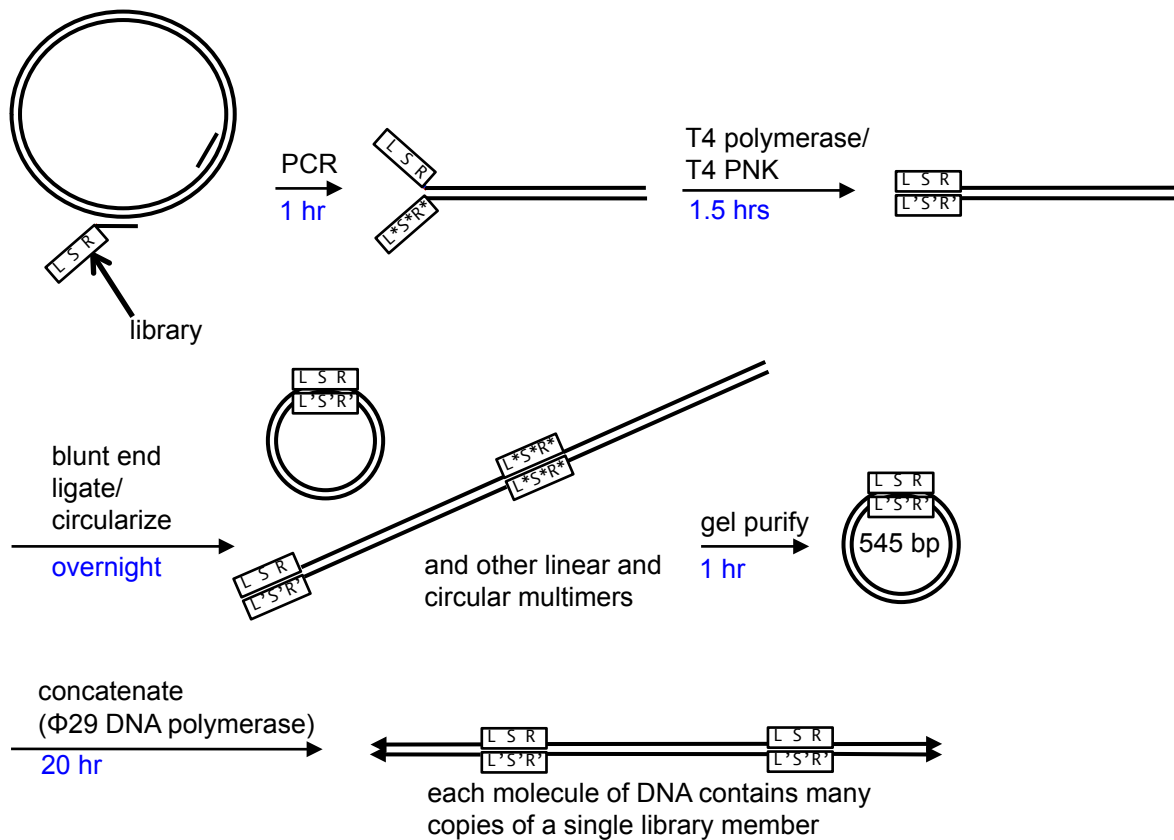
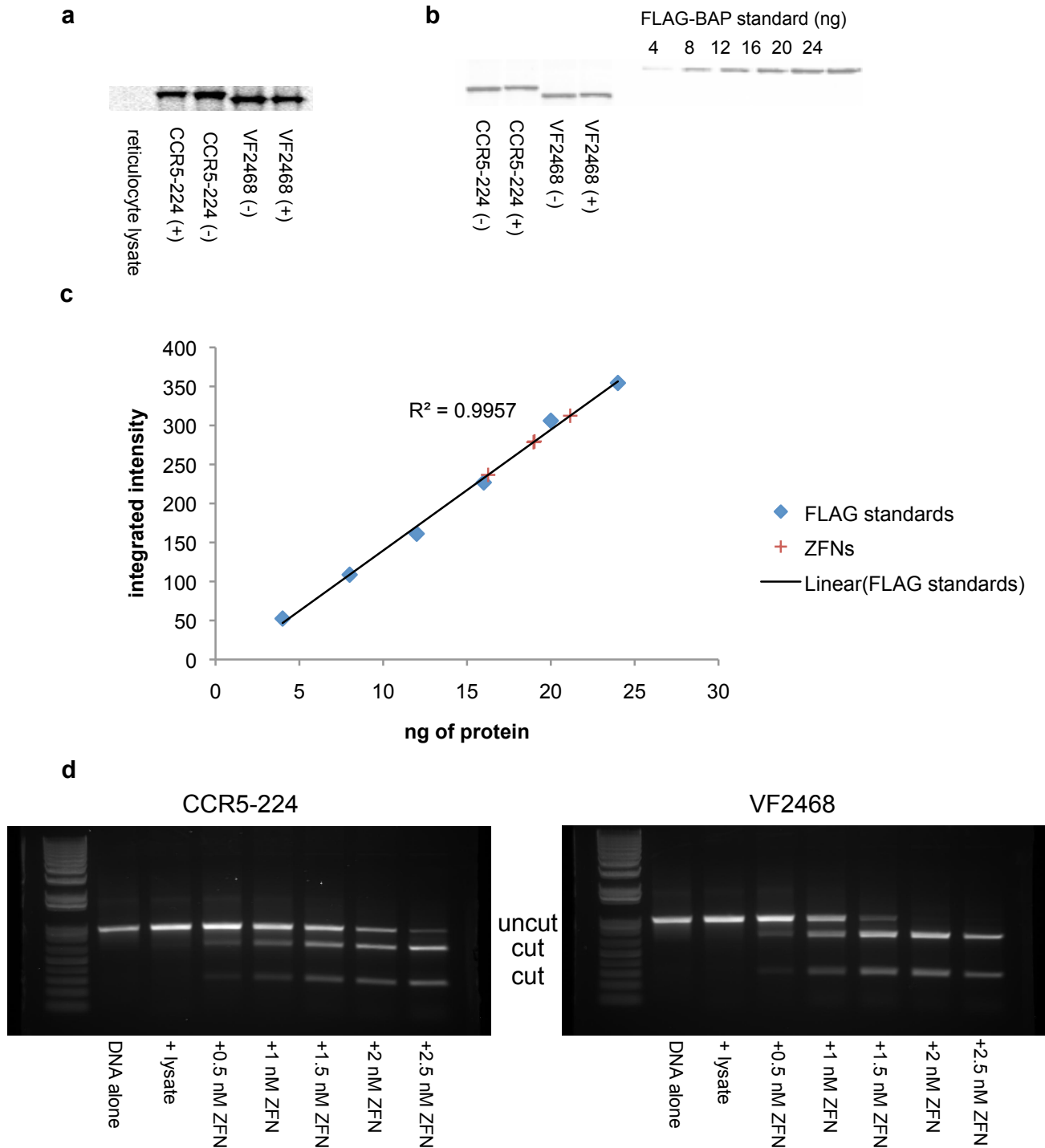


Supplementary Figure S1



***In vitro* synthesis of target site library.** Library members consist of a partially randomized left-half site (L), a fully randomized 4-7 nucleotide spacer sequence (S), and a partially randomized right-half site (R). Library members present on DNA primers were incorporated into a linear ~545 base pair double-stranded DNA by PCR. During PCR, a primer with a library member (L S R) can anneal to a DNA strand with a different library member (L* S* R*), resulting in a double-strand DNA with two different library members at one end. The 3'->5' exonuclease and 5'->3' polymerase activities of T4 DNA polymerase removed mismatched library members and replaced them with complementary, matched library members (L' S' R'). After 5' phosphorylation with T4 polynucleotide kinase, the library DNA was subjected to blunt-end ligation, resulting in a mixture of linear and circular monomeric and multimeric species. Circular monomers were purified by gel electrophoresis and concatenated through rolling-circle amplification with phi29 DNA polymerase.

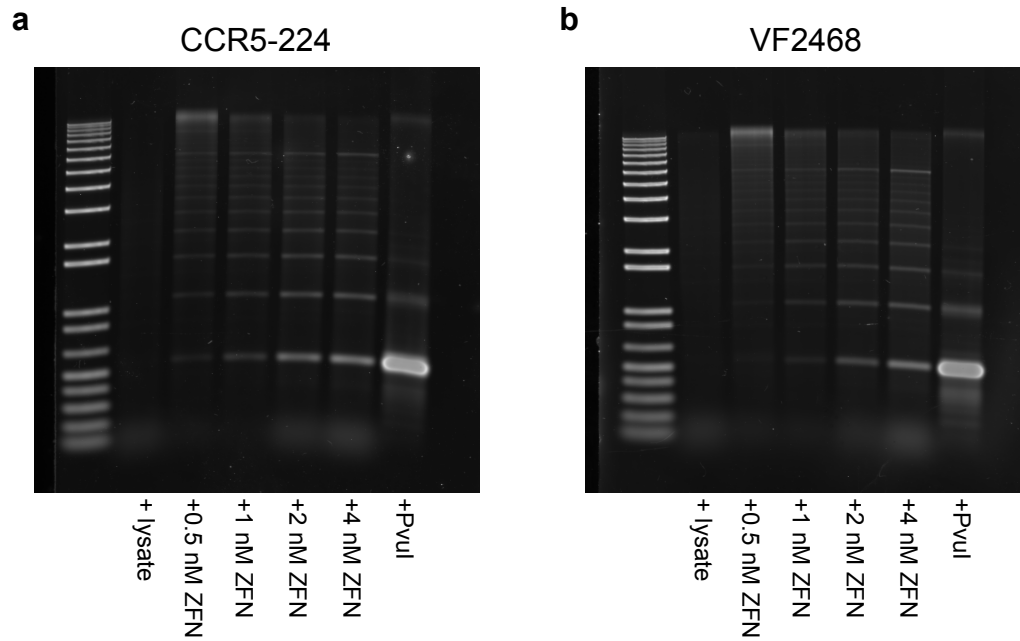
Supplementary Figure S2



Expression and quantification of ZFNs. Western blots for CCR5-224 and VF2468 are shown (a) for the ZFN samples used in the *in vitro* selection, and (b) for quantification. (c) Known quantities of N-terminal FLAG-tagged bacterial alkaline phosphatase (FLAG-BAP) were used to generate a standard curve for ZFN quantification. Blue diamonds represent the intensities of FLAG-BAP standards from the Western blot shown in (b), red plus signs represent the intensities of bands of ZFNs, and the black line shows the best-fit curve of FLAG-BAP standards that was used to quantify ZFNs. (d) Gels are shown of activity assays of CCR5-224 and VF2468 on an 8 nM linear substrate containing one target cleavage site. The ZFNs were each incubated with their respective substrate for 4 hours at 37°C. DNA in the “+ lysate” lane

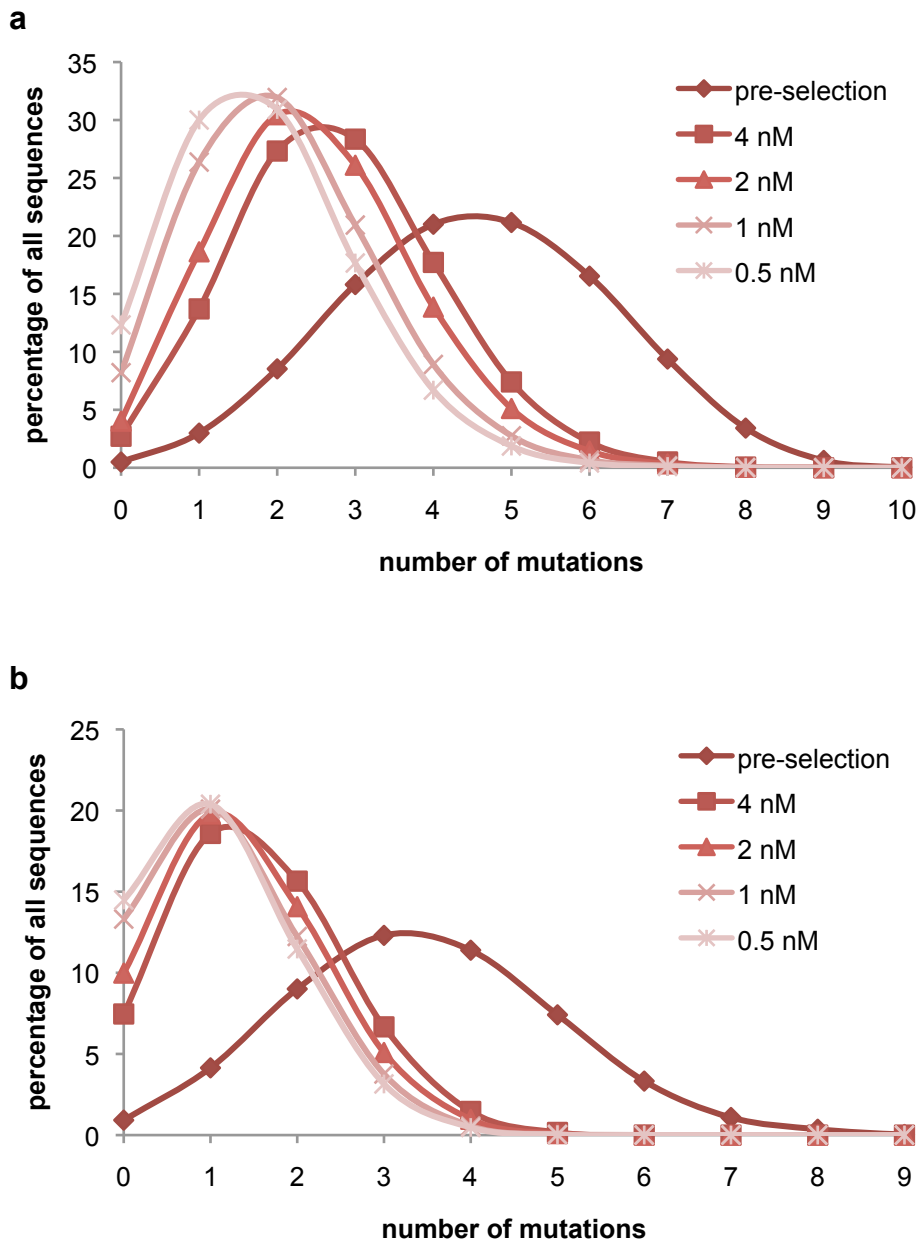
was incubated with an amount of *in vitro* transcription/translation mixture equivalent to that used in the 2.5 nM ZFN reaction. ZFN-mediated cleavage results in two linear fragments approximately 700 bp and 300 bp in length. 2 nM CCR5-224 and 1 nM VF2468 were the amounts required for 50% cleavage of the linear substrate.

Supplementary Figure S3



Library cleavage with ZFNs. Cleavage of 1 μg of concatemeric libraries of CCR5-224 (**a**) or VF2468 (**b**) target sites are shown with varying amounts CCR5-224 or VF2468, respectively. The lane labeled “+ lysate” refers to pre-selection concatemeric library incubated with the volume of *in vitro* transcription/translation mixture contained in the samples containing 4 nM CCR5-224 or 4 nM of VF2468. Uncut DNA, which would be observed in the “+ lysate” lane, is of length >12 kb and is lost upon purification due to its size and therefore is not present on the gel. The lane labeled “+PvuI” is a digest of the pre-selection library at PvuI sites introduced adjacent to library members. The laddering on the gels result from cleavage of pre-selection DNA concatamers at more than one site. There is a dose-dependent increase in the amount of the bottom band, which corresponds to cleavage at two adjacent library sites in the same pre-selection DNA molecule. This bottom band of DNA was enriched by PCR and gel purification before sequencing.

Supplementary Figure S4

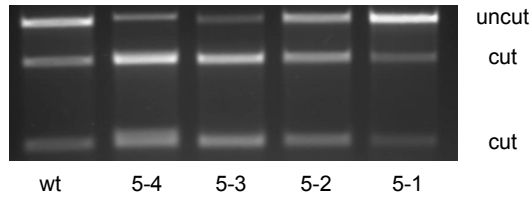


ZFN off-target cleavage is dependent on enzyme concentration. For both (a) CCR5-224 and (b) VF2468 the distribution of cleavable sites revealed by *in vitro* selection shifts to include sites that are less similar to the target site as the concentration of ZFN increases. Both CCR5-224 and VF2468 selections enrich for sites that have fewer mutations than the pre-selection library. For comparisons between pre-selection and post-selection library means for all combinations of selection stringencies, *P*-values are 0 with the exception of the comparison between 0.5 nM and 1 nM VF2468 selections, which has a *P*-value of 1.7×10^{-14} .

Supplementary Figure S5

a

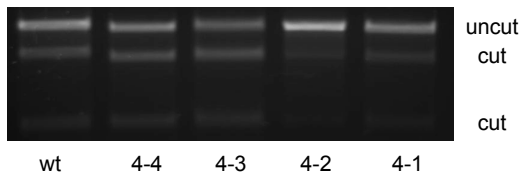
CCR5-224



	(+ site (5'→3'))		(-) site (5'→3')		4 nM	2 nM	1 nM	0.5 nM
wt	GAT	GAG GAT GAC	AAA	CTG CAA AAG	X	X	X	X
5-4	GAT	GAG Ggg cga	AAA	CTG CAA AAG	X	X	X	X
5-3	GAT	GAG Gca cga	AAA	CTG CAA AAG	X	X	X	
5-2	GcT	GAG GAT aAC	AAA	aTG gAA cAG	X	X		
5-1	GAT	aca GAT GAC	AAA	CTG gAA AAa	X			

b

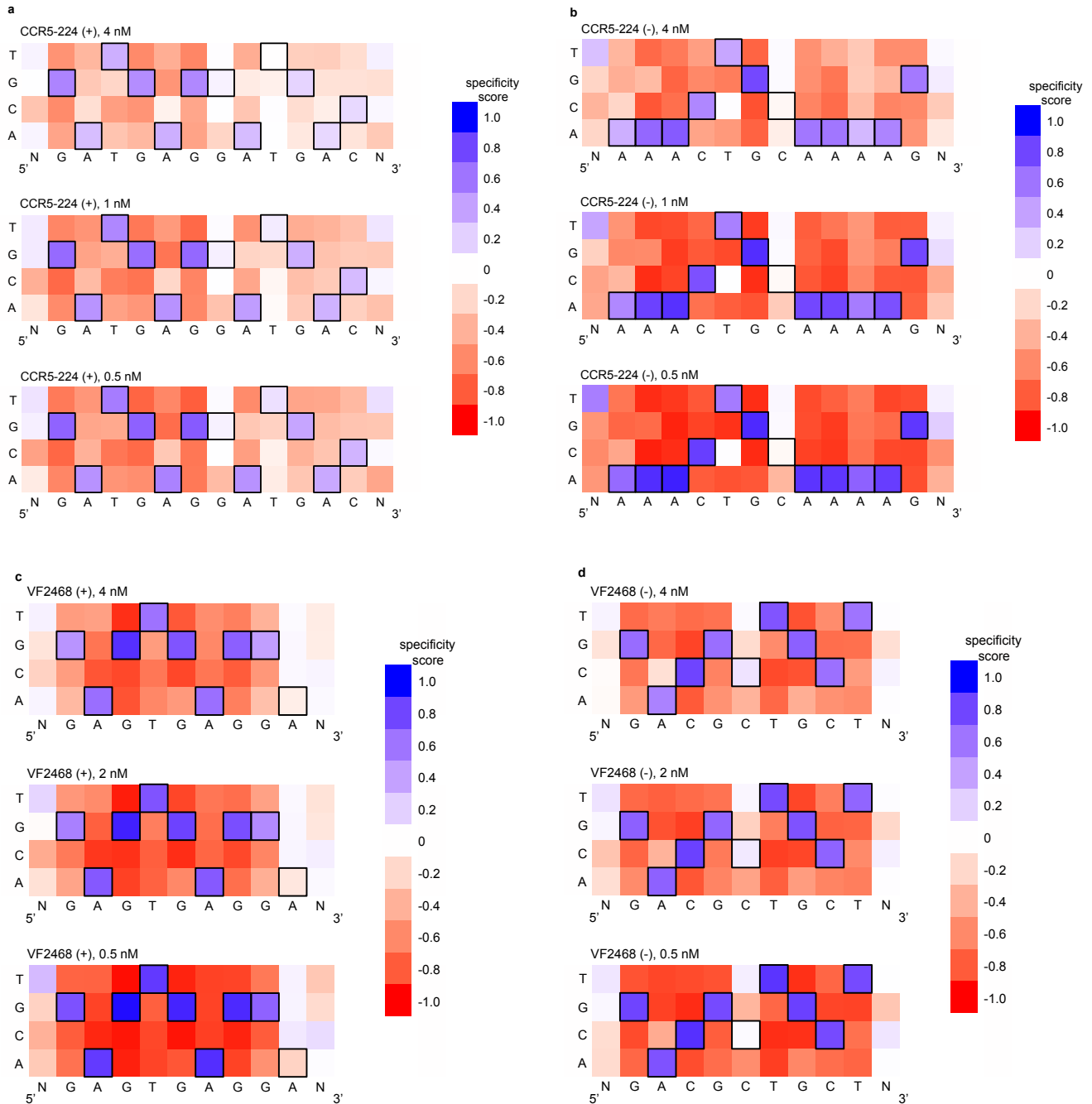
VF2468



	(+ site (5'→3'))		(-) site (5'→3')		4 nM	2 nM	1 nM	0.5 nM
wt	GAG	TGA GGA	GAC	GCT GCT	X	X	X	X
4-4	GAG	TGA aac	GAC	GtT GCT	X	X	X	X
4-3	GAG	TGA Gtc	GAC	GtT aCT	X	X	X	
4-2	GtG	TGA aaA	GAC	GtT GCT	X	X		
4-1	GAG	TGA GGA	GAC	Gaa aCc	X			

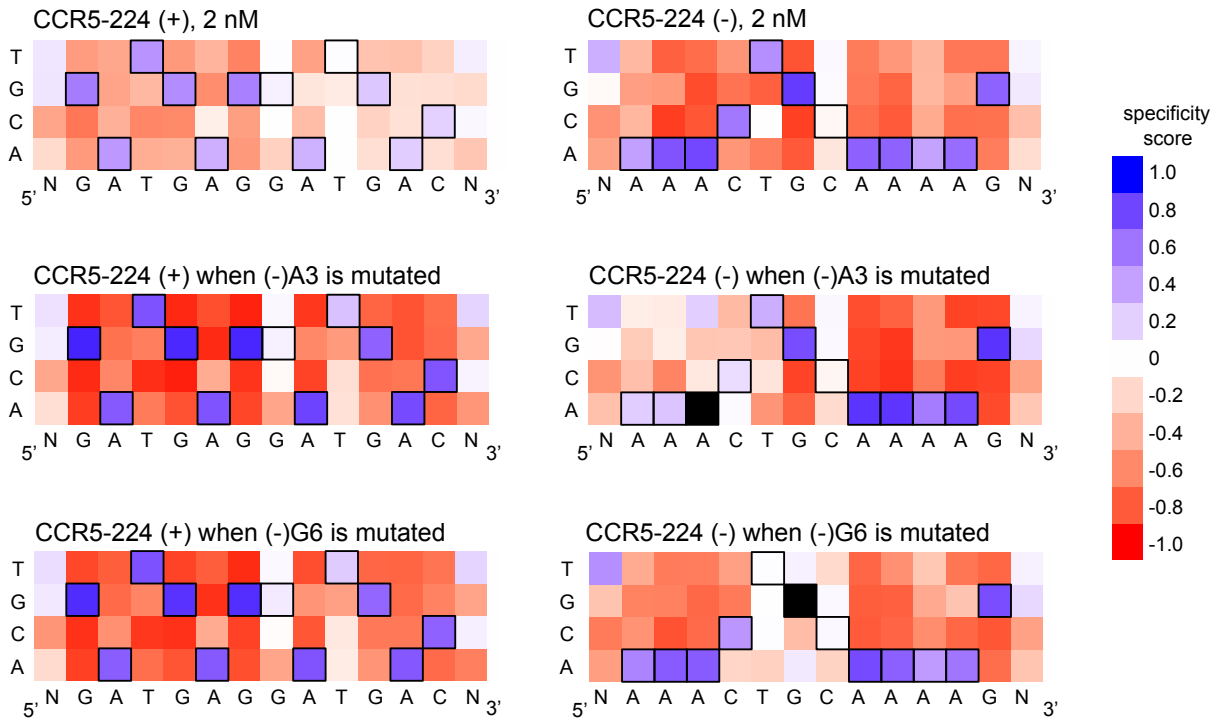
Cleavage efficiency of individual sequences is related to selection stringency. *In vitro* DNA digests were performed on sequences identified in selections of varying stringencies (marked with 'X's). 2 nM CCR5-224 (**a**) or 1 nM VF2468 (**b**) was incubated with 8 nM of linear substrate containing the sequence shown. The 1 kb linear substrate contained a single cleavage site with the spacer sequence found in the genomic target of CCR5-224 ("CTGAT") or VF2468 ("TCGAA") and the indicated (+) and (-) half-sites. Mutant base pairs are represented with lowercase letters. CCR5-224 sites and VF2468 sites that were identified in the highest stringency selections (0.5 nM ZFN) are cleaved most efficiently, while sites that were identified only in the lowest stringency selections (4 nM ZFN) are cleaved least efficiently.

Supplementary Figure S6



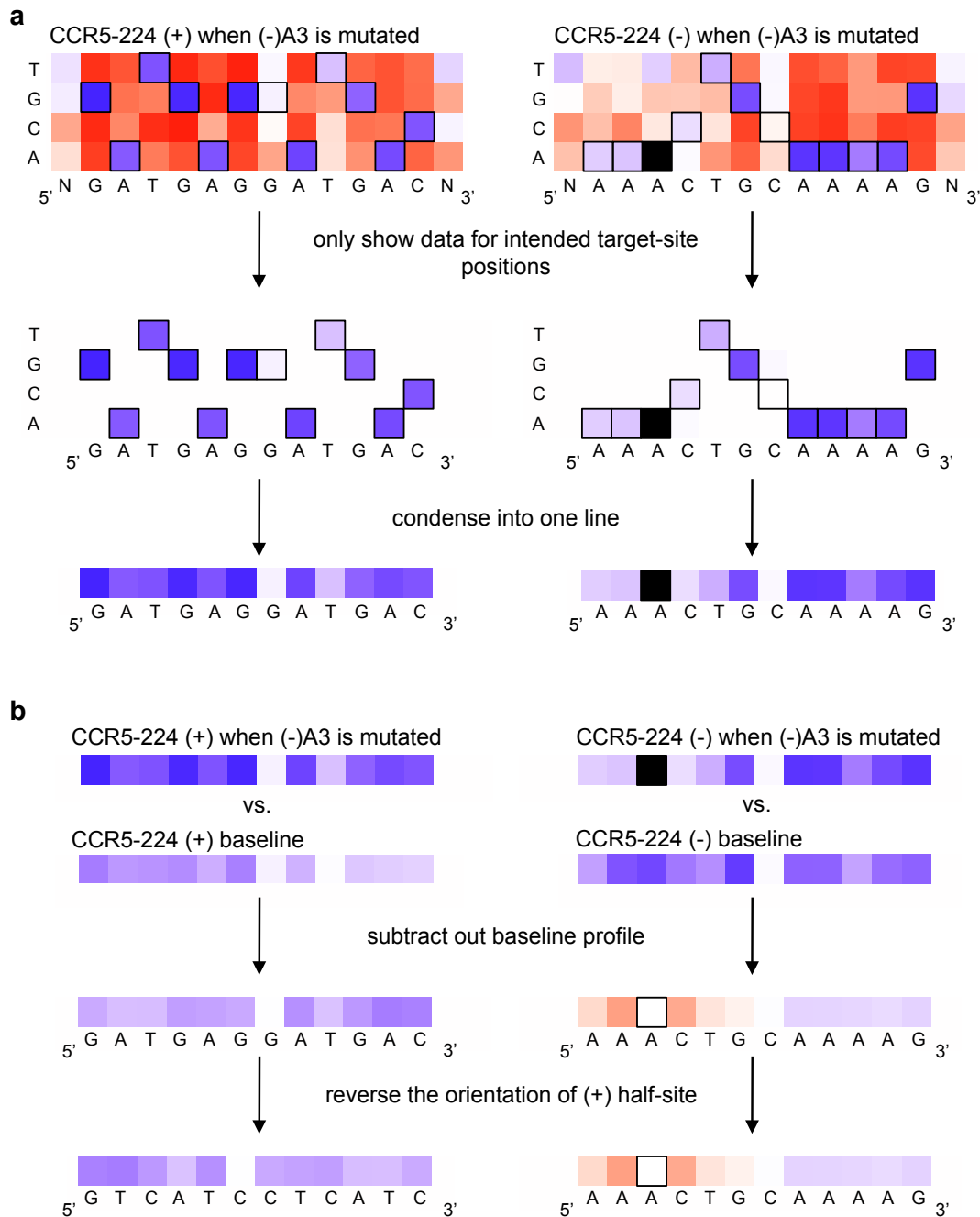
Concentration-dependent sequence profiles for CCR5-224 and VF2468 ZFNs. The heat maps show specificity scores for the cleavage of 14 nM of total DNA library with varying amounts of **(a)** CCR5-224 or **(b)** VF2468. The target DNA sequence is shown below each half-site. Black boxes indicate target base pairs. Specificity scores were calculated by dividing the change in frequency of each base pair at each position in the post-selection DNA pool compared to the pre-selection pool by the maximal possible change in frequency of each base pair at each position. Blue boxes indicate specificity for a base pair at a given position, white boxes indicate no specificity, and red boxes indicate specificity against a base pair at a given position. The darkest blue shown in the legend corresponds to absolute preference for a given base pair (specificity score = 1.0), while the darkest red corresponds to an absolute preference against a given base pair (specificity score = -1.0).

Supplementary Figure S7



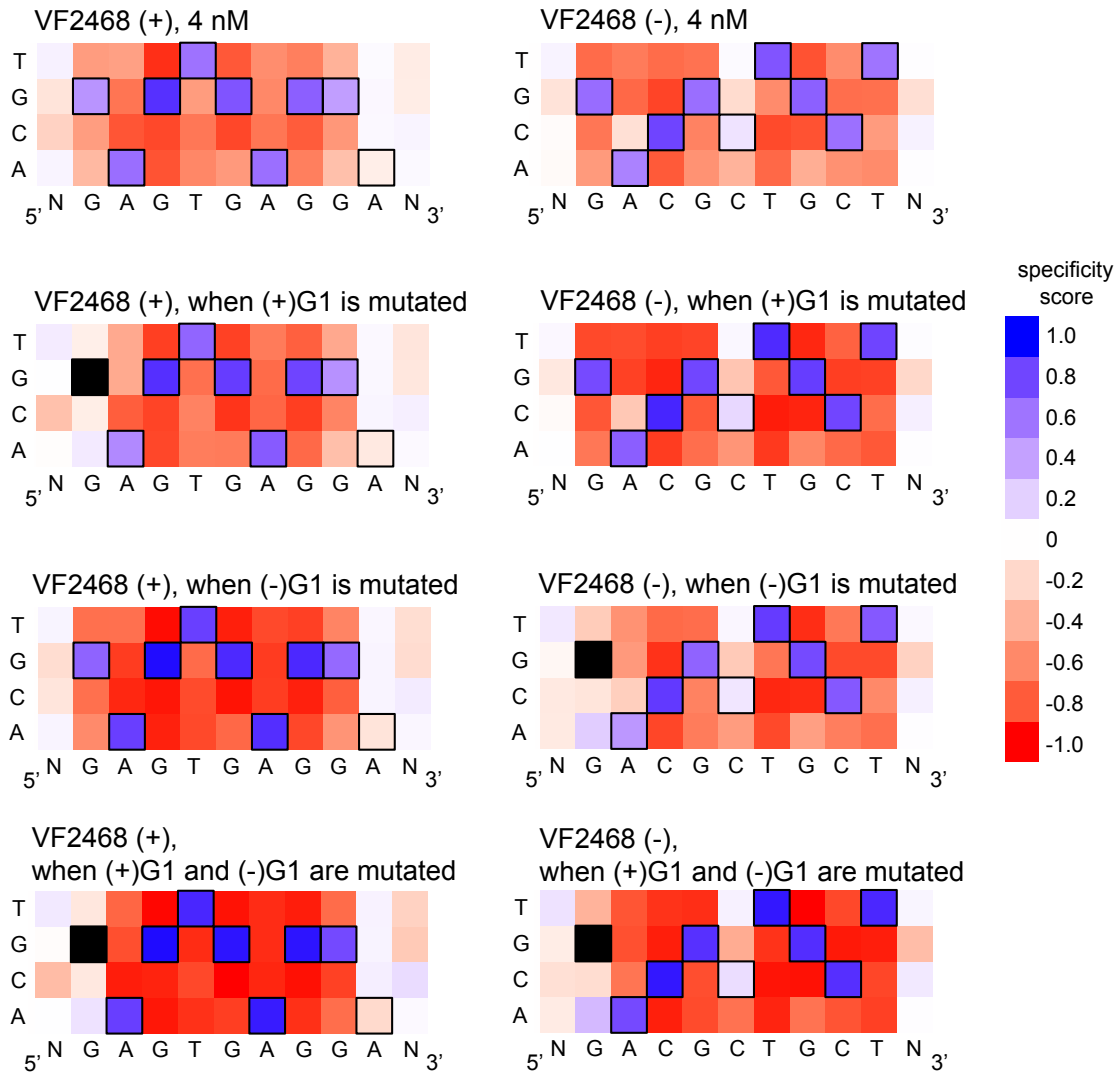
Stringency at the (+) half-site increases when CCR5-224 cleaves sites with mutations at highly specified base pairs in the (-) half-site. The heat maps show specificity scores for sequences identified in the *in vitro* selection with 2 nM CCR5-224. For (-)A3 and (-)G6, indicated by filled black boxes, both pre-selection library sequences and post-selection sequences were filtered to exclude any sequences that contained an A at position 3 in the (-) half-site or G at position 6 in the (-) half-site, respectively, before specificity scores were calculated. For sites with either (-) half-site mutation, there is an increase in specificity at the (+) half-site. Black boxes indicate target base pairs. Specificity scores were calculated by dividing the change in frequency of each base pair at each position in the post-selection DNA pool compared to the pre-selection pool by the maximal possible change in frequency of each base pair at each position. Blue boxes indicate specificity for a base pair at a given position, white boxes indicate no specificity, and red boxes indicate specificity against a base pair at a given position. The darkest blue shown in the legend corresponds to absolute preference for a given base pair (specificity score = 1.0), while the darkest red corresponds to an absolute preference against a given base pair (specificity score = -1.0).

Supplementary Figure S8



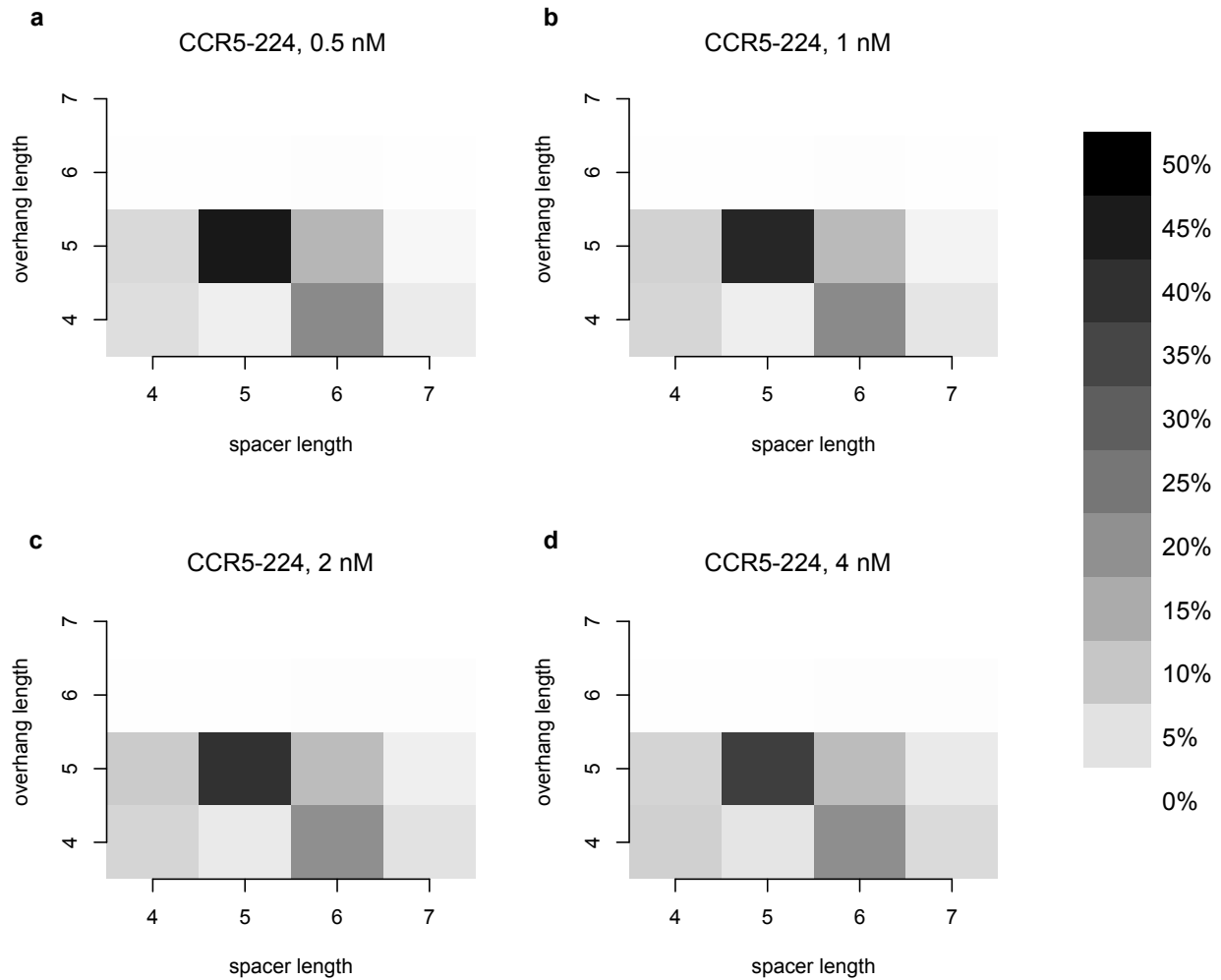
Data processing steps used to create mutation compensation difference maps. The steps to create each line of the difference map in Figure 3 are shown for the example of a mutation at position (-)A3. **(a)** Heat maps of the type described in Supplementary Figure S7 are condensed into one line to show only the specificity scores for intended target site nucleotides (in black outlined boxes in Supplementary Figure S7). **(b)** The condensed heat maps are then compared to a condensed heat map corresponding to the unfiltered baseline profile from Figure 2, to create a condensed difference heat map that shows the relative effect of mutation at the position specified by the white box with black outline on the specificity score profile. Blue boxes indicate an increase in sequence stringency at positions in cleaved sites that contain mutations at the position indicated by the white box, while red boxes indicate a decrease in sequence stringency and white boxes, no change in sequence stringency. The (+) half-site difference map is reversed to match the orientation of the (+) half-site as it is found in the genome rather than as it is recognized by the zinc finger domain of the ZFN.

Supplementary Figure S9



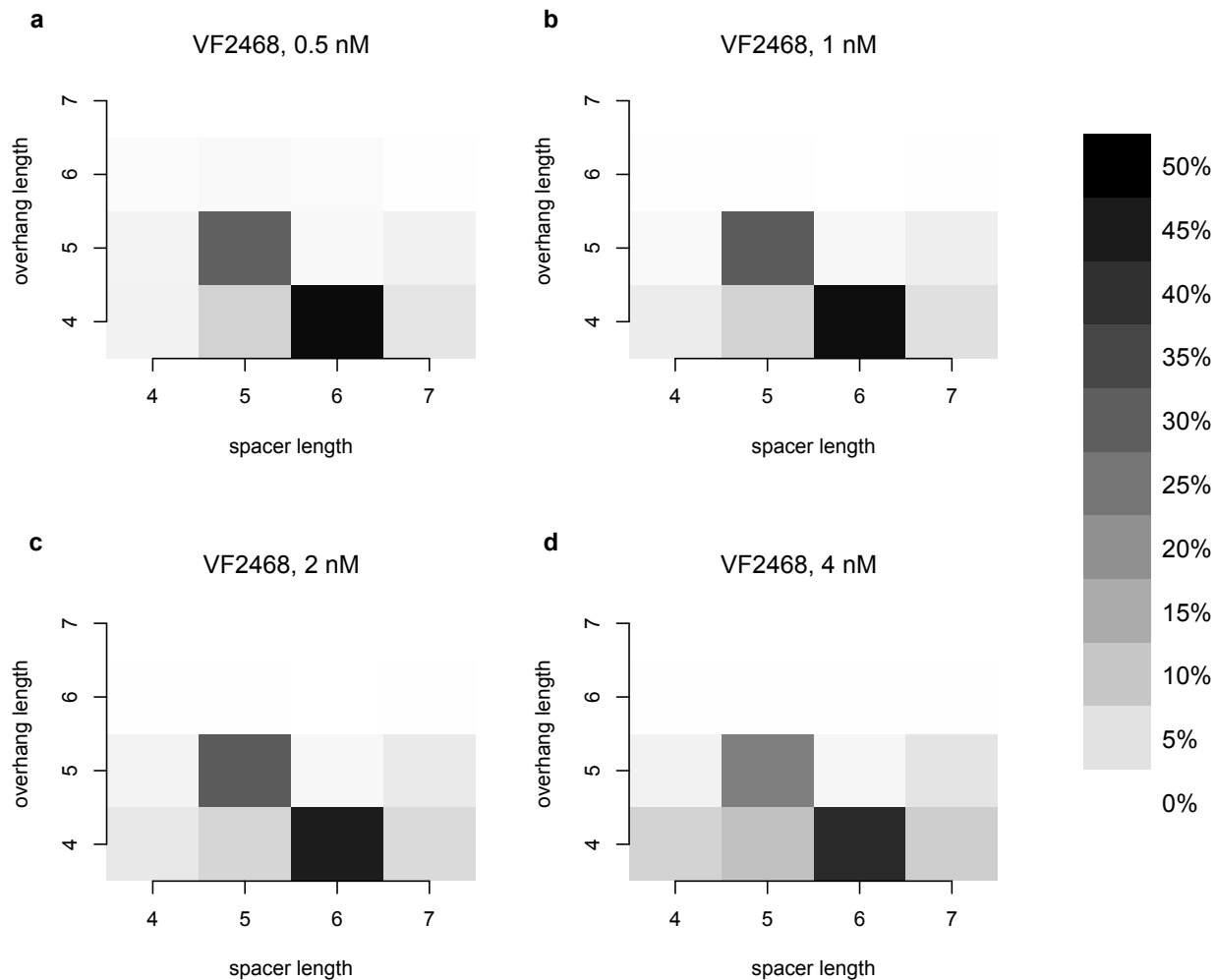
Stringency at both half-sites increases when VF2468 cleaves sites with mutations at the first base pair of both half-sites. The heat maps show specificity scores for sequences identified in the *in vitro* selection with 4 nM VF2468. For (+)G1, (-)G1, and (+)G1/(-)G1, indicated by filled black boxes, both pre-selection library sequences and post-selection sequences were filtered to exclude any sequences that contained an G at position 1 in the (+) half-site and/or G at position 1 in the (-) half-site, before specificity scores were calculated. For sites with either mutation, there is decrease in mutational tolerance at the opposite half-site and a very slight decrease in mutational tolerance at the same half-site. Sites with both mutations show a strong increase in stringency at both half-sites. Black boxes indicate on-target base pairs. Specificity scores were calculated by dividing the change in frequency of each base pair at each position in the post-selection DNA pool compared to the pre-selection pool by the maximal possible change in frequency of each base pair at each position. Blue boxes indicate specificity for a base pair at a given position, white boxes indicate no specificity, and red boxes indicate specificity against a base pair at a given position. The darkest blue shown in the legend corresponds to absolute preference for a given base pair (specificity score = 1.0), while the darkest red corresponds to an absolute preference against a given base pair (specificity score = -1.0).

Supplementary Figure S11



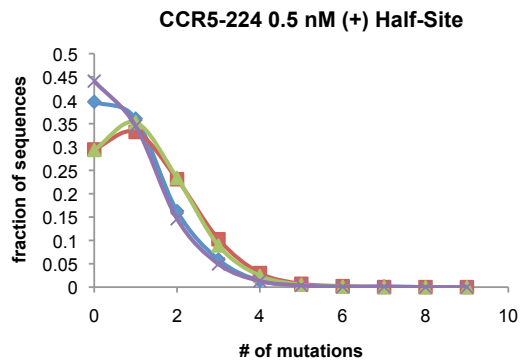
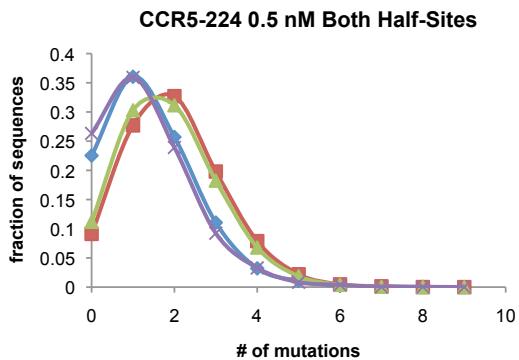
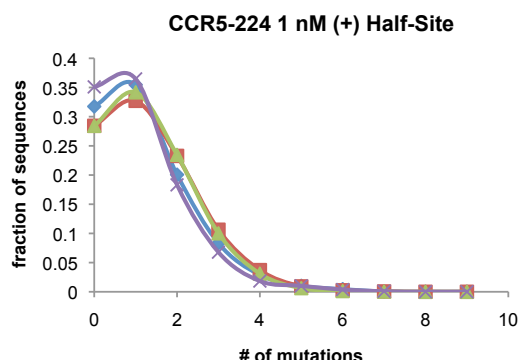
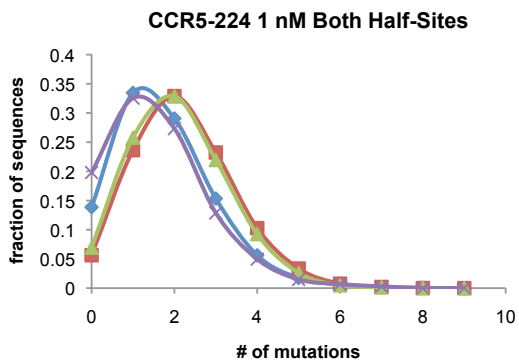
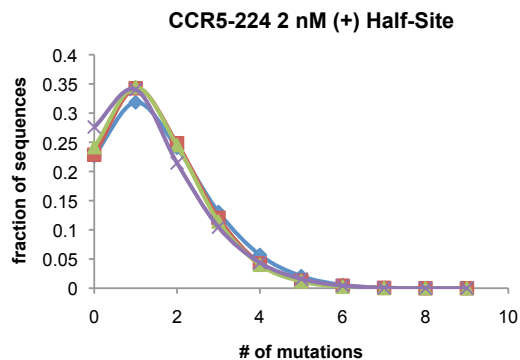
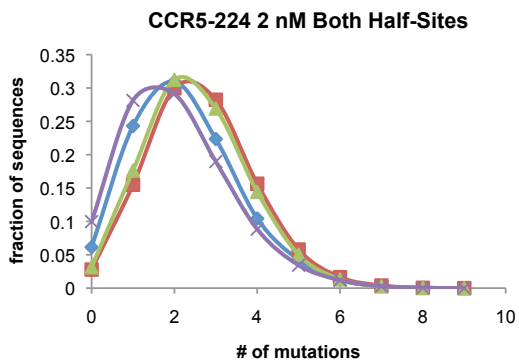
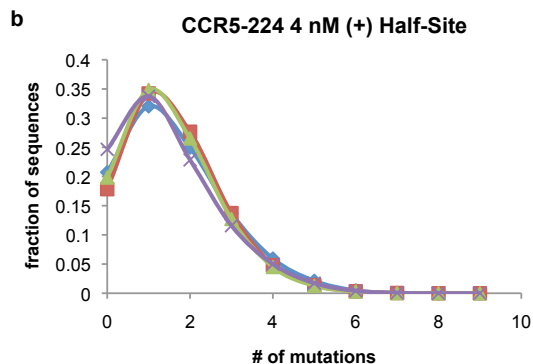
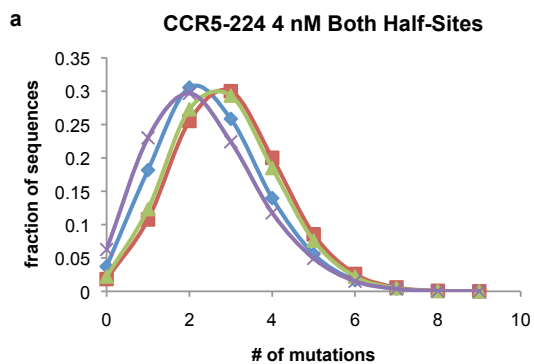
CCR5-224 preferentially cleaves five- and six-base pair spacers and cleaves five-base pair spacers to leave five-nucleotide overhangs. The heat maps show the percentage of all sequences surviving each of the four CCR5-224 *in vitro* selections (**a-d**) that have the spacer and overhang lengths shown.

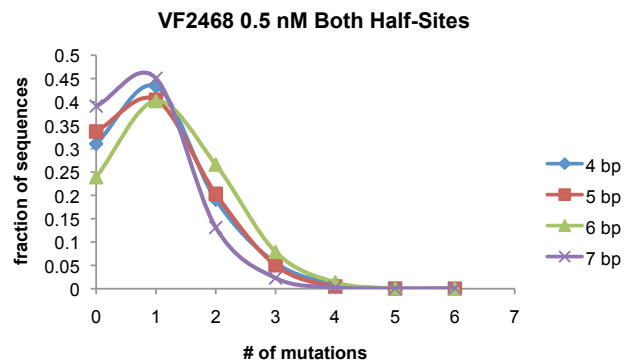
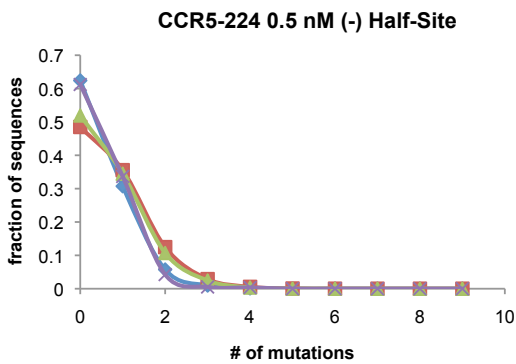
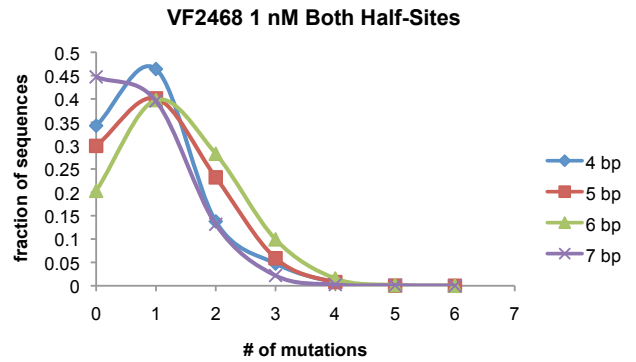
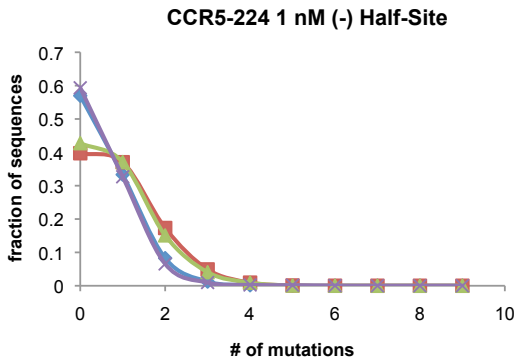
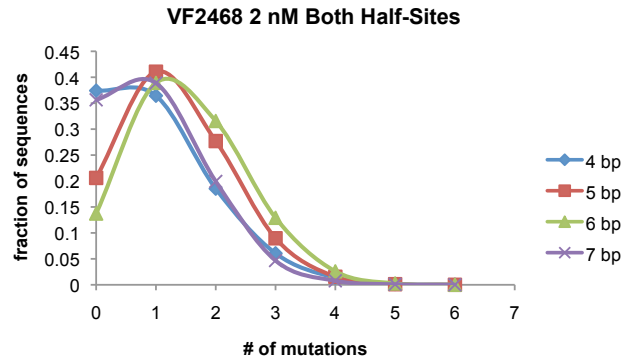
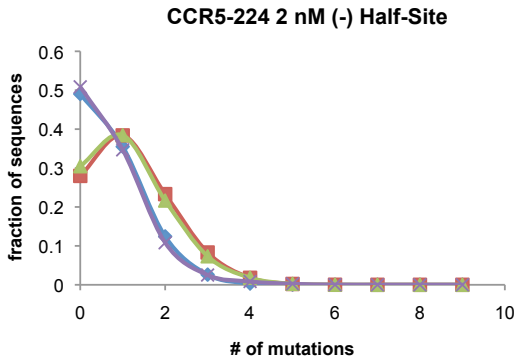
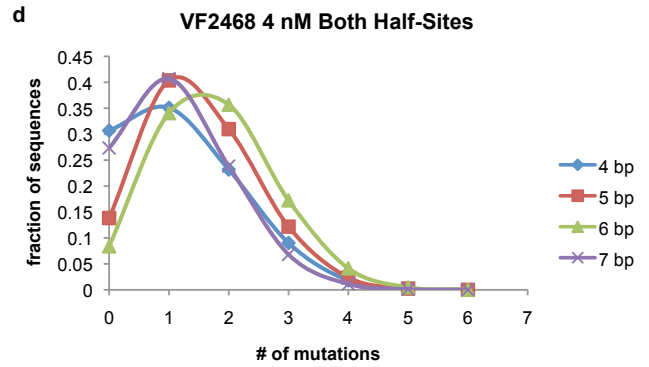
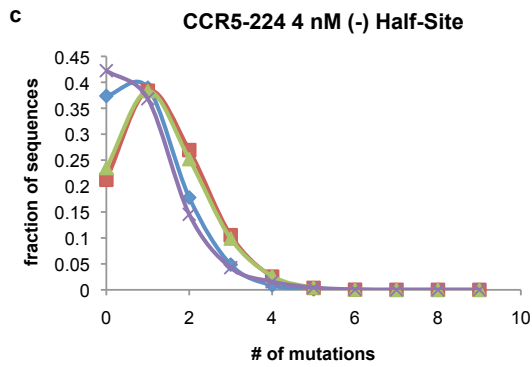
Supplementary Figure S12

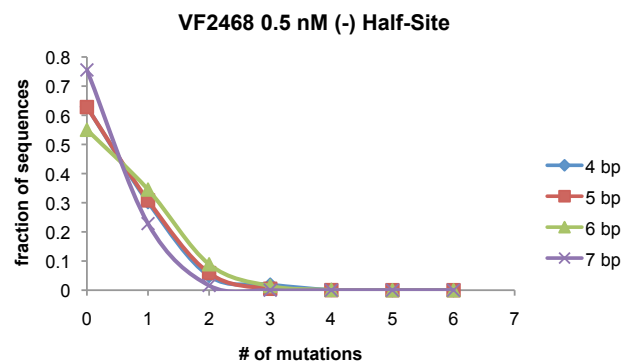
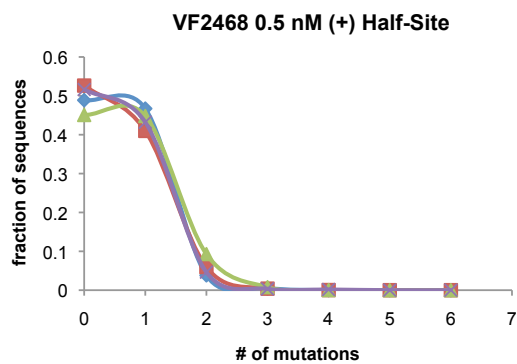
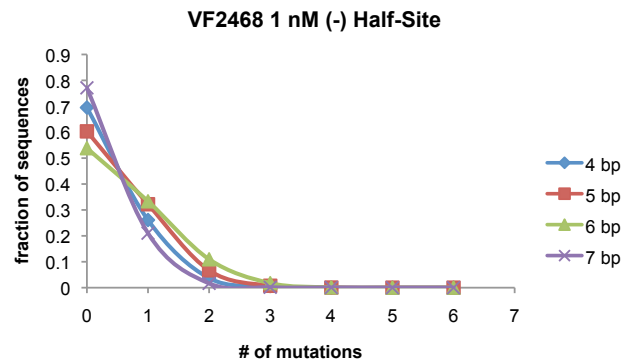
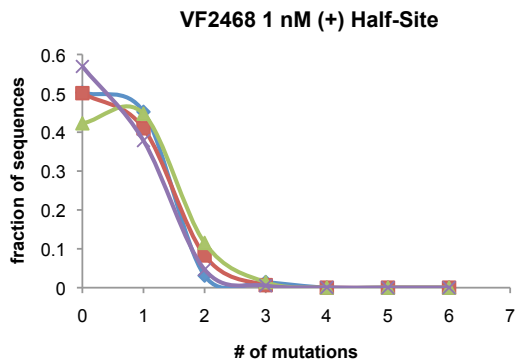
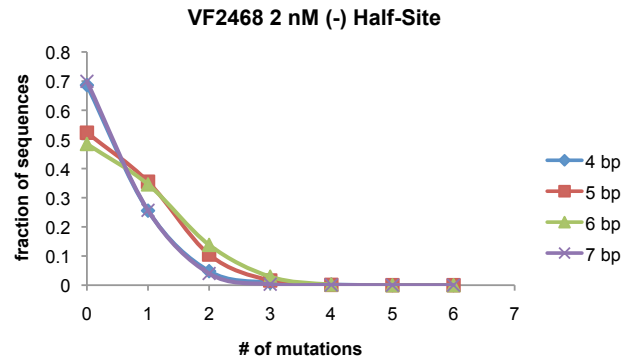
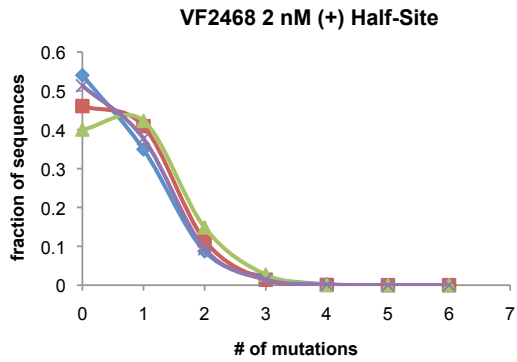
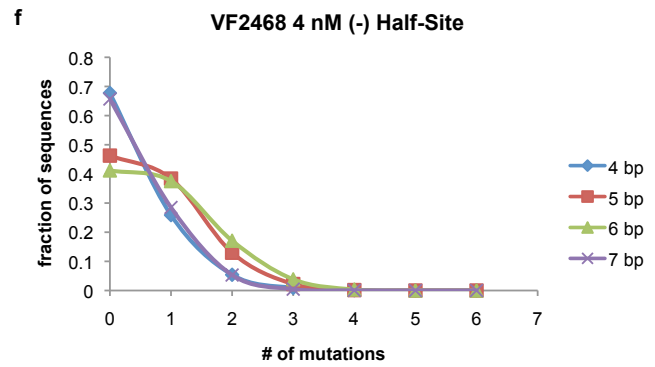
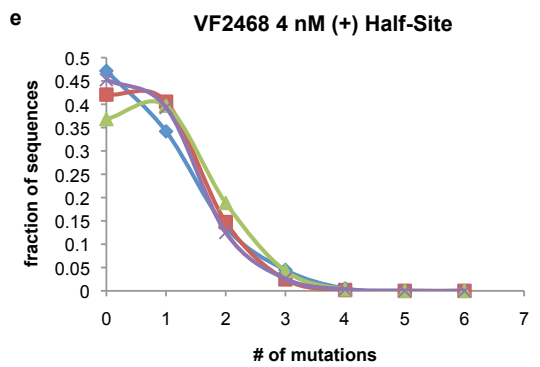


VF2468 preferentially cleaves five- and six-base pair spacers, cleaves five-base pair spacers to leave five-nucleotide overhangs, and cleaves six-base pair spacers to leave four-nucleotide overhangs. The heat maps show the percentage of all sequences surviving each of the four VF2468 *in vitro* selections (a-d) that have the spacer and overhang lengths shown.

Supplementary Figure S13

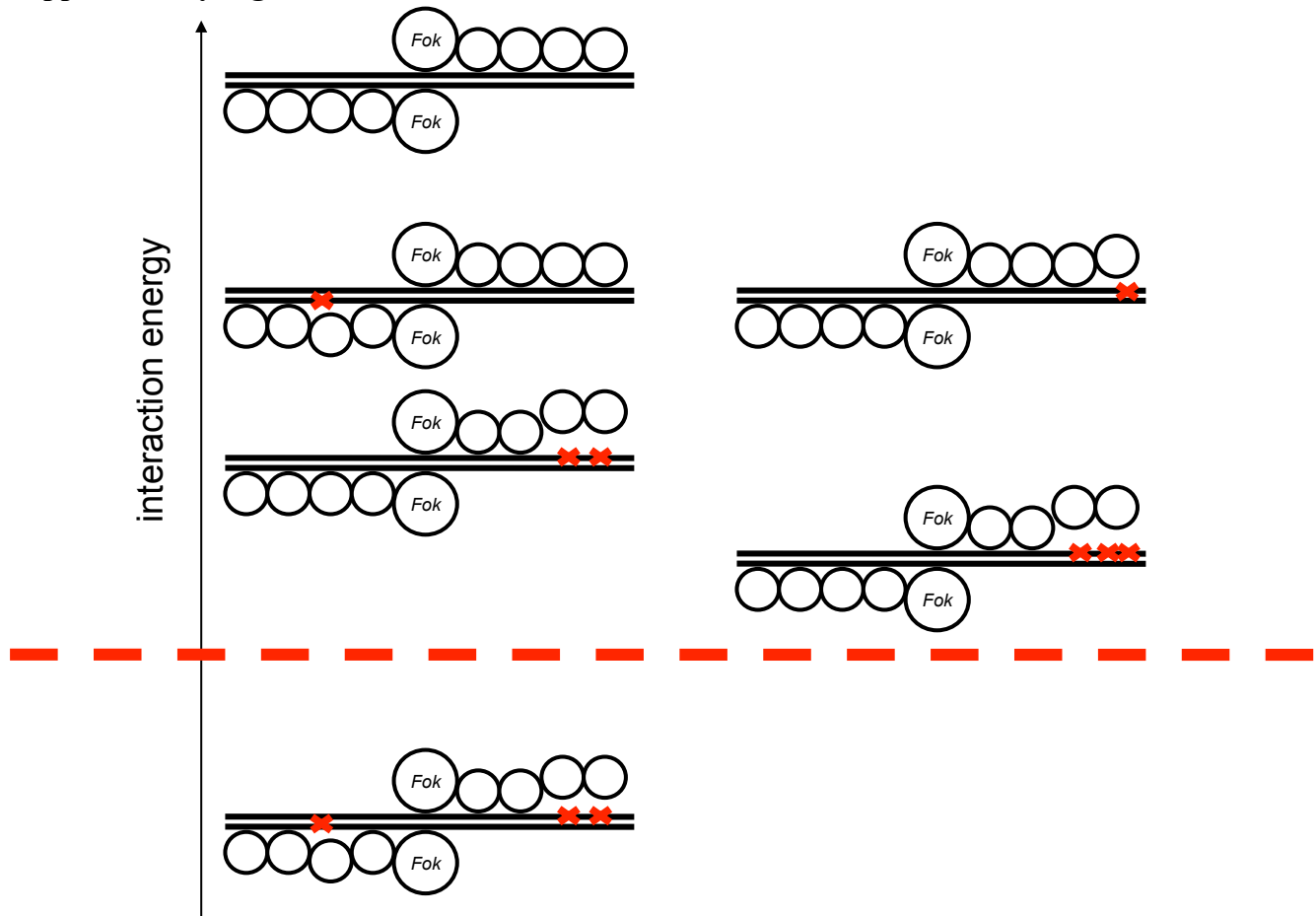






ZFNs show spacer length-dependent sequence preferences. Both CCR5-224 (a-c) and VF2468 (d-f) show increased specificity for half-sites flanking four- and seven-base pair spacers than for half-sites flanking five- and six-base pair spacers. For both ZFNs, one half-site has a greater change in mutational tolerance than the other, and the change in mutational tolerance is concentration dependent.

Supplementary Figure S14



Model for ZFN tolerance of off-target sequences. Our results suggest that some ZFNs recognize their intended target sites (top, black DNA strands with no red Xs) with more binding energy than is required for cleavage under a given set of conditions (red dotted line). Sequences with one or two mutations (one or two red Xs) are generally tolerated since they do not decrease the ZFN:DNA binding energy below the threshold necessary for cleavage. Some sequences with additional mutations can still be cleaved if the additional mutations occur in regions of the zinc-finger binding interface that have already been disrupted (three red Xs above the red dotted line), as long as optimal interactions present at other locations in the ZFN:DNA binding interface maintain binding energies above threshold values. Additional mutations that disrupt key interactions at other locations in the ZFN:DNA interface, however, result in binding energies that fall short of the cleavage threshold.

Supplementary Figure S15

CCR5-224 (+)

DNA sequence:

taatacgactcactatagggagacccaagctggctagccaccatggactacaaagaccatgacgggtgattataaagatcatgacatcgattacaaggatg
acgatgacaagatggccccaagaagaagaggaaggtgggcattcacggggtacccgccgctatggctgagaggccctccagtgtcgaatctgcat
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protein sequence:

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIIHGVPAAAMAERPFQCRICMRNFSDRSNLS
RHIRTHTGEKPFACDICGRKFAISSNLNSHTKIHTGSQKPFQCRICMRNFSRSDNLARHIRTHTGEK
PFACDICGRKFATSGNLTRHTKIHLRGSQLVKSELEEKSELRHKLKYPHEYIELIEIARNSTQDR
ILEMKVMEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDYGVIVDTKAYSGGYNLPIGQADEM
QRYVKENQTRNKHINPNEWKVPSSVTEFKFLFVSGHFKGNYKAQLTRLNHKTNCNGAVLSV
EELLIGGEMIKAGTLTLEEVRRKFNNGEINF

CCR5-224 (-)

DNA sequence:

taatacgactcactatagggagacccaagctggctagccaccatggactacaaagaccatgacgggtgattataaagatcatgacatcgattacaaggatg
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ATTGGTGGAGAAATGATTAAGCCGGCACATTAACCTAGAGGAAGTGAGACGGAAATTTAATAACGGCGAGATAAACTTTAA

CCR5-224 (-)

protein sequence:

MDYKDHDGDYKDHDIDYKDDDDKMAPKKRKRKVGIIHGVPAAAMAERPFQCRICMRNFSRSDNLS
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ERYVEENQTRNKHLNPNEWVKVYPSSVTEFKFLFVSGHFKGNYKAQLTRLNHITNCNGAVLSV
EELLIGGEMIKAGTLTLEEVRRKFNNGEINF

VF2468 (+)

DNA sequence:

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cttagttagaagagctttaattggtggagaaatgattaaagccggcacattaaccttagaggaagtgagacggaaatttaataacggcgagataaacttt
aa

protein sequence:

MDYKDHDGDYKDHDIDYKDDDDKMAPKKRKRKVGIIHGVPSPRGERPFQCRICMRNFSRQDRDL
RHTRTHTGEKPFQCRICMRNFSQKEHLAHLRHTHTGEKPFQCRICMRNFSRRDNLNRHLKTHLR
GSQLVKSELEEKKSELRHKLKYVPHEYIELIEIARNSTQDRILEMKVMEFFMKVYGYRGKHLGGS
RKPDGAIYTVGSPIDYGVIVDTKAYSGGYNLPIGQADEMQRYVKENQTRNKHINPNNEWVKVYP
SSVTEFKFLFVSGHFKGNYKAQLTRLNHKTNCNGAVLSVEELLIGGEMIKAGTLTLEEVRRKFN
GEINF

VF2468 (-)

DNA sequence:

taatacgactcactatagggagacccaagctggctagccaccat**gg**actacaaagaccatgacgggtgattataaagatcatgacatcgattacaaggatg
acgatgacaagatggccccaagaagaagaggaaggtgggcattcacgggggtccgtctagaccgggggagcggccctccagtgtcgatttgc
gcggaacttttcgaccggccagatccttgaccgccatacccgactcataccggtgaaaaaccgttcagtgctggatctgtatgcgaaatttccgtggc
gcacagctgaagaggcatctacgtacgcacaccggcgagaagccattccaatgccgaatgcatgacgcaactcagtgaccccagcaacctgcggc
gccacctaanaaccacctgaggggatccaactagtcaaaagtgaactggaggagaagaaatctgaactcgtcataaattgaaatgtgcctcatga
atataatgaattaattgaaatgccagaaatccactcaggatagaatcttgaaatgaaggtaatggaatTTTTATGAAAGTTATGGATAGAGGTAACATT
tgggtgatcaaggaaaccggacggagcaattatactgtcggatcctattgattacgggtgtgatcgtggatactaaagcttatagcggaggtataatct
gccaattggccaagcagatgaaatggagcgatattcgaagaaatcaaacacgaaacaaacatctcaaccctaatgaatggaggaaagtctatccatct
tctgtaacggaatttaagTTTTATTGTGAGTGGTCACTTAAAGGAACTACAAAGCTCAGCTTACACGATTAAATCATATCACTAATTGTAATGGAGCTGTTCT
agtgtagaagagctTTAATTGGTGGAGAAATGATTAAGCCGGCACATTAACCTTAGAGGAAGTGAGACGGAAATTAATAACGGCGAGATAAACCCTTAA

protein sequence:

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHGVPSRPGERPFQCRICMRNFSTGQILDR
HTRTHTGEKPFQCRICMRNFSVAHSLKRHLRTHHTGEKPFQCRICMRNFSDPSNLRRHLKTHLRGS
QLVKSELEEKKSELRHKLYVPHEYIELIEIARNSTQDRILEMKVMEFFMKVYGYRGKHLGGSRK
PDGAIYTVGSPIDYGVIVDTKAYSGGYNLPIGQADEMERYVEENQTRNKHLNPNEWWKVYPSSV
TEFKFLFVSGHFKGNYKAQLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLTLEEVRRKFNNGEI
NF

Sequences of ZFNs used in this study. DNA and protein sequences are shown for the ZFNs used in this study. The T7 promoter is underlined, and the start codon is in bold.

Supplementary Table S1

	Total Sequences	Analyzed Sequences	Rejected Sequences		Uncalled Bases in Half-Sites
			Incompatible Overhangs	Repeated Sequences	
CCR5-224 Pre-Selection	1,426,442	1,392,576	0	33,660	206
CCR5-224 0.5 nM	649,348	52,552	209,442	387,299	55
CCR5-224 1 nM	488,798	55,618	89,672	343,442	66
CCR5-224 2 nM	1,184,523	303,462	170,700	710,212	149
CCR5-224 4 nM	1,339,631	815,634	352,888	170,700	159
Total	5,088,742	2,619,842	822,702	1,645,563	635
VF2468 Pre-Selection	1,431,372	1,393,153	0	38,128	91
VF2468 0.5 nM	297,650	25,851	79,113	192,671	15
VF2468 1 nM	148,556	24,735	19,276	104,541	4
VF2468 2 nM	1,362,058	339,076	217,475	805,433	74
VF2468 4 nM	1,055,972	397,573	376,364	281,991	44
Total	4,295,608	2,180,388	692,228	1,422,764	228

Sequencing statistics. The total number of interpretable sequences (“total sequences”) and the number of analyzed sequences for each *in vitro* selection condition are shown. Analyzed sequences are non-repeated sequences containing no ambiguous nucleotides that, for post-selection sequences, contained reverse complementary overhang sequences of at least four bases, a signature used in this study as a hallmark of ZFN-mediated cleavage. “Incompatible overhangs” refer to sequences that did not contain reverse complementary overhang sequences of at least four bases. The high abundance of repeated sequences in the 0.5 nM, 1 nM, and 2 nM selections indicate that the number of sequencing reads obtained in those selections, before repeat sequences were removed, was larger than the number of individual DNA sequences that survived all experimental selection steps.

Supplementary Table S2

a

CCR5-224	4 nM (wt EF = 5.48)			2 nM (wt EF = 8.11)			1 nM (wt EF = 16.6)			0.5 nM (wt EF = 24.9)		
	1 mut	2 muts	3 muts	1 mut	2 muts	3 muts	1 mut	2 muts	3 muts	1 mut	2 muts	3 muts
EF > 0	100%	99.96%	76%	100%	99%	49%	100%	83%	14%	100%	75%	11%
EF > 1	100%	93%	55%	100%	84%	42%	100%	68%	14%	100%	58%	11%
EF > 2	100%	78%	37%	100%	70%	31%	99%	55%	14%	96%	46%	11%
EF > (.5 x wt EF)	100%	63%	28%	93%	40%	17%	51%	15%	8%	31%	8%	4%
EF > wt EF	14%	9%	10%	8%	6%	6%	3%	2%	3%	6%	1%	2%

b

VF2468	4 nM (wt EF = 16.7)			2 nM (wt EF = 22.5)			1 nM (wt EF = 30.2)			0.5 nM (wt EF = 33.1)		
	1 mut	2 muts	3 muts	1 mut	2 muts	3 muts	1 mut	2 muts	3 muts	1 mut	2 muts	3 muts
EF > 0	100%	95%	38%	100%	92%	26%	100%	47%	5%	100%	44%	4%
EF > 1	98%	49%	17%	93%	34%	11%	83%	24%	5%	80%	21%	4%
EF > 2	89%	31%	10%	83%	23%	7%	74%	17%	5%	61%	14%	4%
EF > (.5 x wt EF)	57%	15%	4%	30%	10%	2%	11%	6%	1%	9%	5%	1%
EF > wt EF	7%	1%	1%	7%	1%	0.4%	7%	1%	0.4%	7%	1%	0.3%

Both ZFNs tested have the ability to cleave a large fraction of target sites with three or fewer mutations. The percentage of the set of sequences with 1, 2, or 3 mutations (mut) that can be cleaved by (a) the CCR5-224 ZFN and (b) the VF2468 ZFN is shown. Enrichment factors (EFs) were calculated for each sequence identified in the selection by dividing the observed frequency of that sequence in the post-selection sequenced library by the observed frequency of that sequence in the pre-selection library. The enrichment factors for the wild-type sequence (wt EFs) calculated for each *in vitro* selection stringency are shown in the first row of the table.

Supplementary Table S3

mutations		gene	build 36 coordinates	(+)-half-site	spacer	(-)-half-site	<i>in vitro</i> selection stringency				empty vector		active CCR5-224						
T	(+)						(-)	4 nM	2 nM	1 nM	0.5 nM	indels	total	mutation frequency	indels	total	mutation frequency	p-value	
CCR5-224	1	0	0	CCR5 (coding)	chr3:46389548-46389576	GTCATCCTCATC	CTGAT	AAACTGCAAAAG	X	X	X	X	1	226676	0.00044%	105639	240966	44%	0
CCR5-224	2	1	1	CCR2 (coding)	chr3:46374209-46374237	GTCgTCCTCATC	TTAAT	AAACTGCAAAAG	X	X	X	X	0	114904		12856	130496	10%	0
CCR5-224	3	2	1	BTBD10 (promoter)	chr11:13441738-13441766	GTtTCCTCATC	AAAGC	AAACTGCAAAAG	X	X			1	283015	0.00035%	155	224000	0.070%	0
CCR5-224	4	0	4		chr10:29604352-29604380	GTCATCCTCATC	AGAGA	AAACTGgctAAAt	X	X			2	297084	0.00067%	3	245078	0.0012%	0.26
CCR5-224	5	4	3	SLC4A8	chr12:50186653-50186682	taaATCCTCATC	TCTATA	AAAaTGCAAAAG	X	X			0	147246		0	138979		
CCR5-224	6	3	2	Z83955 RNA	chr12:33484433-33484462	GTCATCCcaATC	GAAAGAA	AAACTGaaAAAG	X		X		0	147157		1	146283	0.00068%	0.16
CCR5-224	7	3	1	DGKK	chrX:50149961-50149989	cTCATCCTCATC	CATGC	AcAaTGCAAAAG	X				0	316468		0	313981		
CCR5-224	8	3	1	GALNT13	chr2:154567664-154567692	GTCATCCTCAgC	ATGGG	AAACoGAgAAAG	X				0	136684		0	94657		
CCR5-224	9	3	1		chr17:61624429-61624457	GTCATCtTCATC	AAAAG	gAACTGCAAAAG	X				0	178692		52	146525	0.035%	2.7E-13
CCR5-224	10	4	0		chrX:145275453-145275481	GTCATCCTCATC	CAATA	AAAGaaCAAAAG	X				0	296730		0	276961		
CCR5-224	11	4	1	TACR3	chr4:104775175-104775203	GTCATCtTCATC	AGCAT	AAACTGAAAgt	X				0	273436		1045	308726	0.34%	0
CCR5-224	12	4	1	PIWIL2	chr8:22191670-22191698	GTCATCCTCATa	CATAA	AAACTGccttAG	X				0	168244		1	171618	0.00058%	0.16
CCR5-224	13	4	1		chr9:76194351-76194379	aTCATCCTCATC	CATCC	AAAtgTtCAAAAG	X				0	168244		1	171618	0.00058%	0.16
CCR5-224	14	4	3		chr6:52114315-52114343	GTCcTgCTCAgC	AAAAG	AAACTGAAAAG	X				0	66317		35	138728	0.025%	1.6E-09
CCR5-224	15	4	3	KCNB2	chr8:73899370-73899398	aTgtTCCTCATC	TCCCG	AAACTGAAAgt	X				1	427161	0.00023%	280	393899	0.071%	0
CCR5-224	16	4	3		chr8:4865886-4865914	GTCtTCCTgATg	CTACC	AAACTGAAAAG	X				0	190993		32	171160	0.019%	7.7E-09
CCR5-224	17	4	3		chr9:14931072-14931100	aaCATCCCaATC	ATGAA	AAACTGCAAAAG	X				0	163704		0	146176		
CCR5-224	18	6	3		chr13:65537258-65537286	aTCtTCCTCATt	ACAGG	AAAaTGAAAAG	X				0	109939		0	100948		
CCR5-224	19	6	4	CUBN	chr10:17044849-17044877	GgCtTCCTgAcC	CACGG	AAAtGtAAAAG	X				0	109939		0	100948		
CCR5-224	20	6	5	NID1	chr1:234244827-234244855	GTtTgCcaATt	TCAAT	tAACTGCAAAAG	X				0	114743		0	120169		
CCR5-224	21	3	2		chr9:80584200-80584229	GTCaAcCTCAAc	ACCTAC	AgACTGCAAAAG	X				0	188149		127	213248	0.060%	0
CCR5-224	22	4	1	WWOX	chr16:77185306-77185335	GTCATCCTCCTC	CAACTC	CAAtGCtAAAAG	X				0	366156		0	354878		
CCR5-224	23	4	2	AMBRA1	chr11:46422800-46422829	GTCtTCCTCCTC	TGCACA	tCACTGCAAAAG	X				0	237240		0	227568		
CCR5-224	24	4	2		chr1:99456616-99456645	GTgATaCTCATC	ATCAGC	AACTGCtAAAAG	X				0	129468		0	144274		
CCR5-224	25	4	2	WBSCR17	chr7:70557254-70557283	GTtATCCTCAgC	AAACTA	AAACTGAAAAG	X				0	172543		486	417198	0.12%	0
CCR5-224	26	4	2	ITSN	chr21:34098210-34098239	cTCATgCTCATC	ATTGTG	tAACTGCAAAAG	X				0	267772		0	308093		
CCR5-224	27	4	4		chr9:106457399-106457428	GcCagtCTCAgC	ATTGGT	AAACTGCAAAAG	X				0	350592		0	338281		
CCR5-224	28	4	4		chr17:49929141-49929170	cTCATtCTgTtC	ATGAAA	AAACTGCAAAAG	X				0	105012		0	99968		
CCR5-224	29	5	3		chr15:96714952-96714981	gaagTCCTCATC	CCGAAG	AAACTGgAAAG	X				0	356674		0	338910		
CCR5-224	30	5	3	ZNF462	chr9:108684858-108684887	GTCtTCCTtTtC	CACATA	AAAACgCAAAAG	X				0	173646		1	152744	0.00065%	0.16
CCR5-224	31	5	4		chr5:101113644-101113673	aTaatCCTtTtC	TGTTTA	AAAAGCAAAAG	X				1	245650	0.00041%	0	185572		0.84
CCR5-224	32	5	4		chr17:43908810-43908839	gaCATCCaaATt	ACATGG	AAACTGaaAAAG	X				0	482635		2	413317	0.00048%	0.079
CCR5-224	33	5	5	SDK1	chr7:3446932-3446961	GTCtTgCTgTtC	CACCTC	AAACTGCAAAAG	X				0	237791		0	200398		
CCR5-224	34	4	1	SPTB(coding)	chr14:64329872-64329901	GTCATCCgCATC	GCCTTG	gAACTGgAAAG	X		X		0	180783		0	167885		
CCR5-224	35	4	2		chr10:54268729-54268758	aTCATCCTCAAc	AAACTA	AAACoGgAAAG	X				0	180783		0	167885		
CCR5-224	36	4	0	KIAA1680	chr4:92322851-92322880	GgaATgCCATC	ACCACA	AAACTGCAAAAG	X				0	165657		2	153995	0.0013%	0.079
CCR5-224	37	5	0		chr5:114708142-114708171	GTtTtTgCTCtTg	TACTTC	AAACTGCAAAAG	X				0	152083		0	183305		

Potential CCR5-224 genomic off-target sites. The human genome was searched for DNA sequences surviving *in vitro* selection for CCR5-224 cleavage. Sites marked with an ‘X’ were found in the *in vitro* selection dataset. ‘T’ refers to the total number of mutations in the site, and ‘(+)’ and ‘(-)’ to the number of mutations in the (+) and (-) half-sites, respectively. Chromosomal coordinates from build 36 of the human genome are listed. Mutation frequency for each site is the percentage of sequences with insertions or deletions (indels) in the sequenced DNA from cultured K562 cells expressing active CCR5-224. Bolded red sites have significantly enriched indel percentages in the active nuclease sample compared to cells containing empty vector. The sequences of the sites are listed as 5’ (+) half-site/spacer/(-) half-site 3’, therefore the (+) half-site is listed in the reverse sense as it is in the sequence profiles. Three sites were not tested since they did not yield site-specific PCR amplification products. Indels and totals are not shown for those sites that were not tested. *P*-values shown are for the one-sided alternative hypothesis that the indel frequency is greater for active ZFN treated cells than for cells not expressing ZFN.

Supplementary Table S4

CCR5-224		VF2468	
# of mutations	# of sites in genome	# of mutations	# of sites in genome
0	1	0	1
1	0	1	3
2	1	2	245
3	6	3	3,201
4	99	4	35,995
5	964	5	316,213
6	9,671	6	2,025,878
7	65,449		
8	372,801		
9	1,854,317		

There are many more potential genomic VF2468 target sites than CCR5-224 target sites. The human genome was computationally searched for sites up to nine mutations away from the canonical CCR5-224 target site and up to six mutations away from the canonical VF2468 target site. The number of occurrences of sites containing five or six base pair spacers in the genome, including repeated sequences, is listed in the table.

Supplementary Table S5

	# of sequences		# of sequences
BTBD10 (promoter) ATTTTGCAGTTT <u>GCTTT</u> GATGAGGAAAAC		chr6:52114315-52114343 CTTTTTCAGTTT <u>CTTTT</u> GCTGAGCAGGAC	
ATTTTGCAGTTT <u>GCTTT</u> <u>GATG</u> AGGAAAAC	63	CTTTTTCAGTTT <u>CTTTT</u> GCTGAGCAGGAC	35
ATTTTGCAGTTT <u>GCTTT</u> GCTTT GATGAGGAAAAC	86		
ATTTTGCAGTTT <u>GgTTT</u> GCTTT GATGAGGAAAAC	1		
ATTTTGCAGTTT <u>GCTTT</u> GCTTT GgTGAGGAAAAC	1	KCNB2	
gTTTTGCAGTTT <u>GCTTT</u> GCTTT GATGAGGAAAAC	1	CATTTGCAGTTT <u>CGGGA</u> GATGAGGAACAT	
cTTTTGCAGgTT <u>GCTTT</u> GCTTT GATGAGGAAAAC	1		
ATTTTGCAGTTT <u>GCTTT</u> GCTTT GATGtGGAAAAC	1	CATTTGCAGTTT <u>CGGGA</u> <u>GA</u> GATGAGGAACAT	158
ATTTTGCAGTTT <u>GCTTT</u> GATGAGGAAAAC	1	CATTTGCAGTTa <u>CGGGA</u> <u>GA</u> GATGAGGAACAT	1
		CATTTGCAGTTT <u>CGGGGA</u> GATGAGGgACAT	1
		CATTTGacGcTT <u>CGGGGA</u> <u>GA</u> GgTGAGGgACAT	1
chr17:61624429-61624457		CATTTGCAGTTT <u>CGGG</u> <u>CGGGA</u> GATGAGGAACAT	109
GTTTTGCAGTTC <u>CTTTT</u> GATGAAGATGAC		CATTTGCAGTTT <u>CGGG</u> <u>CGGGA</u> GATGcGGAACAT	1
		CATTTGCAGTTT <u>CGGG</u> <u>CGGGc</u> GATGAGGAACAT	1
GTTTTGCAGTTC <u>CTTTT</u> <u>GATGAAG</u> ATGAC	51	CATTTGCAGTTT <u>CGGG</u> <u>CGGGA</u> GgTGAGGAACAT	1
GTTTTGCAGgTC <u>CTTTT</u> <u>GATGAAG</u> ATGAC	1	CgTTTTGCAGTTT <u>CGGG</u> <u>CGGGA</u> GATGAGGAACAT	2
		CATTTGcIGTTT <u>CGGG</u> <u>CGGGA</u> GATGAGGAACAT	1
		CATTTGCAGTTT <u>CGGG</u> <u>CGGGA</u> GATGAGGAcCAT	1
TACR3		CATTTGCAGTTT <u>CGGG</u> <u>CGGGA</u> GgTGAGGAACAT	1
ACTTTACAGTTT <u>ATGCT</u> GATGAAGATGAC		CcTTTTGCAGTTT <u>CGGG</u> <u>CGGGA</u> GATGAGGAACAT	1
		CATTTGCAGTTg <u>CGGG</u> <u>CGGGA</u> GATGAGGAACAT	1
ACTTTACAGT <u>TT</u> <u>ATGCT</u> GATGAAGATGAC	5		
ACTTTACAGTTT <u>ATGCT</u> GATGAAGATGAC	169		
gCTTTACAGTTT <u>ATGCT</u> GATGAAGATGAC	1	chr8:4865886-4865914	
ACTTTACAGTTT <u>ATGCT</u> GATGAAGaATAC	1	GTCTTCCTGATG <u>CTACC</u> AAACCTGAAAAG	
ACTTTACAGTTT <u>ATGCT</u> GATGAAGATGt	1		
ACTTTACAGTTT <u>ATGCT</u> GATGAAGATGAC	34	GTCTTCCTGATG <u>CTACC</u> AAACCTGAAAAG	30
ACTTTACgTTTT <u>ATGCT</u> GATGAAGATGAC	1	GTCTTCCTGATG <u>CTACC</u> AAACCTgAAAAG	1
ACTTTACAGTTT <u>ATGCT</u> GATGAAGATGAC	180	GTCTTCaTGATG <u>CTACC</u> AAACCTGAAAAG	1
ACTTTACAGTTT <u>ATGCT</u> GATGAAGATGcC	1		
ACTTTACAGTTT <u>ATGCT</u> <u>ATGCT</u> GATGAAGATGAC	507		
gCTTTACAGTTT <u>ATGCT</u> <u>ATGCT</u> GATGAAGATGAC	1	chr9:80584200-80584229	
ACTTTACgTTTT <u>ATGCT</u> <u>ATGCT</u> GATGAAGATGAC	1	CTTTTGCAGTCT <u>GTAGGT</u> GTTGAGGTTGAC	
ACTTTACAGTTT <u>ATGCT</u> <u>ATGCT</u> GATGAtGATGAC	1		
ACgTTACAGTTT <u>ATGCT</u> <u>ATGCT</u> GATGAAGATGAC	1	CTTTTGCAGTCT <u>GTAGGT</u> GTTGAGGTTGAC	125
ACTTTACAGTTT <u>ATGCT</u> <u>GATGAA</u> GATGAC	140	CTTTTGCAGTCT <u>GTAGGT</u> GTTGAGGTTGAC	1
ACTTTACAGTTT <u>ATGCT</u> <u>GATGAA</u> GATGtC	1	CTTTTGCAGTCT <u>GTAGGT</u> GTTGAGGTTGAC	1
WBSCR17			
GTTATCCTCAGC <u>AAACTA</u> AAACCTGGAACAG			
GTTATCCTCAGC <u>AAACTA</u> <u>ACTA</u> AAACCTGGAACAG	128		
GTTATCCTCAGC <u>AAACTA</u> AAACCTGGAACAG	118		
GTTATCCTCAGC <u>AAACTA</u> AAACCTGGgACAG	1		
GTTATCCTCAGC <u>AAACTA</u> AAACCTGGAcCAG	1		
GTTATaCTCAGC <u>AAACTA</u> AAACCTGGAACAG	1		
GTTATCCTCAGC <u>AAACTA</u> AAACCTGGAACAG	116		
aTTATCCTCAGC <u>AAACTA</u> AAACCTGGAACAG	1		
GTTATCCTtAGC <u>AAACTA</u> AAACCTGGAACAG	1		
GTTATCCTCAGC <u>AAACTA</u> AAACCTGGAACAG	118		
GaTATCCTCAGC <u>AAACTA</u> AAACCTGGAACAG	1		

Sequences of CCR5-224-mediated genomic DNA modifications identified in cultured human K562 cells. Sequences with insertions (blue) and deletions (red) identified after sequencing potential CCR5-224 off-target sites from cultured K562 cells expressing CCR5-224 are shown. The numbers of occurrences are shown to the right of each sequence. Other mutations are indicated with lowercase letters and likely reflect mutations that arose during PCR or sequencing. The unmodified site is listed under the gene name or coordinates (build 36), and the spacer sequence is underlined.

Supplementary Table S6

VF2468	mutations		gene	build 36 coordinates	(+/-) half-site		in vitro selection stringency				empty vector		active VF2468		p-value				
	T	(+)			(-)	spacer	(-) half-site	4 nM	2 nM	1 nM	0.5 nM	indels	total	mutation frequency		indels	total	mutation frequency	
VF2468 1	0	0	0	VEGF-A (promoter)	chr6:43,845,393-43,845,415	AGCAGCGTC	TTTCA	GAGTGAAGG	X	X	X	X	125	147187	0.085%	27057	186785	14%	0
VF2468 2	1	0	1		chr1:168,832,650-168,832,672	AGCAGCGTC	AATAC	GAGTGAAGG	X	X	X	X	0	57855		1	62195	0.0016%	0.16
VF2468 3	1	1	0		chr1:242,574,122-242,574,144	AGCAGCGTC	TGCTT	GAGTGAAGG	X	X	X	X	0	167447		0	147340		
VF2468 4	1	1	0	ZNF683	chr1:26,599,668-26,599,690	AGCAGCGTC	GGGAG	GAGTGAAGG	X	X	X	X	0	111340		0	109365		
VF2468 5	2	0	2	GSGL1	chr16:27,853,984-27,854,006	AGCAGCGTC	AAAAA	cAGTGAAGG	X	X	X	X	0	80047		0	69080		
VF2468 6	2	0	2	C9orf98	chr9:134,636,934-134,636,956	AGCAGCGTC	GTGTG	GcGTGAAGG	X	X	X	X	0	202694		0	204809		
VF2468 7	2	0	2	EFHD1	chr2:233,205,384-233,205,407	AGCAGCGTC	GTTCTC	aAGTGAAGG	X	X	X	X	0	160769		1	158886	0.00063%	0.16
VF2468 8	2	0	2	KIAA0841 (exon-intron)	chr20:30,234,845-30,234,868	AGCAGCGTC	TAGGCA	GcGTGAAGG	X	X	X	X	0	160769		1	158886	0.00063%	0.16
VF2468 9	2	0	2	CES7	chr16:54,501,918-54,501,941	AGCAGCGTC	TCAAAA	GAGTGCcCA	X	X	X	X	1	168501	0.00059%	0	144701		0.84
VF2468 10	2	0	2	PTK2B	chr8:27,339,955-27,339,978	AGCAGCGTC	TCCCTT	GAGTGAAGG	X	X	X	X	0	179502		56	138649	0.040%	3.6E-14
VF2468 12	2	0	2		chr9:137,315,499-137,315,521	AGCAGCGTC	TGAAA	GAGTGAAGG	X	X	X	X	0	285530		165	254714	0.065%	0
VF2468 13	2	1	1		chr20:7,985,471-7,985,493	AGcAGCGTC	ATCGA	GAGTGAAGG	X	X	X	X	0	166914		0	148547		
VF2468 14	2	1	1		chrY:8,461,018-8,461,041	AGCAcCGTC	AGATAG	GcGTGAAGG	X	X	X	X	0	157651		0	136373		
VF2468 15	2	1	1		chr1:53,720,668-53,720,690	AGCAcCGTC	ATATT	cAGTGAAGG	X	X	X	X	0	329599		145	290700	0.050%	0
VF2468 16	2	1	1		chrX:122,132,519-122,132,541	AGCAcCGTC	GTAGT	GcTGAAGG	X	X	X	X	0	157651		0	136373		
VF2468 17	2	1	1	F4HA1	chr10:74,506,346-74,506,368	AGCAcCGTC	TTTTT	tAGTGAAGG	X	X	X	X	0	157651		0	136373		
VF2468 18	2	1	1	DFKZp686L07201	chrX:56,830,910-56,830,933	AGCAcCGTC	AGACTT	GAGTGAAGG	X	X	X	X	0	13660		13	12386	0.10%	0.00015
VF2468 19	2	1	1	TTC4	chr1:54,881,895-54,881,917	AGCAcCGTC	TCTGA	GAGTGAAGG	X	X	X	X	0	175808		163	191327	0.085%	0
VF2468 20	2	1	1		chr1:175,847,668-175,847,690	AGCAGCGTC	AGTGA	GAGTGAAGG	X	X	X	X	1	286818	0.00035%	0	343497	0.00087%	0.20
VF2468 21	2	1	1		chr1:50,490,333-50,490,356	AGCAGCGTC	TCCAAA	GAGTGAAGG	X	X	X	X	0	168032		0	183289		
VF2468 22	2	1	1		chr4:128,244,847-128,244,870	AGCAGCGTC	TGCATC	GAGTGAAGG	X	X	X	X	0	86347		0	87663		
VF2468 23	2	1	1		chr13:27,399,187-27,399,210	AGCAGCGTC	GCCTGG	GAGTGAAGG	X	X	X	X	0	23198		394	34455	1.1%	0
VF2468 24	2	1	1		chr16:62,603,303-62,603,326	AGCAGCGTC	TCAAT	GAGTGAAGG	X	X	X	X	0	57001		283	63841	0.44%	0
VF2468 25	2	1	1		chr11:69,063,501-69,063,523	AGCAGCGTC	CCAAA	GAGTGAAGG	X	X	X	X	0	181022		0	221989		
VF2468 26	2	1	1	TNR	chr1:173,885,442-173,885,465	AGCAGCGTC	AGGGGA	GcGTGAAGG	X	X	X	X	0	132693		0	139071		
VF2468 27	2	1	1	PTPRM	chr18:3,320,310-3,320,332	AGCAGCGTC	CTTTT	GAGTGAAGG	X	X	X	X	0	73084		0	100249		
VF2468 28	2	1	1		chr12:25,724,566-25,724,589	AGCAGCGTC	TCCTGG	GAGTGAAGG	X	X	X	X	0	323231		1116	353441	0.32%	0
VF2468 29	2	1	1		chr3:82,039,140-82,039,163	AGCAGCGTC	AGGGCT	GAGTGAAGG	X	X	X	X	0	156241		439	168937	0.26%	0
VF2468 30	2	1	1		chr3:131,201,895-131,201,918	AGCAGCGTC	AGGGCT	GAGTGAAGG	X	X	X	X	0	77427		1960	92791	2.1%	0
VF2468 31	2	1	1		chr3:75,709,387-75,709,410	AGCAGCGTC	AGGGCT	GcGTGAAGG	X	X	X	X	0	34408		114	33070	0.34%	0
VF2468 32	2	1	1		chr11:3,556,299-3,556,322	AGCAGCGTC	AGGGCT	GcGTGAAGG	X	X	X	X	0	19630		19	17409	0.11%	6.5E-06
VF2468 33	2	1	1		chr3:126,970,762-126,970,785	AGCAGCGTC	AGGGCT	GcGTGAAGG	X	X	X	X	0	89679		2570	90901	2.8%	0
VF2468 34	2	1	1		chr11:71,030,884-71,030,907	AGCAGCGTC	AGGGCT	GcGTGAAGG	X	X	X	X	0	112449		231	150275	0.15%	0
VF2468 35	2	1	1	SBF2/U80769	chr19:9,884,211-9,884,234	AGCAGCGTC	CTAAGG	GcGTGAAGG	X	X	X	X	0	418083		695	532165	0.13%	0
VF2468 36	2	1	1	KRI1 (coding)	chr19:10,534,492-10,534,515	AGCAcCGTC	ATCAGA	cAGTGAAGG	X	X	X	X	0	141739		0	139368		
VF2468 37	2	1	1		chr6:112,421,476-112,421,499	AGCAcCGTC	TGAAGT	GAGTGAAGG	X	X	X	X	0	153897		1174	178559	0.66%	0
VF2468 38	2	1	1	MICAL3/KIAA1364	chr22:16,718,914-16,718,937	AGCAcCGTC	TTCTGT	GAGTGAAGG	X	X	X	X	0	267705		175	283796	0.062%	0
VF2468 39	2	1	1	MUC16 (exon-intron)	chr19:8,894,218-8,894,241	AGcAGCGTC	TCACCT	GAGTGAAGG	X	X	X	X	0	212038		0	219913		
VF2468 40	2	2	0		chr8:6,638,000-6,638,023	AaCAGcTC	ATCTCG	GAGTGAAGG	X	X	X	X	0	132803		0	147070		
VF2468 41	2	2	0	PREX1	chr20:46,733,644-46,733,667	AaCAGcTC	TCCGGG	GAGTGAAGG	X	X	X	X	0	204408		0	227091		
VF2468 42	2	2	0	CDH20	chr18:57,303,454-57,303,477	AaCAGcTC	TCTGAG	GAGTGAAGG	X	X	X	X	1	313747	0.00032%	1	403382	0.00025%	0.57
VF2468 43	2	2	0		chr20:6,213,500-6,213,522	AGCAaCGTC	AAACA	GAGTGAAGG	X	X	X	X	1	154154	0.00065%	0	183644		0.84
VF2468 44	2	2	0		chr5:85,841,308-85,841,331	AGCAaCGTC	TGGAAA	GAGTGAAGG	X	X	X	X	0	205890		0	297104		
VF2468 45	2	2	0		chr8:20,481,270-20,481,292	AGCAcCGTC	AATTG	GAGTGAAGG	X	X	X	X	0	274402		1	319493	0.00031%	0.16
VF2468 46	2	2	0		chr5:95,417,045-95,417,068	AGCAGcCGTC	ATAGCA	GAGTGAAGG	X	X	X	X	0	270263		1	358704	0.00028%	0.16
VF2468 47	2	2	0	RORA	chr15:59,165,302-59,165,325	AGCAGcCGTC	GATATG	GAGTGAAGG	X	X	X	X	0	103878		0	176333		
VF2468 48	2	2	0		chr6:24,504,489-24,504,511	AGCAGcCGTC	TCAGG	GAGTGAAGG	X	X	X	X	0	542052		0	708517		
VF2468 49	2	2	0		chr3:31,085,287-31,085,309	AGCAGcCGTC	AAAGA	GAGTGAAGG	X	X	X	X	0	177732		0	212250	0.00047%	0.16
VF2468 50	2	2	0		chr6:27,579,690-27,579,712	AGCAGcCGTC	CTTAG	GAGTGAAGG	X	X	X	X	0	294783		0	302167		
VF2468 51	2	2	0		chr12:113,410,592-113,410,615	AGCAGcCGTC	CTTCAA	GAGTGAAGG	X	X	X	X	0	482765		1	402831	0.00025%	0.16
VF2468 52	2	2	0		chr1:11,399,534-11,399,556	AGCAGcCGTC	CTAAA	GAGTGAAGG	X	X	X	X	0	183510		1	202083	0.00049%	0.16
VF2468 53	2	2	0	MCTP1	chr15:94,590,016-94,590,038	AGCAGcCGTC	TAAAG	GAGTGAAGG	X	X	X	X	0	88944		0	105879		
VF2468 54	2	2	0		chr1:13,394,902-13,394,924	AGCAGcCGTC	ATGAG	GAGTGAAGG	X	X	X	X	0	360710		0	351215		
VF2468 55	2	2	0	PRAMEF20	chr1:13,615,741-13,615,763	AGCAGcCGTC	ATGAG	GAGTGAAGG	X	X	X	X	0	140671		0	157922		
VF2468 56	2	2	0		chr20:59,154,784-59,154,806	AGCAGcCGTC	CACAG	GAGTGAAGG	X	X	X	X	0	196624		0	209781		
VF2468 57	2	2	0		chr14:100,903,675-100,903,697	AGCAGcCGTC	TTGGA	GAGTGAAGG	X	X	X	X	0	223714		0	246196		
VF2468 58	2	2	0		chrX:141,701,170-141,701,192	AGTAgCGc	AAATT	GAGTGAAGG	X	X	X	X	0	2032495		0	383303		
VF2468 59	2	2	0	GTF3C1	chr16:27,452,953-27,452,975	AGTAgCGc	CCAGT	GAGTGAAGG	X	X	X	X	0	84153		0	113996		
VF2468 60	2	2	0	DNMBP/AK089111	chr10:101,688,981-101,688,983	gGCAGCGTC	CTAGA	GAGTGAAGG	X	X	X	X	0	184513		1	212085	0.065%	0
VF2468 61	2	2	0		chr6:137,852,455-137,852,478	tCCAGCGTC	CTCCA	GAGTGAAGG	X	X	X	X	0	176551		2	438355	0.00046%	0.33
VF2468 62	2	2	0	SARDH	chr9:135,592,239-135,592,262	tCCAGCGc	TAGGG	GAGTGAAGG	X	X	X	X	0	191187		138	212085	0.065%	0
VF2468 63	2	2	0		chr7:19,683,400-19,683,423	tCCAGCGTC	AAAAA	GAGTGAAGG	X	X	X	X	1	372808	0.00027%	2	438355	0.00046%	0.33
VF2468 64																			

with insertions or deletions (indels) in the sequenced DNA from cultured K562 cells expressing active VF2468. Bolded red sites have significantly enriched indel percentages in the active nuclease sample compared to cells not expressing nuclease. The sequences of the sites are listed as 5' (+) half-site/spacer/(-) half-site 3', therefore the (+) half-site is listed in the reverse sense as it is in the sequence profiles. Seven sites were not tested since they did not yield site-specific PCR amplification products. Indels and totals are not shown for those sites that were not tested. *P*-values shown are for the one-sided alternative hypothesis that the indel frequency is greater for active ZFN treated cells than for cells not expressing ZFN.

Supplementary Table S7

oligonucleotide name	oligonucleotide sequence (5'→3')		
N5-PvuI	NNNNNCGATCGTTGGGAACCGGA		
CCR5-224-N4	NG* <i>T</i> *C* <i>A</i> * <i>T</i> *C* <i>C</i> * <i>T</i> *C* <i>A</i> * <i>T</i> *C* <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>A</i> * <i>A</i> *C* <i>T</i> *G* <i>C</i> * <i>A</i> * <i>A</i> * <i>A</i> * <i>G</i> *NCAGTGGAACGAAAACTCACG		
CCR5-224-N5	NG* <i>T</i> *C* <i>A</i> * <i>T</i> *C* <i>C</i> * <i>T</i> *C* <i>A</i> * <i>T</i> *C* <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>A</i> * <i>A</i> *C* <i>T</i> *G* <i>C</i> * <i>A</i> * <i>A</i> * <i>A</i> * <i>G</i> *NCAGTGGAACGAAAACTCACG		
CCR5-224-N6	NG* <i>T</i> *C* <i>A</i> * <i>T</i> *C* <i>C</i> * <i>T</i> *C* <i>A</i> * <i>T</i> *C* <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>A</i> * <i>A</i> *C* <i>T</i> *G* <i>C</i> * <i>A</i> * <i>A</i> * <i>A</i> * <i>G</i> *NCAGTGGAACGAAAACTCACG		
CCR5-224-N7	NG* <i>T</i> *C* <i>A</i> * <i>T</i> *C* <i>C</i> * <i>T</i> *C* <i>A</i> * <i>T</i> *C* <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>A</i> * <i>A</i> *C* <i>T</i> *G* <i>C</i> * <i>A</i> * <i>A</i> * <i>A</i> * <i>G</i> *NCAGTGGAACGAAAACTCACG		
VF2468-N4	NA* <i>G</i> *C* <i>A</i> * <i>G</i> *C* <i>G</i> * <i>T</i> *C* <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>G</i> * <i>A</i> * <i>G</i> * <i>T</i> *G* <i>A</i> * <i>G</i> * <i>G</i> * <i>A</i> *NCAGTGGAACGAAAACTCACG		
VF2468-N5	NA* <i>G</i> *C* <i>A</i> * <i>G</i> *C* <i>G</i> * <i>T</i> *C* <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>G</i> * <i>A</i> * <i>G</i> * <i>T</i> *G* <i>A</i> * <i>G</i> * <i>G</i> * <i>A</i> *NCAGTGGAACGAAAACTCACG		
VF2468-N6	NA* <i>G</i> *C* <i>A</i> * <i>G</i> *C* <i>G</i> * <i>T</i> *C* <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>G</i> * <i>A</i> * <i>G</i> * <i>T</i> *G* <i>A</i> * <i>G</i> * <i>G</i> * <i>A</i> *NCAGTGGAACGAAAACTCACG		
VF2468-N7	NA* <i>G</i> *C* <i>A</i> * <i>G</i> *C* <i>G</i> * <i>T</i> *C* <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>N</i> <i>G</i> * <i>A</i> * <i>G</i> * <i>T</i> *G* <i>A</i> * <i>G</i> * <i>G</i> * <i>A</i> *NCAGTGGAACGAAAACTCACG		
test fwd	GCGACACGGAAATGTTGAATACTCAT		
test rev	CAGCGAGTCAGTGAGCGA		
adapter1	ACACTCTTCCCTACACGACGCTCTTCCGATCTT		
adapter1(AAT)	ACACTCTTCCCTACACGACGCTCTTCCGATCTAATT		
adapter1(ATA)	ACACTCTTCCCTACACGACGCTCTTCCGATCTATAT		
adapter1(TAA)	ACACTCTTCCCTACACGACGCTCTTCCGATCTTAAT		
adapter1(CAC)	ACACTCTTCCCTACACGACGCTCTTCCGATCTCACT		
adapter2	/5Phos/AGATCGGAAGAGCGGTTCAGCAGGAATGCCGAG		
adapter2(AAT)	/5Phos/ATTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAG		
adapter2(ATA)	/5Phos/TATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAG		
adapter2(TAA)	/5Phos/TTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAG		
adapter2(CAC)	/5Phos/GTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAG		
PE1	CAAGCAGAAGACGGCATAACGAGATCGGTCTCGGCATTCTGCTGAACCGCTCTTCCGATC		
PE2	AATGATACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTTCCGATCT		
CCR5-224 1 fwd	ATACATCGGAGCCCTGCCAA	CCR5-224 1 rev	GGAAAAACAGGTCAGAGATGGC
CCR5-224 2 fwd	TCCTGCCTCCGCTCTACTCG	CCR5-224 2 rev	ACCCCAAAGGTGACCGTCTCT
CCR5-224 3 fwd	TCCACGTTTTCCCTTGAC	CCR5-224 3 rev	GTCCCTCACGACGACCGACT
CCR5-224 4 fwd	GCACTGCCCCAGAAATATTGGTT	CCR5-224 4 rev	TGGTTTGTGGGGGATCAGG
CCR5-224 5 fwd	ATGCCACCCCTGCCAGATAA	CCR5-224 5 rev	GCCTACCTCAATGCAGGCAAA
CCR5-224 6 fwd	TCTGCTTCTGCCCTTCTGGA	CCR5-224 6 rev	GGAGGATCGCAAAGCCTGA
CCR5-224 7 fwd	CCCCAGTGCTTAACATAGTTCTTGG	CCR5-224 7 rev	ACTCCAGACAAAACCCCTG
CCR5-224 8 fwd	GGCACCAGAACTTACTACTGCC	CCR5-224 8 rev	TGTGAAGGCCAAAACCCCTG
CCR5-224 9 fwd	GTTTTGGGGTGCATGGCAAA	CCR5-224 9 rev	TGGGCAGCCCTAGGTCCTTT
CCR5-224 10 fwd	TTCCCTGGTGATGCACTCCT	CCR5-224 10 rev	TGATGAGTAACTTGGGCGAAAA
CCR5-224 11 fwd	TTGGGGGAATGAGATTGGGA	CCR5-224 11 rev	GGAAAATCCAGCAAGGTGAAA
CCR5-224 13 fwd	CCTTCCCATGGTCACAGAGG	CCR5-224 13 rev	CAACTCTTAACAGCAAAGTGCCA
CCR5-224 14 fwd	TCTCCCGTTGAGGAAGCAC	CCR5-224 14 rev	GCCTCAAAGCATAAACAGCA
CCR5-224 15 fwd	CAGACCGCTGCTGCTGAGAC	CCR5-224 15 rev	AGGGCGGACTCATTGCTTTG
CCR5-224 16 fwd	TGGGTTCTCGGGTTCTCTG	CCR5-224 16 rev	GAAACCAGAAGTTCACAACAATGCTT
CCR5-224 17 fwd	AGGCATAAGCCACTGCACC	CCR5-224 17 rev	TGGCAATGCCTAATCAGACCA
CCR5-224 18 fwd	GAGGATATTTATTGCTGGCTCTTGC	CCR5-224 18 rev	GAGTTTGGGGAAAAGCCACTT
CCR5-224 20 fwd	TGTAGGCCCACCTTTCCCTT	CCR5-224 20 rev	TGCTAGGCCCAACTGTGAGGG
CCR5-224 21 fwd	TGTTTTGGGTGCATGTGGGT	CCR5-224 21 rev	TCCAGGAGTGAGGTGAAGACA
CCR5-224 22 fwd	CTGGGTCAGCTGGGCCATAC	CCR5-224 22 rev	TCACATCTCCGCCTCAGCAT
CCR5-224 23 fwd	CCAGCCTTGGAAAAATGGACA	CCR5-224 23 rev	CTGACACAGTGGCCAGCAGC
CCR5-224 24 fwd	CATGGATGTAATGGGTTGTATCTGC	CCR5-224 24 rev	GAGGGCAGAAGGGGGTGAGT
CCR5-224 25 fwd	AGGATGCATTGTCCCCAGA	CCR5-224 25 rev	TGGAGTGACATGTATGAAGCCA
CCR5-224 26 fwd	CGTTGGCTTGAGAAGGGAC	CCR5-224 26 rev	TGAACCCCGGATTTTTCAACC
CCR5-224 27 fwd	TGACCCAATAAGTCTGTGACCC	CCR5-224 27 rev	TTGGGAAAGCTTTGATGCTGG
CCR5-224 28 fwd	TGGGTTGTTTTTGACTGACAGA	CCR5-224 28 rev	CCCTAGGGGTCACTGGAGCA
CCR5-224 29 fwd	CACCCCATGCAGGAAAATG	CCR5-224 29 rev	TTGGCTGCTGGCAATTTGGTA
CCR5-224 30 fwd	GGCCATTGGTTCTGGAGGAA	CCR5-224 30 rev	TCCGTTGCTTCATCCTTCCAA
CCR5-224 31 fwd	AGTCAGCAATGCCCCAGAGC	CCR5-224 31 rev	TGGAGAGGGTTTACTTTCCAGA
CCR5-224 32 fwd	CCTGGGAGGGTGACTAGTTGGA	CCR5-224 32 rev	GCTCAGGGCCTGGCTTACAG
CCR5-224 33 fwd	TGGCAATTAGGATGTGCCAG	CCR5-224 33 rev	TCCACTCACAAATTTACCTTTCCAC
CCR5-224 34 fwd	TGCCCCACATCTTACCAGA	CCR5-224 34 rev	CCGCATAAAGGAGGTGTCCG
CCR5-224 36 fwd	GTTGCATCTGCGGTCTTCCA	CCR5-224 36 rev	GGAGAGTCTTCCGCTGTGTT
CCR5-224 37 fwd	TAGTGGCCCAACATGCAAAA	CCR5-224 37 rev	GCACATATCATGCACTGTGACTGTAA
VF2468 1 fwd	CCTTTCCAAAGCCCAATCCC	VF2468 1 rev	CAACCCACACGCACACAC

VF2468 2 fwd	TTCACGCTTCAGGCCTCC	VF2468 2 rev	AATGGCCAGAAAATCCCAA
VF2468 3 fwd	CACAGGGACCCAGGACTGCT	VF2468 3 rev	TGACTGGAACCGTGCAGCAT
VF2468 4 fwd	GCACCAGGCTTCTTGCCAT	VF2468 4 rev	TCGGGGGTCCATGGTATTTG
VF2468 5 fwd	CCAAGGCGAGGACATTGAGG	VF2468 5 rev	CCCCAAGTCAGACCCTGCAT
VF2468 7 fwd	ACCATAGTCCAGCGGGTCA	VF2468 7 rev	TTCTCCCCAAGGAAGGCTGA
VF2468 8 fwd	AGAAAGGGTGGTCGGGGAAG	VF2468 8 rev	GCCACCATGCCAGTCTACA
VF2468 9 fwd	TTCCCATGGGGTCTCAGCTC	VF2468 9 rev	ATGGCCTTCCCCAACTGTGA
VF2468 10 fwd	CAGCAAGGATGCCCTTACC	VF2468 10 rev	CGTTGTGATTGAGGAGACGAGG
VF2468 11 fwd	GGCTTGAGCTGGAAGGACCA	VF2468 11 rev	TGGAGCAACTGAACATCTTGGG
VF2468 12 fwd	AACCGAGTTTGCACCGTCT	VF2468 12 rev	CATAACCACCAGGACATCCGC
VF2468 13 fwd	TATCCTCCCCTTCCCCTGA	VF2468 13 rev	TGTTGCCAGAAGTATCAGGTCCC
VF2468 15 fwd	AGAACC CGAATCCCCTTGC	VF2468 15 rev	GCAGAGAAGGCAGCAGACA
VF2468 16 fwd	GGTCTCTGCCATGCCAACT	VF2468 16 rev	TGGAGGAAGCAGGAAAGGCAT
VF2468 18 fwd	CCCCTGGGATCCTTGTCT	VF2468 18 rev	TCAACAGGCAGCTACAGGGC
VF2468 19 fwd	CTAGGCCTGTGGCTGAGGA	VF2468 19 rev	CAAATGTTGGGGTGTGGGTG
VF2468 20 fwd	TACCTGAAACCCCTGGCCCT	VF2468 20 rev	CAAGCTGGATGTGGATGCAGAG
VF2468 21 fwd	CGGGGGCTGACATTAGTGA	VF2468 21 rev	GCCTGAAGATGCATTTGCC
VF2468 22 fwd	TGCATTGGCTCAAGAATTGGG	VF2468 22 rev	TCACACAGTGGTAATGGACAGGAA
VF2468 23 fwd	GCGCTCCCTGTGTTAGTACC	VF2468 23 rev	GCGCAAGTCCCCTTTCTGA
VF2468 24 fwd	TGTTTGGGTTATGGGGGAC	VF2468 24 rev	TCCAGCATCTGCTCCTGGTG
VF2468 25 fwd	AAGGAGACTTCTCAGGCCCA	VF2468 25 rev	TGAAGGGAAGCCACAGTCTC
VF2468 26 fwd	CTTGGGGGCAGACAGTACT	VF2468 26 rev	GCCATGGGATGGCAGTTAGG
VF2468 27 fwd	TGGCCTCAAGCAATCCTCCT	VF2468 27 rev	TTCCATGGCAGTGAAGGGTG
VF2468 28 fwd	CCAAAGAGCCTGGAGGAGCA	VF2468 28 rev	CAGAGGGTGTGGTGGTGTGCG
VF2468 29 fwd	CCAGCCTGTGAAGCTGGAAGTAA	VF2468 29 rev	CCAGTGGGCTGAGTGGATGA
VF2468 30 fwd	CATCTGAATGCCCATGCTGC	VF2468 30 rev	CCGCCACACCCATTCTC
VF2468 31 fwd	CCTCAAAGAAACGGCTGCTGA	VF2468 31 rev	GCCGCTCGAAAAGAGGGAA
VF2468 32 fwd	CGGGCTCTCCTCCTCAAAGA	VF2468 32 rev	GGCCCTTGAAGAGGGAA
VF2468 33 fwd	GGAATCGCATGACCTGAGGC	VF2468 33 rev	CGGGCTCTCCTCCTCAAAGA
VF2468 34 fwd	CCCGCCAGACACATTCTCT	VF2468 34 rev	CATCTGAATGCCCATGCTGC
VF2468 35 fwd	CCGACCTTTTCTATGTGGT	VF2468 35 rev	TCAGATGTGTAGGACACAGATGAC
VF2468 36 fwd	GGTACATGGGCGCAGTTTC	VF2468 36 rev	GGACAGCTGGGAATTGGTG
VF2468 37 fwd	TTACACCTGCTGGCAGGCAA	VF2468 37 rev	GCTGGTGTGAGCAAGAGGCA
VF2468 38 fwd	TGGCCAAGCCTGCCTAACTC	VF2468 38 rev	TGATCAGTTAGCCCTGGGGG
VF2468 39 fwd	CCCCTTCTGCTCCTGCTTCA	VF2468 39 rev	CCTTCTTGCAGCTCAAACCC
VF2468 40 fwd	TGATTTTCAGCGTGGAGGGC	VF2468 40 rev	ACGGCAAAGCCAGAGCAAAG
VF2468 41 fwd	AAGCTGGCAGCCACTCTTCA	VF2468 41 rev	TCTCAGGGCTTCTGTGTGCG
VF2468 42 fwd	TCGATTCTCCATACCCATCAAT	VF2468 42 rev	GCAACCAACTCCCAACAGGG
VF2468 43 fwd	AGGTCCTGGCATTGTCTGGG	VF2468 43 rev	TGGTTGCCCTGTTTACACCC
VF2468 45 fwd	CTGGGAGGCAGCCAGTCAAG	VF2468 45 rev	GCCCTGTAAGCTGAAGCTGGA
VF2468 46 fwd	CAGGTGTGCATTTTGTGCCA	VF2468 46 rev	GCCTGCCAGGTATTTCTGTGT
VF2468 47 fwd	TGGCCTGGTCTATGTGAAAA	VF2468 47 rev	AACTGCAAGTGCCTCCCAG
VF2468 48 fwd	TTGATAAGGGCGGTGCCACT	VF2468 48 rev	TAGAGGGAGGTGCTTGCCCA
VF2468 49 fwd	CATCCCCTTGACCAACAGGC	VF2468 49 rev	GCTTGGGCACTGATCCTGCT
VF2468 50 fwd	ACTGCCAATGGACCCTCTCG	VF2468 50 rev	GAGTTGCCCAGGTGAGCCAT
VF2468 51 fwd	GGGGAGCTAGAATGGTGGGC	VF2468 51 rev	CAAGGTACACAGCTGCCAGG
VF2468 52 fwd	CCCATGCTGGTCTGCTGTT	VF2468 52 rev	GGAGGCTCAGCGGAGAGGAT
VF2468 53 fwd	GGGGTACCAGGGAAGGTTT	VF2468 53 rev	AGTTGCGGGGAGGTGCTACA
VF2468 54 fwd	TGCCCAGAGACCTTCCAAGC	VF2468 54 rev	TGGCCAAGGCCTCTTAAGC
VF2468 56 fwd	GCCAATGTGCAATCGAGACG	VF2468 56 rev	TGCATGCCTCTGACTGATGCT
VF2468 57 fwd	TGACTTGAACCTGGTCCCCC	VF2468 57 rev	CTGGGGCTACAGCCCTCCTT
VF2468 58 fwd	CCCAATCCAGACACCACAGC	VF2468 58 rev	TGCAGATTTTAGGGTTGCCA
VF2468 59 fwd	GGTGAGGAAGGATGGGGTT	VF2468 59 rev	GTAGGCTCTGCCACGCCAGT
VF2468 60 fwd	TGCCCATGTTGTTGCTCCAC	VF2468 60 rev	GACAAGTTAGACCATCCTAGCCCTCA
VF2468 61 fwd	TCACAGCTCCCCTTTCTCGG	VF2468 61 rev	TGTGCTCCTGACTGACGCATT
VF2468 62 fwd	CCTAGGCACAGTGGGGGATG	VF2468 62 rev	GGGCTGACACACTGAGGGCT
VF2468 63 fwd	CCATGAGCACAATTGCCAAAA	VF2468 63 rev	TGAGTTATTTGAAAGAGGAAACAGTG
VF2468 64 fwd	CTGCCAAGAACAGGAGGGGA	VF2468 64 rev	AGCCCATCTACCATCCAGCG
VF2468 66 fwd	ATCGGGGCAGGGCTAGAGTC	VF2468 66 rev	CCCCTGGCATTCCCTACACA
VF2468 67 fwd	GCCGTTAGTGCATTTGCCTG	VF2468 67 rev	TCCCTTCAACCCCTGTAGTGC
VF2468 68 fwd	GTTCTCCAGAGTGGGGCT	VF2468 68 rev	ACTGAGGGAGGCAGACTGG
VF2468 69 fwd	AGGCCTGGCGTAACCTTG	VF2468 69 rev	AAGCTCCAGCCCTGTACCCC
VF2468 70 fwd	GGGATCCTACAGGATGGGACAA	VF2468 70 rev	CAGCCCAGGACAAGGGTAGC

VF2468 71 fwd	GCCACCAAATGTCCACTGGTT	VF2468 71 rev	TTCCCCAAGCAGTCCAGCTC
VF2468 72 fwd	GCACCAGCCTCTTCGATGGT	VF2468 72 rev	CCTTTGGCAGACTGTGGCCT
VF2468 73 fwd	AATGGGGCAAAGGCAAGAAA	VF2468 73 rev	CAGACCTCGTGGTGCATGTG
VF2468 74 fwd	TGGCGAGATAGGCTCTGCTACA	VF2468 74 rev	TGGACAGGGAATTACTCAGACCAG
VF2468 75 fwd	TGTGGGCATGAGACCACAGG	VF2468 75 rev	TTTGACTIONCCCCGCATTGTT
VF2468 76 fwd	TCCTATTTTTAGATGCACTCGAACC	VF2468 76 rev	GTGCTCACTGAAGCCCACCA
VF2468 77 fwd	GGACCTTCTTGCCCTCATGATTC	VF2468 77 rev	GGGAACTGTGCCTTTGCGTC
VF2468 78 fwd	CCTTGCAAAGGCTTGCCTAAA	VF2468 78 rev	GGCAGGCACCTGTAGTCCCA
VF2468 79 fwd	TGGCTTGCAGAGGAGGTGAG	VF2468 79 rev	CAGGGAAGGGTGTGGCTTG
VF2468 80 fwd	GCTTCAGCACATCAGTGGCG	VF2468 80 rev	TTCGCCAGCTCATCAACAA
VF2468 81 fwd	GGTAGGCCACTGTAAGCCAA	VF2468 81 rev	TGGGTGCCATGACAAACAG
VF2468 83 fwd	GAGTTGAGCTGTCAGCGGGG	VF2468 83 rev	GAAGCCAACTGCCTTTGTGAGC
VF2468 84 fwd	TGTTTTCTGCAGTTTTGCAGGG	VF2468 84 rev	GGCTCAGGGAGTTTGAGCCA
VF2468 85 fwd	GCTCTGGCACCAGGCACACT	VF2468 85 rev	GGGAGAGAACCATGAATTTCCCA
VF2468 86 fwd	GCCAAACCCTTTCCAGGGAG	VF2468 86 rev	CCCACCCTATGCACAGAGCC
VF2468 87 fwd	CCTCAGCCAGTTGGAATCGG	VF2468 87 rev	CAACGGTTTAGTTTAGTTCCGGTTT
VF2468 88 fwd	TGGGTGGTGAAAATGGGGTT	VF2468 88 rev	GGTGGGGTATGCACTGGTCA
VF2468 89 fwd	GGAATGTGTGGAACCTCAATTTCTTT	VF2468 89 rev	TTGCTTGCAGGGTGTGGAAA
VF2468 90 fwd	CCACAAGGGTCATCTGGGGA	VF2468 90 rev	CGGAGGCATCATCCACTGAG
VF2468 91 fwd	CCTGGAGTGGTTTGGCTTCG	VF2468 91 rev	TGGAGCCCTGGAGTTCTTGG
VF2468 92 fwd	GGCTCCTGGGGTCATTTTCC	VF2468 92 rev	TGTGCTCCATCCTCCTCCT
VF2468 93 fwd	GTGTGTTTCCGCACACCCTG	VF2468 93 rev	GCTCTTGGCTTCCCAACCCT
VF2468 94 fwd	CCATCGCCGTGTCTGAGTGT	VF2468 94 rev	CAGCAGGAACATCATCCCCC
VF2468 95 fwd	AGGCAATGGCACCAAAAATGG	VF2468 95 rev	GCAGCCTTACCATACTGTGA
VF2468 96 fwd	TTTTGACTTTGAGAACCCCTGA	VF2468 96 rev	CCTTGTCTTTCTCAGTTAGACACA
VF2468 97 fwd	GCTGAGTGCAAAGCTCAGGGA	VF2468 97 rev	GGCAACACAGCAAGACCCCT

Oligonucleotides used in this study. Oligonucleotides “[ZFN] [#] fwd/rev” were ordered from Invitrogen. All other oligonucleotides were ordered from Integrated DNA Technologies. ‘N’ refers to machine mixed incorporation of ‘A’, ‘C’, ‘G’, or ‘T.’ An asterisk indicates that the preceding nucleotide was incorporated as a mixture containing 79 mol % of that nucleotide and 7 mol % each of the other canonical nucleotides. “/5Phos” denotes a 5’ phosphate group installed during synthesis.

Supplementary Note 1. Design of an *In Vitro* Selection for ZFN-Mediated DNA Cleavage

To characterize comprehensively the DNA cleavage specificity of active ZFNs, we first generated a large library of potential DNA substrates that can be selected for DNA cleavage in one step without requiring iterative enrichment steps that could amplify noise and introduce bias. We designed the substrate library such that each molecule in the library is a concatemer of one of $>10^{11}$ potential substrate sequences (Methods; Supplementary Figure S1). Incubation with ZFN results in some molecules that are uncut, some that have been cut once, and some that have been cut at least twice. Those molecules that have been cleaved at least twice have ends consisting of each half of the cleaved DNA sequence (Figure 1).

Cut library members are enriched relative to uncut library members in three ways (Figure 1). First, sequences that have been cleaved twice have two complementary 5' overhangs, which can be identified computationally following DNA sequencing as hallmarks of bona fide cleavage products. Second, since ZFN-mediated cleavage reveals 5' phosphates that are not present in the pre-selection library, only DNA that has undergone cleavage is amenable to sequencing adapter ligation. Third, after PCR using primers complementary to the sequencing adapters, a gel purification step ensures that all sequenced material is of a length consistent with library members that have been cleaved at two adjacent sites. This gel-purified material is subjected to high-throughput DNA sequencing using the Illumina method¹.

Ideally, the library used in a ZFN cleavage selection would consist of every possible DNA sequence of the length recognized by the ZFN. Only one out of every 10^5 members of such a library, however, would contain a sequence that was within seven mutations of a 24-base pair recognition sequence. Since off-target recognition sequences most likely resemble target recognition sites, we used instead a biased library that ensures > 10 -fold coverage of all half-site sequences that differ from the wild-type recognition sequences by up to seven mutations. Library members consist of a fully randomized base pair adjacent to the 5' end of the recognition site, two partially randomized half sites flanking a 4-, 5-, 6-, or 7-bp fully randomized spacer, and another fully randomized base pair adjacent to the 3' end of the recognition site. A fully randomized five-base pair tag follows each library member. This tag, along with the randomized flanking base pairs and the randomized spacer sequence, was used as a unique identifier "key" for each library member. If this unique key was associated with more than one sequence read containing identical library members, these duplicate sequencing reads likely arose during PCR amplification and were therefore treated as one data point.

Supplementary Note 2. Analysis of CCR5-224 and VF2468 ZFNs Using the DNA Cleavage Selection

Each member of a sequence pair consisted of a fragment of the spacer, an entire half-site, an adjacent nucleotide, and constant sequence. One end of the spacer was generally found in one sequence and the other end in its corresponding paired sequence, with the overhang sequence present in both paired sequence reads because overhangs were blunted by extension prior to ligation of adapters. The spacer sequences were reconstructed by first identifying the shared overhang sequence and then any nucleotides present between the overhang sequence and the half-site sequence. Only sequences containing no ambiguous nucleotides and overhangs of at least 4 nucleotides were analyzed. Overall, this computational screen for unique sequences that originated from two cleavage events on identical library members yielded 2.0 million total reads of cleaved library members (Supplementary Table S1). There are far fewer analyzed sequences for the 0.5 nM, 1 nM, and 2 nM CCR5-224 and VF2468 selections compared to the 4 nM selections due to the presence of a large number of sequence repeats, identified through the use of the unique identifier key described above. The high abundance of repeated sequences in the 0.5 nM, 1 nM, and 2 nM selections indicate that the number of sequencing reads obtained in those selections, before repeat sequences were removed, was larger than the number of individual DNA sequences that survived all experimental selection steps. We estimated the error rate of sequencing to be 0.086% per nucleotide by analysis of a constant nucleotide in all paired reads. Using this error rate, we estimate that 98% of the post-selection ZFN target site sequences contain no errors.

Supplementary Notes Reference

1. Bentley, D.R. et al. Accurate whole human genome sequencing using reversible terminator chemistry. *Nature* **456**, 53-9 (2008).

Supplementary Protocol 1. Quality score filtering and sequence binning

- 1) search each position of both pairs of sequencing read for quality score, reject if any position has quality score = 'B'
- 2) output to separate files all sequence reads where the first sequence in the pair start with barcodes ("AAT", "ATA", "TAA", "CAC", "TCG") and count the number of sequences corresponding to each barcode

Supplementary Protocol 2. Filtering by ZFN ("AAT", "ATA", "TAA", "CAC")

For each binned file,

- 1) accept only sequence pairs where both sequences in the pair start with the same barcode
- 2) identify orientation of sequence read by searching for constant regions
 - orientation 1 is identified by the constant region "CGATCGTTGG"
 - orientation 2 is identified by the constant region "CAGTGGAACG"
- 3) search sequences from position 4 (after the barcode) up to the first position in the constant region for the subsequence that has the fewest mutations compared to the CCR5-224 and VF2468 half-site that corresponds to the identified constant region
 - search sequences with orientation 1 for "GATGAGGATGAC" (CCR5-224(+)) and "GACGCTGCT" (VF2468(-))
 - search sequences with orientation 2 for "AAACTGCAAAAG" (CCR5-224(-)) and "GAGTGAGGA" (VF2468(+))
- 4) bin sequences as CCR5-224 or VF2468 by testing for the fewest mutations across both half-sites
- 5) the positions of the half-sites and constant sequences are used to determine the overhang/spacer sequences, the flanking nucleotide sequences, and the tag sequences
 - the subsequence between the half-site of orientation 1 and the constant region is the tag sequence
 - o if there is no tag sequence, the tag sequence is denoted by 'X'
 - the overhang sequence is determined by searching for the longest reverse-complementary subsequences between the subsequences of orientation 1 and orientation 2 that start after the barcodes
 - the spacer sequence is determined by concatenating the reverse complement of the subsequence in orientation 1 that is between the overhang and the half-site (if any), the overhang, and the subsequence in orientation 2 that is between the overhang and the half-site
 - o if there is overlap between the overhang and half-site, only the non-overlapping subsequence present in the overhang is counted as part of the spacer
- 6) to remove duplicate sequences, sort each sequence pair into a tree
 - each level of the tree corresponds to a position in the sequence
 - each node at each level corresponds to a particular base (A, C, G, T, or X = not(A, C, G, or T)) and points to the base of the next position (A,C,G,T,X)
 - the sequence pairs are encoded in the nodes and a subsequence consisting of the concatenation of the spacer sequence, flanking nucleotide sequence, and tag sequence is sorted in the tree
 - at the terminal nodes of the tree, each newly entered sequence is compared to all other sequences in the node to avoid duplication
- 7) the contents of the tree are recursively outputted into separate files based on barcode and ZFN

Supplementary Protocol 3. Library filtering (“TCG”)

- 1) accept only sequence pairs where both sequences in the pair start with the same barcode
- 2) analyze the sequence pair that does not contain the sequence "TCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGAC" (the other pair contains the library sequence)
- 3) search sequences for ZFN half-sites and bin by the ZFN site that has fewer mutations
 - search for "GTCATCCTCATC" and "AAACTGCAAAAG" (CCR5-224) and "AGCAGCGTC" and "GAGTGAGGA" (VF2468)
- 4) identify the spacer, flanking nucleotide, and nucleotide tag sequences based on the locations of the half-sites
- 5) use the tree algorithm in step 6 under **Filtering by ZFN** to eliminate duplicate sequences

Supplementary Protocol 4. Sequence profiles

- 1) analyze only sequences that contain no ‘N’ positions and have spacer lengths between 4 and 7
- 2) tabulate the total number of mutations, the spacer length, the overhang length, the nucleotide frequencies for the (+) and (-) half-sites, the nucleotide frequencies for spacers that are 4-bp, 5-bp, 6-bp, and 7-bp long, and the nucleotide frequencies for the flanking nucleotide and the tag sequence
- 3) repeat steps 1 and 2 for library sequences
- 4) calculate specificity scores at each position using

positive specificity score = (frequency of base pair at position[post-selection]-frequency of base pair at position[pre-selection])/(1-frequency of base pair at position[pre-selection])

negative specificity score = (frequency of base pair at position[post-selection]-frequency of base pair at position[pre-selection])/(frequency of base pair at position[pre-selection])

Supplementary Protocol 5. Genomic matches

- 1) the human genome sequence was searched with 24 and 25 base windows (CCR5-224) and 18 and 19 base windows (VF2468) for all sites within nine mutations (CCR5-224) or six mutations (VF2468) of the canonical target site with all spacer sequences of five or six bases being accepted
- 2) each post-selection sequence was compared to the set of genomic sequences within nine and six mutations of CCR5-224 and VF2468, respectively

Supplementary Protocol 6. Enrichment factors for sequences with 0, 1, 2, or 3 mutations

- 1) for each sequence, divide the frequency of occurrence in the post-selection library by the frequency of occurrence in the pre-selection library

Supplementary Protocol 7. Filtered sequence profiles

- 1) use the algorithm described above in **Sequence profiles**, except in addition, only analyze sequences with off-target bases at given positions for both pre- and post-selection data

Supplementary Protocol 8. Compensation difference map

- 1) use **Filtered sequence profiles** algorithm for mutation at every position in both half-sites
- 2) calculate

$\Delta(\text{specificity score}) = \text{filtered specificity score} - \text{non-filtered specificity score}$

Supplementary Protocol 9. NHEJ search

- 1) identify the site by searching for exact flanking sequences
- 2) count the number of inserted or deleted bases by comparing the length of the calculated site to the length of the expected site and by searching for similarity to the unmodified target site (sequences with 5 or fewer mutations compared to the intended site were counted as unmodified)
- 3) inspect all sites other than CCR5, CCR2, and VEGF-A promoter by hand to identify true insertions or deletions

Supplementary Data

Potential VF2468 genomic off-target sites. The human genome was searched for DNA sequences surviving in vitro selection for VF2468 cleavage. Sites marked with an 'X' were found in the in vitro selection dataset. 'T' refers to the total number of mutations in the site, and '(+)' and '(-)' to the number of mutations in the (+) and (-) half-sites, respectively. The sequences of the sites are listed as they appear in the genome, therefore the (-) half-site is listed in the reverse sense as it is in the sequence profiles.

# of muts			(-) site	spacer	(+) site	[VF2468]			
	T	(-) (+)				4 nM	2 nM	1 nM	0.5 nM
0	0	0	AGCAGCGTC	TTCGA	GAGTGAGGA	X	X	X	X
1	0	1	AGCAGCGTC	AATAC	GAGTGAAGA	X	X	X	X
1	1	0	AGCAGCGTT	GGGAG	GAGTGAGGA	X	X	X	X
1	1	0	AGCAGCCTC	TGCTT	GAGTGAGGA	X	X	X	X
2	0	2	AGCAGCGTC	GTTCTC	AAGTGGGGA	X	X	X	X
2	0	2	AGCAGCGTC	TCCCTT	GAGTGATGG	X	X	X	X
2	0	2	AGCAGCGTC	GTGTG	GTGTGAGGT	X	X	X	X
2	0	2	AGCAGCGTC	AAAAA	CAGTGAGCA	X	X	X	X
2	0	2	AGCAGCGTC	TAGGCA	GAGGGAAGA	X	X	X	X
2	0	2	AGCAGCGTC	TGAAA	GAGTGAAAA	X	X	X	X
2	0	2	AGCAGCGTC	TCAAAA	GAGTGTGCA	X	X	X	X
2	0	2	AGCAGCGTC	TAGGGG	GAGGGAGGG	X	X	X	X
2	1	1	AGCAGAGTC	TCTGA	GAGTGAGGC	X	X	X	X
2	1	1	AGCAGTGTC	AGGCTG	GTGTGAGGA	X	X	X	X
2	1	1	AGCAGTGTC	AGGCTG	GTGTGAGGA	X	X	X	X
2	1	1	AGCAGCCTC	TGCATC	GAGTGAGGT	X	X	X	X
2	1	1	AGCATCGTC	TGAAGT	GAGTGAGGC	X	X	X	X
2	1	1	AGCACCGTC	TTTTC	TAGTGAGGA	X	X	X	X
2	1	1	AGCAGCGTG	CCCAA	GAGTGAGGC	X	X	X	X
2	1	1	AGCAGTGTC	AGGCTG	GTGTGAGGA	X	X	X	X
2	1	1	AGGAGCGTC	TCACCT	GAGTGAGGC	X	X	X	X
2	1	1	AGAAGCGTC	ATCGA	GAGTGAGGT	X	X	X	X
2	1	1	AGCATCGTC	TTCTGT	GAGTGAGTA	X	X	X	X
2	1	1	AGCAGTGTC	AGGCTG	GTGTGAGGA	X	X	X	X
2	1	1	AGCAGAGTC	AGACTT	GAGTGAGGT	X	X	X	X
2	1	1	AGCAACGTC	AGATAG	GGGTGAGGA	X	X	X	X
2	1	1	AGCAGCCTC	TCCAAA	GAGTGAGGC	X	X	X	X
2	1	1	AGCAACGTC	ATATT	CAGTGAGGA	X	X	X	X
2	1	1	AGCAGCTTC	AGGGGA	GTGTGAGGA	X	X	X	X
2	1	1	AGCAGCATC	AGTGA	GAGTGAGGC	X	X	X	X
2	1	1	AGCAGTGTC	AGGCTG	GTGTGAGGA	X	X	X	X
2	1	1	AGCAGTGTC	AGGCTG	GTGTGAGGA	X	X	X	X
2	1	1	AGCAGTGTC	AGGCTG	GTGTGAGGA	X	X	X	X
2	1	1	AGCAGTGTC	CTAAGG	GGGTGAGGA	X	X	X	X
2	1	1	AGCAGCTTC	TCCTGG	GAGTGAGGG	X	X	X	X
2	1	1	AGCAGCGAC	GCCTGG	GAGTGAGGT	X	X	X	X
2	1	1	AGCAGGGTC	AGGGCT	GAGTGAGGC	X	X	X	X
2	1	1	AGCAGCGTA	TCACAT	GAGTGAGGG	X	X	X	X

2	1	1	AGCAGCTTC	CTTTT	GAGTGAGAA	X	X	X	X
2	1	1	AGCATCGTC	ATCAGA	CAGTGAGGA	X	X	X	X
2	1	1	AGCAACGTC	GTAGT	GATTGAGGA	X	X	X	X
2	2	0	AGCTGGGTC	ATGAG	GAGTGAGGA	X	X	X	X
2	2	0	AGCTGGGTC	ATGAG	GAGTGAGGA	X	X	X	X
2	2	0	AGCAACTTC	TGGAAA	GAGTGAGGA	X	X	X	X
2	2	0	AGCTGAGTC	TTAAG	GAGTGAGGA	X	X	X	X
2	2	0	TCCAGCGTC	CTCCCA	GAGTGAGGA	X	X	X	X
2	2	0	TGCAGCGTT	AAAATA	GAGTGAGGA	X	X	X	X
2	2	0	AGCACCTTC	AATTG	GAGTGAGGA	X	X	X	X
2	2	0	TGCAGCGGC	GTAGGG	GAGTGAGGA	X	X	X	X
2	2	0	AGCAGGGTT	CTTCAA	GAGTGAGGA	X	X	X	X
2	2	0	AGCAGCATA	GATATG	GAGTGAGGA	X	X	X	X
2	2	0	AACAGCTTC	TCTGAG	GAGTGAGGA	X	X	X	X
2	2	0	TGCAGGGTC	GGGCAG	GAGTGAGGA	X	X	X	X
2	2	0	AGCAAAGTC	AAACA	GAGTGAGGA	X	X	X	X
2	2	0	AACAGCTTC	TCGGGA	GAGTGAGGA	X	X	X	X
2	2	0	AGTAGCGGC	AAATT	GAGTGAGGA	X	X	X	X
2	2	0	AGCTGAGTC	CTAAA	GAGTGAGGA	X	X	X	X
2	2	0	AGCAGCGAG	AAAGA	GAGTGAGGA	X	X	X	X
2	2	0	TGCAGTGTC	CACAA	GAGTGAGGA	X	X	X	X
2	2	0	AGCAGCATA	ATAGCA	GAGTGAGGA	X	X	X	X
2	2	0	AGCAGCATA	TCAGG	GAGTGAGGA	X	X	X	X
2	2	0	AGCAGCGGT	CTTAG	GAGTGAGGA	X	X	X	X
2	2	0	AACAGCTTC	ATCTCG	GAGTGAGGA	X	X	X	X
2	2	0	GGCAGAGTC	CTAGA	GAGTGAGGA	X	X	X	X
2	2	0	AGCTGTGTC	TTGGA	GAGTGAGGA	X	X	X	X
2	2	0	AGTGCGTC	CCAGT	GAGTGAGGA	X	X	X	X
2	2	0	AGCTGTGTC	CACAG	GAGTGAGGA	X	X	X	X
3	1	2	AGCAGCGGC	TTAAGG	GGGTGAGGT	X	X	X	X
3	1	2	AGCAACGTC	TAACCC	GAGTGTTGA	X	X	X	X
3	1	2	AGCACCGTC	CCCCT	CAGTGAGGC	X	X	X	X
3	1	2	AGCAGCGGC	GGCTG	CAGTGAGGC	X	X	X	X
3	1	2	AGCAGTGTC	TAAAAG	GAGTGAGAT	X	X	X	X
3	1	2	AGCAACGTC	CATAGT	GTGTGAGAA	X	X	X	X
3	2	1	AGAAACGTC	GTGGAG	GAGTGAGGG	X	X	X	X
3	2	1	AGCATAGTC	TAGGCC	GAGTGAGGC	X	X	X	X
3	2	1	AGCAACTTC	ATCTT	GAGTGAGGG	X	X	X	X
3	2	1	AGCAGGGTG	GCGTG	GAGTGAGGC	X	X	X	X
3	2	1	AGCACGGTC	ATGAT	GAGTGAGGC	X	X	X	X
3	2	1	AGCATTGTC	TCCTG	GAGTGAGGG	X	X	X	X
3	2	1	AGCACCGTG	GCTTC	GAGTGAGGC	X	X	X	X
3	2	1	AGCAACTTC	CTGGC	GAGTGAGGG	X	X	X	X
3	2	1	AGCAACATC	TGGTTG	GAGTGAGGG	X	X	X	X
3	2	1	GGCAGCGGC	CGCTGT	GAGTGAGGT	X	X	X	X
3	2	1	AGCATTGTC	TCATGT	GAGTGAGGT	X	X	X	X
3	2	1	AGCAGCAGC	TAGGG	GAGTGAGGG	X	X	X	X
3	2	1	AGCAGCAGC	CCACAG	GAGTGAGGG	X	X	X	X
3	2	1	ATCAGAGTC	TCTGG	GAGTGAGGC	X	X	X	X
3	2	1	ATCAGTGTC	CCTCAG	GAGTGAGGC	X	X	X	X
3	2	1	AGCAACATC	ATCTT	GAGTGAGGG	X	X	X	X
3	2	1	AGCATGGTC	CCAAG	GAGTGAGGG	X	X	X	X
3	2	1	AGCAAAGTC	TGTACT	GAGTGAGGG	X	X	X	X

3	2	1	AGCAGCTCC	TCTCC	GAGTGAGGT	X	X	X	X
3	2	1	AGCAATGTC	AAAAA	GAGTGAGGC	X	X	X	X
3	2	1	AGTAGCGTT	TTTAG	GAGTGAGGT	X	X	X	X
3	2	1	GGCAGAGTC	AGGGCT	GAGTGAGGC	X	X	X	X
3	2	1	TGCAGCTTC	ATGGT	GAGTGAGGC	X	X	X	X
3	3	0	AGCATAGTT	ACCTGG	GAGTGAGGA	X	X	X	X
3	3	0	AGTAAAGTC	TAAGTA	GAGTGAGGA	X	X	X	X
3	3	0	AGCATTGTT	CTGCG	GAGTGAGGA	X	X	X	X
4	3	1	TGCAGTCTC	CTTGG	GAGTGAGGT	X	X	X	X
2	0	2	AGCAGCGTC	CACTTC	CAGAGAGGA	X	X	X	
2	1	1	AGCAGCGTG	GACCCA	GAGTGAGCA	X	X	X	
2	1	1	AGCAGCGCC	AATCC	GAGTGAGAA	X	X	X	
2	1	1	AGCAGCGGC	AGGCT	GAGAGAGGA	X	X	X	
2	1	1	AGCAGCTTC	TGCCTT	GAGTGAGTA	X	X	X	
2	1	1	AGCAGCTTC	ACTGT	CAGTGAGGA	X	X	X	
2	1	1	ATCAGCGTC	TTCAG	AAGTGAGGA	X	X	X	
2	1	1	AGCAGCGTG	GACCCA	GAGTGAGCA	X	X	X	
2	1	1	AGCAGGGTC	AAGAAA	GAGTGAGTA	X	X	X	
2	1	1	AGCAGCGTT	ACACA	GAGTGGGGA	X	X	X	
2	1	1	AGCAGCGGC	AAGAGA	GAATGAGGA	X	X	X	
2	1	1	AGCAGAGTC	CAGGC	AAGTGAGGA	X	X	X	
2	1	1	AGCAGAGTC	CAGGC	AAGTGAGGA	X	X	X	
2	1	1	AGCAGGGTC	TGGGTA	GAGTGATGA	X	X	X	
2	1	1	AGCAGCGTG	GACCCA	GAGTGAGCA	X	X	X	
2	2	0	AGCAGCAGC	TAGCTA	GAGTGAGGA	X	X	X	
2	2	0	AGGAGCTTC	ACTAA	GAGTGAGGA	X	X	X	
2	2	0	AGCAGCCTG	CAATA	GAGTGAGGA	X	X	X	
2	2	0	ACCAAGTGC	TGAGCT	GAGTGAGGA	X	X	X	
2	2	0	AACAGAGTC	CCCAT	GAGTGAGGA	X	X	X	
2	2	0	AGCAGCCTG	GCCAGG	GAGTGAGGA	X	X	X	
2	2	0	AGCAGCAGC	AGTGA	GAGTGAGGA	X	X	X	
2	2	0	ATCAGAGTC	TTAGG	GAGTGAGGA	X	X	X	
2	2	0	AGCGGGGTC	TAGGGG	GAGTGAGGA	X	X	X	
2	2	0	AGCAGCGGA	CAAGT	GAGTGAGGA	X	X	X	
3	0	3	AGCAGCGTC	CCTGCC	TAGGGAGGG	X	X	X	
3	0	3	AGCAGCGTC	TTTTCT	ATGTGAGGC	X	X	X	
3	0	3	AGCAGCGTC	ACCTCT	GTGTGGGGC	X	X	X	
3	0	3	AGCAGCGTC	TAAGG	GAGGGGGGT	X	X	X	
3	0	3	AGCAGCGTC	TTGGG	GTGTGGGGC	X	X	X	
3	0	3	AGCAGCGTC	TAGAG	TAGAGAGGT	X	X	X	
3	1	2	AGCAGGGTC	TCCCAG	GAGTGTGAA	X	X	X	
3	1	2	AGCAGTGTG	TATTT	CAGTGAGGG	X	X	X	
3	1	2	AGCAGGGTC	AGCCCA	GAGTGGGGG	X	X	X	
3	1	2	AGCAGGGTC	AGGCA	CAGTGAGGC	X	X	X	
3	1	2	AGCAGGGTC	CTCTG	GAGTGGGGG	X	X	X	
3	1	2	GGCAGCGTC	CGGAG	GAGTGAAGG	X	X	X	
3	1	2	GGCAGCGTC	ACTCCA	GAGTTAGGT	X	X	X	
3	1	2	AGCAGGGTC	ATTCAT	CAGTGAGGC	X	X	X	
3	1	2	AGCAGAGTC	CTGTCA	GAGGGAGGC	X	X	X	
3	1	2	AGCAGCATC	TTCTG	GAGTGAGAC	X	X	X	
3	1	2	AGCATCGTC	TTTCT	GTGTGAGGC	X	X	X	
3	1	2	AGCAGTGTG	TCACAG	GAGGGAGGG	X	X	X	
3	1	2	GGCAGCGTC	CAGGA	GAGAGAGGT	X	X	X	

3	1	2	AGCAGCGGC	CCCGG	GAGTTAGGT	X	X	X
3	1	2	AGCAGCGGC	GGGTGG	GAGTGGGGG	X	X	X
3	1	2	AGCAGTGTC	CAGAC	GAGGGAGGT	X	X	X
3	1	2	AGCAGTGTC	TATGA	GAGGGAGGG	X	X	X
3	1	2	AGCAGTGTC	AGCCAT	GAGGGAGGG	X	X	X
3	1	2	AGCAGTGTC	CCTGTG	GAGGGAGGT	X	X	X
3	1	2	AGCACCGTC	TGCCA	GAGTGGGCA	X	X	X
3	2	1	AGCCACGTC	CACAC	TAGTGAGGA	X	X	X
3	2	1	AGTAGCGCC	AAAAG	GAGTGAGGT	X	X	X
3	2	1	AACAGGGTC	TTTGAC	GAGTGAGGC	X	X	X
3	2	1	GGCAGGGTC	TCAAT	GAGTGAGGG	X	X	X
3	2	1	AACAGGGTC	CCTGA	GAGTGAGGG	X	X	X
3	2	1	AGGAGAGTC	CAGGT	GAGTGAGGG	X	X	X
3	2	1	AGCAGCCGC	CAACA	GAGTGAGGG	X	X	X
3	2	1	GGCAGAGTC	AGTGTT	GAGTGAGGG	X	X	X
3	2	1	AGCAGTGTG	TGAGCT	GAGTGAGGC	X	X	X
3	2	1	AGCATCTTC	CAGTG	GAGTGAGGG	X	X	X
3	2	1	AGCAGAGTG	GTTGA	GAGTGAGGT	X	X	X
3	2	1	ATCAGTGTC	CCAGA	GAGTGAGGG	X	X	X
3	2	1	TTCAGCGTC	CAAGAA	GAGTGAGGT	X	X	X
3	2	1	AGCAACTTC	CGGACA	GAGTAAGGA	X	X	X
3	2	1	AGCAGCGGG	AGATG	GAGTGAGGC	X	X	X
3	2	1	AGTAGCGTG	GAGAG	GAGTGAGGT	X	X	X
3	2	1	AGCTGCATC	TTTGG	GAGTGAGGT	X	X	X
3	2	1	ATCAGAGTC	AAAGAA	GAGTGAGGT	X	X	X
3	2	1	AGCAGGATC	TGAAAT	GAGTGAGGT	X	X	X
3	2	1	AGCCACGTC	CAGTTT	TAGTGAGGA	X	X	X
3	2	1	AGCAATGTC	TCAAAT	CAGTGAGGA	X	X	X
3	2	1	AGCAATGTC	TGAAA	CAGTGAGGA	X	X	X
3	2	1	GGCTGCGTC	ATCGG	GAGTGAGGT	X	X	X
3	2	1	GGCAGAGTC	AAAAT	GAGTGAGGT	X	X	X
3	2	1	AGCAGTGTG	CATGT	GAGTGAGGT	X	X	X
3	3	0	GGCAACATC	AAACAG	GAGTGAGGA	X	X	X
3	3	0	CCCAGCGGC	TGGCAG	GAGTGAGGA	X	X	X
3	3	0	AGCCTGGTC	GGAGAG	GAGTGAGGA	X	X	X
3	3	0	TGCAGTCTC	TATGG	GAGTGAGGA	X	X	X
3	3	0	AGCATTGTA	GAGGC	GAGTGAGGA	X	X	X
3	3	0	AGCCTGGTC	TCACA	GAGTGAGGA	X	X	X
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3	3	0	AGCAAAGGC	ACCAG	GAGTGAGGA	X	X	X
3	3	0	AACATGGTC	CACGT	GAGTGAGGA	X	X	X
3	3	0	AGCTTTGTC	AACCTA	GAGTGAGGA	X	X	X
3	3	0	AGCAAAGGC	AAAAA	GAGTGAGGA	X	X	X
3	3	0	ATCAAGGTC	TTTTG	GAGTGAGGA	X	X	X
3	3	0	GCCAGTGTC	TCGTCT	GAGTGAGGA	X	X	X
3	3	0	TGCAAAGTC	AGATCT	GAGTGAGGA	X	X	X
4	1	3	AGCAACGTC	TACAG	GAGGAAGGT	X	X	X
4	1	3	AGCAACGTC	CCAGGA	AAGTGAAGG	X	X	X
4	2	2	GGCAGTGTC	CAGTAG	GAGTGAGAT	X	X	X
4	2	2	AGCAAAGTC	TCACA	AAGTGAGGT	X	X	X
4	3	1	TGCTGTGTC	AAACCC	GAGTGAGGT	X	X	X
4	3	1	GGCAAGGTC	TCTGTG	GAGTGAGGG	X	X	X
4	3	1	ATCAACGTC	TCTCA	GAGTGAGGC	X	X	X

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2	0	2	AGCAGCGTC	TGCATG	GTGTGGGGA	X	X	X
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2	1	1	AGCAGCTTC	ATTTAT	GAGTGAGCA	X	X	X
2	1	1	GGCAGCGTC	CTTCT	GAGTGAGCA	X	X	X
2	1	1	AGCAGTGTC	GTGAA	GAGTCAGGA	X	X	X
2	1	1	AGCAGCTTC	CGGGGA	GAGAGAGGA	X	X	X
2	2	0	AGCAGCTGC	GGACC	GAGTGAGGA	X	X	X
2	2	0	AGCAGTGGC	ATTAA	GAGTGAGGA	X	X	X
2	2	0	AGCAGCATG	CACAT	GAGTGAGGA	X	X	X
2	2	0	AGCAGCATG	ACCAA	GAGTGAGGA	X	X	X
2	2	0	ACCAGGGTC	TGTGGG	GAGTGAGGA	X	X	X
2	2	0	AGCAGCATG	AAAAGG	GAGTGAGGA	X	X	X
2	2	0	AGCAGGGTG	ATGGA	GAGTGAGGA	X	X	X
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2	2	0	AGCGCCGTC	CACAGG	GAGTGAGGA	X	X	X
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3	0	3	AGCAGCGTC	CAGTGG	GAGTGGGCC	X	X	X
3	0	3	AGCAGCGTC	CTTCCT	CAGTGAGAC	X	X	X
3	1	2	AGCAGCGGC	GGCGGG	GAGGGAGGC	X	X	X
3	1	2	AGCAGAGTC	TGTTGA	GAGTGAGAC	X	X	X
3	1	2	TGCAGCGTC	AGAAG	GTGTGAGGC	X	X	X
3	1	2	AGCAGCGTG	CCTCT	GGGTGAGGC	X	X	X
3	1	2	AGCAGCTTC	CATCTG	GAGTGAGTC	X	X	X
3	1	2	AGCAGCATC	TGCTCT	TAGTGAGGC	X	X	X
3	1	2	AGCAACGTC	CTGCA	GAGGGAGAA	X	X	X
3	1	2	AGCAGCGGC	CCGCA	GAGGGAGGC	X	X	X
3	1	2	AGCAACGTC	AGCAA	CAGTGAGAA	X	X	X
3	1	2	AGTAGCGTC	TCGAA	GAGAGAGGC	X	X	X
3	1	2	AGCAGCGTT	TTCAG	GAGGGAGGG	X	X	X
3	1	2	AGCAGCGGC	ACCCT	GGGTGAGGC	X	X	X
3	2	1	AGCAAGGTC	AACTCA	GAGTGAGAA	X	X	X
3	2	1	AGCATGGTC	AGTTTC	TAGTGAGGA	X	X	X
3	2	1	AGTAGGGTC	ACGCCA	GAGTGAGGC	X	X	X
3	2	1	ATCAGGGTC	CTGTT	GAGTGAGGG	X	X	X
3	2	1	AGCATGGTC	TTTTTC	TAGTGAGGA	X	X	X
3	2	1	AGCAGGGTA	AGAGGG	GAGTGAGGG	X	X	X
3	2	1	GGCAACGTC	AACTCA	GAGTGAGAA	X	X	X
3	2	1	GCCAGCGTC	TTGGGT	GAGTGAGGT	X	X	X
3	2	1	AGCAGCTTT	CTGCT	GAGTGAGGC	X	X	X
3	2	1	AGCAGTGGC	TGCGG	GAGTGAGGC	X	X	X
3	2	1	GGCAGCATC	TGGGC	GAGTGAGGC	X	X	X
3	2	1	GGCAGCATC	TGAAT	GAGTGAGGC	X	X	X
3	2	1	AGCAGTGTA	TGTGG	GAGTGAGGT	X	X	X
3	2	1	AGGAGAGTC	CCTGG	GAGTGAGGC	X	X	X
3	2	1	AGCATGGTC	AGATTC	TAGTGAGGA	X	X	X
3	2	1	ATCAGGGTC	TTGAGG	GAGTGAGGT	X	X	X
3	2	1	AACAGCGTG	CTGTA	GAGTGAGGT	X	X	X
3	2	1	AGTAGCTTC	TGTGG	GAGTGAGGC	X	X	X
3	2	1	AGCAACTTC	TTGAT	GAGTGAGAA	X	X	X

3	2	1	AGCATGGTC	AGGTTC	TAGTGAGGA	X	X	X
3	2	1	AGAAGTGTC	AGAGTA	GAGTGAGGC	X	X	X
3	2	1	AACAGCGGC	ATGGG	GAGTGAGGC	X	X	X
3	2	1	AGCAGTGGC	ATCTAG	GAGTGAGGC	X	X	X
3	3	0	AAAAGTGTC	ATATAG	GAGTGAGGA	X	X	X
3	3	0	AGCAATGGC	TGGAT	GAGTGAGGA	X	X	X
3	3	0	GCCACCGTC	GGTGAG	GAGTGAGGA	X	X	X
3	3	0	AAAAGTGTC	AGTAGA	GAGTGAGGA	X	X	X
3	3	0	AACATTGTC	TAGTGG	GAGTGAGGA	X	X	X
3	3	0	AACATTGTC	TAGTGA	GAGTGAGGA	X	X	X
3	3	0	AACATTGTC	TAGTGG	GAGTGAGGA	X	X	X
3	3	0	AACATTGTC	TAGTGA	GAGTGAGGA	X	X	X
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3	3	0	AACATTGTC	TAGTGA	GAGTGAGGA	X	X	X
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3	3	0	AACATTGTC	TAGTGA	GAGTGAGGA	X	X	X
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3	3	0	AGCATGGTG	ATTAA	GAGTGAGGA	X	X	X
4	3	1	AGTAGTCTC	TGGCT	GAGTGAGGT	X	X	X
4	3	1	AGCATTGTT	TCTCA	GAGTGAGGT	X	X	X
4	3	1	AGCAAGGTT	AGGCT	GAGTGAGGG	X	X	X
4	3	1	AGCAGTCTT	CCACCA	GAGTGAGGC	X	X	X
4	3	1	AGCATTGTT	TGAGT	GAGTGAGGT	X	X	X
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2	0	2	AGCAGCGTC	ACTACA	GAGGCAGGA	X	X	
2	1	1	GGCAGCGTC	TCTCTG	GGGTGAGGA	X	X	
2	1	1	AGCAGAGTC	TTGAA	GAGTGAGTA	X	X	
2	1	1	AGCAGCATC	TATGC	CAGTGAGGA	X	X	
2	1	1	AGCAGAGTC	TGGCA	GAGAGAGGA	X	X	
2	1	1	AGCAGTGTC	CCTCA	GAGTGTGGA	X	X	
2	1	1	AGCAGCATC	TTGGA	GTGTGAGGA	X	X	
2	1	1	AGCTGCGTC	TTCTG	GAGGGAGGA	X	X	
2	1	1	AGCAGCTTC	AGAAGA	GAATGAGGA	X	X	
2	1	1	AGCAGGGTC	GAGGG	GAGGGAGGA	X	X	
2	1	1	AGCAGGGTC	TGGTG	CAGTGAGGA	X	X	
2	1	1	AGCAGCATC	CATGT	CAGTGAGGA	X	X	
2	1	1	AGCAGAGTC	CCAAG	GGGTGAGGA	X	X	
2	1	1	AGCAGCCTC	TGAAC	AAGTGAGGA	X	X	
2	1	1	AGCAGCCTC	TAGGT	AAGTGAGGA	X	X	
2	1	1	AGCAGCTTC	AGATTT	GAGTTAGGA	X	X	
2	1	1	AGCAGCCTC	ACAGG	CAGTGAGGA	X	X	
2	1	1	AGCAGCATC	AACAC	CAGTGAGGA	X	X	
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2	1	1	AGCAGCATC	TATGC	CAGTGAGGA	X	X	
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2	1	1	AGCAGAGTC	ACCCA	GTGTGAGGA	X	X	
2	1	1	GGCAGCGTC	TGGGAG	GAGTTAGGA	X	X	

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2	1	1	AGCAGAGTC	AGAGAG	GAGAGAGGA	X	X
2	1	1	AGCAGAGTC	ACTGAC	CAGTGAGGA	X	X
2	1	1	AGCAGTGTC	TCCCA	GAGTGTGGA	X	X
2	1	1	AGCAGTGTC	TGAGTA	GAGTGTGGA	X	X
2	1	1	AGCAGCATC	CCGGG	GAGTGAAGA	X	X
2	1	1	AACAGCGTC	AAGGCA	GAGTGAAGA	X	X
2	1	1	AGCAGCGCC	ATCTT	GAGCGAGGA	X	X
2	1	1	AGCAGCGCC	ATCTT	GAGCGAGGA	X	X
2	1	1	AGCAGCGCC	ATCTT	GAGCGAGGA	X	X
2	1	1	AGCAGCGCC	ATCTT	GAGCGAGGA	X	X
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2	1	1	AGCAGCGCC	ATCTT	GAGCGAGGA	X	X
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2	1	1	AGCAGCATC	GTGAGT	GAGTGTGGA	X	X
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2	1	1	AGCAGCGTG	GTTAA	GAGTCAGGA	X	X
2	1	1	ACCAGCGTC	TGGTGA	GAGTGGGGA	X	X
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2	2	0	AGCAGAGTA	CCCAT	GAGTGAGGA	X	X
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3	0	3	AGCAGCGTC	AGGGT	TTGAGAGGA	X	X
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3	0	3	AGCAGCGTC	AGCCTC	TAGAGGGGA	X	X
3	0	3	AGCAGCGTC	CGCAG	GAGGTAGGG	X	X
3	0	3	AGCAGCGTC	CAAGA	GTGTTACGA	X	X
3	0	3	AGCAGCGTC	CTAGC	CTGTGAGGG	X	X
3	0	3	AGCAGCGTC	CTCCTG	GAGGGAGAG	X	X
3	0	3	AGCAGCGTC	AGGGAG	GAGGGGAGA	X	X

3	0	3	AGCAGCGTC	CCCCCG	CAGTGATGG	X	X
3	0	3	AGCAGCGTC	TCCTGA	GAGAGAAGG	X	X
3	0	3	AGCAGCGTC	TGTCCT	GAGTCCAGA	X	X
3	0	3	AGCAGCGTC	AAGGAT	TAGAGAGTA	X	X
3	0	3	AGCAGCGTC	TCCTGA	GAGAGAAGG	X	X
3	1	2	AGTAGCGTC	CTAAT	GAGTGTGAA	X	X
3	1	2	AGCAGCTTC	TCCATG	GAGTGAGAC	X	X
3	1	2	AGCAGGGTC	GGGGA	GAGGGAGGG	X	X
3	1	2	AGCAGCATC	CAGACT	CAGTGAGGT	X	X
3	1	2	AGCAGGGTC	AGCTAA	GAGGGAGGC	X	X
3	1	2	AGCAGCGGC	AGCGA	GAGTGATGT	X	X
3	1	2	GGCAGCGTC	TGACG	GAGTGAGTG	X	X
3	1	2	AGCAGTGTC	AGGTAG	GAGAGAGGC	X	X
3	1	2	AGCAGGGTC	TGAGTG	GAGTAAGGT	X	X
3	1	2	AGCAGTGTC	AGCTGG	TAGTGAGAA	X	X
3	1	2	AGCACCGTC	TGGGG	GAGGGAAGA	X	X
3	1	2	AGCAGCATC	AGCATG	GAGGGAGGC	X	X
3	1	2	AGCAGCCTC	GGTCAA	GAGTGAGAG	X	X
3	1	2	GGCAGCGTC	AATAA	AAGTGAGGG	X	X
3	1	2	AGCAACGTC	GGCAG	CAGTGGGGA	X	X
3	1	2	AGCAACGTC	AGCAA	GTCTGAGGA	X	X
3	1	2	AGCAGGGTC	AGTGTC	TAGTGAGAA	X	X
3	1	2	AGCAGGGTC	AGGATG	GAGTGGGGT	X	X
3	1	2	AGCAGTGTC	AGTGAA	CAGTGAGGT	X	X
3	1	2	AGCAGGGTC	AGTGCC	TAGTGAGGG	X	X
3	1	2	AGCAGCGTA	CGGACT	GAGTGAGCC	X	X
3	1	2	AGCAGCTTC	CCCAGT	AAGTGAGAA	X	X
3	1	2	AGCAGCGGC	ACCTC	GAGAGAGAA	X	X
3	1	2	AGCAGTGTC	CTCAC	CAGTAAGGA	X	X
3	1	2	AGCAGGGTC	TGTTA	GAGTGAGTG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCACCGTC	ATCTAA	GGGTGAGGC	X	X
3	1	2	AGCATCGTC	CTGTG	GAGCGAGGG	X	X
3	1	2	AGCAGGGTC	CTTACT	CAGTGAGGT	X	X
3	1	2	AGCAGAGTC	TGAGA	GTGTGAGGT	X	X
3	1	2	AGCAGCGTG	CAGTGA	CAGTGAGGC	X	X
3	1	2	AGCACCGTC	ATTGGA	GAGGGAGAA	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGAGTC	GCTGCA	GAGTGAGCC	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGAGTC	CTTGG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCGTA	TGCATA	CAGTGAGGG	X	X
3	1	2	AGCAGTGTC	AGGCTG	GTGTGAGAA	X	X
3	1	2	AGCAGAGTC	GGCGTC	TAGTGAGGG	X	X
3	1	2	AGCAGCGTG	GGCCGG	GAGGGAGGT	X	X
3	1	2	GGCAGCGTC	CGATT	CAGTGAGGG	X	X
3	1	2	AGCAGCTTC	ACTGAA	GAGGGAGGC	X	X

3	1	2	ATCAGCGTC	TCTGG	GAGTGGGGC	X	X
3	1	2	AGCAGCGGC	AGGCGA	GAGTGACAA	X	X
3	1	2	AGCAGCTTC	AACGT	GAGTGATGT	X	X
3	1	2	AGCAGCTTC	CTGGG	GAGTGAGTT	X	X
3	1	2	AGCAGCATC	TCGTG	GAGGGAGGC	X	X
3	1	2	AGCAGAGTC	TTCAG	GAGAGAGGC	X	X
3	1	2	AGCAGGGTC	AAGTTC	CAGTGAGGG	X	X
3	1	2	AGCAGAGTC	AGTCTT	GAGTGAGTT	X	X
3	1	2	AGCAGAGTC	AGACTT	GAGTGAGTT	X	X
3	1	2	TGCAGCGTC	CAGAT	GAGGGAGGT	X	X
3	1	2	AGCATCGTC	AGAAT	GGGTGAGGG	X	X
3	1	2	AGCAGTGTC	CAGCTC	CAGTGAGGC	X	X
3	1	2	AGCAGCTTC	TAAAAG	GAGAGAGGT	X	X
3	1	2	AGCAGGGTC	CATGAG	GAGTGAGCC	X	X
3	1	2	AGCAGTGTC	ACCACA	GAGTGAAGG	X	X
3	1	2	AGCAGGGTC	AGGTTT	TAGTGAGGG	X	X
3	1	2	AGCAGCATC	AATGTC	TAGTGAGGG	X	X
3	1	2	AGCAGTGTC	CCGCAC	GAGGAAGGA	X	X
3	1	2	AGCAGCTTC	TTGTGA	GAGAGAGGT	X	X
3	1	2	AGCAGAGTC	CTAAGC	GGGTGAGGG	X	X
3	1	2	AGCAGTGTC	AAGTA	GAGTGAAGG	X	X
3	1	2	AGCATCGTC	AAGTTC	TGGTGAGGA	X	X
3	1	2	AGCAGGGTC	CCTGCT	GAGAGAGGG	X	X
3	1	2	AGCAGAGTC	AAGTCA	GAGAGAGGC	X	X
3	1	2	AGCAGCGGC	TGATG	GA CTGAGGC	X	X
3	1	2	AGCAGAGTC	CAGTGG	GTGTGAGGC	X	X
3	1	2	AGCAGCGGC	TGATG	GA CTGAGGC	X	X
3	1	2	AGCAGCGGC	AGCCGA	GAGAGAGGG	X	X
3	1	2	AGCAGCGGC	TGATG	GA CTGAGGC	X	X
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3	1	2	AGCAGCGGC	TGATG	GA CTGAGGC	X	X
3	1	2	AGCAGCGGC	TGATG	GA CTGAGGC	X	X
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3	1	2	AGCAGCGGC	AGCCGA	GAGAGAGGG	X	X
3	1	2	AGCAGCGGC	TGATG	GA CTGAGGC	X	X
3	1	2	TGCAGCGTC	TTGTT	TAGTGAGGC	X	X
3	1	2	AGCAGTGTC	AGGCTG	GTGTGAGAA	X	X
3	1	2	AGCAGCGTA	GAGTGG	GAATGAGGG	X	X
3	1	2	AGCATCGTC	ACAGGA	GGGTGAGGT	X	X
3	1	2	AGCAGCGGC	ACCCA	GAATGAGGG	X	X
3	1	2	AGCAGCGTT	ATTTCA	GAGTGTGGT	X	X
3	1	2	AGCAGAGTC	GCTCCA	GAGTGAGCC	X	X
3	1	2	AGCAGTGTC	ATCTTT	GAGTGGGAA	X	X
3	1	2	AGCAGCATC	TCCTAG	CAGTGAGGG	X	X
3	1	2	AGCAACGTC	AGTGG	GA CTGAGGG	X	X
3	1	2	AGCACCGTC	ATCTT	GAGTGAGCT	X	X
3	1	2	AGCAGGGTC	CTGAG	GGGAGAGGA	X	X
3	1	2	GGCAGCGTC	AGGAGA	GAGTGATGT	X	X
3	1	2	AGCATCGTC	GGGGAG	GAGTGGGAA	X	X
3	1	2	AGCAGTGTC	TGTGCT	CAGTGAGGT	X	X
3	1	2	AGCAGTGTC	AGTCCT	GAGAGAGCA	X	X
3	1	2	AGCAGCGTT	GCTTTC	TAGTGAGGT	X	X
3	1	2	AGCAGCGGC	GACAGG	GAGAGAGGG	X	X

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3	1	2	AGCAGTGTC	TGCTGG	GAGGGTGGA	X	X
3	1	2	AGCAGCGCC	CTGTGG	GAGGGAGGT	X	X
3	1	2	AGCAGAGTC	AGAAA	GAGTAAGGC	X	X
3	1	2	AGCAGCTTC	TCTAAG	GAGTGGGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGCTTC	ATCTG	GAGGGAGGG	X	X
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3	1	2	AGCAGCTTC	CTGCTC	CAGTGAGGG	X	X
3	1	2	AGCAGCTTC	ACCTG	GAGGGAGGG	X	X
3	1	2	AGCAGAGTC	AAGAGG	GTGTGAGGG	X	X
3	1	2	AGCAGGGTC	CTGAAG	GAGGGAGGG	X	X
3	1	2	AGCAGGGTC	AGCCCA	GAGGGAGGC	X	X
3	1	2	GGCAGCGTC	ATTTT	GAGTGGGGG	X	X
3	1	2	AGCAGCGTG	TGGCA	GAGAGAGGG	X	X
3	1	2	AGCACCGTC	CCCGAG	GTGGGAGGA	X	X
3	1	2	AGCAGCTTC	CCATC	GGGTGAGGG	X	X
3	1	2	AGCAGCATC	TGTGGA	CAGTGAGGT	X	X
3	1	2	AGCAGCGTG	CTGGAT	GAGTGTGGT	X	X
3	1	2	AGCAGCGGC	AGGCAC	CAGTGAGGG	X	X
3	1	2	AGCAGGGTC	AGGGGT	GAGTGGGGT	X	X
3	1	2	AGCAGCGGC	GAACA	GAGCGGGGA	X	X
3	1	2	AGCTGCGTC	TCTGGG	AAGTGAGGG	X	X
3	1	2	AGCAGGGTC	ATGACA	GAGAGAGGG	X	X
3	1	2	AGCAGCATC	TGGCA	GAGTAAGGG	X	X
3	1	2	AGCAGTGTC	CACCT	GAGTTAGGT	X	X
3	1	2	AGCAGCGAC	GGCGG	GTGTGAGGC	X	X
3	1	2	AGCAGGGTC	ACACTA	AAGTGAGGC	X	X
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3	2	1	AGCTGGGTC	ATGTG	AAGTGAGGA	X	X
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3	2	1	GGCAGCGGC	CGGAAA	AAGTGAGGA	X	X
3	2	1	AGCATGGTC	AATGA	CAGTGAGGA	X	X
3	2	1	ATCAGCCTC	TTGTAG	GAGTGAGGG	X	X
3	2	1	AGCATGGTC	ATGAA	CAGTGAGGA	X	X
3	2	1	AGCAGGGGC	ATGAGA	GAGTGAGGT	X	X
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3	2	1	AACAGAGTC	CAGGAA	GAGTGAGGT	X	X
3	2	1	AACAGCATC	AGCTCT	GAGTGAGGC	X	X
3	2	1	ATCAGTGTC	AGTGAG	CAGTGAGGA	X	X
3	2	1	AGCAGCTGC	ATGAT	GAGTGAGGT	X	X
3	2	1	AGCAGGGTT	GATCA	GAGGGAGGA	X	X
3	2	1	AGCATAGTC	CAGAT	TAGTGAGGA	X	X
3	2	1	AGCAGCAAC	CTTAA	GAGTGAGGG	X	X
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3	2	1	AGCATTGTC	ATGAA	GAGGGAGGA	X	X
3	2	1	AGCAGCACC	TGGCCT	GAGTGAGGG	X	X
3	2	1	AGCAGGGTT	GGGCA	GAGGGAGGA	X	X
3	2	1	AGTAGAGTC	TGACTA	AAGTGAGGA	X	X
3	2	1	AGCAACGTG	AGTGT	GAGCGAGGA	X	X
3	2	1	AGCAAGGTC	CCACT	CAGTGAGGA	X	X
3	2	1	AGCAGCCAC	AAGGT	GAGTGAGGG	X	X
3	2	1	AGCAATGTC	AGGGA	AAGTGAGGA	X	X
3	2	1	AGCAGCTAC	TCCAGA	GAGTGAGGT	X	X
3	2	1	AGCAGCTGC	AGCAG	GGGTGAGGA	X	X
3	2	1	AGCAGGGGC	AGCAT	GAGTGAGGT	X	X
3	2	1	AGCAACGTG	ACCTAC	TAGTGAGGA	X	X
3	2	1	AACAGCGTA	AGTAC	AAGTGAGGA	X	X
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3	2	1	AGCAGCTGC	AATTAT	GAGAGAGGA	X	X
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3	2	1	AGCAAGGTC	AGAAG	GAGTAAGGA	X	X
3	2	1	AGCTGCGTG	GGAGCA	GAGTGAGGC	X	X
3	2	1	AGCAAGGTC	CTAGT	GAGTGAAGA	X	X
3	2	1	AGCAGATTC	AGAAG	GAGTGAGGG	X	X
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3	2	1	TGCAGGGTC	TTCCC	GAGTGAGGG	X	X
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3	2	1	AGCTGAGTC	CCTAGA	GAGGGAGGA	X	X
3	2	1	AGCATTGTC	CAGAAA	CAGTGAGGA	X	X
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3	2	1	AGCTGTGTC	AAAGG	AAGTGAGGA	X	X
3	2	1	AACAGCATC	TTAGGG	GAGTGAGGG	X	X
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3	2	1	AGCAGCCCC	ATCCT	GAGTGAGGG	X	X
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3	2	1	AGCACCTTC	CTGGCT	GAGTGAGGG	X	X
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3	2	1	AGCAGATTC	TGGTA	GAGTGAGGG	X	X
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3	2	1	AGCAAAGTC	CTAGAT	GAGGGAGGA	X	X
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3	2	1	AGCAGAGAC	TGAATG	GAGTGAGGG	X	X
3	2	1	AGCAGAGGC	TTAAAG	GAGTGAGGG	X	X
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3	2	1	AGTAGAGTC	TTCCA	GAGTGAGAA	X	X
3	2	1	TGCAGCGAC	AACAG	GAGTGAGGT	X	X
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3	2	1	AGCAACATC	TGCTA	CAGTGAGGA	X	X
3	2	1	ACCAGCTTC	CTGCT	GAGTGAGGT	X	X
3	2	1	AGCAGCATT	ATTCT	GAGTGAGGG	X	X
3	2	1	AGGAGTGTC	GACAAG	GAGTGAGGG	X	X
3	2	1	AGAAGCGGC	TGCAG	GAGTGAGGG	X	X
3	2	1	AGCAGCCAC	AGACTA	GAGTGAGGC	X	X

3	2	1	AGCAGCAGC	AGCAG	GAGTGAGGC	X	X
3	2	1	AGCACAGTC	CGCAGG	GAGGGAGGA	X	X
3	2	1	AGCTGCGGC	GAATGA	GAGTGAGGG	X	X
3	2	1	AGCAAGGTC	TTATA	GGGTGAGGA	X	X
3	2	1	AGCACCTTC	TCCAT	GAGTGGGGA	X	X
3	2	1	AGCAGCATG	ATCCTG	GAGTGAGGC	X	X
3	2	1	AGCAAGGTC	AAGAGA	GAGTGAGCA	X	X
3	2	1	AGCATGGTC	AAAGCT	GAGTGAGAA	X	X
3	2	1	AGCAGCATG	ATCTTG	GAGTGAGGC	X	X
3	2	1	AGCAGGGTG	GGGTGT	GAGTGAGGT	X	X
3	3	0	AGAGGTGTC	GCCAT	GAGTGAGGA	X	X
3	3	0	GTCAGGGTC	ATCAG	GAGTGAGGA	X	X
3	3	0	TGCACTGTC	TCTCCC	GAGTGAGGA	X	X
3	3	0	TGCGGAGTC	GAGGGT	GAGTGAGGA	X	X
3	3	0	AGAAACGTT	CTTGCT	GAGTGAGGA	X	X
3	3	0	AGGAGCAAC	ATGCT	GAGTGAGGA	X	X
3	3	0	CGCTGTGTC	CCCGGG	GAGTGAGGA	X	X
3	3	0	AGCGTGGTC	ACTAGG	GAGTGAGGA	X	X
3	3	0	AGCAGGTCC	TTGAA	GAGTGAGGA	X	X
3	3	0	GGCTGTGTC	ATTCAG	GAGTGAGGA	X	X
3	3	0	TGCAGAGTT	AGAGGT	GAGTGAGGA	X	X
3	3	0	ATCATGGTC	AGAAAA	GAGTGAGGA	X	X
3	3	0	AGCAACGCG	GTGAGG	GAGTGAGGA	X	X
3	3	0	TGAAGTGTC	AGCTC	GAGTGAGGA	X	X
3	3	0	AGCAACTCC	GTCTT	GAGTGAGGA	X	X
3	3	0	AGAAATGTC	TTCCAG	GAGTGAGGA	X	X
3	3	0	GGCAGGGTA	TCACAG	GAGTGAGGA	X	X
3	3	0	AGCAACATG	GAGTT	GAGTGAGGA	X	X
3	3	0	GACAGCGTG	GCCAGT	GAGTGAGGA	X	X
3	3	0	GGCTGAGTC	ACTCT	GAGTGAGGA	X	X
3	3	0	TGCAGAGTT	TTGTG	GAGTGAGGA	X	X
3	3	0	AGCTGAGTG	CTGGAT	GAGTGAGGA	X	X
3	3	0	AACTGAGTC	TCTGA	GAGTGAGGA	X	X
3	3	0	AACATAGTC	TGTACA	GAGTGAGGA	X	X
3	3	0	AGCTGGGTG	ACAGT	GAGTGAGGA	X	X
3	3	0	AGCACCATA	TGGCT	GAGTGAGGA	X	X
3	3	0	ATCAGGTTT	CTTCT	GAGTGAGGA	X	X
3	3	0	ACCACGGTC	AGGTCT	GAGTGAGGA	X	X
3	3	0	ACCACGGTC	AGGTCT	GAGTGAGGA	X	X
3	3	0	ACCACGGTC	AGGTCT	GAGTGAGGA	X	X
3	3	0	ACCACGGTC	AGGTCT	GAGTGAGGA	X	X
3	3	0	ACCACGGTC	AGGTCT	GAGTGAGGA	X	X
3	3	0	ACCATGGTC	AAGTCT	GAGTGAGGA	X	X
3	3	0	AGAAACTTC	CTCTC	GAGTGAGGA	X	X
3	3	0	CACAGCTTC	TCACAG	GAGTGAGGA	X	X
3	3	0	ATCATGGTC	TTAGA	GAGTGAGGA	X	X
3	3	0	AGCAGTGAT	TGAGG	GAGTGAGGA	X	X
3	3	0	ACCAAGGTC	ACACT	GAGTGAGGA	X	X
3	3	0	AGCCCCTTC	CTAGAG	GAGTGAGGA	X	X
3	3	0	CTCAGTGTC	TAAGCA	GAGTGAGGA	X	X
3	3	0	AGTTGCTTC	CTGAG	GAGTGAGGA	X	X
3	3	0	AAGAGAGTC	TGAAA	GAGTGAGGA	X	X
3	3	0	GGCAGTGTC	GTCACC	GAGTGAGGA	X	X
3	3	0	TGCAGAGTT	GGGTCA	GAGTGAGGA	X	X

3	3	0	AGCCTCGTT	GCCAGA	GAGTGAGGA	X	X
3	3	0	ATCATCTTC	AAGTAA	GAGTGAGGA	X	X
3	3	0	AGTAGTGTG	TGAAGG	GAGTGAGGA	X	X
3	3	0	AGCCTCGTG	TCCTCA	GAGTGAGGA	X	X
3	3	0	AAAAGCGTT	TGGGAA	GAGTGAGGA	X	X
3	3	0	ACTAGAGTC	CCCCAA	GAGTGAGGA	X	X
3	3	0	GGCGGCGGC	GAAGG	GAGTGAGGA	X	X
3	3	0	ATGAGAGTC	CTGGG	GAGTGAGGA	X	X
3	3	0	AGCACAGTG	GCCTGA	GAGTGAGGA	X	X
3	3	0	TACAGGGTC	CTCGGT	GAGTGAGGA	X	X
3	3	0	AGCAGAGGT	GCTGA	GAGTGAGGA	X	X
3	3	0	GGAAGAGTC	CAGGG	GAGTGAGGA	X	X
3	3	0	GGAAGAGTC	CAGGG	GAGTGAGGA	X	X
3	3	0	AGTGGGGTC	TGTTGG	GAGTGAGGA	X	X
3	3	0	ATGAGGGTC	ACTGAG	GAGTGAGGA	X	X
3	3	0	GTCAGAGTC	CTAGG	GAGTGAGGA	X	X
3	3	0	GCCAGGGTC	TGGGAG	GAGTGAGGA	X	X
3	3	0	AGCAACTCC	ATCTT	GAGTGAGGA	X	X
3	3	0	AGGGGAGTC	GACAG	GAGTGAGGA	X	X
3	3	0	GTCAGGGTC	ATCAG	GAGTGAGGA	X	X
3	3	0	GTCAGGGTC	ATCAG	GAGTGAGGA	X	X
3	3	0	AGCATAGTA	GTTAA	GAGTGAGGA	X	X
3	3	0	GTCAGAGTC	CAAAA	GAGTGAGGA	X	X
3	3	0	GGCAGTGTT	ACAAA	GAGTGAGGA	X	X
3	3	0	GCCATCGTC	ACCCA	GAGTGAGGA	X	X
3	3	0	CTCAGTGTC	GAGAGA	GAGTGAGGA	X	X
3	3	0	GGAAGAGTC	AAGGGA	GAGTGAGGA	X	X
3	3	0	AGCAACTCC	AGAAGA	GAGTGAGGA	X	X
3	3	0	AGCCTCGGC	GGCCCT	GAGTGAGGA	X	X
3	3	0	GACAGGGTC	ACTTTA	GAGTGAGGA	X	X
3	3	0	AGAATAGTC	CTGGG	GAGTGAGGA	X	X
3	3	0	AGTAGAGTA	GTAAAG	GAGTGAGGA	X	X
3	3	0	GGGAGGGTC	GGTCAG	GAGTGAGGA	X	X
3	3	0	AACAGGGTT	ATCCA	GAGTGAGGA	X	X
3	3	0	GCCAGGGTC	ACCCA	GAGTGAGGA	X	X
3	3	0	GGAAGAGTC	TTACCT	GAGTGAGGA	X	X
3	3	0	AGTGGAGTC	ACCGTA	GAGTGAGGA	X	X
3	3	0	GCCAGAGTC	ACCCTT	GAGTGAGGA	X	X
3	3	0	GGCAGTGTA	ACTTAA	GAGTGAGGA	X	X
3	3	0	CTCAGTGTC	GTTGT	GAGTGAGGA	X	X
3	3	0	AGATGGGTC	TACAGA	GAGTGAGGA	X	X
3	3	0	GCCAGAGTC	TGAGTG	GAGTGAGGA	X	X
3	3	0	AGTAGGGTT	TGAAT	GAGTGAGGA	X	X
3	3	0	CACTGCGTC	CTTGGT	GAGTGAGGA	X	X
3	3	0	AACTGGGTC	CCTGAG	GAGTGAGGA	X	X
3	3	0	AGTAACATC	AGTAGT	GAGTGAGGA	X	X
3	3	0	GACAGAGTC	CACAGA	GAGTGAGGA	X	X
3	3	0	ATCAGGTTT	CAATA	GAGTGAGGA	X	X
3	3	0	AGCATGGTA	GTGGG	GAGTGAGGA	X	X
3	3	0	AGCAACTGC	CCTTCT	GAGTGAGGA	X	X
3	3	0	GGCTGAGTC	TTGCAG	GAGTGAGGA	X	X
3	3	0	AGCAGCCCA	GGGGGT	GAGTGAGGA	X	X
3	3	0	AGCAAAGTG	TCAAT	GAGTGAGGA	X	X

3	3	0	AGAAAAGTC	CACAGG	GAGTGAGGA	X	X
3	3	0	AACAAC TTC	TCCTG	GAGTGAGGA	X	X
3	3	0	TGCGGAGTC	CCTGGG	GAGTGAGGA	X	X
3	3	0	AGAATGGTC	TCTGAT	GAGTGAGGA	X	X
3	3	0	AGCAGCAGA	ACAAC T	GAGTGAGGA	X	X
3	3	0	AGCAGCAGA	TATTG	GAGTGAGGA	X	X
3	3	0	AGTTGCTTC	TTCTAA	GAGTGAGGA	X	X
3	3	0	GACAGGGTC	CTGGA	GAGTGAGGA	X	X
3	3	0	GGAAGAGTC	CGGGG	GAGTGAGGA	X	X
3	3	0	GGAAGAGTC	CAAAG	GAGTGAGGA	X	X
3	3	0	AGGGGGGTC	AAGAGT	GAGTGAGGA	X	X
3	3	0	AACAAC TTC	CATGT	GAGTGAGGA	X	X
3	3	0	ACCAAGGTC	AGCAGG	GAGTGAGGA	X	X
3	3	0	GGCCACGTC	GCACAG	GAGTGAGGA	X	X
3	3	0	AGCAAGGTT	AGGAAG	GAGTGAGGA	X	X
3	3	0	AGTAGGGTT	GGAGGG	GAGTGAGGA	X	X
4	0	4	AGCAGCGTC	ACAAAA	TAGCAAGGT	X	X
4	0	4	AGCAGCGTC	AAGGG	GAGACAAGT	X	X
4	0	4	AGCAGCGTC	CGTCCC	GAGAGGCGC	X	X
4	1	3	AGCAGCGGC	CTAGC	GGGTGAGTC	X	X
4	1	3	AGCAGCGTT	GCTAT	GAGAAAGGT	X	X
4	1	3	AGCAACGTC	ATGTGC	TGGGGAGGA	X	X
4	1	3	AGCAGCGGC	CGGAG	AAGTGTGGG	X	X
4	1	3	AGCAACGTC	TGTTT	GTGTAAGGC	X	X
4	1	3	AGCAACGTC	ACCTG	GAGTCACGC	X	X
4	1	3	AGCAGTGTC	ATGATG	GTGTGTGAA	X	X
4	1	3	AGCAGCGGC	CACATA	GTGTGTGAA	X	X
4	1	3	AGCAACGTC	CAGTCC	AAGTGTGGC	X	X
4	1	3	AGCAACGTC	GGATGC	AGGTGAGCA	X	X
4	1	3	ATCAGCGTC	CAGATG	GTGTGAGTC	X	X
4	1	3	AGCAACGTC	CTTAC	TAGTGAATA	X	X
4	1	3	AGCAACGTC	GTGAC	GTGCGATGA	X	X
4	1	3	AGCAGTGTC	TGTCTG	GAGTGTTGC	X	X
4	1	3	AGCAGCGTT	GTTTTG	ATGTGAGGC	X	X
4	1	3	AGCAACGTC	TGTGT	GAGTGACAG	X	X
4	1	3	AGCACCGTC	TGCCG	GTGTGCGGT	X	X
4	1	3	AGCAACGTC	CAGTCC	AAGTGTGGC	X	X
4	2	2	AGCATTGTC	TTGTGG	GAGTAAGGC	X	X
4	2	2	AGCAGCGAT	GGGGTT	GAGTGAGAC	X	X
4	2	2	AGCTGTGTC	ATCCAT	GAGTGAGTC	X	X
4	2	2	AGCATGGTC	AAGTTC	TAGTGAGGG	X	X
4	2	2	AGCATGGTC	AAGTTC	TAGTGAGGG	X	X
4	2	2	AGCATCTTC	ATATG	GAGTGAGAG	X	X
4	2	2	AGCATGGTC	AGGTTC	TAGTGAGGG	X	X
4	2	2	AGCATAGTC	AAGGG	GAGTGAGAG	X	X
4	2	2	AGCATGGTC	TCTTTC	TAGTGAGGG	X	X
4	2	2	AGCATGGTC	AGGTTC	TAGTGAGGG	X	X
4	2	2	AGCATAGTC	TTTATT	GAGTGAGAG	X	X
4	2	2	AGCAAAGTC	CTGAAG	GAGTGAGAG	X	X
4	2	2	AGCAGCGCA	AAGCAC	GTGTGAGGC	X	X
4	2	2	ATCAACGTC	TGGAC	TAGTGAGGG	X	X
4	2	2	AGTAGTGTC	CACAG	AAGTGAGGG	X	X
4	2	2	AGCAAAGTC	CCTTG	GAGTGAGTG	X	X

4	2	2	AGCCACGTC	TATGCT	TTGTGAGGA	X	X
4	2	2	AGCATGGTC	GGGTTC	TAGTGAGGG	X	X
4	2	2	AGCAGAGTT	GGGAAA	AAGTGAGGG	X	X
4	2	2	AGCATTGTC	ACTGT	GAGTGAGAG	X	X
4	2	2	AGCATGGTC	AGGTTC	TAGTGAGGG	X	X
4	2	2	AGCATGGTC	AGGTTC	TAGTGAGGG	X	X
4	2	2	AGCATGGTC	TAGCA	GAGTGAGTC	X	X
4	2	2	AGCTGTGTC	ATCCAT	GAGTGAGTC	X	X
4	2	2	AGTAGAGTC	TGGGTG	GAGTGAGAC	X	X
4	2	2	AGCATGGTC	AGGTTC	TAGTGAGGG	X	X
4	2	2	AGCTGTGTC	CAGGAG	GAGTGAGTC	X	X
4	2	2	AGCAACTTC	TGATC	TAGTGAGGT	X	X
4	2	2	AGCTGAGTC	AACCT	GAGTAAGGG	X	X
4	2	2	AGTAGGGTC	ATCAG	AAGTGAGGT	X	X
4	2	2	AGCTGTGTC	ACCTT	GAGTGAGTC	X	X
4	2	2	AGCAACATC	TGGAA	GAGTGAGAG	X	X
4	2	2	AGCATCGTG	TTTGA	AAGTGAGGC	X	X
4	2	2	AGCATGGTC	AGGTTC	TAGTGAGGG	X	X
4	2	2	AGCAACTTC	AGGGG	AAGTGAGGG	X	X
4	2	2	AGCATGGTC	AGATTA	TAGTGAGGG	X	X
4	2	2	AGCATGGTC	CGTGTC	TAGTGAGGG	X	X
4	2	2	AGCAAGGTC	ACCTGA	GAGTGAGAG	X	X
4	2	2	AGCATGGTC	AAGTTC	TAGTGAGGG	X	X
4	2	2	AGCAGGGTA	TAGGG	GAGTGAGAT	X	X
4	2	2	GGCAGAGTC	CAAGCA	GAGTGAGAG	X	X
4	2	2	AGTAACGTC	AAAGGT	GAGTGAAAA	X	X
4	2	2	AGCATGGTC	AATTTC	TAGTGAGGG	X	X
4	2	2	AGCAGTGTG	GAGTG	GAGTGAGAG	X	X
4	2	2	AGCACCATC	CCCAT	GAGTGAGTC	X	X
4	2	2	AGCAACGTG	AGACAG	TAGTGAGAA	X	X
4	2	2	AGCAACGGC	CCTGGG	CAGTGAGGG	X	X
4	2	2	AGTAGAGTC	ATGGA	GAGTGAGAG	X	X
4	2	2	GGCACCGTC	GCTGA	GAGTGAGTC	X	X
4	2	2	AGCATGGTC	AGGTTC	TAGTGAGGG	X	X
4	2	2	AGCATAGTC	AGGTTC	TAGTGAGGG	X	X
4	2	2	AGTAACGTC	TCCCT	GAGTGTGGG	X	X
4	3	1	AGCATAGTG	GTTAG	GAGTGAGGG	X	X
4	3	1	ATCAGGGTG	GGTAG	GAGTGAGGC	X	X
4	3	1	TACAGAGTC	TCCAG	GAGTGAGGG	X	X
4	3	1	ATGAGGGTC	TCATA	GAGTGAGGT	X	X
4	3	1	AGCAAATTC	TTCAG	GAGTGAGGT	X	X
4	3	1	AGCAAAGTG	CTCAA	GAGTGAGGC	X	X
4	3	1	ATAAGTGTC	ATTGAA	GAGTGAGGC	X	X
4	3	1	AGTAGTCTC	TTGAT	GAGTGAGGG	X	X
4	3	1	CGCAGCAAC	AGCGGT	GAGTGAGGG	X	X
4	3	1	AGCAATGTG	TGCTT	GAGTGAGGC	X	X
4	3	1	ACCAAAGTC	TTTGAT	GAGTGAGGG	X	X
4	3	1	AGTAGTGTT	TCAAGA	GAGTGAGGC	X	X
4	3	1	AGCATAGTG	GGGTAG	GAGTGAGGG	X	X
4	3	1	ATCACCATC	CTAAGT	GAGTGAGGG	X	X
4	3	1	AGAATCGTT	TGAAA	GAGTGAGGG	X	X
4	3	1	AGTAACATC	GGAAAA	GAGTGAGGT	X	X
4	3	1	AGGACAGTC	AGTTG	GAGTGAGGT	X	X

4	3	1	GGCAGTGTT	GACAG	GAGTGAGGC	X	X
4	3	1	AGTTGTGTC	GTTTT	GAGTGAGGT	X	X
4	3	1	CCCACCGTC	CCGCCC	GAGTGAGGG	X	X
4	3	1	AGTACCGGC	TTCACA	GAGTGAGGT	X	X
4	3	1	AGCAACTTT	GGAATG	GAGTGAGGG	X	X
4	3	1	AGCAAGGGC	AGTGA	GAGTGAGGC	X	X
4	3	1	GTCAGGGTC	ATAAGA	GAGTGAGGC	X	X
4	3	1	AGGAAAGTC	TAACA	GAGTGAGGT	X	X
4	3	1	CACAGTGTC	AGGCT	GAGTGAGGT	X	X
4	3	1	GTCAGTGTC	CAAGAA	GAGTGAGGT	X	X
4	3	1	ATCACCATC	CAGAGA	GAGTGAGGG	X	X
4	3	1	ATCAACATC	TTTGG	GAGTGAGGC	X	X
4	3	1	CCGAGCGTC	TGAAA	GAGTGAGGT	X	X
4	3	1	AGCACAGTG	AGCACT	GAGTGAGGG	X	X
4	3	1	AACATTGTC	TAAGG	GAGTGAGGT	X	X
4	3	1	AACATTGTC	TAAGG	GAGTGAGGT	X	X
4	3	1	AACATTGTC	TAAGG	GAGTGAGGT	X	X
4	3	1	AGTACCGGC	ATCCAT	GAGTGAGGT	X	X
4	3	1	AGTACAGTC	TCTGTT	GAGTGAGAA	X	X
4	3	1	AACAACATC	ACGGG	GAGTGAGGT	X	X
4	3	1	TCCCGCGTC	CGGGAA	GAGTGAGGT	X	X
4	3	1	AGGGGAGTC	AGATGC	GAGTGAGGG	X	X
4	3	1	AGTAGCTGC	GGCCA	GAGTGAGGC	X	X
4	3	1	GGAAGGGTC	AGTGC	GAGTGAGGG	X	X
4	3	1	GGAAGGGTC	AGTGC	GAGTGAGGG	X	X
4	3	1	GGAAGGGTC	AGTGC	GAGTGAGGG	X	X
4	3	1	GGAAGGGTC	AGTGC	GAGTGAGGG	X	X
4	3	1	GGAAGGGTC	AGTGC	GAGTGAGGG	X	X
4	3	1	GGAAGGGTC	AGTGC	GAGTGAGGG	X	X
4	3	1	GGAAGGGTC	AGTGC	GAGTGAGGG	X	X
4	3	1	CTCAGTGTC	TCCCA	GAGTGAGGC	X	X
4	3	1	AGTAAAGTC	ACAAG	GAGTGAGGT	X	X
4	3	1	AACGGGGTC	TGGGA	GAGTGAGGT	X	X
4	3	1	GGGAGGGTC	CCCAT	GAGTGAGGG	X	X
4	3	1	GGCAGGGTT	AAGATT	GAGTGAGGC	X	X
4	3	1	AGGGGAGTC	TGAGGG	GAGTGAGGG	X	X
4	3	1	AACAATGTC	ATGTT	GAGTGAGGG	X	X
4	3	1	AGCTTGGTC	TGGCT	GAGTGAGGT	X	X
4	3	1	ATGAGGGTC	TCATA	GAGTGAGGT	X	X
4	3	1	GCCAGTGTC	TCTTAG	GAGTGAGGT	X	X
4	3	1	ATCACAGTC	TCTGG	GAGTGAGGC	X	X
4	3	1	GACAGGGTC	TTAAT	GAGTGAGGC	X	X
4	3	1	AGCCTTGTC	GTA ACT	GAGTGAGGT	X	X
4	3	1	GGCAGCGGT	GTTCA	GAGTGAGGG	X	X
4	3	1	TCCAGTGTC	TATGG	GAGTGAGGC	X	X
4	3	1	AGCAGCTGT	GATGT	GAGTGAGGG	X	X
4	3	1	AGCAGCTCA	CATGG	GAGTGAGGT	X	X
4	3	1	GGCAACGGC	ACACA	GAGGGAGGA	X	X
4	3	1	AGCTGAGTT	AAGCA	GAGTGAGGT	X	X
4	3	1	AGCAGCACA	AAGCTG	GAGTGAGGG	X	X
4	3	1	AGCAACCTT	GAGAT	GAGTGAGGC	X	X
4	3	1	AGCAAATTC	GGGCCC	GAGTGAGGT	X	X
4	3	1	AGACGGGTC	GGCCC	GAGTGAGGT	X	X
4	3	1	GCCAGAGTC	TGCACA	GAGTGAGGG	X	X

4	3	1	AGCAACAGC	ATTTGG	GAGTGAGGG	X	X		
4	3	1	AACCGAGTC	ACTCAA	GAGTGAGGG	X	X		
4	3	1	AGCAGCTCA	CCAGCA	GAGTGAGGT	X	X		
4	3	1	GGAAGGGTC	CTGTGT	GAGTGAGGG	X	X		
4	3	1	AGAACGGTC	CAGCA	GAGTGAGGC	X	X		
4	3	1	AGCAAGGTA	AGGAA	AAGTGAGGA	X	X		
4	3	1	AGAATGGTC	AGTGGG	GAGTGAGGG	X	X		
4	3	1	AGAATGGTC	CAAAT	GAGTGAGGG	X	X		
4	3	1	AGCAAGGGC	TCCGT	GAGTGAGGG	X	X		
4	3	1	TGCTGAGTC	TCCATG	GAGTGAGGG	X	X		
4	3	1	AGCATTGTT	TCTGGG	GAGTGAGGG	X	X		
4	3	1	AGCATTGTG	GTGAG	GAGTGAGGG	X	X		
4	3	1	GCTAGCGTC	CATGG	GAGTGAGGC	X	X		
4	3	1	AGCAACTTT	CCACTG	GAGTGAGGC	X	X		
4	3	1	AGTAGGGTT	GGTGG	GAGTGAGGG	X	X		
4	3	1	GGCAGTGTT	TCCCAG	GAGTGAGGC	X	X		
4	3	1	AACTGAGTC	TCTGG	GAGTGAGGT	X	X		
4	3	1	AGCATTGTG	ATGAG	GAGTGAGGG	X	X		
4	3	1	AGCAAGGTT	TATGT	GAGTGAGCA	X	X		
4	3	1	GGCAACGTT	TGTAT	GAGTGAGGT	X	X		
4	3	1	AACAACCTC	GCCTAT	GAGTGAGGG	X	X		
4	3	1	AGGGACGTC	CAAGG	GAGTGAGGG	X	X		
4	3	1	TCCAGTGTC	ACATCA	GAGTGAGGC	X	X		
4	3	1	AGCATGGTT	GGAGTA	GAGTGAGGG	X	X		
4	3	1	AATAGGGTC	AAAAT	GAGTGAGGT	X	X		
4	3	1	AGTATAGTC	TTTAGG	GAGTGAGGC	X	X		
4	3	1	TGCAATGTC	CTTGG	GAGTGAGGC	X	X		
4	3	1	AGCTACATC	TACAGG	GAGTGAGGG	X	X		
4	3	1	AGCAAAGTA	AAGAGA	GAGTGAGGC	X	X		
4	4	0	CACCCCGTC	TACCTG	GAGTGAGGA	X	X		
4	4	0	AGGCACGTT	AGGCA	GAGTGAGGA	X	X		
4	4	0	CACCCCGTC	GACGTC	GAGTGAGGA	X	X		
4	4	0	GCAAGAGTC	TGGCT	GAGTGAGGA	X	X		
4	4	0	AGTGCAGTC	CCTTA	GAGTGAGGA	X	X		
4	4	0	ATCCACGTT	ATGCTG	GAGTGAGGA	X	X		
4	4	0	ATCCACGTT	TTGGG	GAGTGAGGA	X	X		
3	1	2	AGCAGCTTC	TGCCAT	GAGTGAAGT	X		X	
3	1	2	AGCAGGGTC	TGCAGT	GAGAGAGGC	X		X	
3	1	2	AGCAGCTTC	CAGGA	GAGTGAAGT	X		X	
3	1	2	AGCAGGGTC	TGTTTT	GAGTGAGTT	X		X	
4	3	1	AGCAACTGC	ATTTT	GAGTGAGGG	X		X	
4	3	1	AGCAACTGC	ATCTT	GAGTGAGGG	X		X	
3	1	2	AGCAGCTTC	CCAAAA	ATGTGAGGA	X			X
3	3	0	AGGTGCCTC	CCCATG	GAGTGAGGA	X			X
5	3	2	AGCTCAGTC	CACAG	GAGTGAGTC	X			X
2	1	1	AGCAGCGTG	CAGAA	GAGAGAGGA	X			
2	1	1	AGCAGCGTG	GATGGA	GAGAGAGGA	X			
2	1	1	AGCAGCGTG	GATGGA	GAGAGAGGA	X			
2	1	1	AGCAGCGTG	GATGGA	GAGAGAGGA	X			
2	1	1	AGCAGCCTC	TGCCAG	GGGTGAGGA	X			
2	1	1	AGCAGCCTC	CCATA	GAGGGAGGA	X			
2	1	1	AGGAGCGTC	CCTTGG	GAGTGATGA	X			
2	1	1	AGCAGCGAC	AGCCA	GAGTGACGA	X			

2	1	1	AGCTGCGTC	CTGTA	GCGTGAGGA	X
2	1	1	AGCAGGGTC	TGCCT	GAGTCAGGA	X
2	1	1	AGCAGCATC	TGGGA	GAATGAGGA	X
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2	1	1	AGCAGCGTG	GATGGA	GAGAGAGGA	X
2	1	1	AGCAGCATC	ACAGAC	GCGTGAGGA	X
2	1	1	ACCAGCGTC	TGCTTT	GGGTGAGGA	X
2	1	1	AGCAGGGTC	ATTGA	GAATGAGGA	X
2	2	0	AGGAGCGAC	GGGGG	GAGTGAGGA	X
2	2	0	AGGAGCGAC	GGGGG	GAGTGAGGA	X
2	2	0	AGGAGCGAC	GGGGG	GAGTGAGGA	X
2	2	0	AGGAGCGAC	GGGGG	GAGTGAGGA	X
2	2	0	AGGAGCGAC	GGGGG	GAGTGAGGA	X
2	2	0	AGGAGCGAC	GGGGG	GAGTGAGGA	X
2	2	0	AGGAGCGAC	GGGGG	GAGTGAGGA	X
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2	2	0	AGGAGCGAC	GGGGG	GAGTGAGGA	X
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3	2	1	ATCAGAGTC	AGAGA	AAGTGAGGA	X
3	2	1	AGCAGTGGC	AGAAT	AAGTGAGGA	X
3	2	1	AGGAGTGTC	TGCAA	AAGTGAGGA	X
3	2	1	TGCAGGGTC	AAGCC	AAGTGAGGA	X
3	2	1	AGCAGGTTC	AGTGTC	TAGTGAGGA	X
3	2	1	AGCAGCGGA	AATAA	GGGTGAGGA	X
3	2	1	AGCAGGGTG	CTCGG	GAGGGAGGA	X
3	2	1	AGCAACCTC	CCCACA	GAGGGAGGA	X
3	2	1	AGCAGGGTG	GGGGA	GAGGGAGGA	X
3	2	1	AGCAACCTC	TGCTCA	GAGAGAGGA	X
3	2	1	TGCAGGGTC	TGCGG	AAGTGAGGA	X
3	2	1	AGCAGGTTC	AGACTG	AAGTGAGGA	X
3	2	1	AGCAATGTC	ACCAT	GAGTGTGGA	X
3	2	1	AGCACGGTC	CCCAAG	GAGGGAGGA	X
3	2	1	AGCAGCGCT	CGGGC	GAGCGAGGA	X
3	2	1	AGCAGGGAC	TGGTCA	GAGTGAGGT	X
3	2	1	AGCAGCCAC	ACAATC	CAGTGAGGA	X
3	2	1	AGTAGAGTC	AAGAGG	GAGTGAGTA	X
3	2	1	AGCCTCGTC	TTGGT	GAGGGAGGA	X
3	2	1	GGCAGCGGC	CTGGAG	GGGTGAGGA	X
3	2	1	AGCAGAGTT	GGTTTC	TAGTGAGGA	X
3	2	1	AGCATCTTC	ACCTG	AAGTGAGGA	X
3	2	1	AGCAACATC	ATAAT	GAGTGGGGA	X
3	2	1	AGCACAGTC	CCTAA	GAGTGAGCA	X
3	3	0	AGGAGTTTC	CAGTT	GAGTGAGGA	X
3	3	0	GGCAGCAGC	CATCA	GAGTGAGGA	X
3	3	0	AGCAGGTTG	TTGGAG	GAGTGAGGA	X
3	3	0	AACAGTGCC	CTGGT	GAGTGAGGA	X

3	3	0	TGGAGCGTG	GGGGGA	GAGTGAGGA	X
3	3	0	TGGAGCGTG	GAAGAG	GAGTGAGGA	X
3	3	0	AGCTGAGGC	ACAGG	GAGTGAGGA	X
3	3	0	TGCAGGGTG	GACCCA	GAGTGAGGA	X
3	3	0	AACAGAGTG	AGGCT	GAGTGAGGA	X
3	3	0	AGCAACTTA	TTGCT	GAGTGAGGA	X
3	3	0	AGCACAATC	TTTTTG	GAGTGAGGA	X
3	3	0	TGGAGGGTC	GGTGGA	GAGTGAGGA	X
3	3	0	AGCCGTGTG	GCTACG	GAGTGAGGA	X
3	3	0	TGCTGCTTC	TGCCGT	GAGTGAGGA	X
3	3	0	AACAGAGTA	ACACA	GAGTGAGGA	X
3	3	0	ACCAACTTC	ATGTA	GAGTGAGGA	X
3	3	0	AGGAGAGTG	AGTGT	GAGTGAGGA	X
3	3	0	GGCAGGGTG	GCGAAG	GAGTGAGGA	X
3	3	0	GGCAGGGTG	GCCGGG	GAGTGAGGA	X
3	3	0	AGCAGGGCT	CCTGGT	GAGTGAGGA	X
3	3	0	TACAGTGTC	AGCAGT	GAGTGAGGA	X
3	3	0	ATCACCTTC	TTTCAT	GAGTGAGGA	X
3	3	0	TTCAGTGTC	TGACGG	GAGTGAGGA	X
3	3	0	AGCAGCTCA	GGTTAG	GAGTGAGGA	X
3	3	0	AGGAGAGTA	GGGCT	GAGTGAGGA	X
3	3	0	ACCTGGGTC	TGAGCA	GAGTGAGGA	X
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3	3	0	GGCAGGGTG	CGAGG	GAGTGAGGA	X
3	3	0	AGGAGAGTG	AATGT	GAGTGAGGA	X
3	3	0	AGCAGTGCA	CCCAA	GAGTGAGGA	X
3	3	0	AGCAGGTTG	AAGACT	GAGTGAGGA	X
3	3	0	AGGAGAGTG	AGAAGT	GAGTGAGGA	X
3	3	0	AGCAGCCGT	AACAAA	GAGTGAGGA	X
3	3	0	AGCAGGGCA	GGGCA	GAGTGAGGA	X
3	3	0	GCCAGCCTC	AGGCT	GAGTGAGGA	X
3	3	0	AGCAGGGCT	TGGTGG	GAGTGAGGA	X
3	3	0	AGTAGCAAC	TATTA	GAGTGAGGA	X
3	3	0	AACAGCGGA	GATTT	GAGTGAGGA	X
3	3	0	AGGACCATC	CGAGA	GAGTGAGGA	X
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3	3	0	AGGACCATC	CCAGG	GAGTGAGGA	X
3	3	0	AGGACCATC	CCAGG	GAGTGAGGA	X
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3	3	0	TGCAGGGTG	AGCCT	GAGTGAGGA	X
3	3	0	AGAAGGGTA	GAAAG	GAGTGAGGA	X
3	3	0	AGATGCGGC	CAGTA	GAGTGAGGA	X
3	3	0	AATAGGGTC	AGGTAG	GAGTGAGGA	X
3	3	0	AGCAGTGAA	GGTGG	GAGTGAGGA	X
3	3	0	AGAAACGTG	GAAAA	GAGTGAGGA	X
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3	3	0	AGCAAGGAC	TTAAA	GAGTGAGGA	X
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3	3	0	GGCAGTGCC	AGTGG	GAGTGAGGA	X

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3	3	0	TGCAGGGTG	TAGTG	GAGTGAGGA	X
3	3	0	AGGAGGTTC	TGGGAG	GAGTGAGGA	X
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3	3	0	AGTAGCTGC	CTTTGG	GAGTGAGGA	X
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3	3	0	GGCAGGGTG	GGGGT	GAGTGAGGA	X
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3	3	0	TGGAGCGTG	GGAGGA	GAGTGAGGA	X
3	3	0	TCCAGGGTC	ACTAAT	GAGTGAGGA	X
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3	3	0	AGCAGGTTG	GGGAA	GAGTGAGGA	X
3	3	0	AGCTGAGGC	TGGCA	GAGTGAGGA	X
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3	3	0	GGCAGTGCC	TGAAGG	GAGTGAGGA	X
3	3	0	GGCAGTGCC	TGAAGG	GAGTGAGGA	X
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3	3	0	TGAAGAGTC	CAAGG	GAGTGAGGA	X
3	3	0	ACGAGGGTC	CATAG	GAGTGAGGA	X
3	3	0	AGAAGCGGT	GGAGT	GAGTGAGGA	X
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4	1	3	AGCAGCGGC	TGTGG	CAGTGTGGT	X
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4	1	3	AGCAGCGGC	TCCCAG	GAGAGGGGC	X
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4	2	2	AGCCGTGTC	CCCTT	AAGTGAGGG	X
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4	2	2	AGCATAGTC	ACTTA	GAGTGTGGG	X
4	2	2	AGCATGGTC	AGGTTC	CAGTGAGGG	X
4	2	2	TCCAGCGTC	GTGACA	GAGTGAGAC	X
4	2	2	AGCACTGTC	CTGTCA	GAGTGTGGC	X
4	2	2	AGCATAGTC	CAGTT	CAGTGAGGC	X
4	2	2	AGCAGTGTG	CACCAC	GAGAGAGGC	X
4	2	2	AGCAACGGC	AGGAGA	GAGAGGGGA	X
4	2	2	AGCCGGGTC	ACCGA	GAGTGAGTG	X
4	2	2	AGCAATGTC	AATTTT	CAGTGAGCA	X
4	2	2	AGCAACGTG	TGGAG	CAGTGAGGG	X
4	2	2	AGCACGGTC	AGTCTT	CAGTGAGGG	X
4	2	2	AGCATGGTC	ATGTTA	TAGTGAGTA	X
4	2	2	AGCAGGGTA	GGGAG	GAGTGAGTG	X
4	2	2	AGCGGTGTC	TGAAAA	AAGTGAGGG	X
4	2	2	AGCAAGGTC	CATCCA	GAGAGAGGC	X
4	2	2	AGCACCTTC	TAGGGA	GTGTGAGGC	X
4	2	2	AGCAAAGTC	TCACAG	GAGGGAGGC	X
4	2	2	AGCAAGGTC	TGGGA	GAGTGATGT	X
4	2	2	AGCAGCAGC	TGCCGG	GAGCGAGGC	X
4	2	2	AGCAACCTC	CTGGG	GAGTGTGGG	X
4	2	2	TGCAGCGAC	TGAAGT	GAGTGAGTG	X
4	2	2	GGCAGCTTC	CCAGT	GAGTAAGGT	X
4	2	2	AACAGTGTC	AGTGAT	TAGTGAGGG	X
4	2	2	AGCTTCGTC	CAGAG	CAGTGAGGG	X
4	2	2	AGCAGCATT	GACAT	GAGTGAGAT	X
4	2	2	AGCAACGTG	ATGAAA	GAGTGAGAT	X
4	2	2	AGCAATGTC	AGTCTC	AAGTGTGGA	X
4	2	2	TGCAGTGTC	CCTGG	GAGGGAGGT	X
4	2	2	AGCAACGGC	CAGTCC	CAGGGAGGA	X
4	2	2	AGCATCGGC	TCCTC	AAGTGAGGC	X
4	2	2	AGCATCGGC	TCCTC	AAGTGAGGC	X
4	2	2	AGCATCGGC	TCCTC	AAGTGAGGC	X
4	2	2	AGCAAGGTC	AGAGA	GTGTGAGGC	X
4	2	2	AGCGGAGTC	CAGAG	AAGTGAGGG	X
4	2	2	AGCACCATC	AGCAC	CAGTGAGGT	X
4	2	2	AGCTGCTTC	CCCTA	GAGTGAGAG	X
4	2	2	AGCAACATC	ACTTT	GAGTAAGGC	X
4	2	2	AACAGTGTC	AAATC	AAGTGAGGT	X
4	2	2	AGCATCGTA	CCTCAA	GAGACAGGA	X
4	2	2	AGCATGGTC	GGTTTC	CAGTGAGGG	X
4	2	2	AACAGCTTC	CCAGCT	TAGTGAGGC	X
4	2	2	AGCAACTTC	CCTGGA	GGGTGAGGG	X
4	2	2	AGCAGCATT	GACAT	GAGTGAGAT	X
4	2	2	AGCAGGGTG	GGGTGT	GAGGGAGGC	X
4	2	2	AGCATTGTC	TGAAG	GAGAGGGGA	X
4	2	2	GGCAGCGTG	TGTGA	GAGTGAGCT	X
4	2	2	AGCTGTGTC	CCCCA	GAGTGAGAG	X
4	2	2	AGCAGCATT	CATGT	GAGTGAGAT	X
4	2	2	AGCAGTGTT	TCTCT	GAGTGTGGC	X
4	2	2	AGCACAGTC	ACCCA	TAGTGAGGC	X

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4	2	2	AGCATTGTC	ATAATA	GAGAGAGGT	X
4	2	2	AGCATGGTC	ATGGA	AAGTGAGTA	X
4	2	2	AGCAGGGTG	GTAAA	GAGGGAGGT	X
4	2	2	AGCAACTTC	TCCAC	TAGTGAGGG	X
4	2	2	AGCAGCAGC	CGGTG	GTGTGAGGC	X
4	2	2	TGCAGGGTC	TCTTA	GAGTGAGTT	X
4	2	2	TGCAGCGTT	GGGCT	CAGTGAGGG	X
4	2	2	AGCAGCATA	TAATA	GAGTGAGTC	X
4	2	2	AGCAGTGTG	CTAAG	GAGAGAGGC	X
4	2	2	AACAGCATC	TCAGCT	GGGTGAGGC	X
4	2	2	AGCAGTGTG	CCTTGG	GTGTGAGGG	X
4	2	2	AACAGAGTC	GTTCA	GTGTGAGGC	X
4	2	2	AGCAACGTT	AGCAG	GAGTGTGGT	X
4	2	2	AGCAAAGTC	TGTAAA	GAGTGTGTA	X
4	2	2	TGCATCGTC	CTATG	GAGGGAGGT	X
4	2	2	AGCAAGGTC	TTGTTG	GAGGGAGGG	X
4	2	2	GGCACCGTC	ATCCT	GAGTGGGGC	X
4	2	2	AGCAGAGTA	AGGGAG	GAGTGAGAG	X
4	2	2	AGCAAAGTC	ACAGG	GAGTGAGCG	X
4	2	2	AGAAGTGTC	ACTGTC	CAGTGAGGC	X
4	2	2	AGCAGCATT	GACAT	GAGTGAGAT	X
4	2	2	AGCAAAGTC	AGCCA	GAGGGAGAA	X
4	2	2	AGCAAAGTC	TGGAGT	GAGTGTGTA	X
4	2	2	GGCAGTGTC	CGGCT	GAGGGAGGG	X
4	2	2	AGCAGCAAC	AGTGT	GAGTGAGTT	X
4	2	2	AGCATTGTC	TAGCA	GGGTGAGAA	X
4	2	2	AGCAAGGTC	ACTGAG	GAGGGAGGC	X
4	2	2	AGCATCGGC	AGCTTG	GAGAGAGGT	X
4	2	2	AGCAGGGTG	GTAGGG	GAGGGAGGT	X
4	2	2	AGCAGCGCT	TCTCA	AAGTGAGGC	X
4	2	2	AGCAGGGTG	GTGTGA	GAGTGAGTG	X
4	2	2	TGCAGCGTG	GCCACA	GAGTGAGAC	X
4	2	2	TGCAGTGTC	ATTTGA	GAGTAAGGT	X
4	2	2	AGCAGGGTG	AGCACT	AAGTGAGGC	X
4	2	2	AACAGGGTC	AGTGGG	GAGAGAGGC	X
4	2	2	AACAGCGGC	CTATT	GTGTGAGGG	X
4	2	2	AGCAACGTT	CAGCT	CAGTGAGGT	X
4	2	2	AGCAGTGTT	GCCCCA	GGGTGAGGT	X
4	2	2	AGCACCGTG	TGGGGA	GAGGGAGGT	X
4	2	2	AGCAACGTT	CTGTG	GAATGAGCA	X
4	2	2	AGCCACGTC	GAATG	GATTGAGGG	X
4	2	2	AGCAGGGTG	GAGCGC	GAGGGAGGC	X
4	2	2	TGCAGCGGC	CTCAG	AAGTGAGGG	X
4	2	2	AGCATTGTC	TCCCTT	GAGTATGGA	X
4	2	2	GGCACCGTC	CTTTG	CAGTGAGGT	X
4	2	2	AGCATGGTC	GGGCAC	TAGTGAGGC	X
4	2	2	AGCACCTTC	ATGAAT	GTGTGAGGC	X
4	2	2	AGTAGTGTC	TAATAG	GTGTGAGGT	X
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4	2	2	AGCCACGTC	ACCTG	AGGTGAGGA	X
4	2	2	AGCAACATC	TGTGTA	GAGCGAGGT	X
4	2	2	AGCCGAGTC	CTTGT	GGGTGAGGC	X

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4	2	2	AGCAACGAC	GGGCT	GCGTGTGGA	X
4	2	2	AGCAGCATT	GACCT	GAGTGAGAT	X
4	2	2	AGCAGCATT	GACCT	GAGTGAGAT	X
4	2	2	CGCAGTGTC	TTCCC	CAGTGAGGC	X
4	2	2	TGCATCGTC	AGAGA	GTGTGAGGG	X
4	2	2	AGCTGAGTC	CCCGGC	AAGTGAGGC	X
4	2	2	AGCAACGTG	TGCCA	GTGTGAGGG	X
4	2	2	AGCAGTGGC	TGGGCA	TAGTGAGGC	X
4	2	2	AGCAGCATT	GACAT	GAGTGAGAT	X
4	2	2	AGCACCATC	TAGGCA	GAGGGAGGC	X
4	2	2	AGCACAGTC	ATGGTG	GAGTAAGGG	X
4	2	2	AGCATGGTC	AGGTTC	CAGTGAGGG	X
4	2	2	AGCATGGTC	AGGTTC	CAGTGAGGG	X
4	2	2	AGTAACGTC	ATTTCA	GAGTGCAGA	X
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4	2	2	AGCAGCATT	GACAT	GAGTGAGAT	X
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4	2	2	AGCAGCGAT	CTAAT	GAGGGAGAA	X
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4	2	2	AGCAACTTC	CACTA	GAGAGAGGC	X
4	2	2	AGCAACGTG	GCAGAT	GAGAGAGGT	X
4	2	2	AACAGCATC	AAATGC	GGGTGAGGC	X
4	2	2	ACAAGCGTC	TGTAA	GAGTGAGTC	X
4	2	2	TCCAGCGTC	ACCTA	AAGTGAGGG	X
4	2	2	AGCAAGGTC	AGGAA	GAGAGAGGC	X
4	2	2	AGTAGCGTT	TTGTC	CAGTGAGGT	X
4	2	2	AGCAGTGTT	TGCTAA	CAGTGAGGC	X
4	2	2	AGCATGGTC	AGGTTC	CAGTGAGGG	X
4	2	2	AGCAGCGGA	GGTCA	GAGTGAGTT	X
4	2	2	AGCACCGAC	TCCAT	CAGTGAGGT	X
4	2	2	AGCAGTGAC	ATGAG	GAGTGAGCC	X
4	2	2	AGCAGGGTT	TCTGCA	GTGTGAGGT	X
4	2	2	AGCAGCATG	GTTAG	GAGTGAGAT	X
4	2	2	ATCAGAGTC	AAAGG	GAGGGAGGC	X
4	2	2	AGCAGGGTT	GGAAGA	AAGTGAGGG	X
4	2	2	AGCAGGGTG	GGCAA	GAGGGAGGC	X
4	2	2	GGCAGTGTC	TCAAAC	GAGGGAGGG	X
4	2	2	GGCATCGTC	ACTCTT	GAGTGAGAG	X
4	2	2	AGCACCGTG	ACTTC	GAGGGAGGT	X
4	2	2	AGCAGAGTT	TAAAA	TAGTGAGGG	X
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4	3	1	AGGGGGGTC	TTGGGA	GAGTGAGGT	X
4	3	1	AGCCTGGTC	CGTGA	GTGTGAGGA	X
4	3	1	GGCAGCGAT	GAGATT	GAGTGAGGG	X
4	3	1	AACAAGGTC	ATAAA	GAGGGAGGA	X
4	3	1	AGCTGAGAC	TTAGA	GAGTGAGGT	X

4	3	1	AGCTGAGAC	TTAGA	GAGTGAGGT	X
4	3	1	GGCAGAGTG	GAGGAA	GAGTGAGGC	X
4	3	1	AGCTGGGTT	GGAGTG	GAGTGAGGG	X
4	3	1	AGCAAAGGC	TAAAGA	GTGTGAGGA	X
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4	3	1	AGCATTGTT	CTCAG	AAGTGAGGA	X
4	3	1	CACAGCATC	AGCAG	GAGTGAGGG	X
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4	3	1	AGCAGCACA	CAGGCC	GAGTGAGGT	X
4	3	1	AGCATTGCC	TTTTG	GAGTGAGGG	X
4	3	1	AGAAGTGCC	ATCTGG	GAGTGAGGG	X
4	3	1	ATCAGCATA	CAGGG	GAGTGAGGC	X
4	3	1	AGCAGGTAC	GTGCCT	GAGTGAGGC	X
4	3	1	AACTACGTC	CACCA	GAGTGGGGA	X
4	3	1	AGAAGTGCC	ATCTAG	GAGTGAGGG	X
4	3	1	AGGAGTCTC	ATACT	GAGTGAGGT	X
4	3	1	TCCAGCGGC	CACAG	GAGTGAGGT	X
4	3	1	AGCTCAGTC	TCCCA	GGGTGAGGA	X
4	3	1	AGCTCAGTC	TCTCA	GGGTGAGGA	X
4	3	1	AACAGTATC	TATTCT	GAGTGAGGC	X
4	3	1	GGAAGTGTC	TTACTG	GAGTGAGGT	X
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4	3	1	AACAGTGTT	TTGGCC	GAGTGAGGG	X
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4	3	1	AGCAGCTGT	AGGGA	GAGTGAGGT	X
4	3	1	AGCTGTGTG	ATCCT	GAGTGAGGG	X
4	3	1	AGGTGTGTC	TTTGGA	GAGTGAGGC	X
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4	3	1	AGCCGGCTC	GCGAGT	GAGTGAGGG	X
4	3	1	AGCACCAGC	CCGGGT	GAGTGAGGT	X
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4	3	1	AGCTCCTTC	GAGGA	GAGTGAGGC	X
4	3	1	AAGAGTGTC	CTGGTT	GAGTGAGGC	X
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4	3	1	AGGATCATC	CAGAGT	GAGTGAGGC	X
4	3	1	GTCTGCGTC	CGAAGG	GAGTGAGGG	X
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4	3	1	CCCAGGGTC	CACAGA	GAGTGAGGC	X
4	3	1	AGTACAGTC	CATTTG	GAGGGAGGA	X
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4	3	1	AGAAGTGCC	TCCTG	GAGTGAGGG	X
4	3	1	GGCAGAGTG	GATCA	GAGTGAGGC	X
4	3	1	AGCAGTTCC	TAAAA	GAGTGAGGG	X
4	3	1	GGCACTGTC	GCTCA	GAGTGAGGT	X
4	3	1	AGCAGGCAC	AGCCTG	GAGTGAGGC	X
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4	3	1	AGGACAGTC	GCAGA	GAGTGAGGC	X
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4	3	1	TGCTGTGTC	CCCAGT	GAGTGAGGG	X
4	3	1	GGCACAGTC	TGACA	GAGAGAGGA	X
4	3	1	AGCTCAGTC	TCACA	GGGTGAGGA	X
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4	3	1	AGCGGTTTC	AGTGA	GAGTGAGGC	X
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4	3	1	AGCCACCTC	CCCTGC	GAGTAAGGA	X
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4	3	1	AGCCGGGTA	GGGGAT	GAGTGAGGC	X
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4	3	1	ACCCGTGTC	ACAGTT	GAGTGAGGG	X
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4	3	1	AGAAACTTC	AAGAAG	GAGTGAGGT	X
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4	3	1	AGCAAAGTT	TAACAA	GAGTGAGAA	X
4	3	1	AGCAAAGTT	TAACAA	GAGTGAGAA	X
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4	3	1	AGCTGAGAC	TTAGA	GAGTGAGGT	X
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4	3	1	AGCAGCTCG	CTGAG	GAGTGAGGG	X
4	3	1	AGCTGAGAC	TTAGA	GAGTGAGGT	X
4	3	1	AGCAATGTG	AGTTGT	GAGTGAGGG	X
4	3	1	AGAAGCGGT	GCGTCT	GAGTGAGGT	X
4	3	1	AGAAGTGCC	ATCTGT	GAGTGAGGG	X
4	4	0	GGATGAGTC	TGGAG	GAGTGAGGA	X
4	4	0	ACAGGTGTC	CAAGAT	GAGTGAGGA	X
4	4	0	CTGGGCGTC	CCTCCA	GAGTGAGGA	X
4	4	0	CCCGGGGTC	TTCAGT	GAGTGAGGA	X
4	4	0	TGGCACGTC	TGAGG	GAGTGAGGA	X
4	4	0	AGCTCAGTA	CAAAAA	GAGTGAGGA	X
4	4	0	AAAAGGTTT	AGAGG	GAGTGAGGA	X
4	4	0	GACATCATC	AGAACT	GAGTGAGGA	X
4	4	0	AGCACTATT	CTATTA	GAGTGAGGA	X
4	4	0	CCCTGAGTC	TGAGG	GAGTGAGGA	X
4	4	0	TGGGGAGTC	AGTGC	GAGTGAGGA	X
4	4	0	AACAGGGCT	TCTGA	GAGTGAGGA	X
4	4	0	AGCAAAGCT	CGAGA	GAGTGAGGA	X
4	4	0	AACATTGTT	TCAGT	GAGTGAGGA	X
4	4	0	AGACACTTC	ATGAAT	GAGTGAGGA	X

4	4	0	GCCCACGTC	TTCGTG	GAGTGAGGA	X
4	4	0	AACATGGTT	GTGTGG	GAGTGAGGA	X
4	4	0	GGTACAGTC	TTCGCC	GAGTGAGGA	X
4	4	0	GGCATGGTG	AGAGTG	GAGTGAGGA	X
4	4	0	GGAAGTCTC	AGGAT	GAGTGAGGA	X
4	4	0	ATCTTGGTC	AGGGCA	GAGTGAGGA	X
4	4	0	ATCAGGTCC	CAATT	GAGTGAGGA	X
4	4	0	GGCATGGTG	TAAAGA	GAGTGAGGA	X
4	4	0	TGAAACGTT	GCAGG	GAGTGAGGA	X
4	4	0	TGAATCGGC	AACAA	GAGTGAGGA	X
4	4	0	ATACACGTC	TCCTG	GAGTGAGGA	X
4	4	0	GGGAAGGTC	CTTGG	GAGTGAGGA	X
4	4	0	CACTGTGTC	GGGTGA	GAGTGAGGA	X
4	4	0	ATCTTTGTC	TTCCT	GAGTGAGGA	X
4	4	0	CTGAGGGTC	ATTGG	GAGTGAGGA	X
4	4	0	ATGTGAGTC	TTCTT	GAGTGAGGA	X
4	4	0	AAAGTCGTC	AGCTAT	GAGTGAGGA	X
4	4	0	AACAATGTT	CGCCT	GAGTGAGGA	X
4	4	0	GGGAAGGTC	CTATGG	GAGTGAGGA	X
4	4	0	GGATGTGTC	TTCAGG	GAGTGAGGA	X
4	4	0	TCCACAGTC	TGGGT	GAGTGAGGA	X
4	4	0	AGCAAAGCT	ATATGG	GAGTGAGGA	X
4	4	0	CCCTGGGTC	CCAGGG	GAGTGAGGA	X
4	4	0	GTGAGGGTC	TCTGGA	GAGTGAGGA	X
4	4	0	AGCCAGGTT	GAAAAG	GAGTGAGGA	X
4	4	0	AGCATGGCT	TATGG	GAGTGAGGA	X
4	4	0	AGCTCAGGC	AGGGG	GAGTGAGGA	X
4	4	0	CCCTGGGTC	TGCTG	GAGTGAGGA	X
4	4	0	AGCAACAGA	TGAAG	GAGTGAGGA	X
4	4	0	AGCATGGCT	GGAATG	GAGTGAGGA	X
4	4	0	AGCTAAGTT	CTTGTA	GAGTGAGGA	X
4	4	0	AACTTTGTC	CTGAA	GAGTGAGGA	X
4	4	0	AACATGGTT	CCTTCT	GAGTGAGGA	X
4	4	0	CGCCACGGC	TGGGAG	GAGTGAGGA	X
4	4	0	CTCATTGTC	CAGGA	GAGTGAGGA	X
4	4	0	CCCTGGGTC	ATGTGA	GAGTGAGGA	X
5	1	4	AGCAACGTC	AAAGAT	CACTGATCA	X
5	1	4	AGCAGCGGC	GACAGC	AGAGGAGGA	X
5	1	4	AGCAGCGGC	AAGTGG	GAGTAGGAT	X
5	1	4	AGCAGCGGC	GGCACC	ACGTGCGCA	X
5	1	4	AGCACCGTC	AATCAG	GTGCGAGTC	X
5	1	4	AGCACCGTC	AAGAGT	CAGTGTTTA	X
5	2	3	AGCACAGTC	ACCTCT	GAGTGACAC	X
5	2	3	AGCAACGTA	TCGAT	GAGGGTAGA	X
5	2	3	AGCATCGGC	AGGCA	GAGTAAGTC	X
5	2	3	AACAACGTC	CTGAAC	GTGAGAGAA	X
5	2	3	AGCATAGTC	CGTGTA	GTGAGAGAA	X
5	2	3	AGCATGGTC	TTAATG	GAGTGATAG	X
5	2	3	AGCTGTGTC	TGCCTT	GGGTGATGC	X
5	2	3	AGCAATGTC	ATGTC	CAGTGAGCC	X
5	2	3	AGCATTGTC	CAAGGA	GAGTAAGTG	X
5	2	3	AGCAGCTGC	TCTCAA	GAGTATGGG	X
5	2	3	TGCAGTGTC	TGGAGT	GTGTCAGGC	X

5	2	3	AGCATTGTC	CTCCTC	TGGTGAGGT	X
5	2	3	AGCATTGTC	CCAAAA	GTGAGGGGA	X
5	2	3	AGCAATGTC	TACCA	CAGTGAGAC	X
5	2	3	AGCAACGTT	CTTTAT	GTAAGAGGA	X
5	2	3	AGCAACTTC	ACTTAG	GCGTGGGAA	X
5	3	2	AGGCGAGTC	TCTTTA	GTGTGAGGC	X
5	3	2	AGCCACGTT	AGGGGT	AAGTGAGGG	X
5	3	2	AGTATCGTG	ATTGA	AAGTGAGGC	X
5	3	2	AGCAAGGTA	GCTTG	GAGTGAGAC	X
5	3	2	TGCAGCTGC	AAAAG	AAGTGAGGG	X
5	3	2	AGTATCTTC	TGGTGT	GAGTGAGAT	X
5	3	2	TGCAGTTTC	TCAAAG	GAGAGTGA	X
5	3	2	ATCAGGGGC	CCACTA	GAGTAAGGG	X
5	3	2	AGTTGCTTC	TGCATT	GAGTAACGA	X
5	3	2	AGCTACGTG	CCCGGC	CAGTGAGGG	X
5	3	2	AGCTTAGTC	TGAGT	GTGTGAGGT	X
5	3	2	ATCAGGGGC	TGAAG	GAGTAAGGG	X
5	3	2	ATCAGGGGC	TGAAG	GAGTAAGGG	X
5	3	2	AGCAACCCC	TCTGCT	GAGGGAGGC	X
5	3	2	AGCATGGTA	TGATGT	AAGTGAGGG	X
5	3	2	CATAGCGTC	AGATTG	GAGTAAGGT	X
5	3	2	TGCAGCTGC	TGTCAG	AAGTGAGGG	X
5	3	2	AGCTAGGTC	CCCTG	CAGTGAGGG	X
5	3	2	AGCTTGGTC	AGTGAA	GAGAGAGGT	X
5	3	2	AGCAACTAC	ATATCT	GTGTGAGGC	X
5	3	2	AGCAACCCC	TCTGCT	GAGGGAGGC	X
5	3	2	GTCAGTGTC	CTGGAA	AAGTGAGGG	X
5	3	2	TGCAGTGTA	GCTGGA	GAGGGAGGT	X
5	3	2	CTCATCGTC	CAGGCT	GAGTGAGTC	X
5	3	2	AGTAACATC	AAGTCA	TAGTGAGGC	X
5	3	2	AGCTATGTC	CTAAAG	AAGTGAGGG	X
5	3	2	GTCCGCGTC	TTGTTT	GAGTAAGGG	X
5	3	2	AGCCTTGTC	ACTGA	AAGTGAGGC	X
5	3	2	AGCACAGCC	ACATCT	GTGTGAGGC	X
5	3	2	AGCAACATT	CTAAGC	GAGTGAGTC	X
5	4	1	AGTGTGGTC	GGAGCA	GAGTGAGGG	X
5	4	1	ACTAATGTC	ATGCTA	GAGTGAGGT	X
5	4	1	TACATTGTC	TAGGAG	GAGTGAGGG	X
5	4	1	ATCAATGGC	CAGAT	GAGTGAGGG	X
5	4	1	CGGGGAGTC	CCAGGG	GAGTGAGGG	X
5	4	1	AGCAGGTCA	CATCG	GAGTGAGGG	X
5	4	1	AGCTAGGTT	GGCCC	GAGTGAGGC	X
5	4	1	AGTGTGGTC	AGAGAG	AAGTGAGGA	X
5	4	1	AGTATGGTA	ACAGCA	GAGTGAGGG	X
5	4	1	ATCCGTCTC	TTCTG	GTGTGAGGA	X
5	4	1	AACAGTATT	GCAAT	GAGTGAGGG	X
5	4	1	ATCAGCAGT	GAACA	AAGTGAGGA	X
5	4	1	GGCCAAGTC	AGCGG	GAGTGAGGC	X
5	4	1	GCCAGTGTT	TCTCA	GAGTGAGGT	X
5	4	1	ATCAGGGCA	GGCCAG	GAGTGAGGG	X
5	4	1	AGTAGATGC	AGTTA	GAGTGAGGT	X
5	4	1	GGCCTGGTC	AGGAGG	GAGTGAGGG	X
5	4	1	AGCAACTCA	TTCTGT	GAGTGAGGG	X

5	4	1	GGGGGAGTC	TTGCGG	GAGTGAGGT	X			
5	4	1	ATCAGTCTA	GCAGCA	GAGTGAGGC	X			
5	4	1	AGTAGATGC	ATAGG	GAGTGAGGT	X			
5	4	1	ACCAGTGGT	GGGGGT	GAGTGAGGT	X			
5	4	1	GGCCTTGTC	CCCTA	GAGTGAGGG	X			
5	4	1	CTCATTGTC	TTGCTG	GAGTGAGGC	X			
5	4	1	AGTATGGTA	AAAGGA	GAGTGAGGG	X			
5	4	1	AGAGAGGTC	AGGGTA	GAGTGAGGG	X			
5	4	1	GGCCTGGTC	AGATTT	GAGTGAGGG	X			
5	4	1	TGTTGAGTC	CGTATG	GAGTGAGGG	X			
5	4	1	AGCACCCT	GACAG	GAGTGAGGG	X			
5	4	1	AAAACAGTC	ATCCT	GAGTGAGGG	X			
5	4	1	AACAGTATT	AAGGA	GAGTGAGGG	X			
5	4	1	GCCAACATC	CACAT	GAGTGAGGT	X			
5	4	1	GGCCAAGTC	TCTCA	GAGTGAGGC	X			
5	4	1	AAAACAGTC	TTTCGA	GAGTGAGGG	X			
5	4	1	AATCCCGTC	ATGGA	GAGTGAGGT	X			
6	4	2	GGTTACGTC	CGGAA	AAGTGAGGC	X			
6	4	2	AGTTACTTC	TATAA	AAGTGAGGG	X			
6	4	2	AGTTACTTC	CCTCA	AAGTGAGGG	X			
3	2	1	GGCATCGTC	CACTC	CAGTGAGGA		X	X	
4	2	2	ATCAGGGTC	CAGCT	CAGTGAGGC		X	X	
4	3	1	AGCTCAGTC	ACTCCT	GAGTGAGGG		X	X	
4	3	1	AGCTCAGTC	CTGGG	GAGTGAGGG		X	X	
4	3	1	AGCATGGTT	TTCTG	GAGTGAGGC		X	X	
4	3	1	AGATGGGTC	TTGCT	GAGTGAGGC		X		X
4	3	1	AGATGGGTC	TTGCT	GAGTGAGGC		X		X
2	1	1	AGCAGAGTC	AGGAT	GAATGAGGA		X		
2	1	1	AGCAGAGTC	ATGAA	GATTGAGGA		X		
3	0	3	AGCAGCGTC	TGAAAG	TAGAGATGA		X		
3	0	3	AGCAGCGTC	AGCTTC	AAGTATGGA		X		
3	0	3	AGCAGCGTC	AACATT	TAGTAATGA		X		
3	0	3	AGCAGCGTC	AACATT	TAGTAATGA		X		
3	1	2	AGCAGTGTC	TTAGGA	AAGAGAGGA		X		
3	1	2	AGCAGCTTC	AGATGG	GAGAGAGAA		X		
3	1	2	AGCAGTGTC	CAGCA	AAGAGAGGA		X		
3	1	2	TGCAGCGTC	AATGT	GAGTGAAAA		X		
3	1	2	AGCAGTGTC	AGGTAT	GAGAGGGGA		X		
3	1	2	AGCAGCTTC	AGGGA	GAGTGTGGG		X		
3	1	2	AGCAGTGTC	CTTGCC	GAAGGAGGA		X		
3	1	2	AGCAGCTTC	ATGAAG	GAGAGAGAA		X		
3	1	2	AGCAGCGTG	GAGGT	GAGTGGGGT		X		
3	1	2	AGCAGCGTT	ACTCAG	GAGAGAGAA		X		
3	1	2	AGAAGCGTC	ACTGA	GAGTGAGTT		X		
3	1	2	AGCAGCATC	TTGAG	GGGTGAGGC		X		
3	1	2	AGCAGCGGC	ACAAA	GAGGGACGA		X		
3	1	2	AGCATCGTC	TGAAG	GGGTGAGCA		X		
3	1	2	AGCAGCTTC	CACCA	GAGGGAGTA		X		
3	1	2	AGCAGCGTT	CTGTCT	AAGTGAAGA		X		
3	1	2	AGCAGCATC	TGCTTC	GGGTGAGGC		X		
3	1	2	AGCAGGGTC	GGGGA	GGGTGAGAA		X		
3	1	2	AGCAGGGTC	AGCTGG	GAGTAAGAA		X		
3	1	2	AGCAGCGCC	GGAAGA	GAGCGAGGG		X		

3	1	2	AGCACCGTC	CCTAA	GACTGAGCA	X
3	1	2	AGCAGAGTC	ACAGCT	GAATGAGGC	X
3	1	2	AGCAGCGTG	GACCCA	AAGAGAGGA	X
3	1	2	AGCAGGGTC	CACAT	GAGTCAGGG	X
3	1	2	AGCAGGGTC	GGGGTG	GAGGGAGAA	X
3	1	2	GGCAGCGTC	CAGGTA	GACTGAGGG	X
3	1	2	AGCAGTGTC	CTAAAG	GAAGGAGGA	X
3	1	2	AGCAGCCTC	TTCTG	TAATGAGGA	X
3	1	2	AGCAGCGTT	GGGAA	GAGAGAGAA	X
3	1	2	AGCAGCGAC	AGGGCA	GAATGAGGC	X
3	1	2	AGCAGAGTC	GAGCA	AGGTGAGGA	X
3	1	2	AGCAGCATC	GAGTGG	AAGTGGGGA	X
3	2	1	AGCTGAGTC	CAGAA	GAGTGGGGA	X
3	2	1	GGCAGTGTC	AGTAG	GTGTGAGGA	X
3	2	1	AGCAACTTC	AGAAT	GAGTTAGGA	X
3	2	1	AGCATCTTC	AGCTA	TAGTGAGGA	X
3	2	1	GGCAGGGTC	ACCCGA	AAGTGAGGA	X
3	2	1	AGCAGTGTC	TGCCCA	GAGTGAGTA	X
3	2	1	AGCAGTGTA	CCATGC	GAGTGAGCA	X
3	2	1	AGCTGGGTC	TATTTG	GAGTCAGGA	X
3	2	1	AGCAGCGAG	GTGGG	GAGTGAGTA	X
3	2	1	AGCAGCTTG	GATTCA	GAGTGAGAA	X
3	2	1	AGCAGCAGC	AACGAG	GAGCGAGGA	X
3	2	1	AGCACCATC	TTTGAA	AAGTGAGGA	X
3	2	1	AGCAGAGTT	TGAATT	GAGTTAGGA	X
3	2	1	GGCAGGGTC	AAGGA	AAGTGAGGA	X
3	2	1	GGCAGTGTC	CAGGAG	GTGTGAGGA	X
3	2	1	TGCAACGTC	ACAAGT	GAGAGAGGA	X
3	2	1	AACAGTGTC	TTTCAA	AAGTGAGGA	X
3	2	1	AGCAGTGTA	GACCCA	GAGTGAGCA	X
3	2	1	AGCTGTGTC	CCCTT	GAGAGAGGA	X
3	2	1	AGCAGCGGA	GGTGGG	GAGGGAGGA	X
3	2	1	AACAGCTTC	TCATT	GAGTGAGTA	X
3	2	1	AGTAGAGTC	AGGCCT	GAATGAGGA	X
3	2	1	AGCAGCGAA	GCCGG	AAGTGAGGA	X
3	2	1	AACTGCGTC	CCAGG	AAGTGAGGA	X
3	2	1	AGAAGCCTC	TGCTAT	GAGTGAGGC	X
3	2	1	AGCAGTGTC	CAATG	GAGTGAGTA	X
3	2	1	AGTAGAGTC	CCTGG	GAGTGAGCA	X
3	2	1	GGCAGTGTC	ATGTGT	GAGGGAGGA	X
3	2	1	AGCACTGTC	ACTGTT	GAGTGATGA	X
3	2	1	AGCTGGGTC	TGGGAG	GAGTCAGGA	X
3	2	1	AGCAGCTTT	CCAAGA	GAGTGAGAA	X
3	2	1	AGCAGTGTA	GACCCA	GAGTGAGCA	X
3	2	1	GGCAGCGTG	GGGATG	CAGTGAGGA	X
3	2	1	AGCAGCAGC	AGAGG	GAGCGAGGA	X
3	2	1	AGTAGCTTC	CCTCT	GTGTGAGGA	X
3	2	1	TGCGGCGTC	TCCTGG	GAGTGAAGA	X
3	2	1	AACAGAGTC	TGGCA	GAGTGAGCA	X
3	2	1	GGCAGCGGC	CTGGG	GAGTGTGGA	X
3	2	1	AGCAGGCTC	CTTGT	TAGTGAGGA	X
3	3	0	ATCACCATC	ATACCT	GAGTGAGGA	X
3	3	0	AGCAGTTTA	ATTCT	GAGTGAGGA	X

3	3	0	AACAGCAAC	AAAAA	GAGTGAGGA	X
3	3	0	AGCTGAGTA	GAATG	GAGTGAGGA	X
3	3	0	AGCAACCTG	GGGCT	GAGTGAGGA	X
3	3	0	AGCAACCTG	GAAAA	GAGTGAGGA	X
3	3	0	TGCAGGCTC	CTGTG	GAGTGAGGA	X
3	3	0	CGCAGTATC	CCACT	GAGTGAGGA	X
3	3	0	AGAAACATC	AGATG	GAGTGAGGA	X
3	3	0	ACCTGTGTC	TCCTG	GAGTGAGGA	X
3	3	0	GGCAGGGCC	TCAAGG	GAGTGAGGA	X
3	3	0	AGAAACATC	TAAGAG	GAGTGAGGA	X
3	3	0	AGGTGCATC	CCTCA	GAGTGAGGA	X
3	3	0	GGCAGGGCC	TTCTT	GAGTGAGGA	X
3	3	0	GGCAGCTGC	TTTTT	GAGTGAGGA	X
3	3	0	AGCATGGCC	CAGGAG	GAGTGAGGA	X
4	0	4	AGCAGCGTC	TTCAGC	AAGTGGAGG	X
4	0	4	AGCAGCGTC	TGGGGC	AGTGGAGGA	X
4	0	4	AGCAGCGTC	TCATA	GAGTTAACC	X
4	0	4	AGCAGCGTC	CCTGA	AATTGTGCA	X
4	1	3	AGCAACGTC	AGGGAA	GAGGGACCA	X
4	1	3	AGCAGGGTC	CACTCA	GAGGGAGTC	X
4	1	3	AGCAGCGTG	TGGCT	GTGTGTGGC	X
4	1	3	AGCAGCGTT	GGCTGA	AACTGAGGT	X
4	1	3	AGCAACGTC	TCCAGG	GACTIONAGC	X
4	1	3	AGCAGGGTC	ATTTAG	GAGTGACAT	X
4	1	3	AGCAGTGTC	TTGTCA	GAGTGTGTC	X
4	1	3	AGCAACGTC	CTCAAG	GAGGCAAGA	X
4	1	3	AGCATCGTC	CACCTG	GCGAGAGGC	X
4	1	3	AGCAGCTTC	TAACA	AAGTGAGAC	X
4	1	3	AGCAACGTC	AGGGAG	GAGAGGGCA	X
4	1	3	AGCAGCGTT	TTCAT	GTGTGTGTA	X
4	1	3	AGCAGCGTT	TAACT	GAGTGAAAG	X
4	1	3	AGCAGGGTC	AGCAG	GAGGGAGTC	X
4	1	3	AGCAGTGTC	ATTAC	GAGTGCGAC	X
4	1	3	AGCAGTGTC	AGTGC	AAGTGCGGG	X
4	1	3	AGCAGCTTC	CATCG	TGGTGTGGA	X
4	1	3	GGCAGCGTC	TAGGG	GTGTGATAA	X
4	1	3	AGCAGCTTC	CGGTC	GAGTGATTT	X
4	1	3	AGCAGGGTC	CGGCTT	GTGTGCGGC	X
4	1	3	AGCAGCGGC	AAGAA	GAGGGTGGT	X
4	1	3	AGCAGCCTC	ACTCA	GAGTGGGAC	X
4	1	3	AGCAACGTC	TCCACA	GAGACAGGC	X
4	1	3	AGCAGCGTG	GGGGGA	GTGTGGGGG	X
4	1	3	AGCAGGGTC	TGCAGG	GACTIONAGAG	X
4	1	3	AGCAGTGTC	TTTTC	CAGTAAGGT	X
4	1	3	AGCAGCGGC	AAGCAC	AAGCAAGGA	X
4	1	3	AGCAGCTTC	CTCCAG	GGGAGAGGT	X
4	1	3	AGCAGCTTC	GCCTGC	TGGTGTGGA	X
4	1	3	AGCAGCGAC	TCACAC	AAGTGAGAT	X
4	1	3	AGCAGCGGC	CCCAGC	GAGTGTGTC	X
4	1	3	AGCAGTGTC	TGCAAC	TAGTGAGCT	X
4	1	3	AGCAGCGGC	CTGGGG	ACGAGAGGA	X
4	1	3	AGCAGCGGC	TGCCA	GAGGGTGGT	X
4	1	3	AGCAACGTC	CATTCT	GAGGCAAGA	X

4	2	2	AGCATTGTC	GGATTC	TGGTGAGGA	X
4	2	2	AGCATGGTC	ACAAA	GGGTGAGGT	X
4	2	2	AGCAACATC	ACAGA	GAGAGAGGG	X
4	2	2	AGCAATGTC	CCTTG	GAGTGTGGG	X
4	2	2	AGCAGCTGC	CAGAG	GAGGGAGGC	X
4	2	2	AGCTGGGTC	CTAGA	AAGTGAGGT	X
4	2	2	AGCAGCTGC	AGTGA	GAGTGAGCT	X
4	2	2	AGCATTGTC	AATGA	CAGTGAGAA	X
4	2	2	AGCAAAGTC	TAAGA	GAGTGTGGC	X
4	2	2	AGCAGGGTG	GAGAA	GAGCGAGGG	X
4	2	2	ATCAACGTC	CTTTGA	GAGAAAGGA	X
4	2	2	AGCAGCTTT	TTTCC	GAGTGAGAG	X
4	2	2	GGCAGCGTT	TCCTGT	GAGCAAGGA	X
4	2	2	AGCACCATC	AGGAG	GAGGGAGGG	X
4	2	2	ATCAGAGTC	TGCAG	GCGTGAGGC	X
4	2	2	AGCACCGGC	CTCTTG	GAGGGAGGT	X
4	2	2	GGCAGGGTC	AGTGG	GAGTGAGTC	X
4	2	2	AGCACCTTC	TCCTGG	TAGTGAGGC	X
4	2	2	AGCGGTGTC	ATCCAG	GAGTGAGCG	X
4	2	2	AGCAATGTC	TATAA	AAGTGAGGC	X
4	2	2	AGCAGGGTA	AGTAC	AAGTGAGGC	X
4	2	2	AGCAACGTG	ATCGG	GAGGGAGGG	X
4	2	2	AGCAGGGTA	GATGG	GAGAGAGGG	X
4	2	2	AGCAATGTC	TGGGT	GAGTGTGGG	X
4	2	2	AGCAATGTC	TGAAA	TAGTGAGTA	X
4	2	2	TGCAGAGTC	AAGGAA	GAGTGAGAT	X
4	2	2	AGCATAGTC	TCCTAG	GAGAGAGGC	X
4	2	2	AGCAGGGTA	ATGGG	GAGAGAGGG	X
4	2	2	ATCACCGTC	GAGGG	GAGGGAGGG	X
4	2	2	GGCAGCTTC	GGTGTC	CAGTGAGGC	X
4	2	2	AGCTGGGTC	TCATTG	CAGTGAGGT	X
4	2	2	AGCAACGTA	CTGTT	AAGTGAGAA	X
4	2	2	AGCAAAGTC	AAGAA	GAGTGAAAA	X
4	2	2	GGCAGGGTC	TCTCA	AAGTGAGGT	X
4	2	2	TGCAGGGTC	ATGCAA	GTGTGAGGT	X
4	2	2	AGCAAAGTC	AGAGCT	GAGTGAGCC	X
4	2	2	GGCAGTGTC	ATTTTT	GAGTAAGGG	X
4	2	2	AGCAGCTGC	TGTGG	GAGGGAGGC	X
4	2	2	AGCAGCGGT	GGTATC	TAGTGAGGC	X
4	2	2	AGCAACATC	TGGAAC	GAGTGAATA	X
4	2	2	AGCAGTGTG	ATCTT	GAGTAAGGC	X
4	2	2	GGCAGCTTC	AGCAC	CAGTGAGGC	X
4	2	2	AGCAGAGTT	GCTTAA	GAGTGAGAG	X
4	2	2	AGCACCTTC	TGCCAA	GAGTGAGAT	X
4	2	2	AGCAGCTGC	GGGCA	GAGTGAGCT	X
4	2	2	AGTAGAGTC	TTTGTT	GTGTGAGGT	X
4	2	2	AGCATGGTC	GTTGGG	GGGTGAGGC	X
4	2	2	AGCATTGTC	TCTTGT	GTGTGAGGT	X
4	2	2	ATCAGAGTC	AATTTG	TAGTGAGGT	X
4	2	2	AGCAGCTTA	GAGGG	GAGAGAGGT	X
4	2	2	GACAGCGTC	CTCCG	GGGTGAGGC	X
4	2	2	TGCAGAGTC	AGCCCT	GAGTGAGAT	X
4	2	2	AGCAGAGTT	GGAAG	GAGTGAGAG	X

4	2	2	AGCAGGGTA	GGTCA	GAGAGAGGG	X
4	3	1	TGCAGTGAC	TGTCCA	GAGTGAGGC	X
4	3	1	AGCAGAGGT	GAGGT	GAGTGAGGG	X
4	3	1	AGCAGTTTA	AATTT	GAGTGAGGC	X
4	3	1	AGAAAGGTC	ATAAT	GAGTGAGGG	X
4	3	1	AGCACAATC	CCAAAG	GAGTGAGGC	X
4	3	1	AGCAAAGGC	AGGAG	GAGTGAGGT	X
4	3	1	AGCCACATC	CCCTA	GAGTGAGGT	X
4	3	1	TGCTGGGTC	TACAG	GAGTGAGGC	X
4	3	1	GGCAGTGTG	AGCTG	GAGTGAGGG	X
4	3	1	AGTAGTGTG	CTGAA	GAGTGAGGG	X
4	3	1	TGCATGGTC	AGAGGT	GAGTGAGGG	X
4	3	1	AGCATAGTT	TAGGAT	CAGTGAGGA	X
4	3	1	AGCAGCAGG	ATGAGA	GAGTGAGGC	X
4	3	1	AGCACCATT	AAATTG	GAGTGAGGC	X
4	3	1	ATCAGGGTT	AAGCA	GAGTGAGGG	X
4	3	1	AGCAAAGTG	GAGAG	GAGGGAGGA	X
4	3	1	AGCAACACC	AATGAA	GAGTGAAGA	X
4	3	1	GGCAGTGGC	TCTGT	GAGTGAGGT	X
4	3	1	AGTATCGGC	TGTGGT	GAGTGAGGG	X
4	3	1	GGCAGCTCC	GCCTCC	GAGTGAGGG	X
4	3	1	AGCAAAGGC	TGGGTG	GAGTGAGGT	X
4	3	1	AGCAAGTTC	CACTG	GAGTGTGGA	X
4	3	1	AGCAAAGGC	AGTCA	GAGTGAGGG	X
4	3	1	CGCAGCAAC	GCTCTG	GAGTGAGGC	X
4	3	1	GGCAGCGGT	TGGGG	GAGTGAGGC	X
4	3	1	AGCAACTGC	TTTTA	GAGTGAGCA	X
4	3	1	AGAAGAGTA	AAGCA	GAGTGAGGT	X
4	3	1	AGCAACATA	ATAACA	GAGTGAGGT	X
4	3	1	CGCACCTTC	CTGTAT	GAGTGAGGC	X
4	3	1	GTCCGCGTC	GCCCA	GAGTGAGAA	X
4	3	1	GGCAGTGTG	CTTGAT	GAGTGAGGG	X
4	3	1	CCCACCGTC	CTAAAG	AAGTGAGGA	X
4	3	1	AACAACGTG	AAACCA	GAGTGAGGC	X
4	3	1	AGCAACCAC	AAAAA	AAGTGAGGA	X
4	3	1	AGCCCCTTC	AGCATA	GAGTGAGGG	X
4	3	1	AGCCGCTGC	AGCAGG	GAGTGAGGT	X
4	3	1	AGCCGCTGC	AGCAGG	GAGTGAGGT	X
4	3	1	AGCCGCTGC	AGCAGG	GAGTGAGGT	X
4	3	1	AGCCGCTGC	AGCAGG	GAGTGAGGT	X
4	3	1	AGAGGGGTC	TGCAG	GAGTGAGGG	X
4	3	1	AGCAAAGGC	AAATA	GAGTGAGGG	X
4	3	1	GGCAACTTC	CAAGA	AAGTGAGGA	X
4	3	1	GCCAGCTTC	CATACA	GAGTGAGGC	X
4	3	1	AGAAGGGTG	ATTAG	GAGTGAGGC	X
4	3	1	AGCTACGAC	TCAGGA	GAGTGAGGT	X
4	3	1	AGCAAGGTG	GGCGG	GAGTGAGGG	X
4	3	1	AGGAGAGTT	AGAAGA	GAGTGAGGT	X
4	3	1	TGCTCCGTC	CTGGCT	GAGTGAGGT	X
4	3	1	AGCACTGTT	TGCCC	GAGTGAGGC	X
4	3	1	AGTACCATC	AGGGCT	GAGTGAGGC	X
4	3	1	AGCAGCAGG	GCAGT	GAGTGAGGC	X
4	3	1	GGCAGGGAC	CATAT	GAGTGAGGC	X

4	3	1	AGCAAGGTT	CCCCG	GAGTGAGTA	X
4	3	1	AGCATGGGC	AGGGG	GAGTGAGGC	X
4	3	1	AGCTGAGTA	GCTAA	GAGTGAGGC	X
4	3	1	AGCGACTTC	ATATCT	GAGTGAGGT	X
4	3	1	AGGAGAGTT	TAAAG	GAGTGAGGT	X
4	3	1	GACAGCATC	AGTCTG	GAGTGAGGG	X
4	3	1	AGCAACTCC	ATTC	GAGTGAGGC	X
4	3	1	AGTCGCTTC	ACTTTG	GAGTGAGAA	X
4	3	1	AGTAACATC	TTTACT	GAGGGAGGA	X
4	3	1	AGCAACTGC	AATGGT	GAGTGAGCA	X
4	3	1	AGCATTGTG	CTAGG	CAGTGAGGA	X
4	3	1	AGAAAAGTC	TTGAAG	GAGTGAGGG	X
4	3	1	GGCAGTGTA	GGGAG	GAGTGAGGT	X
4	3	1	AGCAAGGTA	AAGGAG	GAGTGAGGT	X
4	3	1	AGCATCTGC	AGATG	GAGTGAGGC	X
4	3	1	TGCATAGTC	TTGGG	GAGTGAGGG	X
4	3	1	AGAAGGGTG	AGGTGG	GAGTGAGGC	X
4	3	1	AGCCGAGTG	GTTAA	GAGTGAGGG	X
4	3	1	CTCAGGGTC	ATTAGT	GAGTGAGGG	X
4	3	1	AACAGGGTT	GGCCT	GAGTGAGGC	X
4	3	1	AGCCTAGTC	ACACCT	GAGTGAGGG	X
4	3	1	AGCAATGTT	TTGCT	GAGTGAGAA	X
4	3	1	AGCAGCAAA	TCTGCT	GAGTGAGGT	X
4	3	1	AGCAGTCCC	TGCCCA	GAGTGAGGC	X
4	3	1	TGCAATGTC	TTTGA	GAGTGAGGT	X
4	3	1	TGCAGGTTT	TTTGG	GAGTGAGGG	X
4	3	1	AGCTAAGTC	TGTAGG	CAGTGAGGA	X
4	3	1	AGCATAGTT	GGGAG	CAGTGAGGA	X
4	3	1	AGCATGGTA	GAGACT	GAGTGAGGG	X
4	3	1	AGCAAGGAC	TGGGCT	GAGTGAGGC	X
4	3	1	AGGTGGGTC	CCCAGA	GAGTGAGGC	X
4	3	1	AGCAGCTGT	CAATCA	GAGTGAGGC	X
4	3	1	TGCATGGTC	CTGGAG	GAGTGAGGG	X
4	3	1	AGCATAGTA	CTTAA	GAGTGAGGG	X
4	3	1	AGCAAGGTA	ATTAG	GAGTGAGTA	X
4	3	1	TGCACCTTC	ATGCCT	GAGTGAGGG	X
4	3	1	AGCACCGAG	GTCGGA	GAGTGAGGG	X
4	3	1	TGGAGAGTC	AGCAG	GAGTGAGTA	X
4	3	1	AGAAGAGTT	AGGTGG	GAGTGAGGT	X
4	3	1	ATCAGGGTT	AGGAT	GAGTGAGGG	X
4	3	1	GGCAGTGCC	CAGCAG	GAGTGAGGC	X
4	3	1	AGTAAGGTC	TTAAA	TAGTGAGGA	X
4	3	1	AGCAGCAGG	CCAGT	GAGTGAGGC	X
4	4	0	AGCCATGTG	CAAGT	GAGTGAGGA	X
4	4	0	GGTAGTGTT	ATGAAT	GAGTGAGGA	X
4	4	0	TACAAAGTC	GATGA	GAGTGAGGA	X
4	4	0	AGCCATGTA	CATGT	GAGTGAGGA	X
4	4	0	GACTGGGTC	TGTCAT	GAGTGAGGA	X
4	4	0	AGCACAGCA	GATGA	GAGTGAGGA	X
4	4	0	TGAATAGTC	TTGGAA	GAGTGAGGA	X
4	4	0	GTCAGGTTT	ACACAT	GAGTGAGGA	X
4	4	0	GGTAAAGTC	TGGTCA	GAGTGAGGA	X
4	4	0	AGTATAGTG	GCAGA	GAGTGAGGA	X

4	4	0	ATGGGGGTC	AGAGGG	GAGTGAGGA	X
4	4	0	CCCAAAGTC	GTAAG	GAGTGAGGA	X
4	4	0	CAAATCGTC	TACAT	GAGTGAGGA	X
4	4	0	AATAAGGTC	ATAGCA	GAGTGAGGA	X
4	4	0	AGTATAGTT	CAGAT	GAGTGAGGA	X
4	4	0	AGAGAGGTC	AAGGA	GAGTGAGGA	X
4	4	0	TGGTGAGTC	ACCAC	GAGTGAGGA	X
4	4	0	TGCCTGGTC	ACTTGG	GAGTGAGGA	X
4	4	0	AGCCATGTG	GGAAG	GAGTGAGGA	X
4	4	0	AACAAGGTT	CGCAGA	GAGTGAGGA	X
4	4	0	AGCAATTTA	TGTACA	GAGTGAGGA	X
4	4	0	AGGCATGTC	TCAGCA	GAGTGAGGA	X
4	4	0	TACAAAGTC	CTTAG	GAGTGAGGA	X
4	4	0	AATAAGGTC	AGAGAG	GAGTGAGGA	X
4	4	0	AATAAAGTC	AGATAG	GAGTGAGGA	X
4	4	0	AATAAGGTC	AGATAG	GAGTGAGGA	X
4	4	0	AATAAGGTC	AAATAG	GAGTGAGGA	X
4	4	0	AATAAGGTC	AGATG	GAGTGAGGA	X
4	4	0	AATAAGGTC	AGATAG	GAGTGAGGA	X
4	4	0	AGCACAGCA	GGCAG	GAGTGAGGA	X
4	4	0	GGAAAGGTC	AGTTAT	GAGTGAGGA	X
4	4	0	AGCCATTTT	AACAA	GAGTGAGGA	X
4	4	0	AATAAGGTC	ACGGTG	GAGTGAGGA	X
4	4	0	ATCAGCACT	TCAGA	GAGTGAGGA	X
4	4	0	GGTGGGGTC	ATGGA	GAGTGAGGA	X
4	4	0	CACACAGTC	AGTGTA	GAGTGAGGA	X
4	4	0	AATATTGTC	TCTGT	GAGTGAGGA	X
4	4	0	GGAATAGTC	TGGTTA	GAGTGAGGA	X
4	4	0	AGCAACAAT	CGTAC	GAGTGAGGA	X
4	4	0	AATAAGGTC	ACAGTG	GAGTGAGGA	X
4	4	0	GACTGTGTC	CTTCA	GAGTGAGGA	X
4	4	0	AATAAAGTC	AGATAG	GAGTGAGGA	X
4	4	0	AATAAGGTC	AGAGAG	GAGTGAGGA	X
4	4	0	AATAAGGTC	AGACAA	GAGTGAGGA	X
4	4	0	AATAAGGTC	AGATAG	GAGTGAGGA	X
4	4	0	AATAAGGTC	AGATG	GAGTGAGGA	X
5	1	4	AGCAGCTTC	CCCTG	CAGAAAGGT	X
5	2	3	GGCAACGTC	ATCTC	TAGTGAGAC	X
5	2	3	AGCAGTTTC	TTTTAC	TTGTGAGGG	X
5	2	3	AGCAGTTTC	AGTATC	TTGTGAGGG	X
5	2	3	AGCAGCAGC	CGAAC	GAGGGAGAT	X
5	2	3	AGCAGCAGC	CCAGG	GAGGGAGAT	X
5	2	3	AGCAACTTC	TCTAA	TTGTGAGGT	X
5	2	3	AGCAACTTC	CACAG	TTGTGAGGT	X
5	2	3	AGCAAGGTC	AGTGA	TAGTGAATA	X
5	2	3	AGCAGTTTC	GGTGTT	TTGTGAGGG	X
5	2	3	AGCAGCAGC	AGGAA	GAGGGAGAT	X
5	2	3	AGCATTGTC	TTAGA	AAGTAAGGG	X
5	3	2	AGCCCAGTC	TCAGG	GAGTGAGAG	X
5	3	2	AGCTACATC	TGCATT	GAGTGAGTC	X
5	3	2	AGCATGGTT	TGAAAG	GAGTGAGCC	X
5	3	2	GACAGGGTC	CACTTG	GAGTGAGTC	X
5	3	2	ATCCTCGTC	CTGCA	GAGTGAGTC	X

5	3	2	CAGAGCGTC	CAGGT	GAGTGAGTC	X	
5	3	2	AGCAAAGGC	CTGAAG	GAGTAAGGG	X	
5	3	2	AGCATCGAT	TAAAA	GAGTGAGAG	X	
5	3	2	ATCATGGTC	ACTTT	GAGGGAGGG	X	
5	3	2	AGCCCAGTC	CCCCTA	GAGTGAGAG	X	
5	3	2	TGCATAGTC	AATTT	GAGTGAGAT	X	
5	3	2	AGCCATGTC	AGCTT	GAGGGAGGT	X	
5	3	2	AGCATTGTA	GGGGAC	GAGTGTGGT	X	
5	3	2	ATCATGGTC	CAGGA	GAGGGAGGG	X	
5	3	2	AGCAAAGGC	CAAGT	GAGTAAGGG	X	
5	3	2	ATAAGAGTC	ATGCAG	GAGTGAGTG	X	
5	3	2	AGCCATGTC	CCAAGG	GAGGGAGGT	X	
5	3	2	AGCAAAGGC	AATGA	GAGTAAGGG	X	
5	3	2	AGCCCAGTC	AGGAT	GAGTGAGAG	X	
5	4	1	TTCCACGTC	AACAT	GAGTGAGGG	X	
5	4	1	AGTCAGGTC	CCCACA	GAGTGAGGT	X	
5	4	1	CTGAGGGTC	GGTAG	GAGTGAGGC	X	
5	4	1	ATGACAGTC	TATGCA	GAGTGAGGC	X	
5	4	1	AACAGTCTA	CCTGA	GAGTGAGGC	X	
5	4	1	CTCAGTTTC	CTGAG	GAGTGAGGG	X	
5	4	1	AGTCAGGTC	TTCCAT	GAGTGAGGG	X	
5	4	1	GTGGGCGTC	CACTAA	GAGTGAGGC	X	
5	4	1	GGTGGGGTC	CTTGAA	GAGTGAGGC	X	
5	4	1	AGTTAAGTC	TCTAGA	GAGTGAGGG	X	
5	4	1	TTCACCTTC	CACCAT	GAGTGAGGC	X	
5	4	1	TCCTGAGTC	TTGGTA	GAGTGAGGC	X	
5	4	1	ATAATAGTC	TCCAT	GAGTGAGGC	X	
5	4	1	AGCAAAGGT	GGGGTG	GAGTGAGGT	X	
5	4	1	AGTTTAGTC	CTTGG	GAGTGAGGT	X	
5	4	1	ACAAAGGTC	CTCCA	GAGTGAGGC	X	
5	4	1	TGCAGTCCC	AATCA	GAGTGAGGT	X	
5	4	1	AGTCATGTC	GTTAA	GAGTGAGGC	X	
5	4	1	CACCACGTC	AAGGTA	GAGAGAGGA	X	
5	4	1	CTCAGTTTC	AAAAGC	GAGTGAGGG	X	
5	4	1	GAAAGTGTC	CAAGTG	GAGTGAGGC	X	
5	4	1	GGGTGGGTC	TAGAGG	GAGTGAGGT	X	
5	4	1	AGAGTTGTC	CCCCAA	GAGTGAGGC	X	
6	4	2	AGAAGGGGT	AGGAG	GAGTGAGAG	X	
3	1	2	AGCAGAGTC	ATATT	GAGTCAGGG		X
3	3	0	ACCATCTTC	ATCAG	GAGTGAGGA		X
4	2	2	AGGAACGTC	TCCAA	GGGTGAGGG		X
4	2	2	AGCACCTTC	AGAGG	GAGTGTGGC		X
4	2	2	GGCAGGGTC	GGTCA	GAGTGAGAG		X
4	2	2	GGCAGGGTC	ACAGGT	GAGTGAGAG		X
4	2	2	AGCACAGTC	AAGCT	GAGGGAGGT		X
4	2	2	GGCAGGGTC	TAGGCA	GAGTGAGAG		X
4	2	2	AGCAAGGTC	TACTCG	GGGTGAGGC		X
4	3	1	AGCAAGTTC	CGTTAA	GAGTGAGGT		X
4	3	1	AGCAGTTTT	TGCAGT	GAGTGAGGC		X
2	1	1	AGCTGCGTC	ACATG	GA CTGAGGA		X
3	1	2	AGCAGGGTC	TGAGCT	GTGTGGGGA		X
3	1	2	AGCAGGGTC	AGCTG	GTGTGGGGA		X
3	2	1	AGAAGCCTC	AAGGAT	GAGTGAGGT		X

3	2	1	AGAAGCCTC	ATAAGT	GAGTGAGGT	X
3	3	0	AGCATTTC	AATTT	GAGTGAGGA	X
4	0	4	AGCAGCGTC	CCTCC	GACACTGGA	X
4	1	3	AGCAGTGTC	ACCGAC	AGGTGAGGC	X
4	1	3	AGCAGTGTC	TGGGA	GAGGGTAGA	X
4	2	2	AGCAACTTC	TTCCT	GGGTGAGGC	X
4	3	1	AGCCCGGTC	TGAAAG	GAGTGAAGA	X
4	3	1	AGTAACTTC	TGAGTG	GAGTGAGGC	X
4	3	1	AGTAACTTC	AAAAT	GAGTGAGGC	X
4	3	1	ACCTGCTTC	AAAGT	GAGTGAGGG	X
4	3	1	AGCATTTC	CCCCTA	AAGTGAGGA	X
4	3	1	AGTAACTTC	AGTATA	GAGTGAGGC	X
4	3	1	AGCAATGTT	TGAGT	GAGTGATGA	X
4	3	1	AGCATTTC	CTTTA	AAGTGAGGA	X
4	3	1	AGCCACGGC	TGCCTG	GAGTGAGGG	X
4	4	0	CCTAGAGTC	CAGGA	GAGTGAGGA	X
5	4	1	ATCATAGTG	ACCAC	GAGTGAGGC	X