

Recombined BAC Vectors to add Polymorphic V-regions to the Mouse Genome

1. Cassette Exchange — Replace existing V-regions

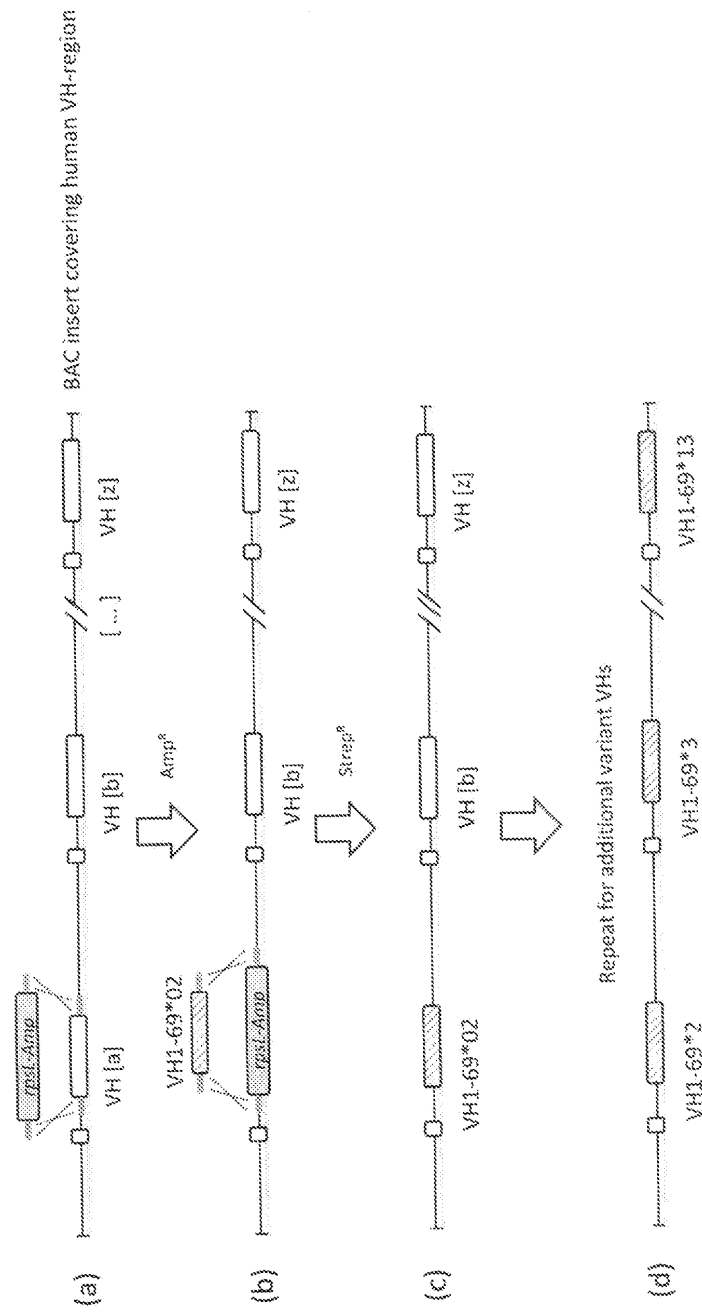


Figure 1

Recombineered BAC Vectors to add
Heterogeneous V-regions to the Mouse Genome

2. Insertion of V-regions into Heterologous Genomic DNA

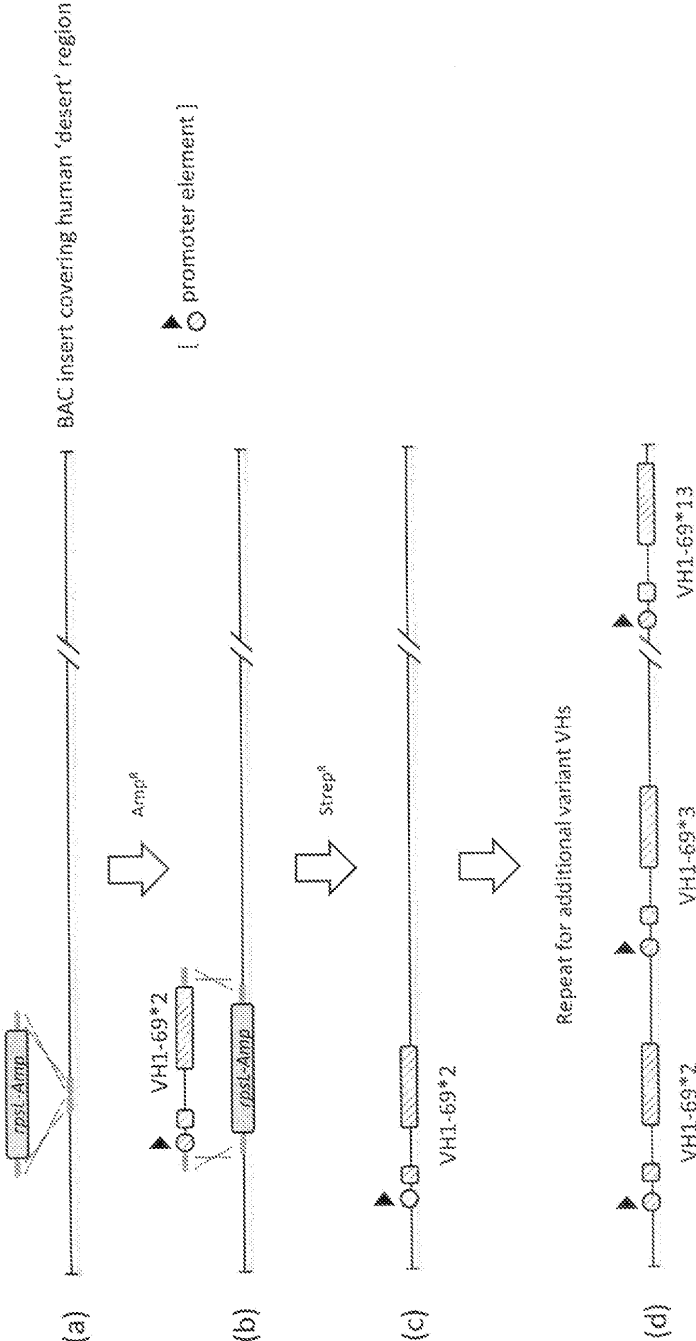


Figure 2

Recombineered BAC Vectors to add Heterogeneous V-regions to the Mouse Genome

3. Single Strand Nucleotide Changes

[Single Stranded targeting fragment with 2 nucleotide changes]

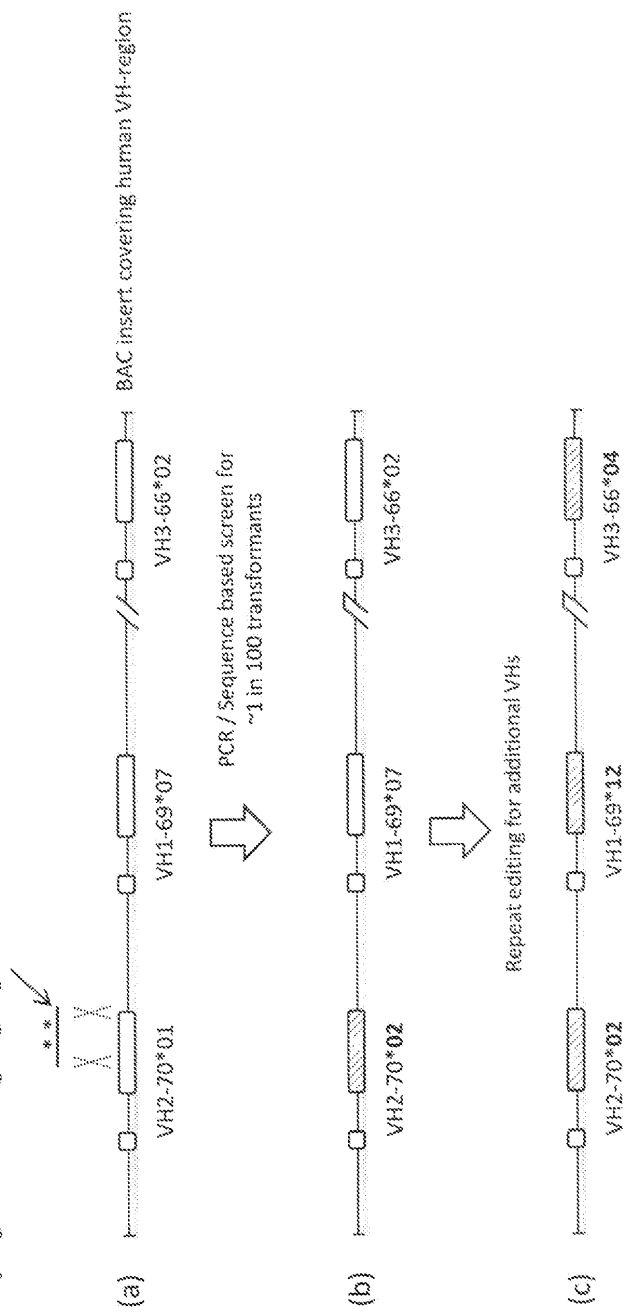


Figure 3

Adding Polymorphic V-regions to the Genome using SRMCE of Modified BACs

1. Insertion at a 'Landing Pad' site during SRMCE

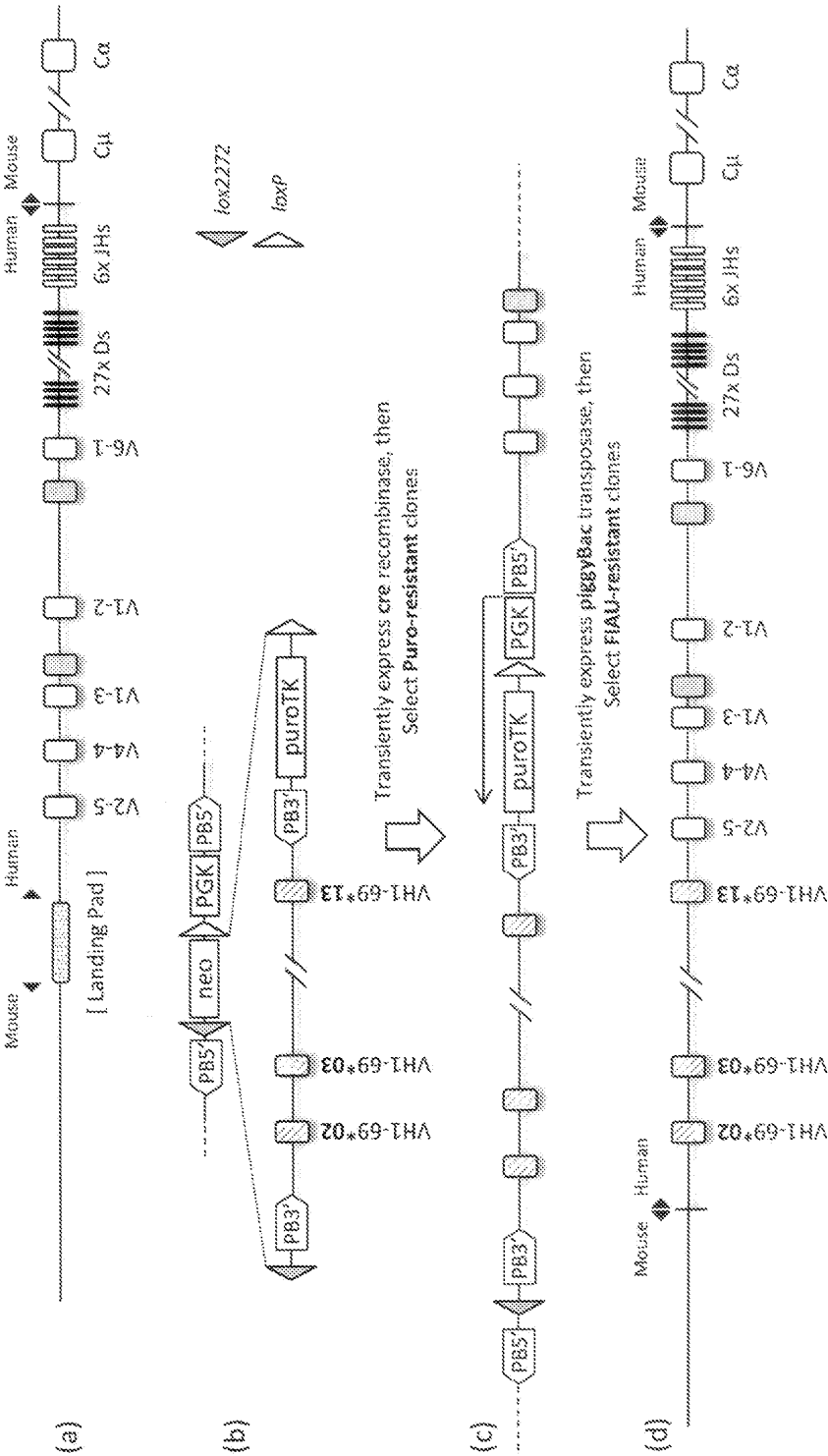


Figure 4

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	E	G	S	S	V	K	V	S	C	K	A	S	
122582 ,IGHV1-69*01, h01051	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GCG	GCT	...	GAG	GTG	AAG	AAG	CCT	GCG	TCC	TCC	GTC	AGC	ATC	TGC	TGC	AAG	GCT	TCT
217506 ,IGHV1-69*02, y15H6(YAC7)	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
X92340 ,IGHV1-69*03, SPGZA6	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
N83132 ,IGHV1-69*04, h01263	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
X67803 ,IGHV1-69*05, BR.VH1.2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
122503 ,IGHV1-69*06, b01051K	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
Z29978 ,IGHV1-69*07, DA-2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
Z14309 ,IGHV1-69*08	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
Z14307 ,IGHV1-69*09	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
Z14300 ,IGHV1-69*10	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
Z14296 ,IGHV1-69*11	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
Z14301 ,IGHV1-69*12	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
Z14214 ,IGHV1-69*13	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	

Alignment of 13 IGHV1-69 alleles showing the variable (V) coding region only. Nucleotides that differ from VH1-69 allele *01 are indicated at the appropriate position whereas identical nucleotides are marked with a dash. Where nucleotide changes result in amino acid differences, the encoded amino acid is shown above the corresponding triplet. Boxed regions correspond to CDR1, CDR2 and CDR3 as indicated.

Figure 5 (part 1 of 4)

	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53
	G	G	T	F	S	S	Y	A					I	S	W	V	R	Q	A	P	S	Q	G	L	S	W	M
	GGA	GGC	ACC	ATC	AGC	AGC	TAT	ACT					ATC	ATC	TGG	GTG	CGA	CAG	GCC	CCT	GGA	CAA	GCG	CCT	GAG	TGG	ATG
L22582 ,IGHV1-69*01, hV1051																											
227506 ,IGHV1-69*02, YIGH6(YAC7)								A																			
X92340 ,IGHV1-69*03, 57GT88																											
N83132 ,IGHV1-69*04, hV1363																											
X87905 ,IGHV1-69*05, RR.VH1.0																											
L22563 ,IGHV1-69*06, hV1051K																											
229978 ,IGHV1-69*07, DA-2								T																			
214309 ,IGHV1-69*08								A																			
214307 ,IGHV1-69*09																											
214300 ,IGHV1-69*10																											
214296 ,IGHV1-69*11																											
214301 ,IGHV1-69*12																											
214213 ,IGHV1-69*13																											

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Figure 5 (part 2 of 4)

	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
	G	G	I	I	F	I	F	G	T	A			N	Y	A	Q	K	F	Q		G	R	V	T	I	T	A
L22582	GGA	GGA	ATC	ATC	CCT	ATC	ATC	TTT	GGT	ACA	GCA	...	...	AAC	TAC	GCA	CAG	AAG	TTC	CAG	...	GGC	AGA	ATC	ACC	GGC	GGC
	A	A						L	I																		
Z17506								C																			
X92340																											
M83130																											
X67905																											
L22583																											
Z13979																											
Z14309																											
Z14307																											
Z14300																											
Z14296																											
Z14301																											
Z14214																											

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Figure 5 (part 3 of 4)

	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	CDR3									
D	S	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	Y	C	A	R					
L22592 ,IGHV1-69*01, hv1051	GAC	GAA	TTC	ACG	AGC	ACA	ACC	TAC	AAC	GAG	CTG	AGC	ATG	AGA	TCT	GAG	GAC	ACG	GCC	ATG	TAT	TAC	TTC	GCG	AGA	GA
	K																									
Z27506 ,IGHV1-69*02, YIGH6(YAC7)		A																								
X92340 ,IGHV1-69*03, 576TA8																										
X93132 ,IGHV1-69*04, b91063		A																								
X67905 ,IGHV1-69*05, KR.VH1.2		R																								
L23583 ,IGHV1-69*06, hv1051K		A																								
Z23978 ,IGHV1-69*07, DR-2		K																								
Z14309 ,IGHV1-69*08		A																								
Z14307 ,IGHV1-69*09		K																								
Z14300 ,IGHV1-69*10		A																								
Z14296 ,IGHV1-69*11		K																								
Z14301 ,IGHV1-69*12		A																								
Z14214 ,IGHV1-69*13		K																								

Alignment of 13 IGHV1-69 alleles showing the variable (V) coding region only. Nucleotides that differ from VH1-69 allele *01 are indicated at the appropriate position whereas identical nucleotides are marked with a dash. Where nucleotide changes result in amino acid differences, the encoded amino acid is shown above the corresponding triplet. Boxed regions correspond to CDR1, CDR2 and CDR3 as indicated.

Figure 5 (part 4 of 4)

Figure 6

