

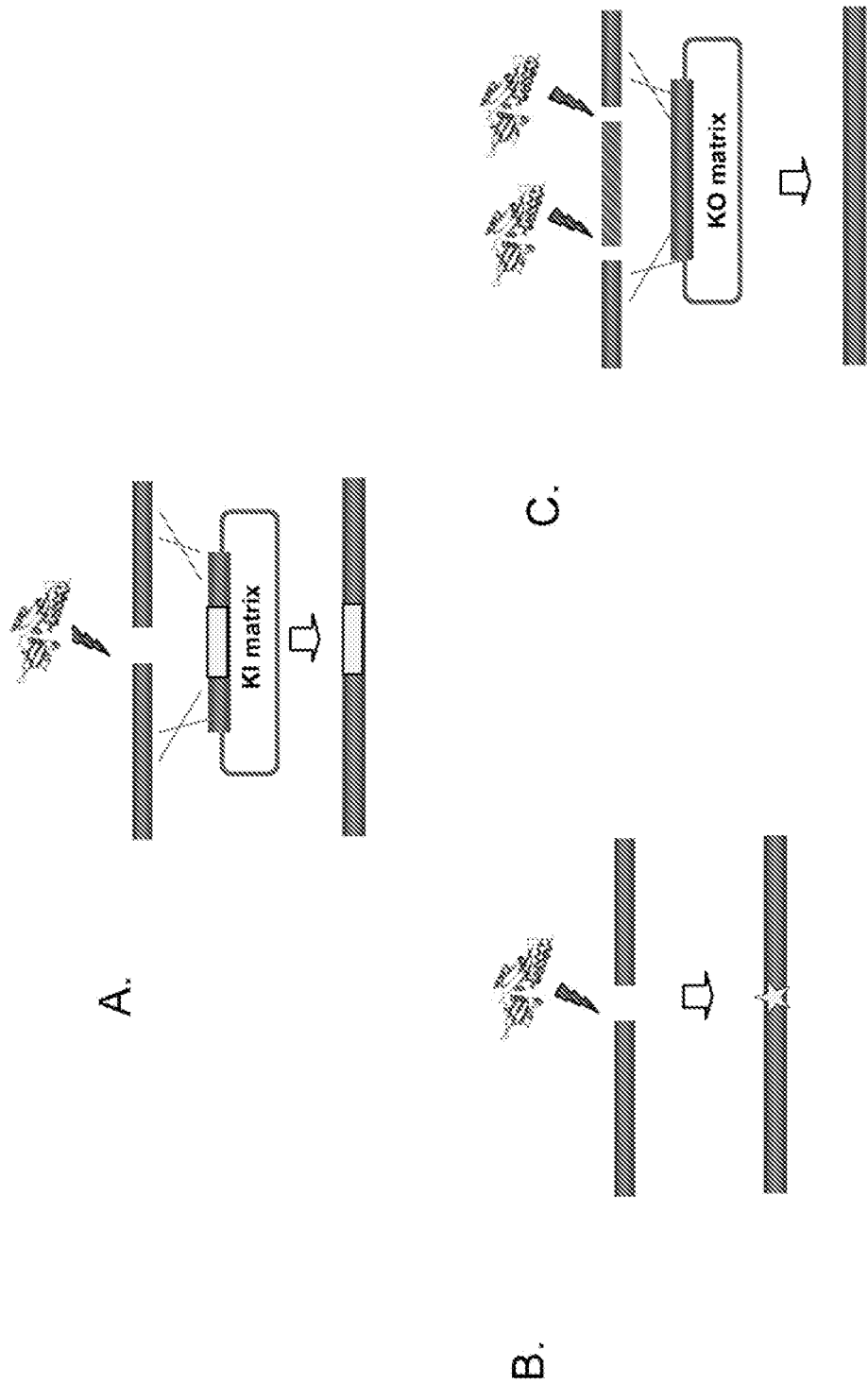


Figure 1

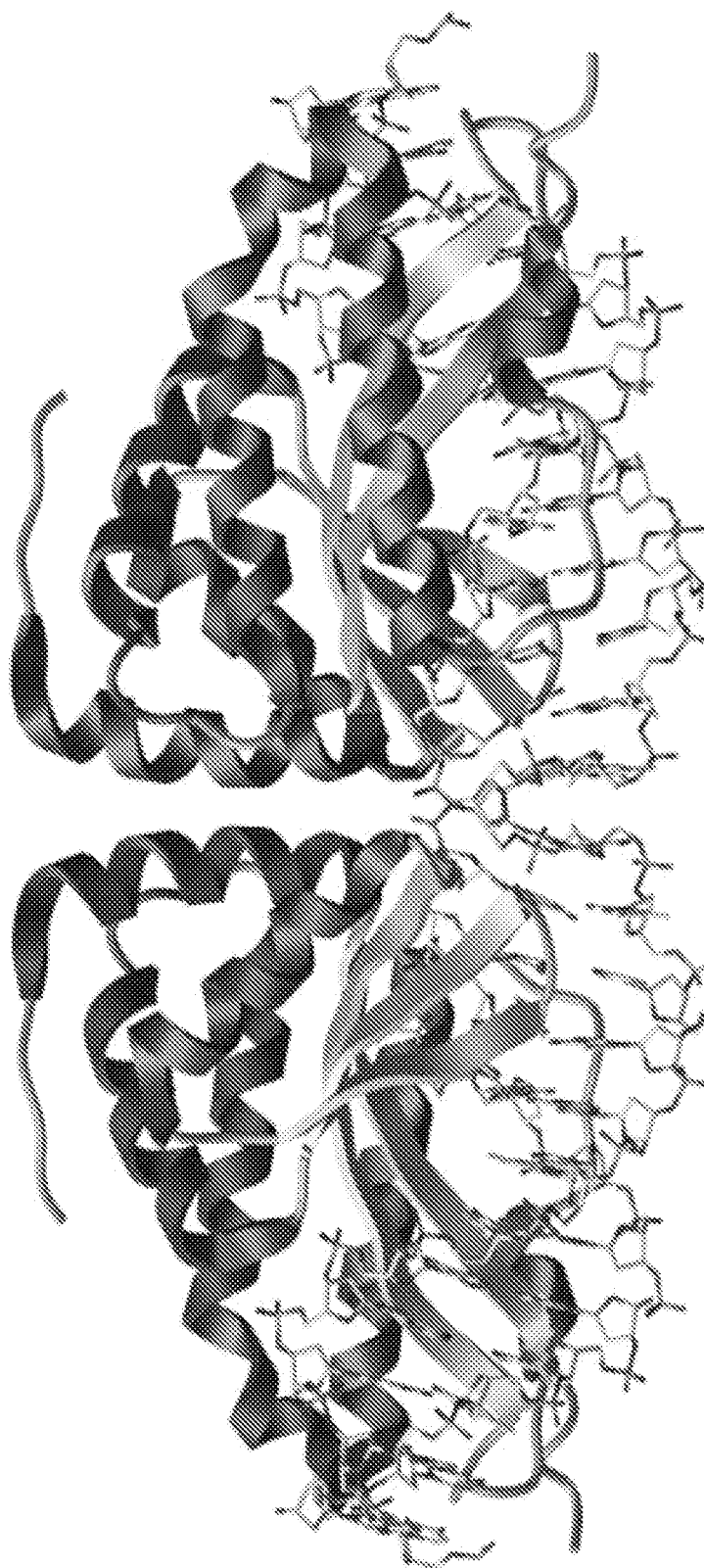


Figure 2A

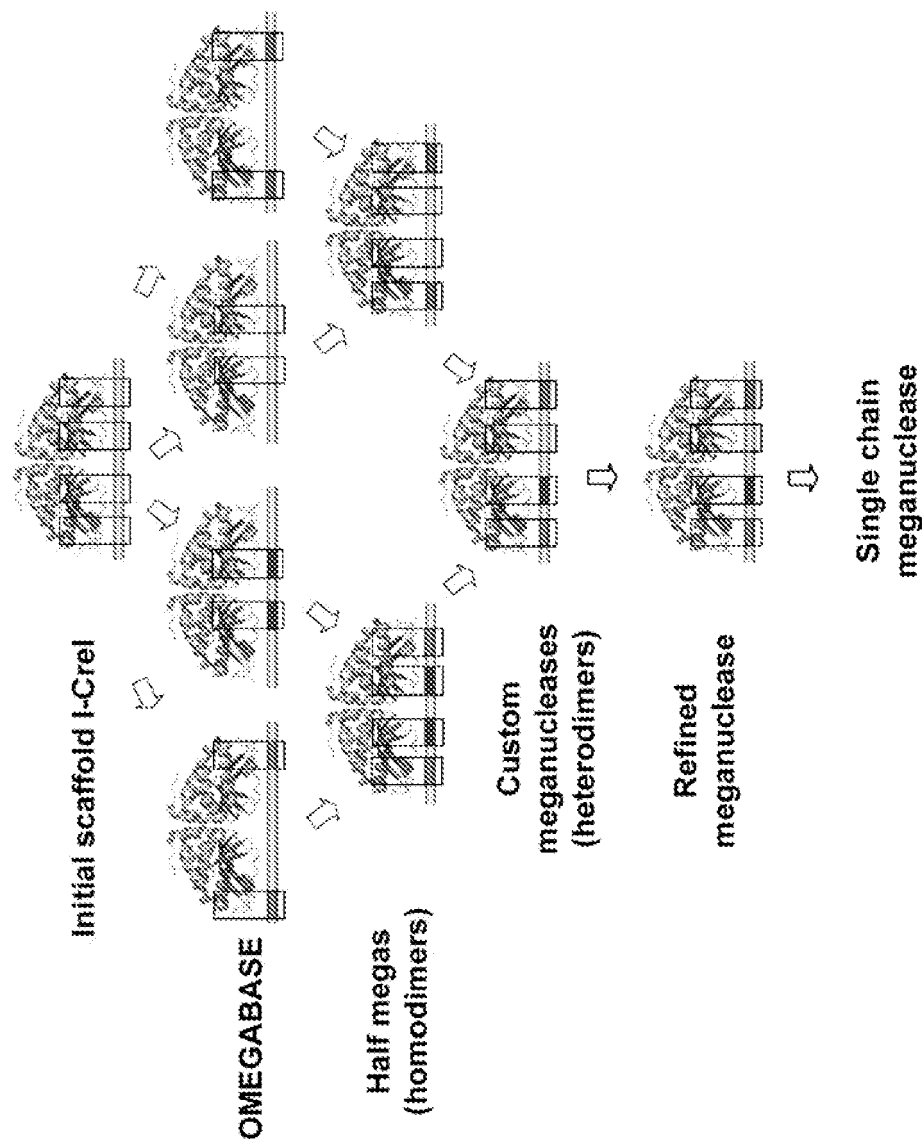


Figure 2B

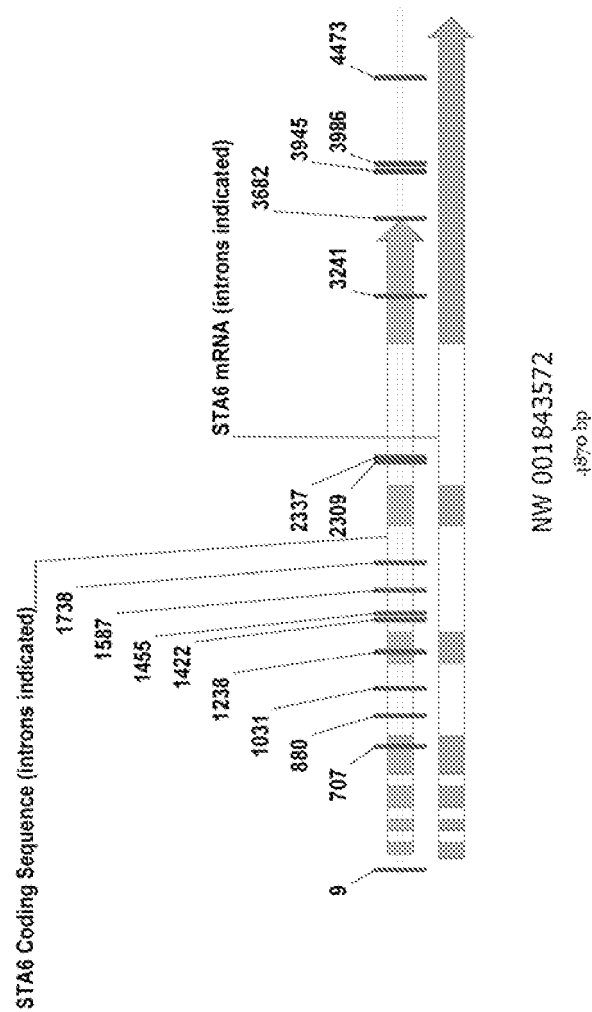


Figure 3

Target Name	Location (start-end)	Meganuclease Recognition Site	Seq ID No.
STA6-1	9-32	TGGGCACGACTTGCAATTGTGACT	4
STA6-2	707-730	ATTTACTGCTCACCAGTTCAC	5
STA6-3	880-903	TCCGCTAGGGGCACAGGAGCGAAC	6
STA6-4	1031-1054	ACCGCACACCGTACCGCGTCCACA	7
STA6-5	1238-1261	GTCCGCCAACAAAGAGCTGGTTCCA	8
STA6-6	1422-1445	TTCCTCTGCGCAAGGCAGCGGAGG	9
STA6-7	1455-1478	TGAGGCCGCCGTAACTGGGGGTGG	10
STA6-8	1587-1610	GTGCCACTGGGCACGGTGGCCTGC	11
STA6-9	1738-1761	ACGGCTGGTACACGGAGGGGTAC	12
STA6-10	2309-2332	TGGGATATGGTTCCAGGGCTAAT	13
STA6-11	2337-2360	CTGGATGGGTCAAGGTGGAGGGG	14
STA6-12	3241-3264	ACGCCGATCTACACCATGTGCG	15
STA6-13	3682-3705	TCGGGCCGGGAAGAGGCGCGCGG	16
STA6-14	3945-3968	CTGGCTGCGTTTTTGGGTTGGAA	17
STA6-15	3986-4009	ACTCTATAGAGTAGGGGGGATTGA	18
STA6-16	4473-4496	GTGGGATGCCGTAGGAGGGGCGGG	19

Figure 4

Identifier	Start	End	Meganuclease Recognition site	SEQ ID NO:	Localisation	Protein function (defined if annotated)
chr_2	498723	498746	TCGIGAIGCTGTAAAGGATTTTGA	20	Within exon	Undefined protein
chr_2	652741	652764	TTTGTACGTGTACGGTGTCTCCG	21	< 100 bp 5' from ATG	Undefined protein
chr_4	279666	279689	GAAGGATACCGTAAGTAGGTTTGG	22	Intron	Undefined protein
chr_4	429224	429247	ACAAGCCATTGTACGTTGTTCCTG	23	Exon	Undefined protein
chr_4	612222	612245	ATTGAACTCTTTACAAGAGCAAGG	24	Exon	Undefined protein
chr_7	172171	172194	TTTGTCTCTGTACGGCGTCTCTGG	25	Exon	Endodeoxyribonuclease
chr_8	301278	301301	TCAAAACTTTGTACAGAATGTTGT	26	Exon	Cathepsin S
chr_9	45476	45499	ACCAGACCCCGTAAAGAGATGGA	27	Exon	Undefined Protein
chr_9	736640	736663	ACGAACTACGTACTCCATTTGG	28	Intergenic	Landing pad
chr_12	505323	505346	GAAAACTGTCGTACAGGGTCTCGA	29	Exon	DNA directed RNA polymerase
chr_16	162706	162729	GCAAACTCTGTACATAGTACAAC	30	Intergenic	Landing pad
chr_17	269399	269422	GCAAACTGAGTTAAGGGATCCGAA	31	Exon	Adenylate cyclase
chr_18	153869	153892	CCGAGACCCCTGTAAAAGGTGGAAG	32	Intron	Undefined protein
chr_18	351359	351382	CCTGGCCCTGGTAAATAGTCTTGG	33	Exon	Undefined protein
chr_18	527270	527293	TTTGTCTTTTGTAAAGACAGACAAT	34	Intergenic	Landing pad
chr_19	534794	534817	ACAACTGGCGTAACGCAGTTTAT	35	Intergenic	Landing pad
chr_20	467336	467359	CCAAACCGTTTACAGTATATTCA	36	Intergenic	Landing pad
chr_21	97848	97871	ACGGGACTACGTACGACGGAATGC	37	Exon	Undefined protein
chr_21	463944	463967	GCAAAATGGTTTACGACAGTACGA	38	Intergenic	Landing pad
chr_28	116204	116227	GTTTACGTTGTACGACGCTAGC	39	Exon	Undefined protein

Figure 5

Identifier	Start	End	Meganuclease Recognition site	SEQ ID NO:	Localisation	Protein function (defined if annotated)
chr_2	2102510	2102533	TCCTTCTTCGGTACGTCATTCT	40	Intergenic	Landing pad
chr_3	653225	653248	ACAAGACGCTCACGTTGTTCCGT	41	Within Exon	Undefined protein
chr_3	1415073	1415096	TTTGGCCGAGGTACAGGGTACAAA	42	Exon	Undefined protein
chr_3	2313099	2313122	GCTACATGTCGTAACCAAGTACGGA	43	Intergenic	Landing pad
chr_4	1113577	1113600	ACAATATGGCTTACAAAAGACAGG	44	Intergenic	Landing pad
chr_5	1974540	1974563	ACAAGCTATTTTACAAGGGTCGGC	45	Intergenic	Landing pad
chr_6	1222972	1222995	TCCCTCTCTTGACAAATGTAAA	46	Exon	Undefined protein
chr_6	1483412	1483435	TCCTGCTCCTGTAAAGAAAGATTGC	47	Exon	Exo-alpha-sialidase
chr_6	1558881	1558904	ATAGGATCCATCACGACGTTTCAC	48	Intergenic	Landing pad
chr_8	73868	73891	ACTGGCCGATGTAAAGACGTCACAC	49	Intergenic	Landing pad
chr_8	439705	439728	GTGAAACTATGTAAAAAGGCAATT	50	Intergenic	Landing pad
chr_13	21020	21043	ATGAACGACGTACGAAGTATGG	51	Intergenic	Landing pad
chr_13	894899	894922	TCAATCTCAGGTGAAACAGAGCGT	52	Intergenic	Landing pad
chr_14	520457	520480	TCTGGCTCTGGTACGTTATCTTGT	53	Intron	Undefined protein
chr_15	170546	170569	ATGACATCCGTTACCGAAGAAAGAT	54	Exon	Undefined protein
chr_15	390968	390991	ATTAGACGAGGTGAGACGCTCTTGT	55	Intron	Undefined protein
chr_16a	339557	339580	ACAGGACGATGTACGACAGCGCAG	56	Intergenic	Landing pad
chr_17	273924	273947	TCAACCTTCTTTACAAGATCTGAC	57	Exon	Undefined protein
chr_23	287963	287986	GTGATACGTTGTGAGAAAGATTAA	58	Intron	Undefined protein

Figure 6

Identifier	Start	End	Meganuclease Recognition site	SEQ ID NO:	Localisation	Protein function (defined if annotated)
scaffold_1	1123137	1123160	ATTTTAIGTTIGGAAGAAGGTTGG	59	Within intron	Adenosine triphosphatase
scaffold_1	2142150	2142173	ACCTTCTCCATTACCCCATCCCCC	60	Intergenic	Landing pad
scaffold_12	1090579	1090602	GCGACCTCIGGTGAGGGGTTTGG	61	Within intron	Undefined protein
scaffold_19	486930	486953	AGGGCTGTGGTACGACGTCTGGG	62	Intergenic	Landing pad
scaffold_20	681363	681386	ACAAACGTCGTACAGGATGCAAG	63	Intergenic	Landing pad
scaffold_20	937919	937942	CCTGCCCTGTTTACCCCGTTTGG	64	Intergenic	Landing pad
scaffold_24	606974	606997	ACTGCCCTGTTTACAACGTGCAGC	65	Within exon	Undefined protein
scaffold_32	294535	294558	ACCTGCCCTGTACCCAGGCTTGC	66	Intergenic	Landing pad
scaffold_33	314696	314719	ATTGAACCTTTGTAAGTAGTTTGG	67	Intergenic	Landing pad
scaffold_40	49219	49242	GCTTCATCATGTACAACGGATCAC	68	Intergenic	Landing pas

Figure 7

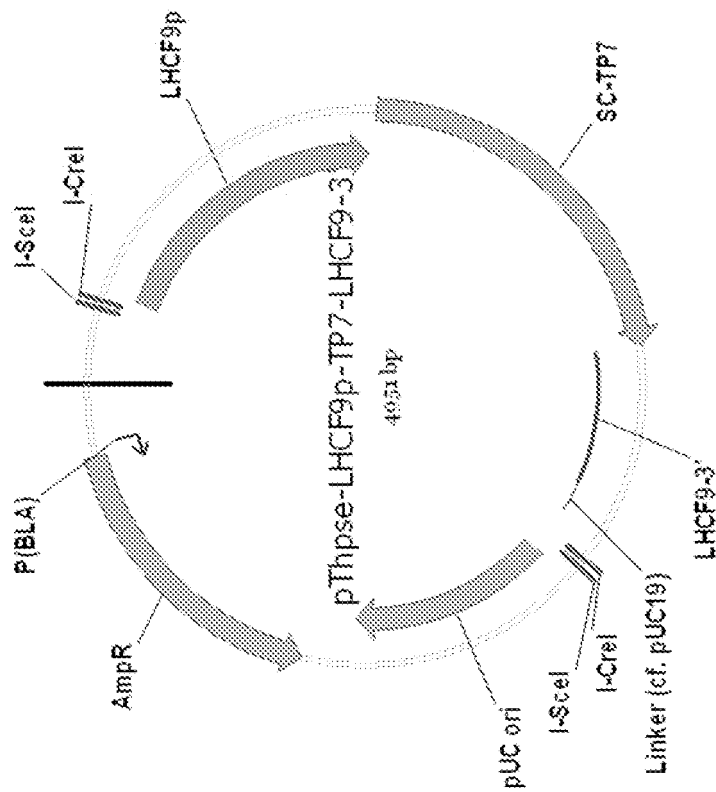


Figure 8

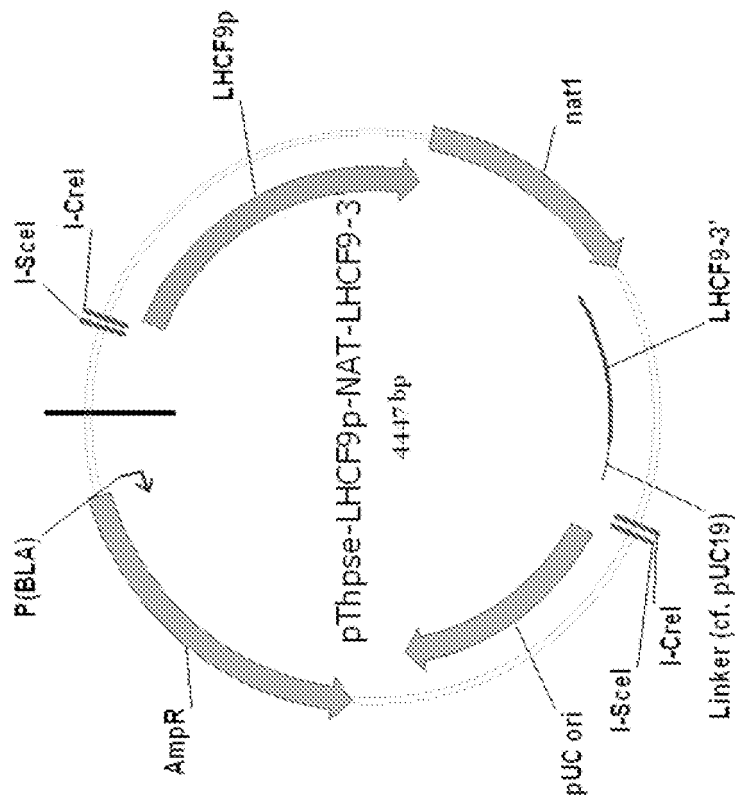
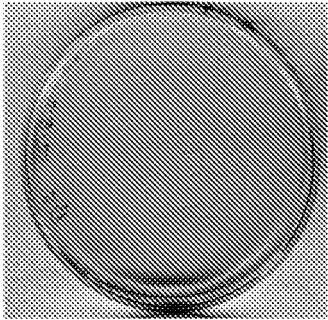


Figure 9

A



B

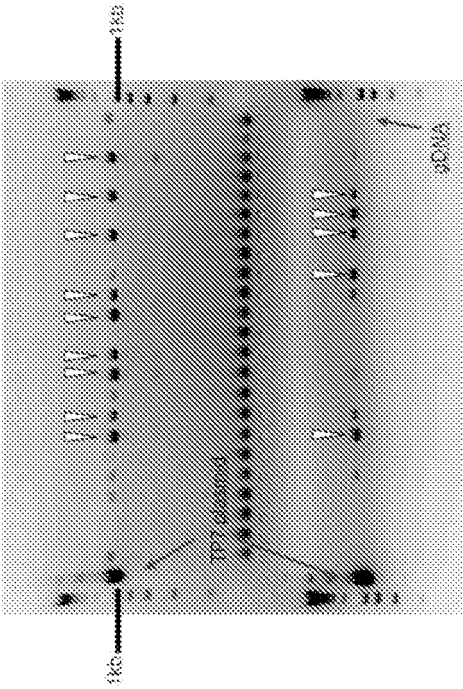


Figure 10

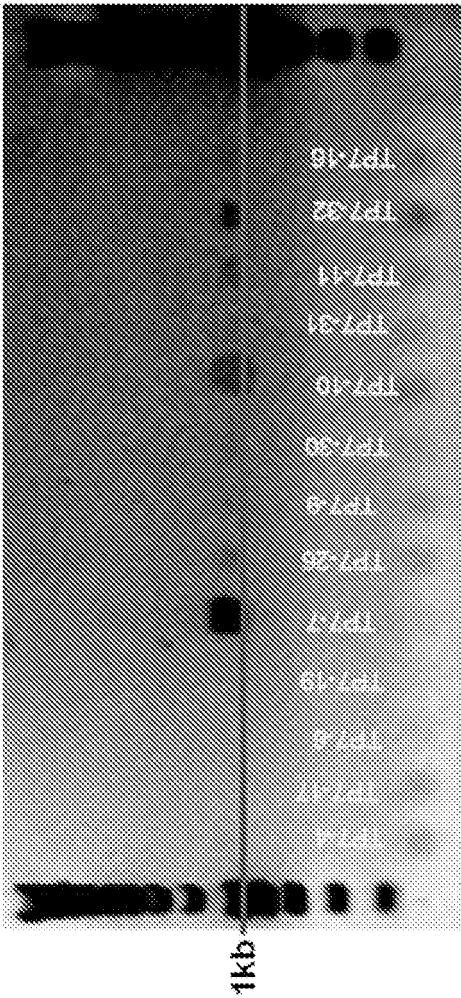


Figure 11

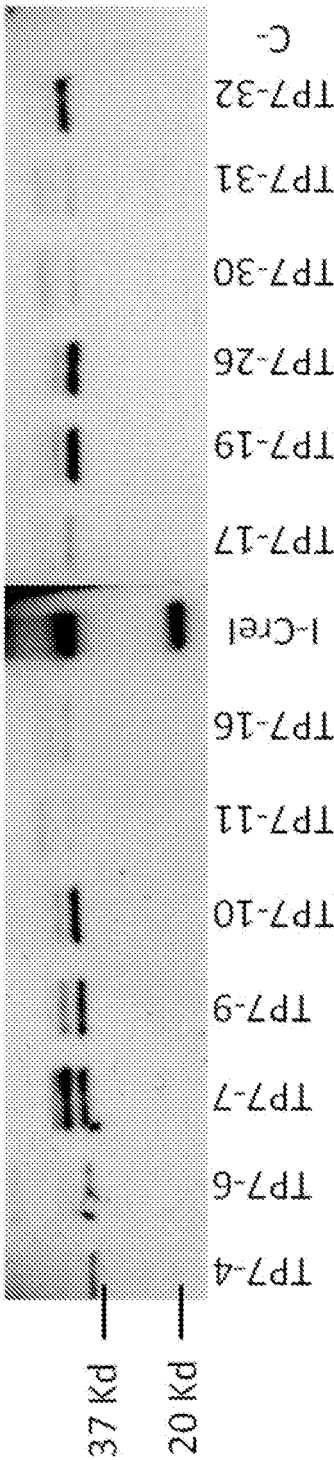


Figure 12

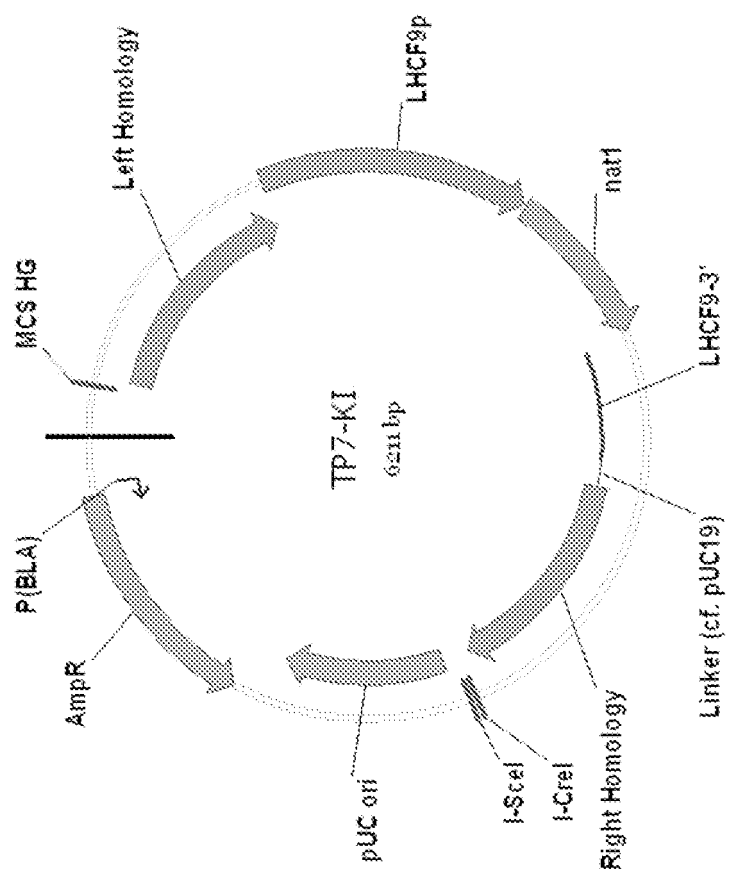


Figure 13