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Score	Expect	Method	Identities	Positives	Gaps
697 bits(1798)	0.0	Compositional matrix adjust.	341/531(64%)	415/531(78%)	2/531(0%)
Query 1	MELKNIIVNSYNITNILGYLRRSRQDMEREKRTGEDTLTEQKELMNKILTAIEIPYELKME	60			
Sbjct 1	MELK+IVNSYN+T I+GYLRRSRQD+EREKRTGEDTLTEQKELMNKILT IEIPYE + E	60			
Query 61	IGSGESIDGRPVFKECLKDLEEGKYQAIHAVKEITRLSRGSYSYDAGQIVNLLQSKRLIIIT	120			
Sbjct 61	IGSGESI+GRPVFK CL DL GK+QAIHAVKEITRLSRGSYSYDAG+IVNLL KR+IIIT	120			
Query 121	PYKVYDPRNPVDMRQIRFELFMAREEFEMTRERMTGAKYTYAAQGKWISGLAPYGYQLNK	180			
Sbjct 121	PYK+YDPRNPVD RQIRFELFMAREEFEMTRERM GAK+TYAAQGKWISGLAP+GY+LNK	180			
Query 181	KTSKLDPVEDEAKVVQLIFNIFLNGLNGKDYSYTAIAASHLTNLQIPTPSGKKRWNYTIK	240			
Sbjct 181	+TS+L+P +++ VV+LIF+IFLNGL+GKD SYTAIA+HL+ LQ TP G KRW++ T++	240			
Query 241	AILQNEVYIGTVKYKVREKTKDGKRTIRPEKEQIVVQDAHAPIIDKEQFQSQVKIANKV	300			
Sbjct 241	ILQNE Y+G V+YK RE TKDGK+ RPE E IVV DAH PII+KE F+ Q KI NKV	300			
Query 301	PLLPNKDEFELSELAGVCTCSKCGEPLSKYESKRIRKNKDGTSVYHVKSLTCKKNKCTY	360			
Sbjct 301	PLL P +E +ELAG+C CS CG+ L K+ES+ RKNKDGT S +HVK L CK NKCT	360			
Query 361	VRYNDVENAILDYLSLNDLNDSTLTKHINSMLSKYEDDNSNMKTKKQMSEHLSQKEKEL	420			
Sbjct 361	VRYEYVEEAILEYLEQLIALENNKLKAIIEKSMEAAETNNSE-KTSEQMLVQANQKQKEL	419			
Query 421	KNKENFIFDKYESGIYSDELFLKRKAALDEEFKELQNAKNELNGLQDTQSEIDSNTVRNN	480			
Sbjct 420	+NK FIF+K+ESGIY+DE+FL+RKAA+++E +++ K EL+ + + E D N R N	478			
Query 481	INKIIDQYHIESSEKKNELLRMVLKDVIVNMTQKRKGPIPAQFEITPILR	531			
Sbjct 479	I+ ++ Y S KNE LR + +++ MT+KR+GPIPA+F I P+LR	529			

Figure 1

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Score	Expect	Identities	Gaps	Strand
874 bits(473)	0.0	483/488(99%)	0/488(0%)	Plus/Minus
Query 113	ACTGACAAAGCGGTTTCTCCAACGAATGCCATGGGTGCAACAAAATTGATTTTCAGAAAAA	172		
Sbjct 464839	ACTGACAAAGCGGTTTCTCCAACGAATGCCATGGGTGCAACAAAATTGATTTTCAGAAAAA	464780		
Query 173	CTATTTTTCGAAGCAAACGAAAGTATTCCGAATCAAAAAACGAGGTTTGTCTCTGTACGC	232		
Sbjct 464779	CTATTTTTCGAAGCAAACGAAAGTATTCCAAATAAAAAACCAAGTTTGTCTCTGTACGC	464720		
Query 233	TTTGGCAATGTGCTTGGATCTAGAGGTTCCGTTATTCCGATCATGCTCCAGCAGCTATTA	292		
Sbjct 464719	TTTGGCAATGTGCTTGGATCTAGAGGTTCCGTGATTCCGATCATGCTCCAGCAGCTATTA	464660		
Query 293	AATGAAAAACCTTTGACCGTGACTGATCCTCATATGACACGCTTTTATGTCCATTGAA	352		
Sbjct 464659	AATGAAAAACCTTTGACCGTGACTGATCCTCATATGACACGTTTTTTTATGTCCATTGAA	464600		
Query 353	GAGGCTGTTTCCCTCACACTTCAAGCAGCAATCATGATGAAAGCGGCGAAACCTTCATT	412		
Sbjct 464599	GAGGCTGTTTCCCTCACACTTCAAGCAGCAATCATGATGAAAGCGGCGAAACCTTCATT	464540		
Query 413	CTCAAGATGGAGTCCTTACAGCTTGCCGATCTCCTAAAAGCGTTTCATGAATATGCCGCT	472		
Sbjct 464539	CTCAAGATGGAGTCCTTACAGCTTGCCGATCTCCTAAAAGCGTTTCATGAATATGCCGCT	464480		
Query 473	CAAATCAATGCTAAATCTCCGGATATTCTTGTAGTCGGAAAAAGACCTGGCGAAAAGCTT	532		
Sbjct 464479	CAAATCAATGCTAAATCTCCGGATATTCTTGTAGTCGGAAAAAGACCTGGCGAAAAGCTT	464420		
Query 533	CACGAGGAGCTCACATTTCCGCACGAAGCAGATGCACTGTTGAACATGAACAATTTTAT	592		
Sbjct 464419	CACGAGGAGCTCACATTTCCGCACGAAGCAGATGCACTGTTGAACATGAACAATTTTAT	464360		
Query 593	GCCATTTT 600			
Sbjct 464359	GCCATTTT 464352			

Figure 2

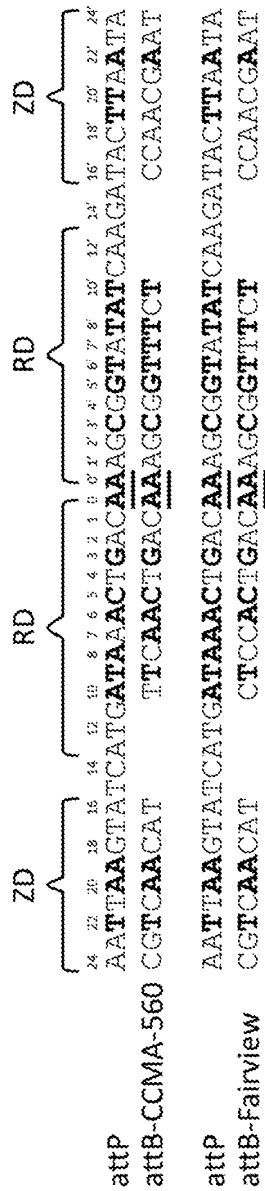


Figure 3

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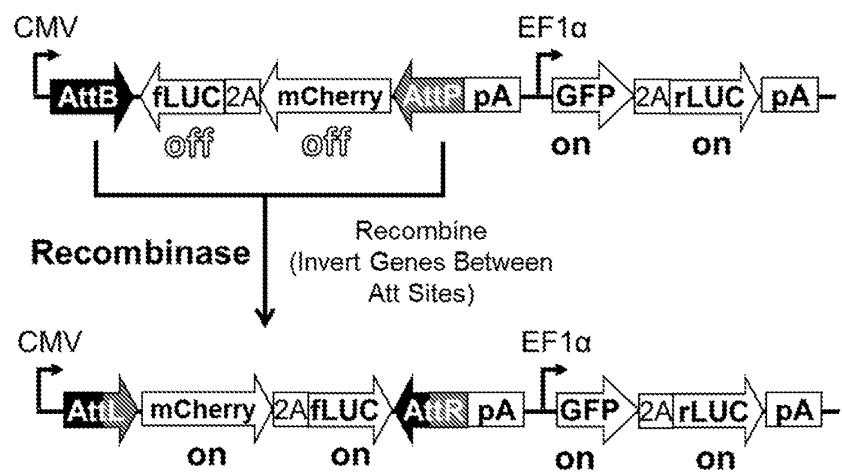


Figure 4

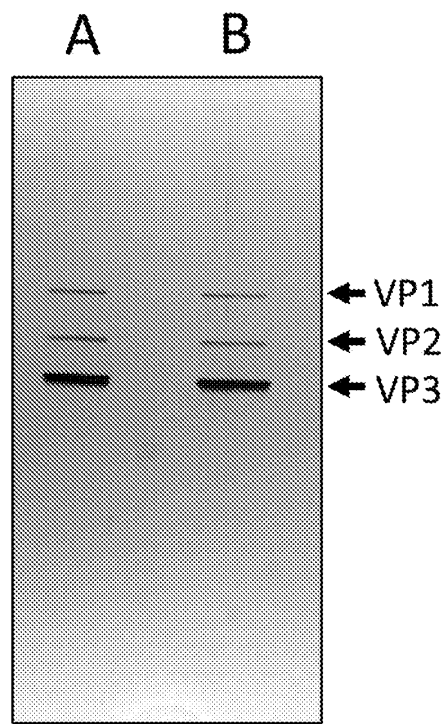


Figure 5

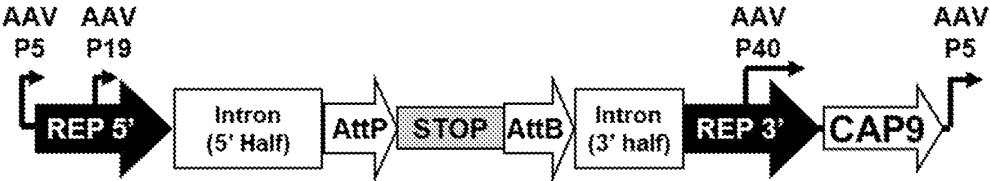


Figure 6

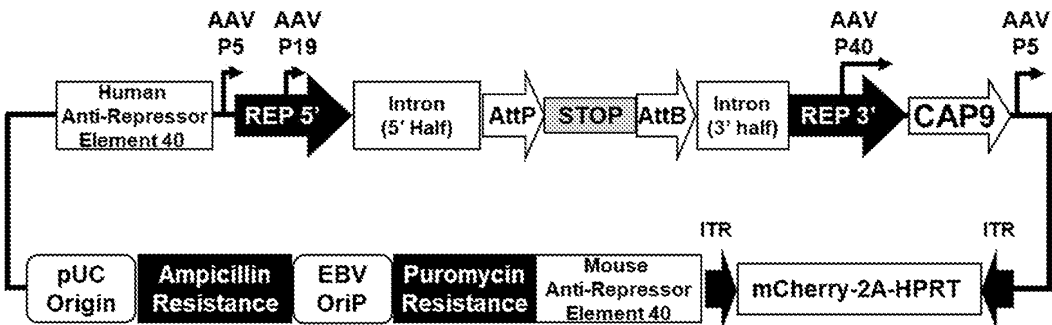
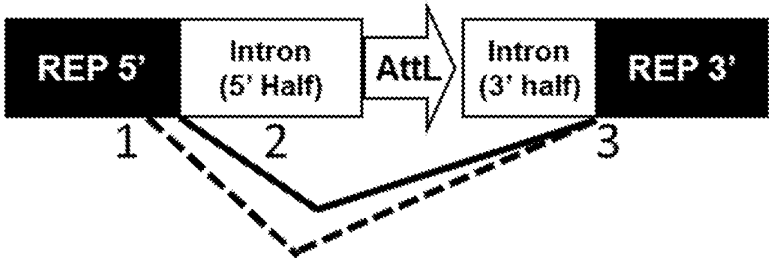


Figure 7



- | | |
|-------------------------------|----------------------|
| 1) REP-derived Splice Donor | CTTCAGCCAGgtacatggag |
| 2) Beta-Actin Splice Donor | GTGGATCCAGgtgggtgtc |
| 3) Beta-Actin Splice Acceptor | ccctcctcagGAGGACCAG |

Figure 8

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P600

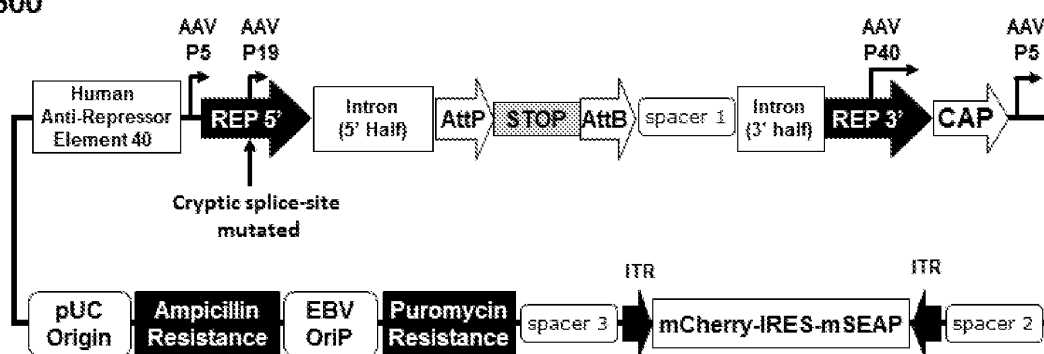


Figure 9