Figure 1

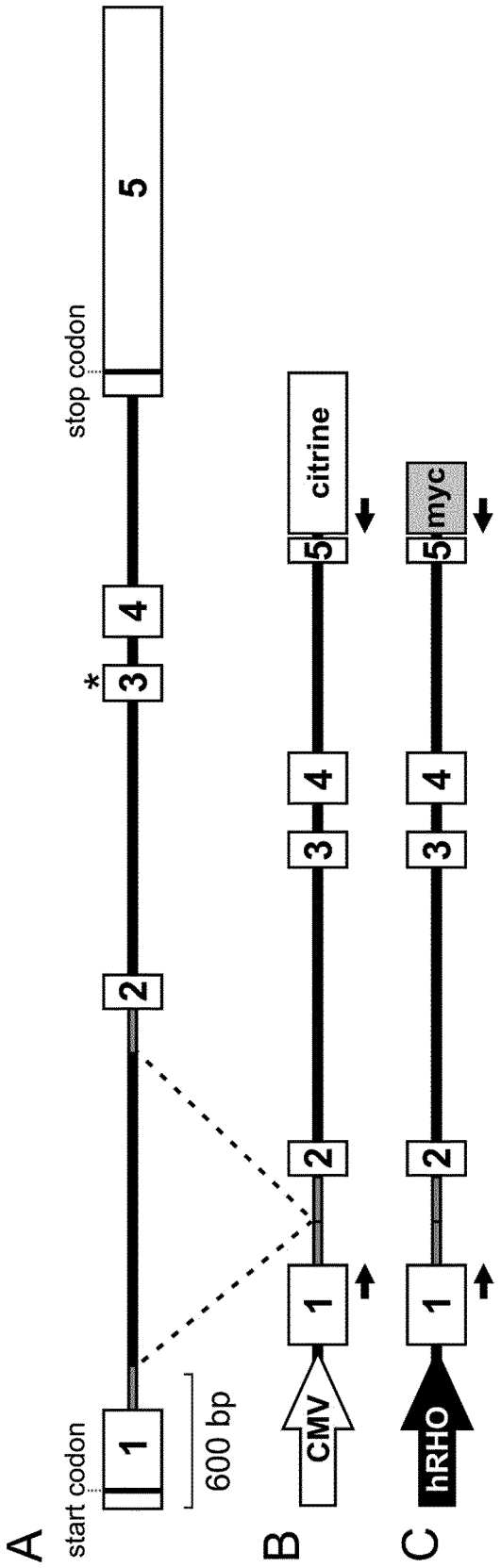

A
start codon
1
600 bp
2
*
3
4
stop codon
5
B
CMV
1
2
3
4
citrine
5
C
hRHO
1
2
3
4
myc
5

Figure 1 (cont')

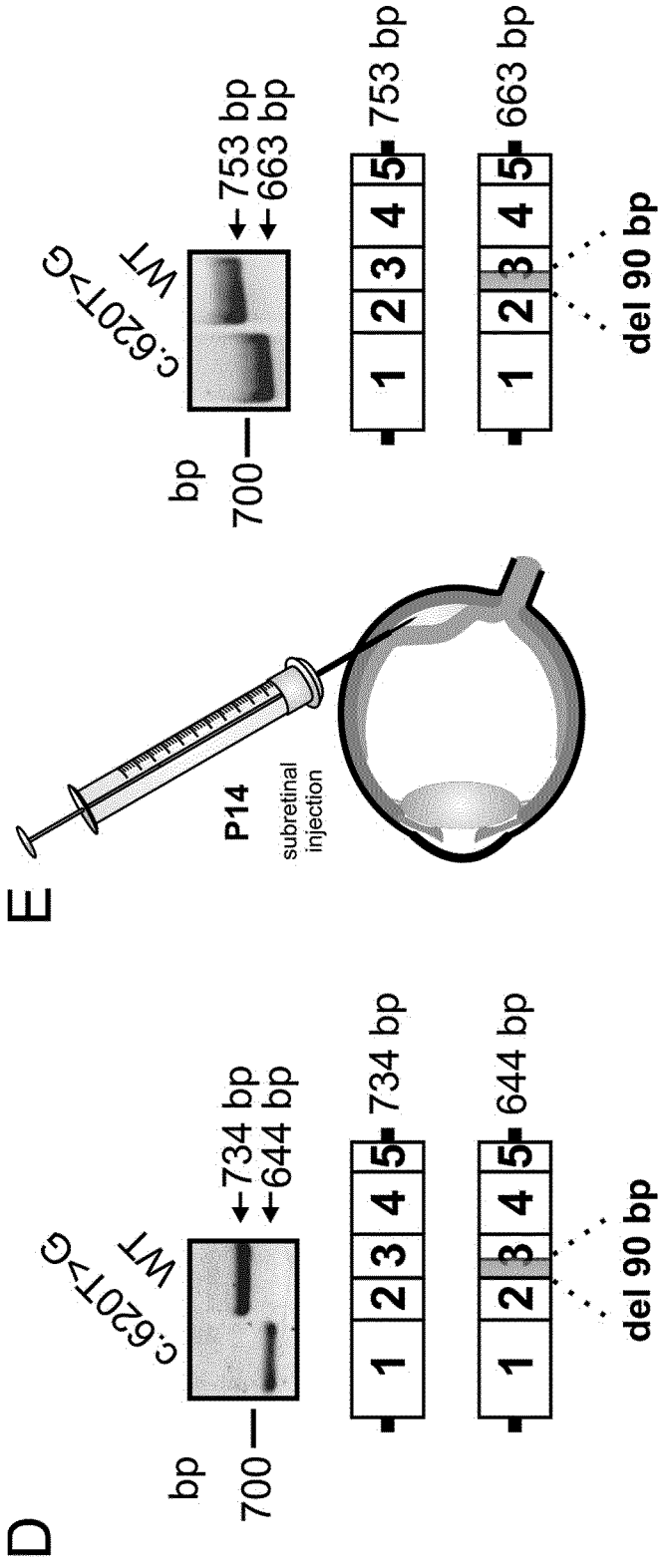


Figure 2

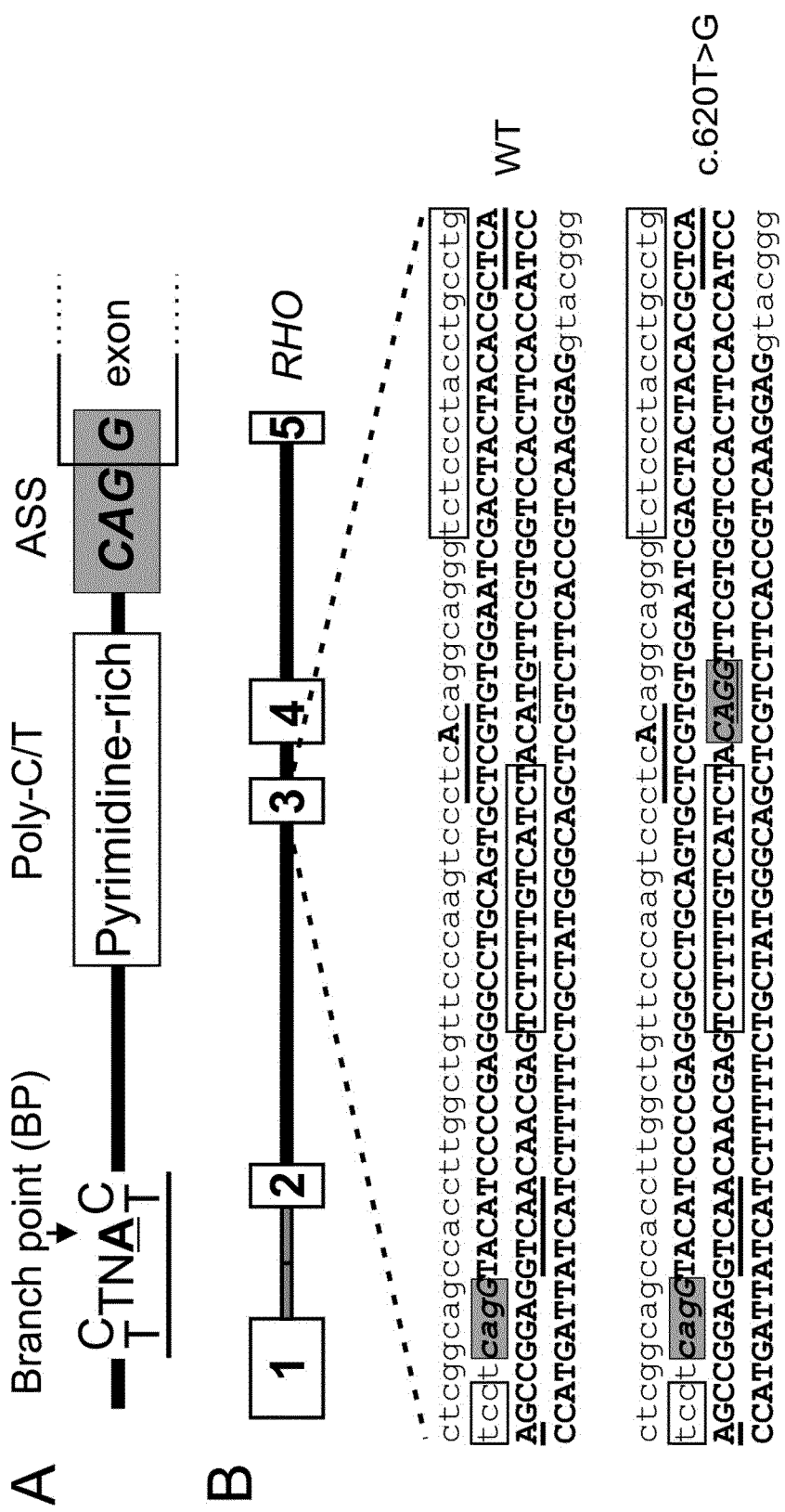

A
Branch point (BP)
Poly-C/T
ASS
exon
Pyrimidine-rich
CAG G
C
TTNAC
T
B
1
2
3
4
5
RHO
WT
c.620T>G

Figure 2 (cont')

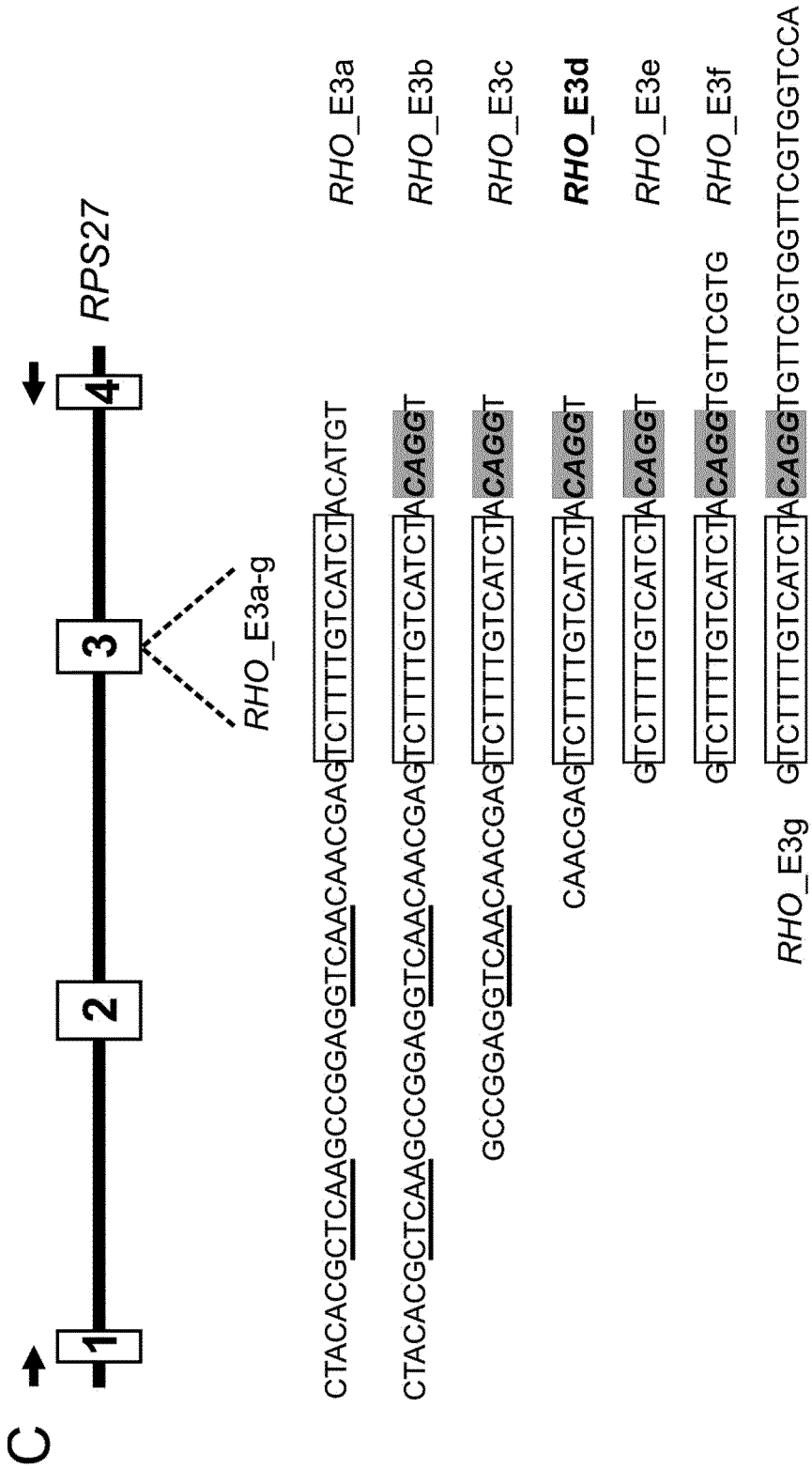


Figure 2 (cont')

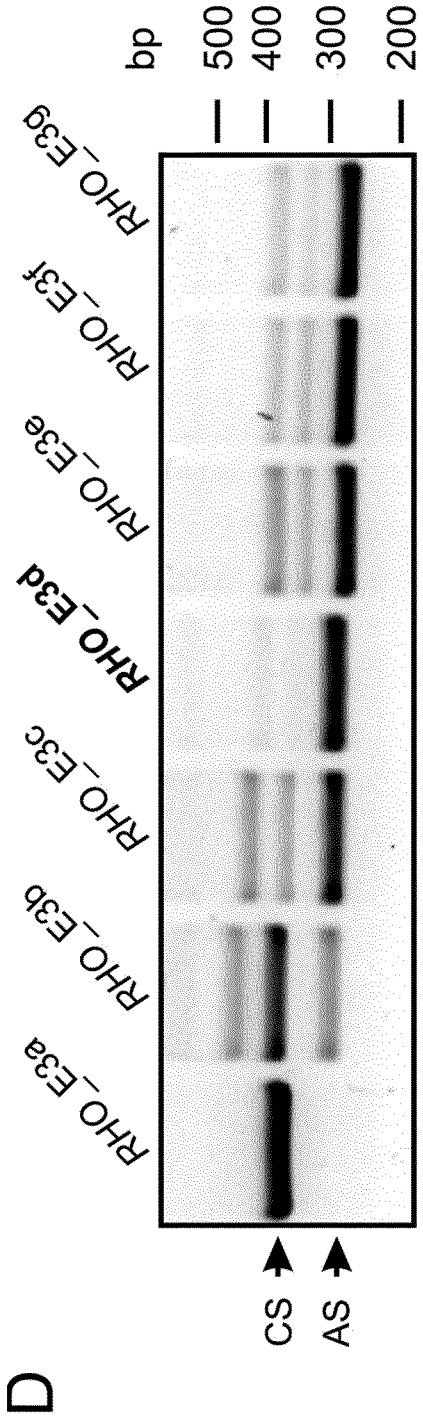


Figure 3

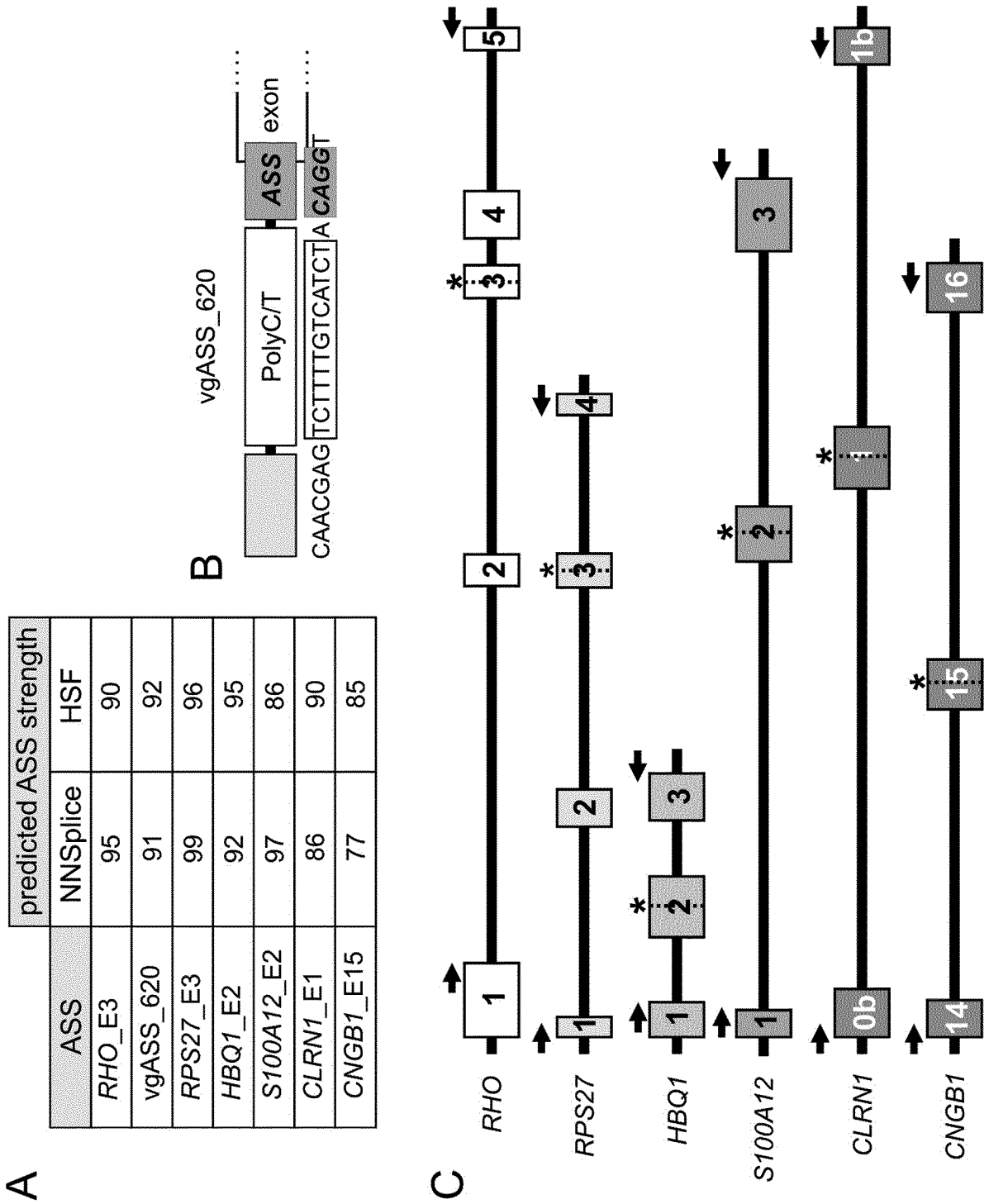
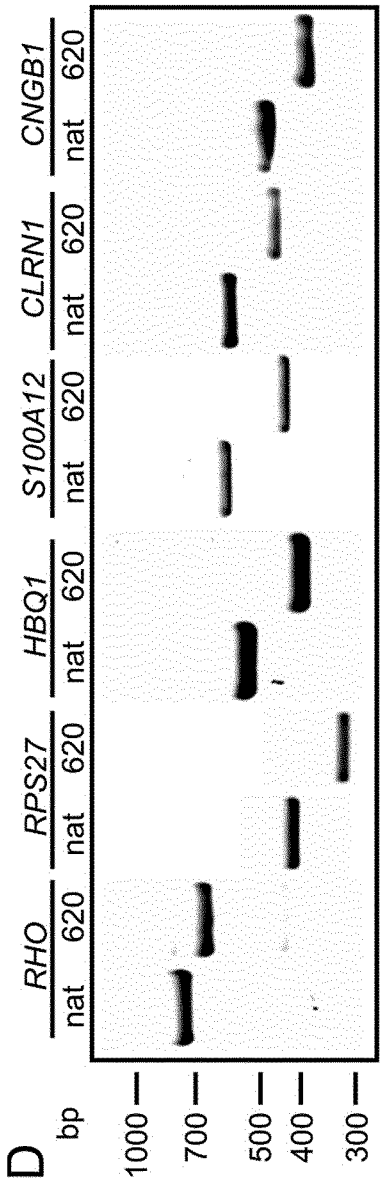

A
predicted ASS strength
ASS
NNSplice
HSF
RHO_E3
95
90
vgASS_620
91
92
RPS27_E3
99
96
HBQ1_E2
92
95
S100A12_E2
97
86
CLRN1_E1
86
90
CNGB1_E15
77
85
B
vgASS_620
PolyC/T
ASS
exon
CAACGAG
TCTTTTGTCATCT
A
CAGGT
C
RHO
RPS27
HBQ1
S100A12
CLRN1
CNGB1

Figure 3 (cont')



E

	length [bp]	
gene	native ASS	vgASS_620
RHO	756	666
RPS27	431	334
HBQ1	548	402
S100A12	582	458
CLRN1	572	475
CNGB1	486	388

Figure 4

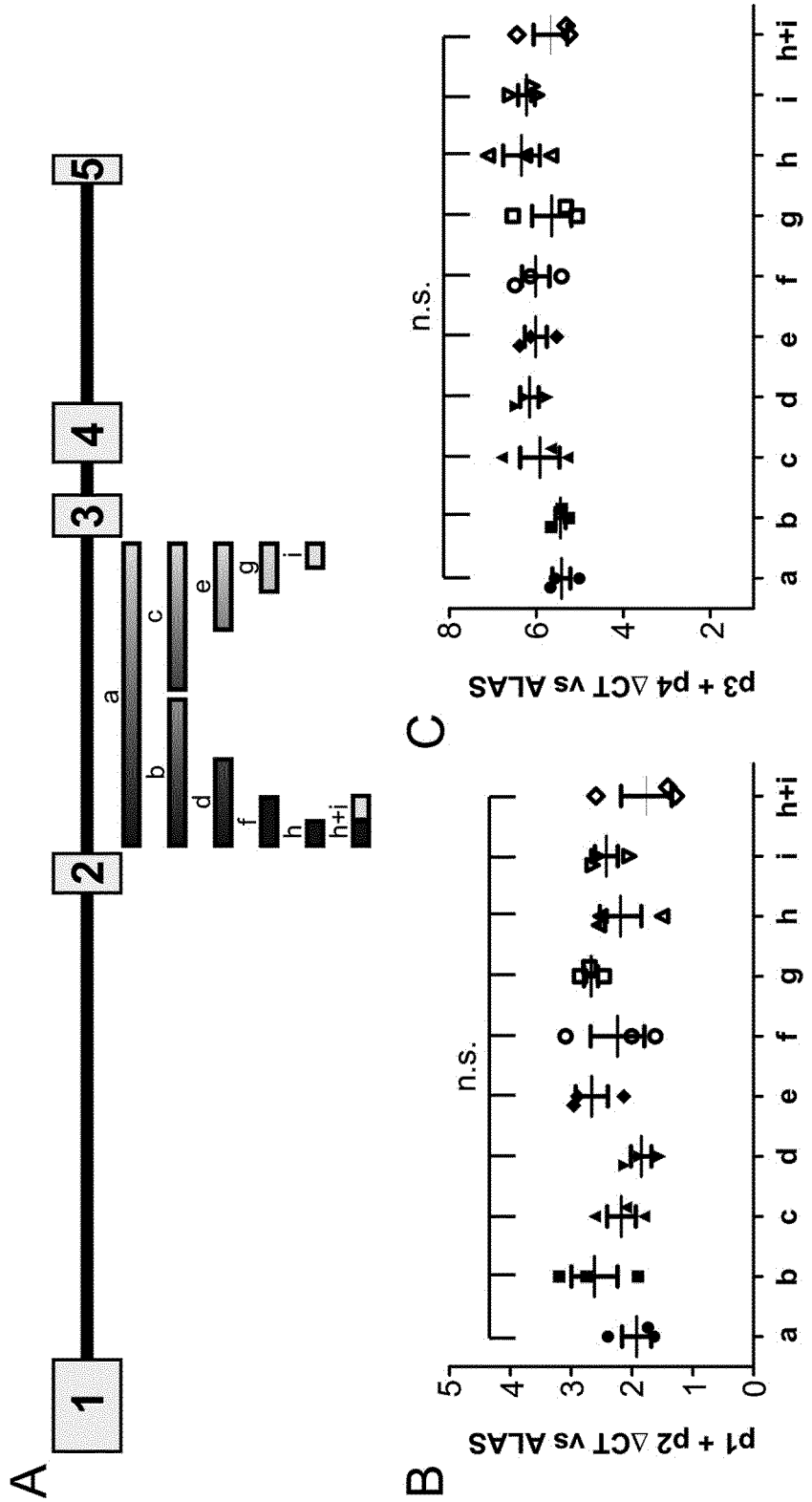
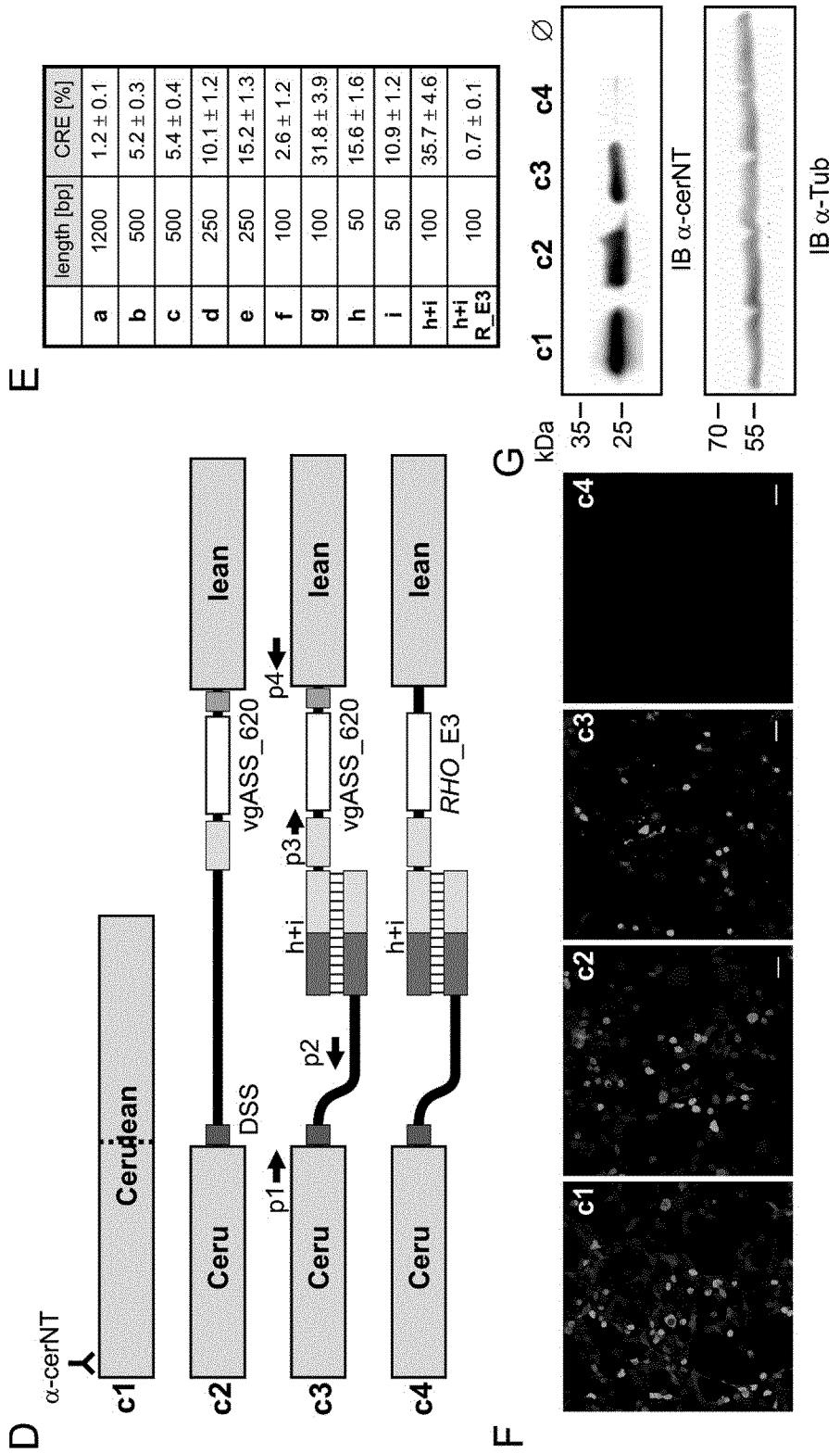

A
1
2
3
4
5
a
b
c
d
e
f
g
h
h+i
i
B
p1 + p2 ΔCT vs ALAS
n.s.
0
1
2
3
4
5
a b c d e f g h i h+i
C
p3 + p4 ΔCT vs ALAS
n.s.
2
4
6
8
a b c d e f g h i h+i

Figure 4 (cont')



	length [bp]	CRE [%]
a	1200	1.2 ± 0.1
b	500	5.2 ± 0.3
c	500	5.4 ± 0.4
d	250	10.1 ± 1.2
e	250	15.2 ± 1.3
f	100	2.6 ± 1.2
g	100	31.8 ± 3.9
h	50	15.6 ± 1.6
i	50	10.9 ± 1.2
h+i	100	35.7 ± 4.6
h+i R_E3	100	0.7 ± 0.1

Figure 5

Dual AAV comprising the 5' coding sequence of ABCA4 (SEQ ID NO: 19):

CTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCGTCGGGCGACCTTTGGTCGCCC
GGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTtgtagt
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gggcgcgccgtttaaatagctagcGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGG
TCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTG
ACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTAT
CATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTA
CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGA
TGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCAC
CCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAA
CTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTggta
ccaccggtgccaccATGGGCTTCGTGAGACAGATACAGCTTTTGCTCTGGAAGAACTGGACCCTGCGG
AAAAGGCAAAAGATTCGCTTTGTGGTGGAACTCGTGTGGCCTTTATCTTTATTTCTGGTCTTGATCTG
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CAGGAATGCTGCCGTGGCTCCAGGGGATCTTCTGCAATGTGAACAATCCCTGTTTTCAAAGCCCCACC
CCAGGAGAATCTCCTGGAATTGTGTCAAACTATAACAACTCCATCTTGGCAAGGGTATATCGAGATTT
TCAAGAACTCCTCATGAATGCACCAGAGAGCCAGCACCTTGGCCGTATTTGGACAGAGCTACACATCT
TGTCCCAATTCATGGACACCCTCCGGACTCACCCGGAGAGAATTGCAGGAAGAGGAATACGAATAAGG
GATATCTTGAAAGATGAAGAAACACTGACACTATTTCTCATTAAAAACATCGGCCTGTCTGACTCAGT
GGTCTACCTTCTGATCAACTCTCAAGTCCGTCCAGAGCAGTTCGCTCATGGAGTCCCGGACCTGGCGC
TGAAGGACATCGCCTGCAGCGAGGCCCTCCTGGAGCGCTTCATCATCTTCAGCCAGAGACGCGGGGCA
AAGACGGTGCGCTATGCCCTGTGCTCCCTCTCCCAGGGCACCCTACAGTGGATAGAAGACACTCTGTA
TGCCAACGTGGACTTCTTCAAGCTCTTCCGTGTGCTTCCCACACTCCTAGACAGCCGTTCTCAAGGTA
TCAATCTGAGATCTTGGGGAGGAATATTATCTGATATGTCACCAAGAATTCAAGAGTTTATCCATCGG
CCGAGTATGCAGGACTTGCTGTGGGTGACCAGGCCCCTCATGCAGAATGGTGGTCCAGAGACCTTTAC
AAAGCTGATGGGCATCCTGTCTGACCTCCTGTGTGGCTACCCCGAGGGAGGTGGCTCTCGGGTGCTCT
CCTTCAACTGGTATGAAGACAATAACTATAAGGCCTTTCTGGGGATTGACTCCACAAGGAAGGATCCT
ATCTATTCTTATGACAGAAGAACAACATCCTTTTGTAATGCATTGATCCAGAGCCTGGAGTCAAATCC
TTTAACCAAAATCGCTTGGAGGGCGGCAAAGCCTTTGCTGATGGGAAAAATCCTGTACACTCCTGATT
CACCTGCAGCACGAAGGATACTGAAGAATGCCAACTCAACTTTTGAAGAACTGGAACACGTTAGGAAG
TTGGTCAAAGCCTGGGAAGAAGTAGGGCCCCAGATCTGGTACTTCTTTGACAACAGCACACAGATGAA
CATGATCAGAGATACCCTGGGGAACCCAACAGTAAAAGACTTTTTGAATAGGCAGCTTGGTGAAGAAG
GTATTACTGCTGAAGCCATCCTAAACTTCCTCTACAAGGGCCCTCGGGAAAGCCAGGCTGACGACATG
GCCAACTTCGACTGGAGGGACATATTTAACATCACTGATCGCACCCTCCGCCTGGTCAATCAATACCT
GGAGTGCTTGGTCCTGGATAAGTTTGAAAGCTACAATGATGAAACTCAGCTCACCCAACGTGCCCTCT
CTCTACTGGAGGAAAACATGTTCTGGGCCGGAGTGGTATTCCCTGACATGTATCCCTGGACCAGCTCT
CTACCACCCCACGTGAAGTATAAGATCCGAATGGACATAGACGTGGTGGAGAAAACCAATAAGATTAA

Figure 5 (cont')

AGACAGGTATTGGGATTCTGGTCCCAGAGCTGATCCCGTGGAAGATTTCCGGTACATCTGGGGCGGGT
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GGAATCTACCTCCAGCAGATGCCCTACCCCTGCTTCGTGGACGATTCTTTCATGATCATCCTGAACCG
CTGTTTCCCTATCTTCATGGTGCTGGCATGGATCTACTCTGTCTCCATGACTGTGAAGAGCATCGTCT
TGGAGAAGGAGTTGCGACTGAAGGAGACCTTGAAAAATCAGGGTGTCTCCAATGCAGTGATTTGGTGT
ACCTGGTTCCTGGACAGCTTCTCCATCATGTCGATGAGCATCTTCCTCCTGACGATATTCATCATGCA
TGGAAGAATCCTACATTACAGCGACCCATTCATCCTCTTCCTGTTCTTGTTGGCTTTCTCCACTGCCA
CCATCATGCTGTGCTTTCTGCTCAGCACCTTCTTCTCCAAGGCCAGTCTGGCAGCAGCCTGTAGTGGT
GTCATCTATTTCACCCTCTACCTGCCACACATCCTGTGCTTCGCCTGGCAGGACCGCATGACCGCTGA
GCTGAAGAAGGCTGTGAGCTTACTGTCTCCGGTGGCATTTGGATTTGGCACTGAGTACCTGGTTCGCT
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TGATCAGGTGTTTCCAGGAGACTATGGAACCCCACTTCCTTGGTACTTTCTTCTACAAGAGTCGTATT
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GAAACGGAGGATCCAGAGCACCCAGAAGGAATACACGACTCCTTCTTTGAACGTGAGCATCCAGGGTG
GGTTCCTGGGGTATGCGTGAAGAATCTGGTAAAGATTTTTGAGCCCTGTGGCCGGCCAGCTGTGGACC
GTCTGAACATCACCTTCTACGAGAACCAGATCACCGCATTCCTGGGCCACAATGGAGCTGGGAAAACC
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CATTGAAACCAGCCTGGATGCAGTCCGGCAGAGCCTTGGCATGTGTCCACAGCACAACATCCTGTTCC
ACCACCTCACGGTGGCTGAGCACATGCTGTTCTATGCCCAGCTGAAAGGAAAGTCCCAGGAGGAGGCC
CAGCTGGAGATGGAAGCCATGTTGGAGGACACAGGCCTCCACCACAAGCGGAATGAAGAGGCTCAGGA
CCTATCAGGTGGCATGCAGAGAAAGCTGTCGGTTGCCATTGCCTTTGTGGGAGATGCC*AAGgtaag*gg
cactgagcagaagggaagaagctccgggggctctttgtagggtaagcttAGTGCATCAAGGCGATCAC
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AGGTGGTCAGATGaagcttattctcgagttaagggcgaattcccgattaggatcttcctagagcatgg
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CTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTT
GCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAG

Figure 6

Dual AAV comprising the 3' coding sequence of ABCA4 (SEQ ID NO:20):

CTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCGTCGGGCGACCTTTGGTCGCCC
GGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTtgtagt
taatgattaacccgccatgctacttatctacgtagccatgctctaggaagatcggaattcgcccttaa
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TCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTG
ACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTAT
CATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTA
CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGA
TGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCAC
CCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAA
CTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTggta
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TAACCGCCTGTCTGGCTTTTTTTCACTGATGTGATCGCCTTGATGCACTaagcttCAACGAGTCTTTT
GTCATCTACAGGTGGTGATTCTGGACGAACCCACCTCTGGGGTGGACCCTTACTCGAGACGCTCAATC
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CGACCTCCTTGGGGACCGCATTGCCATCATTGCCCAGGGAAGGCTCTACTGCTCAGGCACCCCACTCT
TCCTGAAGAACTGCTTTGGCACAGGCTTGTACTTAACCTTGGTGCGCAAGATGAAAAACATCCAGAGC
CAAAGGAAAGGCAGTGAGGGGACCTGCAGCTGCTCGTCTAAGGGTTTCTCCACCACGTGTCCAGCCCA
CGTCGATGACCTAACTCCAGAACAAGTCCTGGATGGGGATGTAAATGAGCTGATGGATGTAGTTCTCC
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GGTCCCAGAGAGAAGGCTGGACAGACACCCCAGGACTCCAATGTCTGCTCCCCAGGGGCGCCGGCTGC
TCACCCAGAGGGCCAGCCTCCCCCAGAGCCAGAGTGCCCAGGCCCGCAGCTCAACACGGGGACACAGC
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TCCTTTTGGCGAATACCCCGCTTTGACCCTTCACCCCTGGATATATGGGCAGCAGTACACCTTCTTCA
GCATGGATGAACCAGGCAGTGAGCAGTTCACGGTACTTGCAGACGTCCTCCTGAATAAGCCAGGCTTT
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TCCTTCTGTGTCCCCAAACATCACCCAGCTGTTCCAGAAGCAGAAATGGACACAGGTCAACCCTTCAC
CATCCTGCAGGTGCAGCACCAGGGAGAAGCTCACCATGCTGCCAGAGTGCCCCGAGGGTGCCGGGGGC
CTCCCGCCCCCCCAGAGAACACAGCGCAGCACGGAAATTCTACAAGACCTGACGGACAGGAACATCTC
CGACTTCTTGGTAAAAACGTATCCTGCTCTTATAAGAAGCAGCTTAAAGAGCAAATTCTGGGTCAATG
AACAGAGGTATGGAGGAATTTCCATTGGAGGAAAGCTCCCAGTCGTCCCCATCACGGGGGAAGCACTT

Figure 6 (cont')

GTTGGGTTTTTAAGCGACCTTGGCCGGATCATGAATGTGAGCGGGGGCCCTATCACTAGAGAGGCCTC
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CAGTTTATCAGTGGAGTGAGCCCCACCACCTACTGGGTGACCAACTTCCTCTGGGACATCATGAATTA
TTCCGTGAGTGCTGGGCTGGTGGTGGGCATCTTCATCGGGTTTCAGAAGAAAGCCTACACTTCTCCAG
AAAACCTTCCTGCCCTTGTGGCACTGCTCCTGCTGTATGGATGGGCGGTCATTCCCATGATGTACCCA
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CATCAACAGCAGTGCTATTACCTTCATCTTGGAATTATTTGAGAATAACCGGACGCTGCTCAGGTTCA
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GCACTGAGCCAGGCTGTGACAGATGTCTATGCCCGGTTTGGTGAGGAGCACTCTGCAAATCCGTTCCA
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GCAATAAACAAGTTctcgagttaagggcgaattcccgattaggatcttcctagagcatggctacgtag
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CTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGC
GGCCTCAGTGAGCGAGCGAGCGCGCAG

Figure 7

Dual AAV comprising the 5' coding sequence of ABCA4 (SEQ ID NO: 21):

CTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCGTCGGGCGACCTTTGGTCGCCC
GGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTtgtagt
taatgattaacccgccatgctacttatctacgtagccatgctctaggaagatcggaattcgcccttaa
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CCCCTCAGGAACCCCTCTCATGGAGGAGAGTGCCTGAGGGTCTTGGTTTCCCATTGCATCCCCCACCT
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CAGTGTCGGCCTCCTCTCCCCAACTAAGGGCTTATGTGTAATTAAAAGGGATTATGCTTTGAAGGGGA
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CAGCAGGAATGCTGCCGTGGCTCCAGGGGATCTTCTGCAATGTGAACAATCCCTGTTTTCAAAGCCCC
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TCTCTCTACTGGAGGAAAACATGTTCTGGGCCGGAGTGGTATTCCCTGACATGTATCCCTGGACCAGC
TCTCTACCACCCCACGTGAAGTATAAGATCCGAATGGACATAGACGTGGTGGAGAAAACCAATAAGAT
TAAAGACAGGTATTGGGATTCTGGTCCCAGAGCTGATCCCGTGGAAGATTTCCGGTACATCTGGGGCG

Figure 7 (cont'):

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GGTGTCATCTATTTCACCCTCTACCTGCCACACATCCTGTGCTTCGCCTGGCAGGACCGCATGACCGC
TGAGCTGAAGAAGGCTGTGAGCTTACTGTCTCCGGTGGCATTTGGATTTGGCACTGAGTACCTGGTTC
GCTTTGAAGAGCAAGGCCTGGGGCTGCAGTGGAGCAACATCGGGAACAGTCCCACGGAAGGGGACGAA
TTCAGCTTCCTGCTGTCCATGCAGATGATGCTCCTTGATGCTGCTGTCTATGGCTTACTCGCTTGGTA
CCTTGATCAGGTGTTTCCAGGAGACTATGGAACCCCACTTCCTTGGTACTTTCTTCTACAAGAGTCGT
ATTGGCTTGGCGGTGAAGGGTGTTCAACCAGAGAAGAAAGAGCCCTGGAAAAGACCGAGCCCCTAACA
GAGGAAACGGAGGATCCAGAGCACCCAGAAGGAATACACGACTCCTTCTTTGAACGTGAGCATCCAGG
GTGGGTTCCTGGGGTATGCGTGAAGAATCTGGTAAAGATTTTTGAGCCCTGTGGCCGGCCAGCTGTGG
ACCGTCTGAACATCACCTTCTACGAGAACCAGATCACCGCATTCCTGGGCCACAATGGAGCTGGGAAA
ACCACCACCTTGTCCATCCTGACGGGTCTGTTGCCACCAACCTCTGGGACTGTGCTCGTTGGGGGAAG
GGACATTGAAACCAGCCTGGATGCAGTCCGGCAGAGCCTTGGCATGTGTCCACAGCACAACATCCTGT
TCCACCACCTCACGGTGGCTGAGCACATGCTGTTCTATGCCCAGCTGAAAGGAAAGTCCCAGGAGGAG
GCCCAGCTGGAGATGGAAGCCATGTTGGAGGACACAGGCCTCCACCACAAGCGGAATGAAGAGGCTCA
GGACCTATCAGGTGGCATGCAGAGAAAGCTGTCGGTTGCCATTGCCTTTGTGGGAGATGCC*AAGgtaa*
*g*ggcactgagcagaagggaagaagctccgggggctctttgtagggtaagcttAGTGCATCAAGGCGAT
CACATCAGTGAAAAAAAGCCAGACAGGCGGTTAAACCAACGCAGATTAAACAGCAGGATGCAAAAATT
CGCAGGTGGTCAGATGaagcttattctcgagttaagggcgaattcccgattaggatcttcctagagca
tggctacgtagataagtagcatggcgggttaatcattaactacaAGGAACCCCTAGTGATGGAGTTGG
CCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGC
TTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAG

Figure 8

Dual AAV comprising the 3' coding sequence of ABCA4 (SEQ ID NO: 22):

CTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCGTCGGGCGACCTTTGGTCGCCC
GGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTtgtagt
taatgattaacccgccatgctacttatctacgtagccatgctctaggaagatcggaattcgcccttaa
gggcgcgccgtttaaatagctagcAAAAGACTAAAAGAGGGAGGGATCACTTCAGATCTGCCGAGTGA
GTCGATTGGACTTAAAGGGCCAGTCAAACCCTGACTGCCGGCTCATGGCAGGCTCTTGCCGAGGACAA
ATGCCCAGCCTATATTTATGCAAAGAGATTTTGTTCCAAACTTAAGGTCAAAGATACCTAAAGACATC
CCCCTCAGGAACCCCTCTCATGGAGGAGAGTGCCTGAGGGTCTTGGTTTCCCATTGCATCCCCCACCT
CAATTTCCCTGGTGCCCAGCCACTTGTGTCTTTAGGGTTCTCTTTCTCTCCATAAAAGGGAGCCAACA
CAGTGTCGGCCTCCTCTCCCCAACTAAGGGCTTATGTGTAATTAAAAGGGATTATGCTTTGAAGGGGA
AAAGTAGCCTTTAATCACCAGGAGAAGGACACAGCGTCCGGAGCCAGAGGCGCTCTTAACGGCGTTTA
TGTCCTTTGCTGTCTGAGGGGCCTCAGCTCTGACCAATCTGGTCTTCGTGTGGTCATTAGCGGTACCg
gtaccaccggtagaaagcttCATCTGACCACCTGCGAATTTTTGCATCCTGCTGTTTAATCTGCGTTG
GTTTAACCGCCTGTCTGGCTTTTTTTCACTGATGTGATCGCCTTGATGCACTaagcttCAACGAGTCT
TTTGTCATCTACAGGTGGTGATTCTGGACGAACCCACCTCTGGGGTGGACCCTTACTCGAGACGCTCA
ATCTGGGATCTGCTCCTGAAGTATCGCTCAGGCAGAACCATCATCATGTCCACTCACCACATGGACGA
GGCCGACCTCCTTGGGGACCGCATTGCCATCATTGCCCAGGGAAGGCTCTACTGCTCAGGCACCCCAC
TCTTCCTGAAGAACTGCTTTGGCACAGGCTTGTACTTAACCTTGGTGCGCAAGATGAAAAACATCCAG
AGCCAAAGGAAAGGCAGTGAGGGGACCTGCAGCTGCTCGTCTAAGGGTTTCTCCACCACGTGTCCAGC
CCACGTCGATGACCTAACTCCAGAACAAGTCCTGGATGGGGATGTAAATGAGCTGATGGATGTAGTTC
TCCACCATGTTCCAGAGGCAAAGCTGGTGGAGTGCATTGGTCAAGAACTTATCTTCCTTCTTCCAAAT
AAGAACTTCAAGCACAGAGCATATGCCAGCCTTTTCAGAGAGCTGGAGGAGACGCTGGCTGACCTTGG
TCTCAGCAGTTTTGGAATTTCTGACACTCCCCTGGAAGAGATTTTTCTGAAGGTCACGGAGGATTCTG
ATTCAGGACCTCTGTTTGCGGGTGGCGCTCAGCAGAAAAGAGAAAACGTCAACCCCCGACACCCCTGC
TTGGGTCCCAGAGAGAAGGCTGGACAGACACCCCAGGACTCCAATGTCTGCTCCCCAGGGGCGCCGGC
TGCTCACCCAGAGGGCCAGCCTCCCCCAGAGCCAGAGTGCCCAGGCCCGCAGCTCAACACGGGGACAC
AGCTGGTCCTCCAGCATGTGCAGGCGCTGCTGGTCAAGAGATTCCAACACACCATCCGCAGCCACAAG
GACTTCCTGGCGCAGATCGTGCTCCCGGCTACCTTTGTGTTTTTGGCTCTGATGCTTTCTATTGTTAT
CCCTCCTTTTGGCGAATACCCCGCTTTGACCCTTCACCCCTGGATATATGGGCAGCAGTACACCTTCT
TCAGCATGGATGAACCAGGCAGTGAGCAGTTCACGGTACTTGCAGACGTCCTCCTGAATAAGCCAGGC
TTTGGCAACCGCTGCCTGAAGGAAGGGTGGCTTCCGGAGTACCCCTGTGGCAACTCAACACCCTGGAA
GACTCCTTCTGTGTCCCCAAACATCACCCAGCTGTTCCAGAAGCAGAAATGGACACAGGTCAACCCTT
CACCATCCTGCAGGTGCAGCACCAGGGAGAAGCTCACCATGCTGCCAGAGTGCCCCGAGGGTGCCGGG
GGCCTCCCGCCCCCCCAGAGAACACAGCGCAGCACGGAAATTCTACAAGACCTGACGGACAGGAACAT
CTCCGACTTCTTGGTAAAAACGTATCCTGCTCTTATAAGAAGCAGCTTAAAGAGCAAATTCTGGGTCA
ATGAACAGAGGTATGGAGGAATTTCCATTGGAGGAAAGCTCCCAGTCGTCCCCATCACGGGGGAAGCA
CTTGTTGGGTTTTTAAGCGACCTTGGCCGGATCATGAATGTGAGCGGGGGCCCTATCACTAGAGAGGC

Figure 8 (cont')

CTCTAAAGAAATACCTGATTTCCTTAAACATCTAGAAACTGAAGACAACATTAAGGTGTGGTTTAATA
ACAAAGGCTGGCATGCCCTGGTCAGCTTTCTCAATGTGGCCCACAACGCCATCTTACGGGCCAGCCTG
CCTAAGGACAGGAGCCCCGAGGAGTATGGAATCACCGTCATTAGCCAACCCCTGAACCTGACCAAGGA
GCAGCTCTCAGAGATTACAGTGCTGACCACTTCAGTGGATGCTGTGGTTGCCATCTGCGTGATTTTCT
CCATGTCCTTCGTCCCAGCCAGCTTTGTCCTTTATTTGATCCAGGAGCGGGTGAACAAATCCAAGCAC
CTCCAGTTTATCAGTGGAGTGAGCCCCACCACCTACTGGGTGACCAACTTCCTCTGGGACATCATGAA
TTATTCCGTGAGTGCTGGGCTGGTGGTGGGCATCTTCATCGGGTTTCAGAAGAAAGCCTACACTTCTC
CAGAAAACCTTCCTGCCCTTGTGGCACTGCTCCTGCTGTATGGATGGGCGGTCATTCCCATGATGTAC
CCAGCATCCTTCCTGTTTGATGTCCCCAGCACAGCCTATGTGGCTTTATCTTGTGCTAATCTGTTCAT
CGGCATCAACAGCAGTGCTATTACCTTCATCTTGGAATTATTTGAGAATAACCGGACGCTGCTCAGGT
TCAACGCCGTGCTGAGGAAGCTGCTCATTGTCTTCCCCCACTTCTGCCTGGGCCGGGGCCTCATTGAC
CTTGCACTGAGCCAGGCTGTGACAGATGTCTATGCCCGGTTTGGTGAGGAGCACTCTGCAAATCCGTT
CCACTGGGACCTGATTGGGAAGAACCTGTTTGCCATGGTGGTGGAAGGGGTGGTGTACTTCCTCCTGA
CCCTGCTGGTCCAGCGCCACTTCTTCCTCTCCCAATGGATTGCCGAGCCCACTAAGGAGCCCATTGTT
GATGAAGATGATGATGTGGCTGAAGAAAGACAAAGAATTATTACTGGTGGAAATAAAACTGACATCTT
AAGGCTACATGAACTAACCAAGATTTATCCAGGCACCTCCAGCCCAGCAGTGGACAGGCTGTGTGTCG
GAGTTCGCCCTGGAGAGTGCTTTGGCCTCCTGGGAGTGAATGGTGCCGGCAAAACAACCACATTCAAG
ATGCTCACTGGGGACACCACAGTGACCTCAGGGGATGCCACCGTAGCAGGCAAGAGTATTTTAACCAA
TATTTCTGAAGTCCATCAAAATATGGGCTACTGTCCTCAGTTTGATGCAATTGATGAGCTGCTCACAG
GACGAGAACATCTTTACCTTTATGCCCGGCTTCGAGGTGTACCAGCAGAAGAAATCGAAAAGGTTGCA
AACTGGAGTATTAAGAGCCTGGGCCTGACTGTCTACGCCGACTGCCTGGCTGGCACGTACAGTGGGGG
CAACAAGCGGAAACTCTCCACAGCCATCGCACTCATTGGCTGCCCACCGCTGGTGCTGCTGGATGAGC
CCACCACAGGGATGGACCCCCAGGCACGCCGCATGCTGTGGAACGTCATCGTGAGCATCATCAGAGAA
GGGAGGGCTGTGGTCCTCACATCCCACAGCATGGAAGAATGTGAGGCACTGTGTACCCGGCTGGCCAT
CATGGTAAAGGGCGCCTTTCGATGTATGGGCACCATTCAGCATCTCAAGTCCAAATTTGGAGATGGCT
ATATCGTCACAATGAAGATCAAATCCCCGAAGGACGACCTGCTTCCTGACCTGAACCCTGTGGAGCAG
TTCTTCCAGGGGAACTTCCCAGGCAGTGTGCAGAGGGAGAGGCACTACAACATGCTCCAGTTCCAGGT
CTCCTCCTCCTCCCTGGCGAGGATCTTCCAGCTCCTCCTCTCCCACAAGGACAGCCTGCTCATCGAGG
AGTACTCAGTCACACAGACCACACTGGACCAGGTGTTTGTAAATTTTGCTAAACAGCAGACTGAAAGT
CATGACCTCCCTCTGCACCCTCGAGCTGCTGGAGCCAGTCGACAAGCCCAGGACTGAgtcgacgcggc
CGCGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAA
GCTGCAATAAACAAGTTctcgagttaagggcgaattcccgattaggatcttcctagagcatggctacg
tagataagtagcatggcgggttaatcattaactacaAGGAACCCCTAGTGATGGAGTTGGCCACTCCC
TCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCG
GGCGGCCTCAGTGAGCGAGCGAGCGCGCAG

Figure 9

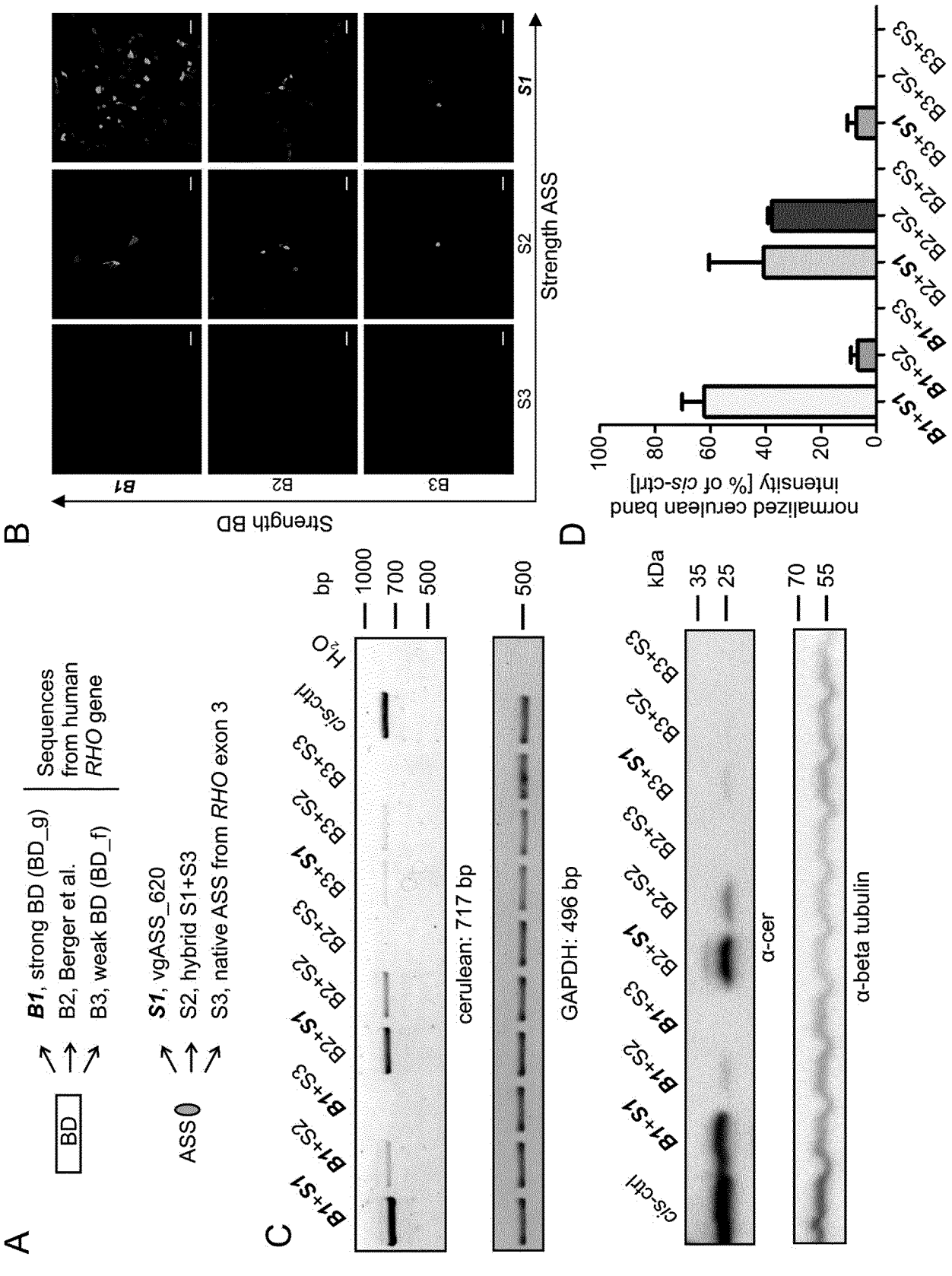

A
BD
B1, strong BD (BD_g)
B2, Berger et al.
B3, weak BD (BD_f)
Sequences from human RHO gene
ASS
S1, vgASS_620
S2, hybrid S1+S3
S3, native ASS from RHO exon 3
B
Strength BD
B1
B2
B3
S1
S2
S3
Strength ASS
C
bp
1000
700
500
H2O
cis-ctrl
B3+S3
B3+S2
B3+S1
B2+S3
B2+S2
B2+S1
B1+S3
B1+S2
B1+S1
cerulean: 717 bp
500
GAPDH: 496 bp
D
kDa
35
25
α-cer
70
55
α-beta tubulin
normalized cerulean band intensity [% of cis-ctrl]
100
80
60
40
20
0

Figure 10

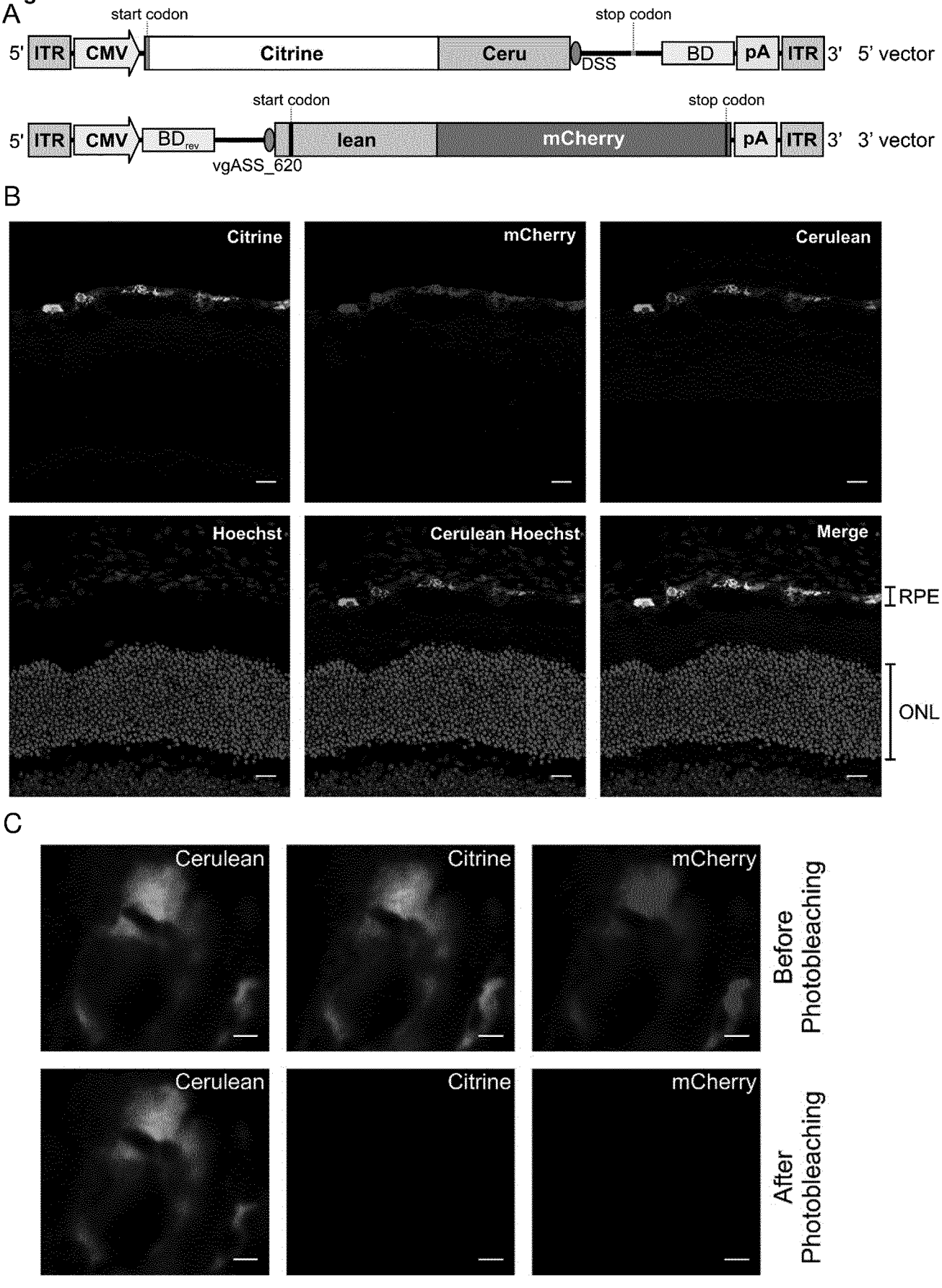

A
start codon
stop codon
5'
ITR
CMV
Citrine
Ceru
DSS
BD
pA
ITR
3'
5' vector
start codon
stop codon
5'
ITR
CMV
BD rev
vgASS_620
lean
mCherry
pA
ITR
3'
3' vector
B
Citrine
mCherry
Cerulean
Hoechst
Cerulean Hoechst
Merge
RPE
ONL
C
Cerulean
Citrine
mCherry
Before Photobleaching
Cerulean
Citrine
mCherry
After Photobleaching

Figure 11

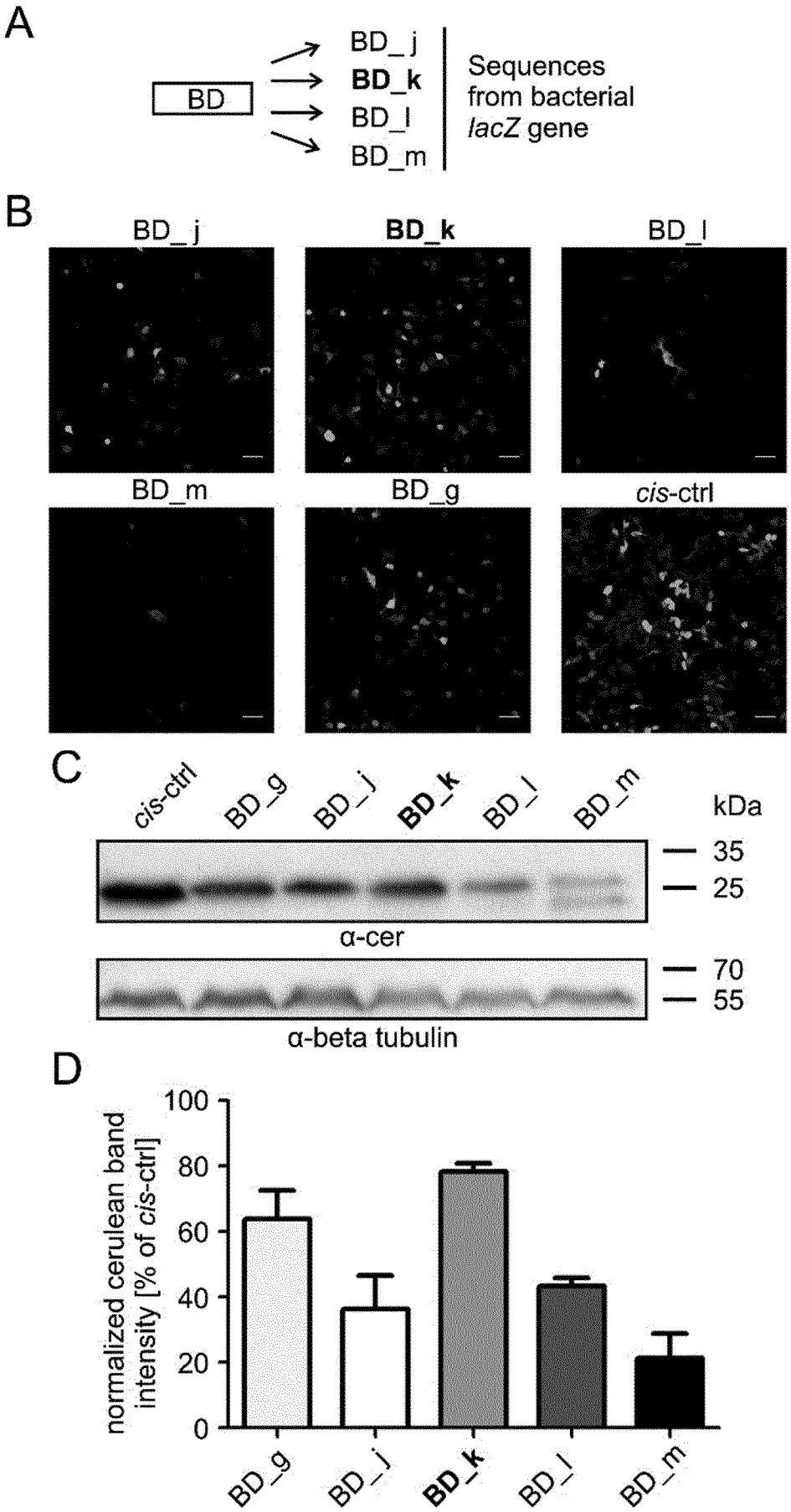

A
BD
BD_j
BD_k
BD_l
BD_m
Sequences from bacterial lacZ gene
B
BD_j
BD_k
BD_l
BD_m
BD_g
cis-ctrl
C
cis-ctrl
BD_g
BD_j
BD_k
BD_l
BD_m
kDa
35
25
α-cer
70
55
α-beta tubulin
D
normalized cerulean band intensity [% of cis-ctrl]
100
80
60
40
20
0
BD_g
BD_j
BD_k
BD_l
BD_m

Figure 12

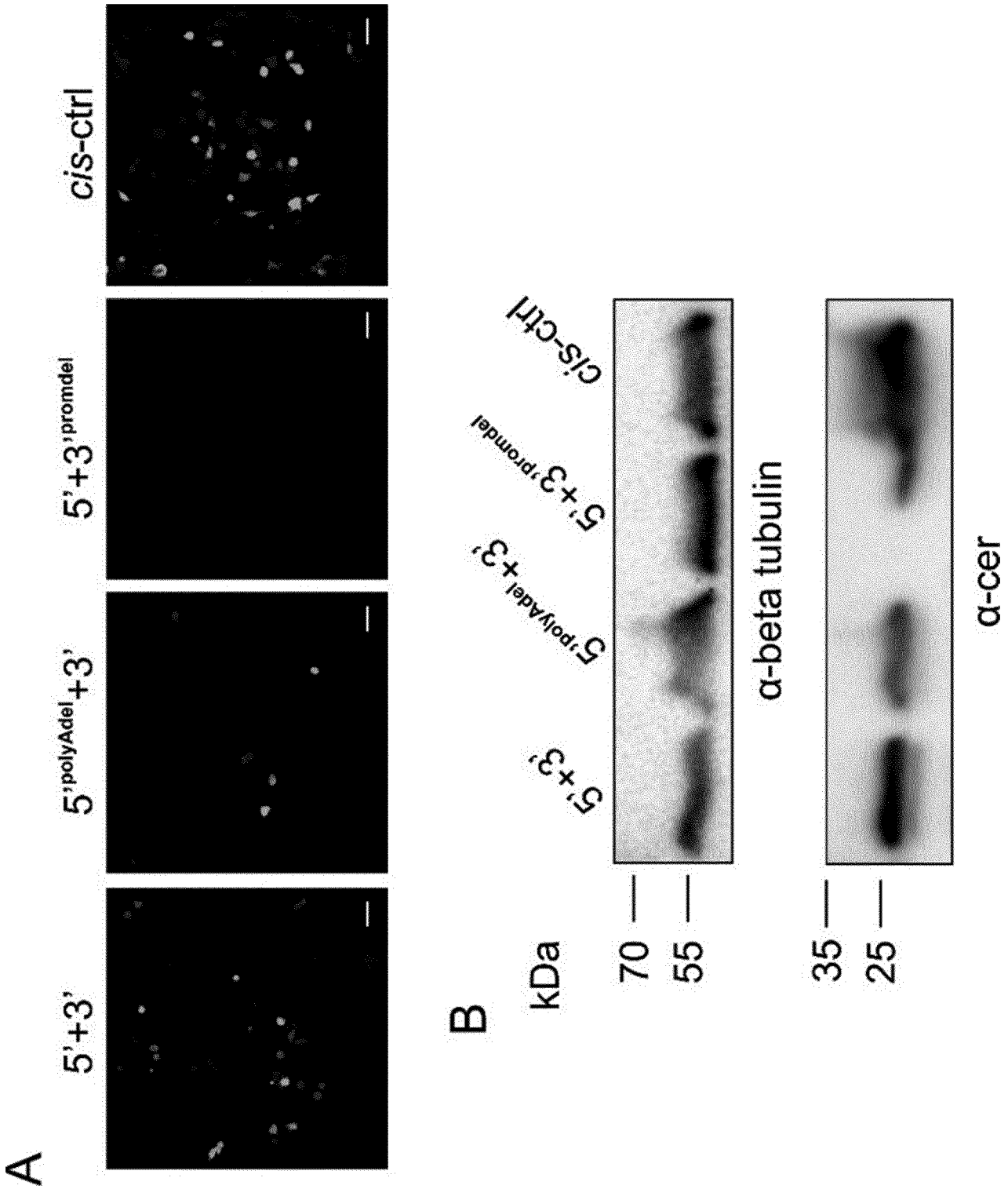

A
5'+3'
5'polyAdel+3'
5'+3'promdel
cis-ctrl
B
kDa
70
55
35
25
5',3'
5',polyAdel+3'
5',3',promdel
cis-ctrl
α-beta tubulin
α-cer

Figure 13

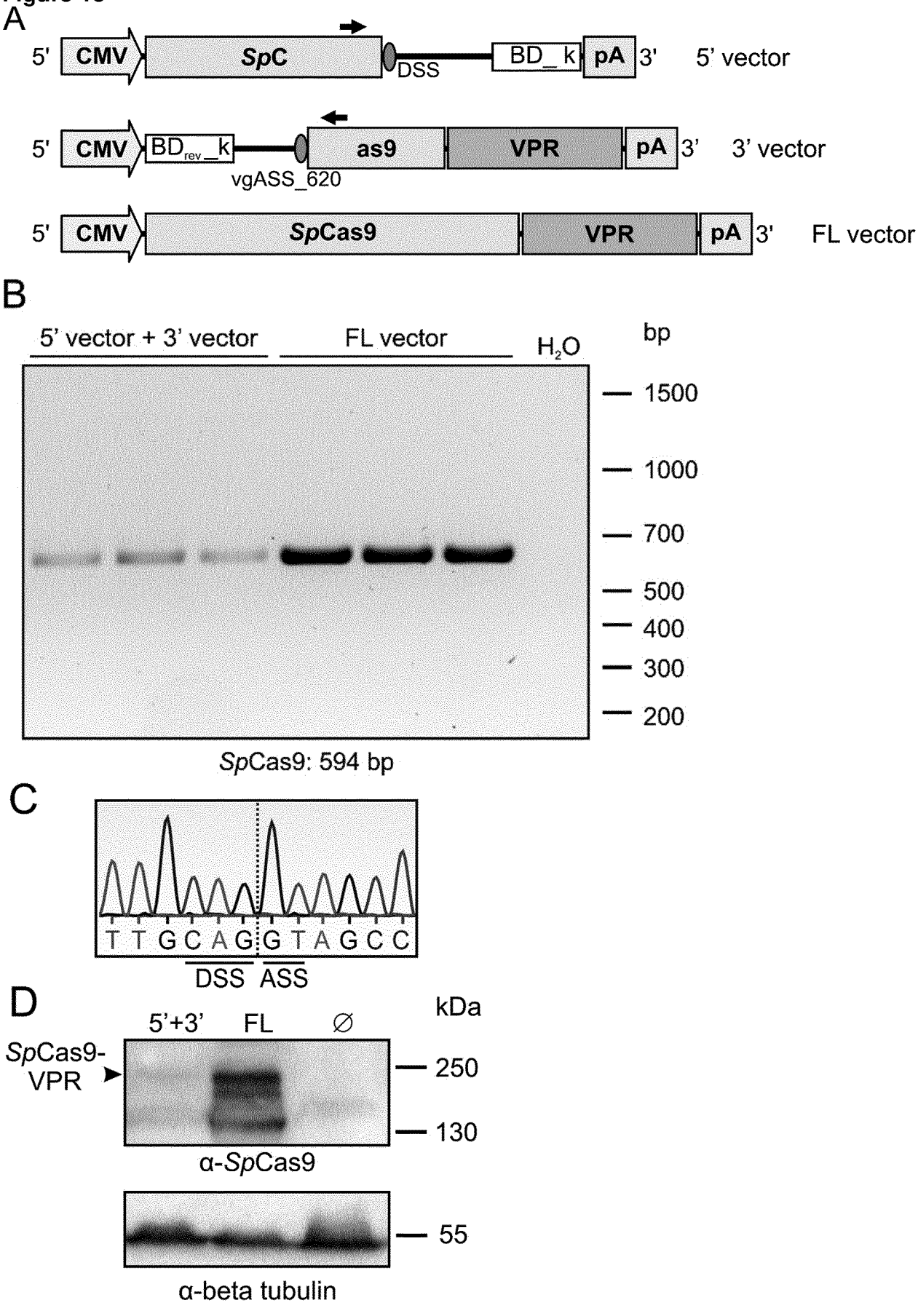

A
5'
CMV
SpC
DSS
BD_ k
pA
3'
5' vector
5'
CMV
BDrev_k
vgASS_620
as9
VPR
pA
3'
3' vector
5'
CMV
SpCas9
VPR
pA
3'
FL vector
B
5' vector + 3' vector
FL vector
H2O
bp
1500
1000
700
500
400
300
200
SpCas9: 594 bp
C
T T G C A G G T A G C C
DSS
ASS
D
kDa
5'+3'
FL
∅
SpCas9-VPR
250
130
α-SpCas9
55
α-beta tubulin

Figure 14

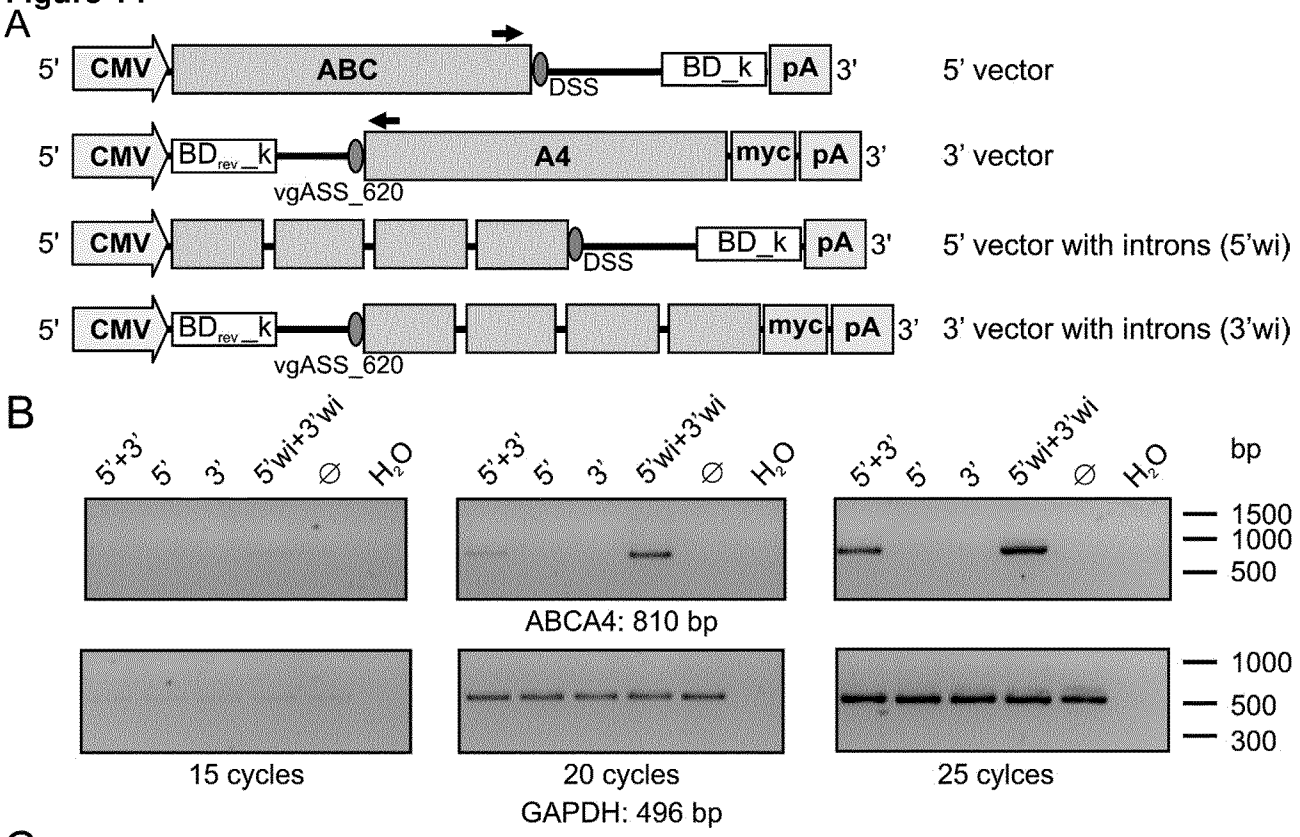

A
5' CMV ABC DSS BD_k pA 3' 5' vector
5' CMV BDrev_k vgASS_620 A4 myc pA 3' 3' vector
5' CMV DSS BD_k pA 3' 5' vector with introns (5'wi)
5' CMV BDrev_k vgASS_620 myc pA 3' 3' vector with introns (3'wi)
B
5'+3' 5' 3' 5'wi+3'wi ∅ H2O
bp
1500
1000
500
ABCA4: 810 bp
1000
500
300
15 cycles
20 cycles
25 cylces
GAPDH: 496 bp
C
GC CA A G G T G G T G
DSS ASS

Figure 15

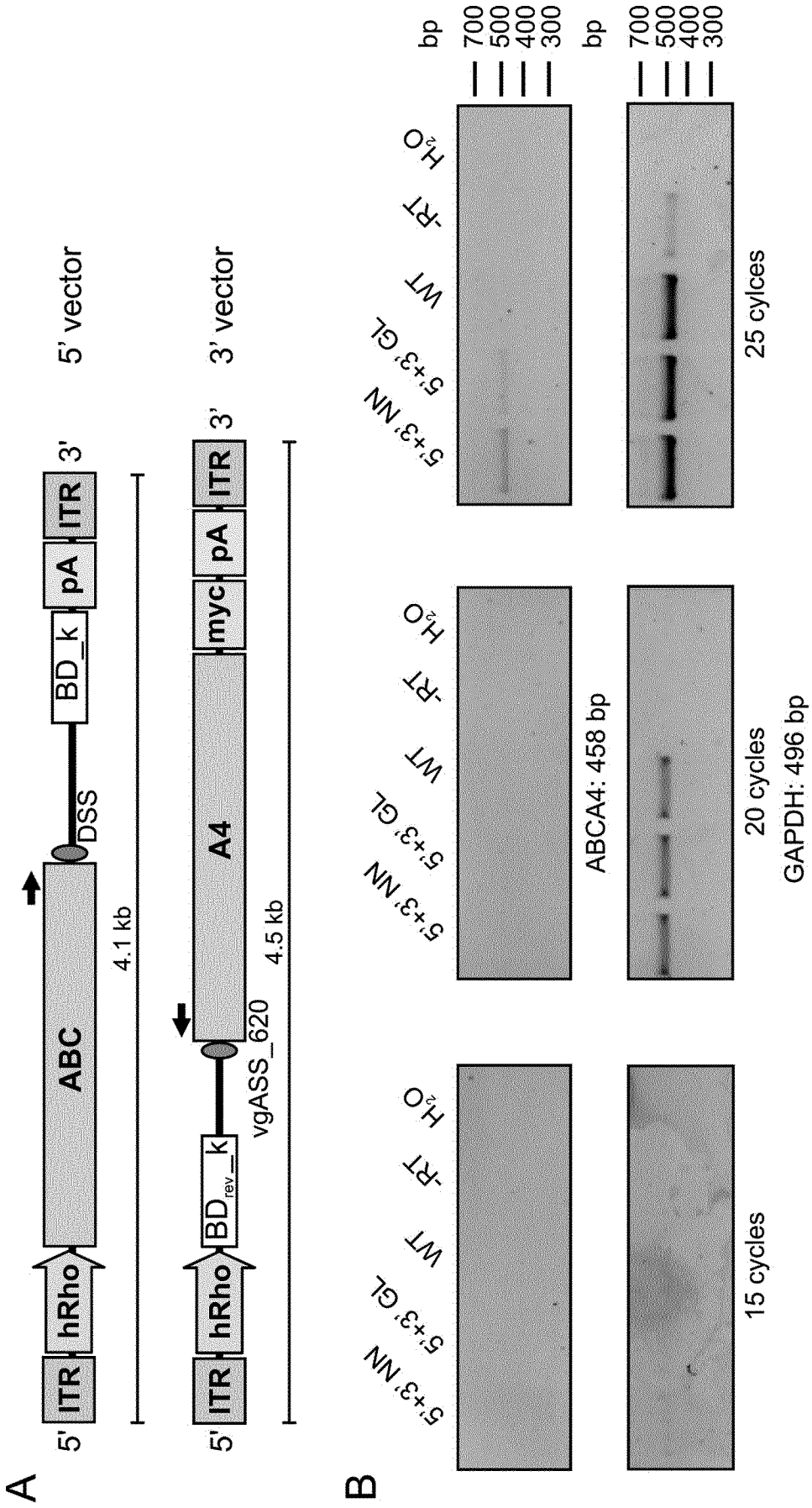

A
5' vector
5'
ITR
hRho
ABC
DSS
BD_k
pA
ITR
3'
4.1 kb
3' vector
5'
ITR
hRho
BD rev_k
vgASS_620
A4
myc
pA
ITR
3'
4.5 kb
B
bp
700
500
400
300
H2O
-RT
WT
5'+3' GL
5'+3' NN
25 cycles
ABCA4: 458 bp
20 cycles
GAPDH: 496 bp
15 cycles

Figure 15 (cont')

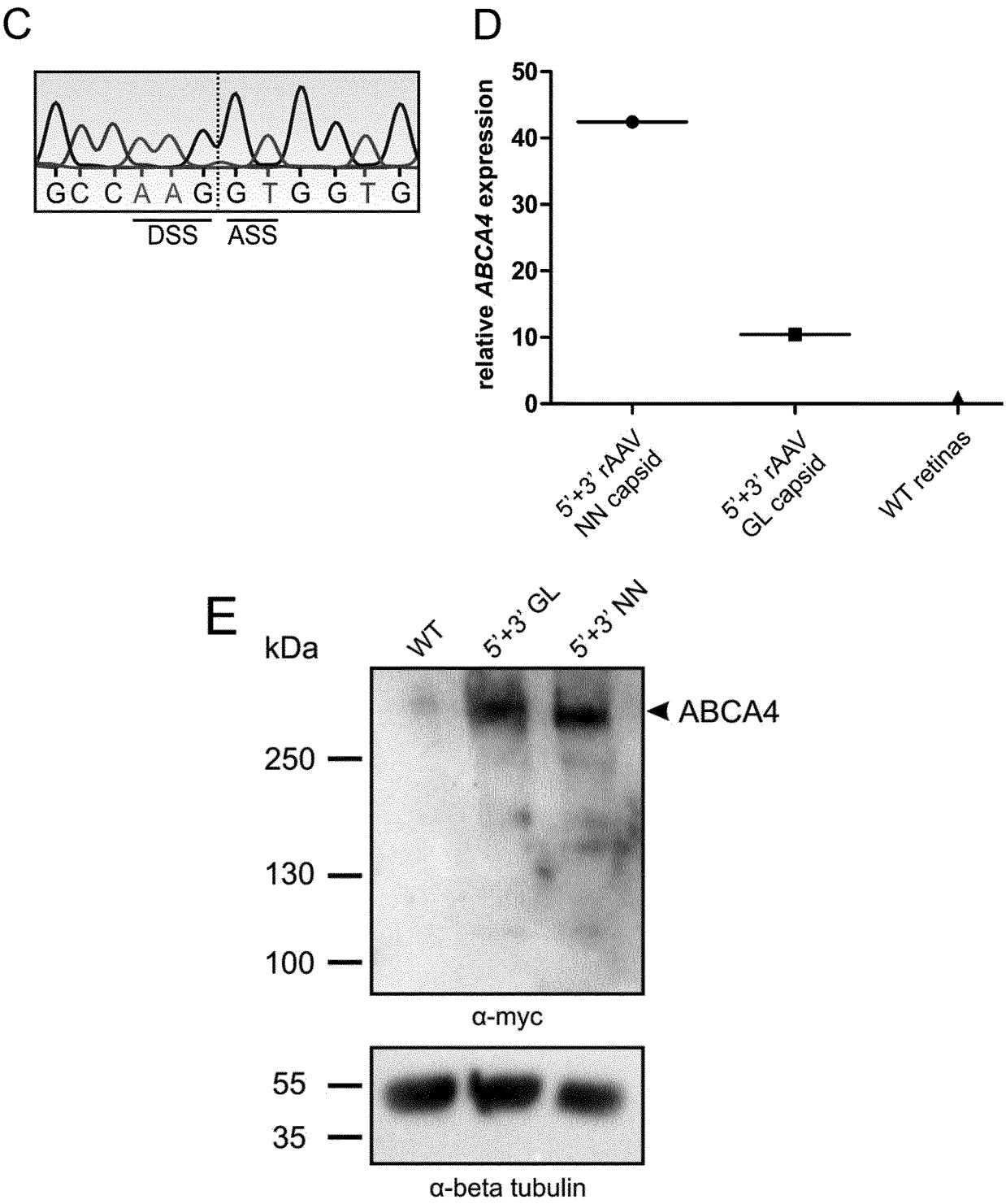


Figure 16

5' Cerulean + BD_g (SEQ ID NO: 35):

GACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCA
TATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGA
CCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCC
ATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTAT
CATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGC
CCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGG
GGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACG
GGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTAC
GGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAGAGAACCCACTGCTTACTGGCTT
ATCGAAATTAATACGACTCACTATAGGGAGACCCAAGCTGGCTAGTTAAGCTT**ATGGTGAGC**
AAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAA
CGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCC
TGAAGTTCATCTGCACCACAGGTAAGGGCACTGAGCAGAAGGGAAGAAGCTCCGGGGGCTCT
TTGTAGGGTGGATCC*CCCTGCCTGTGAGGGACTTGGGAACAGCCAAGGTGGCTGCCGAGCTA*
*GCGAATTCCACCTGGCGCTGGCCCTTTCTGGGGCTTCACATTCCCTCCCTGGAAC*GGATCCC
TCGAGGTCACCCATTCGAACAAAAACTCATCTCAGAAGAGGATCTGAATATGCATACCGGTC
ATCATCACCATCACCATTGAGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC
CAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAC
TGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTC
TGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCT
GGGGATGCGGTGGGCTCTATGG

Figure 17

3' Cerulean + BD_g (SEQ ID NO: 36):

GACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCA
TATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGA
CCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCC
ATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTAT
CATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGC
CCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGG
GGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACG
GGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTAC
GGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAGAGAACCCACTGCTTACTGGCTT
ATCGAAATTAATACGACTCACTATAGGGAGACCCAAGCTGGCTAGTTAAGCTTGGATCC*GTT*
CCAGGGAGGGAATGTGAAGCCCCAGAAAGGGCCAGCGCCAGGTGGAATTCGCTAGCTCGGCA
*GCCACCTTGGCTGTTCCCAAGTCCCTCACAGGCAGGG*GGATCC**CAACGAGTCTTTTGTCATC**
TACAGGTAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTGGGGCGTGCAGT
GCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA
GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGA
GGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGG
AGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACGCCATCAGCGACAACGTCTATATC
ACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGA
CGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGC
TGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAG
CGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGA
GCTGTACAAGTAACTCGAGGTCACCCATTCGAACAAAAACTCATCTCAGAAGAGGATCTGAA
TATGCATACCGGTCATCATCACCATCACCATTGAGTTTAAACCCGCTGATCAGCCTCGACTG
TGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAA
GGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACA
ATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGG

Figure 18

5'*Sp*Cas9-VPR + BD_k (SEQ ID NO: 37):

GACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCA
TATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGA
CCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCC
ATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTAT
CATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGC
CCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGG
GGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACG
GGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTAC
GGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGAACCGGTCGACTAGAGGA
TCC**ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAGCCGACAAGAA**
GTACTCCATTGGGCTCGCTATCGGCACAAACAGCGTCGGCTGGGCCGTCATTACGGACGAGT
ACAAGGTGCCGAGCAAAAAATTCAAAGTTCTGGGCAATACCGATCGCCACAGCATAAAGAAG
AACCTCATTGGCGCCCTCCTGTTCGACTCCGGGGAAACGGCCGAAGCCACGCGGCTCAAAAG
AACAGCACGGCGCAGATATACCCGCAGAAAGAATCGGATCTGCTACCTGCAGGAGATCTTTA
GTAATGAGATGGCTAAGGTGGATGACTCTTTCTTCCATAGGCTGGAGGAGTCCTTTTTGGTG
GAGGAGGATAAAAAGCACGAGCGCCACCCAATCTTTGGCAATATCGTGGACGAGGTGGCGTA
CCATGAAAAGTACCCAACCATATATCATCTGAGGAAGAAGCTTGTAGACAGTACTGATAAGG
CTGACTTGCGGTTGATCTATCTCGCGCTGGCGCATATGATCAAATTTCGGGGACACTTCCTC
ATCGAGGGGGACCTGAACCCAGACAACAGCGATGTCGACAAACTCTTTATCCAACTGGTTCA
GACTTACAATCAGCTTTTCGAAGAGAACCCGATCAACGCATCCGGAGTTGACGCCAAAGCAA
TCCTGAGCGCTAGGCTGTCCAAATCCCGGCGGCTCGAAAACCTCATCGCACAGCTCCCTGGG
GAGAAGAAGAACGGCCTGTTTGGTAATCTTATCGCCCTGTCACTCGGGCTGACCCCCAACTT
TAAATCTAACTTCGACCTGGCCGAAGATGCCAAGCTTCAACTGAGCAAAGACACCTACGATG
ATGATCTCGACAATCTGCTGGCCCAGATCGGCGACCAGTACGCAGACCTTTTTTTGGCGGCA
AAGAACCTGTCAGACGCCATTCTGCTGAGTGATATTCTGCGAGTGAACACGGAGATCACCAA
AGCTCCGCTGAGCGCTAGTATGATCAAGCGCTATGATGAGCACCACCAAGACTTGACTTTGC
TGAAGGCCCTTGTCAGACAGCAACTGCCTGAGAAGTACAAGGAAATTTTCTTCGATCAGTCT
AAAAATGGCTACGCCGGATACATTGACGGCGGAGCAAGCCAGGAGGAATTTTACAAATTTAT
TAAGCCCATCTTGGAAAAAATGGACGGCACCGAGGAGCTGCTGGTAAAGCTTAACAGAGAAG
ATCTGTTGCGCAAACAGCGCACTTTCGACAATGGAAGCATCCCCCACCAGATTCACCTGGGC
GAACTGCACGCTATCCTCAGGCGGCAAGAGGATTTCTACCCCTTTTTGAAAGATAACAGGGA
AAAGATTGAGAAAATCCTCACATTTCGGATACCCTACTATGTAGGCCCCCTCGCCCGGGGAA
ATTCCAGATTCGCGTGGATGACTCGCAAATCAGAAGAGACCATCACTCCCTGGAACTTCGAG
GAAGTCGTGGATAAGGGGGCCTCTGCCCAGTCCTTCATCGAAAGGATGACTAACTTTGATAA
AAATCTGCCTAACGAAAAGGTGCTTCCTAAACACTCTCTGCTGTACGAGTACTTCACAGTTT
ATAACGAGCTCACCAAGGTCAAATACGTCACAGAAGGGATGAGAAAGCCAGCATTCCTGTCT
GGAGAGCAGAAGAAAGCTATCGTGGACCTCCTCTTCAAGACGAACCGGAAAGTTACCGTGAA
ACAGCTCAAAGAAGACTATTTCAAAAAGATTGAATGTTTCGACTCTGTTGAAATCAGCGGAG
TGGAGGATCGCTTCAACGCATCCCTGGGAACGTATCACGATCTCCTGAAAATCATTAAAGAC
AAGGACTTCCTGGACAATGAGGAGAACGAGGACATTCTTGAGGACATTGTCCTCACCCTTAC

GTTGTTTGAAGATAGGGAGATGATTGAAGAACGCTTGAAAACTTACGCTCATCTCTTCGACG
ACAAAGTCATGAAACAGCTCAAGAGGCGCCGATATACAGGATGGGGGCGGCTGTCAAGAAAA
CTGATCAATGGGATCCGAGACAAGCAGAGTGGAAAGACAATCCTGGATTTTCTTAAGTCCGA
TGGATTTGCCAACCGGAACTTCATGCAGTTGATCCATGATGACTCTCTCACCTTTAAGGAGG
ACATCCAGAAAGCACAAGTTTCTGGCCAGGGGGACAGTCTTCACGAGCACATCGCTAATCTT
GCAGGTAAGGGCACTGAGCAGAAGGGAAGAAGCTCCGGGGGCTCTTTGTAGGGTGCGGCCGC
AGTGCATCAAGGCGATCACATCAGTGAAAAAAAGCCAGACAGGCGGTTAAACCAACGCAGAT
*TAAACAGCAGGATGCAAAAATTCGCAGGTGGTCAGATG*GCGGCCGCTCTAGACTCGATGAGT
TTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCT
ATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT

Figure 19

3'*Sp*Cas9-VPR + BD_k (SEQ ID NO: 38):

GACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCA
TATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGA
CCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCC
ATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTAT
CATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGC
CCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGG
GGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACG
GGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTAC
GGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGAGGTACCACCGGTCGACT
AGAGGATCCCGGCCGC*CATCTGACCACCTGCGAATTTTTGCATCCTGCTGTTTAATCTGCGT*
*TGGTTTAACCGCCTGTCTGGCTTTTTTTCACTGATGTGATCGCCTTGATGCACT*CGGCCGC**C**
AACGAGTCTTTTGTCATCTACAGGTAGCCCAGCTATCAAAAAGGGAATACTGCAGACCGTTA
AGGTCGTGGATGAACTCGTCAAAGTAATGGGAAGGCATAAGCCCGAGAATATCGTTATCGAG
ATGGCCCGAGAGAACCAAACTACCCAGAAGGGACAGAAGAACAGTAGGGAAAGGATGAAGAG
GATTGAAGAGGGTATAAAAGAACTGGGGTCCCAAATCCTTAAGGAACACCCAGTTGAAAACA
CCCAGCTTCAGAATGAGAAGCTCTACCTGTACTACCTGCAGAACGGCAGGGACATGTACGTG
GATCAGGAACTGGACATCAATCGGCTCTCCGACTACGACGTGGATCATATCGTGCCCCAGTC
TTTTCTCAAAGATGATTCTATTGATAATAAAGTGTTGACAAGATCCGATAAAAATAGAGGGA
AGAGTGATAACGTCCCCTCAGAAGAAGTTGTCAAGAAAATGAAAAATTATTGGCGGCAGCTG
CTGAACGCCAAACTGATCACACAACGGAAGTTCGATAATCTGACTAAGGCTGAACGAGGTGG
CCTGTCTGAGTTGGATAAAGCCGGCTTCATCAAAAGGCAGCTTGTTGAGACACGCCAGATCA
CCAAGCACGTGGCCCAAATTCTCGATTCACGCATGAACACCAAGTACGATGAAAATGACAAA
CTGATTCGAGAGGTGAAAGTTATTACTCTGAAGTCTAAGCTGGTcTCAGATTTCAGAAAGGA
CTTTCAGTTTTATAAGGTGAGAGAGATCAACAATTACCACCATGCGCATGATGCCTACCTGA
ATGCAGTGGTAGGCACTGCACTTATCAAAAAATATCCCAAGCTTGAATCTGAATTTGTTTAC
GGAGACTATAAAGTGTACGATGTTAGGAAAATGATCGCAAAGTCTGAGCAGGAAATAGGCAA
GGCCACCGCTAAGTACTTCTTTTACAGCAATATTATGAATTTTTTCAAGACCGAGATTACAC
TGGCCAATGGAGAGATTCGGAAGCGACCACTTATCGAAACAAACGGAGAAACAGGAGAAATC
GTGTGGGACAAGGGTAGGGATTTCGCGACAGTCCGGAAGGTCCTGTCCATGCCGCAGGTGAA
CATCGTTAAAAAGACCGAAGTACAGACCGGAGGCTTCTCCAAGGAAAGTATCCTCCCGAAAA
GGAACAGCGACAAGCTGATCGCACGCAAAAAAGATTGGGACCCCAAGAAATACGGCGGATTC
GATTCTCCTACAGTCGCTTACAGTGTACTGGTTGTGGCCAAAGTGGAGAAAGGGAAGTCTAA
AAAACTCAAAAGCGTCAAGGAACTGCTGGGCATCACAATCATGGAGCGATCAAGCTTCGAAA
AAAACCCCATCGACTTTCTCGAGGCGAAAGGATATAAAGAGGTCAAAAAAGACCTCATCATT
AAGCTTCCCAAGTACTCTCTCTTTGAGCTTGAAAACGGCCGGAAACGAATGCTCGCTAGTGC

GGGCGAGCTGCAGAAAGGTAACGAGCTGGCACTGCCCTCTAAATACGTTAATTTCTTGTATC
TGGCCAGCCACTATGAAAAGCTCAAAGGGTCtCCCGAAGATAATGAGCAGAAGCAGCTGTTC
GTGGAACAACACAAACACTACCTTGATGAGATCATCGAGCAAATAAGCGAATTCTCCAAAAG
AGTGATCCTCGCCGACGCTAACCTCGATAAGGTGCTTTCTGCTTACAATAAGCACAGGGATA
AGCCCATCAGGGAGCAGGCAGAAAACATTATCCACTTGTTTACTCTGACCAACTTGGGCGCG
CCTGCAGCCTTCAAGTACTTCGACACCACCATAGACAGAAAGCGGTACACCTCTACAAAGGA
GGTCCTGGACGCCACACTGATTCATCAGTCAATTACGGGGCTCTATGAAACAAGAATCGACC
TCTCTCAGCTCGGTGGAGACAGCAGGGCTGACCCCAAGAAGAAGAGGAAGGTGTCGCCAGGG
ATCCGTCGACTTGACGCGTTGATATCAACAAGTTTGTACAAAAAAGCAGGCTACAAAGAGGC
CAGCGGTTCCGGACGGGCTGACGCATTGGACGATTTTGATCTGGATATGCTGGGAAGTGACG
CCCTCGATGATTTTGACCTTGACATGCTTGGTTCGGATGCCCTTGATGACTTTGACCTCGAC
ATGCTCGGCAGTGACGCCCTTGATGATTTCGACCTGGACATGCTGATTAACTCTAGAAGTTC
CGGATCTCCGAAAAAGAAACGCAAAGTTGGTAGCCAGTACCTGCCCGACACCGACGACCGGC
ACCGGATCGAGGAAAAGCGGAAGCGGACCTACGAGACATTCAAGAGCATCATGAAGAAGTCC
CCCTTCAGCGGCCCCACCGACCCTAGACCTCCACCTAGAAGAATCGCCGTGCCCAGCAGATC
CAGCGCCAGCGTGCCAAAACCTGCCCCCCAGCCTTACCCCTTCACCAGCAGCCTGAGCACCA
TCAACTACGACGAGTTCCCTACCATGGTGTTCCCCAGCGGCCAGATCTCTCAGGCCTCTGCT
CTGGCTCCAGCCCCTCCTCAGGTGCTGCCTCAGGCTCCTGCTCCTGCACCAGCTCCAGCCAT
GGTGTCTGCACTGGCTCAGGCACCAGCACCCGTGCCTGTGCTGGCTCCTGGACCTCCACAGG
CTGTGGCTCCACCAGCCCCTAAACCTACACAGGCCGGCGAGGGCACACTGTCTGAAGCTCTG
CTGCAGCTGCAGTTCGACGACGAGGATCTGGGAGCCCTGCTGGGAAACAGCACCGATCCTGC
CGTGTTCACCGACCTGGCCAGCGTGGACAACAGCGAGTTCCAGCAGCTGCTGAACCAGGGCA
TCCCTGTGGCCCCTCACACCACCGAGCCCATGCTGATGGAATACCCCGAGGCCATCACCCGG
CTCGTGACAGGCGCTCAGAGGCCTCCTGATCCAGCTCCTGCCCCTCTGGGAGCACCAGGCCT
GCCTAATGGACTGCTGTCTGGCGACGAGGACTTCAGCTCTATCGCCGATATGGATTTCTCAG
CCTTGCTGGGCTCTGGCAGCGGCAGCCGGGATTCCAGGGAAGGGATGTTTTTGCCGAAGCCT
GAGGCCGGCTCCGCTATTAGTGACGTGTTTGAGGGCCGCGAGGTGTGCCAGCCAAAACGAAT
CCGGCCATTTCATCCTCCAGGAAGTCCATGGGCCAACCGCCCACTCCCCGCCAGCCTCGCAC
CAACACCAACCGGTCCAGTACATGAGCCAGTCGGGTCACTGACCCCGGCACCAGTCCCTCAG
CCACTGGATCCAGCGCCCGCAGTGACTCCCGAGGCCAGTCACCTGTTGGAGGATCCCGATGA
AGAGACGAGCCAGGCTGTCAAAGCCCTTCGGGAGATGGCCGATACTGTGATTCCCCAGAAGG
AAGAGGCTGCAATCTGTGGCCAAATGGACCTTTCCCATCCGCCCCCAAGGGGCCATCTGGAT
GAGCTGACAACCACACTTGAGTCCATGACCGAGGATCTGAACCTGGACTCACCCCTGACCCC
GGAATTGAACGAGATTCTGGATACCTTCCTGAACGACGAGTGCCTCTTGCATGCCATGCATA
TCAGCACAGGACTGTCCATCTTCGACACATCTCTGTTTtgacAATAAAATATCTTTATTTTC
ATTACATCTGTGTGTTGGTTTTTTGTGT

Figure 20

Dual AAV vector comprising 5'ABCA4 with introns (SEQ ID NO: 39):

CTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCGTCGGGCGACCTTTGG
TCGCCCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGG
GTTCCTtgtagttaatgattaacccgccatgctacttatctacgtagccatgctctaggaag
atcggaattcgcccttaagggcgcgccgtttaaatagctagcGACATTGATTATTGACTAGT
TATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTAC
ATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAA
TAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAG
TATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCC
TATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTT
TGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCC
CATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGC
AGAGCTggtaccaccggtgccaccATGGGCTTCGTGAGACAGATACAGCTTTTGCTCTGGAA
GAACTGGACCCTGCGGAAAAGGCAAAAGATTCGCTTTGTGGTGGAACTCGTGTGGCCTTTAT
CTTTATTTCTGGTCTTGATCTGGTTAAGGAATGCCAACCCACTCTACAGCCATCATGAATGC
CATTTCCCCAACAAGGCGATGCCCTCAGCAGGAATGCTGCCGTGGCTCCAGGGGATCTTCTG
CAATGTGAACAATCCCTGTTTTCAAAGCCCCACCCCAGGAGAATCTCCTGGAATTGTGTCAA
ACTATAACAACTCCATCTTGGCAAGGGTATATCGAGATTTTCAAGAACTCCTCATGAATGCA
CCAGAGAGCCAGCACCTTGGCCGTATTTGGACAGAGCTACACATCTTGTCCCAATTCATGGA
CACCCTCCGGACTCACCCGGAGAGAATTGCAGGTAAGTGGCGACCGTGCCCCACAGCCCTAG
CCGCCCTCCCCACTGCCCGGGCTTACCCTGGTCCTGCTCCCGCAGGAAGAGGAATACGAATA
AGGGATATCTTGAAAGATGAAGAAACACTGACACTATTTCTCATTAAAAACATCGGCCTGTC
TGACTCAGTGGTCTACCTTCTGATCAACTCTCAAGTCCGTCCAGAGCAGTTCGCTCATGGAG
TCCCGGACCTGGCGCTGAAGGACATCGCCTGCAGCGAGGCCCTCCTGGAGCGCTTCATCATC
TTCAGCCAGAGACGCGGGGCAAAGACGGTGCGCTATGCCCTGTGCTCCCTCTCCCAGGGCAC
CCTACAGTGGATAGAAGACACTCTGTATGCCAACGTGGACTTCTTCAAGCTCTTCCGTGTGC
TTCCCACACTCCTAGACAGCCGTTCTCAAGGTATCAATCTGAGATCTTGGGGAGGAATATTA
TCTGATATGTCACCAAGAATTCAAGAGTTTATCCATCGGCCGAGTATGCAGGACTTGCTGTG
GGTGACCAGGCCCCTCATGCAGAATGGTGGTCCAGAGACCTTTACAAAGCTGATGGGCATCC
TGTCTGACCTCCTGTGTGGCTACCCCGAGGGAGGTGGCTCTCGGGTGCTCTCCTTCAACTGG
TATGAAGACAATAACTATAAGGCCTTTCTGGGGATTGACTCCACAAGGAAGGATCCTATCTA
TTCTTATGACAGAAGAACAACATCCTTTTGTAATGCATTGATCCAGAGCCTGGAGTCAAATC
CTTTAACCAAAATCGCTTGGAGGGCGGCAAAGCCTTTGCTGATGGGAAAAATCCTGTACACT
CCTGATTCACCTGCAGCACGAAGGATACTGAAGAATGCCAACTCAACTTTTGAAGAACTGGA
ACACGTTAGGAAGTTGGTCAAAGCCTGGGAAGAAGTAGGGCCCCAGATCTGGTACTTCTTTG

ACAACAGCACACAGATGAACATGATCAGAGATACCCTGGGGAACCCAACAGTAAAAGACTTT
TTGAATAGGCAGCTTGGTGAAGAAGGTATTACTGCTGAAGCCATCCTAAACTTCCTCTACAA
GGGCCCTCGGGAAAGCCAGGCTGACGACATGGCCAACTTCGACTGGAGGGACATATTTAACA
TCACTGATCGCACCCTCCGCCTGGTCAATCAATACCTGGAGTGCTTGGTCCTGGATAAGTTT
GAAAGCTACAATGATGAAACTCAGCTCACCCAACGTGCCCTCTCTCTACTGGAGGAAAACAT
GTTCTGGGCCGGAGTGGTATTCCCTGACATGTATCCCTGGACCAGCTCTCTACCACCCCACG
TGAAGTATAAGATCCGAATGGACATAGACGTGGTGGAGAAAACCAATAAGATTAAAGACAGG
TGAGTGGACTGGAGCCTGGGCACGAGGTGTGGGGTGGCCCCTGCCCTGCCACTTACACCACC
TGCCTCTTCCTGCAGGTATTGGGATTCTGGTCCCAGAGCTGATCCCGTGGAAGATTTCCGGT
ACATCTGGGGCGGGTTTGCCTATCTGCAGGACATGGTTGAACAGGGGATCACAAGGAGCCAG
GTGCAGGCGGAGGCTCCAGTTGGAATCTACCTCCAGCAGATGCCCTACCCCTGCTTCGTGGA
CGATTCTTTCATGATCATCCTGAACCGCTGTTTCCCTATCTTCATGGTGCTGGCATGGATCT
ACTCTGTCTCCATGACTGTGAAGAGCATCGTCTTGGAGAAGGAGTTGCGACTGAAGGAGACC
TTGAAAAATCAGGGTGTCTCCAATGCAGTGATTTGGTGTACCTGGTTCCTGGACAGCTTCTC
CATCATGTCGATGAGCATCTTCCTCCTGACGATATTCATCATGCATGGAAGAATCCTACATT
ACAGCGACCCATTCATCCTCTTCCTGTTCTTGTTGGCTTTCTCCACTGCCACCATCATGCTG
TGCTTTCTGCTCAGCACCTTCTTCTCCAAGGCCAGTCTGGCAGCAGCCTGTAGTGGTGTCAT
CTATTTCACCCTCTACCTGCCACACATCCTGTGCTTCGCCTGGCAGGACCGCATGACCGCTG
AGCTGAAGAAGGCTGTGAGCTTACTGTCTCCGGTGGCATTTGGATTTGGCACTGAGTACCTG
GTTCGCTTTGAAGAGCAAGGCCTGGGGCTGCAGTGGAGCAACATCGGGAACAGTCCCACGGA
AGGGGACGAATTCAGCTTCCTGCTGTCCATGCAGATGATGCTCCTTGATGCTGCTGTCTATG
GCTTACTCGCTTGGTACCTTGATCAGGTGTTTCCAGGAGACTATGGAACCCCACTTCCTTGG
TACTTTCTTCTACAAGAGTCGTATTGGCTTGGCGGTGAAGGTAAGTAGTCTGATTATACACA
AGATATTGTCTAGAACTTGATGAGACTGTGGATATGAATATTTCACTCTTTTCTCAGGGTGT
TCAACCAGAGAAGAAAGAGCCCTGGAAAAGACCGAGCCCCTAACAGAGGAAACGGAGGATCC
AGAGCACCCAGAAGGAATACACGACTCCTTCTTTGAACGTGAGCATCCAGGGTGGGTTCCTG
GGGTATGCGTGAAGAATCTGGTAAAGATTTTTGAGCCCTGTGGCCGGCCAGCTGTGGACCGT
CTGAACATCACCTTCTACGAGAACCAGATCACCGCATTCCTGGGCCACAATGGAGCTGGGAA
AACCACCACCTTGTCCATCCTGACGGGTCTGTTGCCACCAACCTCTGGGACTGTGCTCGTTG
GGGGAAGGGACATTGAAACCAGCCTGGATGCAGTCCGGCAGAGCCTTGGCATGTGTCCACAG
CACAACATCCTGTTCCACCACCTCACGGTGGCTGAGCACATGCTGTTCTATGCCCAGCTGAA
AGGAAAGTCCCAGGAGGAGGCCCAGCTGGAGATGGAAGCCATGTTGGAGGACACAGGCCTCC
ACCACAAGCGGAATGAAGAGGCTCAGGACCTATCAGGTGGCATGCAGAGAAAGCTGTCGGTT
GCCATTGCCTTTGTGGGAGATGCC*AAGgtaag*ggcactgagcagaagggaagaagctccggg
ggctctttgtagggtaagcttAGTGCATCAAGGCGATCACATCAGTGAAAAAAAGCCAGACA
GGCGGTTAAACCAACGCAGATTAAACAGCAGGATGCAAAAATTCGCAGGTGGTCAGATGaag
cttattgtcgagGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTAT
TTGTAACCATTATAAGCTGCAATAAACAAGTTctcgagttaagggcgaattcccgattagga

tcttcctagagcatggctacgtagataagtagcatggcgggttaatcattaactacaAGGAA
CCCCTAGTGATGGAGTTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCG
ACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCA
G

Figure 21

Dual AAV vector comprising 3'ABCA4 with introns (SEQ ID NO: 40):

CTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCGTCGGGCGACCTTTGG
TCGCCCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGG
GTTCCTtgtagttaatgattaacccgccatgctacttatctacgtagccatgctctaggaag
atcggaattcgcccttaagggcgcgccgtttaaatagctagcGACATTGATTATTGACTAGT
TATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTAC
ATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAA
TAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAG
TATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCC
TATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTT
TGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCC
CATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGC
AGAGCTggtaccaccggtagaaagcttCATCTGACCACCTGCGAATTTTTGCATCCTGCTGT
TTAATCTGCGTTGGTTTAACCGCCTGTCTGGCTTTTTTTCACTGATGTGATCGCCTTGATGC
ACTaagctt*CAACGAGTCTTTTGTCATCTACAGGT*GGTGATTCTGGACGAACCCACCTCTGG
GGTGGACCCTTACTCGAGACGCTCAATCTGGGATCTGCTCCTGAAGTATCGCTCAGGCAGAA
CCATCATCATGTCCACTCACCACATGGACGAGGCCGACCTCCTTGGGGACCGCATTGCCATC
ATTGCCCAGGGAAGGCTCTACTGCTCAGGCACCCCACTCTTCCTGAAGAACTGCTTTGGCAC
AGGCTTGTACTTAACCTTGGTGCGCAAGATGAAAAACATCCAGAGCCAAAGGAAAGGCAGTG
AGGTGAGTCAGGCTGGGCGCCCCCGCCCCCAGGGGCCCTCCCTCCCCAAGCCCCCCGGACGC
GCCTCACCCACGTTCCTCTCGCAGGGGACCTGCAGCTGCTCGTCTAAGGGTTTCTCCACCAC
GTGTCCAGCCCACGTCGATGACCTAACTCCAGAACAAGTCCTGGATGGGGATGTAAATGAGC
TGATGGATGTAGTTCTCCACCATGTTCCAGAGGCAAAGCTGGTGGAGTGCATTGGTCAAGAA
CTTATCTTCCTTCTTCCAAATAAGAACTTCAAGCACAGAGCATATGCCAGCCTTTTCAGAGA
GCTGGAGGAGACGCTGGCTGACCTTGGTCTCAGCAGTTTTGGAATTTCTGACACTCCCCTGG
AAGAGATTTTTCTGAAGGTCACGGAGGATTCTGATTCAGGACCTCTGTTTGCGGGTGGCGCT
CAGCAGAAAAGAGAAAACGTCAACCCCCGACACCCCTGCTTGGGTCCCAGAGAGAAGGCTGG
ACAGACACCCCAGGACTCCAATGTCTGCTCCCCAGGGGCGCCGGCTGCTCACCCAGAGGGCC
AGCCTCCCCCAGAGCCAGAGTGCCCAGGCCCGCAGCTCAACACGGGGACACAGCTGGTCCTC
CAGCATGTGCAGGCGCTGCTGGTCAAGAGATTCCAACACACCATCCGCAGCCACAAGGACTT
CCTGGCGCAGATCGTGCTCCCGGCTACCTTTGTGTTTTTGGCTCTGATGCTTTCTATTGTTA
TCCCTCCTTTTGGCGAATACCCCGCTTTGACCCTTCACCCCTGGATATATGGGCAGCAGTAC
ACCTTCTTCAGCATGGATGAACCAGGCAGTGAGCAGTTCACGGTACTTGCAGACGTCCTCCT
GAATAAGCCAGGCTTTGGCAACCGCTGCCTGAAGGAAGGGTGGCTTCCGGAGTACCCCTGTG
GCAACTCAACACCCTGGAAGACTCCTTCTGTGTCCCCAAACATCACCCAGCTGTTCCAGAAG

CAGAAATGGACACAGGTCAACCCTTCACCATCCTGCAGGTGCAGCACCAGGGAGAAGCTCAC
CATGCTGCCAGAGTGCCCCGAGGGTGCCGGGGGCCTCCCGCCCCCCCAGAGAACACAGCGCA
GCACGGAAATTCTACAAGACCTGACGGACAGGAACATCTCCGACTTCTTGGTAAAAACGTAT
CCTGCTCTTATAAGAAGCAGCTTAAAGAGCAAATTCTGGGTCAATGAACAGAGGTATGGAGG
AATTTCCATTGGAGGAAAGCTCCCAGTCGTCCCCATCACGGGGGAAGCACTTGTTGGGTTTT
TAAGCGACCTTGGCCGGATCATGAATGTGAGCGGGGGCCCTATCACTAGAGAGGCCTCTAAA
GAAATACCTGATTTCCTTAAACATCTAGAAACTGAAGACAACATTAAGGTGTGGTTTAATAA
CAAAGGCTGGCATGCCCTGGTCAGCTTTCTCAATGTGGCCCACAACGCCATCTTGTAAGTCC
TACCTTTTTTGTTCCTTTGAAAGCCTCCTGGAAAGCTTTTCCTGAAGTGTTTGTTCTGTAAT
TTCTTTGCAGACGGGCCAGCCTGCCTAAGGACAGGAGCCCCGAGGAGTATGGAATCACCGTC
ATTAGCCAACCCCTGAACCTGACCAAGGAGCAGCTCTCAGAGATTACAGTGCTGACCACTTC
AGTGGATGCTGTGGTTGCCATCTGCGTGATTTTCTCCATGTCCTTCGTCCCAGCCAGCTTTG
TCCTTTATTTGATCCAGGAGCGGGTGAACAAATCCAAGCACCTCCAGTTTATCAGTGGAGTG
AGCCCCACCACCTACTGGGTGACCAACTTCCTCTGGGACATCATGAATTATTCCGTGAGTGC
TGGGCTGGTGGTGGGCATCTTCATCGGGTTTCAGAAGAAAGCCTACACTTCTCCAGAAAACC
TTCCTGCCCTTGTGGCACTGCTCCTGCTGTATGGATGGGCGGTCATTCCCATGATGTACCCA
GCATCCTTCCTGTTTGATGTCCCCAGCACAGCCTATGTGGCTTTATCTTGTGCTAATCTGTT
CATCGGCATCAACAGCAGTGCTATTACCTTCATCTTGGAATTATTTGAGAATAACCGGACGC
TGCTCAGGTTCAACGCCGTGCTGAGGAAGCTGCTCATTGTCTTCCCCCACTTCTGCCTGGGC
CGGGGCCTCATTGACCTTGCACTGAGCCAGGCTGTGACAGATGTCTATGCCCGGTTTGGTGA
GGAGCACTCTGCAAATCCGTTCCACTGGGACCTGATTGGGAAGAACCTGTTTGCCATGGTGG
TGGAAGGGGTGGTGTACTTCCTCCTGACCCTGCTGGTCCAGCGCCACTTCTTCCTCTCCCAA
TGGATTGCCGAGCCCACTAAGGAGCCCATTGTTGATGAAGATGATGATGTGGCTGAAGAAAG
ACAAAGAATTATTACTGGTGGAAATAAAACTGACATCTTAAGGCTACATGAACTAACCAAGA
TTTATCCAGGCACCTCCAGCCCAGCAGTGGACAGGCTGTGTGTCGGAGTTCGCCCTGGAGAG
TGCTTTGGCCTCCTGGGAGTGAATGGTGCCGGCAAAACAACCACATTCAAGATGCTCACTGG
GGACACCACAGTGACCTCAGGGGATGCCACCGTAGCAGGCAAGAGTATTTTAACCAATATTT
CTGAAGTCCATCAAAATATGGGCTACTGTCCTCAGTTTGATGCAATTGATGAGCTGCTCACA
GGACGAGAACATCTTTACCTTTATGCCCGGCTTCGAGGTGTACCAGCAGAAGAAATCGAAAA
GGTAAGTGATTCCTAGGGCTGGGGAAGGTGGGTGGGAATCCTCTCCTGCTCACCTCCTCTCT
CCTGCCCCACAGGTTGCAAACTGGAGTATTAAGAGCCTGGGCCTGACTGTCTACGCCGACTG
CCTGGCTGGCACGTACAGTGGGGGCAACAAGCGGAAACTCTCCACAGCCATCGCACTCATTG
GCTGCCCACCGCTGGTGCTGCTGGATGAGCCCACCACAGGGATGGACCCCCAGGCACGCCGC
ATGCTGTGGAACGTCATCGTGAGCATCATCAGAGAAGGGAGGGCTGTGGTCCTCACATCCCA
CAGCATGGAAGAATGTGAGGCACTGTGTACCCGGCTGGCCATCATGGTAAAGGGCGCCTTTC
GATGTATGGGCACCATTCAGCATCTCAAGTCCAAATTTGGAGATGGCTATATCGTCACAATG
AAGATCAAATCCCCGAAGGACGACCTGCTTCCTGACCTGAACCCTGTGGAGCAGTTCTTCCA
GGGGAACTTCCCAGGCAGTGTGCAGAGGGAGAGGCACTACAACATGCTCCAGTTCCAGGTCT

CCTCCTCCTCCCTGGCGAGGATCTTCCAGCTCCTCCTCTCCCACAAGGACAGCCTGCTCATC
GAGGAGTACTCAGTCACACAGACCACACTGGACCAGGTGTTTGTAAATTTTGCTAAACAGCA
GACTGAAAGTCATGACCTCCCTCTGCACCCTCGAGCTGCTGGAGCCAGTCGACAAGCCCAGG
ACTGAgtcgacgcggccgcGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATT
GCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTctcgagttaagggcgaattcccg
attaggatcttcctagagcatggctacgtagataagtagcatggcgggttaatcattaacta
caAGGAACCCCTAGTGATGGAGTTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGG
CCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGA
GCGCGCAG