

## Supplementary Data

SUPPLEMENTARY TABLE S1. PRIMER SEQUENCES FOR FIBER MODIFICATIONS

A. PRIMERS USED TO GENERATE DNA FRAGMENTS FOR INSERTION THROUGH HOMOLOGOUS RECOMBINATION	
Primer	Sequence (5'-3')
GE11 F	<u>CTTAA</u> CGGAGACAAA <u>AACTAA</u> ACCTGTAAACACTAACCATTAACACTAAACGGTACACAGGAAACATACCCTGGTACGGCTACACCCCCAGAACGTGATC
GE11 R	TGTAGTTGGCCAGACCAGTCCCATGAAAATGACATAGAGTATGCACCTGGAGTTGTCTCCGATCACGTTCTGGGGGTGTAGCCGTACCAGTGGTA
M* F	TGTCAGTCAAGTTTACTTAAACGGGAGACAAAACCTGTAAACACTAACCATTAACACTAAACGGTACACAGGAAACAATGCAGCTGCCCTGGCCACC
M* R	CAAAATTTTCATTAATGTAGTTGGCCAGACCAGTCCCATGAAAATGACATAGAGTATGCACCTGGAGTTGTCTCCGGTGGCCAGGGCAGCTGCAT
LS F	TGTCAGTCAAGTTTACTTAAACGGGAGACAAAACCTGTAAACACTAACCATTAACACTAAACGGTACACAGGAAACAACACTGTCCCCCCCGGTACCCC
LS R	CAAAATTTTCATTAATGTAGTTGGCCAGACCAGTCCCATGAAAATGACATAGAGTATGCACCTGGAGTTGTCTCCGGGGTAACGGGGGGGGACAG
Scramble F	TGTCAGTCAAGTTTACTTAAACGGGAGACAAAACCTGTAAACACTAACCATTAACACTAAACGGTACACAGGAAACAACACTGTATGCCCTGGCCAGCCC
Scramble R	ATGAGTTAGTCCCAAATGTTGCTCCGATATAGCTTCCGTTAGTCCAGGTGATGAAAATGACATTTGAGTATGCACCTGGTGGCTGGGCCAGGGTTCATCAG
RPSL-neo	<u>GTCAGTCAAGTTTACTTAAACGGGAGACAAAACCTAA</u> ACCTGTAAACACTAACCATTAACACTAAACGGTACACAGGAAACAACCTGTGACGGAAAGATCACTTCG
HI loop F	<u>CAAAATTTTCATTAATGTAGTTGGCCAGACCAGTCCCATGAAAATGACATAGAGTATGCACCTGGAGTTGTCTCCCTGAGGTTCTTATGGCTCTTG</u>
HI loop R	<u>AGTTTTGACAGCACAGGTGCCATTACAGTAGGAAACAAAATAATGATAAGCTAACTTTGTGGACCACACCAGCTCCACCCTGTGACGGAAAGATCACTTCG</u>
RPSL-neo	<u>CTGTAGCAAGTATTTGACTGCCACA</u> TTTTGTTAAGACCAAAAGTGAGTTTAGCATCTTCTCTGCAATTTAGTCTACAGTTCTGAGGTTCTTTATGGCTCTTG
AB loop F	<u>GAAACAAAATAATGATAAGCTAACTTTGTGGACCACACCAGTCCAGGGCCAACTGTAGACTAAATGCAGAGAAAAGATGCTAAACTCACTTTGGTCTT</u>
AB loop R	
KO1 mutation oligo	

  

B. SEQUENCING PRIMERS	
Primer	Sequence (5'-3')
HI loop	GCCTATACAAAACGGCTGTTGG
AB loop	GTTACCTAATGCACCAACAC

Regions with homology to Ad5.Luc DNA sequence are underlined. F, forward primer; GE11, YHWYGYTPQNV; KO1, hCAR-binding mutation; LS, LSPRYP; M\*, MQLPLAT; R, reverse primer; scramble, LMTLAQP.

Ad5 fiber knob HI loop was sequenced to verify successful peptide insertions and AB loop was sequenced to verify the KO1 (S408E, P409A) mutation.