

Supplementary materials

General cloning protocols

The Q5 High-Fidelity 2X Master Mix (New England Biolabs, catalog number: M0492) was used for all polymerase chain reactions (PCR) according to the manufacturer's protocol. All oligonucleotides were ordered from Sigma-Aldrich and were listed in **Supplementary Table S1**. The plasmids were constructed using PCR amplification, restriction digest (all restriction enzymes were ordered from New England Biolabs), and ligation with T4 DNA ligase (New England Biolabs, catalog number: M0202). Gel purification and PCR purification were performed with QIAquick Gel Extraction kit (Qiagen, catalog number: 28707) and PCR Purification kit (Qiagen, catalog number: 28104). Transformations were performed using NEB 5-alpha electrocompetent *Escherichia Coli* cells (New England Biolabs, catalog number: C2987). The minipreps were performed using QIAprep Spin Miniprep kit (Qiagen, catalog number: 27106). The final plasmids were confirmed by both restriction enzyme digestions and direct Sanger sequencings.

DNA constructs

PCMV-spCas9-U6-sgRNA.left: The U6-sgRNA.left sequence was first PCR amplified from PCMV-spCas9-U6-sgRNA.PUF (unpublished results) using primers P7 and P8, and the PCR product was subsequently subjected to the second round PCR using primers P7 and P9. The PCR product was then cloned into the PCMV-spCas9-U6-sgRNA.PUF vector using KpnI and XbaI sites.

PCMV-spCas9-U6-sgRNA.right: The U6-sgRNA.right sequence was first PCR amplified from PCMV-spCas9-U6-sgRNA.PUF (unpublished results) using primers P7 and P10, and the PCR product was subsequently subjected to the second round PCR using primers P7 and P9. The PCR product was then cloned into the PCMV-spCas9-U6-sgRNA.PUF vector using KpnI and XbaI sites.

Homologous Recombination (HR) repair template: The NAB2-STAT6 left homologous arm was PCR amplified using HCT116 genomic DNA as the template and primers P11 and P12. The PCR product was then cloned into the PGK1-Hygromycin resistance gene vector (unpublished results) using ClaI and FseI sites. The resulting plasmid was named Step1. Next, the NAB2-STAT6 right homologous arm was PCR amplified using HCT116 genomic DNA as the template and primers P13 and P14. The PCR product was then cloned into the Step1 plasmid using NotI and MscI sites. The resulting plasmid was named Step2. Next, to add new restriction enzyme sites for later knock-in sequences, a PCR reaction was performed using Step2 plasmid as the template and primers P15 and P16. The PCR product was then cloned into Step2 plasmid using ClaI and FseI sites. The resulting plasmid was named Step3. Next, one portion of the knock-in sequence was PCR amplified using HCT116 genomic DNA as the template and primers P17 and P18. The PCR product was then cloned into Step3 plasmid using XhoI and SmaI sites. The resulting plasmid was named Step4. Next, another portion of the knock-in sequence was PCR amplified using HCT116 genomic DNA as the template and primers P19 and P20. The PCR product was then cloned into Step4 plasmid using FseI and SmaI sites. The resulting plasmid was named Step5. Finally, the last portion of the knock-in sequence was synthesized at Genewiz and cloned into Step5 plasmid using MluI and XhoI sites.

PCMV-CasRx-U6-sgRNA.NAB2STAT6: The GFAP-CasRx-U6-sgRNA was ordered from Addgene (catalog number: 154001). The CMV promoter sequence was PCR amplified from D1 (unpublished results) using primers P27 and P28. The PCR product was then cloned into GFAP-CasRx-U6-sgRNA using XbaI and SgrAI sites. The resulting plasmid was named NS4.1.1. Next, the U6-sgRNA.NAB2STAT6 sequence was first PCR amplified from NS4.1.1 using primers P29 and P30, and the PCR product was subsequently subjected to the second round PCR using primers P2 and P31. The PCR product was then cloned into NS4.1.1 vector using BglII and EcoRI sites.

PCMV-ATG-target.NAB2STAT6-YFP-PEST: The target.NAB2STAT6-YFP-PEST was PCR amplified from B12 (unpublished results) using primers P32 and P33. The PCR product was then cloned into B12 using NheI and XmnI sites.

PCMV-CasRx-U6-sgRNA.AAVS1: The U6-sgRNA.AAVS1 sequence was PCR amplified from NS4.1.1 using primers P29 and P34, and the PCR product was subsequently subjected to the second round PCR using primers P2 and P35. The PCR product was then cloned into NS4.1.1 vector using BglII and EcoRI sites.

Homologous Recombination (HR) repair template sequence:

TCGACATCGATGCCAGCCCATGGGCTATGGAGCCGACACATCCTGCAGCAGACACTGATGGACGAGGGGCTGCG
GCTCGCCCGCCTCGTCTCCACGACCGCGTGGGCCGCTCAGCCCCTGTGTGCCTGCGAAGCCACCTCTCGCAGGT
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TCTTCCTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGA
AAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGG

Blue: left homologous arm

Auburn: knock-in sequence

Red: FRT (flippase recognition target) site

Purple: PGK1-Hygromycin resistance gene

Green: right homologous arm

PCMV-CasRx-U6-sgRNA.NAB2STAT6 sequence:

ATTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTACGGTTCCTGGC
CTTTTGTGCTTTTGTCTACATGTCTGCAGGCAGCTGCGCGCTCGCTCGCTCACTGAGGCCGCGCGGCGTCCG
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Red: AAV2 ITR

Green: CMV promoter

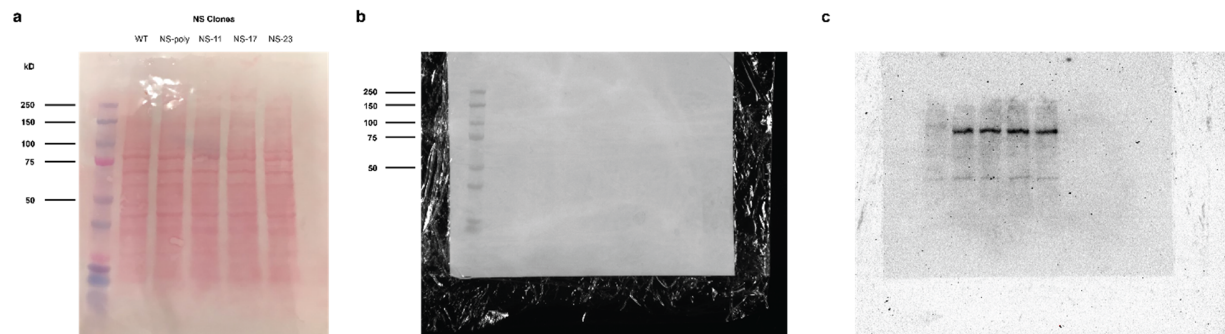
Purple: SV40 NLS

Auburn: CasRx

Orange: U6 promoter

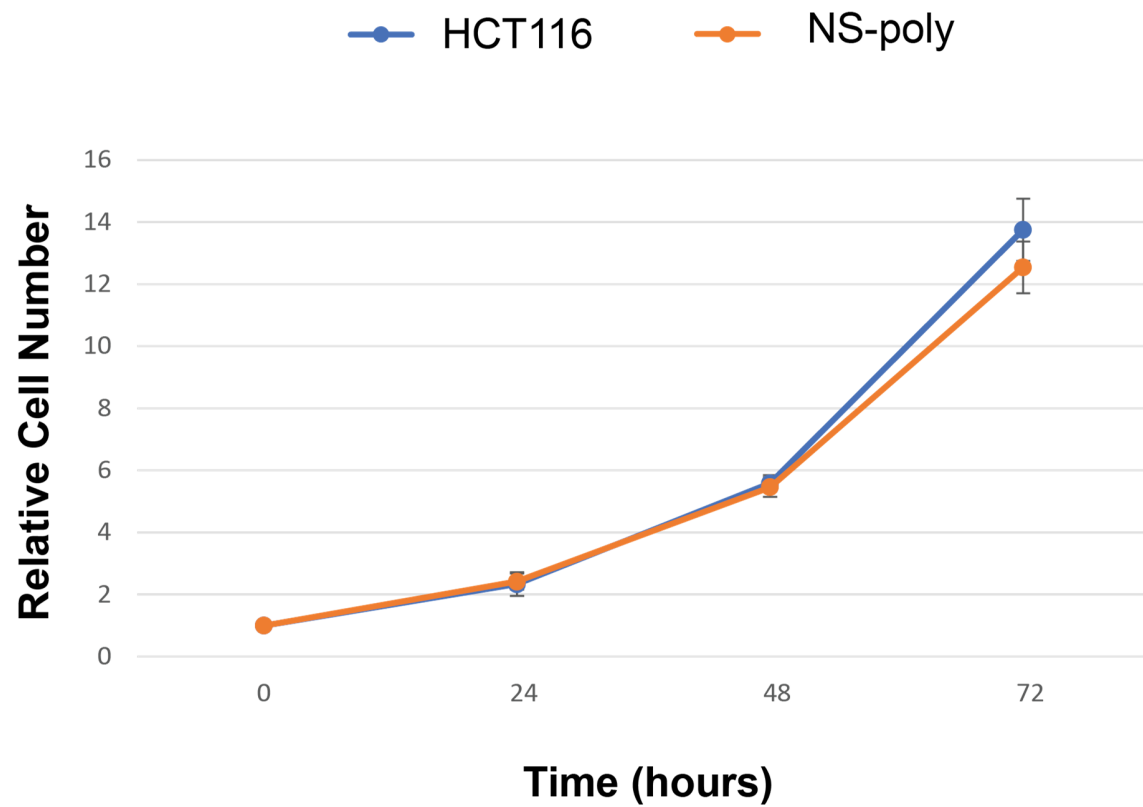
Yellow: sgRNA.NAB2STAT6

Supplementary Figure S1



Supplementary Figure S1. Original data for Western blot. (a) Ponceau staining of the whole cell lysates prepared from HCT116 wild type and NAB2-STAT6 fusion cell lines. **(b)** Full Western blot image (bright field). **(c)** Full Western blot image (chemiluminescence).

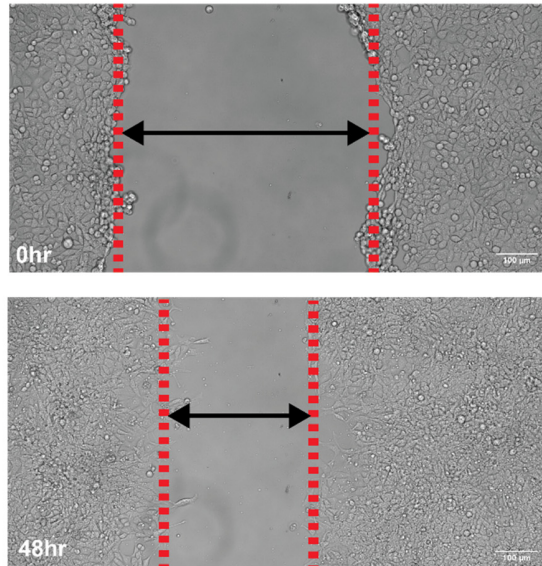
Supplementary Figure S2



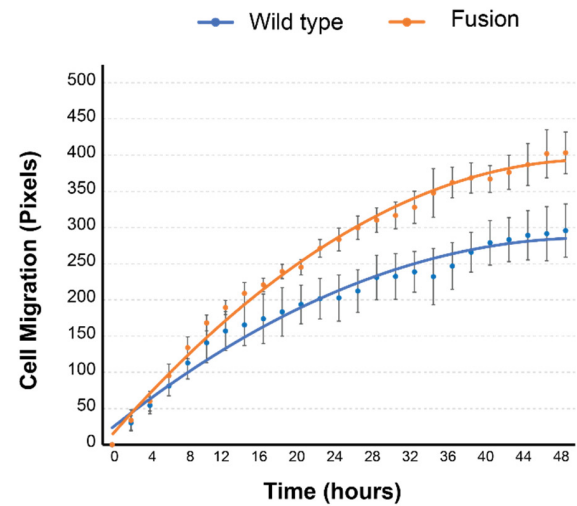
Supplementary Figure S2. Cell proliferation assays for wild type HCT116 and NS-poly cells. No significantly different proliferation rate was observed between wild type HCT116 and NS-poly cells.

Supplementary Figure S3

a



b



Supplementary Figure S3. *In vitro* characterization of NS-poly cell model. (a) Representative wound healing assay images for wild type HCT116 cells at 0 and 48 hours. **(b)** Wound healing assay results for both wild type HCT116 and NS-poly cells. The NS-poly cells showed higher motility rate compared to wild type HCT116.

Supplementary Table S1: Summary sequencing statistics of the RNA-seq assay.

Supplementary Table S2: Primers used in this study.

Supplementary Table S3: Wound healing assays using HCT116 and NS-poly cells.

Supplementary Table S4: Differentially expressed genes between wild type HCT116 and NAB2-STAT6 fusion cells from RNA-seq. Negative values in the log2FoldChange reflected fold changes observed in the control samples (HCT116 parental cells) compared to experimental samples (our engineered NAB2-STAT6 fusion cells). Therefore, negative values indicated that expression levels of such genes were elevated in the engineered NAB2-STAT6 fusion cells.

Supplementary Table S5: Differentially expressed genes used for PANTHER signaling pathway analysis.

Supplementary Table S6: NAB2-STAT6 fusion-related signaling pathways identified by the PANTHER classification system.

Supplementary Table S7: NAB2-STAT6 fusion-specific ASOs with 2'-O-methoxyethyl modifications.

prepDE.py: The python script used to quantify both expressed genes and transcripts.

DESeq2.r: The R script used to identify differentially expressed genes and prepare for the corresponding heatmap.