

Supplemental Information

**CRISPR/Cas9-Mediated Knockin Application
in Cell Therapy: A Non-viral Procedure
for Bystander Treatment of Glioma in Mice**

Oscar Meca-Cortés, Marta Guerra-Rebollo, Cristina Garrido, Salvador Borrós, Nuria Rubio, and Jeronimo Blanco

SUPPLEMENTAL FIGURES

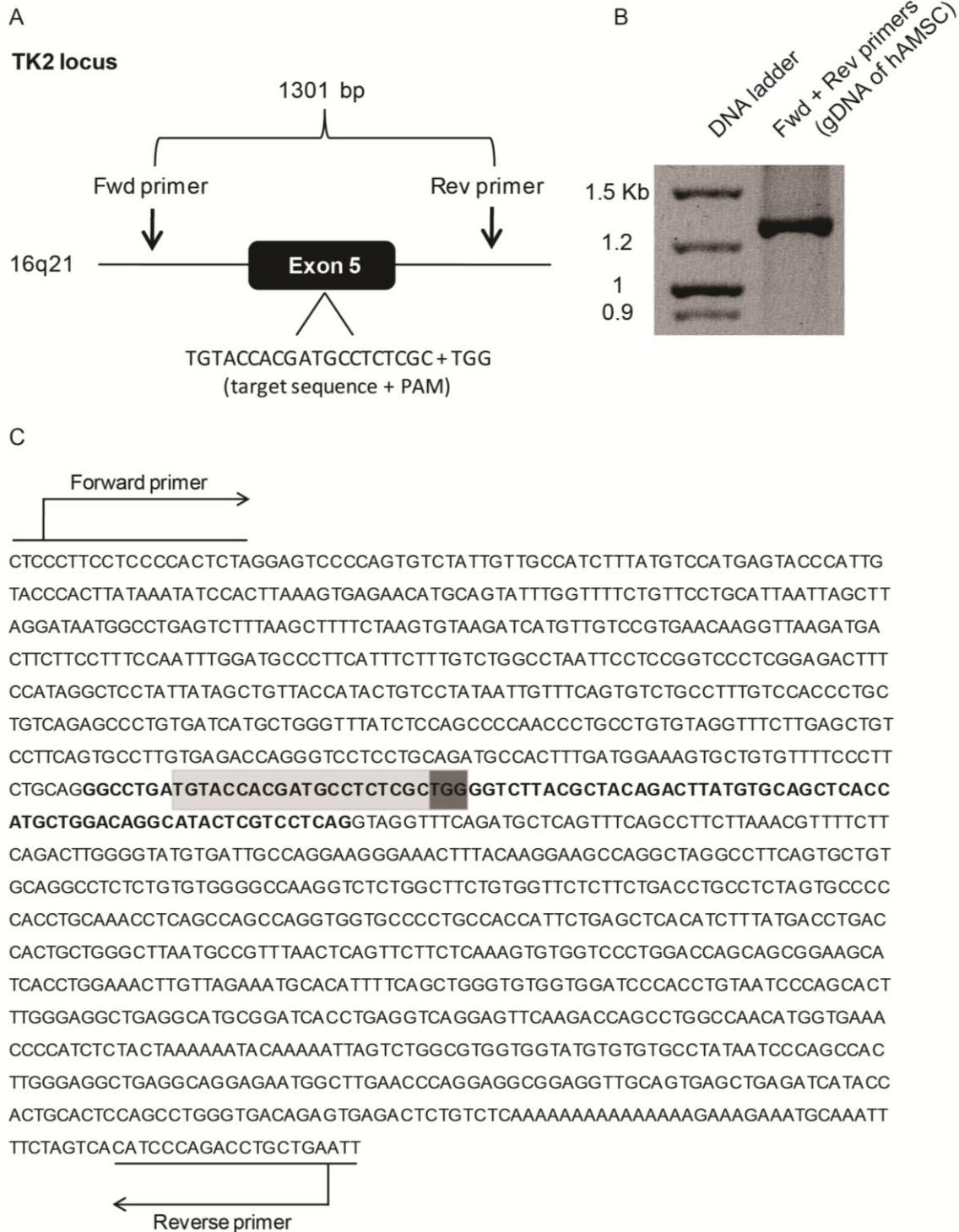


Figure S1. Assessment of the integrity of the selected target sequence in exon 5 of the TK2 gene in hAMSCs. (A) Diagram showing the chosen Cas9 nuclease target sequence within exon 5 of TK2 locus and the expected PCR amplicon size. (B) Agarose gel showing PCR generated amplicon. (C) Sequence corresponding to PCR amplicon. Exon 5 is highlighted (bold), including Cas9 nuclease target sequence (grey-shaded) and PAM (dark grey-shaded).

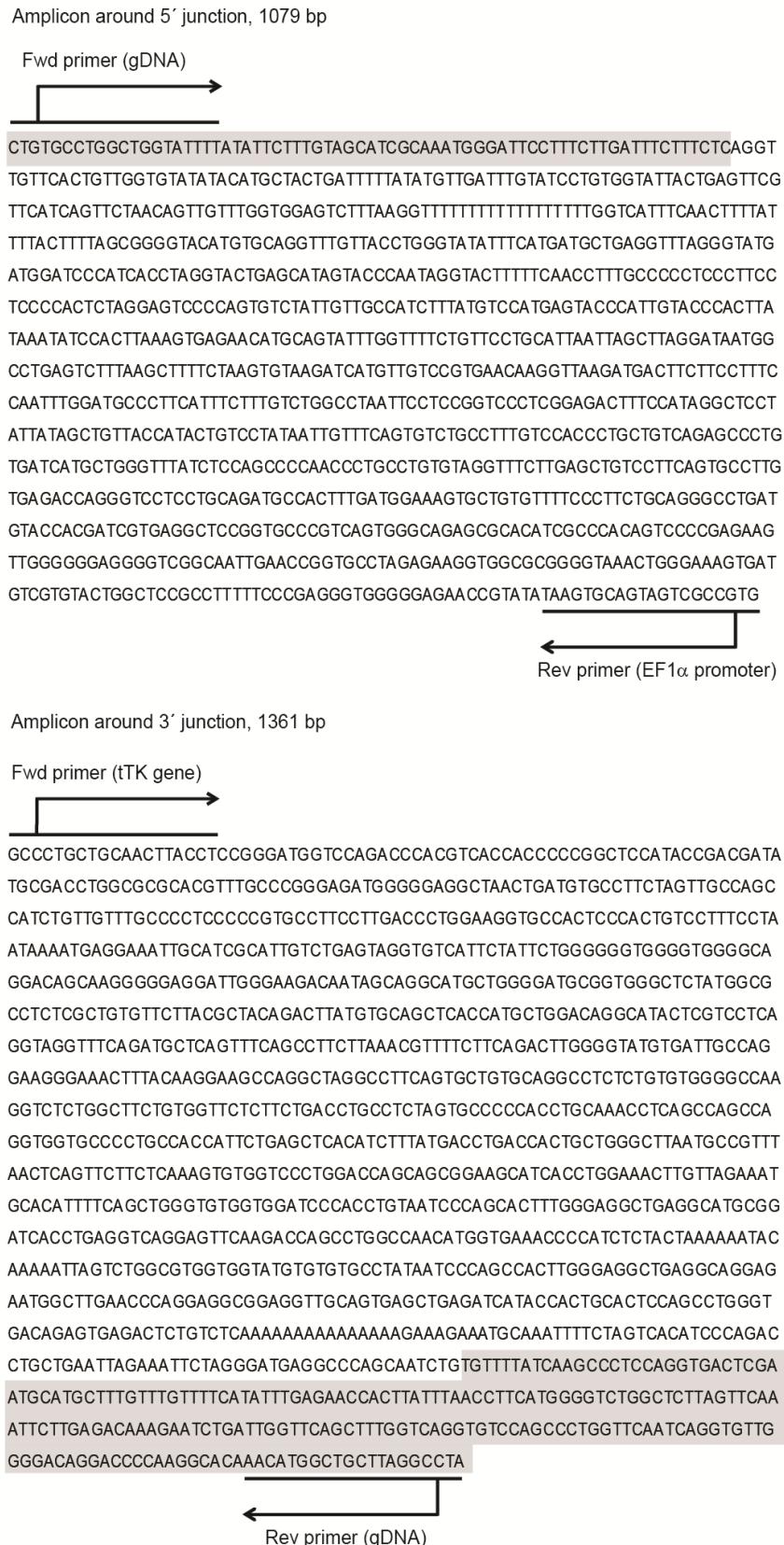


Figure S2. DNA sequence of predicted amplicons indicating integration of donor plasmid elements in exon 5 of TK2 locus in hAMSCs. Amplicon sequences were obtained by PCR amplification of genomic DNA from putative CRISPR/Cas9-engineered hASMCs using primers (underlined) flanking 5' and 3' junctions of integrated and genomic sequences (indicated as transition from non-shaded and grey-shaded nucleotides).

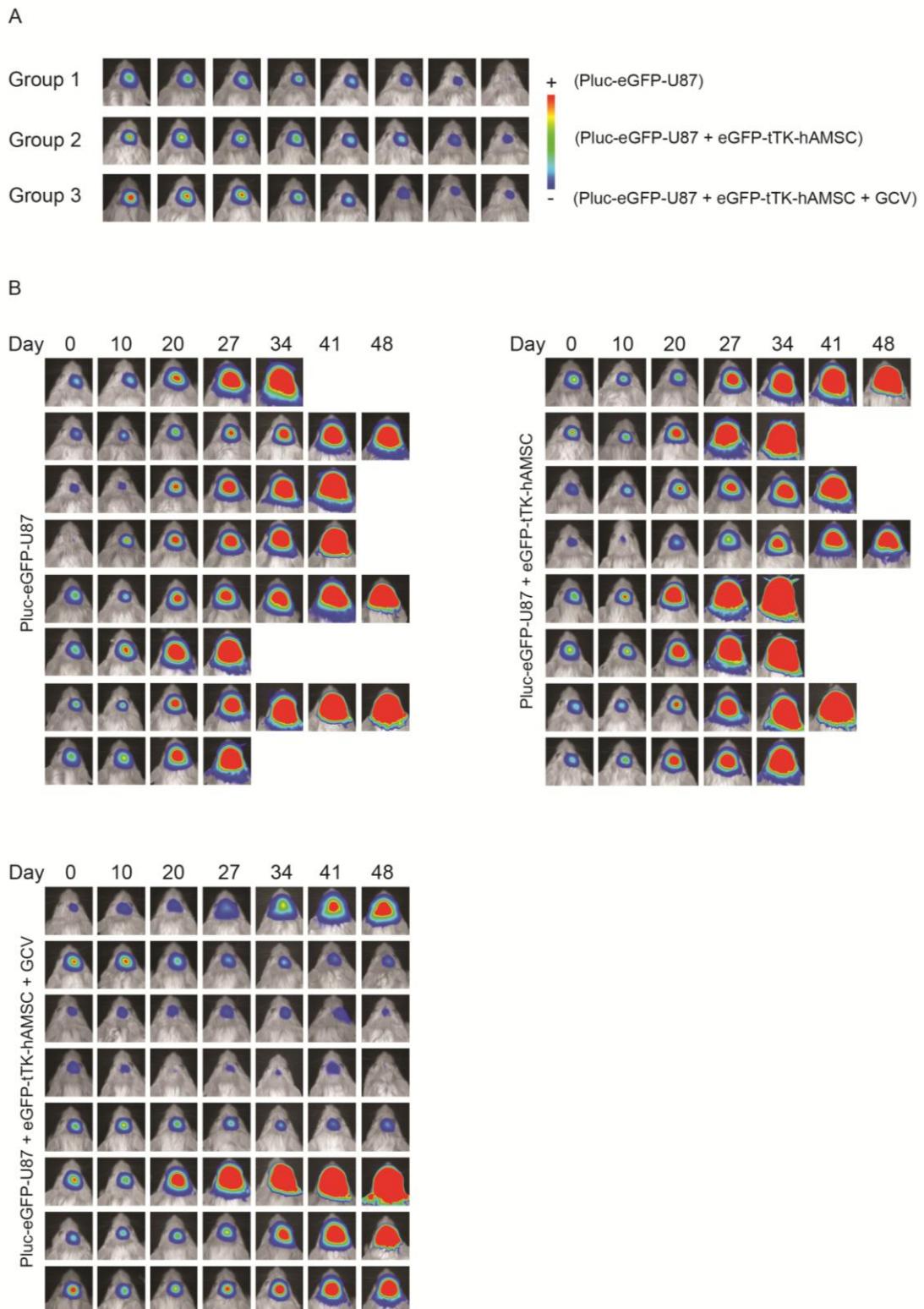
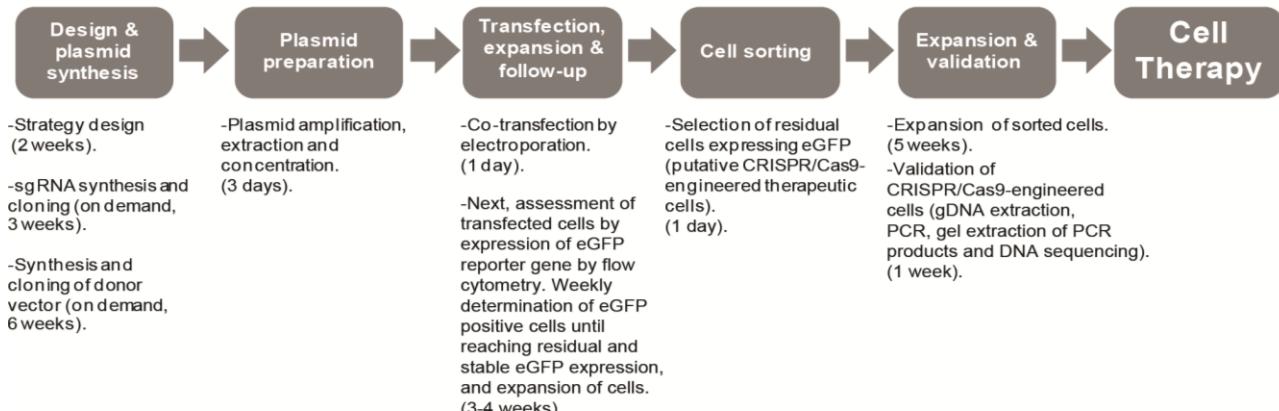


Figure S3. Initial homogenization of experimental groups for *in vivo* assessment of bystander glioblastoma therapy of CRISPR/Cas9-modified hAMSCs and tumor growth development in all mice until day 48. (A) Non-invasive BLI images were acquired as described above 5 days post-implantation of tumor cells and animals were separated in 3 groups with similar light emission capacity. (B) 48 day non-invasive BLI monitoring of tumor growth. Images show all mice from (A). BLI images (false color palette ranging from blue = low intensity, to red = high intensity light emission) are overlaid on bright field images.

Time-scale of CRISPR/Cas9-mediated knock-in in hAMSCs for glioma cell therapy



Working time aprox. 8 weeks

Figure S4. Flow diagram showing the strategy for generating therapeutic hAMSCs through CRISPR/Cas9-mediated knock-in in this study.

SUPPLEMENTAL DATA FILES

5' homology arm, including 5'-end exon 5 of *TK2* gene (**bold**) and 11 of 20 nucleotides of target sequence (underlined)

```

AGGTTGTTCACTGTTGGTATATACATGCTACTGATTTCATATGTTGATTGTATCCTGTGG
TATTACTGAGTCGTTCATCAGTTAACAGTTGTTGGAGTCTTAAGGTTTTTTTT
TTTTTTGGTCATTCAACTTTATTTACTTTAGCAGGGTACATGTGCAGGTTGTTACCTG
GGTATATTGATGCTGAGGTTAGGGTATGATGGATCCCATCACCTAGGTACTGAGCAT
AGTACCCAATAGTACTTTCAACCTTGCCCCCTCCCTCCCTCCCCACTCTAGGAGTCCCC
AGTGTCTATTGTTGCCATCTTATGTCATGAGTACCCATTGTACCCACTATAAATATCCAC
TTAAAGTGAGAACATGCAGTATTGGTTCTGTTCTGCATTAATTAGCTTAGGATAATGGC
CTGAGTCTTAAGCTTCTAAGTGTAAAGATCATGTTGTCGTGAACAAGGTTAAGATGACTT
CTTCCTTCCAATTGGATGCCCTCATTTCTGCTGGCCTAATTCTCCGGTCCCTCGGAG
ACTTCCATAGGCTCTATTATAGCTGTTACCATACTGTCCTATAATTGTTCACTGTCGCT
TTGTCCACCCCTGCTGTCAAGAGCCCTGTGATCATGCTGGGTTATCTCCAGCCCCAACCTGCC
TGTGTAGGTTCTTGAGCTGTCCTCAGTCCTGTGAGACCAGGGCTCTGCAGATGCCA
CTTGATGAAAGTGTGTTCCCTCTGCAGGGCCTGATGTACCACGAT

```

EF1 α promoter

```

CGTGAGGCTCCGGTCCCCGTCACTGGCAGAGCGCACATGCCACAGTCCCCGAGAAGTT
GGGGGGAGGGGTCGGCAATTGAACCGGTGCCTAGAGAAGGTGGCGCGGGTAAACTGGGA
AAAGTGTGTCGTGACTGGCTCCGCCTTTCCCGAGGGTGGGGAGAACCGTATATAAGTG
CACTAGTCGCCGTGAACGTTCTTTCGCAACGGTTGCGCCAGAACACAGGTAACTGCC
GTGTGTGGTTCCCGGGGCTGGCTCTTACGGGTATGGCCCTGCGTGCCTGAATTACT
TCCACCTGGCTGCACTGATTCTGATCCCAGCTCGCTCGTGAAGTTGAGGCCTGGCTGGC
TTCGAGGCCTTGCCTTAAGGAGCCCTTCGCGCTCGTGAAGTTGAGGCCTGGCTGGC
GCTGGGGCCGCCGTGCAATCTGGTGGCACCTTCGCGCCTGCTCGCTGCTTCAAG
TCTCTAGCCATTAAAATTGATGACCTGCTGCGACGCTTTCTGCAAGATAGTCTT
GTAAATGCGGGCCAAGATCTGCACACTGGTATTGCGTTGGGGCCGGCGACGG
GGCCCGTGCCTCCAGCGCACATGTTGGCAGGCAGGGCCTGCGAGCGCGGCCACCGAGA
ATCGGACGGGGTAGTCTCAAGCTGGCCGGCTGCTGGTGCCTGGCCTCGCGCCCGTG
TATCGCCCCGCCCTGGGCGCAAGGCTGGCCGGTGGCACCAGTTGCGTGAGCGGAAAGA
TGGCCGCTCCGGCCCTGCTGCAGGGAGCTCAAATGGAGGACGCAGCGCTGGGAGAGC
GGCGGGGTGAGTCACCCACACAAAGGAAAAGGGCCTTCCGTCCTCAGCCGTCGCTTCA

```

GAATCCACGGAGTACCGGGCGCCGCCAGGCACCTCGATTAGTCGAGCTTTGGAGTAC
GTCGTCTTAGTTGGGGGGAGGGGTTTATGCGATGGAGTTCCCCACACTGAGTGGGTGG
AGACTGAAGTTAGGCCAGCTGGCACTTGATGTAATTCTCCTTGAATTGCCCTTTGAGT
TTGGATCTGGTCATTCTCAAGCCTCAGACAGTGGTCAAAGTTTTCTTCATTCAGGT
GTCGTGAGGAATTAGCC

eGFP gene

ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGTGGTGCCTGCCATCCTGGTCGAGCTGGACG
GCGACGTAACCGGCCACAAGTTCAGCGTCCGGCAGGGCGAGGGCGATGCCACCTACGG
CAAGCTGACCTGAAGTTCATCTGCACCACCGCAAGCTGCCGTGCCCTGGCCCACCCCTCG
TGACCAACCTGACCTACGGCGTGCAGTGCTCAGCCCTACCCGACCACATGAAGCAGCAC
GACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCACATCTTCAGGA
CGACGGCAACTACAAGACCCGCCAGGGTAAGTTGAGGGGACACCCCTGGTAACCGC
ATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGACAAGCTGGAGT
ACAACATACAACAGCCACAACGTCTATATCATGGCGACAAGCAGAAGAACGGCATCAAGGT
GAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTGCCGACCACCTACCA
CAGAACACCCCCATCGGCCAGGGCCCGTGTGCTGCCGACAACCAACTACCTGAGCACCCA
GTCCGCCCTGAGCAAAGACCCCAACGAGAACGCGATCACATGGCCTGCTGGAGTTGTG
ACCGCCGCCGGGATCACTCTGGCATGGACGAGCTGTACAAG

Spacer sequence

ACCGCGGGCCGGGATCCGCCAC

Herpes simplex virus 1 truncated thymidine kinase gene (tTK)

ATGCCACGCTACTGCCGGTTATAGACGGTCCCACGGGATGGGAAAACCACCA
CGCAACTGCTGGTGGCCCTGGGTTCGCGCAGCATATCGTCTACGTACCCGAGCCGATGACT
TAATGGCGGGTGTGGGGCTCCGAGACAATCGCAACATCTACACCACACAACACCGCCT
CGACCAAGGTGAGATATCGGCCGGGACGCCGGTGGTAATGACAAGGCCAGATAACA
ATGGGCATGCCTTATGCCGTGACCGACGCCCTCTGGCTCCTCATATCGGGGGAGGCTGG
GAGCTCACATGCCCGCCCCCGGCCCTCACCATCTTCCTCGACCCCATCCATGCCCTCAT
GCTGTGCTACCCGGCCGGGTACCTTATGGCAGCATGACCCCCCAGGCCGTGTGGCGT
TCGTGGCCCTCATCCGCCGACCTGCCGGCACCAACATCGTGTGCTGGGCCCTCCGGAG
GACAGACACATCGACCGCCTGGCAAACGCCAGGCCGGAGCGGCTGGACCTGGCTA
TGCTGGCTGCGATTGCCCGTGTACGGCTACTTGCCAATACGGTGCAGTATCTGAGTGC
GGCAGGGCTGTGGCGGGAGGACTGGGACAGCTTCGGGACGCCGTGCCGCCAGGGTG
CCGAGCCCCAGAGCAACGCCGGCCACGCCATATCGGGGACACGTTATTACCCCTGTT
CGGGCCCCCGAGTTGCTGCCCTAACGCCAGCTGTATAACGTGTTGCCCTGGGCTTGG
CGTCTGGCCAAACGCCCTCCGTCCATGCACTGCTTTATCCTGGATTACGACCAATGCCCG
CGGCTGCCGGGACGCCCTGCTGCAACTTACCTCCGGATGGTCCAGACCCACGTACCACCC
CCGGCTCCATACCGACGATATGCAACCTGCCGCCACGTTGCCCGGAGATGGGGAGGC
TAACGTGA

BGH pA signal

TGTGCCCTCTAGTTGCCAGCCATCTGTTGTTGCCCTCCCCGTGCCTTCTTGACCCCTGGA
AGGTGCCACTCCACTGTCCTTCTTAATAAAATGAGGAAATTGCATCGCATTGTCAGTA
GGTGTCAATTCTATTCTGGGGGTGGGGCAGGACAGCAAGGGGAGGATTGGGAAGA
CAATAGCAGGCATGCTGGGATGCCGTGGCTATGGC

3' homology arm, including 3'-end exon 5 of TK2 gene (bold**), 9 of 20 nucleotides of target sequence (underlined) and PAM mutations (lower case)**

GCCTCTCG**CTGtGtTCTTACG**CTACAGACTTATGTGCAG**CTCACCATG**TGGACAGGCAT
ACTCGT**CCTCAGG**TAGTTCA**GATG**CTCAGTT**CAGC**CTTCTAAACGTTTCTCAGACTT
GGGGTATGTGATTGCCAGGAAGGGAAACTTACAAGGAAGCCAGGCTAGGCCTTCAGTGCT
GTGCAGGCCCTCTGTGTGGGCCAAGGTCTCTGGCTCTGTGGTTCTTCTGACCTGCC
TAGTGCCCCACCTGCAAACCTCAGCCAGGCCAGGTGGTGCCACCATTCTGAGCTCA
CATTTTATGACCTGACCACTGCTGGCTTAATGCCGTTAAC**TCA**GTTCTCTCAAAGTGTG
GTCCCTGGACCAGCAGCAGGAAGC**ATCAC**CTGGAAACTTGTAGAAATGCACATTTCAGCTG
GGTGTGGTGGATCCACCTGTAATCCAGCACTTGGGAGGCTGAGGACATGCCGAGTACCTG
AGGTCAAGGAGTTCAAGACCAGCCTGCCAACATGGTAAACCCATCTACTAAAAATA

CAAAAATTAGTCTGGCGTGGTGGTATGTGTGCCTATAATCCCAGCCACTGGGAGGCTGA
GGCAGGAGAATGGCTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCTGAGATCATACCACTG
CACTCCAGCCTGGGTGACAGAGTGAGACTCTGTCTAAAAAAAAAAAGAAAGAAATG
CAAATTTCAGTCACATCCCAGACCTGCTGAATTAGAAATTCTAGGGATGAGGCCAGCAA
TCTG

Data file S1. Sequence of donor fragment designed for integration via HDR pathway after DNA cleavage exerted by CRISPR/Cas9 nuclease in hAMSCs.