| Primer             | Sequence                                                                 |
|--------------------|--------------------------------------------------------------------------|
| Map2 sgRNA F       | GAAATTAATACGACTCACTATAGGAATGCCACGCTGGACCTGGCTTTTAGAGCTAGAAATAGC          |
| sgRNA common       | AAAAGCACCGACTCGGTGCCACTTTTCAAGGGTTGATAACCGGACTCCTTTAATTCTTCAGCTCTAAAC  |
| Cas9 Forward       | TTATTACGACTCACTATAGGGAGAATGGACTATAAGGACCACGAC                            |
| Cas9 Reverse       | GCGAGCTCTAGGAATTCTTTAC                                                   |
| Repair oligo       | \*T\*G\*TTTCTCTTTCAACAGATGACAGGCCAAAAGTTGAACCTTCAGAGGACATGCAAAGGCGGG    |
|                    | TAGATCAGGGAGGGCTGAGATCATACACAGAGCCAAAGCAGGTCCAGCGTGGCATCACCCCGACGA*C*T*C |
| MAP2 F1            | TGAACAGGGATGGGAAAGAGCT                                                   |
| MAP2 R1            | TGTCCTTGTTGGATGGGAA                                                     |

All sequences are written in the 5' to 3' direction. Underlined sequences mark gRNA sites. Sequences in **bold** are T7 promoter. Glu knockin codon sequences are marked in **red text** in repair oligo. Phosphorothioate linkages are marked with \* in repair oligo.
| Offtarget Seq                  | Mismatch Count | Offtarget Score | Chrom   | Locus Description                      |
|-------------------------------|----------------|-----------------|---------|----------------------------------------|
| ATGCCACACAGGGCCTGCTTGGG       | 3              | 0.559006211     | chr17   | intron:Kdm4b                            |
| ATGCCACACTGACCAGCTATGG        | 4              | 0.511363636     | chr18   | intergenic:Zeb1-Arhgap12               |
| GTGAGACCTGGACCTGCTTGGG        | 4              | 0.505263158     | chr14   | intergenic:Lmo7-Gm22347                |
| AGGCCTTGGACCTGCTTGGG          | 3              | 0.4875          | chr15   | intergenic:Rims2-Dcstmp                |
| CTGCCACTTTGGACGCTTGGG         | 4              | 0.426136364     | chr19   | intergenic:Slc22a30-Gm6425             |
| CTGCCAAGCTAGCTTGCTAAGG        | 4              | 0.361607143     | chr3    | intron:Zfhx4                           |
| ATGCCACTGAGGACCTGCTTGGG       | 3              | 0.331632653     | chr16   | intergenic:Mrps6-Kcne2                 |
| CTGCCCTGCTGGACCTGCTTGGG       | 3              | 0.316558442     | chr15   | intron:Cacna1i                         |
| TTGCCACGCTGGAACAACTTGGG       | 4              | 0.296969697     | chr1    | intergenic:Wdr64-Exo1                  |
| ATGCCACTCAGCACCTGCTTGGG       | 3              | 0.283613445     | chr7    | intergenic:Glrx3-Gm25798               |