

Figure S1

wt allele (exon3)

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AAT AAT CTC ATT AGT AGT ATA GAC CCA GGT GCC TTT TGG GGA CTG TCA TCG CTA AAA CGA
N N L I S S I D P G A F W G L S S L K R

TTG GAT CTG ACA AAC AAT CGA ATA GGA TGT CTG AAT GCA GAC ATA TTC CGA GGA CTC ACC
L D L T N N R I G C L N A D I F R G L T

AAC CTG GTC AGG CTA AAC CTT TCA GGG AAT TTG TTT TCT TCA TTA TCT CAA GGA ACT TTT
N L V R L N L S G N L F S S L S Q G T F

GAT TAT CTT GGC TCA TTA CGG TCT TTA GAA TTT CAG ACT GAA TAT CTT TTG TGT GAT TGT
D Y L G S L R S L E F Q T E Y L L C D C

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KO allele 1

1 base insertion

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AAT AAT | CTC ATT AGT AGT ATA GCA CCC AGG TGC CTT TTG GGG ACT GTC ATC GCT AAA ACG
N N L I S S I A P R C L L G T V I A K T

ATT GGA TCT GAC AAA CAA TCG AAT AGG ATG TCT GAA TGC AGA CAT ATT CCG AGG ACT CAC
I G S D K Q S N R M S E C R H I P R T H

CAA CCT GGT CAG GCT AAA CCT TTC AGG GAA TTT GTT TTC ATT ATC TCA AGG AAC TTT
Q P G Q A K P F R E F V F F I I S R N F

TGA TTA TCT TGG CTC ATT ACG GTC TTT AGA ATT TCA GAC TGA ATA TCT TTT GTG TGA TTG
* L S W L I T V F R I S D * I S F V * L
stop

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KO allele 2

2 base deletion

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AAT AAT | CTC ATT AGT AGT ATA GAC AGG TGC CTT TTG GGG ACT GTC ATC GCT AAA ACG ATT
N N L I S S I D R C L L G T V I A K T I

GGA TCT GAC AAA CAA TCG AAT AGG ATG TCT GAA TGC AGA CAT ATT CCG AGG ACT CAC CAA
G S D K Q S N R M S E C R H I P R T H Q

CCT GGT CAG GCT AAA CCT TTC AGG GAA TTT GTT TTC ATT ATC TCA AGG AAC TTT TGA
P G Q A K P F R E F V F F I I S R N F *
stop

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wt allele (exon15)

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CTG CAC | CCC GTG GTT TAT ACG ACC GCC GTC ATC CTC CTC TTA AGC CTC TTG GCG GTC ATC
L H P V V Y T T A V I L L L S L L A V I

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KO allele 1

1 base deletion

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CTG CAC | CCC GTG TTT ATA CGA CCG CCG TCA TCC TCC TCT TAA GCC TCT TGG CGG TCA TCG
L H P V F I R P P S S S S * A S W R S S
stop

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KO allele 2

1 base deletion

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CTG CAC | CCC GTG GTT ATA CGA CCG CCG TCA TCC TCC TCT TAA GCC TCT TGG CGG TCA TCG
L H P V V I R P P S S S S * A S W R S S
stop

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Supplemental Figure S1. Genomic sequence of GPR125-knockout (KO) cells revealed frameshift mutations resulting in premature stop codons (stop). The target and PAM sequences are highlighted in yellow and green, respectively (see also Fig. 7). The inserted or deleted nucleotides in KO alleles are indicated in magenta.