Data S1. Sanger sequences of KKU-M213B cells with detected CRISPR-mediated mutation in *RARG* in exon 1 (NM_000966.6). Bold sequence is primer position; underlined sequence is target sequence of RARG CRISPR Guide RNA.

- Sequence for RARG CRISPR 385 bp

CCCCTTACCCGCATGCAGCCCAGCGCCCTATGCTAGCCCTCCCCCTCCCCCCCTGC
TGGAGCGGGGCGCCGCCGGGGGAGGAGGGGGAATCGGCTGCGGGTCCTTGGTGTTT
CCAGCACCCAGTTTCCCTTCAAGCCGGGTCGCGATGTACGACTGTATGGAAACGTTT
GCCCCGGGTCCGCGACGGCTGTACGGGGCGGCCGGGCCCGGGGCCGGCTTGCTGCG
CAGAGCCACCGGCGGCTCCTGTTTCGCCGGACTTGAATCTTTTGCCTGGCCGCAACC
CGCCAGCCTGCAATGTAGGTACCGGAGTCCGGGGCTGGGGTGTAGGGTGCAGGAGA
GGGTGGGATTTACTCTTTCCGTGTGTA**AAGAGTGGAACTGAGGTGCA**

Reference sequence for RARG NM_000966.6

ATGCTAGCCCTCCCCCTCCCCCCCTGCTGGAGCGGGGCGCCGCCGGGGGAGGAGGG
GGAATCGGCTGCGGGTCCTTGGTGTTTCCAGCACCCAGTTTCCCTTCAAGCCGGGTC
GCGATGTACGACTGTATGGAAACGTTTGCCCCGGGTCCGCGACGGCTGTACGGGGC
GGCCGGGCCCGGGGCCGGCTTGCTGCGCAGAGCCACCGGCGGCTCCTGTTTCGCCG
GACTTGAATCTTTTGCCTGGCCGCAACCCGCCAGCCTGCAATGGCTTCTTTCGCCGA
AGCATCCAGAAGAACATGGTGTACACGTGTCACCGCGACAAAAACTGTATCATCAA
CAAGGTGACCAGGAATCGCTGCCAGTACTGCCGGCTACAGAAGTGCTTCGAAGTGG
GCATGTCCAAGGAAGCTGTGCGAAATGACCGGAACAAGAAGAAGAAAGAGGTGAA
GGAAGAAGGGTCACCTGACAGCTATGAGCTGAGCCCTCAGTTAGAAGAGCTCATCA
CCAAGGTCAGCAAAGCCCATCAGGAGACTTTCCCCTCGCTCTGCCAGCTGGGCAAGT
ATACCACGAACTCCAGTGCAGACCACCGCGTGCAGCTGGATCTGGGGCTGTGGGAC
AAGTTCAGTGAGCTGGCTACCAAGTGCATCATCAAGATCGTGGAGTTTGCCAAGCG
GTTGCCTGGCTTTACAGGGCTCAGCATTGCTGACCAGATCACTCTGCTCAAAGCTGC
CTGCCTAGATATCCTGATGCTGCGTATCTGCACAAGGTACACCCCAGAGCAGGACAC
CATGACCTTCTCCGACGGGCTGACCCTGAACCGGACCCAGATGCACAATGCCGGCTT
CGGGCCCCTCACAGACCTTGTCTTTGCCTTTGCTGGGCAGCTCCTGCCCCTGGAGAT
GGATGACACCGAGACAGGGCTGCTCAGCGCCATCTGCCTCATCTGCGGAGACCGCA

TGGACCTGGAGGAGCCCGAAAAAGTGGACAAGCTGCAGGAGCCACTGCTGGAAGC
CCTGAGGCTGTACGCCCGGCGCCGGCGGCCCAGCCAGCCCTACATGTTCCCAAGGA
TGCTAATGAAAATCACCGACCTCCGGGGCATCAGCACTAAGGGAGCTGAAAGGGCC
ATTACTCTGAAGATGGAGATTCCAGGCCCGATGCCTCCCTTAATCCGAGAGATGCTG
GAGAACCCTGAAATGTTTGAGGATGACTCCTCGCAGCCTGGTCCCCACCCCAATGCC
TCTAGCGAGGATGAGGTTCCTGGGGGCCAGGGCAAAGGGGGCCTGAAGTCCCCAGC
CTGA

- The in-frame sequence for RARG is 432 amino acid (Predicted Protein using https://web.expasy.org/translate/)

MLALPLPPCWSGAPPGEEGESAAGPWCFQHPVSLQAGSRCTTVWKRLPRVRDGCTGRP
GPGPACCAEPPAAPVSPDLNLLPGRNPPACNGFFRRSIQKNMVYTCHRDKNCIINKVTRN
RCQYCRLQKCFEVGMSKEAVRNDRNKKKKEVKEEGSPDSYELSPQLEELITKVSKAHQ
ETFPSLCQLGKYTTNSSADHRVQLDLGLWDKFSELATKCIIKIVEFAKRLPGFTGLSIADQ
ITLLKAACLDILMLRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFAGQLL
PLEMDDTETGLLSAICLICGDRMDLEEPEKVDKLQEPLLEALRLYARRRRPSQPYMFPR
MLMKITDLRGISTKGAERAITLKMEIPGPMPPLIREMLENPEMFEDDSSQPGPHPNASSED
EVPGGQGKGGLKSPA-

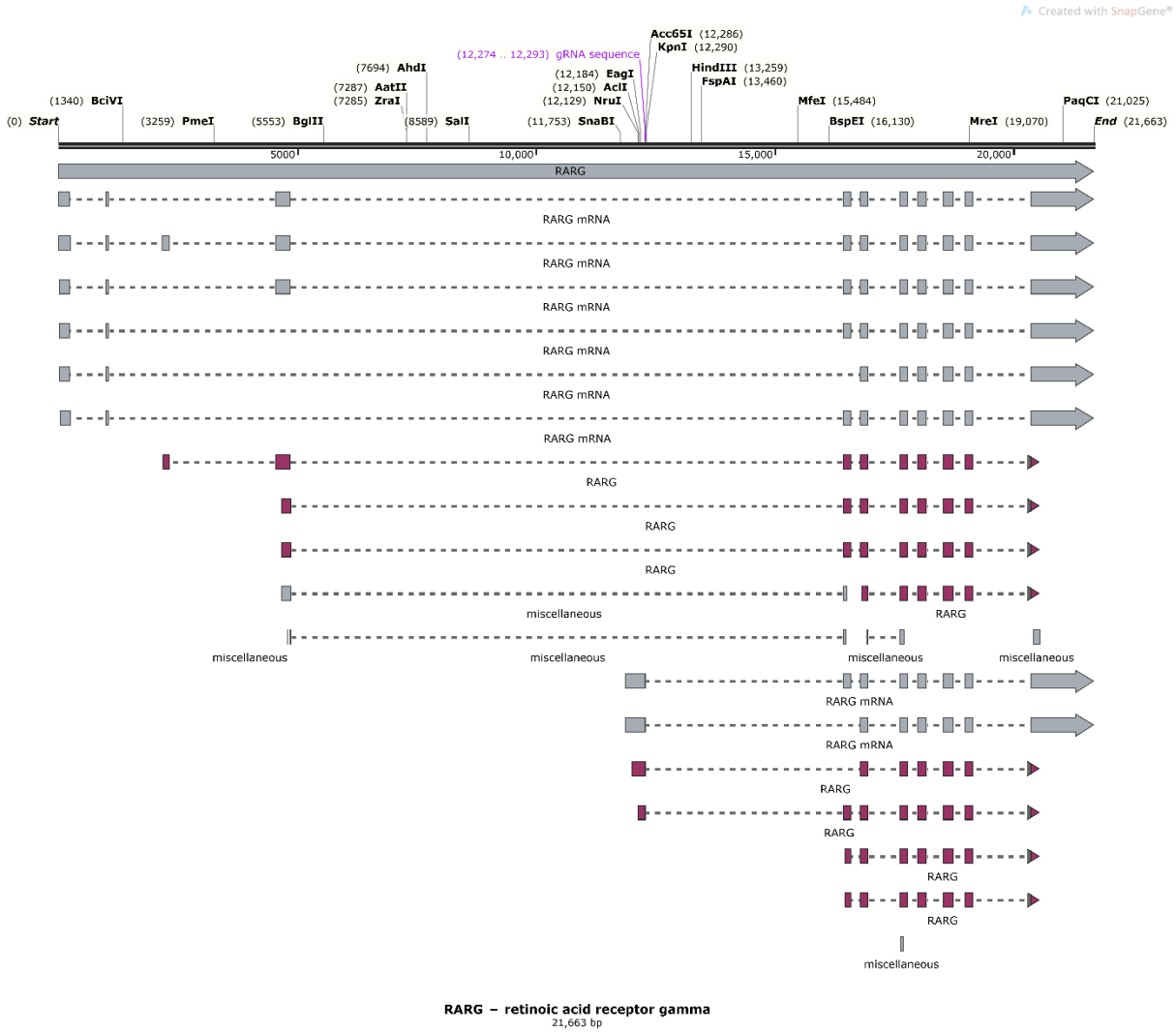
- Predicted sequence for RARG CRISPR, which induced indel mutation

ATGCTAGCCCTCCCCCTCCCCCCCTGCTGGAGCGGGGCGCCGCCGGGGGAGGAGGG
GGAATCGGCTGCGGGTCCTTGGTGTTTCCAGCACCCAGTTTCCCTTCAAGCCGGGTC
GCGATGTACGACTGTATGGAAACGTTTGCCCCGGGTCCG

Predicted translate sequence for RARG CRISPR is a truncated protein with 50 amino acid (Predicted Protein using https://web.expasy.org/translate/)

MLALPLPPCWSGAPPGEEGESAAGPWCFQHPVSLQAGSRCTTVWKRLPRV

RARG gene map with location of gDNA sequence (RARG CRISPR guide RNA 2; Cat. No. SC1805, GenScript®) (More details regarding the sequence can be referred to the following link: https://www.ncbi.nlm.nih.gov/nuccore/NC_000012.12?report=genbank&from=53210569&to=53232231&strand=true)



RARG – retinoic acid receptor gamma
21,663 bp