Name of Mouse model or mutation:
Gldc-S956Y-EM1-B6N

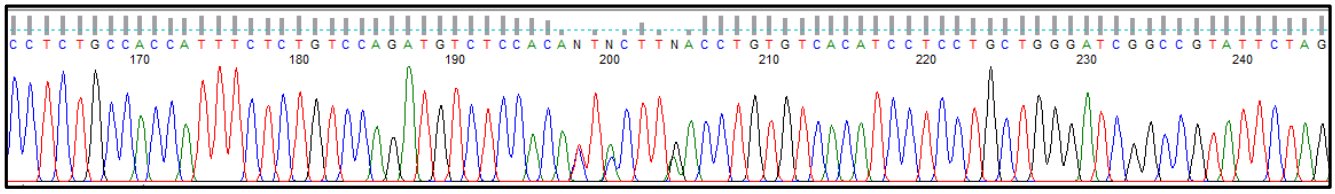
Description:
Point mutation model made using CRISPR/Cas9.

Type of mutation:
SNP: S956Y

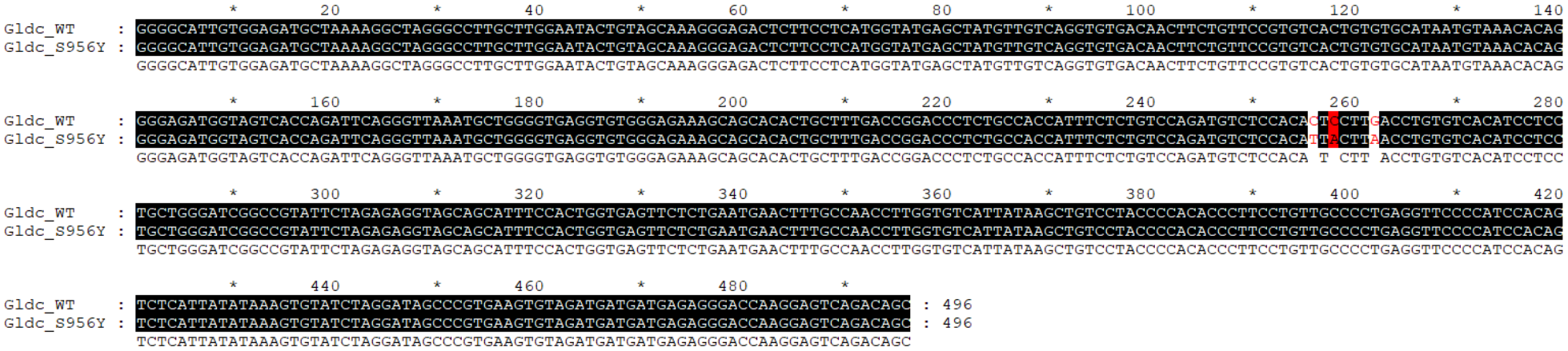
Sequence details
Gldc WT
GGGGCATTGTGGAGATGCTAAAAGGCTAGGGCCTTGCTTGGAATACTGTAGCAAAGGGAGACTCTT
CCTCATGGTATGAGCTATGTTGTCAGGTGTGACAACTTCTGTTCCGTGTCACTGTGTGCATAATGTAA
ACACAGGGGAGATGGTAGTCACCAGATTCAGGGTTAAATGCTGGGGTGAGGTGTGGGAGAAAGCA
GCACACTGCTTTGACCGGACCCTCTGCCACCATTTCTCTGTCCAGATGTCTCCACACTCCTTGACCTGT
GTCACATCCTCCTGCTGGGATCGGCCGTATTCTAGAGAGGTAGCAGCATTTCCACTGGTGAGTTCTC
TGAATGAACTTTGCCAACCTTGGTGTCATTATAAGCTGTCCTACCCCACACCCTTCCTGTTGCCCCTGA
GGTTCCCCATCCACAGTCTCATTATATAAAGTGTATCTAGGATAGCCCGTGAAGTGTAGATGATGAT
GAGAGGGACCAAGGAGTCAGACAGC

Gldc S956Y Mutant
GGGGCATTGTGGAGATGCTAAAAGGCTAGGGCCTTGCTTGGAATACTGTAGCAAAGGGAGACTCTT
CCTCATGGTATGAGCTATGTTGTCAGGTGTGACAACTTCTGTTCCGTGTCACTGTGTGCATAATGTAA
ACACAGGGGAGATGGTAGTCACCAGATTCAGGGTTAAATGCTGGGGTGAGGTGTGGGAGAAAGCA
GCACACTGCTTTGACCGGACCCTCTGCCACCATTTCTCTGTCCAGATGTCTCCACATTACTTAACCTGT
GTCACATCCTCCTGCTGGGATCGGCCGTATTCTAGAGAGGTAGCAGCATTTCCACTGGTGAGTTCTC
TGAATGAACTTTGCCAACCTTGGTGTCATTATAAGCTGTCCTACCCCACACCCTTCCTGTTGCCCCTGA
GGTTCCCCATCCACAGTCTCATTATATAAAGTGTATCTAGGATAGCCCGTGAAGTGTAGATGATGAT
GAGAGGGACCAAGGAGTCAGACAGC

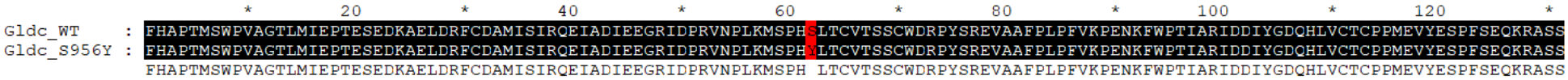
Gldc-S956Y-EM1-B6N Heterozygous F1 animal sequence trace:



Nucleotide Alignment:



Predicted Protein Alignment:



QC strategy employed at Harwell to check the edited allele:

Genomic DNA was extracted from ear clip biopsies and amplified in a PCR reaction using the following conditions/primer sequences:

Geno_ Gldc_F1 (5'-3')	GGGGCATTGTGGAGATGCTA
Geno_Gldc _R1 (5'-3')	GCTGTCTGACTCCTTGGTCC
Taq Polymerase used	Roche Expand Long Range DNTPack
Annealing Temperature (°C)	63
Elongation time (min)	1
WT product size (bp)	496
Mutant product size (bp)	496
Notes	Forward sequencing carried our using primer Geno_Gldc_F2 (GCTAGGGCCTTGCTTGGAAT)

All amplicons were sent for Sanger sequencing in both directions to check for integration of the donor oligo sequence at the target site. F1 sequences should be heterozygous unless on Y chromosome.

Copy counting of the donor sequence was carried out by ddPCR at the F1 stage to confirm donor oligos were inserted once on target into the genome. The following Taqman assay was used to copy count the donor sequence compared against a VIC-labelled reference assay for Dot1l:

Assay name	Gldc-S956Y-DONOR-MUT1
Forward Primer (5'-3')	CTCTGTCCAGATGTCTCCACATTA
Reverse Primer (5'-3')	GGAAATGCTGCTACCTCTCTAGAATA
Probe (5'-3')	ACCTGTGTCACATCCTCCTGCTGGG
Label	FAM-BHQ1

This ddPCR assay is a mutant assay specific to the Gldc-S956Y mutation. WT controls are expected to call at 0 copies and correct mutants are expected to call at 1 copy for F1 (HET) animals.

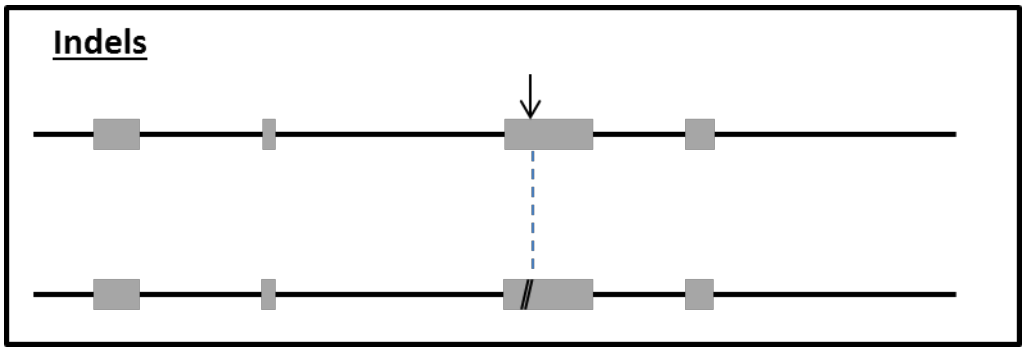
Assay name	Gldc-S956Y-DONOR-UNIV1
Forward Primer (5'-3')	TGGGAGAAAGCAGCACACTG
Reverse Primer (5'-3')	TCCCAGCAGGAGGATGTGA
Probe (5'-3')	TTTGACCGGACCCTCTGCCAC
Label	FAM-BHQ1

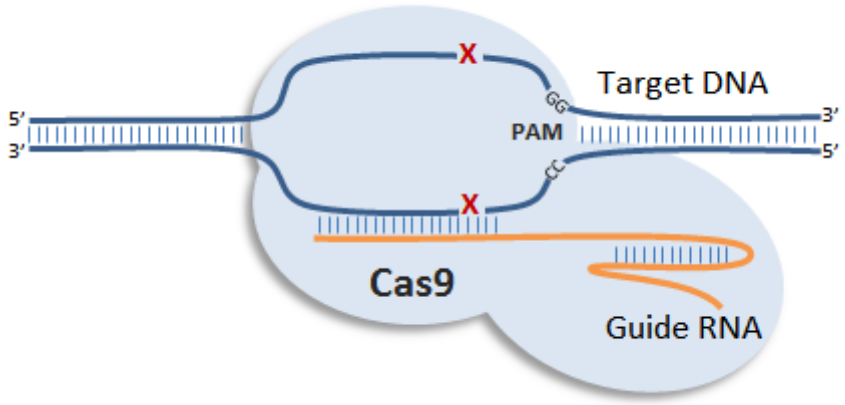
This ddPCR assay is a universal assay to the Gldc gene i.e. will detect both mutant and WT alleles. Correct mutants and WT controls are expected to call at 2 copies.

One of the silent mutations added to this design (c.3029G>A) gives rise to a new MseI site in the PCR amplicon using primers Geno_ Gldc_F1 and Geno_ Gldc_R1 detailed above. Gldc WT amplicons generated using primers Geno_ Gldc_F1 and Geno_ Gldc_R1 give a product of 496 bp and should be cut once by MseI to give two products 168 bp and 328 bp in size. Gldc S956Y amplicons generated using primers Geno_ Gldc_F1 and Geno_ Gldc_R1 give a product of 496 bp and should be cut twice by MseI to give three products; 236 bp, 168 bp and 92 bp in size. Please note this genotyping has not been tested at MRC Harwell as we do not use restriction enzymes for genotyping.

Gldc-S956Y Genotyping Strategy

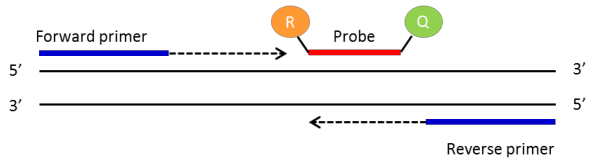
Animals have been engineered using the CRISPR/Cas9 technology. Most of the knockout alleles generated through this method will be obtained by deletion of a critical exon or by introduction of an indel (insertion/deletion) within the coding sequence of a critical exon (see picture below).



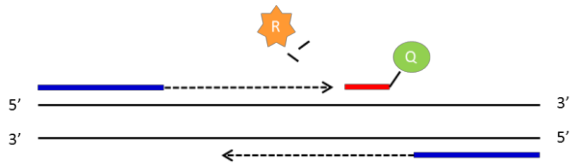


qPCR genotyping strategy

Standard PCR is the amplification of DNA between a pair of primers. Quantitative PCR employs the same principal as standard PCR, although it actually monitors the progress of the DNA synthesis as it occurs. The progress of the reaction is measured by using a Taqman probe. This is a short DNA oligo that is complimentary to part of the DNA sequence between the forward and reverse primers. At the 5' end of the probe there is a fluorescent reporter (R) and at the 3' end a quencher (Q). Whilst they are in close contact with each other there is no fluorescent signal.



As the forward primer is extended the reporter is cleaved from the probe resulting in a fluorescent signal being detected. Once the primer extends enough to release the quencher this signal is blocked. By using probes with different fluorescent signals multiple PCR assays can be multiplexed and run together.



Allele specific primer and probe amplification assay (ASPPAA) PCR

This is a new real-time PCR method (Billard *etal.,* 2012) in which an allele specific primer and an allele specific probe designed specific to the SNPs. The primer is designed such a way that its 3' end ends with a specific SNP. The probe is also designed specific to the SNPs at its 3' end giving a primer probe overlap. A maximum of 3nt overlap between a primer and probe is allowed.

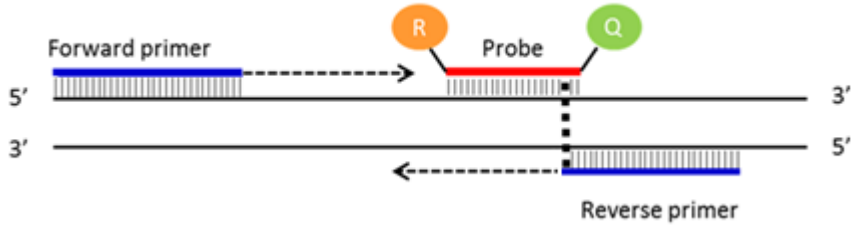
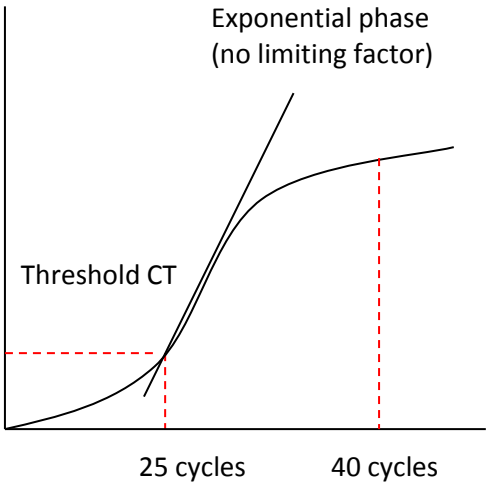


Figure1: Figure showing principle of ASPPAA PCR. The dotted line indicates the position of the SNP.

PCR reaction plot



The number of cycles the PCR takes to reach a set threshold is known as the CT value. This is inversely correlated to the amount of template DNA in the sample.

e.g. CT 25 = 2 x template DNA
CT 26 = 1 x template DNA
CT above 30 = no template represented in the sample

CT value can be used to determine how many copies of a particular allele samples have.

All our qPCR are run in duplicate. A FAM labelled genotyping assay is run in multiplex with a VIC labelled internal control Dot1l.

References:

Billard A., Laval V., Fillinger S., Leroux P., Lachaise H., Beffa R., et al. (2012).
The allele-specific probe and primer amplification assay, a new real-time PCR method for fine quantification of single-nucleotide polymorphisms in pooled DNA.
Appl. Environ. Microbiol. 78 1063–1068. 10.1128/AEM.06957-11

Gldc-S956Y Genotyping Strategy

Samples are genotyped with both WT and Mutant assays. These are FAM labelled assays that are designed to detect the critical exon that has been modified. If the animal contains the modified allele the copy number of the WT assay should drop by 1 and the mutant assay should raise by 1. For autosomal genes that have been targeted this means the following

WT= 2 copies of the WT assay and 0 copies of the Mutant assay
HET = 1 copy of the WT assay and 1 copy of the Mutant assay
HOM = 0 copies of the WT assay and 2 copies of the Mutant assay

Gldc-S956Y CRISPR/Cas9 mutant in which SNPs are as highlighted

WT TGTCTCCACACTCCTTGACCTGTGTCA
Mutant TGTCTCCACATTACTTAACCTGTGTCA

Gldc-S956Y-WT1 assay (FAM labelled probe)

AGTCACCAGATTCAGGGTTAAATGCTGGGGTGAGGTGTGGGAGAAAGCAGCACACTGCTTTGACCGGACCCTCTG
CCACCATTTCTCTGTCCAGATGTCTCCACACTCCTTGACCTGTGTCACATCCTCCTGCTGGGATCGGCCGTATTC
TAGAGAGGTAGCAGCATTTCCACTGGTGAGTTCTCTGAATGAACTTTGCCAACCTTGGTGTCATTATAAGCTGTC

Gldc-S956Y-WT1 primers and probe

Primer 1 = ACCCTCTGCCACCATTTCTC
Primer 2 = CAGGAGGATGTGACACAGGTC
Probe = ATGTCTCCACACTCCTTGAC

Allele specific primer and probes

GLDC-S956Y-DONOR-MUT1 assay (FAM labelled probe)

AGTCACCAGATTCAGGGTTAAATGCTGGGGTGAGGTGTGGGAGAAAGCAGCACACTGCTTTGACCGGACCCTCTG
CCACCATTTCTCTGTCCAGATGTCTCCACATTACTTAACCTGTGTCACATCCTCCTGCTGGGATCGGCCGTATTC
TAGAGAGGTAGCAGCATTTCCACTGGTGAGTTCTCTGAATGAACTTTGCCAACCTTGGTGTCATTATAAGCTGTC

GLDC-S956Y-DONOR-MUT1 primers and probe

Primer 1 = CTCTGTCCAGATGTCTCCACATTA
Primer 2 = GGAAATGCTGCTACCTCTCTAGAATA
Probe = ACCTGTGTCACATCCTCCTGCTGGG

Dot1l internal control (VIC labelled)

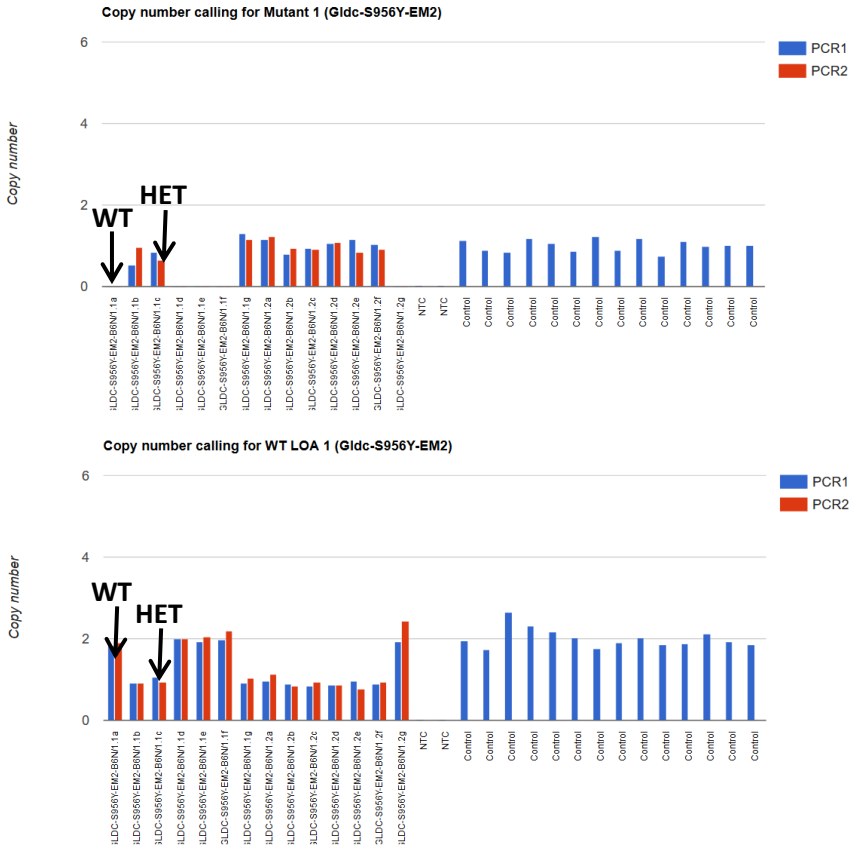
CCCCTCTAGTCGTTTTCTGTTAGTAGTTGGCATCCTTATGCTTCATCTTACAGTCGACTTGAGAGCTGGCCCTGA
ATGGTCGTGCTGGGGCAAGGCTTTATTTCAGGCGTAGCACACATGGTGGCCAATGGGACTCTGTAGGATCTGCCC

Primer 1 = GCCCCAGCACGACCATT
Primer 2 = TAGTTGGCATCCTTATGCTTCATC
Probe = CCAGCTCTCAAGTCG

qPCR master mix

ABI GTX Taqman master mix	5µl
Primers Dot1L_2F (20µM)	0.225µl
Primers Dot1L_R (20µM)	0.225µl
Probe DotL_2M (5µM)	0.2µl
FAM Assay (probe 5µM & primers 15µM each)	0.3µl
ddH20	1.55µl
DNA (1/10 dilution of ABI Sample-to-SNP prep)	2.5µl

Gldc-S956Y copy called result, image showing both replicates and controls



Version No. 1

Date: 30.07.2018

Created/Updated by: Ramakrishna Kurapati

Approved by: Debbie Williams