



Allele Description

This is a CRISPR/Cas9 induced mutation creating a series of point mutations; E167A, Q168A and N169A in *Pttg1ip*. The stock was generated at MRC Harwell via microinjection of CRISPR/Cas9 reagents into 1-cell stage embryos.

qPCR Copy Counting Genotyping Strategy

The genotyping strategy presented here has been optimized for reagents and conditions used by the Genotyping Core at MRC Harwell. To genotype animals, we recommend researchers validate the assay independently. PCR cycling temperature and times may require additional optimization based on the specific genotyping reagents used.

Samples are genotyped using qPCR copy counting with both a wild type and a mutant assay against a known reference assay (*Dot1l* on chromosome 10; 2 copies present). Samples for this line are genotyped using the following primers and probe:

- Wild type (WT) assay with probe and reverse primer binding to the WT bases mutated in the mutant allele.
- Mutant assay with probe and reverse primer binding to the G601R, F606Y and R609H point mutations.

For autosomal genes that have been targeted, the following results would be expected:

Genotype of the Modified allele	WT Assay	Mutant Assay
Wildtype	2	0
Heterozygous	1	1
Homozygous mutant	0	2



Pttg1ip-EQN167AAA

Pttg1ip-EQN167AAA-WT1 assay (FAM labelled)

GCTATACATTGCTTTTGTGAGCTTATTTCCAGTTGAGTGAGTGAATTTGTAAACCGAGTTCTTTTTTCC
 CTTTCTCCCTCAGGTCTGTTTAAA**GaacAaaaCCCGTAtGAgAAGTTCTAAGGTGGCTGGCACACACTT**
GTGGTGGATCGTGCAGTTCCAG**AGTTTCTGGGAATGCACTC**CCCCAGCAGAGCCTGCAGAGACCTC

Lower case letters denote bases changed in the mutant allele.
 Probe sequence is in bold and shaded grey.
 Primer sequences are in bold and underlined.

Oligo Pttg1ip-EQN167AAA	5' label	Sequence 5' → 3'	3' label	Oligo Type
Pttg1ip-EQN167AAA-WT_F	n/a	<u>GAACAAAACCCGTATGAGAAGTTC</u>	n/a	Wild type Forward
Pttg1ip-EQN167AAA-WT_PROBE	FAM	ACACTTGTGGTGGATCGTGCAGTT	ZEN/IBFQ	Wild type Probe
Pttg1ip-EQN167AAA-WT_R	n/a	<u>GAGTGCATTCCCAGGAAACT</u>	n/a	Wild type Reverse

Pttg1ip-EQN167AAA-MUT1 assay (FAM labelled)

GCTATACATTGCTTTTGTGAGCTTATTTCCAGTTGAGTGAGTGAATTTGTAAACCGAGTTCTTTTTTCC
 CTTTCTCCCTCAGGTCTGTTTAAA**GccgcAgctCCGTAcGAaAA**GTTCTAAGGTGGCTGGCAC**ACACTT**
GTGGTGGATCGTGCAGTTCCAG**AGTTTCTGGGAATGCACTC**CCCCAGCAGAGCCTGCAGAGACCTC

Lower case letters denote bases changed in the mutant allele.
 Probe sequence is in bold and shaded grey.
 Primer sequences are in bold and underlined.

Oligo Pttg1ip-EQN167AAA	5' label	Sequence 5' → 3'	3' label	Oligo Type
Pttg1ip-EQN167AAA-MUT_F	n/a	<u>GCCGCAGCTCCGTACGAAAA</u>	n/a	Mutant Forward
Pttg1ip-EQN167AAA-MUT_PROBE	FAM	ACACTTGTGGTGGATCGTGCAGTT	ZEN/IBFQ	Mutant Probe
Pttg1ip-EQN167AAA-MUT_R	n/a	<u>AGTGCATTCCCAGGAAACTCTG</u>	n/a	Mutant Reverse



Dot1l internal control (VIC labelled)

CTGATGGGTGTGGGCAGATCCTACAGAGTCCCATTGGCCACCATGTGTGCTACGCCTGAAATAAAGCCTT**GCC**
CCAGCACGACCATTCAGGG**CCAGCTCTCAAGTCG**ACTGTAAGATGAAGCATAAGGATGCCAACTACTAACA
GAAAACGACTAGAGGGGAAAAGAACAAGGAAACAGAAGACGCAGCACTCCGGCTTCCCTGGGTTGGCCAGT
CACCTATGA

Oligo Pttg1ip-EQN167AAA	5' label	Sequence 5' → 3'	3' label	Oligo Type
Dot1l_Forward	n/a	<u>GCCCCAGCACGACCATT</u>	n/a	WT Forward
Dot1l_Probe	VIC	CCAGCTCTCAAGTCG	BHQ	WT Probe
Dot1l_Reverse	n/a	<u>TAGTTGGCATCCTTATGCTTCATC</u>	n/a	WT Reverse

Probe sequence is in bold and shaded grey
Primer sequences are in bold and underlined

DNA extraction method

DNA is extracted from ear clips using Applied Biosystems Taqman Sample-to-SNP Kit and qPCR run using 1:10 dilution from the crude preparation.

qPCR master mix 1X

Applied Biosystems GTX Taqman master mix	5 µl
Dot1l_Forward (20 µM)	0.225 µl
Dot1l_Reverse (20 µM)	0.225 µl
Dot1l_Probe (5 µM)	0.2 µl
FAM Assay (probe 5 µM & primers 15 µM each)	0.3 µl
ddH2O	1.55 µl
DNA (1:10 dilution of ABI Sample-to-SNP prep)	2.5 µl

Each sample is ran in technical duplicate. Seven WT and/or mutant controls are also included in duplicate along with non-template controls.

qPCR cycling conditions

qPCR instrument: Applied Biosystems 7500/7900 or ThermoFisher QuantStudio 7

95°C for 20 sec
Then 40 cycles of;
95°C for 3 sec
60°C for 30 sec



Analysis

The results are analysed using CopyCaller software v2.0 from Applied Biosystems or in-house software that is based on CopyCaller v2.0.

Pttg1ip-EQN167AAA-WT1 and Pttg1ip-EQN167AAA -MUT1 assays copy called results, image showing copy number chart for WT and Mutant assays (Task 291118 results)



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Created/Updated by: Daniel Ford

Approved by: Rumana Zaman