

# AP2S1-R10W

## Allele Description

This is a CRISPR/Cas9 induced mutation creating a series of point mutations; R10W in exon ENSMUSE00000336284 of *AP2S1*. 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

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## AP2S1-R10W-EM3-WT1 assay (FAM labelled)

GGGAGAGCCTGGGCCCTGACATATCTCCCATAGAATGTCTCGTGGTGCCACCCCTGAGCTGTGTCCC  
 CCCGCATCTCTCATTCCCTCCCCTGCTTGCTCTAGAT**CCGATTCATCCTTATCCAGAAcc**GGGCAGGCA  
 AGACGCGCCTGGCCAAGTGGTACAT**GCAGTTCGATGACGACGAGAAGCA**GAAAGCTGATCGAGGA  
 GGTGCACGCCGT**TGGTCACCGTCAGGGAT**GCCAAGCACACCAACTTTGTGGAGGTGACTGACACCCT

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 AP2S1-R10W	5' label	Sequence 5' → 3'	3' label	Oligo Type
AP2S1-R10W-WT_F	n/a	<b><u>CCGATTCATCCTTATCCAGAAACC</u></b>	n/a	Wild type Forward
AP2S1-R10W-WT_PROBE	FAM	<b>TGCTTCTCGTCGTCATCGAACTGC</b>	ZEN/IBFQ	Wild type Probe
AP2S1-R10W-WT_R	n/a	<b><u>ATCCCTGACGGTGACCA</u></b>	n/a	Wild type Reverse

## AP2S1-R10W-MUT1 assay (FAM labelled)

GGGAGAGCCTGGGCCCTGACATATCTCCCATAGAATGTCTCGTGGTGCCACCCCTGAGCTGTGTCCC  
 CCCGCATCTCTCATTCCCTCCCCTGCTTGCTCTAGAT**TCCGATTCATCCTTATCCAGAAAtt**GGGCAGGCA  
 AGACGCGCCT**GGCCAAGTGGTACATGCAGTTCGA**TGACGAC**GAGAAGCAGAAGCTGATCGAGGA**  
 GGTGCACGCCGTGGTCACCGTCAGGGATGCCAAGCACACCAACTTTGTGGAGGTGACTGACACCCT

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 AP2S1-R10W	5' label	Sequence 5' → 3'	3' label	Oligo Type
AP2S1-R10W-MUT_F	n/a	<b><u>TCCGATTCATCCTTATCCAGAAATT</u></b>	n/a	Mutant Forward
AP2S1-R10W-MUT_PROBE	FAM	<b>TCGAACTGCATGTACCACTTGCC</b>	BHQ	Mutant Probe
AP2S1-R10W-MUT_R	n/a	<b><u>CTCGATCAGCTTCTGCTTCTC</u></b>	n/a	Mutant Reverse

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## Dot1l internal control (VIC labelled)

CTGATGGGTGTGGGCAGATCCTACAGAGTCCCATTGGCCACCATGTGTGCTACGCCTGAAATAAAGCCTT**GCC**  
**CCAGCACGACCATT**CAGGG**CCAGCTCTCAAGTCG**ACTGTAAGATGAAGCATAAGGATGCCAACTACTAACA  
GAAAACGACTAGAGGGGAAAAGAACAAGGAAACAGAAGACGCAGCACTCCGGCTTCCCTGGGTTGGCCAGT  
CACCTATGA

Oligo AP2S1-R10W	5' label	Sequence 5' → 3'	3' label	Oligo Type
Dot1l_Forward	n/a	<b><u>GCCCCAGCACGACCATT</u></b>	n/a	WT Forward
Dot1l_Probe	VIC	<b>CCAGCTCTCAAGTCG</b>	BHQ	WT Probe
Dot1l_Reverse	n/a	<b><u>TAGTTGGCATCCTTATGCTTCATC</u></b>	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

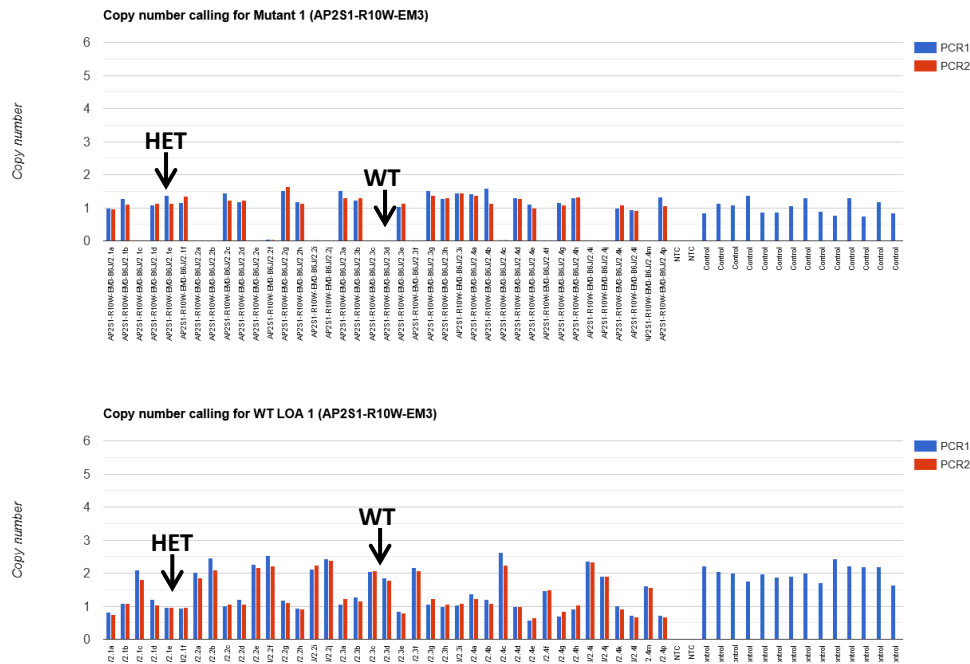
95°C for 20 sec  
Then 40 cycles of;  
95°C for 3 sec  
60°C for 30 sec

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## Analysis

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

AP2S1-R10W-WT1 and AP2S1-R10W -MUT1 assays copy called results, image showing copy number chart for WT and Mutant assays (Task 350031 results)



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