



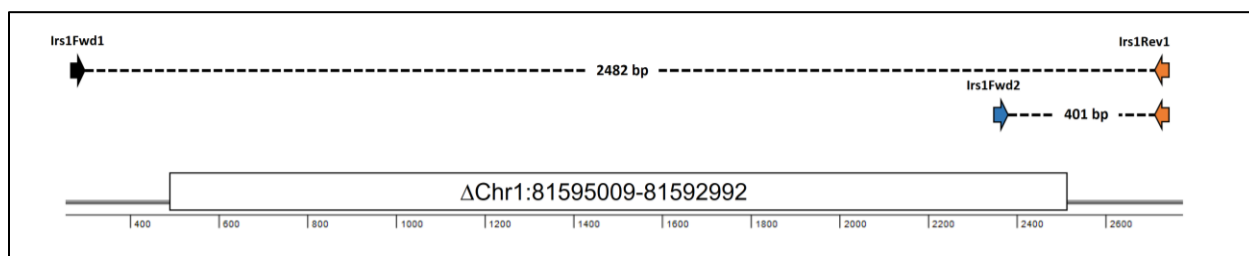
# Vanderbilt Genome Editing Resource

## GENOTYPING PROTOCOL: *Rr*<sup>413em1Mgn/Vu</sup>

**Investigator:** Mark Magnuson

**Genome edit:**  $\Delta$ Chr1:81595009-81592992 (mm10)

**Common allele name:** *Rr*413<sup>em1Mgn/Vu</sup>



### PCR Primers:

Irs1Fwd1: ACCTGCTTTCTGCTCTCCTCTC

Irs1Rev1: AGCTCTGCCCAAATGTTAAGGAG

Irs1CRFwd2: CCACCTCCACTACCACCTATATG

### Predicted PCR product sizes:

Homozygous *Rr*413<sup>em1Mgn/Vu</sup> = 464 bp (= 2482 bp – 2018 bp)

Heterozygous *Rr*413<sup>em1Mgn/Vu</sup> = 464 bp + 401 bp + weak or absent 2482 bp

WT = 401 bp + weak or absent 2482 bp

Component	25 ul reaction	Final concentration	PCR program
5X Phusion Reaction Buffer (NEB #M0530S)	5.0 µL	1X	98°C, 30 seconds
10 mM dNTPs	0.5 µL	200 µM	98°C, 10 seconds
10 µM Irs1Rev1	1.25 µL	0.5 µM	66°C, 10 seconds
10 µM Irs1Fwd1	0.625 µL	0.25 µM	72°C, 30 seconds
10 µM Irs1CRFwd2	0.625 µL	0.25 µM	Go to 2, 38 X
Phusion DNA Polymerase (NEB #M0530S)	0.25 µL	0.02 U/µl	72°C, 2 minutes
Nuclease-free water	16.25 µL		4°C, ∞
Genomic DNA	0.5 µL	Less than 1 µg	

