



Gene: Cd96

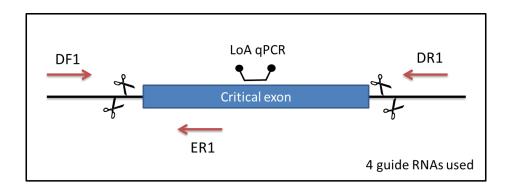
Colony prefix: DAEH

Allele: Cd96em1(IMPC)Wtsi

Allele type: Crispr/Cas9 mediated deletion

#### Allele information:

Further information about the allele can be found on the 'International Mouse Phenotyping Consortium' (IMPC) web site at <a href="http://www.mousephenotype.org/data/genes/MGI:1934368">http://www.mousephenotype.org/data/genes/MGI:1934368</a>



#### **Mouse QC information**

Loss of WT Allele (LOA) qPCR	Pass	Mutation Sequence confirmed	Pass
Mutant Specific SR-PCR	Pass	Off-target analysis complete	na

### **Mutant Allele sequence:**

GCTTATTCTATTAGCTGAATAATTATTCTTTAGCCTTCCACCCTTGTCCCTACCCTCAATGAGAATGATA GGAATTAAGGCAAACAGAATTGCAGGAGTTGCTGGTTTGAGATACCCAATGTACCATTTCCTCTGGAA GAGCAACAGGGACTTTAAAATGGGTTAAGCATGCGTTAAAAATGGGGAGAGACTGAGTATGCT

Deletion size (bp): 512

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### **Guide RNAs used in initial experiment**

Sequence	Chr	Chr Start	Chr End
CCCTACCCTCAATGAGAATGATA	16	46098740	46098762
ATTGCAGGAGTTACCCTGTGTGG	16	46098781	46098803
CGCATGAGGGCAGATTCTTAGGG	16	46099246	46099268
GAATTCACTGGAACTAGAGCTGG	16	46099287	46099309

# Genotyping by end-point PCR

These mice may be genotyped through a combination of separate PCR reactions that detect the gene-specific wild type allele and a mutant allele-specific short range PCR. Interpretation of the consolidated results produces the genotype of the mice. In addition to the expected product, the mutant assay may also amplify the endogenous wild type sequence which will appear as a larger band on an agarose gel. The presence of this extra band will depend on the size of the original deletion.

#### PCRs primer pairs and expected size bands

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Assay Type	Assay	Forward Primer	Reverse Primer	Expected Size Band (bp)
Standard PCR	Wild type	Cd96_DF1	Cd96_ER1	299
Standard PCR	Mutant	Cd96_DF1	Cd96_DR2	313

### **Primer sequences**

Primer Name	Primer Sequence (5' > 3')
Cd96_DF1	TAAAGAGATTTCTGGTACCCTTGGG
Cd96_ER1	CTATGATCTCTTTGCCACCTTTGTG
Cd96_DR2	GCACAGCAATACTTTCTGTAGTAGC

### **Reaction setup**

Reagent	μl
DNA (~50-100 ng)	1
10x Buffer	1.5
MgCl2 (50 mM)	0.45
Platinum Taq (Invitrogen)	0.15
dNTPs (100 mM)	0.15
Primer 1 (10 µM)	0.3
Primer 2 (10 µM)	0.3
ddH20	11.15
Total	15

# **Amplification conditions**

Step	Conditions	Time
1	94°C	5 min
2	94°C	30 sec
3	58°C	30 sec
4	72°C	1:30 sec
5	Go to '2' + 34 cycles	-
6	72°C	5 min
7	12°C	forever

# Links to information and frequently asked questions

MGP mouse phenotype data: <a href="http://www.mousephenotype.org">http://www.mousephenotype.org</a>

## **Useful publications**

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White, J.K., Gerdin, A.-K., Karp, N.A., Ryder, E., Buljan, M., Bussell, J.N., Salisbury, J., Clare, S., Ingham, N.J., Podrini, C., et al. (2013). Genome-wide Generation and Systematic Phenotyping of Knockout Mice Reveals New Roles for Many Genes. Cell 154, 452–464.

Mali P, Yang L, Esvelt KM, et al (2013) RNA-guided human genome engineering via Cas9. Science 339:823–6. doi: 10.1126/science.1232033

Jinek M, Chylinski K, Fonfara I, et al (2012) A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity. Science 337:816–21. doi: 10.1126/science.1225829

Cong L, Ran FA, Cox D, et al (2013) Multiplex genome engineering using CRISPR/Cas systems. Science 339:819–23. doi: 10.1126/science.1231143

Singh P, Schimenti JC, Bolcun-Filas E (2014) A Mouse Geneticist's Practical Guide to CRISPR Applications. Genetics genetics.114.169771—. doi: 10.1534/genetics.114.169771

Brandl C, Ortiz O, Röttig B, et al (2015) Creation of targeted genomic deletions using TALEN or CRISPR/Cas nuclease pairs in one-cell mouse embryos. FEBS Open Bio 5:26–35. doi: 10.1016/j.fob.2014.11.009

Zhou J, Wang J, Shen B, et al (2014) Dual sgRNAs facilitate CRISPR/Cas9 mediated mouse genome targeting. FEBS J. doi: 10.1111/febs.12735

Kraft K, Geuer S, Will AJ, et al (2015) Deletions, Inversions, Duplications: Engineering of Structural Variants using CRISPR/Cas in Mice. Cell Rep. doi: 10.1016/j.celrep.2015.01.016

Shen B, Zhang J, Wu H, et al (2013) Generation of gene-modified mice via Cas9/RNA-mediated gene targeting. Cell Res 23:720–3. doi: 10.1038/cr.2013.46

Wang H, Yang H, Shivalila CS, et al (2013) One-step generation of mice carrying mutations in multiple genes by CRISPR/Cas-mediated genome engineering. Cell 153:910–8. doi: 10.1016/j.cell.2013.04.025

Yang H, Wang H, Shivalila CS, et al (2013) One-Step Generation of Mice Carrying Reporter and Conditional Alleles by CRISPR/Cas-Mediated Genome Engineering. Cell 154:1370–1379. doi: 10.1016/j.cell.2013.08.022

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