

# GENOTYPING PROTOCOL

## MUTANT MOUSE RESOURCE & RESEARCH CENTER: UC DAVIS

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530-754-MMRRC

**Protocol Name:** CR11530 AI429214 EXDEL

**Protocol:** GoTaq® G2 Colorless Master Mix(Promega)

Reagent/Constituent	Volume (μL)
Water	4.5
GoTaq® G2 Colorless Master Mix,2X	7.5
Primer 1. (stock concentration is 20μM) comF	0.5
Primer 2. (stock concentration is 20μM) wtR	0.5
Primer 3. (stock concentration is 20μM) mutR	0.5
DNA (example) extracted w/ "Qiagen DNeasy columns or other similar silica based kits"	1.5
<b>TOTAL VOLUME OF REACTION:</b>	<b>15.00 μL</b>

**Comments on protocol:**

- Protocol may work with other DNA extraction methods.

**Strategy:**

Steps	Temp (°C )	Time (m:ss)	# of Cycles
1. Initiation/Melting HOT START? <input type="checkbox"/>	94	2:00	1x
2. Denaturation	94	0:10	
3. Annealing steps 2-3-4 cycle in sequence	65 (↓1°C/cycle)	0:30	10x
4. Elongation	68	2:00	
5. Denaturation	94	0:15	
6. Annealing steps 5-6-7 cycle in sequence	55	0:30	25x
7. Elongation	68	2:00 (↑20sec/cycle)	
8. Finish	4	∞	n/a

**Primers:**

**Electrophoresis Protocol:**

Name	Nucleotide Sequence (5' - 3')	Agarose: 1.5%	V: 90
1. CR_AI429214_comF	GAATTACACACAGCAGCCTGAGG	Estimated Running Time: 90 min.	
2. CR_AI429214_wtR*	CTGTAAGAGTGAAAGTTCTGACTGC	<b>Primer Combination</b>	<b>Band (bp)</b>
3. CR_AI429214_mutR	GTCTTCCATAATGTGAAAAATCTATTGG	1 & 2, 1 & 3	519, 1420
		1 & 3	695
			wildtype
			mutant

**Allele Description:** Exon 1 ENSMUSE00000637279 and flanking splicing regions were constitutively deleted from the AI429214 Gene ENSMUSG00000074384 using CRISPR Cas9 gene editing technology in mouse zygotes. The subsequent 725bp deletion from Chr 8: 37461061 - 37461785 GRCm39 was screened by PCR analysis. **Note: Not all of the coding region is deleted. 208bp including ATG is still present.** The selected founder animal was backcrossed to C57BL6/N to produce sequence confirmed heterozygous animals for establishing and archiving the line.

\*wtR primer untested (ePCR verified)

