

**GENOTYPING BY PCR PROTOCOL**  
**MUTANT MOUSE REGIONAL RESOURCE CENTER: UC DAVIS**

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530-754-MMRRC

NAME OF PCR: C57BL/6JSfdAnu-Kcnv1<sup>vibe</sup>/ApbMmucd MMRRC # 036420-UCD

**Protocol:**

Reagent/Constituent	Volume ( $\mu$ L)
Water	11.275
10x Buffer	2.5
MgCl <sub>2</sub> (stock concentration is 25mM)	1.7
Betaine (stock concentration is 5M) <i>Optional</i>	6.5
dNTPs (stock concentration is 10mM)	0.5
DMSO <i>Optional</i>	0.325
Primer 1 (stock concentration is 20 $\mu$ M)	0.5
Primer 2 (stock concentration is 20 $\mu$ M)	0.5
Taq Polymerase 5Units/ $\mu$ L	0.2
DNA (50-200ng/ $\mu$ L) extracted w/ "Qiagen DNeasy columns or other similar silica based kits"	1.0
<b>TOTAL VOLUME OF REACTION:</b>	<b>26.000 <math>\mu</math>L</b>

**Comments on protocol:**

- Protocol may work with other DNA extraction methods.
- Use Touch-Down cycling protocol-first 10 cycles anneal at 65°C decreasing in temperature by 1.0°C; next 30 cycles anneal at 55°C.
- Betaine and DMSO have been standardized due to high GC content. Protocol may be tested without. Also, may adjust MgCl<sub>2</sub> to increase reaction or decrease non-specific amplifications.

**Strategy:**

Steps	HOT START? <input type="checkbox"/>	Temp (°C)	Time (m:ss)	# of Cycles
1. Initiation/Melting		94	5:00	1
2. Denaturation		94	0:15	
3. Annealing	steps 2-3-4 cycle in sequence	65 to 55 ( $\downarrow 1^{\circ}\text{C}/\text{cycle}$ )	0:30	40x
4. Elongation		72	0:40	
5. Amplification		72	5:00	1
6. Finish		15	$\infty$	n/a

**Primers:**

Name	Nucleotide Sequence (5' - 3')
1. 36420-snpF	CTTCCCAGCTGAGTGATGTGTG
2. 36420-snpR	GGCAATAAGGAAATCCTTGTAAAGC
3. 36420-snpFS	CATAAGTGGAAATATGTTGGATGACATC

**Electrophoresis Protocol:**

Agarose: 1.5% V: 90

Estimated Running Time: 90 min.

\* Sequence with 36420-snpFS: agacatT/Cgtgaaa

Primer Combination	Band	Genotype
1 and 2	457 bp	*
	bp	KO or MT/-

~140nt of sequence. **T=WT, C=Mutant**