

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

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 530-754-MMRRC

NAME OF PCR: C57BL/6-Unc13d^{Jinx}/Mmc^d, (Jinx)

MMRRC # 016137-UCD

Protocol:

Reagent/ Constituent	Volume (μ L)
Water	12.675
10x Buffer (contains 15mM MgCl ₂)	2.5
Betaine (stock concentration is 5M) <i>Optional</i>	6.5
dNTPs (stock concentration is 25mM)	0.5
DMSO <i>Optional</i>	0.325
Primer 1 (stock concentration is 20 μ M) jinx PCR F1	0.5
Primer 2 (stock concentration is 20 μ M) jinx PCR R1	0.5
Taq Polymerase	0.5
DNA sample extracted with <input type="checkbox"/> NaOH <input type="checkbox"/> Proteinase K <input checked="" type="checkbox"/> Other: Any	1.0
TOTAL VOLUME OF REACTION:	25μL

Comments on protocol:

- PCR products are verified to contain the correct amplicon size by running ~10 μ l of the reaction on a gel and the remaining 15 μ l purified via column based PCR purification method for sequencing.
- 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 MgCl₂ 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 will cycle in sequence	65 to 55 (↓1°C/cycle)	0:30	10x
4. Elongation		72	0:40	
5. Denaturation		94	0:15	
6. Annealing	} steps 5-6-7 will cycle in sequence	55	0:30	30x
7. Elongation		72	0:40	
8. Amplification		72	5:00	1
9. Finish		15	∞	n/a

Primers:

Name	Nucleotide Sequence (5' - 3')
1: jinx PCR F1	CTA CAT GAA CAC CAA CCT GGT CCA GGA G
2: jinx PCR R1	GGA TCA TGA AGA GGA AGG AGA TGC AGT TAG G
3: jinx_Seq (F)	TAC ATG AAC ACC AAC CTG GTC C-
4: jinx_Seq (R)	AGA GGA AGG AGA TGC AGT TAG G

Electrophoresis Protocol:

Agarose: 2% mV: 80 Estimated Running Time: 90 min

Primer Combination	Band	Genotype
1 and 2	775 bp	jinx
SNP found at position ~ 96 of sequencing		

Mutation site (red) and flanking sequence:

WT cacgagt**C**agtggcatgttg
 jinx cacgagt**A**agtggcatgttg