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# SAPAP3 Genotyping Protocol

kajsbr<sup>1</sup><sup>1</sup>University of California, San Francisco

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[dx.doi.org/10.17504/protocols.io.36wgq7d7kvk5/v1](https://dx.doi.org/10.17504/protocols.io.36wgq7d7kvk5/v1)

Lisa Gunaydin Lab



kajsbr

Protocol for SAPAP3 KO Mouse Model Genotyping from Dr. Lisa Gunaydin's Lab,  
University of California, San Francisco

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kajsbr 2022. SAPAP3 Genotyping Protocol. **protocols.io**  
<https://dx.doi.org/10.17504/protocols.io.36wgq7d7kvk5/v1>



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## 1 Cut the tails.

To cut the tails and mark the animals, keep in mind to:

- cut as little amount of the tail as possible;
- always clean the scissors properly in between animals (EtOH and bleach);
- tattoo the animals at the same time as cutting the tails;
- use iso if needed.

## 2 Digest the tails.

Incubate the tails O/N at 55 C (water bath) in 200 ul 1x PBND buffer with Proteinase K at 0.25 mg/ml. Vortex before.

$200\text{ul} * (54+1) = 11000\text{ul} \rightarrow 11\text{ml PBND}$

$0.25\text{mg/ml} * 11\text{ml} = 2.75\text{mg} \rightarrow 0.00275\text{g Proteinase K}$

PBND (250 ml 1x, stored at 4 C)  
 2.5 ml 1M TrisHCl pH 8.3  
 1.125 ml IGEPAL  
 1.125 ml Tween 20  
 0.935 g KCl  
 0.125 g MgCl<sub>2</sub>·6H<sub>2</sub>O  
 0.025 g Gelatin  
 Fill remainder with H<sub>2</sub>O  
 \*Gelatin will dissolve only after heated

### 3 Inactivate Proteinase K.

After taking the tails out of the bath, see if they are digested. If so, vortex and boil them for 10 min. Vortex again and centrifuge at max speed for 5 min (table top centrifuge, something like 14,000 rpm).

### 4 PCR reaction.

We use the KAPABiosystems HotStart ReadyMix (2x) which contains DNA Polymerase, rxn buffer, dNTPs and MgCl<sub>2</sub>.

Pipette 24 ul of Master Mix into each PCR tube

Add 1 ul of DNA from each sample into each tube

Sap3 KO F1, Forward primer, 5' - 3': ATTGGTAGGCAATACCAACAGG

Sap3 KO R1, Reverse Primer 5' - 3': GCAAAGGCTCTTCATATTGTTGG

Extra Primer, TKF2: CTTTGTGGTTCTAAGTACTGTGG

A	B	C	D	E
	1 rxn	MM SAPAP (___ rxns)	Primer name	Total Rxns
Forward primer	1		Sap3 KO F1	
Reverse primer	1		Sap3 KO R1	
Extra primer	1		TKF2	
Rxn mix	12.5			
H <sub>2</sub> O	8.5			
DNA	1.0			
PCR program		Sap3		

PCR Program for SAPAP3 Genotyping:

1. 95C for 4 minutes
2. 30 times:
  - 94C for 30 seconds

- 62C for 30 seconds
- 72C for 60 seconds
- 3. 72C for 5 minutes
- 4. 4C hold

Expected band lengths:

WT: one band at ~147 bp

Het: one band at ~147 bp and one band at ~222 bp

KO: one band at ~222 bp

## 5 Run the 1% agarose gel

200 ml TAE

2g agarose

2ul sybr safe gel stain

24ul DNA per well. 5ul DNA ladder before each new line