



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ567	Date of Submission:	7/22/05
Lexicon Contract Name:	DNA309	Mutation Type:	X Standard Knock out
LexVision Name:	SEC553N1		☐ Conditional
Reference accessions:	NM_146050	Is this gene X-linked?	No

Required Materials: X pKOS clone DNA(s) __pKOS56_____
 X Target Vector DNA __pKOS56.TV_____
 X Targeted ES Cell DNA __2A12_____
 X Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' Internal</u>
Name of Probe:	15+16	3+4
Restriction Enzyme for Genomic Digest:	EcoRI	NcoI
Predicted Wild-type Band (kb):	9.5 kb	8.1 kb
Predicted Mutant Band (kb):	8.7 kb	6.3 kb
Probe Size:	358 bp	306 bp

PCR Strategies:*For standard knockouts, give wildtype and mutant-specific strategies**For conditionals, give 5' loxP and cre-excision strategies*

Wild type-specific (absent in targeted allele)		Mutation-specific product (absent in wt)	
5' Primer Name:	DNA309-1	5' Primer Name:	DNA309-1
3' Primer Name:	DNA309-33	3' Primer Name:	GT ires
Predicted Wild-type Band (bp):	326 bp	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	427 bp

5' loxP strategy		Distinguish Cre-excised and wt	
5' Primer Name:		5' Primer Name:	
3' Primer Name:		3' Primer Name:	
Predicted Wild-type Band (bp):		Predicted Wild-type Band (bp):	
Predicted mutant band (bp)		Predicted mutant band (bp)	

Primer sequences:**Southern probes**

DNA309-3 5' – GAAAACACCCTTAGGATGTGG
 DNA309-4 5' – TCATGGTTAAGTTGGGAGCC
 DNA309-15 5' – AGAAGTGTTATCACCAAAGGC
 DNA309-16 5' – CTATAAACTGGCCAAGAGGC

PCR Genotyping

DNA309-1 5' – GATCCCTGGAGATGTTGAGG
 DNA309-33 5' – CACTGATGATAGCAAAGTGAGC
 GT ires 5' – CCCTAGGAATGCTCGTCAAGA

Genomic Sequence Deleted:

CTTCACTTCAACAGGATGAGAGTGGCAGGTACCAGGGATCTGCAGTTTTGACAGGGGGTGGGGGGTGGGGGGTGGAGGGGGGGGGTGGGGAGTCCGGC
TCTAAAAATTTGTTTGGGCTCACTTTGCTATCATCAGTGTCTACCTATCCCAGCCTCAGAGATGGTTCACTATCTCTGTCTAAGGCCCCAGCAAGAACTC
CAGGAGGACATCACGCAGGGAAACCTGGGAGAACAGAGGACAAGACCTTATCCCTATTGGTGTGTCCAACCTTTGGATACTGTGACATAACTGTGTCA
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GGCTGGGTGAGTGGGGCTCGTGGC

Genomic Locus: (The deleted sequence represents nt13488-15787 in the sequence below. KOS56 used to generate the TV represents nt-9912-19764 in the sequence below.)

GCTAGCTCCAGTATGCACGTGCATGCTAATAAATGTTTTCTCTTGATATGATGGGTAGGGAAGAGACTGCCTCCTTTTCTGCCCATACAATAGTAATGTT
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[illegible]

[illegible]

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Selection Cassette:

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[illegible]