



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ1886	Date of Submission:	11/05/04
Lexicon Contract Name:	DNA011	Mutation Type:	☒ Standard Knock out
LexVision Name:	MEM631N1		☐ Conditional
Reference accessions:	AF168680, ENSMUST00000024876	Is this gene X-linked?	No

Required Materials: ☒ pKOS clone DNA(s) __pKOS/52_____
 ☒ Target Vector DNA __DNA011-pKOS 52-FTV 1_____
 ☒ Targeted ES Cell DNA __1E1_____
 ☒ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	18 + 19	20 + 21
Restriction Enzyme for Genomic Digest:	Acc65I (KpnI)	SpeI
Predicted Wild-type Band (kb):	12.0 kb	9.7 kb
Predicted Mutant Band (kb):	9.6 kb	12.3 kb
Probe Size:	219 bp	300 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:	DNA011-7	5' Primer Name:	Neo3a
3' Primer Name:	DNA011-8	3' Primer Name:	DNA011-8
Predicted Wild-type Band (bp):	233 bp	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	343 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**

DNA011-18	5' – TGGAGTGTATAGTCAATCAC
DNA011-19	5' – CACTGCCCAGGTGTCATTGG
DNA011-20	5' – GATGCTTCTCTGTAACCTGC
DNA011-21	5' – GGGATGCATCATTTCAGAGG

PCR Genotyping

DNA011-7	5' – CTCAATGGCGACTCCATCAC
DNA011-8	5' – TATGCGTGTTCCGAGCTCAC
Neo3a	5' – GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

CGGCGCGGCCCGCAGGGGCGGGGGGCGCTCGCCCCGCGAGGGGAGGAGCGCCCCGGGGGGCCCTAGTGGGGACAGAGGACCGCGGGCTGCGGGTG
CGGCGCGGGCGCGGTGTCCCCGCGCAGGGGAGGGCGCCCCGCTCCGGCCCGGCTGCGAGGAGGAGCGCGCGCAGGAGGTACTTGGT
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GCCTGCCCTGTGACGAGTCCAAGTGCAGGAGCCTCGGAGCTGCCAGGAAGCATCGTGCAGGGCGTCTGCGGCTGTGCTACATGTGCGCCGCCAG
AGGAACGAGAGCTGCGGTGGAGCCTATGGGCTCCATGGAGCCTGCGACCGGGGGCTGCGCTGTGTCATCCGCCCCCGCTCAATGGCGACTCCATCAC
CGAGTACGAAGTGGGCGTCTGCGAAGGTACGGTGC

Genomic Locus: (the deleted sequence represents nt 9806 – 10328 in the sequence below. KOS52 used to generate the TV represents nt 950 - 11833 in the sequence below.)

CAAACACACATATGTACACAGAAACATAAAGTAAAAATGAAATCTTCTTTATTGAGCATCTATTATATGTTCTGTCTATAAACAGTAATTTATCTAGTG
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[illegible]

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Targeted Locus:

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