



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ1921	Date of Submission:	2/10/04
Lexicon Contract Name:	DNA469	Mutation Type:	X Standard Knock out
LexVision Name:	SEC248N1		☐ Conditional
Reference accessions:	ENSMUST00000062744, NM_178793	Is this gene X-linked?	No

Required Materials: X pKOS clone DNA(s) __KOS.86_____
 X Target Vector DNA __KOS.86 FTV_____
 X Targeted ES Cell DNA __ES cell 2A3_____
 X Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	DNA469-17/20	DNA469-23/24
Restriction Enzyme for Genomic Digest:	EcoR V	Xma I
Predicted Wild-type Band (kb):	17 kb	6.6 kb
Predicted Mutant Band (kb):	14 kb	11 kb
Probe Size:	371 bp	540 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:	DNA469-2	5' Primer Name:	Neo3a
3' Primer Name:	DNA469-9	3' Primer Name:	DNA469-15
Predicted Wild-type Band (bp):	652 bp	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	385 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**

DNA469-17 5' – ATGCCCTTCACGTTCTTTCAC
 DNA469-20 5' – TTTGCCGTGTGAGGGACTAA
 DNA469-23 5' – ATGCCTTGTTTCTGGATGCTTCT
 DNA469-24 5' – CCGTGGAGGGTTGACAGTTAT

PCR Genotyping

DNA469-2 5' – GGGGGCCGAGAAGAAGC
 DNA469-9 5' – GAAGCACGTGGTGAGCTCG
 DNA469-15 5' – CACCCACAATCCAATCCGC
 Neo3a 5' – GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

GATGGTGCCGCCGCTCTTCCGAGCCGGGGAGGAGCAGCCAAGAGGCAGCTGGGCAAGAGCCTGGGGCCGCTGCTGCTACTCCTGGCGC
TGGGACACACGTGGACCTACCGAGAGGAACCCGAGGACCGCGACAGGTAAGGGCCACCTGCCCTAGAGGGAGGAGGAGCTGGGTGCGAT
CAGGACTGGCTGGCGGGGTGCAGACGATCACATGTGGCGGATCCACAGATCTCTGTGCGCTGAGCCACTGGCGGAGAGGTTAGCTGATC
CAGGTGACTTTTCATCTCATGCGGAACCGCCTCGGCGCTCCCAGTTGTGAGTTGGGACGCTGGATGCCCTCTGTCTCTGCTTTCCCGCCG
CGCTCGGGTGCAGACTTCTTTGATTTTTCTTGTGCTTGGTAGTGGGATCGCTCTGTGCAGGGACACTGTCTGTCTCCTCCCGGGACC
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CTCCCTTAGAGAAGTGTGCTCTGAAAACAAGATCACCACGACCAAATACCCATGTCTGAAGTCTTCGGGCGAGCTCACCACGTGCTTCA
GGTAAAGTTGGGGCCCTGCGGAGTCTAGAGGGACAGGCGTCTGCTGTCAAGC

Genomic Locus: (the deleted sequence represents nt-4116 to 4789 (exons 1 (ATG) and 2)-in the sequence below)

GATCTGATCTGATGCAGGGCCGGGGCCTCTGCGCTTACAGTCTACTGGTCAGAATCTATCCAACCTTCATTCTCAGTCTGACTTTTTCTT
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Selection Cassette: The IRES-lacZ/MC1neo was inserted to replace nt 4116 to 4789 of the contig above.

GGCCGCTCTAGAGGCCATAGCGGCCATTTAAATGGCGCGCCGGATCCCGGGCCGCTCTAGCTAGACTAGTCTAGCTAGAGGAATTCGCG
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Targeted Locus:

GATCTGATCTGATGCAGGGCCGGGGCCTCTGCGCTTACAGTCTACTGGTCAGAATCTATCCAACCTTCATTCTCAGTCCTGACTTTTCTT
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