



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ430	Date of Submission:	12-23-04
Lexicon Contract Name:	DNA249	Mutation Type:	X Standard Knock out
LexVision Name:	SEC521N1		☐ Conditional
Reference accessions:	ENSMUST00000023260	Is this gene X-linked?	No

Required Materials: X pKOS clone DNA(s) __pKOS-74_____
 XTarget Vector DNA __pKOS-74 TVneo_____
 XTargeted ES Cell DNA __1E6_____
 X Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	<u>12/18</u>	<u>Neo 2/5</u>
Restriction Enzyme for Genomic Digest:	Nhe I	XbaI
Predicted Wild-type Band (kb):	7.1 kb	-----
Predicted Mutant Band (kb):	12.7 kb	12.4 kb
Probe Size:	287 bp	609 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:	DNA249-1	5' Primer Name:	Neo3a
3' Primer Name:	DNA249-6	3' Primer Name:	DNA249-10
Predicted Wild-type Band (bp):	293	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	404

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**

DNA249-12	5' – ATCAAAATCCCCACCCATCAAT
DNA249-18	5' – CATAGCCGCGGACATCTGC
Neo-2	5' – CCTCAGAAGAACTCGTCAAG
Neo-5	5' – GGCAGCGCGGCTATCGTG

PCR Genotyping

DNA249-1	5' – AGCGGGCCCCAGGACTATTCTC
DNA249-6	5' – ATGTCGCCACTTGTTTGTCTCACC
DNA249-10	5' – GCGTGGTTCCAGCAGGAGAGG
Neo3a	5' – GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

ATGCAGGGGACCTGGATGGTGTCTGTTGGCACTGATATTGGGCACCTTCGGGGAGCTTGGTGAGCATGGGGGAGCACGG
AAGTGGGCCCCAGGACTATTCTCAGAGAGAGATTCTCATGGGGGAGTTTCAGAGAAGGAGAACGCTGAGCCGGGACTG
GCCAGGCGGGCAGAAGCCGGCACCAAAGCCCTAGGTGCCAGCGGAGAGCCTCAGGATACTGGTGTGTTTGCTAGTGCA
AGCCTTTCAGCAGGAGAAGAGGGGAGATCTCGGATGCTGGGGCAGATGGCCTGGGACTCTGGATATGATGGAATGTA
ATTGGGGAAGGACATCCAGAAATGTCCAGAGACAGGGTGAGACAAACAAGTGGCGACATGATGTTGACTGTCAGCCT
GTTATGTGCTCAGTGATGAGGGCTCAAGCCAGGCTGTTCCATACAGTTCTTGGAGAGGTTGACTGAACCAGAGGCAGA
GGCCCTACCAGGTCACTGTCTGTGTGGGGTTAGGGGAGGGATGACTTCCCTGTGTGCCTGAATTGCTTGGAGACAAGCT
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GGCCTGCTCCTTGGCCTGGCACTTCTCTTGTCTTGGGTGTCTGCTGTAAAGCCATGGCCATCTAGCTCCGCTCCCTTG
TCCCTGACATCCCAGTTCCTAATGCCTAGAAGAAATACAATGGCCATCTGCATGGGTCTCCTGAGTCTCGTTTCTGGGT
ACTGATCTGCCTTGTGGGC

Genomic Locus: (The deleted sequence represents nt-9179-11252 in the sequence below. KOS74 used to generate the TV represents nt-4982-15906 in the sequence below.)

ATGCCACCTGTGCAAGGGATTTGGAGGATGCTCTCGCCCGTCTAGCTGCCCATGGAGCTCCACCCACTGTGTCATCATT
GCCACCCGTGAGTGTGATGAGAGGGATGGGCTGGACACACCCTTCTTGAACAGAGAGCTGGCTCACTGGGCAGGCAGA
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Selection Cassette:

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