



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ3096	Date of Submission:	2/6/04
Lexicon Contract Name:	DNA479	Mutation Type:	X Standard Knock out
LexVision Name:	TGFB9_2		☐ Conditional
Reference accessions:	AF458063, ENSMUST00000059174	Is this gene X-linked?	NO

Required Materials: X pKOS clone DNA(s) ___pKOS 67_____
 X Target Vector DNA ___TV 67_____
 X Targeted ES Cell DNA ___DNA479- 73_____
 X Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' Internal</u>
Name of Probe:	32/37	43/44
Restriction Enzyme for Genomic Digest:	EcoRI	KpnI
Predicted Wild-type Band (kb):	8.5 kb	7 kb
Predicted Mutant Band (kb):	5.1 kb	6.6 kb
Probe Size:	364 bp	344 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:	DNA379-3	5' Primer Name:	Neo3a
3' Primer Name:	DNA379-50	3' Primer Name:	DNA479-43
Predicted Wild-type Band (bp):	387 bp	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	818 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**

DNA479-37	5' – CCTCTCTGGATGCTGCTG
DNA479-32	5' – TGACTGTGTGTGAGCATGTATGTG
DNA479-43	5' – GTTCACAGTTTAAACACCGGAG
DNA479-44	5' – GATAATGAGTGCTCCGGATCTGG

PCR Genotyping

Neo3a	5' – GCAGCGCATCGCCTTCTATC
DNA479-43	5' – GTTCACAGTTTAAACACCGGAG
DNA479-3	5' – CCGAACACTACATCACCATCC
DNA479-50	5' – GATGTGTGTGATGTGCTTGTATATC

Genomic Sequence Deleted:

GCAGTGATGCTCCTGCTGCGGCCCTCACTCTCTCGCTCTGTCTGCAGGATTTCTACGACCCTGCTCGCTTTCCGAGGTAC
CTGCCCCGAAGCCTACTGCCTGTGCCGAGGCTGCCTGACCGGGCTCTACGGGGAGGAGGACTTCCGCTTTTCGCAGCACAC
CCGTCTTCTCTCCAGCCGTGGTGCTGCGGCGCACAGCGGCCCTGCGCGGGCGGCCGCTCTGTGTACGCCGAACACTACAT
CACCATCCCGGTGGGCTGCACCTGCGTGCCCGAGCCGGACAAGTCCGCGGACAGTGCGAACTCCAGCATGGACAAGCT
GCTGCTGGGGCCCCGCCGACAGGCCTGCGGGGCGCTGATGCCGGGGACTGCCCGCCATGGCCCAGCTTTCCTGCATGCAT
CAG

Genomic Locus: (the deleted sequence represents nt 5530-5926 in the sequence below)

GTGCGCCACCACGCCCGGGCTGTCCCACTGTCTTTAATCTCATCCAGTCTCTCGGACACTTAAGCCCCCTCATTCTCCCT
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Selection Cassette:

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