



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ253	Date of Submission:	3-23-05
Lexicon Contract Name:	DNA320	Mutation Type:	X Standard Knock out
LexVision Name:	SEC561N1		☐ Conditional
Reference accessions:	XM_150243	Is this gene X-linked?	No

Required Materials: X pKOS clone DNA(s) __pKOS55, pKOS57_____
 X Target Vector DNA __pKOS57TV_____
 X Targeted ES Cell DNA __1H6_____
 X Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' Internal</u>	<u>3' External</u>
Name of Probe:	5+6	16+17
Restriction Enzyme for Genomic Digest:	HindIII	HindIII
Predicted Wild-type Band (kb):	13.0 kb	13.0 kb
Predicted Mutant Band (kb):	4.2 kb	12.1 kb
Probe Size:	134 bp	294 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:	DNA320-18	5' Primer Name:	DNA320-18
3' Primer Name:	DNA320-19	3' Primer Name:	IRES-GT
Predicted Wild-type Band (bp):	223 bp	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	401 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**

DNA320-5 5' – GTCCTGGAATTGGCATTAAAGTT
 DNA320-6 5' – GCCTAGGGAAAATATGCAAGAC
 DNA320-16 5' – TGGGCACCGCACAAACGACAACC
 DNA320-17 5' – CCCAGGCTACACAGGACCCTTA

PCR Genotyping

DNA320-18 5' – GTCCTGCTTGACCTACCGTC
 DNA320-19 5' – CAGGGAGGATAACGAGATAGTCTT
 IRES-GT 5' – CCTAGGAATGCTCGTCAAGA

Genomic Sequence Deleted:

TGCAGCAATGGCTGAAGGCCTTTGTGGGTGTCTTCGAGAAGACTATCTCGTTATCCTCCCTGGAACCTCGAAGGTAAGG
CTGAGCCTGCACAGAGGCCAGGGCCAGGCAGGTAGGACTGCCCTTCGGCACTCAGCATCTCTCGCTCCCCTCTTCCAGG
CCAGAGGAGGCAGGTGCGGAAGTGCCTCTGCTACCCCTAGATGCTCTACATGCACTAGCGGAGCAGCTGGACCAGGAC
GACCTGGATCAAGCCCTGCTGTTGCTGAAGCTCTTTATCATCTCTGCAGGTGGTTTCTCCCTGCTGTCCTCCCAGGGTG
GCCAGAGGCACGGATGGGTGGGCCCCGGGAGTGAGGGAGACCTCAGCATTAGCATGACTTCTCCTGTTCTTACCCCCC
CCCCCAGGAACCTAGAGAACGTAGAGGCTGGTTGGGGCCAGGTAAGTGGTGGCCCGTGTGCTGGCGTTGCTCACTGTAT
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AGGCTGGAGGAGAATGACCACTGACCCGACCAAGGCAGCGGTGACAGTTTACAGCTGATGGATCCCAGTGCCCACTGCCCC
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CAAGTTCCCTCCGGCCGCTTGGCCTGTGAATTTGGAGCCTTCTTCCAAGGTTAGGCTCCACCCTGATTTCCCAGGGCC
CACCTGGTCTGCTCCAAAACCTAGTTGCCTAATCCCATCACTAGACAGGGAAGTCTTGGTGGTCTGGCCTGAGACAC
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TCCGTATCCCTGGAGGAGTGAAGCCCAGAAGCCCTTCTGGCCGTTTGTCTCCCTGGCTGTATTCACTAAGTGTTCATC
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TGATGCTGGCGTGTGAGGACCGCCAGTGCTACAAGCCACCTTCTTAGCAACAATTGCTTTGAGCATCTTATTCGCT
CATCCAGAACAGCAAGGTGGGTGGGGTCCACCCGAGGTTGA

Genomic Locus: *(The deleted sequence represents nt 9250-12210 in the sequence below. KOS57 used to generate the TV represents nt 7517-15654 in the sequence below.)*

ATGGCCGCTCGGAGCGGCTCTACGAGTTGTGGCTGCTCTACTACGCGCAGGTGAGCCCGTCTCGCCCCTGGTCCGCGG
GGTCCCCAGATCCGCGCACGCAGTGTCTGCTGCACCTGCGTCCGGCTCCCCCGGGCCGAGATCGGCGCGCGCACGC
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CCGGTGAGCGCTGTATTGCAAGTCTCAGCGAGACCGCGCAGCCTCAGTTGCCCTGGCCAGTCAGTTCTACCCCTTTTC
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TGCAATGGGCCAGGGAGGATGGTGAGGTGAGGAGGATGGCTGAAAGGGACCCTCGTTTCAGGCTGACTCCGCTGGTA
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[illegible]

[illegible]

GGCTCCTCCCAGGCACTGTTCCCTTGTCAGTCTCTCTGCCCTGTAGTCTCTACCCAGGCTCTACCCCCCTCCAGCCCC
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Selection Cassette:

CGCTCTAGAGGCCATAGCGGCCATTAAATGGCGCGCCGGATCCGAATTCCTCGAGGCTAGAACTAGCGATAAGCTTC
GAGCGGGATCAATTCCGCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGAATAAAGGCCGGTGTGCGTTTGTCTATA
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GGGT