



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ571	Date of Submission:	10/22/04
Lexicon Contract Name:	DNA089	Mutation Type:	☒ Standard Knock out
LexVision Name:	SEC436N1		☐ Conditional
Reference accessions:	NM_030699	Is this gene X-linked?	NO

Required Materials: ☒ pKOS clone DNA(s) __pKOS-34,45_____
☒ Target Vector DNA __pKOS-34TVpuro_____
☒ Targeted ES Cell DNA __2B7_____
☒ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	14+4	15+16
Restriction Enzyme for Genomic Digest:	HindIII	BamHI
Predicted Wild-type Band (kb):	17.6	16.5
Predicted Mutant Band (kb):	11.3	14.7
Probe Size (bp):	248	324

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:	1	5' Primer Name:	1
3' Primer Name:	9	3' Primer Name:	GT-IRES
Predicted Wild-type Band (bp):	222	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	406

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**

14 5' – CTGAGCACTGCTCTCATCTCTAGC
 4 5' – GAATTAACCATGAGTGATAGATGCC
 15 5' – CTACATCTTGCTCTTGCAGTTGCTCGTG
 16 5' – GCTGATTAAGGAATCTCTCCCCTGG

PCR Genotyping

1 5' – GGCTGTTGTACAGGAGAATCCAG
 9 5' – CATCAGCTCAGGAGGGTGTGC
 GT-IRES 5' – CCCTAGGAATGCTCGTCAAGA

ATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAACTGGCACACCCTCTGAGCTGATGTTTGATTTGAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCTACTTGGGAAGGAGTACCCCCAACTCTCCAGGTTAACTACTCTGTCTGGAGCAAAACCTTGAACCTCAGACAGCAACATAGTTATTACCTTTGAATCGGGGGCTCCAGACCAAAATGATCTCAGAAAATCTCTGCACTACGGAACAACTGGCAGCCCTATCAGTATTATGCCACAGACTGGCTCCATATGCATTCCACATGGACCCGAAATCCGTGAAGGATTTATCTCAGCACACGGTCTTGAAATCATTTGCACGGAAGAGTACTCCACTGGGTACTCCACGAATAGCAAAATAATCCACTTTCGAGATCAAAGACAGGTTTTCGCTTTTCGCTGGACCTCGGCTACGAAATATGGCTTCCCTCTATGGACAGCTGGATACAACCAAGAAACTCAGAGATTTCTCACTGTACAGACCTGAGGATCAGGCTGTGAGACCCGCCGTGGGGAAATATTTGTAGATGAACATACATTTGGCACGTTACTTTTATGCGATCTCAGACATAAAGGTGCGAGGAAGGTAAGAGAACA

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Selection Cassette: IRES BGeo-PGK Puro

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[illegible]

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GA CTGTG C C T T C T A G T T G C C A G C C A T C T G T T G T T T G C C C C T C C C C G T G C C T T C C T T G A C C C T G G A A G G T G C C A C T C C C A C T G T C C T T T C C T A A T A A A A T
G A G G A A A T T G C A T C G C A T T G T C T A G T A G G T G T C A T T C T A T T C T T G G G G G T G G G G T G G G G C A G G A C A G C A A G G G G A G G A T T G G G A A G A C A A T A G C A
G G C A T G C T G G G A T G C G G T G G G C T C T A T G C T T C T G A G G C G G A A A A C C A G C T G A T T A C C C T G T T A T C C C T A C T C G A C C T C G A G G G C G C C A T T T A A
T G G C C A G C G A G G C C G G T A C C C A A T T C G C C C T A T A G C A T G C C C A T C T T G A A T T G G T G G G G A C G G G G A G A C C A T G T C C A A A A A T T A T G C C C A C A A T T A
T A A A G T G A C T T A G G T C C A T T T T A T T T C C T G A T T T C T G A G G A G C A C C A C T A T G C A A G T A T A T T C T C A A G G C A T T T T G A G A C C C T T T G G C T C A A C A A T G A T
T T G T A A A C C C A C A T T A G C T A C T C T T T A G G C A G T C T A G C T T T T A A C A A A A G A A A C A T A A G T A T C T T A C T G G A A G C A A C A A C T C C C T A G G C G A G
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A C C T G G T T T T A G A A A T A T A T A T A T A T A T A C A C T G T A A T T A A G T T A C A A A G A A T T T G A A G C T G T T T G A A T G A A A A A C T C C A A T A A T G A G A A C A A A C A C T
A C C A A C A T T G A G A T T T T C A T T C A G C A A G G C A T G A T G G G A A T G G A A G C A T G C T G G G T A G G A A A T A A A G A A A T A A A G C A A A A A G A A G T A A C C A T T C T A A
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C A C A G T T C A G A G A C A A C T T A G T C A A A G A C T A T C A A T T C A A A T G T G A T C C T A T T T A T T C T T T T T G T A T A T G C T A T A T A A A A T G T T T A G T A T T T T A A C A
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ATACTTATAAAAGATTCATCGGTTCACTTCTACAGTTCTTACATTGTCACCTTGACTCACAGTGACAGTATCATGATATTCATCGACCCTGATGGTCATTT
CAAAGGAGGAGGAAATGTCTCAGGATCCCTCTAAGAGAGAAATAGTTTCTTTCCACAGGATGCAATAACTCAGGCAATCTTTAGTTCTGTTTTTCCTT
TGACTTTAAGATGCGTGTA AAAAGTCAGCAAAACCCCAAGTGTCTAAGGGAGTGTGACAGGGCTACTAGCTTGAGAAGCAAGTACAGGTTAGGGGGGAA
TCCATGAGGTATAAGAGAATTGCAACTTAGTTTGAGTAGGTGACAGGGTACAGTTATATGGGTCAATTAAAGAGTACAAGTGATAAGATTAAGAAGGA
ATTATGCTGTTAATAAAATTTGACATTCAAAACCCAATTAAATGAGCCATTCTTTGACATCACTTTTTCATTAGCAGTCTTACTTCATATCCACTTTGTGC
AAAGGACAGCCCACTTTGCAGGTGCGATAGACCACTTG