



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ1879	Date of Submission:	10-1-04
Lexicon Contract Name:	DNA323	Mutation Type:	X Standard Knock out
LexVision Name:	MEM763N1		☐ Conditional
Reference accessions:	NM_145562	Is this gene X-linked?	No

Required Materials: ☐ pKOS clone DNA(s) __KOS52, KOS72_____
☐ Target Vector DNA __pKOS72TV_____
☐ Targeted ES Cell DNA __1A12_____
☐ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' Internal</u>
Name of Probe:	11+12	7+8
Restriction Enzyme for Genomic Digest:	Acc65I	SpeI
Predicted Wild-type Band (kb):	12.3 kb	6.8 kb
Predicted Mutant Band (kb):	10.3 kb	10.1 kb
Probe Size:	328 bps	309 bps

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:	14	5' Primer Name:	Neo3A
3' Primer Name:	13	3' Primer Name:	13
Predicted Wild-type Band (bp):	452 bps	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	375 bps

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**

- 11 5' – CACATCATGCCTGCTAATGTC
 12 5' – CTGAAACTGAGCACTTGATGTC
 7 5' – CAAGATTAGTGGCACAGTTGGG
 8 5' – GCCATCTTGGTTTGTTCTTAGG

PCR Genotyping

- 14 5' – CGCAACTTCCCTATCGGAGTCTC
 13 5' – CAGACAGTGGCCAACGACTATGA
 Neo3A 5' – GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

AGTCCCATTTGCCTGTCTCTCTCATGACAAAAAGTTCAGCACCTGTGGCCACCTGGACTACCTCTGCTCCACACACTGCTA
GGGCCACCACCCCTGTAGCCAGTGCCACTCACAACGCCTCAGTTCTCCGCACCACTGCCGCATCCCTGACATCTCAGCT
CCCCACTGACCACAGAGAAGAAGCTGTACCAGCCCACCTTTGAAGAGGGATGTCAACAGCACAGACTCCTCACCTGC
CGGGTTCCCTCAACAAGCAGTGATGGCCACTTGGCACCCACACCTGAGGAACACAGTCTTGGAAGTCCTGAAGCAAC
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CAAGGAGAAATCACCCCAAGACACTGAACCTGGCAAAGTGATCTGTGAGTCTGAGACCACCACCCCTTCTGATCAT

Genomic Locus: (the deleted sequence represents nt9,735-10,364-in the sequence below)

CTGTGTTACCATAGCCACCAACCAAAAGAGTACACATGGAGGGTCCCATGGCTCCAACCCGCATATGTAGCAGAGGATG
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[illegible]

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Selection Cassette:

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Targeted Locus:

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