



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ2436	Date of Submission:	7/20/05
Lexicon Contract Name:	DNA404	Mutation Type:	<input checked="" type="checkbox"/> Standard Knock out
LexVision Name:	MSC347N1		<input type="checkbox"/> Conditional
Reference accessions:	NM_026192	Is this gene X-linked?	No

Required Materials: pKOS clone DNA(s) __pKOS-69_____
 Target Vector DNA __pKOS-69 TV Neo_____
 Targeted ES Cell DNA __1G3_____
 Genomic Map

Southern Blot Analysis:
External/Internal Probe Strategies

	<u>5' Internal</u>	<u>3' External</u>
Name of Probe:	23+24	25+26
Restriction Enzyme for Genomic Digest:	BamHI	NsiI
Predicted Wild-type Band (kb):	7.8	8.2
Predicted Mutant Band (kb):	6.4	12.8
Probe Size:	308	164

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:	DNA404-8	5' Primer Name:	DNA404-29
3' Primer Name:	DNA404-6	3' Primer Name:	GT IRESext
Predicted Wild-type Band (bp):	345	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	197

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**

DNA404-23 5' – CCCAGAAGCTCTCGCGTCACTC
DNA404-24 5' – GTGAGGACAATGCGGGCTACTC
DNA404-25 5' – TGGGTTTGCTTTCTTAGTTATA
DNA404-26 5' – CTTGGGACATTTATATTGCACT

PCR Genotyping

DNA404-6 5' – CCCGGAGGCAAAGTGTAGTGAC
DNA404-8 5' – GTAAGCCAAAGAGGATACAACA
DNA404-29 5' – GGCCTGGAAACCTGTTTAGTGA
GT IRESext 5' – GCTAGACTAGTCTAGCTAGAGCGG

Genomic Sequence Deleted:

CATGGAAGAGTCATCACTAAGCCGGGCACCATCCCCGGGGTGGAGTCAACTTCCTGAATGTGGCCCCGCACCTACATCCC
CAACACCAAGGTGGAATGTCACTACACTTTGCCTCCGGGTACCATGCCAGTGCCAGTGACTGGATTGGCATTTTTAAAG
GTATCCCTAGACCCTCTTCTAGCTCAAGATTATGGGACACAGGTTGGTTAGACTATGAGGAGTGGCTAAGTCCTTACAT
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CGTTCGAGATTATCACACGTTTCGTGTGGTCTCAGTGCCAGAAAGTACAACCTGATGGCTCCCCACCCATGCCAGTGTC
CAATTCCAAGG

**Genomic Locus: (The deleted sequence represents nt6787-7492-in the sequence below. KOS69 used to generate the TV
represents nt3013-12323 in the sequence below.)**

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Selection Cassette:

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