



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ720	Date of Submission:	10-8-04
Lexicon Contract Name:	DNA211	Mutation Type:	x Standard Knock out
LexVision Name:	SEC534N1		☐ Conditional
Reference accessions:	NM_178780.2	Is this gene X-linked?	no

Required Materials: ☐ pKOS clone DNA(s) __kos75_____
☐ Target Vector DNA __DNA211-FTV75_____
☐ Targeted ES Cell DNA __2G10_____
☐ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	DNA211 7 + 8	DNA211 11 + 12
Restriction Enzyme for Genomic Digest:	BamHI	EcoRV
Predicted Wild-type Band (kb):	7.2	8.0
Predicted Mutant Band (kb):	4.0	9.7
Probe Size:	285 bp	245 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:	DNA211-13	5' Primer Name:	Neo3a
3' Primer Name:	DNA211-6	3' Primer Name:	DNA211-6
Predicted Wild-type Band (bp):	280	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	376

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**

DNA211-7 5' – GTCATAAGCCACCCACGGAG
 DNA211-8 5' – GTAATATGGGGATGGAGGAC
 DNA211-11 5' – AGAACTGGCATCCAGGGAG
 DNA211-12 5' – GACATTAAGGCAAAAGGCAAG

PCR Genotyping

DNA211-13 5' – TGCTGCCCAAGGCCTTCTTGTC
 DNA211-6 5' – CTAAGAGGCAACAAGAGGCTG
 Neo3a 5' – GCAGCGCATCGCCTTCTATC

TACG CAGCCATGGCGTACTCCACGGTGCAGAGAGTGGCGCTGGCCTCGGGGCTCGTCTGGCCGTGTCGCTGCTGCTGCCCAAGGCCCTTCTTGCTCGC
GGGAAGCGACCGGAGCCGCCGCCGGGCCCGGAAGGTGAGCGCC

[illegible]

[illegible]

[illegible]

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CGAACCGGTAACGCGAATGGTGCAGCGCGATCGTAATACCCGAGTGATCATCTGGTCTGGGGAATGAATCAGGCCACGGCGCTAATCACGACG CGCTGTATCGCTGGATCAAATCTGTGATCTTCCCGCCGGTGTCAGTATGAAGCGCGGAGCGGCACACCCACCGCATATTATTATGGCCGATGT AGCGCGCTGGATGAAGACCGCCTTCCCGGCTGTCGCCGAATGGTCCATCAAAAATGGCTTTTCGCTACCTGGAGAGACGCGCCGCTGATCCTT TCGCAATACGCCACCGCATGGGTAAACGTTCTGGCGTTTTCGCTAAATCTGGCAGGCGTTTCGTCAGTATCCCCGTTTACAGGGCGGCTCTGCTTGG GACTGGGTGGATCAGTCGCTGATTAAATATGATGAAAACGGCAACCCGTGGTGGCTTACGGCGGTGATTTTGGCGATACGCCGAACGATCGCCAGTT CTGTATGAACGGTCTGGTCTTTGCCGACCGCACGCGCATCCAGCGCTGACGGAAGCAAAACACCAGCAGCAGTTTTCAGTTCCGTTTATCCGGGCA AACCATCGAAGTGACCGCAATAACCTTCCGTCATGAGGATAACGAGCTCTGCACTGGATGGTGCGCTGGATGGTAAGCCGCTGGCAAGCGGTG AAGTGCTCTGGATGTCGCTCAACAGGTAAACAGTGTGATTGAATGCTGTAACCTACCGCGGAGCGCGGCACTCTGGCTGCAAGTACGTAACG CAGTGCAACCGAAGCGGACCGCATGGTCAGAAGCGGGCACATCAGCGCTGGCAGCAGTGGCGTCTGGCGGAAACCTCAGTGTGACGCTCCCG CCGCGTCCACGCCATCCCGCATCTGACCACAGCGAAATGGATTTTGCATCGAGCTGGGTAATAAGCGTTGGCAATTTAACCGCCAGTCAGGCTTTC 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