



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ2424	Date of Submission:	10-11-05
Lexicon Contract Name:	DNA510	Mutation Type:	X Standard Knock out
LexVision Name:	ENZ915N1		☐ Conditional
Reference accessions:	NM_011303	Is this gene X-linked?	NO

Required Materials: pKOS clone DNA(s) N/A
 X Target Vector DNA pKOScrambler TV neo
 X Targeted ES Cell DNA 2E5
 X Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' Internal</u>	<u>3' External</u>
Name of Probe:	13/14	27/28
Restriction Enzyme for Genomic Digest:	Bam HI	Xba I
Predicted Wild-type Band (kb):	5.5	8.1
Predicted Mutant Band (kb):	3.9	12.3
Probe Size:	315	335

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:	35	5' Primer Name:	NEO 3A
3' Primer Name:	36	3' Primer Name:	36
Predicted Wild-type Band (bp):	396	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	375

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**

13 5' – CCTGAAATGAACCCCTTGGCGACCC
14 5' – TCTGAGTGGCTGCGGCGACTTC
27 5' – GTTTGGAAGAATTTGGGTAAC
28 5' – TCAAGGCAACGGTGAGC

PCR Genotyping

35 5' – GGACGCCACCTCGCTCGGGAGT
36 5' – TTAGAGAAAGAGTCATGCGGCAGA
Neo3a5' – GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

AATTCCTGAGCCCAAGAATAGCAATGAGTCGGGAGACTTTCGCGGACTGAAATTGGGAGCTGCAATCACTCCCCAGG
TTTTGTGTGTGGTGTTTTTGTGTGTGGTTTTTCCCCCTTTCTTTTTCTGGAGAAAGTTGGAGGGGGGCGCTACAATTGG
GAAACAGCTTTTTGTTTGTTTGTGTTTGTAAATCTTGCACCTTTGAAACCGCGGACTGTAGCTGTGTGCGCGCTGTGGTTG
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CCCAATCTTCTGAGACGCTTTTTACCTCTCCGCCAGAGCAGAGTTTATCTTTTTTTCTTTTTCTTTTTTTTTCTTTTTCTT
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CATCACCGGCGGTGGGAGAGGCATCGGACGCCACCTCGCTCGGGAGTTCGCAGAGCGTGGCGCCAGAAAGGTACACG
GCGTGGGGGCGGGGTGGCACTGCGACACCTGGAGTGGGCGCTGAGGGTAAAGGGACTCTGGCACGCAGGGAGGGGTA
GGCAGTCGTGGGGGATGTTCCACCTGCTGCGGGTGC

Genomic Locus: 10kb flanking the deletion (the deleted sequence represents nt-12882-13874 in the sequence below. KOS scrambler used to generate the TV represents nt 9199-16663 in the sequence below.))

AAGTGGGGCTATGTGCTTTCCAAGAGAGAGTATGGGAAAGTAAGACACATCCAAGTGTGAATGCAGGCTCCTCGGGAGGGAATGAG
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Selection Cassette:

CCAGCGAGGCC

Targeted Locus:

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