Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ828	**Date of Submission:**	11-10-04
Lexicon Contract Name:	DNA259	**Mutation Type:**	X Standard Knock out
LexVision Name:	SEC496N1		☐ Conditional
Reference accessions:	NM_175696	**Is this gene X-linked?**	No

Required Materials:
☐ pKOS clone DNA(s) __pKOS29, pKOS69_____
☐ Target Vector DNA __pKOS29TV_____
☐ Targeted ES Cell DNA __1F2_____
☐ Genomic Map

Southern Blot Analysis:
External/Internal Probe Strategies

	5' External	**3' Internal**
Name of Probe:	**12+13**	**3+14**
Restriction Enzyme for Genomic Digest:	**EcoRI**	**BamHI**
Predicted Wild-type Band (kb):	**7.0 kb**	**13.3 kb**
Predicted Mutant Band (kb):	**3.3 kb**	**6.7 kb**
Probe Size:	**302 bps**	**238 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:	15	5' Primer Name:	Neo3A
3' Primer Name:	11	3' Primer Name:	11
Predicted Wild-type Band (bp):	415 bps	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	286 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
12 5' – CTAAGTGAGCCCGTGTAGAC
13 5' – CATTCTCCCTGAAGCAACCC
3 5' – GTCGCAATTCTAGGTTTGGC
14 5' – CATGGAGGCAGGTACATTCCG

PCR Genotyping
15 5' – GACCTCTTTCCTTATGATGCACA
11 5' – CTTGGAGAGGATCTGACCAGC
Neo3A 5' – GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

GTGCAGAATGTGGTAAGTTTGGCCCAGCAGAGGGAGCTTGCTTGGAGACCACTTTCCCTGGGGGATTGGGCCCTTTCCT
GCCTAGGCCAACTTGGGGCCTATTAAGGACTGGCCCCTTGGGAAGAGACAAAATGGGGCCAGGGTCTTCCTAACACAC
CTGCTCAAGCAGAGAAACCTGGAGGGAGGTACCCAAGACTCCTGGTGCAAACCTACCCTTTTCTACATGAGCCATCGC
CTGGGTCTCACCTGCTTTTTCTCCCTTCCTATAGGTCTGCTCAACTGCTGTCCCAACTCCTCCCTCTCTGGCCACTGCTGT
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Genomic Locus: ***(The deleted sequence represents nt5487-8217-in the sequence below. KOS29 used to generate the TV represents nt 2836-12899 in the sequence below.)***

GTGCTCCACCAGTGACTCACGCTTCGAGCTTATCACGTGATGGCTCACTGTCTCTCTTACTAAATTGTAAGTCACGAGGA
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Selection Cassette:

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Targeted Locus:

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