



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ499	Date of Submission:	11.2.04
Lexicon Contract Name:	DNA417A	Mutation Type:	x Standard Knock out
LexVision Name:	ENZ240N1		☐ Conditional
Reference accessions:	ENSMUST00000024594; NM_026644	Is this gene X-linked?	No

Required Materials: x pKOS clone DNA(s) __KOS35_____
 x Target Vector DNA __TV35-2_____
 x Targeted ES Cell DNA __1F9 and 1A9_____
 x Genomic Map

Southern Blot Analysis: External/Internal Probe Strategies

	<u>5' External</u>	<u>3' Internal</u>
Name of Probe:	16+17	5+6
Restriction Enzyme for Genomic Digest:	EcoRV/Bgl II	HindIII
Predicted Wild-type Band (kb):	13.5 kb	16.4 (~15.1 kb)
Predicted Mutant Band (kb):	9.3 kb	11.3 (~10.0 kb)
Probe Size:	148 bp	252 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:	DNA417A-25	5' Primer Name:	Neo3a
3' Primer Name:	DNA417A-26	3' Primer Name:	DNA417A-12
Predicted Wild-type Band (bp):	216 bp	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	344 bp

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**

DNA417A-16 5' – CATGCAGGCTAACTCTGAG

DNA417A-17 5' – CCAACCATGAGAGAGTCAC

DNA417A-5 5' – CAAAATGTCTAAATATACAAACGC

DNA417A-6 5' – GTCAAACGATCTTGTACCCTAC

PCR Genotyping

DNA417A-25 5' – TTAGCATAGTGGGCGAAGTTC

DNA417A-26 5' – GGTAGTGGCCAAGTTAATAGTCCT

DNA417A-12 5' – GAAAGAGCTGGAAGGGACGGCATC

Neo3a 5' – GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

CAAAGTCCTGGCCAAGAAAGAACTGGCTTATGTCCCAATCATTGGCTGGATGTGGTACTTCGTGGAAATGATCTTTTGCACACGCAAGTGGGAGCAAG
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GCACTTTGGGGCTGATCTGGCGTCAAGTGTGACTATGAACTTCTTTGGCACTGTGGCCTCTGGTTGAGCTTGGGGTTGTGTGAGCGTGGGATCCTCCTGT
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Genomic Locus: (*The deleted sequence represents nt 23106-26457 in the sequence below. KOS35 used to generate the TV represents nt 16633-27476 in the sequence below.*)

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[illegible]

[illegible]

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Selection Cassette: LacZ/Neo

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Targeted Locus:

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