



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ6124	Date of Submission:	6-24-05
Lexicon Contract Name:	DNA488	Mutation Type:	X Standard Knock out
LexVision Name:	SEC617N1		☐ Conditional
Reference accessions:	ENSMUST00000058595	Is this gene X-linked?	No

Required Materials:

☐ pKOS clone DNA(s) __pKOS44_____
☐ Target Vector DNA __pKOS44 TVneo_____
☐ Targeted ES Cell DNA __2C10_____
☐ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	11+12	19+20
Restriction Enzyme for Genomic Digest:	BamHI	EcoRI
Predicted Wild-type Band (kb):	10.2 kb	7.4 kb
Predicted Mutant Band (kb):	6.0 kb	9.6 kb
Probe Size:	274 bp	322 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:	2	5' Primer Name:	Neo3a
3' Primer Name:	5	3' Primer Name:	10
Predicted Wild-type Band (bp):	425 bp	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	331 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**

DNA488-11 5' – GCTTTGCCCATACAAGT
 DNA488-12 5' – CGCAGAACGATAGAAGATAACT
 DNA488-19 5' – CAGAAAGGGCCAAATGACTTAC
 DNA488-20 5' – GCAGAAGTTACGGAATGTGATCGC

PCR Genotyping

DNA488-2 5' – GGCTCCATCCCTCCAGTGAC
 DNA488-5 5' – AAGCCTCCAAGACAGCAAACATTA
 DNA488-10 5' – GCTAGTAACATAAACGCCATAATG
 Neo3a 5' – GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

TCCAAAGTTTTATGGCTGGTGGCCCTTGTGGCTCTATACATTCCGCCCATCCAATCTCTGAACGTGTGTTTACCTGGATG
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TTTTAAGTTTCCTAAAGAGATTTTGCCATACATCCAGCATATGAAAAGGGAGATAAACGCCGCTCCTATCGTATATCC
TCTCTGGCACTAACTATCTTCAATCTTAAAGGCTCCATCCCTCCAGTGACAGAGGAACACTGGGAACGTATCAGATCGG
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TGCAATTGCTCAAATGTCTCCAAGAACGCTTTATTCTAAAGCCAT

Genomic Locus: (The deleted sequence represents nt 15578-17366 in the sequence below. KOS-44 used to generate the TV represents nt 10650-20328 in the sequence below.)

GACAAGGGCAAAAAGCAGCCACAATCTTTGCCAAAATGTTACTAGAATGGTCTCAAGCCTGGTTGCTAATAGTTTCCCT
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[illegible]

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Selection Cassette:

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Targeted Locus:

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