



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ332	Date of Submission:	10-5-04
Lexicon Contract Name:	DNA068	Mutation Type:	X Standard Knock out
LexVision Name:	MEM641N1		☐ Conditional
Reference accessions:	NM_053141	Is this gene X-linked?	No

Required Materials:

☐ pKOS clone DNA(s) __KOS18, KOS23, KOS46__

☐ Target Vector DNA __pKOS46TV__

☐ Targeted ES Cell DNA __2A10__

☐ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	24+25	20+21
Restriction Enzyme for Genomic Digest:	BamHI	KpnI
Predicted Wild-type Band (kb):	35.7 kb	19.7 kb
Predicted Mutant Band (kb):	8.1 kb	11.5 kb
Probe Size:	582 bps	893 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:	32	5' Primer Name:	Neo3A
3' Primer Name:	33	3' Primer Name:	26
Predicted Wild-type Band (bp):	235 bps	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	502 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**

24 5' – CTGTGGCAGAGGAAACCGAG
 25 5' – CCAAGGCTGTCCCAGATCTG
 21 5' – GCTGAGGTAACTCTGACAGC
 20 5' – AGATGAGCGAGTCCAGGGCCA

PCR Genotyping

32 5' – GGGCACACAATGGAGAGGTAC
 33 5' – GCCAAGGCTATGACCAGGTACAAT
 Neo3A 5' – GCAGCGCATCGCCTTCTATC
 26 5' – TTGAGCATTGCTATGTCGGGTGT

Genomic Sequence Deleted:

GCAGGAAGCTCATTTGCAGACAAAGGCAAGTCCTTTTTTCTTTCTCCTATTAGGCTTCCCTCTAACGACTGCAGGGGAA
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Genomic Locus: (the deleted sequence represents nt15,108-17,515-in the sequence below)

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Selection Cassette:

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[illegible]

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