



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ385	Date of Submission:	10-21-05
Lexicon Contract Name:	DNA315	Mutation Type:	x Standard Knock out
LexVision Name:	MEM761N1		☐ Conditional
Reference accessions:	NM_172883	Is this gene X-linked?	no

Required Materials:

- x pKOS clone DNA(s) __pKOS16____
- x Target Vector DNA __pKOS16 TV____
- x Targeted ES Cell DNA __1D10____
- x Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	13 + 14	15 + 16
Restriction Enzyme for Genomic Digest:	NdeI	HindIII
Predicted Wild-type Band (kb):	9.0	8.6
Predicted Mutant Band (kb):	11.4	11.6
Probe Size:	232	253

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:	DNA315-7	5' Primer Name:	Neo3a
3' Primer Name:	DNA315-8	3' Primer Name:	12
Predicted Wild-type Band (bp):	323	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	366

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**

DNA315-13 5' – CTTGAGTCTGGGTAACCTTG
 DNA315-14 5' – TCTGATCTGGGTGTGTTTCC
 DNA315-15 5' – GATTCTCAGATACCCATGGG
 DNA315-16 5' – CCAGGCTACCTAGTCTCAC

PCR Genotyping

DNA315-7 5' – CTGGATGTCTGTAATCTGCTCC
 DNA315-8 5' – CCACTATGGAGATGATGCTAAC
 Neo3a 5' – GCAGCGCATCGCCTTCTATC
 DNA315-12 5' – GCTGGATTTGTGTCAGAGTC

Genomic Sequence Deleted:

AGCTTTGCACCTGTAGCAGACACCATAGCACAGCACTTCTTCTGCTCCATGGATCAGGTCAACTGGCTGTCACTAATATACTTTGTGTTATCCATCCCAT
TTGGCATGGCTGCCATCTGGGTTCTGGACTCTGTTGGCCTCCGTGGAGCGGTAAGTCAGACTTCATTTCCCATTTCTGGCTGGGTGGGCTGGGGA
CCCTTTGACTTTGAATGCAAAACCTTCATCCCTTCAGATTAGACTCCACAGCCCTACCTGCTAGGCTCCCCAGCAAGCAGCTTGGGGAGTAGGTAG
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Genomic Locus: (The deleted sequence represents nt 7792 – 10860 in the sequence below. KOS16 used to generate the TV represents nt 3613 – 13809 in the sequence below.)

GATCTTATTTTATTTTATGTGTAAGAGTGTGTTGACTGTATGTATATATGTGCACCATATGCATGCCTGGTGTGCGGTAAAGTCATAAGAAGGAGGCATTGT
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Selection Cassette:

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Targeted Locus:

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[illegible]

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