



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ248	Date of Submission:	11/7/04
Lexicon Contract Name:	DNA042	Mutation Type:	☒ Standard Knock out
LexVision Name:	MEM651N1		☐ Conditional
Reference accessions:	NM_133211.2, IPI00009812	Is this gene X-linked?	Yes

Required Materials:

- ✓ pKOS clone DNA(s) __pKOS26_____
- ✓ Target Vector DNA __pKOS26 FTV13_____
- ✓ Targeted ES Cell DNA __1F1 _____
- ✓ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' Internal</u>
Name of Probe:	20/21	Puro C/D
Restriction Enzyme for Genomic Digest:	EcoRI	NheI
Predicted Wild-type Band (kb):	11.0 kb	---
Predicted Mutant Band (kb):	9.4 kb	15.8 kb
Probe Size:	382 bp	949 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:	DNA042-3	5' Primer Name:	DNA042-16
3' Primer Name:	DNA042-11	3' Primer Name:	GT-IRES
Predicted Wild-type Band (bp):	324 bp	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	633 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**

DNA042-20 5' – GTTCATTTCTGCGCCATTGG
 DNA042-21 5' – CCCTATCATGGTCACCAAAC
 PuroC 5'-GCGCCAGCTTACCATGACCGAGTA
 PuroD 5'-CAGCTGGTTCTTTCCGCCTCAGA

PCR Genotyping

DNA042-3 5' – GGGCAGACCTTAGACTTAAG
 DNA042-11 5' –CATGAGTTTGTCCAGAAGCC
 DNA042-16 5' –GACGGAGGTGCTGTTTACAC
 GT IRES-2 5' –GGCCGCTATGGCCTCTAGAGCG

Genomic Sequence Deleted:

AAATCCCTGAGGGCATTCCCACTAACACCACCAATCTTACCCTTACCATCAACCACATACCAAGCATCTCTCCAGATTCCCTCCGTAGGCTGAACCATC
TGGAAGAAATCGAATTTAAGATGCAATTTGTACCTGTCTACTGGGGTCCAAAGCCAATGTGTGTACCAAGAGGCTGCAGATTAGACCTGGAAGCTTT
AGTGGACTCTCTGACTTAAAGGCCCTTTACCTGGATGGAAACCAACTCTGGAGATACCACAGGATCTGCCATCCAGCTTACATCTTCTGAGCCTTGAG
GCTAACAAACATCTTCTCCATCACGAAGGAGAATCTAACAGAACTGGTCAACATTGAAACACTCTACCTGGGTCAAAACTGTTATTATCGAAATCCTTGC
AATGTTTCTATTCTATTGAAAAAGATGCTTTCTTAGTTATGAGAAATTTGAAGGTTCTCTCACTAAAAGATAACAATGTCACAGCTGTCCCCACCACTT
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CCTCAAACTCATAGACCTTTTCAGTGAATAAGATATCTCTTCAGAAAGAGTCAAGAGAAGTTGGCTTTTGTCTAATGCTCAAACTTCTGTAGACCGTCA
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TGTCATGGCTCAGATTGGTGGGAAATCATCAATATATG

Genomic Locus: (the deleted sequence represents nt10114 – 13226 in the sequence below. KOS26 used to generate the TV represents nt 8846 – 19487 in the sequence below.)

TTTCACAAGTTCAGTGCATGTCTTCTCTCACATCCTGTTTGCAAGAGCTGGGTCACATGGTCACATTTATTGGCAACAGAGCATGGGAATGCAAGCAT
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[illegible]

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