



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ649	Date of Submission:	5/17/06
Lexicon Contract Name:	DNA514	Mutation Type:	☒ Standard Knock out
LexVision Name:	PRT426N1		☐ Conditional
Reference accessions:	NM_019974, AK009360	Is this gene X-linked?	No

Required Materials: ☒ pKOS clone DNA(s) __pKOS-15_____
☒ Target Vector DNA __pKOS-15TV floxed neo_____
☒ Targeted ES Cell DNA __1B11, 1D11_____
☒ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	24+25	30+31
Restriction Enzyme for Genomic Digest:	EcoRI	EcoRV
Predicted Wild-type Band (kb):	13.9 kb	13.3 kb
Predicted Mutant Band (kb):	8.2 kb	14.5 kb
Probe Size:	452 bp	556 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:	DNA514-9	5' Primer Name:	Neo3A
3' Primer Name:	DNA514-10	3' Primer Name:	DNA514-6
Predicted Wild-type Band (bp):	477	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	339

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**

DNA514-24 5' – GCAGTAGAGGGCATAGAAGTAGC
 DNA514-25 5' – TTCGTGTAGACTCCTGGAATACCTTTT
 DNA514-30 5' – GGAGGATGGCTGAAACCTGGGTGTCTAC
 DNA514-31 5' – TACCTTGGAACAGCTCAGGCTCCTATT

PCR Genotyping

DNA514-9 5' – CGCCTCTTAAAGTGATTAGACC
 DNA514-10 5' –TAACCCCTTGATGATCCTCGTCTCT
 DNA514-6 5' –TCTTCATGGGTGGCAGAGTTG
 Neo3A 5' –GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

GCTCTGGTAACAGGTACGGTGGGGCTTAGAGGGAAGGGGGGCTCCCTATTCTACTTCTAAGGCCCCCAGCTACAGTG
ACACCTGCTTGGAGATCACCCCCATGAAGTAGTCTGAGCTATACCAGGCATAATCAAGTGGGACTAAGAGGAGGAATG
GGGGTGGGGGTTGGGTCCCCCTCAAAATCTTAGGACAGCCACTAATGACCTGGAAGTATAGTCTTATGCCAGCACGTGA
CAGCTAAGAATGAGAACAGCTATTCTTTTGCTTACTTTTCATTTCTGGGGTCTCTCTACCAGCCTACCCCCTCTTATGCTTG
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GTGGTCTTAGAATAGATGATGGCCTTAGTCCAGGATGAGGATGAAGGAGCGAGTGTGGTAGATGGGTCTGGGTGTTCA
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TGCGATGTGCCAATGTCTCCATCATCGAACACAAGGAGTGTGAGAAGGCCTACCCGGGCAACATCACAGACACCATGC
TGTGCGCCAGTGTTCGGAAAGAGGGCAAGGACTCCTGTCAGGTCAGCAGGCAGGG

Genomic Locus: (The deleted sequence represents nt 10,081-12,019-in the sequence below. KOS15 used to generate the TV represents nt6906-16,572- in the sequence below.)

TAAAATACTTTCAACATCAAAATGTAAAAAAACAAAATAGGTTGGATAACTGGCTATATTGTGTTTCAGTTCTAAATGGA
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Selection Cassette:

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Targeted Locus:

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