



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ782	Date of Submission:	11-8-04
Lexicon Contract Name:	DNA429	Mutation Type:	X Standard Knock out
LexVision Name:	PRT354N1		☐ Conditional
Reference accessions:	XM_196763	Is this gene X-linked?	No

Required Materials:

☐ pKOS clone DNA(s) __pKOS 20_____
☐ Target Vector DNA __FTV 20_____
☐ Targeted ES Cell DNA __1E2_____
☐ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	12+13	14+15
Restriction Enzyme for Genomic Digest:	ApaI	EcoRI
Predicted Wild-type Band (kb):	7.0 kb	11.3 kb
Predicted Mutant Band (kb):	6.1 kb	9.2 kb
Probe Size:	401 bp	351 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:	DNA429-16	5' Primer Name:	Neo3a
3' Primer Name:	DNA429-11	3' Primer Name:	DNA429-11
Predicted Wild-type Band (bp):	291p	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	237

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**

DNA429-12 5'-- GCAGCTCCTTGGCCTTAGACAC
DNA429-13 5' – GACACCGTTAGCCCTCTAGCA
DNA429-14 5' – ACCTGATGTTGCCCGCTCTG
DNA429-15 5' – GCATTTGACGCCATCCCGATT

PCR Genotyping

DNA429-16 5' – TGTATGACCTCATGACTTCAGG
DNA429-11 5' – CCCAGCCCCACAAGTAAATTAA
Neo3a 5' – GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

CTACATTGTTGGAGGCCATGAGGTAACGCCACATTCCCGGCCCTATATGGCCTCTGTGAGCTTCGAGGGCCATCACTAC
TGTGGAGGCTTGCTGATTCATACCCATTGGGTGGTGTCAGCTGCCCATTTGCTTCAGTGACAGGTGACATGCTGGGGCCA
CTGAGGGATAAACTTAAGGCCATCAGGAAGCCAGGATGTGACACAGACAGGACCAACTCTCTACCCCCACGCCCCGGG
ACTTCTGGTGATAACAATCAAACATAATAACTATGATCATCTTCGACACAAGCGACATGTGCTACTGTTTGGACTCACA
TTAACTGTGGGGAGAGCAGCACAGTCCGGGGACTCCAGCTACCCAGAGGCTGGCTCAGGGGGATGGA AAAATGAAGC
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CCTCTTGTGGCCTGCAGGGACCCCTCCATGGGGCTGGTGGTGCTGGGGGCCACGCACTGCTCGCCCCAGAGCCCACA
CAGCAGACATTTAGCATTGCAGCTGCTGTCAGCCATCCTGATTTCAGCCTGCCACACAGGCCAACGATATCTGCCTGC
TAAGGGTGAGCTGGGCTGCA

Genomic Locus: *(The deleted sequence represents nt 10,015-11,773-in the sequence below. KOS20 used to generate the TV represents nt 5484-15106 in the sequence below.)*

CAGTCTGACCCAGGGTCAGGCACGCTCGCACGTTCTGGCTCCCGGGGCCAGCCTGCCCCCCTCGCCCCACCGCGCCT
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[illegible]

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Selection Cassette:

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