



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ1835	Date of Submission:	6/21/05
Lexicon Contract Name:	DNA435	Mutation Type:	X Standard Knock out
LexVision Name:	SEC563N1		☐ Conditional
Reference accessions:	NM_009979	Is this gene X-linked?	No

Required Materials:

☐ pKOS clone DNA(s) __pKOS20_____
☐ Target Vector DNA __pKOS20TVneo_____
☐ Targeted ES Cell DNA __1D3_____
☐ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	8+9	10+11
Restriction Enzyme for Genomic Digest:	HindIII	BglII
Predicted Wild-type Band (kb):	9.9 kb	16.3 kb
Predicted Mutant Band (kb):	8.1 kb	6.6 kb
Probe Size:	379 bp	192 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:	DNA435-13	5' Primer Name:	Neo3a
3' Primer Name:	DNA435-7	3' Primer Name:	DNA435-7
Predicted Wild-type Band (bp):	204 bp	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	310 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**

DNA435-8	5' – GGCTGGTTTAGATCTACAGG
DNA435-9	5' – AAGGGGGTGAGACCATGAAG
DNA435-10	5' – TGAGTTTTTGTGGGTGGTACA
DNA435-11	5' – GGCAAAGGAAGAGTCAGTC

PCR Genotyping

DNA435-7	5' – ACCTCCACATTGTGGCTCAG
DNA435-13	5' – GGAGAGTCTCGATATTTGCC
Neo3a	5' –GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

TGTCCTGTCCACTGAGAAAGAAAGCTCTGCCTCTCACCATGCTGCTGCTTCTGCTGAGTTTTTCATGTTCTCATCACTCCTGTCTCGAAGGCCAATAAAGA
AACAAACAGTCTGTCTTTCATTTCATTCCTCCACAGGTGGAATTTGCCGTGAACACATTTCAACCAGGAAAGTCAGGATGAATATGCCTACAGGATGGAACATA
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AAGTTACACATTGTCTAGGAGCCATAAAGGGACAAGCTAATCACTAGCAGGTGGTCACTATCCTGAATGGCCTGCTTCGGATTATTATATAATCTGCAACA
GGCATGCCCTTATTAAGCAAGGCTGTAAGGGACTCATTTTAGGAAATATTCTGCTATTAATGTGCTTTTCTGTTATTATTAATAAATATATAACAATCA
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GGCTTCAGCTGCGTAGAACCATATGCAAGAAATTTGAGGAGAGTCTCGATATTTGCCCTTTTCAGGAGAGCCATGGTCTGAATAATGTAAGGCAGG

Genomic Locus: (The deleted sequence represents nt 15066-16651 in the sequence below. KOS20 used to generate the TV represents nt 11833-20396- in the sequence below.)

[illegible]

[illegible]

AACTTGTGGTACATTTACACAAATGAAGTACTATGCAGCTATTAAAAACAATGAATTTATGAAATTTTTAGACAAGTGGATGGATCTGGAGGATATCAT
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Targeted Locus:

CCGCACGCCGCATCCAGCGCTGACGGAAGCAAAACACCAGCAGCAGTTTTTCCAGTTCGGTTTATCCGGGCAAACCATCGAAGTGACCAGCGAATACC
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