



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ786	Date of Submission:	11-10-04
Lexicon Contract Name:	DNA430	Mutation Type:	X Standard Knock out
LexVision Name:	ENZ802N1		☐ Conditional
Reference accessions:	NM_175098	Is this gene X-linked?	No

Required Materials: ☐ pKOS clone DNA(s) __pKOS13, pKOS16____
☐ Target Vector DNA __pKOS16TV____
☐ Targeted ES Cell DNA __1H6____
☐ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	20+21	16+17
Restriction Enzyme for Genomic Digest:	EcoRV	EcoRV
Predicted Wild-type Band (kb):	18.2 kb	18.2 kb
Predicted Mutant Band (kb):	13.9 kb	10.3 kb
Probe Size:	245 bps	374 bps

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:	22	5' Primer Name:	30
3' Primer Name:	23	3' Primer Name:	GT-ires
Predicted Wild-type Band (bp):	234 bps	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	487 bps

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**

20 5' – GCATCAGAGCTGCTCCTACA
 21 5' – CTGTATGGTGTCCGAAGCTTC
 16 5' – GGCAGGTGCACACCTGACCA
 17 5' – GTGTGTAGTTTCAGAACAGCTAC

PCR Genotyping

22 5' – TGAAGATGGACAGACGGCAGT
 23 5' – CGGCTGTTGCAAAGTGTAGTGA
 30 5' – GGGCAGTGGTGGCATACT
 GT-ires 5' – CCCTAGGAATGCTCGTCAAGA

Genomic Sequence Deleted:

GCAGCCCTGCTGAAGATGGACAGACGGCAGTAGTCAGCTGTTCCCTCCTCTCTCCTCTCAAAAGACTTGATCGTTTGGTG
TCTTGTTCAGCCACTGCTCCTCGATCAAGTCTGTCTGCTTCCTTCGTAGACATGTTCCGTACAATCTCAAGGAAAAA
TATGTCCCAGAAGCTGAGCTTCCTGTTGTTGGTGTTCGGACTCATCTGGGGGCTGATGCTACTTCACTACACTTTGCAAC
AGCCGCGGCGGCAGAGCAGCGTCAAGCTTCGTGAGCAAATCCTAGATTTAAGCAAAAGATACGTGAAAGCTCTGGCGG
AGGAGAGCAGGAGCACGGCGGATGTGGACAGCGGCGGTCCATGGCAGGCTATGGTAAGAACCTG

Genomic Locus: *(The deleted sequence represents nt15516-15897-in the sequence below. KOS16 used to generate the TV
represents nt 9218-18302 in the sequence below.)*

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[illegible]

[illegible]

Selection Cassette:

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