



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ737	Date of Submission:	11/24/04
Lexicon Contract Name:	DNA330	Mutation Type:	X Standard Knock out
LexVision Name:	MSC335N1		☐ Conditional
Reference accessions:	ENSMUST00000043437, ENSMUST00000049569	Is this gene X-linked?	No

Required Materials: X pKOS clone DNA(s) __pKOS20_____
X Target Vector DNA __TV20_____
X Targeted ES Cell DNA __1A2_____
X Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	16/17	20/21
Restriction Enzyme for Genomic Digest:	BglI	HindIII
Predicted Wild-type Band (kb):	6.7 Kb	6.6 Kb
Predicted Mutant Band (kb):	5.2 Kb	8.9 Kb
Probe Size:	504 bp	569 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:	DNA330-25	5' Primer Name:	Neo3A
3' Primer Name:	DNA330-24	3' Primer Name:	DNA330-24
Predicted Wild-type Band (bp):	371	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	488

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**

DNA330-16 5' – GCAGCGTGACCCACCGTACA
 DNA330-17 5' – TTCTGGGCACGAGGCA
 DNA330-20 5' – CTGCACATGTAGTGTTTCGGCTAT
 DNA330-21 5' – TTCACTCTGTCCCGTGTAGCTG

PCR Genotyping

DNA330-24 5' – AAATTTAGCAGGTACTCATTGCG
 DNA330-25 5' – CACTTTGGTTCAAAGATCTGAG
 Neo3A 5' –GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

ATGACGACCGCCGCCCGCCCGAAAAAGTGTAGATTGTGCCACAGAAAAAGGGATTCTTGTGAGGTCTAGGGGAGCGGAGGGAGGCC
CGTGGGCTCTCGACTCCGGGTGGGTACAGGGAGTGGCAAGGAGGTTAAAGCCTAACATAGAAGAAACCGAAGAAAC
AGCCCAGCCTCTTTGCGGGCCCCGCCCTCACCGCTCCCTGTGAGGTGTTTTGTAGGTCCCCACGCCGAGGAGTGGGG
TACCAGGCGAGAATCCTCACCTCTCTTTCTTAATCCTACAGGTGAAGCCAGCCCAGGAGGTTAAACTTCGCTTTTTTGA
GCAGCTGAGCATCCTTCAGACCCGGCAGCAGAGGGAGGCGGATCTACTGGAGGACATCAGGTAGCCCTAGACCCCTCA
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Genomic Locus: *(The deleted sequence represents nt-6794-9696---in the sequence below. KOS 20 used to generate the TV represents nt-3521-13055- in the sequence below.)*

GTAACTTTAGCTTATAGGACAGCATCACACACACACACACACACACACACACACACACACTTAAAA
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Selection Cassette:

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[illegible]

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