

GENOTYPING BY PCR PROTOCOL

MUTANT MOUSE REGIONAL RESOURCE CENTER: UC DAVIS

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530-754-MMRRC

NAME OF PCR: B6;129S5-Bpifb1^{tm1Lex}/Mmucd MMRRC # 032698-UCD

Protocol:

Reagent/Constituent	Volume (μL)
Water	10.275
10x Buffer	2.5
MgCl ₂ (stock concentration is 25mM)	1.7
Betaine (stock concentration is 5M) <i>Optional</i>	6.5
dNTPs (stock concentration is 10mM)	0.5
DMSO <i>Optional</i>	0.325
Primer 1 (stock concentration is 20μM)	0.5
Primer 2 (stock concentration is 20μM)	0.5
Primer 3 (stock concentration is 20μM)	0.5
Primer 4 (stock concentration is 20μM)	0.5
Taq Polymerase 5Units/μL	0.2
DNA (50-200ng/ μL) extracted w/ "Qiagen DNeasy columns or other similar silica based kits"	1.0
TOTAL VOLUME OF REACTION:	25.000 μL

Comments on protocol:

- Protocol may work with other DNA extraction methods.
- Use Touch-Down cycling protocol-first 10 cycles anneal at 65°C decreasing in temperature by 1.0°C; next 30 cycles anneal at 55°C.
- Betaine and DMSO have been standardized due to high GC content. Protocol may be tested without. Also, may adjust MgCl₂ to increase reaction or decrease non-specific amplifications.

Strategy:

Steps	Temp (°C)	Time (m:ss)	# of Cycles
1. Initiation/Melting HOT START? ☐	94	5:00	1
2. Denaturation	94	0:15	
3. Annealing steps 2-3-4 cycle in sequence	65 to 55 (↓1°C/cycle)	0:30	40x
4. Elongation	72	0:40	
5. Amplification	72	5:00	1
6. Finish	15	∞	n/a

Primers:

Name	Nucleotide Sequence (5' - 3')
1. Neo3A	GCAGCGCATCGCCTTCTATC
2. DNA114-16 (Corrected Primer)	CAACATCAGCTAGGCAGTCAACG
3. DNA114-14	GACAGACCAGACTAAGTC
4. DNA114-15	CCCTACTGTCCTGTCATC

Electrophoresis Protocol:

Agarose: 1.5% V: 90

Estimated Running Time: 90 min.

Primer Combination	Band	Genotype
1 and 2	419 bp	KO
3 and 4	272 bp	WT

The Lexicon PCR Protocol is attached below.

Please note: the primer DNA114-16, CGTTGACTGCCTAGCTGATG listed on the Lexicon Protocol is incorrect. Use the primers listed above to ensure correct results.



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ706	Date of Submission:	3.1.04.
Lexicon Contract Name:	DNA114	Mutation Type:	☒ Standard Knock out
LexVision Name:	SEC464N1		☐ Conditional
Reference accessions:	ENSMUST00000028987, NM_153418	Is this gene X-linked?	No

Required Materials: ☐ pKOS clone DNA(s) pKOS-92
☐ Target Vector DNA pTV-92
☐ Targeted ES Cell DNA 1G11
☐ Genomic Map

Southern Blot Analysis:
External/Internal Probe Strategies

	5' External	3' External
Name of Probe:	8+9	12+13
Restriction Enzyme for Genomic Digest:	BglII	ApaI
Predicted Wild-type Band (kb):	11.9 kb	7.8 kb
Predicted Mutant Band (kb):	17.2 kb	11.1 kb
Probe Size:	156 bp	129 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:	14	5' Primer Name:	Neo3A
3' Primer Name:	15	3' Primer Name:	16* —DNA114-16
Predicted Wild-type Band (bp):	272 bp	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	459 bp* 419 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: *Please note: the primer sequence for DNA114-16 is incorrect. It should be 5' CAACATCAGCTAGGCAGTCAACG. The MMRRC at UC Davis recommends using the protocol above to ensure correct results.

Southern probes

DNA114-8 5' – GAGACACCAGACATCAACC
 DNA114-9 5' – CCTCTGCTTCCTTCTGAG
 DNA114-12 5' – GCTGTGTCGATGTTAGGC
 DNA114-13 5' – GTCAGACTCTAGGACAGAG

PCR Genotyping

DNA114-14 5' – GACAGACCAGACTAAGTC
 DNA114-15 5' – CCCTACTGTCCTGTCATC
~~DNA114-16 5' – CGTTGACTGCCTAGCTGATC*~~ Corrected primer DNA114-16 5'- CAACATCAGCTAGGCAGTCAACG
 Neo3A 5' – GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

GGCACTGAAGGACCATGATGCCACTGCCATCCTCCAGGAGTTGCCACTGCTCAGAGCCATGCAAGATAAGTCTGGCAG
TATCCCCATACTGGACAGCTTCGTGCACACCGTTCTGAGATACATCATATGGTGAGTGGGCCCCGACAGCATTGGGAGCC
ATCTCTTCCCCACACCTCTGCCTACACATTGTGCAGCTGTCAATCAACAGTTATGAAGACAGACCAGACTAAGTCTCTC
TTTTGATAAGCCCCCAGAATGGCTAGTGGTGTCCATAAGGCAGTGTCACTGGTACCTCTAAGAGGGAAGCCACTTAGGA
AGGTTCCCCAGAGTGCTGGAACCTGGAGGTGCTTTTTAATGGAGGTCATGGTTAAGCCAGGGACACCAAGAACTGAT
GTTTCAGGCAAAGGGGCCAGTGGGGCAAAACCATGGAGGGGCAAGAATCACACAATTGGAACCCCAACAGCAAAGGA
TGACAGGACAGTAGGGTCAGGTCATGGAGGAGCTCTGTCAGCCCCAACAGGCTGAGGCTAGAAGCCGAGGAACCTGAA
GAGAAGCAAGCGAGGGTGAAGGGGAGAGACAGAGGTAGGGCCATGATGGAAAGGATTAGTAACTAGGCTTGGGATC
CAGGCTCTGCTCAGGTGTGAGGAAGTCAGGGGAAAGGATGGGAGCAGGCTTGGGGCTGACTCTCGTCCGAGTGTGAAC
ATGATTCTCATCCCCCTGCACCCTGTCCAGGATGAAGGTACCTCTGCTAACATCCTCCAGCTGGATGTGCAGCCTTCA
ACTTATGACCAGGAGCTGGTGGTCAGAATCCCCCTGGACATGGTGGCTGGACTAAACACGTGAGTGTCCCTGAGTCA
GACACAGTAACCTAACAGTTTCAGCTACTCGCTCTCCATGCAGATGTCTAGAAACAAATCCCAGCATTAGATGAACAA
GTGCAAAGGCCCTGAGGCAGAAATGACAACAAGAAGGGAAGGGGTGGGGTTAGAGATGAGGTCAGCAAGCCGCTGAG
GACTGATGGTGCCGGACCTTATGTGACAAGATGAGAACTAGGCTTTAATGGAATATGAGGGCCAAAAGCAACAGAAGG
TCTGAGCTTAGGGGAAAACAGTGTGGTGCAGAGTGGAAGTGGGACCACCACATGGAAGGCCCTGCTCTAGGGGAGAC
AGAAGTGGCTGAGGTAGCCAGGCAGTGGTGGCACACACCTTT:AATCC:CAGCACTTGGGAAGCAGAGGCAGGCGGATT
TCTGAGTTTGAGGGCAGCCTGGTCTACAAAGAGAGTTCCAGGACAGCCAGGGCTATACAGAGAAACCCTGTCTCGGGG
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AAGCAGGCAGAAACAACAGGGATTCTGTGAGTTGGATATGGAGAGAGATCAAGGATGACTTCAGGGTCTGCTCCAC
AACAATCCGGGAGGAACAGCCAGCAGCCAAGACGACAAGGTTTGAAGAGGCAGGCCAGGAGACAATGTGGTGTGAC
TTGGAATCCCCTGGCATCCATAAGTGGTGAGATCCGGAGAAAACCTCTGGGACTCCAGATCTGGGAGAGATAATGGGAA
CCAGCAAAAGAGATAGTGAAGGACAGATAGACTGCTGTGGCACACAGACTTCAACAGCACCCCTTTCTCACTGCTGTTG
TCCCCTCAGACCACTGATCAAGACCATAGTGGAGTTCCAAATGAGCACCGAGGTCCAAGCCCTCATCCGGGTGGAGAG
GAGCAAGAGCGGCCCCGCCACCTGAATCTCAGCGACTGCTCCAGCAATGAGAGCACCCCTGCGCCTCAGCCTGCTTCA
CAAGTGAGTGTTGGGCTCCTGGTCGGAGGG

Genomic Locus: (The deleted sequence represents nt 6379-8280 in the sequence below. KOS92 used to generate the FTV represents nt 115-9704 in the sequence below.)

AAACCACACTTTCCTCCATGACCAGCCAGAGACTGTATGACCTCAGGGACACTGCCCCCTCTCTCATCACCATACAGAT
GGGGACACGACTTAACAATGGATCTCCTAGCCCTAATCCATAGTTTACCCTTCCAGATAGAAGCCAAGACAAGCGCC
CAAAGGTCACATCAATATCCCTACTGACCCTAACATTAACCAGGTGTCACCAGGGCAGAGTGGTCAGGAGTGTGTGGC
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Selection Cassette:

GGCGCGCCGGATCCCGGGCCGCTCTAGCTAGACTAGTCTAGCTAGAGAATTCCGCCCCCCCCCCCCCCCCCTC
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