



## Lexicon Genetics Incorporated – Genentech Project Materials

|                               |                                  |                               |                                                        |
|-------------------------------|----------------------------------|-------------------------------|--------------------------------------------------------|
| <b>Genentech ID:</b>          | UNQ2239                          | <b>Date of Submission:</b>    | Jan 15, 2004                                           |
| <b>Lexicon Contract Name:</b> | DNA031                           | <b>Mutation Type:</b>         | <input checked="" type="checkbox"/> Standard Knock out |
| <b>LexVision Name:</b>        | TRA267N1                         |                               | <input type="checkbox"/> Conditional                   |
| <b>Reference accessions:</b>  | ENSMUST00000045557,<br>NM_011404 | <b>Is this gene X-linked?</b> |                                                        |

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**Required Materials:**    ☒ pKOS clone DNA(s)    \_\_pKOS-31, 54\_\_\_\_  
                                   ☒ Target Vector DNA    \_\_54TV\_\_\_\_  
                                   ☒ Targeted ES Cell DNA    \_\_1C8\_\_\_\_  
                                   ☒ Genomic Map

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### Southern Blot Analysis: *External/Internal Probe Strategies*

|                                        | <u><b>5' External</b></u> | <u><b>3' External</b></u> |
|----------------------------------------|---------------------------|---------------------------|
| Name of Probe:                         | <b>11+12</b>              | <b>13+14</b>              |
| Restriction Enzyme for Genomic Digest: | <b>BamHI</b>              | <b>EcoRV</b>              |
| Predicted Wild-type Band (kb):         | <b>12.2</b>               | <b>7.2</b>                |
| Predicted Mutant Band (kb):            | <b>8.4</b>                | <b>9.3</b>                |
| Probe Size:                            | <b>238 bp</b>             | <b>253 bp</b>             |

**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:                                | 3    | 5' Primer Name:                          | Neo3A |
| 3' Primer Name:                                | 5    | 3' Primer Name:                          | 7     |
| Predicted Wild-type Band (bp):                 | 344  | Predicted Wild-type Band (bp):           | none  |
| Predicted mutant band (bp)                     | none | Predicted mutant band (bp)               | 312   |

| 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**

11 5' – CCTATGGTGTCAACAGCCTGCAGC  
 12 5' – CCTGACCCTCTCATACTCTGTTGC  
 13 5' – GGCACATATGCATGGCTTCTGC  
 14 5' – GCAGCTCCACAAACTCCATCCGG

**PCR Genotyping**

3 5' – CTGCAGCGCAATATCACGCTGCTC  
 5 5' – GACCGGCTTGAGCAAGTAGGTGG  
 7 5' – CGAAAGCATAGACACTATGAATG  
 Neo3A 5' – GCAGCGCATCGCCTTCTATC

**Genomic Sequence Deleted:**

AGAGCATGGCGGTCGCGGGCGCCAAGAGGCGCGCGGTTGCGACCCCGCGGCGGCGGCGGCGGAGGAGGAGCGGCAG  
GCGCGGGAGAAGATGTTGGAGGCGCGGCGCGGGGACGGCGCGGACCCCGAGGGCGAAGGCGTGACCCTGCAGCGCAA  
TATCACGCTGCTCAACGGTGTGGCCATCATCGTGGGCACCATCATCGGCTCTGGCATCTTCGTGACGCCCACCGGCGTG  
CTCAAGGAAGCGGGGTGCCCCGGA CTGTCGCTCGTGGTGTGGGCTGTGTGCGGCGTCTTCTCCATCGTGGGCGCACTCT  
GCTACGCGGAGCTGGGCACCACCATCTCCAAGTCGGGCGGCGACTACGCCTACATGCTGGAGGTCTACGGCTCGTTGC  
CCGCCTTCTCAAGCTCTGGATCGAGCTGCTCATTCGGCCCTCCTCGCAGTACATCGTGGCGCTGGTCTTCGCCACC  
TACTTGCTCAAGCCGGTCTTCCCCACTTGTCGGTGCCCGAGGAAGCTGCCAAGCTCGTGGCCTGCCTCTGCGTGCGTA  
AGTAGGGGTCCGGGCTGGGGTGGGGCCGGGCTGGGGCGGGGCCGGGTGGGCG

**Genomic Locus: (the deleted sequence represents nt 11905-12505 in the sequence below)**

[illegible]

GCCCAAGTCATAGACACAGTGAGAAGGACAGAGACAGAGAACTTAAGTTTATAGAGTACAACCTCTGAGCAGAAGAC  
CCAAGATAGGTACAAGGTGGCCTTCAAGACTGAGCAAACCTGTGGAATGTGGTGGCTCATGCCTTTAATCCCAGTACTGG  
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[illegible]

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#### **Targeted Locus:**

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