



## Lexicon Genetics Incorporated – Genentech Project Materials

|                               |          |                               |                                      |
|-------------------------------|----------|-------------------------------|--------------------------------------|
| <b>Genentech ID:</b>          | UNQ2542  | <b>Date of Submission:</b>    | 7-15-04                              |
| <b>Lexicon Contract Name:</b> | DNA047   | <b>Mutation Type:</b>         | X Standard Knock out                 |
| <b>LexVision Name:</b>        | SEC430N1 |                               | <input type="checkbox"/> Conditional |
| <b>Reference accessions:</b>  | AK083229 | <b>Is this gene X-linked?</b> | No                                   |

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**Required Materials:** ☐ pKOS clone DNA(s) \_\_KOS8, KOS26\_\_\_\_\_  
☐ Target Vector DNA \_\_KOS8TV\_\_\_\_\_  
☐ Targeted ES Cell DNA \_\_1E7\_\_\_\_\_  
☐ 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>18+19</b>              | <b>22+23</b>              |
| Restriction Enzyme for Genomic Digest: | <b>SpeI</b>               | <b>NheI</b>               |
| Predicted Wild-type Band (kb):         | <b>8.7 kb</b>             | <b>10.5 kb</b>            |
| Predicted Mutant Band (kb):            | <b>7.5 kb</b>             | <b>21.0 kb</b>            |
| Probe Size:                            | <b>318 bp</b>             | <b>187 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:                                | 7    | 5' Primer Name:                          | Neo3A |
| 3' Primer Name:                                | 11   | 3' Primer Name:                          | 11    |
| Predicted Wild-type Band (bp):                 | 497  | Predicted Wild-type Band (bp):           | none  |
| Predicted mutant band (bp)                     | none | Predicted mutant band (bp)               | 220   |

| 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**

18 5' – TGACAGCTCCCGAACTGAGTGC  
19 5' – CTCTGAACTCTGGGCTAACTTC  
22 5' – CTAGGGCATAGGGTGTAACC  
23 5' – CATCCAGGATATACAACAGCC

**PCR Genotyping**

7 5' – GCCCAGCAACACAGTCATAGC  
11 5' – GCTTTGCCAGCATATCCTCGC  
Neo3A 5' – GCAGCGCATCGCCTTCTATC

**Genomic Sequence Deleted:**

GCCCCGGTAGCCCGCTGGACAAGGGGGGACAATGAGCTGACCGGGTCCGCTCCGAGGAGAGCCAGGAGACCACCACG  
TCCACCATCGTCACTACCACCATCATCACCACGGAGCAGGCCCCAGGTATAGGAGGCTCATCTCCCCTCCTGAAGTCT  
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**Genomic Locus:** *(the deleted sequence represents nt12979-14804-in the sequence below)*

[illegible]

CGGGTCTCCCAGCTTATTACAGGGAGGGAGGATTTCAGTGGCCAGCCAGCTTGCTGATGAAATGTAAATGAACTTAAA  
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[illegible]

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### Selection Cassette:

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### **Targeted Locus:**

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