



## Lexicon Genetics Incorporated – Genentech Project Materials

|                               |           |                               |                                      |
|-------------------------------|-----------|-------------------------------|--------------------------------------|
| <b>Genentech ID:</b>          | UNQ3043   | <b>Date of Submission:</b>    | 8/22/05                              |
| <b>Lexicon Contract Name:</b> | DNA511    | <b>Mutation Type:</b>         | X Standard Knock out                 |
| <b>LexVision Name:</b>        | TRA418N1  |                               | <input type="checkbox"/> Conditional |
| <b>Reference accessions:</b>  | NM_029875 | <b>Is this gene X-linked?</b> | No                                   |

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**Required Materials:** ☐ pKOS clone DNA(s) \_\_pKOS-73\_\_\_\_\_  
☐ Target Vector DNA \_\_pKOS73-TVNeo\_\_\_\_\_  
☐ Targeted ES Cell DNA \_\_2C7\_\_\_\_\_  
☐ Genomic Map

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

|                                        | <u><b>5' Internal</b></u> | <u><b>3' External</b></u> |
|----------------------------------------|---------------------------|---------------------------|
| Name of Probe:                         | 5/6                       | 22/23                     |
| Restriction Enzyme for Genomic Digest: | <b>Bgl II</b>             | <b>Bgl I</b>              |
| Predicted Wild-type Band (kb):         | <b>11.1 kb</b>            | <b>9.9 kb</b>             |
| Predicted Mutant Band (kb):            | <b>14.9 kb</b>            | <b>8.3 kb</b>             |
| Probe Size:                            | <b>315 bp</b>             | <b>316 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:                                | DNA511-3 | 5' Primer Name:                          | DNA511-1    |
| 3' Primer Name:                                | DNA511-4 | 3' Primer Name:                          | IRES-GT.Ext |
| Predicted Wild-type Band (bp):                 | 463 bp   | Predicted Wild-type Band (bp):           | none        |
| Predicted mutant band (bp)                     | none     | Predicted mutant band (bp)               | 258 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:****Southern probes**

|           |                              |
|-----------|------------------------------|
| DNA511-5  | 5' – GGGCAGAGACATAAGCA       |
| DNA511-6  | 5' – CAGGCTAGACTCGATCTCAAT   |
| DNA511-22 | 5' – GATTAGGAATACCATGCCATAGT |
| DNA511-23 | 5' – CCAGAAGAGGGTGTGTAATTC   |

**PCR Genotyping**

|             |                               |
|-------------|-------------------------------|
| DNA511-3    | 5' – CGCCCTTGGTGTGGTAGTCA     |
| DNA511-4    | 5' – GAGGCCCATGAGCAAGTCGTA    |
| DNA511-1    | 5' – AATCGGCCACAGAACTAATC     |
| IRES-GT.Ext | 5' – GCTAGACTAGTCTAGCTAGAGCGG |

CCGGGACCCGGCTGGCGCATGCCTGTCTCCGGCCGGACCGTGGAGCGGGCGGCTGCGGGGCGCGCGGCGCGGAGAGACCGGGACAGCGGGAGAGCGCTCGAGCGCCCCCGGGGAGGCTGGACAGCCCGGGCTCGGCCGAGGACGCTGCTCCGACGCCGCGGGGCATATGCGCATCGCTGGCGACCCGGTCCGGGGAGCAACGGGCGCATCGCCGCGGGCTCTGTTCACCTGCTGTGTTCATCTGCATCTGTTGTTCACAACAAATGGATATGTATACACCGGCTCCCCAACATGAGCCTGACCCCTGGTGCACCTTCTGTGGTACCTGGCTGGGCTTGTACATCTGCCAGAAACTGAACATCTTTGCCCCCAAAAGTCTGCCGCTCTCC AAGCTCCTCTCTCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTACCAACAGCTTTCTCTGCGAACAACACCATAGGCACCTATAGCTGGCCAAGGCCATGACCAACCGGCTGATCATAGCCATCCAAACCTTCTGGTACCGAAGAGATTCTCCGTGAGAATACAGCTACGCTGGTGTAGTAGCTGCCGCTGCCGCTGCGCGAGCCTGTCCCTGCCAGCTACCTGGCTGCTTCCCCGGGAAAACTGAATACACCTTGTTATAGCCTGGCAGCAGCGGAAGCCCATTCCTAATCTTTACTCCACACAGGCCAGGCCCTTATAAAGACCTTGTTTGGGGAGGGGTGAAAAAGGCCATCTCGACACTCCGCTGCTATTTAGTAAATGGGTGTGTCTCTGATAGAAATCTTTAACTGCTGGGATTGATGAGGGAGAGAGCTGCCTTAATGGAACAGTTCAGTGTGTGACGGATATCTGCGAAAGCTCAACCTGGAAGAAAAAGAAATATCCCCAGGAAAACTCGAACCAGAAGTGATAAACATGAAATGGTTTAGCATAAAAATACCTCGGAATACACCTTCAGTGGGCACTGCTGGGGTGCCCTGTGTGTTACATAAAAGGAGATTGTTAAAAATACATTAGCACTAGTGTTTTTCGTTTTTCCAGTCATAATGCTTTCTCCTCTCTGTGTTATGCTTATGTGTAAAGTACTGGTTTTGGGGGATTATTTTATTCCCTGTAAATGTGTGTCCTGTTTCCCTTACAAAGCACACGCACGGATTTCATATTTCTTCCAGATGTAGAGTTGTATGTGAATCTCTGTAGAGAAGGATTGGCAGTTTTCCCCAAAGAAAACTTACAGTGCTCCCCACCCAGCCCCACTGTTATGTTTCTCTAGTGTGTGAAGACATACCTTGAATTTAATCTTCACAGCATTTGCCTCTTTGTCTTTGACAGATTCTTACTGTAGGTGTAATCCTAATAATCTTATACGATGTGAAGTTTCAATCGCTTGAATGGTGTTTGCCGCCCTGGTGTGGTAGTCACGTCCTTTATCAAGTGGTGGTAACTTTTTTTTTCCTTTTTTGCCCTTTTAGTAGACTTTGTAATTTTGAAGCTGTAACCAAGGTTTAGAGACTACAAGTATAGAGACAACAGAC

[illegible]

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[illegible]

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**Selection Cassette:**

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[illegible]

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