



## Lexicon Genetics Incorporated – Genentech Project Materials

|                               |             |                               |                                      |
|-------------------------------|-------------|-------------------------------|--------------------------------------|
| <b>Genentech ID:</b>          | UNQ659      | <b>Date of Submission:</b>    | 10/5/04                              |
| <b>Lexicon Contract Name:</b> | DNA300      | <b>Mutation Type:</b>         | X Standard Knock out                 |
| <b>LexVision Name:</b>        | PSC210N1    |                               | <input type="checkbox"/> Conditional |
| <b>Reference accessions:</b>  | NM_178594.2 | <b>Is this gene X-linked?</b> | No                                   |

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**Required Materials:** X pKOS clone DNA(s) \_\_pKOS/2\_\_\_\_\_  
 X Target Vector DNA \_\_DNA300-FTV1\_\_\_\_\_  
 X Targeted ES Cell DNA \_\_1B9\_\_\_\_\_  
 X Genomic Map

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

|                                        | <u>5' External</u> | <u>3' External</u> |
|----------------------------------------|--------------------|--------------------|
| Name of Probe:                         | 15 + 16            | 19 + 20            |
| Restriction Enzyme for Genomic Digest: | Bam HI             | HpaI               |
| Predicted Wild-type Band (kb):         | 21.8 kb            | 19.5 kb            |
| Predicted Mutant Band (kb):            | 17.0 kb            | 9.9 kb             |
| Probe Size:                            | 329 bp             | 534 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:                                | DNA300 - 28 | 5' Primer Name:                          | Neo3a       |
| 3' Primer Name:                                | DNA300 - 14 | 3' Primer Name:                          | DNA300 - 14 |
| Predicted Wild-type Band (bp):                 | 335 bp      | Predicted Wild-type Band (bp):           | none        |
| Predicted mutant band (bp)                     | none        | Predicted mutant band (bp)               | 405 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**

|             |                            |
|-------------|----------------------------|
| DNA300 - 15 | 5' – GACAGCAAGTAAGACCCTGG  |
| DNA300 -16  | 5' – CAAACTGAATGCATGTGGACC |
| DNA300 -19  | 5' – GGAGTCACATCTGTCATACC  |
| DNA300 -20  | 5' – CCTGACACGCCTACATTACC  |

**PCR Genotyping**

|            |                           |
|------------|---------------------------|
| DNA300 -28 | 5' – GGCAGATCATCTTTTGGAGG |
| DNA300 -14 | 5' – TGAACATCTCAGCTGAGTCC |
| Neo3a      | 5' – GCAGCGCATCGCCTTCTATC |

ATGGCTTCCTTGGGCGAGATCATCTTTTGAGGTAATCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCCTAAATTGAGAACA  
GGGGTGG

[illegible]

[illegible]

[illegible]

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**Selection Cassette:**

GGCCGCTCTAGAGGCCATAGCGGCCATTTAAATGGCGCGCGGGATCCCGGGCCGCTCTAGACTAGACTAGTCTAGCTAGAGAATTCGGCCCCCCCCCCCC  
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**Targeted Locus:**

[illegible]

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[illegible]

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