# CHAPTER 8: APPENDICES

## Appendix A

Blast Analysis

| **Locus name** | **Blast similarites (NCBI)** | **E- value** |
|---|---|---|
| SFO-VJ2-H12 | -unnamed protein product [Tetraodon nigroviridis] | 3E-12 |
| | -hypothetical protein LOC100192208 [Danio rerio]. | 1E-4 |
| | -PREDICTED: similar to paired box gene 6b [Danio rerio]. | 1E-4 |
| SFO-VJ2-H14 | -novel protein similar to vertebrate potassium voltage-gated channel, subfamily H (eag-related) family [Danio rerio]. | 6.3 |
| | -PREDICTED: similar to potassium voltage-gated channel, subfamily H (eag-related), member 3 [Danio rerio]. | 6.3 |
| SFO-T110-H3 | -unnamed protein product [Tetraodon nigroviridis] | 4E-29 |
| | -Cdkn1bl protein [Danio rerio]. | 6E-19 |
| | -PREDICTED: cyclin-dependent kinase inhibitor 1b, like [Danio rerio]. | 8E-19 |
| SFO-T110-H4 | -unnamed protein product [Tetraodon nigroviridis]. | 4.E-1 |
| SFO-T110-H6 | -unnamed protein product [Tetraodon nigroviridis] | 3E-19 |
| SFO-T110-H9 | -unnamed protein product [Tetraodon nigroviridis] | 4E-1 |
| SFO-T110-H10 | -brain specific homeobox | 5.E-28 |
| SFO-T112-H9 | -FTSH11 membrane AAA-metalloprotease **[** *Chlamydomonas reinhardtii* **]** | 1.6 |
| | **-** Mfsd8 major facilitator superfamily domain containing 8 [ *Rattus norvegicus* ] | 3.5 |
| | - FAM27D1 family with sequence similarity 27, member D1 [ *Homo sapiens* ] | 2.7 |
| | -MUT6 DEAH-box RNA helicase [ *Chlamydomonas reinhardtii* ] | 1.E-3 |

| **Locus name** | **Blast similarities (MGRC-Synablast)** | **E value** |
|---|---|---|
| SFO-VJ2-H1 | Danio rerio chromosome 6 genomic contig, reference assembly (based on Zv7_scaffold586)<br>(35670 bp at 5' side: similar to novel pim oncogene family protein)<br>(2000 bp at 3' side: gastrulation brain homeo box 2) | 1e-114 |
| SFO-VJ2-H4 | Danio rerio chromosome 4 genomic contig, reference assembly (based on Zv7_scaffold333) | 0.001 |
|  | Danio rerio chromosome 5 genomic contig, reference assembly (based on Zv7_scaffold416) | 0.005 |
| SFO-VJ2-H5 | Danio rerio chromosome 4 genomic contig, reference assembly (based on Zv7_scaffold333) | 0.001 |
|  | Danio rerio chromosome 5 genomic contig, reference assembly (based on Zv7_scaffold416) | 0.004 |
| SFO-VJ2-H12 | Danio rerio chromosome 3 genomic contig, reference assembly (based on Zv7_scaffold247)<br>Length=5038135<br>(similar to paired box gene 6b) | 9e-12 |
| SFO-VJ2-H13 | Danio rerio chromosome 8 genomic contig, reference assembly (based on Zv7_scaffold793)<br>Length=6180980<br>(YTH domain family, member 1) | 0.0 |
|  | Danio rerio chromosome 24 genomic contig, reference assembly (based on Zv7_scaffold2328)<br>Length=4000201<br>(YTH domain family 3) | 2e-126 |
|  | Danio rerio chromosome 17 genomic contig, reference assembly (based on Zv7_scaffold1711)<br>Length=1168751<br>(YTH domain family 2) | 8e-106 |

| Locus name | Blast similarities (MGRC Synablast) | E value |
|---|---|---|
| SFO-VJ2-H14 | Danio rerio chromosome 9 genomic contig, reference assembly (based on Zv7_scaffold913)<br>Length=1350117<br>(similar to potassium voltage-gated channel, subfamily H) | 4e-17 |
| SFO-VJ2-H15 | Danio rerio chromosome 17 genomic contig, reference assembly (based on Zv7_scaffold1681)<br>Length=717845<br>(similar to KIAA0311) | 3e-21 |
| SFO-VJ2-H21 | Danio rerio chromosome 16 genomic contig, reference assembly (based on Zv7_scaffold1600)<br>Length=58112 | 5e-41 |
| | Danio rerio chromosome 10 genomic contig, reference assembly (based on Zv7_scaffold990)<br>Length=1710968<br>(6795 bp at 5' side: hypothetical protein LOC474330) | 8e-13 |
| | Danio rerio genomic contig, reference assembly (based on Zv7_NA177)<br>Length=193181 | 3e-05 |
| | Danio rerio chromosome 22 genomic contig, reference assembly (based on Zv7_scaffold2147)<br>Length=317542<br>(9920 bp at 5' side: similar to fibrillin 2)<br>(53470 bp at 3' side: translocase of inner mitochondrial membrane 44 homolog) | 0.001 |
| SFO-VJ2-H26 | Danio rerio chromosome 3 genomic contig, reference assembly (based on Zv7_scaffold247)<br>Length=5038135<br>(similar to paired box gene 6b) | 9e-12 |
| SFO-VJ2-H30 | Danio rerio chromosome 19 genomic contig, reference assembly (based on Zv7_scaffold1896)<br>Length=2436711<br>(271679 bp at 5' side: KH domain containing RNA binding signal transduction)<br>(193209 bp at 3' side: similar to karyopherin alpha 6 (importin alpha 7) | 0.004 |

| **Locus name** | **Blast similarities (MGRC Synablast)** | **E value** |
|---|---|---|
| SFO-VJ2-H34 | Danio rerio chromosome 17 genomic contig, reference assembly (based on Zv7_scaffold1712)<br>Length=4649994<br>( 60060 bp at 5' side: similar to protein kinase D1)<br>(11806 bp at 3' side: hypothetical protein LOC368848)<br><br>Danio rerio chromosome 7 genomic contig, reference assembly (based on Zv7_scaffold717)<br>Length=2772546<br>(similar to putative serine/threonine kinase SADA alpha) | 2e-21<br><br>0.001 |
| SFO-VJ2-H36 | Danio rerio chromosome 10 genomic contig, reference assembly (based on Zv7_scaffold1034)<br>Length=413261<br>(hypothetical protein) | 2e-07 |
| SFO-VJ2-H37 | Danio rerio chromosome 6 genomic contig, reference assembly (based on Zv7_scaffold586)<br>Length=669280<br>(35670 bp at 5' side: similar to novel pim oncogene family protein)<br>(2000 bp at 3' side: gastrulation brain homeo box 2) | 9e-116 |
| SFO-VJ2-H41 | Danio rerio chromosome 6 genomic contig, reference assembly (based on Zv7_scaffold586)<br>Length=669280<br>(35670 bp at 5' side: similar to novel pim oncogene family protein)<br>(2000 bp at 3' side: gastrulation brain homeo box 2) | 5e-113 |
| SFO-VJ2-H42 | Danio rerio chromosome 17 genomic contig, reference assembly (based on Zv7_scaffold1712)<br>Length=4649994<br>(60060 bp at 5' side: similar to protein kinase D1)<br>(11806 bp at 3' side: hypothetical protein LOC368848)<br><br>Danio rerio chromosome 7 genomic contig, reference assembly (based on Zv7_scaffold717)<br>Length=2772546<br>(similar to putative serine/threonine kinase SADA alpha) | 2e-21<br><br>0.005 |

| Locus name | Blast similarities (MGRC Synablast) | E value |
|---|---|---|
| SFO-BP8-H1 | Danio rerio chromosome 17 genomic contig, reference assembly<br>(based on Zv7_scaffold1747)<br>Length=194841 | 0.004 |
| SFO-BP8-H2 | Danio rerio chromosome 23 genomic contig, reference assembly<br>(based on Zv7_scaffold2249)<br>Length=481531<br>(similar to pol polyprotein) | 0.005 |
| SFO-BP8-H3 | Danio rerio chromosome 1 genomic contig, reference assembly<br>(based<br>on Zv7_scaffold54)<br>Length=1059805<br>(65544 bp at 5' side: lymphocyte enhancer binding factor 1) | 0.001 |
| SFO-BP8-H4 | Danio rerio chromosome 1 genomic contig, reference assembly<br>(based<br>on Zv7_scaffold54)<br>Length=1059805<br>(65544 bp at 5' side: lymphocyte enhancer binding factor 1) | 0.001 |
| SFO-BP8-H7 | Danio rerio chromosome 10 genomic contig, reference assembly<br>(based on Zv7_scaffold1013)<br>Length=3691107<br>(Iglon2<br>hypothetical protein LOC678534) | 0.004 |
| SFO-BP8-H10 | Danio rerio chromosome 15 genomic contig, reference assembly<br>(based on Zv7_scaffold1492)<br>Length=2670667<br>(neuro-oncological ventral antigen 2) | 0.005 |

# Appendix B

Allele sizes and allele frequency comparison over six populations of *Channa striata*

| Locus | Allele (bp) | Allele Frequency | | | | | |
|---|---|---|---|---|---|---|---|
| | | N. Sembilan | Johor | Penang | Selangor | Terengganu | Kedah |
| SFO-T112-H4 | A (167) | 0.67 | 0.78 | 0.82 | 0.92 | - | 0.78 |
| | B (197) | 0.33 | 0.22 | 0.18 | 0.08 | | 0.22 |
| SFO-T112-H6 | A (268) | 0.28 | - | - | - | - | - |
| | B (278) | 0.72 | | | | | |
| SFO-T112-H6I | A (160) | 0.77 | 0.57 | 0.82 | 0.71 | 0.77 | 0.67 |
| | B (196) | 0.23 | 0.43 | 0.18 | 0.29 | 0.23 | 0.33 |
| SFO-T112-H6F | A (256) | 0.72 | 0.92 | 0.83 | 0.96 | - | 0.97 |
| | B (296) | 0.28 | 0.08 | 0.17 | 0.04 | | 0.03 |
| SFO-BP8-H1 | A (250) | 0.77 | 0.95 | 0.78 | 0.69 | 0.93 | 0.85 |
| | B (270) | 0.20 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | C (280) | 0.03 | 0.05 | 0.22 | 0.00 | 0.07 | 0.15 |
| | D (300) | 0.00 | 0.00 | 0.00 | 0.31 | 0.00 | 0.00 |
| MFW 5 | A (176) | 0.00 | 0.82 | 0.00 | 0.00 | 0.00 | 0.00 |
| | B (192) | 0.53 | 0.18 | 0.00 | 0.00 | 0.00 | 0.00 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
|  | C (210) | 0.47 | 0.00 | 0.00 | 0.00 | 0.00 | 0.73 |
|  | D (226) | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.27 |
|  | E (246) | 0.00 | 0.00 | 0.67 | 0.73 | 0.22 | 0.00 |
|  | F (276) | 0.00 | 0.00 | 0.33 | 0.27 | 0.78 | 0.00 |
| MFW 1 | A (168) | 0.75 | 0.00 | 0.00 | 0.00 | 0.00 | 0.78 |
|  | B (172) | 0.00 | 0.00 | 0.87 | 0.71 | 0.00 | 0.00 |
|  | C (176) | 0.25 | 0.72 | 0.00 | 0.00 | 0.00 | 0.00 |
|  | D (180) | 0.00 | 0.02 | 0.00 | 0.00 | 0.00 | 0.00 |
|  | E (182) | 0.00 | 0.00 | 0.13 | 0.00 | 0.67 | 0.22 |
|  | F (188) | 0.00 | 0.27 | 0.00 | 0.29 | 0.00 | 0.00 |
|  | G (210) | 0.00 | 0.00 | 0.00 | 0.00 | 0.33 | 0.00 |
| MFW 7 | A (176) | 0.43 | 0.13 | 0.00 | 0.00 | 0.00 | 0.00 |
|  | B (188) | 0.00 | 0.87 | 0.28 | 0.00 | 0.00 | 0.00 |
|  | C (194) | 0.57 | 0.00 | 0.72 | 0.00 | 0.87 | 0.00 |
|  | D (204) | 0.00 | 0.00 | 0.00 | 0.00 | 0.13 | 0.00 |
|  | E (246) | 0.00 | 0.00 | 0.00 | 0.90 | 0.00 | 0.93 |
|  | F (268) | 0.00 | 0.00 | 0.00 | 0.10 | 0.00 | 0.00 |
|  | G (274) | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.07 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| MFW 15 | A (151) | 0.00 | - | 0.23 | 0.00 | 0.00 | 0.00 |
| | B (167) | 0.00 | | 0.00 | 0.00 | 0.83 | 0.00 |
| | C (171) | 0.00 | | 0.38 | 0.00 | 0.00 | 0.13 |
| | D (176) | 0.43 | | 0.00 | 0.00 | 0.00 | 0.87 |
| | E (181) | 0.00 | | 0.38 | 0.00 | 0.17 | 0.00 |
| | F (194) | 0.57 | | 0.00 | 0.00 | 0.00 | 0.00 |
| | G (231) | 0.00 | | 0.00 | 0.13 | 0.00 | 0.00 |
| | H (251) | 0.00 | | 0.00 | 0.87 | 0.00 | 0.00 |
| MFW 2 | A (167) | 0.72 | 0.82 | 0.82 | 0.94 | 0.82 | 0.80 |
| | B (181) | 0.28 | 0.18 | 0.18 | 0.06 | 0.18 | 0.20 |

# APPENDIX C

Sequences of an Isolated Fragment of *Channa striata*

GTAGTACAAATCATCATCATCATCTGTACTATAGTAAGACCGGAGGCAGTAGCAGTAACAGATTAAA
GAAGAACATTTTAACGTAAATCTGAATAGATGACTTTTTAAAAATACGTATTTACACACATTTGTAC
AGATTCTAAATGGGAAAGATTTTTATTAGCAGACACTGATATGCTTCATGCTTCCTCTCATGCTTGAA
TCAGATTTAAACTTTCATTTATGCCTGCTATGCATCAAATCAGTGTCTGTAATAAACATGGAAGCTGC
TCTGTTACAGTGGTTAAGAGAACATCACGGATGCAAAACACTTTAATATTCATCAAATCCTTAGAGA
TTTTAAAACACCTGCAACAGCTTCAACTTCTGTATTGTTTTGTTCTGTCAACACTTCAATTGCTGTTTA
TTGTGGTAGAGGTAGCGTACGGAACATACAACTAAAAATACACACTATGAGCAACACATCTATCAG
TGGGATGTGAACAGTTTAACCTGTAGATGTAAAAGTTGATGTCGCTGAATTAGATGCGATGGGACAC
AACACTAAATGAATTAAACCGAGGTCAAGGTGGGTGTGAAGAGAACAGGAAGTGATATGAGTGATG
AGAGTCACCATGGCAGCATTGTCTTTTAGTGCTGCTGATCTGTCATACATGTTCTCTTTACCACCATG
ACACCCTGGAGTGCAAGAAAGTGTGTGTGTGTGTGTGTAGATAAGAGAAAGCCAGAGATAGGGAGA
ACCATAACTTGATGACAGCCCACTGCTGAGTTCAGCTCACTGGGTGTAAAATTATCATTATGATGAT
GATGATGATCGGTAAGGG

Sequence of an isolated fragment, containing microsatellites (indicated in red). The positions of primers are indicated in blue.

(Primer SFO-T112-H4)

```
CCCTAAGCGATCATCATCATCATCTTTTTAACCTTCCTCCTCCTAGACATCGCAGTGGTGGACATGAGC
GACGTGTTCCGCCAGCCCTCGTTATTCTACCACCTGGGCGTGAGGGAGAGCTTCGACATGGCCAATAA
TGTCATCCTGTACCACGACACTGACCTCGACACCGCACAGTCACTGAAGGTAACACACACACACACAC
ACACATGCACACACGCACACAGACACACACCTCTATTCCATGGATGCCATTCCTTCACAGTTCCTTGG
AACAAAGTGATCCGCTAAGTTATTTACAGACAAGTGTGAGTGTGGTAATACTGGTCAGGCCTGCACTG
AGCTGCCGGCTGTTGCCAGCAGGACTGCAGCAGTGCAGCTCAAAAACACACAAGAACGCACAACATA
CGGCGGCTTCCGATGTTTGGACCCAGTCTCACAGCTGTTTGTCTCCTTGCAGGACATGGTGGCACAGA
AAAACACAGTAAGTTTCTGAGTGGCTGCGTGTGATTTACGCGCACGCTCTGTCCCGTGCTATTTGTGGA
ATAATATTCGTGACAAGTGCTGTTGGTCCTCTCATGCACACATGCTTACATGAATTCATGTCTACACGC
TTCCCCTTCCTCTCTCTCTCATGCATCCACATTATTACACACACACACACACACACACACACACACA
CACACACACACACACACAACAAAACATGTGTGGCAGACTTGTGTAATAGTGTGTTGAAAAATACATTA
AACACAATAACCTTACTTTTATTGGGGTGTATGGTGTTTGTGTGTGTGTGCGTGCGTGCGTGCGTGCTT
GTGTGTGTGTGTGTGTGTGTGTGGAATAGGCTGCTCGTTCTCCAGCATTAGGTTTTCCATGGGTTCAGT
TGCCTCCAGAGTACAGAGGCTCTGGATTGCGCAAAAAAGTAGGTACCGTTCTGCAGCAAAGCATGCTG
GGAGTTTTACGCAAAACTTACTACTAATAATAGCAAACATGGAGGAGGGCTCCAGGCCACTGACCTCC
CCCATGGGGATGTTGTGTTGAAACAAAAAATGAAAATCCCCTTTAAACAAACATGGCAACTTCCTAAA
AGCACCGGGAAAACAAATTGGAAATGAGTTTTGGACCGTGGGAGATATCCGGTGTTTTTGGAAGAAA
AGAAGAAGAGAATTGGCCCCCACACCGGGA
```

Sequence of an isolated fragment, containing microsatellites (indicated in red). The positions of primers are indicated in blue.

(Primer SFO-T112-H6)

CCCTAAGCGATCATCATCATCATCTTTTTAACCTTCCTCCTCCTAGACATCGCAGTGGTGGACA
TGAGCGACGTGTTCCGCCAGCCCTCGTTATTCTACCACCTGGGCGTGAGGGAGAGCTTCGACA
TGGCCAATAATGTCATCCTGTACCACGACACTGACCTCGACACCGCACAGTCACTGAAGGTAA
CACACACACACACACACACATGCACACACGCACACAGACACACACCTCTATTCCATGGATGCC
ATTCCTTCACAGTTCCTTGGAACAAAGTGATCCGCTAAGTTATTTACAGACAAGTGTGAGTGTG
GTAATACTGGTCAGGCCTGCACTGAGCTGCCGGCTGTTGCCAGCAGGACTGCAGCAGTGCAGC
TCAAAAACACACAAGAACGCACAACATACGGCGGCTTCCGATGTTTGGACCCAGTCTCACAGC
TGTTTGTCTCCTTGCAGGACATGGTGGCACAGAAAAACACAGTAAGTTTCTGAGTGGCTGCGT
GTGATTTACGCGCACGCTCTGTCCCGTGCTATTTGTGGAATAATATTCGTGACAAGTGCTGTTG
GTCCTCTCATGCACACATGCTTACATGAATTCATGTCTACACGCTTCCCCTTCCTCTCTCTCTCA
TGCATCCACATTATTACACACACACACACACACACACACACACACACACACACACACACACAC
ACAACAAAACATGTGTGGCAGACTTGTGTAATAGTGTGTTGAAAAATACATTAAACACAATAA
CCTTACTTTTATTGGGGTGTATGGTGTTTGTGTGTGTGTGCGTGCGTGCGTGCGTGCTTGTGTGT
GTGTGTGTGTGTGTGTGGAATAGGCTGCTCGTTCTCCAGCATTAGGTTTTCCATGGGTTCAGTT
GCCTCCAGAGTACAGAGGCTCTGGATTGCGCAAAAAAGTAGGTACCGTTCTGCAGCAAAGCAT
GCTGGGAGTTTTACGCAAAACTTACTACTAATAATAGCAAACATGGAGGAGGGCTCCAGGCCA
CTGACCTCCCCCATGGGGATGTTGTGTTGAAACAAAAAATGAAAATCCCCTTTAAACAAACAT
GGCAACTTCCTAAAAGCACCGGGAAAACAAATTGGAAATGAGTTTTGGACCGTGGGAGATATC
CGGTGTTTTTGGAAGAAAAGAAGAAGAGAATTGGCCCCCACACCGGGA

Sequence of an isolated fragment, containing microsatellites (indicated in red). The positions of primers are indicated in blue.

(Primer SFO-T112-H6I)

CCCTAAGCGATCATCATCATCATCTTTTTAACCTTCCTCCTCCTAGACATCGCAGTGGTGGACA
TGAGCGACGTGTTCCGCCAGCCCTCGTTATTCTACCACCTGGGCGTGAGGGAGAGCTTCGACA
TGGCCAATAATGTCATCCTGTACCACGACACTGACCTCGACACCGCACAGTCACTGAAGGTAA
CACACACACACACACACACATGCACACACGCACACAGACACACACCTCTATTCCATGGATGCC
ATTCCTTCACAGTTCCTTGGAACAAAGTGATCCGCTAAGTTATTTACAGACAAGTGTGAGTGTG
GTAATACTGGTCAGGCCTGCACTGAGCTGCCGGCTGTTGCCAGCAGGACTGCAGCAGTGCAGC
TCAAAAACACACAAGAACGCACAACATACGGCGGCTTCCGATGTTTGGACCCAGTCTCACAGC
TGTTTGTCTCCTTGCAGGACATGGTGGCACAGAAAAACACAGTAAGTTTCTGAGTGGCTGCGT
GTGATTTACGCGCACGCTCTGTCCCGTGCTATTTGTGGAATAATATTCGTGACAAGTGCTGTTG
GTCCTCTCATGCACACATGCTTACATGAATTCATGTCTACACGCTTCCCCTTCCTCTCTCTCTCA
TGCATCCACATTATTACACACACACACACACACACACACACACACACACACACACACACACAC
ACAACAAAACATGTGTGGCAGACTTGTGTAATAGTGTGTTGAAAAATACATTAAACACAATAA
CCTTACTTTTATTGGGGTGTATGGTGTTTGTGTGTGTGTGCGTGCGTGCGTGCGTGCTTGTGTGT
GTGTGTGTGTGTGTGTGGAATAGGCTGCTCGTTCTCCAGCATTAGGTTTTCCATGGGTTCAGTT
GCCTCCAGAGTACAGAGGCTCTGGATTGCGCAAAAAAGTAGGTACCGTTCTGCAGCAAAGCAT
GCTGGGAGTTTTACGCAAAACTTACTACTAATAATAGCAAACATGGAGGAGGGCTCCAGGCCA
CTGACCTCCCCCATGGGGATGTTGTGTTGAAACAAAAAATGAAAATCCCCTTTAAACAAACAT
GGCAACTTCCTAAAAGCACCGGGAAAACAAATTGGAAATGAGTTTTGGACCGTGGGAGATATC
CGGTGTTTTTGGAAGAAAAGAAGAAGAGAATTGGCCCCCACACCGGGA

Sequence of an isolated fragment, containing microsatellites (indicated in red). The positions of primers are indicated in blue.

(Primer SFO-T112-H6F)

CGAATTCCAAGCTAAGGTTTGTTGTTGTTGTTGTTGCTGTTTGTGGTTTAGCAGAGCAAGTATA
GAAAATAGACACATTTATCTACTGTATATTGCATATGTTGCAGCATGTTCGTCAACAATGAATG
AGGTCATCATGTCCAGTTGAGTTTTGCACAAAAGATCCCCTGCCACCAGAAAGAAAATTCAAA
ACACACAATAAATTAAACTGACCTGCCTGACTCCCTGACAATGTGGTGTGAAACTGGGAATTA
TAACAGTAACAAACAAAAAAATGGTGCAAAAATATTCCAGAGATGAAAGATTCTGCTTACAA
CTCGACAAGATGAAGCCAAAGTTTTTGTGGACCAGGGCGGCTGCAGGTTGTCCCATGACGACC
CCCCCAGGTCCTCGATTCAGTACCCAGTGCTACAGTTACTTGACTCACGAGTAGGGCTGCAAA
CGACTTCACGTCACTAACTTTTTATTGTGGGGGGTACTGGTGATTCCATTTTTCCACATTAGAC
AAAACAGCTGAAATACTTTCTCTTTTTGACTTGGGGACATTGACCATTTATCTATCTCTAAGGC
AAAAACTTTATGGACCACAGACACGCTCAGCTATTTCTCTCACTCTCTCTTTCTGTGAATACTG
GCTTTTCTTTTCTTTGGTTATTTAAAACTTAATTGGTAGTGTAGAGAACATCAGCAGAAAACAT
GTCAGCACTTTAACAGGTCCTCTTTTTTCTCCCCTCAGATGTGTTGCACAAGCACCTTATCCTTC
ACGGCTCTGCGCCAAAAATTGAGATGAACAGTGGTATCCAGATTCTTATTTAAAACTAAACAA
CAACAACAACAAATATA

Sequence of an isolated fragment, containing microsatellites (indicated in red). The positions of primers are indicated in blue.

(Primer SFO-BP8-H1)

TAATTAGAGACTCCTCCTCCTCCTATTACGCACAGCAGCTCATGTCCTCCTACCTCCAGCTC
AAAGCAATGTCAAATCATTTCAATTAAGCAGAAATCAATAAATCACCTCCTATCAACCGGCTA
TGTATGAAATTACCCCGTGTGGCGCATTTATTGATTTAGCAGAAATTAAAAATGCTGCTGGAA
GTGCGGCTCGTTCGGGCTCACGCGCTGTTAAAAAGGAAATTCATAACCAAGACGCGTAAAAAA
GGGGGGGAAATTAATAGAGAGCACGAACCCTGAATTAGCTCAGTAAACCAATCACCCAAATA
CTTTCCCGGACTCGTTTTTGGTCGGCGCTTCTGTTTGAGGTGACACCGACGAGCCGAGCACGTG
GCCCCGCTGATTGCATTGTGTGAACTTCCTACAGCGACAGTCCTTTAAAAAACTCGGCAAAACT
CGCGTCCCGTCCAGCAAACGCCTCTAAATGTGTGAAACAACGCAGGTGCAGAGTTTCAAAGGT
GTTTCCATGAGCCATAACCGCTTCCTCGAATTTTTTTCTAATTTAATTGTGCACGGACGCAAATT
GTCTAATTATAATACGTCCTAGCAAATCAGAGAAGTGCTCGTTTCCGTTTTTAAAATTTAGTCG
CAGTGCAAAGCAACGTTTCCAGCCTCGTGATGACATTATGGCATAAAATTCTACACAAACACA
CATAAAACACACACTCTGCTGCTGTTTACCTTGTTTTATGGCGTGGATAAAGTAAAACGTCGGC
ATTGCTGGAGAGGCATTCGTGTGTCGGATAAAGTGTCCCGCATCAAACGCATCCCTGTCCACT
GTCCTCTGTCCTCCATGCGGGGCCACACAGGTAGTTGGACGGTATAGCGTTAACCCCCCATCCC
TCGAATGCACCAACTCAGCAAANACTCGAACAGGGGAGGAGGAGGAGAATCTGAAAAGAGAT
CTGGATCCCTCAAAGTCACCTGCAGGCATGCAACCTGGCTAATCTGGTCTAGCTGTTCCTGGTG
AAATGTTATCCGCTCCAATTCCC

Sequence of an isolated fragment, containing microsatellites (indicated in red). The positions of primers are indicated in blue.

(Primer SFO-VJ2-H38)

TCAGTGAAAGTTGTTGTTGTTGTTTTTGCCTTGACTTTTTAAGGACAAGGGAAATTCAATTCAA
TAATTCAAATCATATTTGATCTGTATTGATTTTAACATGAAGTATTATGCCAAAACATGTTTTTC
TACTCTGCATTGCCTTTTCTTTTGATACACTAGTACCAATAAACCGGATTTGTAAGTCTGTCTCT
ATTTCATTTTATATAAACACAATTTTCTGGCCGACATTTCCTTAAGTGAATAAAGAACTTTTGTT
ATGGAGCAATATGAATCTCTTTTTATAAATATTTTAGCTACGTGGCAATTTTTAACATATTGTAT
CAAACAGCTTTCAACCCCCGTGTGTTTCTCCCCAGGTGAAACCTCTTCAGCTTTACAGTTTCCA
AAGTCTGGCTACCTGTCTCAGAGCAAGGGACAAGCAAAGCGAAAGAAGACAGCGGGAATGAG
AGAAAGAGACAGTCATGGTCTAGCCAATGAATTCAGACAAAGGGCAAGCAGAGGAGACACTG
TCTGAGGGAAGAGGAGGGAGAAAAAGTGCTCTGTTTTATGATAGCAACAATTTTAGTAAAATT
ACACAAAGCATTAAAAAGAATGGTCACTGAGGGAGATGGAAAAATCGGTAGGCCATCAAAAA
GTCAATGGGAGCAGTGAGATCATAAAGTGGACAAAGGCAGTAAAGTGCCAAACGATAGGTAA
GATATGAAAAATATCTAAGCTTTGTTATCATTCTACATGTATGTAGCATGTGAGAGAGCTGACA
AGCTCCAGATCGACGTGACACAGGTGTGCTACTAACACCAGGGGAAGAGAGGACAGGGTCGT
AACACTGTCCACGGTGTGTGGACACTGACGTTGTGTTTGATTCTTTTTGTAAAGCCCTTTCTCTG
CCTTAGTGTCTGTGGTTCATTGTCTGGTCGCTGTACTGGCTGAATGTGTGTGTGTGTGTGTGTGT
GTGTAAATGTGATATCGTTGGCATCATTGTGCCAAATCCTCCCCACATGCTTTCAGTCCCTCCA
CTCGCTGCATGTGAATTTTTCTTTCACAATATGCACAATCCAGTCAAACGTATTTCCTTGTTTCT
TGAACGTCAT

Sequence of an isolated fragment, containing microsatellites (indicated in red). The positions of primers are indicated in blue.

(Primer SFO-BP8-H2)