### Tetranucleotide repeat polymorphism at the human beta-actin related pseudogene 2 (ACTBP2) detected using the polymerase chain reaction

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**Source/Description:** The polymorphic repetitive sequence (AAA-G)\textsubscript{T1} AA (AAAG)\textsubscript{T1} is located in the 5' flanking sequence of human beta-actin pseudogene 2, beginning at base 176 (1). The sequence was identified from a search of the EMBL and GenBank DNA sequence databases (GenBank V00481). The predicted amplified sequence length is 519 bp.

**Primer Sequences:**

- 5'GAGAGAGAGAAAGGAAGG3'
- 5'ATGGGTACTTCAGAGTCAG3'

**Frequency:**

<table>
<thead>
<tr>
<th>Allele</th>
<th>Size (bp)</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1</td>
<td>519</td>
<td>0.14</td>
</tr>
<tr>
<td>A2</td>
<td>513</td>
<td>0.24</td>
</tr>
<tr>
<td>A3</td>
<td>501</td>
<td>0.32</td>
</tr>
<tr>
<td>A4</td>
<td>485</td>
<td>0.08</td>
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<tr>
<td>A5</td>
<td>467</td>
<td>0.22</td>
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</tbody>
</table>

Heterozygosity 68% (estimated using 40 unrelated Caucasian individuals)

**Mendelian Inheritance:** Observed in CEPH families 1029 (Utah pedigree K1345) and 982 (Utah pedigree K1331).

**Other Comments:** 30 cycles of PCR were performed (2) using 200–300 ng of genomic DNA and 150 ng of each primer in a final reaction volume of 50 μl. The reaction mix contained a final magnesium concentration of 2.5 mM, and 10% dimethyl sulfoxide (DMSO). Primers were designed using the program PRIMER (3).

**Chromosomal Localization:** 5.

**References:**


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### Dinucleotide repeat polymorphism in the human alpha-cardiac actin gene, intron IV (ACTC), detected using the polymerase chain reaction

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**Source/Description:** The polymorphic sequence (TG)\textsubscript{T1} lies in intron IV, 61 bases 5' from the start of exon 5 of the human alpha-cardiac actin gene (1). The sequence was identified from a search of the EMBL and GenBank DNA sequence databases (GenBank J00072). The predicted amplified sequence length is 233 bp.

**Primer Sequences:**

- 5'TCAGAGACAAATGTTACACACG3'
- 5'GACATTGTTGGCATACAGG3'

**Frequency:**

<table>
<thead>
<tr>
<th>Allele</th>
<th>Size (bp)</th>
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<tbody>
<tr>
<td>C1</td>
<td>239</td>
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<tr>
<td>C2</td>
<td>221</td>
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<tr>
<td>C3</td>
<td>219</td>
<td>0.23</td>
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</table>

Heterozygosity 41% (estimated using 40 unrelated Caucasian individuals)

**Mendelian Inheritance:** Observed in CEPH families 1029 (Utah pedigree K1345) and 982 (Utah pedigree K1331).

**Other Comments:** 30 cycles of PCR were performed (2) using 200–300 ng of genomic DNA and 150 ng of each primer in a final reaction volume of 50 μl. The reaction mix contained a final magnesium concentration of 2.0 mM, and 10% dimethyl sulfoxide (DMSO). Primers were designed using the program PRIMER (3).

**Chromosomal Localization:** 15q11-qter.

**References:**