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<!DOCTYPE HTML PUBLIC "-//W3C//DTD HTML 4.0 Transitional//EN">
<html>

  <head>
    <title>Mouse Medaka MHC - Vertebrate Genomics</title>
    <meta http-equiv="Content-Type" content="text/html;
charset=iso-8859-1">
    <meta http-equiv="content-language" content="en">
    <meta http-equiv="Reply-to"
content="wwwadm@molgen.mpg.de">
    <meta name="robots" content="index, follow">
    <meta name="allow-search" content="yes">
    <meta http-equiv="Content-Script-Type"
content="text/javascript">
    <meta http-equiv="Content-Style-Type" content="text/css">
    <link rel="stylesheet" type="text/css" href="ags2001.css">
    <script language="JavaScript" src="mainjs2001.js"
type="text/javascript">
<!--
    self.defaultStatus = document.title;
// -->
</script>
  </head>

  <body bgcolor="#FFFFFF" text="#000000" link="#007B70" alink="#
990000" vlink="#2E90B4" leftmargin="0" topmargin="0" marginwidth="0"
marginheight="0">
    <table cellpadding="0" cellspacing="0" border="0"
width="100%" height="120">
      <tr valign="top" align="left" height="88">
        <td rowspan="2" width="7%" valign="middle"
align="center"></td>
        <td align="left" rowspan="2" valign="middle"
width="83%">
          <div align="left">
            <font
face="Verdana,Arial,Helvetica,sans-serif" size="+2">MAX PLANCK
INSTITUTE for MOLECULAR GENETICS</font></div>
          </td>
        <td align="left" rowspan="2" valign="middle"
width="10%"><a href="http://www.molgen.mpg.de/"><font size="-3">home
</font></a>
          <p><a
href="http://www.molgen.mpg.de/contact.html"><font size="-3">contact
</font></a></p>
          <p><a
href="http://www.molgen.mpg.de/search.html"><font size="-3">search
</font></a></p>
        </td>
      </tr>
      <tr valign="top" align="left"></tr>
      <tr valign="top" align="left">
        <td height="36" colspan="2" align="left"
bgcolor="#E3E4E0" background="mhead2001_brownline_back.gif">
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border="0" height="36">
            <tr valign="top" align="left">
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valign="middle" height="36" nowrap background="mhead2001
_titlesmall_blank.gif"><font class="catsmalltitle"
face="Verdana,Arial,Helvetica,sans-serif" color="#FFFFFF" size="-2">
&nbsp;<a href="http://www.molgen.mpg.de/research/lehrach/"></a>Vertebrate Genomics</font></td>
        <td height="36"
valign="middle" nowrap align="left"><font class="catsubtitle"
face="Verdana,Arial,Helvetica,sans-serif" color="#000000" size="+1">
Mouse - Medaka - MHC</font></td>
        <td height="36"
valign="middle" nowrap width="10" align="left"></td>
        <td height="36"
valign="middle" nowrap align="left"><font size="+1">/Projects/Medaka
transcriptome analysis</font></td>
    </tr>
</table>
</td>
    <td height="36" align="left"
bgcolor="#E3E4E0" background="mhead2001_brownline_back.gif"
width="10%"></td>
</tr>
</table>
<br>
<br>
<table cellpadding="0" cellspacing="0" border="0">
    <tr valign="top" align="left">
        <td width="197">
<br>
        </td>
        <td class="tdmain"><!-- START OF CONTENTS -->
        <p class="maintext">
        <h2>HELP - How to use EST Medaka
database</h2><br>
        <table width = "80%">
        <tr><td><b>Search for clone or cluster
information</b></td></tr>
        <tr><td valign = "top">Clone_id</td>
        <td>Searches for clones matching the input pattern. Clone ids are
saved
        <td>
        according to their cDNA library
        (gastrula clones match Med1015*; neurula clones match Med1028;
        organogenesis clones match Med1030*;
        ovary clones match Med1029*; OL clones match Med2000*). You do
        not need to use wild cards, just type
        Med1015 to get all gastrula clones.</td></tr>
        <tr><td valign = "top">
        UniqueSequence_id</td><td>Searches for EST clusters. EST cluster
        follow the pattern
        CL*Contig* (example: CL1Contig1).
        Singletons keep their tracefile identity. Only these clusters or
        singletons were annotated.</td></tr>
        <tr><td valign = "top">Rearray1_id</td>
        <td>Searches for clones according to their coordinates in first
        rearray. Identifiers are build like
        ReI_*, where * are normal plate and well coordinates (example:
        ReI_1A01 for Rearray1 clone in plate 1,
        well A01). Matching clones are separaed in those having
        sequences and those for which no
        sequence is available.</td></tr>
        <tr><td valign = "top">Rearray2_id</td>
        <td>Searches for clones according to their coordinates in second
        rearray. Identifiers are build like
        ReII_*, where * are normal plate and well coordinates (example:
        ReII_1A1 for Rearray1 clone in plate 1,

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well A01). Matching clones are separated in those having
sequences and those for which no
sequence is available.</td></tr>
<tr><td td valign = "top">OFPcluster_id
</td><td>Searches for clusters obtained by <a
href="http://www.molgen.mpg.de/
~rodent/OFP_project_mod.html"> Oligonucleotide fingerprinting
(OFP)</a> analysis. Cluster should
represent one gene. According to EST clustering results
fingerprinting clusters were changed,
so some OFP clusters were put together, therefore you will find
"old" and "new" OFP cluster. In our
analysis we included clones from four different libraries,
gastrula, neurula, organogenesis and
ovary. Their appearance in different fingerprinting clusters was
statistically evaluated and
overexpressed or underexpressed clusters or no changes were recorded.
This was only
applied to "new" OFP clusters. Clones
left as singletons after fingerprinting analysis are identified
by their clone name.</td></tr>
<tr><td td valign = "top">Trace_id</td>
<td>Search for clones according to their traces. Identifiers match
McF00*-MGRbdl, where * stands for plate
coordinates like 21A11; identifiers for plate 1 are different
with McF0001MGR-*bdl</td></tr>
<tr><td td valign = "top">
AnnotationKeyword</td><td>Searches for any keyword you may think of.
</td></tr>
<tr><td><b>Search for abundance profile
</b></td></tr>
<tr><td td valign = "top">Expression
</td><td>Searches for clusters obtained by <a
href="http://www.molgen.mpg.de/
~rodent/OFP_project_mod.html"> Oligonucleotide fingerprinting
(OFP)</a> analysis which show a certain
abundance profile. In our analysis we included clones from four
different libraries,
gastrula, neurula, organogenesis and
ovary. Their appearance in different fingerprinting clusters was
statistically evaluated and
overexpressed ("1") or underexpressed ("-1") clusters or no changes
("0")
were recorded. If you are not
interested for abundances of one library you may choodes the "x"
option.</td></tr>
<tr><td><b>Blast your sequence</b></td>
<td>This is not working, yet!</td></tr>
</table>
<br>
NA always stands for 'not available'.
</p>
</td>
</tr>
</table>
<!-- PAGE FOOTER -->
</body>
</html>

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