Troubleshooting for Variant Confirmation

Test Code: SVTBL
Turnaround time: 3 weeks
CPT Codes: 81479 x1

Condition Description

THIS PAGE IS FOR BOTH OF THE FOLLOWING TESTS

VARIANT CONFIRMATION BY SANGER SEQUENCING (SVCNF)

TROUBLESHOOTING FOR VARIANT CONFIRMATION (SVTBL)

Test definition:

This test includes primer design, PCR amplification and Sanger sequencing to confirm variants that fall into the different categories listed below:

a. Single nucleotide variants corresponding to a single genomic position.
b. A genomic region of interest corresponding to a single amplicon.
c. Small (less than 33 bp) deletion, duplication or indel.

Process:

Variant confirmation by Sanger sequencing (test code SVCNF) includes primer design, PCR amplification, Sanger sequencing, and sequence analysis to detect the presence or absence of a given variant detected by NGS. Most variants can be detected by this routine analysis.

A separate custom test, “troubleshooting for variant confirmation” (test code SVTBL), will confirm variants that are not detected by routine analysis and require additional troubleshooting for accurate identification. These include variants located within DNA segments that are difficult to amplify or sequence due to DNA composition (e.g., highly repetitive sequences, regions where primer design is challenging, etc.). Our team assesses variant requests to determine the likelihood of success and will notify you if the variants cannot be accepted.

Results are reported in a spreadsheet format without interpretation about variant classification. A formal report is not issued with these tests.

reported in a spreadsheet format without interpretation about variant classification. A formal report is not issued with these tests.
Indications

Variant confirmation by Sanger sequencing (SVCNF) and Troubleshooting for variant confirmation (SVTBL) are custom test services. These services are for clinical or research laboratories that require confirmation of variants detected by NGS platforms. Certain variants may not be amenable to confirmation. Prior to initiation of testing, our team assesses each variant request to determine the likelihood of success and to assign the proper SVCNF or SVTBL test code.

Methodology

Suitable primers are designed to amplify the region of the genomic DNA surrounding the variant, or the region of interest, by PCR. Amplicons are sequenced in both the forward and reverse directions.

Detection

Detection rate is determined by the sequence characteristics of the region(s) of interest.

Specimen Requirements

Type: Saliva
Specimen Requirements:
Oragene™ Saliva Collection Kit
Orangene™ Saliva Collection Kit used according to manufacturer instructions. Please contact EGL for a Saliva Collection Kit for patients that cannot provide a blood sample.

Specimen Collection and Shipping:
Please do not refrigerate or freeze saliva sample. Please store and ship at room temperature.

Type: DNA, Isolated

Specimen Requirements:
Microtainer
8µg
Isolation using the Perkin Elmer™Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping:
Refrigerate until time of shipment in 100 ng/µL in TE buffer. Ship sample at room temperature with overnight delivery.

Type: Whole Blood (EDTA)

Specimen Requirements:
EDTA (Purple Top)
Infants and Young Children (2 years of age to 10 years old): 3-5 ml
Older Children & Adults: 5-10 ml
Autopsy: 2-3 ml unclotted cord or cardiac blood

Specimen Collection and Shipping:
Ship sample at room temperature for receipt at EGL within 24 hours of collection. Do not refrigerate or freeze.

Special Instructions

To order the test, clients are asked to fill out a template spreadsheet. Request a digital copy of this template by emailing eglcm@egl-eurofins.com

Assessment and test code assignment will be performed by EGL Genetics prior to initiation. Note that results are reported back in a spreadsheet as well.

Spreadsheet Template for Test Order:

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
<th>G</th>
<th>H</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Sample ID 1 (optional)</td>
<td>Sample ID 2</td>
<td>Genomic Start (GRCh37/human genome build 19)</td>
<td>Genomic End (GRCh37/human genome build 19)</td>
<td>Variant</td>
<td>Transcript (e.g. NM_000492.3)</td>
<td>Notes (unipositivity, mosaicism?)</td>
</tr>
<tr>
<td>2</td>
<td>C1XXX-KB-XXXX</td>
<td>A-00XXXX-D</td>
<td>3141495</td>
<td>3141495</td>
<td>c.215C&gt;G (p.S72X)</td>
<td>NM_002627.4</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>C1XXX-xx-XXXX</td>
<td>5XXXDD1</td>
<td>44103704</td>
<td>44103704</td>
<td>deep intronic</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Disclaimer: This information is confidential and subject to change without notice. It may not be reproduced in whole or part unless authorized in writing by an authorized EGL representative.

09-11-2019 3 / 3