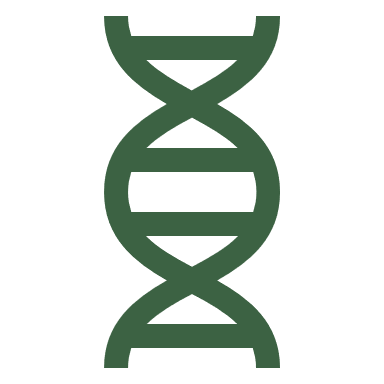
检测报告

**Testing Report**

|  |  |  |  |
| --- | --- | --- | --- |
| **方案编号Protocol ID：** | **JAB-21822-1007** | **厦维项目编号Project ID：** | **XW2402** |

**送检信息 General Information**

|  |  |  |  |
| --- | --- | --- | --- |
| 受试者信息 Patient Information | | | |
| 研究中心Site Name | **{{sample.site\_name}}** | **中心编号Site ID** | **{{sample.site\_ID}}** |
| 受试者编号Subject ID | **{{sample.subject\_ID}}** | **疾病类型Disease Type** | **{{sample.primary\_disease}}** |
| 性别Gender | **{%if sample.gender==”男”%}☑男Male □女Female{%elif sample.gender==”女”%}□男Male ☑女Female {%else%}□男Male □女Female {%endif%}** | **出生年份Year of Birth** | **{{sample.birthday}}** |

|  |  |  |  |
| --- | --- | --- | --- |
| 样本信息 Sample Information | | | |
| 样本编码Sample ID | **{{sample.specimen\_parent\_id}}** | **样本类型Sample Type** | **{%if sample.specimen\_type == “手术”%}☑ 手术 □ 活检{%else%}□ 手术 ☑ 活检{% endif%}** |
| 样本数量Sample Amount | **{{sample.tissue\_specimen\_amount}}** | **采集日期Sample Collection Date** | **{{sample.tissue\_collection\_date}}** |
| 接收日期 Reception Date | **{{sample.tissue\_date\_received}}** | **切片日期Sectioning Date** | **{{sample.section\_date}}** |
| 报告日期 Report Date | **{{sample.report\_date}}** | **取材部位Anatomic Site** | **{{sample.anatomic\_site}}** |
| 检测实验室  Testing laboratory name | **上海厦维医学检验实验室有限公司**  **Shanghai Xiawei Medical Laboratory** | | |

**备注 NOTE**

{%p if lib\_quality\_control.macrodissection\_performed==”是”%}

{%p if lib\_quality\_control.lib\_dna\_qc.tumor\_content\_macrodissection\_performed\_num>= 0.2 and qc.dna\_data\_qc.final == “T”and lib\_quality\_control.lib\_dna\_qc.library\_concn\_num>= 10%}

□ 检测结果通过。即关键质控点合格（如肿瘤含量≥20%、文库浓度合格且数据QC合格）。

**This is a PASS report. The key quality control parameters are pass (e.g., tumor content ≥20% , library concentration and pass data QC).**

{%p elif lib\_quality\_control.lib\_dna\_qc.tumor\_content\_macrodissection\_performed\_num < 0.2 or qc.dna\_data\_qc.final != “T”or lib\_quality\_control.lib\_dna\_qc.library\_concn\_num >= 5%}

□ 检测结果合格。此样本由于某些原因，关键质控点低于合格标准（肿瘤含量＜20%或文库浓度低于合格标准或数据QC低于合格标准）。本报告可以确认检测出的基因变异，但是不能确认是否有其它变异未能检出。

**This is a QUALIFIED report. For some reasons, the key quality control parameter of this specimen is lower than the PASS standard (tumor content <20% or the Library concentration is lower than the PASS standard or the data QC is lower than the PASS standard). We can confirm the presence of genomic alterations detailed in this report, but we cannot confirm the absence of other alterations.**

{%p endif%}

{%p else%}

{%p if lib\_quality\_control.lib\_dna\_qc.tumor\_content\_num>=0.2 and qc.dna\_data\_qc.final == “T”and lib\_quality\_control.lib\_dna\_qc.library\_concn\_num>= 10%}

□ 检测结果通过。即关键质控点合格（如肿瘤含量≥20%、文库浓度合格且数据QC合格）。

**This is a PASS report. The key quality control parameters are pass (e.g., tumor content ≥20% , library concentration and pass data QC).**

{%p elif lib\_quality\_control.lib\_dna\_qc.tumor\_content\_num < 0.2 or qc.dna\_data\_qc.final != “T”or lib\_quality\_control.lib\_dna\_qc.library\_concn\_num >= 5%}

□ 检测结果合格。此样本由于某些原因，关键质控点低于合格标准（肿瘤含量＜20%或文库浓度低于合格标准或数据QC低于合格标准）。本报告可以确认检测出的基因变异，但是不能确认是否有其它变异未能检出。

**This is a QUALIFIED report. For some reasons, the key quality control parameter of this specimen is lower than the PASS standard (tumor content <20% or the Library concentration is lower than the PASS standard or the data QC is lower than the PASS standard). We can confirm the presence of genomic alterations detailed in this report, but we cannot confirm the absence of other alterations.**

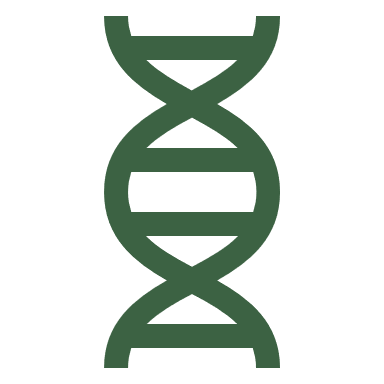
{%p else%}

□ 检测结果失败。本例受试者提供样本不足或质量欠佳以致无法完成实验，不能够满足测序环节的最低要求。

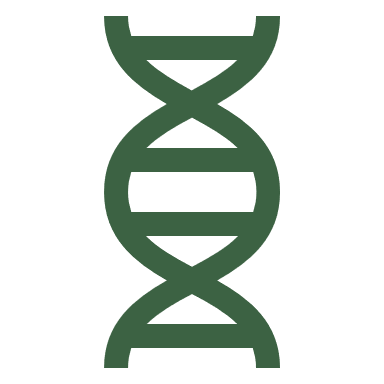
**This is a FAIL report. This sample cannot meet the minimum requirements for sequencing process due to low amount or poor quality.**

{%p endif%}

{%p endif%}

**检测内容Test content**

|  |  |
| --- | --- |
| **检测试剂** Reagents | 人类癌症多基因突变检测试剂盒（高通量测序法）  AmoyDx ® HANDLE Classic NGS Panel |
| **检测方法**  Method | 基于Handle法的高通量测序法  High-throughput sequencing method based on Handle method |
| **检测仪器**  Instrument | NextSeq CN500 / NextSeq 500  NextSeq CN500 / NextSeq 500 |
| **分析软件** Analyzing System | 人类癌症多基因突变分析软件（版本号：v2.0.0）  ADXHS-Classic (Version number: v2.0.0) |
| **检测范围**  Scope | 检测KRAS G12C基因变异  Gene list of the assay is ：KRAS G12C |
|  |  |

**检测结果Results**

**{%p if var.var\_somatic.level\_I+var.var\_somatic.level\_II+var.var\_somatic.level\_onco\_nodrug+var.var\_somatic.level\_III%}**

|  |  |  |
| --- | --- | --- |
| **基因名称**  **Gene** | **基因变异分类**  **Genetic Alteration** | **检测结果**  **Result detected (Yes/No)** |
| KRAS | G12C | *检测出*  *Yes* |

* **详细结果 Detail results:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **变异类型**  **Variation type** | **基因名称**  **Gene** | **转录本**  **Transcript ID** | **外显子/内含子**  **Exon/Intron** | **碱基变化**  **NT Change** | **氨基酸变化**  **AA Change** | **突变丰度**  **Alteration Frequency** |
| {%tr for a in var.var\_somatic.level\_I+var.var\_somatic.level\_II+var.var\_somatic.level\_onco\_nodrug+var.var\_somatic.level\_III%} | | | | | | |
| SNV | *KRAS* | {{a.transcript\_primary}} | {{a.gene\_region}} | {{a.hgvs\_c}} | {{a.hgvs\_p}} | {{a.freq\_str}} |
| {%tr endfor%} | | | | | | |

**{%p else%}**

|  |  |  |
| --- | --- | --- |
| **基因名称**  **Gene** | **基因变异分类**  **Genetic Alteration** | **检测结果**  **Result detected (Yes/No)** |
| KRAS | G12C | *未检出*  *No* |

* **详细结果 Detail results:**

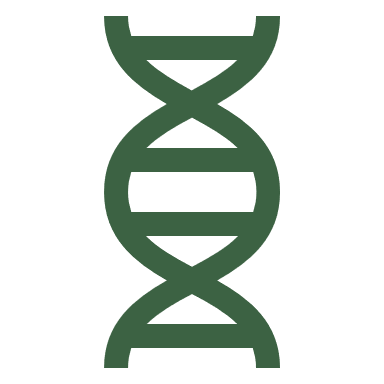
|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **变异类型**  **Variation type** | **基因名称**  **Gene** | **转录本**  **Transcript ID** | **外显子/内含子**  **Exon/Intron** | **碱基变化**  **NT Change** | **氨基酸变化**  **AA Change** | **突变丰度**  **Alteration Frequency** |
| SNV | *KRAS* | N/A | N/A | N/A | N/A | N/A |

**{%p endif%}**

**检测人** Test by**： 复核人**Review by**： 审批人**Approve by**：**

**注：本报告仅针对本次送检标。**

Note: This report is only for the samples received this time.

**数据质控QC Results**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **质控内容**  **QC parameter** | | | **合格标准**  **QC Criteria** | **质控结果**  **QC Result** | **是否合格**  **Pass/Risk/Fail** |
| 病理质控  Pathology QC | 肿瘤细胞含量  Tumor cell content | | ≥20％ | {%p if lib\_quality\_control.lib\_dna\_qc.macrodissection\_performed==”是”%}  {{lib\_quality\_control.lib\_dna\_qc.tumor\_content\_macrodissection\_performed}}  {%p else%}  {{lib\_quality\_control.lib\_dna\_qc.tumor\_content}}  {%p endif%} | {%p if lib\_quality\_control.lib\_dna\_qc.macrodissection\_performed==”是”%}  {%p if lib\_quality\_control.lib\_dna\_qc.tumor\_content\_macrodissection\_performed\_num >= 0.2%}  合格 Pass  {%p else%}  不合格 Fail  {%p endif%}  {%p else%}  {%p if lib\_quality\_control.lib\_dna\_qc.tumor\_content\_num >= 0.2%}  合格 Pass  {%p else%}  不合格 Fail  {%p endif%}  {%p endif%} |
| 提取质控  DNA Extraction QC | 样本DNA  DNA | 总量  Amount | ≥50ng | {{lib\_quality\_control.lib\_dna\_qc.dna\_qty|replace(“.00”, “”)}} | {%p if lib\_quality\_control.lib\_dna\_qc.dna\_qty\_num>=50%}  合格Pass  {%p else%}  不合格 Fail  {%p endif%} |
| 浓度  Conc | ≥6.25ng/µL | {{lib\_quality\_control.lib\_dna\_qc.dna\_concn|replace(“.00”, “”)}} | {%p if lib\_quality\_control.lib\_dna\_qc.dna\_concn\_num>=6.25%}  合格Pass  {%p else%}  不合格 Fail  {%p endif%} |
| 样本RNA  RNA Amount | 总量  Amount | ≥30ng | {{lib\_quality\_control.lib\_dna\_qc.rna\_qty|replace(“.00”,””)}} | {%p if lib\_quality\_control.lib\_dna\_qc.rna\_qty\_num>=30%}  合格Pass  {%p else%}  不合格 Fail  {%p endif%} |
| 浓度  Conc | ≥4ng/µL | {{lib\_quality\_control.lib\_dna\_qc.rna\_concn|replace(“.00”,””)}} | {%p if lib\_quality\_control.lib\_dna\_qc.rna\_concn\_num>=4%}  合格Pass  {%p else%}  不合格 Fail  {%p endif%} |
| 文库质控  Library QC | 文库浓度  Conc of Library | | ≥10ng/µL | {{lib\_quality\_control.lib\_dna\_qc.library\_concn|replace(“.00”,””)}} | {%p if lib\_quality\_control.lib\_dna\_qc.library\_concn\_num>=10%}  合格Pass  {%p elif lib\_quality\_control.lib\_dna\_qc.library\_concn\_num>=5%}  风险 Risk  {%p else%}  不合格 Fail  {%p endif%} |
| 数据质控  Output QC | Q30 | | ≥75％ | {{qc.dna\_data\_qc.cleandata\_q30|replace(“.00%”, “%”)}} | {%p if qc.dna\_data\_qc.cleandata\_q30\_num>=0.75%}  合格Pass  {%p else%}  不合格 Fail  {%p endif%} |
| 平均有效深度  Mean Effective Depth | DNA | ≥400X | {{qc.dna\_data\_qc.depth\_ssbc|replace(“.00”,””)}} | {%p if qc.dna\_data\_qc.depth\_ssbc\_num>=400%}  合格Pass  {%p else%}  不合格 Fail  {%p endif%} |
| RNA | ≥20X | {{qc.dna\_data\_qc.depth\_rna\_ctrl|replace(“.00”,””)}} | {%p if qc.dna\_data\_qc.depth\_rna\_ctrl\_num>=20%}  合格Pass  {%p else%}  不合格 Fail  {%p endif%} |

* **名词解释 Noun Interpretation**

富集后的手术组织，肿瘤细胞含量只报告富集前的含量，肿瘤细胞含量填写为“富集前肿瘤细胞含量值（富集）”，如“15%（富集）”。富集后的样本肿瘤细胞含量理论上远远大于20%。

Notes: For the surgical tissue after macro dissection, we only report tumor cell content only before macro-dissection here. We will fill in the tumor cell content as "tumor cell content value before macro dissection (macro dissection)", such as "15% (macro dissection)". The tumor cell content after macro dissection is theoretically much more than 20%.

Q30: 测序的准确率高于99.9%的碱基的比例

Q30: This means that the base call accuracy (i.e., the probability of a correct base call) is 99.9%

平均有效深度：对所有reads进行校正后，目标区域每个碱基被覆盖到的次数的平均值

Mean Effective Depth: The average of the depth of all the individual base of target region, after single strand base