NGS检测报告

**NGS Test Report**

 **送检信息 General Information**

|  |  |  |  |
| --- | --- | --- | --- |
| **受试者信息 Patient Information** | | | |
| **研究中心** Site Name：**{{sample.site\_name}}** | | | |
| **疾病类型**Disease Type：非小细胞肺癌NSCLC | | **受试者编号**Subject ID：**{{sample.subject\_ID}}** | |
| **出生年份** Year of Birth：**{{sample.birthday }}** | | **性别** Gender： **{%if sample.gender==”男”%}☑男**Male **□女**Female **{%else%}□男**Male **☑女**Female **{%endif%}** | |
| **样本信息 Specimen Information** | | | |
| **厦维样本编****号:**  Xiawei Sample ID | **{{sample.specimen\_parent\_id}}** | **样本类型****:**  Specimen Type: | **{%p if “手术” in sample.specimen\_type%}**  **☑手术**Surgical **活检**Biopsy  **{%p else%}**  **手术**Surgical **☑活检**Biopsy  **{%p endif%}** |
| **组织采集日期:**  Biopsy Collection Date | **{{sample.tissue\_collection\_date}}** | **切片日期:**  Slide Section Date | **{{sample.section\_date}}** |
| **接收日期:**  Reception Date | **{{sample.receive\_data }}** | **报告日期:**  Report Date | **{{sample.report\_date}}** |

**纯合缺失检测结果**Homozygous Deletion test results

|  |  |  |
| --- | --- | --- |
| **基因**  **Gene** | **外显子**  **Exon** | **结果判定**  **Result** **Judgment** |
| {%tr if hd%} | | |
| {%tr for a in hd%} | | |
| {%tr if a.hd\_mcs|float>0%} | | |
| *{{a.gene\_symbol}}* | {{a.region}} | 阳性 Positive |
| {%tr else%} | | |
| *{{a.gene\_symbol}}* | / | 阴性 Negative |
| {%tr endif%} | | |
| {%tr endfor%} | | |
| {%tr else%} | | |
| *MTAP* | / | 阴性 Negative |
| {%tr endif%} | | |

**注：**“/”表示阴性，没有相关结果输出；“N/A”表示不适用或无法评估。

**Note:** "/" indicates negative, no relevant results are output; "N/A" indicates not applicable or unable to assess.

编制人 Reported by**：** 复核人Reviewed by**：**

**注：本报告仅针对本次送检标本。**

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

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**质控标准Quality Control Standard**

|  |  |  |  |
| --- | --- | --- | --- |
| **质控参数**  **Quality control（QC） content** | | **合格标准**  **Pass quality control standard** | **质控数值**  **Quality control value** |
| **病理评估**  **Pathology QC** | **肿瘤细胞含量占比**  **Tumor cell content** | ≥20% | {%p if lib\_quality\_control and lib\_quality\_control.lib\_dna\_qc and 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%} |
| **核酸**  **Nucleic acid QC** | **DNA浓度**  **Con.（ng/μL）** | ≥3.75 | {%p if lib\_quality\_control and lib\_quality\_control.lib\_dna\_qc and lib\_quality\_control.lib\_dna\_qc.dna\_concn%}  {{lib\_quality\_control.lib\_dna\_qc.dna\_concn|replace(“.00”,””)}}  {%p else%}  N/A  {%p endif%} |
| **DNA 总量**  **Amount (ng)** | ≥30 | {%p if lib\_quality\_control and lib\_quality\_control.lib\_dna\_qc and lib\_quality\_control.lib\_dna\_qc.dna\_qty%}  {{lib\_quality\_control.lib\_dna\_qc.dna\_qty|replace(“.00”,””)}}  {%p else%}  N/A  {%p endif%} |
| **文库**  **library QC** | **文库浓度**  **library Con.（ng/μL）** | ≥5 | {%p if lib\_quality\_control and lib\_quality\_control.lib\_dna\_qc and lib\_quality\_control.lib\_dna\_qc.library\_concn%}  {{lib\_quality\_control.lib\_dna\_qc.library\_concn|replace(“.00”,””)}}  {%p else%}  N/A  {%p endif%} |
| **测序数据**  **Sequencing**  **Data QC** | **单个文库Q30碱基占比**  **Percentage of Q30 bases in a single library** | ≥80% | {%p if lib\_quality\_control and lib\_quality\_control.lib\_dna\_qc and lib\_quality\_control.lib\_dna\_qc.note%}  {{lib\_quality\_control.lib\_dna\_qc.note|replace(“.00”,””)}}  {%p else%}  N/A  {%p endif%} |
| **Clean Q30** | ≥80% | {{qc.dna\_data\_qc.cleandata\_q30|replace(“.00%”,”%”)}} |
| **覆盖率**  **（****Coverage(50x)）** | ≥95% | {{qc.dna\_data\_qc.cover\_ratio|replace(“.00%”,”%”)}} |

**注：**

1. 样本质控数值低于合格标准时，影响纯合缺失结果的准确性。

When the quality control values of the sample are below the acceptable standards, the test results may affect the accuracy of Homozygous Deletion (HD) results.

1. “N/A”表示不适用或无法评估。

"N/A" indicates not applicable or unable to assess.

1. 本文中若英文和中文有不一致处，以中文为准。

If there is any inconsistency between English and Chinese, the Chinese shall prevail.

**检测内容 Test Description**

* **检测方法 Test Method**

**样本核酸提取后采用“人类MTAP基因纯合缺失检测试剂盒（高通量测序法）”进行文库构建，测序平台为****ADx-SEQ200 Plus，采用****ADx-SEQ200 Plus配套的分析软件对检测数据进行分析。**

After nucleic acid extraction, the library is constructed using the " AmoyDx® MTAP Homozygous Deletion Panel" and the sequencing platform is the ADx-SEQ200 Plus. The analysis is performed using the ADx-SEQ200 Plus analysis software.

* **检测局限性 Limitation of the Test**

1. **本检测仅在DNA水平进行检测，检测的变异类型仅为纯合缺失（HD）；不包含其他水平(如蛋白水平)的变异或其他类型的突变。**

This test can only detect Homozygous Deletion at DNA level, other types of variant and other levels，such as protein level, are not included in this test.

1. **未检出的特定基因变异，可能由于该样本关键质控点低于合格标准。**

Failing to meet the key quality control parameter may lead to false-negative result.

1. **阴性结果不能完全排除目标基因变异的存在，样本中肿瘤细胞过少或样本过度降解亦可造成阴性结果。**

A negative result does not completely rule out the presence of target gene mutations. An insufficient number of tumor cells in the sample or excessive degradation of the sample can also lead to a negative result.