[**检测报告**] - **${runId}**

**基本信息**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| 姓　　名 | ${patient.patientName} | 样本编号 | ${sample.sampleNumber} | 测序平台 | ${sample.instrumentType} |
| 性　　别 | ${patient.patientGender} | 样本类型 | ${sample.sampleType} | 取样时间 | ${collectDate} |
| 年　　龄 | ${patient.patientAge==null?"":patient.patientAge} | 取样方法 | ${sample.sampleMethod} | 收样时间 | ${receiveDate} |
| 患者编号 | ${patient.patientNumber} | 取样部位 | ${sample.samplePosi} | 报告时间 | ${reportDate} |
| 诊断信息 | ${patient.patientDiag} | 样本来源 | ${sample.sampleSource} | | |
| 临床信息 | ${patient.patientClinic} | | | | |
| 备　　注 | 本报告中的诊断信息及临床信息来自受检者送检时提供的信息，而非来自检测结果。本检测报告不对以上信息的准确性负责。 | | | | |

**质控信息**

| **质量参数** | | **质控标准** | **样本数据** | **配对数据** |
| --- | --- | --- | --- | --- |
| 测序质量评估 | 测序总Reads数(M) | >=50.00 | ${variation['QC'].get(0).get('totalReadsM')} | ${variation['QC'].get(1).get('totalReadsM')} |
| Q20比例 | >=95.00% | ${variation['QC'].get(0).get('Q20Rate')} | ${variation['QC'].get(1).get('Q20Rate')} |
| Q30比例 | >=85.00% | ${variation['QC'].get(0).get('Q30Rate')} | ${variation['QC'].get(1).get('Q30Rate')} |
| GC比例 | 45%~48% | ${variation['QC'].get(0).get('GCRate')} | ${variation['QC'].get(1).get('GCRate')} |
| Mapping Reads数(M) | >=49.50 | ${variation['QC'].get(0).get('mappedReadsM')} | ${variation['QC'].get(1).get('mappedReadsM')} |
| 文库Mapping率 | >=99.00% | ${variation['QC'].get(0).get('mappedRate')} | ${variation['QC'].get(1).get('mappedRate')} |
| 平均插入片段长度(bp) | >=200 | ${variation['QC'].get(0).get('meanInsertSize')} | ${variation['QC'].get(1).get('meanInsertSize')} |
| Duplicate Reads 比例 | <=30% | ${variation['QC'].get(0).get('dupPercent')} | ${variation['QC'].get(1).get('dupPercent')} |
| 平均测序深度 | >=1000 | ${variation['QC'].get(0).get('depthMean')} | ${variation['QC'].get(1).get('depthMean')} |
| 中位数测序深度 | >=1000 | ${variation['QC'].get(0).get('depthMedian')} | ${variation['QC'].get(1).get('depthMedian')} |
| 深度>(0.2x目标测序深度)占比 | >=95% | ${variation['QC'].get(0).get('200xCoverage')} | ${variation['QC'].get(1).get('200xCoverage')} |
| 深度>(1.0x目标测序深度)占比 | >=80% | ${variation['QC'].get(0).get('1000xCoverage')} | ${variation['QC'].get(1).get('1000xCoverage')} |

**检测结果**

1. **SNV & INDEL 突变信息：**

| **CHROM** | **START** | **END** | **REF** | **ALT** | **GENE** | **TYPE** | **VAF** |
| --- | --- | --- | --- | --- | --- | --- | --- |
| ${['Chr']} | ${['Start']} | ${['End']==null?"-":['End']} | ${['Ref']} | ${['Alt']} | ${['Gene']} | ${['Type']} | ${['VAF']} |

本项检测结果为：**阴性**

1. **CNV 突变信息：**

| **CHROM** | **START** | **END** | **GENE** | **REGION** | **TYPE** | **CN** |
| --- | --- | --- | --- | --- | --- | --- |
| ${['CHROM']} | ${['START']} | ${['END']} | ${['GENE']} | ${['REGION']} | ${['TYPE']} | ${['CN']} |

|  |
| --- |
|  |
| ${image['${sample.sampleNumber}/cnv/${sample.sampleNumber}\_cnv\_scatter.png']} |

本项检测结果为：**阴性**

1. **SV 突变信息：**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **CHROM1** | **BREAKPOINT1** | **GENE1** | **CHROM2** | **BREAKPOINT2** | **GENE2** | **TYPE** | **VAF** | **ANNOTATION** |
| ${['CHROM']} | ${['BREAKPOINT1']} | ${['GENE1']} | ${['CHROM2']} | ${['BREAKPOINT2']} | ${['GENE2']} | ${['TYPE']} | ${['VAF']} | ${['ANNOTATION']} |

本项检测结果为：**阴性**