[**检测报告**]

1. **基本信息**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| 姓　　名 | ${patient.patientName} | 样本编号 | ${sample.sampleNumber} | 测序平台 | ${sample.instrumentType==null?"":sample.instrumentType} |
| 性　　别 | ${patient.patientGender} | 样本类型 | ${sample.sampleType==null?"":sample.sampleType} | 取样时间 | ${collectDate} |
| 年　　龄 | ${patient.patientAge==null?"":patient.patientAge} | 取样方法 | ${sample.sampleMethod==null?"":sample.sampleMethod} | 收样时间 | ${receiveDate} |
| 患者编号 | ${patient.patientNumber} | 取样部位 | ${sample.samplePosi==null?"":sample.samplePosi} | 报告时间 | ${reportDate} |
| 诊断信息 | ${patient.patientDiag} | 样本来源 | ${sample.sampleSource==null?"":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。 | | | | |

1. **软件信息：**

|  | **软件名称** | **软件版本** |
| --- | --- | --- |
| 分析软件信息 | fastp | 0.23.2 |
| bwa | 0.7.17 |
| samtools | 1.16.1 |
| sambamba | 0.8.2 |
| gatk（gatk） | 4.3.0.0 |
| HTSJDK（gakt） | 3.0.1 |
| Picard（gatk） | 2.27.5 |
| Ensemble vep | 108.2 |
|  | genome reference | GRCh38（hg38） |

1. **质控信息：**

| **质量参数** | | **质控标准** | **质控数据** |
| --- | --- | --- | --- |
| 测序质量评估 | 测序总Reads数(M) | >=1.00M | ${variation['QC'].get(0).get('TotalReadsMBeforeFiltering')}M |
| Q20比例 | >=95.00% | ${variation['QC'].get(0).get('Q20RateBeforeFiltering')} |
| Q30比例 | >=85.00% | ${variation['QC'].get(0).get('Q30RateBeforeFiltering')} |
| GC比例 | 45%~53% | ${variation['QC'].get(0).get('GCRateBeforeFiltering')} |
| 文库Mapping率 | >=99.00% | ${variation['QC'].get(0).get('MappingRate')} |
| 平均插入片段长度(bp) | >=100 | ${variation['QC'].get(0).get('MeanInsertSize')} |
| Duplicate Reads 比例 | <=30% | ${variation['QC'].get(0).get('DuplicateRate')} |
| 平均测序深度 | >=100 | ${variation['QC'].get(0).get('AverageDepth')} |
| 深度>( 1 x目标测序深度)占比 | >=95% | ${variation['QC'].get(0).get('1xCoverage')} |
| 深度>( 10 x目标测序深度)占比 | >=80% | ${variation['QC'].get(0).get('10xCoverage')} |
| 深度>( 20 x目标测序深度)占比 | >=80% | ${variation['QC'].get(0).get('20xCoverage')} |
| 深度>( 30 x目标测序深度)占比 | >=80% | ${variation['QC'].get(0).get('30xCoverage')} |
| 深度>(100 x目标测序深度)占比 | >=80% | ${variation['QC'].get(0).get('100xCoverage')} |

1. **检测结果：**

|  |  |  |
| --- | --- | --- |
| **Chrom :** ${['Chr']}:${['Start']}-${['End']}  **Gene :** ${['Gene']}  **cHGVS :** ${['cHGVS']}  **pHGVS :** ${['pHGVS']} | **REF :** ${['Ref']}  **Type :** ${['Type']}  **BioType :** ${['BioType']}  **CLNSIG : ${['CLNSIG']}** | **ALT :** ${['Alt']}  **Exon :** ${['Exon']}  **Depth :** ${['DP']}  **VAF :** ${['VAF']} |

本项检测结果为：**未发现致病突变**