检测信息

**关于本检测** OncoDrug-Seq™结直肠癌基因检测是一种基于高通量测序（NGS）的检测方法，可鉴定14个与结直肠癌高度相关的基因中的基因变异，和33个与化疗药物代谢相关基因中的基因多态性, 及微卫星状态。检测基因列表如下：

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 靶向药物相关基因17个 | | | | | | | |

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| --- | --- | --- | --- | --- | --- | --- | --- |
| 检测基因单碱基变异、小片段插入缺失 | | | | | | | |

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| --- | --- | --- | --- | --- | --- | --- | --- |
| AKT1 | BRAF | EGFR | ERBB2 | HRAS | KRAS | NRAS | NTRK1 |
| NTRK2 | NTRK3 | PIK3CA | PTEN | SMAD4 | MLH1 | MSH2 | MSH6 |
| PMS2 |  |  |  |  |  |  |  |

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| --- | --- | --- | --- | --- | --- | --- | --- |
| 检测基因重排 | | | | | | | |

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| --- | --- | --- | --- | --- | --- | --- | --- |
| NTRK1 | NTRK2 | NTRK3 |  |  |  |  |  |

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| --- | --- | --- | --- | --- | --- | --- | --- |
| 检测基因拷贝数变异 | | | | | | | |

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| --- | --- | --- | --- | --- | --- | --- | --- |
| EGFR | ERBB2 |  |  |  |  |  |  |

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| --- | --- | --- | --- | --- | --- | --- | --- |
| 肿瘤遗传易感相关基因4个 | | | | | | | |

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| --- | --- | --- | --- | --- | --- | --- | --- |
| MLH1 | MSH2 | MSH6 | PMS2 |  |  |  |  |

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| --- | --- | --- | --- | --- | --- | --- | --- |
| 化疗药物相关基因33个 | | | | | | | |

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| 检测基因多态性 | | | | | | | |

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| ABCB1 | ABCC2 | CASP7 | CBR3 | CDA | CYP19A1 | CYP2B6 | CYP2C8 |
| CYP2D6 | CYP3A4 | DHFR | DPYD | DYNC2H1 | ERCC1 | ERCC2 | ESR1 |
| GALNT14 | GSTM1 | GSTP1 | GSTT1 | MTHFR | MTR | NQO1 | RRM1 |
| SLC28A3 | SLCO1B1 | SOD2 | TP53 | TPMT | TYMS | UGT1A1 | XPC |
| XRCC1 |  |  |  |  |  |  |  |

检测方法 本检测基于液相探针杂交法的核酸序列靶向捕获及高通量测序技术，测序平台为Illumina NextSeq500/NovaSeq。检测覆盖100%的碱基替换突变 (95%CI=82-100) 及95%的小片段插入缺失突变 (95%CI=98.5-100)。数据通过BWA软件与人类参考基因组进行比对，Variant calls采用GATK软件分析。数据校准与突变注释使用的软件为TOPGEN自主知识产权分析软件（version 20190115），突变注释的主要参考数据库包括Clinvar (version 20181225)、Intervar (version 20180118)、COSMIC (version 83)、1000g2015aug (version 20150824)、EXAC03 (version 20160423)、dbnsfp35a (version 20180921)、avsnp (version 20170929)、OncoKB (version 1.15)、 PharmGKB (version 4.0)等、TOPGEN自建中国人群数据库（version即时更新）等。

检测限 对于单碱基变异，小片段插入缺失，基因融合等变异类型，检测灵敏度≤1%