



NCT

NATIONAL CENTER
FOR TUMOR DISEASES
PARTNER SITE DRESDEN
UNIVERSITY CANCER CENTER UCC

Supported by:
German Cancer Research Center
University Hospital Carl Gustav Carus Dresden
Carl Gustav Carus Faculty of Medicine, TU Dresden
Helmholtz-Zentrum Dresden-Rossendorf

Core Unit for Molecular Tumor Diagnostics

Input Recommendation for selected Protocol

Protocol	Quality Check RNA
Input Material	RNA
Minimum Input	0,1 ng
Standard Input	-
Maximum Volume	3,0 µL
Minimal Concentration	0,02 ng/µL
Standard Concentration	-

Extraction derived from **FFPE/Non-FFPE**

RNA Qualityparameters

RIN **will be determined**

DV200 **will be determined**

Special Considerations **Please provide an estimated concentration (photometric, e.g. Nanodrop)**

For more Information please visit the manufacturers homepage

<https://www.agilent.com/en/product/automated-electrophoresis/fragment-analyzer-systems/fragment-analyzer-systems-rna-analysis-kits>

<https://www.agilent.com/en/product/automated-electrophoresis/fragment-analyzer-systems/fragment-analyzer-systems/5200-fragment-analyzer-system-365720>

The CMTD is not responsible for the consequences/results, if an ordering work group wants to sequence RNA/DNA samples that failed the predefined quality parameters for sequencing!

Possible, risks which can occur are for example bad sequencing quality, no sequencing possible due to failure in library generation, introducing false signals of gene expression or allele frequency.

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