



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	illumina stranded mRNA
Input Material	RNA
Minimum Input	100,0 ng
Standard Input	1000,0 ng
Maximum Volume	50,0 µL
Minimal Concentration	2,00 ng/µL
Standard Concentration	20,00 ng/µL

Extraction derived from **Non-FFPE**

### *RNA Qualityparameters*

RIN	>8
DV200	not relevant

For more Information please visit the manufacturers homepage

<https://emea.illumina.com/products/by-type/sequencing-kits/library-prep-kits/stranded-mrna-prep.html>

[https://emea.support.illumina.com//sequencing/sequencing\\_kits/illumina-stranded-mrna-ligation.html](https://emea.support.illumina.com//sequencing/sequencing_kits/illumina-stranded-mrna-ligation.html)

**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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