

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 Recomendation for selected Protocol

Protocol	Illumina RNA Exom
Input Material	RNA
Minimum Input	10,0 ng
Standard Input	depends on Quality
Maximum Volume	8,5 μL
Minimal Concentration	1,18 ng/μL
Standard Concentration	depends on Quality
Extraction derived from	FFPE/Non-FFPE
RNA Qualityparameters	
RIN	not considered
DV200	>30 %

For more Information please visit the manufacturers homepage

https://emea.illumina.com/products/by-type/sequencing-kits/library-prep-kits/truseq-rna-access.html

https://emea.support.illumina.com/sequencing/sequencing_kits/truseq-rna-exome.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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