Core Unit for Molecular Tumor Diagnostics

Input Recomendation 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

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.