

# ISO/TS 22690:2021-10 (E)

## Genomics informatics - Reliability assessment criteria for high-throughput gene-expression data

---

<b>Contents</b>		<b>Page</b>
Foreword .....		iv
Introduction .....		v
1	Scope .....	1
2	Normative references .....	1
3	Terms and definitions .....	1
4	From sample to RNA .....	3
4.1	General .....	3
4.2	RNA integrity .....	3
4.3	RNA concentration .....	4
4.4	RNA purity .....	4
5	Expression profiling .....	4
6	Quality control metrics in RNA-seq analysis .....	4
6.1	General .....	4
6.2	Sequencing read .....	4
6.2.1	Total number of reads .....	4
6.2.2	Read length .....	5
6.2.3	Base call quality .....	5
6.2.4	GC content .....	5
6.2.5	Overrepresented sequence .....	5
6.2.6	Adapter residue .....	5
6.3	Alignment .....	5
6.3.1	Alignment ratio .....	5
6.3.2	Gene body coverage uniformity .....	5
6.3.3	Strand specificity .....	6
6.3.4	Insert size .....	6
6.3.5	Mismatch .....	6
6.3.6	Contamination from other sources .....	6
6.4	Expression .....	6
6.4.1	Expression distribution .....	6
6.4.2	Expressed genes .....	6
6.4.3	Saturation .....	7
6.4.4	Reproducibility .....	7
6.5	Differentially expressed genes .....	7
6.6	Biological interpretation of differentially expressed genes .....	7
6.7	Sample certificate of origin .....	8
6.8	Quality control of batch effects .....	8
7	Spike-in controls .....	8
8	Proficiency testing .....	8
8.1	General .....	8
8.2	RNA sources .....	9
8.3	Experimental design .....	9

<b>9</b>	<b>Process management .....</b>	<b>9</b>
<b>Bibliography .....</b>		<b>10</b>