

CLAIMS

1. A composition comprising at least 3 RNA molecules, wherein the at least 3 RNA molecules are selected from a group consisting of RNA molecules having a nucleotide sequence according to SEQ ID NO: 1 to SEQ ID NO: 4, a fragment thereof, and a sequence having at least 80% sequence identity thereto.
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2. The composition of claim 1, wherein the composition comprises 4 RNA molecules, wherein the 4 RNA molecules are selected from a group consisting of RNA molecules having a nucleotide sequence according to SEQ ID NO: 1 to SEQ ID NO: 4, a fragment thereof, and a sequence having at least 80% sequence identity thereto.
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3. The composition of claims 1 or 2, wherein the composition comprises RNA molecules having a nucleotide sequence according to
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 - (i) SEQ ID NO: 1, SEQ ID NO: 2, and SEQ ID NO: 3,
 - (ii) SEQ ID NO: 2, SEQ ID NO: 3, and SEQ ID NO: 4,
 - (iii) SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 4,
 - (iv) SEQ ID NO: 1, SEQ ID NO: 2, and SEQ ID NO: 4, or
 - (v) SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, and SEQ ID NO: 4.
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4. The composition of any one of claims 1 to 3, wherein the composition comprises at least 3 RNA molecules and wherein
the first RNA molecule is comprised in an amount of about 3400 amol, the second RNA molecule is comprised in an amount of about 725 amol, and the third RNA molecule is comprised in an amount of about 20 amol, or
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the first RNA molecule is comprised in an amount of about 1360 amol, the second RNA molecule is comprised in an amount of about 290 amol, and the third RNA molecule is comprised in an amount of about 80 amol.
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5. The composition of claim 4, wherein the composition comprises 4 RNA molecules and wherein
the first RNA molecule is comprised in an amount of about 3400 amol, the second RNA molecule is comprised in an amount of about 725 amol, the third RNA molecule is comprised in an amount of about 20 amol, and the fourth RNA molecule is comprised in an amount of about 7 amol, or
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the first RNA molecule is comprised in an amount of about 1360 amol, the second RNA molecule is comprised in an amount of about 290 amol, the third RNA molecule is comprised in an amount of about 80 amol, and the fourth RNA molecule is comprised in an amount of about 27 amol.

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6. The composition of any one of claims 1 to 5, wherein the RNA molecules are artificial RNA molecules (which do not exist in nature).

7. A kit comprising the composition of any one of claims 1 to 6.

- 10 8. Use of the composition of any one of 1 to 6 or the kit of claim 7 (as standard) for process control, sample examination, normalization, and/or data processing control.

- 15 9. A method for examining a sample comprising the step of: evaluating a sample with respect to the at least 3 RNA molecules comprised in/from the composition of any one of claims 1 to 6.

10. The method of claim 9, wherein the evaluation comprises determining whether the at least 3 RNA molecules show a characteristic distribution.

- 20 11. The method of claim 10, wherein, if the characteristic distribution is given, the sample is further processed and/or analysed.

- 25 12. The method of claim 11, wherein the characteristic distribution is given if the at least 3 RNA molecules are present in their expected level, the at least 3 RNA molecules are present at their expected order/rank (defined by the relation of the levels, in particular amounts, of the at least 3 RNA molecules), and/or the at least 3 RNA molecules are present in their expected linearity.

- 30 13. The method of claim 12, wherein the expected order results in a Spearman's rank correlation coefficient (Spearman's ρ) of ≥ 0.95 and/or the expected linearity results in a Pearson's correlation coefficient (Pearson's r) of ≥ 0.66 .

14. The method of any one of claims 9 to 13, wherein the evaluation comprises identifying 5'end and/or 3'end additions of the at least 3 RNA molecules comprised in/from the composition of any one of claims 1 to 6.

5 15. The method of claim 14, wherein the 5'end and/or 3' end additions are the result of RNA molecule/adapter fusion, RNA molecule/RNA molecule fusion, adapter/adapter fusion.

10 16. The method of any one of claims 9 to 15, wherein the sample comprises target RNA molecules, and, wherein the presence of 5'end and/or 3'end additions identified with respect to the at least 3 RNA molecules comprised in/from the composition of any one of claims 1 to 6 is indicative for the presence of 5'end and/or 3'end additions in the target RNA molecules.

15 17. The method of claim 16, wherein target RNA molecules with 5'end and/or 3'end additions comprised in the sample are excluded from further analyses/are not further used.

20 18. A method for
(i) optimized processing of biological samples
(ii) optimized RNA preparation from or RNA analysis of biological samples, or
(iii) improving RNA data set quality
comprising the step of:
carrying out the method of any one of claims 9 to 17.

25 19. A method for improving RNA data set quality comprising the steps of:
(i) determining the sequence of RNA molecules in a sample,
(ii) determining 5'end and/or 3'end additions to the RNA molecules, which are not part of the RNA molecules in naturally occurring form, and
(iii) excluding RNA molecules having 5'end and/or 3'end additions from RNA data set analysis/removing RNA molecules having 5'end and/or 3'end additions from the RNA data set.

30 20. The method of claim 19, wherein the determination of the sequence of RNA molecules in the sample encompasses:
denaturation of RNA molecules and ligation of 5'adapters and/or 3'adapters to the denatured RNA molecules,

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reverse transcription of RNA molecules (having 5'adapters and/or 3'adapters ligated thereon) into cDNA molecules,
amplification of (said) cDNA molecules, and/or
sequencing, preferably next generation sequencing, of (said) cDNA molecules.