

## EVALUATING THE IMPACT OF RNA PURIFICATION KIT AND BLOOD COLLECTION TUBE IN THE EXTRACELLULAR RNA QUALITY CONTROL STUDY – IMPORTANT CONSIDERATIONS FOR LIQUID BIOPSIES

exRNAQC Consortium

CONCEPTUALIZATION: Decock A (1,2), De Wever O (2,4), Everaert C (1,2,3), Helsmoortel H (1,2), Hendrix A (2,4), Mestdagh P (1,2,3,6), Vandesompele J (1,2,3,6), Van Paemel R (1,2,11)

DATA CURATION: Avila Cobos F (1,2,3), Decock A (1,2), Everaert C (1,2,3), Morlion A (1,2), Van Paemel R (1,2,11)

FORMAL ANALYSIS: Avila Cobos F (1,2,3), Everaert C (1,2,3), Fierro C (6), Mestdagh P (1,2,3,6), Morlion A (1,2), Vandesompele J (1,2,3,6), Van Paemel R (1,2,11)

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INVESTIGATION: Decock A (1,2), Deleu J (1,2), Dhondt B (2,4,5), Helsmoortel H (1,2), Hulstaert E (1,2,7), Nijs N (6), Nuytens J (1,2), Philippron A (2,9,10), Schoofs K (1,2), Vanden Eynde E (1,2), Van der Schueren C (1), Van Paemel R (1,2,11), Verniers K (1,2), Yigit N (1,2)

METHODOLOGY: Avila Cobos F (1,2,3), Decock A (1,2), Dhondt B (2,4,5), Everaert C (1,2,3), Fierro C (6), Mestdagh P (1,2,3,6), Nijs N (6), Philippron A (2,9,10), Vandesompele J (1,2,3,6), Van Paemel R (1,2,11)

PROJECT ADMINISTRATION: Decock A (1,2), Helsmoortel H (1,2)

RESOURCES: Dhondt B (2,4,5), Hulstaert E (1,2,7), Kuersten S (8), Philippron A (2,9,10), Schroth G (8), Van Paemel R (1,2,11)

SOFTWARE: Anckaert J (1,2), Avila Cobos F (1,2,3), Everaert C (1,2,3), Morlion A (1,2), Van Paemel R (1,2,11)

SUPERVISION: Mestdagh P (1,2,3,6), Vandesompele J (1,2,3,6)

VISUALIZATION: Avila Cobos F (1,2,3), Everaert C (1,2,3), Morlion A (1,2), Van Paemel R (1,2,11)

(1) Center for Medical Genetics – Department of Biomolecular Medicine, Ghent University, Ghent, Belgium

(2) Cancer Research Institute Ghent (CRIG), Ghent, Belgium

(3) Bioinformatics Institute Ghent from Nucleotides to Networks (BIG N2N), 9000 Ghent, Belgium

(4) Laboratory of Experimental Cancer Research, Ghent University, Ghent, Belgium

(5) Department of Urology, Ghent University Hospital, Ghent, Belgium

(6) Biogazelle, Zwijnaarde, Belgium

(7) Department of Dermatology, Ghent University Hospital, Ghent, Belgium

(8) Illumina Inc., San Diego, California, USA

(9) Lab for Experimental Surgery, Ghent University, Ghent, Belgium

(10) Department of Gastrointestinal Surgery, Ghent University Hospital, Ghent, Belgium

(11) Department of Pediatrics, Ghent University Hospital, Ghent, Belgium

In search of easily accessible biomarkers, extracellular RNAs (exRNAs) have emerged as potential candidates. Unfortunately, exRNA quantification is influenced by many pre-analytical variables and a comprehensive quality control study for blood-based liquid biopsies, evaluating pre-analytical variables in a controlled and systematic manner, is currently lacking. Therefore, we initiated the exRNA quality control (exRNAQC) study. We evaluate the effect of the type of blood collection tube (n=10), time between blood draw and plasma preparation (n=3), centrifugation speed during plasma preparation (n=5), input volume and RNA purification method (n=8). The impact of these factors is assessed by unbiased transcriptome exRNA profiling of all microRNAs and messenger RNAs from healthy donors' plasma using established RNA-sequencing workflows. In the first phase of our study, we observed large differences in RNA purification kit performance in terms of reproducibility, yield and transcriptome complexity. We are currently analyzing the blood collection tube exRNA profiles. Once all pre-analytical variables are evaluated separately, we will integrate our findings into a full factorial experiment and plan dedicated follow-up experiments to validate our findings. Using this systematic approach, we aim to develop quality control metrics and guidelines for the study of exRNA in order to facilitate further progress in the field.