

## Annelien Morlion

### DRAMATIC DIFFERENCES IN RNA PURIFICATION KIT PERFORMANCE IN THE EXTRACELLULAR RNA QUALITY CONTROL STUDY – IMPORTANT CONSIDERATIONS FOR LIQUID BIOPSIES

exRNAQC Consortium

*Conceptualization:* Anneleen Decock (1,2), Olivier De Wever (2,4), Celine Everaert (1,2,3), Hetty Helmoortel (1,2), An Hendrix (2,4), Pieter Mestdagh (1,2,3,6), Jo Vandesompele (1,2,3,6)

*Data curation:* Francisco Avila Cobos (1,2,3), Anneleen Decock (1,2), Celine Everaert (1,2,3), Annelien Morlion (1,2)

*Formal analysis:* Francisco Avila Cobos (1,2,3), Celine Everaert (1,2,3), Carolina Fierro (6), Pieter Mestdagh (1,2,3,6), Annelien Morlion (1,2), Jo Vandesompele (1,2,3,6)

*Funding acquisition:* Anneleen Decock (1,2), Pieter Mestdagh (1,2,3,6), Jo Vandesompele (1,2,3,6)

*Investigation:* Anneleen Decock (1,2), Bert Dhondt (2,4,5), Hetty Helmoortel (1,2), Eva Hulstaert (1,2,7), Nele Nijs (6), Justine Nuytens (1,2), Annouck Philippron (2,9,10), Eveline Vanden Eynde (1,2), Ruben Van Paemel (1,2,11), Kimberly Verniers (1,2), Nurten Yigit (1,2)

*Methodology:* Francisco Avila Cobos (1,2,3), Anneleen Decock (1,2), Bert Dhondt (2,4,5), Celine Everaert (1,2,3), Carolina Fierro (6), Pieter Mestdagh (1,2,3,6), Nele Nijs (6), Annouck Philippron (2,9,10), Jo Vandesompele (1,2,3,6)

*Project administration:* Anneleen Decock (1,2), Hetty Helmoortel (1,2)

*Resources:* Bert Dhondt (2,4,5), Eva Hulstaert (1,2,7), Scott Kuersten (8), Annouck Philippron (2,9,10), Gary Schroth (8), Ruben Van Paemel (1,2,11)

*Software:* Jasper Anckaert (1,2), Francisco Avila Cobos (1,2,3), Celine Everaert (1,2,3), Annelien Morlion (1,2)

*Supervision:* Pieter Mestdagh (1,2,3,6), Jo Vandesompele (1,2,3,6)

*Visualization:* Francisco Avila Cobos (1,2,3), Celine Everaert (1,2,3), Annelien Morlion (1,2)

(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 whose impact is still unknown and therefore complicate the comparison and integration of research findings. A comprehensive quality control study for blood-based liquid biopsies, evaluating these pre-analytical variables in a controlled and systematic manner, is currently lacking. Therefore, we initiated the exRNA quality control (exRNAQC) study to systematically 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 assessed the impact of each pre-analytical variable separately. We observed differences in RNA purification kit performance in terms of reproducibility, yield (up to 37-fold) and transcriptome complexity (2500 vs 15 000 genes detected). 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 results. 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.