# RNA-based liquid biopsies for better clinical management of Barrett's esophagus and esophageal adenocarcinoma

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## Abstract

In the past decades the incidence of esophageal adenocarcinoma (EAC) has increased dramatically in most Western populations. Due to the lack of symptoms EAC is often detected in a late stage, contributing to a poor 5-year survival rate. The potential of RNA (coding and miRNA) as circulating biomarker in blood has already been shown for many cancer entities but requires further investigation for EAC. In this study we will explore several RNA types in blood, including microRNA, messenger RNA, long non-coding RNA and circular RNA as a potential liquid biomarker to facilitate early diagnosis, prognosis and monitoring of esophageal adenocarcinoma

We have been collecting blood and tissue samples from patients with non-dysplastic Barrett's esophagus (NDBE), high-grade dysplasia (HGD) and EAC. Currently, our biobank includes >5000 samples from 120 patients. A proof-of-concept study was conducted including 17 patients from three groups (EAC, HGD and NDBE). For each patient, biopsies from diseased tissue and healthy tissue as well as blood were collected and analyzed using small RNA and total RNA sequencing.

Gene expression analysis was performed to identify differentially expressed genes across the three groups. The highest number of significantly differentially expressed m(i)RNAs were present in the tissues of EAC versus NDBE patients, while these differences were much lower or even absent in the plasma samples. Moreover, we have identified between 1500 and 7500 unique circular RNAs in individual EAC cancer patients' plasma, indicating promising opportunities for a blood-based liquid biomarker for BE and EAC. Currently, we are collecting additional samples to significantly increase the power of the differential expression study as well as to verify the results of our proof-of-concept study.