121 plasma samples from healthy volunteers, CC patients, and CIN patients.

- Isolation of plasma exosomes and exosomal miRNAs
- Preparation of exosomal small RNA libraries
- miRNA sequencing
- Read alignment
- miRNA quantification and normalization
- Differential expression analysis
- 37 DEmiRs

8 DEmiRs in the best panel for discriminating between CINI- and CINI+ were identified by the Random Forest algorithm

46 paired cancerous and para-carcinoma tissues from new CC patients

- qTR-PCR analysis

let-7a-3p, let-7d-3p and miR-30d-5p showed significantly consistent variation trends observed in plasma exosomes

203 independent plasma samples

- ddPCR analysis
  
  let-7d-3p and miR-30d-5p is highly predictive of CINI- and CINI+ in the validation set

- Figure S1 Flow chart for the study design.