55) **Endometriosis** Associated-miRNome Analysis of Blood Samples: A Prospective Study. Bendifallah S, Dabi Y, Suisse S, Delbos L, Poilblanc M, Descamps P, Golfier F, Jornea L, Bouteiller D, Touboul C, Puchar A, Daraï E.Diagnostics (Basel). 2022 May 5;12(5):1150. doi: 10.3390/diagnostics12051150.PMID: 35626305 **Free PMC article.**

**Abstract**

The aim of our study was to describe the bioinformatics approach to analyze miRNome with Next Generation Sequencing (NGS) of 200 plasma samples from patients with and without endometriosis. Patients were prospectively included in the ENDO-miRNA study that selected patients with pelvic pain suggestive of endometriosis. miRNA sequencing was performed using an Novaseq6000 sequencer (Illumina, San Diego, CA, USA). Small RNA-seq of 200 plasma samples yielded ~4228 M raw sequencing reads. A total of 2633 miRNAs were found differentially expressed. Among them, 8.6% (*n* = 229) were up- or downregulated. For these 229 miRNAs, the F1-score, sensitivity, specificity, and AUC ranged from 0-88.2%, 0-99.4%, 4.3- 100%, and 41.5-68%, respectively. Utilizing the combined bioinformatic and NGS approach, a specific and broad panel of miRNAs was detected as being potentially suitable for building a blood signature of endometriosis.

**Keywords:** NGS; bioinformatics; endometriosis; miRNA.