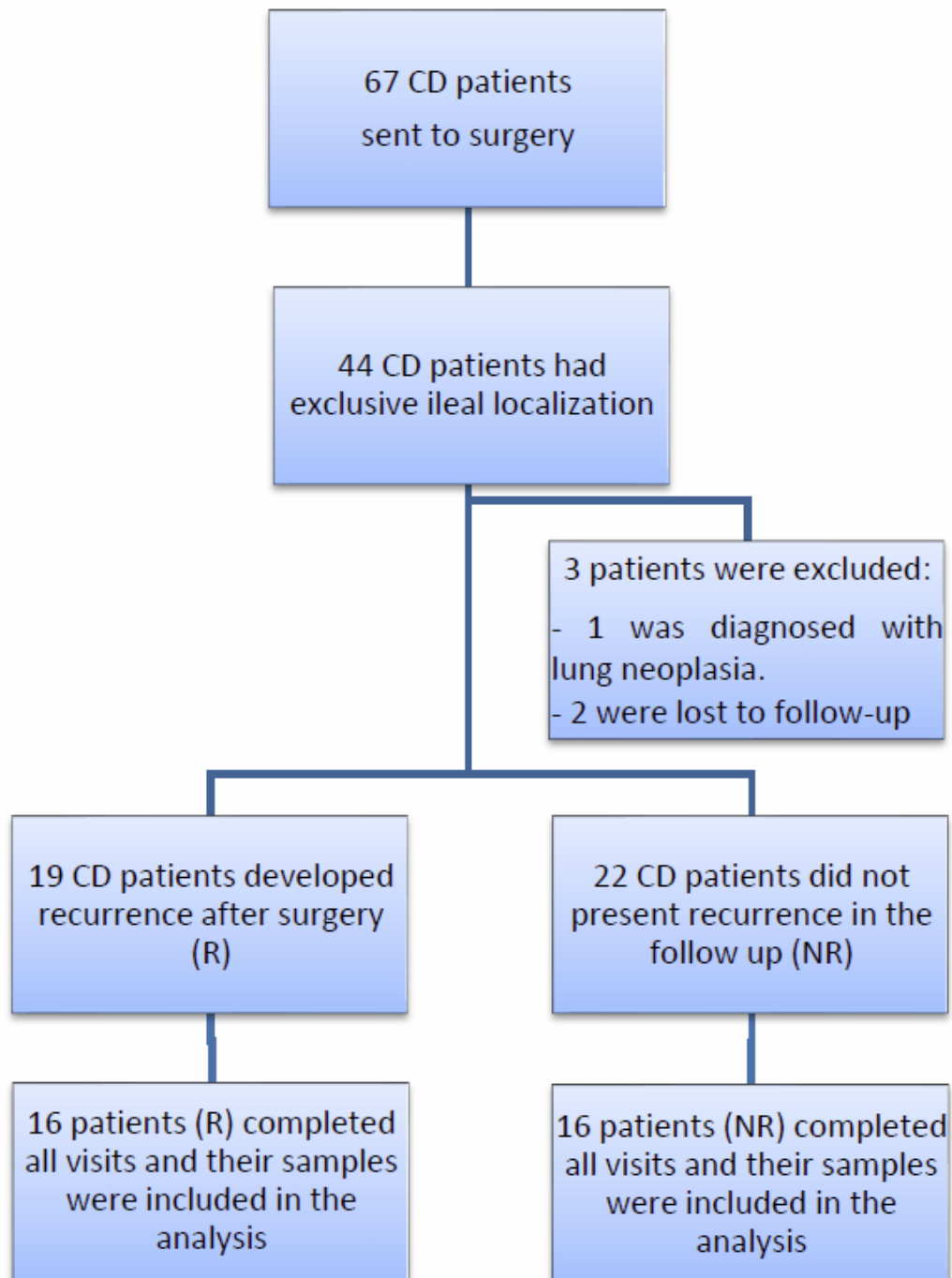
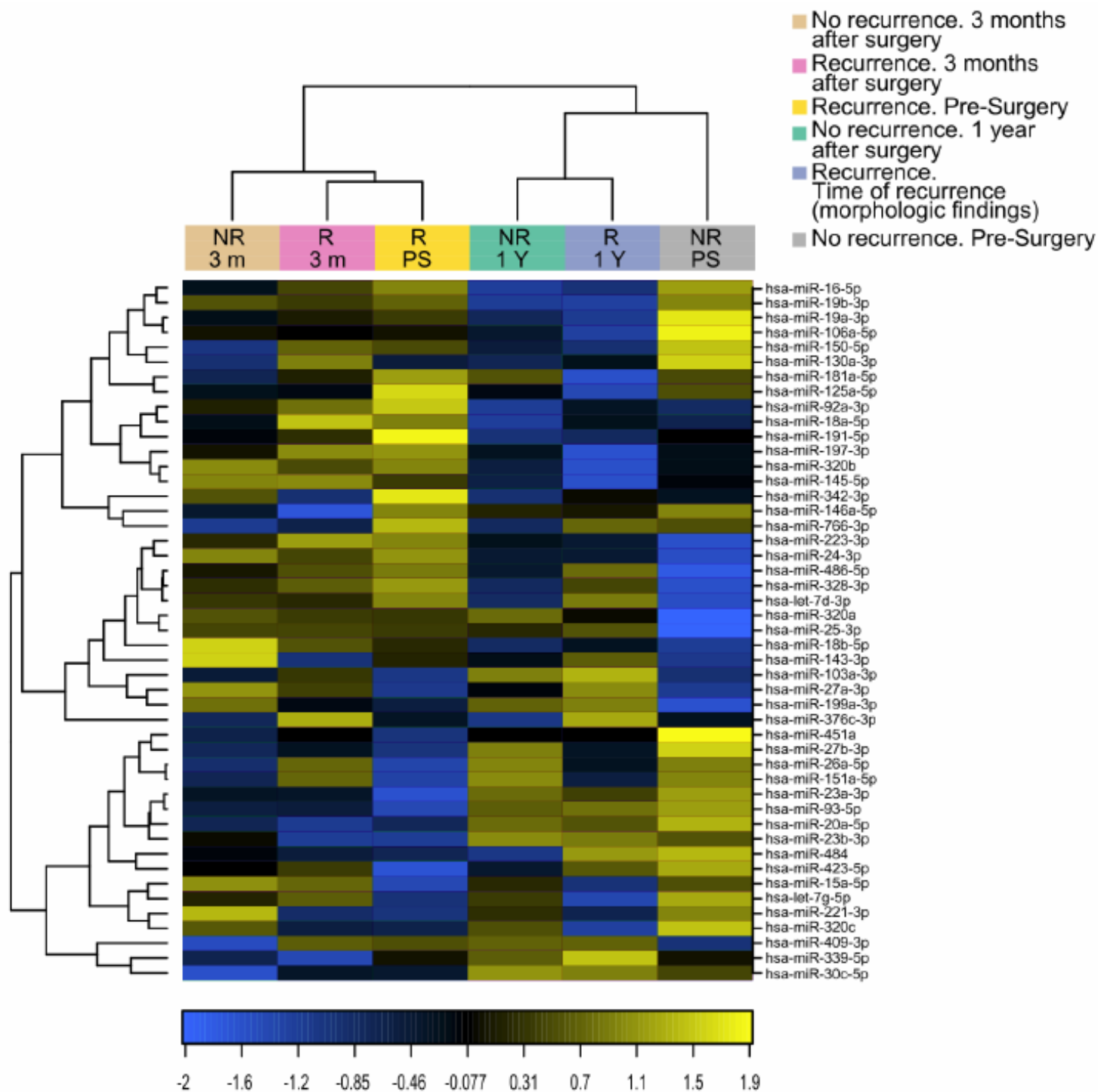


**Figure S1.** Flowchart showing the steps followed for the selection of patients and samples for the study

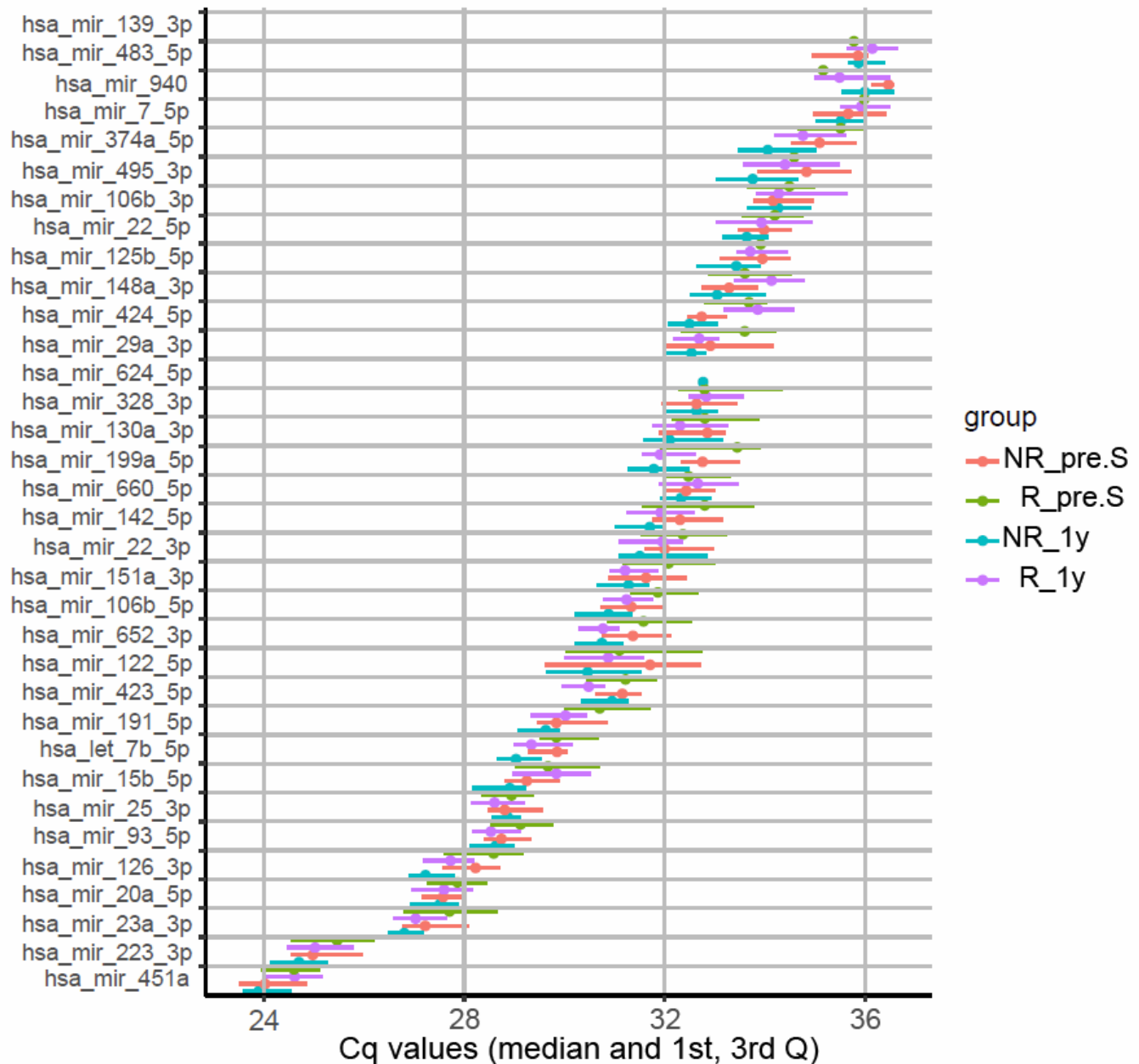


Workflow figure summarizing the sample selection for the experimental cohort. For the inferential cohort, samples for no recurrence and recurrence were included.

**Figure S2.** Heatmap of the 2-way hierarchical clustering of miRNAs and samples. The top 47 miRNAs with the highest standard deviation are depicted. Rows for each miRNA, columns for each sample. Yellow represents a miRNA expression level above mean, whereas blue represents expression lower than the mean. Each row represents 1 miRNA, and each column represents 1 pooled sample (NR PS, no recurrence presurgery; R PS, recurrence presurgery; NR 3 m, no recurrence 3 months after surgery; R 3 m, recurrence 3 months after surgery; NR 1 y, no recurrence 1 year after surgery; R 1 y, recurrence at the time of morphological recurrence confirmation).

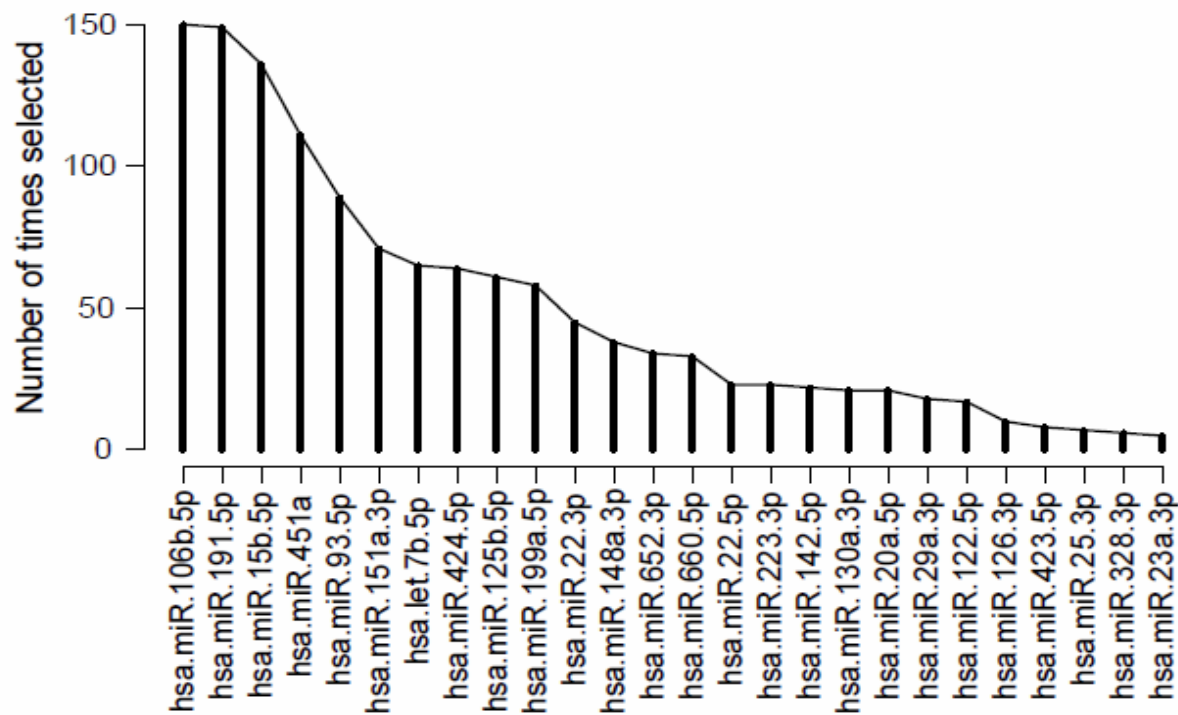


**Figure S3.** Experimental results and Cq values in plasma samples from the inferential cohort. Depicted values are median and first and third quartile. Depicted Cq values are background filtered.

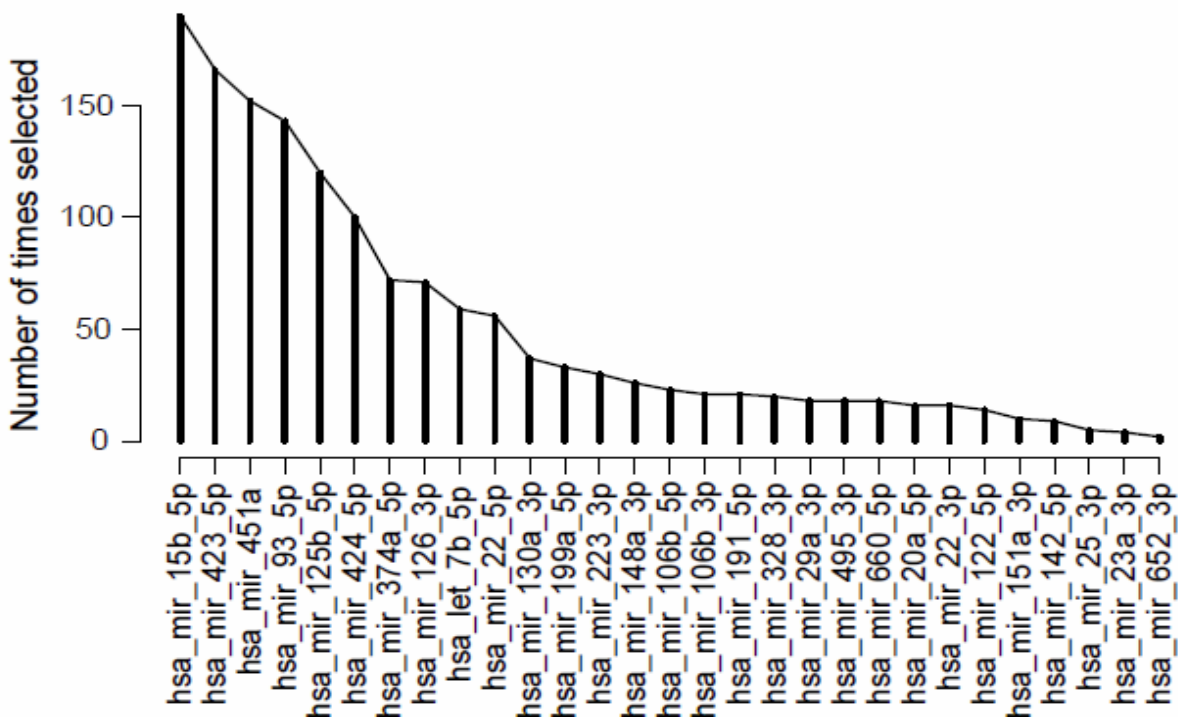


**Figure S4.** Selection of the microRNAs in the bootstrap validation of the relaxed elastic net results. A) presurgical and B) postsurgical CD samples.

A.

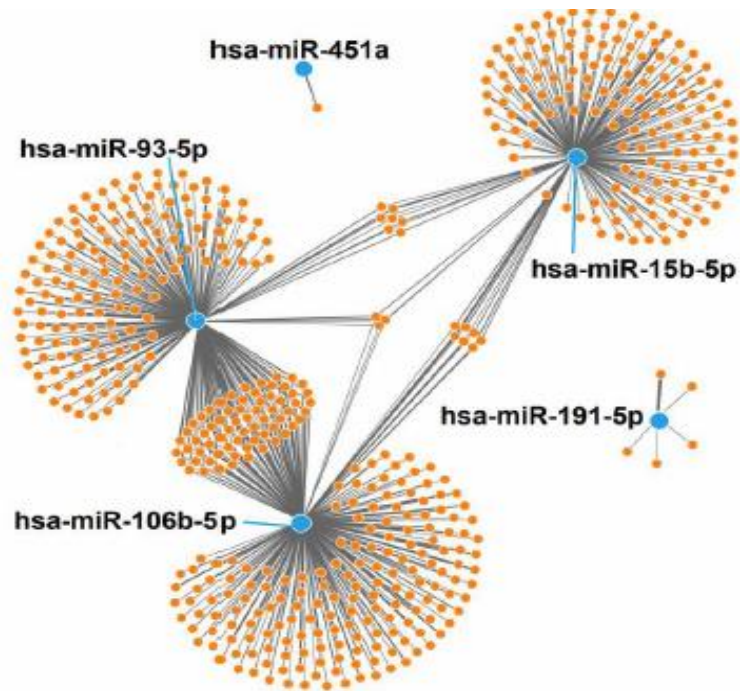


B.



**Figure S5.** Graphical networks of potential target genes from the selected miRNAs in the presurgical (A) and postsurgical (B) CD samples. Predicted miRNA target genes were obtained from miRWalk, version 3.0.

A.



B.

