

# MicroRNA expression in normal and malignant prostate tissues

The aim of this study was to identify a set of miRNAs that could be used as a prognostic and diagnostic tool for prostate cancer

## Introduction

Distinct signatures of miRNA expression can be found for each cancer type [1], and an accurate and reproducible profile of the miRNA expression in malignant prostate tissue would potentially be a valuable medical tool for diagnosis of prostate cancer.

## Material and Methods

Malignant and adjacent normal FFPE prostate tissue from 20 patients in the Swedish Watchful waiting cohort was used in this study with Gleason scores 6 (6), 7 (7), 8 (1), 9 (4) and 10 (2). We performed quantitative RT-PCR on 768 miRNAs, followed by statistical significance analysis to identify differentially expressed miRNAs, principal component analysis (PCA), and hierarchical clustering analysis.

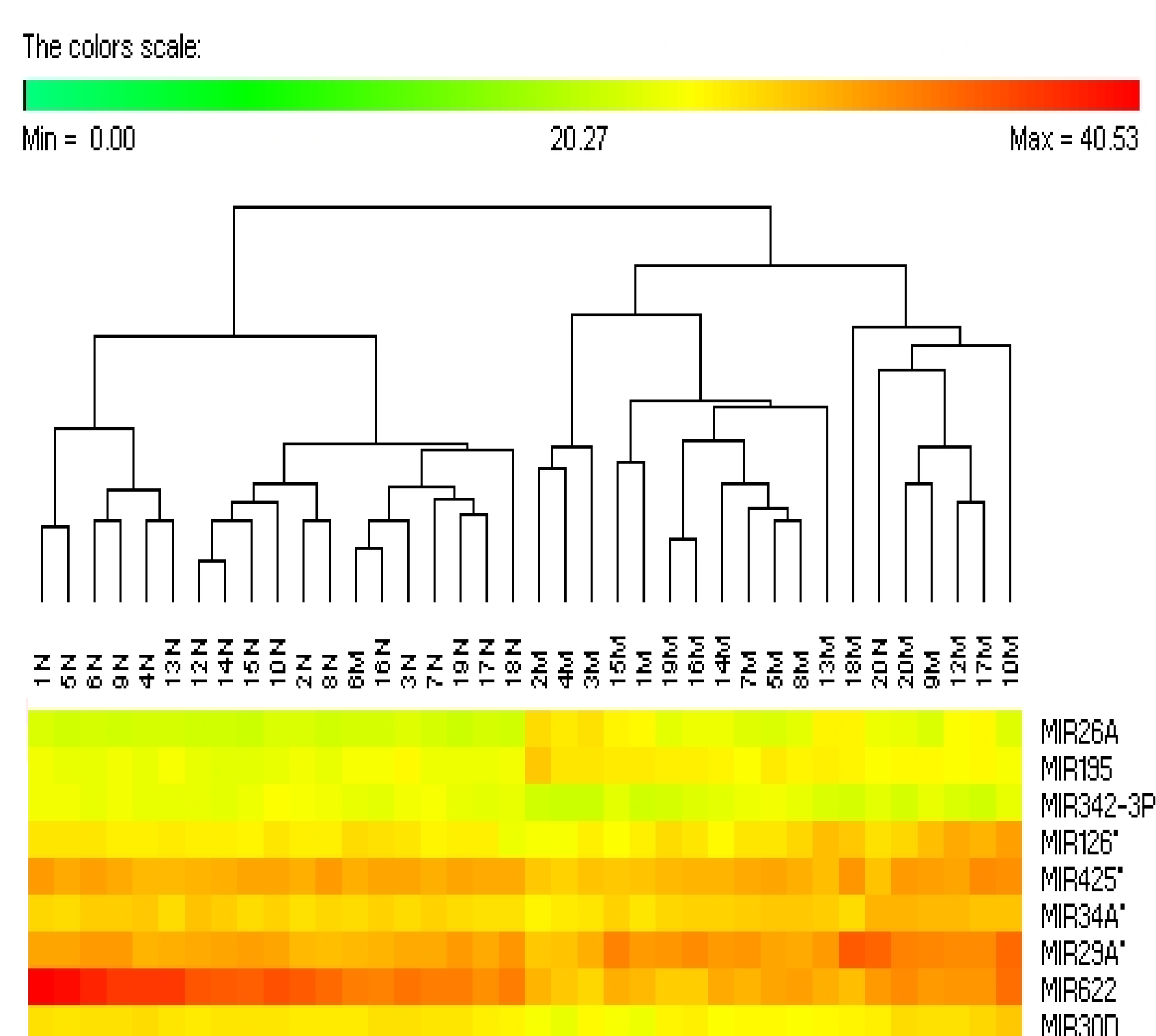


Figure 1: Nine miRNAs separates between normal and malignant prostate tissues with the exception for one normal and one malignant sample.

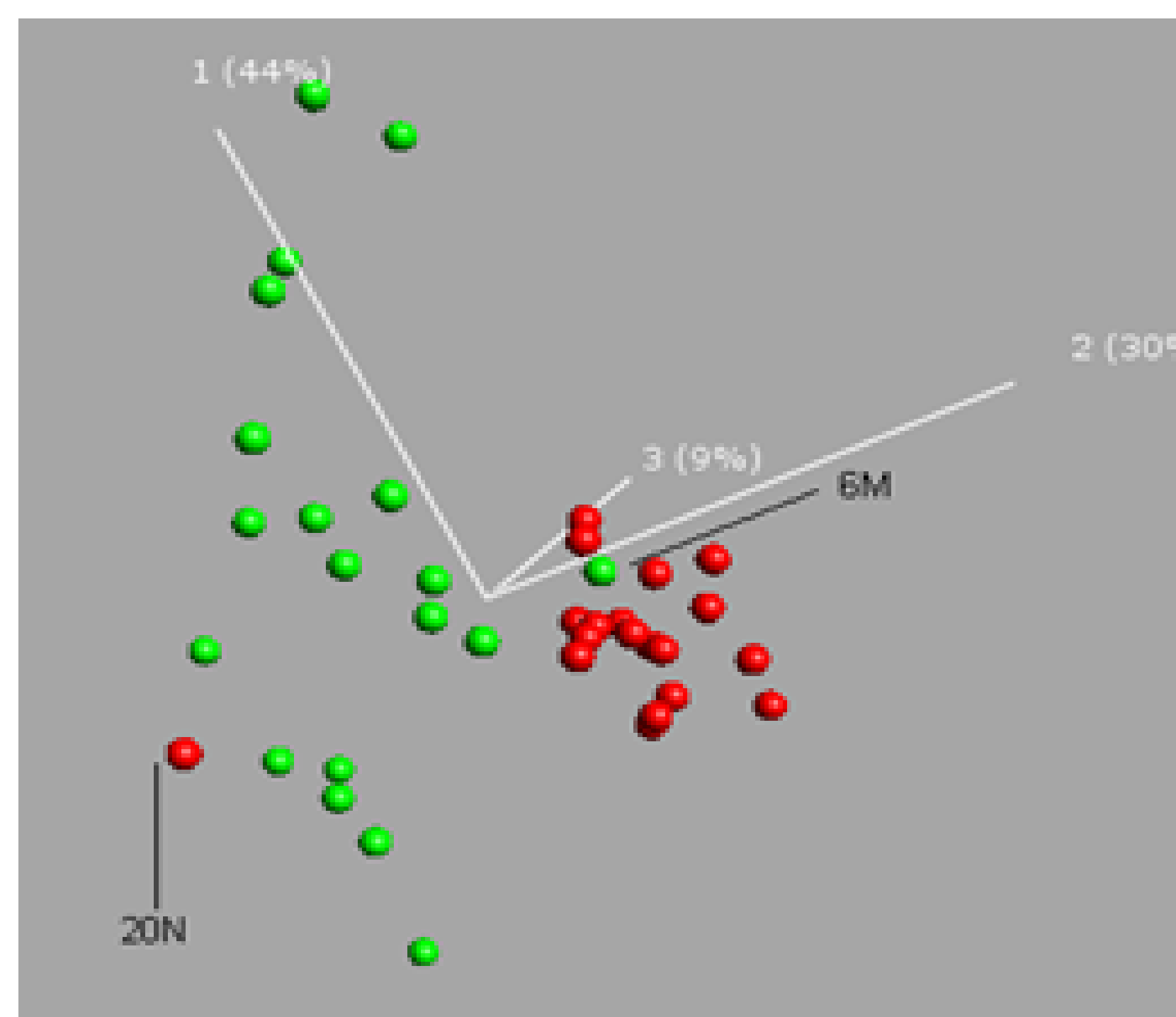


Figure 2: Separation between normal (red) and malignant (green) prostate tissues identified by PCA using a miRNA expression signature of 9 miRNAs.

## Results

Nine miRNAs were found to be differentially expressed at a 0.00001 significance level. Hierarchical clustering and PCA revealed that this expression profile could separate between normal and malignant prostate tissue with the exception for one malignant sample and one normal sample (6M, 20N) (Figure 1,2).

PCA using 16 miRNAs as input also revealed four subgroups within the malignant samples that correlated well with Gleason scores (Figure 3) [2].

A generalization test was performed on the expression profile, showing that the average error rate was 15 %.

## Conclusion

A set of only nine miRNAs was enough to separate between the normal and malignant prostate tissues with the exception of two samples, making the identified miRNA expression signature a good candidate biomarker for diagnosis of prostate cancer. The results from this study will now be validated in a new and larger cohort study.

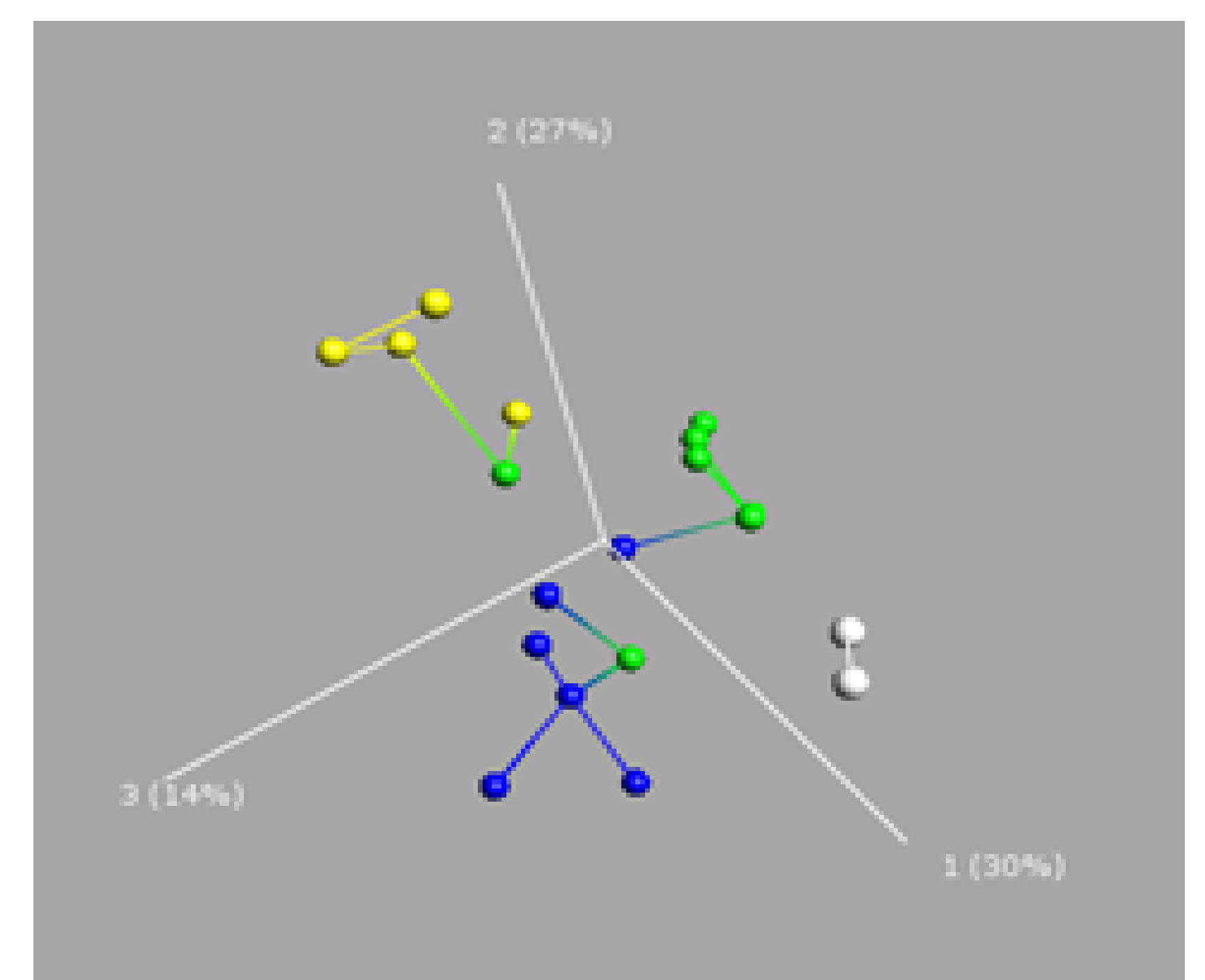


Figure 3: Sixteen miRNAs was found to divide malignant samples into four subgroups which correlated well with Gleason score (GS). Blue = GS 6, Green = GS 7, Yellow = GS 9 and White = GS 10. Gleason 8 was excluded due to loss of PCR data. Lines between samples indicate the nearest neighbours.

## References

- [1] Stahlhut Espinosa, C. & Slack, J. (2006) The role of MicroRNAs in cancer. *Yale journal of biology and medicine*; 79: 131-140
- [2] Carlsson et al. (2010) A miRNA expression signature that separates between normal and malignant prostate tissues. *Cancer cell international* 2011, 11:14

Jessica Carlsson, [jessica.carlsson@his.se](mailto:jessica.carlsson@his.se)

Tumor biology and Bioinformatics researchs group, University of Skövde in collaboration with the University Hospital of Örebro  
Funded by FMB and Lions Cancer Foundation



Systems Biology  
RESEARCH CENTRE