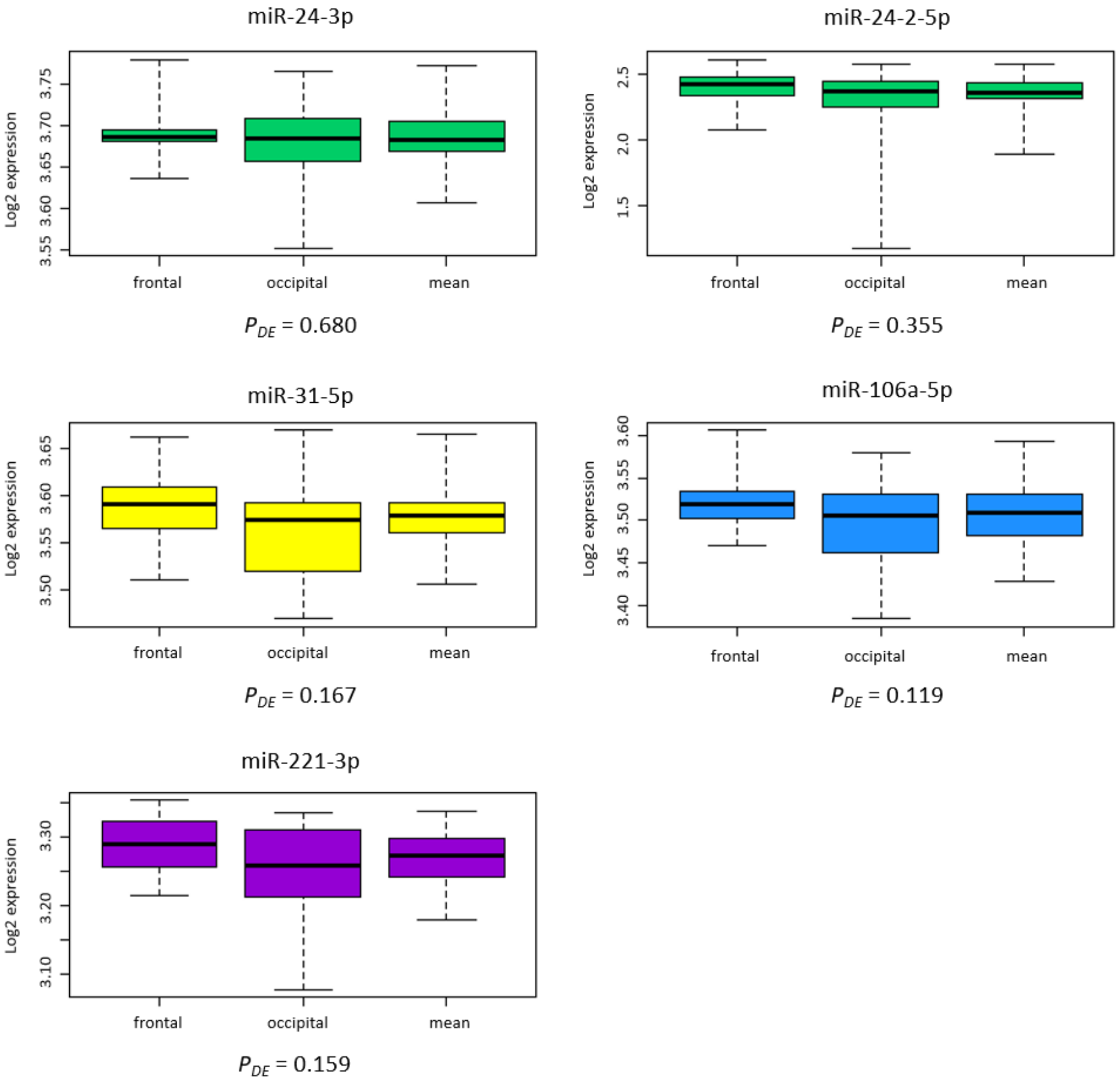
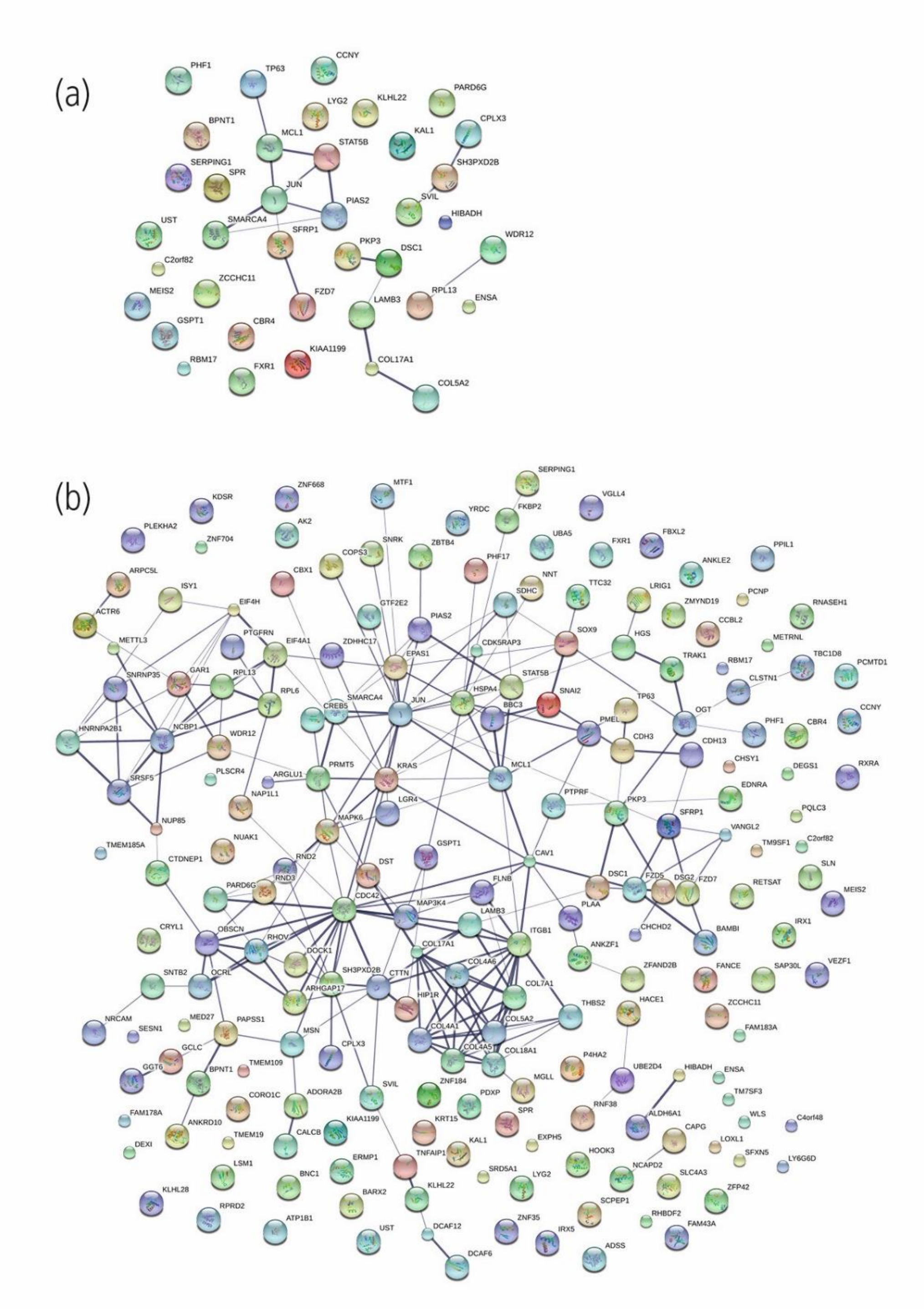
Supplementary Figures:

Expression profiling and bioinformatic analyses suggests new target genes and pathways for human hair follicle related microRNAs



Supplementary Figure 1. **Single tissue analysis of miRNA Expression in the human hair follicle.** Boxplots representing frontal-, occipital- and the mean of frontal and occipital miRNA $\log_2$ expression in the human hair follicle. For those candidate miRNAs that show a significant mRNA correlation (miR-24, miR-31, miR106a, miR-221) no differential expression between hair follicles from the frontal and the occipital scalp areas is observed (Wilcoxon Rank-Sum Test, $P_{DE} < 0.001$ (Benjamini-Hochberg corrected)).



Supplementary Figure 2. **STRING query.** Protein-protein interaction network of: **(a)** the 40 shared target genes; and **(b)** all target genes of miR-24, miR-31, miR-106a and miR-221.