

## Results of Next generation sequencing – Overview of the most dysregulated exomiRs

| Name                   | Log2 fold change | Fold change  | P-value     | FDR p-value |
|------------------------|------------------|--------------|-------------|-------------|
| <b>hsa-miR-4516</b>    | 2.301979591      | 4.93133954   | 2.60E-04    | 0.044631791 |
| <b>hsa-miR-16-5p</b>   | 0.601698752      | 1.517502352  | 0.056039447 | 0.056039447 |
| <b>hsa-miR-143-3p</b>  | 1.205078117      | 2.305497525  | 1.70E-03    | 0.097596967 |
| <b>hsa-miR-451a</b>    | 1.234470352      | 2.352949491  | 4.46E-03    | NaN         |
| <b>hsa-miR-151a-5p</b> | -0.859726972     | -1.814694849 | 5.46E-03    | 0.076437562 |
| <b>hsa-miR-223-3p</b>  | 1.329213947      | 2.512657354  | 9.57E-04    | 0.099003501 |
| <b>hsa-miR-12135</b>   | -2.37776282      | -5.19730174  | 1.36E-04    | 0.044631791 |