**Table 1:** Top two KEGG pathways associated with the most miRNAs. The KEGG pathway ID is shown in brackets.

|  |  |  |
| --- | --- | --- |
| **Number of miRNAs** | **KEGG Pathway** | **Associated miRNAs** |
| 15 | Signalling pathways regulating pluripotency of stem cells (hsa04550) | hsa-miR-4698, hsa-let-7b-5p, hsa-miR-106b-5p, hsa-miR-20a-5p, hsa-miR-548n, hsa-let-7d-5p, hsa-miR-320a, hsa-miR-186-5p, hsa-miR-320b, hsa-miR-320d, hsa-let-7a-3p, hsa-miR-548d-5p, hsa-let-7f-5p, hsa-let-7i-5p, hsa-let-7f-2-3p |
| 11 | TGF-beta signalling pathway (hsa04350) | hsa-miR-4698, hsa-miR-106a-5p, hsa-miR-106b-5p, hsa-miR-20a-5p, hsa-miR-519d-3p, hsa-miR-548n, hsa-miR-101-3p, hsa-miR-186-5p, hsa-let-7a-3p. hsa-miR-548d-5p, hsa-let-7f-2-3p |

**A screenshot of a computer screen

Description automatically generated with low confidenceFigure 1:** Heatmap of the miRNA versus KEGG pathway analysis. This heatmap shows the various miRNAs that are linked to the differentially expressed lncRNAs and their levels of enrichment in KEGG pathways. p-value<0.05; microT<0.8; Fischer’s Test analysis method with fold discovery rate (FDR) correction. Lower log(p-values) is associated with higher enrichment and a deeper red colour. The miRNAs are shown to be associated with various disease pathways, including PCa which is significantly enriched by the hsa-miR-320 family mainly. The hsa-miR-320 family is linked to TERC lncRNA, which is overexpression in PCa.

**Table 2:** Top two GO categories associated with the most miRNAs in the biological process subcategory, and the miRNA names. These miRNAs are associated with the differentially expressed lncRNAs in OCa. The GO category IDs are shown in brackets.

|  |  |  |
| --- | --- | --- |
| **Number of miRNAs** | **GO Category** | **Associated miRNAs** |
| 30 | Biosynthetic process (GO:0009058) and cellular nitrogen compound metabolic process (GO:0034641) | hsa-miR-4698, hsa-let-7b-5p, hsa-miR-485-5p, hsa-miR-106a-5p, hsa-miR-106b-5p, hsa-miR-17-5p, hsa-miR-20a-5p, hsa-miR-20b-5p, hsa-miR-519d-3p, hsa-miR-93-5p, hsa-miR-92b-3p, hsa-miR-548n, hsa-miR-143-3p, hsa-miR-196a-5p, hsa-miR-196b-5p, hsa-let-7d-5p, hsa-miR-320a, hsa-miR-101-3p, hsa-miR-125b-2-3p, hsa-miR-92a-3p, hsa-miR-186-5p, hsa-miR-382-5p, hsa-miR-320b, hsa-miR-320d, hsa-let-7a-3p, hsa-miR-548d-5p, hsa-miR-25-3p, hsa-let-7f-5p, hsa-let-7i-5p, hsa-let-7f-2-3p |

Chart

Description automatically generated with medium confidence**Figure 2:** Heatmap showing the miRNAs that are associated with the differentially expressed lncRNAs versus the biological process GO subcategory (generated by DIANA-miRPath v3.0). p-value<0.05; microT<0.8; Fischer’s Test analysis method with FDR correction. The intensity of the red colour indicates higher enrichment.

A picture containing text, diagram, screenshot, design

Description automatically generated

**Figure 3:** Heatmap of the miRNA versus the molecular function GO subcategory (generated by DIANA-miRPath v3.0). p-value<0.05; microT<0.8; Fischer’s Test analysis method with FDR correction.

A picture containing text, diagram, screenshot, design

Description automatically generated

**Figure 4**: Heatmap of the miRNA versus the cellular component GO subcategory generated by DIANA-miRPath v3.0. p-value<0.05; microT<0.8; Fischer’s Test analysis method with FDR correction.