towards better prediction, prognosis and diagnosis of the disease. Moreover, such an approach would be of interest as part of a combination therapy.

**PO-350** MIRNAS AND THEIR RELATION TO BIOLOGICAL PATHWAYS IN LEFT- AND RIGHT-SIDED COLORECTAL CANCER

S. Sundaramoorthy, S. Heikkinen, M. Hartikainen, T. Kuopio, P. Mecklin, K. Kosma, M. Marranmaa. University of Eastern Finland, School of Medicine- Institute of Clinical Medicine- Clinical Pathology and Forensic Medicine, Kuopio, Finland; University of Eastern Finland, School of Medicine- Institute of Biomedicine, Kuopio, Finland; University of Eastern Finland, Translational Cancer Research Area, Kuopio, Finland; University of Jyväskylä, Biological and Environmental Sciences, Jyväskylä, Finland; Central Finland Health Care District, Department of Pathology, Jyväskylä, Finland; University of Jyväskylä, Sport and Health Sciences, Jyväskylä, Finland; Central Finland Health Care District, Department of Education and Science, Jyväskylä, Finland; Kuopio University Hospital, Department of Clinical Pathology, Kuopio, Finland.

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**Introduction** MicroRNAs (miRNAs) are involved in the regulation of gene expression in colorectal cancer (CRC), which has specific biological pathways that are predominant in either left- or right-sided CRC. However, it is unclear how miRNAs are associated with biological pathways in these two forms of CRC. Our hypothesis is that a comprehensive understanding of the fundamental biological signalling pathways in the two sides of CRC may aid in developing a decisive step towards precision medicine. We aim to clarify specific biological pathway differences of differentially expressed miRNAs between left- and right-sided CRC.

**Material and methods** We extracted total RNA from 24 of left- and right-sided CRC tumour samples from Finnish patients using the mirVana™ miRNA Isolation Kit (Thermo Fisher Scientific) in the discovery cohort. Libraries for small RNA sequencing were prepared using TruSeq® Small RNA Library Prep Kit (Illumina) and run on Illumina MiSeq. Differentially up-regulated miRNAs were identified using DeSeq2. For validation purposes, we used the mature miRSeq dataset of 201 CRC samples from The Cancer Genome Atlas. We analysed biological pathways of site-specific miRNAs from the discovery and validation cohorts using the DIANA/mirPath tool.

**Results and discussions** We found 17 and 15 differentially up-regulated miRNAs in left- and right-sided CRC, respectively, in the discovery cohort. The left miRNAs were involved in the mTOR, Wnt, PI3K-Akt signalling pathways. These pathways are the predominant pathways in left-sided CRC. The Wnt signalling pathway was also significant (false discovery rate <0.05) in the left miRNAs from the validation cohort. In the discovery cohort, the right miRNAs were involved in the TGF-β signalling pathway. This pathway is dominant in right-sided CRC also in earlier reports. Alongside with the pathway findings, we found that the discovery and validation cohorts share six miRNAs. One of these (hsa-miR-196b-5p) was differentially up-regulated in left-sided CRC and the rest of them (hsa-miR-625-3p, hsa-miR-155-5p, hsa-miR-625-5p, hsa-miR-31-5p and hsa-miR-330-5p) in right-sided CRC.

**Conclusion** Our findings highlight that there are site-specific miRNAs in left and right-sided CRC. The results also indicate the involvement of these left and right miRNAs in different predominant biological pathways of the two forms of CRC. This exploration may be useful for further studies on the development of diagnosis in left- and right-sided CRC.

**PO-351** MELATONIN SUPPRESSES TPA-INDUCED ORAL CANCER CELL MIGRATION VIA LINCRNA-LNC310-MEDIATED PRUNE2 ACTIVATION

S. Yang, C. Yeh. Institute of Medicine, Chung Shan Medical University, Taichung, Taiwan; Department of Medical Research, Chung Shan Medical University Hospital, Taichung, Taiwan; Department of Otolaryngology-Head and Neck Surgery, Changhua Christian Hospital- Changhua, Taichung, Taiwan.

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**Introduction** Long non-coding RNAs (lncRNAs) are kind of non-coding RNAs (ncRNAs). The length of IncRNAs is more than 200 nucleotides. A few decades ago, IncRNAs were regarded as useless parts of the genome, but more and more studies demonstrate that IncRNAs play an important role in growth, development, metabolism and cancer. Very few IncRNAs have been characterised in detail at the present time. However, it is clear that IncRNAs are important regulators of gene expression and have a wide range of functions in cellular and developmental processes. Previous studies have shown that development of cancers is accompanied by abnormal expression of IncRNAs that participate in the regulation of cancer metastasis, apoptosis and proliferation. Melatonin is a hormone secreted from pineal gland and play an important role in the regulation of the immune system. Melatonin is also a potent antioxidant agent. Previous studies have shown that melatonin inhibits the growth and metastasis of breast cancer cells, cervical cancer cells and ovarian cancer cells. However, the detailed effects and mechanisms of melatonin and IncRNAs on oral cancer cell metastasis were still unclear.

**Material and methods** RNA-seq and quantitative real-time PCR analyses were used to detect the IncRNAs and mRNAs expression in HSC-3, HSC-4 and OECD-1 oral cancer cells. Transwell migration assay was performed to evaluate the migration of tumour cells. Fluorescent in situ hybridization (FISH) assay was used for determining the IncRNAs levels in oral cancer cell. Protein levels were accessed by western blotting assay.

**Results and discussions** The results show that melatonin could induce the PRUNE2 through decreasing lncRNA-LNC310 to improve the migration inhibition of oral cancer cells. On the other hand, melatonin could partially inactivate Src/STAT3 signalling cascade targeting LNC310 to induce the expression of PRUNE2 in oral cancer cells. Additionally, LNC310 knockdown upregulated PRUNE2 expression and suppressed cell migration in oral cancer cells.

**Conclusion** This results suggested that melatonin inhibited oral cancer migration by inducing lncRNA-LNC310-mediated PRUNE2 expression and indicated that melatonin could be a promising treatment for oral cancer.

**PO-352** THE EFFECTS OF LAPATINIB RESPONSIVE MIRNA ON CELL PROLIFERATION AND CELL INVASION IN HER2 + BREAST CANCER CELL LINE

EE Cilek, H Gurdal, G Gur Dedegolu. Ankara University Biotechnology Institute, System Biotechnology, Ankara, Turkey; Ankara University Medical School, Department of Pharmacology, Ankara, Turkey.

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**Introduction** Lapatinib is a dual receptor tyrosine kinase inhibitor that blocks EGFR (HER1) and HER2 activation in breast cancer. microRNAs (miRNA) are non-coding RNAs involved in the regulation of protein-coding genes and these regulatory
Material and methods To identify tumour-suppressive miRNAs in neuroblastoma, we performed a high-throughput functional screening using 2048 individual miRNAs. Cell proliferation and viability were analysed by crystal violet staining, FACS and western-blot. MiRNA-target prediction analysis was performed in silico and further validated by quantitative real-time PCR, western blot and luciferase-reporter assays. The therapeutic potential of miRNA-restoration therapies in vivo was validated using xenograft models. Statistical significance was determined by two-tailed unpaired Student’s t-test.

Results and discussions Several miRNA whose overexpression reduced cell proliferation and viability in multiple chemoresistant NB cell lines in vitro and in vivo were identified. Those with the highest therapeutic potential were found to target several genes related to cancer, cell cycle and cell survival.

Conclusion MicroRNA-based restoration therapies could be a therapeutic alternative against neuroblastomas resistant to conventional therapies.