swabs (AS) were provided by 45 participants. Shotgun metagenomics sequencing was conducted with the Illumina NovaSeq 6000 System. NGS data analysis was performed using CosmosID, Human3, and R/Bioconductor. **Results** In AS *HPV types* were among the most frequent virus, while *Prevotella copri* and *Prevotella corporis* were among the most abundant bacteria. OS were characterized by the prevalence of *KSHV*, *EBV*, *HSV-2* and *HHV-7*, among others; while species of *Haemophilus*, *Rothia*, and *Neisseria* were the most frequent bacteria. Comparisons between HIV+ and HIV-, considering MSM and TGW, together or separately, indicated a distinctive set of differentially abundant taxa for each comparison (LogFC>1.5, p<0.001). In OS *KSHV* was predominantly abundant in HIV+ patients independently of sexual orientation. AS of HIV+ patients showed enrichment mainly in *HPV* types. For bacteria, species of *Prevotella*, *Leptotrichia*, *Veillonella*, *Fusobacterium, Dialister* were significantly abundant in HIV+ patients independently of the condition MSM or TGW. Next, we analyzed the functional profiling to describe the metabolic potential of the microbial community in a multivariable association between phenotypes and microbial features. Distinctive pathways (n~200) defined OS and AS (q < 0.05). Moreover, we identified differential pathways (q<0.05) associated with HIV condition and anal intraepithelial lesions, such as *ADP-L-glycero-beta-D-mannoheptose* and *preQ0 biosynthesis,* respectively. **Conclusion** Our results reinforce the occurrence of oncogenic viromes in this high HIV-risk population and show that metabolic pathways generated by bacteria associated with HIV-infection could modulate environmental conditions related to inflammation and carcinogenesis.

14. (066) **IDENTIFICATION OF LONG NON-CODING RNAS ASSOCIATED TO THE CMS MOLECULAR SUBTYPES AS PREDICTIVE BIOMARKERS OF RESPONSE TO THERAPY IN COLORECTAL CANCER.**

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The consensus molecular subtypes (CMSs) of colorectal cancer (CRC) define tumor heterogeneity at the gene-expression level. The clinical utility of the CMS classification resides in the possibility to estimate survival (prognostic value) and select patients for both chemotherapy and currently used targeted agents (predictive value). Long Non-coding RNAs (lncRNA) have been largely associated with cancer constituting an essential approach for the search and identification of these biomarkers. **Aim**: To identify lncRNA signatures with prognostic and predictive value associated with each CMS subtype. **Methods**: We performed an integrative bioinformatics analysis on GDC-TCGA-CRC dataset (n=674), considering CMS and SFM based-classification that discriminate tumor microenvironment and drug sensitivity. We first classify tumors in CMSs. We annotated lncRNAs (n=14084) and applied DESeq2 for the comparison of each CMS (CMSk) versus the rest (CMSK-k; pvalue <0.01, LogFC> 1). The obtained lists of the up-modulated lncRNAs exclusive of each CMS were evaluated according to CRC molecular features; the immune, stromal or epithelial tumor component; and the prognostic and predictive value (p<0.05). Furthermore, we evaluated their association to systemic and targeted therapies (SFM) and the potential to be detected in peripheral blood of CRC patients. **Results**: we identified lncRNAs that recapitulate the intrinsic features of the CMS: lncRNA-CMS1 associated with poor prognosis, immune component, resistance to chemotherapy and response to anti-EGFR therapies. LncRNA-CMS2/CMS3 associated with good prognosis, epithelial component and response to anti-EGFR/VEGF. LncRNA-CMS4 showed high expression in mesenchymal-like tumors with poor prognosis but responsive to traditional chemotherapies. Many of these lncRNAs are detected in peripheral blood of CRC patients. **Conclusion**: CMS-lncRNA signatures predictive of therapy response constitute valuable biomarkers to be assessed in preclinical models.

15. (078) **BIOINFORMATIC CHARACTERIZATION OF IMMUNE CELL TYPES IN THE BONE MARROW OF CHILDHOOD ACUTE LYMPHOBLASTIC LEUKEMIA PATIENTS FROM ARGENTINA THROUGH ANALYSIS OF TRANSCRIPTOME DATA**

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Acute lymphoblastic leukemia (ALL), the most incident pediatric cancer, is characterized by the overproduction of immature lymphoid blasts in the bone marrow (BM). While considerable progress has been made on treatment efficacy and survival rates, about 15-30% of patients relapse and/or die. Immunotherapies are promising as complementary treatments to chemotherapy, yet the most relevant therapy targets and patient subsets remain unclear. *Aims*: To characterize immune cell types in the BM microenvironment of ALL samples using predictive bioinformatic tools on transcriptome data. *Methods*: we performed RNA-seq on BM samples collected at ALL diagnosis (N=32). The proportion of immune cells was estimated using MIXTURE through two gene expression signatures (LM22, TIL10). A "cytolytic score" reflecting $CD8^+$ cytotoxic T lymphocytes (CTLs) and Natural Killer cells (NK) abundance was calculated as the geometric mean of 5 genes specifically expressed in CTLs/NK. Gene set enrichment analysis using ImmuneSigDB and Reactome was performed with GSVA package in R. *Results*: Relative proportions of B and T cells were concordant with B- and T-cell ALL subtype, respectively. Cytolytic score was positively correlated with $CD8^+$ T cells and NK proportions (Spearman Rho>0.38, p-val<0.05). Higher $CD8^+$ T cell and NK could be associated with worse event-free survival (hazard ratio=5.39, 95%CI: 0.64-44.98, CoxP p-val=0.08). 12.5% (4/32) of samples showed a cytolytic Z-score > 1, and half of them relapsed or died. Gene set enrichment analysis for >1 vs. <1 cytolytic Z-score resulted in statistically significant enrichment in genesets related to activation of $CD8^+$ T cells, immune cell trafficking, and BM niche signaling. *Conclusions*: we identified a subset of B-ALL patients with increased abundance of $CD8^+$ T cells/NK, suggesting potential candidates for immunotherapies. Given the small sample size, these observations should be confirmed in additional patients.

16. (135) **GENOMIC ANALYSIS OF CLUSTER *FX-MIR*: POSSIBLE IMPLICATIONS IN FRAGILE X-ASSOCIATED DISORDERS**

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The Fragile X Mental Retardation-1 (*FMR1*) gene consists of 17 exons spanning 38 kb of the Xq27.3 chromosome and codes for the protein fragile X mental retardation protein (FMRP).
FMR1 is involved, by different molecular mechanisms, in 3 genetic disorders. The absence of FMRP due to an expansion of > 200 CGG repeats in the 5′UTR of the gene (full mutation), is responsible for the Fragile X syndrome (FXS) while the premutation state is associated with the Fragile X-associated Tremor/Ataxia Syndrome (FXTAS) and Fragile X-associated Primary Ovarian Insufficiency (FXPOI).
Recently, a microRNA (miRNA) cluster adjacent to *FMR1* (*Fx-mir*) has been described in placental mammals and it has been shown that a number of miRNAs in the cluster target *FMR1* in human and mouse, regulating its expression. In this work we described the *Fx-mir* cluster and the putative targets of its miRNAs in *Rattus norvegicus* (rat). In particular, we were interested in studying whether some of the *Fx- mir* miRNAs target *Fmr1* in the rat as well.
We used public access databases and performed a reciprocal best