

ANTICIPATED RESULTS: Progenitor markers are related to extracellular matrix, eg DCN (logFC progenitors vs other cells types=3.17, expressed in 99.7% (pct.1) of progenitors, 26.1% (pct.2) of others). Endothelial and pericytes shared markers like RBP7 (logFC=1.67, pct.1 0.88, pct.2 0.39); pericytes also showed unique markers, eg RGS5 (logFC=2.29, pct.1 0.89, pct.2 0.17). Progenitors are further divided into 11 sub-clusters, one of which showed enrichment of CD36 (high proliferation potential), FABP4 (differentiation), and of the novel marker PALMD (logFC=7.13, pct.1 0.94, pct.2 0.48). All $p < 10E-5$. GSEA analysis suggests that inflammatory pathways are downregulated in both adipose progenitors and endothelial/pericyte cells in the femoral compared to the abdominal depot. DISCUSSION/SIGNIFICANCE OF FINDINGS: Single cell RNA sequencing provides unique insights into the molecular profile of cell types and the identification of novel subsets of cells within the human adipose tissue. Such cellular heterogeneity may explain differences in adipose function between individuals and eventually in the risk of obesity-associated metabolic diseases.

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Differential chromatin accessibility at dorsal root ganglia enhancers is associated with nerve injury

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ABSTRACT IMPACT: Our improved understanding of the changes in chromatin accessibility that occur in persistent pain states may identify regulatory genomic elements that play essential roles in modulating gene expression in the DRG. OBJECTIVES/GOALS: Efforts to understand genetic variability involved in an individual's susceptibility to persistent pain support a role for upstream regulation by epigenetic mechanisms. Our objective was to examine the transcriptomic and epigenetic basis of persistent pain following nerve injury. METHODS/STUDY POPULATION: We used a multiomic approach to identify novel molecular pathways associated with nerve injury-induced pain hypersensitivity. Adult Sprague Dawley rats were randomized to Chronic Constriction Injury (CCI) to the sciatic nerve or no treatment (naive). The ipsilateral L4-L6 dorsal root ganglia (DRG)s were removed on Day 14 and used for ChIP-seq for H3K4me1, ATAC-seq, and RNA-seq. We assessed for differential chromatin accessibility, transcription factor motifs, and enrichment for biological processes in chromatin accessible regions associated with cis-regulatory regions identified by ATAC-seq and H3K4me1 enrichment. Luciferase assays determined the functional significance of these sequences. RESULTS/ANTICIPATED RESULTS: We identified 58,446 genomic regions where H3K4me1 enrichment overlapped with chromatin accessibility. Differential analysis identified 2145 of these 58,446 regions that had changes in accessibility after CCI. The majority of these regions were located in introns or intergenic regions. Functional annotation of the differentially accessible regions identified disparate molecular functions enriched following nerve injury which suggests that altered

chromatin structure plays a role in the development of mechanical hypersensitivity. Motif analysis identified specific transcription factor families whose binding sequences were enriched in regions of increased or decreased accessibility. Luciferase assays showed significant enhancement or repression of gene transcription. DISCUSSION/SIGNIFICANCE OF FINDINGS: Our data provides a comprehensive map of chromatin accessibility changes in the DRG after CCI and emphasizes the importance of chromatin structure in the development and maintenance of chronic pain.

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The role of the bromodomain and extra-terminal motif (BET) family of proteins in head and neck cancer tumorigenic phenotype

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ABSTRACT IMPACT: Understanding the biology underpinning head and neck cancer invasion and metastasis could lead to novel targeted therapies that are both effective and tolerable for patients with this debilitating disease. OBJECTIVES/GOALS: The bromodomain and extra-terminal (BET) family of epigenetic regulators has been implicated in the tumorigenesis of various cancers. In head and neck squamous cell carcinoma (HNSCC), the majority of morbidity is due to invasion and metastasis, so there is special interest in understanding the development of these phenotypes in HNSCC cells. METHODS/STUDY POPULATION: Stable SCC9 knockdown cell lines were generated by infecting cells with a lentivirus encoding Cas9-KRAB and a lentivirus encoding gRNA targeting each of the candidate BET proteins: BRD2, BRD3, BRD4, and BRDT. Knockdown was confirmed by qRT-PCR. Next, standard assays for proliferation (CellTiter-glo), invasion (Matrigel), and migration (scratch-wound healing assay) were performed for all candidate knockdowns and compared to a non-target control. RESULTS/ANTICIPATED RESULTS: Proliferation assay results revealed that BRD4 knockdown had a significant negative effect on the proliferative capacity of SCC9 cells in vitro. Similarly, BRD4 knockdown SCC9 cell lines were less invasive and less migratory. Interestingly, knockdown of BRD2, BRD3, and BRDT had no effect on proliferation, invasiveness, or migration. DISCUSSION/SIGNIFICANCE OF FINDINGS: We have identified BRD4 as a key driver of the HNSCC tumorigenic phenotype. In the future, we plan to investigate the role of JQ1, a pan-BET inhibitor, on HNSCC cell phenotypes. Additionally, we will identify the downstream targets of BRD4, which may serve as potential therapeutic targets for both HNSCC as well as other cancers more broadly.

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Multiple epidemics of multidrug-resistant tuberculosis revealed by spatial disease mapping and whole-genome sequencing analysis in urban China

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ABSTRACT IMPACT: Our study will integrate state-of-the-art methods in pathogen genomics, epidemiology, and geospatial analysis to identify both host- and pathogen-factors driving the MDR-TB transmission and the study outcome can inform the design of