

The Skeletal Atlas: A holistic approach to transcriptomics in the skeleton.

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Gene expression atlases are powerful bioinformatics tools that allow access to the scientific community to explore omics data. In biomedicine, numerous gene expression databases are available, yet none provide enough information about localized transcriptomics in the skeletal system. In this work we try to solve this gap of knowledge by creating a transcriptomic atlas which brings together different works across the skeletal system, analyzing several key tissue compartments in normal and pathological conditions from mouse and human after analyzing more than 200 studies. Our atlas shows a user-friendly representation which allows the comparison of multiple genes across the different tissues of the skeleton: bone, cartilage, tendon, ligament, growth plate and skeletal muscle. As expected, our first finding was the identification of a significant heterogeneity between experiments from similar studies but from different labs, so we have created a dataset processing pipeline with inclusive/exclusive criteria of RNAseq experiments based in sequencing quality and purity of the analyzed tissues in search of a normalization protocol. We believe that this atlas will allow the homogenization of the public transcriptomic studies in the skeleton and will settle the basis to incorporate the upcoming data from single cell transcriptomics studies.