Identifying novel drug targets for Pain using Machine Learning approaches

Pain Neurobiology Research Group

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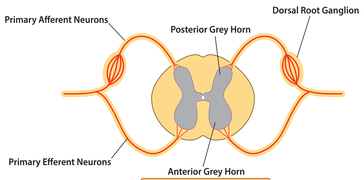
Abstract

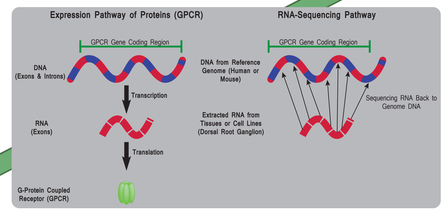
Chronic neuropathic pain is characterized as a dysfunction of the nervous system due to nerve injury or tissue damage. It has become an increasingly more common pathological state in humans, with a prevalence of 30% in the general population (up to 7% being attributed to neuropathy)[1]. Such damage often causes nerves to send incorrect pain signals to the Central Nervous System resulting in unrelenting chronic pain and a severely lessened quality of life. Neuropathic pain is hard to treat, with only 11 - 14% of those affected achieving partial relief through treatment[2]. We aim to characterize the molecular biology of chronic neuropathic pain by performing high-throughput **RNA sequencing**[5,9] for profiling gene expression in human pain-sensing tissues[3] (specifically **Dorsal Root Ganglia** / DRG). Using statistical, **entropy-based measures** and hierarchical clustering, we identify DRG-specific pain receptors by contrasting DRG gene expression against other excitable tissues. A similar profiling for *Mus musculus*[4,7], combined with sophisticated **evolutionary analysis**[6,10], then allows us to pinpoint drug targets compatible with mouse models. Functional analytic[8] studies can then be performed with the aim of taking the first chronic pain drug to market.

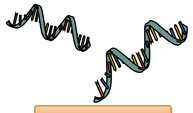


DRG Tissue Sample Donor

RNA preserved in RNA Later

RNA-seq PERFORMED BY Active Motif, Inc



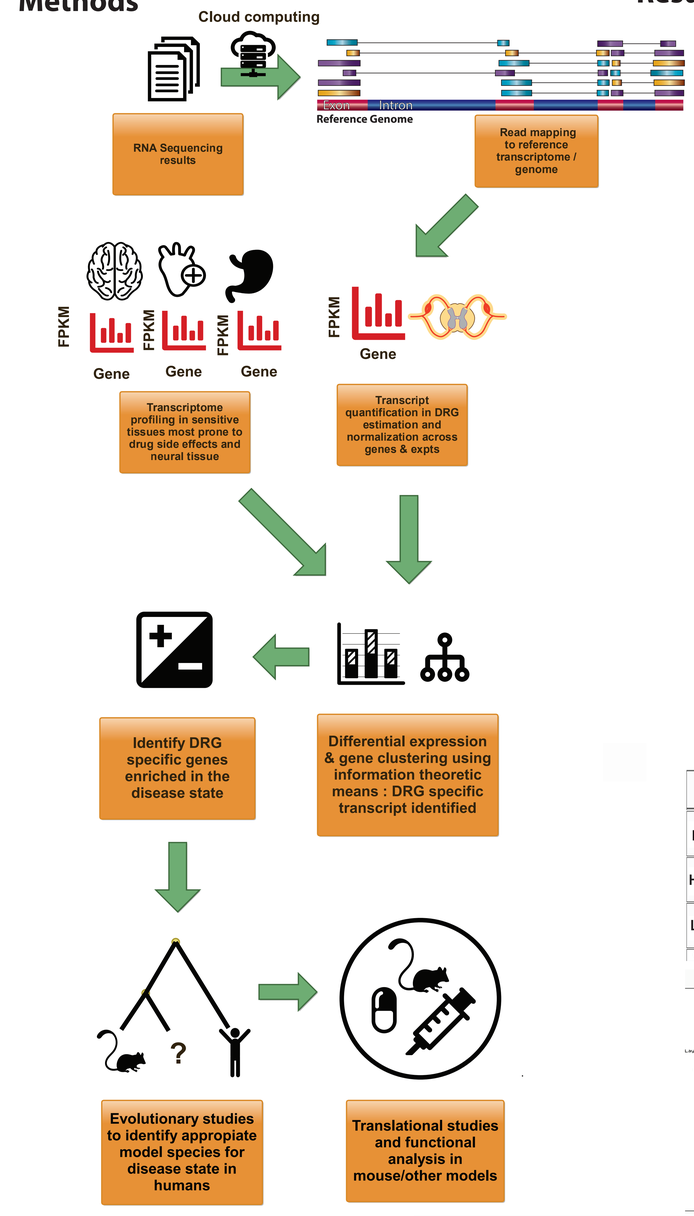


RNA extraction, purification, library selection of Poly A+ RNA

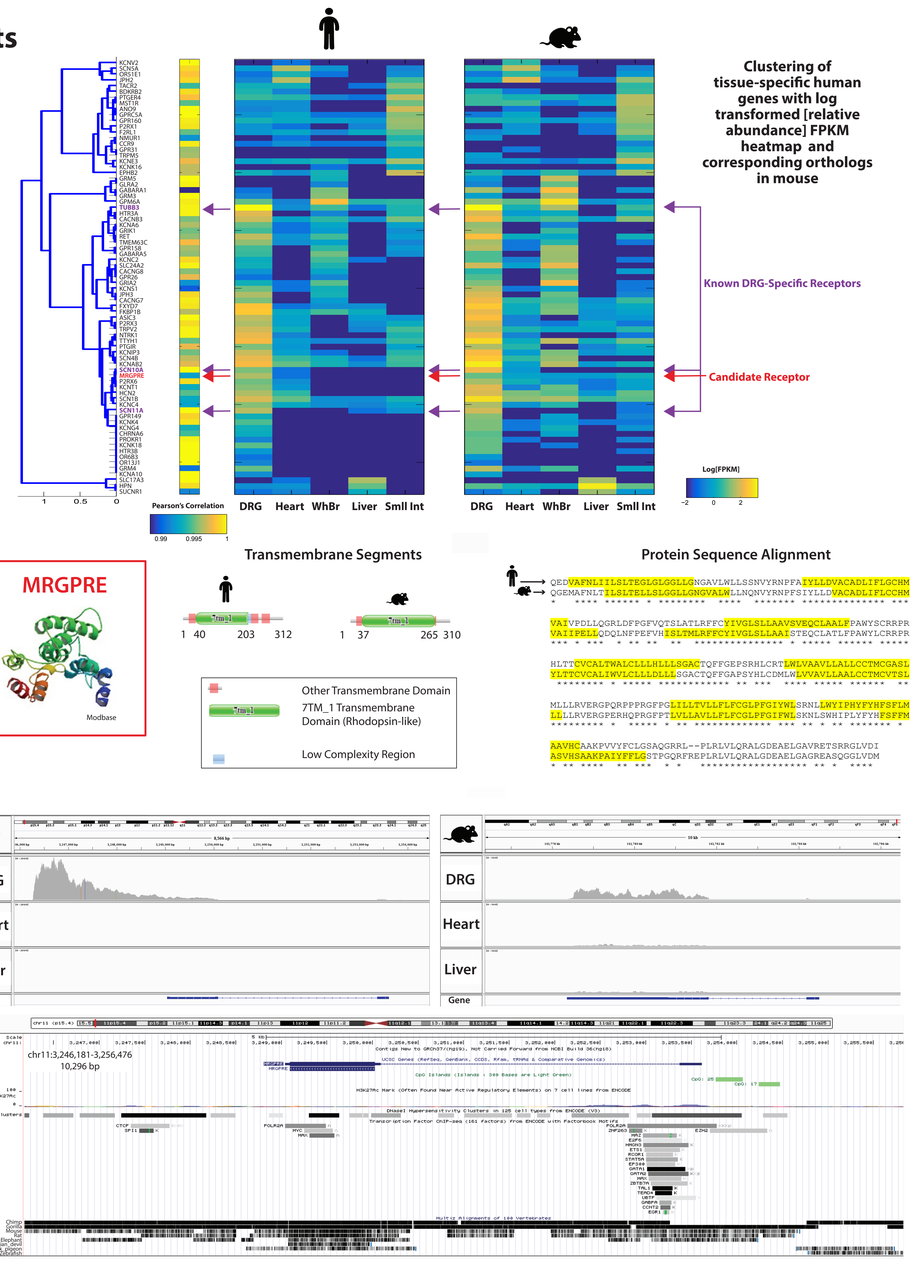
Creation of complementary DNA from RNA

RNA Sequencing results

Methods



Results



Citations

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SRAToolkit (http://www.ncbi.nlm.nih.gov/books/NBK158900/) & SamTools (http://samtools.sourceforge.net/) were used for NGS data processing

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