ABSTRACT

Establishing gene expression profiles across various tissues or cells, under different conditions, is essential for accomplishing many goals of research in life sciences, including the understanding of mechanisms of gene expression and identification of candidate molecules for better diagnostics, prognostics and therapeutics. However, while transcription profiles have been reported for many mammalian tissues and conditions, the molecular mechanisms of transcriptional control are still not understood completely.

Analyzing different sets of promoters of co-expressed genes might provide insights about the specific elements involved in differential transcription control. The current work attempted to make the best possible use of the publicly available mammalian gene expression profiles for an eventual analysis of the promoters corresponding to different sets of similarly transcribed genes. Considering the volume of data available and the work needed, only selected tissues/conditions were addressed in the beginning. The testis tissue and a specific testicular disorder, viz., the non obstructive azoospermia, were prioritized in the current study. Specific elements in and around promoters were identified to be strongly associated with different sets of genes (the testis-specific and ubiquitous genes). Potential biomarkers have also been suggested for the non-obstructive azoospermia disorder in men. Multiple databases and software were also developed as part of the study, and some of them have already been published in peer-reviewed journals.