THOR: a database for the management and analysis of regulatory regions functional assays

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Current efforts to identify functional DNA variants were essentially oriented towards the coding regions of candidate genes since these variants have a direct impact on the structure and function of the affected proteins. Furthermore, abnormal expression of finely regulated genes can lead to disequilibria in different metabolic pathways and/or biological processes. Thus, the investigation of the functional impact of single nucleotide polymorphisms (SNPs) as well as the determination of the importance of evolutionary conservation in the regulatory regions of candidate genes should improve our knowledge on complex disease aetiologies. As part of a Genome Quebec/Canada funded project, this will be done by integrating *in-silico* analysis together with results from electrophoretic mobility shift (EMSA) and *in-vitro/in-vivo* promoter activity assays. Here, we present the THOR MySQL database, a framework for the management of pre- and post- experiment data as well as for the evaluation and distribution of the results. This will help to achieve a better annotation of gene regulatory regions.