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VitExpress, an open interactive transcriptomic platform for grapevine

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We developed VitExpress, an open interactive transcriptomic platform for grapevine, using our newly assembled and annotated Chasselas genome as a reference. This platform provides a genome browser and integrated web tools for expression profiling, and a set of statistical tools (StatTools) for the identification of highly correlated genes. The implementation of the correlation finder tool for *MybA1*, a major regulator of the anthocyanin pathway, identified candidate genes associated with anthocyanin metabolism, whose expression patterns were experimentally validated as discriminating between black and white grapes. These resources and innovative tools for mining genome-related data are anticipated to foster advances in several areas of grapevine research.

Keywords: Transcriptomic platform, RNA-seq, Statistics, Data mining, Anthocyanin pathway.