

DE NOVO RECONSTRUCTION OF THE *VITIS VINIFERA* CV. *CORVINA* TRANSCRIPTOME

VENTURINI L., FERRARINI A., NOEL D., TONONI P., BUSON G., ZENONI S., BELLIN D., PEZZOTTI M., DELLEDONNE M.

Department of Biotechnology, School of Applied Biotechnology, University of Verona, Strada Le Grazie 15, 37134 Verona (Italy)

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The widespread adoption of NGS technologies has created in recent years an unparalleled inflow of sequence data, which can be leveraged to obtain clear information on the genetics and transcriptome of various organisms. In agronomics, these new methods can be used to gather information on cultivars of sequenced organisms. In particular we were interested in identifying putative specific genes represented in *Vitis vinifera* cv Corvina and not in the sequence grape clone (Pinot Noir 40024). These genes could be of interest in order to investigate the molecular bases of specific quality characteristics. To this end, we have pooled RNA of *Vitis vinifera* cv. Corvina samples taken from 45 different tissues and/or development stages, and sequenced it with an Illumina HiSeq platform. We obtained more than 100 million reads, which were filtered and assembled with the Velvet/Oases software suite. To facilitate the assembly, we provided the software with the alignment of the reads against the *Vitis vinifera* 12X genome (performed with the TopHat software). The reconstructed transcripts were compared to known genes already annotated and ESTs, to identify potential genes specific of this cultivar. Moreover, in order to estimate the expression levels of these genes, we performed another sequencing experiment encompassing five developmental fruit stages, with three biological replicate each. Using Bowtie and Cufflinks we calculated gene expression levels and identified putative novel genes which are differentially modulated during berry development and withering.