SUPPLEMENTARY MATERIALS

"Good Wine Makes Good Blood": An Integrated Approach To Characterize Autochthonous Apulian Grapevines As Promising Candidates For Healthy Wines

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Table S1: Untrimmed and trimmed sequences for the different cultivars.

Table S2: Paired-end (PE) and mapped reads, with relative percentage, obtained after sequence alignment.

Table S3: Target genes and specific primer pairs used for qRT-PCR.

Figure S1: Classification of expressed DEGs in the investigated cultivars between pairwise NA vs NT, NA vs SM and NT vs SM, according to molecular function (MF) and biological process (BP).

Table S1. Untrimmed and trimmed sequences for the different cultivars. Biological replicates are indicated in the sample-id column as NA for Negramaro cv, NT for Nero di Troia cv and SM for Susumaniello cv.

Sample-id	Untrimmed sequences	Trimmed sequences
NA_1	72.474.666	64.278.602
NA_2	83.498.082	73.995.480
NA_4	93.439.632	83.434.718
NT_3	73.514.034	64.894.852
NT_5	72.558.438	64.219.248
NT_9	77.299.542	66.473.998
SM_6	67.765.598	59.719.112
SM_7	72.167.418	63.647.554
SM_8	78.083.724	67.947.888

Table S2. Paired-end (PE) and mapped reads, with relative percentage, obtained after sequence alignment.Biological replicates are indicated in the sample-id column as NA for Negramaro cv, NT for Nero di Troia cv and SM for Susumaniello cv.

Sample-id	Input reads (PE)	Mapped reads	%
NA_1	32.139.301	30.137.507	93.77
NA_2	36.997.740	33.136.426	89.56
NA_4	41.717.359	39.401.207	94.45
NT_3	32.447.426	30.773.205	94.84
NT_5	32.109.624	30.408.021	94.70
NT_9	33.236.999	31.327.726	94.26
SM_6	29.859.556	28.004.595	93.79
SM_7	31.823.777	29.684.781	93.28
SM_8	33.973.944	31.808.945	93.63

Table S3. Primer sequences for qRT-PCR analysis.

Gene		Primer sequence (5'→3')	Amplicone size (bp)	Reference
VvF3'H	Fw	GAGAAGAGGTGGACGGAGCAAATC	167	Zhang et al., 2018
	Rv	GCCTCCGTTGCCGCTCAGTT		
VvF3'5'H	Fw	AAACCGCTCAGACCAAAACC	100	Azuma et al., 2012
	Rv	ACTAAGCCACAGGAAACTAA		
VvOMT	Fw	CTCTGCAGGCGCCTCTATTA	139	Cutanda-Perez et al., 2009
	Rv	CCCAAAACAGAGTCTGGACA		
VvANAT	Fw	CACCATTACCAGGCATTT	120	Sun et al., 2016
	Rv	CCTCCCTTAGTAGACCCAC		
VvMybA1	Fw	GTCCTTGATTGCGGGTAG	149	Sun et al., 2016
	Rv	GAGGCTTTATAGCTTTGGTT		
VvMybA2	Fw	CCAGTAAGCCATCATCCACG	140	by authors
	Rv	TGTCCAGAGGCTTGCGATAA		
VvEF1γ	Fw	CAAGAGAAACCATCCCTAGCTG	92	Hichri et al., 2010
	Rv	TCAATCTGTCTAGGAAAGGAAG		

Figure S1: Classification of expressed DEGs in the investigated cultivars between pairwise NA vs NT, NA vs SM and NT vs SM, according to molecular function (MF) and biological process (BP). Abbreviations: NA, Negramaro; SM, Susumaniello; NT, Nero di Troia; UP, Upregulated DEGs; DOWN, Downregulated DEGs.