SUPPLEMENTARY DATA
Berger, M.M.J., Lailheugue, V., Zhelyazova, G., Stammitti, L., Lauvergeat, V., Barrieu, F. & Gallusci, P. (2022).
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Supplementary Material

SUPPLEMENTARY INFORMATION 1. Buffer composition and details.

Extraction Buffer (EB): 300 mM Tris HCL (pH 8.0), 25 mM EDTA, 2M NaCl prepared with Diethyl pyrocarbonate (DEPC) water, 2 % Cetyl trimethylammonium bromide (CTAB), 2 % PVPP, and just prior to use, add 2 % β-mercaptoethanol. DEPC prepared water is prepared overnight by adding 0.1 % (v/v)% of DEPC with gentle stirring and autoclaved in order to eliminate potential RNAseq contamination from water.

Extraction buffer is composed of products that aim at enhancing DNA yield extraction and integrity. Tris-EDTA buffer is a commonly used buffer to prevent DNA from nuclease activity since EDTA is a chelator of bivalent cations. The use of β-mercapto-ethanol, which is a potent antioxidant, limits oxidation of nucleic acids. It also denatures proteins and prevents polymerisation of tannins which can co-precipitate with DNA and interfere with subsequent enzyme activity. PVPP forms complexes with polyphenolic compounds through hydrogen bonding. It allows the polyphenolics to be separated from the DNA, and removed after the centrifugation step. Combination of CTAB and high quantity of NaCl forms soluble complexes with both DNA and protein, thus keeping them in the supernatant (Varma *et al*., 2007).

Chloroform: Isoamyl alcohol: IAA (24/1) was used to separate nucleic acids from proteins that groups at the interphase thanks to the organic solvent (Chloroform-IAA). Protein contamination of nucleic acid is limited by avoiding pipetting the interphase at this step.

Sodium Acetate: NaOAc prepared at 3M (pH 5.2) salt is used to neutralise the negative charge of nucleic acids by breaking up in Na+ ions formed by NaOAc breaks in solution and neutralising the negative charge carried by nucleic acids, making the molecule far less hydrophylic. Subsequent addition of pure isopropanol here facilitates the interaction between Na+ and nucleic acid negative charges which make them drop out of the solution and precipitate. (https://bitesizebio.com/253/the-basics-how-ethanol-precipitation-of-dna-and-rna-works/)

Lithium Chloride: The LiCl solution was prepared at a 10 M concentration with nuclease free water. LiCl solution is known to precipitate RNA specifically by modifying RNA density (ThermoFisher, Technical bulletin #160).

70 % Ethanol (EtOH): solution was prepared with nuclease-free water.

Ammonium acetate: solution was prepared at 7.5M concentration, pH 7.7 with nuclease free water. Combinations of salt and absolute ethanol are used to precipitate DNA in the same way as NaOAc and isopropanol.

Tris-EDTA: TE solution used for nucleic acid resuspension was prepared with 10 mM TrisHCL, 1 mM EDTA at pH 7.5, in depc treated water.

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SUPPLEMENTARY TABLE S1. Extraction results on grapevine leaves obtained with different kits and protocols.

Material	Sample weight (mg)	Methods	Quantification method	DNA yields	A280	A230	Reference
Leaf	50	Thomas *et al*. (1993)	Spectrometry	~ 60,75 (ng/µL)	~ 1,43	-	Akkurt M, 2012
		Lodhi *et al*. (1994)		~ 426 (ng/µL)	~ 1,67	-	
		Lefort *et al*. (1998)		~ 617 (ng/µL)	~ 1,72	-	
		Kit 1 (Nonenzymatic)		~ 140,65 (ng/µL)	~ 1,28	-	
		Kit 2 (Salt precipitation)		~ 189,71 (ng/µL)	~1,47	-	
		Kit 3 (Spin column chromatography)		~ 222,97 (ng/µL)	~ 1,66	-	
Leaf	200–300	Lo Piccolo *et al*. (2012)	Spectrometry	~ 246,25 (ng/µL)	~ 1,85	~ 2,11	Lo Piccolo *et al*. (2012)
Leaf	750	Doyle and Doyle (1987)	Spectrometry	~ 231 (µg.gFW-1)	~ 1,3	-	Marsal *et al*. 2013
	200	Marsal *et al*. (2011)		~ 483 (µg.gFW-1)	~ 2,0	-	
	200	Modified Marsal *et al*. (2011)		~ 445 (µg.gFW-1)	~ 1,9	-	
	100	Dneasy Plant Mini Kit		~ 378 (µg.gFW-1)	~ 1,9	-	
	35	MasterPure Plant Kit		~ 19 (µg.gFW-1)	~ 1,3	-	

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SUPPLEMENTARY TABLE S2. Details of Extraction results.

Tissue	Cultivar	Replicates	DNA µg.gFW-1	260/280	260/230	RNA µg.gFW-1	260/280	260/230	RIN score	Fresh Weight (mg)	[DNA] (60 µL)	[RNA] (50 µL)
Leaf_10	RGM	3	21.1 ± 2.7	1.81 ± 0.37	0.98 ± 0.23	50.45 ± 14.14	2.35 ± 0.10	2.22 ± 0.12	-	11 ± 0	3.87 ± 0.49	11.1 ± 3.52
Leaf_30	RGM	3	41.9 ± 1.7	1.65 ± 0.02	0.93 ± 0.09	248.88 ± 66.16	2.11 ± 0.08	2.37 ± 0.09	-	29 ± 1	20.03 ± 1.14	142.25 ± 39.93
Leaf_50	RGM	6	25.3 ± 1.4	1.69 ± 0.05	1.09 ± 0.22	276.74 ± 39.50	2.05 ± 0.03	2.37 ± 0.07	-	52 ± 2	21.7 ± 1.14	284.9 ± 32.82
Leaf_160	RGM	3	26.9 ± 2.1	1.9 ± 0.02	1.62 ± 0.10	268.19 ± 26.085	2.06 ± 0.01	2.38 ± 0.01	-	157 ± 9	70.17 ± 6.46	839.13 ± 83.40
Leaf	1103P	4	23.7 ± 5.3	1.86 ± 0.03	1.49 ± 0.15	320.3 ± 61.7	2.08 ± 0.01	2.31 ± 0.08	-	152 ± 5	60.1 ± 15.0	974.4 ± 200.2
Leaf	RGM	4	25.1 ± 3.8	1.9 ± 0.02	1.63 ± 0.08	268.2 ± 29.5	2.08 ± 0.03	2.37 ± 0.035	-	160 ± 9	66.5 ± 8.7	681.1 ± 321.8
Leaf	CS	9	17.4 ± 2.8	1.89 ± 0.01	2.13 ± 0.09	184.3 ± 67.2	2.08 ± 0.02	2.35 ± 0.02	7.8 ± 0.2	164 ± 8	47.0 ± 6.6	602.2 ± 218.6
Young Leaf	CS	29	35.6 ± 8.7	1.91 ± 0.01	2.13 ± 0.16	225.5 ± 39.2	2.08 ± 0.02	2.34 ± 0.04	7.7 ± 0.1	228 ± 7	132.4 ± 30.2	1013.6 ± 167.7
Stem	1103P	4	12.9 ± 5.3	1.78 ± 0.07	1.35 ± 0.09	173.1 ± 30.8	2.05 ± 0.02	2.29 ± 0.11	-	206 ± 6	44.5 ± 9.9	715.3 ± 145.6
Stem	RGM	4	21.5 ± 2.2	1.88 ± 0.01	1.57 ± 0.04	214.0 ± 32.2	2.09 ± 0.02	2.34 ± 0.01	-	211 ± 8	75.6 ± 9.6	906.1 ± 165.5
Root	1103P	4	13.4 ± 1.1	1.61 ± 0.05	1.17 ± 0.03	116.0 ± 10.1	1.97 ± 0.01	2.22 ± 0.08	-	207 ± 7	46.2 ± 2.7	479.9 ± 38.8
Root	RGM	4	11.7 ± 1.0	1.74 ± 0.03	1.23 ± 0.07	126.3 ± 14.9	2.00 ± 0.02	2.31 ± 0.06	-	212 ± 12	41.3 ± 4.9	536.9 ± 86.7
In vitro plant	1103P	3	43.0 ± 12.5	1.60 ± 0.01	1.46 ± 0.1	204.2 ± 16.1	2.02 ± 0.01	2.16 ± 0.04	-	101 ± 6	73.2 ± 23.0	413.5 ± 52.8
In vitro plant	RGM	3	32.8 ± 3.9	1.71 ± 0.02	1.25 ± 0.07	143.8 ± 11.4	2.02 ± 0.01	2.33 ± 0.05	-	113 ± 5	61.7 ± 5.6	325.6 ± 37.1
Berry Pulp	CS	3	0.9 ± 0.4	2.03 ± 0.06	0.71 ± 0.05	24.5 ± 4.1	2.08 ± 0.05	2.38 ± 0.05	-	240 ± 20	3.6 ± 1.4	117.2 ± 19.5
Berry Pulp	PN	4	0.8 ± 0.3	1.95 ± 0.06	0.74 ± 0.16	22.3 ± 7.1	2.07 ± 0.04	2.44 ± 0.06	-	239 ± 9	3.0 ± 1.3	107.0 ± 36.1
Berry Skin	CS	3	2.1 ± 0.3	2.00 ± 0.04	0.65 ± 0.04	24.9 ± 8.0	1.97 ± 0.08	2.46 ± 0.15	-	198 ± 3	6.9 ± 1.2	98.7 ± 36.5
Berry Skin	PN	4	1.9 ± 0.2	2.03 ± 0.02	0.75 ± 0.08	26.8 ± 3.9	2.08 ± 0.06	2.36 ± 0.08	-	219 ± 17	6.8 ± 0.8	118.1 ± 23.7

*Protocol efficiency and reliability validation performed on vegetative organs, berry tissues and entire *in vitro* grown plants coming from different grapevine cultivars (RGM, 1103P, CS, PN). Riparia Gloire de Montpellier (RGM), 1103 Paulsen (1103P), Cabernet-Sauvignon (CS), Pinot noir (PN).

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SUPPLEMENTARY TABLE S3. Quality report of DNA samples performed at BGI for Whole genome bisulfite sequencing (WGBS).

No.	Sample Name	Cultivar	Tissue	Concentration (ng/μL)	Volume (μL)	Total Mass (μg)	Sample Integrity	Library Type	Test Result	Remark
1	PHY1	CS	Young leaf	66.2	48	3.18	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
2	PHY2	CS	Young leaf	120	46	5.52	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
3	PHY3	CS	Young leaf	25.8	44	1.14	Degraded slightly	WGBS	Qualified	
4	PHY4	CS	Young leaf	66.4	45	2.99	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
5	PHY5	CS	Young leaf	86.8	45	3.91	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
6	PHY6	CS	Young leaf	49.8	45	2.24	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
7	PHY7	CS	Young leaf	28	43	1.2	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
8	PHY10	CS	Young leaf	100	51	5.1	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
9	PHY11	CS	Young leaf	204	46	9.38	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
10	PHY12	CS	Young leaf	92.6	50	4.63	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
11	PHY13	CS	Young leaf	50.4	46	2.32	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
12	PHY15	CS	Young leaf	165	46	7.59	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
13	PHY16	CS	Young leaf	173	44	7.61	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins. Slightly contaminated with proteins.
14	PHY17	CS	Young leaf	248	44	10.91	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
15	PHY18	CS	Young leaf	65.6	40	2.62	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.

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No.	Sample Name	Cultivar	Tissue	Concentration (ng/μL)	Volume (μL)	Total Mass (μg)	Sample Integrity	Library Type	Test Result	Remark
16	PHY20	CS	Young leaf	60.8	44	2.68	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
17	PHY21	CS	Young leaf	26.8	42	1.13	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
18	PHY22	CS	Young leaf	78.2	44	3.44	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
19	A3_12FC3	CS	Young leaf	34.6	40	1.38	Degraded slightly	WGBS	Qualified	
20	A3_3FC3	CS	Young leaf	134	46	6.16	Degraded slightly	WGBS	Qualified	
21	A3_3FC5	CS	Young leaf	87.4	43	3.76	Degraded slightly	WGBS	Qualified	
22	A3_3FC7A	CS	Young leaf	55.8	42	2.34	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
23	A3_3FC2	CS	Young leaf	85.6	41	3.51	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
24	A3_3FC7B	CS	Young leaf	224	43	9.63	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
25	A3_12FC5	CS	Young leaf	28	43	1.2	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
26	A3_3FC8	CS	Young leaf	147	45	6.62	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
27	A3_3FC1	CS	Young leaf	111	43	4.77	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
28	A2_3FC1	CS	Young leaf	41.2	40	1.65	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
29	A3_12FC2	CS	Young leaf	85.4	46	3.93	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
30	FV_R18C18	CS	Mature leaf	32.4	41	1.33	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
31	FV_R37C8	CS	Mature leaf	22.8	40	0.91	Degraded slightly	WGBS	Risky	m < 1 μg, proposed to resend the sample. Slightly contaminated with proteins.
32	FV_R39C19	CS	Mature leaf	28.2	39	1.1	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.

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No.	Sample Name	Cultivar	Tissue	Concentration (ng/μL)	Volume (μL)	Total Mass (μg)	Sample Integrity	Library Type	Test Result	Remark
33	FES_R18C18	CS	Mature leaf	40.4	42	1.7	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
34	FES_R37C8	CS	Mature leaf	18.1	43	0.78	Degraded slightly	WGBS	Risky	m < 1 μg, proposed to resend the sample. Slightly contaminated with proteins.
35	FES_R39C19	CS	Mature leaf	33.8	43	1.45	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
36	AS_R37C11	CS	Mature leaf	24.6	43	1.06	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
37	AS_R38C20	CS	Mature leaf	31.4	40	1.26	Degraded slightly	WGBS	Qualified	Slightly contaminated with proteins.
38	AS_R39C20	CS	Mature leaf	21.2	41	0.87	Degraded slightly	WGBS	Risky	m＜1μg, proposed to resend the sample

Samples were extracted from young and mature CS leaves for WGBS analysis.

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SUPPLEMENTARY TABLE S4. Quality report of RNA samples performed at BGI.
Samples were extracted from young and mature CS leaves for RNAseq analysis.

No.	Cultivar	Tissue	Concentration (ng/µL)	Volume (µL)	Total Mass (µg)	RIN	28S/18S	Library Type	Test Result
1	CS	Young leaf	1200	17	20.4	7.9	2.0	DNBSEQ Transcriptome	Qualified
2	CS	Young leaf	1350	17	22.95	7.8	1.5	DNBSEQ Transcriptome	Qualified
3	CS	Young leaf	580	17	9.86	7.7	2.3	DNBSEQ Transcriptome	Qualified
4	CS	Young leaf	1370	17	23.29	7.8	2.2	DNBSEQ Transcriptome	Qualified
5	CS	Young leaf	1370	17	23.29	7.9	2.1	DNBSEQ Transcriptome	Qualified
6	CS	Young leaf	910	17	15.47	7.5	2.3	DNBSEQ Transcriptome	Qualified
7	CS	Young leaf	580	17	9.86	7.8	2.3	DNBSEQ Transcriptome	Qualified
8	CS	Young leaf	2230	17	37.91	7.5	1.5	DNBSEQ Transcriptome	Qualified
9	CS	Young leaf	2080	17	35.36	7.8	1.2	DNBSEQ Transcriptome	Qualified
10	CS	Young leaf	990	14	13.86	8.2	2.6	DNBSEQ Transcriptome	Qualified
11	CS	Young leaf	2440	17	41.48	7.2	2.0	DNBSEQ Transcriptome	Qualified
12	CS	Young leaf	3050	17	51.85	8	1.6	DNBSEQ Transcriptome	Qualified
13	CS	Young leaf	2620	17	44.54	7.8	1.2	DNBSEQ Transcriptome	Qualified
14	CS	Young leaf	2760	17	46.92	8	1.1	DNBSEQ Transcriptome	Qualified
15	CS	Young leaf	1320	17	22.44	7.3	2.1	DNBSEQ Transcriptome	Qualified
16	CS	Young leaf	920	17	15.64	8.1	2.6	DNBSEQ Transcriptome	Qualified

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No.	Cultivar	Tissue	Concentration (ng/µL)	Volume (µL)	Total Mass (µg)	RIN	28S/18S	Library Type	Test Result
17	CS	Young leaf	368	17	6.26	7.9	2.4	DNBSEQ Transcriptome	Qualified
18	CS	Young leaf	1430	17	24.31	8.3	2.0	DNBSEQ Transcriptome	Qualified
19	CS	Young leaf	550	17	9.35	7.3	1.9	DNBSEQ Transcriptome	Qualified
20	CS	Young leaf	990	17	16.83	7.5	1.4	DNBSEQ Transcriptome	Qualified
21	CS	Young leaf	1010	17	17.17	7.7	1.7	DNBSEQ Transcriptome	Qualified
22	CS	Young leaf	820	17	13.94	8	2.5	DNBSEQ Transcriptome	Qualified
23	CS	Young leaf	930	17	15.81	7.4	2.2	DNBSEQ Transcriptome	Qualified
24	CS	Young leaf	1480	17	25.16	7.6	1.0	DNBSEQ Transcriptome	Qualified
25	CS	Young leaf	570	17	9.69	7.1	2.2	DNBSEQ Transcriptome	Qualified
26	CS	Young leaf	1090	17	18.53	7.9	1.3	DNBSEQ Transcriptome	Qualified
27	CS	Young leaf	1420	17	24.14	8.2	1.9	DNBSEQ Transcriptome	Qualified
28	CS	Young leaf	306	17	5.2	7.5	2.4	DNBSEQ Transcriptome	Qualified
29	CS	Young leaf	1100	17	18.7	7.6	2.0	DNBSEQ Transcriptome	Qualified
30	CS	Mature leaf	790	17	13.43	8	2.4	DNBSEQ Transcriptome	Qualified
31	CS	Mature leaf	420	17	7.14	8.1	2.5	DNBSEQ Transcriptome	Qualified
32	CS	Mature leaf	420	17	7.14	7.8	2.9	DNBSEQ Transcriptome	Qualified
33	CS	Mature leaf	400	17	6.8	8.1	2.7	DNBSEQ Transcriptome	Qualified
34	CS	Mature leaf	171	17	2.91	7.8	2.4	DNBSEQ Transcriptome	Qualified

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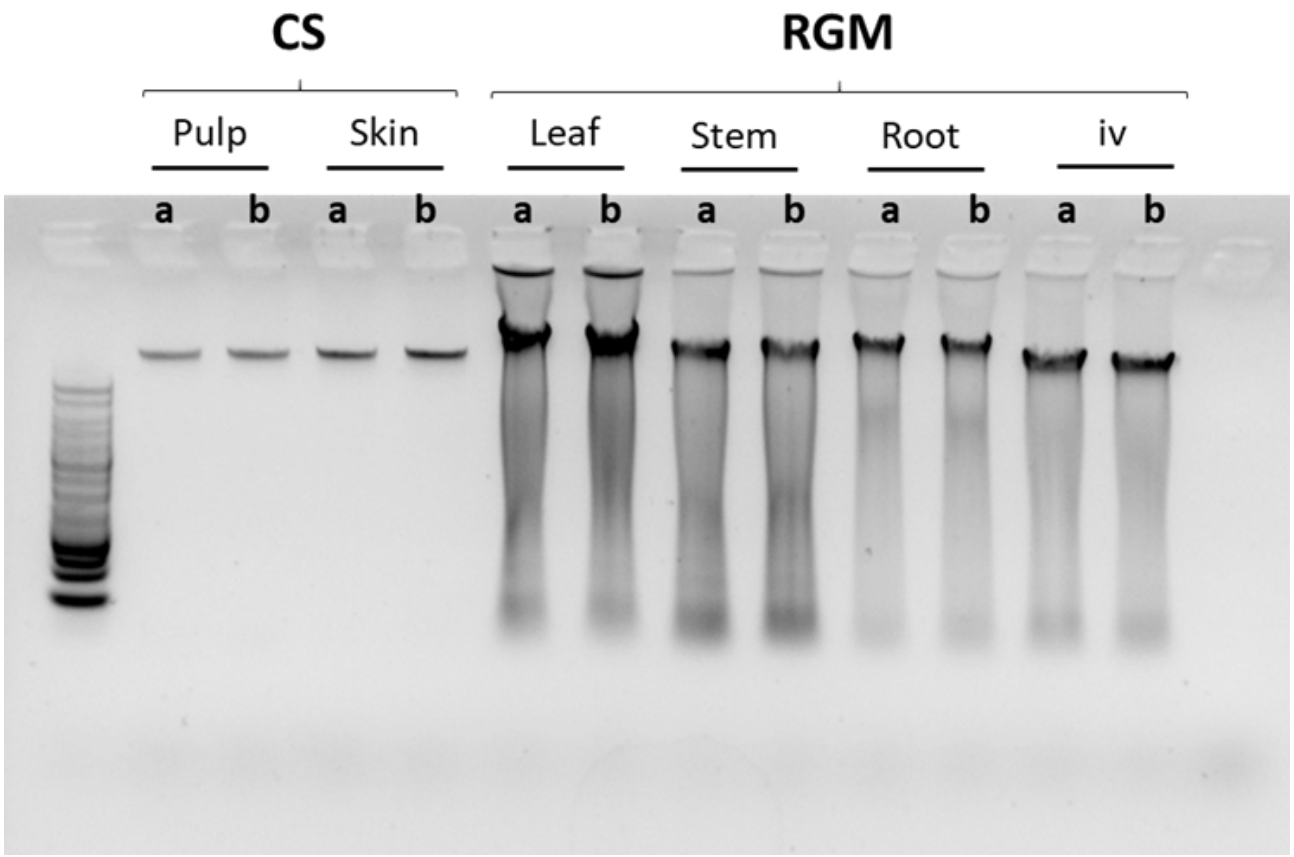
No.	Cultivar	Tissue	Concentration (ng/µL)	Volume (µL)	Total Mass (µg)	RIN	28S/18S	Library Type	Test Result
35	CS	Mature leaf	200	17	3.4	7.3	2.1	DNBSEQ Transcriptome	Qualified
36	CS	Mature leaf	500	17	8.5	8.1	2.6	DNBSEQ Transcriptome	Qualified
37	CS	Mature leaf	590	17	10.03	7.8	2.5	DNBSEQ Transcriptome	Qualified
38	CS	Mature leaf	390	17	6.63	7.7	3.7	DNBSEQ Transcriptome	Qualified

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SUPPLEMENTARY TABLE S5. Extraction results performed on grapevine cells and buds tissues, and from tomato and rapeseed leaves. DNA and RNA yields, quality, samples weights and final nucleic acid concentrations obtained respectively in 50µL and 60µL elution volume from Cabernet-Sauvignon (cells, bud), and leaves coming from tomato and rapeseed.

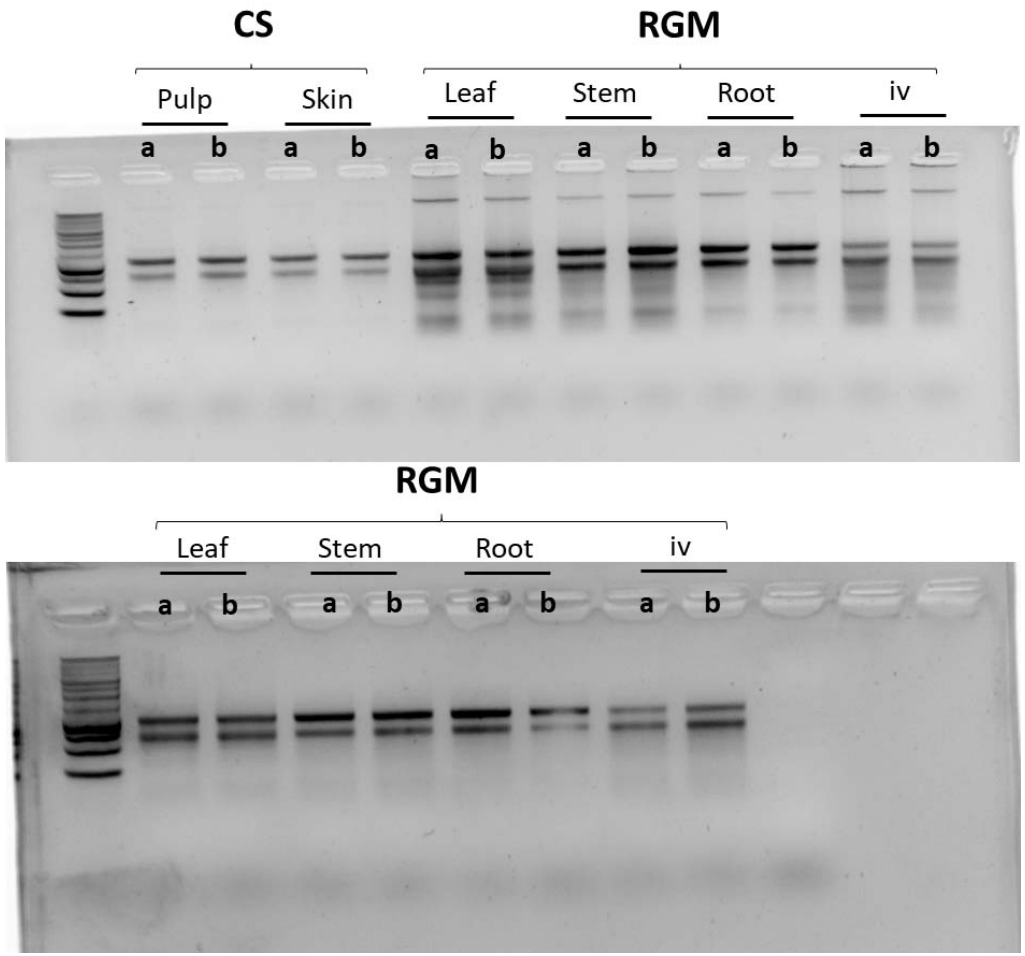
Tissue	Cultivar	Replicates	DNA µg.gFW-1	DNA A280	DNA A230	RNA µg.gFW-1	RNA A280	RNA A230	FW (mg)	[DNA] ng/µL	[RNA] ng/µL
Cells	CS	8	11.2 ± 4.5	1.97 ± 0.01	2.34 ± 0.07	265.7 ± 48.7	2.10 ± 0.01	2.37 ± 0.02	200 ± 14	37.3 ± 14.8	1054.5 ± 178.4
Bud (a,b,c)	CS	3	184.64 ± 70.89	1.70 ± 0.02	2.00 ± 0.04	661.99 ± 29.51	2.03 ± 0.07	2.30 ± 0.08	(a) 19	33	264.5
									(b) 55	194	708.4
									(c) 62	246	800.95
Leaf (Tomato)	-	4	9.2 ± 0.4	1.86 ± 0.01	1.92 ± 0.18	427.9 ± 127.2	2.10 ± 0.02	2.40 ± 0.05	150 ± 4	23.1 ± 0.9	1286.0 ± 394.7
Leaf (Rapeseed)	-	4	8.8 ± 0.5	1.90 ± 0.1	1.92 ± 0.48	31.0 ± 7.5	2.12 ± 0.01	2.42 ± 0.01	148 ± 3	21.6 ± 1.0	96.6 ± 21.3

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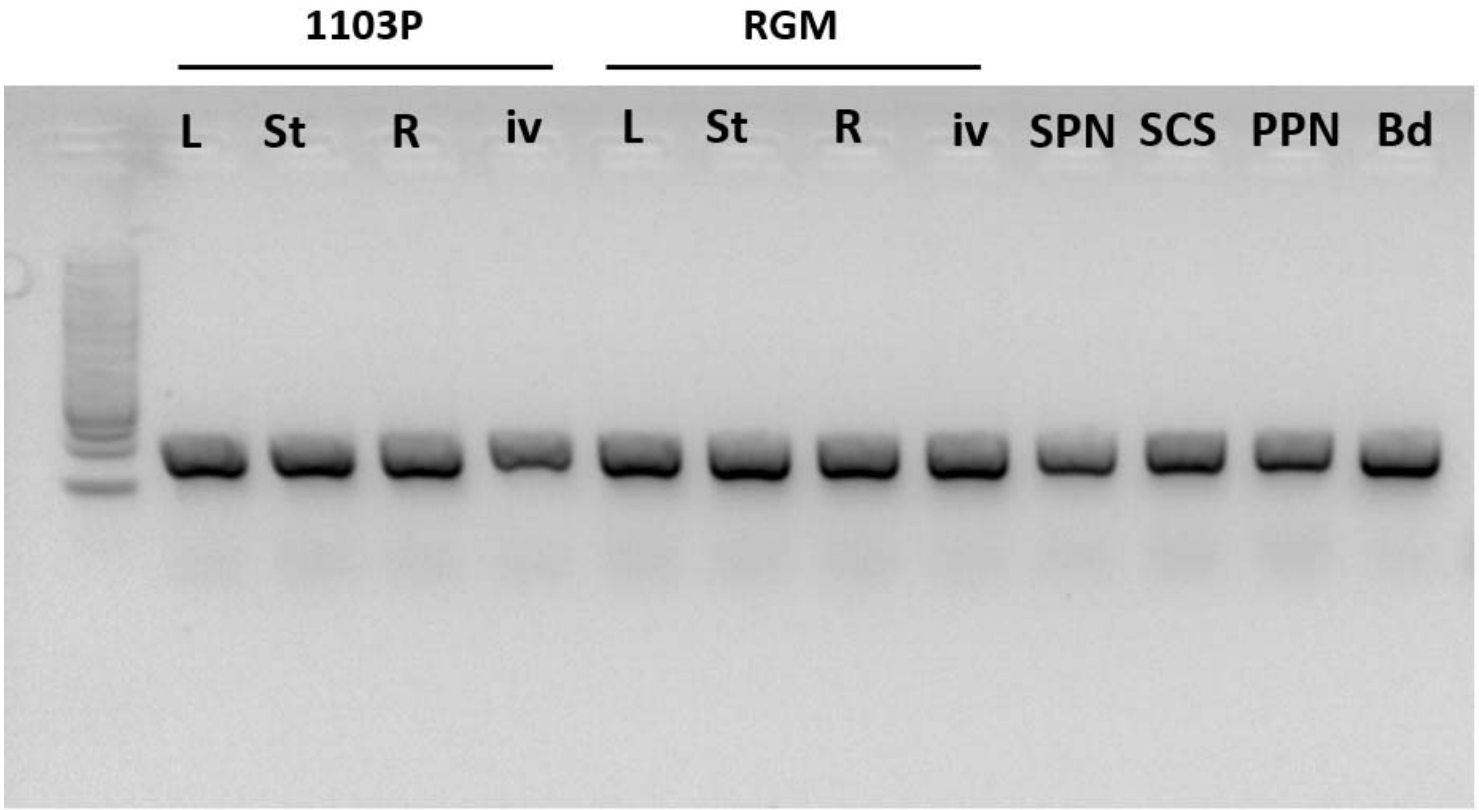
SUPPLEMENTARY FIGURE S1. Genomic DNA (5 µL) electrophoresis on 0.8 % agarose gel extracted from F6 berries and vegetative tissues presented in Table 1.

SUPPLEMENTARY DATA
Berger, M.M.J., Lailheugue, V., Zhelyazova, G., Stammitti, L., Lauvergeat, V., Barrieu, F. & Gallusci, P. (2022).
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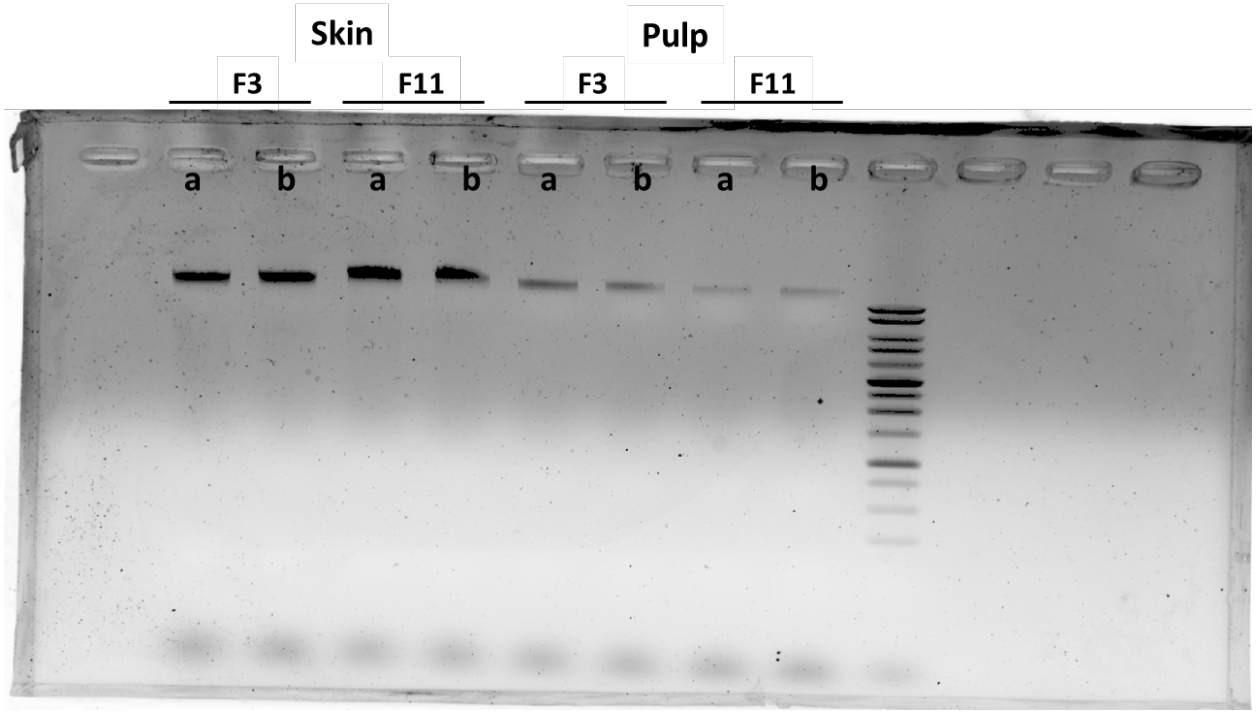
SUPPLEMENTARY FIGURE S2. RNA (5 µL) electrophoresis on 1 % (W/V) native agarose gel before (top) and after (bottom) DNAse treatment. RNA was obtained from RGM vegetative tissues as presented in Table 1. Due to the limited amount of material obtained from berry tissues, DNAse treatments were not performed on DNA extracted from berry Pulp and Skin.

SUPPLEMENTARY DATA
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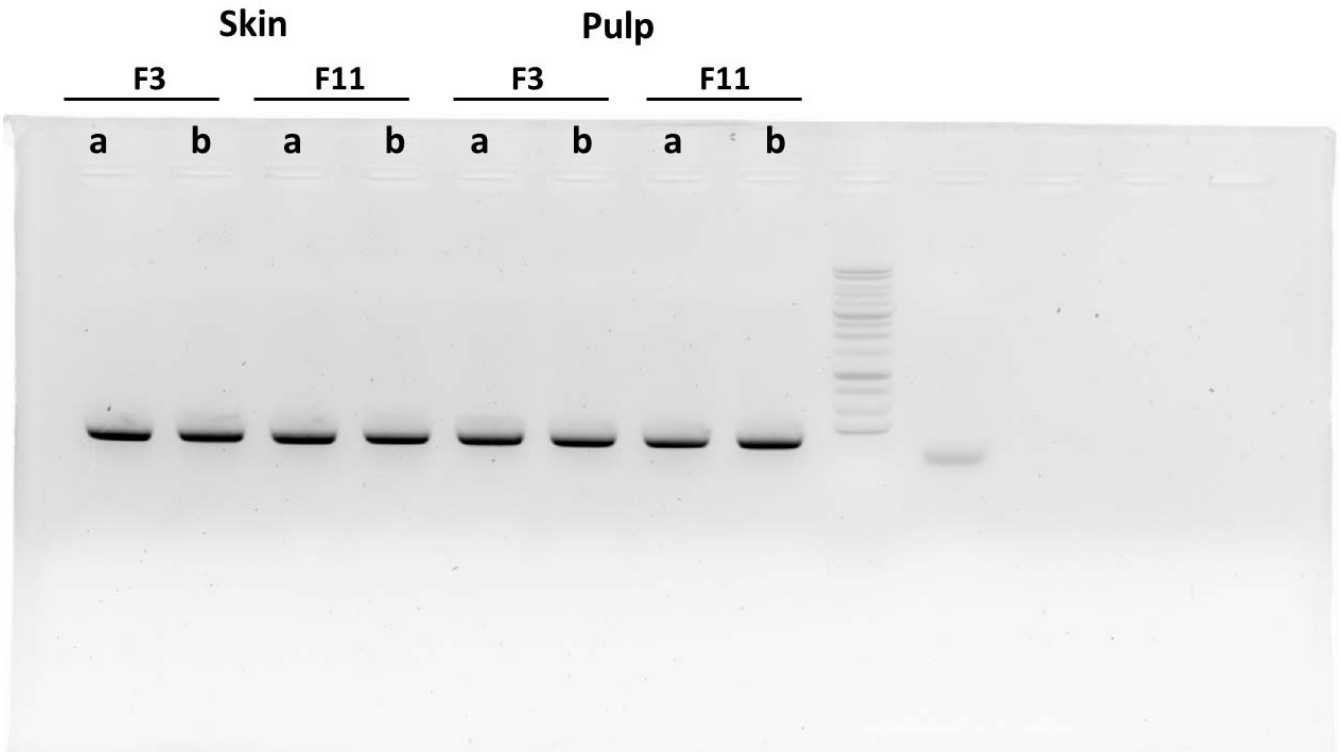
SUPPLEMENTARY FIGURE S3. Electrophoresis gel after PCR performed on GAPDH gene.
PCR results obtained on DNA samples (presented in SD2 and Table 2) diluted at 20ng.µL-1 from vegetative tissues of RGM and 1103P, and F6 Berry skin of PN and CS (SPN, SCS) and pulp of PN (PPN) and Buds (Bd) – amplification of grapevine GAPDH gene. L: leaf, St: Stem, R: root, iv: *in vitro* plants, SCS: skin from F6 Pinot noir berries SPN: skin from F6 Pinot noir berries, PPN: pulp from F6 Pinot noir berries, Bd: CS buds.

SUPPLEMENTARY DATA
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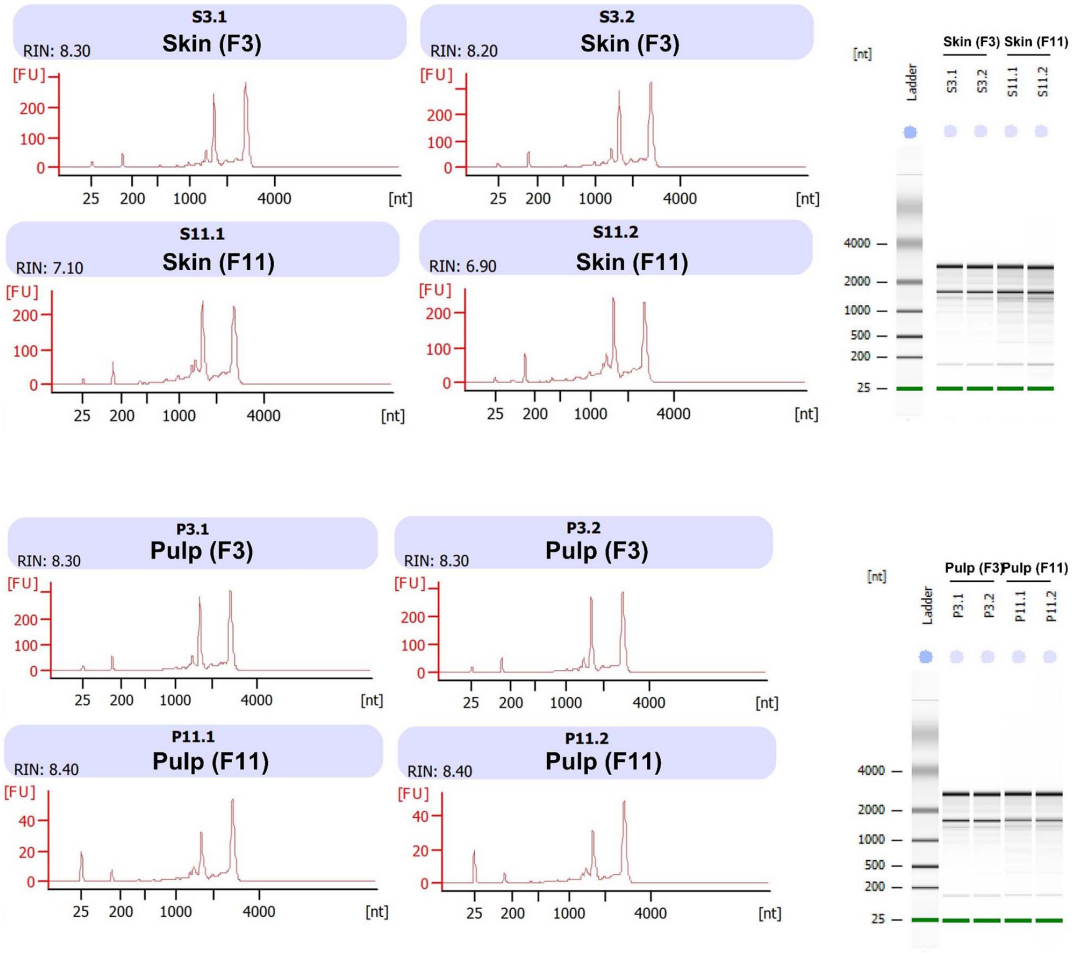
SUPPLEMENTARY FIGURE S4. Electrophoresis gel of DNA (5µL) extracted from berry tissues. (Results presented in Table 1).
F3: Fruit set + 3 weeks, F11: Fruit set + 11 weeks.

SUPPLEMENTARY DATA
Berger, M.M.J., Lailheugue, V., Zhelyazova, G., Stammitti, L., Lauvergeat, V., Barrieu, F. & Gallusci, P. (2022).
One prep to catch them all: "2 in 1", an efficient method for the simultaneous extraction of DNA and RNA from Grapevine tissues. *OENO One*, *56(*1).
https://doi.org/10.20870/oeno-one.2022.56.1.5000



SUPPLEMENTARY FIGURE S5. Electrophoresis gel after PCR amplification of GAPDH gene on DNA extracted from berry tissues presented in Table 1. F3: Fruit set + 3 weeks, F11: Fruit set + 11 weeks.

SUPPLEMENTARY DATA
Berger, M.M.J., Lailheugue, V., Zhelyazova, G., Stammitti, L., Lauvergeat, V., Barrieu, F. & Gallusci, P. (2022).
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SUPPLEMENTARY FIGURE S6. Agilent quality check of RNAs extracted from technical duplicates (1, 2) obtained from skin and pulp of CS berry harvested 3 or 11 weeks after fruit set, respectively named F3 and F11.