SUPPLEMENTARY DATA

Table S1. Elemental and biochemical composition and nutrients present in *Rugulopteryx okamurae* aqueous extract (RO).

RO	Average (standard deviation)
C content (%)	30.57 (0.15)
N content (%)	0.92 (0.01)
S content (%)	2.14 (0.03)
P (mg/kg lyophilized)	1669.8 (157.8)
K (mg/kg lyophilized)	36719 (348.0)
Ca (mg/kg lyophilized)	9049.7 (799.6)
Mg (mg/kg lyophilized)	5638.7 (729.1)
Si (mg/kg lyophilized)	921.6 (99.8)
Cl (mg/kg lyophilized)	36719 (3548.0)
Fe (mg/kg lyophilized)	164.5 (44.5)
Mn (mg/kg lyophilized)	16.66 (1.86)
Br (mg/kg lyophilized)	619.3 (26.6)
Cu (mg/kg lyophilized)	5.6 (1.21)
Zn (mg/kg lyophilized)	7.16 (1.16)
Ashes (%)	26.98 (1.48)
Total carbohydrates (%)	12.37 (0.04)
Total lipids (%)	5.81 (0.34)
Total proteins (%)	5.72 (0.04)

Average (n=3), standard deviations between brackets.

Table S2. Physiological characterization of plants at the initial time point (S_0).

	VN40	RJ43
Stem height	58.43 (2.68) a	55.57 (2.87) a
Number of leaves/principal stem	20.5 (1.07) b	17.07 (0.683) a
Number of stems/plant	2.43 (0.14) b	1.77 (0.133) a
Greeness (SPAD values)	31.77 (0.36) a	31.35 (0.42) a
φ_{PSII}	0.781 (0.001) a	0.780 (0.0019) a

Average (n=30) per clone, standard deviations between brackets. Different letters for the same parameter denote significant differences (ANOVA, $p < 0.05$).

Table S3. List of genes included in the NeoViGen96 chip.

	Gene Functions	Gene Names	N° accession	Primer Sens - 5' > 3' (F)	Primer AntiSens - 5' > 3' (R)	PCR Efficiency Moyenne
reference genes	γ Chain Elongation factor 1	*EF1 γ*	*AF176496*	GAAGGTTGACCTCTCGGATG	AGAGCCTCTCCCTCAAAAGG	1.09
		PP2A	XM_002276144	TCCGGCGGCTCTCGACGATT	TTCGCGTGCTCAACACCTCCG	0.97
		SAND	XM_002285134	GCCCCACAGCCAAACCCCTC	ACGATCCGTTTGCGACCCCG	1.05
		Unknown	XM_002274855	TGGTGAACTTGAGGCTGCAAGGG	ACCATTTGGGGAGTAGCCCTTCCTC	1.01
	UBIQUITIN CONJUGATING ENZYME 9	*UBC9*	XM_002274238	TCCTCCTGACAGTCCATATGCTGGT	GGGCTGGGCTCCACTGCTCC	1.00
		TIP41	XM_002270674	CAGCGGGCAGCGATCGAAGA	CATTTCCGCTCCGGCAGCCTT	1.05
	catalytic thioredoxin-like protein 4A	*THIORYLS8*	XM_002283586	TCACTCTGGATGGGCCGTCG	TCCCAATCGTGGCCGAACCG	1.14
	Tubuline Alpha	*TuA*	XM_002285685.1	GTCGGCGCTGAAGGTGTGGA	GAGGTGGCGGGCAAACCCTC	0.97
	Tubuline Beta	*bTub*		TGAACCACTTGATCTCTGCGACTA	CAGCTTGCGGAGGTCTGAGT	0.99
	Tubuline Beta	*TuB*	XM_02275270.1	CGCCACCCGAGTCTCACTGC	CACACCGTGCTCGTCGGCAGA	1.04
	Actine	*ACT*	XM_002282480.1	GCACCCCAAGCCCATCGTCT	CCTGGGAGCATCATCACCCGC	0.72
	Glyceraldehyde 3-phosphate dehydrogenase	*GADPH*	CB973647	TTCTCGTTGAGGGCTATTCCA	CCACAGACTTCATCGGTGACA	
		GADPH	XM_002263109.1	GAAATCAACGGCCCAGCGCG	CCGGTGGATACTGGGGCGGA	0.83
PR proteins	PR1 Unknown function	*PR1*	AJ536326	CCCAGAACTCTCCACAGGAC	GCAGCTACAGTGTCGTTCCA	1.00
		PR1 bis	XM_002273752.1	GGGGTTGTGTAGGAGTCCATTAGCA	TGGGCACAGCAGATGTGAGCT	1.13
	Beta-1,3-glucanase (PR2)	*GLU*	AF239617	GGGGAGATGTGAGGGGTTAT	TGCAGTGAACAAAGCGTAGG	1.18
		PR2	XM_002277475	CAACTTGCCACCGCCAGGGC	AGGGCTTGGAGAGCAGCTTGG	0.96
	Endochitinase (Chitinase IV) (PR3)	*PR3*	U97522.1	ACTACGGCGCTGCTGGAAACA	TGGCACCGAAACCTTGGCTTAG	1.16
		CHIT4a	U97521.1	TATCCATGTGTCTCCGGTCA	TGAATCCAATGCTGTTTCCA	1.14
	PR4 -chitin binding Chitinases type I, II	*PR4*	XM_002264684.1	CCCAGAGCGCCAGCAATGTGA	TTGCTGCGCCATGCCAAGGG	0.95
		PR4bis	XM_002264611.1	TGGCTACTGCGGAACAACGGC	CAAGTGGCGCAGTAGGCGCT	1.02
	PR5 - thaumatin-like / Osmotin	*PR5bis*	XM_002282874.1	CCCCGGCACCACCAATGCTC	TGGGGGAGAACCGTAGCCCTG	1.18
	proteinase inhibitor PR6	*PIN*	XM_002284418	ACGAAAACGGCATCGTAATC	TCTTACTGGGGCACCATTTC	1.23
		PR6	XM_002277772	TGGGAAGCAGGCTTGGCCTGA	ACCTGGCTCTCACCGAAGGG	0.99
	subtilisin-like endoprotease	*PR7 bis*	XM_002275435.1	CGTTAAGCAGCTGGAAAGGAGCA	TCCTCCGTCAGTCTGGCTGCAA	1.04
	Chitinase 3 - PR8	*CHIT3*	Z68123	AATGATGCCCAAAACGTAGC	ATAAGGCTCGAGCAAGGTCA	0.98
		PR8	XM_002276329	GCAACAAAGCTCAATGGCACACCAC	CAGCCAAGCTGCCCTCGTTCC	0.96
	Lignin-forming peroxidase	*POX*	XM_002285687.1	ACTGCACCAAGAAAGAGCACCAG	AGCTGTGCATGTGCCATCCCC	1.14
		PER	XM_002274762.1	TAAGCGCCACAAGAACACTG	GGACCTCCTTGTTGAGTCCA	0.93
	PR protein - class 10 (PR10)	*PR10*	*AJ291705*	GCTCAAAGTGGTGGCTTCTC	CTCTACATCGCCCTTGGTGT	0.99
	PR11	*PR11*	XM_002270543.1	CTCCACTGCGCAAACCGTGGT	TTTGCGTTTTCGGAGGAAATCGTGA	1.10
	Defensin	*PR12*	XM_002281153	GTGCAAGAACTGGGAGGGTGCC	GCAGAAGCATGCAACTCCCGGG	0.88
	Lipid Transfert Protein	*PR14*	XM_002271080	ACAGTTGATCGCCAGGCCGC	GCCCGGAAGCCCACTTGCAA	1.18
		PR 14bis	XM_002270934	CGCCACCACACAAGACCGCA	AGGGAGGCCAGCAGCCAGAC	1.01
	Germin like Protein	*PR15*		GTTTCCTGGCCCTCATGGAATTGGC	GTGTCCTGCAGTGGGCTTGGA	1.19
	Polygalacturonase Inhibiting Protein	*PGIP*	XM_002263487.1	GAGCGATGCCACCCCAGTGA	CCGTTGAGTCGGACGCTCGAC	0.96
phenylpropanoid pathway	Phenylalanine Ammonialyase	*PAL*	X75967 /XM_002268220.1	ACAACAATGGACTGCCATCA	CACTTTCGACATGGTTGGTG	1.10
	Stilbene synthase (resveratrol synthase)	*STS*	X76892.1	ATCGAAGATCACCCACCTTG	CTTAGCGGTTCGAAGGACAG	0.95
	Resveratrol-*O* -methyl-transferases	*ROMT*	FM178870	TGCCTCTAGGCTCCTTCTAA	TTTGAAACCAAGCACTCAGA	0.96
	Chalcone Synthase	*CHS*	X75969.1	CCAACAATGGTGTCAGTTGC	CTCGGTCATGTGCTCACTGT	1.01
		CHS2	XM_002276885.1	GCATTTTCCGACGAAGTTCACACTG	GTGCCGATGGCCAGAACCGT	1.04
	Chalcone Isomerase	*CHI*	*X75963*	AGAAGCCAAAGCCATTGAGA	CCAAGGGGAGAATGAGTGAA	1.04
		CHI2	XM_002280122	TGTGGGCCATCTGCAACCATGG	GCACTCTCTAGCTGCACCCCG	1.12
	DFR	*DFR*	XM_002281822.1	GGCCACCGTTCGCGATCCAA	GAAGACGCCGGTGCAGCCTT	1.05
	Anthocyanidine Synthase	*LDOX*	X75966	TGGTGGGATGGAAGAGCTAC	CCCACTTGCCCTCATAGAAA	0.84
	Polyphenol Oxidase	*PPO*	XM_002275806.1	GGTCCCTCGTTATGGGGCCGA	CCTGGATGGAAATCAGGGCGCC	0.98
	3-hydroxy-3-methylglutaryl Coenzyme A reductase	*HMGR*	XM_002275791.1	AACGCACACTCCGCTCCACG	GCGGCGGCGATCTTCATCGA	0.93
	Farnesyl Pyrophosphate Synthase	*FPPS*	XM_002272605.1	TCGCCAATGGGTCGAGCGTA	TGCCTGCCTTGCAGCAACTTGT	1.03
	(*E,E*)-alpha-farnesene synthase	*FAR2*	XM_002264969.1	TTGCGAGGCAGAAGCTGGCC	TTTGGCCCACGAAAGGCGGG	1.08
	Flavanone-3-hydroxylase	*F3H*	*X75965.1*	TGACTCGCTCTCTTCAAGCA	CACCTTGGGACGTTCATCTT	0.87
Indole biosynthesis	Antranilate Synthase (ANTS)	*ANTS*	*XM 002281597*	AAAAATCCAAGAGGGGTGCT	AAGCTTCTCCGATGCACTGT	0.84
	Chorismate mutase	*CHORM*	*FJ604854*	TCATTGAGAGGGCCAAATTC	AGGAGGCAGAAAAAGCATCA	1.05
		CHORM2	XM_002284083.1	GGCAAGTTCGTGGCAGAGGCA	GCCGCTGGCTGTCTTGTGCT	1.11
	Chorismate Synthase	*CHORS*	*FJ604855*	GCCTTCACATGCAGATGCTA	CTGCAACTCTCCCAATGGTT	1.00
		CHORS2	XM_002282263	TGTTATGGCGCGCGGTGACT	GCAGCTCTGGCCAGTTGAGCT	1.11
Redox status	GST (glutathione *S* -transferase - GST)	*GST1*	AY156048.1	GGGATCTCAAAGGCAAAACA	AAAAGGGCTTGCGGAGTAAT	0.99
		GST2	AY156049	CATGAAGGCCGGCCAGCACA	CGCGAAGAATTCGCTCTGGCCA	0.84
		GST3	XM_002283178	TGTTTGGCCGCAAACGGGGT	TCCCCAGCCAGGTACTTGCTCT	1.06
		GST4	XM_002271673	AGCTGGAATGGCGCACTTGGT	TGGAAAGGTGCATACATGGCCACG	1.00
		GST5	XM_002283173	CCTTGAGCTCTACCCTGCCCCA	AGCAGCCAGCCCTAGACATGGA	0.86
Lipoxygenase	Lipoxygenase	*LOX2*	XM_002285538	AAACCGTGCATTCCCGGCCC	GGCAGGGACGTAGCCAACCC	1.02
		LOX9	AY159556	GACAAGAAGGACGAGCCTTG	CATAAGGGTACTGCCCGAAA	0.92
		LOX3	XM_002284499.2	GGACCGGGTTCATGAGCTGTTGG	TGAATGCAGACTCGCCAGCGGT	1.09
	Carboxylesterase	*HSR-203J*	XM_002285050.1	TGGAGGAAACATCGTTCACA	CCTGGACAATTCTGCCATCT	1.02
Cell wall reinforcement	Alliinase	*Alli*	XM_002265837.1	CGGCTCAGCCTCATCAAGACCC	GGCATGCATGTCATCTTCCTCAGCC	1.04
		Alli2	XM_002266017.1	AGCCCTTCTGGATGCAGCATGC	TGTAGCTTGCGGATGAGCTTCACT	1.00
	Ascorbate peroxidase	*APOX*	XM_002284731.1	AGCTCAGAGGCCTCATCGCTGA	TACCGGCAGAGTGCCATGCG	1.07
		APOX2	XM_002278245.1	TCGAAGCTCAGCAGACGCCG	ACGTCCCCGCATCATGCCAC	1.14
	Glycosyl transferase	*CAGT*	*XM02273320.1*	TCGGAAGGGAATGCAATAAG	TGTAGGAGGAACCACCCTTG	0.81
	Callose Synthase	*CALS*	AJ430780.1	TGGAAATGCAATTCAAACGA	CGAATGCCATGTCTGTATGG	0.86
		CALS2	XM_002283262 (CS like 12)	ATGGCGTCCAGAAGCGGCTC	GCCGTCTGTGTCCGCGTGAT	0.86
		CALS3	(CS like-10)	GCAGCAGATTGCCACTGCCCA	AGGCAGAATGAGGTGCTCGCC	1.14
	Pectine methyl esterase	*PECT2*	XM_002283905.1	GGGTTGCGCCCTGAGGACAC	CAATCACCCGAGCCGCCTGG	1.08
	CAD Cinnamyl alcool dehydrogenase	*CAD*	XM_002285332.1	AGTCCGATTGGAAGACGGCAGT	TGCCCCTGTCACACACACCA	1.05
		CAD2	XM_002268086.1	TCCGGGTATCCCAGGAGAAAGCA	TCCACGGTATCCTTCATGCTCACC	1.07
signalisation	Lipase 3 / enhanced disease susceptibility 1	*EDS1a*	XM_002281059.1	CAGGTCACAGCCTGGGTGCG	TCGGGCGGGACGATCTCGTT	1.01
		EDS1b	XM_002281871.1	GGAGACGGGGCTGAACGTGC	CCATCGCCGGCACTTGCTCA	0.89
		EDS1c	XM_002275822.1	CCAGCACTGCTTGCAGGCGT	TGCTGTGTTCCTGAGTGCCCC	1.04
	Transcription Factors	*WRKY1*	AY585679.1	GGAAATATGGGCAGAAAGCA	ATCTTTTGAGAGGCGTTGGA	1.00
		WRKY2	AY596466	AGAGGCAAGGCGATGTAGAA	CTGGGGAACAAGCCTTCATA	1.01
Signaling pathways	JAR (Jasmonate resistant 1)	*JAR*	XM_002283193.1	GCAACGGGGCACGACTACTGT	GCCGTGGCGGTGCAAGTACT	0.89
		JAR2	XM_002280702.1	CCGAAGTGCTGGCCCCAGAG	AACGCTCACTTCGCCGCTGA	1.00
	ACCO 1	*ACO1*	XM_002273394.1	GCCGGTTTGAAGTTCCAGGCCA	ACTCAAACTGTGGCAATGGGACCC	1.06
		ACO1b	XM_002275305.1 / XM_002275284.1	CGAGCCCACACTGATGCCGG	TTGAGGAGCTGGAGGCCGCT	1.00
		ACC	XM_002273394.3	GAAGGCCTTTTACGGGTCTC	CCAGCATCAGTGTGTGCTCT	0.86
	EIN3-BINDING F BOX PROTEIN 1	*EIN3*	XM_002285090.1	TTGGCTCTGAACGCGTCCGA	CCCCGGGGCAGAAGGCATCA	0.88
		EIN3bis	XM_02285213.1	CCTCGCAAGCGGTCTCGCAT	TGGAGACCCGAGCGCAGGAG	0.98
	Salicylic acid methyl transferase	*SAMT1*				
	Isochorismate synthase	*ICS a*				
		ICS b				
	Salicylic acid binding protein	*SAPB2 a*				
Photosynthesis	*NADH-plastoquinone oxidoreductase subunit 6*	*NADH*	XM_010654925.2			0.95
Krebbs Cycle	Malate Dehydrogenase, cytoplasmic	MDH	XM_002278676.3			1.28
	Isocitrate Dehydrogenase	IDH42	XM_002270581.3			1.08
	Citrate synthase, mitochondrial	CS	XM_002271415.2			0.97
Nitrogen metabolism	Nitrate Reductase	NR	NM_001281120.			1.02
	Nitrite Reductase	NiR	NM_001281265.1			1.01
	Nitrate/nitrite transporter	NrT1	KF649633.1			1.18
	Nitrate transporter	NrT2	XM_002277091.2			1.2
Glycolysis	*Hexose transporter*	VvHT5	NM_00128127			0.97
Sugar metbolism	*Fructose-bisphosphate aldolase*	PLAST	XM_003631825			0.97

The array contained five reference genes, a total of 89 targeted genes, 74 from Dufour et al., (2016) and 15 from Bodin *et al*. (2020), and NADH and RNAse P as negative and positive control, respectively.

Table S4. Viniferin concentrations in grapevine leaves (mg/kg leaves dw) at S_2 sampling point.

	VN40			RJ43		
	W	BB	RO	W	BB	RO
e-Viniferin	21.99 ab (2.19)	22.63 b (5.53)	26.26 a (4.45)	18.90 b (1.91)	20.18 ab (1.98)	30.09 a (5.38)
w-Viniferin	16.58 a (0.74)	16.31 a (1.12)	17.43 a (0.44)	17.04 a (1.30)	17.56 a (1.38)	22.29 a (2.28)

W, water treated plants; BB, Copper treated plants; RO, *Rugulopteryx okamurae* treated plants. Average (n=5). Standard deviations between brackets. Different letters for the same parameter denote significant differences (ANOVA, $p < 0.05$).

Table S5. Photosynthetic pigments and photochemical parameters in clones after *Plasmopara viticola* inoculation (S_2, 1dPI).

	VN40			RJ43		
	W	BB	RO	W	BB	RO
Chlorophyll a (mg/g DW)	8.41 ab (0.33)	9.03 a (0.60)	7.02 b (0.46)	8.62 (0.58)	8.97 (0.71)	9.22 (1.10)
Chlorophyll b (mg/g DW)	3.89 (0.15)	3.95 (0.18)	3.45 (0.10)	4.05 (0.55)	3.93 (0.25)	4.37 (0.54)
Carotenes + xanthophylls (mg/g DW)	1.55 ab (0.11)	1.74 a (0.14)	1.17 b (0.09)	1.53 (0.19)	1.61 (0.16)	1.70 (0.24)
PQa	1.48 ab (0.01)	1.49 a (0.01)	1.45 b (0.02)	1.51 (0.01)	1.49 (0.01)	1.50 (0.02)
Greenness (SPAD values)	31.81 (0.58)	30.38 (0.59)	29.9 (1.19)	27.98 (1.31)	30.96 (1.04)	29.5 (1.63)
φ_{PSII}	0.720 (0.006)	0.720 (0.004)	0.726 (0.005)	0.720 (0.007)	0.737 (0.009)	0.722 (0.013)

W, water treated plants; BB, Copper treated plants; RO, *Rugulopteryx okamurae* treated plants. PQa, Phaeophytinization Quotient Chlorophyll a; φ_{PSII}: maximum photochemical efficiency in the light of photosystem II. Average (n=5). Standard deviations between brackets. Different letters for the same parameter and clone denote significant differences (ANOVA, $p < 0.05$).