Supplemental Table S2. RNA-Seq validation: primer sequences and Real-time RT-PCR parameters.

<table>
<tr><th>Gene Ensembl ID</th><th>Primer sequence</th><th colspan="2">Real-time RT-PCR parameter</th></tr>
<tr><td rowspan="2">Bcin08g00340</td><td>Forward 5' - CGGTTCCCTCAGTTTTGTGT</td><td colspan="2" rowspan="2">Polymerase activation and denaturation:
95 °C
2 min</td></tr>
<tr><td>Reverse 5' - CGAGACTGAATAACGCGACA</td></tr>
<tr><td rowspan="2">Bcin13g02250</td><td>Forward 5' - TAGGTGACGGCCATTGTGTA</td></tr>
<tr><td>Reverse 5' - CGAATACTCCCCGAAACAAA</td></tr>
<tr><td rowspan="2">Bcin13g02210</td><td>Forward 5' - CAGTGCTACCCTTACACCGT</td><td rowspan="8">Denaturation:
95 °C
10 sec</td><td rowspan="16">Number of cycles used: 40</td></tr>
<tr><td>Reverse 5' - AGAGTAAGGTTGGGGTCGGT</td></tr>
<tr><td rowspan="2">Bcin14g03170</td><td>Forward 5' - CATTGCCAATATGGATGCTG</td></tr>
<tr><td>Reverse 5' - TTGAAGTGCGTTGCTACACC</td></tr>
<tr><td rowspan="2">Bcin04g00060</td><td>Forward 5' - CCTCAGAAGGCACCTCACAA</td></tr>
<tr><td>Reverse 5' - GCCCAAGGTTCGCCATTAGA</td></tr>
<tr><td rowspan="2">VIT_07s0151g00130</td><td>Forward 5' - AGCAGCAGTCACAAATTGGC</td></tr>
<tr><td>Reverse 5' - GGGCTGAGAAGTTGAGGGAT</td></tr>
<tr><td rowspan="2">VIT_07s0005g00740</td><td>Forward 5' - TCATCACTGCCCTCAATTGC</td><td rowspan="8">Annealing and extention:
60 °C
30 sec</td></tr>
<tr><td>Reverse 5' - GTCGATGGCTCTGATTGCTC</td></tr>
<tr><td rowspan="2">VIT_07s0141g00690</td><td>Forward 5' - TAGGTTGGATGCGGTGGATT</td></tr>
<tr><td>Reverse 5' - TCACCATCAAGCTTCGGAGA</td></tr>
<tr><td rowspan="2">VIT_06s0004g05700</td><td>Forward 5' - GCGAGAGGAAGCGATTGAAG</td></tr>
<tr><td>Reverse 5' - AGGCTCCCAACCGAACTTTA</td></tr>
<tr><td rowspan="2">VIT_05s0062g00310</td><td>Forward 5' - TTGGAACCAGAGGCCCTAAG</td></tr>
<tr><td>Reverse 5' - TGCTTTGATAACACCGCGAG</td></tr>
</table>

Supplemental Table S3. Real-time RT-PCR verification of RNA-Seq results. Transcript abundance fold-changes between healthy and noble rot-affected Furmint samples are shown after $\log_2$ transformation.

	Consecutive stages of noble rot					
	I.		**II.**		**III.**	
	RNA–Seq	**Real–time RT-PCR**	**RNA–Seq**	**Real–time RT-PCR**	**RNA–Seq**	**Real–time RT-PCR**
VIT_07s0141g00690	5.08	4.80	6.00	6.06	5.31	4.64
VIT_06s0004g05700	4.06	4.13	4.62	4.29	4.85	4.29
VIT_05s0062g00310	6.79	6.88	7.52	7.31	6.75	5.22
VIT_07s0151g00130	3.41	4.74	3.44	4.86	–0.14	0.29
VIT_07s0005g00740	4.88	5.98	5.51	6.76	3.44	3.57
BCIN_08g00340	4.43	3.74	4.85	4.86	1.56	3.11
BCIN_13g02250	4.16	4.64	4.05	4.65	2.74	4.49
BCIN_13g02210	2.84	1.64	3.47	2.19	2.24	1.86
BCIN_14g03170	3.54	3.91	3.27	3.54	2.33	2.85
BCIN_04g00060	0.61	–1.91	1.93	0.17	4.67	3.38
Correlation	**0.93**		**0.90**		**0.85**	

Supplemental Table S4. Details of targeted abscisic acid, phaseic acid and dihydrophaseic acid analysis by UPLC-US-MS/MS method - According to Vrhovsek et al 2012. and Pál et al. 2019, with modifications.

UPLC:	**Waters Acquity I-class**		
Column:	Waters HSS T3 column (1.8 µm, 100 mm × 2.1 mm) at 40°C		
inj vol.:	2 µl	**Autosampler temperature:**	10 °C

Gradient conditions			
A: Water (0.1 v/v% formic acid)	**B: Acetonitrile (0.1 v/v% formic acid)**		
Time (min)	Flow rate (ml/min)	A%	B%
0	0.4	95	5
3	0.4	80	20
4.3	0.4	80	20
9	0.4	55	45
11	0.4	0	100
13	0.4	0	100
13.01	0.4	95	5
15	0.4	95	5

Detector:	**Xevo TQ-XS with Unispray source**
Resolution:	Unit mass (+/- 0.8 Da)
Impactor voltage:	2 kV
Desolvation temperature:	550°C
Nebulizer gas:	6.5 bar N_2
Desolvation gas flow:	1000 L/h N_2
Cone gas flow:	450 L/h N_2
Collision gas flow:	0.15 ml/min Argon 5.0

Component name	**Unispray Impactor voltage polarity**	**quant. MS/MS transition**	**Pred.RT (min)**	**RT found (min)**	**Cone voltage (V)**	**Collision ennergy (eV)**	**Calibrated to**	**QC**
[2H6](+)-cis,trans-abscisic acid Internal standard	negative	269.1 > 159.1	7.13	7.13	20	10	external	spike recovery
abscisic acid	negative	**263.1 > 153**	**7.18**	**7.16**	20	10	external	IS recovery and spike recovery
phaseic acid	negative	**279.12 > 139**	**5.24**	**5.18**	25	12	external	spike recovery
dihydrophaseic acid	negative	**281.14 > 237.2**	**3.56**	**3.52**	25	12	external	spike recovery

References:

Vrhovsek, U., Masuero, D., Gasperotti, M., Franceschi, P., Caputi, L., Viola, R., et al. (2012). A versatile targeted metabolomics method for the rapid quantification of multiple classes of phenolics in fruits and beverages. J. Agric. Food Chem. 60, 8831–8840. doi:10.1021/jf2051569.

Pál, M., Ivanovska, B., Oláh, T., Tajti, J., Hamow, K. Á., Szalai, G., et al. (2019). Role of polyamines in plant growth regulation of *Rht* wheat mutants. Plant Physiol. Biochem. 137, 189–202. doi:10.1016/j.plaphy.2019.02.013.