

**Table S1. Endogenous content of brassinosteroids (pmol/g DW) in different tissues of cv. Cabernet sauvignon grapevines throughout development.** Quantification of different brassinosteroid metabolites by UHPLC-MS/MS is shown. Mean  $\pm$  standard deviation of three biological and three technical replicates are tabulated. Each biological replicate corresponds to a pool of tissue collected from five different plants.

[illegible]



**Table S3. Genic model for putative genes involved in BRs biosynthesis pathway in grapevines.** The code (ID), primer sequence, Tm and efficiency of primers for RT-qPCR and size of fragment amplified by PCR are shown.

| Gene              | ID                 | Primer sequence (5'-3')                                      | TM (°C) | Ef (%) | Size (bp) | Reference |
|-------------------|--------------------|--|---------|--------|-----------|-----------|
| <i>VviCPD</i>     | VIT_213s0067g00660 | Fw: GACCAGCCGGATCTTACTTATGG<br>Rv: TTCTCAGAGACTCAGTCCACTCC   | 58      | 100    | 107       | This work |
| <i>VviDET2.1</i>  | VIT_213s0067g01830 | Fw: CACTACAGCTCTTACCATCCATT<br>Rv: CCATAAACCCCTTGAGCAATGTG   | 62      | 91.7   | 167       | This work |
| <i>VviDET2.2</i>  | VIT_219s0014g00080 | Fw: GCCCTTTTCCCAGATGAGAG<br>Rv: GAGATAACAATGGCAGCATCG        | 62      | 96     | 140       | This work |
| <i>VviDWF4</i>    | VIT_204s0023g01630 | Fw: GAGCTGAAGATGGAAGAGAGGA<br>Rv: AGCAAAGAGCAAGCTCAGTACC     | 58      | 99.2   | 147       | This work |
| <i>VviROT3</i>    | VIT_204s0023g02650 | Fw: AGGCAGCTAGTGTCAACAACAA<br>Rv: GACGGTGATGGGTAACCTCTTCC    | 57      | 98.6   | 200       | This work |
| <i>VviCYP90D1</i> | VIT_209s0002g02080 | Fw: GACTGGCCTTATCAGTTCAACCC<br>Rv: CCACCCACCTGAATTGAGTAACA   | 57      | 93.8   | 166       | This work |
| <i>VviBR6OX1</i>  | VIT_214s0083g01110 | Fw: GGGGAGACCACTGAGTTTCTTA<br>Rv: TCTAACATGGACTGTGGGTAGC     | 58      | 99.8   | 191       | This work |
| <i>VviBR6OX2</i>  | VIT_201s0011g00190 | Fw: GATAAGCTGGTGGGAAGGAACACT<br>Rv: TAGCCTAACATGTCATCTTGGGTC | 58      | 102    | 158       | This work |
| <i>VviBR11</i>    | VIT_207s0031g01850 | Fw: GGGTCTTTGATTTTCTGGACC<br>Rv: TGTCCCTTGAAGCCTATTGTAG      | 58      | 103.6  | 192       | This work |
| <i>VviBIN2.1</i>  | VIT_210s0003g01480 | Fw: GGTCTTGAAGCACTACAGCAAC<br>Rv: TCAAATCCCTATGGCAAACCTCC    | 58      | 101.9  | 128       | This work |
| <i>VviBIN2.2</i>  | VIT_212s0028g01810 | Fw: CCATCAGTTACATGGCAGAGC<br>Rv: TTCAGGGTGACCACATTTGG        | 62      | 99.3   | 181       | This work |
| <i>VviBIN2.3</i>  | VIT_214s0060g00600 | Fw: CAATAAGTTACATGGCTGAGCG<br>Rv: CTTCAAGGAGACAACATTAGGGT    | 56      | 104    | 182       | This work |
| <i>VviBES1</i>    | VIT_204s0023g01250 | Fw: CAAGTCCTGTACCCTCTTACCA<br>Rv: CCGCTTTGAACCTCTCGAAGTA     | 56      | 100.4  | 129       | This work |
| <i>VviBZR1</i>    | VIT_218s0001g12020 | Fw: CTATCGTCTTCCAAAACACTGCG<br>Rv: GGAAGTTCTTGCAATCTCAGTT    | 56      | 97.9   | 142       | This work |
| <i>VviUBI</i>     | VIT_216s0098g01190 | Fw: TCTGAGGCTTCGTGGTGGTA<br>Rv: AGGCGTGCATAACATTTGCG         | 55      | 99     | 99        | [48,49]   |

**Table S4. CDS FASTA sequences for gene selected coding for BRs pathways in grapevines.**

> *VviCPD\_VIT\_213s0067g00660*

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GGAGTGGACTGAGTCTCTGAGAAAAGAATATGTGCTTGTGATTGAAGGCTTCTTTACCGTCCCTTTCCC  
TCTCTTCTCCGCCACCTACCGCAGAGCCATCCAAGCAAGGACGAAGGTAGCAGAGGCACTGAACCTGG  
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ATAGGTGGGATTTTCAGGCGAGTAACCACTGACATCCATGTCAAAGGTTACACAATTCCTAAGGGATG  
GAAGGTGTTTGCATCATTTTCGAGCTGTACACCTGGACCATGAATACTTCAAGGATGCTCGTACTTTTAA  
TCCCTGGAGATGGCAGAATAATTCTGGACCCACGGTTCAGGGAGTGGTGTGAATGTGTTACACCAT  
TTGGAGGAGGGCCGCGCCTGTGCCCTGGCTATGAGCTTGCAAGGGTGGTGTCTCGGTTTTCTTCACC  
GCATGGTCACTCGATACAGCTGGGCTCCTGCAGAGGAGGATAAGTTGGTGTCTTTTCCAACCACTAGG  
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GATGA

> *VviDET2.1\_VIT\_213s0067g01830*

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AAAGGTTTCCGACCTCTGTTGGTCACTACAGCTCTTACCATCCATTTCTTCAAGAGAGTTTTGGAGGTG  
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CCCACACTATCTTTTTGAGATTCTAGAGTTTGTGGGGTATTCTTCATCTCTCAAACACTCTATTCATTA  
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> *VviDET2.2\_VIT\_219s0014g00080*

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CGTGTGTTATACTCCAGCATTTCTTGCTGGTGTGGCCTCTTTTGCCCTTTTCCCAGATGAGAGTTTCAGG  
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AATACAGTGGTGGGATGGCTCTCGATGCTGCCATTGTTATCTCTCTTAGCTACTTCATCTCTACTGCAA  
CTATGATCTATGCCAACACCTCTCTCGAGATTTTCCGGAGCCGCTAATGGATCTCAAGTATCCAGGAA  
TGGCCAAGGGTGAGAGAGAGTATAAGATTCCCAAGGGCACAGCCTTGATTTGATGGGAAGAAGTTA  
TTCTACTAGGAGATGGTATGTTTCCAAGTTTGAAAACCTTTCCCAATAATGTCAAGGCGCTTATTCCATA  
CATTCTCTAA

> *VviDWF4\_VIT\_204s0023g01630*

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CGGAGAAATCTACAAGTCCAATCTGTTTGGCGAGCCAACCATAGTCTCAGCGGATTCTGGGCTGAACA  
GATTCATACTACAGAACGAAGGAAAATTGTTTGAATGCAGCTATCCCAGAAGCATAGGTGGAATTCTT  
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