**Supplementary Table S9:** Genes with a potential involvement in the accumulation of monoterpenes during Moscato Bianco berry ripening. Probes marked with $ were not differentially expressed in the pairwise comparison between time points (with a cut-off of 2-fold change and a false discovery rate < 1%). Functional annotation was derived from Additional file 1 by Grimplet *et al.* (2012). Abbreviation: BC = bicluster.

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| **Probe ID** | **V1 gene prediction** | **Functional annotation** | **Evidences from the present work** | **Evidences from the literature** |
| **Terpene biosynthesis** | | | | |
| Vv\_10000446$ | VIT\_03s0063g02030 | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase | Profile: 2vs1,4vs1,5vs1up (qRT-PCR\_2016)  Cluster 5 (like free OxA) | HDR plays a major role in controlling the production of MEP-derived precursors for plastid isoprenoid biosynthesis in tomato and *Arabidopsis thaliana* (Botella-Pavía *et al.*, 2004)  The expression of *VvHDR* parallels monoterpene accumulation in Gewürztraminer and Muscat Blanc à petits grains (Martin *et al.*, 2012; Wen *et al.*, 2015) |
| Vv\_10000710$ | VIT\_10s0003g00880 | Nudix hydrolase 15 | Profile: 4vs1up (qRT-PCR\_2016)  Positive correlation with bound *trans*-8-HO-linalool and OxC  Cluster 4 | RhNUDX1 is part of a newly discovered pathway for the biosynthesis of free monoterpene alcohols. It shows geranyl diphosphate diphosphohydrolase activity *in vitro* and supports geraniol biosynthesis *in planta* (Magnard *et al.*, 2015)  VIT\_10s0003g00880 is predicted to be localized also in the chloroplast |
| Vv\_10004183 | VIT\_18s0001g04280 VIT\_18s0001g04530  and others | (-)-germacrene D synthase | Profile: 5vs1up | VIT\_18s0001g04280 and VIT\_18s0001g04530 correlate with linalool and α-terpineol in Tocai Friulano under water deficit (Savoi *et al.*, 2016) |
| **Monoterpene metabolism** | | | | |
| Vv\_10009587 | VIT\_01s0137g00410 | CYP86A2 | Profile: 3vs1,4vs1down  Positive correlation with free 6-methyl-5-hepten-2-one  Cluster 5 (like free OxA and 6-methyl-5-hepten-2-one)  BCs 209 (like free 6-methyl-5-hepten-2-one), 353, 370 (like free OxA, 6-methyl-5-hepten-2-one, bound OxC, HO-diendiol I + HO-trienol) | In apple 6-methyl-5-hepten-2-one is an oxidation product of α-farnesene (Whitaker and Saftner, 2000)  VIT\_01s0137g00410 is predicted to be localized in the chloroplast |
| Vv\_10009014 | VIT\_00s0389g00040 (70/70)  VIT\_00s0389g00030 (67/70)  (chr2) | CYP72A1 | Profile: 5vs1down  Clusters 8+3+7 (like free OxD, HO-diendiol I + HO-trienol, rose oxide II)  BCs 219, 274, 302 (like free HO-diendiol I + HO-trienol, bound OxC) | VIT\_00s0389g00030 and VIT\_00s0389g00040 fall into the confidence interval of a QTL for linalool, linalool/nerol and nerol/geraniol (Doligez *et al.*, 2006; Battilana *et al.*, 2009)  In VTCdb VIT\_00s0389g00030 is coexpressed with genes enriched in the category ‘Chloroplast part’, like *VvDXS1* (VIT\_05s0020g02130) and the linalool/nerolidol synthase *VvRiLinNer*/*VvPNLinNer2*/*VvCSLinNer*  VIT\_00s0389g00030 is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014); it is predicted to be localized in the chloroplast |
| Vv\_10001518  Vv\_10001519$ | VIT\_15s0048g01490 | Geraniol 10-hydroxylase (CYP76) | Profile: 3vs1,4vs1up  Cluster 8 (like free OxD and rose oxide II)  BCs 197 (like bound OxC, HO-diendiol I + HO-trienol), 253, 267, 270 (like free HO-diendiol I+ HO-trienol, bound OxC, HO-diendiol I + HO-trienol), 323 (like free HO-diendiol I + HO-trienol) | Members of the CYP76 family metabolize linalool in *Arabidopsis thaliana* (Ginglinger *et al.*, 2013; Höfer *et al.*, 2014; Boachon *et al.*, 2015) and grapevine (Ilc *et al.*, 2017)  VIT\_15s0048g01490 is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014)  The expression of *CYP76T21* increases along Gewürztraminer berry ripening.CYP76T21 is able to convert linalool to *trans*-8-HO-linalool, to metabolize *trans*-8-HO-linalool and to oxidize *trans*-8-oxo-linalool to *trans*-8-carboxy-linalool *in vitro*. It is also able to metabolize linalool and to produce *trans*-8-carboxy-linalool *in planta* (Ilc *et al.*, 2017)  VIT\_15s0048g01490 is predicted to be localized in the chloroplast |
| Vv\_10002015 | VIT\_15s0048g01590 | CYP76B1 | Profile: 3vs1down  Cluster 7  BCs 340 and 403, like free OxA | Members of the CYP76 family metabolize linalool in *Arabidopsis thaliana* (Ginglinger *et al.*, 2013; Höfer *et al.*, 2014; Boachon *et al.*, 2015) and grapevine (Ilc *et al.*, 2017)  In VTCdb VIT\_15s0048g01590 is coexpressed with the linalool/nerolidol/geranyl linalool synthases *VvPNLNGl1*, *VvPNLNGl2*, *VvPNLNGl3* *VvPNLNGl4*, and the 1,8-cineole synthase VIT\_00s0572g00020  VIT\_15s0048g01490 is predicted to be localized in the chloroplast |
| Vv\_10006928$ | VIT\_15s0048g01700 | CYP86A1 | Cluster 9 (like free linalool, OxB, OxC)  BC 345 (like bound OxB) | In VTCdb VIT\_15s0048g01700 is coexpressed with the linalool/nerolidol/geranyl linalool synthase *VvPNLNGl3*  VIT\_15s0048g01700 is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014); it is predicted to be localized in the chloroplast |
| Vv\_10006984$ | VIT\_16s0039g00880 | CYP89H3 | Positive correlation with free linalool, OxB, α terpineol, bound citronellol  Cluster 9 (like free linalool, OxB, OxC  BCs 4 (like bound OxB), 35 (like bound OxB, OxC), 98 (like bound OxB) | VIT\_16s0039g00880 is up-regulated at E-L 36 vs E-L 35 in three aromatic varieties (Agudelo-Romero *et al.*, 2013)  VIT\_16s0039g00880 is predicted to be localized also in the chloroplast |
| Vv\_10007610 | VIT\_18s0001g06230 | No hit (NADPH-cytochrome P450 reductase) | Profile: 2vs1,3vs1,4vs1,5vs1down  Positive correlation with free linalool, *trans*-8-HO-linalool, α-terpineol, HO-diendiol II, rose oxide I, bound nerol, citronellol  Cluster 9, like free linalool, OxB, OxC  BCs 4 (like bound OxB), 15 (like free *cis*-8-HO-linalool, HO-diendiol I + HO-trienol, *trans*-geranic acid, bound OxB), 35 (like bound OxB, OxC) | - |
| Vv\_10004784 | VIT\_18s0001g13790 | Cytochrome P450, family 83, subfamily B, polypeptide 1 (CYP71) | Profile: 3vs1up,4vs1up,5vs1up  Positive correlation with several oxidized monoterpenes (bound *cis*/*trans* 8-HO-linalool, OxA, OxD, *trans*-geranic acid, HO-diendiol I and II)  Cluster 4  BCs 10, 39 (like free *cis*-8-HO-linalool, *trans*-geranic acid, HO-diendiol I + HO-trienol), 20 (like free *cis*-8-HO-linalool, OxB, *trans*-geranic acid, HO-diendiol I + HO-trienol) | Members of the CYP71 family metabolize linalool in *Arabidopsis thaliana* (Ginglinger *et al.*, 2013)  The expression of *CYP71AT7* increases along Gewürztraminer berry ripening. CYP71AT7 is able to consume low amounts of linalool and *trans*-8-HO-linalool *in vitro* (Ilc *et al.*, 2017)  VIT\_18s0001g13790 is predicted to be localized in the chloroplast |
| Vv\_10006996 | VIT\_04s0023g02610 | Epoxide hydrolase 2 | Profile: 5vs1up (array) | VIT\_04s0023g02610 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.*, unpublished data) and is predicted to be localized also in the chloroplast. It correlates with nerol in Tocai Friulano under water deficit (Savoi *et al.*, 2016) |
| Vv\_10009847$ | VIT\_07s0005g00700 | Epoxide hydrolase | Positive correlation with free linalool, α-terpineol, HO-diendiol II, rose oxide I, bound linalool, geraniol, nerol, *cis*-8-hydroxy-linalool, OxD, citronellol  Clusters 4 (like free HO-diendiol II, bound *cis*/*trans*-8-HO-linalool, OxA, OxC, OxD, HO-diendiol I + HO-trienol, HO-diendiol II, rose oxide I and II) +9 (like free OxB, OxC) +6 (like bound *trans*-geranic acid)  BC 15 (like free *cis*-8-HO-linalool, HO-diendiol I + HO-trienol, *trans*-geranic acid, bound OxB) | VIT\_07s0005g00700 is predicted to be localized also in the chloroplast |
| Vv\_10003763 | VIT\_06s0061g01350 | Cyclase | Profile: 4vs1up  Cluster 8 (like free rose oxide II)  BCs 219 (like bound 4-terpineol), 383, 392 | Rose oxide and 4-terpineol are cyclic monoterpenoids |
| Vv\_10010475$  Vv\_10004634  Vv\_10013426 | VIT\_03s0091g00040  (*VvgGT1*-*VvGT11*)  VIT\_03s0180g00200  (*VvgGT2*-*VvGT9*)  VIT\_03s0180g00320  (*VvgGT3*-*VvGT10*) | Limonoid UDP-glucosyltransferase  Limonoid UDP-glucosyltransferase  Indole-3-acetate beta-glucosyltransferase | Cluster 2 (like bound OxB)  BCs 273, 277, 292, 349, like bound OxB, rose oxide I and II, 3-oxo-α-ionol, benzyl alcohol  Profile: 3vs1down  Cluster 5  BCs 230, 253, 267, 392, like bound OxC, HO-diendiol I + HO-trienol, *cis*-3-hexen-1-ol  Profile: 3vs1down  Cluster 5  BCs 197, 230, 253, 267, 270, like bound OxC, HO-diendiol I + HO-trienol, 4-terpineol, *cis*-3-hexen-1-ol | CitLGT regulates the conversion of limonoid aglycones (triterpenes) to glucosides in citrus fruit (Kita *et al.*, 2000)  The expression levels of VIT\_03s0091g00040, VIT\_03s0180g00200 and VIT\_03s0180g00320 gradually decrease during berry development in 5 different varieties and clones; only in Muscat the expression of VIT\_03s0180g00200 rises at late ripening stages (Bönisch *et al.*, 2014a)  In Sémillon VIT\_03s0180g00320 is up-regulated by noble rot, along with an increase in terpene biosynthesis (Blanco-Ulate *et al.*, 2015)  VIT\_03s0091g00040, VIT\_03s0180g00200 and VIT\_03s0180g00320 are predicted to be localized in the chloroplast |
| Vv\_10010567$ | VIT\_03s0180g00280 (*VvGT18*) | Indole-3-acetate β-glucosyltransferase | Cluster 1  BCs 0 (like bound OxB), 13 (like bound OxB), 19 (like bound OxB), 199 (like bound OxB, OxC, α-terpineol) | AtGT84B1 and AtGT84B2 show *in vitro* activity towards model linalool (Caputi *et al.*, 2008)  CsUGT1 is a putative terpenoid UGT from sweet orange (Fan *et al.*, 2010)  The expression of VIT\_03s0180g00280 decreases after *veraison* in 5 different varieties and clones (Bönisch *et al.*, 2014b) |
| Vv\_10006855$  Vv\_10008432$ | VIT\_05s0062g00430 (*VvGT20*)  VIT\_05s0062g00520 | UDP-glucose:flavonoid 7-O-glucosyltransferase | Cluster 1 (like bound 3-hydroxy-β-damascone, 6-methyl-5-hepten-2-one)  BCs 0 and 119, like bound OxB, 3-hydroxy-β-damascone, 6-methyl-5-hepten-2-one  Clusters 7+1  BCs 317, 355, 377, like bound 3-hydroxy-β-damascone, 6-methyl-5-hepten-2-one, *cis*/*trans*-3-hexen-1-ol | VIT\_05s0062g00430 matches to two monoterpene glucosyltransferases from Eucalyptus (Nagashima *et al.*, 2005)  The expression of VIT\_05s0062g00430 decreases after *veraison* in 5 different varieties and clones (Bönisch *et al.*, 2014b)  VIT\_05s0062g00430 and VIT\_05s0062g00520 are predicted to be localized in the chloroplast |
| Vv\_10010104$ | VIT\_05s0062g00630  (*VvGT8*)  VIT\_05s0062g00640 | UDP-glucose transferase (UGT75B2)  UDP-glucose:flavonoid 7-O-glucosyltransferase | Cluster 3 (like bound *cis*-3-hexen-1-ol)  BCs 82, 90, 92, 107, 116, 124, 141, 152, like bound *trans*-8-HO-linalool, OxB, OxC, α-terpineol, HO-diendiol I + HO-trienol, *cis*-3-hexen-1-ol | VIT\_05s0062g00640 matches to two monoterpene glucosyltransferases from *Eucalyptus* (Nagashima *et al.*, 2005) and a linalool glucosyltransferase from *Arabidopsis* (Caputi *et al.*, 2008)  The expression level of VIT\_05s0062g00630 gradually decreases during berry development in 5 different varieties and clones (Bönisch *et al.*, 2014a)  VIT\_05s0062g00640 is predicted to be localized in the chloroplast |
| Vv\_10013486$ | VIT\_07s0141g00580 | Glycosyl transferase family 8 protein | Positive correlation with free linalool, *trans*-8-HO-linalool, OxB, α-terpineol, rose oxide I, bound citronellol  Cluster 9  BCs 35, 95, like bound OxB, OxC, HO-diendiol I + HO-trienol, 3-hydroxy-β-damascone, 6-methyl-5-hepten-2-one | In VTCdb VIT\_07s0141g00580 is coexpressed with *GPPS* (VIT\_06s0009g03090, VIT\_00s0283g00050) and a CYP76C (VIT\_15s0048g01480) |
| Vv\_10009861 | VIT\_16s0050g01580 (*VvGT7*) | UDP-glucose: anthocyanidin 5,3-O-glucosyltransferase | Profile: 3vs1,4vs1,5vs1down  Cluster 5  BCs 204 (like bound HO-diendiol I + HO-trienol), 209, 283 (like bound HO-diendiol I + HO-trienol) | VIT\_16s0050g01580 matches to a *Arabidopsis* citronellol/geraniol glucosyltransferase (Caputi *et al.*, 2008)  VvGT7 may contribute to the production of geranyl and neryl glucoside during grape ripening; it glucosylates a variety of substrates (Bönisch *et al.*, 2014a)  *VvGT7* transcript accumulation correlates significantly with the accumulation of glycosylated monoterpenes in Riesling ripening grapes (Friedel *et al.*, 2016)  VIT\_16s0050g01580 falls within the confidence interval of a QTL for geraniol and nerol (Doligez *et al.*, 2006) and is predicted to be localized in the chloroplast |
| Vv\_10009347 | VIT\_14s0006g00430 | Carboxylesterase | Profile: 3vs1,4vs1,5vs1up  Positive correlation with free OxC, bound rose oxide I, benzylic alcohol  Cluster 9 | Carboxylesterases are involved in the hydrolysis of esters into acids and alcohols and may contribute to flavor development; VIT\_14s0006g00430 is up-regulated at E-L 36 vs E-L 35 in three aromatic varieties (Agudelo-Romero *et al.*, 2013) |
| **Monoterpene transport** | | | | |
| Vv\_10003051  Vv\_10012513  Vv\_10001796$ | VIT\_02s0012g01630  VIT\_00s0287g00080  (chr 2) | Transmembrane protein 41B (SNARE associated Golgi protein)  Vesicle-associated membrane protein | Profile: 2vs1,3vs1,4vs1,5vs1down Cluster 9  Positive correlation with free nerol, bound *trans*-geranic acid, 7-HO-nerol and α-terpineol  Cluster 6 | Inhibition of vesicle fusion was shown to strongly interact with ectopic expression of certain terpenes, including linalool (Ting *et al.*, 2015)  VIT\_02s0012g01630 and VIT\_00s0287g00080 fall within the confidence interval of a QTL for linalool, linalool/nerol and nerol/geraniol (Doligez *et al.*, 2006; Battilana *et al.*, 2009)  VIT\_00s0287g00080 is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014); it is predicted to be localized in the chloroplast |
| Vv\_10002561$  Vv\_10011974 | VIT\_01s0011g04670  VIT\_16s0039g00010 | ABC transporter G member 2  ABC transporter G member 7 | Positive correlation with free OxB  Cluster 9  Profile: 5vs1up  Cluster 5 | Plant ABCG transporters have been shown to transport terpenoids (Kang *et al.*, 2011)  In VTCdb VIT\_16s0039g00010 is coexpressed with nine monoterpene synthases (including the linalool/nerolidol synthases *VvPNLinNer1* and *VvPNLNGl3*), which determines a significant enrichment in the category ‘S-linalool synthase activity’ for the coexpressed genes  VIT\_01s0011g04670 and VIT\_16s0039g00010 are significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) |
| Vv\_10004737 | VIT\_08s0040g03040 | Glutathione S-transferase GSTO1 | Profile: 5vs1up  Positive correlation with bound *trans*-8-HO-linalool, OxD, *trans*-geranic acid, α-terpineol, HO-diendiol II  Cluster 4 | In VTCdb VIT\_08s0040g03040 is coexpressed with ABCG/PDR12 transporters (VIT\_09s0002g05370, VIT\_09s0002g05410, VIT\_09s0002g05600), which causes a significant enrichment in the category ‘Isoprenoid transport’  VIT\_08s0040g03040 is predicted to be localized also in the chloroplast |
| Vv\_10008655 | VIT\_06s0009g01140 | Amino acid permease | Profile: 2vs1,3vs1,4vs1,5vs1up (array and qRT-PCR\_2016)  Positive correlation with free linalool, *trans*-8-HO-linalool, α-terpineol, HO-diendiol II, rose oxide I, bound linalool, geraniol, nerol, *cis*-8-HO-linalool, citronellol  Clusters 4+6+9 | VIT\_06s0009g01140 falls within the confidence interval of a QTL for nerol/geraniol (Battilana *et al.*, 2009) and is a putative ‘switch gene’ in the immature-to-mature transition during grapevine development (Palumbo *et al.*, 2014)  In VTCdb VIT\_06s0009g01140 is coexpressed with linalool synthase (VIT\_00s0372g00020), 1,8-cineole synthase (VIT\_00s0266g00020, VIT\_00s0271g00010), and CYP76C4s (VIT\_02s0012g02820, VIT\_03s0097g00460) |
| Vv\_10002691 | VIT\_08s0007g05210 | Amino acid permease | Profile: 5vs1up  Positive correlation with free geraniol and bound α-terpineol  Cluster 6 | VIT\_08s0007g05210 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.*, unpublished data)  In VTCdb VIT\_08s0007g05210 is coexpressed with CYP76Cs (VIT\_02s0025g04880, VIT\_15s0048g01480 and VIT\_15s0048g01490) |
| Vv\_10000443  Vv\_10011370 | VIT\_08s0007g04900 | Unknown protein | Profile: 5vs1up  Positive correlation with several monoterpenes  Cluster 4 | VIT\_08s0007g04900 is annotated with the GO term ‘Cytoplasmic membrane-bounded vesicle’; it falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) and is predicted to be localized in the chloroplast |
| **Transcriptional regulation and signaling** | | | | |
| Vv\_10002171 | VIT\_16s0100g00400 | Ethylene-responsive transcription factor ERF025 | Profile: 2vs1,3vs1,5vs1down  Clusters 9+7  Correlated with Vv\_10003051 (correlation > 0.99 between differential gene expression ratios)  Correlated with con Vv\_10003051, Vv\_10006855, Vv\_10007610, Vv\_10009014, Vv\_10009587, Vv\_10012513 (correlation > 0.90 between microarray channel intensities) | VIT\_16s0100g00400 is a candidate master regulator of grape berry maturation (Palumbo *et al.*, 2014)  In VTCdb VIT\_16s0100g00400 is coexpressed with CYP76C4s (VIT\_02s0012g02810, (VIT\_03s0097g00460) and the 9-*cis*-epoxycarotenoid dioxygenase *VvCCD4b* (VIT\_02s0087g00930) |
| Vv\_10008748 | VIT\_18s0001g05250 | DREB sub A-6 of ERF/AP2 transcription factor (RAP2.4) | Profile: 2vs1,3vs1,4vs1,5vs1down  Cluster 9  Correlated with Vv\_10002015, Vv\_10003051, Vv\_10006855, Vv\_10007610, Vv\_10009014, Vv\_10009587, Vv\_10012513 (correlation > 0.90 between microarray channel intensities) | In Wen *et al.* (2015) XM\_002285766.2 is coexpressed with the linalool/nerolidol synthase *VvCSLinNer* |
| Vv\_10006673$ | VIT\_10s0003g04100 | Auxin response factor 3 | Positive correlation with free OxA  Cluster 5 | *AtARF6* promotes volatile sesquiterpene production by activating jasmonate biosynthesis and *AtMYB21* expression (Reeves *et al.*, 2012)  In VTCdb VIT\_10s0003g04100 is coexpressed with the linalool/nerolidol synthase *VvPNLinNer2*, a myrcene synthase (VIT\_00s0271g00030), a putative monoterpene glycosyltransferase (VIT\_08s0007g04590), and three CYPs involved in monoterpenoid biosynthesis or coexpressed with linalool synthase genes (VIT\_10s0092g00500, VIT\_00s0389g00030, VIT\_00s0389g00040)  VIT\_10s0003g04100 is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) |
| Vv\_10006719  Vv\_10007868$ | VIT\_14s0066g01090 | Myb domain protein 24 | Profile: 5vs1up (array)  Positive correlation with bound OxC  Cluster 4  Vv\_10007868 correlated with Vv\_10004183 (correlation > 0.99 between differential gene expression ratios)  Vv\_10006719 correlated with Vv\_10004183 (correlation > 0.95 between microarray channel intensities) | VIT\_14s0066g01090 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data); it is significantly induced by UV radiation in the berry skin of Tempranillo (Carbonell-Bejerano *et al.*, 2014b); candidate transcriptional regulator of monoterpene biosynthesis (Savoi *et al.*, 2016); it is highly co-expressed with flower and fruit specific *TPS* genes (Wong *et al.*, 2016) |
| Vv\_10006438$  Vv\_10003977  Vv\_10007346$ | VIT\_01s0146g00280  VIT\_19s0014g03300 | NAC domain-containing protein 83  NAC domain containing protein 2 | Positive correlation with free nerol, bound *trans*-geranic acid, 7-OH-nerol, α-terpineol  Cluster 6  Correlated with Vv\_10001796 (correlation > 0.99 between differential gene expression ratios)  Profile: 5vs1up (array)  Positive correlation with bound *trans*-8-HO-linalool, OxC, rose oxide II  Cluster 4  Correlated with Vv\_10006996 and Vv\_10000710 (correlation > 0.99 between differential gene expression ratios)  Positive correlation with bound rose oxide II  Cluster 4 | Tomato mutant fruit at the *NOR* locus fails to produce climacteric ethylene or ripen (Giovannoni, 2004)  NAC TFs (AaNAC2, AaNAC3 and AaNAC4) are involved in controlling monoterpene production in kiwifruit through transcriptional activation of *TPS1* (Nieuwenhuizen *et al.*, 2015)  VIT\_01s0146g00280 and VIT\_19s0014g03300 are up-regulated in both flesh and skin throughout Muscat Hamburg ripening (Lijavetzky *et al.*, 2012)  In Sémillon VIT\_19s0014g03300 is up-regulated by noble rot, along with an increase in terpene biosynthesis (Blanco-Ulate *et al.*, 2015) |
| Vv\_10008821 | VIT\_15s0046g01440 | BZip transcription factor G- box binding factor 3 | Profile: 3vs1,4vs1,5vs1down  Negative correlation with several monoterpenes  Cluster 1 | CrGBF1 acts as a transcriptional repressor of the *Str* promoter (Sibéril *et al.*, 2001)  VIT\_15s0046g01440 is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) |
| Vv\_10004421 | VIT\_18s0001g09230 | Salt tolerance zinc finger | Profile: 5vs1down  Negative correlation with bound 4-terpineol  Cluster 7 | ZCT proteins act as repressors in the regulation of elicitor-induced secondary metabolism in *Catharanthus roseus*. In particular, they repress the *Str* and *Tdc* gene expression (Pauw *et al.*, 2004)  VIT\_18s0001g09230 is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) |
| Vv\_10007020 | VIT\_04s0008g05210 | BZIP protein HY5 (HY5) | Profile: 4vs1,5vs1up (array)  Cluster 9  Correlated with Vv\_10008655 (correlation > 0.90 between microarray channel intensities) | *HY5* is a key gene involved in light perception transduction  LeHY5 is a positive regulator of thylakoid organization and carotenoid accumulation (Liu *et al.*, 2004; Toledo-Ortiz *et al.*, 2014)  AaHY5 interacts with the promoter of a pinene synthase gene in modulating its rhythmic expression (Zhou *et al.*, 2015)  *VvHY5*/*HYH* are coexpressed with genes involved in the biosynthesis of monoterpenes, including four *TPS* (Loyola *et al.*, 2016)  The expression of VIT\_04s0008g05210 is induced by UV radiation (Carbonell-Bejerano *et al.*, 2014b; Liu et al., 2015; Loyola *et al.,* 2016) and is higher in Verdejo (aromatic) than in Tempranillo samples (Carbonell-Bejerano *et al.*, 2014a)  VIT\_04s0008g05210 is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) |
| Vv\_10002904$  Vv\_10001238$ | VIT\_06s0061g01140  VIT\_10s0003g04490 | Phototropic-responsive NPH3  Phototropic-responsive NPH3 | Cluster 9  Correlated with Vv\_10013486 (correlation > 0.99 between differential gene expression ratios)  Positive correlation with free linalool, *trans*-8-HO-linalool, α-terpineol, rose oxide I  Clusters 6+8+9+4  Correlated with Vv\_10002691 and Vv\_10000710 (correlation > 0.90 between microarray channel intensities) | In VTCdb VIT\_10s0003g04490 is coexpressed with genes that determine a significant enrichment in the category ‘Chloroplast part’; it is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) |
| Vv\_10000275$  Vv\_10005663$  Vv\_10006303$  Vv\_10010958 | VIT\_15s0048g02410 | Myb CCA1 (circadian clock associated 1) | Cluster 6  Profile: 4vs1down  Clusters 6+5+4 | *Myb CCA1* encodes a protein of the circadian oscillator, which regulates the isoprenoid pathway (Vranová *et al.*, 2012)  In VTCdb VIT\_15s0048g02410 is coexpressed with genes that determine a significant enrichment in the category ‘Plastid’ |
| **New candidate genes** | | | | |
| Vv\_10000182$ | VIT\_01s0010g03900 | SEPALLATA3 | Positive correlation with free OxC  Cluster 9  Correlated with Vv\_10000443 and Vv\_10004737 (correlation > 0.90 between microarray channel intensities) | *VvMADS4* may have an important role in fruit development besides floral organ formation (Boss *et al.*, 2002) |
| Vv\_10011420  Vv\_10000707 | VIT\_01s0026g01970 | RNA-binding region RNP-1 (RNA recognition motif) | Profile: 2vs1,3vs1,4vs1,5vs1down  Cluster 4  Correlated with Vv\_10003051, Vv\_10006855, Vv\_10007610, Vv\_10009587, Vv\_10012513 (correlation > 0.90 between microarray channel intensities)  Profile: 2vs1,3vs1,4vs1,5vs1down  Clusters 5+4 | Chloroplast RNA-recognition motif proteins are candidates for regulating chloroplast RNA processing under shifting environmental conditions (Ruwe *et al.*, 2011)  VIT\_01s0026g01970 falls within the confidence interval of a QTL for nerol/geraniol (Battilana *et al.*, 2009) and is predicted to be localized also in the chloroplast |
| Vv\_10010907 Vv\_10013994$ | VIT\_02s0012g01040 | NAC domain-containing protein 71 | Profile: 2vs1,3vs1,4vs1,5vs1up (array and qRT-PCR\_2016)  Positive correlation with free OxC, bound linalool, *trans*-8-HO linalool, OxA, HO-diendiol I and II, rose oxide I and II  Cluster 4  Vv\_10010907 correlated with Vv\_10008655 and Vv\_10009347 (correlation > 0.90 between microarray channel intensities) | VIT\_02s0012g01040 falls within the confidence interval of a QTL for linalool, linalool/nerol and nerol/geraniol (Doligez *et al.*, 2006; Battilana *et al.*, 2009). It is up-regulated in both flesh and skin throughout Muscat Hamburg ripening (Lijavetzky *et al.*, 2012) and is a candidate master regulator of grape berry maturation (Palumbo *et al.*, 2014) |
| Vv\_10002682$ Vv\_10009852$ Vv\_10012211  Vv\_10013897$ | VIT\_02s0012g01240 (2 gene predictions in V2: Vv\_10012211 matches to VIT\_202s0012g01235 = ring fyve phd zinc finger-containing protein) | PHD finger transcription factor | Profile: 5vs1up  Positive correlation with free geraniol, bound α-terpineol  Cluster 6  Vv\_10012211 correlated with Vv\_10002691 (correlation > 0.99 between differential gene expression ratios) and Vv\_10008655 (correlation > 0.90 between microarray channel intensities) | VIT\_02s0012g01240 falls within the confidence interval of a QTL for linalool, linalool/nerol and nerol/geraniol (Doligez *et al.*, 2006; Battilana *et al.*, 2009) |
| Vv\_10006791$ | VIT\_02s0087g00770 | ABC transporter E member 1 | Cluster 9 | ABCE is a suppressor of RNA silencing (Kärblane *et al.*, 2015)  VIT\_02s0087g00770 falls within the confidence interval of a QTL for linalool/nerol and nerol/geraniol, which is the second QTL on chromosome 2 (Battilana *et al.*, 2009) |
| Vv\_10014336$ | VIT\_02s0087g00830 | CBF1 interacting corepressor CIR | Positive correlation with bound *trans*-8-HO-linalool, OxA, OxD, HO-diendiol I and II, rose oxide II  Cluster 4  Correlated with Vv\_10006996 (correlation > 0.99 between differential gene expression ratios) | VIT\_02s0087g00830 falls within the confidence interval of a QTL for linalool/nerol and nerol/geraniol, which is the second QTL on chromosome 2 (Battilana *et al.*, 2009) |
| Vv\_10003472 | VIT\_02s0234g00100 | Ubiquitinyl hydrolase 1 | Profile: 5vs1up  Positive correlation with several bound monoterpenes  Cluster 4  Correlated with Vv\_10000443 and Vv\_10011370 (correlation > 0.99 between differential gene expression ratios)  Correlated with Vv\_10000443, Vv\_10000710 and Vv\_10002691 (correlation > 0.90 between microarray channel intensities) | VIT\_02s0234g00100 is predicted to be localized also in the chloroplast |
| Vv\_10013322$ | VIT\_00s0341g00050 (chr2) | ATMYB66/WER/WER1 (WEREWOLF 1) | Clusters 6+5+4 | VIT\_00s0341g00050 falls within the confidence interval of a QTL for linalool, linalool/nerol and nerol/geraniol (Doligez *et al.*, 2006; Battilana *et al.*, 2009) and is predicted to be localized also in the chloroplast |
| Vv\_10000578 | VIT\_03s0038g02500 | SKP1 | Profile: 5vs1up  Correlated with Vv\_10000710 and Vv\_10006996 (correlation > 0.99 between differential gene expression ratios) | AtASK1is part of the SCF complex that regulates the expression of jasmonate (JA) responsive genes (Devoto *et al.*, 2002)  JA treatment of grapes induces the expression of genes from the MVA and MEP pathways and the formation of volatile compounds, especially terpenes and norisoprenoids (D’Onofrio *et al.*, 2009; Gómez-Plaza *et al.*, 2012; May and Wüst, 2015)  VIT\_03s0038g02500 is predicted to be localized also in the chloroplast |
| Vv\_10001186$ Vv\_10006289$ | VIT\_04s0008g07340 | Constans-like 4 | Vv\_10006289 positively correlated with bound *trans*-8-HO-linalool, OxD, HO-diendiol II  Cluster 4  Vv\_10006289 correlated with Vv\_10000443 and Vv\_10000710 (correlation > 0.90 and 0.95 between microarray channel intensities, respectively) | At5g24930 correlates with isoprenoid biosynthetic genes (Mannen *et al.*, 2014)  VIT\_04s0008g07340 is annotated with the GO terms ‘Jasmonic acid mediated signaling pathway’ and ‘Red light signaling pathway’ among others; it is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) and is predicted to be localized in the chloroplast |
| Vv\_10009141 | VIT\_04s0023g00130 | Unknown protein | Profile: 4vs1,5vs1up (array), 3vs1,4vs1,5vs1up (qRT-PCR\_2016)  Positive correlation with free OxC, bound OxA, HO-diendiol I, rose oxide I and II  Cluster 4 | VIT\_04s0023g00130 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) and is predicted to localize also in the chloroplast. It is up-regulated in both flesh and skin throughout Muscat Hamburg ripening (Lijavetzky *et al.*, 2012) and is a putative ‘switch gene’ in the immature-to-mature transition during grapevine development (Palumbo *et al.*, 2014) |
| Vv\_10011003$ | VIT\_04s0023g00440 | Zinc finger (C2H2 type) family | Clusters 6+4 | VIT\_04s0023g00440 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) |
| Vv\_10001872 | VIT\_04s0023g01250 | Brassinosteroid signaling positive regulator (BZR1) | Profile: 2vs1,3vs1,5vs1down  Positive correlation with free OxB  Cluster 9  Correlated with Vv\_10002561 (correlation > 0.99 between differential gene expression ratios)  Correlated with Vv\_10003051, Vv\_10007610, Vv\_10009014 (correlation > 0.90 between microarray channel intensities) | The over-expression of *BZR1-D* in tomato leads to the up-regulation of carotenoid biosynthetic genes (including *DXS*) and increased carotenoid content in ripe fruit (Liu *et al.*, 2014)  Brassinosteroids are involved in grapevine berry development at early fruit development stages or around *veraison* (Fortes *et al.*, 2015)  VIT\_04s0023g01250 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) |
| Vv\_10009982 | VIT\_04s0023g01380 | Scarecrow-like | Profile: 2vs1,3vs1down  Positive correlation with bound rose oxide II  Cluster 4 | VIT\_04s0023g01380 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) and is predicted to be localized in the chloroplast |
| Vv\_10002444  Vv\_10012072$ | VIT\_04s0023g02950 | Zinc finger (CCCH-type) family protein | Profile: 2vs1,3vs1,4vs1down  Clusters 4+5  Correlated with Vv\_10003051, Vv\_10007610, Vv\_10009587, Vv\_10012513 (correlation > 0.90 between microarray channel intensities)  Positive correlation with bound OxC  Cluster 4  Correlated with Vv\_10003051, Vv\_10006855, Vv\_10007610, Vv\_10009587, Vv\_10012513 (correlation > 0.90 between microarray channel intensities) | VIT\_04s0023g02950 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) and is up-regulated in both flesh and skin throughout Muscat Hamburg ripening (Lijavetzky *et al.*, 2012) |
| Vv\_10000933 | VIT\_04s0023g03120 | Histone H3 | Profile: 3vs1,4vs1,5vs1up  Positive correlation with bound linalool, *trans*-8-HO-linalool, OxA, OxD, HO-diendiol I and II, rose oxide I and II  Cluster 4 | VIT\_04s0023g03120 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) |
| Vv\_10003073$  Vv\_10008371$  Vv\_10010478$  Vv\_10014421$  Vv\_10006882$ | VIT\_04s0044g00070  VIT\_14s0066g01310 | RAB GDP dissociation inhibitor 1 ATGD1 (rab proteins geranylgeranyltransferase component a 2-like)  CAAX farnesyltransferase beta subunit | Positive correlation with bound linalool, *trans*-8-HO-linalool, OxA, OxC, OxD, HO-diendiol I and II, rose oxide I and II  Cluster 4  Vv\_10003073 correlated with Vv\_10000710 (correlation > 0.99 between differential gene expression ratios)  Vv\_10014421 correlated with Vv\_10000710 and Vv\_10006996 (correlation > 0.99 between differential gene expression ratios)  Positive correlation with bound *trans*-8-HO-linalool, OxC  Cluster 4  Vv\_10006882 correlated with Vv\_10000710 and Vv\_10006996 (correlation > 0.99 between differential gene expression ratios) | Protein prenylation is implicated in the regulation of TIA terpene mojety biosynthesis through the activation of *ORCA3* and MEP (*DXS*, *DXR*) gene expression in response to jasmonate (Courdavault *et al.*, 2009)  VIT\_04s0044g00070 is predicted to be localized also in the chloroplast  VIT\_14s0066g01310 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) |
| Vv\_10005693  Vv\_10008803  Vv\_10013342 | VIT\_00s0214g00090 (chr4) | F-box protein PP2-B10 (Protein phloem protein 2-like B10) | Profile: 3vs1,4vs1,5vs1up (array), 4vs1up (qRT-PCR\_2016)  Positive correlation with several monoterpenes  Clusters 4+6  Correlated with Vv\_10009847 (correlation > 0.99 between differential gene expression ratios)  Correlated with Vv\_10008655 (correlation > 0.90 between microarray channel intensities)  Profile: 3vs1,4vs1up  Positive correlation with free OxD  Cluster 8  Profile: 3vs1,4vs1up  Positive correlation with free OxD  Cluster 8  Correlated with Vv\_10000443 and Vv\_10001518 (correlation > 0.90 between microarray channel intensities) | VIT\_00s0214g00090 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) and is a putative ‘switch gene’ in the immature-to-mature transition during grapevine development (Palumbo *et al.*, 2014) |
| Vv\_10002798$ | VIT\_06s0004g03590 | TOE1 (target of eat1 1) related to apetala2 7 (ethylene signaling) | Cluster 9 | In Wen *et al.* (2015) XM\_002284713.2 is coexpressed with the linalool/nerolidol synthase *VvCSLinNer* and the pinene synthase *VvPNaPin*  VIT\_06s0004g03590 is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) |
| Vv\_10002670$ | VIT\_06s0004g04980 | Scarecrow transcription factor 14 (SCL14) | Cluster 9 | VIT\_06s0004g04980 falls within the confidence interval of a QTL for nerol/geraniol (Battilana *et al.*, 2009) |
| Vv\_10009860 | VIT\_06s0004g07550 | Wound-induced protein WI12 | Profile: 2vs1,3vs1,4vs1,5vs1up (array), 2vs1,4vs1,5vs1up (qRT-PCR\_2016)  Positive correlation with free OxC, HO-diendiol II, bound linalool, geraniol, nerol, OxA, citronellol, HO-diendiol I, rose oxide I  Clusters 9+4  Correlated with Vv\_10008655 and Vv\_10009347 (correlation > 0.95 and 0.90 between microarray channel intensities, respectively) | VIT\_06s0004g07550 falls within the confidence interval of a QTL for nerol/geraniol (Battilana *et al.*, 2009) and is predicted to localize in the chloroplast  It is up-regulated in both flesh and skin throughout Muscat Hamburg ripening (Lijavetzky *et al.*, 2012) and is a putative ‘switch gene’ in the immature-to-mature transition during grapevine development (Palumbo *et al.*, 2014)  In VTCdb VIT\_06s0004g07550 is coexpressed with the 9-cis-epoxycarotenoid dioxygenase *VvCCD4b* (VIT\_02s0087g00930) |
| Vv\_10003323$ | VIT\_06s0009g01000 | Zinc finger (C3HC4-type ring finger) CIC7E11 | Cluster 9  Correlated with Vv\_10003051 (correlation > 0.99 between differential gene expression ratios) | VIT\_06s0009g01000 falls within the confidence interval of a QTL for nerol/geraniol (Battilana *et al.*, 2009) |
| Vv\_10003411$ | VIT\_06s0009g01570 | C2H2 zinc-finger protein SERRATE (SE) | Positive correlation with bound *trans*-8-HO-linalool, OxC  Cluster 4  Correlated with Vv\_10000710 and Vv\_10006996 (correlation > 0.99 between differential gene expression ratios) | VIT\_06s0009g01570 falls within the confidence interval of a QTL for nerol/geraniol (Battilana *et al.*, 2009) |
| Vv\_10009328$ | VIT\_06s0009g02550 | Chaperonin | Cluster 6 | Involved in protein folding and associated to the GO term ‘Isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway’  VIT\_06s0009g02550 falls within the confidence interval of a QTL for nerol/geraniol (Battilana *et al.*, 2009) |
| Vv\_10012857$ | VIT\_07s0005g01560 | PAPA-1 | Positive correlation with free geraniol  Cluster 6 | VIT\_07s0005g01560 is annotated with the GO term ‘Chloroplast’ and falls within the confidence interval of a QTL for nerol/geraniol (Battilana *et al.*, 2009) |
| Vv\_10014365$ | VIT\_07s0005g02570 | WRKY DNA-binding protein 47 | Positive correlation with free OxB, OxD  Cluster 8, like free OxD | In VTCdb VIT\_07s0005g02570 is coexpressed with *HMGR* (VIT\_03s0038g04100) and a CYP76C (VIT\_02s0025g04880)  VIT\_07s0005g02570 is more highly up-regulated in the skin than in the flesh throughout Muscat Hamburg ripening (Lijavetzky *et al.*, 2012)  VIT\_07s0005g02570 is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) |
| Vv\_10013932 | VIT\_07s0031g01320 | TGA-type basic leucine zipper protein TGA1.1 (jasmonate signaling) | Profile: 2vs1,3vs1,4vs1,5vs1down  Positive correlation with bound *trans*-8-HO-linalool, OxD, HO-diendiol II  Cluster 4  Correlated with Vv\_10003051, Vv\_10006855, Vv\_10007610, Vv\_10009014, Vv\_10009587, Vv\_10012513 (correlation > 0.90 between microarray channel intensities) | In Wen *et al.* (2015) XM\_002280746.2 is coexpressed with *VvHMGR1* and the pinene synthase *VvPNaPin*  VIT\_07s0031g01320 is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) |
| Vv\_10009798  Vv\_10010260  Vv\_10014254 | VIT\_07s0031g01930 | Myb TKI1 (TSL-kinase interacting protein 1) | Profile: 2vs1,3vs1,4vs1,5vs1up (Vv\_10009798), 3vs1,4vs1,5vs1up (Vv\_10010260 and Vv\_10014254), 4vs1,5vs1up (qRT-PCR\_2016)  Positive correlation with several monoterpenes (free linalool with high significance)  Clusters 4+6+9  Vv\_10009798 correlated with Vv\_10007610, Vv\_10013486 (correlation > 0.99 between differential gene expression ratios) and Vv\_10008655 (correlation > 0.90 between microarray channel intensities)  Vv\_10010260 and Vv\_10014254 correlated with Vv\_10008655 and Vv\_10009847 (correlation > 0.99 between differential gene expression ratios)  Vv\_10014254 correlated with Vv\_10008655 (correlation > 0.90 between microarray channel intensities) | VIT\_07s0031g01930 is up-regulated in both flesh and skin throughout Muscat Hamburg ripening (Lijavetzky *et al.*, 2012) and is a candidate master regulator of grape berry maturation (Palumbo *et al.*, 2014) |
| Vv\_10010364 | VIT\_07s0104g01050 | Homeobox protein | Profile: 4vs1,5vs1up  Positive correlation with several monoterpenes  Clusters 9+4  Correlated with Vv\_10008655 and Vv\_10009347 (correlation > 0.90 between microarray channel intensities) | - |
| Vv\_10004273$ | VIT\_07s0191g00180 | Homeobox-leucine zipper protein ATHB-6 (ABA signaling) | Clusters 9+8 | In Wen *et al.* (2015) XM\_003632428.1 is coexpressed with *VvHMGR1*, *VvHMGR3* and the pinene synthase *VvPNaPin* |
| Vv\_10004635$ | VIT\_08s0007g03910 | CTR1 serine/threonine protein kinase | Positive correlation with bound 4-terpineol  Clusters 6+2 | *LeCTR1* is involved in ethylene signaling downstream of ethylene receptor; it is up-regulated during tomato ripening (Leclercq *et al.*, 2002)  VIT\_08s0007g03910 is predicted to be localized also in the chloroplast |
| Vv\_10001158 | VIT\_08s0007g05790 | Calmodulin | Profile: 2vs1,3vs1,4vs1,5vs1down  Cluster 9 | VIT\_08s0007g05790 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data); it is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) and is predicted to be localized also in the chloroplast |
| Vv\_10004111 | VIT\_08s0007g05880 | Dehydration-induced protein (ERD15) (ABA signaling) | Profile: 2vs1,3vs1,4vs1,5vs1down  Cluster 9  Correlated with Vv\_10002015, Vv\_10003051, Vv\_10006855, Vv\_10007610, Vv\_10009014, Vv\_10009587, Vv\_10012513 (correlation > 0.90 between microarray channel intensities) | Limited water availability promotes the accumulation of monoterpenes such as HO-trienol, linalool, nerol, and α-terpineol (Koundouras *et al.*, 2006; Savoi *et al.*, 2016)  VIT\_08s0007g05880 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) |
| Vv\_10002459$ | VIT\_08s0007g06530 | DnaJ homolog, subfamily B, member 6 (dnaj heat shock n-terminal domain-containing protein heat shock protein binding) | Cluster 6 | VIT\_08s0007g06530 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) and is predicted to be localized also in the chloroplast |
| Vv\_10007395$ | VIT\_08s0007g07060 | Unknown protein (Ubiquitin carboxyl-terminal hydrolase) | Clusters 4+9 | VIT\_08s0007g07060 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) and is predicted to be localized in the chloroplast |
| Vv\_10000712$ | VIT\_08s0007g07160 | Transcriptional co-activator | Positive correlation with several monoterpenes  Cluster 4  Correlated with Vv\_10000443 and Vv\_10011370 (correlation > 0.90 between microarray channel intensities) | VIT\_08s0007g07160 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) |
| Vv\_10002372$ | VIT\_08s0007g07670 | NAC domain containing protein 47 | Positive correlation with free OxB  Clusters 9+8  Correlated with Vv\_10013486 (correlation > 0.90 between microarray channel intensities) | VIT\_08s0007g07670 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) and is a candidate master regulator of grape berry maturation (Palumbo *et al.*, 2014)  VIT\_08s0007g07670 is up-regulated in both flesh and skin throughout Muscat Hamburg ripening (Lijavetzky *et al.*, 2012); in Sémillon it is up-regulated by noble rot, along with an increase in terpene biosynthesis (Blanco-Ulate *et al.*, 2015)  In VTCdb VIT\_08s0007g07670 is coexpressed with *VvGT14* |
| Vv\_10007880 | VIT\_08s0007g08160 | Telomere repeat binding factor Like TRFL10 | Profile: 2vs1,3vs1,4vs1,5vs1up  Positive correlation with bound linalool, geraniol, *trans*-8-HO-linalool, OxA, OxD, HO-diendiol I, rose oxide I and II  Cluster 4 | VIT\_08s0007g08160 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data) |
| Vv\_10011970$ | VIT\_08s0058g00200 | Transcription factor | Positive correlation with free nerol, bound *cis*-8-HO-linalool, OxD, *trans*-geranic acid, 7-HO-nerol, α-terpineol, HO-diendiol II  Clusters 4+6  Correlated with Vv\_10004737 (correlation > 0.99 between differential gene expression ratios) | - |
| Vv\_10001632  Vv\_10007070$ | VIT\_09s0054g01780  VIT\_11s0016g02620 | HAC1 (P300/CBP acetyltransferase-related protein 2 gene)  Histone acetyltransferase HAG2 | Profile: 3vs1,4vs1,5vs1up  Positive correlation with bound *trans*-8-HO-linalool, rose oxide II  Cluster 4  Correlated with Vv\_10006996 (correlation > 0.99 between differential gene expression ratios)  Positive correlation with bound OxC  Cluster 4  Correlated with Vv\_10004183 (correlation > 0.99 between differential gene expression ratios) | Histone acetylation by histone acetyltransferases increases the accessibility of chromatin to the transcription machinery. In *Arabidopsis thaliana* many metabolic proteins are acetylated (Shen *et al.*, 2015) |
| Vv\_10005633$ | VIT\_10s0003g00190 | DNA-binding protein | Clusters 4+5 | VIT\_10s0003g00190 falls within the confidence interval of a QTL for linalool, linalool/geraniol and linalool/nerol (Battilana *et al.*, 2009) and is predicted to be localized in the chloroplast |
| Vv\_10003356$ | VIT\_10s0003g00210 | Unknown | Clusters 6+4  Correlated with Vv\_10000710 and Vv\_10002691 (correlation > 0.90 between microarray channel intensities) | VIT\_10s0003g00210 falls within the confidence interval of a QTL for linalool, linalool/geraniol and linalool/nerol (Battilana *et al.*, 2009) |
| Vv\_10012485$ | VIT\_10s0003g00270 | Homeobox-1 | Positive correlation with bound OxC  Cluster 4 | VIT\_10s0003g00270 falls within the confidence interval of a QTL for linalool, linalool/geraniol and linalool/nerol (Battilana *et al.*, 2009) |
| Vv\_10005202$ | VIT\_10s0003g01770 | Heat shock transcription factor A4A | Positive correlation with bound *trans*-8-HO-linalool, OxD, *trans*-geranic acid, HO-diendiol II  Cluster 4  Correlated with Vv\_10004737 (correlation > 0.99 between differential gene expression ratios) | In Wen *et al.* (2015) XM\_002267135.2 is coexpressed with the linalool/nerolidol synthase *VvPNLinNer1* |
| Vv\_10008513 | VIT\_10s0003g03190 | RNA recognition motif (RRM)-containing | Profile: 2vs1,3vs1,4vs1,5vs1up (array)  Cluster 9  Correlated with Vv\_10008655 and Vv\_10009347 (correlation > 0.90 between microarray channel intensities) | VIT\_10s0003g03190 falls within the confidence interval of a QTL for linalool, linalool/geraniol and linalool/nerol (Battilana *et al.*, 2009)  It is up-regulated in both flesh and skin throughout Muscat Hamburg ripening (Lijavetzky *et al.*, 2012)  In VTCdb VIT\_10s0003g03190 is coexpressed with *HDR* (VIT\_03s0063g02030) |
| Vv\_10001832$ | VIT\_10s0003g03710 | Cullin-4 | Positive correlation with free linalool and bound citronellol  Cluster 9  Correlated with Vv\_10002561 (correlation > 0.90 between microarray channel intensities) | Cullin is part of the SCF complex that regulates the expression of jasmonate responsive genes (Devoto *et al.*, 2002)  JA treatment of grapes induces the expression of genes from the MVA and MEP pathways and the formation of volatile compounds, especially terpenes and norisoprenoids (D’Onofrio *et al.*, 2009; Gómez-Plaza *et al.*, 2012; May and Wüst, 2015) |
| Vv\_10002850$ | VIT\_00s0454g00030  (chr10) | Subtilisin protease | Positive correlation with free OxB  Cluster 9 | VIT\_00s0454g00030 falls within the confidence interval of a QTL for linalool, linalool/geraniol and linalool/nerol (Battilana *et al.*, 2009); it is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) and is predicted to be localized in the chloroplast |
| Vv\_10002430$ Vv\_10012066$ | VIT\_00s0463g00010 (chr10) | WRKY DNA-binding protein 20 | Positive correlation with free geraniol  Cluster 6 | VIT\_00s0463g00010 falls within the confidence interval of a QTL for linalool, linalool/geraniol and linalool/nerol (Battilana *et al.*, 2009) |
| Vv\_10009872 | VIT\_00s0463g00020  (chr10) | Scarecrow transcription factor 5 (SCL5) | Profile: 2vs1,3vs1,4vs1,5vs1down  Clusters 5+6+4  Correlated with Vv\_10003051, Vv\_10007610, Vv\_10009014, Vv\_10009587, Vv\_10012513 (correlation > 0.90 between microarray channel intensities) | VIT\_00s0463g00020 falls within the confidence interval of a QTL for linalool, linalool/geraniol and linalool/nerol (Battilana *et al.*, 2009)  In Wen *et al.* (2015) XM\_002272365.2 is coexpressed with the linalool/nerolidol synthase *VvCSLinNer* and the nerolidol synthase *VvNerL8* |
| Vv\_10013923$ | VIT\_00s0475g00040  (chr 10) | Myb family | Positive correlation with bound *trans*-8-HO-linalool, OxC  Cluster 4  Correlated with Vv\_10000710 (correlation > 0.99 between differential gene expression ratios) | VIT\_00s0475g00040 falls within the confidence interval of a QTL for linalool, linalool/geraniol and linalool/nerol (Battilana *et al.*, 2009) |
| Vv\_10001911$ | VIT\_11s0016g03290 | SNW domain-containing protein 1 SNW1 | Positive correlation with several monoterpenes  Cluster 4  Correlated with Vv\_10011370 (correlation > 0.99 between differential gene expression ratios) | - |
| Vv\_10004782$  Vv\_10008760$ | VIT\_12s0028g03130 | Proteasome 26S regulatory subunit S2 (RPN1) | Positive correlation with free geraniol, nerol, bound α-terpineol  Cluster 6  Correlated with Vv\_10002691 and Vv\_10000710 (correlation > 0.90 between microarray channel intensities)  Cluster 9  Correlated with Vv\_10012513 (correlation > 0.99 between differential gene expression ratios) | VIT\_12s0028g03130 falls within the confidence interval of a QTL for geraniol and linalool/geraniol (Battilana *et al.*, 2009) |
| Vv\_10008596 | VIT\_12s0028g03860 | Zinc finger (C3HC4-type ring finger) protein (RMA1) | Profile: 4vs1,5vs1up (array), 2vs1,3vs1,5vs1up (qRT-PCR\_2016)  Positive correlation with bound OxC  Cluster 4  Correlated with Vv\_10000710 (correlation > 0.99 between differential gene expression ratios) | VIT\_12s0028g03860 falls within the confidence interval of a QTL for geraniol and linalool/geraniol (Battilana *et al.*, 2009) and is predicted to localize also in the chloroplast  VIT\_12s0028g03860 is up-regulated in both flesh and skin throughout Muscat Hamburg ripening (Lijavetzky *et al.*, 2012) and is a candidate master regulator of grape berry maturation (Palumbo *et al.*, 2014)  In VTCdb VIT\_12s0028g03860 is coexpressed with three CYP71s involved in monoterpenoid biosynthesis (VIT\_01s0137g00540, VIT\_01s0137g00550, VIT\_01s0137g00560) (Ginglinger *et al.*, 2013) |
| Vv\_10004541 | VIT\_13s0019g00860 | Small heat-shock protein HSP17.5 Cytosolic class I | Profile: 2vs1,3vs1down  Clusters 9+4 | Involved in protein folding |
| Vv\_10002554$ | VIT\_13s0064g00640 | PHD finger transcription factor | Cluster 9 | VIT\_13s0064g00640 falls within the confidence interval of a QTL for geraniol and nerol (Doligez *et al.*, 2006)  In VTCdb VIT\_13s0064g00640 is coexpressed with *GPPS* (VIT\_06s0009g03090) |
| Vv\_10000441$ | VIT\_13s0064g00920 | Zinc finger (CCCH-type) family protein | Positive correlation with several bound monoterpenes  Cluster 4  Correlated with Vv\_10000443 and Vv\_10011370 (correlation > 0.99 between differential gene expression ratios)  Correlated with Vv\_10000710 (correlation > 0.90 between microarray channel intensities) | VIT\_13s0064g00920 falls within the confidence interval of a QTL for geraniol and nerol (Doligez *et al.*, 2006) |
| Vv\_10010154$ | VIT\_14s0083g00940 | Auxin-independent growth promoter | Positive correlation with free geraniol, bound α-terpineol  Cluster 6 | VIT\_14s0083g00940 is a putative ‘switch gene’ in the immature-to-mature transition during grapevine development (Palumbo *et al.*, 2014) and is predicted to localize also in the chloroplast |
| Vv\_10012816$ | VIT\_14s0219g00200 | Pentatricopeptide (PPR) repeat-containing protein | Cluster 9  Correlated with Vv\_10000443, Vv\_10009847 and Vv\_10011974 (correlation > 0.90 between microarray channel intensities) | PPR proteins take part in the post-transcriptional regulation of organelle gene expression. For example, the post-transcriptional regulation of mitochondrial RNA by the PPR protein LOI1is likely involved in isoprenoid biosynthesis *via* both the MVA and MEP pathways (Kobayashi *et al.*, 2007)  VIT\_14s0219g00200 falls within the confidence interval of a QTL for geraniol and nerol (Battilana *et al.* 2009, unpublished data); it is significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014) and is predicted to be localized in chloroplast |
| Vv\_10010750 | VIT\_16s0050g01150 | Heat shock protein 90-1 | Profile: 3vs1down  Clusters 9+7 | Involved in protein folding |
| Vv\_10011630$ | VIT\_16s0148g00420  VIT\_00s2365g00010  VIT\_00s0258g00040  VIT\_16s0148g00260  VIT\_16s0050g02740  VIT\_16s0039g01210  VIT\_00s2248g00010  and others | Rust resistance kinase Lr10  Kinase  Ser/Thr receptor-like kinase1  Ser/Thr receptor-like kinase1  Receptor-like protein kinase  Ser/Thr receptor-like kinase1  Rust resistance kinase Lr10 | Positive correlation with bound 4-terpineol  Clusters 6+5  Correlated with Vv\_10002691 (correlation > 0.90 between microarray channel intensities) | Based on the IASMA annotation, Vv\_10011630 falls within the confidence interval of a QTL for nerol/geraniol on chromosome 1 (Battilana *et al.*, 2009)  In VTCdb the corresponding V1 gene predictions are coexpressed with genes that determine a significant enrichment in the category ‘Isoprenoid metabolic process’, including ‘ 1-deoxy-D-xylulose-5-phosphate synthase activity’ and ‘S-linalool synthase activity’  VIT\_00s2365g00010 has a constant expression in the skin and is repressed in the fleshthroughout Muscat Hamburg ripening (Lijavetzky *et al.*, 2012)  VIT\_16s0148g00420, VIT\_00s2365g00010, VIT\_00s0258g00040, VIT\_16s0148g00260, VIT\_16s0050g02740, VIT\_16s0039g01210 and VIT\_00s2248g00010 are significantly more expressed in the skin than in the pulp of Cabernet Sauvignon berries at 23 °Brix (Cramer *et al.*, 2014)  VIT\_00s2365g00010 and VIT\_00s2248g00010 are predicted to be localized also in the chloroplast |
| Vv\_10000260 | VIT\_18s0001g03580 | Ubiquitin-fold modifier 1 precursor | Profile: 4vs1,5vs1up  Positive correlation with bound linalool, *trans*-8-HO-linalool, OxA, OxD, HO-diendiol I and II, rose oxide I and II  Cluster 4 | VIT\_18s0001g03580 is predicted to be localized also in the chloroplast |
| Vv\_10003319 | VIT\_18s0001g15270 | SCL1 (scarecrow-like 1) | Profile: 2vs1,3vs1,4vs1,5vs1down  Cluster 6  Correlated with Vv\_10007610 and Vv\_10009014 (correlation > 0.90 between microarray channel intensities) | In Wen *et al.* (2015) XM\_002266379.2 is coexpressed with the linalool/nerolidol synthase *VvCSLinNer* and the nerolidol synthase *VvNerL8*  VIT\_18s0001g15270 is predicted to be localized in the chloroplast |
| Vv\_10002436$ | VIT\_19s0014g00860 | Zinc finger (FYVE type) | Positive correlation with free nerol, bound *trans*-geranic acid, 7-HO-nerol, α-terpineol  Cluster 6 | - |
| Vv\_10013790$ | VIT\_19s0090g01430 | EDM2 | Positive correlation with free nerol, bound *cis*-8-HO-linalool, OxD, *trans*-geranic, 7-HO-nerol  Clusters 6+4 | In VTCdb VIT\_19s0090g01430 is coexpressed with three CYP71s involved in monoterpenoid biosynthesis (VIT\_01s0137g00540, VIT\_01s0137g00550, VIT\_01s0137g00560) (Ginglinger *et al.*, 2013) |

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