Alterations in grapevine leaf metabolism occur prior to esca apoplexy appearance.

Maryline Magnin-Robert[1], Marielle Adrian[2], Sophie Trouvelot[2], Alessandro Spagnolo[1], Lucile Jacquens[2], Patricia Letousey[1], Fanja Rabenoelina[1], Mourad Harir[3], Chloé Roullier-Gall[4], Christophe Clément[1], Philippe Schmitt-Kopplin[3,4], Armelle Vallat[5], Eliane Abou-Mansour[6], and Florence Fontaine[1*]

[1]SFR Condorcet, Université de Reims Champagne-Ardenne, URVVC EA 4707, Laboratoire Stress, Défenses et Reproduction des Plantes, BP 1039, 51687 Reims Cedex 2, France.

[2]UMR Agroécologie, AgroSup Dijon, INRA, Université Bourgogne Franche-Comté, 17 rue Sully, BP 86510 - 21065 Dijon cedex, France.

[3] Analytical BioGeoChemistry, Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg, Germany

[4]Chair of Analytical Food Chemistry, Technische Universität München, Freising-Weihenstephan, Germany

[5]Université de Neuchâtel, Institut de chimie, NPAC, Avenue de Bellevaux 51, 2000 Neuchâtel, Switzerland

[6]Plant Biology Department, University of Fribourg, Chemin du Musée 10, 1700 Fribourg, Switzerland.

*To whom the correspondence should be addressed. Florence FONTAINE, E-mail: florence.fontaine@univ-reims.fr, Phone: 3 33 26 91 33 18, Fax : 3 33 26 91 33 39

ABSTRACT

Esca disease is one of the major grapevine trunk diseases in Europe and the aetioloy is complex since several inhabiting fungi are identified to be associated with this disease. Among the foliar symptom expression, apoplectic form may be distinguished and characterized by sudden dieback of shoots, leaf drop and shriveling of grape clusters in few days that can ultimately induce the plant death. To further understand this drastic event, we conducted transcriptomic and metabolomic analyses to characterize responses of leaves during the period preceding symptom appearance (twenty and seven days before foliar symptoms expression) and at the day of apoplexy expression. Transcriptomic and metabolomic provide signatures for the apoplectic leaves and most of changes concern the metabolism of carbohydrates, amino acids, and phenylpropanoids. Deciphering on glutathione-S-transferase, its preferential location in phloem, correlated with the upregulation of *GST* genes and a decrease of the glutathione level, offer further support to the putative role of glutathione during apoplexy expression.

KEY-WORDS

Apoplexy, metabolomic, transcriptomic, targeted genes, *in situ* hybridization, glutathione, *Vitis vinifera,* esca.

INTRODUCTION

The 21st century is the burst of re-emerging diseases, among with the grapevine trunk diseases (GTDs) due to a complex of fungi. Over the past decade, their symptom incidence has drastically increased in Europe, *i.e.* the cumulated symptomatic grapevines (foliar symptoms) in French vineyards is close to 13 % (Bruez et al. 2013) and may reach up to 10% in Spain and 50 % in Italian ones (Romanazzi et al. 2009). A recent estimation of the economic cost of GTDs due to decrease of both quality and quantity of wine and the replacement of died vines, evaluates the lost for more than 1.1 billion euros (Hofstetter et al. 2013). In Europe, GTDs are now stated as the major preoccupation for winegrowers since no efficient control is available. Outside Europe, GTDs are also generally of great concern and induces for example economic losses of up to US$ 260 million per year in California and $ 8.3 billion in Australia (De la Fuente et al. 2016).

Esca disease is one of the major GTDs in Europe and esca aetiology is complex since several fungi are known to be associated to this disease, especially *Phaeomoniella chlamydospora*, *Phaeoacremonium minimum* and *Fomitiporia mediterranea* (Bertsch et al. 2013). They are xylem-inhabiting fungi and they induce various wood symptoms such as brown necrosis and black streaking (Larignon and Dubos 2001). For the foliar symptom expression, either a chronic or apoplectic form may be distinguished. The chronic form is typically characterized by spots appearing between the leaf veins or along the edges, which expand and become confluent, finally resulting in chlorotic and necrotic strips with only a narrow green stripe along the midrib (Mugnai et al. 1999; Bertsch et al. 2013). In most cases, the affected leaf finally assumes a “tiger stripe” appearance. The apoplexy form is characterized by the dieback of one or more shoots and is accompanied by leaf drop and the shrivelling and drying of fruit clusters (Mugnai et al. 1999). Usually, this violent event occurs in midsummer, particularly when dry, hot weather follows rainfall (Mugnai et al.

1999; Surico et al. 2006). After such an event, the affected vines can resume growth in the following season or even in the current one, but they can also ultimately die.

To further understand the apoplexy expression, studies have been conducted on related grapevine responses in different organs (Fontaine et al. 2015). In the trunk, healthy wood was mainly characterized by down-expression of proteins involved in cell growth and defense response (Magnin-Robert et al. 2014). Conversely, in black streaked wood, characterized by an extensive presence of GTD agents, the proteome analysis revealed over-expression of proteins involved in defense. For green shoots, various quantitative expressions are triggered upon the onset of apoplexy, although no pathogens associated with GTDs have been isolated from these organs (Spagnolo et al. 2012). In leaves, the period preceding symptom appearance was especially investigated by following physiological and targeted genes associated to photosynthesis and stress responses (Letousey et al. 2010). Within the week preceding symptoms, drastic alterations of photosynthesis were registered in pre-apoplectic vines, as revealed by a decrease in gas exchanges, changes in chlorophyll fluorescence, and repression of photosynthesis-related genes. In the meantime, expression of a set of defense-related genes was induced and amplified during symptom expression (Letousey et al. 2010). Such a characterization of the events preceding apoplexy needs to get new insights of gene regulation and metabolic changes associated to apoplexy expression.

In the present study, transcriptomic and metabolomic analyses were performed in grapevine cv. Chardonnay leaves, before and at the time of apoplexy appearance, in comparison with asymptomatic leaves as controls. This was completed by the qRT-PCR analysis of the expression of 18 targeted genes, selected from the previous transcriptomic study, on healthy and diseased samples collected fifty, thirty, twenty and seven days before apoplexy expression. Focus was given to glutathione metabolism and localization of the glutathione-S-transferase by *in situ* hybridization to characterize its role in detoxification process in response to fungal toxins production. The findings are discussed with respect to the current knowledge about grapevine physiology and plant responses to fungal pathogen attacks.

RESULTS

Differentially-expressed genes detected by Illumina mRNA at T0-20, T0-7 and T0 apoplexy event

Analysis of gene expression was conducted on leaves from diseased plants at various times before apoplectic symptom appearance and on control plants (C) at the same development stage. A total number of 1,216,959 raw reads were generated by 454 GS FLX of a cDNA mix of different leaf samples. After filtering, 1,210,565 clean reads were obtained with an average length of 150 pb. The total length of clean reads was about 314 millions bases (314,141,226).

A selection of genes based on a differential expression between diseased and control leaves (ratio ≥ 2 for up-regulation and ≤0.5 for down-regulation) was done through all the time points. The number of up- and / or down-regulated genes was 2,122. Overall, 51.8% of these genes showed a constant induction of their expression, 35.7% a constant repression and 12.5% had an induction or a repression of their expression at least at two points of the kinetic. The evolution of the expression of the regulated genes (induced and / or repressed) depending on the kinetic was summarized in Fig. 1. Results indicated that 262 genes exhibit a modified expression 20 days before apoplexy event (T0-20). The number of genes with regulated expression increased with the imminent onset of the symptoms, 629 genes for healthy apparent (vh) leaves 7 days before apoplexy (T0-7vh), 1508 genes for turgorless (tg) leaves 7 days apoplexy (T0-7tg) and 1690 genes at the onset of the apoplexy

(T0). Interestingly, the majority of the genes with modified expression at T0-20 were down-regulated (60%) (Fig. 1). This repartition was completely reversed on vh leaves of diseased plants at T0-7 with 25% of down-regulated genes. At the onset of symptoms, the number of down- or up-regulated genes is equivalent. Genes regulated in diseased leaves were grouped into 9 functional categories (Fig. 2), with about 69% (181), 70% (440), 56% (844) and 55% (929) of genes remaining unfortunately not yet known for T0-20, T0-7vh, T0-7tg and T0, respectively. Globally, from T0-20 to T0, there was an increasing number of regulated genes involved in both stress and defense reactions, lipid metabolism and in protein metabolism and a decreasing number of genes involved in amino acid and secondary metabolism. Few modifications were observed for the other pathways. In regard to the 9 functional categories reported namely 1- carbohydrate metabolism; 2- amino acid metabolism; 3- lipid metabolism; 4- growth, replication and DNA damage repair; 5- signalisation, hormonal regulation, transduction, transcriptor factor; 6- protein metabolim; 7- cellular process; 8- secondary metabolism and 9- stress and defense reaction (Table 2, Supplementary Table 2), we focused on 5 ones representing key functions in grapevine physiology and / or already known to be affected by wood trunk diseases in previous studies: carbohydrate metabolism, amino acid metabolism, lipid metabolism, secondary metabolism and stress and defense reactions (Table 2, Koussa et al. 1998; Rifai et al. 2005; Petit et al. 2006; Letousey et al. 2010; Lima et al. 2010, Magnin-Robert et al. 2011). For carbohydrate metabolism, genes involved in energy synthesis, starch degradation, glucose metabolism, and photosynthesis system were globally up-regulated at the beginning of the kinetic (T0-20), in diseased leaves, before symptoms emergence. Among them were the genes encoding succinate dehydrogenase (XM_002269371), lysosomal-beta-glucosidase (XM_002278327), zeta-carotene desaturase (XM_002277312), UTP-glucose 1-phosphate uridyltransferase (XM_002282240); alpha-glucan phosphorylase (XM_002280696), ribulose biphosphate carboxylase small chain (XM_002276931), glucan endo-1,3-beta-glucosidase (XM_002279561). In opposite, the *sucrose synthase 2* (XM_002271494) encoding a protein involved in sucrose synthesis and two *galactose oxidase* genes (XM_01065799 and XM_002274727) encoding two proteins involved in galactose metabolism were clearly repressed in T-20/T0-7tg/T0 and T0-7tg/T0 samples, respectively. At T0, the up-regulated genes were mainly involved in cell wall formation / modification (*beta-xylosidase/alpha-L-arabinofuranosidase* - XM_002264147; *UDP-arabidopyranose mutase* - XM_002263454) whereas several genes involved in glycolysis, photosynthesis and starch degradation were downregulated (*violaxanthin de-epoxidase* XM_010650663; *alpha-amylase* XM_002285177 and XM_0106655795).

Genes involved in amino acid metabolism appeared to be also modulated during the kinetic, especially those involved in methionine and polyamine metabolism. As example, *cysthathionine beta-lyase* (XM_002281384), aspartate aminotransferase, mitochondrial (XM_002281728), *thermospermine synthase* (XM_002281075), *tropinone reductase homolog* (XM_002277799), S-*adenosyl-L-methionine decarboxylase* (XM_002277280), *deoxyhypusine synthase* (XM_002282885) were down-regulated, while S-*adenosyl-L-methionine decarboxylase* (XM_002278114) and *asparte aminotransferase* (XM_002284100) were up-regulated (Table 2).

In lipid metabolism, changes were observed at both T0-7 and T0, especially at T0-7tg. There was an up-regulation of genes associated with alkaloids and terpenoids synthesis, such as *beta-amyrin synthase* (XM_002270898), *secologanin synthase* (XM_003634726), VvCSbOciM (HM8807387), *abietadienol/abietadienal oxidase* (XM_010663730), *hydroxymethylglutaryl-CoA synthase* (XM_002282398) and *3-epi-6-deoxocasthasterone 23 monooxygenase* (XM_010650788). Conversely, the expression of *1-deoxy-D-xylulose-5-phosphate synthase* (XM_002277883) and *jmjC domain-containing protein 7*

(XM_010646063) was down-regulated at the last three points of the kinetic, when the expression of *alpha-terpineol synthase* (XM_002266772) and *alpha-terpineol synthase-like* (XM_ 010660749) was both down-regulated at T0-7tg and T0 (Table 2). Some of the genes involved in the octadecanoid pathway were differently regulated as *12-oxophytodienoate reductase 2-like* (XM_002281312) (upregulation at T0 and T0) and *allene oxide synthase* (XM_002283744), *lipoxygenase 1* (KF033130), *jasmonate-O-methyltransferase* (XM_002281543) (down-regulation especially at T0) (Table 2).

Three genes related to phenylpropanoid metabolism were up-regulated at all time points. Among them were the *salicylate–O-methyltransferase* (XM_002262640), *flavonoid-3'-monooxygenase-like* (XM_0022842115) and *bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase* (XM_002277359). Additionally, a downregulation of the expression of flavonoid-related R2R3MYB4 repressor transcription factor (XM_002278186) was observed at T0-7. Several genes encoding proteins involved in anthocyanidin, flavonoid and lignin biosynthesis were also up-regulated at T0-7tg and T0: *malonate CoA* (XM_002279103), *anthocyanidin 3-O-glucosyl transferase* (XM_002264962), *UDP-glucose/flavonoid 3-O-glucosyltransferase* (AB047093), *chalcone synthase* (XM_001280950), *second bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase* (XM_010651497), *cinnamyl alcohol dehydrogenase* (XM_002285370), *naringenin 2-oxoglutarate 3-dioxygenase* (XM_002284856), and *caffeoyl shikimate esterase* (XM_003634810).

For the "stress and defense reactions" category, the *epoxide hydrolase* gene (XM_003632333) encoding a protein involved in detoxification process was up-regulated from T0-20 to T0. Except for the down-regulation of the gene encoding a putative disease resistance RPP13, 12 genes encoding proteins involved in stress and defense reactions, and detoxification process were up-regulated in leaves at T0-7vh, T0-7tg and T0. Among them were genes encoding glutathione-S-transferase (XM_003634217 and XM_002262806) or haloacid dehalogenase (XM_002267523) and pathogenesis-related proteins (PR) like thaumatin (XM_002274101), PR10 (XM_002273754) or class I β-1,3-glucanase (XM_002277133) (Table 2). At T0-7tg and T0, the expression of genes related to multidrug transports was altered, such as pleiotropic drug resistance (XM_010655751, XM_010656419) and multidrug efflux transporter (MATE) (XM_002274772, XM_002280176) encoding genes. At T0-7, the expression of genes involved in detoxification process was also regulated, as indicated by the induction of two epoxide hydrolase (GSVIVT00025835001, XM_010650793), the repression of two other glutathione–S-transferase (XM_002269082, XM_002275302) and one superoxide dismutase (XM_010661684). Moreover, a down-regulation of *chaperone protein dnaJ 20* (XM_002264118), *hsp70-hsp90 protein 3* (XM_0036355638), chaperone protein ClpB4 (XM_002282844) and an up-regulation for heat shock 70kDa (XM_0022834967), 20kDa chaperonin (XM_002277825) were reported. The expression of 24 genes encoding disease resistance proteins and 10 genes encoding PR proteins was also modulated at T0-7tg and T0 (Table 2).

Validation of candidate genes by RT-PCR

Eighteen genes selected on their expression pattern at the three times of apoplexy event (Supplementary Table 1) were followed in leaves of diseased plants to validate these genes as precocious molecular markers of apoplexy expression. The samples used were the same ones as for the transcriptomic analyses, to which we added others obtained from diseased plants (n=3) cultivated in the same vineyard during the same year. These genes were selected in regard to the regulation of their expression during apoplectic kinetic (transcriptomic data at T0-20 and T0-7tg/vh) and their involvement in various pathways (carbohydrate metabolism, amino acid metabolism, lipid metabolism, hormonal regulation, cellular processes, phenylpropanoid pathway and detoxification processes) (Table 2 and Supplementary Table 2). Results correspond to means ± standard deviation of 3 plants sampled. These genes code for UTP-glucose-1-phosphate uridyltransferase (*gluPuriT*-XM_002282240), sucrose synthase (*SucS2*-XM_002271494), succinate deshydrogenase flavoprotein (*SucDHFla*-XM_002269371), thermospermine synthase (*SperS*-XM_002281075), 1-deoxy-D-xylulose-5-phosphate (*xylPS*-XM_002277883), jmjC domain-containing protein 7 (*jmjc7*-XM_010646063), auxin-induced protein 10A5 (*Aux10A5*-XM_002271727), myosin-H heavy chain (*Myochain*-XM_0022815579), F-box/WD40 repeat-containing protein (*FboxWD40*-XM_002271652), casein kinase (*CasK*-XM_002284008), V-type proton ATPase subunit B (*HatpZ*-XM_002280255), flavonoid-related R2R3 MYB4a repressor transcription factor (*MYB4A*-XM_002278186), shikimate deshydrogenase (*ShiDH*- XM_002277359), epoxide hydrolase (*epoxHF*-XM_003632333) and haloacid dehalogenase hydrolase (*Hahl*-XM_002267523). Three of the four genes encoding a glutathione-S-transferase identified by the transcriptomic study were also selected: (*GSTA* – XM_003634217, *GSTB* – XM8002262806 and *GSTC* – XM8002269082). No significant regulation of the selected genes involved in protein phosphorylation (cellular processes), amino acid metabolism, lipid metabolism and transports was observed in our samples, suggesting they might be not retained as markers of pre-apoplectic event. Among the three selected genes involved in carbohydrate metabolism, only *SucS2* was down-regulated on leaves at T0-20. Similarly to the transcriptomic results, *Aux10A5* was down-regulated at 2 time points, T0-7 and T0 (Table 3). Moreover, the repression of *MYB4A* expression at T0-7 and T0 was confirmed whereas no modifications were monitored at T0-20, 30 and 50. For the detoxification process, *EpoxHF* was up-regulated at T0 and *Hahl* was down-regulated at T0-30 and then up-regulated at T0-7 and T0. Concerning the GST encoding genes, , the *GSTC* expression was not modified during the kinetic whereas *GSTA* and *GSTB* were down-regulated, at T0 for *GSTA* and at T0 and T0-7 for *GSTB* (Table 3). Moreover, these two genes appeared to be up-regulated in our conditions 50 days before apoplexy event (Table 3).

Changes in the metabolome during apoplexy event expression

FT-ICR-MS was used in the negative-ion ESI mode for the non-targeted analysis of the low molecular weight metabolites present in the sample sets. A total of 40,149 raw mass values was first obtained and reduced for masses occurring in minimum of 10% of all samples and by the calculation of elemental formulas with NetCalc software (Tziotis *et al*., 2010). The dataset containing 7,309 masses assigned to an elementary composition was thus obtained, among with only 1,255 m/z could be annotated to putative metabolites after KEGG, HMDB and LipidMaps database query. OPLS-DA analysis allowed the discrimination of three sample groups with a good statistical significance: control, T0-20 and T0-7, and T0 diseased samples (Fig. 3A). Among the 7,309 elementary compositions obtained, 4,220 were common to the three groups whereas 1,206 were specific to control, 87 to diseased T0-20 and T0-7 samples and 32 to diseased T0 samples (Fig. 3B). The chemical composition and VK diagrams obtained from all these m/z highlighted a wide chemical diversity, with a significant contribution of CHO and, to a lesser extent, of CHONS elemental formulas (Fig. 3C). Masses with the highest regression coefficient values in each sample group (specific and common masses with a variable importance in projection (VIP) value > 1; thereafter called “top *m/z*”) were next used for comparison, allowing the visualization of clear differences between the three sample groups (Figs. 3D-E-F). CHO elemental formulas remained the most abundant in all groups, followed by CHONS and CHON ones (Figs. 3D-E-F, chemical composition diagrams on the right part).

CHO and CHON ones were more abundant in diseased T0 samples whereas CHO and CHONS ones were more abundant in control ones. VK diagrams highlighted noteworthy differences in the nature and the number of formulas assigned to masses between the three sample groups, leading to specific fingerprints (Figs. 3D-E-F, VK diagrams on the left part).

KEGG query (*Vitis vinifera* organism) with the MassTRIX interface allowed the assignment of top m/z to metabolic pathways. A rather limited number of pathways were associated to diseased samples, especially for T0-20 and T0-7 ones (6 pathways, Fig. 4). For this sample group, they were related to amino acid metabolism (tyrosine, phenylalanine, cysteine and methionine), biosynthesis of secondary metabolites, flavone and flavonol biosynthesis, ubiquinone and other terpenoid-quinone biosynthesis. In diseased T0 samples, a higher number of pathways were identified (more than 10). The main ones were biosynthesis of secondary metabolites, starch and sucrose metabolism, galactose metabolism, phenylpropanoid biosynthesis, flavone and flavonol biosynthesis, flavonoid biosynthesis, monoterpenoid biosynthesis, phenylalanine metabolism and oxocarboxylic acid metabolism (Fig. 4). The number of pathways associated to the control samples was higher (more than 18) and the main ones were biosynthesis of secondary metabolites, starch and sucrose metabolism, and flavonoid biosynthesis, galactose metabolism and amino sugar and nucleotide sugar metabolism (Fig. 4).

A mass difference network analysis based on series of biochemical transformations (Adrian et al. 2017, Moritz et al. 2017) was performed to obtain an additional overview of the global metabolism in the different grapevine leaf groups (data not shown). A total of 469 transformations were found to connect masses. Those having the highest z-score were represented in histogram in Fig. 5. Four types of differences allowed the discrimination between samples: opposite z-scores for diseased samples at T0, opposite z-scores for diseased samples at T0-7 and T0-20, higher z-scores of control samples, higher z-scores of diseased samples either at T0-7 and T0-20 or T0 time. Transformations in T0 samples were highly different to those of the two other sample groups, with the absence of biochemical reactions involving the conjugation of pteridine, phenylpyruvic and coumaric acids, and an increased number of reactions involving phosphorylation, phosphoric acid addition and ring opening, decarboxylation, tri-prenylation/farnesylation, and also linoleic acid metabolism and condensation (Fig. 5).

Dynamics of glutathione during apoplexy event expression

Attention was paid to the dynamics of glutathione in the samples. The query in the KEGG database (*Vitis vinifera* organism) with the MassTRIX interface first confirmed the importance of the glutathione pathway in diseased leaves (Fig. 6A); the m/z=306,07655 correspond to the formula $[C_{10}H_{17}N_3O_6S]^-$ confirmed with the isotopologues. The signal intensity of putative glutathione in the different sample series was next assessed using the peak intensities of the spectra. Independently of the kinetic, the amount of this metabolite was about three times lower in apoplectic than in control samples (Fig. 6B). No mass corresponding to the reduced form of glutathione could be found. A metabolic network was built from S-containing compounds (41.07% of all masses) and allowed the visualization of the central role of $[C_{10}H_{17}N_3O_6S]^-$ and metabolic connectivity (Fig. 6C). Masses containing 1, 2, 3 and 4 S represented 20.32, 16.74, 3.60 and 0.41% of the total masses, respectively. Masses associated to glutathione could be extracted from this network (Fig. 6D). Most of them were common to the three sample groups and were mainly condensations and additions (Fig. 6E).

In situ hybridization visualization of *GST1* expression in leaves

Since apparent modification of glutathione metabolism was observed with transcriptomic and metabolomic analysis, glutathione-S-transferase 1 (GST1) was further analysed and located in plant tissues. *GST1* has been reported to be induced in pre-symptomatic and symptomatic leaves, green shoots, cordon and trunk of diseased grapevine affected by GLSD or apoplexy external symptoms appearance (Letousey et al. 2010; Magnin-Robert et al. 2011, 2016). Moreover, the expression pattern of *GST1* was monitored by RT-PCR at T0, T0-7, 20, 30 and 50 days before apoplexy event and this analysis reported that *GST1* was up-regulated during this apoplexy kinetic (Table 4) in grapevine leaves, excepted at T0-30. To analyze in depth the cell type-specific expression of *GST1*, *in situ* hybridization experiments were performed in leaves of control or pre-apoplectic grapevines (Figs. 7 and 8). The results revealed a signal preferentially located in veins (Fig. 7G), especially in pre-apoplectic vines. None or only a slight signal was detected in leaf tissues of control vines (Fig. 7E). Visualization of the *GST1* transcripts matched with the cells of phloem complexes in the secondary bundles (Fig. 7G, red arrow heads), and was exclusively revealed with the antisense probe (Figs. 7F-G). Magnification of the principal vein (primary bundles) hybridization allowed the localization of *GST1* expression in the phloem complexes of pre-apoplectic leaves (Fig. 8G). Again, no (or only a slight) signal was detected in primary veins of asymptomatic leaves (Fig. 8E). In comparison to the *Rib* antisense probe (Figs. 7C and 8C), no signal was detected in the epidermis, parenchyma, and xylem cells for the *GST1* gene, thus confirming the preferential phloem-specific expression of the *GST1*-gene.

DISCUSSION

Esca disease is complex, not only since several fungi are causal agents, but also because pathogens are localized in xylem vessels and fibers of mature wood whereas visible symptoms appear at foliar level from July to August (Larignon et al. 2001; Bertsch et al. 2013). Apoplectic form has serious impact on the vineyard safeguard since it leads quickly to the death of the plant and its incidence is increasing, partly due to the climate fluctuation. To further understand the drivers leading to this status, the apoplectic form and the leaf responses before symptoms emergence and at the onset of symptoms were particularly followed. More precisely, to follow the chronology of the onset of apoplexy appearance, leaves were sampled at 50, 30, 20 and 7 days preceding apoplexy event with a focus from T0-20 to the day of expression (T0).

Our study clearly demonstrates changes in plant metabolism from 20 days before symptoms appearance on leaves. Transcriptomic analyses revealed an increase of the number of genes whose expression was altered as the apoplexy event was close: less than 300 ones at T0-20D to about 1,700 ones at T0. Modifications were mainly reported in metabolisms of carbohydrates, amino acids, lipids, phenylpropanoids, and stress and defense responses. The expression of carbohydrate genes involved in energy synthesis, starch degradation and photosynthesis was induced at T0-20D and then repressed at T0 while those involved in plant defense response were up-regulated from T0-7 to T0. This is in agreement with previous results obtained on leaves developing various grapevine trunk diseases (Letousey et al. 2010; Lima et al. 2010; Camps et al. 2010). Regarding amino acid metabolism, especially methionine and polyamine, an alteration was observed during the kinetic, as described in leaves affected by Eutypa dieback (Rifai et al. 2005). This metabolic pathway could be crucial for grapevine immune responses towards the pathogens, as observed for grapevine response to *B. cinerea* (Hatmi et al. 2015). In addition, the grapevine response is strengthened by an induction of defenses, especially related to the phenylpropanoid pathway, during the apoplexy emergence, which are generally up-regulated following a pathogen attack including those involved in trunk diseases (Valtaud et al. 2009; Lima et al. 2010, Magnin-Robert et al. 2011; Lambert et al. 2013; Calzarano et al. 2014) and other diseases (Romero-Perez et al. 2001; Gruau et al. 2015).

In the meantime, a metabolic signature of apoplectic leaves was observed. FT-ICR-MS was used to analyze and compare the metabolome of the different leaf samples (the same as those used for transcriptomic). OPLS discriminant analysis allowed the distinction of three sample groups: samples from asymptomatic leaves (control), samples of pre-apoplectic diseased leaves (T0-20 and T0-7) and samples of leaves at the time of apoplexy expression (T0). The leaf metabolome was therefore affected by esca disease, and in a different manner before and at the time of apoplexy expression. The Venn diagram revealed the occurrence of specific m/z in diseased leaves (87 for T0-20 and T0-7 and 32 for T0 samples), suggesting that either new compounds accumulated before and at the time of apoplexy expression in diseased samples, and / or that compounds initially present were metabolized during symptom appearance. The lower number of these specific m/z at T0 than at T0-20 / T0-7, may be due to apoplexy expression (stop of the metabolism and sap movement). Moreover, both apoplectic sample groups have a lower number of specific m/z than C one, indicating a reduced diversity of the metabolic composition.

VK diagrams obtained from discriminant masses provided a metabolic fingerprint for each of the three distinct groups. KEGG query (*Vitis vinifera* organism) with the MassTRIX interface allowed to associate amino acid metabolism (tyrosine and phenylalanine), biosynthesis of secondary metabolites, ubiquinone and other terpenoid-quinone biosynthesis pathways to the T0-20 / T0-7 sample group. The amino acid phenylalanine plays a crucial role, among others, as the precursor of the phenylpropanoid pathway leading to the biosynthesis of lignin, stilbenes and flavonoids. All these compounds are known to play a role against biotic stresses (Mouradov and Spangenberg 2014).

Terpenoids are also involved in plant / pathogen interactions (Jansen et al. 2011). In grapevine, they may be involved in defense against downy mildew (Chalal et al. 2015; Algarra Alarcon et al. 2015). At T0, discriminant masses were mainly related to biosynthesis of secondary metabolites, starch and sucrose metabolism, galactose metabolism, phenylpropanoid biosynthesis and flavonoid biosynthesis metabolisms. The defensive secondary metabolism still remain activated, despite the terpene one did no more contribute to diseased sample specificity. It therefore seems that primary metabolism, mainly related to amino acids, is highly mobilized at T0-20/T0-7 whereas secondary metabolism is rather activated at T0. All these results suggest a mobilization of the stress responsive secondary metabolism and are in accordance with the previously reported activation of the expression of defense genes before apoplexy and their implication during disease progression in leaves (Letousey et al. 2010) and in wood (Magnin-Robert et al. 2014).

As pathogen propagules and by-products are able to diffuse from the infected woody tissue of the trunk and branches to the crown of the affected vines, some of their metabolites were shown to occur in the xylem sap of naturally infected grapevines (Bruno et al. 2007). As we are not able to distinguish plant metabolites from microbe ones, we can therefore not exclude that microbe metabolites contribute directly to the metabolic signature of the discriminated sample groups. Moreover, esca associated fungi may also contribute to the evolution of some compounds. As example, previous studies conducted with trees have indeed reported the adaptation capability of fungi to metabolize terpenoids and stilbenes and use them as carbon sources for wood colonization (Diguistini et al. 2011; Hammerbacher et al. 2013). This could be also a hypothesis in esca-affected grapevine since phytoalexins were not significantly increased in apoplectic leaves as described below.

VK and chemical composition diagrams indicated that sulfur containing compounds contributed to the metabolite fingerprint of the sample groups. Sulfur containing compounds are known to play an important role in plant response to stress (Capaldi et al. 2015). More specifically, glutathione is probably involved in esca symptom expression (Letousey et al. 2010; Valtaud et al. 2009). In our study, assessment of the evolution of putative glutathione showed a lower accumulation in diseased samples than in control ones, correlated with a higher expression of GST encoding genes. Valtaud et al. (2009) also reported a lower glutathione content in leaves expressing the chronic form of the disease. However, conversely to what they reported, no mass corresponding to the reduced form of glutathione could be found in our conditions. This might be explained by the difference in the disease expression (apoplectic / chronic). A network analysis allowed the identification of transformations involving glutathione as substrate or products. As glutathione is known to play a role in detoxification process, the occurrence of putative glutathione conjugates to toxins previously identified in esca disease was investigated using their *m/z* values and predicted raw formulas. However, no calculated mass corresponding to putative glutathione-conjugated toxins commonly associated to trunk diseases could be found.

In situ hybridization was performed to localize *GST1* gene. A preferential phloem-specific expression of this gene was observed. In this sense, Fukuda et al. (2004) have reported the activity of a phloem-specific glutathione-S-transferase in rice leaves. To our knowledge, an immune FITC–labelling targeted two various GST protein, GSTF and GSTU, have already localized these proteins in veins and particularly in phloem (Valtaud et al. 2009). Moreover, the tau GSTU protein, encoded by the *GST1* gene, was mainly found in the plastids (Valtaud *et al.*, 2009), which suggest an important role in detoxification processes to avoid oxidative damage in chloroplasts (Kuzniak and Sklodowska 2001). GST proteins were proposed to detoxify reactive molecules, such as membrane lipid peroxides, by conjugation to GSH

(Marrs 1996) and some GSTs also function as glutathione peroxidases to detoxify reactive oxygen species directly (Bartling et al. 1993). Sieve elements, which have lost most of their organelles, could therefore defend themselves against oxidative stresses by inducing GST activity. Indeed, the expression of GST in the phloem sap of pre-apoplectic vines could permit the protection of sieve tubes from oxidative damage, especially as this type of stress is frequently described in response to esca (Bertsch et al. 2013). Moreover GSTs modify toxic compounds into less toxic and more water soluble conjugates (Marrs 1996). Therefore, as discussed by Fukuda et al. (2004) in the case of rice, the presence of GST activity in grapevine phloem sap of pre-apoplectic individuals suggests the possibility of GSH-conjugation of endogenous compounds in sieve tubes. One of the possible functions of GST in the vascular cells could be in changing hydrophobic compounds into hydrophilic ones conjugated with GSH, making these modified compounds more mobile in the sieve tubes and easily distributed along the plant tissues. Otherwise, some plant GSTs showed flavonoid-, auxin-, and cytokinin- binding activities, suggesting that these proteins could act as ligands and support the intracellular transport of flavonoids and plant hormones (Bilang and Sturm 1995; Gonneau et al. 1998; Mueller et al. 2000). In this context, and since phloem represents a way for signaling and defense (van Bel et al. 2013), one could imagine that this contribute to deliver throughout the plant (since the phloem circulates up and down manner) a long-distance alert message of a physiological disorder. Valtaud et al. (2009) observed an enhanced expression of both GST genes (phi *GSTF* and tau *GSTU1*) in plants attacked by esca. The expression of these genes was greatest in leaves that were visually healthy, suggesting that the GSTs are the first enzymes induced in the response to esca.

In this study, we show that transcriptomic and non-targeted metabolomic analyses proved to be very effective in discriminating the profiles of apoplectic and healthy leaves of diseased plants, thus demonstrating the great potential of these tools in the understanding of the complex grapevine trunk diseases. Among the changes reported, most of them concern the metabolism of carbohydrates, amino acids, phenylpropanoids, and plant defense responses. Gene expression such as *SucS2*, *Aux10A5*, *MYB4A*, *EpoxHF*, *Hahl* could be identified as markers of the pre-apoplectic event in cv. Chardonnay. Our results support also the hypothesis that glutathione could be an early actor during apoplexy appearance because its amount is lower in apoplectic leaf compared to the control and that *GST1* gene expression is preferentially noted in phloem, suggesting a long-distance transport of glutathione which reinforces the toxin hypothesis of symptom development. In turn, such markers need to be validated in other cultivars, more or less susceptible to trunk diseases, and also in other climatic conditions since abiotic stresses could affect the plant response.

MATERIALS AND METHODS

Plant material

Experiments were performed on Chardonnay grapevines (*Vitis vinifera* L.) planted in 1986, grafted on 41B rootstock, and trained according to the Chablis method. The experimental site was located in the Moët and Chandon vineyard in Avize (Champagne region, France). The site is characterized by an average annual temperature of 10.8°C, reaching an average of 19°C during apoplexy expression, and 480.7 mm annual precipitation. From 2005 to 2007, two groups of vines were defined in the plot: (1) vines which did not show any esca symptoms; visually healthy and considered as unaffected controls; (2) vines which developed acute chronic or apoplexy symptoms; considered as diseased. In the wood of all plants, the major causal agents of esca disease were previously isolated (Magnin-Robert et al. 2014).

To investigate vines before and during acute esca expression, plants with a high potential to develop the apoplectic form were selected, i.e. plants of group 2 (see above) which have expressed symptoms during the previous summer. Since the first apoplectic form symptoms appear in July in the Champagne region, all measurements and sample harvests were performed twice a week from mid-June to the end of July in both 2008 and 2009. Numerous plants were therefore followed in June but only those expressing apoplexy in July were used for the study. At the appearance of foliar symptoms, a retrospective chronology of the disease could be established, as described in Letousey et al. (2010). The analyzed leaf samples were thus harvested (i) twenty days before apoplexy appearance (T0-20), leaves were visually healthy, as control ones; (ii) seven days before (T0-7), leaves were either without symptoms (vh for visually healthy) or turgorless (tg), and (iii) at the day of apoplexy symptom expression starting (T0), leaves were visually healthy, neither turgorless nor drying. Turgorless leaves at T0-7 were dried at T0 and not sampled. In the meantime, leaves were collected from asymptomatic (control) plants, *i.e.* vines from group 1 (see above).

Harvested leaves were immediately frozen in liquid nitrogen in vineyard, then stored at -80°C until extraction. Samples were ground in liquid nitrogen to a fine powder and prepared differently according to the analysis performed.

Next Generation sequencing: 454- and Illumina sequencings

In this study 454- and Illumina sequencing techniques were combined, (i) 454-sequencing was used to constitute a Unigene set from the pool of extracted RNA from various conditions and (ii) illumina sequencing is used to create a RNA sequences data for each treatments, the Illumina sequences were secondly mapping onto the Unigene set previously generating and on genome databases. In the case of 454 sequencing, RNA extraction and cDNA synthesis and size fractionation were realized by Express Genomics Inc (Frederick, Maryland, USA). Total RNA was extracted using the Concert^{TM} Plant RNA Reagent (Thermo Fischer Scientific –previously Invitrogen, Carlsbad, California, USA) according to the manufacturer's protocol. To generate the cDNA, nucleic molecules were digested with *Not I* and *in vitro* RNA transcripts were produced using the SP6 RNA polymerase promoter according to Express Genomics Inc adapted protocol. First strand cDNA was made from these transcripts using a modified primer adapter that reduces the size of the polyA sequence (to about 20 As). After the second strand synthesized, the double strand cDNA is blunt ended and size fractionated. The 454 library was made by Beckman Coulters Genomics (Danvers, Maryland, USA) and created by ligating the Roche titanium adaptators on the Beckman Coulter SPRI-TE instrument. Sequencing was performed on the Genome Sequencer FLX with GS FLX Titanium series reagents using 35,000,000 beads. In the case of Illumina sequencing, also realized by Beckman Coulters Genomics, cDNA was generated from polyA^{+}-purified total RNA (Illumina mRNA Sequencing Sample Preparation Guide, part #1004898 rev. D.; Illumina, Inc., San Diego, California, USA), followed by adaptator ligation on the Beckman Coulter SPRI-TE Instrument. Sequencing was performed on the Illumina HiSeq2000 instrument at 1X50bp read length using v3 chemistry.

Read mapping, assembly, and differential-expression analysis. The mapping assembly was performed with Mira version 3 (http://chevreux.org/projects_mira .html) with the 454 sequences and the consensus sequences compiled by the university of Harvard (VvGi, from 350,000 available EST, http://compbio.dfci.harvard.edu/cgi-bin/tgi/gimain.pl?gudb=grape). In addition, the Illumina mapping was done with Eland program (CASAVA v1.7.0). For amelioration of transcripts annotation BLASTx on the

KOG of NCBI base (http://www.ncbi.nlm.nih.gov/COG/) was used. The mapping of Illumina sequences on the genome was done with the software TopHat (http://tophat.cbcb.umd.emd/). Analyses of mapping were performed with software Cufflinks, Cuffcompare and Cuffdiff (http://cufflinks.cbcb.umd.edu/) with reference the data gtf and fasta form EnsemblePlants. The Cuffdiff analyses were made chronologically and separately between the control and the diseased plant for detecting genes whose expression varies during the follow kinetics. Gene expression was considered as significantly up- or down-regulated to the control, when changes in relative expression were >2× or <0.5× and were colored in grey color.

Quantitative RT-PCR analysis

The analysis was performed on leaves of diseased and control plants collected at T0-20, T0-7 and T0, as for other analyses. Comparing to the Illumina study, some of samples used were the same and others obtained from diseased plants (n=3) cultivated in the same vineyard during the same year were used. Moreover, leaves were also collected at T0-50 and T0-30 in order to extend the kinetic study. Total RNA was isolated using a Plant RNA Purification Reagent (Invitrogen^{TM}, Cergy Pontoise, France) according to Magnin-Robert et al. (2011). In total 150 ng of total RNA was reverse-transcribed using Verso cDNA Synthesis Kit (Thermo Fischer Scientific, Surrey, UK) according to the manufacturer's protocol. PCR conditions were those described by Bézier et al. (2002). The expression of 18 genes selected from transcriptomic analysis was tracked by quantitative RT-PCR using the primers newly designed (Supplementary Table 1). The data were analyzed using CFX Manager software, and the relative levels of gene expression were determined following the method of Hellemans et al. (2007) with EF1-α and 60SRP as internal reference genes. Results represent the relative expression of genes in leaves of pre-apoplectic plants at T0-

50, T0-30, T0-20, T0-7 and T0 versus those corresponding to control (C) ones. The analyzed genes were considered significantly up-or down-regulated when change of their expression was >2X or <0.5X respectively.

FT-ICR-MS analysis

Fifteen milligrams of each leaf sample were suspended in 1 mL methanol (LC-MS grade, Fluka Analytical, Sigma-Aldrich, St. Louis, USA) and sonicated for 30 min. After centrifugation (25 000g, 10 min, room temperature), the supernatant was collected and diluted in methanol (1/50 v/v) prior to analysis. Ultra high-resolution mass spectra were acquired using an Ion Cyclotron Resonance Fourier Transform Mass Spectrometer (FT-ICR-MS) (solariX, BrukerDaltonics GmbH, Bremen, Germany) equipped with a 12 Tesla superconducting magnet (Magnex Scientific Inc., Yarnton, GB) and an APOLO II ESI source (Bruker Daltonics GmbH, Bremen, Germany) operated in the negative ionization mode. Samples were introduced into the micro electrospray source at a flow rate of 120 $\mu L.h^{-1}$. Spectra were acquired with a time domain of 4 mega words over a mass range of m/z 100 to 1000 and 300 scans were accumulated per sample. Spectra were externally calibrated on clusters of arginine (10 $mg.L^{-1}$ in methanol). Further internal calibration was performed for each sample by using a list of ubiquitous fatty acids and recurrent wine compounds, allowing mass accuracies of 0.1 ppm (Gougeon et al. 2009). The *m/z* peaks with a signal-to-noise ratio (S/N) of 4 and higher were exported to peak lists. Exact masses were then subjected to Netcalc algorithm and in-house software tool to obtain chemical formulas (Tziotis *et al.*, 2011). Elemental formulas attributed to *m/z* values were next represented using two-dimensional van Krevelen (VK) diagrams, which sort them onto two axes according H/C and O/C atomic ratios (Tziotis et al. 2011). Their distribution according to their elemental compositions (CHO, CHOS, CHON, CHONS, CHOP, CHONP CHONSP) was represented using histograms. All the processes were done with SIMCA-P+12 (Umetrics, Umea, Sweden). The metabolic pathways associated to selected masses were obtained by KEGG query with *Vitis vinifera* (vvi) as organism using the web server MassTRIX. Network analysis performed from the complete data set and the sulfur containing compounds, was performed as previously described (Adrian et al. 2017). Nodes represent *m/z* values (metabolite candidates) and edges represent chemical reactions. The statistical occurrence of each reaction (mass differences) was tracked through the network and the frequencies of these reactions associated to each group are indicated in terms of z-scores. Z-scores > 1.9 correspond to p-values < 0.05 and z-scores > 2.6 correspond to p-values < 0.01.

OPLS-DA (Orthogonal Projections to Latent Structures-Discriminant Analysis) was applied to the dataset in order to discriminate sample groups. The overfitting was checked by the p-value calculated with the CV-ANOVA (Cross Validation ANOVA). From the classification models, the m/z values with the highest regression coefficient were extrapolated in different lists as representative masses for the different clusters (called "top *m/z*"). These analyses were performed with SIMCA-P+13.0.3 (Umetrics, Umea, Sweden).

In situ *hybridization* analysis

In situ hybridization was carried out on leaf samples collected on control plants and on pre-apoplectic (tg and vh) ones at T0-7. Samples were fixed into a fresh mixture of 4% paraformaldehyde in potassium phosphate buffer (PBS 10mM, pH 7.4) and then embedded in paraffin (Colas et al., 2010). Wax sections at 10 µm thickness were obtained using a microtome and deposited on silanized slides. Primers were designed for PCR amplification of specific regions of *GST1* cDNAs (Table 1) and 26 S ribosomic RNA sequence (Rib) was used as controls. Sense and antisense probes were labeled according to Colas et al.

(2010). To increase signals of the GST probe, the Dig oligonucleotide Tailing kit (Roche) was used to add poly-Dig UTP tail at the 3' end of the amplified RNA sequence (Garcia et al. 2013). Hybridization was performed as previously described by Colas *et al.* (2010).

AKNOWLEDGEMENTS

This work was funded by the interprofessional comity of vine in France (CNIV), and especially supported by those of Champagne (CIVC) and Burgundy areas (BIVB). The company Moët & Chandon is thanked for making available the vineyard used as the experimental plot in this study.

LITERATURE CITED

Adrian, M., Lucio, M., Roullier-Gall, C., Héloir, M.C., Trouvelot, S., Daire, X., Kanawati, B., Lemaître-Guillier, C., Poinssot, B., Gougeon, R., and Schmitt-Kopplin P. 2017. Metabolic fingerprint of PS3-induced resistance of grapevine leaves against *Plasmopara viticola* revealed differences with elicitor-triggered defenses. *Front Plant Sci* 8: 101.

Algarra Alarcon, A., Lazazzara, V., Cappellin, L., Bianchedi, P.L., Schuhmacher, R., Wohlfahrt, G., Pertot, I., Biasioli, F., and Perazzolli, M. 2015. Emission of volatile sesquiterpenes and monoterpenes in grapevine genotypes following *Plasmopara viticola* inoculation in vitro. *J Mass Spectrom* 50: 1013-1022.

Andolfi, A., Mugnai, L., Luque, J., Surico, G., Cimmino, A., and Evidente, A. 2011. Phytotoxins produced by fungi associated with grapevine trunk diseases. Toxins 3: 1569−1605.

Bartling, D., Radzio, R., Steiner, U., and Weiler, E.W. 1993. A glutathione S-transferase with glutathione peroxidase activity from *Arabidopsis thaliana*: molecular cloning and functional characterization. *Eur J Biochem* 216: 579–586.

Bertsch, C., Ramirez-Suero, M., Magnin-Robert, M., Larignon, P., Chong, J., Abou-Mansour, E., Spagnolo, A., Clément, C., and Fontaine, F. 2013. Grapevine trunk diseases: complex and still poorly understood. *Plant Pathol* 62: 243−265.

Bézier, A., Lambert, B., and Baillieul, F. 2002. Study of defence-related gene expression in grapevine leaves and berries infected with *Botrytis cinerea*. *Eur J Plant Pathol* 108: 111-120.

Bilang, J. and Sturm, A. 1995. Cloning and characterization of a glutathione S-transferase that can be photolabeled with 5-azido-indole-3-acetic acid. *Plant Physiol* 109: 253–260.

Bruez, E., Lecomte, P., Grosman, J., Doublet, B., Bertsch, C., Fontaine, F., Ugaglia, A., Teissedre, P. L., Da Costa, J. P., Guerin-Dubrana, L., and Rey, P. 2013. Overview of grapevine trunk diseases in France in the 2000s. *Phytopat Med* 52: 262−275.

Bruno, G., Sparapano, L., and Graniti, A. 2007. Effects of three esca-associated fungi on *Vitis vinifera* L.: IV. Diffusion through the xylem of metabolites produced by two traceiphilous fungi in the woody tissue of grapevine leads to esca-like symptoms on leaves and berries. *Physiol Mol Plant Pathol* 71: 106-124.

Calzarano, F., Di Marco, S., D'Agostino, V., Schiff, S., and Mugnai, L. 2014. Grapevine leaf stripe disease symptoms (esca complex) are reduced by a nutrients and seaweed mixture. *Phytopat Med* 53: 543–558.

Camps, C., Kappel, C., Lecomte, P., Léon, C., Gomès, E., Coutos-Thévenot, P., and Delrot, S. 2010. A transcriptomic study of grapevine (*Vitis vinifera* cv. Cabernet-Sauvignon) interaction with the vascular ascomycete fungus *Eutypa lata*. *J Exp Bot* 61: 1719−1737.

Capaldi, F.R., Lupino Gratão, P., Reis, A., Lima, L. W., and Azevedo, R. A. 2015. Sulfur metabolism and stress defense responses in plants. *Trop Plant Biol* 8: 60-73.

Chalal, M., Barbro Winkler, J., Gourrat, K., Trouvelot, S., Adrian, M., Schnitzler, J. P., Jamois, F., and Daire, X. 2015. Sesquiterpene volatile organic compounds (VOCs) are markers of elicitation by sulfated laminarine in grapevine. *Front Plant Science* 6: 1-9.

Colas, S., Jacquens, L., Manteau, S., Devy, J., Conéjéro, G., Clément, C., Baillieul, F., Mazerat-Gourbeyre, F., and Monti-Dedieu, L. 2010. Expression analysis in grapevine by *in situ* hybridization and immunochemistry. In: Delrot S, Medrano H, Or E, Bavaresco, L., Grando, S., editors. Methodologies and Results in Grapevine Research. 361-374.

De la Fuente, M., Fontaine, F., Gramaje, D., Armengol, J., Smart, R., Nagy, Z. A., Borgo, M., Rego, C., and Corio-Costet, M. F. 2016. Grapevine trunk diseases, a review. OIV publications, 1rst Edition, Paris, France. ISBN: 979-10-91799-60-7.

DiGuistini, S., Wang, Y., Liao, N. Y., Taylor, G., Tanguay, P., Feau, N., Henrissat, B., Chan, S. K., Hesse-Orce, U., Alamouti, S. M., Tsui, C. K., Docking, R; T., Levasseur, A., Haridas, S., Robertson, G., Birol, I., Holt, R. A., Marra, M. A., Hamelin, R. C., Hirst, M., Jones, S. J., Bohlmann, J., and Breuil, C. 2011. Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont *Grosmannia clavigera*, a lodgepole pine pathogen. *Proc Natl Acad Sci USA*:10.1073/pnas.1011289108.

Fontaine, F., Pinto, C., Vallet, J., Clément, C., Gomes, A., and Spagnolo, A. 2015. The effects of Grapevine Trunk Diseases (GTDs) on vine physiology. *Eur J Plant Pathol* 104: 707-721.

Fukuda, A., Okada, Y., Suzui, N., Fujiwara, T., Yoneyama, T., and Hayashi, H. 2004. Cloning and characterization of the gene for a phloem-specific glutathione *S*-transferase from rice leaves. *Physiol Plantarum* 120: 595–602.

Garcia, K., Haider, M. Z., Delteil, A., Corratgé-Faillie, C., Conéjero, G., Tatry, M. V., Becquer, A., Amenc, L., Sentenac, H., Plassard, C., and Zimmermann, S. 2013. Promoter-dependent expression of fungal transporter *HcPT1.1* under Pi shortage and its spatial localization in ectomycorrhiza. *Fungal Genet Biol* 58-59: 53-61.

Gonneau, M., Mornet, R., and Laloue, M. 1998. A *Nicotiana plumbaginifolia* protein labeled with an azido cytokinin agonist is a glutathione S-transferase. *Physiol Plantarum* 103: 114–124.

Gougeon, R. D., Lucio, M., Frommberger, M., Peyron, D., Chassagne, D., Alexandre, H., Feuillat, F., Voilley, A., Cayot, P., Gebefügi, I., Hertkorn, N., and Schmitt-Kopplin, P. 2015. The chemodiversity of wines can reveal a metabologeography expression of cooperage oak wood. Proceedings of the National Academy of Sciences of the United States of America 106: 9174-9179.

Gruau, C., Trotel-Aziz, P., Villaume, S., Rabenoelina, F., Clément, C., Baillieul, F., and Aziz, A. 2015. *Pseudomonas fluorescens* PTA-CT2 triggers local and systemic immune response against *Botrytis cinerea* in grapevine. *Mol Plant-Microbe In* 10: 1117-1129.

Hammerbacher, A., Schmidt, A., Wadke, N., Wright, L. P., Schneider, B., Bohlmann, J., Brand, W. A., Fenning, T. M., Gershenzon, J., and Paetz, C. 2013. A common fungal associate of the spruce bark beetle metabolizes the stilbene defenses of Norway spruce. *Plant Physiol* doi:10.1104/pp.113.218610.

Hofstetter, V., Buyck, B., Croll, D., Viret, O., Couloux, A., and Gindro, K. 2012. What if esca disease of grapevine were not a fungal disease? *Fungal Diversity* 54: 51−67.

Jansen, R. M. C., Wildt, J., Kappers, I.F., Bouwmeester, H.J., Hofstee, J. W., and van Henten, E. J. 2011. Detection of diseased plants by analysis of volatile organic compound emission. *Annu Rev Phytopathol* 49: 157-17.

Koussa, T., Cherrad, M., Zaoui, D., and Broquedis M. 1998. Composition et tenru en acides gras des feuilles de *Vitis vinifera* L. var Cabernet Sauvignon atteintes d'eutypiose. *J Int Sci Vigne Vin* 32 (1) 11-16.

Kuzniak, E., and Sklodowska, M., 2001. Ascorbate, glutathione and related enzymes in chloroplasts of tomato leaves infected by *Botrytis cinerea*. *Plant Sci* 160 (4): 723-731.

Lambert, C., Kim Khiook, I. L., Lucas, S., Télef-Micoleau, N., Mérillon, J. M., and Cluzet, S. 2013. A faster and stronger defense response: one of the key elements in grapevine explaining its lower susceptibility to esca? *Phytopathol* 103: 1028−1034.

Larignon, P., Fulchic, R., Cere, L., and Dubos, B. 2001. Observation on black dead arm in French vineyards. *Phytopathol Med* 40S: 336–342.

Letousey, P., Baillieul, F., Perrot, G., Rabenoelina, C., Boulay, M., Vaillant-Gaveau, N., Clément, C., and Fontaine, F. 2010. Early events prior to visual symptoms in apopletic form of esca disease. *Phytopathol* 100: 424–431.

Lima, M. R. M., Felgueiras, M., Graca, G., Rodrigues, J. E. A., Barros, A. S., Gil, A. M., and Dias, ACP. 2010. NMR metabolomics of esca-disease-affected *Vitis vinifera* cv. Alvarinho leaves. *J Exp Bot* 61: 4033-4042.

Magnin-Robert M, Letousey P, Spagnolo A, Rabenoelina F, Jacquens L, Mercier L, Clément C, Fontaine F. 2011. Leaf strip of esca induces alteration of photosynthesis and defence reactions in presymptomatic leaves. *Funct Plant Biol* 38, 856−866.

Magnin-Robert, M., Spagnolo, A., Alayi, T. D., Cilindre, C., Mercier, L., Schaeffer-Reiss, C., Van Dorsselaer, A., Clément, C., and Fontaine, F. 2014. Proteomic insights into changes in wood of *Vitis vinifera* L. in response to esca proper and apoplexy. *Phytopathol Med* 53 (1) : 168-187.

Magnin-Robert, M., Spagnolo, A., Boulanger, A., Joyeux, C., Clément, C., Abou-Mansour, E., and Fontaine, F. 2016. Changes in plant metabolism and accumulation of fungal metabolites in response to esca proper and apoplexy expression in the whole grapevine. *Phytopathol* 106: 541-553.

Marrs, K.A. 1996. The functions and regulation of glutathione S-transferases in plants. *Annu Rev Plant Physiol Plant Mol Biol* 47: 127–158.

Moritz, F., Kaling, M., Schnitzler, J.P., and Schmitt-Kopplin, P. 2017. Characterization of poplar metabotypes via mass difference enrichment analysis. *Plant, Cell Env*, Online first

Mouradov, A., and Spangenberg, G. 2014. Flavonoids: a metabolic network mediating plants adaptation to their real estate. *Front Plant Sci* 5: 620 doi: 10.3389/fpls.2014.00620

Mueller, L. A., Goodman, C. D., Silady, R. A., and Walbot, V. 2000. AN9, a petunia glutathione S-transferase required for anthocyanin sequestration, is a flavonoid-binding protein. *Plant Physiol* 23: 1561–1570.

Mugnai, L., Graniti, A., and Surico, G. 1999. Esca (Black measles) and brown wood-streaking: Two old and elusive diseases of grapevines. *Plant Dis* 83 : 404−418.

Petit, A.-N., Vaillant, N., Boulay, M., Clément, C., and Fontaine, F. 2006. Alteration of photosynthesis in grapevines affected by esca. Phytopathology 96 (10) : 1060-1066.

Rifai, L. A., Koussa, T., Geny, L., Fassouane, A., Broquedis, M., and Dubos, B. 2005. Evolution des teneurs en polyamines libres et conjuguées dans les feuilles de vigne (*Vitis vinifera* ‘Cabernet Sauvignon’) saine et atteinte d’eutypiose. *Can J Bot* 83: 194–201.

Romanazzi, G., Murolo, S., Pizzichini, L., and Nardi S. 2009. Esca in young and mature vineyards, and molecular diagnosis of the associated fungi. *Eur J Plant Pathol* 25: 277-209.

Romero-Perez, A. I., Lamuela-Raventos, R. M., Andres-Lacueva, C., and De la Torre-Boronat, C. 2001. Method for quantitative extraction of resveratrol and piceid isomers in grape berry skins. Effect of powdery mildew on the stilbene content. *J Agri Food Chem* 49: 210-215.

Spagnolo, A., Magnin-Robert, M., Alayi, T. D., Cilindre, C., Mercier, L., Schaeffer-Reiss, C., Van Dorsselaer, A., Clément, C., and Fontaine, F. 2012. Physiological changes in green stems of *Vitis vinifera* L. cv. Chardonnay in response to Esca proper and apoplexy revealed by proteomic and transcriptomic analyses. *J Proteome Res* 11: 461−475.

Surico, G., Mugnai, L., and Marchi, G. 2006. Older and more recent observations on esca: a critical overview. *Phytopathol Med* 45: S68−S86.

Tziotis, D., Hertkorn, N., and Schmitt-Kopplin, P. 2011. Kendrick-analogous network visualisation of ion cyclotron resonance Fourier transform mass spectra: Improved options for the assignment of elemental compositions and the classification of organic molecular complexity. *Eur J Mass Spectrom* 17: 415–421.

Van Bel, A. J. E., Helariutta, Y., Thompson, G. A., Ton, J., Dinant, S., Ding, B., and Patrick J. W. 2013. Phloem: the integrative avenue for resource distribution, signaling, and defense. *Front Plant Sci* 4: 471. doi:10.3389/fpls.2013.00471

Valtaud, C., Foyer, C. H., Fleurat-Lessard, P., and Bourbouloux, A. 2009. Systemic effects on leaf glutathione metabolism and defence protein expression caused by esca infection in grapevines. *Funct Plant Biol* 36: 260−279.

Table 1. Primers used to generated template DNA for synthesize of RNA probes

Gene	Accession no.	Primer sequences	Product (bp)
Glutathione-S transferase (GST1)	**AY156048**	5’- TTCGAAACTTTTGGGAAGTTCAAC-3’ 5’- TCAAACAACCGCAATAATATCCCT-3’	**243**
26S rRNA	**AY847628.1**	5’- CCGACCTCGATCTTATGAGAAGGG-3’ 5’- CCAAGTCAGACGAACGATTTGCACG-3’	**150**

Table 2. Functional classification of the genes differentially expressed between control and diseased plants and whose expression is altered precociously and during apoplectic expression (at T0-20 and/or T0-7vh or tg and/or T0) and implicated in carbohydrate, amino acids, lipids and phenylpropanoid metabolism, stress and defense pathways. Values indicating over- or down-expressed (ratio |2|) are highlighted in light or dark gray, respectively.

Fold Change				**Functional annotation**	**ID**	**Accession**
T0-20	**T0-7vh**	**T0-7tg**	**T0**		**genoscope**	**Number (NCBI)**
Carbohydrate metabolism						
5.1	**13.5**	**0.8**	**4.7**	PREDICTED: succinate dehydrogenase [ubiquinone] flavoprotein subunit 1	GSVIVT01018976001	XM_002269371
2.1	**11.4**	**2.6**	**4.6**	PREDICTED: lysosomal beta glucosidase-like		XM_002278327
4.2	**0.4**	**0.0**	**0.3**	PREDICTED: uncharacterized LOC100243957		XM_002279899
0.5	**4.2**	**29.0**	**46.6**	PREDICTED: zeta-carotene desaturase, chloroplastic/chromoplastic-like	GSVIVT01021843001	XM_002277312
0.5	**12.5**	**123.4**	**87.6**	PREDICTED: UTP-glucose-1-phosphate uridylyltransferase-like	GSVIVT00034877001	XM_002282240
0.4	**2.0**	**10.8**	**7.2**	PREDICTED: protein THYLAKOID FORMATION1, chloroplastic-like	GSVIVT00029202001	XM_002275650
0.3	**4.1**	**0.1**	1.2	PREDICTED: serine/threonine-protein kinase STN7, chloroplastic-like	GSVIVT00030286001	XM_003631179
0.2	1.5	**0.0**	**0.0**	PREDICTED: sucrose synthase 2-like	GSVIVT00033041001	XM_002271494
1.7	**6.4**	**2.0**	**34.7**	PREDICTED: alcohol dehydrogenase-like 6	GSVIVT01024246001	XM_002263489
0.7	**3.6**	**8.6**	**12.9**	PREDICTED: UDP-glycosyltransferase 74E2-like		XM_002275297
0.7	**3.4**	**3.4**	**12.0**	PREDICTED: starch synthase V precursor		EU661370
0.5	**3.3**	**12.1**	**39.8**	PREDICTED: alpha-glucan phosphorylase, H isozyme-like	GSVIVT01024804001	XM_002280696
0.7	**2.9**	**8.6**	**22.5**	PREDICTED: probable ribose-5-phosphate isomerase-like		XM_002284043
0.9	0.7	**27.4**	**63.4**	PREDICTED: Vitis vinifera glucan endo-1,3-beta-glucosidase 1	GSVIVT00019655001	XM_002279561
0.7	1.7	**4.8**	**3.9**	PREDICTED: Vitis vinifera probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha	GSVIVT00019014001	XM_002269078
0.6	1.9	**4.3**	**4.1**	PREDICTED: Vitis vinifera ribulose bisphosphate carboxylase small chain, chloroplas	GSVIVT00017680001	XM_002276931
1.2	0.9	**2.5**	**0.5**	PREDICTED: Vitis vinifera BTB/POZ domain-containing protein	GSVIVT00029147001	XM_002270766
0.9	1.6	**0.4**	**6.2**	PREDICTED: Vitis vinifera probable ribose-5-phosphate isomerase 3, chloroplastic	GSVIVT00031147001	XM_002278261
1.3	0.8	**0.4**	**0.3**	PREDICTED: Vitis vinifera mavicyanin-like	GSVIVT00011941001	XM_010664298
0.7	0.8	**0.4**	**0.2**	PREDICTED: Vitis vinifera probable beta-D-xylosidase 7	GSVIVT00019689001	XM_002285769
1.1	0.7	**0.3**	**0.4**	PREDICTED: Vitis vinifera germin-like protein subfamily T member 2		XM_002267471
0.8	0.7	**0.3**	**0.2**	PREDICTED: Vitis vinifera mavicyanin	GSVIVT00019955001	XM_002281638
0.5	1.4	**0.3**	**0.2**	PREDICTED: Vitis vinifera putative callose synthase 8	GSVIVT00009059001	XM_010646472
0.8	0.7	**0.3**	**0.1**	PREDICTED: Vitis vinifera glucan endo-1,3-beta-glucosidase 2-like	GSVIVT00032980001	XM_002265360
1.3	0.7	**0.2**	**0.1**	PREDICTED: Vitis vinifera glutamyl-tRNA reductase 1, chloroplastic-like	GSVIVT00015045001	
1.4	0.5	**0.1**	**0.1**	PREDICTED: Vitis vinifera protein DCL, chloroplastic-like	GSVIVT00019490001	XM_002282442
0.9	0.7	**0.1**	**0.2**	PREDICTED: Vitis vinifera mannose-1-phosphate guanyltransferase alpha-like	GSVIVT00020858001	XM_002281923
1.3	0.7	**0.1**	**0.2**	PREDICTED: Vitis vinifera probable gluconokinase	GSVIVT00014074001	XM_002275978
1.5	0.6	**0.1**	**0.1**	PREDICTED: Vitis vinifera putative amidase C869.01	GSVIVT00036077001	XM_003631524
1.0	0.5	**0.1**	**0.0**	PREDICTED: Vitis vinifera galactose oxidase	GSVIVT00016700001	XM_010657990
0.9	0.6	**0.1**	**0.0**	PREDICTED: Vitis vinifera cryptochrome-1	GSVIVT00011744001	XM_002285133
1.2	0.6	**0.0**	**0.1**	PREDICTED: Vitis vinifera galactose oxidase	GSVIVT00021405001	XM_002274727
0.7	1.1	**3.1**	1.8	PREDICTED: Vitis vinifera phosphoenolpyruvate carboxylase kinase 1	GSVIVT00002205001	XM_002265916
0.8	1.4	**2.8**	0.8	PREDICTED: Vitis vinifera plastocyanin	GSVIVT00015518001	XM_002285868
0.9	1.1	**2.7**	0.7	PREDICTED: Vitis vinifera uncharacterized (LOC100247488)	GSVIVT00036876001	XM_002270359
1.7	0.8	**2.6**	1.2	PREDICTED: Vitis vinifera protein SENSITIVITY TO RED LIGHT REDUCED 1	GSVIVT00017343001	XM_010653294
0.8	1.0	**2.6**	0.6	PREDICTED: Vitis vinifera pyridine nucleotide-disulfide oxidoreductase domain-cont	GSVIVT00024927001	XM_010650846
0.7	1.2	**2.3**	1.3	PREDICTED: Vitis vinifera carbonic anhydrase 2-like	GSVIVT00016078001	XM_002282645
1.6	1.8	**0.1**	0.8	PREDICTED: Vitis vinifera uncharacterized (LOC100268021)	GSVIVT00016580001	XM_002282345
0.6	7.2	**0.0**	0.6	PREDICTED: Vitis vinifera zinc finger protein CONSTANS-LIKE 5	GSVIVT00031464001	XM_002277917
1.1	1.2	0.5	**6.7**	PREDICTED: Vitis vinifera GDSL esterase/lipase	GSVIVT00026974001	XM_002276489
0.8	1.9	1.1	**6.3**	PREDICTED: Vitis vinifera pentatricopeptide repeat-containing protein	GSVIVT00032631001	XM_003632946
1.0	1.6	1.8	**3.0**	PREDICTED: Vitis vinifera alkaline/neutral invertase CINV1-like	GSVIVT00034936001	XM_010660432
0.6	1.0	1.2	**3.0**	PREDICTED: Vitis vinifera dolichyldiphosphatase 1-like	GSVIVT00024892001	XM_002263866
1.1	1.0	0.8	**2.8**	PREDICTED: Vitis vinifera beta-xylosidase/alpha-L-arabinofuranosidase 2-like	GSVIVT00027149001	XM_002264147
0.7	1.8	0.8	**2.8**	PREDICTED: Vitis vinifera UDP-arabinopyranose mutase 1	GSVIVT00000015001	XM_002263454
0.7	1.3	0.7	**2.1**	PREDICTED: Vitis vinifera phosphoglycerate kinase, cytosolic-like	GSVIVT00035677001	XM_002263914
1.6	0.9	0.9	**0.4**	PREDICTED: Vitis vinifera activating signal cointegrator 1complex subunit 3	GSVIVT00016213001	XM_010664950
1.3	0.8	0.8	**0.4**	PREDICTED: Vitis vinifera adenosine kinase	GSVIVT00013977001	XM_002271617
1.0	1.0	0.7	**0.4**	Vitis vinifera GDP-mannose-3',5'-epimerase	GSVIVT00034578001	NM_001281039
1.2	1.0	0.7	**0.3**	PREDICTED: Vitis vinifera beta-fructofuranosidase, insoluble isoenzyme CWINV1	GSVIVT00032196001	XM_002278844
0.8	0.8	1.3	**0.3**	PREDICTED: Vitis vinifera alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosam	GSVIVT00003980001	XM_010648923
0.8	0.7	0.9	**0.3**	PREDICTED: Vitis vinifera plastid division protein PDV2-like	GSVIVT00036442001	XR_785443
0.5	1.1	1.9	**0.3**	PREDICTED: Vitis vinifera NADPH--cytochrome P450 reductase	GSVIVT00031360001	XM_002270696
1.0	0.8	1.3	**0.2**	PREDICTED: Vitis vinifera pyruvate kinase	GSVIVT00033621001	XM_002266124
0.8	1.2	0.5	**0.2**	PREDICTED: Vitis vinifera violaxanthin de-epoxidase, chloroplastic	GSVIVT00007662001	XM_010650663
0.7	0.5	0.7	**0.2**	PREDICTED: Vitis vinifera patellin-3	GSVIVT00001819001	XM_002267392
0.7	0.8	0.8	**0.2**	PREDICTED: Vitis vinifera alpha-amylase	GSVIVT00036595001	XM_002285177
0.6	0.8	0.7	**0.2**	PREDICTED: Vitis vinifera UDP-glucose:glycoprotein glucosyltransferase	GSVIVT00026475001	XM_010659381
0.6	1.2	0.7	**0.2**	PREDICTED: Vitis vinifera probable alpha-amylase 2	GSVIVT00015532001	XM_010665795
0.6	0.9	1.0	**0.1**	PREDICTED: Vitis vinifera probable polygalacturonase	GSVIVT00037722001	XM_002273633
1.0	0.8	0.8	**0.1**	PREDICTED: Vitis vinifera beta-glucosidase 12	GSVIVT00024686001	XM_002285548

Table 2 (continued)

Fold Change				Functional annotation	ID	Accession
T0-20	T0-7vh	T0-7tg	T0		genoscope	Number (NCBI)
0.8	0.7	0.8	**0.1**	PREDICTED: Vitis vinifera UDP-glycosyltransferase 86A1	GSVIVT00023233001	XM_002276822
Amino acid metabolism						
0.5	**4.2**	**11.2**	**20.0**	PREDICTED: prolyl 4-hydroxylase subunit alpha-1-like	GSVIVT00020832001	XM_002281384
2.1	**0.4**	0.8	**0.2**	PREDICTED: cystathionine beta-lyase, chloroplastic-like	GSVIVT01033607001	XM_002274277
2.1	0.7	**0.1**	**0.2**	PREDICTED: Glutamyl-tRNA(Gln) amidotransferase subunit A, chloro/mito.	GSVIVT01020788001	XM_002278114
0.4	**5.3**	**22.1**	**79.0**	PREDICTED: S-adenosyl-L-methionine decarboxylase, transcript variant 2 (SAMDC)	GSVIVT00038126001	XM_002282672
0.6	**3.3**	**8.5**	**3.9**	PREDICTED: threonine dehydratase biosynthetic, chloroplastic-like		XM_002264275
0.7	**2.4**	**11.3**	**18.3**	PREDICTED: sulfite reductase [ferredoxin]-like	GSVIVT01025246001	XM_002285362
0.6	**2.2**	**4.3**	**27.2**	PREDICTED: LL-diaminopimelate aminotransferase, chloroplastic-like	GSVIVT01029761001	XM_002268730
0.7	**2.3**	**6.7**	**18.4**	PREDICTED: aspartate aminotransferase, chloroplastic-like	GSVIVT00032463001	XM_002284100
0.0	0.9	**0.2**	1.2	PREDICTED: thermospermine synthase ACAULIS5-like	GSVIVT00032257001	XM_002281075
0.6	1.9	**6.0**	**3.9**	PREDICTED: Vitis vinifera glycine--tRNA ligase 2, chloroplastic/mitochondrial	GSVIVT00019071001	XM_002270738
0.9	1.7	**6.0**	**3.7**	PREDICTED: Vitis vinifera cytochrome b561, DM13 and DOMON domain-containing	GSVIVT00032699001	XM_002285257
0.9	1.6	**4.3**	**5.0**	PREDICTED: Vitis vinifera histone-lysine N-methyltransferase ATX1	GSVIVT00011386001	XM-010652171
1.2	1.4	**3.7**	**4.2**	PREDICTED: Vitis vinifera N6-adenosine-methyltransferase MT-A70-like	GSVIVT00000538001	XM_002272901
1.0	0.4	**3.6**	**3.1**	PREDICTED: Vitis vinifera ketol-acid reductoisomerase, chloroplastic-like	GSVIVT00009175001	XM_002280058
1.9	0.9	**0.4**	**0.4**	PREDICTED: Vitis vinifera S-adenosylmethionine decarboxylase proenzyme 4	GSVIVT00019871001	XM_002277280
1.2	0.9	**0.4**	**0.3**	PREDICTED: Vitis vinifera aspartate aminotransferase, mitochondrial	GSVIVT00018772001	XM_002281728
1.1	0.7	**0.4**	**0.1**	PREDICTED: Vitis vinifera cytosolic sulfotransferase 15	GSVIVT00000004001	XM_002265101
1.0	0.7	**0.4**	**0.1**	PREDICTED: Vitis vinifera uncharacterized (LOC100251769)	GSVIVT00022225001	XM_010653521
1.1	0.7	**0.1**	**0.2**	PREDICTED: Vitis vinifera probable diphthine synthase	GSVIVT00014439001	XM_002280113
0.9	0.7	**0.1**	**0.2**	PREDICTED: Vitis vinifera mannose-1-phosphate guanyltransferase alpha-like	GSVIVT00020858001	XM_002281923
1.0	0.9	**2.5**	**0.4**	PREDICTED: Vitis vinifera protein fluG	GSVIVT00000594001	XM_010655695
0.8	0.7	**2.5**	**0.1**	PREDICTED: Vitis vinifera serine hydroxymethyltransferase, mitochondrial	GSVIVT00008180001	XM_010648100
1.0	1.9	**4.8**	0.5	PREDICTED: Vitis vinifera lysine-specific histone demethylase 1 homolog 3	GSVIVT00014490001	XR_788316
0.8	1.0	**2.6**	0.6	PREDICTED: Vitis vinifera pyridine nucleotide-disulfide oxidoreductase domain-cont	GSVIVT00024927001	XM_010650846
0.2	1.8	1.9	**12.3**	PREDICTED: Vitis vinifera histone-lysine N-methyltransferase ATX1	GSVIVT00032732001	XM_010652169
1.6	1.4	1.2	**3.0**	PREDICTED: Vitis vinifera asparagine--tRNA ligase, cytoplasmic 1	GSVIVT00016615001	XM_003633067
0.7	1.4	1.2	**2.8**	PREDICTED: Vitis vinifera histone-lysine N-methyltransferase, H3 lysine-9 specific S	GSVIVT00033960001	XR_787250
0.7	1.4	1.2	**2.1**	PREDICTED: Vitis vinifera branched-chain-amino-acid aminotransferase 2, chloropla	GSVIVT00015014001	XM_010666170
1.5	0.9	1.6	**0.5**	PREDICTED: Vitis vinifera tropinone reductase homolog At1g07440	GSVIVT00024253001	XM_002277799
0.9	1.5	0.9	**0.4**	PREDICTED: Vitis vinifera probable serine incorporator	GSVIVT00025214001	XM_002270574
0.9	1.0	1.2	**0.4**	PREDICTED: Vitis vinifera deoxyhypusine synthase	GSVIVT00017873001	XM_002282885
0.5	0.7	0.9	**0.3**	PREDICTED: Vitis vinifera dolichyldiphosphatase 1-like	GSVIVT00001717001	XM_002263866
0.6	1.0	1.3	**0.2**	PREDICTED: Vitis vinifera threonine synthase, chloroplastic	GSVIVT00032716001	XM_002285330
0.6	0.8	0.6	**0.2**	PREDICTED: Vitis vinifera tyrosine aminotransferase	GSVIVT00018628001	XM_002276515
0.6	0.8	0.6	**0.2**	PREDICTED: Vitis vinifera aspartate-semialdehyde dehydrogenase	GSVIVT00030599001	XM_003631135
0.6	0.8	0.5	**0.2**	PREDICTED: Vitis vinifera aspartyl-tRNA synthetase-like	GSVIVT00038606001	XM_002271322
0.8	0.9	0.6	**0.2**	PREDICTED: Vitis vinifera glutamate dehydrogenase	GSVIVT00014101001	XM_002278852
Lipid metabolism						
3.0	**55.2**	**20.8**	**117.3**	PREDICTED: 14 kDa proline-rich protein DC2.15	GSVIVT00035368001	XM_002271835
2.7	**6.6**	**46.7**	**29.9**	PREDICTED: 12-oxophytodienoate reductase 2-like	GSVIVT00021911001	XM_002281312
0.5	**3.0**	**5.2**	**5.9**	PREDICTED: GDSL esterase/lipase At5g03820-like		XM_002284051
0.5	**2.3**	**7.8**	**1.2**	PREDICTED: fatty acid desaturase 3-like	GSVIVT00026952001	XM_002279191
0.8	**2.9**	**3.7**	**20.9**	PREDICTED: secologanin synthase-like		XM_003634726
0.6	**2.5**	**8.2**	**19.4**	PREDICTED: beta-amyrin synthase-like	GSVIVT00029666001	XM_002270898
0.5	**2.1**	**9.1**	**6.6**	PREDICTED: 3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase-like	GSVIVT00028244001	XM_002281493
1.3	**0.3**	**0.1**	**0.2**	PREDICTED: probable 1-deoxy-D-xylulose-5-phosphate synthase, chloroplastic	GSVIVT01017832001	XM_002277883
0.8	**0.3**	**0.0**	**0.0**	PREDICTED: jmjC domain-containing protein 7-like		XM_010646063
0.5	1.6	**32.3**	**25.5**	PREDICTED: Vitis vinifera cytochrome P450 714C2	GSVIVT00019034001	XM_002269271
1.1	1.5	**9.5**	**5.4**	PREDICTED: Vitis vinifera glycerophosphodiester phosphodiesterase GDPD6	GSVIVT00033015001	XM_002283909
0.9	1.2	**5.5**	**2.7**	PREDICTED: Vitis vinifera non-specific lipid-transfer protein-like protei	GSVIVT00020023001	XM_010651623
1.2	1.4	**3.8**	**2.4**	PREDICTED: Vitis vinifera isolate VvCSbOciM cultivar Cabernet Sauvignon (E)-beta	GSVIVT00011433001	HM807387
1.0	1.6	**3.1**	**4.2**	PREDICTED: Vitis vinifera phospholipid:diacylglycerol acyltransferase 1	GSVIVT00016485001	XM_002275759
0.9	1.3	**2.7**	**2.9**	PREDICTED: Vitis vinifera 7-deoxyloganetin glucosyltransferase	GSVIVT00008150001	XM_002285735
0.8	1.9	**2.3**	**2.3**	PREDICTED: Vitis vinifera phosphatidylinositol-3-phosphatase myotubularin-1	GSVIVT00035008001	XM_002271313
0.7	1.5	**7.2**	**0.5**	PREDICTED: Vitis vinifera membrane steroid-binding protein 2-like	GSVIVT00009206001	XM_002262744
0.7	0.6	**3.1**	**0.2**	PREDICTED: Vitis vinifera beta-amyrin 28-oxidase	GSVIVT00031766001	XM_002280933
0.9	0.9	**2.3**	**0.3**	PREDICTED: Vitis vinifera probable 2-oxoglutarate/Fe(II)-dependent dioxygenase	GSVIVT00031267001	XM_002267979
1.5	0.6	**0.4**	**0.3**	PREDICTED: Vitis vinifera non-specific lipid-transfer protein	GSVIVT00029443001	XM_002275071
1.4	0.7	**0.4**	**0.3**	PREDICTED: Vitis vinifera abietadienol/abietadienal oxidase	GSVIVT00013859001	XM_010663730
1.2	0.8	**0.4**	**0.3**	PREDICTED: Vitis vinifera short-chain type dehydrogenase/reductase	GSVIVT00025488001	XM_002282165
0.8	1.1	**0.4**	**0.3**	PREDICTED: Vitis vinifera phosphatidylinositol-glycan biosynthesis class F protein	GSVIVT00025250001	XM_003632871
0.8	0.8	**0.4**	**0.3**	PREDICTED: Vitis vinifera putative lipid phosphate phosphatase 3, chloroplastic	GSVIVT00038277001	XM_010662090

Table 2 (continued)

Fold Change				Functional annotation	ID	Accession
T0-20	T0-7vh	T0-7tg	T0		genoscope	Number (NCBI)
0.5	1.0	**0.4**	**0.3**	PREDICTED: Vitis vinifera non-specific lipid-transfer protein-like	GSVIVT00011714001	XM_003635261
1.3	0.5	**0.4**	**0.2**	PREDICTED: Vitis vinifera allene oxide synthase	GSVIVT00036457001	XM_002283744
1.1	0.8	**0.4**	**0.2**	PREDICTED: Vitis vinifera hydroxymethylglutaryl-CoA synthase	GSVIVT00013734001	XM_002282398
1.1	0.7	**0.4**	**0.2**	PREDICTED: Vitis vinifera cytochrome P450 CYP72A219	GSVIVT00011015001	XM_002263573
1.1	0.7	**0.4**	**0.1**	PREDICTED: Vitis vinifera cytosolic sulfotransferase 15	GSVIVT00000004001	XM_002265827
1.0	0.7	**0.3**	**0.3**	PREDICTED: Vitis vinifera (-)-alpha-terpineol synthase	GSVIVT00008933001	XM_002266772
0.9	0.8	**0.3**	**0.3**	PREDICTED: Vitis vinifera valencene synthase	GSVIVT00021793001	XM_002277315
0.8	0.8	**0.3**	**0.2**	PREDICTED: Vitis vinifera phosphatidylinositol:ceramide inositolphosphotransferas	GSVIVT00033769001	XM_002276175
0.8	1.1	**0.2**	**0.4**	PREDICTED: Vitis vinifera strictosidine synthase 1	GSVIVT00003163001	XM_002273728
1.1	0.7	**0.2**	**0.3**	PREDICTED: Vitis vinifera acyl-[acyl-carrier-protein] desaturase, chloroplastic	GSVIVT00012872001	XM_002274672
0.8	0.9	**0.2**	**0.3**	PREDICTED: Vitis vinifera probable acyl-activating enzyme 18, peroxisomal	GSVIVT00024773001	XM_010653061
1.8	0.5	**0.2**	**0.2**	PREDICTED: Vitis vinifera probable mannitol dehydrogenase	GSVIVT00013367001	XM_003635388
1.0	0.7	**0.2**	**0.1**	PREDICTED: Vitis vinifera valencene synthase	GSVIVT00027447001	XM_002277315
1.4	0.9	**0.1**	**0.2**	PREDICTED: Vitis vinifera (-)-alpha-terpineol synthase-like	GSVIVT00008934001	XM_010660749
1.4	0.6	**0.1**	**0.2**	PREDICTED: Vitis vinifera probable ATP synthase 24 kDa subunit, mitochondrial	GSVIVT00019377001	XM_002279353
0.8	0.5	**0.1**	**0.1**	PREDICTED: Vitis vinifera phospholipase D Z	GSVIVT00012872001	XM_002285482
0.8	1.3	**6.1**	0.8	PREDICTED: Vitis vinifera cytochrome P450 CYP716A15	GSVIVT00008991001	NM_001281186
0.8	0.9	**3.3**	1.7	PREDICTED: Vitis vinifera acetyl-CoA carboxylase 1-like	GSVIVT00015269001	XM_010666001
0.6	1.5	**3.2**	1.0	PREDICTED: Vitis vinifera 3-epi-6-deoxocathasterone 23-monooxygenase	GSVIVT00036865001	XM_010650788
0.8	1.5	**3.1**	1.1	PREDICTED: Vitis vinifera uncharacterized (LOC100248919)	GSVIVT00026419001	XM_010663378
1.5	0.8	**2.7**	0.6	PREDICTED: Vitis vinifera phosphomethylethanolamine N-methyltransferase	GSVIVT00030533001	XM_002282146
0.9	1.7	**2.6**	1.1	PREDICTED: Vitis vinifera alpha-dioxygenase 1	GSVIVT00020782001	XM_002279848
1.1	1.2	1.1	**4.8**	PREDICTED: Vitis vinifera phosphatidylinositol N-acetylglucosaminyltransferase sub	GSVIVT00032065001	XM_010662959
0.7	1.5	0.8	**3.4**	PREDICTED: Vitis vinifera GATA transcription factor 8-like	GSVIVT00018182001	XM_002273466
0.8	1.6	1.0	**2.6**	PREDICTED: Vitis vinifera NADPH:quinone oxidoreductase	GSVIVT00030913001	XM_002264823
1.0	1.2	1.3	**2.4**	PREDICTED: Vitis vinifera oleoyl-acyl carrier protein thioesterase 1, chloroplastic-like	GSVIVT00010636001	XM_010648264
0.7	1.9	1.8	**2.1**	PREDICTED: Vitis vinifera (3S,6E)-nerolidol synthase 1, chloroplastic-like	GSVIVT00007997001	XM_010648617
0.7	0.8	0.5	**2.1**	PREDICTED: Vitis vinifera acyl-coenzyme A oxidase, peroxisomal	GSVIVT00009919001	XM_002269614
1.1	1.1	1.5	**0.5**	PREDICTED: Vitis vinifera probable acyl-activating enzyme 16, chloroplastic	GSVIVT00027058001	XM_010654898
0.9	0.7	0.9	**0.3**	PREDICTED: Vitis vinifera cultivar Cabernet Sauvignon lipoxygenase 1(LOX1) mRNA	GSVIVT00022800001	KF033130
0.5	0.9	1.1	**0.3**	PREDICTED: Vitis vinifera peroxisomal fatty acid beta-oxidation multifunctional prote	GSVIVT00016719001	XM_002284247
1.0	0.6	0.8	**0.2**	PREDICTED: Vitis vinifera glycerol-3-phosphate acyltransferase, chloroplastic	GSVIVT00015673001	XM_002276065
0.9	0.8	0.7	**0.2**	PREDICTED: Vitis vinifera N-acylphosphatidylethanolamine synthase-like	GSVIVT00029235001	XM_010660002
0.7	0.9	0.5	**0.2**	PREDICTED: Vitis vinifera jasmonate O-methyltransferase	GSVIVT00014572001	XM_002281543
0.6	0.6	1.5	**0.2**	PREDICTED: Vitis vinifera serine/threonine-protein kinase-like protein CCR1	GSVIVT00018209001	XM_002276007
0.7	0.7	1.2	**0.1**	PREDICTED: Vitis vinifera polyprenol reductase 2	GSVIVT00035975001	XM_002269282
Phenylpropanoid metabolism						
2.4	**2.0**	**15.6**	**59.5**	PREDICTED: salicylate O-methyltransferase	GSVIVT00024874001	XM_002262640
2.4	**3.9**	**7.7**	**16.8**	PREDICTED: flavonoid 3'-monooxygenase-like	GSVIVT00016215001	XM_002284115
2.3	**8.7**	**11.6**	**8.5**	PREDICTED: bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase		XM_002277359
0.0	**8.2**	**64.9**	**79.6**	PREDICTED: peroxidase 24-like		XM_003631913
0.7	**2.6**	**15.9**	**5.4**	PREDICTED: 1-Cys peroxiredoxin	GSVIVT00019700001	XM_002265561
0.7	**2.4**	**5.8**	**7.9**	PREDICTED: probable iron/ascorbate oxidoreductase DDB_G0283291-like	GSVIVT01022069001	XM_002283156
1.7	**0.2**	**0.1**	**0.1**	PREDICTED: flavonoid-related R2R3 MYB 4a repressor transcription factor	GSVIVT00036110001	XM_002278186
1.3	0.7	**12.5**	**5.2**	PREDICTED: Vitis vinifera probable carboxylesterase 11	GSVIVT00027407001	XM_002267052
0.7	1.6	**25.6**	**24.0**	PREDICTED: Vitis vinifera malonate--CoA ligase	GSVIVT00034366001	XM_002279103
1.3	1.1	**5.6**	**4.7**	PREDICTED: Vitis vinifera anthocyanidin 3-O-glucosyltransferase 2-like	GSVIVT00031485001	XM_002264962
1.0	1.4	**4.7**	**4.9**	PREDICTED: Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase UFGT2	GSVIVT00031443001	AB047093
0.7	2.0	**4.5**	**3.7**	PREDICTED: Vitis vinifera chalcone synthase (CHS)	GSVIVT00009232001	NM_001280950
0.9	2.0	**4.1**	**2.6**	PREDICTED: Vitis vinifera laccase-14	GSVIVT00010170001	XM_002265308
0.9	1.8	**2.6**	**2.2**	PREDICTED: Vitis vinifera beta-glucosidase 12-like	GSVIVT00028756001	XM_002276015
0.8	0.8	**0.3**	**0.2**	PREDICTED: Vitis vinifera isoflavone 2'-hydroxylase-like	GSVIVT00019593001	XM_010654455
1.0	0.6	**0.2**	**0.2**	PREDICTED: Vitis vinifera 4-coumarate--CoA ligase-like 5	GSVIVT00018101001	XM_002285884
0.8	1.0	**0.2**	**0.1**	PREDICTED: Vitis vinifera (RS)-norcoclaurine 6-O-methyltransferase-like	GSVIVT00011171001	XM_002281074
1.7	0.5	**0.1**	**0.2**	PREDICTED: Vitis vinifera laccase-11	GSVIVT00024910001	XM_003632588
1.8	0.6	**0.1**	**0.1**	PREDICTED: Vitis vinifera tryptophanyl-tRNA synthetase-like	GSVIVT00032095001	XM_002272993
0.7	1.4	**9.8**	0.9	PREDICTED: Vitis vinifera peroxidase 3	GSVIVT00026053001	XM_002280238
0.7	1.7	**5.0**	1.4	PREDICTED: Vitis vinifera cytochrome P450 82C4	GSVIVT00036466001	XM_002283995
1.2	1.8	**4.8**	0.9	PREDICTED: Vitis vinifera chalcone synthase (CHS)	GSVIVT00009226001	NM_001280950
1.0	1.0	**3.8**	1.6	PREDICTED: Vitis vinifera naringenin,2-oxoglutarate 3-dioxygenase	GSVIVT00036513001	XM_002284856
0.8	1.5	**3.7**	1.0	PREDICTED: Vitis vinifera probable cinnamyl alcohol dehydrogenase 1	GSVIVT00019568001	XM_002285370
0.8	1.4	**3.6**	0.6	PREDICTED: Vitis vinifera (RS)-norcoclaurine 6-O-methyltransferase	GSVIVT00011172001	XM_002281084
0.9	1.2	**2.7**	0.9	PREDICTED: Vitis vinifera caffeoylshikimate esterase	GSVIVT00013671001	XM_003634810
0.9	1.5	**2.6**	1.8	PREDICTED: Vitis vinifera bifunctional 3-dehydroquinate dehydratase/shikimate dehy	GSVIVT00008900001	XM_010651497

Table 2 (continued)

Fold Change				**Functional annotation**	**ID**	**Accession**
T0-20	**T0-7vh**	**T0-7tg**	**T0**		**genoscope**	**Number (NCBI)**
1.1	1.8	**0.4**	1.7	PREIDCTED: Vitis vinifera 1-Cys peroxiredoxin	GSVIVT00019700001	NM_001281268
0.8	1.5	0.8	**2.0**	PREDICTED: Vitis vinifera probable carboxylesterase 2	GSVIVT00019941001	XM_002284551
0.5	0.8	2.0	**0.4**	PREDICTED: Vitis vinifera uncharacterized acetyltransferase At3g50280-like	GSVIVT00014857001	XM_002284880
1.0	1.0	0.7	**0.4**	PREDICTED: Vitis vinifera GDP-mannose-3',5'-epimerase	GSVIVT00034578001	NM_001281039
0.8	1.8	0.5	**0.4**	PREDICTED: Vitis vinifera flavonoid 3'-monooxygenase-like	GSVIVT00016437001	XM_002284115
0.9	1.2	1.7	**0.4**	PREDICTED: Vitis vinifera flavonol synthase/flavanone 3-hydroxylase	GSVIVT00016437001	XM_002285802
0.7	0.8	1.1	**0.1**	PREDICTED: Vitis vinifera flavonol synthase/flavanone 3-hydroxylase	GSVIVT00015347001	XM_002285802
Stress and Defense reactions						
2.3	**8.6**	**2.9**	**46.7**	PREDICTED: epoxide hydrolase 2-like		XM_003632333
0.5	**2.7**	**8.5**	**8.2**	PREDICTED: epoxide hydrolase 2-like		XM_003632333
0.7	**19.9**	**53.4**	**49.1**	PREDICTED: homolog haloacid dehalogenase hydrolase	GSVIVT00021335001	XM_002267523
1.0	**14.7**	**87.0**	**56.5**	PREDICTED: glutathione S-transferase U9-like		XM_003634217
1.0	**12.4**	**13.0**	**5.5**	PREDICTED: germin-like protein subfamily 1 member 14	GSVIVT00022776001	XM_002284264
1.1	**10.1**	**8.7**	**42.9**	PREDICTED: glutathione S-transferase	GSVIVT00027957001	XM_002262806
1.8	**4.2**	**29.3**	**7.6**	PREDICTED: class I beta-1,3-glucanase		XM_002277133
0.5	**3.5**	**16.2**	**9.3**	PREDICTED: serine/threonine-protein phosphatase 7-like	GSVIVT00005999001	XM_002263704
0.8	**3.4**	**2.0**	**6.7**	PREDICTED: TMV resistance protein N-like		XM_002276039
0.6	**3.3**	**25.5**	**10.6**	PREDICTED: pathogenesis-related protein 10.7		XM_002273754
0.9	**3.0**	**2.0**	**5.6**	PREDICTED: probable disease resistance protein RDL6/RF9-like		XM_003633403
0.9	**3.0**	**4.5**	**8.4**	PREDICTED: probable disease resistance protein At5g66900-like		XM_002268171
1.0	**2.6**	**12.4**	**8.0**	PREDICTED: thaumatin-like protein 1	GSVIVT01009928001	XM_002274101
1.2	**2.7**	**2.3**	**7.0**	Uncharacterized LOC100262931	GSVIVT00017866001	XM_002282796
0.8	**2.2**	**87.1**	**37.9**	PREDICTED: disease resistance RPP13-like protein 4	GSVIVT00036904001	XM_002268904
1.0	**2.0**	**0.4**	**4.3**	PREDICTED: probable disease resistance protein At5g63020-like		XM_002263638
1.9	**0.4**	**0.2**	**0.3**	PREDICTED: putative disease resistance RPP13-like protein		XM_003633332
1.9	1.8	**66.1**	**30.1**	PREDICTED: Vitis vinifera ultraviolet-B receptor UVR8	GSVIVT00038080001	NM_111097
0.8	1.4	**16.1**	**5.4**	PREDICTED: Vitis vinifera putative disease resistance RPP13-like protein 1	GSVIVT00031023001	
0.9	1.8	**14.6**	**4.2**	PREDICTED: Vitis vinifera pleiotropic drug resistance protein 2	GSVIVT00034947001	XM_010655751
1.7	1.3	**12.1**	**7.0**	PREDICTED: Disease resistance protein (TIR-NBS-LRR class)	GSVIVT00008753001	
1.2	0.9	**9.4**	**4.8**	PREDICTED: Vitis vinifera leucine-rich repeat receptor-like serine/threonine-protein k	GSVIVT00036586001	XM_002282105
1.0	1.9	**7.8**	**3.8**	PREDICTED: Vitis vinifera TMV resistance protein N	GSVIVT00028940001	XM_010654467
0.6	1.0	**5.9**	**2.5**	PREDICTED: Vitis vinifera RRP15-like protein	GSVIVT00029062001	XM_010659195
0.7	1.3	**5.5**	**3.0**	PREDICTED: Vitis vinifera receptor-like protein 12	GSVIVT00011664001	
1.1	1.3	**4.5**	**2.9**	PREDICTED: Vitis vinifera MATE efflux family protein 6	GSVIVT00001094001	XM_002274772
0.8	1.6	**4.4**	**2.0**	PREDICTED: Vitis vinifera disease resistance protein	GSVIVT00033316001	XM_010646027
1.2	1.3	**3.7**	**3.5**	PREDICTED: Vitis vinifera disease resistance protein	GSVIVT00006778001	XM_010646027
0.8	1.7	**3.5**	**4.4**	PREDICTED: Vitis vinifera gene for chitinase III	GSVIVT00020672001	AB105374
0.7	1.4	**3.0**	**18.5**	PREDICTED: Vitis vinifera germin-like protein subfamily 1 member 17	GSVIVT00029796001	XM_002284248
1.1	1.1	**2.4**	**5.4**	PREDICTED: Epoxide hydrolase	GSVIVT00025835001	
1.0	1.5	**2.4**	**3.6**	PREDICTED: Vitis vinifera B-cell receptor-associated protein 31-like	GSVIVT00012113001	XM_002270265
1.3	1.2	**2.0**	**2.1**	PREDICTED: Vitis vinifera gene for chitinase II	GSVIVT00026961001	AB105374
0.9	1.0	**3.6**	**0.4**	PREDICTED: Vitis vinifera TMV resistance protein N-like	GSVIVT00021897001	XR_788432
0.9	0.9	**2.5**	**0.4**	PREDICTED: Vitis vinifera putative disease resistance protein	GSVIVT00034601001	
0.7	1.4	**0.5**	**2.9**	PREDICTED: Vitis vinifera stromal cell-derived factor 2-like protein	GSVIVT00032696001	XM_002285252
1.0	1.5	**0.2**	**10.5**	PREDICTED: Vitis vinifera pleiotropic drug resistance protein 1-like	GSVIVT00034505001	XM_010656419
1.0	0.8	**0.5**	**0.4**	PREDICTED: Vitis vinifera chaperone protein dnaJ 20, chloroplastic	GSVIVT00031635001	XM_002264118
1.2	0.7	**0.5**	**0.2**	PREDICTED: Vitis vinifera cysteine proteinase inhibitor 1-like	GSVIVT00011952001	XM_003634968
1.0	0.7	**0.5**	**0.1**	PREDICTED: Defense - Dirigent protein	GSVIVT00024746001	XM_002285647
0.9	1.0	**0.4**	**0.4**	PREDICTED: Vitis vinifera MLO-like protein 10	GSVIVT00019324001	XM_002276572
1.0	0.7	**0.4**	**0.2**	PREDICTED: integrase	GSVIVT00008063001	
1.0	0.6	**0.4**	**0.2**	PREDICTED: Vitis vinifera uncharacterized LOC100248098	GSVIVT00026485001	XR_139826
0.9	0.7	**0.4**	**0.2**	PREDICTED: transducin protein	GSVIVT00012724001	
0.8	0.6	**0.4**	**0.1**	PREDICTED: Disease resistance protein (TIR-NBS-LRR class)	GSVIVT00021828001	
1.1	0.6	**0.3**	**0.3**	PREDICTED: Vitis vinifera glutathione S-transferase U9	GSVIVT00000140001	XM_002269082
1.6	0.8	**0.3**	**0.2**	PREDICTED: Vitis vinifera putative disease resistance RPP13-like protei	GSVIVT00034920001	
1.1	0.9	**0.3**	**0.2**	PREDICTED: ACCELERATED CELL DEATH 1 ACD1	GSVIVT00024785001	XM_002283556
1.0	1.0	**0.3**	**0.2**	PREDICTED: Vitis vinifera uncharacterized (LOC100245966)	GSVIVT00012890001	XM_010656905
1.1	0.8	**0.3**	**0.1**	PREDICTED: Pathogenesis- - Bet v I allergen - abscisic acid receptor PYL11	GSVIVT00035869001	XM_002272743
0.9	0.5	**0.3**	**0.1**	PREDICTED: endochitinase PR4	GSVIVT00034644001	XM_002274722
0.8	0.6	**0.3**	**0.0**	PREDICTED: Vitis vinifera hsp70-Hsp90 organizing protein 3-like	GSVIVT00012628001	XM_003635638
1.4	0.7	**0.2**	**0.4**	PREDICTED: Vitis vinifera probable receptor-like protein kinase	GSVIVT00013403001	XM_010662106
1.2	0.5	**0.2**	**0.3**	PREDICTED: Vitis vinifera probable NAD(P)H dehydrogenase (quinone) FQR1-like 2	GSVIVT00024987001	XM_002272994
1.1	0.9	**0.2**	**0.3**	PREDICTED: Glutathione S-transferase U10-like	GSVIVT00036965001	XM_002275302
1.1	0.8	**0.2**	**0.3**	PREDICTED: Vitis vinifera polyadenylate-binding protein-interacting protein 4	GSVIVT00034112001	XM_010656176

Table 2 (continued)

Fold Change				Functional annotation	ID	Accession
T0-20	T0-7vh	T0-7tg	T0		genoscope	Number (NCBI)
0.4	0.5	**0.2**	**0.3**	PREDICTED: Disease resistance - PMR5 (Powdery Mildew Resistant 5)	GSVIVT00018816001	XM_002277193
1.1	0.7	**0.2**	**0.2**	PREDICTED: Vitis vinifera glycine-rich protein 2-like	GSVIVT00036773001	XM_002266079
1.1	0.6	**0.2**	**0.1**	PREDICTED: Vitis vinifera putative disease resistance RPP13-like protein 1	GSVIVT00035449001	XM_003633332
0.7	1.1	**0.2**	**0.1**	PREDICTED: Vitis vinifera uncharacterized (LOC100248098)	GSVIVT00026485001	XR_139826
1.5	0.6	**0.1**	**0.2**	PREDICTED: retrotransposon protein, Ty1-copia subclass	GSVIVT00029789001	
1.7	0.7	**0.1**	**0.1**	PREDICTED: Vitis vinifera chaperone protein ClpB4, mitochondrial	GSVIVT00032702001	XM_002282844
1.2	0.8	**0.0**	**0.2**	PREDICTED: Disease resistance : Receptor kinase TRKa	GSVIVT00018767001	XM_010666231
0.7	1.4	**5.0**	1.3	PREDICTED: Disease resistance protein (TIR-NBS-LRR class)	GSVIVT00021884001	
0.7	1.3	**3.7**	1.1	PREDICTED: Vitis vinifera putative disease resistance RPP13-like protein 1	GSVIVT00025723001	
0.6	1.9	**3.5**	1.0	PREDICTED: Vitis vinifera heat shock 70kDa protein 1/8-like	GSVIVT00021301001	XM_002283496
1.4	0.5	**3.2**	1.8	PREDICTED: Vitis vinifera 20 kDa chaperonin, chloroplastic	GSVIVT00017690001	XM_002277825
0.6	1.3	**3.2**	0.7	PREDICTED: Vitis vinifera uncharacterized (LOC100255258)	GSVIVT00008635001	XM_010663660
0.8	1.0	**3.0**	1.3	PREDICTED: Vitis vinifera pathogenesis-related protein 10 (PR10.2)	GSVIVT00033076001	XM_002274206
0.7	1.7	**2.9**	1.9	PREDICTED: Vitis vinifera dolichyl-diphosphooligosaccharide--protein glycosyltrans	GSVIVT00015676001	XM_002277380
0.9	1.1	**2.8**	0.5	PREDICTED: Vitis vinifera pleiotropic drug resistance protein 1-like	GSVIVT00034512001	XM_010656419
0.8	1.4	**2.8**	1.4	PREDICTED: Vitis vinifera gene for chitinase III	GSVIVT00026948001	AB105374
1.1	1.2	**2.7**	1.7	PREDICTED: Vitis vinifera bifunctional epoxide hydrolase 2	GSVIVT00025831001	XM_010650793
1.0	1.5	**2.7**	1.5	PREDICTED: Vitis vinifera probable protein phosphatase 2C 55	GSVIVT00015482001	XM_010666364
0.8	1.5	**2.7**	0.9	PREDICTED: Vitis vinifera germin-like protein 5 (GER5)	GSVIVT00022771001	NM_001281199
0.9	1.2	**2.5**	0.8	PREDICTED: Wound induced protein [Vitis vinifera]	GSVIVT00013090001	
1.3	0.9	**2.3**	0.6	PREDICTED: Disease resistance	GSVIVT00025182001	
0.9	1.3	**2.1**	0.8	PREDICTED: Vitis vinifera gamma-interferon-inducible lysosomal thiol reductase (L	GSVIVT00024041001	XM_002275247
1.6	1.2	**2.0**	1.0	PREDICTED : Disease resistance protein	GSVIVT00025170001	
0.8	1.3	**2.0**	0.5	PREDICTED: Vitis vinifera zeaxanthin epoxidase, chloroplastic-like	GSVIVT00008708001	XR_785224
0.9	1.0	**0.5**	1.9	PREDICTED: Vitis vinifera superoxide dismutase [Cu-Zn]	GSVIVT00032849001	XM_010661684
0.9	0.9	**0.4**	0.6	PREDICTED: Vitis vinifera reticuline oxidase-like protein	GSVIVT00029833001	XM_002270103
0.6	1.7	0.8	**3.9**	PREDICTED: Vitis vinifera probable LRR receptor-like serine/threonine-protein kinas	GSVIVT00029260001	XM_010659989
0.6	1.5	0.6	**3.4**	PREDICTED: Vitis vinifera respiratory burst oxidase homolog protein E	GSVIVT00016386001	XM_002277504
0.9	1.5	1.4	**3.0**	PREDICTED: Vitis vinifera beta-glucosidase 11-like	GSVIVT00027994001	XM_002267559
1.1	1.3	0.8	**2.7**	PREDICTED: Vitis vinifera FAD-linked sulfhydryl oxidase ERV1	GSVIVT00011077001	XM_002263782
0.8	1.6	0.8	**2.5**	PREDICTED: Vitis vinifera dehydration-responsive protein RD22-like	GSVIVT00032491001	XM_010650235
0.6	0.8	1.7	**2.5**	PREDICTED: Vitis vinifera 66 kDa stress protein	GSVIVT00017796001	XM_002281430
0.8	1.6	1.1	**2.4**	PREDICTED: Vitis vinifera cultivar Riesling thaumatin-like protein mRNA	GSVIVT00001108001	DQ406687
0.7	1.2	0.8	**2.4**	PREDICTED: Vitis vinifera pathogenesis-related protein 10	GSVIVT00033084001	XM_002274206
0.6	1.6	0.8	**2.3**	PREDICTED: Vitis vinifera uncharacterized (LOC100263302)	GSVIVT00035913001	XM_002279165
0.9	1.7	1.1	**2.2**	PREDICTED: Vitis vinifera MLP-like protein 34	GSVIVT00030515001	XM_002284534
1.0	0.9	1.2	**0.5**	PREDICTED: Vitis vinifera elicitor-responsive protein 1	GSVIVT00018476001	XM_002283449
0.5	1.0	0.7	**0.5**	PREDICTED: Vitis vinifera pleiotropic drug resistance protein 1-like	GSVIVT00008910001	XM_010656419
1.2	0.7	1.3	**0.4**	PREDICTED: Vitis vinifera protein NEDD1-like	GSVIVT00015386001	XM_010665913
1.2	0.7	0.7	**0.4**	PREDICTED: Vitis vinifera cleavage stimulating factor 64-like	GSVIVT00017689001	XM_010665298
1.1	0.9	1.8	**0.4**	PREDICTED: Vitis vinifera cysteine proteinase inhibitor 1-like	GSVIVT00013094001	XM_003634968
0.8	1.4	0.8	**0.4**	PREDICTED: Vitis vinifera probable protein phosphatase 2C 25	GSVIVT00029318001	XM_010652586
0.8	1.3	0.8	**0.4**	PREDICTED: Vitis vinifera basic form of pathogenesis-related protein 1	GSVIVT00038580001	XM_002265014
0.7	1.3	1.9	**0.4**	PREDICTED: Vitis vinifera MATE efflux family protein 5	GSVIVT00030436001	XM_002280176
0.7	1.8	1.8	**0.3**	PREDICTED: Vitis vinifera heat shock factor protein HSF30	GSVIVT00032192001	XR_785545
0.7	1.3	0.8	**0.3**	PREDICTED: Vitis vinifera probable disease resistance protein	GSVIVT00009711001	XM_002268171
0.7	0.9	1.5	**0.3**	PREDICTED: Vitis vinifera monothiol glutaredoxin-S2	GSVIVT00019806001	XM_002275348
0.6	1.1	1.5	**0.3**	PREDICTED: Vitis vinifera 15.7 kDa heat shock protein, peroxisomal-like	GSVIVT00018510001	XM_002283824
0.6	0.8	0.6	**0.3**	PREDICTED: Vitis vinifera patatin-like protein 1	GSVIVT00019467001	XM_002277269
1.3	0.9	0.9	**0.2**	PREDICTED: Vitis vinifera disease resistance protein	GSVIVT00032853001	XM_010646027
0.7	0.7	0.7	**0.2**	PREDICTED: Vitis vinifera uncharacterized LOC100264617	GSVIVT00020796001	XM_002275240
0.9	1.1	1.1	**0.2**	PREDICTED: Vitis vinifera putative disease resistance protein	GSVIVT00026613001	
0.9	0.9	0.7	**0.2**	PREDICTED PMR5 (powdery mildew resistant 5)	GSVIVT00033105001	
1.0	0.7	0.5	**0.2**	PREDICTED: Disease resistance RPP13	GSVIVT00031272001	
0.9	1.0	1.0	**0.2**	PREDICTED: Vitis vinifera pleiotropic drug resistance protein 1-like	GSVIVT00034494001	XM_010656419
0.8	0.8	0.6	**0.2**	PREDICTED: Vitis vinifera disease resistance protein	GSVIVT00031272001	XM_010646027
1.1	0.6	0.6	**0.1**	PREDICTED: Vitis vinifera putative disease resistance RPP13-like protein 1	GSVIVT00029984001	XM_003633332

Table 3. Relative expression of 18 selected genes in the visually healthy leaves of pre-apoplectic vines of cultivar Chardonnay 50 (T0-50), 30 (T0-30), 20 (T0-20) and 7 (T0-7) days before symptoms emergence and at the onset of symptoms (T0). Analyses were performed by both Illumina sequencing and RT-PCR. Gene expression was considered as significantly up- or down-regulated to the 1× control, when changes in relative expression were >2× or <0.5×, respectively. The values obtained for regulated gene expression appear in bold. The ratio values correspond to the mean of three biological replicates.

			Relative expression of targeted genes					
Functional classification	Selection as marker		T0-50	T0-30	T0-20	T0-7vh	T0	Methods
Carbohydrate metabolism	no	gluPuriT	1.07	1.01	1.23	0.72	1.26	RT-PCR
					0.50	**12.50**	**87.60**	Illumina
	no	SucS2	0.92	0.88	**0.36**	0.56	0.72	RT-PCR
					0.20	1.50	**0.00**	Illumina
	no	SucDHFla	1.11	1.09	1.00	0.80	0.88	RT-PCR
					5.10	**13.50**	**4.70**	Illumina
Amino acid metabolism	no	SperS	1.81	1.29	1.29	0.97	0.57	RT-PCR
					0.00	0.90	1.20	Illumina
Lipid metabolism	no	xylPS	1.16	0.79	1.12	0.78	1.20	RT-PCR
					1.30	**0.50**	**0.20**	Illumina
	no	jmjc7	1.00	1.07	1.27	0.70	0.71	RT-PCR
					0.80	**0.30**	**0.00**	Illumina
Hormonal regulation, signalisation	ok	Aux10A5	1.25	**0.48**	1.60	**0.29**	**0.22**	RT-PCR
					1.10	**0.40**	**0.20**	Illumina
	no	Myochain	1.59	1.26	1.14	0.88	0.80	RT-PCR
					9.20	**9.30**	**2.10**	Illumina
	no	FboxWD40	0.69	0.76	0.88	0.80	1.02	RT-PCR
					4.20	1.20	**51.20**	Illumina
Cellular processes	no	CasK	1.08	0.93	1.10	0.96	1.05	RT-PCR
					3.90	**0.90**	**0.10**	Illumina
	no	HatpZ	1.27	0.93	0.91	1.25	0.97	RT-PCR
					3.20	**11.40**	**61.30**	Illumina
Phenylpropanoid metabolism	no	ShikDH	0.96	0.85	0.83	1.23	1.11	RT-PCR
					2.30	**8.70**	**8.50**	Illumina
	ok	MYB4A	0.64	1.25	0.81	**0.41**	**0.27**	RT-PCR
					1.70	**0.20**	**0.10**	Illumina
Detoxification	no	epoxHF	0.98	1.06	1.71	1.42	**2.29**	RT-PCR
					2.30	**8.60**	**46.70**	Illumina
	ok	HALH	1.40	**0.46**	1.73	**2.49**	**3.23**	RT-PCR
					0.70	**19.90**	**49.10**	Illumina
	no	GSTA	**2.91**	1.66	1.63	0.62	**0.26**	RT-PCR
					1.00	**14.70**	**56.50**	Illumina
	no	GSTB	**3.94**	1.90	1.11	**0.26**	**0.21**	RT-PCR
					1.10	**10.10**	**42.90**	Illumina
	no	GSTC	1.09	1.31	1.01	1.37	1.35	RT-PCR
					1.10	0.60	**0.30**	Illumina

Table 4. Relative expression by RT-PCR analysis of *GST1* gene in the visually healthy leaves of pre-apoplectic vines of cultivar Chardonnay 50 (T0-50), 30 (T0-30), 20 (T0-20) and 7 (T0-7) days before symptoms emergence and at the onset of symptoms (T0). Gene expression was considered as significantly up- or down-regulated to the 1× control, when changes in relative expression were >2× or <0.5×, respectively and the value appear in bold. The ratio values correspond to the mean of three biological replicates.

	Relative expression of GST1 (glutathion-S-transferase)				
Marker	T0-50	T0-30	T0-20	T0-7vh	T0
GST1	**2.9**	1.91	**3.8**	**2.99**	**36**

FIGURE CAPTIONS

Figure 1: **Repartition of up- or down-regulated genes in grapevine leaf tissues (cv Chardonnay) at 20 days and 7 days before symptoms appearance and at the onset of apoplexy.** The number of the genes differentially expressed in leaf tissues of future apoplectic plant in comparison to those of control (asymptomatic) plants for each time point is reported at the top. The expression of a same gene can be altered at different points of kinetics and therefore counted several times. The percentage indicates the repartition of genes characterized by an up- or a down-regulation of their expression for each point of kinetic (in red or blue, respectively). T0-20: visually healthy leaves sampled 20 days before apoplexy event, T0-7vh: visually healthy leaves sampled 7 days before apoplexy event, T0-7tg: turgorless leaves sampled 7 days before apoplexy event, T0: visually healthy leaves sampled at the onset of apoplexy event.

Figure 2: **Distribution into functional categories of genes differentially expressed in leaves of vines of cultivar Chardonnay affected by apoplexy event.** The percentage of each category is reported in the figure. Only genes with a known function were integrated in this figure, which represents 31% of the total differentially expressed genes in T0-20 leaves (**A**), 30% in T0-7vh leaves (**B**), 44% in T0-7tg leaves (**C**) and 45% in T0 leaves (**D**) of plants affected by apoplexy event.

Figure 3: **Discrimination of FT-ICR-MS data samples and detailed visualization of the samples.**

OPLS-DA analysis showing the discrimination of control, T0-20 / T0-7 diseased samples and T0 diseased samples (A). Venn diagrams showing the distribution of the *m/z* obtained by (-) FT-ICR-MS analysis of the samples (B). Van Krevelen diagrams representing the elemental formulas attributed to the top m/z of total samples (C), control (D), T0-20 / T0-7 (E), and T0 samples (F) onto two axes according H/C and O/C atomic ratios. Dots are colored according to their elemental composition (CHO, CHOS, CHON, CHONS, CHOP, CHONP, CHONSP) and sized according to their relative intensity in mass spectra. Diagrams (on the right) indicate the number of these formula and show their distribution according to their elemental composition (CHO, CHOS, CHON, CHONS, CHOP, CHONP or CHONSP). Top *m/z* correspond to *m/z* with the highest regression coefficient value (VIP ≥1).

Figure 4: **Metabolic pathways associated to the top *m/z* identified in the different sample groups**

The metabolic pathways corresponding to the top *m/z* of control, T0-20 / T0-7, and T0 were obtained after KEGG query with the MassTRIX interface using *Vitis vinifera* organism (vvi). The x axis correspond to the number of annotated formulas obtained for each pathway.

Figure 5: **Possible transformations of the complete *m/z* data set.**

Figure 6: **Focus on glutathione metabolism**

Partial metabolic pathway obtained after KEGG query with the MassTRIX interface using *Vitis vinifera* organism (vvi) focused on glutathione metabolism (A), signal intensity of putative glutathione (B), network analysis of S containing compounds (C) with a focus on glutathione (D) and an example of transformations involving glutathione (E).

Figure 7: **Visualization of *GST1* expression in grapevine leaf tissues**

A control without probe (A) was made to be sure that colorimetric (blue) signal further observed correspond to a specific detection of the probe. The transcripts were localized using a digoxigenin-labelled antisense probe (C, E, G) and the specificity of hybridization was checked with the corresponding sense probe as negative control (B, D, F). *VvGST1* localization (E, G) was compared with the 26S ribosomic (Rib) RNA probe pattern, which was known to be constitutively express in all tissues (C). *VvGST1* transcripts were not detected in asymptomatic (control) leaves (E), whereas visualized in phloem cells of pre-apoplectic ones (G, red arrow heads). Bars represent 100 µm.

Figure 8: **Visualization of *GST1* expression in leaf primary bundles**

A control without probe (A) was made to be sure that colorimetric (blue) signal further observed correspond to a specific detection of the probe. The transcripts were localized using a digoxigenin-labelled antisense probe (C, E and G) and the specificity of hybridization was checked with the corresponding sense probe as negative control (B, D and F). *VvGST1* localization (E and G) was compared with the 26S ribosomic (Rib) RNA probe pattern, which was known to be constitutively express in all tissues (C). *VvGST1* transcripts were not detected in primary bundles asymptomatic leaves (E), whereas appeared to be exclusively localized in phloem cells of pre-apoplectic ones (G). Bars represent 100 µm.

SUPPLEMENTARY DATA

Supplementary Table 1: Primers of genes analyzed by real-time reverse-transcription polymerase chain reaction used in this research.

Supplementary Table 2: Functional classification of the genes differentially expressed between control and diseased plants and whose expression is altered tardily and/ or during apoplectic expression (at T0-20 and/ or T0-7 and / or T0). Values indicating over- or down-expressed (ratio |2|) are highlighted in light or dark gray, respectively.

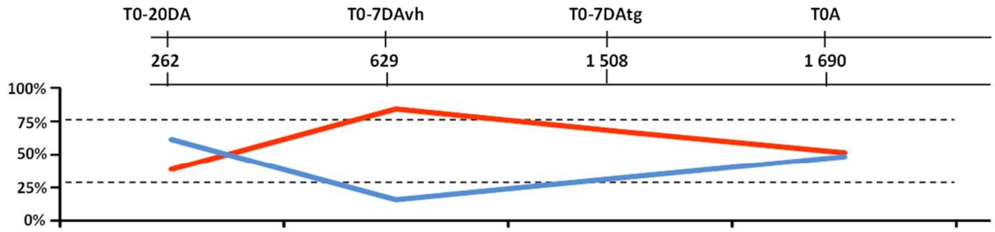


Fig 1. Repartition of up- or down-regulated genes in grapevine leaf tissues (cv Chardonnay) at 20 days and 7 days before symptoms appearance and at the onset of apoplexy.

194x47mm (150 x 150 DPI)

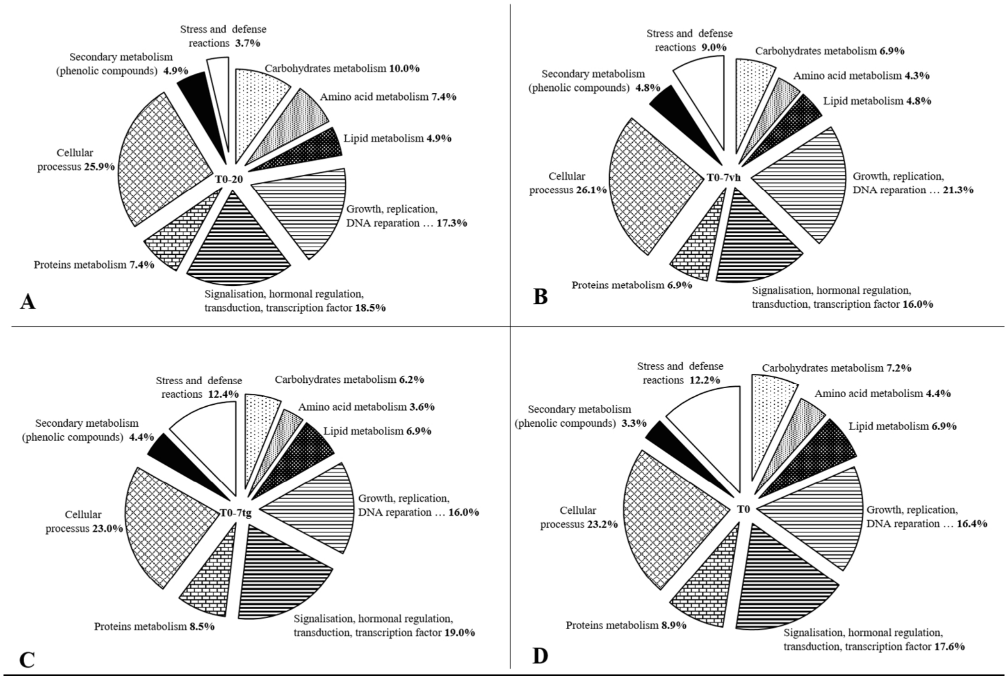


Fig. 2. Distribution into functional categories of genes differentially expressed in leaves of vines of cultivar Chardonnay affected by apoplexy event.

281x191mm (150 x 150 DPI)

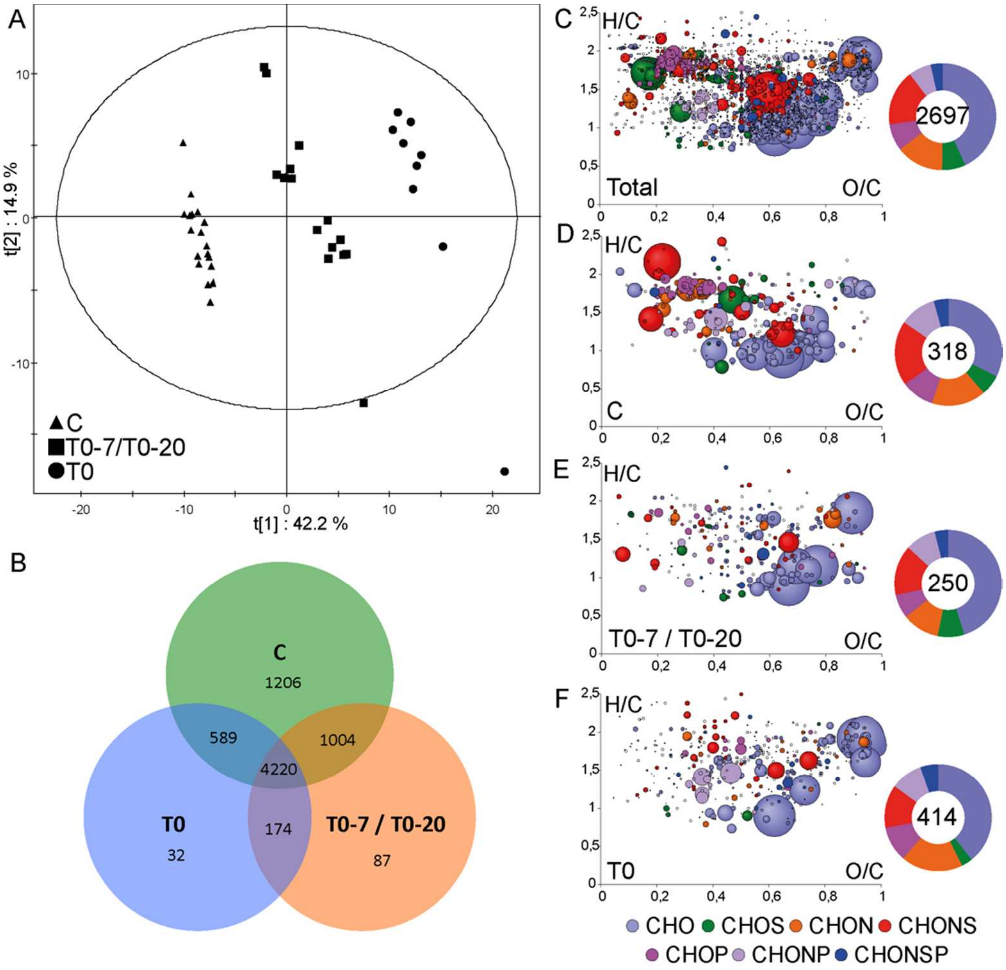


Fig 3. Discrimination of FT-ICR-MS data samples and detailed visualization of the samples.

188x182mm (150 x 150 DPI)

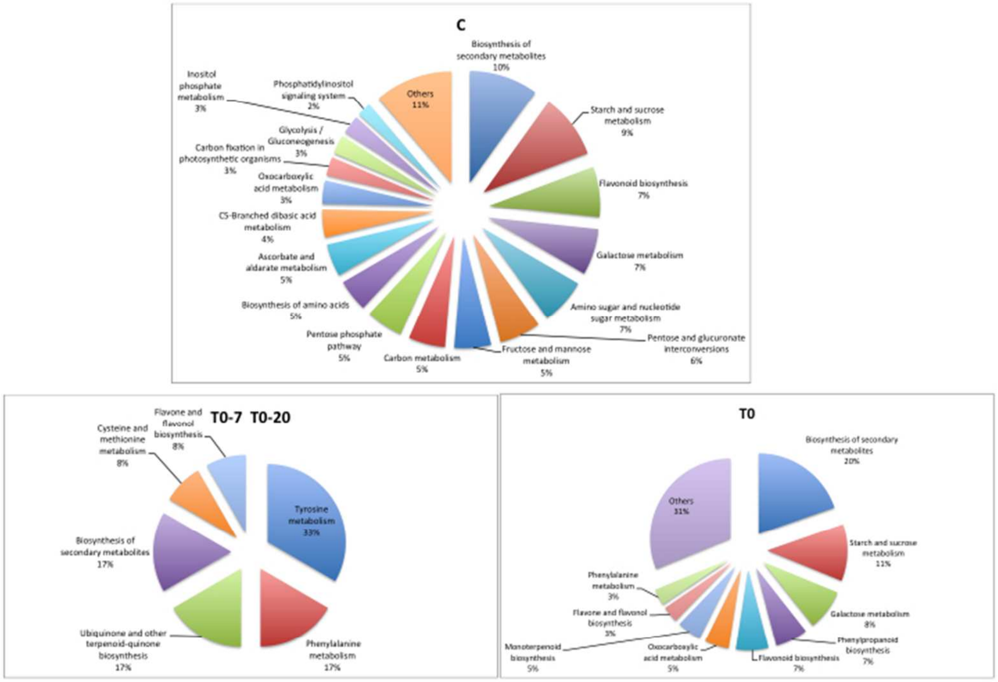


Fig 4. Metabolic pathways associated to the top m/z identified in the different sample groups

254x190mm (72 x 72 DPI)

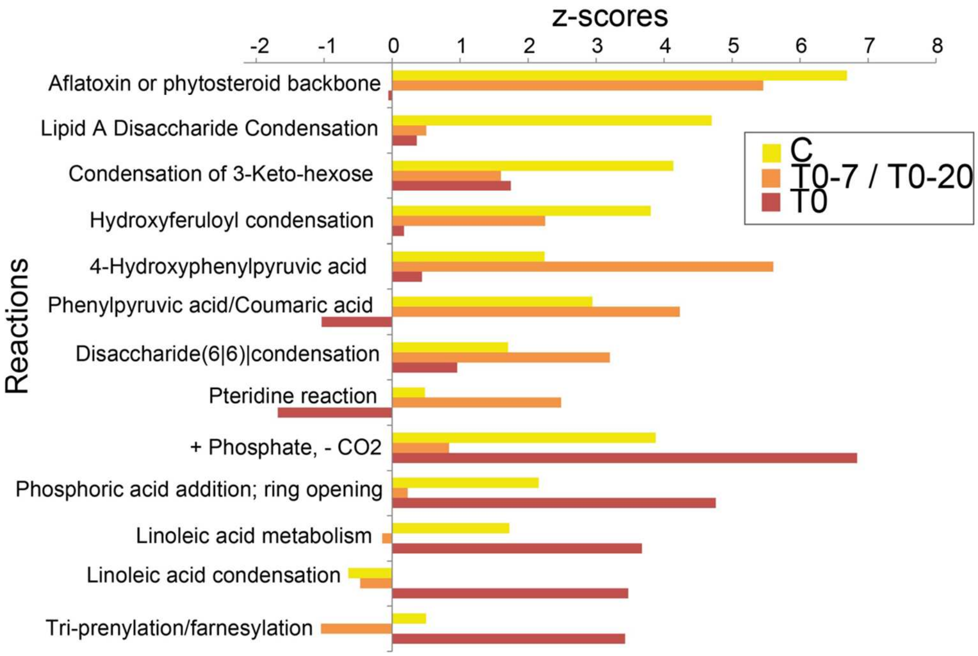
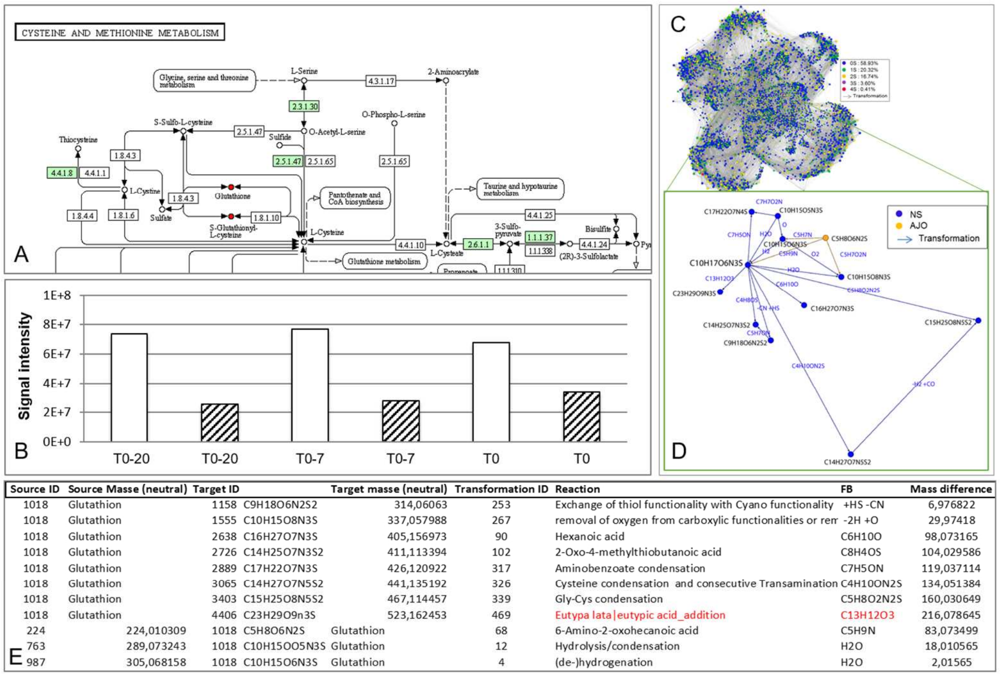


Fig 5. Possible transformations of the complete m/z data set.

228x149mm (150 x 150 DPI)



Source ID	Source Masse (neutral)	Target ID		Target masse (neutral)	Transformation ID	Reaction	FB	Mass difference
1018	Glutathion	1158	C9H18O6N2S2	314,06063	253	Exchange of thiol functionality with Cyano functionality	+HS -CN	6,976822
1018	Glutathion	1555	C10H15O8N3S	337,057988	267	removal of oxygen from carboxylic functionalities or rem	-2H +O	29,97418
1018	Glutathion	2638	C16H27O7N3S	405,156973	90	Hexanoic acid	C6H10O	98,073165
1018	Glutathion	2726	C14H25O7N3S2	411,113394	102	2-Oxo-4-methylthiobutanoic acid	C8H4OS	104,029586
1018	Glutathion	2889	C17H22O7N3S	426,120922	317	Aminobenzoate condensation	C7H5ON	119,037114
1018	Glutathion	3065	C14H27O7N5S2	441,135192	326	Cysteine condensation and consecutive Transamination	C4H10ON2S	134,051384
1018	Glutathion	3403	C15H25O8N5S2	467,114457	339	Gly-Cys condensation	C5H8O2N2S	160,030649
1018	Glutathion	4406	C23H29O9n3S	523,162453	469	Eutypa lata|eutypic acid_addition	C13H12O3	216,078645
224	224,010309	1018	C5H8O6N2S	Glutathion	68	6-Amino-2-oxohecanoic acid	C5H9N	83,073499
763	289,073243	1018	C10H15OO5N3S	Glutathion	12	Hydrolysis/condensation	H2O	18,010565
987	305,068158	1018	C10H15O6N3S	Glutathion	4	(de-)hydrogenation	H2O	2,01565

Fig 6. Focus on glutathione metabolism.

251x170mm (150 x 150 DPI)

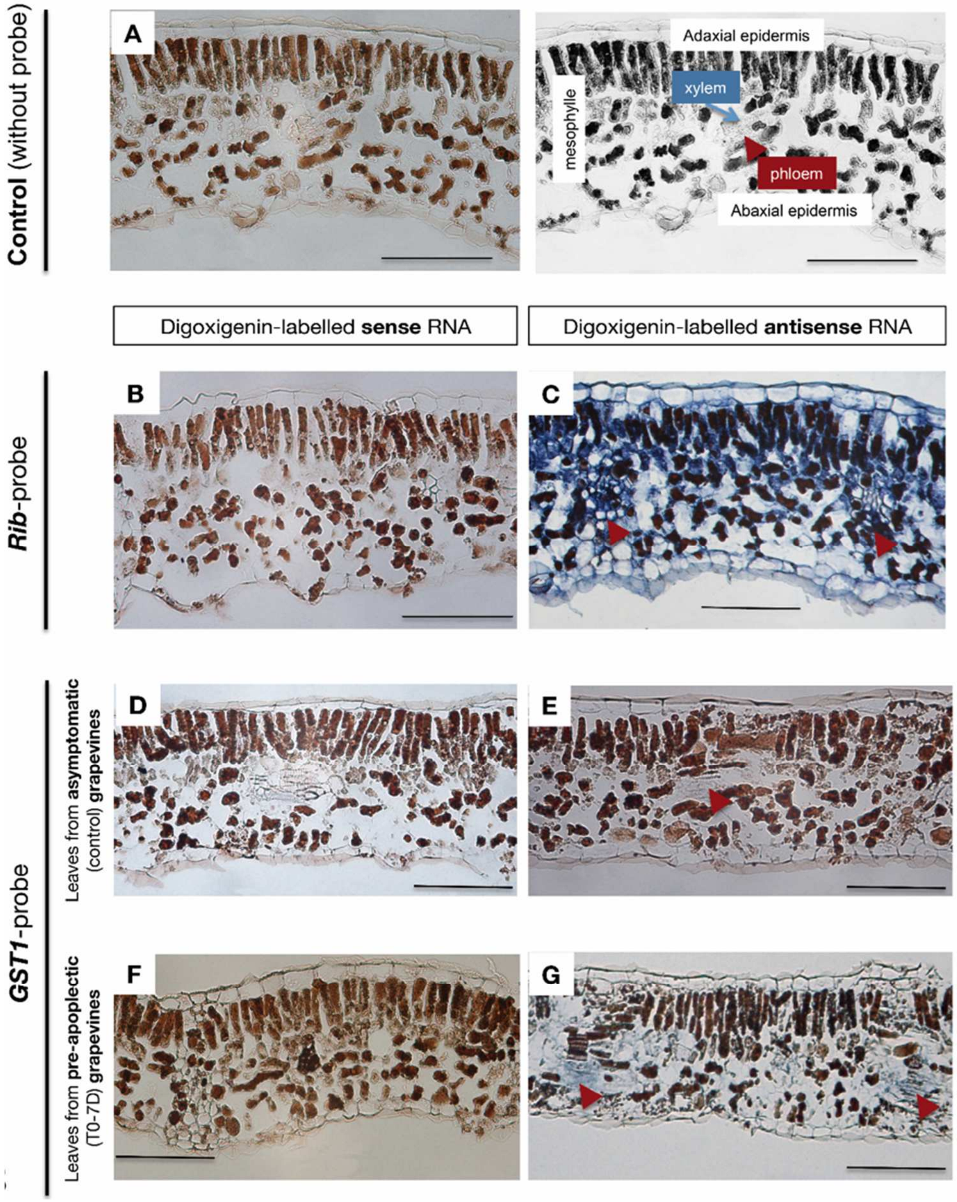


Fig 7. Visualization of VvGST1 expression in grapevine leaf tissues.

148x186mm (150 x 150 DPI)

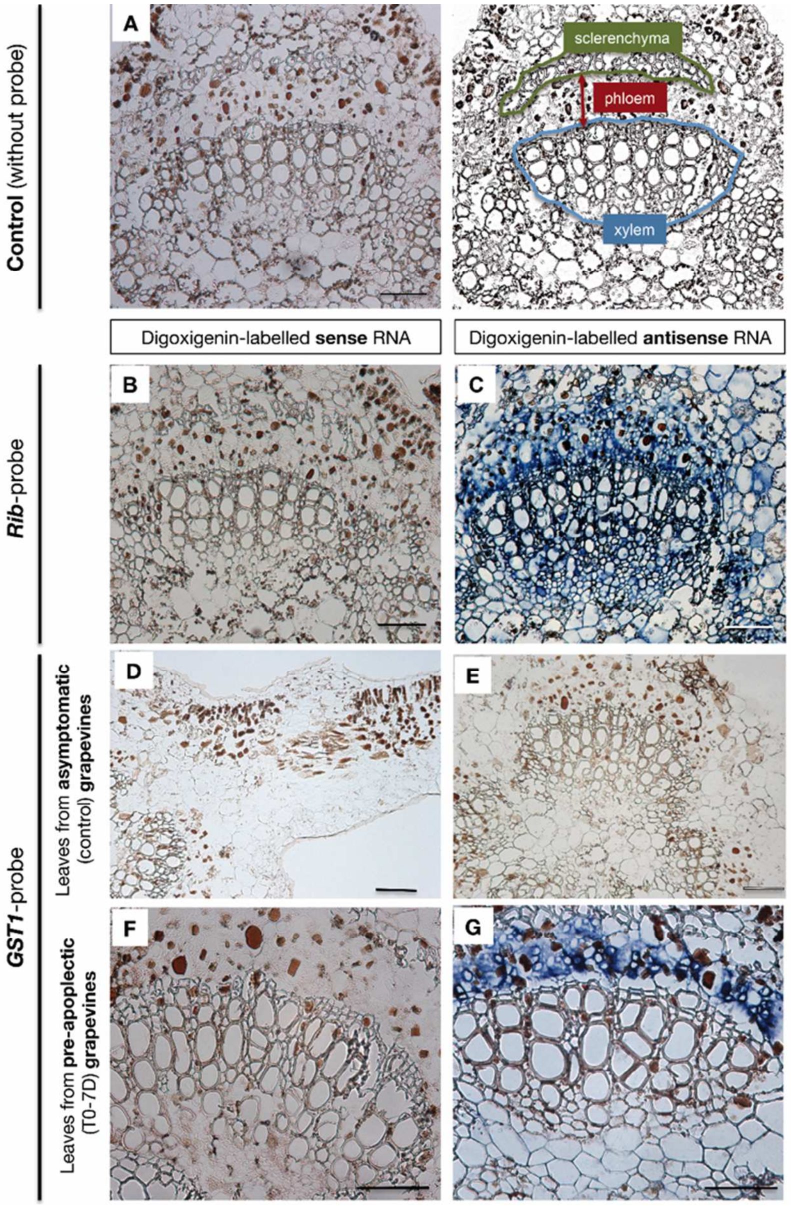


Fig 8. Visualization of VvGST1 expression in leaf primary bundles.

126x189mm (150 x 150 DPI)

Table 1: Primers of genes analyzed by real-time reverse-transcription polymerase chain reaction.

Genes		Primer sequences	Genbank or NCBI accession numbers
Housekeeping genes	*EF1-α* (elongation factor 1-α)	5'-GAACTGGGTGCTTGATAGGC-3' 5'-AACCAAAATATCCGGAGTAAAAGA-3'	GU585871
	60SRP (60S ribosomal protein L18)	5'-ATCTACCTCAAGCTCCTAGTC-3' 5'-CAATCTTGTCCTCCTTTCCT-3'	XM_002270599
Carbohydrate metabolism	*gluPuriT* (UTP-glucose-1-phosphate uridylyltransferase-like)	5'-AAATTGCACAGGTCCCAGATG3' 5'-TCAGCCTCCACAAGCCTCTT-3'	XM_002285070
	SucS2 (sucrose synthase 2)	5'-TGTGGGCTTCCTACATTTGCT-3' 5'-CCTTCTGGCATCGTTCAAAGA-3'	XM_002271494
	SucDHFla (Succinate dehydrogenase flavoprotein subunit 1)	5'-TGCCCGTGAAGATTTTACGAA-3' 5'-ATCGTCCAATGGGTTCATGTG-3'	XM_ 002269371
Amino acid metabolism	*SperS* (thermospermine synthase ACAULIS5-like)	5'-TGCAGGCATTTTTACCCACAA -3' 5'-AAGACGGAACATGAGCTGCAT-3'	XM_002281075
Lipid metabolism	*xylPS* (1-deoxy-d-xylulose 5-phosphate synthase)	5'- GCAGAAGCTGCCAGTGAAATT -3' 5'- GGCAAGCCATGAAAGTGACA -3'	XM_002277883
	jmjc7 (jmjC containing-domain protein 7-like))	5'- TGCCTTGGTGCAGTGTGAAT-3' 5'-AATCTCCCCAGCCTTGACTGT-3'	XM_0010646063
Hormonal regulation, signalisation	*Aux10A5* (auxin-induced protein 10A5)	5'-CCTTCATTCAGATCCTTGCTTTG-3' 5'-TCAAGAAAAGCATGTTCCTCACA-3'	XM_002271727
	Myochain (myosin-H heavy chain-like)	5'-AAAGAGCAACCACCCTGGATT-3' 5'TGTAGGTGTGGGAGACTCAAATACAG-3'	XM_002281579
	FboxWD40 (Fbox / WD 40 repeat-containing protein At2g52030-like))	5'-TAGACGGCGTGTTACGCATTT-3' 5'-GTCGGTTTTCTGGGAGGAAGT-3'	XM_002271652
Cellular processes	*CasK* (casein kinase I isoform delta-like)	5'-CTGCTGCTAGTTCTGGCATACG-3' 5'-CATGTGTGCATCGCTCACAATA-3'	XM_002284008
	HatpZ (V type H transporting ATPase subunit B)	5'- GCCTATGACACCCGCAACAT-3' 5'- GTACTGGTCGAGGGTCTTTGCT-3'	XM_002280255
Phenylpropanoid metabolism	*ShiKDH* (bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase)	5'-GTGGTTCCCCCTTAGCTGGTA-3' 5'-GCATAAGTGCGATTGGCAATC-3'	XM_002277359
	MYB4A (flavonoid-related R2R3 MYB 4a repressor)	5'-TCAGAATCAGCCCACCATACC-3' 5'-GGTATTCCCAAACTGCATGCA-3'	XM_002278186
Detoxication	*epoxHF* (epoxide hydrolase 2-like)	5'-TGCTCGTCTTGGCACTGAGA-3' 5'-TGAGCGCACCACTGTACCAT-3'	XM_003632333
	Hahl (haloacid dehalogenase hydrolase)	5'-CCCTCAGGATAGCCAACATCA-3' 5'-AGGTGCCAACCAGAACTGTGT-3'	XM_002267523
	GSTA (glutathion-S-transferase U9-like)	5'-AGGGGGCACTCCTTCCATTA-3' 5'-TGAACAAGGCCCACGAGTTT-3'	XM_003634217
	GSTB (glutathion-S-transferase)	5'-CCCCTGAAAATCTTGCTCTCGTT-3' 5'-AGAGCTTCAGGTCTCCGTCT-3'	XM_002262806
	GSTC (glutathion-S-transferase U9)	5'-GAAACGCCCCTCACTGATCT-3' 5'-ACAAGGCCATCAGCGTAACC-3'	XM_002269082
Detoxication	*GST1* (glutathion-S-transferase, tau form)	5'-TGCATGGAGGAGGAGTTCGT-3' 5'-CAAGGCTATATCCCCATTTTCTTC-3'	AY156048

Supplemental Table 2: Functional classification of the genes differentially expressed between control and diseased plants and whose expression is altered precociously and during apoplectic expression (at D-20 and/or D-7 and D0) and implicated in growth, replication, DNA repair, signalisation, hormonal regulation, transduction, transcription factor, proteins metabolism, cellular processes. Values indicating over- or down-expressed (ratio |2|) are highlighted in light or dark gray, respectively.

Fold Change				**Functional annotation**	**ID**	**Accession**
T0-20D	**T0-7Dvh**	**T0-7Dtg**	**T0**		**genoscope**	**Number (NCBI)**
Growth, replication and DNA damage repair						
30.7	**43.7**	**8.5**	**7.6**	minichromosome maintenance complex component 6 (MCM6),		XM_003634960
8.5	**4.2**	**11.9**	**9.5**	uncharacterized LOC100264054		XM_002283016
4.6	**16.8**	**19.0**	**15.7**	probable S-acyltransferase At3g51390-like	GSVIVT00011882001	XM_002270945
2.0	**2.4**	**20.5**	**15.1**	vinifera myosin-Vb-like		XM_002278992
2.3	**7.8**	**2.4**	**0.4**	mps one binder kinase activator-like 1, transcript variant 2	GSVIVT01026291001	XM_003631810
0.5	**4.0**	**23.4**	**8.8**	guanylate kinase-like, transcript variant 2	GSVIVT00019884001	XM_003631933
0.4	**14.2**	**46.1**	**36.4**	ATP-dependent RNA helicase dhx8-like		XM_002266606
0.4	**2.1**	**6.3**	**22.9**	homeobox-leucine zipper protein ATHB-13-like		XM_002276853
0.4	**2.1**	**6.6**	**3.2**	uncharacterized protein LOC100265514		XM_002281757
2.0	**5.0**	1.4	**29.4**	intron-binding protein aquarius-like		XM_002268267
5.4	**0.4**	1.2	**0.2**	methyl-CpG-binding domain-containing protein 4-like, (LOC100245968)		XM_002273034
2.4	0.5	**0.2**	**0.4**	DNA-directed RNA polymerase III subunit	GSVIVT01028933001	XM_002267628
0.5	**2.9**	1.6	**8.7**	WD repeat-containing protein 89 homolog-like	GSVIVT00027980001	XM_002264768
0.4	1.5	**139.0**	**25.9**	DNA repair protein RAD50-like (LOC100243413),		XM_002266629
0.8	**12.9**	**14.4**	**15.5**	histone H3-like, transcript variant 2	GSVIVT00008852001	XM_003631870
0.7	**9.7**	**21.9**	**43.5**	probable polygalacturonase-like		XM_002269001
1.0	**7.7**	**12.5**	**23.3**	histone H4-like, transcript variant 1		XM_002262809
1.0	**6.4**	**26.3**	**14.5**	putative DNA repair protein RAD23-3-like	GSVIVT01011907001	XM_002282316
0.6	**5.6**	**4.6**	**28.2**	PREDICTED: uncharacterized protein LOC100251250	GSVIVT00018369001	XM_002281489
0.8	**4.6**	**11.7**	**9.8**	adenylate kinase B-like	GSVIVT00017909001	XM_002283472
0.9	**3.9**	**3.1**	**10.1**	uncharacterized LOC100260605		XM_002282782
0.6	**3.5**	**18.1**	**3.1**	ankyrin repeat domain-containing protein 17-like		XM_002270388
0.8	**3.0**	**11.3**	**15.1**	putative RING-H2 finger protein ATL21A-like (LOC100241420),	GSVIVT00027027001	XM_002277351
1.2	**3.0**	**6.5**	**4.2**	AMP deaminase-like	GSVIVT01011185001	XM_002263270
0.7	**2.9**	**6.7**	**3.9**	PREDICTED: uncharacterized protein LOC100250482		XM_002284581
0.8	**2.8**	**7.1**	**7.1**	PREDICTED: uncharacterized protein LOC100260841 isoform 2		XM_002268890
1.4	**2.7**	**5.0**	**6.2**	PREDICTED: uncharacterized protein LOC100266794 isoform 1	GSVIVT00021270001	XM_002275143
1.5	**2.7**	**3.7**	**11.0**	protein gamma response 1-like		XM_003633526
0.6	**2.5**	**7.8**	**8.8**	uncharacterized LOC100265613	GSVIVT00024846001	XM_002285721
1.0	**2.4**	**3.8**	**8.3**	cellulose synthase-like protein G3	GSVIVT00006720001	XM_002265090
1.0	**2.3**	**9.8**	**10.5**	kinesin-like protein KIF22-like		XM_002271967
0.8	**2.2**	**3.8**	**7.3**	tubulin beta-1chain-like	GSVIVT00009147001	XM_002267344
1.1	**2.1**	**6.9**	**5.4**	PREDICTED: L-type lectin-domain containing receptor kinase IX.1	GSVIVT00008560001	XM_002265265
0.8	**2.1**	**6.3**	**4.5**	histone H2A.6-like	GSVIVT00027438001	XM_002282759
1.4	**2.0**	**2.0**	**7.4**	PREDICTED: uncharacterized protein LOC100247647		XM_002274932
0.9	**0.5**	**0.4**	**0.1**	uncharacterized LOC100257061		XM_002285579
1.3	**0.5**	**0.0**	**0.1**	cyclin-dependent kinase C-1-like (LOC100263383),		XM_002272393
0.8	**0.4**	**0.1**	**0.2**	probable pectinesterase/pectinesterase inhibitor 6-like		XR_078082
1.3	**0.4**	**0.0**	**0.0**	putative DNA repair and recombination protein RAD26-like	GSVIVT01020568001	XM_002274604
1.4	**0.3**	**0.0**	**0.0**	ribonucleases P/MRP protein subunit POP1-like		XM_003633219
1.6	**0.3**	**0.0**	**0.1**	uncharacterized LOC100249046		XM_002278976
1.0	2.0	**18.0**	**100.7**	Transposon	GSVIVT00036279001	
0.6	1.3	**12.9**	**9.5**	PREDICTED: Vitis vinifera replication factor C subunit 3	GSVIVT00015413001	XM_002285832
0.6	1.5	**11.9**	**5.4**	PREDICTED: Vitis vinifera uncharacterized (LOC100852985)	GSVIVT00016286001	XM_003634257
1.1	1.7	**9.9**	**2.6**	PREDICTED: Vitis vinifera kinesin-13A	GSVIVT00016749001	XM_002284557
0.8	1.5	**9.7**	**4.8**	PREDICTED: Vitis vinifera RING-H2 finger protein ATL54	GSVIVT00031255001	XM_003634369
0.7	1.5	**9.0**	**3.7**	PREDICTED: Vitis vinifera uncharacterized (LOC100263121)	GSVIVT00035144001	XM_010657619
0.9	1.0	**6.2**	**4.4**	PREDICTED: Vitis vinifera uncharacterized (LOC100247647)	GSVIVT00012114001	XM_010651384
0.7	1.5	**6.2**	**3.1**	PREDICTED: Vitis vinifera uncharacterized (LOC100249461)	GSVIVT00023645001	XM_002273352
0.8	1.7	**6.1**	**7.8**	PREDICTED: Vitis vinifera centrosomal protein of 63 kDa	GSVIVT00023930001	XM_010652507
0.6	1.8	**6.1**	**2.7**	PREDICTED: Vitis vinifera probable xyloglucan endotransglucosylase/hydro	GSVIVT00031402001	XM_002274118
0.6	1.0	**5.9**	**2.5**	PREDICTED: Vitis vinifera RRP15-like protein	GSVIVT00029062001	XM_010659195
1.1	1.3	**5.8**	**3.9**	PREDICTED: Vitis vinifera villin-1	GSVIVT00024116001	XM_010652608
0.9	1.7	**5.5**	**2.5**	PREDICTED: Vitis vinifera phragmoplast orienting kinesin-1	GSVIVT00019702001	XM_010651367
0.8	1.5	**4.5**	**6.2**	PREDICTED: Vitis vinifera Mre11 DNA repair/recombination protein	GSVIVT00027588001	XM_002281690
0.9	1.7	**3.9**	**2.7**	PREDICTED: Vitis vinifera uncharacterized (LOC100250156)	GSVIVT00024750001	XM_010653049
0.9	1.6	**3.9**	**2.1**	PREDICTED: Vitis vinifera uncharacterized (LOC100853685)	GSVIVT00028344001	XM_003632985
0.6	1.5	**3.0**	**9.5**	PREDICTED: Vitis vinifera DNA repair endonuclease UVH1	GSVIVT00010719001	XM_010648930
0.9	1.8	**3.0**	**7.7**	PREDICTED: Vitis vinifera elongator complex protein 4	GSVIVT00011637001	XM_010648137
0.8	1.5	**2.9**	**2.9**	PREDICTED: Vitis vinifera senescence-associated carboxylesterase 101-like	GSVIVT00033062001	XM_010651259

Supplemental Table 2 (continued)

Fold Change				Functional annotation	ID	Accession
T0-20D	T0-7Dvh	T0-7Dtg	T0		genoscope	Number (NCBI)
1.3	1.5	**2.8**	**2.3**	PREDICTED: Vitis vinifera la-related protein 1C	GSVIVT00014357001	XM_010648570
0.6	1.2	**2.7**	**2.9**	PREDICTED: Vitis vinifera uncharacterized (LOC100262931)	GSVIVT00021226001	XM_010665402
0.6	1.9	**2.6**	**4.4**	PREDICTED: Vitis vinifera kinetochore protein ndc80-like	GSVIVT00026619001	XM_002273906
0.9	1.8	**2.6**	**3.3**	PREDICTED: Vitis vinifera protein DA1	GSVIVT00025021001	XM_010666339
1.2	0.8	**2.5**	**4.4**	PREDICTED: Vitis vinifera GRIP and coiled-coil domain-containing protein 2	GSVIVT00000755001	XM_010650551
0.9	1.6	**2.5**	**3.2**	PREDICTED: Vitis vinifera probable RNA polymerase II transcription factor	GSVIVT00033473001	XM_002276021
0.9	1.6	**2.4**	**3.8**	PREDICTED: Vitis vinifera cyclin-dependent kinase G-2	GSVIVT00017899001	XM_010656984
1.5	0.9	**3.8**	**0.5**	PREDICTED: Vitis vinifera kinesin-13A	GSVIVT00019756001	XM_002271729
1.5	0.9	**3.8**	**0.5**	PREDICTED: Vitis vinifera kinesin-13A	GSVIVT00019756001	XM_002271729
0.8	0.9	**3.7**	**0.5**	PREDICTED: Vitis vinifera protein CHUP1, chloroplastic	GSVIVT00019730001	XM_010651400
0.6	1.4	**3.5**	**0.4**	PREDICTED: Vitis vinifera pumilio homolog 24	GSVIVT00033058001	XM_010651263
2.0	0.7	**0.3**	**2.2**	PREDICTED: Vitis vinifera DNA mismatch repair protein MSH3	GSVIVT00009202001	XM_010664189
0.7	0.9	**0.5**	**0.2**	PREDICTED: Vitis vinifera uncharacterized (LOC104879951)	GSVIVT00031053001	XM_010654716
1.1	0.9	**0.4**	**0.3**	PREDICTED: Vitis vinifera eukaryotic translation initiation factor 3 subunit K	GSVIVT00016373001	XM_002274950
0.9	0.7	**0.4**	**0.2**	PREDICTED: Vitis vinifera telomerase Cajal body protein 1	GSVIVT00012724001	XM_002277010
0.9	0.6	**0.4**	**0.1**	PREDICTED: Vitis vinifera replication factor C subunit 3	GSVIVT00024904001	XM_002263177
1.1	0.8	**0.3**	**0.4**	PREDICTED: Vitis vinifera uncharacterized (LOC100264366)	GSVIVT00014457001	XM_010666487
0.8	0.9	**0.3**	**0.3**	PREDICTED: Vitis vinifera rhodanese-like domain-containing protein 4, chlo	GSVIVT00027006001	XM_010663599
1.6	0.7	**0.3**	**0.3**	PREDICTED: Vitis vinifera nuclear pore complex protein NUP58-like	GSVIVT00008483001	XM_003635588
1.2	0.7	**0.3**	**0.1**	PREDICTED: Vitis vinifera deoxycytidylate deaminase	GSVIVT00017944001	XM_002283781
0.9	0.7	**0.3**	**0.1**	PREDICTED: Vitis vinifera actin-related protein 2/3 complex subunit 5-like	GSVIVT00019114001	XM_003633846
1.1	0.5	**0.3**	**0.0**	PREDICTED: Vitis vinifera ankyrin-2-like	GSVIVT00033277001	XM_010657416
1.3	0.8	**0.2**	**0.5**	PREDICTED: Vitis vinifera polygalacturonase	GSVIVT00028122001	XM_002266063
0.6	1.7	**0.2**	**0.4**	PREDICTED: Vitis vinifera UDP-D-xylose:L-fucose alpha-1,3-D-xylosyltransf	GSVIVT00014656001	XM_002283185
1.4	0.7	**0.2**	**0.2**	PREDICTED: Vitis vinifera adenylyl-sulfate kinase 3-like	GSVIVT00019663001	XM_002265482
1.1	0.6	**0.1**	**0.3**	PREDICTED: Vitis vinifera probable xyloglucan glycosyltransferase 5	GSVIVT00000743001	XM_002274363
1.5	0.6	**0.1**	**0.2**	PREDICTED: Vitis vinifera uncharacterized (LOC104880805)	GSVIVT00029789001	XM_010658622
0.7	0.6	**0.1**	**0.2**	PREDICTED: Vitis vinifera regulator of nonsense transcripts UPF3	GSVIVT00035287001	XM_010659667
0.6	1.2	**0.1**	**0.1**	PREDICTED: Vitis vinifera elongator complex protein 2	GSVIVT00030407001	XM_002282904
0.7	1.2	**7.0**	1.0	PREDICTED: Vitis vinifera UDP-D-xylose:L-fucose alpha-1,3-D-xylosyltransf	GSVIVT00018144001	XM_002273119
0.7	1.3	**6.5**	1.1	PREDICTED: Vitis vinifera exocyst complex component SEC8	GSVIVT00018143001	XM_010660069
0.9	1.1	**4.4**	1.9	PREDICTED: Vitis vinifera protein ACCUMULATION AND REPLICATION	GSVIVT00035128001	XM_010656659
0.8	1.7	**4.1**	0.9	PREDICTED: Vitis vinifera N-acetyltransferase 9-like protein	GSVIVT00029152001	XM_010659117
0.8	1.2	**4.0**	1.9	PREDICTED: Vitis vinifera protein misato homolog 1	GSVIVT00009705001	XM_010654349
0.7	1.5	**4.0**	1.3	Retrotransposon gag protein	GSVIVT00019016001	
0.7	1.4	**3.8**	1.0	PREDICTED: Vitis vinifera mitochondrial inner membrane protease ATP23	GSVIVT00020602001	XM_002269076
0.5	1.5	**3.4**	0.9	PREDICTED: Vitis vinifera formin-like protein 4	GSVIVT00028920001	XM_010654581
0.8	1.5	**3.3**	1.0	PREDICTED: Vitis vinifera putative pectinesterase/pectinesterase inhibitor 4	GSVIVT00028250001	XM_010657774
0.8	1.5	**3.3**	1.0	PREDICTED: Vitis vinifera putative pectinesterase/pectinesterase inhibitor 4	GSVIVT00028250001	XM_010657774
1.0	1.2	**3.2**	0.7	PREDICTED: Vitis vinifera polygalacturonase QRT3	GSVIVT00030119001	XM_010650873
0.7	1.4	**3.1**	1.0	PREDICTED: Vitis vinifera histone acetyltransferase GCN5-like	GSVIVT00023828001	XM_002275110
0.6	1.6	**3.0**	1.4	Retrotransposion protein	GSVIVT00025150001	
0.6	1.4	**2.8**	1.2	PREDICTED: Vitis vinifera actin-7	GSVIVT00025385001	XM_002282480
1.2	1.3	**2.3**	0.8	PREDICTED: Vitis vinifera mannosyl-oligosaccharide 1,2-alpha-mannosidas	GSVIVT00008673001	XM_010657347
0.8	1.7	**2.2**	0.6	PREDICTED: Vitis vinifera biotin carboxyl carrier protein of acetyl-CoA carb	GSVIVT00026587001	XM_002278115
0.7	1.3	**2.2**	0.7	PREDICTED: Vitis vinifera wee1-like protein kinase	GSVIVT00023546001	XR_786155
0.7	1.5	**2.1**	0.8	PREDICTED: Vitis vinifera tether containing UBX domain for GLUT4	GSVIVT00020575001	XM_002266616
0.8	1.9	**0.5**	0.6	Vitis vinifera partial rpl2 gene for putative ribosomal protein L2	GSVIVT00014647001	AJ441290
1.5	1.2	**0.3**	1.0	PREDICTED: Vitis vinifera expansin-like	GSVIVT00029445001	XM_002280264
1.0	1.4	**0.2**	1.4	PREDICTED: Vitis vinifera uncharacterized (LOC100255472)	GSVIVT00025573001	XM_010655489
1.1	1.4	0.9	**9.2**	PREDICTED: Vitis vinifera structural maintenance of chromosomes protein	GSVIVT00029974001	XM_002269818
0.8	1.9	1.1	**6.3**	PREDICTED: Vitis vinifera pentatricopeptide repeat-containing protein At4g	GSVIVT00032631001	XM_003632946
0.8	1.7	1.3	**4.0**	PREDICTED: Vitis vinifera kelch domain-containing protein 3	GSVIVT00022593001	XM_010665160
0.9	1.7	0.7	**3.8**	PREDICTED: Vitis vinifera probable xyloglucan endotransglucosylase/hydro	GSVIVT00031397001	XM_002270380
0.7	1.9	0.8	**3.7**	Transposon - integrase		
0.8	1.6	1.0	**3.3**	PREDICTED: Vitis vinifera uncharacterized LOC100253096	GSVIVT00018177001	XM_002273014
1.2	1.4	1.7	**3.2**	PREDICTED: Vitis vinifera protein MEI2-like 4	GSVIVT00018040001	XM_010665500
0.8	1.1	1.4	**2.9**	Retrotransposon protein, unclassified	GSVIVT00017639001	
0.8	0.9	1.4	**2.9**	PREDICTED: Vitis vinifera GLABRA2 expression modulator	GSVIVT00011458001	XM_002263437
0.8	1.4	1.0	**2.8**	PREDICTED: Vitis vinifera uncharacterized CRM domain-containing protein	GSVIVT00001969001	XM_010652295
1.1	1.3	0.9	**2.5**	PREDICTED: Vitis vinifera myosin-1	GSVIVT00003146001	XM_010657729

Supplemental Table 2 (continued)

Fold Change				Functional annotation	ID	Accession
T0-20D	T0-7Dvh	T0-7Dtg	T0		genoscope	Number (NCBI)
1.1	1.5	1.2	**2.5**	PREDICTED : Pectinesterase inhibitor	GSVIVT00033172001	
0.8	1.9	1.2	**2.3**	PREDICTED: Vitis vinifera LIM domain-containing protein WLIM 2b	GSVIVT00018297001	XM_010660182
1.3	1.7	1.7	**2.2**	PREDICTED: Vitis vinifera DNA (cytosine-5)-methyltransferase DRM 2	GSVIVT00019681001	XM_010651351
0.9	1.5	0.7	**2.2**	PREDICTED: Vitis vinifera translin	GSVIVT00023218001	XM_002281872
0.6	1.8	1.2	**2.2**	PREDICTED: Vitis vinifera probable 28S rRNA (cytosine-C(5))-methyltransfe	GSVIVT00033387001	XM_002266076
1.8	0.6	1.2	**0.4**	PREDICTED: Vitis vinifera polyadenylate-binding protein RBP45-like	GSVIVT00011496001	XM_002280565
1.4	1.0	1.1	**0.4**	PREDICTED: Vitis vinifera probable polygalacturonase	GSVIVT00037720001	XM_002273633
1.4	0.6	0.6	**0.4**	PREDICTED: Vitis vinifera uncharacterized LOC100242981	GSVIVT00034123001	XR_786537
0.9	1.5	0.9	**0.4**	PREDICTED: Vitis vinifera probable serine incorporator	GSVIVT00025214001	XM_010656831
0.8	1.1	1.1	**0.4**	PREDICTED: Vitis vinifera DNA replication licensing factor MCM3 homolog	GSVIVT00003433001	XM_010657342
0.7	1.3	1.8	**0.4**	PREDICTED: Vitis vinifera uncharacterized LOC100262931	GSVIVT00033238001	XM_010665402
1.1	0.7	0.8	**0.3**	PREDICTED: Vitis vinifera chromatin assembly factor 1subunit FAS1	GSVIVT00012871001	XM_010648823
1.1	0.6	0.5	**0.3**	PREDICTED: Vitis vinifera ribonucleoside-diphosphate reductase small chai	GSVIVT00019890001	XM_002279907
0.9	1.1	1.3	**0.3**	PREDICTED: Vitis vinifera xyloglucan galactosyltransferase KATAMARI1ho	GSVIVT00033532001	XM_003632384
0.8	0.8	0.7	**0.3**	PREDICTED: Vitis vinifera uncharacterized LOC100267366	GSVIVT00024524001	XM_010653154
0.7	1.2	1.9	**0.3**	PREDICTED: Vitis vinifera protein PHR1-LIKE 1	GSVIVT00025352001	XM_002278639
0.7	1.0	1.5	**0.3**	PREDICTED: Vitis vinifera putative UDP-rhamnose:rhamnosyltransferase 1	GSVIVT00011805001	XM_002273927
1.1	0.7	0.7	**0.2**	PREDICTED: Vitis vinifera helicase and polymerase-containing protein TEB	GSVIVT00032488001	XM_010650234
0.9	0.9	0.7	**0.2**	PREDICTED: Vitis vinifera wall-associated receptor kinase 2-like	GSVIVT00015471001	XM_010665406
0.9	0.6	0.8	**0.2**	PREDICTED: Vitis vinifera UDP-N-acetylglucosamine transferase subunit A	GSVIVT00022866001	XM_010661525
0.8	0.9	0.6	**0.2**	PREDICTED: Vitis vinifera transcription factor JUNGBRUNNEN 1	GSVIVT00025717001	XM_002283215
0.7	1.0	1.1	**0.2**	PREDICTED: Vitis vinifera NAC domain-containing protein 7	GSVIVT00029905001	XM_010663928
0.6	0.8	0.5	**0.2**	PREDICTED: Vitis vinifera DNA-directed RNA polymerase I subunit RPA2	GSVIVT00002001001	XM_010660782
0.9	1.0	1.6	**0.2**	Retrotransposon *gag -pol precursor* pseudogene.	GSVIVT00022426001	
1.2	0.9	0.6	**0.1**	Zinc finger (C2H2 type) family	GSVIVT00016268001	
0.7	0.9	0.7	**0.1**	PREDICTED: Vitis vinifera uncharacterized LOC104880805	GSVIVT00032650001	XM_010658622
Signalisation, hormonal regulation, transduction, transcription factor						
9.2	**9.3**	**11.2**	**2.1**	myosin-H heavy chain-like		XM_002281579
3.4	**65.4**	**77.9**	**34.6**	embryogenesis-associated protein EMB8-like	GSVIVT00000521001	XM_002280146
2.8	**10.9**	**0.3**	**0.3**	squamosa promoter-binding-like protein 8, transcript variant 2	GSVIVT00019158001	XM_003633858
0.4	**9.5**	**22.6**	**13.7**	GATA transcription factor 18-like		XM_002266628
0.5	**3.0**	**12.2**	**12.1**	probable receptor-like protein kinase At1g80640-like		XM_002285350
0.4	**2.3**	**21.1**	**17.6**	auxin-induced protein PCNT115-like, transcript variant 2	GSVIVT00033541001	XM_003632000
0.3	**2.3**	**13.3**	**25.9**	uncharacterized LOC100258132		XM_002269459
0.4	**2.3**	**7.0**	**2.9**	two-component response regulator-like APRR2	GSVIVT00015824001	XM_002279114
0.3	**2.9**	**9.3**	**0.5**	ethylene-responsive transcription factor RAP2-11-like	GSVIVT00024804001	XM_002283591
0.0	**0.0**	**0.1**	**0.1**	DUF246 domain-containing protein At1g04910-like	GSVIVT01034027001	XM_002277113
4.2	1.2	**51.8**	**51.2**	F-box/WD-40 repeat-containing protein At3g52030-like		XM_002271652
3.5	0.6	**0.2**	**0.1**	NEDD8-conjugating enzyme Ubc12-like		XM_003631580
3.3	0.6	**0.2**	**0.1**	hypothetical protein VITISV_004773		XM_002272888
2.2	1.1	**0.1**	**0.2**	auxin response factor 19-like		XM_002276601
0.2	1.1	**2.3**	**0.1**	eukaryotic translation initiation factor 3 subunit I-like	GSVIVT00030682001	XM_002285245
1.0	**10.9**	**176.9**	**45.6**	PREDICTED: bidirectional sugar transporter SWEET2	GSVIVT00027922001	XM_002285600
1.6	**8.3**	**9.4**	**11.8**	uncharacterized protein LOC100259554	GSVIVT01017826001	XM_002277726
0.9	**5.7**	**10.7**	**12.7**	zinc finger CCCH domain-containing protein 62-like		XM_002262791
0.6	**4.5**	**2.1**	**15.1**	PRA1family protein F2-like		XM_002279736
0.9	**4.2**	**7.4**	**4.4**	bHLH-like DNA binding protein (MYC1)		XM_002277472
0.7	**3.8**	**9.2**	**5.7**	ethylene-responsive transcription factor ERF021-like	GSVIVT01036389001	XM_002275835
0.9	**2.9**	**4.3**	**8.7**	putative ETHYLENE INSENSITIVE 3-like 4 protein-like		XM_002262623
0.5	**2.8**	**21.7**	**5.4**	translation initiation factor IF-2-like		XM_002279454
1.0	**2.6**	**9.0**	**7.8**	transcription factor bHLH25-like		XM_002263010
0.8	**2.1**	**3.8**	**15.0**	auxin-induced protein 5NG4		XM_002284416
1.5	0.5	**0.3**	**0.2**	PREDICTED: Vitis vinifera abhydrolase domain-containing protein 3	GSVIVT00035401001	XM_002263734
1.3	**0.5**	**0.2**	**0.1**	uncharacterized protein LOC100248606		XM_002268051
1.2	**0.5**	**0.2**	**0.1**	myb-related protein 330-like		XM_002268423
0.8	**0.4**	**0.4**	**0.2**	PREDICTED: flotillin-like protein 4	GSVIVT00032735001	XM_002283041
1.1	**0.4**	**0.2**	**0.2**	PREDICTED: auxin-induced protein 10A5	GSVIVT00025082001	XM_002271727
1.0	**0.4**	**0.1**	**0.1**	eukaryotic initiation factor 4A-2-like	GSVIVT00034135001	XM_002277667
1.8	**0.4**	**0.0**	**0.1**	LOB domain-containing protein 11-like	GSVIVT00024480001	XM_002282034
1.6	**0.4**	**0.0**	**0.1**	PREDICTED: ethylene-responsive transcription factor ABR1	GSVIVT00019350001	XM_002278190
1.8	**0.4**	**0.0**	**0.1**	LOB domain-containing protein 11-like	GSVIVT00024480001	XM_002282034

Supplemental Table 2 (continued)

Fold Change				Functional annotation	ID	Accession
T0-20D	T0-7Dvh	T0-7Dtg	T0		genoscope	Number (NCBI)
1.6	**0.4**	**0.0**	**0.1**	uncharacterized LOC100262406		XM_002264761
0.6	1.6	**91.4**	**108.0**	PREDICTED: Vitis vinifera F-box/LRR-repeat protein	GSVIVT00025001001	XM_002283859
0.8	0.6	**53.3**	**7.9**	PREDICTED: Vitis vinifera F-box protein SKIP31	GSVIVT00001173001	XM_002270845
0.6	1.6	**16.5**	**6.9**	PREDICTED: Vitis vinifera F-box protein SKIP22-like	GSVIVT00038619001	XM_002276120
0.8	1.8	**6.6**	**2.5**	PREDICTED: Vitis vinifera transcription factor bHLH80-like	GSVIVT00001847001	XM_002271354
0.8	1.5	**5.8**	**4.7**	PREDICTED: Vitis vinifera ethylene-responsive transcription factor ERF105	GSVIVT00032652001	XM_002281876
0.9	1.4	**5.8**	**2.6**	PREDICTED: Vitis vinifera transcription factor bHLH3	GSVIVT00023884001	XM_002282548
1.3	1.5	**4.8**	**2.9**	PREDICTED: Vitis vinifera O-glucosyltransferase rumi homolog	GSVIVT00000391001	XM_010664454
0.6	1.8	**4.6**	**5.8**	PREDICTED: Vitis vinifera squamosa promoter-binding-like protein 1	GSVIVT00028195001	XM_010654006
1.1	1.8	**4.5**	**3.6**	PREDICTED: Vitis vinifera general transcription factor IIE subunit 2	GSVIVT00025001001	XM_002283521
1.0	1.2	**4.4**	**2.9**	PREDICTED: Vitis vinifera uncharacterized (LOC100266659)	GSVIVT00011146001	XM_010648067
0.8	2.0	**4.2**	**3.0**	PREDICTED: Vitis vinifera transcription initiation factor TFIID subunit 1	GSVIVT00008042001	XM_010658662
1.9	2.0	**4.2**	**5.6**	PREDICTED: Vitis vinifera uncharacterized (LOC100243147)	GSVIVT00022100001	XM_010653438
0.6	1.3	**4.0**	**2.5**	PREDICTED: Vitis vinifera probable ADP-ribosylation factor GTPase-activa	GSVIVT00027600001	XM_003634640
0.6	1.6	**3.2**	**4.2**	PREDICTED: Vitis vinifera phytochrome A-associated F-box protein	GSVIVT00027993001	XM_002266123
0.9	1.8	**3.1**	**6.7**	PREDICTED: Vitis vinifera protein unc-45 homolog A	GSVIVT00012842001	XM_002266009
0.9	1.6	**3.1**	**5.8**	PREDICTED: Vitis vinifera protein phosphatase 2C 16	GSVIVT00016669001	XM_010656199
0.8	1.1	**2.5**	**2.1**	PREDICTED: Vitis vinifera golgin subfamily B member 1-like	GSVIVT00000573001	XM_010663504
0.8	1.7	**2.4**	**7.6**	PREDICTED: Vitis vinifera GTP-binding protein ERG	GSVIVT00030112001	XM_002274185
1.2	1.1	**2.4**	**2.4**	PREDICTED: Vitis vinifera calcium-binding protein PBP1-like	GSVIVT00015817001	XM_002283267
0.7	0.9	**2.3**	**8.7**	PREDICTED: Vitis vinifera putative pentatricopeptide repeat-containing prot	GSVIVT00024893001	XM_002265990
0.9	1.8	**2.3**	**8.2**	PREDICTED: Vitis vinifera probable protein phosphatase 2C 33	GSVIVT00025063001	XM_002277357
0.5	1.1	**2.3**	**5.2**	PREDICTED: Vitis vinifera ethylene-responsive transcription factor SHINE 2	GSVIVT00032652001	XM_002285071
0.8	1.7	**2.3**	**3.5**	PREDICTED: Vitis vinifera putative dual specificity protein phosphatase DSF	GSVIVT00031649001	XM_010663081
0.8	1.3	**2.3**	**2.5**	PREDICTED: Vitis vinifera uncharacterized (LOC100263199)	GSVIVT00009688001	XM_010648613
0.7	0.9	**2.1**	**0.2**	PREDICTED: Vitis vinifera transcription factor MYC4	GSVIVT00000514001	XM_002279937
1.0	1.9	**2.0**	**7.5**	PREDICTED: Vitis vinifera probable F-box protein	GSVIVT00003940001	XM_002266444
0.9	1.8	**3.7**	**0.4**	PREDICTED: Vitis vinifera ammonium transporter 1 member 1		
0.7	0.8	**3.6**	**0.5**	PREDICTED: Vitis vinifera LOB domain-containing protein 1-like	GSVIVT00008636001	XM_002265506
0.7	1.1	**3.0**	**0.3**	PREDICTED: Vitis vinifera squamosa promoter-binding-like protein 8	GSVIVT00019158001	XM_003633858
0.9	1.0	**2.7**	**0.5**	PREDICTED: Vitis vinifera probable indole-3-pyruvate monooxygenase YUC	GSVIVT00020401001	XM_002282612
0.8	1.3	**2.6**	**0.5**	PREDICTED: Vitis vinifera probable serine/threonine-protein kinase WNK4	GSVIVT00023951001	XM_002268264
0.8	1.4	**2.5**	**0.5**	PREDICTED: Vitis vinifera polycomb group protein EMBRYONIC FLOWER	GSVIVT00014223001	XM_010663942
0.9	1.0	**2.3**	**0.5**	PREDICTED: Vitis vinifera probable protein phosphatase 2C 15	GSVIVT00030385001	XM_010646121
1.0	1.1	**2.3**	**0.5**	PREDICTED: Vitis vinifera BEL1-like homeodomain protein 3	GSVIVT00023896001	XM_003631538
1.0	0.8	**2.3**	**0.4**	PREDICTED: Vitis vinifera Aux/IAA protein	GSVIVT00012510001	XM_010665767
1.2	0.7	**0.1**	**5.5**	PREDICTED: Vitis vinifera F-box protein SKIP16-like	GSVIVT00010294001	XR_785899
0.9	0.8	**0.0**	**34.5**	PREDICTED: Vitis vinifera dof zinc finger protein DOF5.1	GSVIVT00018482001	XM_002269995
1.3	0.9	**0.5**	**0.3**	PREDICTED: Vitis vinifera SWR1-complex protein 4	GSVIVT00028159001	XM_010653983
1.8	0.5	**0.5**	**0.2**	PREDICTED: Vitis vinifera eukaryotic translation initiation factor NCBP	GSVIVT00025466001	XM_002281661
1.5	0.7	**0.4**	**0.4**	PREDICTED: Vitis vinifera agamous-like MADS-box protein AGL12	GSVIVT00021903001	XM_002278203
1.5	0.7	**0.4**	**0.4**	PREDICTED: Vitis vinifera agamous-like MADS-box protein AGL12	GSVIVT00012221001	XM_002278203
1.0	0.6	**0.4**	**0.2**	PREDICTED: Vitis vinifera uncharacterized (LOC100248098)	GSVIVT00026485001	XR_139826
0.6	0.9	**0.3**	**0.4**	PREDICTED: Vitis vinifera serine/threonine protein phosphatase 2A 57 kDa	GSVIVT00032527001	XM_010650251
1.4	0.7	**0.3**	**0.3**	PREDICTED: Vitis vinifera uncharacterized (LOC100258629)	GSVIVT00028864001	XM_002265724
1.3	0.7	**0.3**	**0.3**	PREDICTED: Vitis vinifera uncharacterized (LOC100253058)	GSVIVT00021520001	XM_010658593
1.0	0.7	**0.3**	**0.3**	PREDICTED: Vitis vinifera zinc finger CCCH domain-containing protein 24	GSVIVT00024526001	XM_002282278
0.9	0.6	**0.3**	**0.1**	PREDICTED: Vitis vinifera protein IQ-DOMAIN 14	GSVIVT00008074001	XM_002265424
1.5	0.8	**0.2**	**0.4**	PREDICTED: Vitis vinifera uncharacterized (LOC100265991) / MYB family tra	GSVIVT00024052001	XM_002268019
0.9	0.8	**0.2**	**0.3**	PREDICTED: Vitis vinifera probable protein phosphatase 2C 59	GSVIVT00008801001	XM_010650484
1.3	0.7	**0.2**	**0.3**	PREDICTED: Vitis vinifera probable BOI-related E3 ubiquitin-protein ligase 2		XM_010666262
1.3	0.7	**0.2**	**0.2**	PREDICTED: Vitis vinifera transcription initiation factor TFIID subunit 6	GSVIVT00025841001	XM_002264254
1.1	0.7	**0.2**	**0.2**	PREDICTED: Vitis vinifera expansin-A4	GSVIVT00000596001	XM_002283322
1.1	0.6	**0.2**	**0.1**	PREDICTED: Vitis vinifera homeobox-leucine zipper protein HAT4	GSVIVT00012221001	XM_002263157
1.2	0.7	**0.2**	**0.1**	PREDICTED: Vitis vinifera KH domain-containing protein	GSVIVT00015027001	XM_002283555
1.1	0.8	**0.1**	**0.2**	PREDICTED: Vitis vinifera 1-aminocyclopropane-1-carboxylate oxidase (ACC	GSVIVT00021584001	XM_003632599
1.9	1.0	**0.1**	**0.2**	PREDICTED: Vitis vinifera MADS-box protein SVP	GSVIVT00008993001	XM_010648493
1.7	0.9	**0.1**	**0.1**	PREDICTED: Vitis vinifera inactive protein kinase SELMODRAFT_444075	GSVIVT00034194001	XM_010656246
0.5	0.6	**0.0**	**0.1**	PREDICTED: Vitis vinifera trihelix transcription factor GT-3b	GSVIVT00007624001	XR_786356
0.5	0.6	**0.0**	**0.1**	PREDICTED: Vitis vinifera trihelix transcription factor GT-3b	GSVIVT00007624001	XR_786356
0.9	1.9	**7.0**	1.9	PREDICTED: Vitis vinifera primary amine oxidase	GSVIVT00019977001	XM_002278208

Supplemental Table 2 (continued)

Fold Change				Functional annotation	ID	Accession
T0-20D	T0-7Dvh	T0-7Dtg	T0		genoscope	Number (NCBI)
0.8	1.3	**6.9**	1.0	PREDICTED: Vitis vinifera homeobox-leucine zipper protein HAT22	GSVIVT00011041001	XM_010649008
1.6	0.8	**6.2**	1.0	PREDICTED: Vitis vinifera serine/threonine-protein kinase EDR1	GSVIVT00017808001	XM_003634237
1.6	0.8	**6.2**	1.0	PREDICTED: Vitis vinifera serine/threonine-protein kinase EDR1	GSVIVT00017808001	XM_003634237
1.0	0.6	**5.9**	1.4	PREDICTED: Vitis vinifera transcription factor bHLH36	GSVIVT00008249001	XM_003635317
0.9	1.2	**5.2**	0.5	PREDICTED: Vitis vinifera trihelix transcription factor ASIL1-like	GSVIVT00025282001	XM_002264740
0.7	1.6	**5.1**	0.5	PREDICTED: Vitis vinifera transcriptional activator Myb	GSVIVT00014316001	XM_002279243
1.1	1.2	**4.9**	0.6	PREDICTED: Vitis vinifera guanine nucleotide-binding protein subunit beta-li	GSVIVT00017791001	XM_002281243
1.0	1.9	**4.8**	0.5	PREDICTED: Vitis vinifera lysine-specific histone demethylase 1 homolog 3	GSVIVT00014490001	XR_788316
0.7	1.3	**4.8**	1.7	PREDICTED: Vitis vinifera sacsin	GSVIVT00037657001	XM_010650117
0.8	0.9	**4.5**	1.9	PREDICTED: Vitis vinifera WD repeat-containing protein 61	GSVIVT00001149001	XM_002280687
0.8	1.6	**4.2**	0.5	PREDICTED: Vitis vinifera myb-related protein 3R-1-like		XM_002281492
0.7	1.9	**4.0**	3.8	PREDICTED: Vitis vinifera serine/threonine-protein kinase pakB	GSVIVT00035977001	XM_010649265
1.2	1.5	**4.0**	0.9	PREDICTED: Vitis vinifera transcription elongation factor SPT6	GSVIVT00008954001	XM_010655357
0.8	1.4	**3.7**	1.1	PREDICTED: Vitis vinifera uncharacterized (LOC100267848)	GSVIVT00014864001	XM_010666257
0.8	1.3	**3.4**	0.8	PREDICTED: Vitis vinifera PRA1 family protein F2-like	GSVIVT00023862001	XM_002279736
1.1	1.3	**3.2**	0.6	PREDICTED: Vitis vinifera putative zinc finger protein	GSVIVT00029230001	XM_002272888
0.7	1.9	**3.0**	1.6	PREDICTED: Vitis vinifera ras-related protein RABH1e	GSVIVT00012066001	XM_002271184
0.6	1.3	**3.2**	0.7	PREDICTED: Vitis vinifera uncharacterized (LOC100255258)	GSVIVT00008635001	XM_010663660
1.1	1.4	**3.0**	0.6	PREDICTED: Vitis vinifera TIMELESS-interacting protein	GSVIVT00021265001	XM_010656341
0.7	1.4	**2.9**	0.9	PREDICTED: Vitis vinifera zinc finger protein NUTCRACKER	GSVIVT00023802001	XM_010647827
1.0	0.7	**2.8**	1.2	PREDICTED: Vitis vinifera auxin-induced protein X15-like	GSVIVT00036007001	XM_003631505
1.2	0.9	**2.5**	0.5	PREDICTED: Vitis vinifera BTB/POZ domain-containing protein	GSVIVT00029147001	XM_002270766
0.9	1.2	**2.4**	0.8	PREDICTED: Vitis vinifera HVA22-like protein j	GSVIVT00021528001	XM_002281002
1.0	1.3	**2.2**	0.6	PREDICTED: Vitis vinifera CCR4-NOT transcription complex subunit 1-like	GSVIVT00029978001	XM_010663024
0.6	1.2	**0.4**	1.0	PREDICTED: Vitis vinifera F-box/kelch-repeat protein SKIP11-like	GSVIVT00000121001	XM_010653935
1.2	0.9	**0.3**	1.3	PREDICTED: Vitis vinifera auxin-induced protein X15	GSVIVT00035991001	XM_010649207
1.2	0.9	**0.3**	1.3	PREDICTED: Vitis vinifera auxin-induced protein X15	GSVIVT00035991001	XM_010649207
1.4	0.5	**0.2**	1.3	PREDICTED: Vitis vinifera zinc finger CCCH domain-containing protein 14	GSVIVT00025374001	XM_002279035
0.7	0.9	0.9	**9.3**	PREDICTED: Vitis vinifera equilibrative nucleotide transporter 3-like	GSVIVT00011005001	XM_010648063
1.6	2.0	0.9	**4.6**	PREDICTED: Vitis vinifera HD domain-containing protein 2	GSVIVT00030235001	XR_785531
0.8	1.1	1.0	**3.1**	PREDICTED: Vitis vinifera protein ROOT HAIR DEFECTIVE 3 homolog 2	GSVIVT00035518001	XM_010647065
1.0	1.4	0.7	**3.1**	PREDICTED: Vitis vinifera probable protein phosphatase 2C 49	GSVIVT00028179001	XM_002279654
0.8	1.8	0.6	**3.1**	PREDICTED: Vitis vinifera protein ULTRAPETALA 1	GSVIVT00026010001	XM_002278628
1.1	1.0	0.9	**3.1**	PREDICTED: Vitis vinifera AT-rich interactive domain-containing protein 2	GSVIVT00026942001	XM_010659834
1.1	1.0	0.9	**3.1**	PREDICTED: Vitis vinifera AT-rich interactive domain-containing protein 1	GSVIVT00026942001	XM_010663552
0.7	1.5	0.8	**2.9**	PREDICTED: Vitis vinifera zinc finger CCCH domain-containing protein 14	GSVIVT00024576001	XM_002279035
0.9	1.5	1.1	**2.8**	PREDICTED: Vitis vinifera mavicyanin	GSVIVT00020596001	XM_002275021
1.1	1.0	1.4	**2.4**	PREDICTED: Vitis vinifera probable WRKY transcription factor 47	GSVIVT00028232001	XM_002281158
1.1	1.7	1.1	**0.5**	PREDICTED: Vitis vinifera auxin-repressed 12.5 kDa protein	GSVIVT00034028001	XM_010656093
0.5	1.1	1.6	**0.4**	PREDICTED: Vitis vinifera pentatricopeptide repeat-containing protein	GSVIVT00028346001	XM_002272907
0.9	1.0	1.9	**0.4**	PREDICTED: Vitis vinifera uncharacterized (LOC100249460)	GSVIVT00025852001	XM_002270874
1.1	0.9	0.7	**0.4**	PREDICTED: Vitis vinifera F-box-like/WD repeat-containing protein TBL1X	GSVIVT00019607001	XM_010654454
0.9	0.9	1.1	**0.3**	PREDICTED: Vitis vinifera transcription factor IIIA-like	GSVIVT00035536001	XM_002278791
0.5	1.0	0.7	**0.3**	PREDICTED: Vitis vinifera NAC domain-containing protein 18	GSVIVT00031526001	XM_002266784
0.8	0.8	0.5	**0.3**	PREDICTED: Vitis vinifera GATA transcription factor 2-like	GSVIVT00025490001	XM_002282189
0.9	0.9	1.1	**0.3**	PREDICTED: Vitis vinifera R2R3 MYB transcription factor (MYBA6)	GSVIVT00022409001	XM_002274956
0.6	0.9	1.9	**0.3**	PREDICTED: Vitis vinifera BEL1-like homeodomain protein 9	GSVIVT00021404001	XM_010655932
1.1	0.6	0.5	**0.3**	PREDICTED: Vitis vinifera putative pentatricopeptide repeat-containing prot	GSVIVT00024376001	XM_002281300
0.7	1.2	1.9	**0.3**	PREDICTED: Vitis vinifera protein PHR1-LIKE 1	GSVIVT00025352001	XM_002278639
0.9	0.8	1.1	**0.3**	PREDICTED: Vitis vinifera probable UDP-N-acetylglucosamine--peptide N-a	GSVIVT00015910001	XM_002275575
0.6	1.1	0.9	**0.2**	PREDICTED: Vitis vinifera BEL1-like homeodomain protein 11	GSVIVT00014547001	XM_010666430
0.8	0.9	0.6	**0.2**	PREDICTED: Vitis vinifera transcription factor JUNGBRUNNEN 1	GSVIVT00025717001	XM_002283215
0.7	0.9	1.0	**0.2**	PREDICTED: Vitis vinifera ethylene-responsive transcription factor RAP2-4	GSVIVT00010923001	XM_010648970
0.6	0.6	1.5	**0.2**	PREDICTED: Vitis vinifera serine/threonine-protein kinase-like protein CCR	GSVIVT00018209001	XM_002276007
0.8	0.7	1.3	**0.2**	PREDICTED: Vitis vinifera putative ER lumen protein-retaining receptor C28	GSVIVT00014422001	XM_002273297
0.8	0.8	1.1	**0.2**	PREDICTED: Vitis vinifera uncharacterized (LOC100247524)	GSVIVT00020760001	XM_002279063
0.6	1.1	2.0	**0.2**	PREDICTED: Vitis vinifera nuclear transcription factor Y subunit A-1	GSVIVT00024601001	XM_002282742
0.6	1.0	0.6	**0.2**	PREDICTED: Vitis vinifera probable WRKY transcription factor 75	GSVIVT00037881001	XM_002275540
0.6	0.8	1.1	**0.2**	PREDICTED: Vitis vinifera transcription factor UNE12	GSVIVT00023837001	XM_002281590
0.7	1.0	0.7	**0.2**	PREDICTED: Vitis vinifera protein EMBRYONIC FLOWER 1	GSVIVT00032454001	XM_010650207
1.0	0.8	1.7	**0.1**	Vitis vinifera MADS-box protein 2 (MADS2)	GSVIVT00038077001	NM_001281180

Supplemental Table 2 (continued)

Fold Change				Functional annotation	ID	Accession
T0-20D	T0-7Dvh	T0-7Dtg	T0		genoscope	Number (NCBI)
1.0	0.8	0.5	**0.1**	PREDICTED: Vitis vinifera zinc finger protein WIP2	GSVIVT00024637001	XM_002277501
0.6	0.9	1.0	**0.1**	PREDICTED: Vitis vinifera probable protein phosphatase 2C 25	GSVIVT00025384001	XM_010655586
0.8	0.7	0.8	**0.1**	PREDICTED: Vitis vinifera UDP-glycosyltransferase 86A1/ cytokinin-O- glyc	GSVIVT00023233001	XM_002276822
0.9	0.8	0.9	**0.1**	PREDICTED: Vitis vinifera transcription factor DIVARICATA-like	GSVIVT00024157001	XM_010655884
Proteins metabolism						
2.7	**2.5**	**8.9**	**9.9**	SKP1-like protein 1A	GSVIVT00036131001	XM_002279196
2.2	**5.5**	**2.5**	**9.1**	T-complex protein 1 subunit beta-like	GSVIVT00015538001	XM_002285876
3.4	**0.4**	**0.1**	**0.2**	methionine aminopeptidase 1B, chloroplastic-like	GSVIVT01011946001	XM_002278712
0.3	**11.3**	**86.8**	**71.1**	ubiquitin-like domain-containing CTD phosphatase		XM_002265755
3.5	0.6	**0.2**	**0.1**	NEDD8-conjugating enzyme Ubc12-like		XM_003631580
0.5	1.1	**6.2**	**2.5**	polyubiquitin-like	GSVIVT00003823001	XM_002270097
1.2	**4.2**	**59.6**	**17.8**	60S ribosomal protein L19-like	GSVIVT00028043001	XM_002272321
0.7	**4.4**	**3.4**	**10.4**	serine carboxypeptidase-like 2-like		XM_002283377
1.2	**3.6**	**26.2**	**9.8**	pumilio homolog 12-like		XM_002283711
0.7	**11.7**	**26.4**	**7.0**	inactive rhomboid protein 1-like	GSVIVT00021327001	XM_002270606
0.5	**3.7**	**10.5**	**7.6**	ATP-dependent zinc metalloprotease FtsH-like		XM_002283718
1.9	**41.3**	**231.0**	**388.8**	protein bem46-like		XM_002280177
0.9	**3.5**	**4.3**	**7.3**	E3 ubiquitin-protein ligase COP1-like	GSVIVT00025955001	XM_002271379
0.5	2.0	**12.5**	**8.0**	PREDICTED: Vitis vinifera proteasome subunit alpha type-5-like	GSVIVT00033998001	XM_010656068
0.7	1.1	**9.7**	**2.6**	PREDICTED: Vitis vinifera ubiquitin-like-specific protease ESD4	GSVIVT00019757001	XM_010651415
1.0	1.3	**8.4**	**4.9**	PREDICTED: Vitis vinifera 60S ribosomal protein L13a-4-like	GSVIVT00031707001	XM_002268865
0.6	1.2	**6.8**	**3.2**	PREDICTED: Vitis vinifera ATP-dependent zinc metalloprotease FTSH 2	GSVIVT00038548001	XM_010657177
0.7	1.9	**6.6**	**5.3**	PREDICTED: Vitis vinifera protein LURP-one-related 8	GSVIVT00033620001	XM_002269152
0.8	1.5	**6.3**	**7.6**	PREDICTED: Vitis vinifera probable cytosolic oligopeptidase A	GSVIVT00022112001	XM_002270183
0.7	2.0	**5.2**	**48.5**	PREDICTED: Vitis vinifera E3 ubiquitin-protein ligase UPL1	GSVIVT00033388001	XM_010646285
1.3	1.4	**4.9**	**4.0**	PREDICTED: Vitis vinifera serine carboxypeptidase-like	GSVIVT00018114001	XM_010660041
0.8	1.9	**4.7**	**3.7**	PREDICTED: Vitis vinifera PCI domain-containing protein-like	GSVIVT00016574001	XM_002282266
0.8	1.8	**3.7**	**6.1**	PREDICTED: Vitis vinifera E3 ubiquitin-protein ligase MBR2	GSVIVT00019515001	XM_002282341
1.1	2.0	**2.2**	**4.1**	PREDICTED: Vitis vinifera uncharacterized (LOC100241484)	GSVIVT00012831001	XM_010648591
0.8	1.8	**2.1**	**7.4**	PREDICTED: Vitis vinifera ubiquitin-conjugating enzyme E2 variant 1D	GSVIVT00021532001	XM_002271736
0.9	1.1	**2.1**	**2.8**	PREDICTED: Vitis vinifera 20 kDa chaperonin, chloroplastic	GSVIVT00019006001	XM_002267310
1.3	1.0	**2.1**	**2.1**	PREDICTED: Vitis vinifera 26S proteasome non-ATPase regulatory subunit	GSVIVT00009324001	XM_010648116
0.6	1.4	**3.5**	**0.4**	PREDICTED: Vitis vinifera pumilio homolog 24	GSVIVT00033058001	XM_010651263
0.7	1.0	**2.9**	**0.4**	PREDICTED: Vitis vinifera xaa-Pro dipeptidase	GSVIVT00016599001	XM_002282743
0.8	1.3	**2.5**	0.5	PREDICTED: Vitis vinifera OTU domain-containing protein DDB_G0284757-	GSVIVT00023222001	XM_010655298
0.5	1.2	**2.4**	**0.4**	PREDICTED: Vitis vinifera 60S ribosomal protein L17-2-like	GSVIVT00021788001	XM_002279257
1.6	0.7	**2.1**	**0.5**	PREDICTED: Vitis vinifera polyubiquitin 9	GSVIVT00017850001	XM_010665386
1.0	1.6	**2.1**	**0.3**	PREDICTED: Vitis vinifera 26S proteasome non-ATPase regulatory subunit	GSVIVT00014791001	XM_002284530
0.6	1.2	**0.4**	**2.5**	PREDICTED: Vitis vinifera 40S ribosomal protein S18	GSVIVT00031714001	XM_002262666
1.8	0.5	**0.5**	**0.2**	PREDICTED: Vitis vinifera eukaryotic translation initiation factor NCBP	GSVIVT00025466001	XM_002281661
0.9	0.8	**0.5**	**0.2**	*A. thaliana* - carboxyl-terminal peptidase	GSVIVT00001148001	
1.1	0.9	**0.4**	**0.3**	PREDICTED: Vitis vinifera eukaryotic translation initiation factor 3 subunit K	GSVIVT00016373001	XM_002274950
0.8	1.1	**0.4**	**0.3**	PREDICTED: Vitis vinifera 60S ribosomal protein L27a-3-like	GSVIVT00020666001	XM_002274062
1.0	0.9	**0.3**	**0.3**	PREDICTED: Vitis vinifera thioredoxin-like protein CDSP32, chloroplastic	GSVIVT00015512001	XM_002285866
0.9	0.6	**0.3**	**0.2**	PREDICTED: Vitis vinifera U-box domain-containing protein 43	GSVIVT00008662001	XM_002273185
1.2	0.9	**0.2**	**0.4**	PREDICTED: Vitis vinifera uncharacterized (LOC100853755)	GSVIVT00001353001	XR_786361
1.4	0.5	**0.2**	**0.3**	PREDICTED: Vitis vinifera eukaryotic translation initiation factor 2 subunit al	GSVIVT00024042001	XM_002275276
0.7	0.9	**0.2**	**0.3**	PREDICTED: Vitis vinifera endoplasmic reticulum metallopeptidase 1	GSVIVT00010855001	XM_002279204
1.0	0.6	**0.2**	**0.2**	PREDICTED: Vitis vinifera ribosome biogenesis protein BRX1	GSVIVT00028481001	XM_002269993
0.9	0.7	**0.1**	**0.3**	PREDICTED: Vitis vinifera heterogeneous nuclear ribonucleoprotein H2	GSVIVT00008733001	XM_010651148
1.4	0.9	**0.1**	**0.2**	PREDICTED: Vitis vinifera microtubule-associated protein TORTIFOLIA1	GSVIVT00017006001	XM_010658410
1.4	0.6	**0.1**	**0.1**	PREDICTED: Vitis vinifera 40S ribosomal protein S15-like	GSVIVT00020133001	XM_002282258
0.8	1.0	**0.1**	**0.1**	PREDICTED: Vitis vinifera heterogeneous nuclear ribonucleoprotein H2	GSVIVT00032030001	XM_010651148
1.1	1.4	**4.6**	1.6	PREDICTED: Vitis vinifera pentatricopeptide repeat-containing protein	GSVIVT00029079001	XM_002267911
0.9	1.3	**3.1**	1.5	PREDICTED: Vitis vinifera aspartic proteinase PCS1-like	GSVIVT00032938001	XM_002263584
0.9	1.3	**3.1**	1.5	PREDICTED: Vitis vinifera uncharacterized (LOC100250825)	GSVIVT00030177001	XM_010650393
0.9	0.6	**2.9**	1.1	PREDICTED: Vitis vinifera eukaryotic translation initiation factor 1A	GSVIVT00034754001	XM_002285808
0.7	1.5	**2.8**	0.6	PREDICTED: Vitis vinifera eukaryotic peptide chain release factor subunit 1-3	GSVIVT00001852001	XM_002271620
0.9	1.2	**2.5**	0.9	PREDICTED: Vitis vinifera pentatricopeptide repeat-containing protein	GSVIVT00030057001	XM_002274396
0.6	1.2	**2.1**	1.0	PREDICTED: Vitis vinifera uncharacterized (LOC100247715)	GSVIVT00001036001	XM_002269463
0.8	0.6	**0.2**	1.7	PREDICTED: Vitis vinifera nucleolar GTP-binding protein 1	GSVIVT00027086001	XM_002265220

Supplemental Table 2 (continued)

Fold Change				Functional annotation	ID	Accession
T0-20D	T0-7Dvh	T0-7Dtg	T0		genoscope	Number (NCBI)
1.1	2.9	1.4	**10.1**	PREDICTED: Vitis vinifera 26S protease regulatory subunit 8 homolog A	GSVIVT00032563001	XM_002284711
0.6	1.5	0.9	**4.0**	PREDICTED: Vitis vinifera serine carboxypeptidase-like 16	GSVIVT00038626001	XM_002272080
0.8	1.3	1.9	**4.0**	PREDICTED: Vitis vinifera RWD domain-containing protein 1	GSVIVT00034208001	XM_002281127
1.1	0.8	1.2	**3.4**	PREDICTED: Vitis vinifera putative 60S ribosomal protein L30-1	GSVIVT00015281001	XM_002285777
1.1	0.8	1.2	**3.4**	PREDICTED: Vitis vinifera putative 60S ribosomal protein L30-1	GSVIVT00015281001	XM_002285777
0.6	1.6	1.2	**3.2**	PREDICTED: Vitis vinifera putative pentatricopeptide repeat-containing prot	GSVIVT00033662001	XM_010654833
0.8	1.4	1.0	**2.8**	PREDICTED: Vitis vinifera uncharacterized CRM domain-containing protein	GSVIVT00001969001	XM_010652295
1.2	1.4	0.7	**2.8**	PREDICTED: Vitis vinifera PITH domain-containing protein At3g04780	GSVIVT00031148001	XM_002278284
0.7	2.0	1.7	**2.4**	PREDICTED: Vitis vinifera oligoribonuclease	GSVIVT00022313001	XM_002279417
0.8	1.4	0.7	**2.1**	PREDICTED: Vitis vinifera pentatricopeptide repeat-containing protein At3g	GSVIVT00016595001	XM_010657918
0.7	1.4	0.9	**2.0**	PREDICTED: Vitis vinifera subtilisin-like protease	GSVIVT00001053001	XM_002278256
0.7	1.4	0.9	**2.0**	PREDICTED: Vitis vinifera subtilisin-like protease	GSVIVT00001055001	XM_002284065
1.7	1.0	1.0	**0.5**	PREDICTED: Vitis vinifera 40S ribosomal protein S3-3	GSVIVT00016476001	XM_002279914
1.4	0.7	1.0	**0.3**	PREDICTED: Vitis vinifera T-complex protein 1 subunit delta	GSVIVT00017754001	XM_002280198
0.6	1.1	0.7	**0.3**	PREDICTED: Vitis vinifera oligoribonuclease	GSVIVT00017340001	XM_002271292
0.9	1.0	1.3	**0.3**	PREDICTED: Vitis vinifera protein CYPRO4	GSVIVT00036588001	XM_002282124
1.1	0.6	0.5	**0.3**	PREDICTED: Vitis vinifera ribosome biogenesis regulatory protein homolog	GSVIVT00026149001	XM_002264612
0.8	0.8	0.9	**0.2**	PREDICTED: Vitis vinifera putative E3 ubiquitin-protein ligase LIN-1	GSVIVT00016710001	XM_010657996
0.6	1.0	1.1	**0.2**	PREDICTED: Vitis vinifera pentatricopeptide repeat-containing protein	GSVIVT00031640001	XM_010652032
1.1	0.7	0.7	**0.2**	PREDICTED: Vitis vinifera lysosomal Pro-X carboxypeptidase	GSVIVT00022128001	XM_002271697
Cellular processes						
3.2	**11.4**	**4.5**	**61.3**	V-type proton ATPase subunit B 1-like	GSVIVT01023982001	XM_002280255
0.5	**18.1**	**104.7**	**174.0**	ABC transporter B family member 13-like		XM_002279435
0.5	**3.5**	**17.0**	**2.8**	putative metallophosphoesterase At3g03305-like		XM_002266850
0.4	**5.1**	**30.7**	**7.8**	coatomer subunit beta'-2-like		XM_002284737
0.4	1.6	**6.9**	**17.4**	uncharacterized LOC100263597		XM_002276971
0.2	**7.9**	**72.9**	**104.7**	Di-glucose binding protein with Leucine-rich repeat domain-like	GSVIVT01011948001	XM_002281632
0.3	**3.5**	**6.2**	**11.8**	probable serine/threonine-protein kinase At4g35230-like	GSVIVT00036214001	XM_002281577
3.1	**9.3**	**0.5**	**4.2**	uncharacterized LOC100247996		XM_002279521
3.7	**0.3**	**0.0**	**0.2**	PREDICTED: serine/threonine-protein phosphatase 7	GSVIVT00005999001	XM_002263704
7.3	**0.5**	**0.0**	**0.0**	AP-1 complex subunit gamma-2-like	GSVIVT01020209001	XM_002265154
4.5	18.7	**3.2**	**10.4**	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130	GSVIVT00029223001	XM_002277183
2.6	1.8	**9.9**	**26.3**	V-type proton ATPase subunit C-like	GSVIVT01033006001	XM_002275474
8.2	1.0	**0.4**	**2.6**	potassium transporter 5-like		XM_003631177
4.0	0.7	**0.1**	**0.0**	cation/calcium exchanger 4-like	GSVIVT00034062001	XM_002272544
3.9	0.9	**0.3**	**0.1**	casein kinase I isoform delta-like		XM_002284008
0.5	**0.5**	0.7	**0.1**	erd6-like transporter	GSVIVT00006082001	XM_002263382
0.4	1.3	**27.2**	**3.8**	uncharacterized LOC100257476		XM_002271055
0.3	0.8	**0.4**	**8.6**	UDP-glycosyltransferase 87A2-like		XM_002274384
0.1	1.3	**0.4**	**0.1**	cysteine-rich receptor-like protein kinase 25-like		XM_003631474
0.5	**35.0**	**208.7**	**11.1**	protein SEC13 homolog-like	GSVIVT00020856001	XM_002281820
1.3	**16.6**	**21.8**	**115.0**	12S seed storage globulin 1-like	GSVIVT00026049001	XM_002280155
0.7	**10.0**	**8.4**	**6.5**	ATP synthase subunit beta, mitochondrial-like		XM_002283915
0.6	**9.8**	**62.4**	**38.1**	probable LRR receptor-like serine/threonine-protein kinase At1g29720-like		XM_002264038
0.5	**9.3**	**11.9**	**6.8**	probable LRR receptor-like serine/threonine-protein kinase At1g53430	GSVIVT01020456001	XM_002268701
0.9	**9.0**	**3.2**	**2.7**	uncharacterized LOC100243620	GSVIVT00027784001	XM_002282951
0.8	**8.9**	**74.8**	**71.4**	probable LRR receptor-like serine/threonine-protein kinase At1g56130	GSVIVT01029718001	XM_002267093
1.9	**7.5**	**2.3**	**4.7**	uncharacterized LOC100260760	GSVIVT00018781001	XM_002281940
1.1	**7.3**	**22.3**	**70.5**	cation/calcium exchanger 4-like	GSVIVT00034062001	XM_002272544
1.5	**6.7**	**7.9**	**25.8**	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1	GSVIVT00003760001	XM_002268983
0.6	**6.6**	**4.7**	**55.1**	cytochrome c oxidase assembly protein COX19-like	GSVIVT00034344001	XM_002284132
0.9	**6.5**	**41.7**	**58.2**	endo-1,4-beta-xylanase A		XM_002283514
0.7	**6.4**	**13.7**	**8.9**	quinone oxidoreductase-like protein 2 homolog	GSVIVT00029244001	XM_002267141
1.3	**5.9**	**29.3**	**36.3**	ras-related protein Rab7-like	GSVIVT00034372001	XM_002284372
1.1	**5.9**	**18.5**	**10.4**	coatomer subunit beta'-2-like		XM_002284737
1.6	**5.5**	**5.6**	**4.3**	pentatricopeptide repeat-containing protein At2g32230		XM_002267869
0.8	**5.4**	**14.0**	**18.2**	casein kinase I isoform delta-like		XM_002277477
1.1	**4.9**	**20.8**	**14.5**	probable LRR receptor-like serine/threonine-protein kinase	GSVIVT01020456001	XM_002268701
0.5	**4.4**	**19.1**	**4.5**	TPR repeat-containing thioredoxin TTL1-like		XM_002283061
0.6	**4.1**	**16.7**	**13.9**	probable LRR receptor-like serine/threonine-protein kinase At4g08850-like		XM_002278525
0.9	**3.7**	**7.4**	**9.4**	cytochrome P450 82C4-like	GSVIVT01009590001	XM_002283995

Supplemental Table 2 (continued)

Fold Change				**Functional annotation**	**ID**	**Accession**
T0-20D	**T0-7Dvh**	**T0-7Dtg**	**T0**		**genoscope**	**Number (NCBI)**
0.6	**3.6**	**64.4**	**96.0**	probable LRR receptor-like serine/threonine-protein		XM_002267636
1.3	**3.4**	**48.7**	**107.2**	uncharacterized LOC100255442	GSVIVT00031820001	XM_002267832
0.8	**3.2**	**3.6**	**13.3**	ABC transporter B family member 26		XM_002272024
1.2	**3.1**	**8.2**	**3.5**	uncharacterized LOC100241221		XM_002285181
1.2	**3.1**	**8.2**	**3.5**	uncharacterized LOC100241221		XM_002285181
1.6	**2.6**	**6.3**	**5.5**	sulfate transporter	GSVIVT00015271001	XM_002285774
0.9	**2.5**	**8.3**	**11.1**	flavin-containing monooxygenase YUCCA6-like	GSVIVT00032480001	XM_002281561
0.9	**2.4**	**34.9**	**3.4**	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290-like		XM_002280681
0.3	**2.4**	**6.6**	**6.9**	sorting nexin-1-like	GSVIVT00021573001	XM_002281974
1.3	**2.1**	**25.4**	**9.1**	copper-transporting ATPase RAN1-like		XM_002275968
0.9	**2.1**	**6.4**	**8.5**	membrane-bound O-acyltransferase C24H6.01c-like	GSVIVT00004222001	XM_002268808
1.4	**0.5**	**0.0**	**0.1**	peptide/nitrate transporter	GSVIVT00018397001	XM_002277546
1.8	**0.4**	**0.0**	**0.1**	leucine-rich repeat receptor-like serine/threonine-protein kinase BAM3	GSVIVT00021105001	XM_002264916
1.1	**0.3**	**0.1**	**0.0**	nitrate transporter 1.3-like		XM_002274191
1.5	**0.4**	**0.1**	**0.0**	ankyrin repeat-containing protein At5g02620-like		XM_002284486
1.1	**0.5**	**0.2**	**0.1**	PREDICTED: Vitis vinifera UDP-glycosyltransferase 85A3-like	GSVIVT00015205001	XM_002285731
1.7	**0.5**	**0.4**	**0.1**	dehydrogenase/reductase SDR family member 4-like	GSVIVT00011718001	XM_002264461
0.4	1.7	**52.5**	**195.6**	PREDICTED: Vitis vinifera ATP-dependent zinc metalloprotease FtsH	GSVIVT00022916001	XM_002266039
0.8	1.5	**32.5**	**12.8**	PREDICTED: Vitis vinifera mitogen-activated protein kinase kinase kinase 7	GSVIVT00026986001	XM_010660668
0.7	1.4	**21.0**	**16.5**	PREDICTED: Vitis vinifera uncharacterized (LOC100254866)	GSVIVT00034368001	XM_010656352
0.7	1.2	**15.6**	**9.3**	PREDICTED: Vitis vinifera probable LRR receptor-like serine/threonine-prot	GSVIVT00033651001	XM_010654820
0.8	1.8	**12.6**	**5.2**	PREDICTED: Vitis vinifera G-type lectin S-receptor-like serine/threonine-pro	GSVIVT00021390001	XM_002277183
0.9	1.5	**9.7**	**3.2**	PREDICTED: Vitis vinifera cytochrome P450 94B3-like	GSVIVT00017932001	XM_002279945
0.8	1.8	**8.8**	**2.9**	PREDICTED: Vitis vinifera cytochrome b5 domain-containing protein RLF	GSVIVT00028750001	XM_010661135
1.2	1.1	**8.3**	**2.4**	PREDICTED: Vitis vinifera serine/threonine-protein kinase Nek5	GSVIVT00017494001	XM_010653343
0.9	1.8	**7.6**	**12.8**	PREDICTED: Vitis vinifera probable L-type lectin-domain containing recepto	GSVIVT00022018001	XM_002275483
1.2	1.7	**7.6**	**2.4**	PREDICTED: Vitis vinifera receptor-like serine/threonine-protein kinase	GSVIVT00016952001	XM_002285354
0.9	1.3	**5.9**	**5.4**	PREDICTED: Vitis vinifera uncharacterized (LOC100264257)	GSVIVT00015663001	XR_787976
1.4	1.0	**5.7**	**6.2**	PREDICTED: Vitis vinifera uncharacterized protein At4g18255 (LOC10488050	GSVIVT00003435001	XM_010657343
0.7	1.7	**5.6**	**2.8**	PREDICTED: Vitis vinifera ras-related protein RGP1	GSVIVT00022294001	XR_787339
0.7	1.3	**5.4**	**2.3**	PREDICTED: Vitis vinifera probable sodium/metabolite cotransporter BASS	GSVIVT00010615001	XM_002263648
0.6	1.5	**4.8**	**3.1**	PREDICTED: Vitis vinifera probable LRR receptor-like serine/threonine-prot	GSVIVT00032664001	XM_010659263
0.8	0.9	**4.6**	**2.1**	PREDICTED: Vitis vinifera ABC transporter C family member 10-like	GSVIVT00000264001	XM_010664289
0.8	1.7	**4.3**	**10.7**	PREDICTED: Vitis vinifera receptor-like protein 12	GSVIVT00001351001	XM_010659216
0.9	0.8	**3.9**	**2.1**	PREDICTED: Vitis vinifera ATP-dependent zinc metalloprotease FTSH 2, ch	GSVIVT00035051001	XM_010657177
0.8	1.0	**3.8**	**2.1**	PREDICTED: Vitis vinifera LRR receptor-like serine/threonine-protein kinase	GSVIVT00028256001	XM_010654045
1.7	1.6	**3.3**	**9.0**	PREDICTED: Vitis vinifera CBL-interacting protein kinase 18	GSVIVT00016733001	XM_010653183
1.1	1.7	**3.3**	**2.6**	PREDICTED: Vitis vinifera vacuolar amino acid transporter 1	GSVIVT00018153001	XM_010660076
1.0	1.2	**3.2**	**3.3**	PREDICTED: Vitis vinifera cysteine-rich receptor-like protein kinase 10	GSVIVT00008005001	XM_010648597
0.8	1.3	**3.1**	**2.5**	PREDICTED: Vitis vinifera G-type lectin S-receptor-like serine/threonine-pro	GSVIVT00027480001	XM_010645996
0.8	1.6	**2.9**	**3.8**	PREDICTED: Vitis vinifera reticuline oxidase-like protein		XM_002269426
0.7	1.9	**2.7**	**5.7**	PREDICTED: Vitis vinifera organic cation/carnitine transporter 4	GSVIVT00027463001	XM_002280273
0.7	0.9	**2.7**	**4.6**	PREDICTED: Vitis vinifera protein HOTHEAD	GSVIVT00034174001	XM_010656222
0.7	1.5	**2.7**	**2.8**	PREDICTED: Vitis vinifera uncharacterized (LOC100243646)	GSVIVT00008694001	XM_002277023
0.7	1.8	**2.1**	**2.5**	PREDICTED: Vitis vinifera nicotinate-nucleotide pyrophosphorylase [carbox	GSVIVT00030474001	XM_010659813
1.0	1.4	**2.0**	**2.1**	PREDICTED: Vitis vinifera calcineurin B-like protein 07	GSVIVT00032178001	XM_010649971
0.8	1.1	**5.3**	**0.4**	PREDICTED: Vitis vinifera vacuolar protein sorting-associated protein 22 ho	GSVIVT00027355001	XM_002281094
1.0	1.3	**4.4**	**0.5**	PREDICTED: Vitis vinifera probable sugar phosphate/phosphate translocato	GSVIVT00001039001	XM_002281587
0.9	1.1	**4.2**	**0.2**	PREDICTED: Vitis vinifera rho GTPase-activating protein 1	GSVIVT00021595001	XM_010653575
0.8	1.2	**3.3**	**0.5**	PREDICTED: Vitis vinifera protein kinase PVPK-1	GSVIVT00020660001	XM_002272675
1.0	0.9	**3.0**	**0.5**	PREDICTED: Vitis vinifera ABC transporter A family member 7	GSVIVT00031557001	XM_002274267
1.1	1.3	**2.7**	**0.5**	PREDICTED: Vitis vinifera frataxin, mitochondrial	GSVIVT00029229001	XM_002277055
0.7	1.0	**2.9**	**0.4**	PREDICTED: Vitis vinifera xaa-Pro dipeptidase	GSVIVT00016599001	XM_002282743
0.6	1.0	**2.5**	**0.3**	PREDICTED: Vitis vinifera endoplasmic reticulum-Golgi intermediate compa	GSVIVT00018943001	XM_010658644
0.8	1.5	**0.4**	**2.8**	PREDICTED: Vitis vinifera fe-S cluster assembly factor HCF101, chloroplasti	GSVIVT00016780001	XM_002281317
0.6	1.4	**0.4**	**2.3**	PREDICTED: Vitis vinifera probable purine permease 5	GSVIVT00008067001	XM_002266443
0.7	0.9	**0.3**	**17.6**	PREDICTED: Vitis vinifera uncharacterized (LOC100267710)	GSVIVT00034903001	XR_785718
1.4	1.2	**0.5**	**0.3**	PREDICTED: Vitis vinifera glutamate receptor 2.8-like	GSVIVT00000721001	XM_002266180
1.0	1.0	**0.5**	**0.3**	PREDICTED: Vitis vinifera G-type lectin S-receptor-like serine/threonine-pro	GSVIVT00012561001	XM_010659090
0.7	0.9	**0.5**	**0.3**	PREDICTED: Vitis vinifera uncharacterized transporter YBR287W-like	GSVIVT00038733001	XM_010651032
0.9	0.9	**0.5**	**0.2**	PREDICTED: Vitis vinifera probable serine/threonine protein kinase IRE4 (LO	GSVIVT00014640001	XM_002282922

Supplemental Table 2 (continued)

Fold Change				Functional annotation	ID	Accession
T0-20D	T0-7Dvh	T0-7Dtg	T0		genoscope	Number (NCBI)
0.9	0.7	**0.5**	**0.2**	PREDICTED: Vitis vinifera potassium transporter 1	GSVIVT00035544001	XM_010652583
0.8	0.7	**0.5**	**0.2**	PREDICTED: Vitis vinifera ankyrin repeat-containing protein At5g02620-like	GSVIVT00018558001	XM_002266996
1.2	1.0	**0.4**	**0.5**	PREDICTED: Vitis vinifera cytochrome P450 76A1	GSVIVT00009931001	XM_010655729
0.8	0.8	**0.4**	**0.4**	PREDICTED: Vitis vinifera probable L-type lectin-domain containing recepto	GSVIVT00027870001	XM_002275483
0.9	1.0	**0.4**	**0.4**	PREDICTED: Vitis vinifera glutamate receptor 2.8-like	GSVIVT00000720001	XM_002266180
1.7	0.8	**0.4**	**0.3**	PREDICTED: Vitis vinifera probable metal-nicotianamine transporter YSL7	GSVIVT00037055001	XM_002266621
1.2	0.7	**0.4**	**0.3**	PREDICTED: Vitis vinifera NADH kinase	GSVIVT00027917001	XM_002283633
1.7	0.6	**0.4**	**0.1**	PREDICTED: Vitis vinifera L-type lectin-domain containing receptor kinase I	GSVIVT00011490001	XM_010648556
1.5	0.7	**0.3**	**0.2**	PREDICTED: Vitis vinifera G-type lectin S-receptor-like serine/threonine-pro	GSVIVT00027519001	XM_010649231
1.1	0.8	**0.3**	**0.4**	PREDICTED: Vitis vinifera WD repeat-containing protein 74	GSVIVT00015713001	XM_010664964
1.1	0.8	**0.3**	**0.3**	PREDICTED: Vitis vinifera uncharacterized (LOC100260982)	GSVIVT00017071001	XR_785635
0.9	0.6	**0.3**	**0.2**	PREDICTED: Vitis vinifera mitochondrial import inner membrane translocas	GSVIVT00016660001	XM_002283601
0.6	1.0	**0.3**	**0.2**	PREDICTED: Vitis vinifera protein EXORDIUM-like 5	GSVIVT00036277001	XM_003631510
1.1	0.9	**0.3**	**0.2**	PREDICTED: Vitis vinifera protochlorophyllide-dependent translocon comp	GSVIVT00024785001	XM_002283556
1.2	0.5	**0.3**	**0.1**	Vitis vinifera hexose transporter	GSVIVT00038182001	NM_001281111
1.1	0.5	**0.3**	**0.0**	PREDICTED: Vitis vinifera ankyrin-2-like	GSVIVT00033277001	XM_010657416
1.4	0.7	**0.2**	**0.4**	PREDICTED: Vitis vinifera probable receptor-like protein kinase	GSVIVT00013403001	XM_010662106
1.3	0.6	**0.2**	**0.3**	PREDICTED: Vitis vinifera ankyrin repeat-containing protein At2g01680	GSVIVT00030584001	XM_002284866
1.0	0.8	**0.2**	**0.2**	PREDICTED: Vitis vinifera UDP-galactose/UDP-glucose transporter 5	GSVIVT00024400001	XM_002281418
0.5	1.1	**0.2**	**0.2**	PREDICTED: Vitis vinifera polyadenylate-binding protein 2	GSVIVT00014106001	XM_002279112
1.2	0.8	**0.2**	**0.2**	PREDICTED: Vitis vinifera nicotinamide adenine dinucleotide transporter 1, c	GSVIVT00030386001	XM_010645902
1.9	0.9	**0.2**	**0.1**	PREDICTED: Vitis vinifera ABC transporter C family member 8-like	GSVIVT00034195001	XM_010656248
1.2	0.8	**0.2**	**0.1**	PREDICTED: Vitis vinifera protein TIC 55 (Translocon at the inner envelope	GSVIVT00032812001	XM_002283397
0.6	0.7	**0.2**	**0.0**	PREDICTED: Vitis vinifera transmembrane emp24 domain-containing protei	GSVIVT00033393001	XM_002265269
0.9	0.7	**0.1**	**0.2**	PREDICTED: Vitis vinifera equilibrative nucleotide transporter 3-like	GSVIVT00013175001	XM_010648063
1.9	0.6	**0.1**	**0.2**	PREDICTED: Vitis vinifera beta-hexosaminidase 3-like	GSVIVT00007781001	XM_010648158
1.4	0.6	**0.1**	**0.2**	PREDICTED: Vitis vinifera probable ATP synthase 24 kDa subunit, mitocho	GSVIVT00019377001	XM_002279353
1.3	0.5	**0.1**	**0.1**	PREDICTED: Vitis vinifera vesicle transport v-SNARE 13	GSVIVT00016295001	XM_010662789
1.8	0.4	**0.0**	**0.1**	PREDICTED: Vitis vinifera leucine-rich repeat receptor-like serine/threonine-	GSVIVT00035385001	XM_002264916
0.8	1.2	**5.9**	1.8	PREDICTED: Vitis vinifera oligopeptide transporter 2	GSVIVT00015062001	XM_002283655
1.2	1.5	**4.8**	0.6	PREDICTED: Vitis vinifera probable aquaporin NIP-type	GSVIVT00011149001	XM_003633656
0.7	1.3	**4.2**	1.1	PREDICTED: Vitis vinifera mitochondrial carrier protein MTM1	GSVIVT00009710001	XM_010664299
0.7	1.3	**4.1**	1.3	PREDICTED: Vitis vinifera probable receptor-like protein kinase	GSVIVT00011563001	XM_010662183
0.8	1.4	**3.9**	0.8	PREDICTED: Vitis vinifera TOM1-like protein 2	GSVIVT00027891001	XM_010645783
0.7	1.5	**3.3**	0.9	PREDICTED: Vitis vinifera ankyrin-2-like	GSVIVT00030146001	XM_010657417
0.8	1.5	**3.3**	1.2	PREDICTED: Vitis vinifera clathrin coat assembly protein AP180	GSVIVT00025947001	XM_002271201
0.5	1.2	**3.2**	1.0	PREDICTED: Vitis vinifera pentatricopeptide repeat-containing protein At3g	GSVIVT00012784001	XM_010657590
1.1	1.3	**3.0**	0.7	PREDICTED: Vitis vinifera phytanoyl-CoA dioxygenase	GSVIVT00033627001	XM_002284433
0.7	1.1	**3.0**	0.6	PREDICTED: Vitis vinifera ankyrin repeat-containing protein At5g02620	GSVIVT00024413001	XM_002284486
0.3	1.9	**2.9**	1.5	PREDICTED: Vitis vinifera WAT1-related protein At3g28050	GSVIVT00028879001	XM_002279726
1.1	1.3	**2.6**	0.9	PREDICTED: Vitis vinifera G-type lectin S-receptor-like serine/threonine-pro	GSVIVT00010007001	XM_010659090
1.1	1.3	**2.6**	0.9	PREDICTED: Vitis vinifera uncharacterized (LOC100267196)	GSVIVT00010007001	XM_010659075
0.8	1.6	**2.5**	0.8	PREDICTED: Vitis vinifera metal transporter Nramp6	GSVIVT00015428001	XM_010656720
0.7	1.6	**2.4**	0.8	PREDICTED: Vitis vinifera probable receptor-like protein kinase	GSVIVT00013404001	XM_010662183
1.1	1.1	**2.4**	0.6	PREDICTED: Vitis vinifera probable LRR receptor-like serine/threonine-prot	GSVIVT00035813001	XM_010657265
0.6	1.3	**2.3**	0.7	PREDICTED: Vitis vinifera UDP-glycosyltransferase 90A1-like	GSVIVT00016118001	XM_010662632
0.9	1.7	**2.2**	1.0	PREDICTED: Vitis vinifera random slug protein 5	GSVIVT00024935001	XM_010666381
1.3	0.9	**2.1**	1.1	PREDICTED: Vitis vinifera serine/threonine-protein kinase SRK2I	GSVIVT00009710001	XM_002264136
1.1	1.0	**0.4**	0.5	PREDICTED: Vitis vinifera putative clathrin assembly protein At1g25240	GSVIVT00030651001	XM_002281674
1.0	1.0	**0.2**	0.5	PREDICTED: Vitis vinifera casein kinase I	GSVIVT00028561001	XM_010651803
1.1	1.1	**0.0**	1.0	PREDICTED: Vitis vinifera AP-1complex subunit mu-2	GSVIVT00009485001	XM_002274427
1.0	1.6	0.9	**5.0**	PREDICTED: Vitis vinifera endophilin-A3	GSVIVT00007619001	XM_002266198
0.9	1.2	1.6	**3.8**	PREDICTED: Vitis vinifera receptor-like serine/threonine-protein kinase SD1	GSVIVT00029671001	XM_010648578
1.0	1.4	0.6	**3.2**	PREDICTED : NADH dehydrogenase subunit 7	GSVIVT00035567001	
1.6	1.7	1.0	**3.1**	PREDICTED: Vitis vinifera transmembrane 9 superfamily member 5	GSVIVT00037359001	XM_002274218
0.9	1.5	1.4	**3.0**	PREDICTED: Vitis vinifera beta-glucosidase 11-like	GSVIVT00027994001	XM_002268111
0.8	1.0	1.6	**2.9**	PREDICTED: Vitis vinifera probable LRR receptor-like serine/threonine-prot	GSVIVT00008037001	XM_010658778
0.9	1.4	0.9	**2.8**	PREDICTED: Vitis vinifera mitochondrial import inner membrane translocas	GSVIVT00017994001	XM_002284234
1.1	1.3	0.8	**2.7**	PREDICTED: Vitis vinifera FAD-linked sulfhydryl oxidase ERV1	GSVIVT00011077001	XM_002263782
0.9	0.8	0.6	**2.6**	PREDICTED: Vitis vinifera receptor-like serine/threonine-protein kinase SD1	GSVIVT00013447001	XM_010645972
0.9	0.8	0.6	**2.6**	PREDICTED: Vitis vinifera receptor-like serine/threonine-protein kinase SD1	GSVIVT00013447001	XM_010645972

Supplemental Table 2 (continued)

Fold Change				Functional annotation	ID	Accession
T0-20D	T0-7Dvh	T0-7Dtg	T0		genoscope	Number (NCBI)
0.7	1.5	0.8	**2.5**	PREDICTED: Vitis vinifera probable purine permease 5	GSVIVT00012052001	XM_002266443
0.8	1.6	1.0	**2.4**	PREDICTED: Vitis vinifera vesicle-associated protein 2-2	GSVIVT00008892001	XM_010661688
0.8	1.5	1.1	**2.1**	PREDICTED: Vitis vinifera L-type lectin-domain containing receptor kinase S	GSVIVT00001301001	XM_002277979
0.6	1.0	1.6	**0.5**	PREDICTED: Vitis vinifera receptor-like cytosolic serine/threonine-protein k	GSVIVT00019857001	XM_010651519
1.1	0.8	1.9	**0.5**	PREDICTED: Vitis vinifera luminal-binding protein 5	GSVIVT00022356001	XM_002263287
0.9	0.6	0.9	**0.4**	PREDICTED: Vitis vinifera uncharacterized (LOC100243949)	GSVIVT00035507001	XM_002278525
0.8	1.2	1.2	**0.4**	PREDICTED: Vitis vinifera probable LRR receptor-like serine/threonine-prot	GSVIVT00008078001	XM_010648962
0.8	1.2	0.6	**0.4**	PREDICTED: Vitis vinifera ABC transporter C family-like	GSVIVT00028387001	XM_010657404
0.7	1.1	1.4	**0.4**	PREDICTED: Vitis vinifera WAT1-related protein At3g28050	GSVIVT00028877001	XM_002279726
0.9	0.7	0.5	**0.4**	PREDICTED: Vitis vinifera cytochrome P450 82C4	GSVIVT00036470001	XM_002283995
0.9	0.7	0.9	**0.4**	PREDICTED: Vitis vinifera ankyrin repeat-containing protein At5g02620-like	GSVIVT00018555001	XM_010658839
0.6	1.0	0.7	**0.4**	PREDICTED: Vitis vinifera UDP-glucose iridoid glucosyltransferase-like	GSVIVT00018352001	XM_010660352
0.7	0.9	0.6	**0.3**	PREDICTED: Vitis vinifera G-type lectin S-receptor-like serine/threonine-pro	GSVIVT00015350001	XM_010665932
0.8	0.8	0.9	**0.3**	PREDICTED: Vitis vinifera protein TRANSPARENT TESTA 12-like	GSVIVT00033862001	XM_010654867
0.8	1.0	0.9	**0.3**	PREDICTED: Vitis vinifera ABC transporter B family member 15-like	GSVIVT00027398001	XM_010662694
0.6	0.9	0.9	**0.3**	PREDICTED: Vitis vinifera mechanosensitive ion channel protein 6-like	GSVIVT00036185001	XM_010648148
0.8	1.0	1.4	**0.3**	PREDICTED: Vitis vinifera equilibrative nucleotide transporter 3-like	GSVIVT00008459001	XM_010648063
0.6	0.7	0.7	**0.3**	PREDICTED: Vitis vinifera phosphoenolpyruvate/phosphate translocator 2,	GSVIVT00020707001	XM_002276460
1.0	0.9	1.2	**0.3**	PREDICTED: Vitis vinifera magnesium transporter MRS2-5	GSVIVT00030033001	XM_010651475
0.6	0.9	0.3	**0.3**	PREDICTED: Vitis vinifera G-type lectin S-receptor-like serine/threonine-pro	GSVIVT00027036001	XM_010648577
0.9	0.9	0.7	**0.2**	PREDICTED: Vitis vinifera wall-associated receptor kinase 2-like	GSVIVT00015471001	XM_010665406
0.6	1.1	0.9	**0.2**	PREDICTED: Vitis vinifera BEL1-like homeodomain protein 11	GSVIVT00014547001	XM_010666430
1.0	0.7	0.5	**0.2**	PREDICTED: Vitis vinifera probable inactive leucine-rich repeat receptor-like	GSVIVT00017911001	XM_010665428
0.9	0.6	0.8	**0.2**	PREDICTED: Vitis vinifera UDP-N-acetylglucosamine transferase subunit A	GSVIVT00022866001	XM_010661525
1.3	0.7	1.1	**0.2**	PREDICTED: Vitis vinifera ABC transporter G family member 15	GSVIVT00022210001	XM_002274073
0.6	0.7	1.3	**0.2**	PREDICTED: Vitis vinifera proline transporter 2-like	GSVIVT00018303001	XM_002280181
0.9	0.8	1.2	**0.2**	PREDICTED: Vitis vinifera pentatricopeptide repeat-containing protein At3g	GSVIVT00013264001	XM_010657590
0.7	1.3	0.9	**0.2**	PREDICTED: Vitis vinifera probable flavin-containing monooxygenase 1	GSVIVT00032310001	XM_002280356
1.1	0.7	1.1	**0.2**	PREDICTED: Vitis vinifera golgin candidate 3	GSVIVT00026946001	XM_010663555
1.2	0.8	0.8	**0.2**	PREDICTED: Vitis vinifera mitochondrial import inner membrane translocas	GSVIVT00016062001	XM_002284234
1.0	0.9	1.5	**0.2**	PREDICTED: Vitis vinifera phospholipid-transporting ATPase 3	GSVIVT00011966001	XM_010647906
0.8	0.6	0.8	**0.2**	PREDICTED: Vitis vinifera uncharacterized protein OsI_027940 (LOC100258	GSVIVT00027981001	XM_010653877
0.7	0.9	0.6	**0.2**	PREDICTED: Vitis vinifera protein NRT1/ PTR FAMILY 6.3	GSVIVT00009628001	XM_002266915
1.0	0.6	0.6	**0.1**	PREDICTED: Vitis vinifera ammonium transporter 2-like	GSVIVT00019241001	XM_010655111
0.6	0.6	1.5	**0.1**	PREDICTED: Vitis vinifera probable zinc transporter 10	GSVIVT00031911001	XM_002273143
1.4	0.5	0.7	**0.1**	PREDICTED: Vitis vinifera vesicle-associated membrane protein 714	GSVIVT00020446001	XM_002273925
0.9	0.8	1.8	**0.1**	PREDICTED: Vitis vinifera cytochrome b-c1 complex subunit 8	GSVIVT00023918001	XM_002264353
0.9	1.2	1.0	**0.0**	PREDICTED: Vitis vinifera ABC transporter B family member 15-like	GSVIVT00035705001	XM_010662694

11