

**Enhanced Viral Detection in Grapevine via Exome Depletion and Next-
Generation Sequencing (NGS)**

Raúl Andrés Cuello^{1*}, Diego Zavallo¹, Pablo Vera¹, Agustín Sattler⁴, Andrea Puebla¹,
Humberto Debat^{2,3}, Sebastián Gómez Talquenca⁴ & Sebastián Asurmendi^{1*}.

¹ Instituto de Agrobiotecnología y Biología Molecular (IABIMO), CICVyA. Instituto
Nacional de Tecnología Agropecuaria (INTA), Consejo Nacional de investigaciones
Científicas y Técnicas (CONICET), Los Reseros y Nicolas Repetto, Hurlingham,
Buenos Aires, Argentina, 1686.

² Instituto de Patología Vegetal, Centro de Investigaciones Agropecuarias, Instituto
Nacional de Tecnología Agropecuaria (IPAVE-CIAP-INTA), 11 de setiembre 4755,
Córdoba, Argentina, X5020ICA.

³Unidad de Fitopatología y Modelización Agrícola, Consejo Nacional de
Investigaciones Científicas y Técnicas (UFYMA-CONICET), 11 de setiembre 4755,
Córdoba, Argentina, X5020ICA.

⁴Estación Experimental Agropecuaria Mendoza, Instituto Nacional de Tecnología
Agropecuaria (EEA-Mendoza-INTA), San Martín 3853, Luján de Cuyo, Mendoza,
Argentina, 5507.

*Correspondence: R.A. Cuello & S. Asurmendi

e-mail address: cuello.raul@inta.gob.ar

e-mail address: asurmendi.sebastian@inta.gob.ar

Abstract ·

Grapevine (*Vitis vinifera* L.) is highly prone to viral infections that pose a significant threat to global viticulture sustainability. Traditional detection methods, such as PCR and ELISA, are limited to well-known pathogens, highlighting the need for more comprehensive and unbiased approaches. Here, we present the development of a cost-effective viral enrichment system adapted to next-generation sequencing (NGS) for the detection and characterization of grapevine viruses. Our strategy leverages hybridization-based capture using biotin-labeled cDNA probes hereafter named "Chloro-Zero") designed to selectively deplete highly abundant host transcripts particularly plastid and ribosomal RNAs while preserving viral RNA. Probe design was informed by transcriptomic analysis of *V. vinifera*. We evaluated different subtractor-to-target RNA ratios, observing a consistent reduction of host RNA and a moderate enrichment of viral sequences. NGS analysis revealed improved recovery of low-abundance viral transcripts, with coverage levels comparable, to a certain extent, to those obtained using previously available commercial kits, but at a significantly lower cost. Although variability in depletion efficiency was observed, the results demonstrate the potential of this scalable and locally adaptable protocol for virome profiling in grapevines. By addressing key limitations of current depletion methods, our approach facilitates the detection of emerging viral threats and supports the development of more effective certification programs and sustainable management practices. Ongoing improvements in probe design and bioinformatic workflows are expected to enhance performance, providing a robust platform for broader applications in plant virology.

KEYWORDS

Grapevine virome · Next-generation sequencing (NGS) · Exome depletion system ·
Viral RNA enrichment · Chloro-Zero probes · Hybridization-capture techniques

1. INTRODUCTION

Grapevine (*Vitis vinifera* L.) is one of the most economically important fruit crops worldwide, significantly contributing to the agricultural sectors of numerous countries through the production of wine, table grapes, raisins, and related products (Estêvão et al., 2024). In Argentina, the viticulture industry plays a critical role, with more than 220,000 hectares cultivated, primarily in the Andean provinces of Mendoza and San Juan (Alonso et al., 2024). Given the perennial nature of grapevines and their vegetative propagation, these plants are particularly prone to systemic infections caused by viruses and viroids, which have a profound impact on vine health and productivity (Debat et al., 2019a; Fuchs, 2025). The dissemination of viral pathogens poses a significant threat to viticulture sustainability, as viruses reduce grape yield and quality, leading to substantial economic losses (Fuchs, 2025).

More than 100 viruses and several viroids have been identified in grapevine globally, including the Grapevine leafroll-associated virus (GLRaV), Grapevine fanleaf virus (GFLV), Grapevine virus A (GVA), and Grapevine Pinot gris virus (GPGV) (Fuchs, 2025). While traditional methods for virus detection, such as PCR and ELISA, have been used extensively, they are limited to the detection of known pathogens (Javaran et al., 2021). High-throughput sequencing (HTS) technologies have

emerged as a robust alternative, allowing for the comprehensive profiling of the "virome", the entire set of viral agents present in grapevine tissues (Hadidi et al., 2016; Adams et al., 2009). This approach is essential for the identification of emerging viral pathogens and the characterization of mixed infections, which are common in grapevines (Coetzee et al., 2010; Debat et al., 2019b).

Recent advances in next-generation sequencing (NGS) and third-generation sequencing (TGS) technologies, such as Oxford Nanopore sequencing, have further revolutionized the field of grapevine virology (Phannareth et al., 2021). These methods enable the simultaneous detection of viruses and viroids without prior knowledge of their genome sequences, thereby providing a comprehensive and unbiased analysis of the grapevine virome (Miljanić et al., 2022; Fall et al., 2020). The ability to directly sequence RNA molecules and detect viral RNA modifications offers new opportunities to study the interactions between grapevine hosts and their associated pathogens (Badial et al., 2018). Several studies have successfully demonstrated the power of these sequencing techniques in elucidating the complex interactions between viral agents in grapevine tissues (Guček et al., 2017; Al Rwahnih et al., 2009).

In addition to virus detection, advances in bioinformatics tools for the *de novo* assembly of viral genomes have significantly improved our ability to reconstruct complete viral genomes from HTS data (Soltani et al., 2021). Various assembly approaches have been employed to optimize the recovery of viral sequences from metagenomic datasets (Thapa et al., 2024). These tools are essential for identifying unknown viruses and characterizing viral variants, which can have implications for virus evolution and epidemiology (Hily et al., 2020). Studies of grapevine tissues

from different geographical regions have revealed the presence of unique viral species and variants that were previously undetectable using classical approaches (Debat et al., 2019b; Villamor et al., 2019).

To address the persistent challenges in grapevine virus detection and respond to the needs of the wine industry, we developed a comprehensive, cost-effective, and efficient method for detecting grapevine viruses using NGS technologies (Di Gaspero et al., 2022). The proposed methodological framework uses hybridization-capture techniques to enrich viral RNA before sequencing (Maina et al., 2024). This enriches viral RNA, enhancing sequencing coverage and sensitivity (Miozzi et al., 2013).

The potential impact of this work extends beyond virus detection. By characterizing the grapevine virome, it becomes possible to track the evolution of viral pathogens, identify potential quarantine risks, and support certification programs for virus-free propagation material (Maliogka et al., 2018; Abrahamian et al., 2025). This is particularly relevant given the significant costs and regulatory hurdles associated with the international movement of grapevine plant material (Campos et al., 2021). Furthermore, the ability to identify viruses in asymptomatic plants enables more effective disease management, which is critical for maintaining sustainable viticulture practices (Fuchs et al., 2025).

In summary, we developed a comprehensive NGS-based method for the detection and characterization of grapevine viruses, using advanced molecular and bioinformatics tools. This work addresses key challenges in virus diagnostics and contributes to the broader understanding of grapevine virus epidemiology and control (Jeger, 2020). The resulting platform offers versatile applications, from

strengthening certification systems to supporting healthier and more competitive grapevine propagation at both national and international levels.

2. MATERIALS AND METHODS

2.1. Sample Collection and Preparation

Vitis vinifera plant tissues used in this study were obtained from the EEA INTA Mendoza collection. Four accessions, 171, CH40, MB21, and P1103 were selected as putative virus-free sources of RNA for probe template production. In addition, a fifth accession, carrying multiple viral infections and referred to as Torrontés, was included as a test sample. Samples were obtained by tissue disruption and immediately were frozen in liquid nitrogen and stored at -80°C until processing. Frozen tissue was ground into a fine powder using a pre-chilled mortar and pestle.

2.2. RNA Extraction and probe synthesis

The RNA extraction from tissue samples was carried out using the RNeasy Plant Plus Kit (Qiagen Biotech, Beijing, China). Once the RNA was obtained, the samples were quantified and used to synthesize biotin-labeled cDNA probes. For this purpose, Biotin-16-dUTP (Merck) was employed, replacing dTTP in DNA labeling reactions at a ratio of 35% Biotin-16-dUTP and 65% dTTP. The synthesis was performed following the protocol provided by manufacturer (Thermo Fisher, Carlsbad, CA) to synthesize the first strand of cDNA using M-MLV RT starting from 1 µg of total RNA and each corresponding oligonucleotide. The biotinylated RNA-cDNA hybrid was cleaned with RNase H using the protocol suggested by the manufacturer (NEB, Ipswich, MA).

2.3. Enrichment of RNA of interest through hybridization and streptavidin pull-down

Hybridization-based capture of plant RNA to enrich viral RNA (Figure 1) was performed using two components: the biotin-labeled probe (hereafter referred to as the subtractor) and the plant RNA targeted for enrichment (hereafter referred to as the subtracted). Biotinylated cDNA probes (calculated in approximately average length ~300 nt) were hybridized to *Vitis vinifera* total RNA in 30 µl reaction volumes, using RNA:cDNA at different molar ratios (1:1 and 1:2 molar ratios corresponding to 2.27 pmol and 4.55 pmol of biotinylated cDNA, respectively). Hybridization was carried out in a thermal cycler with the following program: 95 °C for 1 min, 85 °C for 30 s, 25 °C for 1 min, followed by a hold at 4 °C.

To capture RNA–cDNA hybrids, 60 µl of streptavidin-coated magnetic beads (10 mg/ml; Roche Diagnostics GmbH, Mannheim Germany) was added, providing approximately 1080 pmol of biotin-binding capacity per reaction (manufacturer specification: $\geq 1800 \text{ pmol biotin/mg} \times 0.60 \text{ mg beads}$). This represents a large molar excess of available binding sites relative to the amount of biotinylated probe, ensuring efficient hybrid recovery.

Before use, streptavidin-coated beads were pre-washed with TEN100 buffer (10 mM Tris-HCl pH 7.5, 1 mM EDTA, 1 M NaCl). After hybrid binding, bead–RNA complexes were placed on a magnetic stand to separate the beads, and washed with at least twice the original reaction volume of TEN100 buffer for 10 min at +15 to +25 °C. The complexes were again immobilized on a magnetic stand, and the resulting supernatant—containing the RNA depleted of complementary plant sequences (i.e., enriched viral RNA)—was collected and used for sequencing.

2.4. Improvement of probe synthesis (Chloro-Zero probes)

Considering the approach described by Forsythe et al. (2022), and to improve the exome-reduction system (Figure 2), specific primers (Supplementary Table 1A) were designed to target approximately 40% of the most highly expressed grapevine genes, based on our transcriptome dataset (Table 1 and Supplementary Table 2). This strategy aimed to objectively enhance the generation of biotin-labeled cDNA, in contrast to using random primers or oligo(dT). cDNA probe synthesis was performed using this primer set following the protocol described in Section 2.2.

2.5. Real time quantitative polymerase chain reaction (qPCR)

All qPCR experiments were carried out in an ABI StepOne Plus Real Time PCR System (Applied Biosystems, California, USA). For each transcript quantification, three biological replicates were used in each treatment. qPCR data analysis and primer efficiencies were obtained using LinReg PCR software (Ruijter et al. 2009). Relative expression ratios and statistical analysis were performed using R software interface (Li et al., 2022), which uses the $2^{-\Delta\Delta Ct}$ method to analyze the relative changes in gene expression (Livak & Schmittgen 2001). A *p*-value below 0.05 was set as the cut-off for statistical significance.

2.6. Equation for Verification of Subtraction Efficiency

To ensure that the values obtained from our subtraction were objective, a modified $\Delta\Delta Ct$ method was applied. The relative abundance of viral RNA was estimated based on the relationship between Ct values for the endogenous transcript (housekeeping) and the viral transcript, using the equation: $2^{(\Delta Ct_{sws}(eg-vg)-\Delta Ct_{ss}(eg-vg))}$, where 'eg' corresponds to the endogenous transcript,

'vg' to the viral transcript, 'sws' to the sample without subtraction, and 'ss' to the subtracted sample (Figure 2c).

2.7. Sequencing and Bioinformatic Analysis

RNA Sequencing

Total RNA was extracted from *Vitis vinifera* tissue samples as described in Section 2.2. The integrity and quality of the RNA were assessed by means of agarose gel electrophoresis and bioanalyzer (Agilent 2100) . The first four libraries were subtracted using RIBO Zero (Ribo-Zero™ Magnetic Kit (Plant Leaf- Cat. No. MRZPL1224, Illumina, San Diego, CA, currently discontinued) and were subjected to Illumina Sequencing up to 100M reads per sample. The second set of four RNA libraries were prepared as follow: two controls—one subtracted with the Ribo-Zero™ as mentioned and the other without any depletion—and two experimental libraries using the Chloro-Zero methodology at “subtractor-to-subtracted” ratios of 1:1 and 2:1. Each library for this second round was sequenced on the Illumina platform to generate a minimum of 20 million paired-end reads, providing sufficient depth for comprehensive transcriptome analysis.

Quality Control and Preprocessing

Raw sequencing reads underwent quality assessment using FastQC (v0.11.9) to identify adapter contamination, low-quality bases, and overrepresented sequences. Subsequent trimming of adapters and low-quality bases was performed with Trimmomatic (v0.39) employing the following parameters: ILLUMINACLIP:TruSeq3-PE.fa:2:30:10, SLIDINGWINDOW:4:28, and MINLEN:50. Post-trimming quality was re-evaluated to confirm the effectiveness of the preprocessing steps.

Custom references Construction, Indexing, and Alignment

To enhance enrichment specificity, a series of custom references were constructed, incorporating highly expressed plastid, ribosomal, and nuclear genes, such as *psbA*, *rbcL*, ribosomal RNAs, as well as plant viral database. High-quality reads were aligned to the custom references and the *Vitis vinifera* genome (GenBank accession GCA_000003745.2) using Bowtie2 (v2.4.5) with sensitive mode parameters.

Alignment statistics, including mapping efficiency, concordant and discordant alignment rates, and coverage depth, were compiled using Samtools (v1.15.1). These metrics ensured the uniformity of alignments across libraries and allowed for an evaluation of the effectiveness of the Chloro-Zero subtraction protocol.

Transcriptomic Analysis

Reads from the RNA libraries of the first set of plant samples (CH40, MB21, 171, and P1103) were aligned to the *Vitis vinifera* reference genome (GenBank accession GCA_000003745.2) using Bowtie2 (v2.4.5) with sensitive mode parameters. Mapping statistics, including genome coverage and mapping efficiency, were calculated to evaluate transcript distribution and identify highly expressed genes. Transcript quantification was performed using eXpress (v1.5.1) (Roberts & Pachter, 2013) which enables rapid and accurate estimation of transcript abundances by modeling fragment assignment uncertainty.

In similar manners were treated the RNA reads from the MB21-derived subtraction treatments (second set of sequenced libraries, control without Ribo-Zero, Ribo-Zero-treated, and Chloro-Zero-treated at 1:1 and 2:1 subtractor-to-target ratios).

The raw data were used for de-novo transcripts assembly by means of

rnaviralSPAdes 3.15.3. From the assembled transcripts the viral ones were selected. The raw data of the four libraries (control without Ribo-Zero, Ribo-Zero-treated, and Chloro-Zero-treated at 1:1 and 2:1) were mapped against the same *Vitis vinifera* genome, the custom references transcripts and the reconstructed viral transcripts. This analysis enabled the assessment of subtraction efficiency by comparing transcript abundances, particularly for ribosomal RNAs, plastid genes, and viral RNAs.

3. RESULTS

3.1. Sensitivity Analysis and Probe Definition for Exome Depletion

To establish the detection limit of the NGS-based system, four test samples previously analyzed by gold-standard PCR were selected (Table 2). These samples, designated as CH40 (*Chardonnay*), MB21 (*Malbec*), and 171 (a recently described cultivar named *Criolla N°1*, Torres R et al., 2022), had been previously tested for the presence of *grapevine leafroll-associated virus 1-4* (GLRaV-1 to -4), *grapevine fanleaf virus* (GFLV), *grapevine fleck virus* (GFkV), *grapevine virus A* (GVA), *grapevine Pinot Gris virus* (GPGV), and *grapevine rupestris stem pitting-associated virus* (GRSPaV) (Table 2a). However, no prior information was available for sample P1103 (*Paulsen 1103*).

All samples were sequenced with a depth exceeding 100 million reads per sample, ensuring robust genome coverage and reliable detection of viral sequences. As expected, approximately 90% of the reads aligned to the *Vitis vinifera* genome, while 10% remained unmapped. The remained reads were mapped to Plant Virus

Database (<http://47.90.94.155/PlantVirusBase/#/home>) and between 0.1% and 1.1% were identified as viral or viroidal sequences (Table 2b).

Through comparative analyses, including *de novo* assemblies as previously described (e.g., Debat et al., 2019b), viral sequences were detected in all samples—even in those initially considered virus-free by PCR (Table 2c). For instance, Grapevine Pinot gris virus (GPGV) was identified in samples 171 and CH40, with over 40,000 reads mapped to this virus, consistent with PCR results. Similarly, low levels of *Grapevine Rupestris stem pitting-associated virus* (GRSPaV) were detected, ranging from 300 to 1,600 reads in CH40 and P1103 (Table 2c). On the other hand, low amounts of GPGV sequences were detected in samples P1103 and MB21 (40 and 53 reads, respectively), despite the absence of amplification in the corresponding PCR tests. A similar case was observed for GRSPaV in sample MB21, where only 3 reads were detected (Table 2c).

To confirm the presence of the detected viruses, specific primers were designed for PCR validation. Viral sequences detected by NGS and confirmed by PCR are indicated in green, while those undetected by PCR are marked in red (Table 2c). The case of sample CH40 and GLRaV-3 appears to be different. Although the virus was not detected by PCR but detected by NGS, the high number of reads mapped to GLRaV-3 suggests that this is more likely a PCR false negative error rather than a sensitivity issue. These results established two key outcomes, the identification of a candidate plant sample with minimal viral content to be used as a pure grapevine transcriptome (MB21), and the estimation of the sensitivity threshold of the NGS technique, which, under the experimental conditions applied, outperformed conventional gold-standard PCR methods in terms of accuracy.

3.2. First Methodology for Subtraction

Using RNA extracted from the MB21 sample—characterized by a minimal viral load—we implemented the subtraction protocol described in Figure 1. The method involved synthesizing biotin-dUTP-labeled probes from the complete grapevine transcriptome, hybridizing them to the RNA targets, and subsequently removing the resulting RNA–probe hybrids with streptavidin-coated magnetic beads. All steps were conducted successfully and without technical issues, confirming the feasibility of the approach.

The results of the genomic RNA subtraction, summarized in Table 3, reveal variability in subtraction efficiency across different experimental rounds. Efficiency was estimated by comparing Ct values for endogenous reference genes and viral targets between subtracted and non-subtracted RNA samples (see formula in the Materials and Methods section). In the first round, a ΔCt of 1.18 was observed in the T sample (Torrentés, high viral load), when using ST351 probes at a subtractor-to-sample ratio of 3.5:1—corresponding to a 2.26-fold enrichment of viral RNA. Similar results were obtained in round four ($\Delta\text{Ct} = 1.32$; 2.49-fold enrichment). In rounds eight and ten, subtraction efficiency improved further, with ΔCt values of 1.93 and 1.92, equivalent to 3.81- and 3.78-fold enrichment, respectively.

These findings demonstrate that the protocol enables enrichment of viral RNA to a degree that could allow the sequencing of up to four samples per run—compared to the single-sample limitation of conventional methods—while maintaining similar sensitivity and significantly reducing costs.

However, the variability observed across experimental replicates highlighted limitations in the reproducibility of the method (Table 3 shows only 4 out of 10

assays). While the results represent a step forward in achieving efficient and cost-effective viral exome enrichment, further optimization is required to improve both the reliability and consistency of the subtraction process, ensuring more effective and reproducible concentration of viral RNA while minimizing host RNA contamination.

3.3. Characterization of Transcripts for Improving Subtraction Probes

To refine subtraction efficiency, transcriptomic data from all four sequenced samples (Table 2) were further analyzed to identify the highly expressed genes. The analysis revealed that all samples exhibited similar expression profiles, with *psbA* (Photosystem II protein D1) being the most abundant transcript (Table 1a). It should be noted that all sequencing libraries analyzed in this section were subjected to rRNA depletion using the Ribo-Zero method prior to sequencing. This extremely high expression level, which is consistent with previous findings by Forsythe et al. (2022), underscores the dominance of plastid transcripts in the cellular mRNA pool. Other highly expressed plastid genes, such as *rbcL* (RuBisCO large subunit), were also observed, alongside ribosomal RNA (rRNA), whose abundance further highlights the challenge of efficient host RNA depletion. The full list of the 200 most expressed genes is provided in Supplementary Table 2.

Building on this analysis, three probes batches were designed (Table 1b): Batch 1, containing 13 rRNA genes and other 10 highly expressed genes from the top 200 list; Batch 2, comprising highly expressed plastid and mitochondrial genes identified in the transcriptomic analysis; and Batch 3, consisting endogenous highly expressed genes along with endogenous nuclear housekeeping genes such as *actin* and *nad5*. Primer batches were designed based on the selected genes and

subsequently used to synthesize cDNA probes targeting the most abundant transcripts. This approach was aimed to increased subtraction efficiency and addressed the limitations inherent to probe synthesis strategies relying on random primers or oligo(dT).

To validate the effectiveness of the improved probes set in the subtraction efficiency, specific PCR primers were designed for key targets genes in each batch (Supplementary Table 1). Genes highlighted in bold were used to assess transcript depletion and to evaluate probe performance. The complete list of primers for probes cDNAs synthesis is provided in Supplementary Table 1B, offering a comprehensive resource for future applications of this methodology.

3.4. Exome Rejection with Specific Primers (Chloro-Zero)

The three primers batches were mixed in a 1:1:1 ratio to generate biotin-labeled cDNA probes. These probes, collectively referred to as “Chloro-Zero,” were used in the hybridization and pull-down steps outlined in Figure 2a and evaluated for their efficiency in depleting highly abundant transcripts. The probes were applied at two subtractor-to-target RNA ratios, 1:1 and 2:1, to assess the subtraction efficiency and reproducibility. This design aims to optimize RNA subtraction without unintentionally depleting viral RNA.

The subtraction process was quantified by RT-qPCR, comparing the abundance of endogenous transcripts (*actin*, *nad5*, *rbcL*, *28s*, and *psbA*) against a region of *GLRaV-2* genome. Figure 2b presents qPCR results for the Actin housekeeping gene and a viral gene, comparing RNA samples before and after subtraction. The data reveals a more pronounced depletion of Actin transcripts relative to the viral gene.

The full results, summarized in Figure 2c, revealed that enrichment efficiency varied

depending on the endogenous gene and subtraction ratio. At the 1:1 ratio, *psbA* and 28s showed significant reductions of 2.07-fold and 274.72-fold, respectively. At the 2:1 ratio, the same genes showed reductions of 2.52-fold and 132.20-fold, respectively. Other genes, such as *actin7* and *nad5*, exhibited lower but consistent reductions across both ratios, ranging from 1- to 5-fold. Notably, 28s showed the highest subtraction efficiency, with reductions exceeding 270-fold under the 1:1 ratio.

The formula used to calculate enrichment efficiency (Figure 2c) ensured accuracy by accounting for the ΔC_t differences between endogenous and viral genes under subtraction or non-subtraction conditions. This approach minimized the risk of artifacts that could result from subtractor probes unintentionally binding to viral transcripts. The results consistently demonstrated significant depletion of abundant transcripts while preserving viral RNA across all replicates, confirming the robustness and reproducibility of the method.

Overall, the Chloro-Zero system effectively reduced host RNAs, enabling the enrichment of viral RNA for downstream analyses. These positive results pave the way for the next phase of research, focusing on RNA integrity and virome profiling using next-generation sequencing (NGS).

To complement the qPCR-based validation of the exome subtraction system and provide an additional layer of analysis, capillary electrophoresis using the Bioanalyzer system was incorporated. The evaluation included a non-subtracted control, and samples subjected to 1:1 and 2:1 subtraction ratios. Bioanalyzer electropherograms revealed a marked reduction in ribosomal RNA peaks (18S and 25S) in the subtracted samples, confirming the effective removal of rRNA by the

Chloro-Zero system (Figures 3b and c). As expected, the RNA Integrity Number (RIN) was only calculated for the intact control sample, where the presence of well-defined rRNA peaks allowed for a reliable assessment of RNA integrity (Figure 3a). Furthermore, the control sample enabled a direct comparison between the Chloro-Zero method and the commercial Ribo-Zero Plus rRNA Depletion Kit (Illumina®). Results suggest that the Chloro-Zero system constitutes a cost-effective alternative for reducing rRNA, tailored to the specific experimental objective of minimizing sequencing costs without compromising RNA quality.

3.6. NGS Analyzed Samples and Enrichment Efficiency

To evaluate the performance of the different tested RNA subtraction strategies, a RNAseq assay was set, four libraries using the same RNA sample were sequenced: a negative control (without Ribo-Zero), a commercial control (with Ribo-Zero subtractions), and two experimental treatments using Chloro-Zero at subtractor-to-target ratios of 1:1 and 2:1. Table 4a summarizes the RNA-seq results, including total read counts, mapping rates to the *Vitis vinifera* chloroplast and mitochondrial genomes, rRNAs genes and remaining *Vitis* nuclear genome. Comparison of Chloro-Zero-treated samples (ratios 1:1 and 2:1) with the negative control revealed a measurable effect on transcript depletion. In particular, the 2:1 Chloro-Zero treatment resulted in approximately a 10% reduction in chloroplast and in mitochondrial genome content (Table 4a). This treatment also contributed to a modest reduction in non-coding and highly expressed rRNAs. Nevertheless, Ribo-Zero® exhibited a stronger overall depletion efficiency.

Furthermore we were able to detect 7 viral RNAs in the test samples, resulting in the identification of grapevine Roditis leaf deformation virus, grapevine rupestris stem

404 pitting virus, grapevine Pinot Gris virus, grapevine fanleaf virus, grapevine virus A,
405 grapevine satellite virus, grapevine leafroll associated virus 2 and 4. Surprisingly
406 not all of them were enriched in a similar way. Chloro-Zero treatments showed their
407 potential by enriching some viral genomes RNA approximately up to 60% at the
408 better ratio showed to GRSPaV. (Table 4b)

409 While not as effective in depleting highly abundant rRNAs as Ribo-Zero (note, this
410 commercial product is no longer available as standalone reagent), the Chloro-Zero
411 system preserved and enhanced viral RNA representation, a key feature for virome
412 profiling. These results shows Chloro-Zero idea as a promising, cost-effective
413 alternative for enriching low-abundance transcripts, particularly viral RNA, without
414 requiring extensive depletion of all highly expressed RNAs.

415 **3.7. Analysis of the Increase in Subtraction Ratio**

416 To evaluate whether the efficiency of subtraction could be enhanced by modifying
417 the ratio between subtractor and target RNA, we conducted a final test using a
418 substantially higher subtractor-to-target ratio of 10:1. Endogenous reference
419 genes, including actin and several 18S rRNAs, were used as internal benchmarks
420 and compared to GLRaV-2 gene to assess the effectiveness of the subtraction.
421 Supplementary Table 3, exhibited a reduction in expression of ribosomal RNA genes
422 (e.g., 18S-2 and 28S) by 3 to 4-fold under these conditions. However, these results
423 lacked reproducibility, with inconsistent outcomes observed even at the same 10:1
424 ratio, and further attempts at a 50:1 ratio (Supplementary Table 3) did not improve
425 reliability.

426 These findings indicate that increasing the concentration of the subtractor relative
427 to the target viral RNA does not enhance the efficiency of the Chloro-Zero system.

On the contrary, such adjustments can negatively impact the methodology by introducing variability and escalating costs due to the higher consumption of labeled probes and streptavidin reagents.

Nevertheless, the ChloroZero system remains a promising approach for transcript subtraction and enrichment. Its ability to target and slightly enrich viral RNA, as demonstrated in earlier tests, highlights its potential for applications requiring cost-effective and customizable methodologies. The flexibility of Chloro-Zero, coupled with its scalability, positions it as an adaptable solution for transcriptomic studies focused on enriching low-abundance RNAs, particularly in resource-limited scenarios. Future refinements in probe design and application protocols may address the reproducibility challenges observed at high subtraction ratios, further unlocking the system's potential for virome profiling and other RNA enrichment applications

4. DISCUSSION

Next Generation Sequencing (NGS) has become an essential tool for the detection and characterization of plant viruses (Navrotskaya et al., 2021; Eichmeier et al., 2016), particularly in crops like *Vitis vinifera*, where mixed infections and asymptomatic viral reservoirs pose significant challenges for disease management. Despite its advantages, a major limitation of RNA sequencing in virome studies is the overwhelming presence of highly expressed host transcripts—particularly non-coding RNAs such as ribosomal RNAs and the unexpectedly abundant plastid-derived mRNAs (Forsythe et al., 2022). These transcripts dominate sequencing reads, often masking low-abundance viral sequences. Commercial rRNA depletion kits, like Ribo-Zero Plant, have been discontinued by the original manufacturer and

are no longer available as standalone reagents (supportassets.illumina.com).

Additionally, the lack of plant-specific formulations in current alternatives underscores the need for developing tailored strategies for plant transcriptomes.

To address these challenges, this study explored the development of a targeted subtraction approach, leveraging transcriptomic data to design customized probes capable of selectively depleting highly expressed host RNAs while preserving viral RNA.

The candidate genes selected for probe design were derived from RNA-seq data of *V.vinifera* samples, ensuring an evidence-driven approach. The most highly expressed transcripts, including *psbA* (Photosystem II protein D1), *rbcS* (RuBisCO small subunit), and multiple rRNA sequences, were consistently among the most abundant across independent biological replicates. These findings were corroborated by previous studies (Forsythe et al., 2022), reinforcing the reliability of transcript selection. Given that high transcript abundance correlates with high sequencing representation, novel transcriptomic analyses in grapevine are expected to yield similar rankings, with only minor variability on relative expression levels.

While the probe-based depletion approach holds theoretical promise, the observed rRNA depletion was limited under the conditions tested. The absence of rRNA peaks in electrophoresis profiles and chromatograms initially suggested successful subtraction, yet NGS data revealed persistent rRNA presence, with mapping percentages exceeding 50% in all Chloro-Zero-treated samples. This discrepancy aligns with previous reports showing that rRNA contamination can remain undetectable in electrophoresis yet still be present in sequencing reads (Zhao et al.,

2018). These findings highlight the importance of complementary validation methods beyond gel electrophoresis when assessing depletion efficiency.

To optimize the protocol, multiple parameters were systematically varied, including subtractor-to-target RNA ratios, probe concentrations, and streptavidin bead volumes. The experimental design ensured precise control over these variables, with rigorous adherence to hybridization and pull-down conditions. However, even at increased subtractor ratios of 10:1 and 50:1, no consistent improvement in rRNA depletion was observed. These results suggest that the hybridization efficiency or probe specificity may be limiting factors, rather than subtractor concentration alone.

The limited efficiency of rRNA depletion observed through NGS suggests that electrophoresis data may provide misleading results. A plausible explanation is that rRNA molecules were partially degraded—producing no visible peaks on electrophoresis gels yet containing fragments that remained detectable during sequencing and contributed to the residual rRNA signal. This latter hypothesis also correlates with qPCR analysis.

Despite these challenges, one of the key findings of this study was the ability of the ChloroZero protocol to enrich viral RNA. While depletion of host transcripts was limited, viral reads, particularly those corresponding to *GLRaV-2*, *-4* and *GRSPaV*, were fairly enriched in ChloroZero-treated samples. Given that RiboZero® is optimized for animal and bacterial rRNA depletion and lacks plant-specific formulations, its efficiency in plant transcriptomes remains suboptimal. The development of organism-specific depletion strategies, such as the one tested here, remains a promising direction for future research.

To further refine this methodology, improvements in probe synthesis and hybridization conditions could be explored. Outsourcing the production of biotin-labeled probes to specialized synthesis services could enhance quality control, ensuring consistent probe-to-target hybridization. Future protocol modifications could include replacing streptavidin bead-based pull-down with enzymatic degradation of hybridized fragments. Alternatives such as DNase II treatment may offer selective RNA degradation while preserving viral RNA integrity, partly due to the structured nature of viral genomes (Zhuang et al., 2024).

In summary, this study highlights the complexities of transcript depletion in plant virome studies and underscores the challenges associated with developing cost-effective alternatives to commercial depletion kits. While the tested approach did not achieve significant rRNA removal, it demonstrated the ability to enrich viral RNA, making it a valuable framework for further optimization. Future refinements in probe design, hybridization conditions, and bioinformatics analyses may ultimately lead to a more effective and reproducible subtraction method, tailored specifically for plant transcriptomes.

Acknowledgements

This work was supported by Instituto Nacional de Tecnología Agropecuaria (INTA) Grant# PD-INTA: 2023-PD-L01-I083, Agencia Nacional de Promoción de la Investigación, el Desarrollo Tecnológico y la Innovación Grants # PID 2018 -021. Additional funding was provided by Catena Institute of Wine.

CONFLICT OF INTEREST STATEMENT

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this article.

ORCID

Sebastián Asurmendi <https://orcid.org/0000-0001-9516-5948>

REFERENCES

1. Estêvão C, Rodrigues L, Rato AE, Garcia R, Cardoso H, Campos C (2024) Applicability of metabolomics to improve sustainable grapevine production. *Front Mol Biosci* 11:1395677. <https://doi.org/10.3389/fmolb.2024.1395677>
2. Alonso R, Bottini R, Piccoli P, Berli FJ (2024) Impact of climate change on Argentine viticulture: as it moves south, what may be the effect of wind? In: Gutiérrez Gamboa G, Fourment M (eds) *Latin American viticulture adaptation to climate change*. Springer, Cham, pp 189–196. https://doi.org/10.1007/978-3-031-51325-1_12
3. Debat H, Zavallo D, Luna F, Moyano S, Asurmendi S, Gomez-Talquenca S (2019a) First report of grapevine virus E infecting grapevine in Argentina. *J Plant Pathol* 101:1221–1222. <https://doi.org/10.1007/s42161-019-00282-x>
4. Fuchs, M. (2025) Grapevine viruses: Did you say more than a hundred?. *J Plant Pathol* 107, 217–227. <https://doi.org/10.1007/s42161-024-01819-5>
5. Mannini, F., Digiario, M. (2017). The Effects of Viruses and Viral Diseases on Grapes and Wine. In: Meng, B., Martelli, G., Golino, D., Fuchs, M. (eds)

- 545 Grapevine Viruses: Molecular Biology, Diagnostics and Management.
 546 Springer, Cham. https://doi.org/10.1007/978-3-319-57706-7_23
- 547 6. Javaran VJ, Moffett P, Lemoyne P, Xu D, Adkar-Purushothama CR, Fall ML
 548 (2021) Grapevine virology in the third-generation sequencing era: from virus
 549 detection to viral epitranscriptomics. *Plants* 10:2355.
 550 <https://doi.org/10.3390/plants10112355>
- 551 7. Hadidi A, Flores R, Candresse T, Barba M (2016) Next-generation sequencing
 552 and genome editing in plant virology. *Front Microbiol* 7:1325.
 553 <https://doi.org/10.3389/fmicb.2016.01325>
- 554 8. Adams IP, Glover RH, Monger WA, Mumford R, Jackeviciene E, Navalinskiene
 555 M, Samuitiene M, Boonham N (2009) Next-generation sequencing and
 556 metagenomic analysis: a universal diagnostic tool in plant virology. *Mol Plant*
 557 *Pathol* 10:537–545. <https://doi.org/10.1111/j.1364-3703.2009.00545.x>
- 558 9. Coetzee B, Freeborough MJ, Maree HJ, Celton JM, Rees DJ, Burger JT (2010)
 559 Deep sequencing analysis of RNAs from a grapevine showing Syrah decline
 560 symptoms reveals a multiple virus infection that includes a novel virus.
 561 *Virology* 400:157–163. <https://doi.org/10.1016/j.virol.2010.01.023>
- 562 10. Phannareth T, Nunziata SO, Stulberg MJ, Galvez ME, Rivera Y (2021)
 563 Comparison of Nanopore Sequencing Protocols and Real-Time Analysis for
 564 Phytopathogen Diagnostics. *Plant Health Progress* 22:31–36.
 565 <https://doi.org/10.1094/PHP-02-20-0013-RS>
- 566 11. Miljanić V, Jakše J, Kunej U, Rusjan D, Škvarč A, Štajner N (2022) First Report
 567 of Grapevine Red Globe Virus, Grapevine Rupestris Vein Feathering Virus,

- 568 and Grapevine Syrah Virus-1 Infecting Grapevine in Slovenia. Plant Dis
569 106:2315. <https://doi.org/10.1094/PDIS-05-21-1069-PDN>
- 570 12. Fall ML, Xu D, Lemoyne P, Moussa IEB, Beaulieu C, Carisse O (2020) A
571 Diverse Virome of Leafroll-Infected Grapevine Unveiled by dsRNA
572 Sequencing. Viruses 12:1142. <https://doi.org/10.3390/v12101142>
- 573 13. Badial AB, Sherman D, Stone A, Gopakumar A, Wilson V, Schneider W, King J
574 (2018) Nanopore Sequencing as a Surveillance Tool for Plant Pathogens in
575 Plant and Insect Tissues. Plant Dis 102:1648–1652.
576 <https://doi.org/10.1094/PDIS-04-17-0488-RE>
- 577 14. Guček T, Trdan S, Jakše J, Javornik B, Matoušek J, Radišek S (2016) Diagnostic
578 techniques for viroids. Plant Pathol 65:799–817.
579 <https://doi.org/10.1111/ppa.12624>
- 580 15. Al Rwahnih M, Daubert S, Golino D, Rowhani A (2009) Deep sequencing
581 analysis of RNAs from a grapevine showing Syrah decline symptoms reveals
582 a multiple virus infection that includes a novel virus. Virology 387:395–401.
583 <https://doi.org/10.1016/j.virol.2009.02.028>
- 584 16. Soltani N, Stevens KA, Klaassen V, Hwang MS, Golino DA, Al Rwahnih M
585 (2021) Quality assessment and validation of high-throughput sequencing for
586 grapevine virus diagnostics. Viruses 13:1130.
587 <https://doi.org/10.3390/v13061130>
- 588 17. Thapa P, Diksha D, Sharma SK, Khan ZA, Gupta N, Mailem YS, Prajapati MR,
589 Holkar SK, Naik S, Saha S, Baranwal VK (2024) Understanding the
590 dissemination of viruses and viroids identified through virome analysis of
591 major grapevine rootstocks and RPA-based detection of prevalent grapevine

- 592 virus B. Sci Hortic 337C:113538.
 593 <https://doi.org/10.1016/j.scienta.2024.113538>
- 594 18. Hily JM, Poulicard N, Candresse T, Vigne E, Beuve M, Renault L, Velt A,
 595 Spilmont AS, Lemaire O (2020) Datamining, genetic diversity analyses, and
 596 phylogeographic reconstructions redefine the worldwide evolutionary
 597 history of Grapevine Pinot gris virus and Grapevine berry inner necrosis virus.
 598 Phytobiomes J 4:41–55. <https://doi.org/10.1094/PBIOMES-10-19-0061-R>
- 599 19. Debat H, Zavallo D, Soltero Brisbane R, Vončina D, Almeida RPP, Blouin AG,
 600 Al Rwahnih M, Gomez-Talquenca S, Asurmendi S (2019b) Grapevine virus L:
 601 a novel vitivirus in grapevine. Eur J Plant Pathol 155:319–328.
 602 <https://doi.org/10.1007/s10658-019-01727-w>
- 603 20. Villamor DEV, Ho T, Al Rwahnih M, Martin RR, Tzanetakis IE (2019) High
 604 throughput sequencing for plant virus detection and discovery.
 605 Phytopathology 109:716–725. [https://doi.org/10.1094/PHYTO-07-18-0257-](https://doi.org/10.1094/PHYTO-07-18-0257-RVW)
 606 [RVW](https://doi.org/10.1094/PHYTO-07-18-0257-RVW)
- 607 21. Di Gaspero G, Radovic S, De Luca E, Spadotto A, Magris G, Falginella L,
 608 Cattonaro F, Marroni F (2022) Evaluation of sensitivity and specificity in RNA-
 609 Seq-based detection of grapevine viral pathogens. J Virol Methods
 610 300:114383. <https://doi.org/10.1016/j.jviromet.2021.114383>
- 611 22. Sidharthan VK, Sevanthi AM, Jaiswal S, Baranwal VK (2020) Robust virome
 612 profiling and whole genome reconstruction of viruses and viroids enabled by
 613 use of available mRNA and sRNA-seq datasets in grapevine (*Vitis vinifera* L.).
 614 Front Microbiol 11:1232. <https://doi.org/10.3389/fmicb.2020.01232>

23. Seguin J, Rajeswaran R, Malpica-López N, Martin RR, Kasschau K, Dolja VV, Otten P, Farinelli L, Pooggin MM (2014) De novo reconstruction of consensus master genomes of plant RNA and DNA viruses from siRNAs. PLoS One 9:e88513. <https://doi.org/10.1371/journal.pone.0088513>
24. Maina S, Donovan NJ, Plett K, Bogema D, Rodoni BC (2024) High-throughput sequencing for plant virology diagnostics and its potential in plant health certification. Front Hortic 9:1388028. <https://doi.org/10.3389/fhort.2024.1388028>
25. Miozzi L, Gambino G, Burgyan J, Pantaleo V (2012) Genome-wide identification of viral and host transcripts targeted by viral siRNAs in Vitis vinifera. Mol Plant Pathol 14:30–43. <https://doi.org/10.1111/j.1364-3703.2012.00828.x>
26. Maliogka VI, Minafra A, Saldarelli P, Ruiz-García AB, Glasa M, Katis N, Olmos A (2018) Recent advances on detection and characterization of fruit tree viruses using high-throughput sequencing technologies. Viruses 10:436. <https://doi.org/10.3390/v10080436>
27. Abrahamian P, Cai W, Nunziata S O, Stevens K, Hu X, Hwang M S, Costa L C, Belanger C A, Atha B, Yang Y, Soltani N, Hurtado-Gonzales O P, Al Rwahnih M, Rivera Y (2025). Interlaboratory Validation of High-Throughput Sequencing for the Detection of Viruses and Viroids in Apple, Grapevine, and Stone Fruits. Phytofrontiers 5:623-634. <https://doi.org/10.1094/phytofr-03-25-0025-r>

28. Campos G, Chialva C, Miras S, Lijavetzky D (2021) New technologies and strategies for grapevine breeding through genetic transformation. *Front Plant Sci* 12:767522. <https://doi.org/10.3389/fpls.2021.767522>
29. Fuchs, M., Al Rwahnih M, Blouin A, Burger J, Chooi K, Constable F, Ertunc F, Fiore N, Habili N, Hily J-M, Katis N, Lemaire O, Maliogka V, Maree H, Minafra A, Naidu R, Pietersen G, Saldarelli P, Schmidt A-M, Šeruga Musić M, Várallyay É (2025) A list of eclectic viruses, virus-like diseases and viroids of grapevines that should not be considered for regulatory oversight: a global plea from virologists. *J Plant Pathol* 107, 847–858. <https://doi.org/10.1007/s42161-025-01871-9>
30. Jeger MJ (2020) The epidemiology of plant virus disease: Towards a new synthesis. *Plants* 9:1768. <https://doi.org/10.3390/plants9121768>
31. Forsythe ES, Grover CE, Miller ER, Sloan DB (2022) Organellar transcripts dominate the cellular mRNA pool across plants of varying ploidy levels. *Proc Natl Acad Sci USA* 119:e2204187119. <https://doi.org/10.1073/pnas.2204187119>
32. Ruijter JM, Ramakers C, Hoogaars WMH, Karlen Y, Bakker O, van den Hoff MJB, Moorman AFM (2009) Amplification efficiency: Linking baseline and bias in the analysis of quantitative PCR data. *Nucleic Acids Res* 37:e45. <https://doi.org/10.1093/nar/gkp045>
33. Li X, Wang Y, Li J, Mei X, Liu Y, Huang H (2022) qPCRtools: an R package for qPCR data processing and visualization. *Front Genet* 13:1002704. <https://doi.org/10.3389/fgene.2022.1002704>

34. Livak KJ, Schmittgen TD (2001) Analysis of relative gene expression data using real-time quantitative PCR and the 2- $\Delta\Delta$ CT method. *Methods* 25:402–408. <https://doi.org/10.1006/meth.2001.1262>
35. Roberts A, Pachter L (2013) Streaming fragment assignment for real-time analysis of sequencing experiments. *Nat. Methods* 10:71–73. <https://doi.org/10.1038/nmeth.2251>
36. Torres R, Aliquó G, Toro A, Fernández F, Tornello S, Palazzo E, Sari S, Fanzone M, De Biazzi F, Oviedo H J, Segura R, Laucou V, Lacombe T, Prieto J A (2022) Identification and recovery of local *Vitis vinifera* L. cultivars collected in ancient vineyards in different locations of Argentina. *Aust Jour of Grape and Wine Res.* 4: 521-657. <https://doi.org/10.1111/ajgw.12561>
37. Navrotskaya E, Porotikova E, Yurchenko E, Galbacs ZN, Varallyay E, Vinogradova S (2021) High-throughput sequencing of small RNAs for diagnostics of grapevine viruses and viroids in Russia. *Viruses* 13:2432. <https://doi.org/10.3390/v13122432>
38. Eichmeier A, Komínková M, Komínek P, Baránek M (2016) Comprehensive virus detection using next generation sequencing in grapevine vascular tissues of plants obtained from the wine regions of Bohemia and Moravia (Czech Republic). *PLoS One* 11:e0167966. <https://doi.org/10.1371/journal.pone.0167966>
39. Zhao S, Zhang Y, Gamini R, Zhang B & von Schack D (2018) Evaluation of two main RNA-seq approaches for gene quantification in clinical RNA sequencing: polyA+ selection versus rRNA depletion. *Sci Rep.* 2018;8(1): 4781. <https://doi.org/10.1038/s41598-018-23226-4>

684 40. Zhuang J, Du X, Liu K, Hao J, Wang H, An R, Liang X (2024) *DNase II can*
685 *efficiently digest RNA and needs to be redefined as a nuclease*. *Cells*
686 13:1525. <https://doi.org/10.3390/cells13181525>
687

Figure legends

Figure 1. Conceptual diagram of expressed exome rejection. Section 1. Starting from our RNA extraction, biotin-labeled cDNA probes are made with a pool of random primers + oligo(dT). **Section 2.** Pull down of the hybrids formed between the labeled cDNA and the plant RNA using streptavidin beads. This captured exome is discarded, leaving the RNA that remains in suspension. **Section 3.** Once ready, the RNA is cleaned, to be used to evaluate the depth of viral enrichment through qPCR.

Figure 2. Conceptual diagram of accurate exome rejection with Chloro-Zero. 2a. Same methodology described in Figure 1 but with the replacement of the cDNA probes made from the primers batches (Chloro-Zero) listed in Table 1b. **2b.** Examples of real-time qPCR analyses of subtractions at different subtractor to target ratios, both 1:1 and 2:1, with the formula for calculating the associated ratios between subtracted RNA and non-subtracted RNA. 'eg' corresponds to the endogenous gene, 'vg' to the viral gene, 'sws' to the sample without subtraction, and 'ss' to the subtracted sample. **2c.** The table shows the differences corresponding to each enrichment rate, comparing some endogenous and ribosomal genes against a viral gene of GLRaV-2.

Figure 3. Contrast between control and subtracted (enriched) samples. Electrophoresis analysis (Bioanalyzer) of RNAs from **a.** Sample of the Torrontés cultivar. **b** and **c**, same sample analyzed after performing exome rejection in a subtraction ratio of 1:1 and 2:1 between subtractor (biotinylated designed probes) and subtracted (target RNA). Note that in both graphs **b** and **c**, unlike in **a**, the peaks associated with ribosomal 18s and 25s disappear, suggesting that these have been eliminated or degraded.

714 Table legends

715

716 **Table 1. Characterization of transcripts associated with plastids and**
717 **ribosomes. 1a:** Abbreviated list of the 200 most expressed genes in grapevine,
718 representing a considerable percentage of reads ($\approx$ 50% of the total reads) with their
719 respective biological functions. **1b:** Chlro-Zero Batches of genes that target
720 ribosomal, plastid, most expressed endogenous genes and some particular
721 reference genes such as Actin and NAD. Primers used to target these genes are to
722 improve the system for constructing labeled probes, replacing random primers and
723 oligo(dT).

724 **Table 2. Analysis of samples by gold standard PCR and Next-Generation**
725 **Sequencing (NGS). 2a.** Grapevine plants whose viruses were characterized by
726 standard PCR detection. These were GLRaV-1,2,3,4 (Grapevine Leafroll associated
727 Virus), GFLV (Grapevine Fanleaf Virus), GFkV (Grapevine Fleck Virus), GVA
728 (Grapevine Virus A). The only grapevine cultivar not tested before was the Paulsen
729 P1103 rootstock. After sequencing, primers were designed to confirm the presence
730 of GPGV (Grapevine Pinot gris Virus) and GRSaV (Grapevine Rupestris Stem pitting-
731 associated Virus). **2b.** Reads exceeding 100 M per sample. Note that 90% or more
732 of the mappings are associated with grapevine, 8% do not map to grapevine, and
733 only 0.12% to 1.12% map to viral sequences. **2c.** Of the sequences that map to
734 viruses, we could establish a detection limit more sensitive than a gold standard
735 PCR. Viruses confirmed by PCR afterwards are marked in green, while those not
736 confirmed are marked in red, establishing a new standard to define virus-free or
737 virus-infected samples

738 **Table 3. Results of subtractions with random primers and Oligo (dt).** Differences
739 in Ct values between control T (Torrontés) and the corresponding subtraction were
740 observed in subtraction rounds 1, 4, 8, and 10: in round 1, the subtraction ratio was
741 3.5:1 between subtractor and subtracted, the same for round 4. In round 8, the ratio
742 was 5:1, and in round 10, it was 2:1.

743

744 **Table 4 - Overview analysis of samples analyzed by NGS**

745 This table presents sequencing results obtained from the same RNA sample under
746 four conditions designed to evaluate different RNA subtraction strategies: a
747 negative control without Ribo-Zero, a commercial control with Ribo-Zero
748 subtraction, and two experimental treatments using Chloro-Zero at subtractor-to-
749 target ratios of 1:1 and 2:1. Panel (a) shows general mapping statistics for the
750 sequenced samples. Panel (b) compares viral genome detection across seven
751 grapevine viruses (GRLDaV, GRSPaV, GPGV, GFLV, GLRaV2, GLRaV3, and GVA)
752 among the four conditions.

753

754 **Supplementary Table 1**

755 Primers sequence list, A Chloro-Zero primers. B qPCR primers.

756 **Supplementary Table 2**

757 Top 200 most expressed transcripts per library (MB21, P1103, CH40, 171), ranked
758 by counts; IDs and descriptions standardized to RefSeq (XM_/XR_/NM_). Here, NM_
759 denotes curated RefSeq mRNAs, XM_ predicted model mRNAs, and XR_ predicted
760 model non-coding RNAs. A small subset of NM_ accessions lacks an associated
761 description in this dataset (left blank).

762 **Supplementary Table 3**

763 **Analysis of the increase in enrichment ratio.** Different subtractions comparing an
764 endogenous gene such as actin and different ribosomal genes (18s 1, 2, 3, and 28s
765 listed in Table 3c) against a viral gene such as GLRaV-2 in a 10:1 fold between
766 subtractor and target. Note that although the results for 18s 2 and 28s appear
767 favorable by reducing the expression of ribosomal genes by 3 to 4, even 5 times,
768 they were not reproducible, neither at the same 10:1 ratio nor at a higher 50:1 ratio.

Figure 1 - First methodology of subtraction

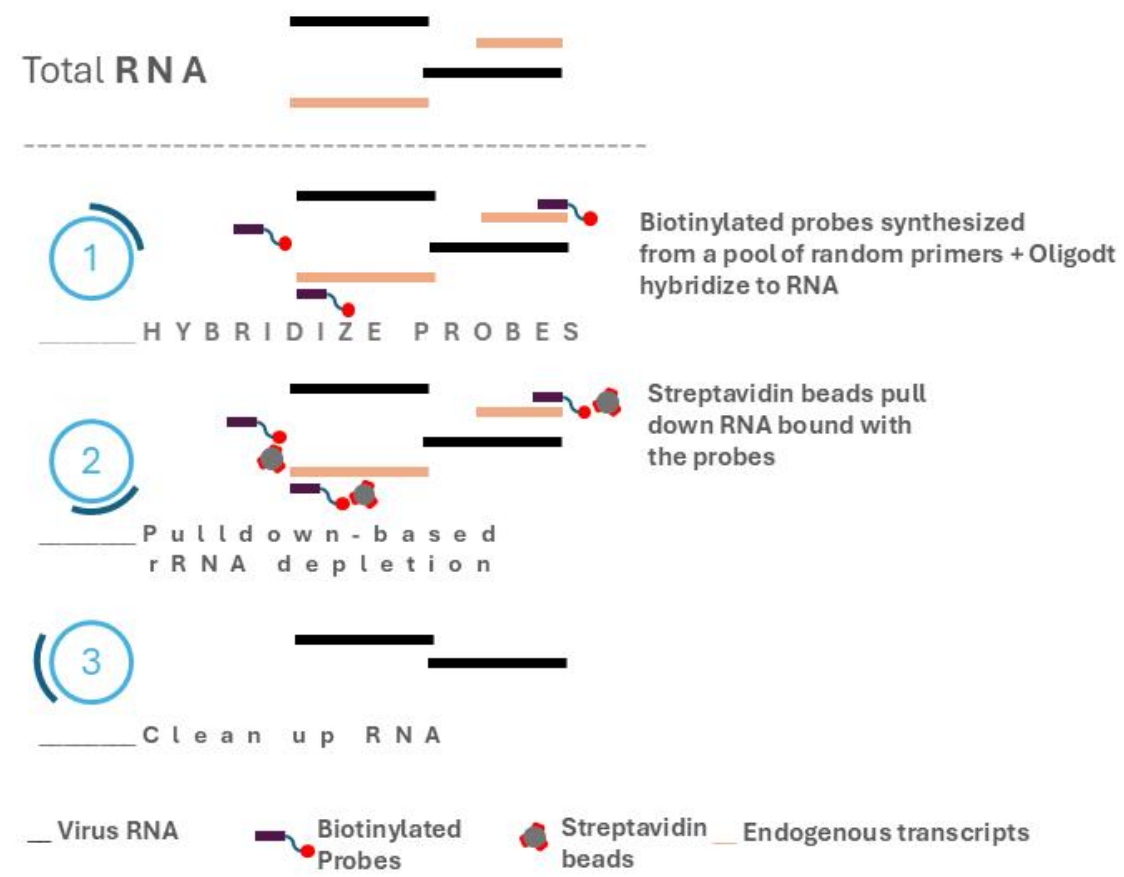


Figure 2 – Conceptual diagram of accurate exon rejection with Chloro-Zero

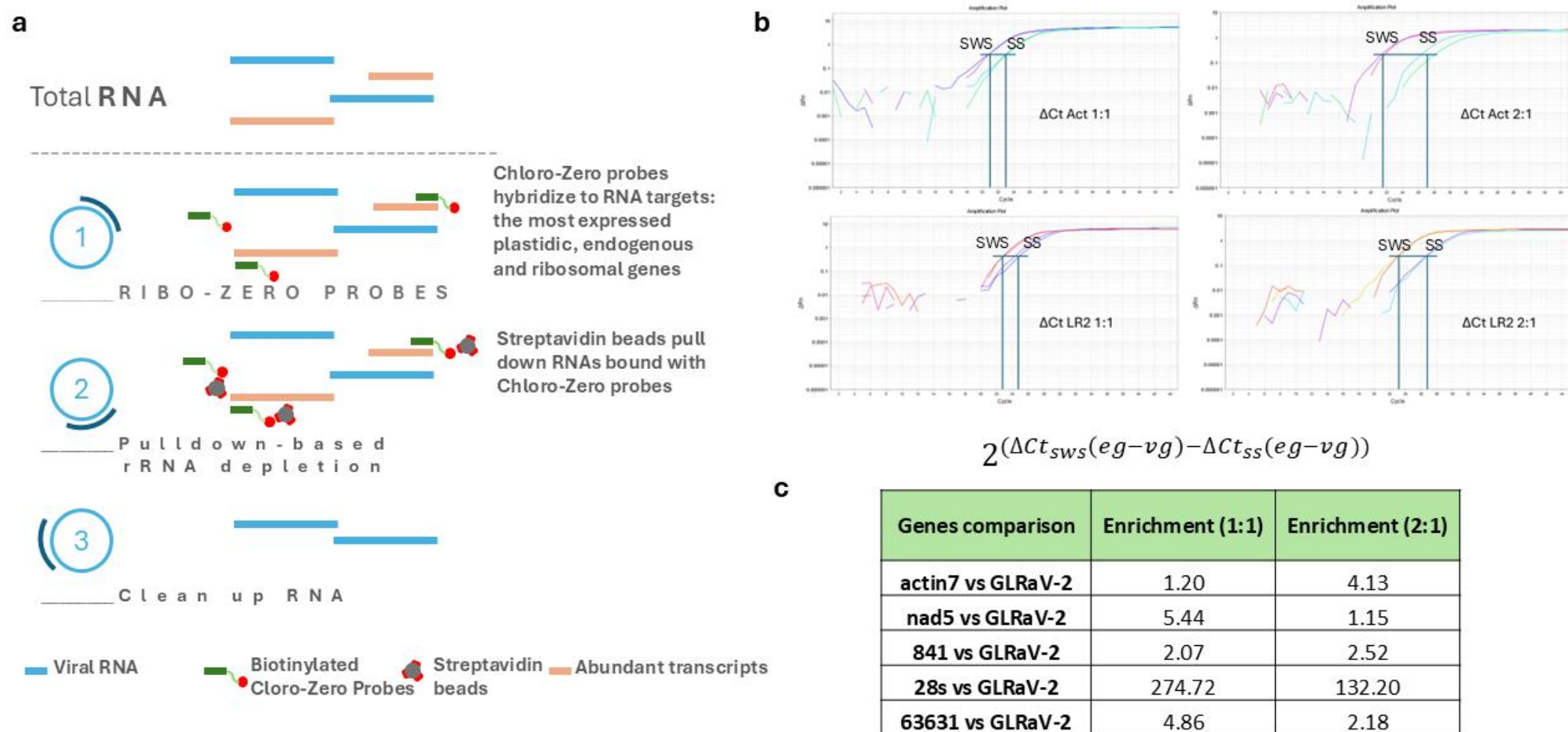


Figure 3 - Contrast between control and sustracted (enriched) samples

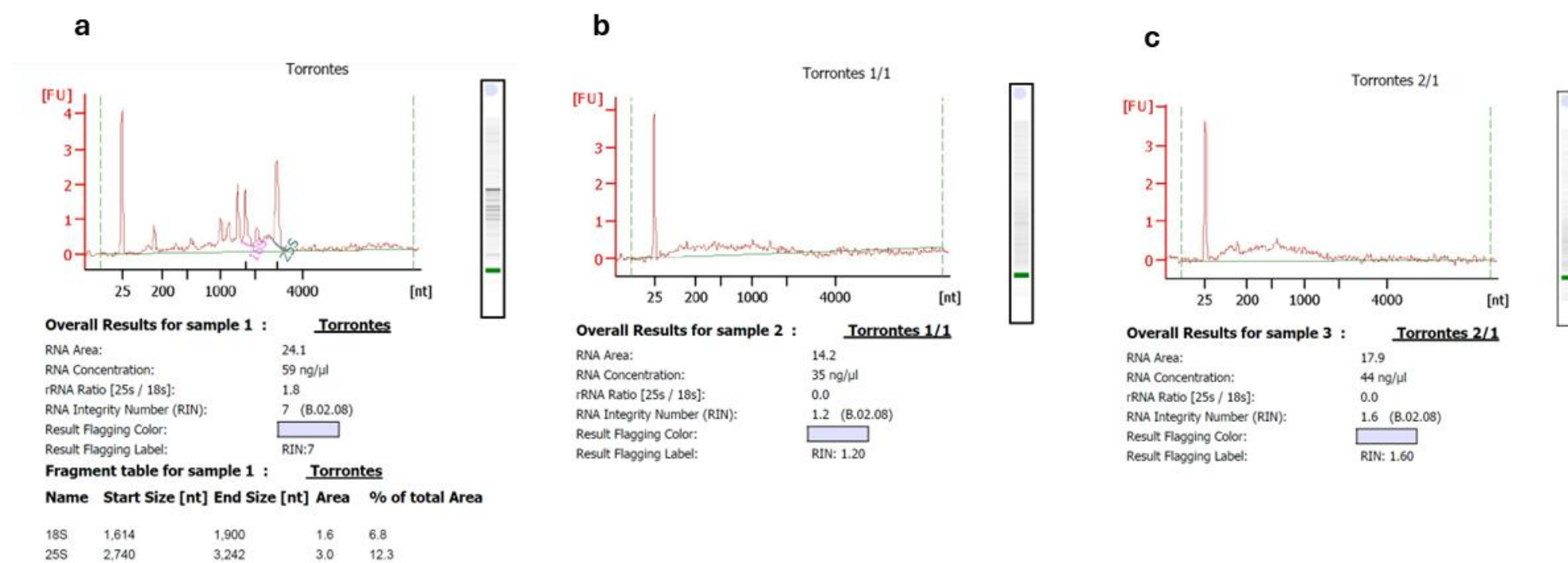


Table 1 - Characterization of transcripts associated with plastids and ribosomes

a

Gene name	Counts	Description
ViviCp001	23273776	psbA photosystem II protein D1
ViviM_p049	5864041	psbA PSII 32 kDa protein
ViviCp029	3718155	rbcL RuBisCO large subunit
ViviCp017	1760935	psbC PSII 43 kDa protein
ViviM_p010	1692599	rbcL ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
ViviCp016	815859	psbD photosystem II protein D2
ViviCp048	733230	psbB photosystem II P680 chlorophyll A apoprotein
ViviCp052	418293	petB cytochrome b6

b

Batch 1	Batch 2	Batch 3
Rv_18S_rRNA_1	Rv_YP_567084.1	VvActinR
Rv_18S_rRNA_2	Rv_YP_567084.2	qVv-nad5-R
Rv_18S_rRNA_3	Rv_YP_567072.1	Rv_YP_567063.1
Rv_18S_rRNA_4	Rv_YP_567072.2	Rv_XM_019225640.1
Rv_18S_rRNA_5	Rv_YP_567071.1	Rv_YP_567056.1
Rv_28S_rRNA_1	Rv_YP_567103.1	Rv_YP_567056.2
Rv_28S_rRNA_2	Rv_YP_567075.1	Rv_YP_567106.1
Rv_28S_rRNA_3	Rv_YP_567107.1	Rv_XM_019218790.1
Rv_5S_rRNA_2	RV_YP_002608363.1	Rv_XM_002267690.4
Rv_5_8S_rRNA_1	Rv_YP_002608363.2	Rv_XM_002284027.3
Rv_5_8S_rRNA_2	Rv_YP_567057.1	Rv_YP_567061.1
Rv_GQ849399.1	Rv_XM_019216320.1	Rv_YP_002608395.1
Rv_KF544886.1	Rv_YP_567108.1	Rv_YP_567138.1
8S_rRNA_498_r	Rv_YP_567074.1	Rv_YP_567083.1
Rv_XM_002271755.3	Rv_XR_002030730.1	Rv_YP_002608358.1
Rv_YP_567129.1	Rv_XR_002031531.1	Rv_YP_567064.1
Rv_YP_002608376.1	Rv_XR_002031185.1	Rv_YP_567102.1
Rv_NM_001281136.1	Rv_XM_003632139.2	Rv_XM_002285821.3
Rv_YP_567131.1	Rv_XM_019216227.1	Rv_YP_567077.1
Rv_XM_002278316.4	Rv_YP_567133.1	Rv_XR_004652793.1
Rv_XM_019220594.1	Rv_YP_567093.1	Rv_XM_002267296.3
Rv_XM_002271651.4	Rv_YP_567059.1	Rv_YP_002608358.1
Ribo + genes	Chloro More expressed	Chloro More expressed 2 + actin + nad5

Table 2 - Analysis of samples by gold standard PCR and Next-Generation Sequencing (NGS)

a

Sample name	GLRaV-1	GLRaV-2	GLRaV-3	GLRaV-4	GFLV	GFkV	GVA	GPGV	GRSPaV
CH 40	(-)	(+)	(-)	(-)	(-)	(-)	(-)	(+)	(+)
MB 21	(-)	(-)	(-)	(-)	(-)	(-)	(-)	(-)	(-)
171	(-)	(-)	(-)	(-)	(-)	(-)	(-)	(+)	NT
P1103	Not tested before							(-)	(+)

b

Sample name	Total lectures (M)	Mapped to grapevine (%)	Not mapped (%)	Mapped to virals in database (%)
CH40	126	92	8	1.12
MB21	113.5	92.52	7.84	0.43
171	128	90	10	0.24
P1103	104	91	9	0.12

c

Sample name	GPGV	GRSPaV	GLRaV-3
171	40,255	0	3
P1103	40	1,638	5
CH40	170,227	308	35,143
B21	53	3	0

Table 3 – Results of subtractions with random primers and Oligo (dt)

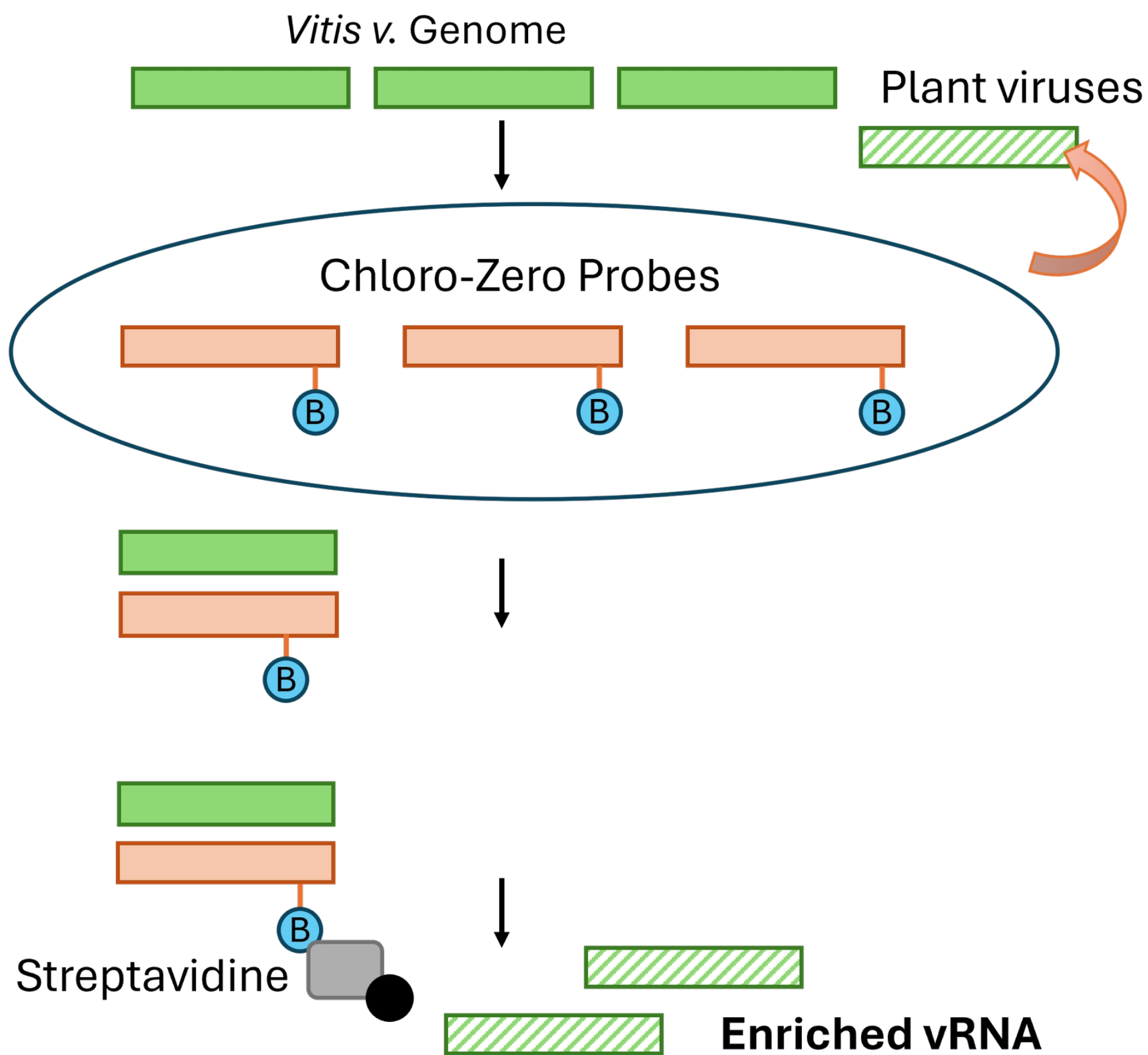
Round	Sample	Ct	Difference between ct's	Level of enrichment
1	T	6.292	1.18	2.26
	ST351	5.116		
4	T	4.77	1.32	2.49
	ST351	3.455		
8	T	7	1.93	3.81
	ST51	5.071		
10	T	8.044	1.92	3.78
	ST21	6.127		

Table 4a - Overview analysis of samples analyzed by NGS

Treatment/ # Total Reads		Mapping to <i>Vitis v.</i> Chloroplast genome	Mapping to <i>Vitis v.</i> Mitochondria genome	Mapping to remaining <i>Vitis v.</i> genome	Mapping to remaining <i>Vitis v.</i>	Unmapped reads	Mapping to Virus Genomes database
Chloro-Zero 1:1	Reads	11,740,939	303,879	13,300,587	2,336,443	4,795,251	59,556
32,477,099	%	36.2%	0.94%	41.0%	7.19%	14.8%	0.18%
	RPM	361,514.40	9,356.72	409,537.41	71,941.25	147,650.23	1,833.78
Chloro-Zero 2:1	Reads	12,014,477	317,528	13,334,000	2,473,549	7,027,758	60,798
35,167,312	%	34.16%	0.90%	37.92%	7.03%	19.98%	0.17%
	RPM	341,637.63	9,029.07	379,158.92	70,336.60	199,837.79	1,728.82
RiboZero®	Reads	11,004,752	355,295	23,963	5,251,144	3,836,218	1,256,729
20,751,288	%	53.03%	1.71%	0.12%	25.31%	18.49%	6.06%
	RPM	530,316.58	171,21.59	1,154.77	253,051.47	184,866.50	60,561.49
Negative Control without Ribozero	Reads	13,995,818	368,919	14,921,595	2,761,800	5,558,118	67,32
37,606,250	%	37.22%	0.98%	39.68%	7.34%	14.78%	0.18%
	RPM	372,167.34	9,810.04	396,784.98	73,439.92	147,797.72	1,790.13

Table 4b - Overview analysis of samples analyzed by NGS

Library/ # Total Reads		Detected Virus						
		GRLDaV	GRSPaV	GPGV	GFLV	GLRaV2	GLRaV3	GVA
Chloro-Zero 1:1	Reads	568.00	8,373.00	2,184.00	47,797.00	313.00	76.00	247.00
32,477,099.00	RPM	17.49	257.81	67.25	1,471.71	9.64	2.34	7.61
	Enrichment compared to Negative Control (untreated samples)	0.93	1.60	1.16	0.96	1.21	1.28	0.93
Chloro-Zero2:1	Reads	578.00	7,222.00	2,188.00	50,181.00	278.00	72.00	295.00
35,167,312.00	RPM	16.44	205.36	62.22	1,426.92	7.91	2.05	8.39
	Enrichment compared to Negative Control (untreated samples)	0.88	1.27	1.07	0.93	0.99	1.12	1.02
RiboZero®	Reads	11,242.00	96,269.00	45,649.00	1,095,921.00	4,191.00	1,002.00	1,838.00
20,751,288.00	RPM	541.75	4,639.18	2,199.82	52,812.19	201.96	48.29	88.57
	Enrichment compared to Negative Control (untreated samples)	28.86	28.77	37.79	34.47	25.32	26.32	10.78
Negative Control with out Ribozero	Reads	706.00	6,065.00	2,189.00	57,614.00	300.00	69.00	309.00
37,606,250.00	RPM	18.77	161.28	58.21	1,532.03	7.98	1.83	8.22



No.	Oligo Name	5' - Oligo Seq - 3'
1	Rv_18S_rRNA_1	ACGAATGTCTCTGACCATCCTT
2	Rv_18S_rRNA_2	AGGCACGACCCGACTAGTTA
3	Rv_18S_rRNA_3	ACTGCGATCCGAACACTTCA
4	Rv_18S_rRNA_4	GTTCCCCTACGGCTACCTTG
5	Rv_18S_rRNA_5	AGTAACGACTTCGGGCATGG
6	Rv_28S_rRNA_1	GCAAGGCCACTCTACCACTT
7	Rv_28S_rRNA_2	GGGCAAAAATCACACTGCGT
8	Rv_28S_rRNA_3	AGGAACCGAACTGTCTCACG
9	Rv_5S_rRNA_1	CAACACGAGGACTTCCCAGG
10	Rv_5S_rRNA_2	ACGAGGACTTCCCAAGAGGT
11	Rv_5_8S_rRNA_1	GTGCCCTCAACCTAATGGCT
12	Rv_5_8S_rRNA_2	TCGGTCTAATGGCTTCAGGC
13	Rv_GQ849399.1	CCAGCGGAGTCCTAAAAGCA
14	Rv_KF544886.1	TTAAACTCAGCGGGTGGTCC
15	VvAtinR	TCCTGTGGACAATGGATGGA
16	qVv-nad5-R	TCCCTCCCATCCCAGGAATAATTG
17	8S_rRNA_498_r	CTGCCTTCCTTGATGTGGTA
18	Rv_YP_567084.1	CCTCACGAGCAAGATCACGT
19	Rv_YP_567084.2	TCACGAGCAAGATCACGTCC
20	Rv_YP_567072.1	GCGTGCCACAAATGACCTAC
21	Rv_YP_567072.2	TTCAAATCCTGCTGCAGCTG
22	Rv_YP_567071.1	ACGGGGTAGAACCTCCTCAG
23	Rv_YP_567103.1	GAGCATCCAAATCCGGGTCA
24	Rv_YP_567075.1	CCCGATGTGGAGGCAATCAA
25	Rv_YP_567107.1	CACACTAGCACTTCCGCGTA
26	Rv_XM_002276931.4	CGTTTACATGGCCACCAACG
27	RV_YP_002608363.1	TAGGGAACGCTCTGCCTAGT
28	Rv_YP_002608363.2	CACGGGTATAGGGAACGCTC
29	Rv_YP_567057.1	GAGCCAAAGTTCGAGCACAA
30	Rv_XM_019216320.1	ACAGACATCCAGCTATGGCT
31	Rv_YP_567108.1	AACGGTTGTCGCTACTGGAC
32	Rv_YP_567074.1	CCAACTTGATCTTGTTGCCCC
33	Rv_XR_002030730.1	AGCTCCTTTCCTTGAGTGGTG
34	Rv_XR_002031531.1	AAACAAGCAGAGCCAGACCA
35	Rv_XR_002031185.1	TGCTTGTTTCATGCCTCCAGA
36	Rv_XM_003632139.2	TGACCAATTCCTCATTCCCCAG
37	Rv_XM_019216227.1	TTGCAGTGCTGTGACAGTCA
38	Rv_YP_567133.1	TGGTCCATTCTCAGCCTAGGT
39	Rv_YP_567093.1	CAAAGGATCAAAACGGCCGG
40	Rv_YP_567059.1	TCGAAAACCTACAGCGGCTTG
41	Rv_YP_567063.1	TGCTAATGCTACAACCAGTCCA
42	Rv_XM_019225640.1	GTTCAACACTCCCCCTCAGG
43	Rv_YP_567056.1	ACCAAGGTTAGCACGGTTGA
44	Rv_YP_567056.2	TCCATACCAAGGTTAGCACGG
45	Rv_YP_567106.1	ATAGAGCCATTGCGACACCC

46	Rv_XM_019218790.1	TCACAGTAGCAGGGTCGCTA
47	Rv_XR_002031186.1	GCTTCCCAAGGGTACAAGGG
48	Rv_XM_002267690.4	TGACTGATCTCATCTGCAGGA
49	Rv_XM_002284027.3	CCTCCAGCAGAAGGACCATC
50	Rv_YP_567061.1	GGTTTCTGCTTCCTCGGTGA
51	Rv_YP_002608395.1	TGGCATTGATCACAGAATCCA
52	Rv_YP_567138.1	TAATTTGCGCACGTGAGGGGT
53	Rv_YP_567083.1	CTTCGCGGTAGCTTCATCGA
54	Rv_YP_567083.1	CTTCGCGGTAGCTTCATCGA
55	Rv_YP_002608358.1	TGTTCAACAGCCCAAGGACT
56	Rv_YP_567064.1	TTCGCCTATATAAGCCGCGG
57	Rv_YP_567102.1	TGGGCTTCTGTTGCTGACAT
58	Rv_XM_002285821.3	GTCACAAATTTCCCGACCCG
59	Rv_YP_567077.1	TTCGAAACGCCTCGTGATCT
60	Rv_XR_004652793.1	ATCTCAGTGGATCGTGGCAG
61	Rv_XM_002267296.3	AAACCAAGCCCAGACACGAA
62	Rv_XM_002271755.3	ACAAGAAGAGCACCCCCAAG
63	Rv_YP_567129.1	TAAGCTAGACCCATGCTGCG
64	Rv_YP_002608376.1	TAAGCTAGACCCATGCTGCG
65	Rv_NM_001281136.1	AGTGCTCAACTCTCTGCGAA
66	Rv_YP_567131.1	GCCACAGCAATTGCACCTAT
67	Rv_XM_002278316.4	AGCCACTACTCCCAAATCCG
68	Rv_XM_019220594.1	GGCAGACAGACAAGAAGCCA
69	Rv_XM_002271651.4	GGCAACAAAGGAGCTGGTCT

70

71

72

73

74

75

76

77

78

79

80

81

No.	Oligo Name	5` - Oligo Seq - 3`
1	Fw_18S_rRNA_1	CCTTCTACTGGCGATGTGCT
2	Rv_18S_rRNA_1	ACGAATGTCTCTGACCATCCTT
3	Fw_28S_rRNA_1	ATCCAGGCTAGAAAGTGACGC
4	Rv_28S_rRNA_1	GCAAGGCCACTCTACCACTT
5	Fw_5S_rRNA_1	TGCGATCATACCAGCACTAATG
6	Rv_5S_rRNA_1	CAACACGAGGACTTCCCAGG
7	VvActinF	CTTGCATCCCTCAGCACCTT
8	VvAtinR	TCCTGTGGACAATGGATGGA
9	qVv-nad5-F	GCTTCTTGGGGCTTCTTGTTCCG
10	qVv-nad5-R	TCCCTCCCATCCCAGGAATAATTG
11	LR 2P19qtF4	CTAACAATTTCTTCTTTGGATCGCAT
12	LR2 P24qtR	AGAATGTCTTCAGCTTCATAAGGAG

Library	ID	Counts	Description
MB21	XM_019221016.1	1733675	Vitis vinifera ribulose biphosphate carboxylase large chain (LOC109122894), partial mRNA
MB21	XM_010654474.1	676187	Vitis vinifera cytochrome P450 81E8-like (LOC100242168), mRNA
MB21	XM_019218790.1	381333	Vitis vinifera photosystem II CP47 reaction center protein-like (LOC109122277), mRNA
MB21	XM_002276931.4	368054	Vitis vinifera ribulose biphosphate carboxylase small chain, chloroplastic-like (LOC100267942), mRNA
MB21	XM_019216320.1	314406	Vitis vinifera pentatricopeptide repeat-containing protein At1g19720 (LOC100255764), mRNA
MB21	XR_002030730.1	307899	Vitis vinifera uncharacterized LOC104880458 (LOC104880458), ncRNA
MB21	XR_002030742.1	251833	Vitis vinifera uncharacterized LOC109123058 (LOC109123058), ncRNA
MB21	XM_019216227.1	246549	Vitis vinifera pentatricopeptide repeat-containing protein At5g40410, mitochondrial (LOC100260830), mRNA
MB21	XM_003632139.2	244681	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100263871), transcript variant X2, mRNA
MB21	XR_002031185.1	244443	Vitis vinifera uncharacterized LOC109123445 (LOC109123445), ncRNA
MB21	XR_788116.2	242292	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X1, ncRNA
MB21	XR_788122.2	242291	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X2, ncRNA
MB21	XR_788121.2	242290	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X3, ncRNA
MB21	XR_788119.2	242285	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X4, ncRNA
MB21	XR_788124.2	242284	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X5, ncRNA
MB21	XR_002031529.1	242283	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X6, ncRNA
MB21	XR_002031531.1	242282	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X7, ncRNA
MB21	XM_002282200.3	229111	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100263871), transcript variant X1, mRNA
MB21	XR_002031186.1	180588	Vitis vinifera uncharacterized LOC109123446 (LOC109123446), ncRNA
MB21	XR_002031525.1	146718	Vitis vinifera uncharacterized LOC109123733 (LOC109123733), ncRNA
MB21	XM_002281184.4	136238	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100242821), mRNA
MB21	XR_002031535.1	134226	Vitis vinifera uncharacterized LOC109123739 (LOC109123739), ncRNA
MB21	XM_002281318.3	131220	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100249533), mRNA
MB21	XM_002281224.4	127565	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100259921), mRNA
MB21	XM_002281358.3	125940	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100244376), mRNA
MB21	XM_002280439.4	125688	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100249153), mRNA
MB21	XM_002280596.3	123876	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100250883), mRNA
MB21	XM_002281249.4	123060	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100265108), mRNA
MB21	XR_078097.3	114068	Vitis vinifera 18.2 kDa class I heat shock protein-like (LOC100266701), misc_RNA
MB21	XM_002281420.3	108063	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100261497), mRNA
MB21	XM_010646105.2	101932	Vitis vinifera polyubiquitin (LOC100267431), mRNA
MB21	XM_019225640.1	98298	Vitis vinifera uncharacterized mitochondrial protein AtMg00810-like (LOC109124071), mRNA
MB21	XM_010649010.2	96334	Vitis vinifera ATP synthase subunit alpha, mitochondrial (LOC104878494), mRNA
MB21	XM_002283496.3	95976	Vitis vinifera heat shock 70kDa protein 1/8-like (LOC100254725), mRNA
MB21	XM_010646102.2	94737	Vitis vinifera polyubiquitin (LOC104877307), mRNA
MB21	XM_002267690.4	93093	Vitis vinifera probable fructose-bisphosphate aldolase 1, chloroplastic-like (LOC100262354), mRNA
MB21	XM_002280461.3	89917	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100254252), mRNA
MB21	XM_002284027.3	88358	Vitis vinifera heat shock cognate 70 kDa protein 2-like (LOC100265651), mRNA
MB21	XM_019220594.1	81802	Vitis vinifera heat shock cognate 70 kDa protein-like (LOC100253562), transcript variant X1, mRNA
MB21	XM_003632976.3	79889	Vitis vinifera chlorophyll a-b binding protein 40, chloroplastic-like (LOC100252004), mRNA
MB21	XM_019220595.1	75609	Vitis vinifera heat shock cognate 70 kDa protein-like (LOC100253562), transcript variant X2, mRNA
MB21	XM_002263563.3	75433	Vitis vinifera heat shock cognate 70 kDa protein 1-like (LOC100259551), mRNA
MB21	XM_002275039.3	73652	Vitis vinifera chlorophyll a-b binding protein of LHCII type 1 (LOC100241745), mRNA
MB21	NM_001281136.1	68211	Vitis vinifera Bcl-2-associated athanogene-like protein (LOC100260747), mRNA
MB21	XM_002280611.4	67404	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100245734), mRNA
MB21	NM_001280938.1	65701	Vitis vinifera small heat shock protein 17.3 kDa (LOC100243983), mRNA
MB21	XM_003634988.3	62311	Vitis vinifera heat shock cognate protein 80 (LOC100246843), mRNA
MB21	XM_002280424.4	61568	Vitis vinifera 17.1 kDa class II heat shock protein (LOC100266315), mRNA
MB21	XM_002280644.3	60322	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100268056), mRNA
MB21	XM_003631877.3	60232	Vitis vinifera catalase isozyme 1 (LOC100853165), mRNA
MB21	NM_001281169.1	60119	Vitis vinifera catalase (GCAT), mRNA
MB21	XM_003631761.3	60089	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100854120), mRNA
MB21	XM_002267296.3	59956	Vitis vinifera 23.6 kDa heat shock protein, mitochondrial (LOC100253548), mRNA
MB21	XM_002270535.3	58794	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100256315), mRNA

MB21	XM_002271651.4	58495	Vitis vinifera chlorophyll a-b binding protein 151, chloroplastic-like (LOC100254533), mRNA
MB21	XM_002278316.4	58092	Vitis vinifera glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic (LOC100246378), mRNA
MB21	XM_010650056.2	52054	Vitis vinifera glycine dehydrogenase (decarboxylating), mitochondrial (LOC100266170), mRNA
MB21	XM_002280449.3	51893	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100261109), mRNA
MB21	XM_002265911.3	51722	Vitis vinifera galactinol synthase 1 (LOC100260266), mRNA
MB21	XM_002271755.3	51443	Vitis vinifera photosystem II 10 kDa polypeptide, chloroplastic (LOC100243967), mRNA
MB21	XM_002280899.4	50280	Vitis vinifera 18.1 kDa class I heat shock protein (LOC100253085), mRNA
MB21	XM_002284928.4	50207	Vitis vinifera elongation factor 1-alpha (LOC100256979), transcript variant X1, mRNA
MB21	XM_010652829.2	50187	Vitis vinifera elongation factor 1-alpha (LOC100256979), transcript variant X2, mRNA
MB21	XM_002283530.4	48614	Vitis vinifera chlorophyll a-b binding protein 40, chloroplastic-like (LOC100250504), mRNA
MB21	XM_002285821.3	48584	Vitis vinifera photosystem II 22 kDa protein, chloroplastic (LOC100245393), mRNA
MB21	XM_002284888.3	48438	Vitis vinifera elongation factor 1-alpha (LOC100246711), mRNA
MB21	XM_002266334.4	48145	Vitis vinifera polyubiquitin 4 (LOC100252768), mRNA
MB21	XM_010657023.2	47286	Vitis vinifera protein TIC 214 (LOC100855294), mRNA
MB21	XM_002280785.4	46639	Vitis vinifera 18.1 kDa class I heat shock protein (LOC100263355), mRNA
MB21	XM_010650493.2	45991	Vitis vinifera 17.9 kDa class II heat shock protein-like (LOC100256023), mRNA
MB21	XM_002263530.4	45824	Vitis vinifera peptidyl-prolyl cis-trans isomerase FKBP62 (LOC100266654), mRNA
MB21	XM_002279798.3	45703	Vitis vinifera chlorophyll a-b binding protein CP29.2, chloroplastic-like (LOC100266604), mRNA
MB21	XR_785545.2	45183	Vitis vinifera heat shock factor protein HSF30 (LOC100245740), transcript variant X3, misc_RNA
MB21	XM_002274760.4	43994	Vitis vinifera oxygen-evolving enhancer protein 1, chloroplastic (LOC100245459), mRNA
MB21	XM_002274343.4	43902	Vitis vinifera uncharacterized LOC100264128 (LOC100264128), mRNA
MB21	XM_002279459.4	43623	Vitis vinifera 17.3 kDa class II heat shock protein-like (LOC100268136), mRNA
MB21	XM_010664718.2	43071	Vitis vinifera heat shock protein 101 (HSP101), transcript variant X1, mRNA
MB21	XM_019226699.1	42504	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X1, mRNA
MB21	XM_019226700.1	42502	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X3, mRNA
MB21	XM_019226702.1	42497	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X5, mRNA
MB21	XM_019224912.1	42121	Vitis vinifera polyubiquitin (LOC100259635), transcript variant X3, mRNA
MB21	XM_002273165.4	42104	Vitis vinifera photosystem I chlorophyll a/b-binding protein 3-1, chloroplastic (LOC100232927), mRNA
MB21	NM_001280893.1	41440	Vitis vinifera heat shock protein 101 (HSP101), mRNA
MB21	XM_002282943.4	41202	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100266698), transcript variant X1, mRNA
MB21	XM_010660236.2	40981	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100266698), transcript variant X2, mRNA
MB21	XM_010657584.1	40742	Vitis vinifera chlorophyll a-b binding protein, chloroplastic (LOC100266036), mRNA
MB21	XM_019224911.1	40507	Vitis vinifera polyubiquitin (LOC100259635), transcript variant X2, mRNA
MB21	XM_002265738.3	40043	Vitis vinifera ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic (LOC100241976), mRNA
MB21	XM_002278673.3	39531	Vitis vinifera heat shock factor protein HSF30 (LOC100245740), transcript variant X2, mRNA
MB21	XM_010650040.2	38295	Vitis vinifera heat shock factor protein HSF30 (LOC100245740), transcript variant X1, mRNA
MB21	XM_019218228.1	38130	Vitis vinifera putative ATP synthase protein YMF19 (LOC104878237), mRNA
MB21	XM_010665664.2	37399	Vitis vinifera catalase isozyme 1 (LOC100244516), mRNA
MB21	XM_010658486.2	36742	Vitis vinifera phenylalanine--tRNA ligase, chloroplastic/mitochondrial (LOC100265994), transcript variant X2, mRNA
MB21	XM_003631825.3	36040	Vitis vinifera fructose-bisphosphate aldolase 1, chloroplastic (LOC100852851), mRNA
MB21	XM_002270596.3	35225	Vitis vinifera 23.6 kDa heat shock protein, mitochondrial (LOC100243757), transcript variant X1, mRNA
MB21	XM_002267378.4	35222	Vitis vinifera thiamine thiazole synthase 2, chloroplastic (THI1-2), mRNA
MB21	XM_002263688.4	35078	Vitis vinifera phosphoribulokinase, chloroplastic (LOC100244092), mRNA
MB21	NM_001281246.1	34862	Vitis vinifera glutamine synthetase (GS), mRNA
MB21	XM_019224594.1	33892	Vitis vinifera 18.1 kDa class I heat shock protein (LOC100254733), mRNA
MB21	NM_001303086.1	33720	Vitis vinifera heat shock factor protein HSF30 (LOC100245740), mRNA
MB21	XM_002285868.4	33461	Vitis vinifera plastocyanin (LOC100248911), mRNA
MB21	XM_010660191.2	33218	Vitis vinifera 18.1 kDa class I heat shock protein (LOC100249611), transcript variant X1, mRNA
MB21	XR_002031623.1	33126	Vitis vinifera 18.1 kDa class I heat shock protein (LOC100249611), transcript variant X2, misc_RNA
MB21	XM_010665493.2	32713	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X2, mRNA
MB21	XM_010665492.2	32712	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X1, mRNA
MB21	XM_002278068.4	32430	Vitis vinifera peroxisomal (S)-2-hydroxy-acid oxidase GLO1 (LOC100232932), mRNA
MB21	XR_002031999.1	31938	Vitis vinifera 23.6 kDa heat shock protein, mitochondrial (LOC100243757), transcript variant X2, misc_RNA
MB21	XM_002280545.4	31697	Vitis vinifera 18.1 kDa class I heat shock protein (LOC100261583), mRNA
MB21	XM_019226465.1	31407	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X3, mRNA

MB21	XM_002282071.4	31005	Vitis vinifera ATP-dependent zinc metalloprotease FTSH 2, chloroplastic (LOC100250511), transcript variant X1, mRNA
MB21	XM_019223684.1	30999	Vitis vinifera ATP-dependent zinc metalloprotease FTSH 2, chloroplastic (LOC100250511), transcript variant X2, mRNA
MB21	XM_002263287.3	30546	Vitis vinifera luminal-binding protein 5 (LOC100251379), mRNA
MB21	XM_002274833.4	30130	Vitis vinifera peptidyl-prolyl cis-trans isomerase-like (LOC100247119), mRNA
MB21	XM_002281733.3	29568	Vitis vinifera thiamine thiazole synthase 1, chloroplastic-like (THI1-1), mRNA
MB21	XM_002273208.4	29206	Vitis vinifera heat shock cognate protein 80 (LOC100261759), mRNA
MB21	XM_002268669.3	29188	Vitis vinifera 17.4 kDa class III heat shock protein (LOC100244609), mRNA
MB21	XM_002277014.3	29040	Vitis vinifera heat shock 70 kDa protein (LOC100265708), mRNA
MB21	XM_002278858.3	28367	Vitis vinifera heat shock protein 83 (LOC100265661), transcript variant X1, mRNA
MB21	XM_010652797.2	28350	Vitis vinifera L-ascorbate peroxidase 2, cytosolic (LOC100233013), transcript variant X1, mRNA
MB21	XM_002284731.4	28215	Vitis vinifera L-ascorbate peroxidase 2, cytosolic (LOC100233013), transcript variant X2, mRNA
MB21	XM_002272029.3	27950	Vitis vinifera 25.3 kDa heat shock protein, chloroplastic-like (LOC100261354), mRNA
MB21	XM_002266458.4	27800	Vitis vinifera transketolase, chloroplastic (LOC100248004), mRNA
MB21	XR_139816.3	27647	Vitis vinifera uncharacterized LOC100853453 (LOC100853453), ncRNA
MB21	XM_002281697.3	27497	Vitis vinifera peroxisomal membrane protein 11A (LOC100243820), mRNA
MB21	NM_001281165.1	27408	Vitis vinifera AlaT1 (LOC100261274), mRNA
MB21	XM_019216300.1	27375	Vitis vinifera heat shock protein 83 (LOC100265661), transcript variant X2, mRNA
MB21	XM_002273718.4	27032	Vitis vinifera glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic (LOC100259814), mRNA
MB21	XM_002281606.3	26576	Vitis vinifera 29 kDa ribonucleoprotein A, chloroplastic (LOC100246501), mRNA
MB21	XM_002269581.3	26574	Vitis vinifera ferredoxin-like (LOC100249080), mRNA
MB21	XM_002263013.3	26515	Vitis vinifera sedoheptulose-1,7-bisphosphatase, chloroplastic (LOC100260169), mRNA
MB21	XM_002284325.3	26116	Vitis vinifera cytochrome b6-f complex iron-sulfur subunit 1, chloroplastic (LOC100258879), mRNA
MB21	XM_002270940.4	25837	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X1, mRNA
MB21	XM_010648098.2	25836	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X1, mRNA
MB21	XM_010647664.2	25833	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X3, mRNA
MB21	XM_010647663.2	25831	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X2, mRNA
MB21	XM_019217932.1	25825	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X4, mRNA
MB21	XM_010648099.2	25820	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X2, mRNA
MB21	XM_010648100.2	25817	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X4, mRNA
MB21	XM_002262836.4	25806	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X3, mRNA
MB21	XM_019217933.1	25805	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X5, mRNA
MB21	XM_002263109.3	25648	Vitis vinifera glyceraldehyde-3-phosphate dehydrogenase, cytosolic (LOC100233024), mRNA
MB21	XM_010648649.2	25553	Vitis vinifera ribosomal protein S4, mitochondrial (LOC104878382), mRNA
MB21	XM_002268125.4	25169	Vitis vinifera peptidyl-prolyl cis-trans isomerase FKBP62 (LOC100249097), partial mRNA
MB21	XM_002275516.2	25014	Vitis vinifera chlorophyll a-b binding protein 6A, chloroplastic-like (LOC100263275), mRNA
MB21	XM_002284207.4	24865	Vitis vinifera chaperone protein ClpB3, chloroplastic (LOC100252611), mRNA
MB21	XM_002283012.4	23933	Vitis vinifera probable oxygen-evolving enhancer protein 2 (PSBP1), transcript variant X1, mRNA
MB21	XM_002278303.3	23623	Vitis vinifera GDP-L-galactose phosphorylase 2 (LOC100253859), mRNA
MB21	XM_002274206.3	23594	Vitis vinifera pathogenesis-related protein 10 (PR10.2), mRNA
MB21	XR_002030515.1	23377	Vitis vinifera uncharacterized LOC109122938 (LOC109122938), ncRNA
MB21	XM_019218694.1	23315	Vitis vinifera hsp70-Hsp90 organizing protein 3-like (LOC100854305), mRNA
MB21	XM_003635638.3	23295	Vitis vinifera hsp70-Hsp90 organizing protein 3 (LOC100855394), mRNA
MB21	XM_010648101.2	23179	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X1, mRNA
MB21	XM_019218132.1	23067	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X2, mRNA
MB21	XM_019223422.1	23067	Vitis vinifera uncharacterized LOC100262484 (LOC100262484), mRNA
MB21	XM_019218133.1	23042	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X3, mRNA
MB21	NM_001281060.1	22242	Vitis vinifera cysteine protease (CYSP), mRNA
MB21	XM_002283856.3	22092	Vitis vinifera magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic-like (LOC100241461), mRNA
MB21	XM_010649856.2	22016	Vitis vinifera cytochrome b6-f complex iron-sulfur subunit 2, chloroplastic (LOC100245219), mRNA
MB21	XR_002031214.1	21825	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X1, ncRNA
MB21	XR_002031215.1	21823	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X2, ncRNA
MB21	XR_002031216.1	21820	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X3, ncRNA
MB21	XM_002266744.4	21804	Vitis vinifera elongation factor 2 (LOC100261253), mRNA
MB21	XM_002278744.3	21640	Vitis vinifera photosystem I reaction center subunit XI, chloroplastic (LOC100242802), mRNA
MB21	XM_002273394.3	21609	Vitis vinifera 1-aminocyclopropane-1-carboxylate oxidase (LOC100232928), mRNA

MB21	NM_001281149.1	21574	Vitis vinifera magnesium chelatase H subunit (CHLH), mRNA
MB21	XM_010653193.2	21530	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X2, mRNA
MB21	XM_002279200.4	21524	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X1, mRNA
MB21	XM_010658776.1	21266	Vitis vinifera uncharacterized LOC100267696 (LOC100267696), transcript variant X2, mRNA
MB21	XM_002282402.4	21227	Vitis vinifera uncharacterized LOC100267696 (LOC100267696), transcript variant X1, mRNA
MB21	XM_002284457.3	21145	Vitis vinifera chlorophyll a-b binding protein 13, chloroplastic (LOC100260599), mRNA
MB21	XM_002285889.4	20853	Vitis vinifera ATP-dependent zinc metalloprotease FTSH, chloroplastic (LOC100250509), mRNA
MB21	XM_002284460.3	20631	Vitis vinifera photosystem I reaction center subunit VI, chloroplastic (LOC100241224), mRNA
MB21	XM_002270560.4	20536	Vitis vinifera small heat shock protein, chloroplastic (LOC100248906), mRNA
MB21	XM_002279548.3	20430	Vitis vinifera BAG family molecular chaperone regulator 6 (LOC100256846), transcript variant X2, mRNA
MB21	XM_010663559.2	20428	Vitis vinifera BAG family molecular chaperone regulator 6 (LOC100256846), transcript variant X1, mRNA
MB21	XM_002277921.4	20315	Vitis vinifera beta carbonic anhydrase 1, chloroplastic (LOC100249137), transcript variant X1, mRNA
MB21	XM_019218224.1	20221	Vitis vinifera NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (LOC109122065), partial mRNA
MB21	XM_019220709.1	20059	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X3, mRNA
MB21	XM_003632975.3	20036	Vitis vinifera dnaJ homolog subfamily B member 13 (LOC100252168), mRNA
MB21	XM_002281359.4	19856	Vitis vinifera chloroplast stem-loop binding protein of 41 kDa b, chloroplastic (LOC100261308), mRNA
MB21	XM_002273986.3	19805	Vitis vinifera heat shock protein 83 (LOC100257736), mRNA
MB21	XM_010658801.1	19542	Vitis vinifera probable oxygen-evolving enhancer protein 2 (PSBP1), transcript variant X2, mRNA
MB21	XR_785679.2	19477	Vitis vinifera uncharacterized LOC100852628 (LOC100852628), transcript variant X2, ncRNA
MB21	XM_002265554.4	19219	Vitis vinifera putative transcription factor (LOC100250281), mRNA
MB21	XM_002275007.3	18879	Vitis vinifera calvin cycle protein CP12-1, chloroplastic (LOC100267103), mRNA
MB21	XM_002285866.3	18879	Vitis vinifera thioredoxin-like protein CDSP32, chloroplastic (LOC100259132), mRNA
MB21	NM_001280913.1	18869	Vitis vinifera chloroplast ELIP early light-induced protein (LOC100263179), mRNA; nuclear gene for chloroplast product
MB21	XR_785678.2	18766	Vitis vinifera uncharacterized LOC100852628 (LOC100852628), transcript variant X1, ncRNA
MB21	XM_002282110.3	18762	Vitis vinifera cell division cycle protein 48 homolog (LOC100265402), mRNA
MB21	XR_785937.2	18427	Vitis vinifera phosphomethylpyrimidine synthase, chloroplastic (LOC100250096), transcript variant X2, misc_RNA
MB21	XM_002270926.4	18426	Vitis vinifera methanol O-anthraniloyltransferase (LOC100243166), mRNA
MB21	XR_785938.2	18413	Vitis vinifera phosphomethylpyrimidine synthase, chloroplastic (LOC100250096), transcript variant X3, misc_RNA
MB21	NM_001280992.1	18404	Vitis vinifera aquaporin-like (PIP1;3), mRNA
MB21	XM_002280191.4	18326	Vitis vinifera phosphomethylpyrimidine synthase, chloroplastic (LOC100250096), transcript variant X1, mRNA
MB21	XM_010650280.2	18304	Vitis vinifera RING finger and CHY zinc finger domain-containing protein 1-like (LOC100252623), transcript variant X1, mRNA
MB21	XM_010652630.2	18299	Vitis vinifera phosphomethylpyrimidine synthase, chloroplastic (LOC100250096), transcript variant X4, mRNA
MB21	XM_002262806.4	17991	Vitis vinifera glutathione S-transferase (LOC100265903), mRNA
MB21	XM_002266384.4	17976	Vitis vinifera methanol O-anthraniloyltransferase (LOC100252759), mRNA
MB21	XM_002267020.3	17712	Vitis vinifera ferredoxin-dependent glutamate synthase, chloroplastic (LOC100233082), mRNA
MB21	XM_002284820.3	17496	Vitis vinifera chlorophyll a-b binding protein 4, chloroplastic (LOC100232934), mRNA

Library	ID	Counts	Description
P1103	XM_019221016.1	2319250	Vitis vinifera ribulose biphosphate carboxylase large chain (LOC109122894), partial mRNA
P1103	XM_010654474.1	903305	Vitis vinifera cytochrome P450 81E8-like (LOC100242168), mRNA
P1103	XM_002276931.4	830428	Vitis vinifera ribulose biphosphate carboxylase small chain, chloroplastic-like (LOC100267942), mRNA
P1103	XM_019218790.1	421063	Vitis vinifera photosystem II CP47 reaction center protein-like (LOC109122277), mRNA
P1103	XM_003632139.2	385429	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100263871), transcript variant X2, mRNA
P1103	XM_002282200.3	359910	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100263871), transcript variant X1, mRNA
P1103	XR_002030730.1	287898	Vitis vinifera uncharacterized LOC104880458 (LOC104880458), ncRNA
P1103	XR_002031185.1	267840	Vitis vinifera uncharacterized LOC109123445 (LOC109123445), ncRNA
P1103	XR_002030742.1	249591	Vitis vinifera uncharacterized LOC109123058 (LOC109123058), ncRNA
P1103	XR_788116.2	241762	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X1, ncRNA
P1103	XR_788121.2	241758	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X3, ncRNA
P1103	XR_788122.2	241758	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X2, ncRNA
P1103	XR_788124.2	241754	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X5, ncRNA
P1103	XR_002031531.1	241753	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X7, ncRNA
P1103	XR_788119.2	241753	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X4, ncRNA
P1103	XR_002031529.1	241752	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X6, ncRNA
P1103	XM_019216227.1	223220	Vitis vinifera pentatricopeptide repeat-containing protein At5g40410, mitochondrial (LOC100260830), mRNA
P1103	XM_019216320.1	213679	Vitis vinifera pentatricopeptide repeat-containing protein At1g19720 (LOC100255764), mRNA
P1103	XM_002267690.4	198798	Vitis vinifera probable fructose-bisphosphate aldolase 1, chloroplastic-like (LOC100262354), mRNA
P1103	XR_002031525.1	166714	Vitis vinifera uncharacterized LOC109123733 (LOC109123733), ncRNA
P1103	XR_002031535.1	148537	Vitis vinifera uncharacterized LOC109123739 (LOC109123739), ncRNA
P1103	XM_019225640.1	134852	Vitis vinifera uncharacterized mitochondrial protein AtMg00810-like (LOC109124071), mRNA
P1103	XM_010660203.2	132935	Vitis vinifera cucumisin (LOC100259879), transcript variant X1, mRNA
P1103	XM_010660204.2	132906	Vitis vinifera cucumisin (LOC100259879), transcript variant X2, mRNA
P1103	XM_019224313.1	120834	Vitis vinifera cucumisin (LOC100259879), transcript variant X3, mRNA
P1103	XR_002031186.1	97887	Vitis vinifera uncharacterized LOC109123446 (LOC109123446), ncRNA
P1103	XM_002278316.4	90255	Vitis vinifera glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic (LOC100246378), mRNA
P1103	XM_002269581.3	88831	Vitis vinifera ferredoxin-like (LOC100249080), mRNA
P1103	XM_010650056.2	83748	Vitis vinifera glycine dehydrogenase (decarboxylating), mitochondrial (LOC100266170), mRNA
P1103	XM_010649010.2	82516	Vitis vinifera ATP synthase subunit alpha, mitochondrial (LOC104878494), mRNA
P1103	XM_002271651.4	82385	Vitis vinifera chlorophyll a-b binding protein 151, chloroplastic-like (LOC100254533), mRNA
P1103	XM_002270535.3	82333	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100256315), mRNA
P1103	XM_010657023.2	81426	Vitis vinifera protein TIC 214 (LOC100855294), mRNA
P1103	XM_010665664.2	77270	Vitis vinifera catalase isozyme 1 (LOC100244516), mRNA
P1103	XM_002282943.4	72257	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100266698), transcript variant X1, mRNA
P1103	XM_002265911.3	71735	Vitis vinifera galactinol synthase 1 (LOC100260266), mRNA
P1103	XM_010660236.2	71058	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100266698), transcript variant X2, mRNA
P1103	XM_019226700.1	63130	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X3, mRNA
P1103	XM_019226699.1	63126	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X1, mRNA
P1103	XM_019226702.1	63126	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X5, mRNA
P1103	XM_002285821.3	60393	Vitis vinifera photosystem II 22 kDa protein, chloroplastic (LOC100245393), mRNA
P1103	XM_002274760.4	59251	Vitis vinifera oxygen-evolving enhancer protein 1, chloroplastic (LOC100245459), mRNA
P1103	XM_003632976.3	57130	Vitis vinifera chlorophyll a-b binding protein 40, chloroplastic-like (LOC100252004), mRNA
P1103	NM_001281246.1	56472	Vitis vinifera glutamine synthetase (GS), mRNA
P1103	XM_002278303.3	56124	Vitis vinifera GDP-L-galactose phosphorylase 2 (LOC100253859), mRNA
P1103	XM_002263688.4	51616	Vitis vinifera phosphoribulokinase, chloroplastic (LOC100244092), mRNA
P1103	XM_002275039.3	51470	Vitis vinifera chlorophyll a-b binding protein of LHCII type 1 (LOC100241745), mRNA
P1103	XM_002277921.4	51156	Vitis vinifera beta carbonic anhydrase 1, chloroplastic (LOC100249137), transcript variant X1, mRNA
P1103	XM_010657584.1	50782	Vitis vinifera chlorophyll a-b binding protein, chloroplastic (LOC100266036), mRNA
P1103	XM_002278068.4	50349	Vitis vinifera peroxisomal (S)-2-hydroxy-acid oxidase GLO1 (LOC100232932), mRNA
P1103	XM_002265738.3	49996	Vitis vinifera ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic (LOC100241976), mRNA
P1103	XM_002283496.3	48511	Vitis vinifera heat shock 70kDa protein 1/8-like (LOC100254725), mRNA
P1103	XM_003631825.3	48373	Vitis vinifera fructose-bisphosphate aldolase 1, chloroplastic (LOC100852851), mRNA
P1103	XM_002282071.4	43657	Vitis vinifera ATP-dependent zinc metalloprotease FTSH 2, chloroplastic (LOC100250511), transcript variant X1, mRNA

P1103	XM_019223684.1	43637	Vitis vinifera ATP-dependent zinc metalloprotease FTSH 2, chloroplastic (LOC100250511), transcript variant X2, mRNA
P1103	XM_010662610.2	42195	Vitis vinifera beta carbonic anhydrase 1, chloroplastic (LOC100249137), transcript variant X2, mRNA
P1103	XM_002273165.4	41993	Vitis vinifera photosystem I chlorophyll a/b-binding protein 3-1, chloroplastic (LOC100232927), mRNA
P1103	NM_001281165.1	41842	Vitis vinifera AlaT1 (LOC100261274), mRNA
P1103	XM_002279798.3	39008	Vitis vinifera chlorophyll a-b binding protein CP29.2, chloroplastic-like (LOC100266604), mRNA
P1103	XM_002284928.4	38749	Vitis vinifera elongation factor 1-alpha (LOC100256979), transcript variant X1, mRNA
P1103	XM_010652829.2	38701	Vitis vinifera elongation factor 1-alpha (LOC100256979), transcript variant X2, mRNA
P1103	XM_010665492.2	38646	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X1, mRNA
P1103	XM_010665493.2	38631	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X2, mRNA
P1103	XM_002283530.4	37144	Vitis vinifera chlorophyll a-b binding protein 40, chloroplastic-like (LOC100250504), mRNA
P1103	XM_019226465.1	37086	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X3, mRNA
P1103	XM_002284888.3	36743	Vitis vinifera elongation factor 1-alpha (LOC100246711), mRNA
P1103	XM_002283856.3	36519	Vitis vinifera magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic-like (LOC100241461), mRNA
P1103	XM_010646105.2	36352	Vitis vinifera polyubiquitin (LOC100267431), mRNA
P1103	XM_010658486.2	35457	Vitis vinifera phenylalanine--tRNA ligase, chloroplastic/mitochondrial (LOC100265994), transcript variant X2, mRNA
P1103	XM_002279200.4	34610	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X1, mRNA
P1103	XM_010653193.2	34581	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X2, mRNA
P1103	NM_001281149.1	34420	Vitis vinifera magnesium chelatase H subunit (CHLH), mRNA
P1103	NM_001281130.1	34310	Vitis vinifera germin-like protein 6 (GER6), mRNA.
P1103	XM_002269394.3	33859	Vitis vinifera zinc finger CCCH domain-containing protein 29-like (LOC100246707), transcript variant X2, mRNA
P1103	XM_002284325.3	33619	Vitis vinifera cytochrome b6-f complex iron-sulfur subunit 1, chloroplastic (LOC100258879), mRNA
P1103	XM_010648098.2	33507	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X1, mRNA
P1103	XM_019224434.1	33488	Vitis vinifera zinc finger CCCH domain-containing protein 29-like (LOC100246707), transcript variant X1, mRNA
P1103	XM_002262836.4	33475	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X3, mRNA
P1103	XM_010648100.2	33466	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X4, mRNA
P1103	XM_010648099.2	33408	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X2, mRNA
P1103	XM_002274206.3	33188	Vitis vinifera pathogenesis-related protein 10 (PR10.2), mRNA
P1103	XM_002285868.4	33099	Vitis vinifera plastocyanin (LOC100248911), mRNA
P1103	XM_002263013.3	32685	Vitis vinifera sedoheptulose-1,7-bisphosphatase, chloroplastic (LOC100260169), mRNA
P1103	XM_002284731.4	32617	Vitis vinifera L-ascorbate peroxidase 2, cytosolic (LOC100233013), transcript variant X2, mRNA
P1103	XM_010652797.2	32475	Vitis vinifera L-ascorbate peroxidase 2, cytosolic (LOC100233013), transcript variant X1, mRNA
P1103	XM_010648101.2	32463	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X1, mRNA
P1103	XM_019218132.1	32397	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X2, mRNA
P1103	XM_019218133.1	32324	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X3, mRNA
P1103	XM_019220709.1	32293	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X3, mRNA
P1103	XM_010660206.2	32273	Vitis vinifera cucumisin (LOC100263317), mRNA
P1103	XM_010646102.2	29931	Vitis vinifera polyubiquitin (LOC104877307), mRNA
P1103	XM_002284460.3	29839	Vitis vinifera photosystem I reaction center subunit VI, chloroplastic (LOC100241224), mRNA
P1103	XM_019218224.1	29611	Vitis vinifera NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (LOC109122065), partial mRNA
P1103	XM_010654521.2	28900	Vitis vinifera inositol-3-phosphate synthase (LOC100259515), mRNA
P1103	XM_010649856.2	28877	Vitis vinifera cytochrome b6-f complex iron-sulfur subunit 2, chloroplastic (LOC100245219), mRNA
P1103	XM_019224309.1	28521	Vitis vinifera cucumisin-like (LOC109123728), transcript variant X2, mRNA
P1103	XM_019224310.1	28224	Vitis vinifera cucumisin-like (LOC109123728), transcript variant X3, mRNA
P1103	XM_002279245.4	28105	Vitis vinifera glycerate dehydrogenase HPR, peroxisomal (LOC100262344), transcript variant X1, mRNA
P1103	XM_019224311.1	27852	Vitis vinifera cucumisin-like (LOC109123728), transcript variant X4, mRNA
P1103	XM_002273718.4	27788	Vitis vinifera glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic (LOC100259814), mRNA
P1103	XM_019224312.1	27555	Vitis vinifera cucumisin-like (LOC109123728), transcript variant X5, mRNA
P1103	XM_010660205.2	27261	Vitis vinifera cucumisin-like (LOC104881130), mRNA
P1103	XM_002281359.4	26680	Vitis vinifera chloroplast stem-loop binding protein of 41 kDa b, chloroplastic (LOC100261308), mRNA
P1103	XM_002281697.3	26596	Vitis vinifera peroxisomal membrane protein 11A (LOC100243820), mRNA
P1103	XM_019224308.1	26475	Vitis vinifera cucumisin-like (LOC109123728), transcript variant X1, mRNA
P1103	XM_002263109.3	26317	Vitis vinifera glyceraldehyde-3-phosphate dehydrogenase, cytosolic (LOC100233024), mRNA
P1103	XM_002277873.4	26026	Vitis vinifera photosystem II 5 kDa protein, chloroplastic-like (LOC100265352), mRNA
P1103	XM_019218228.1	25939	Vitis vinifera putative ATP synthase protein YMF19 (LOC104878237), mRNA
P1103	XR_002031278.1	25721	Vitis vinifera uncharacterized LOC109123537 (LOC109123537), ncRNA

P1103	XM_002274833.4	24774	Vitis vinifera peptidyl-prolyl cis-trans isomerase-like (LOC100247119), mRNA
P1103	XM_002266334.4	24774	Vitis vinifera polyubiquitin 4 (LOC100252768), mRNA
P1103	XM_002273752.3	24472	Vitis vinifera pathogenesis-related protein (PR1), mRNA
P1103	XM_002278744.3	24288	Vitis vinifera photosystem I reaction center subunit XI, chloroplastic (LOC100242802), mRNA
P1103	XM_002275007.3	23937	Vitis vinifera calvin cycle protein CP12-1, chloroplastic (LOC100267103), mRNA
P1103	XM_002281606.3	23650	Vitis vinifera 29 kDa ribonucleoprotein A, chloroplastic (LOC100246501), mRNA
P1103	XM_002266458.4	23238	Vitis vinifera transketolase, chloroplastic (LOC100248004), mRNA
P1103	XM_002274979.4	23124	Vitis vinifera ATP synthase gamma chain, chloroplastic (LOC100264091), mRNA
P1103	XM_019219116.1	23057	Vitis vinifera glycerate dehydrogenase HPR, peroxisomal (LOC100262344), transcript variant X2, mRNA
P1103	XM_002282023.3	22942	Vitis vinifera photosystem II reaction center W protein, chloroplastic (LOC100256361), mRNA
P1103	XM_002283663.3	22861	Vitis vinifera oxygen-evolving enhancer protein 1, chloroplastic (LOC100260811), mRNA
P1103	XM_003632895.2	22845	Vitis vinifera 5'-adenylylsulfate reductase 3, chloroplastic (LOC100854884), mRNA
P1103	XM_002267378.4	22817	Vitis vinifera thiamine thiazole synthase 2, chloroplastic (THI1-2), mRNA
P1103	XM_019224912.1	22777	Vitis vinifera polyubiquitin (LOC100259635), transcript variant X3, mRNA
P1103	XM_002280671.2	22647	Vitis vinifera glycine cleavage system H protein, mitochondrial (LOC100259229), mRNA
P1103	XM_002272665.3	21921	Vitis vinifera aminomethyltransferase, mitochondrial (LOC100250401), mRNA
P1103	XM_002283012.4	21918	Vitis vinifera probable oxygen-evolving enhancer protein 2 (PSBP1), transcript variant X1, mRNA
P1103	NM_001281060.1	21868	Vitis vinifera cysteine protease (CYSP), mRNA
P1103	XM_003631865.3	21728	Vitis vinifera photosystem I reaction center subunit N, chloroplastic (LOC100232935), mRNA
P1103	XR_139816.3	21633	Vitis vinifera uncharacterized LOC100853453 (LOC100853453), ncRNA
P1103	XM_002284457.3	21574	Vitis vinifera chlorophyll a-b binding protein 13, chloroplastic (LOC100260599), mRNA
P1103	XM_002275588.3	21369	Vitis vinifera oxygen-evolving enhancer protein 3, chloroplastic (LOC100240959), mRNA
P1103	XM_002270940.4	21250	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X1, mRNA
P1103	XM_010647663.2	21249	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X2, mRNA
P1103	XM_019217932.1	21249	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X4, mRNA
P1103	XM_010647664.2	21248	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X3, mRNA
P1103	XM_019217933.1	21247	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X5, mRNA
P1103	XM_002270449.3	21005	Vitis vinifera alpha-glucan water dikinase, chloroplastic (LOC100246568), transcript variant X2, mRNA
P1103	XM_010653413.2	20992	Vitis vinifera alpha-glucan water dikinase, chloroplastic (LOC100246568), transcript variant X1, mRNA
P1103	XR_784776.2	20696	Vitis vinifera putative disease resistance protein RGA4 (LOC100251296), transcript variant X6, misc_RNA
P1103	XM_010650075.2	20673	Vitis vinifera uncharacterized LOC104878987 (LOC104878987), mRNA
P1103	XR_784774.2	20650	Vitis vinifera putative disease resistance protein RGA4 (LOC100251296), transcript variant X4, misc_RNA
P1103	XM_002282835.4	20364	Vitis vinifera beta-amylase 3, chloroplastic (LOC100247246), mRNA
P1103	NM_001281242.1	20349	
P1103	XR_784772.2	20331	Vitis vinifera putative disease resistance protein RGA4 (LOC100251296), transcript variant X2, misc_RNA
P1103	XR_784771.2	20305	Vitis vinifera putative disease resistance protein RGA4 (LOC100251296), transcript variant X1, misc_RNA
P1103	XM_003631877.3	19949	Vitis vinifera catalase isozyme 1 (LOC100853165), mRNA
P1103	XM_002284736.4	19948	Vitis vinifera ribulose-phosphate 3-epimerase, chloroplastic (LOC100267206), transcript variant X1, mRNA
P1103	NM_001281169.1	19930	Vitis vinifera catalase (GCAT), mRNA
P1103	XM_019224911.1	19837	Vitis vinifera polyubiquitin (LOC100259635), transcript variant X2, mRNA
P1103	XR_784773.2	19741	Vitis vinifera putative disease resistance protein RGA4 (LOC100251296), transcript variant X3, misc_RNA
P1103	XM_002284820.3	19648	Vitis vinifera chlorophyll a-b binding protein 4, chloroplastic (LOC100232934), mRNA
P1103	XM_002266744.4	19585	Vitis vinifera elongation factor 2 (LOC100261253), mRNA
P1103	XM_002266071.3	19367	Vitis vinifera protein CURVATURE THYLAKOID 1B, chloroplastic (LOC100248815), mRNA
P1103	XM_003634905.2	19246	Vitis vinifera photosystem I reaction center subunit III, chloroplastic (LOC100247987), mRNA
P1103	NM_001281143.1	18982	
P1103	XM_003631644.3	18877	Vitis vinifera malate dehydrogenase, glyoxysomal (LOC100232924), mRNA
P1103	XM_002265986.3	18874	Vitis vinifera thioredoxin (LOC100264263), mRNA
P1103	XM_010658801.1	18722	Vitis vinifera probable oxygen-evolving enhancer protein 2 (PSBP1), transcript variant X2, mRNA
P1103	XM_019226384.1	18712	Vitis vinifera ATP synthase subunit alpha, chloroplastic-like (LOC109124299), mRNA
P1103	XM_002276531.4	18584	Vitis vinifera fructose-1,6-bisphosphatase, chloroplastic (LOC100240924), mRNA
P1103	XM_003633119.3	18555	Vitis vinifera protein TSS (LOC100257033), mRNA
P1103	XM_002267020.3	18422	Vitis vinifera ferredoxin-dependent glutamate synthase, chloroplastic (LOC100233082), mRNA
P1103	XM_002264585.4	18316	Vitis vinifera zinc transporter 8 (LOC100255284), mRNA
P1103	XM_002274330.4	18169	Vitis vinifera ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic (LOC100252241), mRNA

P1103	XM_002277213.4	18115	Vitis vinifera peroxisomal (S)-2-hydroxy-acid oxidase GLO1 (LOC100244701), transcript variant X1, mRNA
P1103	XM_002263165.4	18107	Vitis vinifera chlorophyll a-b binding protein CP24 10A, chloroplastic-like (LOC100241887), mRNA
P1103	XM_019220594.1	18087	Vitis vinifera heat shock cognate 70 kDa protein-like (LOC100253562), transcript variant X1, mRNA
P1103	XM_010646764.2	17991	Vitis vinifera isoflavone reductase-like protein 5 (IFRL5), transcript variant X1, mRNA
P1103	XM_002271755.3	17948	Vitis vinifera photosystem II 10 kDa polypeptide, chloroplastic (LOC100243967), mRNA
P1103	XM_002268994.4	17842	Vitis vinifera arginine decarboxylase (LOC100233080), mRNA
P1103	NM_001281183.1	17776	
P1103	XM_010646363.2	17757	Vitis vinifera pectin acetylesterase 8 (LOC100245856), mRNA
P1103	XM_019216879.1	17528	Vitis vinifera putative disease resistance protein RGA4 (LOC100251296), transcript variant X5, mRNA
P1103	XM_010648649.2	17350	Vitis vinifera ribosomal protein S4, mitochondrial (LOC104878382), mRNA
P1103	XM_002263760.3	16932	Vitis vinifera phosphoglycerate kinase, chloroplastic-like (LOC100249576), mRNA
P1103	XM_003634988.3	16849	Vitis vinifera heat shock cognate protein 80 (LOC100246843), mRNA
P1103	XM_002281733.3	16654	Vitis vinifera thiamine thiazole synthase 1, chloroplastic-like (THI1-1), mRNA
P1103	XR_002030515.1	16198	Vitis vinifera uncharacterized LOC109122938 (LOC109122938), ncRNA
P1103	XM_019220595.1	16195	Vitis vinifera heat shock cognate 70 kDa protein-like (LOC100253562), transcript variant X2, mRNA
P1103	XM_010646514.2	16084	Vitis vinifera peroxisomal (S)-2-hydroxy-acid oxidase GLO1 (LOC100244701), transcript variant X2, mRNA
P1103	XM_019217246.1	16044	Vitis vinifera putative disease resistance protein RGA3 (LOC104877751), mRNA
P1103	XM_010646515.2	15658	Vitis vinifera peroxisomal (S)-2-hydroxy-acid oxidase GLO1 (LOC100244701), transcript variant X3, mRNA
P1103	XM_002265554.4	15586	Vitis vinifera putative transcription factor (LOC100250281), mRNA
P1103	XM_019224652.1	15503	Vitis vinifera GDP-mannose-3',5'-epimerase (LOC100233034), transcript variant X1, mRNA
P1103	XM_002282110.3	15487	Vitis vinifera cell division cycle protein 48 homolog (LOC100265402), mRNA
P1103	XR_002031214.1	15378	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X1, ncRNA
P1103	XR_002031215.1	15378	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X2, ncRNA
P1103	XR_002031216.1	15378	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X3, ncRNA
P1103	XM_002270603.3	15364	Vitis vinifera indole-3-acetic acid-induced protein ARG2 (LOC100260685), mRNA
P1103	XM_010646844.2	15195	Vitis vinifera putative disease resistance protein RGA4 (LOC100251296), transcript variant X7, mRNA
P1103	XM_002280651.4	15085	Vitis vinifera photosystem I reaction center subunit psaK, chloroplastic (LOC100261762), mRNA
P1103	XM_002278592.4	15083	Vitis vinifera carotenoid 9,10(9',10')-cleavage dioxygenase 1 (LOC100249903), mRNA
P1103	XM_002278282.2	15038	Vitis vinifera DEAD-box ATP-dependent RNA helicase 3, chloroplastic (LOC100251060), mRNA
P1103	NM_001281224.1	15014	
P1103	XM_002284828.4	14841	Vitis vinifera subtilisin-like protease SBT1.9 (LOC100248944), mRNA
P1103	XM_002275152.4	14713	Vitis vinifera uncharacterized LOC100263114 (LOC100263114), mRNA
P1103	NM_001280913.1	14670	Vitis vinifera chloroplast ELIP early light-induced protein (LOC100263179), mRNA; nuclear gene for chloroplast product
P1103	XM_002280073.3	14566	Vitis vinifera CSC1-like protein ERD4 (LOC100260008), mRNA
P1103	XM_002285866.3	14525	Vitis vinifera thioredoxin-like protein CDSP32, chloroplastic (LOC100259132), mRNA
P1103	XM_019226537.1	14517	Vitis vinifera ribulose-phosphate 3-epimerase, chloroplastic (LOC100267206), transcript variant X2, mRNA

Library	ID	Counts	Description
CH40	XM_019221016.1	2282291	Vitis vinifera ribulose biphosphate carboxylase large chain (LOC109122894), partial mRNA
CH40	XM_010654474.1	887798	Vitis vinifera cytochrome P450 81E8-like (LOC100242168), mRNA
CH40	XM_002276931.4	667751	Vitis vinifera ribulose biphosphate carboxylase small chain, chloroplastic-like (LOC100267942), mRNA
CH40	XM_019218790.1	485237	Vitis vinifera photosystem II CP47 reaction center protein-like (LOC109122277), mRNA
CH40	XM_019216320.1	326445	Vitis vinifera pentatricopeptide repeat-containing protein At1g19720 (LOC100255764), mRNA
CH40	XR_002031185.1	315038	Vitis vinifera uncharacterized LOC109123445 (LOC109123445), ncRNA
CH40	XM_003632139.2	251696	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100263871), transcript variant X2, mRNA
CH40	XR_002030730.1	241485	Vitis vinifera uncharacterized LOC104880458 (LOC104880458), ncRNA
CH40	XM_002282200.3	236039	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100263871), transcript variant X1, mRNA
CH40	XR_788116.2	231448	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X1, ncRNA
CH40	XR_788124.2	231448	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X5, ncRNA
CH40	XR_788119.2	231447	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X4, ncRNA
CH40	XR_002031529.1	231444	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X6, ncRNA
CH40	XR_002031531.1	231444	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X7, ncRNA
CH40	XR_788121.2	231444	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X3, ncRNA
CH40	XR_788122.2	231442	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X2, ncRNA
CH40	XR_002030742.1	213741	Vitis vinifera uncharacterized LOC109123058 (LOC109123058), ncRNA
CH40	XM_019216227.1	202148	Vitis vinifera pentatricopeptide repeat-containing protein At5g40410, mitochondrial (LOC100260830), mRNA
CH40	XR_002031186.1	152998	Vitis vinifera uncharacterized LOC109123446 (LOC109123446), ncRNA
CH40	XR_002031525.1	152440	Vitis vinifera uncharacterized LOC109123733 (LOC109123733), ncRNA
CH40	XR_002031535.1	144369	Vitis vinifera uncharacterized LOC109123739 (LOC109123739), ncRNA
CH40	XM_019225640.1	104978	Vitis vinifera uncharacterized mitochondrial protein AtMg00810-like (LOC109124071), mRNA
CH40	XM_002267690.4	101633	Vitis vinifera probable fructose-bisphosphate aldolase 1, chloroplastic-like (LOC100262354), mRNA
CH40	XM_010649010.2	92853	Vitis vinifera ATP synthase subunit alpha, mitochondrial (LOC104878494), mRNA
CH40	XM_002278316.4	81403	Vitis vinifera glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic (LOC100246378), mRNA
CH40	XM_002275039.3	80305	Vitis vinifera chlorophyll a-b binding protein of LHClI type 1 (LOC100241745), mRNA
CH40	XM_002270535.3	79450	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100256315), mRNA
CH40	XM_010646105.2	77387	Vitis vinifera polyubiquitin (LOC100267431), mRNA
CH40	XM_003632976.3	73909	Vitis vinifera chlorophyll a-b binding protein 40, chloroplastic-like (LOC100252004), mRNA
CH40	XM_002271651.4	72892	Vitis vinifera chlorophyll a-b binding protein 151, chloroplastic-like (LOC100254533), mRNA
CH40	XM_010646102.2	71954	Vitis vinifera polyubiquitin (LOC104877307), mRNA
CH40	XM_019226700.1	70119	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X3, mRNA
CH40	XM_019226699.1	70117	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X1, mRNA
CH40	XM_019226702.1	70108	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X5, mRNA
CH40	XM_002283496.3	69071	Vitis vinifera heat shock 70kDa protein 1/8-like (LOC100254725), mRNA
CH40	XM_002284928.4	67004	Vitis vinifera elongation factor 1-alpha (LOC100256979), transcript variant X1, mRNA
CH40	XM_010652829.2	66998	Vitis vinifera elongation factor 1-alpha (LOC100256979), transcript variant X2, mRNA
CH40	XM_002284888.3	64415	Vitis vinifera elongation factor 1-alpha (LOC100246711), mRNA
CH40	XM_010657023.2	64174	Vitis vinifera protein TIC 214 (LOC100855294), mRNA
CH40	XM_002283530.4	63419	Vitis vinifera chlorophyll a-b binding protein 40, chloroplastic-like (LOC100250504), mRNA
CH40	XM_002285821.3	62277	Vitis vinifera photosystem II 22 kDa protein, chloroplastic (LOC100245393), mRNA
CH40	XM_002271755.3	60134	Vitis vinifera photosystem II 10 kDa polypeptide, chloroplastic (LOC100243967), mRNA
CH40	XM_002274760.4	56637	Vitis vinifera oxygen-evolving enhancer protein 1, chloroplastic (LOC100245459), mRNA
CH40	XM_002280439.4	53663	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100249153), mRNA
CH40	XM_002280596.3	52638	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100250883), mRNA
CH40	XM_002269581.3	52389	Vitis vinifera ferredoxin-like (LOC100249080), mRNA
CH40	XM_010650056.2	52086	Vitis vinifera glycine dehydrogenase (decarboxylating), mitochondrial (LOC100266170), mRNA
CH40	XM_002277921.4	51394	Vitis vinifera beta carbonic anhydrase 1, chloroplastic (LOC100249137), transcript variant X1, mRNA
CH40	XM_002267378.4	48724	Vitis vinifera thiamine thiazole synthase 2, chloroplastic (THI1-2), mRNA
CH40	XM_003631877.3	46084	Vitis vinifera catalase isozyme 1 (LOC100853165), mRNA
CH40	NM_001281169.1	45903	Vitis vinifera catalase (GCAT), mRNA
CH40	XM_002285868.4	45441	Vitis vinifera plastocyanin (LOC100248911), mRNA
CH40	XM_002282943.4	44697	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100266698), transcript variant X1, mRNA
CH40	XM_002273165.4	44634	Vitis vinifera photosystem I chlorophyll a/b-binding protein 3-1, chloroplastic (LOC100232927), mRNA

CH40	XM_002263109.3	44389	Vitis vinifera glyceraldehyde-3-phosphate dehydrogenase, cytosolic (LOC100233024), mRNA
CH40	XM_010660236.2	44354	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100266698), transcript variant X2, mRNA
CH40	XM_002284027.3	43713	Vitis vinifera heat shock cognate 70 kDa protein 2-like (LOC100265651), mRNA
CH40	XM_010665492.2	43281	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X1, mRNA
CH40	XM_010665493.2	43274	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X2, mRNA
CH40	XM_002265738.3	43215	Vitis vinifera ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic (LOC100241976), mRNA
CH40	XM_010662610.2	43109	Vitis vinifera beta carbonic anhydrase 1, chloroplastic (LOC100249137), transcript variant X2, mRNA
CH40	XM_002278068.4	43089	Vitis vinifera peroxisomal (S)-2-hydroxy-acid oxidase GLO1 (LOC100232932), mRNA
CH40	XM_002279798.3	42899	Vitis vinifera chlorophyll a-b binding protein CP29.2, chloroplastic-like (LOC100266604), mRNA
CH40	XM_010660203.2	42846	Vitis vinifera cucumisin (LOC100259879), transcript variant X1, mRNA
CH40	XM_010660204.2	42830	Vitis vinifera cucumisin (LOC100259879), transcript variant X2, mRNA
CH40	XM_019226465.1	41708	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X3, mRNA
CH40	XM_003634988.3	41505	Vitis vinifera heat shock cognate protein 80 (LOC100246843), mRNA
CH40	XM_010657584.1	40480	Vitis vinifera chlorophyll a-b binding protein, chloroplastic (LOC100266036), mRNA
CH40	XM_002265911.3	40352	Vitis vinifera galactinol synthase 1 (LOC100260266), mRNA
CH40	XM_019218224.1	39584	Vitis vinifera NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (LOC109122065), partial mRNA
CH40	XM_010658486.2	39281	Vitis vinifera phenylalanine--tRNA ligase, chloroplastic/mitochondrial (LOC100265994), transcript variant X2, mRNA
CH40	XM_002263688.4	38794	Vitis vinifera phosphoribulokinase, chloroplastic (LOC100244092), mRNA
CH40	XM_019224313.1	38696	Vitis vinifera cucumisin (LOC100259879), transcript variant X3, mRNA
CH40	XM_002284325.3	38554	Vitis vinifera cytochrome b6-f complex iron-sulfur subunit 1, chloroplastic (LOC100258879), mRNA
CH40	NM_001281130.1	38496	Vitis vinifera germin-like protein 6 (GER6), mRNA
CH40	XM_002280461.3	38260	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100254252), mRNA
CH40	XM_010665664.2	38162	Vitis vinifera catalase isozyme 1 (LOC100244516), mRNA
CH40	XM_019220594.1	36874	Vitis vinifera heat shock cognate 70 kDa protein-like (LOC100253562), transcript variant X1, mRNA
CH40	XM_002263563.3	36219	Vitis vinifera heat shock cognate 70 kDa protein 1-like (LOC100259551), mRNA
CH40	XM_010652797.2	35843	Vitis vinifera L-ascorbate peroxidase 2, cytosolic (LOC100233013), transcript variant X1, mRNA
CH40	XM_002284731.4	35691	Vitis vinifera L-ascorbate peroxidase 2, cytosolic (LOC100233013), transcript variant X2, mRNA
CH40	XM_002263287.3	35570	Vitis vinifera luminal-binding protein 5 (LOC100251379), mRNA
CH40	XM_002281184.4	35149	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100242821), mRNA
CH40	XM_002280644.3	34463	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100268056), mRNA
CH40	XM_019220595.1	33940	Vitis vinifera heat shock cognate 70 kDa protein-like (LOC100253562), transcript variant X2, mRNA
CH40	XM_002281697.3	33487	Vitis vinifera peroxisomal membrane protein 11A (LOC100243820), mRNA
CH40	XM_002282071.4	33363	Vitis vinifera ATP-dependent zinc metalloprotease FTSH 2, chloroplastic (LOC100250511), transcript variant X1, mRNA
CH40	XM_019223684.1	33363	Vitis vinifera ATP-dependent zinc metalloprotease FTSH 2, chloroplastic (LOC100250511), transcript variant X2, mRNA
CH40	XM_002274833.4	33284	Vitis vinifera peptidyl-prolyl cis-trans isomerase-like (LOC100247119), mRNA
CH40	XM_002281318.3	33173	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100249533), mRNA
CH40	XM_010649856.2	32558	Vitis vinifera cytochrome b6-f complex iron-sulfur subunit 2, chloroplastic (LOC100245219), mRNA
CH40	XM_002281224.4	32558	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100259921), mRNA
CH40	XM_019218228.1	32393	Vitis vinifera putative ATP synthase protein YMF19 (LOC104878237), mRNA
CH40	XM_002281358.3	32358	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100244376), mRNA
CH40	XM_002277873.4	32187	Vitis vinifera photosystem II 5 kDa protein, chloroplastic-like (LOC100265352), mRNA
CH40	NM_001281165.1	32128	Vitis vinifera AlaT1 (LOC100261274), mRNA
CH40	XM_002283856.3	31986	Vitis vinifera magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic-like (LOC100241461), mRNA
CH40	NM_001280938.1	31905	Vitis vinifera small heat shock protein 17.3 kDa (LOC100243983), mRNA
CH40	XM_002284460.3	31624	Vitis vinifera photosystem I reaction center subunit VI, chloroplastic (LOC100241224), mRNA
CH40	NM_001281246.1	31493	Vitis vinifera glutamine synthetase (GS), mRNA
CH40	XM_002280611.4	31445	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100245734), mRNA
CH40	XM_002265554.4	31260	Vitis vinifera putative transcription factor (LOC100250281), mRNA
CH40	XM_002266458.4	30763	Vitis vinifera transketolase, chloroplastic (LOC100248004), mRNA
CH40	XM_002281249.4	30756	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100265108), mRNA
CH40	XR_078097.3	30338	Vitis vinifera 18.2 kDa class I heat shock protein-like (LOC100266701), misc_RNA
CH40	XM_002270940.4	29965	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X1, mRNA
CH40	XM_010647663.2	29945	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X2, mRNA
CH40	XM_010647664.2	29942	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X3, mRNA
CH40	XM_019217932.1	29931	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X4, mRNA

CH40	XM_019217933.1	29902	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X5, mRNA
CH40	XM_003631761.3	29864	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100854120), mRNA
CH40	XM_010648098.2	29784	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X1, mRNA
CH40	XM_010648100.2	29759	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X4, mRNA
CH40	XM_010648099.2	29749	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X2, mRNA
CH40	XM_002262836.4	29742	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X3, mRNA
CH40	XM_002281733.3	29715	Vitis vinifera thiamine thiazole synthase 1, chloroplastic-like (THI1-1), mRNA
CH40	XM_002263530.4	28833	Vitis vinifera peptidyl-prolyl cis-trans isomerase FKBP62 (LOC100266654), mRNA
CH40	XM_002281420.3	28679	Vitis vinifera 18.2 kDa class I heat shock protein (LOC100261497), mRNA
CH40	XM_002280424.4	27012	Vitis vinifera 17.1 kDa class II heat shock protein (LOC100266315), mRNA
CH40	XM_010648101.2	26701	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X1, mRNA
CH40	XM_019218132.1	26625	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X2, mRNA
CH40	XM_019218133.1	26566	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X3, mRNA
CH40	XM_002278858.3	26560	Vitis vinifera heat shock protein 83 (LOC100265661), transcript variant X1, mRNA
CH40	NM_001281149.1	26431	Vitis vinifera magnesium chelatase H subunit (CHLH), mRNA
CH40	XM_003631825.3	25924	Vitis vinifera fructose-bisphosphate aldolase 1, chloroplastic (LOC100852851), mRNA
CH40	XM_019216300.1	25667	Vitis vinifera heat shock protein 83 (LOC100265661), transcript variant X2, mRNA
CH40	XM_002281606.3	25548	Vitis vinifera 29 kDa ribonucleoprotein A, chloroplastic (LOC100246501), mRNA
CH40	XM_002271648.2	25392	Vitis vinifera tetraspanin-8 (LOC100243286), mRNA
CH40	XM_002280449.3	25269	Vitis vinifera 17.3 kDa class II heat shock protein (LOC100261109), mRNA
CH40	XM_002279065.4	25164	Vitis vinifera stromal 70 kDa heat shock-related protein, chloroplastic (LOC100249184), mRNA
CH40	XM_002266744.4	25153	Vitis vinifera elongation factor 2 (LOC100261253), mRNA
CH40	XR_002031278.1	25144	Vitis vinifera uncharacterized LOC109123537 (LOC109123537), ncRNA
CH40	XM_002280785.4	25066	Vitis vinifera 18.1 kDa class I heat shock protein (LOC100263355), mRNA
CH40	XM_002284457.3	24602	Vitis vinifera chlorophyll a-b binding protein 13, chloroplastic (LOC100260599), mRNA
CH40	XM_002283012.4	24479	Vitis vinifera probable oxygen-evolving enhancer protein 2 (PSBP1), transcript variant X1, mRNA
CH40	XM_002278744.3	24320	Vitis vinifera photosystem I reaction center subunit XI, chloroplastic (LOC100242802), mRNA
CH40	XM_002279245.4	24019	Vitis vinifera glycerate dehydrogenase HPR, peroxisomal (LOC100262344), transcript variant X1, mRNA
CH40	XM_002273749.4	23347	Vitis vinifera endoplasmic homolog (LOC100267648), mRNA
CH40	XM_002285866.3	23015	Vitis vinifera thioredoxin-like protein CDSP32, chloroplastic (LOC100259132), mRNA
CH40	XR_139816.3	23010	Vitis vinifera uncharacterized LOC100853453 (LOC100853453), ncRNA
CH40	XM_002280899.4	22529	Vitis vinifera 18.1 kDa class I heat shock protein (LOC100253085), mRNA
CH40	XM_002281359.4	22494	Vitis vinifera chloroplast stem-loop binding protein of 41 kDa b, chloroplastic (LOC100261308), mRNA
CH40	XM_002266334.4	22486	Vitis vinifera polyubiquitin 4 (LOC100252768), mRNA
CH40	XM_002284733.4	22237	Vitis vinifera protochlorophyllide reductase, chloroplastic (LOC100255647), mRNA
CH40	XM_010648649.2	22225	Vitis vinifera ribosomal protein S4, mitochondrial (LOC104878382), mRNA
CH40	XM_003634905.2	22084	Vitis vinifera photosystem I reaction center subunit III, chloroplastic (LOC100247987), mRNA
CH40	XM_002267296.3	22076	Vitis vinifera 23.6 kDa heat shock protein, mitochondrial (LOC100253548), mRNA
CH40	XM_019224912.1	21888	Vitis vinifera polyubiquitin (LOC100259635), transcript variant X3, mRNA
CH40	XM_002279459.4	21501	Vitis vinifera 17.3 kDa class II heat shock protein-like (LOC100268136), mRNA
CH40	XM_002279200.4	21449	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X1, mRNA
CH40	XM_010653193.2	21433	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X2, mRNA
CH40	XM_002263013.3	21360	Vitis vinifera sedoheptulose-1,7-bisphosphatase, chloroplastic (LOC100260169), mRNA
CH40	XM_002274979.4	21349	Vitis vinifera ATP synthase gamma chain, chloroplastic (LOC100264091), mRNA
CH40	XM_010658801.1	21141	Vitis vinifera probable oxygen-evolving enhancer protein 2 (PSBP1), transcript variant X2, mRNA
CH40	XM_010650493.2	21056	Vitis vinifera 17.9 kDa class II heat shock protein-like (LOC100256023), mRNA
CH40	XM_002275588.3	20899	Vitis vinifera oxygen-evolving enhancer protein 3, chloroplastic (LOC100240959), mRNA
CH40	NM_001281136.1	20742	Vitis vinifera Bcl-2-associated athanogene-like protein (LOC100260747), mRNA
CH40	XM_010664718.2	20684	Vitis vinifera heat shock protein 101 (HSP101), transcript variant X1, mRNA
CH40	XM_002273718.4	20402	Vitis vinifera glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic (LOC100259814), mRNA
CH40	XM_019220709.1	20220	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X3, mRNA
CH40	XM_002273208.4	20176	Vitis vinifera heat shock cognate protein 80 (LOC100261759), mRNA
CH40	NM_001281060.1	19977	Vitis vinifera cysteine protease (CYSP), mRNA
CH40	XM_010646363.2	19932	Vitis vinifera pectin acetylesterase 8 (LOC100245856), mRNA
CH40	XM_002278303.3	19904	Vitis vinifera GDP-L-galactose phosphorylase 2 (LOC100253859), mRNA

CH40	XM_002282110.3	19813	Vitis vinifera cell division cycle protein 48 homolog (LOC100265402), mRNA
CH40	NM_001280893.1	19716	Vitis vinifera heat shock protein 101 (HSP101), mRNA
CH40	XM_002280073.3	19686	Vitis vinifera CSC1-like protein ERD4 (LOC100260008), mRNA
CH40	XM_019219116.1	19601	Vitis vinifera glycerate dehydrogenase HPR, peroxisomal (LOC100262344), transcript variant X2, mRNA
CH40	XM_002270449.3	19524	Vitis vinifera alpha-glucan water dikinase, chloroplastic (LOC100246568), transcript variant X2, mRNA
CH40	XM_002278282.2	19520	Vitis vinifera DEAD-box ATP-dependent RNA helicase 3, chloroplastic (LOC100251060), mRNA
CH40	XM_010653413.2	19506	Vitis vinifera alpha-glucan water dikinase, chloroplastic (LOC100246568), transcript variant X1, mRNA
CH40	XM_019224911.1	19234	Vitis vinifera polyubiquitin (LOC100259635), transcript variant X2, mRNA
CH40	XM_010660191.2	19233	Vitis vinifera 18.1 kDa class I heat shock protein (LOC100249611), transcript variant X1, mRNA
CH40	XR_002031623.1	19223	Vitis vinifera 18.1 kDa class I heat shock protein (LOC100249611), transcript variant X2, misc_RNA
CH40	XM_002280058.3	19044	Vitis vinifera ketol-acid reductoisomerase, chloroplastic-like (LOC100262542), mRNA
CH40	XM_002275007.3	19035	Vitis vinifera calvin cycle protein CP12-1, chloroplastic (LOC100267103), mRNA
CH40	XM_002284820.3	18734	Vitis vinifera chlorophyll a-b binding protein 4, chloroplastic (LOC100232934), mRNA
CH40	XR_785937.2	18481	Vitis vinifera phosphomethylpyrimidine synthase, chloroplastic (LOC100250096), transcript variant X2, misc_RNA
CH40	XR_785938.2	18452	Vitis vinifera phosphomethylpyrimidine synthase, chloroplastic (LOC100250096), transcript variant X3, misc_RNA
CH40	XM_002280191.4	18377	Vitis vinifera phosphomethylpyrimidine synthase, chloroplastic (LOC100250096), transcript variant X1, mRNA
CH40	NM_001280913.1	18362	Vitis vinifera chloroplast ELIP early light-induced protein (LOC100263179), mRNA; nuclear gene for chloroplast product
CH40	XM_010652630.2	18343	Vitis vinifera phosphomethylpyrimidine synthase, chloroplastic (LOC100250096), transcript variant X4, mRNA
CH40	XM_002280545.4	18273	Vitis vinifera 18.1 kDa class I heat shock protein (LOC100261583), mRNA
CH40	XM_002282835.4	18246	Vitis vinifera beta-amylase 3, chloroplastic (LOC100247246), mRNA
CH40	XM_010658776.1	17908	Vitis vinifera uncharacterized LOC100267696 (LOC100267696), transcript variant X2, mRNA
CH40	XM_002282402.4	17894	Vitis vinifera uncharacterized LOC100267696 (LOC100267696), transcript variant X1, mRNA
CH40	XM_002284207.4	17789	Vitis vinifera chaperone protein ClpB3, chloroplastic (LOC100252611), mRNA
CH40	XR_785679.2	17706	Vitis vinifera uncharacterized LOC100852628 (LOC100852628), transcript variant X2, ncRNA
CH40	XM_002282023.3	17642	Vitis vinifera photosystem II reaction center W protein, chloroplastic (LOC100256361), mRNA
CH40	XR_785678.2	17632	Vitis vinifera uncharacterized LOC100852628 (LOC100852628), transcript variant X1, ncRNA
CH40	XR_002031214.1	17591	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X1, ncRNA
CH40	XR_002031215.1	17588	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X2, ncRNA
CH40	XR_002031216.1	17588	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X3, ncRNA
CH40	NM_001280992.1	17536	Vitis vinifera aquaporin-like (PIP1;3), mRNA
CH40	XM_002262806.4	17430	Vitis vinifera glutathione S-transferase (LOC100265903), mRNA
CH40	XM_002266071.3	17411	Vitis vinifera protein CURVATURE THYLAKOID 1B, chloroplastic (LOC100248815), mRNA
CH40	XM_002279562.4	17375	Vitis vinifera elongation factor 1-alpha-like (LOC100244821), mRNA
CH40	XM_002271875.3	17371	Vitis vinifera uncharacterized LOC100262861 (LOC100262861), mRNA
CH40	XM_002267020.3	17358	Vitis vinifera ferredoxin-dependent glutamate synthase, chloroplastic (LOC100233082), mRNA
CH40	XM_002280676.3	17348	Vitis vinifera uncharacterized LOC100262932 (LOC100262932), transcript variant X1, mRNA

Library	ID	Counts	Description
171	XM_019221016.1	2308839	Vitis vinifera ribulose biphosphate carboxylase large chain (LOC109122894), partial mRNA
171	XM_010654474.1	863546	Vitis vinifera cytochrome P450 81E8-like (LOC100242168), mRNA
171	XM_003632139.2	609921	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100263871), transcript variant X2, mRNA
171	XM_002282200.3	575381	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100263871), transcript variant X1, mRNA
171	XM_019218790.1	514706	Vitis vinifera photosystem II CP47 reaction center protein-like (LOC109122277), mRNA
171	XM_019216320.1	484944	Vitis vinifera pentatricopeptide repeat-containing protein At1g19720 (LOC100255764), mRNA
171	XR_002030730.1	343412	Vitis vinifera uncharacterized LOC104880458 (LOC104880458), ncRNA
171	XR_002030742.1	312697	Vitis vinifera uncharacterized LOC109123058 (LOC109123058), ncRNA
171	XM_019216227.1	291789	Vitis vinifera pentatricopeptide repeat-containing protein At5g40410, mitochondrial (LOC100260830), mRNA
171	XM_002267690.4	237010	Vitis vinifera probable fructose-bisphosphate aldolase 1, chloroplastic-like (LOC100262354), mRNA
171	XR_788116.2	215802	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X1, ncRNA
171	XR_788121.2	215799	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X3, ncRNA
171	XR_788119.2	215791	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X4, ncRNA
171	XR_788124.2	215790	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X5, ncRNA
171	XR_002031529.1	215788	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X6, ncRNA
171	XR_788122.2	215788	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X2, ncRNA
171	XR_002031531.1	215787	Vitis vinifera uncharacterized LOC104882412 (LOC104882412), transcript variant X7, ncRNA
171	XM_002276931.4	215057	Vitis vinifera ribulose biphosphate carboxylase small chain, chloroplastic-like (LOC100267942), mRNA
171	XR_002031185.1	194275	Vitis vinifera uncharacterized LOC109123445 (LOC109123445), ncRNA
171	XM_010649010.2	181282	Vitis vinifera ATP synthase subunit alpha, mitochondrial (LOC104878494), mRNA
171	XM_019225640.1	177972	Vitis vinifera uncharacterized mitochondrial protein AtMg00810-like (LOC109124071), mRNA
171	XM_010665664.2	133847	Vitis vinifera catalase isozyme 1 (LOC100244516), mRNA
171	XR_002031525.1	133379	Vitis vinifera uncharacterized LOC109123733 (LOC109123733), ncRNA
171	XR_002031186.1	127830	Vitis vinifera uncharacterized LOC109123446 (LOC109123446), ncRNA
171	XM_002270535.3	123392	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100256315), mRNA
171	XR_002031535.1	121336	Vitis vinifera uncharacterized LOC109123739 (LOC109123739), ncRNA
171	XM_002283496.3	117271	Vitis vinifera heat shock 70kDa protein 1/8-like (LOC100254725), mRNA
171	XM_003631825.3	114580	Vitis vinifera fructose-bisphosphate aldolase 1, chloroplastic (LOC100852851), mRNA
171	XM_002282943.4	107165	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100266698), transcript variant X1, mRNA
171	XM_010660236.2	106134	Vitis vinifera ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (LOC100266698), transcript variant X2, mRNA
171	XM_010646105.2	100444	Vitis vinifera polyubiquitin (LOC100267431), mRNA
171	XM_010646102.2	91941	Vitis vinifera polyubiquitin (LOC104877307), mRNA
171	XM_010650056.2	91050	Vitis vinifera glycine dehydrogenase (decarboxylating), mitochondrial (LOC100266170), mRNA
171	XM_002265911.3	86356	Vitis vinifera galactinol synthase 1 (LOC100260266), mRNA
171	XR_139816.3	79760	Vitis vinifera uncharacterized LOC100853453 (LOC100853453), ncRNA
171	XM_002278316.4	77337	Vitis vinifera glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic (LOC100246378), mRNA
171	XM_002273718.4	67197	Vitis vinifera glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic (LOC100259814), mRNA
171	XM_002271755.3	66716	Vitis vinifera photosystem II 10 kDa polypeptide, chloroplastic (LOC100243967), mRNA
171	XM_003632895.2	65751	Vitis vinifera 5'-adenylylsulfate reductase 3, chloroplastic (LOC100854884), mRNA
171	XM_002278303.3	65077	Vitis vinifera GDP-L-galactose phosphorylase 2 (LOC100253859), mRNA
171	XM_002273165.4	62302	Vitis vinifera photosystem I chlorophyll a/b-binding protein 3-1, chloroplastic (LOC100232927), mRNA
171	XM_019218228.1	61795	Vitis vinifera putative ATP synthase protein YMF19 (LOC104878237), mRNA
171	XM_002284928.4	61270	Vitis vinifera elongation factor 1-alpha (LOC100256979), transcript variant X1, mRNA
171	XM_010652829.2	61224	Vitis vinifera elongation factor 1-alpha (LOC100256979), transcript variant X2, mRNA
171	XM_002265554.4	58193	Vitis vinifera putative transcription factor (LOC100250281), mRNA
171	XM_002280073.3	58187	Vitis vinifera CSC1-like protein ERD4 (LOC100260008), mRNA
171	XM_002266322.4	58108	Vitis vinifera S-adenosylmethionine synthetase 2 (METK2), mRNA
171	NM_001281149.1	57814	Vitis vinifera magnesium chelatase H subunit (CHLH), mRNA
171	XM_002284888.3	56618	Vitis vinifera elongation factor 1-alpha (LOC100246711), mRNA
171	XM_002266523.4	54028	Vitis vinifera probable mannitol dehydrogenase (LOC100255907), transcript variant X1, mRNA
171	XM_003635388.3	53991	Vitis vinifera probable mannitol dehydrogenase (LOC100255907), transcript variant X2, mRNA
171	XM_019226699.1	52664	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X1, mRNA
171	XM_019226700.1	52664	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X3, mRNA
171	XM_019226702.1	52662	Vitis vinifera pentatricopeptide repeat-containing protein At5g50990 (LOC100247459), transcript variant X5, mRNA

171	XM_003632976.3	51769	Vitis vinifera chlorophyll a-b binding protein 40, chloroplastic-like (LOC100252004), mRNA
171	XM_019225614.1	48982	Vitis vinifera protein LHY (LOC100250535), transcript variant X4, mRNA
171	XM_010663209.2	48187	Vitis vinifera protein LHY (LOC100250535), transcript variant X5, mRNA
171	XM_019225615.1	48104	Vitis vinifera protein LHY (LOC100250535), transcript variant X6, mRNA
171	XM_002270940.4	47832	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X1, mRNA
171	XM_010647664.2	47828	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X3, mRNA
171	XM_010647663.2	47826	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X2, mRNA
171	XM_019217932.1	47823	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X4, mRNA
171	XM_019217933.1	47806	Vitis vinifera probable LRR receptor-like serine/threonine-protein kinase At1g56140 (LOC100242759), transcript variant X5, mRNA
171	XM_010663213.2	47659	Vitis vinifera protein LHY (LOC100250535), transcript variant X9, mRNA
171	XM_010663207.2	47256	Vitis vinifera protein LHY (LOC100250535), transcript variant X2, mRNA
171	XM_010663210.2	47108	Vitis vinifera protein LHY (LOC100250535), transcript variant X7, mRNA
171	XM_010663211.2	46929	Vitis vinifera protein LHY (LOC100250535), transcript variant X8, mRNA
171	XM_019225613.1	46314	Vitis vinifera protein LHY (LOC100250535), transcript variant X1, mRNA
171	XM_010648098.2	46236	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X1, mRNA
171	XM_010658486.2	46235	Vitis vinifera phenylalanine--tRNA ligase, chloroplastic/mitochondrial (LOC100265994), transcript variant X2, mRNA
171	XM_010648100.2	46199	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X4, mRNA
171	XM_002262836.4	46186	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X3, mRNA
171	NM_001281246.1	46174	Vitis vinifera glutamine synthetase (GS), mRNA
171	XM_010648099.2	46164	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100243424), transcript variant X2, mRNA
171	XM_010665376.2	46097	Vitis vinifera calcium-binding allergen Ole e 8-like (LOC100264572), mRNA
171	XM_010663208.2	45956	Vitis vinifera protein LHY (LOC100250535), transcript variant X3, mRNA
171	XM_002275039.3	45933	Vitis vinifera chlorophyll a-b binding protein of LHCII type 1 (LOC100241745), mRNA
171	XM_002278068.4	44996	Vitis vinifera peroxisomal (S)-2-hydroxy-acid oxidase GLO1 (LOC100232932), mRNA
171	XM_002285821.3	44625	Vitis vinifera photosystem II 22 kDa protein, chloroplastic (LOC100245393), mRNA
171	XM_010657584.1	44532	Vitis vinifera chlorophyll a-b binding protein, chloroplastic (LOC100266036), mRNA
171	XM_002274067.4	44018	Vitis vinifera scarecrow-like protein 21 (LOC100250258), transcript variant X1, mRNA
171	XM_010648101.2	42732	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X1, mRNA
171	XM_002279798.3	42700	Vitis vinifera chlorophyll a-b binding protein CP29.2, chloroplastic-like (LOC100266604), mRNA
171	XM_019218132.1	42614	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X2, mRNA
171	XM_010646221.2	42600	Vitis vinifera scarecrow-like protein 21 (LOC100250258), transcript variant X2, mRNA
171	XM_019218133.1	42536	Vitis vinifera serine hydroxymethyltransferase, mitochondrial (LOC100261289), transcript variant X3, mRNA
171	XM_003635387.3	42450	Vitis vinifera probable mannitol dehydrogenase (LOC100855415), mRNA
171	XR_785679.2	42364	Vitis vinifera uncharacterized LOC100852628 (LOC100852628), transcript variant X2, ncRNA
171	XM_010663216.2	41761	Vitis vinifera protein LHY (LOC100250535), transcript variant X11, mRNA
171	XM_010648273.2	41621	Vitis vinifera probable cytochrome c biosynthesis protein (LOC104878236), mRNA
171	XR_785678.2	40893	Vitis vinifera uncharacterized LOC100852628 (LOC100852628), transcript variant X1, ncRNA
171	XM_002263688.4	40811	Vitis vinifera phosphoribulokinase, chloroplastic (LOC100244092), mRNA
171	XM_010648649.2	40019	Vitis vinifera ribosomal protein S4, mitochondrial (LOC104878382), mRNA
171	XM_002271651.4	39905	Vitis vinifera chlorophyll a-b binding protein 151, chloroplastic-like (LOC100254533), mRNA
171	XM_019225580.1	38609	Vitis vinifera uncharacterized LOC100243097 (LOC100243097), mRNA
171	XM_010663214.2	37894	Vitis vinifera protein LHY (LOC100250535), transcript variant X10, mRNA
171	XM_002285883.2	37803	Vitis vinifera dehydrin ERD14 (LOC100254126), mRNA
171	XM_010659535.2	37718	Vitis vinifera anthocyanidin 3-O-glucosyltransferase 2 (LOC100242982), mRNA
171	XM_002271648.2	37101	Vitis vinifera tetraspanin-8 (LOC100243286), mRNA
171	XM_002276741.3	37055	Vitis vinifera inactive beta-amylase 9 (LOC100263193), mRNA
171	XM_002274760.4	36042	Vitis vinifera oxygen-evolving enhancer protein 1, chloroplastic (LOC100245459), mRNA
171	XM_010665492.2	36012	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X1, mRNA
171	XM_010665493.2	35997	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X2, mRNA
171	XM_002265766.4	35916	Vitis vinifera uncharacterized LOC100245618 (LOC100245618), transcript variant X4, mRNA
171	XM_002269581.3	35184	Vitis vinifera ferredoxin-like (LOC100249080), mRNA
171	XM_002279200.4	34865	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X1, mRNA
171	XM_010653193.2	34864	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X2, mRNA
171	XM_002275372.4	34724	Vitis vinifera valencene synthase (LOC100246608), mRNA
171	XM_019226465.1	34702	Vitis vinifera ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (LOC100250896), transcript variant X3, mRNA

171	XM_010660818.2	34598	Vitis vinifera uncharacterized LOC104881268 (LOC104881268), mRNA
171	XM_019219070.1	34144	Vitis vinifera uncharacterized LOC100245618 (LOC100245618), transcript variant X5, mRNA
171	XM_002271875.3	33859	Vitis vinifera uncharacterized LOC100262861 (LOC100262861), mRNA
171	XM_002274745.4	33823	Vitis vinifera valencene synthase-like (LOC100260112), mRNA
171	XM_019218713.1	33543	Vitis vinifera 5'-adenylylsulfate reductase 3, chloroplastic-like (LOC100853787), mRNA
171	XM_010649763.2	33143	Vitis vinifera uncharacterized LOC100245618 (LOC100245618), transcript variant X1, mRNA
171	XM_002264972.4	33089	Vitis vinifera uncharacterized LOC100247569 (LOC100247569), mRNA
171	XR_002031214.1	32901	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X1, ncRNA
171	XR_002031215.1	32900	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X2, ncRNA
171	XR_002031216.1	32895	Vitis vinifera uncharacterized LOC109123515 (LOC109123515), transcript variant X3, ncRNA
171	XM_002263013.3	32821	Vitis vinifera sedoheptulose-1,7-bisphosphatase, chloroplastic (LOC100260169), mRNA
171	XM_002283530.4	32713	Vitis vinifera chlorophyll a-b binding protein 40, chloroplastic-like (LOC100250504), mRNA
171	XM_019220709.1	32640	Vitis vinifera serine--glyoxylate aminotransferase (LOC100261927), transcript variant X3, mRNA
171	XM_002274343.4	32405	Vitis vinifera uncharacterized LOC100264128 (LOC100264128), mRNA
171	XM_010649764.2	31644	Vitis vinifera uncharacterized LOC100245618 (LOC100245618), transcript variant X2, mRNA
171	XM_019220594.1	31639	Vitis vinifera heat shock cognate 70 kDa protein-like (LOC100253562), transcript variant X1, mRNA
171	XM_002282480.4	31562	Vitis vinifera actin-7 (LOC100232866), mRNA
171	XM_002267020.3	31449	Vitis vinifera ferredoxin-dependent glutamate synthase, chloroplastic (LOC100233082), mRNA
171	XM_019218224.1	31199	Vitis vinifera NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (LOC109122065), partial mRNA
171	XM_002265738.3	30662	Vitis vinifera ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic (LOC100241976), mRNA
171	XM_010651412.2	30533	Vitis vinifera translationally-controlled tumor protein homolog (LOC100251175), mRNA
171	NM_001281165.1	30432	Vitis vinifera AlaT1 (LOC100261274), mRNA
171	XM_002277921.4	30156	Vitis vinifera beta carbonic anhydrase 1, chloroplastic (LOC100249137), transcript variant X1, mRNA
171	XM_002283856.3	30120	Vitis vinifera magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic-like (LOC100241461), mRNA
171	XM_002282071.4	30020	Vitis vinifera ATP-dependent zinc metalloprotease FTSH 2, chloroplastic (LOC100250511), transcript variant X1, mRNA
171	XM_019223684.1	30005	Vitis vinifera ATP-dependent zinc metalloprotease FTSH 2, chloroplastic (LOC100250511), transcript variant X2, mRNA
171	XM_002269394.3	29607	Vitis vinifera zinc finger CCCH domain-containing protein 29-like (LOC100246707), transcript variant X2, mRNA
171	XM_002266458.4	29599	Vitis vinifera transketolase, chloroplastic (LOC100248004), mRNA
171	XM_019224434.1	29584	Vitis vinifera zinc finger CCCH domain-containing protein 29-like (LOC100246707), transcript variant X1, mRNA
171	XM_010649765.2	29072	Vitis vinifera uncharacterized LOC100245618 (LOC100245618), transcript variant X3, mRNA
171	XM_019220595.1	28788	Vitis vinifera heat shock cognate 70 kDa protein-like (LOC100253562), transcript variant X2, mRNA
171	XM_010664285.2	28372	Vitis vinifera ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant X1, mRNA
171	XM_010664288.2	28247	Vitis vinifera ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant X2, mRNA
171	XM_010646899.2	28157	Vitis vinifera melanoma-associated antigen D1 (LOC100250684), transcript variant X1, mRNA
171	XM_019225805.1	27825	Vitis vinifera ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant X3, mRNA
171	XM_002263563.3	27799	Vitis vinifera heat shock cognate 70 kDa protein 1-like (LOC100259551), mRNA
171	XM_010664289.2	27652	Vitis vinifera ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant X5, mRNA
171	XM_019225806.1	27601	Vitis vinifera ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant X4, mRNA
171	XM_002273394.3	27576	Vitis vinifera 1-aminocyclopropane-1-carboxylate oxidase (LOC100232928), mRNA
171	XM_002263925.4	27551	Vitis vinifera gibberellin 2-beta-dioxygenase 1 (LOC100264177), mRNA
171	NM_001280968.1	27427	
171	XM_002262806.4	26682	Vitis vinifera glutathione S-transferase (LOC100265903), mRNA
171	NM_001303076.1	26232	
171	XM_002266744.4	26224	Vitis vinifera elongation factor 2 (LOC100261253), mRNA
171	XM_002269656.4	26125	Vitis vinifera UDP-glucose 6-dehydrogenase 3 (LOC100261061), mRNA
171	XM_002283012.4	26025	Vitis vinifera probable oxygen-evolving enhancer protein 2 (PSBP1), transcript variant X1, mRNA
171	XM_002270848.4	25919	Vitis vinifera UDP-D-apiose/UDP-D-xylose synthase 2 (LOC100248193), mRNA
171	XM_010666759.2	25741	Vitis vinifera protein GIGANTEA (LOC100254197), transcript variant X1, mRNA
171	XM_010666760.2	25515	Vitis vinifera protein GIGANTEA (LOC100254197), transcript variant X2, mRNA
171	XM_010662610.2	25413	Vitis vinifera beta carbonic anhydrase 1, chloroplastic (LOC100249137), transcript variant X2, mRNA
171	XM_019224912.1	25264	Vitis vinifera polyubiquitin (LOC100259635), transcript variant X3, mRNA
171	XM_010657023.2	25249	Vitis vinifera protein TIC 214 (LOC100855294), mRNA
171	XM_002268994.4	25050	Vitis vinifera arginine decarboxylase (LOC100233080), mRNA
171	XM_002266334.4	25046	Vitis vinifera polyubiquitin 4 (LOC100252768), mRNA
171	XM_002285889.4	25043	Vitis vinifera ATP-dependent zinc metalloprotease FTSH, chloroplastic (LOC100250509), mRNA

171	XM_019223300.1	24999	Vitis vinifera anthocyanidin 3-O-glucosyltransferase 2-like (LOC100267003), mRNA
171	XM_002284325.3	24735	Vitis vinifera cytochrome b6-f complex iron-sulfur subunit 1, chloroplastic (LOC100258879), mRNA
171	XM_002271000.3	24673	Vitis vinifera glycine-rich protein A3 (LOC100254598), mRNA
171	XM_019217516.1	24584	Vitis vinifera melanoma-associated antigen D1 (LOC100250684), transcript variant X2, mRNA
171	XM_003633507.3	24579	Vitis vinifera zinc finger A20 and AN1 domain-containing stress-associated protein 5 (LOC100852428), mRNA
171	XM_002270926.4	24505	Vitis vinifera methanol O-anthraniloyltransferase (LOC100243166), mRNA
171	XM_002262568.4	24499	Vitis vinifera glutathione S-transferase (LOC100243577), mRNA
171	XM_003634988.3	24227	Vitis vinifera heat shock cognate protein 80 (LOC100246843), mRNA
171	XM_002266384.4	24198	Vitis vinifera methanol O-anthraniloyltransferase (LOC100252759), mRNA
171	XM_002281011.4	24189	Vitis vinifera ADP-ribosylation factor (LOC100242677), transcript variant X2, mRNA
171	XM_003631668.3	24030	Vitis vinifera uncharacterized LOC100854587 (LOC100854587), mRNA
171	XM_002266078.4	23823	Vitis vinifera methanol O-anthraniloyltransferase (LOC100257911), mRNA
171	XM_002268484.4	23320	Vitis vinifera nematode resistance protein-like HSPRO2 (LOC100255226), mRNA
171	XM_003635230.3	23160	Vitis vinifera probable mannitol dehydrogenase (LOC100854583), mRNA
171	XM_002272443.3	23157	Vitis vinifera probable mannitol dehydrogenase (LOC100252642), mRNA
171	NM_001280992.1	23086	Vitis vinifera aquaporin-like (PIP1;3), mRNA
171	XM_003631529.3	23057	Vitis vinifera uncharacterized LOC100243519 (LOC100243519), mRNA
171	XM_002274141.4	23020	Vitis vinifera NAC domain-containing protein 2 (LOC100261123), mRNA
171	NM_001281183.1	22905	
171	XM_010652797.2	22872	Vitis vinifera L-ascorbate peroxidase 2, cytosolic (LOC100233013), transcript variant X1, mRNA
171	XM_002281697.3	22866	Vitis vinifera peroxisomal membrane protein 11A (LOC100243820), mRNA
171	XM_002284731.4	22743	Vitis vinifera L-ascorbate peroxidase 2, cytosolic (LOC100233013), transcript variant X2, mRNA
171	XM_010661442.2	22681	Vitis vinifera S-adenosylmethionine synthetase 4 (METK4), mRNA
171	XM_002279245.4	22681	Vitis vinifera glycerate dehydrogenase HPR, peroxisomal (LOC100262344), transcript variant X1, mRNA
171	XM_003635386.3	22545	Vitis vinifera probable mannitol dehydrogenase (LOC100855376), mRNA
171	XM_003631877.3	22227	Vitis vinifera catalase isozyme 1 (LOC100853165), mRNA
171	XM_002276344.3	22221	Vitis vinifera ETHYLENE INSENSITIVE 3-like 1 protein (LOC100250496), transcript variant X1, mRNA
171	NM_001281169.1	22198	Vitis vinifera catalase (GCAT), mRNA
171	XM_010657066.2	22187	Vitis vinifera calcium permeable stress-gated cation channel 1 (LOC100257332), transcript variant X1, mRNA
171	XM_002284736.4	22129	Vitis vinifera ribulose-phosphate 3-epimerase, chloroplastic (LOC100267206), transcript variant X1, mRNA
171	XM_010658801.1	21886	Vitis vinifera probable oxygen-evolving enhancer protein 2 (PSBP1), transcript variant X2, mRNA
171	XM_002275516.2	21776	Vitis vinifera chlorophyll a-b binding protein 6A, chloroplastic-like (LOC100263275), mRNA
171	XM_002277121.3	21759	Vitis vinifera protein TIFY 10A (LOC100254231), mRNA
171	XM_002265805.4	21683	Vitis vinifera methanol O-anthraniloyltransferase (LOC100263045), mRNA
171	XM_010660723.2	21587	Vitis vinifera ETHYLENE INSENSITIVE 3-like 1 protein (LOC100250496), transcript variant X2, mRNA
171	XM_002266352.2	21587	Vitis vinifera hybrid signal transduction histidine kinase A (LOC100252953), mRNA

Supplementary table 3 - Analysis of the increase in subtraction ratio

Genes comparison	Enrichment 10:1
ACT vs GLRaV-2	0.16706715
18s 1 vs GLRaV-2	0.00280944
18s 2 vs GLRaV-2	4.58683814
18s 3 vs GLRaV-2	0.14890871
28s vs GLRaV-2	3.17663647

Genes comparison	Enrichment 50:1
ACT vs GLRaV-2	0.8288065
18s 1 vs GLRaV-2	0.01393799
18s 2 vs GLRaV-2	2.75586723
18s 3 vs GLRaV-2	0.738754371
28s vs GLRaV-2	5.759668360