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RESEARCH ARTICLE

Comprehensive analysis of copy number variation in diverse bitter gourd (*Momordica charantia* L.) accessions

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Abstract

Copy number variation (CNV), a type of large-scale structural variation, contributes substantially to genetic diversity, impacting phenotypic traits and adaptive evolution in plants. In this study, genome re-sequencing of 146 bitter gourd (*Momordica charantia* L.) accessions revealed over 200,000 unique CNVs, consisting of 33,8031 deletions and 200,714 duplications. A total of 5763 CNV regions (CNVRs) were identified, spanning sizes ranging from 1 to over 400 kb, with notable enrichment on chromosomes 6 and 8. Functional annotation of 992 genes overlapping with CNVRs highlighted processes related to DNA repair, pathogen defense, metabolic regulation, and bioactive compound synthesis, including terpenes and antioxidants. Gene ontology and KEGG pathway enrichment analyses indicated roles in DNA integration, stress resilience, and metabolic pathways. A significant genetic differentiation influenced by domestication and regional adaptation was observed from clustering and population structure analyses. Hierarchical and PCA clustering identified distinct groups based on geographic origin, with a marked divergence between wild and cultivated varieties, particularly among accessions from China and Africa. This comprehensive CNV analysis provides valuable insights into the genetic diversity and adaptive mechanisms of bitter gourd, supporting breeding strategies, conservation efforts, and further exploration of its genomic potential for crop improvement.

Keywords: Copy number variations, bitter gourd, whole-genome re-sequencing, population genetics, functional enrichment

Introduction

Bitter gourd, or bitter melon, is a widely cultivated vegetable-cum-medicinal plant found in regions such as India, China, Malaysia, Africa, and South America (Heiser 1979). Belonging to the family *Cucurbitaceae*, the bitter gourd finds its primary center of origin in India and was domesticated in eastern Asia, potentially in regions of eastern India or southern China (Rathod et al. 2019). Bitter gourd, rich in ascorbic acid, iron, and bioactive compounds such as cucurbitacins, alkaloids, and ribosome-inactivating proteins, is esteemed for its therapeutic potential, including anti-diabetic, anti-carcinogenic, anti-inflammatory, and anti-HIV properties (Varela et al. 2022). This plant exhibits broad phenotypic diversity in Indian germplasm, showcasing variations in growth habit, maturity, fruit characteristics, and sex expression (Robinson and Decker-Walters 1997). Notable botanical varieties include *Momordica charantia* L. var. charantia, known for its large fruits, and *M. charantia* var. muricata, which produces small, round fruits used in culinary preparations and *M. charantia* subsp. *macroloba*, which is characterized by elongated spiny fruits (Rathod et al. 2019). However, the genetic variation, especially the large-scale structural variations, remains largely unknown in bitter gourd to date.

Genetic variation encompasses both sequence variation and structural alteration. Sequence variation typically manifests as SNPs, short sequence insertions and deletions (indels), microsatellites, or transposable elements. Structural variations (SVs), such as deletions, insertions, inversions, and duplications, represent a significant wellspring of genetic diversity (Alkan et al. 2011). Among SVs, copy number variations (CNVs), including deletions and duplications ranging from 1 kb to several Mb (Stankiewicz and Lupski

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2010), constitute a notable source of genetic diversity (Redon et al. 2006). CNVs have been linked to various human disorders such as autism, schizophrenia, and neuroblastoma. In plants, SVs contribute to phenotypic variations like leaf size (Horiguchi et al. 2009), fruit shape (Xiao et al. 2008), and aluminium tolerance (Maron et al. 2013).

Numerous methods have been devised for CNV detection, including fluorescence *in situ* hybridization (FISH), quantitative polymerase chain reaction (qPCR), and microarray. Initially, microarray-based comparative genomic hybridization was the primary method for CNV detection in various species such as humans (Iafrate et al. 2004), rice (Yu et al. 2013), soybean (McHale et al. 2012), and barley (Muñoz-Amatriaín et al. 2013). However, array-based technologies have limitations in detecting novel CNVs accurately due to their dependency on probe homology and inability to determine copy number or breakpoints precisely. Next-generation sequencing (NGS) technologies have revolutionized CNV detection in recent years, with new approaches and algorithms based on strategies like read-pair (RP), split read (SR), read depth (RD), and *de novo* assembly (AS) (Zhao et al. 2013). Several studies have utilized NGS technologies for SV mapping at the population level in plants, including species like *Arabidopsis thaliana* (Cao et al. 2011) and *Zea mays* (Chia et al. 2012). The complexity of crop genomes and the variability in CNV structure and distribution pose challenges in comprehensive and accurate CNV detection across different crop germplasms.

The comprehensive study of CNVs in bitter gourd is warranted in view of the large amount of genomic data available of 146 accessions across different geographical regions. Here, we present a comprehensive analysis elucidating the correlation between CNVs and gene expression levels, uncovering CNVs' role in the genetic diversity of the bitter gourd genome. This high-accuracy CNV dataset promises insights into genome evolution dynamics, offers a deeper understanding of the genetic underpinnings of essential agricultural traits, and holds the potential for enhancing future crop breeding endeavors.

Materials and methods

Collection of bitter gourd whole-genome sequencing data

a total of 146 Whole-Genome Sequencing **(**WGS) accessions of bitter gourd with clear pedigree information (Fig. 1A) were downloaded from the National Centre for Biotechnology Information (NCBI; https://www.ncbi.nlm.nih.gov/) public database. This dataset consists of re-sequencing data of 131 cultivated bitter gourd accessions and 15 wild accessions of 2 groups, i.e., *Momordica charantia* subsp. *macroloba* and *Momordica charantia* var. muricata. The corresponding bio-project IDs for the 146 accessions are PRJEB24032, PRJEB24033, and PRJNA578358. The data was sequenced on an Illumina HiSeq 2000 sequencer (Illumina Inc.) with 100bp paired-end reads.The reference genome GCA_013281855.1 was downloaded from NCBI. The CNV region determination and the enrichment analysis of the harboring genes were performed after the reads' cleaning and pre-processing. Fig. 1B delineated the whole workflow of the analysis.

Data processing and sequence alignment

After quality control checking of raw reads using FastQC-0.11.8 (Andrews 2010), adapter and low-quality bases of reads were removed by Trimmomatic-0.39(v0.32) to obtain clean

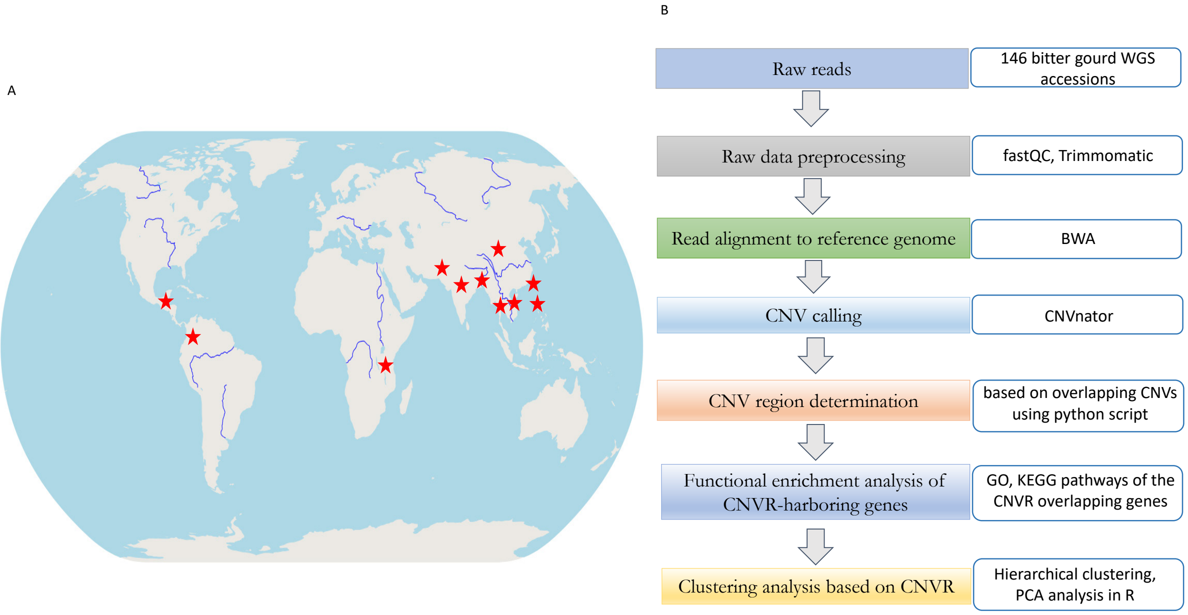

Fig. 1. (A) Map of samples by its geographic locations. (B)Workflow of the CNV identification and analysis

reads, with the parameters set as MINLEN = 50, LEADING = 20, TRAILING = 20, and SLIDING WINDOW = 5, 20(Bolger et al. 2014). Trimmed reads were then mapped to the bitter gourd reference genome using BWA-MEM (v0.7.17) (Li and Durbin 2009)with default parameters, and SAM format files were sorted and indexed into BAM format files using Samtools (v1.5) (Li et al. 2009). Repetitions were removed from the alignment results using the marked up command in SAMTOOLS software. The alignment rate and mean depth were also calculated using SAMTOOLS.

Prediction of CNV and CNVRs in bitter gourd accessions

the CNV prediction was performed using the CNVnator-v0.4 tool (Abyzov et al. 2011), a method based on read depth, relative to the reference genome assembly. With an average read depth of approximately 10× from the realigned BAM files, a uniform bin size of 300 bp was applied across all samples. CNVs were filtered based on *p*-values below 0.01 (calculated using t-test statistics), sizes exceeding 1 kb, and fractions of mapped reads with low quality ($q_0 < 0.5$)(Shi et al. 2023), and were then retained for further analysis.

The CNV region (CNVR) is defined as a combined region of overlapping CNVs in the bitter gourd genome after aggregating and filtering out the ones existed in less than ten accessions. Here, CNVRs were merged from different accessions with at least 90% stringently reciprocal overlap by extending the boundaries of the overlapping CNVs. These CNVRs were used for downstream analysis to remove false-positive results. Then they were further classified as "gain" (*i.e.*, CNVRs merged from duplications across different accessions), "loss" (*i.e.*, CNVRs merged from deletions across different accessions), and "both" (*i.e.*, CNVRs merged from both duplications and deletions within the same regions across different accessions) events according to their types.

CNVR annotation in bitter gourd accessions

Blastx was performed against *the nr* database to identify the genes overlapping with the CNVRs using BLAST2GO(Conesa et al. 2005). Gene Ontology (GO) enrichment and KEGG pathway analyses were conducted through the Database for Annotation, Visualization, and Integrated Discovery (DAVID; https://david.ncifcrf.gov/) on protein-coding genes. GO categories included biological processes, cellular components, and molecular functions, with statistical significance set at $p < 0.05$.

Population structure in bitter gourd accessions

To examine population differentiation based on CNVRs, we utilized clustering analysis and Principal Component Analysis (PCA). We created a sparse matrix of "0"s and "1"s for each CNVRs depending on the presence or absence of a certain CNVR in that particular genotype. Clustering was conducted using the *pvclust* R package, using that binary matrix. The clustering process involved 10,000 multiscale bootstrap resampling using the unweighted pair-group method with arithmetic mean (UPGMA), and statistical significance was assessed through approximately unbiased (AU) *p*-values and bootstrap probabilities (BP). The results were visualized using the *dendextend* R package. Additionally, PCA was performed using the prcomp function of the R package *stats*, and we created the biplot using the R package *factoextra*.

Results

Prediction of CNV and CNVRs in bitter gourd accessions

the retrieved 146 bitter gourd accessions had been sequenced on an average to >6 Gb. Mapping sequencing data to bitter gourd reference genome assembly showed an average mapping rate of 96.87% and a depth of 8.9X, indicating that the data are sufficient and of high quality for CNV detection (Supplementary Table S1). CNVnator reported 200714 duplications and 33,8031 deletions after removing the duplicate CNVs and only keeping the unique in the 146 accessions (Supplementary Table S2)—the highest number of CNVs found in the accession ERR2505455 with 12260 deletions and 11885 duplications. Chromosome 6 has the highest number of deletions with a count of 52368, and Chromosome 8 has the highest number of duplications with a count of 25599. The highest number of CNVs lies within the size range of 1K to 10k bp(Supplementary Table S3, Figs. 2A and 2B).The overlapping regions of CNVs were obtained using the in-house Python code, which consisted of 5763 CNVRs with 4766 deletions sized from 1 kb to 118.2 kb and 564 duplications from 1.7 kb to 415.5 kb and 433 regions with both deletions and duplications. Among the CNVRs combined from 146 samples, 3253 (34.5%) were detected in five individuals, 1327 (10.8%) in six individuals, and 491 (8.4%) in seven individuals, 659 in 8 or more than eight accessions. Of the 5763 CNVRs detected in five or more individuals, a total of 4539 CNVRs were detected only in domesticated cultivars and 69 CNVRs only in wild cultivars—the highest number of CNVRs was found to be within 1K to 10k length. CNVR detected in most individuals was duplication detected in 23accessions, located on chr9 at12.97–13.35 Mb, and second was deletion in 20 individuals, on chr6 at 16.34–16.39 Mb (Supplementary Table S4, Figs. 2C and 2D). We used CNVs with a minimum length of 1 kb in the analysis, and the shortest CNVRs had a length of 1.8 kb. The number of CNVRs on the chromosomes was not significantly different among the breeds. In general, the number of CNVRs detected was proportional to the chromosome size, but chromosomes such as 6 and 8 showed more CNVRs than other chromosomes (Fig. 2E). The highest number of deletions was found in chromosome 6, and the highest number of duplications was found in chromosome 9. Deletion events were significantly more

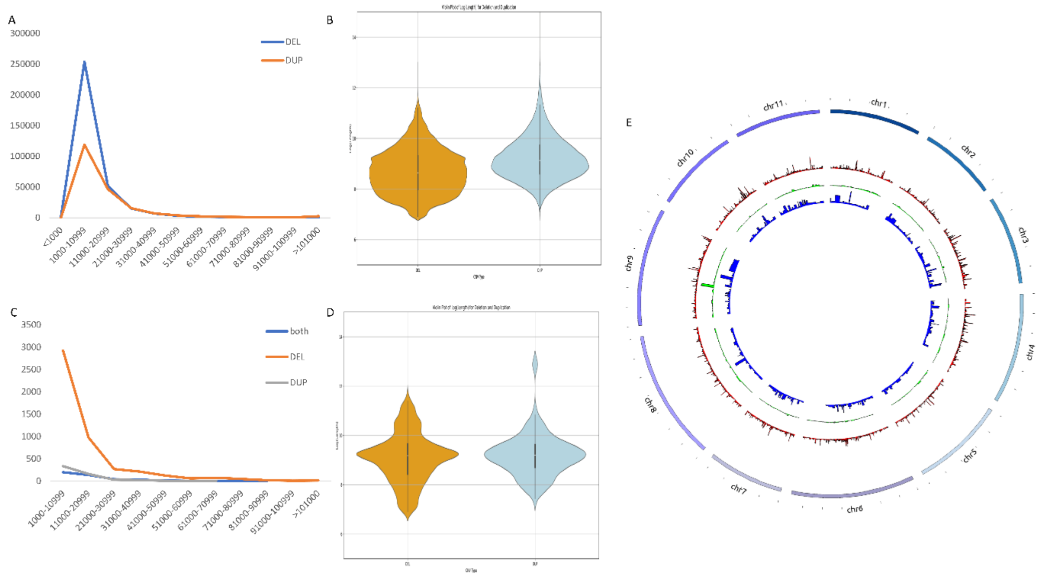

Fig. 2. Properties of the identified CNVs and CNVRs (A)The length distribution of the identified CNV. (B)The length distribution of the identified CNVR. (C) Circos plot showing the chromosome wide frequency distribution of the deletion and duplication events

common than duplication events among the CNVs revealed in this investigation.

Annotation of CNVRs in bitter gourd accessions

As there are no chromosome-level annotations of bitter gourd available to date, the functional analysis of all the identified CNVRs was carried out by homology-based searches using BLASTx against the NCBI non-redundant (*Nr*) database, with an *E*-value threshold set at 10–5 and coverage ≥ 50%. In total, 2788 CNV regions were taken for BLAST, followed by mapping and annotation. Out of these, 1372 regions could BLAST and be mapped; 504 regions could only BLAST but not be mapped, and 1038 regions showed no hits. The top blast-hit species was *Momordica charantia,* and we further discarded the hits with all other species and proceeded with only M. *charantia* for functional analysis. The CNVR region annotation reveals a predominant presence in promoter regions (89.2%), suggesting significant regulatory potential, while smaller proportions are annotated within exons (4.1%), introns (1.1%), intergenic(5.3%), and downstream regions (0.2%) (Fig. 3C). A total of 992 genes were overlapped with the identified CNVRs (Supplementary Table S5). When CNVR and gene overlap more than 1 bp, the relevant gene is annotated. Functional enrichment analysis was performed on GO terms and KEGG pathways through DAVID with 992 protein-coding

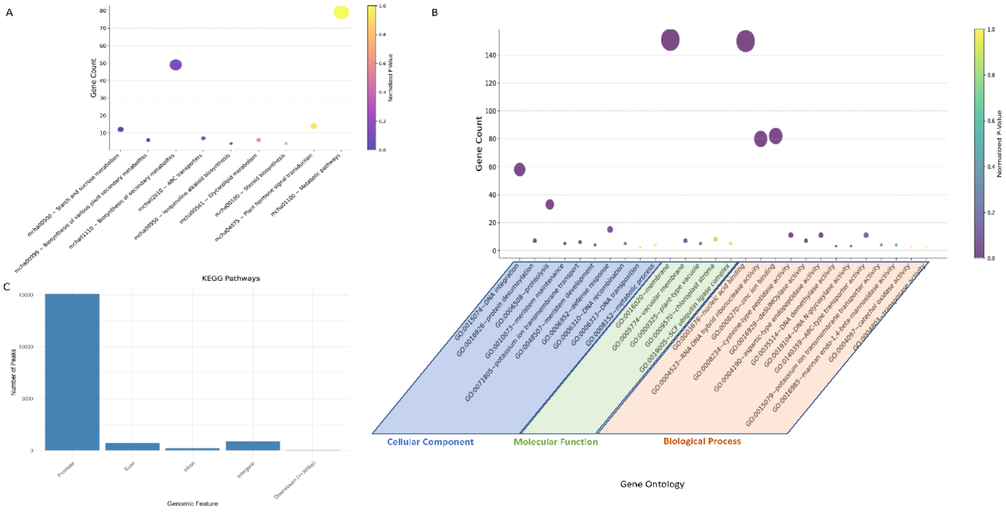

Fig. 3. Functional analysis of the CNVR harbouring genes. (A) The KEGG pathways enriched (p value< 0.05) in the CNVR-harboured genes. (B) The GO terms enriched (p value< 0.05) in the CNVR-harboured genes. (C) The distribution of the annotated peaks of the CNVRs

genes within 1 kb of CNVR. Eight terms in the biological process, three cellular components, ten molecular functions, and five KEGG pathways were significantly enriched (*p*-value < 0.05) (Table 1). They are mainly involved in DNA repair and recombination, stress tolerance and defense responses against pathogens, metabolic regulation, growth through meristem development, and the synthesis of bioactive compounds like terpenes and antioxidants for therapeutic properties.

Several biological processes, such as DNA integration, defense responses, and proteolysis, are central to the stress resilience and adaptive mechanisms in bitter gourd. For instance, GO terms associated with DNA integration (GO:0015074) are crucial for maintaining genomic stability. In contrast, the defense response term (GO:0006952) highlights the plant's ability to defend against pathogens, making it valuable in biotic stress resistance. Furthermore, the molecular functions related to nucleic acid binding (GO:0003676) and RNA-DNA

Table 1. Gene Ontology (GO) and Kegg pathway terms enriched in the genes overlapped with copy number variation regions

Term	ID	Description	Count	P value	Fold Enrichment	Bonferroni	Benjamini
Biological Process	GO:0015074	DNA integration	58	0	16.33	0	0
	GO:0016926	protein desumoylation	7	0	18.17	0	0
	GO:0006508	proteolysis	33	0	2.56	0.001	0
	GO:0010073	meristem maintenance	5	0.001	10.62	0.247	0.071
	GO:0071805	potassium ion transmembrane transport	6	0.002	6.37	0.487	0.133
	GO:0048507	meristem development	4	0.004	11.68	0.707	0.204
	GO:0006952	defense response	15	0.005	2.32	0.824	0.247
	GO:0006310	DNA recombination	5	0.020	4.67	0.999	0.846
Cellular Component	GO:0016020	membrane	151	0	1.32	0.006	0.006
	GO:0005774	vacuolar membrane	7	0.004	4.52	0.348	0.213
	GO:0000325	plant-type vacuole	5	0.011	5.68	0.666	0.364
Molecular Function	GO:0003676	nucleic acid binding	150	0	8.4	0	0
	GO:0004523	RNA-DNA hybrid ribonuclease activity	80	0	15.67	0	0
	GO:0008270	zinc ion binding	82	0	2.71	0	0
	GO:0008234	cysteine-type peptidase activity	11	0	19.75	0	0
	GO:0016929	deSUMOylase activity	7	0	15.23	0	0
	GO:0004190	aspartic-type endopeptidase activity	11	0.001	3.71	0.179	0.033
	GO:0035514	DNA demethylase activity	3	0.008	19.59	0.907	0.296
	GO:0019104	DNA N-glycosylase activity	3	0.008	19.59	0.907	0.296
	GO:0140359	ABC-type transporter activity	11	0.010	2.56	0.960	0.355
	GO:0015079	potassium ion transmembrane transporter activity	4	0.044	4.89	1.000	1.0
Kegg Pathways	mcha00500	Starch and sucrose metabolism	12	0.004	2.75	0.303	0.238
	mcha00999	Biosynthesis of various plant secondary metabolites	6	0.005	5.25	0.379	0.238
	mcha01110	Biosynthesis of secondary metabolites	49	0.012	1.37	0.687	0.310
	mcha02010	ABC transporters	7	0.013	3.55	0.713	0.310
	mcha00950	Isoquinoline alkaloid biosynthesis	4	0.016	7.22	0.792	0.312
	mcha00561	Glycerolipid metabolism	6	0.048	2.99	0.991	0.773

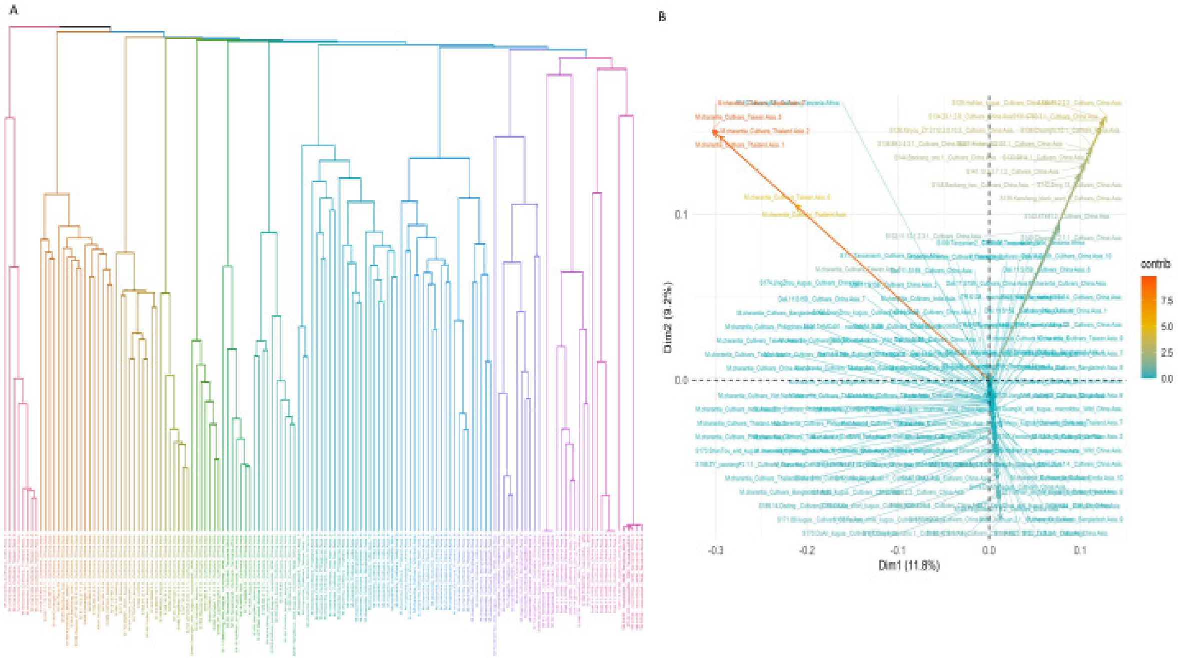

Fig. 4. (A) Hierarchical clustering tree. For every genotype, the absence or presence of CNVs in autosomal CNVRs was converted to vector made of '0's and '1's. The hierarchical clustering was performed on these vectors representing each individual. The bootstrap value was written under the edges of every clustering. The approximately unbiased (AU) and the bootstrap probability (BP) p-value were written in red and green letters on the edges after being multiplied by 100. The branch of hierarchical clustering tree was colored to indicate the group of clades following their region and population. (B)PCA results generated from the matrix of present and absent of CNVR in a particular genotype; the percentage of variance explained by each PC is listed in parenthesis

hybrid ribonuclease activity (GO:0004523) support the plant's response to various environmental stresses and its regulation of cellular functions. Additionally, the presence of terpene synthase activity (GO:0010333) correlates with the synthesis of terpenoid compounds, which are known for their antioxidant and anticancer properties (Fig. 3B). The KEGG pathways include "Starch and sucrose metabolism" (mcha00500), which regulates energy storage and growth, and "Biosynthesis of secondary metabolites" (mcha00999, mcha01110), involved in producing bioactive compounds like cucurbitacins for defense. The "ABC transporters" pathway (mcha02010) plays a role in nutrient and stress resistance, while "Isoquinoline alkaloid biosynthesis" (mcha00950) points to the plant's potential medicinal properties (Fig. 3A). These pathways highlight the metabolic versatility and adaptive functions of bitter gourd.

Population Structure of the bitter gourd accessions revealed by CNV

Clustering analysis was performed on CNVRs identified in 146 genotypes of bitter gourd through the result of each genotype. Hierarchical clustering was created using the sparse matrix which represents the presence or absence of any CNVR in an individual, and the *p*-value was calculated by multiscale bootstrap resampling. The results are shown together with the AU *p*-value and BP value, and it was confirmed that they were significantly clustered within each genotype (Supplementary Table S6). The clustering results of bitter gourd accessions demonstrate significant genetic differentiation shaped by domestication, geographical dispersion, and localized selective breeding practices. Wild accessions from Tanzania clustered distinctly from cultivated Chinese varieties, indicating divergence between wild populations and domesticated lines (Fig. 4A). Furthermore, the sub-grouping of cultivars within China and across Southeast Asia (Taiwan, Thailand, Philippines, Vietnam, India, and Bangladesh) suggests regional adaptation and the impact of intensive breeding programs on genetic structure.

The Principal Component Analysis (PCA) clustering result reveals two primary groups among the samples, distinguished by their geographic origin and cultivar type. Cluster 1 includes samples from diverse regions across Africa, Asia, and the Americas, with African samples (e.g., from Tanzania) clustering closely together, likely due to similar genetic or phenotypic traits. These wild and cultivated varieties display similar values for PCA1 and PCA2, suggesting shared characteristics or selective pressures despite regional variations (Fig. 4B, Supplementary Table S7). Conversely, Cluster 0 predominantly comprises cultivars from China, displaying higher PCA2 values, indicating substantial divergence along this principal component. This separation could signify unique genetic adaptations or breeding selections specific to Chinese cultivars, reflecting distinct lineage or environmental adaptation.

Discussion

Copy Number Variations (CNVs) are a prominent class of structural variations that have been extensively studied for their significant impact on genome diversity and functional traits in plants. In the present investigation, CNVs in bitter gourd (*Momordica charantia*) revealed a distinct prevalence of deletion events over duplication events. This observation aligns with similar findings in studies of other plant species, where deletion events are often detected with greater sensitivity. The higher frequency of deletions may reflect underlying genome dynamics and evolutionary pressures that selectively favor the loss of certain genomic regions (Zhang et al. 2020, Xu et al. 2023). CNVs in bitter gourd reflect patterns observed in other crops, highlighting their role in adaptation and domestication. In rice, CNVs are associated with traits like stress tolerance and pathogen resistance (Yu et al. 2013), while in maize, they influence agronomic traits such as flowering time and kernel composition(Chia et al. 2012). These findings underscore the functional diversity of CNVs across species, shaped by evolutionary and domestication pressures (Zmienko et al. 2020).

The functional annotations of CNVs in bitter gourd highlight their critical roles in various biological processes. Genes affected by these variations are predominantly involved in DNA repair and recombination, stress tolerance, pathogen defense, metabolic regulation, meristem development, and the biosynthesis of bioactive compounds. These findings are consistent with previous studies demonstrating that structural variations often target genes associated with adaptive and essential biological functions(Gayathry and John 2022, Aragón et al. 2021). For instance, the biosynthesis of terpenes and antioxidants, which confer therapeutic properties, underscores the medicinal potential of bitter gourd. Pathway enrichment analysis further supports the multifunctional impact of CNVs on bitter gourd biology. Key enriched pathways in the CNVRs are “Starch and sucrose metabolism” (Rathi et al. 2002), “Biosynthesis of secondary metabolites” (Reshi et al. 2023), “ABC transporters” (Tao et al. 2024), “Isoquinoline alkaloid biosynthesis” (Ning et al. 2024) which has been previously reported in the copy number variation regions of other crops. These enriched pathways collectively underscore the metabolic versatility and adaptive functions of bitter gourd, reflecting its ecological and agricultural significance.

Genetic clustering based on CNV regions (CNVRs) revealed the presence of mixed regional clusters, indicating potential historical gene flow, introgression, and hybridization events. These genetic exchanges have likely contributed to the observed trait variability within bitter gourd populations(Chomicki et al. 2020). The genetic differentiation observed among accessions also underscores the importance of maintaining diverse genetic pools for breeding and conservation. Such diversity is critical for developing resilient cultivars that can withstand environmental stresses and changing climatic conditions. The clustering pattern in PCA highlights significant regional and genetic diversity within the samples, likely influenced by both natural selection in wild populations and human-driven selection in cultivated varieties. This genetic differentiation is consistent with observations in other domesticated crops where geographic and anthropogenic factors played pivotal roles in shaping genetic structure(Meyer and Purugganan 2013; Sauvage et al. 2017). In bitter gourd, the role of local adaptation, particularly in response to environmental pressures, appears to be a significant driver of genetic differentiation. This is consistent with studies in other crops that link genetic structuring to both climatic and anthropogenic influences (Meyer and Purugganan 2013; Sauvage et al. 2017). This spatial genetic structuring also underscores the role of local adaptation in shaping the genetic makeup of bitter gourd accessions, particularly in response to climatic and environmental pressures (Allaby et al. 2008).

The findings from this study provide a foundation for understanding the evolutionary dynamics and adaptive significance of CNVs in bitter gourd. The clustering analysis of CNVRs based on CNV frequency variations across individuals offers valuable insights into the population structure and evolutionary background of bitter gourd accessions. Advances in genome analysis are uncovering trait-associated structural variants, which hold immense potential for improving crop resilience and sustainability (Gabur et al. 2019). Integrating CNV data with Genome-Wide Association Studies (GWAS) and Quantitative Trait Loci (QTL) analysis could further identify key loci associated with significant phenotypic traits in crop plants (Cheng et al. 2020). These findings pave the way for future research aimed at harnessing genetic diversity for crop improvement, thereby contributing to food security and sustainable agricultural practices.

Supplementary material

Supplementary Tables S1 to S7 are provided, which can be accessed at www.isgpb.org

Author’s contribution

Conceptualization of research (PD, SJ, MAI); Designing of the experiments (PD); Contribution of experimental materials (PD, SJ, MAI, UA, DK); Execution of field/lab experiments and data collection (PD); Analysis of data and interpretation (PD); Preparation of the manuscript (PD, SJ, MAI, UA, DK).

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Supplementary Table 1. Number of deletion and duplication events identified in 146 accessions of bittergourd

Accessions	DEL	DUP	Total CNVs
ERR2505445	3157	5380	8537
ERR2505446	3131	1499	4630
ERR2505447	5184	9458	14642
ERR2505448	671	3966	4637
ERR2505449	522	2494	3016
ERR2505450		18	18
ERR2505451	590	80	670
ERR2505452	9232	737	9969
ERR2505453	3792	1977	5769
ERR2505454	4273	135	4408
ERR2505455	12260	11885	24145
ERR2505456	501	749	1250
ERR2505457	2589	3061	5650
ERR2505458	2675	3047	5722
ERR2505459	1254	1235	2489
ERR2505460	759	494	1253
ERR2505461	3739	3221	6960
ERR2505462	2800	1845	4645
ERR2580681	3218	3407	6625
ERR2580682	2605	3537	6142
ERR2580683	3835	6436	10271
ERR2580684	5366	5988	11354
ERR2580685	5592	6913	12505
ERR2580686	4259	3697	7956
ERR2580687	5384	5515	10899
ERR2580688	2849	2369	5218
ERR2580689	5151	3458	8609
ERR2580690	3056	1941	4997
ERR2580691	3781	2024	5805
ERR2580692	1967	416	2383
ERR2580693	4170	3174	7344
ERR2580694	4723	3607	8330
ERR2580695	5502	4129	9631
ERR2580696	3716	2040	5756
ERR2580697	3234	1778	5012
ERR2580698	1738	635	2373
ERR2580699	2966	1133	4099
ERR2580700	1455	303	1758
ERR2580701	1475	178	1653
ERR2580702	1253	198	1451
ERR2580703	1270	227	1497
ERR2580704	1578	380	1958
ERR2580767	1668	353	2021
ERR2580768	1669	338	2007
ERR2580769	3296	1600	4896
ERR2581984	2082	746	2828
ERR2581985	1860	493	2353
ERR2581986	1363	231	1594
ERR2581987	1374	298	1672
ERR2581988	1642	329	1971
ERR2581989	1568	196	1764
ERR2581990	1609	362	1971
ERR2581991	2997	1617	4614
ERR2581992	1365	215	1580
ERR2581993	1435	360	1795
ERR2581994	2272	1125	3397
ERR2581995	1241	284	1525
ERR2581996	1203	248	1451
ERR2581997	2665	1562	4227
ERR2581998	5813	5855	11668
ERR2581999	1968	384	2352
ERR2582000	3292	1618	4910
ERR2582001	3176	1447	4623
ERR2582002	4719	3116	7835
ERR2582003	3257	1793	5050
ERR2582005	3366	2080	5446
ERR2582006	2300	814	3114
ERR2582007	4980	3835	8815
ERR2582008	2372	867	3239
ERR2582009	3211	1842	5053
ERR2582010	3134	4738	7872
ERR2582011	4826	3458	8284
ERR2582012	2932	1077	4009
ERR2582013	1702	683	2385
ERR2582014	2020	627	2647
ERR2582015	2659	1004	3663
ERR2582016	1469	350	1819
ERR2582017	3378	2155	5533
ERR2582018	2762	1342	4104
ERR2582019	3430	2061	5491
ERR2582020	2126	567	2693
ERR2582021	1988	758	2746
ERR2582022	2749	1800	4549
ERR2582023	2265	729	2994
ERR2631406	4254	3304	7558
SRR10309996	1266	394	1660
SRR10309997	1207	384	1591
SRR10309998	976	253	1229
SRR10309999	2	14	16

SRR10310000	711	509	1220
SRR10310001	1688	401	2089
SRR10310002	3717	706	4423
SRR10310003	3609	731	4340
SRR10310004	3620	461	4081
SRR10310005	3430	709	4139
SRR10310006	3503	717	4220
SRR10310007	1346	1560	2906
SRR10310008	2911	459	3370
SRR10310009	3218	722	3940
SRR10310010	4069	617	4686
SRR10310011	824	252	1076
SRR10310012	4153	874	5027
SRR10310013	2789	589	3378
SRR10310014	3507	610	4117
SRR10310015	3459	1268	4727
SRR10310016	3544	595	4139
SRR10310017	711	224	935
SRR10310018	477	213	690
SRR10310019	554	397	951
SRR10310020	494	143	637
SRR10310021	548	223	771
SRR10310022	806	198	1004
SRR10310023	467	175	642
SRR10310024	514	203	717
SRR10310025	555	188	743
SRR10310026	610	216	826
SRR10310027	478	142	620
SRR10310028	678	149	827
SRR10310029	717	233	950
SRR10310030	914	356	1270
SRR10310031	1188	286	1474
SRR10310032	1092	353	1445
SRR10310033	587	228	815
SRR10310034	1117	371	1488
SRR10310035	840	348	1188
SRR10310036	649	325	974
SRR10310037	1070	267	1337
SRR10310038	568	143	711
SRR10310039	1082	410	1492
SRR10310040	547	241	788
SRR10310041	485	130	615
SRR10310042	594	200	794
SRR10310043	744	220	964
SRR10310044	769	364	1133
SRR10310045	2444	942	3386
SRR10310046	1249	339	1588
SRR10310047	1068	1361	2429
SRR10310048	2841	1159	4000
SRR10310049	761	225	986
SRR10310050	841	221	1062
SRR10310051	1130	288	1418
SRR10310052	831	417	1248
SRR10310053	2236	1787	4023
SRR10310054	969	260	1229
SRR10310055	584	153	737
SRR10310056	943	365	1308
Grand Total	338030	200713	538743

Supplementary Table 2. Genes overlapped with the copy number variation regions.

David Gene Name	Gene ID	CNVRs	CNVR Count
uncharacterized protein LOC111024419	LOC111024419	CNVR21, CNVR24, CNVR35, CNVR48, CNVR61, CNVR69, CNVR76, CNVR105, CNVR231, CNVR756, CNVR799, CNVR803, CNVR996, CNVR1040, CNVR1090, CNVR1111, CNVR1127, CNVR1142, CNVR1146, CNVR1187, CNVR1234, CNVR1240, CNVR1251, CNVR1263, CNVR1265, CNVR1269, CNVR1271, CNVR1290, CNVR1301, CNVR1310, CNVR1337, CNVR1346, CNVR1371, CNVR1381, CNVR1387, CNVR1388, CNVR1433, CNVR1437, CNVR1452, CNVR1464, CNVR1465, CNVR1487, CNVR1493, CNVR1505, CNVR1511, CNVR1517, CNVR1555, CNVR1558, CNVR1609, CNVR1623, CNVR1629, CNVR1636, CNVR1646, CNVR1691, CNVR1745, CNVR1836, CNVR1846, CNVR1869, CNVR1879, CNVR1944, CNVR1952, CNVR1960, CNVR2006, CNVR2038, CNVR2052, CNVR2107, CNVR2146, CNVR2186, CNVR2191, CNVR2206, CNVR2309, CNVR2345, CNVR2892, CNVR3134, CNVR3198, CNVR3234, CNVR3403, CNVR3419, CNVR3499, CNVR3512, CNVR3556, CNVR3563, CNVR3567, CNVR3575, CNVR3584, CNVR3591, CNVR3597, CNVR3620, CNVR3654, CNVR3703, CNVR3707, CNVR3739, CNVR3740, CNVR3780, CNVR3827, CNVR3834, CNVR3930, CNVR3998, CNVR4036, CNVR4038, CNVR4042, CNVR4044, CNVR4052, CNVR4055, CNVR4072, CNVR4116, CNVR4132, CNVR4148, CNVR4205, CNVR4227, CNVR4259, CNVR4299, CNVR4357, CNVR4369, CNVR4379, CNVR4388, CNVR4427, CNVR4432, CNVR4504, CNVR4509, CNVR4554, CNVR4560, CNVR4568, CNVR4580, CNVR4615, CNVR4642, CNVR4652, CNVR4662, CNVR4704, CNVR4935, CNVR4985, CNVR5028, CNVR5035, CNVR5172, CNVR5173, CNVR5204, CNVR5278, CNVR5326, CNVR5336, CNVR5370, CNVR5484, CNVR5568, CNVR5646, CNVR5656, CNVR5730	145
uncharacterized protein LOC111008813	LOC111008813	CNVR17, CNVR20, CNVR36, CNVR40, CNVR59, CNVR60, CNVR70, CNVR133, CNVR141, CNVR178, CNVR263, CNVR284, CNVR1036, CNVR1060, CNVR1077, CNVR1092, CNVR1095, CNVR1096, CNVR1103, CNVR1105, CNVR1143, CNVR1178, CNVR1191, CNVR1217, CNVR1249, CNVR1252, CNVR1267, CNVR1293, CNVR1317, CNVR1389, CNVR1401, CNVR1440, CNVR1485, CNVR1497, CNVR1507, CNVR1518, CNVR1521, CNVR1708, CNVR1712, CNVR1718, CNVR1757, CNVR1774, CNVR1797, CNVR1819, CNVR1825, CNVR1840, CNVR1907, CNVR1924, CNVR1967, CNVR1979, CNVR2015, CNVR2135, CNVR2184, CNVR2220, CNVR2488, CNVR3095, CNVR3145, CNVR3431, CNVR3537, CNVR3546, CNVR3573, CNVR3581, CNVR3582, CNVR3585, CNVR3622, CNVR3666, CNVR3672, CNVR3674, CNVR3742, CNVR3759, CNVR3819, CNVR3832, CNVR3874, CNVR3926, CNVR3974, CNVR4031, CNVR4034, CNVR4074, CNVR4081, CNVR4092, CNVR4108, CNVR4121, CNVR4183, CNVR4224, CNVR4230, CNVR4248, CNVR4264, CNVR4286, CNVR4292, CNVR4330, CNVR4342, CNVR4382, CNVR4393, CNVR4395, CNVR4400, CNVR4414, CNVR4444, CNVR4463, CNVR4476, CNVR4493, CNVR4543, CNVR4556, CNVR4593, CNVR4598, CNVR4681, CNVR4713, CNVR4717, CNVR4802, CNVR4826, CNVR4852, CNVR5072, CNVR5091, CNVR5113, CNVR5163, CNVR5188, CNVR5195, CNVR5228, CNVR5241, CNVR5329, CNVR5363, CNVR5474, CNVR5726, CNVR5745, CNVR5757, CNVR5761	125

uncharacterized protein LOC111023451	LOC111023451	CNVR14, CNVR37, CNVR47, CNVR62, CNVR110, CNVR139, CNVR172, CNVR198, CNVR238, CNVR269, CNVR293, CNVR1067, CNVR1072, CNVR1073, CNVR1110, CNVR1129, CNVR1195, CNVR1205, CNVR1311, CNVR1347, CNVR1348, CNVR1374, CNVR1375, CNVR1379, CNVR1398, CNVR1409, CNVR1421, CNVR1443, CNVR1586, CNVR1600, CNVR1628, CNVR1660, CNVR1681, CNVR1739, CNVR1763, CNVR1780, CNVR1801, CNVR1812, CNVR1889, CNVR1896, CNVR1915, CNVR1974, CNVR1984, CNVR2117, CNVR2155, CNVR2156, CNVR2194, CNVR2215, CNVR2618, CNVR2759, CNVR3199, CNVR3444, CNVR3544, CNVR3553, CNVR3590, CNVR3599, CNVR3653, CNVR3659, CNVR3664, CNVR3665, CNVR3685, CNVR3691, CNVR3693, CNVR3719, CNVR3730, CNVR3734, CNVR3747, CNVR3751, CNVR3787, CNVR3814, CNVR3828, CNVR3912, CNVR3948, CNVR3949, CNVR3963, CNVR3964, CNVR4021, CNVR4050, CNVR4158, CNVR4176, CNVR4191, CNVR4192, CNVR4200, CNVR4203, CNVR4214, CNVR4216, CNVR4247, CNVR4273, CNVR4329, CNVR4346, CNVR4370, CNVR4446, CNVR4452, CNVR4453, CNVR4489, CNVR4492, CNVR4496, CNVR4502, CNVR4529, CNVR4545, CNVR4617, CNVR4632, CNVR4644, CNVR4656, CNVR4675, CNVR4676, CNVR4694, CNVR4699, CNVR4705, CNVR4766, CNVR4831, CNVR4871, CNVR5030, CNVR5128, CNVR5154, CNVR5443, CNVR5478, CNVR5512, CNVR5657	119
uncharacterized protein LOC111019515	LOC111019515	CNVR136, CNVR143, CNVR165, CNVR166, CNVR243, CNVR318, CNVR661, CNVR790, CNVR791, CNVR825, CNVR977, CNVR998, CNVR1013, CNVR1323, CNVR1327, CNVR1328, CNVR1331, CNVR1416, CNVR1454, CNVR1508, CNVR1509, CNVR1613, CNVR1689, CNVR1741, CNVR1772, CNVR1793, CNVR1870, CNVR1969, CNVR2106, CNVR2123, CNVR2189, CNVR2337, CNVR2432, CNVR2754, CNVR2761, CNVR3093, CNVR3188, CNVR3189, CNVR3232, CNVR3239, CNVR3241, CNVR3296, CNVR3326, CNVR3486, CNVR3601, CNVR3645, CNVR3697, CNVR3980, CNVR4015, CNVR4166, CNVR4229, CNVR4233, CNVR4250, CNVR4327, CNVR4331, CNVR4356, CNVR4368, CNVR4374, CNVR4428, CNVR4435, CNVR4442, CNVR4449, CNVR4620, CNVR4624, CNVR4628, CNVR4688, CNVR4743, CNVR4744, CNVR4745, CNVR4760, CNVR4844, CNVR4906, CNVR4960, CNVR4986, CNVR4988, CNVR5011, CNVR5015, CNVR5026, CNVR5067, CNVR5124, CNVR5131, CNVR5193, CNVR5206, CNVR5280, CNVR5282, CNVR5297, CNVR5342, CNVR5343, CNVR5434, CNVR5462, CNVR5492, CNVR5505, CNVR5529, CNVR5570, CNVR5586, CNVR5602, CNVR5631, CNVR5632, CNVR5659, CNVR5676, CNVR5729	101
uncharacterized protein LOC111025502	LOC111025502	CNVR63, CNVR176, CNVR1066, CNVR1074, CNVR1445, CNVR1501, CNVR1536, CNVR1665, CNVR2972, CNVR3136, CNVR3538, CNVR3555, CNVR3565, CNVR3708, CNVR3712, CNVR3738, CNVR3743, CNVR3746, CNVR3758, CNVR3774, CNVR3776, CNVR3863, CNVR3873, CNVR3877, CNVR3893, CNVR3918, CNVR3920, CNVR3932, CNVR3969, CNVR3973, CNVR3977, CNVR3992, CNVR4051, CNVR4080, CNVR4198, CNVR4208, CNVR4211, CNVR4223, CNVR4246, CNVR4283, CNVR4308, CNVR4311, CNVR4339, CNVR4351, CNVR4439, CNVR4445, CNVR4470, CNVR4477, CNVR4520, CNVR4521, CNVR4530, CNVR4531, CNVR4532, CNVR4567, CNVR4608, CNVR4612, CNVR4651, CNVR4695, CNVR4736, CNVR5023, CNVR5175, CNVR5220, CNVR5227, CNVR5398, CNVR5518, CNVR5551	66
uncharacterized protein LOC111024897	LOC111024897	CNVR90, CNVR120, CNVR649, CNVR965, CNVR993, CNVR1023, CNVR1093, CNVR1182, CNVR1344, CNVR1356, CNVR1403, CNVR1458, CNVR1749, CNVR1898, CNVR1987, CNVR2028, CNVR2036, CNVR2243, CNVR2504, CNVR2649, CNVR2849, CNVR2905, CNVR2997, CNVR3196, CNVR3365, CNVR3477, CNVR3896, CNVR3905, CNVR3923, CNVR3981, CNVR3996, CNVR4013, CNVR4085, CNVR4086, CNVR4249, CNVR4256, CNVR4280, CNVR4319, CNVR4340, CNVR4440, CNVR4505, CNVR4563, CNVR4619, CNVR4785, CNVR4800, CNVR4862, CNVR4883, CNVR4894, CNVR4950, CNVR5110, CNVR5277, CNVR5323, CNVR5419, CNVR5481, CNVR5520, CNVR5527, CNVR5544, CNVR5614	58

uncharacterized protein LOC111025045	LOC111025045	CNVR3, CNVR150, CNVR270, CNVR1053, CNVR1229, CNVR1313, CNVR1411, CNVR1693, CNVR1785, CNVR1811, CNVR1830, CNVR1843, CNVR1868, CNVR1930, CNVR1938, CNVR1943, CNVR2018, CNVR2029, CNVR2032, CNVR2037, CNVR2138, CNVR2285, CNVR3331, CNVR3414, CNVR3583, CNVR3684, CNVR3717, CNVR3879, CNVR4310, CNVR4516, CNVR4552, CNVR4614, CNVR4841, CNVR4854, CNVR4867, CNVR4913, CNVR5049, CNVR5098, CNVR5271, CNVR5509, CNVR5626, CNVR5717, CNVR5747	43
uncharacterized protein LOC111024115	LOC111024115	CNVR374, CNVR801, CNVR856, CNVR961, CNVR984, CNVR1274, CNVR1463, CNVR1510, CNVR1715, CNVR1746, CNVR2053, CNVR2310, CNVR2586, CNVR2783, CNVR3137, CNVR3194, CNVR3281, CNVR3626, CNVR3638, CNVR3643, CNVR3794, CNVR3909, CNVR4756, CNVR4758, CNVR4992, CNVR5033, CNVR5079, CNVR5122, CNVR5321, CNVR5322, CNVR5324, CNVR5438, CNVR5477, CNVR5532, CNVR5622, CNVR5713	36
uncharacterized protein LOC111019899	LOC111019899	CNVR195, CNVR566, CNVR674, CNVR1018, CNVR1094, CNVR1097, CNVR1134, CNVR1449, CNVR1634, CNVR1910, CNVR3031, CNVR3472, CNVR3589, CNVR3689, CNVR3792, CNVR3829, CNVR3878, CNVR3931, CNVR3987, CNVR4145, CNVR4153, CNVR4172, CNVR4355, CNVR4384, CNVR4497, CNVR4566, CNVR4629, CNVR4638, CNVR4639, CNVR4683, CNVR4730, CNVR5407, CNVR5485, CNVR5645, CNVR5654	35
uncharacterized protein LOC111018823	LOC111018823	CNVR19, CNVR71, CNVR246, CNVR637, CNVR1232, CNVR1404, CNVR1482, CNVR1569, CNVR1615, CNVR1740, CNVR1791, CNVR2024, CNVR2083, CNVR2171, CNVR2192, CNVR2908, CNVR3105, CNVR3238, CNVR3449, CNVR3542, CNVR3568, CNVR3621, CNVR3686, CNVR4167, CNVR4189, CNVR4240, CNVR4275, CNVR4524, CNVR4627, CNVR4692, CNVR4978, CNVR5215, CNVR5229	33
uncharacterized protein K02A2.6-like	LOC111018311	CNVR97, CNVR129, CNVR1025, CNVR1099, CNVR1166, CNVR1223, CNVR1438, CNVR1525, CNVR2179, CNVR2544, CNVR2651, CNVR3059, CNVR3099, CNVR3408, CNVR3795, CNVR4448, CNVR4601, CNVR4691, CNVR4770, CNVR4858, CNVR5076, CNVR5198, CNVR5214, CNVR5281, CNVR5335, CNVR5396, CNVR5650	27
uncharacterized protein K02A2.6-like	LOC111023782	CNVR97, CNVR129, CNVR1025, CNVR1099, CNVR1166, CNVR1223, CNVR1438, CNVR1525, CNVR2179, CNVR2544, CNVR2651, CNVR3059, CNVR3099, CNVR3408, CNVR3795, CNVR4448, CNVR4601, CNVR4691, CNVR4770, CNVR4858, CNVR5076, CNVR5198, CNVR5214, CNVR5281, CNVR5335, CNVR5396, CNVR5650	27
uncharacterized protein K02A2.6-like	LOC111010888	CNVR97, CNVR129, CNVR1025, CNVR1099, CNVR1166, CNVR1223, CNVR1438, CNVR1525, CNVR2179, CNVR2544, CNVR2651, CNVR3059, CNVR3099, CNVR3408, CNVR3795, CNVR4448, CNVR4601, CNVR4691, CNVR4770, CNVR4858, CNVR5076, CNVR5198, CNVR5214, CNVR5281, CNVR5335, CNVR5396, CNVR5650	27
uncharacterized protein K02A2.6-like	LOC111020114	CNVR97, CNVR129, CNVR1025, CNVR1099, CNVR1166, CNVR1223, CNVR1438, CNVR1525, CNVR2179, CNVR2544, CNVR2651, CNVR3059, CNVR3099, CNVR3408, CNVR3795, CNVR4448, CNVR4601, CNVR4691, CNVR4770, CNVR4858, CNVR5076, CNVR5198, CNVR5214, CNVR5281, CNVR5335, CNVR5396, CNVR5650	27
uncharacterized protein K02A2.6-like	LOC111023037	CNVR97, CNVR129, CNVR1025, CNVR1099, CNVR1166, CNVR1223, CNVR1438, CNVR1525, CNVR2179, CNVR2544, CNVR2651, CNVR3059, CNVR3099, CNVR3408, CNVR3795, CNVR4448, CNVR4601, CNVR4691, CNVR4770, CNVR4858, CNVR5076, CNVR5198, CNVR5214, CNVR5281, CNVR5335, CNVR5396, CNVR5650	27

uncharacterized protein LOC111023448	LOC111023448	CNVR1063, CNVR1211, CNVR1451, CNVR1480, CNVR1619, CNVR1880, CNVR2115, CNVR2177, CNVR2273, CNVR2564, CNVR3415, CNVR3521, CNVR3728, CNVR3818, CNVR3831, CNVR3902, CNVR4185, CNVR4488, CNVR4490, CNVR4536, CNVR4851, CNVR5059, CNVR5318, CNVR5655, CNVR5752	25
uncharacterized protein LOC111020753	LOC111020753	CNVR372, CNVR857, CNVR1456, CNVR1461, CNVR1596, CNVR1883, CNVR2079, CNVR2970, CNVR3702, CNVR3725, CNVR3771, CNVR4177, CNVR4557, CNVR4728, CNVR4755, CNVR4840, CNVR5020, CNVR5041, CNVR5052, CNVR5437, CNVR5479, CNVR5663, CNVR5734	23
uncharacterized protein LOC111018360	LOC111018360	CNVR216, CNVR976, CNVR1125, CNVR1391, CNVR1680, CNVR2066, CNVR3399, CNVR3682, CNVR3815, CNVR3959, CNVR4098, CNVR4150, CNVR4156, CNVR4582, CNVR4838, CNVR4879, CNVR5085, CNVR5411, CNVR5545, CNVR5569, CNVR5677, CNVR5751	22
uncharacterized protein LOC111024751	LOC111024751	CNVR676, CNVR1136, CNVR1333, CNVR1392, CNVR1514, CNVR1549, CNVR1598, CNVR1713, CNVR1768, CNVR1778, CNVR1848, CNVR2004, CNVR2150, CNVR2199, CNVR3033, CNVR3982, CNVR4154, CNVR4900, CNVR5029, CNVR5149, CNVR5428, CNVR5439	22
uncharacterized protein LOC111023249	LOC111023249	CNVR164, CNVR289, CNVR789, CNVR960, CNVR1085, CNVR1326, CNVR1610, CNVR1653, CNVR2336, CNVR2992, CNVR3187, CNVR4892, CNVR4958, CNVR4987, CNVR5162, CNVR5435, CNVR5476, CNVR5620	18
uncharacterized protein LOC111023816	LOC111023816	CNVR1140, CNVR1172, CNVR1312, CNVR1316, CNVR1467, CNVR1753, CNVR1804, CNVR1882, CNVR2104, CNVR2164, CNVR2203, CNVR2968, CNVR3183, CNVR3910, CNVR4731, CNVR5276	16
serine carboxypeptidase-like	LOC111006031	CNVR201, CNVR550, CNVR595, CNVR705, CNVR736, CNVR1701, CNVR2425, CNVR3019, CNVR3116, CNVR3453, CNVR3610, CNVR4045, CNVR4707, CNVR4914, CNVR5237, CNVR5679	16
uncharacterized protein LOC111025738	LOC111025738	CNVR559, CNVR2623, CNVR3796, CNVR3885, CNVR3944, CNVR3961, CNVR4118, CNVR4129, CNVR4144, CNVR4187, CNVR4271, CNVR4478, CNVR4853, CNVR5369, CNVR5445, CNVR5736	16
uncharacterized protein LOC111020479	LOC111020479	CNVR99, CNVR275, CNVR292, CNVR792, CNVR1022, CNVR1059, CNVR1177, CNVR1329, CNVR1764, CNVR1939, CNVR3056, CNVR4660, CNVR4903, CNVR4969, CNVR5168	15
uncharacterized protein LOC111020149	LOC111020149	CNVR920, CNVR1552, CNVR1838, CNVR1863, CNVR2165, CNVR2465, CNVR2637, CNVR2848, CNVR3038, CNVR3363, CNVR4910, CNVR5014, CNVR5093, CNVR5467, CNVR5504	15
uncharacterized protein LOC111025293	LOC111025293	CNVR1137, CNVR1161, CNVR1662, CNVR1751, CNVR1947, CNVR2141, CNVR3046, CNVR4215, CNVR4764, CNVR4905, CNVR5208, CNVR5427, CNVR5449, CNVR5557	14
uncharacterized protein LOC111021029	LOC111021029	CNVR525, CNVR536, CNVR701, CNVR1442, CNVR2277, CNVR3398, CNVR3421, CNVR4309, CNVR4933, CNVR5230, CNVR5590, CNVR5723	12
serine/threonine-protein phosphatase 7 long form homolog	LOC111021487	CNVR528, CNVR994, CNVR1345, CNVR2129, CNVR2381, CNVR2875, CNVR3175, CNVR3197, CNVR3467, CNVR3490, CNVR4819, CNVR5315	12
serine/threonine-protein phosphatase 7 long form homolog	LOC111019957	CNVR528, CNVR994, CNVR1345, CNVR2129, CNVR2381, CNVR2875, CNVR3175, CNVR3197, CNVR3467, CNVR3490, CNVR4819, CNVR5315	12
serine/threonine-protein phosphatase 7 long form homolog	LOC111018266	CNVR528, CNVR994, CNVR1345, CNVR2129, CNVR2381, CNVR2875, CNVR3175, CNVR3197, CNVR3467, CNVR3490, CNVR4819, CNVR5315	12
serine/threonine-protein phosphatase 7 long form homolog	LOC111023038	CNVR528, CNVR994, CNVR1345, CNVR2129, CNVR2381, CNVR2875, CNVR3175, CNVR3197, CNVR3467, CNVR3490, CNVR4819, CNVR5315	12

serine/threonine-protein phosphatase 7 long form homolog	LOC111018366	CNVR528, CNVR994, CNVR1345, CNVR2129, CNVR2381, CNVR2875, CNVR3175, CNVR3197, CNVR3467, CNVR3490, CNVR4819, CNVR5315	12
uncharacterized protein LOC111025033	LOC111025033	CNVR262, CNVR1175, CNVR1899, CNVR1975, CNVR2201, CNVR2543, CNVR3054, CNVR3947, CNVR4123, CNVR5071, CNVR5579	11
uncharacterized protein LOC111025302	LOC111025302	CNVR826, CNVR1384, CNVR1744, CNVR3434, CNVR3493, CNVR3722, CNVR4832, CNVR5087, CNVR5366, CNVR5524	10
UPF0496 protein At2g18630-like	LOC111021486	CNVR1135, CNVR2149, CNVR2232, CNVR2630, CNVR3032, CNVR4965, CNVR5148, CNVR5413, CNVR5675, CNVR5688	10
BURP domain protein USPL1-like	LOC111007566	CNVR15, CNVR583, CNVR713, CNVR1683, CNVR2113, CNVR3081, CNVR3608, CNVR4973, CNVR5421, CNVR5502	10
UPF0496 protein At2g18630-like	LOC111021511	CNVR1135, CNVR2149, CNVR2232, CNVR2630, CNVR3032, CNVR4965, CNVR5148, CNVR5413, CNVR5675, CNVR5688	10
protein FAR-RED ELONGATED HYPOCOTYL 3-like	LOC111024830	CNVR106, CNVR437, CNVR898, CNVR1527, CNVR2439, CNVR2818, CNVR3456, CNVR3726, CNVR5353, CNVR5666	10
uncharacterized protein LOC111023977	LOC111023977	CNVR1047, CNVR1275, CNVR1278, CNVR1554, CNVR2124, CNVR2313, CNVR2406, CNVR3140, CNVR3636, CNVR3862	10
uncharacterized protein LOC111024860	LOC111024860	CNVR682, CNVR1407, CNVR4162, CNVR4171, CNVR4727, CNVR4829, CNVR5008, CNVR5153, CNVR5433, CNVR5755	10
UPF0415 protein C7orf25 homolog	LOC111020434	CNVR252, CNVR474, CNVR1007, CNVR1570, CNVR2470, CNVR2913, CNVR2923, CNVR3631, CNVR4792, CNVR5603	10
uncharacterized protein LOC111020110	LOC111020110	CNVR966, CNVR1091, CNVR1098, CNVR1147, CNVR2100, CNVR3394, CNVR3466, CNVR4630, CNVR4959, CNVR5293	10
uncharacterized mitochondrial protein AtMg00810-like	LOC111019945	CNVR107, CNVR439, CNVR900, CNVR1528, CNVR2174, CNVR2440, CNVR3706, CNVR4621, CNVR4773, CNVR5335	10
uncharacterized protein LOC111013362	LOC111013362	CNVR125, CNVR1589, CNVR2489, CNVR3382, CNVR3637, CNVR4125, CNVR4874, CNVR4955, CNVR5114, CNVR5543	10
uncharacterized protein LOC111019842	LOC111019842	CNVR49, CNVR1270, CNVR1410, CNVR1649, CNVR2007, CNVR4084, CNVR4373, CNVR4658, CNVR4882	9
putative nuclease HARBI1	LOC111009055	CNVR580, CNVR711, CNVR1204, CNVR2268, CNVR3077, CNVR3607, CNVR3956, CNVR4673, CNVR5181	9
uncharacterized protein LOC111004939	LOC111004939	CNVR604, CNVR760, CNVR1276, CNVR1890, CNVR2573, CNVR2895, CNVR2985, CNVR3131, CNVR3139	9
uncharacterized protein LOC111020516	LOC111020516	CNVR573, CNVR704, CNVR1192, CNVR2259, CNVR2653, CNVR3060, CNVR3533, CNVR5058, CNVR5177	9
uncharacterized protein LOC111016200	LOC111016200	CNVR435, CNVR522, CNVR641, CNVR834, CNVR2762, CNVR4469, CNVR4591, CNVR4677, CNVR5112	9
beta-amyrin 11-oxidase-like	LOC111022631	CNVR2094, CNVR3709, CNVR4954, CNVR5017, CNVR5084, CNVR5106, CNVR5108, CNVR5641	8
beta-amyrin 11-oxidase-like	LOC111014773	CNVR2094, CNVR3709, CNVR4954, CNVR5017, CNVR5084, CNVR5106, CNVR5108, CNVR5641	8

probable endo-1,3(4)-beta-glucanase ARB_01444	LOC111025628	CNVR956, CNVR1071, CNVR2494, CNVR3506, CNVR3713, CNVR4803, CNVR5116, CNVR5609	8
L-type lectin-domain containing receptor kinase S.6	LOC111011959	CNVR734, CNVR1243, CNVR1700, CNVR3115, CNVR4043, CNVR4706, CNVR5063, CNVR5236	8
uncharacterized protein LOC111021922	LOC111021922	CNVR94, CNVR510, CNVR959, CNVR3566, CNVR4857, CNVR5117, CNVR5541, CNVR5643	8
protein TRIGALACTOSYLDIACYLGLYCEROL 4, chloroplastic	LOC111025174	CNVR840, CNVR1426, CNVR2578, CNVR2768, CNVR3253, CNVR3623, CNVR4928, CNVR5310	8
uncharacterized protein LOC111025424	LOC111025424	CNVR923, CNVR1617, CNVR3790, CNVR4375, CNVR4788, CNVR5132, CNVR5347, CNVR5376	8
TMV resistance protein N	LOC111022384	CNVR128, CNVR506, CNVR1010, CNVR2495, CNVR2871, CNVR3387, CNVR5404, CNVR5610	8
pentatricopeptide repeat-containing protein At1g06270	LOC111011343	CNVR203, CNVR554, CNVR1122, CNVR2532, CNVR2880, CNVR3022, CNVR4860, CNVR5144	8
uncharacterized protein LOC111004740	LOC111004740	CNVR342, CNVR1427, CNVR2389, CNVR2770, CNVR4293, CNVR4836, CNVR5090, CNVR5311	8
potassium transporter 8-like	LOC111018367	CNVR366, CNVR846, CNVR1444, CNVR2402, CNVR2780, CNVR3273, CNVR4929, CNVR5316	8
berberine bridge enzyme-like 15	LOC111020167	CNVR1199, CNVR1678, CNVR3067, CNVR4668, CNVR4972, CNVR5179, CNVR5563	7
berberine bridge enzyme-like 15	LOC111020159	CNVR1199, CNVR1678, CNVR3067, CNVR4668, CNVR4972, CNVR5179, CNVR5563	7
TMV resistance protein N-like	LOC111012057	CNVR128, CNVR506, CNVR1010, CNVR2495, CNVR3387, CNVR5404, CNVR5610	7
pleiotropic drug resistance protein 2-like	LOC111014246	CNVR549, CNVR772, CNVR985, CNVR2320, CNVR2713, CNVR3160, CNVR3817	7
disease resistance protein RGA2-like	LOC111019843	CNVR421, CNVR532, CNVR765, CNVR2043, CNVR3148, CNVR3518, CNVR4961	7
pleiotropic drug resistance protein 2-like	LOC111014283	CNVR549, CNVR772, CNVR985, CNVR2320, CNVR2713, CNVR3160, CNVR3817	7
cytochrome P450 CYP736A12-like	LOC111005927	CNVR95, CNVR132, CNVR1119, CNVR1903, CNVR3012, CNVR5139, CNVR5687	7
uncharacterized protein LOC111025310	LOC111025310	CNVR796, CNVR2068, CNVR3192, CNVR3825, CNVR5002, CNVR5066, CNVR5300	7
uncharacterized protein LOC111014151	LOC111014151	CNVR429, CNVR893, CNVR1520, CNVR3330, CNVR3628, CNVR5047, CNVR5665	7
zinc finger CCCH domain-containing protein 31-like	LOC111025050	CNVR515, CNVR963, CNVR1086, CNVR2993, CNVR4893, CNVR5126, CNVR5612	7
protein PHLOEM PROTEIN 2-LIKE A9-like	LOC111012691	CNVR1198, CNVR2111, CNVR3065, CNVR3606, CNVR4884, CNVR5501, CNVR5762	7
pleiotropic drug resistance protein 2-like	LOC111011031	CNVR549, CNVR772, CNVR985, CNVR2320, CNVR2713, CNVR3160, CNVR3817	7
cytochrome P450 CYP736A12-like	LOC111005393	CNVR95, CNVR132, CNVR1119, CNVR1903, CNVR3012, CNVR5139, CNVR5687	7
TMV resistance protein N-like	LOC111022364	CNVR128, CNVR506, CNVR1010, CNVR2495, CNVR3387, CNVR5404, CNVR5610	7
alpha carbonic anhydrase 7-like	LOC111025178	CNVR534, CNVR2110, CNVR2537, CNVR3409, CNVR4666, CNVR4863, CNVR5176	7
uncharacterized protein LOC111024922	LOC111024922	CNVR569, CNVR684, CNVR1158, CNVR2236, CNVR3605, CNVR3884, CNVR4655	7
alpha carbonic anhydrase 7-like	LOC111020526	CNVR534, CNVR2110, CNVR2537, CNVR3409, CNVR4666, CNVR4863, CNVR5176	7
arogenate dehydratase/prephenate dehydratase 6, chloroplastic-like	LOC111020559	CNVR214, CNVR574, CNVR975, CNVR1674, CNVR3063, CNVR4667, CNVR5653	7
glyoxylate/hydroxypyruvate reductase HPR3-like	LOC111025775	CNVR2158, CNVR3670, CNVR4710, CNVR4982, CNVR5077, CNVR5240, CNVR5510	7

TMV resistance protein N-like	LOC111012131	CNVR128, CNVR506, CNVR1010, CNVR2495, CNVR3387, CNVR5404, CNVR5610	7
thaumatin-like protein 1b	LOC111013752	CNVR535, CNVR719, CNVR1212, CNVR1934, CNVR1935, CNVR2549	6
squamosa promoter-binding-like protein 1	LOC111025506	CNVR769, CNVR1048, CNVR1287, CNVR2789, CNVR3158, CNVR3613	6
polygalacturonase-like	LOC111018280	CNVR623, CNVR1690, CNVR2055, CNVR2056, CNVR4911, CNVR5192	6
uncharacterized protein LOC111022006	LOC111022006	CNVR174, CNVR1696, CNVR3103, CNVR3972, CNVR4141, CNVR4919	6
probable splicing factor 3A subunit 1	LOC111025286	CNVR1914, CNVR3482, CNVR3603, CNVR3839, CNVR4640, CNVR5151	6
desumoylating isopeptidase 1-like	LOC111020707	CNVR871, CNVR1490, CNVR2142, CNVR2802, CNVR3497, CNVR5637	6
uncharacterized protein LOC111024874	LOC111024874	CNVR606, CNVR2009, CNVR2261, CNVR2565, CNVR3781, CNVR5644	6
probable serine/threonine-protein kinase At1g54610	LOC111011253	CNVR1123, CNVR2881, CNVR3023, CNVR3735, CNVR4637, CNVR5617	6
thaumatin-like protein 1b	LOC111025694	CNVR535, CNVR719, CNVR1212, CNVR1934, CNVR1935, CNVR2549	6
berberine bridge enzyme-like 14	LOC111025613	CNVR159, CNVR1770, CNVR4924, CNVR5037, CNVR5295, CNVR5661	6
trihelix transcription factor GT-2-like	LOC111021134	CNVR501, CNVR945, CNVR1587, CNVR2611, CNVR2959, CNVR3633	6
beta-amyrin synthase	LOC111022720	CNVR308, CNVR375, CNVR2364, CNVR2785, CNVR3226, CNVR3285	6
ent-copalyl diphosphate synthase, chloroplastic	LOC111025355	CNVR815, CNVR1365, CNVR1762, CNVR2572, CNVR5073, CNVR5521	6
protein DMR6-LIKE OXYGENASE 1-like	LOC111011533	CNVR3540, CNVR3727, CNVR4483, CNVR4779, CNVR5667, CNVR5668	6
uncharacterized protein LOC111023821	LOC111023821	CNVR658, CNVR693, CNVR1167, CNVR2244, CNVR4881, CNVR5624	6
berberine bridge enzyme-like 14	LOC111015841	CNVR159, CNVR1770, CNVR4924, CNVR5037, CNVR5295, CNVR5661	6
uncharacterized protein LOC111006766	LOC111006766	CNVR1245, CNVR3669, CNVR4046, CNVR4708, CNVR4915, CNVR5689	6
probable splicing factor 3A subunit 1	LOC111009168	CNVR1914, CNVR3482, CNVR3603, CNVR3839, CNVR4640, CNVR5151	6
uncharacterized protein LOC111018267	LOC111018267	CNVR1156, CNVR1302, CNVR1669, CNVR2175, CNVR3657, CNVR4261	6
FT-interacting protein 1-like	LOC111022063	CNVR523, CNVR1104, CNVR3396, CNVR4631, CNVR5055, CNVR5134	6
uncharacterized protein LOC111025777	LOC111025777	CNVR463, CNVR2025, CNVR3352, CNVR3505, CNVR5012, CNVR5361	6
zinc finger protein WIP2-like	LOC111019571	CNVR197, CNVR526, CNVR970, CNVR2045, CNVR2511, CNVR3397	6
U11/U12 small nuclear ribonucleoprotein 48 kDa protein	LOC111019602	CNVR968, CNVR1621, CNVR2368, CNVR4083, CNVR4897, CNVR5133	6
beta-D-glucosyl crocetin beta-1,6-glucosyltransferase-like	LOC111022962	CNVR547, CNVR2049, CNVR2530, CNVR2878, CNVR3016	5
(-)-germacrene D synthase-like	LOC111021373	CNVR73, CNVR189, CNVR1877, CNVR2851, CNVR4534	5
uncharacterized protein At1g04910	LOC111021383	CNVR490, CNVR596, CNVR933, CNVR2322, CNVR2482	5
squamosa promoter-binding-like protein 17	LOC111025846	CNVR769, CNVR1048, CNVR1287, CNVR3158, CNVR3613	5
CBS domain-containing protein CBSX5-like	LOC111010644	CNVR706, CNVR1679, CNVR2657, CNVR4669, CNVR5702	5

oligopeptide transporter 4-like	LOC111007884	CNVR1046, CNVR1584, CNVR2946, CNVR4795, CNVR5111	5
uncharacterized protein LOC111023421	LOC111023421	CNVR918, CNVR1083, CNVR1861, CNVR2994, CNVR4455	5
Ycf2	ycf2	CNVR298, CNVR807, CNVR1154, CNVR1758, CNVR3209	5
(-)-germacrene D synthase-like	LOC111013811	CNVR73, CNVR189, CNVR1877, CNVR2851, CNVR4534	5
uncharacterized protein LOC111022320	LOC111022320	CNVR3913, CNVR4312, CNVR5431, CNVR5464, CNVR5539	5
uncharacterized protein LOC111023003	LOC111023003	CNVR519, CNVR1622, CNVR2873, CNVR4898, CNVR5482	5
UPF0481 protein At3g47200-like	LOC111005028	CNVR635, CNVR1430, CNVR2771, CNVR3257, CNVR5450	5
uncharacterized protein LOC111023016	LOC111023016	CNVR696, CNVR1601, CNVR2496, CNVR2869, CNVR2984	5
ubiquitin carboxyl-terminal hydrolase 5	LOC111025728	CNVR4665, CNVR5174, CNVR5499, CNVR5500, CNVR5651	5
BURP domain-containing protein BNM2A-like	LOC111025544	CNVR1256, CNVR1258, CNVR1260, CNVR1710, CNVR5243	5
vesicle-associated membrane protein 722-like	LOC111009770	CNVR335, CNVR1800, CNVR2385, CNVR2766, CNVR3249	5
ribonuclease MC-like	LOC111025771	CNVR1002, CNVR2077, CNVR2078, CNVR4348, CNVR4754	5
uncharacterized protein LOC111016201	LOC111016201	CNVR1576, CNVR1711, CNVR2352, CNVR3213, CNVR3233	5
Ycf2	ycf2	CNVR298, CNVR807, CNVR1154, CNVR1758, CNVR3209	5
uncharacterized protein LOC111022007	LOC111022007	CNVR723, CNVR3858, CNVR3921, CNVR4459	4
probable L-ascorbate peroxidase 6, chloroplastic	LOC111011899	CNVR1699, CNVR2682, CNVR3113, CNVR3416	4
uncharacterized protein LOC111012566	LOC111012566	CNVR1196, CNVR1677, CNVR4970, CNVR5178	4
tryptophan--tRNA ligase, cytoplasmic	LOC111015924	CNVR440, CNVR1531, CNVR2441, CNVR3336	4
uncharacterized protein LOC111025268	LOC111025268	CNVR832, CNVR1321, CNVR1399, CNVR5344	4
homeobox-leucine zipper protein HAT5	LOC111018349	CNVR365, CNVR845, CNVR2401, CNVR2778	4
DNA repair protein XRCC3 homolog	LOC111020868	CNVR1828, CNVR2416, CNVR2794, CNVR3302	4
basic leucine zipper 4	LOC111004726	CNVR347, CNVR842, CNVR2772, CNVR3496	4
uncharacterized protein At1g04910-like	LOC111015133	CNVR490, CNVR596, CNVR2322, CNVR2482	4
ABC transporter C family member 14-like	LOC111013247	CNVR383, CNVR2423, CNVR2807, CNVR3317	4
uncharacterized protein LOC111025324	LOC111025324	CNVR294, CNVR319, CNVR373, CNVR2431	4
disease resistance response protein 206-like	LOC111008378	CNVR458, CNVR913, CNVR2838, CNVR3349	4
EIN3-binding F-box protein 1-like	LOC111014530	CNVR616, CNVR779, CNVR2561, CNVR2720	4
probable polygalacturonase	LOC111016350	CNVR274, CNVR768, CNVR2706, CNVR3515	4
crocetin glucosyltransferase, chloroplastic-like	LOC111016219	CNVR835, CNVR1419, CNVR1796, CNVR3245	4
uncharacterized protein LOC111024851	LOC111024851	CNVR955, CNVR1887, CNVR2041, CNVR4956	4
high affinity nitrate transporter 2.5	LOC111019669	CNVR1851, CNVR3630, CNVR4778, CNVR5359	4

uncharacterized protein LOC111025448	LOC111025448	CNVR864, CNVR1475, CNVR4265, CNVR4354	4
serine carboxypeptidase-like 51	LOC111020504	CNVR201, CNVR550, CNVR705, CNVR3019	4
uncharacterized protein LOC111012032	LOC111012032	CNVR957, CNVR1602, CNVR2497, CNVR2870	4
uncharacterized protein LOC111025665	LOC111025665	CNVR930, CNVR4353, CNVR4376, CNVR5265	4
uncharacterized protein LOC111025666	LOC111025666	CNVR855, CNVR1455, CNVR4930, CNVR5320	4
putative ribosome-inactivating protein	LOC111024731	CNVR1765, CNVR4741, CNVR4742, CNVR5582	4
uncharacterized protein LOC111012228	LOC111012228	CNVR1519, CNVR2121, CNVR3329, CNVR3788	4
uncharacterized protein LOC111019025	LOC111019025	CNVR276, CNVR2332, CNVR2731, CNVR3429	4
glycosyltransferase-like KOBITO 1	LOC111010107	CNVR443, CNVR2021, CNVR2446, CNVR3337	4
aspartyl protease family protein At5g10770-like	LOC111009289	CNVR488, CNVR937, CNVR2480, CNVR2940	4
uncharacterized protein LOC111021128	LOC111021128	CNVR82, CNVR1999, CNVR5005, CNVR5530	4
exopolygalacturonase-like	LOC111024445	CNVR1690, CNVR2055, CNVR2056, CNVR4911	4
uncharacterized protein LOC111020765	LOC111020765	CNVR32, CNVR2085, CNVR5332, CNVR5392	4
uncharacterized protein At1g04910-like	LOC111006206	CNVR490, CNVR596, CNVR2322, CNVR2482	4
isoleucine N-monooxygenase 2-like	LOC111017495	CNVR619, CNVR783, CNVR1734, CNVR2728	4
uncharacterized protein LOC111023247	LOC111023247	CNVR2145, CNVR3785, CNVR4585, CNVR4626	4
terpene synthase 10-like	LOC111025107	CNVR196, CNVR512, CNVR2501, CNVR2872	4
protein SMAX1-LIKE 6	LOC111018991	CNVR685, CNVR2640, CNVR3744, CNVR4810	4
uncharacterized protein LOC111025764	LOC111025764	CNVR1320, CNVR3432, CNVR4689, CNVR5096	4
ABC transporter C family member 14-like	LOC111017962	CNVR383, CNVR2423, CNVR2807, CNVR3317	4
serine carboxypeptidase-like 51	LOC111011336	CNVR201, CNVR550, CNVR705, CNVR3019	4
F-box/kelch-repeat protein At3g06240-like	LOC111025804	CNVR1612, CNVR2042, CNVR2502, CNVR3600	4
uncharacterized protein At1g04910-like	LOC111012925	CNVR490, CNVR596, CNVR2322, CNVR2482	4
proteinaceous RNase P 1, chloroplastic/mitochondrial-like	LOC111025808	CNVR2163, CNVR4149, CNVR4984, CNVR5577	4
Ycf1	ycf1	CNVR235, CNVR1424, CNVR2722, CNVR5429	4
C2 domain-containing protein At1g53590-like	LOC111006337	CNVR496, CNVR942, CNVR2484	3
uncharacterized protein LOC111017548	LOC111017548	CNVR1213, CNVR1656, CNVR5599	3
3-hydroxy-3-methylglutaryl-coenzyme A reductase 1	LOC111007941	CNVR1931, CNVR2666, CNVR3527	3
probable GTP-binding protein OBGM, mitochondrial	LOC111019488	CNVR1019, CNVR1165, CNVR3049	3

uncharacterized protein LOC111025517	LOC111025517	CNVR802, CNVR1341, CNVR2567	3
proteasome activator subunit 4	LOC111013390	CNVR926, CNVR2090, CNVR2855	3
uncharacterized protein LOC111013435	LOC111013435	CNVR2235, CNVR2636, CNVR3037	3
phytochrome E	LOC111010794	CNVR1201, CNVR3070, CNVR4864	3
protein ROS1-like	LOC111014286	CNVR339, CNVR773, CNVR2714	3
cation/H(+) antiporter 15-like	LOC111023706	CNVR2500, CNVR3098, CNVR3997	3
potassium transporter 5-like	LOC111014129	CNVR412, CNVR866, CNVR877	3
basic helix-loop-helix protein A	LOC111022687	CNVR2363, CNVR2748, CNVR3492	3
pentatricopeptide repeat-containing protein At1g25360-like	LOC111013956	CNVR4837, CNVR5588, CNVR5589	3
calmodulin-like	LOC111013084	CNVR395, CNVR747, CNVR2303	3
pentatricopeptide repeat-containing protein At5g02860	LOC111017386	CNVR584, CNVR1684, CNVR3084	3
cleavage and polyadenylation specificity factor subunit 3-II	LOC111022502	CNVR438, CNVR899, CNVR2601	3
potassium transporter 5-like	LOC111013191	CNVR412, CNVR866, CNVR877	3
receptor-like protein kinase FERONIA	LOC111006051	CNVR1702, CNVR2620, CNVR3121	3
linoleate 9S-lipoxygenase 6-like	LOC111018861	CNVR870, CNVR2799, CNVR3306	3
polyphenol oxidase, chloroplastic-like	LOC111010634	CNVR708, CNVR2265, CNVR2659	3
potassium transporter 5-like	LOC111015563	CNVR412, CNVR866, CNVR877	3
phosphoenolpyruvate carboxykinase (ATP)-like	LOC111008216	CNVR911, CNVR2837, CNVR3345	3
uncharacterized protein LOC111024176	LOC111024176	CNVR721, CNVR2276, CNVR2673	3
uncharacterized protein LOC111018708	LOC111018708	CNVR2169, CNVR4360, CNVR4936	3
uncharacterized protein LOC111025834	LOC111025834	CNVR87, CNVR113, CNVR5232	3
uncharacterized protein LOC111018892	LOC111018892	CNVR74, CNVR2650, CNVR3860	3
uncharacterized protein LOC111019634	LOC111019634	CNVR331, CNVR3812, CNVR3890	3
polyphenol oxidase, chloroplastic-like	LOC111010674	CNVR708, CNVR2265, CNVR2659	3
uncharacterized protein LOC111025653	LOC111025653	CNVR4433, CNVR5003, CNVR5213	3
VQ motif-containing protein 22-like	LOC111010357	CNVR91, CNVR495, CNVR2951	3
protein TRANSPORT INHIBITOR RESPONSE 1	LOC111018428	CNVR878, CNVR4843, CNVR5330	3
uncharacterized protein LOC111010521	LOC111010521	CNVR2126, CNVR2862, CNVR5248	3
protein BIC1	LOC111014324	CNVR613, CNVR770, CNVR2712	3

uncharacterized protein LOC111015181	LOC111015181	CNVR5027, CNVR5092, CNVR5244	3
uncharacterized protein LOC111020095	LOC111020095	CNVR1737, CNVR3856, CNVR4335	3
protein FAR1-RELATED SEQUENCE 2	LOC111006163	CNVR494, CNVR2950, CNVR4542	3
LOB domain-containing protein 1-like	LOC111010151	CNVR442, CNVR2821, CNVR3457	3
protein RST1	LOC111019939	CNVR363, CNVR1810, CNVR2399	3
uncharacterized protein LOC111023591	LOC111023591	CNVR989, CNVR4889, CNVR5712	3
cytochrome P450 CYP82D47-like	LOC111023576	CNVR2935, CNVR3462, CNVR3571	3
uncharacterized protein LOC111023818	LOC111023818	CNVR2558, CNVR3144, CNVR5700	3
cytochrome b561 and DOMON domain-containing protein At3g25290-like	LOC111023610	CNVR417, CNVR2910, CNVR3454	3
uncharacterized protein LOC111024473	LOC111024473	CNVR116, CNVR1573, CNVR2925	3
uncharacterized protein LOC111019949	LOC111019949	CNVR3276, CNVR4751, CNVR5662	3
probable leucine-rich repeat receptor-like protein kinase At2g33170	LOC111016044	CNVR1705, CNVR4709, CNVR5573	3
uncharacterized protein LOC111017306	LOC111017306	CNVR2272, CNVR2889, CNVR3083	3
transcription factor bHLH35-like	LOC111018151	CNVR2082, CNVR2792, CNVR3301	3
uncharacterized protein LOC111013375	LOC111013375	CNVR1155, CNVR1396, CNVR2105	3
upstream activation factor subunit spp27-like	LOC111022603	CNVR2231, CNVR3030, CNVR3400	3
uncharacterized protein LOC111023248	LOC111023248	CNVR901, CNVR5393, CNVR5741	3
RING-H2 finger protein ATL1-like	LOC111022611	CNVR691, CNVR2646, CNVR3048	3
uncharacterized protein LOC111016620	LOC111016620	CNVR1845, CNVR4237, CNVR5553	3
uncharacterized protein LOC111008302	LOC111008302	CNVR157, CNVR1466, CNVR3745	3
protein ROS1-like	LOC111009900	CNVR339, CNVR773, CNVR2714	3
uncharacterized protein LOC111018268	LOC111018268	CNVR4948, CNVR5266, CNVR5364	3
NDR1/HIN1-like protein 13	LOC111024089	CNVR1297, CNVR3615, CNVR5252	3
putative receptor-like protein kinase At4g00960	LOC111010733	CNVR3660, CNVR4671, CNVR5180	3
exocyst complex component SEC10b	LOC111016312	CNVR742, CNVR2555, CNVR2686	3
uncharacterized protein LOC111018820	LOC111018820	CNVR949, CNVR2612, CNVR2966	3
probable disease resistance protein At4g19060	LOC111025943	CNVR1363, CNVR1761, CNVR3514	3
uncharacterized protein LOC111015505	LOC111015505	CNVR266, CNVR560, CNVR3470	3
MLP-like protein 43	LOC111022325	CNVR896, CNVR1523, CNVR2437	3
uncharacterized protein LOC111022333	LOC111022333	CNVR1736, CNVR2333, CNVR3430	3

cycloartenol-C-24-methyltransferase-like	LOC111020366	CNVR283, CNVR2397, CNVR3263	3
probable protein phosphatase 2C 4	LOC111017092	CNVR974, CNVR2534, CNVR3025	3
mitochondrial import inner membrane translocase subunit PAM16 like 2-like	LOC111024104	CNVR800, CNVR1641, CNVR1748	3
uncharacterized protein LOC111025754	LOC111025754	CNVR2101, CNVR3714, CNVR5129	3
tubby-like F-box protein 7	LOC111012926	CNVR465, CNVR2844, CNVR3353	3
cytochrome P450 CYP82D47-like	LOC111009608	CNVR2935, CNVR3462, CNVR3571	3
brefeldin A-inhibited guanine nucleotide-exchange protein 1	LOC111007998	CNVR4674, CNVR5182, CNVR5763	3
beta-amyrin synthase-like	LOC111018501	CNVR375, CNVR2785, CNVR3285	3
uncharacterized protein LOC111025802	LOC111025802	CNVR171, CNVR805, CNVR4997	3
cation/H(+) antiporter 15-like	LOC111017799	CNVR2500, CNVR3098, CNVR3997	3
uncharacterized mitochondrial protein AtMg00810-like	LOC111022102	CNVR647, CNVR1599, CNVR2854	3
uncharacterized protein LOC111018538	LOC111018538	CNVR3891, CNVR4307, CNVR4485	3
uncharacterized protein LOC111025504	LOC111025504	CNVR3588, CNVR3775	2
acetylajmalan esterase-like	LOC111013753	CNVR188, CNVR3875	2
disease resistance protein LAZ5	LOC111012886	CNVR251, CNVR3356	2
proton pump-interactor 1-like	LOC111010381	CNVR310, CNVR2914	2
uncharacterized protein LOC111009371	LOC111009371	CNVR744, CNVR2301	2
uncharacterized protein LOC111025501	LOC111025501	CNVR716, CNVR1767	2
snRNA-activating protein complex subunit	LOC111012694	CNVR2262, CNVR3066	2
agamous-like MADS-box protein AGL17	LOC111018474	CNVR4940, CNVR5458	2
uncharacterized protein LOC111023667	LOC111023667	CNVR4787, CNVR5373	2
RNA polymerase beta'' subunit	rpoC2	CNVR808, CNVR2166	2
transketolase, chloroplastic-like	LOC111022787	CNVR279, CNVR334	2
uncharacterized protein LOC111010771	LOC111010771	CNVR578, CNVR2266	2
pentatricopeptide repeat-containing protein At2g03880, mitochondrial	LOC111011143	CNVR551, CNVR2809	2
uncharacterized protein LOC111022954	LOC111022954	CNVR1307, CNVR4458	2
telomere repeat-binding protein 3	LOC111010243	CNVR441, CNVR2443	2
serine carboxypeptidase-like 21	LOC111013428	CNVR2425, CNVR3453	2

phospholipid-transporting ATPase 2	LOC111016739	CNVR2663, CNVR3078	2
cytochrome P450 81D1-like	LOC111010788	CNVR3652, CNVR5387	2
K(+) efflux antiporter 6	LOC111004724	CNVR2393, CNVR3258	2
uncharacterized protein LOC111005481	LOC111005481	CNVR3246, CNVR3844	2
protein STRUBBELIG-RECEPTOR FAMILY 2	LOC111021536	CNVR4115, CNVR5514	2
uncharacterized protein LOC111013441	LOC111013441	CNVR177, CNVR5001	2
bZIP transcription factor TGA10-like	LOC111021530	CNVR1286, CNVR3157	2
membrane steroid-binding protein 2-like	LOC111019874	CNVR2703, CNVR3487	2
probable polygalacturonase At3g15720	LOC111021549	CNVR768, CNVR2706	2
auxin-responsive protein IAA16-like	LOC111022235	CNVR804, CNVR2902	2
acetylajmalan esterase-like	LOC111023320	CNVR188, CNVR3875	2
probable WRKY transcription factor 71	LOC111012424	CNVR546, CNVR2526	2
uncharacterized protein LOC111007442	LOC111007442	CNVR1291, CNVR2323	2
RHOMBOID-like protein 1	LOC111022268	CNVR689, CNVR3526	2
basic form of pathogenesis-related protein 1-like	LOC111017389	CNVR1207, CNVR4974	2
basic form of pathogenesis-related protein 1-like	LOC111025079	CNVR1207, CNVR4974	2
sugar transport protein 8-like	LOC111018947	CNVR2642, CNVR3475	2
putative Myb family transcription factor At1g14600	LOC111025236	CNVR2143, CNVR3327	2
uncharacterized protein LOC111024332	LOC111024332	CNVR5469, CNVR5670	2
endoglucanase-like	LOC111025829	CNVR422, CNVR5352	2
uncharacterized protein LOC111018172	LOC111018172	CNVR3763, CNVR4548	2
uncharacterized protein LOC111024352	LOC111024352	CNVR3777, CNVR4723	2
uncharacterized protein LOC111023976	LOC111023976	CNVR2428, CNVR3323	2
uncharacterized protein LOC111008210	LOC111008210	CNVR290, CNVR462	2
OTU domain-containing protein 3	LOC111005897	CNVR539, CNVR2915	2
delta(12)-fatty-acid desaturase FAD2	LOC111024845	CNVR666, CNVR2709	2
uncharacterized protein LOC111018186	LOC111018186	CNVR5043, CNVR5683	2
uncharacterized protein LOC111025019	LOC111025019	CNVR45, CNVR5340	2
long chain acyl-CoA synthetase 4-like	LOC111008230	CNVR2839, CNVR3350	2
uncharacterized protein LOC111023849	LOC111023849	CNVR1842, CNVR4181	2

gibberellin 20 oxidase 1-D-like	LOC111023125	CNVR630, CNVR817	2
uncharacterized protein LOC111025624	LOC111025624	CNVR4350, CNVR5285	2
ornithine decarboxylase-like	LOC111013933	CNVR2583, CNVR5714	2
benzyl alcohol O-benzoyltransferase-like	LOC111017178	CNVR3027, CNVR5146	2
LRR receptor-like serine/threonine-protein kinase GSO1	LOC111020436	CNVR253, CNVR3651	2
serine/threonine-protein kinase SMG1-like	LOC111017174	CNVR205, CNVR2226	2
probable F-box protein At5g04010	LOC111021321	CNVR530, CNVR1625	2
universal stress protein PHOS34-like	LOC111016397	CNVR876, CNVR2806	2
NAD(P)H-quinone oxidoreductase subunit M, chloroplastic	LOC111010476	CNVR2864, CNVR2958	2
protein NYNRIN-like	LOC111017848	CNVR114, CNVR1968	2
uncharacterized protein LOC111024680	LOC111024680	CNVR4201, CNVR5159	2
sulfate transporter 1.3-like	LOC111012207	CNVR218, CNVR3089	2
ABC transporter C family member 3-like	LOC111010499	CNVR500, CNVR943	2
thiamine biosynthetic bifunctional enzyme TH1, chloroplastic	LOC111023892	CNVR894, CNVR3503	2
kinesin-like protein KIN-7D, mitochondrial	LOC111015460	CNVR657, CNVR2624	2
amino acid permease 3	LOC111012015	CNVR594, CNVR2294	2
protein SMAX1-LIKE 4-like	LOC111007146	CNVR2717, CNVR3300	2
guanine nucleotide-binding protein-like NSN1	LOC111018449	CNVR413, CNVR3498	2
uncharacterized protein LOC111024737	LOC111024737	CNVR4798, CNVR5395	2
uncharacterized protein LOC111024735	LOC111024735	CNVR1781, CNVR5669	2
uncharacterized protein LOC111024734	LOC111024734	CNVR4995, CNVR5221	2
subtilisin-like protease SBT5.4	LOC111012693	CNVR2655, CNVR3064	2
protein TIC 20-I, chloroplastic	LOC111019474	CNVR213, CNVR1644	2
putative disease resistance protein RGA4	LOC111016078	CNVR287, CNVR406	2
putative glucuronosyltransferase PGSIP8	LOC111021355	CNVR2474, CNVR2929	2
uncharacterized protein LOC111010533	LOC111010533	CNVR2890, CNVR3086	2
uncharacterized protein LOC111020066	LOC111020066	CNVR729, CNVR2289	2
pentatricopeptide repeat-containing protein At5g55740, chloroplastic	LOC111014489	CNVR617, CNVR2721	2

uncharacterized mitochondrial protein AtMg00810-like	LOC111022111	CNVR1874, CNVR2605	2
uncharacterized protein LOC111017807	LOC111017807	CNVR4725, CNVR5270	2
uncharacterized protein LOC111007859	LOC111007859	CNVR3851, CNVR5325	2
auxin response factor 4	LOC111011210	CNVR2879, CNVR3020	2
protein NYNRIN-like	LOC111012813	CNVR114, CNVR1968	2
pentatricopeptide repeat-containing protein At3g22690	LOC111009484	CNVR227, CNVR2299	2
E3 ubiquitin-protein ligase RMA1H1-like	LOC111010843	CNVR2264, CNVR3072	2
uncharacterized protein LOC111022880	LOC111022880	CNVR1647, CNVR4815	2
protein BEARSKIN2-like	LOC111015190	CNVR664, CNVR982	2
uncharacterized protein LOC111012821	LOC111012821	CNVR3650, CNVR4075	2
uncharacterized mitochondrial protein AtMg00310-like	LOC111004787	CNVR3436, CNVR5672	2
cellulose synthase-like protein H1	LOC111011080	CNVR4636, CNVR5145	2
uncharacterized protein At1g66480-like	LOC111013306	CNVR1824, CNVR2790	2
uncharacterized protein LOC111012466	LOC111012466	CNVR1562, CNVR3811	2
uncharacterized protein LOC111010906	LOC111010906	CNVR2263, CNVR3069	2
protein TIFY 9-like	LOC111015215	CNVR2556, CNVR3483	2
berberine bridge enzyme-like 8	LOC111010911	CNVR577, CNVR3068	2
uncharacterized protein LOC111023822	LOC111023822	CNVR212, CNVR3039	2
MADS-box transcription factor 8-like	LOC111022564	CNVR995, CNVR1369	2
uncharacterized protein LOC111023817	LOC111023817	CNVR2571, CNVR3755	2
uncharacterized protein LOC111013520	LOC111013520	CNVR948, CNVR3380	2
pentatricopeptide repeat-containing protein At4g04370	LOC111026115	CNVR2747, CNVR3437	2
uncharacterized mitochondrial protein AtMg00810-like	LOC111006944	CNVR1003, CNVR2811	2
transcription factor MYB80	LOC111013345	CNVR4790, CNVR5378	2
uncharacterized protein LOC111025405	LOC111025405	CNVR1037, CNVR2031	2
formin-like protein 20	LOC111006954	CNVR986, CNVR1292	2
lysM domain receptor-like kinase 4	LOC111005993	CNVR1902, CNVR5022	2

uncharacterized ATP-dependent helicase C29A10.10c-like	LOC111012310	CNVR121, CNVR939	2
uncharacterized protein LOC111022579	LOC111022579	CNVR2699, CNVR3146	2
proton pump-interactor 1-like	LOC111022582	CNVR310, CNVR2914	2
30S ribosomal protein S21, chloroplastic	LOC111021467	CNVR361, CNVR2777	2
uncharacterized mitochondrial protein AtMg00810-like	LOC111013365	CNVR3108, CNVR4468	2
uncharacterized protein LOC111023433	LOC111023433	CNVR316, CNVR2752	2
4-coumarate--CoA ligase 1-like	LOC111020820	CNVR2417, CNVR3303	2
pectinesterase-like	LOC111020634	CNVR399, CNVR2419	2
uncharacterized protein LOC111024128	LOC111024128	CNVR1400, CNVR3516	2
cytochrome P450 CYP72A219-like	LOC111023453	CNVR2965, CNVR3634	2
uncharacterized protein LOC111013372	LOC111013372	CNVR2353, CNVR5351	2
triacylglycerol lipase 2	LOC111021471	CNVR2585, CNVR3269	2
replication protein A 70 kDa DNA-binding subunit E-like	LOC111022373	CNVR3206, CNVR3389	2
uncharacterized protein LOC111025431	LOC111025431	CNVR67, CNVR5451	2
uncharacterized protein LOC111024898	LOC111024898	CNVR1183, CNVR5728	2
uncharacterized protein LOC111024415	LOC111024415	CNVR505, CNVR3970	2
benzyl alcohol O-benzoyltransferase-like	LOC111017247	CNVR3027, CNVR5146	2
exportin-2	LOC111016290	CNVR600, CNVR2298	2
F-box/kelch-repeat protein At1g23390	LOC111005008	CNVR1031, CNVR1996	2
pentatricopeptide repeat-containing protein At2g03380, mitochondrial	LOC111018771	CNVR2829, CNVR3340	2
ornithine decarboxylase-like	LOC111013993	CNVR2583, CNVR5714	2
calmodulin-like protein 3	LOC111014628	CNVR747, CNVR2303	2
uncharacterized protein LOC111016631	LOC111016631	CNVR158, CNVR2701	2
diphthine methyltransferase	LOC111007485	CNVR232, CNVR2716	2
uncharacterized protein LOC111005015	LOC111005015	CNVR2391, CNVR3255	2
60S ribosomal protein L6, mitochondrial-like	LOC111024915	CNVR3716, CNVR4813	2
protein FAR-RED IMPAIRED RESPONSE 1	LOC111008127	CNVR459, CNVR2841	2
cytochrome P450 705A22-like	LOC111015491	CNVR2084, CNVR3315	2

isoflavone reductase homolog	LOC111025718	CNVR813, CNVR3223	2
probable carboxylesterase 2	LOC111020502	CNVR2478, CNVR2937	2
uncharacterized protein LOC111025158	LOC111025158	CNVR565, CNVR2628	2
uncharacterized protein LOC111008135	LOC111008135	CNVR461, CNVR2457	2
probable protein S-acyltransferase 15	LOC111006718	CNVR737, CNVR2295	2
protein RALF-like 19	LOC111009733	CNVR999, CNVR1994	2
uncharacterized protein LOC111025147	LOC111025147	CNVR1164, CNVR1666	2
1-aminocyclopropane-1-carboxylate synthase 7-like	LOC111016473	CNVR987, CNVR1727	2
glutamate receptor 2.8-like	LOC111010574	CNVR498, CNVR2610	2
receptor-like serine/threonine-protein kinase NCRK	LOC111011323	CNVR654, CNVR2531	2
protein ECERIFERUM 2	LOC111008780	CNVR1583, CNVR2483	2
uncharacterized protein LOC111022059	LOC111022059	CNVR3004, CNVR5483	2
uncharacterized protein LOC111018144	LOC111018144	CNVR3866, CNVR5226	2
tubby-like F-box protein 5	LOC111008190	CNVR2455, CNVR3348	2
uncharacterized protein LOC111023060	LOC111023060	CNVR2698, CNVR3142	2
putative lipid-transfer protein DIR1	LOC111023061	CNVR416, CNVR2426	2
uncharacterized protein LOC111022081	LOC111022081	CNVR521, CNVR1900	2
DNA polymerase zeta processivity subunit	LOC111017977	CNVR556, CNVR1124	2
calcium-dependent protein kinase 20-like	LOC111019358	CNVR2319, CNVR2899	2
uncharacterized mitochondrial protein AtMg00810-like	LOC111020391	CNVR3935, CNVR4194	2
uncharacterized protein LOC111022071	LOC111022071	CNVR3976, CNVR4856	2
protein GRAVITROPIC IN THE LIGHT 1	LOC111016170	CNVR291, CNVR328	2
RAB6A-GEF complex partner protein 1-like	LOC111016171	CNVR330, CNVR2763	2
protein FLUORESCENT IN BLUE LIGHT, chloroplastic	LOC111016954	CNVR358, CNVR2918	2
uncharacterized protein LOC111023969	LOC111023969	CNVR368, CNVR3765	2
dof zinc finger protein DOF1.2-like	LOC111011931	CNVR1946, CNVR2553	2
uncharacterized protein LOC111016198	LOC111016198	CNVR4140, CNVR5400	2
pentatricopeptide repeat-containing protein At1g59720, chloroplastic/mitochondrial	LOC111019179	CNVR1850, CNVR4777	2

elongation factor 2-like	LOC111017983	CNVR557, CNVR3508	2
uncharacterized protein LOC111025577	LOC111025577	CNVR4333, CNVR4334	2
putative disease resistance protein At4g19050	LOC111021012	CNVR2739	1
(S)-coclaurine N-methyltransferase-like	LOC111010373	CNVR936	1
protein ANTI-SILENCING 1	LOC111007160	CNVR2944	1
UDP-glucose flavonoid 3-O-glucosyltransferase 7-like	LOC111022761	CNVR3962	1
uncharacterized protein LOC111022935	LOC111022935	CNVR5170	1
probable pectinesterase/pectinesterase inhibitor 25	LOC111018622	CNVR2827	1
uncharacterized protein LOC111022932	LOC111022932	CNVR2120	1
serine/threonine-protein kinase SRK2I	LOC111017916	CNVR2885	1
uncharacterized protein LOC111021825	LOC111021825	CNVR4604	1
methionine aminopeptidase 1D, chloroplastic/mitochondrial	LOC111017911	CNVR2627	1
receptor protein kinase TMK1	LOC111011885	CNVR261	1
inositol oxygenase 4-like	LOC111016907	CNVR2775	1
uncharacterized protein LOC111023653	LOC111023653	CNVR2733	1
probable WRKY transcription factor 51	LOC111025535	CNVR5150	1
phenolic glucoside malonyltransferase 1-like	LOC111019505	CNVR4324	1
pentatricopeptide repeat-containing protein At4g02820, mitochondrial	LOC111018472	CNVR103	1
uncharacterized protein LOC111025522	LOC111025522	CNVR5275	1
uncharacterized protein C6orf132 homolog	LOC111013573	CNVR2832	1
uncharacterized protein LOC111025516	LOC111025516	CNVR5616	1
berberine bridge enzyme-like 18	LOC111020173	CNVR576	1
magnesium-chelatase subunit ChlH, chloroplastic	LOC111020006	CNVR3800	1
zinc finger protein CONSTANS-LIKE 6	LOC111022043	CNVR2539	1
aminodeoxychorismate synthase, chloroplastic	LOC111010216	CNVR444	1
cystatin-1-like	LOC111012734	CNVR138	1
PLASMODESMATA CALLOSE-BINDING PROTEIN 3-like	LOC111008636	CNVR2269	1
MLO-like protein 6	LOC111010208	CNVR2824	1

probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SPINDLY	LOC111005450	CNVR538	1
uncharacterized protein LOC111021683	LOC111021683	CNVR4120	1
nucleolar complex protein 2 homolog	LOC111006372	CNVR738	1
glutamate receptor 3.7-like	LOC111011141	CNVR4861	1
long-chain-alcohol oxidase FAO4A	LOC111012719	CNVR492	1
transcriptional activator DEMETER	LOC111010054	CNVR2449	1
uncharacterized protein LOC111011908	LOC111011908	CNVR2552	1
E3 ubiquitin-protein ligase RHF2A-like	LOC111019328	CNVR3422	1
protein tesmin/TSO1-like CXC 2	LOC111004863	CNVR5313	1
alpha-amylase 3, chloroplastic	LOC111019134	CNVR449	1
dynamin-2A-like	LOC111020185	CNVR3122	1
uncharacterized protein LOC111024362	LOC111024362	CNVR3604	1
WAT1-related protein At4g15540-like	LOC111018340	CNVR5715	1
UDP-glycosyltransferase 73C1-like	LOC111014275	CNVR971	1
uncharacterized protein LOC111014277	LOC111014277	CNVR2321	1
cellulose synthase A catalytic subunit 2 [UDP-forming]-like	LOC111020024	CNVR4801	1
protein SCAI	LOC111022810	CNVR2384	1
alpha-dioxygenase 1-like	LOC111018335	CNVR3519	1
putative oxidoreductase C1F5.03c	LOC111005277	CNVR1626	1
respiratory burst oxidase homolog protein A-like	LOC111015291	CNVR301	1
subtilisin-like protease SBT4.15	LOC111014270	CNVR1288	1
uncharacterized protein LOC111022971	LOC111022971	CNVR2538	1
uncharacterized protein LOC111022972	LOC111022972	CNVR5558	1
uncharacterized protein LOC111023488	LOC111023488	CNVR5167	1
UDP-sulfoquinovose synthase, chloroplastic	LOC111006075	CNVR2939	1
fluoride export protein 2	LOC111011796	CNVR1241	1
pre-mRNA-splicing factor cwc22-like	LOC111010998	CNVR5142	1
uncharacterized protein LOC111013439	LOC111013439	CNVR5693	1
uncharacterized protein LOC111013438	LOC111013438	CNVR2536	1
probable RNA-binding protein ARP1	LOC111010248	CNVR2820	1

ethylene-responsive transcription factor ABR1-like	LOC111006073	CNVR2916	1
CDPK-related kinase 3	LOC111024369	CNVR321	1
F-box protein At1g47056-like	LOC111005479	CNVR485	1
protein NSP-INTERACTING KINASE 2-like	LOC111017591	CNVR448	1
uncharacterized protein LOC111007775	LOC111007775	CNVR2812	1
uncharacterized protein LOC111021063	LOC111021063	CNVR356	1
F-box protein At3g07870-like	LOC111005288	CNVR3015	1
arogenate dehydrogenase 1, chloroplastic	LOC111013055	CNVR3307	1
uncharacterized protein LOC111020044	LOC111020044	CNVR981	1
4-alpha-glucanotransferase DPE2	LOC111021744	CNVR3532	1
naringenin,2-oxoglutarate 3-dioxygenase-like	LOC111023502	CNVR2758	1
aladin	LOC111019858	CNVR3151	1
uncharacterized protein LOC111020715	LOC111020715	CNVR4386	1
probable protein S-acyltransferase 4	LOC111019862	CNVR2702	1
defensin-like protein 1	LOC111025288	CNVR679	1
universal stress protein A-like protein	LOC111023305	CNVR392	1
ent-kaurenoic acid oxidase 2-like	LOC111022826	CNVR3248	1
uncharacterized protein LOC111005306	LOC111005306	CNVR541	1
protein DETOXIFICATION 14-like	LOC111020042	CNVR731	1
cleavage stimulation factor subunit 77	LOC111021740	CNVR2516	1
probable LRR receptor-like serine/threonine-protein kinase At1g05700	LOC111022244	CNVR400	1
uncharacterized protein LOC111012433	LOC111012433	CNVR3469	1
U-box domain-containing protein 35-like	LOC111007629	CNVR3080	1
uncharacterized protein LOC111025065	LOC111025065	CNVR5224	1
uncharacterized protein LOC111025316	LOC111025316	CNVR3922	1
transcription factor bHLH62	LOC111022233	CNVR419	1
uncharacterized protein LOC111006110	LOC111006110	CNVR223	1
molybdate transporter 1	LOC111004614	CNVR345	1
beta-glucosidase BoGH3B-like	LOC111022483	CNVR2062	1
zinc finger CCCH domain-containing protein 30	LOC111021554	CNVR3155	1

uncharacterized protein LOC111014310	LOC111014310	CNVR771	1
probable mitochondrial-processing peptidase subunit beta, mitochondrial	LOC111014126	CNVR1477	1
uncharacterized protein LOC111013454	LOC111013454	CNVR5711	1
magnesium-chelatase subunit ChlI, chloroplastic-like	LOC111012251	CNVR545	1
peroxidase P7-like	LOC111016753	CNVR2270	1
probable inactive receptor-like protein kinase At3g56050	LOC111015959	CNVR4606	1
probable nucleoredoxin 1	LOC111016584	CNVR2563	1
UDP-glycosyltransferase 91C1-like	LOC111005320	CNVR3011	1
uncharacterized protein LOC111024587	LOC111024587	CNVR4944	1
uncharacterized protein LOC111021367	LOC111021367	CNVR480	1
uncharacterized protein LOC111021544	LOC111021544	CNVR5209	1
protein argonaute 10	LOC111009218	CNVR743	1
purple acid phosphatase 23	LOC111015982	CNVR151	1
leucine-rich repeat extensin-like protein 4	LOC111024215	CNVR638	1
ATP-dependent helicase NAM7-like	LOC111014153	CNVR3502	1
protein phosphatase 2C 29	LOC111014810	CNVR1580	1
alpha-1,4 glucan phosphorylase L isozyme, chloroplastic/amyloplastic	LOC111014157	CNVR3298	1
uncharacterized protein LOC111018954	LOC111018954	CNVR5290	1
oxysterol-binding protein-related protein 2A-like	LOC111023341	CNVR1360	1
uncharacterized protein LOC111022267	LOC111022267	CNVR4260	1
cadmium/zinc-transporting ATPase HMA3-like	LOC111007462	CNVR233	1
transcription factor MYC4-like	LOC111014145	CNVR2414	1
uncharacterized protein LOC111014147	LOC111014147	CNVR5061	1
protein CHROMATIN REMODELING 8-like	LOC111022691	CNVR277	1
putative clathrin assembly protein At2g01600	LOC111022501	CNVR2819	1
protein SIEVE ELEMENT OCCLUSION B	LOC111004559	CNVR2579	1
uncharacterized protein LOC111022403	LOC111022403	CNVR2741	1
nuclear transcription factor Y subunit B-1-like	LOC111008372	CNVR3346	1

monogalactosyldiacylglycerol synthase 2, chloroplastic	LOC111013024	CNVR2595	1
endoglucanase 7	LOC111018160	CNVR387	1
uncharacterized protein LOC111024991	LOC111024991	CNVR1663	1
uncharacterized protein LOC111024135	LOC111024135	CNVR1001	1
TORTIFOLIA1-like protein 3	LOC111007376	CNVR775	1
AP2-like ethylene-responsive transcription factor AIL5	LOC111007391	CNVR777	1
uncharacterized protein LOC111024824	LOC111024824	CNVR5341	1
uncharacterized protein LOC111022426	LOC111022426	CNVR3595	1
major allergen Pru ar 1-like	LOC111009801	CNVR341	1
DNA-directed RNA polymerase III subunit rpc6-like	LOC111023984	CNVR5491	1
alanine--glyoxylate aminotransferase 2 homolog 1, mitochondrial	LOC111008389	CNVR455	1
putative pentatricopeptide repeat-containing protein At3g16890, mitochondrial	LOC111009187	CNVR2689	1
copper methylamine oxidase	LOC111006817	CNVR3163	1
major extracellular endoglucanase-like	LOC111023982	CNVR3531	1
uncharacterized protein LOC111009028	LOC111009028	CNVR2662	1
defensin Ec-AMP-D2-like	LOC111015561	CNVR5235	1
beta-amyrin 28-oxidase-like	LOC111006822	CNVR2161	1
pentatricopeptide repeat-containing protein At1g71210	LOC111023275	CNVR390	1
DExH-box ATP-dependent RNA helicase DExH18, mitochondrial	LOC111024354	CNVR332	1
putative GTP diphosphokinase RSH1, chloroplastic	LOC111022415	CNVR865	1
auxin-responsive protein SAUR23-like	LOC111015411	CNVR3824	1
putative ABC transporter C family member 15	LOC111019797	CNVR2453	1
GPI ethanolamine phosphate transferase 2	LOC111005904	CNVR200	1
uncharacterized protein LOC111025032	LOC111025032	CNVR4175	1
uncharacterized protein LOC111018900	LOC111018900	CNVR5488	1
aluminum-activated malate transporter 2-like	LOC111012160	CNVR3173	1
protein SUPPRESSOR OF MAX2 1	LOC111007233	CNVR234	1

uncharacterized protein LOC111024004	LOC111024004	CNVR1637	1
ribonuclease E/G-like protein, chloroplastic	LOC111007590	CNVR2665	1
thyroid adenoma-associated protein homolog	LOC111005108	CNVR852	1
non-specific lipid-transfer protein-like protein At5g64080	LOC111012165	CNVR718	1
probable glycosyltransferase At3g07620	LOC111014547	CNVR3166	1
uncharacterized protein LOC111009035	LOC111009035	CNVR2888	1
uncharacterized protein LOC111024165	LOC111024165	CNVR732	1
ribosomal protein S12, mitochondrial	LOC111007417	CNVR3632	1
probable kinetochore protein NUF2	LOC111024175	CNVR3986	1
uncharacterized protein LOC111025021	LOC111025021	CNVR3769	1
5’-3’ exoribonuclease 3-like	LOC111013945	CNVR2396	1
cytochrome P450 71A14-like	LOC111017184	CNVR2787	1
BTB/POZ domain-containing protein At2g30600	LOC111019636	CNVR953	1
uncharacterized protein LOC111017193	LOC111017193	CNVR5619	1
methyltransferase-like protein 2	LOC111013949	CNVR350	1
uncharacterized protein LOC111016223	LOC111016223	CNVR329	1
lipase-like PAD4	LOC111017842	CNVR969	1
calmodulin-binding protein 60 A-like	LOC111026027	CNVR2362	1
uncharacterized protein LOC111023847	LOC111023847	CNVR309	1
uncharacterized protein LOC111018723	LOC111018723	CNVR1537	1
zinc finger CCCH domain-containing protein 14-like	LOC111024859	CNVR2708	1
F-box protein At2g17036-like	LOC111025629	CNVR3629	1
uncharacterized protein LOC111024676	LOC111024676	CNVR4285	1
late embryogenesis abundant protein D-34-like	LOC111009658	CNVR5448	1
uncharacterized protein LOC111019624	LOC111019624	CNVR3805	1
uncharacterized protein LOC111019629	LOC111019629	CNVR1038	1
uncharacterized protein LOC111017181	LOC111017181	CNVR3386	1
uncharacterized protein LOC111023841	LOC111023841	CNVR1005	1
uncharacterized protein LOC111023843	LOC111023843	CNVR3934	1

pentatricopeptide repeat-containing protein At4g30825, chloroplastic	LOC111007115	CNVR614	1
uncharacterized protein LOC111018906	LOC111018906	CNVR3097	1
histidine kinase 4-like	LOC111015621	CNVR2291	1
probable fructokinase-4	LOC111018577	CNVR5442	1
uncharacterized protein LOC111025643	LOC111025643	CNVR4371	1
pentatricopeptide repeat-containing protein At2g13600-like	LOC111025648	CNVR3322	1
protein DETOXIFICATION 30	LOC111019813	CNVR2921	1
probable glucuronoxylan glucuronosyltransferase F8H	LOC111020450	CNVR2255	1
uncharacterized protein LOC111012186	LOC111012186	CNVR2786	1
acetylornithine deacetylase-like	LOC111025871	CNVR2746	1
probable LRR receptor-like serine/threonine-protein kinase At3g47570	LOC111020480	CNVR3479	1
uncharacterized protein LOC111021158	LOC111021158	CNVR5010	1
B3 domain-containing protein Os01g0234100-like	LOC111017874	CNVR2229	1
uncharacterized protein LOC111012212	LOC111012212	CNVR3088	1
uncharacterized protein LOC111011249	LOC111011249	CNVR2617	1
uncharacterized protein LOC111025451	LOC111025451	CNVR2969	1
uncharacterized protein LOC111020475	LOC111020475	CNVR22	1
uncharacterized protein LOC111020469	LOC111020469	CNVR2093	1
zinc finger BED domain-containing protein DAYSLEEPER-like	LOC111014589	CNVR2560	1
phenolic glucoside malonyltransferase 2-like	LOC111016863	CNVR3266	1
uncharacterized protein LOC111023870	LOC111023870	CNVR5567	1
cellulose synthase-like protein G3	LOC111008102	CNVR2840	1
uncharacterized protein LOC111018736	LOC111018736	CNVR935	1
uncharacterized protein LOC111019463	LOC111019463	CNVR1112	1
putative pentatricopeptide repeat-containing protein At5g59900	LOC111017039	CNVR5412	1
uncharacterized protein LOC111016277	LOC111016277	CNVR741	1
uncharacterized protein LOC111016890	LOC111016890	CNVR4462	1

E3 ubiquitin-protein ligase PUB23-like	LOC111012220	CNVR622	1
NAC transcription factor 29-like	LOC111025473	CNVR5403	1
1-phosphatidylinositol-3-phosphate 5-kinase FAB1B-like	LOC111018061	CNVR2803	1
23 kDa jasmonate-induced protein-like	LOC111023882	CNVR5262	1
uncharacterized protein LOC111008116	LOC111008116	CNVR2456	1
trihelix transcription factor ASR3-like	LOC111023888	CNVR2435	1
CBL-interacting serine/threonine-protein kinase 5-like	LOC111011090	CNVR254	1
probable copper-transporting ATPase HMA5	LOC111022922	CNVR2360	1
probable LRR receptor-like serine/threonine-protein kinase At4g36180	LOC111018446	CNVR4405	1
uncharacterized protein LOC111008576	LOC111008576	CNVR497	1
RPM1-interacting protein 4-like	LOC111012692	CNVR575	1
APO protein 3, mitochondrial-like	LOC111013546	CNVR411	1
uncharacterized protein LOC111013735	LOC111013735	CNVR2521	1
uncharacterized protein LOC111020513	LOC111020513	CNVR2545	1
protein GRAVITROPIC IN THE LIGHT 1-like	LOC111007922	CNVR291	1
probable aquaporin TIP2-2	LOC111021982	CNVR628	1
ribosome-inactivating protein bryodin I-like	LOC111024724	CNVR4922	1
uncharacterized protein LOC111010172	LOC111010172	CNVR2445	1
quinolinate synthase, chloroplastic	LOC111008585	CNVR2660	1
dynein light chain 1, cytoplasmic-like	LOC111009552	CNVR340	1
2S albumin-like	LOC111022124	CNVR1550	1
uncharacterized protein LOC111017816	LOC111017816	CNVR75	1
IAA-amino acid hydrolase ILR1-like 6	LOC111011964	CNVR2293	1
uncharacterized protein LOC111021292	LOC111021292	CNVR3008	1
TVP38/TMEM64 family membrane protein slr0305-like	LOC111020425	CNVR2472	1
3beta-hydroxysteroid-dehydrogenase/decarboxylase	LOC111009273	CNVR3417	1
expansin-A18	LOC111020426	CNVR2034	1
uncharacterized protein LOC111021911	LOC111021911	CNVR2801	1

ABC transporter G family member 22	LOC111019388	CNVR611	1
heat stress transcription factor A-6b-like	LOC111022847	CNVR104	1
uncharacterized protein LOC111004755	LOC111004755	CNVR2390	1
auxin-responsive protein IAA4-like	LOC111012980	CNVR2909	1
uncharacterized protein LOC111024651	LOC111024651	CNVR4479	1
pathogen-related protein-like	LOC111012790	CNVR3545	1
ABC transporter G family member 9-like	LOC111012812	CNVR914	1
uncharacterized protein LOC111004493	LOC111004493	CNVR2609	1
ammonium transporter 3 member 1	LOC111004759	CNVR1429	1
homeobox-leucine zipper protein GLABRA 2	LOC111022137	CNVR3311	1
uncharacterized protein LOC111018559	LOC111018559	CNVR1881	1
bidirectional sugar transporter SWEET5-like	LOC111025616	CNVR364	1
long chain acyl-CoA synthetase 6, peroxisomal-like	LOC111009493	CNVR2687	1
GDSL esterase/lipase 1-like	LOC111020259	CNVR4298	1
uncharacterized protein LOC111019405	LOC111019405	CNVR3895	1
pentatricopeptide repeat-containing protein At2g03880, mitochondrial-like	LOC111018419	CNVR2809	1
basic 7S globulin 2	LOC111018418	CNVR1831	1
uncharacterized protein LOC111019909	LOC111019909	CNVR5600	1
WD repeat-containing protein 3	LOC111023565	CNVR2911	1
transcription factor RAX2-like	LOC111013686	CNVR533	1
kirola-like	LOC111009302	CNVR651	1
aquaporin PIP2-1-like	LOC111010114	CNVR2447	1
uncharacterized protein LOC111015183	LOC111015183	CNVR1815	1
F-box/kelch-repeat protein At5g60570-like	LOC111023783	CNVR1188	1
VQ motif-containing protein 10-like	LOC111012826	CNVR464	1
histidine kinase 2-like	LOC111011062	CNVR552	1
probable N-acetyltransferase HLS1	LOC111009312	CNVR745	1
protein DEFECTIVE IN EXINE FORMATION 1	LOC111019425	CNVR2519	1
zinc finger protein ZAT9	LOC111021966	CNVR3211	1
shikimate O-hydroxycinnamoyltransferase	LOC111021609	CNVR403	1

nardilysin-like	LOC111012652	CNVR3941	1
acetyl-CoA carboxylase 1-like	LOC111011862	CNVR593	1
pentatricopeptide repeat-containing protein At1g09900-like	LOC111016014	CNVR599	1
ABC transporter C family member 10	LOC111011692	CNVR909	1
two-pore potassium channel 1	LOC111010336	CNVR2486	1
probable sugar phosphate/phosphate translocator At5g25400	LOC111011518	CNVR1008	1
uncharacterized protein LOC111020115	LOC111020115	CNVR3474	1
uncharacterized protein LOC111005544	LOC111005544	CNVR3374	1
uncharacterized protein LOC111023802	LOC111023802	CNVR3442	1
protein SMG7	LOC111020767	CNVR2729	1
F-box/LRR-repeat protein 4	LOC111019922	CNVR3272	1
protein SLOW GREEN 1, chloroplastic	LOC111005371	CNVR1016	1
BEACH domain-containing protein C2	LOC111016011	CNVR273	1
P-loop NTPase domain-containing protein LPA1 homolog 1-like	LOC111011076	CNVR202	1
uncharacterized protein LOC111013514	LOC111013514	CNVR3381	1
transcription factor DICHOTOMA-like	LOC111024260	CNVR147	1
acyltransferase-like protein At3g26840, chloroplastic	LOC111023398	CNVR359	1
uncharacterized protein LOC111007674	LOC111007674	CNVR2271	1
uncharacterized protein LOC111008483	LOC111008483	CNVR1854	1
pentatricopeptide repeat-containing protein At3g22150, chloroplastic	LOC111010146	CNVR2861	1
transcriptional corepressor LEUNIG_HOMOLOG	LOC111016027	CNVR272	1
uncharacterized protein LOC111015217	LOC111015217	CNVR5680	1
respiratory burst oxidase homolog protein D-like	LOC111020130	CNVR4077	1
uncharacterized protein LOC111019946	LOC111019946	CNVR1782	1
uncharacterized protein LOC111006168	LOC111006168	CNVR2684	1
peptidyl-prolyl cis-trans isomerase CYP38, chloroplastic	LOC111025383	CNVR2400	1
protein NPGR2-like	LOC111015207	CNVR224	1

kynurenine--oxoglutarate transaminase 1-like	LOC111020964	CNVR3316	1
uncharacterized protein LOC111022900	LOC111022900	CNVR379	1
DNA (cytosine-5)-methyltransferase DRM2	LOC111019935	CNVR285	1
uncharacterized protein LOC111022347	LOC111022347	CNVR5731	1
ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	LOC111021429	CNVR404	1
protein ABSCISIC ACID-INSENSITIVE 5	LOC111014388	CNVR1959	1
F-box protein At5g03970	LOC111013139	CNVR2800	1
probable L-type lectin-domain containing receptor kinase VII.2	LOC111016666	CNVR140	1
vacuolar iron transporter 1-like	LOC111015869	CNVR2442	1
peptide methionine sulfoxide reductase A1-like	LOC111011724	CNVR1852	1
uncharacterized protein LOC111017468	LOC111017468	CNVR4870	1
probable phosphoribosylformylglycinamidine synthase, chloroplastic/mitochondrial	LOC111015874	CNVR644	1
uncharacterized protein LOC111014861	LOC111014861	CNVR483	1
oligopeptide transporter 7	LOC111004497	CNVR3224	1
uncharacterized protein LOC111023609	LOC111023609	CNVR2188	1
probable WRKY transcription factor 75	LOC111023408	CNVR2776	1
probable alkaline/neutral invertase D	LOC111013535	CNVR123	1
ABC transporter G family member 25	LOC111013533	CNVR193	1
cyclin-dependent kinase G-2-like	LOC111004676	CNVR2769	1
probable carboxylesterase 15	LOC111005401	CNVR2622	1
monoacylglycerol lipase abhd6-A-like	LOC111008351	CNVR1853	1
uncharacterized protein At5g39865-like	LOC111015887	CNVR905	1
immune-associated nucleotide-binding protein 9-like	LOC111015058	CNVR2715	1
uncharacterized protein LOC111023625	LOC111023625	CNVR244	1
mitogen-activated protein kinase kinase kinase 3	LOC111005414	CNVR3009	1
CDPK-related kinase 5-like	LOC111007701	CNVR2670	1
uncharacterized protein LOC111015239	LOC111015239	CNVR4739	1
probable inactive receptor kinase At5g67200	LOC111005862	CNVR540	1

polygalacturonase QRT2	LOC111015052	CNVR874	1
dCTP pyrophosphatase 1-like	LOC111024481	CNVR885	1
uncharacterized protein DDB_G0271670-like	LOC111009149	CNVR601	1
protein SAR DEFICIENT 1-like	LOC111023256	CNVR2796	1
phospholipid-transporting ATPase 1-like	LOC111013881	CNVR199	1
uncharacterized protein LOC111025215	LOC111025215	CNVR892	1
uncharacterized protein LOC111023250	LOC111023250	CNVR5708	1
uncharacterized protein LOC111009964	LOC111009964	CNVR2947	1
uncharacterized protein LOC111023450	LOC111023450	CNVR5649	1
uncharacterized protein LOC111013370	LOC111013370	CNVR5075	1
uncharacterized protein LOC111013369	LOC111013369	CNVR725	1
chlorophyll a-b binding protein of LHCII type 1-like	LOC111012353	CNVR1200	1
uncharacterized protein LOC111015892	LOC111015892	CNVR3504	1
protein MEI2-like 6	LOC111007720	CNVR2669	1
copper-transporting ATPase RAN1	LOC111015725	CNVR653	1
ATP-dependent DNA helicase PIF1-like	LOC111022374	CNVR2193	1
5′-nucleotidase domain-containing protein DDB_G0275467	LOC111007365	CNVR2718	1
uncharacterized protein LOC111024114	LOC111024114	CNVR4239	1
chromatin modification-related protein EAF1 B	LOC111014167	CNVR398	1
probable 1-acyl-sn-glycerol-3-phosphate acyltransferase 4	LOC111013982	CNVR349	1
zinc transporter 8-like	LOC111014796	CNVR941	1
uncharacterized protein LOC111025110	LOC111025110	CNVR4326	1
probable 3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase	LOC111024900	CNVR3133	1
uncharacterized protein LOC111021593	LOC111021593	CNVR4014	1
pentatricopeptide repeat-containing protein At3g06920	LOC111009241	CNVR2688	1
SWI/SNF complex subunit SWI3D	LOC111007653	CNVR5183	1
centromere-associated protein E	LOC111005948	CNVR2943	1
uncharacterized protein LOC111025121	LOC111025121	CNVR3927	1

pentatricopeptide repeat-containing protein At1g18485	LOC111007464	CNVR2325	1
magnesium transporter MRS2-5	LOC111005161	CNVR3647	1
dehydration-responsive element-binding protein 3	LOC111015808	CNVR401	1
aldehyde dehydrogenase family 3 member F1-like	LOC111017407	CNVR3017	1
uncharacterized protein LOC111024891	LOC111024891	CNVR2069	1
ribosomal L1 domain-containing protein 1-like	LOC111026071	CNVR2361	1
ATP sulfurylase 1, chloroplastic-like	LOC111009889	CNVR338	1
polyol transporter 5-like	LOC111024218	CNVR5457	1
putative NAC domain-containing protein 94	LOC111021578	CNVR3154	1
uncharacterized protein LOC111022280	LOC111022280	CNVR3993	1
uncharacterized protein LOC111025102	LOC111025102	CNVR5591	1
uncharacterized protein LOC111016288	LOC111016288	CNVR226	1
uncharacterized protein LOC111013826	LOC111013826	CNVR4186	1
interaptin	LOC111018078	CNVR204	1
uncharacterized protein LOC111023375	LOC111023375	CNVR307	1
protein MRG1-like	LOC111004999	CNVR2479	1
tryptophan aminotransferase-related protein 2-like	LOC111007309	CNVR774	1
uncharacterized protein LOC111023906	LOC111023906	CNVR4597	1
protein BONZAI 3	LOC111018242	CNVR2415	1
gamma aminobutyrate transaminase 1, mitochondrial	LOC111008130	CNVR2842	1
protein WVD2-like 3	LOC111009911	CNVR838	1
protein PHLOEM PROTEIN 2-LIKE A10	LOC111012299	CNVR2938	1
uncharacterized mitochondrial protein AtMg00810-like	LOC111013815	CNVR4525	1
uncharacterized protein LOC111017421	LOC111017421	CNVR247	1
protein WVD2-like 7	LOC111006710	CNVR1246	1
uncharacterized protein LOC111022541	LOC111022541	CNVR3204	1
uncharacterized protein LOC111018973	LOC111018973	CNVR5306	1
beta-amylase 1, chloroplastic-like	LOC111009907	CNVR3495	1

uncharacterized protein LOC111022300	LOC111022300	CNVR88	1
G-type lectin S-receptor-like serine/threonine-protein kinase At1g34300	LOC111015682	CNVR1236	1
endoribonuclease Dicer homolog 2	LOC111018265	CNVR624	1
E3 ubiquitin-protein ligase UPL1	LOC111013839	CNVR922	1
uncharacterized mitochondrial protein AtMg00310-like	LOC111014662	CNVR4062	1
vinorine synthase-like	LOC111005025	CNVR2580	1
uncharacterized protein LOC111022321	LOC111022321	CNVR3942	1
uncharacterized protein LOC111022318	LOC111022318	CNVR4869	1
uncharacterized protein LOC111024750	LOC111024750	CNVR4082	1
receptor-like protein 12	LOC111009124	CNVR2894	1
AAA-ATPase At5g17760-like	LOC111008317	CNVR1542	1
pentatricopeptide repeat-containing protein At1g80270, mitochondrial-like	LOC111016638	CNVR2316	1
uncharacterized protein LOC111014651	LOC111014651	CNVR822	1
uncharacterized protein LOC111005036	LOC111005036	CNVR281	1
uncharacterized protein LOC111025149	LOC111025149	CNVR2312	1
bifunctional pinoresinol-lariciresinol reductase 2-like	LOC111022994	CNVR2130	1
uncharacterized protein LOC111008952	LOC111008952	CNVR5564	1
BTB/POZ domain-containing protein At3g44820	LOC111020544	CNVR2260	1
uncharacterized protein Mb2253c-like	LOC111019518	CNVR1393	1
DEAD-box ATP-dependent RNA helicase 35	LOC111017080	CNVR2596	1
beta-1,6-galactosyltransferase GALT31A	LOC111025945	CNVR3489	1
uncharacterized protein LOC111007960	LOC111007960	CNVR2667	1
IQ domain-containing protein IQM1-like	LOC111016465	CNVR236	1
formin-like protein 6	LOC111017931	CNVR1631	1
uncharacterized protein LOC111017925	LOC111017925	CNVR2626	1
probable inactive receptor kinase At5g10020	LOC111024090	CNVR1298	1
uncharacterized mitochondrial protein AtMg00810-like	LOC111024092	CNVR42	1
ER lumen protein-retaining receptor-like	LOC111025934	CNVR814	1

uncharacterized protein LOC111018639	LOC111018639	CNVR3452	1
uncharacterized protein At1g28695-like	LOC111016134	CNVR2554	1
uncharacterized protein LOC111024970	LOC111024970	CNVR1315	1
BEL1-like homeodomain protein 7	LOC111015329	CNVR102	1
protein NRT1/ PTR FAMILY 1.2-like	LOC111020557	CNVR3310	1
eukaryotic translation initiation factor 4G-like	LOC111016126	CNVR3125	1
uncharacterized protein LOC111023942	LOC111023942	CNVR2744	1
caffeic acid 3-O-methyltransferase-like	LOC111025741	CNVR3983	1
B3 domain-containing protein At4g01580-like	LOC111024773	CNVR1633	1
uncharacterized protein LOC111024105	LOC111024105	CNVR4243	1
protein TsetseEP-like	LOC111024967	CNVR170	1
probable aminotransferase TAT2	LOC111010585	CNVR2952	1
NAC domain-containing protein 35	LOC111008182	CNVR280	1
uncharacterized protein LOC111022065	LOC111022065	CNVR3658	1
DNA mismatch repair protein MLH3	LOC111024800	CNVR5604	1
protein RALF-like 33	LOC111009595	CNVR634	1
uncharacterized protein LOC111010588	LOC111010588	CNVR257	1
alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1	LOC111007356	CNVR255	1
VQ motif-containing protein 4-like	LOC111009767	CNVR3375	1
uncharacterized protein LOC111021236	LOC111021236	CNVR2529	1
uncharacterized protein LOC111014698	LOC111014698	CNVR3130	1
structural maintenance of chromosomes protein 1-like	LOC111023062	CNVR4499	1
uncharacterized protein LOC111023952	LOC111023952	CNVR811	1
uncharacterized protein LOC111023053	LOC111023053	CNVR2671	1
polyamine oxidase 1	LOC111018503	CNVR408	1
transcription factor bHLH87-like	LOC111016961	CNVR2398	1
probable bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1 1	LOC111010423	CNVR499	1
GTPase HflX	LOC111011354	CNVR2933	1

uncharacterized protein LOC111020215	LOC111020215	CNVR2685	1
pentatricopeptide repeat-containing protein At3g62890-like	LOC111017771	CNVR453	1
protein TPX2	LOC111020393	CNVR2927	1
ethylene-responsive transcription factor RAP2-11-like	LOC111016335	CNVR3126	1
protein DETOXIFICATION 19-like	LOC111010608	CNVR5686	1
kinesin-like protein KIN-7C, mitochondrial	LOC111011929	CNVR2683	1
argininosuccinate lyase, chloroplastic-like	LOC111004891	CNVR344	1
L-type lectin-domain containing receptor kinase VII.1-like	LOC111010621	CNVR3410	1
LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.3	LOC111016973	CNVR184	1
UDP-glucuronic acid decarboxylase 4-like	LOC111009636	CNVR3252	1
serine/threonine-protein kinase prpf4B-like	LOC111018688	CNVR2830	1
uncharacterized protein LOC111018362	LOC111018362	CNVR2198	1
periodic tryptophan protein 2	LOC111021076	CNVR1000	1
probable LRR receptor-like serine/threonine-protein kinase At1g12460	LOC111020408	CNVR477	1
uncharacterized protein LOC111025585	LOC111025585	CNVR2122	1
putative phospholipid:diacylglycerol acyltransferase 2	LOC111011365	CNVR3018	1
protein kinase PINOID 2	LOC111012966	CNVR3308	1
uncharacterized protein LOC111025810	LOC111025810	CNVR5205	1
probable strigolactone esterase DAD2	LOC111014472	CNVR780	1
methyltransferase-like protein 13	LOC111010269	CNVR109	1

Supplementary Table 3. Approximately unbiased (AU) p-value and bootstrap probability (BP) values of clustering obtained through 10,000 multiscale bootstrap

si	au	bp	se.si	se.au	se.bp	v	c	pchi
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.466	0.924	0.24	0.054	0.013	0.004	-0.363	1.069	0.571
0	0.608	0.242	0	0.033	0.004	0.213	0.486	0.59
0	0.629	0.019	0	0.078	0.001	0.871	1.201	0.029
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.967	0.993	0.8	0.006	0.002	0.004	-1.651	0.809	0.201
0.956	0.988	0.856	0.008	0.003	0.004	-1.659	0.597	0.864
0.948	0.988	0.793	0.009	0.003	0.004	-1.532	0.715	0.682
0.501	0.859	0.471	0.04	0.017	0.005	-0.501	0.574	0.115
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.96	0.99	0.833	0.008	0.002	0.004	-1.648	0.682	0.433
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.967	0.992	0.847	0.007	0.002	0.004	-1.712	0.689	0.676
0.359	0.837	0.366	0.047	0.02	0.005	-0.321	0.663	0.178
0.961	0.99	0.854	0.007	0.002	0.004	-1.686	0.634	0.882
0.959	0.989	0.856	0.008	0.003	0.004	-1.675	0.611	0.887
0.405	0.847	0.389	0.045	0.019	0.005	-0.371	0.652	0.589
0.607	0.889	0.529	0.035	0.015	0.005	-0.646	0.573	0.179
0.928	0.985	0.709	0.011	0.003	0.005	-1.361	0.81	0.242
0.898	0.974	0.731	0.015	0.005	0.005	-1.281	0.664	0.884
0.83	0.956	0.664	0.021	0.007	0.005	-1.062	0.639	0.984
0.952	0.986	0.858	0.009	0.003	0.004	-1.641	0.57	0.838
0.953	0.987	0.858	0.009	0.003	0.004	-1.642	0.571	0.837
0.368	0.82	0.412	0.045	0.021	0.005	-0.347	0.569	0.808
0.913	0.978	0.747	0.013	0.004	0.005	-1.344	0.678	0.815
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.833	0.96	0.63	0.021	0.007	0.005	-1.042	0.709	0.157
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.958	0.989	0.854	0.008	0.003	0.004	-1.668	0.614	0.759
0.409	0.814	0.472	0.042	0.021	0.005	-0.411	0.48	0.673
0.896	0.98	0.631	0.015	0.004	0.005	-1.191	0.856	0.863
0.935	0.985	0.76	0.01	0.003	0.005	-1.436	0.73	0.721
0.758	0.932	0.628	0.026	0.01	0.005	-0.91	0.583	0.045
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.742	0.938	0.548	0.028	0.01	0.005	-0.831	0.71	0.829
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833

0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.945	0.987	0.798	0.009	0.003	0.004	-1.523	0.691	0.947
0.957	0.991	0.779	0.008	0.002	0.005	-1.561	0.792	0.743
0.969	0.993	0.838	0.006	0.002	0.004	-1.716	0.729	0.751
0.953	0.987	0.858	0.009	0.003	0.004	-1.644	0.573	0.84
0.759	0.934	0.621	0.026	0.01	0.005	-0.906	0.598	0.712
0.592	0.903	0.449	0.037	0.014	0.005	-0.585	0.713	0.934
0.929	0.982	0.772	0.011	0.004	0.005	-1.426	0.68	0.985
0.564	0.894	0.441	0.039	0.014	0.005	-0.552	0.699	0.411
0.312	0.83	0.34	0.049	0.021	0.005	-0.271	0.682	0.527
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.959	0.99	0.837	0.008	0.002	0.004	-1.647	0.663	0.908
0.954	0.987	0.858	0.009	0.003	0.004	-1.649	0.579	0.848
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.538	0.911	0.348	0.043	0.013	0.005	-0.478	0.869	0.818
0.957	0.991	0.773	0.008	0.002	0.005	-1.554	0.807	0.913
0.967	0.993	0.788	0.006	0.002	0.004	-1.636	0.836	0.855
0.966	0.992	0.824	0.006	0.002	0.004	-1.676	0.744	0.971
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.961	0.99	0.85	0.007	0.002	0.004	-1.68	0.641	0.869
0.957	0.988	0.857	0.008	0.003	0.004	-1.664	0.596	0.871
0.922	0.983	0.711	0.012	0.003	0.005	-1.341	0.784	0.585
0.39	0.871	0.32	0.05	0.017	0.005	-0.331	0.799	0.96
0.333	0.806	0.406	0.045	0.022	0.005	-0.312	0.551	0.11
0.794	0.956	0.547	0.024	0.007	0.005	-0.911	0.794	0.355
0.171	0.801	0.285	0.055	0.024	0.005	-0.139	0.707	0.509
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0	0.754	0.082	0	0.037	0.003	0.353	1.041	0.732
0.959	0.992	0.772	0.007	0.002	0.005	-1.57	0.823	0.714
0.293	0.78	0.415	0.045	0.023	0.005	-0.279	0.493	0.676
0.906	0.982	0.647	0.013	0.004	0.005	-1.232	0.856	0.858
0.159	0.828	0.241	0.06	0.022	0.004	-0.121	0.825	0.464
0	0.701	0.179	0	0.032	0.004	0.196	0.724	0.098
0.959	0.991	0.78	0.007	0.002	0.005	-1.578	0.805	0.114
0.699	0.943	0.432	0.032	0.009	0.005	-0.703	0.874	0.85
0.859	0.971	0.607	0.018	0.005	0.005	-1.08	0.81	0.399
0.67	0.923	0.486	0.033	0.011	0.005	-0.697	0.73	0.086
0.535	0.879	0.454	0.039	0.016	0.005	-0.528	0.644	0.458
0.966	0.994	0.734	0.006	0.001	0.005	-1.577	0.952	0.041
0	0.782	0.165	0	0.028	0.004	0.097	0.878	0.193

0.965	0.991	0.845	0.007	0.002	0.004	-1.701	0.684	0.975
0.857	0.978	0.49	0.019	0.004	0.005	-0.994	1.018	0.79
0.159	0.828	0.24	0.061	0.022	0.004	-0.12	0.826	0.997
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.885	0.983	0.503	0.016	0.003	0.005	-1.068	1.061	0.441
0	0.598	0.057	0	0.05	0.002	0.666	0.914	0.706
0.876	0.971	0.668	0.017	0.005	0.005	-1.166	0.732	0.746
0.889	0.981	0.574	0.015	0.004	0.005	-1.129	0.942	0.118
0	0.85	0.141	0	0.024	0.004	0.021	1.056	0.08
0.479	0.918	0.267	0.052	0.013	0.005	-0.386	1.008	0.023
0.881	0.974	0.656	0.016	0.005	0.005	-1.17	0.767	0.992
0.321	0.84	0.328	0.05	0.02	0.005	-0.274	0.721	0.396
0.484	0.926	0.248	0.052	0.013	0.004	-0.382	1.064	0.134
0.859	0.972	0.581	0.018	0.005	0.005	-1.062	0.857	0.706
0.203	0.886	0.177	0.072	0.019	0.004	-0.139	1.065	0.298
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833
0.614	0.916	0.43	0.037	0.012	0.005	-0.6	0.776	0.987
0.576	0.91	0.401	0.039	0.013	0.005	-0.544	0.794	0.83
0.383	0.901	0.242	0.057	0.015	0.004	-0.295	0.995	0.096
0.277	0.919	0.15	0.077	0.015	0.004	-0.182	1.219	0.583
0.419	0.914	0.235	0.057	0.014	0.004	-0.321	1.042	0.457
0.819	0.964	0.538	0.022	0.006	0.005	-0.949	0.854	0.964
0.953	0.989	0.802	0.008	0.003	0.004	-1.569	0.72	0.643
0.464	0.952	0.154	0.067	0.01	0.004	-0.321	1.339	0.374
0.86	0.968	0.635	0.018	0.006	0.005	-1.102	0.757	0.285
0.88	0.97	0.704	0.016	0.006	0.005	-1.207	0.672	0.6
0.805	0.965	0.489	0.024	0.006	0.005	-0.894	0.922	0.33
0.532	0.928	0.281	0.047	0.012	0.005	-0.441	1.021	0.239
0.949	0.99	0.725	0.008	0.002	0.005	-1.465	0.868	0.103
0.952	0.986	0.858	0.009	0.003	0.004	-1.64	0.569	0.833

Supplementary Table 4. Principal component values of the 146 cultivars based on the CNVRs

Sample	PCA1	PCA2	Cluster
TR(S108) (macroloba)_Wild_Tanzania(Africa)	-4.09696378	-5.1354314	1
TR(S108) (macroloba)_Wild_Tanzania(Africa).1	-4.09125586	-5.1242924	1
TR(S108) (macroloba)_Wild_Tanzania(Africa).2	-4.10254709	-5.1461849	1
TR(S108) (macroloba)_Wild_Tanzania(Africa).3	-4.09684074	-5.1350507	1
TR(S108) (macroloba)_Wild_Tanzania(Africa).4	-4.09684074	-5.1350507	1
TR(S108) (macroloba)_Wild_Tanzania(Africa).5	-3.64528335	-4.2465923	1
Dali-11(S159)_Cultivars_China(Asia)	-3.65659108	-4.2684433	1
Dali-11(S159)_Cultivars_China(Asia).1	-3.77669606	-4.4961091	1
Dali-11(S159)_Cultivars_China(Asia).2	-3.75728237	-4.4558236	1
Dali-11(S159)_Cultivars_China(Asia).3	-3.75728237	-4.4558236	1
Dali-11(S159)_Cultivars_China(Asia).4	-3.75728237	-4.4558236	1
Dali-11(S159)_Cultivars_China(Asia).5	-3.74122032	-4.4257203	1
Dali-11(S159)_Cultivars_China(Asia).6	-3.87075044	-4.7002698	1
Dali-11(S159)_Cultivars_China(Asia).7	-4.16276817	-5.3209918	1
Dali-11(S159)_Cultivars_China(Asia).8	-4.54151401	-6.1132222	1
Dali-11(S159)_Cultivars_China(Asia).9	-4.3922922	-5.8035644	1
Dali-11(S159)_Cultivars_China(Asia).10	-4.64773784	-6.3343634	1
Dali-11(S159)_Cultivars_China(Asia).11	-4.57341972	-6.1804052	1
S106(THMC401) (macroloba)_Wild_Columbia(America)	-4.25525297	-5.511505	1
S107(THMC402) (macroloba)_Wild_Columbia(America)	-4.21651162	-5.4295206	1
S108(TR) (macroloba)_Wild_Tanzania(Africa)	-4.21330209	-5.4312008	1
S109(Tanzanian2)_Cultivars_Tanzania(Africa)	-3.72265064	-4.4146707	1
S110(Tanzanian3)_Cultivars_Tanzania(Africa)	-3.72265064	-4.4146707	1
S111(Tanzanian4)_Cultivars_Tanzania(Africa)	-3.72265064	-4.4146707	1
S112(Tanzanian5)_Cultivars_Tanzania(Africa)	-5.64874476	-10.39773	1
S113(Tanzanian6)_Cultivars_Tanzania(Africa)	-6.20471934	-12.221787	1
S114(9809-3-9)_Cultivars_China(Asia)	-6.64124802	-13.59616	1
S115(YunNan_small_kugua) (muricata)_Wild_China(Asia)	-6.34941184	-12.676087	1
S116(9825-18-2) _Cultivars_China(Asia)	-6.64784545	-13.61183	1
S117(BaoTing_wild_kugua) (muricata)_Wild_China(Asia)	-4.70295924	-7.4794253	1
S118(83_kugua)_Cultivars_China(Asia)	-6.61420483	-13.512846	1
S119(DaXin_kugua)_Cultivars_China(Asia)	-6.64314611	-12.594414	1
S120(Qiong-2)_Cultivars_China(Asia)	-5.94109695	-10.420425	1
S121(YangShuo_wild_kugua) (muricata)_Wild_China(Asia)	-6.12841362	-10.897465	1
S122(YunNan_langya_kugua)_Cultivars_China(Asia)	-5.86224762	-10.202651	1
S123(HaiNan_small_kugua) (muricata)_Wild_China(Asia)	-5.30176924	-8.5948653	1
S124(K44)_Cultivars_China(Asia)	-5.83437949	-10.089138	1
S125(JiangMen_dading-2)_Cultivars_China(Asia)	-4.95642883	-7.5724564	1
S126(68-2-1-2-1)_Cultivars_China(Asia)	-4.62825717	-6.6912367	1
S127(Red_seed_dading-3-3)_Cultivars_China(Asia)	-4.6304515	-6.7067291	1

S128(HuiZhou_dading-1-2-3-1)_Cultivars_China(Asia)	-4.96150428	-4.8064084	1
S129(HaiNan_kugua)_Cultivars_China(Asia)	-12.6410871	67.9526591	0
S130(89-2-2-2)_Cultivars_China(Asia)	-13.1285259	71.9034997	0
S131(9780-3-1)_Cultivars_China(Asia)	-12.743657	68.6908343	0
S132(11-13-1-2-3-1)_Cultivars_China(Asia)	-9.0970175	38.1941198	0
S133(9814-1)_Cultivars_China(Asia)	-11.6552792	59.3456711	0
S134(29-1-2-8)_Cultivars_China(Asia)	-12.8829359	69.7311087	0
S135(Kansheng_black_seed-1)_Cultivars_China(Asia)	-10.7188903	52.1053411	0
S136(89-2-4-3-1)_Cultivars_China(Asia)	-11.7623124	60.7926452	0
S137(Xiutian_BG101-1)_Cultivars_China(Asia)	-11.7785691	60.8443757	0
S138(Xinyou_ZY-3112-2-0-10-3)_Cultivars_China(Asia)	-12.3657083	65.7997128	0
S139(Chuangfu-10-1)_Cultivars_China(Asia)	-11.7838388	60.7255878	0
S140(Chuangfu-2-1-1)_Cultivars_China(Asia)	-9.5093182	41.4483649	0
S141(10-3-2-7-1-2)_Cultivars_China(Asia)	-11.0213767	54.5937479	0
S142(Zeng-13)_Cultivars_China(Asia)	-10.8961296	53.0520375	0
S143(XT491-2)_Cultivars_China(Asia)	-9.3364739	40.1601417	0
S144(Baokang_one-1)_Cultivars_China(Asia)	-11.140423	55.5743353	0
S145(Baokang_two)_Cultivars_China(Asia)	-10.6556258	51.5600521	0
S146(10-5-1-1-1)_Cultivars_China(Asia)	-6.69255814	-8.5477321	1
S147(10-4-1-1-2)_Cultivars_China(Asia)	-6.79404238	-13.637636	1
S148(Meiyu_kugua)_Cultivars_China(Asia)	-5.04760044	-8.3475128	1
S149(TingShan-2-1-5-2)_Cultivars_China(Asia)	-6.80625651	-13.656095	1
S150(Jinchuan-2-1)_Cultivars_China(Asia)	-6.77878361	-13.570601	1
S151(ZYUXF3-810-1-1-1)_Cultivars_China(Asia)	-6.91446679	-13.97722	1
S152(ZY-9-3-1)_Cultivars_China(Asia)	-6.63077638	-13.138527	1
S154(DY951-1-11-2)_Cultivars_China(Asia)	-5.95147643	-10.693737	1
S155(Yaoxiang-6-1-2-2)_Cultivars_China(Asia)	-5.20549747	-8.5144379	1
S156(Nongbo-1-2-1-1-3)_Cultivars_China(Asia)	-5.69965779	-9.9045046	1
S157(25-4-1-4)_Cultivars_China(Asia)	-5.37889815	-9.0025075	1
S158(ZY_yaoxiangF2-1-1)_Cultivars_China(Asia)	-5.71330286	-9.9357154	1
S160(GuangXi_wild_kugua) (macroloba)_Wild_China(Asia)	-5.04414583	-8.072827	1
S161(Jiangke_texuan-1)_Cultivars_China(Asia)	-6.23629225	-12.188316	1
S162(47-2-1-1-3)_Cultivars_China(Asia)	-8.14500571	-22.456811	1
S163(9808-2-2)_Cultivars_China(Asia)	-6.6088111	-16.086291	1
S164(9825-10-1-1)_Cultivars_China(Asia)	-7.12523285	-18.246539	1
S165(FuJian_white_kugua)_Cultivars_China(Asia)	-7.32743037	-19.129967	1
S166(14-Dading)_Cultivars_China(Asia)	-5.82073194	-12.860119	1
S167(Cuiyu_zhenzhu-1)_Cultivars_China(Asia)	-7.53482285	-19.966711	1
S168(UX203)_Cultivars_China(Asia)	-7.51936404	-19.898239	1
S170(DuAn_kugua)_Cultivars_China(Asia)	-7.43722289	-19.557382	1
S171(88-kugua)_Cultivars_China(Asia)	-6.82307769	-16.975941	1

S172(DaXin_short_kugua)_Cultivars_China(Asia)	-6.7599689	-16.738012	1
S173(ShanTou_wild_kugua) (macroloba)_Wild_China(Asia)	-4.73413257	-7.9961784	1
S174(JingZhou_kugua)_Cultivars_China(Asia)	-3.88766177	-4.791312	1
S169(QuanZhou_kugua)_Cultivars_China(Asia)	-3.85436807	-4.7087101	1
M.charantia_Cultivars_Bangladesh(Asia)	-4.20192161	-5.5310385	1
M.charantia_Cultivars_Bangladesh(Asia).1	-4.22930627	-5.5922971	1
M.charantia_Cultivars_Bangladesh(Asia).2	-4.16713439	-5.4310773	1
M.cochinchinensis_Cultivars_Taiwan(Asia)	-3.64528335	-4.2465923	1
M.charantia_Cultivars_India(Asia)	-4.00920456	-5.0555424	1
M.charantia_Cultivars_Philippines(Asia)	-4.34013013	-5.9314258	1
M.charantia_Cultivars_Taiwan(Asia)	-4.56516724	-6.5056721	1
M.charantia_Cultivars_Taiwan(Asia).1	-4.56707825	-6.5037801	1
M.charantia_Cultivars_Taiwan(Asia).2	-2.02391114	-6.4302999	1
M.charantia_Cultivars_Taiwan(Asia).3	144.2778756	8.65744859	2
M.charantia_Cultivars_Taiwan(Asia).4	143.1147708	8.54863933	2
M.charantia_Cultivars_Taiwan(Asia).5	42.79889941	-0.4247669	1
M.charantia_Cultivars_Taiwan(Asia).6	97.31538657	4.46757028	2
M.charantia_Cultivars_Thailand(Asia)	97.81647606	4.58293356	2
M.charantia_Cultivars_Thailand(Asia).1	139.8968194	8.28703158	2
M.charantia_Cultivars_India(Asia).1	0.224977639	-3.9557036	1
M.charantia_Cultivars_Thailand(Asia).2	140.161988	8.32267805	2
M.charantia_Cultivars_Thailand(Asia).3	-3.93876332	-6.8885331	1
M.charantia_Cultivars_Taiwan(Asia).7	-4.61935538	-6.4369592	1
M.charantia_Cultivars_Taiwan(Asia).8	-4.65958835	-6.5277369	1
M.charantia_Cultivars_Taiwan(Asia).9	-4.69883711	-6.6117392	1
M.charantia_Cultivars_Bangladesh(Asia).3	-4.57418535	-6.2982867	1
M.charantia_Cultivars_China(Asia)	-4.6072402	-6.3540731	1
M.charantia_Cultivars_China(Asia).1	-4.61436837	-6.3656285	1
M.charantia_Cultivars_China(Asia).2	-4.72150948	-6.6064398	1
M.charantia_Cultivars_China(Asia).3	-4.5214748	-6.1661692	1
M.charantia_Cultivars_India(Asia).2	-4.61458578	-6.3868229	1
M.charantia_Cultivars_China(Asia).4	-4.56078954	-6.2504824	1
M.charantia_Cultivars_China(Asia).5	-4.44717097	-5.9962948	1
M.charantia_Cultivars_Philippines(Asia).1	-4.37841113	-5.8496776	1
M.charantia_Cultivars_China(Asia).6	-4.60186606	-6.3390334	1
M.charantia_Cultivars_China(Asia).7	-4.66869473	-6.4912923	1
M.charantia_Cultivars_Viet Nam(Asia)	-4.60203286	-6.3431733	1
M.charantia_Cultivars_Viet Nam(Asia).1	-4.50621027	-6.1339462	1
M.charantia_Cultivars_Bangladesh(Asia).4	-4.66949665	-6.5171852	1
M.charantia_Cultivars_Bangladesh(Asia).5	-4.8636926	-6.9702743	1
M.charantia_Cultivars_Bangladesh(Asia).6	-4.99139742	-7.2575458	1

M.charantia_Cultivars_Thailand(Asia).4	-4.56093751	-6.2831023	1
M.charantia_Cultivars_Bangladesh(Asia).7	-5.89162198	-9.7647763	1
M.charantia_Cultivars_Philippines(Asia).2	-4.52499434	-6.3256497	1
M.charantia_Cultivars_Viet Nam(Asia).2	-4.84229351	-7.1193347	1
M.charantia_Cultivars_Thailand(Asia).5	-5.45076165	-8.6505886	1
M.charantia_Cultivars_Viet Nam(Asia).3	-4.77479704	-6.9573651	1
M.charantia_Cultivars_Bangladesh(Asia).8	-5.51765003	-8.8245131	1
M.charantia_Cultivars_Philippines(Asia).3	-4.54671716	-6.3898881	1
M.charantia_Cultivars_Philippines(Asia).4	-4.64746663	-6.6350281	1
M.charantia_Cultivars_Pakistan(Asia)	-5.30310856	-8.284209	1
M.charantia_Cultivars_India(Asia).3	-5.3236093	-8.3361669	1
M.charantia_Cultivars_Thailand(Asia).6	-4.70950571	-6.7932635	1
M.charantia_Cultivars_Taiwan(Asia).10	-4.75603926	-6.9106605	1
M.charantia_Cultivars_India(Asia).4	-5.65923163	-9.1873651	1
M.charantia_Cultivars_India(Asia).5	-5.38068075	-8.4973131	1
M.charantia_Cultivars_Thailand(Asia).7	-4.88952947	-7.2379234	1
M.charantia_Cultivars_India(Asia).6	-5.41210715	-8.5618659	1
M.charantia_Cultivars_India(Asia).7	-5.29750929	-8.2810051	1
M.charantia_Cultivars_India(Asia).8	-5.12741707	-7.8432559	1
M.charantia_Cultivars_India(Asia).9	-5.37464402	-8.4604116	1
M.charantia_Cultivars_Belize(America)	-4.774783	-6.9551545	1
M.charantia_Cultivars_Bangladesh(Asia).9	-5.5194143	-8.8301214	1
M.charantia_Cultivars_Philippines(Asia).5	-4.66675894	-6.7007361	1
M.charantia_Cultivars_India(Asia).10	-5.14363801	-7.8907131	1