



Analysis of Clade V *MLO* Gene Expressions in Hazelnut Leaves during Exposure to Powdery Mildew

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ABSTRACT

Text Powdery mildew affecting European hazelnut *Corylus avellana* L. in Turkey is caused by the obligate biotrophic fungus *Erysiphe corylacearum*. This fungal disease causes significant economic losses by reducing the yield and quality of hazelnuts. Loss-of-function mutations in the *mildew resistance locus o* (*MLO*) gene family of many plants confer high levels of broad-spectrum resistance to powdery mildew. The proteins encoded by the genes at the *MLO* locus are divided into approximately seven different conserved clades. Among them, phylogenetic clade V has been found to be involved in PM susceptibility, as inactivation of these genes leads to long-term disease resistance in dicots. In this study, we examined the temporal expression pattern of three hazelnut *MLO* genes, previously identified as clade V, in response to powdery mildew infection in *C. avellana* cv. Tombul. Leaves are the main tissue affected by the powdery mildew pathogen in hazelnut plants. Analysis of *MLO* expression in hazelnut leaves showed that *CavMLO2* and *CavMLO6* were significantly upregulated after challenge with *E. corylacearum*, providing preliminary evidence that they may be involved in PM susceptibility. Thus, these results present a basis for the isolation and use of relevant genes in plant breeding for disease resistance. In addition, gene expression profiles of clade V *MLO* are also important for identifying candidate genes that need to be silenced or modified for future molecular studies to obtain resistant hazelnut varieties.

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Introduction

Powdery mildew (PM) is a widespread and harmful disease of plants, including economically important European hazelnuts (*Corylus avellana* L.). Recently, the pathogen responsible for PM fungal disease in *C. avellana* L. has been identified as *Erysiphe corylacearum* (Sezer et al., 2017). Disease control is important to avoid serious economic losses for hazelnuts. PM in hazelnut fields is controlled with fungal pesticides, but the disease is not eradicated. Due to environmental damage and the possibility of emergence of new resistant races of the pathogen, investigation of PM-resistant hazelnut varieties or identification of *MLO* genes responsible for susceptibility of hazelnut plants is necessary to produce resistant varieties for breeding or genetic engineering.

PM pathogens break down the plant defense through plant susceptibility genes (S-genes), *Mildew Locus O* (*MLO*) genes. *MLO* genes encode seven transmembrane domain proteins containing a C-terminal calmodulin-binding domain (CaMBD) (Büsches et al., 1997; Devoto et al.,

1999; Kim et al., 2002a). The number of amino acids in *MLO* proteins ranges from 400 to 600. Their biological functions mainly include modulating the host response to powdery mildew. Analysis of the expression pattern of the *MLO* gene family is important to identify the candidate gene for engineering its function. *MLO* genes have been isolated from several species based on their similarity to well-characterized barley and *Arabidopsis*. As a natural loss-of-function (*Mlo*) mutation in barley (*Hordeum vulgare*), it leads to broad-spectrum resistance to *Blumeria graminis* f. sp. *hordei* (*Bgh*) (Kusch and Panstruga, 2017; Jørgensen, 1992). Complete resistance to *Golovinomyces orontii* in *Arabidopsis thaliana* has been obtained by mutation of the *AtMLO2*, *AtMLO6*, and *AtMLO12* genes [transfer-DNA (T-DNA insertion), chemical mutagenesis] (Consonni et al., 2007). Subsequently, only a few *MLO* sequences have been functionally characterized in different plants and found to be involved in plant-powdery mildew interactions such as a natural loss-of-function mutation in tomato (*Solanum*

lycopersicum L. var. *cerasiforme*) *SIMLO1* has provided resistance to the tomato PM pathogen *Oidium neolycopersici* (Bai et al., 2008); reduced susceptibility to *Leveillula taurica* has been demonstrated in pepper (*Capsicum annuum*) with an RNAi loss-of-function mutant of an *Mlo* ortholog, *CaMLO2* (Zheng et al., 2013); bread wheat (*Triticum aestivum*) has acquired long-lasting resistance to *Blumeria graminis* f.sp. *tritici* (*Bgt*) in the presence of mutants of the *TaMLO1* gene generated either using transcription activator-like effector nucleases (TALLEN) or targeting induced lesions in genomes (TILLING) technologies (Wang et al, 2014; Acevedo-Garcia et al, 2017); in grapevine (*Vitis vinifera*), the combination of RNAi knock-down of *VvMLO6* and *VvMLO7* has significantly reduced the severity of the powdery mildew pathogen *Erysiphe necator* (Pessina et al., 2016b); RNAi knock-down of *MdMLO19* expression from apple (*Malus domestica*) has led to resistance to *Podosphaera leucotricha* (Pessina et al., 2014; Pessina et al., 2016a).

This study describes the identification of potential candidates for hazelnut *MLO* genes associated with powdery mildew susceptibility based on analysis of the transcriptional response of hazelnut to powdery mildew infection by semi-quantitative polymerase chain reaction (qPCR). The results obtained would be useful for developing resistant varieties for hazelnut breeding or for making mutations in specific genes with gene editing tools (Gaj et al., 2013; Lozano-Juste and Cutler, 2014; Puchta and Fauser, 2014).

Materials and Methods

Plant Material and Growth Conditions

Hazelnut (*Corylus avellana* cv. Tombul) suckers (~50 cm in length) were collected from a hazelnut field and planted in pots (39×35 cm dimensions). Plants were maintained in a growth chamber at 25°C and 60–65% humidity with a 16 h photoperiod provided by cool white fluorescent rods with a light intensity of 120 $\mu\text{mol m}^{-2} \text{s}^{-1}$. The soil was fertilized once using 20:20:20. Plants were

irrigated with tap water until fresh, healthy leaves were obtained for pathogen inoculation.

Isolation of Powdery Mildew Pathogen and Leaf Inoculation

PM pathogenic fungus *E. corylacearum* was collected from hazelnut plants in a field in Giresun, Türkiye, and regularly preserved on the leaves of *Corylus avellana* cv. Tombul plants in the growth chamber. Hazelnut leaves were inoculated by brushing conidia from heavily infected leaves. For hazelnut *MLO* gene expression analysis, three different plants were sampled at two different time points; 9 hours post inoculation (hpi) and 24 hpi. Uninfected leaves were used as experimental controls at 0 hpi. Collected leaf samples were frozen directly in liquid nitrogen and used immediately for RNA extraction.

Total RNA Extraction and Gene Expression Analysis by Semi-Quantitative RT-PCR

Total RNA was extracted from frozen young hazelnut leaves using the Plant/Fungi RNA Isolation Kit (Norgen Biotek) according to the manufacturer's instructions. RNA quality and quantity were assessed using a 1% agarose gel assay. Semi-quantitative RT-PCR was used to analyze gene expressions of the hazelnut clade V *MLO* (*CavMLO*) in *C. avellana* cv. Tombul. Total RNA was used to synthesize single stranded cDNA using the Superscript III reverse transcriptase kit (Invitrogen, Thermo Fisher Scientific). Each 20 μl reaction mix contained 1 μg of total RNA, oligo primers (dT18), and other components according to the manufacturer's instructions. In semi-quantitative RT-PCR, *C. avellana MLO* gene-specific primers spanning a partial coding region of *MLO* genes were used to monitor gene expression in infected and uninfected individuals at defined time points (0, 9, 24, hpi). The coding sequences of the genes were obtained from a project deposited in the NCBI database [*Corylus avellana*, Transcriptome Shotgun Assembly (TSA), BioProject: PRJNA316492] (Kavas et al., 2019) used to design pairs of clade V *MLO* gene-specific primers.

Table 1. List of the primers used in this study.

Gene	GenBank accession number	Primer pair sequences (5'–3')	Al (base pairs)
<u>CavMLO2</u> (<u>Cav10g09700</u>)	GGSA01064561.1	CoravMLO2-Forward GGTGGGGACGAACTACAGGTGATC	720
		CoravMLO2-Reverse GGAAGCGGAGCCACTTGACTTGAG	
<u>CavMLO6</u> (<u>Cav07g19540</u>)	GGSA01025153.1	CoravMLO6-Forward ACACCTGTGGTACAGCCAGGTGATG	720
		CoravMLO6-Reverse CATCTGCGAAATGTGAATTCCGAG	
<u>CavMLO12</u> (<u>Cav07g19590</u>)	GGSA01055436.1	CoravMLO12-Forward TGCCAACGCATATGGATGGCATTC	720
		CoravMLO12-Reverse CGTGTTGGGTTCTGAATGGTTCCTAG	
<u>CavACT</u> (on chr <u>11</u>)	GGSA01045693.1	CoravACT-Forward TGCTGGATTCTGGTGATGGTGTGAG	589
		CoravACT-Reverse GATGCAAGGATTGATCCTCCGATCC	

Al: Amplicon length. The name of the full length clade V *Corylus avellana* cv. Tombul Mildew Locus O (*MLO*) genes and *ACTIN* as a reference gene with GenBank accession numbers, the primer sequences used to amplify part of the genes by RT-PCR reaction and the length of the products. The chromosomes on which the genes are located were underlined.

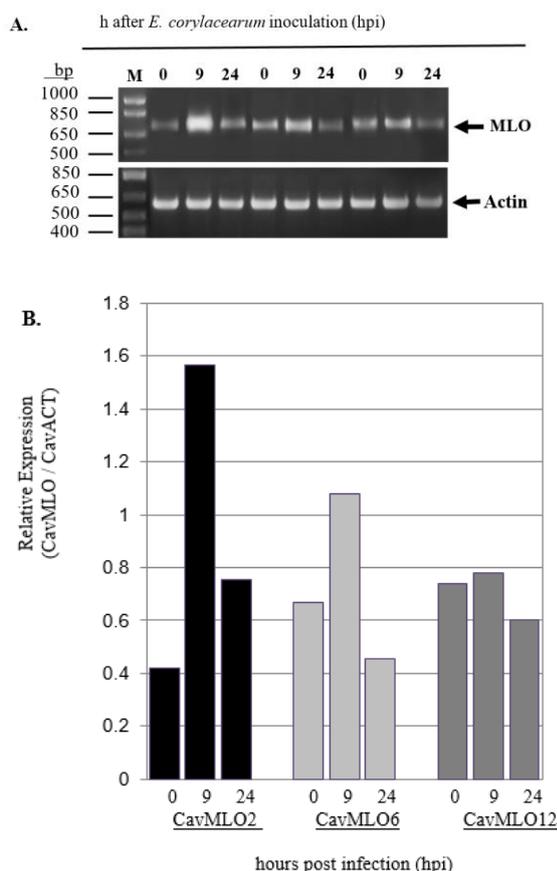


Figure 1. Expression analysis of the clade V *CavMLO* at transcript level, which was measured by semi-quantitative RT-PCR at three time points: 0-hpi (hours post inoculation), 9 hpi and 24 hpi in hazelnut leaves when exposed to *E. corylacearum*. (A.) *CavMLO* transcript accumulation in hazelnut leaves upon exposure to *E. corylacearum*. RT-PCR products from different time points were separated on a 1 % agarose gel. M represents 1 kb plus DNA size marker. A total of three leaves were collected for each time point and pooled for RNA isolation. The RT-PCR reaction was performed using *CavMLO* primer sets and yielded different amounts of the same size fragment (720 bp). Amplification of the reference *CaACT* gene using a pair gene-specific primers resulted in a 589 bp fragment. (B.) Transcript accumulation was measured as band intensity of amplified fragments using Image J software. The relative expression of *CaMLO* genes was calculated by normalizing the expression of the *CaMLO* genes against the housekeeping gene *CaACT*.

As a reference housekeeping gene, a putative gene sequence of *C. avellana* L. *Actin* was obtained from GenBank by blasting the *Arabidopsis Actin2* gene, *AtACT2* (GenBank ID: AY096381.1) against *Corylus avellana*, Transcriptome Shotgun Assembly (TSA) and then a gene specific primer pair was designed. The primer pair, *CavACT-F* and *CavACT-R* was used to amplify a fragment of the hazelnut *Actin* (*CavACT*) coding sequence as a reference housekeeping gene for relative quantification of hazelnut *MLO* genes. A 50 μ l RT-PCR reaction was set up and performed at 94°C for 3 min; 35 cycles at 94°C for 1 min, 55°C for 1 min, 72°C for 1 min and final extension at 72°C for 10 min for clade V *CaMLO* and *CavACT* cDNA amplification. PCR products were visualized by 1 % agarose gel electrophoresis and sequenced for confirmation. RT-PCR products were quantified by measuring the band intensity using Image J software (<https://imagej.nih.gov>). The relative transcript abundance of the three, clade V hazelnut genes was assessed using *Actin* as the reference gene for target normalization. The primers used in the experiments were listed in Table 1.

Results and Discussions

Erysiphe corylacearum has severely affected hazelnut fields in the Black Sea Region of Türkiye. Since none of the hazelnuts grown in Türkiye have been reported to be genetically resistant to powdery mildew pathogens, control of this pathogen is currently achieved through the application of fungicides (Lucas et al., 2018). The possibility of emergence of races resistant to fungicides has increased interest in the development of new hazelnut varieties with improved genetic resistance to powdery mildew. Thus, the hazelnut *MLO* homologues responsible for mediating susceptibility to *E. corylacearum* have been identified in *C. avellana* cv. Tombul by next-generation whole genome sequencing (WGS) (Lucas et al., 2021). Before Lucas et al. (2021) published their results on the identification of target genes, including *MLOs*, for hazelnut crop improvement using *C. avellana* cv. Tombul WGS data, we also identified clade V hazelnut *MLO* sequences that would be responsible for susceptibility in hazelnuts using information from the NCBI database, *Corylus avellana*, Transcriptome Shotgun Assembly (TSA), BioProject: PRJNA316492 (Kavas et al., 2019). Our results were similar to previous study in terms of phylogenetic analysis showing that *MLOs* named *CavMLO2*, *CavMLO6* and *CavMLO12* (Lucas et al., 2021) contain all sequence signatures that are considered diagnostic for *MLOs* and grouped in clade V. As shown in Table 1, two different IDs were used for the same gene from two different projects in NCBI [TSA (BioProject: PRJNA316492) and WGS (BioProject: PRJEB31933; Assembly GCA_901000735.2)] and relevant publications to avoid confusion.

For the temporal expression profile, hazelnut leaves were sampled before and at 9 and 24 h post inoculation. The accumulation of *MLO* transcripts was determined by PCR on reverse-transcribed total RNA using gene-specific primers. Amplification specificity was checked for each primer pair such that each primer pair generated a single amplification band with no non-specific products. Primer pairs for *MLO* genes amplified a 720 bp *MLOs*-specific fragment from cDNA templates (Table 1; Figure 1a). Amplified *MLO* fragments were confirmed by sequencing. The sequencing results showed some discrepancies from the source used to design the primer sets (BioProject: PRJNA316492). At the coding sequence (CDS) level, the sequenced fragments showed almost 100% similarity to those reported by Lucas et al. (2021), after delineating exon/intron boundaries using full length CDS from BioProject: PRJNA316492.

As a reference, the coding sequence of the *C. avellana* L. *Actin* gene was identified by blasting the *Arabidopsis Actin2* gene, *AtACT2* (GenBank ID: AY096381.1), which is commonly used as a reference for qRT-PCR reactions. The putative hazelnut *Actin* (GenBank ID: GGSA01044805.1), showed 84.1 % and 92.8% identity to *Arabidopsis ACT2* at the nucleotide and amino acid levels, respectively. *CavACT-F* and *CavACT-R* primers were designed and used to amplify the 589 bp fragment of the hazelnut *Actin* gene (*CavACT*) coding sequence. The amplified *CaACT* gene fragment was confirmed by sequencing. It was identical to the sequence obtained from WGS data. Only three base pair differences were identified between the sequences from TSA (BioProject: PRJNA316492) and WGS (BioProject: PRJEB31933) data.

The relative expressions of *CavMLO2*, *CavMLO6* and *CavMLO12* were determined using semi-quantitative RT-PCR (Figure 1). Gene expression analysis revealed that *CavMLO2* and *CavMLO6* transcript levels were upregulated more than 3- and 1.5-fold, respectively at 9 hpi (Figure 1b). In contrast, no significant difference was observed in *CavMLO12* transcript abundance at any time compared to the transcript abundance before inoculation. The results showed that *CavMLO2* and *CavMLO6* could play an important role in susceptibility during interactions between hazelnut plant and powdery mildew pathogen and provide useful information to study mechanisms of susceptibility to powdery mildew.

CavMLO2 and *CavMLO6* were anticipated as PM susceptibility genes in hazelnut, the discovery of loss-of-function mutations leading to resistance in these genes of wild and other cultivated accessions could be useful in breeding for the development of resistant hazelnut germplasm. The other method of acquiring powdery mildew resistance using this information could be gene editing such as CRISPR/Cas9 (Wan et al., 2020). Gene editing is a technique of targeted gene manipulation. Therefore, the breeding problem arises from crossing mutants and economically important varieties can be eliminated.

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Supplementary File: Sequence Alignments

Figure S1. Sequence alignment of the putative *Corylus avellana* actin gene (*CavACT*) from the TSA (BioProject: PRJNA316492) in the NCBI database with the *Arabidopsis thaliana* actin gene (*AtACT2*) from the TAIR database for comparison.

	1	11	21	31	41	51	61	71	81	91
CavACT	ATGGCCGATGCCGAGGATATTCAGCCCTTGTGTTGTGACAATGGAAC	TGCAATGGTGAAGGCTGGTTTGGCTGGTATGATGCTCCAGGGCAGTGTTC								
AtACT2	ATGGCTGAGGCTGATGATATTCACCAATCGTGTGTGACAATGGTACCG	TATGGTGAAGGCTGGAATTTGCAGGAGATGCTCCAGGGCTGTTTTTC								
Consensus	atggc ga gc ga gatattca cc t gt tgtgacaatgg ac gg atggtgaaggctgg	tttgc gg gatgatgctcccagggc gt tttc								
	101	111	121	131	141	151	161	171	181	191
CavACT	CTAGTATTGTGGTAGGCCCCCTCACACTGGTGTATGGTTGGGATGGGCAAAA	AGATGCTTATGTTGGTGAAGCTCAATCCAAGAGGGTATTCT								
AtACT2	CCAGTGTGTGTTGGTAGGCCAAGACATCATGGTGTCTATGGTTGGGATGAA	CCAGAAAGGATGCATATGTTGGTGAAGCAATCCAAGAGAGGATTCT								
Consensus	c agt ttgt ggtaggcc g ca tgggtgt atggttgggatg cca aa gatgc	tatggttggatgaagc caatccaagag ggtattct								
	201	211	221	231	241	251	261	271	281	291
CavACT	TACCTTGAAATATCCTATTGAGCATGGTATTGTCACTAATGGGATGACATGG	AAGATGCGCATCACAAATTTCTACAATGAGCTTCGAGTTGCTCCT								
AtACT2	TACCTTGAAATATCCTATTGAGCATGGTATTGTAGCAACTGGGATGATATGG	AAAAGATCTGGCATCACAAATTTCTACAATGAGCTTCGATATTGCTCCT								
Consensus	taccttgaa taccctattgagcatggt ttgt ag aa tggatga atgga aagatc	tggcatcacaa tttctacaatgagcttcgatattgctcct								
	301	311	321	331	341	351	361	371	381	391
CavACT	GAAGAGCACCCAGTGTCTTCTCACTGAAAGCTCCTCTCAACCTTAAGGCC	AACAGAGAAAGATGACTCAAATCATGTTTGAGACCTTCAA	TGTGCTGCCA							
AtACT2	GAAGAGCACCCCTGTTCTTCTTACCAGGCTCCTCTTAACCCAAAGGCC	AACAGAGAAAGATGACTCAAATCATGTTTGAGACCTTAACTCTCCGCTA								
Consensus	gaagagcacc gt cttct ac ga gctcctct aacc aaggccaacagaga	aagatgactcaaatcatgtttgagacctt aa cc gc a								
	401	411	421	431	441	451	461	471	481	491
CavACT	TGTATGTGTGATATCCAGGCTGTTCTCTCCCTGTATGCCAGTGGTCTGTA	CAACTGGTATTGTGCTGGATCTGGTGTGAGTTCACACTGTGCCAAT								
AtACT2	TGTATGTGCGCATCCAAAGCTGTTCTCTCTTGTACGCCAGTGGTCTGTA	CAACTGGTATTGTGCTGGATCTGGTGTGAGTTCACACTGTGCCAAT								
Consensus	tgtatgt gc atcca gctgtctctcc tgyta gccagtggtcgtacaac	ggtattgtgctggattcgtggtggtgty tcaactgtgccaat								
	501	511	521	531	541	551	561	571	581	591
CavACT	CTATGAAAGGATGACCCTCCACATGCCATCCTACGTTTGACACTTGGCTGG	TCTGATCTCACTGACGCTTTGATGAAGATTCTCACTGAGAGAGGGTAT								
AtACT2	CTACGAGGTTCTCTCTTCTCCTCATGCCATCCTCCGCTTTCACCTTGGTGG	ACCTTACTGATTACCTCATGAAGATCTTACAGAGAGAGGTTAC								
Consensus	cta ga gg t c ct cc catgccatcct cgt t gaccttggctgg cgtga ct	actga t atgaagat ct ac gagagagg ta								
	601	611	621	631	641	651	661	671	681	691
CavACT	ATGTTTACCACCCTGCCGAAACGGGAAATGTCCCTGACATGAAGGAGAAGCT	TGCATATGTTGGCCCTTGACTATGAGCAGGAACTTGAGACTGCCAAGA								
AtACT2	ATGTTTACCACAAACAGCAGAGCGGAAATGTAAAGACATCAAGGAGAAGCT	TCTCTTTGTTGCTGTTGACTACGAGCAGGAGATGGAACCTCAAAGA								
Consensus	atgttcaccac ac gc ga cgggaaattgt g gacat aaggagaagct c t	tgttgc ttgacta gagcagga t ga ac c aaga								
	701	711	721	731	741	751	761	771	781	791
CavACT	GCAGCTCCTGTTGAGAAGAACTATGAATTGCCTGATGGCAAGTCATCACAA	TCCGAGCTGAGAGATTCCCTTGCCCCAGAAAGTCTCTTCCAGCCATC								
AtACT2	CEAGCTCTTCCATCGAGAAGAACTATGAATTAACCGATGGCAAGTCATCAC	GAATGGTGTGAGAGATTCAGATGCCCCAGAAAGTCTTGTCCAGCCCTC								
Consensus	cagctc tc t gagaagaactatgaatt cc gatgg caagtcatcac at gg	gctgagagattc g tggccagaagtc t ttccagcc tc								
	801	811	821	831	841	851	861	871	881	891
CavACT	GCTGATTGGAATGGAAGCTGGTGGAAATCCACGAGACCACCTACAACCT	TATCATGAAATGTGACGTGGATATCAGAAAGGATCTTACGGAAACATTGTT								
AtACT2	GTITGTGGAAATGGAAGCTGCTGGAATCCACGAGACAACCTATAACTCAAT	CATGAAATGTGATGTGGATATCAGAAAGGATCTGTACCGTAACATTGTTG								
Consensus	g t t ggaatggaagctgctggaatccacgagac accta aactc atcatgaa	tgtga gttgatcatcag aaggatct tacgg aacattgt								
	901	911	921	931	941	951	961	971	981	991
CavACT	CTCAGTGGTGGCTCAACCATGTTCCAGGTAITGCTGACCGGATGAGCAA	GGAGATCACTGCTTTGGCCCAAGCAGCATGAAGATTAAGGTTGTGGCAC								
AtACT2	CTCAGTGGTGGAAACCATATGTTCTCAGGTATCGCTGACCTATGAGCAA	GAAGATCACTGCTTTGGCCCAAGCAGCATGAAGATTAAGGTTGTGGCAC								
Consensus	ctcagtggtgg c ac atgttc caggtat gctgaccg atgagcaa ga atcac	gc cttgc ccaagcagcatgaagattaaggt gt gcac								
	1001	1011	1021	1031	1041	1051	1061	1071	1081	1091
CavACT	CACCAGAGAGGAAGTACAGTGTCTGGATCGGAGGATCAATCCTTGGCAT	CCCTCAGCACCTTCCAGCAGATGTGGATTTCCAAGGGCCGACTACGACGATC								
AtACT2	CACCTGAAAGGAAGTACAGTGTCTGGATCGGTGGTCCATTCTTGGCTCC	CTCAGCACATTCAGCAGATGTGGATTTCCAAGGGCCGAGTATGATGAGGC								
Consensus	cacc ga aggaagtacagtgctggatcggatcgaatc cttggc tccctcagca	attccagcagatgtggat tccaagggccgagtatgatgaggc								
	1101	1111	1121	1131	1141	1151	1161	1171	1181	1191
CavACT	TGGTCCATCTATTGTCCACAGGAAGTGCTTCTAA									
AtACT2	AGGTCCAGGAATCGTTCACAGAAAATGTTTCTAA									
Consensus	ggtcca at gt cacag aa tg ttctaa									

Figure S2. Sequence alignment of the putative *C. avellana* actin protein (CavACT) from the TSA (BioProject: PRJNA316492) in the NCBI database with the *A. thaliana* actin protein (AtACT2) the TAIR database for comparison.

	1	11	21	31	41	51	61	71	81
CavACT	MADAEDIQPLVCDNGTGMVKAGFAGDDAPRAVFP	SIWGRPRHTGVMVGMGQKDAYVVGDEAQS	KRGILTLKYP	IEHGI	VSNWDDMEKI	WHH			
AtACT2	MAEADDIQPIVCDNGTGMVKAGFAGDDAPRAVFP	SVWGRPRHGVMVGMNQKDAYVVGDEAQS	KRGILTLKYP	IEHGV	VSNWDDMEKI	WHH			
Consensus	ma a diqp vcdngtgmvkagfagddapravfps	vgrprh gvmvgm qkdayvvgdeaqskrgiltlky	piehg vsnwddmeki	whh					
	91	101	111	121	131	141	151	161	171
CavACT	TFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFN	VPAMYVAIQAVLSLYASGRITGIVLDSGDGVSHTVPIYEGYALPHAILRL							
AtACT2	TFYNELRIAPEEHPVLLTEAPLNPKANREKMTQIMFETFN	SPAMYVAIQAVLSLYASGRITGIVLDSGDGVSHTVPIYEGFSLPHAILRL							
Consensus	tfynelr apeehpvllteaplmpkanrekmtqimfetfn	pamyvaiqavlslyasgrttgivldsgdgvsh	twpiyeg yalphailrl						
	181	191	201	211	221	231	241	251	261
CavACT	DLAGRDLTDALMKILTERGYMFTTTAEREIVRDMKEKLAYVALDYEQ	LETAKESSSSVEKNYELPDGQVITIGAERFRCPEVLFQPSLIG							
AtACT2	DLAGRDLTDYLMKILTERGYMFTTTAEREIVRDIKEKLSFVAVDYEQ	EMETSRTSSIEKNYELPDGQVITIGAERFRCPEVLFQPSFVG							
Consensus	dlagrldtd lmkiltergymftttaereivrd kekl	va dyeqe et k sss eknypeldgqvitigaerfr	cevlfqps lig						
	271	281	291	301	311	321	331	341	351
CavACT	MEAAGIHETTYNSIMKCDVDIRKDLGNIVLSGGSTMFGIADRMSKEITALAPSSMKIKVVAPPERKYSVWIGGSILASLSTFQQMWIS								
AtACT2	MEAAGIHETTYNSIMKCDVDIRKDLGNIVLSGGTTFMFGIADRMSKEITALAPSSMKIKVVAPPERKYSVWIGGSILASLSTFQQMWIS								
Consensus	meaagihettynsimkcdvdirkdlygnivlsgg tmf	giadrmskeitalapssmkikvvapperkysvw	iggsilaslstfqqmwis						
	361	371	381	391	401	411	421	431	441
CavACT	KGEYDESGPSIVHRKCF								
AtACT2	KAEYDEAGPGIVHRKCF								
Consensus	k eyde gp ivhrkcf								

	1401	1411	1421	1431	1441	1451	1461	1471	1481	1491
ML02-GGSA010	-----ATCCAGAGCGATTAGGTTTGAAGGGACACGTCATTTGGGAGAAGGCACCTTAAGCTTCTGGACCAACACACCTGCCCTC									
ML02-Cav10g0	TGTTGTTGCATGTGTGACAGATCCAGAGCGATTAGGTTTGAAGGGACACGTCATTTGGGAGAAGGCACCTTAAGCTTCTGGACCAACACACCTGCCCTC									
Consensus	atccagagcgatttaggtttgcaagggacacgtcatttgggagaaggcacttaagcttctggaccaaacacacctgccctc									
	1501	1511	1521	1531	1541	1551	1561	1571	1581	1591
ML02-GGSA010	-----ATGTGGATAGT-----									
ML02-Cav10g0	ATGTGGATAGTAAGCAATTCITTCCTCCTCAGTTAAATGCAATAGAAATCCTAACAATTATGTTATTCAGATTGCTAATAATTCAAGCAATAATTCAAG									
Consensus	atgtggatagt									
	1601	1611	1621	1631	1641	1651	1661	1671	1681	1691
ML02-GGSA010	-----									
ML02-Cav10g0	CAGTAGGGCTTATAAGTAGGCTCTGCATAGTTCATCTTTTGTTCGGCAAGCGGACGACTCCTTAAGAGCTTTTACGTTTGCTGCTTAGATTGTTAG									
Consensus	-----									
	1701	1711	1721	1731	1741	1751	1761	1771	1781	1791
ML02-GGSA010	-----									
ML02-Cav10g0	TAATTCAAACAACAATAATAGAAATTTGGATCTGTTTAAAACTCACGCTCGTGCATCATGCTGAAATGTTGGAAAGCACAAAAATTAATTTTGAAT									
Consensus	-----									
	1801	1811	1821	1831	1841	1851	1861	1871	1881	1891
ML02-GGSA010	-----									
ML02-Cav10g0	CAATAAACTGCACACAAACTTTACAAGGGGACGTTAGATAGATCCAAATCCCTATCAATGGCTTTCCATTTCCGTAGAGCTAGGTAGAGAACTAAAAATC									
Consensus	-----									
	1901	1911	1921	1931	1941	1951	1961	1971	1981	1991
ML02-GGSA010	-----									
ML02-Cav10g0	TCTAGACTCTCCATATTCTATATTGTCTGAACGACCTCTTTAGTAGTACAAATATACACCATTAGATCAGAGGATTGATAAACTTTGCTTAGGAATAGT									
Consensus	-----									
	2001	2011	2021	2031	2041	2051	2061	2071	2081	2091
ML02-GGSA010	-----									
ML02-Cav10g0	GCTATTCGATCAGTTGCTTCCGCCCCAAAAATTAGAGTGTGAATCAGATTTAATTGAGTAATGATTACTAGTAATAATTAACGAACATAATTAAT									
Consensus	-----									
	2101	2111	2121	2131	2141	2151	2161	2171	2181	2191
ML02-GGSA010	-----									
ML02-Cav10g0	AAATTAATGGCTTTGGCTTCATTAATATTATTTCAAGTTGAACTCCATTATAGGATGTTGAAAGAAAGAACCCAAAGTACGTAATTTCTAAGGATATA									
Consensus	-----									
	2201	2211	2221	2231	2241	2251	2261	2271	2281	2291
ML02-GGSA010	-----									
ML02-Cav10g0	TCATGCATAGTTGATGTGTTTATGACGATTCAATAATGATGTGGGGGATTGACCACTTCAATCAGAACTAAGATTTTTACCGGTTTATTAGAGTA									
Consensus	-----									
	2301	2311	2321	2331	2341	2351	2361	2371	2381	2391
ML02-GGSA010	-----									
ML02-Cav10g0	TTCAGTTAGATATTCGTA AAAAAGTGAAAAAAGTAACTACTTTTCCACATTACACATGGAGCAGTTACCTAACAAAGGATACAAATTCAGGCAACAGAAAGAA									
Consensus	-----									
	2401	2411	2421	2431	2441	2451	2461	2471	2481	2491
ML02-GGSA010	-----									
ML02-Cav10g0	ACGGTCATAACACGGCAGTTAAAAAGAAAACGAGTAATAAACCTCTTACCGTGCATTTGACTTTTTTGAAGTGCATTTGGATTGCGTGAACAATGTTTCC									
Consensus	-----									
	2501	2511	2521	2531	2541	2551	2561	2571	2581	2591
ML02-GGSA010	-----TTGT									
ML02-Cav10g0	TACTCCAATATCTTAATTAATTAATTAACAGGGCATTTCITTTGCACGAACTCTGTTTTCACACTAATCTGTTTATTATTATTATTATTGTCAGGTTTGT									
Consensus	-----ttgt									
	2601	2611	2621	2631	2641	2651	2661	2671	2681	2691
ML02-GGSA010	-----TTCTTCAGGCAGTTTGTAGATCGGTTCCCTAAAGTTGATTACTTGGACTCTGCGACATGGATTTATCATGG									
ML02-Cav10g0	TTCTTCAGGCAGTTTGTAGATCGGTTCCCTAAAGTTGATTACTTGGACTCTGCGACATGGATTTATCATGGTAATCTTCTACTAATTAATTTGCGATTTC									
Consensus	-----ttcttcaggcagtttgttagatcggttccctaaagttgattacttggactctgcgacatggatttatcatgg									
	2701	2711	2721	2731	2741	2751	2761	2771	2781	2791
ML02-GGSA010	-----CACACTGGCACCTCAAAGTCACCAAGATTGACTTCCAAAAGTATATCA									
ML02-Cav10g0	AAAAAATAATGTTGTTATCTTCTTAATTTCTATGCAAAAATCAGGCACACTGGCACCTCAAAGTCACCAAGATTGACTTCCAAAAGTATATCA									
Consensus	-----cacactggcacctcaaagtcaccaagattgacttccaaaagtatatca									
	2801	2811	2821	2831	2841	2851	2861	2871	2881	2891
ML02-GGSA010	-----AGAGATCATTGGAGGAGGATTTCAAG									
ML02-Cav10g0	AGAGATCATTGGAGGAGGATTTCAAGGTTGTTGTGGGGATTAGGTTGGTCTTTTCGATTATGAATTAATATTATCTCCAGTTTATTGAAATTAGATAAT									
Consensus	-----agagatcattggaggaggatttcaag									
	2901	2911	2921	2931	2941	2951	2961	2971	2981	2991
ML02-GGSA010	-----									
ML02-Cav10g0	ATCGAGTTAGTTATATTAGAAGGATATTTTATCTATAAAAAAGTAAATGACAAAAATACCATTCCAATATAATTAAGTGGATATTATCTAGTTCAAAT									
Consensus	-----									

	3001	3011	3021	3031	3041	3051	3061	3071	3081	3091
ML02-GGSA010	-----									CCCACCGATCTGGTTTTTCG
ML02-Cav10g0	GAACTGGAGAGGATCTTGTTCCTCCATCACACCCTTATGTTCAAGTCTAACAATTAATCATTTTTTCTTTTCAATTTTCAG									CCCACCGATCTGGTTTTTCG
Consensus										cccaccgatctggttttttcg
	3101	3111	3121	3131	3141	3151	3161	3171	3181	3191
ML02-GGSA010	CTGTGGTATTCTTACTCTTTAACTACTCAGG									-----
ML02-Cav10g0	CTGTGGTATTCTTACTCTTTAACTACTCAGG									TGGGTAAAGAATAATTAATTTGAATCATGAGAGGATGAAAAATGTGAAAAGTTTCAGAACTTTTTTTTTT
Consensus	ctgtggtattcttactctttaactactcag									
	3201	3211	3221	3231	3241	3251	3261	3271	3281	3291
ML02-GGSA010	-----									CTGGAAATCTTATCTATGGCTGCCATTTATCCCATTGCTT
ML02-Cav10g0	TTTTTTTGACTAAGTTGCTTGTCTTGTTCAGG									CTGGAAATCTTATCTATGGCTGCCATTTATCCCATTGCTT
Consensus	ctggaaatcttactctatggctgccatttatcccattgctt									GTAAGCAAATTATATATCTCTCCTA
	3301	3311	3321	3331	3341	3351	3361	3371	3381	3391
ML02-GGSA010	-----									ATCATCTACTGTTGGGGACGAAA
ML02-Cav10g0	TCCATCACATGCTGATATAATATAATTATAGCAGCTAGCTAGCAGATGATCTAACGGCTAAATATGGCTGCAG									ATCATCTACTGTTGGGGACGAAA
Consensus										atcatcctactggtggggacgaaa
	3401	3411	3421	3431	3441	3451	3461	3471	3481	3491
ML02-GGSA010	CTACAGGTGATCATAACCAAAATGGCATTGAGAATCCAGGAGAGAGAGGTTGTGCAGGGGGTCCAGTGGTGCAGCCAGGTGACGA									ACTCTTCTGGT
ML02-Cav10g0	CTACAGGTGATCATAACCAAAATGGCATTGAGAATCCAGGAGAGAGAGGTTGTGCAGGGGGTCCAGTGGTGCAGCCAGGTGACGA									ACTCTTCTGGT
Consensus	ctacaggtgatcataaaccaaaatggcattgagaatccaggagagagaggttgtgcagggggtccagtgggtgcagccaggtgacga									ctctctggt
	3501	3511	3521	3531	3541	3551	3561	3571	3581	3591
ML02-GGSA010	TCAACCGCCCTCGCCTCACTCTACCTCATCAACTTTGTTCTCTTTCAG									-----
ML02-Cav10g0	TCAACCGCCCTCGCCTCACTCTACCTCATCAACTTTGTTCTCTTTCAG									GTTCCTTTTCCATAATCTTTGCCTTAATTTCTTACATAAAATACGCTAA
Consensus	tcaaccgccctcgccctcactctacccatcaactttgttctctttcag									
	3601	3611	3621	3631	3641	3651	3661	3671	3681	3691
ML02-GGSA010	-----									
ML02-Cav10g0	ATATTTAGCAAGACTCTTATACAACCTGCATACAATCTAATAATGTGGCTCGTGAATAATGATATTTAAGATTATTAAGATTATCACTAGCAGTGACGGAG									
Consensus										
	3701	3711	3721	3731	3741	3751	3761	3771	3781	3791
ML02-GGSA010	-----									
ML02-Cav10g0	CCAGAAATTACTATGGGGAGGGTCCAGGAGTCAAAAAAATTGTTACTAGGAGTCCGGTGGCTGATTTATTATTGTTATTATTATTATTATTATTATT									
Consensus	ccagaaattactatggggaggggtccaggagtcaaaaaaattgttactaggagtccggggctgattttattattgttattattattattattattatt									
	3801	3811	3821	3831	3841	3851	3861	3871	3881	3891
ML02-GGSA010	-----									
ML02-Cav10g0	CCTTAAAAATTTGTTGTTGTTAGGAATTGGAGAGGGGCCATGGCCAACCAATCTCCCTCCCTCCGCTCTTCATCACTAGTATAACAATCGTATAATA									
Consensus	ccttaaaaatTTGTTGTTGTTAGGAATTGGAGAGGGGCCATGGCCAACCAATCTCCCTCCCTCCGCTCTTCATCACTAGTATAACAATCGTATAATA									
	3901	3911	3921	3931	3941	3951	3961	3971	3981	3991
ML02-GGSA010	-----									
ML02-Cav10g0	ATTTTCATTGACATGTTACCTAGTATATATATACAGTCTACTAAATAATATTATTACTATTAATTTTACTTAATCCACCATCATAGTATGCTAATAATTCT									
Consensus	atTTTCATTGACATGTTACCTAGTATATATATACAGTCTACTAAATAATATTATTACTATTAATTTTACTTAATCCACCATCATAGTATGCTAATAATTCT									
	4001	4011	4021	4031	4041	4051	4061	4071	4081	4091
ML02-GGSA010	-----									AATGCCCTTTCAGCTTGCCTTTCTTTGTCATGGGCTTGG
ML02-Cav10g0	TTCCCATCTTTGCTTTTCCCGTTTCAG									AATGCCCTTTCAGCTTGCCTTTCTTTGTCATGGGCTTGG
Consensus	aatgccctttcagcttgcctttctttgtcatgggcttgg									GTAAGTACCATCATATATATAATATCCATGTCC
	4101	4111	4121	4131	4141	4151	4161	4171	4181	4191
ML02-GGSA010	-----									TATCAATTCCGGGTTGA
ML02-Cav10g0	CTATATATGCTTAAACTTCAATAGTACGTGTGAAAAATTAATTAATAAGTAATATTGATAATTACTGTTATGATTTTCAG									TATCAATTCCGGGTTGA
Consensus	ctatataTgctTAAACTTCAATAGTACGTGTGAAAAATTAATTAATAAGTAATATTGATAATTACTGTTATGATTTTCAG									tatcaattccgggttga
	4201	4211	4221	4231	4241	4251	4261	4271	4281	4291
ML02-GGSA010	AATCTTGTTTCCACGACCATACTGAGGATATTGTCATTAGAAATCTCAATGGGG									-----
ML02-Cav10g0	AATCTTGTTTCCACGACCATACTGAGGATATTGTCATTAGAAATCTCAATGGGG									TACGCTCTCATTAATTATCACTTTCTATATTTATGATCTGAAATTA
Consensus	aatcttgtttccacgaccatactgaggatattgtcatttagaaatctcaatgggg									
	4301	4311	4321	4331	4341	4351	4361	4371	4381	4391
ML02-GGSA010	-----									GTCCTCATACAAATTTTGTGCAGCTACGTAACCTCTCCACTCTATGCCCT
ML02-Cav10g0	ATTAATTCAAATGTTCTAATACAATTAATAAATGTTGGCTCTTTATCAGG									GTCCTCATACAAATTTTGTGCAGCTACGTAACCTCTCCACTCTATGCCCT
Consensus	atTAATTCAAATGTTCTAATACAATTAATAAATGTTGGCTCTTTATCAGG									gtcctcatacaaatTTTgtgcagctacgtaacctctccactctatgccct
	4401	4411	4421	4431	4441	4451	4461	4471	4481	4491
ML02-GGSA010	TGTAACACAG									-----
ML02-Cav10g0	TGTAACACAG									GTAACAAAATTAATTTTGTGATCAAAATATGCATAGAAAGAGTTCAACATTACATGCAGATCGAGCCTGATTTCTCTTTTGTATGATA
Consensus	tgtaacacag									
	4501	4511	4521	4531	4541	4551	4561	4571	4581	4591
ML02-GGSA010	-----									ATGGGTTTCATCCATGAAACCAACCATATTCAACGAAAAGAGTGGCGGGCTCTACGCAACTGGCACCACACGGCGAGGAAGAACCTAAAGCAG
ML02-Cav10g0	TGAGTAG									ATGGGTTTCATCCATGAAACCAACCATATTCAACGAAAAGAGTGGCGGGCTCTACGCAACTGGCACCACACGGCGAGGAAGAACCTAAAGCAG
Consensus	atgggtttcacatccatgaaaccaaccatattcaacgaaaagagtggcgggctctacgcaactggcaccacacggcgaggaagaacctaaagcag									

	4601	4611	4621	4631	4641	4651	4661	4671	4681	4691
ML02-GGSA010	AACAAAGGGCTCGGTGACGGGGACCCCGATGTCTAGCAGACCCGCCACCCCGTCCCACCACATGTCCCCGGTTCACCTCCTCCGTCACTACCGGAGCGAGG									
ML02-Cav10g0	AACAAAGGGCTCGGTGACGGGGACCCCGATGTCTAGCAGACCCGCCACCCCGTCCCACCACATGTCCCCGGTTCACCTCCTCCGTCACTACCGGAGCGAGG									
Consensus	aacaagggctcgggtgacggggaccccgatgtctagcagacccgccaccccggtcccaccacatgtccccggttcacctcctccgtcaactaccggagcgagg									
	4701	4711	4721	4731	4741	4751	4761	4771	4781	4791
ML02-GGSA010	CGGACAGCCTCCACACATCACCGAGACGATCCAATTTTGACATTGAGCATTGGGAAACTGAATCTCCGTCCCCCTCGCACCACCACCCTGGTCGGCGA									
ML02-Cav10g0	CGGACAGCCTCCACACATCACCGAGACGATCCAATTTTGACATTGAGCATTGGGAAACTGAATCTCCGTCCCCCTCGCACCACCACCCTGGTCGGCGA									
Consensus	cggacagcctccacacatcacccgagacgatccaatTTTGacattgagcattgggaaactgaatctccgtccccctcgaccaccaccactggtcggcgga									
	4801	4811	4821	4831	4841	4851	4861	4871	4881	4891
ML02-GGSA010	GGGTTTCATCCTCGCATCACAAACGGCCACCAAAATGGGCCAAAAGGAATTATATTGAGTATGATGTAAAAGAGCTGAACCTCAAGTCAAGTGGCTCCGCTTCCA									
ML02-Cav10g0	GGGTTTCATCCTCGCATCACAAACGGCCACCAAAATGGGCCAAAAGGAATTATATTGAGTATGATGTAAAAGAGCTGAACCTCAAGTCAAGTGGCTCCGCTTCCA									
Consensus	gggttcacctcgcacacaaacggccaccaaaatgggccaaggaattatattgagtatgatgtaaaagagctgaacctcaagtcaagtggtccgcttcca									
	4901	4911	4921	4931	4941	4951	4961	4971	4981	4991
ML02-GGSA010	CAAACAGACCGCTTGGAAACCCAAATTGATATCGGCCACCAAAAGGACTTTTCATTGATAAAAAGAACAAAGTTTGTGA									
ML02-Cav10g0	CAAACAGACCGCTTGGAAACCCAAATTGATATCGGCCACCAAAAGGACTTTTCATTGATAAAAAGAACAAAGTTTGTGA									
Consensus	caaacagaccgcttggaaacccaaattgatatcgggccaccaaaaggacttttcatttgataaaaagaacaagtttgtga									

Figure S5. Sequence alignment of the putative *C. avellana* *MLO6* gene(*CavMLO6*) from the TSA (BioProject: PRJNA316492) and the WGS (BioProject: PRJEB31933; Assembly GCA_901000735.2) in the NCBI database. Overlapping regions were exons and highlighted in yellow.

	1	11	21	31	41	51	61	71	81	91
ML06-GGSA010	ATGGCGGTCGCGGAGAAAGGAAAGTACAATGGAGGAAACTTCAACATGGGCAGTTGCGGCGGTGTGCTTCGCTTTGCTTGCCGTTTCAATCTTCATTGAAC									
ML06-Cav07g1	ATGGCGGACAAAGCAGAAGGAAAGTACAATGGAGGAAACTTCAACATGGGCAGTTGCGGCGGTGTGCTTCGCTTTGCTTGCCATTCAATCTTCATTGAAC									
Consensus	atggcgg c g agaaggaagatacaatggaggaacttcaacatgggcagttgcgcggtgtgcttcgctttgcttgccgtttcaatcttcattgaac									
	101	111	121	131	141	151	161	171	181	191
ML06-GGSA010	ATATTCTTCATTCTATTGGAAAG-----									
ML06-Cav07g1	ATATTCTTCATGCTATTGGAAAGGTAAGCTGCTCTGCTCTGCTCAGCTCTCTGTTTTGTTGTTGTTGTTAAATTAATGCTGAAATCATTTCTTGATT									
Consensus	atattcttcat ctattggaaag									
	201	211	221	231	241	251	261	271	281	291
ML06-GGSA010	-----TGGCTAAAAACAACAACAAAACGAGCTCTTTACGAAGCGCTTGAAAAGATCAAAGCAG-----									
ML06-Cav07g1	CCTTTAATAGTGGCTAAAAACAACAACAAAACGAGCTCTTTACGAAGCGCTTGAAAAGATCAAAGCAGGTATCTCTAGATTCTTACCTCACACATTAAG									
Consensus	tggctaaaa acaaacacaacagagctctttacgaagcgcttgaaaagatcaaagcag									
	301	311	321	331	341	351	361	371	381	391
ML06-GGSA010	-----AGCTTATGCTGTTGGGATTTCATATCCTTGCTCCTGACAGTGT									
ML06-Cav07g1	ATGATCGATCAGGATTCAGTCGCCTAACCATTTTTCTTCATGGTTTTTTTGGGAGAGCTTATGCTGTTGGGATTTCATATCCTTGCTCCTGACAGTGT									
Consensus	agcttatgctggtggattccatctctgctcctgacagtgt									
	401	411	421	431	441	451	461	471	481	491
ML06-GGSA010	TACAAGATCCCATTTCTACCATATGCATACCACAAGAGAGTCGGAGCCACGTGGCATCCCTGTGAAACGGTGAAGAATGGGACGACCAAAAAGATTCTGG									
ML06-Cav07g1	TACAAGATCCCATTTCTACCATATGCATACCACAAGAGAGTCGGAGCCACGTGGCATCCCTGTGAAACGGTGAAGAATGGGACAAACCAATAGATTCTGG									
Consensus	tacaagatcccatttctaccatatgcataccacaagagagtcggagccacgtggcatccctgtgaaacggtgaagaatgggac accaa a agattctgg									
	501	511	521	531	541	551	561	571	581	591
ML06-GGSA010	AGATTCCGAGGATTCTGAGGACAGCAATGGTCGGAAACTGCTCCAATTTTTGGATTCTGGCTTCTCTGCTCGTCGGAGATTAGCTACAAAAGGATACGAC									
ML06-Cav07g1	AGATTCCGAGGATTCTGAGGACAGCAATGGTCGGAAACTGCTCCAATTTTTGGATTCTGGCTTCTCTGCTCGTCGGAGATTAGCTACAAAAGGATACGAC									
Consensus	agattccgagatttctgaggacagcaatggtcggaaactgctccaatTTTTGGATTCTGGCTTCTCTGCTCGTCGGAGATTAGCTACAAAAGGATACGAC									
	601	611	621	631	641	651	661	671	681	691
ML06-GGSA010	AAGTGCACAAAAATG-----									
ML06-Cav07g1	AAGTGCACAAAGAAAATGTAATTTCTTTCTTTCTTTCTTTCTTTCCAAATGGGTATTACCAATGAAGATCTAATGATTTAATCCATGGAATAATCA									
Consensus	aagtgcac aaaaatg									
	701	711	721	731	741	751	761	771	781	791
ML06-GGSA010	-----GAAAAGTGGCTTTCATGTCTGCATATGCAATTCACCAGCTCCATGTGTTTCATCTTCGCTTTGGCCGTTTTTCATGTGA									
ML06-Cav07g1	TTTGGGTTGCCTATTTTGCAGGAAAAGTTGCTTTCATGTCTGCATATGCAATTCACCAGCTCCATGTGTTTCATCTTCGCTTTGGCACTTTTTCATGTGA									
Consensus	gaaaagt gcttctcatgtctgcatatgc attcaccagctccatgttctcatctctgctttggccg ttttctcatgtga									
	801	811	821	831	841	851	861	871	881	891
ML06-GGSA010	TTTTTCCATACTACCCTGGCTTTGGGCAGAACGAAG-----									
ML06-Cav07g1	TTTTTTGCATACTACCCTTGCTTTGGGCAGAACGAAGGTACCCTTTTACCCTTTCTCCTTCTATGGAGATCTATAAATTTCTTCTTTTGAATTTGTGA									
Consensus	tttt t catactcacctt gctttgggcagaaacgaag									
	901	911	921	931	941	951	961	971	981	991
ML06-GGSA010	-----ATGAGAAGATGGAAGGCTTTGGGAGGATGAAACAAGAACAATTGAATATCAATATCATAATG-----									
ML06-Cav07g1	GATTCTAAATCCCTCTTTGAATTCAGATGAGAAGATGGAAGGCTTTGGGAGGACGAAACGAGAACAATTGAATATCAATATCATAATGTAACCTCTCTT									
Consensus	atgagaagatggaag ttgggagga gaaac agaacacttgaatatcaatatcataatg									
	1001	1011	1021	1031	1041	1051	1061	1071	1081	1091
ML06-GGSA010	-----									
ML06-Cav07g1	TGACTTTCAAACCATCTACTCAGCTCTCTAAATCAATTGCTTTTCCACTTAATTTAAATTAATACTTATCCGTTTGCTGACGTGGAACCTAAAA									
Consensus										
	1101	1111	1121	1131	1141	1151	1161	1171	1181	1191
ML06-GGSA010	-----									
ML06-Cav07g1	TGCACATCGGCTCTTCCAAAATTTCTTTAAAAAAAAGTGTGTTGTTAAGAGATTATGATTAATTAGTAAAATGATTAAGAAAAAATATACCCTCCAAT									
Consensus										
	1201	1211	1221	1231	1241	1251	1261	1271	1281	1291
ML06-GGSA010	-----									
ML06-Cav07g1	CTAATTTGTTATTAACCACTTTTTAATTATTTACTAATTATAAAITAITACGTCCATTTGTA AAAACATTATAGTCAATTTGCCAACATTTTATGGA									
Consensus										
	1301	1311	1321	1331	1341	1351	1361	1371	1381	1391
ML06-GGSA010	-----									
ML06-Cav07g1	CTTGGTCAGTGTCTACAGAGGAATCAGGCACCCCTCTTTCTTGA AAAAGTGATAACAACAACAATAAATTTACCAAGAGTGACTCACATTGTCAAC									
Consensus										

	1401	1411	1421	1431	1441	1451	1461	1471	1481	1491
ML06-GGSA010	-----									
ML06-Cav07g1	TGATTAGATGACTTTGCATCCCATCATCTTTCTTTATTTATTTTGTCTTAATGCAAAGTCAACTAATAGATGACTTTGTAAATTCCTTT									
Consensus										
	1501	1511	1521	1531	1541	1551	1561	1571	1581	1591
ML06-GGSA010	-----									
ML06-Cav07g1	TGTGACCAAATCTGTATGAAAAATCTTTAAATTTTTTTTAAAAAATTTGATAGTGTGGTGAAGAGATCATATGGACTTCAAGGGGGTGACA									
Consensus										
	1601	1611	1621	1631	1641	1651	1661	1671	1681	1691
ML06-GGSA010	-----									
ML06-Cav07g1	TATGCTTATGGAATGATTTATTTGATGCAGATCCAGAGAGGTTTAGGTTTGCAAAGGAACTTCATTTGGGCGAAGGCATATGAGCTTCTGGAGCAAG									
Consensus	atcca agaggttttaggtttgcaa ggaacttcatttggggaagggcatatgagcttctggagcaag									
	1701	1711	1721	1731	1741	1751	1761	1771	1781	1791
ML06-GGSA010	-----									
ML06-Cav07g1	TCAACGGTTTCTCTTTGGGTGGT-----CAGTAATGTCTCATCAGGATTATGTGACTTTTACAATCATAAATTAACAAAGACTCAGGAATTAAGTTGATTTGGAT									
Consensus	tcaacggtttctctttgggtgggt									
	1801	1811	1821	1831	1841	1851	1861	1871	1881	1891
ML06-GGSA010	-----									
ML06-Cav07g1	GATTTGTTACATAAAATTTACTCTGTATATTTATAATACGTACCTAACGTGCTTTCAAAATATGCGAATTTGACCAATATTTTAAAGCATAATTTTTTTTTT									
Consensus										
	1901	1911	1921	1931	1941	1951	1961	1971	1981	1991
ML06-GGSA010	-----									
ML06-Cav07g1	TTTTTTTTGTGTTTGAACCAATTATTTTGTTCAACTGCACITTTAAACGGGATACTTTAGGCAATTTTGTTTAAAAATGCATATTTATCTTGCAAAATTT									
Consensus										
	2001	2011	2021	2031	2041	2051	2061	2071	2081	2091
ML06-GGSA010	-----									
ML06-Cav07g1	GCAGGTCAAACGCATTCTTTAGGTAATTTTCAAAATGATCATTTTGAAGTGGCCGACTGACTGGTTGCCTCATCAAAGTTTGAGTAGGCCCATCAAT									
Consensus										
	2101	2111	2121	2131	2141	2151	2161	2171	2181	2191
ML06-GGSA010	-----									
ML06-Cav07g1	CTTCTGTCTGCATCACCACAAGTTTCTAAAAGTGACTAGTTTAAAGTATAATAGGACGTCCAAGTACCTTTTCTTAATAACGAGAACTTGTGTTTATT									
Consensus										
	2201	2211	2221	2231	2241	2251	2261	2271	2281	2291
ML06-GGSA010	-----									
ML06-Cav07g1	TTTCAATTTTGAACITTAAGGGCATAAAGAGTTGTTGTGTACACTTGTTTGAAAGACCTTTTCTCCTCCTTATCAGGTGTGTTTCTTCCAGACAAT									
Consensus	gtgtttcttcagacaat									
	2301	2311	2321	2331	2341	2351	2361	2371	2381	2391
ML06-GGSA010	-----									
ML06-Cav07g1	TCGTCAAACCGTTACTAAGGTTGATTACCTTACGCTGAGACATGGATTTATTGTGG-----TCGTCAAGAACGTTACTAAGGTTGATTACATTACACTTAGACATGGATTTATCATGGTACGTTTAAITTAGAAATAATGCTAGAAATCACACTTTTATCC									
Consensus	tcgtca aac gttactaaggttgattac ttac ct agacatggatttat tgg									
	2401	2411	2421	2431	2441	2451	2461	2471	2481	2491
ML06-GGSA010	-----									
ML06-Cav07g1	TACAACATTTTATTTTGTGATGTGATGAACCAATGCCAATCAGTCTTGGTTAAAAATAAAAAATTCAAAGGTTGATTGTGCACCTTGGGATTCCAATT									
Consensus										
	2501	2511	2521	2531	2541	2551	2561	2571	2581	2591
ML06-GGSA010	-----									
ML06-Cav07g1	CACATTGATAATTGAAGCTCCAATGTTATGTGACTTAAGGCACACTTGGCCACCGAAAAGTGAAAATAAGTTTGATTTTCAAAAGTACATCAAGAGATCAC									
Consensus	cacacttggcacc gaaagtga aaagtgtgattttcaaaagtacatcaagagatcac									
	2601	2611	2621	2631	2641	2651	2661	2671	2681	2691
ML06-GGSA010	-----									
ML06-Cav07g1	TTGAAGAGGAATTTAAAGTTGTGGTGCAGATCAG-----TTGAAGAGGAATTTAAAGTTGTGGTGCAGATCAGGTTGGTCTCAAGAACTTAAAGGGGTTGCTTCTTTGATTGATTTCAATATCTTAAATTTCTA									
Consensus	ttgaagagga ttaaagttgtggtg agatcag									
	2701	2711	2721	2731	2741	2751	2761	2771	2781	2791
ML06-GGSA010	-----									
ML06-Cav07g1	ACCTTACTTTTCATGTGCAGTCCAATCATATGGGGCTTTGCAGTGTATTTCCTACTGTCCAATGCATATAG-----TCCAATCATATGGGGCTTTGCAGTGTATTTCCTACTGTCCAATGCATATAG									
Consensus	tccaatcatatggggctttgcagtgatttccctactgtccaatgcatatg									
	2801	2811	2821	2831	2841	2851	2861	2871	2881	2891
ML06-GGSA010	-----									
ML06-Cav07g1	TGTATCAGTTGAGTGAAGACTCGAACAGTTGATTTCTGGTATTAACCAACAGAGTCCGACATTCGAGCTAATCTCGGAGCCCGATTCTCATTATTTTC									
Consensus										

	2901	2911	2921	2931	2941	2951	2961	2971	2981	2991
ML06-GGSA010	-----									ATGGCATTCTTCTCTATGGCTACCA
ML06-Cav07g1	TGAGTCCAAATTTATCATAGATTGCCTTGGGGACTACAAGTACTGACTAAGACATGTTTCCCTGTACGTGTCGACAGG									ATGGCATTCTTCTCTATGGCTACCA
Consensus	atggcattcttctctatggctacca									
	3001	3011	3021	3031	3041	3051	3061	3071	3081	3091
ML06-GGSA010	TTTGTACCATTGTTT-----									
ML06-Cav07g1	TTTGTACCATTGTTT									GTAAGCTCCAAAACAGAGACAAACTTGTTCCTACATTCTTTTATCTGGGTTGGAGCTCTTTATACAATCTAAGCATTGGGTT
Consensus	tttgtaccattgttt									
	3101	3111	3121	3131	3141	3151	3161	3171	3181	3191
ML06-GGSA010	-----									ATAATCCTGTTGGTGGGGACAAAGCTACAAGTAATAATTACAAAAATGGGGCTA
ML06-Cav07g1	GTTGGTTTAATAGAAAGATTCATGTAGTTTGCTGTGACTTTTACAGATAAATCCTGTTGGTGGGGACAAAGCTACAAGTGATAAATTACAAAAATGGGGCTA									
Consensus	ataatcctgttggggtgggacaaagctacaagtataattacaaaaatggggcta									
	3201	3211	3221	3231	3241	3251	3261	3271	3281	3291
ML06-GGSA010	AGAATTC AAGAGAGAGAGATGTGATT AAGGGTACACCTGTGGTACAGCCAGGTGATGACCTCTTCTGGTTTGGACGCCCTCGGTTCTCTTTCTCA									
ML06-Cav07g1	AGAATTC AAGAGAGAGAGATGTGATC AAGGGTACACCTGTGGTACAGCCAGGTGATGACCTCTTCTGGTTTGGACGCCCTCGGTTCTCTTTCTCA									
Consensus	agaatcaagagagaggagatgtgat aagggtacacctgtggtacagccaggtgatgacctcttctggtttggaagccctcggttctctctctctctca									
	3301	3311	3321	3331	3341	3351	3361	3371	3381	3391
ML06-GGSA010	TTCACTTCGTTCTCTTTTCAG-----									
ML06-Cav07g1	TTCACTTCGTTCTCTTTTCAG									GTCACAATTTCTCACATTCATCGATAAATTACATAAATAGTCTATCTGGGATACTAATTCTAACATCTTCTTTTGTCTTT
Consensus	ttcaacttctctctctttcag									
	3401	3411	3421	3431	3441	3451	3461	3471	3481	3491
ML06-GGSA010	-----									AATGCATTTCAACTGGCCCTCTTTGCTTGGGGTGTG
ML06-Cav07g1	GCCCTCTTAATTGCAGAAATGCATTTCAACTGGCCCTCTTTGCTTGGGGTGTG									GTAATTAGCCTTTCACCTTCTACTTATCTATTCTATCAATTTGGTGCA
Consensus	aatgcatttcaactggccctctttgcttgggggtgtg									
	3501	3511	3521	3531	3541	3551	3561	3571	3581	3591
ML06-GGSA010	-----									TATGAATTTGGCACAGATTCTTGCTTCCACGAA
ML06-Cav07g1	TGCTTAGAAGATGCCAACACTGCTTTTCCCTAACTTTCCGCCATATGTTTCTTCTCTTTTCAG									TATGAATTTGGCACAGATTCTTGCTTCCACGAA
Consensus	tatgaatttggcacagattcttgcctccacgaa									
	3601	3611	3621	3631	3641	3651	3661	3671	3681	3691
ML06-GGSA010	CGCACTGCAGATAAAGTTCATCAAACTCTCAATGGGG-----									
ML06-Cav07g1	CGCACTGCAGATAAAGTTCATCAAACTCTCAATGGGG									TGAGTTCTTATCAAITAATCCATATGCTGCTGCCATTGTTAAGATGTTATTATCTGGCTGATT
Consensus	cgcactgcagataaagttcatcaaaactctcaatgggg									
	3701	3711	3721	3731	3741	3751	3761	3771	3781	3791
ML06-GGSA010	-----									GTCATCATAAAGTTCTCTGCGATTATGTGACTTTGCCACTCTATGCTCTAGTGACTCAG
ML06-Cav07g1	AACATTAATTGCCACTTAATTTCTTCAGGG									GTCATCATAAAGTTCTCTGCGATTATGTGACTTTGCCACTCTATGCTCTAGTGACTCAGGTGAGACATGA
Consensus	gtcatcatacaagttctctgacgttatgtgactttgccactctatgctctagtgactcag									
	3801	3811	3821	3831	3841	3851	3861	3871	3881	3891
ML06-GGSA010	-----									ATGGGGTCTTCCATGAAGCCC
ML06-Cav07g1	TTACACATTAACACAACAAAACATGTTATGATAATTAACAACAACCTTGAGACTAATGATTCTTTGCTTTGATTGACAG									ATGGGGTCTTCCATGAAGCCC
Consensus	atgggggtcttccatgaagccc									
	3901	3911	3921	3931	3941	3951	3961	3971	3981	3991
ML06-GGSA010	ACCATCTTCAACGATGGAGTGGCGGATGCATTAAAGAGCTGGCATCGGACTGCCAGAAAGAACACAAGGCAAAAGCCATCATCTTCTGAGACAAATTCAC									
ML06-Cav07g1	ACCATCTTCAACGATCGAGTGGCGGATGCATTAAAGAGCTGGCATCGGACTGCCAGAAAGAACACAAGGCAAAAGCCATCATCTTCTGAGACAAATTCAC									
Consensus	accatcttcaacgat gagggtggcgatgcattaaagagctggcatcggactgccagaaagaacaagggcaaaagccatcatcttctgagacaaattcac									
	4001	4011	4021	4031	4041	4051	4061	4071	4081	4091
ML06-GGSA010	CATTITCAAGTAGGCCGGCTCTCCACGCACGGGATGTCCCTGTTCACTCTCTGCATAACTATCAGCACAGTAGCCTCGACAGCTTGCACACGTTCTCC									
ML06-Cav07g1	CATTITCAAGTAGGCCGGCTCTCCACGCACGGGATGTCCCTGTTCACTCTCTGCATAACTATCAGCACAGTAGCCTCGACAGCTTGCACACGTTCTCC									
Consensus	cattttcaagtaggccggcc ctcccacgcacgggatgtccctgttcaactctctgcataactatcagcacagtagcctcgacagcttgcacacgcttctcc									
	4101	4111	4121	4131	4141	4151	4161	4171	4181	4191
ML06-GGSA010	AAGAAAGTCAAATGTTGAGAATGATCATTAGGCGTGGTGGAGTTGGGATTCGGTAGGAAACAAATAGTGGAGAAGAAGATTCTTCGCATTATTCATAC									
ML06-Cav07g1	AAGAAAGTCAAATGTTGAGAATGATCATTAGGCGTGGTGGAGTTGGGATTCGGTAGGAAACAAATAGTGGAGAAGAAGATTCTTCGCATTATTCATAC									
Consensus	aagaaagtcaaattgttgaagaatgatcatttaggcgtggtggagttgggattccgtaggaaacaattagtgagaagaagattcttgcattatccatcac									
	4201	4211	4221	4231	4241	4251	4261	4271	4281	4291
ML06-GGSA010	AAAAAAGAAAGATTCTGTGCACTCTGAGCAGCAGCAAGAGAGGGAGATTCAAGAGCAAAGCCATTGCAATTGGCCGAAACACCGGGAGCCATCCGTACCC									
ML06-Cav07g1	AAAAAAGAAAGATTCTGTGCACTCTGAGCAGCAGCAAGAGAGGGAGATTCAAGAGCAAAGCCATTGCAATTGGCCGAAACACCGGGAGCCATCCGTACCC									
Consensus	aaaaaagaagattctgtgcaactctgagcagcagcaagagaggagattcaagagcaaaagccattgcaattggccgaaacacgggagccatccgtaccc									
	4301	4311	4321	4331	4341	4351	4361	4371	4381	4391
ML06-GGSA010	AACATGAAGTCAACAATAGTCTCTCGGAATTCACATTTCCGAGATGA									
ML06-Cav07g1	AACATGAAGTCAACAATAGTCTCTCGGAATTCACATTTCCGAGATGA									
Consensus	aacatgaagtcaaca tagtctctcggaattcacatttccgagatga									

Figure S6. Sequence alignment of the putative *C. avellana* *MLO12* gene (*CavMLO12*) from the TSA (BioProject: PRJNA316492) and the WGS (BioProject: PRJEB31933; Assembly GCA_901000735.2) of the NCBI database. A 211 nt fragment is missing from the 5'-end of the sequence obtained from the TSA. Overlapping regions were exons and highlighted in yellow.

	1	11	21	31	41	51	61	71	81	91
ML012-GGSA01	-----									
ML012-Cav07g	ATGGACAAATGTGAGTATGATGAACGTACAATGGCGGAAACTCCAACATGGGCAGTTGCGGGTGGTGTGCTTCATGTTGCCATTTCAATCTTCATTG									
Consensus	-----									
ML012-GGSA01	101	111	121	131	141	151	161	171	181	191
ML012-Cav07g	AACATATTATTGAAGCTACTGAAAAGGTAATATTATTGATTAAGGTTGTATATATATTCTCTTTTGTATTGTTTTCTTGATTGATTACTGAAAAT									
Consensus	-----									
ML012-GGSA01	201	211	221	231	241	251	261	271	281	291
ML012-Cav07g	TCTTGCATGCTTTATATATTAATTATAGTGGCTAAAAGCCAAACACAAGGGACCTTTCACGAAGCCCTTGAAAAGATCAAATCAGGTACCTCTATATAT									
Consensus	-----									
ML012-GGSA01	301	311	321	331	341	351	361	371	381	391
ML012-Cav07g	ATATCTCACACATTAAGATCATCAACAAATGGTCAATTAATTAACCATTTTTCTTAATTTATTGGGTTTTTTTTTTTTTTTTTTTCGGTCAGAGATTAT									
Consensus	-----									
ML012-GGSA01	401	411	421	431	441	451	461	471	481	491
ML012-Cav07g	-----TGCTCCTAACAGTGTTCCAAAGAGCCCATTTCTGGGATGTGTATACCCATGAGTGTGGAGACACTTGGCATCCCTGTATA									
Consensus	-----tgctcctaacaagtgttccaagagcccatttctgggatgtgtatacccatgagtggtggagacacttggcatccctgtata									
ML012-GGSA01	501	511	521	531	541	551	561	571	581	591
ML012-Cav07g	GGTGAGAAGAAATATTCGGACAAAAGTGGTCGAAAAGTCTCCAGTTATTTGATTCTGGCTTCAGTGGTCGTCGAAGATTAGCTACAAAAGGATGCGACA									
Consensus	-----ggtgagaagaatattccggacaaaagtggtcgaaaagtctccagttatTTGATTCTGGCTTCAGTGGTCGTCGAAGATTAGCTACAAAAGGATGCGACA									
ML012-GGSA01	601	611	621	631	641	651	661	671	681	691
ML012-Cav07g	AATGCAAAAAGG-----GT									
Consensus	-----aatgcaaaaagg-----gt									
ML012-GGSA01	701	711	721	731	741	751	761	771	781	791
ML012-Cav07g	AAAGTGGCCTTCATGCTGCGTATTCGATTACCAGCTGCATATATTCATCTTTGTCTTAGCCGTTTTTCATGTGCTCTACTGCATAATCACCCCTGGCTT									
Consensus	-----aaagtggccttcattgctgctgctatttcgattaccagctgcataatattcatctTTGTCTTAGCCGTTTTTCATGTGCTCTACTGCATAATCACCCCTGGCTT									
ML012-GGSA01	801	811	821	831	841	851	861	871	881	891
ML012-Cav07g	TAGGCACAACCAAG-----TAGGCACAACCAAGGTAGTACTTTTTTAACATATATACATGCACAAATTGCAACCCCTTTCTTTCTCTCGAGATCTAAATCTTCTTTGAATAGATT									
Consensus	-----taggcacaaccaag-----taggcacaaccaag									
ML012-GGSA01	901	911	921	931	941	951	961	971	981	991
ML012-Cav07g	CTTGTAGAAATATATTATAGGATTTAATTTTCAGCATTGATTGTAATCGGATTTGATGAATCTTCTTGGAAATTCAGATCAAAAAGATGGAAGGCTTTGGG									
Consensus	-----atcaaaaagatggaaggctttggg									
ML012-GGSA01	1001	1011	1021	1031	1041	1051	1061	1071	1081	1091
ML012-Cav07g	AGGAAGAAACAAGGACACTTGAATCTCAAGTTCATATTG-----GTAACAAATCGGCTCTCAAAAACCTGCTTAAAAACAAGGACTACTTCTAAGTGTACATA									
Consensus	-----aggaagaacaaggacacttgaatctcaagttcatattg-----gtaacaaatcggctctcaaaaacctgcttAAAAACAAGGACTACTTCTAAGTGTACATA									
ML012-GGSA01	1101	1111	1121	1131	1141	1151	1161	1171	1181	1191
ML012-Cav07g	GTTTTATTATAAGTTTTCTTAGGCTATAATTGATGAAATAATTAAGAAGGTTTTTTTTTTTTTTTTTTTCAATTAATTAAGTACTAGTACTGCTG									
Consensus	-----									
ML012-GGSA01	1201	1211	1221	1231	1241	1251	1261	1271	1281	1291
ML012-Cav07g	TTTTAACCATACATTCTTTAATTATGTACGTTAATTTGTAAAATAAATTATAGTAAAAGCAGTAGTAATTCAAACATCTTCTCATTTAATGAAATTAAT									
Consensus	-----									
ML012-GGSA01	1301	1311	1321	1331	1341	1351	1361	1371	1381	1391
ML012-Cav07g	GTCACCTTATGGACTTGGTCAGGTGCTCCACAGAGTAGTCAAACCCCTCTTTCTTGGATAATGCTATGAACACAAAACAAAGTTACCGAAAAGTGACTCA									
Consensus	-----									

	1401	1411	1421	1431	1441	1451	1461	1471	1481	1491
ML012-GGSA01	-----									
ML012-Cav07g	CACTGTCAATCTATGCGGTTAAAGACTTGTCCACTTTTTTATACTACAAAGTCAACATTAAGATGACTTTGTAATTTGCTTTTGTGAGCAAATTTTGT									
Consensus										
	1501	1511	1521	1531	1541	1551	1561	1571	1581	1591
ML012-GGSA01	-----									
ML012-Cav07g	ATGAAAAAAAAAAGATTAATATCTCTTTTTTATTTTTTATTTTTTATTTTCATGTGTCCAGATTGCTGTTGCTAATTTAATTTAAAATAAATTTGTAGGA									
Consensus										
	1601	1611	1621	1631	1641	1651	1661	1671	1681	1691
ML012-GGSA01	-----									
ML012-Cav07g	TTTTTTTATTTTTTATTTTTTTTATATAGTTTGGTAAAAGAGATCATATATGTTATGGAAAATGATTATATATGATGAGATCAGCGCGGTTTAGGTTT									
Consensus	atcacgagcggttagggttt									
	1701	1711	1721	1731	1741	1751	1761	1771	1781	1791
ML012-GGSA01	-----									
ML012-Cav07g	GCAAGGGAAACATCATTGGACGAAGGCACCTTAACCTACTGGAGCAAGTCAACGGTTTCCCTTTGGATGGT-----									
Consensus	gcaagggaaacatcatttggacgaaggcacttaacctactggagcaagtcaacggtttccctttggatggtcagtattgaaatcctataattaactactt									
	1801	1811	1821	1831	1841	1851	1861	1871	1881	1891
ML012-GGSA01	-----									
ML012-Cav07g	AACTATGCTTGCATAGTTAGTTTGTGCTTAATAATAATATTAAGTTAGTATATGTTTATATTAAGTTATTATATATATATATAAATGTTTATATG									
Consensus										
	1901	1911	1921	1931	1941	1951	1961	1971	1981	1991
ML012-GGSA01	-----									
ML012-Cav07g	TGTATGTATGAGTTAGGCTCACAACTTAATCGAGTCGGGCGAGTAAACCGAGTATGTATCACTTAATAATCAAGCGAGTTTCTACCGTCATGAGCCAG									
Consensus										
	2001	2011	2021	2031	2041	2051	2061	2071	2081	2091
ML012-GGSA01	-----									
ML012-Cav07g	TTTCTGCAATCAGAGTCAAGTTAAGATCGAGTTTAAACAAACCGATTGTCGACGAGACTAGTTTATTACAACCTATTCTAGGCTTTAGTCCCGCAAT									
Consensus										
	2101	2111	2121	2131	2141	2151	2161	2171	2181	2191
ML012-GGSA01	-----									
ML012-Cav07g	TAAAGCAATTATCAATGGGTGAGGTGGGAGGAATGATAAACATGGAATAATATCAGTCTCCCCAAAATGTATGCCATAACTAATAATTTGGTGGAGCGCT									
Consensus										
	2201	2211	2221	2231	2241	2251	2261	2271	2281	2291
ML012-GGSA01	-----									
ML012-Cav07g	CTATATTACATGTTGGATTTATTTATTTTTATCTTAAGTACAATGTTCAATTTTCAAGATATCATTAGCGTAAACACTCTAGTTTCATGTTGAGAAAAGAT									
Consensus										
	2301	2311	2321	2331	2341	2351	2361	2371	2381	2391
ML012-GGSA01	-----									
ML012-Cav07g	GTGTAAGTCACACAGAGTTAATAGTTTATAAGATATGTTTCATTGGTGTAAAGTTGTTCCACATTGCTTATTTATTAGTAAAATTGAACTTTAAAAGTAA									
Consensus										
	2401	2411	2421	2431	2441	2451	2461	2471	2481	2491
ML012-GGSA01	-----									
ML012-Cav07g	TTTTAAGGAAGTTTCAAATTGACTAAATGTGCCAACGTGGGCAACTCATCTTTTTAATATGGAAGTGGGTTTACAAATTCCTCTCTTAAAACCCCTG									
Consensus										
	2501	2511	2521	2531	2541	2551	2561	2571	2581	2591
ML012-GGSA01	-----									
ML012-Cav07g	AAGTCACCATCTACGTGGAGAAATGTAGAAGAAAGGATATCCGCATCCACATAATGCAATTACTATCTACATCTGCACAGTCTACATCACAGCTAAAAA									
Consensus										
	2601	2611	2621	2631	2641	2651	2661	2671	2681	2691
ML012-GGSA01	-----									
ML012-Cav07g	CATTTTTTGAGAAAAAATTTGATGCCGAAACAAACAAAGCCTTAGTAATGAAACTTGTGTTATTTTTCAATTTTGAATTTAAGGGCATAAAAGGTTA									
Consensus										
	2701	2711	2721	2731	2741	2751	2761	2771	2781	2791
ML012-GGSA01	-----									
ML012-Cav07g	GTTATGTTACAGTTGTTTGAAGTCTTTTCTCCTCTATCAGGTTTGTTCCTCAGACAATTCTTCAGATCAATTACTAAGGTTGATTACATTACGTTG									
Consensus	ttgtttcttcagacaattcttcagatcaattactaaggttgattacattacggtt									
	2801	2811	2821	2831	2841	2851	2861	2871	2881	2891
ML012-GGSA01	-----									
ML012-Cav07g	AGATATGGATTTATCGTGG-----									
Consensus	agatatggatttatcgtgg									

	2901	2911	2921	2931	2941	2951	2961	2971	2981	2991
ML012-GGSA01	-----CACATTGGCACCCGGAAGTGAACAACGTTTGATTTTCAAAAATACATCCAGAGAGCACTTGAAGCTGATTTTAAATTCGTGGTGGGGATA									
ML012-Cav07g	ACTTCAGGCACATTGGCACCCGGAAGTGAACAACGTTTGATTTTCAAAAATACATCCAGAGAGCACTTGAAGCTGATTTTAAATTCGTGGTGGGGATA									
Consensus	cacatttggcaccccggaagtgaacaacgtttgattttcaaaaatacatccagagagcacttgaagctgattttaaattcgtgggtggggata									
	3001	3011	3021	3031	3041	3051	3061	3071	3081	3091
ML012-GGSA01	AG-----TCCAAAAATATGG									
ML012-Cav07g	AGGTTGGTGTGCTGAAGCACTTAAAGGCCTTTCCTCTTTGATTGATTTTAAATATCTTAAATTCACACTTTACCTCTCATTGGCAGTCCAAAAATATGG									
Consensus	ag tccaaaaatattgg									
	3101	3111	3121	3131	3141	3151	3161	3171	3181	3191
ML012-GGSA01	TGCTTTGCAGTTTTATCCCTATTGTCCAACGCATATGG-----									
ML012-Cav07g	TGCTTTGCAGTTTTATCCCTATTGTCCAACGCATATGGTAAGCTAAATACTACCTTTTGGTTATCATACTATCTCTCTTTTAAATGACGTGGAACCCCTTG									
Consensus	tgctttgcagttttatccctattgtccaacgcatatgg									
	3201	3211	3221	3231	3241	3251	3261	3271	3281	3291
ML012-GGSA01	AAGGCCAAGGCCACTTCTGATATTCTTGTGGGCAAACTCTAAATACACGACCTTGTCCGTAAGAACCGTGTATCGGTTGAGTGACGACTCGAATAACCG									
ML012-Cav07g	AAGGCCAAGGCCACTTCTGATATTCTTGTGGGCAAACTCTAAATACACGACCTTGTCCGTAAGAACCGTGTATCGGTTGAGTGACGACTCGAATAACCG									
Consensus	aaggccaaaggccacttctgatattcttgtgggcaaaactctaaatacacgaccttgtccgtaagaaccggtgtatcggttgagtgacgactcgaataaccg									
	3301	3311	3321	3331	3341	3351	3361	3371	3381	3391
ML012-GGSA01	ATGATATTAAGCAAATGAGTCGATCATTGACGCTGCTCCCTGGGGCCAAAGTAGTGTTCATTCTTTGTGTGCCATTCTCATTTTGGAGCCAAATATGTT									
ML012-Cav07g	ATGATATTAAGCAAATGAGTCGATCATTGACGCTGCTCCCTGGGGCCAAAGTAGTGTTCATTCTTTGTGTGCCATTCTCATTTTGGAGCCAAATATGTT									
Consensus	atgatattaagcaaatgagtcgatcattgacgctgctccctggggccaaagtagtgttcattctttgtgtgccattctcatTTTGGAGCCAAATATGTT									
	3401	3411	3421	3431	3441	3451	3461	3471	3481	3491
ML012-GGSA01	-----ATGGCATTCTTATCTATGGCTACCATTTCCTCCATTGATTG									
ML012-Cav07g	GTGGGCTGCCTTAGTAATACTACTGACTAAGAAATGTTCCATCGATGTTGGACAGGATGGCATTCTTATCTATGGCTACCATTTCCTCCATTGATTG									
Consensus	atggcattcttattctatggctaccatttcctccattgattg									
	3501	3511	3521	3531	3541	3551	3561	3571	3581	3591
ML012-GGSA01	TAA-----									
ML012-Cav07g	TAAAGCTCAATTACAGAAACCAACTGGTTTCCTAAATTTTTCTTTGTCGGGTCTCCCAACCCATTTTAAATAGCCAGGGTTTTGGAGGAAAACCTTTGTTC									
Consensus	taa									
	3601	3611	3621	3631	3641	3651	3661	3671	3681	3691
ML012-GGSA01	-----TCCTCTTGGTGGGTAC									
ML012-Cav07g	TTTTATCGGCTTTGTTTACAATCTAAGCTTTTGGGTTGTTGGTTTAAATGGAAAAATCATGTGTTTGTGTGATTTTACAGGTAATCCTCTTGGTGGGTAC									
Consensus	tcctcttgggtgggtac									
	3701	3711	3721	3731	3741	3751	3761	3771	3781	3791
ML012-GGSA01	ACAGCTACAAGTAATAATTACAAAAATGGGGCTAAGAATTCAAGAGAGAGGAGATGTGATTAAGGGTACACCTGTGGTACAGCCAGGTGATGACCTCTTC									
ML012-Cav07g	ACAGCTACAAGTAATAATTACAAAAATGGGGCTAAGAATTCAAGAGAGAGGAGATGTGATTAAGGGTACACCTGTGGTACAGCCAGGTGATGACCTCTTC									
Consensus	acagctacaagtaataattacaaaaatggggctaaagaattcaagagagagaggatgtgattaaagggtacacctgtggtaca ccaggtgatgacctcttc									
	3801	3811	3821	3831	3841	3851	3861	3871	3881	3891
ML012-GGSA01	TGGTTTGGAAACCCTCGGTTCTCTATCTCATTCACTTCGTTCTCTTTTCAG-----									
ML012-Cav07g	TGGTTTGGAAACCCTCGGTTCTCTATCTCATTCACTTCGTTCTCTTTTCAGGTATTTCTCAAATACATCAACAAATACATATTACAGCCTCTTTGA									
Consensus	tggtttgaaaaccctcggttctctatctcattcaacttcggttctcttttcag									
	3901	3911	3921	3931	3941	3951	3961	3971	3981	3991
ML012-GGSA01	GATTGCGTCGAGAAATAGAGCTTTTGTTCACAGAAAAGTCTAAAATAACTTTTATAGGAAAAAGAAAGAAAGAAAACCTCATTTTCAAGCTTTTCTC									
ML012-Cav07g	GATTGCGTCGAGAAATAGAGCTTTTGTTCACAGAAAAGTCTAAAATAACTTTTATAGGAAAAAGAAAGAAAGAAAACCTCATTTTCAAGCTTTTCTC									
Consensus	gattgctgcgagaaatagagcttttgttccacagaaaagtctaaaataacttttataggaaaaagaaagaaagaaaacctcatTTTCAAGCTTTTCTC									
	4001	4011	4021	4031	4041	4051	4061	4071	4081	4091
ML012-GGSA01	AAAAATGCAGTTTTGAGTTTTTTTAGAGCAAAAAGTCAAAAAGTCTTTTAAAGTTTTTACCATCAGATCCATTTTGTGTTGGTACATCTTTTTATGT									
ML012-Cav07g	AAAAATGCAGTTTTGAGTTTTTTTAGAGCAAAAAGTCAAAAAGTCTTTTAAAGTTTTTACCATCAGATCCATTTTGTGTTGGTACATCTTTTTATGT									
Consensus	aaaaatgcagttttgagtttttttagagcaaaaagtcaaaaagtctttttaaagtttttaccatcagatccattttgtgttgggtacatctTTTTATGT									
	4101	4111	4121	4131	4141	4151	4161	4171	4181	4191
ML012-GGSA01	-----									
ML012-Cav07g	ACTAAAAATGCTTTTTTAAACTTTTTAACGTAATCTCAACCGCTTTCGAGCTCTCTGGATTCTAATATCAGCCTTTGGCTTTTGGCATCTTTGTCTTGACT									
Consensus	actaaaaatgctTTTTTAAACTTTTTAACGTAATCTCAACCGCTTTCGAGCTCTCTGGATTCTAATATCAGCCTTTGGCTTTTGGCATCTTTGTCTTGACT									
	4201	4211	4221	4231	4241	4251	4261	4271	4281	4291
ML012-GGSA01	-----AATGCATTCAACTGGCCTTCTATGCGTGGAGTGTG-----									
ML012-Cav07g	TTAATTGCAGAAATGCATTCAACTGGCCTTCTATGCGTGGAGTGTGTAAGCCTTTCACTTCTTTAATTCATTAATTCACAAAGTACTTAGGGACTGTTT									
Consensus	aatgcatttcaactggccttctatgCGTGGAGTGTG									
	4301	4311	4321	4331	4341	4351	4361	4371	4381	4391
ML012-GGSA01	-----									
ML012-Cav07g	GAGTTGCGTTTAAAGGAGCCTAAAAGTGCATTTAATACTCAAAAAGTTCATTTAAAAAAGAAAGTATCGGTTTCGTAAAAAATTTTGAAGCGTTTTTGA									
Consensus	gagttgCGTTTAAAGGAGCCTAAAAGTGCATTTAATACTCAAAAAGTTCATTTAAAAAAGAAAGTATCGGTTTCGTAAAAAATTTTGAAGCGTTTTTGA									

	4401	4411	4421	4431	4441	4451	4461	4471	4481	4491
ML012-GGSA01	-----									
ML012-Cav07g	GGATCCAAGAAGTCAAAAAATGACTAAAACGTACTTTTGGCAAAAACCTTAAAAATGATGCTTTTGTCAAAAAATGCTTTTGTATTTAAAAGCTCTATTTT									
Consensus										
	4501	4511	4521	4531	4541	4551	4561	4571	4581	4591
ML012-GGSA01	-----									
ML012-Cav07g	TCAAAATGCAATCACAACATGCTTTTAAATGGTGTCTGTACTACGAAACAAAGTCCCATCACATGTGACATTGGCATTGCTCAAAAGCATCTACTTTTAGA									
Consensus										
	4601	4611	4621	4631	4641	4651	4661	4671	4681	4691
ML012-GGSA01	-----									
ML012-Cav07g	AITTAGAATTAAGCAACAAGTGAAGCTTATGCTAAGAGCTTTCCTAACTTTCTGTCTATTTTTTCTTCTTTTCAGTATGCAATTTGGCATAAAATCT									
Consensus	tatgcatttggcataaaattct									
	4701	4711	4721	4731	4741	4751	4761	4771	4781	4791
ML012-GGSA01	-----									
ML012-Cav07g	TGCTTCCATAAAGCGCACTGAAGATAAAGGTCATCAGACTCTCAACGGGGTGAGTTCTTTCACAAATGCACATCCATGGAAATCCATATGCCATGCATGGTG									
Consensus	tgcttccataaagcgcaactgaagataaaggtcatcagactctcaacgggg									
	4801	4811	4821	4831	4841	4851	4861	4871	4881	4891
ML012-GGSA01	-----									
ML012-Cav07g	CCATTGTTAAGATGTAGTTATTTGGATGATTAATGTGTTAATTAAGTTTAAAGAATTGCTAATGCTATACGACTTTGGCACTTTCTTCAGGATCATCACAC									
Consensus	atcatcacac									
	4901	4911	4921	4931	4941	4951	4961	4971	4981	4991
ML012-GGSA01	-----									
ML012-Cav07g	AAGTTCTATGCAGTTATGTGACTTTGCCTCTCTATGCTCTAGTGATTCCGGAAGTTGAGAAATTAATGATGACATGGCTTCAAGGTTAAATAATACAAATATA									
Consensus	aagttctatgcagttatgtgactttgcctctctatgctctagtgattccgg									
	5001	5011	5021	5031	5041	5051	5061	5071	5081	5091
ML012-GGSA01	-----									
ML012-Cav07g	GAAGCAAATATATTAGCAAACAATACAAATCATTAAAAAGCAGTTTTCACATTTATAGAGAAATATAAGAAAAACAAATTTTTTTAAAAAAAATTTTAT									
Consensus										
	5101	5111	5121	5131	5141	5151	5161	5171	5181	5191
ML012-GGSA01	-----									
ML012-Cav07g	GATGGAGAAGGGTTTTTCGGACCTACCTTTATAGAGTAAACCTCGAACCCGTGATTGCATTCTCGAAAGTTTCTTTACACGGACAGGGTAAATACCTG									
Consensus										
	5201	5211	5221	5231	5241	5251	5261	5271	5281	5291
ML012-GGSA01	-----									
ML012-Cav07g	ACTTTTGCACCAAGGGGTGTGGCGCCCTAATGGGGTGTTTGTACCTAGCAAGTCTCAAACTTGAGATCTAATGCCGTGATCTCCCTAAGACCACAAAGCCT									
Consensus										
	5301	5311	5321	5331	5341	5351	5361	5371	5381	5391
ML012-GGSA01	-----									
ML012-Cav07g	CAACCACTAGGGCAGCCCTTTGGGGTAAAAAATAAAAAATTAATATGCATAGCCCTTTGACTAATATTCTTTGGACTGATTTTTTTCGACATGG									
Consensus	atgg									
	5401	5411	5421	5431	5441	5451	5461	5471	5481	5491
ML012-GGSA01	-----									
ML012-Cav07g	GCTCTTCCATGAATTTCTACCATTTTTAATGATGGAGTGGCAACAGCATTAAAGAGCTGGCATCGAAGGCCAAGAAGAAATCTAAGCATGCCATCATTC									
Consensus	gctcttccatgaatttctaccatTTTTAATGATGGAGTGGCAACAGCATTAAAGAGCTGGCATCGAAGGCCAAGAAGAAATCTAAGCATGCCATCATTC									
	5501	5511	5521	5531	5541	5551	5561	5571	5581	5591
ML012-GGSA01	-----									
ML012-Cav07g	TGAGGCAAATTCACCAATTCACCTCTTGCATAACTATCAGCATCGCAGCCTTGATAGCTTGCACACATCTCCTAATGATCATTITGAAATGGAAGACTTA									
Consensus	tgaggcaaattcaccatttcacctcttgcataactatcagcatcgagccttgatagcttgcacacatctcctaattgatcattitgaaatggaagactta									
	5601	5611	5621	5631	5641	5651	5661	5671	5681	5691
ML012-GGSA01	-----									
ML012-Cav07g	GAATTCCAAAGGAAACAAAGTGGACACGAAGACTCTATGCATTCTGAGCAAGAGAAGGAGATTCAAGAGCAAAGATCATCGCAATTGCCTCCATCACTAG									
Consensus	gaattccaaaggaaacaaagtggacacgaagactctatgcattctgagcaagagaaggagattcaagagcaaagatcatcgcaattgcctccatcactag									
	5701	5711	5721	5731	5741	5751	5761	5771	5781	5791
ML012-GGSA01	-----									
ML012-Cav07g	GAACCATTCGAACCCAACACGAAATCAACGTTAGTCCGTCAGATTTCTCTTTTCGCAGATGA									
Consensus	gaaccatttcgaacccaacacgaaatcaacgtttagtccgtcagatTTCTCTTTTCGCAGATGA									