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

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ARTICLE INFO	A B S T R A C T
Research Article	Text Powdery mildew affecting European hazelnut <i>Corylus avellana</i> L. in Turkey is caused by the obligate biotrophic fungus <i>Erysiphe corylacearum</i> . This fungal disease causes significant economic
Received : 16/09/2021 Accepted : 14/02/2022	losses by reducing the yield and quality of hazelnuts. Loss-of-function mutations in the <i>mildew resistance locus o</i> (<i>MLO</i>) gene family of many plants confer high levels of broad-spectrum resistance to powdery mildew. The proteins encoded by the genes at the <i>MLO</i> 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
<i>Keywords:</i> Hazelnut Corylus avellana Mildew resistance locus o (MLO) Powdery mildew Semi-quantitative PCR	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) (Büschges 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 wellcharacterized barley and Arabidopsis. As a natural loss-offunction (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

lycospersicum L. var. cerasiforme) SlMLO1 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 µmol m⁻² s⁻¹. The soil was fertilized once using 20:20:20. Plants were

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

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 semiquantitative 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 [Corvlus avellana, Transcriptome Shotgun Assembly (TSA), BioProject: PRJNA316492] (Kavas et al., 2019) used to design pairs of clade V MLO gene-specific primers.

Gene	GenBank accession number	Primer pair sequences $(5'-3')$	Al (base pairs)
C NIL 02 (C) 10,00700)	000401064561.1	CoravMLO2-Forward GGTGGGGACGAAACTACAGGTGATC	700
CavMLO2 (Cav <u>10</u> g09700)	GGSA01064561.1	CoravMLO2-Reverse GGAAGCGGAGCCACTTGACTTGAG	720
		CoravMLO6-Forward	
CavMLO6 (Cav07g19540)	GGSA01025153.1	ACACCTGTGGTACAGCCAGGTGATG	720
		CoravMLO6-Reverse CATCTGCGAAATGTGAATTCCGAG	
		CoravMLO12-Forward	
CavMLO12 (Cav07g19590)	GGSA01055436-1	TGTCCAACGCATATGGATGGCATTC	720
Cavini2012 (Cav <u>075</u> 19390)	000101055450.1	CoravMLO12-Reverse	720
		CGTGTTGGGTTCGAATGGTTCCTAG	
		CoravACT-Forward	
CavACT (on chr 11)	GGSA01045693.1	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.



hours post infection (hpi)

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 µl 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

Ervsiphe corvlacearum 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 each primer pair generated a single amplification band with no non-specific products. Primer pairs for MLO genes amplified a 720 bp MLOsspecific 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 tothose reported by Lucas et al. (2021), after delineating exon/inton 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 analyisis 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 AtACT2	ATGGCCGA ATGGCTGA	T <mark>GCCGAGGAT</mark> G <mark>GCTGATGAT</mark>	<mark>ATTCAGCC</mark> CC	TTGTTTGTGA TCGTGTGTGA	CAATGGAACTI CAATGGTACCI	GG <mark>A</mark> ATGGTGA <i>I</i> GGTATGGTGA <i>I</i>	AGGCTGG <mark>TTTT</mark> AGGCTGG <mark>ATTT</mark>	GCTGGTGATG GCAGGAGATG	ATGCTCCCA	GGCAGTGTTTC
Consensus	atggc ga	gc ga gat	attca cc	t gt tgtga	caatgg ac (yg atggtgas	aggetgg ttt	gc gg gatg	atgetecca	gggc gt tttc
and the second	101	111	121	131	141	151	161	171	181	191
CavACT AtACT2	CTAGTATT CCAGTGTT	GTGGGTAGGC GTTGGTAGGC	CCCGTCACAC CAAGACATCA	TGGTGTTATG	GTTGGGATGGI GTTGGGATG <mark>A</mark> J	G <mark>CCAAAAAGAT</mark> A <mark>CCAGAA</mark> GGAT	IGCTTATGTTG IGCATATGTTG	GTGATGAAGC GTGATGAAGC	TCAATCCAA	GAGGGGGTATTCT
Consensus	c agt tt	gt ggtaggo	c g ca	tggtgt atg	gttgggatg	cca aa gat	tgc tatgttg	gtgatgaagc	caatccaa	yag ggtattet
	201	211	221	231	241	251	261	271	281	291
CavACT	TACCTTGA	AATATCCTAT	TGAGCATGGT	ATTGTCAGTA	ATTGGGATGA	CATGGAGAAG	ATCTGGCATCA	CACATTCTAC	AATGAGCTT	CGAGTTGCTCCT
AtACT2	TACCTTGA	AGTATCCTAT	TGAGCATGGT	GTTGTTAGCA	ACTGGGATGAT	T <mark>ATGGAAAAG</mark>	ATCTGGCATCA	CACTTTCTAC	AATGAGCTT	CGTATTGCTCCT
Consensus	taccttga	a tatcctat	tgagcatggt	; ttgt ag a	a tgggatga	atgga aaga	atctggcatca	cac ttctac	aatgagett	eg ttgeteet
	301	311	321	331	341	351	361	371	381	391
CavACT	GAAGAGCA	CCCAGTGCTI	CTCACTGAAG	CTCCTCTCAA	CCCTAAGGCC	ACAGAGAA	AGATGACTCAA	ATCATGTTTG	AGACCTTCA	ATGTG <mark>CC</mark> TGCCA
AtACT2	GAAGAGCA	CCCTGTTCTI	CTTACCGAG	CTCCTCTTAA	CCC <mark>AAAGGCC</mark>	AACAGAGA <mark>G</mark> AA	AGATGACTCAA	ATCATGTTTG	AGACCTTTA	ACTCT <mark>CC</mark> CGCTA
Consensus	gaagagca	ccc gt ctt	ct ac ga g	ctcctct aa	ccc aaggcc:	aacagaga aa	agatgactcas	atcatgtttg	agacett a	a cogoa
	401	411	421	431	441	451	461	471	481	491
CavACT	TGTATGT	GCTATCCAG	CTGTTCTCTC	CCTGTATGCC.	AGTEGTEGTA	CAACTGGTATT	FGTGCTGGATI	CTGGTGATGG	TGTGAGTCA	CACTGTGCCAAT
AtACT2	TGTATGTC	GCCATCCAAG	CTGTTCTCTC	CTTGTACGCC.	AGTGGTCGTA	CAACCGGTATI	FGTGCTGGATI	CTGGTGATGG	TGTGTCTCA	CACTGTGCCAAT
Consensus	tgtatgt	gc atcca g	ctgttctctc	c tgta gcc	agtggtcgta	caac ggtati	tgtgctggatt	ctggtgatgg	itgtg tca	cactgtgccaat
	501	511	521	531	541	551	561	571	581	591
CavACT	CTATGAAG	GGTATGCCCT	CCCACATGCC	ATCCTACGTT	TGGACCTTGC	FGGTCGTGAT(CTCACTGACGC	TTTGATGAAG	ATTCTCACT	GAGAGAGGGTAT
Congongua	CIALGAGG	erricicici	ILLILAIGU	AILLILLUI	IIGALLIIGU	IGGALGIGAL	LI IALIGATIA	t ofgood	AILLIIALA	GAGAGAGGGIIAL
consensus	cca ya y		, cc cacyce	accor cyc	c yaccecyc.	lyg cycya (allya	c acyaay		yayayayy ca
0	5UI	611	621	631	641	651	551	671	681	691
AtACT2	ATGTTCAC	CACAACAGCA	GAGCGGGGAAA	TTGTAAGAGA	CATCAAGGAG	AGCTCTCCT	TGTTGCCCT1	GACTACGAGE	AGGAGATGG	AAACCTCAAAGA
Consensus	atgttcac	cac ac gc	ga cgggaas	ittgt g ga	cat aaggag	aaget e t	tgttgc tt	gacta gago	agga tg	a ac caaga
	701	711	721	731	741	751	761	771	781	791
CavACT	GCAGCTCC	TCTGTTGAGA	AGAACTATGA	ATTGCCTGAT	GGACAAGTCA	CACAATC GGA	AGCTGAGAGAT	TCCGTTGCCC	AGAAGTCCT	TTCCAGCCATC
AtACT2	c <mark>cagete</mark> t	TCCATCGAGA	AGAACTATGA	ATTACCCGAT	GGGCAAGTCAT	FCACGATTGG1	r <mark>gctgagagat</mark>	TCAGATGCCC	AGAAGTCTT	G <mark>TTCCAGCC</mark> CTC
Consensus	cagete	tc t gaga	agaactatga	att cc gat	gg caagtca	tcac at gg	gctgagagat	tc g tgccc	agaagtc t	ttccagcc tc
	801	811	821	831	841	851	861	871	881	891
CavACT	<mark>GCTGATTG</mark>	GAATGGAAGC	TGCTGGAATC	CACGAGACCA	CCTAC <mark>AACTC</mark>	r <mark>atcatgaa</mark> at	<mark>FGTGA</mark> CGTGGA	TATCAG <mark>A</mark> AAG	GATCTCTAC	<mark>ggaaacattgt</mark> t
AtACT2	GTTTGTGG	GAATGGAAGC	TGCTGGAATC	CACGAGACAA	CCTATAACTC	ATCATGAAG	<mark>FGTGA</mark> TGTGGA	TATCAG <mark>G</mark> AAG	GATCTGTAC	GGTAACATTGTG
Consensus	gt tg	gaatggaago	tgctggaato	cacgagac a	ccta aactc	atcatgaa t	tgtga gtgga	tatcag aag	gatet tac	gg aacattgt
	901	911	921	931	941	951	961	971	981	991
CavACT	CTCAGTGG	TGGCTCAACC	ATGTTCCCAG	GTATTGCTGA	CCGGATGAGC	AGGAGATCA	TGCTCTTGCC	CCAAGCAGCA	TGAAGATTA.	AGGTTGTGGCAC
AtACT2	CTUAGTEG	TGGAAUCAUT	ATGTTUTUAG	GTATUGUTGA	CCGTATGAGCI	AAGAAATUAU	CAGUAUTTGUA	CUAAGUAGUA	TGAAGATTA	AGGTUGTIGUAU
Lonsensus	ctcagtgg	tgg c ac	atgttc cag	igtat getga	ccg atgage	aa ga atcad	c gc cttgc	ccaagcagca	itgaagatta:	aggt gt gcac
	1001	1011	1021	1031	1041	1051	1061	1071	1081	1091
CavACT AtACT2	CACCAGAG	AGGAAGTACA	GTGTCTGGAT	CGGAGGATCA	ATCUTTGCAT	CCTUAGCAC	ATTCCAGCAGA	TGTGGATTTC	CAAGGCCCA	TAUGACGAGTC
Consensus	cacc da	aggaagtacs	atatetaaat	caa aa re	at otter to	cotcancac	ttccarcara	tatagat to	caadd cda	ta ga gan c
	1101	1111	1121	1101	1141	1151	1161	1171	1101	1101
Cavicr	TGGTCCAT	CTATTCTCCA	CAGGAAGTEC	TTCTAL	1141	1131	1101	11/1	1101	1191
AtACT2	AGGTCCAG	GAATCGTTCA	CAGAAAATGT	TTCTAA						
	No. Constanting	- Constanting and	a and a constant of the							8

Consensus ggtcca

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	MADAEDIQI	PLVCDNGTGN	IVKAGFAGDDA	PRAVFPSIVG	RPRH <mark>T</mark> GVMVGI	MGQKDAYVGI	EAQSKRGILT	LKYPIEHGI <mark>V</mark>	'SNWDDMERIWHH
AtACT2	MAEADDIQ	PIVCDNGTGN	IVKAGFAGDDA	PRAVFPSVVG	RPRHHGVMVG	MNQKDAYVGI	EAQSKRGILT	LKYPIEHGVV	SNUDDMEKIUHH
Consensus	ma a diq	o vedngtgn	nvkagfagdda	pravfps vg	rprh gvmvgi	m qkdayvgo	leaqskrgilt	lkypiehg v	snwddmekiwhh
	91	101	111	121	131	141	151	161	171
CavACT	TFYNELRV	APEEHPVLLT	EAPLNPKANR	EKMTQIMFET	FNV <mark>PAMYVAI</mark>	QAVLSLYAS	GRTTGIVLDSG	DGVSHTVPIY	EGYALPHAILRL
AtACT2	TFYNELR I	APEEHPVLLT	EAPLNPKANR	EKMTQIMFET	FNSPAMYVAI)	QAVLSLYAS	GRTTGIVLDSG	DGVSHTVPIY	EGFS <mark>LPHAILRL</mark>
Consensus	tfynelr a	apeehpvllt	eaplnpkanr	ekmtqimfet.	fn pamyvai	qavlslyasç	grttgivldsg	dgvshtvpiy	eg lphailrl
	181	191	201	211	221	231	241	251	261
CavACT	DLAGRDLTI	ALMKILTER	GYMFTTTAER	EIVRDMKEKL.	AY <mark>VALDYEQE</mark> I	LETAKSSSS	EKNYELPDGQ	VITIGAERFR	CPEVLFQPSLIG
AtACT2	DLAGRDLTI	YLMKILTER	GYMFTTTAER	EIVRDIKEKL	SF <mark>VA</mark> VDYEQEI	M <mark>et</mark> sktsss]	EKNYELPDGQ	VITIGAERFR	CPEVLFQPSFVG
Consensus	dlagrdlt	i lmkilter	gymftttaer:	eivrd kekl	va dyeqe	et k sss	eknyelpdgq	vitigaerfr	cpevlfqps g
	271	281	291	301	311	321	331	341	351
CavACT	MEAAGIHE'	TYNSIMKCI	VDIRKDLYGN	IVLSGGSTMF	PGIADRMSKE:	ITALAPSSM	XIKVVAPPERK	YSVWIGGSIL	ASLSTFQQMUIS
AtACT2	MEAAGIHET	FTYNSIMKCI	VDIRKDLYGN	IVLSGGTTMF:	S <mark>GIADRMSKE</mark>	ITALAPSSM	XIKVVAPPERK	YSVWIGGSIL	ASLSTFQQMWIS
Consensus	meaagihe	ttynsimkco	lvdirkdlygn	ivlsgg tmf	giadrmske:	italapssmk	rikvvapperk	ysvwiggsil	aslstfqq m wis.
	361	371	381	391	401	411	421	431	441
CavACT	KGEYDESGI	PSIVHRKCF							
AtACT2	KAEYDEAGI	PGIVHRKCF							
Conconque	la errele en	imbrhaf							

Consensus k eyde gp ivhrkcf

Figure S3. Sequence alignment of the putative *C. avellana* actin gene (*CavACT*) 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. For simplicity, our amplified 589 nt sequence was not included in the alignment as it had the same sequence as *CavACT*-WGS.

	1	11	21	31	41	51	61	71	81	91	
CavACT-TSA	ATGGCCGI	ATGCCGAGGA	TATTCAGCCCC	CTTGTTTGTG.	ACAATGGAAC	TGGAATGGTO	BAAGG				3
CavACT-WGS	ATGGCCG	ATGCCGAGGA	TATTCAGCCCO	CTTGTTTGTG.	ACAATGGAAC	TGGAATGGTO	<mark>BAAGG</mark> TTAGTC	AATACATTTO	ATGCTTATTA	ATTTGGACCAAGTT	
consensus	acggeegs	acgeegagga	Latteageeet		acaacggaac	Lggaalgglg	jaagg		101	101	
AVACT-TSA	101		121	131	141	151	161 CTGG	171 TTTGCTGCI	181 CATGATGETC	191 CCASSSCASTSTT	
ACT-WGS	CTGTTCT	TTATTACTA	ITTAGTTATTI	TGAAACGCT	тстаататат	TGTTTTTGTG	GTGCAGG <mark>CTGG</mark>	TTTTGCTGGT	GATGATGCTC	CCAGGGCAGTGTT	
nsensus	02						ctgg	itttgctggt	gatgatgcto	ccagggcagtgtt	
	201	211	221	231	241	251	261	271	281	291	
-TSA	TCCTAGT	ATTGTGGGTA(GGCCCCGTCA	CACTGGTGTT.	ATGGTTGGGA	TGGGCCAAAA	AGATGCTTAT	GTTGGTGATO	GAAGCTCAATC	CAAGAGGGGTATT	1
CT-WGS	TCCTAGTA	ATTGTGGGTA	GGCCCCGTCA	CACTGGTGTT.	ATGGTTGGGA	TGGGCCAAAA	AGATGCTTAT	GTTGGTGATO	GAAGCTCAATC	CAAGAGGGGTATT	
sensus	tcctagta	attgtgggta	ggccccgtcad	cactggtgtt	atggttggga	.tgggccaaas	agatgettat	gttggtgatg	gaageteaate	caagaggggtatt	ŝ
	301	311	321	331	341	351	361	371	381	391	2
-TSA	CTTACCT	IGAAATATUU IGAAATATUU	TATTGAGCATO TATTGAGCATO	GTATTGTCA	GTAATTGGGA GTAATTGGGA	TGACATGGAU	AAGATUTGGU AAGATUTGGU	ATCACACATI	CTACAATGAU	CTTCGAGTTGCTC CTTCGAGTTGCTC	
nsus	cttaccti	tgaaatatcci	tattgagcato	ggtattgtca	gtaattggga	tgacatggad	aagatetgge	atcacacatt	ctacaatgac	gettegagttgete	
10000000000	401	411	421	431	441	451	461	471	481	491	
-TSA	CTGAAGAG	GCACCCAGTG	CTTCTCACTG	AGCTCCTCT	CAACCCTAAG	GCCAACAGAG	GAAAAGATGAC	TCAAATCATO	TTTGAGACCT	TCAATGTGCCTGC	1
r-wgs	CTGAAGAG	GCACCCAGTG	CTTCTCACTG	AGCTCCTCT	CAACCCTAAG	GCCAACAGAG	GAAAAGATGAC	TCAAATCATO	TTTGAGACCT	TCAATGTGCCTGC	
nsus	ctgaagag	gcacccagtg	cttctcactga	agctcctct	caaccctaag	gccaacagag	yaaaagatgac	tcaaatcato	gtttgagacct	tcaatgtgcctgc	1000
	501	511	521	531	541	551	561	571	581	591	22
-TSA	CATGTATO	GTTGCTATCC/	AGGCTGTTCTO	TCCCTGTAT	GCCAGTGGTC	GTACAACTGO GTACAACTGO	T				
1-W65	Catotate	TIGUIAIUU	aggetattete	tccctatet	accentante	diacaactor	<mark>FI</mark> IAGIAILAL 17	IAILILLAIL	IGAAAIICAI	AAACIIGICIIIG	-
11343	cauguati	eri			gecaytyytt zan	glalaatigg gen		671	601	601	
-750	0U1	<u>ьтт</u>	621	631	641	-ATTGTOCTO	DD1	5/I ATGGTGTGAG	661 TCACACTOTO	591 591	
WGS	AATCACAG	CTGAGCCTCT(GACCCTGACTI	FGGCTCCTCA	TTGGAATAGG	TATTGTGCTG	GATTCTGGTG	ATGGTGTGA	TCACACTOTO	GCCAATCTATGAAG	
ensus	0.					attgtgctg	gattctggtg	atggtgtga	ftcacactgtg	gccaatcta gaag	
	701	711	721	731	741	751	761	771	781	791	251
TSA	GGTATGCO	CTCCCACAT	GCCATCCT <mark>T</mark> CO	GTTTGGACCT	TECTEETCET	GATCTCACTO	GACGCTTTGAT	GAAGATTCTO	ACTGAGAGAG	GGTATATGTTCAC	
-WGS	GGTATGCO	CTCCCACAT	GCCATCCTACO	GTTTGGACCT	TGCTGGTCGT	GATETCACTO	GACGCTTTGAT	GAAGATTCTO	ACTGAGAGAG	GGTATATGTTCAC	
asus	ggtatgco	ctcccacat	gccateet eq	ytttggacct	tgctggtcgt	gateteacto	jacgctttgat	gaagattete	actgagagag	ggtatatgttcac	ŝ.
	801	811	821	831	841	851	861	871	881	891	
WGS	CACCACTO	GCCGAACGGG	AAATTGTCCGT	IGACATGAAG	GAGAAGCTTG GAGAAGCTTG	CATATGTTG	COTTGACTAT	GAGCAGGAAC	TTGAGACTGO	CAAGAGCAGCTCC	
nsus	caccacto	jccgaacggg	aaattgtccgt	tgacatgaag	gagaagcttg	catatgttgc	ccttgactat	gagcaggaad	ttgagactgo	caagagcagctcc	
	901	911	921	931	941	951	961	971	981	991	
r-TSA	TCTGTTG	AGAAGAACTAT	TGAATTGCCT	GATGGACAAG	TCATCACAAT	CGGAGCTGAG	AGATTCCGTT	GCCCAGAAGT	CCTCTTCCAG	GCCATCGCTGATTG	
-WGS	TCTGTTG	AGAAGAACTA	TGAATTGCCTO	GATGGACAAG	TCATCACAAT	CGGAGCTGAG	GAGATTCCGTT	GCCCAGAAGT	TCCTCTTCCAG	CCATCGCTGATTG	
nsus	tctgttga	agaagaacta	tgaattgeeto	gatggacaag	tcatcacaat	cggagctgag	gagattccgtt	gcccagaagt	cetetteca	gccatcgctgattg	1999
	1001	1011	1021	1031	1041	1051	1061	1071	1081	1091	2
-TSA	GAATGGA	AGCTGCTGGA	ATCCACGAGAG	CACCTACAA	CTCTATCATG	AAATGTGACG	TGGATATCAG	AAAGGATCTO	TACGGAAACA	ATTGTTCTCAGTGG	-
-#65	maatage	adctactace	atccaccacca	cacctaces	ctctatcate	aaatotoaco	togalalcab	AAAooAltil	TACGGAAALA	attatteteeataa	
1949	1101	1111	1121	1101	11/11	1101	1121	1171	1101	1101	Ŕ
-TSA	TGGCTCAL	ACCATGTTCC	CAGGTATTGC	TIST TGACCGGATG	AGCAAGGAGA	TEACTGETET	TIGECCCAAGE	AGCATGAAGI	TTAAGGTTCT	II91 IGGCACCACCAGAG	
-WGS	TGGCTCA	ACCATGTTCC	CAGGTATTGCT	FGACCGGATG.	AGCAAGGAGA	TCACTGCTCT	TGCCCCAAGC	AGCATGAAGA	TTAAGGTTGT	GGCACCACCAGAG	
nsus	tggctcas	accatgttcc	caggtattgct	tgaccggatg	agcaaggaga	tcactgetet	ctgccccaage	agcatgaaga	attaaggttgt	cggcaccaccagag	
	1201	1211	1221	1231	1241	1251	1261	1271	1281	1291	
-TSA	AGGAAGT	ACAGTGTCTG	GATCGGAGGAT	FCAATCCTTG	CATCCCTCAG	CACCTTCCAG	GCAG				• 5
-WGS	AGGAAGTI	ACAGTGTCTG	GATCGGAGGAT	FCAATCCTTG	CATCCCTCAG	CACCTTCCAG	<mark>GCAG</mark> GTGAATA	.00000000000000000000000000000000000000	TCCATGATTA	AGGCTCCTTTCTGC	1
ensus	aggaagta	acagtgtctg	gatoggaggat	tcaatcottg	catccctcag	cacettecaç	lcad				
	1301	1311	1321	1331	1341	1351	1361	1371	1381	1391	
T-TSA	ATT A 177						ATGTGGATTT	CCAAGGGCGA	GTACGACGAC	TETEGTECATETA	
T-WGS	ATATTCT	TIGGUCAGG	AUIGAUAATGO	LIGUITTGT	TITGTTTTGC	TITGTAATAG	atorogati	CCAAGGGGGG	AGTACGACGAG	HCTGGTCCATCTA	
:11343	1 407						acgrggattt		igcacgacgag	Jurggueeateta	Щ.
	1401	1411	1421	1431	1441	1451	1461	1471	1481	1491	2
-TSA -WGS	TTGTCCA	CAGGAAGTGC	TTCTAA								
ensus	ttgtccar	aggaagtor	ttctaa								1
000000000000000000000000000000000000000			12076 Birbh								

Figure S4. Sequence alignment of the putative *C. avellana MLO2* gene (*CavMLO2*) 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
ML02-GGSA010	ATGGCAG	GGGCCAGCGG	AGGAAGATCT	TTGGAACAAA	CGCCGACATO	GGCTGTCGC	GTTGTCTGT	FTTGTTTTGGT	CGTAATATCO	ATATTCATCGAGC
ML02-Cav10g0	ATGGCAG	GGGCCAGCGG	AGGAAGATCT	TTGGAACAAA	CGCCGACATO	GGCTGTCGC	GTCGTCTGT	FTTGTTTTGGI	CGTAATATCO	ATATTCATCGAGC
Consensus	acygcag	јууссаусуу 111	ayyaayatti	logyaacaad	icyccyacacy 1 au	1990 0900 900		171	101	Jacacccaccyayc
MI.02-665A010	ACATCAT	CACCTGATA	GGAAAG	151	141	151	101	1/1	101	191
ML02-Cav10g0	ACATCAT	CACCTGATA	GGAAAGGTAA	ATAAATATCI	CCAACAATAT	TAATTAATCO	GGCTTTTGT	GATTCTGAGTI	FGGAATATAA T	AGAAGTAATTTCT
Consensus	acatcat	ccacctgata	ggaaag							
	201	211	221	231	241	251	261	271	281	291
ML02-GGSA010		<mark>TG</mark>	GCTGAAGAAG	GAAACATAAAA	GAGCTTTAT	ATGAGGCGCTI	AGAAAAGATC <i>I</i>	AAATCAG		
ML02-Cav10g0	TGCGCCA	ATTTGCAG <mark>TG</mark>	GCTGAAGAAG	GAAACATAAAA	GAGCTTTATA	ATGAGGCGCTA	AGAAAAGATCA	AAATCAGGTCO	CGTACAACACA	GCACCTCTTCGTG
Consensus		tg	gctgaagaag	yaaacataaaa	agagetttata	atgaggegeta	agaaaagatca	aatcag		
M 00 0003010	301	311	321	331	341	351	361	371	381	391
ML02-GGSA010 ML02-Cav10g0	TTCATCA		ΑΤΑΤΤΑΑΤΤΙ	 \ATTAATATT	TTGTTTTG		AGCI GATGCAGAGCI	TATECTATIC	GGATTTATCI	CETTGETTETAAC
Consensus							aget	tatgetatto	ggatttatct	ccttgcttctaac
	401	411	421	431	441	451	461	471	481	491
ML02-GGSA010	GGTCGGA	CAAGGGATAA	TATCGAATAT	TTGCGTATCO	CAGAAAGTTO	GAGCGTCGT	GCATCCATG	CAGCAAGGAAA	AAGAACTCA	GTTGGACGAGGCG
ML02-Cav10g0	GGTCGGA	CAAGGGATAA	TATCGAATAT	FTTGCGTATCO	CAGAAAGTTO	GGAGCGTCGT	GCATCCATG	CAGCAAGGAAA	AAAGAACTCGA	GTTGGA
Consensus	ggtcgga	caagggataa	tatogaatat	ttgcgtatco	gcagaaagtto	gagegtegt	gcatccatgo	cagcaaggaaa	aaagaactc a	lgttgga
	501	511	521	531	541	551	561	571	581	591
ML02-GGSA010	GAGGAAA	CGGATTCTGA	TGATTCCAAT	CGACGGAAGC	TACTGATGT	FGTCGAACTCO	GGTGAAACTI	FTCCGACGCTI	TTTGGCGTCC	GCTTCGTCCAATT
ML02-Cav10g0	GGAAA	CGGATTCTGA	TGATTCCAAT	regaeggaage	TACTGATGT	FGTCGAACTCO	GGTGAAACTI	FTCCGACGCTI	FFFFGGCGTCC	GETTEGTECAATT
Consensus	ggaaa	cggattetga	tgattccaat	ccgacggaago	cactgatgtt	cgtcgaactco	cggtgaaacti	tteegaegett	rttggcgtci	Igettegtecaatt
M 00 0003010	601	611	621	631	641	651	661	671	681	691
ML02-GGSA010 ML02-Cav10g0	CCACTGA	TAAATGIGIA	GCCAAGGTGT	IGTCCCACACT	TATACGCCAT	TGGTGTGTT	TCTTTAAGAT	TTTTTTCTGTA	AAAACAACTO	TCATCCACACATT
Consensus	ccactga	taaatgtgta	gccaagg							
	701	711	721	731	741	751	761	771	781	791
ML02-GGSA010										
ML02-Cav10g0	GGACATA	FATATATAT	CATGAATTT	GATGTGAGAA	GAATTTTATA	ATATAGAGAA	GATTAGATTAT	ГСААААБАААА	ACAAAACAAGI	ATGAGACAAAATG
Consensus										
	801	811	821	831	841	851	861	871	881	891
ML02-GGSA010	TTTCANT	 \ \ \ TTC \ TCC	AGTTOTOTA			TCCCAACAT(TTCTACCCC	A ACTACCOACTT
Consensus	TITOAATI	MATICATOO	AUTIOIOIA	JAATOOOOACP	ICHIOACAAO	TOOCAACAT	JIOOINICIA	IOTTOTOACAC	JIICINCCCO	ANDIACCOACITI
	901	911	921	931	941	951	961	971	981	991
ML02-GGSA010										
ML02-Cav10g0	GATTTTT	нттттаа	TCACGTGAG	ACTITCTAAT	TTCAAGATAT	ГТАААСАТТТ <i>і</i>	AAAATCTATAT	rgaaaatcgac	CAGTCTAGATT	GTTATTAAAAAAA
Consensus										
	1001	1011	1021	1031	1041	1051	1061	1071	1081	1091
ML02-GGSA010						GTAAA(STCCCATTTG1	FATCGTCGGAT	FGGTATTCAT	AACTACACATATT
MLU2-Caviligu	ААААААА	HAAAAAAAAA	CAAGAAAIAI	AIAIIIIGAIA	IIGGAAAIIII	at a a a	HULLAIIIG	TAILGILGGAI	GGGIALICAL	AACTACALATATT
consensus	1101	1111	1121	1101	11.01	ycaaa.	11c1	1191	1101	.aactacatatat
MT.02-6654010	TATCTTC	TGTTGGCTG	TTTTCACG	TIST	TT41	TGGTTTTGG	TAGAGCCAA	11/1	1101	
ML02-Cav10g0	TATCTTC	GTGTTGGCTA	TTTTTCACGT	GCTTTATTGO	GTCATCACCO	TGGTTTTGG	GTAGAGCCAA	GTACGTAATI	ГААТААТТААТ	CCTTCTTAATTAC
Consensus	tatette	gtgttggct	tttttcacgt	getttattge	gtcatcacco	tggttttgg	gtagagccaaq	1		
	1201	1211	1221	1231	1241	1251	1261	1271	1281	1291
ML02-GGSA010							-ATGAGGCGT	TEGAAGCATI	FGGGAAATAGA	GACAAGAACTGCT
ML02-Cav10g0	TTATTTA	ATTACTTCAT	ATTCATATAT	TAATTAATCAA	TTAAGGGCTO	GTTTGGCTAC	AGATGAGGCGT	TEGAAGCATI	IGGGAAATAGA	GACAAGAACTGCT
Consensus							atgaggogt	ttggaagcatt	tgggaaataga	igacaagaactgct
	1301	1311	1321	1331	1341	1351	1361	1371	1381	1391
ML02-GGSA010 ML02-Cav10e0	GAGTACCI	AGTTUTUTUA AGTTUTUTUA	CGGTTAGCCT			 ГАТАТАТАТАТА	 ГАТАТАТАТАТ	 ГАТАТАТАТА	 	АТАТЕСТСАСАСС
Consensus	gagtacca	agttctctca	ca							

	1401	1411	1421	1431	1441	1451	1461	1471	1481	1491
ML02-GGSA010			<mark>ATCCAGA</mark>	GCGATTTAGG	TTTGCAAGGG	ACACGTCATI	TGGGAGAAGG	CACTTAAGCT	TCTGGACCAA	CACACCTGCCCTC.
ML02-Cav10g0	TGGTGTTG	CATGTGTGA	CAG <mark>ATCCAGA</mark>	GCGATTTAGG	TTTGCAAGGG	ACACGTCATI	TGGGAGAAGG	CACTTAAGCT	TCTGGACCAA	CACACCTGCCCTC
Consensus			atccaga	gcgatttagg	tttgcaaggg	acacgtcatt	tgggagaagg	cacttaagct	tctggaccaa	cacacctgccctc
	1501	1511	1521	1531	1541	1551	1561	1571	1581	1591
ML02-GGSA010	ATGTGGAT	AGT								
ML02-Cav10g0	ATGTGGAT	AGTAAGCAA	ттеттесте	CTCAGTTAAA	ATGCAATAGA	AATCCTAACA	ATTATGTTAT	TCAGATTGCT	AATAATTCAA	GCAATAATTCAAG
Consensus	atgtggat	agt								
	1601	1611	1621	1631	1641	1651	1661	1671	1681	1691
ML02-GGSA010										
ML02-Cav10g0	CAGTAGGG	CTTATAAGTA	AGGTCTCGCA	TAGTTCATCT	TTTTGTTCGG	GCAAGCGGAC	GACTCCTTAA	GAGCTTTTTT	ACGTTTGCTG	CTTAGATTGTTAG
Consensus										
	1701	1711	1721	1731	1741	1751	1761	1771	1781	1791
ML02-GGSA010										
ML02-Cav10g0	TAATTCAA	ACAACAAAT	TAATAGAAAT	TTGGATCTGT	ТТАААААСТС	ACGCTCGTGC	ATCATGCTGA	AATGTTGGAA	AGCACAAAAA	TTAAATTTTGAAT
Consensus										
	1801	1811	1821	1831	1841	1851	1861	1871	1881	1891
ML02-GGSA010										
ML02-Cav10g0	СААТАААА	CTGCACACA	AACTITACAA	GGGGACGTTA	GATAGATCCA	ATCCCTATCA	ATGGCTTTCC	ATTTCCGTAG	AGCTAGGTAG	AGAAACTAAAATC
Consensus										
	1901	1911	1921	1931	1941	1951	1961	1971	1981	1991
ML02-GGSA010										
ML02-Cav10g0	TCTAGACT	CTCCATATT	CTATATTGTC	TGAACGACCT	CTTTAGTAGT	ACAACATATA	CACCATTAGA	TCAGAGGATT	GATAAACTIT	GTCTAGGAATAGT
Consensus										
	2001	2011	2021	2031	2041	2051	2061	2071	2081	2091
ML02-GGSA010										
ML02-Cav10g0	GCTATTCG	ATCAGTTCG	TTGCCTTCGG	CCCCAAAAAT	TAGAGTGTTG	AATCAGATTI	AATTGAGTAA	TGATTACTAG	ТААТААТТАА	CGAACTAATTAAT
Consensus										
	2101	2111	2121	2131	2141	2151	2161	2171	2181	2191
MI.02-665A010										
ML02-Cav10g0	AAATTAAA	TGGCTTTGG	CTTCATTAAT.	ATTATTTCAA	GTTGAAACTC	CATTATAGGA	TGTTGAAAGA	AGAACCACCA	AGTACGTAAT	TTCTAAGGATATA
Consensus										
	2201	2211	2221	2231	2241	2251	2261	2271	2281	2201
MT 02-6654010										
ML02-Cav10g0	TCATGCAT	AGTTGATGT	GTTTATGACG.	ATTCAATAAT	GATGTGGGCG	GGATTTGACC	ACTTCAATCA	GAACTAAGAT	TTTTCACCGG	TTCATTTAGAGTA
Consensus										
	2301	2211	2221	2221	2241	2351	2261	2271	2291	2201
MT 02-CCSA010	2301	6J11	6361	2331	2341	2001	2301	2371	2301	
ML02-Cav10g0	TTCAGTTA	GATATTCGT	AAAAAAGTGA	AAAAACTACT	TITCACACAT	TACACATGGA	GCAGTTACCT	AACAAAGGAT	ACAAATTCAG	GCAACAGAAGAAA
Consensus										
	2401	2411	2421	2421	2441	2451	2461	2471	2401	2401
MT 02-6654010		6411	4461	2401		2401	2401		2401	
ML02-Cav10g0	ACGGTCAT	AACACGGCA	GTTAAAAAGA	AAACGACGTA	ATTAACCTCT	TACCGTGCAT	TTGACTTTTT	TGAACTGTCA	TTGGATTCGT	GAACAATGTTTCC
Consensus	1									
	2501	2511	2521	2531	2541	2551	2561	2571	2581	2501
MI.02-6652010		6J11		2001	2041	2001	2301		2301	
ML02-Cav10g0	TACTCCAA	TATCTTAAT	 ГААТТААТТА	ACAGGGCATT	TTCTTTGCAC	GAACTCTGTT	ТТСАСАСТАА	TCTTGTTTAT	 TTATTTATTT	ATTGCAGGTTTGT
Consensus										ttat
	2601	2611	2621	2621	2641	2651	2661	2671	2601	2601
M 00 0008010	2601	2011	Z0Z1	2031	2041	ZOSI	2001	20/1	2001	2691
ML02-GGSA010 ML02-Cav10g0	TTETTEAG	GCAGITIGI	TAGATEGGTT	CCTAAAGTIG	ATTACTICAC	TETGEGACAT	GGATTTATCA	TEETAATCTT	 ТСТАСТААТТ	AATTTGCGATTTC
Consensus	ttettead	acaatttati	tagategatt	rctasagttg	attacttoac	tetgegacat	ugatttatca	taa		
- one chode	2702	0.001		0.000	07.0	ogen	0741		0701	2701
M 00 000101-	2701	2711	2721	2731	2741	2751	2761	2771	2781	2791
ML02-665A010	111111	. ስጥር ምጥር ምጥል	 <u> </u> <u> </u>	 TATTTCTATC	 Гаааластсь	CACAUTTG	GCACCTCAAA	GTCACCAAAG	ATTTGACTTC	CAAAAGTATATCA
Concercie		anorioria.	ICIIAAI	ALLICIALD	CARARACICA	caractta	urcaceteeeo	atcaccese	atttractta	Casaagtatatata
consensus	0001	10000	100000		000000	Cacactog	igcaccicaaa	gecaccaaag	accegadede	Jaaaaytatattta
	2801	2811	2821	2831	2841	2851	2861	2871	2881	2891
ML02-GGSA010	AGAGATCA	TTGGAGGAG	GATITCAAG-	memora				·····		
MLU2-CaviugU	AGAGATCA	III GGAGGAGI	GATITCAAGG	1161161666	GATTAGGTTG	6166111166	ATTATGAATT	AATATTATUT	UCAGITIAIT	IGAATIAGATAAT
consensus	agagatca	iccààaààaài	yatttcaag							
	2901	2911	2921	2931	2941	2951	2961	2971	2981	2991
ML02-GGSA010										
ML02-Cav10g0	ATCGAGTI	AGTTATATTA	AGAAGGATAT	ITTTATCTAT.	аааааастаа	AATGACAAAA	ATACCATTCC	AATATAATTA	ACTGGATATT	ATCTAGTTCAAAT

Consensus

	3001	3011	3021	3031	3041	3051	3061	3071	3081	3091
ML02-GGSA010									CCCACCG	ATCTGGTTTTTCG
ML02-Cav10g0	GAACTGGA	GAGGATCTTO	TTTCTCCAT	CACACCCTTA	TGTTCAAGTC	ТААСААТТАА	TCATTTTTC	TTTTCAATTI	CAG <mark>CCCACCG</mark>	ATCTGGTTTTTCG
Consensus									cccaccg	atctggtttttcg
	3101	3111	3121	3131	3141	3151	3161	3171	3181	3191
ML02-GGSA010	CTGTGGTA	FICTIFACTO	TTAACACTC	ACGG	 እስርእስጥስጥጥ	••	TENENCENTO			
Consensus	ctataata	ttettactet	ttaacacto	acua	ANOAATATTA	MILIOANICA	TONONOONTO	AAAAAIOIOA	INANOTITICAC	AACITITITI
	3201	3211	3221	3231	3241	3251	3261	3271	3281	3201
ML02-GGSA010		J211	J661	CT	GGAAATCTTA	TETATGGETG	CCATTTATCC	CATTGETT		5291
ML02-Cav10g0	TTTTTTTG.	ACTAAGTTGI	CTTGCTTGT	TTTGCAGG <mark>CT</mark>	GGAAATCTTA	TCTATGGCTG	CCATTTATCC	CATTGCTTGT	TAAGCAAATTA	тататстстсста
Consensus				ct	ggaaatctta	itctatggctg	ccatttatcc	cattgctt		
	3301	3311	3321	3331	3341	3351	3361	3371	3381	3391
ML02-GGSA010								<mark>A</mark>	TCATCCTACT	GGTGGGGGACGAAA
ML02-Cav10g0	TCCATCAC.	ATGTCTGAT	ТААТАТАТА	ATTATAGCAG	CTAGCTAGCA	GATGATCTAA	CGGCTAAATA	TGGCTGCAG <mark>A</mark>	ATCATCCTACT	GGTGGGGGACGAAA
Consensus								8	atcatcctact	ggtggggacgaaa
	3401	3411	3421	3431	3441	3451	3461	3471	3481	3491
ML02-GGSA010	CTACAGGT	GATCATAACO	CAAAATGGCA	TTGAGAATCC.	AGGAGAGAGG	AGAGGTTGTG	CAGGGGGGTGC	CAGTGGTGCA	GCCAGGTGAC	GAACTETTETGGT
MLU2-Cav1UgU	UTACAGGT	GATUATAAUU	AAAATGGCA	TTGAGAATUU.	AUGAGAGAGU	AGAGGTTGTG	CAGGGGGGTGC	CAGTGGTGCA	AGUUAGGTGAU	GAUCTUTTUTGGT
consensus	ctacaggt	gatcataaco	aaaatggca	ttgagaatcc	aggagagagg	lagaggttgtg	caggggggtgc	cagtggtgca	igccaggtgac	ga ctcttctggt
M 00 0058010	3501	3511	3521	3531	3541	3551	3561	3571	3581	3591
ML02-Cav10g0	TCAACCGC	CCTCGCCTC	TTCTCTACC	TCATCAACTT	TGTTCTCTTT	CAGGTTCTTT	TCCCATAATT	CTTTGCCTTA	ATTTCTTACA	TAAATAACGCTAA
Consensus	tcaaccgc	cctcgcctca	attetetace	tcatcaactt	tgttctcttt	cag				
	3601	3611	3621	3631	3641	3651	3661	3671	3681	3691
ML02-GGSA010										
ML02-Cav10g0	ATATTTAG	CAAGACTCTT	TATACAACTG	TCATACAATC	TAATAATGTG	GTCGTGAAAA	TGATATTTAA	GATTATTTAA	GATTATCACT	AGCAGTGACGGAG
Consensus										
	3701	3711	3721	3731	3741	3751	3761	3771	3781	3791
ML02-GGSA010										
ML02-Cav10g0	CCAGAAAT	TACTATGGGG	GAGGGGTCAG	GAGTCAAAAA	AAATTGTTAC	TAGGAGTCGG	TGGGCTGATT	TATTATTGTI	TATTATTATTA	TTATTATTATTTA
Consensus										
	3801	3811	3821	3831	3841	3851	3861	3871	3881	3891
ML02-GGSA010 ML02-Cav10g0	CCTTAAAA		GTTAGGAAT	TGGAGAGGGG	CCATGGCCAA	CACCAATCTC	CCTCCCCTCC	GTEETTEATE	ACTAGTATAA	CAATCGTATAATA
Consensus										
	3901	3911	3921	3931	3941	3951	3961	3971	3981	3991
ML02-GGSA010										
ML02-Cav10g0	ATTITCAT	TGACATGTT <i>I</i>	ACCTAGTATA	TATATCAGTC	ТАСТАААТАА	ТАТТАТТАСТ	аттаатттта	CTTAATCCAC	CATCATAGTA	TGCTAATAATTCT
Consensus										
	4001	4011	4021	4031	4041	4051	4061	4071	4081	4091
ML02-GGSA010				AATGCCTTTC.	AGCTTGCTTI	CTTTGCATGG	GCTTGG			
MLU2-Cavilugu	IILLLAIL	1116101111	JULGIIILAG	AAIGUUIII.	agettgettt	ctttgcetgg	<mark>GUIIGG</mark> GIAA	GUIAUUAIUA	AIAIAIAIAIA	AIAIICCAIGICC
consensus	4101	4111	4101	4101	aye cege cee	ALE1	41.61	4171	4101	4101
MT.02-6654010	4101	4111	4121	4131	4141	4151	4101	41/1	4101	CAATTOGGGTTGA
ML02-Cav10g0	CTATATAT	GCTTAAAACI	TCAATAGTA	CGTGTGAAAA	ATTATTTAAA	TTAAGTAATA	TTGATAATTA	CTGTTATGAT	TTTTCAGTAT	CAATTCGGGTTGA
Consensus									tat	caattcgggttga
	4201	4211	4221	4231	4241	4251	4261	4271	4281	4291
ML02-GGSA010	AATCTTGT	TTCCACGACO	ATACTGAGG	ATATTGTCAT	TAGAATCTCA	ATGGGG				
ML02-Cav10g0	AATCTTGT	FTCCACGACO	CATACTGAGG	ATATTGTCAT	TAGAATCTCA	ATGGGGTACG	TCTCATTAAT	TATCACTTTC	TATATTTATG	ATTCTGAAATTAA
Consensus	aatcttgt	ttccacgaco	catactgagg	atattgtcat	tagaatetea	latgggg				
	4301	4311	4321	4331	4341	4351	4361	4371	4381	4391
ML02-GGSA010						GTCCTCA	TACAAATTIT	GTGCAGCTAC	GTAACTCTCC	CACTCTATGCCCT
Consensus	ATTAATTO	MAAIGIICIA	MINCANIIA	AAAA101100	CICILIIAIC	atcetca	tacaaatttt	atacaactac	ataactetee	cactctatgccct
oonbenbab	4401	4411	4421	4421	4441	A4E1	AA61	4471	лло1	4401
ML02-GGSA010	TGTAACAC	4411 AG	4421	16##		1049F			4401	4471
ML02-Cav10g0	TGTAACAC.	AGGTAACAAA	ATTATTTT	GATCAAAATA	TGCATAGAAA	GAGTTCAACA	TTACATGCAG	ATCGAGCCTG	ATTTTCTTCT	TTTTGTTATGATA
Consensus	tgtaacac	ag								
	4501	4511	4521	4531	4541	4551	4561	4571	4581	4591
ML02-GGSA010	A	FGGGTTCATO	CATGAAACC	AACCATATTC.	AACGAAAGAG	TGGCGGCGGC	TCTACGCAAC	TGGCACCACA	CGGCGAGGAA	GAACCTAAAGCAG
ML02-Cav10g0	TGAGTAGA	FEGETTCATO	CATGAAACC	AACCATATTC.	AACGAAAGAG	TGGCGGCGGC	TCTACGCAAC	TGGCACCACA	ACGGCGAGGAA	GAACCTAAAGCAG
Consensus	a	tgggttcato	catgaaacc	aaccatattc	aacgaaagag	ırddeddedde	tctacgcaac	tggcaccaca	acggcgaggaa	gaacctaaagcag

	4601	4611	4621	4631	4641	4651	4661	4671	4681	4691
ML02-GGSA010	AACAAGGGC	TEGGTGACO	GGGACCCCGAT	FGTCTAGCAG	ACCCGCCACO	CCGTCCCACC	ACATGTCCCC	GGTTCACCTC	CTCCGTCACT	ACCGGAGCGAGG
ML02-Cav10g0	AACAAGGGC	TEGGTGAC	GGGACCCCGA	FGTCTAGCAG	ACCCGCCACO	CCGTCCCACC	ACATGTCCCC	GGTTCACCTC	CTCCGTCACT	ACCGGAGCGAGG
Consensus	aacaagggc	toggtgao	igggaccccgat	tgtctagcag	accogcoaco	ccgtcccacc	acatgtcccc	ggttcaccto	ctccgtcact	accggagcgagg
	4701	4711	4721	4731	4741	4751	4761	4771	4781	4791
ML02-GGSA010	CGGACAGCC	TCCACACAT	CACCGAGACG	ATCCAATTTT	GACATTGAG	ATTGGGAAAC	TGAATCTCCG	TCCCCCTCGC	ACCACCACCA	CCTGGTCGGCGA
ML02-Cav10g0	CGGACAGCC	TCCACACAT	CACCGAGACG	ATCCAATTTT	GACATTGAG	ATTGGGAAAC	TGAATCTCCG	TCCCCCTCGC	ACCACCACCA	CCTGGTCGGCGA
Consensus	cggacagcc	tccacacat	caccgagacg	atccaatttt	gacattgago	cattgggaaac	tgaatctccg	teccetege	accaccacca	cctggtcggcga
	4801	4811	4821	4831	4841	4851	4861	4871	4881	4891
ML02-GGSA010	GGGTTCATC	CTCGCATC	CAACGGCCAC	CAAATGGGCC	AAAGGAATT <i>I</i>	TATTGAGTAT	GATGTAAAAG	AGCTGAACTC	AAGTCAAGTG	GCTCCGCTTCCA
ML02-Cav10g0	GGGTTCATC	CTCGCATC!	CAACGGCCAC	CAAATGGGCC	AAACGAATT#	ATATTGAGTAT	GATGTAAAAG	AGCTGACCTC	AAGTCAAGTG	GCTCCGCTTCCA
Consensus	gggttcatc	ctcgcatca	caacggccac	caaatgggcca	aaa gaatta	atattgagtat	gatgtaaaag	agetga etc	aagtcaagtg	gctccgcttcca
	4901	4911	4921	4931	4941	4951	4961	4971	4981	4991
ML02-GGSA010	CAAACAGAC	CGCTTGGA	CACCAAATTG	ATATCGGCCC	ACCAAAGGAG	TTTTCATTTG	ATAAAAGAAC	AAGTTTGTGA		
ML02-Cav10g0	CAAACAGAC	CGCTTGGA	CACCAAATTG	ATATCGGCCC	ACCAAAGGAG	TTTTCATTTG	ATAAAAGAAC	AAGTTTGTGA		
Consensus	caaacagac	cgcttggaa	caccaaattg	atatoggood	accaaaggad	cttttcatttg	ataaaagaac	aagtttgtga		

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.

Bit 0.6-663A010 ATTOCOS JANOS (0.6.00 GABAGADATA LATOGO ADATA LATOGO ADATA LATOGO ADTOGO CONTINUE TO UTUTO TTUE AUTUT TATU TATA AUTUT LATURAL AUTUAL AU		1	11	21	31	41	51	61	71	81	91	
HUB - Georg 741 TODOGRAPHIC EXAMPLANCY ANTICAGOUNDER CITEMENT CONTROL CUTENT CONTENT C	ML06-GGSA010	ATGGCGGT	'CGCGG <mark>AGAA</mark>	GGAAAGTACI	AATGGAGGAA <i>l</i>	CTTCAACATO	GGCAGTTGC	GGCGGTGTGCI	TTCGTCTTGC	TTGCC <mark>GTTT</mark> C	AATCTTCATTGAAC	
Conservator argeorgy of y agaagsaacabagaacabacab	ML06-Cav07g1	ATGGCGGA	CAAGCAGAA	GGAAAGTACI	AATGGAGGAAI	CTTCAACATO	GGCAGTTGC	GGCGGTGTGC	TCGTGTTGC	ITGCCATTTC	AATCTTCATTGAAC	
101 111 121 131 141 151 161 171 181 391 110.6 65.001 ATATETCA TO CATAGOGAAL Consensus 201 211 221 231 241 251 261 271 281 291 110.6 605.001	Consensus	atggcgg	c g agaa	ggaaagtaca	aatggaggaas	ncttcaacato	ggcagttgc	ggcggtgtgct	tegt ttge	ttgcc tttc	aatetteattgaae	
M. 06 - 6058010 AVAIT TELA TOLATICIA TOLATICIA TOLATORADO M. 06 - 6058010 AVAIT TELA TOLATICIA TOLATORADO CONTRACTOCIONECTONICA CASTOCTEVITI TOTTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTU		101	111	121	131	141	151	161	171	181	191	
NLID=Cartoria Constraint Cons	ML06-GGSA010	ATATTCTT	CATTCTATT	GGAAAG								
Consensus 201 211 221 231 241 251 261 271 281 291 ML 06-062701	Conconque	ATATICT	CAIGUIAII	GGAAAGGIAA	46616616161	,ILIGUILALA	GIUIUIGIII	11161116161	IGIIIAAII	AAIIGUIGAA	AICAIIICIIGAII	
201 211 221 231 241 231 231 241 231 241 231 241 231 231 231 231 231 231 231 231 231 231 231 231 331 341 351 361 371 381 391 M. 06 - 665A010 M. 05 - 665A010	consensus		.cat ttatt	yyaaay								
H105-005K010 International control and control in account of the control and contro and control and control and control and cont	NR 06 0003010	201	211	221	231	241	251	261	271	281	291	
Column Under Grade 0.0 311 321 331 341 351 361 371 391 391 M.0.6-GCANO791 ATSATCONTOCONTINUODATTCATACCONTOCONTACATACCTUCTOCALACIST September 2010 391 391 391 M.0.6-GCANO791 ATSATCONTOCONTCATACCTUTOCONTACATIC September 2010 September	ML06-GGSAUIU ML06-Cav07g1	COTTRAAT	AGTEECTAA	ААААСАААСИ ААГАГААААСИ	ACAAACGAGCI ACAAACGAGCI	CTITACGAAU CTITACGAAU	CGUTTGAAA	AGATCAAAGC <i>i</i> Agatcaaagc <i>i</i>	GGTATCTCT	адаттетета	CCTCACACATTAAG	
301 311 321 341 351 361 371 381 391 HL 06-G6SA019 ATGATCAGCATTCAGCATTCAGCATTCATCCCTAGCATTTTTTTT	Consensus		taactaa	aa acaaaca	tonenceese	ctttacraar	cacttaaaa	agatcaaagca	aa	NONTTOTOTA	COTORCACATIANO	
Sub Sub <th></th> <th>201</th> <th>211</th> <th>221</th> <th>221</th> <th>241</th> <th>251</th> <th>261</th> <th>271</th> <th>201</th> <th>201</th>		201	211	221	221	241	251	261	271	201	201	
ML 06 - CAV0721 ATGATEGATCASGATTCASTCCCTTATCCATTCTCTTCCAGGGTTTTTTCTGGGGATTGTTTGGGGATTCATATCCTTGCTCGGATTGATAGTGCTGGGATCGATGGAGGGATGGGAGGGA	MT 06-GGSA010	301	311	321	551	341	331	AGCTTATG	TETTERAT	JOI TCATATCCTT	GCTCCTGACAGTGT	
agettatgetgttgggatteatstetttgetectgacagtgt MI.06-665X010 MI.06-05X010 MI.06-05X010 MI.06-05X010 MI.06-05X010 Consensus Consensus <th co<="" th=""><th>ML06-Cav07g1</th><th>ATGATCGA</th><th>TCAGGATTC</th><th>AGTEGEETAA</th><th>ACCATTTTTC</th><th>TTCATGGGT</th><th>TTTTTGGGC</th><th>AGAGCTTATGO</th><th>TGTTGGGAT</th><th>TCATATCOTT</th><th>GCTCCTGACAGTGT</th></th>	<th>ML06-Cav07g1</th> <th>ATGATCGA</th> <th>TCAGGATTC</th> <th>AGTEGEETAA</th> <th>ACCATTTTTC</th> <th>TTCATGGGT</th> <th>TTTTTGGGC</th> <th>AGAGCTTATGO</th> <th>TGTTGGGAT</th> <th>TCATATCOTT</th> <th>GCTCCTGACAGTGT</th>	ML06-Cav07g1	ATGATCGA	TCAGGATTC	AGTEGEETAA	ACCATTTTTC	TTCATGGGT	TTTTTGGGC	AGAGCTTATGO	TGTTGGGAT	TCATATCOTT	GCTCCTGACAGTGT
401 411 421 431 441 451 461 471 491 491 HL 06-6658.010 FARAGATCCATTTICACATACCATACCAAGAGATTOGACCACTTCCTTTTGAALCOFTAAGAGATTOGACCACCAAATAGATTACCAATAGAGATTOGACCACTCCAATATACCAATAGAGATTOGACCACTCCAATATACCAATACCAAGATTOGACCACTCCAATATACCAATACCAAGATTOGACCACTCCAATATACCAATAGAGATTOGACAACCAACTACACTAC	Consensus	-						agettatge	tgttgggat	tcatatcctt	gctcctgacagtgt	
HL 06-66SA010 ALAGATCCATTTTACCATATICACTATCCAAGAGATCCOAGCACCTOCATCTTTTGAACCOTTAGAACAGATCAACATAGATCCAACTAGATTCTCA HL 06-6CAV071 ALAGATCCATTTTACCATATCCATACCCAAGAGATCCOAGCACCTOCGATCTTCTTTGAACCOTTAGAACATAGAACTAGAACAACATAGATTCCAATTTACCAATATCCAATTCCAATTTCACATATCCAATACCAAGATCCAACTATCCAATTCCAA		401	411	421	431	441	451	461	471	481	491	
IND.06-Cav0791 TACAAGATCCCATTTCTACCATATCCATAGCCAAGATCGGAGCCACCTUCTUTGAAAGGTTGAAGATCGGAGAAGCCATCATTTCTGGATCGGATCACCTUTTGAAGACGGAGAAGCGATCGGAGAAGCGATCGGATCG	ML06-GGSA010	TACAAGAT	CCCATTTCT	ACCATATGC	ATACCCAAGAG	AGTEGGAGEC	ACGTGGCAT	CCCTGTGAAAG	GGTGAAGAA	TGGGACGACC	AAAAAAGATTCTGG	
Consensus tacaagatcccatttotaccatatgcatacccaagagatggggacaccctytygaacggtggaagaatggyac accaa a agattctyg 501 511 521 531 541 551 561 571 581 591 M1.66-66X007071 AATTCCGAGCATTCTCTGCAGCAACCACCAATGCTCCAATTTTTGCATTCGCTTCCTCGCGCGACATTAGCTACAAAAGGATACGAC AATTCCGAGCATTCTCAGGACACCAATGGTCGCAAACTGCTCCAATTTTTGGCTTCTCTGTCTG	ML06-Cav07g1	TACAAGAT	CCCATTTCT	ACCATATGC	ATACCCAAGA	AGTEGGAGE	ACGTGGCAT	CCCTGTGAAAO	GGTGAAGAA	TGGGAC <mark>A</mark> ACC	AACATAGATTCTGG	
S01 S11 S21 S31 S41 S51 S61 S71 S81 S91 ML06-Ce3V010 AMATTCGAGGATTTCAGGACACCAATGGTCGAAATCGTCGAAATTGGTCGAAATCGTCCAATGGTCGAATGGCGAAATGGTCGAATGGCGAAATGGTCGAATGGCGAAATGGTCGAATGGCGAAATGGTCGAATGGCGAATGGCGAAGGTCGAATGGCGAAGGGTAGTAAGAAGGTCGAATGGAATGGAATGGTCGAATGGAAGAAGAAAA	Consensus	tacaagat	cccatttct	accatatge	atacccaaga	agtoggagod	acgtggcat	ccctgtgaaaa	ggtgaagaa	tgggac acc	aa a agattctgg	
H1.06-06SA010 (H.06-Cav07q) AGATTCCGAGGATTCTGGAGAAGCATGGTGGGAAATTGTTGGCTACTAGATGGTGTGGGGGATTGCTGCGAGATTAGCTACAAAAGGATAGGA AGATTCCGAGGATTCTGGAGAACGAATGGTGGGAAATTGTTGCGTTTTTGGATTCTGCTTTTGTTCTGTCGGGGGAGTTGGCTACAAAAGGATAGGA GGTGCGAGGGAGAGGACGACAGCAATGGTGGGAGAGTGCCCAATTTTTGGATTCTGGTTTGTTGTGTGTG		501	511	521	531	541	551	561	571	581	591	
INL 06 - Cav 0791 AGATTECCAGGATTECTGAGGACAGCAGCAGCAGACGACGACCGAATTGETTGGATTETTGGATTECTGETCGTGGAGATTAGCTACAAAAGGATACGAC Consensus AGATTECCAGGATTAGCTACGAGGACAGCACGACGACGACGAATTGETTGGATTETTGGATTETTGGTTCGTGGTGGTGGTGGTGGGGGGGGGG	ML06-GGSA010	AGATTCCG	AGGATTCTG	AGGACAGCA	ATGGTCGGAAI	CTGCTCCAAT	TTTTGGATT	CTGGCTTCTCT	GCTCGTCGG	AGATTAGCTA	CAAAAGGATACGAC	
Consensus agattccgaggattctgaggacagcagcagcagggggggg	ML06-Cav07g1	AGATTCCG	AGGATTCTG	AGGACAGCA	ATGGTCGGAAI	CTGCTCCAAT	TTTTGGATTO	CTGGCTTCTCT	GCTCGTCGG	AGATTAGCTA	CAAAAGGATACGAC	
501 611 621 631 641 651 661 671 681 691 HL 06-GGSA010 AATTECA (AAAATTE AATTECA (AAAATTE AATTECA (AAAATTE AATTECA (AAAATTECATTECTTTECTTTECTTTECTTTECTTTECT	Consensus	agattccg	aggattetg	aggacagcas	atggtcggaas	actgetecaat	ttttggatto	etggettetet	getegtegg	agattagcta	caaaaggatacgac	
HL06-G6SA010 AAGTCACAAAAATGTAATTGTTTTTTTTTTTTTTTTTTT		601	611	621	631	641	651	661	671	681	691	
ML06-Cav07g1 AAGTGCAALGAAAATGTAATTTCTTTTTTTTTTTTTTTTT	ML06-GGSA010	AAGTGCAC	AAAAAATG-									
Consensus aagtgca a aaaatg ML06-GGSA010 711 721 731 741 751 761 771 781 791 ML06-GGSA010 711 721 731 741 751 761 771 781 791 ML06-GGSA010 TTTGGGTTGCCTATTTGCAGGAAAAGTTGCCTTCATGTCTGCATTCCCATTCAGCAGCCCATGGTCATCTCATCTTCGCTTTGGCAGTTTTGCAGGAAAAGTGCCAGAGG 891 910 910 910 <th>ML06-Cav07g1</th> <th>AAGTGCAA</th> <th>AGAAAATGT</th> <th>AATTTCTTT</th> <th>CTTTCTTTCT</th> <th>TCTITCTIC</th> <th>CAAATGGGT</th> <th>ATTACCAATG</th> <th>AGATCTAAT</th> <th>TGATTTAATT</th> <th>CCATGGAATAATCA</th>	ML06-Cav07g1	AAGTGCAA	AGAAAATGT	AATTTCTTT	CTTTCTTTCT	TCTITCTIC	CAAATGGGT	ATTACCAATG	AGATCTAAT	TGATTTAATT	CCATGGAATAATCA	
701 711 721 731 741 751 761 771 781 791 ML06-G6SA010 Consensus Gaaaast GeeCTTCATGTCGCATTGCGATTGCAGTCCAGGCCCACGCCCCGTGTGTTCATCTTGGCTGGC	Consensus	aagtgca	a aaaatg									
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Consensus 1301 1311 1321 1331 1341 1351 1361 1371 1381 1391 ML06-GGSA010	Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010	801 TTTTCTCC TTTTTTGC tttt t c 901 GATTCTAA 1001 TGACTTTC 1101 TGCACATC 1201	811 ATACTCACC ATACTCACC Satactcacc 911 ATCCCTCTT 1011 SAAACCATCT 1111 GGCTCTTCC 1211	gaaas 821 CTGGCTTTG CTTGCTTTG ct gctttg 921 TGAATTGCA 1021 ACTCACGTCT 1121 AAAATTTTCT 1221	agt gccttcs 831 GCCAGAACGAJ GCCAGAACGAJ ggcagaacgas 931 ATGAGAAGAA ATGAGAAGAA atgagaagat 1031 TCCTAAATCAJ 1131 TTTAAAAAAAA 1231	atgtetgeats 841 GGTACCCTTT ag 941 GGAAGGCTTT GGAAGGCTTTC GGAAGCTTTT 1041 ATTGETTCTTTT 1141 AGTGTGTGTTGTT 1241	atgc attcad 851 TACCCTTTCT 951 GGAGGACGATGAJ GGAGGACGACGAT 1051 TCCACTTAAT 1151	CCAGCCCCALC 861 TCCTTCTATGO 961 AACCAAGAACAO AACGAGAACAO AACGAGAACAO 1061 TTTAAATTTAAJ 1161 TGATTAATTAC 1261	SAGATCTATA 971 CTTGAATATCA CTTGAATATCA CTTGAATATCA CTTGAATATCA 1071 1171 STAAAATGAT 1271	tcgtcttggc 881 AATTCTTCTT 981 AATATCATAA AATATCATAA aatatcataa 1081 CGTTTGCTGA 1181 TAAGAAAAAA 1281	tttttcatgtga 891 CTITGAATTGTGTA 991 TG TGGTAACTCCTCTT tg 1091 CGTGGAACTCAAAA 1191 ATATACCCTCCAAT 1291	
1301 1311 1321 1331 1341 1351 1361 1371 1381 1391 ML06-GGSA010	Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-CGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010	801 TTTTCTCC TTTTTTGC tttt t c 901 GATTCTAA 1001 TGACTTTC 1101 TGCACATC 1201 CTAATTGC	811 ATACTCACC ATACTCACC SATACTCACC SATACTCACC 911 ATCCCTCTT 1011 SAAACCATCT 1111 SGGCTCTTCC 1211	gaaa: 821 CTGGCTTTG CTTGCTTTG ct gctttg; 921 TGAATTGCA(1021 1021 ACTCACGTC 1121 AAAATTTTC 1221 AAAATTTTC	agt gccttcs 831 GCCAGAACGAJ GCCAGAACGAJ GCCAGAACGAJ ggcagaacgas 931 ATGAGAAGAA ATGAGAAGAA 1031 ICCTAAATCAJ II31 ITTAAAAAAAJ 1231 ATTATTTTAC	atgtotgcate 841 GGTACCCTTT Ag 941 GGAAGGCTTTC GGAAGCTTTC GGAAGCTTTC 1041 ATTGCTTCTTT 1141 AGTGTGTGTTGTT 1241 CAATTATAAAA	atgc attcad 851 TACCCTTTCT 951 GGAGGACGATGAJ GGAGGACGACGAI 1051 TCCACTTAAT 1151 TAAGAGATTAT 1251 TATTACGTCG	CCAQCECCALC 861 FCCTTCTATGG 961 AACCAAGAACAG AACGAGAACAG AACGAGAACAG 1061 FTTAAATTAAT 1161 FGATTAATTAG 1261 CATTTGTAAAA	SAGATCTATA 971 SAGATCTATA 971 STTGAATATC, STTGAATATC, 1071 1171 STAAAATGAT 1271 AACATTATAG	tcgtcttggc 881 AATTCTTCTT 981 AATATCATAA AATATCATAA aatatcataa 1081 CGTTTGCTGA 1181 TAAGAAAAAA 1281 TCAATTTGGC	tttttcatgtga 891 CTTTGAATTGTGTA 991 TG TGGTAACTCCTCTT tg 1091 CGTGGAACTCAAAA 1191 ATATACCCTCCAAT 1291 CAACATTTTATGGA	
ML06-GGSA010 ML06-Cav07g1 CTTGGTCAGCTGCTCTACAGAGGAATCAGGCACCCCTCTTTCTT	Consensus ML 06-GGSA010 ML 06-Cav 07g1 Consensus ML 06-GGSA010 ML 06-GGSA010	801 TTTTCTCC TTTTTTGC tttt t c 901 GATTCTAA 1001 TGACTTTC 1101 TGCACATC 1201 CTAATTTG	811 ATACTCACC ATACTCACC Satactcacc 911 ATCCCTCTT 1011 AAACCATCT 1111 SGGCTCTTCC 1211	gaaa: 821 CTGGCTTTG CTTGCTTTG ct gctttg 921 	agt gccttcs 831 GCCAGAACGAJ GCCAGAACGAJ ggcagaacgas 931 ATGAGAAGAA ATGAGAAGAA ATGAGAAGAA 1031 FCCTAAATCAJ 1131 FTTAAAAAAAJ 1231 ATTATTTTACT	Atgtetgeate 841 GGTACCCTTT Ag 941 GGAAGGCTTC GGAAGCTTTC GGAAGCTTTC 1041 ATTGCTTCTTT 1141 AGTGTGTGTTGTT 1241 	atgc attcad 851 TACCCTTTCT 951 GGAGGACGATGAJ GGAGGACGACGAJ J051 TCCACTTAAT 1151 TAAGAGATTAT 1251 TATTACGTCC	CCAQCECCALC 861 TCCTTCTATGG 961 AACCAAGAACAG AACGAGAACAG AACGAGAACAG 1061 TTTAAATTAAT 1161 TGATTAATTAG 1261 CATTTGTAAAJ	SAGATCTATA 971 SAGATCTATA 971 STTGAATATC, STTGAATATC, 1071 AATACTTATC 1171 STAAAATGAT 1271 AACATTATAG	tegtettgge 881 AATTETTETT 981 AATATEATAA AATATEATAA AATATEATAA 1081 CGTTTGETGA 1181 TAAGAAAAAA 1281 FEAATTTGGE	tttttcatgtga 891 CTTTGAATTGTGTA 991 TG TGGTAACTCCTCTT tg 1091 CGTGGAACTCAAAA 1191 ATATACCCTCCAAT 1291 	
ML06-Cav07g1 CTTGGTCAGCTGCTCTACAGAGGAATCAGGCACCCCTCTTTCTT	Consensus ML 06-GGSA010 ML 06-Cav 07g1 Consensus ML 06-GGSA010 ML 06-GGSA010	801 TTTTCTCC TTTTTTGC tttt t c 901 GATTCTAA 1001 TGACTTTC 1101 TGCACATC 1201 1301	811 ATACTCACC ATACTCACC Satactcacc 911 ATCCCTCTT 1011 AAACCATCT 11111 CGGCTCTTCC 1211 TTATTAACC	gaaa: 821 CTGGCTTTG CTTGCTTTG ct gctttg 921 	agt gccttcs 831 GCCAGAACGAJ GCCAGAACGAJ ggcagaacgas 931 ATGAGAAGAA ATGAGAAGAA ATGAGAAGAA 1031 TCCTAAATCAJ 1131 TTTAAAAAAAJ 1231	Atgtotgoate 841 GGTACCCTTI Ag 941 GGAAGGCTTC GGAAGCTTCC GGAAGCTTCC GGAAGCTTCC 1041 1141 ATTGCTTCTTT 1141 	atgc attcad 851 TACCCTTTCT 951 GGAGGATGAJ GGAGGACGATGAJ GGAGGACGATGAJ TCCACTTAAT 1151 TAAGAGATTAT 1251 TATTACGTCC 1351	CCAQCCCCALC 861 TCCTTCTATG(961 AACAAGAACA(AACGAGAACA(AACGAGAACA(1061 TTTAAATTAAT 1161 TGATTAATTA(1261 CATTTGTAAAA 1361	SAGATCTATA 971 SAGATCTATA 971 STTGAATATC. STTGAATATC. 1071 1171 STAAAATGAT 1271 AACATTATAG 1371	tegtettgge 881 AATTETTETT 981 AATATCATAA AATATCATAA aatatcataa 1081 CGTTTGCTGA 1181 TAAGAAAAAA 1281	tttttcatgtga 891 CTTTGAATTGTGTA 991 TG TGGTAACTCCTCTT tg 1091 CGTGGAACTCAAAA 1191 ATATACCCTCCAAT 1291 CAACATTTTATGGA 1391	
	Consensus ML 06-GGSA010 ML 06-Cav07g1 Consensus ML 06-GGSA010 ML 06-GGSA010 ML 06-GGSA010 ML 06-GGSA010 ML 06-GGSA010 ML 06-GGSA010 ML 06-GGSA010 ML 06-GGSA010 ML 06-GGSA010 ML 06-GGSA010	801 TTTTCTCC TTTTTTGC Uttt t c 901 GATTCTAA 1001 TGACTTTC 1101 TGCACATC 1201 CTAATTTG 1301	811 ATACTCACC ATACTCACC atactcacc 911 ATCCCTCTT 1011 AAACCATCT 1111 CGGCTCTTCC 1211 TTATTAACC 1311	gaaa: 821 CTGGCTTTG CTGGCTTTG ctgcttg; 921 	agt gccttcs 831 GCCAGAACGAJ GCCAGAACGAJ ggcagaacgas 931 ATGAGAAGAA ATGAGAAGAA ATGAGAAGAA 1031 TCCTAAATCAJ 1131 1231 ATTATTTTTACT 1331	Atgtotgoate 841 GGTACCCTTT Ag 941 GGAAGGCTTC GGAAGCTTCC GGAAGCTTCC GGAAGCTTCC 1041 1141 ATTGCTTCTTT 1241 TAATTATAAAT 1341	ALGC ALLCAG 851 TACCCTTTCT 951 GGAGGACGATGAJ GGAGGACGACGAJ 1051 TCCACTTAAT 1151 TAAGAGATTAT 1251 TATTACGTCG 1351	CCAGGCCCCALG 861 FCCTTCTATGG 961 AACGAGAACAG AACGAGAACAG 1061 FTTAAATTAAJ 1161 FGATTAATTAG 1261 CATTTGTAAAJ 1361	SAGATCTATA 971 SAGATCTATA 971 TTGAATATC. TTGAATATC. 1071 AATACTTATCI 1171 STAAAAATGAT 1271 AACATTATAG 1371	tegtettgge 881 AATTCTTCTT 981 AATATCATAA AATATCATAA aatatcataa 1081 CGTTTGCTGA 1181 TAAGAAAAAA 1281 TCAATTTGGC 1381	tttttcatgtga 891 CTTTGAATTGTGTA 991 TG TGGTAACTCCTCTT tg 1091 CGTGGAACTCCAAAA 1191 ATATACCCTCCAAT 1291 CAACATTTTATGGA	

Consensus

	1401	1411	1421	1431	1441	1451	1461	1471	1481	1491
ML06-GGSA010 ML06-Cav07g1	 ТБАТТАБА	TGACTTTGC	 АТСССАТСАТ	CTTTTA	 TTTTATTTATT			АСТСААСТАА	ТАБАТБАСТТ	 TGTAAATTGCTTT
Consensus										
	1501	1511	1521	1531	1541	1551	1561	1571	1581	1591
ML06-GGSA010										
ML06-Cav07g1	TGTGAGCA	AATTCTGTA	<u>FGAAAAAATC</u>	TITAATITIT	ТГГГГААААА	AAAAATTTGA	TAGTGTGGTG	AAAGAGATCA	TATGGACTTC	AAGGGGGGGTGACA
consensus	1601	1611	1621	1621	1641	1651	1661	1671	1691	1601
ML06-GGSA010	1001	1011		ATCCA	CAGAGGTTTA	GGTTTGCAAA	GGAAACTTCA	TTTGGGCGAA	GGCATATGAG	CTTCTGGAGCAAG
ML06-Cav07g1	TATGCTTA	TGGAAAATG	ATTTATTTGA	TGCAG <mark>ATCCA</mark>	GAGAGGTTTA	GGTTTGCAAG	GGAAACTTCA	TTTGGGCGAA	GGCATATGAG	GCTTCTGGAGCAAG
Consensus				atcca	agaggttta	iggtttgcaa	ggaaacttca	itttgggcgaa	aggcatatgag	gettetggageaag
	1701	1711	1721	1731	1741	1751	1761	1771	1781	1791
ML06-GGSA010 ML06-Cav07g1	TCAACGGT	TTCTCTTTG	GGTGGT	AATGTCTCAT	CACGATTATO	TGACTITIAC	AATCATAATT	ААСАААБАСТ	САББААТТАА	GTTGTATTTGGAT
Consensus	tcaacggt	ttetetttg	ggtggt							
	1801	1811	1821	1831	1841	1851	1861	1871	1881	1891
ML06-GGSA010										
ML06-Cav07g1	GATTTGTI	'ACATAAATT'	FACTCTGTAT	ΆΤΤΤΑΤΑΑΤΑ	CGTACCTAAC	GTGCTTTCAA	AATATGCGAT	TTGACCAATA	TTTTAAAGCA	TAATTTTTTTTTTT
Consensus	1001	1011	1001	1001	1041	1051	1051	1071	1001	1001
ML06-GGSA010	1901	1911	1921	1931	1941	1951	1961	1971	1981	1991
ML06-Cav07g1	TITITI	GTGTTTTGC	AACCATTATT	TTGTTCAACT	GCACTTTTAA	ACGGGATACT	TTAGGCAATI	ттсттаааа	ATGCATATTI	TATCTTGCAAAATT
Consensus										
	2001	2011	2021	2031	2041	2051	2061	2071	2081	2091
ML06-GGSA010	GCAGGTCA		 ТТТАССТААА		CATCATTTC			тесстсатса		ТАСССССАТСААТ
Consensus	CENSOTER	INCOUNTIO.	TTROOTAAA		OAICAIIIIC	MOINCOUCCO	ACTOACTOCT	TOCCIONICA	MANOTITORO	TROOCCORTORNI
	2101	2111	2121	2131	2141	2151	2161	2171	2181	2191
ML06-GGSA010										
ML06-Cav07g1	CTTCTGTC	TGCATCACCA	ACAAGTTTCT	AAAAGTGACT	AGTTTTAAGT	ATAATAGGGA	CGTCCAAGTA	CCTTTTCTTA	ATAACGAGAA	ACTTGTGTTTATT
ML06-Cav07g1 Consensus	CTTCTGTC	TGCATCACC	ACAAGTTTCT	AAAAGTGACT	AGTTTTAAGT	ATAATAGGGA	CGTCCAAGTA	CCTTTTCTTA	ATAACGAGAA	ACTTGTGTTTATT
ML06-Cav07g1 Consensus ML06-GGSA010	CTTCTGTC 2201	2211	2221	AAAAGTGACT 2231	2241	ATAATAGGGA	CGTCCAAGTA 2261	2271	ATAACGAGAA 2281	ACTTGTGTTTATT 2291 TTCTTCAGACAAT
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1	CTTCTGTC 2201 TTTCAATT	ZZ11 TTGAACTTTA	ACAAGTITCT 2221 AAGGGCATAA	AAAAGTGACT 2231 AGAGTTGGTT	2241 GTGTTACACT	ATAATAGGGA 2251 TGTTTGAAAG	2261 ACCCTTTTCT	2271 CCTCCTCTTA	ATAACGAGAA 2281 <mark>GTGT</mark> ATCAGGT <mark>GTGT</mark>	2291 TTCTTCAGACAAT
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus	CTTCTGTC 2201 TTTCAATI	2211 TTGAACTTTA	ACAAGTTTCT 2221 AAGGGCATAA	2231 AGAGTTGGTT	AGTTTTAAGT 2241 GTGTTACACT	2251 TGTTTGAAAG	2261 GACCCTTTTCT	2271	2281 2281 <mark>GTGT</mark> ATCAGGT <mark>GTGT</mark> gtgt	2291 TTCTTCAGACAAT TTCTTCAGACAAT StCtCtcagacaat
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus	<u>CTTCTGTC</u> 2201 <u>TTTCAATT</u> 2301	2211 TTGAACTTTA 2311	2221 2221 AAGGGCATAA 2321	2231 AGAGTTGGTT 2331	2241 GTGTTACACT 2341	2251 TGTTTGAAAG 2351	2261 34000000000000000000000000000000000000	2271 2271 CCTCCTCTTA 2371	2281 GTGT ATCAGGTGTGT gtgt 2381	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT ttcttcagacaat 2391
ML06-Cav07g1 Consensus ML06-G6SA010 ML06-Cav07g1 Consensus ML06-G6SA010 ML06-Cav07g1	<u>2201</u> <u>1117CAAT1</u> 2301 <u>TCGTCAAA</u> TCGTCAGA	2211 7TGAACTT7/ 2311 ACCGTTACT/ ACAGTTACT/	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT	2231 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT	AGTTTTAAG1 2241 GTGTTACACT 2341 GAGACATGGA	2251 TGTTTGAAAG 2351 TTTATTGTGG TTTATCATGG	2261 2261 ACCCTTTTCT 2361	2271 2271 CCTCCTCTTA 2371	2281 GTGT ATCAGGTGTGT gtgt 2381 	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT LtCttCagacaat 2391
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus	CTTCTGTC 2201 TTTCAATT 2301 TCGTCAAA TCGTCAGA	2211 2211 TTGAACTIT 2311 ACCGTTACTI ACAGTTACTI iac gttacti	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT aaggttgatt	AAAAGTGACT 2231 	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga	2251 2251 TGTTTGAAAG 2351 TTTATTGTGG TTTATCATGG itttat tgg	2261 2261 ACCCTTTTCT 2361 TACGTTTAAT	2271 	2281 2281 TCAGGTGTGT gtgt 2381 TGCTAGAAAT	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT SttCttcagacaat 2391 TCACACTTTTATCC
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus	CTTCTGTC 2201 TTTCAATI 2301 TCGTCAAA TCGTCAGA tCgtCa a 2401	2211 2211 TTGAACTTTA 2311 ACCGTTACTA ACAGTTACTA AC gttacta 2411	ACAAGTITCT 2221 AAGGGCCATAA 2321 AAGGTTGATT AAGGTTGATT 3aggttgatt 2421	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ac ttac ct 2431	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA Agacatgga 2441	2251 2251 TGTTTGAAAG 2351 TTTATTGTGG TTTATCATGG itttat tgg 2451	2261 2261 ACCCTTTTCT 2361 TACGTTTAAT 7 2461	2271 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471	2281 GTGT TCAGGTGTGT gtgt 2381 	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT 2391 TCACACTTTTATCC 2491
ML06-Cav07g1 Consensus ML06-G6SA010 ML06-Cav07g1 Consensus ML06-G6SA010 ML06-Cav07g1 Consensus ML06-G6SA010	CTTCTGTC 2201 TTTCAATT 2301 TCGTCAAA TCGTCAGA tCGTCAGA 2401	2211 TTGAACTTT 2311 ACCGTTACT ACAGTTACT ac gttact 2411	ACAAGTITCT 2221 AAGGGCCATAA 2321 AAGGTTGATT AAGGTTGATT aaggttgatt 2421	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ac ttac ct 2431	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441	2251 TGTTTGAAAG 2351 XTTTATTGTGG XTTTATCATGG Itttat tgg 2451	2261 2261 GACCCTTTTCT 2361 TACGTTTAAT (2461	2271 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471	ATTAACGAGAA 2281 GTGT ATCAGGTGTGT gtgt 2381 	2291 TTCTTCAGACAAAT TTCTTCAGACAAAT TTCTTCAGACAAAT 2391 TCACACTTTTATCC 2491
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus	CTTCTGTC 2201 TTTCAATT 2301 TCGTCAAA TCGTCAGA tcgtca a 2401 TACAACTA	2211 TTGAACTITA 2311 ACCGTTACTA ACAGTTACTA ac gttacta 2411 TTTTATTTT	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT aaggttgatt 2421 GCTGATGTGA	AAAAGTGACT 2231 	AGTTTTAAG1 2241 GTGTTACACT 2341 GAGACATGGA Agacatgga 2441 CCAATCAGTO	2251 TGTTTGAAAG 2351 TTTATTGTGG TTTATCATGG Lttat tgg 2451 TTGGTTAAAAA	2261 2261 2361 74CCCTTTTCT 2361 74CGTTTAAT 2461 2461	2271 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA	2281 CTCACCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT 2391 TCACACTTTTATCC 2491
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus	CTTCTGTC 2201 TTTCAATI 2301 TCGTCAAA TCGTCAGA tCgtca a 2401 TACAACTA 2501	2211 2211 TTGAACTTT7 2311 ACCGTTACT7 ACAGTTACT7 Iac gttact0 2411 TTTTATTTT(2511	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT aaggttgatt 2421 GCTGATGTGA	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ac ttac ct 2431 TGAACCAATG	AGTTTTAAGI 2241 GTGTTACACI 2341 GAGACATGGA agacatgge 2441 CCAATCAGTC 2541	2251 2251 TGTTTGAAAG 2351 TTTATTGTGG TTTATCATGG Lttat tgg 2451 TTGGTTAAAA	2261 2261 2361 7ACCCTTTTCT 7ACGTTTAAT 7 2461 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	2271 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571	ATTAACGAGAA 2281 GTGT GTGT GTGT 2381 ATGCTAGAAAT 2481 ATTGTGCACTT	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT 2391 CACACTTTTATCC 2491 TGGGGATTCCAATT
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010	CTTCTGTC 2201 TTTCAATT 2301 TCGTCAAA TCGTCAGA tcgtca a 2401 TACAACTA 2501	2211 TTTGAACTTT7 2311 ACCGTTACT7 ACAGTTACT7 IAC gttact7 2411 TTTTATTTTC 2511	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT aaggttgatt 2421 GCTGATGTGA GCTGATGTGA	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ac ttac ct 2431 TGAACCAATG 2531	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441 	2251 TGTTTGAAAG 2351 TTATTGTGG TTATCATGG Lttat tgg 2451 TTGGTTAAAA 2551 GGCACCGGAA	2261 2261 ACCCTTTTCT 2361 TACGTTTAAT (2461 ATAAAAAATT 2561 AGTGAAACAA	2271 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571 AGTTTGATTT	ATTAACGAGAA 2281 GTGT GTGT 2381 	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT CLCCLCagacaat 2391 TCACACTTTTATCC 2491 TGGGGATTCCAATT 2591 CATCAAGAGATCAC
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus	CTTCTGTC 2201 TTTCAATT 2301 TCGTCAAA TCGTCAAA tCGTCAAA 2401 TACAACTA 2501 CACATTGA	2211 TTGAACTTTA 2311 ACCGTTACTA ACCGTTACTA ACAGTTACTA ACAGTTACTA ACAGTTACTA ACAGTTACTA ACAGTTACTA ACAGTTACTA ACAGTTACTA ACAGTTACTA ACAGTTACTA ACAGTACTA ACAGTTACTACTA ACAGTTACTACTA ACAGTTACTA ACAGTTACTACTACTA ACAGTTACTACTACTACTACTACTACTACTACTACTACTACTAC	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT aaggttgatt 2421 GCTGATGTGA GCTGATGTGA 2521 TCCAATGTT	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ac ttac ct 2431 TGAACCAATG 2531 	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441 	2251 TGTTTGAAAG 2351 TTATTGTGG TTATCATGG Lttat tgg 2451 TTGGTTAAAA 2551 TGGCACCGGAA TGGCACCGGAA	2261 2261 3ACCCTTTTCT 2361 7ACGTTTAAT (2461 4ATAAAAAAATT 2561 4AGTGAAACAA 4AGTGAAACAA	2271 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571 AGTTTGATTT AGTTTGATTT	ATTAACGAGAA 2281 GTGT STCAGGTGTGT 2381 	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT CACACATTTAGCACAAT 2391 TCACACTTTTATCC 2491 TGGGGGATTCCAATT 2591 CATCAAGAGATCAC CATCAAGAGATCAC
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus	CTTCTGTC 2201 TTTCAATI 2301 TCGTCAAA TCGTCAGA tcgtca a 2401 TACAACTA 2501 CACATTGA	2211 TTGAACTTTA 2311 ACCGTTACTA ACAGTTACTA IAC GTTACTA IAC GTTACTACTA IAC GTTACTA IAC GTTACTA IAC GTTACTA IAC GT	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT aaggttgatt 2421 GCTGATGTGA GCTGATGTGA 2521 CTCCAATGTT	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ac ttac ct 2431 TGAACCAATG 2531 ATGTGACTTA	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441 CCAATCAGTC 2541 CACACTT AGGCACACTT cacactt	2251 TGTTTGAAAG 2351 TTTTATTGTGG TTTATTGTGG TTTATCATGG 1000 2451 TTGGTTAAAA 2551 TGGCACCGGAA CGCACCAGAA	2261 2261 2361 7ACCCTTTTCT 2361 7ACGTTTAAT 2261 4ATAAAAAATT 2561 4AGTGAAACAA 4AGTGAAACAA 4AGTGAAACAA	2271 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571 AGTTTGATTT AGTTTGATTT agtttgattt	2281 2281 GTGT GTGT UTCAGGTGTGT gtgt 2381 UTGCTAGAAAT 2481 UTGGCACTT 2581 TTCAAAAGTAC CTCAAAAGTAC	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT 2391 TCACACTTTTATCC 2491 TGGGGGATTCCAATT 2591 CATCAAGAGATCAC CATCAAGAGATCAC CATCAAGAGATCAC
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010	CTTCTGTC 2201 TTTCAATI 2301 TCGTCAAA TCGTCAAA tCgtca a 2401 TACAACTA 2501 CACATTGA 2601	2211 2211 TTGAACTTT, 2311 ACCGTTACT, ACAGTAC, ACAGTAC, ACAGTAC, ACAGTAC, ACAGTAC, ACAGTAC, ACAGTAC, ACAGTAC, ACAGTAC, ACAGTAC, ACAGTAC, ACAGTAC, ACAGTAC, ACAGT, ACAGTAC, ACAGT, ACAGTAC, ACAGT,	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT aaggttgatt 2421 GCTGATGTGA 2521 CTCCAATGTT 2621	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ACATTACACT ac ttac ct 2431 TGAACCAATG 2531 ATGTGACTTA 2631	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441 	2251 TGTTTGAAAG 2351 TGTTTATGTGG 2351 TTTATTGTGG TTTATCATGG 2451 TTGGTTAAAA 2551 TGGCACCGGAA TGGCACCGGAA TGGCACCAGAA 2651	2261 2261 2361 2361 7ACCCTTTTCT 2361 7ACGTTTAAT 2261 4AGTGAAAATT 2561 4AGTGAAACAA 4AGTGAAACAA 4AGTGAAAATAA 4AGTGAAAATAA	CCTCTTTCTTA 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571 AGTTTGATTI AGTTTGATTI agtttgattt 2671	ATTAACGAGAA 2281 GTGT TCAGGTGTGT gtgt 2381 ATGCTAGAAAT 2481 	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT 2391 TCACACTTTTATCC 2491 TCACACTTTTATCC 2491 TCGGGGATTCCAATT 2591 CACCAGGGATCCAC CATCAAGAGATCAC CACCAGGGATCAC CACCAGGGATCAC
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010	CTTCTGTC 2201 TTTCAATT 2301 TCGTCAAA TCGTCAAA CGTCAAA 2401 TACAACTA 2501 CACATTGA 2601 TTGAAGAG TTGAAGAG	2211 TTGAACTTT, 2311 ACCGTTACT, ACCGTT	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT aaggttgatt 2421 GCTGATGTGAT GCTGATGTGA CTCCAATGTT 2621 YTTGTGGTGG YTTGTGGTGG	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ACATTACACT TGAACCAATG 2531 	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441 	ATAATAGGGA 2251 TGTTTGAAAG 2351 CTTATGTGG CTTATCATGG 1tttat tgg 2451 CTTGGTTAAAA 2551 CGCACCGGAA CGCACCGGAA CGCACCAGAA CGCACCAGAA	2261 2261 ACCCTTTTCT 2361 TACGTTTAAT (2461 AGTGAAATT 2561 AGTGAAATAA agtgaaa aa 2661 3666TTTGCTT	CCTTTTGATTGATCGA	ATTAACGAGAA 2281 GTGT STCAGGTGTGT gtgt 2381 	2291 TTCTTCAGACAAAT TTCTTCAGACAAAT TTCTTCAGACAAAT TTCTTCAGACAAAT CACACACTTTTATCC 2391 TCACACTTTTATCC 2491 CACACACTTTTATCC 2591 CATCAAGAGATCAC CATCAAGAGATCAC CACCAGAGAACACC CACAGAGAACACC
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010	CTTCTGTC 2201 TTTCAATI 2301 TCGTCAAA TCGTCAAA tcgtca a 2401 TACAACTA 2501 CACATTGA 2601 TTGAAGAG TTGAAGAG ttgaagag	2211 2211 7TTGAACTTT7 2311 ACCGTTACT7 ACCGTTACT7 ACCGTTACT7 ACCGTTACT7 ACCGTTACT7 ACCGTTACT7 ACCGTTACT7 ACCGTTACT7 ACCGTTACT7 ACCGTTACT7 ACCGTTTAAAA (GATTTAAAA (GATTTAAAA) (GA TTTAAAA)	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT AAGGTTGATT AAGGTTGATT CTCCAATGTT 2621 CTCCCAATGTT 2621 CTCCGATGGTGG STTCTGGTGG STTCTGGTGG	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ac ttac ct 2431 	AGTTTTAAGI 2241 GTGTTACACI 2341 GAGACATGGA agacatgga 2441 CACACTI AGGCACACTI cacactt 2541 CACACTI cacactt 2641 GAGACTI	2251 TGTTTGAAAG 2351 TTTTATTGTGG TTTATTGTGG TTTATCATGG 2451 TTGGTTAAAA 2551 TGGCACCGGAA 2555 TGGCACCGGAA 2651 	2261 2261 ACCCTTTTCT 2361 TACGTTTAAT 2261 ACCCTTTAAT 2261 ACCCTTAAAAAAATT 22561 ACCCAAACAA AGTGAAACAA AGTGAAACAA AGTGAAACAA AGTGAAACAA AGTGAAACAA AGTGAAACAA AGTGAAACAA AGTGAAACAA	CCTTTTCTTA 2271 CCTCCTCTTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571 AGTTTGATTT AGTTTGATTT agtttgattt 2671 	ATTAACGAGAA 2281 GTGT GTGT GTGT 2381 ATGCTAGAAAT 2481 ATTGTGCACTT 2581 TTCAAAAGTAC CTCAAAAGTAC CTCAAAAGTAC CTCAAAAGTAC CCCAAAGTAC	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT 2391 TCACACTTTTATCC 2491 TCACACTTTTATCC 2491 TCGGGGATTCCAATT 2591 CATCAAGAGATCAC CATCAAGAGATCAC CATCAAGAGATCAC CATCAAGAGATCAC
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus	CTTCTGTC 2201 TTTCAATI 2301 TCGTCAAA TCGTCAAA tCGTCAGA tCGTCAGA tCGTCAGA CGTCAGA CACATTGA 2601 TTGAAGAG TTGAAGAG ttgaagag 2701	2211 2211 TTGAACTTT, 2311 ACCGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, CONTRA	ACAAGTTTCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT AAGGTTGATT AAGGTTGATT CTCCAATGTT 2621 JTGTGGTGG JTGTGG JTGTGG JTGTGGTGG JTGTGGTGG JTGTGGTGG JTGTGG JTGTGG JTGTGG JTGTGG JTGTGG JTGTGG JTGTGG JTGTGG JTGTGG JTGTGG JTGTGG JTGTGG JTGTG JTGTGG JTGT	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ACATTACACT ac ttac ct 2431 	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441 	ATAATAGGGA 2251 TGTTTGAAAG 2351 TGTTTGAAAG 2351 TTTATTGTGG CTTTATCATGG 2451 TGGCACCGGAA 2551 TGGCACCGGAA 2551 TGGCACCGGAA 2651 GGCACCAGAA 2651 GGCACCAGAA 2751	2261 2261 2361 2361 7ACCTTTTTT 2361 7ACGTTTAAT 2261 4AGTGAAACAA 4AGTGAAACAA 4AGTGAAACAA 4AGTGAAACAA 2661 3GGGTTTGCTT 2761	CCTCTTTCTTA 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571 AGTTTGATTG AGTTTGATTT 1agtttgattt 2671 CTTTGATTGATTG 2771	ATTAACGAGAA 2281 GTGT gtgt 2381 GTGT gtgt 2381 	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT 2391 CACACACTTTTATCC 2491 CACACACTTTTATCC 2491 CGGGGATTCCAATT 2591 CATCAAGAGATCAC CATCAAGAGATCAC CACCAGGGATCAC CACCAGGGATCAC CACCAGGGATCAC
ML06-Cav07g1 Consensus ML06-GGSA010	CTTCTGTC 2201 TTTCAATT 2301 TCGTCAAA TCGTCAAA tCGTCAGA tCGTCAGA 100 100 100 100 100 100 100 10	2211 TTTGAACTTT, 2311 ACCGTTACT, ACCGTTACA, ACCGTTACA, ACCGTTTAAA, ACCGTTTAAA, ACCGTTTAAA, ACCGTTTAAA, ACCGTTACA, A	ACAAGTTTCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT AAGGTTGATT AAGGTTGATT 2421 GCTGATGTGAT GCTGATGTGAT 2521 CTCCAATGTT 2621 GTTGTGGTGG GTTGTGGTGG GTTGTGGTGG GTTGTGGTGG GTTGTGGTGG GTTGTGGTGG GTTGTGGTGG GTTGTGGTGG	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ACATTACACT ACATTACACT ACATTACACT ACATTACACT ACATTACAGT 2531 TGAACCAATG 2531 AGATCAGCTTA AGATCAGGTT agatcag 2731 ATATGGGGCCT	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441 	ATAATAGGGA 2251 TGTTTGAAAG 2351 TGTTTGAAAG 2351 TTATCATGG 1000 1	2261 2261 ACCCTTTTCT 2361 TACGTTTAAT 2361 TACGTTTAAT 2461 407GAAACAAA 407GAAACAA 407GAAACAA 407GAAACAA 407GAAACAAA 407GAAAAAAAAAAAAAAAAA 407GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	CCTUTTCTTA 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571 AGTTTGATTGA 2571 AGTTTGATTGA 2671 CTTTGATTGA 2771 ATAG	ATTAACGAGAA 2281 GTGT TCAGGTGTGT gtgt 2381 ATGCTAGAAAT 2481 	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT CLCCLCagacaat 2391 CACACACTITTATCC 2491 CGGGGATTCCAATT 2591 CATCAAGAGATCAC CATCAAGAGATCAC CATCAAGAGATCAC CACCACAGAGATCAC CACCAGAGATCAC CACCACAGAGATCAC CACCAGAGATCAC CACCAGAGATCAC CACCAGAGATCAC CACCAGAGATCAC CACCAGAGATCAC CACCAGAGATCAC
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010	CTTCTGTC 2201 TTTCAATT 2301 TCGTCAAA TCGTCAAA TCGTCAGA tCGTCAGA CGC	2211 TTTGAACTTT, 2311 ACCGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, CAGTTTAAAG (GATTTAAAG (GATTTAAAG (GATTTAAAG) CATTTAAAG (GATTTAAAG) CATTTAAAG	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT AAGGTTGATT AAGGTTGATT CTCCAATGTC CTCCAATGTT 2621 STTGTGGTGG STTGTGGTGG STTGTGGTGG STTGTGGTGG STTGTGGTGG STTGTGGTGG STTGTGGTGG STCCAATG CAGTCCAATG	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACGCT ACATTACACT ACATTACACT ACATTACACT ACATTACACT AGATCAGCACTTA 2531 AGATCAGCACTTA 2631 AGATCAGCACTTA AGATCAGGTT agatcag 2731 ATATGGGGCT	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441 CACACTG 2541 CACACTG AGGCACACTG 2641 CACACTG CGGGCTCAAG GGTGCTCAAG	ATAATAGGGA 2251 TGTTTGAAAG 2351 TGTTTGTGGG (TTATGTGG (TTATGTGGG (TTATCATGGG 2451 TGGCACCGGAA 2551 TGGCACCGGAA 2651 CGCACCGGAA 2651 CGCACCGGAA 2751 CGCACTAAAAG 2751	2261 2261 ACCCTTTTCT 2361 TACGTTTAAT (2461 4076AAATAA 4076AAATAA 4076AAATAA 4076AAATAA 4076AAATAA 4076AAATAA 4076AAATAA 4076AAATAA 4076AAATAA 4076AAATAA 4076AAATAA	2271 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571 AGTTTGATTG AGTTTGATTGA 2671 CTTTGATTGATTGA 2771 ATGG ATGGTAAGCA	ATTAACGAGAA 2281 GTGT STCAGGTGTGT 2381 GTGT 2381 	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT TCACACTTTTATCC 2391 CACACTTTTATCC 2491 CGGGGATTCCAATT 2591 CATCAAGAGATCAC CATCAAGAGATCAC CATCTAAAATTCTA 2791 CATGCAAAAACTG
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010	CTTCTGTC 2201 TTTCAATI 2301 TCGTCAAA TCGTCAAA tCGTCAGA tCGTCAGA tCGTCAGA CGTCAGA CGTCAGA CGTCAGA CACATTGA 2601 TTGAAGAG TTGAAGAG TTGAAGAG CACATTGA 2201 2001 200	2211 2211 TTGAACTTT, 2311 ACCGTTACT, ACCGTTACT, ACAGTTACT, ac gttacta 2411 TTTTATTTT 2511 CAATTTAAAG GATTTAAAG (GATTTAAAG (GATTTAAAG (GATTTAAAG) 2711 TTTCATGTGG	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTCATTA AAGGTTGATT AAGGTTGATT AAGGTTGATT AAGGTTGATTGAT CTCCAATGTT 2621 CTCCCAATGTT 2621 CTCCCAATGTT 2621 CTCTCGGTGG GTTGTGGGTGG GTTGTGGGTGG GTTGTGGGTGG	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ac ttac ct 2431 AGACCAATG 2531 ATGTGACCAATG 2631 AGATCAG AGATCAGGTTA agatcag 2731 ATATGGGGCT ATATGGGGCT ATATGGGGCT ATATGGGGCT ATATGGGGCT ATATGGGGCT	AGTTTTAAGI 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441 	ATAATAGGGA 2251 TGTTTGAAAG 2351 TTTTTGTAGG 1TTATTGTGG 1TTATCATGG 1TTATCATGG 1TTATCATGG 1TTGGTTAAAA 2551 TGGCACCGGAA 2551 TGGCACCGGAA 2651 TGGCACCGGAA 2651 TGGCACCGGAA 2751 TATTCCTACTG TATTCCTACTG TATTCCTACTG 1ATTCCTACTG 1ATTCCTACTG 1ATTCCTACTG 1ATTCCTACTG 1ATTCCTACTG 1ATTCCTACTG	2261 2261 2361 TACCTTTTCT 2361 TACGTTTAAT 2261 ACCCTTTAAT 2261 AGTGAAACAA AGTGAAACAA AGTGAAACAA AGTGAAACAA AGTGAAACAA CAACTGAAACAA CAACTGAAACAA CAACTGAAACAA CAACTGAAACAA CAACTGAAACAA CAACTGAAACAA CAACTGAAACAA CAACTGAAACAA CAACTGAAACAA CAACTGAAACAA CAACTGAAACAA CAACTGAATGCAT TCCAATGCAT TCCAATGCAT	CCTCTTTCTTA 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571 AGTTTGATTGA AGTTTGATTG AGTTTGATTG 2671 CTTTGATTGA 2771 TAG CTTTGATAGA 2771 CTTTGATAGA 2771	ATTAACGAGAA 2281 2281 GTGT GTGT GTGT GTGT 2381 ATGCTAGAAAT 2481 ATGCTAGAAAT 2481 ATGCTAGAAAT 2481 ATGCTAGAAAT 2581 TCAAAAGTAC 2581 TCAAAAGTAC 2681 ATTATGGCACTT 2581 ATGCTAGAAAGTAC 2681 ATTATGGCACAA	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT 2391 CACACTTTTATCC 2491 CACACTTTTATCC 2491 CACAGGATCACAATT 2591 CATCAAGAGATCAC CATCAAGAGATCAC CATCAAGAGATCAC 2691 CATCAAGAGATCAC 2791 CATGCAAAAACTG
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010	CTTCTGTC 2201 TTTCAATT 2301 TCGTCAAA TCGTCAGA tCgtCa a 2401 TCGTCAGA tCgtCa a 2401 CACATTGA 2501 TCAAACTA 2501 TTGAAGAG TTGAAGAG ttgaagag 2701 ACCTTACT 2801	2211 2211 TTTGAACTTT, 2311 ACCGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, ACAGTTACT, 2511 TTTTATTTTCA 2511 CAGATTTAAAG (GATTTTAAAG) (GATTTTAAG) (GATTTTAAG) (GATTTTAAG) (GATTTTAAAG) (GATTAAAG) (GATTTTAAAG) (GATTTTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTTAAAG) (GATTTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG) (GATTAAAG)	ACAAGTITCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT AAGGTTGATT AAGGTTGATT CTCCAATGTT 2621 CTCCAATGTT 2621 CTCCGATGTGG GTTGTGGTGG GTTGTGGTGG GTTGTGGTGG GTTGTGGTGG GTTGTAGTCG AGTCCAATG 2821 	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ACATTACACT ACATTACACT ACATTACACT ACATCACAATG 2531 	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441 	ATAATAGGGA 2251 TGTTTGAAAG 2351 TGTTTGAAAG 2351 TTATTGTGG ATTATTGTGG 2451 CTTGGTTAAAA 2551 CGCACCGGAA CGCACCGGAA CGCACCAGAA CAGAA CGCACCAGAA CAGAA CGCACCAGAA CAGAAA CGCACCAGAA CAGAAA CGCACCAGAA CAGAAA CGCACCAGAA CAGAAA CGCACCAGAA CGCACAAA CGCACAAA CGCACAAA CGCACAAAA CGCACAAAAA CAGAAAAAAAA	2261 2261 2261 2361 7ACCCTTTTCT 2361 7ACGTTTAAT 2261 2461 2561 AGTGAAACAA AGTGAAACAA AGTGAAATAA agtgaaa aa 2661 3GGGTTTGCTT 2761 7CCCAATGCAT 7CCCAATGCAT 7CCCAATGCAT 7CCCAATGCAT	CCTTTTCTTA 2271 CCTCCTCTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571 AGTTTGATTGA CAAAGGTTGA 2571 AGTTTGATTGA 2571 CATTGATTGATTGA 2671 CTTTTGATTGATTGA 2771 ATAG	ATTAACGAGAA 2281 GTGT gtgt 2381 ATGCTAGGAGTG ATGCTAGAAAT 2481 	2291 TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT TTCTTCAGACAAT 2391 TCACACTTTTATCC 2491 TCACACTTTTATCC 2491 TCGGGGATTCCAATT 2591 TCACAGAGATCAC CATGAAGAGATCAC CACAGAGATCAC 2691 TCTTTAAAATTCTA 2791
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus	CTTCTGTC 2201 TTTCAATT 2301 TCGTCAAA TCGTCAAA TCGTCAGA tCGTCAGA 2401 TACAACTA 2501 CACATTGA 2601 TTGAAGAG TTGAAGAG 2601 TTGAAGAG 2701 ACCTTACT 2801 	2211 TTTGAACTTT, 2311 ACCGTTACT, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTTACA, ACCGTCA, ACCGTCA, ACCGTCA, ACCGTTACA,	ACAAGTTTCT 2221 AAGGGCATAA 2321 AAGGTTGATT AAGGTTGATT AAGGTTGATT AAGGTTGATTGATT 2421 GCTGATGTGAT 2521 CTCCAATGTT 2621 CTCCGATGTGGTGG GTTGTGGTGG GTTGTGGTGG GTTGTGGTGG GTTCTGGTGG 2721 TCCAATC 2622 2721 TCCAATC 2621 CTCCGATGTCG CTCCGATGTGGTGG CTCCGATGT CCCCATCG CTCCGATCC CTCCGATCC 2821	AAAAGTGACT 2231 AGAGTTGGTT 2331 ACCTTACGCT ACATTACACT ACATTACACT ACATTACACT ACATTACACT ACATTACACT ACATTACAGT 2531 TGAACCAATG 2531 AGATCAGCTTA AGATCAGGTT agatcag 2731 ATATGGGCCT ATATGGCCCT ATATGGCCCT ATATGGCCCT ATATGGCCCT ATATGGCCCT ATATGGCCCT ATATGGCCCT ATATGGCCCT ATATGCGCCT ATATCGCCCT ATATCGCCCT ATATGCGCCT ATATGCCCCC ATATGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	AGTTTTAAGT 2241 GTGTTACACT 2341 GAGACATGGA agacatgga 2441 	ATAATAGGGA 2251 TGTTTGAAAG 2351 TGTTTGAAAG 2351 TTATCATGG 1000 1	2261 2261 ACCCTTTTCT 2361 TACGTTTAAT 2361 2461 2461 2461 AGTGAAACAA AGTGAAACAA AGTGAAACAA AGTGAAATAA agtgaaa aa 2661 36GGTTTGCTT 2761 TCCAATGCAT TCCAATGCAT TCCAATGCAT CCATGCAT	CCTTTTCTTA 2271 CCTCCTCTTTA 2371 TTAGAAATAA 2471 CAAAGGTTGA 2571 AGTTTGATTGA 2571 AGTTTGATTGA 2571 AGTTTGATTGA 2671 CTTTGATTGATTGA 2771 ATAG 2771 ATAG 2771 ATAG 2771 ATAG 2771 ATAG 2771 ATAG 2771 ATAG 2771 ATAG 2771 ATAG 2771 ATAG 2771 ATAG 2771 CAAAGCATTGATTGA 2771 CTTTGCTTAG 2771 CTTTGCTTAG 2771 CTTTGCTTAG 2771 CTTTGCTTAG 2771 CTTTGCTTAG CTTTCA 2771 CTTTGCTTAG 2771 CTTTGCTTAG 2771 CTTTGCTTAG 2771 CTTTGCTTAG 2771 CTTTGCTTAG CTTTCCTTCCTTCCTCCCCCCCCCCCCC	ATTAACGAGAA 2281 GTGT GTGT 3CAGGTGTGT 2381 ATGCTAGAAATA 2481 	2291 TTCTTCAGACAAAT TTCTTCAGACAAAT TTCTTCAGACAAAT TTCTTCAGACAAAT TTCTTCAGACAAAT TCACACTTTTATCC 2391 TCACACTTTTATCC 2491 TGGGGATTCCAATT 2591 ATCAAGAGAATCAC CATCAAGAGATCAC CATCAAGAGAATCAC 2691 TCTTAAAAATTCTA 2791 ACATGCAAAAAACTG 2891

	2901	2911	2921	2931	2941	2951	2961	2971	2981	2991
ML06-GGSA010								<mark>RA</mark>	GGCATTCTTC	TCTATGGCTACCA
ML06-Cav07g1	TGAGTCCA	AATTTATCA	TAGATTGCCI	TGGGGACTAC	AACTGACTAA	GACATGTTTC	CTTGTACGTO	TCGACAGG <mark>AT</mark>	GGCATTCTTC	TCTATGGCTACCA
Consensus								at	ggcattette	tctatggctacca:
	3001	3011	3021	3031	3041	3051	3061	3071	3081	3091
ML06-GGSA010	TTTGTACC	ATTGTTT	 \ \ CCTCC \ \ I		ACTTETTE	 TACATTCT	TTATCTCCCT	TERACETET	 ••••••••••••••••••••••••••••••••	A CC ATTTCCCTT
Consensus	tttataco	attatt	ANOCICCAAP	INCHONONCAN	ACTIOTITCC	INCHITCIII	TIMICIOUDI	TOCHOCICII	ININGANICI	ANOCATTIOUUTI
compensation	2101	2111	2121	2121	21.41	21.51	2161	2171	2101	2101
MT 06-GGSA010	3101	3111	5121	3131	<u>1</u>	TAATCOTOT	101C	JAGCTACAAG	JIOI TATTAATTAC	191 AAAAATGGGGCTA
ML06-Cav07g1	GTTGGTTI	AATAGAAGA	TCTCATGTAG	TTTGCTGTGA	CTTTTACAGA	TAATCCTGTI	GGTGGGGGACA	AAGCTACAAG	TGATAATTAC	AAAAATGGGGCTA
Consensus	· · · · · · · · · · · · · · · · · · ·				а	taatcctgtt	ggtggggaca	aagctacaag	ft ataattac	aaaaatggggcta
	3201	3211	3221	3231	3241	3251	3261	3271	3281	3291
ML06-GGSA010	AGAATTCA	AGAGAGAGG	AGATGTGAT	AAGGGTACAC	CTGTGGTACA	GCCAGGTGAT	GACCTCTTCT	GGTTTGGACG	CCCTCGGTTC	CTTCTCTTTCTCA
ML06-Cav07g1	AGAATTCA	AGAGAGAGAG.	AGATGTGAT	AAGGGTACAC	CTGTGGTACA	GCCAGGTGAT	GACCTCTTCI	GGTTTGGACG	CCCTCGGTTC	CTTCTCTTTCTCA
Consensus	agaattca	agagagagg	agatgtgat	aagggtacac	ctgtggtaca	igccaggtgat	gacctcttct	ggtttggacg	peceteggtte	cttctctttctca
	3301	3311	3321	3331	3341	3351	3361	3371	3381	3391
ML06-GGSA010	TTCACTTC	GTTCTCTTT	CAG							
ML06-Cav07g1	TTCACTTC	GTTCTCTTT	<mark>CAG</mark> GTACAAT	TTTCTCACAT	TCATCGATAA	АТТАСАТААТ	AGTCTATCTO	GGATACTAAT	TCTAACATCT	TCCTTTTGCTTTT
Consensus	ttcacttc	gttetettt	cag							
	3401	3411	3421	3431	3441	3451	3461	3471	3481	3491
ML06-GGSA010		TA ATTOCAC	AATGCATTTO	AACTGGCCTT	CTITECTICS	GGTGTG				
Conservat	GUULIUI	TAATIGLAG	AAIGCAIIIC	AALIGGULII	atttaattaa	GGIGIGGGIAA	IIAGUUIIIU	ACTICIACII	AILIAIILIA	ICAAIIIGGIGCA
consensus	0.501	0511	aatytattu	aat tyyttet	ora	orei	0.5.63	0.571	0.501	0.501
MT OF CC58010	3501	3511	3521	3531	3541	3551	3561	3571	3581	3591
ML06-Cav07g1	TGCTTAGA	AGATGCCAA	CACACTGCTT	TTCCCTAACT	TTCCCGCCAT	ATTGTTTTCT	TCTCTTTCAG	TATGAATTTG	GCACAGATIC	TTGCTTCCACGAA
Consensus								tatgaatttg	gcacagatto	ttgcttccacgaa
	3601	3611	3621	3631	3641	3651	3661	3671	3681	3691
MT 06_CCS8010	0001									
TTT00-002W010	LULAL IUL	AGAIAAGGI	CATCAAACTU	TCAATGGGG-						
ML06-Cav07g1	CGCACTGC	AGATAAGGT AGATAAGGT	CATCAAACTU CATCAAACTU	TCAATGGGG- TCAATGGGGT	GAGTTCTTAT	CAATTAATTO	CATATGCTGC	TGCCATTGTT	AAGATGTTAT	TATCTGGCTGATT
ML06-Cav07g1 Consensus	CGCACTGC CGCACTGC cgcactgc	AGATAAGGT AGATAAGGT agataaggt	CATCAAACTO CATCAAACTO Catcaaacto	:TCAATGGGG- :TCAATGGGGT :tcaatgggg	GAGTTCTTAT	CAATTAATTO	CATATGCTGC	TGCCATTGTI	AAGATGTTAT	TATCTGGCTGATT
ML06-Cav07g1 Consensus	CGCACTGC CGCACTGC cgcactgc 3701	AGATAAGGT AGATAAGGT agataaggt 3711	CATCAAACTO CATCAAACTO catcaaacto 3721	TCAATGGGG- TCAATGGGGGT tcaatgggg 3731	GAGTTCTTAT	CAATTAATTO 3751	CATATGCTGC 3761	TGCCATTGTI 3771	TAAGATGTTAT 3781	TATCTGGCTGATT 3791
ML06-Cav07g1 Consensus ML06-GGSA010	CGCACTGC CGCACTGC cgcactgc 3701	AGATAAGGT agataaggt 3711	CATCAAACTO CATCAAACTO catcaaacto 3721	TCAATGGGG- TCAATGGGGT tCaatgggg 3731 <mark>GTCATCAT</mark>	GAGTTCTTAT 3741 ACAAGTTCTC	CAATTAATTO 3751 TGCAGTTATO	CATATGCTGC 3761 TGACTTTGCC	TGCCATTGTT 3771 ACTCTATGCT	CAAGATGTTAT 3781 CTAGTGACTC	TATCTGGCTGATT 3791
ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1	CGCACTGC CGCACTGC CgCaCtgc 3701 AACATTAA	AGATAAGGT AGATAAGGT agataaggt 3711 ATTGCCACTT	CATCAAACTO CATCAAACTO Catcaaacto 3721 AATTTCTTCA	TCAATGGGG- TCAATGGGGT tcaatgggg 3731 <mark>GTCATCAT AGGGTCATCAT</mark>	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC	CAATTAATTO 3751 TGCAGTTATO TGCAGTTATO	3761 TGACTITGCC	TGCCATTGTT 3771 ACTCTATGCT ACTCTATGCT	AAGATGTTAT 3781 CCTAGTGACTC	TATCTGGCTGATT 3791 AG AGGTGAGACATGA
ML06-GeSA010 ML06-GeSA010 ML06-GeSA010 ML06-Cav07g1 Consensus	CGCACTGC CGCACTGC 3701 AACATTAA	AGAINAGGT AGATAAGGT agataaggt 3711 	CATCAAACT CATCAAACT catcaaacto 3721 AATTTCTTCA	TCAATGGGG TCAATGGGGT stcaatgggg 3731 GTCATCAT AGGGTCATCAT gtcatcat	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC acaagttctc	CAATTAATTO 3751 TGCAGTTATO TGCAGTTATO tgcagttato	3761 TGACTTTGCC TGACTTTGCC	3771 3771 ACTCTATGCT ACTCTATGCT actctatgct	3781 CTAGTGACTC CTAGTGACTC CTAGTGACTC	TATCTGGCTGATT 3791 AG AGGTGAGACATGA ag
ML06-GeSA010 ML06-GeSA010 ML06-GeSA010 ML06-Cav07g1 Consensus	CGCACTGC CGCACTGC CgCaCtGC 3701 AACATTAA 3801	CAGATAAGGT CAGATAAGGT 3711 3711 ATTGCCACTT. 3811	CATCAAACTU CATCAAACTU catcaaactu 3721 AATTTCTTCA 3821	TCAATGGGG TCAATGGGGT tteaatgggg 3731 <mark>GTCATCAT GGGTCATCAT gtcatcat 3831</mark>	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC acaagttctc 3841	3751 TGCAGTTATO TGCAGTTATO TGCAGTTATO tgcagttato 3851	3761 TGACTTTGCC TGACTTTGCC TGACTTTGCC (tgactttgcc 3861	3771 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871	3781 CTAGTGACTC CTAGTGACTC CCTAGTGACTC CCTAGTGACTC 3881	3791 36 AGGTGAGACATGA ag 3891
ML06-G6SA010 ML06-G6SA010 ML06-G6SA010 ML06-Cav07g1 Consensus ML06-G6SA010 ML06-G6SA010	CGCACTGC CGCACTGC CgCaCtGC 3701 	AGAIAAGGT SAGATAAGGT 3711 3711 ATTGCCACTT. 3811	CATCAAACTI CATCAAACTI catcaaacto 3721 AATTTCTTC# 3821	TCAATGGGG TCAATGGGGT 3731 GTCATCAT GGGTCATCAT gtcatcat 3831	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC acaagttctc 3841	CAATTAATTC 3751 TGCAGTTATC TGCAGTTATC tgcagttatc 3851	3761 TGACTTTGCC TGACTTTGCC TGACTTTGCC 1tgactttgcc 3861	TGCCATTGTT 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871	TAAGATGTTAT 3781 CTAGTGACTC CTAGTGACTC CCTAGTGACTC CCTAGTGACTC 3881 	3791 36
ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1	CGCACTGC CGCACTGC CGCACTGC 3701 AACATTAA 3801 TTACACAT	AGATAAGGT Sagataaggt 3711 ATTGCCACTT. 3811 TAACACAAC.	CATCAAACTI CATCAAACTI catcaaacto 3721 AATTTCTTCA 3821 AAAACATGTT	TCAATGGGG- TCAATGGGGT StCaatgggg 3731 GTCATCAT GGGTCATCAT gtCatCat 3831 	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC acaagttctc 3841 ACAACAACTT	CAATTAATTC 3751 TGCAGTTATC TGCAGTTATC tgcagttatc 3851 	3761 TGACTTTGCC TGACTTTGCC TGACTTTGCC 1tgactttgcc 3861	TGCCATTGTT 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871 TTGATTTGAC	TAAGATGTTAT 3781 TCTAGTGACTC CTAGTGACTC CCTAGTGACTC CCTAGTGACTC 3881 	TATCTGGCTGATT 3791 AG
ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus	CGCACTGC CGCACTGC CGCACTGC 3701 AACATTAA 3801 TTACACAT	AGATAAGGT Agataaggt 3711 ATTGCCACTT. 3811 TAACACAAAC.	CATCAAACTI CATCAAACTI catcaaacto 3721 AATTTCTTCA 3821 AAAACATGTT	TCAATGGGG- TCAATGGGGT StCaatgggg 3731 GTCATCAT GGGTCATCAT gtCatCat 3831 	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC ACAAGTTCTC 3841 ACAACAACTT	CAATTAATTC 3751 TGCAGTTATC TGCAGTTATC tgCagttatc 3851 GAGACTAATC	3761 TGACTTTGCC TGACTTTGCC TGACTTTGCC 3861 CATTCTTTGCT	TGCCATTGTT 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871 TTGATTTGAC	TAAGATGTTAT 3781 TTAGTGACTC TTAGTGACTC CTAGTGACTC CAGUGGGCC 3881 ATGGGGCC AGATGGGGCC atggggtc 2001	TATCTGGCTGATT 3791 AG AGGTGAGACATGA ag 3891 TTCCATGAAGCCC TTCCATGAAGCCC ttCcatgaagccc 2001
ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010	CGCACTGC CGCACTGC cgcactgc 3701	AGATAAGGT AGATAAGGT 33711 ATTGCCACTT. 3811 TAACACAAAC. 3911	CATCAAACTI CATCAAACTI catcaaacto 3721 AAATTTCTTCA 3821 AAAACATGTT 3921	TCAATGGGG- TCAATGGGGT StCaatgggg 3731 GTCATCAT GGGTCATCAT gtCatCAT 3831 	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC acaagttctc 3841 ACAACAACTT 3941	CAATTAATTC 3751 TGCAGTTATC TGCAGTTATC tgCagttatc 3851 GAGACTAATC 3951	3761 TGACTTTGCC TGACTTTGCC 10gactttgcc 3861 SATTCTTTGCT 3961	TGCCATTGTT 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871 TTGATTTGAC 3971	TAAGATGTTAT 3781 CTAGTGACTC CTAGTGACTC CTAGTGACTC 3881 ATGGGGTC AGATGGGGTC atggggtc 3981	TATCTGGCTGATT 3791 AG AGGTGAGACATGA ag 3891 TTCCATGAAGCCC TTCCATGAAGCCC ttccatgaagccc 3991
ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010	CGCACTGC CGCACTGC CGCACTGC 3701 AACATTAA 3801 TTACACAT 3901 ACCATCTT ACCATCTT	AGATAAGGT agataaggt 3711 	CATCAAACTI CATCAAACTI catcaaacto 3721 AATTTCTTCA 3821 AAAACATGTT 3921 AGTGGCGGGAT	TCAATGGGG- TCAATGGGGT StCaatgggg 3731 GTCATCAT GCGGTCATCAT gtCatCAT 3831 	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC acaagttctc 3841 ACAACAACTT 3941 GCTGGCATCG GCTGGCATCG	CAATTAATTO 3751 TGCAGTTATO TGCAGTTATO tgCagttato 3851 GAGACTAATO 3951 GACTGCCAGA GACTGCCAGA	3761 TGACTTTGCC TGACTTTGCC TGACTTTGCC 3861 SATTCTTTGCT 3961 AAGAACACAA	TGCCATTGTI 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871 TTGATTTGAC 3971 GGCAAAGCCA	TAAGATGTTAT 3781 CTAGTGACTC CTAGTGACTC CCTAGTGACTC 3881 ATGGGGTC AGATGGGGTC AtggggtC 3981 XTCATCATTCT XTCATCATTCT	TATCTGGCTGATT 3791 AG
ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus	CGCACTGC CGCACTGC CGCACTGC 3701 AACATTAA 3801 TTACACAT 3901 ACCATCTT ACCATCTT accatctt	AGATAAGGT agataaggt 3711 	CATCAAACTI CATCAAACTI catcaaacto 3721 AATTTCTTCA 3821 AAAACATGTT 3921 AGTGGCGGAT AGTGGCGGAT agtggcggat	TCAATGGGG- TCAATGGGGT StCaatgggg 3731 GTCATCAT GCGCTCATCAT gtcatcat 3831 	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC acaagttctc 3841 ACAACAACTT 3941 GCTGGCATCG GCTGGCATCG gctggcatcg	CAATTAATTC 3751 TGCAGTTATC TGCAGTTATC tgcagttatc 3851 	3761 TGACTTTGCC TGACTTTGCC TGACTTTGCC 3861 ATTCTTTGCT 3961 AAGAACACAA AAGAACACAA	TGCCATTGTI 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871 TTGATTTGAC 3971 GGCAAAGCCA GGCAAAGCCA	TAAGATGTTAT 3781 TTAGTGACTC TTAGTGACTC CTAGTGACTC 3881 ATGGGGTC AGGATGGGGTC atggggtc 3981 TCATCATTCT TCATCATTCT	TATCTGGCTGATT 3791 AG
ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-Cav07g1 Consensus	CGCACTGC CGCACTGC CGCACTGC 3701 AACATTAA 3801 TTACACAT 3901 ACCATCTT ACCATCTT ACCATCTT accatctt 4001	AGATAAGGT Sagataaggt 3711 ATTGCCACTT. 3811 TAACACAAC. 3911 CAACGATGG CAACGATGG CAACGATCG. Caacgat g 4011	CATCAAACTI CATCAAACTI catcaaacto 3721 AATTTCTTCA 3821 AAAACATGTT 3921 AGTGGCGGAT AGTGGCGGGAT AGTGGCGGGAT agtggcggat 4021	TCAATGGGG- TCAATGGGGT StCaatgggg 3731 GTCATCAT GGGTCATCAT gtCatCAT 3831 	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC acaagttctc 3841 ACAACAACTT 3941 GCTGGCATCG GCTGGCATCG GCTGGCATCG Gctggcatcg 4041	CAATTAATTC 3751 TGCAGTTATC TGCAGTTATC tgcagttatc 3851 	3761 TGACTTTGCC TGACTTTGCC TGACTTTGCC 3861 3961 AATCCTTTGCT 3961 AAGAACACAA AAGAACACAA AAGAACACAA AAGAACACAA	TGCCATTGTT 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871 TTGATTTGAC 3971 GGCAAAGCCA GGCAAAGCCA GGCAAAGCCA 4071	TAAGATGTTAT 3781 CTAGTGACTC CTAGTGACTC CCtagtgactc 3881 ATGGGGTC AGATGGGGTC 3981 CCATCATCATTCT CCATCATTCT CCATCATTCT CCATCATTCT CCATCATTCT CCATCATTCT	TATCTGGCTGATT 3791 AGGTGAGACATGA ag 3891 TTCCATGAAGCCC TTCCATGAAGCCC CTCCCATGAAGCCC 3991 GAGACAAATTCAC GAGACAAATTCAC GAGACAAATTCAC Gagacaaattcac 4091
ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010	CGCACTGC CGCACTGC CGCACTGC CGCACTGC 3701 AACATTAA 3801 TTACACAT 3901 ACCATCTT ACCATCTT accatctt 4001 CATTTTCA	AGATAAGGT Sagataaggt 3711 	CATCAAACTI CATCAAACTI catcaaacto 3721 AATTTCTTC/ 3821 AAAACATGTI 3921 AGTGGCGGAT AGTGGCGGAT agtggcggat 4021 GCCTCTCCCA	TCAATGGGG- TCAATGGGGT StCaatgggg 3731 GTCATCAT GGGTCATCAT gtCatCAT 3831 	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC ACAAGTTCTC ACAACAACTT 3841 ACAACAACTT 3941 GCTGGCATCG GCTGGCATCG GCTGGCATCG GCTGGCATCG GCTGGCATCG GCTGGCATCG GCTGCCCTGTT	CAATTAATTC 3751 TGCAGTTATC TGCAGTTATC tgCagttatc 3851 	3761 TGACTTTGCC TGACTTTGCC TGACTTTGCC (tgactttgcc 3861 	TGCCATTGTT 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871 TTGATTTGAC 3971 GGCAAAGCCA GGCAAAGCCA 4071 GCACAGTAGC	TAGATGTTAT 3781 CTAGTGACTC CTAGTGACTC CCAGTGGACTC CAGATGGGGTC AGATGGGGTC 3981 CTCATCATTCT CATCATTCT CATCATCTTCT ACACATTCT ACACATTCT ACACATTCT ACACATTCT ACACATTCT ACACATCC	TATCTGGCTGATT 3791 AG AGGTGAGACATGA ag 3891 TTCCATGAAGCCC TTCCATGAAGCCC CTCCCATGAAGCCC 3991 GAGACAAATTCAC GAGACAAATTCAC Gagacaaattcac 4091 TGCACCGCTCCC
ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010	CGCACTGC CGCACTGC CGCACTGC CGCACTGC 3701 AACATTAA 3801 TTACACAT 3901 ACCATCTT ACCATCTT ACCATCTT accatctt 4001 CATTTTCA	AGATAAGGT SAGATAAGGT SAGATAAGGT SAGATAAGGT SAGATAAGGT SAGATAGACAAC SAGATAGACGATGG CAACGATGG CCAACGATGG CCAACGATGG CCAACGATGG SCGTAGGCCGG	CATCAAACTI CATCAAACTI CATCAAACTI Catcaaacto 3721 AATTTCTTCA 3821 AATTTCTTCA 3821 AAAACATGTT 3921 AGTGGCGGGAT AGTGGCGGGAT agtggcggat 4021 GCCTCTCCCA GCCACTCCCA	TCAATGGGG- TCAATGGGGT StCaatgggg 3731 GTCATCAT GGGTCATCAT gtCatCat 3831 	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC ACAAGTTCTC ACAACAACTT 3841 ACAACAACTT 3941 GCTGGCATCG GCTGGCATCG GCTGGCATCG GCTGGCATCG GCTGCCCTGTT GTCCCCTGTT	CAATTAATTC 3751 TGCAGTTATC TGCAGTTATC tgcagttatg 3851 GAGACTAATC 3951 GACTGCCAGA GACTGCCAGA gactgccaga 4051 CACCTCCTGC CACCTCCTGC	3761 TGACTTTGCC TGACTTTGCC (tgactttgcc 3861 3961 AAAGAACACAA AAAGAACACAA AAAGAACACAA 4061 ATAACTATCA	TGCCATTGTT 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871 TTGATTTGAC 3971 GGCAAAGCCA GGCAAAGCCA GGCAAAGCCA 4071 GCACAGTAGC GCACAGTAGC	TAGATGTTAT 3781 CTAGTGACTC CTAGTGACTC CTAGTGACTC CCAgtggctc 3881 ATGGGGTC AGATGGGGTC 3981 CTCATCATTCT CATCATTCT ACATCATTCT ACATCATTCT ACATCATCATTCT CTCGACAGCT CTCGACAGCT	TATCTGGCTGATT 3791 AG AGGTGAGACATGA ag 3891 TTCCATGAAGCCC TTCCATGAAGCCC TTCCATGAAGCCC 3991 'GAGACAAATTCAC GAGACAAATTCAC Gagacaaattcac 4091 TGCACACGTCTCC TGCACACGTCTCC
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ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010	CGCACTGC CGCACTGC CGCACTGC CGCACTGC 3701 	AGATAAGGT agataaggt 3711 ATTGCCACTT. 3811 TTAACACAAC. 3911 CAACGATGG. CAACGATGG. CAACGATGG. CAACGATGG. CAACGATGG. CAACGATGGCCG. AGTAGGCCG. AGTAGGCCG. AGTAGGCCG. CAAATGTTG. CAAATGTTG. CAAATGTTG. CAAATGTTG. CAAATGTTG. CAAATGTTG. CAAATGTTG. CAAATGTCGT. AGATCTGT. AGATCTGT. AGATCTGT.	ATTCAAACTT CATCAAACTT CATCAAACTT CATCAAACTT Catcaaactc 3721 AATTTCTTCA 3821 AATTTCTTCA 3921 AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGCGAT AGTGGCGGAT AGTGGCGCGAT AGTGGCGCGAT AGTGGCGCGAT AGTGGCGCGAT AGTGGCGCGAT AGTGGCGCGAT AGTGGCGCGAT AGTGGCGCGAT AGTGGCGCGAT AGTGGCGCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCCGAT AGTGGCGGGAT AGTGGCGGGAT AGTGGCGGGAT AGTGGCGGGAT AGTGGCGGGAT AGTGGCGGGAT AGTGGCGGGAT AGTGGCGGGAT AGTGGCGGGAT AGTGGCGGAT AGTGGCGGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGCGGAT AGTGGAT AGTGGAT AGTGGAT AGTGGCGGAT AGTGGAT	TCAATGGGG- TCAATGGGG- TCAATGGGGT StCaatgggg 3731 GTCATCAT GGGTCATCAT gtcatcat 3831 	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC ACAAGTTCTC ACAAGTTCTC ACAACATTTC ACAACAACTT ACAACAACTT 3941 GCTGGCATCG GCTGGCATCG GCTGGCATCG GCTGGCATCG GCTGGCATCG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTTGG GTGGAGTGG GTGGAGTGG ACAACAACAACAACAACAACAACAACAACAACAACAACA	CAATTAATTC 3751 TGCAGTTATC TGCAGTTATC TGCAGTTATC tgcagttatc 3851 GACACTAATC 3951 GACTGCCAGA gactgccaga 4051 CACCTCCTGC cacctcctgc 4151 GATTCCGTAG GATTCCGTAG GATTCCGTAG GATTCCGTAG GATTCCGTAG GATCCGTAG	3761 TGACTTTGCC TGACTTTGCC TGACTTTGCC 3861 3861 3961 AAGAACACAA AAGAACACAA AAGAACACAA 4061 ATAACTATCA AAGAACACAA 4061 ATAACTATCA AAGAACACAA 161 GAAACAAATT	TGCCATTGTT 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871 TTGATTTGAC 3971 GGCAAAGCCA 3971 GGCAAAGCCA 4071 GGCACAGTAGC GGCACAGTAGC GGCACAGTAGC GGCACAGTAGC GGCGAGAGCA AGTGGGGGAGAG AGTGGGGGAGAG AGTGGCGGA AATTGCCGCA AATTGCCGCA AATTGCCGCA AATTGCCGCA	TAGATGTTAT 3781 CTAGTGACTC CTAGTGACTC CTAGTGACTC CAGATGGGCTC Adggggtc 3981 CTCATCATTCT ACCATCATTCT ACCACCATTCT CTCGACAGCT CTCG	TATCTGGCTGATT 3791 AG AGGTGAGACATGA ag 3891 TTCCATGAAGCCC TTCCATGAAGCCC TTCCATGAAGCCC CTCCATGAAGCCC CTCCATGAAGCCC CAGACAAATTCAC GAGACAAATTCAC GAGACAAATTCAC CGACCACGTCTCC CTGCACACGTCTCC CCGCATCATCTATCATAC CGCATTATTCATAC CGCATCGTACCC GCCATCCGTACCC GCCATCCGTACCC CGCCATCCGTACCC CGCCATCCGTACCC CGCCATCCGTACCC CGCCATCCGTACCC CGCCATCCGTACCC
ML06-GGSA010 ML06-Cav07g1 Consensus ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010 ML06-GGSA010	CGCACTGC CGCACTGC CGCACTGC CGCACTGC 3701 	AGATAAGGT SAGATAAGGT SAGATAAGGT SAGATAAGGT SAGATAGCACATT SAGATAGAAGA SAGAT SAGATGAGATGG CAACGATGG CAACGATGG CAACGATGG CGAAGGACGG AGTAGGCCG AGTAGGCCG AGTAGGCCG CAAATGTTG CAAATGTTG CAAATGTTG CAAATGTTG CAAATGTCGT AGATTCTGT AGATTCTGT AGATTCTGT AGATTCTGT AGATTCTGT	ATTCAAACTT CATCAAACTT CATCAAACTT Catcaaactc 3721 AATTTCTTCA 3821 AATTTCTTCA 3921 AGTGGCGGGAT 3921 AGTGGCGGGAT 4021 GCCTCTCCCA GCCACTCCCA GCCACTCCCA GCCACTCCCA GCACTCTGAC GCACTCTGAC GCACTCTGAC GCACTCTGAC GCACTCTGAC GCACTCTGAC	TCAATGGGG- TCAATGGGGT TCAATGGGGT TCAATGGGGT TCAATGGGGT GTCATCAT GTCATCAT gtcatcat 3831 TATGATAATTA 3931 TCCATTAAGAA CCCATTAAGAA CCCATGGGAT ACGCACGGGAT ACGCACGGGAT ACGCACGGGAT ACGCACGGGAT ACGCACGGGAT ACGCACGGGAT ACGCACGGGAT ACGCACGGGAT ACGCACGGGAT ACGCACGGAGAAG CAGCAGCAAGGAAG CAGCAGCAAGAAAG CAGCAGCAAGAAAG CAGCAGCAAGAAAG CAGCAGCAAGAAAG	GAGTTCTTAT 3741 ACAAGTTCTC ACAAGTTCTC ACAAGTTCTC ACAAGTTCTC ACAACATTCTC ACAACAACTT ACAACAACTT 3941 GCTGGCATCG GCTGGCATCG GCTGGCATCG GCTGGCATCG GCTGGCATCG GTGCACTGTT GTCCCCTGTT GTCCCCTGTT GTCCCCTGTT GTCCCCTGTT GTCCCCTGTT GTGCACGTCG GTGGAGTTCG GTGGAGTTCG GTGGAGTTCG ACAGGGGAGAT AGAGGGGAGAT AGAGGGGAGAT AGAGGGAGAT AGAGGGAGAT	CAATTAATTC 3751 TGCAGTTATC TGCAGTTATC TGCAGTTATC tgcagttatc 3851 GACACTAATC 3951 GACTGCCAGA GACTGCCAGA GACTGCCAGA GACTGCCAGA CACCTCCTGC CACCTCCTGC CACCTCCTGC CACCTCCTGC GATTCCGTAG GATTCCGTAG GATTCCGTAG GATTCCGTAG GATTCCGTAG GATTCCGTAG GATTCCGTAG GATTCCGTAG GATTCCGTAG GATTCCGTAG GATTCCGTAG	3761 TGACTTTGCC TGACTTTGCC TGACTTTGCC 3861 3861 3961 AAGAACACAA AAGAACACAA AAGAACACAA AAGAACACAA AAGAACACAA AAGAACACAA AAGAACACAA TAACTATCA AAGAACAAATT GAAACAAATT	TGCCATTGTT 3771 ACTCTATGCT ACTCTATGCT actctatgct 3871 TTGATTTGAC 3971 GGCAAAGCCA GGCAAAGCCA GGCAAAGCCA GGCAAGTAGC GGCACAGTAGC GGCACAGTAGC GGCGAGAAG AGTGGGGAAA AGTGGGGAAA AATTGCCGCA AATTGCCGCA AATTGCCGCA AATTGCCGCA AATTGCCGCA AATTGCCGCA AATTGCCGCA AATTGCCGCA	TAAGATGTTAT 3781 TTAGTGACTC TTAGTGACTC TTAGTGACTC CTAGTGACTC CAGATGGGGTC AUG90901 TCATCATCATTCT AUG81 CTCGACAGCT CT	TATCTGGCTGATT 3791 AG AGGTGAGACATGA ag 3891 TTCCATGAAGCCC TTCCATGAAGCCC TTCCATGAAGCCC 3991 GAGACAAATTCAC 3991 GAGACAAATTCAC 4091 TGCACACGTCTCC 4091 TGCACACGTCTCC 4091 GCATCACGTCTCC 4091 GCATTATTCATAC GCATTATTCATAC GCATTCATACACC GCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC AGCCATCCGTACCC

Consensus aacatgaagtcaaca tagtctctcggaattcacatttcgcagatga

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	ATGGACA	AATGTGAGTA	TGATGAACGI	ACAATGGCGG	GAAACTCCAA	CATGGGCAGT	FGCGGTGGTGT	GCTTCATGTI	IGCTTGCCATI	TCAATCTTCATTG
Consensus										
	101	111	121	131	141	151	161	171	181	191
ML012-GGSA01		 TATTCAACCT			TCATTA ACC	TCTATATAT				
Conconduc	AACATAT	IAIIGAAGUI	ACIGGAAAGG	TAAATATTA	I IGAT TAAGG.	IGIAIAIAI	AIICICIIIIG	-TITGIATIO	IIIICIIGAII	GATTACIGAAAAT
CONSENSUS										
NR 040 000104	201	211	221	231	241	251	261	271	281	291
MLU12-GGSAUI	TOTTOON	 ГССТТТАТАТ		CTCCCTAAAA						 TACCTCTATATAT
Consensus	Torroom		HI IMII IMIE		iocommonoi	mooomooro			110mm10n00	Incororminini
oonbenbab	201		001	221	2.41	0.51	0.51	071	201	201
M 010 CCC201	301	311	321	331	341	351	361	371	381	391
ML012-GGSA01 ML012-Cav07g	ATATCTC	ACACATTAAG	ATCATCAACA	AATGGTCAAT	ТААТТААССИ	ATTTTTCTTA	ATTTATTGGGT			GGTCAGAGATTAT
Consensus										
	401	411	401	421	4.41	451	461	171	401	401
MT 012_CCS801	401	411	441	431	441 CAAGAGCCCI	451	401 FCTCTATACCC	471 MTCACTCTT	401 CAGACACTTO	491 CCATCCCTCTATA
ML012-Cav07g	GCTGTTG	GGATTCATAT	CCCTGCTCCT	AACAGTGTT	CAAGAGCCC	ATTTCTGGGA	IGTGTATACCC	ATGAGTGTT	GAGACACTTO	GCATCCCTGTATA
Consensus	65		tgeteet	aacagtgtto	caagagccca	atttctggga	tgtgtataccc	atgagtgtt	gagacactto	gcatccctgtata
	501	511	521	531	541	551	561	571	581	591
ML012-GGSA01	GGTGAGA	AGAAATATTC	CGACAAAAGT	GGTCGGAAAG	TGCTCCAGT	TATTTGATTC	FGGCTTCAGTG	GTCGTCGAAC	GATTAGCTACA	AAAGGATGCGACA
ML012-Cav07g	GGTGAGA.	AGAAATATTC	CGACAAAAGT	GGTCGGAAAO	TGCTCCAGT	TATTTGATTC	FGGCTTCAGTG	GTCGTCGAA	GATTAGCTACA	AAAGGATGCGACA
Consensus	ggtgaga	agaaatattc	cgacaaaagt	ggtcggaaaq	gtgctccagt	atttgattc	tggcttcagtg	gtcgtcgaaq	gattagetace	aaaggatgcgaca
	601	611	621	631	641	651	661	671	681	691
ML012-GGSA01	AATGCAA	AAAGG								GT
ML012-Cav07g	AATGCAA	<mark>aaagg</mark> taagc	TGAATTTATA	AGTTTGTTT	GTTTGTTTTT.	TCTAGCAGA	GCTTTCATATA	TATGAATTT	AGAGGGATGAG	TTGTTTGCAGG <mark>GT</mark>
Consensus	aatgcaa	aaagg								gt
	701	711	721	731	741	751	761	771	781	791
ML012-GGSA01	AAAGTGG	CETTCATGTE	TGCGTATTCG	ATTCACCAGO	TGCATATAT	CATCTTTGT(TTAGCCGTTT	TTCATGTGCT	FCTACTGCATA	ATCACCCTGGCTT
ML012-Cav07g	AAAGTGG	CCTTCATGTC	TGCGTATTCG	ATTCACCAGO	TGCATATAT	CATCTTTGT(CTTAGCCGTTI	TTCATGTGCT	FCTACTGCATA	ATCACCCTGGCTT
Consensus	aaagtgg	ccttcatgtc	tgcgtattcg	fattcaccago	ctgcatatati	catetttgt	cttagccgttt	ttcatgtgct	cctactgcate	atcaccctggctt
	801	811	821	831	841	851	861	871	881	891
ML012-GGSA01	TAGGCAC.	AACCAAG								
ML012-Cav07g	TAGGCAC.	AACCAAGGTA	.GGTACTTTTI	ТААСАТАТАЗ	FACATGCACA	ATTGCAACCO	CCTTTCTCTTI	CTCTCGAGAT	ICTAAATTCTI	CTTTGAATAGATT
Consensus	taggcac	aaccaag								
	901	911	921	931	941	951	961	971	981	991
ML012-GGSA01									<mark>ATCAAAAGA</mark>	TGGAAGGCTTGGG
ML012-Cav07g	CTTGTTA	GAATATATTA	TAGGATTTAA	TTTCAGCATI	FGATTGTAAT(CGGATTTGAT	GAATTCTTCTI	GGAAATTGCA	AG <mark>ATCAAAAGA</mark>	TGGAAGGCTTGGG
Consensus									atcaaaaga	itggaaggettggg
	1001	1011	1021	1031	1041	1051	1061	1071	1081	1091
ML012-GGSA01	AGGAAGA	AACAAGGACA	CTTGAATCTC	AAGGTCATAT	TTG					
MLUI2-Cavurg	AGGAAGA	AALAAGGALA	CIIGAAICIC	AAGGICAIAI	1661AACAA	41666616111	AAAAALIIGU	IIAAAAAAU	AAAAGAUIAUI	ILIAAGIGLIALA
consensus	ayyaaya	aacaayyaca	cilgaalele	aayyttatat	Jug					
	1101	1111	1121	1131	1141	1151	1161	1171	1181	1191
MLU12-GGSAU1 ML012-Cav07g	GTTTTTA	 ሞዋልጥል ልርረጥጥ	 тсттатассс						 ГГ А АТТГ А А АТТ	AGTTAGTGACTGC
Consensus		THIANOTTI	ICTIMINOUC	TATAATIOA	OAAAIAAIII	HOHHOOTIT			CANTINANII	ACTINOTORCIOC
Compendad	1201	1211	1221	1001	10.41	1051	1001	1001	1201	1202
MI 012-005801	1201	1211	1221	1231	1241	1251	1201	1271	1201	1291
ML012-Cav07a	TTTTAAC	CATACATTCT	TTAATTATGT	CACGTTAATT	TGTAAAATA	ATTATAGTA	AAAGCAGTAGT	AATTCAAACA	ATCTTCTCATT	TAATGAAATTAAT
Consensus										
	1301	1311	1991	1221	1241	1951	1261	1001	1201	1301
ML012-GGSA01				1001	1041	1001	1301	10/1	1001	1071
ML012-Cav07g	GTCACTT	ATGGACTTGG	TCAGGTGCTC	CACAGAGTAG	TCAAACCCCC	CTCTTTCTT(GGATAATGCTA	TGAACACAA	ACTAAGTTAC	CGAAAGTGACTCA
-	17. 17.									1

Consensus

	1401	1411	1421	1431	1441	1451	1461	1471	1481	1491
ML012-GGSA01										
ML012-Cav07g	CACTGTCA	ATCTATGCCG	TTAAAGACTI	GTCCACTIT.	ГТТТАТАСТА	CAAAGTCAAC	ATTAAAGATG	ACTITGTAAA	TTGCTTTTGT	GAGCAAATTTTGT
Consensus										
	1501	1511	1521	1531	1541	1551	1561	1571	1581	1591
ML012-GGSA01										
MLU12-CavU7g	AIGAAAAAAAAAAAAAAAAIIAAIAIUUUIIIIIIIIAIIIIIAIIIIIAIIIIAIIIUAIGTUUUUGATTIGUTGTTGUTAATTTAATT									
Consensus										
DENER BRIDER	1601	1611	1621	1631	1641	1651	1661	1671	1681	1691
ML012-GGSA01				CTTTCCTA A					ATCACGA	GEGETTTAGETTT
MLUI2-CavU7g		IIIIIIAIII	IIIIIAIAIA	GITIGGIAA	AAGAGAICAI.	AIAIGGIIAI	GGAAAAIGAI	TIATAIGAIG	CAGAICACGA	GCGGIIIAGGIII
consensus									accacya	geggeelaggeel
	1701	1711	1721	1731	1741	1751	1761	1771	1781	1791
ML012-GGSA01 ML012-Cav07g	GCAAGGGGA	AACATCATTT AACATCATTT	GGACGAAGGU CCACCAACCO	ACTTAACCT	AUTGGAGUAA	GIUAAUGGII	TECETTEGA	TGGTCACTAT	 TGAAATCCTA'	 ГА АТТА АСТАСТТ
Consensus	dCaaddada	acatcattt	auscassaa	actteactt	actoregase	atceedaatt	tecettinga	taat	IOAAAICCIA	TAATTAACTACT
consensus	ycaayyya	acattattt	yyacyaayyc	acticalities	ac cyyaycaa	yccaacyycc				
NR 04.0 0003.04	1801	1811	1821	1831	1841	1851	1861	1871	1881	1891
ML012-GGSA01 ML012-Cav07g	110	TTGCATAGTT	AGTTTGGTTGC	 TTAATAATA	 \TATTAAGTT	 AGTATATGTT	 ТАТАТТААСТ	 ТАТТАТАТАТ	 ататататаа.	 acatgtttatatg
Consensus	momiou					noiminioii	inini inno i	Int Inthint	ninininini	
	1001	1011	1021	1021	1041	1051	1061	1071	1001	1001
MT 019_CCS801	1901	1911	1921	1931	1941	1951	1961	1971	1981	1991
ML012-Cav07g	TGTATGTAT	 FGAGTTAGGC	ТСАСАААССТ	TAATCGAGT	CGGGCGAGTA	AACCGAGTAT	GTATCACTTA	ATAATCAAGC	GAGTITCTAC	CGTCATGAGCCAG
Consensus										
	2001	2011	2021	2031	20/1	2051	2061	2071	2081	2091
MT 012-GGSA01	2001	2011	2021	2031	2041	2031	2001	2071	2001	2091
ML012-Cav07g	TTTCTGCA	ATCACGAGTC.	AAGTTAAGAT	CGAGTTTAA	ACAAACCGAT	TGTCGACGAG	ACTAGTTTAT	TACAACCCTA	TTTCTAGGTC	FTAGTCCCGCAAT
Consensus	-									
	2101	2111	2121	2131	2141	2151	2161	2171	2181	2191
ML012-GGSA01										
ML012-Cav07g	TAAAGCAA	ITATCAATGG	GTGAGGTGGG	AGGAATGAT	AACGATGGA	AAATATCAGT	CTCCCCCAAA	ATGTATGCCA	ТААСТААТАА	FTGGTGGAGCGCT
Consensus										
	2201	2211	2221	2231	2241	2251	2261	2271	2281	2291
ML012-GGSA01										
ML012-Cav07g	CTATATTA	CATGTTGGAT	TTATTTATTI	TTATCTTAA	JTACAATGTT	CAATTTTCAA	GATATCATTA	GCGTAACACT	CTAGTTTCAT	GTTGAGAAAAGAT
Consensus										
	2301	2311	2321	2331	2341	2351	2361	2371	2381	2391
ML012-GGSA01										
ML012-Cav07g	GTGTAAGT	CACACAGAGT	TAATAGTTTA	TAAGATATG	FTCATTGGTG	CTAAGTTGTT	CCACATTGCT	TATTTATTAG	GTAAAATTGA	ACTTTAAAAGTAA
Consensus										
	2401	2411	2421	2431	2441	2451	2461	2471	2481	2491
ML012-GGSA01										
ML012-Cav07g	TTTTAAGG	AAGTTTCAAA	ТТБАСТАААТ	GTGCCAACG	FGGGCAACTC.	ATCTTTTTAA	TATGGAACTA	GGGTGTTACA	AATTCCTCTC	CTTAAAACCCCTG
Consensus										
	2501	2511	2521	2531	2541	2551	2561	2571	2581	2591
ML012-GGSA01										
ML012-Cav07g	AAGTCACCA	ATCTACGTGG	AGAAATGTAG	AAGAAAGGA'	FATECGCATE	CACATAATGC	AATTACTATC	TACATCTGCA	CAGTECTACA	TCACAGCTAAAAA
Consensus										
	2601	2611	2621	2631	2641	2651	2661	2671	2681	2691
ML012-GGSA01	C & TTTTTTTTTTT									
MLUI2-CavU/g	CATITIT	JAGAAAAAAA	IIIGAIGUUU	AAALAAALAI	AAGUUTTAGI.	AAIGAAAUII	GIGIIIAIII	IICAAIIIIG	AAATTTAAGG	GUATAAAAGGITA
consensus				manage a		1000-000	110000			
	2701	2711	2721	2731	2741	2751	2761	2771	2781	2791
ML012-GGSA01	GTTATOT				TT PATCAGGTTT	GITTUTTCAG	ACAATTETTE	AGATUAATTA	CTAAGGTTGA	TACATTACGTTC
Concensus	JIAIGIN	ACROTICITI	onnnn i i i i		.AICA00111	atttetteea	acaattette	agatceette	ctaagettee	tacattecatta
Consensus	0001	2013		0001	00.00	ace.		agaocaatta	- July Cuya	
M 010 000304	2801	2811	2821	2831	2841	2851	2861	2871	2881	28AT
ML012-665A01 ML012-Cav074	AGATATEC	ATTTATCETC	GTACGTTTAN	TCCACTAAAA	AGTCAGATTT	 TTTGTACATG	ТАСТТСССАА	 AGGGATTCCN	ATGTTATTAT	TTACATTATATC

Consensus agatatggatttatcgtgg

	2901	2911	2921	2931	2941	2951	2961	2971	2981	2991
ML012-GGSA01	[ACATTTGGC	ACCCGGAAGTO	GAAACAACGT	TGATTTTC.	AAAAATACATO	CAGAGAGCA	TTGAAGCT	GATTTTAAATT	CGTGGTGGGGATA
ML012-Cav07g	ACTTCAGG	ACATTTGGCI	ACCCGGAAGTO	GAAACAACGT	ITGATTTTC.	AAAAATACATO	CAGAGAGCA	CTTGAAGCT	GATTTTAAATT	CGTGGTGGGGATA
Consensus	c	acatttggca	accoggaagto	jaaacaacgti	ttgattttc	aaaaatacato	cagagagca	cttgaagct(yattttaaatt	cgtggtggggata
	3001	3011	3021	3031	3041	3051	3061	3071	3081	3091
ML012-GGSA01	AG									TCCAAAAATATGG
ML012-Cav07g	AGGTTGGTO	GCTGAAGCACT	TAAAGGCCTI	TGCTTCTTT	GATTGATTT	ГТААТТАТСТІ	TAAAATTCCA	ACTTTACCT	CTCATTTGCAG	TCCAAAAATATGG
Consensus	ag									tccaaaaatatgg
	3101	3111	3121	3131	3141	3151	3161	3171	3181	3191
MT.012-GGSA01	TECTTTECA	GTTTTATCC	TATTOTOTAL	CGCATATEG-						
ML012-Cav07g	TGCTTTGC	GTTTTATCC	TATTGTCCA	CGCATATGG	TAAGCTAAA'	FACTACCTTT	GGTTATCAT.	ACTATCTCT	CTTTTTAATGA	CGTGGAACCCTTG
Consensus	tgetttgea	agttttatcco	ctattgtccaa	acgcatatgg	-					
	2201	2211	2221	2221	2241	2251	2261	2271	2201	2201
M 010 CC5801	3201	3411	3441	3431	3241	3431	3201	3471	3201	3491
MI.012-Cav07g	AAGGCAAGO	CCACTTCCT	ATATTCTTCT	TGGGCAAAC	ГСТАААТАС.	ACGACCTTGT	CGTAAGAAC	GTGTATCG	TTGAGTGACG	ACTEGAATAACEG
Consensus										
oonochodo		120.29								
NR 04 0 0001 04	3301	3311	3321	3331	3341	3351	3361	3371	3381	3391
MLU12-GGSAU1	ATC ATATT?				meeccec			Percectarr		CCCCAANTATCTT
MLUIZ-Cavurg	AIGAIAIIA	AGCAAAIGA	JICGAICAII	GAGCIGICC	.116666666	LAAGIAGIGI	CALICITIC	IGIGUCATIO	LICATITITOA	GUULAAATAIGII
Lonsensus										
	3401	3411	3421	3431	3441	3451	3461	3471	3481	3491
ML012-GGSA01							ATGGCATT	CTTATCTAT(GGCTACCATTT	CTCCCATTGATTG
ML012-Cav07g	GTGGGCTGC	CTTAGTAACI	FACTACTGACT	TAAGAAATGT.	FTCCATCGA	FGTTTGGACAC	GGATGGCATT	CTTATCTAT(GGCTACCATIT	CTCCCATTGATTG
Consensus							atggcatt	cttatctat	ggctaccattt	ctcccattgattg
	3501	3511	3521	3531	3541	3551	3561	3571	3581	3591
ML012-GGSA01	TAA									
ML012-Cav07g	TAAGCTCAA	TTACAGAAA	CCAACTGGTTT	CCTAAATTT	TCTTTGTC	CGGTTCCTCCA	ACCCATTTT.	AATAGCCAG	GGTTTTTGGAG	GAAAACTTTGTTC
Consensus	taa									
	3601	3611	3621	3631	3641	3651	3661	3671	3681	3691
ML012-GGSA01									TEC	TETTGGTGGGTAC
									100	
ML012-Cav07g	TTTTATCGO	GCTTTGTTTA	СААТСТААССТ	TTTGGGTTG	TGGTTTAA	FGGAAAATCAT	rgtggtttgt	rgtgatttt	ACAGGTAATCC	TCTTGGTGGGTAC
ML012-Cav07g Consensus	TITTATCG	GCTTTGTTTA	CAATCTAAGCI	TTTGGGTTG	TTGGTTTAA	TGGAAAATCAT	rgtggtttgt	rgtgatttt.	ACAGGTAA <mark>TCC</mark> tcc	<mark>TCTTGGTGGGTAC</mark> tcttggtgggtac
ML012-Cav07g Consensus	TTTTATCGC	GCTTTGTTTAG	3721	TTTTGGGTTG	TTGGTTTAA 3741	TGGAAAATCAT 3751	TGTGGTTTGT 3761	TGTGATTTTA 3771	ACAGGTAA <mark>TCC</mark> tcc 3781	TCTTGGTGGGTAC tcttggtgggtac 3791
ML012-Cav07g Consensus ML012-GGSA01	TTTTATCGC 3701 ACAGCTACA	GCTTTGTTTAG 3711 MAGTAATAAT	CAATCTAAGCT 3721 FACAAAAATGO	TTTGGGTTG 3731 GGGCTAAGAAT	TTGGTTTAA 3741 TTCAAGAGA	TGGAAAATCAT 3751 GAGGAGATGTC	GTGGTTTGT 3761 GATTAAGGGT	TGTGATTTTA 3771 ACACCTGTG	ACAGGTAATCC tcc 3781 FTACAGCCAGG	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g	TTTTATCGC 3701 ACAGCTACA ACAGCTACA	CTTTGTTTA 3711 AGTAATAATT AGTAATAATT	CAATCTAAGCT 3721 FACAAAAATGO FACAAAAATGO	TTTTGGGTTG 3731 GGGCTAAGAAT	TTGGTTTAA 3741 TTCAAGAGA TTCAAGAGAGA	TGGAAAATCAT 3751 GAGGAGATGTC GAGGAGATGTC	GTGGTTTGT 3761 SATTAAGGGT. SATTAAGGGT.	IGTGATTTT 3771 ACACCTGTG ACACCTGTG	ACAGGTAATCC tcc 3781 FTACAGCCAGG FTACAACCAGG	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus	TTTTATCGC 3701 ACAGCTACA ACAGCTACA acagctaca	3711 3711 AGTAATAATI AGTAATAATI	CAATCTAAGCT 3721 FACAAAAATGO FACAAAAATGO tacaaaaatgo	TTTGGGTTG 3731 GGCTAAGAA GGCTAAGAA gggctaagaat	TTGGTTTAA 3741 TTCAAGAGA TTCAAGAGA CLCAAGAGAGA	TGGAAAATCAT 3751 GAGGAGATGTO GAGGAGATGTO gaggagatgto	GTGGTTTGT 3761 GATTAAGGGT. GATTAAGGGT. gattaagggt:	3771 3771 ACACCTGTG ACACCTGTG ACACCTGTG	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus	TTTTATCGO 3701 ACAGCTACA ACAGCTACA acagctaca 3801	GCTTTGTTTA 3711 LAGTAATAAT LAGTAATAAT LAGTAATAAT LAGTAATAAT 3811	CAATCTAAGCT 3721 FACAAAAATGO FACAAAAATGO tacaaaaatgo 3821	TTTTGGGTTG 3731 GGGCTAAGAA GGGCTAAGAA Igggctaagaa1 3831	3741 3741 ITCAAGAGAGA ITCAAGAGAGA Itcaagaga 3841	TGGAAAATCAT 3751 GAGGAGATGTO GAGGAGATGTO gaggagatgto 3851	GTGGTTTGT 3761 GATTAAGGGT. GATTAAGGGT. Gattaagggt: 3861	TGTGATTTT 3771 ACACCTGTG ACACCTGTG acacctgtg 3871	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01	3701 ACAGCTACA ACAGCTACA acagctaca 3801 TGGTTTGGA	3711 AGGTAATAAT AAGTAATAAT AAGTAATAAT 3811 AAACCCTCGG	3721 3721 TACAAAAATGO TACAAAAATGO tacaaaatgo 3821 FFECTTCTCT	TTTGGGTTG 3731 GGCTAAGAA GGCTAAGAA gggctaagaa 3831 ATCTCATTCA	3741 3741 TTCAAGAGA TTCAAGAGA CtCaagaga 3841 CTTCGTTCT	TGGAAAATCAT 3751 GAGGAGATGTO GAGGAGATGTO gaggagatgto 3851 CTTTCAG	GTGGTTTGT 3761 GATTAAGGGT. GATTAAGGGT. gattaagggt. 3861	GTGATTTT 3771 ACACCTGTG ACACCTGTG acacctgtg 3871	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g	3701 ACAGCTACA acagctaca 3801 TGGTTTGGA	3711 3711 AGTAATAAT AGTAATAAT AGTAATAAT 3811 AACCCTCGG AACCCTCGG	3721 3721 TACAAAAATGO TACAAAAATGO tacaaaaatgo 3821 FTCCTTCTCTA FTCCTTCTCTA	3731 3731 366CTAAGAA 366CTAAGAA 363CTAAGAA 3831 ATCTCATTCATCA	3741 TTCAAGAGAGA TTCAAGAGAGA CtCAAGAGAGA 3841 CTTCGTTCT CTTCGTTCT	3751 3751 GAGGAGATGTO GAGGAGATGTO gaggagatgto 3851 CTTTCAG CTTTCAGGTAJ	3761 3761 GATTAAGGGT. SATTAAGGGT. Jattaagggt. 3861 TTCTCAAAT.	GTGATTTT 3771 ACACCTGTGG ACACCTGTGG acacctgtg 3871 	ACAGGTAATCC tcc 3781 3TACAGCCAGG 5TACAACCAGG gtaca ccagg 3881 AATTACATATT	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus	3701 ACAGCTACA acagCTACA 3801 TGGTTTGGA tggtttgga	3711 3711 AGTAATAAT AAGTAATAAT AAGTAATAAT 3811 AAACCCTCGG7 AAACCCTCGG7 AAACCCTCGG7	3721 3721 TACAAAAATGO TACAAAAATGO tacaaaaatgo 3821 FTCCTTCTCTA FTCCTTCTCTA	3731 3731 366CTAAGAAT 366CTAAGAAT 366CTAAGAAT 3631 3831 ATCTCATTCAT ATCTCATTCAT	3741 TTCAAGAGAGA TTCAAGAGAGA ttCaagagaga 3841 CTTCGTTCT CTTCGTTCT CTTCGTTCT	3751 3751 GAGGAGATGTC GAGGAGATGTC gaggagatgtc 3851 CTTTCAG CTTTCAGGTAT ctttcag	3761 3761 SATTAAGGGT. SATTAAGGGT. Jattaagggt. 3861 TTCTCAAAT.	3771 3771 ACACCTGTG ACACCTGTG acacctgtg 3871 ACATCAACAA	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA
ML012-Cav07g Consensus ML012-G6SA01 ML012-Cav07g Consensus ML012-G6SA01 ML012-Cav07g Consensus	3701 ACAGCTACA acagctaca 3801 TGGTTTGGA tggtttgga 3901	3711 AGTAATAAT AAGTAATAAT Aagtaataat 3811 AACCCTCGG AACCCTCGG Aaaccctcggt 3911	3721 3721 TACAAAAATGO TACAAAAATGO tacaaaaatgo 3821 FTCCTTCTCTA FTCCTTCTCTA ttccttctcta 3921	3731 3731 366CTAAGAAT 366CTAAGAAT 366CTAAGAAT 3631 3831 ATCTCATTCAT ATCTCATTCAT ATCTCATTCAT 41ctcattcad 3931	3741 TTCAAGAGAGA TTCAAGAGAGA ttCaagagaa 3841 TTCGTTCT TTCGTTCT Sttcgttct 3941	3751 3751 GAGGAGATGTU GAGGAGATGTU gaggagatgtu 3851 CTTTCAG CTTTCAGGTAT CTTTCAGGTAT Ctttcag 3951	3761 3761 SATTAAGGGT. SATTAAGGGT. Jattaagggt. 3861 TTCTCAAAT. 3961	3771 3771 ACACCTGTG ACACCTGTG acacctgtg 3871 ACATCAACAJ 3971	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT 3981	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus	3701 ACAGCTACA acagctaca 3801 TGGTTTGGA tggtttgga 3901	3711 AGTAATAAT AAGTAATAAT Aagtaataat 3811 AACCCTCGG AACCCTCGG Aaaccctcggu 3911	3721 3721 TACAAAAATGO TACAAAAATGO tacaaaaatgo 3821 FTCCTTCTCTA FTCCTTCTCTA ttccttctcta 3921	3731 3731 366CTAAGAAT 366CTAAGAAT 369CTAAGAAT 3831 ATCTCATTCAT ATCTCATTCA ATCTCATTCA AtCtCattCad 3931	3741 TTCAAGAGAGA TTCAAGAGAGA CTCAAGAGAGA CTCCAAGAGAGA 3841 CTTCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTTCT	3751 SAGGAGATGTU SAGGAGATGTU gaggagatgtu 3851 CTTTCAG CTTTCAGGTAT ctttcag 3951	3761 3761 SATTAAGGGT. SATTAAGGGT. Jattaagggt. 3861 FTTCTCAAAT. 3961	3771 3771 ACACCTGTGG ACACCTGTGG acacctgtgg 3871 ACATCAACAJ 3971	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT 3981	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA 3991
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus	3701 ACAGCTACA acagctaCa 3801 TGGTTTGGA tggtttgga 3901 GATTGCGTC	CTTTGTTTA 3711 AGTAATAAT AGTAATAAT Aagtaataat 3811 AACCCTCGG Aaaccctcggu 3911 CGAGAAATAG	3721 TACAAAAATGO TACAAAATGO TACAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAAATGO TACAAAAAATGO TACAAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	3731 3731 366CTAAGAAT 366CTAAGAAT 3831 ATCTCATTCA ATCTCATTCA ATCTCATTCA ATCTCATTCA 3931	3741 TTCAAGAGAGA TTCAAGAGAGA ttCaagagaa 3841 TTCGTTCTT STTCGTTCTT SttCgTtCT 3941 TTCTAAAAAT.	3751 GAGGAGATGTO GAGGAGATGTO gaggagatgto 3851 CTTTCAG CTTTCAGGTAT ctttcag 3951	GGAAAAAAGA	3771 3771 ACACCTGTGG ACACCTGTGG acacctgtgg 3871 ACATCAACAJ 3971	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT 3981	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA 3991 TCAAGCTTTTCTC
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-GGSA01 ML012-Cav07g Consensus	3701 ACAGCTACA acagctaca 3801 TGCTTTGGA tggtttgga 3901 GATTGCGTC	3711 AGTAATAATI AAGTAATAATI AAGTAATAATI AAGTAATAATI AAGCACTCGGT AAACCCTCGGT	3721 TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO 3821 TTCCTTCTCTA ttccttctcta 3921 AGCTTTTGTTT	3731 3731 366CTAAGAAT 366CTAAGAAT 3831 ATCTCATTCA(ATCTCATTCA(ATCTCATTCA(3931 TACAGAAAAAA(3741 TTCAAGAGAGA TTCAAGAGAGA ttCaagagaa 3841 TTCGTTCT TTCGTTCT sttcgttct 3941 TTCTAAAAAT.	3751 GAGGAGATGTU GAGGAGATGTU GAGGAGATGTU gaggagatgtu 3851 CTTTCAG CTTTCAGGTAT Ctttcag 3951 AACTTTTATAC	GGAAAAAAAGA	3771 3771 ACACCTGTGG ACACCTGTGG acacctgtgg 3871 ACATCAACA 3971	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT 3981 AAACCTCATTT	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA 3991 TCAAGCTTTTCTC
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-GGSA01 ML012-Cav07g Consensus	TTTTATCGC 3701 ACAGCTACA acagctaca 3801 TGGTTTGGA tggtttgga 3901 GATTGCGTC 4001	3711 AGTAATAATI AAGTAATAATI AAGTAATAATI AAGTAATAATI AAGCAATAATI AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT CGAGAAATAGJ	3721 TACAAAAATGO TACAAAATGO TACAAAATGO TACAAAAATGO TACAAAATGO TACAAAAATGO TACAAAAATGO TACAAAATGO TACAAAAATGO TACAAAAATGO TACAAAATGO TACATTCO TACAAAATGO TACATTCO TAC	3731 3731 366CTAAGAAT 366CTAAGAAT 3831 ATCTCATTCA(ATCTCATTCA(3931 TACAGAAAAAA(4031	3741 TTCAAGAGAGA TTCAAGAGAGA CTCCAAGAGAGA CTCCAGGAGA CTCCGTTCT CTTCGTTCT CTTCGTTCT CTCCGTTCT	TGGAAAATCAT 3751 GAGGAGATGTC GAGGAGATGTC gaggagatgtc 3851 CTTTCAG CTTTCAGGTAT CTTTCAGGTAT Ctttcag 3951 AACTTTTATAC	GGAAAAAAGA	3771 3771 ACACCTGTGG ACACCTGTGG acacctgtg(3871 ACATCAACAJ 3971 AGAAGAAGAAGA	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT 3981 AAACCTCATTT	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA 3991 TCAAGCTTTTCTC
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus	TTTTATCGC 3701 ACAGCTACA acagctaca 3801 TGGTTTGGA tggtttgga 3901 GATTGCGTC 4001	3711 AGTAATAATI AAGTAATAATI AAGTAATAATI AAGTAATAATI AAGCATCGGT AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT CGAGAAATAGJ 4011	3721 TACAAAAATGO TACAAAATGO TACAAAATGO TACAAAAATGO TACAAAATGO TACAAAAATGO TACAAAAATGO TACAAAATGO TACATCTTATA	3731 3731 366CTAAGAAT 366CTAAGAAT 3831 ATCTCATTCA(ATCTCATTCA(3931 TACAGAAAAAA(4031	3741 TTCAAGAGAGA TTCAAGAGAGA CTCCAAGAGAGA CTCCAAGAGAGA CTCCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTTCT CTCGTTCT 3941 TTCTAAAAAT. 4041	TGGAAAATCAT 3751 GAGGAGATGTC GAGGAGATGTC gaggagatgtc 3851 CTTTCAG CTTTCAGGTAT Ctttcag 3951 AACTTTTATAC 4051	3761 3761 34TTAAGGGT, 34TTAAGGGT, 3861 57TCTCAAAT, 3961 56AAAAAAGA 4061	3771 3771 ACACCTGTGG ACACCTGTGG acacctgtg 3871 ACATCAACA 3971 AGAAGAAGAAGA 4071	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT 3981 AAACCTCATTT 4081	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA 3991 TCAAGCTTTTCTC 4091
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus	TTTTATCGC 3701 ACAGCTACA acagctaca 3801 TGGTTTGGA tggtttgga 3901 GATTGCGTC 4001 AAAATGCAC	3711 AGTAATAATI AAGTAATAATI AAGTAATAATI AAGTAATAATI AAGCAATAATI AAACCCTCGGI AAACCCTCGGI AAACCCTCGGI AAACCCTCGGI CGAGAAATAGJ 4011	3721 3721 TACAAAAATGO TACAAAAATGO TACAAAAATGO tacaaaaatgo 3821 FTCCTTCTCTA FTCCTTCTCTA ttccttctcta 3921 AGCTTTTGTTT 4021	TTTGGGTTG 3731 36GCTAAGAAT 36GCTAAGAAT 36GCTAAGAAT 3631 3831 TTTCATTCAT 4031 4031 2001	3741 TTCAAGAGAGA TTCAAGAGAGA CTCAAGAGAGA CTCCAAGAGAGA CTCCGTTCT CTTCGTTCT CTTCGTTCT CTCCGTTCCGTTCT CTCCGTTCTCT CTCCGTTCTCT CTCCGTTCTCT CTCCGTTCT C	TGGAAAATCAT 3751 GAGGAGATGTU GAGGAGATGTU gaggagatgtu 3851 CTTTCAG CTTTCAGGTAT Ctttcag 3951 AACTTTTATAC 4051	3761 3761 3775 34TTAAGGGT, 34TTAAGGGT, 3861 7777774 3861 7777774 3961 3961 3961 4061	3771 3771 ACACCTGTGG ACACCTGTGG acacctgtg 3871 ACATCAACA 3971 AGAAGAAGAAGA 4071	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT 3981 AAACCTCATTT 4081	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA 3991 TCAAGCTTTTTCC 4091 CATCTTTTTATGT
ML012-Cav07g Consensus ML012-G6SA01 ML012-Cav07g Consensus ML012-Cav07g Consensus	TTTTATCGC 3701 ACAGCTACA acagctaca 3801 TGGTTTGGA tggtttgga 3901 GATTGCGTC 4001 AAAATGCAC	3711 AGTAATAATI AAGTAATAATI AAGTAATAATI AAGTAATAATI AAGTAATAATI AAGTAATAATI AAGTAATAATI AAGTATAATI AAGTATAATI AAGTAATAATI	3721 TACAAAAATGO TACAAAAATGO TACAAAAATGO tacaaaaatgo 3821 TTCCTTCTCTA TTCCTTCTCTA ttccttctcta 3921 AGCTTTTGTTT 4021 TTTTTTAGAGG	TTTGGGTTG 3731 36GCTAAGAAT 36GCTAAGAAT 36GCTAAGAAT 3631 3831 TTTCATTCAT 4031 7ACAGAAAAAGTCJ	3741 TTCAAGAGAA TTCAAGAGAGA CTCAAGAGAGA CTCCAAGAGAGA CTCCAGGAGA 3841 TTCGTTCT TTCGTTCT CTTCGTTCT CTCGTTCT CTCGTTCT 3941 TTCTAAAAAT, 4041	TGGAAAATCAT 3751 GAGGAGATGTU GAGGAGATGTU gaggagatgtu 3851 CTTTCAG CTTTCAGGTAT Ctttcag 3951 AACTTTTAAGTT 4051	3761 3761 3775 377777777777777777777777777777777	3771 3771 ACACCTGTGG ACACCTGTGG acacctgtgg 3871 ACATCAACA 3971 AGAAGAAGAAGA 4071	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT 3981 AAACCTCATTT 4081 FTTGCTTGGTA	TCTTGGTGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA 3991 TCAAGCTTTTTCTC 4091 CATCTTTTTATGT
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ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-GGSA01 ML012-Cav07g Consensus	3701 ACAGCTACA ACAGCTACA acagctaca 3801 TGGTTTGGA TGGTTTGGA tggtttgga 3901 GATTGCGTC 4001 AAAATGCAC 4101 ACTAAAAAT 4201 TTAATTGCA 4301	3711 AGTAATAAT AAGTAATAAT AAGTAATAAT AAGCAATAAT AAGCCTCGG AAACCCTCGG AAACCCTCGG AAACCCTCGG AAACCCTCGG AAACCCTCGG AAACCCTCGG ABAA AACCCTCGG ABAA AACCCTCGG ABAA AACCCTCGG ABAA AACCCTCGG ABAA AACCCTCGG AAATAA AAAAAAAAAAAAAAAAAAAA	3721 TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO 3821 TACATTCTTT 4021 TACATTGTTT 4021 TACATTGCCT TCAACTGGCCT TCAACTGGCCT TCAACTGGCCT TCAACTGGCCT TCAACTGGCCT TCAACTGGCCT	TTTGGGTTG 3731 GGCTAAGAAT GGCTAAGAAT GGCTAAGAAT 36GCTAAGAAT 36GCTAAGAAT 3631 TTTCATTCAT ATTTCATTCAT ATTTCATTCAT 4031 TCAAGAAAAAGTCA 4031 TCAAGAAAAAGTCA 4131 TCTATGCGTG TCTATGCGTG TCTATGCGTG TCTATGCGTG CLCLatgCGTG 4331	3741 TTCAAGAGAA TTCAAGAGAA CTCAAGAGAA CTCCATCAAGAGAA CTCCATCT CTTCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCTC CTTCGTCCTC CTTCGTCCCCCCCC	TGGAAAATCAT 3751 GAGGAGATGTU GAGGAGATGTU 3851 CTTTCAG CTTTCAGGTAT ctttcag 3951 ctttcag 3951 AACTTITATAG 4051 TTTTTAAGTTI 4151 AGCTCTCTGG/ 4251 TAAGCCTTTC/ 4351	3761 3761 SATTAAGGGT. SATTAAGGGT. SATTAAGGGT. 3861 TTTCTCAAAT. 3961 GGAAAAAAGA. 4061 TTTACCCATC. 4161 ATTCTAATATT 4261 ACTTCTTTAA 4361	3771 3771 ACACCTGTG ACACCTGTG acacctgtg 3871 ACATCAACA 3971 ACAACCATCAACA 3971 ACAACCATCAACA 4071 AGAAGAAGAAGA 4071 AGAATCCATT 4171 CAGCCTTTGG 4271 TTCATTAAT 4371	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT 3981 AAATCATATT 4081 TITGCTTGGTA 4181 GCTTTTGCCAT 4281 TCACAAAGTAC 4381	TCTTGGTGGGGAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA 3991 TCAAGCTTTTTCTC 4091 CATCTTTTTATGT 4191 CTTTGTCTTGACT 4291 TTAGGGACTGTTT 4391
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-Cav07g Consensus	TTTTATCGC 3701 ACAGCTACA acagctaca 3801 TGGTTTGGA TGGTTTGGA tggtttgga 3901 GATTGCGTC 4001 AAAATGCAC 4101 ACTAAAAAT 4201 TTAATTGCA 4301	3711 AGTAATAATT AAGTAATAATT AAGTAATAATT AAGTAATAATT AAGCATCCCCGGT AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT AAACCCTCGGT AAATGAATAGAATT GAATGCATTT AAATGCATTT AAATGCATTT AAATGCATTT AAATGCATTT	AATCTAAGCT 3721 TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO TACAAAAATGO 3821 TTCCTTCTCTA AGCTTTTTCTA AGCTTTTTTAGAGO 4021 TTTTTTAGAGO 4121 TCAACTGGCCT TCAACTGGCCT TCAACTGGCCT TCAACTGGCCT TCAACTGGCCT TCAACTGGCCT	TTTGGGTTG 3731 GGCTAAGAAT GGCTAAGAAT GGCTAAGAAT 36GCTAAGAAT 36GCTAAGAAT 3631 TTTCATTCAT ATTTCATTCAT ATTTCATTCAT 4031 TAAAAAAAGTCJ 4031 4031 TTTAATCTCAAJ 4131 TTTTATGCGTG TTTTATGCGTG TCTATGCGTG TCTATGCGTG	3741 TTCAAGAGAA TTCAAGAGAA TTCAAGAGAA CTCCAAGAGAA TTCGTTCTT TTCGTTCTT CTTCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTCTTC CTTCGTCTTCG CTTCGTCTTCG CTTCGTCT CTTCGTCTTCG CTTCGTCT CTTCGTCTCC CTTCGTCTC CTTCGTCTC CTTCGTCTC CTTCGTCTC CTTCGTCTC CTTCGTCTC CTTCGTCTCC CTTCGTCTC CTTCGTCTC CTTCGTCTC CTTCGTCTCC CTTCGTCTC CTTCGTCTC CTTCGTCTC CTTCGTCC	TGGAAAATCAT 3751 GAGGAGATGTU GAGGAGATGTU 3851 CTTTCAG CTTTCAGGTAT ctttcag 3951 ctttcag 3951 AACTTITATAG 4051 FITTTAAGTTI 4151 AGCTCTCTGG/ 4251 TAAGCCTTTC/ 4351	3761 3761 SATTAAGGGT. SATTAAGGGT. SATTAAGGGT. 3861 TTTCTCAAAT. 3961 GGAAAAAAGA. 4061 TTTACCCATC. 4161 ATTCTAATAT 4261 ACTTCTTTAA 4361	3771 3771 ACACCTGTG ACACCTGTG acacctgtg 3871 ACATCAACA 3971 ACAACCATCAACA 3971 ACAACCATCAACA 4071 AGAAGAAGAAGA 4071 AGAATCCATT 4171 CAGCCTTTGG 4271 TTCATTAAT 4371	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT 3981 AAATTACATATT 4081 CTTGCTTGGTA 4181 CTTGCTTGGTA 4281 CCACAAAGTAC 4381	TCTTGGTGGGGAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA 3991 TCAAGCTTTTTTATGT 4091 CATCTTTTTTATGT 4191 CTTTGTCTTGACT 4291 TTAGGGACTGTTT 4391
ML012-Cav07g Consensus ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-GGSA01 ML012-Cav07g Consensus ML012-GGSA01 ML012-GGSA01 ML012-Cav07g Consensus	TTTTATCGC 3701 ACAGCTACA acagctaca 3801 TGCTTTGGA TGGTTTGGA tggtttgga 3901 GATTGCGTC 4001 AAAATGCAC 4101 ACTAAAAAT 4201 TTAATTGCA 4301 GAGTTGCGTC	CTTTGTTTA 3711 AGTAATAATT AGTAATAATT AGTAATAATT AGTAATAATT AGTAATAATT AGTAATAATT AGTAATAATT AGTAATAATT AGACCTCCGG 3911 	AATCTAAGCT 3721 TACAAAAATGC TACAAAAATGC TACAAAAATGC TACAAAAATGC TACAAAAATGC TACAAAAATGC 3821 TTCCTTCTCT ACTTTTCTTA ACTTTTTTAGAGC 4021 TCAACTGGCCT TCAACTGGCCT TCAACTGGCCT TCAACTGGCCT TCAAAAGTGC/	TTTGGGTTG 3731 GGCTAAGAAT GGCTAAGAAT GGCTAAGAAT 36GCTAAGAAT 36GCTAAGAAT 3631 TTTCATTCAT 4031 TCAAGAAAAAGTCA 4031 TCAAGAAAAAGTCA 4131 TCTATGCGTC TCTATGCGTC TCTATGCGTC tCtatgcgtQ 4331	3741 TTCAAGAGAA TTCAAGAGAA TTCAAGAGAA CTCCAAGAGAA CTCCATCT TTCGTTCT TTCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCT CTTCGTCTC CTTCGTCT CT	3751 3751 GAGGAGATGTO GAGGAGATGTO SASI CTTTCAG 3951 ctttcag 3951 ctttcag 3951 ctttcag 3951 ctttcag 4051 FITTTAAGTTI 4151 AGCTCTCTGGA 4251 TAAGCCTTTCA 4351	3761 3761 SATTAAGGGT. SATTAAGGGT. SATTAAGGGT. 3861 TTTCTCAAAT. 3961 GGAAAAAAGA. 4061 TTTACCCATC. 4161 ATTCTAATAT 4261 ACTTCTTTAA 4361	3771 ACACCTGTG ACACCTGTG ACACCTGTG acacctgtg 3871 ACATCAACAJ 3971 ACATCAACAJ 4071 AGAAGAAGAAGA 4071 AGATCCATT 4171 CAGCCTTTG 4271 TTCATTAAT 4371 CGGTTTCGTJ	ACAGGTAATCC tcc 3781 STACAGCCAGG STACAACCAGG gtaca ccagg 3881 AATTACATATT 3981 AAACCTCATTT 4081 CTTGCTTGGTA 4181 CTTGCTTGGTA 4281 CCACAAAGTAC 4381	TCTTGGTGGGGTAC tcttggtgggtac 3791 TGATGACCTCTTC TGATGACCTCTTC tgatgacctcttc 3891 ACAGCCTCTTTGA 4091 CATCTTTTTATGT 4191 CTTTGTCTTGACT 4291 TTAGGGACTGTTT 4391 AAAGCGTTTTTGACT

	4401	4411	4421	4431	4441	4451	4461	4471	4481	4491
ML012-GGSA01										
ML012-Cav07g	GGATCCAA	GAAGTCAAAA	LAATGACTAAA	ACGTACTTT	TGGCAAAAAC	TTAAAAATGA	TGCTTTTGTC	AAAAAATGCT	TTTTGATTTA	AAAGCTCTATTTT
Consensus										
	4501	4511	4521	4531	4541	4551	4561	4571	4581	4591
ML012-GGSA01										
ML012-Cav07g	TCAAATGC	AATCACAAAO	ATGCTTTTAA	TGGTGTCTG	TACTACGAAA	CAAAGTCCCA	TCACATGTGA	CATTGGCATI	FGCTCAAAAGC	ATCTACTITIAGA
Consensus										
	4601	4611	4621	4631	4641	4651	4661	4671	4681	4691
ML012-GGSA01									TATGCATT	TGGCATAAATTCT
ML012-Cav07g	ATTTAGAA	TTAAGCAACA	AGTGAAGCTI	ATGCTAAGA	GCTTTCCCTA	ACTTTCCTGI	CATATTTTT	CTTCTCTTTC	CAGTATGCATT	TGGCATAAATTCT
Consensus									tatgcatt	tggcataaattet
	4701	4711	4721	4731	4741	4751	4761	4771	4781	4791
ML012-GGSA01	TGCTTCCA	TAAGCGCACT	GAAGATAAGO	TCATCAGAC	TCTCAACGGG	<mark>6</mark>				
ML012-Cav07g	TGCTTCCA	TAAGCGCACT	GAAGATAAGO	TCATCAGAC	TCTCAACGGG	GTGAGTTCTI	TCACAAATGC	ACATCCATGO	GAATTCCATAT	GCCATGCATGGTG
Consensus	tgcttcca	taagcgcact	gaagataago	ftcatcagac	tctcaacggg	ıà				
	4801	4811	4821	4831	4841	4851	4861	4871	4881	4891
ML012-GGSA01										ATCATCACAC
ML012-Cav07g	CCATTGTT	AAGATGTAGT	TATTTGGATO	attaatgtg	TTAATTAAGT	TTAAGAATTO	GCTAATGCTAT	ACGACTTTGO	GCACTTTCTTC	AGG <mark>ATCATCACAC</mark>
Consensus										atcatcacac
	4901	4911	4921	4931	4941	4951	4961	4971	4981	4991
ML012-GGSA01	AAGTTCTA	TGCAGTTATO	TGACTTTGCC	TCTCTATGC	TCTAGTGATT	CGG				
ML012-Cav07g	AAGTTCTA	TGCAGTTATO	TGACTTTGCC	TCTCTATGC	TCTAGTGATI	CGGGTGAGAA	ATTAATGATG	ACATGGCTTO	CAAAGGTTAAA	ТААТАСАААТАТА
Consensus	aagttcta	tgcagttato	gtgactttgco	tctctatgc	tctagtgatt	caa				
	5001	5011	5021	5031	5041	5051	5061	5071	5081	5091
ML012-GGSA01										
ML012-Cav07g	GAAGCAAA	TATATTAGCA	AACAATACAA	ATCATTAAA	AAGCAGTTTI	CACATTTATA	TGAGAATATA	AGAAAACACA	ATTTTTTTA	АААААААТТТАТ
Consensus										530
	5101	5111	5121	5131	5141	5151	5161	5171	5181	5191
ML012-GGSA01										
ML012-Cav07g	GATGGAGA	AGGGTTTTTC	GGACCTACCT	TTATAGAGT.	AAACCTCGAA	CCCGTGTATI	GCATTCTCGA	AAGTITCCTI	TACACGGACCA	GGGTAAATACCTG
Consensus										
	5201	5211	5221	5231	5241	5251	5261	5271	5281	5291
ML012-GGSA01										
ML012-Cav07g	ACTTTTGC	ACCAAGGGGT	GTGGCGCCCT	AATGGGGTG	TITGTACCTA	GCAAGTCTCA	AACTTGAGAT	CTAATGCGTO	GATACTCCCTA	AGACCACAAGCCT
Consensus										50
	5301	5311	5321	5331	5341	5351	5361	5371	5381	5391
ML012-GGSA01										ATGG
ML012-Cav07g	CAACCACT	AGGCGAGCCO	TTTGGGGTTA	AAAAAATAA	AAGTAAAAAT	TAATATGCAT	AGCCTTTGAC	ТААТТАТТСТ	TTGGACTGAT	TTTTTGCAG <mark>ATGG</mark>
Consensus										atgg
	5401	5411	5421	5431	5441	5451	5461	5471	5481	5491
ML012-GGSA01	GCTCTTCC	ATGAATTCTA	CCATTTTTAA	TGATGGAGT	GGCAACAGCA	TTAAAGAGCT	GGCATCGCAA	GGCCAAGAAG	GAAATCTAAGC	ATGCCCATCATTC
ML012-Cav07g	GCTCTTCC	ATGAATTCTA	CCATTTTTAA	TGATGGAGT	GGCAACAGCA	TTAAAGAGCT	GGCATCGCAA	GGCCAAGAAG	GAAATCTAAGC	ATGECCATCATTC
Consensus	getettee	atgaatteta	Accattttas	atgatggagt	ggcaacagca	ittaaagagct	ggcatcgcaa	iggccaagaag	yaaatctaagc	atgcccatcattc
	5501	5511	5521	5531	5541	5551	5561	5571	5581	5591
ML012-GGSA01	TGAGGCAA	ATTCACCAAT	TCACCTETTO	CATAACTAT	CAGCATEGEA	GCCTTGATAG	CTTGCACACA	TETECTAATO	ATCATTTGA	AATGGAAGACTTA
ML012-Cav07g	TGAGGCAA	ATTCACCAAT	TCACCTCTTC	CATAACTAT	CAGCATCGCA	GCCTTGATAG	GCTTGCACACA	TCTCCTAATO	GATCATTTTGA	AATGGAAGACTTA
Consensus	tgaggcaa	attcaccaat	tcacctett	gcataactat	cagcatogca	gccttgatag	gettgeacaca	tctcctaato	gatcattttga	aatggaagactta
	5601	5611	5621	5631	5641	5651	5661	5671	5681	5691
MI 012-GGSA01	GAATTOCA	AAGGAAACAA	AGTEGACACI	AAGACTCTA	TGCATTCTGA	GCALGAGAAA	GAGATTCAAG	AGCAAAGATO	ATCGCAATTG	CETECATEAETAG
ML012-Cav07g	GAATTCCA	AAGGAAACAA	AGTEGACACO	AAGACTCTA	TGCATTCTGA	GCAAGAGAAG	GAGATTCAAG	AGCAAAGATO	ATCGCAATTG	CCTCCATCACTAG
Consensus	gaattcca	aaggaaacaa	agtggacaco	aagactcta	tgcattctga	igcaagagaac	gagattcaad	agcaaagato	atogcaatto	cctccatcactag
	5701	5711	5721	5731	5741	5751	5761	5771	5781	5791
MI.012-005201	GAACCATT	CGAACCCAAC	ALEVAL	CGTTAGTCC	GTCAGATTE	TETTTEREN	GATGA	0771	3701	0/21
ML012-Cav07g	GAACCATT	CGAACCCAAC	ACGAAATCA	CGTTAGTCC	GTCAGATTTC	TCTTTTCGCA	GATGA			

Consensus gaaccattcgaacccaacacgaaatcaacgttagtccgtcagatttctcttttcgcagatga