

UNIVERSIDADE FEDERAL DO RIO GRANDE DO SUL  
CENTRO DE BIOTECNOLOGIA  
PROGRAMA DE PÓS-GRADUAÇÃO EM BIOLOGIA CELULAR E MOLECULAR

**ESTRUTURA DO GENE *VvAGL11* E ANÁLISE DA EXPRESSÃO DURANTE A  
MORFOGÊNESE DA SEMENTE DE VIDEIRA**

Dissertação de Mestrado

**Jaiana Malabarba**

Porto Alegre, outubro de 2014

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Dissertação submetida ao Programa de Pós-graduação em Biologia Celular e Molecular do Centro de Biotecnologia da Universidade Federal do Rio Grande do Sul como requisito parcial para obtenção do título de Mestre.

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Porto Alegre, outubro de 2014

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“There are many hypotheses in science which are wrong.  
That is perfectly all right: it’s the aperture to finding out what’s right.  
Science is a self-correcting process.”

*Carl Sagan*

“There's real poetry in the real world.  
Science is the poetry of reality.”

*Richard Dawkins*

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## ÍNDICE

<b>LISTA DE ABREVIATURAS, SÍMBOLOS E UNIDADES.....</b>	<b>8</b>
<b>RESUMO.....</b>	<b>11</b>
<b>ABSTRACT.....</b>	<b>12</b>
<b>1 INTRODUÇÃO.....</b>	<b>13</b>
1.1 MORFOGÊNESE DE SEMENTES E APIRENIA.....	14
<b>1.1.1 Anatomia das Sementes em Desenvolvimento.....</b>	<b>14</b>
<b>1.1.2 Apirenia.....</b>	<b>16</b>
<b>1.1.3 Mecanismos Moleculares da Morfogênese de Sementes.....</b>	<b>17</b>
1.1.3.1 Os genes <i>MADS-BOX</i> .....	17
1.1.3.1.2 Genes <i>MIKC<sup>c</sup></i> responsáveis pelo desenvolvimento de óvulo e de semente.....	20
1.2 A CULTURA DA VIDEIRA.....	22
<b>1.2.1 A Cultivar Sultanina.....</b>	<b>24</b>
<b>1.2.2 Controle Genético e Molecular da Apirenia em Videira.....</b>	<b>26</b>
<b>2 OBJETIVOS.....</b>	<b>30</b>
2.1 OBJETIVO GERAL.....	30
2.2 OBJETIVOS ESPECÍFICOS.....	30
<b>3 CAPÍTULO I.....</b>	<b>31</b>
Manuscrito a ser submetido ao periódico .....	32
<b>4 CONCLUSÕES.....</b>	<b>80</b>
<b>5 PERSPECTIVAS.....</b>	<b>82</b>
<b>6 REFERÊNCIAS BIBLIOGRÁFICAS.....</b>	<b>83</b>
<b>7 CURRICULUM VITAE.....</b>	<b>91</b>

## **LISTA DE ABREVIATURAS, SÍMBOLOS E UNIDADES**

% - percentagem

3' - extremidade 3' -hidroxila de DNA ou RNA

5' - extremidade 5' -fosfato de DNA ou RNA

A – adenilato ou ácido adenílico

*AG* - gene *AGAMOUS*

*AGL6* – gene *AGAMOUS-LIKE 6*

*AGL11* – gene *AGAMOUS-LIKE 11*

*AGL15* – gene *AGAMOUS-LIKE 15*

*AGL17* – gene *AGAMOUS-LIKE 17*

*API* – gene *APETALA 1*

*AP2* – gene *APETALA 2*

*AP3* – gene *APETALA 3*

*AtAGL11* - gene *AGAMOUS-like* de *Arabidopsis thaliana*

*AVAG2* - gene *AGAMOUS 2* de *Aspargus*

*BPC1* - gene *BASIC PENTACYSTEINE 1*

*BS* - gene *B SISTER*

C – citidilato ou ácido citidílico

cDNA – DNA complementar (do inglês, *complementary DNA*)

Col-0 - *Arabidopsis thaliana* acesso Columbia-0

DNA – ácido desoxirribonucleico (do inglês, *deoxyribonucleic acid*)

*DEF* - gene *DEFICIENS*

DNase – desoxirribonuclease

*EgMADS1* - gene *MADS-Box 1* de *Eustoma grandiflorum*

ESTs – etiquetas ou marcas de sequências expressas (do inglês, *Expressed Sequence Tags*)

F1 - primeira geração filial (do inglês, *First Filial Generation*)

FAO – Organização das Nações Unidas para Agricultura e Alimentação (do inglês, *Food and Agriculture Organization of the United Nations*)

*FBP7* - gene codificador da *FLORAL BINDING PROTEIN 7*

*FBP11* - gene codificador da *FLORAL BINDING PROTEIN 11*

*FLC* - gene *FLOWERING LOCUS C*

*FUL* - gene *FRUITFULL*

G – guanidilato ou ácido guanidílico

INDEL- mutação de inserção ou deleção de nucleotídeos (do inglês *Insertion* e *Deletion*)

*LMADS2* – gene *MADS-Box 2* de *Lilium*

*Mcm1* - gene *minichromossome maintenance 1*

MAS - seleção assistida por marcadores (do inglês, *marker assisted selection*)

mRNA – RNA mensageiro (do inglês, *messenger RNA*)

OIV - Organização Internacional da Uva e do Vinho (do francês, *Organization Internationale de la Vigne e du Vin*)

*OsMADS13* - gene *MADS-Box 13* de *Oryza sativa*

pb – par (es) de bases

PCR – reação em cadeia da DNA polimerase (do inglês, *polymerase chain reaction*)

*PhalAG2* - gene *AGAMOUS 2* de *Phalaenopsis*

*PI* - gene *PISTILATTA*

Place – do inglês, *Plant Cis-acting Regulatory DNA Elements*

*QTL*- *locus* de característica quantitativa (do inglês, *quantitative trait locus*)

RNA – ácido ribonucleico (do inglês, *ribonucleic acid*)

RT-qPCR – PCR quantitativa precedida de transcrição reversa (do inglês, *reverse transcription-quantitative PCR*)

*SdI* - inibidor do desenvolvimento da semente (do inglês *Seed Development Inhibitor*)

*SEP1* – gene *SEPALLATA 1*

*SEP2* - gene *SEPALLATA 2*

*SEP3* - gene *SEPALLATA 3*

*SEP4* - gene *SEPALLATA 4*

*SHP1* - gene *SHATTERPROOF 1*

*SHP2* - gene *SHATTERPROOF 2*

SNP- polimorfismo de nucleotídeo único (do inglês *Single Nucleotide Polymorphism*)

*SOC* - gene *SUPPRESSOR OF OVEREXPRESSION OF CONSTANCE 1*

*SRF* - gene *SERUM RESPONSE FACTOR*

*STK* - gene *SEEDSTICK*

*stk* - mutante que não expressa o gene *STK/AtAGL11*

*SVF* - gene *SHORT VEGETATIVE PHASE*

T – timidilato ou ácido timidílico

UTR - região não traduzida (do inglês, *untranslated region*)

*VvAG3* - gene *AGAMOUS 3* de *Vitis vinifera* (*VvAGL11*)

*VvAGL11* - gene *AGAMOUS-LIKE 11* de *Vitis vinifera* (*VvAG3*)

WT - tipo-selvagem (do inglês, *wild-type*)

*ZAG2* - gene *AGAMOUS 2* de *Zea mays*

*ZMM1* - gene *MADS-BOX 1* de *Zea mays* (*ZMADS1*)

## RESUMO

A videira é uma frutífera de origem antiga e atualmente é a mais cultivada do mundo, sendo de extrema importância econômica para diversos países. Certos genótipos de *Vitis vinifera* L., como a ‘Sultanina’, produzem bagas com apenas traços de sementes. Esta característica, denominada de apirenia, é classificada como estenoespermocarpia uma vez que a fecundação ocorre para a formação do fruto, porém é seguida de aborto do embrião devido à degeneração do endosperma. A apirenia é uma das características mais apreciadas para a uva de mesa e a compreensão dos mecanismos genéticos e moleculares controladores dessa característica é justificada pelo crescimento e pela exigência do mercado de uvas *in natura*. Estudos anteriores de nosso grupo permitiram identificar o gene *VvAGL11* como principal candidato atuante no controle do desenvolvimento de sementes em videira. Foi nosso objetivo, pelo presente trabalho, avaliar o gene *VvAGL11* nas cultivares pirênicas Chardonnay e apirênicas Sultanina, visando uma maior compreensão de seu papel durante a morfogênese da semente. Por meio de sequenciamento alelo-específico, foi possível caracterizar as variações alélicas do gene, o qual apresenta duas isoformas transcritas na cultivar pirênicas Chardonnay. Em ‘Sultanina’, uma das isoformas identificadas possui mutações únicas. Pela avaliação do perfil transcracional de *VvAGL11* em diferentes estádios de desenvolvimento, da flor e do fruto, foi observado um grande acúmulo de transcritos em sementes de 2, 4 e 6 semanas em comparação com tecidos de flor e polpa. Na cultivar Sultanina, a expressão de *VvAGL11* foi extremamente baixa em todos os estádios e tecidos analisados. Análises morfo-anatômicas foram empregadas para comparar a semente e o traço de semente. Foram identificadas alterações anatômicas que sugerem a perda da identidade da camada de integumento médio do traço de semente de Sultanina, uma vez que esta camada não apresentou o padrão de diferenciação normal. O padrão de expressão espaço-temporal de *VvAGL11* foi determinado pela técnica de hibridização *in situ*. Foram utilizadas amostras das cultivares Chardonnay e Sultanina nos mesmos estádios de desenvolvimento analisados por RT-qPCR. Os níveis de transcritos de *VvAGL11* aumentaram significativamente em frutos de ‘Chardonnay’ com 2 e 4 semanas de desenvolvimento, especificamente na camada dupla do integumento médio da semente. Em ‘Sultanina’, não houve detecção de transcritos do gene em quaisquer estádios de desenvolvimento.

## ABSTRACT

Grapevine have ancient origins and is currently the most widely cultivated fruit in the world, with high economic importance to many countries. Certain genotypes of *Vitis vinifera* L. like 'Sultanina' produce berries with only seed traces. This characteristic, termed apireny, is classified as stenospermocarpy since fertilization occurs aiming the formation of fruits but it is followed by the abortion of the embryo due to endosperm degeneration. Seedlessness is one of the most appreciated features for table grapes. Thereby the understanding of genetic and molecular mechanisms that control this feature is justified by the growth and the demand of *in natura* grapes' market. Our previous studies allowed us to identify a candidate gene, *VvAGL11*, possibly involved in the control of seed development in grapevine. Our objective with the present study was to evaluate *VvAGL11* in a pirenic cultivar, Chardonnay, and in an apirenic cultivar, Sultanina, in order to better understand its role during seed morphogenesis. By allele-specific sequencing, it was possible to characterize the allelic variations of *VvAGL11*, which exhibited two transcript isoforms in 'Chardonnay'. In 'Sultanina' one of the isoforms was identified with unique mutations. Evaluation of transcriptional profiles of *VvAGL11* during different developmental stages, from flowers to mature fruits, it showed a large accumulation of transcripts in seeds of 2, 4 and 6 weeks old compared to flower and pulp tissues in the Chardonnay cultivar. In 'Sultanina' the expression of *VvAGL11* was extremely low in all stages and tissues examined. Anato-morphological analyzes were performed in order to compare the seed and the seed trace. It was identified a loss of identity of the medium integument layer in the Sultanina seed trace since this layer neither elongated nor doubled in size as it should. The spatial-temporal expression pattern of *VvAGL11* was determined by an *in situ* hybridization technique. Samples of 'Chardonnay' and 'Sultanina' in the same stages of development analyzed by RT-qPCR were employed. *VvAGL11* transcript levels were significantly increased in 'Chardonnay' seeds with 2 and 4 weeks of development, specifically in the dual layer medium integument of the seed. In 'Sultanina', gene transcripts were undetectable during all stages of development.

## 1 INTRODUÇÃO

O desenvolvimento e a seleção de variedades de uva de mesa (*Vitis vinifera*) são considerados investimentos de longo prazo e de alto custo. A técnica de melhoramento clássico comumente utilizada envolve a geração de centenas de indivíduos F1 (do inglês, *First Filial Generation*) a cada ano, os quais necessitam de muito espaço para avaliação em campo e de longo período de cultivo para a obtenção de frutos (CABEZAS *et al.*, 2006). Todo este processo gera perdas de produtividade pela demora excessiva, de até seis anos, para a avaliação da qualidade dos frutos. Visando a inovação deste sistema, a geração de plantas que apresentem caracteres de interesse por técnicas de engenharia genética é vantajosa para os grandes mercados produtores de frutíferas de desenvolvimento prolongado, como a videira, além da utilização de ferramentas biotecnológicas, como marcadores moleculares, que auxiliem na aceleração da geração e seleção de novas cultivares.

Muitos programas de melhoramento têm mantido o foco na geração de uvas de mesa que combinem ausência de sementes com outros caracteres de interesse agronômico no fruto tais como aumento do tamanho da baga, sabor moscatel e crocância (LOOMIS & WEINBERG, 1979; CAMARGO *et al.*, 2005). A compreensão dos mecanismos genéticos e moleculares controladores da apirenia ou ausência de sementes em uvas de mesa possui grande relevância econômica, uma vez que o mercado consumidor desta fruta vem crescendo significativamente nas últimas décadas, além de ter aumentado sua preferência por uvas apirênicas (VITTI, 2009).

Diversos autores e grupos de pesquisa buscaram compreender as bases genéticas e moleculares da apirenia. A presença de um alelo dominante na região do *locus SdI* (Inibidor do desenvolvimento da semente, do inglês, *Seed development Inhibitor*), na extremidade do cromossomo 18 de *Vitis vinifera*, foi identificada como o principal QTL (*QTL*, do inglês, *Quantitative Trait Locus*) associado à apirenia, responsável por 50 a 70% da variância fenotípica total (BOUQUET E DANGLOT, 1996; LAHOGUE *et al.*, 1998; DOLIGEZ *et al.*, 2002; CABEZAS *et al.*, 2006; MEJÍA *et al.*, 2007; COSTANTINI *et al.*, 2008). O gene *VvAGL11* (*AGAMOUS-LIKE 11*; acesso no genoma em <http://genomes.cribi.unipd.it/grape/:Vv18s0041g01880>) está localizado no mesmo *contig* do *Locus SdI* e foi proposto como um forte candidato responsável pela ausência de sementes

em videira (COSTANTINI *et al.*, 2008; MEJÍA *et al.*, 2011; REVERS *et al.*, 2010). *VvAGL11* codifica um fator de transcrição do tipo MADS-box. Análises *in silico* permitiram sugerir uma possível ortologia entre *VvAGL11* e *SEEDSTICK* (*STK* ou *AtAGL11*) de *Arabidopsis thaliana* (acesso no genoma [www.Arabidopsis.org](http://www.Arabidopsis.org): AT4G09960), o qual está envolvido no controle da identidade do óvulo (PINYOPICH *et al.*, 2003).

A identificação do gene *VvAGL11* localizado dentro de um *Locus* de Características Quantitativas significativamente associado à apirenia, aliado à sua ortologia com o gene *SEEDSTICK* de *Arabidopsis* justifica a caracterização deste gene no contexto da apirenia em videira. A compreensão de seu papel na morfogênese de sementes em uvas poderá ser útil no desenvolvimento de novas cultivares de uvas de mesa que atendam às exigentes demandas do mercado de consumo nacional e internacional.

## 1.1 MORFOGÊNESE DE SEMENTES E APIRENIA

### 1.1.1 Anatomia das Sementes em Desenvolvimento

As angiospermas apresentam uma estrutura especializada altamente complexa responsável pela propagação e manutenção de suas espécies, a semente. Esta é composta por três partes principais, cada qual com sua função: os integumentos, que protegem o endosperma e o embrião de situações adversas até que haja condições favoráveis para a germinação; o endosperma, que possui os nutrientes necessários para o desenvolvimento inicial do embrião; e o embrião, que se divide em duas partes, a radícula e o cotilédone, que germinarão para a formação de uma nova planta (Figura 1a; HAUGHN & CHAUDHURY, 2005).

As diversas camadas de integumentos que compõem a casca da semente (Figura 1b) possuem origem materna. Esta estrutura é formada, geralmente, por uma cutícula que se localiza acima de uma camada de epiderme e por três regiões tegumentares: integumento externo; uma camada dupla de integumento médio; e três camadas de integumento interno (PRATT, 1971; Figura 1b). Por outro lado, o endosperma e o embrião são gerados por dupla fecundação, sendo o primeiro triploide, proveniente da fecundação da célula central

homodiplóide, e o segundo diploide, originado da fecundação da célula ovo haplóide (SITTE *et al.*, 2002).

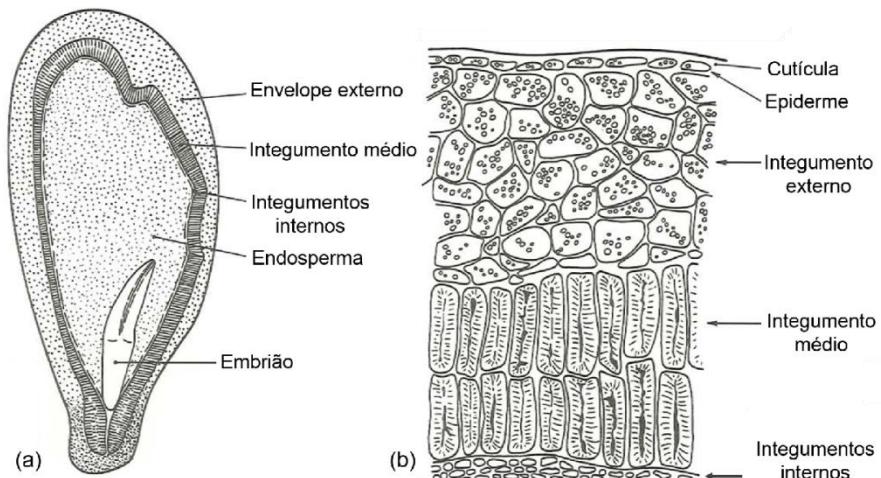


Figura 1. Ilustração da semente de *Vitis*. (a) A semente madura apresentada em corte longitudinal onde são visualizadas as camadas externas seguidas do integumento médio e de camadas de integumento interno. A porção central é composta pelo embrião circundado pelo endosperma. (b) Ilustração das camadas da casca da semente composta por uma camada de cutícula, uma camada de epiderme seguida pelo integumento externo e pelo integumento médio. Abaixo destes, iniciam-se as camadas de integumentos internos. Adaptado de PRATT (1971).

Em *A. thaliana*, o desenvolvimento da semente pode ser dividido em duas fases. A primeira é caracterizada pela proliferação e crescimento do endosperma, que aumenta o tamanho da semente em cerca de 100 vezes e traz grande contribuição para o seu tamanho final (VAROQUAUX *et al.*, 2000). Em contraste, o crescimento do embrião ocorre durante a segunda fase, quando há a expansão do endosperma (JÜRGENS & MAYER, 1994). O fluxo de nutrientes ocorre de forma centrípeta, do integumento externo para o interno, passando através de apoplastos para o endosperma e para o embrião em rotas que ainda não são completamente compreendidas (STADLER *et al.*, 2005). Ao fim da maturação da semente as camadas de integumentos morrem devido à sua lignificação, com exceção do endotélio (HAUGHN & CHAUDHURY, 2005). O crescimento da semente é, portanto, ditado pelo desenvolvimento conjunto do endosperma e dos integumentos (GARCIA *et al.*,

2005). Estudos já demonstraram que existe um forte efeito materno dos integumentos no controle e na determinação do tamanho da semente, por consequência de seu alongamento (BERGER *et al.* 2006). Deste modo, uma coordenação temporal e espacial de crescimento entre estes diferentes tecidos é crítica para o desenvolvimento correto da semente (UNGRU *et al.*, 2010).

### **1.1.2 Apirenia**

Os processos que regem o desenvolvimento de sementes estão bem caracterizados do ponto de vista fisiológico (EGLI, 1998). Diversas culturas que possuem apelo comercial voltado para a produtividade de grãos dependem deste conhecimento, bem como do seu entendimento do ponto de vista genético e molecular, para a obtenção de boas safras ano a ano. Entretanto, em culturas onde o produto final é o fruto, uma das características mais apreciadas pelos consumidores é a ausência de sementes.

Uma planta é considerada apirênica quando é capaz de produzir frutos sem sementes, com traços de sementes ou com sementes reduzidas em número e tamanho (VAROQUAUX *et al.*, 2000). Duas formas de apirenia podem ser observadas dependendo do estádio em que a semente cessa o seu desenvolvimento, partenocarpia e estenoespermocarpia. Na partenocarpia, o ovário é capaz de se desenvolver em fruto sem que haja fecundação, apenas a partir do desenvolvimento dos tecidos maternos. Os frutos partenocápicos são caracterizados pela ausência total de sementes. Por outro lado, na estenoespermocarpia, a fecundação ocorre normalmente e o desenvolvimento da semente se inicia. Porém, após o início de sua formação, ocorre aborto do embrião ainda imaturo devido à ausência ou má formação do endosperma, caracterizando a estenoespermocarpia pela produção de frutos com apenas traços de sementes (STOUT, 1936; BOUQUET & DANGLOT, 1996; VAROQUAUX *et al.*, 2000; MEJÍA *et al.*, 2011). Na maioria dos casos, o aborto do embrião ocorre oito semanas após a fecundação (EMERSHAD *et al.*, 1989).

Frutíferas altamente comercializadas como videiras, laranjeiras, tomateiros e caquizeiros realizam, com mais frequência, a estenoespermocarpia. Este fator agrega valor aos frutos produzidos. Por consequência, os mecanismos moleculares que regem o cessar do

desenvolvimento da semente na estenoespermocarpia são de grande importância para que haja um entendimento maior deste fenótipo.

### 1.1.3 Mecanismos Moleculares da Morfogênese de Sementes

O desenvolvimento dos órgãos florais e o processo de transição floral são bem conhecidos do ponto de vista molecular (SMACZNIAK *et al.*, 2012). Entre diversos componentes deste processo, os genes da família *MADS-box* possuem papel fundamental na regulação dos mecanismos que definem a identidade dos meristemas florais como sépalas, pétalas, estames, carpelos e óvulos, sendo que seus representantes são muito estudados na área de genética molecular vegetal com mais de 2.600 estudos publicados em revistas internacionais (SMACZNIAK *et al.*, 2012).

#### 1.1.3.1 Os genes *MADS-box*

Os fatores de transcrição da família MADS-box possuem papéis de extrema importância no desenvolvimento de plantas, pois são responsáveis pelo controle da identidade dos órgãos florais. A origem do nome MADS deve-se à alta similaridade desses fatores de transcrição com a proteína humana SRF (do inglês, *Serum Response Factor*; NORMAN *et al.*, 1988), com o gene *Mcm1* (do inglês, *Minichromosome maintenance 1*) de *Saccharomyces cerevisiae* (PASSMORE *et al.*, 1988), com o gene *AGAMOUS* (AG; YANOFSKY *et al.*, 1990) de *A. thaliana* e com o gene *DEFICIENS* (DEF) de *Antirrhinum majus* (SOMMER *et al.*, 1990). Por este motivo, estes fatores de transcrição foram denominados de genes da família MADS (de **MCM1**, **AG**, **DEF** e **SRF**; SCHWARZ-SOMMER *et al.*, 1990).

Os fatores de transcrição MADS-box contêm domínios de ligação ao DNA e de dimerização conservados em diversas espécies, chamados de domínio MADS (SCHWARZ-SOMMER *et al.*, 1992; PELLEGRINI *et al.*, 1995; HUANG *et al.*, 2000). Os genes *MADS-box* são divididos em dois grupos tendo-se por base a estrutura dos seus domínios proteicos, denominadas de tipo I e de tipo II (SMACZNIAK *et al.*, 2012). Os genes *MADS-box* de estruturas do tipo I constituem um grupo bem diversificado, contendo apenas ~180 pares de bases (pb) de sequências do domínio MADS em comum (DE BODT *et al.*, 2003;

PARENICOVÁ *et al.*, 2003). Estudos recentes permitiram demonstrar que os genes pertencentes a este grupo possuem funções relacionadas com a gametogênese feminina e com o desenvolvimento de sementes (WUEST *et al.*, 2010).

Por outro lado, os genes *MADS-box* do tipo II foram mais bem estudados e caracterizados. Estes são genes homeóticos que atuam principalmente no desenvolvimento floral, na embriogênese e no desenvolvimento do fruto. Este grupo é caracterizado por sua estrutura denominada *MIKC*, na qual a porção N-terminal é composta pelo domínio MADS (M) de ligação ao DNA, seguido por dois domínios essenciais para a interação com proteínas, as porções I (*intervening*) e K (*keratin-like*). O domínio C-terminal é responsável pela formação e atividade de complexos proteicos e pela regulação transcricional (KAUFMANN *et al.*, 2005). Com base nas características estruturais deste domínio, os genes *MADS-box* do tipo *MIKC* foram ainda divididos em *MIKC<sup>C</sup>* (forma canônica) e *MIKC\**. Este último apresenta alterações no domínio K, possivelmente pela duplicação de exons desta região, e forma uma rede de interação de proteínas responsável pela maturação do pólen (ADAMCZYK & FERNANDEZ, 2009).

Na planta-modelo *A. thaliana*, 107 genes *MADS-box* foram identificados nos últimos 20 anos, sendo que os genes do tipo *MIKC<sup>C</sup>* compõem o modelo de desenvolvimento floral ABCDE (THEISSEN, 2001; THEISSEN & SAEDLER, 2001; PARENICOVA *et al.*, 2003; SMACZNIAK *et al.*, 2012). Os genes da classe A (*APETALA1 - API*) determinam a identidade de sépalas, os genes da classe A juntamente com genes da classe B (*APETALA3 - AP3* - e *PISTILLATA - PI*) determinam a identidade das pétalas, ao passo que os genes da classe B somados aos genes da classe C (*AG*) são responsáveis pela formação de estames. Os genes da classe C possuem papel na identidade de carpelos (LOHMANN & WEIGEL, 2002), enquanto os genes da classe D (*SEEDSTICK-SHATTERPROOF1 - SHATTERPROOF2*) atuam no desenvolvimento dos óvulos (Figura 2; COLOMBO *et al.*, 1995). Os genes *MADS-box* das classes A, B, C e D realizam interações com os genes da classe E (*SEPALATTAA1-SEP2-SEP3-SEP4*), formando o modelo de quartetos florais (THEISSEN & SAEDLER, 2001 DORNELAS & DORNELAS, 2005). Interessantemente, as proteínas *MADS-box* formam complexos de alta ordem, normalmente em junções tetraméricas formadas por dois dímeros, como demonstrado na Figura 2.

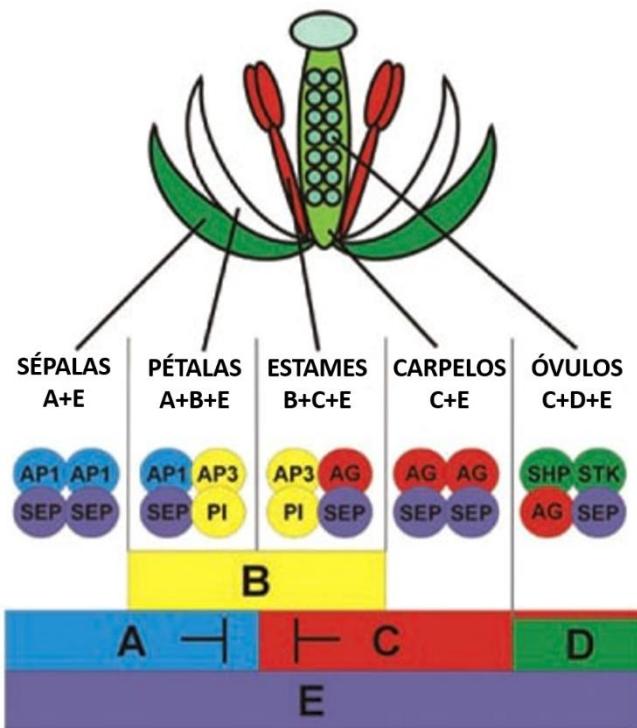


Figura 2. Modelo ABCDE de determinação da identidade dos órgãos florais por proteínas *MIKC<sup>C</sup>* em *Arabidopsis thaliana*. Os genes *MIKC<sup>C</sup>* da classe A (*API*) determinam a formação de sépalas; genes da classe B (*AP3* e *PI*), juntamente com genes da classe A, são necessários para a formação de pétalas. Os genes da classe B também são necessários para a formação de estames junto com os genes da classe C (*AG*), que por sua vez são necessários para a formação de carpelos. Os genes da classe D (*STK*, *SHP1* e *SHP2*) são responsáveis pelo desenvolvimento de óvulos. Todas as classes (ABCDE) necessitam de, ao menos, um dos genes da classe E (*SEP1*, *SEP2*, *SEP3* e *SEP4*) para realizarem sua função. Adaptado de DORNELAS & DORNELAS (2005).

Os complexos quartenários das proteínas MADS-box normalmente ligam-se a duas sequências de DNA consenso denominadas CArG-box (CC(A/T)<sub>6</sub>GG) separadas por até 300 pb (LIU *et al.*, 2008). Essa interação entre complexos MADS-box e CArG-box é responsável pela geração de um *loop* de DNA entre os dois sítios CArG-box (THEISSEN, 2001; THEISSEN & SAEDLER, 2001; MENDES *et al.*, 2013). A formação das diferentes interações proteicas determina a diferenciação e o crescimento dos órgãos florais criando, assim, inúmeras combinações de multimerização de proteínas que aumentam a diversificação de ligação dos complexos MADS-box ao DNA e, consequentemente, a

promoção da transcrição de genes por essas proteínas (MELZER & THEISSEN, 2009; SMACZNIAK *et al.*, 2012).

#### 1.1.3.2 Genes *MIKC<sup>C</sup>* responsáveis pelo desenvolvimento de óvulo e de semente

Os genes *MIKC<sup>C</sup>* das classes C e D formam a subfamília monofilética AG, pertencendo a clados irmãos uma vez que foram gerados por um evento de duplicação ocorrido no início da evolução das angiospermas (KRAMER *et al.* 2004). As proteínas codificadas por genes destas duas classes possuem dois motivos na região C-terminal conhecidos como AGI e II, os quais atuam na formação de complexos quaternários das proteínas MADS-box (YUN *et al.*, 2004; SONG *et al.*, 2006).

Os genes *MIKC<sup>C</sup>* da classe D primeiramente caracterizados foram *FBP7* e *Fbp11* (*FLORAL BINDING PROTEIN 7* e *11*) de *Petunia hybrida*, expressos especificamente nos óvulos. A geração de duplos mutantes destes genes levou à formação alterada destas estruturas (ANGENENT *et al.*, 1995; COLOMBO *et al.*, 1995; ANGENENT & COLOMBO 1996; COLOMBO *et al.*, 1997). No estudo de COLOMBO *et al.* (1995), foi demonstrado que a expressão ectópica de *Fbp7* ou de *Fbp11* em *Petunia* induziu a formação de óvulos em pétalas e sépalas, mostrando o papel destes genes no desenvolvimento dos óvulos. Foram propostos ortólogos à *Fbp7* e *Fbp11* em outras espécies como *AGL11* (*STK*) em *A. thaliana* (ROUNSLEY *et al.*, 1995; PINYOPICH *et al.*, 2003), *ZAG2* e *ZMM1* em *Zea* (SCHMIDT *et al.*, 1993; THEISSEN *et al.*, 1995), *OsMADS13* em *Oryza* (LOPEZ-DEE *et al.*, 1999), *PhaLAG2* em *Phalaenopsis* (SONG *et al.*, 2006), *AVAG2* em *Asparagus* (YUN *et al.*, 2004), *LMADS2* em *Lilium* e *EgMADS1* em *Lisianthus* (TZENG *et al.* 2002). Todos estes genes tendem a especificar a identidade dos tecidos da quarta camada da flor.

Em *A. thaliana*, o gene *AtAGL11* é responsável pela identidade do óvulo juntamente com os genes *SHATTERPROOF 1* e *SHATTERPROOF 2* (*SHP1*, *SHP2*), e seu mutante defectivo apresenta fenótipo de sementes diminutas (PINYOPICH *et al.*, 2003; BRAMBILLA *et al.*, 2007). O gene *AtAGL11* é responsável pela expansão e divisão celular do funículo, sendo que a ausência deste gene faz com que esta estrutura se torne mais larga e espessa (ROUNSLEY *et al.*, 1995; PINYOPICH *et al.*, 2003). Este gene é uniformemente

expresso nos integumentos dos óvulos e ao longo do funículo nas fases iniciais de desenvolvimento da semente. Na fase de maturação, *AtAGL11* é fortemente expresso no funículo e fracamente nos integumentos (ROUNSLEY *et al.*, 1995; PINYOPICH *et al.*, 2003; MATIAS-HERNANDEZ *et al.*, 2010). Seu mutante (*stk*), além de demonstrar diminuição no tamanho das sementes e aumento da espessura do funículo (Figura 3d-e), possui siliques menores com apenas metade da quantidade normal de sementes (Figura 3a). O mutante *stk* também apresenta o fenótipo de não abscisão das sementes (Figura 3f), provavelmente pela estrutura diferenciada do funículo que as mantém fortemente ligadas à rafe (PINYOPICH *et al.*, 2003).

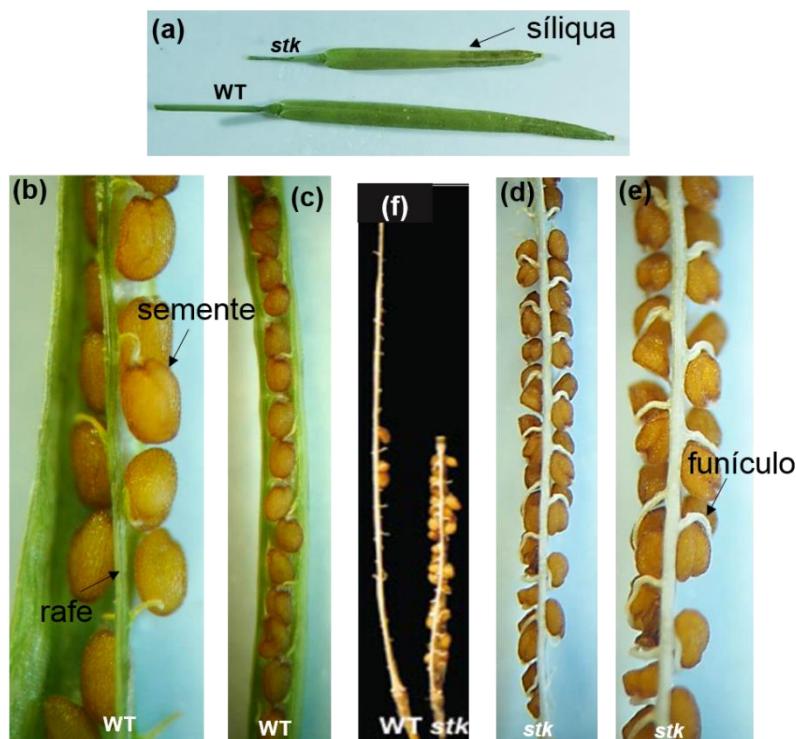


Figura 3. Comparação entre *Arabidopsis thaliana* Col-0 selvagem (WT, do inglês, *wild-type*) e *A. thaliana* Col-0 mutante para o gene *AtAGL11* (*stk*). (a) Diferença entre o tamanho de siliqua; (b-c) formato e tamanho da semente de WT e espessura e comprimento do funículo de WT; (d-e) formato e tamanho da semente de *stk* e espessura e comprimento do funículo de *stk*; (f) diferença entre WT e *stk* em relação à abscisão das sementes da rafe. Imagem f realizada por PINYOPICH *et al.* (2003).

A regulação da expressão tecido-específica do gene *AG* é dependente de elementos *cis* presentes no seu segundo ítron, conhecido por sua grande extensão (3 quilobases ou kb, do inglês, *kilobase*) (DEYHOLOS 2000; HONG *et al* 2003). Da mesma maneira, o gene *AtAG11 (STK)* é regulado por elementos *cis* localizados em sua região promotora e em seu grande primeiro ítron (1,3 kb). Esses elementos regulatórios são ricos em G-A, no qual a proteína BASIC PENTACYSTEINE 1 (BPC1) se liga e gera uma mudança conformacional do DNA que auxilia na formação do precomplexo de ativação da transcrição deste gene (KOOIKER *et al.*, 2005).

A compreensão da regulação da expressão de genes responsáveis pelo desenvolvimento de semente em plantas modelos como *A. thaliana* avançou significativamente nos últimos anos (MATIAS-HERNANDEZ *et al.*, 2010). Do mesmo modo, estudos abordando este tema também vêm sendo conduzidos em outras espécies tais como videira, tomateiro, laranjeira, entre outros (VAROQUAUX *et al.*, 2000). Uma das plantas que têm sido extensivamente estudadas com o intuito de buscar uma maior compreensão do processo de apirenia é a videira. Nesta planta, a subfamília AG foi previamente caracterizada, sendo composta por três membros, dois deles mais similar a *AG* (*VvAG1* e *VvAG2*) e um terceiro, *VvAGL11* ou *VvAG3*, mais similar de *AGL11/STK* (BOSS *et al.*, 2001 e 2002). Porém, nenhum gene foi identificado como ortólogo de *SHP1* e *SHP2* (DÍAZ RIQUELME *et al.*, 2009). A confirmação da ortologia entre *AtAGL11* e *VvAGL11* auxiliaria no processo de compressão da ausência de semente em *V. vinifera*.

## 1.2 A CULTURA DA VIDEIRA

A videira (*Vitis* spp. L.) é uma planta de origem antiga, proveniente de áreas caucasianas e que se propagou inicialmente na área mediterrânea. Sua grande expansão mundial ocorreu graças a sua habilidade de se adaptar a diversos solos e condições climáticas (LACIRIGNOLA & DIGIARO, 1999). Atualmente, a videira é a frutífera mais cultivada mundialmente, cobrindo 7,8 milhões de hectares em 2011 e sendo a 5<sup>a</sup> fruta mais produzida no mundo com 67,5 milhões de toneladas de frutos em 2012 (OIV, 2011; FAO, 2012). A videira possui grande apelo comercial uma vez que as suas bagas são utilizadas para as mais diversas finalidades tais como produção de vinhos (68%), consumo de uvas de mesa *in natura* (30%), produção de uvas passas (2%) e produtos de menor impacto como sucos,

geleias, etanol, vinagre, óleo de sementes, ácido tartárico e fertilizantes (FASOLI *et al.*, 2012).

A viticultura é uma atividade tradicional em países de clima temperado e, recentemente, tem ganhado grande significância em diversas regiões de clima subtropical e tropical. Esta característica abre perspectivas para uma grande expansão na viticultura tropical, principalmente para a produção de uvas de mesa (AMARAL *et al.*, 2012). A produção mundial de uva de mesa atingiu 2,1 milhões de toneladas em 2010, sendo que o Brasil ocupa o 6º lugar na produção mundial de uva de mesa (FAO, 2010).

A apirenia é uma das características mais apreciadas em uvas de mesa, em concomitância com frutos de tamanho elevado. Estas duas qualidades constituem principais objetivos de programas de melhoramento de uvas de mesa (VAROQUAUX *et al.*, 2000; CABEZAS *et al.*, 2006). Nos Estados Unidos da América, as uvas apirênicas já dominam o mercado enquanto que, na Europa, é crescente a demanda por uvas sem sementes. Dados de 2012 da Organização Internacional da Uva e do Vinho (OIV, do francês, *Organisation Internationale de la Vigne et du Vin* e da Organização das Nações Unidas para Agricultura e Alimentação (FAO, do inglês, *Food and Agriculture Organization of the United Nations*), permitiram comprovar que nas últimas duas décadas a comercialização mundial de uva *in natura* aumentou cerca de 26% ao ano, enquanto que a produção de uvas para esta finalidade cresceu a taxas anuais próximas de 13%. Essa expansão comercial gerou oportunidades de crescimento aos países produtores e a competitividade entre os mercados exportadores das melhores uvas apirênicas (LAZZAROTTO & FIORAVANÇO, 2012).

A produção de uvas brasileiras *in natura* está baseada, predominantemente, na cultivar Niágara Rosada, no caso de uvas de mesa comuns. Em contrapartida, as uvas finas de mesa são, essencialmente, as cultivares Itália, Rubi, Benitaka, Brasil e Red Globe, que são uvas pirênicas, e as cultivares Centennial Seedless, Superior Seedless, Sultanina, Catalunha e Crimson Seedless, que são uvas apirênicas (PROTAS, 2005). Dentre estas, a cultivar Sultanina destaca-se devido à sua boa adaptação ao cenário europeu e estado-unidense de cultivo, onde foi amplamente utilizada em cruzamentos visando a geração de novas cultivares apirênicas e, por isso, vêm sendo estudada como modelo de apirenia em videira.

### **1.2.1 A Cultivar Sultanina**

Atualmente, diversas variedades de uvas apirênicas são produzidas no mundo, cada qual sendo escolhida por sua adaptabilidade às condições locais. As principais cultivares estenoespermocárpicas são, em sua maioria, descendentes de ‘Sultanina’, também chamada de ‘Thompson Seedless’. Esta é uma das cultivares mais importantes comercialmente e é, até hoje, utilizada em cruzamentos como doadora de seu fenótipo apirênico (ADAM-BLONDON *et al.*, 2001; GENOVA *et al.*, 2014). Na Figura 4, é possível visualizar o contraste entre uma cultivar pirênica, neste caso ‘Chardonnay’, e ‘Sultanina’, que é estenoespermocárpica e, portanto, origina frutos com traços de sementes pouco desenvolvidos e macios, imperceptíveis ao consumidor, sendo fortemente apreciada no mercado de uvas de mesa (STOUT, 1936). A mutante somática natural Sultanina possui coloração mais clara e estava entre um grupo de variedades inicialmente cultivadas em Nova York e, em 1872, em Marysville, Califórnia, por Willian Thompson do qual descende seu nome mais comum. Originalmente, a cultivar Sultanina é proveniente da Pérsia da Ásia Menor, atualmente áreas do Irã e da Turquia, onde era conhecida como ‘Oval Kechmish’ (CHRISTENSEN, 2000).

Para a determinação do fenótipo de apirenia de uma determinada cultivar de videira é utilizada uma classificação determinada pela OIV sobre a norma descritora 243 (Figura 5). De acordo com esta norma utiliza-se dados de matéria seca de 100 sementes aleatoriamente amostradas, classificadas pela seguinte ordem: classe 1 - muito baixa ( $\leq 10$  mg/semente); classe 3 - baixa (21-29 mg/semente); classe 5 - média (36-44 mg/semente); classe 7 - alta (51-59 mg/semente) e classe 9 - muito alta ( $> 65$  mg/semente) como mostrado na Figura 6. As variedades que se encaixam nas classes 1, 3 e 5 são consideradas apirênicas, enquanto que as cultivares com notas 7 e 9 são consideradas pirênicas.

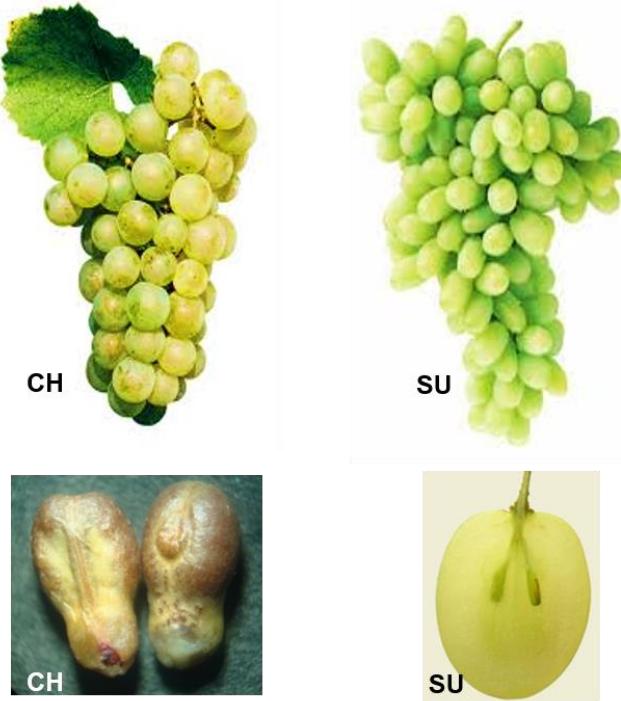


Figura 4. Comparação entre a cultivar pirênica Chardonnay (CH) e a cultivar apirênica Sultanina (SU), ambas em estádio de maturação dos frutos. ‘Chardonnay’ apresenta sementes de tamanho adequado e lignificadas enquanto que ‘Sultanina’ (baga) contém apenas o traço de uma semente. Imagem de ‘Chardonnay’ proveniente de Ternuta dei Mille (2011), e de ‘Sultanina’ proveniente de Agrofresh (2013). Semente de ‘Chardonnay’ com aumento de 40X.

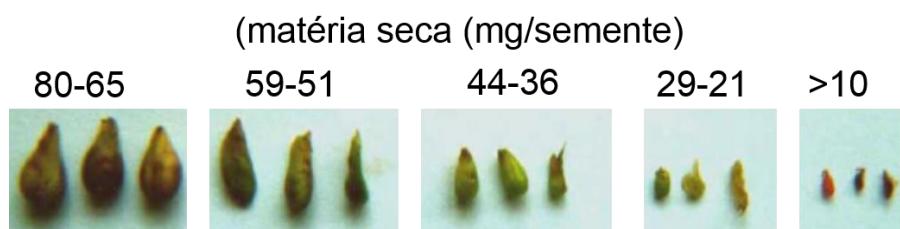


Figura 5. Classificação da pirenia e apirenia em videira segundo o descritor OIV 243. Distribuição das classes fenotípicas para a determinação de apirenia. Peso de matéria seca entre 44 - >10 mg/semente, abrangendo as classes 1, 3 e 5, classifica a cultivar como apirênica. Peso de matéria entre 51 - < 65, classes 7 e 9, determina que a cultivar é pirênica. Imagem proveniente de Acervo EMBRAPA Uva e Vinho. Adaptado de BOUQUET & DANGLOT (1996).

### **1.2.2 Controle Genético e Molecular da Apirenia em Videira**

*V. vinifera* possui seu genoma completamente sequenciado em sua forma quase homozigota e, também, em sua forma altamente heterozigota, ambas obtidas a partir da cultivar Pinot Noir (PN40024; JAILLON *et al.*, 2007; VELASCO *et al.*, 2007), caracterizando o genoma-referência de videira (<http://genomes.cribi.unipd.it/grape/>). Este conjunto de dados genômicos auxilia em estudos de desenvolvimento de cultivares por métodos não tradicionais, concomitantemente com o entendimento da função de seus mais de 23 mil genes.

A identificação e a compreensão dos mecanismos genéticos e moleculares que regem o desenvolvimento de espécies com ausência de sementes são essenciais para a obtenção de culturas comerciais de alta qualidade e competitividade no mercado (CAMARGO *et al.*, 1999). Como alternativa biotecnológica, muitos pesquisadores focaram seus esforços na busca de marcadores moleculares que pudessem ser utilizados para a detecção do fenótipo de apirenia prematuramente, utilizando-os em estratégias de seleção assistida por marcadores (MAS, do inglês, *Marker Assisted Selection*) em populações segregantes (STRIEM *et al.*, 1996; LAHOGUE *et al.*, 1998; ADAM-BLONDON *et al.*, 2001; MEJÍA *et al.*, 2007; MEJÍA *et al.*, 2011).

O método de obtenção de mapas genéticos baseados na estratégia do duplo pseudocruzamento-teste, desenvolvido por GRATTAPAGLIA & SEDEROFF (1994), permitiu identificar QTLs com grandes efeitos fenotípicos. Esta estratégia é muito utilizada para espécies altamente heterozigotas e de demorado desenvolvimento como *V. vinifera*, sendo que os indivíduos avaliados são a progênie do cruzamento, plantas F1. Deste modo, a produção de mapas genéticos de videira aumentou consideravelmente (LODHI *et al.*, 1995; DALBO *et al.*, 2000; DOLIGEZ *et al.*, 2002; RIAZ *et al.*, 2003; ADAM-BLONDON *et al.*, 2004; FISCHER *et al.*, 2004; CABEZAS *et al.*, 2006).

Diversos graus de tamanho de sementes podem ser observados em cultivares de videiras estenospermocárpicas e em suas progêneres, o que demonstra que a estenospermocarpia é um caractere quantitativo. BOUQUET & DANGLOT (1996) geraram um modelo de controle desta característica. Neste modelo, alelos recessivos de três *loci* independentes são regulados por um alelo dominante em um único *locus*, o qual inibiria

o desenvolvimento da semente. Posteriormente, este *locus* foi denominado *SdI* (Inibidor do desenvolvimento da semente, do inglês, *Seed development Inhibitor*) (LAHOGUE *et al.*, 1998).

Em estudos genéticos com populações geradas a partir de variedades de videira pirênicas (doadora materna) e apirênicas (doador paterno), foram detectados QTLs para tamanho de baga, peso e tamanho de sementes em *V. vinifera*. Os QTLs estão localizados no grupo de ligação 18, na porção distal do cromossomo, e explica de 50 a 70% da variância fenotípica para esses caracteres (DOLIGEZ *et al.*, 2002; FANIZZA *et al.*, 2005; CABEZAS *et al.*, 2006; MEJÍA *et al.*, 2007; CONSTANTINI *et al.*, 2008; REVERS *et al.*, 2010). Este QTL corresponde ao *locus SdI* proposto anteriormente no modelo de BOUQUET & DANGLOT (1996) (MEJÍA *et al.*, 2011).

A partir deste *QTL*, o gene *AGAMOUS-LIKE 11* (*VvAGL11*) foi mapeado *in silico* no mesmo *contig* que o *locus SdI* e também colocalizou com o marcador molecular SSR (repetição de sequência simples, do inglês, *Simple Sequence Repeat*) VMC7F2, que se encontra 463 pb a montante do códon de início de tradução de *VvAGL11*. Este marcador é altamente polimórfico, identificando diferenças entre os alelos do gene *VvAGL11* por amplificar uma região que apresenta tamanhos desiguais. Assim, é possível detectar cada um dos dois alelos de ‘Sultanina’, no caso um dos alelos é idêntico ao do genoma referência (‘Pinot Noir’) e é chamado de alelo selvagem, enquanto que o outro alelo, chamado de alelo mutado, possui diferenças em sua região promotora. VMC7F2 é utilizado com 95% de eficácia para detecção de apirenia em videira (CONSTANTINI *et al.*, 2008). Pelo emprego deste marcador na técnica de MAS é possível identificar o genótipo de cada indivíduo, podendo este ser homozigoto para o alelo normal (pirênico), heterozigoto (apirênico) ou homozigoto para o alelo mutado (apirênico).

*VvAGL11* (acesso no genoma em <http://genomes.cribi.unipd.it/grape/>: Vv18s0041g01880), também chamado por BOSS *et al.* (2002) de *VvMADS5* e por DÍAZ-RIQUELME *et al.* (2009) de *VvAG3*, é um possível ortólogo do gene *AtAGL11/STK* de *A. thaliana* que, por sua vez, atua no controle da identidade do óvulo (FAVARO *et al.*, 2003; PINYOPICH *et al.*, 2003). Em um estudo contemplando a família MADS-box em videira, DÍAZ-RIQUELME *et al.* (2009) demonstrou que *VvAGL11* é induzido em tecidos florais e em frutos, enquanto que é reprimido em raiz, ramo, folha, gavinha e gema. Ainda nesse estudo, foi demonstrada uma possível ortologia entre *VvAGL11* (*VvAG3* na Figura 6),

*AtAGL11* e *PMADS21* de álamo. Estes genes agruparam-se na subfamília AG (Figura 6), na qual os genes *MADS-box MIKC* de videira, álamo e *A. thaliana* foram agrupados em uma árvore filogenética que se mostrou dividida em 13 subfamílias (SEPALLATA, AGAMOUS-LIKE 6, APETALA1-FRUITFULL, FLOWERING LOCUS C, AGAMOUS, AGAMOUS-LIKE 12, TM 8, AGAMOUS-LIKE 15, AGAMOUS-LIKE 17, SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1, SHORT VEGETATIVE PHASE, APETALA-PISTILLATA, B SISTER) dentro de 10 clados maiores.

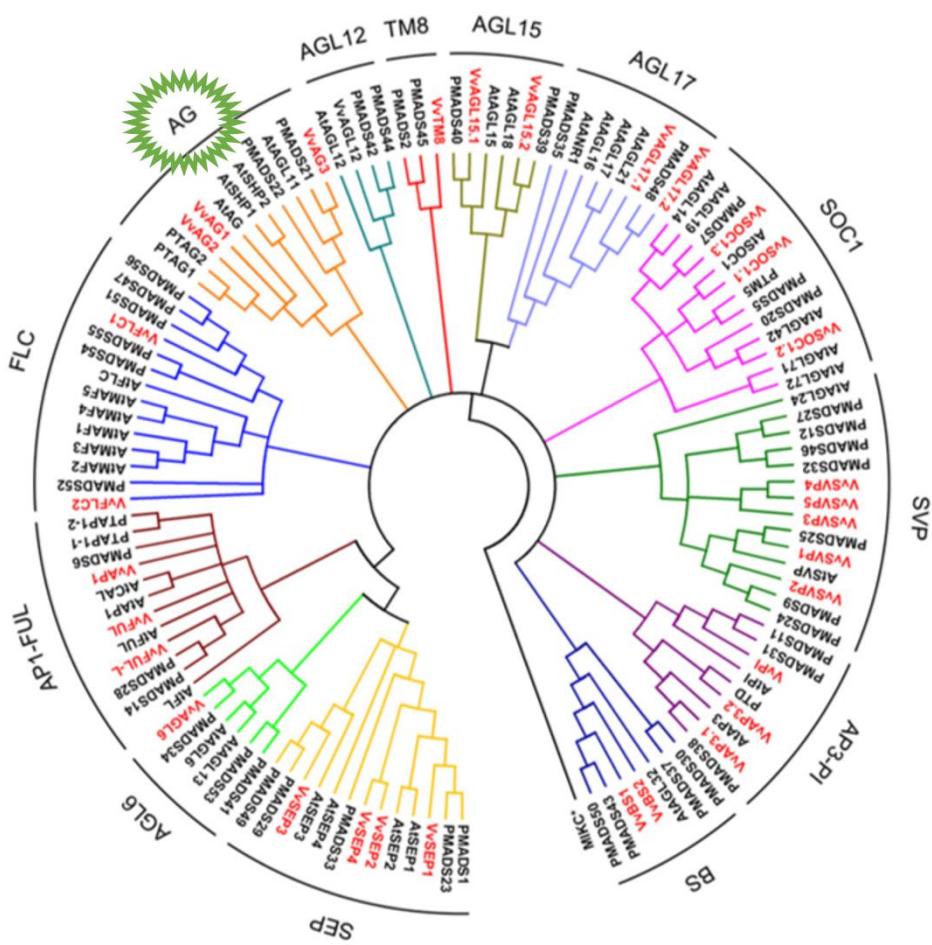


Figura 6. Árvore filogenética da família de genes *MIKC* de *Vitis* (em vermelho), *Arabidopsis* e *Populus*. Árvore gerada pelo alinhamento das sequências completas de aminoácidos das proteínas de cada gene. O método junção de vizinhos (NJ, do inglês, *neighbor-joining*) foi utilizado para o alinhamento. As proteínas *MIKC* agruparam-se em 13 subfamílias. As proteínas MADS-box *MIKC\** foram utilizadas como um grupo externo. Adaptado de DÍAZ-RIQUELME *et al.* (2009).

Com o objetivo de caracterizar a expressão do gene *VvAGL11*, MEJÍA *et al.* (2011), por meio de ensaios de PCR quantitativa precedida de transcrição reversa (*RT-qPCR*, do inglês, *reverse transcription-quantitative PCR*), observaram que transcritos de *VvAGL11* são 25 vezes mais abundantes no estádio de fruto em comparação com os estádios de prefloração e floração em genótipos de videira sem sementes. Outro dado interessante refere-se ao fato de que, no estádio de fruto, a expressão do gene é acentuada em genótipos homozigotos para o alelo normal de *VvAGL11*, mostrando uma expressão 25 vezes maior do que em genótipos homozigotos para o alelo mutado, enquanto que os genótipos heterozigotos demonstraram um nível intermediário da expressão do gene. O sequenciamento da região promotora e codificadora de *VvAGL11* realizado por estes autores não permitiu concluir se as variações alélicas identificadas são responsáveis pelo fenótipo de apirenia e não foram realizadas análises funcionais neste trabalho (MEJÍA *et al.*, 2011).

Paralelamente a estes estudos, nosso grupo analisou uma progênie de videira gerada a partir do cruzamento de uma cultivar apirênica ‘Crimson Seedless’ com o híbrido complexo resistente ao míldio ‘Villard Blanc’. Os resultados obtidos a partir do mapa genético construído entre estas duas cultivares permitiram confirmar o QTL para a ausência de sementes dentro do *locus SdI* na extremidade do cromossomo 18 e com LOD (do inglês, *Linked Open Data*) máximo associado ao marcador molecular microssatélite VMC7F2 (REVERS *et al.*, 2010).

Na presente Dissertação de Mestrado, a hipótese de trabalho foi fundamentada na seguinte afirmação: a extrema diminuição da expressão de *VvAGL11* encontrada em genótipos apirênicos de videira é a causa do fenótipo de apirenia, uma vez que o gene é essencial para a morfogênese da semente em uvas.

## **2 OBJETIVOS**

### **2.1 OBJETIVO GERAL**

Caracterizar as estruturas do gene *VvAGL11* na cultivar pirênia Chardonnay e na cultivar apirênia Sultanina por meio do sequenciamento de suas variações alélicas e da exploração da sua expressão gênica diferencial, visando uma maior compreensão de seu papel durante a morfogênese das sementes em videira.

### **2.2 OBJETIVOS ESPECÍFICOS**

- Caracterizar as variações alélicas do gene *VvAGL11* em videira apirênia e pirênia;
- Caracterizar o perfil transcracional do gene *VvAGL11* em diferentes estádios de desenvolvimento do fruto;
- Analisar morfologicamente a semente de ‘Chardonnay’ e o traço de semente de ‘Sultanina’;
- Determinar o padrão de expressão espaço-temporal de *VvAGL11* em videira apirênia e com semente durante o desenvolvimento reprodutivo.

### **3 CAPÍTULO I**

#### **THE AGAMOUS-LIKE 11 TRANSCRIPTION IS ESSENTIAL FOR SEED MORPHOGENESIS IN GRAPEVINE**

*Manuscrito a ser submetido ao periódico ‘Journal of Experimental Botany’*

**Title**

The *AGAMOUS-LIKE 11* transcription is essential for seed morphogenesis in grapevine

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**Footnotes:**

The nucleotide sequences reported in this paper have been submitted to GenBank under the accession numbers KM401845, KM401846, KM401847 and KM401848.

## **Abstract**

Despite the wide and extensive appreciation of seedless grapes, little is known about the mechanisms that drive apireny. *VvAGL11* is a candidate gene involved in *Vitis vinifera* seed morphogenesis and studies showed that its expression is mainly localized in fruits of seeded grapes, while seedless varieties exhibits significantly lower levels of transcripts. Grapevine *AGL11* is a MADS-box gene, possibly orthologous to *Arabidopsis AGL11*, with an important role in ovule development. Our study aimed to characterize *VvAGL11* allelic variations in a seeded (Chardonnay) and in a seedless (Sultanina) grapevine cultivars, allowing us to observe several mutations that might be responsible for gene's loss of function. *VvAGL11* transcript levels corresponding to each phenotype were evaluated by RT-qPCR during grapevine flower and fruit development. *VvAGL11* relative expression was significantly higher in seeds of 2, 4 and 6 weeks after fruit-set of the seeded variety whereas in the seedless grape its transcription was extremely low in all stages analyzed. We further characterized the patterns of *VvAGL11* spatial and temporal expression via *in situ* hybridization. Transcript accumulation was specifically detected in the dual medium integument layer of the seeds, which is responsible for the elongation of seed coat and necessary to determine final seed size. Nevertheless, in seedless grape, no hybridization signals were visible and a morphological analysis showed an apparent loss of identity of the medium integument layer of the seed traces. Our data provide insights of the important role of *VvAGL11* in seed morphogenesis suggesting that depletion of its expression may be the main responsible for the erroneous development of a highly essential seed layer therefore culminating in the typical apirenic phenotype.

**Keywords:** apireny, grapevine, *in situ* hybridization, seed, Sultanina, *VvAGL11*.

## Introduction

Seedlessness is one of the most appreciated features in table grapes along with enlarged fruit size, both being main goals in breeding programs (Varoquaux *et al.*, 2000; Cabezas *et al.*, 2006; Lazzarotto and Fioravanço, 2012). In the past two decades, the worldwide market of *in natura* grapes increased about 26% per year, while the production of such grapes grew at a 13% annual rate (OIV, 2012; FAO, 2012). In grapevine, the absence of seeds, also called apireny, is divided in two biological processes. One is known as parthenocarpy, when fecundation does not occur and there is no seed formation, as in raisins. The second process is called stenospermocarpy, in which fertilization takes place to form the fruit but it is followed by embryo abortion due to the cease of endosperm development, normally after four weeks of fruit growth. The consequence of stenospermocarpy is the production of berries with reduced seed size, known as seed traces (Bouquet and Danglot, 1996; Mejía, 2011).

Several studies have shown that the presence of a dominant allele in the region of the *Seed Development Inhibitor (SdI)* locus, located in *Vitis vinifera* distal portion of chromosome 18, is responsible for 50 to 90% of the total phenotypic variance of seedlessness (Bouquet and Danglot, 1996; Lahogue *et al.*, 1998; Cabezas *et al.*, 2006; Costantini *et al.*, 2008; Doligez *et al.*, 2002; Mejía *et al.*, 2007). *In silico* analysis allowed the identification of a gene, named *Vitis vinifera AGAMOUS-LIKE 11 (VvAGL11)*, that mapped to the same locus contig *SdI* (Constantini *et al.*, 2008). The same work has also co-located *VvAGL11* with the molecular microsatellite marker VMC7F2, which was known to be a highly polymorphic marker capable of an efficiency of 95% in the detection of seedlessness in grapes (Constantini *et al.*, 2008).

The *VvAGL11* gene (Vv18s0041g01880; Boss *et al.*, 2002) was proposed as a strong candidate gene involved in the absence of seeds in grapevine (Costantini *et al.*, 2008; Mejía *et al.*, 2011; Revers *et al.*, 2010). This MADS-box gene was shown to be a possible ortholog of *AGL11 (STK)* of *Arabidopsis thaliana*, which acts on the identity and control of ovule and seed development (Favaro *et al.*, 2003; Pinyopich *et al.*, 2003; Díaz-Riquelme *et al.*, 2009). *AtAGL11* mutant (*stk*) presents reduced number and size of seeds (Pinyopich *et al.*, 2003; Brambilla *et al.*, 2007).

The transcription factors of the MADS-box family have extremely important roles in the development of plants. They are responsible for controlling the identity of floral organs (Smaczniak *et al.*, 2012). In a study covering the MADS-box family in grapevine, Díaz-Riquelme *et al.* (2009) demonstrated that *VvAGL11* is induced in floral and fruit tissues, whereas it is repressed in roots, branches, leaves, buds and tendrils. More recently, another study showed that *VvAGL11* is 25 times more expressed at the stage of fruit compared to flower stages in genotypes homozygous for seedless in grapes. In heterozygous genotypes, an intermediate level of *VvAGL11* expression was observed (Mejía *et al.*, 2011).

We therefore hypothesized that *VvAGL11* might be responsible for controlling seed morphogenesis in grapevine since the decrease of its expression would cause the apirenic phenotype. In this work we report the identification of differences between *VvAGL11* allele sequences in apirenic and pirenic grapevines, observing several mutations in intragenic regions and a set of *SNPs* in the coding region of the gene exclusively in the apirenic genotypic background. We characterized the *VvAGL11* transcript levels, observing a 65-fold increase in expression in grapevine seeds compared to apirenic grapevine fruits. We also described its spatial and temporal expression patterns in reproductive tissues by *in situ* hybridization that allowed us to establish a correlation between the development of a specific seed layer with normal or decreased *VvAGL11* expression.

## Materials and methods

### *Plant material*

All samples were harvested from grapevines located at Embrapa Grape and Wine experimental areas in Bento Gonçalves, Rio Grande do Sul, Brazil ( $29^{\circ} 09' 48''$  S,  $51^{\circ} 31' 42''$  O and 616 m altitude). The phenological scale followed was the one described by Baggioini (1952; Supplementary Table 2). ‘Chardonnay’ was chosen for comparison with ‘Sultanina’ because of its similar phenological development. For *VvAGL11* transcriptional profile, ‘Chardonnay’ (seeded) and ‘Sultanina’ (seedless) organ and tissue samples were harvested at the stages of preanthesis flower, fruit set and fruits at 2, 4 and 6 weeks after fruit set in 2010/2011. For *in situ* hybridization and morphological assays, ‘Chardonnay’ and ‘Sultanina’ samples were harvested at H1, preanthesis flower, fruit set and fruits at 2, 4 and

6 weeks after fruit set in 2012/2013 harvest. Both cultivars were grafted on Paulsen 1103 rootstock.

### *Sequencing*

Twenty-two sets of primers were designed to amplify sequences in the promoter and in exon/intron regions of *VvAGL11* (Supplementary Table 1) in order to sequence the whole gene. Each region exhibited a 300-500 bp overlapping sequence. PCR amplifications were performed with 10 to 25 ng of grapevine genomic DNA using Platinum® Pfx DNA polymerase (Applied Biosystems) as recommended by the manufacturer. RACE amplifications were done with the SMARTer™ RACE cDNA Amplification Kit (Clontech). PCR products were cloned into pGEM®-T Easy Vector (Promega) following the manufacturer instructions. Plasmid DNA was extracted by the alkaline lysis miniprep protocol modified by a CIA step (Maniatis, Fritsch and Sambrook, 1987). PCR products were treated with the Illustra ExoProStar reagent (GE Healthcare) as recommended by the manufacturer, and were sequenced in an ABI Prism® 310 Genetic Analyser (Applied Biosystems) using standard sequencing protocols described by Falavigna *et al.*, 2014.

### *Identification of Putative CArG Sequences*

Genomic regions located 3 kb upstream of the *VvAGL11* ATG start codon, 377 bp downstream of the stop codon, and exons and introns were analyzed to identify CArG-Box sequences with the New Place bioinformatic program available at the Sogo website (<http://sogo.dna.affrc.go.jp>).

### *RNA extraction*

Total RNA samples were extracted from frozen material (approximately 200 mg) by LiCl precipitation using the Zeng and Yang (2002) protocol modified by a purification scale adapted to 2 mL microcentrifuge tubes. Each extraction was conducted using three tubes that had their volumes pooled before the LiCl precipitation step. Genomic DNA in total RNA samples was removed using the TURBO DNA-free Kit (Ambion) according to the manufacturer's protocol. RNA integrity and quantity was monitored by agarose gel electrophoresis and spectrophotometric quantitation, respectively.

#### *RT-qPCR analyses*

Complementary DNAs were synthesized using the GeneAmp RNA PCR Core Kit (Applied Biosystems) according to manufacturer's instructions. Gene-specific primer pairs were designed for the two forms of the candidate gene (*VvAGL1F* 5'-CACTTAATGGGTGATTCCTGGC-3', *VvAGL1R* 5'-AGCAACTCATGCTTCTCGACC-3'; and *VvAGL3F* 5'-ATTGTTCATCTGGGCATTCG-3', *VvAGL3R* 5'-GGAGATGAAGTTGGCGGATA-3') and evaluated by Oligo Analyzer (IDT, <http://www.idtdna.com>). RT-qPCR was performed in a StepOnePlus Real-Time PCR System (Applied Biosystems). SYBR Green (Invitrogen) was used to monitor dsDNA synthesis and ROX (Invitrogen) was employed as passive fluorescence reference. Each biological sample was analyzed in technical triplicates. Cycling protocol consisted of one step at 95 °C for 10 min followed by 40 cycles of 95 °C for 15 s, 60 °C for 1 min, and finished by a dissociation curve between 60 °C and 95 °C. The specificity of PCR amplifications was assessed by the presence of a single peak in melting curves and by the visualization of single amplification products of expected size in 1% ethidium bromide gel electrophoresis. Primer efficiency was calculated by LinRegPCR (version 11.0, Ruijter *et al.*, 2009). Mean relative gene expression was calculated by the Pfaffl (2001) method with the *actin* gene (GenBank EC969944) as reference (Reid *et al.*, 2006). Statistical analysis was performed using Prism 5.1 with One-way ANOVA and Tukey test.

#### *Seed morphological assay*

Seeds and seed traces were transferred into a fixation solution under vacuum (McDowell and Trump, 1976). Thereafter, samples were dehydrated in an increasing gradient of ethanol as described by Gabriel (1982), and embedded in 2-hydroxyethyl methacrylate resin according to Gerrits and Smid (1983). The 5 µm sections were obtained by a Leica RM 2255 microtome. The metachromatic reagent Toluidine Blue O (Feder and O'Brien, 1968) was used to determine seed structure. For the staining procedure, slides with sections were placed on a hot plate at 45 °C, and the reagent was added. After 15 min, slides were rinsed with 95% ethanol and dried at room temperature.

### *In situ hybridization analysis*

‘Chardonnay’ and ‘Sultanina’ samples were fixed in 4% formaldehyde for 16 hours. To submerge the samples, vacuum was applied (approximately 600 mmHg) for 20 min. The material was stored under refrigeration (4 to 10 °C) after fixation. Thereafter, the tissues were dehydrated in ethanolic series and embedded in paraffin. Longitudinal and transversal sections (8-10 µm) were prepared with a rotary microtome and mounted on silanized microscope slides. Gene-specific sense and antisense probes were designed at 3'UTR region (*VvAGL3F* 5'-ATTGTTCATCTGGGCATTCG-3', *VvAGL3R* 5'-GGAGATGAAGTTGGCGGATA-3') corresponding to 185 nucleotides of the 3' UTR of *VvAGL11* gene. Probes were generated by digoxigenin (DIG)-labeling using T7 or SP6 RNA polymerase of the DIG RNA Labeling Kit (Roche). After the detection of the hybridization signals by immunostaining, slides were washed, dehydrated, and mounted using Entellan® (Merck).

## Results

### *Sequencing of VvAGL11*

To further characterize the structural organization of the *VvAGL11* gene, allelic variations were PCR amplified with specific primers from genomic DNA extracted from an apirenic grapevine, ‘Sultanina’, and a pirenic grapevine, ‘Chardonnay’ as previously described. A total of six PCR fragments were assembled, formed by overlapping primers sets showed in figure 1. The gene sequence is composed by the promoter, coding and intragenic regions (8 exons and 7 introns). After allele specific isolation and sequencing, we were allowed to identify two alleles for each cultivar. Because ‘Chardonnay’ is a direct offspring of Pinot Noir, the comparison with the ‘Pinot Noir’ (PN40024) sequence in the publicly available genome base was possible ([http://genomes.cribi.unipd.it/gb2/gbrowse/public/Vitis\\_vinifera/](http://genomes.cribi.unipd.it/gb2/gbrowse/public/Vitis_vinifera/)).

The two *VvAGL11* alleles of ‘Chardonnay’ showed 99% sequence identity with the corresponding ‘Pinot Noir’ genome sequence for *VvAGL11*. One allele from ‘Sultanina’ also exhibited 99% identity with PN40024. However the other ‘Sultanina’ *VvAGL11* allele, the one with the molecular microsatellite marker VMC7F2 described with shorter length (198 bp; Constantini *et al.*, 2008), presented a group of polymorphisms that differed this allele

from the others, and due to that it was named the mutant allele (*Sultanina mut*), as shown in Fig. 1. The group of polymorphisms was composed by 28 INDELs and 105 SNPs.

Among the observed alterations in *Sultanina mutant VvAGL11 allele*, two SNPs give rise to two amino acid substitutions (R590L and T628A) as shown in Fig. 2. A sequence alignment of the four *VvAGL11* alleles, PN40024, and the newest sequence of *VvAGL11* from Sultanina (Di Genova *et al.*, 2014) is presented in Supplementary Fig. 1. With high fidelity amplification and sequencing, we were confident to define all *VvAGL11* alleles' modifications. We also searched for CArG-box sequences, perfect CArG-boxes and CArG sequences with one mismatch deduced by a probability matrix. These *cis* elements are known to be the sites of MADS-box protein complex binding (Smacznia *et al.*, 2012). We identified ten putative CArG sequences in *VvAGL11*. One of them is located in the promoter region, eight in the second intron and one in the 3'-UTR region. The seventh CArG-box putative sequence of 'Sultanina' *VvAGL11 mut* has a nucleotide modification (Supplementary Fig. 1, black arrow). Sequence modification in these *cis* elements could disrupt *VvAGL11* transcription activation.

#### *VvAGL11 expression isoforms*

The 3'- and 5'-RACE experiments allowed us to visualize the mRNA isoforms of *VvAGL11* in apirenic and pirenic grapevines. Two products of amplification differing in size were obtained from 'Chardonnay' and one product was obtained from 'Sultanina'. After sequencing them, it was possible to confirm the specificity of the amplicons and to characterize each transcript form present in the cultivars.

The results revealed that 'Chardonnay' has two isoforms of *VvAGL11* mRNA. One isoform, named CH-1, is longer with 1,454 bp, being 732 bp of coding region. This alternative form increases the coding region in 60 nucleotides. The second 'Chardonnay' allele, named CH-2, has 958 bp and a coding sequence of 672 pb. 'Sultanina' also has two transcript forms, both with the same length (958 bp) and coding sequence (672 bp). The dissemblance of the two *VvAGL11* isoforms derived from 'Sultanina' is the ten SNPs found in the mutant allele (*SU mut*). The coding regions of CH-2 and 'Sultanina' allele 1 are identical to the *VvAGL11* gene predicted in the Pinot Noir reference genome. However, none of the Sultanina isoforms are completely identical to the 'Pinot Noir' gene since their 5'-UTR are different in size, as shown in Fig. 3.

### *Transcription profile of VvAGL11*

Aiming to evaluate the expression of *VvAGL11* and its isoforms, we performed RT-qPCR analysis with mRNA samples extracted from the reproductive organs of ‘Chardonnay’ and ‘Sultanina’ at critical developing stages. Besides a pair of primers designed for regions of the actin reference gene, we employed two sets of primers in RT-qPCR studies to differentiate *VvAGL11* mRNA isoforms. The first *VvAGL11* primer set was composed of a forward primer designed to anneal in the last intronic region and a reverse primer that annealed in the 3'-UTR, therefore allowing the amplification of the longer CDS isoform (CH1). The second pair of primers was designed to anneal in the first (forward) and in the second (reverse) exons that allowed us to amplify simultaneously the two isoforms of *VvAGL11* (the shorter (CH1) and longer (CH2) CDS). Considering that in ‘Sultanina’ the isoforms differ in point mutations (10 SNPs) only, we employed the primer set flanking the first and second exons for the analysis of both isoforms (SU1 and SU mut).

The reproductive tissues evaluated were divided into initial and advanced developmental stages. The initial stages of development were represented by flowers at preanthesis and fruit-set. The advanced stages were represented by fruits at 2, 4 and 6 weeks of development after fruit establishment (fruit-set). Seeds were separated from the pulp in ‘Chardonnay’ berry samples and the whole berry was evaluated in ‘Sultanina’ samples. The amplicons were sequenced for determination of their specificity. Actin gene *VvACT* (Gen Bank EC969944) was used as reference.

Our RT-qPCR results showed that *VvAGL11* relative expression was similarly low at all stages sampled from the ‘Sultanina’ variety for both isoforms SU1 and SU mut. ‘Chardonnay’ flowers and berry pulps also demonstrated low transcript levels of *VvAGL11* for both isoforms CH1 and CH2. RT-qPCR with primers designed to the intronic region was also performed with ‘Sultanina’ mRNA samples and a minor level of expression was detected, probable descendent from residual from pre-mRNA during cDNA synthesis. Nevertheless, seeds of ‘Chardonnay’ from fruits at 2, 4 and 6 weeks after fruit set exhibited much higher accumulation of *VvAGL11* CH2 transcripts, an increase 15-fold higher than CH2 transcripts in berries at fruit set and 65-fold higher than ‘Sultanina’ whole berries. ‘Chardonnay’ CH1 allele relative expression was unstable through seed stages, fluctuating from 5 to 11 fold higher than fruit-set (Fig. 4).

### *Morphological analysis of seeds from apirenic and pirenic grapevines*

*V. vinifera* seeds possess a particular shape resembling a pear, being triangular in cross sections (Fig. 5). The seeds are composed of a cuticle, an epidermis, two layers corresponding to the outer integument and the medium integument, both forming the seed coat at the ripening stage, and yet three inner integument layers that are positioned around the endosperm and embryo (Ribereau-Gayon and Peynaud, 1980). The structure of the seeds from ‘Chardonnay’ and seed traces from ‘Sultanina’ were found to be very different in shape, size and hardness (Fig. 5). For that reason, a morphological analysis was conducted to better characterize the development of endosperm, embryo and seed layers of both cultivars at 2, 4 and 6 weeks of fruit development. Descriptions of the structures as they evolve, examined with the metachromatic reagent toluidine blue O staining, are presented below and in Fig. 6.

*Endosperm and Embryo.* A normal and complete development of the endosperm and the embryo was observed in ‘Chardonnay’ seeds after 6 weeks of fruit development. ‘Sultanina’ seed traces showed an unevolved endosperm and no embryo could be distinguished at that stage.

*Outer Integument.* Parenchyma cells are the main constituent of the outer integument and cell layers are thicker in the ventral face of the seed. At the time of ripening there is an increase in parenchyma cell volume in ‘Chardonnay’, but the number of cells do not seem to change (Fig. 6A, 6C and 6E). In ‘Sultanina’ seed traces, no differences were observed in this layer, since there is no visible evolution of the seeds in this variety (Fig. 6B, 6D and 6F). Along with the outer integument, the epidermis covers the outer integument in both varieties.

*Medium Integument.* After 2 weeks of fruit development, one layer of rectangular palisade cells was observed in the seeds of both varieties (Fig. 6A and 6B). After 4 weeks, two layers of this integument were observed in ‘Chardonnay’ seeds (Fig. 6C), but this duplication was not observed in ‘Sultanina’ seed traces (Fig. 6D). After 6 weeks of fruit development, ‘Chardonnay’ seeds showed a sclerified and thicker medium integument (Fig. 6E) opposed to ‘Sultanina’ seed traces that exhibited the same structures of the initial stage of development.

*Inner Integument.* Three layers of inner integument were observed in the seeds at the initial stage of fruit development in both varieties (Fig. 6A and 6B), although only two layers

were present in later stages in ‘Chardonnay’ (Fig. 6C and 6E) and in ‘Sultanina’ (Fig. 6D and 6F).

#### *Spatial and temporal accumulation of VvAGL11 transcripts*

*In situ* hybridization (ISH) of the reproductive tissues of both grapevine varieties were performed in order to better characterize *VvAGL11* spatial and temporal expression patterns at the level of transcript accumulation. The stages of development analyzed were those described by Baggioini (1952; Supplementary Table 2) including flower formation (H1), preanthesis (PA), fruit-set (FS), seeds at 2, 4 and 6 weeks after flower fertilization.

After ISH with the complementary (antisense) probe, no expression of *VvAGL11* was detected at the stages H1 (Fig. 7B), PA (Fig. 7C), FS (Fig. 7D) and at 6 weeks of fruit development (Fig. 7L) in ‘Chardonnay’. *VvAGL11* transcripts exhibited a high accumulation in seeds after 2 (Fig. 7E and 7F) and 4 weeks (Fig. 7G to 7J) of development in ‘Chardonnay’. The ISH signal was clearly visible in the medium integument layer of the seeds (Fig. 7K). In ‘Sultanina’, no gene expression was observed at any reproductive tissue/organ or stage of development (Fig. 8A to 8F). Important to mention, the ISH slides with the antisense probe were always compared with slides hybridized with the sense *VvAGL11* probe as control in the analysis of ‘Chardonnay’ and ‘Sultanina’ (Supplementary Fig. 2 and 3, respectively).

## **Discussion**

Spontaneous somatic variants have been selected all the way through grapevine domestication, hence creating new and different cultivars with interesting traits such as berry size, taste, color, and seedlessness (This *et al.*, 2006). Grapevine somatic variants have also been useful tools for studies of gene function, whereas they result from single mutation events in a given genetic background (Fernandez *et al.*, 2010). *VvAGL11* was proposed as a candidate gene involved in the absence of seeds (Costantini *et al.*, 2008; Revers *et al.*, 2010; Mejía *et al.*, 2011). With the attempt to better evidence the essentiality of *VvAGL11* in grapevine apireny, we described here *VvAGL11* gene structure in apirenic (‘Sultanina’) and pirenic (‘Chardonnay’) grapevines, its transcript isoforms and profiles of accumulation, and

its spatial-temporal expression pattern during reproductive organ/tissue development and seed morphogenesis.

By means of a PCR strategy based on a high fidelity polymerase, sequencing of *VvAGL11* allelic variants from ‘Sultanina’ and ‘Chardonnay’ was performed, allowing the identification of a group of polymorphisms (Fig. 1). No transposon or large sequence insertion or deletion was found in ‘Sultanina’ that could explain the gene loss of transcription observed in previous data (Mejía *et al.*, 2011). Sequences were compared with the grapevine reference (‘Pinot Noir’) genome and to a recent work that reported the whole genome sequence of ‘Sultanina’, producing a catalog of structural variants for grapevine (Di Genova *et al.*, 2014). We found two amino acid modifications in ‘Sultanina’s’ *VvAGL11* coding region (Fig. 2). Arginine and threonine were substituted by two more hydrophobic amino acids, leucine and alanine, respectively. These amino acid substitutions were localized in the C-terminal portion of the *VvAGL11* protein, a well known region responsible for activity and ternary complex formation (Egea-Cortines *et al.*, 1999). Furthermore, 17 INDELs and 53 additional SNPs were identified in the second intron of the ‘Sultanina’ mutant allele (Supplementary Fig. 1). The second intron of MADS-box AG subfamily members is known to present a quite large size (*AtAG* ~3 kb, *AtAGL11* ~1,8 kb, and *VvAGL11* ~4 kb) and to be a region with important *cis* elements that may control tissue specific expression of AG and AG-like genes (Deyholos, 2000; Hong *et al.*, 2003). Interestingly, MADS-box proteins form complexes of high order, often in tetrameric junctions made by two dimers that bind to two DNA consensus sequences called CArG-box [CC(A/T)<sub>6</sub>GG] separated by up to 300 bp (Liu *et al.*, 2008). A CArG-box modification was observed in ‘Sultanina’ *mut* allele, in the seventh putative sequence. This *cis* element is only 84 bp distant from another CArG-box what would suggest their relevance in gene regulation.

We performed the first analysis of *VvAGL11* transcript isoforms and compared them to the genome gene-predicted models (Fig. 3). The transcription profile of *VvAGL11* isoforms provided complete data for each expression isoform during the development of flowers, fruits and seeds. ‘Sultanina’ alleles presented a low level of expression in all organs and stages of development, including berries, while the ‘Chardonnay’ alleles were expressed at very low levels in the pulp, but highly expressed in seeds (Fig. 4). Of the two ‘Chardonnay’ alleles, one possesses a larger coding region, able to encode 20 additional amino acids (CH1). The sequence of CH1 transcripts was also found in a ‘Cabernet Sauvignon’ cDNA

library derived from berries (GenBank CB974197.1). This could cause conformational changes in the C-terminal portion of VvAGL11 protein, yet no abnormal seed morphogenesis is observed in Chardonnay neither in Cabernet Sauvignon cultivars. Thus it is clear that this 60 nucleotides may not be relevant to seed phenotype, therefore the biological relevance of these 20 additional amino acids in the C-terminal VvAGL11 protein remains to be elucidated. The relative expression of CH1 allele in seeds showed a fluctuation between 5 to 11-fold compared to fruit-set (Fig. 4). This instability was possibly due to the random amplification of *VvAGL11* pre-mRNA since primers employed allowed the amplification of intronic regions. Taken together, our results suggested that *VvAGL11* has indeed a major role in seed development. Without its expression (transcript accumulation), there is no normal seed formation.

The interaction of proteins encoded by MADS-box genes of classes A, B, C, D, and E forms the model of floral quartets (Theissen and Saedler, 2001; Dornelas and Dornelas, 2005). The AGAMOUS subfamily of *MADS-box* genes is known to have redundant functions in *A. thaliana* since *AtAGL11* is the major responsible gene in the regulation of ovule development along with other two genes of class D, *SHATTERPROOF1* and *SHATTERPROOF2* (Colombo *et al.*, 1995; Pinyopich *et al.*, 2003). The *VvAGL11* gene was proposed as a possible ortholog of *AtAGL11*, however no gene has been identified yet as orthologous to *SHP1* or *SHP2* in grapevine (Díaz-Riquelme *et al.*, 2009). These data suggest that *VvAGL11* might be the only class D gene in grapevine and a possible model of floral quartet would be composed by *VvAG1* and *VvAG2* (*AGAMOUS* genes), and one of the *SEPALLATA* genes of grapevine (*VvSEP1*, *VvSEP2*, *VvSEP3*, and *VvSEP4*) as previously described by Boss *et al.* (2002) and Díaz-Riquelme *et al.* (2008). Additional studies of the VvAGL11 protein are necessary to confirm this hypothesis.

Previous studies have described grapevine's seed anatomy (Pratt, 1971; Ribereau-Gayon and Peynaud, 1980) as well as the changes of internal layers towards seed ripening (Cadot *et al.*, 2006), but, as much as we are concerned, no study has demonstrated detailed morphological parameters in seeds of stenospermocarpic grapevines, specially seed traces. The main objective of our morphological assay was to compare normal seeds from 'Chardonnay' and seed traces from 'Sultanina' as they resemble so differently from each other (Fig. 5). Our analysis showed that the most substantial difference was at the medium integument of the seed coat, which did not develop normally in 'Sultanina' seed traces,

preserving its initial features until the complete maturation of the fruits. As expected, ‘Chardonnay’ seeds developed correctly with the elongation and duplication of the medium integument, along with normal endosperm growth (Fig. 6). The nutrient flux in seeds occurs in a centripetal way, from the outer integument to the inner, going through apoplasts to the endosperm and to the embryo (Stadler *et al.*, 2005). Garcia *et al.* (2005) have previously shown that there is a strong maternal effect of the integuments in the control and determination of final seed size, due to the elongation of these layers and, in case of elongation absence, there is a compensation effect promoted by the duplication of these layers. Seed traces formation are likely originated due to disruption of seed tissues normal development. Probably the erroneous formation of the medium integument seed layer that occurs in stenospermocarpic grapevines could interfere in seed nutrient intake and cause the degeneration of some tissues during seed development, like the endosperm.

ISH assays were performed for better characterization of *VvAGL11* spatial and temporal expression patterns, in ‘Chardonnay’ and ‘Sultanina’, during seed morphogenesis in order to identify its transcription specific tissue localization. At the time of ISH assays the transcription isoforms were not known and the probe used for hybridization was designed according to the *VvAGL11* gene predicted model (GSVIVT01025945001) available at <http://www.genoscope.cns.fr>. Therefore, the whole probe (185 bp) hybridizes with CH1 mRNA isoform while 38 nucleotides hybridizes with CH2, SU1 and SU *mut* mRNA isoforms. The transcripts accumulation were localized in the medium integument layer of ‘Chardonnay’ seeds of 2 and 4 weeks (Fig. 7), while no accumulation of transcripts was found in ‘Sultanina’ seed traces (Fig. 8). After 6 weeks of ‘Chardonnay’ seed development, no hybridization signals were detected (Fig. 7L), this is due probably because the medium integument layer has already started lignification process, once it will be part of the mature and hard seed coat (Haughn & Chaudhury, 2005). This data is in agreement with *VvAGL11* RT-qPCR transcriptional profile, where ‘Sultanina’ shows almost no expression in any of the stages evaluated. The particular accumulation of *VvAGL11* transcripts in a specific layer of the seed coat in Chardonnay cultivar, combined with the morphological differences in this same layer when comparing Chardonnay and Sultanina cultivars, suggest that this gene is essential for the elongation and duplication of the medium integument of the seed coat. Furthermore, seed growth is dictated by the coordinated development of endosperm and

integuments and, hence, a spatial and temporal coordination of endosperm and integument growth is critical for normal seed development (Garcia *et al.*, 2005).

Taken together, our results allow us to propose that the absence of *VvAGL11* expression, a MADS-box class D gene of grapevine, is responsible for the erroneous development of seeds. The extreme diminution of final seed size could be due to the non-differentiation of the medium integument seed layer, causing the cease of the elongation and duplication of the seed coat. Within this loss of identity, the endosperm would have no normal development as well, stopping its growth and causing the death of the embryo leading to the formation of a seed trace.

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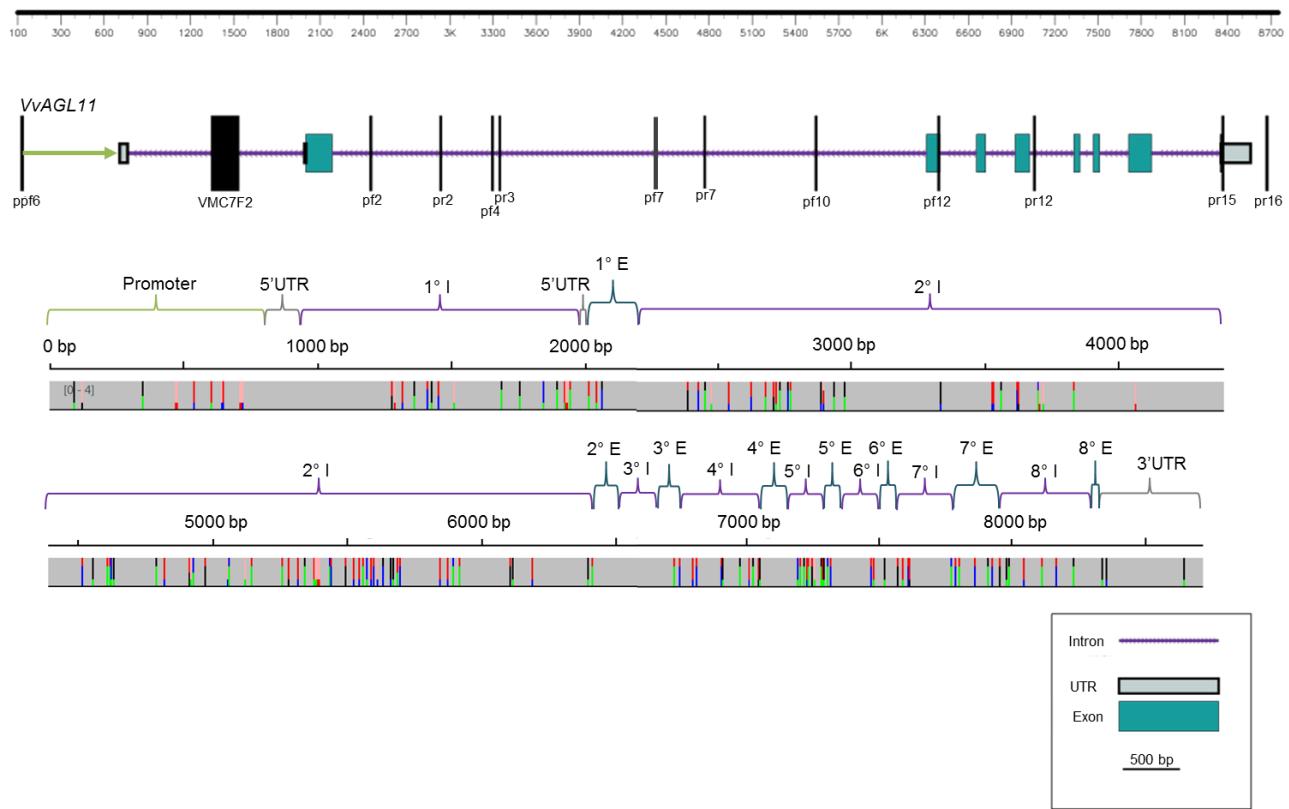
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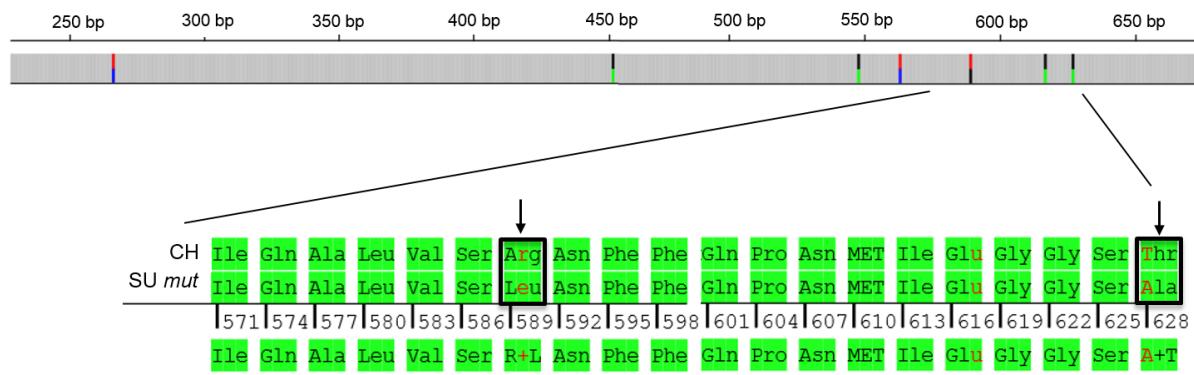
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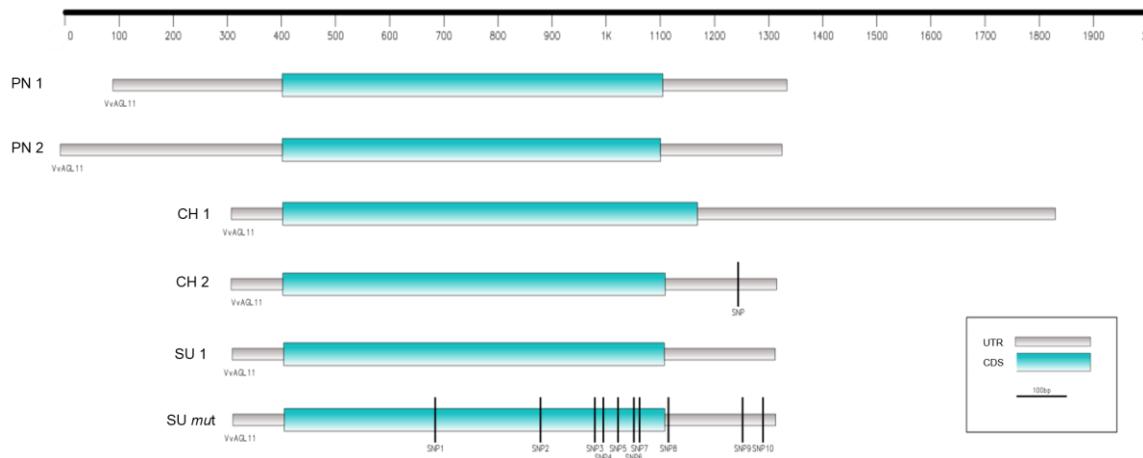
## FIGURES



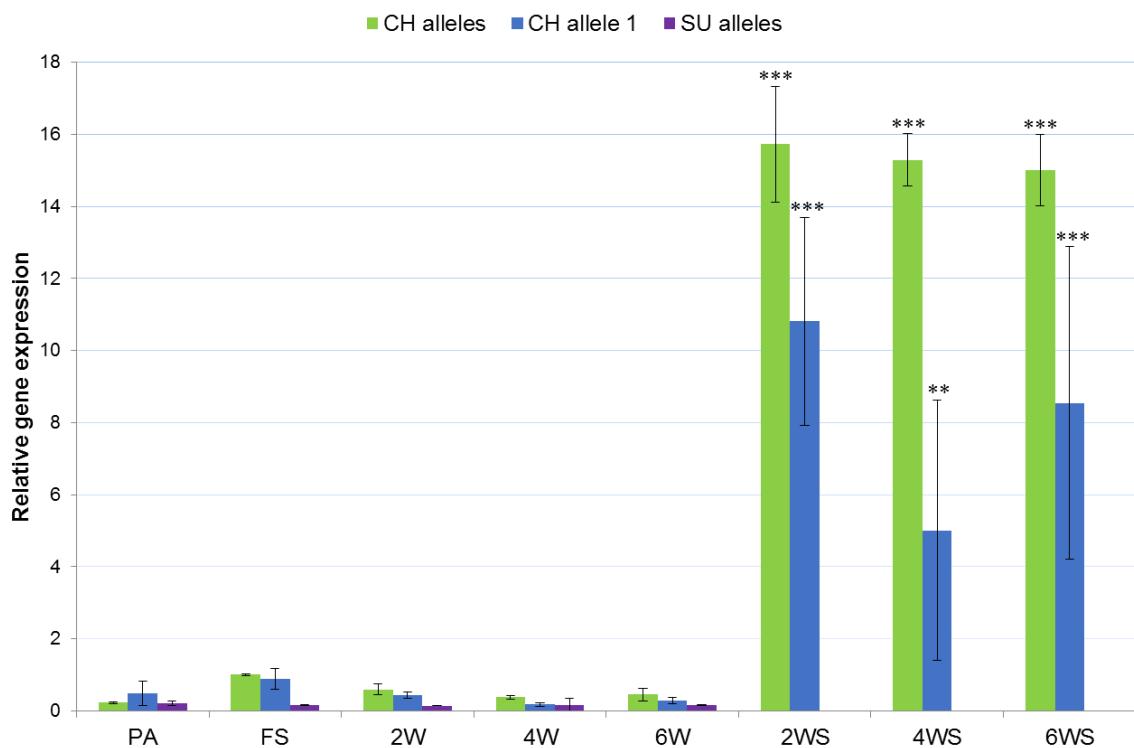
**Fig. 1.** Representative image of *VvAGL11*. DNA structure is composed by a promoter region, 5'-UTR, 8 introns, 8 exons and 3'-UTR. The black lines represents the localization of the primers used for allele amplification. Below, the alignment with the set of polymorphisms derived from ‘Sultanina’ and ‘Chardonnay’ *VvAGL11* alleles. Colors stripes represent SNPs (A-green, C-blue, T-red, G-black), and the salmon color indicates INDELs.



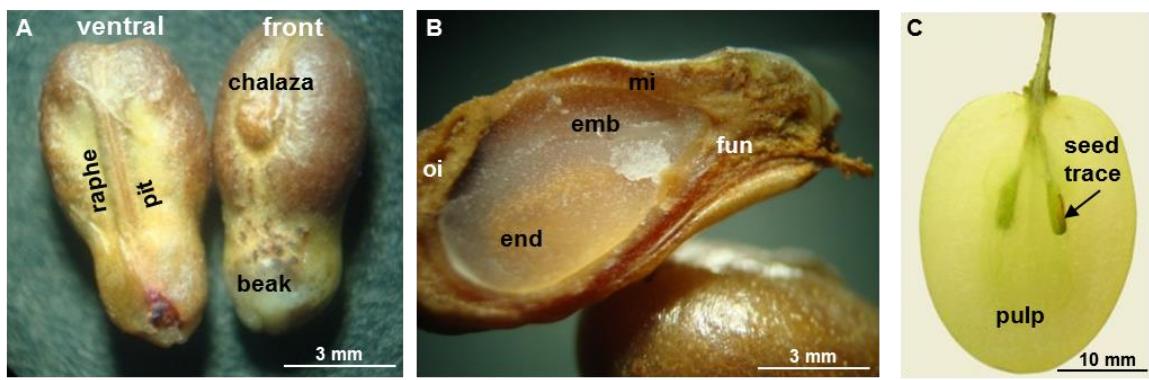
**Fig. 2.** Alignment of the coding regions of *VvAGL11* alleles where two amino acid modifications were observed. Alleles from ‘Pinot Noir’ (PN40024), ‘Chardonnay’ (both *VvAGL11* alleles) and ‘Sultanina’ normal and mutant allele. Colors stripes represent SNPs (A-green, C-blue, T-red, G-black).



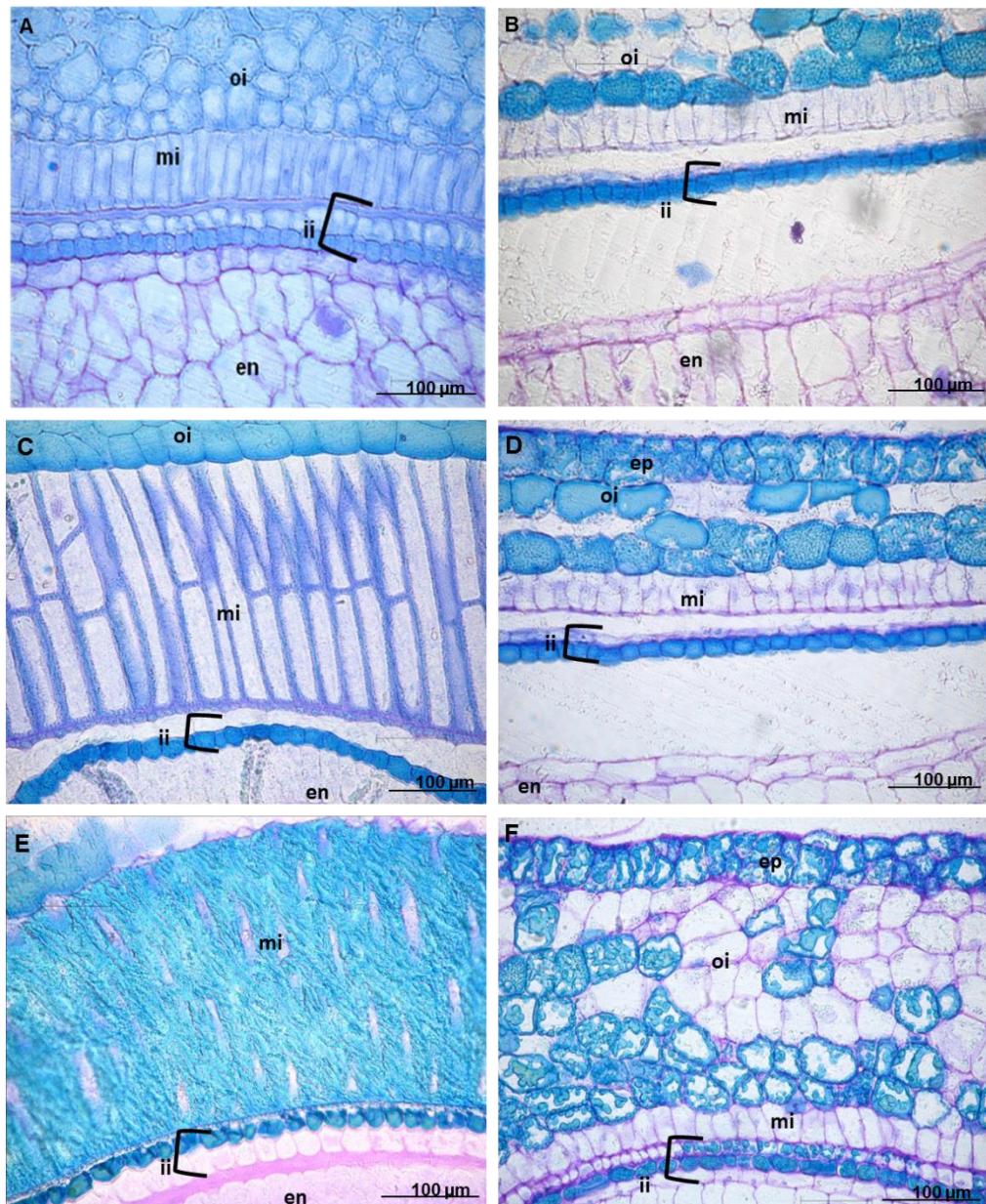
**Fig. 3.** Comparison between *VvAGL11* mRNA forms. PN 1 and PN 2 represent mRNA versions of *VvAGL11* from the Pinot Noir reference cultivar (VIT\_218s0041g01880.1 and VIT\_218s0041g01880.2, respectively). ‘Chardonnay’ allele 1 (CH1), ‘Chardonnay’ allele 2 (CH2), ‘Sultanina’ allele 1 (SU1) are compared with the ‘Sultanina’ mutant allele (SU mut). SNPs represented by black stripes (GenBank KM401845, KM401846, KM401847 and KM401848).



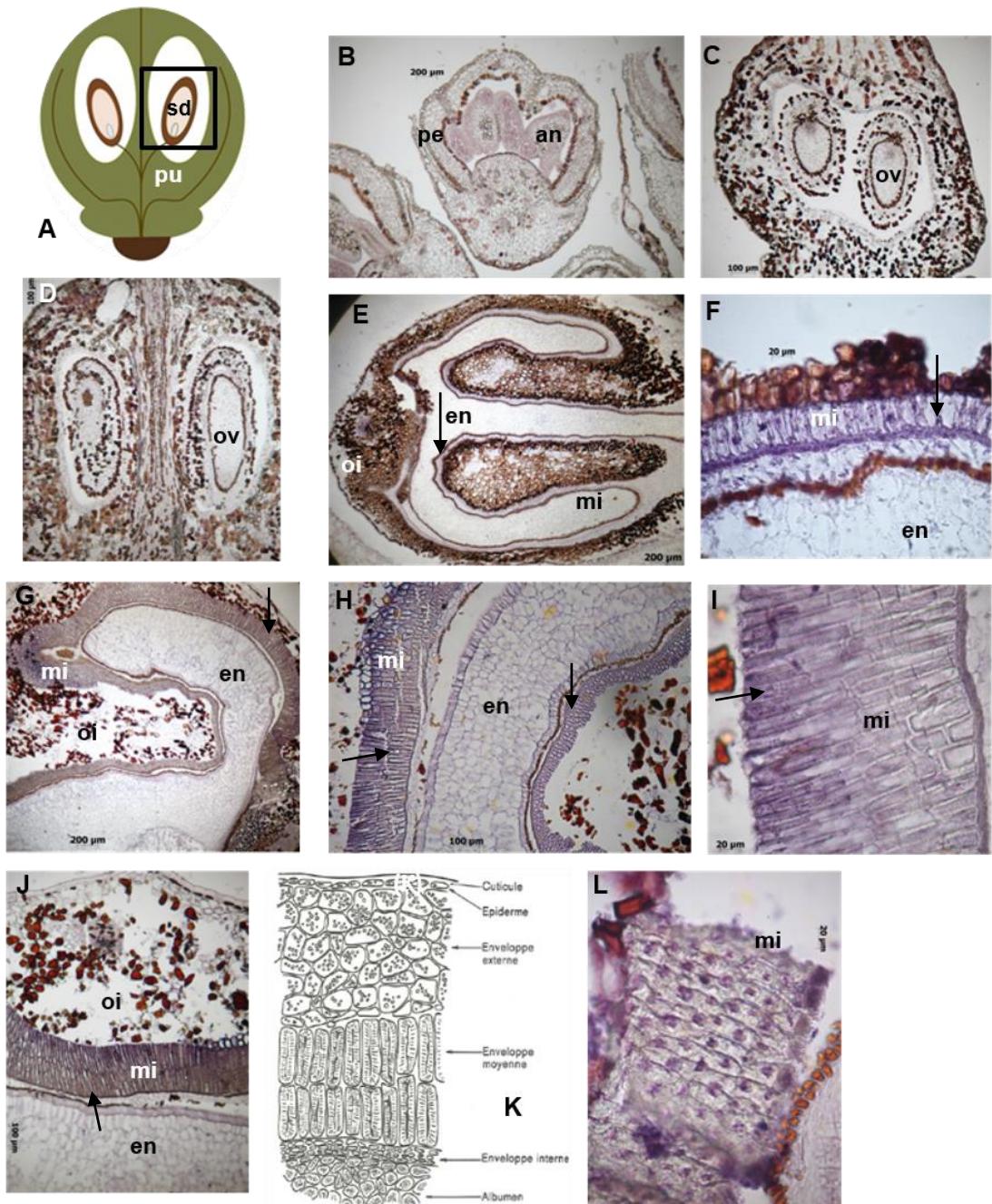
**Fig. 4.** Relative gene expression of *VvAGL11* alleles from ‘Chardonnay’ and ‘Sultanina’ via RT-qPCR. The developmental stages sampled are shown in the x-axis: (**PA**) pre anthesis flower; (**FS**) fruit set; (**2W-4W-6W**) fruits at 2, 4 and 6 weeks after fruit set and ‘Chardonnay’ seed stages (**2WS-4WS-6WS**). ‘Chardonnay’ fruit-set was used as reference. The relative expression expressed in the y-axis was calculated by the Pfaffl (2001) method. Standard deviation is showed for each stage and sample. Asterisks indicate statistical significance between ‘Chardonnay’ alleles in seed stages to others stages evaluated for the ‘Chardonnay’ and ‘Sultanina’ alleles (Tukey test: \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ ).



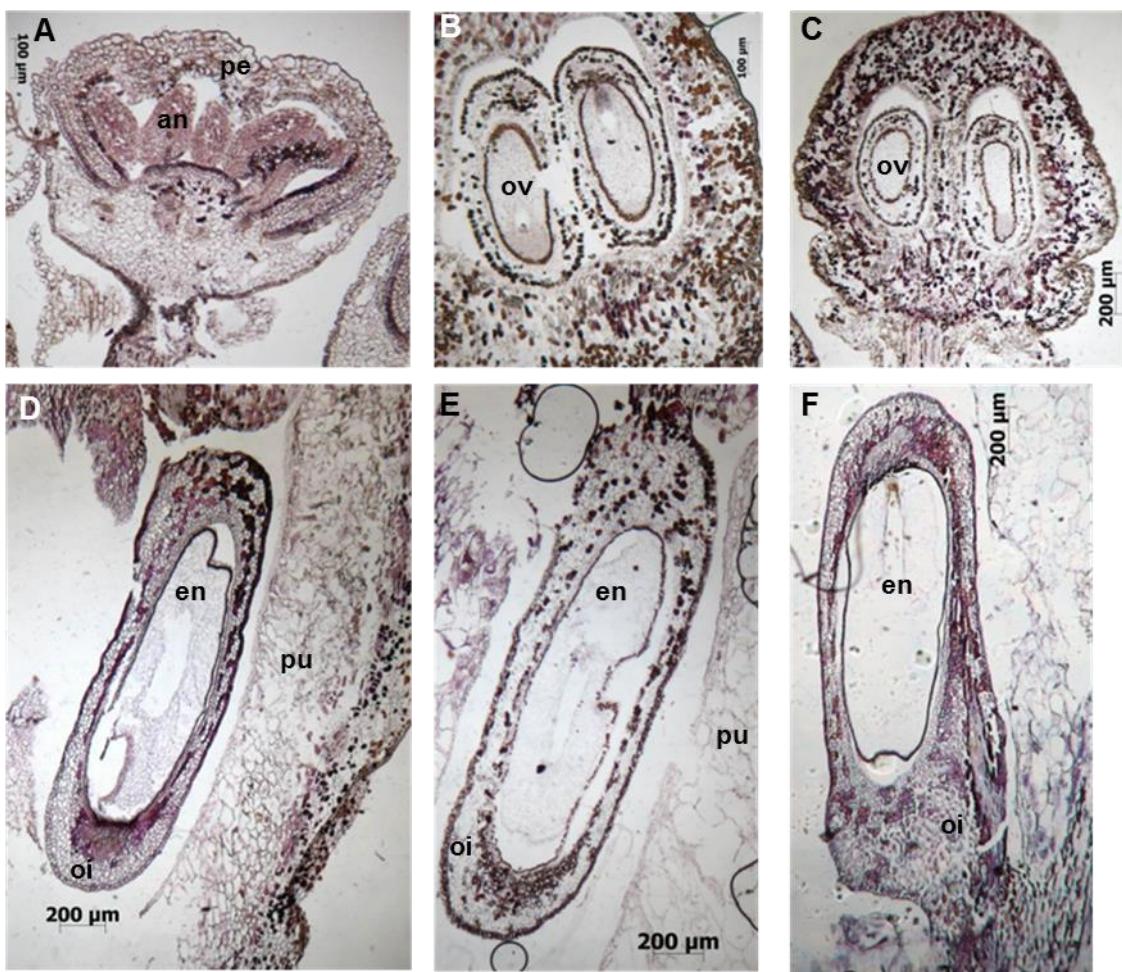
**Fig. 5.** Seeds and seed traces in *V. vinifera*. (A) Mature ‘Chardonnay’ (CH) seeds at their ventral and frontal view. Main structures are indicated. (B) CH seed cross section, with the internal view exhibiting outer integument (oi), medium integument (mi), endosperm (end), embryo (emb), and funiculus (fun). (C) Mature ‘Sultana’ (SU) berry showing its seed traces.



**Fig. 6.** Grapevine seed structure development from 2 to 6 weeks after fruit set. Light micrographs of grape seed cross sections were stained with toluidine blue O. The cross sections in the median area of the seeds of ‘Chardonnay’ and seed traces of ‘Sultanina’ enable the visualization of three defined integuments. ‘Chardonnay’ seed: 2 weeks (A), 4 weeks (C) and 6 weeks (E). ‘Sultanina’ seed trace: 2 weeks (B), 4 weeks (D) and 6 weeks (F). Endosperm (en), epidermis (ep), internal integument (ii), medium integument (mi), outer integument (oi).



**Fig. 7.** *In situ* hybridization of *VvAGL11* in ‘Chardonnay’ reproductive tissues and organs, from flowers to seeds after 6 weeks of fruit development. (A) Schematic berry. No hybridization signal is visible in (B) H1 flower stage, (C) pre anthesis flower stage and (D) fruit set flower stage. *VvAGL11* expression is detectable in the medium integument of (E-F) 2 weeks seeds and (G-J) 4 weeks seeds (black arrows). No hybridization signal is visible in (L) 6 week seeds, compared to the control slides (Supplementary Fig. 2). (K) Schematic figure of the grapevine seed layers (Pratt, 1971). Anther (an), endosperm (en), medium integument (mi), outer integument (oi), petal (pe), pulp (pu), seed (sd).



**Fig. 8.** *In situ* hybridization of *VvAGL11* in ‘Sultanina’ from flowers to 6 weeks of fruit development. No hybridization signal is visible in H1 flower stage (A), pre anthesis flower stage (B), fruit set flower stage (C) and in 2 (D), 4 (E) and 6 (F) weeks of fruit development. All samples compared with control slides (Supplementary Fig. 3). Anther (an), endosperm (en), medium integument (mi), outer integument (oi), petal (pe), pulp (pu).

## Supplementary Material

**Supplementary Table 1.** Primers designed for the amplification and sequencing of *VvAGL11*.

CDS+INTRON_AGL11_R_1	CAT CAG CAG ATG CCA GAT
CDS+INTRON_AGL11_F_1	CAA TAA ACC TAA CAG TGT AGT GAA C
CDS+INTRON_AGL11_R_2	GGA CAG TGG AAT ACA GAT TC
CDS+INTRON_AGL11_F_2	TAG GAA GGG ATT ACA TGG G
CDS+INTRON_AGL11_R_3	GAT GGC ATT GAG CAA ACA
CDS+INTRON_AGL11_F_3	CTA GGC AAC AAC CAG TTA G
CDS+INTRON_AGL11_R_4	ATA AGG AAG ACT TCT CCC C
CDS+INTRON_AGL11_F_4	CCC ATT ACA TCT TTG TGT GG
CDS+INTRON_AGL11_R_5	CTT TTT CTC CTA CTT TTC CTC
CDS+INTRON_AGL11_F_5	CGA TCT TAC ATG AGA TTT TAC C
CDS+INTRON_AGL11_R_6	TTG GAG CAT CGT CTT AGA G
CDS+INTRON_AGL11_F_6	GAGGAAAAGTAGGAGAAAAAG
CDS+INTRON_AGL11_R_7	AAA CCC CAC TGT GAT AGG
CDS+INTRON_AGL11_F_7	GGA TGG TGT CAT AAT GAT AGG
CDS+INTRON_AGL11_R_8	GAA ATA TCA TAG TCA TCC TCA C
CDS+INTRON_AGL11_F_8	TAA GGT GTC GAA GCC ATG
CDS+INTRON_AGL11_R_9	TGA GTT TCT TTG TGT GGA C
CDS+INTRON_AGL11_F_9	GAG AGC CTA TTT GGG ATA AC
CDS+INTRON_AGL11_R_10	GAG TTT GTA TGG AGA ATA GCA G
CDS+INTRON_AGL11_F_10	GCA AAG CAG TTA TTG AAA GC
CDS+INTRON_AGL11_R_11	GGA TTT GGA TTG ATT CAT TAA C
CDS+INTRON_AGL11_F_11	AGG AGA AAC CAG GAC AAG
CDS+INTRON_AGL11_R_12	CAA ATG CTC AGC CAG ATT AG
CDS+INTRON_AGL11_F_12	TGC CCA AGT AAG AAA ACT TC
CDS+INTRON_AGL11_R_13	CGG TAT CAA CTG TTG TGC
CDS+INTRON_AGL11_F_13	GGT AAC GAC ACC TAG ACA C
CDS+INTRON_AGL11_R_14	GCT TGA AAT GTC TCA TTA AGC
CDS+INTRON_AGL11_F_14	CGT ATA TCT CCG AAC CAA G
CDS+INTRON_AGL11_R_15	GGC GGA TAT TTT CTC CCA TC
CDS+INTRON_AGL11_F_15	CTC GGG TAC ACT CAT CTT TC
CDS+INTRON_AGL11_R_16	TGA TTA TCA ACA CCA AAC ATG GC
CDS+INTRON_AGL11_F_16	TTC AAG TTC GAC CTA ATT CCT GG
Promo_AGL11_R_1	GAT CTC GAT CTT TCC TCT CCC
Promo_AGL11_F_1	CCT CAC CCT ATT TTT CGA ACA AC
Promo_AGL11_R_2	GAG ATC TGA ATG ATG ATA GAC TGA G
Promo_AGL11_F_2	CTT GAG GGG AAA AAG CCA G
Promo_AGL11_R_3	CAT AAA CCC AGG ATA TGG ATG AG
Promo_AGL11_F_3	TTG CCT ACA TAT GAA CAT CTG C
Promo_AGL11_R_4	ATT TGG AGA GAT GGG CAC TG
Promo_AGL11_F_4	AAA GTC ACT TTC TAC ATC TGC AC
Promo_AGL11_R_5	GGA GAG ATG TGA GAC GGA TAT G

Promo_AGL11_F_5	AGA AGA AAG TTT GCA GTT TGT G
Promo_AGL11_R_6	CAA AGT CGG ATA CAA GAC ATA GTA G
Promo_AGL11_F_6	CCA CTG ATA TGG ATT GAT TTG CC

**Supplementary Table 2.** Stages of development of grapevine reproductive organs sampled for the evaluation of *VvAGL11* transcriptional profile (except H1) and for the *in situ* hybridization experiment. Dates of harvesting, the phenological stage according to Baggioolini (1952), grapevine cultivars and a representative picture of each sample are represented.

Dates	Phenological stage (Baggiolini, 1952)	Sample	Cultivar	
09/11/12	<b>H1</b>	Flowers at initial development	Chardonnay	
08/30/12			Sultanina	
10/08/12	<b>Pre anthesis</b>	Flowers before anthesis	Chardonnay	
10/08/12			Sultanina	
10/22/12	<b>Fruit-set</b>	Flowers in anthesis	Chardonnay	
10/08/12			Sultanina	
11/05/12	<b>2 weeks of development</b>	Fruits (Pulp and seeds)	Chardonnay	
11/22/12			Sultanina	
11/19/12	<b>4 weeks of development</b>	Fruits (Pulp and seeds)	Chardonnay	
11/05/12			Sultanina	
12/03/12	<b>6 weeks of development</b>	Fruits (Pulp and seeds)	Chardonnay	
11/19/12			Sultanina	
01/02/13	<b>Maturation</b>	Fruits (Pulp and seeds)	Chardonnay	
12/17/12			Sultanina	

CLUSTAL multiple sequence alignment by MUSCLE (3.8)

su_mut	CCACTGATATGGATTGATTGCCTTTAATTGAAGACCCCTTCTGGTAACCTTG
su_Di Genova	CCACTGATATGGATTGATTGCCTTTAATTGAAGACCCCTTCTGGTAACCTTG
ch2	CCACTGATATGGATTGATTGCCTTTAATTGAAGACCCCTTCTGGTAACCTTG
VIT_218S0041G01880.2	CCACTGATATGGATTGATTGCCTTTAATTGAAGACCCCTTCTGGTAACCTTG
su_wt	CCACTGATATGGATTGATTGCCTTTAATTGAAGACCCCTTCTGGTAACCTTG
ch1	CCACTGATATGGATTGATTGCCTTTAATTGAAGACCCCTTCTGGTAACCTTG
	*****
su_mut	GAAGGCATGAACGAAGTTGATTACTGAAAATATTAGCAACATTACTAGGGTTTGGCGGA
su_Di Genova	GAAGGCATGAACGAAGTTGATTACTGAARATATTAGCAACATTACTAGGGTTTGGCGGA
ch2	GAAGGCATGAACGAAGTTGATTACTGAAGATATTAGCAACATTACTAGGGTTT---GGA
VIT_218S0041G01880.2	GAAGGCATGAACGAAGTTGATTACTGAAGATATTAGCAACATTACTAGGGTTT---GGA
su_wt	GAAGGCATGAACGAAGTTGATTACTGAAGATATTAGCAACATTACTAGGGTTT---GGA
ch1	GAAGGCATGAACGAAGTTGATTACTGAAGATATTAGCAACATTACTAGGGTTT---GGA
	*****
su_mut	GATGAGACTGTAAAGTGGCTAAACCCCTAGAGGCATGTTTTAATAATTGGAGAT
su_Di Genova	GATGAGACTGTAAAGTGGCTAAACCCCTAGAGGCATGTTTTAATAATTGGAGAT
ch2	GATGAGACTGTAAAGTGGCTAAACCCCTAGAGGCATGTTTTAATAATTGGAGAT
VIT_218S0041G01880.2	GATGAGACTGTAAAGTGGCTAAACCCCTAGAGGCATGTTG-TTTTAATAATTGGAGAT
su_wt	GATGAGACTGTAAAGTGGCTAAACCCCTAGAGGCATGTTG-TTTTAATAATTGGAGAT
ch1	GATGAGACTGTAAAGTGGCTAAACCCCTAGAGGCATGTTG-TTTTAATAATTGGAGAT
	*****
su_mut	ACCATATATGTATGTCGAGTCAGATATACGTGAAAGCACAAAACCTAACCTGTT
su_Di Genova	ACCATATATGTATGTCGAGTCAGATATACGTGAAAGCACAAAACCTAACCTGTT
ch2	ACCATATATGTATGTCGAGTCAGATATACGTGAAAGCACAAAACCTAACCTGTT
VIT_218S0041G01880.2	ACCATATATGTATGTCGAGTCAGATATACGTGAAAGCACAAAACCTAACCTGTT
su_wt	ACCATATATGTATGTCGAGTCAGATATACGTGAAAGCACAAAACCTAACCTGTT
ch1	ACCATATATGTATGTCGAGTCAGATATACGTGAAAGCACAAAACCTAACCTGTT
	*****
su_mut	AAACTGTAATTGGGAAGATATTGTTCTTACGTGTTGGATACAACATTGGTTG
su_Di Genova	AAACTGTAATTGGGAAGATATTGTTCTTACGTGTTGGATACAACATTGGTTG
ch2	AAACTGTAATTGGGAAGATATTGTTCTTACGTGTTGGATACAACATTGGTTG
VIT_218S0041G01880.2	AAACTGTAATTGGGAAGATATTGTTCTTACGTGTTGGATACAACATTGGTTG
su_wt	AAACTGTAATTGGGAAGATATTGTTCTTACGTGTTGGATACAACATTGGTTG
ch1	AAACTGTAATTGGGAAGATATTGTTCTTACGTGTTGGATACAACATTGGTTG
	*****
su_mut	GGCCTGAAGAAAATAAGAGAGAAGAAAGTTGCAGTTATGGTGGGAATTGGAAC
su_Di Genova	GGCCTGAAGAAAATAAGAGAGAAGAAAGTTGCAGTTATGGTGGGAATTGGAAC
ch2	GGCCTGAAGAAAATAAGAGAGAAGAAAGTTGCAGTTATGGTGGGAATTGGAAC
VIT_218S0041G01880.2	GGCCTGAAGAAAATAAGAGAGAAGAAAGTTGCAGTTATGGTGGGAATTGGAAC
su_wt	GGCCTGAAGAAAATAAGAGAGAAGAAAGTTGCAGTTATGGTGGGAATTGGAAC
ch1	GGCCTGAAGAAAATAAGAGAGAAGAAAGTTGCAGTTATGGTGGGAATTGGAAC
	*****
su_mut	GCAAAGCTTTACATTATAAAACTACTATGTCTGTATCCGACTTGGTAATAAGCCA
su_Di Genova	GCAAAGCTTTACATTATAAAACTACTATGTCTGTATCCGACTTGGTAATAAGCCA
ch2	GCAAAGCTTTACATTATAAAACTACTATGTCTGTATCCGACTTGGTAATAAGCCA
VIT_218S0041G01880.2	GCAAAGCTTTACATTATAAAACTACTATGTCTGTATCCGACTTGGTAATAAGCCA
su_wt	GCAAAGCTTTACATTATAAAACTACTATGTCTGTATCCGACTTGGTAATAAGCCA
ch1	GCAAAGCTTTACATTATAAAACTACTATGTCTGTATCCGACTTGGTAATAAGCCA
	*****
su_mut	TTCGGAAGTCTTCTTCCTCAACCC-----CTCTCTCTCTCTCTCTTGAAGAAG
su_Di Genova	TTCGGAAGTCTTCTTCCTCAACCC-----CTCTCTCTCTCTCTCTTGAAGAAG
ch2	TTCGGAAGTCTTCTTCCTCAACCC-----CTCTCTCTCTCTCTCTCTCTCTTGAAGAAG
VIT_218S0041G01880.2	TTCGGAAGTCTTCTTCCTCAACCC-----CTCTCTCTCTCTCTCTCTCTCTCTTGAAGAAG
su_wt	TTCGGAAGTCTTCTTCCTCAACCC-----CTCTCTCTCTCTCTCTCTCTCTTGAAGAAG
ch1	TTCGGAAGTCTTCTTCCTCAACCC-----CTCTCTCTCTCTCTCTCTCTCTTGAAGAAG
	*****

su\_mut TCATTTCTTCATCTGCACCGCCCATTCTCTCGTATTGTCATCTTCCCTC--CTC  
 su\_Di Genova TCATTTCTTCATCTGCACCGCCCATTCTCTCGTATTGTCATCTTCCCTCCTC  
 ch2 TCATTTCTTCATCTGCACCGCCCATTCTCTCGTATTGTCATCTTCCCTC--  
 VIT\_218S0041G01880.2 TCATTTCTTCATCTGCACCGCCCATTCTCTCGTATTGTCATCTTCCCTC--TTC  
 su\_wt TCATTTCTTCATCTGCACCGCCCATTCTCTCGTATTGTCATCTTCCCTC--TTC  
 ch1 TCATTTCTTCATCTGCACCGCCCATTCTCTCGTATTGTCATCTTCCCTC--TTC  
 \*\*\*\*

su\_mut TCTCTCTCTCTCTCTCTCTCTCTCTCTATTGTAATCTCTCTCTCTATCTCTCT  
 su\_Di Genova TCTCTCTCTCTCTCTCTCTCTCTATTGTAATCTCTCTCTCTATCTCTCT  
 ch2 ----TTCTCTCTCTCTCTCTCTCTATTGTAATCTCTCTCTCTATCTCTCA  
 VIT\_218S0041G01880.2 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATCTCTCT  
 su\_wt TCTCTCTCTCTCTCTCTCTCTCTATTGTAATCTCTCTCTCTATCTCTCT  
 ch1 TCTCTCTCTCTCTCTCTCTCTCTATTGTAATCTCTCTCTCTATCTCTCT  
 \*\*\*\*

su\_mut TTATTGCTCTCTCTCCCTTCCCTCTCCCTCTCCCTCCCTCTCTCTCTCTCT  
 su\_Di Genova TTATTGCTCTCTCTCCCTTCCCTCTCCCTCTCC--CTCCCTCTCTCT  
 ch2 TTATTGCTCTCTCTCCCTTCCCTCTCCCTCTCC--CTCCCTCTCTCTCT  
 VIT\_218S0041G01880.2 TTATTGCTCTCTCCCTTCCCTCTCC--CTCCCTCTCTCT  
 su\_wt TTATTGCTCTCTCTCCCTTCCCTCTCC--CTCCCTCTCTCTCT  
 ch1 TTATTGCTCTCTCTCCCTTCCCTCTCC--CTCCCTCTCTCTCTCTCT  
 \* \* \* \* \*

su\_mut CAAAGTCACTTCTACATCTGCACCACCCACTCTCTCTCTCTCTCTCTCTCT  
 su\_Di Genova CAAAGTCACTTCTACATCTGCACCACCCACTCTCTCTCTCTCT  
 ch2 CAAAGTCACTTCTACATCTGCACCACCCACTCTCTCTCTCTCTCT  
 VIT\_218S0041G01880.2 CAAAGTCACTTCTACATCTGCACCACCCACTCTCTCTCTCT  
 su\_wt CAAAGTCACTTCTACATCTGCACCACCCACTCTCTCTCTCTCT  
 ch1 CAAAGTCACTTCTACATCTGCACCACCCACTCTCTCTCTCTCT  
 \*\*\*

su\_mut TATCCGTCTCACATCTCCATTGGTATATATATAAGGACTAACACAAGTCTAA  
 su\_Di Genova TATCCGTCTCACATCTCCATTGGTATATATATAAGGACTAACACAAGTCTAW  
 ch2 TATCCGTCTCACATCTCCATTGGTATATATATAAGGACTAACACAAGTCTAA  
 VIT\_218S0041G01880.2 TATCCGTCTCACATCTCCATTGGTATATATATAAGGACTAACACAAGTCTAA  
 su\_wt TATCCGTCTCACATCTCCATTGGTATATATATAAGGACTAACACAAGTCTAA  
 ch1 TATCCGTCTCACATCTCCATTGGTATATATATAAGGACTAACACAAGTCTAA  
 \*\*\*\*

su\_mut GGCACTTGGCTCATTGGGATACCGGTTTGACAGCCGAAATTTCGAAAGCTGA  
 su\_Di Genova GGCACTTGGCTCATTGGGATACCGGTTTGACAGCCGAAATTTCGAAAGCTGA  
 ch2 GGCACTTGGCTCATTGGGATACCGGTTTGACAGCCGAAATTTCGAAAGCTGA  
 VIT\_218S0041G01880.2 GGCACTTGGCTCATTGGGATACCGGTTTGACAGCCGAAATTTCGAAAGCTGA  
 su\_wt GGCACTTGGCTCATTGGGATACCGGTTTGACAGCCGAAATTTCGAAAGCTGA  
 ch1 GGCACTTGGCTCATTGGGATACCGGTTTGACAGCCGAAATTTCGAAAGCTGA  
 \*\*\*\*

su\_mut AGTCGCCGATTGGAAACAGGTGTAGGTATTTAACAGAACGTTCACAC  
 su\_Di Genova AGTCGCCGATTGGAAACAGGTGTAGGTATTTAACAGAACGTTCACAC  
 ch2 AGTCGCCGATTGGAAACAGGTGTAGGTATTTAACAGAACGTTCACAC  
 VIT\_218S0041G01880.2 AGTCGCCGATTGGAAACAGGTGTAGGTATTTAACAGAACGTTCACAC  
 su\_wt AGTCGCCGATTGGAAACAGGTGTAGGTATTTAACAGAACGTTCACAC  
 ch1 AGTCGCCGATTGGAAACAGGTGTAGGTATTTAACAGAACGTTCACAC  
 \*\*\*\*

su\_mut CAAAATTCACAACTAACCATCTCTCTGTGAAAAACGTTCGTCATAACTGGTAA  
 su\_Di Genova CAAAATTCACAACTAACCATCTCTCTGTGAAAAACGTTCGTCATAACTGGTAA  
 ch2 CAAAATTCACAACTAACCATCTCTCTGTGAAAAACGTTCGTCATAACTGGTAA  
 VIT\_218S0041G01880.2 CAAAATTCACAACTAACCATCTCTCTGTGAAAAACGTTCGTCATAACTGGTAA  
 su\_wt CAAAATTCACAACTAACCATCTCTCTGTGAAAAACGTTCGTCATAACTGGTAA  
 ch1 CAAAATTCACAACTAACCATCTCTCTGTGAAAAACGTTCGTCATAACTGGTAA  
 \*\*\*\*

su\_mut TCTTAGATCTGCTCCCTCCACACCACAGAATCTACTTTGCCTACATATGAACATCTGC  
 su\_Di Genova TCTTAGATCTGCTCCCTCCACACCACAGAATCTACTTTGCCTACATATGAACATCTGC  
 ch2 TCTTAGATCTGCTCCCTCCACACCACAGAATCTACTTTGCCTACATATGAACATCTGC  
 VIT\_218S0041G01880.2 TCTTAGATCTGCTCCCTCCACACCACAGAATCTACTTTGCCTACATATGAACATCTGC  
 su\_wt TCTTAGATCTGCTCCCTCCACACCACAGAATCTACTTTGCCTACATATGAACATCTGC  
 ch1 TCTTAGATCTGCTCCCTCCACACCACAGAATCTACTTTGCCTACATATGAACATCTGC

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su_mut	TTTCCATTCTCCTCTTCTTGTCACTGCCATCTCTCAAATTACTCCACCTCT
su_Di Genova	TTTCCATTCTCCTCTTCTTGTCACTGCCATCTCTCAAATTACTCCACCTCT
ch2	TTTCCATTCTCCTCTTCTTGTCACTGCCATCTCTCAAATTACTCCACCTCT
VIT_218S0041G01880.2	TTTCCATTCTCCTCTTCTTGTCACTGCCATCTCTCAAATTACTCCACCTCT
su_wt	TTTCCATTCTCCTCTTCTTGTCACTGCCATCTCTCAAATTACTCCACCTCT
ch1	TTTCCATTCTCCTCTTCTTGTCACTGCCATCTCTCAAATTACTCCACCTCT

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su_mut	TACATTTCTTACCATCTTTAGATTCTTGCTGATTTACTCTCTTCTTGCAA
su_Di Genova	TACATTTCTTACCATCTTTAGATTCTTGCTGATTTACTCTCTTCTTGCAA
ch2	TACATTTCTTACCATCTTTAGATTCTTGCTGATTTACTCTCTTCTTGCAA
VIT_218S0041G01880.2	TACATTTCTTACCATCTTTAGATTCTTGCTGATTTACTCTCTTCTTGCAA
su_wt	TACATTTCTTACCATCTTTAGATTCTTGCTGATTTACTCTCTTCTTGCAA
ch1	TACATTTCTTACCATCTTTAGATTCTTGCTGATTTACTCTCTTCTTGCAA

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su_mut	CACTTACTCTTCAGTTCTGATTCTCTTGCCTCTTCATGCATTGTTCCATT <sub>CTT</sub>
su_Di Genova	CACTTACTCTTCAGTTCTGATTCTCTTGCCTCTTCATGCATTGTTCCATT <sub>CTT</sub>
ch2	CACTTACTCTTCAGTTCTGATTCTCTTGCCTCTTCATGCATTGTTCCATT <sub>CTT</sub>
VIT_218S0041G01880.2	CACTTACTCTTCAGTTCTGATTCTCTTGCCTCTTCATGCATTGTTCCATT <sub>CTT</sub>
su_wt	CACTTACTCTTCAGTTCTGATTCTCTTGCCTCTTCATGCATTGTTCCATT <sub>CTT</sub>
ch1	CACTTACTCTTCAGTTCTGATTCTCTTGCCTCTTCATGCATTGTTCCATT <sub>CTT</sub>

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su_mut	<b>TAATTAGTCATTCTTATTCTAAACTTCTTCCCTTTTCGTTATTTCAGAATGC</b>
su_Di Genova	<b>TAATTAGTCATTCTTATTCTAAACTTCTTCCCTTTTCGTTATTTCAGAATGC</b>
ch2	<b>TAATTAGTCATTCTTATTCTAAACTTCTTCCCTTTTCGTTATTTCAGAATGC</b>
VIT_218S0041G01880.2	<b>TAATTAGTCATTCTTATTCTAAACTTCTTCCCTTTTCGTTATTTCAGAATGC</b>
su_wt	<b>TAATTAGTCATTCTTATTCTAAACTTCTTCCCTTTTCGTTATTTCAGAATGC</b>
ch1	<b>TAATTAGTCATTCTTATTCTAAACTTCTTCCCTTTTCGTTATTTCAGAATGC</b>

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su_mut	AGTTGATTATTTCGCTTTTCATGTTAACAGTATTGTTGGTAGTTCTAG
su_Di Genova	AGTTGATTATTTCGCTTTTCATGTTAACAGTATTGTTGGTAGTTCTAG
ch2	AGTTGATTATTTCGCTTTTCATGTTAACAGTATTGTTGGTAGTTCTAG
VIT_218S0041G01880.2	AGTTGATTATTTCGCTTTTCATGTTAACAGTATTGTTGGTAGTTCTAG
su_wt	AGTTGATTATTTCGCTTTTCATGTTAACAGTATTGTTGGTAGTTCTAG
ch1	AGTTGATTATTTCGCTTTTCATGTTAACAGTATTGTTGGTAGTTCTAG

\*\*\*\*\*

su_mut	TTTATTTTCCATAAATTCTGTTCAAAAACCTTGAAGGGAAAAAGCCAGAATTTC
su_Di Genova	TTTATTTTCCATAAATTCTGTTCAAAAACCTTGAAGGGAAAAAGCCAGAATTTC
ch2	TTTATTTTCCATAAATTCTGTTCAAAAACCTTGAAGGGAAAAAGCCAGAATTTC
VIT_218S0041G01880.2	TTTATTTTCCATAAATTCTGTTCAAAAACCTTGAAGGGAAAAAGCCAGAATTTC
su_wt	TTTATTTTCCATAAATTCTGTTCAAAAACCTTGAAGGGAAAAAGCCAGAATTTC
ch1	TTTATTTTCCATAAATTCTGTTCAAAAACCTTGAAGGGAAAAAGCCAGAATTTC

\*\*\*\*\*

su_mut	TTTCCTCGTTCTGGCTTAAGCTCTCATCCATCTGGGTTATGGGAAATGTGTT
su_Di Genova	TTTCCTCGTTCTGGCTTAAGCTCTCATCCATCTGGGTTATGGGAAATGTGTT
ch2	TTTCCTCGTTCTGGCTTAAGCTCTCATCCATCTGGGTTATGGGAAATGTGTT
VIT_218S0041G01880.2	TTTCCTCGTTCTGGCTTAAGCTCTCATCCATCTGGGTTATGGGAAATGTGTT
su_wt	TTTCCTCGTTCTGGCTTAAGCTCTCATCCATCTGGGTTATGGGAAATGTGTT
ch1	TTTCCTCGTTCTGGCTTAAGCTCTCATCCATCTGGGTTATGGGAAATGTGTT

\*\*\*\*\*

su_mut	AAGGGTCATGGGGTTTGAGAAATGTG---GAGAGAGAGAGAGAGAGAGAGAGA
su_Di Genova	AAGGGTTATGGGGTTTGAGAAATGTG---GAGAGAGAGAGAGAGAGAGAGAGA
ch2	AAGGGTCATGGGGTTTGAGAAATGTG---GAGAGAGAGAGAGAGAGAGAGAGA
VIT_218S0041G01880.2	AAGGGTTATGGGGTTTGAGAAATGTG-----GAGAGAGAGA
su_wt	AAGGGTTATGGGGTTTGAGAAATGTG-----GAGAGAGAGA
ch1	AAGGGTTATGGGGTTTGAGAAATGTG-----GAGAGAGAGA

\*\*\*\*\*

su_mut	GAGAGAGATGTAGACATGCACCCACTTGTAGTAGTATTAGTAGTGGAGATAGATCCTG
su_Di Genova	GAGAGAGATGTAGACATGCACCCACTTGTAGTAGTATTAGTAGTGGAGATAGATCCTG
ch2	GAGAGAGATGTAGACATGCACCCACTTGTAGTAGTATTAGTAGTGGAGATAGATCCTG

VIT\_218S0041G01880.2 GAGAGAGATGTAGACATGCACCCACTTGTAGTAGTATTAGTAGTGGAGATAGATCCTG  
 su\_wt  
 ch1  
 \*\*\*\*  
 su\_mut GGTGATTTCAAAATGGTAGATCATGTTCTCTCTTGTCTCATCTTCATGTTC  
 su\_Di Genova GGTGATTTCAAAATGGTAGATCATGTTCTCTCTTGTCTCATCTTCATGTTC  
 ch2 GGTGATTTCAAAATGGTAGATCATGTTCTCTCTTGTCTCATCTTCATGTTC  
 VIT\_218S0041G01880.2 GGTGATTTCAAAATGGTAGATCATGTTCTCTCTTGTCTCATCTTCATGTTC  
 su\_wt GGTGATTTCAAAATGGTAGATCATGTTCTCTCTTGTCTCATCTTCATGTTC  
 ch1 GGTGATTTCAAAATGGTAGATCATGTTCTCTCTTGTCTCATCTTCATGTTC  
 \*\*\*\*  
 su\_mut TTTTCCCTCAGTGGCTTACAGATTTCTGTCCTCCAACTTTGGTTCCATCTTTT  
 su\_Di Genova TTTTCCCTCAGTGGCTTACAGATTTCTGTCCTCCAACTTTGGTTCCATCTTTT  
 ch2 TTTTCCCTCAGTGGCTTACAGATTTCTGTCCTCCAACTTTGGTTCCATCTTTT  
 VIT\_218S0041G01880.2 TTTTCCCTCAGTGGCTTACAGATTTCTGTCCTCCAACTTTGGTTCCATCTTTT  
 su\_wt TTTTCCCTCAGTGGCTTACAGATTTCTGTCCTCCAACTTTGGTTCCATCTTTT  
 ch1 TTTTCCCTCAGTGGCTTACAGATTTCTGTCCTCCAACTTTGGTTCCATCTTTT  
 \*\*\*\*  
 su\_mut CCAAGATCCTTATTTCTACATTATCATCATTATTTATTATACACAAGCCTCAC  
 su\_Di Genova CCAAGATCCTTATTTCTACATTATCATCATTATTTATTATACACAAGCCTCAC  
 ch2 CCAAGGTCTCTTATTTCTACATTATCATCATTATTTATTATACACAAGCCTCAC  
 VIT\_218S0041G01880.2 CCAAGATCCTTATTTCTACATTATCATCATTATTTATTATACACAAGCCTCAC  
 su\_wt CCAAGATCCTTATTTCTACATTATCATCATTATTTATTATACACAAGCCTCAC  
 ch1 CCAAGATCCTTATTTCTACATTATCATCATTATTTATTATACACAAGCCTCAC  
 \*\*\*\*  
 su\_mut CCTATTTCAAAACATCTAACCTTCTCATTTCTCAGTCTATCATCATTCTCAGA-----  
 su\_Di Genova CCTATTTCGAACACATCTAACCTTCTCATTTCTCAGTCTATCATCATTCTCAGA-----  
 ch2 CCTATTTCAAAACATCTAACCTTCTCATTTCTCAGTCTATCATCATTCTCAGA-----  
 VIT\_218S0041G01880.2 CCTATTTCGAACACATCTAACCTTCTCATTTCTCAGTCTATCATCATTCTCAGA-----  
 su\_wt CCTATTTCGAACACATCTAACCTTCTCATTTCTCAGTCTATCATCATTCTCAGA-----  
 ch1 CCTATTTCGAACACATCTAACCTTCTCATTTCTCAGTCTATCATCATTCTCAGA-----  
 \*\*\*\*  
 su\_mut --TCTCTCTCTCTCCTCTTACCCCTCTACCAAAAACACACATTTCGGTAGATCTC  
 su\_Di Genova CCTCTCTCTCTCCTCTTACCCCTCTACCAAAAACACACATTTCGGTAGATCTC  
 ch2 CCTCTCTCTCTCCTCTTACCCCTCTACCAAAAACACACATTTCGGTAGATCTC  
 VIT\_218S0041G01880.2 CCTCTCTCTCTCCTCTTACCCCTCTACCAAAAACACACATTTCGGTAGATCTC  
 su\_wt CCTCTCTCTCTCCTCTTACCCCTCTACCAAAAACACACATTTCGGTAGATCTC  
 ch1 CCTCTCTCTCTCCTCTTACCCCTCTACCAAAAACACACATTTCGGTAGATCTC  
 \*\*\*\*  
 su\_mut TCTCACAAATTACATGCATTATTACCCCTCATATGTCACTCATACTTCATT-----TT  
 su\_Di Genova TCTCACAAATTACATGCATTATTACCCCTCATATGTCACTCATACTTCATT-----TT  
 ch2 TCTCACAAATTACATGCATTATTACCCCTCATATGTCACTCATACTTCATT-----TT  
 VIT\_218S0041G01880.2 TCTCACAAATTACATGCATTATTACCCCTCATATGTCACTCATACTTCATT-----TT  
 su\_wt TCTCACAAATTACATGCATTATTACCCCTCATATGTCACTCATACTTCATT-----TT  
 ch1 TCTCACAAATTACATGCATTATTACCCCTCATATGTCACTCATACTTCATT-----TT  
 \*\*\*\*  
 su\_mut TTTTTTTAAAGCTGAACAGATCTCAAACCTTCTAGTATTGTAATCTTAG  
 su\_Di Genova TTTTTTTAAAGCTGAACAGATCTCAAACCTTCTAGTATTGTAATCTTAG  
 ch2 TTTTTTTAAAGCTGAACAGATCTCAAACCTTCTAGTATTGTAATCTTAG  
 VIT\_218S0041G01880.2 TTTTTTTAAAGCTGAACAGATCTCAAACCTTCTAGTATTGTAATCTTAG  
 su\_wt TTTTTTTAAAGCTGAACAGATCTCAAACCTTCTAGTATTGTAATCTTAG  
 ch1 TTTTTTTAAAGCTGAACAGATCTCAAACCTTCTAGTATTGTAATCTTAG  
 \*\*\*\*  
 su\_mut CAGTTTCATAAAGAGATGCTTGGTAATTCTAATATTTCACTGGGTGATATAATA  
 su\_Di Genova CAGTTTCATAAAGAGATGCTTGGTAAWTTCTAATATTTCACTGGGTGATATAATA  
 ch2 CAGTTTCATAAAGAGATGCTTGGTAATTCTAATATTTCACTGGGTGATATAATA  
 VIT\_218S0041G01880.2 CAGTTTCATAAAGAGATGCTTGGTAATTCTAATATTTCACTGGGTGATATAATA  
 su\_wt CAGTTTCATAAAGAGATGCTTGGTAATTCTAATATTTCACTGGGTGATATAATA  
 ch1 CAGTTTCATAAAGAGATGCTTGGTAATTCTAATATTTCACTGGGTGATATAATA  
 \*\*\*\*

su_mut	AAACAATGTATAGTACTACAAAATTGTTCTTATACCTAACGCCATTTCCTTGG
su_Di Genova	WAACAATGTATAGTACTACAAAATTGTTCTTATACCTAACGCCATTTCCTTGG
ch2	TAACAATGTATAGTACTACAAAATTGTTCTTATACCTAACGCCATTTCCTTGG
VIT_218S0041G01880.2	TAACAATGTATAGTACTACAAAATTGTTCTTATACCTAACGCCATTTCCTTGG
su_wt	TAACAATGTATAGTACTACAAAATTGTTCTTATACCTAACGCCATTTCCTTGG
ch1	TAACAATGTATAGTACTACAAAATTGTTCTTATACCTAACGCCATTTCCTTGG
	*****
su_mut	GTGCAATAACCTAACAG <b>TGTAGTGAA</b> CATGGGGAGAGGAAGATCGAGATCAAGAGGAT
su_Di Genova	GTGCAATAACCTAACAG <b>TGTAGTGAA</b> CATGGGGAGAGGAAGATCGAGATCAAGAGGAT
ch2	GTGCAATAACCTAACAG <b>TGTAGTGAA</b> CATGGGGAGAGGAAGATCGAGATCAAGAGGAT
VIT_218S0041G01880.2	GTGCAATAACCTAACAG <b>TGTAGTGAA</b> CATGGGGAGAGGAAGATCGAGATCAAGAGGAT
su_wt	GTGCAATAACCTAACAG <b>TGTAGTGAA</b> CATGGGGAGAGGAAGATCGAGATCAAGAGGAT
ch1	GTGCAATAACCTAACAG <b>TGTAGTGAA</b> CATGGGGAGAGGAAGATCGAGATCAAGAGGAT
	*****
su_mut	<b>CGAAAACACGACCAACC</b> GTCAGGTACATCTGCAAGCGAAGGAATGGGCTTTGAAGAA
su_Di Genova	<b>CGAAAACACGACCAACC</b> GTCAGGTACATCTGCAAGCGAAGGAATGGGCTTTGAAGAA
ch2	<b>CGAAAACACGACCAACC</b> GTCAGGTACATCTGCAAGCGAAGGAATGGGCTTTGAAGAA
VIT_218S0041G01880.2	<b>CGAAAACACGACCAACC</b> GTCAGGTACATCTGCAAGCGAAGGAATGGGCTTTGAAGAA
su_wt	<b>CGAAAACACGACCAACC</b> GTCAGGTACATCTGCAAGCGAAGGAATGGGCTTTGAAGAA
ch1	<b>CGAAAACACGACCAACC</b> GTCAGGTACATCTGCAAGCGAAGGAATGGGCTTTGAAGAA
	*****
su_mut	GGCTTATGAATTATCAGTGCTATGTGATGCAGAAGTTGCCCTCATCGTCTTCTCCAGCCG
su_Di Genova	GGCTTATGAATTATCAGTGCTATGTGATGCAGAAGTTGCCCTCATCGTCTTCTCCAGCCG
ch2	GGCTTATGAATTATCAGTGCTATGTGATGCAGAAGTTGCCCTCATCGTCTTCTCCAGCCG
VIT_218S0041G01880.2	GGCTTATGAATTATCAGTGCTATGTGATGCAGAAGTTGCCCTCATCGTCTTCTCCAGCCG
su_wt	GGCTTATGAATTATCAGTGCTATGTGATGCAGAAGTTGCCCTCATCGTCTTCTCCAGCCG
ch1	GGCTTATGAATTATCAGTGCTATGTGATGCAGAAGTTGCCCTCATCGTCTTCTCCAGCCG
	*****
su_mut	<b>CGGTCGAGTCTATGAGTACTCAAACAA</b> GAATAATTTCTCCACCATTCTCAACC
su_Di Genova	<b>CGGTCGAGTCTATGAGTACTCAAACAA</b> GAATAATTTCTCCACCATTCTCAACC
ch2	<b>CGGTCGAGTCTATGAGTACTCAAACAA</b> GAATAATTTCTCCACCATTCTCAACC
VIT_218S0041G01880.2	<b>CGGTCGAGTCTATGAGTACTCAAACAA</b> GAATAATTTCTCCACCATTCTCAACC
su_wt	<b>CGGTCGAGTCTATGAGTACTCAAACAA</b> GAATAATTTCTCCACCATTCTCAACC
ch1	<b>CGGTCGAGTCTATGAGTACTCAAACAA</b> GAATAATTTCTCCACCATTCTCAACC
	*****
su_mut	ATCTGCTGAATTTCATGTTCATCTTCTCCATTGGTGCATCATACGGCAATTAAT
su_Di Genova	ATCTGCTGAATTTCATGTTCATCTTCTCCATTGGTGCATCATACGGCAATTAAT
ch2	ATCTGCTGAATTTCATGTTCATCTTCTCCATTGGTGCATCATACGGCAATTAAT
VIT_218S0041G01880.2	ATCTGCTGAATTTCATGTTCATCTTCTCCATTGGTGCATCATACGGCAATTAAT
su_wt	ATCTGCTGAATTTCATGTTCATCTTCTCCATTGGTGCATCATACGGCAATTAAT
ch1	ATCTGCTGAATTTCATGTTCATCTTCTCCATTGGTGCATCATACGGCAATTAAT
	*****
su_mut	GGTTTATATTGATGAGATTAATATCATCAGAAGTTGCAGAACCTAATGTTATTAAGC
su_Di Genova	GGTTTATATTGATGAGATTAATATCATCAGAAGTTGCAGAACCTAATGTTATTAAGC
ch2	GGTTTATATTGATGAGATTAATATCATCAGAAGTTGCAGAACCTAATGTTATTAAGC
VIT_218S0041G01880.2	GGTTTATATTGATGAGATTAATATCATCAGAAGTTGCAGAACCTAATGTTATTAAGC
su_wt	GGTTTATATTGATGAGATTAATATCATCAGAAGTTGCAGAACCTAATGTTATTAAGC
ch1	GGTTTATATTGATGAGATTAATATCATCAGAAGTTGCAGAACCTAATGTTATTAAGC
	*****
su_mut	AAAG-AAAAAAAAGAACAGTGGAGGGAGAGTCAATAAATTGAAAATCTAACTC
su_Di Genova	AAAG-AAAAAAAAGAACAGTGGAGGGAGAGTCAATAAATTGAAAATCTAACTC
ch2	AAAG-AAAAAAAAGAACAGTGGAGGGAGAGTCAATAAATTGAAAATCTAACTC
VIT_218S0041G01880.2	AAAG-AAAAAAAAGAACAGTGGAGGGAGAGTCAATAAATTGAAAATCTAACTC
su_wt	AAAG-AAAAAAAAGAACAGTGGAGGGAGAGTCAATAAATTGAAAATCTAACTC
ch1	AAAG-AAAAAAAAGAACAGTGGAGGGAGAGTCAATAAATTGAAAATCTAACTC
	*****
su_mut	ACTGCAGATTATGATTTTACGAGGGGAGTCAGATTCTTTGCTTTATTTAGGAAGGG
su_Di Genova	ACTGCAGATTATGATTTTACGAGGGGAGTCAGATTCTTTGCTTTATTTAGGAAGGG
ch2	ACTGCAGATTATGATTTTACGAGGGGAGTCAGATTCTTTGCTTTATTTAGGAAGGG
VIT_218S0041G01880.2	ACTGCAGATTATGATTTTACGAGGGGAGTCAGATTCTTTGCTTTATTTAGGAAGGG
su_wt	ACTGCAGATTATGATTTTACGAGGGGAGTCAGATTCTTTGCTTTATTTAGGAAGGG
ch1	ACTGCAGATTATGATTTTACGAGGGGAGTCAGATTCTTTGCTTTATTTAGGAAGGG

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*****
su_mut ATTACATGGGTACCTGCTTGATATTATGAT-ATTTCTTCATCAAATTAATTAAT
su_Di Genova ATTACATGGGTACCTGCTTGATATTATGAT-ATTTCTTCATCAAATTAATTAAT
ch2 ATTACATGGGTACCTGCTTGATATTATGAT-ATTTCTTCATCAAATTAATTAAT
VIT_218S0041G01880.2 ATTACATGGGTACCTGCTTGATATTATGATAAATTCTTATCAAATTTA---AAT
su_wt ATTACATGGGTACCTGCTTGATATTATGATAAATTCTTATCAAATTTA---AAT
ch1 ATTACATGGGTACCTGCTTGATATTATGATAAATTCTTATCAAATTTA---AAT
*****
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su_mut GAAGGAAAATGCAGATAATATTCTGACATTCATCAGGCATCTGCTGATGAATCTGAGAA
su_Di Genova GAAGGAAAATGCAGATAATATTCTGACATTCATCAGGCATCTGCTGATGAATCTGAGAA
ch2 GAAGGAAAATGCAGATAATATTCTGACATTCATCAGGCATCTGCTGATGAATCTGAGAA
VIT_218S0041G01880.2 GAAGGAAAATGCAGATAATATTCTGACATTCATCAGGCATCTGCTGATGAATCTGAGAA
su_wt GAAGGAAAATGCAGATAATATTCTGACATTCATCAGGCATCTGCTGATGAATCTGAGAA
ch1 GAAGGAAAATGCAGATAATATTCTGACATTCATCAGGCATCTGCTGATGAATCTGAGAA
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su_mut AACAAATGTCTTCTCAAGATTTCACTAATTACATCTTGACTGATATAAGGAAAATAT
su_Di Genova AACAAATGTCTTCTCAAGATTTCACTAATTACATCTTGACTGATATAAGGAAAATAT
ch2 AACAAATGTCTTCTCATGATTTCACTAATTACATCTTGACTGATATAAGGAAAATAT
VIT_218S0041G01880.2 AACAAATTCTTCTCATGATTTCACTAATTACATCTTGACTGATATAAGGAAAATAT
su_wt AACAAATTCTTCTCATGATTTCACTAATTACATCTTGACTGATATAAGGAAAATAT
ch1 AACAAATTCTTCTCATGATTTCACTAATTACATCTTGACTGATATAAGGAAAATAT
*****
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su_mut GAGAAAGAACACTATACCTATAGTTAGAAACTCTTCAAGAGATTAACATCAGAGGGTT
su_Di Genova SAGAAAGAACACTATACCTATAGTTAGAAACTCTTCAAGAGATTAACATCAGAGGGTT
ch2 CAGAAAGAACACTTACCTATAGTTAGAAACTCTTCAAGAGATTAACATCAGAGGGTT
VIT_218S0041G01880.2 CAGAAAGAACACTATACCTATAGTTAGAAACTCTTCAAGAGATTAACATCAGAGGGTT
su_wt CAGAAAGAACACTATACCTATAGTTAGAAACTCTTCAAGAGATTAACATCAGAGGGTT
ch1 CAGAAAGAACACTATACCTATAGTTAGAAACTCTTCAAGAGATTAACATCAGAGGGTT
*****
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su_mut TTTTATTCATGTTAGTGCATTAAAA----AAAATTATAATGAAAAAATAAAAATA
su_Di Genova TTTTATTCATGTTAGTGCATTAAAAAAAATAAAAATTATAATGAAAAAATAAAAATA
ch2 TTTTATTCATGTTAGTGCATTAAAAAAAATAAAAATTATAATGAAAAAATAAAAATA
VIT_218S0041G01880.2 TTTTATTCATGTTAGTGCATTAAAAAAAATAAAAATTATAATGAAAAAATAAAAATA
su_wt TTTTATTCATGTTAGTGCATTAAAAAAAATAAAAATTATAATGAAAAAATAAAAATA
ch1 TTTTATTCATGTTAGTGCATTAAAAAAAATAAAAATTATAATGAAAAAATAAAAATA
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```

su_mut AAATA-GCAAAAAAACGAAAAAGTTGAAATCCAACATCAGTTACACTGGTAGTACTGA
su_Di Genova AAATAGGAAAAAAATCGAAAAGTTGAAATCCAACATCAGTTACACTGGTAGTACTGA
ch2 AAATAGGAAAAAAACGAAAAGTTGAAATCCAACATCAGTTACACTGGTAGTACTGA
VIT_218S0041G01880.2 AAATAGGAAAAAAATCGAAAAGTTGAAATCCAACATCAGTTACACTGGTAGTACTGA
su_wt AAATAGGAAAAAAATCGAAAAGTTGAAATCCAACATCAGTTACACTGGTAGTACTGA
ch1 AAATAGGAAAAAAATCGAAAAGTTGAAATCCAACATCAGTTACACTGGTAGTACTGA
*****
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su_mut TATGCATGCAAGGGAAGACAATCTAGGCAACAGCCAGTTAGGGTTCTGCTCTAGCTAG
su_Di Genova TATGCATGCAAGGGAAGACAATCTAGGCAACARCCAGTAGGGTTCTGCTCTAGCTAG
ch2 TATGCATGCAAGGGAAGACAATCTAGGCAACAGCCAGTTAGGGTTCTGCTCTAGCTAG
VIT_218S0041G01880.2 TATGCATGCAAGGGAAGACAATCTAGGCAACACAACAGTTAGGGTTCTGCTCTAGCTAG
su_wt TATGCATGCAAGGGAAGACAATCTAGGCAACACAACAGTTAGGGTTCTGCTCTAGCTAG
ch1 TATGCATGCAAGGGAAGACAATCTAGGCAACACAACAGTTAGGGTTCTGCTCTAGCTAG
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su_mut TTCTTCCCCTCTCCTTACTGTTCTTCAATAATATTAACATTGTAATCTGTGAGA
su_Di Genova TTCTTCCCCTCTCCTTACTGTTCTTCAATAATATTAACATTGTAATCTGTGAGA
ch2 TTCTTCCCCTCTCCTTACTGTTCTTCAATAATATTAACATTGTAATCTGTGAGA
VIT_218S0041G01880.2 TTCTTCCCCTCTCCTTACTGTTCTTCAATAATATTAACATTGTAATCTGTGAGA
su_wt TTCTTCCCCTCTCCTTACTGTTCTTCAATAATATTAACATTGTAATCTGTGAGA
ch1 TTCTTCCCCTCTCCTTACTGTTCTTCAATAATATTAACATTGTAATCTGTGAGA
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su_mut ATCTGTATTCCACTGTCCACAGTACAGTATTAAAGAAAAGGGTTATGCCCTTCCCT
su_Di Genova ATCTGTATTCCACTGTCCACAGTACAGTATTAAAGAAAAGGGTTATGCCCTTCCCT
ch2 ATCTGTATTCCACTGTCCACAGTACAGTATTAAAGAAAAGGGTTATGCCCTTCCCT

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VIT\_218S0041G01880.2 ATCTGTATTCCACTGTCCACAGTACAGTATTAAGAAAAGGGTTATGCCCTTCCCT  
 su\_wt ATCTGTATTCCACTGTCCACAGTACAGTATTAAGAAAAGGGTTATGCCCTTCCCT  
 ch1 ATCTGTATTCCACTGTCCACAGTACAGTATTAAGAAAAGGGTTATGCCCTTCCCT  
 \*\*\*\*

su\_mut TCCACTCTTGTCAAGTCTCAGTTCTCGCTCTCTCTTCCATTCCAGCTTGGGA  
 su\_Di Genova TCCACTCTTGTCAAGTCTCAGTTCTCGCTCTCTCTTCCATTCCAGCTTGGGA  
 ch2 TCCACTCTTGTCAAGTCTCAGTTCTCGCTCTCTCTTCCATTCCAGCTTGGGA  
 VIT\_218S0041G01880.2 TCCACTCTTGTCAAGTCTCAGTTCTCGCTCTCTCTTCCATTCCAGCTTGGGA  
 su\_wt TCCACTCTTGTCAAGTCTCAGTTCTCGCTCTCTCTTCCATTCCAGCTTGGGA  
 ch1 TCCACTCTTGTCAAGTCTCAGTTCTCGCTCTCTCTTCCATTCCAGCTTGGGA  
 \*\*\*\*

su\_mut GGCTTGGAGCCCAGTATCATAAATCCTCCCTGTTTCTCCATCTTTGTTTGGG  
 su\_Di Genova GGCTTGGAGCCCAGTATCATAAATCCTCCCTGTTTCTCCATCTTTGTTTGGG  
 ch2 GGCTTGGAGCCCAGTATCATAAATCCTCCCTGTTTCTCCATCTTTGTTTGGG  
 VIT\_218S0041G01880.2 GGCTTGGAGCCCAGTATCATAAATCCTCCCTGTTTCTCCATCTTTGTTTGGG  
 su\_wt GGCTTGGAGCCCAGTATCATAAATCCTCCCTGTTTCTCCATCTTTGTTTGGG  
 ch1 GGCTTGGAGCCCAGTATCATAAATCCTCCCTGTTTCTCCATCTTTGTTTGGG  
 \*\*\*\*

su\_mut TTTCTTCAGCCTAAAGCTGTGAACCTTCAATGGAGTCTTGGCCTCTCTCTT  
 su\_Di Genova TTTCTTCAGCCTAAAGCTGTGAACCTTCAATGGAGTCTTGGCCTCTCTCTT  
 ch2 TTTCTTCAGCCTAAAGCTGTGAACCTTCAATGGAGTCTTGGCCTCTCTCTT  
 VIT\_218S0041G01880.2 TTTCTTCAGCCTAAAGCTGTGAACCTTCAATGGAGTCTTGGCCTCTCTCTT  
 su\_wt TTTCTTCAGCCTAAAGCTGTGAACCTTCAATGGAGTCTTGGCCTCTCTCTT  
 ch1 TTTCTTCAGCCTAAAGCTGTGAACCTTCAATGGAGTCTTGGCCTCTCTCTT  
 \*\*\*\*

su\_mut CCCATTCTCATTTAAAGTGCAGTAAAGTGATCACCTTCACTGCTCTTGGTTTTCAC  
 su\_Di Genova CCCATTCTCATTTAAAGTGCAGTAAAGTGATCASCTTCACTGCTCTTGGTTTTCAC  
 ch2 CCCATTCTCATTTAAAGTGCAGTAAAGTGATCAGCTTCACTGCTCTTGGTTTTCAC  
 VIT\_218S0041G01880.2 CCCATTCTCATTTAAAGTGCAGTAAAGTGATCAGCTTCACTGCTCTTGGTTTTCAC  
 su\_wt CCCATTCTCATTTAAAGTGCAGTAAAGTGATCAGCTTCACTGCTCTTGGTTTTCAC  
 ch1 CCCATTCTCATTTAAAGTGCAGTAAAGTGATCAGCTTCACTGCTCTTGGTTTTCAC  
 \*\*\*\*

su\_mut TTGGTGTGGCAATTGTGGATATCAA--TCAGAAATGGGACGGGTACATCAGCACCC  
 su\_Di Genova TTGGTGTGGCAATTGTGGATATCAA--TCAGAAATGGGACGGGTACATCAGCACCC  
 ch2 TTGGTGTGGCAATTGTGGATATCAA--TCAGAAATGGGACGGGTACATCAGCACCC  
 VIT\_218S0041G01880.2 TTGGTGTGGCAATTGTGGATATCAAATCTCAGAAATGGGACGGGTACATCAGCACCC  
 su\_wt TTGGTGTGGCAATTGTGGATATCAAATCTCAGAAATGGGACGGGTACATCAGCACCC  
 ch1 TTGGTGTGGCAATTGTGGATATCAAATCTCAGAAATGGGACGGGTACATCAGCACCC  
 \*\*\*\*

su\_mut ATTACATTTGTGTGGTTGAATAAAATATTCATATCAATCATTGTTGCTCAA  
 su\_Di Genova ATTACATTTGTGTGGTTGAATAAAATATTCATATCAATCATTGTTGCTCAA  
 ch2 ATTACATTTGTGTGGTTGAATAAAATATTCATATCAATCATTGTTGCTCAA  
 VIT\_218S0041G01880.2 ATTACATTTGTGTGGTTGAATAAAATATTCATATCAATCATTGTTGCTCAA  
 su\_wt ATTACATTTGTGTGGTTGAATAAAATATTCATATCAATCATTGTTGCTCAA  
 ch1 ATTACATTTGTGTGGTTGAATAAAATATTCATATCAATCATTGTTGCTCAA  
 \*\*\*\*

su\_mut TGCCATCCAAGATTTCTTCACCTCATGTCATTTCCCTCCGATTCTCCCT  
 su\_Di Genova TGCCATCCAAGATTTCTTCACCTCATGTCATTTCCCTCCGATTCTCCCT  
 ch2 TGCCATCCAAGATTTCTTCACCTCATGTCATTTCCCTTGATTCTCCCT  
 VIT\_218S0041G01880.2 TGCCATCCAAGATTTCTTCACCTCATGTCATTTCCCTTGATTCTCCCT  
 su\_wt TGCCATCCAAGATTTCTTCACCTCATGTCATTTCCCTTGATTCTCCCT  
 ch1 TGCCATCCAAGATTTCTTCACCTCATGTCATTTCCCTTGATTCTCCCT  
 \*\*\*\*

su\_mut GTTCAAGGAAAATTGAAGATCTCATAGTTGAGATAGTATTTAAAGGACATTGAT  
 su\_Di Genova GTTCAAGGAAAATTGAAGATCTCATAGTTGAGATAGTATTTAAAGGACATTGAT  
 ch2 GTTCAAGGAAAATTGAAGATCTCATAGTTGAGATAGTATTTAAAGGACATTGAT  
 VIT\_218S0041G01880.2 GTTCAAGGAAAATTGAAGATCTCATAGTTGAGATAGTATTTAAAGGACATTGAT  
 su\_wt GTTCAAGGAAAATTGAAGATCTCATAGTTGAGATAGTATTTAAAGGACATTGAT  
 ch1 GTTCAAGGAAAATTGAAGATCTCATAGTTGAGATAGTATTTAAAGGACATTGAT  
 \*\*\*\*

su_mut	CTTACATGAGATTTACTTTGTTTCAAATTTAAATTATTTTACACTTTAA
su_Di Genova	CTTACATGAGATTTACTTTGTTTCAAATTTAAATTATTTTACACTTTAA
ch2	CTTACATGAGATTTACCTTTTCAAATTTAAATTATTTTACACTTTAA
VIT_218S0041G01880.2	CTTACATGAGATTTACCTTTTCAAATTTAAATTATTTTACACTTTAA
su_wt	CTTACATGAGATTTACCTTTTCAAATTTAAATTATTTTACACTTTAA
ch1	CTTACATGAGATTTACCTTTTCAAATTTAAATTATTTTACACTTTAA *****
su_mut	AAATACTTGTCCCCCTTAATCAATTAAACAAAAAATAAAATGAAAAAAAGAC
su_Di Genova	AAATACTTGTCCCCCTTAATCAATTAAACAAAAAATAAAATGAAAAAAAGAC
ch2	AAATACTTGTCCCCCTTAATCAATTAAACAAAAAATGA-AAAATG-AAAAAAAGAC
VIT_218S0041G01880.2	AAATACTTGTCCCCCTTAATCAATTAAACAAAAAATGA-AAAATG-AAAAAAAGAC
su_wt	AAATACTTGTCCCCCTTAATCAATTAAACAAAAAATGA-AAAATG-AAAAAAAGAC
ch1	AAATACTTGTCCCCCTTAATCAATTAAACAAAAAATGA-AAAATG-AAAAAAAGAC *****
su_mut	CAATTGAACTTTTTTTAATGTTGAGGGTGC-----TGGGGGTGGGGGG
su_Di Genova	CAATTGAACTTTTTTTAATGTTGAGGGTGC-----TGGGGGTGGGGGG
ch2	CAATTGAACTTTTTTTAATGTTGAGGGTGC-----TGGGGGTGGGGGTGGAGGG
VIT_218S0041G01880.2	CAATTGAACTTTTTTTAATGTTGAGGGTGCATGGGGGTGGGGGTGGAGGG
su_wt	CAATTGAACTTTTTTTAATGTTGAGGGTGC-----TGGGGGTGGGGGTGGAGGG
ch1	CAATTGAACTTTTTTTAATGTTGAGGGTGC-----TGGGGGTGGGGGTGGAGGG *****
su_mut	AGAAGTCTCCTTATTATTTAAATTAAATGCATTATTTAGTCAAATCCAATTAA
su_Di Genova	AGAAGTCTCCTTATTATTTAAATTAAATGCATTATTTAGTCAAATCCAATTWA
ch2	AGAAGTCTCCTTATTATTTAAATTAAATGCATTATTTAGTCAAATCCAATTATA
VIT_218S0041G01880.2	AGAAGTCTCCTTATTATTTAAATTAAATGCATTATTTAGTCAAATCCAATTATA
su_wt	AGAAGTCTCCTTATTATTTAAATTAAATGCATTATTTAGTCAAATCCAATTATA
ch1	AGAAGTCTCCTTATTATTTAAATTAAATGCATTATTTAGTCAAATCCAATTATA *****
su_mut	TTGCATAAAATTAAACATCATCTTGATCATCTTAAATCATATGGATTAAATCGTA
su_Di Genova	TTGCATAAAATTAAACATCATCTTGATCATCTTAAATCATATGGATTAAATCGTA
ch2	TTGCATAAAATTAAACATCATCTTGATCATCTTAAATCATATGGATTAAATCGTA
VIT_218S0041G01880.2	TTGCATAAAATTAAACATCATCTTGATCATCTTAAATCATATGGATTAAATCGTA
su_wt	TTGCATAAAATTAAACATCATCTTGATCATCTTAAATCATATGGATTAAATCGTA
ch1	TTGCATAAAATTAAACATCATCTTGATCATCTTAAATCATATGGATTAAATCGTA *****
su_mut	TTGGTGCCTTATTTCCTTATTCAAATAGAATAAAAATTATTTAAGATTCTTATTCTT
su_Di Genova	TTGGTGCCTTATTTCCTTATTCAAATAGAATAAAAATTATTTAAGATTCTTATTCTT
ch2	TTGGTGCCTTATTTCCTTATTCAAATAGAATAAAAATTATTTAAGATTCTTATTCTT
VIT_218S0041G01880.2	TTGGTGCCTTATTTCCTTATTCAAATAGAATAAAAATTATTTAAGATTCTTATTCTT
su_wt	TTGGTGCCTTATTTCCTTATTCAAATAGAATAAAAATTATTTAAGATTCTTATTCTT
ch1	TTGGTGCCTTATTTCCTTATTCAAATAGAATAAAAATTATTTAAGATTCTTATTCTT *****
su_mut	ATATATGAGAGAAAATAAAGAAATAATTGATAAAATATGTGAAAAAATTATTAAGT
su_Di Genova	ATATATGAGAGAAAATAAAGAAATAATTGATAAAATATGTGAAAAAATTATTAAGT
ch2	ATATATGAGAGAAAATAAAGAAATAATTGATAAAATATGTGAAAAAATTATTAAGT
VIT_218S0041G01880.2	ATATATGAGAGAAAATAAAGAAATAATTGATAAAATATGTGAAAAAATTATTAAGT
su_wt	ATATATGAGAGAAAATAAAGAAATAATTGATAAAATATGTGAAAAAATTATTAAGT
ch1	ATATATGAGAGAAAATAAAGAAATAATTGATAAAATATGTGAAAAAATTATTAAGT *****
su_mut	TCAAGCTTTTATTATTTATTTCATCATTTTTGTTCTTTTTC
su_Di Genova	TCAAGCTTTTATTATTTATTTCATCATTTTTGTTCTTTTTC
ch2	TCAAGCTTTTATTATTTATTTCATCA-TTTTTTTGTTCTTTTTC
VIT_218S0041G01880.2	TCAAGCTTTTATTATTTATTTCATCA-TTTTTTTGTTCTTTTTC
su_wt	TCAAGCTTTTATTATTTATTTCATCA-TTTTTTTGTTCTTTTTC
ch1	TCAAGCTTTTATTATTTATTTCATCA-TTTTTTTGTTCTTTTTC *****
su_mut	TCTCTCTAAATTTGAAGATTAAATGCAACCCCTACACTTACACCTAACAGAGAGTT
su_Di Genova	TCTCTCTAAATTTGAAGATTAAATGCAACCCCTACACTTACACCTAACAGAGAGTT
ch2	TCTCTCTAAATTTGAAGATTAAATGCAACCCCTACACTTACACCTAACAGAGAGTT
VIT_218S0041G01880.2	TCTCTCTAAATTTGAAGATTAAATGCAACCCCTACACTTACACCTAACAGAGAGTT
su_wt	TCTCTCTAAATTTGAAGATTAAATGCAACCCCTACACTTACACCTAACAGAGAGTT
ch1	TCTCTCTAAATTTGAAGATTAAATGCAACCCCTACACTTACACCTAACAGAGAGTT

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su_mut	GAGGAAAAGTAGGAGAAAAGAAAACAAGAAGAAAATGAAAGAAGAAAAGAAAAAT
su_Di Genova	GAGGAAAAGTAGGAGAAAAGAAAACAAGAAGAAAATGAAAGAAGAAAAGAAAAAT
ch2	GAGGAAAAGTAGGAGAAAAGAAAACAAGAAGAAAATGAAAGAAGAAAAGAAAAAT
VIT_218S0041G01880.2	GAGGAAAAGTAGGAGAAAAGAAAACAAGAAGAAAATGAAAGAAGAAAAGAAAAAT
su_wt	GAGGAAAAGTAGGAGAAAAGAAAACAAGAAGAAAATGAAAGAAGAAAAGAAAAAT
chl	GAGGAAAAGTAGGAGAAAAGAAAACAAGAAGAAAATGAAAGAAGAAAAGAAAAAT

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su_mut	AAAGAAATATGTTAAATT CAATAAATTGTTATTACTTATTTCTAAAATTATTTTAT
su_Di Genova	AAAGAAATATGTTAAATT CAATAAATTGTTATTACTTATTTCTAAAATTATTTTAT
ch2	AAAGAAATATGTTAAATT CAATAAATTGTTATTACTTATTTCTAAAATTATTTTAT
VIT_218S0041G01880.2	AAAGAAATATGTTAAATT CAATAAATTGTTATTACTTATTTCTAAAATTATTTTAT
su_wt	AAAGAAATATGTTAAATT CAATAAATTGTTATTACTTATTTCTAAAATTATTTTAT
chl	AAAGAAATATGTTAAATT CAATAAATTGTTATTACTTATTTCTAAAATTATTTTAT

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su_mut	TCTTTCTCTCATATACAACCAACAAAATTTCAAAATGTAAAATTGGATATAGTT
su_Di Genova	TCTTTCTCTCATATACAACCAACAAAATTTCAAAATGTAAAATTGGATATAGTT
ch2	TCTTTCTCTCATATACAACCAACAAAATTTCAAAATGTAAAATTGGATATAGTT
VIT_218S0041G01880.2	TCTTTCTCTCATATACAACCAACAAAATTTCAAAATGTAAAATTGGATATAGTT
su_wt	TCTTTCTCTCATATACAACCAACAAAATTTCAAAATGTAAAATTGGATATAGTT
chl	TCTTTCTCTCATATACAACCAACAAAATTTCAAAATGTAAAATTGGATATAGTT

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su_mut	TCATTAGATTGATTTTCATACTTTCCATAATAATCCAACAGATCAATTAAACC
su_Di Genova	TCATTAGATTGATTTTCATACTTTCCATAATAATCCAACAGATCAATTAAACC
ch2	TCATTAGATTGATTTTCATACTTTCCATAATAATCCAACAGATCAATTAAACC
VIT_218S0041G01880.2	TCATTAGATTGATTTTCATACTTTCCATAATAATCCAACAGATCAATTAAACT
su_wt	TCATTAGATTGATTTTCATACTTTCCATAATAATCCAACAGATCAATTAAACC
chl	TCATTAGATTGATTTTCATACTTTCCATAATAATCCAACAGATCAATTAAACC

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su_mut	GAAACAAAACCTACAATGACTTCATAATAACGGAAGTTAAAGGAACTAAGGATGAATTG
su_Di Genova	GAAACAAAACCTACAATGACTTCATAATAACGGAAGTTAAAGGAACTAAGGATGAATTG
ch2	GAAACAAAACCTACAATGACTTCATAATAACGGAAGTTAAAGGAACTAAGGATGAATTG
VIT_218S0041G01880.2	GAAACAAAACCTACAATGACTTCATAATAACGGAAGTTAAAGGAACTAAGGATGAATTG
su_wt	GAAACAAAACCTACAATGACTTCATAATAACGGAAGTTAAAGGAACTAAGGATGAATTG
chl	GAAACAAAACCTACAATGACTTCATAATAACGGAAGTTAAAGGAACTAAGGATGAATTG

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su_mut	AGATAGATTCGAGGATGGTGTCAAATGATAGGAGT CCAAATTGGAGGTAAGAACAAAC
su_Di Genova	AGATAGATTCGAGGATGGTGTCAAATGATAGGAGT CCAAATTGGAGGTAAGAACAAAC
ch2	AGATAGATTCGAGGATGGTGTCAAATGATAGGAGT CCAAATTGGAGGTAAGAACAAAC
VIT_218S0041G01880.2	AGATAGATTCGAGGATGGTGTCAAATGATAGGAGT CCAAATTGGAGGTAAGAACAAAC
su_wt	AGATAGATTCGAGGATGGTGTCAAATGATAGGAGT CCAAATTGGAGGTAAGAACAAAC
chl	AGATAGATTCGAGGATGGTGTCAAATGATAGGAGT CCAAATTGGAGGTAAGAACAAAC

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su_mut	TTAAATAAACTCTAAGATGATGCTCAAATGATGAATTCTTTTAAATATTGAGTAG
su_Di Genova	TTAAATAAACTCTAAGATGATGCTCAAATGATGAATTCTTTTAAATATTGAGTAG
ch2	TTAAATAAACTCTAAGACGATGCTCAAATGATGAATTCTTTTAAATATTGAGTAG
VIT_218S0041G01880.2	TTAAATAAACTCTAAGACGATGCTCAAATGATGAATTCTTTTAAATATTGAGTAG
su_wt	TTAAATAAACTCTAAGACGATGCTCAAATGATGAATTCTTTTAAATATTGAGTAG
chl	TTAAATAAACTCTAAGACGATGCTCAAATGATGAATTCTTTTAAATATTGAGTAG

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su_mut	ACATTGTCTTAAATTCTAACTACAAATAGATT CCAAATAAAATGATCATTATCCCT
su_Di Genova	GCATTGTCTTAAATTCTAACTACAAATAGATT CCAAATAAAATGATCATAATCCCT
ch2	GCATTGTCTTAAATTCTAACTACAAATAGATT CCAAATAAAATGATCATAATCCCT
VIT_218S0041G01880.2	GCATTGTCTTAAATTCTAACTACAAATAGATT CCAAATAAAATGATCATAATCCCT
su_wt	GCATTGTCTTAAATTCTAACTACAAATAGATT CCAAATAAAATGATCATAATCCCT
chl	GCATTGTCTTAAATTCTAACTACAAATAGATT CCAAATAAAATGATCATAATCCCT

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su_mut	TTCTACAGAACTTGTGATTGTTGATTGTTTTATGATATTTTATGTAACATGTTAA
su_Di Genova	TTCAACCGAACTTGTGCGTTGTTGATTGTTTTATGATATTTTATGTAACATGTTAA
ch2	TTCAACCGAACTTGTGCGTTGTTGATTGTTTTATGATATTTTATGTAACATGTTAA

VIT\_218S0041G01880.2 TTCAACCGAACTGTCGGTTGTATTGTTTATGATATTTATGTAACATGTTAA  
 su\_wt TTCAACCGAACTGTCGGTTGTATTGTTTATGATATTTATGTAACATGTTAA  
 ch1 TTCAACCGAACTGTCGGTTGTATTGTTTATGATATTTATGTAACATGTTAA  
 \*\*\* \* \*\*\*\*\*  
  
 su\_mut ATTATAAAAATAAATAAAGTTATAAGAAGAAGAAAAACCAATTCAATTCCAATAAA  
 su\_Di Genova ATTATAAAAATAAATAAAGTTATAAGAAGAAGAAAAACCAATTCAATTCCAATAAA  
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 su\_wt ATTATAAAAATAAATAAAGTTATAAGAAGAAGAAAAACCAATTCAATTCCAATAAA  
 ch1 ATTATAAAAATAAATAAAGTTATAAGAAGAAGAAAAACCAATTCAATTCCAATAAA  
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 su\_Di Genova AACCTTGAAATAATAAATGGTGGGATATGTGATAGAGGTGCAAAGTCTGGGTTGAT  
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 su\_wt AACCTTGAAATAATAAATGGTGGGATATGTGATAGAGGTGCAAAGTCTGGGTTCAAT  
 ch1 AACCTTGAAATAATAAATGGTGGGATATGTGATAGAGGTGCAAAGTCTGGGTTCAAT  
 \*\*\*\*\*  
  
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 su\_Di Genova TACCATCATTAAGAACATCCCTGGATTACTCGGAGTTGATTCTAATGGGTGCGTTGGAATC  
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 su\_Di Genova CCTAAGGTGTCGAAGCCATGGTGGATTGAAAGGCCCTATCACAGTGGGTTCCGGGT  
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 su\_mut TATCAAAAAAAACACACACACACAATTTCATAATAGAAGGTAGAAAAATTGAG  
 su\_Di Genova TATCAAAAAAAACACACACACACAATTTCATAATAGAAGGTAGAAAAAKTGAG  
 ch2 TAT---AAAAAACACACACACACACAATTTCATAATAGAAGGTAGAAAAAKTGAG  
 VIT\_218S0041G01880.2 TAT---AAAAAACACACACACACACAATTTCATAATAGAAGGTAGAAAAAKTGAG  
 su\_wt TAT---AAAAAACACACACACACACAATTTCATAATAGAAGGTAGAAAAAKTGAG  
 ch1 TAT---AAAAAACACACACACACACAATTTCATAATAGAAGGTAGAAAAAKTGAG  
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 su\_mut AATAAGGTAGAGAAGATGTTTTCC----TAGTACTCTAGGTTTGATAATAG  
 su\_Di Genova AATAAGGTAGAGAAGATGTTTTCTAGCTATAGTACTCTAGGTTTGATAATAG  
 ch2 AATAAGGTAGAGAAGATGTTTTCTAGCTATAGTACTCTAGGTTTGATAATAG  
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 su\_Di Genova ATTTGGATTTTCCCCAATAATTCAATTATAATTCAATTATAATAATATAAAAA  
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 ch1 ATTTGGATTTTCCCATAATTAAATTATAATTCAATTATAATAATATAAAAA  
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 su\_Di Genova TCAATGAGAAATCCATGGAAAACCAAATCAAATGTTGCAATATAGATCAAGATTAGCA  
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su\_mut TTTACTTATGCATGCTTAATTAGTTGACCTAAAGATCTTAGTACTGGTCC  
 su\_Di Genova TTTACTTATGCATGCTTAATTAGTTGACCTAAAGATCTTAGTACTGGTCC  
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 VIT\_218S0041G01880.2 TTTACTTATGCATGCTTAATTAGTTGACCTAAAGATCTTAGTACTGGTCC  
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 ch1 TTTACTTATGCATGCTTAATTAGTTGACCTAAAGATCTTAGTACTGGTCC  
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su\_mut CAATATAAAAATGAGAGCCTATTGGGATAACTTTAACCTGCATCTAGTAATTAGA  
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 ch1 CAATATAAAAATGAGAGCCTATTGGGATAACTTTAACACCTGCATCTAGTAATTAGA  
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su\_mut GATGAAACAGACATTATTGTATTATGTAATCTATTTACWCGCATCTAGTAATTAGA  
 su\_Di Genova GATGAAACAGACATTATTGTATTATGTAATCTATTTACWCGCATCTAGTAATTAGA  
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 VIT\_218S0041G01880.2 GATGAAACACATACATTATTGTATTATGTAATCTATTTACWCGCATCTAGTAATTAGA  
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su\_mut TTTAATAAGTAGTGAGGATGACTATGATATTCAAAAAAATTATTAATTAAAAAATT  
 su\_Di Genova TTTAATAATAGTGAGGATGACTATGATATTCAAAAAAATTATTAATTAAAAAATT  
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 su\_wt TTTAATAATAGTGAGGATGACTATGATATTCA-----AAAAAATT  
 ch1 TTTAATAATAGTGAGGATGACTATGATATTCA-----AAAAAATT  
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su\_mut ACTAACAAAATGTCGATAATCATTATACTACATGCCCTAAAATCACTT  
 su\_Di Genova ACTAACAAAATGTCGATAATCATTATACTACATGCCCTAAAATCACTT  
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 VIT\_218S0041G01880.2 ACTAACAAAATGTCGATAATCATTATACTACATGCCCTAAAATCACTT  
 su\_wt ACTAACAAAATGTCGATAATCATTATACTACATGCCCTAAAATCACTT  
 ch1 ACTAACAAAATGTCGATAATCATTATACTACATGCCCTAAAATCACTT  
 \*\*\*\*

su\_mut ATTTAAATAAGAAATTAGCTAGATTAATGAATTAAAAGAAA----AAAAATT  
 su\_Di Genova ATTTAAATAAGAAATTAGCTAGATTAATGAATTAAAAGAAA----AAAAATT  
 ch2 ATTTAAATAAGAAATTAGCTAGATTAATGAATTAAAAGAAA----AAAAATT  
 VIT\_218S0041G01880.2 ATTTAAATAAGAAATTAGCTAGATTAATGAATTAAAAGAAA----AAAAATT  
 su\_wt ATTTAAATAAGAAATTAGCTAGATTAATGAATTAAAAGAAA----AAAAATT  
 ch1 ATTTAAATAAGAAATTAGCTAGATTAATGAATTAAAAGAAA----AAAAATT  
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su\_mut GTACAAACCATCCAGTTAGTACTGGTCCGAACCCCTCTAGCTCAAAGGTCAATAGG  
 su\_Di Genova GTACAAACCATCCAGTTAGTACTGGTCCGAACCCCTCTAGCTCAAAGGTCAATAGG  
 ch2 GTACAAACCATCCAGTTAGTACTGGTCCGAACCCCTCTAGCTCAAAGGTCAATAGG  
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 su\_wt GTACAAACCATCCAGTTAGTACTGGTCCGAACCCCTCTAGCTCAAAGGTCAATAGG  
 ch1 GTACAAACCATCCAGTTAGTACTGGTCCGAACCCCTCTAGCTCAAAGGTCAATAGG  
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su\_mut ATTGGACTAGGATCCGGTCAATAGTCGATTGATTAAATCGATCAATT-GGTCCGATGTT  
 su\_Di Genova ATTGGACTAGGATCTGGTCAACAGTCGATTGATT----GATCAATTGGTCCGATCTT  
 ch2 ATTGGACTAGGATCTGGTCAACAGTCGATTGATT----GATCAATTGGTCCGATCTT  
 VIT\_218S0041G01880.2 ATTGGACTAGGATCTGGTCAACAGTCGATTGATT----GATCAATTGGTCCGATCTT  
 su\_wt ATTGGACTAGGATCTGGTCAACAGTCGATTGATT----GATCAATTGGTCCGATCTT  
 ch1 ATTGGACTAGGATCTGGTCAACAGTCGATTGATT----GATCAATTGGTCCGATCTT  
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su\_mut TAAACACATTACAATAACTTATCTGAGTTTGATGCATCTCATACATGCAAAGTA  
 su\_Di Genova TAAACACATTACAATAACTTATCTGAGTTTGATGCATCTCATACATGCAAAGCA  
 ch2 TAAACACATTACAATAACTTATCTGAGTTTGATGCATCTCATACATGCAAAGCA  
 VIT\_218S0041G01880.2 TAAACACATTACAATAACTTATCTGAGTTTGATGCATCTCATACATGCAAAGCA  
 su\_wt TAAACACATTACAATAACTTATCTGAGTTTGATGCATCTCATACATGCAAAGCA  
 ch1 TAAACACATTACAATAACTTATCTGAGTTTGATGCATCTCATACATGCAAAGCA

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su_mut	GTTATTGAAAGCCAATACATATTCATACAAAGTCCACACAAAGAACTCAAATAAAAAA
su_Di Genova	GTTATTGAAAGCCAATACATATTCATACAAAGTCCACACAAAGAACTCAAATAAAAAA
ch2	GTTATTGAAAGCCAATACATATTCATACAAAGTCCACACAAAGAACTCAAATAAAAAA
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su_wt	GTTATTGAAAGCCAATACATATTCATACAAAGTCCACACAAAGAACTCAAATAAAAAA
ch1	GTTATTGAAAGCCAATACATATTCATACAAAGTCCACACAAAGAACTCAAATAAAAAA
***** * ***** * ***** * ***** * *****	
su_mut	ATAAAAAAATCAGAGAATAAAATCCTCATGGTAAAGTTGCACCAATAAGACCTATACTGC
su_Di Genova	ATAAAAAAATCAGAGAATAAAATCCTCATGGTAAAGTTGCACCAATAAGACCTATACTGC
ch2	ATAAAAAAATCAGAGAATAAAATCCTCATGGTAAAGTTGCACCAATAAGACCTATACTGC
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su_wt	ATAAAAAAATCAGAGAATAAAATCCTCATGGTAAAGTTGCACCAATAAGACCTATACTGC
ch1	ATAAAAAAATCAGAGAATAAAATCCTCATGGTAAAGTTGCACCAATAAGACCTATACTGC
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su_mut	ATACAGTTGCAGAGTGGCAGTGCTCTCCATTGTTCTTCTTGCTTTCAGTGGTGCAA
su_Di Genova	ATACAGTTGCAGAGTGGCAGTGCTCTYCATGTTCTTCTTGCTTTCAGTGGTGCAA
ch2	ATACAGTTGCAGAGTGGCAGTGCTCTCATGTTCTTCTTGCTTTCAGTGGTGCAA
VIT_218S0041G01880.2	ATACAGTTGCAGAGTGGCAGTGCTCTCATGTTCTTCTTGCTTTCAGTGGTGCAA
su_wt	ATACAGTTGCAGAGTGGCAGTGCTCTCATGTTCTTCTTGCTTTCAGTGGTGCAA
ch1	ATACAGTTGCAGAGTGGCAGTGCTCTCATGTTCTTCTTGCTTTCAGTGGTGCAA
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su_mut	TCCATGAGAATCTGAACCCTCTGGCAGTGTCTGAAAAGGGTGGTCATAGCAGTACAACC
su_Di Genova	TCCATGAGAATCTGAACCCTCTGGCAGTGTCTGAAAAGGGTGGTCATAGCAGTACAACC
ch2	TCCATGAGAATCTGAACCCTCTGGCAGTGTCTGAAAAGGGGAGGTCAAGCAGTACAACC
VIT_218S0041G01880.2	TCCATGAGAATCTGAACCCTCTGGCAGTGTCTGAAAAGGGGAGGTCAAGCAGTACAACC
su_wt	TCCATGAGAATCTGAACCCTCTGGCAGTGTCTGAAAAGGGGAGGTCAAGCAGTACAACC
ch1	TCCATGAGAATCTGAACCCTCTGGCAGTGTCTGAAAAGGGGAGGTCAAGCAGTACAACC
***** * ***** * ***** * ***** * *****	
su_mut	AACCACTATTTCATCTTCCCTGTATCTCCCTGTTGCAAATCTCAGTTTCT
su_Di Genova	AACCACTATTTCATCTTCCCTGTATCTCCCTGTTGCAAATCTCAGTTTCT
ch2	AACCACTATTTCATCTTCCCTGTATCTCCCTGTTGCAAATCTCAGTTTCT
VIT_218S0041G01880.2	AACCACTATTTCATCTTCCCTGTATCTCCCTGTTGCAAATCTCAGTTTCT
su_wt	AACCACTATTTCATCTTCCCTGTATCTCCCTGTTGCAAATCTCAGTTTCT
ch1	AACCACTATTTCATCTTCCCTGTATCTCCCTGTTGCAAATCTCAGTTTCT
***** * ***** * ***** * ***** * *****	
su_mut	GGTTGTTCTTCCACTTTGGTTCCGCAAACCTTGAATGGAGTCTGGGTCTTTCT
su_Di Genova	GGTTGTTCTTCCACTTTGGTTCCGCAAACCTTGAATGGAGTCTGGGTCTTTCT
ch2	GGTTGTTCTTCCACTTTGGTTCCGCAAACCTTGAATGGAGTCTGGGTCTTTCT
VIT_218S0041G01880.2	GGTTGTTCTTCCACTTTGGTTCCGCAAACCTTGAATGGAGTCTGGGTCTTTCT
su_wt	GGTTGTTCTTCCACTTTGGTTCCGCAAACCTTGAATGGAGTCTGGGTCTTTCT
ch1	GGTTGTTCTTCCACTTTGGTTCCGCAAACCTTGAATGGAGTCTGGGTCTTTCT
***** * ***** * ***** * ***** * *****	
su_mut	CTTGCCTCTCAAAGCTGCAATCACTGCTTTTAGTGCTGGAGAGTAGAAACCAAGA
su_Di Genova	CTTGCCTCTCAAAGCTGCAATCACTGCTTTTAGTGCTGGAGAGTAGAAACCAAGA
ch2	CTTGCCTCTCAAAGCTGCAATCACTGCTTTTAGTGCTGGAGAGGAGAAACCAAGGA
VIT_218S0041G01880.2	CTTGCCTCTCAAAGCTGCAATCACTGCTTTTAGTGCTGGAGAGGAGAAACCAAGGA
su_wt	CTTGCCTCTCAAAGCTGCAATCACTGCTTTTAGTGCTGGAGAGGAGAAACCAAGGA
ch1	CTTGCCTCTCAAAGCTGCAATCACTGCTTTTAGTGCTGGAGAGGAGAAACCAAGGA
***** * ***** * ***** * ***** * *****	
su_mut	CAAGACTTTCAACTGCTATTCTCCATACAAACTCATGAAACTGATGAACAATTGAGCAG
su_Di Genova	CAAGACTTTCAACTGCTATTCTCCATACAAACTCATGAAACTGATGAACAATTGAGCAG
ch2	CAAGACTTTCAACTGCTATTCTCCATACAAACTCATGAAACTGATGAACAATTGAGCAG
VIT_218S0041G01880.2	CAAGACTTTCAACTGCTATTCTCCATACAAACTCATGAAACTGATGAACAATTGAGCAG
su_wt	CAAGACTTTCAACTGCTATTCTCCATACAAACTCATGAAACTGATGAACAATTGAGCAG
ch1	CAAGACTTTCAACTGCTATTCTCCATACAAACTCATGAAACTGATGAACAATTGAGCAG
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su_mut	TAGGGTCACTGTGCATACTGTATAGTGATTAACTGATTTAAT	CATTTTATGTCATAACTGTGG
su_Di Genova	TAGGGTCACTGTGYATACTGTATAGTGATTAACTGATTTAAT	CATTTTATGTCATAACTGTGG
ch2	TAGGGTCACTGTGTATACTGTATAGTGATTAACTGATTTAAT	CATTTTATGTCATAACTGTGG
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su_wt	TAGGGTCACTGTGTATACTGTATAGTGATTAACTGATTTAAT	CATTTTATGTCATAACTGTGG
chl	TAGGGTCACTGTGTATACTGTATAGTGATTAACTGATTTAAT	CATTTTATGTCATAACTGTGG
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su_mut	GTGTTTGTACTGTTACTTCATCTTCTCATATCAAGTCATAGTCCTTCACAAACTTG	
su_Di Genova	GTGTTTGTACTGTTACTTCATCTTCTCATATCAAGTCATAGTCCTTCACAAACTTG	
ch2	GTGTTTGTACTGTTACTTCATCTTCTCATATCAAGTCATAGTCCTTCACAAACTTG	
VIT_218S0041G01880.2	GTGTTTGTACTGTTACTTCATCTTCTCATATCAAGTCATAGTCCTTCACAAACTTG	
su_wt	GTGTTTGTACTGTTACTTCATCTTCTCATATCAAGTCATAGTCCTTCACAAACTTG	
chl	GTGTTTGTACTGTTACTTCATCTTCTCATATCAAGTCATAGTCCTTCACAAACTTG	
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su_mut	CTGTCATCTCCCATCATATATGGTTCCCTCCTTAGGGTTTGCTTCCGCCCTCACTTT	
su_Di Genova	CTGTCATCTCCCATCATATATGGTTCCCTCCTTAGGGTTTGCTTCCGCCCTCACTTT	
ch2	CTGTCATCTCCCATCATATATGGTTCCCTCCTTAGGGTTTGCTTCCGCCCTCACTTT	
VIT_218S0041G01880.2	CTGTCATCTCCCATCATATATGGTTCCCTCCTTAGGGTTTGCTTCCGCCCTCACTTT	
su_wt	CTGTCATCTCCCATCATATATGGTTCCCTCCTTAGGGTTTGCTTCCGCCCTCACTTT	
chl	CTGTCATCTCCCATCATATATGGTTCCCTCCTTAGGGTTTGCTTCCGCCCTCACTTT	
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su_mut	TGACTACTTTGGAGCAATTTCCTCTTGAAATTCTATCATATGTAATTTCATCCAT	
su_Di Genova	TGACTACTTTGGAGCAATTTCCTCTTGAAATTCTATCATATGTAATTTCATCCAT	
ch2	TGACTACTTTGGAGCAATTTCCTCTTGAAATTCTATGGTATGTAATTTCATCCAT	
VIT_218S0041G01880.2	TGACTACTTTGGAGCAATTTCCTCTTGAAATTCTATGGTATGTAATTTCATCCAT	
su_wt	TGACTACTTTGGAGCAATTTCCTCTTGAAATTCTATGGTATGTAATTTCATCCAT	
chl	TGACTACTTTGGAGCAATTTCCTCTTGAAATTCTATGGTATGTAATTTCATCCAT	
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su_mut	TTTGCAACAATTTTTAATTCTATTTTATATATTGGAAAACAGCATAAATCAA	
su_Di Genova	TTTGCAACAATTTTTAATTCTATTTTATATATTGGAAAACAGCATAAATCAA	
ch2	TTTGCAACAATTTTTAATTCTATTTTATATATTGGAAAACAGCATAAATCAA	
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su_wt	TTTGCAACAATTTTTAATTCTATTTTATATATTGGAAAACAGCATAAATCAA	
chl	TTTGCAACAATTTTTAATTCTATTTTATATATTGGAAAACAGCATAAATCAA	
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su_mut	CCATAGATAGGTACAAGAAGGCCAGCTCAGATAGTACAATGGAGGCTTACCATGGAGA	
su_Di Genova	CCATAGATAGGTACAAGAAGGCCAGCTCAGATAGTACAATGGAGGCTTACCATGGAGA	
ch2	CCATAGATAGGTACAAGAAGGCCAGCTCAGATAGTACAATGGAGGCTTACCATGGAGA	
VIT_218S0041G01880.2	CCATAGATAGGTACAAGAAGGCCAGCTCAGATAGTACAATGGAGGCTTACCATGGAGA	
su_wt	CCATAGATAGGTACAAGAAGGCCAGCTCAGATAGTACAATGGAGGCTTACCATGGAGA	
chl	CCATAGATAGGTACAAGAAGGCCAGCTCAGATAGTACAATGGAGGCTTACCATGGAGA	
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su_mut	TCAATGCCAAAGTAAGAAAACCTCCATTATGATAGTAAATGAATCAATCCAATCCTA	
su_Di Genova	TCAATGCCAAAGTAAGAAAACCTCCATTATGATAGTAAATGAATCAATCCAATCCTA	
ch2	TCAATGCCAAAGTAAGAAAACCTCCATTATGATAGTAAATGAATCAATCCAATCCTA	
VIT_218S0041G01880.2	TCAATGCCAAAGTAAGAAAACCTCCATTATGATAGTAAATGAATCAATCCAATCCTA	
su_wt	TCAATGCCAAAGTAAGAAAACCTCCATTATGATAGTAAATGAATCAATCCAATCCTA	
chl	TCAATGCCAAAGTAAGAAAACCTCCATTATGATAGTAAATGAATCAATCCAATCCTA	
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su_mut	TATGGTTTACTGATCAGATGTCTTATCCACCATGGCTGTTAGAACATCTCAATCCATTCT	
su_Di Genova	TATGGTTTACTGATCAGATGTCTTATCCACCATGGCTGTTAGAACATCTCAATCCATTCT	
ch2	TATGGTTTACTGATCAGATGTCTTATCCACCATGGCTGTTAGAACATCTCAATCCATTCT	
VIT_218S0041G01880.2	TATGGTTTACTGATCAGATGTCTTATCCACCATGGCTGTTAGAACATCTCAATCCATTCT	
su_wt	TATGGTTTACTGATCAGATGTCTTATCCACCATGGCTGTTAGAACATCTCAATCCATTCT	
chl	TATGGTTTACTGATCAGATGTCTTATCCACCATGGCTGTTAGAACATCTCAATCCATTCT	
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su_mut	GTTGATTGAAAAGTGCACATTTCATTAGGCTGGCCACAAATTAAACCCCTCATCATGC	
su_Di Genova	GTTGATTGAAAAGTGCACATTTCATTAGGCTGGCCACAAATTAAACCCCTCATCATGC	
ch2	GTTGATTGAAAAGTGCACATTTCATTAGGCTGGCCACAAATTAAACCCCTCATCATGC	
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su_wt	GTTGATTGAAAAGTGCACATTTCATTAGGCTGGCCACAAATTAAACCCCTCATCATGC	
chl	GTTGATTGAAAAGTGCACATTTCATTAGGCTGGCCACAAATTAAACCCCTCATCATGC	

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su_mut	TTAGCCATAAACAAATTGTTAAAATCATTATTCTACTTCTTTCTTTGGATTAT
su_Di Genova	TTAGCCATAAACAAATATGTTAAAATCATTATCCTACTTCTTTCTTTGGATTAT
ch2	TTAGCCATAAACAAATATGTTAAAATCATTATCCTACTTCTTTCTTTGGATTAT
VIT_218S0041G01880.2	TTAGCCATAAACAAATATGTTAAAATCATTATCCTACTTCTTTCTTTGGATTAT
su_wt	TTAGCCATAAACAAATATGTTAAAATCATTATCCTACTTCTTTCTTTGGATTAT
ch1	TTAGCCATAAACAAATATGTTAAAATCATTATCCTACTTCTTTCTTTGGATTAT
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su_mut	CCCATTGAACCTTCGAATTCTCGTGAACATAGTATTACCAGCAAGAACATCAGCAA
su_Di Genova	CCCATTGAACCTTCGAATTCTCGTGAACATAGTACTACCAGCAAGAACATCAGCAA
ch2	CCCATTGAACCTTCGAATTCTCGTGAACATAGTACTACCAGCAAGAACATCAGCAA
VIT_218S0041G01880.2	CCCATTGAACCTTCGAATTCTCGTGAACATAGTACTACCAGCAAGAACATCAGCAA
su_wt	CCCATTGAACCTTCGAATTCTCGTGAACATAGTACTACCAGCAAGAACATCAGCAA
ch1	CCCATTGAACCTTCGAATTCTCGTGAACATAGTACTACCAGCAAGAACATCAGCAA
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su_mut	GCTGCCAGCAAATACAGATGCTGCAGAATTCTAACAGGTACCCCTGATTCATATTCA
su_Di Genova	GCTGCCAGCAAATACAGATGCTGCAGAATTCTAACAGGTACCCCTGATTCATATTCA
ch2	GCTGCCAGCAAATACAGATGCTGCAGAATTCTAACAGGTACCCCTGATTCATATTCA
VIT_218S0041G01880.2	GCTGCCAGCAAATACAGATGCTGCAGAATTCTAACAGGTACCCCTGATTCATATTCA
su_wt	GCTGCCAGCAAATACAGATGCTGCAGAATTCTAACAGGTACCCCTGATTCATATTCA
ch1	GCTGCCAGCAAATACAGATGCTGCAGAATTCTAACAGGTACCCCTGATTCATATTCA
	*****
su_mut	TTTTCTCACATGAAATTGAGGTGATATATATATGCAATTGCATTTCCTCTGCTTG
su_Di Genova	TTTTCTCACATGCAGTTGAGGTGATATATATATGCAATTGCATTTCCTCTGCTTG
ch2	TTTTCTCACATGCAGTTGAGGTGATATATATATGCAATTGCATTTCCTCTGCTTG
VIT_218S0041G01880.2	TTTTCTCACATGCAGTTGAGGTGATATATATATGCAATTGCATTTCCTCTGCTTG
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ch1	TTTTCTCACATGCAGTTGAGGTGATATATATATGCAATTGCATTTCCTCTGCTTG
	*****
su_mut	TGTCTTAACAGGTTTGGCATCAGTCCCCATGAAAAATTCAAATATTACTAACG
su_Di Genova	TGTCTTAACAGGTTTGRCATCAGTCCCCATGAAAAATTCAAATATTACTAACG
ch2	TGTCTTAACAGGTTTGCACATCAGTCCCCATGAAAAATTCAAATATTACTAACG
VIT_218S0041G01880.2	TGTCTTAACAGGTTTGCACATCAGTCCCCATGAAAAATTCAAATATTACTAACG
su_wt	TGTCTTAACAGGTTTGCACATCAGTCCCCATGAAAAATTCAAATATTACTAACG
ch1	TGTCTTAACAGGTTTGCACATCAGTCCCCATGAAAAATTCAAATATTACTAACG
	*****
su_mut	ATCTTAATTAGGTATGTTAAGACTTAAGAGCAGGTATACTAACGACATTGTCTGTGTT
su_Di Genova	ATCTTAATTAGGTATGTTAAGACTTAAGATCAGGTGACTAACGACATTGTCTGTGTT
ch2	ATCTTAATTAGGTATGTTAAGACTTAAGATCAGGTGACTAACGACATTGTCTGTGTT
VIT_218S0041G01880.2	ATCTTAATTAGGTATGTTAAGACTTAAGATCAGGTGACTAACGACATTGTCTGTGTT
su_wt	ATCTTAATTAGGTATGTTAAGACTTAAGATCAGGTGACTAACGACATTGTCTGTGTT
ch1	ATCTTAATTAGGTATGTTAAGACTTAAGATCAGGTGACTAACGACATTGTCTGTGTT
	*****
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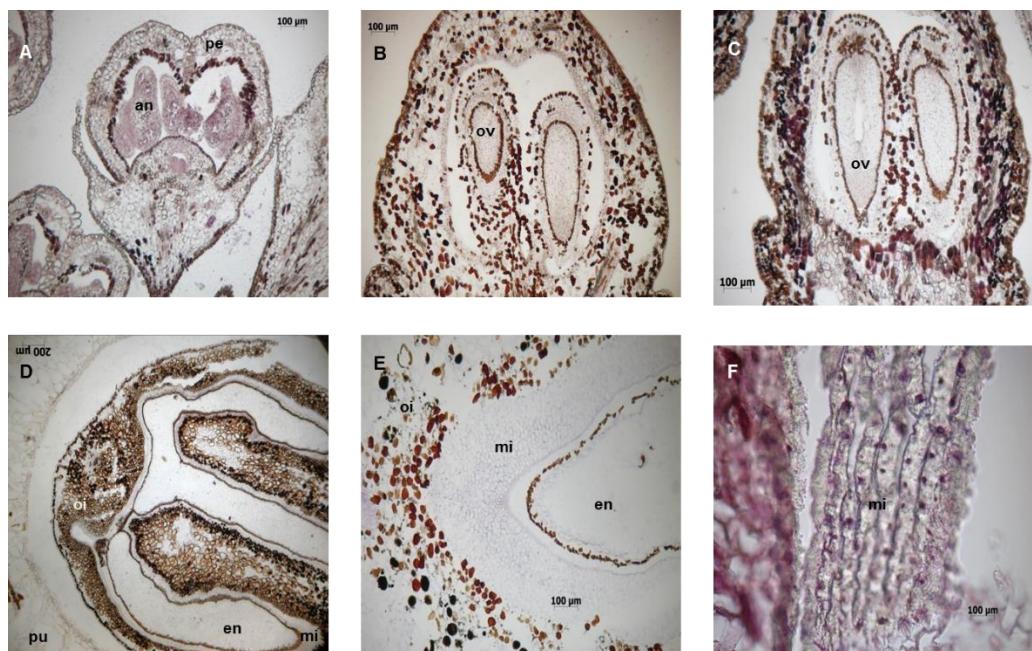
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su_wt	TTTTTTGATGTATGAAAACATCCATATCCATACTACTACTCTTCATTGAGCTCTGCTG
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su_wt	CTTCGTCTTTAGAATACTGCATAGTCATTGACTACCCTATATAATCTGCTGTGAATTA
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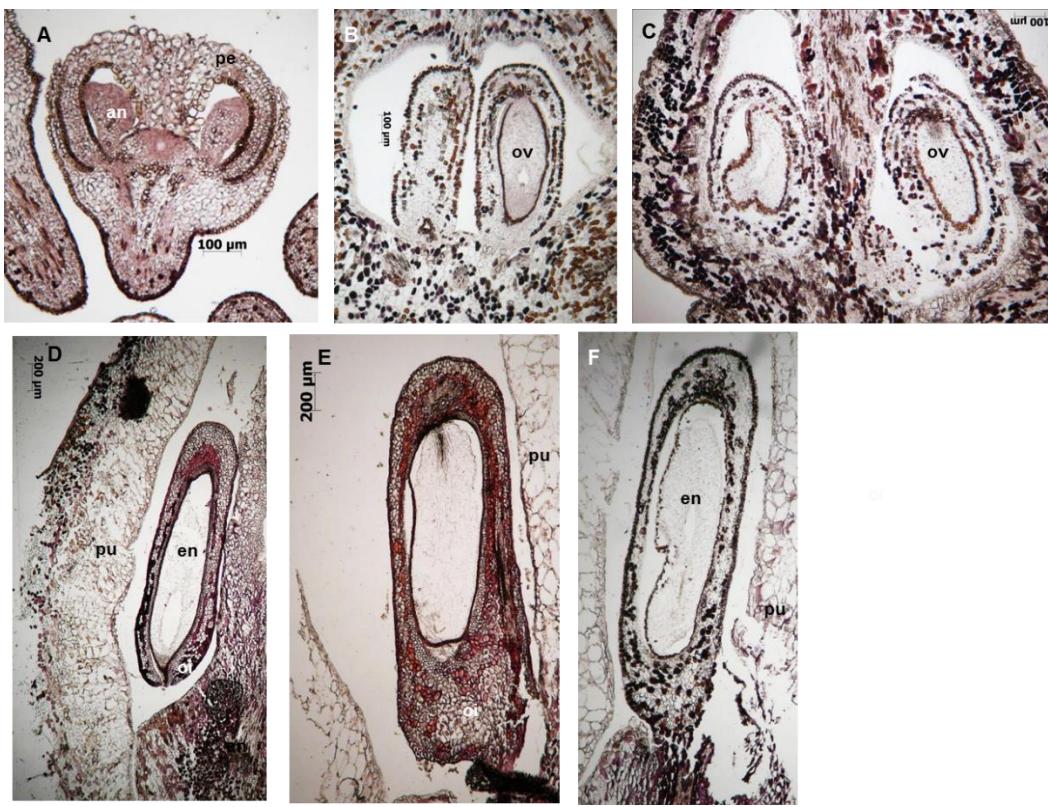
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*****
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**Supplementary Fig. 1.** Complete alignment of *VvAGL11* alleles. The sequences presented in the alignment are *VvAGL11* PN40024 (VIT\_218S0041G01880.2), *VvAGL11*

‘Chardonnay allele 1’ (CH1), *VvAGL11* ‘Chardonnay allele 2’ (CH2), *VvAGL11* ‘Sultanina’ mutant allele (*SU mut*), *VvAGL11* ‘Sultanina wt allele’ (*SU wt*) and the available sequence from ‘Sultanina’ by Di Genova (2014). Underlined sequence represents the SSR marker VMC7F2, blue sequence marks represent UTRs, red sequences comprise exons and green enhancement are indicating putative CArG-Box sequences.



**Supplementary Fig. 2.** *In situ* hybridization of *VvAGL11* sense probe (control) in ‘Chardonnay’. H1 flower stage (A), pre anthesis flower stage (B), fruit set flower stage (C), 2 weeks (D), 4 weeks (E) and 6 weeks (F) of fruit development. Anther (an), endosperm (en), medium integument (mi), outer integument (oi), ovule (ov), petal (pe), pulp (pu).



**Supplementary Fig. 3.** *In situ* hybridization of *VvAGL11* sense probe (control) in ‘Sultanina’. H1 flower stage (**A**), pre anthesis flower stage (**B**), fruit set flower stage (**C**), 2 weeks (**D**), 4 weeks (**E**) and 6 weeks (**F**) of fruit development. Anther (an), endosperm (en), medium integument (mi), outer integument (oi), ovule (ov), petal (pe), pulp (pu).

## 4 CONCLUSÕES

A utilização da técnica de sequenciamento alelo-específica mostrou-se eficiente na identificação das variações alélicas de *VvAGL11* em ‘Chardonnay’ e ‘Sultanina’. Foram identificados conjuntos de *SNPs* e *INDELS* que permitem diferenciar os alelos avaliados. Com isso, foi possível discernir dois alelos para ‘Chardonnay’ e dois para ‘Sultanina’. Um dos alelos de ‘Sultanina’, o alelo SU *mut*, é o único que possui mutações pontuais em seu RNA mensageiro, estas compostas por 10 *SNPs*, dois deles realizando modificações de aminoácidos na região codificadora. O sequenciamento por *RACE* permitiu a identificação dos *mRNAs* de *VvAGL11* de cada cultivar, mostrando que os quatro alelos são transcritos, porém ‘Chardonnay’ possui um alelo, CH1, com uma região codificante 60 nucleotídeos maior do que os outros alelos avaliados.

A quantificação de transcritos por meio da técnica de *RT-qPCR* permitiu a avaliação das isoformas de transcritos de *VvAGL11* previamente identificadas por meio de *RACE*. A expressão gênica relativa de cada isoforma foi avaliada em amostras de ambas as cultivares nos estádios fenológicos de flores e frutos. As isoformas de *VvAGL11* identificadas em ‘Sultanina’ são igualmente pouco expressas em todos os estádios analisados, enquanto que as isoformas de ‘Chardonnay’ também são pouco expressas em flores e polpa. Em contraste, os alelos de CH1 e CH2 possuem uma expressão 15-65 vezes maior em sementes em comparação com flores e frutos tanto de ‘Chardonnay’ como de ‘Sultanina’.

Para a investigação de diferenças morfológicas entre as sementes de ‘Chardonnay’ e o traço de semente de ‘Sultanina’, o emblocamento dos tecidos em resina plástica foi realizado. Isto permitiu a observação da provável perda de identidade da camada de integumento médio do traço de semente, o qual não se alongou nem se duplicou como

esperado em quatro semanas, mantendo sua forma original indiferenciada durante todo o desenvolvimento do fruto.

A caracterização da expressão tecido-específica de *VvAGL11* foi realizada com sucesso por meio da investigação do padrão de expressão espaço temporal do gene pela técnica de hibridização *in situ*. Ambas as cultivares e os estádios de desenvolvimento de flor e fruto utilizadas nos ensaios de *RT-qPCR* foram analisados. O acúmulo dos transcritos de *VvAGL11* foi detectado especificamente na camada de integumento médio da semente de ‘Chardonnay’, a qual é responsável pelo alongamento da casca em quatro semanas. Esta é justamente a camada que apresentou atraso de desenvolvimento na cultivar estenoespermocárpica Sultanina. Todavia, não foi detectada hibridização do gene na cultivar apirênica ‘Sultanina’, nem mesmo no traço de semente analisado. Os resultados são consistentes com a hipótese que a expressão de *VvAGL11* é necessária para a formação da semente e a análise dos dados permite sugerir que a diminuição de sua expressão pode estar relacionada à perda de identidade da camada de integumento médio da semente o que afeta seu tamanho final e leva ao fenótipo de apirenia.

## 5 PERSPECTIVAS

- \* Caracterizar a funcionalidade de *VvAGL11* por meio de complementação em modelo heterólogo (*A. thaliana*);
- \* Avaliar a ortologia de *VvAGL11* e *AtAGL11* por meio da complementação de mutante *stk* (*seedstick*);
- \* Caracterizar funcionalmente *VvAGL11* em videiras por meio da expressão do gene em cultivares apirênicas e do seu silenciamento em cultivares pirênicas;
- \* Caracterizar as interações da proteína *VvAGL11* com seus genes-alvo e os elementos *cis* (CArG-box) críticos às interações;
- \* Identificar as proteínas que constituem complexos quaternários de transcrição juntamente com *VvAGL11*;
- \* Identificar um haplótipo associado com potencial para seleção assistida da apirenia em videira;
- \* Desenvolver e testar um marcador definitivo para apirenia a partir de SNPs do alelo *VvAGL11* de Sultanina mutado, almejando a geração de patente sobre essas marcas;
- \* Avaliar cinco populações segregantes para o fenótipo de apirenia (1.000 indivíduos) com os haplótipos de marcadores microssatélites e com o marcador definitivo.

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## **7 CURRICULUM VITAE**

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### **FORMAÇÃO**

2013 – 2014

**Mestrado em Biologia Celular e Molecular,** PPGBCM, Universidade Federal do Rio Grande do Sul, UFRGS, Brasil. Estrutura do gene *VvAGL11* e análise da expressão durante a morfogênese da semente de videira. Orientador: Dr. Giancarlo Pasquali.

2009 – 2013

**Graduação em Ciências Biológicas.** Universidade do Vale do Rio dos Sinos, UNISINOS, São Leopoldo, RS, Brasil. Autoecologia De *Aulacoseira Granulata* Ehrenberg (Bacillariophyta) Em Ambientes Lóticos Subtropicais Com Diferentes Graus De Preservação. Dr<sup>a</sup> Luciane Oliveira Crossetti.

### **FORMAÇÃO COMPLEMENTAR**

2011 – 2013

Estágio de Iniciação Científica no **Laboratório de Genética Molecular Vegetal**. EMBRAPA Uva e Vinho, Bento Gonçalves/RS.

Orientação: Dr. Luís Fernando Revers.

Pesquisa inserida no projeto: “Uvas do Brasil: Programa de Melhoramento Genético”.

2010 – 2012

Bolsista de Iniciação Científica Petrobras no **Laboratório de Ecofisiologia e Cultura Vegetal**. UNISINOS, São Leopoldo/RS.

Orientação: Dr<sup>a</sup>. Luciane Oliveira Crossetti.

Atuando nos seguintes temas: Estudo das comunidades fitoplâncticas de diferentes arroios da Bacia do Rio dos Sinos através da avaliação da influência da composição de mata ciliar.

2010 – 2011

Estágio de Iniciação Científica no **Laboratório de Enoquímica**. EMBRAPA Uva e Vinho, Bento Gonçalves/RS.

Orientação: Dr. Celito Crivellaro Guerra.

Atuando nos seguintes temas: Acompanhamento e análises da maturação fenólica, com determinação de taninos e antocianinas presentes em cascas e sementes de diversas variedades de uva provenientes de regiões produtoras dos estados do Rio Grande do Sul e de Santa Catarina no projeto “Novas Regiões Vitivinícolas”.

## **PRÊMIOS E TÍTULOS**

**2013**

1º lugar da Pós-graduação com o trabalho 'Padrão de expressão espaço-temporal do gene *VvAGL1* em tecidos reprodutivos de videira por hibridização *in situ*', Embrapa Uva e Vinho.

**2013**

Proficiência em leitura da Língua Inglesa, Universidade Federal do Rio Grande do Sul.

**2012**

Laureada como Jovem Cientista em Fruticultura Brasileira, Sociedade Brasileira de Fruticultura.

**2012**

Distinção em Trabalho de Conclusão de Curso, Universidade do Vale do Rio dos Sinos.

## **2012**

Menção honrosa com o trabalho "Avaliação De Marcadores SSR Com Potencial Para Seleção Assistida De Videiras Apirênicas e Resistentes Ao Míldio" no 2º Prêmio Jovem Cientista em Fruticultura Brasileira, Sociedade Brasileira de Fruticultura.

## **2011**

Destaque em Mostra de Iniciação Científica, Universidade do Vale do Rio dos Sinos.

## **RESUMOS PUBLICADOS EM ANAIS DE CONGRESSOS**

- \* MALABARBA, J.; BUFFON, V.; PASQUALI, G.; REVERS, L. F. Estudo estrutural e funcional do gene *VvAGL11* e seu papel na morfogênese de sementes de *Vitis vinifera*. In: 12º Encontro de Iniciação Científica e 8º Encontro de Pós-Graduandos da Embrapa Uva e Vinho, Bento Gonçalves. 2014.
- \* MALABARBA, J.; BUFFON, V.; WAIRICH, A.; MARIATH, J.; GAETA, M.; DORNELAS, M. C.; REVERS, L. F.; PASQUALI, G. Padrão de Expressão Espaço-temporal do Gene *VvAGL11* em Tecidos Reprodutivos de Videira por Hibridização *In situ*. In: X Reunião Anual do Programa de Pós-Graduação em Biologia Celular e Molecular. Porto Alegre: UFRGS, 2013.
- \* MALABARBA, J.; BUFFON, V.; WAIRICH, A.; MARIATH, J.; GAETA, M.; DORNELAS, M. C.; REVERS, L. F. Gene expression analysis of *VvAGL11* in grapevine reproductive tissues by *In situ* hybridization. In: IV Simpósio Brasileiro de Genética Molecular de Plantas, Bento Gonçalves, RS. 2013.
- \* WAIRICH, A.; MALABARBA, J.; BUFFON, V.; REVERS, L. F. Evaluation of resistance to *Plasmopara viticola* in a self-fertilized segregating population from Villard Blanc (*Vitis* spp.). In: IV Simpósio Brasileiro de Genética Molecular de Plantas, Bento Gonçalves, RS. 2013.

- \* MALABARBA, J.; BUFFON, V.; WAIRICH, A.; MARIATH, J.; GAETA, M.; DORNELAS, M. C.; PASQUALI, G.; REVERS, L. F. Padrão de expressão espaço-temporal do gene *VvAGL11* em tecidos reprodutivos de videira por hibridização *In situ*. *In:* 11º Encontro de Iniciação Científica e 7º Encontro de Pós-Graduandos da Embrapa Uva e Vinho, Bento Gonçalves. 2013.
- \* WAIRICH, A.; MALABARBA, J.; BUFFON, V.; REVERS, L. F.; WELTER, L. J. Avaliação da resistência ao *Plasmopara viticola* em uma população segregante para a resistência auto-fertilizada de 'Villard Blanc' (*Vitis* spp.). *In:* 11º Encontro de Iniciação Científica e 5º Encontro de Pós-Graduandos da Embrapa Uva e Vinho, 2012, Bento Gonçalves. 2013.
- \* MALABARBA, J.; WAIRICH, A.; BUFFON, V.; CZERMAINSKI, A.; REVERS, L. F. Avaliação de marcadores SSR com potencial para seleção assistida de videiras apirênicas e resistentes ao míldio. *In:* XXII Congresso Brasileiro de Fruticultura, 2012, Bento Gonçalves. XXII CBF, 2012.
- \* WAIRICH, A.; MALABARBA, J.; BUFFON, V.; CZERMAINSKI, A.; REVERS, L. F. Análise do perfil transcripcional de genes candidatos associados à resistência ao míldio em videira, presentes no locus Rpv3. *In:* XXII Congresso Brasileiro de Fruticultura, 2012, Bento Gonçalves. XXII CBF, 2012.
- \* WAIRICH, A.; MALABARBA, J.; BUFFON, V. ; PORTO, D. D. ; REVERS, L. F. Análise do perfil transcripcional de genes candidatos associados à resistência ao míldio em videira, presentes no locus Rpv3. *In:* 10º Encontro de Iniciação Científica e 6º Encontro de Pós-Graduandos da Embrapa Uva e Vinho, Bento Gonçalves. 2012.
- \* MALABARBA, J.; WAIRICH, A.; BUFFON, V.; CZERMAINSKI, A.; REVERS, L. F. Avaliação de marcadores SSR com potencial para seleção assistida de videiras apirênicas e resistentes ao míldio. *In:* 10º Encontro de Iniciação Científica e 6º

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- \* MALABARBA, J.; BUFFON, V.; CZERMAINSKI, A.; REVERS, L. F. Caracterização do perfil transcricional de um gene associado à estenoespermocarpia em videira (*Vitis vinifera* L.). III Simpósio de Biodiversidade, UFSM, Santa Maria, RS. 2011.
- \* MALABARBA, J.; BUFFON, V.; CZERMAINSKI, A.; REVERS, L. F. Caracterização do perfil transcricional de genes associados à estenoespermocarpia em videira (*Vitis vinifera* L.). In: 9º Encontro de Iniciação Científica e 5º Encontro de Pós-Graduandos da Embrapa Uva e Vinho, Bento Gonçalves. 2011.

## PARTICIPAÇÃO EM CURSOS

- \* I Workshop Interno De Biologia Molecular De Plantas. Universidade Federal do Rio Grande do Sul. 2014.
- \* Theoretical and practical aspects of gene silencing in plants. Peter Waterhouse & Rogério Margis. PPGBCM, Universidade Federal do Rio Grande do Sul. 2013.
- \* Sequenciamento e Análise de Fragmentos através da Eletroforese Capilar na Plataforma 310. Embrapa Uva e Vinho, Bento Gonçalves. Life Technologies Brasil. 2013.
- \* REVERS, L.F.; PORTO, D.D.; FALAVIGNA, V.S.; BUFFON, V.; MALABARBA, J. Genética Molecular Vegetal: mapeamento genético, identificação de QTLs, genes candidatos e suas aplicações tecnológicas. 2012. (Curso de curta duração ministrado/Extensão).

- \* Manejo e uso de recursos genéticos de uva. Embrapa Uva e Vinho, Bento Gonçalves. 2011.
  
- \* PCR em Tempo Real - Princípios e Aplicações. Life Technologies Brasil. 2011.

**ATIVIDADES DESENVOLVIDAS NO PROGRAMA DE PÓS-GRADUAÇÃO EM  
BIOLOGIA CELULAR E MOLECULAR - UFRGS**

Período Letivo	Atividade de Ensino	Créditos	Conceito
2014/1	Atividade Didática	3	A
2014/1	Redação Científica Manuscrito	1	A
2014/1	Seminário do Centro de Biotecnologia	2	A
2014/1	Seminários de Dados Experimentais Apresentação	1	A
2014/1	Seminários de Dados Experimentais Frequência	1	A
2014/1	Tópicos Avançados	3	A
2013/2	Biologia Molecular	4	B
2013/2	Estrutura e Estratégias de Análise Genômica Vegetal	3	A
2013/1	Biologia Celular	3	A
2013/1	Curso- Theoretical and practical aspects of gene silencing in plants	2	A
2013/1	Fundamentos de Análise de Proteínas	2	A