

Modulation of the antioxidant/biofumigant properties of glucosinolates by regulation of *BoAOP2* expression in *B.oleracea*

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Name	Michele Bandecchi
Supervisors	Dr.Diana Zuluaga Dr.Mark Aarts
Laboratory of Genetics	

Modulation of the antioxidant/biofumigant properties of glucosinolates by regulation of *BoAOP2* expression in *B.oleracea*

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Name :	Michele Bandecchi
Registration Nr.	850730034050
University:	Wageningen Univeristy, Wageningen, The Netherlands
Supervisors/Examiners:	Dr. Diana Zuluaga Dr. Mark Aarts

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This work is firstly dedicated to my parents that always have been supporting the choices I made in my life. This work is also dedicated to all of those who never believed in me and in my field of study.

Everything that I am, everything that I now possess, is because of you all.

Questa tesi è innanzitutto dedicata ai miei genitori, che mi hanno sempre supportato nelle scelte fatte durante la mia vita. Questa tesi è anche dedicata a tutti coloro che non hanno mai creduto in me e nei miei studi.

Tutto quello che sono, tutto quello che adesso possiedo, è grazie a voi tutti.

Abstract

Glucosinolates are sulfur-containing compounds presents in several *Brassicaceae* vegetables, including *B.oleracea*. *AOP2* is a glucosinolate pathway gene that plays a central role in the conversion of methylsulfinylalkyl glucosinolates (glucoiberin and glucoraphanin) into alkenyl glucosinolates (siningrin and gluconapin). The functional or not-functional allele of *AOP2* directly influences the accumulation of substrates and products, with ecological and practical implications, such as plant-insect interactions, biofumigation and functional food applications. This project aims to study the genomic regulation of the *AOP2* gene involved in the glucosinolates pathway in *Brassica oleracea*, through the transformation of *B.oleracea* var. DHAG1012 with the *AOP2_2* gene from the wild-type Winspit 7. The GATEWAYTM Binary Destination Vectors pH7WG2 and pK7WG2D are the destination vectors used in this experiment, together with *Agrobacterium tumefaciens* strain AGL1 used as transformation vector. A copy number polymorphisms analysis of *AOP2* among four different genotype of *B.oleracea* (Winspit, Double Haploid AG1012 (DHAG), Savoy Cabbage var. Wintessa (Savoy), and Purple Sprouting Broccoli var. Sante (PSB) was investigating, using both PCR and qRT-PCR. Moreover the presence of conserved elements in the *MYB29* regulator factor among four different genotype was carried out. No regeneration of transformed *Brassica oleracea* DHAG1012 was obtained. Indeed most of the transformed cotyledons either grew in dimensions without develop any callus or develop tissue culture blackening. Concerning the isolation of *MYB29* regulator factor, the final cloning procedure failed and no results are available for this reasons. A 2-bp deletions was found in the *AOP2* sequence of Winspit, confirming the result of Li and Quiros (2003) and the functionality of *AOP2* in Winspit. The *AOP2* polymorphisms analysis among the four genotypes showed that Winspit has three copies of *AOP2*, PSB and DHAG1012 have two copies and Savoy has one copy. Dimension and number of all of these copies are in agreement with Gao *et al.* (2004) expect for Winspit, that resulted with an extra third copy of *AOP2*. Sequence analysis of key pathway genes, their promoter and/or regulator factors analysis, as well as over-expression transformation of these genes *in planta* are nowadays important and fundamental research methodologies. Therefore further research aimed to demonstrate the functionality of *AOP2* in *B.oleracea* is needed.

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1. Introduction

1.1 Brassicaceae and Brassica oleracea

The *Brassicaceae* family contains about 338 genera and more than 3,700 species (Hasan *et al.*, 2006; King, 2007; Warwick *et al.*, 2009) in which *Brassica* and *Arabidopsis* represent the two major genera. *Brassica* and *Arabidopsis* genera diverged approximately 14.5 to 20.4 million years ago (Yang *et al.*, 1999) and because of that they were subjected to comparative genomics studies. *Brassicaceae* is one of the 10 most economically important plant families because of their wide range of use (Warwick *et al.*, 2009). Examples of their extended use are the oilseed species *Brassica napus* (rapeseed), *B. rapa* (turnip rape), *B. juncea* (Indian mustard) and the cruciferous species such as *B. oleracea* (broccoli, cabbage, cauliflower and collard green) and *B. nigra* (mustard). Agricultural breeding and selection, as well as natural evolution have produced a large diversity on species in the *Brassicaceae* family. A large part of these species resulted from crosses between three major *Brassica* diploid plants: *B. rapa* (genome AA: $n=10$), *B. nigra* (genome BB: $n=8$) and *B. oleracea* (genome CC: $n=9$). These crosses resulted in economically important amphidiploid hybrids: *B. napus* (genome AACC: $n=19$) from the cross between *B. rapa* and *B. oleracea*, *B. carinata* (genome BBCC: $n=17$) from the cross between *B. nigra* and *B. oleracea* and *B. juncea* (genome AABB: $n=18$) from *B. rapa* x *B. nigra* (Hayward, 2012). *Brassica oleracea* represents the *Brassica* 'C' genome, with a genome size of 600-650 Mbp (King, 2007). *B. oleracea* has been divided into six different phenfigureotypes: cabbage, kales, inflorescence kales, branching bush kales, Chinese kales and kohlrabi (Rakow 2004; Warwick *et al.* 2009).

1.2 Glucosinolates: general aspects and biosynthesis

Glucosinolates (GSLs) are presents in several *Brassicaceae* vegetables, such as broccoli, cauliflower, cabbage, Chinese cabbage, turnip, and oilseed rape among others (Gao *et al.*, 2006). The specific presence of glucosinolate within the *Brassicaceae* family is related to two relevant applications among all these crops: cancer-prevention and biofumigation. Glucosinolate compounds have a common chemical structure consisting of (Figure 1):

1. β -D-glucopyranose residue;
2. Sulphur atom acts a linker;
3. (Z)-N-hydroximosulfate ester;
4. Variable R group derived from 8 amino acids (Ala, Leu, Ile, Met, Val, Phe, Tyr, Trp).

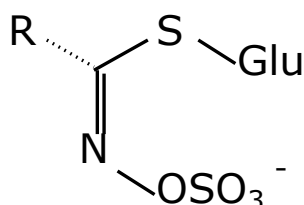


Figure 1 Glucosinolate chemical structure

Glucosinolates are therefore thioglucosides consisting of β -thioglucose, a sulfonated oxime and a variable side chain derived from an amino acid. Depending on the origin of amino acid side chain they can be classified as either aliphatic, aromatic or indole glucosinolates (Larson 1981; Mithen 2001).

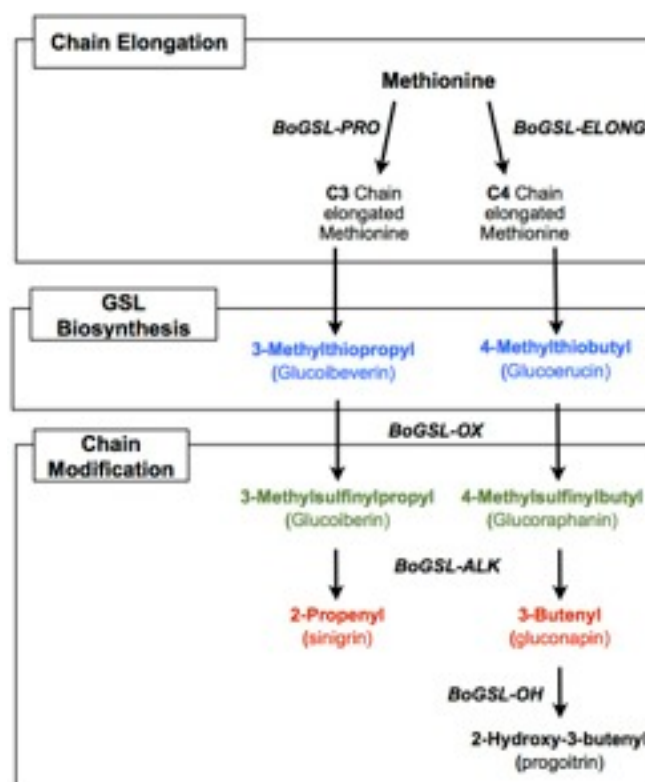


Figure 2. Model for aliphatic glucosinolate in *Brassica oleracea*, including the major genes (Li and Quiros, 2003). Products colored in blue are **Methylthioalkyl-GSL**. Products colored in green are **Methylsulfinylalkyl-GSL**. Products colored in red are **Alkenyl-GSL**.

Glucosinolates are synthesised in a three steps process (Figure 2) involving: (1) amino acid side chain elongation (mostly derived from methionine), (2) synthesis of the core glucosinolate, and (3) side chain modification. The primary (elongation) and secondary (oxidation, hydroxylation and esterification) modifications give rise to methylsulfinylalkyl-GSL (3-methylthiopropyl or 4-methylthiobutyl) (Schrantz *et al.*, 2012). In the aliphatic glucosinolates pathway (Figure 2) different genes are responsible for the expression of a series of enzymes that work in cascade. According to Li and Quiros (2002) the expression of one of the two genes in the chain elongation step, either *BoGSL-ELONG* or *BoGSL-PRO*, will respectively result in four-carbon (4C) or three-carbon (3C) GSL. In a plant with dominant *BoGSL-ELONG* allele, methionine will be chain-elongated to form glucoerucin (4-methylthiobutyl), whereas a dominant *BoGSL-PRO* allele will produce glucoibeverin (3-methylthiopropyl). At this point glucoerucin and glucoibeverin will be oxidated by *BoGSL-OX* to form gluconaphanin (4-methylsulphinybutyl) and glucoiberin (3-methylsulphinypropyl) respectively. In the last step *BoGSL-ALK* will use glucoiberin as substrate to form sinigrin (2-propenyl). In contrast, a plant with a strong 4C glucosinolate profile *BoGSL-ALK* will use gluconaphanin to produce gluconapin (3-butenyl) that will be converted by *BoGSL-OH* into progoitrin (2-hydroxy-3-butenyl). As the glucosinolate pathway elucidates, glucoiberin is the precursor of sinigrin and this conversion is undertaken by *BoGSL-ALK* (*AOP2*) gene product. These side-chain modifications of basic GSL have both biological and biochemical interest because they influence the direction of hydrolysis and therefore the resulting activity of reaction's product. Genetic studies in *Arabidopsis* have characterized a cluster of three genes that is encoding 2-oxoacid-dependent dioxygenase (*AOP*, previously called *GSL-ALK*) proteins and therefore responsible for the secondary oxidative transformation of methionine-derived GSL (oxidation of the side chain of GSL): *AOP1*, *AOP2* and *AOP3* (Hall *et al.*, 2001, Kliebenstein *et al.*, 2001). *AOP2* controls the conversion of methylsulfinylalkyl glucosinolates to alkenyl glucosinolates, *AOP3* converts methylsulfinylalkyl glucosinolates to their hydroxyalkyl form, whereas the function of *AOP1* is unknown (Kliebenstein *et al.*, 2001). *AOP2* is pointed out as one of the major genes that control the level of gluconaphanin in *Brassica* crops. The presence of a non-functional allele of *AOP2* in broccoli is responsible for the

accumulation of glucoraphanin (Li and Quiros, 2003)._Sulforaphane (SF), hydrolytic products of glucosinolates has been identified as powerful cancer-prevention agent. SF is a phytochemical that was isolated from broccoli in the early 1990s as an inducer of phase 2 enzymes, such as NAD(P)H:quinone oxidoreductase1 and glutathione S-transferase (Zhang *et al.*, 2007). SF is largely derived from glucoraphanin (β -thioglucoside N-hydroxysulfate) and the conversion is catalyzed by myrosinase (thioglucoside glucohydrolase) an enzyme that is physically separated from glucosinolates in normal plants (Zhang *et al.*, 2007). SF is a promising antiangiogenic drug that is able to inhibit the metastasis of cancer cells. No drugs presently available are able to inhibit the metastasis of cancer cells (Fimognari and Hrelia, 2007). However antimetastatic effects of sulforaphane were obtained in xenograft models, which cannot fully recapitulate the situation in humans.

1.3 Metabolic engineering of glucosinolates

Presently is available a body of literature with several examples of glucosinolate-engineering plants, aimed to improve favourable properties such as flavour taste, pathogens/insect resistance, biofumigation and anti-cancer substance accumulation (Mikkelsen *et al.*, 2000; Hansen *et al.*, 2001; Reintanz *et al.*, 2001; Celenza *et al.* 2005; Halkier and Gershenzon, 2006; Gigolashvili *et al.* 2007; Hirai *et al.*, 2007). Most of the studies concerning glucosinolates biosynthesis involve the model plant *Arabidopsis*, as it contains more than 20 different glucosinolates and belong to the *Brassicaceae* family. One of the first metabolic engineering experiment involving glucosinolates aimed to alter the expression of cytochromes P450 of the CYP79 enzyme family, responsible for the conversion of amino acids into aldoxime, during the first enzymatic reaction of GSL biosynthesis (Hansen *et al.*, 2001). Hansen *et al.*, (2001) demonstrated that over- or down-expression of *CYP79F1* transcripts in *A.thaliana* respectively enhance or decrease the level of aliphatic glucosinolate in the plant. They confirmed that *CYP79F1* in *A.thaliana* converted dihomomethionine and trihomomethionine into 5-methylthiopentanaloxime and 6-methylthiohexanaloxime respectively. Moreover, in plants with a low content of aliphatic glucosinolates there is accumulation of *CYP79F1* substrates (dihomomethionine and trihomomethionine), suggesting that this pathway is not subject to feed-back inhibition by products of the chain elongation step. Reintanz *et al.* (2001) also confirmed these results, showing that GSL that are formed from methionine are mediated by *CYP79F1* gene (improve with analysis of glucosinolate patterns). Celenza *et al.* (2005) tried a different approach in the metabolic engineering of glucosinolates, aimed to overexpress GSL transcript regulator. In fact, they demonstrated that an over-expression of *atr1D*, a MYB transcription factor of *A.thaliana*, activates the expression of genes implicated in the production of indolic glucosinolate (*CYP79B2*, *CYP79B3* and *CYP83B1*). Moreover, they proved a reduction of indolic glucosinolate synthesis genes expression in *atr1* loss-of-function mutant, and consequently a decline in the indolic glucosinolate level. *Arabidopsis* plants transformed with *35S::ATR1* produced a much higher level of transcripts than *atr1D*, but the level of indole glucosinolates is just two-fold higher compared with wild-type plant (Celenza *et al.* 2005). Mikkelsen *et al.* (2000) found that *35S::CYP79B2 Arabidopsis* plant produced five times more indole glucosinolates than the wild-type. In this sense, glucosinolate metabolic engineering with a specific gene conferring a gain-of-function is optimal than ectopic expression of gene regulators (Halkier and Gershenzon, 2006). Zuluaga *et al.* (2012, data not published) investigated the AGSL pathway of *B.oleracea* aiming to produce metabolic engineering plants with an increased content of sinigrin, engineering the regulator factor *MYB28* and *MYB29*.

MYB28 is a key positive regulator gene, that shown to regulate the aliphatic methionine-derived glucosinolate biosynthesis in *A. thaliana* (Gigolashvili *et al.* 2007). Hirai *et al.*, (2007) overexpressed *MYB28* in Arabidopsis cell suspension cultures and demonstrated that the expression of this transcription factor is correlated with a large production of GSLs. *MYB28* gene from *A.thaliana* was over-expressed in the *B.oleracea* Double Haploid AG1012 (DHAG1012) accession, resulting in the 2-fold up-regulation of all the target genes in *B.oleracea* (Transgenic plant number 4, TP4) except for *BoST5* (Zuluaga *et al.*, 2012 data not published). *BoPRO*, *BoCYP79F1*, *BoCYP83A1*, *BoC-S lyase* and *BoST5b* genes were up-regulated in three 35S::*AtMYB28* *B.oleracea* plants, whereas *BoST5c* was still not expressed. During the over expression experiment of *AtMYB28* the higher transcript level of the target genes were reach during analysis of the plant when they were in vitro. Unfortunately after the transfer from the in-vitro conditions to green-house, the level of transcript dramatically decreased in all the samples. Because of that, the HPLC analysis for the glucosinolate showed only a small significant difference ($p=0.0275$) between the TP4 and the wild type (WT2). *MYB29*, as well as *MYB28*, is a transcription factor that regulates positively the aliphatic GSL in the cell, but it might play an accessory role in the regulation (Hirai *et al.*, 2007). Zuluaga *et al.*, (2012, data not published) expressed *WinMYB29* from WinSpit 7 in *B.oleracea* 'DHAG1012' genotype. qRT-PCR analysis shows that *AOP2* and *MYB29(2)* (the second copy of *MYB29*) expression levels are higher in Winspit if compared with the other three genotypes, and these expression levels seem to be correlated. Because of that, *AOP2* expression can be hypothetically regulated by *MYB29* transcription factor (Zuluaga *et al.*, 2012 data not published). A transformation experiment was carried out in order to test this hypothesis. When *MYB29(2)* gene from Winspit was transformed into DHAG1012 plant a higher expression of the transcription factor was detected together with an over-expression of *AOP2* gene (data compared with non-transformed plant). This result confirmed that *AOP2* gene expression is controlled by *MYB29* transcription factor. After the transformation, qRT-PCR analysis of transcript level of genes resulted in the over-expression of all the genes involved glucosinolate biosynthesis pathway, with the exception of *BoC-S lyase*, *BoUGT74B1*, and *BoUGT74C1*. Concerning the aliphatic glucosinolate profile of 35S::*MYB29* plants, was reported a significant increase of glucoraphanin and a radical increase of glucoiberin (transgenic plant *MYB29-6* produce 8 times more glucoiberin than Empty vector-1 and about 3 times more than wild-type-1). The accumulation of methylsulfinylpropyl-GSL (glucoraphanin and glucoiberin in the case of 35S::*MYB29* transformants) can be explained by the presence of a null allele in the DHAG1012 genotype, that codifies for a non-functional copy of *AOP2*. This hypothesis has to be proven by the expression of a functional copy of *AOP2* in DHAG1012, that should convert methylsulfinylpropyl-GSL (glucoiberin) into the correspondent alkenyl-GSLs (sinigrin).

1.4 Characterization of *AOP2*

In *B.oleracea* two tandemly repeated copies of *AOP2* that contain 2 bp deletions at the third exon are present (Zang *et al.*, 2009). According to Zang *et al.*, (2009) this is the reason for the high accumulation of glucoraphanin in *B.oleracea* and therefore the glucoraphanin quantity both in *B.rapa* and *B.oleracea* 'could be elevated by inhibiting *AOP2* expression via antisense or RNA interference approaches.' Neal *et al.* (2010) identified three alleles of *AOP2* in five *Arabidopsis* accessions (Col, Cvi, Ler, Pi and St). The allele present in the Cvi and St accessions was named allele 1 (*AOP2-1*), the allele presents in the Pi accession which contains two polymorphisms (18 bp and 9 bp deletions) was named allele 2 (*AOP2-2*), and finally the allele present in the Col and Ler accessories that contains these two polymorphisms and an additional 5 bp frame shift deletion was

named *AOP2-3*. In *AOP2-2* the two deletions (18 and 9 bp) cause a difference of nine amino acids between the *AOP2-1* and *AOP2-2* encoded protein (432 and 423 amino acids, respectively). The 5 bp frame shift deletion in *AOP2-3* allele results in the production of a truncated protein of 172 amino acids. This latter result agreed with the non-functionality of *AOP2-3* allele in the Col accession.

Table 1. Schematic representation about 5' regulatory region analysis (according to Neal *et al.*, 2010)

Col(-) = Pi (+)

Ler (-) = St (-) ≈ Cvi (+)

= identical sequences; ≈ high similarity with only some minor differences

The *AOP2-2* allele transcribed in the Pi accession contains two in-frame 18 bp and 9 bp deletion polymorphisms, whereas the *AOP2-3* contains a 5 bp deletion that causes the introduction of a series of stop codons in the transcript. According to Neal *et al.* (2010) and Kliebenstein *et al.* (2001) both *AOP2-1* and *AOP2-2* are coding for functional protein products. Interestingly, both Cvi and St contain the *AOP2-1* allele but this is only expressed in Cvi (Table 1). The St *AOP2-1* does not contain the 5 bp deletion and therefore other regulation mechanisms behind this not expression to be investigated, because mRNA instability from shift mutation is not responsible for the lack of expression in St. Gao *et al.*, (2004) in his comparison study of a long genetic sequence between *B.oleracea* and *A.thaliana* found a rearrangement of the *AOP* gene family in broccoli and collard. In these two genotypes both *AOP2* and *AOP1* genes have been duplicated, while *AOP3* is absent. The arrangement of the *AOP* gene family found in the research is as follows: *Bo-AOP2.1* (*BoGSL-ALKa*) – pseudogene – *AOP2.2* (*BoGSL-ALKb*) – *AOP1.1* – *AOP1.2*. In *Brassica* both *AOP1* and *AOP2* have three exons as well as in *Arabidopsis*. The two copies of *AOP2* that are present in functional-*AOP2* plants, such as collard, do not have a 2-bp deletion in exon 2 that indeed characterized non-functional plants, such as broccoli (Li and Quiros, 2004). Neal *et al.*, (2010) analysed the regulatory regions upstream (2kb) the *AOP2* structural gene in four accessions of *Arabidopsis*, two expressing (Cvi/Pi) and two not-expressing (Ler/St) the gene. In this work they aim to identify any polymorphisms in the promoter regions that could explain the differences in *AOP2* gene expression. Northern blot analysis of *AOP2* transcript level in the leaves of Col, Cvi, Ler, Pi and St indicated that Pi and Cvi have high level of gene expression, whereas Ler, St and Col show low or no detectable expression. Surprisingly Col (*AOP2*-) and Pi (*AOP2*+) accessions have identical 5' regulatory region sequences; this result diverges with the difference in *AOP2* gene expression of the two accessions. Ler (*AOP2*-) and St (*AOP2*+) accessions were also found to have identical *AOP2* 5' regulatory region sequences and highly similar to Cvi regulatory sequence (Tab.1) (Neal *et al.*, 2005). Regulatory regions in expressing (Cvi/Pi) and non-expressing (Ler/St) accessions shown to have only small differences (single/double bp substitutions and insertion/deletion) and all clustered between nucleotides 1184 and 1232 upstream the ATG. The comparison of the 5' regulatory regions of the two expressing accession (Cvi and Pi) shows a 37bp deletion and 45bp and 3 bp insertions. However, these differences are not crucial for *AOP2* expression profiles of the two alleles. *Cis*-elements were not identified in this region and because of that reasons behind the difference in the leaf level of *AOP2* transcript are missing (Neal *et al.*, 2010). Therefore further investigation concerning regulatory *cis*-elements is needed. Wang *et al.* (2011) conducted a comparative analysis of the genome of *A. thaliana* and *Brassica rapa* and

identifying 52 homologous glucosinolate biosynthetic genes of *Arabidopsis*. Concerning the transcription factors, three copies of *MYB28* were identifying (Bra012961, Bra035929, Bra029311) with 79.1, 81.5, 72.5% identity respectively. *MYB29* was found to have two copies (Bra009245, Bra005949) with 92.1 and 75.7% of identity. Concerning the regulation of *AOP2* gene expression, no proof of transcriptional regulation was found by Neal *et al.* (2010), therefore the *AOP2* gene regulation can be a post-transcriptional (RNA interference) or a post-translation (dephosphorylation, glycosilation, acetylation etc.) event, or might occur during translation (presence of 5' cap or 3' poly adenosine monophosphate tail).

1.5 Project Background and Implications

Biofumigation is the practice in which harvested plant material is cut and incorporated in the soils in order to suppress pathogens, nematodes or weeds (Brown and Morra, 1995; Zasada and Ferris, 2004; Vaughn *et al.*, 2005). Crops from the *Brassicaceae* family are able to release, upon mechanics damage of cells, toxic compounds for soil organisms and therefore influence both the direct and indirect nutrients balance in the soil, the so-called 'detritus food web' (Zuluaga *et al.*, 2012, data not published). Zuluaga *et al.* (2012, data not published) used cruciferous plants able to affect the detritus food web (through GSLs degradation products) in order to develop a soil quality monitoring system. This cruciferous monitoring system is used as decision matrix in agriculture policy for assessing the impact of GM or not-GM crops on soil ecosystem processes. More precisely, the project aims to establish a decision matrix that can be used as tool for analysing the risk of GM crops on beneficial soil invertebrates (Collembolans, Isopods and Earthworms). A cross collaboration between the Department of Genetic of Wageningen University Research (WUR) and the Department of Animal ecology of the Free University of Amsterdam (VU) was established in order to meet this objective. In the specific case WUR has to produce an over-expressing GSLs metabolic engineering *B.oleracea* plant. This plant would be successively used by VU in order to determine direct and indirect effects of increased level of glucosinolates on four target soil invertebrates (in the specific case *Folsomia candida*, *Protaphorura armata*, *Porcellio scaber* and *Eisenia fetida*). Four *Brassica oleracea* accessions were used in this study and were either wild species Winspit, Double Haploid AG1012 (DHAG) or obtained from commercial varieties: Savoy Cabbage var. Wintessa (Savoy), and Purple Sprouting Broccoli var. Sante (PSB). AGDH1012 accession (*B.oleracea italica* x *B.oleracea albogabra*) was selected as the most efficient genotype for transformation with *A.tumefaciens*, based on the following parameters: *A.tumefaciens* susceptibility, shoot regeneration potential (expressed with the percentage of inoculated explants that successfully produced transgenic plants) and shoot regeneration. The last parameter was considered the most relevant. In fact the transformation success depended both on multiple shoot regeneration through swelling of callus and absence of tissue culture blackening (Sparrow *et al.* 2004). Moreover, this study aims to characterise the glucosinolate synthesis pathway in *B.oleracea* investigating the *AOP2* gene, and consequently provide a better understanding of the biochemical and molecular mechanisms behind glucosinolates synthesis. Elucidations on glucosinolates in *Brassica* have several practical implications. GSL knowledge can be used to establish a model system for understanding secondary plant products pathways. In this sense the impact of a modification in specific part of the biosynthetic pathway can be assess both at the whole metabolic processes level (accumulation, transport, turnover), and at the related compounds level (Selmar, 2010). A better knowledge about GSL will enable the modification of the quantity and of the distribution of glucosinolates in plants. Genetic engineering plants, with a modified glucosinolate profile can be indeed used for delineate the complex ecological interactions among herbivores, pathogenic microorganisms and plants. Moreover GSL-engineering plants will find interesting

opportunities in the functional food sector. Increase of beneficial glucosinolate product (e.g. glucoraphanin) in commercial *Brassicaceae* plants, as well as rapeseed with low content of anti-nutritional glucosinolates, will produce various commercially valuable products, both for human (e.g. chemoprotection SF-content products against cancer) and animal nutrition (e.g. low-GSL content rapeseed meal). In fact according to Hansen *et al.* (2001) the presence of 2-hydroxy-3-butenylglucosinolate in *B.napus* limits the use of rapeseed meal as animal feed. The bio-fumigation use of metabolic engineering plants, together with the functional food application, represents a major implication of this study. In fact, an optimal combination of myrosinase and glucosinolates in plants will make the pest-control in field less dependent by pesticides, with both ecological and human health benefits. According to Halkier and Gershenzon (2006) an optimal metabolic engineering strategy should aims for the combination of chain-elongation pathway genes, aldoxime-production *CYP79s* genes and key chain modification genes transformation, in order to obtain crops plants with higher preferred glucosinolate and not improper glucosinolates.

1.7 Goal of this project

This project aims to study the genomic regulation of the *AOP2* gene involved in the glucosinolates pathway in *Brassica oleracea*. Such information will clarify the genetic basis that control important agronomic traits such as nutritional properties, resistance to pests and to abiotic stress. Based on the hypothesis that a functional or not-functional *AOP2* gene in *B.oleracea* caused a production or non-production of the product sinigrin, and in order to characterise the modulation of glucosinolates pathway, the goals of this projects are 1) to transform *B.oleracea* var. DHAG1012 with *AOP2_2* gene from Winspit 7, in order to demonstrate that the over-expression of *AOP2_2* in *Brassica* enhances the production of Alkenyl-GSLs (sinigrin), 2) to investigate the presence of conserved elements, distal regulatory elements and corresponding *trans*-activating factors (transcriptional factors) among the four accessions for the promoter of *MYB29* regulator factor and, 3) to analyze copy number polymorphisms of *AOP2* using two primers from Gao *et al.*, (2004) and quantitative RT-PCR in order to assess a direct correlation between quantitative number of *AOP2* copies and expression of the gene product.

2. Materials and Methods

2.1 Over-expression transformation of *Brassica oleracea* DHAG1012

2.1.1 Construction of binary plant expression vectors

Agrobacterium tumefaciens strain AGL1 was used as transformation vector. The GATEWAY™ Binary Destination Vectors pH7WG2 and pK7WG2D were the destination vectors used in this experiment. These destination vectors contain the CaMV35S promoter followed by CmR-ccdB selection gene flanked by *attR1* and *attR2* recombination sites, that allow the recombination of the CmR-ccdB gene with the gene of interest contained in the entry clone (in this experiment pENTR/D-TOPO). Vector pH7WG2 contains the hygromycin phosphotransferase (*hpt*) gene selection marker, whereas pK7WG2D contains the kanamycin resistance gene for selection of transformants plant with kanamycin. The pENTR™ Directional TOPO® method (Invitrogen) was used for cloning *AOP2* gene inside pENTR/D-TOPO entry vector (2580 bp, Invitrogen). *AOP2* gene was amplified by PCR using a CACC sequence upstream of the forward primer. This 4-bases sequence allowed compulsory directional cloning of *AOP2*. The pENTR/D-TOPO entry vector has the entry site flanked by *attL1* and *attL2* sequences. After the GATEWAY™ LR clonase enzyme mix reaction the gene flanked by *attL1* and *attL2* in the entry vector is recombined in the destination vector where it replaces the CmR-ccdB selection gene.

2.1.2 PCR amplification of *AOP2*

To amplify *AOP2* gene, genomic DNA from Winspit accession number 7 was used as template. According to Zuluaga *et al.*, (2012, data not published) Winspit accession 7 is the accession that among others showed a higher content of total aliphatic GSL (from 2 to 4 times more than the other accessions) and higher content of the specific aliphatic GSL sinigrin as well as gluconapin. In the present work the *AOP2_2* gene sequence (second copy of *AOP2*) was isolated from the wild species Winspit 7 and transformed into *B.oleracea* var. DHAG1012. Specific primers were designed to amplify *AOP2_2* with a CACC sequence upstream the forward primer. Amplification was carried out in a 30µL total volume reaction containing 3µL of Pfu 10x buffer, 1,8µL of dNTP, 1,5µL of each primer (10 µmol), 3 µL of cDNA (1ng/µL) template, 0,6µL of Pfu DNA polymerase and demineralised water (DW) to the total volume. The primers used were *AOP2* D-TOPO FW and *AOP2* D-TOPO RV (Table 11). This amplification mixture was used to amplify *AOP2* for cloning as well as confirming the transformed colonies. The PCR preceded with 95°C for 2 min, followed by 35 cycles of 95°C for 0,5 min, 75°C for 0,5 min, 72°C for 3 min and with a final extension of 72°C for 10 min. The PCR products were checked by 1% agarose gel electrophoresis for 1,5 h at 90V. cDNA was obtained from Dr.Diana Zuluaga, Department of Genetics, WUR, and where either obtained from different RNA's accession mix or from one accession. The samples used were Winspit 7 (RNA from accession number 7), Savoy 2 (mix RNA from accession number 2, 5, 14), PSB 3 (mix RNA from accession number 3, 11,14) and DHAG1012 1 (mix RNA from accession number 1, 2, 3). The expected band (Winspit band of around 1300 bp, Figure 10) was cut and extracted with QIAquick gel extraction kit (QIAGEN). To check the orientation, primer odd12 reverse was used together with *AOP2* D-TOPO forward. Primer odd12 attached in the first intron of *AOP2*, sequencing the sequence upstream the insert. PCR products from these amplifications were aligned using Lasergene® SeqMan™ program and compared with *GS-ALK* gene from *Brassica rapa* (EF611253.1) and the sequence of the destination vector (pH7WG2 and pK7WG2D).

A second PCR amplification of *AOP2* was repeated and run in agarose 1% for 1,5 hours at 90V (Figure 10). The expected band of ~1300bp for all the four genotypes was excised and isolated from the gel, as well as the second band (~900bp) of Winspit. These bands were extracted with QIAquick gel extraction kit (QIAGEN) and sequenced with Eurofins MWG Operon (Ebersberg, Germany). The sequences were analyzed using DNASTar Lasergene Seqman program. Thereafter, the contig sequences were compared with the on-line program CLUSTAL 2.1. multiple sequence alignment (<http://www.ebi.ac.uk/Tools/clustalw2/index.html>). The PCR reaction, the extraction and the sequencing was repeated four times for each PCR fragments obtained.

2.1.3 Transformation of *E.coli* (heat shock) and *Agrobacterium tumefaciens* (electroporation)

E.coli DH5 α competent cells (from Dr.Diana Zuluaga, Department of Genetics, WUR, The Netherlands) were mixed with *AOP2* DNA on ice for 30 minutes. In this phase was used a 2:1 molar ratio of PCR product:TOPO[®] vector (total amount: 5ng of DNA). The mixture was heat-shocked for 50 seconds in a water bath at exactly 42°C and immediately return in ice for 2 minutes. The cells were mixed with 950 μ L of S.O.C. medium and incubated without antibiotics for 1.5 hours at 37°C with shaking (150-200 rpm). The mixture was afterwards spread on Lysogeny Broth (LB) agar plate with kanamycin selection (50mg/L) and growth overnight at 37°C. A total of 24 colonies were picked (20 colonies of *E.coli* with pENTR/D-TOPO and 4 'vector only' control colonies) and cultured in 3 mL LB containing 50mg/L kanamycin at 37°C overnight in a shaker (300rpm). The plasmid DNA was extracted using QIAprep Spin Miniprep Kit (QIAGEN) and check by double restriction enzyme digestion with *Ascl* and *NotI* (Fermentas), followed by the analyze of their sequence (using 'Greenomics' company, Wageningen, The Netherlands). The sequences were aligned with *GSL-ALK* gene of *B.rapa* (NCBI ID: EF611253.1) and pENTR/D-TOPO sequence to confirm the presence of *AOP2*. The colonies with a positive alignment were used for the GATEWAY[™] LR clonase enzyme mix reaction, obtaining as products two expression vector: pH7WG2::*AOP2* and pK7WG2D::*AOP2* (Figures 3 and 4, for sequences see Appendix II). These expression vectors were transformed in *E.coli* DH5 α competent cells according to the method in the protocol (GATEWAY[™] LR clonase enzyme, Invitrogen), and the resulted transformed bacteria were plated on LB plates containing spectinomycin (100mg/L). 20 colonies were picked up and cultured in 3 mL LB containing 100mg/L of spectinomycin at 37°C overnight in a shaker (300rpm). The plasmid DNA was extracted using QIAprep Spin Miniprep Kit (QIAGEN) and first analyzed with the restriction enzyme *NcoI* (Fermentas), and second with sequencing (using 'Greenomics' company, Wageningen, The Netherlands). Finally, the two desired constructs were transferred into *Agrobacterium tumefaciens* by electroporation (electroporation protocol by Dr. Mark Aarts, Department of Genetics, WUR, The Netherlands), and then plated in LB-agar plates with spectinomycin (100mg/L) and carbenicillin (100mg/L) at 28°C for 48 hours. Positive colonies of *Agrobacterium* were picked up (5 colonies containing pH7WG2::*AOP2* and 5 colonies containing pK7WG2D::*AOP2*) and cultured in 3 mL LB medium containing spectinomycin (100mg/L) and carbenicillin (100mg/L) at 28°C for 48 hours in shaker (300rpm). The plasmid DNA was extracted using QIAprep Spin Miniprep Kit (QIAGEN) and check by sequencing (using 'Greenomics' company, Wageningen, The Netherlands). For sequencing were used primer odd12 reverse and *AOP2* D-TOPO forward, in order to check the right orientation of *AOP2* in the expression vectors.

2.1.4 Plant Materials

B.oleracea cv. 'DHAG1012' seeds were used for transformation. Seeds were sterilized with surface-sterilization in 100% ethanol for 2 minutes, and in 100% sodium hypochlorite for 15 min. Then, the seeds were rinsed three time for 10 minutes with distilled sterile water, sown on germination medium at a density of 20 seed per 90-mm Petri dish, sealed with Micropore tape, and transferred to a 10°C cold room overnight. The seeds were transferred for 4 days to a 23°C culture room under 16-h day length of 70 $\mu\text{mol}/\text{m}^2/\text{s}$ (Sparrow *et al.*, 2006).

2.1.4 Agrobacterium preparation

A single colony of *A.tumefaciens* strain AGL1 containing pH7WG2::AOP2 as well as pK7WG2D::AOP2 was cultured in 3 ml LB medium containing spectinomycin (100mg/L) and carbenicillin (100mg/L) at 28°C for 48 hours in a shaker (300rpm). A 50 μL aliquot of the culture liquid was transferred to 10 μL new LB medium containing no selection and grow overnight at 28°C in a shaker (300rpm). Overnight suspension of $\text{OD}_{650} = 0.07\text{-}0.1$ were used for inoculation. Dilution were made with LB medium and the following formula: $1/\text{Abs} \cdot 300 = \text{X}\mu\text{L}$ (where Abs is the measurement of absorbance that is obtain from the overnight culture, and X the μL of overnight liquid culture to use). The inoculation is done with 5 mL of LB medium and overnight liquid culture (5000 μL LB medium minus X μL obtained from the previous formula).

2.1.5 Explant Isolation, inoculation, cocultivation and selection

The explant isolation, inoculation, and cocultivation as well as the selection part was done according to Sparrow *et al.*, (2006) section 3.3 and 3.4. Concerning the selection medium, this experiment deviate from Sparrow *et al.* (2006) protocol, because two types of selection medium plates with antibiotics were made. For selection of *A.tumefaciens* pK7WG2D::AOP2 were add to the medium 15 mg/L of kanamycin and 500mg/L of ticarcillin. On the other hand, for selection of *A.tumefaciens* pH7WG2::AOP2 were add to the medium 10 mg/L of hygromycin (according to Kong *et al.* 2009) and 500mg/L of ticarcillin. In this work two transformation experiments were undertaken, both resulted with no transformants plants. In the first transformation were used a total of 540 cotyledons (excluded the control plates), 310 inoculated with *A.tumefaciens* pK7WG2D::AOP2 and 230 inoculated with *A.tumefaciens* pH7WG2::AOP2. In the second transformation a total of 960 cotyledons were used (included the control plates), in which 890 cotyledons were inoculated with just *A.tumefaciens* pK7WG2D::AOP2. This experiment included two kind of controls: one plate contains cotyledons inoculated with *Agrobacterium* (500mg/L of ticarcillin; no kanamycin) and one with cotyledons not inoculated but transferred directly to co-cultivation media (no ticarcillin; no kanamycin). Both experiments were ended after three to five weeks from inoculation, due to no emergence of green shots and severe blackening.

2.2 AOP2 polymorphism analysis among different *B.oleracea* genotypes

Gao *et al.* (2004) in their work designed two primers (odd12, odd48) based on the putative promoter region and exon 1 of each *BoGSL-ALK* duplicate in order to confirm the two copies of the *BoGSL-ALK* gene. In this work primers odd12 and odd48 (Table 8) were used in order to analyse the polymorphism on AOP2 copy number in the four genotype of *B.oleracea*.

Genomic DNA was extracted from the four genotype (Winspit, PSB, DHAG1012 and Savoy) according to Zuluaga *et al.*, (2012, data not published). Amplification was carried out in a 30 μL total volume reaction containing 3 μL of Pfu 10x buffer, 1,8 μL of dNTP, 1,5 μL of each primer (10 μmol), 3 μL of DNA (2ng/ μL) template, 0,6 μL of Pfu DNA polymerase and DW to the total volume. The PCR

preceded with 95°C for 2 min, followed by 30 cycles of 95°C for 0,5 min, 50°C for 0,5 min, 72°C for 3 min and with a final extension of 72°C for 10 min. The PCR products were checked by 1,5% agarose gel electrophoresis for 6 h at 70V (Figure 11). Bands were cut and extracted with QIAquick gel extraction kit (QIAGEN) and sequenced with Eurofins MWG Operon (Ebersberg, Germany). The sequences were analyzed using DNASTar Lasergene Seqman program. Thereafter, the contig sequences were compared with the on-line program CLUSTAL 2.1. multiple sequence alignment (<http://www.ebi.ac.uk/Tools/clustalw2/index.html>). The PCR, the extraction and the sequencing was repeated three times for each PCR fragments obtained.

2.3 Estimation of AOP2 gene copy number among different *B.oleracea* genotypes by using qRT-PCR on genomic DNA

To estimate the copy number of AOP2 among different *B.oleracea* genotypes, genomic DNA was isolated from leaf tissue for a quantitative gene expression analysis according to the methodology of Zuluaga *et al.* (2012, data not published). The samples used for the DNA extraction were stored at -80°C by Dr. Diana Zuluaga, Department of Genetics, WUR. For each genotype, three different accessions were used and three replica of the qRT-PCR were performed: Savoy (accession number: 3, 6, 13), PSB (accession number: 2, 4, 8), DHAG1012 (accession number: 9, 11, 12), Winspit (accession number 8, 9, 14) and *B.rapa* (DNA from recombinant inbred line number: 97V, 64V, 113V, from Hedayat Bagheri, Department of Genetics, WUR, The Netherlands). According to Livak and Schmittgen (2001) one internal control gene was selected as reference gene: *RPS2* (virus resistance gene) which is a single copy in *Brassica oleracea* and *A.thaliana* according to Quiros *et al.* (2001).

Before starting the experiment, a preliminary trial was carried out with two purposes: validate *RPS2* as reference gene (check that is not affected by experimental treatment) and assess the right set of primers to be used with qRT-PCR. Zuluaga *et al.* (2012, data not published) developed three sets of primers for qRT-PCR analysis, one for every copy of AOP2 (Tab.10). In this initial trial were used only one genomic DNA from Savoy (accession nr. 2), PSB (accession nr. 3), DHAG1012 (accession nr. 1), Winspit (accession nr. 7) and *B.rapa* (accession nr. 95V). All the quantitative RT-PCR analyses were performed in a 10µL volume real time PCR of 5µL iQTM SYBR® Green Supermix (Bio-Rad), 0.2 µL of each primers (10 µmol), 2µL of DNA (10ng/µL) and 2.6 µL of DW in CFX96™ Real-Time system machine (BIO-RAD). C_T values from samples of qRT-PCR were analyzed according to Livak and Schmittgen (2001) ΔC_T method. After the preliminary trial, the experiment with three accessions for each genotypes was run. Each DNA sample (4 genotypes times 3 accessions each equal to 12 samples) was analysed three times in separate reactions.

2.4 MYB29 promoter analysis

All the four genotypes of *B.oleracea* previously discusses were included in this MYB29 promoter analysis (Winspit, DHAG1012, PSB, Savoy), that aims to gather knowledge about the regulation of AOP2 by the transcription factor MYB29. In order to isolate the MYB29 promoter, the APAGene™ GOLD Genome Walking kit (BIOS&T) was used. This kit enables the isolation of unknown sequences that flank known genetic sequences, and uses four degenerate random tagging primers (DRT) together with two short universal tagging primers (UAP), both included in the kit, together with 3 gene-specific primers (GSP) specifically designed for MYB29 promoter isolation (Table 6). The APAGene™ GOLD Genome Walking Kit (RT) performed three reactions (primary PCR and two nested PCR) in order to amplify targeted sequences. The first GSP primer (GSPa) was design to

anneal 153 bp from the end of the known sequence, the second GSP primer (GSPb) anneals at 144bp from the end of the known sequence and the third primer (GSPc) at 69 bp from the end of the know sequence. Wang *et al.* (2011) found two copies of *MYB29* (Bra009245, Bra005949) with 92.1 and 75.7% of identity during their comparative study of the glucosinolate biosynthetic pathways between *A.thaliana* and *B.rapa*. The two copies were analysed using the online database BLASTn (nucleotide BAST – National Center of Biotechnology Information). Bra009245 highly matched with *Brassica rapa* subsp. *pekinensis* MYB domain protein 29-2 (gene partial cds; GenBank: FJ584291.1), scoring 99% of max identity value. Bra005949 matched completely with *Brassica rapa* subsp. *pekinensis* MYB domain protein 29-1 gene (complete cds; GenBank: FJ584290.1), scoring 100% of max identity value. The cDNA sequence of *MYB29* isolated from Winspit (Zuluaga *et al.*, 2012 data not published) was used to designed 3 sets of gene specific primers (Table 6). **Primer3plus** and **Net Primer** programs were utilised during the design and the evaluation of primers (right T_m temperature, absence or no presence of hairpins). These primers were also tested with both copies of *MYB29* (Bra009245, Bra005949) from Wang *et al.* (2011). After the second nested PCR (Figure 22) a 1% agarose gel was run and 12 bands (respectively 6 bands for Winspit, 1 band for Savoy, 2 bands for DHAG1012 and 3 bands for PSB) were cut and extracted with QIAquick gel extraction kit (QIAGEN). Purified fragment were cloned with pGEM®-T Easy Vector System (Promega) cloning kit. The cloned fragments were transformed in *E.coli* DH5 α heat shock competent cells (Department of Genetics, WUR, The Netherlands). After the transformation the colonies were incubate overnight at 37°C on LB agar plates containing 100 μ g/ml Ampicillin, 80 μ g/ml X-Gal and 0.5 mM IPTG. This transformation were repeated two times, but unfortunately both time the transformation failed.

3. Results

3.1 Over-expression transformation of *Brassica oleracea* DHAG1012

During the two transformation experiments carried out in this work (~1.400 cotyledons inoculated with *Agrobacterium*) only one explant regenerate in the control (Figure 19). No cotyledons inoculated with *Agrobacterium* was able to regenerate. Most of these cotyledons did grow in dimension (Figures 14, 20, 21) or start to develop plant tissue blackening (Figures 15, 17). A relevant observation is that all the cotyledons started to fold on themselves during the first weeks of selection (Figure 12, 13, 14) and this made the following step in which they have to be dip in the medium harder. Despite two transformation experiments, no transgenic *B.oleracea* plant was obtained.

3.1.1 PCR amplification of *AOP2*

AOP2 gene from the genotypes Winspit, Savoy, PSB and DHAG1012 was amplified, separated in gel electrophoresis and the resulted bands were sequenced. The different *AOP2* sequences of Winspit (higher and intermediate bands), Savoy (higher band), PSB (higher band) and DHAG1012 (higher band) were compared with *Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene* (Collard, complete cds of 2869bp, GenBank ID: AY044425.1), with *Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene* (Broccoli, null allele complete cds of 2939bp, GenBank ID: AY044424.1), with *Brassica rapa subsp. rapa glucosinolate GS-ALK (GSL-ALK) gene* (mRNA, complete cds of 1296 bp, GenBank ID: EF611253.1) and *Brassica rapa subsp.rapa glucosinolate GS-ALK (GSL-ALK) gene* (genomic DNA, compled cds, 1781 bp, GenBank ID: EF611252.1) with the on-line program CLUSTAL 2.1 multiple sequence alignment (Appendix II). The *AOP2* genomic DNA sequences of collard (AY044425.1) and broccoli (AY044424.1) were compared with the *AOP2* mRNA sequence of *B.rapa* (EF611253.1) and the second exon of the gene was identified. According to Li and Quiros (2003) a 2-bp deletion presents in exon 2 is responsible for the non-functional gene in broccoli, because it causes a frameshift in the coding sequence and produces a shorted protein (the functional collard coding sequence is 1,317 nucleotides; the non-functional broccoli coding sequence is 957 nucleotides). Exon 2 of *AOP2* in broccoli starts at nucleotide 938 and ends at nucleotide 1626. In this exon was identified a 2-bp deletion in broccoli at nucleotides 1503-1504 (when broccoli sequence is blasted with collard) replaced in collard with two adenine. The first band of Winspit presents these 2 adenine at positions 926-927 (Appendix II, highlighted in blue), whereas the second band does not (position 747-748, Appendix II, highlighted in blue). Savoy is presented as two sequences (Savoy forward and Savoy reverse) due to not overlapping sequences during the contig in DNASTar Lasergene Seqman. However is possible to identify just in the sequence Savoy reverse the positions in which either the deletion of 2 base pair or the 2 adenine were supposed to be (position 351-352 of Savoy reverse, Appendix II highlighted in blue). Both PSB and DHAG1012 are presented as only reverse sequence obtained from DNASTar Lasergene Seqman. This was due to not reliable results of the sequence in forward as well as the not overlap of the forward and reverse sequences. For this reason at the position of the 2-bp deletion in broccoli, no sequence of DHAG1012 and PSB is present and therefore no results (Appendix II, highlighted in blue).

3.2 AOP2 polymorphism analysis among different *B.oleracea* genotypes

Figure 11 shows the gel electrophoresis separation of the PCR products obtained from Winspit, PSB, Savoy and DHAG1012 using odd12 and odd48 as primers. These two primers were developed and previously used by Gao *et al.*, (2004) to confirm the duplication of *BoGSL-ALK* gene in their work. According to figure 11, three copies of AOP2 were obtained from Winspit genotype, two copies from PSB and DHAG1012 and one copy from Savoy; the higher band of Winspit, PSB, Savoy and DHAG1012 is ~580bp, the intermediate band of Winspit ~510-520bp, and the lower band of Winspit, PSB and DHAG1012 ~490bp. However the sequenced band obtained are much shorter if compared with the gel electrophoresis (Appendix II: Contings of sequenced bands from odd12/odd48 PCR amplification) are this was due to not reliable results for the first 50-60 bp at the beginning and at the end of each sequence. However the sequenced bands from the odd12/odd48 amplification were analysed using the online database BLASTn (nucleotide BAST – National Center of Biotechnology Information) and compared with *Brassica oleracea* 2-oxoglutarate-dependent dioxygenase gene, (Collard, complete cds of 2869bp, GenBank ID: AY044425.1) in which AOP2 is known to be functional and *Brassica oleracea* 2-oxoglutarate-dependent dioxygenase gene (Broccoli, null allele complete cds of 2939bp, GenBank ID: AY044424.1) in which AOP2 is not functional.

Results (Appendix II) show that all the bands scored a higher query coverage and max identity when compared with the broccoli sequence. An interesting result is that also all the three bands of Winspit (which have a functional AOP2 gene) have a higher identity with the broccoli sequence (from 97 to 100% of query coverage and from 96 to 100% of max identity value) than with the collard sequence (from 68 to 70% of query coverage and from 94 to 97% of max identity value).

3.3 Estimation of AOP2 gene copy number among different *B.oleracea* genotypes by using q-PCT on genomic DNA

To estimate the copy number of AOP2 among different *B.oleracea* genotypes, genomic DNA was isolated from leaf tissue of three accessions for each genotype (samples from Dr. Diana Zuluaga, Department of Genetics, WUR, stored at -80°C). A preliminary trial experiment was done for the validation of the reference gene (*RPS2*) and for assessing the right set of primer to be used (Table 7). In this preliminary experiment no amplification of the third copy of AOP2 was detected for all the genotype analysed (data not shown), and neither for the *Brassica rapa* genotype resulted when was used the set of primers AOP2_1 (Figure 5). A relevant result comes from the second set of primers AOP2_2 (Figure 6) where around three copies of AOP2 for *Brassica rapa* were identified. A second qRT-PCR with AOP2_2 was run in order to confirm these results (Figure 7). After validating the reference gene *RPS2* and testing the primers, quantitative RT-PCR was run with Savoy (accession number: 3, 6, 13), PSB (accession number: 2, 4, 8), DHAG1012 (accession number: 9, 11, 12), Winspit (accession number 8, 9, 14) and *B.rapa* (accession number: 97V, 64V, 113V). For each genotypes three different accessions were used and three replica of the qRT-PCR were performed. Figure 8 shows the results of this experiment for Savoy (accession number: 3, 6, 13), PSB (accession number: 2, 4, 8), DHAG1012 (accession number: 9, 11, 12), Winspit (accession number 8, 9, 14) and *B.rapa* (accession number: 97V, 64V, 113V). The three accession of Winspit are show in Figure 9, because of the great variability in this population. On the other hand Savoy, PSB, DHAG1012 samples were homogeneous accessions, obtained as F1. Results indicated that Savoy has relative 1.5-fold higher, PSB and DHAG1012 have relative two-fold higher and Winspit and *B.rapa* have 3-fold higher (Figure 8). Figure 8 also shows that the value of Savoy is significant different from the values of the other samples (Standard Errors bars). No significant

difference was observed between PSB and DHAG1012, whereas both were significantly different from Savoy, Winspit and *B.rapa*. Finally the values of Winspit and *B.rapa* are not significant different, but they are significant different from Savoy PSB and DHAG1012.

3.4 MYB29 promoter analysis

Figure 22 shows that 12 fragments were isolated by chromosome walking, respectively six fragments from Winspit, one fragment from Savoy, two fragments from DHAG1012 and three fragments from PSB. Cloning of these fragments failed two times.

The first time the antibiotic selection did not work, and no selection was possible on the plates. The second time the ligation was probably suboptimal or failed, as showed by the positive control plate (Figure 26) in which no white colonies are present. Therefore this experiment was stopped and no further continued. Figure 25 shows the background control plate in this experiment. In the appendix are included also two plates resulted from the transformation of respectively the first and forth fragments of Winspit (figure 23 and 24).

4. Discussions and Conclusion

4.1 No regeneration of transformed *Brassica oleracea* DHAG1012

With the aim to have a better understanding of the glucosinolate pathway, and especially proving the essential role of *AOP2* in the production of sinigrin, *AOP2* gene from Winspit 7 was engineering in two expression vectors (pH7WG2::*AOP2* and pK7WG2D::*AOP2*). Two transformation experiment were carried on in order to engineer *B.oleracea* cv. DHAG1012 with *AOP2*. About 1.400 cotyledons were inoculated with *Agrobacterium*, but no plant regeneration was obtained. On the other hand, most of the cotyledons either grew in dimensions without develop any callus or develop tissue culture blackening. According to Sparrow *et al.* (2004) culture blackening results in necrosis of the plant cells and is due to the contact between the cut part of the plant and the culture medium. However, in the current work results showed how cotyledons developed blackening from parts that were not damaged and either in contact or not in contact with the medium (Figures 14, 15, 17). According to Sparrow *et al.* (2004) the absence of tissue blackening is a key factor for a successful production of transgenic plants, mostly because the blackening suppress shoot regeneration. However, *B.oleracea* genotype DHAG1012 showed to be the most efficient genotype with an average of 15% of transgenic shoots regeneration. Zuluaga *et al.* (2012, data not published) in her experiment utilised the same genotype as Sparrow *et al.* (2004), and was able to obtain a transformation efficiency of 5%. The explant tissue blackening represented in this experiment the main limitation factor, and probably the major reason of shoot regeneration suppressions. During the transformation process, explants are under different stresses, such as post-inoculation stress, antibiotic stress, *Agrobacterium* susceptibility as well as light stress. Each explant had an increased dimensions and was folded and therefore it was deeply dipped in the medium, during the transfer of the third week. This had increased the area of the explant in direct contact with the antibiotic, and probably this could be an increasing factor to the blackening of the cotyledons (for details about the procedure Sparrow *et al.*, 2004). Figures 12 and 13 showed that the cotyledons were inserted very deeply in the medium, and this increased the area of the cotyledons that was in contact with the medium and therefore with the antibiotic, increasing the stress for the explant. This hypothesis is supported by the different colour of explants in figure 12 (plate with 15 mg/L of kanamycin and 500mg/L of ticarcillin) and in figures 20 and 21 (control plate, no kanamycin no ticarcillin). Moreover because of the tendency of the explant to fold on itself, the cut surface of the cotyledon was either hanging outside of the medium or in contact with the plastic of the bottom of the petri disc. In both cases it was not in contact with the media and this also might results in necrosis of the tissue. However this experiment was done according to the *B.oleracea* transformation protocol used by Zuluaga *et al.*, (2012) and beside all the factors previously discussed, the only difference between this experiment and the transformation undertake by Zuluaga *et al.* is the period of the year. Although both explants were grow in a growth chamber in the same light and temperature conditions as Zuluaga *et al.*, the two transformations in this experiment were carried out in winter, whereas Zuluaga transformed *B.oleracea* in spring.

4.2 *AOP2* polymorphism analysis among different *B.oleracea* genotypes

In order to assess any correlation between quantitative number of *AOP2* copies and expression of this gene product, *AOP2* was amplified in the four *B.oleracea* genotypes Winspit, DHAG1012, Savoy, and PSB using odd48 and odd12 primers (Gao *et al.*, 2004).

Based on the gel electrophoresis results of *AOP2* (Figure 11) Winspit has three copies of *AOP2*, PSB and DHAG1012 have two copies and Savoy has one copy. According to the dimension

evaluated in the figure gel, the higher band for the four genotype is ~580bp, and this correspond with *BoGSL-ALKb* (567bp) in the paper of Gao *et al.*, (2004). Winspit is the only genotype that has an intermediate band at ~510-520bp, that corresponds with the intermediate migration band *BoGSL-ALKc* (510bp) of Gao *et al.*, (2004). Finally, the lower band in Winspit, PSB and DHAG1012 ~490bp corresponds with the smaller band (491 bp) *BoGSL-ALKa* of Gao *et al.*, (2004). Therefore the sample DHAG1012 has *BoGSL-ALKa* and *BoGSL-ALKb*, and this is supported by Gao *et al.*, (2004). According Li and Quiros (2003), the *BoGSL-ALKa* and *BoGSL-ALKb* copies in broccoli have a 2-bp deletion in the second exon, and this deletion could find place also in the DHAG1012 sample analysed. Interestingly, no *B.oleracea* accessions analysed by Gao *et al.*, (2004) resulted to have three copies of *AOP2* from the odd12/odd48 analysis, as was obtained in this experiment with Winspit. However, the intermediate band of Winspit cannot be pointed out as the reason for the functionality of *AOP2* in this wild-type genotype. As stated by Gao *et al.*, (2004) the polymorphisms of *BoGSL-ALK* in term of size and number is not related to the functionality. Further analysis aimed to investigate the role of the third copy of *AOP2* in Winspit 7 are necessary. According to the AGSL content analysis of Zuluaga *et al.*, (2012, data not published) Winspit 7 (the sample analyzed in this study) is the genotype with the higher production of total AGSL (4.19 $\mu\text{mol/g}$ fresh weight) if compared with other wild-types (e.g. Winspit 9 has 1.36 $\mu\text{mol/g}$ fresh weight). A relevant experiment in this sense could analysed the polymorphisms of *AOP2* among different wild-type accessions, and investigate any differences in copy number related to higher or lower production of total AGSL. In fact, according to Kim *et al.* (2006) tandem gene duplication in *Brassica* are controlling specific function and are acting in an additive manner. According to the BLAST analysis of the sequences, all the samples resulted to be more similar to the broccoli sequence than to the collard one. This result indicated that even if polymorphisms analysis with odd12/odd 48 is an effective way for analysed the copy number of *AOP2*, sequencing the short sequence amplified by odd12/odd48 does not provide enough data to deduce if *AOP2* is functional or not.

4.3 Estimation of *AOP2* gene copy number among different *B.oleracea* genotypes by using q-PCT on genomic DNA

The four different genotypes of *B.oleracea* were analyzed with qRT-PCR and results showed that different copy numbers of *AOP2* gene existing among Winspit, PSB, DHAG1012 and Savoy. The data obtained were normalised using the cycle threshold (C_T) value of *RPS2*, a single copy according to Quiros *et al.* (2001), which means that *RPS2* copy number in the different samples was defined as one. According to figure 8, three copies in of *B.rapa* were identified, and this agreed with Wang *et al.* (2011). Moreover according to Gao *et al.* (2004) there are two copies of *AOP2* in the DH line of *B.oleracea* var. *italica*, and this results is confirmed using primers *AOP2_2*. The higher value of Winspit is due to the heterogeneity of wild-type samples (Figures 9). An increased copy number of glucosinolate is an important advantage of plant during evolution, firstly because genes can active in an additive manner and therefore produce more transcripts, and furthermore because it allows one of the copies of the gene to mutate, while other copies of the gene are still maintaing the original function. *AOP2* duplication in Winspit can be explained with the two whole genome duplication (WGD) that the order *Brassicales* have undertaken during their evolution (Soltis *et al.*, 2009). In fact, genes that are involved in highly-connected signaling and regulatory networks are preserved with WGDs events, instead of been just duplicated with no-WGDs events.

4.4 No cloning of *MYB29* cis-elements

During this experiment the ligation of fragments failed and therefore should be repeated. An upgrade experiment in this direction could aim at the *MYB29* and *AOP2* cis-elements comparison in order to find correlation of the regulation between these two genes. However in doing such experiment is important to take into account the paper of Neal *et al.* (2010) concerning the regulation of *AOP2* gene expression. In fact Neal *et al.* (2010) did not find any promoter differences when they compared two kb of 5' regulatory upstream region of *AOP2* gene between *AOP2*-expressing accessions and *AOP2*-no expressing accession. Therefore the *AOP2* gene regulation can be a post-transcriptional (RNA interference) or a post-translation (dephosphorylation, glycosilation, acetylation etc.) event, or might occur during translation (presence of 5' cap or 3' poly adenosine monophosphate tail).

4.5 PCR amplification of *AOP2*

The *AOP2* sequences from Winspit, Savoy, PSB and DHAG1012 were amplified using *AOP2* D-TOPO FW and *AOP2* D-TOPO RV primers, and the fragments were separated in gel electrophoresis 1%. Figure 10 shows the gel electrophoresis separation of PCR-amplified fragments performed with *AOP2* gene-specific primer. The dimension of the first band of Winspit genotypes is according to Li and Quiros (2003), and correspond to the functional *BoGSL-ALK* described in their paper. In fact, band 1 of Winspit does not have a 2-bp deletion in exon 2 as broccoli, but it has two adenine as the functional allele of collard (Appendix II). Therefore this results is supported by Li and Quiros (2003) but not by (Zang *et al.*, 2009) who found a 2-bp deletion in the third exon of *AOP2*. Li and Quiros (2003) stated that a non-functional *BoGSL-ALK* gene has 957 nucleotides, and this is caused by the 2-bp deletions and the resulted sequence frameshift. Therefore a band of this dimension was expected from amplification with the other three genotypes, especially from the DHAG102 genotype (it carries a non-functional gene as broccoli), but not obtained. Indeed a band of around 957 bp was obtained from Winspit, and the CLUSTER analysis shows the presence of a base substitution (A into G, at position 747, Appendix II, highlighted in blue) and a base deletion (at position 748, Appendix II, highlighted in blue). This band seems to correspond to the non-functional *BoGSL-ALK* allele of Li and Quiros (2003). Sequencing inefficiency of the higher bands of PSB, of Savoy and of DHAG1012 made not possible to infer any conclusion concerning these sequences. However this experiment confirmed the functionality of the Winspit band isolated and cloned into the destination vectors (pH7WG2 and pK7WG2D) in section 2.1.1. Further analysis of the PSB, Savoy and DHAG1012 sequences are needed in order to confirm the presence of the 2-bp deletions.

4.5 Conclusions

This project major aim was the modulation of the glucosinolate pathway by regulation of *AOP2* expression in *B.oleracea*. Despite two transformation experiments, no transgenic *B.oleracea* plant was obtained and the hypothesis of a direct correlation between a functional *AOP2* gene in *B.oleracea* and an increase production of sinigrin is not answered. Moreover also the experiment aimed at the promoter characterization of *MYB29* did not succeed, and therefore no information about the 5' regulatory upstream region of *MYB29* is available. Concerning the analysis of the *AOP2* sequences among the four *B.oleracea* genotypes (Winspit, Savoy, DHAG1012 and PSB), a 2-bp deletions was found in the first band of Winspit, confirmed the result of Li and Quiros (2003) and the functionality of *AOP2* in Winspit. The *AOP2* polymorphisms analysis among the four genotypes showed that Winspit has three copies of *AOP2*, PSB and DHAG1012 have two copies

and Savoy has one copy. Dimension and number of all of these copies are in agreement with Gao *et al.* (2004) expect for Winspit, that resulted with an extra third copy of *AOP2*. Sequence analysis of key pathway genes, their promoter and/or regulator factors analysis, as well as over-expression transformation of these genes *in planta* are nowadays important and fundamental research methodologies. These methods are aimed to develop a correlation between metabolite production and biosynthetic genes, as well as provide a deeper and wider understanding concerning the regulation of important pathways in plants.

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Appendix I

Table 2. MS basal medium, pH 5.8 (Sparrow *et al.*, 2004)

Murashige and Skoog salts	4.3 g/L
Phytoagar (Duchefa, cat. nl. P1003)	8 g/L
Sucrose	30 g/L

Autoclave at 120°C for 20 min

Table 3. Composition of germination medium (Sparrow *et al.*, 2004)

MS basal medium	1 L
10 g/L myoinositol (Sigma, cat. no. I-3011)	1 mL
10 mg/L thiamine-HCl (Sigma, cat. no. T-3902)	1 mL
1 mg/L pyridoxine (Sigma, cat. no. P-8666)	1 mL
1mg/L nicotinic acid (Sigma, cat. no. N-0765)	1 mL

Vitamins are indicated with the stock solution concentration. Vitamins are added before pouring the medium. All vitamins are made with distilled water, filter sterilized and store at 4°C, with the exception of myoinositol, store at room temperature. One liter is typically enough for 30 Petri plates (15 x 90 mm)

Table 4. Composition of cocultivation medium (Sparrow *et al.*, 2004)

MS basal medium	1 L
10 g/L myoinositol (Sigma, cat. no. I-3011)	1 mL
10 mg/L thiamine-HCl (Sigma, cat. no. T-3902)	1 mL
1 mg/L pyridoxine (Sigma, cat. no. P-8666)	1 mL
1mg/L nicotinic acid (Sigma, cat. no. N-0765)	1 mL
4 mg/mL 6-Benzylaminopurine (BAP; Sigma, cat. no. B-9395)	0.5 mL

BAP is added before autoclaving the medium. Vitamins are indicated with the stock solution concentration. Vitamins are added before pouring the medium. All vitamins are made with distilled water, filter sterilized and store at 4°C, with the exception of myoinositol, store at room temperature. One liter is typically enough for 30 Petri plates (15 x 90 mm)

Table 5. Composition of selection medium (Sparrow *et al.*, 2004)

MS basal medium	1 L
10 g/L myoinositol (Sigma, cat. no. I-3011)	1 mL
10 mg/L thiamine-HCl (Sigma, cat. no. T-3902)	1 mL
1 mg/L pyridoxine (Sigma, cat. no. P-8666)	1 mL
1mg/L nicotinic acid (Sigma, cat. no. N-0765)	1 mL
4 mg/mL 6-Benzylaminopurine (BAP; Sigma, cat. no. B-9395)	0.5 mL
Kanamycin (15mg/L) or Hygromycin (10mg/L)	
Ticarcillin 500mg/L	

BAP is added before autoclaving the medium. Vitamins are indicated with the stock solution concentration. Vitamins are added before pouring the medium. All vitamins are made with distilled water, filter sterilized and store at 4°C, with the exception of myoinositol, store at room temperature. One liter is typically enough for 30 Petri plates (15 x 90 mm)

Table 6. Gene Specific Primers (GSP) used for *MYB29* walking to promoter isolation

GSPa	5' – TTCCCACATCGTTTTAGTCCAGCTTT – 3'
GSPb	5' – CGTTTTAGTCCAGCTTTTTGGGGAATG – 3'
GSPc	5' – TGTCTTCTTCGATGGTCCATACTCCTT – 3'



Figure 3. Expression clone **pH7WG2** containing *AOP2* gene sequence.

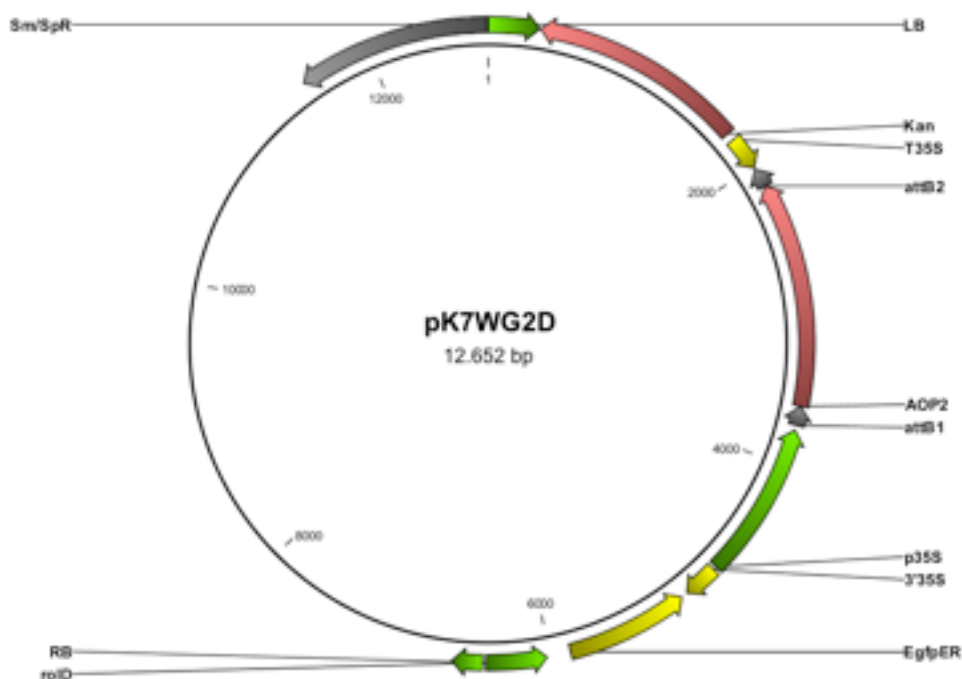


Figure 4. Expression clone **pK7WG2D** containing *AOP2* gene sequence.

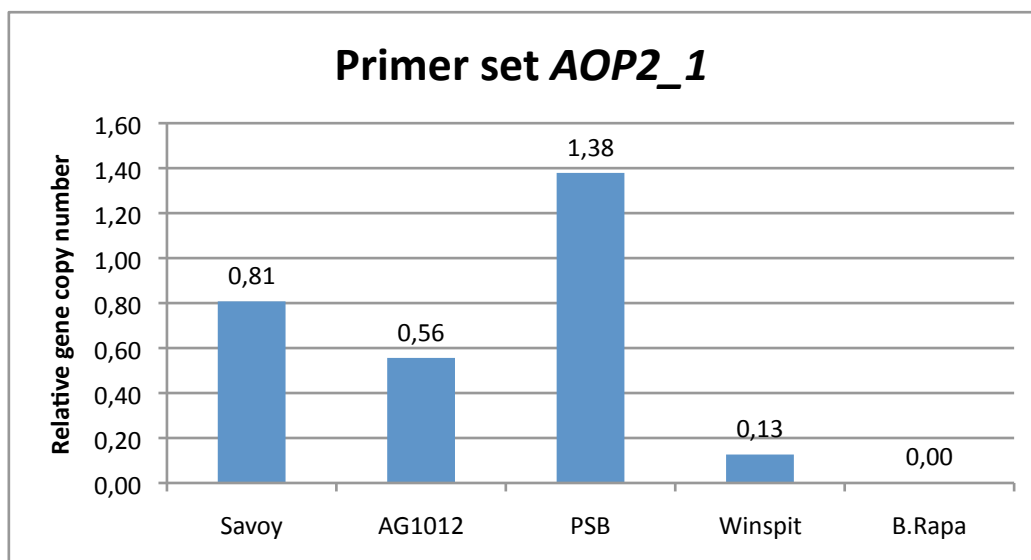


Figure 5. Relative *AOP2_1* copy number in genomic DNA of difference genotypes. The one copy gene *RPS2* was used as C_T normalization reference gene.

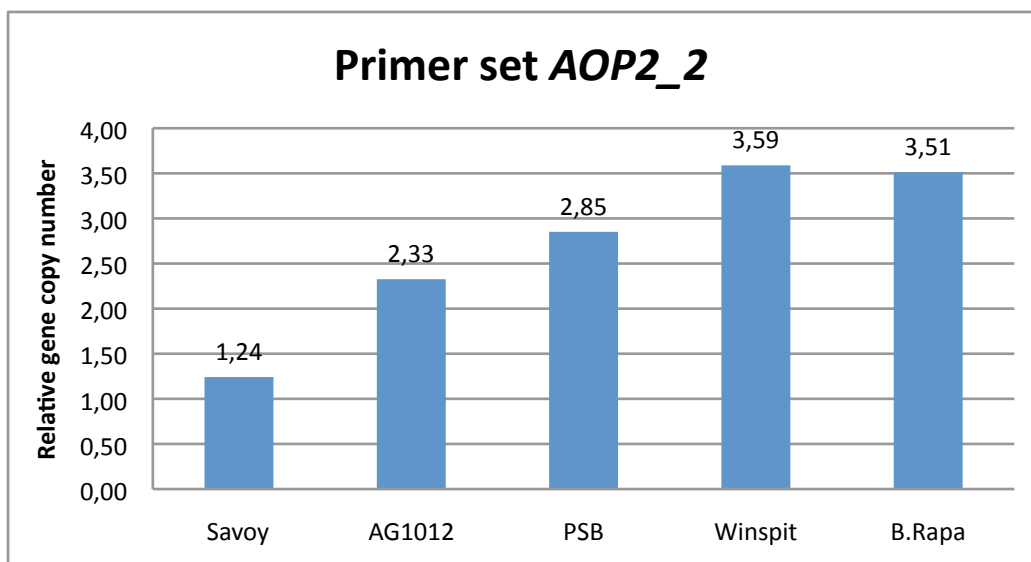


Figure 6. Relative *AOP2_2* copy number in genomic DNA of difference genotypes. The one copy gene *RPS2* was used as C_T normalization reference gene.

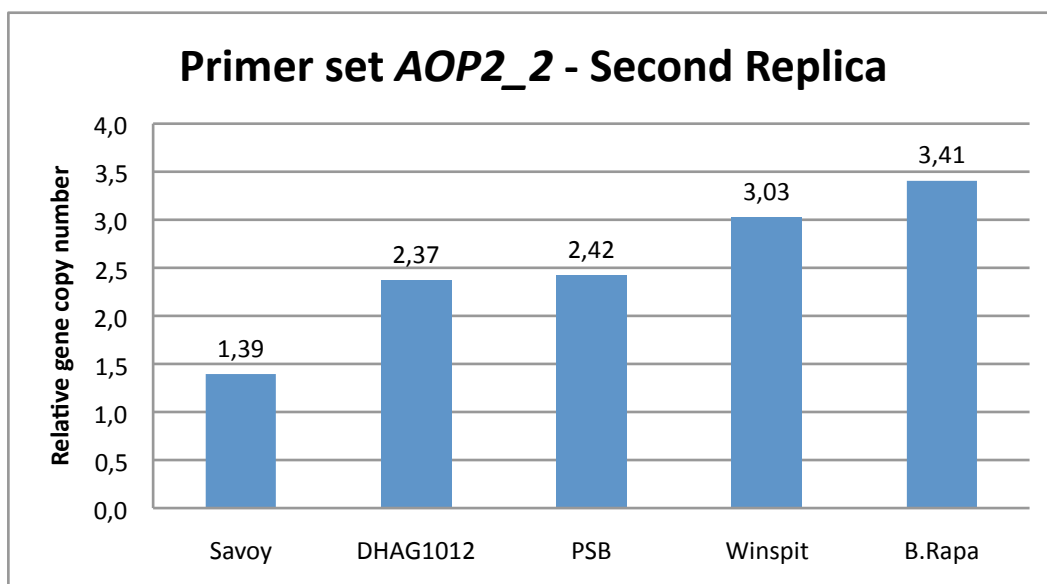


Figure 7. Relative *AOP2_2* copy number in genomic DNA of difference genotypes, second replica. The one copy gene *RPS2* was used as C_T normalization reference gene.

Table 7. Quantitative Real-Time PCR gene specific primers used for copy number estimation of *AOP2_1*, *AOP2_2*, and *AOP2_3*.

<i>AOP2_1</i> *	FW 5' – CTTCGTCCACAAGCTCTTCC – 3'
	RV 5' – ATTCTCCACGTCACCGAGTC – 3'
<i>AOP2_2</i> *	FW 5' – AGGAACTTGTGGACGAGCAG – 3'
	RV 5' – GGAGACGGCACAATAAGCAT – 3'
<i>AOP2_3</i> *	FW 5' – CAACTGCTACGCCCTGATTT – 3'
	RV 5' – CCCAAAGCTCTCCATAACCA – 3'

* sequences from Diana Zuluaga *et al.* (2012, data not published)

Table 8. PCR gene specific primers used for *AOP2* cloning and *AOP2* polymorphisms analysis.

BoAOP2 D-TOPO FW	5' – CACCATGGGTGCAGACACTCCTCAACTTCCAG – 3'
BoAOP2 D-TOPO RV	5' – TTATGCTCCAGAGACGGCACAATAAGCGTG – 3'
odd48 forward	5' – TTCCATCATTTACTTTCTCAG – 3'
odd12 reverse	5' – TTGAATATCCAGTGTAAGGTT – 3'

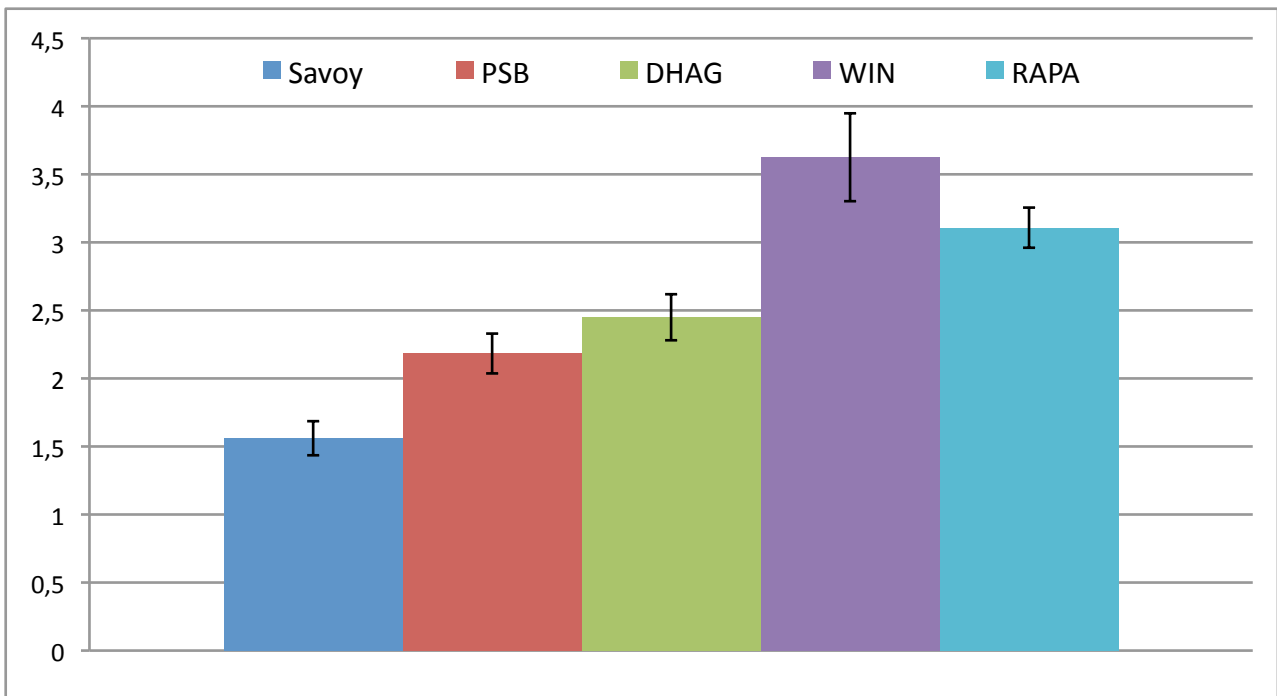


Figure 8. Genomic copy number of *AOP2_2* in four genotypes of *B.oleracea* and in *B.rapa* normalized with C_T values for *BoRPS2*, determined using quantitative real-time PCR. Error bars represent $\pm$ SEs.

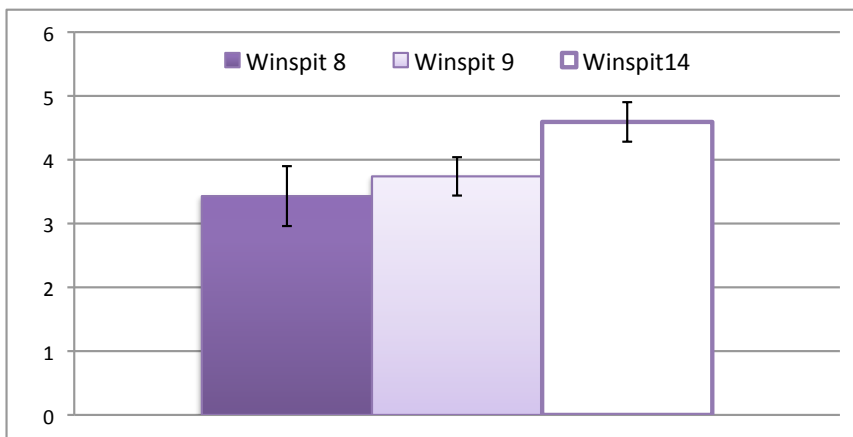


Figure 9. Genomic copy number of *AOP2_2* in three accession of Winspit normalized with C_T values for *BoRPS2*, determined using quantitative real-time PCR. Error bars represent $\pm$ SEs.

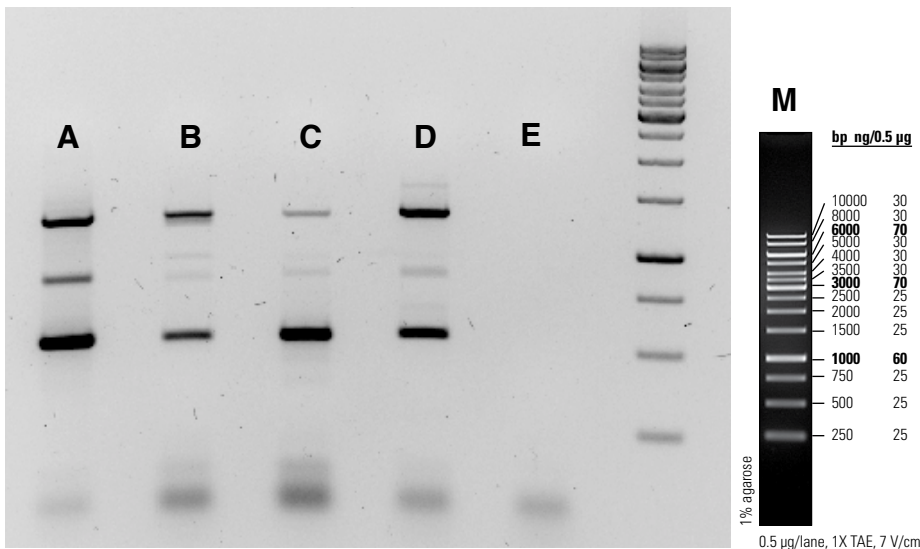


Figure 10. Gel electrophoresis separation of PCR-amplified fragments performed with *AOP2* gene-specific primer. This PCR reaction used genomic DNA from Winspit (A), PSB (B), Savoy (C), DHAG1012 (D). Line E represents the negative control. M is the 1 kb DNA market (GeneRuler™ 1 kb DNA Ladder, ThermoScientific).

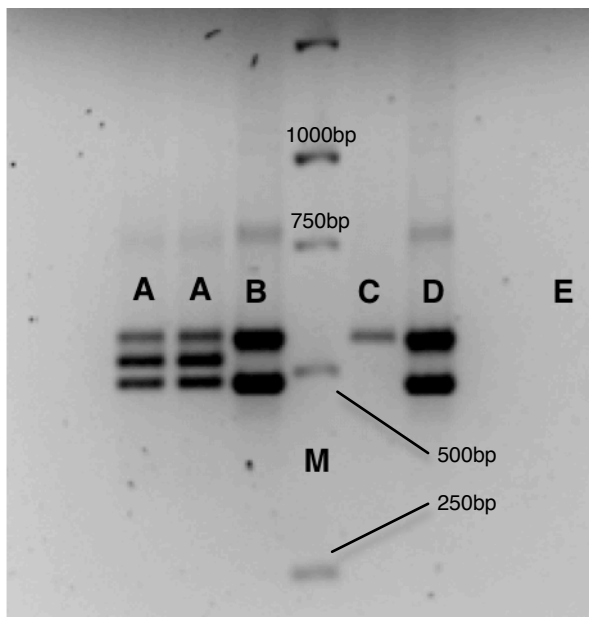


Figure 11. Gel electrophoresis separation of PCR-amplified fragments performed with *odd12* and *odd48* primers (Gao *et al.*, 2004). This PCR reaction used genomic DNA from Winspit (A), PSB (B), Savoy (C), DHAG1012 (D). Line E represents the negative control. Line M is the 1 kb DNA market (GeneRuler™ 1 kb DNA Ladder, ThermoScientific).

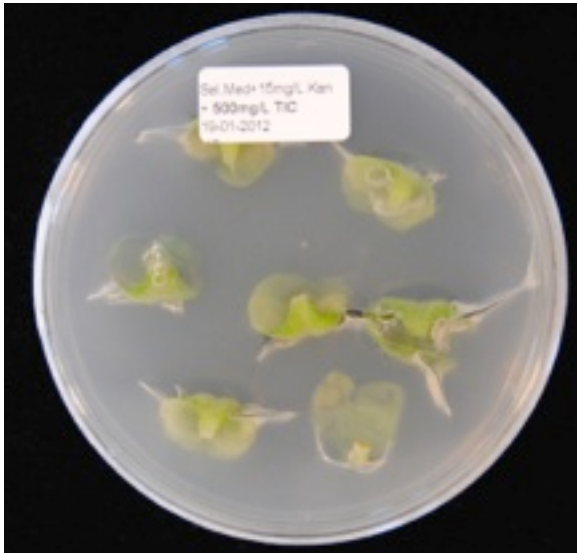


Figure 12. Plate with selection medium plus 15 mg/L of kanamycin and 500mg/L of ticarcillin. Figure was done after 3-4 weeks from inoculation.

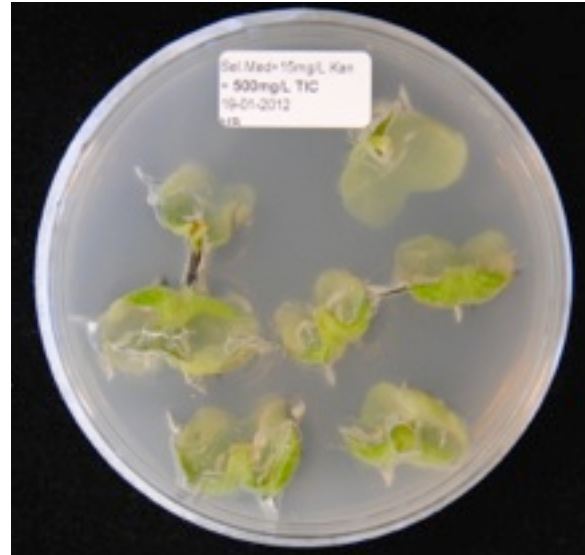


Figure 13. Plate with selection medium plus 15 mg/L of kanamycin and 500mg/L of ticarcillin. Figure was done after 3-4 weeks from inoculation.

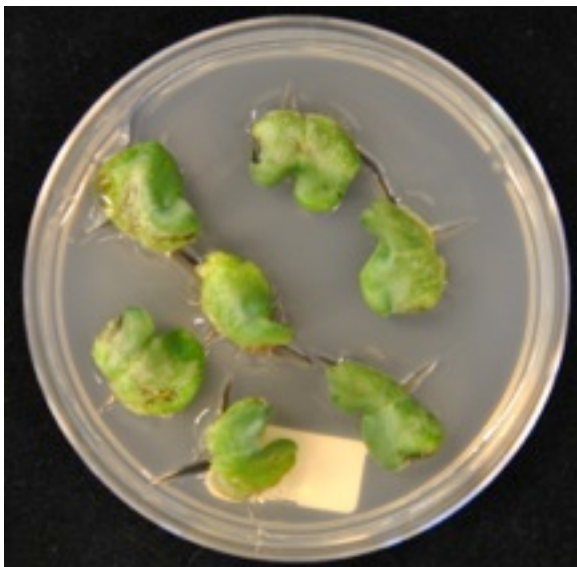


Figure 14. Plate with selection medium plus 15 mg/L of kanamycin and 500mg/L of ticarcillin. Figure was done after 3-4 weeks from inoculation.



Figure 15. Plate with selection medium plus 15 mg/L of kanamycin and 500mg/L of ticarcillin. Figure was done after 3-4 weeks from inoculation.

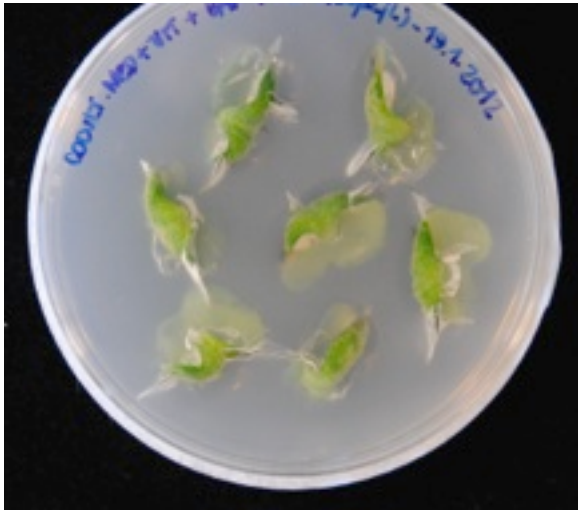


Figure 16. Control plate with selection medium with 500mg/L of ticarcillin and without kanamycin. Figure was done after 3-4 weeks from inoculation.



Figure 17. Control plate with selection medium with 500mg/L of ticarcillin and without kanamycin. Figure was done after 3-4 weeks from inoculation.



Figure 18. Control plate with selection medium without antibiotics. Figure was done after 3-4 weeks from inoculation.



Figure 19. Control plate with selection medium without antibiotics. Figure was done after 3-4 weeks from inoculation. Zoom in of the only green shoot obtain in the control plates.



Figure 20. Control plate with selection medium without antibiotics. Figure was done after 3-4 weeks from inoculation.



Figure 21. Control plate with selection medium without antibiotics. Figure was done after 3-4 weeks from inoculation.

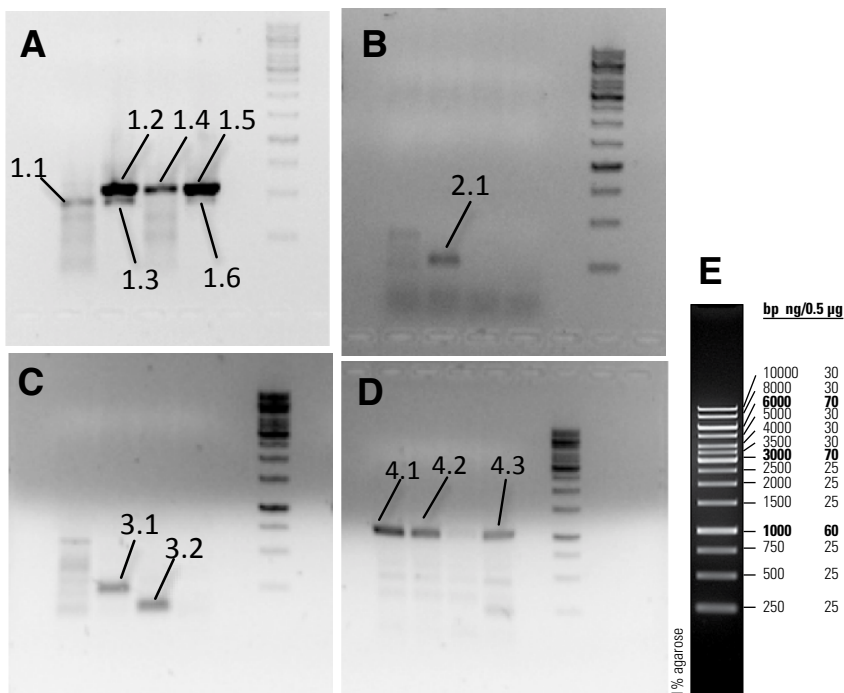


Figure 22. Agarose gel (1%) of the amplified fragments of the second nested PCR from MYB29 walking for promoter isolation. Fragments labels with numbers were excised and isolated from gel and cloned in *E.coli*. A: Winspit genotype; B: Savoy genotype; C: DHAG1012 genotype; D: PSB genotype. E: GeneRuler™ 1kb DNA ladder (ThermoScientific), marker used in the gel electrophoresis.

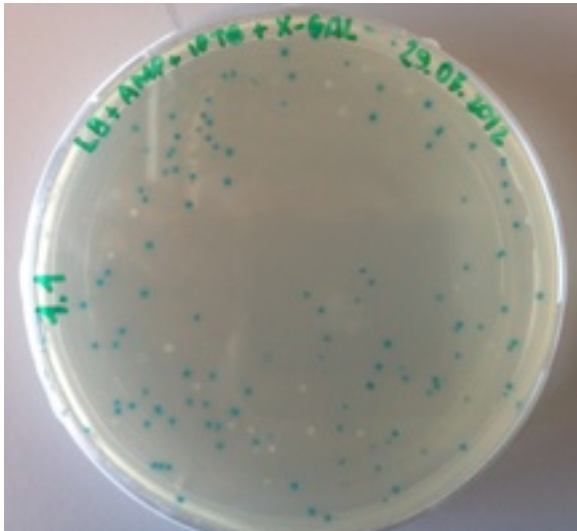


Figure 23. Cloning plate of Winspit band 1.1. (Figure 25). *MYB29* promoter analysis experiment.

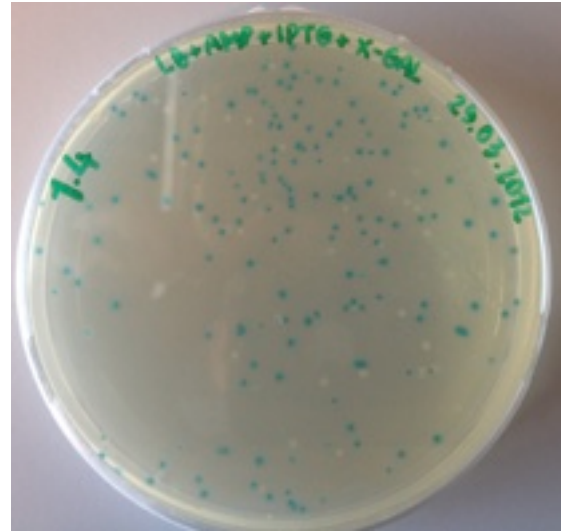


Figure 24. Cloning plate of Winspit band 1.4. (Figure 25). *MYB29* promoter analysis experiment.

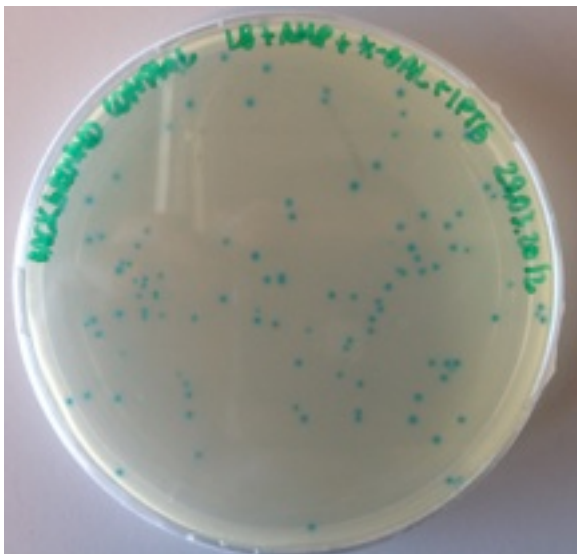


Figure 25. Background control plate from *MYB29* promoter analysis. Medium according to pGEM®-T Easy Vector System (Promega) cloning kit.

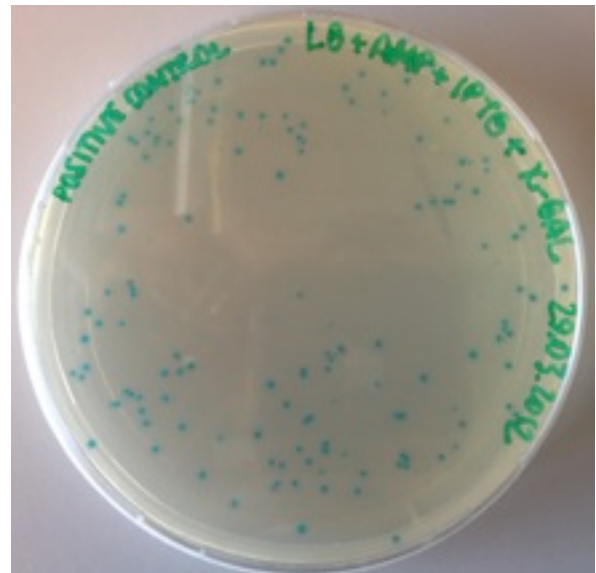


Figure 26. Positive control plate from *MYB29* promoter analysis. Medium according to pGEM®-T Easy Vector System (Promega) cloning kit.

Appendix II

Sequence of Expression clone pH7WG2 with Winspit7_AOP2 gene

Circular Sequence

GTACAAAAAGCAGGCTCCGCGGCCGCCCTTCACCATGGGTGCAGACACTCCTCAACTTCCAGTCTATCTCTCGGACCAAAACC
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Sequence of Expression clone pH7WG2 with Winspit 7_AOP2 gene

Circular Sequence

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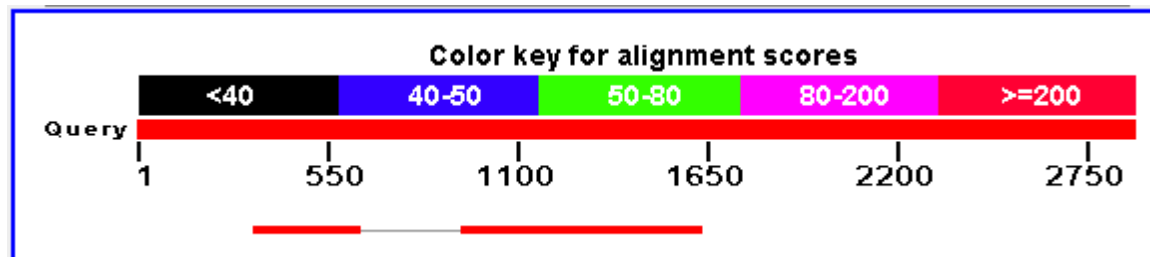
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BLAST *B.oleracea* collard (AY044425.1), *B.oleracea* broccoli (AY044424.1), *B.rapa* mRNA (EF611253.1) *B.rapa* genomic DNA (EF611252.1) and the first band of Winspit.

AY044425.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene,
Complete cds (2869bp)

AOP2 Winspit Band1



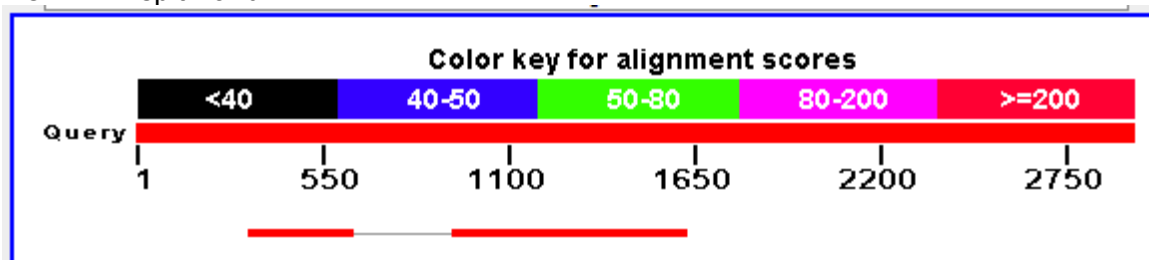
Query Coverage 34%

E value 0.0

Max identity 99%

AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene,
null allele, Complete cds (2939bp)

AOP2 Winspit Band1



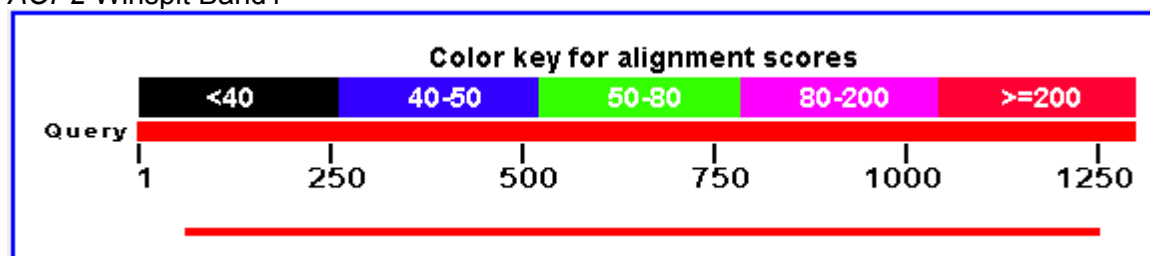
Query Coverage 34%

E value 0.0

Max identity 99%

EF611253.1 Brassica rapa subsp. rapa glucosinolate GS-Alk (GSL-Alk) mRNA,
complete cds (1296bp)

AOP2 Winspit Band1



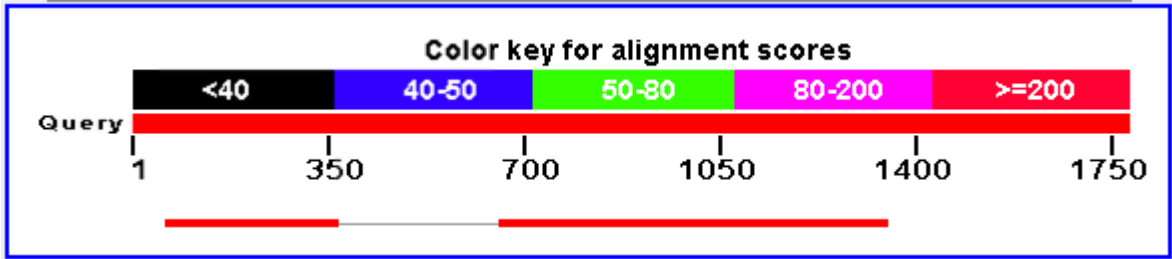
Query Coverage 91%

E value 0.0

Max identity 91%

EF611252.1 Brassica rapa subsp. rapa glucosinolate GS-Alk gene, complete cds (1781bp)

AOP2 Winspit Band1

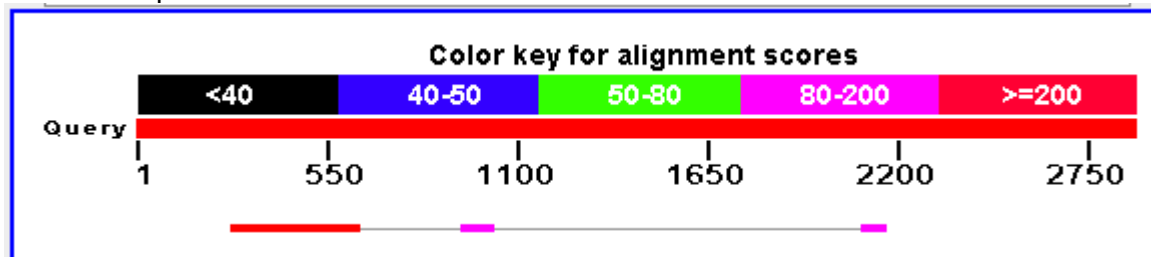


Query Coverage 56%
E value 0.0
Max identity 97%

BLAST *B.oleracea* collard (AY044425.1), *B.oleracea* broccoli (AY044424.1), *B.rapa* mRNA (EF611253.1) *B.rapa* genomic DNA (EF611252.1) and the second band of Winspit.

EF611252.1 *Brassica rapa* subsp. *rapa* glucosinolate GS-Alk gene, complete cds (1781bp)

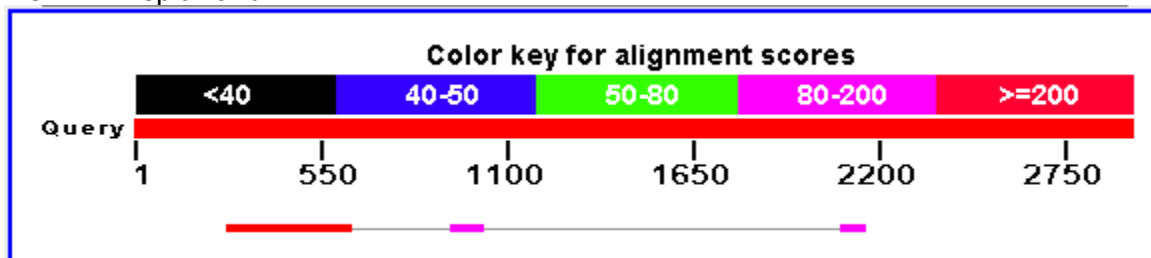
AOP2 Winspit Band2



Query Coverage 19%
E value 0.0
Max identity 100%

AY044424.1: *Brassica oleracea* 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)

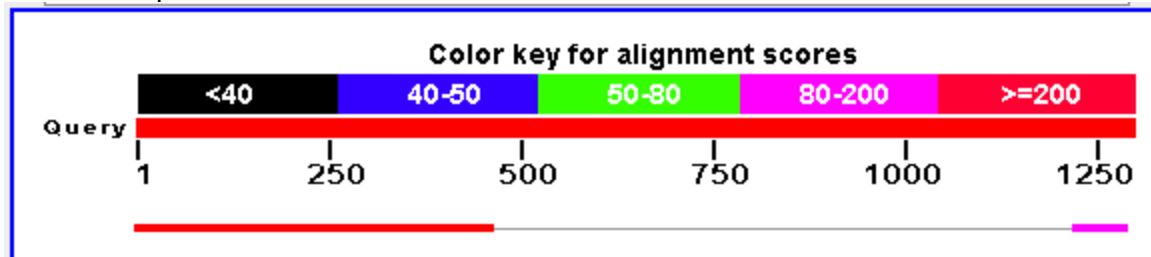
AOP2 Winspit Band2



Query Coverage 18%
E value 0.0
Max identity 100%

EF611253.1 *Brassica rapa* subsp. *rapa* glucosinolate GS-Alk (GSL-Alk) mRNA, complete cds (1296bp)

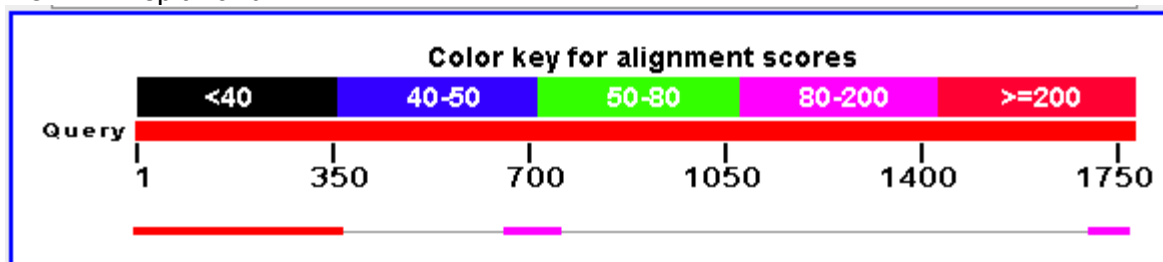
AOP2 Winspit Band2



Query Coverage 41%
E value 0.0
Max identity 97%

EF611252.1 Brassica rapa subsp. rapa glucosinolate GS-Alk gene, complete cds
(1781bp)

AOP2 Winspit Band2



Query Coverage 30%

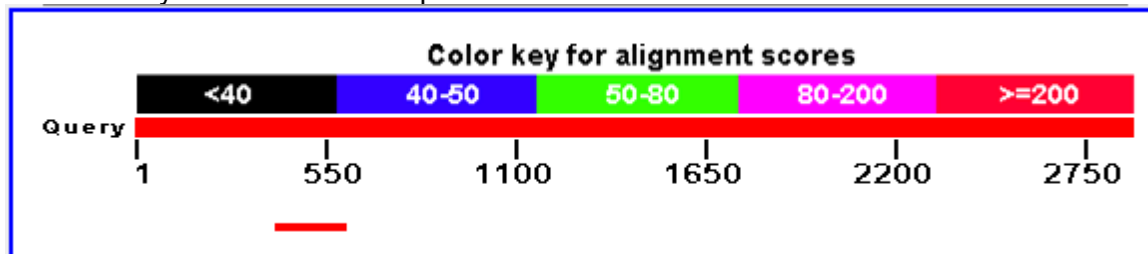
E value 0.0

Max identity 99%

BLAST *B.oleracea* collard (AY044425.1), *B.oleracea* broccoli (AY044424.1), *B.rapa* mRNA (EF611253.1) *B.rapa* genomic DNA (EF611252.1) and the forward sequence of the band of Savoy.

EF611252.1 Brassica rapa subsp. rapa glucosinolate GS-Alk gene, complete cds (1781bp)

AOP2 Savoy band - forward sequence



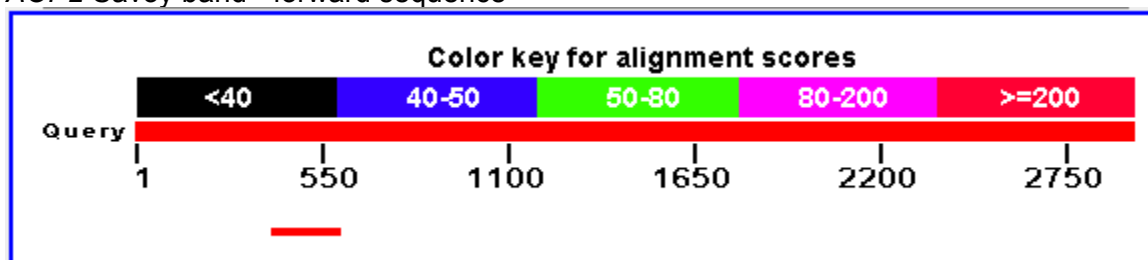
Query Coverage 7%

E value 8e-82

Max identity 89%

AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)

AOP2 Savoy band - forward sequence



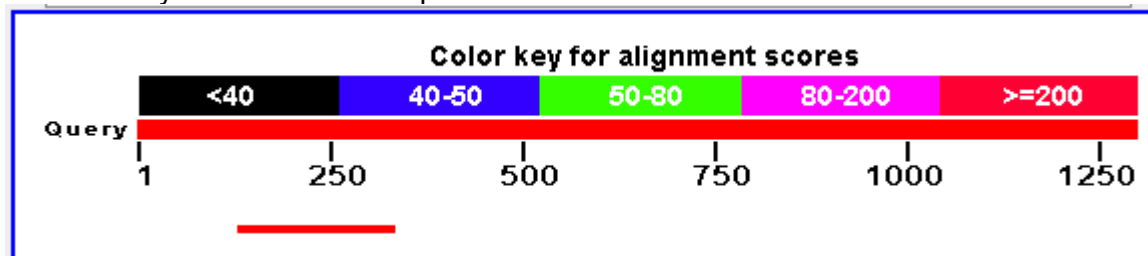
Query Coverage 7%

E value 8e-82

Max identity 89%

EF611253.1 Brassica rapa subsp. rapa glucosinolate GS-Alk (GSL-Alk) mRNA, complete cds (1296bp)

AOP2 Savoy band - forward sequence



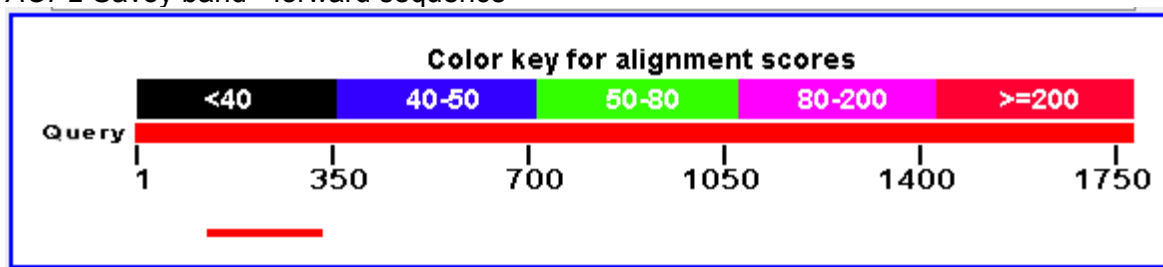
Query Coverage 15%

E value 3e-78

Max identity 88%

EF611252.1 Brassica rapa subsp. rapa glucosinolate GS-Alk gene, complete cds (1781bp)

AOP2 Savoy band - forward sequence



Query Coverage 11%

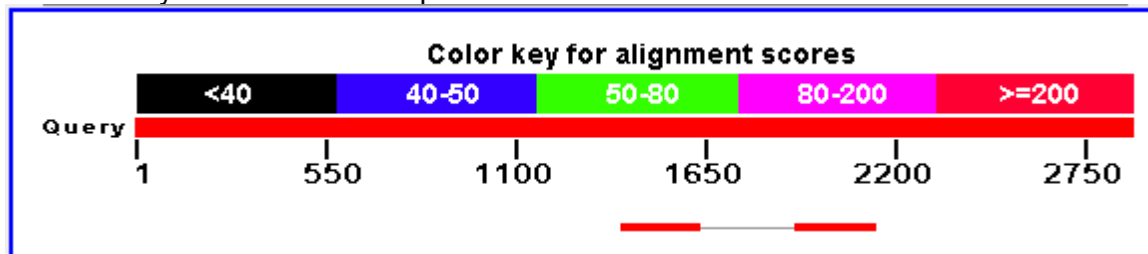
E value 4e-78

Max identity 88%

BLAST *B.oleracea* collard (AY044425.1), *B.oleracea* broccoli (AY044424.1), *B.rapa* mRNA (EF611253.1) *B.rapa* genomic DNA (EF611252.1) and the reverse sequence of the band of Savoy.

EF611252.1 Brassica rapa subsp. rapa glucosinolate GS-Alk gene, complete cds (1781bp)

AOP2 Savoy band - reverse sequence



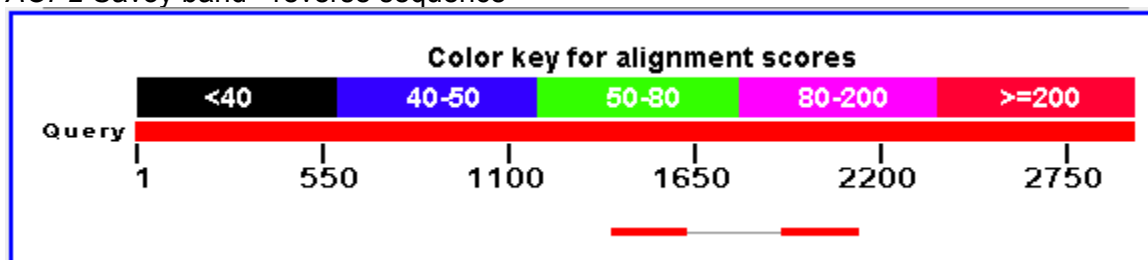
Query Coverage 15%

E value 7e-99

Max identity 93%

AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)

AOP2 Savoy band - reverse sequence



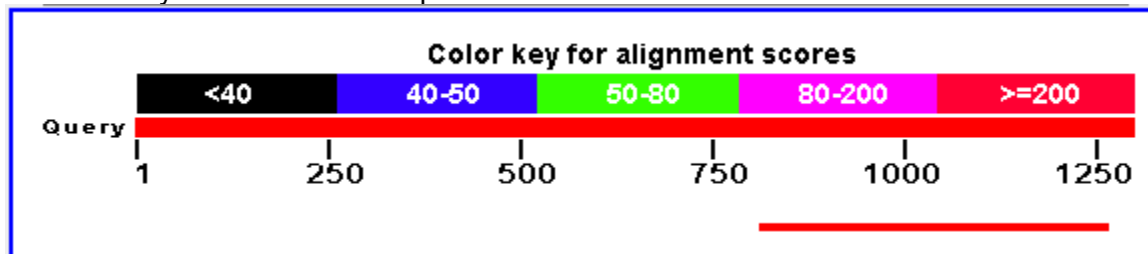
Query Coverage 15%

E value 9e-98

Max identity 93%

EF611253.1 Brassica rapa subsp. rapa glucosinolate GS-Alk (GSL-Alk) mRNA, complete cds (1296bp)

AOP2 Savoy band - reverse sequence



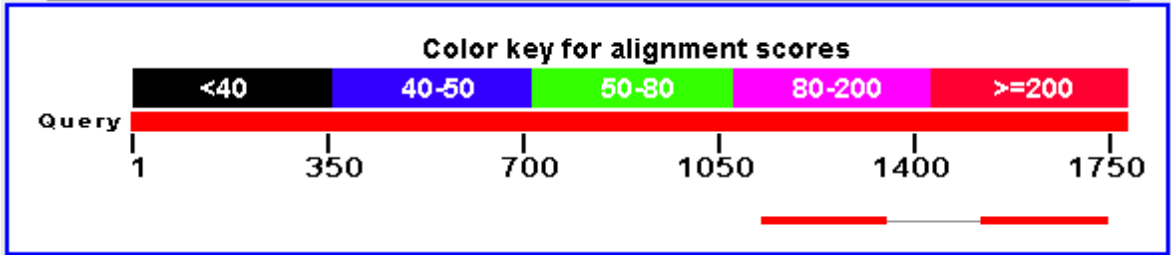
Query Coverage 35%

E value 0.0

Max identity 92%

EF611252.1 Brassica rapa subsp. rapa glucosinolate GS-Alk gene, complete cds (1781bp)

AOP2 Savoy band - reverse sequence

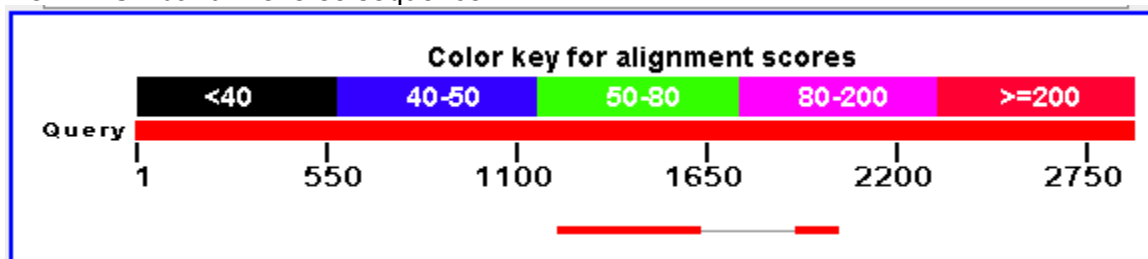


Query Coverage 25%
E value 2e-102
Max identity 94%

BLAST *B.oleracea* collard (AY044425.1), *B.oleracea* broccoli (AY044424.1), *B.rapa* mRNA (EF611253.1) *B.rapa* genomic DNA (EF611252.1) and the reverse sequence of the band of PSB.

EF611252.1 Brassica rapa subsp. rapa glucosinolate GS-Alk gene, complete cds (1781bp)

AOP2 PSB band - reverse sequence



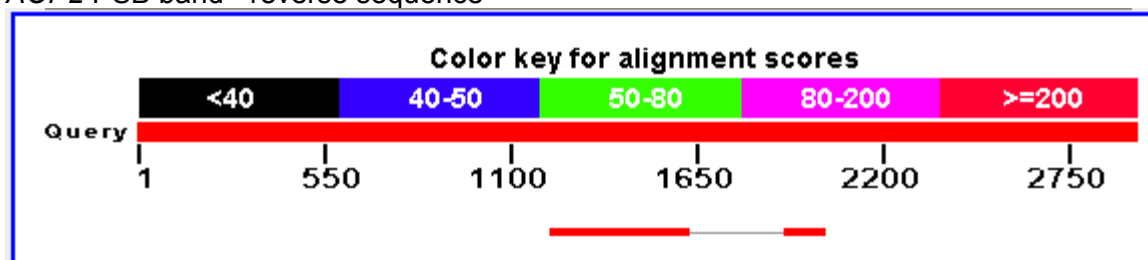
Query Coverage 18%

E value 8e-179

Max identity 98%

AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)

AOP2 PSB band - reverse sequence



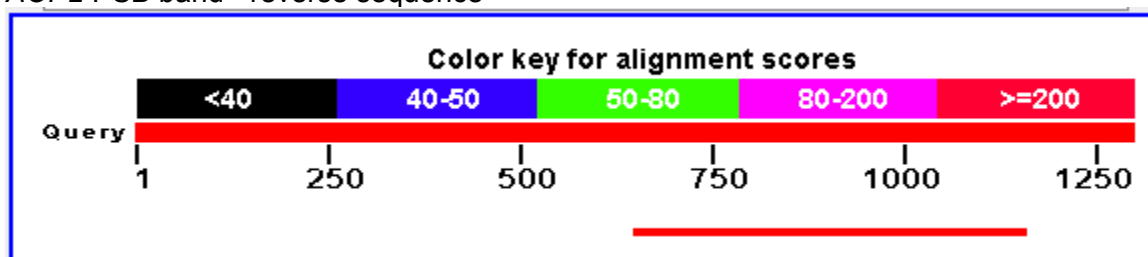
Query Coverage 18%

E value 0.0

Max identity 98%

EF611253.1 Brassica rapa subsp. rapa glucosinolate GS-Alk (GSL-Alk) mRNA, complete cds (1296bp)

AOP2 PSB band - reverse sequence



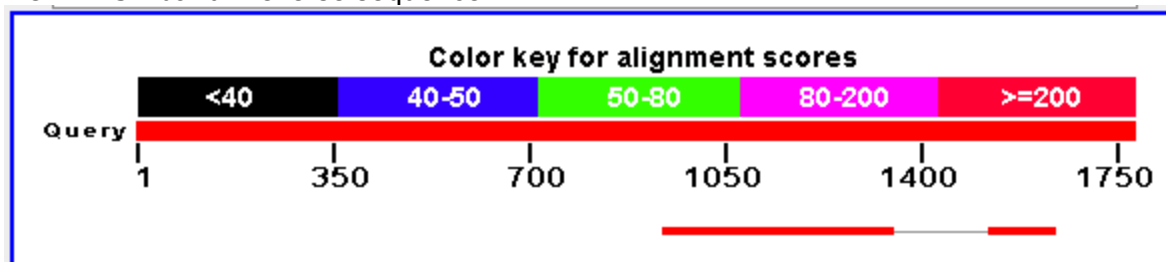
Query Coverage 39%

E value 0.0

Max identity 90%

EF611252.1 Brassica rapa subsp. rapa glucosinolate GS-Alk gene, complete cds (1781bp)

AOP2 PSB band - reverse sequence



Query Coverage 30%

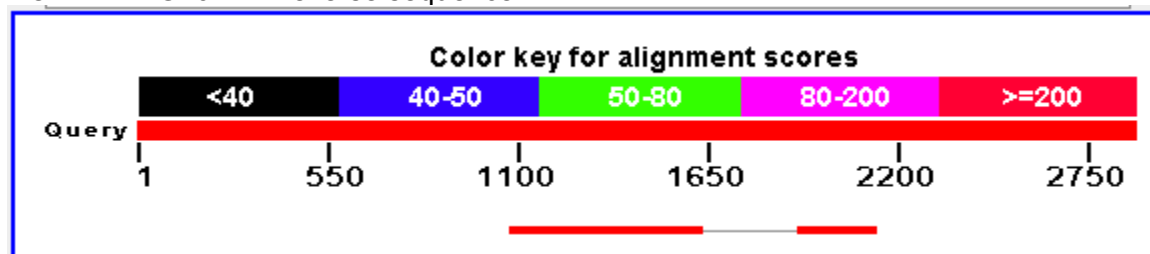
E value 2e-172

Max identity 97%

BLAST *B.oleracea* collard (AY044425.1), *B.oleracea* broccoli (AY044424.1), *B.rapa* mRNA (EF611253.1) *B.rapa* genomic DNA (EF611252.1) and the reverse sequence of the band of DHAG1012.

EF611252.1 *Brassica rapa* subsp. *rapa* glucosinolate GS-Alk gene, complete cds (1781bp)

AOP2 DHAG1012 - Reverse sequence



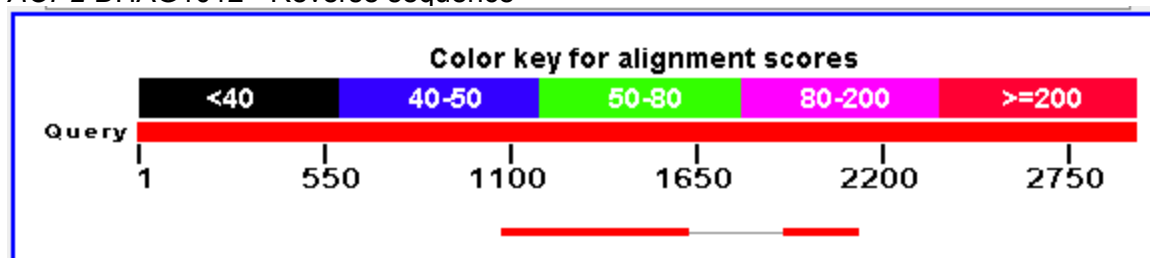
Query Coverage 27%

E value 0.0

Max identity 96%

AY044424.1: *Brassica oleracea* 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)

AOP2 DHAG1012 - Reverse sequence



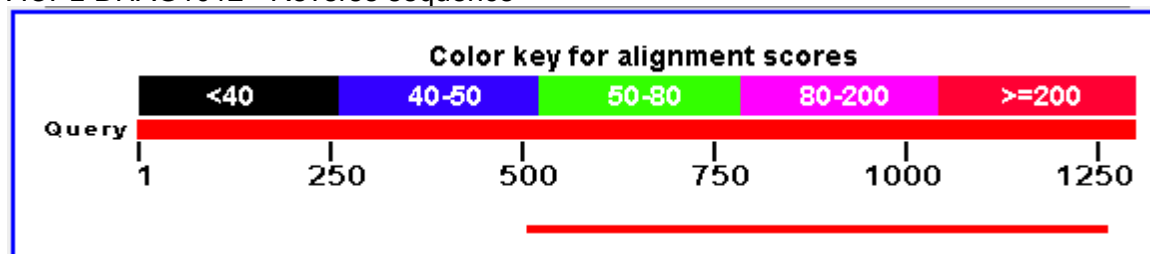
Query Coverage 26%

E value 0.0

Max identity 96%

EF611253.1 *Brassica rapa* subsp. *rapa* glucosinolate GS-Alk (GSL-Alk) mRNA, complete cds (1296bp)

AOP2 DHAG1012 - Reverse sequence



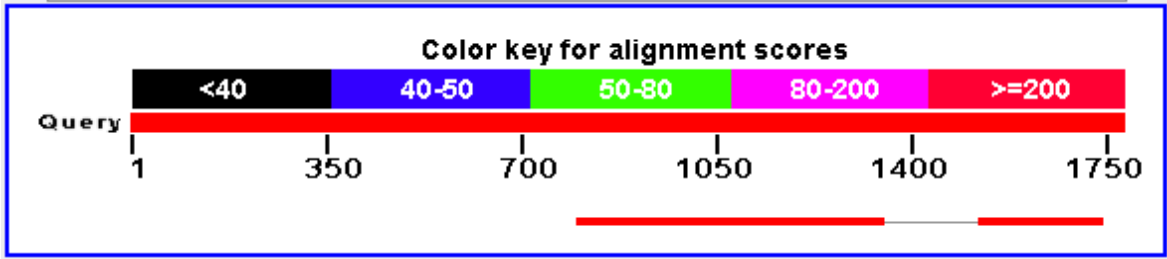
Query Coverage 58%

E value 0.0

Max identity 91%

EF611252.1 Brassica rapa subsp. rapa glucosinolate GS-Alk gene, complete cds (1781bp)

AOP2 DHAG1012 - Reverse sequence

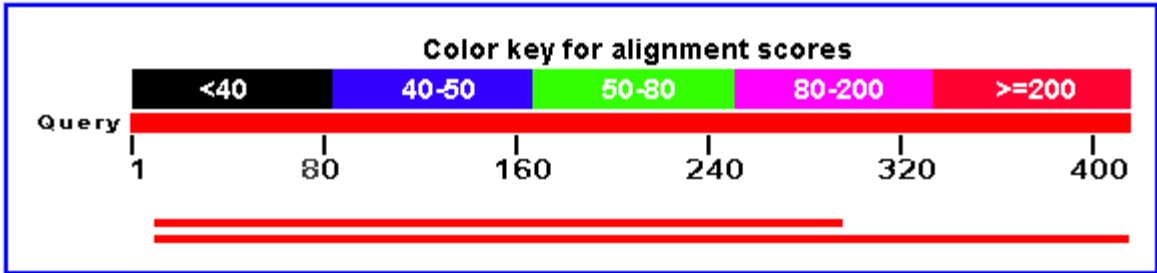


Query Coverage 43%
E value 0.0
Max identity 94%

BLAST *B.oleracea* collard (AY044425.1), *B.oleracea* broccoli (AY044424.1), *B.rapa* mRNA (EF611253.1) *B.rapa* genomic DNA (EF611252.1) and the three bands of Winspit obtained with PCR amplification with primer odd12/odd48.

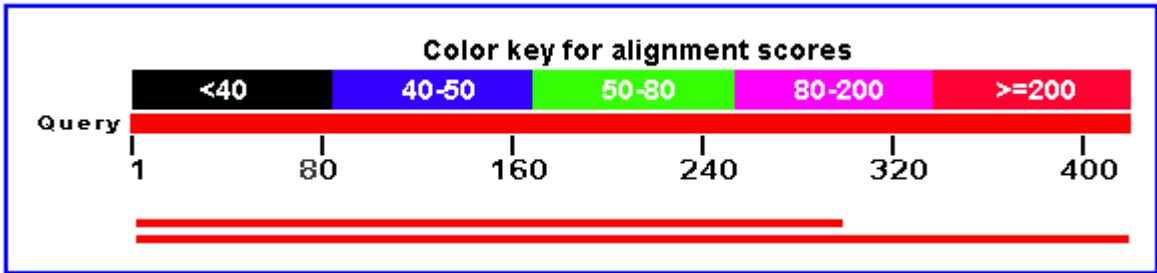
Winspit band 1 - odd12/odd48 primers amplification

AY044425.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, complete cds (2869bp)	Query Coverage 68% E value 4e-130 Max identity 94%
AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)	Query Coverage 97% E value 0.0 Max identity 96%



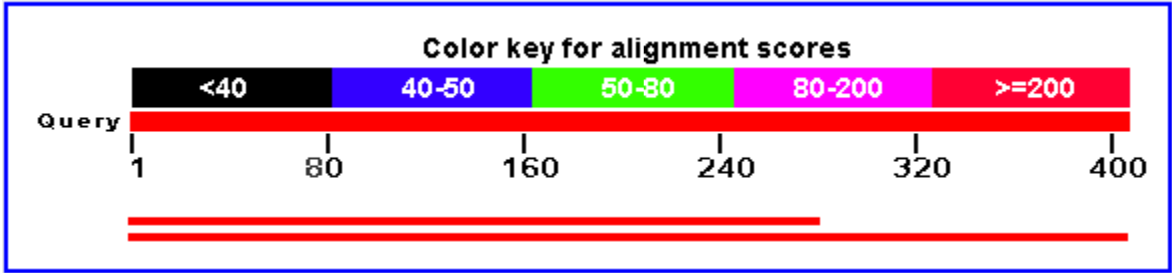
Winspit band 2 - odd12/odd48 primers amplification

AY044425.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, complete cds (2869bp)	Query Coverage 70% E value 4e-140 Max identity 96%
AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)	Query Coverage 99% E value 0.0 Max identity 98%



Winspit band 3 - odd12/odd48 primers amplification

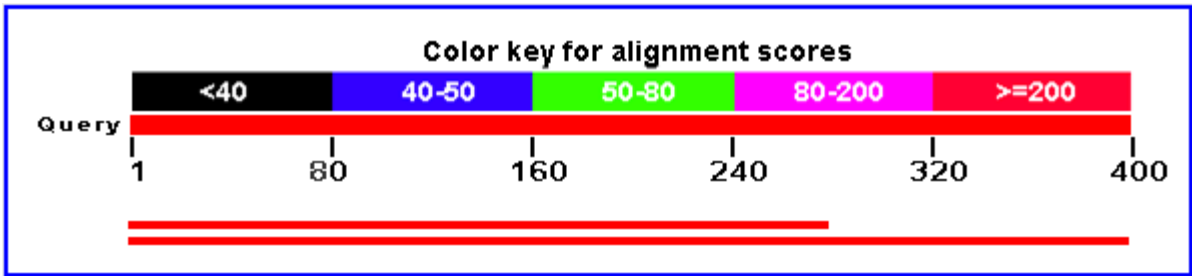
AY044425.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, complete cds (2869bp)	Query Coverage 69% E value 2e-138 Max identity 97%
AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)	Query Coverage 100% E value 0.0 Max identity 100%



BLAST *B.oleracea* collard (AY044425.1), *B.oleracea* broccoli (AY044424.1), *B.rapa* mRNA (EF611253.1) *B.rapa* genomic DNA (EF611252.1) and the two bands of PSB obtained with PCR amplification with primer odd12/odd48.

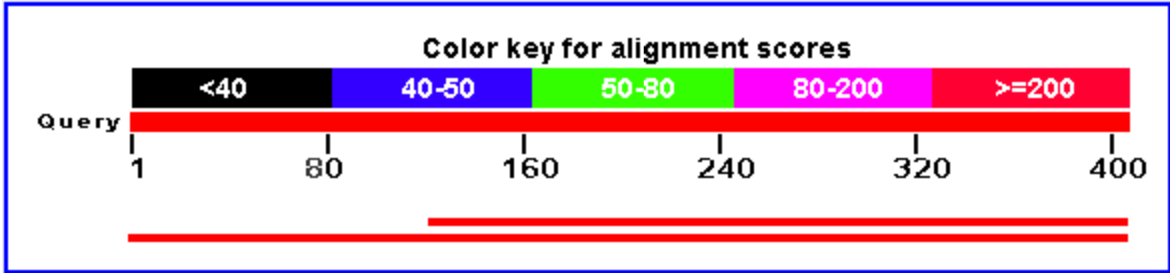
PSB band 1 - odd12/odd48 primers amplification

AY044425.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, complete cds (2869bp)	Query Coverage 70% E value 3e-136 Max identity 97%
AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)	Query Coverage 100% E value 0.0 Max identity 99%



PSB band 2 - odd12/odd48 primers amplification

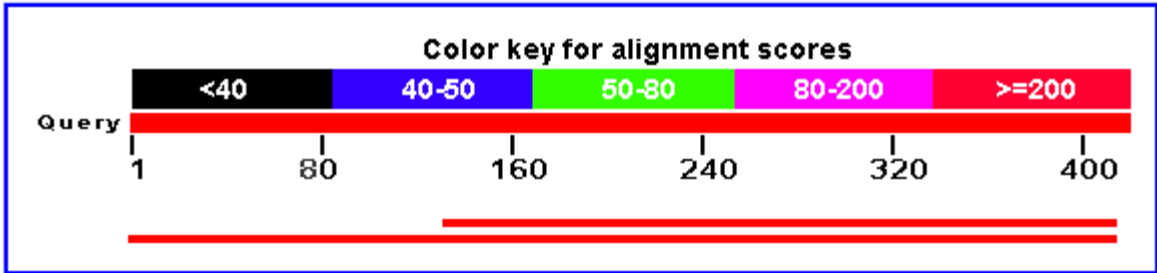
AY044425.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, complete cds (2869bp)	Query Coverage 69% E value 2e-139 Max identity 97%
AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)	Query Coverage 100% E value 0.0 Max identity 100%



BLAST *B.oleracea* collard (AY044425.1), *B.oleracea* broccoli (AY044424.1), *B.rapa* mRNA (EF611253.1) *B.rapa* genomic DNA (EF611252.1) and the two bands of DHAG1012 obtained with PCR amplification with primer odd12/odd48.

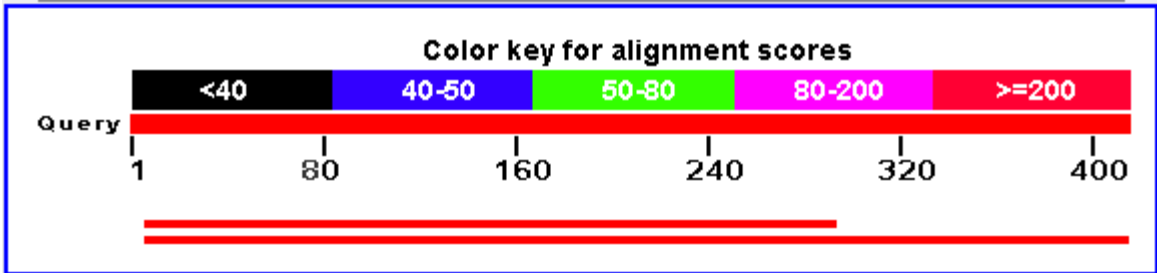
DHAG1012 band 1 - odd12/odd48 primers amplification

AY044425.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, complete cds (2869bp)	Query Coverage 67% E value 4e-135 Max identity 96%
AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)	Query Coverage 98% E value 0.0 Max identity 98%



DHAG1012 band 2 - odd12/odd48 primers amplification

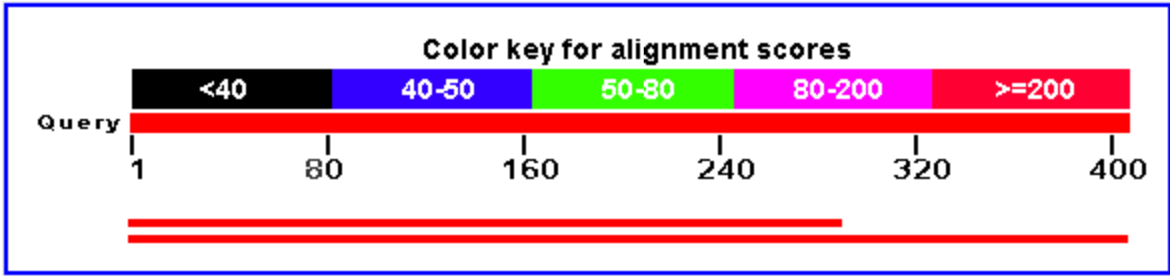
AY044425.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, complete cds (2869bp)	Query Coverage 69% E value 7e-138 Max identity 97%
AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)	Query Coverage 98% E value 0.0 Max identity 99%



BLAST *B.oleracea* collard (AY044425.1), *B.oleracea* broccoli (AY044424.1), *B.rapa* mRNA (EF611253.1) *B.rapa* genomic DNA (EF611252.1) and the one band of Savoy obtained with PCR amplification with primer odd12/odd48.

Savoy band 1 - odd12/odd48 primers amplification

AY044425.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, complete cds (2869bp)	Query Coverage 71% E value 2e-138 Max identity 97%
AY044424.1: Brassica oleracea 2-oxoglutarate-dependent dioxygenase gene, null allele, Complete cds (2939bp)	Query Coverage 100% E value 0.0 Max identity 99%



Contings of sequenced bands from odd12/odd48 PCR amplification.

LEGEND:

K: T/G

Y: T/C

R: G/A

M: A/C

S: G/C

W: A/T

Winspit band1 – 464 bp

TGCGCGGACMGTTCTCTGTTtAGCCTCACTGGTAACCSAAAAGCTCTATCATGGCATCCAAAAGTACTTCTTAAGCTCTTCTGACWcTCT
ATCATATGACACCTCAAAAGCGCCGKASTCTKCARGAGCTYTACGGACATCACTCCTCACTTCAACCCACTTCTCACCTCCTGGTTTTAG
GGTTTGGTCCGAGAGATAGATGACTGGAAGTTGAGGAGTGTCTGCACCCATTCTTTTYKICCTTTGGTGCAAATCCAAAAATATATTYATAA
AAKGTTAATTAGCTTTATATTTTAACCCGAAAGAAAATRTTTAAGTRRCTTTAATCATCACAAACAAAAGAAAACATTAATAAACTCATAAGAC
AAaCTACCTTTGGAGTTTTCTTTGATTCAAAaGAGATCAAGCTGGT

Winspit band2 – 426 bp

GYYtCGGAGAcacGTTTTtCTGTTAGCCTCACTGGKWACTCGAAAAGCTCTATCATGGCATCCAAAAGTACTTCTTAAGCTCTTCTGACAC
TCTATCATATGACACCTCAAAAGCGCCGTAGTCTTCAAGAGCTTTACGGACATCACTCCTCACTTCAACCCACTTCTCACCTCCTGGTTTT
AGGGTTTGGTCCGAGAGATAGATGACTGGAAGTTGAGGAGTGTCTGCACCCATTCTTTTTTCTTTGGTGCAAATCCAAAAATATATTTAT
AAAATGTTAATTAGCTTTATATTTTAACCCGAAAGAAAATGTTAAGTMSCTCTTTAATCATCACWACAAAAGAAAACATTAATAAACTCATAAR
ACAACCTACCTTTGGAGTTTTCTTTGATTCAAAGAGATCAAGCTGGTTtC

Winspit band3 – 408 bp

TGTTtAGCCTCAaCTGGTAaCTCGaAAAGCTCTATCATGGCATCCAAAAGTACTTCTTAAGCTCTTCTGACACTCTATCATATGACACCTCA
AAAGCGCCGTAGTCTTCAAGAGCTTTACGGACATCACTCCTCACTTCAACCCACTTCTCACCTCCTGGTTTTAGGGTTTGGTCCGAGAGA
TAGATGACTGGAAGTTGAGGAGTGTCTGCACCCATTCTTTTTTCTTTGGTGCAAATCCAAAAATATATTTATAAAATGTTAATTAGCTTTAT
ATTTAACCCGAAAGAAAATGTTAAGTAGCTCTTTAATCATCACAAACAAAAGAAAACATTAATAAACTCATAAGACAACCTACCTTTGGAGTTT
TTCTTTGATTCAAAGAGATCAAGCTGGTTtCTTTtC

PSB band1 – 400bp

GTTtAGCCTCaACTGGTAaCTCGaAAAGCTCTATCATGGCATCCAAAAGTACTTCTTAAGCTCTTCTGACACTCTATCATATGACACCTCAA
AAGCGCCGTAGTCTTCAAGAGCTTTACGGACATCACTCCTCACTTCAACCCACTTCTCACCTCCTGGTTTTAGGGTTTGGTCCGAGAGAT
AGATGACTGGAAGTTGAGGAGTGTCTGCACCCATTCTTTTTTCTTTGGTGCAAATCCAAAAATATATTTATAAAATGTTAATTAGCTTTATA
TTTTAACCCGAAAGAAAATGTTAAGTAGCTCTTTAATCATCACAAACAAAAGAAAACATTAATAAACTCATAAGACAACCTACCTTTGGAGTTT
TCTTTGATTCAAAGAGATCAAGCTGGTTtC

PSB band2 - 406bp

AAGaaAACCAGCTTGATCTCTTTGAATCAAAGAAAAACTCCAAAGGTAGTTGTCTTATGAGTTTTTAATGTTTTCTTTTGTGTGATGATTAA
AGAGCTACTTAACATTTTTCTTTGGGTTAAATATAAAGCTAATTAACATTTTATAAATATATTTTTGGATTTGCACCAAAGGAAAAAAGAAT
GGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAAACCCTAAAACCAGGAGGTGAGAAGTGGGTTGAAGTGAGGAGT
GATGTCCGTAAAGCTCTTGAAGACTACGGCGCTTTTGAGGTGTATATGATAGAGTGTGAGAAGAGCTTAAGAAGTCAGTTTTGGATGCC
ATGATAGAGCTTTtCGAGTTACCAGTtGAGGCTAAaCAGA

DHAG1012 band1 – 466bp

ACTAaGGAAAAAGAAAACYAGCTTGATCTCTTTGAATCAAAGAAAAACTCCAAAGGTAGTTKTCTTATGARTTTTTAATGTTTTCTTTTGTGT
GATGATTAAAGAGCTACTTAACATTTTTCTTTGGGTTAAATATAAAGCTAATTAACATTTTATAAATATATTTTTGGATTTGCACCAAAGGAA
AAAAAGAATGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAAACCCTAAAACCAGGARGTGAGAAGTGGGTTGAAG
TGAGGAGTGATGTCCGTAAAGCTCTTGAAGACTACGGCGCTTTTGAGGTGTATATGATAGAGTGTGAGAAGAGCTTAAGAAGTCAGTTT
TGGATGCCATGATAGAGCTTTTTCGAGTACCAGTGAGCTAMACAGAGAACKTBC

DHAG1012 band 2– 419bp

MCASGTgTTCTCtGgTTTAGCCTCACTGGTaACTCGAAAAGCTCTATCATGGCATCCAAAAGTACTTCTTAAGCTCTTCTGACACTCTATCA
TATGACACCTCAAAAGCGCCGTAGTCTTCAAGAGCTTTACGGACATCACTCCTCACTTCAACCCACTTCTCACCTCCTGGTTTTAGGGTTT
GGTCCGAGAGATAGATGACTGGAAGTTGAGGAGTGTCTGCACCCATTCTTTTTTTCCTTTGGTGCAAATCCAAAAATATATTATAAAATGT
TAATTAGCTTTATATTTTAACCCGAAAGAAAATGTTTAAGTAGCTCTTTAATCATCACAAACAAAAGAAAACATTAAAAACTCATAAGACAAC
TA
CCTTTGGAGTTTTTCTTTGATTCAAAGAGATCAAGCTGGTTTTCT

SAV – 409bp

TTCTCTGTtAGCCTCaACTGGgTAACTCGcAAAAGCTCTATCATGGCATCCAAAAGTACTTCTTAAGCTCTTCTGACACTCTATCATATGAC
ACCTCAAAAGCGCCGTAGTCTTCAAGAGCTTTACGGACATCACTCCTCACTTCAACCCACTTCTCACCTCCTGGTTTTAGGGTTTGGTCC
GAGAGATAGATGACTGGAAGTTGAGGAGTGTCTGCACCCATTCTTTTTTTCCTTTGGTGCAAATCCAAAAATATATTATAAAATGTTAATTA
GCTTTATATTTTAACCCGAAAGAAAATGTTTAAGTAGCTCTTTAATCATCACAAACAAAAGAAAACATTAAAAACTCATAAGACAAC
TACCTTTG
GAGTTTTTCTTTGATTCAAAGAGATCAAGCTGGT

CLUSTAL 2.1 multiple sequence alignment

WINSPIT Band1 AOP2

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BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  AAAAAAAAAAATAGAAATGTTTCTGTCTATAAATGGGCATTCCATCATTT 50
BoCollardCompleteCDS         -----
WinspitBand1                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  ACTTCTCTAGTACGGAAGCAAAAAAAAAAACTAAGGAAAAGAAAACAGCT 100
BoCollardCompleteCDS         -----AAAAAACCTAAGGAAAAGAAAACAGCT 29
WinspitBand1                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  TGATCTCTTTGAATCAAGAAAAA----- 123
BoCollardCompleteCDS         TGATCTCTTTGAATCAAGAAAACTCCAAGGTAATTTTGGTAAAATGTT 79
WinspitBand1                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  ---ACTCCAAAGGTAGTTGT-CTTATGAGTTTTTAATGTTTTCTTTTGT 168
BoCollardCompleteCDS         AAATACTCCAAAGGTAGTTTTTCTTATGAATTTTGAAATGTTTCTTTTGT 129
WinspitBand1                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  TGTGATGATTAAAGAGCTACTTAACATTTTCTTTCGGGTAAAAATA--- 215
BoCollardCompleteCDS         GTGGGTGATTAAAGAGTTACTTAATATTTTCTTTCGGGTAAAAATAAG 179
WinspitBand1                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  -----TAAAGCTAATT 226
BoCollardCompleteCDS         CTAAATTAATTAGTTTACTAAAAAAAAATTAAAAAAAAATAAAGCTAATT 229
WinspitBand1                  -----

BrCompleteCDSGenomicDNA      -----A 1
BrCompleteCDSmDNA             -----A 1
BoBroccoliNullAlleleGenomicDNA  AACATTTTATAAATATATTTTTT--GGATTTGCACCAAAGGAAAAAAGAA 274
BoCollardCompleteCDS         AACATTTTATGAATATATTTTTTTGGATTTGCACCAAAGGCGAAAA-GAA 278
WinspitBand1                  -----

BrCompleteCDSGenomicDNA      TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 51
BrCompleteCDSmDNA             TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 51
BoBroccoliNullAlleleGenomicDNA  TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 324
BoCollardCompleteCDS         TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 328
WinspitBand1                  -----WAWAWNNT--NCDTGSWTTCTACTCTSTCT-GACGCRWCM 38
                                *  *  *      **  *  *  *  *  *  *

BrCompleteCDSGenomicDNA      CTAAAAACAG---GAAGTGAGAAGT-GGGTTGAAGTGAGGAGTGATGTCC 97
BrCompleteCDSmDNA             CTAAAAACAG---GAAGTGAGAAGT-GGGTTGAAGTGAGGAGTGATGTCC 97
BoBroccoliNullAlleleGenomicDNA  CTAAAAACAG---GAGGTGAGAAGT-GGGTTGAAGTGAGGAGTGATGTCC 370
BoCollardCompleteCDS         CTAAAAACAG---GAAGTGAGAAGT-GGGTTGAAGTGAGGAGTGATGTCC 374
WinspitBand1                  CTRWRRCAGAGARATGTGAGAAGTAGGGTTGAAGTGAGGAGTGATGTCC 88
                                **      ****      *  *****  *****

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BrCompleteCDSGenomicDNA	GTAAAGCTCTTGAAGACTACGGCGGTTTTGAGGTGTCATATGATAGAGTG	147
BrCompleteCDSmDNA	GTAAAGCTCTTGAAGACTACGGCGGTTTTGAGGTGTCATATGATAGAGTG	147
BoBroccoliNullAlleleGenomicDNA	GTAAAGCTCTTGAAGACTACGGCGGTTTTGAGGTGTCATATGATAGAGTG	420
BoCollardCompleteCDS	GTAAAGCTCTTGAAGACTACGGCGGTTTTGAGGTGTCATATGATAGAGTG	424
WinspitBand1	GTAAAGCTCTTGAAGACTACGGCGGTTTTGAGGTGTCATATGATAGAGTG	138

BrCompleteCDSGenomicDNA	TCAGAGGAGCTGAAGAAGTCAGTTTGGATGCCATGATAGAGCTTTTCGA	197
BrCompleteCDSmDNA	TCAGAGGAGCTGAAGAAGTCAGTTTGGATGCCATGATAGAGCTTTTCGA	197
BoBroccoliNullAlleleGenomicDNA	TCAGAAGAGCTTAAGAAGTCAGTTTGGATGCCATGATAGAGCTTTTCGA	470
BoCollardCompleteCDS	TCAGAAGAGCTTAAGAAGTCAGTTTGGATGCCATGATAGAGCTTTTCGA	474
WinspitBand1	TCAGAAGAGCTTAAGAAGTCAGTTTGGATGCCATGATAGAGCTTTTCGA	188

BrCompleteCDSGenomicDNA	GTTACCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTG	247
BrCompleteCDSmDNA	GTTACCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTG	247
BoBroccoliNullAlleleGenomicDNA	GTTACCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTG	520
BoCollardCompleteCDS	GTTACCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTG	524
WinspitBand1	GTTACCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTG	238

BrCompleteCDSGenomicDNA	GATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAAATTC	297
BrCompleteCDSmDNA	GATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAAATTC	297
BoBroccoliNullAlleleGenomicDNA	GATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAAATTC	570
BoCollardCompleteCDS	GATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAAATTC	574
WinspitBand1	GATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAAATTC	288

BrCompleteCDSGenomicDNA	AATGTTTT-GGAGAAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATT	346
BrCompleteCDSmDNA	AATGTTTT-GGAGAAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATT	346
BoBroccoliNullAlleleGenomicDNA	AATGTTTT-GGAGAAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATT	619
BoCollardCompleteCDS	AATGTTTT-GGAGAAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATT	623
WinspitBand1	AATGTTTTGGAGAAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATT	338

BrCompleteCDSGenomicDNA	GTGAGGGTAACAAGAGTATGAGGTAAACGTCATGTCAAAAAAAAAAAAACT	396
BrCompleteCDSmDNA	GTGAGGGTAACAAGAGTATGAG-----	368
BoBroccoliNullAlleleGenomicDNA	GTGAGGGTAACAAGACTATGAGGTAAACGTCATGTCAAAAAAAAAAAAACT	669
BoCollardCompleteCDS	GTGAGGGTAACAAGACTATGAGGTAAACGTCATGTCAAAAAAAAAAA--CT	671
WinspitBand1	GTGAGGGTAACAAGACTATGAG-----	360

BrCompleteCDSGenomicDNA	AAGTAATGCTTCGTAGAGTATATT---GTTTCGTAACCTCCTGTTATTTT	442
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	CAGTAATGCTTCATAGAGTAAATTAATTGTTTCGTAATTCCTGTTAATCT	719
BoCollardCompleteCDS	CAGTAATGCTTCATAGAGTAAATTAATTGTTTCGTAATTCCTGTAA--TC	719
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	TTAATCAAAAAATATTTTCGTAATTTTTTTGTTAGTTGCTTTT-ATAAGCT	491
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TTCATCAAAAAATATTTTCGTAACTTTTT-GCTAGTTGTTTTTCATAAGTT	768
BoCollardCompleteCDS	TTCATCAAAAAATATTT-CGTAACTTTTT-GCTAGTTGTTTTT-ATAAGGT	766
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	ATGTAAACAATTTTCTATATAAACCTTGTTTTTATTTTTATTTTTTTGGA	541
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ATGTGACAAATTTCTATAAAAAACCTTGTTTTTATCTTTATTTTTTTGGA	818
BoCollardCompleteCDS	ATGTGACAAATTTCTATA-AAAACCTTGTTTTTATCTTTATTTTTTTGGA	815
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	AAAAATGTCAGTTCCTTATATAGTAATGAACTGAAATTTGTTTTCAATC	591
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AAAAATGTTAGTTCCTCATATAGTAATGAACTGAAATTTGTTTTCAATC	868
BoCollardCompleteCDS	AAAAATGTTAGTTCCTCATATAGTAATGAACTGAAATTTGTTTTCAATC	865
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	TCACGTTTCTCGCATTTTATTTTCTGTTTCTATTAAAAATAGCTATATAA	641

BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TCACGTTTCACGCATTT--TTTTTGTCTTCTATTAAAATAGCTATATAA	915
BoCollardCompleteCDS	TCACGTTTCACGCATTT--TTTTTGTCTTCTATTAAAATAGCTATATAA	912
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	--TTTTCTTTGTGTTGAAAACAGCGAAACGATCCAGAATTTTTCAGAGAA	689
BrCompleteCDSmDNA	-----CGAAACGATCCAGAATTTTTCAGAGAA	395
BoBroccoliNullAlleleGenomicDNA	A-TTTTCTTTGTGTTGAAAACAGCGAAACGATCCAGAAGTTTTCAGAGAA	964
BoCollardCompleteCDS	ATTTTCTTTGTGTTGAAAACAGCGAAACGATCCAGAAGTTTTCAGAGAA	962
WinspitBand1	-----CGAAACGATCCAGAAGTTTTCAGAGAA	387

BrCompleteCDSGenomicDNA	GTTAGCAGAATTGGATGTAATGGTGAGAAGAATGGTCATAGAGAGCTTTG	739
BrCompleteCDSmDNA	GTTAGCAGAATTGGATGTAATGGTGAGAAGAATGGTCATAGAGAGCTTTG	445
BoBroccoliNullAlleleGenomicDNA	GTTAGCAGAATTGGATGTAATGGTGAGAAGAATGGTCATAGAGAGCTTTG	1014
BoCollardCompleteCDS	GTTAGCAGAATTGGATGTAATGGTGAGAAGAATGGTCATAGAGAGCTTTG	1012
WinspitBand1	GTTAGCAGAATTGGATGTAATGGTGAGAAGAATGGTCATAGAGAGCTTTG	437

BrCompleteCDSGenomicDNA	GGATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAA-TTACCGTTT	788
BrCompleteCDSmDNA	GGATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAA-TTACCGTTT	494
BoBroccoliNullAlleleGenomicDNA	GGATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAA-TTACCGTTT	1063
BoCollardCompleteCDS	GGATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAA-TTACCGTTT	1061
WinspitBand1	GGATAGAAAACACTTTTGATGAAYWCCTCWMGTCMWCGAAGTTPSCGTCW	487

BrCompleteCDSGenomicDNA	GCGACTGATGAAATATGTAGCACCACTGACGTTGATGCTAATGTTGCGG	838
BrCompleteCDSmDNA	GCGACTGATGAAATATGTAGCACCACTGACGTTGATGCTAATGTTGCGG	544
BoBroccoliNullAlleleGenomicDNA	GCGACTGATGAAATATGTAGCACCACTGATGTTGATGCTAATGTTGCGG	1113
BoCollardCompleteCDS	GCGACTGATGAAATATGTAGCACCACTGATGTTGATGCTAATGTTGCGG	1111
WinspitBand1	GCSACTGATGAASTMTGYASCMCCACYKARTGTTTATGTAATGTTGCGG	537
	** ***** * ** * * ***** ** ** *****	
BrCompleteCDSGenomicDNA	TTGGTACTAAAGATTCTGATGATGGTGCTAATACGAATACAACGCTAAT	888
BrCompleteCDSmDNA	TTGGTACTAAAGATTCTGATGATGGTGCTAATACGAATACAACGCTAAT	594
BoBroccoliNullAlleleGenomicDNA	TCAGTACTAAAGATTCTGTTGATGGTGCTAATACGAATACAACGCTAAT	1163
BoCollardCompleteCDS	TCAGTACTAAAGATTCTGTTGATGGTGCTAATACGAATACAACGCTAAT	1161
WinspitBand1	TTGGTACTAAAGATTCTGATGATGGTGCTAATACGAATACAACGCTAAT	587
	* ***** ***** *****	
BrCompleteCDSGenomicDNA	GCTGATGCTGATGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGA	938
BrCompleteCDSmDNA	GCTGATGCTGATGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGA	644
BoBroccoliNullAlleleGenomicDNA	GCTGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGA	1213
BoCollardCompleteCDS	GCTGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGA	1211
WinspitBand1	GCTGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGA	637
	***** *****	
BrCompleteCDSGenomicDNA	CGATGCTGATGCCAAGGGTGACGTTTGCACGTTGCTGGTACCAATCATA	988
BrCompleteCDSmDNA	CGATGCTGATGCCAAGGGTGACGTTTGCACGTTGCTGGTACCAATCATA	694
BoBroccoliNullAlleleGenomicDNA	CGATGCTAATGCCAAGGGTGACGTTTGCACGTTGCTGGTACCAATCATA	1263
BoCollardCompleteCDS	CGATGCTAATGCCAAGGGTGACGTTTGCACGTTGCTGGTACCAATCATA	1261
WinspitBand1	CGATGCTAATGCCAAGGGTGACGTTTGCACGTTGCTGGTACCAATCATA	687
	***** *****	
BrCompleteCDSGenomicDNA	ATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTC	1038
BrCompleteCDSmDNA	ATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTC	744
BoBroccoliNullAlleleGenomicDNA	ATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTC	1313
BoCollardCompleteCDS	ATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTC	1311
WinspitBand1	ATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTC	737

BrCompleteCDSGenomicDNA	GACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAA	1088
BrCompleteCDSmDNA	GACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAA	794
BoBroccoliNullAlleleGenomicDNA	GACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAA	1363
BoCollardCompleteCDS	GACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAA	1361
WinspitBand1	GACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAA	787

BrCompleteCDSGenomicDNA	CACTGGCACTATTGATGATGTTAATGCTAATGCTGGTACTCGTAGTAGTG	1138
BrCompleteCDSmDNA	-----TGCTAATGCTGGTACTCGTAGTAGTG	820
BoBroccoliNullAlleleGenomicDNA	CATTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACTCGTAGTAGTG	1413
BoCollardCompleteCDS	CATTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACTCGTAGTAGTG	1411
WinspitBand1	CATTGGCACTATTGCTGATGTTWAGGCTAATACTGGTACTCGTAGTAGTG	837

BrCompleteCDSGenomicDNA	CTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGAT	1188
BrCompleteCDSmDNA	CTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGAT	870
BoBroccoliNullAlleleGenomicDNA	CTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGAT	1463
BoCollardCompleteCDS	CTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGAT	1461
WinspitBand1	CTACTGTTGGCGTTAGTGATAGTGTTCAAGCTAATGGTGGCGCAGATGAT	887

BrCompleteCDSGenomicDNA	GAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGAC	1238
BrCompleteCDSmDNA	GAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGAC	920
BoBroccoliNullAlleleGenomicDNA	GAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAA--ACCTTTTGAC	1511
BoCollardCompleteCDS	GAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGAC	1511
WinspitBand1	GAGGAGAAGAAATTAGGTCTACCTTCTCACACTGATAAAACCTTTTGAC	937

BrCompleteCDSGenomicDNA	GGTACTTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATG	1288
BrCompleteCDSmDNA	GGTACTTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATG	970
BoBroccoliNullAlleleGenomicDNA	GGTGCTTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATG	1561
BoCollardCompleteCDS	GGTGCTTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATG	1561
WinspitBand1	GGTACTTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAAMCAAAGATG	987

BrCompleteCDSGenomicDNA	AAAAGTGGATCAGGTT-AAAACCATCTCATAACTCTTTCGTTGTTATGGC	1337
BrCompleteCDSmDNA	AAAAGTGGATCAGGTT-AAAACCATCTCATAACTCTTTCGTTGTTATGGC	1019
BoBroccoliNullAlleleGenomicDNA	AAAAGTGGATCAGGTT-AAAACCATCTCATAACTCTTTCGTTGTTATGGC	1610
BoCollardCompleteCDS	AAAAGTGGATCAGGTT-AAAGCCATCTCATAACTCTTTCGTTGTTATGGC	1610
WinspitBand1	AAAAGTGGATCAGGTTTAAAACCATGTCTAACTCTTTCGTTGTTATGGC	1037

BrCompleteCDSGenomicDNA	TGGAGATTC-TCTATATGTAAGTTCTAACTTATTTTATTTTAAATGGGA	1386
BrCompleteCDSmDNA	TGGAGATTC-TCTATATG-----	1036
BoBroccoliNullAlleleGenomicDNA	TGGAGATTC-TCTATATGTAAGTTCTAACTTATTTTATTTTAAATGGGA	1659
BoCollardCompleteCDS	TGGAGATTC-TCTATATGTAAGTTCTAACTTATTTTATTTTAAATGGGA	1659
WinspitBand1	TGGAGATTCSTCTATATGCA-----	1057

BrCompleteCDSGenomicDNA	TGCACC-----	1392
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TGCACCATAATATCTTAATTGCGATCATCATAATAATCATAAAGTTTATTA	1709
BoCollardCompleteCDS	TGCACCATAATATCTTAATTGCGATCATCATAATAATCATAAAGTTTATTA	1709
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TGATATATATTATAACTTTATGATATACATATTCATAAAGTTTATGATATA	1759
BoCollardCompleteCDS	TGATATATATTATAACTTTATGATATACATATTCATAAAGTTTATGATATA	1759
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----TTTTTATTTTTCCTATCACTTTTACAAATGC	1424
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AATATTACATAAATTCACCTTTTTATTTATTTCTTATCACTTTTACAAATGC	1809
BoCollardCompleteCDS	AATATTACATAAATTCACCTTTTTATTTATTTCTTATCACTTTTACAAATGC	1809
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	ATGTCTTTTCTTTACTAAAGTGTATACATTAACATTATATGTTTTCTT	1474
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ATGTCTG--ACGTTACTAAAGTGTATACATTAACATTA--TGTTTTCTT	1855
BoCollardCompleteCDS	ATGTCTG--ACGTTACTAAAGTGTATACATTAACATTA--TGTTTTCTT	1855
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	CTCATCATGAAACTTGTTTTGATTTTGTATTATT-TTGTTTGCAGGCA	1523
BrCompleteCDSmDNA	-----CA	1038

BoBroccoliNullAlleleGenomicDNA	CTCATCATGAATCTTGTGTTGGTTTTTTTATTATTATTTTTTGCAGGCA	1905
BoCollardCompleteCDS	CTCATCATGAATCTTGTGTTGGTTTTTTTATTATTATTTTTTGCAGGCA	1905
WinspitBand1	-----R	1058
BrCompleteCDSGenomicDNA	CTTATGAATGGTAGA-CTGT-CTCGTCCG-TTTCATAGAGTAAGAGTAAC	1570
BrCompleteCDSmDNA	CTTATGAATGGTAGA-CTGT-CTCGTCCG-TTTCATAGAGTAAGAGTAAC	1085
BoBroccoliNullAlleleGenomicDNA	CTTATGAATGGTAGA-CTAT-CTCGTCCG-TTTCATAGAGTAAGAGTAAC	1952
BoCollardCompleteCDS	CTTATGAATGGTAGA-CTAT-CTCGTCCG-TTTCATAGAGTAAGAGTAAC	1952
WinspitBand1	CTTATGAATGGTAGAACTATTCTCGTCCGATWTCATAGAGTAAGAGTAAC	1108
	***** ** *	
BrCompleteCDSGenomicDNA	GGAAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACG	1620
BrCompleteCDSmDNA	GGAAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACG	1135
BoBroccoliNullAlleleGenomicDNA	GGAAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACG	2002
BoCollardCompleteCDS	GGAAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACG	2002
WinspitBand1	GGAAAGAAASMMGACAAGGTATTCAATAGCATTGTTSSWSGACTCCAAWCS	1158
	***** ***** *	
BrCompleteCDSGenomicDNA	G-AGATTACATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCC	1669
BrCompleteCDSmDNA	G-AGATTACATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCC	1184
BoBroccoliNullAlleleGenomicDNA	G-AGATTACATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCC	2051
BoCollardCompleteCDS	G-AGATTACATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCC	2051
WinspitBand1	RGAGAKTACATCATCGAAYYACCAAAAGASCWTGTGGACGAGAAGCACCC	1208
	*** ***** *	
BrCompleteCDSGenomicDNA	ACGTCTCTTCAAACCATTCACCTACGTTGACTTGATGAGTTTCTATCACA	1719
BrCompleteCDSmDNA	ACGTCTCTTCAAACCATTCACCTACGTTGACTTGATGAGTTTCTATCACA	1234
BoBroccoliNullAlleleGenomicDNA	ACGTCTCTTCAAATCATTCACCTACGTTGACTTGATGAGTTTCTATCACA	2101
BoCollardCompleteCDS	ACGTCTCTTCAAACCATTCACCTACGTTGACTTGATGAGTTTCTATCACA	2101
WinspitBand1	AYGTCTSWTCAAACCTKCWCKTAMRYTGACTTGAYMGTYTCTATCMCA	1258
	* **** * * * *	
BrCompleteCDSGenomicDNA	CTGAGGCTGGTCGTAGAGCTCGTTCTACTCTTACGCTTATTGTGCCGTC	1769
BrCompleteCDSmDNA	CTGAGGCTGGTCGTAGAGCTCGTTCTACTCTTACGCTTATTGTGCCGTC	1284
BoBroccoliNullAlleleGenomicDNA	CTGAGGCTGGTCGTAGACCTCGTTCTACTCTTACGCTTATTGTGCCGTC	2151
BoCollardCompleteCDS	CTGAGGCTGGTCGTAGACCTCGTTCTACTCTTACGCTTATTGTGCCGTC	2151
WinspitBand1	VYGAGGCTGGTCGTAGACCTACGWMTAY-SYSTGGHGNANNBY----	TB 1303
	***** ** * *	
BrCompleteCDSGenomicDNA	TCTGGAGCATAA-----	1781
BrCompleteCDSmDNA	TCTGGAGCATAA-----	1296
BoBroccoliNullAlleleGenomicDNA	TCTGGAGCATAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTA	2201
BoCollardCompleteCDS	TCTGGAGCATAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTA	2201
WinspitBand1	YTW-----	1306
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AGTAGTTTCATGGTTCAACTAATATCAAGAAGTGCATGTAGTACTAAA-T	2250
BoCollardCompleteCDS	AGTAGTTTCATGGTTCAACTAATATCAAGAAGTGCATGTAGTACTAAAA	2251
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AAGAGTTTTTGGATTAGTTGAGTATATGTGTTTTATTTCCGGGAGAAGCAA	2300
BoCollardCompleteCDS	AAGAGTTTTTGGATTAGTTGAGTATATGTGTTTTATTTCCGGGAGAAGCAA	2301
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TCAAGTCTCTCTTTTGTATGAAAAATCAATAAAA-ATATGTGTATGAGCA	2349
BoCollardCompleteCDS	TCAAGTCTCTCTTTTGTATGAAAAATCAATAATGTGTATGTGTATGAGCA	2351
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TGTTCAATAATGTAAATGAATTTGGTTGGATCTGTTGGTTTACAAGATGTC	2399
BoCollardCompleteCDS	TGTTCAATAATGTAAATGAATTTGGTTGGATCTGTTGGTTTACAAGATGTC	2401
WinspitBand1	-----	

BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AAGATCGTAAATAGGTTAATTAAATAGGTTAATTTCTTCTTCTTTTAA	2449
BoCollardCompleteCDS	AAGATCGTAAATAGGTTAATTAAATAGGTTAATTTCTTCTTCTTTTAA	2451
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ACTAAATTAAATTCATTTTTTTTTTATAAAAAATACTAGTTTAATTCAG	2499
BoCollardCompleteCDS	ACTAAATTAAATTCATTTTTTTTTTCTAAAAATACTAGTTTAATTCAG	2501
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	GAGATGGGAAACGAGTGTGGAACATATAAAAACTGGTGTGCGATTTC	2549
BoCollardCompleteCDS	GAGATGGGAAACGAGTGTGGAACATATAAAAAACGGGTGTGCGATTTC	2551
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AACATTAAACGCTAAATAAGTGAATGATTTACTTTCATGTTATCGTAGCG	2599
BoCollardCompleteCDS	AACATTAAACGCTAAATAAGTGAATGATTTACTTTCATGTTATCGTAGCG	2601
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ACAGTGGTTTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTT	2649
BoCollardCompleteCDS	ATAGTGGTCTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTT	2651
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TGTTTGCAAAATGCCAAAATCGTAAATAGTAGTAAATAGTAATGTTATT	2699
BoCollardCompleteCDS	TGTTTGCAAAATGCCAAAATCGTAAATAGT---AAATTAATAATGTTATT	2698
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TAAAGTTTGACTGGTTTAATTGCAGTAGGTGTATGTGCTGTGGTCCAAAA	2749
BoCollardCompleteCDS	TAAAGTTTGACCGGTTTACTTGCAATAGGTGTATGTGCTGTGGTCCAAAA	2748
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ATTAGTGAAACGAATAATT-CAATTGTAAATTAGTAATGTTATTTAAAA	2798
BoCollardCompleteCDS	ATTAGTGAACTAATAATTACAATTGTAAATTAGTAATGTTATTTAAAA	2798
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ATAGACATGCATTGTCTCATGAACAAAAGTGGTTGAAATAGCGATTTGCAA	2848
BoCollardCompleteCDS	ATAGACATGCATTGTCTCATGAACAAAAGTGGTTGAAATAGCGATTTGCAA	2848
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	GTGCCAACTCTCTTCTTATGAACAACGTTACAAATTAGGACCGGCTTGGG	2898
BoCollardCompleteCDS	GTGCCAACTCTCTTCTCATGA-----	2869
WinspitBand1	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	

BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
WinspitBand1

CAAACCTAACGAAACATTACCTTTAATAAATCACCTTGC 2939

CLUSTAL 2.1 multiple sequence alignment

WINSPIT Band2 AOP2

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BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  AAAAAAAAAAATAGAAATGTTTCTGTCTATAAATGGGCATTCCATCATTT  50
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  ACTTTCTCAGTACGGAAGCAAAAAAAAAACTAAGGAAAAGAAAACAGCT  100
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  TGATCTCTTTGAATCAAGAAAACTCCAAGGTAAATTTGGTAAAAATGTT  79
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  TGATCTCTTTGAATCAAGAAAA  123
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  AAATACTCCAAAGGTAGTTTTCTTATGAATTTTGAAATGTTTCTTTTGT  129
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  ---ACTCCAAAGGTAGTTGT-CTTATGAGTTTTTAATGTTTCTTTTGT  168
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  GTGGGTGATTAAAGAGTTACTTAAATATTTTCTTTCGGGTTAAAAATAAG  179
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  TGTGATGATTAAAGAGCTACTTAAACATTTTCTTTCGGGTTAAAAATA  215
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  CTAATTAATTAGTTTACTAAAAAAAAATTAAAAAAAAATAAGCTAATT  229
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  ---TAAAGCTAATT  226
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  A  1
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  AACATTTTATGAATATATTTTTTTTGGATTTGCACCAAAGGCGAAAAA-GAA  278
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  AACATTTTATAAATATATTTT--TGGATTTGCACCAAAGGAAAAAAGAA  274
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  TGGGTGCAGACACTCCTCAACTTC-CAGTCATCTATCTCTCGGACCAAAC  50
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  TGGGTGCAGACACTCCTCAACTTC-CAGTCATCTATCTCTCGGACCAAAC  50
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  TGGGTGCAGACACTCCTCAACTTC-CAGTCATCTATCTCTCGGACCAAAC  327
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  TGGGTGCAGACACTCCTCAACTTC-CAGTCATCTATCTCTCGGACCAAAC  323
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  ---CGCCGATTTTCAAGTTTTTTTTTGTCTCGAGCGA---  33
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  CCTAAAACAGGAAGTGAGAAGTGGGTTGAAGTGAGGAGTGATGTCCGTA  100
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  CCTAAAACAGGAAGTGAGAAGTGGGTTGAAGTGAGGAGTGATGTCCGTA  100
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  CCTAAAACAGGAAGTGAGAAGTGGGTTGAAGTGAGGAGTGATGTCCGTA  377
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  CCTAAAACAGGAAGTGAGAAGTGGGTTGAAGTGAGGAGTGATGTCCGTA  373
WinspitBand2                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmdDNA            -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  ---TAGGAGAAGAAAAATCG--CGACCCCCGGCTCTG--CG-A  70
WinspitBand2                  -----

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BrCompleteCDSGenomicDNA	AAGCTCTTGAAGACTACGGCGGTTTTGAGGT--GTCATATGATAGAGTGT	148
BrCompleteCDSmDNA	AAGCTCTTGAAGACTACGGCGGTTTTGAGGT--GTCATATGATAGAGTGT	148
BoCollardCompleteCDS	AAGCTCTTGAAGACTACGGCGCTTTTGAGGT--GTCATATGATAGAGTGT	425
BoBroccoliNullAlleleGenomicDNA	AAGCTCTTGAAGACTACGGCGCTTTTGAGGT--GTCATATGATAGAGTGT	421
WinspitBand2	GAGCGTCAACAGGTAATA--GATTGTGTGGTCCATCATCTAAACACCGGT	118
	*** ** *	
BrCompleteCDSGenomicDNA	CAGAGGAGCTGAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAG	198
BrCompleteCDSmDNA	CAGAGGAGCTGAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAG	198
BoCollardCompleteCDS	CAGAAGAGCTTAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAG	475
BoBroccoliNullAlleleGenomicDNA	CAGAAGAGCTTAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAG	471
WinspitBand2	CA-----AGTACTCCTTTTT---CTGTGGCTTAGACTTTCTAT	153
	** * * * *	
BrCompleteCDSGenomicDNA	TTACCAAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTGG	248
BrCompleteCDSmDNA	TTACCAAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTGG	248
BoCollardCompleteCDS	TTACCAAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCTTACACTGG	525
BoBroccoliNullAlleleGenomicDNA	TTACCAAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCTTACACTGG	521
WinspitBand2	TT----GTT---CTAATCCTTCATAAATATCTTTGAG-CTAT-TGCTGT	193
	** *** * * *	
BrCompleteCDSGenomicDNA	-ATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAAATCC	297
BrCompleteCDSmDNA	-ATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAAATCC	297
BoCollardCompleteCDS	-ATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGGATTC	574
BoBroccoliNullAlleleGenomicDNA	-ATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGGATTC	570
WinspitBand2	TATTTTTGGTTT-TACTCTTTCCCTGCGG---GGGATCAGGAGATTT	238
	** * * * *	
BrCompleteCDSGenomicDNA	AATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTG	347
BrCompleteCDSmDNA	AATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTG	347
BoCollardCompleteCDS	AATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTG	624
BoBroccoliNullAlleleGenomicDNA	AATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTG	620
WinspitBand2	--TCTTTTA--AAAGTT-----CCCCAATTCCTGTTTC	268
	* **** * * *	
BrCompleteCDSGenomicDNA	TGAGGGTAACAAGAGTATGAGGTAACGTCATGTCAAAAAAAAAAACTA	397
BrCompleteCDSmDNA	TGAGGGTAACAAGAGTATGAG-----	368
BoCollardCompleteCDS	TGAGGGTAACAAGACTATGAGGTAACGTCATGTCAAAAAAAAAAA--CTC	672
BoBroccoliNullAlleleGenomicDNA	TGAGGGTAACAAGACTATGAGGTAACGTCATGTCAAAAAAAAAAACTC	670
WinspitBand2	TCCGAGCTCCCCGA-CAT-----	285
	* * * * *	
BrCompleteCDSGenomicDNA	AGTAATGCTTCGTAGAGTATATT----GTTTCGTAACCTCCTGTTATTTTT	443
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AGTAATGCTTCATAGAGTAAATTAAATTGTTTCGAAATTCCTGTAATCTTC	722
BoBroccoliNullAlleleGenomicDNA	AGTAATGCTTCATAGAGTAAATTAAATTGTTTCGTAATTCCTGTTAATCTTC	720
WinspitBand2	-----CTTC-----	289
BrCompleteCDSGenomicDNA	TAAATCAAAAATATTTTCGTAATTTTTTTGTTAGTTGCTTTT-ATAAGCTA	492
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	--ATCAAAAATATTT-CGTAACTTTTT-GCTAGTTGTTTTT-ATAAGGTA	767
BoBroccoliNullAlleleGenomicDNA	TCATCAAAAATATTTTCGTAACTTTTT-GCTAGTTGTTTTT-CATAAGGTA	769
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	TGTAAACAATTTTCTATATAAAACCTTGTTTTTATTTTTATTTTTTTGGAA	542
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TGTGACAAATTTCTATA-AAAACCTTGTTTTTATCTTTATTTTTTTGGAA	816
BoBroccoliNullAlleleGenomicDNA	TGTGACAAATTTCTATAAAAACCTTGTTTTTATCTTTATTTTTTTGGAA	819
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	AAATGTCAGTTCACCTTATATAGTAATGAACGAAAAATTTGTTTCAATCT	592
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AAATGTTAGTTCACCTCATATAGTAATGAACGAAAAATTTGTTTCAATCT	866
BoBroccoliNullAlleleGenomicDNA	AAATGTTAGTTCACCTCATATAGTAATGAACGAAAAATTTGTTTCAATCT	869
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	CACGTTTCTCGCATTTTATTTTCTGTTTCTATTAAAAAGCTATATAA-	641


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BrCompleteCDSDNA
BoCollardCompleteCDS
BoBroccoliNullAlleleGenomicDNA
WinspitBand2
-----
CACGTTTCACGCATTT--TTTTTTGTTTCTATTAAAAAGCTATATAAA 913
CACGTTTCACGCATTT--TTTTTTGTTTCTATTAAAAAGCTATATAAA 916
-----

BrCompleteCDSDNA
BrCompleteCDSDNA
BoCollardCompleteCDS
BoBroccoliNullAlleleGenomicDNA
WinspitBand2
-----
-TTTTCTTTGTGTTGAAAAACAGCGAAACGATCCAGAATTTTTCAGAGAAG 690
-----CGAAACGATCCAGAATTTTTCAGAGAAG 396
TTTTTCTTTGTGTTGAAAAACAGCGAAACGATCCAGAAGTTTTCAGAGAAG 963
-TTTTCTTTGTGTTGAAAAACAGCGAAACGATCCAGAAGTTTTCAGAGAAG 965
-----AAACGACCC---CCCCTCGAGGA-309
***** ** **

BrCompleteCDSDNA
BrCompleteCDSDNA
BoCollardCompleteCDS
BoBroccoliNullAlleleGenomicDNA
WinspitBand2
TTAGCAGAATTGGATGTAAATGGTGAGAAGAATGGTCATAGAGAGCTTTGG 740
TTAGCAGAATTGGATGTAAATGGTGAGAAGAATGGTCATAGAGAGCTTTGG 446
TTAGCAGAATTGGATGTAAATGGTGAGAAGAATGGTCATAGAGAGCTTTGG 1013
TTAGCAGAATTGGATGTAAATGGTGAGAAGAATGGTCATAGAGAGCTTTGG 1015
TTATCTTC-TTGTGTGGAACTTTATTTTTTTTTTTTCTGTAA--TTCTAA 356
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BrCompleteCDSDNA
BrCompleteCDSDNA
BoCollardCompleteCDS
BoBroccoliNullAlleleGenomicDNA
WinspitBand2
GATAGAAAACACTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGC 790
GATAGAAAACACTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGC 496
GATAGAAAACACTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGC 1063
GATAGAAAACACTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGC 1065
TCAGGAAAACCTCTCTCCACGTCCTCC--CCAAAGGGGTTCATTAC 403
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BrCompleteCDSDNA
BrCompleteCDSDNA
BoCollardCompleteCDS
BoBroccoliNullAlleleGenomicDNA
WinspitBand2
GACTGATGAAATATGTAGCACCACCTGACGTTGATGCTAATGTTGCGGTT 840
GACTGATGAAATATGTAGCACCACCTGACGTTGATGCTAATGTTGCGGTT 546
GACTGATGAAATATGTAGCACCACCTGATGTTGATGCTAATGTTGCGGTC 1113
GACTGATGAAATATGTAGCACCACCTGATGTTGATGCTAATGTTGCGGTC 1115
-----TTTTTAACCATC--CTTAGGTGT--ACCCCCACCC 437
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BrCompleteCDSDNA
BrCompleteCDSDNA
BoCollardCompleteCDS
BoBroccoliNullAlleleGenomicDNA
WinspitBand2
GGTACTAAAGATTCTGATGATGGTGCTAATACGAATACAACCTGCTAACGC 890
GGTACTAAAGATTCTGATGATGGTGCTAATACGAATACAACCTGCTAACGC 596
AGTACTAAAGATTCTGTTGATGGTGCTAATACGAATACAACCTGCTAACGC 1163
AGTACTAAAGATTCTGTTGATGGTGCTAATACGAATACAACCTGCTAACGC 1165
GG-GCCGGTGGTTTTCCTCACCATGGT--CGCAGAT-CAGTT-----C 476
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BrCompleteCDSDNA
BrCompleteCDSDNA
BoCollardCompleteCDS
BoBroccoliNullAlleleGenomicDNA
WinspitBand2
TGATGCTGATGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGACG 940
TGATGCTGATGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGACG 646
TGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGACG 1213
TGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGACG 1215
TCATTTCCCTTACCTTTCT-----TCCCCACCGTCCAT-----GGAA 513
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BrCompleteCDSDNA
BrCompleteCDSDNA
BoCollardCompleteCDS
BoBroccoliNullAlleleGenomicDNA
WinspitBand2
ATGCTGATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATCATAAT 990
ATGCTGATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATCATAAT 696
ATGCTAATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATCATAAT 1263
ATGCTAATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATCATAAT 1265
TTTTTGCCCCCAAAGCT--CTCCATAACCAAGT-----CATCTATACCAAT 556
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BrCompleteCDSDNA
BrCompleteCDSDNA
BoCollardCompleteCDS
BoBroccoliNullAlleleGenomicDNA
WinspitBand2
--GGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTC 1038
--GGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTC 744
--GGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTC 1311
--GGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTC 1313
TGGGTCA-GACACTMTM-----AACTCCMGTCATCTATC 591
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BrCompleteCDSGenomicDNA	GACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAA	1088
BrCompleteCDSmDNA	GACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAA	794
BoCollardCompleteCDS	GACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAA	1361
BoBroccoliNullAlleleGenomicDNA	GACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAA	1363
WinspitBand2	--TCTCGG-ACCAA-----ACCCTAAAACAGGA--GGTGA-GAAGTGGG	630
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BrCompleteCDSGenomicDNA	CACTGGCACTATTGATGATGTTAATGCTAATGCTGGTACTCGTAGTAGTG	1138
BrCompleteCDSmDNA	-----TGCTAATGCTGGTACTCGTAGTAGTG	820
BoCollardCompleteCDS	CATTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACTCGTAGTAGTG	1411
BoBroccoliNullAlleleGenomicDNA	CATTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACTCGTAGTAGTG	1413
WinspitBand2	-----TTGAAGTGAGGAGTGATGTCCGTAA-AGCT	659
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BrCompleteCDSGenomicDNA	CT--AATGTT--GGCGTTAGTGATAGTGTTAAAGCTAATGGTGCGCAGA	1184
BrCompleteCDSmDNA	CT--AATGTT--GGCGTTAGTGATAGTGTTAAAGCTAATGGTGCGCAGA	866
BoCollardCompleteCDS	CT--AATGTT--GGCGTTAGTGATAGTGTTAAAGCTAATGGTGCGCAGA	1457
BoBroccoliNullAlleleGenomicDNA	CT--AATGTT--GGCGTTAGTGATAGTGTTAAAGCTAATGGTGCGCAGA	1459
WinspitBand2	CTTGAAAGACTACGGCGCTTTTGA-GGTGTCATA----TGATAGAGTGTC	703
	** ** * ***** ** ***** * * ** * *	
BrCompleteCDSGenomicDNA	TGATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTT	1234
BrCompleteCDSmDNA	TGATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTT	916
BoCollardCompleteCDS	TGATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTT	1507
BoBroccoliNullAlleleGenomicDNA	TGATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAA--CCTTT	1507
WinspitBand2	AGAAGAGCTTAAGAGTCAGTTTTGGATGC-CAT---GATAGAG--CCTTT	748
	* *** ***** * * * * * * * * * * *	
BrCompleteCDSGenomicDNA	TGACGGTACTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAA	1284
BrCompleteCDSmDNA	TGACGGTACTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAA	966
BoCollardCompleteCDS	TGACGGTGCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAA	1557
BoBroccoliNullAlleleGenomicDNA	TGACGGTGCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAA	1557
WinspitBand2	CGAG-----TTACCACTG-TGAGGCTAAACAGAGAAACGTGTCT-CCGAA	790
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BrCompleteCDSGenomicDNA	GATGAAAAGTGGATCAGGTTAAAACCATCTCATAAATCTTTTCGTTGTTAT	1334
BrCompleteCDSmDNA	GATGAAAAGTGGATCAGGTTAAAACCATCTCATAAATCTTTTCGTTGTTAT	1016
BoCollardCompleteCDS	GATGAAAAGTGGATCAGGTTAAAACCATCTCATAAATCTTTTCGTTGTTAT	1607
BoBroccoliNullAlleleGenomicDNA	GATGAAAAGTGGATCAGGTTAAAACCATCTCATAAATCTTTTCGTTGTTAT	1607
WinspitBand2	ACCTTACACTGGAT-----ATTCAACTCATAATGGTCTCTCTGAGA-	831
	* * ***** * * * ***** * * * * *	
BrCompleteCDSGenomicDNA	GGCTGGAGATTC-----TCTATATGTAAGTTCTAACTATTTTATTTTAA	1379
BrCompleteCDSmDNA	GGCTGGAGATTC-----TCTATATG-----	1036
BoCollardCompleteCDS	GGCTGGAGATTC-----TCTATATGTAAGTTCTAACTATTTTATTTTAA	1652
BoBroccoliNullAlleleGenomicDNA	GGCTGGAGATTC-----TCTATATGTAAGTTCTAACTATTTTATTTTAA	1652
WinspitBand2	GTCTAGGGATCCAGGATTCCA-ATGT-----	856
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BrCompleteCDSGenomicDNA	AATGGGATGCACC-----	1392
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AATGGGATGCACCATAATATCTTAATTGCGATCATCATAATAATCATAAAC	1702
BoBroccoliNullAlleleGenomicDNA	AATGGGATGCACCATAATATCTTAATTGCGATCATCATAATAATCATAAAC	1702
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TTTTTTATGATATATATTATAACTTTATGATATACATATTCATAACTTTA	1752
BoBroccoliNullAlleleGenomicDNA	TTTTTTATGATATATATTATAACTTTATGATATACATATTCATAACTTTA	1752
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----TTTTTATTTTTTCCTATCACTTTCA	1417
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TGATATAAATATTACATAAATTCACCTTTTTATTATTTCTTATCACTTTCA	1802
BoBroccoliNullAlleleGenomicDNA	TGATATAAATATTACATAAATTCACCTTTTTATTATTTCTTATCACTTTCA	1802
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	CAAAATGCATGTCTTTTCTTTACTAAAGTGTTTATACATTAAACATTATATG	1467

BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	CAAAATGCATGTCG--ACGTTACTAAAGTGTTTATACATTAACATTA--TG	1848
BoBroccoliNullAlleleGenomicDNA	CAAAATGCATGTCG--ACGTTACTAAAGTGTTTATACATTAACATTA--TG	1848
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	TTTTCTTCTCATCATGAAACTTGTTTTGATTTTTGTATTATT-TTTGTTT	1516
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TTTTCTTCTCATCATGAATCTTGTTGGTTTTTTTTATTATTATTTTTTTT	1898
BoBroccoliNullAlleleGenomicDNA	TTTTCTTCTCATCATGAATCTTGTTGGTTTTTTTTATTATTATTTTTTTT	1898
WinspitBand2	-----TTT	859
BrCompleteCDSGenomicDNA	GCAGGCACTTA-TGAAT--GGTAGACTGTCTCGTCCGTTTCAT-AGAGTA	1562
BrCompleteCDSmDNA	-----CACTTA-TGAAT--GGTAGACTGTCTCGTCCGTTTCAT-AGAGTA	1077
BoCollardCompleteCDS	GCAGGCACTTA-TGAAT--GGTAGACTATCTCGTCCGTTTCAT-AGAGTA	1944
BoBroccoliNullAlleleGenomicDNA	GCAGGCACTTA-TGAAT--GGTAGACTATCTCGTCCGTTTCAT-AGAGTA	1944
WinspitBand2	GGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTGTGAGGGTA	909
	* * * * *	
BrCompleteCDSGenomicDNA	A---GAGTA---ACGGAAGAA--AGAAGA---CAAGGTATTCAATAGCA	1601
BrCompleteCDSmDNA	A---GAGTA---ACGGAAGAA--AGAAGA---CAAGGTATTCAATAGCA	1116
BoCollardCompleteCDS	A---GAGTA---ACGGAAGAA--AGAAGA---CAAGGTATTCAATAGCA	1983
BoBroccoliNullAlleleGenomicDNA	A---GAGTA---ACGGAAGAA--AGAAGA---CAAGGTATTCAATAGCA	1983
WinspitBand2	ACAAGACTATGAGCGAAACGATCCAGAAGTTTTCAGAGAAGTTAGCAGAA	959
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BrCompleteCDSGenomicDNA	TTGTTCTCGACTCCAAACGGAGATTACATCATCGAACCACCA-AAAGAGC	1650
BrCompleteCDSmDNA	TTGTTCTCGACTCCAAACGGAGATTACATCATCGAACCACCA-AAAGAGC	1165
BoCollardCompleteCDS	TTGTTCTCGACTCCAAACGGAGATTACATCATCGAACCACCA-AAAGAGC	2032
BoBroccoliNullAlleleGenomicDNA	TTGTTCTCGACTCCAAACGGAGATTACATCATCGAACCACCA-AAAGAGC	2032
WinspitBand2	TTG-----GATGT--AATGGTGAGAA-----GAATGGTCATAGAGAGC	995
	* * * * *	
BrCompleteCDSGenomicDNA	TTGTGGACGAGAAGCACCCACGTCTCTTCAAACCATTCACTTACGTTGAC	1700
BrCompleteCDSmDNA	TTGTGGACGAGAAGCACCCACGTCTCTTCAAACCATTCACTTACGTTGAC	1215
BoCollardCompleteCDS	TTGTGGACGAGAAGCACCCACGTCTCTTCAAACCATTCACTTACGTTGAC	2082
BoBroccoliNullAlleleGenomicDNA	TTGTGGACGAGAAGCACCCACGTCTCTTCAAATCATTCACTTACGTTGAC	2082
WinspitBand2	TT-TGGGATAGAA-----AACTACT-----	1014
	* * * * *	
BrCompleteCDSGenomicDNA	TTGATGAGTTTCTATCACACTGAGGCTGGTCGTAGAGCTCGTTCTACTCT	1750
BrCompleteCDSmDNA	TTGATGAGTTTCTATCACACTGAGGCTGGTCGTAGAGCTCGTTCTACTCT	1265
BoCollardCompleteCDS	TTGATGAGTTTCTATCACACTGAGGCTGGTCGTAGACCTCGTTCTACTCT	2132
BoBroccoliNullAlleleGenomicDNA	TTGATGAGTTTCTATCACACTGAGGCTGGTCGTAGACCTCGTTCTACTCT	2132
WinspitBand2	TTGATGAGTTTCTATCACACTGAGGCTGGTCGTAGACCTCGTTCTACTCT	1064

BrCompleteCDSGenomicDNA	TCACGCTTA-TTGTGCCGTCTCTGG--AGCAT-AA-----	1781
BrCompleteCDSmDNA	TCACGCTTA-TTGTGCCGTCTCTGG--AGCAT-AA-----	1296
BoCollardCompleteCDS	TCACGCTTA-TTGTGCCGTCTCTGG--AGCAT-AAATGTGTGCGCTTACT	2178
BoBroccoliNullAlleleGenomicDNA	TCACGCTTA-TTGTGCCGTCTCTGG--AGCAT-AAATGTGTGCGCTTACT	2178
WinspitBand2	TCACGCTKNATTGTGCCGTCTCTGGSMAYCATCAARRRRCYAGCCTWWWK	1114

BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TACGAGAGTTTCAACAATGTTTAAAGTAGTTTCATGGTTCAACTAATATCA	2228
BoBroccoliNullAlleleGenomicDNA	TACGAGAGTTTCAACAATGTTTAAAGTAGTTTCATGGTTCAACTAATATCA	2228
WinspitBand2	ATTYTGAAGWTSTTSMWMTMSCAGTM-----CMASTKMTAAMRT	1154

BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AGAACTTCATGTAGTACTAAAATAAGAGTTTTTGGATTAGTTGAGTATAT	2278
BoBroccoliNullAlleleGenomicDNA	AGAACTGCATGTAGTACTAAA-TAAGAGTTTTTGGATTAGTTGAGTATAT	2277
WinspitBand2	CSGACTGCAGGTGATTTTGGCAAAGGGAG-----	1183
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GTGTTTTATTTCCGGAGAAGCAATCAAGTCTCTCTTTGTATGAAAAATC	2328
BoBroccoliNullAlleleGenomicDNA	GTGTTTTATTTCCGGAGAAGCAATCAAGTCTCTCTTTGTATGAAAAATC	2327
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AATAATGTGTATGTGTATGAGCATGTTCAATAATGTAAATGAATTTGGTTG	2378
BoBroccoliNullAlleleGenomicDNA	AATAA-AAATATGTGTATGAGCATGTTCAATAATGTAAATGAATTTGGTTG	2376
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GATCTGTTGGTTCACAAGATGTCAAGATCGTAAATAGGTTAATTAAATAG	2428
BoBroccoliNullAlleleGenomicDNA	GATCTGTTGGTTCACAAGATGTCAAGATCGTAAATAGGTTAATTAAATAG	2426
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GTTAATTTCTTCTTCTTTTTTAACTAAATTAATTCATTTTTTTTTCTA	2478
BoBroccoliNullAlleleGenomicDNA	GTTAATTTCTTCTTCTTTTTTAACTAAATTAATTCATTTTTTTTTATA	2476
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AAAAAATACTAGTTTAATTTTCAGGAGATGGGAAACGAGTGTGGAACATAT	2528
BoBroccoliNullAlleleGenomicDNA	AAAAAATACTAGTTTAATTTTCAGGAGATGGGAAACGAGTGTGGAACATAT	2526
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AAAAACGGGTGTTTGCCATTTCAAACATTAAACGCTAAATAAGTGAAATGA	2578
BoBroccoliNullAlleleGenomicDNA	AAAAACTGGTGTTTGCCATTTCAAACATTAAACGCTAAATAAGTGAAATGA	2576
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TTTACTTTTCATGTTATCGTAGCGATAGTGGTCTTGAGTCGACATGTAGAT	2628
BoBroccoliNullAlleleGenomicDNA	TTTACTTTTCATGTTATCGTAGCGACAGTGGTTTTGAGTCGACATGTAGAT	2626
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	CCCCCTTACCTTAGGAATTTGTTTGTTTGCAAAATGCCAAAATCGTAAAT	2678
BoBroccoliNullAlleleGenomicDNA	CCCCCTTACCTTAGGAATTTGTTTGTTTGCAAAATGCCAAAATCGTAAAT	2676
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AGTA--AATTAATAATGTTATTTAAAGTTTGACCGGTTTACTTGCAATA	2725
BoBroccoliNullAlleleGenomicDNA	AGTAGTAAATTAGTAATGTTATTTAAAGTTTGACTGGTTTAATTGCAATA	2726
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	

BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GGTGTATGTGCTGTGGTCCAAAAATTAGTGAACTAATAATTACAAATTGT	2775
BoBroccoliNullAlleleGenomicDNA	GGTGTATGTGCTGTGGTCCAAAAATTAGTGAAACGAATAATT-CAATTGT	2775
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AAATTAGTAATGTTATTTAAATATAGACATGCATTGTCTCATGAACAAA	2825
BoBroccoliNullAlleleGenomicDNA	AAATTAGTAATGTTATTTAAATATAGACATGCATTGTCTCATGAACAAA	2825
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GTGTTTGAATAGCGATTTGCAAGTGCCAACTCTTCTCATGA-----	2869
BoBroccoliNullAlleleGenomicDNA	GTGTTTGAATAGCGATTTGCAAGTGCCAACTCTTCTTATGAACAACG	2875
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	-----	
BoBroccoliNullAlleleGenomicDNA	TTACAAATTAGGACCGGCTTGGGCAAAACCTAACGAAACATTACCTTTAA	2925
WinspitBand2	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	-----	
BoBroccoliNullAlleleGenomicDNA	TAAATCACCTTTGC	2939
WinspitBand2	-----	

CLUSTAL 2.1 multiple sequence alignment
Savoy Band1 AOP2 - Forward Sequence

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BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  AAAAAAAAAAATAGAAATGTTTCTGTCTATAAATGGGCATTCCATCATTT  50
SavoyFW                        -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  ACTTTCTCAGTACGGAAGCAAAAAAAAAACTAAGGAAAAGAAAACAGCT  29
SavoyFW                        -----
                                -AAAAAACCTAAGGAAAAGAAAAGCT  100

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          TGAATCTCTTTGAATCAAGAAAACTCCAAAGGTAATTTTGGTAAAAATGTT  79
BoBroccoliNullAlleleGenomicDNA  TGAATCTCTTTGAATCAAGAAAA  123
SavoyFW                        -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          AAATACTCCAAAGGTAGTTTTTCTTATGAATTTTGAATGTTTCTTTTGT  129
BoBroccoliNullAlleleGenomicDNA  ---ACTCCAAAGGTAGTTGT-CTTATGAGTTTTTAATGTTTCTTTTGT  168
SavoyFW                        -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          GTGGGTGATTAAAGAGTTACTTAAATATTTTCTTTCGGGTAAAAATAAAG  179
BoBroccoliNullAlleleGenomicDNA  TGTGATGATTAAAGAGCTACTTAAACATTTTCTTTCGGGTAAAAATA---  215
SavoyFW                        -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          CTAATTAATTAGTTTACTAAAAAAAAATTAAAAAAAAATAAAGCTAATT  229
BoBroccoliNullAlleleGenomicDNA  -----TAAAGCTAATT  226
SavoyFW                        -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          AACATTTTATGAATATATTTTTTTGGATTTGCACCAAGGCGAAAA-GAA  278
BoBroccoliNullAlleleGenomicDNA  AACATTTTATAAATATATTTT--TGGATTTGCACCAAGGAAAAAAGAA  274
SavoyFW                        -----

BrCompleteCDSGenomicDNA      TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGAC-CAAAC  50
BrCompleteCDSmDNA             TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGAC-CAAAC  50
BoCollardCompleteCDS          TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGAC-CAAAC  327
BoBroccoliNullAlleleGenomicDNA  TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGAC-CAAAC  323
SavoyFW                        -----GNAATTTT-----WCTATCTCTCGNGCACAAAC  28
                                **  ***  *****  *  *****

BrCompleteCDSGenomicDNA      CCTAAAC-CAGGAAGTGAGAAGTGGGTGAAGTGAGGAG--TGATGTCC  97
BrCompleteCDSmDNA             CCTAAAC-CAGGAAGTGAGAAGTGGGTGAAGTGAGGAG--TGATGTCC  97
BoCollardCompleteCDS          CCTAAAC-CAGGAAGTGAGAAGTGGGTGAAGTGAGGAG--TGATGTCC  374
BoBroccoliNullAlleleGenomicDNA  CCTAAAC-CAGGAGGTGAGAAGTGGGTGAAGTGAGGAG--TGATGTCC  370
SavoyFW                        CTTAAACACCGNAGGTGAGWAGTGGGTGAAGTKAGVMGGTCGAYG-CC  77
                                *  *****  *  *  *****  *****  *  *  *  *

BrCompleteCDSGenomicDNA      GTAAAGCT--CTTG-AAGACT-ACGGCGGTTTTGAGGTGTCATATGATA  142
BrCompleteCDSmDNA             GTAAAGCT--CTTG-AAGACT-ACGGCGGTTTTGAGGTGTCATATGATA  142
BoCollardCompleteCDS          GTAAAGCT--CTTG-AAGACT-ACGGCGGTTTTGAGGTGTCATATGATA  419
BoBroccoliNullAlleleGenomicDNA  GTAAAGCT--CTTG-AAGACT-ACGGCGGTTTTGAGGTGTCATATGATA  415

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SavoyFW	KBAAAGYTTGCMYSTRASACTTAYGG-GSTTKTSASGKGTCATATGATA 126 * * * * *
BrCompleteCDSGenomicDNA	GAGTGTCAAGAGAGCTGAAGAAGTCAGTTTTGGATGCCATGATAGAGCTT 192
BrCompleteCDSmDNA	GAGTGTCAAGAGAGCTGAAGAAGTCAGTTTTGGATGCCATGATAGAGCTT 192
BoCollardCompleteCDS	GAGTGTCAAGAGAGCTTAAGAAGTCAGTTTTGGATGCCATGATAGAGCTT 469
BoBroccoliNullAlleleGenomicDNA	GAGTGTCAAGAGAGCTTAAGAAGTCAGTTTTGGATGCCATGATAGAGCTT 465
SavoyFW	GASTGTCTGARGASCTTAAGAASTYWKTTTTGGATGCCMTGATAKAKCTT 176 * * * * *
BrCompleteCDSGenomicDNA	TTTCGAGTTACCAAGTTGAGGCTAAACAGAGAAACGTGCTCCGAAACCGTA 242
BrCompleteCDSmDNA	TTTCGAGTTACCAAGTTGAGGCTAAACAGAGAAACGTGCTCCGAAACCGTA 242
BoCollardCompleteCDS	TTTCGAGTTACCAAGTTGAGGCTAAACAGAGAAACGTGCTCCGAAACCTTA 519
BoBroccoliNullAlleleGenomicDNA	TTTCGAGTTACCAAGTTGAGGCTAAACAGAGAAACGTGCTCCGAAACCTTA 515
SavoyFW	TTCSAGTY-CCAGTTGAGGCTAWHCM-AGAAACGTGCTCCGAAACCTTA 224 * * * * *
BrCompleteCDSGenomicDNA	CACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGA 292
BrCompleteCDSmDNA	CACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGA 292
BoCollardCompleteCDS	CACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGG 569
BoBroccoliNullAlleleGenomicDNA	CACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGG 565
SavoyFW	CWCTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGG 274 * * * * *
BrCompleteCDSGenomicDNA	ATTCCAATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCT 342
BrCompleteCDSmDNA	ATTCCAATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCT 342
BoCollardCompleteCDS	ATTCCAATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCT 619
BoBroccoliNullAlleleGenomicDNA	ATTCCAATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCT 615
SavoyFW	ATTCCAATGTTTTGGAGAAAGTTCAAAATTTACTCAACTGCTACG---- 320 * * * * *
BrCompleteCDSGenomicDNA	GATTGTGAGGGTAACAAGAGTATGAGGTAACGTCATGTCAAAAAAAAAA 392
BrCompleteCDSmDNA	GATTGTGAGGGTAACAAGAGTATGAG----- 368
BoCollardCompleteCDS	GATTGTGAGGGTAACAAGACTATGAGGTAACGTCATGTCGAAAAAAAAAA 669
BoBroccoliNullAlleleGenomicDNA	GATTGTGAGGGTAACAAGACTATGAGGTAACGTCATGTCAAAAAAAAAA 665
SavoyFW	-----
BrCompleteCDSGenomicDNA	AACTAAGTAATGCTTCGTAGAGTATATT---GTTTCGTAAACTCCTGTTA 438
BrCompleteCDSmDNA	-----
BoCollardCompleteCDS	--CTCAGTAATGCTTCATAGAGTAAATTAATTGTTTCGGAATTCCTGTAA 717
BoBroccoliNullAlleleGenomicDNA	AACTCAGTAATGCTTCATAGAGTAAATTAATTGTTTCGTAATTCCTGTTA 715
SavoyFW	-----
BrCompleteCDSGenomicDNA	TTTTTTAATCAAAAATATTTTCGTAATTTTTTTTGTAGTTGCTTTT-ATA 487
BrCompleteCDSmDNA	-----
BoCollardCompleteCDS	TCTTC--ATCAAAAATATTT-CGTAACCTTTTT-GCTAGTTGTTTTT-ATA 762
BoBroccoliNullAlleleGenomicDNA	ATCTTTCATCAAAAATATTTTCGTAACCTTTTT-GCTAGTTGTTTTT-CATA 764
SavoyFW	-----
BrCompleteCDSGenomicDNA	AGCTATGTAACAATTTTCTATATAAAACCTTGTTTTTATTTTTATTTTTT 537
BrCompleteCDSmDNA	-----
BoCollardCompleteCDS	AGGTATGTGACAAATTTCTATA-AAAAACCTTGTTTTTATCTTTATTTTTT 811
BoBroccoliNullAlleleGenomicDNA	AGTTATGTGACAAATTTCTATAAAAAACCTTGTTTTTATCTTTATTTTTT 814
SavoyFW	-----
BrCompleteCDSGenomicDNA	TGGAAAAATGTCAGTTCACCTTATATAGTAATGAACGAAAAATTTGTTTTT 587
BrCompleteCDSmDNA	-----
BoCollardCompleteCDS	TGGAAAAATGTTAGTTCACCTCATATAGTAATGAACGAAAAATTTGTTTTT 861
BoBroccoliNullAlleleGenomicDNA	TGGAAAAATGTTAGTTCACCTCATATAGTAATGAACGAAAAATTTGTTTTT 864
SavoyFW	-----
BrCompleteCDSGenomicDNA	AATCTCACGTTTCTCGCATTTTATTTTCTTGTCTATTAAAATAGCTAT 637
BrCompleteCDSmDNA	-----
BoCollardCompleteCDS	AATCTCACGTTTTCACGCATTT---TTTTTGTCTTATTAAAATAGCTAT 908
BoBroccoliNullAlleleGenomicDNA	AATCTCACGTTTTCACGCATTT---TTTTTGTCTTATTAAAATAGCTAT 911
SavoyFW	-----

BrCompleteCDSGenomicDNA	ATAA--TTTTCTTTGTGTTGAAAACAGCGAAACGATCCAGAATTTTTTCAG	685
BrCompleteCDSmDNA	-----CGAAACGATCCAGAATTTTTTCAG	391
BoCollardCompleteCDS	ATAAAATTTTTCTTTGTGTTGAAAACAGCGAAACGATCCAGAAGTTTTTCAG	958
BoBroccoliNullAlleleGenomicDNA	ATAAA--TTTTCTTTGTGTTGAAAACAGCGAAACGATCCAGAAGTTTTTCAG	960
SavoyFW	-----	
BrCompleteCDSGenomicDNA	AGAAGTTAGCAGAAATTGGATGTAATGGTGAGAAGAAATGGTCATAGAGAGC	735
BrCompleteCDSmDNA	AGAAGTTAGCAGAAATTGGATGTAATGGTGAGAAGAAATGGTCATAGAGAGC	441
BoCollardCompleteCDS	AGAAGTTAGCAGAAATTGGATGTAATGGTGAGAAGAAATGGTCATAGAGAGC	1008
BoBroccoliNullAlleleGenomicDNA	AGAAGTTAGCAGAAATTGGATGTAATGGTGAGAAGAAATGGTCATAGAGAGC	1010
SavoyFW	-----	
BrCompleteCDSGenomicDNA	TTTGGGATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAATTACCG	785
BrCompleteCDSmDNA	TTTGGGATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAATTACCG	491
BoCollardCompleteCDS	TTTGGGATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAATTACCG	1058
BoBroccoliNullAlleleGenomicDNA	TTTGGGATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAATTACCG	1060
SavoyFW	-----	
BrCompleteCDSGenomicDNA	TTTGCGACTGATGAAATATGTAGCACCACTGACGTTGATGCTAATGTTG	835
BrCompleteCDSmDNA	TTTGCGACTGATGAAATATGTAGCACCACTGACGTTGATGCTAATGTTG	541
BoCollardCompleteCDS	TTTGCGACTGATGAAATATGTAGCACCACTGATGTTGATGCTAATGTTG	1108
BoBroccoliNullAlleleGenomicDNA	TTTGCGACTGATGAAATATGTAGCACCACTGATGTTGATGCTAATGTTG	1110
SavoyFW	-----	
BrCompleteCDSGenomicDNA	CGGTTGGTACTAAAGATTCTGATGATGGTGCTAATACGAATACAACCTGCT	885
BrCompleteCDSmDNA	CGGTTGGTACTAAAGATTCTGATGATGGTGCTAATACGAATACAACCTGCT	591
BoCollardCompleteCDS	CGGTCAGTACTAAAGATTCTGTTGATGGTGCTAATACGAATACAACCTGCT	1158
BoBroccoliNullAlleleGenomicDNA	CGGTCAGTACTAAAGATTCTGTTGATGGTGCTAATACGAATACAACCTGCT	1160
SavoyFW	-----	
BrCompleteCDSGenomicDNA	AACGCTGATGCTGATGATATTGCTAATGGTATTGCTAAAGTTTCATATTGA	935
BrCompleteCDSmDNA	AACGCTGATGCTGATGATATTGCTAATGGTATTGCTAAAGTTTCATATTGA	641
BoCollardCompleteCDS	AACGCTGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTTCATATTGA	1208
BoBroccoliNullAlleleGenomicDNA	AACGCTGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTTCATATTGA	1210
SavoyFW	-----	
BrCompleteCDSGenomicDNA	TGACGATGCTGATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATC	985
BrCompleteCDSmDNA	TGACGATGCTGATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATC	691
BoCollardCompleteCDS	TGACGATGCTAATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATC	1258
BoBroccoliNullAlleleGenomicDNA	TGACGATGCTAATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATC	1260
SavoyFW	-----	
BrCompleteCDSGenomicDNA	ATAATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAAT	1035
BrCompleteCDSmDNA	ATAATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAAT	741
BoCollardCompleteCDS	ATAATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAAT	1308
BoBroccoliNullAlleleGenomicDNA	ATAATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAAT	1310
SavoyFW	-----	
BrCompleteCDSGenomicDNA	GTCGACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGT	1085
BrCompleteCDSmDNA	GTCGACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGT	791
BoCollardCompleteCDS	GTCGACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGT	1358
BoBroccoliNullAlleleGenomicDNA	GTCGACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGT	1360
SavoyFW	-----	
BrCompleteCDSGenomicDNA	TAACTGGCACTATTGATGATGTTAATGCTAATGCTGGTACTCGTAGTA	1135
BrCompleteCDSmDNA	TAA-----TGCTAATGCTGGTACTCGTAGTA	817
BoCollardCompleteCDS	TAACTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACTCGTACTA	1408
BoBroccoliNullAlleleGenomicDNA	TAACTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACTCGTACTA	1410
SavoyFW	-----	
BrCompleteCDSGenomicDNA	GTGCTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGAT	1185

BrCompleteCDSDNA	GTGCTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGAT	867
BoCollardCompleteCDS	GTGCTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGAT	1458
BoBroccoliNullAlleleGenomicDNA	GTGCTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGAT	1460
SavoyFW	-----	
BrCompleteCDSGenomicDNA	GATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTT	1235
BrCompleteCDSDNA	GATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTT	917
BoCollardCompleteCDS	GATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTT	1508
BoBroccoliNullAlleleGenomicDNA	GATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAA--CCTTTT	1508
SavoyFW	-----	
BrCompleteCDSGenomicDNA	GACGGTACTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAG	1285
BrCompleteCDSDNA	GACGGTACTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAG	967
BoCollardCompleteCDS	GACGGTGCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAG	1558
BoBroccoliNullAlleleGenomicDNA	GACGGTGCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAG	1558
SavoyFW	-----	
BrCompleteCDSGenomicDNA	ATGAAAAGTGGATCAGGTTAAAACCATCTCATAACTCTTTCGTTGTTATG	1335
BrCompleteCDSDNA	ATGAAAAGTGGATCAGGTTAAAACCATCTCATAACTCTTTCGTTGTTATG	1017
BoCollardCompleteCDS	ATGAAAAGTGGATCAGGTTAAAGCCATCTCATAACTCTTTCGTTGTTATG	1608
BoBroccoliNullAlleleGenomicDNA	ATGAAAAGTGGATCAGGTTAAAACCATCTCATAACTCTTTCGTTGTTATG	1608
SavoyFW	-----	
BrCompleteCDSGenomicDNA	GCTGGAGATTCTCTATATGTAAGTTCTAACTTATTTTATTTTTAAATGGG	1385
BrCompleteCDSDNA	GCTGGAGATTCTCTATATG-----	1036
BoCollardCompleteCDS	GCTGGAGATTCTCTATATGTAAGTTCTAACTTATTTTATTTTTAAATGGG	1658
BoBroccoliNullAlleleGenomicDNA	GCTGGAGATTCTCTATATGTAAGTTCTAACTTATTTTATTTTTAAATGGG	1658
SavoyFW	-----	
BrCompleteCDSGenomicDNA	ATGCACC-----	1392
BrCompleteCDSDNA	-----	
BoCollardCompleteCDS	ATGCACCATAATATCTTAATTGCGATCATCATAAATCATAACTTTTTT	1708
BoBroccoliNullAlleleGenomicDNA	ATGCACCATAATATCTTAATTGCGATCATCATAAATCATAACTTTTTT	1708
SavoyFW	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSDNA	-----	
BoCollardCompleteCDS	ATGATATATATTATAACTTTATGATATACATATTCATAACTTTATGATAT	1758
BoBroccoliNullAlleleGenomicDNA	ATGATATATATTATAACTTTATGATATACATATTCATAACTTTATGATAT	1758
SavoyFW	-----	
BrCompleteCDSGenomicDNA	-----TTTTTATTTTTTCCTATCACTTTCACAAATG	1423
BrCompleteCDSDNA	-----	
BoCollardCompleteCDS	AAATATTACATAAATTCACCTTTTTATTATTTCTTATCACTTTCACAAATG	1808
BoBroccoliNullAlleleGenomicDNA	AAATATTACATAAATTCACCTTTTTATTATTTCTTATCACTTTCACAAATG	1808
SavoyFW	-----	
BrCompleteCDSGenomicDNA	CATGTCTTTTCTTTACTAAAGTGTTTATACATTAACATTATATGTTTCT	1473
BrCompleteCDSDNA	-----	
BoCollardCompleteCDS	CATGTCTG--ACGTTACTAAAGTGTTTATACATTAACATTA--TGTTTTCT	1854
BoBroccoliNullAlleleGenomicDNA	CATGTCTG--ACGTTACTAAAGTGTTTATACATTAACATTA--TGTTTTCT	1854
SavoyFW	-----	
BrCompleteCDSGenomicDNA	TCTCATCATGAACCTGTTTTGATTTTGTATTATT--TTGTTTGCAGGC	1522
BrCompleteCDSDNA	-----C	1037
BoCollardCompleteCDS	TCTCATCATGAATCTTGTGTTGGTTTTTTTATTATTATTTTTTGCAGGC	1904
BoBroccoliNullAlleleGenomicDNA	TCTCATCATGAATCTTGTGTTGGTTTTTTTATTATTATTTTTTGCAGGC	1904
SavoyFW	-----	
BrCompleteCDSGenomicDNA	ACTTATGAATGGTAGACTGTCTCGTCCGTTTCATAGAGTAAGAGTAACGG	1572
BrCompleteCDSDNA	ACTTATGAATGGTAGACTGTCTCGTCCGTTTCATAGAGTAAGAGTAACGG	1087
BoCollardCompleteCDS	ACTTATGAATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAACGG	1954

BoBroccoliNullAlleleGenomicDNA SavoyFW	ACTTATGAATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAACGG	1954

BrCompleteCDSGenomicDNA	AAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGA	1622
BrCompleteCDSmDNA	AAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGA	1137
BoCollardCompleteCDS	AAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGA	2004
BoBroccoliNullAlleleGenomicDNA SavoyFW	AAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGA	2004

BrCompleteCDSGenomicDNA	GATTACATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCACG	1672
BrCompleteCDSmDNA	GATTACATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCACG	1187
BoCollardCompleteCDS	GATTACATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCACG	2054
BoBroccoliNullAlleleGenomicDNA SavoyFW	GATTACATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCACG	2054

BrCompleteCDSGenomicDNA	TCTCTTCAAACCATTCACCTACGTTGACTTGATGAGTTTCTATCACA CTG	1722
BrCompleteCDSmDNA	TCTCTTCAAACCATTCACCTACGTTGACTTGATGAGTTTCTATCACA CTG	1237
BoCollardCompleteCDS	TCTCTTCAAACCATTCACCTACGTTGACTTGATGAGTTTCTATCACA CTG	2104
BoBroccoliNullAlleleGenomicDNA SavoyFW	TCTCTTCAAATCATTCACCTACGTTGACTTGATGAGTTTCTATCACA CTG	2104

BrCompleteCDSGenomicDNA	AGGCTGGTCGTAGAGCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCT	1772
BrCompleteCDSmDNA	AGGCTGGTCGTAGAGCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCT	1287
BoCollardCompleteCDS	AGGCTGGTCGTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCT	2154
BoBroccoliNullAlleleGenomicDNA SavoyFW	AGGCTGGTCGTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCT	2154

BrCompleteCDSGenomicDNA	GGAGCATAA-----	1781
BrCompleteCDSmDNA	GGAGCATAA-----	1296
BoCollardCompleteCDS	GGAGCATAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTAA GT	2204
BoBroccoliNullAlleleGenomicDNA SavoyFW	GGAGCATAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTAA GT	2204

BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AGTTTCATGGTTCAACTAATATCAAGAACTTCATGTAGTACTAAAATAAG	2254
BoBroccoliNullAlleleGenomicDNA SavoyFW	AGTTTCATGGTTCAACTAATATCAAGAACTGCATGTAGTACTAAA-TAAG	2253

BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AGTTTTTGGATTAGTTGAGTATATGTGTTTTATTTCCGGAGAAGCAATCA	2304
BoBroccoliNullAlleleGenomicDNA SavoyFW	AGTTTTTGGATTAGTTGAGTATATGTGTTTTATTTCCGGAGAAGCAATCA	2303

BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AGTCTCTCTTTTGTATGAAAAATCAATAATGTGTATGTGTATGAGCATGT	2354
BoBroccoliNullAlleleGenomicDNA SavoyFW	AGTCTCTCTTTTGTATGAAAAATCAATAA-AAATATGTGTATGAGCATGT	2352

BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TCAATAATGTAATGAATTTGGTTGGATCTGTTGGTTCAAGATGTCAAG	2404
BoBroccoliNullAlleleGenomicDNA SavoyFW	TCAATAATGTAATGAATTTGGTTGGATCTGTTGGTTCAAGATGTCAAG	2402

BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	ATCGTAAATAGGTTAATTAAATAGGTTAATTTCTTCTCTTTTTTAAACT	2454
BoBroccoliNullAlleleGenomicDNA SavoyFW	ATCGTAAATAGGTTAATTAAATAGGTTAATTTCTTCTCTTTTTTAAACT	2452

BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AAATTAAATTCATTTTTTTTTCTAAAAAATACTAGTTTAATTCAGGAG	2504
BoBroccoliNullAlleleGenomicDNA	AAATTAAATTCATTTTTTTTTTATAAAAAAATACTAGTTTAATTCAGGAG	2502
SavoyFW	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	ATGGGAAACGAGTGTGGAACATATAAAAAACGGGTGTTTGCCATTTCAAAC	2554
BoBroccoliNullAlleleGenomicDNA	ATGGGAAACGAGTGTGGAACATATAAAAACTGGTGTTTGCGATTTCAAAC	2552
SavoyFW	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	ATTAAACGCTAAATAAGTGAATGATTTACTTTCATGTTATCGTAGCGATA	2604
BoBroccoliNullAlleleGenomicDNA	ATTAAACGCTAAATAAGTGAATGATTTACTTTCATGTTATCGTAGCGACA	2602
SavoyFW	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GTGGTCTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTTTGT	2654
BoBroccoliNullAlleleGenomicDNA	GTGGTTTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTTTGT	2652
SavoyFW	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TTGCAAAATGCCAAAATCGTAAATAGTA--AATTAAATGTTATTTAA	2701
BoBroccoliNullAlleleGenomicDNA	TTGCAAAATGCCAAAATCGTAAATAGTAGTAAATTAGTAATGTTATTTAA	2702
SavoyFW	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AGTTTGACCGGTTTACTTGCAATAGGTGTATGTGCTGTGGTCCAAAAATT	2751
BoBroccoliNullAlleleGenomicDNA	AGTTTGACTGGTTTAATTGCAGTAGGTGTATGTGCTGTGGTCCAAAAATT	2752
SavoyFW	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AGTGAAACTAATAATTACAATTGTAAATTAGTAATGTTATTTAAATATA	2801
BoBroccoliNullAlleleGenomicDNA	AGTGAAACGAATAATT-CAATTGTAAATTAGTAATGTTATTTAAATATA	2801
SavoyFW	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GACATGCATTGTCTCATGAACAAAGTGGTTGAAATAGCGATTTGCAAGTG	2851
BoBroccoliNullAlleleGenomicDNA	GACATGCATTGTCTCATGAACAAAGTGGTTGAAATAGCGATTTGCAAGTG	2851
SavoyFW	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	CCAACTCTTCTCATGA-----	2869
BoBroccoliNullAlleleGenomicDNA	CCAACTCTTCTTATGAACAACGTTACAAATTAGGACCGGCTTGGGCAA	2901
SavoyFW	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	-----	
BoBroccoliNullAlleleGenomicDNA	AACCTAACGAAACATTACCTTTAATAAATCACCTTTGC	2939
SavoyFW	-----	

CLUSTAL 2.1 multiple sequence alignment
Savoy Band1 AOP2 - Reverse Sequence

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BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  AAAAAAAAAAATAGAAATGTTTCTGTCTATAAATGGGCATTCCATCATTT 50
SavoyRV                        -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  ACTTCTCAGTACGGAAGCAAAAAAAAAACTAAGGAAAAGAAAACCAAGCT 100
SavoyRV                        -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  TGATCTCTTTGAATCAAGAAAACTCCAAAGGTAAATTTGGTAAAAATGTT 79
SavoyRV                        TGATCTCTTTGAATCAAGAAAA----- 123

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  AAATACTCCAAAGGTAGTTTTTCTTATGAATTTTGAAATGTTTCTTTTGT 129
SavoyRV                        ----ACTCCAAAGGTAGTTGT-CTTATGAGTTTTTAATGTTTTCTTTTGT 168

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  GTGGGTGATTAAAGAGTTACTTAAATATTTTCTTTCGGGTTAAAAATAAG 179
SavoyRV                        TGTGATGATTAAAGAGCTACTTAAACATTTTCTTTCGGGTTAAAAATA--- 215

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  CTAATTAATTAGTTTACTAAAAAAATTAATAAAAAAATAAAGCTAATT 229
SavoyRV                        -----TAAAGCTAATT 226

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoCollardCompleteCDS          -----
BoBroccoliNullAlleleGenomicDNA  AACATTTTATGAATATATTTTTTTTGGATTTGCACCAAAGGCGAAAA-GAA 278
SavoyRV                        AACATTTTATAAATATATTTT--TGGATTTGCACCAAAGGAAAAAAGAA 274

BrCompleteCDSGenomicDNA      TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 51
BrCompleteCDSmDNA             TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 51
BoCollardCompleteCDS          TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 328
BoBroccoliNullAlleleGenomicDNA TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 324
SavoyRV                        -----

BrCompleteCDSGenomicDNA      CTAAAACAGGAAGTGAGAAGTGGGTTGAAGTGAGGAGTGATGTCCGTAA 101
BrCompleteCDSmDNA             CTAAAACAGGAAGTGAGAAGTGGGTTGAAGTGAGGAGTGATGTCCGTAA 101
BoCollardCompleteCDS          CTAAAACAGGAAGTGAGAAGTGGGTTGAAGTGAGGAGTGATGTCCGTAA 378
BoBroccoliNullAlleleGenomicDNA CTAAAACAGGAGGTGAGAAGTGGGTTGAAGTGAGGAGTGATGTCCGTAA 374
SavoyRV                        -----GGAAT-----TCGA-----GAGT----- 14
                               *** * * ** *

BrCompleteCDSGenomicDNA      AGCTCTTGAAGACTACGGCGGTTTTGAGGTGTCATATGATAGAGTGTGAG 151
BrCompleteCDSmDNA             AGCTCTTGAAGACTACGGCGGTTTTGAGGTGTCATATGATAGAGTGTGAG 151
BoCollardCompleteCDS          AGCTCTTGAAGACTACGGCGGTTTTGAGGTGTCATATGATAGAGTGTGAG 428
BoBroccoliNullAlleleGenomicDNA AGCTCTTGAAGACTACGGCGGTTTTGAGGTGTCATATGATAGAGTGTGAG 424

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SavoyRV	-----AGAC-----GAKGTC-TACGACAG-----	32
	*** * ** *	
BrCompleteCDSGenomicDNA	AGGAGCTGAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAGTTA	201
BrCompleteCDSmDNA	AGGAGCTGAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAGTTA	201
BoCollardCompleteCDS	AAGAGCTTAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAGTTA	478
BoBroccoliNullAlleleGenomicDNA	AAGAGCTTAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAGTTA	474
SavoyRV	-----CC-----TCA	37
	** *	
BrCompleteCDSGenomicDNA	CCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTGGATA	251
BrCompleteCDSmDNA	CCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTGGATA	251
BoCollardCompleteCDS	CCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCTTACACTGGATA	528
BoBroccoliNullAlleleGenomicDNA	CCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCTTACACTGGATA	524
SavoyRV	CY-SCTGA-----TAGATP	50
	* *** *	
BrCompleteCDSGenomicDNA	TTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAATTCCAATG	301
BrCompleteCDSmDNA	TTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAATTCCAATG	301
BoCollardCompleteCDS	TTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGGATTCCAATG	578
BoBroccoliNullAlleleGenomicDNA	TTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGGATTCCAATG	574
SavoyRV	HKCA--TCAN---GTC-----RAYGTAAG-----YGAATG	75
	** *** ** *	
BrCompleteCDSGenomicDNA	TTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTGTGAG	351
BrCompleteCDSmDNA	TTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTGTGAG	351
BoCollardCompleteCDS	TTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTGTGAG	628
BoBroccoliNullAlleleGenomicDNA	TTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTGTGAG	624
SavoyRV	GTYTGAGA--GWYGWGAGT-----GCTTCT-----	100
	* * * * *	
BrCompleteCDSGenomicDNA	GGTAACAAGAGTATGAGGTAACGTCATGTCAAAAAAAAAAACTAAGTA	401
BrCompleteCDSmDNA	GGTAACAAGAGTATGAG-----	368
BoCollardCompleteCDS	GGTAACAAGACTATGAGGTAACGTCATGTCAAAAAAAAAAA--CTCAGTA	676
BoBroccoliNullAlleleGenomicDNA	GGTAACAAGACTATGAGGTAACGTCATGTCAAAAAAAAAAACTCAGTA	674
SavoyRV	-----	
BrCompleteCDSGenomicDNA	ATGCTTCGTAGAGTATATT---GTTCGTAAACTCCTGTTATTTTTTAA	447
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	ATGCTTCATAGAGTAAATTAATTGTTTCGGAAATTCCTGTAATCTTC--AT	724
BoBroccoliNullAlleleGenomicDNA	ATGCTTCATAGAGTAAATTAATTGTTTCGTAAATTCCTGTTAATCTTTCA	724
SavoyRV	-----	
BrCompleteCDSGenomicDNA	CAAAAAATATTTTCGTAAATTTTTTTTGTAGTTGCTTT-TATAAGCTATGTA	496
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	CAAAAAATATTTTCGTAA--CTTTTTGCTAGTTGTTTTT-CATAAGGTATGTG	771
BoBroccoliNullAlleleGenomicDNA	CAAAAAATATTTTCGTAA-CTTTTTGCTAGTTGTTTTTTCATAAGTTATGTG	773
SavoyRV	-----	
BrCompleteCDSGenomicDNA	ACAATTTTCTATATAAAACCTTGTTTTTATTTTTATTTTTTTGGAAAAAT	546
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	ACAAATTTCTATA-AAACCTTGTTTTTATCTTTATTTTTTTGGAAAAAT	820
BoBroccoliNullAlleleGenomicDNA	ACAAATTTCTATAAAAAACCTTGTTTTTATCTTTATTTTTTTGGAAAAAT	823
SavoyRV	-----	
BrCompleteCDSGenomicDNA	GTCAGTTCACTTATATAGTAATGAACTGAAAATTTGTTTTCAATCTCACG	596
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GTTAGTTCACTCATATAGTAATGAACTGAAAATTTGTTTTCAATCTCACG	870
BoBroccoliNullAlleleGenomicDNA	GTTAGTTCACTCATATAGTAATGAACTGAAAATTTGTTTTCAATCTCACG	873
SavoyRV	-----	
BrCompleteCDSGenomicDNA	TTTCTCGCATTTTATTTTCTGTTTCTATTTAAATAGCTATATAA--TTT	644
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TTTACGCGATTT--TTTTTGTCTTCTATTTAAATAGCTATATAAATTTT	917
BoBroccoliNullAlleleGenomicDNA	TTTACGCGATTT--TTTTTGTCTTCTATTTAAATAGCTATATAA--TTT	919
SavoyRV	-----	

BrCompleteCDSGenomicDNA	TCTTTGTGTTGAAAAACAGCGAAACGATCCAGAATTTTTCAGAGAAGTTAG	694
BrCompleteCDSmDNA	-----CGAAACGATCCAGAATTTTTCAGAGAAGTTAG	400
BoCollardCompleteCDS	TCTTTGTGTTGAAAAACAGCGAAACGATCCAGAAGTTTTCAGAGAAGTTAG	967
BoBroccoliNullAlleleGenomicDNA	TCTTTGTGTTGAAAAACAGCGAAACGATCCAGAAGTTTTCAGAGAAGTTAG	969
SavoyRV	-----CGGTCCACAAGCTCTT-----TTGG	120
	** ** ** * * ** *	
BrCompleteCDSGenomicDNA	CAGAAATTGGATGTAAATGGTGAGAAGAAATGGTCATAGAGAGCTTTGGGATA	744
BrCompleteCDSmDNA	CAGAAATTGGATGTAAATGGTGAGAAGAAATGGTCATAGAGAGCTTTGGGATA	450
BoCollardCompleteCDS	CAGAAATTGGATGTAAATGGTGAGAAGAAATGGTCATAGAGAGCTTTGGGATA	1017
BoBroccoliNullAlleleGenomicDNA	CAGAAATTGGATGTAAATGGTGAGAAGAAATGGTCATAGAGAGCTTTGGGATA	1019
SavoyRV	TGG--TTCGATG--ATG-----TAACTCTCCG----TTTGGAGTC	151
	* ** ** ** ** * ** * ***** *	
BrCompleteCDSGenomicDNA	GAAAACTACTTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCAGCT	794
BrCompleteCDSmDNA	GAAAACTACTTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCAGCT	500
BoCollardCompleteCDS	GAAAACTACTTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCAGCT	1067
BoBroccoliNullAlleleGenomicDNA	GAAAACTACTTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCAGCT	1069
SavoyRV	GAGAACAAATGCTATTGAATACCTT--GTC-----TTCTTTCTTTT----	189
	** ** * * ** ** ** ** ** *	
BrCompleteCDSGenomicDNA	GATGAAATATGTAGCACACCTGACGTTGATGCTAATGTTGCGGTTGGTA	844
BrCompleteCDSmDNA	GATGAAATATGTAGCACACCTGACGTTGATGCTAATGTTGCGGTTGGTA	550
BoCollardCompleteCDS	GATGAAGTATGTAGCACACCTGATGTTGATGCTAATGTTGCGGTCAGTA	1117
BoBroccoliNullAlleleGenomicDNA	GATGAAGTATGTAGCACACCTGATGTTGATGCTAATGTTGCGGTCAGTA	1119
SavoyRV	-----CGTT-----	193

BrCompleteCDSGenomicDNA	CTAAAGATTCTGATGATGGTGCTAATACGAATACAACCTGCTAACGCTGAT	894
BrCompleteCDSmDNA	CTAAAGATTCTGATGATGGTGCTAATACGAATACAACCTGCTAACGCTGAT	600
BoCollardCompleteCDS	CTAAAGATTCTGTTGATGGTGCTAATACGAATACAACCTGCTAACGCTGAT	1167
BoBroccoliNullAlleleGenomicDNA	CTAAAGATTCTGTTGATGGTGCTAATACGAATACAACCTGCTAACGCTGAT	1169
SavoyRV	-----ACTCT-----TACT-----CTA---TGAA	209
	* ** * * *** ***	
BrCompleteCDSGenomicDNA	GCTGATGATATTGCTAATGGTATTGCTAAAGTTCATATTGATGACGATGC	944
BrCompleteCDSmDNA	GCTGATGATATTGCTAATGGTATTGCTAAAGTTCATATTGATGACGATGC	650
BoCollardCompleteCDS	GCTGGTGATATTGCTAATGGTATTGCTAAAGTTCATATTGATGACGATGC	1217
BoBroccoliNullAlleleGenomicDNA	GCTGGTGATATTGCTAATGGTATTGCTAAAGTTCATATTGATGACGATGC	1219
SavoyRV	ACGGACGA-----GATAGT----CTACCATTTCATA-----AGTGC	240
	* * ** ** ** *** ***** ***	
BrCompleteCDSGenomicDNA	TGATGCCAAGGGTGACGTTTGCACCTGGTGCTGGTACCAATCATAATGGTG	994
BrCompleteCDSmDNA	TGATGCCAAGGGTGACGTTTGCACCTGGTGCTGGTACCAATCATAATGGTG	700
BoCollardCompleteCDS	TAAATGCCAAGGGTGACGTTTGCACCTGGTGTTGGTACCAATCATAATGGTG	1267
BoBroccoliNullAlleleGenomicDNA	TAAATGCCAAGGGTGACGTTTGCACCTGGTGTTGGTACCAATCATAATGGTG	1269
SavoyRV	--ATATAGAGAAT-----CT-----CCAGCCATAACAACG	268
	** ** * ** *** ***** *	
BrCompleteCDSGenomicDNA	ATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGACGTT	1044
BrCompleteCDSmDNA	ATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGACGTT	750
BoCollardCompleteCDS	ATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGACGTT	1317
BoBroccoliNullAlleleGenomicDNA	ATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGACGTT	1319
SavoyRV	AAAGAGTTA-----KGACAKGGTT---TTAA-CCTGAT-----	297
	* **** ** * * *** ** **	
BrCompleteCDSGenomicDNA	GGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAACACTGG	1094
BrCompleteCDSmDNA	GGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAA-----	794
BoCollardCompleteCDS	GGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAACATTGG	1367
BoBroccoliNullAlleleGenomicDNA	GGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAACATTGG	1369
SavoyRV	---CCACTTTT-----ATCT---TTGGT-----	315
	* * * * **** *****	
BrCompleteCDSGenomicDNA	CACTATTGATGATGTTAATGCTAATGCTGGTACTCGTAGTAGTGCTAATG	1144
BrCompleteCDSmDNA	-----TGCTAATGCTGGTACTCGTAGTAGTGCTAATG	826
BoCollardCompleteCDS	CACTATTGCTGATGTTAAGGCTAATACTGGTACTCGTAGTAGTGCTAATG	1417
BoBroccoliNullAlleleGenomicDNA	CACTATTGCTGATGTTAAGGCTAATACTGGTACTCGTAGTAGTGCTAATG	1419
SavoyRV	-----TARCAC-----CTC-----	324
	** * ***	
BrCompleteCDSGenomicDNA	TTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAGGAG	1194

BrCompleteCDSmDNA	TTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAGGAG	876
BoCollardCompleteCDS	TTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAGGAG	1467
BoBroccoliNullAlleleGenomicDNA	TTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAGGAG	1469
SavoyRV	-----CAAACCT-----	331
	*** **	
BrCompleteCDSGenomicDNA	AAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGACGGTACT	1244
BrCompleteCDSmDNA	AAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGACGGTACT	926
BoCollardCompleteCDS	AAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGACGGTGCT	1517
BoBroccoliNullAlleleGenomicDNA	AAGAAATTAGGTCTACCTTCTCATACTGATAAA--CCTTTTGACGGTGCT	1517
SavoyRV	-----TCAA--TCTCATATTGATAAA-----GTAC-	354
	** * ***** ** *	
BrCompleteCDSGenomicDNA	TTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAAAGT	1294
BrCompleteCDSmDNA	TTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAAAGT	976
BoCollardCompleteCDS	TTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAAAGT	1567
BoBroccoliNullAlleleGenomicDNA	TTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAAAGT	1567
SavoyRV	-CGTCAA-----AAGGTTY-----TTA-----	370
	***** ** *	
BrCompleteCDSGenomicDNA	GGATCAGGTTAAACCACATCTCATAACTCTTTCGTTGTTATGGCTGGAGAT	1344
BrCompleteCDSmDNA	GGATCAGGTTAAACCACATCTCATAACTCTTTCGTTGTTATGGCTGGAGAT	1026
BoCollardCompleteCDS	GGATCAGGTTAAAGCCATCTCATAACTCTTTCGTTGTTATGGCTGGAGAT	1617
BoBroccoliNullAlleleGenomicDNA	GGATCAGGTTAAACCACATCTCATAACTCTTTCGTTGTTATGGCTGGAGAT	1617
SavoyRV	---TCAG-----TGTTG-----	378
	*** ** *	
BrCompleteCDSGenomicDNA	TCTCTATATGTAAGTTCTAACTTATTTTATTTTAAATGGGATGCACC--	1392
BrCompleteCDSmDNA	TCTCTATATG-----	1036
BoCollardCompleteCDS	TCTCTATATGTAAGTTCTAACTTATTTTATTTTAAATGGGATGCACCAT	1667
BoBroccoliNullAlleleGenomicDNA	TCTCTATATGTAAGTTCTAACTTATTTTATTTTAAATGGGATGCACCAT	1667
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AATATCTTAATTGCGATCATCATAATAATCATAACTTTTTTATGATATAT	1717
BoBroccoliNullAlleleGenomicDNA	AATATCTTAATTGCGATCATCATAATAATCATAACTTTTTTATGATATAT	1717
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	ATTATAACTTTTATGATATACATATTCATAACTTTTATGATATAAATATTAC	1767
BoBroccoliNullAlleleGenomicDNA	ATTATAACTTTTATGATATACATATTCATAACTTTTATGATATAAATATTAC	1767
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----TTTTTATTTTTTCCTATCACTTTCACAAATGCATGTCTTT	1432
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	ATAATTCACCTTTTTATTATTTCTTATCACTTTCACAAATGCATGTCTG--	1815
BoBroccoliNullAlleleGenomicDNA	ATAATTCACCTTTTTATTATTTCTTATCACTTTCACAAATGCATGTCTG--	1815
SavoyRV	-----	
BrCompleteCDSGenomicDNA	TCTTTACTAAAGTGTTTATACATTAACATTATATGTTTCTTCTCATCAT	1482
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	ACGTTACTAAAGTGTTTATACATTAACATTA--TGTTTCTTCTCATCAT	1863
BoBroccoliNullAlleleGenomicDNA	ACGTTACTAAAGTGTTTATACATTAACATTA--TGTTTCTTCTCATCAT	1863
SavoyRV	-----	
BrCompleteCDSGenomicDNA	GAAACTTGTTTTGATTTTTGTATTATT--TTGTTTGCAGGCACCTTATGAA	1531
BrCompleteCDSmDNA	-----CACTTATGAA	1046
BoCollardCompleteCDS	GAACTTGTTGTTGGTTTTTTTATTATTATTTTTTGCAGGCACCTTATGAA	1913
BoBroccoliNullAlleleGenomicDNA	GAACTTGTTGTTGGTTTTTTTATTATTATTTTTTGCAGGCACCTTATGAA	1913
SavoyRV	-----	
BrCompleteCDSGenomicDNA	TGGTAGACTGTCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAGAAAAGA	1581
BrCompleteCDSmDNA	TGGTAGACTGTCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAGAAAAGA	1096
BoCollardCompleteCDS	TGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAGAAAAGA	1963

BoBroccoliNullAlleleGenomicDNA	TGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAAGAAA	1963
SavoyRV	-----AGAAAGW	385
	*** *	
BrCompleteCDSGenomicDNA	AGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGAGATTACATC	1631
BrCompleteCDSmDNA	AGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGAGATTACATC	1146
BoCollardCompleteCDS	AGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGAGATTACATC	2013
BoBroccoliNullAlleleGenomicDNA	AGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGAGATTACATC	2013
SavoyRV	AGAC-----CTAAT---TKCTTCTC---CTC-----ATC	408
	*** * * * * *	
BrCompleteCDSGenomicDNA	ATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCACGTCTCTTCAA	1681
BrCompleteCDSmDNA	ATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCACGTCTCTTCAA	1196
BoCollardCompleteCDS	ATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCACGTCTCTTCAA	2063
BoBroccoliNullAlleleGenomicDNA	ATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCACGTCTCTTCAA	2063
SavoyRV	ATC-----TGCG-----CCAC-----	419
	** * * * *	
BrCompleteCDSGenomicDNA	ACCATTCACTTACGTTGACTTGATGAGTTTCTATCACACTGAGGCTGGTC	1731
BrCompleteCDSmDNA	ACCATTCACTTACGTTGACTTGATGAGTTTCTATCACACTGAGGCTGGTC	1246
BoCollardCompleteCDS	ACCATTCACTTACGTTGACTTGATGAGTTTCTATCACACTGAGGCTGGTC	2113
BoBroccoliNullAlleleGenomicDNA	ATCATTCACCTTACGTTGACTTGATGAGTTTCTATCACACTGAGGCTGGTC	2113
SavoyRV	-----CATTAGCTTAAACA---CYATCAC--TAACGCCMACA	451
	* * * * * *	
BrCompleteCDSGenomicDNA	GTAGAGCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGCATAA	1781
BrCompleteCDSmDNA	GTAGAGCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGCATAA	1296
BoCollardCompleteCDS	GTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGCATAA	2163
BoBroccoliNullAlleleGenomicDNA	GTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGCATAA	2163
SavoyRV	GTA-----CCACTAGCTACG-----	466
	* * * * *	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	ATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTAAGTAGTTTCATG	2213
BoBroccoliNullAlleleGenomicDNA	ATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTAAGTAGTTTCATG	2213
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GTTCAACTAATATCAAGAACTTCATGTAGTACTAAAAAAGAGTTTTTGG	2263
BoBroccoliNullAlleleGenomicDNA	GTTCAACTAATATCAAGAACTGCATGTAGTACTAAA-TAAGAGTTTTTGG	2262
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	ATTAGTTGAGTATATGTGTTTTATTTCCGGAGAAGCAATCAAGTCTCTCT	2313
BoBroccoliNullAlleleGenomicDNA	ATTAGTTGAGTATATGTGTTTTATTTCCGGAGAAGCAATCAAGTCTCTCT	2312
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TTTGTATGAAAAATCAATAATGTGTATGTGTATGAGCATGTTCAATAATG	2363
BoBroccoliNullAlleleGenomicDNA	TTTGTATGAAAAATCAATAA-AAATATGTGTATGAGCATGTTCAATAATG	2361
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TAAATGAAATTTGGTTGGATCTGTTGGTTCACAAGATGTCAGATCGTAAAT	2413
BoBroccoliNullAlleleGenomicDNA	TAAATGAAATTTGGTTGGATCTGTTGGTTCACAAGATGTCAGATCGTAAAT	2411
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AGGTTAATTAATAGGTTAATTTCTTCTTTTTTAACTAAATTAAT	2463
BoBroccoliNullAlleleGenomicDNA	AGGTTAATTAATAGGTTAATTTCTTCTTTTTTAACTAAATTAAT	2461
SavoyRV	-----	

BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TCATTTTTTTTTCTAAAAAATACTAGTTTAATTTCAAGGAGATGGGAAAC	2513
BoBroccoliNullAlleleGenomicDNA	TCATTTTTTTTTTATAAAAAAATACTAGTTTAATTTCAAGGAGATGGGAAAC	2511
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GAGTGTGGAACATATAAAAAACGGGTGTTTGCCATTTCAAACATTAAACGC	2563
BoBroccoliNullAlleleGenomicDNA	GAGTGTGGAACATATAAAAACTGGTGTGTTGCGATTTCAAACATTAAACGC	2561
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TAAATAAGTGAATGATTTACTTTTCATGTTATCGTAGCGATAGTGGTCTTG	2613
BoBroccoliNullAlleleGenomicDNA	TAAATAAGTGAATGATTTACTTTTCATGTTATCGTAGCGACAGTGGTTTTG	2611
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTTGTTTGCAAAAT	2663
BoBroccoliNullAlleleGenomicDNA	AGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTTGTTTGCAAAAT	2661
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GCCAAAATCGTAAATAGTA---AATTAATAATGTTATTTAAAGTTTGACC	2710
BoBroccoliNullAlleleGenomicDNA	GCCAAAATCGTAAATAGTAGTAAATTAGTAATGTTATTTAAAGTTTGACT	2711
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	GGTTTACTTGCAATAGGTGTATGTGCTGTGGTCCAAAAATTAGTGAAACT	2760
BoBroccoliNullAlleleGenomicDNA	GGTTTAATTGCAGTAGGTGTATGTGCTGTGGTCCAAAAATTAGTGAAACG	2761
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	AATAATTACAATTGTAAATTAGTAATGTTATTTAAAAATATAGACATGCAT	2810
BoBroccoliNullAlleleGenomicDNA	AATAATT-CAATTGTAAATTAGTAATGTTATTTAAAAATATAGACATGCAT	2810
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TGTCTCATGAACAAAGTGTGTTGAAATAGCGATTTGCAAGTGCCAACACTC	2860
BoBroccoliNullAlleleGenomicDNA	TGTCTCATGAACAAAGTGTGTTGAAATAGCGATTTGCAAGTGCCAACACTC	2860
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	TTCTCATGA-----	2869
BoBroccoliNullAlleleGenomicDNA	TTCTTATGAACAACGTTACAAATTAGGACCGCTTGGGCAAAACCTAACG	2910
SavoyRV	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoCollardCompleteCDS	-----	
BoBroccoliNullAlleleGenomicDNA	AAACATTACCTTTAATAAATCACCTTTGC	2939
SavoyRV	-----	

CLUSTAL 2.1 multiple sequence alignment

PSB Band1 AOP2 - Reverse Sequence

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BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  AAAAAAAAAAATAGAAATGTTTCTGTCTATAAATGGGCATTCCATCATTT 50
BoCollardCompleteCDS         -----
PSBrv                         -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  ACTTTCTCAGTACGGAAGCAAAAAAAAAAACTAAGGAAAAGAAAACCACT 100
BoCollardCompleteCDS         -----AAAAAAACCTAAGGAAAAGAAAACCTAGCT 29
PSBrv                         -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  TGATCTCTTTGAATCAAAGAAAA----- 123
BoCollardCompleteCDS         TGATCTCTTTGAATCAAAGAAAACCTCCAAAGGTAATTTTGGTAAATGT 79
PSBrv                         -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  ----ACTCCAAAGGTAGTTGT-CTTATGAGTTTTTAATGTTTTCTTTTGT 168
BoCollardCompleteCDS         AAATACTCCAAAGGTAGTTTTTCTTATGAATTTTGATGTTTTCTTTTGT 129
PSBrv                         -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  TGTGATGATTAAAGAGCTACTTAAACATTTTCTTTTCGGGTAAAAATA--- 215
BoCollardCompleteCDS         GTGGGTGATTAAAGAGTTACTTAAATATTTTCTTTTCGGGTAAAAATAAG 179
PSBrv                         -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  -----TAAAGCTAATT 226
BoCollardCompleteCDS         CTAATTAAATTAGTTTACTAAAAAAAATTAATAAAAAAATAAAGCTAATT 229
PSBrv                         -----

BrCompleteCDSGenomicDNA      -----A 1
BrCompleteCDSmDNA             -----A 1
BoBroccoliNullAlleleGenomicDNA  AACATTTTATAAATATATTTT--GGATTTGCACCAAGGAAAAAAGAA 274
BoCollardCompleteCDS         AACATTTTATGAATATATTTTTTTGGATTTGCACCAAGGCGAAAA-GAA 278
PSBrv                         -----

BrCompleteCDSGenomicDNA      TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 51
BrCompleteCDSmDNA             TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 51
BoBroccoliNullAlleleGenomicDNA  TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 324
BoCollardCompleteCDS         TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 328
PSBrv                         -----TCTACGACCAAGCC-TCAGTGTGATAGA---AACT 30
                               ** ** * * * * * * * * * *

BrCompleteCDSGenomicDNA      CTAAAACCAAGGAGTGAGAAGTGGGTGAAGTGAGGAGTGATGTCCGTAA 101
BrCompleteCDSmDNA             CTAAAACCAAGGAGTGAGAAGTGGGTGAAGTGAGGAGTGATGTCCGTAA 101
BoBroccoliNullAlleleGenomicDNA  CTAAAACCAAGGAGTGAGAAGTGGGTGAAGTGAGGAGTGATGTCCGTAA 374
BoCollardCompleteCDS         CTAAAACCAAGGAGTGAGAAGTGGGTGAAGTGAGGAGTGATGTCCGTAA 378
PSBrv                         C----AKCAGTCWDYGT-AHSWGRRT-GATGTGCA-ARWGA----SKBK 69
                               *   * * * *   *   *   * * * * *   *   *

BrCompleteCDSGenomicDNA      AGCTCTTGAAGACTA-CGGCGGTTTTGAGGTGTCATATGATAGAGTGTC 150
BrCompleteCDSmDNA             AGCTCTTGAAGACTA-CGGCGGTTTTGAGGTGTCATATGATAGAGTGTC 150
BoBroccoliNullAlleleGenomicDNA  AGCTCTTGAAGACTA-CGGCGGTTTTGAGGTGTCATATGATAGAGTGTC 423
BoCollardCompleteCDS         AGCTCTTGAAGACTA-CGGCGGTTTTGAGGTGTCATATGATAGAGTGTC 427
PSBrv                         GRCT-TTGMMSGASWGTCGCGC-MTTYTG--GTGTTCCGATGATGTAATCTCC 115
                               ** * * *   *   *   * * * *   * * * *

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BrCompleteCDSGenomicDNA	GA--GGAGCTGAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAG	198
BrCompleteCDSmDNA	GA--GGAGCTGAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAG	198
BoBroccoliNullAlleleGenomicDNA	GA--AGAGCTTAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAG	471
BoCollardCompleteCDS	GA--AGAGCTTAAGAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAG	475
PSBrv	GTTTGGAGTCSAGAACAAATGCTATTGAATACCTTG-----TCTTC---	155
	* *** * * * *** * * *	
BrCompleteCDSGenomicDNA	TTACCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTGG	248
BrCompleteCDSmDNA	TTACCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTGG	248
BoBroccoliNullAlleleGenomicDNA	TTACCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCTTACACTGG	521
BoCollardCompleteCDS	TTACCAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCTTACACTGG	525
PSBrv	TTTC-----TTTCCG-----TTACTCT--	172
	** * * * * *** * * *	
BrCompleteCDSGenomicDNA	ATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAATTCCA	298
BrCompleteCDSmDNA	ATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAATTCCA	298
BoBroccoliNullAlleleGenomicDNA	ATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGGATTCCA	571
BoCollardCompleteCDS	ATATTCAACTCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGGATTCCA	575
PSBrv	-TACTCTA--TGAAACGGAC-----GAGA--TAG--TCTACCATTCAA	208
	* * * * * * * * * * * *	
BrCompleteCDSGenomicDNA	ATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTGT	348
BrCompleteCDSmDNA	ATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTGT	348
BoBroccoliNullAlleleGenomicDNA	ATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTGT	621
BoCollardCompleteCDS	ATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTGT	625
PSBrv	AAGT---GCATA---TAGAGAATCT--CCAGCCA-----	234
	* * * * * * * * *	
BrCompleteCDSGenomicDNA	GAGGGTAACAAGAGTATGAGGTAAACGTCATGTCAAAAAAAAAAAACTAA	398
BrCompleteCDSmDNA	GAGGGTAACAAGAGTATGAG-----	368
BoBroccoliNullAlleleGenomicDNA	GAGGGTAACAAGACTATGAGGTAAACGTCATGTCAAAAAAAAAAAACTCA	671
BoCollardCompleteCDS	GAGGGTAACAAGACTATGAGGTAAACGTCATGTCGAAAAAAAAAAAA--CTCA	673
PSBrv	-----TAACAA-----	240

BrCompleteCDSGenomicDNA	GTAAATGCTTCGTAGAGTATATT---GTTCGTAAACTCCTGTTATTTTTT	444
BrCompleteCDSmDNA	GTAAATGCTTCGTAGAGTATATT---GTTCGTAAACTCCTGTTATTTTTT	
BoBroccoliNullAlleleGenomicDNA	GTAAATGCTTCATAGAGTAAATTAATTGTTTCGTAAATTCCTGTTAACTTTT	721
BoCollardCompleteCDS	GTAAATGCTTCATAGAGTAAATTAATTGTTTCGTAAATTCCTGTTAA--TCTT	721
PSBrv	-----	
BrCompleteCDSGenomicDNA	AATCAAAAATATTTTCGTAAATTTTTTTGTTAGTTGCTTTTATAAGCTATG	494
BrCompleteCDSmDNA	AATCAAAAATATTTTCGTAAATTTTTTTGTTAGTTGCTTTTATAAGCTATG	
BoBroccoliNullAlleleGenomicDNA	CATCAAAAATATTTTCGTAACTTTTTTGCTAGTTGTTTTTCATAAGTTATG	771
BoCollardCompleteCDS	CATCAAAAATATTT--CGTAACTTTTT--GCTAGTTGTTTTTCATAAGGTATG	769
PSBrv	-----	
BrCompleteCDSGenomicDNA	TAACAATTTTCTATATAAAACCTTGTTTTTATTTTTATTTTTTTGGAAAA	544
BrCompleteCDSmDNA	TAACAATTTTCTATATAAAACCTTGTTTTTATTTTTATTTTTTTGGAAAA	
BoBroccoliNullAlleleGenomicDNA	TGACAAATTTTCTATATAAAACCTTGTTTTTATCTTTATTTTTTTGGAAAA	821
BoCollardCompleteCDS	TGACAAATTTTCTATA--AAACCTTGTTTTTATCTTTATTTTTTTGGAAAA	818
PSBrv	-----	
BrCompleteCDSGenomicDNA	ATGTCAGTTCACCTATATAGTAATGAACCTGAAATTTGTTTTCAATCTCA	594
BrCompleteCDSmDNA	ATGTCAGTTCACCTATATAGTAATGAACCTGAAATTTGTTTTCAATCTCA	
BoBroccoliNullAlleleGenomicDNA	ATGTTAGTTCACCTCATATAGTAATGAACCTGAAATTTGTTTTCAATCTCA	871
BoCollardCompleteCDS	ATGTTAGTTCACCTCATATAGTAATGAACCTGAAATTTGTTTTCAATCTCA	868
PSBrv	-----	
BrCompleteCDSGenomicDNA	CGTTTCTCGCATTTTATTTTCTGTTTCTATTAATAAGCTATATAA--T	642
BrCompleteCDSmDNA	CGTTTCTCGCATTTTATTTTCTGTTTCTATTAATAAGCTATATAA--T	
BoBroccoliNullAlleleGenomicDNA	CGTTTCACGCATTT---TTTTTGTTCCTATTAATAAGCTATATAA--T	917
BoCollardCompleteCDS	CGTTTCACGCATTT---TTTTTGTTCCTATTAATAAGCTATATAAATT	915
PSBrv	-----	
BrCompleteCDSGenomicDNA	TTTCTTTGTGTTGAAAAAGCGAAACGATCCAGAAATTTTTCAGAGAGTT	692

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BrCompleteCDSDNA          -----CGAAACGATCCAGAAATTTTTCAGAGAAAGTT 398
BoBroccoliNullAlleleGenomicDNA TTTCTTTGTGTTGAAAAACAGCGAAACGATCCAGAAAGTTTTCAGAGAAAGTT 967
BoCollardCompleteCDS      TTTCTTTGTGTTGAAAAACAGCGAAACGATCCAGAAAGTTTTCAGAGAAAGTT 965
PSBrv                     -----CAAAGAGTT 250
                               ** * ****

BrCompleteCDSDNA          AGCAGAAATTGGATGTAATGGTGAGAAAGATGGTCATAGAGAGCTTTGGGA 742
BrCompleteCDSDNA          AGCAGAAATTGGATGTAATGGTGAGAAAGATGGTCATAGAGAGCTTTGGGA 448
BoBroccoliNullAlleleGenomicDNA BoBroccoliNullAlleleGenomicDNA AGCAGAAATTGGATGTAATGGTGAGAAAGATGGTCATAGAGAGCTTTGGGA 1017
BoCollardCompleteCDS      AGCAGAAATTGGATGTAATGGTGAGAAAGATGGTCATAGAGAGCTTTGGGA 1015
PSBrv                     AGGAGA--TGGTTTTAA-----ACTGATC-----CCCTTTTCA 281
                               ** *** ** * ** * * * * *

BrCompleteCDSDNA          TAGAAAACACTCTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCGA 792
BrCompleteCDSDNA          TAGAAAACACTCTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCGA 498
BoBroccoliNullAlleleGenomicDNA BoBroccoliNullAlleleGenomicDNA TAGAAAACACTCTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCGA 1067
BoCollardCompleteCDS      TAGAAAACACTCTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCGA 1065
PSBrv                     T-----CTTTGGTTAGCACCTC---CAA--ACCTTCAATCTCAGA 316
                               * ***** * * **** * * * * *

BrCompleteCDSDNA          CTGATGAAATATGTAGCACACCTGACGTTGATGCTAATGTTGCGGTTGG 842
BrCompleteCDSDNA          CTGATGAAATATGTAGCACACCTGACGTTGATGCTAATGTTGCGGTTGG 548
BoBroccoliNullAlleleGenomicDNA BoBroccoliNullAlleleGenomicDNA CTGATGAAGTATGTAGCACACCTGATGTTGATGCTAATGTTGCGGTCAG 1117
BoCollardCompleteCDS      CTGATGAAGTATGTAGCACACCTGATGTTGATGCTAATGTTGCGGTCAG 1115
PSBrv                     TTGATAAA---GCAGCGTC---CAAAGGTTTATCAGAATGACAAGGT--- 357
                               *** ** * * * * * * * * * *

BrCompleteCDSDNA          TACTAAAGATTCTGATGATGGTGCTAATACGAATACAACCTGCTAACGCTG 892
BrCompleteCDSDNA          TACTAAAGATTCTGATGATGGTGCTAATACGAATACAACCTGCTAACGCTG 598
BoBroccoliNullAlleleGenomicDNA BoBroccoliNullAlleleGenomicDNA TACTAAAGATTCTGTTGATGGTGCTAATACGAATACAACCTGCTAACGCTG 1167
BoCollardCompleteCDS      TACTAAAGATTCTGTTGATGGTGCTAATACGAATACAACCTGCTAACGCTG 1165
PSBrv                     ---AAA---CCTAAT-----TTCTTCTCTCAT-CATCTGC----- 386
                               *** ** * * * * * * * * *

BrCompleteCDSDNA          ATGCTGATGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGACGAT 942
BrCompleteCDSDNA          ATGCTGATGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGACGAT 648
BoBroccoliNullAlleleGenomicDNA BoBroccoliNullAlleleGenomicDNA ATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGACGAT 1217
BoCollardCompleteCDS      ATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTTCATATTGATGACGAT 1215
PSBrv                     --GCCACCATTAACCTTTAACTATCACTATCGCCACATTAG---CACT 431
                               ** * * * * * * * * * *

BrCompleteCDSDNA          GCTGATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATCATAATGG 992
BrCompleteCDSDNA          GCTGATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATCATAATGG 698
BoBroccoliNullAlleleGenomicDNA BoBroccoliNullAlleleGenomicDNA GCTAATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATCATAATGG 1267
BoCollardCompleteCDS      GCTAATGCCAAGGGTGACGTTTGCACTGGTGCTGGTACCAATCATAATGG 1265
PSBrv                     ACT-----AGGAT-----TACCGGTA----- 447
                               ** *** * * * *

BrCompleteCDSDNA          TGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGACG 1042
BrCompleteCDSDNA          TGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGACG 748
BoBroccoliNullAlleleGenomicDNA BoBroccoliNullAlleleGenomicDNA TGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGACG 1317
BoCollardCompleteCDS      TGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGACG 1315
PSBrv                     TGAT--CCTTAACATCAACGATAGTGCCAAATGTTAA-----CA 483
                               **** * **** * * * * * * * * *

BrCompleteCDSDNA          TTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAACT 1092
BrCompleteCDSDNA          TTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAA---- 794
BoBroccoliNullAlleleGenomicDNA BoBroccoliNullAlleleGenomicDNA TTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAACT 1367
BoCollardCompleteCDS      TTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTGCTGATGTTAACT 1365
PSBrv                     TCAGCACCAA-----CACTGAATTTAGC----- 506
                               * * * * * * * * *

BrCompleteCDSDNA          GGCACATTGATGATGTTAATGCTAATGCTGGTACTCGTAGTAGTGCTAA 1142
BrCompleteCDSDNA          -----TGCTAATGCTGGTACTCGTAGTAGTGCTAA 824
BoBroccoliNullAlleleGenomicDNA BoBroccoliNullAlleleGenomicDNA GGCACATTGCTGATGTTAAGGCTAATACTGGTACTCGTAGTAGTGCTAA 1417
BoCollardCompleteCDS      GGCACATTGCTGATGTTAAGGCTAATACTGGTACTCGTAGTAGTGCTAA 1415
PSBrv                     -----ACTAACATTAGTACC 523
                               *** * * * * *

BrCompleteCDSDNA          TGTGCGGCTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAGG 1192
BrCompleteCDSDNA          TGTGCGGCTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAGG 874
BoBroccoliNullAlleleGenomicDNA BoBroccoliNullAlleleGenomicDNA TGTGCGGCTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAGG 1467

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BoCollardCompleteCDS	TGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAGG	1465
PSBrv	CGTCGACATTAG-----ACTTAACATTAGCACAA-----	552
	* * * * *	
BrCompleteCDSGenomicDNA	AGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGACGGTA	1242
BrCompleteCDSmDNA	AGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGACGGTA	924
BoBroccoliNullAlleleGenomicDNA	AGAAGAAATTAGGTCTACCTTCTCATACTGATAA--ACCTTTTGACGGTG	1515
BoCollardCompleteCDS	AGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGACGGTG	1515
PSBrv	-----	
BrCompleteCDSGenomicDNA	CTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAAA	1292
BrCompleteCDSmDNA	CTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAAA	974
BoBroccoliNullAlleleGenomicDNA	CTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAAA	1565
BoCollardCompleteCDS	CTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAAA	1565
PSBrv	--TCACCAAGTAT-----TAAC-----	566
	* * * * *	
BrCompleteCDSGenomicDNA	GTGGATCAGGTTAAAACCATCTCATAACTCTTTCGTTGTTATGGCTGGAG	1342
BrCompleteCDSmDNA	GTGGATCAGGTTAAAACCATCTCATAACTCTTTCGTTGTTATGGCTGGAG	1024
BoBroccoliNullAlleleGenomicDNA	GTGGATCAGGTTAAAACCATCTCATAACTCTTTCGTTGTTATGGCTGGAG	1615
BoCollardCompleteCDS	GTGGATCAGGTTAAAGCCATCTCATAACTCTTTCGTTGTTATGGCTGGAG	1615
PSBrv	-----GTCATCACCAT-----	577
	* * *	
BrCompleteCDSGenomicDNA	ATTCTCTATATGTAAGTTCTAACTTATTTTATTTTAAATGGGATGCACC	1392
BrCompleteCDSmDNA	ATTCTCTATATG-----	1036
BoBroccoliNullAlleleGenomicDNA	ATTCTCTATATGTAAGTTCTAACTTATTTTATTTTAAATGGGATGCACC	1665
BoCollardCompleteCDS	ATTCTCTATATGTAAGTTCTAACTTATTTTATTTTAAATGGGATGCACC	1665
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ATAATATCTTAATTGCGATCATCATAATAATCATAACTTTTTTATGATAT	1715
BoCollardCompleteCDS	ATAATATCTTAATTGCGATCATCATAATAATCATAACTTTTTTATGATAT	1715
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ATATTATAACTTTATGATATACATAATTCATAACTTTATGATATAAATATT	1765
BoCollardCompleteCDS	ATATTATAACTTTATGATATACATAATTCATAACTTTATGATATAAATATT	1765
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----TTTTTATTTTTTCCTATCACTTTCACAAATGCATGTCT	1430
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ACATAATTCACCTTTTTATTATTTCTTATCACTTTCACAAATGCATGTCT	1815
BoCollardCompleteCDS	ACATAATTCACCTTTTTATTATTTCTTATCACTTTCACAAATGCATGTCT	1815
PSBrv	-----	
BrCompleteCDSGenomicDNA	TTTCTTTACTAAAGTGTTTATACATTAACATTATATGTTTTCTTCTCATC	1480
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	--ACGTTACTAAAGTGTTTATACATTAACATTA--TGTTTTCTTCTCATC	1861
BoCollardCompleteCDS	--ACGTTACTAAAGTGTTTATACATTAACATTA--TGTTTTCTTCTCATC	1861
PSBrv	-----	
BrCompleteCDSGenomicDNA	ATGAAACTTGTTTTGATTTTTGTATTATT-TTGTTTGCAGGCATTATG	1529
BrCompleteCDSmDNA	-----CACTTATG	1044
BoBroccoliNullAlleleGenomicDNA	ATGAATCTTGTTGTTGGTTTTTTTATTATTATTTTTTGCAGGCATTATG	1911
BoCollardCompleteCDS	ATGAATCTTGTTGTTGGTTTTTTTATTATTATTTTTTGCAGGCATTATG	1911
PSBrv	-----TATG	581
	* * * *	
BrCompleteCDSGenomicDNA	AATGGTAGACTGTCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAGAAA	1579
BrCompleteCDSmDNA	AATGGTAGACTGTCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAGAAA	1094
BoBroccoliNullAlleleGenomicDNA	AATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAGAAA	1961
BoCollardCompleteCDS	AATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAGAAA	1961
PSBrv	ATTGGTA-----	588

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BrCompleteCDSGenomicDNA      GAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGAGATTACA 1629
BrCompleteCDSmDNA             GAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGAGATTACA 1144
BoBroccoliNullAlleleGenomicDNA GAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGAGATTACA 2011
BoCollardCompleteCDS         GAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGAGATTACA 2011
PSBrv                         -----CCAA----- 592
                               * * * *

BrCompleteCDSGenomicDNA      TCATCGAACCACCAAAAAGAGCTTGTGGACGAGAAGCACCACGTCTCTTC 1679
BrCompleteCDSmDNA             TCATCGAACCACCAAAAAGAGCTTGTGGACGAGAAGCACCACGTCTCTTC 1194
BoBroccoliNullAlleleGenomicDNA TCATCGAACCACCAAAAAGAGCTTGTGGACGAGAAGCACCACGTCTCTTC 2061
BoCollardCompleteCDS         TCATCGAACCACCAAAAAGAGCTTGTGGACGAGAAGCACCACGTCTCTTC 2061
PSBrv                         -----CACCA-----GTG-----C 601
                               * * * * * * * * *

BrCompleteCDSGenomicDNA      AAACCATTCACTTACGTTGACTTGATGAGTTTCTATCACACTGAGGCTGG 1729
BrCompleteCDSmDNA             AAACCATTCACTTACGTTGACTTGATGAGTTTCTATCACACTGAGGCTGG 1244
BoBroccoliNullAlleleGenomicDNA AAATCATTCACTTACGTTGACTTGATGAGTTTCTATCACACTGAGGCTGG 2111
BoCollardCompleteCDS         AAACCATTCACTTACGTTGACTTGATGAGTTTCTATCACACTGAGGCTGG 2111
PSBrv                         AAAC-----G 606
                               * * * * *

BrCompleteCDSGenomicDNA      TCGTAGAGCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGCAT 1779
BrCompleteCDSmDNA             TCGTAGAGCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGCAT 1294
BoBroccoliNullAlleleGenomicDNA TCGTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGCAT 2161
BoCollardCompleteCDS         TCGTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGCAT 2161
PSBrv                         TC-----ACCTTGGCATT-----AGCA- 624
                               * * * * * * * * *

BrCompleteCDSGenomicDNA      AA----- 1781
BrCompleteCDSmDNA             AA----- 1296
BoBroccoliNullAlleleGenomicDNA AAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTAAAGTAGTTTCA 2211
BoCollardCompleteCDS         AAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTAAAGTAGTTTCA 2211
PSBrv                         -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA TGGTTCAACTAATAATCAAGAACTGCATGTAGTACTAAA-TAAGAGTTTTT 2260
BoCollardCompleteCDS         TGGTTCAACTAATAATCAAGAACTTCATGTAGTACTAAAATAAGAGTTTTT 2261
PSBrv                         -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA GGATTAGTTGAGTATATGTGTTTTATTTCCGGGAGAAACAATCAAGTCTCT 2310
BoCollardCompleteCDS         GGATTAGTTGAGTATATGTGTTTTATTTCCGGGAGAAACAATCAAGTCTCT 2311
PSBrv                         -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA CTTTTGTATGAAAAATCAATAAAA-ATATGTGTATGAGCATGTTCAATAA 2359
BoCollardCompleteCDS         CTTTTGTATGAAAAATCAATAATGTGTATGTGTATGAGCATGTTCAATAA 2361
PSBrv                         -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA TGTAAATGAATTTGGTTGGATCTGTTGGTTCACAAGATGTCAAGATCGTAA 2409
BoCollardCompleteCDS         TGTAAATGAATTTGGTTGGATCTGTTGGTTCACAAGATGTCAAGATCGTAA 2411
PSBrv                         -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA ATAGGTTAATTAAATAGGTTAATTTCTTCTTTTAACTAAATTAA 2459
BoCollardCompleteCDS         ATAGGTTAATTAAATAGGTTAATTTCTTCTTTTAACTAAATTAA 2461
PSBrv                         -----

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BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ATTCAATTTTTTTTATAAAAAAATACTAGTTTAATTCAGGAGATGGGAA	2509
BoCollardCompleteCDS	ATTCAATTTTTTTTCTAAAAAATACTAGTTTAATTCAGGAGATGGGAA	2511
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ACGAGTGTGGAACATATAAAAACTGGTGTTCGATTTCAAACATTAAAC	2559
BoCollardCompleteCDS	ACGAGTGTGGAACATATAAAAACTGGTGTTCGATTTCAAACATTAAAC	2561
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	GCTAAATAAGTGAAATGATTTACTTTTCATGTTATCGTAGCGACAGTGGTTT	2609
BoCollardCompleteCDS	GCTAAATAAGTGAAATGATTTACTTTTCATGTTATCGTAGCGATAGTGGTCT	2611
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTTTGTTCGAAA	2659
BoCollardCompleteCDS	TGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTTTGTTCGAAA	2661
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ATGCCAAAATCGTAAATAGTAGTAAATTAGTAATGTTATTTAAAGTTTGA	2709
BoCollardCompleteCDS	ATGCCAAAATCGTAAATAGT---AAATTAATAATGTTATTTAAAGTTTGA	2708
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	CTGGTTTAATTGCAGTAGGTGTATGTGCTGTGGTCCAAAAATTAGTGAAA	2759
BoCollardCompleteCDS	CCGGTTTACTTGCAATAGGTGTATGTGCTGTGGTCCAAAAATTAGTGAAA	2758
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	CGAATAAATT-CAATTGTAAATTAGTAATGTTATTTAAAAATATAGACATGC	2808
BoCollardCompleteCDS	CTAATAAATTACAATTGTAAATTAGTAATGTTATTTAAAAATATAGACATGC	2808
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ATTGTCTCATGAACAAAGTGTGTTGAAATAGCGATTTGCAAGTGCCAACTC	2858
BoCollardCompleteCDS	ATTGTCTCATGAACAAAGTGTGTTGAAATAGCGATTTGCAAGTGCCAACAC	2858
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TCTTCTTATGAACAACGTTACAAATTAGGACCGGCTTGGGCAAAACCTAA	2908
BoCollardCompleteCDS	TCTTCTCATGA-----	2869
PSBrv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	CGAAACATTACCTTTAATAAATCACCTTTGC	2939
BoCollardCompleteCDS	-----	
PSBrv	-----	

CLUSTAL 2.1 multiple sequence alignment

DHAG1012 Band1 - Reverse Sequence

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BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  AAAAAAAAAAATAGAAATGTTTCTGTCTATAAATGGGCATTCCATCATTT 50
BoCollardCompleteCDS         -----
DHAG1012rv                    -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  ACTTTCTCAGTACGGAAGCAAAAAAAAAAACTAAGGAAAAGAAAACCACT 100
BoCollardCompleteCDS         -----AAAAAAACCTAAGGAAAAGAAAACCTAGCT 29
DHAG1012rv                    -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  TGATCTCTTTGAATCAAAGAAAACTCCAAAGGTAGTTG----- 139
BoCollardCompleteCDS         TGATCTCTTTGAATCAAAGAAAACTCCAAAGGTAATTTTGGTAAATGTT 79
DHAG1012rv                    -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  -----TCTTATGAGTTTTTAAATGTTTTCTTTTGT 168
BoCollardCompleteCDS         AAATACTCCAAAGGTAGTTTTTCTTATGAATTTTGAAATGTTTCTTTTGT 129
DHAG1012rv                    -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  TGTGATGATTAAAGAGCTACTTAAACATTTTCTTTCGGGTAAAAATA--- 215
BoCollardCompleteCDS         GTGGGTGATTAAAGAGTTACTTAAATATTTTCTTTCGGGTAAAAATAAG 179
DHAG1012rv                    -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA             -----
BoBroccoliNullAlleleGenomicDNA  -----TAAAGCTAATT 226
BoCollardCompleteCDS         CTAATTAAATTAGTTTACTAAAAAAAATTAATAAAAAAATAAAGCTAATT 229
DHAG1012rv                    -----

BrCompleteCDSGenomicDNA      -----A 1
BrCompleteCDSmDNA             -----A 1
BoBroccoliNullAlleleGenomicDNA  AACATTTTATAAATATATTTT--GGATTTGCACCAAGGAAAAAAGAA 274
BoCollardCompleteCDS         AACATTTTATGAATATATTTTTTTGGATTTGCACCAAGGCGAAAA-GAA 278
DHAG1012rv                    -----

BrCompleteCDSGenomicDNA      TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 51
BrCompleteCDSmDNA             TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 51
BoBroccoliNullAlleleGenomicDNA  TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 324
BoCollardCompleteCDS         TGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCGGACCAAACC 328
DHAG1012rv                    -GGGT--AGACGAGGGTCTACGACCAAGCC-TCAGTGTGATAGA--RACTS 44
                                * * * * * * * * * * * * * * * * * * * * * *

BrCompleteCDSGenomicDNA      CTAAAACCAAGGAGTGAGAAGTGGGTGAAGTGAGGAGTGATGTCCGTAA 101
BrCompleteCDSmDNA             CTAAAACCAAGGAGTGAGAAGTGGGTGAAGTGAGGAGTGATGTCCGTAA 101
BoBroccoliNullAlleleGenomicDNA  CTAAAACCAAGGAGTGAGAAGTGGGTGAAGTGAGGAGTGATGTCCGTAA 374
BoCollardCompleteCDS         CTAAAACCAAGGAGTGAGAAGTGGGTGAAGTGAGGAGTGATGTCCGTAA 378
DHAG1012rv                    RTCAAGTCARCGTAHGWGAR-TGATKTGMA--GAGRCGTGG-GTGCTT-- 88
                                * * * * * * * * * * * * * * * * * * * * * *

BrCompleteCDSGenomicDNA      AGCTCTTGAAGACTACGGCGGTTTTGAGGTGTCATATGATAGAGTGTGAC 151
BrCompleteCDSmDNA             AGCTCTTGAAGACTACGGCGGTTTTGAGGTGTCATATGATAGAGTGTGAC 151
BoBroccoliNullAlleleGenomicDNA  AGCTCTTGAAGACTACGGCGCTTTTGAGGTGTCATATGATAGAGTGTGAC 424
BoCollardCompleteCDS         AGCTCTTGAAGACTACGGCGCTTTTGAGGTGTCATATGATAGAGTGTGAC 428
DHAG1012rv                    --CTCGTCCASAM--GSTCTTTTGGTG-GTTCGATGATGTAATCTCCG 131
                                * * * * * * * * * * * * * * * * * * * * * *

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BrCompleteCDSGenomicDNA	A--GGAGCTGAAGAAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAGT	199
BrCompleteCDSmDNA	A--GGAGCTGAAGAAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAGT	199
BoBroccoliNullAlleleGenomicDNA	A--AGAGCTTAAGAAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAGT	472
BoCollardCompleteCDS	A--AGAGCTTAAGAAAGTCAGTTTTGGATGCCATGATAGAGCTTTTCGAGT	476
DHAG1012rv	TTTGGAGTCSAGAAACAATGCTATTGAATACCTTGTCTTCTTTCTTTCCGT	181
	*** * *	
BrCompleteCDSGenomicDNA	TACCAAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTGGA	249
BrCompleteCDSmDNA	TACCAAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTGGA	249
BoBroccoliNullAlleleGenomicDNA	TACCAAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTGGA	522
BoCollardCompleteCDS	TACCAAGTTGAGGCTAAACAGAGAAACGTGTCTCCGAAACCGTACACTGGA	526
DHAG1012rv	TACTCTT-----AC-----TCTATGAAACGG-----ACGARA	208
	*** *	
BrCompleteCDSGenomicDNA	TATTCAAC--TCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAAATTC	297
BrCompleteCDSmDNA	TATTCAAC--TCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGAAATTC	297
BoBroccoliNullAlleleGenomicDNA	TATTCAAC--TCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGGATTC	570
BoCollardCompleteCDS	TATTCAAC--TCATAATGGTCTCTCTGAGAGTCTAGGGATCCAGGATTC	574
DHAG1012rv	TAKTCTACATTCTAAGTGCATATMK-AGAATC-----TCCAG-----CC	247
	** * * * *	
BrCompleteCDSGenomicDNA	AATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTG	347
BrCompleteCDSmDNA	AATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTG	347
BoBroccoliNullAlleleGenomicDNA	AATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTG	620
BoCollardCompleteCDS	AATGTTTTGGAGAAAGTTAACGAATTTACTCAACTGCTACGCCCTGATTG	624
DHAG1012rv	A-----	248
	*	
BrCompleteCDSGenomicDNA	TGAGGGTAACAAGAGTATGAGGTAAACGTCATGTCAAAAAAAAAAAAACTA	397
BrCompleteCDSmDNA	TGAGGGTAACAAGAGTATGAG-----	368
BoBroccoliNullAlleleGenomicDNA	TGAGGGTAACAAGACTATGAGGTAAACGTCATGTCAAAAAAAAAAAAACTC	670
BoCollardCompleteCDS	TGAGGGTAACAAGACTATGAGGTAAACGTCATGTCAAAAAAAAAAAAACTC	672
DHAG1012rv	-----TAACAA-----	254

BrCompleteCDSGenomicDNA	AGTAATGCTTCGTAGAGTATATT---GTTTCGTAAACTCCTGTTATTTTT	443
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AGTAATGCTTCATAGAGTAAATTAAATTGTTTCGTAAATTCCTGTTAACTCT	720
BoCollardCompleteCDS	AGTAATGCTTCATAGAGTAAATTAAATTGTTTCGAAATTCCTGTAA--TCT	720
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	TAAATCAAAAATATTTTCGTAATTTTTTTGTTAGTTGCTTTTATAAGCTAT	493
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TCATCAAAAATATTTTCGTAACTTTTTGTAGTTGTTTTCATAAGTTAT	770
BoCollardCompleteCDS	TCATCAAAAATATTT--CGTAACTTTTT--GCTAGTTGTTTTCATAAGGTAT	768
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	GTAAACAATTTTCTATATAAAAACCTTGTTTTTATTTTTTATTTTTTTGGAAA	543
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	GTGACAAATTTTCTATATAAAAACCTTGTTTTTATCTTTATTTTTTTGGAAA	820
BoCollardCompleteCDS	GTGACAAATTTTCTATA--AAAACCTTGTTTTTATCTTTATTTTTTTGGAAA	817
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	AATGTCAGTTCACTTATATAGTAATGAAGTGAATTTGTTTTCAATCTC	593
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AATGTTAGTTCACTCATATAGTAATGAAGTGAATTTGTTTTCAATCTC	870
BoCollardCompleteCDS	AATGTTAGTTCACTCATATAGTAATGAAGTGAATTTGTTTTCAATCTC	867
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	ACGTTTCTCGCATTTTATTTTCTTGTCTATTAAAAATAGCTATATAA--	641
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ACGTTTACGCATTT---TTTTTGTCTTCTATTAAAAATAGCTATATAA--	916
BoCollardCompleteCDS	ACGTTTACGCATTT---TTTTTGTCTTCTATTAAAAATAGCTATATAA--	914
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	TTTTCTTTGTGTTGAAAAAGCGAAACGATCCAGAAATTTTTCAGAGAAGT	691

BrCompleteCDSDNA		CGAAACGATCCGAATTTTTCAGAGAAGT	397
BoBroccoliNullAlleleGenomicDNA	TTTTCTTTGTGGTAAAAACAGCGAACGATCCAGAAGTTTTTCAGAGAAGT	966	
BoCollardCompleteCDS	TTTTCTTTGTGGTAAAAACAGCGAACGATCCAGAAGTTTTTCAGAGAAGT	964	
DHAG1012rv	-----CAAAGAGT	263	
		* * *	
BrCompleteCDSDNA	TAGCAGAAATTGGATGTAATGGTGAGAAGAATGGTCATAGAGAGCTTTGGG	741	
BrCompleteCDSDNA	TAGCAGAAATTGGATGTAATGGTGAGAAGAATGGTCATAGAGAGCTTTGGG	447	
BoBroccoliNullAlleleGenomicDNA	TAGCAGAAATTGGATGTAATGGTGAGAAGAATGGTCATAGAGAGCTTTGGG	1016	
BoCollardCompleteCDS	TAGCAGAAATTGGATGTAATGGTGAGAAGAATGGTCATAGAGAGCTTTGGG	1014	
DHAG1012rv	TAGGAGAG--GGTTTAAACC-----TGATC-----CCCTTTTC	294	
	* * * * *	* * *	* * *
BrCompleteCDSDNA	ATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCG	791	
BrCompleteCDSDNA	ATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCG	497	
BoBroccoliNullAlleleGenomicDNA	ATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCG	1066	
BoCollardCompleteCDS	ATAGAAAACACTTTTGATGAACACCTCAAGTCAACGAATTACCGTTTGCG	1064	
DHAG1012rv	AT-----CTTTGGTTAACACCTC---CAA--ACCTTCAATCTCAG	329	
	**	*****	* * * * *
BrCompleteCDSDNA	ACTGATGAAATATGTAGCACCACTGACGTTGATGCTAATGTTGCGGTTG	841	
BrCompleteCDSDNA	ACTGATGAAATATGTAGCACCACTGACGTTGATGCTAATGTTGCGGTTG	547	
BoBroccoliNullAlleleGenomicDNA	ACTGATGAAGTATGTAGCACCACTGATGTTGATGCTAATGTTGCGGTTG	1116	
BoCollardCompleteCDS	ACTGATGAAGTATGTAGCACCACTGATGTTGATGCTAATGTTGCGGTTG	1114	
DHAG1012rv	ATTGATAAA---GCAGCGTC--CAAAGGTTTATCAGAATGAGAAGGTAG	373	
	* * * * *	* * * * *	* * * * *
BrCompleteCDSDNA	GTAATAAGATTCTGATGATGGTGCTAATACGAATACAACCTGCTAACGCT	891	
BrCompleteCDSDNA	GTAATAAGATTCTGATGATGGTGCTAATACGAATACAACCTGCTAACGCT	597	
BoBroccoliNullAlleleGenomicDNA	GTAATAAGATTCTGTTGATGGTGCTAATACGAATACAACCTGCTAACGCT	1166	
BoCollardCompleteCDS	GTAATAAGATTCTGTTGATGGTGCTAATACGAATACAACCTGCTAACGCT	1164	
DHAG1012rv	AC-CTAAT--TTCTTCTC-----CTCAT-----CATCTGC-----	400	
	* * * *	* * * *	* * * * *
BrCompleteCDSDNA	GATGCTGATGATATTGCTAATGGTATTGCTAAAGTTCATATTGATGACGA	941	
BrCompleteCDSDNA	GATGCTGATGATATTGCTAATGGTATTGCTAAAGTTCATATTGATGACGA	647	
BoBroccoliNullAlleleGenomicDNA	GATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTCATATTGATGACGA	1216	
BoCollardCompleteCDS	GATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTCATATTGATGACGA	1214	
DHAG1012rv	---GCCACCTTTACCTTTAACTATCACTAA-----	429	
	**	**	*** ** *
BrCompleteCDSDNA	TGCTGATGCCAAGGGTGACGTTTGCTGCTGGTACCAATCATAATG	991	
BrCompleteCDSDNA	TGCTGATGCCAAGGGTGACGTTTGCTGCTGGTACCAATCATAATG	697	
BoBroccoliNullAlleleGenomicDNA	TGCTAATGCCAAGGGTGACGTTTGCTGCTGGTACCAATCATAATG	1266	
BoCollardCompleteCDS	TGCTAATGCCAAGGGTGACGTTTGCTGCTGGTACCAATCATAATG	1264	
DHAG1012rv	-----CGCCAA-----CATTAGCACT-----	445	
	* * * * *	* * * * *	
BrCompleteCDSDNA	GTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGAC	1041	
BrCompleteCDSDNA	GTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGAC	747	
BoBroccoliNullAlleleGenomicDNA	GTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGAC	1316	
BoCollardCompleteCDS	GTGATGACGTTAATACTGGTGATTGTGCTAATGTTAAGTCTAATGTGCGAC	1314	
DHAG1012rv	-----ACTAG-GATTA--CCGGTATTAGCCTTAACATCAAC	478	
	* * *	* * * * *	* * * * *
BrCompleteCDSDNA	GTTGGTACTAATGTTAGTGCTAAATCTAGTGTGGTGCTGATGTTAACAC	1091	
BrCompleteCDSDNA	GTTGGTACTAATGTTAGTGCTAAATCTAGTGTGGTGCTGATGTTAA---	794	
BoBroccoliNullAlleleGenomicDNA	GTTGGTACTAATGTTAGTGCTAAATCTAGTGTGGTGCTGATGTTAACAT	1366	
BoCollardCompleteCDS	GTTGGTACTAATGTTAGTGCTAAATCTAGTGTGGTGCTGATGTTAACAT	1364	
DHAG1012rv	AATAGGGCCAATGTTA----ACATC-AGCAACGCTGAT-----	514	
	* * *	* * * * *	* * * * *
BrCompleteCDSDNA	TGGCACTATTGATGATGTTAATGCTAATGCTGGTACTCGTAGTAGTGCTA	1141	
BrCompleteCDSDNA	-----TGCTAATGCTGGTACTCGTAGTAGTGCTA	823	
BoBroccoliNullAlleleGenomicDNA	TGGCACTATTGCTGATGTTAAGGCTAATACTGGTACTCGTAGTAGTGCTA	1416	
BoCollardCompleteCDS	TGGCACTATTGCTGATGTTAAGGCTAATACTGGTACTCGTAGTAGTGCTA	1414	
DHAG1012rv	-----TTAGCACTAACATTAGTACCA	535	
		* * * * *	* * * * *
BrCompleteCDSDNA	ATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAG	1191	
BrCompleteCDSDNA	ATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAG	873	
BoBroccoliNullAlleleGenomicDNA	ATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAG	1466	

BoCollardCompleteCDS	ATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGATGATGAG	1464
DHAG1012rv	ACGTCGACATTAG-----ACTTAACATTAGCACAA-----	565
	* * * * *	
BrCompleteCDSGenomicDNA	GAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGACGGT	1241
BrCompleteCDSmDNA	GAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGACGGT	923
BoBroccoliNullAlleleGenomicDNA	GAGAAGAAATTAGGTCTACCTTCTCATACTGATAA--ACCTTTTGACGGT	1514
BoCollardCompleteCDS	GAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAACCTTTTGACGGT	1514
DHAG1012rv	-----TC-----ACCAGTA-----TTAACGTC	582
	* * * * *	
BrCompleteCDSGenomicDNA	ACTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAA	1291
BrCompleteCDSmDNA	ACTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAA	973
BoBroccoliNullAlleleGenomicDNA	GCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAA	1564
BoCollardCompleteCDS	GCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACCAAAGATGAAA	1564
DHAG1012rv	A--TCACCATTATGA-----TT---GGTACCAAC-----	606
	* * * * *	
BrCompleteCDSGenomicDNA	AGTGGATCAGGTTAAAACCATCTCATAACTCTTTCGTTGTTATGGCTGGA	1341
BrCompleteCDSmDNA	AGTGGATCAGGTTAAAACCATCTCATAACTCTTTCGTTGTTATGGCTGGA	1023
BoBroccoliNullAlleleGenomicDNA	AGTGGATCAGGTTAAAACCATCTCATAACTCTTTCGTTGTTATGGCTGGA	1614
BoCollardCompleteCDS	AGTGGATCAGGTTAAAGCCATCTCATAACTCTTTCGTTGTTATGGCTGGA	1614
DHAG1012rv	-----ACCAGTGC AAA-----CGTCACCCTT--GGCATTAGCATCG--	640
	* * * * *	
BrCompleteCDSGenomicDNA	GATTCTCTATATGTAGTTCTAACTTATTTTATTTTAAATGGGATGCAC	1391
BrCompleteCDSmDNA	GATTCTCTATATG-----	1036
BoBroccoliNullAlleleGenomicDNA	GATTCTCTATATGTAGTTCTAACTTATTTTATTTTAAATGGGATGCAC	1664
BoCollardCompleteCDS	GATTCTCTATATGTAGTTCTAACTTATTTTATTTTAAATGGGATGCAC	1664
DHAG1012rv	--TCATCAATATG-----	651
	* * * * *	
BrCompleteCDSGenomicDNA	C-----	1392
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	CATAATATCTTAATTGCGATCATCATAATAATCATAACTTTTTTATGATA	1714
BoCollardCompleteCDS	CATAATATCTTAATTGCGATCATCATAATAATCATAACTTTTTTATGATA	1714
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TATATTATAACTTTATGATATACATATTCATAACTTTATGATATAAATAT	1764
BoCollardCompleteCDS	TATATTATAACTTTATGATATACATATTCATAACTTTATGATATAAATAT	1764
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	-----TTTTTATTTTTCCTATCAGTTTCACAAATGCATGTC	1429
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TACATAATTCACCTTTTTATTATTTCTTATCAGTTTCACAAATGCATGTC	1814
BoCollardCompleteCDS	TACATAATTCACCTTTTTATTATTTCTTATCAGTTTCACAAATGCATGTC	1814
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	TTTTCTTTACTAAAGTGTTTATACATTAAACATTATATGTTTCTTCTCAT	1479
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	G--ACGTTACTAAAGTGTTTATACATTAAACATTA--TGTTTTCTTCTCAT	1860
BoCollardCompleteCDS	G--ACGTTACTAAAGTGTTTATACATTAAACATTA--TGTTTTCTTCTCAT	1860
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	CATGAAACTTGTTTTGATTTTTGTATTATT-TTGTGTTGCAGGCACTTAT	1528
BrCompleteCDSmDNA	-----CACTTAT	1043
BoBroccoliNullAlleleGenomicDNA	CATGAATCTTGTTGGTTTTTTTTATTATTATTTTTTGCAGGCACTTAT	1910
BoCollardCompleteCDS	CATGAATCTTGTTGGTTTTTTTTATTATTATTTTTTGCAGGCACTTAT	1910
DHAG1012rv	-----AACTT--	656
	* * * *	
BrCompleteCDSGenomicDNA	GAAATGGTAGACTGTCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAGAA	1578
BrCompleteCDSmDNA	GAAATGGTAGACTGTCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAGAA	1093
BoBroccoliNullAlleleGenomicDNA	GAAATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAGAA	1960
BoCollardCompleteCDS	GAAATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAGAA	1960
DHAG1012rv	---TAGCAA--TA-----CCATT-----AGCAATATCACCAGCAT---	686

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BrCompleteCDSGenomicDNA      AGAAGACAAGGTATTCAATAGCA-TTGTTCGACTCCAAACGGAGATTA 1627
BrCompleteCDSmDNA            AGAAGACAAGGTATTCAATAGCA-TTGTTCGACTCCAAACGGAGATTA 1142
BoBroccoliNullAlleleGenomicDNA AGAAGACAAGGTATTCAATAGCA-TTGTTCGACTCCAAACGGAGATTA 2009
BoCollardCompleteCDS        AGAAGACAAGGTATTCAATAGCA-TTGTTCGACTCCAAACGGAGATTA 2009
DHAG1012rv                  -----CAGCGT-----TAGCAGTTGTATTCGT-----ATTA 712
                               **  **          * * * * * * * *          * * * *

BrCompleteCDSGenomicDNA      CATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCCACGTCTCT 1677
BrCompleteCDSmDNA            CATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCCACGTCTCT 1192
BoBroccoliNullAlleleGenomicDNA CATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCCACGTCTCT 2059
BoCollardCompleteCDS        CATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCCACGTCTCT 2059
DHAG1012rv                  -----GCACCATCAACAGAATCTTT-----AGTACTGAC-----C 742
                               * * * * * * * *          * *          * * * *

BrCompleteCDSGenomicDNA      TCAAACCATTCACCTACGTTGACTTGATGAGTTTCTATCACACTGAGGCT 1727
BrCompleteCDSmDNA            TCAAACCATTCACCTACGTTGACTTGATGAGTTTCTATCACACTGAGGCT 1242
BoBroccoliNullAlleleGenomicDNA TCAAACCATTCACCTACGTTGACTTGATGAGTTTCTATCACACTGAGGCT 2109
BoCollardCompleteCDS        TCAAACCATTCACCTACGTTGACTTGATGAGTTTCTATCACACTGAGGCT 2109
DHAG1012rv                  GCAA-----CATTAGCATCAAC-----ATCA----- 763
                               * * *          * * * *          * * * *

BrCompleteCDSGenomicDNA      GGTCGTAGAGCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGC 1777
BrCompleteCDSmDNA            GGTCGTAGAGCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGC 1292
BoBroccoliNullAlleleGenomicDNA GGTCGTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGC 2159
BoCollardCompleteCDS        GGTCGTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAGC 2159
DHAG1012rv                  GGTGGTG-----CTACATACT----- 779
                               * * * *          * *          * *

BrCompleteCDSGenomicDNA      ATAA----- 1781
BrCompleteCDSmDNA            ATAA----- 1296
BoBroccoliNullAlleleGenomicDNA ATAAATGTTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTAAAGTAGTTT 2209
BoCollardCompleteCDS        ATAAATGTTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTAAAGTAGTTT 2209
DHAG1012rv                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA            -----
BoBroccoliNullAlleleGenomicDNA CATGGTTCAACTAATATCAAGAACTGCATGTAGTACTAAA-TAAGAGTTT 2258
BoCollardCompleteCDS        CATGGTTCAACTAATATCAAGAACTTCATGTAGTACTAAAATAAGAGTTT 2259
DHAG1012rv                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA            -----
BoBroccoliNullAlleleGenomicDNA TTGGATTAGTTGAGTATATGTGTTTTATTTCCGGAGAAGCAATCAAGTCT 2308
BoCollardCompleteCDS        TTGGATTAGTTGAGTATATGTGTTTTATTTCCGGAGAAGCAATCAAGTCT 2309
DHAG1012rv                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA            -----
BoBroccoliNullAlleleGenomicDNA CTCTTTTGTATGAAAAATCAATAAAA-ATATGTGTATGAGCATGTTCAAT 2357
BoCollardCompleteCDS        CTCTTTTGTATGAAAAATCAATAATGTGTATGTGTATGAGCATGTTCAAT 2359
DHAG1012rv                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA            -----
BoBroccoliNullAlleleGenomicDNA AATGTAATGAATTTGGTTGGATCTGTTGGTTCACAAGATGTCAAGATCGT 2407
BoCollardCompleteCDS        AATGTAATGAATTTGGTTGGATCTGTTGGTTCACAAGATGTCAAGATCGT 2409
DHAG1012rv                  -----

BrCompleteCDSGenomicDNA      -----
BrCompleteCDSmDNA            -----
BoBroccoliNullAlleleGenomicDNA AAATAGGTTAATTAATAGGTTAATTTCTTCTTCTTTTTTAAACTAAATT 2457
BoCollardCompleteCDS        AAATAGGTTAATTAATAGGTTAATTTCTTCTTCTTTTTTAAACTAAATT 2459
DHAG1012rv                  -----

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BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AAATTCATTTTTTTTATAAAAAATACTAGTTTAATTCAGGAGATGGG	2507
BoCollardCompleteCDS	AAATTCATTTTTTTTCTAAAAAATACTAGTTTAATTCAGGAGATGGG	2509
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AAACGAGTGTGGAACATATAAAAACTGGTGTTCGATTTCAAACATTAA	2557
BoCollardCompleteCDS	AAACGAGTGTGGAACATATAAAAAACGGGTGTTCGATTTCAAACATTAA	2559
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	ACGCTAAATAAGTGAAATGATTTACTTTCATGTTATCGTAGCGACAGTGGT	2607
BoCollardCompleteCDS	ACGCTAAATAAGTGAAATGATTTACTTTCATGTTATCGTAGCGATAGTGGT	2609
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTTTGTTCGA	2657
BoCollardCompleteCDS	CTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTTTGTTCGA	2659
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AAATGCCAAAATCGTAAATAGTAGTAAATTAGTAATGTTATTTAAAGTTT	2707
BoCollardCompleteCDS	AAATGCCAAAATCGTAAATAGT---AAATTAATAATGTTATTTAAAGTTT	2706
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	GACTGGTTTAATTGCAGTAGGTGTATGTGCTGTGGTCCAAAAATTAGTGA	2757
BoCollardCompleteCDS	GACCGGTTTACTTGCAATAGGTGTATGTGCTGTGGTCCAAAAATTAGTGA	2756
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AACGAATAATT-CAATTGTAAATTAGTAATGTTATTTAAAAATATAGACAT	2806
BoCollardCompleteCDS	AACGAATAATTACAATTGTAAATTAGTAATGTTATTTAAAAATATAGACAT	2806
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	GCATTGTCTCATGAACAAAGTGTGTTGAAATAGCGATTTGCAAGTGCCAAC	2856
BoCollardCompleteCDS	GCATTGTCTCATGAACAAAGTGTGTTGAAATAGCGATTTGCAAGTGCCAAC	2856
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	TCTCTTCTTATGAACAACGTTACAAATTAGGACCGCTTGGGCAAAACCT	2906
BoCollardCompleteCDS	ACTCTTCTCATGA-----	2869
DHAG1012rv	-----	
BrCompleteCDSGenomicDNA	-----	
BrCompleteCDSmDNA	-----	
BoBroccoliNullAlleleGenomicDNA	AACGAAACATTACCTTTAATAAATCACCTTTGC	2939
BoCollardCompleteCDS	-----	
DHAG1012rv	-----	

CLUSTAL 2.1 multiple sequence alignment

Winspit band 1, band 2, band 3 - odd12/odd48 primers amplification

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W1_odd      -----
W2_odd      -----
W3_odd      -----
BoBroccoliNullAlleleGenomicDNA  AAAAAAAAAAATAGAAATGTTTCTGTCTATAAATGGGCATTCCATCATTT 50
BoCollardCompleteCDS             AAAAAAACCTAAGGAAAAG-----AAACTAG-----CTTGATCT 35

W1_odd      -----
W2_odd      -----
W3_odd      -----
BoBroccoliNullAlleleGenomicDNA  ACTTTCTCAGTACGGAAGCAAAAAAAAAAACTAAGGAAAAGAAAACCAAGCT 100
BoCollardCompleteCDS             -CTTT-----GAATCAAAGAAAACCTCAAAGG----- 61

W1_odd      -----
W2_odd      -----
W3_odd      -----
BoBroccoliNullAlleleGenomicDNA  TGATCTCTTTGAATCAAAGAAAACTCCAAAGGTAGTTGT-CTTATGAGT 149
BoCollardCompleteCDS             TAAATTTTGGTAAATGTT-AAATACTCCAAAGGTAGTTTTTCTTATGAAT 110

W1_odd      -----
W2_odd      -----
W3_odd      -----
BoBroccoliNullAlleleGenomicDNA  TTTTAATGTTTTCTTTGTTGTGA-TGATTAAAGAGCTACTTAAACATTT 198
BoCollardCompleteCDS             TTTGAATGTTT-CTTTGTTGTGGGTGATTAAAGAGTTACTTAAATATTT 159

W1_odd      -----
W2_odd      -----
W3_odd      -----
BoBroccoliNullAlleleGenomicDNA  TCTTTCGGGTAAAAATA----- 215
BoCollardCompleteCDS             TCTTTCGGGTAAAAATAAGCTAATTAAATTAGTTTACTAAAAAAAATTA 209

W1_odd      -----
W2_odd      -----
W3_odd      -----
BoBroccoliNullAlleleGenomicDNA  -----TAAAGCTAATTAACATTTTATAAATATATTTTTT--GGATTT 254
BoCollardCompleteCDS             AAAAAAAATAAAGCTAATTAACATTTTATGAATATATTTTTTTGGATTT 259

W1_odd      -----
W2_odd      -----
W3_odd      -----
BoBroccoliNullAlleleGenomicDNA  GCACCAAAGGAAAAAAGAAATGGGTGCAGACACTCCTCAACTTCCAGTCA 304
BoCollardCompleteCDS             GCACCAAAGGCGAAAA-GAATGGGTGCAGACACTCCTCAACTTCCAGTCA 308

W1_odd      -----
W2_odd      -----
W3_odd      -----
BoBroccoliNullAlleleGenomicDNA  TCTATCTCTCGGACCAAAACCTAAAAACAGGAGGTGAGAAGTGGGTTGAA 354
BoCollardCompleteCDS             TCTATCTCTCGGACCAAAACCTAAAAACAGGAAGTGAGAAGTGGGTTGAA 358

W1_odd      -----
W2_odd      -----
W3_odd      -----
BoBroccoliNullAlleleGenomicDNA  GTGAGGAGTGATGTCCGTAAAGCTCTTGAAGACTACGGCGCTTTTGAGGT 404
BoCollardCompleteCDS             GTGAGGAGTGATGTCCGTAAAGCTCTTGAAGACTACGGCGCTTTTGAGGT 408

W1_odd      -----
W2_odd      -----
W3_odd      -----
BoBroccoliNullAlleleGenomicDNA  GTCATATGATAGAGTGTGAGAAGAGCTTAAGAAGTCAGTTTTGGATGCCA 454
BoCollardCompleteCDS             GTCATATGATAGAGTGTGAGAAGAGCTTAAGAAGTCAGTTTTGGATGCCA 458

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W1_odd      -----TG-----CGCGGACM-GT----- 12
W2_odd      -----GYYT-----CGGAGACACGT----- 15
W3_odd
BoBroccoliNullAlleleGenomicDNA  TGATAGAGCTTTTCGAGTTACCAAGTTGAGGCTAAACAGAGAAACGTGTCT 504
BoCollardCompleteCDS           TGATAGAGCTTTTCGAGTTACCAAGTTGAGGCTAAACAGAGAAACGTGTCT 508

W1_odd      -----TCTCTG----- 18
W2_odd      -----TTTTCT----- 21
W3_odd      -----TG----- 2
BoBroccoliNullAlleleGenomicDNA  CCGAAACCTTACACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCT 554
BoCollardCompleteCDS           CCGAAACCTTACACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCT 558

W1_odd      -----TTTAGC-----CTCA-C 29
W2_odd      -----GTTAGC-----CTCA-C 32
W3_odd      -----TTTAGC-----CTCAAC 14
BoBroccoliNullAlleleGenomicDNA  AGGGATCCAGGATTCCAATGTTTTGGAGAAAGTTAACGAATTTACTCAAC 604
BoCollardCompleteCDS           AGGGATCCAGGATTCCAATGTTTTGGAGAAAGTTAACGAATTTACTCAAC 608
                                   *** *      *****

W1_odd      TG-----GTAAC-----C 37
W2_odd      TG-----GKWAC-----TC 41
W3_odd      TG-----GTAAC-----TC 23
BoBroccoliNullAlleleGenomicDNA  TGCTACGCCCTGATTGTGAGGGTAACAAGACTATGAGGTAACGTCATGTC 654
BoCollardCompleteCDS           TGCTACGCCCTGATTGTGAGGGTAACAAGACTATGAGGTAACGTCATGTC 658
                                   **      * **

W1_odd      SAAAAG-----CTC--TA----TCATGG----- 54
W2_odd      GAAAAG-----CTC--TA----TCATGG----- 58
W3_odd      GAAAAG-----CTC--TA----TCATGG----- 40
BoBroccoliNullAlleleGenomicDNA  AAAAAAAAAAAAACTCAGTAATGCTTCATAGAGTAAATTAATTGTTTCGTA 704
BoCollardCompleteCDS           GAAAAAAAAAAAA--CTCAGTAATGCTTCATAGAGTAAATTAATTGTTTCGGA 706
                                   ****      ** *      *****

W1_odd      -----CATCCAAAC-----TGA CTTCTTA--AGCT 78
W2_odd      -----CATCCAAAC-----TGA CTTCTTA--AGCT 82
W3_odd      -----CATCCAAAC-----TGA CTTCTTA--AGCT 64
BoBroccoliNullAlleleGenomicDNA  AATTCCCTGTTAATCTTTTCATCAAAAATATTTTCGTAAC TTTTGTCTAGTT 754
BoCollardCompleteCDS           AATTCCCTGT-AACTCTT-CATCAAAAATATTT-CGTAAC TTTTGTCTAGTT 753
                                   *****      * ***** **

W1_odd      CTTCT-----GACW---CTCTAT----- 93
W2_odd      CTTCT-----GACA---CTCTAT----- 97
W3_odd      CTTCT-----GACA---CTCTAT----- 79
BoBroccoliNullAlleleGenomicDNA  GTTTTTCATAAGTTATGTGACAAATTTCTATAAAAAACCTTGTTTTTATC 804
BoCollardCompleteCDS           GTTTT-CATAAGGTATGTGACAAATTTCTATAAAAA-CCTTGTTTTTATC 801
                                   ** *      *** *****

W1_odd      -----CATATGACA----- 102
W2_odd      -----CATATGACA----- 106
W3_odd      -----CATATGACA----- 88
BoBroccoliNullAlleleGenomicDNA  TTTATTTTTTTTGGAAAAATGTTAGTTCACTCATATAGTAATGAACGAAA 854
BoCollardCompleteCDS           TTTATTTTTTTTGGAAAAATGTTAGTTCACTCATATAGTAATGAACGAAA 851
                                   *****

W1_odd      -----CCTCA-----AAA 110
W2_odd      -----CCTCA-----AAA 114
W3_odd      -----CCTCA-----AAA 96
BoBroccoliNullAlleleGenomicDNA  TTTTGTTTTCAATCTCACGTTTCACGCATTTTTTTTTGTTTCTATTAAAA 904
BoCollardCompleteCDS           TTTTGTTTTCAATCTCACGTTTCACGCATTTTTTTTTGTTTCTATTAAAA 901
                                   ****      ***

W1_odd      GCGCCGKA-----S 119
W2_odd      GCGCCGTA-----G 123
W3_odd      GCGCCGTA-----G 105
BoBroccoliNullAlleleGenomicDNA  TAGCTATATAAAATTTT-CTTTGTGTTGAAAACAGCGAAACGATCCAGAAG 953
BoCollardCompleteCDS           TAGCTATATAAAATTTTCTTTGTGTTGAAAACAGCGAAACGATCCAGAAG 951
                                   ** *

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W1_odd	TCTKCA-----	125
W2_odd	TCTTCA-----	129
W3_odd	TCTTCA-----	111
BoBroccoliNullAlleleGenomicDNA	TTTTCAGAGAAGTTAGCAGAATTGGATGTAATGGTGAGAAGAATGGTCAT	1003
BoCollardCompleteCDS	TTTTCAGAGAAGTTAGCAGAATTGGATGTAATGGTGAGAAGAATGGTCAT	1001
	* * *	
W1_odd	--RGAGCTYT--ACGGACATC-----ACTCCTCACTTCAAC--	157
W2_odd	--AGAGCTTT--ACGGACATC-----ACTCCTCACTTCAAC--	161
W3_odd	--AGAGCTTT--ACGGACATC-----ACTCCTCACTTCAAC--	143
BoBroccoliNullAlleleGenomicDNA	AGAGAGCTTTGGGATAGAAAACACTTTGATGAACACCTCAAGTCAACGA	1053
BoCollardCompleteCDS	AGAGAGCTTTGGGATAGAAAACACTTTGATGAACACCTCAAGTCAACGA	1051
	***** * * * * *	
W1_odd	---CCTT---CT-----CACCTCCTGGTTTT-----	179
W2_odd	---CCTT---CT-----CACCTCCTGGTTTT-----	183
W3_odd	---CCTT---CT-----CACCTCCTGGTTTT-----	165
BoBroccoliNullAlleleGenomicDNA	ATTACCGTTTGGGACTGATGAAGTATGTAGCACCACTGATGTTGATGCT	1103
BoCollardCompleteCDS	ATTACCGTTTGGGACTGATGAAGTATGTAGCACCACTGATGTTGATGCT	1101
	* * * * *	
W1_odd	-----	
W2_odd	-----	
W3_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AATGTTGCGGTCAGTACTAAAGATTCTGTTGATGGTGCTAATACGAATAC	1153
BoCollardCompleteCDS	AATGTTGCGGTCAGTACTAAAGATTCTGTTGATGGTGCTAATACGAATAC	1151
W1_odd	-----	
W2_odd	-----	
W3_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AACTGCTAACGCTGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTC	1203
BoCollardCompleteCDS	AACTGCTAACGCTGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTC	1201
W1_odd	-----AGGGT-----TTGGT	189
W2_odd	-----AGGGT-----TTGGT	193
W3_odd	-----AGGGT-----TTGGT	175
BoBroccoliNullAlleleGenomicDNA	ATATTGATGACGATGCTAATGCCAAGGGTGACGTTTGCACTGGTGTTGGT	1253
BoCollardCompleteCDS	ATATTGATGACGATGCTAATGCCAAGGGTGACGTTTGCACTGGTGTTGGT	1251
	* * * * *	
W1_odd	CC-----	191
W2_odd	CC-----	195
W3_odd	CC-----	177
BoBroccoliNullAlleleGenomicDNA	ACCAATCATAATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAA	1303
BoCollardCompleteCDS	ACCAATCATAATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAA	1301
	*	
W1_odd	-----	
W2_odd	-----	
W3_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GTCTAATGTGCGACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTG	1353
BoCollardCompleteCDS	GTCTAATGTGCGACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTTGGTG	1351
W1_odd	-----	
W2_odd	-----	
W3_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CTGATGTTAACATTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACT	1403
BoCollardCompleteCDS	CTGATGTTAACATTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACT	1401
W1_odd	-----	
W2_odd	-----	
W3_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CGTACTAGTGCTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTG	1453
BoCollardCompleteCDS	CGTACTAGTGCTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTG	1451
W1_odd	-----GAGA-----GATAGA-	201
W2_odd	-----GAGA-----GATAGA-	205

W3_odd	-----GAGA-----GATAGA-	187
BoBroccoliNullAlleleGenomicDNA	CGCAGATGATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAA-	1502
BoCollardCompleteCDS	CGCAGATGATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAA	1501
	*****	***** *
W1_odd	-----TGAC-----TGGAAGT----	212
W2_odd	-----TGAC-----TGGAAGT----	216
W3_odd	-----TGAC-----TGGAAGT----	198
BoBroccoliNullAlleleGenomicDNA	-CCTTTTGACGGTGCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTA	1551
BoCollardCompleteCDS	ACCTTTTGACGGTGCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTA	1551
	*****	***** **
W1_odd	-----TGAGGAGTG--TC-----	223
W2_odd	-----TGAGGAGTG--TC-----	227
W3_odd	-----TGAGGAGTG--TC-----	209
BoBroccoliNullAlleleGenomicDNA	ACCAAAGATGAAAAGTGGATCAGGTTAAAACCATCTCATAACTCTTTCGT	1601
BoCollardCompleteCDS	ACCAAAGATGAAAAGTGGATCAGGTTAAAGCCATCTCATAACTCTTTCGT	1601
	*** ***** *	
W1_odd	-----	
W2_odd	-----	
W3_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TGTTATGGCTGGAGATTCTCTATATGTAAGTTCTAACTTATTTTATTTTT	1651
BoCollardCompleteCDS	TGTTATGGCTGGAGATTCTCTATATGTAAGTTCTAACTTATTTTATTTTT	1651
W1_odd	-----TGCACC-----CATT-----	233
W2_odd	-----TGCACC-----CATT-----	237
W3_odd	-----TGCACC-----CATT-----	219
BoBroccoliNullAlleleGenomicDNA	AAATGGGATGCACCATAATATCTTAATTGCGATCATCATAATAATCATAA	1701
BoCollardCompleteCDS	AAATGGGATGCACCATAATATCTTAATTGCGATCATCATAATAATCATAA	1701
	*****	***
W1_odd	CTTTTYK-----TC----CTTT	246
W2_odd	CTTTT---TC----CTTT	250
W3_odd	CTTTT---TC----CTTT	232
BoBroccoliNullAlleleGenomicDNA	CTTTTATGATATATATTATAACTTTATGATATACATATTCATAACTTT	1751
BoCollardCompleteCDS	CTTTTATGATATATATTATAACTTTATGATATACATATTCATAACTTT	1751
	*****	** *****
W1_odd	--GGTGCAAAT-----CC	257
W2_odd	--GGTGCAAAT-----CC	261
W3_odd	--GGTGCAAAT-----CC	243
BoBroccoliNullAlleleGenomicDNA	ATGATATAAATATTACATAATTCACCTTTTTATTATTTCTTATCACTTTC	1801
BoCollardCompleteCDS	ATGATATAAATATTACATAATTCACCTTTTTATTATTTCTTATCACTTTC	1801
	* * ***** *	
W1_odd	AAAAATATAT-----TYA-TAAAKGTTAAT---TAGCTTTATATTT	295
W2_odd	AAAAATATAT-----TTA-TAAATGTTAAT---TAGCTTTATATTT	299
W3_odd	AAAAATATAT-----TTA-TAAATGTTAAT---TAGCTTTATATTT	281
BoBroccoliNullAlleleGenomicDNA	ACAAATGCATGTCGACGTTACTAAAGTGTTTATACATTAAACATTATGTTT	1851
BoCollardCompleteCDS	ACAAATGCATGTCGACGTTACTAAAGTGTTTATACATTAAACATTATGTTT	1851
	* ***** * * * * * * * * * * * * *	
W1_odd	T-----AACCC-----	301
W2_odd	T-----AACCC-----	305
W3_odd	T-----AACCC-----	287
BoBroccoliNullAlleleGenomicDNA	TCTTCTCATCATGAATCTTGTTGGTTTTTTTATTATTATTTTTTTGCA	1901
BoCollardCompleteCDS	TCTTCTCATCATGAATCTTGTTGGTTTTTTTATTATTATTTTTTTGCA	1901
	* * * *	
W1_odd	-----	
W2_odd	-----	
W3_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GGCACTTATGAATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAA	1951
BoCollardCompleteCDS	GGCACTTATGAATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAA	1951
W1_odd	--GAAAGAAA-----	309
W2_odd	--GAAAGAAA-----	313
W3_odd	--GAAAGAAA-----	295
BoBroccoliNullAlleleGenomicDNA	CGGAAAGAAAGAGACAAGGTATTCAAATAGCATTGTTCTCGACTCCAAAC	2001

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BoCollardCompleteCDS      CGGAAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAAC 2001
                          *****

W1_odd                    -----
W2_odd                    -----
W3_odd                    -----
BoBroccoliNullAlleleGenomicDNA  GGAGATTACATCATCGAACCAACCAAAAGAGCTTGTGGACGAGAAGCACCC 2051
BoCollardCompleteCDS      GGAGATTACATCATCGAACCAACCAAAAGAGCTTGTGGACGAGAAGCACCC 2051


W1_odd                    -----
W2_odd                    -----
W3_odd                    -----
BoBroccoliNullAlleleGenomicDNA  ACGTCTCTTCAAATCATTCATTACGTTGACTTGATGAGTTTCTATCACA 2101
BoCollardCompleteCDS      ACGTCTCTTCAAACCATTCATTACGTTGACTTGATGAGTTTCTATCACA 2101


W1_odd                    -----
W2_odd                    -----
W3_odd                    -----
BoBroccoliNullAlleleGenomicDNA  CTGAGGCTGGTCGTAGACCTCGTTCTACTCTTACGCTTATTGTGCCGTC 2151
BoCollardCompleteCDS      CTGAGGCTGGTCGTAGACCTCGTTCTACTCTTACGCTTATTGTGCCGTC 2151


W1_odd                    -----
W2_odd                    -----
W3_odd                    -----
BoBroccoliNullAlleleGenomicDNA  TCTGGAGCATAAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTA 2201
BoCollardCompleteCDS      TCTGGAGCATAAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTA 2201
                          **  ****


W1_odd                    -----
W2_odd                    -----
W3_odd                    -----
BoBroccoliNullAlleleGenomicDNA  AGTRR-----ATRTTTA 316
W2_odd                    -----ATGTTTA 320
W3_odd                    -----ATGTTTA 302
BoBroccoliNullAlleleGenomicDNA  TCTGGAGCATAAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTA 2201
BoCollardCompleteCDS      TCTGGAGCATAAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTA 2201
                          **  ****


W1_odd                    AGTRR----- 321
W2_odd                    AGTMS----- 325
W3_odd                    AGTAG----- 307
BoBroccoliNullAlleleGenomicDNA  AGTAGTTTCATGGTTCAACTAATATCAAGAACTGCATGTAGTACTAAA-T 2250
BoCollardCompleteCDS      AGTAGTTTCATGGTTCAACTAATATCAAGAACTTCATGTAGTACTAAAAA 2251
                          ***


W1_odd                    -----
W2_odd                    -----
W3_odd                    -----
BoBroccoliNullAlleleGenomicDNA  AAGAGTTTTTTGGATTAGTTGAGTATATGTGTTTTATTTCCGGGAGAAGCAA 2300
BoCollardCompleteCDS      AAGAGTTTTTTGGATTAGTTGAGTATATGTGTTTTATTTCCGGGAGAAGCAA 2301


W1_odd                    -----
W2_odd                    -----
W3_odd                    -----
BoBroccoliNullAlleleGenomicDNA  TCAGTCTCTCTTTTGTATGAAAAATCAATAAAA-ATATGTGTATGAGCA 2349
BoCollardCompleteCDS      TCAGTCTCTCTTTTGTATGAAAAATCAATAATGTGTATGTGTATGAGCA 2351
                          *****

W1_odd                    -----
W2_odd                    -----
W3_odd                    -----
BoBroccoliNullAlleleGenomicDNA  TGTTCAATAATGTAATGAATTTGGTTGGATCTGTTGGTTCACAAGATGTC 2399
BoCollardCompleteCDS      TGTTCAATAATGTAATGAATTTGGTTGGATCTGTTGGTTCACAAGATGTC 2401
                          *****

W1_odd                    -----
W2_odd                    -----
W3_odd                    -----
BoBroccoliNullAlleleGenomicDNA  AAGATCGTAAATAGGTTAATTAAATAGGTTAATTTCTTCTCTTTTTTAA 2449
BoCollardCompleteCDS      AAGATCGTAAATAGGTTAATTAAATAGGTTAATTTCTTCTCTTTTTTAA 2451


W1_odd                    -----
W2_odd                    -----
W3_odd                    -----
BoBroccoliNullAlleleGenomicDNA  ACTAAATTAAATTCATTTTTTTTTTATAAAAAATACTAGTTTAATTTTCAG 2499
BoCollardCompleteCDS      ACTAAATTAAATTCATTTTTTTTTTATAAAAAATACTAGTTTAATTTTCAG 2501
                          *****

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W1_odd	-----AACAT-TAAAAAC-----TCA	361
W2_odd	-----AACAT-TAAAAAC-----TCA	365
W3_odd	-----AACAT-TAAAAAC-----TCA	347
BoBroccoliNullAlleleGenomicDNA	GAGATGGGAAACGAGTGTGGAACATATAAAAACTGGTGTTCGATTTC	2549
BoCollardCompleteCDS	GAGATGGGAAACGAGTGTGGAACATATAAAAAACGGGTGTTCGCATTTC	2551

W1_odd	-----TAAG--ACAACTACCTTTG-----	379
W2_odd	-----TAAG--ACAA-CTACCTTTG-----	382
W3_odd	-----TAAG--ACAA-CTACCTTTG-----	364
BoBroccoliNullAlleleGenomicDNA	AACATTAAACGCTAAATAAGTGAATGATTTACTTTTCATGTTATCGTAGCG	2599
BoCollardCompleteCDS	AACATTAAACGCTAAATAAGTGAATGATTTACTTTTCATGTTATCGTAGCG	2601
	*** * *	
W1_odd	-----GAGTT-----TTTCTT	390
W2_odd	-----GAGTT-----TTTCTT	393
W3_odd	-----GAGTT-----TTTCTT	375
BoBroccoliNullAlleleGenomicDNA	ACAGTGGTTTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTT	2649
BoCollardCompleteCDS	ATAGTGGTCTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTT	2651
	*** **	
W1_odd	TGATT-CAAAA---GAGATC-----	406
W2_odd	TGATT-CAAA---GAGATC-----	408
W3_odd	TGATT-CAAA---GAGATC-----	390
BoBroccoliNullAlleleGenomicDNA	TGTTTGCAAAATGCCAAAATCGTAAATAGTAGTAAATAGTAATGTTATT	2699
BoCollardCompleteCDS	TGTTTGCAAAATGCCAAAATCGTAAATAGTA---AATTAATAATGTTATT	2698
	* * * * *	
W1_odd	--AAG---CTGGT-----	414
W2_odd	--AAG---CTGGTTTTTC-----	420
W3_odd	--AAG---CTGGTTTTCTTTTC-----	407
BoBroccoliNullAlleleGenomicDNA	TAAAGTTTGACTGGTTTAATTGCAGTAGGTGTATGTGCTGTGGTCCAAAA	2749
BoCollardCompleteCDS	TAAAGTTTGACCGGTTTACTTGCAATAGGTGTATGTGCTGTGGTCCAAAA	2748
	*** * *	
W1_odd	-----	
W2_odd	-----	
W3_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ATTAGTGAAACGAATAATT-CAATTGTAAATTAGTAATGTTATTTAAAAAT	2798
BoCollardCompleteCDS	ATTAGTGAAACTAATAATTACAATTGTAAATTAGTAATGTTATTTAAAAAT	2798
W1_odd	-----	
W2_odd	-----	
W3_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ATAGACATGCATTGTCTCATGAACAAAGTGTTCGAAATAGCGATTTGCAA	2848
BoCollardCompleteCDS	ATAGACATGCATTGTCTCATGAACAAAGTGTTCGAAATAGCGATTTGCAA	2848
W1_odd	-----	
W2_odd	-----	
W3_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GTGCCAACTCTCTTCTTATGAACAACGTTACAAATTAGGACCGGCTTGGG	2898
BoCollardCompleteCDS	GTGCCAACTCTCTCTCATGA-----	2869
W1_odd	-----	
W2_odd	-----	
W3_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CAAAACCTAACGAAACATTACCTTTAATAAATCACCTTTGC	2939
BoCollardCompleteCDS	-----	

PSB band 1, band 2 - odd12/odd48 primers amplification

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PSB2_odd
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
PSB1_odd
-----
AAAAAAAAAAAAATAGAATGTTTCTGTCTATAAATGGGCATTCCATCATTT 50

PSB2_odd
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
PSB1_odd
-----
-----AAGAA--AACCAG 11
ACTTCTCTAGTACGGAAGCAAAAAAAAAAACTAAGGAAAAGAA--AACCAG 98
-----AAAAAACCTAAGGAAAAGAA--AACTAG 27
-----GTTTAGCCTCAACTGG 16
          **   ***   *

PSB2_odd
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
PSB1_odd
-----
---CTTGATCTCTTTGAATCAAAGAAAA----- 36
---CTTGATCTCTTTGAATCAAAGAAAA----- 123
---CTTGATCTCTTTGAATCAAAGAAAAGTAAATTTTGGTAAA 74
TAACTCGAAAGCTCT--ATCATGGCA----- 40
      * * *   * *   * * *   * *

PSB2_odd
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
PSB1_odd
-----
-----ACTCCAAAGGTAGTTGT-CTTATGAGTTTTTAATGTTTTCT 76
-----ACTCCAAAGGTAGTTGT-CTTATGAGTTTTTAATGTTTTCT 163
ATGTTAAATACTCCAAAGGTAGTTTTCTTATGAATTTTGAATGTTT-CT 123
-----TCCAAACTGACT-T-CTTAAGCTCTTCTGACACTCTAT 77
          * * * * *   *   *   * * * * *   * *   *   *

PSB2_odd
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
PSB1_odd
-----
TTTGTGTGTA-TGATTAAAGAGCTA---CTTAAACATTTTCTTTCCGGGT 121
TTTGTGTGTA-TGATTAAAGAGCTA---CTTAAACATTTTCTTTCCGGGT 208
TTTGTGTGGGTGATTAAAGAGTTA---CTTAAATATTTTCTTTCCGGGT 169
CATATGACACCTCA--AAAGCGCGTAGTCTTCAAGAGCTT--TACGGAC 123
      * *   * *   * * * * *   * * * * *   * * * *

PSB2_odd
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
PSB1_odd
-----
TAAAAATA-----T 129
TAAAAATA-----T 216
TAAAAATAAAGCTAATTAATTAGTTTACTAAAAAAAAAATAAAAAAAAAAT 219
ATCACTCC-----T 132
      * *   *

PSB2_odd
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
PSB1_odd
-----
AAAGCTAATTAACATTTTATAAATATATTTTT--GGATTTGCACCAAAGG 177
AAAGCTAATTAACATTTTATAAATATATTTTT--GGATTTGCACCAAAGG 264
AAAGCTAATTAACATTTTATGAATATATTTTTTTGGATTTGCACCAAAGG 269
CACTTCAACCCACTTCTCACCTCCTGGTTTTTA--GGGTTTGGTCCGAGAG 180
      *   **   * *   * *   * * * * *   * * * * *   *

PSB2_odd
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
PSB1_odd
-----
AAAAAAGAATGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTC 227
AAAAAAGAATGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTC 314
CGAAAA-GAATGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTC 318
ATAGAT-GACTGGAAGTTGAGGAGTGTCTGCACCAATCTTTTTTTCCTT 229
      * *   * * * * *   * *   * *   * * * * *   *

PSB2_odd
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
PSB1_odd
-----
GGAC-CAAACCCATAAAACCAGGAGGTGAGAAGTGGGTTGAAGTGAGGAGT 276
GGAC-CAAACCCATAAAACCAGGAGGTGAGAAGTGGGTTGAAGTGAGGAGT 363
GGAC-CAAACCCATAAAACCAGGAAGTGAGAAGTGGGTTGAAGTGAGGAGT 367
TGGTGCAAAATCCAAAAATATATTTATAAAATGTTAAATAGCTTTATATTT 279
      *   * * * * *   * *   * *   * *   * *   *

PSB2_odd
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
PSB1_odd
-----
GATGTCCGTAA--AGCTCTTGAAGACTACGGCGCTTTTGAGGTGTCATAT 324
GATGTCCGTAA--AGCTCTTGAAGACTACGGCGCTTTTGAGGTGTCATAT 411
GATGTCCGTAA--AGCTCTTGAAGACTACGGCGCTTTTGAGGTGTCATAT 415
TA-ACCCGAAAGAAAAATGTTTAAAG--TA---GCTCTTTAATCATCACA- 321
      *   * * * * *   * *   * *   * *   * *   *

PSB2_odd
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
PSB1_odd
-----
GATAGAGTGTGAGAAGAGCTTAAGAAGTCAGTTTTTGA---TGCCATGA 370
GATAGAGTGTGAGAAGAGCTTAAGAAGTCAGTTTTTGA---TGCCATGA 457
GATAGAGTGTGAGAAGAGCTTAAGAAGTCAGTTTTTGA---TGCCATGA 461
-ACAAA-----AGAAAACATTAAAACTCA--TAAGACAACCTACCTT-- 360
      * * *   * * * *   * * * *   * *   *   *

PSB2_odd
-----
TAGAGCTTTTC---GAGTTACCAGTTGAGGCTAAACAGA----- 406

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BoBroccoliNullAlleleGenomicDNA	TAGAGCTTTTC---GAGTTACCAAGTTGAGGCTAAACAGAGAAACGTGTCT	504
BoCollardCompleteCDS	TAGAGCTTTTC---GAGTTACCAAGTTGAGGCTAAACAGAGAAACGTGTCT	508
PSB1_odd	TGGAGTTTTTCTTTGATTCA--AA--GAGATCAAGCTGGTTTTTC-----	400
	* *	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CCGAAACCTTACACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCT	554
BoCollardCompleteCDS	CCGAAACCTTACACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCT	558
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AGGGATCCAGGATTCCAATGTTTTGGAGAAAGTTAACGAATTTACTCAAC	604
BoCollardCompleteCDS	AGGGATCCAGGATTCCAATGTTTTGGAGAAAGTTAACGAATTTACTCAAC	608
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TGCTACGCCCTGATTGTGAGGGTAACAAGACTATGAGGTAACGTCATGTC	654
BoCollardCompleteCDS	TGCTACGCCCTGATTGTGAGGGTAACAAGACTATGAGGTAACGTCATGTC	658
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AAAAAAAAAAAACTCAGTAATGCTTCATAGAGTAAATTAATTGTTTCGTA	704
BoCollardCompleteCDS	GAAAAAAAAAACTCAGTAATGCTTCATAGAGTAAATTAATTGTTTCGAAA	708
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AATTCCTGTTAATCTTTCATCAAAAAATATTTTCGTAACTTTTGTCTAGTT	754
BoCollardCompleteCDS	TTCTGTAAATCTTTCATCAAAAAATATTTTCGTAACTTTTGTCTAGTTGTTT	758
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GTTTTTCATAAGTTATGTGACAAATTTCTATAAAAAACCTTGTTTTTATC	804
BoCollardCompleteCDS	CATAAGGTATGTGACAAATTTCTATAAAAAACCTTGTTTTTATCTTTATTT	808
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TTTATTTTTTTGGAAAAATGTTAGTTCACTCATATAGTAATGAAGTAAA	854
BoCollardCompleteCDS	TTTTGGAAAAATGTTAGTTCACTCATATAGTAATGAAGTAAATTTTGTT	858
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TTTTGTTTTCAATCTCACGTTTCACGCATTTTTTTTTGTTTCTATTAAAA	904
BoCollardCompleteCDS	TTCAATCTCACGTTTCACGCATTTTTTTTTGTTTCTATTAAATAGCTAT	908
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TAGCTATATAAATTTTCTTTGTGTTGAAAACAGCGAAACGATCCAGAAGT	954
BoCollardCompleteCDS	ATAAATTTTTCTTTGTGTTGAAAACAGCGAAACGATCCAGAAGTTTTCAG	958
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TTTCAGAGAAGTTAGCAGAATTGGATGTAATGGTGAGAAGAATGGTCATA	1004
BoCollardCompleteCDS	AGAAGTTAGCAGAATTGGATGTAATGGTGAGAAGAATGGTCATAGAGAGC	1008
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GAGAGCTTTGGGATAGAAAACACTTTGATGAACACCTCAAGTCAACGAA	1054
BoCollardCompleteCDS	TTTGGGATAGAAAACACTTTGATGAACACCTCAAGTCAACGAATTACCG	1058
PSB1_odd	-----	
PSB2_odd	-----	

BoBroccoliNullAlleleGenomicDNA	TTACCGTTTGCGACTGATGAAGTATGTAGCACCACTGATGTTGATGCTA	1104
BoCollardCompleteCDS	TTTGCGACTGATGAAGTATGTAGCACCACTGATGTTGATGCTAATGTTG	1108
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ATGTTGCGGTCAGTACTAAAGATTCTGTTGATGGTGCTAATACGAATACA	1154
BoCollardCompleteCDS	CGGTCAGTACTAAAGATTCTGTTGATGGTGCTAATACGAATACAACTGCT	1158
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ACTGCTAACGCTGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTCA	1204
BoCollardCompleteCDS	AACGCTGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTCATATTGA	1208
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TATTGATGACGATGCTAATGCCAAGGGTGACGTTTGCACTGGTGTGGTA	1254
BoCollardCompleteCDS	TGACGATGCTAATGCCAAGGGTGACGTTTGCACTGGTGTGGTACCAATC	1258
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CCAAATCATAATGGTGATGACGTTAACTGCTGATTGTGCTAATGTTAAG	1304
BoCollardCompleteCDS	ATAATGGTGATGACGTTAACTGCTGATTGTGCTAATGTTAAGTCTAAT	1308
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TCTAATGTGCGACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTGGTGTC	1354
BoCollardCompleteCDS	GTCCGACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTGGTGCTGATGT	1358
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TGATGTTAACATTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACTC	1404
BoCollardCompleteCDS	TAAATTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACTCGTACTA	1408
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GTAAGTGTGCTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGC	1454
BoCollardCompleteCDS	GTGCTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGGCGCAGAT	1458
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GCAGATGATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAACC	1504
BoCollardCompleteCDS	GATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAAACCTTTT	1508
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TTTTGACGGTGCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACC	1554
BoCollardCompleteCDS	GACGGTGCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTAACC	1558
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AAAGATGAAAAGTGGATCAGGTTAAACCATCTCATAACTCTTCGTTGT	1604
BoCollardCompleteCDS	ATGAAAAGTGGATCAGGTTAAAGCCATCTCATAACTCTTCGTTGTTATG	1608
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TATGGCTGGAGATTCTCTATATGTAAGTTCTAACTATTTTATTTTAAA	1654
BoCollardCompleteCDS	GCTGGAGATTCTCTATATGTAAGTTCTAACTATTTTATTTTAAATGGG	1658
PSB1_odd	-----	
PSB2_odd	-----	

BoBroccoliNullAlleleGenomicDNA	TGGGATGCACCATAATATCTTAATTGCGATCATCATAATAATCATAACTT	1704
BoCollardCompleteCDS	ATGCACCATAATATCTTAATTGCGATCATCATAATAATCATAACTTTTTT	1708
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TTTTATGATATATATTATAACTTTATGATATACATATTCATAACTTTATG	1754
BoCollardCompleteCDS	ATGATATATATTATAACTTTATGATATACATATTCATAACTTTATGATAT	1758
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ATATAAATATTACATAATTCACCTTTTTATTATTTCTTATCACTTTCACA	1804
BoCollardCompleteCDS	AAATATTACATAATTCACCTTTTTATTATTTCTTATCACTTTCACAAATG	1808
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AATGCATGTCGACGTTACTAAAGTGTTTATACATTAAACATTATGTTTTCT	1854
BoCollardCompleteCDS	CATGTCGACGTTACTAAAGTGTTTATACATTAAACATTATGTTTTCTTCTC	1858
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TCTCATCATGAATCTTGTTGGTTTTTTTATTATTATTTTTTTGCAAGGC	1904
BoCollardCompleteCDS	ATCATGAATCTTGTTGGTTTTTTTATTATTATTTTTTTGCAAGGCACCTT	1908
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ACTTATGAATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAACGG	1954
BoCollardCompleteCDS	ATGAATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAACGGAAAG	1958
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGA	2004
BoCollardCompleteCDS	AAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAACGGAGATT	2008
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GATTACATCATCGAACCACAAAAGAGCTTGTGGACGAGAAGCACCCACG	2054
BoCollardCompleteCDS	ACATCATCGAACCACAAAAGAGCTTGTGGACGAGAAGCACCCACGTCCTC	2058
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TCTCTTCAAATCATTCACCTTACGTTGACTTGATGAGTTTCTATCACA	2104
BoCollardCompleteCDS	TTCAAACCATTCACCTTACGTTGACTTGATGAGTTTCTATCACA	2108
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AGGCTGGTCGTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCT	2154
BoCollardCompleteCDS	TGGTCGTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTCTCTGGAG	2158
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GGAGCATAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTAAAGT	2204
BoCollardCompleteCDS	CATAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTAAAGTAGTT	2208
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AGTTTCATGGTTCAACTAATATCAAGAACTGCATGTAGTACTAAATAAGA	2254
BoCollardCompleteCDS	TCATGGTTCAACTAATATCAAGAACTGCATGTAGTACTAAATAAGAGTT	2258
PSB1_odd	-----	
PSB2_odd	-----	

BoBroccoliNullAlleleGenomicDNA	GTTTTTGGATTAGTTGAGTATATGTGTTTTATTTCCGGAGAAGCAATCAA	2304
BoCollardCompleteCDS	TTTGGATTAGTTGAGTATATGTGTTTTATTTCCGGAGAAGCAATCAAGTC	2308
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GTCTCTCTTTTGTATGAAAAATCAATAAAAAATATGTGTATGAGCATGTTTC	2354
BoCollardCompleteCDS	TCTCTTTTGTATGAAAAATCAATAATGTGTATGTGTATGAGCATGTTCAA	2358
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AATAATGTAATGAATTTGGTTGGATCTGTTGGTTCACAAGATGTCAAGAT	2404
BoCollardCompleteCDS	TAAATGTAATGAATTTGGTTGGATCTGTTGGTTCACAAGATGTCAAGATCG	2408
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CGTAAATAGGTTAATTAAATAGGTTAATTTCTTCTTCTTTTTTAACTAA	2454
BoCollardCompleteCDS	TAAATAGGTTAATTAAATAGGTTAATTTCTTCTTCTTTTTTAACTAAAT	2458
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ATTAAATTCATTTTTTTTTTATAAAAAAATACTAGTTTAATTTTCAGGAGAT	2504
BoCollardCompleteCDS	TAAATTCATTTTTTTTTTCTAAAAAATACTAGTTTAATTTTCAGGAGATGG	2508
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GGGAAACGAGTGTGGAACATATAAAAACTGGTGTGTTGCGATTTCAAACAT	2554
BoCollardCompleteCDS	GAAACGAGTGTGGAACATATAAAAAACGGGTGTTTGCCATTTCAAACATTA	2558
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TAAACGCTAAATAAGTGAATGATTTACTTTCATGTTATCGTAGCGACAGT	2604
BoCollardCompleteCDS	AACGCTAAATAAGTGAATGATTTACTTTCATGTTATCGTAGCGATAGTGG	2608
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GGTTTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTTTGTTT	2654
BoCollardCompleteCDS	TCTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTTTGTTTGC	2658
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GCAAAATGCCAAAATCGTAAATAGTAGTAAATTAGTAATGTTATTTAAAG	2704
BoCollardCompleteCDS	AAAATGCCAAAATCGTAAATAGTAAATTAATAATGTTATTTAAAGTTTGA	2708
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TTTGACTGGTTTAAATTGCAGTAGGTGTATGTGCTGTGGTCCAAAAATTAG	2754
BoCollardCompleteCDS	CCGGTTTACTTGCAATAGGTGTATGTGCTGTGGTCCAAAAATTAGTGAAA	2758
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TGAAACGAATAATTCAATTGTAAATTAGTAATGTTATTTAAAATATAGAC	2804
BoCollardCompleteCDS	CTAATAATTACAATTGTAAATTAGTAATGTTATTTAAAATATAGACATGC	2808
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ATGCATTGTCTCATGAACAAAGTGTGAAATAGCGATTTGCAAGTGCCA	2854
BoCollardCompleteCDS	ATTGTCTCATGAACAAAGTGTGAAATAGCGATTTGCAAGTGCCAAACAC	2858
PSB1_odd	-----	
PSB2_odd	-----	

BoBroccoliNullAlleleGenomicDNA	ACTCTCTTCTTATGAACAACGTTACAAATTAGGACCGGCTTGGGCAAAAC	2904
BoCollardCompleteCDS	TCTTCTCATGA-----	2869
PSB1_odd	-----	
PSB2_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CTAACGAAACATTACCTTTAATAAATCACCTTTGC	2939
BoCollardCompleteCDS	-----	
PSB1_odd	-----	

DHAG1012 band 1, band 2 - odd12/odd48 primers amplification

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DHAG1012_1
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
DHAG1012_2
-----
AAAAAAAAAAAAATAGAAATGTTTCTGTCTATAAATGGGCATTCCATCATTT 50
-----

DHAG1012_1
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
DHAG1012_2
-----
-----ACTAAGGGAAAAGAAAACYAGC 22
ACTTTCTCAGTACGGAAGCAAAAAAAAAAACTAAGG-AAAAGAAAACCAGC 99
-----AAAAAACCTAAGGAAAAGAAAACCTAGC 28
-----MC-ASG-----TGTTCTCTGGT 16
              * * * * *

DHAG1012_1
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
DHAG1012_2
TTGATCTCTTTG--AATCAAAGAAAA----- 46
TTGATCTCTTTG--AATCAAAGAAAA----- 123
TTGATCTCTTTG--AATCAAAGAAAACTCCAAAGGTAATTTTGGTAAAA 76
TTAGCCTCACTGGTAACTCGAAAAGCTCTATCATG----- 51
**   ***   *   *   *   *

DHAG1012_1
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
DHAG1012_2
-----AC-TCCAAAGGTAGTTKT-CTTATGARTTTTTAATGTTTTCTT 87
-----AC-TCCAAAGGTAGTTGT-CTTATGAGTTTTTAATGTTTTCTT 164
GTTAAATAC-TCCAAAGGTAGTTTTTCTTATGAATTTGAATGTTT-CTT 124
-----GCATCCAAAACGACTT--CTTAAGCTCTCTGACACTCTATC 92
              * * * * * * * * * *

DHAG1012_1
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
DHAG1012_2
TTGTTGTGA-TGATTAAGAGCTA---CTTAAACATTTTCTTTCGGGTT 132
TTGTTGTGA-TGATTAAGAGCTA---CTTAAACATTTTCTTTCGGGTT 209
TTGTTGTGGGTGATTAAGAGTTA---CTTAAATATTTTCTTTCGGGTT 170
ATATGACACCTCA--AAAGCGCCGTAGTCTTCAAGAGCT--TTACGACA 138
      * *      * *      * * * *      * * * * *

DHAG1012_1
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
DHAG1012_2
AAAAAATA-----TA 140
AAAAAATA-----TA 217
AAAAATAAGCTAATTAATTAGTTTACTAAAAAAAAAATAAAAAAAAAATA 220
TCACTCC-----TC 147
      * * * * *

DHAG1012_1
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
DHAG1012_2
AAGCTAATTAACATTTTATAAATATATTTTT--GGATTGACCAAAAGGA 188
AAGCTAATTAACATTTTATAAATATATTTTT--GGATTGACCAAAAGGA 265
AAGCTAATTAACATTTTATGAATATATTTTTTTGGATTGACCAAAAGGC 270
ACTTCAACCCACTTCTCACCTCCTGGTTTTTA--GGGTTTGGTCCGAGAGA 195
*   **   * * * *   * * * * *

DHAG1012_1
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
DHAG1012_2
AAAAAAGAATGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCG 238
AAAAAAGAATGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCG 315
GAAAA-GAATGGGTGCAGACACTCCTCAACTTCCAGTCATCTATCTCTCG 319
TAGAT-GACTGGAAGTTGAGGAGTGTCTGCACCCATTCTTTTTTTCCTTT 244
      * *   * * * *   * *   * * * * *

DHAG1012_1
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
DHAG1012_2
GAC-CAAACCCTAAAAACAGGAGTGAGAAAGTGGGTTGAAGTGAGGAGTG 287
GAC-CAAACCCTAAAAACAGGAGGTGAGAAAGTGGGTTGAAGTGAGGAGTG 364
GAC-CAAACCCTAAAAACAGGAAGTGAGAAAGTGGGTTGAAGTGAGGAGTG 368
GGTGCAAATCCAAAAATATATTTATAAAATGTTAATTAGCTTTATATTTT 294
*   * * * * * * * *   * * * * *

DHAG1012_1
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
DHAG1012_2
ATGTCCGTAA--AGCTCTTGAAGACTACGGCGCTTTTGAGGTGTCATATG 335
ATGTCCGTAA--AGCTCTTGAAGACTACGGCGCTTTTGAGGTGTCATATG 412
ATGTCCGTAA--AGCTCTTGAAGACTACGGCGCTTTTGAGGTGTCATATG 416
A-ACCCGAAAGAAAAATGTTTAAAG--TA----GCTCTTTAATCATCACA-- 335
*   * * * * * * * *   * * * * *

DHAG1012_1
BoBroccoliNullAlleleGenomicDNA
BoCollardCompleteCDS
DHAG1012_2
ATAGAGTGTCAGAAAGAGCTTAAGAAGTCAGTTTTGGA---TGCCATGAT 381
ATAGAGTGTCAGAAAGAGCTTAAGAAGTCAGTTTTGGA---TGCCATGAT 458
ATAGAGTGTCAGAAAGAGCTTAAGAAGTCAGTTTTGGA---TGCCATGAT 462
ACAAA-----AGAAAAATTAAAACTCA---TAAGACAACACTACCTT--T 375
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DHAG1012_1	AGAGCTTTTC---GAGT-ACCAGT--GAGCT-AMACAGAGAA-CKTBC--	421
BoBroccoliNullAlleleGenomicDNA	AGAGCTTTTC---GAGTTACCAGTTGAGGCT-AAACAGAGAAACGTGTCT	504
BoCollardCompleteCDS	AGAGCTTTTC---GAGTTACCAGTTGAGGCT-AAACAGAGAAACGTGTCT	508
DHAG1012_2	GGAGTTTTTCTTTGATT---CAAA--GAGATCAAGCTGG---TTTTCT-	415
	*** ***** * * * * * * * * *	

DHAG1012_1	-----	
BoBroccoliNullAlleleGenomicDNA	CCGAAACCTTACACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCT	554
BoCollardCompleteCDS	CCGAAACCTTACACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCT	558
DHAG1012_2	-----	

No more alignment until the end of *BoBroccoliNullAlleleGenomicDNA*, *BoCollardCompleteCDS*.

Savoy band 1 - odd12/odd48 primers amplification

BoBroccoliNullAlleleGenomicDNA	AAAAAAAAAAAAATAGAAATGTTTCTGTCTATAAATGGGCATTCCATCATTT	50
BoCollardCompleteCDS	AAAAAACCTAAGGAAAAG-----AAACTAG-----CTTGATCT	35
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ACTTTCTCAGTACGGAAGCAAAAAAAAAAACTAAGGAAAAGAAAACCAAGCT	100
BoCollardCompleteCDS	-CTTT-----GAATCAAAGAAAACCTCAAAGG-----	61
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TGATCTCTTTGAATCAAAGAAAACTCCAAAGGTAGTTGT-CTTATGAGT	149
BoCollardCompleteCDS	TAAATTTTGGTAAAATGTT-AAATACTCCAAAGGTAGTTTTTCTTATGAAT	110
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TTTTAATGTTTTCTTTTGTGTGA-TGATTAAAGAGCTACTTAAACATTT	198
BoCollardCompleteCDS	TTTGAAATGTTT-CTTTTGTGTGGGTGATTAAAGAGTTACTTAAATATTT	159
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TCTTTCGGGTAAAAATA-----	215
BoCollardCompleteCDS	TCTTTCGGGTAAAAATAAAGCTAATTAATTAGTTTACTAAAAAAAATTA	209
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	-----TAAAGCTAATTAACATTTTATAAATATATTTTT--GGATTT	254
BoCollardCompleteCDS	AAAAAAAATAAAGCTAATTAACATTTTATGAATATATTTTTTTGGATTT	259
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GCACCAAAGGAAAAAAGAATGGGTGCAGACACTCCTCAACTTCCAGTCA	304
BoCollardCompleteCDS	GCACCAAAGGCGAAAA-GAATGGGTGCAGACACTCCTCAACTTCCAGTCA	308
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TCTATCTCTCGGACCAAAACCCTAAAACAGGAGGTGAGAAGTGGGTTGAA	354
BoCollardCompleteCDS	TCTATCTCTCGGACCAAAACCCTAAAACAGGAAGTGAGAAGTGGGTTGAA	358
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GTGAGGAGTGATGTCCGTAAAGCTCTTGAAGACTACGGCGCTTTTGAGGT	404
BoCollardCompleteCDS	GTGAGGAGTGATGTCCGTAAAGCTCTTGAAGACTACGGCGCTTTTGAGGT	408
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GTCATATGATAGAGTGTCAGAAGAGCTTAAGAAGTCAGTTTGGATGCCA	454
BoCollardCompleteCDS	GTCATATGATAGAGTGTCAGAAGAGCTTAAGAAGTCAGTTTGGATGCCA	458
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TGATAGAGCTTTTCGAGTTACCAAGTTGAGGCTAAACAGAGAAACGTGTCT	504
BoCollardCompleteCDS	TGATAGAGCTTTTCGAGTTACCAAGTTGAGGCTAAACAGAGAAACGTGTCT	508
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CCGAAACCTTACACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCT	554
BoCollardCompleteCDS	CCGAAACCTTACACTGGATATTCAACTCATAATGGTCTCTCTGAGAGTCT	558
SAV_odd	-----TTCTCTG---TTT	10
	***** * *	
BoBroccoliNullAlleleGenomicDNA	AGGGAATCCAGGATTCCAATGTTTTGGAGAAAGTTAACGAATTTACTCAAC	604
BoCollardCompleteCDS	AGGGAATCCAGGATTCCAATGTTTTGGAGAAAGTTAACGAATTTACTCAAC	608
SAV_odd	AGC-----CTCAAC	19
	** *****	
BoBroccoliNullAlleleGenomicDNA	TGCTACGCCCTGATTGTGAGGGTAACAAGACTATGAGGTAAAGTCATGTC	654
BoCollardCompleteCDS	TGCTACGCCCTGATTGTGAGGGTAACAAGACTATGAGGTAAAGTCATGTC	658
SAV_odd	TG-----GGTAAC-----TC	29
	** ***** *	

BoBroccoliNullAlleleGenomicDNA	AAAAAAAAAAAACTCAGTAATGCTTCATAGAGTAAATTAATTGTTTCGTA	704
BoCollardCompleteCDS	AAAAAAAAAAAA--CTCAGTAATGCTTCATAGAGTAAATTAATTGTTTCGGA	706
SAV_odd	GCAAAAG-----CTC--TA-----TCATGG-----	47
	**** * * *	
BoBroccoliNullAlleleGenomicDNA	AATTCCTGTTAATCTTTCATCAAAATATTTTCGTAACCTTTTGGCTAGTT	754
BoCollardCompleteCDS	AATTCCTGT-AATCTT-CATCAAAATATTT-CGTAACCTTTTGGCTAGTT	753
SAV_odd	-----CATCCAAAC-----TGACTTCTTA--AGCT	71
	**** * * *	
BoBroccoliNullAlleleGenomicDNA	GTTTTTCATAAGTTATGTGACAAATTTCTATAAAAAACCTTGTTTTATC	804
BoCollardCompleteCDS	GTTTT-CATAAGGTATGTGACAAATTTCTATAAAAA-CCTTGTTTTATC	801
SAV_odd	CTTCT-----GACA--CTCTAT-----	86
	* * *	
BoBroccoliNullAlleleGenomicDNA	TTTATTTTTTTGGAAAAATGTTAGTTCACCTCATATAGTAATGAACGAAA	854
BoCollardCompleteCDS	TTTATTTTTTTGGAAAAATGTTAGTTCACCTCATATAGTAATGAACGAAA	851
SAV_odd	-----CATATGACA-----	95
	**** *	
BoBroccoliNullAlleleGenomicDNA	TTTTGTTTTCAATCTCACGTTTCACGCATTTTTTTTTGTTTCTATTAAAA	904
BoCollardCompleteCDS	TTTTGTTTTCAATCTCACGTTTCACGCATTTTTTTTTGTTTCTATTAAAA	901
SAV_odd	-----CCTCAA-----	101

BoBroccoliNullAlleleGenomicDNA	TAGCTATATAAAATTTT-CTTTGTGTTGAAAACAGCGAAACGATCCAGAAG	953
BoCollardCompleteCDS	TAGCTATATAAAATTTTCTTTGTGTTGAAAACAGCGAAACGATCCAGAAG	951
SAV_odd	-----AAGCG--CCGTAG	112
	* * * * *	
BoBroccoliNullAlleleGenomicDNA	TTTTCAGAGAAGTTAGCAGAATTGGATGTAATGGTGAGAAGAATGGTCAT	1003
BoCollardCompleteCDS	TTTTCAGAGAAGTTAGCAGAATTGGATGTAATGGTGAGAAGAATGGTCAT	1001
SAV_odd	TCTTCA-----	118
	* * * * *	
BoBroccoliNullAlleleGenomicDNA	AGAGAGCTTTGGGATAGAAAACACTTTGATGAACACCTCAAGTCAACGA	1053
BoCollardCompleteCDS	AGAGAGCTTTGGGATAGAAAACACTTTGATGAACACCTCAAGTCAACGA	1051
SAV_odd	--AGAGCTTTACGG--ACATCACT-----CCTCACTTCAAC--	150
	***** * * * *	
BoBroccoliNullAlleleGenomicDNA	ATTACCGTTTGCGACTGATGAAGTATGTAGCACCACCTGATGTTGATGCT	1103
BoCollardCompleteCDS	ATTACCGTTTGCGACTGATGAAGTATGTAGCACCACCTGATGTTGATGCT	1101
SAV_odd	---CCACTT---CT-----CACCTCCTGGTTTT---	172
	* * * *	
BoBroccoliNullAlleleGenomicDNA	AATGTTGCGGTCACTACTAAAGATTCTGTTGATGGTGCTAATACGAATAC	1153
BoCollardCompleteCDS	AATGTTGCGGTCACTACTAAAGATTCTGTTGATGGTGCTAATACGAATAC	1151
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	AACTGCTAACGCTGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTC	1203
BoCollardCompleteCDS	AACTGCTAACGCTGATGCTGGTGATATTGCTAATGGTATTGCTAAAGTTC	1201
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ATATTGATGACGATGCTAATGCCAAGGGTGACGTTTGCACTGGTGTTGGT	1253
BoCollardCompleteCDS	ATATTGATGACGATGCTAATGCCAAGGGTGACGTTTGCACTGGTGTTGGT	1251
SAV_odd	-----AGGGT-----TTGGT	182

BoBroccoliNullAlleleGenomicDNA	ACCAATCATAATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAA	1303
BoCollardCompleteCDS	ACCAATCATAATGGTGATGACGTTAATACTGGTGATTGTGCTAATGTTAA	1301
SAV_odd	CC-----	184
	*	
BoBroccoliNullAlleleGenomicDNA	GTCTAATGTGCGACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTGGTG	1353
BoCollardCompleteCDS	GTCTAATGTGCGACGTTGGTACTAATGTTAGTGCTAAATCTAGTGTGGTG	1351
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CTGATGTTAACATTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACT	1403
BoCollardCompleteCDS	CTGATGTTAACATTGGCACTATTGCTGATGTTAAGGCTAATACTGGTACT	1401

SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CGTACTAGTGCTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGG	1453
BoCollardCompleteCDS	CGTACTAGTGCTAATGTTGGCGTTAGTGATAGTGTTAAAGCTAATGGTGG	1451
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CGCAGATGATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAA-	1502
BoCollardCompleteCDS	CGCAGATGATGAGGAGAAGAAATTAGGTCTACCTTCTCATACTGATAAAA	1501
SAV_odd	-----GAGA-----GATAGA-	194
	***	*** *
BoBroccoliNullAlleleGenomicDNA	-CCTTTTGACGGTGCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTA	1551
BoCollardCompleteCDS	ACCTTTTGACGGTGCTTTATCAATATGAGATTGAAGGTTTGGAGGTGTTA	1551
SAV_odd	-----TGAC-----TGAAGT-----	205
	***	*** *
BoBroccoliNullAlleleGenomicDNA	ACCAAAGATGAAAAGTGGATCAGGTTAAAACCATCTCATAACTCTTTCGT	1601
BoCollardCompleteCDS	ACCAAAGATGAAAAGTGGATCAGGTTAAAGCCATCTCATAAGCTCTTTCGT	1601
SAV_odd	-----TGAGGAGTG-----	214
	** *	***
BoBroccoliNullAlleleGenomicDNA	TGTTATGGCTGGAGATTCTCTATATGTAAGTTCTAACTTATTTTATTTTT	1651
BoCollardCompleteCDS	TGTTATGGCTGGAGATTCTCTATATGTAAGTTCTAACTTATTTTATTTTT	1651
SAV_odd	-----TCT-----	217

BoBroccoliNullAlleleGenomicDNA	AAATGGGATGCACCATAATATCTTAATTGCGATCATCATAATAATCATAA	1701
BoCollardCompleteCDS	AAATGGGATGCACCATAATATCTTAATTGCGATCATCATAATAATCATAA	1701
SAV_odd	-----GCACC-----CATT-----	226
	*****	** *
BoBroccoliNullAlleleGenomicDNA	CTTTTTTATGATATATATTATAACTTTATGATATACATATTCATAACTTT	1751
BoCollardCompleteCDS	CTTTTTTATGATATATATTATAACTTTATGATATACATATTCATAACTTT	1751
SAV_odd	CTTTTTTT-----TC-----CTTT	239
	*****	** *
BoBroccoliNullAlleleGenomicDNA	ATGATATAAATATTACATAATTCACCTTTTTATTATTTCTTATCACTTTC	1801
BoCollardCompleteCDS	ATGATATAAATATTACATAATTCACCTTTTTATTATTTCTTATCACTTTC	1801
SAV_odd	--GGTGCAAAT-----CC	250
	* * *	*
BoBroccoliNullAlleleGenomicDNA	ACAAATGCATGTCGACGTTACTAAAGTGTTTATACATTAAACATTATGTTT	1851
BoCollardCompleteCDS	ACAAATGCATGTCGACGTTACTAAAGTGTTTATACATTAAACATTATGTTT	1851
SAV_odd	AAAAATATAT-----TTA-TAAATGTTAA---TTAGCTTTATATTT	288
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BoBroccoliNullAlleleGenomicDNA	TCTTCTCATCATGAATCTTGTGTTGGTTTTTTTATTATTATTTTTTTGCA	1901
BoCollardCompleteCDS	TCTTCTCATCATGAATCTTGTGTTGGTTTTTTTATTATTATTTTTTTGCA	1901
SAV_odd	T-----AACCC-----	294
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BoBroccoliNullAlleleGenomicDNA	GGCACTTATGAATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAA	1951
BoCollardCompleteCDS	GGCACTTATGAATGGTAGACTATCTCGTCCGTTTCATAGAGTAAGAGTAA	1951
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CGGAAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAAC	2001
BoCollardCompleteCDS	CGGAAAGAAAGAAGACAAGGTATTCAATAGCATTGTTCTCGACTCCAAAC	2001
SAV_odd	--GAAAGAAA-----	302

BoBroccoliNullAlleleGenomicDNA	GGAGATTACATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCC	2051
BoCollardCompleteCDS	GGAGATTACATCATCGAACCACCAAAAGAGCTTGTGGACGAGAAGCACCC	2051
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ACGTCTCTTCAAATCATTCACCTTACGTTGACTTGATGAGTTTCTATCACA	2101
BoCollardCompleteCDS	ACGTCTCTTCAAACCATTCACCTTACGTTGACTTGATGAGTTTCTATCACA	2101
SAV_odd	-----	

BoBroccoliNullAlleleGenomicDNA	CTGAGGCTGGTCGTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTC	2151
BoCollardCompleteCDS	CTGAGGCTGGTCGTAGACCTCGTTCTACTCTTCACGCTTATTGTGCCGTC	2151
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TCTGGAGCATAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTA	2201
BoCollardCompleteCDS	TCTGGAGCATAAATGTGTGCGCTTACTTACGAGAGTTTCAACAATGTTTA	2201
SAV_odd	-----ATGTTTA	309

BoBroccoliNullAlleleGenomicDNA	AGTAGTTTCATGGTTCAACTAATATCAAGAACTGCATGTAGTACTAAA-T	2250
BoCollardCompleteCDS	AGTAGTTTCATGGTTCAACTAATATCAAGAACTGCATGTAGTACTAAAAAT	2251
SAV_odd	AGTAG-----	314

BoBroccoliNullAlleleGenomicDNA	AAGAGTTTTTGGATTAGTTGAGTATATGTGTTTTATTTCCGGGAGAAGCAA	2300
BoCollardCompleteCDS	AAGAGTTTTTGGATTAGTTGAGTATATGTGTTTTATTTCCGGGAGAAGCAA	2301
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	TCAAGTCTCTCTTTTGTATGAAAAATCAATAAAA-ATATGTGTATGAGCA	2349
BoCollardCompleteCDS	TCAAGTCTCTCTTTTGTATGAAAAATCAATAATGTGTATGTGTATGAGCA	2351
SAV_odd	-----CTCTTT-----AATCA-----	325
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BoBroccoliNullAlleleGenomicDNA	TGTTCAATAATGTAATGAATTTGGTTGGATCTGTTGGTTCACAAGATGTC	2399
BoCollardCompleteCDS	TGTTCAATAATGTAATGAATTTGGTTGGATCTGTTGGTTCACAAGATGTC	2401
SAV_odd	-----TCACAA-----	331

BoBroccoliNullAlleleGenomicDNA	AAGATCGTAAATAGGTTAATTAATAGGTTAATTTCTTCTCTTTTTTTAA	2449
BoCollardCompleteCDS	AAGATCGTAAATAGGTTAATTAATAGGTTAATTTCTTCTCTTTTTTTAA	2451
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ACTAAATTAAATTCATTTTTTTTTTATAAAAAAATACTAGTTTAATTTTCAG	2499
BoCollardCompleteCDS	ACTAAATTAAATTCATTTTTTTTTTATAAAAAAATACTAGTTTAATTTTCAG	2501
SAV_odd	-----CAAAAGAA-----	339
	*****	**
BoBroccoliNullAlleleGenomicDNA	GAGATGGGAAACGAGTGTGGAACATATAAAAACTGGTGTGCGATTTC	2549
BoCollardCompleteCDS	GAGATGGGAAACGAGTGTGGAACATATAAAAAACGGTGTGCGATTTC	2551
SAV_odd	-----AACAT-TAAAAAC-----TCA	354
	*****	*****
BoBroccoliNullAlleleGenomicDNA	AACATTAAACGCTAAATAAGTGAATGATTTACTTTTCATGTTATCGTAGCG	2599
BoCollardCompleteCDS	AACATTAAACGCTAAATAAGTGAATGATTTACTTTTCATGTTATCGTAGCG	2601
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	ACAGTGGTTTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTT	2649
BoCollardCompleteCDS	ATAGTGGTCTTGAGTCGACATGTAGATCCCCCTTACCTTAGGAATTTGTT	2651
SAV_odd	-----TAAGACAAC-----TACCTTTGGAGTT--TT	378
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BoBroccoliNullAlleleGenomicDNA	TGTTTGCAAAATGCCAAAATCGTAAATAGTAGTAAATAGTAATGTTATT	2699
BoCollardCompleteCDS	TGTTTGCAAAATGCCAAAATCGTAAATAGTA--AATTAATAATGTTATT	2698
SAV_odd	TCTTTG-----ATT	387
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BoBroccoliNullAlleleGenomicDNA	TAAAGTTTGACTGGTTTAATTGCAGTAGGTGTATGTGCTGTGGTCCAAAA	2749
BoCollardCompleteCDS	TAAAGTTTGACCGTTTACTTGCAATAGGTGTATGTGCTGTGGTCCAAAA	2748
SAV_odd	CAAAG-----AG	394
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BoBroccoliNullAlleleGenomicDNA	ATTAGTGAAACGAATAATT-CAATTGTAATAGTAATGTTATTTAAAAAT	2798
BoCollardCompleteCDS	ATTAGTGAACTAATAATTACAATTGTAATAGTAATGTTATTTAAAAAT	2798
SAV_odd	ATCA-----AGCTGGT-----	405
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BoBroccoliNullAlleleGenomicDNA	ATAGACATGCATTGTCTCATGAACAAAAGTGGTTGAAATAGCGATTTGCAA	2848

BoCollardCompleteCDS	ATAGACATGCATTGTCTCATGAACAAAGTGTTGAAATAGCGATTTGCAA	2848
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	GTGCCAACTCTCTTCTTATGAACAAAGTTACAAATTAGGACCGGCTTGGG	2898
BoCollardCompleteCDS	GTGCCAACTCTTCTCATGA-----	2869
SAV_odd	-----	
BoBroccoliNullAlleleGenomicDNA	CAAAACCTAACGAAACATTACCTTTAATAAATCACCTTGC	2939
BoCollardCompleteCDS	-----	
SAV_odd	-----	