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(54) Title: *BRASSICA PLANT COMPRISING A MUTANT INDEHISCENT ALLELE*

(57) Abstract: This invention relates to crop plants of which the fruit dehiscence properties are modulated. More specifically the invention relates to improved methods and means for reducing seed shattering, or delaying seed shattering until after harvest, while maintaining at the same time an agronomically relevant treshability of the pods, and for increasing yield.



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Brassica* plant comprising a mutant *INDEHISCENT* allele*FIELD OF THE INVENTION**

[1] This invention relates to the field of agriculture, more specifically to the use of molecular biology techniques to alter dehiscent seed plants, particularly of the *Brassicaceae* family, in particular *Brassica* species, and/or accelerate breeding of such dehiscent seed plants. More specifically the invention relates to improved methods and means for reducing seed shattering, or delaying seed shattering until after harvest, in plants such as *Brassicaceae* plants, particularly *Brassicaceae* plants grown for seed production, while maintaining at the same time an agronomically relevant treshability of the pods. Methods are also provided to identify molecular markers associated with reduced or delayed seed shattering in a population of dehiscent seed plants. Also provided are methods and means to increase the yield, particularly grain and seed yield. The yield increase phenotype may be separate from the reduced or delayed seed shatter phenotype.

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BACKGROUND OF THE INVENTION

[2] Siliques or pods from *Brassica* plants release their seeds through a process called fruit dehiscence. A silique consists of two carpels joined margin to margin. The suture between the margins forms a thick rib, called replum. As pod maturity approaches, the two valves separate progressively from the replum, along designated lines of weakness in the pod, eventually resulting in the shattering of the seeds that were attached to the replum. The dehiscence zone defines the exact location of the valve dissociation.

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[3] Shedding of seed (also referred to as “seed shatter” or “pod shatter”) by mature pods before or during crop harvest is a universal phenomenon with crops that develop dry dehiscent fruits. Premature seed shatter results in a reduced seed recovery, which represents a problem in crops that are grown primarily for the seeds, such as oil-producing *Brassica* plants, particularly oilseed rape. Another problem related to premature seed shattering is an increase in volunteer growth in the subsequent crop year. In oilseed rape, pod shatter-related yield losses are on average 20% (Child *et al.*, 1998, *J Exp Bot* 49: 829-838), but can reach up to 50%, depending on the weather conditions (MacLeod, 1981, *Harvesting in Oilseed Rape*, pp. 107-120, Cambridge Agricultural Publishing, Cambridge).

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[4] Current commercial oilseed rape varieties are extremely susceptible to shattering. There is little variation for resistance to shattering within existing breeding programs of *B. napus* but

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resistant lines have been found within the diploid parents of *B. napus* (*B. oleracea* and *B. rapa*) as well as within other members of the *Brassica* genus, notably *B. juncea*, *B. carinata* and *B. nigra*. Kadkol *et al.* (1986, Aust. J. Botany 34 (5): 595-601) report increased resistance towards shattering in certain accessions of *B. campestris* that was associated with the absence of a separation layer in the region of attachment of the siliqua valves to the replum. Prakash and Chopra (1988, Plant breeding 101: 167-168) describe the introgression of resistance to shattering in *Brassica napus* from *Brassica juncea* through non-homologous recombination. Spence *et al.* (1996, J of Microscopy 181: 195-203) describe that some lines of *Brassica juncea* show a reduced tendency to shatter as compared to *Brassica napus* lines. Morgan *et al.*, 1998 (Fields Crop Research 58, 153-165) describe genetic variation for pod shatter resistance among lines of oilseed rape developed from synthetic *B. napus* and conclude that lines which required much energy to open their pods appeared to have increased vascularisation in the dehiscence zone and to have reduced cell wall degradation within the dehiscence zone. They further found a significant negative correlation between the length of the pod beak and the force needed to cause pod shattering. Child and Huttly (1999, Proc 10th Int. Rapeseed Congress) describe variation in pod maturation in an irradiation-induced mutant *B. napus* and a population of its parent cultivar, Jet Neuf, wherein the most resistant wild-type and mutant plants showed much lignification of groups of cells throughout the dehiscence zone and wherein vascular traces situated close to the inner edge of the dehiscence zone in the mutant were described to help to secure the valves. Child *et al.* (2003, J Exp Botany 54 (389): 1919-1930) further describe the association between increased pod shatter resistance and changes in the vascular structure in pods of a resynthesized *Brassica napus* line. However, the traditional methods for breeding have been unsuccessful in introducing shatter resistance into rape cultivars, without interference with other desirable traits such as early flowering, maturity and blackleg resistance (Prakash and Chopra, 1990, Genetical Research 56: 1-2).

[5] Several genes, which promote or inhibit pod dehiscence, have been identified in *Arabidopsis thaliana* through mutant analysis: Combined mutants in both *SHATTERPROOF1* (*SHP1*; initially referred to as *AGL1*) and *SHATTERPROOF2* (*SHP2*; initially referred to as *AGL5*) result in indehiscent siliques (i.e. siliques which remain closed upon maturity in *Arabidopsis thaliana*) (Liljegren *et al.*, 2000, Nature 404, 766-770). Similarly, mutants in the *INDEHISCENT* gene (referred to as *INDI*) in *Arabidopsis thaliana* (Liljegren *et al.*, 2004, Cell 116: 843-853; PCT publication WO 01/79517), as well as in *ALCATRAZ* (referred to as *ALC*; Rajani *et al.* 2001, Current Biology 11, 1914-1922) interfered with pod dehiscence leading to pod shatter resistance. Constitutive expression of *FRUITFUL* (*FUL*), a repressor of *SHP* and

IND, in *Arabidopsis thaliana* also resulted in indehiscent siliques (Ferrandiz *et al.*, 2000, Science, 289, 436-438). These transcription factors are believed to form a non-linear transcriptional network that controls valve margin identity and pod shatter. Liljegren *et al.* (2004, Cell 116: 843-853) further describe that *IND*, an atypical basic helix-loop-helix (bHLH) gene, directs the differentiation of the valve margin into the separation and lignified layers in *Arabidopsis thaliana*. The layer of lignified cells adjacent to the separation layer along with the endocarp *b* layer (a single lignified cell layer in each valve) produce a spring-like tension within the drying fruit that contributes to its opening. Lignification of the valve endodocarp *b* layer requires the activities of *IND*, *SHP*, *ALC*, and *FUL*, a MADS-domain transcription factor that is expressed throughout the valves (Liljegren *et al.*, 2004, *supra*; Mandel and Yanofsky, 1995, Plant Cell 7, 1763-1771). *FUL* and *REPLUMLESS* (*RPL*), a homeodomain transcription factor that is expressed in the replum (Roeder *et al.*, 2003, Curr Biol 13, 1630-1635), have been found to set the boundaries of the genes that confer valve margin identity (Gu *et al.*, 1998, Development 125, 1509-1517; Ferrandiz *et al.*, 2000, Science, 289, 436-438; Roeder *et al.*, 2003, *supra*). Finally, *FILAMENTOUS FLOWER* (*FIL*) and *YABBY3* (*YAB3*), two *YABBY*-family transcription factors (Sawa *et al.*, 1999, Genes Dev 13, 1079-1088; Siegfried *et al.*, 1999, Development 126, 4117-4128), and *JAGGED* (*JAG*), a C2H2 zinc-finger transcription factor (Dinneny *et al.*, 2004, Development 131, 1101-1110; Ohno *et al.*, 2004, Development 131, 1111-1122), were identified to redundantly contribute to proper valve and valve margin development by promoting the expression of *FUL* and *SHP* in a region-specific manner (Dinneny *et al.*, 2005, Development 132, 4687-4696). Genes for a number of hydrolytic enzymes, such as endopolygalacturonases, which play a role, during pod dehiscence, in the programmed breakdown of the dehiscence zone in pods from *Brassica* plants have also been identified (see e.g. WO 97/13865; Petersen *et al.*, Plant. Mol. Biol., 1996, 31:517-527).

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[6] Liljegren *et al.* (2004, Cell 116: 843-853) describe five mutant alleles of *Arabidopsis* *IND*. The lignified cells in the dehiscence zone are either absent or present in plants comprising these mutant alleles depending on the severity of the mutations (severe *ind* mutants do not contain lignified cells in the region corresponding to the inner part of the valve margin in wild-type plants), but in all cases the silique is indehiscent. Wu *et al.* (2006), Planta 224, 971-979) describe a sixth mutant allele of *Arabidopsis* *IND*. Plants comprising this mutant allele show no lignified cells at the junctions of the valve margin and the replum, contain fewer cells in a region of seven layers of cells, which appeared to encompass the commonly known dehiscence zone and replum border in wild-type plants, and exhibit incomplete cytokinesis in this layer.

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[7] US 2005/0120417 and US 2007/0006336 describe the identification and isolation of two *IND1* orthologs from *Brassica napus*.

5 [8] WO99/00503, WO01/79517 and WO0159122 describe down-regulation of the expression of the *Arabidopsis ALC*, *IND*, *AGL1* and *AGL5* genes and orthologs thereof using gene-silencing techniques (such as antisense suppression or cosuppression) and mutagenesis.

[9] Vancanneyt *et al.*, 2002 (XIII International Conference on *Arabidopsis* Research, Sevilla, Spain June 28-July 2; 2002) reported that the expression of *FUL* from *A. thaliana* under control
10 of a CaMV 35S promoter in oilseed rape resulted in a number of pod shatter resistant transformants. Pods of such pod shatter resistant lines had no dehiscence zone, and opening of the pods could only be achieved by random fracture of the valves by applying considerable pressure.

15 [10] Vancanneyt *et al.*, 2002 (XIII International Conference on *Arabidopsis* Research, Sevilla, Spain June 28-July 2; 2002) also reported that silencing of the *IND* gene in *Arabidopsis thaliana* using so-called dsRNA silencing techniques resulted in almost complete pod shatter resistance. Ninety-eight percent of the transgenic *Arabidopsis* lines developed siliques, which did not open
20 along the valve suture, and could only be opened by applying considerable pressure to the valves.

[11] It is important to realize that while seed shattering constitutes an important problem in oilseed rape culture, which may be solved by developing pod shatter resistant lines, ultimately, separation of the seeds from the pods is still required. In normal agricultural practice this is
25 achieved by treshing of the pods by a combine harvester. Treshing of the pods by a combine harvester must be complete and must cause minimum damage to the seeds thus released. However, as pod strength increases, the more severe action required to tresh them causes an unacceptable level of damage to the seed. The pods of pod shatter resistant *Brassicaceae* plants should thus not be so strong that they cannot be treshed in a combine harvester (Bruce *et al.*
30 2001, J. Agric. Engng Res. 80, 343-350).

[12] WO 2004/113542 describes that moderate dsRNA gene silencing of genes involved in the development of the dehiscence zone and valve margins of pods in *Brassicaceae* plants allows the isolation of transgenic lines with increased pod shatter resistance and reduced seed

shattering, the pods of which however may still be opened along the dehiscence zone by applying limited physical forces.

[13] WO09/068313 (claiming priority of European patent application EP 07023052) discloses *Brassica* plants comprising at least two *IND* genes, in particular *Brassica napus* plants, characterized in that they comprise three full knock-out mutant *IND* alleles in their genome and wherein the pod shatter resistance of the plants is significantly increased compared to the pod shatter resistance of a plant not comprising mutant *IND* alleles, but wherein the plant preferably maintains an agronomically relevant treshability of the pods.

[14] The inventions described hereinafter in the different embodiments, examples and claims provide further improved methods and means for modulating dehiscence properties in dehiscent seed plants. More specifically, the present invention describes further improved methods and means for reducing seed shattering, or delaying seed shattering until after harvest, in plants such as *Brassicaceae* plants, particularly *Brassicaceae* plants grown for seed production, while maintaining at the same time an agronomically relevant treshability of the pods. In particular, the present application discloses *Brassica* plants comprising at least two *IND* genes, in particular *Brassica napus* plants, characterized in that they comprise two partial knock-out mutant *IND* alleles in their genome or two partial and two full knock-out mutant *IND* alleles and wherein the pod shatter resistance of the plants is significantly increased compared to the pod shatter resistance of a plant not comprising mutant *IND* alleles, but wherein the plant preferably maintains an agronomically relevant treshability of the pods. Also provided are methods and means to increase the yield, particularly grain and seed yield. The yield increase phenotype may be separate from the reduced or delayed seed shatter phenotype.

SUMMARY OF THE INVENTION

[15] The inventors found that *Brassica napus* plants with a pod shatter phenotype similar to the *Brassica* plants described in WO09/068313 (claiming priority of European patent application EP 07023052), i.e. which combine an increased pod shatter resistance with an agronomically relevant treshability of the pods, can also be obtained by combining two partial knock-out mutant *IND* alleles with or without two full knock-out mutant *IND* alleles instead of combining three full knockout mutant *IND* alleles.

[16] Thus, in a first aspect, the present invention provides a *Brassica* plant comprising at least two *IND* genes, or a cell, part, seed or progeny thereof, characterized in that it comprises at least

two partial knockout mutant *IND* alleles in its genome. In one embodiment, the *IND* genes are *IND-A1* or *IND-C1* genes. In another embodiment, the *IND* genes comprise a nucleic acid molecule selected from the group consisting of: a nucleic acid molecule which comprises at least 90% sequence identity to SEQ ID NO: 1, SEQ ID NO: 3 from the nucleotide at position 46 to the nucleotide at position 633, SEQ ID NO: 3, SEQ ID NO: 5, or SEQ ID NO: 7; and a nucleic acid molecule encoding an amino acid sequence comprising at least 90% sequence identity to SEQ ID NO: 2, SEQ ID NO: 4 from the amino acid at position 16 to the amino acid at position 21 or SEQ ID NO: 4. In a further embodiment, the partial knockout mutant *IND* alleles are mutant *IND* alleles of the *IND-C1* gene. In still a further embodiment, the partial knockout mutant *IND* alleles are selected from the group consisting of *ind-a1-EMS06*, *ind-a1-EMS09*, *ind-a1-EMS13*, *ind-c1-EMS04*, *ind-c1-EMS08* and *ind-c1-EMS09*. In yet a further embodiment, the plant further comprises at least one full knockout mutant *IND* allele in its genome. In still a further embodiment, the full knockout mutant *IND* allele is a mutant *IND* allele of the *IND-C1* gene. In another embodiment, the full knockout mutant *IND* allele is selected from the group consisting of *ind-a1-EMS01*, *ind-a1-EMS05*, *ind-c1-EMS01* and *ind-c1-EMS03*. In yet another embodiment, the plant is homozygous for the partial and/or for the full knockout mutant *IND* allele. In still another embodiment, the plant produces a significantly reduced amount of functional *IND* protein compared to the amount of functional *IND* protein produced by a corresponding plant not comprising mutant *IND* alleles. In a further embodiment, the seed shattering of the plant is significantly reduced or delayed compared to the seed shattering of a corresponding plant not comprising mutant *IND* alleles. In an even further embodiment, the plant maintains an agronomically relevant treshability of the pods. In yet another embodiment, the plant is a plant from a *Brassica* crop species, preferably *Brassica napus*, *Brassica juncea*, *Brassica carinata*, *Brassica rapa* or *Brassica oleracea*. In still another embodiment, the plant is a plant from a *Brassica* oilseed species, preferably *Brassica napus*, *Brassica juncea* or *Brassica rapa*.

[17] In another aspect, the invention provides a plant, or a cell, part, seed or progeny thereof, comprising at least one partial knockout mutant allele of an *IND* gene in its genome, wherein the *IND* gene comprises a nucleic acid molecule selected from the group consisting of: a nucleic acid molecule which comprises at least 90% sequence identity to SEQ ID NO: 1, SEQ ID NO: 3 from the nucleotide at position 46 to the nucleotide at position 633, SEQ ID NO: 3, SEQ ID NO: 5, or SEQ ID NO: 7; and a nucleic acid molecule encoding an amino acid sequence comprising at least 90% sequence identity to SEQ ID NO: 2, SEQ ID NO: 4 from the amino acid at position 16 to the amino acid at position 21 or SEQ ID NO: 4. In one embodiment, the partial knockout

mutant *IND* allele is selected from the group consisting of *ind-a1*-EMS06, *ind-a1*-EMS09, *ind-a1*-EMS13, *ind-cl*-EMS04, *ind-cl*-EMS08 and *ind-cl*-EMS09. In another embodiment, the mutant *IND* allele is derived from a plant of a *Brassica* species. In yet another embodiment, the plant is a plant from a *Brassica* species.

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[18] In a further aspect, a seed pod obtainable from the plants of the invention is provided.

[19] In still a further aspect, a partial knockout mutant allele of an *IND* gene is provided, wherein the *IND* gene comprises a nucleic acid molecule selected from the group consisting of: a
10 nucleic acid molecule which comprises at least 90% sequence identity to SEQ ID NO: 1, SEQ ID
NO: 3 from the nucleotide at position 46 to the nucleotide at position 633, SEQ ID NO: 3, SEQ
ID NO: 5, or SEQ ID NO: 7; and a nucleic acid molecule encoding an amino acid sequence
comprising at least 90% sequence identity to SEQ ID NO: 2, SEQ ID NO: 4 from the amino acid
15 at position 16 to the amino acid at position 21 or SEQ ID NO: 4. In one embodiment, the mutant
allele is selected from the group consisting of *ind-a1*-EMS06, *ind-a1*-EMS09, *ind-a1*-EMS13,
ind-cl-EMS04, *ind-cl*-EMS08 and *ind-cl*-EMS09. In another embodiment, the mutant allele is
derived from a plant of a *Brassica* species, preferably from a *Brassica* crop species or a *Brassica*
oilseed species. In yet a further aspect, a mutant *IND* protein is provided encoded by the mutant
20 *IND* alleles of the invention.

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[20] In even a further aspect, a method for identifying a mutant *IND* allele according to the
invention in a biological sample is provided comprising determining the presence of a mutant
IND specific region in a nucleic acid present in the biological sample. In one embodiment, the
method further comprises subjecting the biological sample to a polymerase chain reaction assay
25 using a set of at least two primers, said set being selected from the group consisting of: a set of
primers, wherein one of said primers specifically recognizes the 5' flanking region of the mutant
IND allele and the other of said primers specifically recognizes the 3' flanking region of the
mutant *IND* allele, respectively; a set of primers, wherein one of said primers specifically
recognizes the 5' or 3' flanking region of the mutant *IND* allele and the other of said primers
30 specifically recognizes the mutation region of the mutant *IND* allele; and a set of primers,
wherein one of said primers specifically recognizes the 5' or 3' flanking region of the mutant
IND allele and the other of said primers specifically recognizes the joining region between the 3'
or 5' flanking region and the mutation region of the mutant *IND* allele, respectively. In another
embodiment, the primer which specifically recognizes the 5' or 3' flanking region of the mutant
35 *IND* allele consist of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from

the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or the primer which specifically recognizes the mutation region of the mutant *IND* allele consists of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or the primer which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele consists of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof, wherein said 17 to 200 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences. In still a further embodiment, the primer which specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele comprises at its extreme 3' end a nucleotide sequence of at least 17 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or the primer which specifically recognizes the mutation region of the mutant *IND* allele comprises at its extreme 3' end a nucleotide sequence of at least 17 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or the primer which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele comprises at its extreme 3' end a nucleotide sequence of at least 17 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof, wherein said 3'-located 17 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences. In yet a further embodiment, the method further comprises subjecting the biological sample to an hybridization assay using a set of specific probes comprising at least one specific probe, said set being selected from the group consisting of : a set of specific probes, wherein one of said probes specifically recognizes the 5' flanking region of the mutant *IND* allele, and the other of said probes specifically recognizes the 3' flanking region of the mutant *IND* allele; a set of specific probes, wherein one of said probes specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele, and the other of said probes specifically recognizes the mutation region of the mutant *IND* allele; a set of specific probes, wherein one of said probes specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele and the other of said probes specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the mutant *IND* allele, respectively; and a specific probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele. In still a further embodiment, the probe which specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele consists of a

nucleotide sequence of 13 to 1000 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or a sequence having at least 80% sequence identity therewith, or the probe which specifically recognizes the mutation region of the mutant *IND* allele consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or a sequence having at least 80% sequence identity therewith, or the probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof, respectively, wherein said 13 to 1000 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences, or a sequence having at least 80% sequence identity therewith. In a particular embodiment, the probe which specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or the probe which specifically recognizes the mutation region of the mutant *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or the probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof, respectively, wherein said at least 13 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences. In another particular embodiment, the 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 929 or 931 to 1622 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 930 of SEQ ID NO: 5 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 930 or 930 to 1622 or of the complement thereof, respectively; or the 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 995 or 997 to 1622 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 996 of SEQ ID NO: 5 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 996 or 996 to 1622 or of the complement thereof, respectively; or the 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to

1035 or 1037 to 1622 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 1036 of SEQ ID NO: 5 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1036 or 1036 to 1622 or of the complement thereof, respectively; or the 5' or 3' flanking region
5 comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 902 or 904 to 1593 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 903 of SEQ ID NO: 7 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 903 or 903 to 1593 or of the complement thereof, respectively; or the 5' or 3' flanking region comprises the nucleotide
10 sequence of SEQ ID NO: 7 from nucleotide 1 to 910 or 912 to 1593 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 911 of SEQ ID NO: 7 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 911 or 911 to 1593 or of the complement thereof, respectively; or the 5' or 3' flanking region comprises the nucleotide sequence of SEQ
15 ID NO: 7 from nucleotide 1 to 919 or 921 to 1593 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 920 of SEQ ID NO: 7 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 920 or 920 to 1593 or of the complement thereof, respectively. In still another particular embodiment, the set of probes is selected from the group consisting of: a set of
20 probes comprising one probe comprising the sequence of SEQ ID NO: 11 and/or one probe comprising the sequence of SEQ ID NO: 12; a set of probes comprising one probe comprising the sequence of SEQ ID NO: 14 and/or one probe comprising the sequence of SEQ ID NO: 15; a set of probes comprising one probe comprising the sequence of SEQ ID NO: 17 and/or one probe comprising the sequence of SEQ ID NO: 18; a set of probes comprising one probe
25 comprising the sequence of SEQ ID NO: 20 and/or one probe comprising the sequence of SEQ ID NO: 21; a set of probes comprising one probe comprising the sequence of SEQ ID NO: 23 and/or one probe comprising the sequence of SEQ ID NO: 24; and a set of probes comprising one probe comprising the sequence of SEQ ID NO: 26 and/or one probe comprising the sequence of SEQ ID NO: 27.

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[21] In yet another aspect, a method for determining the zygosity status of a mutant *IND* allele according to the invention in a plant, or a cell, part, seed or progeny thereof, is provided comprising determining the presence of a mutant and/or a corresponding wild type *IND* specific region in the genomic DNA of said plant, or a cell, part, seed or progeny thereof. In one
35 embodiment, the method further comprises subjecting the genomic DNA of said plant, or a cell,

part, seed or progeny thereof, to a polymerase chain reaction assay using a set of at least two or at least three primers, wherein at least two of said primers specifically recognize the wild type *IND* allele, said at least two primers being selected from the group consisting of: a first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second primer which specifically recognizes the 3' or 5' flanking region of the mutant and the wild type *IND* allele, respectively; a first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second primer which specifically recognizes the mutation region of the wild type *IND* allele; and a first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second primer which specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the wild type *IND* allele, respectively; and wherein at least two of said primers specifically recognize the mutant *IND* allele, said at least two primers being selected from the group consisting of: the first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and the second primer which specifically recognizes the 3' or 5' flanking region of the mutant and the wild type *IND* allele, respectively; the first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a third primer which specifically recognizes the mutation region of the mutant *IND* allele; and the first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a third primer which specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the mutant *IND* allele, respectively. In a further embodiment, the primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele consist of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant and the wild type *IND* allele or from the complement thereof, respectively; or the primers which specifically recognizes the mutation region of the mutant or the wild type *IND* allele consists of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from the mutation sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively; or the primers which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele, consists of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele or from the complement thereof, respectively, wherein said 17 to 200 consecutive nucleotides are not derived exclusively from either the mutation region or from the flanking sequences. In yet a further embodiment, the primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele

comprises at its extreme 3' end a nucleotide sequence of 17 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant and the wild type *IND* allele or from the complement thereof, respectively; or the primers which specifically recognizes the mutation region of the mutant or the wild type *IND* allele comprises at its extreme 3' end a nucleotide sequence of 17 consecutive nucleotides selected from the mutation sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively; or the primers which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele comprises at its extreme 3' end a nucleotide sequence of 17 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele or from the complement thereof, respectively, wherein said 3'-located 17 consecutive nucleotides are not derived exclusively from either the mutation site or region or from the flanking sequences. In still a further embodiment, the method further comprises subjecting the genomic DNA of said plant, or a cell, part, seed or progeny thereof, to an hybridization assay using a set of at least two specific probes, wherein at least one of said specific probes specifically recognizes the wild type *IND* allele, said at least one probe selected from the group consisting of: a first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second probe which specifically recognizes the 3' and 5' flanking region of the mutant and the wild type *IND* allele, respectively; a first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second probe which specifically recognizes the mutation region of the wild type *IND* allele; a first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second probe which specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the wild type *IND* allele, respectively; and a probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the wild type *IND* allele; and wherein at least one of said specific probes specifically recognize(s) the mutant *IND* allele, said at least one probe selected from the group consisting of: the first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and the second probe which specifically recognizes the 3' or 5' flanking region of the mutant and the wild type *IND* allele, respectively; the first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a third probe which specifically recognizes the mutation region of the mutant *IND* allele; the first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a third probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele; and a

probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele. In a particular embodiment, the probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or a sequence having at least 80% sequence identity therewith, or the probe which specifically recognizes the mutation region of the mutant or the wild type *IND* allele consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from the sequence of the mutation region of the mutant or the wild type *IND* allele, respectively, or a sequence having at least 80% sequence identity therewith, or the probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele, respectively, or a sequence having at least 80% sequence identity therewith, wherein said 13 to 1000 consecutive nucleotides are not derived exclusively from either the mutation site or region or from the flanking sequences. In another particular embodiment, the probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or the probe which specifically recognizes the mutation region of the mutant or the wild type *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from the mutation sequence of the mutant or the wild type *IND* allele or from the complement thereof, or the probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele or from the complement thereof, respectively, wherein said at least 13 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences. In a further particular embodiment, the 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 929 or 931 to 1622 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 930 of SEQ ID NO: 5 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence a or the complement thereof; said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 930 or 930 to 1622 or

of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 929 followed by a or a followed by the nucleotide sequence SEQ ID NO: 5 from nucleotide 931 to 1622 or of the complement thereof, respectively; or the 5' or 3' flanking region comprises the nucleotide
5 sequence of SEQ ID NO: 5 from nucleotide 1 to 995 or 997 to 1622 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 996 of SEQ ID NO: 5 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence a or the complement thereof; said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to
10 996 or 996 to 1622 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 995 followed by a or a followed by the nucleotide sequence SEQ ID NO: 5 from nucleotide 997 to 1622 or of the complement thereof, respectively; or the 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1035 or 1037 to 1622 or of the
15 complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 1036 of SEQ ID NO: 5 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence t or the complement thereof; said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1036 or 1036 to 1622 or of the complement thereof, respectively; and said
20 joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1035 followed by t or t followed by the nucleotide sequence SEQ ID NO: 5 from nucleotide 1037 to 1622 or of the complement thereof, respectively; or the 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 902 or 904 to 1593 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele
25 has the nucleotide sequence of nucleotide 903 of SEQ ID NO: 7 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence t or the complement thereof; and said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 903 or 903 to 1593 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7
30 from nucleotide 1 to 902 followed by t or t followed by the nucleotide sequence SEQ ID NO: 7 from nucleotide 904 to 1593 or of the complement thereof, respectively; or the 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 910 or 912 to 1593 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 911 of SEQ ID NO: 7 or of the complement thereof;
35 said mutation region of the mutant *IND* allele has the sequence a or the complement thereof; and

said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 911 or 911 to 1593 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 910 followed by a or a followed by the nucleotide sequence SEQ ID NO: 7 from nucleotide 912 to 1593 or of the complement thereof, respectively; or the 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 919 or 921 to 1593 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 920 of SEQ ID NO: 7 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence t or the complement thereof; and said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 920 or 920 to 1593 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 919 followed by t or t followed by the nucleotide sequence SEQ ID NO: 7 from nucleotide 921 to 1593 or of the complement thereof, respectively. In a specific embodiment, the set of at least three specific probes is selected from the group consisting of: a set of probes comprising one probe comprising the sequence of SEQ ID NO: 11, one probe comprising the sequence of SEQ ID NO: 12, and/or one probe comprising the sequence of SEQ ID NO: 13; a set of probes comprising one probe comprising the sequence of SEQ ID NO: 14, one probe comprising the sequence of SEQ ID NO: 15, and/or one probe comprising the sequence of SEQ ID NO: 16; a set of probes comprising one probe comprising the sequence of SEQ ID NO: 17, one probe comprising the sequence of SEQ ID NO: 18, and/or one probe comprising the sequence of SEQ ID NO: 19; a set of probes comprising one probe comprising the sequence of SEQ ID NO: 20, one probe comprising the sequence of SEQ ID NO: 21 and/or one probe comprising the sequence of SEQ ID NO: 22; a set of probes comprising one probe comprising the sequence of SEQ ID NO: 23, one probe comprising the sequence of SEQ ID NO: 24 and/or one probe comprising the sequence of SEQ ID NO: 25; and a set of probes comprising one probe comprising the sequence of SEQ ID NO: 26, one probe comprising the sequence of SEQ ID NO: 27 and/or one probe comprising the sequence of SEQ ID NO: 28.

[22] Kits for identifying a mutant *IND* allele according to the invention in a biological sample, and kits for determining the zygosity status of a mutant *IND* allele according to the invention in a plant, or a cell, part, seed or progeny thereof comprising the primers or probes as described above are also provided, as are methods for combining the mutant *IND* alleles according to the invention in one plant, methods for transferring the mutant *IND* alleles according to the invention

from one plant to another plant, and methods for making a (hybrid) plant or seed according to the invention.

[23] In another embodiment of the invention, the mutant *IND* alleles of the invention are used to increase the yield of harvested seed or grain from *Brassica* plants. The increased yield may be a consequence of reducing or delaying seed shattering, but may also be independent from the reduced or delayed seed shatter. In particular, *Brassica* plants are provided comprising at least two *IND* genes, or a cell, part, seed or progeny thereof, characterized in that these plants comprise two mutant homozygous *IND* alleles as herein described in their genome.

GENERAL DEFINITIONS

[24] "Increase of pod shatter resistance" and "reduction of seed shattering", as used herein, refers to a decreased seed shatter tendency and/or a delay in the timing of seed shattering, in particular until after harvest, of *Brassica* plants, the fruits of which normally do not mature synchronously, but sequentially, so that some pods burst open and shatter their seeds before or during harvest. The level of resistance to pod shattering is positively correlated with and can, for example, be measured by determining the force needed to break pods in the 'tensile separation test' (Davies and Bruce, 1997, *J Mat Sci* 32: 5895-5899; Morgan *et al.*, 1998, *Fields Crop Research* 58, 153-165), the number of intact pods remaining after e.g. 20 sec ('IP20'; Morgan *et al.*, 1998, *supra*), 9.7 or 17 sec (Bruce *et al.*, 2002, *Biosystems Eng* 81(2): 179-184) in a 'random impact test', the pod sample half-life (hereinafter also referred to as 'LD50') in a random impact test, i.e. the treatment time needed to cause the opening of 50% of the pods in tested pod samples, and the 'field score for shattering' (Morgan *et al.*, 1998, *supra*). Random impact tests (RITs) and algorithms to define the pod sample half-lives in such RITs have been described in Bruce *et al.*, 2002 (*supra*), Morgan *et al.*, 1998 (*supra*) and the Examples below. Both publications are hereby incorporated by reference. Briefly, a sample of intact mature pods is placed in a closed drum together with steel balls and the drum is then vigorously agitated for increasing periods of times (e.g. 10 s, 20 s, 40 s, 80 s). After each period, the drum is opened and the number of broken and damaged pods is counted. The most accurate estimation of the level of shattering resistance for each line is calculated by fitting a linear x linear curve to all the available data and estimating the time taken for half of the pods within a sample to be broken ("pod sample half-life" or "LD50"). It is important however that pods open mainly along the dehiscence zone, and are not simply pulverized, as may occur with indehiscent pods.

[25] An “agronomically relevant increase of pod shatter resistance”, as used herein, refers to an increase of pod shatter resistance in a plant which results in pod shatter-related yield losses in the field (pre-harvest) below those normally observed for that plant in the field. For oilseed rape, pod shatter-related yield losses in the field are reported to be about 11% for a season with on average good growth conditions and about 25% for a season with on average bad growth conditions. A positive correlation has been found between these levels of seed loss and the level of seed loss at 9.7 s and 17 s treatment time, respectively, in the random impact test as described by Bruce *et al.*, 2002 (Biosystems Eng 81(2): 179-184). Alternatively, to determine whether the level of resistance to pod shattering in a plant is agronomically relevant, the pod sample half-life (‘LD50’, see above) of the plant can be compared with the pod sample half-life of a plant known to have an average level of pod shatter resistance, such as, for oilseed rape, all currently commercially available oilseed rape varieties.

[26] As used herein, “pod or seed shattering” or “fruit or pod dehiscence” refers to a process that takes place in a fruit after seed maturation, whereby the valves detach from the central septum freeing the seeds. The region that breaks (i.e. the “dehiscence zone”) runs the entire length of the fruit between the valves and the replum (external septum). At maturity, the “dehiscence zone” is essentially a non-lignified layer of cells between a region of lignified cells in the valve and the replum. Shattering occurs due to the combination of cell wall loosening in the dehiscence zone and the tensions established by the differential mechanical properties of the drying cells in the silique.

[27] A *Brassica* “fruit”, as used herein, refers to an organ of a *Brassica* plant that develops from a gynoeceium composed of fused carpels, which, upon fertilization, grows to become a “(seed) pod” or “silique” that contains the developing seeds. A *Brassica* “(seed) pod” or “silique” consists of a fruit wall (carpel) enclosing two locules separated by the septum. The “dehiscence zones” develop at the carpel margins adjacent to the septum and run the length of the silique. The cells of the dehiscence zone eventually begin to degrade and this weakens the contact between the carpel walls or valves and the septum. The loss of cellular cohesion is confined to the cells of the dehiscence zone and results from middle lamella breakdown (Meakin and Roberts, 1990, J Exp Bot 41, 995-1011).

[28] “Dehiscence zones”, as used herein, refers to layers of simple, parenchymatous cells, contained in the sutures situated on both sides of the bi-valved pod of plants, in particular *Brassica* plants. The dehiscence zones are situated between the pod valve edge and a central

replum that contains the main vascular bundle to the stalk or pedicel. Dissociation of the cells in the dehiscence zone takes place during pod senescence and is complete by the time the pods reach full maturity (Meakin and Roberts, 1990, *supra*). Valve separation can then take place. The dehiscence zone contains vascular traces, which pass from the pod wall to the pedicel (stalk) and the replum. The process of pod shatter takes place only after external force fractures the delicate vascular threads, allowing the valves to separate and the seeds to fall to the ground. This occurs during disturbance of the canopy, for example by contact with the combine during harvesting. The vascular tissue contains thickened, lignified cells, which form the collenchymatous groups of cells found adjacent to the conductive cells (Meakin and Roberts, 1990, *supra*). This provides rigidity to the tissue and presumably, some resistance to fracturing.

[29] As used herein, “an agronomically relevant treshability” refers to the resistance of a pod, particularly an oilseed rape pod, to opening along the dehiscence zone of the pod with concurrent release of the seeds, upon application of physical forces that allow complete opening of the pods while preventing damage to the seeds, as they are used e.g. in a combine harvester. A positive correlation has been found between a pod sample half-life (‘LD50’) in a random impact test and their treshability. Oilseed rape pod sample half-lives, as determined in a RIT performed as described in the Examples, which correspond to agronomically relevant treshability should not exceed 80 seconds. Typical sample half-life values for control lines of commercially available oilseed rape varieties are about 10 seconds. Thus, lines with significantly increased pod shatter resistance with agronomically relevant treshability have a pod sample half-life in RIT between about 10 and about 80 seconds, between about 10 and about 70 seconds, between about 15 and about 70 seconds, between about 10 and about 60 seconds, between about 10 and about 50 seconds, between about 20 and about 60 seconds, between about 20 and about 50 seconds, between about 40 and about 60 seconds, or about 57 seconds.

[30] “Dehiscent seed plant” means a plant that produces a dry dehiscent fruit, which has fruit walls that open to permit escape of the seeds contained therein. Dehiscent fruits commonly contain several seeds and include the fruits known, for example, as legumes, capsules and siliques.

[31] “Crop plant” refers to plant species cultivated as a crop, such as *Brassica napus* (AACC, 2n=38), *Brassica juncea* (AABB, 2n=36), *Brassica carinata* (BBCC, 2n=34), *Brassica rapa* (syn. *B. campestris*) (AA, 2n=20), *Brassica oleracea* (CC, 2n=18) or *Brassica nigra* (BB, 2n=16). The definition does not encompass weeds, such as *Arabidopsis thaliana*.

[32] The term “nucleic acid sequence” (or nucleic acid molecule) refers to a DNA or RNA molecule in single or double stranded form, particularly a DNA encoding a protein or protein fragment according to the invention. An “endogenous nucleic acid sequence” refers to a nucleic acid sequence within a plant cell, e.g. an endogenous allele of an *IND* gene present within the nuclear genome of a *Brassica* cell. An “isolated nucleic acid sequence” is used to refer to a nucleic acid sequence that is no longer in its natural environment, for example *in vitro* or in a recombinant bacterial or plant host cell.

[33] The term “gene” means a DNA sequence comprising a region (transcribed region), which is transcribed into an RNA molecule (e.g. into a pre-mRNA, comprising intron sequences, which is then spliced into a mature mRNA, or directly into a mRNA without intron sequences) in a cell, operable linked to regulatory regions (e.g. a promoter). A gene may thus comprise several operably linked sequences, such as a promoter, a 5' leader sequence comprising e.g. sequences involved in translation initiation, a (protein) coding region (cDNA or genomic DNA) and a 3' non-translated sequence comprising e.g. transcription termination sites. “Endogenous gene” is used to differentiate from a “foreign gene”, “transgene” or “chimeric gene”, and refers to a gene from a plant of a certain plant genus, species or variety, which has not been introduced into that plant by transformation (i.e. it is not a “transgene”), but which is normally present in plants of that genus, species or variety, or which is introduced in that plant from plants of another plant genus, species or variety, in which it is normally present, by normal breeding techniques or by somatic hybridization, e.g., by protoplast fusion. Similarly, an “endogenous allele” of a gene is not introduced into a plant or plant tissue by plant transformation, but is, for example, generated by plant mutagenesis and/or selection or obtained by screening natural populations of plants.

[34] “Expression of a gene” or “gene expression” refers to the process wherein a DNA region, which is operably linked to appropriate regulatory regions, particularly a promoter, is transcribed into an RNA molecule. The RNA molecule is then processed further (by post-transcriptional processes) within the cell, e.g. by RNA splicing and translation initiation and translation into an amino acid chain (protein), and translation termination by translation stop codons. The term “functionally expressed” is used herein to indicate that a functional protein is produced; the term “not functionally expressed” to indicate that a protein with significantly reduced or no functionality (biological activity) is produced or that no protein is produced (see further below).

[35] The term “protein” refers to a molecule consisting of a chain of amino acids, without reference to a specific mode of action, size, 3-dimensional structure or origin. A “fragment” or “portion” of an IND protein may thus still be referred to as a “protein”. An “isolated protein” is used to refer to a protein that is no longer in its natural environment, for example *in vitro* or in a recombinant bacterial or plant host cell. “Amino acids” are the principal building blocks of proteins and enzymes. They are incorporated into proteins by transfer RNA according to the genetic code while messenger RNA is being decoded by ribosomes. During and after the final assembly of a protein, the amino acid content dictates the spatial and biochemical properties of the protein or enzyme. The amino acid backbone determines the primary sequence of a protein, but the nature of the side chains determines the protein's properties. “Similar amino acids”, as used herein, refers to amino acids that have similar amino acid side chains, i.e. amino acids that have polar, non-polar or practically neutral side chains. “Non-similar amino acids”, as used herein, refers to amino acids that have different amino acid side chains, for example an amino acid with a polar side chain is non-similar to an amino acid with a non-polar side chain. Polar side chains usually tend to be present on the surface of a protein where they can interact with the aqueous environment found in cells (“hydrophilic” amino acids). On the other hand, “non-polar” amino acids tend to reside within the center of the protein where they can interact with similar non-polar neighbors (“hydrophobic” amino acids”). Examples of amino acids that have polar side chains are arginine, asparagine, aspartate, cysteine, glutamine, glutamate, histidine, lysine, serine, and threonine (all hydrophilic, except for cysteine which is hydrophobic). Examples of amino acids that have non-polar side chains are alanine, glycine, isoleucine, leucine, methionine, phenylalanine, proline, and tryptophan (all hydrophobic, except for glycine which is neutral).

[36] The term “transcription factor” is used to refer to a protein consisting of at least two discrete domains – a DNA binding domain and an activation or repression domain - that operate together to modulate the rate of transcriptional initiation from target gene promoters (Ptashne, 1988, Nature 335, 683-689). The term “basic helix-loop-helix (bHLH) domain transcription factor” is used to refer to a transcription factor comprising, apart from the bHLH DNA binding domain (Heim *et al.*, 2003, Mol Biol Evol 20, 735-747; Toledo-Ortiz *et al.*, 2003, Plant Cell 15, 1749-1770), domains which are known to be important for the regulation of gene expression which may be conserved at the amino acid level in related proteins from different species (Quong *et al.*, 1993, Mol Cell Biol 13, 792-800). Transcriptional regulators comprising a bHLH domain bind DNA through residues in the basic region while the helix-loop-helix domain promotes dimerization, allowing family members to form hetero- or homodimers (Murre *et al.*, 1989, Cell 56, 777-783).

[37] The term “*IND* gene” refers herein to a nucleic acid sequence encoding an INDEHISCENT (*IND*) protein, which is a basic helix-loop-helix (bHLH) domain transcription factor required for seed dispersal (Liljgren *et al.*, 2004, Cell 116: 843-853).

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[38] As used herein, the term “allele(s)” means any of one or more alternative forms of a gene at a particular locus. In a diploid (or amphidiploid) cell of an organism, alleles of a given gene are located at a specific location or locus (loci plural) on a chromosome. One allele is present on each chromosome of the pair of homologous chromosomes.

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[39] As used herein, the term “homologous chromosomes” means chromosomes that contain information for the same biological features and contain the same genes at the same loci but possibly different alleles of those genes. Homologous chromosomes are chromosomes that pair during meiosis. “Non-homologous chromosomes”, representing all the biological features of an organism, form a set, and the number of sets in a cell is called ploidy. Diploid organisms contain two sets of non-homologous chromosomes, wherein each homologous chromosome is inherited from a different parent. In amphidiploid species, essentially two sets of diploid genomes exist, whereby the chromosomes of the two genomes are referred to as “homeologous chromosomes” (and similarly, the loci or genes of the two genomes are referred to as homeologous loci or genes). A diploid, or amphidiploid, plant species may comprise a large number of different alleles at a particular locus.

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[40] As used herein, the term “heterozygous” means a genetic condition existing when two different alleles reside at a specific locus, but are positioned individually on corresponding pairs of homologous chromosomes in the cell. Conversely, as used herein, the term “homozygous” means a genetic condition existing when two identical alleles reside at a specific locus, but are positioned individually on corresponding pairs of homologous chromosomes in the cell.

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[41] As used herein, the term “locus” (loci plural) means a specific place or places or a site on a chromosome where for example a gene or genetic marker is found. For example, the “*IND-A1* locus” refers to the position on a chromosome of the A genome where the *IND-A1* gene (and two *IND-A1* alleles) may be found, while the “*IND-C1* locus” refers to the position on a chromosome of the C genome where the *IND-C1* gene (and two *IND-C1* alleles) may be found.

[42] Whenever reference to a “plant” or “plants” according to the invention is made, it is understood that also plant parts (cells, tissues or organs, seed pods, seeds, severed parts such as roots, leaves, flowers, pollen, etc.), progeny of the plants which retain the distinguishing characteristics of the parents (especially the fruit dehiscence properties), such as seed obtained
5 by selfing or crossing, e.g. hybrid seed (obtained by crossing two inbred parental lines), hybrid plants and plant parts derived there from are encompassed herein, unless otherwise indicated.

[43] A “molecular assay” (or test) refers herein to an assay that indicates (directly or indirectly) the presence or absence of one or more particular *IND* alleles at one or both *IND* loci
10 (e.g. at one or both of the *IND-A1* or *IND-C1* loci). In one embodiment it allows one to determine whether a particular (wild type or mutant) *IND* allele is homozygous or heterozygous at the locus in any individual plant.

[44] “Wild type” (also written “wildtype” or “wild-type”), as used herein, refers to a typical
15 form of a plant or a gene as it most commonly occurs in nature. A “wild type plant” refers to a plant with the most common phenotype of such plant in the natural population. A “wild type allele” refers to an allele of a gene required to produce the wild-type phenotype. By contrast, a “mutant plant” refers to a plant with a different rare phenotype of such plant in the natural population or produced by human intervention, e.g. by mutagenesis, and a “mutant allele” refers
20 to an allele of a gene required to produce the mutant phenotype.

[45] As used herein, the term “wild type *IND*” (e.g. wild type *IND-A1* or *IND-C1*), means a naturally occurring *IND* allele found within plants, in particular *Brassicaceae* plants, especially *Brassica* plants, which encodes a functional *IND* protein (e.g. a functional *IND-A1* or *IND-C1*,
25 respectively). In contrast, the term “mutant *IND*” (e.g. mutant *IND-A1* or *IND-C1*), as used herein, refers to an *IND* allele, which does not encode a functional *IND* protein, i.e. an *IND* allele encoding a non-functional *IND* protein (e.g. a non-functional *IND-A1* or *IND-C1*, respectively), which, as used herein, refers to an *IND* protein having no biological activity or a significantly reduced biological activity as compared to the corresponding wild-type functional *IND* protein,
30 or encoding no *IND* protein at all. A “full knock-out” or “null” mutant *IND* allele, as used herein, refers to a mutant *IND* allele, which encodes an *IND* protein having no biological activity as compared to the corresponding wild-type functional *IND* protein or which encodes no protein at all. Such a “full knock-out mutant *IND* allele” is, for example, a wild-type *IND* allele, which comprises one or more mutations in its nucleic acid sequence, for example, one or more non-
35 sense or mis-sense mutations. In particular, such a full knock-out mutant *IND* allele is a wild-

type IND allele, which comprises a mutation that preferably result in the production of an IND protein lacking at least one functional domain, such as the activation domain, the DNA binding domain and/or the dimerization domain, or lacking at least one amino acid critical for its function, such as an amino acid critical for DNA binding, e.g. the arginine at position 127 in SEQ ID NO: 2 or at position 140 in SEQ ID NO: 4 and the like, or the glutamine at position 122 in SEQ ID NO: 2 or at position 135 in SEQ ID NO: 4 and the like, such that the biological activity of the IND protein is completely abolished, or whereby the mutation(s) preferably result in no production of an IND protein. A “partial knock-out” mutant *IND* allele, as used herein, refers to a mutant *IND* allele, which encodes an IND protein having a significantly reduced biological activity as compared to the corresponding wild-type functional IND protein. Such a “partial knock-out mutant *IND* allele” is, for example, a wild-type *IND* allele, which comprises one or more mutations in its nucleic acid sequence, for example, one or more mis-sense mutations. In particular, such a partial knockout mutant IND allele is a wild-type IND allele, which comprises a mutation that preferably result in the production of an IND protein wherein at least one conserved and/or functional amino acid is substituted for another amino acid, such that the biological activity is significantly reduced but not completely abolished. Such full or partial knock-out mutant IND allele may also encode a dominant negative IND protein, which is capable of adversely affecting the biological activity of other IND proteins within the same cell. Such a dominant negative IND protein can be an IND protein that is still capable of interacting with the same elements as the wild-type IND protein, but that blocks some aspect of its function. Examples of dominant negative IND proteins are IND proteins that lack the activation domain and/or dimerization domain or specific amino acid residues critical for activation and/or dimerization, but still contain the DNA binding domain, such that not only their own biological activity is reduced or abolished, but that they further reduce the total IND activity in the cell by competing with wildtype and/or partial knockout IND proteins present in the cell for DNA binding sites. Other examples of dominant negative IND proteins are IND proteins that lack the activation domain and/or DNA binding domain or specific amino acid residues critical for activation and/or DNA binding but still contain the dimerization domain, such that not only their own biological activity is reduced or abolished, but that they further reduce the total IND activity in the cell by producing protein dimers lacking at least one functional domain. Mutant alleles of the IND protein-encoding nucleic acid sequences are designated as “*ind*” (e.g. *ind-a1* or *ind-cl*, respectively) herein. Mutant alleles can be either “natural mutant” alleles, which are mutant alleles found in nature (e.g. produced spontaneously without human application of mutagens) or “induced mutant” alleles, which are induced by human intervention, e.g. by mutagenesis.

[46] A “significantly reduced amount of functional IND protein” (e.g. functional IND-A1 or IND-C1 protein) refers to a reduction in the amount of a functional IND protein produced by the cell comprising a mutant *IND* allele by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 100% (i.e. no functional IND protein is produced by the cell) as compared to the amount of the functional IND protein produced by the cell not comprising the mutant *IND* allele. This definition encompasses the production of a “non-functional” IND protein (e.g. truncated IND protein) having no biological activity *in vivo*, the reduction in the absolute amount of the functional IND protein (e.g. no functional IND protein being made due to the mutation in the *IND* gene), the production of an IND protein with significantly reduced biological activity compared to the activity of a functional wild type IND protein (such as an IND protein in which one or more amino acid residues that are crucial for the biological activity of the encoded IND protein, as exemplified below, are substituted for another amino acid residue) and/or the adverse effect of dominant negative IND proteins on other functional and/or partially functional IND proteins.

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[47] The term “mutant IND protein”, as used herein, refers to an IND protein encoded by a mutant *IND* nucleic acid sequence (“*ind* allele”) whereby the mutation results in a significantly reduced and/or no IND activity *in vivo*, compared to the activity of the IND protein encoded by a non-mutant, wild type *IND* sequence (“*IND* allele”).

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[48] “Mutagenesis”, as used herein, refers to the process in which plant cells (e.g., a plurality of *Brassica* seeds or other parts, such as pollen, etc.) are subjected to a technique which induces mutations in the DNA of the cells, such as contact with a mutagenic agent, such as a chemical substance (such as ethylmethylsulfonate (EMS), ethylnitrosourea (ENU), etc.) or ionizing radiation (neutrons (such as in fast neutron mutagenesis, etc.), alpha rays, gamma rays (such as that supplied by a Cobalt 60 source), X-rays, UV-radiation, etc.), or a combination of two or more of these. Thus, the desired mutagenesis of one or more *IND* alleles may be accomplished by use of chemical means such as by contact of one or more plant tissues with ethylmethylsulfonate (EMS), ethylnitrosourea, etc., by the use of physical means such as x-ray, etc, or by gamma radiation, such as that supplied by a Cobalt 60 source. While mutations created by irradiation are often large deletions or other gross lesions such as translocations or complex rearrangements, mutations created by chemical mutagens are often more discrete lesions such as point mutations. For example, EMS alkylates guanine bases, which results in base mispairing: an alkylated guanine will pair with a thymine base, resulting primarily in G/C to A/T transitions.

35 Following mutagenesis, *Brassica* plants are regenerated from the treated cells using known

techniques. For instance, the resulting *Brassica* seeds may be planted in accordance with conventional growing procedures and following self-pollination seed is formed on the plants. Alternatively, doubled haploid plantlets may be extracted to immediately form homozygous plants, for example as described by Coventry *et al.* (1988, Manual for Microspore Culture
5 Technique for *Brassica napus*. Dep. Crop Sci. Techn. Bull. OAC Publication 0489. Univ. of Guelph, Guelph, Ontario, Canada). Additional seed that is formed as a result of such self-pollination in the present or a subsequent generation may be harvested and screened for the presence of mutant *IND* alleles. Several techniques are known to screen for specific mutant alleles, e.g., DeleteageneTM (Delete-a-gene; Li *et al.*, 2001, Plant J 27: 235-242) uses polymerase
10 chain reaction (PCR) assays to screen for deletion mutants generated by fast neutron mutagenesis, TILLING (targeted induced local lesions in genomes; McCallum *et al.*, 2000, Nat Biotechnol 18:455-457) identifies EMS-induced point mutations, etc. Additional techniques to screen for the presence of specific mutant *IND* alleles are described in the Examples below.

15 [49] As used herein, the term "non-naturally occurring" or "cultivated" when used in reference to a plant, means a plant with a genome that has been modified by man. A transgenic plant, for example, is a non-naturally occurring plant that contains an exogenous nucleic acid molecule, e.g., a chimeric gene comprising a transcribed region which when transcribed yields a biologically active RNA molecule capable of reducing the expression of an endogenous gene,
20 such as an *IND* gene, and, therefore, has been genetically modified by man. In addition, a plant that contains a mutation in an endogenous gene, for example, a mutation in an endogenous *IND* gene, (e.g. in a regulatory element or in the coding sequence) as a result of an exposure to a mutagenic agent is also considered a non-naturally plant, since it has been genetically modified by man. Furthermore, a plant of a particular species, such as *Brassica napus*, that contains a
25 mutation in an endogenous gene, for example, in an endogenous *IND* gene, that in nature does not occur in that particular plant species, as a result of, for example, directed breeding processes, such as marker-assisted breeding and selection or introgression, with a plant of the same or another species, such as *Brassica juncea* or *rapa*, of that plant is also considered a non-naturally occurring plant. In contrast, a plant containing only spontaneous or naturally occurring
30 mutations, i.e. a plant that has not been genetically modified by man, is not a "non-naturally occurring plant" as defined herein and, therefore, is not encompassed within the invention. One skilled in the art understands that, while a non-naturally occurring plant typically has a nucleotide sequence that is altered as compared to a naturally occurring plant, a non-naturally occurring plant also can be genetically modified by man without altering its nucleotide sequence,
35 for example, by modifying its methylation pattern.

[50] The term “ortholog” of a gene or protein refers herein to the homologous gene or protein found in another species, which has the same function as the gene or protein, but is (usually) diverged in sequence from the time point on when the species harboring the genes diverged (i.e. the genes evolved from a common ancestor by speciation). Orthologs of the *Brassica napus* *IND* genes may thus be identified in other plant species (e.g. *Brassica juncea*, etc.) based on both sequence comparisons (e.g. based on percentages sequence identity over the entire sequence or over specific domains) and/or functional analysis.

[51] A “variety” is used herein in conformity with the UPOV convention and refers to a plant grouping within a single botanical taxon of the lowest known rank, which grouping can be defined by the expression of the characteristics resulting from a given genotype or combination of genotypes, can be distinguished from any other plant grouping by the expression of at least one of the said characteristics and is considered as a unit with regard to its suitability for being propagated unchanged (stable).

[52] The term “comprising” is to be interpreted as specifying the presence of the stated parts, steps or components, but does not exclude the presence of one or more additional parts, steps or components. A plant comprising a certain trait may thus comprise additional traits.

[53] It is understood that when referring to a word in the singular (e.g. plant or root), the plural is also included herein (e.g. a plurality of plants, a plurality of roots). Thus, reference to an element by the indefinite article "a" or "an" does not exclude the possibility that more than one of the element is present, unless the context clearly requires that there be one and only one of the elements. The indefinite article "a" or "an" thus usually means "at least one".

[54] For the purpose of this invention, the "sequence identity" of two related nucleotide or amino acid sequences, expressed as a percentage, refers to the number of positions in the two optimally aligned sequences which have identical residues (x100) divided by the number of positions compared. A gap, i.e., a position in an alignment where a residue is present in one sequence but not in the other, is regarded as a position with non-identical residues. The “optimal alignment” of two sequences is found by aligning the two sequences over the entire length according to the Needleman and Wunsch global alignment algorithm (Needleman and Wunsch, 1970, J Mol Biol 48(3):443-53) in The European Molecular Biology Open Software Suite (EMBOSS, Rice *et al.*, 2000, Trends in Genetics 16(6): 276—277; see e.g.

<http://www.ebi.ac.uk/emboss/align/index.html>) using default settings (gap opening penalty = 10 (for nucleotides) / 10 (for proteins) and gap extension penalty = 0.5 (for nucleotides) / 0.5 (for proteins)). For nucleotides the default scoring matrix used is EDNAFULL and for proteins the default scoring matrix is EBLOSUM62.

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[55] "Substantially identical" or "essentially similar", as used herein, refers to sequences, which, when optimally aligned as defined above, share at least a certain minimal percentage of sequence identity (as defined further below).

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[56] "Stringent hybridization conditions" can be used to identify nucleotide sequences, which are substantially identical to a given nucleotide sequence. Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequences at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typically stringent conditions will be chosen in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least 60°C. Lowering the salt concentration and/or increasing the temperature increases stringency. Stringent conditions for RNA-DNA hybridizations (Northern blots using a probe of e.g. 100nt) are for example those which include at least one wash in 0.2X SSC at 63°C for 20min, or equivalent conditions.

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[57] "High stringency conditions" can be provided, for example, by hybridization at 65°C in an aqueous solution containing 6x SSC (20x SSC contains 3.0 M NaCl, 0.3 M Na-citrate, pH 7.0), 5x Denhardt's (100X Denhardt's contains 2% Ficoll, 2% Polyvinyl pyrrolidone, 2% Bovine Serum Albumin), 0.5% sodium dodecyl sulphate (SDS), and 20 µg/ml denaturated carrier DNA (single-stranded fish sperm DNA, with an average length of 120 - 3000 nucleotides) as non-specific competitor. Following hybridization, high stringency washing may be done in several steps, with a final wash (about 30 min) at the hybridization temperature in 0.2-0.1× SSC, 0.1% SDS.

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[58] "Moderate stringency conditions" refers to conditions equivalent to hybridization in the above described solution but at about 60-62°C. Moderate stringency washing may be done at the hybridization temperature in 1x SSC, 0.1% SDS.

[59] "Low stringency" refers to conditions equivalent to hybridization in the above described solution at about 50-52°C. Low stringency washing may be done at the hybridization temperature in 2x SSC, 0.1% SDS. See also Sambrook *et al.* (1989) and Sambrook and Russell (2001).

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[60] "Increased harvested yield" or "increased seed or grain yield" refers to the larger amount of seed or grain harvested from a plurality of plants, each comprising mutant *IND* alleles according to the invention, when compared to the amount of seed or grain harvested from a similar number of isogenic plants without the mutant *IND* alleles. Yield is typically expressed in volume units of harvested seed per surface units, such as bushels/acre or kg/ha. The yield increase is typically expressed in percentage, whereby the yield of the reference or control plant is referred to as 100% and the yield of the plants according to the inventions is expressed in % relative to the yield of the control plant. Observed yield increases in *Brassica* plants according to the invention ranged from at least 101% to at least 124% and it is expected that higher yield increases are feasible. Yield increase may also range from 104% to 108% or 105% to 110%.

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DETAILED DESCRIPTION

[61] As described in WO09/068313 (claiming priority of European patent application EP 07023052), it was found before that *Brassica napus* plants, which are homozygous for a full knockout *ind* allele in only one of their two *IND* genes, i.e. in *IND-A1* or *IND-C1*, did not show a significant increase in pod shatter resistance compared to *Brassica napus* plants not comprising mutant *IND* alleles, while in *Brassica napus* plants, which were homozygous for a full knockout *ind* allele in both *IND* genes, pod shatter resistance was significantly increased, but the level of pod shatter resistance was too high to maintain an agronomically relevant treshability. By contrast, pod shatter resistance was significantly increased in *Brassica napus* plants comprising three full knockout *ind* alleles of the two *Brassica napus* *IND* genes, to a level whereby the plants maintain an agronomically relevant treshability of the pods.

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[62] The inventors surprisingly found that *Brassica napus* plants with a pod shatter phenotype similar to the *Brassica* plants described in WO09/068313 (claiming priority of European patent application EP 07023052), i.e. which combine an increased pod shatter resistance with an agronomically relevant treshability of the pods, can also be obtained by combining two partial knock-out mutant *IND* alleles with two full knock-out mutant *IND* alleles instead of combining three full knockout mutant *IND* alleles. It was further found that mutations in the *IND-C1* gene resulted in a stronger increase in pod shatter resistance than mutations in the *IND-A1* gene. A

stronger increase in pod shatter resistance in *Brassica napus* plants was, for example, observed when the two full knock-out mutant *IND* alleles were full knock-out mutant *IND* alleles from the *IND-C1* gene and the two partial knock-out mutant *IND* alleles were partial knock-out mutant *IND* alleles from the *IND-A1* gene than when the two full knock-out mutant *IND* alleles were from the *IND-A1* gene and the partial knock-out mutant *IND* alleles were from the *IND-C1* gene. Surprisingly, *Brassica napus* plants which combine an increased pod shatter resistance with an agronomically relevant treshability of the pods could also be obtained by introducing two partial knock-out mutant *IND* alleles, in particular of the *IND-C1* gene, alone.

[63] Thus in one embodiment of the invention, a *Brassica* plant comprising at least two *IND* genes, in particular a *Brassica napus* plant comprising an *IND-A1* and an *IND-C1* gene, characterized in that it comprises two partial knock-out mutant *IND* alleles in its genome, in particular of an *IND-A1* and/or an *IND-C1* gene, preferably of an *IND-C1* gene, is provided herein, whereby the *ind* alleles result in a significantly reduced amount of functional *IND* protein of the type encoded by the wild-type equivalent of these mutant alleles and thus an overall significantly reduced amount of the functional *IND* proteins produced in the plant cells, specifically in the developing seed pods, *in vivo*.

[64] In another embodiment, the *Brassica* plant further comprises two full knock-out mutant *IND* alleles in its genome, in particular of an *IND-C1* and/or an *IND-A1* gene, respectively, preferably of an *IND-C1* gene, such as those described in WO09/068313 (claiming priority of European patent application EP 07023052), e.g. *ind-a1-ems01*, *ind-a1-ems05*, *ind-c1-ems01*, or *ind-c1-ems03*, and the like.

[65] It is thought that by combining sufficient copies of specific partial knock-out mutant *IND* alleles with sufficient copies of specific full knock-out mutant and/or wild type *IND* alleles in one plant, in particular a *Brassica* plant, it is possible to fine tune the amount and/or type of functional *IND* proteins made, which in turn influences the fruit dehiscence properties of the plant. The absolute and relative amount of the *IND* proteins can thus be tuned in such a way as to provide plants that produce sufficient *IND* protein(s) to enable an agronomically relevant treshability of the seed pods, while reducing seed shattering before or during harvest.

[66] Thus in another embodiment of the invention, a plant, in particular a *Brassica* plant, is provided comprising at least one partial knock-out mutant *IND* allele, which encodes a partially functional *IND* protein, such as those described below, e.g. *ind-a1-ems06*, *ind-a1-ems09*, *ind-*

a1-ems13, *ind-c1-ems04*, *ind-c1-ems08*, or *ind-c1-ems09*, and the like, while the remaining alleles may be partial knock-out, full knock-out and/or wild-type *IND* alleles.

5 [67] In one aspect of the invention a *Brassica* plant comprising at least two *IND* genes, in particular a *Brassica napus* plant, comprising two partial knockout *ind* alleles and n-tuple full knockout *ind* alleles of the two *IND* genes in that *Brassica* plant, in particular of the *Brassica napus* *IND-A1* and/or *IND-C1* genes, preferably the *IND-C1* gene, is provided, whereby $n \leq 2$ (e.g. $n = 0, 1, \text{ or } 2$), so that at least one allele produces at least partially functional *IND* protein.

10 [68] In a further aspect of the invention an homozygous *IND* single mutant- ($n=2$, i.e. homozygous for a partial knockout mutant allele of one *IND* gene), and/or an homozygous *IND* double mutant- ($n=4$, i.e. homozygous for a full and/or a partial knockout mutant allele of two *IND* genes) plant of a *Brassica* species comprising at least two *IND* genes, in particular of *Brassica napus*, is provided, whereby the mutant alleles are mutant alleles of the two *IND* genes
15 in that *Brassica* plant, in particular of the *IND-A1* and/or *IND-C1* genes. Such mutant plants may, according to this invention, be used for breeding purposes.

[69] Thus in one embodiment of the invention, an homozygous *IND* single partial knockout mutant *Brassica napus* plant is provided herein, wherein the genotype of the plant can be
20 described as *ind-a1^P/ind-a1^P*, *IND-C1/IND-C1*, or *IND-A1/IND-A1*, *ind-c1^P/ind-c1^P*. In another embodiment of the invention, an homozygous *IND* double partial mutant *Brassica napus* plant is provided herein, wherein the genotype of the plant can be described as *ind-a1^P/ind-a1^P*, *ind-c1^P/ind-c1^P*. In yet a further embodiment of the invention, an homozygous *IND* double partial and full mutant *Brassica napus* plant is provided herein, wherein the genotype of the plant can be
25 described as or *ind-a1^F/ind-a1^F*, *ind-c1^P/ind-c1^P* or *ind-a1^P/ind-a1^P*, *ind-c1^F/ind-c1^F*.

[70] Further provided herein are novel nucleic acid sequences of partial knockout mutant *IND* genes/alleles from *Brassica* species, as well as the partial knockout mutant *IND* proteins. Also provided are methods of generating and combining partial knockout mutant *IND* alleles in
30 *Brassica* plants, as well as *Brassica* plants and plant parts comprising specific combinations of full and partial knockout mutant *IND* alleles in their genome, whereby seed shattering is reduced in these plants. The use of these plants for transferring partial knockout mutant *IND* alleles to other plants is also an embodiment of the invention, as are the plant products of any of the plants described. In addition kits and methods for marker assisted selection (MAS) for combining or

detecting *IND* genes and/or alleles are provided. Each of the embodiments of the invention is described in detail herein below.

[71] The *Brassica* plants described herein which exhibit reduced or delayed seed shattering
5 have an increase in the yield of harvested seed. However, it was observed that not only the harvested seed yield from *Brassica* plants comprising only the *ind-c1-09* allele in homozygous state (that show an observable reduced or delayed seed shatter phenotype), but also the harvested seed yield from other *Brassica* plants comprising only two mutant *IND* alleles in homozygous state, i.e. wherein the genotype of the plant can be described as *ind-a1^P/ind-a1^P*, *IND-C1/IND-C1*, or *IND-A1/IND-A1*, *ind-c1^P/ind-c1^P* was also significantly increased, when compared to
10 isogenic *Brassica* plants not comprising the mutant *IND* alleles, despite the absence of an observable reduced or delayed seed shatter phenotype in the *Brassica* plants comprising the mutant *IND* alleles. The invention thus also provides *Brassica* plants comprising at least two *IND* genes, wherein at least two alleles produce a functional *IND* protein, which plants have a
15 higher seed yield. It will be clear that the two mutant alleles at the *IND-A* locus or at the *IND-C* locus may be the same mutant allele or a different mutant allele.

[72] Nucleic acid sequences according to the invention

[73] Provided are partial knockout mutant *ind* nucleic acid sequences encoding partially
20 functional *IND* proteins, i.e. *IND* proteins with a significantly reduced biological activity (i.e., *IND* nucleic acid sequences comprising one or more mutations, which result in a significantly reduced biological activity of the encoded *IND* protein) of *IND* genes from *Brassicaceae*, particularly from *Brassica* species, especially from *Brassica napus*, but also from other *Brassica* crop species. For example, *Brassica* species comprising an A and/or a C genome may comprise
25 alleles of *IND-A1* or *IND-C1* genes, which are essentially similar to the partial knockout mutant *IND* alleles of the present invention and which can be identified and combined in a single plant according to the invention. In addition, mutagenesis methods can be used to generate mutations in wild type *IND* alleles, thereby generating mutant *ind* alleles essentially similar to the partial knockout mutant *IND* alleles of the present invention for use according to the invention. Because
30 specific *IND* alleles are preferably combined in a plant by crossing and selection, in one embodiment the *ind* nucleic acid sequences are provided within a plant (i.e. endogenously), e.g. a *Brassica* plant, preferably a *Brassica* plant which can be crossed with *Brassica napus* or which can be used to make a "synthetic" *Brassica napus* plant. Hybridization between different *Brassica* species is described in the art, e.g., as referred to in Snowdon (2007, Chromosome
35 research 15: 85-95). Interspecific hybridization can, for example, be used to transfer genes from,

e.g., the C genome in *B. napus* (AACC) to the C genome in *B. carinata* (BBCC), or even from, e.g., the C genome in *B. napus* (AACC) to the B genome in *B. juncea* (AABB) (by the sporadic event of illegitimate recombination between their C and B genomes). “Resynthesized” or “synthetic” *Brassica napus* lines can be produced by crossing the original ancestors, *B. oleracea* (CC) and *B. rapa* (AA). Interspecific, and also intergeneric, incompatibility barriers can be successfully overcome in crosses between *Brassica* crop species and their relatives, e.g., by embryo rescue techniques or protoplast fusion (see e.g. Snowdon, above).

[74] However, isolated *ind* nucleic acid sequences (e.g. isolated from the plant by cloning or made synthetically by DNA synthesis), as well as variants thereof and fragments of any of these are also provided herein, as these can be used to determine which sequence is present endogenously in a plant or plant part, whether the sequence encodes a functional, a partially functional, a non-functional or no protein (e.g. by expression in a recombinant host cell as described below) and for selection and transfer of specific alleles from one plant into another, in order to generate a plant having the desired combination of partial and/or full knockout mutant *IND* alleles.

[75] Novel partial knockout mutant *IND* nucleic acid sequences of wild-type *IND-A1* and *IND-C1* have been isolated from *Brassica napus*. The wild type *IND* sequences as described in WO09/068313 (claiming priority of European patent application EP 07023052) are depicted in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 7 of the sequence listing, while the novel partial knockout mutant *ind* sequences of these sequences, and of sequences essentially similar to these, are described herein below and in the Examples, with reference to the wild type *IND* sequences. The genomic *IND* protein-encoding DNA from *Brassica napus* does not comprise any introns.

[76] “*IND-A1* nucleic acid sequences” or “*IND-A1* variant nucleic acid sequences” according to the invention are nucleic acid sequences encoding an amino acid sequence having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, 98%, 99% or 100% sequence identity with SEQ ID NO: 2 or nucleic acid sequences having at least 80%, at least 85%, at least 90%, at least 95%, 96%, 97%, 98%, 99% or 100% sequence identity with SEQ ID NO: 1 or SEQ ID NO: 5. These nucleic acid sequences may also be referred to as being “essentially similar” or “essentially identical” to the *IND* sequences provided in the sequence listing.

[77] “IND-C1 nucleic acid sequences” or “IND-C1 variant nucleic acid sequences” according to the invention are nucleic acid sequences encoding an amino acid sequence having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, 98%, 99% or 100% sequence identity with SEQ ID NO: 4 (IND-C1-long) or with SEQ ID NO: 4 from the amino acid at position 16 to the amino acid at position 210 (IND-C1-short) or nucleic acid sequences having at least 80%, at least 85%, at least 90%, at least 95%, 96%, 97%, 98%, 99% or 100% sequence identity with SEQ ID NO: 3 (*IND-C1-long*), with SEQ ID NO:3 from the nucleotide at position 46 to the nucleotide at position 633 (*IND-C1-short*) or with SEQ ID NO: 7. These nucleic acid sequences may also be referred to as being “essentially similar” or “essentially identical” to the *IND* sequences provided in the sequence listing.

[78] Thus the invention provides novel partial knockout mutant nucleic acid sequences of nucleic acid sequences encoding wild type, functional IND-A1 and IND-C1 proteins, including variants and fragments thereof (as defined further below), whereby the mutation in the nucleic acid sequence preferably results in one or more amino acids being inserted, deleted or substituted in comparison to the wild type IND protein, in particular in one or more amino acids being substituted, and whereby the biological activity of the IND protein is significantly reduced. A significant reduction in the biological activity of the IND protein refers herein to a reduction in the DNA binding activity, the dimerization capacity and/or transcriptional regulating activity of the IND protein, such that the pod shatter resistance of a plant expressing the mutant IND protein is increased as compared to a plant expressing the corresponding wild type IND protein.

[79] To determine the functionality of a specific *IND* allele/protein in plants, particularly in *Brassica* plants, the level of resistance to pod shattering in the plants can be determined by performing macroscopical, microscopical and histological assays on fruits and flowers of the plants comprising the specific *IND* allele/protein and of corresponding wild type plants analogous to the assays performed on *Arabidopsis* fruits and flowers as described by Liljegren *et al.* (2004, *supra*) or as described in the Examples below. Briefly, changes in pod shatter resistance can be evaluated and/or measured, e.g., by macroscopical tests, such as inspection of the seed pods with naked eye to evaluate, e.g., the presence or absence of the valve margins, the length of the beak of the pods, etc.; a Manual Impact Test (MIT) to compare the level of pod shatter resistance between different mutant *IND* lines and corresponding wild type lines by evaluating the ease of pod opening upon gently twisting the pods; a Random Impact Test (RIT) to compare the treshability of seed pods from plants from different mutant *IND* lines and corresponding wild type lines, respectively, by measuring the half-life of pod samples of these

lines; and/or by microscopic tests to examine, e.g., whether and how cells at the valve margin and the dehiscence zone of seed pods are affected by mutations in *IND*. Once the dimerization partner of the IND protein (e.g., the IND protein itself in case its functioning depends on the formation of an homodimer or another protein in case its functioning depends on the formation of an heterodimer) and/or the gene(s) the transcription of which is regulated by the IND protein are identified and characterized, the functionality of a specific *IND* allele/protein can alternatively be evaluated by recombinant DNA techniques as known in the art, e.g., by co-expressing both partners of the dimer in a host cell (e.g. a bacterium, such as *E. coli*) and evaluating if dimers can still be formed, if the dimers can still bind to the bHLH binding site of the regulated gene(s), and/or if the transcription of these gene(s) is still regulated by this binding.

[80] Both endogenous and isolated nucleic acid sequences are provided herein. Also provided are fragments of the mutant *IND* sequences and mutant *IND* variant nucleic acid sequences defined above, for use as primers or probes and as components of kits according to another aspect of the invention (see further below). A "fragment" of an *ind* nucleic acid sequence or variant thereof (as defined) may be of various lengths, such as at least 10, 12, 15, 18, 20, 50, 100, 200, 500, 600 contiguous nucleotides of the *IND* or *ind* sequence (or of the variant sequence).

[81] *Nucleic acid sequences encoding functional IND proteins*

[82] The nucleic acid sequences depicted in the sequence listing encode wild type, functional IND proteins from *Brassica napus*. Thus, these sequences are endogenous to the *Brassica napus* plants from which they were isolated. Other *Brassica* crop species, varieties, breeding lines or wild accessions may be screened for other *IND* alleles, encoding the same IND proteins or variants thereof. For example, nucleic acid hybridization techniques (e.g. Southern blot analysis, using for example stringent hybridization conditions) or PCR-based techniques may be used to identify *IND* alleles endogenous to other *Brassica* plants, such as various *Brassica napus* varieties, lines or accessions, but also *Brassica juncea* (especially *IND* alleles on the A-genome), *Brassica carinata* (especially *IND* alleles on the C-genome) and *Brassica rapa* (A-genome) and *Brassica oleracea* (C-genome) plants, organs and tissues can be screened for other wild type *IND* alleles. To screen such plants, plant organs or tissues for the presence of *IND* alleles, the *IND* nucleic acid sequences provided in the sequence listing, or variants or fragments of any of these, may be used. For example whole sequences or fragments may be used as probes or primers. For example specific or degenerate primers may be used to amplify nucleic acid sequences encoding IND proteins from the genomic DNA of the plant, plant organ or tissue. These *IND* nucleic acid sequences may be isolated and sequenced using standard molecular

biology techniques. Bioinformatics analysis may then be used to characterize the allele(s), for example in order to determine which *IND* allele the sequence corresponds to and which *IND* protein or protein variant is encoded by the sequence.

5 [83] Whether a nucleic acid sequence encodes a functional *IND* protein can be analyzed by recombinant DNA techniques as known in the art, e.g., by a genetic complementation test using, e.g., an *Arabidopsis* plant, which is homozygous for a full knock-out *ind* mutant allele or a *Brassica napus* plant, which is homozygous for a full knock-out *ind* mutant allele of both the *IND-A1* and *IND-C1* gene.

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[84] In addition, it is understood that *IND* nucleic acid sequences and variants thereof (or fragments of any of these) may be identified *in silico*, by screening nucleic acid databases for essentially similar sequences. Likewise, a nucleic acid sequence may be synthesized chemically. Fragments of nucleic acid molecules according to the invention are also provided, which are described further below. Fragments include nucleic acid sequences encoding only the bHLH domain, or smaller fragments comprising part of the bHLH domain, such as the basic domain or the HLH domain, etc.

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[85] *Nucleic acid sequences encoding mutant IND proteins*

20 [86] The invention provides nucleic acid sequences comprising one or more nucleotide deletions, insertions or substitutions relative to the wild type *IND* nucleic acid sequences depicted in SEQ ID NO: 1, 3, 5 and 7 of the sequence listing, wherein the mutation(s) in the nucleic acid sequence result in a significantly reduced biological activity, i.e. a partial knockout of the biological activity, of the encoded *IND* protein relative to the wild type *IND* protein, as well as fragments of such mutant nucleic acid molecules. Such mutant nucleic acid sequences (referred to as *ind^P* sequences) can be generated and/or identified using various known methods, as described further below. Again, such nucleic acid molecules are provided both in endogenous form and in isolated form.

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30 [87] Basically, any mutation in the wild type *IND* nucleic acid sequences which results in an *IND* protein comprising at least one amino acid insertion, deletion and/or substitution relative to the wild type *IND* protein can lead to significantly reduced or no biological activity. It is, however, understood that certain mutations in the *IND* protein are more likely to result in a complete abolishment of the biological activity of the *IND* protein, such as mutations whereby significant portions of the functional domains, such as the DNA binding domain ('b'), the

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dimerization domain ('HLH') and/or transcription regulating domains, are lacking, or whereby certain critical amino acid residues within these domains, such as the Gln (Q), Ala (A) and Arg (R) amino acids at position 5, 9, and 13 or the basic amino acid residues (in particular Arg (R) residues) at positions 10 and 12 of the consensus bHLH domain sequence defined by Heim *et al.* (2003, Mol Biol Evol 20, 735-747; corresponding to positions 123, 127 and 131, and 128 and 130, respectively, in SEQ ID NO: 10, see Table 1) are lacking or are substituted, preferably by non-similar or non-conservative amino acids, while other mutations in the IND protein are more likely to result in a significant reduction of the biological activity of the IND protein, such as mutations leading to substitutions of specific amino acids, e.g. the conserved amino acids indicated in Table 1, causing a less efficient DNA binding, a less efficient dimerization, and/or a less efficient regulation of transcription without completely abolishing the biological activity of the encoded IND protein. WO09/068313 (claiming priority of European patent application EP 07023052) describes, for example, full knockout mutant IND alleles, in particular *ind-a1-ems01*, *ind-c1-ems01* and *ind-c1-ems03*, comprising a nonsense mutation resulting in the production of truncated IND proteins lacking the bHLH domain, and full knockout mutant IND alleles, in particular *ind-a1-ems05*, encoding a mutant IND protein in which the conserved Arg at position 10 of the consensus bHLH domain is substituted for an aromatic His, while the present invention describes partial knockout mutant IND alleles, in particular, e.g., *ind-c1-ems09*, encoding a mutant IND protein in which the conserved Ala at position 9 of the consensus bHLH domain is substituted for a Thr, and *ind-c1-ems04*, encoding a mutant IND protein in which the conserved Arg at position 12 of the consensus bHLH domain is substituted for a Cys.

[88] The nucleic acid molecules may comprise one or more mutations, such as:

- a "missense mutation", which is a change in the nucleic acid sequence that results in the substitution of an amino acid for another amino acid;
- a "nonsense mutation" or "STOP codon mutation", which is a change in the nucleic acid sequence that results in the introduction of a premature STOP codon and thus the termination of translation (resulting in a truncated protein); plant genes contain the translation stop codons "TGA" (UGA in RNA), "TAA" (UAA in RNA) and "TAG" (UAG in RNA); thus any nucleotide substitution, insertion, deletion which results in one of these codons to be in the mature mRNA being translated (in the reading frame) will terminate translation;
- an "insertion mutation" of one or more amino acids, due to one or more codons having been added in the coding sequence of the nucleic acid;
- a "deletion mutation" of one or more amino acids, due to one or more codons having been deleted in the coding sequence of the nucleic acid;

- a “frameshift mutation”, resulting in the nucleic acid sequence being translated in a different frame downstream of the mutation. A frameshift mutation can have various causes, such as the insertion, deletion or duplication of one or more nucleotides.

5 [89] Table 1 indicates the length of the *Arabidopsis* IND protein in SEQ ID NO: 10, of the *Arabidopsis* IND coding DNA in SEQ ID NO: 9, and of the *Brassica napus* IND-A1 and IND-C1 proteins in SEQ ID NO: 2 and 6 and SEQ ID NO: 4 and 8, respectively; the position of the bHLH domains in the *Brassica napus* IND-A1 and IND-C1 proteins based on the indicated position of pfam domain PF00010, smart domain SM00353, prosite domain PS50888 and
 10 superfam domain G3D.4.10.280.10 or SSF47459 of the *Arabidopsis* IND protein according to The *Arabidopsis* Information Resource (TAIR) database (<http://www.arabidopsis.org/>; locus At4g00120.1, herein incorporated by reference; SEQ ID NO: 10); the position of the bHLH domains and conserved amino acids in the *Brassica napus* IND-A1 and IND-C1 proteins based
 15 on the indicated position of the bHLH domain and conserved amino acids in *Arabidopsis* IND protein according to Heim *et al.* (2003, Mol Biol Evol 20, 735-747), according to Toledo-Ortiz *et al.* (2003, Plant Cell 15: 1749-1770), and according to Liljegren *et al.* (2004, Cell, 116, 843-853), herein incorporated by reference; as further described in WO09/068313 (claiming priority of European patent application EP 07023052), which is herein incorporated by reference.

20 Table 1 IND proteins - amino acids (AA) regions and positions

		AtIND1 (SEQ ID NO: 10)	AtIND1 (SEQ ID NO: 9)	BnIND-A1 (SEQ ID NO: 2/6)	BnIND-C1a/b (SEQ ID 4/8 from 16-210 / SEQ ID 4/8)
<u>Coding region</u>	<u>TAIR:</u>	1-198 (198 AA)	1-594	1-185 (185 AA)	16-210 / 1-210 (195 / 210 AA)
	PF00010	121-168	361-504	120-167	133-180
	SM00353	124-173	370-519	123-172	136-185
	PS50888	112-168	334-504	111-167	124-180
	G3D.4.10.280.10	114-196	340-588	-	127-208
	SSF47459	114-198	340-594	-	127-210
	<u>Liljegren <i>et al.</i></u>	30-198 (169 AA)	88-594		
<u>bHLH:</u>	<u>Heim <i>et al.</i></u>	119-174	355-523	118-173	131-186

	<u>Toledo-Ortiz et al.</u>	115-167	343-501	114-166	127-179
	<u>Liljegren et al.</u>	119-167	355-501	118-166	131-179
b	Heim et al.	119-131	355-393	118-132	131-145
	Toledo-Ortiz et al.	115-131	343-393	114-132	127-145
	Liljegren et al.	119-131	355-393	118-132	131-145
H1	Heim et al.	132-146	394-438	133-145	146-158
	Toledo-Ortiz et al.	132-146	394-438	133-145	146-158
	Liljegren et al.	132-145	394-435	133-144	146-157
L	Heim et al.	147-152	439-456	146-151	159-164
	Toledo-Ortiz et al.	147-152	439-456	146-151	159-164
	Liljegren et al.	146-152	436-456	145-151	158-164
H2	Heim et al.	153-174	457-523	152-173	165-186
	Toledo-Ortiz et al.	153-167	457-501	152-166	165-179
	Liljegren et al.	153-167	457-501	152-166	165-179
<u>Conserved</u>	N (1 ^T)	115	343-345	114	127
<u>AA</u>	V (2 ^T)	116	346-348	115	128
	Q (5 ^H)	123	367-379	122	135
	A (9 ^H - 13 ^T)	127	379-381	126	139
	R (10 ^H - 14 ^T)	128	382-384	127	140
	R (12 ^H - 16 ^T)	130	388-390	129	142
	R (13 ^H)	131	391-393	130	143
	I (16 ^H - 20 ^T)	134	400-403	133	146
	S (21 ^T)	135	404-406	134	147
	I (20 ^H - 24 ^T)	138	412-414	137	150
	L (23 ^H - 27 ^T)	141	421-423	140	153
	K (28 ^T)	142	424-426	141	154
	V (27 ^H)	145	433-435	144	157
	K (39 ^T)	150	448-450	149	162
	T (42 ^T)	153	460-463	152	165
	A (36 ^H)	154	460-462	153	166
	M (45 ^T)	156	466-468	155	168
	L (39 ^H -46 ^T)	157	469-471	156	169
	A (49 ^T)	160	478-480	159	172

	I (43 ^H - 50 ^T)	161	481-483	160	173
	Y (52 ^T)	163	487-489	162	175
	T (53 ^T)	164	490-492	163	176
	L (49 ^H -56 ^T)	167	499-501	166	179
	V (53 ^H)	171	511-513	170	183
	L (56 ^H)	174	580-582	173 (A)	186
<u>At ind</u>	<i>ind-5</i>	42	124-126	25	41
	(W13>STOP) ^L				
	<i>ind-2</i> (A26>FS) ^L	55	163-165	-	-
	<i>ind-6</i> ^W	Insertion	Insertion	-	-
		after 61	after 185		
	<i>ind-4</i>	92	274-276	91	104
	(Q63>STOP) ^L				
	<i>ind-3</i> (R99>H) ^L	128	382-384	127	140
	<i>ind-1</i> (L112>F) ^L	141	421-423	140	153

Heim et al., ^H: Heim *et al.*, 2003, Mol Biol Evol 20, 735-747; Toledo-Ortiz *et al.*, ^T: Toledo-Ortiz *et al.*, 2003, Plant Cell 15: 1749-1770; Liljegen *et al.*, ^L: Liljegen *et al.*, 2004, Cell, 116, 843-853; ^W: Wu *et al.*, 2006, Planta 224, 971-979.

5 [90] Optimal alignment of the *Arabidopsis IND* nucleic acid (SEQ ID NO: 9) and amino acid (SEQ ID NO: 10) sequences with *IND* nucleic acid sequences, in particular the *Brassica IND* nucleic acid (SEQ ID NO: 1 and 3) and amino acid (SEQ ID NO: 2 and 4) sequences of the present invention, allows to determine the positions of the corresponding conserved domains and amino acids in these *Brassica* sequences (see Table 1 for the *Brassica IND* sequences of SEQ ID
10 NO: 1 to 4).

[91] Thus in one embodiment, partial knockout mutant *IND* nucleic acid sequences comprising one or more of any of the types of mutations described above are provided. In another embodiment, partial knockout *ind* sequences comprising one or more stop codon
15 (nonsense) mutations, one or more missense mutations and/or one or more frameshift mutations are provided. Any of the above mutant nucleic acid sequences are provided *per se* (in isolated form), as are plants and plant parts comprising such sequences endogenously. In the tables herein below the most preferred *ind* alleles are described and seed deposits of *Brassica napus* seeds comprising one or more *ind* alleles have been deposited as indicated.

[92] A nonsense mutation in an *IND* allele, as used herein, is a mutation in an *IND* allele whereby one or more translation stop codons are introduced into the coding DNA and the corresponding mRNA sequence of the corresponding wild type *IND* allele. Translation stop codons are TGA (UGA in the mRNA), TAA (UAA) and TAG (UAG). Thus, any mutation (deletion, insertion or substitution) that leads to the generation of an in-frame stop codon in the coding sequence will result in termination of translation and truncation of the amino acid chain. In one embodiment, a partial knockout mutant *IND* allele is provided comprising a nonsense mutation wherein an in-frame stop codon is introduced in the *IND* codon sequence by a single nucleotide substitution, such as the mutation of CAG to TAG, TGG to TAG, TGG to TGA, or CAA to TAA. In another embodiment, a partial knockout mutant *IND* allele is provided comprising a nonsense mutation wherein an in-frame stop codon is introduced in the *IND* codon sequence by double nucleotide substitutions, such as the mutation of CAG to TAA, TGG to TAA, or CGG to TAG or TGA. In yet another embodiment, a partial knockout mutant *IND* allele is provided comprising a nonsense mutation wherein an in-frame stop codon is introduced in the *IND* codon sequence by triple nucleotide substitutions, such as the mutation of CGG to TAA. The truncated protein lacks the amino acids encoded by the coding DNA downstream of the mutation (i.e. the C-terminal part of the *IND* protein) and maintains the amino acids encoded by the coding DNA upstream of the mutation (i.e. the N-terminal part of the *IND* protein). In one embodiment, a partial knockout mutant *IND* allele is provided comprising a nonsense mutation present anywhere in front of the conserved Leu residue of the H2 domain (at position 56 in the consensus bHLH domain sequence as described by Heim *et al.*, 2003, see Table 1), so that at least the conserved Leu residue is lacking. The more truncated the mutant *IND* protein is in comparison to the wild type *IND* protein, the more the truncation may result in a significantly reduced activity of the *IND* protein. It is believed that, in order for the mutant *IND* protein to retain some biological activity, it should at least comprise the DNA binding (b) domain. Thus in another embodiment, a partial knockout mutant *IND* allele is provided comprising a nonsense mutation which results in a truncated protein of less than about 170 amino acids (lacking the conserved Leu), less than about 150 amino acids (lacking the H2 domain), less than about 145 amino acids (lacking the L and H2 domains), or less than about 130 amino acids (lacking the HLH domain)(see Table 1).

[93] The Tables herein below describe a range of possible nonsense mutations in the *Brassica napus* *IND* sequences provided herein:

Table 2a Potential STOP codon mutations in *IND-A1* (SEQ ID NO: 1)

Amino acid position	Nucleotide position	Wild type → mutant codon	Wild type → mutant amino acid
25	74	tgg → tag	TRP → STOP
	75	tgg → tga	TRP → STOP
	74+75	tgg → taa	TRP → STOP
57	169	cag → tag	GLN → STOP
	169+171	cag → taa	GLN → STOP
91	271	caa → taa	GLN → STOP
98	292	cag → tag	GLN → STOP
	292+294	cag → taa	GLN → STOP
122	364	cag → tag	GLN → STOP
	364+366	cag → taa	GLN → STOP
128	382+383	cgg → tag	ARG → STOP
	382+384	cgg → tga	ARG → STOP
	382+383+384	cgg → taa	ARG → STOP
138	412+413	cgg → tag	ARG → STOP
	412+414	cgg → tga	ARG → STOP
	412+413+414	cgg → taa	ARG → STOP
168	502+503	cgg → tag	ARG → STOP
	502+504	cgg → tga	ARG → STOP
	502+503+504	cgg → taa	ARG → STOP
169	505	cag → tag	GLN → STOP
	505+507	cag → taa	GLN → STOP
181	542	tgg → tag	TRP → STOP
	543	tgg → tga	TRP → STOP
	542+543	tgg → taa	TRP → STOP

Table 2b Potential STOP codon mutations in *IND-C1* (SEQ ID NO: 3)

Amino acid position	Nucleotide position	Wild type → mutant codon	Wild type → mutant amino acid
41	122	tgg → tag	TRP → STOP
	123	tgg → tga	TRP → STOP
	122+123	tgg → taa	TRP → STOP
50	148	caa → taa	GLN → STOP
73	271	cag → tag	GLN → STOP
	271+272	cag → taa	GLN → STOP
104	310	caa → taa	GLN → STOP
111	331	cag → tag	GLN → STOP
	331+333	cag → taa	GLN → STOP
135	403	cag → tag	GLN → STOP
	403+405	cag → taa	GLN → STOP
141	421+422	cgg → tag	ARG → STOP
	421+423	cgg → tga	ARG → STOP
	421+422+423	cgg → taa	ARG → STOP
151	451+452	cgg → tag	ARG → STOP

	451+453	cgg → tga	ARG → STOP
	451+452+453	cgg → taa	ARG → STOP
181	541+542	cgg → tag	ARG → STOP
	541+543	cgg → tga	ARG → STOP
	541+542+543	cgg → taa	ARG → STOP
182	544	cag → tag	GLN → STOP
	544+546	cag → taa	GLN → STOP
187	559	cag → tag	GLN → STOP
	559+561	cag → taa	GLN → STOP
191	571	cag → tag	GLN → STOP
	571+573	cag → taa	GLN → STOP

[94] Obviously, mutations are not limited to the ones shown in the above tables and it is understood that analogous STOP mutations may be present in *ind* alleles other than those depicted in the sequence listing and referred to in the tables above.

5

[95] A missense mutation in an *IND* allele, as used herein, is any mutation (deletion, insertion or substitution) in an *IND* allele whereby one or more codons are changed into the coding DNA and the corresponding mRNA sequence of the corresponding wild type *IND* allele, resulting in the substitution of one or more amino acids in the wild type *IND* protein for one or more other amino acids in the mutant *IND* protein. In one embodiment, a partial knockout mutant *IND* allele is provided comprising a missense mutation resulting in a substitution of a valine (Val) residue at position 124 of the *IND* protein in SEQ ID NO: 2, or a sequence essentially similar thereto, in particular by a methionine (Met) residue, such as the *ind-a1*-EMS06 allele (Table 3a). In another embodiment, a partial knockout mutant *IND* allele is provided comprising a missense mutation resulting in a substitution of a glycine (Gly) residue at position 146 of the *IND* protein in SEQ ID NO: 2, or a sequence essentially similar thereto, in particular by a serine (Ser) residue, such as the *ind-a1*-EMS09 allele (Table 3a). In yet another embodiment, a partial knockout mutant *IND* allele is provided comprising a missense mutation resulting in a substitution of an alanine (Ala) residue at position 159 of the *IND* protein in SEQ ID NO: 2, or a sequence essentially similar thereto, in particular by a valine (Val) residue, such as the *ind-a1*-EMS13 allele (Table 3a). In still another embodiment, a partial knockout mutant *IND* allele is provided comprising a missense mutation resulting in a substitution of a threonine (Thr) residue at position 136 of the *IND* protein in SEQ ID NO: 4, or a sequence essentially similar thereto, in particular by a methionine (Met) residue, such as the *ind-c1*-EMS08 allele (Table 3b). In a further embodiment, a partial knockout mutant *IND* allele is provided comprising a missense mutation resulting in a substitution of an alanine (Ala) residue at position 139 of the *IND* protein in SEQ ID NO: 4, or a sequence essentially similar thereto, in particular by a threonine (Thr) residue, such as the *ind-*

c1-EMS09 allele (Table 3b). In still a further embodiment, a partial knockout mutant *IND* allele is provided comprising a missense mutation resulting in a substitution of an arginine (Arg) residue at position 142 of the *IND* protein in SEQ ID NO: 4, or a sequence essentially similar thereto, in particular by a cysteine (Cys) residue, such as the *ind-c1*-EMS04 allele (Table 3b).

- 5 Reference seed comprising *ind-a1*-EMS06, *ind-a1*-EMS09, *ind-a1*-EMS13, *ind-c1*-EMS08, *ind-c1*-EMS09, and *ind-c1*-EMS04 alleles in homozygous state have been deposited at the NCIMB Limited (Ferguson Building, Craibstone Estate, Bucksburn, Aberdeen, Scotland, AB21 9YA, UK) on July 7, 2008, under accession number NCIMB 41570, NCIMB 41571, NCIMB 41572, NCIMB 41573, NCIMB 41574, and NCIMB 41575, respectively.

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Table 3a: Missense mutations in *IND-A1*

Amino acid position	Nucleotide position		Wild type → mutant codon	Wild type → mutant amino acid	Allele name	Deposit number
<i>SEQ ID: 2/6</i>	<i>SEQ ID: 1</i>	<i>SEQ ID: 5</i>				
124	370	930	gtg → atg	VAL → MET	<i>ind-a1</i> -EMS06	NCIMB 41570
146	436	996	ggc → agc	GLY → SER	<i>ind-a1</i> -EMS09	NCIMB 41571
159*	476	1036	gcc → gtc	ALA → VAL	<i>ind-a1</i> -EMS13	NCIMB 41572

Table 3b: Missense mutations in *IND-C1*

Amino acid position	Nucleotide position		Wild type → mutant codon	Wild type → mutant amino acid	Allele name	Deposit number
<i>SEQ ID: 4/8</i>	<i>SEQ ID: 3</i>	<i>SEQ ID: 7</i>				
136	407	903	acg → atg	THR → MET	<i>ind-c1</i> -EMS08	NCIMB 41573
139*	415	911	gct → act	ALA → THR	<i>ind-c1</i> -EMS09	NCIMB 41574
142*	424	920	cgt → tgt	ARG → CYS	<i>ind-c1</i> -EMS04	NCIMB 41575

- 15 [96] In another embodiment, a partial knockout mutant *IND* allele comprising a missense mutation is provided encoding an *IND* protein wherein one or more of the conserved amino acids indicated above or in Table 1 is/are substituted, such as partial knockout mutant *IND* alleles *ind-a1*-EMS13, *ind-c1*-EMS04 and *ind-c1*-EMS09 (indicated with * in Table 3). As described in Heim *et al.* (2003, Mol Biol Evol 20, 735-747), Toledo-Ortiz *et al.* (2003, Plant Cell 15: 1749-20 1770), Liljgren *et al.* (2004, Cell, 116, 843-853), and WO09/068313 (claiming priority of European patent application EP 07023052), some of the conserved amino acids are more critical for the biological activity of the *IND* protein than others. Thus, for example, missense mutations which result in the substitution of, e.g., the amino acids at position 5, 9 (e.g., *ind-c1*-EMS09), and 13 or at positions 10 (e.g., *ind-a1*-EMS05) and 12 (e.g., *ind-c1*-EMS04) of the consensus 25 bHLH domain sequence defined by Heim *et al.* (*supra*) are more likely to result in a significantly reduced activity, due to a reduced ability to bind to the target DNA, of the *IND* protein. Similarly

missense mutations which result in the substitution of, e.g., the amino acids at position 16, 20, 23, 27 in helix1 or at positions 36, 39, 43, 49 (e.g., *ind-a1*-EMS13), 53, and 56 in helix2 of the consensus bHLH domain sequence defined by Heim *et al.* (*supra*) are more likely to result in a significantly reduced activity, due to a reduced dimerization ability, of the IND protein.

5

[97] In still another embodiment, a partial knockout mutant *IND* allele comprising a missense mutation which can be used according to the invention is an *IND* allele comprising a missense mutation corresponding to the missense mutation in the *Arabidopsis* partial knockout *ind-1* (Liljegren *et al.*, 2004, *supra*) alleles (see Table 1).

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[98] A frameshift mutation in an *IND* allele, as used herein, is a mutation (deletion, insertion, duplication, and the like) in an *IND* allele that results in the nucleic acid sequence being translated in a different frame downstream of the mutation.

15 [99] Amino acid sequences according to the invention

[100] Provided are partial knockout mutant IND amino acid sequences (i.e., IND amino acid sequences comprising one or more mutations, which result in a significantly reduced biological activity of the IND protein) from *Brassicaceae*, particularly from *Brassica* species, especially from *Brassica napus*, but also from other *Brassica* crop species. For example, *Brassica* species comprising an A and/or a C genome may encode different IND-A1 or IND-C1 amino acids, which are essentially similar to the novel partial knockout mutant IND proteins of the present invention. In addition, mutagenesis methods can be used to generate mutations in wild type *IND* alleles, thereby generating mutant alleles which can encode further mutant IND proteins, which are essentially similar to the partial knockout mutant IND proteins of the present invention. In one embodiment the mutant IND amino acid sequences are provided within a *Brassica* plant (i.e. endogenously). However, isolated IND amino acid sequences (e.g. isolated from the plant or made synthetically), as well as variants thereof and fragments of any of these are also provided herein.

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30 [101] Amino acid sequences, which are essentially similar to the novel partial knockout mutant IND proteins of the present invention can be obtained by replacing amino acids in the partial knockout IND amino acid sequences of the present invention by other amino acids having similar properties (such as similar hydrophobicity, hydrophilicity, antigenicity, propensity to form or break α -helical structures or β -sheet structures). Conservative substitution tables are well

known in the art (see for example Creighton (1984) Proteins. W.H. Freeman and Company and Table 4 of the present patent application).

Table 4: Examples of conserved amino acid substitutions

Residue	Conservative Substitutions	Residue	Conservative Substitutions
Ala	Ser	Leu	Ile, Val
Arg	Lys	Lys	Arg, Gln
Asn	Gln, His	Met	Leu, Ile
Asp	Glu	Phe	Met, Leu, Tyr
Gln	Asn	Ser	Thr, Gly
Cys	Ser	Thr	Ser, Val
Glu	Asp	Trp	Tyr
Gly	Pro	Tyr	Trp, Phe
His	Asn, Gln	Val	Ile, Leu
Ile	Leu, Val		

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[102] Novel partial knockout mutant IND amino acid sequences of wild-type IND-A1 and IND-C1 proteins have been isolated from *Brassica napus*. The wild type IND sequences as described in WO09/068313 (claiming priority of European patent application EP 07023052) are depicted in SEQ ID NO: 2 and SEQ ID NO: 4, while the novel partial knockout mutant IND sequences of these sequences, and of sequences essentially similar to these, are described herein below and in the Examples, with reference to the wild type IND sequences. As described above, the wildtype IND proteins of *Brassica napus* are about 185-210 amino acids in length and comprise a number of structural and functional domains.

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[103] “IND-A1 amino acid sequences” or “IND-A1 variant amino acid sequences” according to the invention are amino acid sequences having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, 98%, 99% or 100% sequence identity with SEQ ID NO: 2. These amino acid sequences may also be referred to as being “essentially similar” or “essentially identical” to the IND sequences provided in the sequence listing.

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[104] “IND-C1 amino acid sequences” or “IND-C1 variant amino acid sequences” according to the invention are amino acid sequences having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, 96%, 97%, 98%, 99% or 100% sequence identity with SEQ ID NO: 4 (IND-C1-long) or with SEQ ID NO:4 from the amino acid at position 16 to the amino acid at position

210 (IND-C1-short). These amino acid sequences may also be referred to as being “essentially similar” or “essentially identical” the *IND* sequences provided in the sequence listing.

[105] Thus, the invention provides novel partial knockout mutant sequences of amino acid sequences of wild type, functional IND-A1 and IND-C1 proteins, including variants and fragments thereof (as defined further below), whereby the mutation in the amino acid sequence preferably results in a significant reduction in the biological activity of the IND protein as compared to the biological activity of the corresponding wild type IND protein. A significant reduction in the biological activity of the IND protein refers herein to a reduction in the DNA binding activity, the dimerization capacity and/or transcriptional regulating activity of the IND protein, such that the pod shatter resistance of a plant expressing the mutant IND protein is increased as compared to a plant expressing the corresponding wild type IND protein compared to the pod shatter resistance of a corresponding wild type plant.

[106] Both endogenous and isolated amino acid sequences are provided herein. Also provided are fragments of the IND amino acid sequences and IND variant amino acid sequences defined above. A “fragment” of a IND amino acid sequence or variant thereof (as defined) may be of various lengths, such as at least 10, 12, 15, 18, 20, 50, 100, 150, 175, 180 contiguous amino acids of the IND sequence (or of the variant sequence).

[107] *Amino acid sequences of functional IND proteins*

[108] The amino acid sequences depicted in the sequence listing are wild type, functional IND proteins from *Brassica napus*. Thus, these sequences are endogenous to the *Brassica napus* plants from which they were isolated. Other *Brassica* crop species, varieties, breeding lines or wild accessions may be screened for other functional IND proteins with the same amino acid sequences or variants thereof, as described above.

[109] In addition, it is understood that IND amino acid sequences and variants thereof (or fragments of any of these) may be identified in silico, by screening amino acid databases for essentially similar sequences. Fragments of amino acid molecules according to the invention are also provided. Fragments include amino acid sequences of the bHLH domain, or smaller fragments comprising part of the bHLH domain, such as the basic domain or the HLH domain, etc.

[110] *Amino acid sequences of mutant IND proteins*

[111] The invention provides amino acid sequences comprising one or more amino acid deletions, insertions or substitutions relative to the wild type IND amino acid sequences depicted in SEQ ID NO: 2 and 4 of the sequence listing, wherein the mutation(s) in the amino acid sequence result in a significantly reduced biological activity, i.e. a partial knockout of the biological activity, of the encoded IND protein relative to the wild type protein, as well as fragments of such mutant amino acid molecules. Such mutant amino acid sequences can be generated and/or identified using various known methods, as described above. Again, such amino acid molecules are provided both in endogenous form and in isolated form.

[112] As described above, basically, any mutation in the wild type IND amino acid sequences which results in an IND protein comprising at least one amino acid insertion, deletion and/or substitution relative to the wild type IND protein can lead to significantly reduced or no biological activity. It is, however, understood that certain mutations in the IND protein are more likely to result in a complete abolishment of the biological activity of the IND protein, such as mutations leading to truncated proteins, whereby significant portions of the functional domains, such as the DNA binding domain ('b'), the dimerization domain ('HLH') and/or amino acids which are important in the regulation of transcription (See Table 1), are lacking, or mutations whereby certain critical amino acid residues within these domains, such as the Gln (Q), Ala (A) and Arg (R) amino acids at position 5, 9, and 13 or the basic amino acid residues (in particular Arg (R) residues) at positions 10 and 12 of the consensus bHLH domain sequence defined by Heim *et al.* (*supra*; corresponding to positions 123, 127 and 131, and 128 and 130, respectively, in SEQ ID NO: 10, see Table 1) are lacking or are substituted, preferably by non-similar or non-conservative amino acids, while other mutations of the protein are more likely to result in a significant reduction of the biological activity of the IND protein, such as mutations leading to substitutions of specific amino acids, e.g. the conserved amino acids indicated in Table 1, causing a less efficient DNA binding, a less efficient dimerization, and/or a less efficient regulation of transcription without completely abolishing the biological activity of the encoded IND protein.

[113] Thus in one embodiment, partial knockout mutant IND proteins are provided comprising one or more deletion or insertion mutations, whereby the deletion(s) or insertion(s) result(s) in a mutant protein which has significantly reduced activity *in vivo*. Such mutant IND proteins are IND proteins wherein at least 1, at least 2, 3, 4, 5, 10, 20, 30, 50, 100, 100, 150, 175, 180 or more

amino acids are deleted or inserted as compared to the wild type IND protein, whereby the deletion(s) or insertion(s) result(s) in a mutant protein which has significantly reduced activity *in vivo*.

5 [114] In another embodiment, partial knockout mutant IND proteins are provided which are truncated whereby the truncation results in a mutant protein that has significantly reduced activity *in vivo*. Such truncated IND proteins are IND proteins which lack functional domains in the C-terminal part of the corresponding wild type IND protein and which maintain the N-terminal part of the corresponding wild type IND protein. Thus in one embodiment, a partial
10 knockout mutant IND protein is provided comprising the N-terminal part of the corresponding wild type IND protein up to but not including the conserved Leu residue of the H2 domain (at position 56 in the consensus bHLH domain sequence as described by Heim *et al.*, 2003, see above) is provided. The more truncated the mutant protein is in comparison to the wild type protein, the more the truncation may result in a significantly reduced activity of the IND protein.
15 It is believed that, in order for the mutant IND protein to retain some biological activity, it should at least comprise the DNA binding (b) domain. Thus in another embodiment, a partial knockout mutant IND protein is provided comprising the N-terminal part of the corresponding wild type IND protein lacking part or all of the second H domain, and/or lacking part or all of the L domain, and/or lacking part or all of the first H domain(see Table 1).

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[115] In yet another embodiment, partial knockout mutant IND proteins are provided comprising one or more substitution mutations, whereby the substitution(s) result(s) in a mutant protein that has significantly reduced activity *in vivo*. In one embodiment, a partial knockout mutant IND protein is provided comprising a substitution mutation resulting in a substitution of a
25 valine (Val) residue at position 124 of the IND protein in SEQ ID NO: 2, or a sequence essentially similar thereto, in particular by a methionine (Met) residue, such as the partial knockout mutant IND protein encoded by the *ind-a1*-EMS06 allele (Table 3a). In another embodiment, a partial knockout mutant IND protein is provided comprising a substitution mutation resulting in a substitution of a glycine (Gly) residue at position 146 of the IND protein
30 in SEQ ID NO: 2, or a sequence essentially similar thereto, in particular by a serine (Ser) residue, such as the partial knockout mutant IND protein encoded by the *ind-a1*-EMS09 allele (Table 3a). In yet another embodiment, a partial knockout mutant IND protein is provided comprising a substitution mutation resulting in a substitution of an alanine (Ala) residue at position 159 of the IND protein in SEQ ID NO: 2, or a sequence essentially similar thereto, in
35 particular by a valine (Val) residue, such as the partial knockout mutant IND protein encoded by

the *ind-a1*-EMS13 allele (Table 3a). In still another embodiment, a partial knockout mutant IND protein is provided comprising a substitution mutation resulting in a substitution of a threonine (Thr) residue at position 136 of the IND protein in SEQ ID NO: 4, or a sequence essentially similar thereto, in particular by a methionine (Met) residue, such as the partial knockout mutant
5 IND protein encoded by the *ind-c1*-EMS08 allele (Table 3b). In a further embodiment, a partial knockout mutant IND protein is provided comprising a substitution mutation resulting in a substitution of an alanine (Ala) residue at position 139 of the IND protein in SEQ ID NO: 4, or a sequence essentially similar thereto, in particular by a threonine (Thr) residue, such as the partial knockout mutant IND protein encoded by the *ind-c1*-EMS09 allele (Table 3b). In still a further
10 embodiment, a partial knockout mutant IND protein is provided comprising a substitution mutation resulting in a substitution of an arginine (Arg) residue at position 142 of the IND protein in SEQ ID NO: 4, or a sequence essentially similar thereto, in particular by a cysteine (Cys) residue, such as the partial knockout mutant IND protein encoded by the *ind-c1*-EMS04 allele (Table 3b).

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[116] In another embodiment, a partial knockout mutant IND protein is provided comprising a substitution mutation resulting in the substitution of a conserved amino acid residues as indicated above or in Table 1, such as the partial knockout mutant IND protein encoded by *ind-a1*-EMS13, *ind-c1*-EMS04 or *ind-c1*-EMS09 (indicated with * in Table 3).

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[117] Methods according to the invention

[118] In another aspect of the invention, methods are provided for generating and selecting dehiscent seed plants, and cells, parts, seeds and progeny thereof, containing at least one partial and/or at least one full knock-out *ind* allele. In particular, methods are provided for generating
25 and selecting *Brassica* plants comprising at least two *IND* genes, in particular *Brassica napus* plants, and cells, parts, seeds and progeny thereof, containing at least one partial and/or at least one full knock-out *ind* allele at at least one of the at least two different *IND* loci in the genome, for example at at least one of the two different loci of the *Brassica* IND-A1 and IND-C1 gene, and to distinguish between the presence of full knockout *ind* alleles, partial knockout *ind* alleles
30 and wild type *IND* alleles in a dehiscent seed plant or plant part. Thus methods are provided (such as mutagenesis and/or marker assisted selection) for generating and/or identifying partial knockout *ind* alleles and/or full knockout *ind* alleles or dehiscent seed plants or plant parts comprising such *ind* alleles and for combining a suitable number of partial knockout *ind* alleles and/or full knockout *ind* alleles and/or different types of partial knockout *ind* alleles and/or full
35 knockout *ind* alleles in a single dehiscent seed plant to alter the fruit dehiscence properties of the

plants, in particular to reduce seed shattering, or delay seed shattering until after harvest, while maintaining at the same time an agronomically relevant treshability of the pods.

5 [119] Partial and full knockout mutant *ind* alleles according to the invention may be generated (for example induced by mutagenesis) and/or identified using a range of methods, which are conventional in the art, for example using PCR based methods to amplify part or all of the *ind* genomic or cDNA.

10 [120] Following mutagenesis, plants are grown from the treated seeds, or regenerated from the treated cells using known techniques. For instance, mutagenized seeds may be planted in accordance with conventional growing procedures and following self-pollination seed is formed on the plants. Alternatively, doubled haploid plantlets may be extracted from treated microspore or pollen cells to immediately form homozygous plants, for example as described by Coventry *et al.* (1988, Manual for Microspore Culture Technique for *Brassica napus*. Dep. Crop Sci. Techn. Bull. OAC Publication 0489. Univ. of Guelph, Guelph, Ontario, Canada). Additional seed which is formed as a result of such self-pollination in the present or a subsequent generation may be harvested and screened for the presence of mutant *IND* alleles, using techniques which are conventional in the art, for example polymerase chain reaction (PCR) based techniques (amplification of the *ind* alleles) or hybridization based techniques, e.g. Southern blot analysis, 20 BAC library screening, and the like, and/or direct sequencing of *ind* alleles. To screen for the presence of point mutations (so called Single Nucleotide Polymorphisms or SNPs) in mutant *IND* alleles, SNP detection methods conventional in the art can be used, for example oligoligation-based techniques, single base extension-based techniques or techniques based on differences in restriction sites, such as TILLING.

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[121] As described above, mutagenization (spontaneous as well as induced) of a specific wild-type *IND* allele results in the presence of one or more deleted, inserted, or substituted nucleotides (hereinafter called "mutation region") in the resulting mutant *IND* allele. The mutant *IND* allele can thus be characterized by the location and the configuration of the one or more deleted, 30 inserted, or substituted nucleotides in the wild type *IND* allele. The site in the wild type *IND* allele where the one or more nucleotides have been inserted, deleted, or substituted, respectively, is herein also referred to as the "mutation region or sequence". A "5' or 3' flanking region or sequence" as used herein refers to a DNA region or sequence in the mutant (or the corresponding wild type) *IND* allele of at least 20 bp, preferably at least 50 bp, at least 750 bp, at least 1500 bp, 35 and up to 5000 bp of DNA different from the DNA containing the one or more deleted, inserted,

or substituted nucleotides, preferably DNA from the mutant (or the corresponding wild type) *IND* allele which is located either immediately upstream of and contiguous with (5' flanking region or sequence") or immediately downstream of and contiguous with (3' flanking region or sequence") the mutation region in the mutant *IND* allele (or in the corresponding wild type *IND* allele). A "joining region" as used herein refers to a DNA region in the mutant (or the corresponding wild type) *IND* allele where the mutation region and the 5' or 3' flanking region are linked to each other. A "sequence spanning the joining region between the mutation region and the 5' or 3' flanking region thus comprises a mutation sequence as well as the flanking sequence contiguous therewith.

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[122] The tools developed to identify a specific mutant *IND* allele or the plant or plant material comprising a specific mutant *IND* allele, or products which comprise plant material comprising a specific mutant *IND* allele are based on the specific genomic characteristics of the specific mutant *IND* allele as compared to the genomic characteristics of the corresponding wild type *IND* allele, such as, a specific restriction map of the genomic region comprising the mutation region, molecular markers or the sequence of the flanking and/or mutation regions.

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[123] Once a specific mutant *IND* allele has been sequenced, primers and probes can be developed which specifically recognize a sequence within the 5' flanking, 3' flanking and/or mutation regions of the mutant *IND* allele in the nucleic acid (DNA or RNA) of a sample by way of a molecular biological technique. For instance a PCR method can be developed to identify the mutant *IND* allele in biological samples (such as samples of plants, plant material or products comprising plant material). Such a PCR is based on at least two specific "primers": one recognizing a sequence within the 5' or 3' flanking region of the mutant *IND* allele and the other recognizing a sequence within the 3' or 5' flanking region of the mutant *IND* allele, respectively; or one recognizing a sequence within the 5' or 3' flanking region of the mutant *IND* allele and the other recognizing a sequence within the mutation region of the mutant *IND* allele; or one recognizing a sequence within the 5' or 3' flanking region of the mutant *IND* allele and the other recognizing a sequence spanning the joining region between the 3' or 5' flanking region and the mutation region of the specific mutant *IND* allele (as described further below), respectively.

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[124] The primers preferably have a sequence of between 15 and 35 nucleotides which under optimized PCR conditions "specifically recognize" a sequence within the 5' or 3' flanking region, a sequence within the mutation region, or a sequence spanning the joining region between the 3' or 5' flanking and mutation regions of the specific mutant *IND* allele, so that a

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specific fragment ("mutant *IND* specific fragment" or discriminating amplicon) is amplified from a nucleic acid sample comprising the specific mutant *IND* allele. This means that only the targeted mutant *IND* allele, and no other sequence in the plant genome, is amplified under optimized PCR conditions.

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[125] PCR primers suitable for the invention may be the following:

- 10 - oligonucleotides ranging in length from 17 nt to about 200 nt, comprising a nucleotide sequence of at least 17 consecutive nucleotides, preferably 20 consecutive nucleotides selected from the 5' or 3' flanking sequence of a specific mutant *IND* allele or the complement thereof (i.e., for example, the sequence 5' or 3' flanking the one or more nucleotides deleted, inserted or substituted in the mutant *IND* alleles of the invention, such as the sequence 5' or 3' flanking the non-sense, mis-sense or frameshift mutations described above or the sequence 5' or 3' flanking the STOP codon mutations indicated in the above Tables or the substitution mutations indicated above or the complement thereof) (primers recognizing 5' flanking sequences); or
 - 15 - oligonucleotides ranging in length from 17 nt to about 200 nt, comprising a nucleotide sequence of at least 17 consecutive nucleotides, preferably 20 nucleotides selected from the sequence of the mutation region of a specific mutant *IND* allele or the complement thereof (i.e., for example, the sequence of nucleotides inserted or substituted in the *IND* genes of the invention or the complement thereof) (primers recognizing mutation sequences) .
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[126] The primers may of course be longer than the mentioned 17 consecutive nucleotides, and may e.g. be 18, 19, 20, 21, 30, 35, 50, 75, 100, 150, 200 nt long or even longer. The primers may entirely consist of nucleotide sequence selected from the mentioned nucleotide sequences of flanking and mutation sequences. However, the nucleotide sequence of the primers at their 5' end (i.e. outside of the 3'-located 17 consecutive nucleotides) is less critical. Thus, the 5' sequence of the primers may consist of a nucleotide sequence selected from the flanking or mutation sequences, as appropriate, but may contain several (e.g. 1, 2, 5, 10) mismatches. The 5' sequence of the primers may even entirely consist of a nucleotide sequence unrelated to the flanking or mutation sequences, such as e.g. a nucleotide sequence representing restriction enzyme recognition sites. Such unrelated sequences or flanking DNA sequences with mismatches should preferably be not longer than 100, more preferably not longer than 50 or even 25 nucleotides.

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[127] Moreover, suitable primers may comprise or consist of a nucleotide sequence spanning the joining region between flanking and mutation sequences (i.e., for example, the joining region between a sequence 5' or 3' flanking one or more nucleotides deleted, inserted or substituted in the mutant *IND* alleles of the invention and the sequence of the one or more nucleotides inserted or substituted or the sequence 3' or 5', respectively, flanking the one or more nucleotides deleted, such as the joining region between a sequence 5' or 3' flanking non-sense, missense or frameshift mutations in the *IND* genes of the invention described above and the sequence of the non-sense, missense or frameshift mutations, or the joining region between a sequence 5' or 3' flanking a potential STOP codon mutation as indicated in the above Tables or the substitution mutations indicated above and the sequence of the potential STOP codon mutation or the substitution mutations, respectively), provided the nucleotide sequence is not derived exclusively from either the mutation region or flanking regions.

[128] It will also be immediately clear to the skilled artisan that properly selected PCR primer pairs should also not comprise sequences complementary to each other.

[129] For the purpose of the invention, the "complement of a nucleotide sequence represented in SEQ ID No: X" is the nucleotide sequence which can be derived from the represented nucleotide sequence by replacing the nucleotides through their complementary nucleotide according to Chargaff's rules ($A \leftrightarrow T$; $G \leftrightarrow C$) and reading the sequence in the 5' to 3' direction, i.e. in opposite direction of the represented nucleotide sequence.

[130] Examples of primers suitable to identify specific mutant *IND* alleles are described in the Examples.

[131] As used herein, "the nucleotide sequence of SEQ ID No. Z from position X to position Y" indicates the nucleotide sequence including both nucleotide endpoints.

[132] Preferably, the amplified fragment has a length of between 50 and 1000 nucleotides, such as a length between 50 and 500 nucleotides, or a length between 100 and 350 nucleotides. The specific primers may have a sequence which is between 80 and 100% identical to a sequence within the 5' or 3' flanking region, to a sequence within the mutation region, or to a sequence spanning the joining region between the 3' or 5' flanking and mutation regions of the specific mutant *IND* allele, provided the mismatches still allow specific identification of the specific mutant *IND* allele with these primers under optimized PCR conditions. The range of allowable

mismatches however, can easily be determined experimentally and are known to a person skilled in the art.

5 [133] Detection and/or identification of a "mutant *IND* specific fragment" can occur in various ways, e.g., via size estimation after gel or capillary electrophoresis or via fluorescence-based detection methods. The mutant *IND* specific fragments may also be directly sequenced. Other sequence specific methods for detection of amplified DNA fragments are also known in the art.

10 [134] Standard PCR protocols are described in the art, such as in "PCR Applications Manual" (Roche Molecular Biochemicals, 2nd Edition, 1999) and other references. The optimal conditions for the PCR, including the sequence of the specific primers, is specified in a "PCR identification protocol" for each specific mutant *IND* allele. It is however understood that a number of parameters in the PCR identification protocol may need to be adjusted to specific laboratory conditions, and may be modified slightly to obtain similar results. For instance, use of
15 a different method for preparation of DNA may require adjustment of, for instance, the amount of primers, polymerase, MgCl₂ concentration or annealing conditions used. Similarly, the selection of other primers may dictate other optimal conditions for the PCR identification protocol. These adjustments will however be apparent to a person skilled in the art, and are furthermore detailed in current PCR application manuals such as the one cited above.

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[135] Examples of PCR identification protocols to identify specific mutant *IND* alleles are described in the Examples.

[136] Alternatively, specific primers can be used to amplify a mutant *IND* specific fragment
25 that can be used as a "specific probe" for identifying a specific mutant *IND* allele in biological samples. Contacting nucleic acid of a biological sample, with the probe, under conditions that allow hybridization of the probe with its corresponding fragment in the nucleic acid, results in the formation of a nucleic acid/probe hybrid. The formation of this hybrid can be detected (e.g. labeling of the nucleic acid or probe), whereby the formation of this hybrid indicates the
30 presence of the specific mutant *IND* allele. Such identification methods based on hybridization with a specific probe (either on a solid phase carrier or in solution) have been described in the art. The specific probe is preferably a sequence that, under optimized conditions, hybridizes specifically to a region within the 5' or 3' flanking region and/or within the mutation region of the specific mutant *IND* allele (hereinafter referred to as "mutant *IND* specific region").
35 Preferably, the specific probe comprises a sequence of between 10 and 1000 bp, 50 and 600 bp,

between 100 to 500 bp, between 150 to 350bp, which is at least 80%, preferably between 80 and 85%, more preferably between 85 and 90%, especially preferably between 90 and 95%, most preferably between 95% and 100% identical (or complementary) to the nucleotide sequence of a specific region. Preferably, the specific probe will comprise a sequence of about 13 to about 100
5 contiguous nucleotides identical (or complementary) to a specific region of the specific mutant *IND* allele.

[137] Specific probes suitable for the invention may be the following:

- 10 - oligonucleotides ranging in length from 13 nt to about 1000 nt, comprising a nucleotide sequence of at least 13 consecutive nucleotides selected from the 5' or 3' flanking sequence of a specific mutant *IND* allele or the complement thereof (i.e., for example, the sequence 5' or 3' flanking the one or more nucleotides deleted, inserted or substituted in the mutant *IND* alleles of the invention, such as the sequence 5' or 3' flanking the non-sense, mis-sense or frameshift mutations described above or the sequence 5' or 3' flanking the potential STOP
15 codon mutations indicated in the above Tables or the substitution mutations indicated above), or a sequence having at least 80% sequence identity therewith (probes recognizing 5' flanking sequences); or
- 20 - oligonucleotides ranging in length from 13 nt to about 1000 nt, comprising a nucleotide sequence of at least 13 consecutive nucleotides selected from the mutation sequence of a specific mutant *IND* allele or the complement thereof (i.e., for example, the sequence of nucleotides inserted or substituted in the *IND* genes of the invention, or the complement thereof), or a sequence having at least 80% sequence identity therewith (probes recognizing mutation sequences).

25 [138] The probes may entirely consist of nucleotide sequence selected from the mentioned nucleotide sequences of flanking and mutation sequences. However, the nucleotide sequence of the probes at their 5' or 3' ends is less critical. Thus, the 5' or 3' sequences of the probes may consist of a nucleotide sequence selected from the flanking or mutation sequences, as appropriate, but may consist of a nucleotide sequence unrelated to the flanking or mutation
30 sequences. Such unrelated sequences should preferably be not longer than 50, more preferably not longer than 25 or even not longer than 20 or 15 nucleotides.

[139] Moreover, suitable probes may comprise or consist of a nucleotide sequence spanning the joining region between flanking and mutation sequences (i.e., for example, the joining region
35 between a sequence 5' or 3' flanking one or more nucleotides deleted, inserted or substituted in

the mutant *IND* alleles of the invention and the sequence of the one or more nucleotides inserted or substituted or the sequence 3' or 5', respectively, flanking the one or more nucleotides deleted, such as the joining region between a sequence 5' or 3' flanking non-sense, mis-sense or frameshift mutations in the *IND* genes of the invention described above and the sequence of the non-sense, mis-sense or frameshift mutations, or the joining region between a sequence 5' or 3' flanking a potential STOP codon mutation as indicated in the above Tables or the substitution mutations indicated above and the sequence of the potential STOP codon or substitution mutation, respectively), provided the mentioned nucleotide sequence is not derived exclusively from either the mutation region or flanking regions.

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[140] Examples of specific probes suitable to identify specific mutant *IND* alleles are described in the Examples.

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[141] Detection and/or identification of a "mutant *IND* specific region" hybridizing to a specific probe can occur in various ways, e.g., via size estimation after gel electrophoresis or via fluorescence-based detection methods. Other sequence specific methods for detection of a "mutant *IND* specific region" hybridizing to a specific probe are also known in the art.

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[142] Alternatively, plants or plant parts comprising one or more mutant *ind* alleles can be generated and identified using other methods, such as the "Delete-a-geneTM" method which uses PCR to screen for deletion mutants generated by fast neutron mutagenesis (reviewed by Li and Zhang, 2002, *Funct Integr Genomics* 2:254-258), by the TILLING (Targeting Induced Local Lesions IN Genomes) method which identifies EMS-induced point mutations using denaturing high-performance liquid chromatography (DHPLC) to detect base pair changes by heteroduplex analysis (McCallum *et al.*, 2000, *Nat Biotech* 18:455, and McCallum *et al.* 2000, *Plant Physiol.* 123, 439-442), etc. As mentioned, TILLING uses high-throughput screening for mutations (e.g. using Cel 1 cleavage of mutant-wildtype DNA heteroduplexes and detection using a sequencing gel system). Thus, the use of TILLING to identify plants or plant parts comprising one or more mutant *ind* alleles and methods for generating and identifying such plants, plant organs, tissues and seeds is encompassed herein. Thus in one embodiment, the method according to the invention comprises the steps of mutagenizing plant seeds (e.g. EMS mutagenesis), pooling of plant individuals or DNA, PCR amplification of a region of interest, heteroduplex formation and high-throughput detection, identification of the mutant plant, sequencing of the mutant PCR product. It is understood that other mutagenesis and selection methods may equally be used to generate such mutant plants.

[143] Instead of inducing mutations in *IND* alleles, natural (spontaneous) mutant alleles may be identified by methods known in the art. For example, ECOTILLING may be used (Henikoff *et al.* 2004, *Plant Physiology* 135(2):630-6) to screen a plurality of plants or plant parts for the presence of natural mutant *ind* alleles. As for the mutagenesis techniques above, preferably *Brassica* species are screened which comprise an A and/or a C genome, so that the identified *ind* allele can subsequently be introduced into other *Brassica* species, such as *Brassica napus*, by crossing (inter- or intraspecific crosses) and selection. In ECOTILLING natural polymorphisms in breeding lines or related species are screened for by the TILLING methodology described above, in which individual or pools of plants are used for PCR amplification of the *ind* target, heteroduplex formation and high-throughput analysis. This can be followed by selecting individual plants having a required mutation that can be used subsequently in a breeding program to incorporate the desired mutant allele.

[144] The identified mutant alleles can then be sequenced and the sequence can be compared to the wild type allele to identify the mutation(s). Optionally functionality can be tested as indicated above. Using this approach a plurality of mutant *ind* alleles (and *Brassica* plants comprising one or more of these) can be identified. The desired mutant alleles can then be combined with the desired wild type alleles by crossing and selection methods as described further below. Finally a single plant comprising the desired number of mutant *ind* and the desired number of wild type *IND* alleles is generated.

[145] Oligonucleotides suitable as PCR primers or specific probes for detection of a specific mutant *IND* allele can also be used to develop methods to determine the zygosity status of the specific mutant *IND* allele.

[146] To determine the zygosity status of a specific mutant *IND* allele, a PCR-based assay can be developed to determine the presence of a mutant and/or corresponding wild type *IND* specific allele:

[147] To determine the zygosity status of a specific mutant *IND* allele, two primers specifically recognizing the wild-type *IND* allele can be designed in such a way that they are directed towards each other and have the mutation region located in between the primers. These primers may be primers specifically recognizing the 5' and 3' flanking sequences, respectively. This set

of primers allows simultaneous diagnostic PCR amplification of the mutant, as well as of the corresponding wild type *IND* allele.

[148] Alternatively, to determine the zygosity status of a specific mutant *IND* allele, two primers specifically recognizing the wild-type *IND* allele can be designed in such a way that they are directed towards each other and that one of them specifically recognizes the mutation region. These primers may be primers specifically recognizing the sequence of the 5' or 3' flanking region and the mutation region of the wild type *IND* allele, respectively. This set of primers, together with a third primer which specifically recognizes the sequence of the mutation region in the mutant *IND* allele, allow simultaneous diagnostic PCR amplification of the mutant *IND* gene, as well as of the wild type *IND* gene.

[149] Alternatively, to determine the zygosity status of a specific mutant *IND* allele, two primers specifically recognizing the wild-type *IND* allele can be designed in such a way that they are directed towards each other and that one of them specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region. These primers may be primers specifically recognizing the 5' or 3' flanking sequence and the joining region between the mutation region and the 3' or 5' flanking region of the wild type *IND* allele, respectively. This set of primers, together with a third primer which specifically recognizes the joining region between the mutation region and the 3' or 5' flanking region of the mutant *IND* allele, respectively, allow simultaneous diagnostic PCR amplification of the mutant *IND* gene, as well as of the wild type *IND* gene.

[150] Alternatively, the zygosity status of a specific mutant *IND* allele can be determined by using alternative primer sets that specifically recognize mutant and wild type *IND* alleles.

[151] If the plant is homozygous for the mutant *IND* gene or the corresponding wild type *IND* gene, the diagnostic PCR assays described above will give rise to a single PCR product typical, preferably typical in length, for either the mutant or wild type *IND* allele. If the plant is heterozygous for the mutant *IND* allele, two specific PCR products will appear, reflecting both the amplification of the mutant and the wild type *IND* allele.

[152] Identification of the wild type and mutant *IND* specific PCR products can occur e.g. by size estimation after gel or capillary electrophoresis (e.g. for mutant *IND* alleles comprising a number of inserted or deleted nucleotides which results in a size difference between the

fragments amplified from the wild type and the mutant *IND* allele, such that said fragments can be visibly separated on a gel); by evaluating the presence or absence of the two different fragments after gel or capillary electrophoresis, whereby the diagnostic PCR amplification of the mutant *IND* allele can, optionally, be performed separately from the diagnostic PCR amplification of the wild type *IND* allele; by direct sequencing of the amplified fragments; or by fluorescence-based detection methods.

[153] Examples of primers suitable to determine the zygosity of specific mutant *IND* alleles are described in the Examples.

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[154] Alternatively, to determine the zygosity status of a specific mutant *IND* allele, a hybridization-based assay can be developed to determine the presence of a mutant and/or corresponding wild type *IND* specific allele:

[155] To determine the zygosity status of a specific mutant *IND* allele, two specific probes recognizing the wild-type *IND* allele can be designed in such a way that each probe specifically recognizes a sequence within the *IND* wild type allele and that the mutation region is located in between the sequences recognized by the probes. These probes may be probes specifically recognizing the 5' and 3' flanking sequences, respectively. The use of one or, preferably, both of these probes allows simultaneous diagnostic hybridization of the mutant, as well as of the corresponding wild type *IND* allele.

[156] Alternatively, to determine the zygosity status of a specific mutant *IND* allele, two specific probes recognizing the wild-type *IND* allele can be designed in such a way that one of them specifically recognizes a sequence within the *IND* wild type allele upstream or downstream of the mutation region, preferably upstream of the mutation region, and that one of them specifically recognizes the mutation region. These probes may be probes specifically recognizing the sequence of the 5' or 3' flanking region, preferably the 5' flanking region, and the mutation region of the wild type *IND* allele, respectively. The use of one or, preferably, both of these probes, optionally, together with a third probe which specifically recognizes the sequence of the mutation region in the mutant *IND* allele, allow diagnostic hybridization of the mutant and of the wild type *IND* gene.

[157] Alternatively, to determine the zygosity status of a specific mutant *IND* allele, a specific probe recognizing the wild-type *IND* allele can be designed in such a way that the probe

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specifically recognizes the joining region between the 5' or 3' flanking region, preferably the 5' flanking region, and the mutation region of the wild type *IND* allele. This probe, optionally, together with a second probe that specifically recognizes the joining region between the 5' or 3' flanking region, preferably the 5' flanking region, and the mutation region of the mutant *IND* allele, allows diagnostic hybridization of the mutant and of the wild type *IND* gene.

[158] Alternatively, the zygosity status of a specific mutant *IND* allele can be determined by using alternative sets of probes that specifically recognize mutant and wild type *IND* alleles.

[159] If the plant is homozygous for the mutant *IND* gene or the corresponding wild type *IND* gene, the diagnostic hybridization assays described above will give rise to a single specific hybridization product, such as one or more hybridizing DNA (restriction) fragments, typical, preferably typical in length, for either the mutant or wild type *IND* allele. If the plant is heterozygous for the mutant *IND* allele, two specific hybridization products will appear, reflecting both the hybridization of the mutant and the wild type *IND* allele.

[160] Identification of the wild type and mutant *IND* specific hybridization products can occur e.g. by size estimation after gel or capillary electrophoresis (e.g. for mutant *IND* alleles comprising a number of inserted or deleted nucleotides which results in a size difference between the hybridizing DNA (restriction) fragments from the wild type and the mutant *IND* allele, such that said fragments can be visibly separated on a gel); by evaluating the presence or absence of the two different specific hybridization products after gel or capillary electrophoresis, whereby the diagnostic hybridization of the mutant *IND* allele can, optionally, be performed separately from the diagnostic hybridization of the wild type *IND* allele; by direct sequencing of the hybridizing DNA (restriction) fragments; or by fluorescence-based detection methods.

[161] Examples of probes suitable to determine the zygosity of specific mutant *IND* alleles are described in the Examples.

[162] Furthermore, detection methods specific for a specific mutant *IND* allele that differ from PCR- or hybridization-based amplification methods can also be developed using the specific mutant *IND* allele specific sequence information provided herein. Such alternative detection methods include linear signal amplification detection methods based on invasive cleavage of particular nucleic acid structures, also known as InvaderTM technology, (as described e.g. in US patent 5,985,557 "Invasive Cleavage of Nucleic Acids", 6,001,567 "Detection of Nucleic Acid

sequences by Invader Directed Cleavage, incorporated herein by reference), RT-PCR-based detection methods, such as Taqman, or other detection methods, such as SNPlex, Single Base Extension (SBE), and the like. Briefly, in the InvaderTM technology, the target mutation sequence may e.g. be hybridized with a labeled first nucleic acid oligonucleotide comprising the nucleotide sequence of the mutation sequence or a sequence spanning the joining region between the 5' flanking region and the mutation region and with a second nucleic acid oligonucleotide comprising the 3' flanking sequence immediately downstream and adjacent to the mutation sequence, wherein the first and second oligonucleotide overlap by at least one nucleotide. The duplex or triplex structure that is produced by this hybridization allows selective probe cleavage with an enzyme (Cleavase®) leaving the target sequence intact. The cleaved labeled probe is subsequently detected, potentially via an intermediate step resulting in further signal amplification.

[163] A "kit", as used herein, refers to a set of reagents for the purpose of performing the method of the invention, more particularly, the identification of a specific mutant *IND* allele in biological samples or the determination of the zygosity status of plant material comprising a specific mutant *IND* allele. More particularly, a preferred embodiment of the kit of the invention comprises at least two specific primers, as described above, for identification of a specific mutant *IND* allele, or at least two or three specific primers for the determination of the zygosity status. Optionally, the kit can further comprise any other reagent described herein in the PCR identification protocol. Alternatively, according to another embodiment of this invention, the kit can comprise at least one specific probe, which specifically hybridizes with nucleic acid of biological samples to identify the presence of a specific mutant *IND* allele therein, as described above, for identification of a specific mutant *IND* allele, or at least two or three specific probes for the determination of the zygosity status. Optionally, the kit can further comprise any other reagent (such as but not limited to hybridizing buffer, label) for identification of a specific mutant *IND* allele in biological samples, using the specific probe.

[164] The kit of the invention can be used, and its components can be specifically adjusted, for purposes of quality control (e.g., purity of seed lots), detection of the presence or absence of a specific mutant *IND* allele in plant material or material comprising or derived from plant material, such as but not limited to food or feed products.

[165] The term "primer" as used herein encompasses any nucleic acid that is capable of priming the synthesis of a nascent nucleic acid in a template-dependent process, such as PCR.

Typically, primers are oligonucleotides from 10 to 30 nucleotides, but longer sequences can be employed. Primers may be provided in double-stranded form, though the single-stranded form is preferred. Probes can be used as primers, but are designed to bind to the target DNA or RNA and need not be used in an amplification process.

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[166] The term "recognizing" as used herein when referring to specific primers, refers to the fact that the specific primers specifically hybridize to a nucleic acid sequence in a specific mutant *IND* allele under the conditions set forth in the method (such as the conditions of the PCR identification protocol), whereby the specificity is determined by the presence of positive and
10 negative controls.

[167] The term "hybridizing", as used herein when referring to specific probes, refers to the fact that the probe binds to a specific region in the nucleic acid sequence of a specific mutant *IND* allele under standard stringency conditions. Standard stringency conditions as used herein
15 refers to the conditions for hybridization described herein or to the conventional hybridizing conditions as described by Sambrook et al., 1989 (Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbour Laboratory Press, NY) which for instance can comprise the following steps: 1) immobilizing plant genomic DNA fragments or BAC library DNA on a filter, 2) prehybridizing the filter for 1 to 2 hours at 65°C in 6 X SSC, 5 X Denhardt's reagent,
20 0.5% SDS and 20 µg/ml denaturated carrier DNA, 3) adding the hybridization probe which has been labeled, 4) incubating for 16 to 24 hours, 5) washing the filter once for 30 min. at 68°C in 6X SSC, 0.1 %SDS, 6) washing the filter three times (two times for 30 min. in 30ml and once for 10 min in 500ml) at 68°C in 2 X SSC, 0.1 %SDS, and 7) exposing the filter for 4 to 48 hours to X-ray film at -70°C.

25

[168] As used in herein, a "biological sample" is a sample of a plant, plant material or product comprising plant material. The term "plant" is intended to encompass plant tissues, at any stage of maturity, as well as any cells, tissues, or organs taken from or derived from any such plant, including without limitation, any seeds, leaves, stems, flowers, roots, single cells, gametes, cell
30 cultures, tissue cultures or protoplasts. "Plant material", as used herein refers to material that is obtained or derived from a plant. Products comprising plant material relate to food, feed or other products that are produced using plant material or can be contaminated by plant material. It is understood that, in the context of the present invention, such biological samples are tested for the presence of nucleic acids specific for a specific mutant *IND* allele, implying the presence of
35 nucleic acids in the samples. Thus the methods referred to herein for identifying a specific

mutant *IND* allele in biological samples, relate to the identification in biological samples of nucleic acids that comprise the specific mutant *IND* allele.

5 [169] The present invention also relates to the combination of specific *IND* alleles in one plant, to the transfer of one or more specific mutant *IND* allele(s) from one plant to another plant, to the plants comprising one or more specific mutant *IND* allele(s), the progeny obtained from these plants and to plant cells, plant parts, and plant seeds derived from these plants.

10 [170] In one embodiment, a method is provided for combining a suitable number of partial knockout *ind* alleles and/or full knockout *ind* alleles and/or different types of partial knockout *ind* alleles and/or full knockout *ind* alleles in a single dehiscent seed plant to alter the fruit dehiscence properties of the plant, in particular to reduce seed shattering, or delay seed shattering until after harvest, while maintaining at the same time an agronomically relevant treshability of the pods.

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[171] In one aspect, a method is provided for altering the fruit dehiscence properties, in particular for reducing seed shattering, or delaying seed shattering until after harvest, while maintaining at the same time an agronomically relevant treshability of the pods, of a *Brassica* plant comprising at least two *IND* genes, comprising the steps of:

- 20
- generating and/or selecting a *Brassica* plant comprising at least two *IND* genes, wherein at least two alleles of the at least two *IND* genes are partial knockout *ind* alleles, as described above,
 - selecting a plant with altered fruit dehiscence properties, in particular a plant wherein seed shattering is reduced or delayed until after harvest, while the pods maintain at the
- 25 same time an agronomically relevant treshability.

25

[172] In one embodiment of this aspect, the *Brassica* plant comprising at least two *IND* genes is a *Brassica napus* plant comprising an *IND-A1* and an *IND-C1* gene. In a particular aspect of this embodiment, the at least two partial knockout *ind* alleles are partial knockout *ind* alleles of

30 the *IND-C1* gene.

30

[173] In another aspect, the method further comprises the step of generating and/or selecting a *Brassica* plant comprising at least two *IND* genes, wherein at least two further alleles of the at least two *IND* genes are full knockout *ind* alleles, as described above. In one embodiment, the

35 *Brassica* plant comprising at least two *IND* genes is a *Brassica napus* plant comprising an *IND-*

AI and an *IND-C1* gene. In a particular aspect of this embodiment, the at least two partial knockout *ind* alleles are partial knockout *ind* alleles of the *IND-A1* gene and the at least two full knockout *ind* alleles are full knockout *ind* alleles of the *IND-C1* gene.

5 [174] In another embodiment of the invention, a method for making a hybrid *Brassica* crop plant or seed comprising at least two *IND* genes, in particular a hybrid *Brassica napus* plant or seed, wherein the fruit dehiscence properties of the plant or of the plant grown from the seed are altered, in particular wherein seed shattering is reduced or delayed until after harvest, while the pods maintain at the same time an agronomically relevant treshability, comprising the steps of:

- 10
- generating and/or identifying a first plant comprising a first partial knockout *ind* allele in homozygous state and a second plant comprising a second partial knockout *ind* allele in homozygous state, as described above,
 - crossing the first and the second plant and collecting F1 hybrid seeds from the cross comprising two partial knockout *ind* alleles of the at least two *IND* genes.

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[175] In a further embodiment of the invention, the first plant additionally comprises a first full knockout *ind* allele in homozygous state and the second plant additionally comprises a second full knockout *ind* allele in homozygous state, as described above, and F1 hybrid seeds comprising two partial knockout *ind* alleles and two full knockout *ind* alleles of the at least two
20 *IND* genes are collected.

20

[176] The possibility of using parent plants comprising a partial and/or a full knockout *ind* allele in homozygous state to produce hybrid seed from which plants can be grown that show reduced or delayed seed shattering, while maintaining at the same time an agronomically relevant treshability of the pods, provides an advantages over the use of one parent plant comprising two full knockout *ind* alleles in homozygous state and one parent plant comprising one full knockout *ind* allele state as described in WO09/068313 (claiming priority of European patent application EP 07023052), as both parent plants produce pods showing an agronomically relevant treshability, while the pods of the parent plant comprising two full knockout *ind* alleles
25 in homozygous state produces tube-like pods from which it is difficult to harvest the seeds.

30

[177] In one aspect of the invention, the first and the second partial knockout *ind* alleles are the same, such that the F1 hybrid seeds are homozygous for a partial knockout *ind* allele. In another aspect of the invention, the first and the second full knockout *ind* alleles are the same, such that
35 the F1 hybrid seeds are homozygous for a full knockout *ind* allele.

35

[178] Full knockout *ind* alleles (i.e., *IND* alleles the functional expression of which is completely abolished), such as those described in WO09/068313 (claiming priority of European patent application EP 07023052), and/or partial knockout *ind* alleles (i.e., *IND* alleles the functional expression of which is partially abolished) according to the invention can be combined according to standard breeding techniques.

[179] Partial and/or full knockout *ind* alleles can, for example, be combined in a single dehiscent seed plant by

- 10 (a) generating and/or identifying two or more plants each comprising one or more selected partial and/or full knockout *ind* alleles, as described above for the partial and in WO09/068313 (claiming priority of European patent application EP 07023052), for the full knockout *ind* alleles,
- 15 (b) crossing a first plant comprising one or more selected partial and/or full knockout *ind* alleles with a second plant comprising one or more other selected partial and/or full knockout *ind* alleles, collecting F1 seeds from the cross, and, optionally, identifying an F1 plant comprising one or more selected partial and/or full knockout *ind* alleles from the first plant with one or more selected partial and/or full knockout *ind* alleles from the second plant, as described above,
- 20 (c) optionally, repeating step (b) until an F1 plant comprising all selected partial and/or full knockout *ind* alleles is obtained,
- (d) optionally,
 - identifying an F1 plant, which is homozygous or heterozygous for a selected partial and/or full knockout *ind* allele by determining the zygosity status of the mutant *IND* alleles, as described above for the partial and in WO09/068313 (claiming priority of European patent application EP 07023052), for the full knockout *ind* alleles, or
 - generating plants which are homozygous for one or more of the selected partial and/or full knockout *ind* alleles by performing one of the following steps:
 - 25 - extracting doubled haploid plants from treated microspore or pollen cells of F1 plants comprising the one or more selected partial and/or full knockout *ind* alleles, as described above,
 - 30 - selfing the F1 plants comprising the one or more selected partial and/or full knockout *ind* allele(s) for one or more generations (*y*), collecting F1 *S_y* seeds from the selfings, and identifying F1 *S_y* plants, which are homozygous for the one or more partial and/or full knockout *ind* allele, as described above.

[180] Partial and/or full knockout *ind* alleles can, for example, be transferred from one dehiscent seed plant to another by

- 5 (a) generating and/or identifying a first plant comprising one or more selected partial and/or full knockout *ind* alleles, as described above, or generating the first plant by combining the one or more selected partial and/or full knockout *ind* alleles in one plant, as described above (wherein the first plant is homozygous or heterozygous for the one or more partial and/or full knockout *ind* alleles)
- 10 (b) crossing the first plant comprising the one or more partial and/or full knockout *ind* alleles with a second plant not comprising the one or more partial and/or full knockout *ind* alleles, collecting F1 seeds from the cross (wherein the seeds are heterozygous for a partial and/or full knockout *ind* allele if the first plant was homozygous for that partial and/or full knockout *ind* allele, and wherein half of the seeds are heterozygous and half of the seeds are azygous for, i.e. do not comprise, a partial and/or full knockout *ind* allele if the first plant was
- 15 heterozygous for that partial and/or full knockout *ind* allele), and, optionally, identifying F1 plants comprising one or more selected partial and/or full knockout *ind* alleles, as described above,
- (c) backcrossing F1 plants comprising one or more selected partial and/or full knockout *ind* alleles with the second plant not comprising the one or more selected partial and/or full
- 20 knockout *ind* alleles for one or more generations (x), collecting BCx seeds from the crosses, and identifying in every generation BCx plants comprising the one or more selected partial and/or full knockout *ind* alleles, as described above,
- (d) optionally, generating BCx plants which are homozygous for the one or more selected partial and/or full knockout *ind* alleles by performing one of the following steps:
- 25 - extracting doubled haploid plants from treated microspore or pollen cells of BCx plants comprising the one or more desired partial and/or full knockout *ind* allele(s), as described above,
- selfing the BCx plants comprising the one or more desired partial and/or full knockout *ind* allele(s) for one or more generations (y), collecting BCx Sy seeds from the selfings,
- 30 and identifying BCx Sy plants, which are homozygous for the one or more desired partial and/or full knockout *ind* allele, as described above.

[181] The first and the second dehiscent seed plant can be *Brassicaceae* plants, particularly *Brassica* plants, especially *Brassica napus* plants or plants from another *Brassica* crop species.

35 Alternatively, the first plant can be a *Brassicaceae* plant, particularly a *Brassica* plant, especially

a *Brassica napus* plant or a plant from another *Brassica* crop species, and the second plant can be a plant from a *Brassicaceae* breeding line, particularly from a *Brassica* breeding line, especially from a *Brassica napus* breeding line or from a breeding line from another *Brassica* crop species. "Breeding line", as used herein, is a preferably homozygous plant line distinguishable from other plant lines by a preferred genotype and/or phenotype that is used to produce hybrid offspring.

SEQUENCES

- 10 SEQ ID NO: 1: Coding DNA of the *IND-A1* gene encoding a wild-type IND-A1 protein from *Brassica napus*.
SEQ ID NO: 2: wild type IND-A1 protein encoded by SEQ ID NO: 1.
SEQ ID NO: 3: Coding DNA of the *IND-C1* gene encoding a wild-type IND-C1 protein from *Brassica napus*.
- 15 SEQ ID NO: 4: wild type IND-C1 protein encoded by SEQ ID NO: 3.
SEQ ID NO: 5: Genomic DNA of the *IND-A1* gene encoding a wild-type IND-A1 protein from *Brassica napus*.
SEQ ID NO: 6: wild type IND-A1 protein encoded by SEQ ID NO: 5.
SEQ ID NO: 7: Genomic DNA of the *IND-C1* gene encoding a wild-type IND-C1 protein from
- 20 *Brassica napus*.
SEQ ID NO: 8: wild type IND-C1 protein encoded by SEQ ID NO: 7.
SEQ ID NO: 9: Coding DNA of the *Arabidopsis IND1* gene.
SEQ ID NO: 10: *Arabidopsis* IND1 protein encoded by SEQ ID NO: 9.
SEQ ID NO: 11: Oligonucleotide for detection of IND-A1-EMS06 and -WT
- 25 SEQ ID NO: 12: Oligonucleotide for detection of IND-A1-EMS06
SEQ ID NO: 13: Oligonucleotide for detection of IND-A1-WT
SEQ ID NO: 14: Oligonucleotide for detection of IND-A1-EMS09 and -WT
SEQ ID NO: 15: Oligonucleotide for detection of IND-A1-EMS09
SEQ ID NO: 16: Oligonucleotide for detection of IND-A1-WT
- 30 SEQ ID NO: 17: Oligonucleotide for detection of IND-A1-EMS13 and -WT
SEQ ID NO: 18: Oligonucleotide for detection of IND-A1-EMS13
SEQ ID NO: 19: Oligonucleotide for detection of IND-A1-WT
SEQ ID NO: 20: Oligonucleotide for detection of IND-C1-EMS04 and -WT
SEQ ID NO: 21: Oligonucleotide for detection of IND-C1-EMS04
- 35 SEQ ID NO: 22: Oligonucleotide for detection of IND-C1-WT

SEQ ID NO: 23: Oligonucleotide for detection of IND-C1-EMS08 and -WT

SEQ ID NO: 24: Oligonucleotide for detection of IND-C1-EMS08

SEQ ID NO: 25: Oligonucleotide for detection of IND-C1-WT

SEQ ID NO: 26: Oligonucleotide for detection of IND-C1-EMS09 and -WT

5 SEQ ID NO: 27: Oligonucleotide for detection of IND-C1-EMS09

SEQ ID NO: 28: Oligonucleotide for detection of IND-C1-WT

Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard molecular biological techniques as described in Sambrook and Russell
10 (2001) *Molecular Cloning: A Laboratory Manual*, Third Edition, Cold Spring Harbor Laboratory Press, NY, in Volumes 1 and 2 of Ausubel *et al.* (1994) *Current Protocols in Molecular Biology*,
Current Protocols, USA and in Volumes I and II of Brown (1998) *Molecular Biology LabFax*,
Second Edition, Academic Press (UK). Standard materials and methods for plant molecular work
are described in *Plant Molecular Biology Labfax* (1993) by R.D.D. Croy, jointly published by
15 BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications, UK. Standard
materials and methods for polymerase chain reactions can be found in Dieffenbach and Dveksler
(1995) *PCR Primer: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, and in
McPherson *et al.* (2000) *PCR - Basics: From Background to Bench*, First Edition, Springer
Verlag, Germany. Standard procedures for AFLP analysis are described in Vos *et al.* (1995,
20 NAR 23:4407-4414) and in published EP patent application EP 534858.

EXAMPLES

Example 1 - Generation and isolation of partial knockout mutant *IND* alleles (*ind*)

25 Mutations in the *IND* genes depicted in SEQ ID NO: 1 or 3 and 5 or 7 of the sequence listing were generated and identified as follows:

- 30,000 seeds from an elite spring oilseed rape breeding line (M0 seeds) were preimbibed for two hours on wet filter paper in deionized or distilled water. Half of the seeds were exposed to 0.8% EMS and half to 1% EMS (Sigma: M0880) and incubated for 4 hours.
- 30 - The mutagenized seeds (M1 seeds) were rinsed 3 times and dried in a fume hood overnight. 30,000 M1 plants were grown in soil and selfed to generate M2 seeds. M2 seeds were harvested for each individual M1 plant.
- Two times 4800 M2 plants, derived from different M1 plants, were grown and DNA samples were prepared from leaf samples of each individual M2 plant according to the CTAB method
35 (Doyle and Doyle, 1987, *Phytochemistry Bulletin* 19:11-15).

- The DNA samples were screened for the presence of point mutations in the *IND* genes causing the substitution of amino acids in the IND proteins, particularly in the bHLH domain of the IND proteins, by direct sequencing by standard sequencing techniques (Agowa) and analyzing the sequences for the presence of the point mutations using the NovoSNP software (VIB Antwerp).
- The partial knockout mutant *IND* alleles (*ind*) indicated in Table 3a and b above were thus identified.

In conclusion, the above examples show how partial knockout mutant *IND* alleles can be generated and isolated. Also, plant material comprising such mutant alleles can be used to combine selected mutant *IND* alleles in a plant, as described in the following examples.

Example 2 - Identification of a *Brassica* plant comprising a partial knockout mutant *Brassica IND* allele

Brassica plants comprising the mutations in the *IND* genes identified in Example 1 were identified as follows:

- For each mutant *IND* gene identified in the DNA sample of an M2 plant, at least 50 M2 plants derived from the same M1 plant as the M2 plant comprising the *IND* mutation were grown and DNA samples were prepared from leaf samples of each individual M2 plant.
- The DNA samples were screened for the presence of the identified point *IND* mutation as described above in Example 1.
- Heterozygous and homozygous (as determined based on the electropherograms) M2 plants comprising the same mutation were selfed and M3 seeds were harvested.

Example 3 - Analysis of the fruit dehiscence properties of *Brassica* plants comprising a partial and/or full knockout mutant *Brassica IND* gene

To determine the correlation between the presence of partial and/or full knockout mutant *IND* genes in *Brassica* plants and the fruit dehiscence properties of the *Brassica* plants, the fruit dehiscence properties of *Brassica napus* plants comprising a partial knockout mutant *IND* gene in homozygous state alone or both a partial and a full knockout mutant *IND* gene in homozygous state were analyzed in the glass house and in the field and compared with the fruit dehiscence properties of *Brassica napus* plants comprising 2 to 4 full knockout *ind* alleles as described in WO09/068313 (claiming priority of European patent application EP 07023052) as follows:

- To examine whether and how the fruit valve margins and the dehiscence properties of seed pods were affected by the presence of partial and/or full knockout mutant *IND* genes, *ind* fruit was compared to wild-type fruit using the following macroscopic tests:

- (a) Inspection of the seed pods and plants in general with naked eye to determine differences in the phenotype of the pods and plants caused by the presence of different partial and/or full knockout mutant *IND* genes. Determination of the phenotype of the pods: When the pods were fully grown and filled, just prior to yellowing, the degree of sharpness of the zone that delineates the valve and beak at the zone where both valves are not touching anymore (at distal end of pod) of 5 random pods (from different plants if multiple plants per line are available) was assessed and attributed a score from 0 to 10 or from 1 to 5: 0 or 1, respectively, for a clear indentation and fine sharp zone that separates valve and beak; 1-3 or 2, respectively, for some indentation and clear, though more fuzzy, zone that separates valve from beak; 4-6 or 3, respectively, for valves and beak that are still well observable as two different tissues but with a very smooth transition between them; 7-9 or 4, respectively, for valves and beak that are barely observable as different tissues; 10 or 5, respectively, for a completely smoothed transition between valves and beak without any clear differentiation between both tissue types, i.e. the less indentation between the valve and the beak at the distal end of the pods the higher the score. A score of 0 or 1, respectively, (sharp indentation between the valve and the beak) corresponds to a wildtype phenotype of the pods, more specifically a pod shatter sensitive phenotype of the pods; a score of 1 to 9 or 2 to 4, respectively, (more gradual transition between the valve and the beak) corresponds to a pod shatter resistant phenotype of the pods, wherein seed shattering is significantly reduced or delayed while an agronomically relevant treshability of the pods is maintained, such that the pods may still be opened along the dehiscence zone by applying limited physical forces; and a score of 10 or 5, respectively, (no indentation between the valve and the beak) corresponds to a pod shatter resistant phenotype of the pods, wherein seed shattering is reduced or delayed to a degree which does not allow an agronomically relevant treshability of the pods anymore, such that the pods cannot be opened along the dehiscence zone by applying limited physical forces.
- (b) Manual Impact Test (MIT) to determine the increase in pod shatter resistance caused by the presence of different partial and/or full knockout mutant *IND* genes : The level of pod shatter resistance of *Brassica napus* lines comprising a partial knockout mutant *IND* gene in homozygous state alone or both a partial and a full knockout mutant *IND* gene in homozygous state and of *Brassica* lines comprising the corresponding wild type *IND* alleles was compared in a semi-quantitative way by determining the physical forces needed to open closed mature pods by manually applying torsion on the pods. The podshatter resistance of the pods was attributed a score from 1 to 5 based on this physical force: 1 for pods which completely open along the dehiscence zone at the slightest

torsion, 2-4 for pods which open only at the base of the dehiscence zone and need stronger torsion to open completely and 5 for pods which can only be crushed and do not open along the dehiscence zone.

- 5 (c) Random Impact Test (RIT) to determine the increase in pod shatter resistance caused by the presence of different partial and/or full knockout mutant *IND* genes : The level of pod shatter resistance of *Brassica napus* lines comprising a partial knockout mutant *IND* gene in homozygous state alone or both a partial and a full knockout mutant *IND* gene in homozygous state and of *Brassica* lines comprising the corresponding wild type *IND* alleles was compared in a quantitative way by determining the half life of samples of pods from both lines according to Bruce *et al.* (2002, *supra*). More specifically, two
10 replicate samples of 20 intact mature pods from each line were subjected to a RIT. 20 pods were placed together with six steel balls of 12.5 mm diameter in a cylindrical container of diameter 20 cm with its axis vertical. The container was then subjected to simple harmonic motion of frequency 4.98 Hz and of stroke 51 mm in the horizontal
15 plane. The pods, checked for soundness before the test, were shaken for cumulative times of 10, 20, 40, and, if more than 50% of pods remained intact, 80s. The drum was opened after each period and the number of closed pods counted. The pods were examined and classed as "closed" if the dehiscence zone of both valves was still closed. Thus the pods were classed as "opened" if one or both of the valves was detached, so that the seed had
20 been released. If the majority of the pods was broken or damaged without opening of the dehiscence zone, the sample was marked "uncountable" (indicated with * in Table 5b). To give each point equal weighing, the data were made evenly spaced in the independent variable, time, by adding 1 and taking \log_{10} . The percentage of pods opened p was transformed by the logit transformation, i.e. $\text{logit } p = \log_e(p/100-p)$. A linear model was
25 then fitted to the transformed time and percentage data and used to estimate the half-life.
- (d) Field tests to determine the relationship between pod shatter resistance, treshability and yield and the presence of certain mutant *IND* alleles in plants: The level of pod shatter resistance, treshability and yield of *Brassica* lines comprising the mutant *IND* alleles and *Brassica* lines comprising the corresponding wild type *IND* alleles was compared in a
30 semi-quantitative way by determining and comparing the level of seed shattering (SHAT), combiner harvest ability (CHA1) and treshing ability (CHA2) and in a quantitative way by determining and comparing seed yield per plot after combining (YLDP) and seed yield after treshing of straw (YLDS) in the field between plots with *ind* plants and plots with wild-type plants. The plots were attributed a score of 1-9 to indicate
35 the level of seed shattering on the plot before harvest: a score of 1 to indicate that

practically all plants on the plot were shattering before harvest to a score of 9 to indicate that practically no plants on the plot were shattering before harvest. The plots were attributed a score of 1-5 to indicate the level of combiner harvest ability on the plot: a score of 1, to 3 or to 5 to indicate that it was difficult, to feasible, or to easy, respectively, to harvest the plot with a combiner. The plots were attributed a score of 1-5 to indicate the level of threshing ability of the plot: a score of 1, to 3 or to 5 to indicate that it was difficult, to feasible, or to easy, respectively, to manually harvest the seed remaining in the straw after combiner harvest. The seed yield per plot after combining (YLDP; expressed in grams per plot) was determined by harvesting the seeds per plot with a combine harvester and weighing the seeds and the seed yield after threshing of straw (YLDS; expressed in weight% of the straw) was determined by manually harvesting the seeds remaining in the straw after seed harvest with the combine harvester.

- To examine more closely whether and how cells at the valve margin of seed pods are affected by the presence of partial and/or full knockout mutant *IND* genes, sections of *ind* fruit were compared to sections of wild-type fruit by microscopic evaluation of the seed pods:
 - Explants: Explants of about 3 mm taken from the center and the distal ends of pods of similar developmental stage (about 35 days after anthesis (DAA), a stage of development which closely corresponds to the onset of visible pericarp yellowing) and size were harvested from plants grown in a greenhouse (three pods for each genotype). One dehiscence zone was dissected from the pods.
 - Fixation: Fixation was done in 100mM K-phosphate buffer pH7 with 10% formalin and 0.25% glutaraldehyde for a total of 4 hours. Vacuum infiltration was done after 1 and 2 hours for 15 minutes. The fixative was renewed after each vacuum infiltration.
 - Dehydration: The specimen was rinsed 2 times 30 minutes with 100mM K-phosphate buffer pH7. Dehydration was done with technical ethanol diluted with 0.85% NaCl in water: 60 minutes (‘) in 50% ethanol, 90’ in 70% ethanol, 90’ in 80% ethanol, 90’ in 90% ethanol, 90’ in 95% ethanol, 90’ in 100% ethanol at room temperature
 - Embedding: Embedding was done with The Leica 7022-31731 Histo-resin or the Kulzer Histo-Technik 7100 (Heraeus) embedding kits, which are three component resin (a basic resin, an activator and a hardener) kits. The three components were used in the proportions as advised by the manufacturer as follows: the specimen were incubated for 4 hours in 50% ethanol/50% basic resin, overnight in 30% ethanol/70% basic resin (optional: at 4°C), for 2 to 4 hours in 100% basic resin, for one day in 100% basic resin after renewing the basic resin and vacuum infiltration for 20’ (optionally at 4°C), for one

- day in basic resin + activator (1%) (“infiltration medium”) after vacuum infiltration in this medium for 20 minutes. The specimen was washed with basic resin + activator (1%) + hardener (1 ml in 15 ml) (“embedding medium”). The embedding was done in flat embedding moulds (AGAR flat embedding moulds G3531 with cavities of about 300µl: 5 14 mm long x 6 mm wide x 4 mm deep): 100-125 µl of embedding medium/cavity was added, the embedding medium was polymerized at 55°C for about one hour, the tissue was put on the polymerized embedding medium (1 explant/cavity), the cavities were filed with embedding medium, the embedding medium was polymerized for 3 to 5 hours at 10 55°C, the moulds were cooled down, the plastic blocks were removed from the moulds and stored at room temperature in a sealed container (e.g. eppendorf tube).
- Sectioning: The plastic blocks were glued with the flat side on a 1cm³ perspex block and trimmed squarely around the specimen. 4 µm sections (3 to 4 explants per genotype, about 25 sections per explant) were cut with a ralph glass knife (made on -1 position of the histoknifemaker of Reichert-Jung using 6 mm thick glass rods under a cutting angle 15 of about 6°) on the microtome. The sections were attached on glass slides treated with Vectabond (Vector laboratories).
 - Demonstration of lignin: unstained sections mounted in Eukitt were examined using a microscope equipped for fluorescence (with Zeiss filter set 02). Lignin fluoresces clear bluish
 - Evaluation of histology: unstained sections were visualized by using DIC-Normaski or 20 autofluorescence (with Zeiss filter set 18 -- Excitation BP390-420; Emission LP450).

Plant material:

Progeny of a plant line comprising a full knockout mutation in the *IND-A1* gene (indicated as 25 *ind-a1^F*), in particular the *ind-a1-EMS01* allele described in WO09/068313 (claiming priority of European patent application EP 07023052) (indicated as *ind-a1-01* in Table 5), and a partial knockout mutation in the *IND-C1* gene (indicated as *ind-c1^P*), in particular the *ind-c1-EMS04*, -EMS08 and -EMS09 alleles indicated in Table 3b (indicated as *ind-c1-04*, -08, and -09 in Table 5), with genotype *ind-a1^F/ind-a1^F*, *ind-c1^P/ind-c1^P* (i.e., homozygous double mutant plants), 30 *IND-A1/IND-A1*, *ind-c1^P/ind-c1^P* (i.e., homozygous single mutant plants), and *IND-A1/IND-A1*, *IND-C1/IND-C1* (i.e., wildtype plants).

Progeny of a plant line comprising a partial knockout mutation in the *IND-A1* gene (indicated as 35 *ind-a1^P*), in particular the *ind-a1-EMS06*, -EMS09 and -EMS13 alleles indicated in Table 3a (indicated as *ind-a1-06*, -09, and -13 in Table 5), and a full knockout mutation in the *IND-C1*

gene (indicated as *ind-cl^F*), in particular the *ind-cl*-EMS01 allele and the *ind-cl*-EMS03 allele described in WO09/068313 (claiming priority of European patent application EP 07023052) (indicated as *ind-cl-01* and *-03* in Table 5), with genotype *ind-a1^P/ind-a1^P*, *ind-cl^F/ind-cl^F* (i.e., homozygous double mutant plants), *IND-A1/IND-A1*, *ind-cl^F/ind-cl^F* (i.e., homozygous single mutant plants), and *IND-A1/IND-A1*, *IND-C1/IND-C1* (i.e., wildtype plants).

Macroscopical evaluation:

- a) Inspection of the seed pods and plants with naked eye.
- The pods from homozygous double mutant *IND* sibling plants with genotype *ind-a1^F/ind-a1^F*, *ind-cl^P/ind-cl^P* or *ind-a1^P/ind-a1^P*, *ind-cl^F/ind-cl^F* showed a phenotype similar to the pods from plants comprising one full knockout *ind* allele in homozygous state and one full knockout *ind* allele in heterozygous state described in WO09/068313 (claiming priority of European patent application EP 07023052) (genotype: *ind-a1^F/ind-a1^F*, *IND-C1/ind-cl^F* or *IND-A1/ind-a1^F*, *ind-cl^F/ind-cl^F*, wherein *ind-a1^F* is a full knockout *ind-a1* allele, in particular the *ind-a1*-EMS01 or *ind-a1*-EMS05 allele described in WO09/068313 (claiming priority of European patent application EP 07023052), and wherein *ind-cl^F* is a full knockout *ind-cl* allele, in particular the *ind-cl*-EMS01 or *ind-cl*-EMS03 allele described in WO09/068313 (claiming priority of European patent application EP 07023052)). More specifically, the valve margins of the pods of these mutant *IND* sibling plants were in general better defined than in the homozygous double full knockout mutant *IND* sibling plants described in WO09/068313 (claiming priority of European patent application EP 07023052) (which showed a lack of proper valve margin definition, particularly apparent at both the proximal and distal end of the fruit, as compared to the pods from wild-type *IND* sibling plants), but the sharp indentation between the valve and the beak at the distal end of the pods in the wild-type sibling plants was still largely absent in these mutant plants as in the homozygous double full knockout *ind* sibling plants, which also showed a more gradual transition between valve and beak tissue (see also visual score in Table 5a for glasshouse grown plants and in Table 5b for field grown plants).
 - The pods from homozygous single mutant *IND* sibling plants (genotype: *IND-A1/IND-A1*, *ind-cl^P/ind-cl^P* or *ind-a1^P/ind-a1^P*, *IND-C1/IND-C1*) showed a pod morphology similar to pods from wild-type *IND* sibling plants, except for pods from homozygous single mutant *IND* sibling plants with genotype *IND-A1-EMS01/IND-A1-EMS01*, *ind-cl-EMS09/ind-cl-EMS09*, which showed an altered pod morphology similar to pods from the homozygous double mutant *IND* sibling plants with genotype *ind-a1^F/ind-a1^F*, *ind-cl^P/ind-cl^P* or *ind-a1^P/ind-a1^P*, *ind-cl^F/ind-cl^F* (see also visual score in Table 5a for glasshouse grown plants and

in Table 5b for field grown plants). It was further observed that the presence of the *ind-c1-EMS09* allele in heterozygous state in plants (genotype: *IND-A1/IND-A1*, *IND-C1/ind-c1-EMS09*) was sufficient to cause an altered pod morphology similar to pods from the homozygous double mutant *IND* sibling plants with genotype *ind-a1^F/ind-a1^F*, *ind-c1^P/ind-c1^P* or *ind-a1^P/ind-a1^P*, *ind-c1^F/ind-c1^F*. It is thought that the *ind-c1-EMS09* allele, which comprises a substitution mutation in a conserved amino acid of the basic DNA binding domain, might produce a dominant negative IND protein that is still capable of dimer formation, but not capable of binding to the bHLH binding site of the regulated gene(s).

b) Random Impact Test:

- 10 - Table 5 shows that the LD50 value was in general higher for pods from plants comprising a full knockout *ind-c1* allele in homozygous state and a partial knockout *ind-a1* allele in homozygous state than for pods from plants comprising a full knockout *ind-a1* allele in homozygous state and a partial knockout *ind-c1* allele in homozygous state indicating that the mutations in the *IND-C1* allele could have a stronger effect on pod shatter resistance than the mutations in the *IND-A1* allele.
- 15

Table 5a

Genotype	Visual pod Score (0-10)	LD50 (sec)	Corrected Lower 95%	Corrected Upper 95%
<i>IND-A1-06/IND-A1-06, IND-C1-01/IND-C1-01</i>	0	8.06	3.1	1.78
<i>ind-a1-06/ind-a1-06, IND-C1-01/IND-C1-01</i>	0	9.05	2.83	2.15
<i>ind-a1-06/ind-a1-06, ind-c1-01/ind-c1-01</i>	7	26.31	4.83	7.64
<i>IND-A1-06/IND-A1-06, IND-C1-03/IND-C1-03</i>	0	8.86	*	*
<i>ind-a1-06/ind-a1-06, IND-C1-03/IND-C1-03</i>	0	5.74	4.2	2.06
<i>ind-a1-06/ind-a1-06, ind-c1-03/ind-c1-03</i>	7	29.38	3.8	5.18
<i>IND-A1-09/IND-A1-09, IND-C1-01/IND-C1-01</i>	0	9.36	2.6	1.7
<i>ind-a1-09/ind-a1-09, IND-C1-01/IND-C1-01</i>	1	9.05	2.83	2.15
<i>ind-a1-09/ind-a1-09, ind-c1-01/ind-c1-01</i>	8	52.03	8.96	14.03
<i>IND-A1-09/IND-A1-09, IND-C1-03/IND-C1-03</i>	0	8.44	2.74	2.26
<i>ind-a1-09/ind-a1-09, IND-C1-03/IND-C1-03</i>	0	9.05	2.83	2.15
<i>ind-a1-09/ind-a1-09, ind-c1-03/ind-c1-03</i>	8.5	85.57	23.34	64.64
<i>IND-A1-13/IND-A1-13, IND-C1-01/IND-C1-01</i>	3	12.91	2.4	2.46
<i>ind-a1-13/ind-a1-13, IND-C1-01/IND-C1-01</i>	2	14.2	2.2	2.59
<i>ind-a1-13/ind-a1-13, ind-c1-01/ind-c1-01</i>	7	61.21	9.6	15.18
<i>IND-A1-13/IND-A1-13, IND-C1-03/IND-C1-03</i>	0	8.86	*	*
<i>ind-a1-13/ind-a1-13, IND-C1-03/IND-C1-03</i>	0	7.74	3.98	1.54
<i>ind-a1-13/ind-a1-13, ind-c1-03/ind-c1-03</i>	9	56.68	8.9	13.6
<i>IND-A1-01/IND-A1-01, IND-C1-04/IND-C1-04</i>	0	7.89	2.88	2
<i>IND-A1-01/IND-A1-01, ind-c1-04/ind-c1-04</i>	0	10.91	2.5	2
<i>ind-a1-01/ind-a1-01, ind-c1-04/ind-c1-04</i>	9	37.8	5.77	8.4
<i>IND-A1-01/IND-A1-01, IND-C1-08/IND-C1-08</i>	0	8.94	2.78	2.38
<i>IND-A1-01/IND-A1-01, ind-c1-08/ind-c1-08</i>	0	9.8	2.8	2.1

<i>ind-a1-01/ind-a1-01, ind-c1-08/ind-c1-08</i>	8.5	31.81	6.66	10.45
<i>IND-A1-01/IND-A1-01, IND-C1-09/IND-C1-09</i>	0	7.22	3.56	1.82
<i>IND-A1-01/IND-A1-01, ind-c1-09/ind-c1-09</i>	8.5	46.6	7.82	11.48
<i>ind-a1-01/ind-a1-01, ind-c1-09/ind-c1-09</i>	9	90.11	*	*

Table 5b

Genotype	Visual pod score (1-5)	Score based on physical force needed to open closed mature pods (1-5)	LD50 (sec)	
			field 1	field 2
<i>IND-A1-06/IND-A1-06, IND-C1-01/IND-C1-01</i>	1	1	9.7	7.2
<i>ind-a1-06/ind-a1-06, IND-C1-01/IND-C1-01</i>	1	1	6.2	8.3
<i>ind-a1-06/ind-a1-06, ind-c1-01/ind-c1-01</i>	2	2	17.0	16.6
<i>IND-A1-06/IND-A1-06, IND-C1-03/IND-C1-03</i>	1	1	6.5	6.6
<i>ind-a1-06/ind-a1-06, IND-C1-03/IND-C1-03</i>	1	1	7.4	5.3
<i>ind-a1-06/ind-a1-06, ind-c1-03/ind-c1-03</i>	3	2	15.3	12.4
<i>IND-A1-09/IND-A1-09, IND-C1-01/IND-C1-01</i>	1	1	7.5	6.9
<i>ind-a1-09/ind-a1-09, IND-C1-01/IND-C1-01</i>	1	1	5.4	7.2
<i>ind-a1-09/ind-a1-09, ind-c1-01/ind-c1-01</i>	3	4	60.1	77.0
<i>IND-A1-09/IND-A1-09, IND-C1-03/IND-C1-03</i>	1	1	6.6	6.2
<i>ind-a1-09/ind-a1-09, IND-C1-03/IND-C1-03</i>	1	1	7.7	7.0
<i>ind-a1-09/ind-a1-09, ind-c1-03/ind-c1-03</i>	3	4	49.8	63.0
<i>IND-A1-13/IND-A1-13, IND-C1-01/IND-C1-01</i>	1	1	11.7	10.7
<i>ind-a1-13/ind-a1-13, IND-C1-01/IND-C1-01</i>	1	1	10.7	7.9
<i>ind-a1-13/ind-a1-13, ind-c1-01/ind-c1-01</i>	3	3	19.1	22.9
<i>IND-A1-13/IND-A1-13, IND-C1-03/IND-C1-03</i>	1	1	5.4	5.7
<i>ind-a1-13/ind-a1-13, IND-C1-03/IND-C1-03</i>	1	1	9.2	8.3
<i>ind-a1-13/ind-a1-13, ind-c1-03/ind-c1-03</i>	3	3	10.2	38.6
<i>IND-A1-01/IND-A1-01, IND-C1-04/IND-C1-04</i>	1	1	6.5	7.4
<i>IND-A1-01/IND-A1-01, ind-c1-04/ind-c1-04</i>	1	2	9.5	7.2
<i>ind-a1-01/ind-a1-01, ind-c1-04/ind-c1-04</i>	3	5	87.7	126.6
<i>IND-A1-01/IND-A1-01, IND-C1-08/IND-C1-08</i>	1	1	9.7	8.3
<i>IND-A1-01/IND-A1-01, ind-c1-08/ind-c1-08</i>	1	1	4.9	9.0
<i>ind-a1-01/ind-a1-01, ind-c1-08/ind-c1-08</i>	3	3	14.9	23.7
<i>IND-A1-01/IND-A1-01, IND-C1-09/IND-C1-09</i>	1	1	9.1	8.3
<i>IND-A1-01/IND-A1-01, ind-c1-09/ind-c1-09</i>	3	2	7.9	8.3
<i>ind-a1-01/ind-a1-01, ind-c1-09/ind-c1-09</i>	5	5	*	*

* : uncountable

5 c) Field tests

Table 5c shows the level of seed shattering (SHAT), combiner harvest ability (CHA1), threshing ability (CHA2), seed yield per plot after combining (YLDP) and seed yield after threshing of straw (YLDS) determined as described above for field plots with *ind* plants and wild-type plants as indicated. The YieldWTseg% value represents the YLDP as a percentage of the wildtype segregant within one segregating population.

Table 5c
Genotype

Genotype	SHAT (1-9)	CHA1 (1-5)	CHA2 (1-5)	YLDP (in grams per plot)	Yield WTSeg %	YLDS (in wt% of straw)
<i>IND-A1-06/IND-A1-06, IND-C1-01/IND-C1-01</i>	8.3	5.0	5.0	2263.3	100	0.4
<i>ind-a1-06/ind-a1-06, IND-C1-01/IND-C1-01</i>	8.4	4.6	5.0	2274.9	101	0.3
<i>ind-a1-06/ind-a1-06, ind-c1-01/ind-c1-01</i>	8.7	4.4	4.9	2525.1	112	1.1
<i>IND-A1-06/IND-A1-06, IND-C1-03/IND-C1-03</i>	8.6	4.6	4.9	2102.0	100	0.5
<i>ind-a1-06/ind-a1-06, IND-C1-03/IND-C1-03</i>	8.7	4.8	5.0	2292.7	109	0.4
<i>ind-a1-06/ind-a1-06, ind-c1-03/ind-c1-03</i>	8.8	4.1	4.6	2276.2	108	1.3
<i>IND-A1-09/IND-A1-09, IND-C1-01/IND-C1-01</i>	8.3	5.0	4.9	1964.2	100	0.3
<i>ind-a1-09/ind-a1-09, IND-C1-01/IND-C1-01</i>	8.0	4.7	5.0	1872.0	95	0.4
<i>ind-a1-09/ind-a1-09, ind-c1-01/ind-c1-01</i>	9.0	2.7	3.8	2323.3	118	5.7
<i>IND-A1-09/IND-A1-09, IND-C1-03/IND-C1-03</i>	8.6	4.8	5.0	2168.9	100	0.5
<i>ind-a1-09/ind-a1-09, IND-C1-03/IND-C1-03</i>	8.3	4.7	5.0	1985.6	92	0.4
<i>ind-a1-09/ind-a1-09, ind-c1-03/ind-c1-03</i>	9.0	1.9	3.6	1726.7	80	13.6
<i>IND-A1-13/IND-A1-13, IND-C1-01/IND-C1-01</i>	8.3	4.8	5.0	1977.1	100	0.4
<i>ind-a1-13/ind-a1-13, IND-C1-01/IND-C1-01</i>	8.4	4.2	4.9	1929.3	98	0.5
<i>ind-a1-13/ind-a1-13, ind-c1-01/ind-c1-01</i>	8.9	3.6	4.7	2445.6	124	2.0
<i>IND-A1-13/IND-A1-13, IND-C1-03/IND-C1-03</i>	8.3	4.2	5.0	1885.1	100	0.4
<i>ind-a1-13/ind-a1-13, IND-C1-03/IND-C1-03</i>	8.3	4.8	5.0	2137.8	113	0.6
<i>ind-a1-13/ind-a1-13, ind-c1-03/ind-c1-03</i>	8.9	2.8	3.9	2120.9	113	4.8
<i>IND-A1-01/IND-A1-01, IND-C1-04/IND-C1-04</i>	8.8	4.9	4.8	2120.4	100	0.6
<i>IND-A1-01/IND-A1-01, ind-c1-04/ind-c1-04</i>	8.6	4.8	5.0	2136.4	101	0.6
<i>ind-a1-01/ind-a1-01, ind-c1-04/ind-c1-04</i>	9.0	1.8	2.8	1437.0	68	19.1
<i>IND-A1-01/IND-A1-01, IND-C1-08/IND-C1-08</i>	8.0	4.8	5.0	2250.4	100	0.6
<i>IND-A1-01/IND-A1-01, ind-c1-08/ind-c1-08</i>	8.3	4.3	4.9	2131.3	95	0.5
<i>ind-a1-01/ind-a1-01, ind-c1-08/ind-c1-08</i>	8.9	3.0	4.1	2385.1	106	2.5
<i>IND-A1-01/IND-A1-01, IND-C1-09/IND-C1-09</i>	8.7	4.9	5.0	2080.0	100	0.4
<i>IND-A1-01/IND-A1-01, ind-c1-09/ind-c1-09</i>	8.7	4.6	4.6	2447.8	118	1.0
<i>ind-a1-01/ind-a1-01, ind-c1-09/ind-c1-09</i>	9.0	1.1	1.8	589.6	28	28.4

Microscopical evaluation:

- 5 - The pods from homozygous double mutant *IND* sibling plants with genotype *ind-a1^F/ind-a1^F*, *ind-c1^P/ind-c1^P* or *ind-a1^P/ind-a1^P*, *ind-c1^F/ind-c1^F* and the pods from homozygous single mutant *IND* sibling plants with genotype *IND-A1-EMS01/IND-A1-EMS01*, *ind-c1-EMS09/ind-c1-EMS09*, grown under greenhouse conditions, showed at their distal ends lignification throughout the complete dehiscence zone and a poor differentiation of cells belonging to the dehiscence zone from neighboring cell types, such as the vascular tissue cells and the lignified layer of cells normally found at the inner pod wall (i.e. the *enb* cells).
10 At the center of the pods, lignification did not occur throughout the complete dehiscence

Plants containing *ind* are selected using molecular markers for the mutant *IND* allele (*ind*). Individual BC3-6 S1 plants that are homozygous for the mutant *IND* allele (*ind / ind*) are selected using molecular markers for the mutant and the wild-type *IND* alleles. These plants are then used for seed production.

5

To select for plants comprising a point mutation in an *IND* allele, direct sequencing by standard sequencing techniques known in the art, such as those described in Example 1, can be used.

10

Alternatively, PCR assays can be developed to discriminate plants comprising a specific point mutation in an *IND* allele from plants not comprising that specific point mutation. The following discriminating PCR assays can thus be developed to detect the presence or absence and the zygosity status of the mutant alleles identified in Example 1 (see Table 3a and 3b):

- Template DNA:

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- Genomic DNA isolated from leaf material of homozygous or heterozygous mutant *Brassica* plants (comprising a mutant *IND* allele, called hereinafter "IND-Xx-EMSXX").

- Wild type DNA control: Genomic DNA isolated from leaf material of wild type *Brassica* plants (comprising the wild type equivalent of the mutant *IND* allele, called hereinafter "IND-Xx-WT").

20

- Positive DNA control: Genomic DNA isolated from leaf material of homozygous mutant *Brassica* plants known to comprise IND-Xx-EMSXX.

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- Generally, each primer set consists of one primer specific for both the mutant and the wild type target gene (e.g. primer specific for both the IND-A1-EMS06 and the IND-A1-WT allele) and one primer specific for the nucleotide difference (e.g. primer specific for either the IND-A1-EMS06 allele or the IND-A1-WT allele). Usually, the last nucleotide of the latter primer matches with the nucleotide difference, but one (or more) additional target specific nucleotide(s) may be added to improve the annealing between the primer and its target sequence.

30

- PCR mix: 2.5 µl 10x PCR buffer (15mM MgCl₂), 0.25 µl dNTP's (20 mM), 1 µl forward primer (10 µM), 1 µl reverse primer(10 µM), 0.25 µl Taq-polymerase (5U/µl), 19.5 µl Milli-Q H₂O, 0.5 µl DNA (20-50 ng/µl) = Total volume of 25 µl;

35

- Thermocycling profile: 4 min at 95°C; 30x [1min at 95°C (denaturation) and 1 min at annealing temperature and 2 min at 72°C (elongation)]; 5min at 72°C; cool down to 4°C. The optimal annealing temperature can be determined by temperature gradient PCR wherein the annealing temperature can be varied e.g. between 57°C to 70°C on a MJ Research thermocycler PTC-200 (Biozym). The optimal annealing temperature for the wild type *IND*

specific primers is that temperature at which a clear PCR fragment of the expected size can be detected (as described below) for the DNA sample from the wild type *Brassica* plant and not for the DNA sample from the mutant *Brassica* plant. The optimal annealing temperature for the mutant *IND* specific primers is that temperature at which a clear PCR fragment of the expected size can be detected (as described below) for the DNA sample from the mutant *Brassica* plant and not for the DNA sample from the wild type *Brassica* plant.

- After amplification, 5 µl loading dye (orange dye) is added to 15µl of the PCR samples and the samples are loaded on a 1.5% agarose gel.

- The banding patterns obtained after amplification of genomic DNA of mutant *Brassica* plants are evaluated as follows:

- Data from DNA samples isolated from leaf material of the mutant *Brassica* plants within a single PCR run and a single PCR mix should not be accepted unless:

- the wild-type DNA control shows the PCR fragment of the expected size for the *IND - Xx-WT* specific PCR assay and no PCR fragment of the expected size for the *IND-Xx-EMSXX* specific PCR assay

- the positive DNA control shows the PCR fragment of the expected size for the *IND-Xx-EMSXX* specific PCR assay and no PCR fragment of the expected size for the *IND-Xx-WT* specific PCR assay

- Lanes showing no PCR product of the expected size for the *IND-Xx-WT* specific PCR assay and the PCR fragment of the expected size for the *IND-Xx-EMSXX* specific PCR assay, indicate that the corresponding plant from which the genomic template DNA was prepared, is a homozygous mutant for *IND-Xx-EMSXX*.

- Lanes showing the PCR fragment of the expected size for the *IND -Xx-WT* specific PCR assay and the *IND-Xx-EMSXX* specific PCR assay, indicate that the corresponding plant from which the genomic template DNA was prepared, is a heterozygous mutant for *IND-Xx-EMSXX*.

- Lanes showing the PCR fragment of the expected size for the *IND -Xx-WT* specific PCR assay and no PCR product of the expected size for the *IND-Xx-EMSXX* specific PCR assay, indicate that the corresponding plant from which the genomic template DNA was prepared, is a wild type plant.

Alternatively, InvaderTM technology (Third Wave Agbio) can be used to discriminate plants comprising a specific point mutation in an *IND* allele from plants not comprising that specific point mutation. The following discriminating InvaderTM probes were thus developed to detect the

presence or absence and the zygosity status of the mutant alleles identified in Example 4 (see Table 6:

- Probes specific for the mutant or corresponding wild-type target *IND* gene (indicated as “5’ flap1-x” and “5’ flap2-x”, respectively) and “invading” probes which can be used in combination with them are indicated in Table 6. Generally, each probe set consists of one probe specific for the mutant or the wild type target gene of which the first nucleotide after the 5’ flap sequence matches with the nucleotide difference (underlined nucleotide in Table 6) (the so-called “primary probe”; e.g. the probe with SEQ ID NO: 12 is specific for IND-A1-EMS06 and the probe with SEQ ID NO: 13 is specific for IND-A1-WT) and one probe specific for the nucleotides upstream of the nucleotide difference (the so-called “invader® oligo”; e.g. the probe with SEQ ID NO: 11 is specific for the nucleotides upstream of the nucleotide difference between IND-A1-EMS06 and IND-A1-WT). The last nucleotide of the latter primer may match with the nucleotide difference in the mutant (as indicated by the bold nucleotides in Table 6), but other nucleotides may be used as well for this last nucleotide as long as the primary probe and the invader® oligo are still able to form a single base overlap when hybridized to the target DNA to generate the specific invasive structure recognized by the Cleavase® enzymes (Third Wave Agbio).
- The Invader™ assay procedure and interpretation of the data are performed as prescribed by the manufacturer (Third Wave Agbio). Briefly, the nucleotide sequences indicated as “flap1” and “flap2” in Table 6 represent the sequences of the 5’ “flaps” which are cleaved from the primary probes in the primary phase of the Invader™ assay and which are complementary to sequences in FRET™ cassette 1 and 2, respectively, and not complementary to the target mutant or wild type sequences. If the primary probes are cleaved in the primary phase and the flap1-probe and/or flap2-probe hybridise to FRET™ cassette 1 and 2, respectively, in the secondary phase, a signal is generated indicative of the presence in the sample of the mutant or corresponding wild-type target *IND* gene, respectively.

Table 6

Allele No.	Probes	
IND-A1-EMS06	5’ CGTAAGGGTAAGCGACGACCCTCAGACGT 3’	(SEQ ID NO: 11)
	5’ flap1- <u>A</u> TGGTGGCTCGTCG 3’	(SEQ ID NO: 12)
IND-A1-WT	5’ CGTAAGGGTAAGCGACGACCCTCAGACGT 3’	(SEQ ID NO: 11)
	5’ flap2- <u>G</u> TGGTGGCTCGTC 3’	(SEQ ID NO: 13)
IND-A1-EMS09	5’ GGAGGCAGTGTCCATCTTTGCACCGCA 3’	(SEQ ID NO: 14)
	5’ flap1- <u>T</u> TGGCACCATCCTCT 3’	(SEQ ID NO: 15)
IND-A1-WT	5’ GGAGGCAGTGTCCATCTTTGCACCGCA 3’	(SEQ ID NO: 14)
	5’ flap2- <u>C</u> TGGCACCATCCTCT 3’	(SEQ ID NO: 16)
IND-A1-EMS13	5’ CCTGCCGTTTCAAGAACTTGGTGTAGCGGATGT 3’	(SEQ ID NO: 17)

IND-A1-WT	5' flap1- <u>A</u> CTTCGTCGAGCATG 3'	(SEQ ID NO: 18)
	5' GGAGGCAGTGTCCATCTTTGCACCGCA 3'	(SEQ ID NO: 17)
	5' flap2- <u>G</u> CTTCGTCGAGCATG 3'	(SEQ ID NO: 19)
IND-C1-EMS04	5' CATCCTCTTCAATATCCGGATCTTCTCGCTTATCC TTTCTCTACT 3'	(SEQ ID NO: 20)
IND-C1-WT	5' flap1- <u>A</u> CCGACGAGCCAC 3'	(SEQ ID NO: 21)
	5' CATCCTCTTCAATATCCGGATCTTCTCGCTTATCC TTTCTCTACT 3'	(SEQ ID NO: 20)
	5' flap2- <u>G</u> CCGACGAGCCAC 3'	(SEQ ID NO: 22)
IND-C1-EMS08	5' CGTAAGGGTAAGCGAGGACCCCCAGA 3'	(SEQ ID NO: 23)
IND-C1-WT	5' flap1- <u>T</u> GGTGGTGGCTCG 3'	(SEQ ID NO: 24)
	5' CGTAAGGGTAAGCGAGGACCCCCAGA 3'	(SEQ ID NO: 23)
	5' flap2- <u>C</u> GGTGGTGGCTCG 3'	(SEQ ID NO: 25)
IND-C1-EMS09	5' CGAGGACCCCCAGACGGTGGTGT 3'	(SEQ ID NO: 26)
IND-C1-WT	5' flap1- <u>A</u> CTCGTCGGCGTAG 3'	(SEQ ID NO: 27)
	5' CGAGGACCCCCAGACGGTGGTGT 3'	(SEQ ID NO: 26)
	5' flap2- <u>G</u> CTCGTCGGCGT 3'	(SEQ ID NO: 28)

CLAIMS

1. A *Brassica* plant comprising at least two *IND* genes, or a cell, part, seed or progeny thereof, characterized in that it comprises at least two partial knockout mutant *IND* alleles in its genome.
5
2. A plant according to claim 1, wherein the *IND* genes are *IND-A1* or *IND-C1* genes.
3. A plant according to claim 1 or 2, wherein the *IND* genes comprise a nucleic acid molecule selected from the group consisting of:
 - (a) a nucleic acid molecule which comprises at least 90% sequence identity to SEQ ID NO: 1, SEQ ID NO: 3 from the nucleotide at position 46 to the nucleotide at position 633, SEQ ID NO: 3, SEQ ID NO: 5, or SEQ ID NO: 7;
10
 - (b) a nucleic acid molecule encoding an amino acid sequence comprising at least 90% sequence identity to SEQ ID NO: 2, SEQ ID NO: 4 from the amino acid at position 16 to the amino acid at position 21 or SEQ ID NO: 4.
- 15 4. A plant according to claim 2 or 3, wherein the partial knockout mutant *IND* alleles are mutant *IND* alleles of the *IND-C1* gene.
5. A plant according to any one of the preceding claims, wherein the partial knockout mutant *IND* alleles are selected from the group consisting of *ind-a1-EMS06*, *ind-a1-EMS09*, *ind-a1-EMS13*, *ind-c1-EMS04*, *ind-c1-EMS08* and *ind-c1-EMS09*.
- 20 6. A plant according to any one of the preceding claims, which further comprises at least one full knockout mutant *IND* allele in its genome.
7. A plant according to claim 6, wherein the full knockout mutant *IND* allele is a mutant *IND* allele of the *IND-C1* gene.
8. A plant according to claim 6 or 7, wherein the full knockout mutant *IND* allele is selected from the group consisting of *ind-a1-EMS01*, *ind-a1-EMS05*, *ind-c1-EMS01* and *ind-c1-EMS03*.
25
9. A plant according to any one of the preceding claims, which is homozygous for the partial and/or for the full knockout mutant *IND* allele.
10. A plant according to any one of the preceding claims, which produces a significantly reduced amount of functional *IND* protein compared to the amount of functional *IND* protein produced by a corresponding plant not comprising mutant *IND* alleles.
30
11. A plant according to any one of the preceding claims, wherein the seed shattering of the plant is significantly reduced or delayed compared to the seed shattering of a corresponding plant not comprising mutant *IND* alleles.

12. A plant according to claim 11, which maintains an agronomically relevant treshability of the pods.
13. A plant according to any one of the preceding claims, which is a plant from a *Brassica* crop species, preferably *Brassica napus*, *Brassica juncea*, *Brassica carinata*, *Brassica rapa* or
5 *Brassica oleracea*.
14. A plant according to any one of the preceding claims, which is a plant from a *Brassica* oilseed species, preferably *Brassica napus*, *Brassica juncea* or *Brassica rapa*.
15. A plant, or a cell, part, seed or progeny thereof, comprising at least one partial knockout mutant allele of an *IND* gene in its genome, wherein the *IND* gene comprises a nucleic acid
10 molecule selected from the group consisting of:
- (a) a nucleic acid molecule which comprises at least 90% sequence identity to SEQ ID NO: 1, SEQ ID NO: 3 from the nucleotide at position 46 to the nucleotide at position 633, SEQ ID NO: 3, SEQ ID NO: 5, or SEQ ID NO: 7;
- (b) a nucleic acid molecule encoding an amino acid sequence comprising at least 90%
15 sequence identity to SEQ ID NO: 2, SEQ ID NO: 4 from the amino acid at position 16 to the amino acid at position 21 or SEQ ID NO: 4.
16. A plant according to claim 15, wherein the partial knockout mutant *IND* allele is selected from the group consisting of *ind-a1-EMS06*, *ind-a1-EMS09*, *ind-a1-EMS13*, *ind-cl-EMS04*, *ind-cl-EMS08* and *ind-cl-EMS09*.
- 20 17. A plant according to claim 15 or 16, wherein the mutant *IND* allele is derived from a plant of a *Brassica* species.
18. A plant according to any one of claims 15 to 17, which is a plant from a *Brassica* species.
19. A seed pod obtainable from a plant according to any one of claims 1 to 18.
20. A partial knockout mutant allele of an *IND* gene, wherein the *IND* gene comprises a nucleic
25 acid molecule selected from the group consisting of:
- (a) a nucleic acid molecule which comprises at least 90% sequence identity to SEQ ID NO: 1, SEQ ID NO: 3 from the nucleotide at position 46 to the nucleotide at position 633, SEQ ID NO: 3, SEQ ID NO: 5, or SEQ ID NO: 7;
- (b) a nucleic acid molecule encoding an amino acid sequence comprising at least 90%
30 sequence identity to SEQ ID NO: 2, SEQ ID NO: 4 from the amino acid at position 16 to the amino acid at position 21 or SEQ ID NO: 4.
21. An mutant allele according to claim 20, which is selected from the group consisting of *ind-a1-EMS06*, *ind-a1-EMS09*, *ind-a1-EMS13*, *ind-cl-EMS04*, *ind-cl-EMS08* and *ind-cl-EMS09*.

22. An mutant allele according to any one of claims 20 to 21, which is derived from a plant of a *Brassica* species, preferably from a *Brassica* crop species or a *Brassica* oilseed species.
23. A mutant IND protein encoded by a mutant allele according to any one of claims 20 to 22.
24. A method for identifying a mutant *IND* allele according to any one of claims 20 to 22 in a biological sample comprising determining the presence of a mutant *IND* specific region in a nucleic acid present in the biological sample.
25. A method according to claim 24, which further comprises subjecting the biological sample to a polymerase chain reaction assay using a set of at least two primers, said set being selected from the group consisting of:
- 10 - a set of primers, wherein one of said primers specifically recognizes the 5' flanking region of the mutant *IND* allele and the other of said primers specifically recognizes the 3' flanking region of the mutant *IND* allele, respectively,
 - a set of primers, wherein one of said primers specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele and the other of said primers specifically recognizes the mutation region of the mutant *IND* allele,
 - 15 - a set of primers, wherein one of said primers specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele and the other of said primers specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the mutant *IND* allele, respectively.
- 20 26. A method according to claim 25, wherein
- said primer which specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele consist of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or
 - 25 - said primer which specifically recognizes the mutation region of the mutant *IND* allele consists of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or
 - said primer which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele consists of a nucleotide sequence
 - 30 of 17 to 200 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof, wherein said 17 to 200 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences.

27. A method according to claim 25, wherein

- said primer which specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele comprises at its extreme 3' end a nucleotide sequence of at least 17 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or
- said primer which specifically recognizes the mutation region of the mutant *IND* allele comprises at its extreme 3' end a nucleotide sequence of at least 17 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or
- said primer which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele comprises at its extreme 3' end a nucleotide sequence of at least 17 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof, wherein said 3'-located 17 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences.

28. A method according to claim 24, which further comprises subjecting the biological sample to an hybridization assay using a set of specific probes comprising at least one specific probe, said set being selected from the group consisting of :

- a set of specific probes, wherein one of said probes specifically recognizes the 5' flanking region of the mutant *IND* allele, and the other of said probes specifically recognizes the 3' flanking region of the mutant *IND* allele,
- a set of specific probes, wherein one of said probes specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele, and the other of said probes specifically recognizes the mutation region of the mutant *IND* allele,
- a set of specific probes, wherein one of said probes specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele and the other of said probes specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the mutant *IND* allele, respectively,
- a specific probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele.

29. A method according to claim 28, wherein

- said probe which specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected

- from the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or a sequence having at least 80% sequence identity therewith, or
- said probe which specifically recognizes the mutation region of the mutant *IND* allele consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or a sequence having at least 80% sequence identity therewith, or
 - said probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof, respectively, wherein said 13 to 1000 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences, or a sequence having at least 80% sequence identity therewith.

30. A method according to claim 28, wherein

- said probe which specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or
- said probe which specifically recognizes the mutation region of the mutant *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or
- said probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof, respectively, wherein said at least 13 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences.

31. A method according to any one of claims 25 to 30, wherein

- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 929 or 931 to 1622 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 930 of SEQ ID NO: 5 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 930 or 930 to 1622 or of the complement thereof, respectively, or

- 5
- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 995 or 997 to 1622 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 996 of SEQ ID NO: 5 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 996 or 996 to 1622 or of the complement thereof, respectively, or
 - 10 - said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1035 or 1037 to 1622 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 1036 of SEQ ID NO: 5 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1036 or 1036 to 1622 or of the complement thereof, respectively, or
 - 15 - said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 902 or 904 to 1593 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 903 of SEQ ID NO: 7 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 903 or 903 to 1593 or of the complement thereof, respectively, or
 - 20 - said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 910 or 912 to 1593 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 911 of SEQ ID NO: 7 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 911 or 911 to 1593 or of the complement thereof, respectively, or
 - 25 - said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 919 or 921 to 1593 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 920 of SEQ ID NO: 7 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 920 or 920 to 1593 or of the complement thereof, respectively.
- 30
32. A method according to any one of claims 28 to 31, wherein said set of probes is selected from the group consisting of:
- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 11 and/or one probe comprising the sequence of SEQ ID NO: 12,

- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 14 and/or one probe comprising the sequence of SEQ ID NO: 15,
 - a set of probes comprising one probe comprising the sequence of SEQ ID NO: 17 and/or one probe comprising the sequence of SEQ ID NO: 18,
 - 5 - a set of probes comprising one probe comprising the sequence of SEQ ID NO: 20 and/or one probe comprising the sequence of SEQ ID NO: 21,
 - a set of probes comprising one probe comprising the sequence of SEQ ID NO: 23 and/or one probe comprising the sequence of SEQ ID NO: 24,
 - a set of probes comprising one probe comprising the sequence of SEQ ID NO: 26 and/or
 - 10 one probe comprising the sequence of SEQ ID NO: 27.
33. A method for determining the zygosity status of a mutant *IND* allele according to any one of claims 20 to 22 in a plant, or a cell, part, seed or progeny thereof, comprising determining the presence of a mutant and/or a corresponding wild type *IND* specific region in the genomic DNA of said plant, or a cell, part, seed or progeny thereof.
- 15 34. A method according to claim 33, which further comprises subjecting the genomic DNA of said plant, or a cell, part, seed or progeny thereof, to a polymerase chain reaction assay using a set of at least two or at least three primers, wherein at least two of said primers specifically recognize the wild type *IND* allele, said at least two primers being selected from the group consisting of:
- 20 - a first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second primer which specifically recognizes the 3' or 5' flanking region of the mutant and the wild type *IND* allele, respectively,
 - a first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second primer which specifically recognizes the mutation
 - 25 region of the wild type *IND* allele,
 - a first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second primer which specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the wild type *IND* allele, respectively, and
- 30 wherein at least two of said primers specifically recognize the mutant *IND* allele, said at least two primers being selected from the group consisting of:
- the first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and the second primer which specifically recognizes the 3' or 5' flanking region of the mutant and the wild type *IND* allele, respectively,

- the first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a third primer which specifically recognizes the mutation region of the mutant *IND* allele,
- the first primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a third primer which specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the mutant *IND* allele, respectively.

35. A method according to claim 34, wherein

- said primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele consist of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant and the wild type *IND* allele or from the complement thereof, respectively, or
- said primers which specifically recognizes the mutation region of the mutant or the wild type *IND* allele consists of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from the mutation sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or
- said primers which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele, consists of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele or from the complement thereof, respectively, wherein said 17 to 200 consecutive nucleotides are not derived exclusively from either the mutation region or from the flanking sequences.

36. A method according to claim 34, wherein

- said primer which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele comprises at its extreme 3' end a nucleotide sequence of 17 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant and the wild type *IND* allele or from the complement thereof, respectively, or
- said primers which specifically recognizes the mutation region of the mutant or the wild type *IND* allele comprises at its extreme 3' end a nucleotide sequence of 17 consecutive nucleotides selected from the mutation sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or
- said primers which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele comprises at its extreme 3' end a nucleotide sequence of 17 consecutive nucleotides

selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele or from the complement thereof, respectively, wherein said 3'-located 17 consecutive nucleotides are not derived exclusively from either the mutation site or region or from the flanking sequences.

37. A method according to claim 33, which further comprises subjecting the genomic DNA of said plant, or a cell, part, seed or progeny thereof, to an hybridization assay using a set of at least two specific probes, wherein at least one of said specific probes specifically recognizes the wild type *IND* allele, said at least one probe selected from the group consisting of:

- a first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second probe which specifically recognizes the 3' and 5' flanking region of the mutant and the wild type *IND* allele, respectively,
- a first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second probe which specifically recognizes the mutation region of the wild type *IND* allele,
- a first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a second probe which specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the wild type *IND* allele, respectively,
- a probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the wild type *IND* allele, and

wherein at least one of said specific probes specifically recognize(s) the mutant *IND* allele, said at least one probe selected from the group consisting of:

- the first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and the second probe which specifically recognizes the 3' or 5' flanking region of the mutant and the wild type *IND* allele, respectively,
- the first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a third probe which specifically recognizes the mutation region of the mutant *IND* allele,
- the first probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, and a third probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele,
- a probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele.

38. A method according to claim 37, wherein

- said probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or a sequence having at least 80% sequence identity therewith, or
- said probe which specifically recognizes the mutation region of the mutant or the wild type *IND* allele consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from the sequence of the mutation region of the mutant or the wild type *IND* allele, respectively, or a sequence having at least 80% sequence identity therewith, or
- said probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele, respectively, or a sequence having at least 80% sequence identity therewith, wherein said 13 to 1000 consecutive nucleotides are not derived exclusively from either the mutation site or region or from the flanking sequences.

39. A method according to claim 37, wherein

- said probe which specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or
- said probe which specifically recognizes the mutation region of the mutant or the wild type *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from the mutation sequence of the mutant or the wild type *IND* allele or from the complement thereof, or
- said probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele or from the complement thereof, respectively, wherein said at least 13 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences.

40. A method according to any one of claims 34 to 39, wherein

- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 929 or 931 to 1622 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 930 of SEQ ID NO: 5 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence a or the complement thereof; said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 930 or 930 to 1622 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 929 followed by a or a followed by the nucleotide sequence SEQ ID NO: 5 from nucleotide 931 to 1622 or of the complement thereof, respectively, or
- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 995 or 997 to 1622 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 996 of SEQ ID NO: 5 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence a or the complement thereof; said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 996 or 996 to 1622 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 995 followed by a or a followed by the nucleotide sequence SEQ ID NO: 5 from nucleotide 997 to 1622 or of the complement thereof, respectively, or
- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1035 or 1037 to 1622 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 1036 of SEQ ID NO: 5 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence t or the complement thereof; said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1036 or 1036 to 1622 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1035 followed by t or t followed by the nucleotide sequence SEQ ID NO: 5 from nucleotide 1037 to 1622 or of the complement thereof, respectively, or
- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 902 or 904 to 1593 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide

903 of SEQ ID NO: 7 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence t or the complement thereof; and said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 903 or 903 to 1593 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 902 followed by t or t followed by the nucleotide sequence SEQ ID NO: 7 from nucleotide 904 to 1593 or of the complement thereof, respectively, or

- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 910 or 912 to 1593 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 911 of SEQ ID NO: 7 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence a or the complement thereof; and said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 911 or 911 to 1593 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 910 followed by a or a followed by the nucleotide sequence SEQ ID NO: 7 from nucleotide 912 to 1593 or of the complement thereof, respectively, or

- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 919 or 921 to 1593 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 920 of SEQ ID NO: 7 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence t or the complement thereof; and said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 920 or 920 to 1593 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 919 followed by t or t followed by the nucleotide sequence SEQ ID NO: 7 from nucleotide 921 to 1593 or of the complement thereof, respectively.

41. A method according to any one of claims 37 to 40, wherein said set of at least three specific probes is selected from the group consisting of:

- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 11, one probe comprising the sequence of SEQ ID NO: 12, and/or one probe comprising the sequence of SEQ ID NO: 13,

- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 14, one probe comprising the sequence of SEQ ID NO: 15, and/or one probe comprising the sequence of SEQ ID NO: 16,
 - a set of probes comprising one probe comprising the sequence of SEQ ID NO: 17, one probe comprising the sequence of SEQ ID NO: 18, and/or one probe comprising the sequence of SEQ ID NO: 19,
 - a set of probes comprising one probe comprising the sequence of SEQ ID NO: 20, one probe comprising the sequence of SEQ ID NO: 21 and/or one probe comprising the sequence of SEQ ID NO: 22,
 - a set of probes comprising one probe comprising the sequence of SEQ ID NO: 23, one probe comprising the sequence of SEQ ID NO: 24 and/or one probe comprising the sequence of SEQ ID NO: 25, and
 - a set of probes comprising one probe comprising the sequence of SEQ ID NO: 26, one probe comprising the sequence of SEQ ID NO: 27 and/or one probe comprising the sequence of SEQ ID NO: 28.
42. A kit for identifying a mutant *IND* allele according to any one of claims 20 to 22 in a biological sample, comprising a set of primers or probes, said set selected from the group consisting of:
- a set of primers or probes, wherein one of said primers or probes specifically recognizes the 5' flanking region of the mutant *IND* allele and the other of said primers or probes specifically recognizes the 3' flanking region of the mutant *IND* allele,
 - a set of primers or probes, wherein one of said primers or probes specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele and the other of said primers or probes specifically recognizes the mutation region of the mutant *IND* allele,
 - a set of primers or probes, wherein one of said primers specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele and the other of said primers or probes specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the mutant *IND* allele, respectively,
 - a probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele.
43. A kit according to claim 42, wherein
- said primer which specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele consists of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or

- said primer which specifically recognizes the mutation region of the mutant *IND* allele consists of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or
 - said primer which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele consists of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof,, wherein said 17 to 200 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences,
 - said probe which specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele, consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or a sequence having at least 80% sequence identity therewith, or
 - said probe which specifically recognizes the mutation region of the mutant *IND* allele, consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or a sequence having at least 80% sequence identity therewith, or
 - said probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele, consists of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof, respectively, wherein said 13 to 1000 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences, or a sequence having at least 80% sequence identity therewith.
44. A kit according to claim 42, wherein
- said primer which specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele comprises at its extreme 3' end a nucleotide sequence of at least 17 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or
 - said primer which specifically recognizes the mutation region of the mutant *IND* allele comprises at its extreme 3' end a nucleotide sequence of at least 17 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or
 - said primer which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele comprises at its extreme 3' end a

nucleotide sequence of at least 17 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof, wherein said 3'-located 17 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences

- said probe which specifically recognizes the 5' or 3' flanking region of the mutant *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant *IND* allele or from the complement thereof, respectively, or

- said probe which specifically recognizes the mutation region of the mutant *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from the mutation sequence of the mutant *IND* allele or from the complement thereof, or

- said probe which specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele comprises a nucleotide sequence of at least 13 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele or from the complement thereof, respectively, wherein said at least 13 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences.

45. A kit according to any one of claims 42 to 44, wherein

- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 929 or 931 to 1622 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 930 of SEQ ID NO: 5 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 930 or 930 to 1622 or of the complement thereof, respectively, or

- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 995 or 997 to 1622 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 996 of SEQ ID NO: 5 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 996 or 996 to 1622 or of the complement thereof, respectively, or

- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1035 or 1037 to 1622 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 1036 of SEQ ID NO: 5 or of

the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1036 or 1036 to 1622 or of the complement thereof, respectively, or

5 - said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 902 or 904 to 1593 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 903 of SEQ ID NO: 7 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 903 or 903 to 1593 or of the complement thereof, respectively, or

10 - said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 910 or 912 to 1593 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 911 of SEQ ID NO: 7 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 911 or 911 to 1593 or of the complement thereof, respectively, or

15 - said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 919 or 921 to 1593 or of the complement thereof, respectively; said mutation region has the nucleotide sequence of nucleotide 920 of SEQ ID NO: 7 or of the complement thereof; and said joining region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 920 or 920 to 1593 or of the complement thereof, respectively.

46. A kit according to any one of claims 42 to 45, wherein said set of probes is selected from the group consisting of:

25 - a set of probes comprising one probe comprising the sequence of SEQ ID NO: 11 and/or one probe comprising the sequence of SEQ ID NO: 12,

- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 14 and/or one probe comprising the sequence of SEQ ID NO: 15,

- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 17 and/or one probe comprising the sequence of SEQ ID NO: 18,

30 - a set of probes comprising one probe comprising the sequence of SEQ ID NO: 20 and/or one probe comprising the sequence of SEQ ID NO: 21,

- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 23 and/or one probe comprising the sequence of SEQ ID NO: 24,

35 - a set of probes comprising one probe comprising the sequence of SEQ ID NO: 26 and/or one probe comprising the sequence of SEQ ID NO: 27.

47. A kit for determining the zygosity status of a mutant *IND* allele according to any one of claims 20 to 22 in a plant, or a cell, part, seed or progeny thereof, comprising a set of primers or probes, wherein at least two of said primers or at least one of said probes specifically recognize the wild type *IND* allele and wherein at least two of said primers or at least one of said probes specifically recognize the mutant *IND* allele, selected from the group consisting of:

- a set of at least two primers or probes, wherein a first primer or probe specifically recognizes the 5' flanking region of the mutant and the wild type *IND* allele and a second primer or probe specifically recognizes the 3' flanking region of the mutant and the wild type *IND* allele,
- a set of at least three primers or probes, wherein a first primer or probe specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, a second primer or probe specifically recognizes the mutation region of the mutant *IND* allele, and a third primer or probe specifically recognizes the mutation region of the wild type *IND* allele,
- a set of at least three primers or probes, wherein a first primer or probe specifically recognizes the 5' or 3' flanking region of the mutant and the wild type *IND* allele, a second primer or probe specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the mutant *IND* allele, respectively, and a third primer or probe specifically recognizes the joining region between the 3' or 5' flanking region and the mutation region of the wild type *IND* allele, respectively,
- a set of at least two probes, wherein a first probe specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the mutant *IND* allele and a second probe specifically recognizes the joining region between the 5' or 3' flanking region and the mutation region of the wild type *IND* allele.

48. A kit according to claim 47, wherein

- said primers which specifically recognize the 5' or 3' flanking region of the mutant and the wild type *IND* allele consist of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or
- said primers which specifically recognize the mutation region of the mutant or the wild type *IND* allele consist of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from the sequence of the mutation region of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or

- said primers which specifically recognize the joining region between the 5' or 3' flanking region and the mutation region of the wild type or of the mutant *IND* allele,, consist of a nucleotide sequence of 17 to 200 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the wild type or of the mutant *IND* allele or from the complement thereof, respectively, wherein said 17 to 200 consecutive nucleotides are not derived exclusively from either the mutation region or from the flanking sequences, or
- said probes which specifically recognize the 5' or 3' flanking region of the mutant and the wild type *IND* allele, consist of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or a sequence having at least 80% sequence identity therewith, or
- said probes which specifically recognize the mutation region of the mutant or the wild type *IND* allele, consist of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from the mutation sequence of the mutant or the wild type *IND* allele or from the complement thereof, or a sequence having at least 80% sequence identity therewith, or
- said probes which specifically recognize the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele, consist of a nucleotide sequence of 13 to 1000 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele or from the complement thereof, respectively, wherein said 13 to 1000 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences, or a sequence having at least 80% sequence identity therewith.

49. A kit according to claim 47, wherein

- said primers which specifically recognize the 5' or 3' flanking region of the mutant and the wild type *IND* allele comprise at their extreme 3' end a nucleotide sequence of 17 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or
- said primers which specifically recognize the mutation region of the mutant or the wild type *IND* allele comprise at their extreme 3' end a nucleotide sequence of 17 consecutive nucleotides selected from the sequence of the mutation region of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or

- said primers which specifically recognize the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele comprise at their extreme 3' end a nucleotide sequence of 17 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele, respectively, wherein said 3'-located 17 consecutive nucleotides are not derived exclusively from either the mutation region or from the flanking sequences, or
- said probes which specifically recognize the 5' or 3' flanking region of the mutant and the wild type *IND* allele comprise a nucleotide sequence of at least 13 consecutive nucleotides selected from the 5' or 3' flanking sequence of the mutant or the wild type *IND* allele or from the complement thereof, respectively, or
- said probes which specifically recognize the mutation region of the mutant or the wild type *IND* allele comprise a nucleotide sequence of at least 13 consecutive nucleotides selected from the mutation sequence of the mutant or the wild type *IND* allele or from the complement thereof, or
- said probes which specifically recognize the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele comprise a nucleotide sequence of at least 13 consecutive nucleotides selected from a sequence spanning the joining region between the 5' or 3' flanking region and the mutation region of the mutant or the wild type *IND* allele or from the complement thereof, respectively, wherein said at least 13 consecutive nucleotides are not derived exclusively from either the mutation or the flanking sequences.

50. A kit according to any one of claims 47 to 49, wherein

- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 929 or 931 to 1622 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 930 of SEQ ID NO: 5 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence a or the complement thereof; said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 930 or 930 to 1622 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 929 followed by a or a followed by the nucleotide sequence SEQ ID NO: 5 from nucleotide 931 to 1622 or of the complement thereof, respectively, or
- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 995 or 997 to 1622 or of the complement thereof, respectively; said

- mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 996 of SEQ ID NO: 5 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence a or the complement thereof; said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 996 or 996 to 1622 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 995 followed by a or a followed by the nucleotide sequence SEQ ID NO: 5 from nucleotide 997 to 1622 or of the complement thereof, respectively, or
- 5
- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1035 or 1037 to 1622 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 1036 of SEQ ID NO: 5 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence t or the complement thereof; said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1036 or 1036 to 1622 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 5 from nucleotide 1 to 1035 followed by t or t followed by the nucleotide sequence SEQ ID NO: 5 from nucleotide 1037 to 1622 or of the complement thereof, respectively, or
- 10
- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 902 or 904 to 1593 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 903 of SEQ ID NO: 7 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence t or the complement thereof; and said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 903 or 903 to 1593 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 902 followed by t or t followed by the nucleotide sequence SEQ ID NO: 7 from nucleotide 904 to 1593 or of the complement thereof, respectively, or
- 15
- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 910 or 912 to 1593 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 911 of SEQ ID NO: 7 or of the complement thereof; said mutation region of the mutant *IND* allele has the sequence a or the complement thereof; and said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from
- 20
- 25
- 30
- 35

nucleotide 1 to 911 or 911 to 1593 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 910 followed by a or a followed by the nucleotide sequence SEQ ID NO: 7 from nucleotide 912 to 1593 or of the complement thereof, respectively,
5 or

- said 5' or 3' flanking region comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 919 or 921 to 1593 or of the complement thereof, respectively; said mutation region of the wild type *IND* allele has the nucleotide sequence of nucleotide 920 of SEQ ID NO: 7 or of the complement thereof; said mutation region of the mutant
10 *IND* allele has the sequence t or the complement thereof; and said joining region of the wild type *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 920 or 920 to 1593 or of the complement thereof, respectively; and said joining region of the mutant *IND* allele comprises the nucleotide sequence of SEQ ID NO: 7 from nucleotide 1 to 919 followed by t or t followed by the nucleotide sequence
15 SEQ ID NO: 7 from nucleotide 921 to 1593 or of the complement thereof, respectively.

51. A kit according to any one of claims 47 to 50, wherein said set of at least three specific probes is selected from the group consisting of:

- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 11, one probe comprising the sequence of SEQ ID NO: 12, and/or one probe comprising the
20 sequence of SEQ ID NO: 13,
- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 14, one probe comprising the sequence of SEQ ID NO: 15, and/or one probe comprising the sequence of SEQ ID NO: 16,
- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 17, one
25 probe comprising the sequence of SEQ ID NO: 18, and/or one probe comprising the sequence of SEQ ID NO: 19,
- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 20, one probe comprising the sequence of SEQ ID NO: 21 and/or one probe comprising the sequence of SEQ ID NO: 22,
- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 23, one
30 probe comprising the sequence of SEQ ID NO: 24 and/or one probe comprising the sequence of SEQ ID NO: 25, and
- a set of probes comprising one probe comprising the sequence of SEQ ID NO: 26, one probe comprising the sequence of SEQ ID NO: 27 and/or one probe comprising the
35 sequence of SEQ ID NO: 28.

52. A method for combining at least two partial knockout mutant *IND* alleles according to any one of claims 20 to 22 in one plant comprising the steps of:
- (a) identifying at least two plants each comprising at least one partial knockout mutant *IND* allele according to any one of claims 24 to 32,
 - 5 (b) crossing the at least two plants and collecting F1 hybrid seeds from the at least one cross,
 - (c) optionally, identifying an F1 plant comprising at least two partial knockout mutant *IND* alleles according to any one of claims 24 to 32.
53. A method according to claim 52, which further comprises the step of identifying an F1 plant, which is homozygous or heterozygous for a partial knockout mutant *IND* allele by
10 determining the zygosity status of the selected mutant *IND* allele, according to any one of claims 33 to 41.
54. A method for transferring at least one partial knockout mutant *IND* allele from one plant to another plant comprising the steps of:
- (a) identifying a first plant comprising at least one partial knockout mutant *IND* allele
15 according to any one of claims 24 to 32 or generating a first plant comprising at least two partial knockout mutant *IND* alleles according to claim 52,
 - (b) crossing the first plant with a second plant not comprising the at least one partial knockout mutant *IND* allele and collecting F1 seeds from the cross,
 - (c) optionally, identifying F1 plants comprising the at least one partial knockout mutant *IND*
20 allele according to any one of claims 24 to 32,
 - (d) backcrossing F1 plants comprising the at least one partial knockout mutant *IND* allele with the second plant not comprising the at least one partial knockout mutant *IND* allele for at least one generation (x) and collecting BCx seeds from the crosses,
 - (e) identifying in every generation BCx plants comprising the at least one partial knockout
25 mutant *IND* allele according to any one of claims 24 to 32.
55. A method according to claim 54, which further comprises the step of identifying a BCx plant, which is homozygous or heterozygous for a partial knockout mutant *IND* allele by determining the zygosity status of the partial knockout mutant *IND* allele, according to any one of claims 33 to 41.
- 30 56. A method for making a plant according to any one of claims 1 to 18 comprising combining and/or transferring mutant *IND* alleles according to any one of claims 20 to 22 in or to one *Brassica* plant, according to any one of claims 52 to 55.
57. A method according to claim 56, which further comprises combining and/or transferring the partial knockout mutant *IND* alleles according to any one of claims 20 to 22 in one plant with

full knockout mutant *IND* alleles and/or to one plant comprising full knockout mutant *IND* alleles.

58. A method according to claim 57, wherein the full knockout mutant *IND* alleles are selected from the group consisting of *ind-al-EMS01*, *ind-al-EMS05*, *ind-cl-EMS01* and *ind-cl-EMS03*.
59. A method for making a hybrid *Brassica* seed or plant according to any one of claims 1 to 18 comprising the steps of:
- (a) identifying a first plant comprising a first partial knockout mutant *IND* allele in homozygous state and a second plant comprising a second partial knockout mutant *IND* allele in homozygous state according to any one of claims 33 to 41,
 - (b) crossing the first and the second plant and collecting F1 hybrid seeds from the cross.
60. A method according to claim 59, wherein the first and the second partial knockout mutant *IND* allele are the same.
61. A method according to claim 59 or 60, wherein the first plant additionally comprises a first full knockout mutant *IND* allele in homozygous state and the second plant comprising a second full knockout mutant *IND* allele in homozygous state.
62. A method according to claim 61, wherein the first and the second full knockout mutant *IND* allele are the same.
63. *Brassica* seed comprising a partial knockout *ind* allele selected from the group consisting of: seed comprising the *ind-al-EMS06* allele having been deposited at the NCIMB under accession number NCIMB 41570, seed comprising the *ind-al-EMS09* allele having been deposited at the NCIMB under accession number NCIMB 41571, seed comprising the *ind-al-EMS13* allele having been deposited at the NCIMB under accession number NCIMB 41572, seed comprising the *ind-cl-EMS04* allele having been deposited at the NCIMB under accession number NCIMB 41575, seed comprising the *ind-cl-EMS08* allele having been deposited at the NCIMB under accession number NCIMB 41573, seed comprising the *ind-cl-EMS09* allele having been deposited at the NCIMB under accession number NCIMB 41574, and derivatives therefrom.
64. A *Brassica* plant, or a cell, part, seed or progeny thereof, obtained from the seed of claim 63.
65. A *Brassica* plant, or a cell, part, seed or progeny thereof, comprising the *ind-al-EMS06*, *ind-al-EMS09*, *ind-al-EMS13*, *ind-cl-EMS04*, *ind-cl-EMS08* or *ind-cl-EMS09* allele in its genome, obtained by propagation of and/or breeding with a *Brassica* plant grown from the seed of claim 63.
66. A seed comprising the *ind-al-EMS06*, *ind-al-EMS09*, *ind-al-EMS13*, *ind-cl-EMS04*, *ind-cl-EMS08* or *ind-cl-EMS09* allele, reference seed comprising said allele having been

deposited at the NCIMB under accession number NCIMB 41570, NCIMB 41572, NCIMB 41572, NCIMB 41574, NCIMB 41575 and NCIMB 41573, respectively.

67. A plant, or a cell, part, seed or progeny thereof, comprising the *ind-a1*-EMS06, *ind-a1*-EMS09, *ind-a1*-EMS13, *ind-cl*-EMS04, *ind-cl*-EMS08 or *ind-cl*-EMS09 allele, produced
5 from the seed of claim 66.
68. A *Brassica* plant comprising at least two *IND* genes at two loci, or a cell, part, seed or progeny thereof, characterized in that it comprises two mutant *IND* alleles at one locus in its genome.
69. The plant according to claim 68, wherein said two mutant *IND* alleles are homozygous.
- 10 70. The plant according to claim 68, wherein the *IND* genes are *IND-A1* or *IND-C1* genes.
71. The plant according to any one of claims 68 to 70, wherein the *IND* genes comprise a nucleic acid molecule selected from the group consisting of:
- (a) a nucleic acid molecule which comprises at least 90% sequence identity to SEQ ID NO: 1, SEQ ID NO: 3 from the nucleotide at position 46 to the nucleotide at position 633,
15 SEQ ID NO: 3, SEQ ID NO: 5, or SEQ ID NO: 7;
- (b) a nucleic acid molecule encoding an amino acid sequence comprising at least 90% sequence identity to SEQ ID NO: 2, SEQ ID NO: 4 from the amino acid at position 16 to the amino acid at position 21 or SEQ ID NO: 4.
72. The plant according to any one of claims 68 to 71, wherein the mutant *IND* alleles are partial
20 knock-out *IND* alleles.
73. The plant according to any one of claims 68 to 72, wherein the mutant *IND* alleles are selected from the group consisting of *ind-a1*-EMS06, *ind-a1*-EMS09, *ind-a1*-EMS13, *ind-cl*-EMS08, *ind-cl*-EMS09 and *ind-cl*-EMS04.
74. The plant according to any one of claims 68 to 73, which produces a significantly reduced
25 amount of functional *IND* protein compared to the amount of functional *IND* protein produced by a corresponding plant not comprising mutant *IND* alleles.
75. The plant according to any one of claims 68 to 74, wherein the seed yield of the plant is increased, preferably significantly increased compared to the seed yield of a corresponding plant not comprising mutant *IND* alleles.
- 30 76. The plant according to any one of claims 68 to 75, which is a plant from a *Brassica* crop species, preferably *Brassica napus*, *Brassica juncea*, *Brassica carinata*, *Brassica rapa* or *Brassica oleracea*.
77. The plant according to any one of claims 68 to 76, which is a plant from a *Brassica* oilseed species, preferably *Brassica napus*, *Brassica juncea* or *Brassica rapa*.

78. A method to increase the yield of *Brassica* plant comprising at least two *IND* genes, comprising introducing two mutant homozygous *IND* alleles in its genome.
79. Use of a mutant *IND* allele according to any one of claims 20 to 22 to increase the seed yield in a *Brassica* plant.
- 5 80. Use of a mutant *IND* allele according to any one of claims 20 to 22 to increase the shatter resistance of pods in a *Brassica* plant.