

# SEQUENCE LISTING

<110> Bayer BioScience N.V.  
 <120> Brassica plant comprising a mutant INDEHISCENT allele  
 <130> BCS 07-2014  
 <160> 40  
 <170> PatentIn version 3.3  
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 <211> 558  
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 <213> Brassica napus wild type IND-A1 coding sequence

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Met Ser Gly Ser Lys Ala Asp Ala Ala Ile Ala Pro Ile Val Met Met
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gag cat cat cat ctc ctt atg aat tgg aac aaa cct att gat ctc att      96
Glu His His His Leu Leu Met Asn Trp Asn Lys Pro Ile Asp Leu Ile
          20          25          30

aca gaa gaa aac tct ttt aac cac aat cct cat ttc ata gta gat cca     144
Thr Glu Glu Asn Ser Phe Asn His Asn Pro His Phe Ile Val Asp Pro
          35          40          45

cct tcc gaa acc cta agc cac ttc cag ccc ccg ccg aca atc ttc tcc     192
Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Ile Phe Ser
          50          55          60

gat cac gga gga gga gag gaa gca gaa gaa gaa gaa gaa gaa gaa gga     240
Asp His Gly Gly Gly Glu Glu Ala Glu Glu Glu Glu Glu Glu Glu Gly
65          70          75          80

gag gaa gag atg gat ccg atg aag aag atg caa tac gcg att gct gcc     288
Glu Glu Glu Met Asp Pro Met Lys Lys Met Gln Tyr Ala Ile Ala Ala
          85          90          95

atg cag ccc gta gac ctc gat cca gcc acc gtt cct aag ccg aac cgc     336
Met Gln Pro Val Asp Leu Asp Pro Ala Thr Val Pro Lys Pro Asn Arg
          100          105          110

cgt aac gta agg gta agc gac gac cct cag acg gtg gtg gct cgt cgg     384
Arg Asn Val Arg Val Ser Asp Asp Pro Gln Thr Val Val Ala Arg Arg
          115          120          125

cgt aga gaa agg ata agc gag aag atc cgg ata ttg aag agg atg gtg     432
Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met Val
          130          135          140

cca ggc ggt gca aag atg gac act gcc tcc atg ctc gac gaa gcc atc     480
Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile
145          150          155          160

cgc tac acc aag ttc ttg aaa cgg cag gtg agg cta gct tct tca gcc     528
Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Leu Ala Ser Ser Ala
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tca cac tca gct tgg agc tcc tat gtc tga      558
Ser His Ser Ala Trp Ser Ser Tyr Val
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180

185

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 <213> Brassica napus wild type IND-A1 coding sequence

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Met Ser Gly Ser Lys Ala Asp Ala Ala Ile Ala Pro Ile Val Met Met  
 1 5 10 15

Glu His His His Leu Leu Met Asn Trp Asn Lys Pro Ile Asp Leu Ile  
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Thr Glu Glu Asn Ser Phe Asn His Asn Pro His Phe Ile Val Asp Pro  
 35 40 45

Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Ile Phe Ser  
 50 55 60

Asp His Gly Gly Gly Glu Glu Ala Glu Glu Glu Glu Glu Glu Gly  
 65 70 75 80

Glu Glu Glu Met Asp Pro Met Lys Lys Met Gln Tyr Ala Ile Ala Ala  
 85 90 95

Met Gln Pro Val Asp Leu Asp Pro Ala Thr Val Pro Lys Pro Asn Arg  
 100 105 110

Arg Asn Val Arg Val Ser Asp Asp Pro Gln Thr Val Val Ala Arg Arg  
 115 120 125

Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met Val  
 130 135 140

Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile  
 145 150 155 160

Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Leu Ala Ser Ser Ala  
 165 170 175

Ser His Ser Ala Trp Ser Ser Tyr Val  
 180 185

<210> 3  
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<400> 3

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| atg tat aaa aga aag gtc tat gcg tct cta gtc caa aaa ctc tat atg<br>Met Tyr Lys Arg Lys Val Tyr Ala Ser Leu Val Gln Lys Leu Tyr Met<br>1 5 10 15       | 48  |
| tct ggt tca aaa gca gat gca gca gcc ata gcc cca ata gtc atg atg<br>Ser Gly Ser Lys Ala Asp Ala Ala Ala Ile Ala Pro Ile Val Met Met<br>20 25 30        | 96  |
| gag cct cat cat ctc ctt atg aac tgg aac aaa cct att gat ctc att<br>Glu Pro His His Leu Leu Met Asn Trp Asn Lys Pro Ile Asp Leu Ile<br>35 40 45        | 144 |
| aca caa gaa aac tct ttt aac cac aat cct cat ttc atg gta gat cca<br>Thr Gln Glu Asn Ser Phe Asn His Asn Pro His Phe Met Val Asp Pro<br>50 55 60        | 192 |
| cct tcc gaa acc cta agc cac ttc cag ccc ccg ccg aca gtc ttc tcc<br>Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Val Phe Ser<br>65 70 75 80     | 240 |
| gat ccc gga gga gga gag gaa gca gaa gac gaa gaa gga gag gaa gag<br>Asp Pro Gly Gly Gly Glu Glu Glu Ala Glu Asp Glu Glu Gly Glu Glu<br>85 90 95        | 288 |
| ata gat gag atg aag gag atg caa tac gcg att gct gcc atg cag ccc<br>Ile Asp Glu Met Lys Glu Met Gln Tyr Ala Ile Ala Ala Met Gln Pro<br>100 105 110     | 336 |
| gta gac atc gat cca gcc acc gtt cct aag ccg aac cgc cgt aac gta<br>Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn Arg Arg Asn Val<br>115 120 125     | 384 |
| agg gta agc gag gac ccc cag acg gtg gtg gct cgt cgg cgt aga gaa<br>Arg Val Ser Glu Asp Pro Gln Thr Val Val Ala Arg Arg Arg Arg Glu<br>130 135 140     | 432 |
| agg ata agc gag aag atc cgg ata ttg aag agg atg gtg cca ggc ggt<br>Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met Val Pro Gly Gly<br>145 150 155 160 | 480 |
| gca aag atg gac act gcc tcc atg ctt gac gaa gcc atc cgc tac acc<br>Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile Arg Tyr Thr<br>165 170 175     | 528 |
| aag ttc ttg aaa cgg cag gtg agg ctt ctt cag cct cac act cag ctt<br>Lys Phe Leu Lys Arg Gln Val Arg Leu Leu Gln Pro His Thr Gln Leu<br>180 185 190     | 576 |
| ggg gct cct atg tct gac cct tct cgc ctt tgt tat tac cac aac tcg<br>Gly Ala Pro Met Ser Asp Pro Ser Arg Leu Cys Tyr Tyr His Asn Ser<br>195 200 205     | 624 |
| gat acc taa<br>Asp Thr<br>210   | 633 |

<210> 4  
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 <213> Brassica napus wild type IND-C1 coding sequence  
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Met Tyr Lys Arg Lys Val Tyr Ala Ser Leu Val Gln Lys Leu Tyr Met  
1 5 10 15

Ser Gly Ser Lys Ala Asp Ala Ala Ala Ile Ala Pro Ile Val Met Met

| 20   | 25 | 30 |
|--|----|----|
| Glu Pro His His Leu Leu Met Asn Trp Asn Lys Pro Ile Asp Leu Ile<br>35 40 45        |    |    |
| Thr Gln Glu Asn Ser Phe Asn His Asn Pro His Phe Met Val Asp Pro<br>50 55 60        |    |    |
| Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Val Phe Ser<br>65 70 75 80     |    |    |
| Asp Pro Gly Gly Gly Glu Glu Ala Glu Asp Glu Glu Gly Glu Glu Glu<br>85 90 95        |    |    |
| Ile Asp Glu Met Lys Glu Met Gln Tyr Ala Ile Ala Ala Met Gln Pro<br>100 105 110     |    |    |
| Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn Arg Arg Asn Val<br>115 120 125     |    |    |
| Arg Val Ser Glu Asp Pro Gln Thr Val Val Ala Arg Arg Arg Arg Glu<br>130 135 140     |    |    |
| Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met Val Pro Gly Gly<br>145 150 155 160 |    |    |
| Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile Arg Tyr Thr<br>165 170 175     |    |    |
| Lys Phe Leu Lys Arg Gln Val Arg Leu Leu Gln Pro His Thr Gln Leu<br>180 185 190     |    |    |
| Gly Ala Pro Met Ser Asp Pro Ser Arg Leu Cys Tyr Tyr His Asn Ser<br>195 200 205     |    |    |
| Asp Thr<br>210   |    |    |

<210> 5  
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 <213> Brassica napus wild type IND-A1 genomic sequence

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| tttgacaatc tacatacata accaacaaaa agtagaatac cttgaaaatc taaaacccaa  | 60  |
| aatatgatgt aaaactcaag cttgggtccag agcataaaaa aattaaagcc atcgcttttg | 120 |
| tatcacatat ttaaactgca gttttttttt tttttttggg gggggggggg ggggtaatat  | 180 |
| aaaaatataa ttaacaaaaa aaaattatga aacaattagc atgtaaaaca ctaatctttt  | 240 |

|         |        |          |       |         |       |        |        |         |       |          |        |     |     |     |     |      |
|---------|--------|----------|-------|---------|-------|--------|--------|---------|-------|----------|--------|-----|-----|-----|-----|------|
| ggttg   | tgaca  | aaacg    | ttttc | acaaat  | gttcc | tataa  | ataaaa | ttcaa   | gtgca | ttttat   | ctgc   |     |     |     |     | 300  |
| aaaata  | tatata | ctttc    | actca | taaaata | aaga  | gcgttt | taaaa  | cattc   | ataca | cgca     | ctacat |     |     |     |     | 360  |
| tgacat  | gaca   | aaagaa   | atcc  | gcaaata | cac   | atgat  | gtatg  | tcgaaaa | aaaaa | atac     |        |     |     |     |     | 420  |
| acatgat | gta    | tatatag  | aga   | ggatag  | tatc  | taggaa | aataa  | gactat  | atta  | tatatata | aa     |     |     |     |     | 480  |
| gaaaata | gag    | aaaagata | aaa   | aatata  | aaatt | ggtat  | gtata  | aaagaa  | aggt  | ctatgc   | gtct   |     |     |     |     | 540  |
| ctagt   | cctaaa | aactc    | tatat | atg     | tct   | ggc    | tca    | aaa     | gca   | gat      | gca    | gcc | ata | gcc |     | 593  |
|         |        |          |       | Met     | Ser   | Gly    | Ser    | Lys     | Ala   | Asp      | Ala    | Ala | Ile | Ala |     |      |
|         |        |          |       | 1       |       |        |        | 5       |       |          |        |     | 10  |     |     |      |
| cca     | ata    | gtc      | atg   | atg     | gag   | cat    | cat    | cat     | ctc   | ctt      | atg    | aat | tgg | aac | aaa | 641  |
| Pro     | Ile    | Val      | Met   | Met     | Glu   | His    | His    | His     | Leu   | Leu      | Met    | Asn | Trp | Asn | Lys |      |
|         |        |          | 15    |         |       |        |        | 20      |       |          |        |     | 25  |     |     |      |
| cct     | att    | gat      | ctc   | att     | aca   | gaa    | gaa    | aac     | tct   | ttt      | aac    | cac | aat | cct | cat | 689  |
| Pro     | Ile    | Asp      | Leu   | Ile     | Thr   | Glu    | Glu    | Asn     | Ser   | Phe      | Asn    | His | Asn | Pro | His |      |
|         |        | 30       |       |         |       | 35     |        |         |       |          | 40     |     |     |     |     |      |
| ttc     | ata    | gta      | gat   | cca     | cct   | tcc    | gaa    | acc     | cta   | agc      | cac    | ttc | cag | ccc | ccg | 737  |
| Phe     | Ile    | Val      | Asp   | Pro     | Pro   | Ser    | Glu    | Thr     | Leu   | Ser      | His    | Phe | Gln | Pro | Pro |      |
|         | 45     |          |       |         |       | 50     |        |         |       |          | 55     |     |     |     |     |      |
| ccg     | aca    | atc      | ttc   | tcc     | gat   | cac    | gga    | gga     | gga   | gag      | gaa    | gca | gaa | gaa | gaa | 785  |
| Pro     | Thr    | Ile      | Phe   | Ser     | Asp   | His    | Gly    | Gly     | Gly   | Glu      | Glu    | Ala | Glu | Glu | Glu |      |
| 60      |        |          |       |         | 65    |        |        |         | 70    |          |        |     |     |     | 75  |      |
| gaa     | gaa    | gaa      | gaa   | gga     | gag   | gaa    | gag    | atg     | gat   | ccg      | atg    | aag | aag | atg | caa | 833  |
| Glu     | Glu    | Glu      | Glu   | Gly     | Glu   | Glu    | Glu    | Met     | Asp   | Pro      | Met    | Lys | Lys | Met | Gln |      |
|         |        |          |       | 80      |       |        |        | 85      |       |          |        |     |     | 90  |     |      |
| tac     | gcg    | att      | gct   | gcc     | atg   | cag    | ccc    | gta     | gac   | ctc      | gat    | cca | gcc | acc | gtt | 881  |
| Tyr     | Ala    | Ile      | Ala   | Ala     | Met   | Gln    | Pro    | Val     | Asp   | Leu      | Asp    | Pro | Ala | Thr | Val |      |
|         |        |          | 95    |         |       |        |        | 100     |       |          |        |     | 105 |     |     |      |
| cct     | aag    | ccg      | aac   | cg      | cgt   | aac    | gta    | agg     | gta   | agc      | gac    | gac | cct | cag | acg | 929  |
| Pro     | Lys    | Pro      | Asn   | Arg     | Arg   | Asn    | Val    | Arg     | Val   | Ser      | Asp    | Asp | Pro | Gln | Thr |      |
|         |        | 110      |       |         |       |        | 115    |         |       |          |        | 120 |     |     |     |      |
| gtg     | gtg    | gct      | cgt   | cgg     | cgt   | aga    | gaa    | agg     | ata   | agc      | gag    | aag | atc | cgg | ata | 977  |
| Val     | Val    | Ala      | Arg   | Arg     | Arg   | Arg    | Glu    | Arg     | Ile   | Ser      | Glu    | Lys | Ile | Arg | Ile |      |
|         | 125    |          |       |         |       | 130    |        |         |       |          | 135    |     |     |     |     |      |
| ttg     | aag    | agg      | atg   | gtg     | cca   | ggc    | ggg    | gca     | aag   | atg      | gac    | act | gcc | tcc | atg | 1025 |
| Leu     | Lys    | Arg      | Met   | Val     | Pro   | Gly    | Gly    | Ala     | Lys   | Met      | Asp    | Thr | Ala | Ser | Met |      |
| 140     |        |          |       |         | 145   |        |        |         |       | 150      |        |     |     |     | 155 |      |
| ctc     | gac    | gaa      | gcc   | atc     | cg    | tac    | acc    | aag     | ttc   | ttg      | aaa    | cgg | cag | gtg | agg | 1073 |
| Leu     | Asp    | Glu      | Ala   | Ile     | Arg   | Tyr    | Thr    | Lys     | Phe   | Leu      | Lys    | Arg | Gln | Val | Arg |      |
|         |        |          |       | 160     |       |        |        | 165     |       |          |        |     |     | 170 |     |      |
| cta     | gct    | tct      | tca   | gcc     | tca   | cac    | tca    | gct     | tgg   | agc      | tcc    | tat | gtc | tga |     | 1118 |
| Leu     | Ala    | Ser      | Ser   | Ala     | Ser   | His    | Ser    |         |       |          |        |     |     |     |     |      |

gtgttactag ttatataact ggaaaacaaa tgtctggaat aagaattccc gggagaacca 1478  
 agcctttctc taatccctaa gattatagct actgaaacaa tgaaacaatg aagaatcagt 1538  
 tgggcattag taaaaaaaaa agaatcagtt gggttgctta taaaattttg ttataaaatt 1598  
 tatgtcgtat gtgtgttagc cgta 1622

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 <212> PRT  
 <213> Brassica napus wild type IND-A1 genomic sequence

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Met Ser Gly Ser Lys Ala Asp Ala Ala Ile Ala Pro Ile Val Met Met  
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Glu His His His Leu Leu Met Asn Trp Asn Lys Pro Ile Asp Leu Ile  
 20 25 30

Thr Glu Glu Asn Ser Phe Asn His Asn Pro His Phe Ile Val Asp Pro  
 35 40 45

Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Ile Phe Ser  
 50 55 60

Asp His Gly Gly Gly Glu Glu Ala Glu Glu Glu Glu Glu Glu Glu Gly  
 65 70 75 80

Glu Glu Glu Met Asp Pro Met Lys Lys Met Gln Tyr Ala Ile Ala Ala  
 85 90 95

Met Gln Pro Val Asp Leu Asp Pro Ala Thr Val Pro Lys Pro Asn Arg  
 100 105 110

Arg Asn Val Arg Val Ser Asp Asp Pro Gln Thr Val Val Ala Arg Arg  
 115 120 125

Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met Val  
 130 135 140

Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile  
 145 150 155 160

Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Leu Ala Ser Ser Ala  
 165 170 175

Ser His Ser Ala Trp Ser Ser Tyr Val  
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<222> (497)..(1126)

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| tgccatacat | aaccacggat | catagtcgac | acctcaacgt   | gaagcaaatt | tgacaatcta  | 60  |     |     |     |     |     |     |     |     |
| catacataac | caacaaaaag | tagaataccg | tgaaaaccta   | aacccaaaat | atgatgtaaa  | 120 |     |     |     |     |     |     |     |     |
| actcaagctt | ggtccagagc | ataaaaaaat | taaagccatc   | gctttgggat | cacatattta  | 180 |     |     |     |     |     |     |     |     |
| aacgtcagtt | tttttttggg | gaagtaatat | aaaaatataa   | ttaacaagaa | aattttatgaa | 240 |     |     |     |     |     |     |     |     |
| ataattagca | tgtaaaacac | tagtcttttg | gttgtgacaa   | aacgttttca | caaagtgttct | 300 |     |     |     |     |     |     |     |     |
| ataaataaat | tcaagcacat | tttatctgca | aaatatatac   | tttcactcat | aaaataagag  | 360 |     |     |     |     |     |     |     |     |
| cgtttaaaac | attcatatac | gcactacatt | gacatgacaa   | aagaaatccg | caaatacaaa  | 420 |     |     |     |     |     |     |     |     |
| catatttagt | tcggatatat | ctaggaaata | agactatatatt | atatatataa | agaaattaga  | 480 |     |     |     |     |     |     |     |     |
| aaaaaagaaa | attggg     | atg        | tat          | aaa        | aga         | aag | gtc | tat | gcg | tct | cta | gtc | caa | 532 |
|            |            | Met        | Tyr          | Lys        | Arg         | Lys | Val | Tyr | Ala | Ser | Leu | Val | Gln |     |
|            |            | 1          |              |            |             | 5   |     |     |     |     | 10  |     |     |     |

atc cgc tac acc aag ttc ttg aaa cgg cag gtg agg ctt ctt cag cct 1060  
Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Leu Leu Gln Pro  
175 180 185

cac act cag ctt ggg gct cct atg tct gac cct tct cgc ctt tgt tat 1108  
 His Thr Gln Leu Gly Ala Pro Met Ser Asp Pro Ser Arg Leu Cys Tyr  
 190 195 200  
 tac cac aac tcg gat acc taattataat tctatcacgc gtttcatgtt 1156  
 Tyr His Asn Ser Asp Thr  
 205 210  
 gatatatata gataaatggt tgaataagga tttcgatcga agattgtatg gctattgatt 1216  
 acattatata ttgtacaata aatgatgtgt gtatttctat taatgtatat atgatatata 1276  
 tctgttttgca gtatgcattt atattctatt ctttataggg aggcaacatg ccggattagg 1336  
 gctttgatcg tatgcaagtt ttccgaccaa aaatatgaaa tacttgtttg gatataacat 1396  
 atgaatcggg taagtgttac tagttatata actggaaaaa attgtttggt ataagaattc 1456  
 ccgggagAAC caagcctttc tctaattcct aagatcatag ctactgaaat aatgaaaaaa 1516  
 aacaaaaaaa aaacaatgaa gaatcagttg ggcattagtc caaaaaaaaa aaagaatcag 1576  
 ttggattgct tataaaa 1593

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 <212> PRT  
 <213> Brassica napus wild type IND-C1 genomic sequence  
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Met Tyr Lys Arg Lys Val Tyr Ala Ser Leu Val Gln Lys Leu Tyr Met  
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 Ser Gly Ser Lys Ala Asp Ala Ala Ala Ile Ala Pro Ile Val Met Met  
 20 25 30  
 Glu Pro His His Leu Leu Met Asn Trp Asn Lys Pro Ile Asp Leu Ile  
 35 40 45  
 Thr Gln Glu Asn Ser Phe Asn His Asn Pro His Phe Met Val Asp Pro  
 50 55 60  
 Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Val Phe Ser  
 65 70 75 80  
 Asp Pro Gly Gly Gly Glu Glu Ala Glu Asp Glu Glu Gly Glu Glu Glu  
 85 90 95  
 Ile Asp Glu Met Lys Glu Met Gln Tyr Ala Ile Ala Ala Met Gln Pro  
 100 105 110  
 Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn Arg Arg Asn Val  
 115 120 125  
 Arg Val Ser Glu Asp Pro Gln Thr Val Val Ala Arg Arg Arg Arg Glu  
 130 135 140



Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met Val Pro Gly Gly  
145 150 155 160

Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile Arg Tyr Thr  
165 170 175

Lys Phe Leu Lys Arg Gln Val Arg Leu Leu Gln Pro His Thr Gln Leu  
180 185 190

Gly Ala Pro Met Ser Asp Pro Ser Arg Leu Cys Tyr Tyr His Asn Ser  
195 200 205

Asp Thr  
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<220>  
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<222> (1)..(594)

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| Met Glu Asn Gly Met Tyr Lys Lys Lys Gly Val Cys Asp Ser Cys Val |     |
| 1 5 10 15   |     |
| tcg tcc aaa agc aga tcc aac cac agc ccc aaa aga agc atg atg gag | 96  |
| Ser Ser Lys Ser Arg Ser Asn His Ser Pro Lys Arg Ser Met Met Glu |     |
| 20 25 30  |     |
| cct cag cct cac cat ctc ctc atg gat tgg aac aaa gct aat gat ctt | 144 |
| Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu |     |
| 35 40 45  |     |
| ctc aca caa gaa cac gca gct ttt ctc aat gat cct cac cat ctc atg | 192 |
| Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met |     |
| 50 55 60  |     |
| tta gat cca cct ccc gaa acc cta att cac ttg gac gaa gac gaa gag | 240 |
| Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu |     |
| 65 70 75 80   |     |
| tac gat gaa gac atg gat gcg atg aag gag atg cag tac atg atc gcc | 288 |
| Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala |     |
| 85 90 95  |     |
| gtc atg cag ccc gta gac atc gac cct gcc acg gtc cct aag ccg aac | 336 |
| Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn |     |
| 100 105 110   |     |
| cgc cgt aac gta agg ata agc gac gat cct cag acg gtg gtt gct cgt | 384 |
| Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg |     |
| 115 120 125   |     |
| cgg cgt cgg gaa agg atc agc gag aag atc cga att ctc aag agg atc | 432 |
| Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Ile |     |
| 130 135 140   |     |
| gtg cct ggt ggt gcg aag atg gac aca gct tcc atg ctc gac gaa gcc | 480 |
| Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala |     |

| 145   | 150 | 155 | 160 |     |
|---|-----|-----|-----|-----|
| ata cgt tac acc aag ttc ttg aaa cgg cag gtg agg att ctt cag cct |     |     |     | 528 |
| Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro | 165 | 170 | 175 |     |
| cac tct cag att gga gct cct atg gct aac ccc tct tac ctt tgt tat |     |     |     | 576 |
| His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys Tyr | 180 | 185 | 190 |     |
| tac cac aac tcc caa ccc tga                                     |     |     |     | 597 |
| Tyr His Asn Ser Gln Pro   | 195 |     |     |     |

<210> 10  
 <211> 198  
 <212> PRT  
 <213> Arabidopsis thaliana IND1

<400> 10

|   |     |     |     |     |
|---|-----|-----|-----|-----|
| Met Glu Asn Gly Met Tyr Lys Lys Lys Gly Val Cys Asp Ser Cys Val | 1   | 5   | 10  | 15  |
| Ser Ser Lys Ser Arg Ser Asn His Ser Pro Lys Arg Ser Met Met Glu | 20  | 25  | 30  |     |
| Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu | 35  | 40  | 45  |     |
| Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met | 50  | 55  | 60  |     |
| Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu | 65  | 70  | 75  | 80  |
| Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala | 85  | 90  | 95  |     |
| Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn | 100 | 105 | 110 |     |
| Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg | 115 | 120 | 125 |     |
| Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Ile | 130 | 135 | 140 |     |
| Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala | 145 | 150 | 155 | 160 |
| Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro | 165 | 170 | 175 |     |
| His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys Tyr | 180 | 185 | 190 |     |

Tyr His Asn Ser Gln Pro  
195

<210> 11  
<211> 643  
<212> DNA  
<213> Nucleotide sequence of a INDEHISCENT homologue from Brassica napus  
(Bn1-IND - SEQ ID NO: 2 of WO04/113542 )

<400> 11  
gaattcgccc ttgcatgta taaaaagaag ggtctatgcg tctctagtcc aaaaactcta 60  
tatgtctggt tcaaaagcag atgcagcagc catagcccca atagtcatga tggagcctca 120  
tcattctcctt atgaactgga acaaacctat tgatctcatt acacaagaaa actcttttaa 180  
ccacaatcct cttttcatgg tagatccacc ttccgaaacc ctaagccact tccagccccc 240  
gccgacagtc ttctccgac ccggaggagg agaggaagca gaagacgaag aaggagagga 300  
agagatagat gagatgaagg agatgcaata cgcgattgct gccatgcagc ccgtagacat 360  
cgatccagcc accgttccta agccgaaccg ccgtaacgta agggtaagcg aggaccccca 420  
gacggtggtg gctcgtcggc gtagagaaag gataagcgag aagatccgga tattgaagag 480  
gatggtgcca ggcggtgcaa agatggacac tgcctccatg cttgacgaag ccatccgcta 540  
caccaagttc ttgaaacggc aggtgaggct tcttcagcct cacactcagc ttggggctcc 600  
tatgtctgac ctttctcgcc ttgtttatta ccacaactct caa 643

<210> 12  
<211> 660  
<212> DNA  
<213> Nucleotide sequence of a second INDEHISCENT homologue from Brassica napus  
(Bn2-IND - SEQ ID NO: 3 of WO04/113542 )

<400> 12  
gaattcgccc ttggcatgta caagaagaaa ggtctatgcg tctctagtcc aaaaactcta 60  
tatatgtctg gctcaaaagc agatgcagcc atagcccca tagtcatgat ggagcatcat 120  
catctcctta tgaattggaa caaacctatt gatctcatta cagaagaaaa ctcttttaac 180  
cacaatcctc atttcatagt agatccacct tccgaaaccc taagccactt ccagcccccg 240  
ccgacaatct tctccggtca cggaggagga gaggaagcag cagaagaaga agaagaagaa 300  
ggagaggaag agatggatcc gatgaagaag atgcaatacg cgattgctgc catgcagccc 360  
gtagacctcg atccagccac cgttcctaag ccgaaccgcc gtaacgtaag ggtaagcgac 420  
gacctcaga cggtggtggc tcgtcggcgt agagaaagga taagcgagaa gatccggata 480  
ttgaggagga tgggtgccagg cggtgcaaag atggacactg cctccatgct cgacgaagcc 540  
atccgctaca ccaagttctt gaaacggcag gtgaggctag cttcttcagc ctcacactca 600  
gcttggagct cctatgtctg acccttcttg cttttgttat taccataact cgcagccctg 660

<210> 13  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
 <223> forward oligonucleotide for detection of IND-A1-EMS01  
 <400> 13  
 aagggttaagc gacgaccctt 20

<210> 14  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Forward oligonucleotide for detection of IND-A1-WT  
 <400> 14  
 aagggttaagc gacgaccctc 20

<210> 15  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
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 <400> 15  
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<210> 16  
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 <212> DNA  
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<220>  
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 <400> 16  
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<210> 17  
 <211> 20  
 <212> DNA  
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<220>  
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 <400> 17  
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<210> 18  
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<220>  
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<210> 19

<211> 21  
 <212> DNA  
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 <210> 20  
 <211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Reverse oligonucleotide for detection of IND-C1-WT  
  
 <400> 20  
 gtggttaaaa gagttttctt g 21  
  
 <210> 21  
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 <212> DNA  
 <213> Artificial  
  
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 <400> 21  
 attagcatgt aaaacactag 20  
  
 <210> 22  
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 <210> 23  
 <211> 18  
 <212> DNA  
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 <400> 23  
 acgagccacc accgtctg 18  
  
 <210> 24  
 <211> 21  
 <212> DNA  
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 <400> 24  
 gttcaaaagc agatgcagca g 21

<210> 25  
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 <210> 26  
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 <400> 26  
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 <210> 27  
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 <210> 28  
 <211> 34  
 <212> DNA  
 <213> Artificial  
  
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 <400> 28  
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 <210> 29  
 <211> 13  
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 <210> 30  
 <211> 13  
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 <213> Artificial  
  
 <220>  
 <223> oligonucleotide for detection of IND-A1-WT

|  |    |
|--|----|
| <400> 30<br>cgagccacca ccg   | 13 |
|  |    |
| <210> 31<br><211> 48<br><212> DNA<br><213> Artificial                |    |
| <220><br><223> oligonucleotide for detection of IND-C1-EMS01 and -WT |    |
| <400> 31<br>aggtggatct accatgaaat gaggattgtg gttaaaagag ttttcttt     | 48 |
|  |    |
| <210> 32<br><211> 23<br><212> DNA<br><213> Artificial                |    |
| <220><br><223> oligonucleotide for detection of IND-C1-EMS01         |    |
| <400> 32<br>atgtaatgag atcaataggt ttg                                | 23 |
|  |    |
| <210> 33<br><211> 23<br><212> DNA<br><213> Artificial                |    |
| <220><br><223> oligonucleotide for detection of IND-C1-WT            |    |
| <400> 33<br>gtgtaatgag atcaataggt ttg                                | 23 |
|  |    |
| <210> 34<br><211> 29<br><212> DNA<br><213> Artificial                |    |
| <220><br><223> oligonucleotide for detection of IND-C1-EMS03 and -WT |    |
| <400> 34<br>ccgtaacgta agggtagcg aggacccca                           | 29 |
|  |    |
| <210> 35<br><211> 14<br><212> DNA<br><213> Artificial                |    |
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| <400> 35<br>tagacggtgg tggc  | 14 |
|  |    |
| <210> 36<br><211> 14<br><212> DNA<br><213> Artificial                |    |

<220>  
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 cagacggtgg tggc 14

<210> 37  
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<210> 38  
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<210> 39  
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<220>  
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<210> 40  
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 <212> DNA  
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<220>  
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 cgtattgcat ctccttcac t 21