**Table S1** Grain test data of grain length, grain width, 100-grain weight and grain color of the hybrid offspring (F2) of ZY96-3 and GZ1.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sample name** | **100-grain weight** | **Grain length mean** | **Grain width mean** | **Grain color**  **White (0) / Purple (1)** |
| F2-002 | 4.617857143 | 7.757 | 3.412 | 0 |
| F2-007 | 4.744444444 | 7.234 | 3.445 | 1 |
| F2-020 | 3.481081081 | 7.016 | 3.169 | 1 |
| F2-022 | 4.091907514 | 7.036 | 3.386 | 0 |
| F2-025 | 4.65 | 7.817 | 3.400 | 1 |
| F2-030 | 4.997590361 | 7.564 | 3.546 | 1 |
| F2-031 | 4.731506849 | 7.811 | 3.499 | 1 |
| F2-032 | 4.358139535 | 7.823 | 3.324 | 0 |
| F2-033 | 4.789655172 | 7.622 | 3.415 | 1 |
| F2-034 | 4.93877551 | 7.212 | 3.602 | 1 |
| F2-035 | 4.162264151 | 7.535 | 3.248 | 1 |
| F2-036 | 4.075471698 | 7.599 | 3.217 | 0 |
| F2-037 | 4.538043478 | 7.369 | 3.361 | 1 |
| F2-038 | 4.478921569 | 7.827 | 3.447 | 1 |
| F2-039 | 3.703139013 | 7.427 | 3.283 | 1 |
| F2-041 | 4.547916667 | 7.484 | 3.341 | 1 |
| F2-042 | 4.860784314 | 7.763 | 3.526 | 1 |
| F2-047 | 4.254285714 | 7.432 | 3.371 | 1 |
| F2-048 | 3.077931034 | 7.325 | 3.035 | 1 |
| F2-049 | 5.553333333 | 7.510 | 3.721 | 0 |
| F2-054 | 4.007246377 | 7.544 | 3.224 | 0 |
| F2-056 | 4.615909091 | 7.456 | 3.556 | 0 |
| F2-057 | 4.892913386 | 7.767 | 3.506 | 1 |
| F2-058 | 3.547297297 | 7.512 | 3.090 | 1 |
| F2-059 | 5.087719298 | 7.535 | 3.584 | 0 |
| F2-061 | 5.125480769 | 7.751 | 3.538 | 1 |
| F2-063 | 4.565384615 | 7.693 | 3.367 | 0 |
| F2-065 | 4.792929293 | 7.504 | 3.620 | 0 |
| F2-067 | 5.01122449 | 7.577 | 3.841 | 0 |
| F2-068 | 4.448780488 | 7.198 | 3.489 | 1 |
| F2-069 | 4.441603053 | 7.696 | 3.344 | 1 |
| F2-070 | 4.379452055 | 7.519 | 3.238 | 1 |
| F2-071 | 4.861184211 | 7.723 | 3.503 | 0 |
| F2-072 | 5.111447811 | 8.084 | 3.601 | 1 |
| F2-074 | 4.861832061 | 7.329 | 3.449 | 1 |
| F2-075 | 4.160969388 | 7.470 | 3.335 | 0 |
| F2-076 | 4.918589744 | 7.514 | 3.606 | 1 |
| F2-078 | 5.538636364 | 7.771 | 3.655 | 1 |
| F2-079 | 4.803389831 | 7.070 | 3.487 | 1 |
| F2-081 | 5.158479532 | 7.599 | 3.580 | 1 |
| F2-082 | 5.192253521 | 7.820 | 3.589 | 0 |
| F2-083 | 4.064634146 | 7.197 | 3.280 | 1 |
| F2-087 | 4.285 | 7.123 | 3.485 | 1 |
| F2-093 | 4.781944444 | 7.594 | 3.401 | 1 |
| F2-095 | 4.419148936 | 7.344 | 3.449 | 0 |
| F2-099 | 4.849264706 | 7.441 | 3.540 | 0 |
| F2-101 | 4.257216495 | 7.485 | 3.341 | 1 |
| F2-102 | 3.844308943 | 7.433 | 3.360 | 1 |
| F2-104 | 3.527777778 | 7.446 | 3.250 | 0 |
| F2-106 | 4.529545455 | 7.438 | 3.422 | 1 |
| F2-107 | 3.349333333 | 6.972 | 3.221 | 0 |
| F2-108 | 4.139189189 | 7.586 | 3.239 | 1 |
| F2-109 | 4.196761134 | 7.297 | 3.264 | 1 |
| F2-110 | 3.792253521 | 7.444 | 3.208 | 1 |
| F2-111 | 5.607228916 | 7.697 | 3.739 | 0 |
| F2-112 | 4.028391167 | 7.368 | 3.377 | 0 |
| F2-113 | 4.505982906 | 7.415 | 3.408 | 1 |
| F2-115 | 3.521495327 | 7.445 | 3.256 | 1 |
| F2-116 | 4.76185567 | 7.396 | 3.425 | 1 |
| F2-118 | 3.474566474 | 7.241 | 3.159 | 1 |
| F2-121 | 4.379372197 | 7.467 | 3.472 | 1 |
| F2-123 | 5.071710526 | 7.614 | 3.583 | 0 |
| F2-124 | 5.377403846 | 7.791 | 3.679 | 1 |
| F2-126 | 4.270212766 | 7.312 | 3.344 | 1 |
| F2-127 | 4.598019802 | 7.697 | 3.421 | 0 |
| F2-128 | 4.352760736 | 7.672 | 3.381 | 0 |
| F2-130 | 5.181045752 | 7.618 | 3.629 | 0 |
| F2-131 | 3.809708738 | 7.603 | 3.197 | 1 |
| F2-132 | 3.7456621 | 7.608 | 3.194 | 1 |
| F2-133 | 4.198850575 | 7.996 | 3.194 | 1 |
| F2-134 | 3.466423358 | 7.321 | 3.215 | 1 |
| F2-135 | 2.976870748 | 7.149 | 3.025 | 0 |
| F2-137 | 4.434146341 | 7.551 | 3.386 | 0 |
| F2-138 | 3.94516129 | 7.294 | 3.297 | 1 |
| F2-139 | 3.816055046 | 7.458 | 3.286 | 1 |
| F2-140 | 2.885098039 | 6.489 | 3.007 | 0 |
| F2-141 | 3.1 | 6.850 | 2.911 | 0 |
| F2-143 | 3.396052632 | 6.886 | 3.159 | 1 |
| F2-147 | 3.468367347 | 6.774 | 3.237 | 0 |
| F2-150 | 2.36969697 | 7.015 | 2.865 | 1 |
| F2-153 | 3.787134503 | 6.936 | 3.200 | 0 |
| F2-155 | 3.273786408 | 6.810 | 2.960 | 1 |
| F2-156 | 4.429090909 | 7.023 | 3.440 | 1 |
| F2-157 | 4.040506329 | 6.931 | 3.226 | 0 |
| F2-158 | 3.520863309 | 6.840 | 3.093 | 1 |
| F2-159 | 3.061309524 | 6.909 | 3.078 | 1 |
| F2-160 | 3.055 | 6.740 | 3.027 | 1 |
| F2-161 | 4.160147601 | 7.163 | 3.291 | 0 |
| F2-164 | 3.875897436 | 7.428 | 3.248 | 1 |
| F2-165 | 3.233557047 | 6.706 | 3.039 | 1 |
| F2-168 | 4.483850932 | 7.500 | 3.376 | 0 |
| F2-171 | 3.828813559 | 6.979 | 3.037 | 1 |
| F2-172 | 4.313793103 | 7.612 | 3.267 | 0 |
| F2-177 | 3.85375 | 6.974 | 3.222 | 1 |
| F2-182 | 3.462337662 | 7.095 | 3.085 | 0 |
| F2-183 | 4.979268293 | 7.367 | 3.576 | 0 |
| F2-184 | 4.091111111 | 7.462 | 3.194 | 0 |
| F2-185 | 4.556603774 | 7.499 | 3.380 | 0 |
| F2-186 | 3.201204819 | 7.069 | 2.976 | 0 |
| F2-187 | 4.776315789 | 7.753 | 3.370 | 0 |
| F2-188 | 4.658695652 | 8.025 | 3.359 | 1 |
| F2-190 | 4.72260274 | 7.456 | 3.466 | 0 |
| F2-191 | 4.37254902 | 7.090 | 3.408 | 1 |
| F2-192 | 4.651304348 | 7.270 | 3.476 | 1 |
| F2-193 | 4.897959184 | 7.344 | 3.579 | 0 |
| F2-194 | 3.983050847 | 7.187 | 3.285 | 1 |
| F2-198 | 4.17244898 | 7.539 | 3.494 | 1 |
| F2-199 | 3.99800995 | 7.332 | 3.342 | 1 |
| F2-200 | 3.967889908 | 7.465 | 3.180 | 1 |
| F2-202 | 5 | 7.710 | 3.511 | 0 |
| Average Value | 4.266937649 | 7.400327273 | 3.349463636 |  |

**Table S2** Grain test data of grain length, grain width and 100-grain weight of male parent ZY96-3 and female parent GZ1.

|  |  |  |  |
| --- | --- | --- | --- |
| **Sample name** | **100-grain weight** | **Grain length mean** | **Grain width mean** |
| **Male Parent(ZY96-3）** | 6.83 | 7.64 | 3.62 |
|  | 6.84 | 7.59 | 3.61 |
|  | 6.71 | 7.69 | 3.62 |
|  | 6.73 | 7.74 | 3.59 |
|  | 6.67 | 7.59 | 3.59 |
|  | 6.64 | 7.60 | 3.62 |
|  | 6.70 | 7.65 | 3.62 |
|  | 6.66 | 7.61 | 3.60 |
|  | 6.66 | 7.62 | 3.60 |
|  | 6.65 | 7.62 | 3.63 |
| Average Value | 6.7775 | 7.665 | 3.61 |
| **Female Parent(GZ1）** | 3.34 | 6.13 | 2.8 |
|  | 3.27 | 6.11 | 2.79 |
|  | 3.3 | 6.01 | 2.78 |
|  | 3.3 | 6.07 | 2.8 |
|  | 3.34 | 6.06 | 2.81 |
|  | 3.21 | 6.03 | 2.75 |
|  | 3.28 | 6.05 | 2.79 |
|  | 3.36 | 6.08 | 2.84 |
|  | 3.35 | 6.07 | 2.81 |
|  | 3.20 | 5.99 | 2.75 |
| Average Value | 3.3025 | 6.08 | 2.7925 |

**Table S3 Inferentially annotated genes identified within the 7.1-cM candidate interval (chr3A-38613887 to chr3A-43635422) of GW based on IWGSC RefSeq v1.0 (IWGSC et al., 2018).**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene ID** | **Start position (bp)** | **Stop position (bp)** | **Length (bp)** | **Gene description/Predicted function** |
| TraesCS3A01G065600 | 38613887 | 38615552 | 1665 | Amino acid permease |
| TraesCS3A01G065700 | 38621153 | 38622697 | 1544 | E3 ubiquitin-protein ligase |
| TraesCS3A01G065800 | 38628107 | 38628697 | 590 | E3 ubiquitin-protein ligase |
| TraesCS3A01G065900 | 38657457 | 38658404 | 947 | E3 ubiquitin-protein ligase |
| TraesCS3A01G066000 | 38992001 | 38993618 | 1617 | KH domain-containing protein |
| TraesCS3A01G066100 | 39185479 | 39186633 | 1154 | 3'-phosphoinositide-dependent protein kinase 1 |
| TraesCS3A01G066200 | 39574244 | 39575395 | 1151 | L-carnitine/gamma-butyrobetaine antiporter |
| TraesCS3A01G066300 | 39658697 | 39659223 | 526 | TIR-NBS-LRR class disease resistance protein |
| TraesCS3A01G066400 | 39678462 | 39678850 | 388 | L-carnitine/gamma-butyrobetaine antiporter |
| TraesCS3A01G066500 | 39698694 | 39699082 | 388 | Ribose-5-phosphate isomerase A |
| TraesCS3A01G066600 | 40152371 | 40152708 | 337 | Phospholipid phosphatase 5 |
| TraesCS3A01G066700 | 40173113 | 40173509 | 396 | lectin protein kinase family protein |
| TraesCS3A01G066800 | 40181011 | 40184517 | 3506 | Actin cross-linking protein, putative |
| TraesCS3A01G066900 | 40185576 | 40186407 | 831 | Cysteine proteinase RD21a |
| TraesCS3A01G067000 | 40189531 | 40190345 | 814 | S-locus cysteine-rich protein (SCR) |
| TraesCS3A01G067100 | 40284461 | 40285192 | 731 | S-locus cysteine-rich protein (SCR) |
| TraesCS3A01G067200 | 40286499 | 40287120 | 621 | tRNA (guanine(37)-N1)-methyltransferase |
| TraesCS3A01G067300 | 40349182 | 40360520 | 11338 | Threonine--tRNA ligase |
| TraesCS3A01G067400 | 40389534 | 40390079 | 545 | GTP cyclohydrolase 1 |
| TraesCS3A01G067500 | 40555480 | 40556191 | 711 | 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase 1 |
| TraesCS3A01G067600 | 40560558 | 40565782 | 5224 | DNA (Cytosine-5-)-methyltransferase |
| TraesCS3A01G067700 | 40822815 | 40825086 | 2271 | Isoaspartyl peptidase/L-asparaginase |
| TraesCS3A01G067800 | 40826588 | 40831583 | 4995 | F-box/LRR-repeat protein |
| TraesCS3A01G067900 | 40859116 | 40861284 | 2168 | Scarecrow transcription factor family protein |
| TraesCS3A01G068000 | 40871360 | 40873510 | 2150 | Scarecrow transcription factor family protein |
| TraesCS3A01G068100 | 40913403 | 40915343 | 1940 | tRNA N6-adenosine threonylcarbamoyltransferase |
| TraesCS3A01G068200 | 40936378 | 40939434 | 3056 | Disease resistance protein (NBS-LRR class) family |
| TraesCS3A01G068300 | 40945173 | 40948771 | 3598 | NBS-LRR disease resistance protein |
| TraesCS3A01G068400 | 40977707 | 40978127 | 420 | GTPase Der |
| TraesCS3A01G068500 | 41048111 | 41050196 | 2085 | Disease resistance protein (NBS-LRR class) family |
| TraesCS3A01G068600 | 41064235 | 41065650 | 1415 | NBS-LRR disease resistance protein |
| TraesCS3A01G068700 | 41117805 | 41121915 | 4110 | NBS-LRR disease resistance protein |
| TraesCS3A01G068800 | 41149964 | 41153017 | 3053 | NBS-LRR disease resistance protein |
| TraesCS3A01G068900 | 41178317 | 41179372 | 1055 | NBS-LRR disease resistance protein |
| TraesCS3A01G069000 | 41180909 | 41181568 | 659 | Disease resistance protein (TIR-NBS-LRR class) family |
| TraesCS3A01G069100 | 41239119 | 41240093 | 974 | NBS-LRR disease resistance protein |
| TraesCS3A01G069200 | 41368832 | 41372790 | 3958 | Disease resistance protein (NBS-LRR class) family |
| TraesCS3A01G069300 | 41616718 | 41619747 | 3029 | Disease resistance protein (NBS-LRR class) family |
| TraesCS3A01G069400 | 41650569 | 41653161 | 2592 | arginine-tRNA protein transferase 2 |
| TraesCS3A01G069500 | 41658032 | 41658277 | 245 | 3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ |
| TraesCS3A01G069600 | 41953819 | 41957090 | 3271 | transmembrane protein, putative (DUF247) |
| TraesCS3A01G069700 | 41990881 | 41998604 | 7723 | Adenylyl-sulfate kinase |
| TraesCS3A01G069800 | 42016913 | 42019963 | 3050 | NBS-LRR disease resistance protein |
| TraesCS3A01G069900 | 42024221 | 42032372 | 8151 | Helicase, putative |
| TraesCS3A01G070000 | 42206148 | 42206965 | 817 | Cysteine protease |
| TraesCS3A01G070100 | 42209662 | 42211161 | 1499 | Acetate/butyrate--CoA ligase AAE7, peroxisomal |
| **TraesCS3A01G070200** | **42319880** | **42320278** | **398** | **regulatory-associated protein of TOR 2 (RAPTOR2)** |
| TraesCS3A01G070300 | 42336585 | 42355697 | 19112 | WAT1-related protein |
| TraesCS3A01G070400 | 42365645 | 42371268 | 5623 | Serine protease HTRA1 |
| TraesCS3A01G070500 | 42378078 | 42383556 | 5478 | Serine protease HTRA1 |
| TraesCS3A01G070600 | 42442268 | 42444261 | 1993 | Ribosomal protein S24/S35 |
| TraesCS3A01G070700 | 42793181 | 42794166 | 985 | Glutamyl endopeptidase |
| TraesCS3A01G070800 | 42884521 | 42884891 | 370 | Short-chain dehydrogenase TIC 32, chloroplastic |
| TraesCS3A01G070900 | 43011381 | 43012368 | 987 | Acetylornithine aminotransferase, mitochondrial |
| TraesCS3A01G071000 | 43121758 | 43124183 | 2425 | Aminotransferase-like, plant mobile domain-containing protein |
| TraesCS3A01G071100 | 43288437 | 43293339 | 4902 | Serine protease HTRA1 |
| **TraesCS3A01G071200** | **43634217** | **43635422** | **1205** | **Starch synthase, chloroplastic/amyloplastic** |

**Table S4** DNA sequences of chr3A-38613887 and chr3A-43635422 used for designing simple sequence repeat (SSR) markers.

|  |  |
| --- | --- |
| **Position** | **DNA sequence** |
| **Chr3A-38613887** | TTCTTTAACCTAAATGCGTAAAAGAGGATTTTATTGTCAATTCTCCAGTGGTCGATGGCTGAACTTTTTATTAAGAAAGAGAGAGCACTACCGAACGTTTGCAGGGGCATGCATCTGCTCAGCCGTGCTCGGTGGCATGATAGTTTCGTGATCTACAAAGTTATTGAATTTCGTGCGAGGATACACTAAGTTTTAAGTCTTAATTTTCAATACCTGTGATTTTTGTTGTTCTTTTGTATCAAGTTTCAGTAGATGAAACTTAATGAAATTTTAAAAACTCATCAAAATGTATTCGAATTAGGTCTTATTTGAAAGCCTTTGTCACAAGAGACACGAATATGAAAACAAAAAGTAATTGGATATCCGGTTCAAAAGATAAGAAAGATTGAAAATCGAAAGCCAAAAAAAACTGTCGATGGCCCCACCTGCATGCCACAAATCCCCTATCAGAACTCTTTGTTTGTACATATTAATTTCTCCTTCTCTTAGTCGGTTGGCAAAGTTTCTGCCTTTGTTTATCTACCACTACCATAAAACCAGCACACAGAAAGAGCAAGCATACAAGTGTTACTTGCCTCGCTCGCTCACTCTTTTGCAGCAATGGAGAATCCCCGCACCGATCCCAGGGACTACGACGACGACGGCGGCCTGAAGCGCACCGGTGAGGAAGCGGCCGGTGACGTTCGCGTAGCTATCGTGGTTGCAGCAAATCGTCTGATTCTGTGGTGTTGCAGGCACGGTATGGACGGCCACTGCACGCATCATCACGGCCGTGATCGGGTCTGGCGTCCTGGCGCTGCCGTGGGCATCGGCGCAGCTCGGCTGGGTGATCTACCCGATCATGGTGCTGCTCTTCGCCGGCATCATCTGCTACACCTCCGCGCTGCTCTCGGACTGCTACCGATCCGGCGACCCGAGCCACGGCGAGCGCAACTGCACATACATGGACACCGTCAAGGCCAGCCTAGGTACGTGTCCTAAGTTCCTAACTCCTACATCGATGGAGAGGCAGCTATGCCCATGTCTTCAACTTTACGGATCTTAACTAGCACACTCATGTCTACTTTGTCATTTCGCCCATGGATGGATCCAACAGGACGCGCACAGGTTTGGCTATGCCAGTTTTCTGCATACTCCAACGTCTTTGGGGTGGCCATCGGGCATACCATCGCCGCCGGCATGAGCATGTTGGCAATCCAGCGGAGGGCTAGCTGCTTCCAGCACAACAAGGGCCACCGCCACCCGTGCAATTTCCCAATCTGGCCCTATATGATAACCTTCGGCGTGGCGGAGATCTTCTTCTCGCAGATCCCGGAGTACCATACGTGGTGGTTCTCATATCTCGGCCCCGCCATGTCCTTCACCTATTGCTCTATCGGCGTCGGGATCAGCATCGCCAAAGTCGTCGGTAACACACGCACACGCTGCTCAATGAATGATCTATGGCAACGGCATCAATCATGTCATGCTTGAACCTTGGATGCGTGCAGAGAACGGAGTCCTCAAGGGCGGCCTCGTCGGCATCGGCATGACCGCGGTGACCGCGTCCCCGATGAGTAAGGTGTGGGGAAGCCTGGAGGCGCTGGGCGTCATCGCCTTCGTCTACTGCTACTCAAGAATCTTAATCGAGATCCAGGACACCATCAAAGCGCCTCCTCCGCCCGAGTCCAAGGTCATGAAGCTTGCCACCGCCATGGGCGTCGCTGTCACCACGTTCTTATACCTGCTCTTTGGCTTCATGGGGTACGCCGCGCTGGGGGGCGCTACCCCAGGGAACCTGCTCGCGGGGCTCGGCTTCTACGAGCCATACTGGGTCGTCGACATCGCCAACGTGGCAATCATCGTCCACCTCGCCGTCGCTTACCAGGTCTACTGCCGGCCCATTTACGACTTCGTCGAGAGGTGCGCCGCGCGTAGGTGGCCGGAGTCGTCCTACGTCACAAGGGAGTTCGACGTGCTCGTCTTGAGGTCGTCGTACAAGCTGAACCTATTCCGAGCTACGTGGCGGACCGCGTTCGTGGTCACCACCACGGTGGTGGCGGCGCTGCTGCCCTTCTTCCACGACGTGGTGGCGCTCGTCGGCGCACTGGGGTTCTGGCCGTTGTGTGTCTACATCCCAGTGGAGATGTACGTGACCCAGAAGAAGGTGCTTAGGTGGAGCCCCCTGTGGGTGTGGCTGCAGATCCTCAGCCTCGGCTGCCTCTTCGTCTGCTTGGCCGCCATGGCCGCGTCCATCGTCGGTATCATCACTATTCATAAGAAGTAATATTTGGGTGTGCAGGGTGATACTGATACTAGGGTTCTTATCTTGCTGAGGGTGTAATGTTAGGATTTGGCTTGCTATGTACGGCTCTTGTAAACCGGATCCTCTTAGACTGGCTGCAACGGTAGCATCTTGTGCTCGACTAGCCAGCAAGTGAGTTTGTTAAACTTTTTCTTTTTCTTATTGTCGAAAGGAGATCTTTTCTTGTTGTCCAGGGGAGCCTAAAAGCAGCCGATTTTCCAGCTAGGCATGCTTTTCTAGTGTAGGTTAGATTATCGCACACGGTTTAAGCGACGGTGGGAGGTGAGGGGGTGATGATGGTGGTGATGGAGGTGTTAGGACATACTCCCTTCGTTCCTAAATATTTGTCTTTCTAAATATTTCAAATGACTACTACATACGGATATATGTAGACATATTCTAGAATGTAGATTCACTCATTTTGCTTCGTATGTAGTCACTTGTTAAAATGCCTAGAAAGACAAGTATTTAGAAACGGAGGAAGTATATGTAGAAAAACCACGTGCAATTGGACATCAGTTGAGTAGTGCGTTTTATAAAAACAAAACATTAGGGATCCATTGCACATATGGTGAATAACAC |
| **Chr3A-43635422** | GCCAGCGCTGCAGATTTATTTGCTCACATGTGCTGTGCAGATCTGGCTCGCTCTCGCATGGAGCAACATCCGCAGCTAGCTAGCTAGCTAATGTGCTCTGGCTTATCACTTAAAACTTAAAAGCCAGTAGATGCATACAATCACACTTGCATTACTTCATGAACAGATTCGGAGACCGTTCCTAAATATAAGATTTTTTAAAGGTTCCACTATGCATACGGAGCAAAATGCGTGAATCTATATTTTAAGATATGTCTATATACATCCGTATGCAGTCCATAATGCAATATCCAAAAGGTCTTATATTTAAAGACGGAGGAAGTAATAGATTTATGCATACATCATGTGTGTTTAACATGTACGTATTGTTCATTGGAACATTTTTTTTTTACAAGTTGACATCTAAACATGTCCGATGTCATGGATGAAGGTTTATGGTGCGAGCGGGTGTTTAGAGACCATCAACTCTTTGTGGTGCGTCTCCATACCGCTACTGACAATGTTTTTCAAGGCAATGGCTTTATTGTCAGCAACAATAAAACCATCTGTGACATAGTATCATGTCAACATGTCGTCAAGATGCTTCCCGTGGGTGGAACAATGGCTGTTTATTTCTTCAACTCCGACGGATTGATCCCACGCCGATACAATGCAAGAATAATTCGTACTGATGAGGGTCGGGATCTTGCTTGGCTGCGGGCTCAAGATGTCTATGAACCAGTGACTTGTCTGAGGTTCTTCGACCCACCATATGCTTCTGGGTGGAATGTTGTTGCGCTGGCTTATACCACATTGGATGGCTCTTCTGCTACTATTCTAGAGCCAGGGACGTATTCTGGTCAAATAACGTAATGCACTCTTCCGATACTTAGTATCTCTTACTTACTAGAACATGGTACTAGTAGTATAATGTAGCATGAAAATTCCTTTTGTCTCTACTCGTGCTAATCATTAGAATATTTATTTATTGCAGCAATGAACCAGATGAAGTGTCGCTTACCTGCAGTTGTACATCTAAGCAAGGTGCATCAGGTTCACCTCTTATTTTGCCACGGATAGACAGGGTAGTTGGGGTGCTTGCCGGAGCTTCACATGCATCGGTATACGCTGTTCCTGTCACACATATAAGGGAGTTCTTAATAGAGTGGCTTGGTGGAGACGAAGACCTGGTAAAATCCTTGAACTTTATTGCAACATGTTTTATACTCGCTCCGCCTCAAATTACTTGTCGCTCGCTCACATAAATCCATTTGAGCCACAAGTAATTCGGGACGGAGGCAGTATCTAATAAGTATGTTTTTTGGTTTGACTGATTTATAACCTTTCCATTTCATACATTTGTTAGAACGAAGTACGAACTGCTGGGTTGGTTATGCTTGTCGCAAAGGGCCAATAGTACGATGAGGTAATGTATGGGTGCCCTTTCTCAAATTCTCATAAGAAAGACCGTTGTATGTCAATTGATACTAGTTTAAGACCAAATCGTCCTGTATTCAATACGAGTGTTGTATATGGAAGTATAGATAAAAGGCATCCATGCTAGTATGATACATGTGGTAAGCTATCTCAAAACAACAAAAATGTGCAAGTTTGCAAATGTACGCTTTAACTTAACCTGAAGTCTAAATAGTGCACGCACAACGACTACTTTTGACAAGCACCTGCTGCGTGCCCACACAGAGAAAATCATTTGTCATCGTTTATGTAAATAAGTATGACACCGTTTTTTTCCTCTTCCAGATCTAATATACTCTTTGTATGCAGGACTTGAACACTGGACGGAAACTTGGGGAGGAAGAACCATGAGAAGTTGTCAGAATTTATCCTAAAAAAAGTTGACGTGCGCGTGGCGTAGTTCTAGGTTTCATAGTTAGTATGCTGGAATGTTTTAATCCTAGACTTTGTAGCTAGTCATTGGCTGGGCTTTGCTCATTTTAGATTGTATACTGATCTACTACTTATTTCTTTCTTAACTTTGCTACCTTATTGTCTTGCGGTTTGAATTATGTCACCGTATTAATTTCTCTGTGTGTTAGACAAACATGATATGATTAAACGTGTGTTAATTCGTTCCATTGTTAATTGCAGTGCAGTCTCCTCTTTATATGTGGAACTAAATGAACAGCACCAATAGAAGAATGCTGCTATATAATTTTAGACAGCCCAAACAGGGCAATGATGCTCCTCTACGAAGCTTGGCATATTACTACAGGCATGTATTGCTCTCCGCAGCAAAGTTCATGTAGAACATGTTTATGGATAAATGACATTTTTATTAACTCAGAATGTAGCATCAAACGGATACAAAGCATGATGAGTAACACCCAGAGTCCGCATAACAAGATGCACACAGCCAAACACGAACGTTGCGACAAAAGATAAATAAAAAACCGACATGGTGACAAC |

**Table S5** Inferentially annotated genes identified in the 2B candidate interval (chr2B-139340708 to chr2B-189748943) and 3B candidate interval (chro3B-556934804 to chr3B-562274308) of GL based on IWGSC RefSeq v1.0 (IWGSC et al., 2018).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene ID** | **Start position (bp)** | **Stop position (bp)** | **Length (bp)** | **Gene description/Predicted function** |
| TraesCS2B01G166400 | 139340708 | 139343104 | 2396 | zinc transporter-like protein |
| TraesCS2B01G166500 | 139345394 | 139346375 | 981 | Zinc finger MYM-type protein 1 |
| TraesCS2B01G166600 | 139351391 | 139353559 | 2168 | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex |
| TraesCS2B01G166700 | 139361047 | 139363243 | 2196 | Transposase |
| TraesCS2B01G166800 | 139398180 | 139401136 | 2956 | Endonuclease/exonuclease/phosphatase family protein |
| TraesCS2B01G166900 | 139569897 | 139570538 | 641 | transmembrane protein, putative (DUF679) |
| TraesCS2B01G167000 | 139793626 | 139816285 | 22659 | Transcription-associated protein 1 |
| TraesCS2B01G167100 | 139914313 | 139916649 | 2336 | Glycoprotein membrane GPI-anchored |
| TraesCS2B01G167200 | 140244680 | 140245963 | 1283 | F-box protein |
| TraesCS2B01G167300 | 140519813 | 140521039 | 1226 | Cysteine-rich receptor-kinase-like protein |
| TraesCS2B01G167400 | 140747858 | 140749039 | 1181 | F-box/RNI-like superfamily protein |
| TraesCS2B01G167500 | 140750519 | 140756635 | 6116 | Cytochrome P450, putative |
| TraesCS2B01G167600 | 140763452 | 140773200 | 9748 | Pre-mRNA-splicing factor SYF1 |
| TraesCS2B01G167700 | 140775124 | 140777446 | 2322 | Sulfotransferase |
| TraesCS2B01G167800 | 140785911 | 140788521 | 2610 | Ubiquitin-like protein |
| TraesCS2B01G167900 | 140843989 | 140847191 | 3202 | BZIP transcription factor |
| TraesCS2B01G168000 | 140847510 | 140850732 | 3222 | ATP synthase mitochondrial F1 complex assembly factor 2 |
| TraesCS2B01G168100 | 140851844 | 140853271 | 1427 | Bifunctional glutamine synthetase adenylyltransferase/adenylyl-removing enzyme |
| TraesCS2B01G168200 | 140852057 | 140853166 | 1109 | Gibberellin receptor GID1A |
| TraesCS2B01G168300 | 141147392 | 141148435 | 1043 | Gibberellin receptor GID1A |
| TraesCS2B01G168400 | 141203336 | 141205467 | 2131 | Zinc transporter |
| TraesCS2B01G168500 | 141282515 | 141283588 | 1073 | Gibberellin receptor GID1A |
| TraesCS2B01G168600 | 141367316 | 141368528 | 1212 | Gibberellin receptor GID1A |
| TraesCS2B01G168700 | 141559309 | 141564696 | 5387 | RNA binding protein |
| TraesCS2B01G168800 | 141694675 | 141697573 | 2898 | Quinoprotein amine dehydrogenase, beta chain-like; RIC1-like guanyl-nucleotide exchange factor |
| TraesCS2B01G168900 | 141836797 | 141841524 | 4727 | B3 domain-containing protein |
| TraesCS2B01G169000 | 141874974 | 141877590 | 2616 | Cytochrome P450 |
| TraesCS2B01G169100 | 141913537 | 141916152 | 2615 | Cytochrome P450 |
| TraesCS2B01G169200 | 141986139 | 141989354 | 3215 | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase |
| TraesCS2B01G169300 | 142239046 | 142245398 | 6352 | C2 domain-containing protein |
| TraesCS2B01G169400 | 142373560 | 142377649 | 4089 | Stomatal closure-related actin-binding protein 1 |
| TraesCS2B01G169500 | 142446090 | 142446332 | 242 | Cold shock protein |
| TraesCS2B01G169600 | 142675677 | 142675886 | 209 | Cold shock protein |
| TraesCS2B01G169700 | 142863492 | 142865941 | 2449 | Transcription elongation factor-related family protein |
| TraesCS2B01G169800 | 142888444 | 142889331 | 887 | Myb/SANT-like DNA-binding domain protein |
| TraesCS2B01G169900 | 142944550 | 142945721 | 1171 | Peroxidase |
| TraesCS2B01G170000 | 142999224 | 143000898 | 1674 | Cysteine-rich receptor-kinase-like protein |
| TraesCS2B01G170100 | 143025300 | 143025812 | 512 | Lysine--tRNA ligase |
| TraesCS2B01G170200 | 143136294 | 143140205 | 3911 | DNA/RNA helicase protein |
| TraesCS2B01G170300 | 143272877 | 143274763 | 1886 | Pentatricopeptide repeat-containing protein |
| TraesCS2B01G170400 | 143280891 | 143282018 | 1127 | U3 small nucleolar RNA-associated protein 18-like protein |
| TraesCS2B01G170500 | 143483896 | 143485002 | 1106 | U3 small nucleolar RNA-associated protein 18-like protein |
| TraesCS2B01G170600 | 143822573 | 143824765 | 2192 | Pentatricopeptide repeat-containing protein |
| TraesCS2B01G170700 | 143935223 | 143938276 | 3053 | ATP-dependent RNA helicase DeaD |
| **TraesCS2B01G170800** | **144021136** | **144022430** | **1294** | **GDSL esterase/lipase** |
| **TraesCS2B01G170900** | **144034321** | **144035705** | **1384** | **GDSL esterase/lipase** |
| **TraesCS2B01G171000** | **144076886** | **144078584** | **1698** | **GDSL esterase/lipase** |
| TraesCS2B01G171100 | 144427688 | 144431689 | 4001 | S2 self-incompatibility locus-linked pollen 3.2 protein |
| TraesCS2B01G171200 | 144432166 | 144433982 | 1816 | 4-coumarate-CoA ligase |
| TraesCS2B01G171300 | 144596243 | 144597358 | 1115 | Plastid-lipid associated protein PAP / fibrillin family protein |
| TraesCS2B01G171400 | 144603207 | 144605156 | 1949 | 10 kDa chaperonin |
| TraesCS2B01G171500 | 144605519 | 144609277 | 3758 | Methyltransferase family protein, putative |
| TraesCS2B01G171600 | 144650256 | 144654866 | 4610 | protein kinase family protein |
| TraesCS2B01G171700 | 146006936 | 146007832 | 896 | AGAMOUS-like MADS-box protein |
| TraesCS2B01G171800 | 146435615 | 146438453 | 2838 | calcium ion-binding protein |
| TraesCS2B01G171900 | 146440459 | 146442544 | 2085 | Heat shock transcription factor |
| TraesCS2B01G172000 | 146453400 | 146454171 | 771 | nuclear poly(a) polymerase |
| TraesCS2B01G172100 | 146634611 | 146638883 | 4272 | Xylulose kinase |
| TraesCS2B01G172200 | 146660837 | 146664040 | 3203 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 |
| TraesCS2B01G172300 | 146716213 | 146717802 | 1589 | FAD-binding Berberine family protein |
| TraesCS2B01G172400 | 146733967 | 146737128 | 3161 | Small nuclear RNA activating complex (SNAPc), subunit SNAP43 protein |
| TraesCS2B01G172500 | 146779633 | 146781416 | 1783 | Carboxyl methyltransferase |
| TraesCS2B01G172600 | 146901316 | 146904465 | 3149 | Protein arginine methyltransferase |
| TraesCS2B01G172700 | 146904851 | 146906600 | 1749 | Thymidylate kinase |
| TraesCS2B01G172800 | 146913259 | 146915334 | 2075 | Eukaryotic translation initiation factor 6 |
| TraesCS2B01G172900 | 146954784 | 146956562 | 1778 | Pyrrolidone-carboxylate peptidase |
| TraesCS2B01G173000 | 146963926 | 146965041 | 1115 | Peroxidase |
| TraesCS2B01G173100 | 146983050 | 146986186 | 3136 | Transposon Ty3-I Gag-Pol polyprotein |
| TraesCS2B01G173200 | 146992648 | 146993607 | 959 | Peroxidase |
| TraesCS2B01G173300 | 146995858 | 146997330 | 1472 | Peroxidase |
| TraesCS2B01G173400 | 147284902 | 147286249 | 1347 | Peroxidase |
| TraesCS2B01G173500 | 147490875 | 147492494 | 1619 | Peroxidase |
| TraesCS2B01G173600 | 147830010 | 147831164 | 1154 | Peroxidase |
| TraesCS2B01G173700 | 147830405 | 147830761 | 356 | RNA-binding (RRM/RBD/RNP motifs) family protein |
| TraesCS2B01G173800 | 147869763 | 147870917 | 1154 | Peroxidase |
| TraesCS2B01G173900 | 148036672 | 148037909 | 1237 | Peroxidase |
| TraesCS2B01G174000 | 148143928 | 148144645 | 717 | Glutaredoxin-like family protein |
| TraesCS2B01G174100 | 148237525 | 148240812 | 3287 | Leucine--tRNA ligase |
| TraesCS2B01G174200 | 148400928 | 148404388 | 3460 | Phosphoserine phosphatase |
| TraesCS2B01G174300 | 148424043 | 148425272 | 1229 | Peroxidase |
| TraesCS2B01G174400 | 148589670 | 148590518 | 848 | Peroxiredoxin |
| TraesCS2B01G174500 | 148863890 | 148866084 | 2194 | tolB protein-like protein |
| TraesCS2B01G174600 | 149016538 | 149028348 | 11810 | Kinesin-like protein |
| TraesCS2B01G174700 | 149835544 | 149841608 | 6064 | Serine/threonine-protein kinase haspin |
| TraesCS2B01G174800 | 149842731 | 149845969 | 3238 | SNARE |
| TraesCS2B01G174900 | 150140967 | 150142005 | 1038 | Glycine rich protein 3 |
| TraesCS2B01G175000 | 150200275 | 150201326 | 1051 | Glycine rich protein 3 |
| TraesCS2B01G175100 | 150338203 | 150339249 | 1046 | Glycine rich protein 3 |
| TraesCS2B01G175200 | 150535639 | 150538275 | 2636 | Gag polyprotein |
| TraesCS2B01G175300 | 150595853 | 150599894 | 4041 | Pyruvate dehydrogenase kinase, mitochondrial |
| TraesCS2B01G175400 | 150604268 | 150608254 | 3986 | Meiosis arrest female protein 1 |
| TraesCS2B01G175500 | 150704318 | 150707358 | 3040 | Meiosis arrest female protein 1 |
| TraesCS2B01G175600 | 150708593 | 150710534 | 1941 | Chaperone protein DnaJ |
| TraesCS2B01G175700 | 150710719 | 150712551 | 1832 | Pentatricopeptide repeat-containing protein |
| TraesCS2B01G175800 | 150713109 | 150717410 | 4301 | Non-specific serine/threonine protein kinase |
| TraesCS2B01G175900 | 150938651 | 150941879 | 3228 | 50S ribosomal protein L7Ae |
| TraesCS2B01G176000 | 150984844 | 150985518 | 674 | Dirigent protein |
| TraesCS2B01G176100 | 151102885 | 151103481 | 596 | UDP-glycosyltransferase |
| TraesCS2B01G176200 | 151103581 | 151104363 | 782 | UDP-glycosyltransferase |
| TraesCS2B01G176300 | 151460371 | 151460688 | 317 | Zinc finger protein |
| TraesCS2B01G176400 | 151485224 | 151485823 | 599 | Dirigent protein |
| TraesCS2B01G176500 | 151488648 | 151489934 | 1286 | Dirigent protein |
| TraesCS2B01G176600 | 151627559 | 151628146 | 587 | Dirigent protein |
| TraesCS2B01G176700 | 151643652 | 151659393 | 15741 | chromatin remodeling 1 |
| TraesCS2B01G176800 | 151901631 | 151902467 | 836 | Aspartic proteinase cdr1 |
| TraesCS2B01G176900 | 151903298 | 151904431 | 1133 | DNA-binding storekeeper protein-related transcriptional regulator |
| TraesCS2B01G177000 | 152156927 | 152158750 | 1823 | tRNA pseudouridine synthase B |
| TraesCS2B01G177100 | 152175687 | 152175965 | 278 | Low temperature and salt responsive protein |
| TraesCS2B01G177200 | 152183264 | 152185345 | 2081 | Pentatricopeptide repeat-containing protein |
| TraesCS2B01G177300 | 152472323 | 152474152 | 1829 | Cytochrome P450 |
| TraesCS2B01G177400 | 152503304 | 152505168 | 1864 | Cytochrome P450 |
| TraesCS2B01G177500 | 152569091 | 152570845 | 1754 | Cytochrome P450 |
| TraesCS2B01G177600 | 152608437 | 152610784 | 2347 | Cytochrome P450 |
| TraesCS2B01G177700 | 152701590 | 152702222 | 632 | cyclin-dependent kinase inhibitor |
| TraesCS2B01G177800 | 152714502 | 152714837 | 335 | Retrovirus-related Pol polyprotein from transposon 17.6 |
| TraesCS2B01G177900 | 152843210 | 152844722 | 1512 | MYB transcription factor |
| TraesCS2B01G178000 | 153126356 | 153127211 | 855 | MYB transcription factor |
| TraesCS2B01G178100 | 153223831 | 153227230 | 3399 | Pectin acetylesterase |
| TraesCS2B01G178200 | 153549111 | 153549386 | 275 | RNase H family protein |
| TraesCS2B01G178300 | 153580367 | 153583856 | 3489 | B3 domain-containing protein |
| TraesCS2B01G178400 | 153585725 | 153588003 | 2278 | Haloacid dehalogenase-like hydrolase family protein |
| TraesCS2B01G178500 | 153609535 | 153612972 | 3437 | Protein LTV1 like |
| TraesCS2B01G178600 | 153673500 | 153674815 | 1315 | Ras family |
| TraesCS2B01G178700 | 153760061 | 153761866 | 1805 | F-box protein-like |
| TraesCS2B01G178800 | 153855100 | 153859660 | 4560 | Mitochondrial carrier family protein |
| TraesCS2B01G178900 | 153866103 | 153866646 | 543 | Translation initiation factor IF-2 |
| TraesCS2B01G179000 | 153892180 | 153893822 | 1642 | TVP38/TMEM64 family membrane protein |
| TraesCS2B01G179100 | 153894721 | 153895535 | 814 | Genome polyprotein |
| TraesCS2B01G179200 | 153903469 | 153904152 | 683 | transmembrane protein, putative (DUF679) |
| TraesCS2B01G179300 | 153907415 | 153907849 | 434 | Undecaprenyl-diphosphatase 1 |
| TraesCS2B01G179400 | 154140028 | 154140432 | 404 | NADH-ubiquinone oxidoreductase subunit |
| TraesCS2B01G179500 | 154233392 | 154236862 | 3470 | Protein kinase family protein |
| TraesCS2B01G179600 | 154244923 | 154253141 | 8218 | ATP-dependent RNA helicase family protein |
| TraesCS2B01G179700 | 154253822 | 154255987 | 2165 | Anaphase-promoting complex subunit 13 |
| TraesCS2B01G179800 | 154269479 | 154271242 | 1763 | Calcium ion binding |
| TraesCS2B01G179900 | 154485482 | 154489828 | 4346 | ATP-dependent RNA helicase DeaD |
| TraesCS2B01G180000 | 154592475 | 154594845 | 2370 | Calmodulin-binding family protein, putative, expressed |
| TraesCS2B01G180100 | 154594579 | 154594806 | 227 | Phox (PX) domain-containing protein |
| TraesCS2B01G180200 | 154719452 | 154723196 | 3744 | RNA binding protein |
| TraesCS2B01G180300 | 154830810 | 154832452 | 1642 | Glucan endo-1,3-beta-glucosidase 3 |
| TraesCS2B01G180400 | 154838925 | 154840359 | 1434 | DUF1997 family protein |
| TraesCS2B01G180500 | 154900609 | 154905615 | 5006 | Protein kinase, putative |
| TraesCS2B01G180600 | 154912392 | 154914715 | 2323 | Disease resistance protein (NBS-LRR class) family |
| TraesCS2B01G180700 | 154914736 | 154916163 | 1427 | disease resistance family protein / LRR family protein |
| TraesCS2B01G180800 | 154930933 | 154934633 | 3700 | Transmembrane emp24 domain-containing protein |
| TraesCS2B01G180900 | 154985263 | 154994777 | 9514 | Chaperone protein DnaJ |
| TraesCS2B01G181000 | 155034115 | 155034477 | 362 | glutamate synthase 1 |
| TraesCS2B01G181100 | 155043859 | 155047746 | 3887 | DUF630 family protein, putative (DUF630 and DUF632) |
| TraesCS2B01G181200 | 155820013 | 155820860 | 847 | Cysteine protease |
| TraesCS2B01G181300 | 155829416 | 155830162 | 746 | Y-family DNA polymerase H |
| TraesCS2B01G181400 | 156047028 | 156048179 | 1151 | Centrosomal protein of 63 kDa |
| TraesCS2B01G181500 | 156588408 | 156590403 | 1995 | RING finger protein |
| TraesCS2B01G181600 | 156591139 | 156593091 | 1952 | RNA-binding protein |
| TraesCS2B01G181700 | 156593987 | 156597474 | 3487 | Exosome complex component |
| TraesCS2B01G181800 | 156606296 | 156606913 | 617 | Calcium-binding family protein |
| TraesCS2B01G181900 | 156914704 | 156922970 | 8266 | 3-isopropylmalate dehydratase large subunit |
| TraesCS2B01G182000 | 157041051 | 157041650 | 599 | Calcium-binding family protein |
| TraesCS2B01G182100 | 157243309 | 157243839 | 530 | RING/U-box superfamily protein |
| TraesCS2B01G182200 | 157265505 | 157266651 | 1146 | Transmembrane protein, putative |
| TraesCS2B01G182300 | 157284233 | 157284796 | 563 | RING/U-box superfamily protein, putative |
| TraesCS2B01G182400 | 157314410 | 157314793 | 383 | RALF |
| TraesCS2B01G182500 | 157372750 | 157374348 | 1598 | Cytochrome P450 family cinnamate 4-hydroxylase |
| TraesCS2B01G182600 | 157574314 | 157580728 | 6414 | Defective in cullin neddylation protein |
| **TraesCS2B01G182700** | **157639786** | **157644811** | **5025** | **Cellulose synthase-like protein** |
| TraesCS2B01G182800 | 157688966 | 157696282 | 7316 | NBS-LRR disease resistance protein |
| TraesCS2B01G182900 | 157734939 | 157736070 | 1131 | Ribonuclease |
| TraesCS2B01G183000 | 157754799 | 157758719 | 3920 | F-box domain containing protein, expressed |
| TraesCS2B01G183100 | 158146363 | 158147397 | 1034 | Myb factor |
| TraesCS2B01G183200 | 158430980 | 158433397 | 2417 | Origin recognition complex subunit 6 |
| TraesCS2B01G183300 | 158617043 | 158618998 | 1955 | Transcription factor |
| TraesCS2B01G183400 | 158619335 | 158621020 | 1685 | Pentatricopeptide repeat-containing protein |
| TraesCS2B01G183500 | 158621342 | 158624499 | 3157 | 30S ribosomal protein S4 |
| TraesCS2B01G183600 | 158631729 | 158633225 | 1496 | UDP-glycosyltransferase |
| TraesCS2B01G183700 | 158642594 | 158644350 | 1756 | Lipase/lipooxygenase, PLAT/LH2 |
| TraesCS2B01G183800 | 158650388 | 158651163 | 775 | exocyst complex component sec3A |
| TraesCS2B01G183900 | 158863583 | 158868838 | 5255 | Glycosyltransferase |
| TraesCS2B01G184000 | 159098405 | 159099835 | 1430 | Glycosyltransferase |
| TraesCS2B01G184100 | 159203946 | 159208120 | 4174 | GTPase obg |
| TraesCS2B01G184200 | 159255909 | 159256349 | 440 | SAUR-like auxin-responsive protein family |
| TraesCS2B01G184300 | 159300238 | 159300444 | 206 | Chymotrypsin inhibitor |
| TraesCS2B01G184400 | 159319089 | 159319352 | 263 | Chymotrypsin inhibitor |
| TraesCS2B01G184500 | 159363150 | 159367580 | 4430 | Myb-related protein-like |
| TraesCS2B01G184600 | 159485810 | 159488511 | 2701 | Heat shock transcription factor A2 |
| TraesCS2B01G184700 | 159489080 | 159489649 | 569 | TBC1 domain family member 10A |
| TraesCS2B01G184800 | 159601233 | 159602454 | 1221 | RNA-binding (RRM/RBD/RNP motifs) family protein |
| TraesCS2B01G184900 | 159891606 | 159896289 | 4683 | 4-alpha-glucanotransferase |
| TraesCS2B01G185000 | 159969474 | 159971187 | 1713 | Cytochrome P450 |
| TraesCS2B01G185100 | 160199685 | 160201348 | 1663 | Phytoene desaturase |
| TraesCS2B01G185200 | 160280778 | 160282853 | 2075 | Patatin |
| TraesCS2B01G185300 | 160401169 | 160407223 | 6054 | Histone acetyltransferase |
| TraesCS2B01G185400 | 160410294 | 160411599 | 1305 | B3 domain-containing protein |
| TraesCS2B01G185500 | 160668152 | 160669455 | 1303 | B3 domain-containing protein |
| TraesCS2B01G185600 | 160700520 | 160705818 | 5298 | B3 domain-containing protein |
| TraesCS2B01G185700 | 160752634 | 160755004 | 2370 | Purple acid phosphatase |
| TraesCS2B01G185800 | 160900576 | 160905178 | 4602 | Receptor protein kinase, putative |
| TraesCS2B01G185900 | 161018594 | 161020729 | 2135 | Pentatricopeptide repeat-containing protein |
| TraesCS2B01G186000 | 161026470 | 161026880 | 410 | Histone H3 |
| TraesCS2B01G186100 | 161142271 | 161146611 | 4340 | Cytochrome P450 |
| TraesCS2B01G186200 | 161385171 | 161386123 | 952 | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family, putative |
| TraesCS2B01G186300 | 161392035 | 161392622 | 587 | Late embryogenesis abundant protein |
| TraesCS2B01G186400 | 161406533 | 161408712 | 2179 | Chaperone protein dnaJ |
| TraesCS2B01G186500 | 161408988 | 161413376 | 4388 | DNA-directed RNA polymerase II, putative |
| TraesCS2B01G186600 | 161414605 | 161418152 | 3547 | Apoptotic chromatin condensation inducer in the nucleus |
| TraesCS2B01G186700 | 161419500 | 161420262 | 762 | 50S ribosomal protein L7/L12 |
| TraesCS2B01G186800 | 161464233 | 161470041 | 5808 | Mitochondrial import inner membrane translocase subunit TIM44 |
| TraesCS2B01G186900 | 161472834 | 161474533 | 1699 | Heavy-metal-associated domain-containing protein, putative, expressed |
| TraesCS2B01G187000 | 161722416 | 161725366 | 2950 | Trehalose 6-phosphate phosphatase |
| TraesCS2B01G187100 | 162007701 | 162010749 | 3048 | Trehalose 6-phosphate phosphatase |
| TraesCS2B01G187200 | 162445752 | 162448779 | 3027 | Trehalose 6-phosphate phosphatase |
| TraesCS2B01G187300 | 162626321 | 162628411 | 2090 | Adenylate kinase |
| TraesCS2B01G187400 | 162863706 | 162870529 | 6823 | Transducin/WD40 repeat protein |
| TraesCS2B01G187500 | 162872742 | 162873746 | 1004 | Transcription factor WRKY |
| TraesCS2B01G187600 | 162928065 | 162929589 | 1524 | Lipid transfer protein |
| TraesCS2B01G187700 | 163231279 | 163232388 | 1109 | Leucine-rich repeat protein kinase family protein |
| TraesCS2B01G187800 | 163231487 | 163232095 | 608 | Galactose oxidase/kelch repeat superfamily protein |
| TraesCS2B01G187900 | 163402950 | 163403402 | 452 | Leucine-rich repeat (LRR) family protein |
| TraesCS2B01G188000 | 163404652 | 163414644 | 9992 | Glycosyltransferase |
| TraesCS2B01G188100 | 163417518 | 163418156 | 638 | nitric oxide synthase-interacting protein |
| TraesCS2B01G188200 | 163712747 | 163715551 | 2804 | Alpha-ketoglutarate-dependent dioxygenase alkB-like protein 2 |
| TraesCS2B01G188300 | 163741793 | 163743097 | 1304 | Aspartic proteinase nepenthesin-1 |
| TraesCS2B01G188400 | 163977255 | 163978565 | 1310 | Aspartic proteinase nepenthesin-1 |
| TraesCS2B01G188500 | 164082799 | 164085665 | 2866 | Transcription elongation factor SPT4 homolog |
| TraesCS2B01G188600 | 164088726 | 164091514 | 2788 | Serine/arginine rich splicing factor, putative |
| TraesCS2B01G188700 | 164107712 | 164109492 | 1780 | Copper-transporting P-type ATPase |
| TraesCS2B01G188800 | 164419281 | 164427140 | 7859 | Calmodulin-binding transcription activator |
| TraesCS2B01G188900 | 164628813 | 164631575 | 2762 | Multifunctional methyltransferase subunit TRM112-like protein |
| TraesCS2B01G189000 | 164638702 | 164642366 | 3664 | Signal peptidase subunit-12 |
| TraesCS2B01G189100 | 164893446 | 164897232 | 3786 | Alpha/beta-hydrolase superfamily protein |
| TraesCS2B01G189200 | 164904337 | 164906734 | 2397 | Pentatricopeptide repeat-containing protein, putative |
| TraesCS2B01G189300 | 164936804 | 164939999 | 3195 | Phospho-2-dehydro-3-deoxyheptonate aldolase |
| TraesCS2B01G189400 | 165067641 | 165067991 | 350 | Serpin family protein |
| TraesCS2B01G189500 | 165111094 | 165113123 | 2029 | 40S ribosomal protein S6 |
| TraesCS2B01G189600 | 165115608 | 165119793 | 4185 | Kinase family protein |
| TraesCS2B01G189700 | 165244246 | 165246281 | 2035 | Alcohol dehydrogenase, putative |
| TraesCS2B01G189800 | 165250465 | 165253060 | 2595 | Alcohol dehydrogenase, putative |
| TraesCS2B01G189900 | 165273299 | 165275975 | 2676 | Cytochrome c oxidase subunit 6B |
| TraesCS2B01G190000 | 165277697 | 165278302 | 605 | Anthocyanin 3'-O-beta-glucosyltransferase |
| TraesCS2B01G190100 | 165503041 | 165512693 | 9652 | ATP-dependent RNA helicase, putative |
| TraesCS2B01G190200 | 165522452 | 165523693 | 1241 | TNF receptor-associated factor family protein |
| TraesCS2B01G190300 | 165927602 | 165928377 | 775 | Defensin |
| TraesCS2B01G190400 | 166040473 | 166041862 | 1389 | GEM-like protein 1 |
| TraesCS2B01G190500 | 166045455 | 166048692 | 3237 | Pentatricopeptide repeat-containing protein |
| TraesCS2B01G190600 | 166210292 | 166210543 | 251 | Cytochrome b559 subunit alpha |
| TraesCS2B01G190700 | 166291103 | 166292832 | 1729 | Cyclin family protein |
| TraesCS2B01G190800 | 166406777 | 166406887 | 110 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4 |
| TraesCS2B01G190900 | 166429308 | 166464390 | 35082 | Receptor-like protein kinase |
| TraesCS2B01G191000 | 166466358 | 166466468 | 110 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4 |
| TraesCS2B01G191100 | 166468675 | 166471537 | 2862 | ADP-ribosylation factor, putative |
| TraesCS2B01G191200 | 166472490 | 166476532 | 4042 | AP-4 complex subunit mu |
| TraesCS2B01G191300 | 166610880 | 166612414 | 1534 | Chaperone protein DnaJ |
| TraesCS2B01G191400 | 166612820 | 166613359 | 539 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein |
| TraesCS2B01G191500 | 166749395 | 166755925 | 6530 | Purple acid phosphatase |
| TraesCS2B01G191600 | 166809633 | 166810439 | 806 | Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 |
| TraesCS2B01G191700 | 166813270 | 166814418 | 1148 | Fasciclin-like arabinogalactan protein |
| TraesCS2B01G191800 | 167081565 | 167086338 | 4773 | protein kinase family protein |
| TraesCS2B01G191900 | 167465276 | 167469564 | 4288 | Zinc finger CCCH domain-containing protein 62 |
| TraesCS2B01G192000 | 167475838 | 167476948 | 1110 | calmodulin-binding protein (DUF1645) |
| TraesCS2B01G192100 | 167499351 | 167499611 | 260 | Calcium binding family protein |
| TraesCS2B01G192200 | 167796062 | 167796337 | 275 | Calmodulin |
| TraesCS2B01G192300 | 167797799 | 167800434 | 2635 | Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 |
| TraesCS2B01G192400 | 167860263 | 167863533 | 3270 | Calmodulin-related protein |
| TraesCS2B01G192500 | 167895297 | 167896535 | 1238 | F-box family protein |
| TraesCS2B01G192600 | 168117795 | 168123159 | 5364 | Ubiquitin carboxyl-terminal hydrolase-related protein |
| TraesCS2B01G192700 | 168605771 | 168611862 | 6091 | cold regulated protein 27 |
| TraesCS2B01G192800 | 168614433 | 168617377 | 2944 | Ankyrin repeat domain-containing protein |
| TraesCS2B01G192900 | 168621115 | 168622811 | 1696 | Dihydropteroate synthase, putative |
| TraesCS2B01G193000 | 168623900 | 168629978 | 6078 | Receptor-like protein kinase |
| TraesCS2B01G193100 | 168631685 | 168632391 | 706 | Polynucleotidyl transferase, ribonuclease H-like superfamily protein |
| TraesCS2B01G193200 | 168827491 | 168830968 | 3477 | ankyrin repeat protein |
| TraesCS2B01G193300 | 168831609 | 168853380 | 21771 | Trehalose 6-phosphate phosphatase |
| TraesCS2B01G193400 | 169574904 | 169575963 | 1059 | ubiquitin-specific protease 27 |
| TraesCS2B01G193500 | 169864360 | 169865163 | 803 | Ring finger protein, putative |
| TraesCS2B01G193600 | 170388371 | 170393379 | 5008 | Aminotransferase |
| TraesCS2B01G193700 | 170396025 | 170397272 | 1247 | F-box protein |
| TraesCS2B01G193800 | 170851824 | 170852486 | 662 | Dirigent protein |
| TraesCS2B01G193900 | 170969269 | 170970111 | 842 | Ribosomal protein L32 |
| TraesCS2B01G194000 | 170971250 | 170971801 | 551 | Dirigent protein |
| TraesCS2B01G194100 | 171024780 | 171026959 | 2179 | SH3 domain-containing protein |
| TraesCS2B01G194200 | 171030429 | 171034964 | 4535 | Sucrose synthase |
| TraesCS2B01G194300 | 171101284 | 171101523 | 239 | Acetylornithine deacetylase |
| TraesCS2B01G194400 | 171453242 | 171455239 | 1997 | 40S ribosomal protein SA |
| TraesCS2B01G194500 | 171457405 | 171460610 | 3205 | DNA-directed RNA polymerase II family protein |
| TraesCS2B01G194600 | 171461076 | 171466422 | 5346 | Peroxisomal (S)-2-hydroxy-acid oxidase |
| TraesCS2B01G194700 | 171789147 | 171793671 | 4524 | 3-oxoacyl-[acyl-carrier-protein] synthase |
| TraesCS2B01G194800 | 171794441 | 171795535 | 1094 | Hydroxyproline-rich glycoprotein |
| **TraesCS2B01G194900** | **171995910** | **172003669** | **7759** | **Erect panicle 2 protein** |
| TraesCS2B01G195000 | 172175263 | 172175835 | 572 | RING/U-box superfamily protein |
| TraesCS2B01G195100 | 172218863 | 172224563 | 5700 | DNA-directed RNA polymerase subunit |
| TraesCS2B01G195200 | 172672545 | 172679159 | 6614 | Argonaute protein |
| TraesCS2B01G195300 | 172890712 | 172895217 | 4505 | Bromo-adjacent-like (BAH) domain protein |
| TraesCS2B01G195400 | 172980221 | 172984609 | 4388 | RNA-binding protein |
| TraesCS2B01G195500 | 173188626 | 173188934 | 308 | TTF-type zinc finger protein with HAT dimerization domain-containing protein |
| TraesCS2B01G195600 | 173204323 | 173205940 | 1617 | Jasmonate-zim-domain protein |
| TraesCS2B01G195700 | 173439644 | 173445605 | 5961 | cytidinediphosphate diacylglycerol synthase 4 |
| TraesCS2B01G195800 | 173464146 | 173466326 | 2180 | Pentatricopeptide repeat-containing protein |
| TraesCS2B01G195900 | 173485268 | 173486072 | 804 | SPX domain-containing protein |
| TraesCS2B01G196000 | 173755493 | 173757320 | 1827 | Transmembrane protein 87A |
| TraesCS2B01G196100 | 174343695 | 174345408 | 1713 | Elongation factor 1-beta |
| TraesCS2B01G196200 | 174385083 | 174386437 | 1354 | Peptide chain release factor 1 |
| TraesCS2B01G196300 | 174393958 | 174401387 | 7429 | Inter-alpha-trypsin inhibitor heavy chain-like protein |
| TraesCS2B01G196400 | 174588653 | 174591981 | 3328 | Proteasome subunit alpha type |
| TraesCS2B01G196500 | 174592030 | 174593762 | 1732 | Adipocyte plasma membrane-associated protein |
| TraesCS2B01G196600 | 174662658 | 174664205 | 1547 | Adipocyte plasma membrane-associated protein |
| TraesCS2B01G196700 | 174780829 | 174781296 | 467 | DUF1677 family protein (DUF1677) |
| TraesCS2B01G196800 | 174792533 | 174797287 | 4754 | Eukaryotic translation initiation factor 3 subunit G |
| TraesCS2B01G196900 | 174826453 | 174827665 | 1212 | F-box like protein |
| TraesCS2B01G197000 | 174828170 | 174831392 | 3222 | Kinase family protein |
| TraesCS2B01G197100 | 174923251 | 174932535 | 9284 | Exportin-T |
| TraesCS2B01G197200 | 175060227 | 175060664 | 437 | 50S ribosomal protein L15 |
| **TraesCS2B01G197300** | **175067745** | **175071145** | **3400** | **Rela/spot homolog 3 family protein** |
| TraesCS2B01G197400 | 175409701 | 175411810 | 2109 | Alpha/beta-hydrolase superfamily protein |
| TraesCS2B01G197500 | 175413398 | 175414008 | 610 | GRF zinc finger family protein |
| TraesCS2B01G197600 | 175415314 | 175418298 | 2984 | DNA-directed RNA polymerase III subunit |
| **TraesCS2B01G197700** | **175454756** | **175455112** | **356** | **Fibroblast growth factor 6** |
| TraesCS2B01G197800 | 175456899 | 175459012 | 2113 | Contactin-3 |
| TraesCS2B01G197900 | 175537350 | 175540863 | 3513 | Methyltransferase-like protein |
| TraesCS2B01G198000 | 175541278 | 175542529 | 1251 | Transposon protein, putative, Pong sub-class, expressed |
| TraesCS2B01G198100 | 175627020 | 175627820 | 800 | Stress responsive alpha-beta barrel domain protein |
| TraesCS2B01G198200 | 175634053 | 175636972 | 2919 | Small nuclear ribonucleoprotein family protein |
| TraesCS2B01G198300 | 175638457 | 175649555 | 11098 | DNA mismatch repair protein mutS |
| TraesCS2B01G198400 | 175895190 | 175897148 | 1958 | 30S ribosomal protein S3 |
| TraesCS2B01G198500 | 176167985 | 176172676 | 4691 | PHD finger alfin-like protein |
| TraesCS2B01G198600 | 176294981 | 176299996 | 5015 | alpha/beta-Hydrolases superfamily protein |
| TraesCS2B01G198700 | 176406772 | 176409106 | 2334 | Nuclear transcription factor Y subunit |
| TraesCS2B01G198800 | 176407685 | 176412003 | 4318 | 6,7-dimethyl-8-ribityllumazine synthase |
| TraesCS2B01G198900 | 176413503 | 176414909 | 1406 | DUF2996 family protein |
| TraesCS2B01G199000 | 176705722 | 176708590 | 2868 | Acidic leucine-rich nuclear phosphoprotein 32-related protein |
| TraesCS2B01G199100 | 177217530 | 177218818 | 1288 | Ankyrin repeat family protein |
| TraesCS2B01G199200 | 177545062 | 177545817 | 755 | Embryogenesis transmembrane protein |
| TraesCS2B01G199300 | 177583467 | 177584634 | 1167 | sugar transporter, putative (DUF1195) |
| TraesCS2B01G199400 | 177597685 | 177600001 | 2316 | Pectinesterase |
| TraesCS2B01G199500 | 177649553 | 177657471 | 7918 | Agenet domain-containing protein / bromo-adjacent domain-containing protein, putative |
| TraesCS2B01G199600 | 178161075 | 178163460 | 2385 | Heavy metal transport/detoxification superfamily protein |
| TraesCS2B01G199700 | 178167065 | 178168111 | 1046 | Gibberellin receptor GID1A |
| TraesCS2B01G199800 | 178338316 | 178338993 | 677 | Nuclear transcription factor Y subunit B |
| TraesCS2B01G199900 | 178700155 | 178711584 | 11429 | ATP-dependent RNA helicase-like protein |
| TraesCS2B01G200000 | 178723855 | 178724994 | 1139 | Werner Syndrome-like exonuclease |
| TraesCS2B01G200100 | 178730819 | 178731928 | 1109 | Sulfotransferase |
| TraesCS2B01G200200 | 178758874 | 178759101 | 227 | lysine ketoglutarate reductase trans-splicing-like protein (DUF707) |
| TraesCS2B01G200300 | 178775152 | 178775718 | 566 | EGG APPARATUS-1 protein |
| TraesCS2B01G200400 | 178857252 | 178857722 | 470 | Formin-like protein |
| TraesCS2B01G200500 | 179051258 | 179051530 | 272 | EGG APPARATUS-1 protein |
| TraesCS2B01G200600 | 179065057 | 179066502 | 1445 | Werner Syndrome-like exonuclease |
| TraesCS2B01G200700 | 179132443 | 179139519 | 7076 | Dihydroflavonol-4-reductase |
| TraesCS2B01G200800 | 180041243 | 180059836 | 18593 | MADS-box transcription factor |
| TraesCS2B01G200900 | 180420893 | 180423787 | 2894 | Alpha-1,4-glucan-protein synthase [UDP-forming] 1 |
| TraesCS2B01G201000 | 180436705 | 180437221 | 516 | B12D protein |
| TraesCS2B01G201100 | 180539897 | 180540580 | 683 | Mitochondrial import inner membrane translocase subunit Tim17 |
| TraesCS2B01G201200 | 180540855 | 180541544 | 689 | Mitochondrial import inner membrane translocase subunit Tim17 |
| TraesCS2B01G201300 | 180546232 | 180546897 | 665 | Mitochondrial import inner membrane translocase subunit Tim17 |
| TraesCS2B01G201400 | 180558461 | 180560173 | 1712 | COBRA-like protein |
| TraesCS2B01G201500 | 180568782 | 180572059 | 3277 | Protein COBRA, putative |
| TraesCS2B01G201600 | 180605684 | 180607225 | 1541 | Transducin/WD40 repeat protein |
| TraesCS2B01G201700 | 180616692 | 180619271 | 2579 | 6-phosphogluconolactonase |
| TraesCS2B01G201800 | 180822185 | 180823633 | 1448 | Pentatricopeptide repeat-containing protein, putative |
| TraesCS2B01G201900 | 181119111 | 181120782 | 1671 | Cytochrome P450 protein |
| TraesCS2B01G202000 | 181613111 | 181616760 | 3649 | Methyl esterase |
| TraesCS2B01G202100 | 181980712 | 181980999 | 287 | B3 domain-containing protein |
| TraesCS2B01G202200 | 182001226 | 182004885 | 3659 | RNA-binding protein-like |
| TraesCS2B01G202300 | 182011592 | 182016808 | 5216 | Longifolia protein |
| TraesCS2B01G202400 | 182131215 | 182133646 | 2431 | Guanylate-binding protein 2 |
| TraesCS2B01G202500 | 182132876 | 182153140 | 20264 | SKP1-like 7 |
| TraesCS2B01G202600 | 182356504 | 182360936 | 4432 | GPI transamidase subunit PIG-U family protein |
| TraesCS2B01G202700 | 182569319 | 182570997 | 1678 | Ninja-family protein |
| TraesCS2B01G202800 | 182705927 | 182707427 | 1500 | Glycerophosphodiester phosphodiesterase |
| TraesCS2B01G202900 | 182708536 | 182711907 | 3371 | Receptor-like kinase |
| TraesCS2B01G203000 | 182861726 | 182862642 | 916 | Disease resistance protein RGA2 |
| TraesCS2B01G203100 | 182925941 | 182927482 | 1541 | RB-like protein |
| TraesCS2B01G203200 | 182931654 | 182935254 | 3600 | RNA-binding protein |
| TraesCS2B01G203300 | 182936300 | 182954290 | 17990 | Fasciclin-like arabinogalactan-protein-like |
| TraesCS2B01G203400 | 183129194 | 183130366 | 1172 | Fasciclin-like arabinogalactan-protein-like |
| TraesCS2B01G203500 | 183199128 | 183200389 | 1261 | Fasciclin-like arabinogalactan-protein-like |
| TraesCS2B01G203600 | 183211169 | 183212537 | 1368 | RING/U-box superfamily protein |
| TraesCS2B01G203700 | 183262511 | 183263085 | 574 | Myosin-1 |
| TraesCS2B01G203800 | 183313966 | 183314754 | 788 | Fasciclin-like arabinogalactan-protein-like |
| TraesCS2B01G203900 | 183315462 | 183317939 | 2477 | SNF1-related protein kinase regulatory subunit gamma 1 |
| TraesCS2B01G204000 | 183528464 | 183529664 | 1200 | Superoxide dismutase [Cu-Zn] |
| TraesCS2B01G204100 | 183654052 | 183662786 | 8734 | Histone deacetylase |
| TraesCS2B01G204200 | 184114202 | 184119171 | 4969 | Alpha/beta hydrolase, putative |
| TraesCS2B01G204300 | 184133486 | 184135102 | 1616 | Glycosyl hydrolase family protein 43, putative, expressed |
| TraesCS2B01G204400 | 184317654 | 184318234 | 580 | Anthocyanidin reductase |
| TraesCS2B01G204500 | 184326389 | 184331831 | 5442 | Dihydroflavonol-4-reductase |
| TraesCS2B01G204600 | 184365877 | 184370520 | 4643 | Dihydroflavonol-4-reductase |
| TraesCS2B01G204700 | 184407899 | 184410259 | 2360 | Glucan endo-1,3-beta-glucosidase 3 |
| TraesCS2B01G204800 | 184489796 | 184493848 | 4052 | Ribosome biogenesis protein WDR12 homolog |
| TraesCS2B01G204900 | 184494691 | 184495212 | 521 | IgA FC receptor |
| TraesCS2B01G205000 | 184513528 | 184514001 | 473 | IgA FC receptor |
| TraesCS2B01G205100 | 184572540 | 184638093 | 65553 | IgA FC receptor |
| TraesCS2B01G205200 | 184577512 | 184578290 | 778 | IgA FC receptor |
| TraesCS2B01G205300 | 184654961 | 184655743 | 782 | Snake venom serine proteinase 1 |
| TraesCS2B01G205400 | 184661116 | 184661722 | 606 | Hydroxyproline-rich glycoprotein family protein, putative |
| TraesCS2B01G205500 | 184662116 | 184663437 | 1321 | RING/U-box superfamily protein |
| TraesCS2B01G205600 | 184770885 | 184771670 | 785 | Leguminosin group485 secreted peptide |
| TraesCS2B01G205700 | 184772883 | 184775076 | 2193 | RNA binding protein |
| TraesCS2B01G205800 | 184800227 | 184801099 | 872 | IgA FC receptor |
| TraesCS2B01G205900 | 184876969 | 184877841 | 872 | IgA FC receptor |
| TraesCS2B01G206000 | 184899828 | 184900529 | 701 | IgA FC receptor |
| TraesCS2B01G206100 | 184909668 | 184910450 | 782 | IgA FC receptor |
| TraesCS2B01G206200 | 184930648 | 184952290 | 21642 | IgA FC receptor |
| TraesCS2B01G206300 | 184955925 | 184961144 | 5219 | Multifunctional CCA protein |
| TraesCS2B01G206400 | 185080019 | 185084989 | 4970 | Smr domain-containing protein, putative |
| TraesCS2B01G206500 | 185761088 | 185762547 | 1459 | CsAtPR5 |
| TraesCS2B01G206600 | 185769889 | 185772567 | 2678 | F-box family protein |
| TraesCS2B01G206700 | 185793910 | 185794682 | 772 | Plant invertase/pectin methylesterase inhibitor |
| TraesCS2B01G206800 | 185797238 | 185798788 | 1550 | Pentatricopeptide repeat-containing family protein |
| TraesCS2B01G206900 | 185800522 | 185804102 | 3580 | Disease resistance protein (TIR-NBS-LRR class) family |
| TraesCS2B01G207000 | 185806065 | 185809469 | 3404 | Pentatricopeptide repeat-containing protein |
| TraesCS2B01G207100 | 185812484 | 185815947 | 3463 | COBW domain-containing protein 1 |
| TraesCS2B01G207200 | 186311701 | 186313229 | 1528 | Thaumatin |
| TraesCS2B01G207300 | 186314840 | 186375161 | 60321 | DNA ligase |
| TraesCS2B01G207400 | 188020910 | 188023533 | 2623 | Protein DETOXIFICATION |
| **TraesCS2B01G207500** | **188149190** | **188151658** | **2468** | **regulatory-associated protein of TOR 2 (RAPTOR2)** |
| TraesCS2B01G207600 | 188255556 | 188261437 | 5881 | tRNA-specific 2-thiouridylase MnmA 2 |
| TraesCS2B01G207700 | 188460858 | 188462037 | 1179 | F-box family protein |
| TraesCS2B01G207800 | 188469320 | 188470714 | 1394 | Zinc finger family protein |
| TraesCS2B01G207900 | 188714843 | 188717312 | 2469 | Myosin heavy chain-like protein |
| TraesCS2B01G208000 | 188719038 | 188720872 | 1834 | SNAP25 homologous protein SNAP33 |
| TraesCS2B01G208100 | 188812253 | 188814311 | 2058 | Heparanase, putative |
| TraesCS2B01G208200 | 189593144 | 189604410 | 11266 | S phase cyclin A-associated protein in the endoplasmic reticulum |
| TraesCS2B01G208300 | 189606779 | 189608966 | 2187 | F-box family protein |
| TraesCS2B01G208400 | 189617277 | 189632096 | 14819 | DNA/RNA helicase protein |
| TraesCS2B01G208500 | 189745074 | 189745820 | 746 | EID1-like F-box protein 2 |
| TraesCS2B01G208600 | 189748002 | 189748943 | 941 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein |
| TraesCS3B01G347800 | 556934804 | 556939440 | 4636 | Expansin |
| TraesCS3B01G347900 | 556944321 | 556945167 | 846 | Expansin |
| TraesCS3B01G348000 | 556959431 | 556960277 | 846 | Expansin |
| TraesCS3B01G348100 | 557087052 | 557089079 | 2027 | Protein kinase |
| TraesCS3B01G348200 | 557089800 | 557099566 | 9766 | SNF2 domain-containing protein / helicase domain-containing protein |
| TraesCS3B01G348300 | 557171563 | 557173468 | 1905 | Protein FAR1-RELATED SEQUENCE 5 |
| TraesCS3B01G348400 | 557705315 | 557706100 | 785 | B3 domain-containing protein |
| TraesCS3B01G348500 | 558277109 | 558277372 | 263 | ATP-dependent caseinolytic (Clp) protease/crotonase family protein |
| TraesCS3B01G348600 | 558381347 | 558381956 | 609 | evolutionarily conserved C-terminal region 2 |
| TraesCS3B01G348700 | 558500278 | 558500922 | 644 | F-box domain containing protein |
| TraesCS3B01G348800 | 559109105 | 559110311 | 1206 | Immunoglobulin A1 protease autotransporter |
| TraesCS3B01G348900 | 559207086 | 559208448 | 1362 | F-box and associated interaction domains-containing protein |
| TraesCS3B01G349000 | 559327202 | 559334635 | 7433 | Katanin p80 WD40 repeat-containing subunit B1 homolog |
| TraesCS3B01G349100 | 559335783 | 559340330 | 4547 | Secretory carrier-associated membrane protein |
| TraesCS3B01G349200 | 559340808 | 559343631 | 2823 | BTB/POZ domain-containing protein |
| TraesCS3B01G349300 | 559723732 | 559726951 | 3219 | Ultrapetala |
| TraesCS3B01G349400 | 559877343 | 559877987 | 644 | Vacuolar sorting-associated protein 28-like protein |
| TraesCS3B01G349500 | 559882583 | 559884802 | 2219 | Rp1-like protein |
| TraesCS3B01G349600 | 559886838 | 559893111 | 6273 | Disease resistance protein (NBS-LRR class) family |
| TraesCS3B01G349700 | 559889232 | 559890281 | 1049 | ADP-ribosylation factor-related protein 1 |
| TraesCS3B01G349800 | 559890796 | 559892520 | 1724 | Rp1-like protein |
| TraesCS3B01G349900 | 559893857 | 559896666 | 2809 | Sphingosine kinase, putative |
| TraesCS3B01G350000 | 560058746 | 560059633 | 887 | 18S pre-ribosomal assembly protein gar2-like protein |
| TraesCS3B01G350100 | 560116012 | 560120708 | 4696 | Protein downstream neighbor of Son |
| TraesCS3B01G350200 | 560423463 | 560427833 | 4370 | External alternative NAD(P)H-ubiquinone oxidoreductase B2, mitochondrial |
| TraesCS3B01G350300 | 560429931 | 560432513 | 2582 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, putative |
| TraesCS3B01G350400 | 560556356 | 560557681 | 1325 | Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase |
| TraesCS3B01G350500 | 560595001 | 560598315 | 3314 | Cyclic nucleotide-gated channel |
| TraesCS3B01G350600 | 560872961 | 560873917 | 956 | ATP-dependent protease La (LON) domain protein |
| TraesCS3B01G350700 | 561026438 | 561031038 | 4600 | Eukaryotic translation initiation factor 3 subunit L |
| TraesCS3B01G350800 | 561038700 | 561039083 | 383 | LysM domain containing protein |
| TraesCS3B01G350900 | 561044324 | 561044733 | 409 | LysM domain containing protein |
| TraesCS3B01G351000 | 561093445 | 561095454 | 2009 | Pentatricopeptide repeat-containing protein |
| TraesCS3B01G351100 | 561097854 | 561102564 | 4710 | Diacylglycerol kinase |
| TraesCS3B01G351200 | 561229185 | 561231909 | 2724 | DNA cross-link repair protein |
| TraesCS3B01G351300 | 561232713 | 561237144 | 4431 | Adenine nucleotide alpha hydrolases-like superfamily protein |
| TraesCS3B01G351400 | 561537825 | 561540482 | 2657 | Protein CyaY |
| TraesCS3B01G351500 | 561540901 | 561541236 | 335 | Calcium-binding family protein |
| TraesCS3B01G351600 | 561543886 | 561545511 | 1625 | 2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative |
| TraesCS3B01G351700 | 561550353 | 561563424 | 13071 | LysM domain containing protein |
| TraesCS3B01G351800 | 561590530 | 561591713 | 1183 | Receptor protein kinase, putative |
| TraesCS3B01G351900 | 561592592 | 561592992 | 400 | Peptidoglycan-binding lysin domain-containing protein |
| TraesCS3B01G352000 | 561700847 | 561702750 | 1903 | Nucleolar protein |
| TraesCS3B01G352100 | 561840804 | 561841212 | 408 | Peptidoglycan-binding lysin domain-containing protein |
| TraesCS3B01G352200 | 561889208 | 561889605 | 397 | LysM domain containing protein |
| TraesCS3B01G352300 | 561970656 | 561974756 | 4100 | Serine/threonine-protein kinase |
| TraesCS3B01G352400 | 562061867 | 562062496 | 629 | Cytochrome P450 |
| TraesCS3B01G352500 | 562272971 | 562276632 | 3661 | Serine/threonine-protein kinase |
| TraesCS3B01G352600 | 562273088 | 562274308 | 1220 | Zinc finger C-x8-C-x5-C-x3-H type family protein |

**Table S6** DNA sequences of 2B (chr2B-139340708 to chr2B-1897489430) and 3B (chr3B-556934804 to chr3B-562274308) used for designing simple sequence repeat (SSR) markers.

|  |  |
| --- | --- |
| **Position** | **DNA sequence** |
| **Chr2b-139340708** | TAGGCGATCGTGGTACGTAGGCGTGGGCTAGACCCACGCCTGAGTCGACAACAACCCACG  ATCCACGCGTCTAGGATTCGTAGCGCATCGTTTAATGACTCGTAATTAATTCAACTCGAC  TCAATCACGAAACACGACGCGCGCTCAGGCGAGGCAGGCGACGGAGGAGGACCGCGCGGG  AACCACTCTTCTCATGCTCCAACAACACGTGGAAGAGAACCTTTTTACGAAGGTGCAAAT  CTTCACCCGTTCTCGAGATGATACTAAACTTCTCATCACCTATTCATGTCACCCACATAG  AGTTTTAGAGATTTTTTCTGAAATTGTTTTACGGGCCTAAACCCCATCTATATTTGAACG  GTGTAGAGGCGACGTCGATCTTGGTGGGTGCGGATATGGAGCTCCAGAGGGGGGAGGGGC  ACCCCGAAATCTCCCTCAATTTTGTTTCTTGTTTGACATACGAAGTGCGGATTGGTCCAT  GAAAATTTGATGCATGGTGCTGGATGACATAACCAGGTTATCAAATGTTTAGCACCGTTA  TTTTAATGTATGGCGTTGGAGATGACCTAAAATGACAACTATTGGCTGTTTTTTTGGGGT  AGAGTTGCTGTGACCTGTGAGGCCATCTGAAAGGAGAGCAAGTCAAAAAAGACAGGAGAC  CGGGTAGTCCACCGCCGCCCCTGACCACACTCTCCCCGATCCGATCCGCCGGCGATGGCC  GCCCCTCACCGTGCTTTTCCCGATCCGCCGCCGATGGCCGCCTTCCGCTCTGGCCGACAC  GCTGCCCATCTCCGCCTGGCCGTACCGCCGCGGCTGGCCGCCCACCCCTCCTTCCGCTTC  CCCACCACGCCCCTCCCCACCCCATCCAAGACGCGCCTCCCCGCCGCCGGCGCCGCCTCT  CCCTACGCCGCCGCGCTCCTGCGCATCCTCGCGCTCCACTCCCTCTTCCTTCTCGCGCCC  GCCGCCCGAGCGCTCCCCTCCCTGCCCCACCTCTTCCTGCTTCCGCCGCTCCTCGCCATC  ATCTCCGCCGTCGCCATCCTCCTCATCCCCTCCAAGAGCCAGCCCCACCCCTTCCCGGCG  CTCCGCCACCTCTTCCGTCCCGCCCTCCTCCTGGCGGCGTCCCTTCTCCTCCGGCTCTCC  TCCCTCCACCTCATCAGTGACCCCGGTCTCATCGTCCTCGCAGACTCCGCCGGCGCGCTG  CTCGCCCGCGCCCTCAACCGCCCCTCCCGCCGCCGCGTGATCTCCGTCGCTGCCGCCTCC  GTTTCGCTGGCGGTCGTGTCGCCTTCCCACTCCGTGCTTCTTCTCGCACTCCCCTTTGCT  TCCGGCCTCCTCTCCTCGTTCGAGCACTCTGTATCTGCGCGACATGTCACCCGCAGCCGC  CACGCCCGTGCGGCCGTTTTTGCCCTCGCCGCCACCTTCCTCTCGGCGCCGGCACTTGCG  GGCCTCTTCTTTCTTGATGGCACTGACACCAGCGACGGTGTCCCGATTGGCCAGCTCTGG  TGGCTGCTCCTTAACGCGGCTGTCTTTGGCATGGCCTTGGGGCGACGGCAAGCCTACGAC  AGCAGTAGCAGTAGCAGTAGACCAAGCATGAATTTTGCAATGACCTTTGTGTGCACTATT  GTTCTGGAGCTGGTGTACTACCCAAAGCTGTCGTTGCCGGGCTTCTTAATTTGTGGGTTC  ATCTTGTGGATCGCCAGCAGGGAGCTGACTCCTTCAGGATATGTTGAGCTTGGGAGCACT  GACGAGTCCGTGTATGAGGCTGTCATGGGGCCGGTCCGGCATATCCTTAGTGAACGCAAG  TCCAGGAAGATTGCTGCTTTTCTGTTGATCAACACAGCTTACATGTTTGTTGAGTTCGCC  AGCGGTTTCATGAGCGATAGCCTTGGGCTGCTCTCTGACGCTTGCCATATGTTGTTTGAT  TGTGCTGCTCTGGCAATTGGACTATATGCGTCGTACATTGCGAGGCTGCCTGCAAATGGA  TTGTATAACTATGGAAGGGGCAGGTTTGAGGTGCTATCTGGGTATGTTAATGCAGTGTTC  TTGGTGCTTGTTGGGGCCCTGATTGTGTTGGAGTCGTTTGAGAGGATACTCGAGCCTCGG  GAGATATCAACAAGTAGCCTTTTGGCAGTTTCTGTTGGTGGACTTTTTGTAAATATCATT  GGATTGGTTTTCTTTCATGAGGAGCACCATCATGCGCATGGCGGTAGCTGCTCCCACTCC  CATTCACATTCACATTCTCATTCTCATTCACATAATCATGTTCATGAAGATCACCATCAC  CATCATGATCATGTTCATGAAGATCACCATCACCATCATGATCATGTTCATCAGAGTGCT  GATCACGAGAAGACATGTTCTGGTCATCATGGAGACACAAATAAGGGCCATCATCAGAAT  CACCAACATGATAGCAACAATGCAGAGAATCATCATCAACATAACCATGGTTGTAGCCAC  AAGCATGGTCACAATGGCCATATGGAACATCACCAGCAGGGTGTAGATCAGGCTCATCAA  GATTGCAGCAGCAGCAGCAGCGAGCAAGGACTTCTTGAGATTCCACTGATAAATGTGCAC  TCTCATGGCGCAGAATCTCAGTCTTGTAATGGAGAGGTGGAATCGCCAGAAACCGGAAAC  CATGCCAAGCCGGCAAGCCGGCGTCACATTGACCATAACATGGAAGGTATCTTCTTACAT  GTCCTAGCTGACACAATGGGAAGCGTTGGTGTTGTGATCTCAACTCTATTAATCAAGTAC  AAGGGATGGCTAATAGCAGATCCCATTTGCTCTGTATTCATTTCAATAATGATTGTGGCT  TCTGTCCTTCCATTGTTGAGAAATTCTGCTGAAATTTTGTTGCAAAGAGTTCCAAGGAGC  CATGAGAAGGACTTCGAAGCAGCACTGGATGATGTTAAGAAGATTAATGGTGTGATTGGA  GTCCATAATGTTCATTTATGGAACTTGACAAACACTGATATTGTAGGCACTTTTCATCTT  CATATATCAGCCGAAGCTGACAAGTCTGTTATAAGAGAAAGTGCTTCACGGATATTTCAA  GAAGCTGGGGTTCAAGATCTGACTATCCAGATCGAATGTGTCGAAAGATAGCAGTTGTTG  GTATAGCGACACTTGTTGGTAGTTTGATAGGATTTTGGCACAGATCAAATATATCTGTAG  TGCTTAATTCAGGAGCCATCCTTTATGTACCGCTGAAAGGAAATTGCATTAAAATACAGG  TTTGCAGCTTAATCATTTTGGTCTGAGCAACTTAATATTTATATGCTGTATATTGTCCAT  GTCGCATATAGACTTCACAAAAGCTTTCCAATCACATGATGATAAGCAGTTCCAGCTTAA  ACAAGCAGATTAATGAAGAAAACAAAGAGCACAATTCCAGCAGAAAAGAAAGGAAACCAG  AGAATAATGCGAGTTCATTACATGACCATATATAACCAGTTCAAACTTGAGCGAGCAAAT  TAATGGAGAAAGCAAGCTAGGTAGCAATAAACGAGAAGTGAAGCCTCTAAATTAAAGAGG  TACACTGAGTAATGCAAGCGCTAGCATTGTTGGGGCAGAGCGACTGGAGCCTTAGTTCAG  CTAAGATATAATCCGTGTGTATCTTCGACATCGAATTGTATCCATTTCATGCACCCTCTC  TTATTCATCACCTGGTATGTGCCTACATAATACGGGTATGTCTTTCTCCGTCATCCCCAC  TGGCCACCACTGCCGTCGATTGTAGCTGTGGAAGCAATGAAGAAATATGTGGGATCTAAA  ATGAAGCATGTCAAGAATTAATGAAAGAAAGCATCAGATGGATGAGTATAGATACTCCAG  ATCAATCCTTTTTTGTTTATCATCATAAACATCATAATAGTCATCATCATCCTCATCATT  GGTGTCTTAATTTGGAGACTGAGATGCCAAAAGAGCAACAAGTGAGTAATTAATGTCATG  TATTAATTAGGAGGCATGTGCATGTATGTAGGACAACTAGAGGAGTGTAGAAAGATGTAA  TAGAGAAAAGGCACTTAATTCCTCTGTTGATGAATATCGTGTGTTATTAGATGATCATAT  CTAGTTGCGTAATCCTCTGTTTTGCTGCTTACTGGGAGAGCCTATATGCACTAACTATTC  TTGCTATGGAGTCTATAAGTTTGGTCCCGACTCTTCTTGCTGCATGACCTTTTGTTGCTT  GCATCCTCGTGTCTTTAGGCAAGGAGTAATAAACTATCCTATGGAGGGGAAAAGACTGAT  GAAAGCATACAGGATAGTATGCAAAAGACATTCCCTTCAGTTCTTGAATCAGAGTGCAGC  AGTGAAGAACAAGACGCTTTTTTGGTTGATGAGTTGGTCCAAATAGATTGAGACGCCCCG  ACCTTAAGCTTCCTCCATTTTGGTCTGGTGGGGAATGCTCTATTAGGGTGTTCCCGTAGT  GATCGATGTGAGTGAATCTTTCAAGTCCTTTTGATCTGCAAAACACTGTGAATATTATGG  ACTGAATATCATATATGTTAGAGCTATTTGTTACGTAGTATTTTTTCCTAAATGTGCTCC  ACATTGTTTAAGTTCTTGACCATTTTTGTGCTTATAGTTTCAGAGTTCTTTTTTTTCCTT  TTGCCTTCTACAATTTGGATGCCGTTGTGAAATGCCATGATCTGAAGTTTGAGTTTGAGG  CTGTTAAACGCGATGCAGATATGCGCAGACAAGCTGAGATGGAGNNNNNNNNNNNNNNNN  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGTAGCCAAAATTACGTATACAAAAAAA  TACGGTTCGTTTTAGTACATGGGCCAATACATGTGGGGATTTGCAC |
| **Chr2b-189748943** | AAGGAATGCATAATTTACAGTTTGCTCGAAAGTTTTGATCACCTGTTGCTCTTTGATCTG  ACCCAATCAATACGTTTGATACTGAAGGTTTAAACGTGACTTTTCCCTCATCTGGGTGAT  CTGGGTGTTTGGTTGGTGACCATATTTTTCAGCGGATATGCCAGAAGGGAGTTGTAAGCG  TCCAACACCCCCGATCGAGGCCCAAGCACACGCCGACTTTAGGTTCGAACAGACGACTTT  GAGCAGATTTGCAAGTCTCAGTTCAAACGCTGGTATATCCCGTGAACTTTTACTCTTAAC  CATTTATCTGCAGCCGCAATGGCAGGGTGATATCTTGTTATATCCCGTAAACTGGAGGAG  TCCTTCGCTCCAACACCTGGTTTTGCCGTTGCCGCCTCCATTTTAATGCAGGCAATGCCG  TTCAAACGCCGTATCTAAGATCGACTAAGATAAGAGTGACACAAAACAAAACGAAGAGTC  CCATGTTGATGCGATCGACCAGTGCTGTTCAAACGCCCTATCTCGTCCCCATTCCCTCCT  ATAAAATGGCCGTCATGCACCCCGTTGGTTCTTCGCACCACAGACCGCAAACCCAGTAGC  CGACCGTAAACCTCCGCGCAGCGCATGCACGAGATGGCGCCATCCAAGCCCGCCGCCGCC  CTGCTCCTCGCCTTGGCCGTCCTGCTCGCGGCCGCGCAGCCGTCTTCCGCCATCAGAGTC  AAGCCCGCGTGCGCCCCGATTGTTAAGCCATCGCCACCTCCCCCCGCAGCTTCCCCACCG  CCGCCGCCGACCCCGGTGATCAGCAACCCACCCCCATCTGTCCCGTCTGTCCCAGCTTCC  CCGCCGCCACCGAGCCCAGTGATCAGCAACCCACCGCCATCCGTCCCTGCTTCCCCGCCG  CCGCCGAGCCCAGTGATCAGCAACCCAACCCCATCCGTCCCTGCTTCTCCACCGCCGGCC  ACCCCACCACCAGCCCCGGCCTCGCCCGCTACCCCGCCGTCCCAGCCCACGGAGTGCCTG  ACGCCGTTGATGGGACTGACGCCATGCATGGGCTACCTGACCAACACCAGCGTGGCGACG  CCCCCGGCCGCGTGCTGCGGCGCCTTCAAGTCCCTGGTGGACAACGCCCCCATCTGCCTC  TGCCACGGCCTGAACGGCGACATCAACAAGATCATGCCCGCCCCCATGGACTTCATGCGC  ATGATGTCCCTCCCGGGAAACTGCGCCGTCCCGCTGCCAATGCAGACGCTTGCACAGTGC  GCCAGTAAGTCATCGTAGCCGATCTTCACTACTGTATTATGTTTCTATTTTTGGCATTGT  TATTTTGTGAATTACCTGCATGACCGGAGGAAGATTGAATTTTTGTCGATGTTATGACAG  CGGCGCCGGTGCCACCACTGGACCCTCCTACCGCTCCAGCAGCCCCATCTCCAAGTAACT  ACCGTTTCCTTCGGAAATTCTGCCTTCACTAAATAATAATTTGGCCATGCTAGCTAGTGT  TAATTTGTCGTATGATCCACAGTCTGACACGTGTTTTTTTTCTCTCTATCCTTTGCAGAG  CCATGACTGTAGAAGCAAGATGATCCATCGATATGAAGTCCGATCAAGATGATGAATTAG  TTGTCAACCACATACTCCACTAGTTTCGGTATAGTTAGGGATAAGATATATTTATCTTAG  GTTAGTGTTTTATACTATGTTGTGTGCTGGCGATTTAGATCTACAAAGTACCTATTCTGT  AGGAGAATTCTTTTCTTTTCATCACTGTATATATGCGGTGATCAATATTAGTCCATACGT  GCATCGCGAATTCGTAAGTGTCTATATGCATGTGCTTTACGGGTGCCCCTGCGTGTTGGA  TCAGCTCTTGATTCAAATCATTTCTTCCTCTTTCAGTTTCAGGAGCTTGTGAATCTGCAG  GGTACGCGCGTATTTTTTCTCTCTCTGCATTGCAGGCTACGAACGCACTGTGAGGTGCTA  GAGCCCATGTTTTTTTTCTTTTCTTTGAGGTGGATGCTAGAGCCCACGTGTGTTGTGTGC  TGTTCCTCGATGAGGCCCGCTATGATACGTGGGCTTTTTACCAGGCCAGCATAGCCTGCC  GGGTCTCTTGCTGGGAGCGTGCAAGCGGGCGACGATGGTGGCGAGCAACGCAGCGCGCGA  GCGAAAGCGATTGACGGACGCGGTACGGTTGCGGTTGCCAGTTGCCGAGTTGGCCACTTG  GAGAGACCAAGTGGGCACCTGCCGTCCACTTGGCTGATAGGATTTCATCAACCGCAGCGA  GCAGCCTGCCACGGTGTCTCCTGTGCCAACGCGTGCGCATTCTTGATTCTGTCGGCCGCT  GCGGCGGGGTTTCTAGGTGCGGTTGCCGTATGGTGAATTCTGTGGAATAGA |
| **Chr3b-556934804** | CCAACGAGGATTGATTAATCGAAAAAACTGAATAATGTCAAAGAAATGATTTTCGTTCAC  CGCCAAACAGATCGTCACGCTGCTATAGTTGAATTATGATAAACTTGAAAGGACAAGGTC  ACAATCCTCTTCACAAGTTCAGATATCTTGCCTGAAATAACATCACAAGTCTGTCTTTAC  TTCTTTTTTCCCGATAAAGATCATACGCCTGTCTGCCGGCCGGCCTACTAGAACTTCATG  CTTCGTCGGAATATAAGACGTGCCTCCTGCAATTTGATAGGGAAAAACTGCACATGGGTA  TGATCCTGTTTAATCCGCGTACCCGTGTTAGTCTTAACCGTCAAGAGCCAACGGCCATCC  TAAGCAAATCAAGGCATGTTCATCCCAATAATTGTTAAGCTGACCAATCCTAACGAAAAT  CATCACATAGAAAATCTCCATAATCAATCAAGCTTACAATTATTAGCAACCAACACGCAA  GCTCTGATGATGTGAACACTATAAATAGGGACACCATTACCATTGCAAAAGCACAAGACA  TAAACCTTGAGGACTTGTCGGCCTAGCTACATTACTTACTAGGCGTGCTCTGAAATTGAA  ATGGACGCTCCTTCTCTGCTTCTTCTCACCACCTTGTTGGCCTTTGCATTCAAGGCCTCC  GTTGCTCAATGGACGCCTGCATTTGCAACATTCTACGGCGGCAGCGACGCGTCGGACACC  ATGGGTAAGGTTTCTTTTACGCTTGAGCTGCATGCATTATTTGGATGCCGCAGATCCTCG  ATCTTCTTTTACTAAGCAGGACGCAACTTACACAAATATGCAGGTGGTGCGTGCGGGTAC  GGGAACTTGTACAACGCCGGGTACGGGGTTAATTCTTTTTTTTTTTTGAAGCTCGCATAC  TCTTTATTTAAACGTCCCAAGCAGGGATCTCGTCCGAAACAGCCTGCAAAATACAGTCCG  GGGGTTCGGCTAGCCAAACCTTACACAGATTATTTGCCACACTATGTCTAGCTAACAGAT  GAGCTGCATTATTAACAGAACGTCTAACCCAAGTGACTTTCCAGCCATCCCTCAACGCCA  GAAGTTGCTTAACCTCTTCTATGACCGATCCCAGCATAGATAAGTCCCTCTCCTTGTTAT  TCAGCTTGCTGACTATCTCAAGGGAGTCCATCTCCACATGCAGGCGTCCAACATTTAGCT  CCTGAGCTAGTTGTGCTGCCCTTTTGCATGCCTGTATTTCCACCATCGCCGCATCCTTGC  ACCCAGGATAGGCCTGGCACGCCCCGGCCATGAACGCGCCCTCCTGGTTCCTGATGACCA  CTCCTACGCCTCCCAACTCCCCTCCCTTGGACGTAGCTCCGTCCACGTTTGCCTTCACCC  ACCCTTGATCAGGTGGTTGCCATTTTTCCTTCGGAGCAGGGTTGTCTTGCTTGCATTTTC  GACCATGTATGGACTGCCACTCCTCCATTAACTGGAAAACTCTTCTCGCAATAGCTGCAG  CATCCTCGATCCTCCGTCCTTCTCTTGCGTTATTCCTGGCTAACCAGAGTGCATACACAC  CTTGAACCAAGACGGCTTTCTCATCATCGGACACTGTCGGGAGCCACTCCATGAGCCACC  TAGATAATGCACTCTGAGGGCATGCTGACTCCGGTGGGATCGCCACCGGTACCCCCAATT  CCCACTGCATGATCTTCCAGAATTTTGCTGAGTGAAAGCAACCCCAAAATCTATGATAGT  TAGTCTCCTCCCTCCCACAAGCAACACAAACAACTCCCTCCTTGATCTTCCTCCTCTGTA  ACTCTGTGCCCACAGCCAGCCCATTCCGAATGAGACGCCACATATGTATTTTAACCTTGC  CCGGTGCTACAGTATCCCATAGGCTCAGCCAAGATTTATGCTCCGCCACAGGAGATGAAG  TTTCCGGCCTACATGCTTTTAGACGTTTTTGTGCCATTCTCAAGTGGTAGGCTGACCTCA  CCGTGAACACCCCGTTTTTGGTGAAGTTCCAAGCTAAGTAGTCCTCCATGGCTGGCCCCC  CAATCGGAATCTGCAGTATCTCTTCCACCTCATCCGGGGCAAACATGGACTGCACCTTAC  TGTGGTCCCAAGCATTGCCTTGATCATTGAGTAGATCGCATACCCTCGTGATCCCATGTA  TATAGTTCTGGCCCAGTGGCCTTAAACATCCCTTCCGTGGTATCCAATTGTCATGATGTA  TTTTGACTCTCGTCCCATCCCCAATCCTCCAAATGAGCCCATCCAAGAGGAGATTCCTCC  CATGAATAATGCTTCTGAAAGTGAAGGAACCTCCATCCGGGCACGTTGCATTGAGGATCG  ACCCATCCCCAAAGTATCTAGCTTTTAAGACTCGTGCACACAGCGAGTTTGGCACCTGAA  GTATTCTCCAGGCTTGTTTGGCAAGCATCGCTTGGTTAAACGCTTCTGGGTCACGAAACC  CGAGCCCGCCCTCATGCTTCCTAACACACATTTTATCCCAAGCTATCCAATGTACCTTAT  TTTGCCCATTAGCTTCACCCCACCAGAAGTTCGCAGAGATAGATGACAGATTCCCGCACA  TTTTCTTTGTGAGTTGAAAACAGCTCATGGTAAAAGTTGGTGTTGATTGGAGACCCGACT  TGACAAGCATCTCTCTCGCCATCTTGGATAGACCTTGCCCCTTCCATCCGCCTACTTTCC  CTCTTGCACTCTCCTTAACATACTTGAACGTACCCTCCTTTGACTTTCCAACGACAGTGG  GGAGCCCTAGATACCGTTCACTTAGGGCCTCCTCAGAAATGCCAATAATCTGCTTCACCT  CCTGTTTCAATGCATCCGGGCAACCTTTCCCGAAGAAAATAGCAGATTTTTGAAGATTAA  CTTTCTGTCCCGACGCCACTTAATACCCCTGCAAAATGACACGAAGCGCCTCAAAATTAT  CCCGGGATCCCTCCAAGAACACCACACTATCATCTGCAAATAGGAGGTGAGTAACAGTCG  GCCCGGTGCATCCAAACGACACTCCTTTGATTTCCTTCTTACTCTGTGCATTCTTCAGCA  AAGCTGAGAACCCCTCTACACAAAAAAGGAAGAGGTAGGGGGAAAGGGGATCTCCCTGTC  TAAGTCCACGCGACGGCCAAAACCTGTGAGATAGCCCACCATTCAACTTGACCGCAAAGG  TAGCTGATTTCACACACCTCATAATCATCTCCGTCCAGTGACAGGAGAAACCAAATTTGA  GTAACATTTTCTCTAGGAAATCCCACTCCACTCTGTCGTACGCCTTCATCATATCCAGCT  TTACTGCACATAAAGGTTTCCTGCGTTTCCGCTTTCTTATCGCATGCACACACTCATATG  CCACCAAGACATTATCCGTTAGTAGCCTTCCTGGGACGAAGGCACTTTGTTCCTCCGATA  TCATAAAACGTAGCACCTCCTTCAGCCGGTTAGCCAGTGCTTTCGCGGCAACCTTGTATA  GGACATTACAGAGACTAATTGGGCGGAATTGTGAAAGTAGCTCCGGTGAGCTTACCTTCG  GAATCAGCACCAGAGTTGTGCCATTAAATCCATCTGGGGTTGCACCCCCGGCAAGGAACT  CGCGAACAGCGTTGCACACATCATTTTTTACTAACGCCCAATGCTTCTGAAAGAACATGG  CCAGCAGCCCATCTGGCCCCGGCGCCTTCGTGGGGCCCATCTGGAAAAGCGCCTTCTCAA  TTTCATCATCCGTGAACGGTGCCCCCAACTTTGCATTCATCTCCTCTGTGACGCACCCGG  TAATATGCTGCAAAATTGTATCGGCATCACGAGAACCCTCTGATGCGAACAACCTGGCAT  AGAACTCAGCAGCCATCTTCCTCATACCTTCGTCGTCCGTGCACTTAGATCCATCATCTC  TCCTCAAAGCCTTGATAGTGTTTTTCCTTTTACGGTGTGAGGCGCGATTCTGGAAGTACT  TCGTGTTCTGATCCCCCTCTGTTAACCAATCAATCCGGGATCTTTGCTTGTAATATACTT  CTTCTCTTTCATATAATTCATGTAATTGATCCTCTATATCTTTTACCTCCTGTCTGTATC  CCGTCCGAGCGCCCCGTTCTTTAGCATCCACTAACTGAACCTTGAGGTGAGCGATCTATT  TTTTAATTGAGTCGAAGACTTGGCGACTCCATCTGTGCATGGCTCTCGACGTGAACAGGA  GGCGACTGCATGCCGCGCCGAGTGCGCCAGCCTCCTGATTGGCTGCATGGGCTTCGGCCC  ATGCACTGGCCACCATGGTCTCGTATCCCTCGTGCCTTGCCCAAGCGGCTTCATAGATAA  ACGGCCGCTGTCCTCCAGAGTGCGCTGCGACCTGTGTCGCCTGCACTCTGACAACTAGCG  CCTGATGGTCCGACTCCTCTGTCATAATATGCGTCACATCAGTTGCCGGGAATAACTACG  CGAACTCCGCATCGCACGTGGTTAATTCAGCTGCGTTGAGCACGACGCTCTTCAACAACG  GTGCATCGTGCGGCATGTGCTTCACCATCACATGCGACGCAAGCAAGACACCATCGTGCA  AACAGGGCACGTCAATCACCATCACGGCAACCAACTTCTGCCCACCCAACTACGCCCTGG  CCAGCGACAATGACGGATGGTGCAACCCGCCGCGGCAACACTTCGACATGTCGCAGCCCG  CATGGGAGACCATCGCTGTCTATCAAGCCGGCATTGTGCCCGTCAACTACATGAGGGTTC  CCTGCCAGAGGAGTGGGGGCATGAGGTTCACCATCAACGGGAACGACTACTTTGAGCTCG  TCACAGTGGCAAATGTCGGCGGTAGTGGTGTGGTGTCCCAAATGTGGATCAAGGGGTCCA  AGACTGACTGGATGGTAATGAGCAGGAATTGGGGTGCCAGCTGGCAGAGCAATGCTTACC  TCAACGGCCAGAGCCTGTCCTTCAAGGTACAGACCGACGACGGCCGGGTCGTCATGGCCG  ACAATGTTGCACCGTCCAACTGGTGGTTCGGTGGCACCTACACTTCGTGGCAGCAGTTCT  AACATCTTGCGAGGTTGATGTAGGTACTCATCTATGGGTACTCAAATAGTCAGGCCCGAT  GATTTCATCTGAGGCTGTATCTCTTCTTTTATTTCTTTGTATCTCTATTTTGCTTGTCCA  AGTTTGTGTACTTAGCTTCCATTAATTCTCTTGTGGCATAAGATCATTAGATTATATGTA  TGTGCTCAACATCTCAAGAGTAATTTATCTTCAATCAAATCTTTAGTGTTTAATACAGGG  TCGCCTATTTGTGCCTAAATTTTAGTCGATTTTCTTCGCTTTTGGGTTGAAATCCAACGG  ATGGGACAACTTCCACCTCCCGCTTCTTCCTCCTCTAACCAACTACACACTAGATGGCCC  CCTTCAAAGTGTTATATGGACGAAAGTGCCGAACCCCTTTGAACTGGTCAGAAACTGGGG  AACATCCACTCTTCGGTCCAGATATTATCTAACACGCCGAAGAACAAGTTTGCGTTATCC  GCAAGAATCTCAAGATTGCTCAGTCACGTTAGAAAAGTCAGTATGATCGTCATCATAAAG  ACATGGTCTATCAACCTGGCGAAAAGGCTTATCTTCTAGTCACACCAATGAAGGGTGCAC  AA |
| **Chr3b-562274308** | TATAATTATTAGTGTTGAACACTTTGAAGCTAGTTCGTGTTGCACGTTTGATCTTTGTTT  GATGTTGTGGACTGCACTGTGCCTAATCCAGCGATGGCGAATACGTGATACAGACATCCT  ACCAGTAGAAGAATCAATGGCTATTTGCAATTTTATACCCAACGAATGGCTGAGGGCTAC  TGAGCCCATGAAAATCTGCTTATATTTGTTGGTAACCGTCGACATGTATGCTGCGGCAAA  TGAATTCACAAATATAATCTTCAATTGTTTCTCCTCTTGTGTTATCAATATTCTCACCAG  TTCATTCTATTGCATAAAATTTACAGTTATATATCTGCCTTTAAAAAAAATGCTCTCATC  AATTAAGACGTCTAGTTGAATTGGCTGGTGCATATAGAATCCAAAATTGCATGAAATGAA  AGAGGTATTTTAAGATAATTTAGCAGCAATATAATCATGAACATTCAACAAGGTTACTCC  CTCTGTTAAAAAATATTTGAACTAAAACCATGACACTTATTTTGGAATGGAGAGAGTAAT  AGAAAACTGCTTATAATGTGATTTTGCTAATTTTGAACTGTATAACAAGTTAATAACTTA  ATGAAACGCTTTAATAAATCTGTGAAAGTCCTAACCTGCAGCGTTCAAGGCGTCGATCTC  GGAACGCGCGAGCCGGATATACACATCCTGCACGACCACCGGGTACTGCCTCATGTCAAG  CAGATCCACGCCCCAAATGACGCACCCGTGGCTGATTCCCCCGCTAATGTTGGCGGCGGC  GTACGCCCTGCAGCTGCAGTTACCCAGGCACAGCTGCCTGCACTCGGCCAGGGTCATGTC  GGGGCGCACCGTCGCTTCCGTCGCCTCCGGCAGCTTCATCCGGTTCACCGGCCAGAAGCC  GTCTCCAGACCCACAGCTCAGGTTGGCGCTCCTGGTGCAGCCACCGGACCAGCCCCTCTG  CTCCCACTGCTCCGGCGACCGGGGCTTGAACCCCGGCAGGCAGCTACACTTGGGGGGCTG  GCCGACCTCGCACACGCCGAAACCGAATGCCCCGCACTTGTAGTAGCTATCACACGGGTC  GCTCGGGTGGTACCAGTAGCTGCTCCACGCGCCGTTGCCCCACACGTAGCTCTGCAGCTG  CCCCGTCGCGCCGTCCAGGATCAGCCGCGACAGAGCCGACGGGTCGCTGACGTAGTAGGC  ATAGTATGTCTCGTCGGCGTTGGACACGACCATGAACGTGTAGCCCTCGGCGTTGAGGTT  CTGCACGCCGGTGAGCACCACGCCGTTCCACGGCCCGCTCGCGTAGATCCTCTCCGGGCC  GCGGAAAAGGAAGAACTCGGGCAGTCCGCCCATGACCAGCTTGAACGTGTAGGCCCCCGG  CGAGGGGTCGGTCGGGCTTCTACACGACGTGATGTTTCTGGCGATGCCCTTCTTGAGGTC  CACCCCGAGCTTCATGCCGGGCAGCATCGTGTCCGTCGGGTAGTCGAAGCTCTGCCACGC  CACGCTCTGGCTCGACCCACTCCCGTCAGAGCTCAGGACGAAGTTGCCGTCGTCGAGAAG  CTGAGCGGTGACCTTGGTGGTTATATTTCTGGTGGGCGCCGCGGAGGACCAGACTGTGGT  GTTCCGGCCGTCGACGATGACCAGGCGGCCGTCGGGGGAGAGCTTGAGGACGCCGGGGGA  GCTGACGACCGGGCTCCGGCGGTTGGCGACCCACACGACGGTCTGTACAGGGATGCCCGC  GTACCAAATGCCGAGGTAGGCTCTGGCATCGGAGCTTCCGGGCGGGTTGTAGAAGCCGAG  CCTGAAGATTCCACCGGCTGAGATCAGCGTCTGGTTGCCGGTGATGGAGGCGGCATGGTC  GATGGTGTCGGTGGCGATGGAGATGGAGAGGCAGGTGGTGGCAAAGACGACGAGTAGAGC  GCGCGCAGGCGCCCTCATCCTTTCTCCACGCTCCCTCTCTCTGGAATCGAGCGCCCCGCC  AAATACGAGAGTACTGTAATTTGTGACTGAAAGACGGCGTGGTTATCGTGCGAAAGAATG  GATGAGTGGTGGTAACCCATAAACTTCAAATGAGCGTGACAGCGTGGAACAGCAGTGAGA  AGTATTGCAGGTCGACGTTAAGCCTCCGGAACAGCTAGTTTTCGCGCGAGGTTGGCGCTG  CTCAGAGCCACTCTGTACAGTGCTGCAGGGTATTCACAAACTTCAACGGATCTGCCTCGA  TGGCACATGTTCGATATTGCGATATTGTGGTACCGGATCCGAATATTGCGGTAGTGGTGC  ACATGCAAGAGAATGTATCCGGTGCAACCTGTGCGTCCAAGTAAAAAACGAGTGAAATGC  ATAAAAACCACCACAGCCGTGTCACAACTCGTAAAAAACCACCACAATTCAAAAAAGTGG  CAAAATGCACCGAACGTTATC |