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一个新的小麦黄叶位点的分子定位

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摘要：小麦叶片颜色与植株光合效率和籽粒产量密切相关。人工合成小麦Y223表现为生理性黄叶，与正常绿叶品种晋作82的杂种F_1植株叶色表现为中间型，在Y223旗叶抽出17 d后，杂种F_2群体中绿叶、中间和黄叶类型植株数目的分离比例符合1∶2∶1，表明Y223的黄叶表现不完全显性。采用混合分离群体分析法，利用杂种F_2植株构建绿叶池和黄叶池，从分布于小麦21条染色体的569个SSR标记中筛选出12个在亲本间和绿叶/黄叶池间表现多态性的标记。利用9个位于2B染色体的多态性标记扩增F_2群体，最终用5个标记定位了黄叶位点，暂命名为*YL-2B*，其侧翼标记为*Xbarc200*和*Xbarc55*，与*YL-2B*的遗传距离分别为2.3 cM和3.8 cM。通过比较显隐性、黄叶表型和标记连锁程度，证明*YL-2B*与2B染色体上已报道黄叶位点均不相同，是1个新的黄叶位点。本研究初步明确了Y223黄叶位点的遗传规律和染色体位置，为下一步基因克隆以及叶片衰老机制解析奠定了基础。

关键词：人工合成小麦；黄叶；混合分离群体分析；SSR标记；分子定位

Molecular Mapping of a Novel Yellow Leaf Locus in Wheat

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Abstract：Leaf color is closely related to plant photosynthetic efficiency and grain yield of wheat. The physiological yellow leaves were present in an artificially synthesized wheat Y223. The F_1 plants derived from the cross between Y223 and a normal green leaf variety Jinzuo 82 displayed intermediate phenotype in leaf color. Seventeen days after the emergence of Y223's flag leaves，the segregation ratio for green leaf，intermediate，and yellow leaf types in the F_2 population Y223×Jinzuo 82 fits to 1∶2∶1，showing incomplete dominance of Y223's yellow leaves. Using the bulked segregant analysis method，F_2 individuals with contrasting phenotypes were selected to establish green leaf pools and yellow leaf pools. From 569 SSR markers distributed on 21 chromosomes of wheat，12 markers with consistent polymorphism between parents and green/yellow leaf pools were identified. Nine of them were located on chromosome 2B. These markers were used to genotype the F_2 population，and the yellow leaf locus，designated *YL-2B*，was mapped by five markers. *YL-2B* was flanked by markers *Xbarc200* and *Xbarc55*，with genetic distances of 2.3 cM and 3.8 cM，respectively. By comparing the characteristic of dominance/recessiveness，yellow leaf phenotype，and marker linkage，*YL-2B* proved to differ from the reported yellow leaf loci on chromosome 2B，indicating that it is possibly a novel locus. This study clarifies the inheritance mode and chromosome position of the yellow leaf locus carried by Y223，which provides a reference information for gene cloning and understanding leaf senescence mechanism.

Key words：artificially synthesized wheat；yellow leaf；bulked segregant analysis；SSR marker；molecular mapping

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作为世界上三大主粮作物之一，小麦稳产、高产对保障粮食安全具有重要意义。叶片是小麦光合作用的主要器官，叶片颜色、叶面积以及叶夹角的变化均能显著改变植株光合效率，进而影响籽粒产量[1]。叶色主要由叶肉细胞中的叶绿素含量决定。在光合作用中，叶绿素能固定光能并驱动电子传递将其转化为化学能，用于合成碳水化合物[2]。叶绿素含量越高、叶片绿色越深，越有利于小麦高产[3-4]。在未遭受病原菌侵染或逆境胁迫（如干旱、营养元素缺乏等）的情况下，小麦植株有时会出现生理性叶色异常，表现为黄叶、条纹叶或类病斑叶。这些异常叶色通常被认为是叶片早衰表型，而且可以遗传，是由基因突变所致。

小麦第二部分同源群包含多个小麦黄叶早衰位点。例如，Agarwal等[5]利用一个小麦突变体将叶片早衰位点*els*（*early leaf senescence*）定位在2DL染色体上；Li等[6]从一个早衰育种品系中鉴定了控制叶片早衰的隐性位点*els1*，并将其定位在2BS染色体；Wang等[7]从三叶期开始叶片不断黄化的突变体LF2009中鉴定出早衰位点*Els2*，定位在2BL染色体上。此外，在2AL染色体上还检测到一个旗叶早衰主效位点*QFlea-2AL*[8]。Zhang等[9]将黄叶突变株中的早衰位点*Y1718*定位在2BS染色体上。张强[10]从衰老突变体*m68*中鉴定出位于2DL染色体上的隐性衰老位点*TaLS-2D*。其余部分同源群染色体上也检测出了黄叶早衰位点，如4BS染色体上的叶片黄化基因*TaEYL*[11]、7AL染色体上的隐性叶绿体缺陷基因*cn-A1*[12]和6BS染色体上的隐性白色条纹叶基因*Wsl*[13]。类病斑（LM，lesion mimic）叶的研究则较多，鉴定出多个类病斑控制位点，包括位于1BL染色体的*Qlr.pser.1BL*[14]、3BS染色体的*lm1*、4BL染色体的*lm2*[15]、3BL染色体的*lm3*[16]、2DS染色体的*lm4*[17]、2AL染色体的*lm5*[18]、5AL染色体的*lmpa*[19]和3DS染色体的*TaSpl1*[20]。

控制叶片衰老进程的重要基因可通过正向或反向遗传学手段加以验证，例如，NAC转录因子*NAM-B1*[21]和*NAC-S*[22]、WRKY转录因子*TaWRKY42-B*[23]和*TaWRKY40-D*[24]、生长素响应因子*TaARF15-A*[25]、脱镁叶绿素酶基因*TaPPH-7A*[26]和衰老相关基因*TaSAG1~TaSAG9*[27]。

Y223是一个人工合成六倍体小麦，由硬粒小麦MV TD14-00与粗山羊草Y168杂交、幼胚拯救获得单倍体，经秋水仙素人工加倍获得双二倍体创制而成。Y223植株叶片在拔节期出现黄色斑点，后期变为典型黄叶。为了分析黄叶表型的遗传规律和控制位点，本研究利用Y223与正常叶色品种杂交构建了作图群体进行分子定位，以期为黄叶基因克隆和叶片衰老机制解析奠定基础。

1 材料与方法

1.1 试验材料

黄叶品系Y223、正常叶色品种晋作82、晋作82×Y223杂种F_1植株（共18株）和F_2群体（由9个杂种F_1植株收获的所有种子种植而来，共包含245个F_2单株），用于黄叶表型的遗传分析和基因定位。试验于2021-2023年度在山西农业大学东阳试验基地温室进行。

1.2 叶色表型鉴定

2022年10月下旬在温室播种F_2群体及其亲本，行长1.5 m，行宽0.2 m，每行等距种植10粒种子。次年4月在亲本Y223植株旗叶完全展开3 d、10 d和17 d后，分别鉴定遗传群体的旗叶表型。参考Liu等[17]的鉴定标准，将群体表型分为1~5级：亲本晋作82类型的正常绿色旗叶为1级、出现零星黄色斑点叶片为2级、出现黄斑或大量黄色斑点叶片为3级、大面积变黄叶片为4级、亲本Y223类型的完全黄叶表型为5级，并将2~4级定义为中间型。利用Excel进行卡方分析。

1.3 混合分离群体分析

采用SDS法提取三叶期F_2群体单株及其亲本的叶片基因组DNA。根据后期旗叶表型鉴定结果，采用混合分离群体分析法（BSA，bulked segregant analysis）在F_2群体中随机选取1级单株（正常绿色）和5级单株（完全黄叶）各10株，分别将其DNA等量混合建立绿叶池和黄叶池。采用分布于小麦21条染色体的569个SSR标记[28]（https://graingenes.org/cgi-bin/GG3/browse.cgi?class=marker）扩增亲本和绿/黄叶池，筛选多态性标记。PCR反应体系为10 μL：含PCR Mixture（B532061，生工生物，中国上海）5.0 μL，DNA模板1.5 μL，正反向引物共1.5 μL，ddH_2O 2.0 μL。PCR扩增体系为：95℃预变性3 min；95℃变性15 s，引物特定退火温度（表1）退火15 s，72℃延伸30 s，共34个循环；最后72℃延伸10 min。扩增产物在8%非变性聚丙烯酰胺凝胶（Acr：Bis=29：1）中电泳，银染法染色显影，记录带型。

表 1　本研究与黄叶基因连锁的 SSR 标记

Table 1　SSR markers linked to the yellow leaf gene in this study

标记名称 Marker name	上游引物（5'–3'） Forward sequence（5'–3'）	下游引物（5'–3'） Reverse sequence（5'–3'）	产物长度（bp） Product size	退火温度（℃） Tm
Xwmc314	ACACGGGGTCTGATTGCTTTAC	ATCGCTTTTTGACAAGTGAGGC	188	61
Xbarc200	GCGATATGATTTGGAGCTGATTG	GCGATGACGTTAGATGCGGAATTGT	168	52
Xbarc55	GCGGTCAACACACTCCACTCCTCTCTC	CGCTGCTCCCATTGCTCGCCGTTA	131	55
Xgwm374	ATAGTGTGTTGCATGCTGTGTG	TCTAATTAGCGTTGGCTGCC	184	60
Xbarc91	TTCCCATAACGCCGATAGTA	GCGTTTAATATTAGCTTCAAGATCAT	129	50

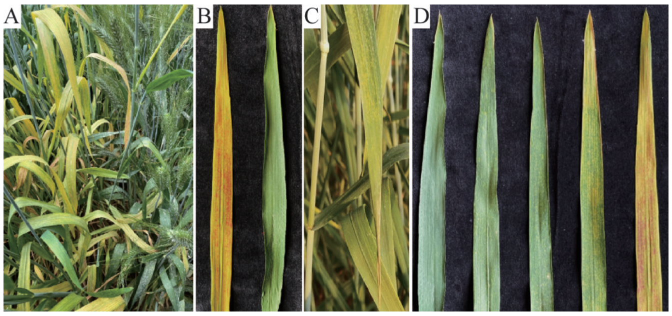
1.4　遗传定位与位点新颖性分析

利用在亲本间和绿/黄叶池间差异多态性一致的 SSR 标记，扩增 F_2 群体 DNA，获得群体基因型数据。将群体表型数据和基因型数据导入 Jionmap 4.0 软件计算基因与标记之间的遗传距离，用 MapDraw V2.1 绘制连锁图。根据定位结果，查阅目标染色体上已报道的黄叶位点及其侧翼连锁标记。合成已知黄叶连锁标记引物，并利用其扩增黄叶亲本 Y223 和正常绿叶亲本晋作 82，观察是否具有多态性；将亲本多态性标记进一步扩增晋作 82×Y223 杂种 F_2 群体的绿/黄叶池，如果标记在亲本和表型池间显示出一致的多态性，则用其扩增全部群体单株，进而将该标记整合到定位图谱中。

2　结果与分析

2.1　Y223 黄叶表型

Y223 幼苗植株叶片保持正常绿色，从拔节期开始，叶片开始出现黄色斑点，从下往上逐渐变为黄叶，至旗叶完全抽出第 10 天后，旗叶完全变黄，整株呈现黄叶表型；此时期与正常绿叶品种晋作 82 相比，Y223 旗叶差异明显，整个叶片呈黄色，原先黄色斑点变为红棕色斑点（图 1A、B）。



A：Y223（左）和晋作 82（右）植株表型；B：Y223（左）和晋作 82（右）旗叶表型；C：杂种 F_1 植株表型；D：杂种 F_2 群体旗叶表型分离，从左到右依次为 1~5 级

A: Phenotypes of Y223 (left) and Jinzuo 82 (right) plants; B: Phenotypes of Y223 (left) and Jinzuo 82 (right) flag leaves; C: Phenotype of F_1 plants; D: Phenotypic separation of flag leaves in the F_2 population, from left to right, leaves with grade 1 to 5

图 1　Y223、晋作 82 以及晋作 82×Y223 杂种后代的旗叶表型

Fig. 1　Flag leaf phenotypes of Y223, Jinzuo 82, and progenies of cross Jinzuo 82×Y223

2.2　晋作 82×Y223 杂种后代黄叶表型遗传特征

Y223 黄叶表型多年来表现稳定，将 Y223 与晋作 82 杂交，杂种 F_1 植株叶片上分布大量黄色斑点，叶片大部分呈淡黄色（图 1C）。杂种 F_2 群体植株的旗叶颜色出现分离。按照 1~5 级方法（图 1D），先后进行 3 次鉴定，第一次（Y223 旗叶抽出 3 d 后）鉴定结果显示，与晋作 82 绿叶类型相似的 1 级单株有 85 株、与 Y223 黄叶类型相似的 5 级单株有 23 株、中间类型 2~4 级单株有 137 株。第二次（Y223 旗叶抽出 10 d 后）鉴定结果显示，1 级单株有 66 株、5 级单株有 45 株、中间类型单株有 134 株。第三次（Y223 旗叶抽出 17 d 后）鉴定结果显示，1 级单株有 59 株、5 级单株有 65 株、中间类型单株有 121 株（表 2）。

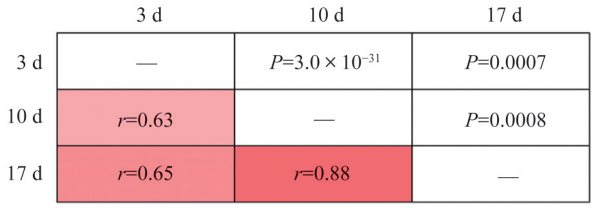
统计分析结果显示，F_2 群体第一次旗叶表型鉴定结果中的绿叶类型、中间类型和黄叶类型单株数目比例不符合 1∶2∶1（$P < 0.05$），而第二次鉴定结果大致符合（$P = 0.06$）、第三次鉴定结果最为符合（$P = 0.85$）（表 2）。三次鉴定结果之间差异极显著

（$P<0.001$），相关系数（r）分别为0.63（3 d与10 d）、0.88（10 d与17 d）和0.65（3 d与17 d）（图2），存在相关性，表明鉴定结果之间的差异可能是由于群体植株旗叶生长变化所致。综合F_1植株和F_2群体的旗叶表型，推测Y223携带1个不完全显性黄叶基因。

表2　晋作82×Y223杂交组合不同世代旗叶表型

Table 2　Flag leaf phenotypes of different generations derived from the cross between Jinzuo 82 and Y223

亲本或世代 Parent or generation	数目 Number	1级 Grade 1	中间型 Intermediate type				5级 Grade 5	$\chi^2_{1:2:1}$	P
			2级 Grade 2	3级 Grade 3	4级 Grade 4	合计 Total			
晋作82 Jinzuo 82	10	10	0	0	0	0	0		
Y223	10	0	0	0	0	0	10		
F_1	18	0	0	0	18	18	0		
F_2（3 d）	245	85	67	41	29	137	23	34.81	2.8×10^{-8}
F_2（10 d）	245	66	45	57	32	134	45	5.76	0.06
F_2（17 d）	245	59	41	43	37	121	65	0.33	0.85



	3 d	10 d	17 d
3 d	—	P=3.0×10^{-31}	P=0.0007
10 d	r=0.63	—	P=0.0008
17 d	r=0.65	r=0.88	—

图2　晋作82×Y223 F_2群体黄叶表型3次鉴定结果相关性分析

Fig. 2　Correlation analysis among three investigation results of yellow leaf phenotype in the Jinzuo 82×Y223 F_2 population

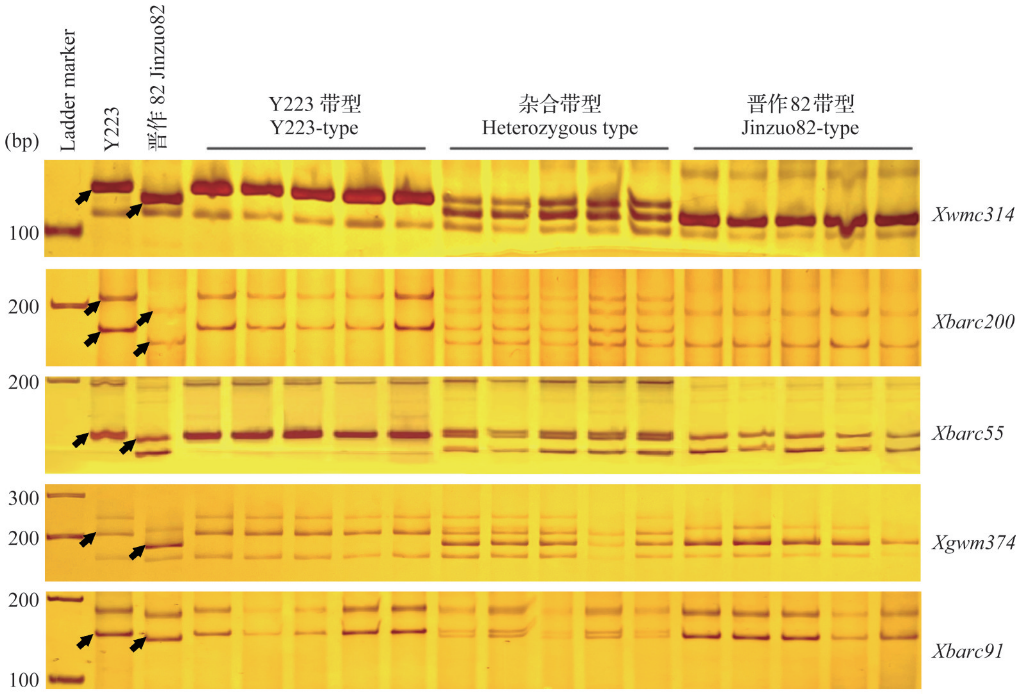
2.3　黄叶连锁标记筛选

通过BSA从569个SSR标记中选出191个（33.57%）在晋作82和Y223间存在多态性的标记，进一步筛选出12个在亲本间多态性和绿叶/黄叶表型池间多态性一致的标记。这12个SSR标记中，*Xgpw2204*和*Xgwm30*位于2A染色体、*Xgwm515*位于2D染色体，其余9个均位于2B染色体，包括*Xgwm47*、*Xgwm374*、*Xgwm382*、*Xwmc314*、*Xwmc474*、*Xbarc200*、*Xbarc55*、*Xbarc91*和*Xbarc101*。使用位于2B染色体的9个标记扩增F_2群体，所有标记均为共显性标记（表3）。每个标记在F_2群体单株中的电泳条带均显示Y233型、杂合型或晋作82型3种类型。其中，*Xgwm374*、*Xwmc314*、*Xbarc55*、*Xbarc91*和*Xbarc200*等5个标记出现3种带型的单株数目之比符合1∶2∶1分离比（$P>0.05$）（图3），而*Xgwm47*、*Xgwm382*、*Xwmc474*和*Xbarc101*等4个标记的带型显示偏分离，不符合1∶2∶1的分离比例（$P<0.05$），可能与黄叶表型不连锁。

表3　小麦2B染色体SSR标记基因型在F_2群体中的分离

Table 3　Genotypic separation of SSR markers on wheat chromosome 2B in the F_2 population of cross Jinzuo 82×Y223

SSR标记 SSR markers	Y223带型数目 No. of Y233-type	杂合带型数目 No. of heterozygous type	晋作82带型数目 No. of Jinzuo82-type	总计 Total	$\chi^2_{1:2:1}$（d=2）	P
Xgwm47	49	114	82	245	10.07	0.006
Xgwm374	69	119	57	245	1.38	0.50
Xgwm382	42	91	112	245	56.20	6.3×10^{-13}
Xwmc314	68	122	55	245	1.38	0.50
Xwmc474	33	104	108	245	51.51	6.5×10^{-12}
Xbarc55	66	121	58	245	0.56	0.76
Xbarc91	73	113	59	245	3.07	0.22
Xbarc101	53	101	91	245	19.33	6.3×10^{-5}
Xbarc200	59	120	66	245	0.50	0.78



箭头指示多态性条带
Arrows show polymorphic bands

图 3　*YL-2B* 连锁标记在 Y223、晋作 82 及其 F_2 单株中的扩增带型

Fig. 3　Amplification banding patterns of markers linked to *YL-2B* in Y223, Jinzuo 82, and their F_2 individuals

2.4　黄叶位点分子定位

将9个2B染色体标记扩增F_2群体的基因型数据与第3次叶色鉴定（Y223旗叶抽出17 d后）表型数据导入软件，选择Kosambi函数计算遗传距离，最终有5个标记*Xgwm374*、*Xwmc314*、*Xbarc55*、*Xbarc91*和*Xbarc200*与黄叶位点连锁。将定位的黄叶位点暂命名为*YL-2B*，其侧翼标记为*Xbarc200*和*Xbarc55*，与*YL-2B*的遗传距离分别为2.3 cM和3.8 cM（图4）。

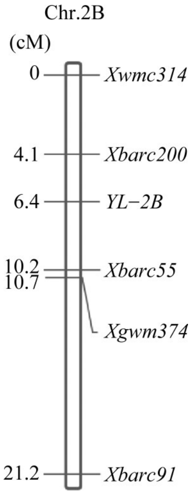


图 4　*YL-2B* 的遗传图谱

Fig. 4　Genetic map of *YL-2B*

2.5　*YL-2B* 与 2B 染色体已报道黄叶位点连锁性分析

目前，小麦2B染色体上报道的黄叶早衰位点有3个：*els1*[6]、*Els2*[7]和*Y1718*[9]（表4）。其中，*els1*为隐性位点，对应的黄叶特点为失绿，不出现黄色斑点，其侧翼连锁标记*WGGB306*和*WGGB307*在本研究所用亲本晋作82和Y223之间均显示出多态性，但在绿叶/黄叶池间没有多态性。*Els2*为不完全显性位点，纯合突变体在三叶期即出现黄色叶片，其一侧标记*Xgpw4043*在本研究所用亲本间无多态性，另一侧标记*Xwmc149*虽在亲本间有多态性，但在绿叶/黄叶池间没有多态性。*Y1718*为不完全显性位点，其纯合突变体与Y223具有类似的黄叶表型，但其侧翼连锁标记*Xwmc25*和*BE498358*在晋作82和Y223之间均没有多态性。综上所述，*YL-2B*与2B染色体上的已知黄叶位点在遗传特性、黄叶表型和连锁标记方面都不完全一致，表明*YL-2B*可能是1个新的黄叶位点。

表4 小麦2B染色体上已定位黄叶位点

Table 4 Yellow leaf loci on chromosome 2B reported in wheat

位点 Loci	显隐性 Dominance/ recessiveness	黄叶表型 Phenotype	来源 Source	连锁标记 Linkage marker		
				名称 Name	亲本多态性 Polymorphism between parents	与表型连锁 Linked to phenotype
YL-2B	不完全显性	拔节期起叶片现黄色斑点，抽穗期旗叶完全变黄	人工合成小麦	*Xbarc200*	+	+
				Xbarc55	+	+
els1[6]	隐性	拔节期起叶片发黄失绿，抽穗期旗叶出现变黄枯死表型	小麦杂交组合F_3突变家系	*WGGB306*	+	−
				WGGB307	+	−
Els2[7]	不完全显性	叶片在三叶期变黄，抽穗期旗叶完全变黄	小麦EMS突变体	*Xgpw4043*	−	−
				Xwmc149	+	−
Y1718[9]	不完全显性	叶片在苗期变为黄绿色，拔节期开始黄色加深，抽穗期旗叶完全变黄	小麦自然突变体	*Xwmc25*	−	−
				BE498358	−	−

+：存在多态性或连锁；−：不存在多态性或连锁

+：Polymorphic or linked；−：Non-polymorphic or unlinked

3 讨论

黄叶是植物衰老的重要表征之一，受叶绿素合成、库-源诱导和内源激素信号转导等途径调控。这些调控途径中的基因如发生突变则会加速或延缓衰老，造成黄叶或滞绿表型。因此，小麦生理性黄叶被认为是由基因突变引起的叶片早衰。例如，小麦脱镁叶绿素酶基因*TaPPH-7A*突变导致叶绿素含量降低、叶片失绿[26]。小麦NAC转录因子基因*NAM-B1*是籽粒蛋白含量(Grain protein content)位点*Gpc-B1*的功能基因，过表达*NAM-B1*能够增加籽粒蛋白含量，但也加速了叶片衰老[21]。生长素响应因子基因*TaARF15-A*则抑制*NAM-1*的表达，*arf15*突变体表现出黄叶早衰特征[25]。在小麦演化过程中，叶片早衰突变概率较小，且对于植株本身属于不利变异，一般会被自然选择所淘汰。而小麦种质创制或品种选育增加了基因组整合机会和基因突变概率，在种质杂交后代中较容易发现黄叶突变体。通常情况下，在品种选育后代发现的黄叶突变是隐性突变，这是由于被选为育种亲本的材料都是正常绿叶表型；而在种质创制过程中的人工杂交、EMS诱变等，有可能获得不完全显性的黄叶突变体。

本研究中的黄叶品系Y223为一个由四倍体硬粒小麦与二倍体粗山羊草杂交人工合成六倍体小麦，不同倍性基因组的整合可能增加了基因突变的频率。Y223植株旗叶在抽出第10天后完全变黄，整株呈现黄叶表型，与正常叶色品种晋作82的杂种F_1植株旗叶表现中间型。以Y223为参照，在Y223旗叶抽出3 d、10 d和17 d后，分别鉴定F_2群体单株的旗叶颜色。结果显示，只有第3次鉴定结果(Y223旗叶抽出17 d)符合不完全显性黄叶基因的分离比例，而前两次的鉴定结果中，绿叶单株偏多。这可能是由于Y223抽穗较晚、晋作82抽穗较早，杂种F_2群体植株旗叶抽出时期发生了偏分离，即在Y223抽出旗叶10 d后，仍有部分F_2植株旗叶未抽出或未完全显示出黄叶，直至Y223抽出旗叶17 d后，F_2群体的旗叶表型基本稳定，黄叶性状得以充分显示。利用SSR标记将Y223携带的黄叶位点*YL-2B*定位在小麦2B染色体上，通过比较显隐性、黄叶表型和标记连锁程度，发现*YL-2B*与2B染色体已报道黄叶位点均不相同，可能是1个新的黄叶位点。

*YL-2B*被定位在标记*Xbarc200*和*Xbarc55*之间约6.1 cM的遗传区段内。在小麦品种中国春参考基因组(IWGSC v1.0版)序列中，*Xbarc200*~*Xbarc55*对应Chr.2B：47.64~133.52 Mb的物理距离，此区间共有744个高置信(High confidence)注释基因(详见https://doi.org/10.13430/j.cnki.jpgr.20240318002，附表1)，包括可能参与调控叶片衰老的NAC转录因子(TraesCS2B01G100600、TraesCS2B01G118200、TraesCS2B01G119000)、WRKY转录因子(TraesCS2B01G121800)和在生长素信号转导通路中抑制ARF的Aux/IAA转录因子(TraesCS2B01G155800)。在接下来对*YL-2B*的精细定位研究中，将重点关注上述基因。

此外，Y223植株在成株期还对白粉病表现为免

疫，白粉菌孢子在其黄叶上不能生长，而相邻种植的正常叶色小麦品种晋作82则重度感病。这种叶片早衰植株的成株抗病性增强的现象已有许多报道，尤其是类病斑叶。例如，携带*Qlr.pser.1BL*的类病斑叶突变体成株期对叶锈病抗性增强[14]，携带*lm3*的突变体对白粉病的成株抗性增强[16]，携带*lm4*的突变体对条锈病的成株抗性增强[17]。这可能是由于早衰叶片中的活性氧等自由基含量较高，不利于病原菌孢子生存和扩散。本研究所种植温室内的白粉病为自然发病，因此尚不明确Y223的黄叶表型是否与抗白粉病表型连锁，接下来将对其F_2遗传群体进行白粉菌接种鉴定。

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附表 1 *YL-2B* 区段内的高置信注释基因

Appendix 1 High confidence annotated genes within the *YL-2B* region

基因编号 Gene ID	注释 Annotation	Pfam 注册号 Pfam accession number
TraesCS2B01G085400	F-box family protein	PF12937
TraesCS2B01G085500	Flavin-containing monooxygenase	PF00743
TraesCS2B01G085600	Secretion apparatus protein BsaZ	PF13968
TraesCS2B01G085700	Flavin-containing monooxygenase	PF00743
TraesCS2B01G085800	Flavin-containing monooxygenase	PF00743
TraesCS2B01G085900	Flavin-containing monooxygenase	PF00743
TraesCS2B01G086000	Flavin-containing monooxygenase	PF00743
TraesCS2B01G086100	Flavin-containing monooxygenase	PF00743
TraesCS2B01G086200	Aspartic proteinase nepenthesin-1	PF14543
TraesCS2B01G086300	Receptor-like protein kinase	PF07714
TraesCS2B01G086400	Response regulator	PF00072
TraesCS2B01G086500	Response regulator	PF00072
TraesCS2B01G086600	Two-component response regulator	
TraesCS2B01G086700	DNA/RNA helicase protein	PF08797
TraesCS2B01G086800	Vacuolar protein sorting-associated protein 54	PF07928
TraesCS2B01G086900	Thylakoid lumenal 15.0 kDa protein 2, chloroplastic	PF04536
TraesCS2B01G087000	response regulator 1	PF00072
TraesCS2B01G087100	Response regulator	PF00072
TraesCS2B01G087200	Envelopment polyprotein	
TraesCS2B01G087300	Receptor-like protein kinase	PF13947
TraesCS2B01G087400	Peroxidase family protein	PF00141
TraesCS2B01G087500	calpain-type cysteine protease family	
TraesCS2B01G087600	GDT1-like protein	PF01169
TraesCS2B01G087700	Kelch repeat and BTB domain-containing protein 1	
TraesCS2B01G087800	Cysteinyl-tRNA synthetase, class Ia family protein	
TraesCS2B01G087900	tRNA N6-adenosine threonylcarbamoyltransferase	
TraesCS2B01G088000	transmembrane protein, putative (DUF1218)	PF06749
TraesCS2B01G088100	Receptor-like protein kinase	PF13947
TraesCS2B01G088200	Citrate-binding protein	PF08787
TraesCS2B01G088300	Leucine-rich repeat receptor-like protein kinase family protein	PF08263
TraesCS2B01G088400	Glycosyltransferase	PF00201
TraesCS2B01G088500	5'-3' exoribonuclease 3	PF03159
TraesCS2B01G088600	F-box family protein	PF00646
TraesCS2B01G088700	Cytochrome P450 family protein, expressed	PF00067
TraesCS2B01G088800	5'-3' exoribonuclease 3	
TraesCS2B01G088900	Glycosyltransferase	PF00201
TraesCS2B01G089000	Ubiquitin thioesterase	PF10275
TraesCS2B01G089100	Ubiquitin thioesterase	PF10275
TraesCS2B01G089200	Protein FAR1-RELATED SEQUENCE 5	
TraesCS2B01G089300	F-box domain containing protein, expressed	
TraesCS2B01G089400	F-box domain containing protein, expressed	
TraesCS2B01G089500	CASP-like protein	PF04535

TraesCS2B01G089600	Ubiquitin thioesterase	PF10275
TraesCS2B01G089700	E3 ubiquitin-protein ligase SINA-like 10	PF02902
TraesCS2B01G089800	Ubiquitin thioesterase	PF10275
TraesCS2B01G089900	F-box protein family	PF08387
TraesCS2B01G090000	F-box protein	
TraesCS2B01G090100	1-deoxy-D-xylulose-5-phosphate synthase, Transketolase	PF00456
TraesCS2B01G090200	F-box family protein	PF12937
TraesCS2B01G090300	Germin-like protein	PF00190
TraesCS2B01G090400	Acyl-[acyl-carrier-protein] desaturase	PF03405
TraesCS2B01G090500	F-box family protein	PF00646
TraesCS2B01G090600	Methyl-CpG-binding domain protein	PF01429
TraesCS2B01G090700	Acyl-[acyl-carrier-protein] desaturase	PF03405
TraesCS2B01G090800	carboxyl-terminal peptidase, putative (DUF239)	PF14365
TraesCS2B01G090900	flocculation FLO11-like protein	
TraesCS2B01G091000	IAA-amino acid hydrolase ILR1	PF01546
TraesCS2B01G091100	carboxyl-terminal peptidase (DUF239)	PF14365
TraesCS2B01G091200	IAA-amino acid hydrolase ILR1	PF01546
TraesCS2B01G091300	Amine oxidase	PF02727
TraesCS2B01G091400	L-lactate dehydrogenase	PF00056
TraesCS2B01G091500	Cytochrome P450	PF00067
TraesCS2B01G091600	Elongation factor 1 alpha	PF00009
TraesCS2B01G091700	FBD-associated F-box protein	PF00646
TraesCS2B01G091800	ER membrane protein complex subunit 8/9-like protein	PF03665
TraesCS2B01G091900	CsAtPR5	
TraesCS2B01G092000	Glycosyltransferase	PF00201
TraesCS2B01G092100	Glycosyltransferase	PF00201
TraesCS2B01G092200	Glycosyltransferase	PF00201
TraesCS2B01G092300	transmembrane protein, putative (DUF594)	PF13968
TraesCS2B01G092400	transmembrane protein, putative (DUF594)	PF13968
TraesCS2B01G092500	DNA topoisomerase	
TraesCS2B01G092600	transmembrane protein, putative (DUF594)	PF13968
TraesCS2B01G092700	NAD-dependent protein deacetylase	PF02146
TraesCS2B01G092800	Glycine-rich cell wall structural protein 2	
TraesCS2B01G092900	Strictosidine synthase	PF03088
TraesCS2B01G093000	Strictosidine synthase	PF03088
TraesCS2B01G093100	Cytochrome P450, putative	PF00067
TraesCS2B01G093200	Cytochrome P450 family protein	PF00067
TraesCS2B01G093300	Cytochrome P450, putative	PF00067
TraesCS2B01G093400	O-glucosyltransferase rumi	PF05686
TraesCS2B01G093500	Protein trichome birefringence	PF14416
TraesCS2B01G093600	Mitochondrial transcription termination factor-like	PF02536
TraesCS2B01G093700	F-box family protein	PF03478
TraesCS2B01G093800	Repetitive proline-rich cell wall protein	
TraesCS2B01G093900	F-box/RNI superfamily protein	
TraesCS2B01G094000	Dof zinc finger protein	PF02701
TraesCS2B01G094100	Kinase family protein	PF00582

TraesCS2B01G094200	Peptide transporter family protein	
TraesCS2B01G094300	2-oxoglutarate dehydrogenase E1 component family protein	PF16078
TraesCS2B01G094400	Kinase family protein	PF12819
TraesCS2B01G094500	Telomere repeat-binding factor like-protein	PF00249
TraesCS2B01G094600	P53/DNA damage-regulated protein	
TraesCS2B01G094700	methyl-coenzyme M reductase II subunit gamma, putative (DUF3741)	PF14383
TraesCS2B01G094800	LPS-induced tumor necrosis factor alpha factor	PF10601
TraesCS2B01G094900	Actin cross-linking protein, putative (DUF569)	PF04601
TraesCS2B01G095000	Actin cross-linking protein, putative (DUF569)	PF04601
TraesCS2B01G095100	DNAJ heat shock N-terminal domain-containing protein-like	PF11926
TraesCS2B01G095200	Actin cross-linking protein, putative (DUF569)	PF04601
TraesCS2B01G095300	epstein-barr nuclear antigen	
TraesCS2B01G095400	actin cross-linking protein, putative (DUF569)	PF04601
TraesCS2B01G095500	Kinase interacting (KIP1-like) family protein	PF07765
TraesCS2B01G095600	Expansin protein	PF03330
TraesCS2B01G095700	Expansin protein	PF03330
TraesCS2B01G095800	UDP-Glycosyltransferase	PF00201
TraesCS2B01G095900	Transcription factor	
TraesCS2B01G096000	Protein kinase-like protein	PF07714
TraesCS2B01G096100	Sporulation protein RMD1	PF02582
TraesCS2B01G096200	Ascorbate peroxidase	PF00141
TraesCS2B01G096300	Arogenate dehydratase	PF00800
TraesCS2B01G096400	Tapetum determinant 1	
TraesCS2B01G096500	UvrABC system protein C	PF14520
TraesCS2B01G096600	Serine/threonine-protein kinase ATM	PF00855
TraesCS2B01G096700	Glycosyltransferases	PF03360
TraesCS2B01G096800	Glycosyltransferases	PF03360
TraesCS2B01G096900	F-box family protein	PF08387
TraesCS2B01G097000	Pyridoxal 5'-phosphate synthase subunit PdxT	PF07762
TraesCS2B01G097100	Elongation factor 1-alpha	PF00009
TraesCS2B01G097200	Nuclear pore complex protein NUP205	
TraesCS2B01G097300	Elongation factor 1-alpha	PF00009
TraesCS2B01G097400	Yellow stripe-like transporter 12	PF03169
TraesCS2B01G097500	Urease subunit gamma	
TraesCS2B01G097600	Yellow stripe-like transporter 12	PF03169
TraesCS2B01G097700	Urease subunit gamma	
TraesCS2B01G097800	MLO-like protein	PF03094
TraesCS2B01G097900	MLO-like protein	PF03094
TraesCS2B01G098000	F-box family protein	
TraesCS2B01G098100	Peroxidase	PF00141
TraesCS2B01G098200	Peroxidase	PF00141
TraesCS2B01G098300	F-box family protein	
TraesCS2B01G098400	Peroxidase	PF00141
TraesCS2B01G098500	Phosphoinositide phospholipase C	PF00388
TraesCS2B01G098600	Peroxidase	PF00141

TraesCS2B01G098700	Peroxidase	PF00141
TraesCS2B01G098800	Symplekin	PF12295
TraesCS2B01G098900	D-ribose-binding periplasmic	PF14009
TraesCS2B01G099000	Transposon protein, putative, CACTA, En/Spm sub-class	
TraesCS2B01G099100	D-ribose-binding periplasmic	PF14009
TraesCS2B01G099200	D-ribose-binding periplasmic	PF14009
TraesCS2B01G099300	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF14223
TraesCS2B01G099400	D-ribose-binding periplasmic	PF14009
TraesCS2B01G099500	Omega-3 fatty acid desaturase	PF11960
TraesCS2B01G099600	Chaperone protein dnaJ	PF00226
TraesCS2B01G099700	Syntaxin-binding protein 5-like protein	PF12894
TraesCS2B01G099800	RING/FYVE/PHD zinc finger protein	PF16135
TraesCS2B01G099900	Mitochondrial import inner membrane translocase subunit Tim17	PF02466
TraesCS2B01G100000	Mitochondrial import inner membrane translocase subunit Tim17	PF02466
TraesCS2B01G100100	F-box domain containing protein	
TraesCS2B01G100200	Disease resistance protein (NBS-LRR class) family	PF00931
TraesCS2B01G100300	receptor kinase 1	PF00069
TraesCS2B01G100400	26S protease regulatory subunit	PF00004
TraesCS2B01G100500	Transferase family protein	PF02458
TraesCS2B01G100600	NAC domain protein,	PF02365
TraesCS2B01G100700	Dirigent protein	PF03018
TraesCS2B01G100800	Dirigent protein	PF03018
TraesCS2B01G100900	U3 small nucleolar RNA-associated protein 18-like protein	PF07893
TraesCS2B01G101000	Transposon protein, putative, Mutator sub-class	
TraesCS2B01G101100	Transducin/WD40 repeat-like superfamily protein	PF07893
TraesCS2B01G101200	Phospho-N-acetylmuramoyl-pentapeptide-transferase	PF07762
TraesCS2B01G101300	NBS-LRR-like resistance protein	
TraesCS2B01G101400	Homeobox leucine zipper protein	
TraesCS2B01G101500	Transmembrane protein 234 like	PF10639
TraesCS2B01G101600	Trichome birefringence-like protein	PF14416
TraesCS2B01G101700	AMP deaminase	PF00962
TraesCS2B01G101800	Protein phosphatase 2C	PF00481
TraesCS2B01G101900	Protein transport protein sec20	PF03908
TraesCS2B01G102000	BTB/POZ and MATH domain-containing protein 2	
TraesCS2B01G102100	HOPW1-1-interacting 2	
TraesCS2B01G102200	BTB/POZ/MATH-domain protein	PF00917
TraesCS2B01G102300	BTB/POZ/MATH-domain protein	
TraesCS2B01G102400	BTB/POZ/MATH-domain protein	PF00917
TraesCS2B01G102500	Importin, putative	PF03810
TraesCS2B01G102600	Divalent ion symporter	
TraesCS2B01G102700	Isoflavone reductase-like protein	PF05368
TraesCS2B01G102800	Isoflavone reductase-like protein	PF05368
TraesCS2B01G102900	Isoflavone reductase-like protein	PF05368
TraesCS2B01G103000	transmembrane protein, putative (DUF594)	PF13968
TraesCS2B01G103100	Isoflavone reductase-like protein	PF05368

TraesCS2B01G103200	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	PF04578
TraesCS2B01G103300	ATP-dependent DNA helicase PIF2	PF13968
TraesCS2B01G103400	Actin cytoskeleton-regulatory complex protein PAN1	PF13968
TraesCS2B01G103500	Isoflavone reductase-like protein	PF05368
TraesCS2B01G103600	Isoflavone reductase-like protein	PF05368
TraesCS2B01G103700	Sulfotransferase	PF00685
TraesCS2B01G103800	Isoflavone reductase-like protein	PF05368
TraesCS2B01G103900	Pyruvate decarboxylase	PF02776
TraesCS2B01G104000	Pyruvate decarboxylase	PF02776
TraesCS2B01G104100	Sulfotransferase	PF00685
TraesCS2B01G104200	Protein kinase family protein, putative, expressed	PF07714
TraesCS2B01G104300	Ubiquitin activating enzyme E1	PF00899
TraesCS2B01G104400	Serine/threonine-protein kinase	PF01453
TraesCS2B01G104500	F-box like protein	PF12937
TraesCS2B01G104600	Chromosome partition protein MukB	
TraesCS2B01G104700	Xyloglucan endotransglucosylase/hydrolase	PF00722
TraesCS2B01G104800	TPX2 (Targeting protein for Xklp2) family protein, putative	
TraesCS2B01G104900	F-box protein (DUF295)	PF03478
TraesCS2B01G105000	Eukaryotic translation initiation factor 2 subunit alpha	PF00575
TraesCS2B01G105100	Heat shock transcription factor	PF00447
TraesCS2B01G105200	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	PF13456
TraesCS2B01G105300	Abscisic acid receptor	PF10604
TraesCS2B01G105400	SNF2 domain-containing protein / helicase domain-containing protein	PF00176
TraesCS2B01G105500	Methyltransferase	PF08241
TraesCS2B01G105600	CASP-like protein	PF04535
TraesCS2B01G105700	26S protease regulatory subunit	PF00004
TraesCS2B01G105800	Receptor-like protein kinase	PF00560
TraesCS2B01G105900	Zinc-finger protein	PF13912
TraesCS2B01G106000	SCAR family protein	
TraesCS2B01G106100	Lectin receptor kinase	PF00069
TraesCS2B01G106200	Lectin receptor kinase	PF00139
TraesCS2B01G106300	Growth/differentiation factor 11	
TraesCS2B01G106400	Short-chain dehydrogenase/reductase family protein	PF13561
TraesCS2B01G106500	Short-chain dehydrogenase/reductase family protein	PF00106
TraesCS2B01G106600	Short-chain dehydrogenase/reductase family protein	PF13561
TraesCS2B01G106700	Wound-induced protein 1	PF07107
TraesCS2B01G106800	Wound-induced protein 1	PF07107
TraesCS2B01G106900	Receptor-like kinase	PF13855
TraesCS2B01G107000	F-box family protein	PF08268
TraesCS2B01G107100	Wound-induced protein 1, putative, expressed	PF07107
TraesCS2B01G107200	D-alanine--D-alanine ligase	PF01820
TraesCS2B01G107300	Ta11-like non-LTR retrotransposon	PF14111
TraesCS2B01G107400	ACT domain-containing protein	PF01842
TraesCS2B01G107500	Pectinesterase	PF04043

TraesCS2B01G107600	UBiQuitin family member	PF00240
TraesCS2B01G107700	Protein COBRA, putative	PF04833
TraesCS2B01G107800	Ubiquitin	PF00240
TraesCS2B01G107900	F-box family protein	PF00646
TraesCS2B01G108000	Membrane-bound lytic murein transglycosylase C	
TraesCS2B01G108100	F-box family protein	PF08268
TraesCS2B01G108200	Protein phosphatase 2C-like	PF00481
TraesCS2B01G108300	Pleckstrin homology domain-containing family A member 8	PF07893
TraesCS2B01G108400	F-box family protein	PF03478
TraesCS2B01G108500	F-box domain containing protein-like	PF03478
TraesCS2B01G108600	F-box domain containing protein-like	
TraesCS2B01G108700	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	
TraesCS2B01G108800	PHD and RING finger domain-containing protein 1	PF13639
TraesCS2B01G108900	DUF3511 domain protein, putative (DUF3511)	PF12023
TraesCS2B01G109000	Ribosomal protein L19	PF01280
TraesCS2B01G109100	vesicle transport V-snare 13	
TraesCS2B01G109200	Retrotransposon protein, putative, unclassified, expressed	PF13456
TraesCS2B01G109300	Alpha-soluble NSF attachment protein	PF14938
TraesCS2B01G109400	Hexosyltransferase	PF01501
TraesCS2B01G109500	DHHC-type zinc finger family protein	PF07762
TraesCS2B01G109600	GRF zinc finger family protein	
TraesCS2B01G109700	Hexosyltransferase	PF01501
TraesCS2B01G109800	Hexosyltransferase	PF01501
TraesCS2B01G109900	BRCT domain-containing protein	PF12738
TraesCS2B01G110000	Defensin	
TraesCS2B01G110100	Defensin	
TraesCS2B01G110200	GRF zinc finger family protein	
TraesCS2B01G110300	DnaJ	
TraesCS2B01G110400	cAMP-regulated phosphoprotein-like protein	PF04667
TraesCS2B01G110500	Protein kinase	PF00069
TraesCS2B01G110600	Multidrug resistance protein ABC transporter family protein, putative	PF14009
TraesCS2B01G110700	O-methyltransferase-like protein	PF08100
TraesCS2B01G110800	Lon protease homolog	PF02190
TraesCS2B01G110900	ATP-binding-cassette transporter family protein	
TraesCS2B01G111000	Dipeptidyl-peptidase, putative	PF00326
TraesCS2B01G111100	Nicotianamine synthase	PF03059
TraesCS2B01G111200	F-box protein family-like	PF03478
TraesCS2B01G111300	F-box protein family-like	PF03478
TraesCS2B01G111400	Aldehyde dehydrogenase, putative	PF00171
TraesCS2B01G111500	F-box family protein	PF00646
TraesCS2B01G111600	Disease resistance protein (NBS-LRR class) family	
TraesCS2B01G111700	Disease resistance protein (NBS-LRR class) family	
TraesCS2B01G111800	Leucine-rich repeat (LRR) family protein	PF13516
TraesCS2B01G111900	Transcription factor protein	
TraesCS2B01G112000	Poly(A) polymerase	PF04928

TraesCS2B01G112100	DELLA protein	PF03514
TraesCS2B01G112200	Beta-glucosidase, putative	PF00232
TraesCS2B01G112300	transmembrane protein	
TraesCS2B01G112400	Importin subunit alpha	PF01749
TraesCS2B01G112500	calcium-dependent protein kinase 29	
TraesCS2B01G112600	MYB transcription factor	PF00249
TraesCS2B01G112700	Pentatricopeptide repeat-containing protein, putative	PF01535
TraesCS2B01G112800	Hexosyltransferase	PF01501
TraesCS2B01G112900	F-box family protein	PF00646
TraesCS2B01G113000	BTB-POZ and MATH domain protein	
TraesCS2B01G113100	Chaperone protein ClpB	
TraesCS2B01G113200	transcription factor-like protein	PF00170
TraesCS2B01G113300	Peptidyl-prolyl cis-trans isomerase	PF13616
TraesCS2B01G113400	Gag-Pol polyprotein	
TraesCS2B01G113500	Guanine nucleotide-binding-like protein	PF08701
TraesCS2B01G113600	DNA primase	PF03121
TraesCS2B01G113700	SNF1-related protein kinase regulatory subunit beta-1	PF16561
TraesCS2B01G113800	Calmodulin	PF13499
TraesCS2B01G113900	Dihydrofolate reductase	PF03959
TraesCS2B01G114000	Non-specific serine/threonine protein kinase	PF00069
TraesCS2B01G114100	Myb/SANT-like DNA-binding domain protein	PF12776
TraesCS2B01G114200	Retrotransposon protein, putative, unclassified	PF14111
TraesCS2B01G114300	Disease resistance protein (TIR-NBS-LRR class) family	
TraesCS2B01G114400	F-box domain containing protein, expressed	PF03478
TraesCS2B01G114500	Alpha-L-arabinofuranosidase 1	PF06964
TraesCS2B01G114600	Retrotransposon protein, putative, unclassified	
TraesCS2B01G114700	2-dehydro-3-deoxyphosphooctonate aldolase	PF00793
TraesCS2B01G114800	RINT1-like protein	PF04437
TraesCS2B01G114900	Protein kinase	PF07714
TraesCS2B01G115000	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	PF03171
TraesCS2B01G115100	VQ motif-containing family protein	PF05678
TraesCS2B01G115200	VQ motif-containing family protein	PF05678
TraesCS2B01G115300	VQ motif family protein	PF05678
TraesCS2B01G115400	CAP-Gly domain-containing linker protein 1	
TraesCS2B01G115500	RING finger protein	PF13639
TraesCS2B01G115600	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	
TraesCS2B01G115700	BZIP transcription factor	PF00170
TraesCS2B01G115800	F-box family protein	PF12937
TraesCS2B01G115900	F-box domain containing protein	
TraesCS2B01G116000	F-box family protein	PF12937
TraesCS2B01G116100	Retrovirus-related Pol polyprotein from transposon TNT 1-94	
TraesCS2B01G116200	Subtilisin-like protease	PF05922
TraesCS2B01G116300	Subtilisin-like protease	PF05922
TraesCS2B01G116400	Subtilisin-like protease	PF00082
TraesCS2B01G116500	Fructose-1,6-bisphosphatase class 1	PF07893

TraesCS2B01G116600	Subtilisin-like protease	PF05922
TraesCS2B01G116700	Short chain dehydrogenase/reductase	PF00106
TraesCS2B01G116800	actin binding protein	
TraesCS2B01G116900	Ethylene insensitive 3	PF04873
TraesCS2B01G117000	Short chain dehydrogenase/reductase	PF00106
TraesCS2B01G117100	Subtilisin-like protease	PF05922
TraesCS2B01G117200	Kunitz-type trypsin inhibitor-like 2 protein	
TraesCS2B01G117300	Serine/threonine-protein kinase	PF01453
TraesCS2B01G117400	Alpha/beta-hydrolase superfamily protein	PF00561
TraesCS2B01G117500	Pectinesterase	PF01095
TraesCS2B01G117600	transmembrane protein, putative (DUF594)	PF13968
TraesCS2B01G117700	Nuclear pore complex	
TraesCS2B01G117800	Myb family transcription factor APL	PF00249
TraesCS2B01G117900	WUSCHEL-related homeobox	PF00046
TraesCS2B01G118000	Dof zinc finger protein	PF02701
TraesCS2B01G118100	Thioredoxin, putative	PF00085
TraesCS2B01G118200	NAC domain-containing protein	PF02365
TraesCS2B01G118300	NAC domain-containing protein	PF02365
TraesCS2B01G118400	NAC domain protein,	PF02365
TraesCS2B01G118500	NAC domain-containing protein	PF02365
TraesCS2B01G118600	Sentrin-specific protease	PF02902
TraesCS2B01G118700	Stress responsive protein	
TraesCS2B01G118800	Ricin B-like lectin R40G2	
TraesCS2B01G118900	Stress responsive protein	
TraesCS2B01G119000	NAC domain protein	PF02365
TraesCS2B01G119100	NAC domain protein	PF02365
TraesCS2B01G119200	Apyrase-like protein	PF01150
TraesCS2B01G119300	Pro-resilin, putative	
TraesCS2B01G119400	RNA-binding domain CCCH-type zinc finger protein	PF00642
TraesCS2B01G119500	Sorting and assembly machinery component 50 like	PF01103
TraesCS2B01G119600	Ferredoxin reductase-like protein	PF00175
TraesCS2B01G119700	Cellulose synthase	PF14569
TraesCS2B01G119800	Cysteine protease	
TraesCS2B01G119900	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	PF13456
TraesCS2B01G120000	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic	PF02902
TraesCS2B01G120100	Serpin family protein	PF00079
TraesCS2B01G120200	Hexosyltransferase	PF01501
TraesCS2B01G120300	Ribonuclease PH	PF01138
TraesCS2B01G120400	30S ribosomal protein S7, putative	PF00177
TraesCS2B01G120500	DUF4283 domain protein	PF14111
TraesCS2B01G120600	ATP-dependent RNA helicase DeaD	PF00270
TraesCS2B01G120700	Polyadenylate-binding protein 1-B-binding protein	
TraesCS2B01G120800	Mediator of RNA polymerase II transcription subunit 33A	
TraesCS2B01G120900	Calcium-binding family protein	PF13405
TraesCS2B01G121000	Cytochrome P450 family protein, expressed	PF00067

TraesCS2B01G121100	Receptor-like kinase	PF08263
TraesCS2B01G121200	Eukaryotic translation initiation factor 2 subunit beta	PF01873
TraesCS2B01G121300	filament-like protein (DUF869)	
TraesCS2B01G121400	F-box family protein	PF12937
TraesCS2B01G121500	Protein kinase	PF00069
TraesCS2B01G121600	extra-large G-like protein, putative (DUF3133)	PF11331
TraesCS2B01G121700	E3 ubiquitin-protein ligase SHPRH	PF00176
TraesCS2B01G121800	WRKY transcription factor	PF03106
TraesCS2B01G121900	WRKY transcription factor	PF03106
TraesCS2B01G122000	Mitochondrial transcription termination factor-like	PF02536
TraesCS2B01G122100	Expansin protein	PF03330
TraesCS2B01G122200	tRNA (Guanine(26)-N(2))-dimethyltransferase	PF02005
TraesCS2B01G122300	Ubiquinol-cytochrome c reductase complex 6.7 kDa protein	
TraesCS2B01G122400	Vacuolar sorting receptor family protein	PF02225
TraesCS2B01G122500	B3 domain transcription factor	PF02362
TraesCS2B01G122600	GRF zinc finger / Zinc knuckle protein	
TraesCS2B01G122700	Transcription factor	PF00170
TraesCS2B01G122800	Poly (A) RNA polymerase cid14	
TraesCS2B01G122900	Alpha-galactosidase	PF16499
TraesCS2B01G123000	transcription repressor	PF04844
TraesCS2B01G123100	Actin-related protein 2/3 complex subunit 5	PF04699
TraesCS2B01G123200	Transcription repressor ofp17	
TraesCS2B01G123300	Transposon protein, putative, Mutator sub-class	
TraesCS2B01G123400	B12D protein	PF06522
TraesCS2B01G123500	Thiamin pyrophosphokinase 1	PF04263
TraesCS2B01G123600	Sentrin-specific protease	PF02902
TraesCS2B01G123700	Potassium transporter	PF02705
TraesCS2B01G123800	Zinc finger, C2H2	
TraesCS2B01G123900	Non-specific serine/threonine protein kinase	PF00069
TraesCS2B01G124000	Non-specific serine/threonine protein kinase	PF03822
TraesCS2B01G124100	Non-specific serine/threonine protein kinase	PF00069
TraesCS2B01G124200	WEAK movement UNDER BLUE LIGHT-like protein	PF05701
TraesCS2B01G124300	Peroxidase	PF00141
TraesCS2B01G124400	Peroxidase	PF00141
TraesCS2B01G124500	Peroxidase	PF00141
TraesCS2B01G124600	Peroxidase	PF00141
TraesCS2B01G124700	Transposon protein, putative, CACTA, En/Spm sub-class, expressed	
TraesCS2B01G124800	Peroxidase	PF00141
TraesCS2B01G124900	Peroxidase	PF00141
TraesCS2B01G125000	transmembrane protein, putative (DUF594)	PF13968
TraesCS2B01G125100	Peroxidase	PF00141
TraesCS2B01G125200	Peroxidase	PF00141
TraesCS2B01G125300	Peroxidase	PF00141
TraesCS2B01G125400	Heat shock 70 kDa protein	PF00012
TraesCS2B01G125500	Peroxidase	PF00141

TraesCS2B01G125600	Peroxidase	PF00141
TraesCS2B01G125700	Peroxidase	PF00141
TraesCS2B01G125800	Peroxidase	PF00141
TraesCS2B01G125900	Peroxidase	PF00141
TraesCS2B01G126000	Peroxidase	PF00141
TraesCS2B01G126100	Peroxidase	PF00141
TraesCS2B01G126200	Peroxidase	PF00141
TraesCS2B01G126300	Peroxidase	PF00141
TraesCS2B01G126400	BHLH transcription factor	
TraesCS2B01G126500	Ribosomal protein L19	PF01280
TraesCS2B01G126600	1,4-dihydroxy-2-naphthoate polyprenyltransferase, chloroplastic	
TraesCS2B01G126700	Ring finger protein, putative	PF13639
TraesCS2B01G126800	GATA transcription factor-like protein	
TraesCS2B01G126900	Pentatricopeptide repeat-containing protein	PF13041
TraesCS2B01G127000	Germin-like protein	PF00190
TraesCS2B01G127100	Aspartic proteinase nepenthesin-1	PF14543
TraesCS2B01G127200	Translation initiation factor 1A	PF01176
TraesCS2B01G127300	NADH-quinone oxidoreductase subunit B	
TraesCS2B01G127400	Eukaryotic aspartyl protease family protein, putative	PF14543
TraesCS2B01G127500	Peroxiredoxin	PF00578
TraesCS2B01G127600	Pectinesterase	PF04043
TraesCS2B01G127700	Acyl-CoA dehydrogenase	PF01636
TraesCS2B01G127800	Ethylene-responsive transcription factor	PF00847
TraesCS2B01G127900	60S ribosomal protein L18	PF17135
TraesCS2B01G128000	F-box family protein	
TraesCS2B01G128100	Leucine-rich repeat protein kinase family protein	
TraesCS2B01G128200	F-box family protein	
TraesCS2B01G128300	Pollen Ole e 1 allergen/extensin	PF01190
TraesCS2B01G128400	ABC transporter G family member	PF00005
TraesCS2B01G128500	cell elongation protein / DWARF1 / DIMINUTO (DIM)	
TraesCS2B01G128600	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	PF13456
TraesCS2B01G128700	ABC transporter G family member	PF00005
TraesCS2B01G128800	ABC transporter G family member	PF00005
TraesCS2B01G128900	ABC-2 type transporter family protein	
TraesCS2B01G129000	Glutamate receptor 2.7	
TraesCS2B01G129100	Ras-specific guanine nucleotide-releasing factor RalGPS2	
TraesCS2B01G129200	Pentatricopeptide repeat-containing protein	PF01535
TraesCS2B01G129300	60S ribosomal protein L22, putative	PF01776
TraesCS2B01G129400	UPF0235 protein	PF02594
TraesCS2B01G129500	DNA-directed RNA polymerases I, II, and III subunit rpabc3	PF03870
TraesCS2B01G129600	UDP-glucuronate decarboxylase	PF16363
TraesCS2B01G129700	NBS-LRR disease resistance protein-like protein	PF00931
TraesCS2B01G129800	NBS-LRR disease resistance protein-like protein	PF00931
TraesCS2B01G129900	B0809H07.3 protein	PF12442
TraesCS2B01G130000	Hypoxia-responsive family protein-like	PF04588

TraesCS2B01G130100	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	
TraesCS2B01G130200	Kelch repeat-containing protein	PF01344
TraesCS2B01G130300	Ultraviolet-B-repressible protein	PF06596
TraesCS2B01G130400	splicing factor-like protein	PF00076
TraesCS2B01G130500	Universal stress protein	PF00582
TraesCS2B01G130600	F-box protein	PF00646
TraesCS2B01G130700	GPI-anchored wall transfer protein 1	PF06423
TraesCS2B01G130800	Retrotransposon protein, putative, unclassified	PF13456
TraesCS2B01G130900	Protein AIG1	PF04548
TraesCS2B01G131000	Retrotransposon protein, putative, unclassified	PF04195
TraesCS2B01G131100	Aspartic proteinase nepenthesin-1	PF14543
TraesCS2B01G131200	Universal stress protein	PF00582
TraesCS2B01G131300	Universal stress protein	PF00582
TraesCS2B01G131400	Universal stress protein	PF00582
TraesCS2B01G131500	THUMP domain-containing protein 1	PF02926
TraesCS2B01G131600	E3 ubiquitin-protein ligase	PF13445
TraesCS2B01G131700	Ubiquitin-like-specific protease ESD4	PF02902
TraesCS2B01G131800	F-actin capping protein alpha subunit	PF01267
TraesCS2B01G131900	Ribosomal protein S8e/ribosomal biogenesis NSA2	PF01201
TraesCS2B01G132000	Zinc finger CCCH domain protein, putative	
TraesCS2B01G132100	UDP-glycosyltransferase	PF00201
TraesCS2B01G132200	RNA polymerase sigma factor sigE, chloroplastic/mitochondrial	
TraesCS2B01G132300	UDP-glycosyltransferase	PF00201
TraesCS2B01G132400	UDP-glycosyltransferase	PF00201
TraesCS2B01G132500	UDP-glycosyltransferase	PF00201
TraesCS2B01G132600	UDP-glycosyltransferase	PF00201
TraesCS2B01G132700	UDP-glycosyltransferase	PF00201
TraesCS2B01G132800	LURP-one-like protein	PF04525
TraesCS2B01G132900	ATP-dependent zinc metalloprotease FtsH 1	PF00004
TraesCS2B01G133000	Divalent metal cation transporter MntH 2	PF01566
TraesCS2B01G133100	Hippocampus abundant transcript-like protein 1	
TraesCS2B01G133200	Rubber elongation factor family protein	PF05755
TraesCS2B01G133300	Protein arginine methyltransferase	PF05185
TraesCS2B01G133400	60S ribosome subunit biogenesis protein NIP7 homolog	PF03657
TraesCS2B01G133500	Photosystem I reaction center subunit N	PF05479
TraesCS2B01G133600	Flowering-promoting factor 1-like protein 1	
TraesCS2B01G133700	Flowering-promoting factor 1-like protein 1	
TraesCS2B01G133800	Uveal autoantigen with coiled-coil domains and ankyrin repeats isoform 2	
TraesCS2B01G133900	Pentatricopeptide repeat-containing protein	PF13041
TraesCS2B01G134000	Fas-binding factor 1 homolog	
TraesCS2B01G134100	Heavy metal transport/detoxification superfamily protein	PF00403
TraesCS2B01G134200	GH3 family protein	PF03321
TraesCS2B01G134300	40S ribosomal protein S21	PF01249
TraesCS2B01G134400	WD repeat domain phosphoinositide-interacting protein	PF00400
TraesCS2B01G134500	WD-repeat protein, putative	PF00400

TraesCS2B01G134600	UPF0194 membrane protein YbhG	
TraesCS2B01G134700	CsAtPR5	
TraesCS2B01G134800	rRNA N-glycosidase	
TraesCS2B01G134900	WD-repeat protein, putative	PF00400
TraesCS2B01G135000	Calcium-dependent lipid-binding (CaLB domain) family protein	PF00168
TraesCS2B01G135100	Calcium-dependent lipid-binding (CaLB domain) family protein	PF00168
TraesCS2B01G135200	Calcium-dependent lipid-binding domain-containing protein	PF00168
TraesCS2B01G135300	Peptidase B	
TraesCS2B01G135400	Aspartic proteinase nepenthesin-1	PF14543
TraesCS2B01G135500	Cation calcium exchanger	PF01699
TraesCS2B01G135600	Two-component response regulator	PF00249
TraesCS2B01G135700	Pentatricopeptide repeat-containing protein	PF01535
TraesCS2B01G135800	MORC family CW-type zinc finger protein 4	PF07496
TraesCS2B01G135900	Potassium transporter	PF02705
TraesCS2B01G136000	E3 ubiquitin-protein ligase	
TraesCS2B01G136100	Ethylene-responsive transcription factor	PF00847
TraesCS2B01G136200	Subtilisin-like protease	PF05922
TraesCS2B01G136300	Retrotransposon polyprotein	PF00098
TraesCS2B01G136400	bZIP transcription factor family protein	
TraesCS2B01G136500	Cytochrome P450 family protein, expressed	PF00067
TraesCS2B01G136600	Cytochrome P450 family protein, expressed	PF00067
TraesCS2B01G136700	AMP deaminase	PF00962
TraesCS2B01G136800	Calcium-dependent lipid-binding domain-containing protein	PF00168
TraesCS2B01G136900	Kinase family protein	
TraesCS2B01G137000	Calcium-dependent lipid-binding domain-containing protein	PF00168
TraesCS2B01G137100	GTPase obg	PF01018
TraesCS2B01G137200	Subtilisin-like protease	PF05922
TraesCS2B01G137300	Xylose isomerase	
TraesCS2B01G137400	DNA polymerase	PF03104
TraesCS2B01G137500	Ankyrin repeat protein-like	PF12796
TraesCS2B01G137600	Ankyrin repeat protein-like	PF12796
TraesCS2B01G137700	Zinc finger protein 512B family	
TraesCS2B01G137800	Kinase family protein	PF00069
TraesCS2B01G137900	Lipase	PF01764
TraesCS2B01G138000	Zinc finger CCCH domain-containing protein	
TraesCS2B01G138100	Zinc finger CCCH domain-containing protein	
TraesCS2B01G138200	Ubiquitin carboxyl-terminal hydrolase 2	PF13968
TraesCS2B01G138300	Lipid transfer protein	
TraesCS2B01G138400	Receptor kinase	PF08263
TraesCS2B01G138500	GDSL esterase/lipase	PF00657
TraesCS2B01G138600	Adenylyl cyclase	
TraesCS2B01G138700	XH/XS domain-containing family protein	PF03470
TraesCS2B01G138800	Cytochrome P450 family protein	PF00067
TraesCS2B01G138900	Protein GAMETE EXPRESSED 1	

TraesCS2B01G139000	Kinase family protein	PF00069
TraesCS2B01G139100	Nucleolar protein	PF08156
TraesCS2B01G139200	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF14223
TraesCS2B01G139300	Pectinesterase	PF01095
TraesCS2B01G139400	Pectinesterase	PF01095
TraesCS2B01G139500	Pectinesterase	PF01095
TraesCS2B01G139600	Pectinesterase	PF01095
TraesCS2B01G139700	F-box protein	PF00646
TraesCS2B01G139800	Embryogenesis transmembrane protein-like	PF13962
TraesCS2B01G139900	Pectinesterase	PF01095
TraesCS2B01G140000	Pectinesterase	PF01095
TraesCS2B01G140100	Pectinesterase	PF01095
TraesCS2B01G140200	S-adenosylmethionine-dependent methyltransferase, putative	
TraesCS2B01G140300	CONSTANS-like zinc finger protein	PF06203
TraesCS2B01G140400	Formamidopyrimidine-DNA glycosylase	
TraesCS2B01G140500	GDSL-like Lipase/Acylhydrolase superfamily protein	
TraesCS2B01G140600	tRNA-specific 2-thiouridylase MnmA	
TraesCS2B01G140700	Dynein assembly factor with WDR repeat domains 1	PF04578
TraesCS2B01G140800	transmembrane protein, putative (DUF594)	PF13968
TraesCS2B01G140900	6-methylsalicylic acid synthase	
TraesCS2B01G141000	Inner membrane ABC transporter permease protein YtfT	
TraesCS2B01G141100	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	
TraesCS2B01G141200	Mediator of DNA damage checkpoint protein 1	
TraesCS2B01G141300	ARID/bright DNA-binding domain protein	
TraesCS2B01G141400	translation initiation factor 3 subunit I	
TraesCS2B01G141500	transmembrane protein, putative (DUF247)	PF03140
TraesCS2B01G141600	Basic helix-loop-helix transcription factor	PF00010
TraesCS2B01G141700	Beta-amylase	PF01373
TraesCS2B01G141800	Tubby-like F-box protein	PF00646
TraesCS2B01G141900	Sodium/hydrogen exchanger	PF00999
TraesCS2B01G142000	Kinase interacting (KIP1-like) family protein	PF07765
TraesCS2B01G142100	F-box family protein	
TraesCS2B01G142200	F-box family protein	PF00646
TraesCS2B01G142300	Glycoprotein hormones alpha chain	
TraesCS2B01G142400	F-box family protein	PF00646
TraesCS2B01G142500	F-box family protein	
TraesCS2B01G142600	Salt-induced protein	
TraesCS2B01G142700	Retrotransposon protein, putative, unclassified	PF14111
TraesCS2B01G142800	F-box family protein	PF00646
TraesCS2B01G142900	F-box family protein	
TraesCS2B01G143000	Dynein light chain	PF01221
TraesCS2B01G143100	F-box family protein	PF13516
TraesCS2B01G143200	F-box family protein	
TraesCS2B01G143300	Lipoxygenase	
TraesCS2B01G143400	Kinase family protein	PF07714

TraesCS2B01G143500	DNA-directed RNA polymerase subunit beta'	
TraesCS2B01G143600	Short-chain dehydrogenase/reductase	PF13561
TraesCS2B01G143700	U3 small nucleolar RNA-associated protein 18-like protein	PF07893
TraesCS2B01G143800	Dirigent protein	PF03018
TraesCS2B01G143900	Short-chain dehydrogenase/reductase	PF13561
TraesCS2B01G144000	Short-chain dehydrogenase/reductase	PF13561
TraesCS2B01G144100	Membrane-associated 30 kDa, chloroplastic	PF04012
TraesCS2B01G144200	Short-chain dehydrogenase/reductase	PF13561
TraesCS2B01G144300	Endo-1,4-beta-xylanase, putative, expressed	PF02018
TraesCS2B01G144400	Tesmin/TSO1-like CXC domain-containing protein	PF03638
TraesCS2B01G144500	C6HC-type zinc finger RING/U-box protein	PF13445
TraesCS2B01G144600	Splicing factor U2AF, large subunit	
TraesCS2B01G144700	Trans-acting enoyl reductase	PF12274
TraesCS2B01G144800	Glutathione S-transferase T3	PF14303
TraesCS2B01G144900	Cellulose synthase, putative	PF14570
TraesCS2B01G145000	Short-chain dehydrogenase/reductase	PF13561
TraesCS2B01G145100	Short-chain dehydrogenase/reductase	PF13561
TraesCS2B01G145200	Short-chain dehydrogenase/reductase	PF13561
TraesCS2B01G145300	FAD-binding Berberine family protein, putative	PF01565
TraesCS2B01G145400	Collagen, type IV, alpha 5	
TraesCS2B01G145500	FAD-binding Berberine family protein, putative	PF01565
TraesCS2B01G145600	phospholipase D alpha 3	
TraesCS2B01G145700	4-alpha-glucanotransferase	PF00686
TraesCS2B01G145800	Tyrosine-specific transport protein, putative	PF03222
TraesCS2B01G145900	Pentatricopeptide repeat-containing protein	PF01535
TraesCS2B01G146000	NAD(P)H dehydrogenase (Quinone)	PF03358
TraesCS2B01G146100	AGAMOUS-like MADS-box protein	PF00319
TraesCS2B01G146200	Membrane-associated zinc metalloprotease family protein, expressed	PF02163
TraesCS2B01G146300	F-box family protein	
TraesCS2B01G146400	F-box domain containing protein	
TraesCS2B01G146500	NADH dehydrogenase subunit 9	PF00329
TraesCS2B01G146600	basic pentacysteine 7	
TraesCS2B01G146700	NADH dehydrogenase subunit 2	PF00361
TraesCS2B01G146800	Mitochondrial DNA orf152b	
TraesCS2B01G146900	pfkB-like carbohydrate kinase family protein	
TraesCS2B01G147000	F-box domain containing protein	
TraesCS2B01G147100	RNA binding	PF00076
TraesCS2B01G147200	Pre-rRNA-processing protein ESF2	PF00076
TraesCS2B01G147300	Homeodomain-like transcriptional regulator	PF02791
TraesCS2B01G147400	Phosducin, thioredoxin-like domain-containing protein	PF02114
TraesCS2B01G147500	Nucleolar pre-ribosomal-associated protein 1	PF11707
TraesCS2B01G147600	Cytochrome P450, putative, expressed	PF00067
TraesCS2B01G147700	Elongation factor 1-beta	PF00736
TraesCS2B01G147800	Pentatricopeptide repeat-containing protein	PF01535
TraesCS2B01G147900	Nucleolar family protein	PF08156
TraesCS2B01G148000	Nucleolar family protein	PF08156

TraesCS2B01G148100	Tetratricopeptide repeat (TPR)-like superfamily protein	
TraesCS2B01G148200	Metallo-beta-lactamase-like	PF13370
TraesCS2B01G148300	Calcium-binding and coiled-coil domain-containing protein 2	
TraesCS2B01G148400	Cysteine proteinase inhibitor	PF16845
TraesCS2B01G148500	Lectin receptor kinase	PF00139
TraesCS2B01G148600	WD40 repeat-like protein	PF00400
TraesCS2B01G148700	RING finger protein	PF13920
TraesCS2B01G148800	Nucleosome-remodeling factor subunit	PF02791
TraesCS2B01G148900	Early response to dehydration 15-like protein	
TraesCS2B01G149000	Ubiquitin carboxyl-terminal hydrolase	PF00443
TraesCS2B01G149100	Phospho-N-acetylmuramoyl-pentapeptide-transferase	PF00953
TraesCS2B01G149200	Cyst nematode resistance protein-like	
TraesCS2B01G149300	E3 ubiquitin-protein ligase	
TraesCS2B01G149400	DUF4283 domain protein	PF14111
TraesCS2B01G149500	Adenosine deaminase-like protein	PF00962
TraesCS2B01G149600	Receptor-kinase, putative	PF08263
TraesCS2B01G149700	Benzyl alcohol O-benzoyltransferase	PF02458
TraesCS2B01G149800	B3 domain-containing protein family	PF02362
TraesCS2B01G149900	Pleiotropic drug resistance ABC transporter	PF00005
TraesCS2B01G150000	Lectin receptor kinase	
TraesCS2B01G150100	Lectin receptor kinase	PF00139
TraesCS2B01G150200	Pseudouridine synthase family protein	PF00849
TraesCS2B01G150300	Glycosyltransferase	PF00201
TraesCS2B01G150400	Sialyltransferase-like protein 2	PF00777
TraesCS2B01G150500	Chromodomain helicase DNA-binding protein, putative	PF00385
TraesCS2B01G150600	ABC transporter, putative	PF00664
TraesCS2B01G150700	carboxyl-terminal peptidase (DUF239)	PF03080
TraesCS2B01G150800	ATP-dependent RNA helicase DDX47	PF00270
TraesCS2B01G150900	Glutaredoxin family protein, expressed	PF00462
TraesCS2B01G151000	Serine/threonine-protein kinase	PF01453
TraesCS2B01G151100	E3 ubiquitin-protein ligase	PF03145
TraesCS2B01G151200	F-box family protein	PF12937
TraesCS2B01G151300	BED zinc finger,hAT family dimerization domain	PF02892
TraesCS2B01G151400	F-box family protein	PF00646
TraesCS2B01G151500	auxin-induced in root cultures-like protein	PF04526
TraesCS2B01G151600	NBS-LRR disease resistance protein	PF00931
TraesCS2B01G151700	Leucine-rich repeat protein kinase family protein	
TraesCS2B01G151800	NAD(P)-binding Rossmann-fold superfamily protein	PF13460
TraesCS2B01G151900	Protein kinase	PF13947
TraesCS2B01G152000	Annexin	PF00191
TraesCS2B01G152100	Condensin complex subunit 1	PF12922
TraesCS2B01G152200	Retrotransposon protein, putative, Ty1-copia subclass	PF14223
TraesCS2B01G152300	Haloacid dehalogenase-like hydrolase domain-containing protein 3	PF13419
TraesCS2B01G152400	DUF4228 domain protein	PF14009
TraesCS2B01G152500	BTB/POZ domain containing protein, expressed	PF00651

TraesCS2B01G152600	Aspartic proteinase nepenthesin-1	PF14543
TraesCS2B01G152700	Phosphatidylinositol 4-phosphate 5-kinase 4	PF02493
TraesCS2B01G152800	Ankyrin repeat family protein	PF13637
TraesCS2B01G152900	Glutamate synthase, putative	PF00310
TraesCS2B01G153000	Zinc finger A20 and AN1 domain stress-associated protein	PF01754
TraesCS2B01G153100	Zinc finger A20 and AN1 domain stress-associated protein	PF01754
TraesCS2B01G153200	Zinc finger A20 and AN1 domain stress-associated protein	PF01754
TraesCS2B01G153300	Zinc finger A20 and AN1 domain-containing stress-associated protein	PF01754
TraesCS2B01G153400	Zinc finger A20 and AN1 domain stress-associated protein	PF01754
TraesCS2B01G153500	CASP-like protein	PF04535
TraesCS2B01G153600	GRF zinc finger family protein, expressed	
TraesCS2B01G153700	F-box protein	
TraesCS2B01G153800	Rho GTPase-activating protein	PF00169
TraesCS2B01G153900	NHL repeat-containing protein	
TraesCS2B01G154000	Pentatricopeptide repeat-containing protein	PF01535
TraesCS2B01G154100	Receptor-like kinase	PF08263
TraesCS2B01G154200	CsAtPR5	
TraesCS2B01G154300	CsAtPR5	
TraesCS2B01G154400	30S ribosomal protein S9	PF00380
TraesCS2B01G154500	Transmembrane protein, putative	
TraesCS2B01G154600	Phospholipase A2 family protein	
TraesCS2B01G154700	Thioredoxin reductase	PF07992
TraesCS2B01G154800	Protein FLOWERING LOCUS T	PF01161
TraesCS2B01G154900	Actin cross-linking protein, putative (DUF569)	PF04601
TraesCS2B01G155000	DNA glycosylase	PF00730
TraesCS2B01G155100	TRAF type zinc finger domain containing 1	
TraesCS2B01G155200	Unknown protein	
TraesCS2B01G155300	Glycosyltransferase	PF04577
TraesCS2B01G155400	TTF-type zinc finger protein with HAT dimerization domain-containing protein	PF05699
TraesCS2B01G155500	Transposon protein, putative, Mutator sub-class	PF03108
TraesCS2B01G155600	Werner Syndrome-like exonuclease	
TraesCS2B01G155700	ubiquitin-conjugating enzyme 33	
TraesCS2B01G155800	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-like protein	PF07893
TraesCS2B01G155900	Translation initiation factor IF-2	
TraesCS2B01G156000	PP2A regulatory subunit TAP46	PF07893
TraesCS2B01G156100	N-alpha-acetyltransferase	
TraesCS2B01G156200	SKP1-like protein 4	
TraesCS2B01G156300	BRI1 suppressor 1 (BSU1)-like 3	PF07893
TraesCS2B01G156400	transducin family protein / WD-40 repeat family protein	PF12931
TraesCS2B01G156500	BRI1 suppressor 1 (BSU1)-like 3	PF07893
TraesCS2B01G156600	Lactoylglutathione lyase	PF00903
TraesCS2B01G156700	UBX domain-containing protein	PF14555
TraesCS2B01G156800	3-oxoacyl-[acyl-carrier-protein] synthase	PF00109
TraesCS2B01G156900	3-oxoacyl-[acyl-carrier-protein] synthase	PF00109
TraesCS2B01G157000	Carboxypeptidase	PF00450

TraesCS2B01G157100	Carboxypeptidase	PF00450
TraesCS2B01G157200	Methyltransferase-like protein	PF08241
TraesCS2B01G157300	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	PF13456
TraesCS2B01G157400	F-box domain containing protein-like	
TraesCS2B01G157500	Structural constituent of ribosome, putative	PF03350
TraesCS2B01G157600	Magnesium-chelatase subunit H	PF11965
TraesCS2B01G157700	transmembrane protein, putative (DUF288)	PF03385
TraesCS2B01G157800	Beta-glucosidase	PF00232
TraesCS2B01G157900	Choline transporter-like protein	PF04515
TraesCS2B01G158000	Glycerol-3-phosphate acyltransferase 3, putative	PF01553
TraesCS2B01G158100	Cysteine-rich receptor-kinase-like protein	PF01657
TraesCS2B01G158200	Protein FAR1-RELATED SEQUENCE 3	PF04434
TraesCS2B01G158300	ATP-dependent Clp protease ATP-binding subunit	PF00004
TraesCS2B01G158400	Protein trichome birefringence	PF14416
TraesCS2B01G158500	TVP38/TMEM64 family membrane protein	PF09335
TraesCS2B01G158600	Late embryogenesis abundant protein	
TraesCS2B01G158700	Lectin receptor kinase	PF00139
TraesCS2B01G158800	Lectin receptor kinase	PF00139
TraesCS2B01G158900	GDSL esterase/lipase	
TraesCS2B01G159000	GDSL esterase/lipase	
TraesCS2B01G159100	GDSL esterase/lipase	
TraesCS2B01G159200	GDSL esterase/lipase	PF00657
TraesCS2B01G159300	Pectinesterase	PF01095
TraesCS2B01G159400	Pectinesterase	PF01095
TraesCS2B01G159500	Hepatoma-derived growth factor-related protein 2	PF00855
TraesCS2B01G159600	Transmembrane protein 115	PF08551
TraesCS2B01G159700	BTB-POZ and MATH domain protein	PF00651