**Table S9** Predicted genes in the interval of the major QTL (TableS9.1-9.3)

**Table S9.1** Predicted genes in the interval of the major QTL *QKL.sicau-2SY-1B* and *QKS.sicau-2SY-1B*

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene ID in CS** | **Annotation** | **Orthologs in Wild emmer** | **References** |
| *TraesCS1B01G349900.1* | **Glycosyltransferase** | *TRIDC1BG056750.1* | [1] |
| *TraesCS1B01G351200.1* | **VQ motif-containing protein** | *TRIDC1BG056890.1* | [2] |
| *TraesCS1B01G338700.1* | **B3 domain-containing protein family** | *TRIDC1BG054930.1* | [3] |
| *TraesCS1B01G349800.1* | **NHL domain-containing protein** | *TRIDC1BG056740.1* | [4] |
| *TraesCS1B01G345000.1* | **Carboxypeptidase** | *TRIDC1BG055900.1* | [5] |
| *TraesCS1B01G344600.1* | **F-box family protein** | *TRIDC1BG055870.1* | [6] |
| *TraesCS1B01G342700.1* | **F-box protein** | *TRIDC1BG055580.1* | [7] |
| *TraesCS1B01G345900.1* | Clavata3/ESR (CLE) gene family member | *TRIDC1BG056090.1* | [8] |
| *TraesCS1B01G347700.1* | Cytochrome P450 | *TRIDC1BG056370.1* | [9] |
| *TraesCS1B01G342500.1* | Ethylene-responsive transcription factor | *TRIDC1BG055500.1* | [10] |
| *TraesCS1B01G350800.1* | Non-symbiotic hemoglobin | *TRIDC1BG056850.1* | [11] |
| *TraesCS1B01G348200.1* | O-methyltransferase | *TRIDC1BG056420.1* | [12] |
| *TraesCS1B01G348400.1* | O-methyltransferase-like protein | *TRIDC1BG056460.1* | [12] |
| *TraesCS1B01G348700.1* | O-methyltransferase-like protein | *TRIDC1BG056540.1* | [12] |
| *TraesCS1B01G344000.1* | Phosphate transporter | *TRIDC1BG055760.1* | [13] |
| *TraesCS1B01G338900.1* | rapid alkalinization factor 23 | *TRIDC1BG054960.1* | [14] |
| *TraesCS1B01G351000.1* | RNA ligase/cyclic nucleotide phosphodiesterase family protein | *TRIDC1BG056860.1* | [15] |
| *TraesCS1B01G349600.1* | rRNA N-glycosidase | *TRIDC1BG056730.1* | [16] |
| *TraesCS1B01G351400.1* | senescence regulator (Protein of unknown function, DUF584) | *TRIDC1BG056910.1* | [17] |
| *TraesCS1B01G340600.1* | Signal recognition particle 54 kDa protein | *TRIDC1BG056380.1* | [18] |
| *TraesCS1B01G338800.1* | Thioredoxin | *TRIDC1BG054950.1* | [19] |
| *TraesCS1B01G339000.1* | Thioredoxin | *TRIDC1BG055020.1* | [19] |
| *TraesCS1B01G343700.1* | Thioredoxin | *TRIDC1BG055690.1* | [19] |
| *TraesCS1B01G350600.1* | Trehalose-6-phosphate synthase 6 | *TRIDC1BG056830.1* | [20] |
| *TraesCS1B01G347200.1* | Tubby-like F-box protein | *TRIDC1BG056320.1* | [21] |
| *TraesCS1B01G343000.1* | Tyrosine decarboxylase | *TRIDC1BG055600.1* | [22] |
| *TraesCS1B01G345200.1* | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | *TRIDC1BG055940.1* | N |
| *TraesCS1B01G339400.1* | 30S ribosomal protein S19 | *TRIDC1BG055080.1* | N |
| *TraesCS1B01G346800.1* | 50S ribosomal protein L33 | *TRIDC1BG056240.1* | N |
| *TraesCS1B01G349400.1* | Anaerobic nitric oxide reductase flavorubredoxin | *TRIDC1BG056700.1* | N |
| *TraesCS1B01G352400.1* | ATP-dependent chaperone ClpB | *TRIDC1BG057070.1* | N |
| *TraesCS1B01G346000.1* | BAG family molecular chaperone regulator 8, chloroplastic | *TRIDC1BG056100.1* | N |
| *TraesCS1B01G343500.1* | Basic-leucine zipper (BZIP) transcription factor family | *TRIDC1BG055660.1* | N |
| *TraesCS1B01G345500.1* | BSD domain containing protein | *TRIDC1BG056040.1* | N |
| *TraesCS1B01G346400.1* | Calcium-transporting ATPase | *TRIDC1BG056190.1* | N |
| *TraesCS1B01G340100.1* | Citrate-binding protein | *TRIDC1BG055200.1* | N |
| *TraesCS1B01G346600.1* | Cleavage stimulation factor subunit | *TRIDC1BG056210.1* | N |
| *TraesCS1B01G340900.1* | DUF1677 family protein | *TRIDC1BG055290.1* | N |
| *TraesCS1B01G352000.1* | DUF506 family protein | *TRIDC1BG057010.1* | N |
| *TraesCS1B01G352100.1* | DUF506 family protein | *TRIDC1BG057030.1* | N |
| *TraesCS1B01G350300.1* | Gamma-glutamyl phosphate reductase | *TRIDC1BG056790.1* | N |
| *TraesCS1B01G345800.1* | Lysine--trna ligase | *TRIDC1BG056070.1* | N |
| *TraesCS1B01G339500.1* | Photosystem II reaction center W protein | *TRIDC1BG055090.1* | N |
| *TraesCS1B01G339700.1* | Photosystem II reaction center W protein, chloroplastic | *TRIDC1BG055160.1* | N |
| *TraesCS1B01G339100.1* | p-loop containing nucleoside triphosphate hydrolases superfamily protein | *TRIDC1BG055050.1* | N |
| *TraesCS1B01G341700.1* | Poly [ADP-ribose] polymerase | *TRIDC1BG055410.1* | N |
| *TraesCS1B01G350200.1* | Ras-like protein | *TRIDC1BG056780.1* | N |
| *TraesCS1B01G352500.1* | Transcriptional regulatory plant protein, putative | *TRIDC1BG057090.1* | N |
| *TraesCS1B01G339300.1* | Ubiquitin carboxyl-terminal hydrolase 2 | *TRIDC1BG055070.1* | N |
| *TraesCS1B01G351500.1* | UPF0502 protein YceH | *TRIDC1BG056920.1* | N |
| *TraesCS1B01G350400.1* | Very long-chain-fatty-acid--CoA ligase bubblegum | *TRIDC1BG056800.1* | N |
| *TraesCS1B01G338600.1* |  | N |  |
| *TraesCS1B01G339200.1* |  | N |  |
| *TraesCS1B01G339600.1* |  | N |  |
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| *TraesCS1B01G342800.1* |  | N |  |
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| *TraesCS1B01G343200.1* |  | N |  |
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| N |  | *TRIDC1BG056810.1* |  |
| N |  | *TRIDC1BG056820.1* |  |
| N |  | *TRIDC1BG056840.1* |  |
| N |  | *TRIDC1BG056870.1* |  |
| N |  | *TRIDC1BG056880.1* |  |
| N |  | *TRIDC1BG056900.1* |  |
| N |  | *TRIDC1BG056930.1* |  |
| N |  | *TRIDC1BG056940.1* |  |
| N |  | *TRIDC1BG056950.1* |  |
| N |  | *TRIDC1BG056960.1* |  |
| N |  | *TRIDC1BG056970.1* |  |
| N |  | *TRIDC1BG056980.1* |  |
| N |  | *TRIDC1BG056990.1* |  |
| N |  | *TRIDC1BG057000.1* |  |
| N |  | *TRIDC1BG057020.1* |  |
| N |  | *TRIDC1BG057040.1* |  |
| N |  | *TRIDC1BG057050.1* |  |
| N |  | *TRIDC1BG057060.1* |  |
| N |  | *TRIDC1BG057080.1* |  |
| N |  | *TRIDC1BG057100.1* |  |
| N |  | *TRIDC1BG057110.1* |  |
| N |  | *TRIDC1BG057120.1* |  |
| N |  | *TRIDC1BG057130.1* |  |
| N |  | *TRIDC1BG057140.1* |  |
| N |  | *TRIDC1BG057150.1* |  |
| N |  | *TRIDC1BG057160.1* |  |
| N |  | *TRIDC1BG055810.1* | 　 |

Note: N represents no orthologs were identified after reciprocal blasting analysis.

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**Table S9.2** Predicted genes in the interval of the major QTL *QKW.sicau-2SY-6D*, *QLWR.sicau-2SY-6D* and *QKS.sicau-2SY-6D*

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene ID in CS** | **Annotation** | **Orthologs in Aegilops tauschii** | **References** |
| *TraesCS6D01G081900.1* | **BURP domain protein RD22** | *AET6Gv20259300.1* | [1] |
| *TraesCS6D01G082000.1* | **BURP domain protein RD22** | *AET6Gv20258800.1* | [1] |
| *TraesCS6D01G088500.1* | **cyclin-dependent kinase inhibitor** | *AET6Gv20246600.1* | [2] |
| *TraesCS6D01G088200.1* | **F-box family protein** | *AET6Gv20247500.1* | [3] |
| *TraesCS6D01G090100.1* | **F-box family protein** | *AET6Gv20266200.1* | [3] |
| *TraesCS6D01G090300.1* | **F-box family protein** | *AET6Gv20266600.1* | [3] |
| *TraesCS6D01G091400.1* | **F-box family protein** | *AET6Gv20269000.1* | [3] |
| *TraesCS6D01G093500.1* | **F-box family protein** | *AET6Gv20273300.1* | [3] |
| *TraesCS6D01G093600.1* | **F-box family protein** | *AET6Gv20274100.1* | [3] |
| *TraesCS6D01G097200.1* | **F-box family protein** | *AET6Gv20282700.1* | [3] |
| *TraesCS6D01G107300.1* | **F-box family protein** | *AET6Gv20303900.1* | [3] |
| *TraesCS6D01G080600.1* | **F-box domain containing protein** | *AET6Gv20240000.1* | [4] |
| *TraesCS6D01G080900.1* | **F-box domain containing protein** | *AET6Gv20240800.1* | [4] |
| *TraesCS6D01G091500.1* | **F-box domain containing protein** | *AET6Gv20269100.1* | [4] |
| *TraesCS6D01G092900.1* | **F-box domain containing protein** | *AET6Gv20272000.1* | [4] |
| *TraesCS6D01G093100.1* | **F-box domain containing protein** | *AET6Gv20272500.1* | [4] |
| *TraesCS6D01G102900.1* | **F-box domain containing protein** | *AET6Gv20292600.1* | [4] |
| *TraesCS6D01G103200.1* | **F-box domain containing protein** | *AET6Gv20294200.1* | [4] |
| *TraesCS6D01G090700.1* | **Glycosyltransferase** | *AET6Gv20267600.1* | [5] |
| *TraesCS6D01G094700.1* | **Glycosyltransferase** | *AET6Gv20276900.1* | [5] |
| *TraesCS6D01G105400.1* | **Glycosyltransferase** | *AET6Gv20299500.1* | [5] |
| *TraesCS6D01G104900.1* | FBD-associated F-box protein | *AET6Gv20297100.1* | [6] |
| *TraesCS6D01G107200.1* | FBD-associated F-box protein | *AET6Gv20303500.1* | [6] |
| *TraesCS6D01G100800.1* | Auxin response factor | *AET6Gv20287800.1* | [7] |
| *TraesCS6D01G102300.1* | Auxin response factor | *AET6Gv20290900.1* | [7] |
| *TraesCS6D01G088600.1* | Chlorophyll a-b binding protein, chloroplastic | *AET6Gv20246500.1* | [8] |
| *TraesCS6D01G088800.1* | Chlorophyll a-b binding protein, chloroplastic | *AET6Gv20245800.1* | [8] |
| *TraesCS6D01G095000.1* | Splicing factor 3B subunit-like protein | *AET6Gv20277400.1* | [9] |
| *TraesCS6D01G104700.1* | Splicing factor 3B subunit 1 | *AET6Gv20296700.1* | [9] |
| *TraesCS6D01G086200.1* | Sequence-specific DNA binding transcription factor | *AET6Gv20251000.1* | [10] |
| *TraesCS6D01G086500.1* | Sequence-specific DNA binding transcription factor | *AET6Gv20250300.1* | [10] |
| *TraesCS6D01G087900.1* | Sequence-specific DNA binding transcription factor | *AET6Gv20248200.1* | [10] |
| *TraesCS6D01G104400.1* | SAUR-like auxin-responsive protein family, putative | *AET6Gv20296300.1* | [11] |
| *TraesCS6D01G104500.1* | SAUR-like auxin-responsive protein family, putative | *AET6Gv20296400.1* | [11] |
| *TraesCS6D01G086300.1* | RING/U-box superfamily protein | *AET6Gv20250900.1* | [12] |
| *TraesCS6D01G087000.1* | RING/U-box superfamily protein | *AET6Gv20249200.1* | [12] |
| *TraesCS6D01G086600.1* | P-loop containing nucleoside triphosphate hydrolases superfamily protein | *AET6Gv20250000.1* | [13] |
| *TraesCS6D01G088400.1* | P-loop containing nucleoside triphosphate hydrolases superfamily protein | *AET6Gv20246700.1* | [13] |
| *TraesCS6D01G083100.1* | Pentatricopeptide repeat-containing protein | *AET6Gv20256200.1* | [14] |
| *TraesCS6D01G083400.1* | Pentatricopeptide repeat-containing protein | *AET6Gv20255400.1* | [14] |
| *TraesCS6D01G101000.1* | Mitochondrial import inner membrane translocase subunit TIM22 | *AET6Gv20288100.1* | [15] |
| *TraesCS6D01G096100.1* | Mitochondrial import inner membrane translocase subunit tim-10 isoform 1 | *AET6Gv20280800.1* | [15] |
| *TraesCS6D01G082700.1* | Lipid transfer protein | *AET6Gv20257800.1* | [16] |
| *TraesCS6D01G084600.1* | Lipid transfer protein | *AET6Gv20253700.1* | [16] |
| *TraesCS6D01G081500.1* | Leucine-rich repeat receptor-like protein kinase family protein | *AET6Gv20262600.1* | [17] |
| *TraesCS6D01G096600.1* | Leucine-rich repeat receptor-like protein kinase family protein | *AET6Gv20281900.1* | [17] |
| *TraesCS6D01G106800.1* | Histone H2A | *AET6Gv20302800.1* | [18] |
| *TraesCS6D01G107000.1* | Histone H2A | *AET6Gv20303400.1* | [18] |
| *TraesCS6D01G098400.1* | Glucan endo-1,3-beta-glucosidase-like protein | *AET6Gv20284600.1* | [19] |
| *TraesCS6D01G099100.1* | Glucan endo-1,3-beta-glucosidase 3 | *AET6Gv20285400.1* | [19] |
| *TraesCS6D01G085800.1* | F-box/LRR-repeat protein | *AET6Gv20252000.1* | [20] |
| *TraesCS6D01G087800.1* | F-box/LRR-repeat protein | *AET6Gv20248300.1* | [20] |
| *TraesCS6D01G084200.1* | Ethylene-responsive transcription factor | *AET6Gv20254600.1* | [21] |
| *TraesCS6D01G084900.1* | Ethylene-responsive transcription factor | *AET6Gv20253100.1* | [21] |
| *TraesCS6D01G085000.1* | Ethylene-responsive transcription factor | *AET6Gv20252800.1* | [21] |
| *TraesCS6D01G092800.1* | Disease resistance protein (NBS-LRR class) family | *AET6Gv20271800.1* | [22] |
| *TraesCS6D01G105100.1* | Disease resistance protein (NBS-LRR class) family | *AET6Gv20297700.1* | [22] |
| *TraesCS6D01G085100.1* | Cytochrome P450 family protein, expressed | *AET6Gv20252600.1* | [23] |
| *TraesCS6D01G103300.1* | Cytochrome P450 family protein, expressed | *AET6Gv20294400.1* | [23] |
| *TraesCS6D01G098600.1* | Terpene cyclase/mutase family member | *AET6Gv20284800.1* | [24] |
| *TraesCS6D01G100000.1* | Terpene cyclase/mutase family member | *AET6Gv20286800.1* | [24] |
| *TraesCS6D01G106100.1* | Harpin-induced protein | *AET6Gv20301600.1* | [25] |
| *TraesCS6D01G106200.1* | Harpin-induced protein | *AET6Gv20301700.1* | [25] |
| *TraesCS6D01G080300.1* | Late embryogenesis abundant protein | *AET6Gv20239000.1* | [26] |
| *TraesCS6D01G082600.1* | Zinc transporter, putative | *AET6Gv20257900.1* | [27] |
| *TraesCS6D01G103100.1* | Zinc finger protein VAR3, chloroplastic | *AET6Gv20292700.1* | [28] |
| *TraesCS6D01G108000.1* | Zinc finger protein CONSTANS-LIKE 2 | *AET6Gv20305800.1* | [29] |
| *TraesCS6D01G103600.1* | Zinc finger BED domain-containing protein DAYSLEEPER | *AET6Gv20294800.1* | [30] |
| *TraesCS6D01G080400.1* | UBX domain-containing protein 1 | *AET6Gv20239100.1* | [31] |
| *TraesCS6D01G104300.1* | U3 small nucleolar RNA-associated protein 18-like protein | *AET6Gv20295600.1* | [32] |
| *TraesCS6D01G092700.1* | transmembrane protein, putative (DUF1218) | *AET6Gv20271600.1* | [33] |
| *TraesCS6D01G084700.1* | Transmembrane protein 53 | *AET6Gv20253300.1* | [34] |
| *TraesCS6D01G105900.1* | transmembrane protein | *AET6Gv20301300.1* | [35] |
| *TraesCS6D01G093700.1* | Transducin family protein / WD-40 repeat family protein | *AET6Gv20274200.1* | [36] |
| *TraesCS6D01G097100.1* | Transcription factor GTE8 | *AET6Gv20282400.1* | [37] |
| *TraesCS6D01G083200.1* | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial | *AET6Gv20255600.1* | [38] |
| *TraesCS6D01G101200.1* | Subtilisin-like protease | *AET6Gv20288200.1* | [39] |
| *TraesCS6D01G098500.1* | Squamosa promoter-binding-like protein | *AET6Gv20284700.1* | [40] |
| *TraesCS6D01G086400.1* | Spindle pole body component SPC42 | *AET6Gv20250600.1* | [41] |
| *TraesCS6D01G088300.1* | Sphingoid base hydroxylase 2 | *AET6Gv20246900.1* | [42] |
| *TraesCS6D01G108200.1* | Sn1-specific diacylglycerol lipase alpha | *AET6Gv20306300.1* | [43] |
| *TraesCS6D01G089600.1* | Signal recognition particle protein | *AET6Gv20265000.1* | [44] |
| *TraesCS6D01G103700.1* | Serine/threonine-protein kinase TAO1 | *AET6Gv20294900.1* | [45] |
| *TraesCS6D01G081100.1* | Serine/threonine-protein kinase ATM | *AET6Gv20241400.1* | [46] |
| *TraesCS6D01G085200.1* | Sec14p-like phosphatidylinositol transfer family protein | *AET6Gv20252400.1* | [47] |
| *TraesCS6D01G086800.1* | RNA binding protein, putative | *AET6Gv20249500.1* | [48] |
| *TraesCS6D01G096800.1* | RNA binding protein | *AET6Gv20282000.1* | [49] |
| *TraesCS6D01G095500.1* | Ribosomal RNA small subunit methyltransferase H | *AET6Gv20278100.1* | [50] |
| *TraesCS6D01G101400.1* | Ribosomal RNA apurinic site specific lyase | *AET6Gv20288500.1* | [51] |
| *TraesCS6D01G092500.1* | Ribosomal protein S4 | *AET6Gv20271200.1* | [52] |
| *TraesCS6D01G096200.1* | Rhamnogalacturonate lyase | *AET6Gv20281100.1* | [53] |
| *TraesCS6D01G085400.1* | Protoheme IX farnesyltransferase | *AET6Gv20252100.1* | [54] |
| *TraesCS6D01G105700.1* | Protein STIP1-like protein | *AET6Gv20301000.1* | N |
| *TraesCS6D01G099700.1* | Protein phosphatase 2c, putative | *AET6Gv20286200.1* | [55] |
| *TraesCS6D01G097500.1* | Protein arginine N-methyltransferase | *AET6Gv20283300.1* | [56] |
| *TraesCS6D01G102200.1* | Protein AIG2 | *AET6Gv20290800.1* | [57] |
| *TraesCS6D01G084800.1* | Proteasome subunit alpha type | *AET6Gv20253200.1* | [58] |
| *TraesCS6D01G092200.1* | Proline-rich protein | *AET6Gv20270900.1* | [59] |
| *TraesCS6D01G105800.1* | Polynucleotide 5'-hydroxyl-kinase NOL9 | *AET6Gv20301200.1* | [60] |
| *TraesCS6D01G094800.1* | Pleiotropic drug resistance ABC transporter | *AET6Gv20277300.1* | [61] |
| *TraesCS6D01G091000.1* | Plant regulator RWP-RK family protein | *AET6Gv20268100.1* | [62] |
| *TraesCS6D01G093800.1* | Plant protein 1589 of unknown function | *AET6Gv20274400.1* | N |
| *TraesCS6D01G095600.1* | Photosystem I assembly protein Ycf3 | *AET6Gv20279400.1* | [63] |
| *TraesCS6D01G084500.1* | Phosphopantetheine adenylyltransferase | *AET6Gv20254200.1* | [64] |
| *TraesCS6D01G108400.1* | Peroxidase | *AET6Gv20306700.1* | [65] |
| *TraesCS6D01G087600.1* | Pentatricopeptide repeat-containing protein | *AET6Gv20248600.1* | [66] |
| *TraesCS6D01G104100.1* | ORMDL family protein-like | *AET6Gv20295300.1* | [67] |
| *TraesCS6D01G089800.1* | Oligopeptide transporter | *AET6Gv20265800.1* | [68] |
| *TraesCS6D01G081400.1* | Nucleotide-sugar transporter family protein | *AET6Gv20241600.1* | [69] |
| *TraesCS6D01G102600.1* | Nuclear pore complex protein Nup160 | *AET6Gv20291700.1* | [70] |
| *TraesCS6D01G089100.1* | Nucellin-like aspartic protease | *AET6Gv20244800.1* | [71] |
| *TraesCS6D01G094600.1* | Nodulin-like / Major Facilitator Superfamily protein | *AET6Gv20276600.1* | [72] |
| *TraesCS6D01G100300.1* | NBS-LRR-like resistance protein | *AET6Gv20287100.1* | [73] |
| *TraesCS6D01G084400.1* | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase | *AET6Gv20254300.1* | [74] |
| *TraesCS6D01G096300.1* | NAC domain-containing protein, putative | *AET6Gv20281500.1* | [75] |
| *TraesCS6D01G098200.1* | Myb family transcription factor-like | *AET6Gv20284300.1* | [76] |
| *TraesCS6D01G108100.1* | Mitogen-activated protein kinase | *AET6Gv20306100.1* | [77] |
| *TraesCS6D01G081200.1* | MALE GAMETOPHYTE DEFECTIVE 1 | *AET6Gv20241500.1* | [78] |
| *TraesCS6D01G097900.1* | low-molecular-weight cysteine-rich 48 | *AET6Gv20283700.1* | [79] |
| *TraesCS6D01G096000.1* | Leucine-rich repeat protein kinase family protein | *AET6Gv20279900.1* | [80] |
| *TraesCS6D01G083900.1* | Kinetochore protein nuf2, putative | *AET6Gv20254800.1* | [81] |
| *TraesCS6D01G091600.1* | Kinesin-like protein | *AET6Gv20269300.1* | [82] |
| *TraesCS6D01G082800.1* | Histone H3 | *AET6Gv20257700.1* | [83] |
| *TraesCS6D01G095400.1* | Histone acetyltransferase | *AET6Gv20278000.1* | [84] |
| *TraesCS6D01G083800.1* | Heat shock transcription factor | *AET6Gv20255000.1* | [85] |
| *TraesCS6D01G095700.1* | guanine nucleotide-binding protein subunit gamma | *AET6Gv20279500.1* | [86] |
| *TraesCS6D01G089700.1* | GRF zinc finger family protein, expressed | *AET6Gv20270800.1* | [87] |
| *TraesCS6D01G091800.1* | Glycine rich protein | *AET6Gv20269600.1* | [88] |
| *TraesCS6D01G090500.1* | Geranylgeranyl pyrophosphate synthase | *AET6Gv20266800.1* | [89] |
| *TraesCS6D01G093000.1* | GDSL esterase/lipase | *AET6Gv20272100.1* | [90] |
| *TraesCS6D01G100700.1* | Gamma-tubulin complex component | *AET6Gv20287500.1* | [91] |
| *TraesCS6D01G102400.1* | Galactokinase | *AET6Gv20291200.1* | [92] |
| *TraesCS6D01G099200.1* | F-box plant-like protein, putative | *AET6Gv20285600.1* | [93] |
| *TraesCS6D01G100200.1* | Fatty acid desaturase 4, chloroplastic | *AET6Gv20287000.1* | [94] |
| *TraesCS6D01G103500.1* | Fasciclin-like arabinogalactan protein | *AET6Gv20294700.1* | [95] |
| *TraesCS6D01G102100.1* | Eukaryotic translation initiation factor | *AET6Gv20290500.1* | [96] |
| *TraesCS6D01G082300.1* | Esterase/lipase/thioesterase-like protein | *AET6Gv20258200.1* | [97] |
| *TraesCS6D01G089000.1* | Endoglucanase 11 | *AET6Gv20245000.1* | [98] |
| *TraesCS6D01G089200.1* | Endoglucanase | *AET6Gv20244600.1* | [99] |
| *TraesCS6D01G108300.1* | E3 ubiquitin-protein ligase SINA-like 10 | *AET6Gv20306400.1* | [100] |
| *TraesCS6D01G087300.1* | E3 ubiquitin-protein ligase MARCH8 | *AET6Gv20248900.1* | [101] |
| *TraesCS6D01G083500.1* | DUF1645 family protein | *AET6Gv20255300.1* | [102] |
| *TraesCS6D01G103900.1* | DTW domain containing protein, expressed | *AET6Gv20295100.1* | N |
| *TraesCS6D01G104800.1* | Dolichol kinase | *AET6Gv20296900.1* | [103] |
| *TraesCS6D01G106700.1* | DNA-binding protein BIN4 | *AET6Gv20302700.1* | [104] |
| *TraesCS6D01G107900.1* | DNA/RNA helicase protein | *AET6Gv20305100.1* | [105] |
| *TraesCS6D01G107800.1* | DNA repair helicase ERCC6-like | *AET6Gv20304400.1* | [106] |
| *TraesCS6D01G089900.1* | DNA polymerase V | *AET6Gv20265900.1* | [107] |
| *TraesCS6D01G106000.1* | DNA mismatch repair protein MutS | *AET6Gv20301400.1* | [108] |
| *TraesCS6D01G106600.1* | disease resistance protein (TIR-NBS-LRR class) | *AET6Gv20302200.1* | [109] |
| *TraesCS6D01G081600.1* | Disease resistance family protein | *AET6Gv20260900.1* | [110] |
| *TraesCS6D01G098000.1* | Dirigent protein | *AET6Gv20284000.1* | [111] |
| *TraesCS6D01G095800.1* | Delta-aminolevulinic acid dehydratase | *AET6Gv20279600.1* | [112] |
| *TraesCS6D01G094000.1* | cytomegalovirus UL139 protein | *AET6Gv20275200.1* | [113] |
| *TraesCS6D01G080800.1* | Cytochrome P450 family protein | *AET6Gv20240500.1* | [114] |
| *TraesCS6D01G090800.1* | CTC-interacting domain 7 | *AET6Gv20267800.1* | [115] |
| *TraesCS6D01G101300.1* | Cortactin-binding protein 2 | *AET6Gv20288400.1* | [116] |
| *TraesCS6D01G102700.1* | Chorismate synthase | *AET6Gv20291900.1* | [117] |
| *TraesCS6D01G084300.1* | Chloride channel protein | *AET6Gv20254500.1* | [118] |
| *TraesCS6D01G106500.1* | Chitinase-like protein 2 | *AET6Gv20302300.1* | [119] |
| *TraesCS6D01G094300.1* | Cellulose synthase-like protein | *AET6Gv20276100.1* | [120] |
| *TraesCS6D01G088000.1* | Cation-transporting ATPase 4 | *AET6Gv20247700.1* | [121] |
| *TraesCS6D01G083000.1* | CASP-like protein | *AET6Gv20256600.1* | [122] |
| *TraesCS6D01G090200.1* | Calreticulin/calnexin | *AET6Gv20266400.1* | [123] |
| *TraesCS6D01G080500.1* | Calmodulin-binding protein-like | *AET6Gv20239300.1* | [124] |
| *TraesCS6D01G093400.1* | Calmodulin-binding family protein, putative, expressed | *AET6Gv20273500.1* | [125] |
| *TraesCS6D01G104000.1* | Calcium-dependent lipid-binding domain protein | *AET6Gv20295200.1* | [126] |
| *TraesCS6D01G102500.1* | CAAX amino terminal protease | *AET6Gv20291600.1* | [127] |
| *TraesCS6D01G087400.1* | BZIP transcription factor | *AET6Gv20248700.1* | [128] |
| *TraesCS6D01G094100.1* | BTB/POZ domain containing protein, expressed | *AET6Gv20275300.1* | [129] |
| *TraesCS6D01G087200.1* | BRCT domain-containing protein | *AET6Gv20249000.1* | [130] |
| *TraesCS6D01G102000.1* | B3 domain-containing protein | *AET6Gv20290200.1* | [131] |
| *TraesCS6D01G103400.1* | ATP-dependent RNA helicase DDX47 | *AET6Gv20294600.1* | [132] |
| *TraesCS6D01G105000.1* | ATP-dependent RNA helicase | *AET6Gv20297200.1* | [133] |
| *TraesCS6D01G090000.1* | AT5G11810-like protein | *AET6Gv20266100.1* |  |
| *TraesCS6D01G091100.1* | Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B | *AET6Gv20268200.1* | [134] |
| *TraesCS6D01G101600.1* | AP-1 complex subunit sigma-like protein | *AET6Gv20289600.1* | [135] |
| *TraesCS6D01G089300.1* | Anthranilate phosphoribosyltransferase | *AET6Gv20244500.1* | [136] |
| *TraesCS6D01G094500.1* | Alpha-amylase/subtilisin inhibitor | *AET6Gv20276400.1* | [137] |
| *TraesCS6D01G082500.1* | Adenylate cyclase | *AET6Gv20258000.1* | [138] |
| *TraesCS6D01G090900.1* | 5'-AMP-activated protein kinase subunit beta-1 | *AET6Gv20268000.1* | [139] |
| *TraesCS6D01G094200.1* | 50S ribosomal protein L3 | *AET6Gv20275400.1* | [140] |
| *TraesCS6D01G086900.1* | 3-isopropylmalate dehydratase large subunit | *AET6Gv20249400.1* | [141] |
| *TraesCS6D01G107100.1* | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | *AET6Gv20303700.1* | [142] |
| *TraesCS6D01G105500.1* | 26S proteasome non-ATPase regulatory subunit-like protein | *AET6Gv20299700.1* | [143] |
| *TraesCS6D01G080700.1* |  | N |  |
| *TraesCS6D01G081000.1* |  | N |  |
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| N |  | *AET6Gv20307000.1* |  |
| N | 　 | *AET6Gv20307100.1* |  |

Note: N represents no orthologs were identified after reciprocal blasting analysis.

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**Table S9.3** Predicted genes in the interval of the major QTL *QKT.sicau-2SY-2D*, *QTKW.sicau-2SY-2D*, *QKS.sicau-2SY-2D* and *QFFD.sicau-2SY-2D*

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene ID in CS** | **Annotation** | **Orthologs in Aegilops tauschii** | **References** |
| *TraesCS2D01G391600.1* | **Expansin** | *AET2Gv20878000.1* | [1] |
| *TraesCS2D01G385000.1* | **Kinesin-like protein** | *AET2Gv20863300.1* | [2] |
| *TraesCS2D01G388300.1* | **F-box family protein** | *AET2Gv20866700.1* | [3] |
| *TraesCS2D01G378100.1* | Kinase family protein | *AET2Gv20852100.1* | [4] |
| *TraesCS2D01G386900.1* | Kinase family protein | *AET2Gv20870900.1* | [4] |
| *TraesCS2D01G388000.1* | Kinase family protein | *AET2Gv20867500.1* | [4] |
| *TraesCS2D01G389200.1* | Kinase family protein | *AET2Gv20873800.1* | [4] |
| *TraesCS2D01G391000.1* | Kinase family protein | *AET2Gv20877000.1* | [4] |
| *TraesCS2D01G396100.1* | Xyloglucan galactosyltransferase KATAMARI1-like protein | *AET2Gv20886900.1* | [5] |
| *TraesCS2D01G396200.1* | Xyloglucan galactosyltransferase KATAMARI1-like protein | *AET2Gv20887000.1* | [5] |
| *TraesCS2D01G377800.1* | SAUR-like auxin-responsive family protein | *AET2Gv20851400.1* | [6] |
| *TraesCS2D01G383200.1* | SAUR-like auxin-responsive family protein | *AET2Gv20860700.1* | [6] |
| *TraesCS2D01G385600.1* | Required to maintain repression 2 | *AET2Gv20864200.1* | [8] |
| *TraesCS2D01G385800.1* | Required to maintain repression 2 | *AET2Gv20864500.1* | [8] |
| *TraesCS2D01G385900.1* | Required to maintain repression 2 | *AET2Gv20865100.1* | [8] |
| *TraesCS2D01G377900.1* | Protein kinase family protein | *AET2Gv20851600.1* | [9] |
| *TraesCS2D01G378000.1* | Protein kinase family protein | *AET2Gv20851900.1* | [9] |
| *TraesCS2D01G389900.1* | Pentatricopeptide repeat-containing protein | *AET2Gv20874700.1* | [10] |
| *TraesCS2D01G391800.1* | Pentatricopeptide repeat-containing protein | *AET2Gv20878800.1* | [10] |
| *TraesCS2D01G388900.1* | Histone H1 | *AET2Gv20873000.1* | [11] |
| *TraesCS2D01G395200.1* | Histone H1 | *AET2Gv20886200.1* | [11] |
| *TraesCS2D01G397000.1* | Dehydration-responsive element binding factor | *AET2Gv20888800.1* | [12] |
| *TraesCS2D01G397100.1* | Dehydration-responsive element binding factor | *AET2Gv20889100.1* | [12] |
| *TraesCS2D01G392800.1* | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | *AET2Gv20881200.1* | [13] |
| *TraesCS2D01G392900.1* | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | *AET2Gv20881400.1* | [13] |
| *TraesCS2D01G377200.1* | Phenylalanine ammonia-lyase | *AET2Gv20850300.1* | [14] |
| *TraesCS2D01G377300.1* | Protein FAR1-RELATED SEQUENCE 3 | *AET2Gv20850700.1* | [15] |
| *TraesCS2D01G386300.1* | Zinc finger, B-box | *AET2Gv20866200.1* | [16] |
| *TraesCS2D01G382700.1* | YABBY protein | *AET2Gv20860100.1* | [17] |
| *TraesCS2D01G390200.1* | WRKY transcription factor | *AET2Gv20875200.1* | [18] |
| *TraesCS2D01G383400.1* | Vacuolar-processing enzyme | *AET2Gv20861200.1* | [19] |
| *TraesCS2D01G396900.1* | Vacuolar protein sorting-associated protein 53 A | *AET2Gv20888700.1* | [20] |
| *TraesCS2D01G383900.1* | Vacuolar iron transporter | *AET2Gv20861700.1* | [21] |
| *TraesCS2D01G387400.1* | Ubiquitin-specific protease family C19-related protein | *AET2Gv20868400.1* | [22] |
| *TraesCS2D01G394900.1* | Ubiquitin fusion degradation 1 protein | *AET2Gv20885800.1* | [23] |
| *TraesCS2D01G387100.1* | Trihelix transcription factor GT-2 | *AET2Gv20869300.1* | [24] |
| *TraesCS2D01G388500.1* | Trihelix transcription factor | *AET2Gv20872600.1* | [24] |
| *TraesCS2D01G382200.1* | Transporter | *AET2Gv20859000.1* | [25] |
| *TraesCS2D01G394300.1* | Transmembrane protein 14C | *AET2Gv20884700.1* | [26] |
| *TraesCS2D01G390300.1* | transcription repressor | *AET2Gv20875900.1* | [27] |
| *TraesCS2D01G394500.1* | TatD family | *AET2Gv20885100.1* | [28] |
| *TraesCS2D01G396500.1* | Superoxide dismutase [Cu-Zn] | *AET2Gv20888100.1* | [29] |
| *TraesCS2D01G396400.1* | Subtilisin-like protease | *AET2Gv20888000.1* | [30] |
| *TraesCS2D01G395700.1* | S-type anion channel | *AET2Gv20886500.1* | [31] |
| *TraesCS2D01G396700.1* | SPX domain-containing family protein | *AET2Gv20888400.1* | [32] |
| *TraesCS2D01G387200.1* | Sphingoid long-chain bases kinase 1 | *AET2Gv20868800.1* | [33] |
| *TraesCS2D01G379200.1* | Sister chromatid cohesion protein PDS5-like protein B | *AET2Gv20853400.1* | N |
| *TraesCS2D01G386200.1* | SH3 domain-containing protein 2 | *AET2Gv20866000.1* | [34] |
| *TraesCS2D01G387500.1* | senescence regulator (Protein of unknown function, DUF584) | *AET2Gv20868000.1* | [35] |
| *TraesCS2D01G397900.1* | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | *AET2Gv20891100.1* | [36] |
| *TraesCS2D01G388400.1* | RNA binding protein, putative | *AET2Gv20872400.1* | [37] |
| *TraesCS2D01G392600.1* | RING/U-box superfamily protein, putative | *AET2Gv20880900.1* | [38] |
| *TraesCS2D01G397200.1* | Ring finger protein, putative | *AET2Gv20889200.1* | [39] |
| *TraesCS2D01G393400.1* | RING finger family protein | *AET2Gv20882700.1* | [40] |
| *TraesCS2D01G394800.1* | Rho GTPase-activating protein | *AET2Gv20885400.1* | [41] |
| *TraesCS2D01G390600.1* | responsive to abscisic acid 28 | *AET2Gv20876400.1* | [42] |
| *TraesCS2D01G378700.1* | Protodermal factor 1 | *AET2Gv20852800.1* | [43] |
| *TraesCS2D01G394000.1* | Protein SPIRAL1 | *AET2Gv20883300.1* | [44] |
| *TraesCS2D01G378300.1* | Protein root UVB sensitive 2, chloroplastic | *AET2Gv20852300.1* | [45] |
| *TraesCS2D01G390900.1* | Protein ROOT PRIMORDIUM DEFECTIVE 1 | *AET2Gv20876900.1* | [46] |
| *TraesCS2D01G397500.1* | Protein DETOXIFICATION | *AET2Gv20890600.1* | [47] |
| *TraesCS2D01G386400.1* | Protein COBRA | *AET2Gv20866400.1* | [48] |
| *TraesCS2D01G381600.1* | Protein BREAST CANCER SUSCEPTIBILITY 1-like protein | *AET2Gv20857900.1* | [49] |
| *TraesCS2D01G392100.1* | p-loop containing nucleoside triphosphate hydrolases superfamily protein, putative | *AET2Gv20879100.1* | [50] |
| *TraesCS2D01G391900.1* | p-loop containing nucleoside triphosphate hydrolases superfamily protein | *AET2Gv20879000.1* | [50] |
| *TraesCS2D01G394600.1* | pleckstrin homology (PH) domain-containing protein | *AET2Gv20885200.1* | [51] |
| *TraesCS2D01G380900.1* | plastid transcriptionally active 5 | *AET2Gv20856400.1* | [52] |
| *TraesCS2D01G384800.1* | Phosphoglucosamine mutase | *AET2Gv20863200.1* | N |
| *TraesCS2D01G380300.1* | Phosducin-like protein | *AET2Gv20855200.1* | N |
| *TraesCS2D01G377400.1* | Phenylalanine ammonia-lyase | *AET2Gv20850500.1* | [53] |
| *TraesCS2D01G396800.1* | Peptidoglycan-binding LysM domain-containing protein | *AET2Gv20888600.1* | [54] |
| *TraesCS2D01G382900.1* | Pathogenesis-related protein 1 | *AET2Gv20860300.1* | [55] |
| *TraesCS2D01G396600.1* | Oxygen-dependent choline dehydrogenase | *AET2Gv20888300.1* | [56] |
| *TraesCS2D01G391700.1* | Oxidative stress 3, putative isoform 2 | *AET2Gv20878300.1* | [57] |
| *TraesCS2D01G394100.1* | Nuclear transport factor 2 (NTF2) family protein | *AET2Gv20884400.1* | [58] |
| *TraesCS2D01G395000.1* | Non-specific serine/threonine protein kinase | *AET2Gv20886000.1* | [59] |
| *TraesCS2D01G385300.1* | NAD(P)H-quinone oxidoreductase subunit M | *AET2Gv20863700.1* | [60] |
| *TraesCS2D01G382800.1* | NAC domain protein, | *AET2Gv20860200.1* | [61] |
| *TraesCS2D01G378800.1* | NAC domain protein | *AET2Gv20853000.1* | [61] |
| *TraesCS2D01G386800.1* | Multiprotein-bridging factor, putative | *AET2Gv20871000.1* | [62] |
| *TraesCS2D01G378600.1* | Mitochondrial import receptor subunit TOM22 | *AET2Gv20852700.1* | [63] |
| *TraesCS2D01G385200.1* | Metallothiol transferase fosB | *AET2Gv20863600.1* | N |
| *TraesCS2D01G383700.1* | Light-independent protochlorophyllide reductase iron-sulfur ATP-binding protein | *AET2Gv20861500.1* | [64] |
| *TraesCS2D01G378900.1* | LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) | *AET2Gv20853200.1* | [65] |
| *TraesCS2D01G379000.1* | L-allo-threonine aldolase | *AET2Gv20853300.1* | [66] |
| *TraesCS2D01G384400.1* | Hydroxyproline-rich glycoprotein family protein | *AET2Gv20862400.1* | [67] |
| *TraesCS2D01G390800.1* | HXXXD-type acyl-transferase family protein, putative | *AET2Gv20876800.1* | [68] |
| *TraesCS2D01G383600.1* | Hsp70-Hsp90 organizing protein 1 | *AET2Gv20861400.1* | [69] |
| *TraesCS2D01G387300.1* | Homeobox protein, putative | *AET2Gv20868600.1* | [70] |
| *TraesCS2D01G385500.1* | Homeobox leucine zipper protein | *AET2Gv20863900.1* | [71] |
| *TraesCS2D01G389100.1* | Histone-lysine N-methyltransferase, H3 lysine-9 specific | *AET2Gv20873200.1* | [72] |
| *TraesCS2D01G391500.1* | Histone H4 | *AET2Gv20877900.1* | [73] |
| *TraesCS2D01G382500.1* | Histidine triad nucleotide binding protein | *AET2Gv20859700.1* | [74] |
| *TraesCS2D01G378200.1* | Hexosyltransferase | *AET2Gv20852200.1* | N |
| *TraesCS2D01G392200.1* | Heavy metal transport/detoxification superfamily protein | *AET2Gv20879800.1* | [75] |
| *TraesCS2D01G389700.1* | HAUS augmin-like complex subunit 6 | *AET2Gv20874200.1* | N |
| *TraesCS2D01G395900.1* | Growth-regulating factor | *AET2Gv20886700.1* | [76] |
| *TraesCS2D01G393200.1* | GRAS transcription factor | *AET2Gv20882500.1* | [77] |
| *TraesCS2D01G388800.1* | Glutamate dehydrogenase | *AET2Gv20872900.1* | [78] |
| *TraesCS2D01G377700.1* | Glucuronoxylan 4-O-methyltransferase | *AET2Gv20851000.1* | N |
| *TraesCS2D01G390000.1* | GATA transcription factor, putative | *AET2Gv20874800.1* | [79] |
| *TraesCS2D01G386100.1* | GATA transcription factor | *AET2Gv20865800.1* | [79] |
| *TraesCS2D01G386600.1* | Formin-like protein | *AET2Gv20871600.1* | [80] |
| *TraesCS2D01G393700.1* | Ferric reduction oxidase 2 | *AET2Gv20883700.1* | [81] |
| *TraesCS2D01G397700.1* | F-box protein PP2-A13 | *AET2Gv20890900.1* | [82] |
| *TraesCS2D01G381800.1* | Fatty acid hydroxylase superfamily protein | *AET2Gv20858100.1* | [83] |
| *TraesCS2D01G396000.1* | Fasciclin-like arabinogalactan protein | *AET2Gv20886800.1* | [84] |
| *TraesCS2D01G388100.1* | Eukaryotic translation initiation factor 4G | *AET2Gv20867400.1* | [85] |
| *TraesCS2D01G391400.1* | Ethylene-responsive transcription factor | *AET2Gv20877800.1* | [86] |
| *TraesCS2D01G381400.1* | Enolase | *AET2Gv20857400.1* | [87] |
| *TraesCS2D01G381500.1* | Embryo sac development arrest 6, putative | *AET2Gv20857700.1* | [88] |
| *TraesCS2D01G383800.1* | Elongation factor G | *AET2Gv20861600.1* | [89] |
| *TraesCS2D01G390400.1* | ELMO domain-containing protein, putative | *AET2Gv20876000.1* | [90] |
| *TraesCS2D01G390500.1* | ELMO domain-containing protein A | *AET2Gv20876200.1* | [90] |
| *TraesCS2D01G393000.1* | DUF1191 superfamily protein | *AET2Gv20882000.1* | [91] |
| *TraesCS2D01G380400.1* | Disease resistance protein (NBS-LRR class) family | *AET2Gv20856000.1* | [92] |
| *TraesCS2D01G380200.1* | Dihydroxy-acid dehydratase | *AET2Gv20855700.1* | N |
| *TraesCS2D01G379600.1* | dCTP pyrophosphatase 1 | *AET2Gv20854100.1* | [93] |
| *TraesCS2D01G386000.1* | Cytochrome P450 family protein | *AET2Gv20865200.1* | [94] |
| *TraesCS2D01G391200.1* | Cysteine-rich receptor-kinase-like protein | *AET2Gv20877200.1* | [95] |
| *TraesCS2D01G384500.1* | Cysteine desulfurase | *AET2Gv20862700.1* | [96] |
| *TraesCS2D01G389800.1* | Cyclin-like | *AET2Gv20874400.1* | [97] |
| *TraesCS2D01G380500.1* | CC-NBS-LRR family disease resistance protein | *AET2Gv20856200.1* | [98] |
| *TraesCS2D01G379300.1* | CASP-like protein | *AET2Gv20853500.1* | N |
| *TraesCS2D01G388200.1* | Casein kinase II subunit beta | *AET2Gv20867200.1* | [99] |
| *TraesCS2D01G382300.1* | Caleosin | *AET2Gv20859200.1* | [100] |
| *TraesCS2D01G385100.1* | BRCT domain-containing protein | *AET2Gv20863500.1* | [101] |
| *TraesCS2D01G390700.1* | Blue copper protein | *AET2Gv20876600.1* | [102] |
| *TraesCS2D01G381300.1* | Beta-glucosidase, putative | *AET2Gv20857000.1* | [103] |
| *TraesCS2D01G381000.1* | Beta-glucosidase | *AET2Gv20856500.1* | [103] |
| *TraesCS2D01G393900.1* | Beta-carotene hydroxylase | *AET2Gv20883500.1* | [104] |
| *TraesCS2D01G393500.1* | Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe | *AET2Gv20884100.1* | N |
| *TraesCS2D01G392400.1* | B3 domain-containing protein | *AET2Gv20880200.1* | [105] |
| *TraesCS2D01G395500.1* | Ankyrin repeat protein-like | *AET2Gv20886300.1* | [106] |
| *TraesCS2D01G395800.1* | Ankyrin repeat and zinc finger domain-containing protein 1 | *AET2Gv20886600.1* | [106] |
| *TraesCS2D01G389600.1* | Alpha/beta-Hydrolases superfamily protein, putative | *AET2Gv20874100.1* | [107] |
| *TraesCS2D01G392300.1* | Alpha/beta-Hydrolases superfamily protein | *AET2Gv20880000.1* | [107] |
| *TraesCS2D01G386700.1* | Aldehyde dehydrogenase | *AET2Gv20871400.1* | [108] |
| *TraesCS2D01G380000.1* | Actin family protein | *AET2Gv20854500.1* | [109] |
| *TraesCS2D01G383100.1* | Acidic leucine-rich nuclear phosphoprotein 32 family B protein | *AET2Gv20860500.1* | [110] |
| *TraesCS2D01G393800.1* | ABC2 homolog 4 | *AET2Gv20883600.1* | [111] |
| *TraesCS2D01G395600.1* | 4-hydroxy-tetrahydrodipicolinate synthase | *AET2Gv20886400.1* | N |
| *TraesCS2D01G379400.1* | 3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ | *AET2Gv20853700.1* | N |
| *TraesCS2D01G394200.1* | 1-aminocyclopropane-1-carboxylate synthase | *AET2Gv20884600.1* | [112] |
| *TraesCS2D01G376700.1* |  | N |  |
| *TraesCS2D01G376800.1* |  | N |  |
| *TraesCS2D01G376900.1* |  | N |  |
| *TraesCS2D01G377000.1* |  | N |  |
| *TraesCS2D01G377100.1* |  | N |  |
| *TraesCS2D01G377500.1* |  | N |  |
| *TraesCS2D01G377600.1* |  | N |  |
| *TraesCS2D01G378400.1* |  | N |  |
| *TraesCS2D01G378500.1* |  | N |  |
| *TraesCS2D01G379100.1* |  | N |  |
| *TraesCS2D01G379500.1* |  | N |  |
| *TraesCS2D01G379700.1* |  | N |  |
| *TraesCS2D01G379800.1* |  | N |  |
| *TraesCS2D01G379900.1* |  | N |  |
| *TraesCS2D01G380100.1* |  | N |  |
| *TraesCS2D01G380600.1* |  | N |  |
| *TraesCS2D01G380700.1* |  | N |  |
| *TraesCS2D01G380800.1* |  | N |  |
| *TraesCS2D01G381100.1* |  | N |  |
| *TraesCS2D01G381200.1* |  | N |  |
| *TraesCS2D01G381700.1* |  | N |  |
| *TraesCS2D01G381900.1* |  | N |  |
| *TraesCS2D01G382000.1* |  | N |  |
| *TraesCS2D01G382100.1* |  | N |  |
| *TraesCS2D01G382400.1* |  | N |  |
| *TraesCS2D01G382600.1* |  | N |  |
| *TraesCS2D01G383000.1* |  | N |  |
| *TraesCS2D01G383300.1* |  | N |  |
| *TraesCS2D01G383500.1* |  | N |  |
| *TraesCS2D01G384000.1* |  | N |  |
| *TraesCS2D01G384100.1* |  | N |  |
| *TraesCS2D01G384200.1* |  | N |  |
| *TraesCS2D01G384300.1* |  | N |  |
| *TraesCS2D01G384600.1* |  | N |  |
| *TraesCS2D01G384700.1* |  | N |  |
| *TraesCS2D01G384900.1* |  | N |  |
| *TraesCS2D01G385400.1* |  | N |  |
| *TraesCS2D01G385700.1* |  | N |  |
| *TraesCS2D01G386500.1* |  | N |  |
| *TraesCS2D01G387000.1* |  | N |  |
| *TraesCS2D01G387600.1* |  | N |  |
| *TraesCS2D01G387700.1* |  | N |  |
| *TraesCS2D01G387800.1* |  | N |  |
| *TraesCS2D01G387900.1* |  | N |  |
| *TraesCS2D01G388600.1* |  | N |  |
| *TraesCS2D01G388700.1* |  | N |  |
| *TraesCS2D01G389000.1* |  | N |  |
| *TraesCS2D01G389300.1* |  | N |  |
| *TraesCS2D01G389400.1* |  | N |  |
| *TraesCS2D01G389500.1* |  | N |  |
| *TraesCS2D01G390100.1* |  | N |  |
| *TraesCS2D01G391100.1* |  | N |  |
| *TraesCS2D01G391300.1* |  | N |  |
| *TraesCS2D01G392000.1* |  | N |  |
| *TraesCS2D01G392700.1* |  | N |  |
| *TraesCS2D01G393100.1* |  | N |  |
| *TraesCS2D01G393300.1* |  | N |  |
| *TraesCS2D01G393600.1* |  | N |  |
| *TraesCS2D01G394400.1* |  | N |  |
| *TraesCS2D01G394700.1* |  | N |  |
| *TraesCS2D01G395100.1* |  | N |  |
| *TraesCS2D01G395300.1* |  | N |  |
| *TraesCS2D01G395400.1* |  | N |  |
| *TraesCS2D01G396300.1* |  | N |  |
| *TraesCS2D01G397300.1* |  | N |  |
| *TraesCS2D01G397400.1* |  | N |  |
| *TraesCS2D01G398000.1* |  | N |  |
| *TraesCS2D01G398100.1* |  | N |  |
| *TraesCS2D01G398200.1* |  | N |  |
| *TraesCS2D01G398300.1* |  | N |  |
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| *TraesCS2D01G398500.1* | 　 | N |  |
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| N |  | *AET2Gv20850900.1* |  |
| N |  | *AET2Gv20852000.1* |  |
| N |  | *AET2Gv20852400.1* |  |
| N |  | *AET2Gv20852500.1* |  |
| N |  | *AET2Gv20852600.1* |  |
| N |  | *AET2Gv20854000.1* |  |
| N |  | *AET2Gv20854800.1* |  |
| N |  | *AET2Gv20857200.1* |  |
| N |  | *AET2Gv20864100.1* |  |
| N |  | *AET2Gv20867600.1* |  |
| N |  | *AET2Gv20867700.1* |  |
| N |  | *AET2Gv20867900.1* |  |
| N |  | *AET2Gv20868700.1* |  |
| N |  | *AET2Gv20869100.1* |  |
| N |  | *AET2Gv20870800.1* |  |
| N |  | *AET2Gv20871800.1* |  |
| N |  | *AET2Gv20872700.1* |  |
| N |  | *AET2Gv20872800.1* |  |
| N |  | *AET2Gv20873400.1* |  |
| N |  | *AET2Gv20875000.1* |  |
| N |  | *AET2Gv20875300.1* |  |
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| N |  | *AET2Gv20881700.1* |  |
| N |  | *AET2Gv20882100.1* |  |
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| N |  | *AET2Gv20883800.1* |  |
| N |  | *AET2Gv20883900.1* |  |
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| N |  | *AET2Gv20858200.1* |  |
| N | 　 | *AET2Gv20858400.1* |  |

Note: N represents no orthologs were identified after reciprocal blasting analysis.

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