**Table S3. The list of possible candidate *Lr*, *Sr* and *Yr* genes, protein-coding genes of *T. aestivum* overlapping with QTL identified in the current study and proteins coded by them.** Orthologue genes and proteins with known functions in other species are listed for proteins whose functions are uncharacterized in *T. aestivum.*

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Trait** | **Marker** | **Chr.1** | **Pos. (cM)1** | **Candidate gene(s)** | **Overlapping gene(s)** | **Protein** | **Orthologue gene(s)3** | **Identity (%)4** | **Orthologue protein3** |
| 1 | LR | BobWhite\_c96\_170 | 1A | 96.3 |  | TraesCS1A02G342900 (exon) | Uncharacterized protein | AET1Gv20821000  (*A. tauschii*) | 97.72 | ABC transporter A family member 2 |
| 2 | LR | BS00078431\_51 | 1B | 70.8 |  | TraesCS1B02G266000 (intron) | Uncharacterized protein | - | - | - |
| 3 | LR | BobWhite\_c14141\_197 | 1BL2 | 90.52 | *Lr46* | TraesCS1B02G350700 (exon) | Folate gamma-glutamyl hydrolase | - | - | - |
| 4 | LR | BobWhite\_c33756\_74 | 1DS2 | 15.82 | *Lr21, Lr60* | TraesCS1D02G024800 (exon) | Uncharacterized protein | AET1Gv20053700  (*A. tauschii*) | 98.03 | tRNA pseudouridine synthase B |
| 5 | LR | BS00063511\_51 | 1D | 167.1 |  | TraesCS1D02G439800 (intron) | Uncharacterized protein | AET1Gv21018700  (*A. tauschii*) | 99.32 | Trimethylguanosine synthase |
| 6 | LR | BobWhite\_c14476\_80 | 2A | 101.9 |  | TraesCS2A02G141400 (exon) | Uncharacterized protein | AET2Gv20287000  (*A. tauschii*) | 96.29 | Zinc transporter 7 |
| 7 | LR | Excalibur\_c20376\_615 | 2BS2 | 76.92 | *Lr13, Lr23* | TraesCS2B02G141800 (exon) | Uncharacterized protein | BRADI\_1g18380v3  (*B. distachyon*) | 79.63 | Tubby-like F-box protein |
| 8 | LR | BS00011630\_51 | 2BL2 | 100.02 | *Lr35, Lr50* | TraesCS2B02G490800 (exon) | Uncharacterized protein | - | - | - |
| 9 | LR | wsnp\_Ex\_c34303\_42642389 | 2B | 145.5 |  | TraesCS2B02G592500 (exon) | Uncharacterized protein | AET2Gv21232800  (*A. tauschii*) | 99.44 | ETO1-like protein 1 |
| 10 | LR | Tdurum\_contig16896\_426 | 4A | 136.3 | *Lr32* | TraesCS4A02G434900 (exon) | Growth regulating factor 5-4A | - | - | - |
| 11 | LR | Excalibur\_c27349\_166 | 4B | 77.9 | *Lr12, Lr31* | TraesCS4B02G328500 (exon) | Uncharacterized protein | AET4Gv20774800  (*A. tauschii*) | 100 | Putative membrane protein |
| 12 | LR | D\_contig23076\_255 | 5A | 53.5 |  | TraesCS5A02G264000 (exon/intron) | Uncharacterized protein | - | - | - |
| 13 | LR | RAC875\_rep\_c112818\_307 | 5A | 98.9 |  | TraesCS5A02G428800 (exon) | Uncharacterized protein | AET5Gv20995500  (*A. tauschii*) | 100 | 25.3 kDa vesicle transport protein |
| 14 | LR | GENE-2307\_1216 | 5B | 147.4 |  | TraesCS5B02G505200 (intron) | Uncharacterized protein | - | - | - |
| 15 | LR | wsnp\_Ex\_rep\_c68175\_66950387 | 6A | 31.9 |  | - | - | - | - | - |
| 16 | LR | TA003021-1057 | 6A | 56.1 |  | - | - | - | - | - |
| 17 | LR | BobWhite\_c17385\_55 | 6A | 99 |  | TraesCS6A02G349000 (exon) | Uncharacterized protein | - | - | - |
| 18 | LR | RAC875\_c93959\_96 | 6A | 117.9 |  | TraesCS6A02G369300 (exon) | Uncharacterized protein | - | - | - |
| 19 | LR | BS00063555\_51 | 7A | 106.8 |  | - | - | - | - | - |
| 20 | LR | BobWhite\_c24063\_231 | 7A | 127.7 |  | TraesCS7A02G250500 (exon) | Uncharacterized protein | TRIUR3\_01974  (*T. urartu*) | 98.18 | Chitinase-like protein 1 |
| 21 | LR | TA003458-0086 | 7A | 134 |  | TraesCS7A02G389100 (intron) | Uncharacterized protein | - | - | - |
| 22 | LR | Kukri\_c12901\_706 | 7B | 98.7 | *Lr14, Lr19* | TraesCS7B02G381300 (exon) | CNNM transmembrane domain-containing protein | - | - | - |
| 23 | LR | TA005127-0595 | 7B | 133.6 |  | TraesCS7B02G432400 (exon) | Uncharacterized protein | AET7Gv21263100  (*A. tauschii*) | 99.32 | Isoleucyl-tRNA synthetase |
| 24 | SR | Tdurum\_contig37488\_126 | 1AS2 | 66.12 |  | TraesCS1A02G060500 (exon) | Uncharacterized protein | - | - | - |
| 25 | SR | RFL\_Contig22\_387 | 1A | 84.3 |  | TraesCS1A02G312000 (exon) | Uncharacterized protein | - | - | - |
| 26 | SR | Tdurum\_contig56188\_569 | 1B | 53.3 |  | TraesCS1B02G048800 (exon) | Uncharacterized protein | - | - | - |
| 27 | SR | BS00078431\_51 | 1B | 70.8 |  | TraesCS1B02G266000 (intron) | Uncharacterized protein | - | - | - |
| 28 | SR | IAAV565 | 1B | 122.5 |  | TraesCS1B02G426300 (exon) | Uncharacterized protein | AET1Gv20952800  (*A. tauschii*) | 99.54 | Ras-related protein Rab11B |
| 29 | SR | Tdurum\_contig10048\_207 | 2A | 154.8 |  | TraesCS2A02G588000 (exon) | Uncharacterized protein | TRIUR3\_06369  (*T. urartu*) | 80.13 | Allantoinase |
| 30 | SR | Excalibur\_c20376\_615 | 2BS2 | 76.92 | *Sr36, Sr40, Sr47, Sr9, Sr28* | TraesCS2B02G141800 (exon) | Uncharacterized protein | BRADI\_1g18380v3  (*B. distachyon*) | 79.63 | Tubby-like F-box protein |
| 31 | SR | D\_contig23076\_255 | 5A | 53.5 |  | TraesCS5A02G264000 (intron) | Uncharacterized protein | - | - | - |
| 32 | SR | TA003021-1057 | 6A | 56.1 |  | - | - | - | - | - |
| 33 | SR | Tdurum\_contig97355\_194 | 6A | 110.8 | *Sr26* | TraesCS6A02G360900 (exon) | Uncharacterized protein | - | - | - |
| 34 | SR | BS00022032\_51 | 6B | 21.7 |  | - | - | - | - | - |
| 35 | SR | wsnp\_Ex\_c9750\_16105678 | 6B | 71.9 | *Sr11* | TraesCS6B02G348700 (exon/intron) | Uncharacterized protein | - | - | - |
| 36 | SR | BobWhite\_c4684\_245 | 7A | 130.3 |  | - | - | - | - | - |
| 37 | SR | Excalibur\_rep\_c75066\_126 | 7B | 133.6 |  | TraesCS7B02G431600 (exon) | Uncharacterized protein | - | - | - |
| 38 | YR | Excalibur\_c63885\_115 | 1B | 112.4 |  | TraesCS1B02G417200 (exon) | Uncharacterized protein | AET1Gv20935500  (*A. tauschii*) | 81.05 | Ribosomal L1 domain-containing protein 1 |
| 39 | YR | Kukri\_rep\_c87640\_135 | 3A | 90.6 |  | TraesCS3A02G328300 (exon) | Uncharacterized protein | - | - | - |
| 40 | YR | BobWhite\_rep\_c63429\_271 | 4A | 52 |  | TraesCS4A02G257800 (exon) | Tubulin alpha chain | - | - | - |
| 41 | YR | RAC875\_rep\_c112818\_307 | 5A | 98.9 | *Yr34, Yr48* | TraesCS5A02G428800 (exon) | Uncharacterized protein | AET5Gv20995500  (*A. tauschii*) | 100 | 25.3 kDa vesicle transport protein |
| 42 | YR | wsnp\_Ex\_rep\_c68175\_66950387 | 6A | 31.9 |  | - | - | - | - | - |
| 43 | YR | BobWhite\_c18566\_106 | 6B | 0.4 | *Yr35* | - | - | - | - | - |
| 44 | YR | wsnp\_Ku\_c1876\_3666308 | 6B | 70.7 |  | TraesCS6B02G310500 (exon) | Uncharacterized protein | AET6Gv20712000  (*A. tauschii*) | 82.88 | E3 ubiquitin-protein ligase makorin |
| 45 | YR | BobWhite\_rep\_c49587\_1290 | 7B | 73.8 | *Yr52, Yr59, Yr67* | TraesCS7B02G266300 (exon) | Uncharacterized protein | HORVU7Hr1G087050 (*H. vulgare*) | 94.63 | Eukaryotic elongation factor 1 gamma |
| Note: 1 – Positions according to 90K array consensus map; 2 – Positions according to the CSS POPSEQ 2014 map; 3 – Genes and proteins with known functions only are included; 4 – Percentage of *T. aestivum’s* sequence matching the sequence of the orthologue. | | | | | | | | | | |