**Supplementary Material**

**QTL mapping for stripe rust and powdery mildew resistance** **in *Triticum durum- Aegilops speltoides* backcross introgression lines**

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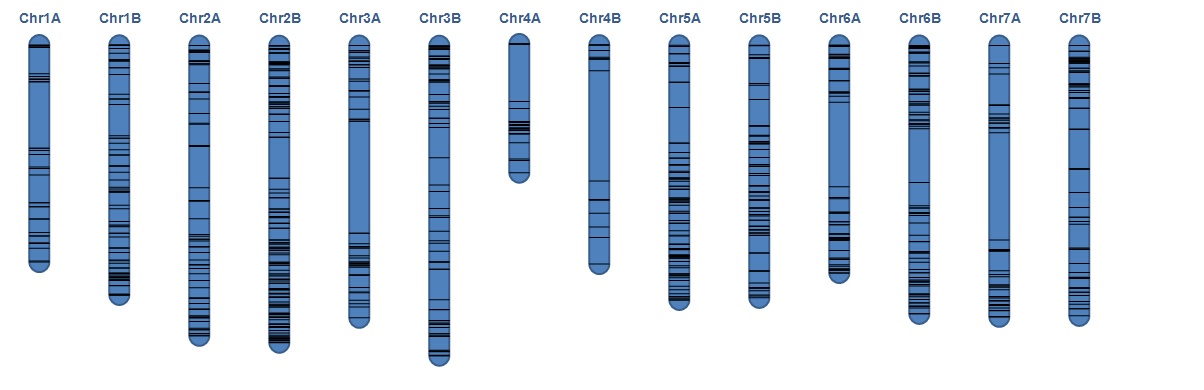


Figure S1: Coverage of filtered 1095 SNPs used for mapping QTLs for various diseases along A and B genome chromosomes. The black lines represent physical positions of the SNPs according to wheat RefSeqv1.0 on blue background of recurrent parent PDW274.

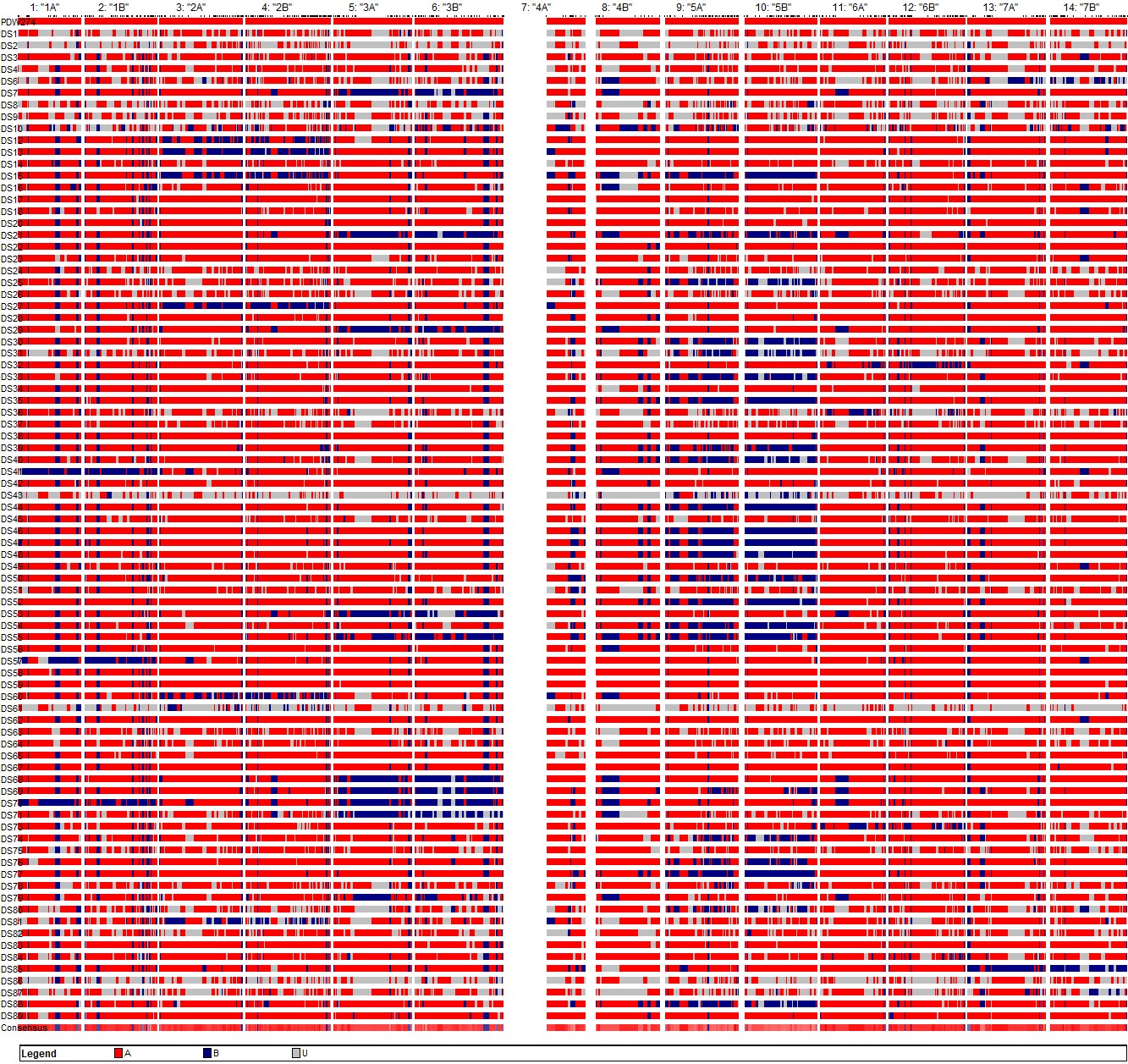


Figure S2: Introgression profile of 89 lines with recurrent parent PDW274 (on top) is given with red colour represents the segment from PDW274 and blue represent the introgression of *Ae. speltoides* in the DS-BILs

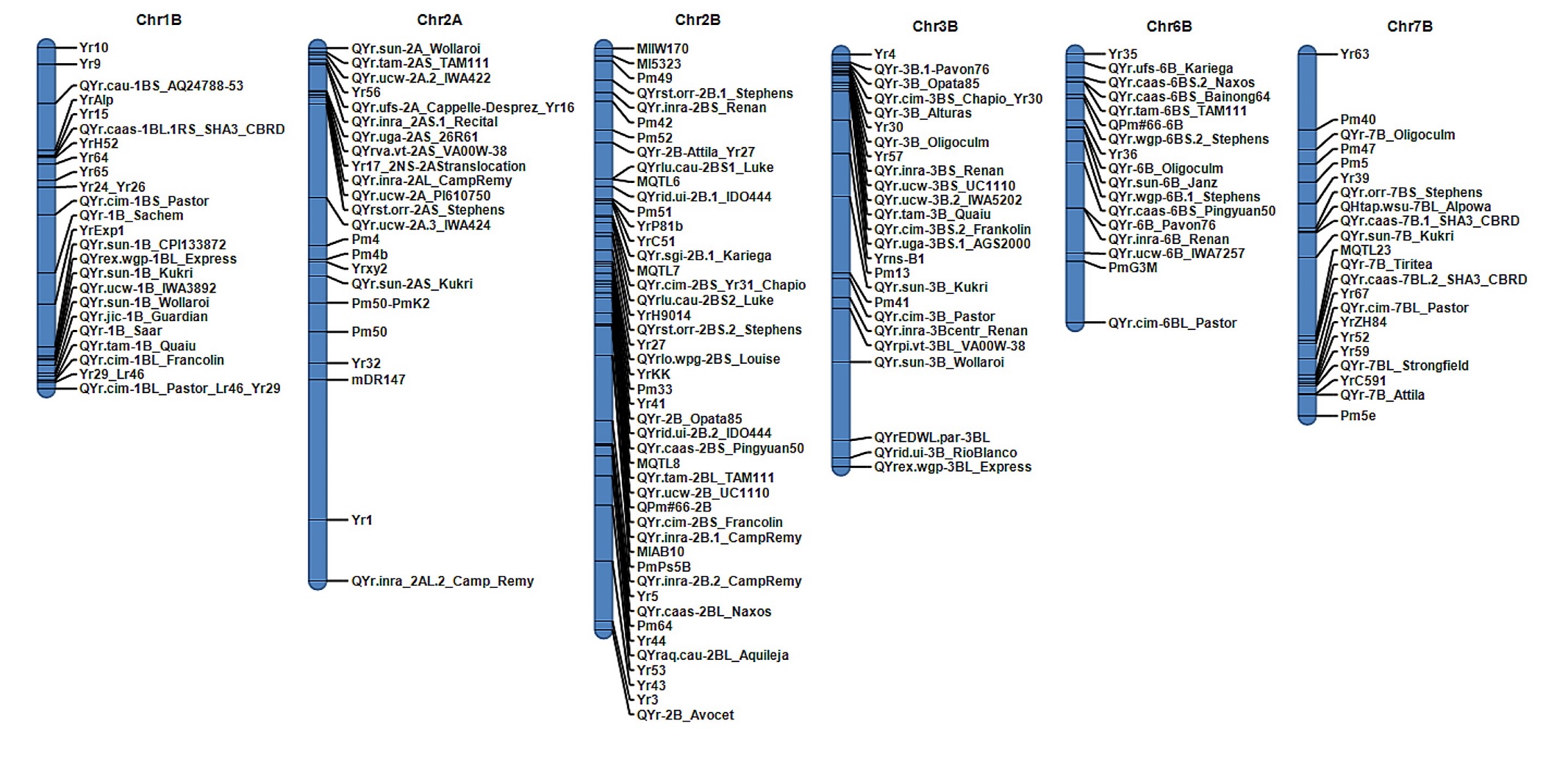


Figure S3: Summary of the designated genes, preliminary reported genes and QTLs on chromosomes harbouring QTL in the present study. The mapped genes/QTL, their linkage positions were retrieved from [www.wheat.pw.usda.gov](http://www.wheat.pw.usda.gov) as has been reported by Maccaferri *et al.* (2015) for stripe rust and Ben-David *et al.* (2014) for powder mildew along with other powder mildew genes reported and chromosome maps were generated in IciMapping V4.1.0.0

Table S1: Postulation of genes present in the survey sequence of wheat genome refseqV1.0

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | SNP marker | Distance  from SNP | Chr | Reference gene Gene ID | Function |
| *QYrAs.pau-1B* | ASR Pst field pathotypes | S1B\_626229235 | +4.598 | chr1B | *TraesCS1B01G393400.1* | RING/U-box superfamily protein(Zinc finger)\* |
|  |  |  | -1.251 | chr1B | *TraesCS1B01G393500.1* | Serine/threonine-protein phosphatase |
|  |  |  | -14.764 | chr1B | *TraesCS1B01G393600.1* | Disease resistance protein (NBS-LRR class) family\* |
|  |  |  | -21.334 | chr1B | *TraesCS1B01G393700.1* | Reticulon-like protein |
| *QYrAs.pau-2A.1* | ASR Pst field pathotypes | S2A\_16016633 | 0 | chr2A | *TraesCS2A01G038100.1* | L-gulonolactone oxidase\* |
|  |  |  | -8.225 | chr2A | *TraesCS2A01G038200.1* | Vascular endothelial growth factor receptor 3 |
|  |  |  | -49.03 | chr2A | *TraesCS2A01G038300.1* | Beta-glucosidase |
| *QPmAS.pau-2A.1* | ASR Bg field pathotypes | S2A\_43146710 | +13.059 | chr2A | *TraesCS2A01G090000.1* | 26S protease regulatory subunit\* |
|  |  |  | +1.31 | chr2A | *TraesCS2A01G090100.1* | Leucine-rich repeat receptor-like protein kinase\* |
|  |  |  | -33.072 | chr2A | *TraesCS2A01G090200.1* | Zinc-finger protein\* |
| *QYrTd.pau-2A.2* | ASR Pst 78S84 | S2A\_766158316 | +6.454 | chr2A | *TraesCS2A01G567300.1* | Auxin response factor\* |
|  |  |  | 0 | chr2A | *TraesCS2A01G567400.1* | CAA30371.1 protein |
| *QPmAS.pau-2A.2* | ASR Bg field pathotypes | S2A\_771507864 | +21.662 | chr2A | *TraesCS2A01G577300.1* | Protein kinase family protein, putative, expressed\* |
|  |  |  | +2.653 | chr2A | *TraesCS2A01G577400.1* | Kinase family protein\* |
|  |  |  | 0 | chr2A | *TraesCS2A01G577500.1* | Pentatricopeptide repeat-containing family protein |
|  |  |  | -4.614 | chr2A | *TraesCS2A01G577600.1* | 3-isopropylmalate dehydrogenase |
|  |  |  | -7.998 | chr2A | *TraesCS2A01G577700.1* | UPF0235 protein |
|  |  |  | -30.782 | chr2A | *TraesCS2A01G577800.1* | Cytochrome P450 family protein, expressed |
|  |  |  | -39.245 | chr2A | *TraesCS2A01G577900.1* | Glutathione S-transferase\* |
| *QYrAs.pau-2B* | ASR Pst field pathotypes | S2B\_27896451 | +8.029 | chr2B | *TraesCS2B01G057200.1* | ELMO domain-containing protein, putative |
|  |  |  | 0 | chr2B | *TraesCS2B01G057300.1* | Zinc finger family protein\* |
| *QPmAS.pau-2B* | ASR Bg field pathotypes | S2B\_791958961 | +1.911 | chr2B | *TraesCS2B01G612700.1* | Dihydroflavonol-4-reductase |
| *QYrTd.pau-3B* | ASR Pst 78S84 | S3B\_743818730 | +5.51 | chr3B | *TraesCS3B01G499200.1* | Glutathione S-transferase\* |
| *QPmAs.pau-3B* | ASR Bg field pathotypes | S3B\_775092221 | -145.056 | chr3B | *TraesCS3B01G535100.1* | GRAS family transcription factor containing protein |
|  |  |  | +83.639 | chr3B | *TraesCS3B01G535200.1* | F-box protein |
|  |  |  | +352.758 | chr3B | *TraesCS3B01G535300.1* | Glutathione S-transferase\* |
|  |  |  | +383.528 | chr3B | *TraesCS3B01G535400.1* | Peroxiredoxin |
|  |  |  | +388.745 | chr3B | *TraesCS3B01G535500.1* | Protein ENHANCED DISEASE RESISTANCE 2\* |
|  |  |  | +444.521 | chr3B | *TraesCS3B01G535600.1* | F-box SKIP23-like protein |
|  |  |  | +469.715 | chr3B | *TraesCS3B01G535700.1* | Glutathione S-transferase\* |
| *QPmAS.pau-6B* | ASR Bg field pathotypes | S6B\_26793381 | +24.086 | chr6B | *TraesCS6B01G044800.1* | receptor kinase 1\* |
|  |  |  | 0 | chr6B | *TraesCS6B01G044900.1* | Mitochondrial transcription termination factor-like\* |
|  |  |  | -47.402 | chr6B | *TraesCS6B01G045000.1* | Mitochondrial transcription termination factor-like\* |
| *QYrAs.pau-7B* | ASR Pst field pathotypes | S7B\_708445814 | +29.704 | chr7B | *TraesCS7B01G443600.1* | RING/U-box superfamily protein (Zinc finger) \* |
|  |  |  | -30.142 | chr7B | *TraesCS7B01G443700.1* | Coatomer subunit beta'-1 |

\* represent genes/ functions which have been well reported to be a part of plant-pathogen interaction or plant-pathogenesis

In column distance from SNP represent the distance of start site of the gene to SNP linked with QTL, where + sign represents the gene was found downstream of the SNP and – sign gene was found upstream, 0 represent the SNP was present inside the gene, and all distances are in kilobase