|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **QTL1** | **Chr.** | **Peak SNP position (bp)2** | **Start (bp)2** | **Stop (bp)2** | **Interval (Mbp)2** | **Genes3** | **Gene percentile rank4** | **Resistance genes5** | **Resistance gene percentile rank6** | ***P*-value7** |
| ***QYr.niab-1A.1*** | 1A | 568,012,820 | 545888499 | 577841123 | 31.953 | 1328 | **100** | 41 | 88 | 0.848 |
| ***QYr.niab-2A.1*** | 2A | 607,827,264 | 543620284 | 677529736 | 133.909 | 2214 | 63 | 57 | 66 | 0.997 |
| ***QYr.niab-2A.2*** | 2A | 762,290,086 | 761248623 | 780798557 | 19.550 | 830 | **99** | 49 | **97** | **0.001** |
| ***QYr.niab-2B.1*** | 2B | 683,047,583 | 635023684 | 748985682 | 113.962 | 2630 | 85 | 95 | 86 | 0.517 |
| ***QYr.niab-2D.1*** | 2D | 638,376,433 | 637636368 | 651852609 | 14.216 | 689 | **100** | 71 | **99** | **0.000** |
| ***QYr.niab-3A.1*** | 3A | 7,920,709 | 1 | 9852685 | 9.853 | 286 | 86 | 14 | 88 | 0.105 |
| *QYr.niab-3D.1* | 3D | 574,773,288 | 536029042 | 596708808 | 60.680 | 2009 | **97** | 102 | **96** | **0.001** |
| *QYr.niab-4B.1* | 4B | 36,642,747 | 28716585 | 132334233 | 103.618 | 1732 | 63 | 43 | 63 | 0.996 |
| *QYr.niab-4D.1* | 4D | 499,108,143 | 482705858 | 509857067 | 27.151 | 1018 | **97** | 34 | 88 | 0.665 |
| *QYr.niab-5A.1* | 5A | 683,342,769 | 682933090 | 709773743 | 26.841 | 857 | 92 | 23 | 80 | 0.927 |
| ***QYr.niab-6A.1*** | 6A | 18,713,189 | 10493377 | 23434335 | 12.941 | 538 | **98** | 47 | **98** | **0.000** |
| ***QYr.niab-6A.2*** | 6A | 27,108,470 | 26977185 | 47106025 | 20.129 | 595 | 88 | 36 | 93 | **0.001** |
| *QYr.niab-6A.3* | 6A | 596,521,256 | 592818078 | 607956733 | 15.139 | 620 | **98** | 25 | 91 | 0.264 |
| *QYr.niab-6B.1* | 6B | 54,662,261 | 41706023 | 121489184 | 79.783 | 1668 | 77 | 77 | 87 | **0.018** |

**Supplementary Table 6.** Analysis of physical intervals and gene content within for the 14 yellow rust resistance quantitative trait loci (QTL). 1‘Major’ YR resistance QTL (each explaining >5% of the phenotypic variance) are highlighted in bold. 2Based on the wheat reference genome (RefSeq v1.0; IWGSC, 2018). 3Gene model build: RefSeq v1.1). 4Calculated using an interval the size of each target QTL, sampling the genome every 100 bp. 5Number of resistance genes, as defined in the Methods section. 6Number of resistance genes, as defined in the Methods section. 7 7‘Resistance gene’ enrichment value (binomial cumulative probability).