**Table S1** The RNAseq datasets, for which transcript count values were downloaded from expVIP. These datasets provide RNAseq data on wheat inoculated with a fungal pathogen or a pathogen associated molecular pattern.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Stress (reference)** | **Cultivar** | **Timepoint** | **Disease** | **Tissue** |
| *Zymoseptoria tritici*  (Yang et al., 2013) | Sevin | 4, 10 and 13 days | Septoria tritici blotch | Leaf |
| *Fusarium graminearum* (Kugler et al., 2013) | NIL1, NIL2, NIL3, NIL4 from CM-82036 BC5 in Remus | 38 and 50 hours | Fusarium head blight | Floret |
| *Puccinia striiformis*  (Zhang et al., 2014) | N9134 | 24, 48 and 82 hours | Stripe rust | Leaf |
| *Blumeria graminis*  (Zhang et al., 2014) | N9134 | 24, 48 and 82 hours | Powdery mildew | Leaf |
| *Fusarium graminearum* (Schweiger et al., 2016) | NIL38 AND NIL51 from Remus in CM-82036 | 3, 6, 12, 24, 46, 48 hours | Fusarium head blight | Head |
| *Fusarium pseudograminearum* (Powell et al., 2017) | Chara | 36 hours | Fusarium crown rot | Coleoptile |
| *Magnaporthe oryzae*  (Islam et al., 2016) | unknown (field) | unknown (field) | Wheat blast | Leaf |
| *Zymoseptoria tritici*  (Rudd et al., 2015) | Riband | 1, 4, 9, 14, 21 days | Septoria tritici blotch | Leaf |
| *Fusarium pseudograminearum* (Ma et al., 2014) | NILs from Janz’\*2/CSCR6 | 3 and 5 days | Fusarium crown rot | Seedling stem |
| Chitin and flg22  (Ramirez-Gonzalez et al., 2018) | Chinese Spring | 30 minutes | PAMP elicitors | Leaf |

**Table S2** The RNAseq datasets for which transcript TMP values were downloaded from expVIP. These datasets provide RNAseq data on wheat heads and the developing grain.

|  |  |
| --- | --- |
| Tissue | Cultivar |
| Spike and grain  (Ramirez-Gonzalez et al. 2018) | Chinese Spring |
| Spike and grain  (Ramirez-Gonzalez et al. 2018) | Westonia x Kauz DH lines |
| Endosperm  (Li et al. 2013) | P271 |
| Spike and grain  (Pearce et al. 2015) | Chinese spring |
| Grain  (Gillies et al. 2012) | Banks |
| Grain  (Pfeifer et al. 2014) | Chinese spring |
| Grain  (Barrero et al. 2015) | MAGIC RILs |

**Figure S1** Serpins genes in differentially regulated in response to infection with *F. graminearum* in multiple cultivars. These nine serpin genes were upregulated by *Fusarium* across two different wheat genotypes. The near-isogenic lines (NILs) NIL38 and NIL51 are derived from a cross between *Triticum aestivum* cvs. CM-82036 and Remus. NIL38 carries resistant alleles for two FHB QTL, and NIL51 carries the susceptible alleles (Schweiger et al. 2016). Blue tiles represent the Log2 fold change in expression of each gene, between samples inoculated with *F. graminearum* or a control solution across three timepoints. The lighter the shade of blue, the higher the fold change, and therefore the more up-regulated that gene is by *Fusarium* application.



**Figure S2** A subclade of the wheat serpin family that contains five *Fusarium graminearum* responsive genes. Colour is red if the serpin is up-regulated by *F. graminearum* inoculation (compared to a mock-treatment), and blue if the gene is not responsive. Five out of nine *Fusarium* responsive serpins belonged to the same clade. Two *Fusarium* responsive serpins in this clade on chromosome 4A are paralogues that share 80% identity in protein sequence. The *Fusarium* responsive genes on the group 3 chromosomes are homoeologues that are 93% identical in protein sequence.