

Supplemental figures

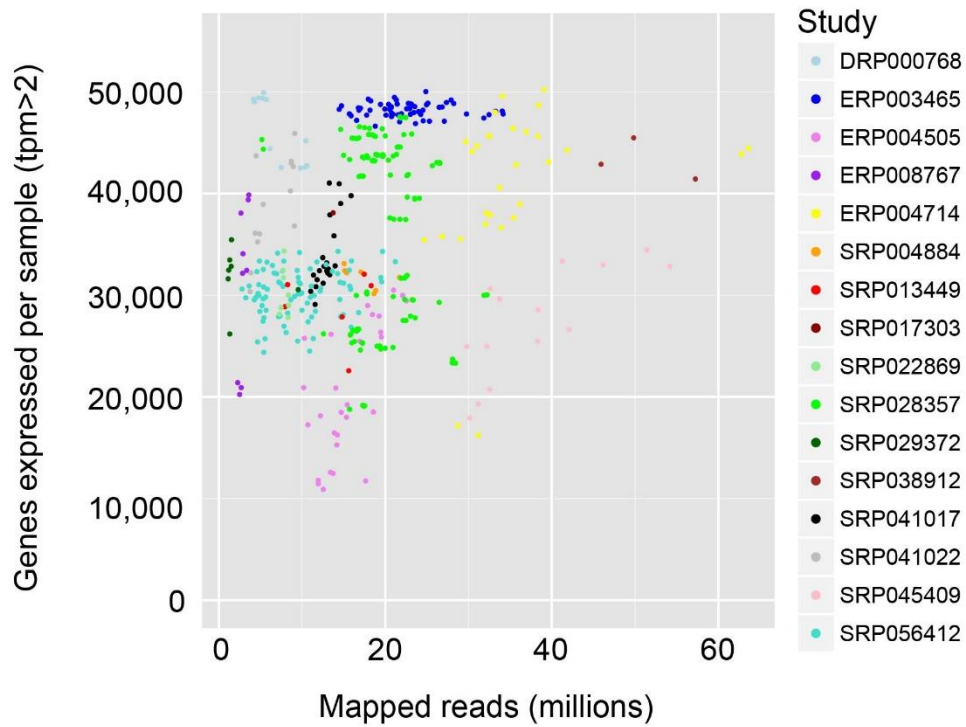


Figure S1. Number of genes expressed per sample compared to the number of mapped reads per sample. Samples are colour coded by study.

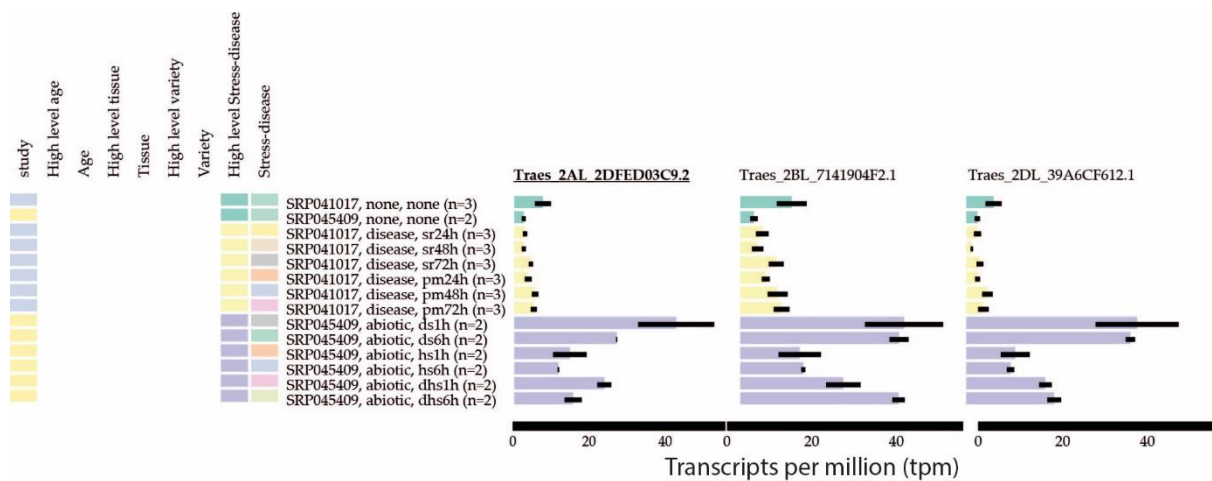


Figure S2. Demonstration of data filtering within expVIP interface. The expression of Traes_2AL_2DFED03C9.2 is shown only from studies which were used for differential gene expression analysis (SRP041017 for disease and SRP045409 for abiotic stress).

Supplemental tables

Tissue	Ensembl transcript ID	Average expression (tpm)	Function
grain	Traes_5BS_FDE980DE1.1	5,808	Grain softness protein
grain	TRAES3BF027700070CFD_t1	6,898	Serine protease inhibitor (annotation of orthologue)
grain	Traes_3DS_D718FF51C1.2	7,042	Alpha-amylase inhibitor 0.19
grain	Traes_1AS_8FAD6A69F.1	9,155	unknown
grain	Traes_1DS_67B7153A8.1	10,350	Glutenin (annotation of orthologue)
grain	Traes_1DS_66B67E9B41.2	20,423	Glutenin (annotation of orthologue)
grain	Traes_4AL_661613B77.1	63,949	Alpha/beta-gliadin MM1
grain	Traes_4AL_4FF5B8837.1	70,002	Alpha/beta-gliadin A-I
grain	Traes_5BL_E68C461B3.1	77,505	Alpha/beta-gliadin (annotation of orthologue)
grain	Traes_1DL_D861501F5.1	96,186	Glutenin, high molecular weight subunit 12
leaf	Traes_4DL_7CF374FEE.1	4,518	Ribulose biphosphate carboxylase large chain (annotation of orthologue)
leaf	Traes_3DS_4EF0DAA39.1	4,794	Photosystem I reaction center subunit XI (annotation of orthologue)
leaf	Traes_3DL_B80EC2366.1	6,041	putative nontranslating CDS
leaf	TRAES3BF032400040CFD_t1	6,402	unknown
leaf	Traes_4DL_85C90C56C.2	7,058	Ribulose biphosphate carboxylase large chain
leaf	TRAES3BF011000020CFD_t1	7,785	Histidine kinase 3 (annotation of orthologue)
leaf	Traes_6BL_5979B5341.1	10,819	unknown
leaf	TRAES3BF007300450CFD_t1	12,421	unknown
leaf	TRAES3BF007300320CFD_t1	21,923	unknown
leaf	Traes_7DS_037CD9FCA.1	23,120	unknown

Table S2. Ten most highly expressed genes in wheat grain and leaf tissues from seven and nine independent studies, respectively.

		Shoots								Roots							
		euploid	N1AT1B	N1AT1D	N1BT1A	N1BT1D	N1DT1A	N1DT1B	euploid	N1AT1B	N1AT1D	N1BT1A	N1BT1D	N1DT1A	N1DT1B		
kallisto	Average gene expression level in shoots for genes located on chromosome (tpm):	1A	16.5	3.0	3.6	42.0	19.5	32.6	22.6	20.7	3.6	4.7	42.9	24.0	38.8	22.0	
		1B	14.0	31.3	16.8	3.0	3.2	16.6	32.0	20.0	40.2	20.9	2.4	3.2	20.4	39.4	
		1D	14.7	17.2	29.7	18.7	29.1	3.1	3.4	21.3	23.9	39.3	25.5	45.7	3.4	4.1	
		1A+ 1B+ 1D															
	Percentage of gene expression originating from:	1A	36.6%	5.8%	7.3%	66.0%	37.6%	62.4%	39.0%	33.4%	5.3%	7.2%	60.5%	32.9%	62.0%	33.6%	
		1B	30.9%	60.7%	33.5%	4.7%	6.3%	31.7%	55.2%	32.3%	59.3%	32.2%	3.4%	4.4%	32.6%	60.2%	
		1D	32.5%	33.5%	59.3%	29.3%	56.1%	5.9%	5.8%	34.4%	35.4%	60.6%	36.0%	62.7%	5.4%	6.2%	
bowtie2 + eXpress	Average gene expression level in shoots for genes located on chromosome (tpm):	1A	9.1	2.2	2.4	20.5	11.0	16.8	11.5	13.5	2.7	3.4	26.3	14.9	24.0	13.9	
		1B	7.4	15.3	8.2	1.8	2.0	8.6	15.8	13.0	24.7	13.2	2.4	2.6	12.9	24.6	
		1D	7.6	8.6	14.8	8.9	14.7	1.9	1.9	13.8	15.2	24.3	16.0	28.1	2.7	3.2	
		1A+ 1B+ 1D															
	Percentage of gene expression originating from:	1A	37.8%	8.5%	9.4%	65.7%	39.6%	61.5%	39.4%	33.6%	6.4%	8.3%	58.8%	32.6%	60.6%	33.4%	
		1B	30.7%	58.5%	32.3%	5.8%	7.2%	31.5%	54.1%	32.2%	58.0%	32.3%	5.3%	5.7%	32.7%	58.9%	
		1D	31.5%	33.0%	58.3%	28.5%	53.2%	7.0%	6.5%	34.2%	35.7%	59.5%	35.8%	61.7%	6.7%	7.7%	

Table S3. Comparison of accuracy for two methods of read alignment and quantification. Reads from nullitetrasonic wheat lines were aligned and quantified using the pseudo aligner and quantifier kallisto (upper part of table) or the conventional aligner bowtie2 combined with eXpress for quantification (lower part of table). Gene expression on chromosome group 1 (the chromosome group for which whole chromosomes were added or deleted in these lines) was compared to assess accuracy of alignment and quantification.