

Table S2. Main genes of wheat (*Triticum aestivum* L.) determining yield components.

Approach / locus	Gene/protein class	Function/Orthologs	Alleles/Modifiers/Regulators	Affected yield components	References
Transcription regulators (floral) – inflorescence architecture – grain number					
QTL, mutant analyses <i>FT FLOWERIN G LOCUS</i>	<i>Ppd-D1a</i> (<i>Photoperiod-1</i>) a member of the pseudo-response regulator gene family (PPR)	Controls photoperiod-dependent floral induction; regulates inflorescence architecture and paired spikelet development by modulating the strength of the floral promoting signal (<i>FT</i>); ortholog in barley	<i>Ppd-1</i> – major inhibitory effect on paired spikelet formation by regulating the expression of <i>FT</i> <i>Ppd-D1a</i> loss of function allele – photoperiod-insensitive, promotes constitutive LD response	Temperate cereals – allelic variation in <i>Ppd-1</i> influences sensitivity to long-day conditions. Modulated expression of <i>Ppd-1</i> and <i>FT</i> can be used to form a wheat inflorescence with a better arrangement and increased number of grains in spikelets	(Beales et al. 2007; Boden et al. 2015; Li et al. 2011; Shaw et al. 2013; Shaw et al. 2012; Turner et al. 2005)
Natural mutants	<i>FRIZZY PANICLE</i> (<i>WFZP</i> ; <i>T. aestivum</i>), <i>branched head</i> [†] (<i>bh</i> [†] <i>T. turgidum</i>) APETALA2/ Ethylene Response Factor	A key player in spikelet development during the floret meristem transition phase; non-canonical spike-branching; orthologs in barley, rice, maize	Three <i>FZP</i> homologous genes <i>WFZP</i> – recessive, coding mutations of <i>WFZP-D</i> – cause the SS phenotype, the most severe in <i>FZP-D</i> lesions + <i>FZP-A</i> frameshift mutants	Multirow spike (MRS) in hexaploid wheat and tetraploid ‘Miracle-Wheat’, significantly more grains per spike, higher spike yield	(Dobrovolskaya et al. 2015; Poursarebani et al. 2015)
Haplotypes, NILs, gene isolation, overexpression in <i>A. thaliana</i>	<i>TaTEF-7A</i> ; TaTEF-7A transcript elongation factor	<i>OsTEF1</i> regulates the tillering process by inducing expression of cytochrome P450	<i>TaTEF-7A</i> allele – the highest expression in young spikes and developing seeds; overexpression in <i>A. thaliana</i>	Increased grain number, enhance grain length, silique number and silique length	(Paul et al. 2012; Zheng et al. 2014)
Genome identification, gene cloning, phylogenetic	<i>NFYAs</i> , <i>NFYBs</i> , <i>NFYCs</i> Nuclear Factor Y (NF-Y): subunits NF-YA, NF-YB, NF-YC	Essential role in root development and nitrogen and phosphorus usage; orthologs in maize (<i>ZmNF-YB2</i>) and other species	Each of the NF-Y subunits is encoded by multiple genes (18 <i>NFYAs</i> , 34 <i>NFYBs</i> , 28 <i>NFYCs</i>). <i>TaNFYA-B1</i> is a low nitrogen and low phosphorus-inducible gene –	Increased grain yield and root development under control, low N and low P conditions, high yield with less fertilizer input	(Qu et al. 2015; Yadav et al. 2015)

analysis, transgenic overexpression of <i>TaNf-YB4</i>	that bind to the CCAAT box, a ubiquitous eukaryotic promoter element		increase in nitrogen and phosphorus uptake, upregulation of the expression of both nitrate and phosphate transporters in roots + down-regulation of miR169	Overexpression stimulates lateral branching. Transgenics increased grain yield by 20–30%.	
QTL <i>Gpc-B1</i> , cloning, RNAi	<i>NAM-B1</i> NAC transcription factor	<i>NAC</i> family genes regulate NAC protein level and localization and participate in transcription complex including microRNA: specific to plants	NAC accelerates senescence and improves grain protein, zinc and iron content; RNA reduction delayed senescence	Grain size	(Uauy et al. 2006 a,b; rev. function Olsen et al. 2005)
Gene isolation, overexpression in transgenic wheat lines	<i>TaNAC2-5A</i> – a nitrate inducible and cereal-specific NAM, ATAF, and CUC (NAC) transcription factor	<i>TaNAC2-5A</i> binds to the promoter regions of the genes encoding nitrate transporter and glutamine synthetase; involved in nitrate signaling; members in other species	Overexpression of <i>TaNAC2-5A</i> in wheat enhanced root growth and nitrate influx rate	Higher grain yield and higher nitrogen accumulation in aerial parts and allocated more nitrogen to grains in a field experiment	(He et al. 2015)
RNAi	<i>TaABCC13</i> ; <i>TaABCC13</i> functional transporter	Functionally important for grain development and detoxification of heavy metals.	Silencing of <i>TaABCC13</i> reduced PA in mature grains and developmental defects	Grain development	(Bhati et al. 2016)
Genes of cytokinin metabolism – plant architecture – grain size					
Haplotype variants	<i>TaCKX6-D1</i> ; CKX – cytokinin dehydrogenase	CKX enzymes irreversibly degrade cytokinins; temporal and spatial control of cytokinin level; orthologs in barley, rice (<i>OsCKX2</i>) and family members in other species	Five haplotypes <i>a-e</i> . Haplotype <i>TaCKX6-D1a</i> associated with higher grain weight – decreased expression relative to haplo b in 8 DAP seeds; novel allele <i>TaCKX6a02</i>	Grain weight, grain size, filling rate	(Lu et al. 2015; Zhang et al. 2012)
Recombinant inbred lines (RIL) QTL	<i>TaCKX4</i> ; CKX - cytokinin dehydrogenase	As above	Significant association of copy number variation of <i>TaCKX4</i> with flag leaf chlorophyll content after anthesis and grain weight	Grain weight	(Chang et al. 2015)
Gibberellin signaling – plant architecture – culm (stem) robustness/hardiness					

Natural mutations	<i>Rht-B1</i> and <i>Rht-D1</i> , <i>Rht-B1c</i> DELLA proteins that share an N-terminal DELLA domain	GR genes, transcriptional regulators that negatively regulate GA signaling, suggested regulation of GATA-like transcription factor; ortholog of <i>Arabidopsis GAI</i> and <i>SLN1</i> in barley	GA insensitive alleles of the <i>Rht-B1</i> and <i>Rht-D1</i> loci; semidominant mutations (more than 20); truncated proteins lacking the DELLA motif cannot respond to GA3; <i>Rht-B1c</i> partially dominant or co-dominant for plant height, differed from <i>Rht-B1a</i> by one 2 kb <i>Veju</i> retrotransposon insertion, primarily responsible for the extreme dwarfing effect	Reduced plant height and a compact lodging-resistance phenotype, effect on seed dormancy, and photosynthesis	(Pearce et al. 2011; Peng et al. 1999; Sun and Gubler 2004; Wen et al. 2013)
Natural mutation, RIL, fine mapping	<i>Rht8</i> ; as above	Reduced cell elongation; reduced sensitivity to brassinosteroids	Not known	Shorter intermodal segments and culm, improved lodging resistance; used in dry environments	(Gasperini et al. 2012)
Cell division/proliferation regulators – grain size					
QTL – rice, comparative genomics, cloning, TILLING	<i>TaGW2</i> (<i>GRAIN WIDTH 2</i>) <i>OsGW2</i> encodes an E3 RING ligase	<i>TaGW2-A</i> and <i>-D</i> act in both the cell division and late grain-filling phase; ortholog in rice	Homologs in the A, B, D genomes <i>TaGW2</i> – down-regulation, significant reduction in endosperm cell number; <i>gw2-A1</i> – significant increase of grain size and weight	Grain size and weight	(Bednarek et al. 2012; Hong et al. 2014; Simmonds et al. 2016; Su et al. 2011)
Comparative genomics, haplotypes	<i>TaTGW6</i> indole-3-acetic acid-glucose hydrolase	Low expression of <i>TaTGW6</i> is associated with low IAA content and high grain weight; ortholog in rice (<i>TGW6</i>)	<i>TaTGW6-a</i> , <i>TaTGW6-A1b</i> – low TGW; <i>TaTGW6-A1a</i> (3 SNPs), <i>TaTGW6-b</i> (InDel mutant), <i>TaTGW6-c</i> (null mutant) – last two low or lack of expression and significant increase in grain size and weight	Thousand grain weight (TGW) and yield	(Hanif et al. 2016; Hu et al. 2016)
Comparative genomics	<i>TaGS-D1</i>	Regulate stigma length and stigma extension in rice; ortholog of rice <i>OsGS3</i>	InDels in the introns of the gene between genotypes – higher or lower TGW	Grain weight and grain length	(Zhang et al. 2014)
VIGS	<i>TaCYP78A3</i>	Affects the extent of	Specifically expressed in wheat	Grain size: 11–48%	(Ma et al.

silencing, overexpression (<i>A. thaliana</i>)	cytochrome P450 CYP78A3 protein	integument cell proliferation	reproductive organs; positively correlated with the final seed size	increase in <i>Arabidopsis</i> seed size	2015b)
Comparative genomics, transgenic rice	<i>TaGS5-3A-T</i> , serine carboxypeptidases (SCPs), members of the <i>a/b</i> hydrolase proteins in the S_10 protein family	Promotes cell division by regulating cell cycle genes resulting in large grain size generated by an increased cell number; ortholog in rice <i>OsGS5</i>	<i>TaGS5-3A-T</i> preferentially expressed in young spikes and developing grains, significantly correlated with larger grain size and higher thousand kernel weight	Larger grain size, larger kernel and yield	(Ma et al. 2015a)
Sucrose, starch metabolism – plant architecture – grain yield					
Transgenic wheat, field trials	<i>HvSUT1</i> , sucrose transporter (SUT)	Stimulates storage protein synthesis	Up-regulated gene expression of positive and negative regulators of sugar signaling and assimilate supply	Increased grain yield and micronutrient concentration	(Saalbach et al. 2014; Weichert et al. 2010)
Comparative genomics, haplotypes	<i>TaSus1</i> and <i>TaSus2</i> sucrose synthase SUS	Sucrose synthase catalysis is the first step in the conversion of sucrose to starch	Loci: <i>TaSus2-2A</i> , <i>TaSus2-2B</i> , <i>TaSus1-7A</i> , and <i>TaSus1-7B</i> main variations within the introns; significant differences between the haplotypes correlated with TKW differences	Larger grain size	(Hou et al. 2014)
Haplotypes	<i>TaCWI</i> , cell wall invertase (CWI),	Wheat anther-specific invertase genes; hydrolyzes sucrose into glucose and fructose; orthologs in rice	<i>TaCWI-4A</i> , <i>TaCWI-5D</i> – SNPs <i>TaCWI-5B</i> – no polymorphism; <i>TaCWI-5D</i> significantly associated with TKW	Higher thousand kernel weight	(Jiang et al. 2015)
Natural mutant	<i>T6P/SnRK1</i> trehalose6-phosphate (T6P)	T6P is the intermediary in TRE synthesis formed from glucose-6-phosphate and UDP-glucose; source/sink interaction	Not known	Expected function to determine grain yield	(reviewed by Lawlor and Paul 2014)
RNAi	<i>GWD</i> GWD – glucan, water-dikinase, the primary enzyme required for starch	unclear	RNAi-mediated down-regulation (endosperm-specific promoter) – a decrease in starch phosphate content and an increase in grain size (+ increased level of α -amylase activity	Increases in grain size, early vigor and plant biomass	(Ral et al. 2013; Ral et al. 2012)

	phosphorylation		in the aleurone layer during grain maturation)		
Induced mutant	<i>Tin</i> (tiller inhibition)	Reduced tillering due to early cessation of tiller bud outgrowth during the transition of the shoot apex from the vegetative to the reproductive stage.	Upregulation of a gene induced by Suc starvation, downregulation of a <i>Suc-inducible</i> gene, and reduced Suc content in dormant tin buds	Reduced tillering (branching)	(Kebrom et al. 2012)