

Table S1. Main genes of barley (*Hordeum vulgare*) determining yield components.

Approach / locus	Locus/gene/protein class	Function/orthologs	Modifiers/regulators	Affected yield components	References
Transcription factors and other regulators – spikelet development, inflorescence architecture and growth – grain number					
Mutant	<i>Vrs1</i> (<i>SIX-ROWED SPIKE 1</i>); a homeodomain-leucine zipper I-class (HD-Zip I) type transcription factor	Cell division and development in the lateral spikelets; no orthologs	<i>Vrs1.b</i> – wild type allele, <i>VRS1</i> – loss of function mutant; modifiers – <i>INT</i> alleles (see below)	<i>VRS1</i> – six-row spikes, reduction in the number of tillers <i>Vrs1.b</i> – two-rowed spikes	(Komatsuda et al. 2007; Lundqvist et al. 1997; Ramsay et al. 2011)
Mutant	<i>INT</i> (<i>INTERMEDIUM</i>); HD-ZIP I-class homeobox transcription factor	Modifier of lateral spikelet fertility; orthologs: maize <i>TEOSINTE BRANCHED 1</i> (<i>TB1</i>) and barley <i>Photoperiod-1</i> (<i>Ppd-H1</i>)	<i>INT-C</i> alleles – quantitative variation; <i>vrs1.a</i> in six-rowed (loss of function allele) is complemented by <i>Int-c.a</i> allele and in two-rowed <i>Vrs1.b</i> is complemented by <i>int-c.b</i>	Variations in male fertility and grain development from two-rowed to six-rowed	(Lundqvist et al. 1997; Lundqvist and Lundqvist 1988; Ramsay et al. 2011)
Mutant, positional cloning	<i>Ppd-H1</i> (<i>Photoperiod-1</i>), a member of pseudo-response regulator (<i>PPR</i>) family genes	The major determinant of photoperiod response; ortholog in wheat	<i>ppd-H1</i> mutant, reduced photoperiod responsiveness altered circadian expression of the photoperiod pathway gene <i>CONSTANS</i> and reduced expression of its downstream target, <i>FT</i>	Induction of flowering, highly advantageous in spring-sown varieties	(Turner et al. 2005)
Natural mutation, positional cloning, gene isolation	<i>com2</i> (<i>compositum 2</i>); AP2/ERF transcription factors	Branch repression pathway; orthologs in tetraploid and hexaploid wheat	<i>COM2</i> expression is regulated by <i>Six-rowed spike 4</i> influencing branch repression; <i>HvIDS1</i> is a putative down-stream target of <i>COM2</i>	Spikelets are replaced by lateral secondary spikes; significantly more grains per spike, higher spike yield	(Poursarebani et al. 2015; Sharman 1994)

Mapping MLOC_43830	<i>HvAP2 (APETALA 2)</i> ; transcription factor two, AP2 DNA-binding domain and miR172-binding site in its last exon	Perturbed interaction between miR172 and its corresponding binding site in the mRNA of <i>AP2</i> like transcription factor; orthologs in rice, wheat and maize	Mutant alleles – internode elongation is reduced in both the culm and the spike	A key controller of barley spike density	(Houston et al. 2013)
Databases MLOC_65101.1	<i>HvNAC005</i> ; NAC-a6 transcription factor	Positive regulator of senescence	Over-expression – delayed development combined with precocious senescence; up regulation of genes involved in secondary metabolism, hormone metabolism, stress, signaling, development and transport	Nutrient remobilization related to senescence process	(Christiansen et al. 2016; 2011)
Mutant, mapping and cloning by sequencing	<i>Blade-On-Petiole 1 (BOP1)</i> and <i>BOP2</i> ; putative transcriptional coactivator in <i>A. thaliana</i>	Developmental growth of vegetative and reproductive organs; partially conserved function between <i>Arabidopsis</i> and barley	<i>BOP1/2</i> controls internode length and causes pleiotropic changes in spike development; haplotype diversity	Internode length, spike development	(Jost et al. 2016)
Natural mutations, mapping	<i>dsp (dense spike)</i>	Controlling the barley spike and spikelet characteristics	28 alleles	A reduction in length of rachis internodes, shorter culms, compact spikes, smaller volume of dew (reduced risk of fungal infections and pre-harvest sprouting)	(Shahinnia et al. 2012)
Spontaneous mutation	<i>ert-a (erectoides-a)</i>	A second dense spike locus	43 alleles, <i>ert-a.6</i> shorter plants and kernels, reduced grain yield	Resistance to lodging, semi-compact spikes with dense basis, reduced culm length, improved culm strength, susceptibility to powdery mildew, virus and nematode diseases	(Druka et al. 2011; Franckowiak and Lundqvist 2012) (mapping)

Induced mutations, mapping	<i>ert-k.32</i> (<i>erectoides-k.32</i>)	Controlling culm length and spike architecture	<i>ert-k.32</i> – induced, approved as a cultivar; eight allelic <i>ert-k</i> mutants	Resistance to lodging; alternative to pleiotropic GR alleles of the <i>Sdw1</i> and <i>Uzu1</i>	(Franckowiak and Lundqvist 2012; Kristensen et al. 2016)
Genes of cytokinin metabolism – plant architecture – grain number					
RNAi	<i>HvCKX1</i> cytokinin dehydrogenase enzyme HvCKX1	CKX enzymes irreversibly degrade cytokinins, temporal and spatial control of cytokinin level; orthologs in wheat and other species	Multigene family Decreased expression of the <i>HvCKX1</i> gene by RNAi silencing and CKX enzyme in the developing spikes	Higher number of seeds and spikes	(Zalewski et al. 2010)
RNAi	<i>HvCKX9</i> cytokinin dehydrogenase enzyme HvCKX9	As above	One of multigene family Decreased expression of the <i>HvCKX9</i> gene by RNAi silencing and CKX enzyme in the developing spikes	Higher number of seeds and spikes	(Zalewski et al. 2014; Zalewski et al. 2012)
Gibberellin signaling and metabolism – plant architecture – culm (stem) robustness/hardiness					
Natural or induced mutations	<i>Sdw</i> (<i>semidwarf</i>); <i>Sdw1/Denso</i> locus	GR gene, GA-insensitive, GA signaling?	53 mutants; numerous different mother cultivars <i>Sdw1/Denso</i> locus – first reported allele <i>sdw1.c</i> ; second allele – <i>sdw1.a</i> ; third <i>sdw1.d</i> the most important – main allele in modern European; fourth <i>sdw1.e</i>	Semi-dwarf, reduction of culm and rachis internode length and increased lodging resistance, reduced grain size	(Druka et al. 2011; Franckowiak and Lundqvist 2012)
Mutant Hv287 Map based cloning	<i>sdw3</i> (<i>semidwarf 3</i>) former <i>gai</i>	GA-insensitive, GA signaling	Monogenic recessive trait; lack of gene identity (unidentified)	Mild semi-dwarf, lodging-resistant	(Börner et al. 1999; Vu et al. 2010)
Mutant	<i>sdw4</i> (<i>semidwarf 4</i>)	GA-insensitive, GA signaling	<i>sdw4.ba</i> – recessive, short-culm mutant with enlarged flag leaves	semi-dwarf, enhanced lodging-resistant; enlarged flag leaf	(Franckowiak and Lundqvist 2012)
Natural mutants	<i>HvSln1</i> (<i>Slender1</i>) – mutation in DELLA proteins	GA-insensitive, GA signaling; ortholog of <i>Rht1</i> in wheat and <i>GAI</i> in	<i>sln1b</i> allele – single amino acid substitution in DELLA domain, recessive loss of function alleles	Pleiotropic effects: semi-dwarf, slender-type plant architecture	(Chandler et al. 2002; Wen et al. 2013)

		<i>Arabidopsis</i>	(translational stop codon)		
Mutants	<i>Grd5</i> (<i>GIBBERELLIN-RESPONSIVE DWARF</i>), CYPSSA – cytochrome P450 <i>ent</i> -kaurenoic acid oxidase	Involved in GA metabolism, the enzyme catalyzes the first step of the gibberellin biosynthetic pathway from <i>ent</i> -kaurenoic acid to GA12; ortholog in maize	<i>grd5</i> – gibberellin-responsive, three independent mutants contain mutations in a gene encoding a member of the CYP88A subfamily of cytochrome P450 enzymes,	Dwarfing	(Helliwell et al. 2001)
Brassinosteroid (BR) signaling and metabolism – plant architecture – culm length					
Natural mutation	<i>Uzu1</i> (MLOC_5176; <i>UZU DWARF</i>) brassinosteroid hormone receptor BRASSINOSTEROID-INSENSITIVE HvBRI1	GR gene, BR insensitive, deficient in brassinosteroid biosynthesis; ortholog of the rice <i>D61</i>	Mutation in the brassinosteroid receptor causing an His-857 to Arg exchange in the kinase domain of the receptor <i>uzu1.a</i> allele – monogenic recessive mutation	Short-culm in six-rowed barley in East Asia, highly resistant to lodging, upright plant architecture, low leaf angles (high photosynthetic efficiency; facilitates dense crop planting, heat sensitive)	(Chono et al. 2003; Dockter et al. 2014)
Mutants	<i>brh</i> (<i>brachytic</i>)	Deficient in brassinosteroid biosynthesis	A group of mutants (27 semidwarf mutants in 18 independent genetic loci, e.g. <i>brh1</i> , <i>bhr4.j</i> , <i>bhr8.ad</i>)	Reduced culm length, shorter kernels with lower weight but with an increased number of kernels per inflorescence, upright plant architecture	(Dahleen et al. 2005; Franckowiak and Lundqvist 2012)
Other – plant architecture (culm and awn length), grain size					
Mutants	<i>ari</i> (<i>breviaristatum</i>) <i>ari-e GP</i> (<i>erectoides</i> in cv. Golden Promise)	Semi dwarfing mutant	32 <i>ari</i> mutant alleles in Bowman near-isogenic lines, several hundred at the Nordic Genetic Resource Centre <i>ari-e</i> recessive mutant – Golden Promise (Liu et al. 2014)	Reduced awn length, a number of mutants have shortened culm, and upright arch	(Druka et al. 2011; Franckowiak and Lundqvist 2012)
Homologs	<i>PcG</i> Polycomb group protein complexes (PcG)	Involved in seed development and in response to external ABA, ultimately leading to	Four homologs: <i>HvFIE</i> , <i>HvE(Z)</i> , <i>HvSu(z)12a</i> , and <i>HvSu(z)12b</i> . Gene expression is responsive to abscisic acid (ABA).	Seed size	(Kapazoglou et al. 2010)

		chromatin compaction and gene silencing			
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