Figure 1 Photoperiod and spectral distribution of three light regimens.
(a) Schematic representation of photoperiod and light spectral quality in SW, LW, and LR treatment. The white and bright red boxes at the top represented the duration of ~320 µmol m^{-2} s^{-1} illumination (12h), the gray and pink boxes represented the duration of ~12 µmol m^{-2} s^{-1} illumination (10h), and the black box represented the duration of darkness (12h or 2h). (b) A real view of the light environment for wheat plants provided by LED lamps in SW, LW, and LR treatment. SW, short photoperiod + white LEDs; LW, long photoperiod + white LEDs; LR, long photoperiod + red LEDs.
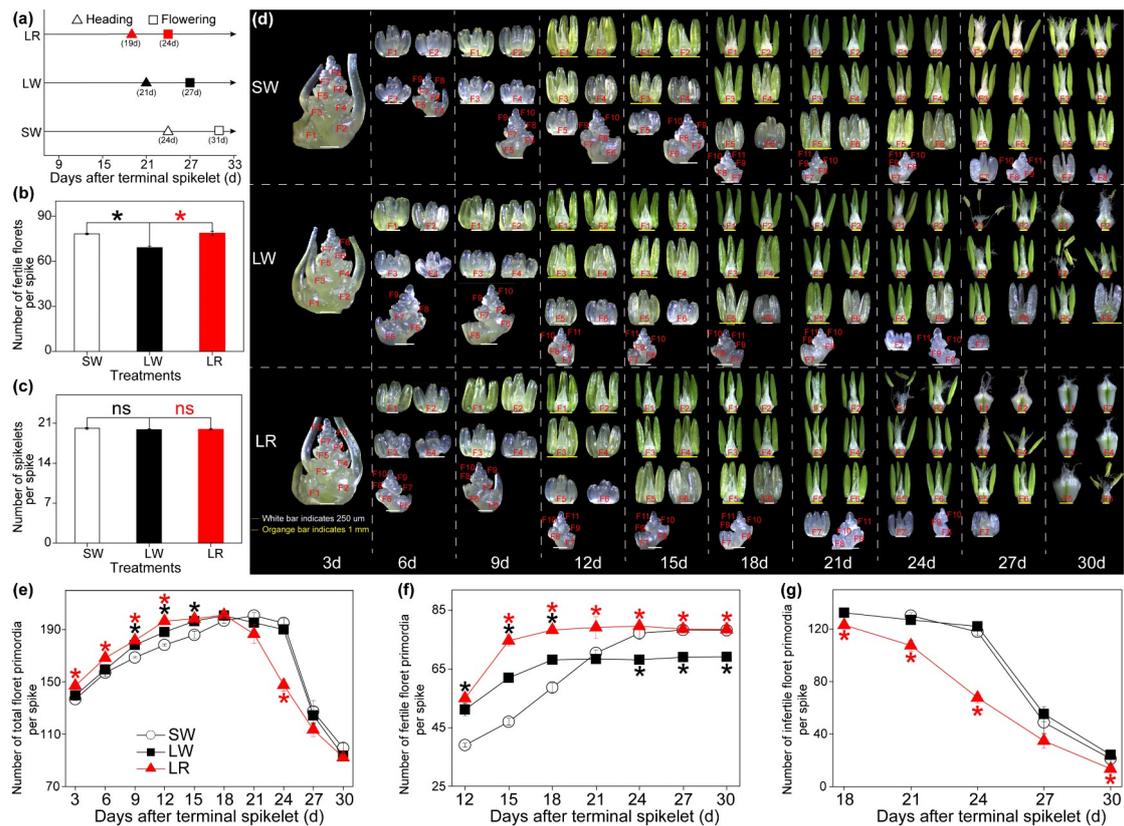
Figure 2 LR treatment accelerated flowering and increased the number of fertile florets per spike (NFFs) at flowering. (a) Representative graph depicting the development stages of wheat under three light regimens. (b) The number of fertile florets per spike at flowering. (c) The number of spikelets per spike at flowering. (d) The morphological changes of floret primordia (*x* axis, days after terminal spikelet stage). The letter + number on floret primordia represented primordia from the most proximal (F1) to the most distal (F11) with respect to the spike rachis. The dynamics of the number of total floret primordia (e), fertile floret primordia (f), and infertile floret primordia (g). Significant differences between treatments were indicated by asterisks (LSD test, *P < 0.05, ns, not significant, black and red asterisks represented the differences between LW *versus* SW and LR *versus* LW, respectively). Bars represented standard error (n = 6).
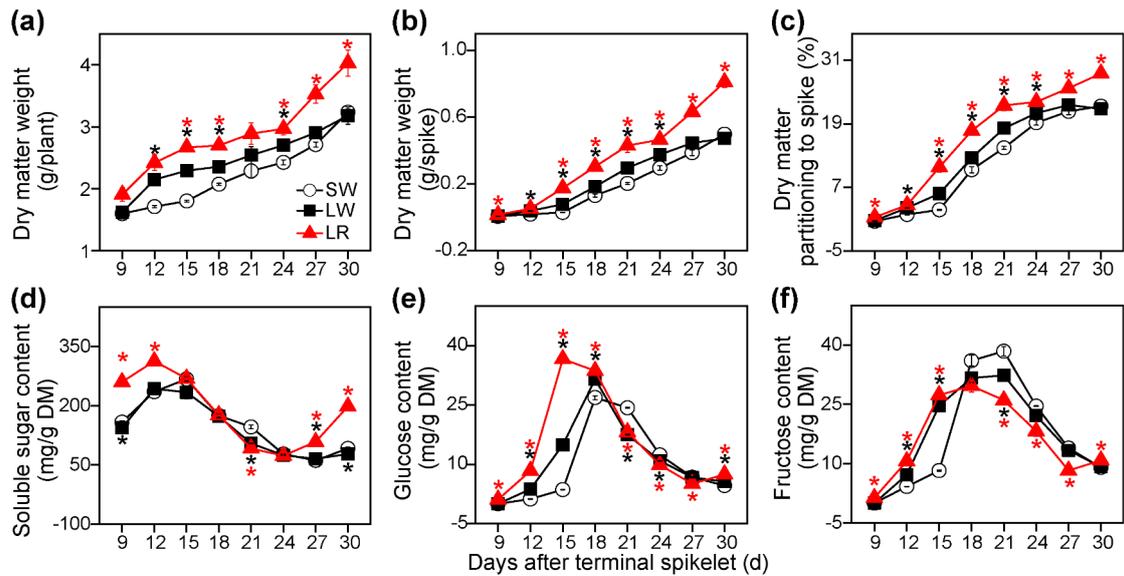
Figure 3 Effect of three light regimens on assimilate accumulation in wheat. (a) Dry plant weight. (b) Dry spike weight. (c) Dry matter partitioning to spike. (d) Soluble sugar content in the spike. (e) Glucose content in the spike. (f) Fructose content in the spike. Significant differences between treatments were indicated by asterisks (LSD test, *$P < 0.05$, black and red asterisks represented the differences between LW *versus* SW and LR *versus* LW, respectively). Bars represented standard error (n = 6 in a, b, and c; n = 3 in d, e, and f).
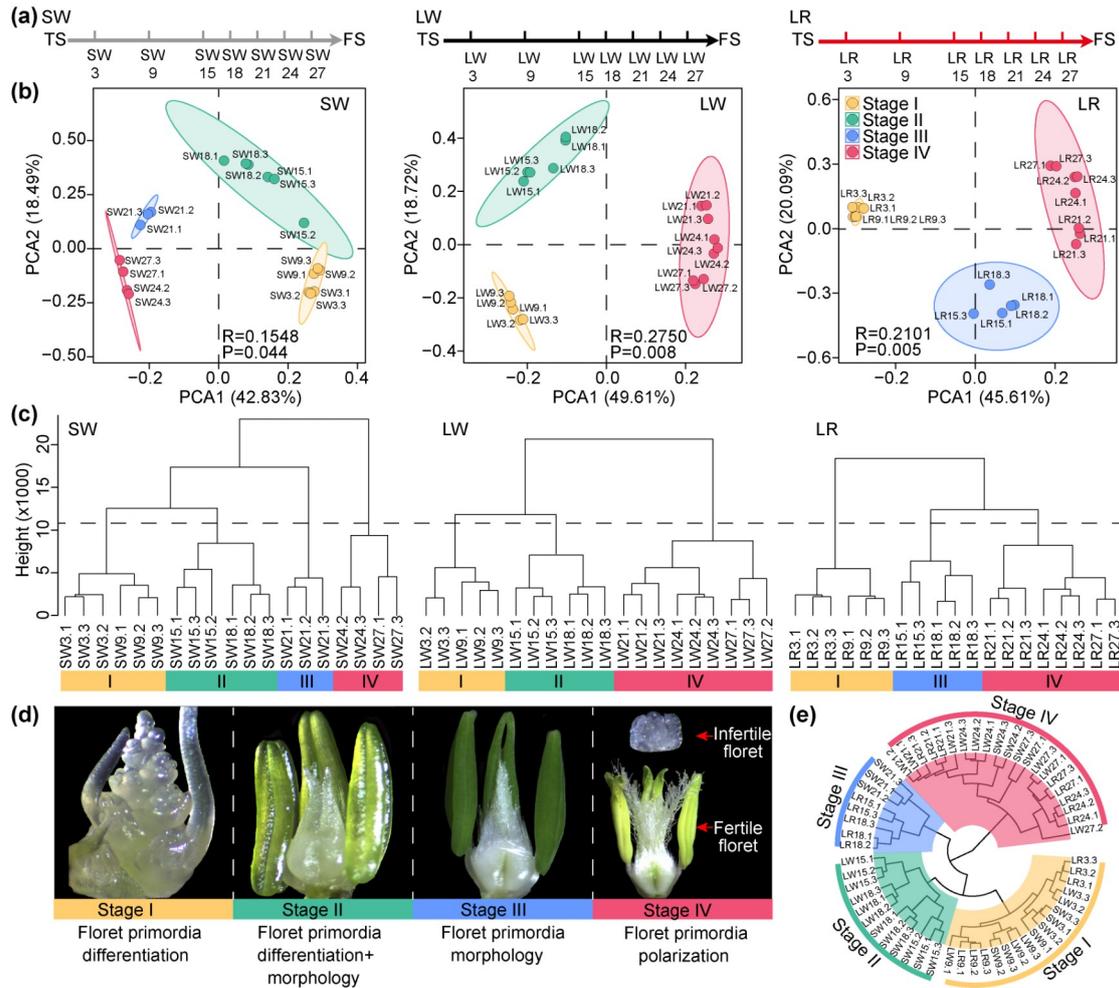
Figure 4 Samples collection and gene expression dynamics under three light regimens. (a) RNA-seq samples collected at an interval of six days (3-15) or three days (15-27) from the terminal spikelet stage (TS) to flowering stage (FS) in SW, LW, and LR treatment. Principal component analysis (PCA, b) and hierarchical clustering (c) of RNA-seq data showed distinct stages of floret primordia development in SW, LW, and LR treatment. Numbers represented sampling time and biological replicate. (d) Representative images of the floret primordium at distinct development stages. (e) A cluster dendrogram of all transcriptomes reflecting the similarity of gene expression in different light regimens.
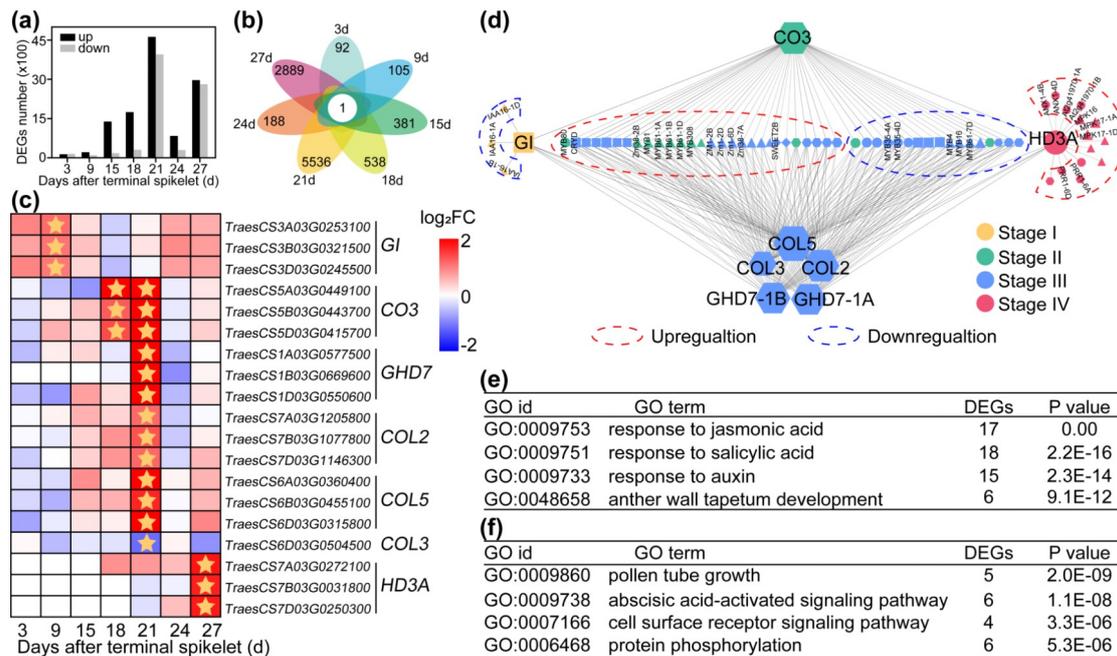
Figure 5 Regulatory network of key genes/homologs involved in long photoperiod-accelerated flowering. (a) The number of differentially expressed genes (DEGs) during floret development. (b) A Venn diagram showing the number of DEGs specifically expressed at different sampling times. (c) A heat map of key genes/homologs involved in the photoperiodic flowering pathway. Colors represented $\log_2$FC in expression levels of LW relative to SW. The star represented a significant level (absolute $\log_2$FC ≥ 1, FDR-adjusted P < 0.05). (d) The protein-protein interaction (PPI) analysis between key genes/homologs and functional DEGs. Node color represented that the gene displayed significantly different expression in Stage I (yellow), Stage II (green), 21 DAT (i.e., Stage III in SW and Stage IV in LW) (blue), and Stage IV (red), respectively. Node shape represented that the gene displayed functional categories, including light response (square), hormone metabolism (triangle), carbohydrate metabolism (diamond), flower development (circular), and more than one of the four functions (hexagon). The genes in the red and blue dotted boxes were up- and down-regulated, respectively, in LW compared to SW. (e) GO terms were significantly enriched in functional DEGs that interact directly with CO-like genes. (f) GO terms were significantly enriched in functional DEGs that interact directly with $HD3A$ gene.

(a)

DEGs number (x100) vs Days after terminal spikelet (d)
- up (black)
- down (gray)

(b) Venn diagram
- 3d: 213
- 9d: 42
- 15d: 5657
- 18d: 938
- 21d: 108
- 24d: 1209
- 27d: 763
- center: 0

(c) Gap statistic (k) vs Number of clusters k

(d) Module / log$_2$FC (−3 to 3)
Modules: i, ii, iii, iv, v, vi, vii
Days after terminal spikelet (d): 3 9 15 18 21 24 27

(e) Z-score — LW (black), LR (red)
Days after terminal spikelet (d): 3 9 15 18 21 24 27

GO_Term	DEGs	P value
i(293)		
ethylene activated signaling pathway	21	2.2E-16
response to chitin	15	2.2E-15
regulation of transcription, DNA templated	45	1.5E-09
salicylic acid mediated signaling pathway	7	2.0E-09
phloem or xylem histogenesis	9	2.5E-09
ii(3458)		
response to light stimulus	90	0.00
sporopollenin biosynthetic process	20	9.6E-24
pollen exine formation	23	7.5E-18
stamen morphogenesis	5	2.9E-04
specification of floral organ number	5	2.1E-03
iii(2818)		
plant type secondary cell wall biogenesis	44	2.2E-16
photosynthesis, light harvesting	50	2.2E-16
phenylpropanoid biosynthetic process	29	5.7E-12
carbohydrate transport	29	1.0E-08
flavonoid biosynthetic process	45	3.0E-06
iv(3174)		
nucleosome assembly	367	0.00
microtubule based movement	49	0.00
chromosome organization	126	5.6E-135
regulation of cell cycle	59	1.3E-43
DNA replication initiation	40	3.1E-38
v(1322)		
peptidyl serine phosphorylation	35	0.00
pectin catabolic process	21	0.00
regulation of pollen tube growth	19	1.1E-16
abscisic acid activated signaling pathway	47	7.2E-15
plant type cell wall loosening	20	1.1E-14
vi(748)		
jasmonic acid mediated signaling pathway	12	2.7E-11
positive regulation of autophagy	6	2.4E-09
stamen filament development	7	3.1E-09
regulation of floral organ abscission	6	2.4E-08
sterol metabolic process	10	4.7E-08
vii(569)		
regulation of cellular respiration	12	0.00
cellular response to red light	18	2.5E-29
fatty acid biosynthetic process	21	1.2E-11
lipid biosynthetic process	7	7.3E-09
carbohydrate metabolic process	18	4.8E-08

Figure 6 Transcriptional signatures of LR *versus* LW reflected flowering acceleration and NFFs increase. (a) The number of DEGs during floret development. (b) A Venn diagram showing the number of DEGs specifically expressed at different sampling times. (c) The optimal number of clusters according to the *k*-means function in R software. (d) Heat maps of coexpression clusters for 12382 DEGs. Colors represented log$_2$FC in expression levels of LR relative to LW. (e) The mean expression level across all genes and Go terms enriched significantly in different coexpression modules.
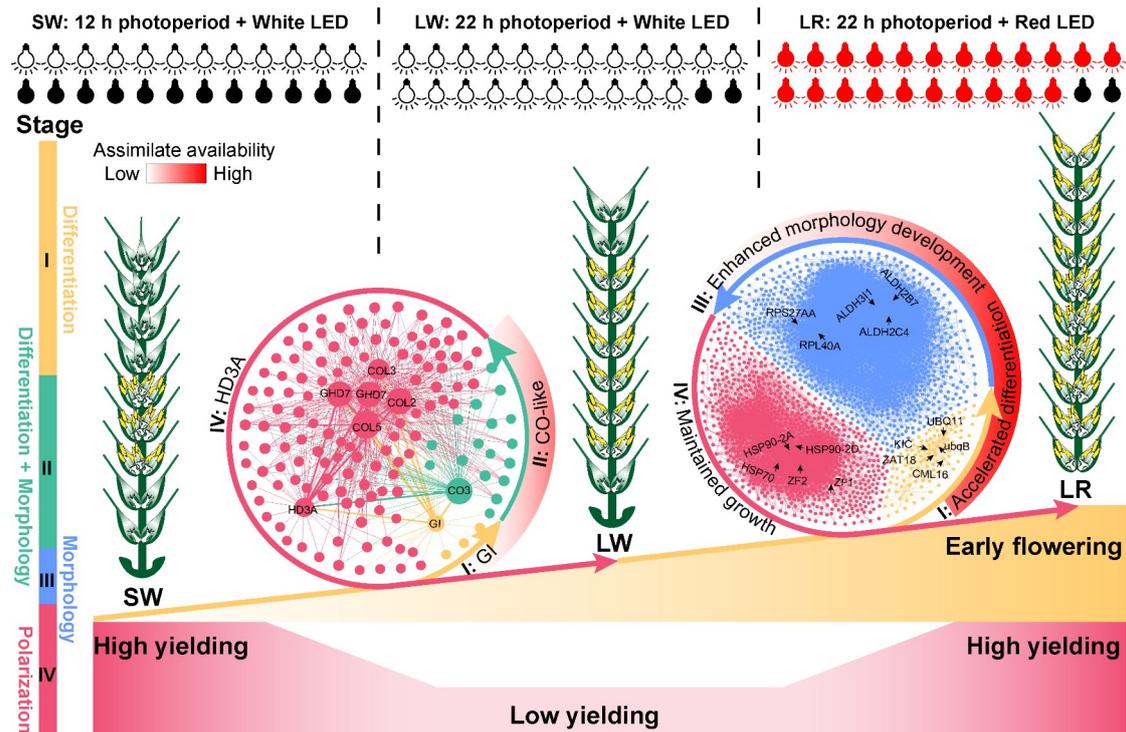
Figure 7 Regulatory network for LR-mediated "early flowering" and "high yielding". The development of all floret primordia in a wheat spike included four distinct stages: differentiation (Stage I), differentiation and morphology development concurrently (Stage II), morphology development (Stage III), and polarization (Stage IV). Compared to SW, LW treatment accelerated flowering by increasing assimilate availability moderately, advancing Stage IV initiation, and shortening the developmental time in Stage III, in which the *GI-CO-like-HD3A* framework played a central role; however, we could not afford to ignore the loss of fertile florets caused by LW treatment. Surprisingly, wheat plants treated with LR treatment flowered early and had high NFFs. LR treatment accelerated the differentiation rate of floret primordia in Stage I, shortened the time required in Stage II, enhanced assimilate availability and morphological development of floret primordia highly in Stage III, and maintained the continuous development of fertile floret primordia in Stage IV until flowering. A dynamic gene network centered on ubiquitin, calcium signaling, *ALDH*s, *ZF*s, and *HSP*s was predicted to play an important role in "early flowering" and "high yielding" in LR treatment.