

Fig. S1a. Breeding procedure of Huaduo 8



Fig. S1b Panicles of Huaduo 1 (H1), Huaduo 8 (H8) and their hybrid

A: Panicles of Huaduo 1 (H1), Huaduo 8 (H8) and their F₁ hybrid (F₁); B: Panicles of Luxiang 97-4x (T445, An autotetraploid rice), Huaduo 8 (H8) and their F₅ generation with high fertility; C: Panicles of Huaduo 3 × Huaduo 8 in F₃ generation

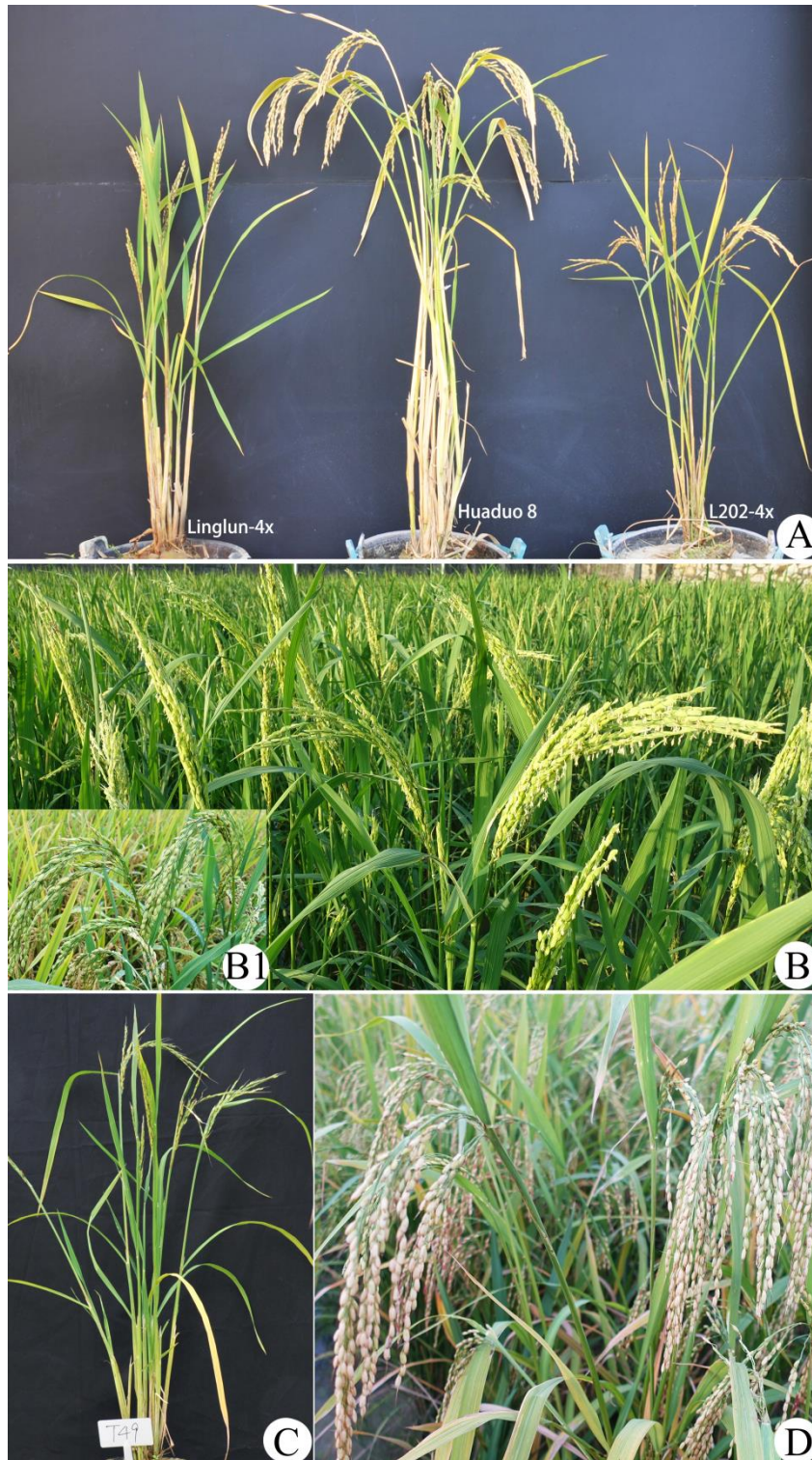


Fig. S1c Plant appearance of parents and F₁ hybrid generated by crossing with Huaduo 8 (H8)

[A: Linglun-4x (T428), Huaduo 8 (H8) and L202-4x (T43); B: Huaduo 8 at flowering stage, B1: Huaduo 8 at 15 days after flowering; C: Bengal-4x (T49, an autotetraploid rice with low fertility); D: F₁ of Bengal-4x × Huaduo 8]

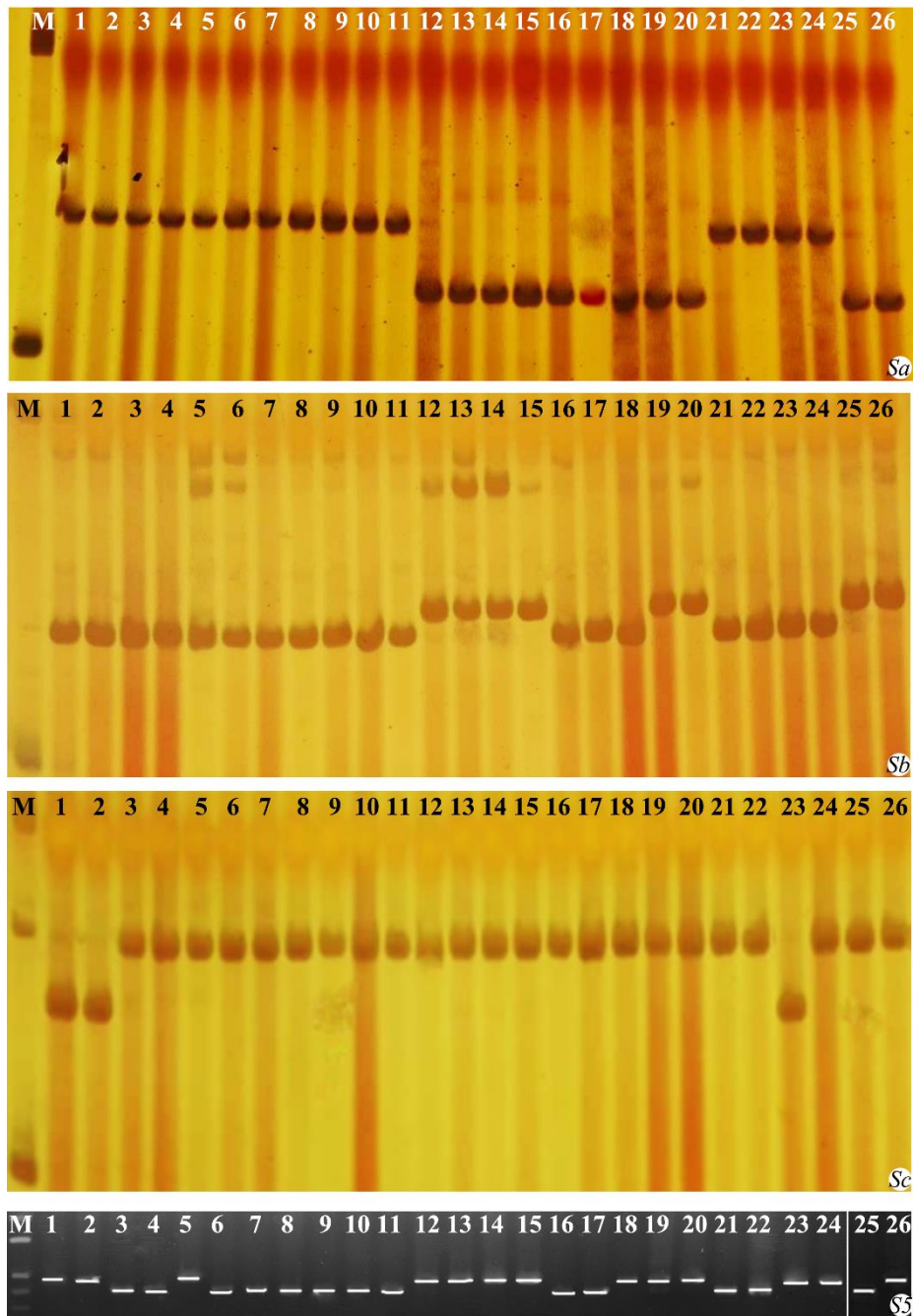


Fig. S2 Original images of genotypes of parental lines at pollen sterility loci (*Sa*, *Sb* and *Sc*) and *S5* locus detected by molecular markers.

First image indicates the genotypes at *Sa* locus, followed by (upper to lower) *Sb*, *Sc* and *S5* locus. M indicates DNA ladder, lanes 1-4 indicate control cultivars (typical *indica* and *japonica* cultivars), while lanes 5-26 indicate neo-tetraploid/autotetraploid rice lines (see the name of materials in Additional file 2: Table S1). Lanes 25 and 26 in *S5* were taken from another gel.

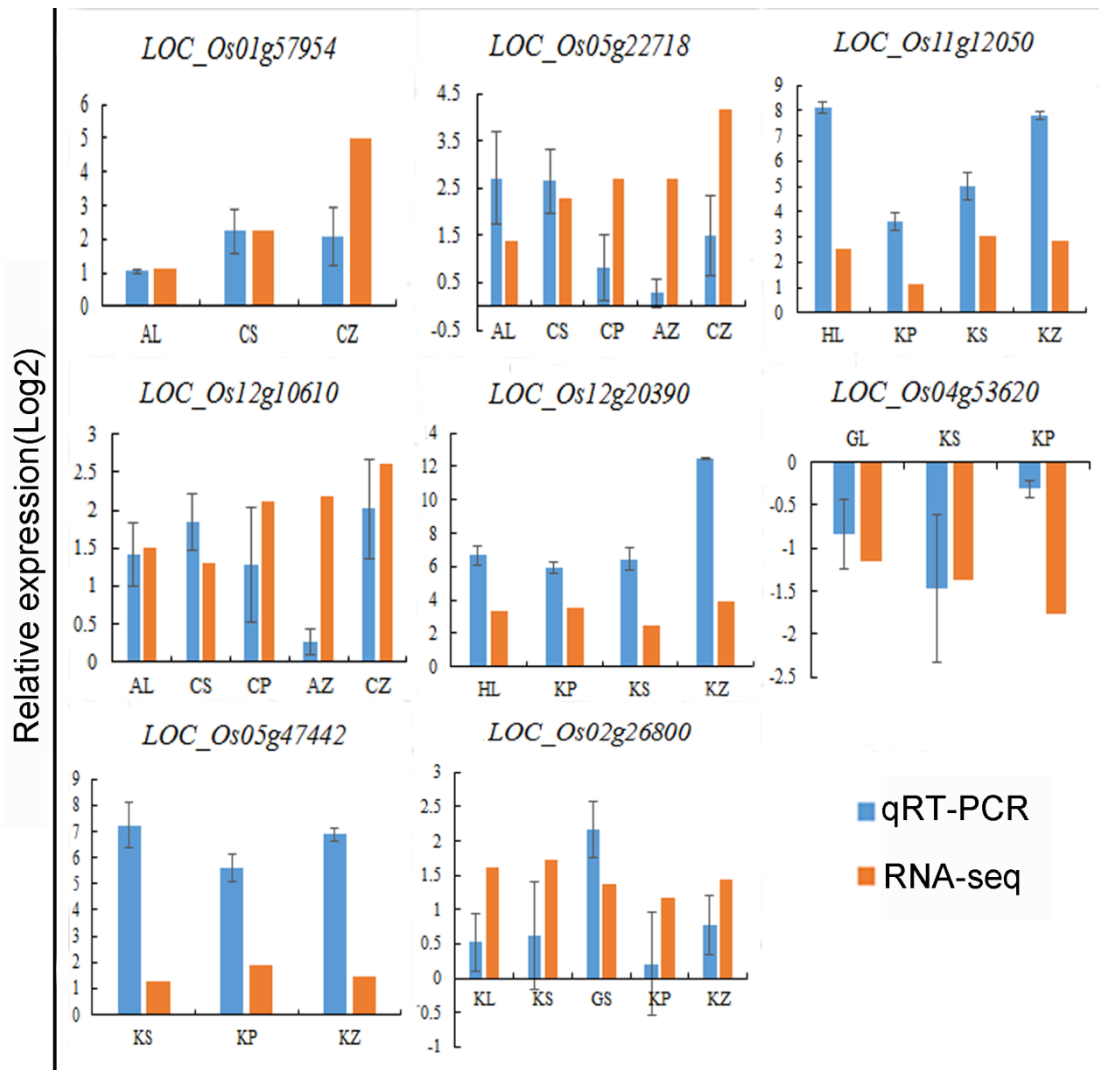


Fig. S3 qRT-PCR validation of the important genes detected in the present study (Codes of all X-axis are listed in Additional file 2: Table S4a)

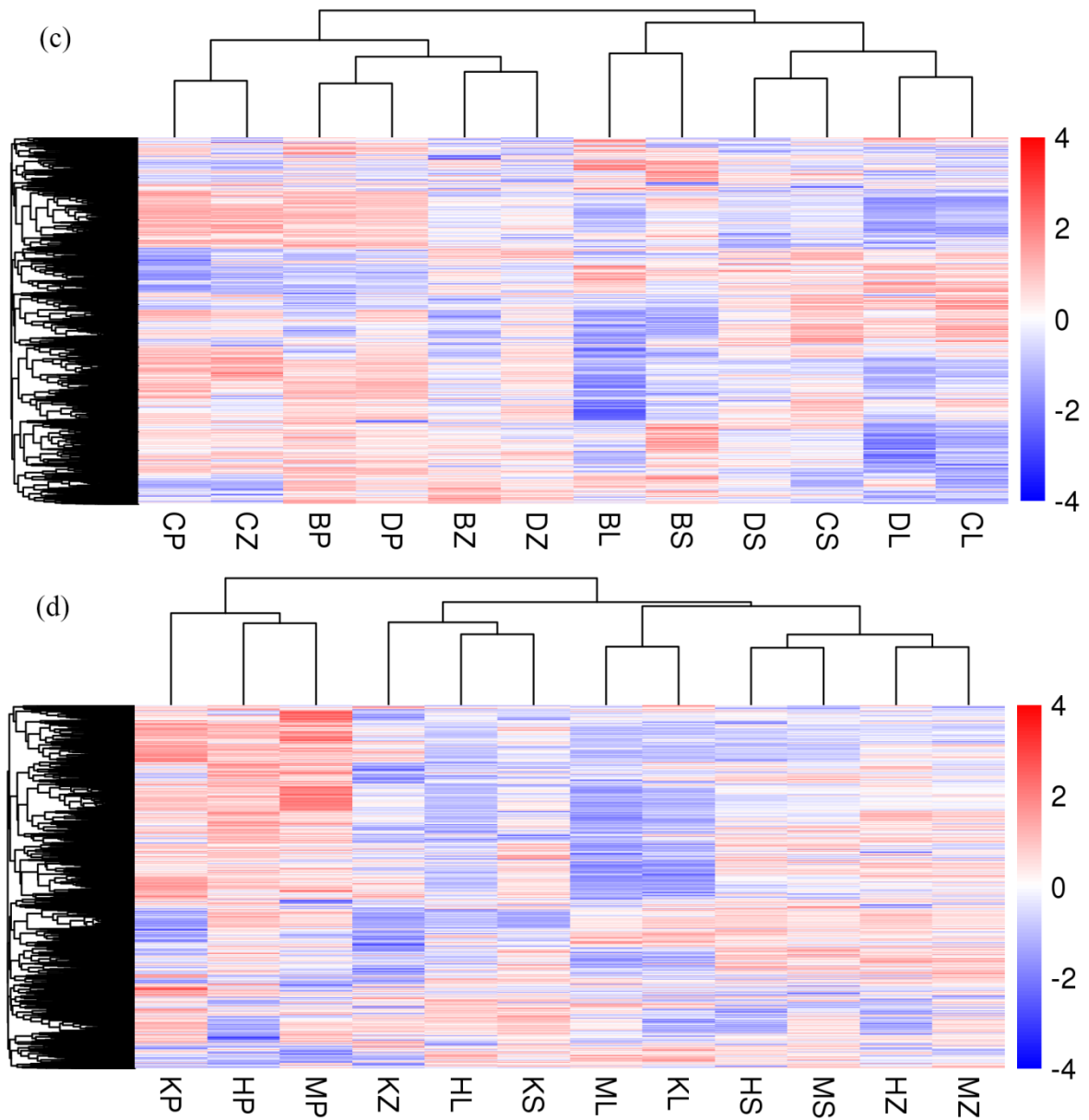


Fig. S4. Hierarchical clustering analysis of all expressed genes in F₁ hybrid and their parents based on transcriptome data

(a): F₁ hybrid (H1×H8) and its parents before flowering; (b): F₁ hybrid (H1×H8) and its parents 5 days after flowering; (c): F₁ hybrid (T485×H8) and its parents before flowering; (d) F₁ hybrid (T485×H8) and its parents 5 days after flowering. Codes of all X-axis are listed in Additional file 2: Table S4a

Hybrids	(H1xH8)F ₁								(T485xH8)F ₁								
	L ₀	S ₀	P ₀	Z ₀	L ₅	S ₅	P ₅	Z ₅	L ₀	S ₀	P ₀	Z ₀	L ₅	S ₅	P ₅	Z ₅	
A. Biological process																	
GO:0055114																	
GO:0005975																	
GO:0044267																	
GO:0016310																	
GO:0006796																	
GO:0006793																	
GO:0058007																	
GO:0043687																	
GO:0006464																	
GO:0043412																	
GO:0006468																	
GO:0050794																	
GO:0010467																	
GO:0050789																	
GO:0006350																	
GO:0044262																	
GO:0006810																	
GO:0051234																	
GO:0051179																	
GO:0043436																	
GO:0019752																	
GO:0006082																	
GO:0042180																	
GO:0009308																	
GO:0044281																	
GO:0015979																	
GO:0065004																	
GO:0006323																	
GO:0034728																	
GO:0065003																	
GO:0043933																	
GO:0019538																	
GO:0022607																	
GO:0006334																	
GO:0034631																	
GO:0046022																	
GO:0031497																	
GO:0071103																	
GO:0006412																	
GO:0031326																	
GO:0000900																	
GO:0009880																	
GO:0010468																	
GO:0045449																	
GO:0051171																	
GO:0060255																	
GO:0019219																	
GO:0031323																	
GO:0010556																	
GO:0019222																	
GO:0055085																	
GO:0006520																	
GO:0034641																	
GO:0005976																	
GO:0006519																	
GO:0009811																	
GO:0044106																	
GO:0006812																	
GO:0009607																	
GO:0016051																	
GO:0034637																	
GO:0046394																	
GO:0044283																	
GO:0044085																	
GO:0016053																	
GO:0034660																	
GO:0006457																	
B. Molecular function																	
GO:0016491																	
GO:0016773																	
GO:0004672																	
GO:0004674																	
GO:0016301																	
GO:0003554																	
GO:0001883																	
GO:0001882																	
GO:0000166																	
GO:0016798																	
GO:0004553																	
GO:0032559																	
GO:0008524																	
GO:0003700																	
GO:0032553																	
GO:0017076																	
GO:0032555																	
GO:0009055																	
GO:0003735																	
GO:0005198																	
GO:0005038																	
GO:0005215																	
GO:0020037																	
GO:0005506																	
GO:0046906																	
GO:0003565																	
GO:0008037																	
GO:0004497																	
GO:0001675																	
GO:00045735																	
GO:0050662																	
C. Cell component																	
GO:0016020																	
GO:0032991																	
GO:0005623																	
GO:0044464																	
GO:0044425																	
GO:0005840																	
GO:0005829																	
GO:0032993																	
GO:0000786																	
GO:0034357																	
GO:0009579																	
GO:0004234																	
GO:0005737																	
GO:0044444																	
GO:0009521																	
GO:0016021																	
GO:0031224																	
GO:0044424																	
GO:0015935																	
GO:0005622																	
GO:0043239																	
GO:0003232																	
GO:0009522																	
GO:0015934																	
GO:0043228																	
GO:0033279																	
GO:0043226																	

Fig. S5. Prominent functional categories of genes in the eight tissues detected by Gene ontology enrichment analysis before and 5 days after flowering in two hybrids
L₀, Flag leaf; S₀, Leaf sheath; P₀, Spikelet; Z₀, Main panicle axis before flowering; L₅, Flag leaf; S₅, Leaf sheath; P₅, Spikelet; Z₅, Main panicle axis 5 days after flowering

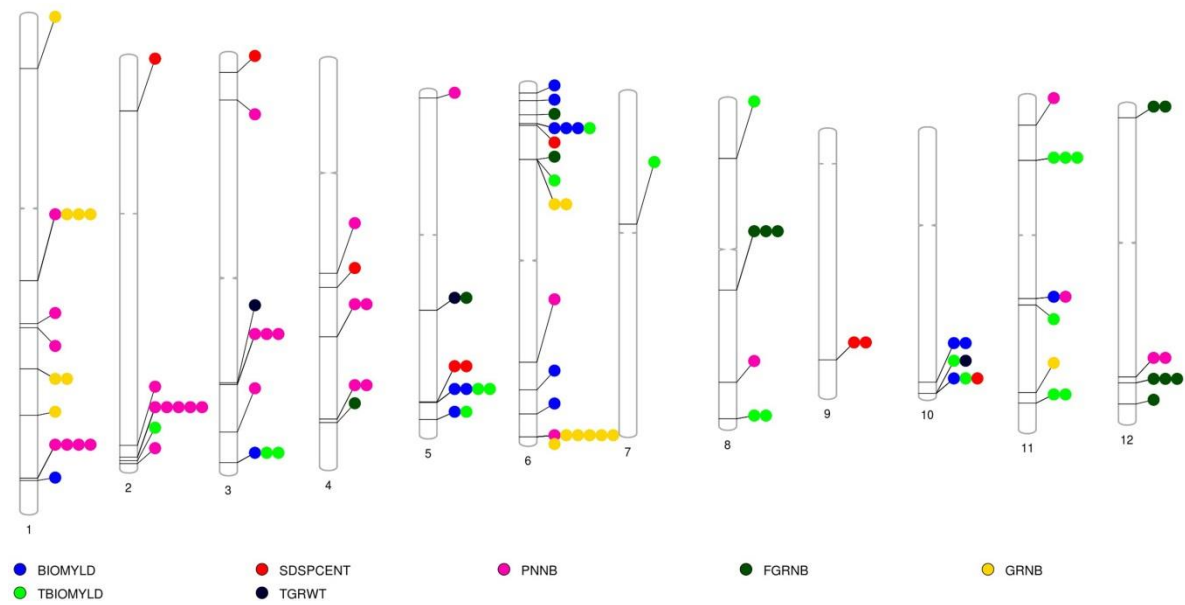


Fig. S6 Distribution of the common seven yield-related QTLs in our two F_1 hybrids, T449 \times H1 [17] and T452 \times H3 [16], compared to the DEGfu-sp-related QTLs detected in the present study. Seven rice yield-related QTLs included biomass yield (TBIOMYLD), biomass yield (BIOMYLD), filled grain number (FGRNB), grain number (GRNB), panicle number (PNNB), seed set percent (SDSPCENT) and 1000-grain weight (TGRWT).



Fig. S8 Samples used for RNA-seq analysis

A. Flag leaf; B. Leaf sheath; C. Spikelets; D. Main panicle axis