Supplementary Material

Novel *OsGRAS19* mutant, *D26*, positively regulates grain shape in rice (*Oryza sativa*)

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Table S1. All primers used in this study

The primer sets D26F and D26R were used to clone the full-length cDNA of *D26* gene. The primer sets of DX-F and DX-R were used to construct the complementation vector, and prime sets of Hyg-F and Hyg-R were used to validate complementation positive lines

Primer ID	Sequence (5' to 3')
RM5813-F	ATGGCGTCCCTCTCCCTTTCC
RM5813-R	AATGCAGCCCTAGCAATTCAGTCC
RM0316-F	GGAGTAGTTATATAGTATGA
RM0316-R	TGGAGAAGAATGTACGTTCG
RM0340-F	GCACCATCACCATCACTTAT
RM0340-R	ATCAATCCATCCACCATAGC
RM0344-F	CTTGTGTCTCCTGGTGTGTG
RM0344-R	CCTATAGAAGGGATGACGGA
RM0347-F	TCAGGGTTTAATCAATTTC
RM0347-R	TCATGTGTGTTGCATGCACA
RM0360-F	GCTAGGCTGCCCATCCATTT
RM0360-R	GGACGAAGGGATTATGTCAG
RM0369-F	TCTGAGAGTGAGAGTGAGAG
RM0369-R	CCAGAGAAGAAGAAGAAGCA
D26F	ATGGCGTACATGTGCGCGGACAGCGG
D26R	TCACCTCCAAGCAGACACAGTAAGCA
DX-F	TGCTCATTTTTTATGTCAGATTCTT
DX-R	AGTCGAAGAGGTCTTTCCAGTTCCAG
Hyg-F	TACACAGCCATCGGTCCAGA
Hyg-R	TAGGAGGGCGTGGATATGTC
GFP-F	ATGGTGAGCAAGGGCGAGGAGCTGT
GFP-R	TTACTTGTACAGCTCGTCCATGCCG
D26G-F	ATGGCGTACATGTGCGCGGACAGCG
D26G-R	TCCTCGCCCTTGCTCACCATCCTCCAAGCAGACACAGTAAGCAAT
DGFP-F	TTACTGTGTCTGCTTGGAGGATGGTGAGCAAGGGCGAGGAGCTGT
DGFP-R	TTACTTGTACAGCTCGTCCATGCCG
D26-Cas91F	CAGTGCCGCTCAGCAACTATGCC
D26-Cas91R	AACGGCATAGTTGCTGAGCGGCA
D26-Cas92F	CAGCCTCGACCTGAGGCTGCAC
D26-Cas91R	AACGTGCAGCCTCAGGTCGAGG
D26-gRNA-seq91F	GGAGAGTACGAGGTCAGCCTGAAC
D26-gRNA-seq91R	CTCCCAGGTTCTATCACAACGCCA
D26-gRNA-seq92R	TCGACTCTGATGGGTGGATGGAG
D26-gRNA-seq92R	CGACTAAGCGCGTCAGCGAAGTAG

OsACTIN1-QPCR-F	CCACTATGTTCCCTGGCATT
OsACTIN1-QPCR-R	GTACTCAGCCTTGGCAATCC
D26-QPCR-F	AGCTGTACCACCTTCTTGGCGACTC
D26-QPCR-R	CGGTTCAGGCTGACCTCGTACTCTC
GW7-QPCR-F	CCCCTAGCATCGACACCAAG
GW7-QPCR-R	CGGGTTCCAGCACTCCTCT
Gl2-QPCR-F	ATGCGGCTGTCGATTCTGTGAAG
GL2-QPCR-R	CCGAGAAGTCAGAGGATGCCATTG
GS5-QPCR-F	AGTGGACTGCTTCCAGGGAAG
GS5-QPCR-R	CACGCAGTACCGAGAACTGA
GW6a-QPCR-F	ACGATGATGAAGGTGTTGGTGAGG
GW6a-QPCR-R	TCTTCTTCTTCGTCTTCGTCTTGGT
GW8-QPCR-F	CCAGCCACTTCTGAAGACGGTAG
GW8-QPCR-R	AGCACTTGTGTCAACCCACCATC
GW2-QPCR-F	TTTTCAGTGCCGTCATACC
GW2-QPCR-R	GAGCCCGCGTAGCTTGTT
GW5-QPCR-F	TCCATCAAAGTGGGATGGATTAG
GW5-QPCR-R	CTTCCCAGATCCAGGACGAG
G53-QPCR-F	GAACTCCTGATCCATTCATAACGATT
G53-QPCR-R	CAAACAGCGAAACTTCTTCAAGAA
TGW6-QPCR-F	CAACGATCTCAGCACGAGCAAGTC
TGW6-QPCR-R	CGGTCAATGCAACGATCAGATGTGT

Table S2. Statistical analysis of agronomic traits

The double asterisks represent the significant difference confirmed by two-tailed t-test at $P<0.01$

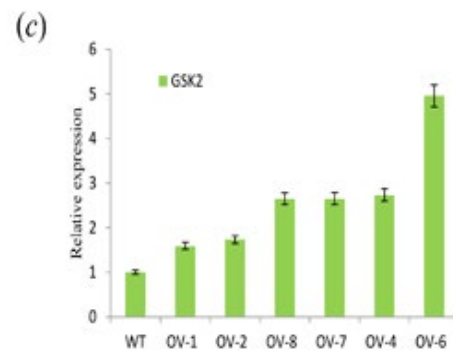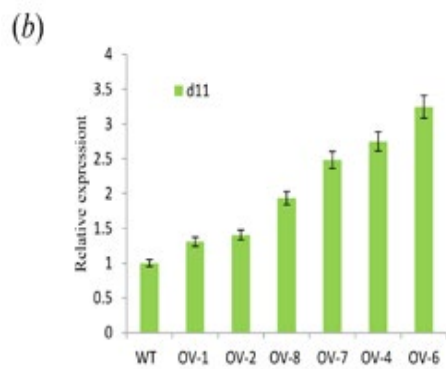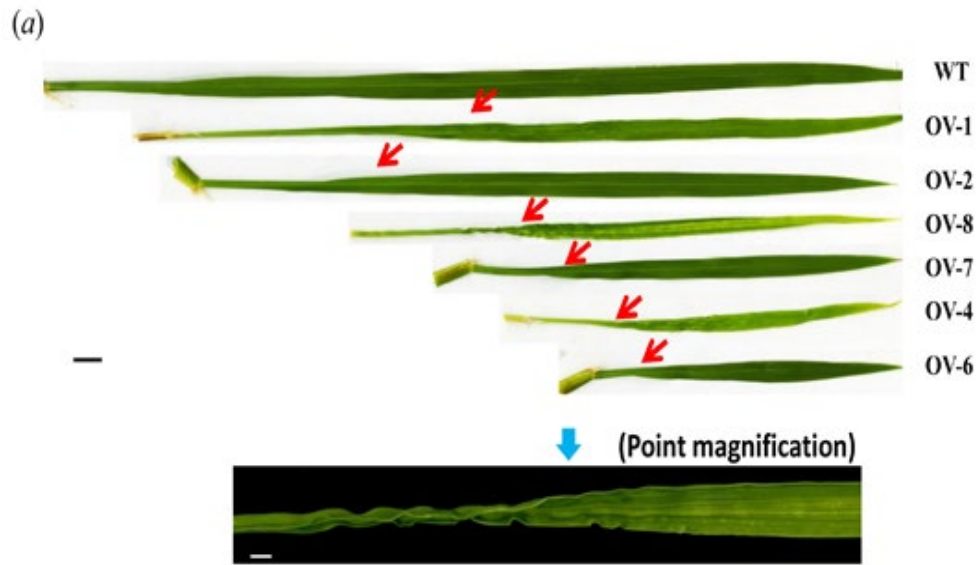|	Height (cm)	Tiller number	Panicle length (cm)	Seed number per panicle	Seed set (%)
D26-2	84.3±7.2**	8.7±2.6**	20.6±2.5**	188.9±47.4	56.7±10.9**
WT	121.5±4.9	13.1±4.1	26.4±3.9	200.2±26.1	69.2±4.6

Fig. S1. Leaf phenotype of overexpressing plants. Comparison of overexpression leaf of six lines and the leaf of WT (*a*). Expression levels of *d11* and *GSK2* gene in overexpression plants leaves of six lines compared with that of WT (*b*, *c*). Scale bar 1 cm.
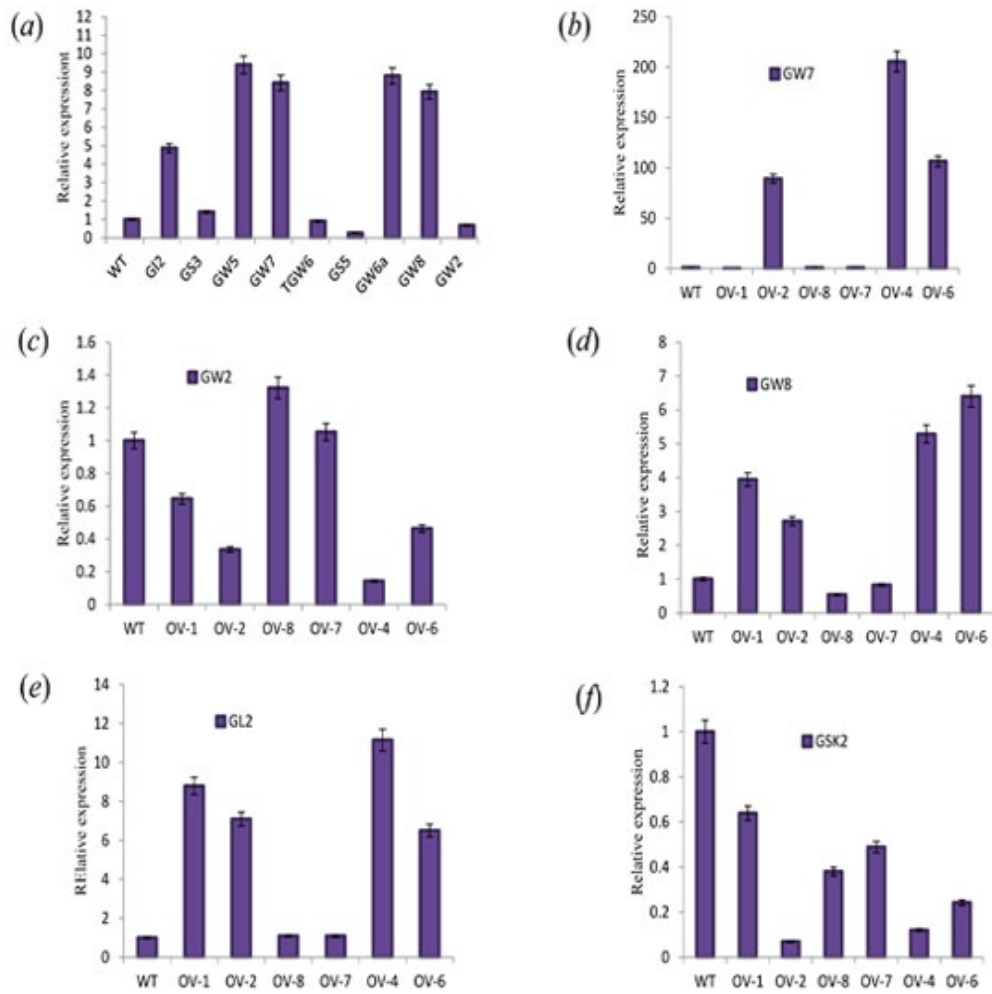
Fig. S2. qRT-PCR analysis of mature seed's expresion levels between the wild-type and overexpression plant. Expression levels of the nine known grain genes in OV-6 (*a*). Expression levels of *GW2* gene in overexpression plants between six lines and WT (*b*). Expression levels of *GL2* gene in overexpression plants between six lines and WT (*c*). Expression levels of *GW7* gene in overexpression plants between six lines and WT (*d*). Expression levels of *GW8* gene in overexpression plants between six lines and WT (*e*). Expression levels of *GSK2* gene in overexpression plants between six lines and WT (*f*).