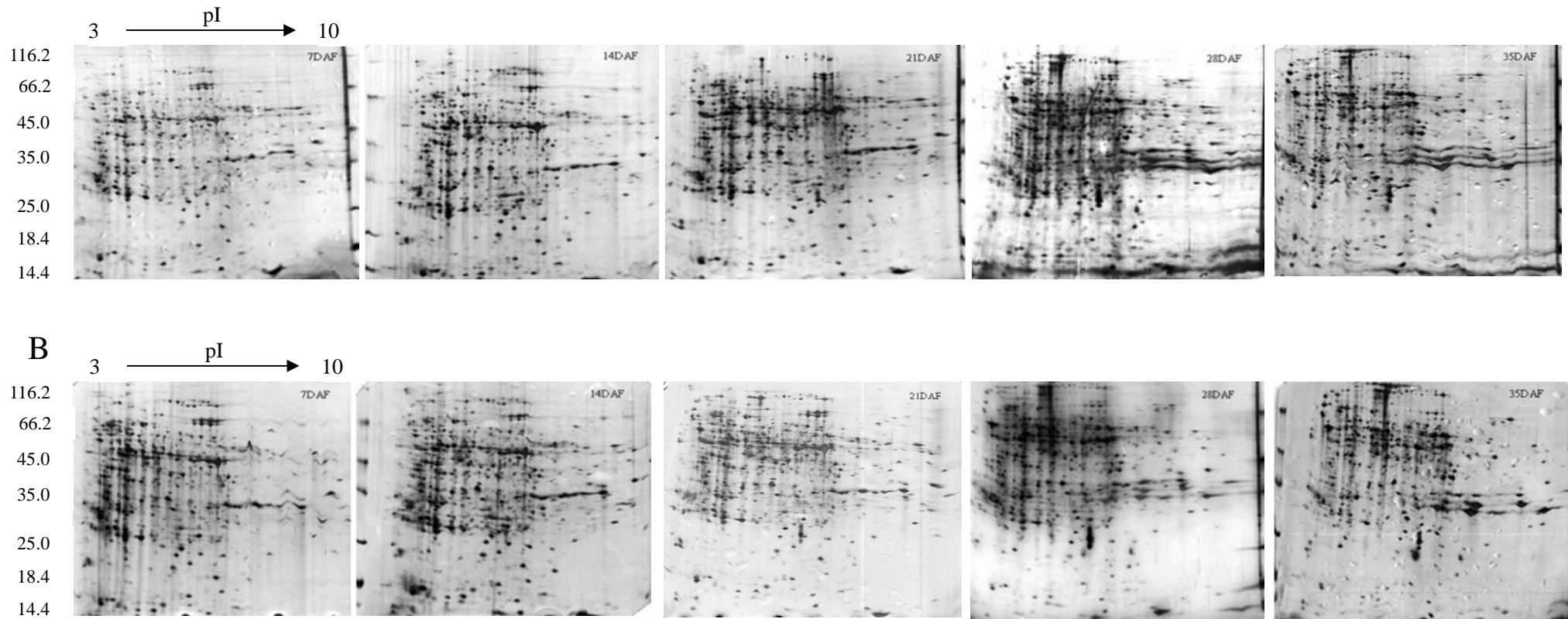


Supplementary Data

Differential proteomic expressions between superior and inferior spikelets of rice in response to varied nitrogen treatments

Supplementary figure



**Fig. S1** Separation of inferior spikelet proteins by 2-DE. **A:** 2-DE map of 5 grain-filling stages of inferior spikelets under TNA treatments. **B:** 2-DE map of 5 grain-filling stages of inferior spikelets under MNA treatment. 7, 14, 21, 28 and 35 DAF are days after flowering of sampled inferior spikelets. Proteins (150mg) were separated in the first and second dimensions by IEF tube gel (17cm×0.02cm) followed by 12% SDS-PAGE then visualized by silver staining. The changes in protein spots were calculated with Image-Master 5.0 software. For details see Materials and methods.

**Table S1. Primers used for qRT-PCR**

Spot No	Gene symbol	Sense primer (5'-3')	Antisense primer (5'-3')
5	Gi 75160868	GTCAACCCAACCTCATTACTG	AACATAGCCACCCGAAAGC
8	Gi 75143191	CGATGGTGATAATGGCTATGG	CCCTTGAGATAACTTTCCTTCC
17	Gi 75286324	GACCTTGCTCTTGCCTCTG	AACGCCTCCATCACTCAAC
29	Gi 122167725	CCGTGGTGAAGGTGGTATC	TGGAGGCAGATGGTTAAGATG
31	Gi 122236836	CCGTGGTGAAGGTGGTATC	TGGAGGCAGATGGTTAAGATG