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Identification of genes related to the regulation of anther and pollen development in Mu-type cytoplasmic male sterile wheat (*Triticum aestivum*) by transcriptome analysis

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Supplementary Tables

Table S1. Primers used for qRT-PCR

Gene ID	Description	Forward primer (5'-3')	Reverse primer (5'-3')
Traes_6BL_973 79BBEE	diacylglycerol kinase 4	ATGCAAATGGATGG GGAGCC	CCGGGCTGGAAG CTAAAAAC
Traes_7BL_CF 0F853C2	Exopolygalacturonase	AGAGCAAAGCCAG GAGATCG	CCGGCACGAGTAT CAACAAG
Traes_7BL_F4 A19E128	Diacylglycerol kinase theta	G TTCACACTGCCTT ACGTCG	GTCATCGTCCTTT GGGAGGG
Traes_5AL_98 E4B09F2	Calmodulin-like protein 1	TAGCCAACGCGAC GAACAAG	AAGCTCGTCCATT TTGCTCC
Traes_4AS_BC 5510ABB	PREDICTED: probable pectinesterase/pectinesteras e inhibitor 21	GTCAAGGAGGGCA CGTACAA	ATGAAGAAGCCG TTGCCGAT
Traes_7AL_351 65D4BE	Exopolygalacturonase	AACCCGACCATCAT CATCCC	GTTGCCTTTGCCA GTGATGG
Traes_4DS_A8 1FE9BC3	Phosphatidylinositol 4- phosphate 5-kinase 6-like	ATCGTCACCCGGAA AGAGTG	ACAGTGCAGGCC AAAGAACT
Actin		CTCCCTCACAACAA CCGC	TACCAGGAACTTC CATACCAAC

Table S2. The seed setting rates at the F₁ generation obtained by crossing between U706A and restorer lines

Male parent	Seed setting rate in Yangling (%)	Seed setting rate in Sanyuan (%)
	(34°29'N, 108°08'E)	(34°62' N, 108°93'E)
85S504	80.53±3.48	70.08±6.66
79107	88.99±1.76	58.46±18.51
223D3	85.79±8.97	57.79±3.33
M806	86.71±6.10	50.32±19.53
TM504	79.55±9.19	66.60±8.77
Annong0822	69.79±22.63	57.58±23.97

Table S3. The clear reads mapped to the reference wheat genome

Sample	U706A-1	U706A-2	U706A-3	706B-1	706B-2	706B-3
Total Pair Reads	21,794,022	19,691,447	16,804,696	16,659,523	22,966,775	19,599,843
Unmapped Pair Reads	7,313,398 (33.56%)	6,777,231 (34.42%)	5,761,231 (34.28%)	6,587,181 (39.54%)	7,738,337 (33.69%)	7,267,611 (37.08%)
Unique Mapped Pair Reads	13,817,410 (63.40%)	12,346,537 (62.70%)	10,553,349 (62.80%)	9,679,183 (58.10%)	14,583,902 (63.50%)	11,857,905 (60.50%)
Multiple Mapped Pair Reads	663,214 (3.04%)	567,679 (2.88%)	490,116 (2.92%)	393,159 (2.36%)	644,536 (2.81%)	474,327 (2.42%)
Mapping Ratio	66.44%	65.58%	65.72%	60.46%	66.31%	62.92%