

Table S1 | Clean-reads in BSA pools

#Sample_ID	Total_Reads	Total_Bases	Total_Reads_with_Ns	N_Reads%	A%	T%	C%	G%	N%	Error%	Q20%	Q30%	GC%
The CK (Weilyu11) pool	196869736	29231893396	63942	0.03	33.07	32.65	17.18	17.1	0	0.0416	97.58	92.02	34.28
Male sterile plants in M <sub>3</sub> pool	213597502	31776404012	68853	0.03	32.94	32.31	17.4	17.34	0	0.0403	97.86	92.97	34.74
Male sterile plants in M <sub>4</sub> pool	193903636	28835330095	61414	0.03	32.94	32.4	17.36	17.3	0	0.0404	97.86	92.91	34.66
Fertile pool in M4 pool	200865064	29766030004	80806	0.04	33.28	32.61	17.05	17.05	0	0.042	91.41	91.84	34.11

**Table S2.** The list of primers used in this study.

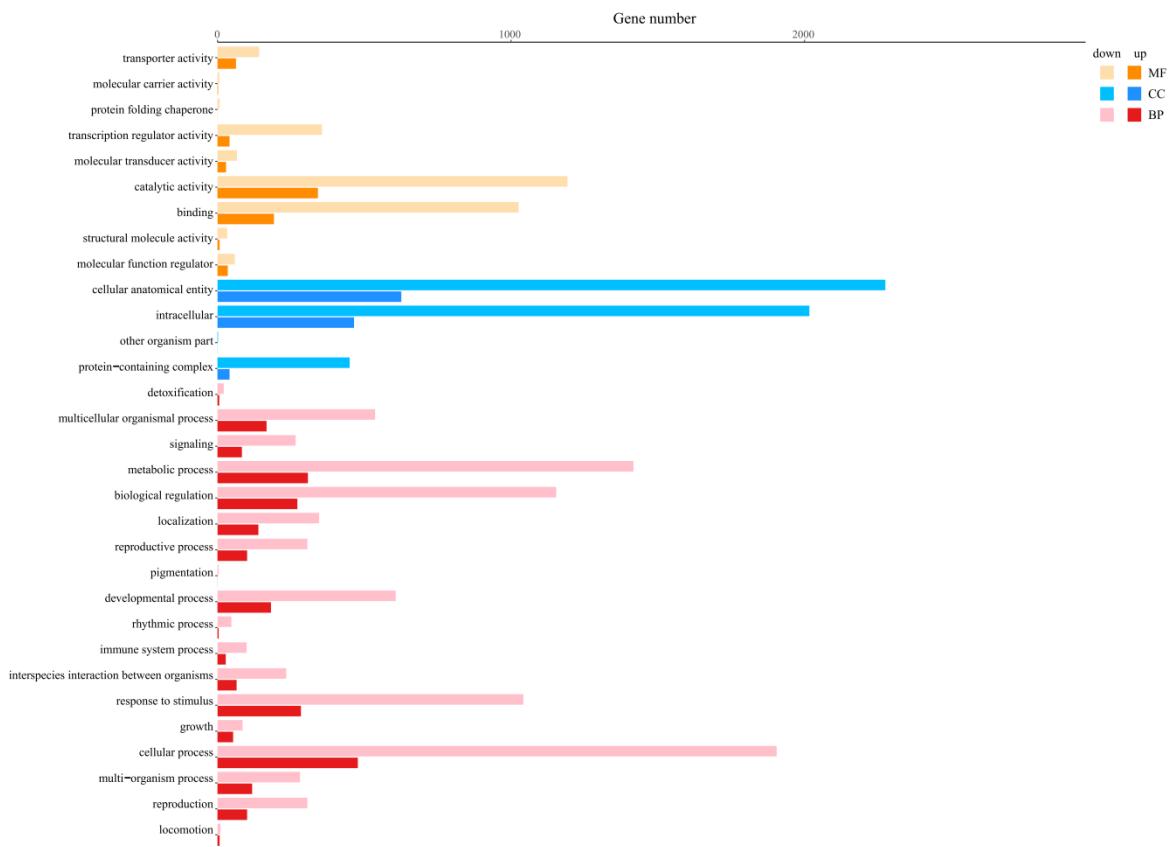
Primer	Sequence (5' to 3')	Purpose	Products (bp)	Primer	Sequence (5' to 3')	Purpose	Products (bp)
EVM0013050 1F	GCCGGAATTCCACTGCCTAT	Quantitative Real time RT-qPCR	162	EVM0030179 7F	TCTCCAAAGAGGCCGCTAC	Quantitative Real time RT-qPCR	187
EVM0013050 1R	TTCCCTAACAGCTTCTCCCC	Quantitative Real time RT-qPCR		EVM0030179 7R	GCCAGTTGAGTCTTCATGGTT	Quantitative Real time RT-qPCR	
EVM0001741 2F	GTAAACACGCTCGCTCGGTC	Quantitative Real time RT-qPCR	175	EVM0000114 8F	GGGTATGACAGACCGAGCAA	Quantitative Real time RT-qPCR	155
EVM0001741 2R	GTGGAAAACAATATTGATC	Quantitative Real time RT-qPCR		EVM0000114 8R	ATGCCCATGTCACTAGACCC	Quantitative Real time RT-qPCR	
EVM0018917 3F	GCGGTACCATGGCGATTCCGATGA	Quantitative Real time RT-qPCR	149	EVM0029279 9F	CGGTTCCCAAACCCGTAACA	Quantitative Real time RT-qPCR	152
EVM0018917 3R	CAGGTCGACTCAGTCAGTTGCCTA	Quantitative Real time RT-qPCR		EVM0029279 9R	ACTGGATTCCCTGCGTGTATG	Quantitative Real time RT-qPCR	
EVM0017094 4F	CCGGGGCGGTACCATGGCTATTGCA	Quantitative Real time RT-qPCR	169	EVM0019079 10F	AAGAGCAATGTCATCGACGCCA	Quantitative Real time RT-qPCR	177
EVM0017094 4R	CAGTGGTCTCACCTGCAGGTCTAGTTTCT	Quantitative Real time RT-qPCR		EVM0019079 10R	AGCCTCATATGTTCCATCTTCCAA	Quantitative Real time RT-qPCR	
EVM0018917 5F	CAGTGGTCTCAGCCCCGGCTCTGAACTATC	Quantitative Real time RT-qPCR	153	EVM0026892 11F	GTTTCCAAGGCACAAGGTGT	Quantitative Real time RT-qPCR	172
EVM0018917 5R	CTCAGGGCTGTCATGGTACTCTGCCAC	Quantitative Real time RT-qPCR		EVM0026892 11R	GGGATCATGGGACGAGA	Quantitative Real time RT-qPCR	
EVM0031043 6F	CTCATACAGTTATGAAAAATAAAATT	Quantitative Real time RT-qPCR	161	EVM0004172 12F	TCTTCGGAACCGACCACCTTG	Quantitative Real time RT-qPCR	149
EVM0031043 6R	ATGGAGAAACTCGAGTCAAATCT	Quantitative Real time RT-qPCR		EVM0004172 12R	TCAGCAATATGATTGAGACGGC	Quantitative Real time RT-qPCR	
Tubulin-R	TTCTTTATGGTTGGGTTGC	Quantitative Real time RT-qPCR	192				
Tubulin-F	GCTCGTCTACCTCCTTG	Quantitative Real time RT-qPCR					

F: forward primers; R: reverse primers. Primers were designed by NCBI, and tested by RCR of Tubulin.

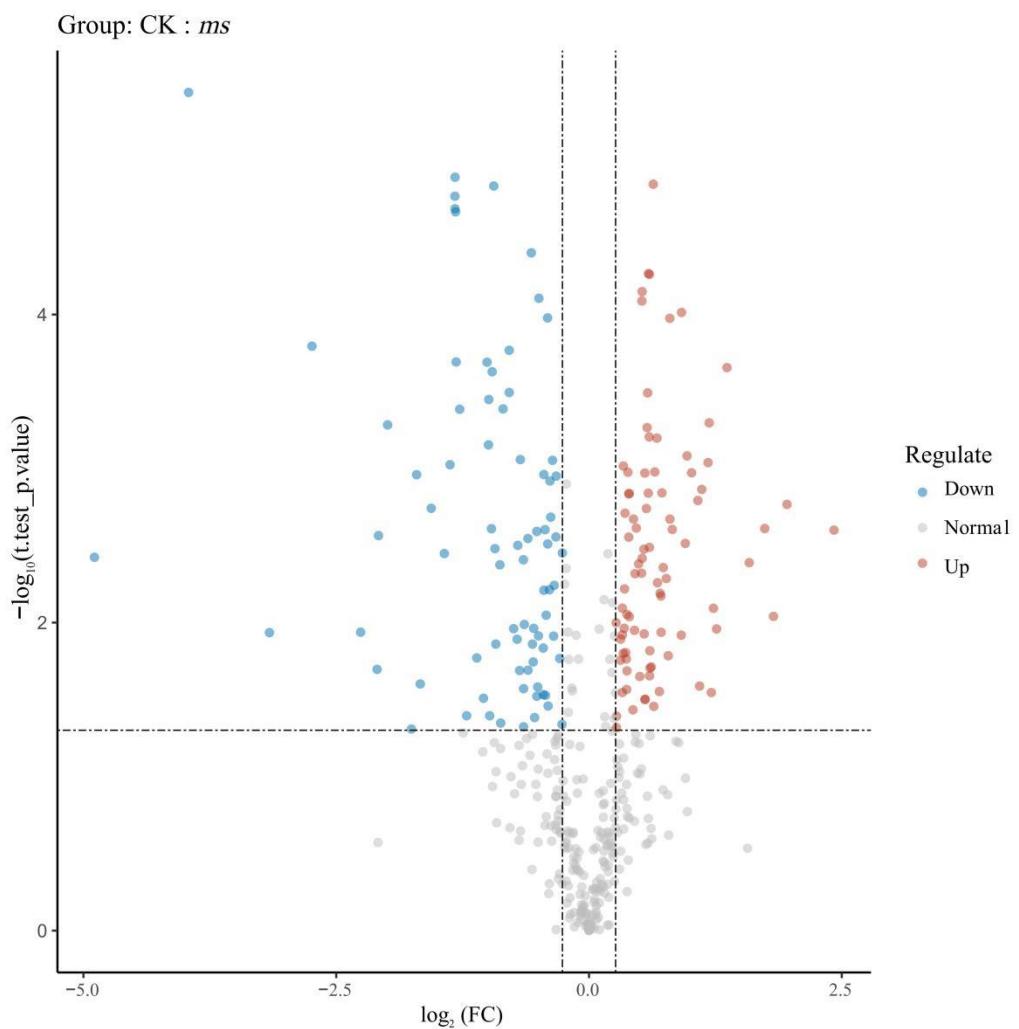
Table S3 | The significant PPI between EVM0001741 and six seed development related genes.

<b>Gene1</b>	<b>Arabidopsis homologs</b>	<b>Gene2 ID</b>	<b>Arabidopsis homologs</b>	<b>score</b>
EVM0001741	AT1G77390	EVM0030179	AT5G67260	0.77
EVM0001741	AT1G77390	EVM0000114	AT3G15030	0.40
EVM0001741	AT1G77390	EVM0029279	AT4G31400	0.46
EVM0001741	AT1G77390	EVM0019079	AT5G48600	0.65
EVM0001741	AT1G77390	EVM0026892	AT5G22800	0.405
EVM0001741	AT1G77390	EVM0004172	AT5G05560	0.67
EVM0004172	AT5G05560	EVM0026892	AT5G22800	0.97

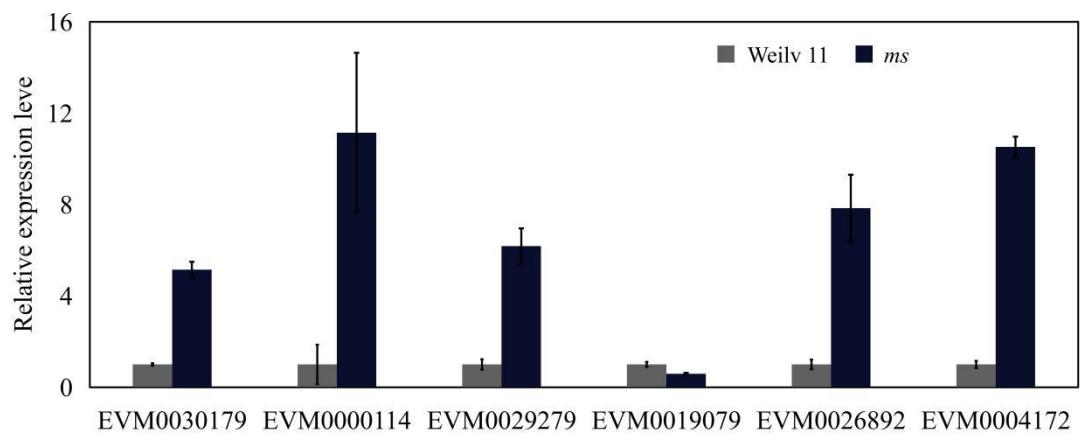
The critical score for protein-by-protein interaction was set at 0.40.



**Figure S1.** Gene ontology (GO) enrichment analysis for up- and down-regulated genes. The ordinate represents the detailed classification of GO term, and the abscissa represents the number of DEGs. MF(Molecular Function), BP (Biological Process) and CC (Cellular Component).



**Figure S2.** Volcano plots are using for visualizing differential metabolites between CK group and *ms* group. Pink and blue points represent the significant differential metabolites with  $p\text{-value}<0.005$  and  $|\log_2\text{FC}|>0.5$ .



**Figure S3.** Real-time PCR analysis of six genes interaction with EVM0001741 in mungbean.