

Supporting Information Available

Figure S1. Length distribution of contigs and transcripts in bitter melon transcriptome

Figure S2. GO annotation (A) and COG functional classification (B) of bitter melon transcripts

Table S1. Sequences of specific primers used for quantitative real-time PCR

Table S2. Summary of the transcriptome of bitter melon

Table S1. Sequences of specific primers used for quantitative real-time PCR

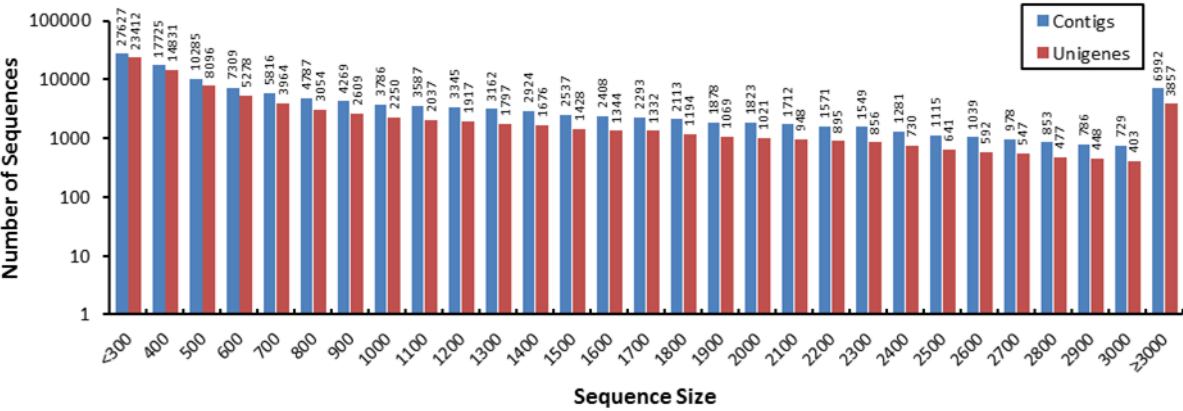
Primers name	Forward primer sequences (5' to 3')	Reverse primer sequences (5' to 3')	Size (bp)
<i>McCYP</i>	GGCAAACCCTAAAGTTTCTTCG	GATGAGCCCTTGTAATGAAGTGG	174
<i>McAACT</i>	TGGCAGCACAGAGTATCCAG	GCCATCTTTCAGCATTCCAT	152
<i>McHMGS</i>	TTCCCTTTCTGACGCTGACT	ATCCCGGCTCTGGTAACTTT	184
<i>McHMGR1</i>	CTGCTGTGAACTGGATCGAA	AGCGAGGTTCTTGAGCATGT	134
<i>McHMGR2</i>	CCTATCTGGAGGAGCCAACA	GGCGCACTTGATGTTCTGTA	190
<i>McMK</i>	TTTTGTGTGCGAGTTTCAGC	CAATTCCAGAGGGTTTCCA	163
<i>McPMK</i>	TGGCAGTCAACGCTATGTTC	TGCTCATGGTTCCACTTCTG	123
<i>McMVD</i>	CCACATCCAGAAACGGAGTT	CGGCCTGGTACAGATGAAAT	171
<i>McIDI</i>	GCGAGCACGAATTGGATTAT	AGCTTCAGCCCTTCTTCTCC	151
<i>McFPS1</i>	TCATTCTACCTTCCGTTTGC	TCCAATCTTCCCGATCACAT	162
<i>McFPS2</i>	GACGCTTCTCGTCAATGGAT	TGGAGCCACTCAATACACCA	173
<i>McSQS</i>	ACCCGCTTGTGAAACTGAAA	GGCTCGCAGAACCAGATAAA	182
<i>McSE</i>	CGCTTATACTCTCGCCAAGG	CAAGCCCTAATTCGATCAGC	128
<i>McCPQ</i>	CTTCACTTATGCGGGTTGGT	CCAGGTGTGGTCTGTTTCCT	194
<i>McCAS1</i>	CCACAGGTTGAGAAGAAGC	GACCATCATCTGCCTGGATT	188
<i>McCAS2</i>	CGGCTGATGGATCTTGGTAT	AACTTTCTCCCCAACCACCT	174

Table S2. Summary of the transcriptome of bitter melon

	Raw reads	Contigs	Transcripts
Total length (bp)	5,173,613,512	130,896,553	79,708,401
Number of sequences	68,073,862	126,279	88,703
Average length (bp)	76	1,036	898
Median length (bp)	76	604	471

Max length (bp)	76	15,750	15,750
Min length (bp)	76	224	224
N50 (bp)	76	1,763	1,600

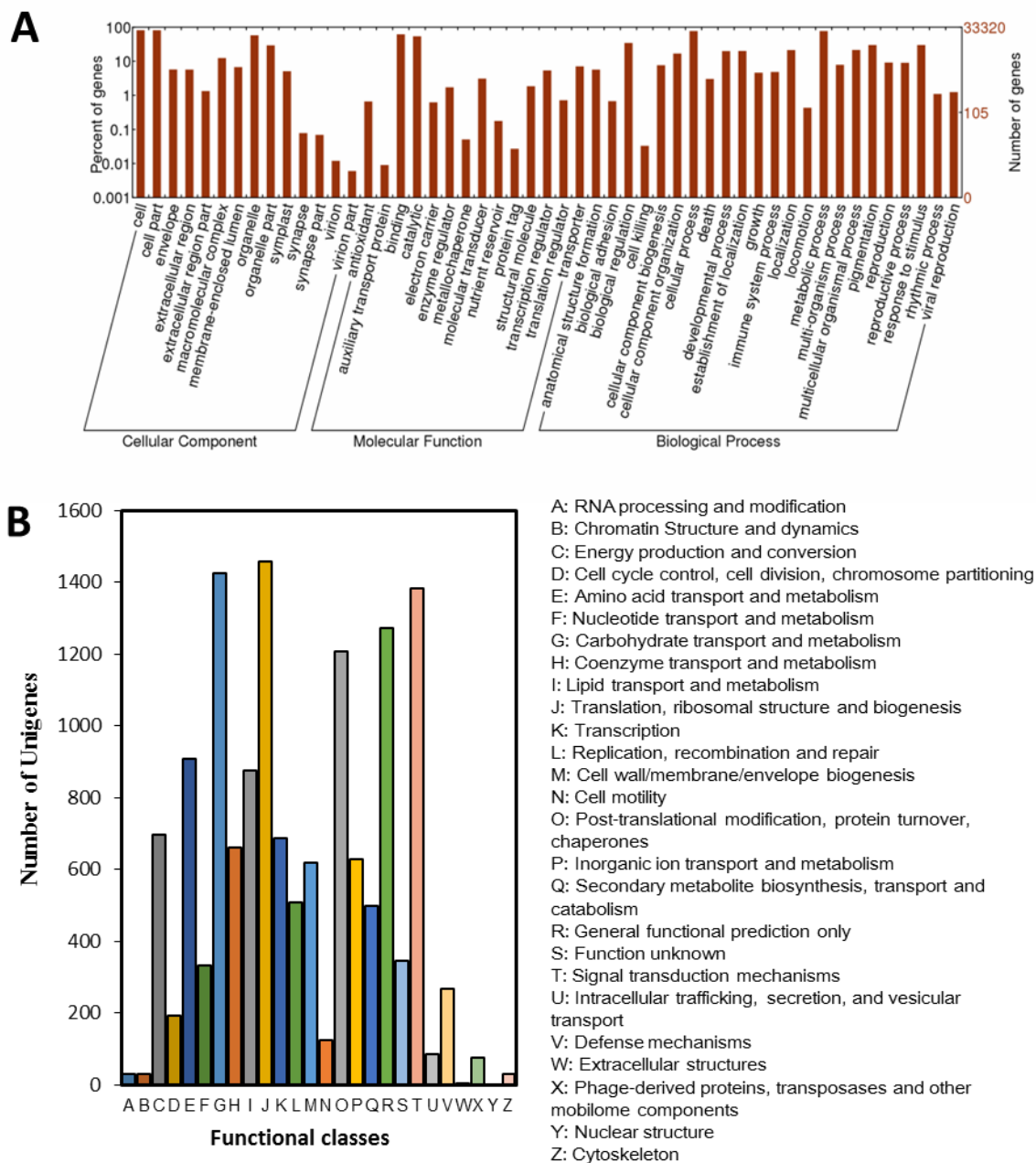
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13 **Figure S1.**

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16 **Figure S2.**