

**Table S1.** Primers and their sequences used for the quantitative real-time PCR (qRT-PCR) analysis.

Primer name	Sequence
<i>ZmCAB1-F</i>	CTTCGTGCAGGCTATCGTCA
<i>ZmCAB1-S</i>	CGTAAGCCCAGGCGTTGT
<i>ZmBCP-F</i>	TTACGGCAGGTCTGCTGGTA
<i>ZmBCP-S</i>	GTCGCTGTAGGACTGGATGGA
<i>ZmPEPC-F</i>	ATCCTGCACATGCTCAACCTC
<i>ZmPEPC-S</i>	TTAGGCACGCCCTTCCATAC
<i>ZmPPDK-F</i>	CCGTCAAGTCGCTAACAAGT
<i>ZmPPDK-S</i>	GCTGCCCTGGGAATCTCAATC
<i>ZmMDH-F</i>	CTCTCCGCCTCCTCCTCTAC
<i>ZmMDH-S</i>	TTCCATTCCCTCCTTCCTGG
<i>ZmrbcLBP-F</i>	CCTGGTGCAGCAGCTAATC
<i>ZmrbcLBP-S</i>	ATCTACCGGCTCGAACTCA
<i>ZmCP12-1-F</i>	GCATCAAGCAGGCGGAGGA
<i>ZmCP12-1-S</i>	GGGTCGTTGGCGTTGGTCT
<i>ZmME-F</i>	ACGGAGAAAGAGCGGGACA
<i>ZmME-S</i>	GCTGCAACGGGATCTGGAA
<i>ZmSOD-F</i>	CATAGCCGAGGCAACCATT
<i>ZmSOD-S</i>	CGTAGCTGCAACTGCAACCC
<i>ZmPOD-F</i>	TGTCGTTGCCGTTGAGATTAC
<i>ZmPOD-S</i>	GTCAGTGAACCCATTTGAGC
<i>ZmGAPDH-F</i>	CGTCCATGCTCTCCGCTACC
<i>ZmGAPDH-S</i>	GCCACCTTCAGCTTCGCCTC

**Table S2.** Global statistics of RNA-seq results between maize monocropping and maize-peanut intercropping.

Treatments	Total reads	Total base (bp)	GC%	Q30%
T1-1	22976739	5787029038	55.62	85.71
T1-2	26424079	6655010166	57.06	85.71
T1-3	25214850	6346506801	56.46	85.24
T2-1	25709362	5192479847	57.91	87.44
T2-2	26107181	5272662740	58.31	88.25
T2-3	24704364	4989329004	58.39	87.94

**Table S3.** Statistical results of protein identification.

Database	Total spectra	Spectra (PSM)	Peptides	Unique peptides	Protein groups
maize	291823	51015	22092	17644	4997