Table 1 Basic features of the assembled putative unique transcripts (PUTs) of cotton plant

Total PUTs	Average length of PUTs (bp)	BLASTX matches against Swiss-Prot data (%)	Total ORFs (%)	Full-length PUTs (%)	Pfam matches (%)	PUTs match with predicted gene models (%)
279050	975	201924 (72.4)	278650 (99.9)	115043 (41.2)	155446 (55.7)	247871 (88.8)