

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

Total PUTs	614 201
Average length of PUTs (bp)	815
BLASTX matche against UniProt/Swiss-Prot database	247 798
Total ORFs	601 196
Full-length PUTs	128 505
PFam matches	166 174
PUTs mapped to genome (%)	320 447 (52.2)
PUTs matched to cDNAs of gene models (%)	298 248 (48.6)
PUTs mapped to genome with gene models (%)	206 593 (33.6)
Unique genes supported with matching PUTs (%)	37 751 (95.6)
AS rate of gene models (%)	20 860 (55.3)