Reviewer Report

Title: Long-read sequencing of the coffee bean transcriptome reveals the diversity of full length transcripts

Version: Revision 1   **Date:** 7/1/2017

Reviewer name: Sandeep Chakraborty

Reviewer Comments to Author:

Cheng, et al. have satisfactorily responded to my comments with respect to contamination and xmt2 gene (my mistake).

However, significant discrepancies in their data still exist - and need to be addressed.

1) The number 1217 of "novel genes" in the paper, and those provided in 7_1271_novel_genes.fa (n=1271) dont match.
Maybe a typo (71 becomes 17?).

2) There are transcripts with really small ORFS - these cannot be taken as genes without proof

>C35828.F1P0.435
MKLGFLGKGFGLKTEDERQKMKKQRRGC
>C14734.F1P0.431
MMTKSPLHLYVARFYTNYSTLETSTPS
>C23681.F3P0.964
MGMNMIYMDFVEGKGFLVEAKWTAFSSPE

There should be a reasonable cutoff - maybe 60.

3) Finally, and most importantly, they are not novel : C57465.F1P0.755 ORF 2 matches to:
https://www.ncbi.nlm.nih.gov/protein/661881444?report=genbank&log$=prottop&blast_rank=1&RID=MFJCCGRX016
with a 100% match.
"The 1,217 sequences without hits to the FOUR databases (NR plant proteins" is therefore incorrect.

4) Also, the 145 sequences in the "6_Long_non-coding_RNAs.fasta" all have long ORF's (>100).
c14217_f2p0_996_1 also an ORF with significant match (1E-25) to XP_019192529.1 (
PREDICTED: uncharacterized protein C6G9.01c-like [Ipomoea nil])

Most of the "novel genes" seem to be long non-coding RNA.

Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Yes

Conclusions

Are the conclusions adequately supported by the data shown? No

Reporting Standards

Does the manuscript adhere to the journal's guidelines on [minimum standards of reporting?](#) YesChoose an item.

Statistics

Are you able to assess all statistics in the manuscript, including the appropriateness of statistical tests used? Yes, and I have assessed the statistics in my report.

Quality of Written English

Please indicate the quality of language in the manuscript: Acceptable

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