General comments

The paper deals with a sediment-fingerprinting tool that uses the 13C signature in organic biomarkers (FAs) allowing sediment source identification via an analytical solution of end-members along a mixing line. This paper presents a simple, but clear and well-developed case (including many previously missed caveats, e.g. use of long chain FAs, checking for tracer conservativeness and use of FA concentration rather %C to assess soil sources).
The paper is very well written and I have no major comments and some specific remarks are listed below. However, I disagree with the statements made in the abstract (Page 14246, line 7-10) and in the conclusions (page 14260, line 10-15). The later statement is clearly driven by the very simple case that was investigated. In reality most catchments are much more complex, as mentioned by the authors in the very first sentence of the abstract. According to me this has to be reformulated. I do not see an analytical constraint (data quality analyses time) to analyze more FAs. Furthermore new Bayesian mixing models (mixSIAR) have now many additional features (e.g. mixed and random effect, concentration dependency, etc.) to allow reliable distribution of estimates of sediment source proportions for complex landscapes (i.e. with >3 land uses), different sediments samples (event, vs. integrated) and samples taken at sub-catchment scale. Hence also aim iii) on page 14248 can only be achieved in this simple case and can not be generalized for other, likely more complex cases.

Specific comments

The title is too general. Please make it more specific towards the case you studied. Also what is CSIA? This is not clear here yet. Further be uniform sometimes you use "CSIA" vs. "CSSI". I think it should be "CSSIA".

Page 14247, line 8-13 is unclear. Please consider revising.

Page 14247, line 25. It is assumed that plant species have different 13C FA signals, but this is far from proven, although it is the basic (black box) assumption of the method used here. Please revise the sentence.

Page 14248, line 19-21. Can you please indicate much better in the results and discussion and maybe the abstract where you show CSSIA signature preservations, hence that the tracers you have used are indeed clearly conservative, which is a crucial assumption in the method.

Page 14250. Maybe a criticism is the rather poor number of replicated samples of the sources. At least the authors could add of these replicates represent composite samples from 3 fields, which I hope it was otherwise this strongly reduces the statistical power of the investigation.

Page 14253, line 13. Explain "SS".

Page 14254, Line 5-6. Please make clear if you refer to the 0.5 per mill for procedural error or to the FA-specific errors given on page 14253, line 8?

Page 14255, line 23-26. Why were the FA-specific errors not considered here? Can you better explain how the "forcing to mixing line" was carried out, i.e. the algebraic solution.

Page 14256, line 6. Replace "bulking" by "averaging"?

Page 14256, Line 21-21. In your simple case (especially site A) Bayesian statistics would not at more info. But I would not generalize it (see comments) above and I would simply remove that sentence. I feel free to add I am not convinced the authors are aware of al recent developments and capacities (isotopic) Bayesian mixing models. The literature is plenty, but don't see any (recent) reference appairing.

Page 14257, Line 12. Indicate this is the 13C signal in FAs