We greatly appreciate the thoughtful and helpful review of our manuscript by the reviewers and editors. We have addressed all the concerns below and in the manuscript. We believe the changes further strengthen the quality and clarity of our manuscript.

Reviewer #1: The author's goal is to demonstrate the clinical utility of next generation sequencing in T-cell lymphomas. They identify patients that have received such testing with a diagnosis of T-cell lymphoma. They seek to identify which mutations relevant both theoretically and by asking their treating physicians if the test changed management. Overall, the study is helpful in understanding the clinical role of these technologies and does give a clinician a sense of how testing would be helpful.
Thank you for your endorsement of our manuscript

Few clarity points:
1. in the first paragraph of the results section, "patients" and "samples" are interchanged. Were there any patients that had more than one sample in the cohort? or were all the samples from unique patients. in the subsequent paragraph, it states that all patients (n=99) had NGS at first presentation and that 21 had it repeated. It's confusing to me where the repeat testing lies within the sample size. It's also confusing if the "duplicate" samples were considered differently in the Figure 1A/B.
Thank you for allowing us to clarify this point. All ninety-nine unique patients had NGS performed at first presentation whose genetic alterations are shown in Figure 1A/B. Then at a later time point, twenty-one of these patients had NGS repeated which are distinct from the ninety-nine patient samples that are depicted in these Figures. To clarify this, we have removed the alternating terminology between patients and samples in the first paragraph and have moved all information about repeated NGS sampling to the second to last paragraph of the results section (Lines 146-149). We have also amended the Figure legends to specify that these genetic alterations were detected at routine NGS at first presentation at our institution (Lines 296-300).

2. supplemental figure 1 ("consort" diagram) is very helpful and would consider elevating it to the manuscript
Thank you for this feedback, we have moved the consort diagram to Figure 2 within the text from Supplemental Figure 1.
3. were physicians of patients who had 2 samples run asked twice about the utility of the NGS?
Thank you for the opportunity to clarify this point. Given the survey was sent out prospectively after the NGS data was collected clinicians were only asked one time per patient whether or not NGS had any impact on their clinical decision making. This has been clarified within the methods section (Lines 106-110).

4. I'm a bit conflicted about excluding the 15 samples that essentially had testing failure. while, yes, no identifiable mutation could be identified and therefore was not helpful, if I'm considering whether to order the test, those samples are relevant. Thus, in reality, 78+15=93 patients with NGS were not used for clinical decision making. further, 18 of

99+15 or 15.8% of patients with NGS were helpful for decision making. Excluding those 15 patients, particularly in the analysis of clinical utility of the test, over sells the test.
-fust FYI, those patients that did not have T-cell lymphoma should be excluded.
Thank you for bringing up this excellent point, we have added a portion to the discussion section discussing this possible overestimation as a limitation to this study (Lines 214-217) . We have also moved up the exclusion of non TCL samples within the Results section (Lines 112-113) to eliminate any possible confusion.

Reviewer #2: This is a very nice article showing the value of routine testing by NGS in T-cell lymphomas. While the article is limited to a single institution experience, relies on a targeted panel from the particular institution, and does not incorporate a large number of cases, it shows the value of routine NGS testing in the management of this complex group of lymphomas.

T-cell lymphomas are a very heterogeneous group of lymphomas with a diverse clinical presentation and variable poor prognosis. The NGS panel utilized shows the advantages of targeting specific therapeutic approaches with particular mutations present (e.g. HIDAC inhibitors in patients with epigenetic mutations, and referral to clinical trials for particular mutations). The key advantage of this study is its relative unique space in the literature, were little data exists in the role of NGS testing in routine management of TCL.

Thank you for your endorsement of our manuscript