**Response to Reviewers**

We would like to thank the reviewers and editor for taking the time to suggest improvements to our manuscript. Please see below for details of the changes we have made to the manuscript. Our comments are in blue.

We used LaTex to create the pdf of our manuscript so a track changes version would have been difficult to produce in this format. Therefore we have attached a track changes Word document to show where changes have been made. The line numbers that mark our responses in this document refer to the line numbers in the track-changes Word file. Please note that this Word document does not contain any references - these can be found in the full pdf file. Our re-submitted pdf file contains all of the new edits to the manuscript including additional references.

**Editor's comments**

Overall, I think this is an excellent, well presented study that will be suitable for publication in Peer J following minor revisions. Both reviewers share a similar, positive view of the manuscript and have provided some helpful suggestions that I ask the authors to please consider carefully when revising their manuscript. Particularly,   
  
1. Reviewer #1 has noted that the bibliography could be improved, and that a number of references are duplicated throughout the text. I agree with this statement, and see several areas where the authors could qualify their statements with stronger referencing. For example, the statement that tenrecs are commonly considered an example of adaptive radiation, needs to be better qualified, or wording needs to be amended accordingly.

We have improved our referencing throughout the text by reducing repetition of papers and adding additional citations (please see our responses to specific comments below for details).

2. Reviewer #1 has also made some important suggestions regarding improving aesthetic of the Figures. Similarly, Reviewer #2 has suggested Fig. 1 could be moved to supplementary information given the extensive details provided on the method (though currently sample size is ommitted?)

We have improved our figures by adding colour to figure 2 and increasing the contrast of the images so that they should not appear as dark. However, we have had difficulty in reducing the darkness of the images because it seems to arise from some steps during the submission process: our PNG copies of these figures appear much lighter than the versions after they have been uploaded to the PeerJ site.

We think that it would be beneficial to keep figure 1 within the main text as an aid for readers who may not be as familiar with morphometric methods. We are glad that the text in our methods section is clear but we feel that the picture helps to clarify some stages of our protocol for readers who may be new to the field. This will also help with the repeatability of our analyses: all of our data and code are publicly available so, with the aid of this figure, other researchers can follow each step of our protocol in detail.

We have added an additional table to the supplementary material which summarises the sample sizes for each species in our three analyses.

3. Reviewer #2 has made an important point regarding the use of “morphological diversity” rather than “disparity” and suggested some key citations that should be included. I am in strong agreement with their statement that at present the authors have over stated the lack of quantitative approach in this area – please check those comments and revisit that statement. Doing so will not detract from the importance of this article.

Please see our response to the reviewer comments below and the additional paragraph we added to the methods section to explain why we refer to morphological diversity rather than disparity. We have also revised the introduction and removed our original over-statement of the lack of quantitative studies of diversity.

4. Reviewer #2 has queried the approach used to quantify disparity, I agree with their comment here, and ask the authors to please either consider extending their analytical approach or providing further justification for their choice of method

We have added an extra paragraph to the results section to justify our choice of method and why we did not follow more conventional disparity approaches. We have also addressed the reviewer’s concerns about the validity of our method (please see below).  
  
In addition to the reviewer comments, please find below some additional points from my review of the manuscript. Importantly, I suggest that the authors should please reconsider to revise their first paragraph, which at the moment does not lead into the paper, or do justice to the importance of your study.   
  
Specific points:  
  
Abstract  
I think that the first statement is not accurate. There exist a large number of studies on morphological diversity (disparity) that encapsulate both extant and extinct groups.

We have removed this first statement and re-phrased the opening of the abstract.

Introduction  
Pg2, ln8-18. I think this first paragraph is generally confused in that the authors deal with research areas that are vast within very few qualified sentences that do not relate directly to the topic in hand. For example, adaptive radiation is not something studied here, (or if it is, then it needs to be signaled much earlier in the paper, directly and with numerous examples for tenrecs). The references do not include classical works such as Schluter 2000, and could easily comprise many review papers (e.g. Gavrilets and Losos 2009;Salzburger 2009; Salzburger et al. 2014; Kocher 2004; Gavrilets and Vose 2005…) rather than a repetition of Olson and Arroyo-Santos 2009. In a related matter, morphological convergence is introduced without a clear explanation about its relationship to adaptive radiation, or ecomorphological variation, niche exploitation.  
I suggest that the authors re-phrase this paragraph to better introduce their study.

On reflection, we agree that it was unnecessary to try to introduce the paper within the context of adaptive radiation and convergent evolution studies. Our aim was to show the wider relevance of studying morphological diversity but we understand that it was confusing and unclear to deal with such broad topics so briefly. We have removed our references to adaptive radiations and convergent evolution - instead we present the manuscript as a study of morphological diversity.

Also, somewhere you should provide a definition of morphological diversity (variation in form) or more commonly referred as, disparity. Consider citing Foote.

We have added a citation to Foote 1997 in our opening sentence. Please see the methods section for our explanation of why we are referring to diversity rather than disparity (ln166).

Pg2, ln22: I think this is a slight over statement, there are really many studies of morphological diversity (disparity). Please see for example papers by Drake and Klingenberg (dogs), Gerber, Polly, Weisbecker, Sears…

We agree. Our original claim that not many studies are qualitative rather than quantitative assessments of diversity related to assessments of the degree of convergent similarities rather than quantifying diversity in general (though we realise now that this was not clear in our manuscript). We have changed this section to include more example references which do quantify morphological diversity to demonstrate that our paper will fit into this literature.

Pg2, ln29: OK, but see e.g. Polly and MacLeod eigensurface, or papers on statistical atlases (e.g. Fatah et al. 2012 AJPA) that allow entire shapes to be appreciated rather than single traits.

We have qualified our original statement and added two additional sentences to show that we are referring to 2D geometric morphometric techniques which are still useful and appropriate for measuring variation in overall 3D shape.

Pg3, ln46: the references cited here do not reflect the statement – I would expect to find cichlids, anoles, icefishes, stickelbacks, Darwin’s finches in any recent review or book on adaptive radiation, could you cite similar references for tenrecs? Also, see Poux et al. 2008 – BMC Evol Biol and their statements on diversification rates in tenrecs. - doi:10.1186/1471-2148-8-102

We recognise that our original phrasing was confusing. We meant that researchers who study tenrecs often claim that they are an example of both an adaptive radiation and convergent evolution - not that general texts on these two topics often include tenrecs as an example (along with cichlids, finches etc.) We have re-phrased this sentence to make it clearer.

We have also added the reference to Poux et al at line 52 introduction:

“Therefore, it appears that tenrecs represent an adaptive radiation of species which filled otherwise vacant ecological niches through gradual morphological specialisations (Poux et al 2008).”

Pg6, ln101: please could you provide specimen numbers here – you mention that much later (ln140), but I think it would be helpful for the reader to have that information right away.

Our reason for mentioning specimen numbers later in the text was because we felt it was necessary to first of all explain the photographic procedure and reasons for having a different total specimen number for each analysis. We have, however, moved the information about specimen numbers to an earlier section of the methods (ln98) and we hope that this is clearer.

Pg7, ln141: should be “the” rather than “that”

Fixed

Figure 2: I suggest the authors use colour here. For instance, you could colour the landmarks e.g. red, which would help distinguish those against the photographs. At present it is difficult to see the landmarks easily.

Good suggestion: we have updated the figure so that the landmarks are red and the curves are marked in blue. The darkness of the figures in our original submission occurred at some stage during the file upload process: our own PNG copies of the figures do not appear as dark as the versions after they were uploaded to PeerJ. We have increased the contrast in our version of the figure so that hopefully the images are clearer even if they go darker during the submission process.

Pg14, ln304: agreed, however it might also equally suggest that a complete 3D GMM approach would also be fitting.

We have added the following sentence: “Future analyses could use 3D geometric morphometric approaches to test whether similar patterns emerge.”

Pg15, ln310 – you may also want to check Goswami’s early papers (e.g. 2006 in Am Nat; 2007 in PLoS ONE) in which she defines a subset of homologous landmarks for a wide variety of mammalian clades.

Thank you for suggesting these additional citations: we have added Goswami 2006 to the reference list.

Pg312: I think you could add citations for papers by Norberto Giannini or David Flores here (extensive work on cranial anatomy)

We added citations to Flores 2010 and Giannini 2010

Pg16, ln3338: agreed, but I think you put your study down here! The skull is an excellent model that shows a high diversity in form related to function, and that has been widely studied.

We changed this sentence to: “While the skull is widely regarded as a good model for studying morphological variation (e.g. citations), quantifying variation in other morphological traits could yield different patterns.”

Pg16, ln345: another suggestion might be to consider exploring the ontogenetic basis for differing levels of morphological diversity? For example, check papers by Daisuke Koyabu on mammalian cranial development. (Nat Comm, PNAS)

We agree that this is a good suggestion for future research however we have not referred to it within the manuscript because we feel that ontogenetic studies are beyond the scope of our current study. However, our data is publicly available so any researchers with an interest in ontogenetic studies could of course use our data as a starting point for their work.

**Reviewer Comments**

**Reviewer 1 (Anonymous)**

**Basic reporting**

The manuscript is well written and well presented. The first two sentences of the abstract, however, do not do the manuscript justice. The first sentence of the introduction has a better hook, so I suggest using something like that.

We agree: we have re-phrased the opening of the abstract to reflect the rest of the manuscript.  
  
The only issue I have in the basic reporting is regarding the comment that nowadays morphological diversity is predominantly studied qualitatively – the palaeobiology and evolutionary literature is rife with studies of quantitative disparity (morphological diversity). Thus I disagree that there are “few examples” (line 21).

The more interesting foci for why this study was done would be to talk about why morphological diversity differs among clades, what it is and isn’t related to and what it means to study it.

We have changed the introduction to reflect the variety of studies which quantify morphological diversity.

We have also re-phrased the abstract and introduction to put our research within the context of studies of morphological diversity and the importance of quantifying patterns of diversity to increase our understanding of ecological and evolutionary patterns (please see our changes made in response to the specific comments above).

**Experimental design**

The study is clearly outlined and well designed. The sampling efforts are seemingly impressive, covering 43 species out of 55 species from the two families under study, however the number of specimens per species is not fully disclosed; only a total of specimens for each view. I suggest a supplementary table summarising how many specimens per species.

We have added the recommended table to the supplementary material and referred to it in the main text (ln102).

The supplementary materials text describes the authors’ diligence in measurement error from digitizing and photographing 3D objects. I applaud their conscientiousness.  
The geometric morphometric analyses have mostly been carried out appropriately. I am concerned by the potentially overkill number of variables in this dataset. The authors should, but do not disclose the total number in the main text, and Figure 2 only shows the fixed landmarks, not the semilandmarks used. From the supplementary materials, I calculate there were for the dorsal view 54 landmarks and semilandmarks, for the ventral view 73 landmarks and semilandmarks and lateral view 44 landmarks and semilandmarks.

We have added this information to the methods section in the main text (ln128): “We used 54 points for skulls in dorsal view (10 landmarks, 44 semilandmarks across 4 curves), 73 points for skulls in ventral view (13 landmarks, 60 semilandmarks) and 44 points for skulls in lateral view (9 landmarks and 35 semilandmarks across 2 curves). See Figure 2 and the supplementary material for more details.”

For 2D data the authors are aware of issues with oversampling (lines 151-153), yet I would be wary that this dataset is indeed oversampling. For the interests of leading by example, I suggest the authors examine the number of principal components that are near zero and reassess the number of semilandmarks used. In particular, it would helpful to show by mantel tests that the distribution of species in the PCA morphospace are not substantially changed by altering the number of landmarks used. Perhaps oversampling has added variation?  
Fortunately, the statistical analyses of morphological disparity, as measured by the amount of shape space occupied, are not directly affected by the greater number of variables than specimens because they use distances between species (thus taking advantage of the Q-mode R mode equivalency, Gower 1966). Therefore my concerns above with oversampling are more about making sure that having so many semilandmarks is not introducing error and thus more shape variation. 

We have conducted a sensitivity analysis to address the reviewer’s concern that the number of semilandmarks we used introduced error into our estimates of shape variation. We tested whether the number of semilandmarks used influenced the number of PC axes which accounted for 95% of the variation. We compared the number of PC axes that account for 95% of the variation in the full data set to the number of axes generated when semilandmarks were randomly re-sampled to reduce their number. If there’s no significant difference in the number of axes used when the semilandmarks are reduced then that indicates that the original number of semilandmarks is not adding error to our calculations. The code for our analyses is available on GitHub.

For each analysis (skulls in dorsal, ventral and lateral view), we randomly re-sampled the number of Procrustes-superimposed semilandmarks. We selected different percentages of the total number of semilandmarks (90%, 80%, 70% etc.) and then continued with the rest of our analysis as described in the paper (find the average shape coordinates for each species, conduct a PCA analysis and select the PC axes that account for 95% of the total variation). We repeated these re-samplings and analyses for 100 replicates of each percentage subsample of semilandmarks (i.e. 100 replicates when semilandmarks were sub-sampled to 90% of their total number, the same for 80% etc.).

Table 1 below is a brief summary of our results (the full results are available on GitHub). There appears to be no issue of semilandmark oversampling for the dorsal skulls analysis. The majority (more than 75%) of our random samplings of 90%, 80% and 70% of the semilandmarks still resulted in the same number of PC axes representing 95% of the total shape variation as when we did the full analysis with all semilandmarks.

There may be some slight issues of oversampling for the ventral and lateral skulls analyses as subsamples of 90% of the landmarks did not necessarily generate the same number of PC axes accounting for 95% of the variation as the full (all semilandmarks) analysis (Table 1). However, in these cases, the number of PC axes that were selected was only one less than the number of PC axes used in the full analysis and therefore would not have significant effects on the overall calculations of relative morphological diversity in each family.

Reducing the number of semilandmarks had a slight (ventral and lateral) or negligible (dorsal) effect on the number of PC axes that accounted for 95% of the total shape variation (and which were then used to calculate morphological diversity in the full analyses). Therefore, we are happy that the number of semilandmarks used is not introducing significant error which would affect our calculations of relative morphological disparity in the two groups.

Table 1: Summary results of our semilandmark resampling (% semilandmarks) calculations (full results are available on GitHub). We resampled the semilandmarks 100 times at each % and for each analysis. Figures represent the number of times (out of those 100) when the number of PC axes that accounted for 95% of the total shape variation was the same (Full PC axes) or one less than the number of PC axes used in the original analysis (when all semilandmarks were included).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Analysis | 90% semilandmarks | | 80% semilandmarks | | 70% sample | |
|  | Full PC axes | One less PC axis | Full PC axes | One less PC axis | Full PC axes | One less PC axis |
| Skulls dorsal | 99 | 1 | 94 | 6 | 79 | 21 |
| Skulls ventral | 12 | 88 | 4 | 96 | 1 | 99 |
| Skulls lateral | 61 | 39 | 27 | 73 | 16 | 84 |

There are several methods in the literature for quantifying morphological diversity/disparity. The authors chose an average centroid size approach, which is taking the square root of the summed square distances of points to the group centroid (center of gravity) and dividing by the number of points in the group. This approach measures the cumulative disparity of points and allows for comparison of groups with different sample sizes. The pros and cons of this approach are: centroid size is the square root of within-group Sums of Squares, and is, therefore, a direct measure of within-group variation. While centroid size is hard to compare among groups with different sample sizes, by taking the average Centroid size allows centroid size to be compared among groups of different size. But, it is not really an average since centroid size is the square root of the summed squared distances, dividing by the number of points only scales this single value. Thus this measure is good as a relative scale; it makes less sense on an absolute scale.  
Why did the authors choose to calculate morphological diversity this way and not using the Procrustes variance or convex hull (e.g. Drake and Klingenberg 2010 Am Nat). How do you think your results would differ if one of these was used? I’m very surprised to see a paper studying disparity that does not reference more of the classic literature, e.g. Foote 1997 Annu. Rev. Ecol. Syst., Foote 1992 Paleobiology , Ciampaglio et al. 2001 Paleobiology.

Thank you for pointing out this omission. We chose to use our centroid size because, as the reviewer points out, it is a good, relative measure of differences in morphological diversity between the two groups. It is also easy to both understand and interpret. While we recognise that there is a diverse literature on measuring morphological disparity, we feel that many non-specialists may find it confusing due to the diversity of methods for measuring disparity and the different assumptions that are inherent among them. We did not include references to the classic disparity literature in our original manuscript because we were trying to avoid the confusion. However, we recognise that this could be perceived as an indication that we were not aware of this work rather than a deliberate choice. Therefore, we have added the following paragraph to the methods section (ln166) to help clarify this issue:

“Morphological diversity (variation in form) is more commonly referred to as morphological disparity (Foote1997). There are many different methods for measuring disparity. Calculations based on summary (principal component) axes of shape variation are popular (e.g. Ruta2013, Foth2012, Brusatte2008, Wainwright2007) while other methods include calculating disparity directly from Procrustes shape variables (Zelditch2012) or rate-based approaches which depend on phylogenetic branching patterns (e.g. Price2013, Price2010, OMeara2006). There is no single best method of measuring disparity (Ciampaglio2001) and each method makes different assumptions which are appropriate for different situations. Therefore, for clarity, we have chosen to measure variation in physical form using a clear, easily-interpretable method which captures variation in morphological diversity.”

**Validity of the findings**

The data presented are robust and statistically sound.

**Comments for the author**

The term “morphological diversity” is used here to refer to morphological disparity which I believe is the more commonly used term. I suggest using disparity at least once, or throughout, to aid this paper being found in computer literature searching.

Please see the additional paragraph we have added to the methods section (ln166)  
  
I would like to see described in the results the biology behind the PC axes, i.e. what shape change the first two PCs of each view describes. Particularly since PC1 delimits the two taxa.

Our analysis focuses on overall patterns of morphological diversity rather than specific biological or anatomical differences among the two families. Therefore, we have not included detailed anatomical descriptions of shape changes because we feel that it is not in-keeping with the main topic of the rest of the paper. We have, however, added the following sentence to the results section (ln232):

“For each analysis, PC1 summarises a morphological change from the foreshortened, "squat" shape of golden mole skulls at one extreme to the rostrally elongated shape of tenrecs (particularly the \textit{Microgale}) at the other extreme.”  
  
Figure 1 is very nicely made. However I do not see that there is any reason for its inclusion, given all of this information is described in the methods. If the author has such strong attachment to it, I suggest it is put in supplementary materials.

While we acknowledge that this figure may be unnecessary for some readers, we think that it is important to keep it in the main text because not all people will be as familiar with our approach. We think that it will help to clarify our methods description.

Figure 2 is well-presented but very dark. Suggest changing the brightness and using colour of the digitized landmark positions so that it is easier to read. Also, the semilandmarks should be depicted on this figure.

Please see our response to the reviewer’s comments above - we have used colour and changed the brightness. We have chosen not to add the semilandmarks individually because we feel it would make the figure cluttered and more difficult to read. However, the curves show the outlines which the semilandmarks summarise and all of our semilandmarks are spaced evenly by distance so we feel that it is straightforward for readers to understand how we summarised the shapes of our specimens.

Figure 3 would benefit from colour.

We feel that figure 3 (distance from centroid) is clear and easy to understand as it remains - we don’t think that making each of the four hypothetical species a different colour would add any relevant information to the interpretation of the figure. Similarly, if the reviewer intended to refer to figure 4 (PCA plots), again we feel that it is clear and easy to interpret in its current state. Adding different colours for tenrecs and golden moles would add unnecessary distraction to an already relatively cluttered figure.  
  
The citation for the R package geomorph is wrong, Emmanuel Paradis is not an author on paper. The proper citation is:  
Adams, D. C., and E. Otárola-Castillo. 2013. geomorph: an r package for the collection and analysis of geometric morphometric shape data. Methods in Ecology and Evolution 4:393-399.  
  
Also, given that software is regularly changed and updated, please cite the version of geomorph used as follows:  
Adams, D. C., E. Otarola-Castillo. 2013. geomorph: Software for geometric morphometric analyses. R package version 1.0: [cran.r-project.org/web/packages/geomorph/index.html](http://cran.r-project.org/web/packages/geomorph/index.html).  
or  
Adams, D. C., E. Otarola-Castillo, and E. Sherratt. 2014. geomorph: Software for geometric morphometric analyses. R package version 2.0: [cran.r-project.org/web/packages/geomorph/index.html](http://cran.r-project.org/web/packages/geomorph/index.html).  
or  
Adams, D. C., M. L. Collyer, E. Otarola-Castillo, and E. Sherratt. 2014. geomorph: Software for geometric morphometric analyses. R package version 2.1: [cran.r-project.org/web/packages/geomorph/index.html](http://cran.r-project.org/web/packages/geomorph/index.html).

We thank the reviewer for identifying our mistake: we have updated the geomorph paper citation and identified that we used version 2.1 of the package.

**Reviewer 2 (Nick Crumpton)**

**Basic reporting**

This is a very interesting, novel investigation into how morphological diversity can be studied and raises important questions about certain methodological techniques.   
The article is, on the whole, written very well, although there are a number of grammatical problems and a few errors that I have highlighted in general comments.   
The article is a fine structure, although a slightly broader bibliography would be of use to the reader. But overall, this is an excellent addition to the literature.

Thank you for your positive comments and for identifying places where we could approve.

**Experimental design**

No comment: research questions were defined well, and investigated rigorously with appropriate techniques and an impressively large data set.

**Validity of the findings**

No comment: findings are clearly set out in the context of the original questions and concluded in a sufficient, easily understandable way.

**Comments for the author**

Throughout the paper, the term 'Afrosoricida' is used to denote the tenrecid-chrysochlorid clade. It is recommended the authors consider using the term 'Tenrecoidea' for this clade. It is the authors' choice, but Asher and Helgen (2010) <http://link.springer.com/article/10.1186/1471-2148-10-102> may be of interest for a detailed history of the prevailing (and relic) nomenclature for tenrecs and golden moles.

While we recognise the debate surrounding the nomenclature of this clade, we have chosen to continue using Afrosoricida instead of Tenrecoidea. This is so that our nomenclature is in-keeping with Wilson and Reeder’s Mammal Species of the World 2005 as this is the taxonomy that we use throughout the rest of the paper.   
  
Abstract:   
The term ‘exceptional’ is used twice in the first and second paragraphs and feels slightly repetitive.

We have rephrased the opening of the abstract to remove this repetition.

Final paragraph:  
First line: ‘We’ should not be capitalized.  
The terms ‘genus’ and ‘family’ should not be capitalized (and throughout the paper).

We have fixed these errors throughout the text  
  
[Page 2, line 18] Losos (2011) is cited as exploring ‘relative’ repeatability of evolution. However, this is after a 2012 and a 2013 reference are cited. Also, the ‘repeatability of evolution’ is an odd phrase. Do the authors mean the repeated evolution of certain morphologies due to certain (e.g. developmental) constraints? Perhaps this needs a slight tweak.

We have removed our references to convergence and adaptive radiation from the opening paragraph.  
  
[Page 2, line 23] Examples of papers ‘qualitatively’ assessing morphological diversity would be useful here, especially as this work seeks to show qualitative work can be bettered.

We have re-phrased this section so that we are placing our work into the context of other studies that quantify morphological diversity instead of claiming that it is unusual to quantify diversity.  
  
[Page 2, line 19 – Page 3, line 26] Five out of the six sentences in this section begin with conjunctions and similar words (Although… However… Unfortunately… In addition… Furthermore) which sets up an unnecessarily apologetic tone.

Agreed: we have re-phrased this paragraph after taking out the claim that not many papers quantify diversity.  
  
[Page 2, line 30] ‘…influenced by the trait being used’. I recommend changing the word ‘used’ to something like ‘measured’ or ‘analysed’ earlier in the sentence. The term ‘used’ led me initially to think this would begin a section on the ‘use’ of an adaptation, e.g. functional role.

We have changed this to read “the trait being measured”  
  
[Page 3, line 34] ‘…unlikely to give a completely accurate representation’. It seems to me that the 'accuracy' could be ‘complete’ regardless the number of measurements. Even a few measurements could still be ‘accurate’ depending on their repeatability. The resolution of the 3-D shape’s description is perhaps the concept the authors are getting at? Although I’m sure there’s a better way to say that.

Thank you for pointing out this confusion: we have changed the sentence to “…unlikely to give a complete representation…”  
  
[Page 3, line 38] As Adams et al. (2004) is a review of 10-years’ worth of work, it might be worth adding ‘and references therein’.

Agreed, we have made this addition  
  
[Page 3, line 47] These two references are in neither alphabetical nor chronological order. If they refer to ‘convergent evolution’ and ‘adaptative radiation’ respectively, it is noticed they appear on the next page in the same order, although the order of convergence and adaptive radiation are reversed.

Both citations include references to convergent evolution and adaptive radiation. We have kept the two citations in the same order (most recent citation first) because this is in-keeping with the style of the rest of the manuscript.  
  
[Page 3, line 3] ‘…which convergently resemble’. The addition of ‘convergently’ makes this sentence is a little grammatically awkward as it /could/ be read that the tenrecs that resemble shrews, moles, and hedgehogs are convergent on each other rather than their lipotyphlan doppelgangers.

Thank you for identifying this issue: we have removed the word convergently and modified the following sentence to read: “The similarities among tenrecs and other small mammal species include…”  
  
[Page 4, line 61] This sentence is a repetition.

We edited this down to reduce the repetition.  
  
[Page 4, line 67-72] ‘Morphological diversity… gain an insight into their evolution’. Feels repetitive from page 2.

We think that this section is less repetitive now that the introduction has been changed.  
  
[Page 4, 76] It is noted that although much is made of the assumed less diverse cranial anatomy of golden moles, no qualitative description of golden mole skull anatomy is presented. A brief overview of broad anatomical differences previously ‘qualitatively’ described from the literature (which, I assume was the germ of this paper) would be useful for a reader unassociated with tenrecid and chrysochlorid morphology. E.g. an illustrative diagram of a few species of tenrecs and golden moles indicating differences would perhaps help the reader - especially as there are no images of chrysochlorids in the paper regardless of them being referred to often.

We agree that it would be useful for readers to compare broad scale morphological differences between tenrecs and golden moles. We have added an additional figure to the supplementary material to show the landmarks we used on an example of a golden mole skull. The reference to this additional figure is on line 125 in the text:

“Detailed descriptions of the landmarks as well as an example figure of landmarks on golden mole skulls, can be found in the supplementary material.”

We have not included a discussion of the specifics of golden mole cranial anatomy because we feel that it is beyond the scope of our current paper. We have focused on broad-based differences in morphology rather than a detailed analysis of specific anatomical features of either tenrecs or golden moles.  
  
[Page 5, 83] ‘though not always’. This is an important caveat and is an interesting avenue of research - but is not referenced. Perhaps this would be a good place to consider, for instance, the decoupling of functional convergence and anatomical convergence e.g. McGee and Wainwright (2012) doi:10.1111/j.1558-5646.2012.01839.x 

The Losos and Mahler 2010 reference was intended to back up this statement. We have moved this citation from the end of the sentence to follow the “not always” qualifier and we have added the McGee and Wainwright citation.

[Page 5, line 99] ‘all of the… in the collections’. Irrespective of damage? This is referenced later in the methods, but would be useful to clarify here.

We changed this to read “all of the intact tenrec and golden mole skulls…”  
  
[Page 6, line 120] Please reference what image software was used.

We added the reference to Canon Digital Photo Professional software.  
  
[Page 7, line 126] ‘Available on request’. As this follows immediately after mentioning the museums, it is unclear whether the request should be made to the authors or the institutions.

Good point: we changed this to “available from the authors on request”  
  
[Page 7, line 131] Scale bar not referenced before this point as part of the photography protocol.

We added “…and a scale bar placed below the specimen” earlier in the methods (ln92)  
  
[Page 7, line 141] ‘depict that’ change to ‘depict the’.

Fixed  
  
[Page 7, 142- Page 8, 149] Consider moving this large block of references to the end of the sentence or after ‘where available’.

Moved references to after “where available”  
  
[Page 9, line 178] ‘that has relatively low morphological diversity’. Qualify that the Microgale genus has previously been qualitatively considered to have low diversity. 

We’re not sure what the reviewer means here: the current two citations at the end of this sentence do qualify the statement that the *Microgale* genus has relatively low morphological diversity.

[Page 9, line 179-180] Reconsider this switch into present tense.

We think the tense of this sentence is appropriate because we’re referring to a continuous situation (*Microgale* similarities may mask signals of higher diversity among other tenrecs) rather than a past hypothesis or occurrence.  
  
[Page 13, line 274] This is the fourth use of either ‘commonly cited’ or ‘often cited’.

We acknowledge this repetition but we feel that our usage of these phrases are sufficiently spread out to justify using “often cited” here.  
  
[Page 14, line 300-301] ‘…particularly diverse palate morphologies’. Are these broad diets similar in terms of them being broad, or similar in terms of the actual breadth of foodstuffs that make up these ‘broad’ dietary preferences? Also, it may be worth mentioning teeth morphology here (obviously linked to diet) as the authors reference so many sources of anatomy between pages 7 and 8, and also any osteological correlates of jaw musculature as well as palate size/shape?

Thank you for identifying this possible source of confusion by using the word “broad”. We have changed this sentence to read: “…most tenrecs have non-specialised insectivorous or faunivorous diets…” (ln266)

We have also added the following mention of teeth morphology (ln264):

“Similarly, while there are anatomical differences among tenrec tooth morphologies (Asher2005) more work is required to determine if and how those differences correspond to variation in diet or feeding ecology.”

[Page 15, line 329-332] ‘the majority of tenrecs are very morphologically similar’. I suppose here the authors are talking about Microgale specifically, but if not, surely this sentence negates the thesis and, moreover, counters the repeated fact that tenrecs are ‘often cited as an example of an exceptionally morphologically diverse group?’ Especially as the authors reference a 2003 paper?   
Sorry for the confusion: yes we were referring to the Microgale here and we have added this to the sentence to be more explicit. (ln291)

[Page 16, line 335-36] Do these three really need to be referenced here again? If so, they should be either chronologically or alphabetically ordered.

We’ve removed these references: we agree that it was unnecessary to repeat them again.  
  
[Page 16, line 352] ‘…restricted to just one axis…’. Consider altering the word ‘axis’ here as it has connotations of the PCAs performed as part of this study rather than the scope of the morphological data collected - as I think is meant.

We changed the word axis to “aspect”

Figure 1  
Some of the labels within the flow chart boxes might need tweaking. Some are descriptions of parts of the methodology (e.g. ‘Landmarks and curves’, ‘PC axes that account for 95% variation’) whereas others are instructions (e.g. ‘Combine data in R’, ‘Compare diversity of groups’).

We agree that these labels refer to different aspects of the methodology but we think that is necessary so that readers can follow all of the steps of our protocol. We have updated the skull pictures in the figure so that they are all from the same specimen (see response to the comment below). We have also changed the contrast of the skull pictures so that they should not appear as dark (although, as mentioned previously, we had the same problem here that the figure appears darker after uploading to the PeerJ site).  
  
Figure 2  
It is a shame this diagram is a chimera of two specimens. Surely out of the vast data set there was one skull from which all three views could be taken?

We have changed the figure so that all three skull views come from one specimen.  
  
‘1cm’ on scale bar has a space in the ventral view.

Fixed - thank you for spotting this mistake.  
  
Due to the darkness of the photograph, the landmarks are difficult to see (esp. 8, 9, and 10). Consider a different colour or shade to show them more easily, or using a diagrammatic skull rather than a photograph.   
The curves are very difficult to see. Consider changing colour or tone.

Please see our responses to reviewer #1’s comments above: we have made the skull pictures lighter and changed to depicting both the landmarks and curves in colour.   
  
Figure 3  
In text – ‘95%’ rather than ‘95\%’

Thank you for spotting this: a left-over from LaTex formatting!  
  
Table 1  
0.04 for 31 lateral is not bold.

This is a mistake: the figure is bold (included within our LaTex commands, though perhaps it is not clear enough)?  
  
Table 2  
Although these are all significant, consider making all p values bold in keeping with Table 1.

We have changed these numbers to be bold  
  
Additional:   
It is very obvious that some references are repeated many times. For instance, Soarimalala and Goodman (2011) is referenced no fewer than ten times throughout the paper. Although the authors are obviously very knowledgeable in all facets of tenrecid biology, this repetition sometimes results in a feeling that these references are cited instead of more salient works from before 2011 – a feeling amplified by the repeated twinning of Soarimalala and Goodman with a paper from 1969. A slightly more diverse bibliography would remedy this.

We agree that over-use of the “key papers” is too repetitive. Some of the edits to the other reviewer comments (above) have reduced this problem. We have also added additional references to represent the wider breadth of the tenrecid literature including Poux et al 2008 and Asher and Sanchez-Villagra 2005.