**We would like to thank the reviewers for their time, and insights through this process. Specific responses to the comments can be found below.**

Reviewer #1: The potential impact of co-medications on gene-expression profiles should be discussed.

**We have mentioned this in the revised discussion section as such:**

**Another potential caveat is the potential confounding effect of anti-diabetic or anti-growth hormone medications. Only one acromegalic patient was on somatostatin, and their IGF-1 levels were non-responsive. Our exclusion criteria included any glucocorticoid or hormone treatment, nor any known hormonal deficiencies. One patient in each group was on metformin as an antidiabetic medication, so we do not feel that this affected our overall conclusions.**

The array data should be made publically available e.g. by uploading the data to the NCBI Gene Expression Omnibus.

**These data are available through the Gene Expression Omnibus (GSE57803).**  
  
Reviewer #2: The revised manuscript by Hochberg et al. has addressed the concerns raised by this reviewer. However, the authors failed to provide another method to further evaluate gene expression profiles. Their reasons are that there is insufficient remaining RNA and tissue and they did not believe that qPCR analyses from the same samples would add any extra validity to the current data analysis. I think this is a judgment call as to if qPCR or other analysis needs to be added to the current manuscript. It is always better to have a second method to validate the analysis of gene expression data since the correlation between the observed phenotypes and gene expression profiles in acromegalic patients presented in the manuscript is purely speculated without any direct proof. Beside this, I have no other concerns.

**We agree with this reviewers concern and have stated the lack of validation as a limitation to our study in the discussion section as such:**

**Another potential limitation was our inability to separately validate our findings at the protein level, due to a lack of sample or in a secondary cohort due to the rarity of this disease.**