

# pathology report addendums

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Inbox

To: Eula Fung <eula@stanford.edu>;

Hey Eula,

I have been trying to get some traction for adding STAMP results to pathology reports as addendums. This has a lot of value, both (I think anyway) to the pathologists who otherwise never see these results, and to the clinicians, as it takes the place (not perfectly) of the “digest” version we wanted to build into the Epic report (the clinicians are notified when we change the pathology report and it gives them another place to quickly find the important mutation information. I’ve been doing this for a while for lung cases, but I’m hoping to get the rotating residents doing them, but as with all tasks that involve some measure of data entry, there is the risk of sadness and consternation from all sides, so I am trying to make it as painless as possible.

Do you think it would be possible to make a script that would take as input the csv file and return as output the formatted addendum (example below)? One problem is that PowerPath, the software we use to make pathology reports, uses Microsoft Word as an intermediary, so ideally the output would be a Word file. But I suspect that might be a lot of extra trouble, so a text file alternative might work OK, although then the user would have to do some formatting after copying it into the Word file for the report. It would also be good if we could put multiple csv files in and have the output a single file with an addendum for each case on each page (maybe with the csv file name or some other identifier at the top).

Let me know if you think this is something that would be practical without requiring too much effort on your part. I can also work on optimizing templates to reduce manual entry within Word if the script would be too painful. I have been using single letter protein descriptions only (as below), but the three letter codes in the CSV would be fine also. The “specimenID” part and the names at the bottom will have to be manually copied from the pathology report or entered; we don’t get that information. Finally, only pathogenic and likely-pathogenic variants would be reported here.

**ADDENDUM COMMENT:** This addendum is issued to describe the results of next generation sequencing-based mutational profiling using the Stanford Solid Tumor Actionable Mutation Panel (STAMP), version <from CSV file>. All variants considered "pathogenic" or "likely pathogenic" are reported here. For additional details on the variants detected as well as the full list of variants (including variants of uncertain significance) and methodologic details, please see the complete report in EPIC.

## **ADDENDUM DIAGNOSIS:**

### **SPECIMENID, MUTATIONAL PROFILING BY STAMP**

- **POSITIVE FOR *NF1* Q236X MUTATION**
- **POSITIVE FOR *TP53* E298X MUTATION**

**RESIDENTNAME/KUNDER/ORIGINALSIGNOUTATTENDING**