FW: STAMP addendums

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

From: Kunder, Christian
Sent: Thursday, April 20, 2017 10:04 AM
To: Fung, Eula
Subject: STAMP addendums

Hey Eula,

I wonder if I might beg a few changes to the addendum script? None of these are deal breakers if it's going to be time-consuming.

1. Automaticity: can each new run have the script run automatically for the cases in that run so that the Word file is already there in the run folder when the resident goes there?
2. Formatting: can the output be single-spaced without 10 pts space after paragraphs?
3. Special variants: If I send you a list of exon 19 deletions, can you have the line for that variant say: **POSITIVE FOR *EGFR* EXON 19 DELETION**
   a. ERBB2 exon 20 insertions: **POSITIVE FOR *ERBB2* EXON 20 INSERTION** (again I can provide a list of variants)
   b. TERT variants: **POSITIVE FOR *TERT* PROMOTER MUTATION**
   c. MET exon 14 skipping variants – not sure how to do this since almost every case is a different variant. Maybe I can give you a genomic range and any variant in that range will show up as **POSITIVE FOR *MET* EXON 14 SKIPPING MUTATION**
4. No variants detected: **NO PATHOGENIC OR LIKELY PATHOGENIC VARIANTS DETECTED**
5. Fusions: can the script look in the filtered fusions file and add a line (the top line) for **POSITIVE FOR *GENE1-GENE2* FUSION**
6. Amplifications: can the script look in the cnvs file and for amplified targets (not CHECK_AMP) add a line after the fusions, SNVs, and indels that says **POSITIVE FOR *GENE* AMPLIFICATION**

Thanks, and again I have no idea how much work this is so please tell me if any or all of these would be a major effort, thanks again,
Christian Kunder, M.D., Ph.D.
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