

**Instructions: - 4Aug23**

**NOTE: In the most updated list, the addition is Fig2 which is produced by the same code as supplemental table 4 and 5 (FNIH-Report-TaskID7&8-20220421-modified.Rmd).**

- A. The following are general purpose functions which are later called by R markdown codes. These functions are used to produce a structured output of the R markdown files. They are meant to be in the folder where the R markdown codes are and are called inside the R markdown codes:
  - 1. Table\_Fun\_ComparsionCandiatevsBiomarkers 220114.R
  - 2. Table\_Fun\_ComparsionCandiatevsBiomarkers.R
  - 3. Table\_Fun\_ComparsionCandiatevsBiomarkers\_modified.R
  - 4. Table\_Fun2\_Space 220114.R
  - 5. Table\_Fun2\_Space.R
  - 6. Table\_Fun2\_Space\_modified.R
- B. Manuscript Table-1: - Selected Outputs from the following R codes:
  - 1. FNIH table1 and supp table-3.R
  - 2. table-1 summary output MS.R
- C. Manuscript Table-2: - Selected outputs from the R Markdown file:
  - 1. FNIH-Report-20210820.Rmd
- D. Manuscript Table-3: - Selected outputs from the R Markdown file:
  - 1. FNIH-Report-TaskId5-20220420.Rmd
- E. Supplemental Table 1 and Table 2 :- Non numeric table (not done by Cytel)
- F. Supplemental Table 3: - Selected outputs from the following R code:
  - 1. FNIH table1 and supp table-3.R
- G. Supplemental Table 4 & 5: - Selected outputs from the R Markdown file
  - 1. FNIH-Report-TaskID7&8-20220421-modified.Rmd
- H. Supplemental Table 6 :- List of IRB protocol approval studies (not done by Cytel)
- I.
- J. Fig1:- Flow chart (not done by Cytel)
- K. Fig2 :- Sensitivity and Specificity plots:
  - 1. FNIH-Report-TaskID7&8-20220421-modified.Rmd