```yaml
name: Validate_wf_docker

inputs:
  - ped_input <- data/toydata.ped
  - map_input <- data/toydata.map
  - bed_input <- data/toydata.bed
  - bim_input <- data/toydata.bim
  - fam_input <- data/toydata.fam
  - pheno_input <- data/toydata.phe
  - known_truth <- data/fakekt.ote

outputs:
  - demonstrate.comptable
  - demonstrate.TPhist
  - demonstrate.FPhist
  - demonstrate.TPvsFP
  - demonstrate.AUCvsMAE

processes:
  fastlmm:
    image: taccsciapps/fastlmm
    description: Analyzes the data to produce GWAS output
    inputs:
      - inputs.ped_input -> /tmp/test.ped
      - inputs.map_input -> /tmp/test.map
      - inputs.bed_input -> /tmp/test.bed
      - inputs.bim_input -> /tmp/test.bim
      - inputs.fam_input -> /tmp/test.fam
      - inputs.pheno_input -> /tmp/pheno.txt
    outputs:
      - /fastlmm/LMM_Docker_Results.csv -> GWAS_out
    command:
      fastlmmc -verboseOutput -bfile /tmp/test
      -fileSim /tmp/test -pheno /tmp/pheno.txt
      -out LMM_Docker_Results.csv


  winnow:
    image: taccsciapps/winnow
    description:
      Produces fit statistics for determining
      appropriateness of GWAS analysis tool
    inputs:
      - fastlmm.GWAS_out -> /samples/GWAS_out.csv
      - inputs.known_truth -> /kt.ote
    outputs:
      - /outputs/YAML_Winnow_Results.txt -> Winnow_out
    command:
      --verbose --Folder /samples --Class /kt.ote
      --Snp SNP --Score Pvalue --beta SNPWeight
      --kttype OTE --seper comma --kttypeseper whitespace
      --filename  /outputs/YAML_Winnow_Results


  demonstrate:
    image: taccsciapps/demonstrate
    description:
      Produce human-readable graphics from the Winnow
      output of the previous step
    inputs:
      - winnow.Winnow_out -> /tmp/results.txt
    outputs:
      - /tmp/ComparisonTable.csv -> comptable
      - /tmp/'TP Histograms.pdf' -> TPhist
      - /tmp/'FP Histograms.pdf' -> FPhist
      - /tmp/Test_Run_Pos_Plot.pdf -> TPvsFP
      - /tmp/Test_Run_Error_Plot.pdf -> AUCvsMAE
    command:
      Rscript /usr/bin/DemonstrateRun.R /tmp TRUE
      Test_Run_Pos_Plot.pdf TRUE Test_Run_Error_Plot.pdf TRUE
```

```yaml
name: Validate_wf_Stampede

inputs:
  - ped_input <- agave://val.storage//data/toydata.ped
  - map_input <- agave://val.storage//data/toydata.map
  - bed_input <- agave://val.storage//data/toydata.bed
  - bim_input <- agave://val.storage//data/toydata.bim
  - fam_input <- agave://val.storage//data/toydata.fam
  - pheno_input <- agave://val.storage//data/toydata.phe
  - known_truth <- agave://val.storage//data/fakekt.ote

outputs:
  - ComparisonTable.csv
  - TP Histograms.pdf
  - FP Histograms.pdf
  - True Positives vs. False Positives.pdf
  - Plot of AUC by MAE.pdf

processes:
  fastlmm:
    app_id: FaST-LMM-2.07
    execution: agave_app
    description: Step 1
    inputs:
      inputFAM: ["inputs.fam_input"]
      inputPED: ["inputs.ped_input"]
      inputBED: ["inputs.bed_input"]
      inputBIM: ["inputs.bim_input"]
      inputMAP: ["inputs.map_input"]
      inputPHENO: ["inputs.pheno_input"]
    parameters:
      MainFileset: "P"
      SimFileset: "BEDBIMFAM"
      output: "YAMLTest_LMM.csv"
      verboseOutput: 0
    outputs:
      - YAMLTest_LMM.csv -> output


  winnow:
    app_id: Winnow-0.9
    execution: agave_app
    inputs:
      Folder: ["fastlmm.output"]
      Class: ["inputs.known_truth"]
    parameters:
      SNP: "SNP"
      Filename: "YAML_Winnow_Results"
      Score: "Pvalue"
      beta: "SNPWeight"
      kttype: "OTE"
      seper: "comma"
      kttypeseper: "whitespace"
    outputs:
      - YAML_Winnow_Results.txt -> output


  demonstrate:
    app_id: Demonstrate-0.9
    execution: agave_app
    inputs:
      dir: ["winnow.output"]
    parameters:
      make_pos_plot: 1
      pos_plot_title: "'Test Run - Pos Plot'"
      make_error_plot: 1
      error_plot_title: "'Test Run - Error Plot'"
      extra_plots: 1
    outputs:
      - ComparisonTable.csv -> comparison_table
      - TP Histograms.pdf -> tp_histograms
      - FP Histograms.pdf -> fp_histograms
      - True Positives vs. False Positives -> tp_vs_fp
      - Plot of AUC by MAE.pdf -> auc_by_mae
```