# 1. 02462 SW Test Report

## 1. Approvers

| Role | Name | Signature and Date |
|---|---|---|
| Technical Lead | Todd Richmond | |
| Quality Representative | Lori Radavich | |
| Tester | Kurt Heilman | |

## 1.2. Reviewers

| Role | Name |
|---|---|
| Research Informatics | Mark D`Ascenzo |

## 1.3. Definitions

Term 1: PS - Product Specification

Term 2: Probe Information File - The probe information or probe info file is a tab-delimited plain text file which is intended to be delivered to HEAT-seq and HEAT-seq Ultra customers. It describes all HEAT-seq probes in a design including primer sequences and genomic target locations. The probe info file is needed during data analysis to determine appropriate read trimming lengths and to match reads to probes using coordinates and sequence. See also: http://wiki.dmd.roche.com/index.php/Probe_Information_File

## 1.4. Scope

Verify that HSQUtils software correctly trims FASTQ formatted sequencing reads given a read set (read one and read two) and a probe information file.

## 1.5. References

| Document | Reference | Version |
|---|---|---|
| Requirements Document | 02642 Product Requirements Doc (PRD) 1200000069949 | 02 |

## 1.6. Plan

| Requirement Type | Requirement Number | Requirement Text |
|---|---|---|
| PS | 60.001.046.001 | The system shall provide a means to perform trimming based on the uid extension, ligation primer and ligation primer lengths defined in the probe information file. |
| PS | 60.001.046.016 | The system shall utilize the following key-value pairs for trimming when presented in the header of the probe information file: extension_uid, ligation_uid, genome. |
| PS | 60.001.046.026 | The system shall allow users to specify an output directory to place all outputted files. |
| PS | 60.001.046.028 | The system shall use the current working directory as the output directory if the output directory is not provided by the user. |
| PS | 60.001.049.068 | The system shall require the following inputs be provided for trimming: raw read one fastq file, raw read two fastq file, probe information file. |

## 1.7. Notes

1) Dataset 5: This is comprised of three simulated datasets with testable combinations of extension_uid and ligation_uid values. The combinations are: a. exenstion_uid=10 and ligation_uid=0 b. extension_uid= 0 and ligation_uid=10 c. extension_uid=10 and ligation_uid=10. Included with the dataset are fastq files before and after trimming and probe_info files that specify corresponding header values for trimming the fastq sequence files using HSQUtils.

# 2. Test Steps

| Step Number | Test Step | Acceptance Criteria | Acceptance Results | Results (Pass/Fail) |
|---|---|---|---|---|
| 1 | Verify that the system shall require the raw read one fastq file, raw read two fastq file, probe information file as inputs for trimming by executing the below command and wait until the prompt is back java -jar [trim, --r1, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step1\S6_86-2_S6_L001_R1_quality_filtered.fastq, --r2, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step1\S6_86-2_S6_L001_R2_quality_filtered.fastq, --probe, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step1\140730_HG19_HotSpotAlpha2_1in4_HSQ_probe_info.txt] | | | |
| | Verify that the system shall use the current working directory as the output directory if the output directory is not provided by the user. Note that the '--outputDir' option was not provided in the arguments. | Three files are in the current working directory. | Trimmed R1[trimmed_S6_86-2_S6_L001_R1_quality_filtered.fastq], Trimmed R2[trimmed_S6_86-2_S6_L001_R2_quality_filtered.fastq] and the Log File[HSQUtils_trim_2016_01_15_15-53-18.log] were all found in the results directory[D:\kurts_space\heatseq\Test_Plans\testplan10_workspace\step1_results_20160115155317]. | Pass |