1. 02462 SW Test Report

1. Approvers

Role	Name	Signature and Date
Technical Lead	Todd Richmond	
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1.2. Reviewers

Role	Name
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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	The system shall run without the 'outputDir' argument being provided. 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 application ran succesfully.	"Trimming has completed successfully." is observed in the console output and no errors are observed in the error output.	The text "Trimming has completed successfully." was observed in the console output. No errors were detected.	Pass
	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.	Both trimmed fastq files and a log file were found in the current working directory.	The following files were found in the results directory[D:\kurts_space\heatseq\Test_Plans\testplan10_workspace\step1_results_20160211092601]: 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_02_11_09-26-01.log].	Pass
2	Trim simulated reads using HSQUtils. Reads contain a 10 bp ligation endu UID only. java -jar [trim, --r1, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step2\sim_extension_uid_0_ligation_uid_10_r1.fastq, --r2, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step2\sim_extension_uid_0_ligation_uid_10_r2.fastq, --probe, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step2\150414_HG19_Cancer_HotSpot_HSU_probe_info_0_10.txt]			
	Verify that the output matches SME generated output.	Diff reports that R1 and R2 results match the corresponding SME generated R1 and R2 results.	The trimmed R1 file[D:\kurts_space\heatseq\Test_Plans\testplan10_workspace\step2_results_20160211092601\trimmed_sim_extension_uid_0_ligation_uid_10_r1.fastq] matches the SME generated trimmed R1 file[D:\kurts_space\heatseq\Test_Plans\testplan10_data\step2\expected_results\trimmed_sim_extension_uid_0_ligation_uid_10_r1.fastq]. The trimmed R2 file[D:\kurts_space\heatseq\Test_Plans\testplan10_workspace\step2_results_20160211092601\trimmed_sim_extension_uid_0_ligation_uid_10_r1.fastq] matches the SME generated trimmed R2 file[D:\kurts_space\heatseq\Test_Plans\testplan10_data\step2\expected_results\trimmed_sim_extension_uid_0_ligation_uid_10_r2.fastq].	Pass
3	Trim simulated reads using HSQUtils. Reads contain both a 10 bp extension and 10 bp ligation end UID. java -jar [trim, --r1, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step3\sim_extension_uid_10_ligation_uid_0_r1.fastq, --r2, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step3\sim_extension_uid_10_ligation_uid_0_r2.fastq, --probe, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step3\150414_HG19_Cancer_HotSpot_HSU_probe_info_10_0.txt]			
	Verify that the output matches SME generated output.	Diff reports that R1 and R2 results match the corresponding SME generated R1 and R2 results.	The trimmed R1 file[D:\kurts_space\heatseq\Test_Plans\testplan10_workspace\step3_results_20160211092601\trimmed_sim_extension_uid_10_ligation_uid_0_r1.fastq] matches the SME generated trimmed R1 file[D:\kurts_space\heatseq\Test_Plans\testplan10_data\step3\expected_results\trimmed_sim_extension_uid_10_ligation_uid_0_r1.fastq]. The trimmed R2 file[D:\kurts_space\heatseq\Test_Plans\testplan10_workspace\step3_results_20160211092601\trimmed_sim_extension_uid_10_ligation_uid_0_r1.fastq] matches the SME generated trimmed R2 file[D:\kurts_space\heatseq\Test_Plans\testplan10_data\step3\expected_results\trimmed_sim_extension_uid_10_ligation_uid_0_r2.fastq].	Pass
4	Trim simulated reads using HSQUtils. Reads contain both a 10 bp extension UID only. java -jar [trim, --r1, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step4\sim_extension_uid_10_ligation_uid_0_r1.fastq, --r2, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step4\sim_extension_uid_10_ligation_uid_0_r2.fastq, --probe, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step4\150414_HG19_Cancer_HotSpot_HSU_probe_info_10_0.txt]			

		Verify that the output matches SME generated output.	Diff reports that R1 and R2 results match the corresponding SME generated R1 and R2 results.	The trimmed R1 file[D:\kurts_space\heatseq\Test_Plans\testplan10_workspace\step4_results_20160211092601\trimmed_sim_extension_uid_10_ligation_uid_0_r1.fastq] matches the SME generated trimmed R1 file[D:\kurts_space\heatseq\Test_Plans\testplan10_data\step4\expected_results\trimmed_sim_extension_uid_10_ligation_uid_0_r1.fastq]. The trimmed R2 file[D:\kurts_space\heatseq\Test_Plans\testplan10_workspace\step4_results_20160211092601\trimmed_sim_extension_uid_10_ligation_uid_0_r1.fastq] matches the SME generated trimmed R2 file[D:\kurts_space\heatseq\Test_Plans\testplan10_data\step4\expected_results\trimmed_sim_extension_uid_10_ligation_uid_0_r2.fastq].	Pass
5		The system shall utilize the provided 'outputDir' argument. java -jar [trim, --r1, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step5\S6_86-2_S6_L001_R1_quality_filtered.fastq, --r2, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step5\S6_86-2_S6_L001_R2_quality_filtered.fastq, --probe, D:\kurts_space\heatseq\Test_Plans\testplan10_data\step5\140730_HG19_HotSpotAlpha2_1in4_HSQ_probe_info.txt, --outputDir, D:\kurts_space\heatseq\Test_Plans\testplan10_workspace\step5_results_20160211092601]			
		Verify that the application ran succesfully.	"Trimming has completed successfully." is observed in the console output and no errors are observed in the error output.	The text "Trimming has completed successfully." was observed in the console output. No errors were detected.	Pass
		Verify that the system shall use the provided working directory as the output directory.	Both trimmed fastq files and a log file were found in the provided working directory.	The following files were found in the results directory[D:\kurts_space\heatseq\Test_Plans\testplan10_workspace\step5_results_20160211092601]: 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_02_11_09-26-49.log].	Pass