

Project Name: RUO LST
Experiment Name: Demo Report
Date: Thu Feb 27 09:15:17 PST 2020
Investigator/Institution: Investigator Name / Institution Name
Number of analysed samples: 11
Number of failed samples: 2
Number of borderline samples: 1
Number of passed samples: 8

The results from this report should be limited to Research Use Only (RUO) and should not be used in any medical decision making where results will go back to patients or patients' physicians, or used as inclusion/exclusion criteria or stratification in a prospective clinical trial.

The dataset was analyzed using the RUO version of the NanoString Lymphoma Subtyping Test (LST) algorithm to determine the Cell-of-Origin molecular subtype of each sample. The LST algorithm measures the geometric mean of 5 housekeeping genes (HK geomean) to ensure RNA quality based on a pre-defined clinical QC threshold of 128. A HK geomean value below 64 was deemed insufficient RNA quality to provide a subtyping result (subtype listed as N/A). A value between 64 and 128 was borderline quality since it meets previously published thresholds for RNA quality within clinical research studies (Scott et. al, Blood, 2014) but does not meet our clinical QC threshold of 128 for individual patients. Each sample meeting the QC threshold is reported as one of the two molecular subtypes, Activated-B- Cell (ABC) or Germinal Center-B- Cell (GCB), or Unclassified within an equivocal zone. The QC Status Statistics Data Table summarizes the QC test result of the samples.

A sample that failed to meet the required RNA quality for the test is indicated as FAIL. A sample that has borderline RNA quality for the test is indicated as BORDERLINE (NanoString has not verified or validated the subtype output for samples of borderline RNA quality). A sample that has met the QC threshold is indicated as PASS and the subtype is reported as ABC, GCB, or UNCLASSIFIED provided by the algorithm. The subtype distribution of the samples providing a borderline or passing RNA quality is shown in the Subtype Statistics Data Table.

QC status of each sample and subtype output for the samples with passing RNA quality are summarized in the LPS Data Table.

Reference. Scott D, Wright G, Williams M, Lih C, Walsh W, Jaffe E, et al; Determining cell-of- origin subtypes of diffuse large B-cell lymphoma using gene expression in formalin-fixed paraffin embedded tissue. Blood 2014;123(8):1214-7.

LPS Data

	Lane Sample Name	File Name	LPS Score	Subtype	HK Geomean	QC Status
1	Sample_001	Sample_0010.RCC	2770	ABC	3417	PASS
2	Sample_002	Sample_0020.RCC	N/A	N/A	7	FAIL
3	Sample_003	Sample_0030.RCC	2886	ABC	1989	PASS
4	Sample_004	Sample_0040.RCC	465	GCB	1837	PASS
5	Sample_005	Sample_0050.RCC	3982	ABC	1892	PASS
6	Sample_006	Sample_0060.RCC	462	GCB	3691	PASS
7	Sample_007	Sample_0070.RCC	28	GCB	100	BORDERLINE
8	Sample_008	Sample_0080.RCC	409	GCB	3615	PASS
9	Sample_009	Sample_0090.RCC	2837	ABC	4160	PASS
10	Sample_010	Sample_0100.RCC	2797	ABC	4162	PASS
11	Sample_011	Sample_0110.RCC	N/A	N/A	20	FAIL

Subtype Statistics Data

Pass and Borderline Subtype calls are represented in the table below, failures are excluded.

	Subtype	Count	Percent
1	ABC	5	56
2	GCB	4	44
3	UNCLASSIFIED	0	0
4	Total	9	100

QC Status Statistics Data

	QC Status	Count	Percent
1	PASS	8	73
2	FAIL	2	18
3	BORDERLINE	1	9
4	Total	11	100