



Original Sample QC

General Information

Order Number	1907UNHS-0108	Name of Customer	Yale Passamaneck	Date of Order	2019-07-18
--------------	---------------	------------------	------------------	---------------	------------

Final QC Result of DNA sample(s)				
Experiment Date	Sample count	Pass	Fail	Hold
N/A	N/A	N/A	N/A	N/A

Final QC Result of RNA sample(s)				
Experiment Date	Sample count	Pass	Fail	Hold
2019-07-18	6	0	0	6

The QC criteria are specified for requirements needed for a single run. Occasionally, we may encounter a shortage of sample volume or amount due to various reasons such as library construction failure or dried samples. In such case, we may notify the client and request for additional samples.

To avoid consequential delays, it is recommended to double the amount of sample, if possible.

*** Pass :** Samples automatically move forward to the next steps.

*** Hold :** A specific instruction should be given by the client for further processing.

Macrogen does not proceed to the next step until we have received the client's confirmation.

*** Fail :** Samples have failed to meet all the criteria set and cannot proceed to the next step.

Sample(s) will be put on hold until further written notice from the client.

As 5 ul was taken from the sample (library) QC purposes, the indicated volume represents 5 ul less than the total volume received.

QC Result of RNA

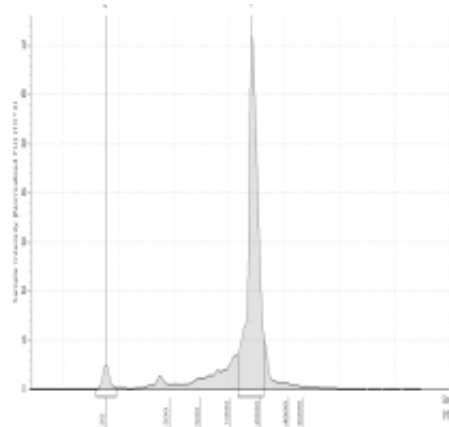
Arrival Date	2019-07-18	Experiment Date	2019-07-18	Tested by	SLC
Comment	All samples are placed on hold because abnormal pattern was observed (missing 28S peak). Please confirm the next step for these samples. Thank you.				

#	Sample Name	MacrogenSID	Conc. (ng/ul)	Volume (ul)	Total Amount (ug)	RIN	Added DW	Result*	
1	Drb-Whole2	S190718-0032	387.32	16	6.2	9.4		Hold	
2	Drb-Whole3	S190718-0033	952.94	17	16.2	8.8		Hold	
3	Drb029-Ovary	S190718-0034	165.79	16	2.65	10		Hold	
4	Drb029-Gill	S190718-0035	245.23	16	3.92	9.7		Hold	
5	Drb006-Foot	S190718-0036	326.44	15	4.9	9		Hold	
6	Drb023-Testes	S190718-0037	506.9	16	8.11	9.1		Hold	

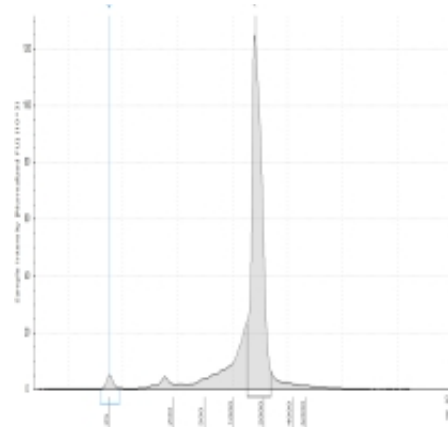
Experiment
Condition

RNA Screen Tape

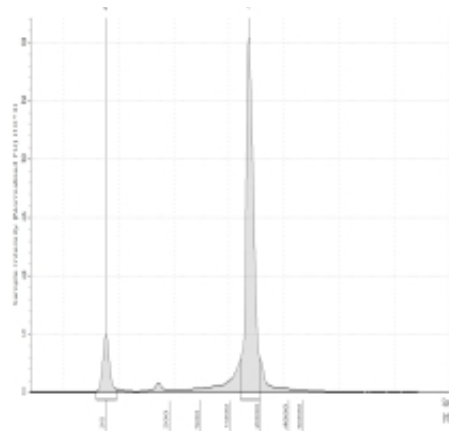
Enlarge=>Drb-Whole2



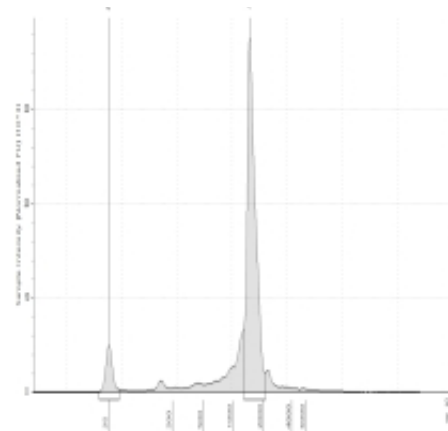
Enlarge=>Drb-Whole3



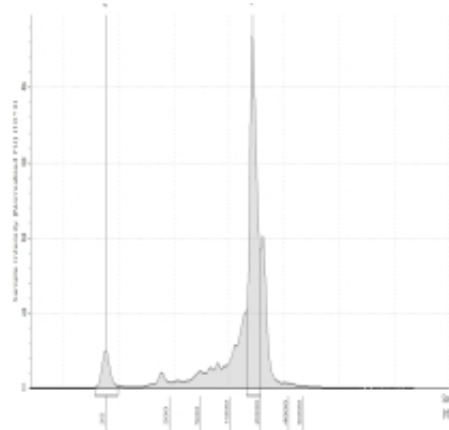
Enlarge=>Drb029-Ovary



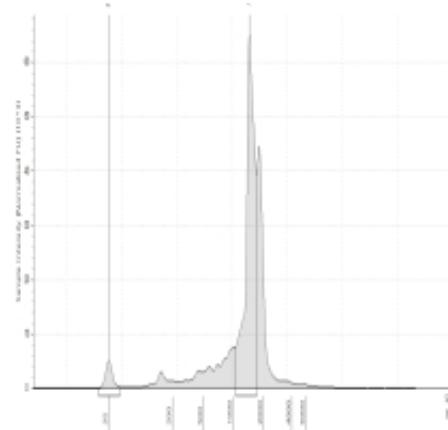
Enlarge=>Drb029-Gill



Enlarge=>Drb006-Foot



Enlarge=>Drb023-Testes



Sample QC Method

1. Quantity of DNA : Completed by picogreen* method using Victor X2 fluorometry.

MacroGen quantifies the starting genomic material by fluorescence-based quantification method, rather than UV-spectrometer-based method.

This is due to fluorescence-based methods accurately quantitate dsDNA even in the presence of common contaminants by employing double-stranded DNA specific dye.

UV spectrometer methods based on 260 OD readings are prone to overestimating the DNA concentration due to the presence of RNA and other contaminants found in gDNA preparations.

* Picogreen (Life technologies, cat# P7589)

2. Integrity of DNA : Completed by Agilent genomic DNA screentape.

The Genomic DNA ScreenTape assay offers a numeric measurement DNA Integrity Number (DIN)

3. Quantify of RNA : Completed by Ribogreen** method using Victor X2 fluorometry.

MacroGen quantifies the starting RNA material by fluorescence-based quantification method. **

** Ribogreen (Life technologies, cat# R11490)

4. Integrity of RNA : Completed by Agilent RNA screentape.

We check total RNA integrity using an Agilent Technologies 2100 Bioanalyzer or TapeStation with an RNA Integrity Number (RIN) value greater than or equal to 7.

We recommend adding DNase at the RNA isolation step to maximize the quality of RNA.

Sample QC Criteria

Platform	Requested Library Type		Sample QC Criteria			
			Conc. (ng/μl)	Vol. (μl)	Total Amount (μg)	DIN (RIN)
HiSeq / HiSeq X	Shotgun Library	TruSeq Nano Library	> 20 ng/μl	10 μl	0.1 μg	> 7.0
HiSeq / HiSeq X	Shotgun Library	TruSeq PCR Free Library	> 20 ng/μl	25 μl	0.5 μg	> 7.0
HiSeq / HiSeq X	Shotgun Library	KAPA Library Preparation (PCR Free)	> 20 ng/μl	20 μl	0.4 μg	> 7.0
HiSeq	Exome Library	SureSelect_V4_Post	> 20 ng/μl	50 μl	1 μg	> 7.0
HiSeq	Exome Library	SureSelect_V4+UTR_Post	> 20 ng/μl	50 μl	1 μg	> 7.0
HiSeq	Exome Library	SureSelect_V5_Post	> 20 ng/μl	50 μl	1 μg	> 7.0
HiSeq	Exome Library	SureSelect_V5+UTR_Post	> 20 ng/μl	50 μl	1 μg	> 7.0
HiSeq	RNA Library	TruSeq RNA Library	> 20 ng/μl	25 μl	0.5 μg	> 7.0
HiSeq	RNA Library	TruSeq Stranded RNA Library	> 20 ng/μl	25 μl	0.5 μg	> 7.0