

Original Sample QC

General Information

Order Number AN00021156 Name of Customer Sam White Date of Order 2024-09-06

Final QC Result of DNA sample(s)										
Order Registered Date	Total Ordered	Sample in Report	Pass	Fail	Hold					
2024-09-06	24	24	8	12	4					

Final QC Result of RNA sample(s)										
Order Registered Date	Total Ordered	Sample in Report	Pass	Fail	Hold					
N/A	N/A	N/A	N/A	N/A	N/A					

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.

 PSOMAGEN, INC. does not proceed to the next step until we have received the client's confirmation.
- st 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 DNA

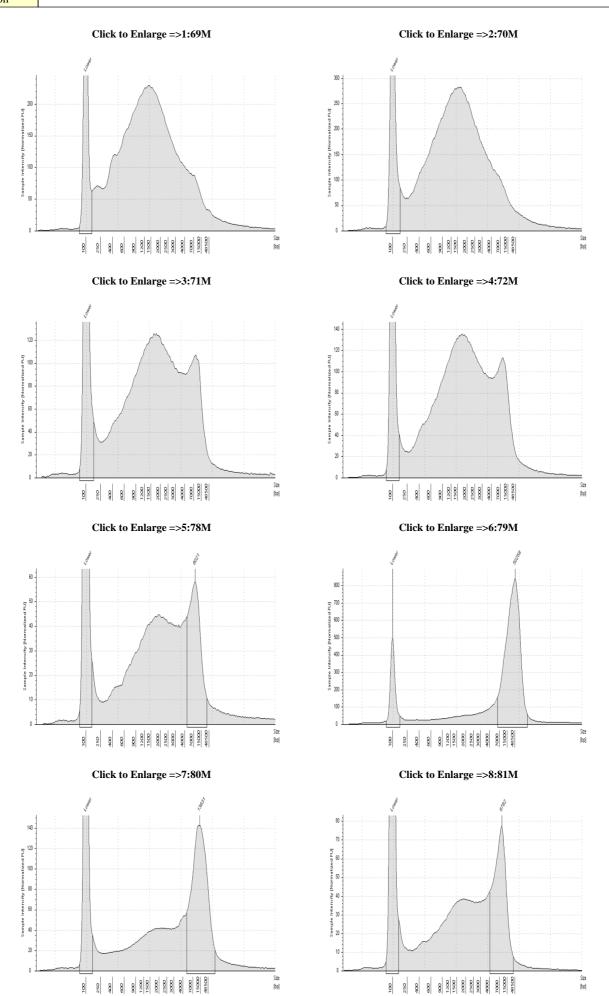
Worksheet Number	ANW240909S006Q003	Test Date	2024-09-09	Tested by	Suyeon Shin
Comment					

^{*} AddVol : We add DW or DEPC. Because of low Sample volume.

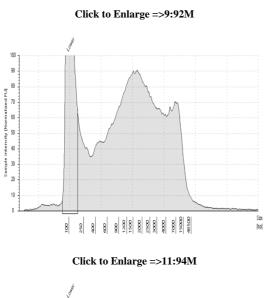
#	Sample Name	WSID	Conc. (ng/ul)	Add_Vol (ul)	Final Volume (ul)	Total Amount (ug)	DIN	Result*	
1	69M	ANW240909S006 AS0000192458	87.87	20	33	2.9	2.8	Fail	DIN
2	70M	ANW240909S006 AS0000192459	62.78	20	33	2.072	3	Fail	DIN
3	71M	ANW240909S006 AS0000192460	22.73	20	31	0.705	3.6	Fail	DIN
4	72M	ANW240909S006 AS0000192461	21.19	20	31	0.657	3.7	Fail	DIN
5	78M	ANW240909S006 AS0000192462	74.29	20	33	2.452	4.4	Fail	DIN
6	79M	ANW240909S006 AS0000192463	341.57	20	33	11.272	7.5	Pass	
7	80M	ANW240909S006 AS0000192464	97.07	20	33	3.203	6.1	Hold	DIN
8	81M	ANW240909S006 AS0000192465	46.3	20	33	1.528	5	Fail	DIN
9	92M	ANW240909S006 AS0000192466	69.28	20	33	2.286	3.5	Fail	DIN

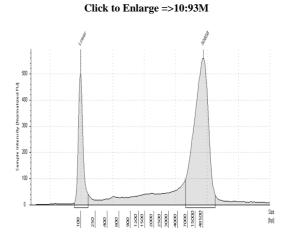
#	Sample Name	WSID	Conc. (ng/ul)	Add_Vol (ul)	Final Volume (ul)	Total Amount (ug)	DIN	Result*	
10	93M	ANW240909S006 AS0000192467	203.79	20	33	6.725	7.3	Pass	
11	94M	ANW240909S006 AS0000192468	120.93	20	33	3.991	3.5	Fail	DIN
12	95M	ANW240909S006 AS0000192469	674.94	20	31	20.923	6.3	Hold	DIN
13	105M	ANW240909S006 AS0000192470	168.65	20	33	5.565	4.5	Fail	DIN
14	106M	ANW240909S006 AS0000192471	319.61	20	31	9.908	7.6	Pass	
15	107M	ANW240909S006 AS0000192472	639.99	20	31	19.84	8	Pass	
16	109M	ANW240909S006 AS0000192473	306.88	20	32	9.82	8.2	Pass	
17	239M	ANW240909S006 AS0000192474	549.05	20	31	17.021	7.1	Pass	
18	240M	ANW240909S006 AS0000192475	17.93	20	31	0.556	2.8	Fail	DIN
19	241M	ANW240909S006 AS0000192476	55.01	20	30	1.65	2.6	Fail	DIN
20	242M	ANW240909S006 AS0000192477	16.99	20	31	0.527	1.6	Fail	DIN
21	269M	ANW240909S006 AS0000192478	98.31	20	31	3.048	6.6	Hold	DIN
22	270M	ANW240909S006 AS0000192479	73.41	20	30	2.202	6.1	Hold	DIN
23	271M	ANW240909S006 AS0000192480	248.79	20	31	7.712	8.6	Pass	
24	272M	ANW240909S006 AS0000192481	23.99	20	30	0.72	8.3	Pass	

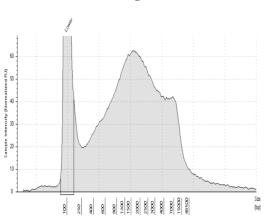
TapeStation gDNA Screen Tape

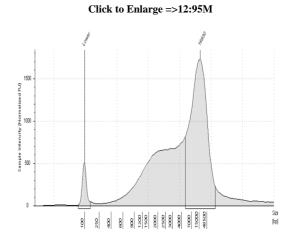


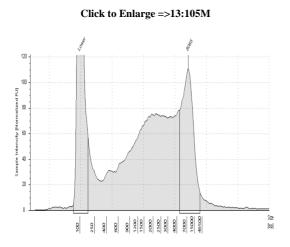
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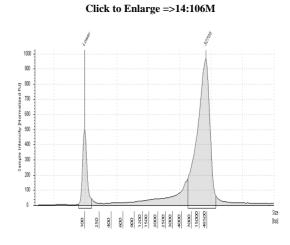


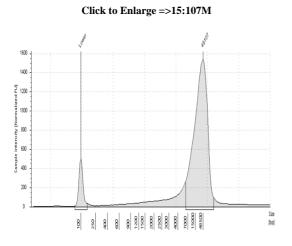


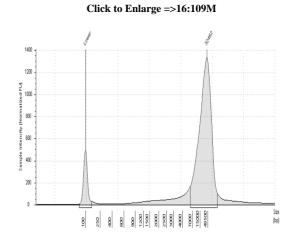




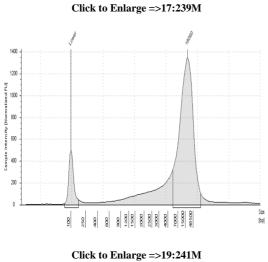


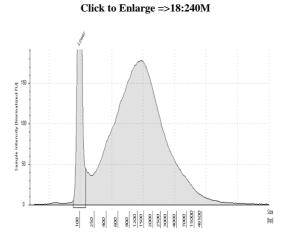


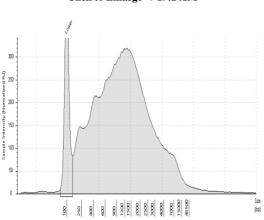


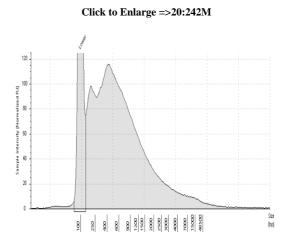


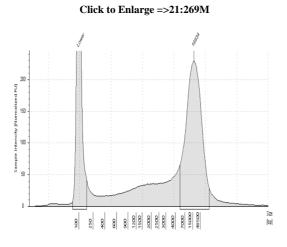
TapeStation gDNA Screen Tape

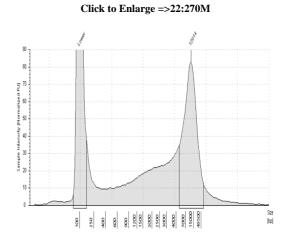


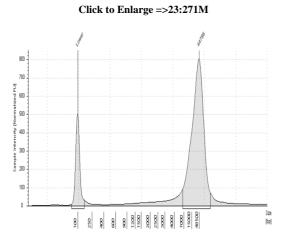


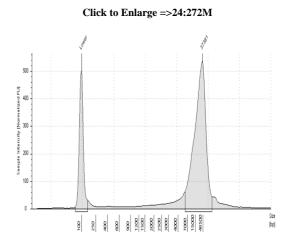












Sample QC Method

1. Quantity of DNA: Completed by *QuantiFluor dsDNA System using Victor X2 fluorometry.

PSOMAGEN, INC. 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.

* QuantiFluor dsDNA System (Promega, cat. E2670)

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.

PSOMAGEN, INC. 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	Library Type	Library Kit	Conc.(ng/ul)	Total Amount	DIN	etc
NovaSeqX	Whole Genome library	TruSeq Nano DNA (350)	-	0.100ug	7	
NovaSeqX	Whole Genome library	TruSeq Nano DNA (550)	-	0.200ug	7	
NovaSeqX	Whole Genome library	TruSeq DNA PCR Free (350)	-	0.500ug	7	
NovaSeqX	Whole Genome library	TruSeq DNA PCR Free (550)	-	1.000ug	7	
NovaSeqX	Whole Genome library	Nextera DNA XT	-	0.001ug	7	
NovaSeqX	Whole Genome library	Accel Methyl-Seq DNA library	-	0.100ug	7	
NovaSeqX	Whole Genome library	TruSeq ChIP-seq library	-	0.010ug	7	
NovaSeqX	Whole Genome library	Plexwell LP384	-	0.010ug	7	
NovaSeqX	Whole Genome library	Plexwell 96	-	0.010ug	7	
NovaSeqX	Whole Genome library	Plexwell 384	-	0.010ug	7	
NovaSeqX	Whole Genome library	Riptide	-	0.050ug	7	
NovaSeqX	Whole Genome library	Nextera DNA flex	-	0.010ug	7	
NovaSeqX	Whole Genome library	KAPAHyper(for SkrybAmp)	-	0.500ug	7	
NovaSeqX	Whole Genome library	KAPA hyper library preparation (std)	-	0.500ug	7	
NovaSeqX	Whole Genome library	Accel-NGS 2S PCR-free(cfDNA)	-	0.010ug	-	