NGS Library QC

General Information

Order Number	HN00155645	Name of Customer	Macrogen Europe	Date of Order	2021-08-10

Final QC Result of DNA sample(s)					
Arrival Date	Experiment Date	Sample count	Pass	Fail	Hold
2021-08-11	2021-08-13	4	0	4	0

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

*** Pass : Proceed with the library construction.**

*** Fail : Further processes are on hold until the replacement samples received.**

We do not recommend in proceeding further steps until a specific instruction was given from the client.

*** Hold : A specific instruction should be given by the client for further processing as the QC pattern may be triggered by the sample nature.**

Macrogen does not proceed the next step until we have received your permission.

As 3 ul was taken from the sample for sample (library) QC purposes, the indicated volume represents 3ul less than the total volume received.

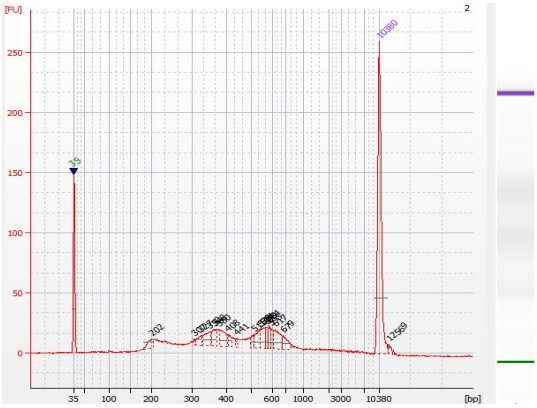
Library QC Result of DNA

Arrival Date	2021-08-11	Experiment Date	2021-08-13	Tested by	JJH
Comment	LightCycle qPCR				

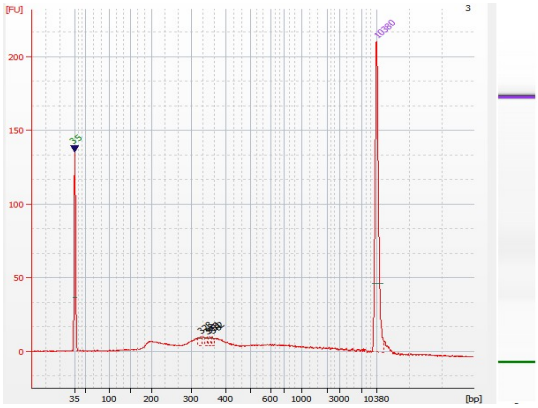
#	Library Name	Library Type	Conc. (ng/ul)	Conc. (nM)	Size (bp)	Result*	
1	DN1_WT_rep1	ETC	0.2	0.72	434	Fail	Low Quantity to (Run or Capture)
2	DN1_WT_rep2	ETC	0.26	0.97	409	Fail	Low Quantity to (Run or Capture)
3	DN1_KO_rep1	ETC	0.85	3.26	403	Fail	Low Quantity to (Run or Capture)
4	DN1_KO_rep2	ETC	0.24	0.88	417	Fail	Low Quantity to (Run or Capture)

Experiment Condition	Bioanalyzer DNA High Sensitivity chip

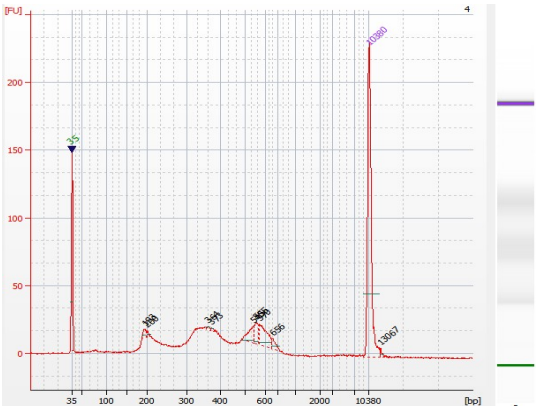
Click to Enlarge =>1:Library : DN1_WT_rep1



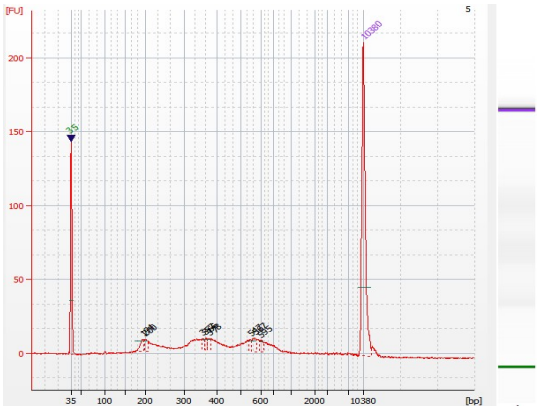
Click to Enlarge =>2:Library : DN1_WT_rep2



Click to Enlarge =>3:Library : DN1_KO_rep1



Click to Enlarge =>4:Library : DN1_KO_rep2



Library QC Method

1. Library Size Check

To verify the size of PCR enriched fragments, we check the template size distribution by running on a Agilent Technologies 2100 Bioanalyzer using a DNA 1000 chip.

2. Library Quanity Check

1) illumina library

In order to achieve the highest quality of data on Illumina sequencing platforms, it is important to create optimum cluster densities across every lane of every flow cell.
This requires accurate quantitation of DNA library templates.
So we quantify prepared libraries using qPCR according to the Illumina qPCR Quantification Protocol Guide.

2) PacBio library

To generate a standard curve of fluorescence readings and calculate the library sample concentration, we use Qubit standard Quantification solution and calculator.

Library DNA QC Criteria

Platform	Library Type	Library Kit	Conc (molecules/	Conc (nM)	Conc (ng/ul)	Size(bp) From	Size(bp) To	etc
NovaSeq	Modified Library	GBS library(single enzyme)	-	5	-	-	-	
NovaSeq	Modified Library	GBS library(double enzyme)	-	5	-	-	-	
NovaSeq	Modified Library	RAD Library(single Library)	-	5	-	-	-	
NovaSeq	Modified Library	RAD Library(double Library)	-	5	-	-	-	
NovaSeq	Modified Library	ETC	-	5	-	-	-	
NovaSeq		NGS library (Ready to Run)	-	10	-	-	-	at least 20ul