



NGS Library QC

General Information

Order Number	1308KFT-0010	Name of Customer	Katherine Hornick	Date of Order	2013-08-16
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Final QC Result of DNA sample(s)					
Arrival Date	Experiment Date	Sample count	Pass	Fail	Hold
2013-08-16	2013-08-28 15:05	2	2	0	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.

Library QC Result of DNA

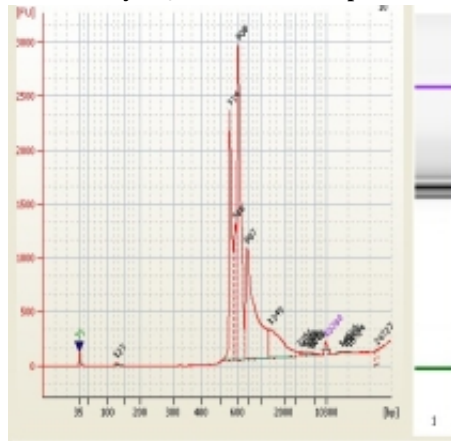
Arrival Date	2013-08-16	Experiment Date	2013-08-28 15:05	Tested by	
Comment					

#	Library Name	Library Type	Conc. (molecules/ul)	Size (bp)	Result*	
1	Quenec_North_Impact_1	Amplicon library (Lib-L Type)	28949116296	600	Pass	
2	Quenec_South_Impacted_3	Amplicon library (Lib-L Type)	12562500034	600	Pass	

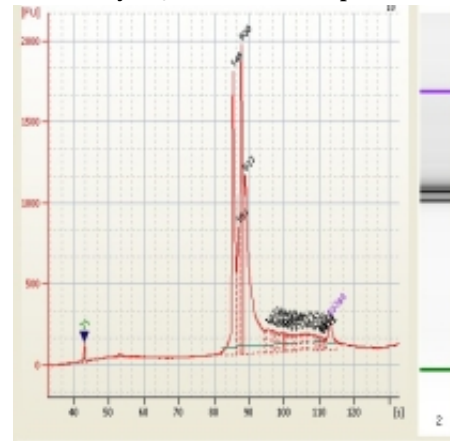
Experiment
Condition

Aglient bioanalyzer & Caliper Labchip GX DNA High Sensitivity

Library : Quenec_North_Impact_1



Library : Quenec_South_Impacted_3



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 Quantity 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) GS FLX library

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

Library DNA QC Criteria

Platform	Requested library type	QC Criteria				etc
		Conc (molecules/ μ l)	Conc (nM)	Conc (ng/ μ l)	Size (bp)	
GS FLX Plus	RL library (>1.5kb)	1.46×10^8			1400~1800	
GS FLX	RL library (>1.5kb)	1.46×10^8			600~900	
GS FLX	PCR product (LMW)	1.46×10^8				
GS FLX	Amplicon library	1.0×10^9				
GS FLX	Mate paired End library (3kb)			>0.2ng/ μ l	500~700	
GS FLX	Mate paired End library (8kb)			>0.2ng/ μ l	500~700	
GS FLX	Mate paired End library (20kb)			>0.2ng/ μ l	500~700	
HiSeq	TruSeq DNA library		5	>1.5ng/ μ l	400~500	
HiSeq	Mate paired End library (2~5kb)		5	>1.5ng/ μ l	350~650	
HiSeq	Mate paired End library (6~10kb)		5	>1.5ng/ μ l	350~650	
HiSeq	Mate paired End library (11~20kb)		5	>1.5ng/ μ l	350~650	
HiSeq	Nextera Mate Pair (Gel-free)		5	1.5 ng/ μ l	600~900	
HiSeq	Nextera Mate Pair (Gel-plus)		5	1.5 ng/ μ l	600~900	
HiSeq	Truseq DNA PCR-free (350bp insert)		2		250~1000	
HiSeq	Truseq DNA PCR-free (550bp insert)		2		450~1200	
HiSeq	Library for Nimblegen EZ Whole Exome	146		>35ng/ μ l	300~400	
HiSeq	Library for Sureselect	67		>17ng/ μ l	250~500	
HiSeq	Library for TruSeq Exome Enrichment		58	>15ng/ μ l	300~400	
HiSeq	ChIP seq library*		5	>1.5ng/ μ l	400~500	
HiSeq	Nextera library		2	-	200~1000	
HiSeq	Nextera XT library		2	-	200~1000	
HiSeq	TruSeq HT library (dual indexing)		5	-	400~500	
HiSeq	Whole Genome Bisulfite treated library		5	-	400~500	
HiSeq	MBD enriched library		2	-	400~500	
HiSeq	Library for nextera Rapid exome capture		58	>15ng/ μ l	250~350	
HiSeq	Amplicon library		2	-	-	

Library RNA QC Criteria

Platform	Requested library type	QC Criteria					etc
		Status	Conc (molecules/ μ l)	Conc (nM)	Conc (ng/ μ l)	Size (bp)	
GS FLX	cDNA Rapid library	Total RNA	1.46×10^8			600~1200	
GS FLX	cDNA Rapid library	purified mRNA	1.46×10^8			600~1200	
HiSeq	mRNA library	total RNA		5	>1.5ng/ μ l	200~400	
HiSeq	mRNA library	mRNA		5	>1.5ng/ μ l	200~400	
HiSeq	Strand-specific RNA library	total RNA		5	>1.5ng/ μ l	300~500	
HiSeq	Strand-specific RNA library	mRNA		5	>1.5ng/ μ l	300~500	
HiSeq	small RNA library	total RNA		2	>0.6ng/ μ l	140~160	
HiSeq	small RNA library	smallRNA		2	>0.6ng/ μ l	140~160	