BGI Sample Testing Report

1. Project Information

Report No.: THKa15101406

Project Name	UW - Sam ***** - Sam White - de-novo genome Panopea generosa			Project No.	F15FTSUSAT0328		
Customer Name	Steven Roberts			Customer Unit	Univ. of Washington		
Lab Sample Collector	YUEN Ka Yiu			Lab Sample Receiving Date	20151013		
Lab Sample Tester	Lam Tsz Tung, Li Wai Cheung, YUEN Ka Yiu			Lab Sample Testing Date	20151013		
Reported by	wongpolam	Inspected by	lamtsztung	Approved by	Wong Wai Man Vivien	Report Date	20151014

2. Sample Test Method

①Method of concentration determination:■Qubit Fluorometer、□NanoDrop、□Microplate Reader
②Method of sample integrity test:■Agarose Gel Electrophoresis

3. Sample Test Result

No.	Sample Name	Sample Number	Tube No.	Concen-tration(ng/μL)	Volume(μL)	Total Mass(μg)	Library type	Test result	Remark
1	gDNA geoduck	8521510002170	1	34	230	7.82	≤800bp Insert Size	Level A	

Note*:

1. The test result based on the 《DNA sequencing sample quality standards》 explains whether the testing sample meets the requirement of library construction.
a) Level A means the sample is qualified, and the amount of sample is sufficient for two or more library constructions.
b) Level B means the sample is qualified, but the amount of sample only satisfies one time library construction.
c) Level C means the sample does not totally meet the requirements of library construction and sequencing. BGI can try to construct the library but the quality of the sequence is not guaranteed
d) Level D means the sample does not meet the requirements of library construction and sequencing. BGI does not suggest in using this sample.
2. According to BGI's data, the one-time successful rate of library construction is more than 95% for samples of level A and level B.
3. According to BGI's data,the risks of library construction for sample of level C or level D are listed below:
a) The deficiency of the quantity: There may be the risk of failure in library construction and the yield of library of experiment may be too low to sequencing,.and the database of low yield for sequencing may lead to poor randomness.
b) Degradation of sample: It may cause high duplication rate of library and insert fragment will be abnormal."
c) Pollution by Protein or Insoluble Impurity: It may affect the fragmentation effect, leads to insert size unstable, influence the SNP analysis
d) RNA contamination: It possibly effects the DNA concentration quantitative accuracy.
4. If the partner insists on using the sample of level C or level D, the risk and responsibility is taken by the cooperative partner.
5. Other notes:
a) Sample is contaminated by protein.

4. Appendix

Appendix 1: Test results of Qubit Fluorometer or Microplate Reader
Appendix 2: Test results of Agarose Gel Electrophoresis
Appendix 3: Original information of sample

5. Statement

1. The results shown in this report refer only to the sample of the report unless otherwise stated.

2. This test report cannot be copied partly without the prior written permission of the Lab.

Appendix 1: Test results of Qubit Fluorometer or Microplate Reader

1. Pre-treatment

After the sample melted the ice, centrifuged and fully mixed, take appropriate samples for testing.

2.Test Result

Sample Name	Sample Number	Test Instrument	Test Kit	Dilution Ratio(×)	Test Volume (μL)	Test Concentration(ng/μL)	Concentration of original sample(ng/μL)	Remark
gDNA geoduck	8521510002170	Qubit	DNA BR	1	1	34	34	

Appendix 2: Test results of agarose gel electrophoresis

1. Pre-treatment

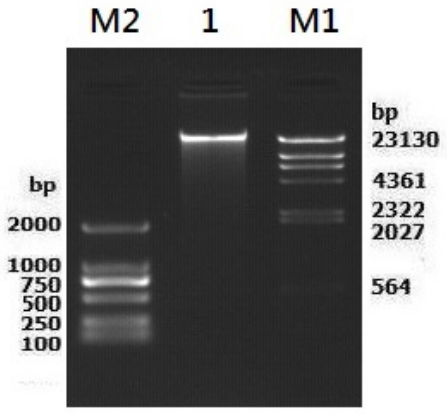
After the sample melted the ice, centrifuged and fully mixed, take appropriate samples for testing.

2. Test Parameter

Concentration of Agarose Gel: 1 %; Voltage: 150 V; Electrophoresis Time: 40 min

3. Test Result

(1)Electrophoretogram:



Lane No.	Sample Name	Dilution Ratio(×)	Test Volume(μL)	Sample Integrity	Remark
M1	λ-Hind III digest(Takara)	1	3		
1	gDNA geoduck	1	2.94		
M2	D2000 (Tiangen)	1	6		

Appendix 3: Original information of sample

Sample Type:									
Genome DNA									
Sample status:									
Dissolved in 10mM Tris-HCl									
Further Information:									
Sample Name	Species	No. of Tubes	Concentration(ng/μL)	Volume(μL)	Total Quantity(μg)	Fragment Size	OD260/280	OD260/230	Remark
gDNA geoduck	Panopea generosa	1	291	255	74.2		2.04	0	Please combine with DNA previously received for this project.

Report End