GLOBAL GENOMIC SERVICES

BGI Genomics

Single Cell Transcriptomics

Product Catalog

GLOBAL GENOMIC SERVICES

Contents

1 Why Smart-Seq2 Single Cell Full Transcriptomics?

Single Cell Transcriptome Sequencing uses SMART-Seq2 single cell full-length transcriptome amplification and high throughput DNBSEQ sequencing for full transcriptome analysis at cellular level. This powerful approach enables increased biological insight into areas not possible with traditional bulk transcriptome sequencing, for example the analysis of scarce cells, highly heterogenous inner tissue cells in early embryo development, stem cells, immune system research and single cell profiling of tumor heterogeneity.

2 Our Service

We do not provide mouth-pipetting single cell isolation services, however we do provide you with lysis buffer formulation. Simply select the cell of your choice and put it in the lysis buffer, then ship your sample to our laboratory with dry ice. We will perform SMART-Seq2 amplification, and if the sample is amplified successfully, we then proceed to sequencing using the DNBSEQ sequencing platform with a PE100 sequencing strategy. Bioinformatics analysis services can be provided. (See Fig 1). The typical turnaround time is around 35 working days.

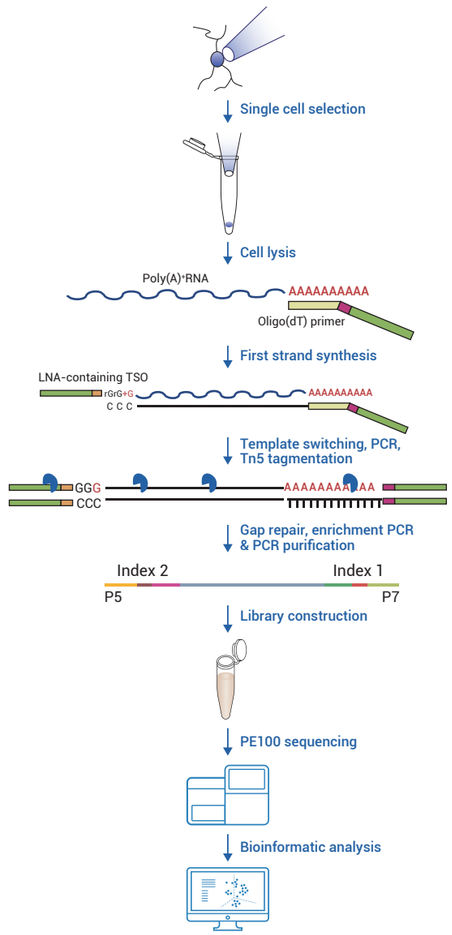

Fig 1. Service Workflow

3 Bioinformatics Workflow

Customers can choose two kinds of bioinformatics analysis service: standardized analysis delivered by Dr. Tom system or customized bioinformatics analysis performed according to customers' needs. (See Fig 2-5)

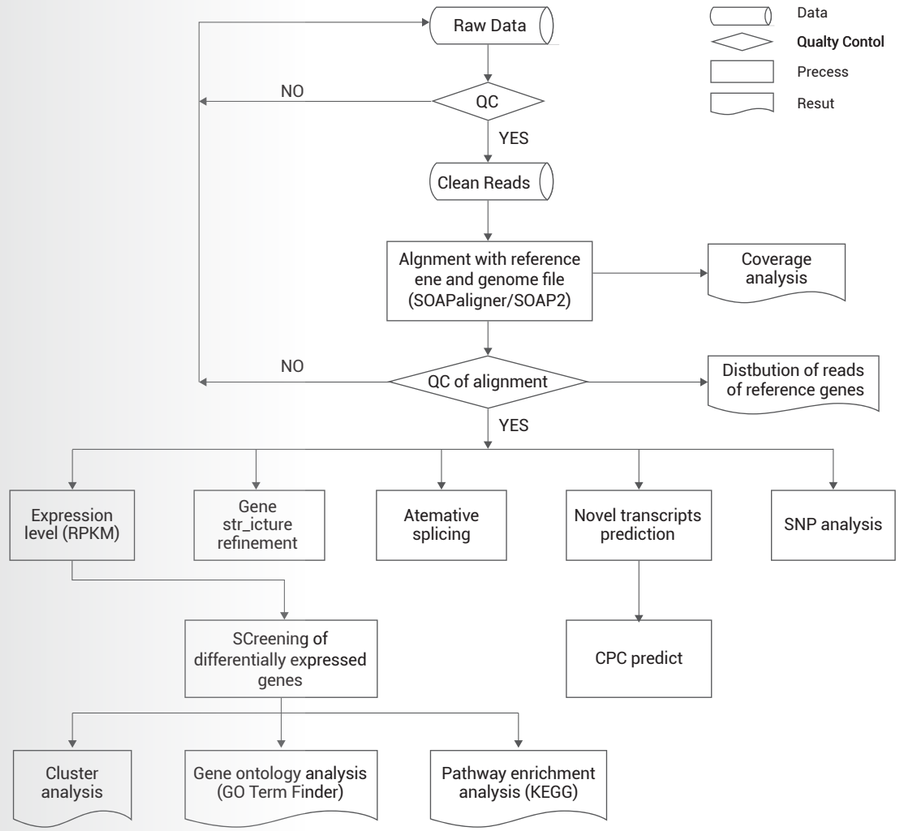

Fig 2. Bioinformatics Workflow

Bioinformatics Analysis	Bioinformatics Analysis Contents
Standard Bioinformatics Analysis	1, Data filtering includes removing adaptors contamination – low quality reads from raw reads. 2, Assessment of sequencing (Alignment statistics, Randomness assessment of sequencing, distribution of reads on the reference genome) 3, Gene expression and annotation (Gene coverage and coverage depth) 4, Gene expression difference analysis 5, Expression pattern analysis of DEGs 6, Gene ontology analysis of DEGs 7, Pathway enrichment analysis of DEGs 8, Refinement of gene structures 9, Identification of alternative spliced transcripts 10, Prediction and annotation of novel transcripts 11, SNP analysis
Advanced Bioinformatics Analysis	12, Gene fusion analysis (only for human) 13, Principal component analysis (PCA) 14, Condition - specific expressed analysis
Customized Bioinformatics Analysis	Customized according to client's needs

Fig 3. Heat Map by Dr. Tom

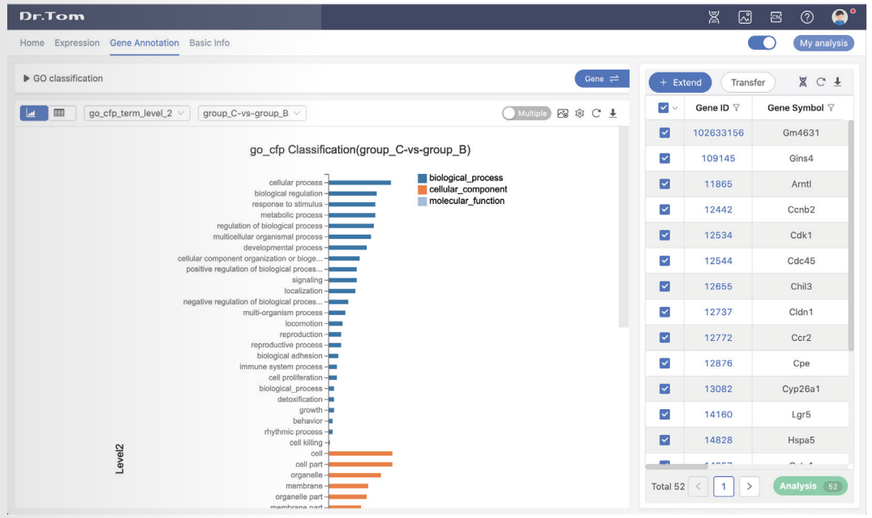

Fig 4. DEG GO Annotation by Dr. Tom

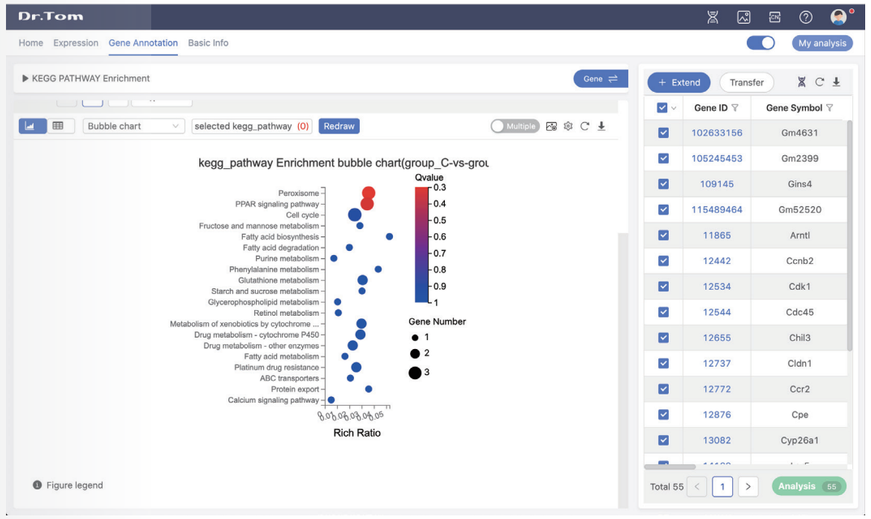

Fig 5. KEGG Pathway Enrichment by Dr. Tom

4 Sample Requirements

You can choose from two types of service: ‘Single Cell Service’ or ‘Few Cell Service’.
For single cell service, you can send samples in 1 or 2 cells per tube with a cell diameter greater than 10um, such as oocyte, single cell isolated from morula or cell lines.
For few cells service, you can send in sample with a few cells per tube, such as morula or blastocyst.
For specific requirement and guideline, please refer to the BGI sample preparation guideline.

Sample	Transcriptome
Single cell	1-2 cells (4μL lysis buffer)
Few cells	2≤X≤200 (4μL lysis buffer)
Total RNA	Total RNA>2ng; RNA 28S/18S≥1, RIN≥7; concentration>50pg/μL

www.bgi.com
info@bgi.com

BGI Americas

One Broadway, 14th Floor
Cambridge, MA 02142
U.S.A.

BGI Japan

Kobe KIMEC Center BLDG. 8F 1-5-2
Minatojima-minamimachi,
Chuo-ku, Kobe 650-0047 Japan

BGI Europe

Ole Maaløes Vej 3,
DK-2200 Copenhagen N,
Denmark

BGI Australia

L6,CBCRC, 300 Heston Road,
erston, Brisbane,
Queensland 4006, Australia

BGI Asia

Building NO.7, BGI Park,
No.21 Hongan 3rd Street,
Yantian District, Shenzhen
518083,China

Visit **www.bgi.com** for more information.

For Research Use Only. Not for use in diagnostic procedures (except as specifically noted).