Detection of copy number variation in single cells using Agilent microarray

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Copy number variation (CNV) exists in the blastomeres from human embryos and accounts for the development of early human embryos. However, few studies have been done concerning the copy number variation in the single cells due to the limited amount of DNA. In this study, we performed the analysis for genome-wide copy number variation detection in single cells using Agilent 244K array.

Two cell lines were used in this study: Epstein barr virus (EBV) transformed lymphoblastoids and blastomeres derived from human embryos. The goal of this study is to quantify the preprocessing methods of the Agilent microarray data derived from single amplified cells; investigate the segmentation algorithms to detect copy number variation in DNA from single amplified cells and compare the resolution of Agilent microarray with BAC array and SNP array.

Two methods were used to preprocess the Agilent microarray data separately: linear polynomial regression and loess regression. M-A plot was used to check the effect of these two normalization methods. Two algorithms were performed to detect the chromosomal segmentations from these two cell lines: Circular Binary Segmentation (CBS) and Adaptive Weights Smoothing (GLAD).

Genome-wide loess method normalized data better than the genome-wide linear polynomial method for amplified single cells. The segmentation results of CBS and GLAD were confirmed by the 3K-BAC array and 250-SNP array data derived from the same cells. Copy number variation can thus be detected in single cells using the Agilent 244K array. Further analysis of the specificity and sensitivity of the detection is needed.