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Single Cell Genomic Analyses of Circulating Tumor Cells

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Award: Pioneer Award

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Cancers are genomic diseases. Point mutation and copy number variation (CNV), which are two major dynamical changes of in cancer genomes, can now be studied at the single cell level by improved whole genome amplification and next generation sequencing [1]. Circulating tumor cells (CTCs) enter the circulation system from primary cancer issues and lead metastasis, which is responsible for 90% cancer related death. We found that CTCs of the same patient exhibit reproducible CNV gain and loss patterns, which are similar to those of the metastatic site. More interestingly, patients of the same cancer exhibit similar CNV patterns, suggesting that the CNV patterns are cancer and tissue dependent [2]. Reproducible for many patients of lung, breast, gastric, prostate and colon cancers, this result provides clues for the genesis of metastasis, as well as the prospect of noninvasive early diagnosis to identify the cancer types.