Copy number variation (CNV) is an important feature of the cancer genome. Blood-based low-pass whole genome sequencing (LP-WGS) has been increasingly used to identify CNVs of large genomic regions in cancer. In this study, we report the development of a proprietary NGS platform to identify segment-based CNVs and CNV abnormality in plasma samples from 500 cancer patients, including breast, prostate, pancreatic and lung cancers. With low volume of plasma sample input, our study demonstrates cancer type-specific pattern of CNV across chromosome arms. The chromosome instability (CIN) score is capable to distinguish cancer patients from healthy individuals and monitor disease progression for longitudinal patient samples.

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**RESULTS**

**CONCLUSIONS**

We have developed a proprietary Predicine LP-WGS assay platform. The assay’s CNV detection LOD is 15% tumor fraction with as low as 0.5ml plasma volume or 0.5ng cfDNA input. The CNV abnormality LOD is 2.5% tumor fraction. Clinical application of the Predicine LP-WGS assay demonstrates high sensitivity to distinguish cancer patients from normal individuals and the CIN score exhibits ability to monitor disease progression and early cancer detection.

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