|  |
| --- |
| **Title** |
| **Cancer detection and monitoring by liquid biopsy** |
| **Author(s)** |
| *Presenting author's name should be underlined and be without degrees or titles.***Duhee Bang** |
| **Affiliation(s)** |
| *Author(s) should be listed by department, institution, city and country.***Yonsei University, College of Science, Seoul, Korea** |
| **Content** |
| While considerable progress has been made in the field of genomics for early cancer detection, most existing studies have primarily focused on single aspects, such as targeted methylation panels or whole-genome sequencing. Our work attempts to build upon these foundations by introducing an integrated platform that employs a single assay for the simultaneous analysis of whole-genome methylation, copy number variations, and other genomic patterns. Utilizing a diverse set of plasma and tissue samples from both healthy individuals and patients suffering from multiple cancer types, we generated high-resolution whole-genome methylation sequencing (WGMS) data. We introduce the concept of a "cancer signature ensemble", which appears to show improved performance over traditional single-feature models. Importantly, the versatility of this integrated approach suggests potential utility not only for early cancer detection but also for monitoring tumor prognosis. We believe our approach represents a promising step toward enhancing cancer care. |