

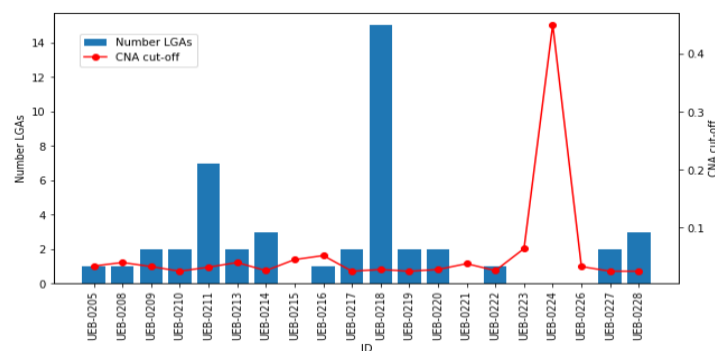


Figure S1. Analysis for homologous recombination detection in shallow WGS in breast cancer patients. The figure shows the number of large-scale genomic recombination events detected by shallowHRD algorithm¹. Values greater than 15 are considered positive to homologous recombination deficiency.

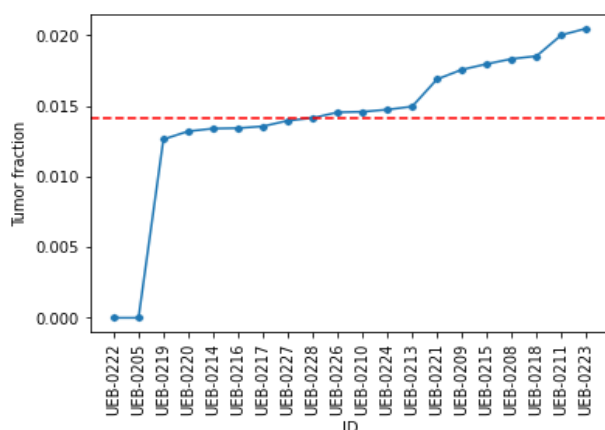


Figure S2. Tumor fraction of cfDNA in shallow WGS in breast cancer patients. The mean tumor fraction detected in this study was 0.014 (range 0-0.02047) evaluated by the ichorCNA algorithm².

References

1. Eeckhoutte, A. *et al.* ShallowHRD: detection of homologous recombination deficiency from shallow whole genome sequencing. *Bioinforma. Oxf. Engl.* **36**, 3888–3889 (2020).
2. Adalsteinsson, V. A. *et al.* Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. *Nat. Commun.* **8**, 1324 (2017).