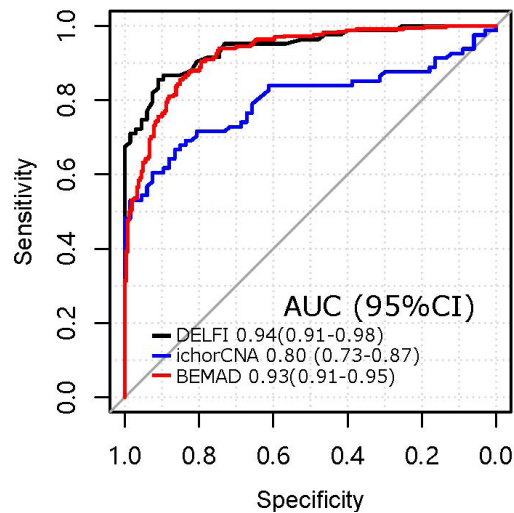
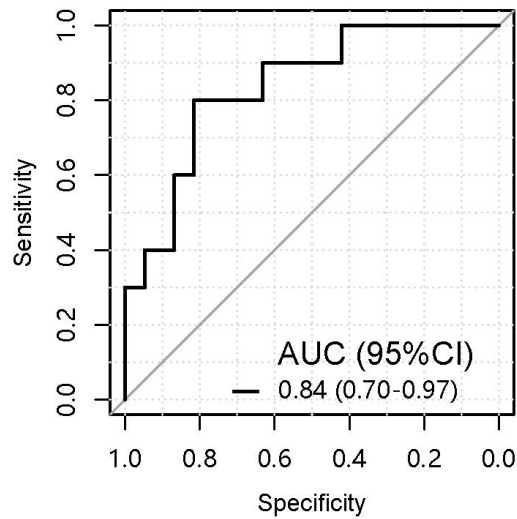


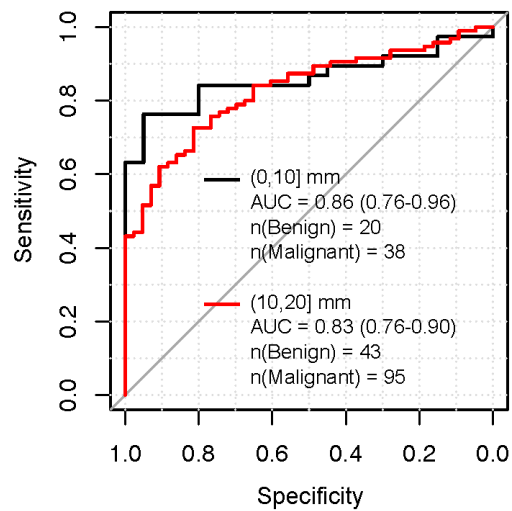
**Figure S1** Workflow of this study. CT, computed tomography; WGS, whole-genome sequencing; LD, low-depth.



**Figure S2** Comparison between the other two methods (ichorCNA and DELFI) to our method using the LUCAS cohort. AUC, area under the receiver operating characteristic curve; CI, confidence interval; DELFI, DNA evaluation of fragments for early interception; CNA, copy number alteration; BEMAD, benign and malignant diagnostic; LUCAS, Longitudinal Urban Cohort Ageing Study.



**Figure S3** An external independent dataset from The CUHK including 38 healthy control and 10 lung cancer patients for validation. AUC, area under the receiver operating characteristic curve; CI, confidence interval; CUHK, Chinese University of Hong Kong.



**Figure S4** Performance of the BEMAD model to diagnose pulmonary nodules of 6–20 mm. AUC, area under the receiver operating characteristic curve; BEMAD, benign and malignant diagnostic.