|  |
| --- |
| **Supplementary Table 5.** Gene abnormality prediction results for cohort 1 and 2, with a combination of six pathomorphological features. |
|  | Validation cohort 1 | Validation cohort 2 |
| Gene abnormality | Coverage | Accuracy | AUC | Coverage | Accuracy | AUC |
| *BRAF*V600E | 0.653  | 0.883  | 0.852  | 0.652  | 0.891  | 0.863  |
| MSI | 0.806  | 0.965  | 0.944  | 0.957  | 0.960  | 0.866  |
| *KRAS* | 0.335  | 0.639  | 0.736  | 0.300  | 0.606  | 0.718  |
| The conditions are as follows; *BRAF*V600E; monotonized images and the primary site is left and cribriform with mucin minus or plus, or monotonized images and the primary site is right and solid nest with large nest consisting of usual cell, or monotonized images and the primary site is left and the percent of tumor content is over 50%. The necessary selected tiles for each patient is over 10. MSI; monotonized images and the primary site is left and the percent of tumor content is over 50%, or monotonized images and the primary site is right and cribriform with mucin plus, or original images and the primary site is left and nuclear shape is elliptic or oval. The necessary selected tiles for each patient is over 0. *KRAS*; monotonized images and the primary site is left and solid nest with large nest regardless of cell type, or monotonized images and the primary site is right and solid nest with small nest regardless of cell type, or monotonized images and solid nest with small nest consisting of usual cells. The necessary selected tiles for each patient is over 20. |