**Supplementary Figure S1. The quantitative performance of the ddPCR assay for the *TERT*-p and *BRAFV600E* mutations.** The mutant PCR products were serially diluted and mixed with the wild-type PCR products to achieve mutation fractions of 0, 1, 5, 10, 50, and 100% in samples with different total DNA copy numbers: (a) *TERT* 500, (b) *TERT* 1,000, (c) *TERT* 3,000, (d) *TERT* 9,000, (e) *BRAF* 500, (f) *BRAF* 1,000, (g) *BRAF* 3,000, and (h) *BRAF* 9,000 copies. Each point represents the mean and standard deviation of eight reactions. The best fit line and the coefficient of determination, R2, are shown.

**Supplementary Figure S2. The detection limit of the ddPCR for the *TERT* promoter mutations.** The *TERT*-p mutant PCR products were serially diluted and mixed with the wild-type PCR products to obtain samples with mutation fractions of 0, 0.125, 0.25, 0.5, and 1% in samples with the total DNA copy numbers of 250, 500, 1,000, 3,000, 6,000, and 12,000. For each sample, the ddPCR was performed in six replicates. To determine the cutoff percentage of the *TERT*-p mutant allele at a given total DNA copy number that achieves statistically significant difference from the wild-type sample, the Kruskal-Wallis test with the Dunnet’s post-test was used. For each point, lines represent median and interquartile range. \*, *p* < 0.05; \*\*, *p* < 0.01; \*\*\*, *p* < 0.001.

**Supplementary Figure S3. The correspondence analysis of the mutational status of FNA and FFPE specimens and clinicopathological features.** The biplotdisplays six types (indicated by the red arrows) of combinations of DNA origin (FNA or FFPE) with their mutational status (TERTwt, TERTmut, BRAFwt and BRAFmut) in principal coordinates. Clinicopathological features (individually labeled black circles) are displayed in contribution coordinates, which are the standard coordinates multiplied by the square root of the corresponding masses. The number of dimensions retained in the present analysis was five, and two major ones are presented: Dimension 1 and 2, which accounted for 95.4% of variance. The analysis was performed in R with the CA and factoextra packages. The colgreen option was used to calculate biplot principal coordinates for the DNA origin/mutation types and contribution coordinates for categorical clinicopathological variables.