Figure S1. Our next-generation sequencing panel performance evaluation. (A) Alternative allelic frequencies obtained with our panel for the nine samples of the 2017 European Molecular Genetics Quality Network quality control run, compared with expected frequencies. (B) Alternative allelic frequencies obtained for eight variants from an internal control in 231 consecutive runs. Vertical bars indicate minimum and maximum values.

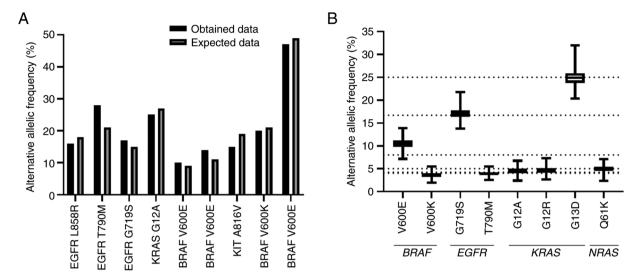


Figure S2. Gain-of-function and loss-of-function variants for each target gene of our next-generation sequencing panel detected in the four tumor types during three years of routine use. Lung cancers appear in white, colorectal cancers in black, melanomas in dark grey, and GISTs in light grey. GIST, gastrointestinal stromal tumor.

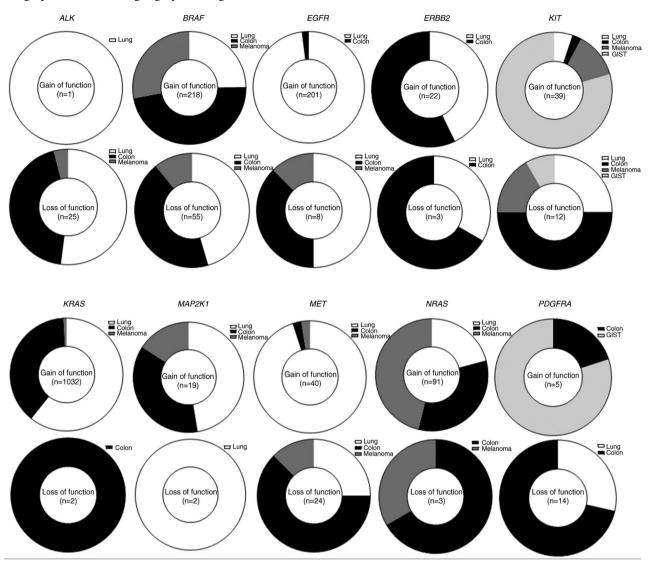


Figure S3. Continued.

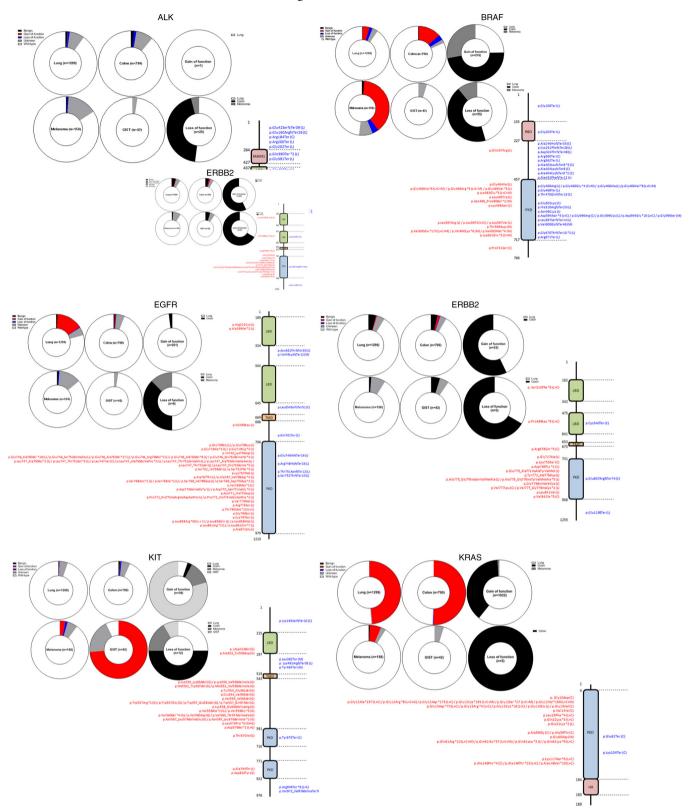


Figure S3. Benign (black), gain-of-function (red), loss-of-function (blue), unknown significance (grey) and wild-type (white) variants in each gene of our next-generation sequencing panel, by tumor type, followed by the distribution of the gain-of-function and loss-of-function variants in the resulting protein. Gain-of-function mutations are listed in red on the left side of the protein outline whereas loss-of-function mutations are in blue and on the right (L), Lung cancer; (C), colorectal cancer; (M), melanoma; (G), gastrointestinal stromal tumor (GIST).

