Supplementary Online Content


**eFigure.** *BRAF* V600E mutation detection sensitivity assayed using two methods

This supplementary material has been provided by the authors to give readers additional information about their work.
**eFigure.** *BRAF* V600E mutation detection sensitivity assayed using two methods

A. The sensitivity of the Sanger sequencing method for *BRAF* V600E detection was tested by mixing genomic DNA extracted from human saliva and MM96L melanoma cell line DNA in ratios of 0:1, 1:0, 1:1, 1:3, 1:5 and 1:10 in a total volume of 100ul for each ratio. The *BRAF* V600E mutation is indicated as A/T in the chromatograms. B, *BRAF* mutation was also independently tested by quantitative MALDI-TOF assay (SA Pathology, Adelaide, Australia) to detect the V600E mutation. The sample column lists the DNA extracted from microbiopsy samples from each dermoscopic area (I-III) of the lesion along with the ratios of genomic DNA from human saliva and MM96L controls that were tested for the mutation. The genotype column indicates the percentage of the V600E mutation detected in the samples.