Supplementary table 1

NRAS primer sequences for successive cycles of enzymatic digestion of wild-type allele and hemi-nested PCR, to selectively amplify mutant allele in mosaic tissue.

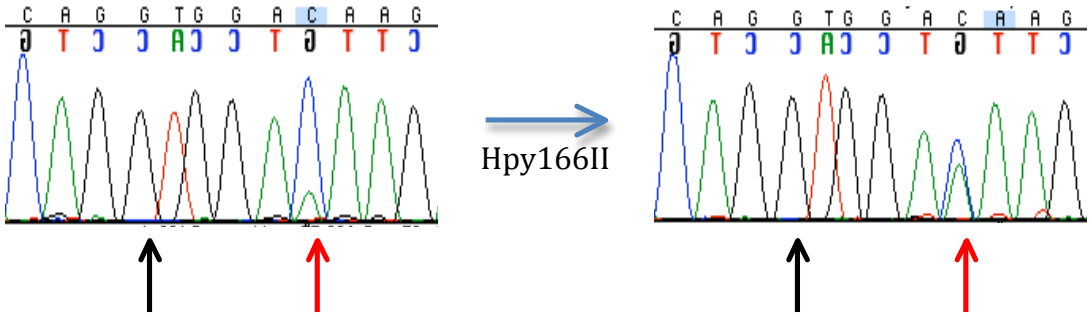
Q61K mosaicism detection	Q61R mosaicism detection
Forward primer: 5'TGTTTGTTGGACATACTGGATACAGC>GTGGA3'	**Forward primer:** 5'TGTTTGTTGGACATACTGGATACAGCTGG>TA3'
Reverse primers: 1. 5'GATAGAGCTTTTTAATTATGG3' 2. 5'GAGGTTACCACACTAGGGAA3' 3. 5'GAATCTTTATGGGGAAAT3' **4.** 5'AAAGGATGATCTTTGTGTTCT3'	**Reverse primers:** as for Q61K

Supplementary figure 1

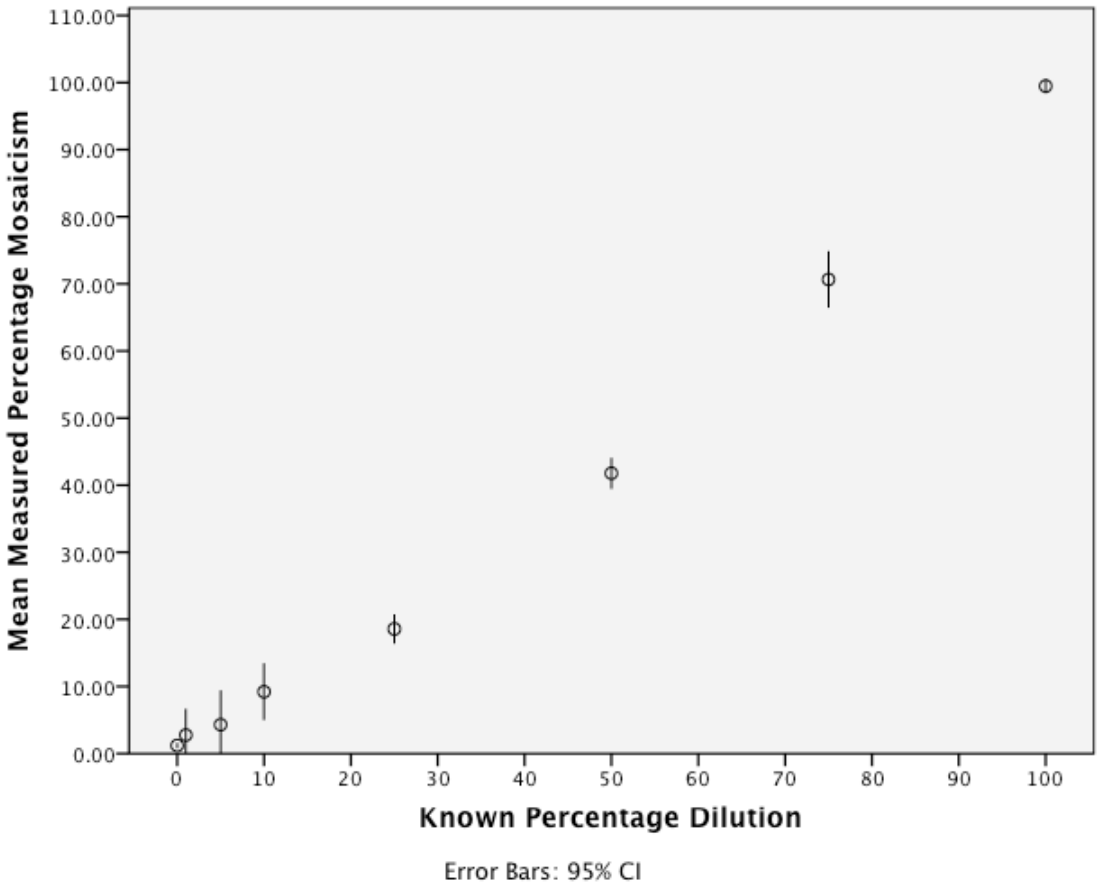
A. An example of forward sequence, showing improvement in detection of a Q61K heterozygous mutation (red arrows) after one cycle of enzymatic digestion of the wild-type allele. The black arrow indicates the position of site directed mutagenesis, introducing the recognition sequence for Hpy166II (GTNNAC).

B. Validation of the measurement of percentage of mosaicism used in this study. Percentage of mosaicism was measured in triplicate in samples of known percentage of *NRAS* Q61K mutation, produced by TA cloning of heterozygous samples. Correlation between mean measured and predicted percentages was high (two-tailed Pearson $r^2 = 0.990$, $p<0.001$).

A



B


Mean Measured Percentage Mosaicism
110.00
100.00
90.00
80.00
70.00
60.00
50.00
40.00
30.00
20.00
10.00
0.00
0
10
20
30
40
50
60
70
80
90
100
Known Percentage Dilution
Error Bars: 95% CI