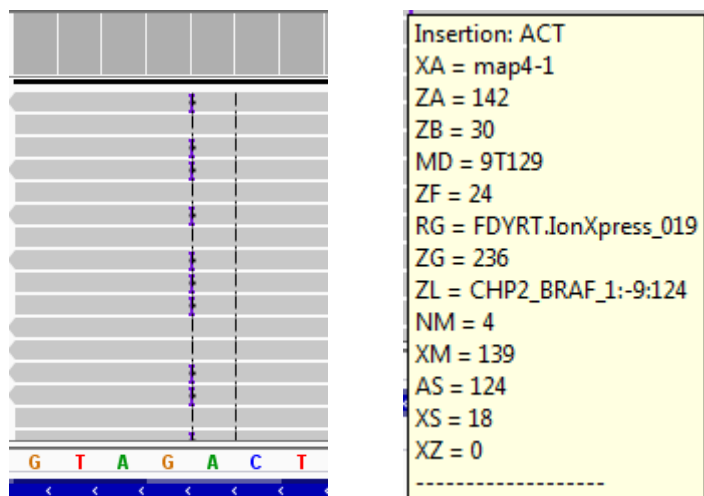


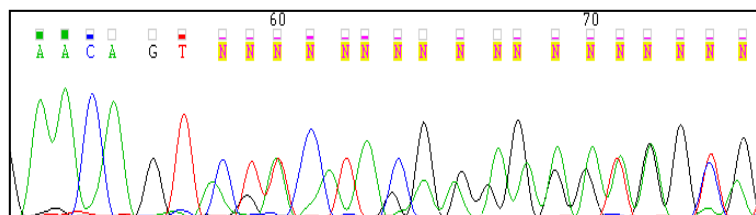
Figure S1: Sanger validation of BRAF mutations

Sample: OMCR18-059TK

NGS



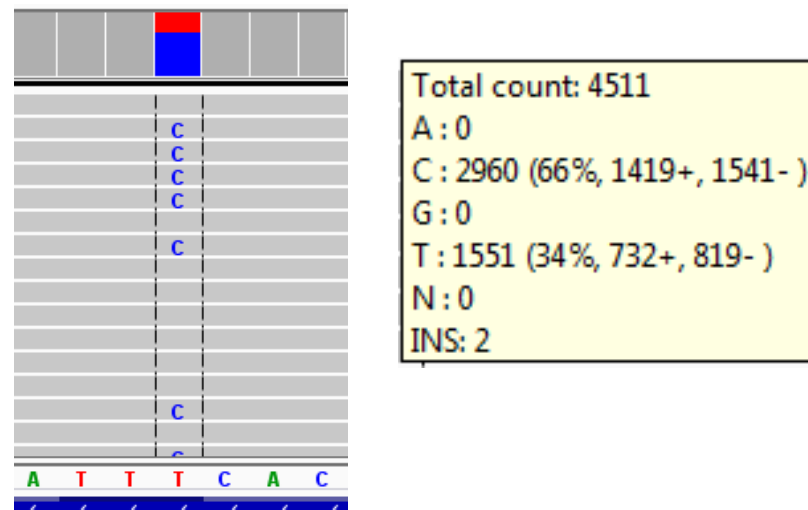
Sanger Seq



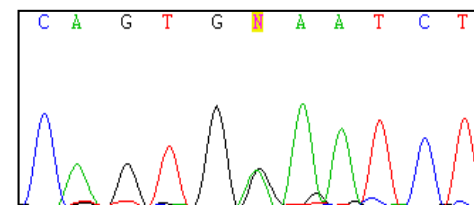
***BRAF* c. 1412_1413insAGT; *BRAF* p.V471dup**

Sample: OMCR13-011TK

NGS



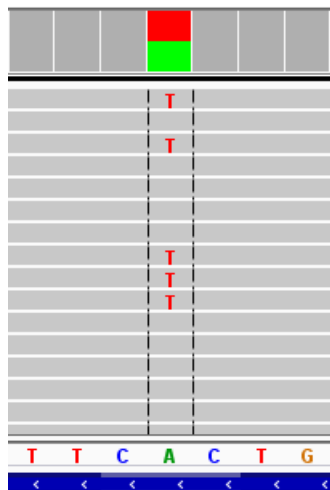
Sanger Seq



***BRAF* c.1801A>G; *BRAF* p.K601E**

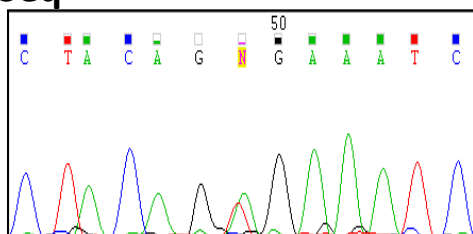
Sample: OMCR16-005TK

NGS

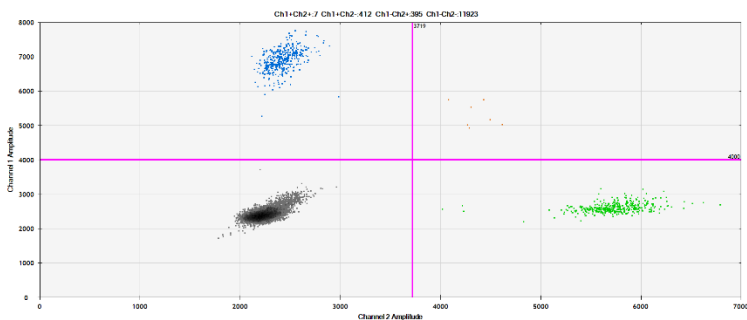


Total count: 6839
A : 3360 (49%, 1574+, 1786-)
C : 6 (0%, 2+, 4-)
G : 3 (0%, 2+, 1-)
T : 3470 (51%, 1548+, 1922-)
N : 0
INS: 3

Sanger Seq



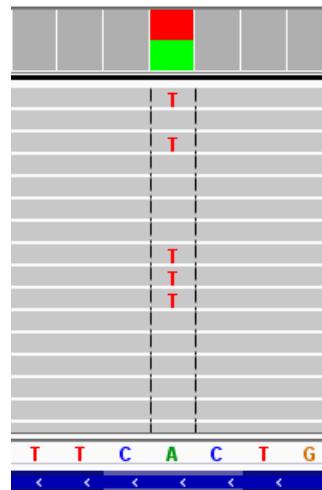
ddPCR (51.5%)



BRAF c.1799T>A; BRAF p.V600E

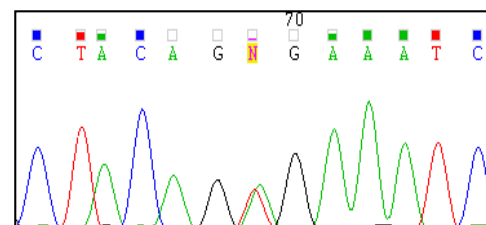
Sample: OMCR18-025TK

NGS

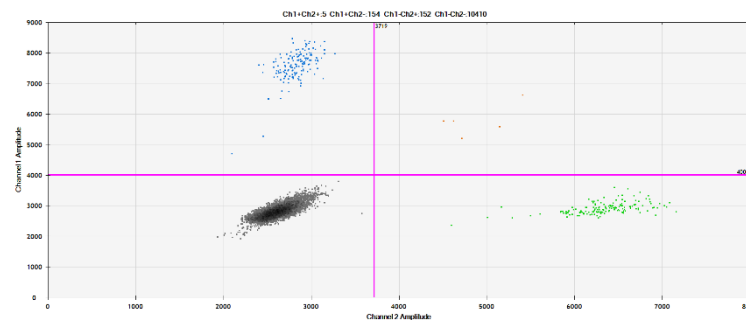


Total count: 4125
A : 2116 (51%, 1102+, 1014-)
C : 4 (0%, 2+, 2-)
G : 3 (0%, 2+, 1-)
T : 2002 (49%, 1011+, 991-)
N : 0
INS: 1

Sanger Seq



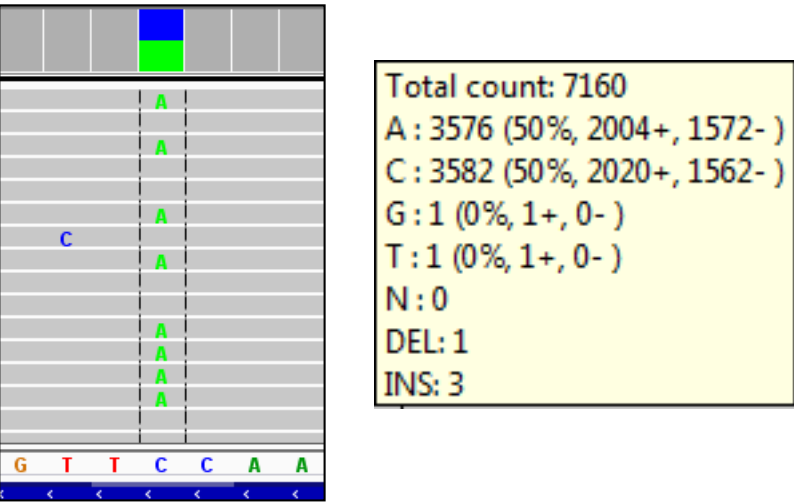
ddPCR (50.6%)



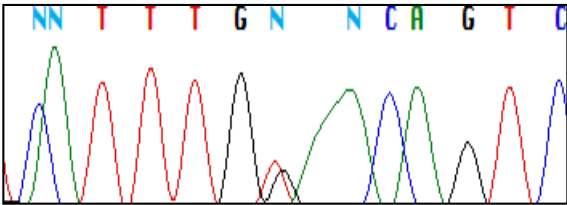
BRAF c.1799T>A; BRAF p.V600E

Sample: OMCR19-011TK

NGS



Sanger Seq



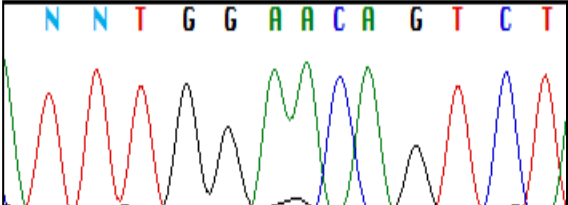
BRAF c.1406G>T; BRAF p.G469V

Sample: OMCR19-060TK

NGS

Wild Type

Sanger Seq



BRAF Wild-type; BRAF Wild-type