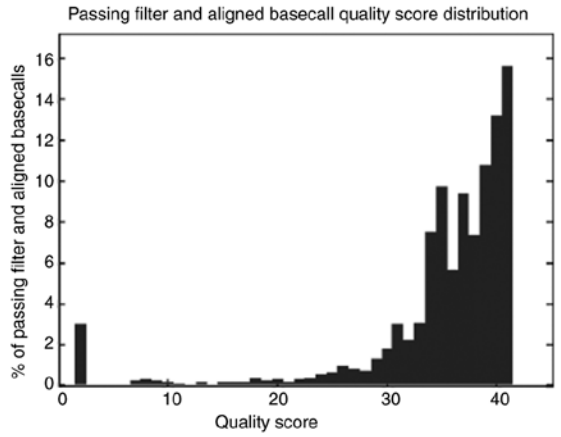
Figure S1. Continued.

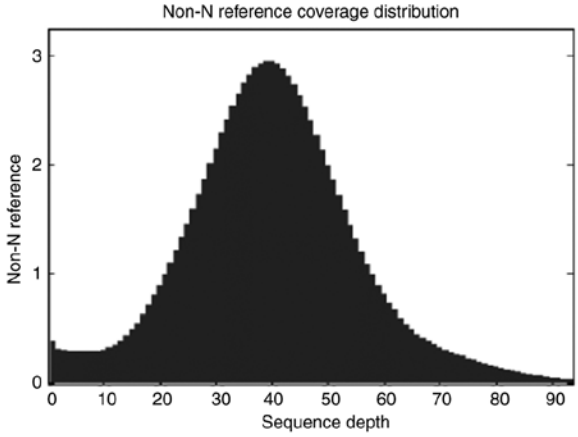
A

B381

	Yield (gigabases)	%Bases>=Q30
Passing filter	137.5	88.3%
Passing filter and aligned	122.3	89.0%

	Mean Coverage	% Positions>=1X Coverage	% Positions>=10X Coverage
Non-N reference	40.7	98.0%	95.2%
Genes	41.4	98.7%	96.9%
Exons	40.7	97.9%	96.6%



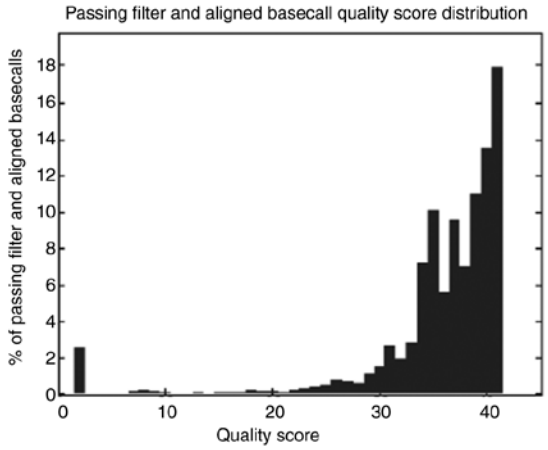


B

B450

	Yield (gigabases)	%Bases>=Q30
Passing filter	116.3	90.2%
Passing filter and aligned	104.0	90.7%

	Mean Coverage	% Positions>=1X Coverage	% Positions>=10X Coverage
Non-N reference	35.0	98.3%	96.0%
Genes	34.9	98.9%	97.1%
Exons	34.1	98.0%	96.8%



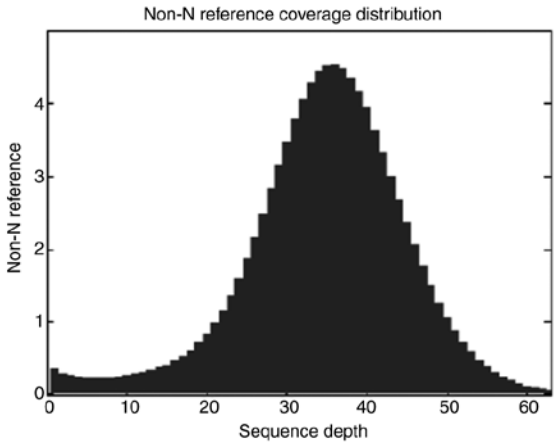


Figure S1. Data volume and coverage summaries. The samples had a high quality score with a percentage base calling of >Q30 indicating a smaller probability of error following alignment to the human reference genome (NCBI37). The passing filters gave the yield in Gigabases of data from the samples input into the NCBI37 reference genome, while the passing filter and aligned reported only the subset of data in Gigabases that aligned to the NCBI37 reference genome. (A) Sample B381 had 89.0% of filtered and aligned reads with a mean depth of coverage of 40.7. (B) Sample B450 had 90.7% of filtered and aligned reads with a mean depth of coverage of 35.0. (C) Sample M456 had 89.3% of filtered and aligned reads with a mean depth of coverage of 33.6. (D) Sample M478 had 88.3% of filtered and aligned reads with a mean depth of coverage of 34.2.

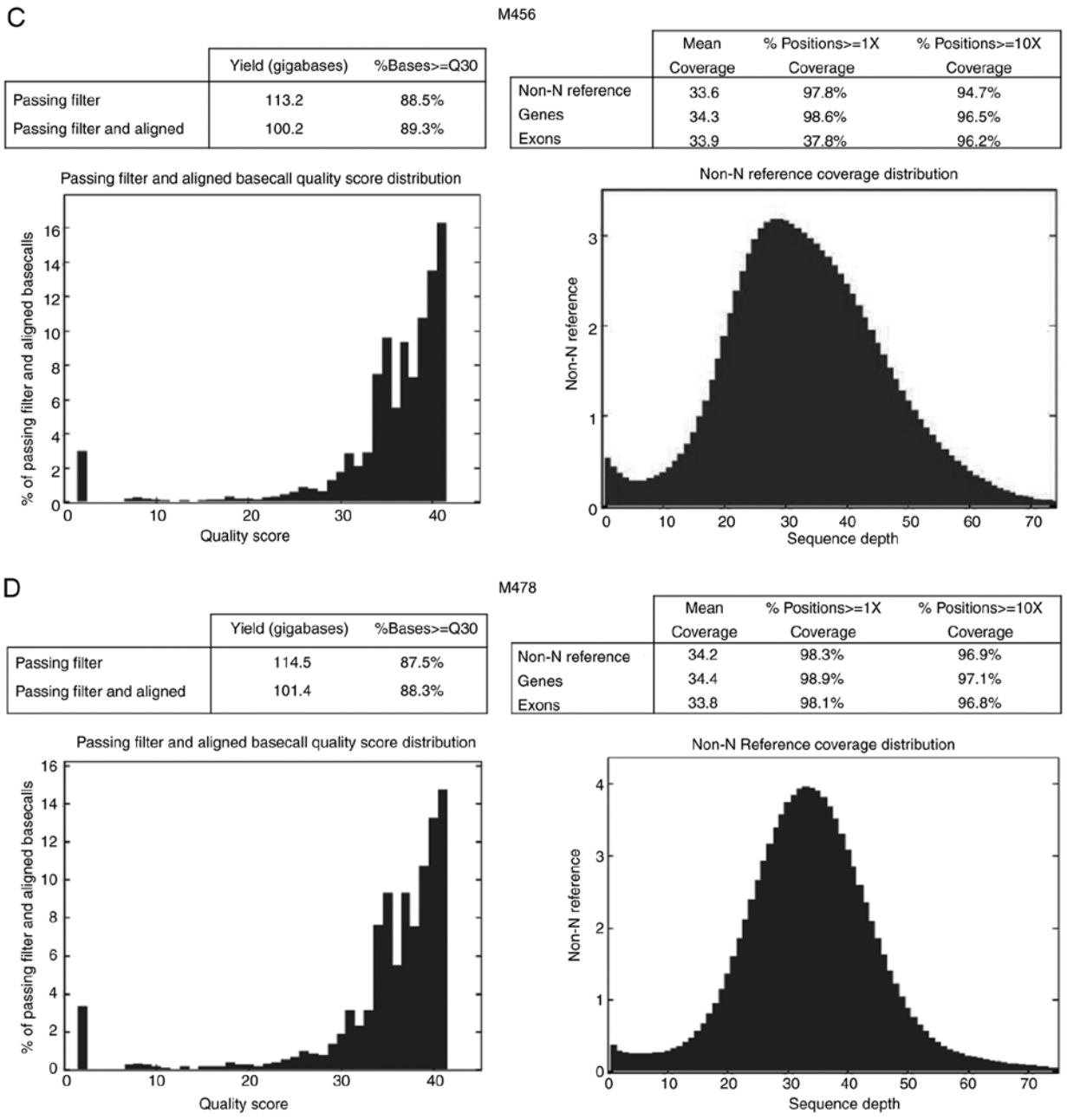


Figure S2. Untrimmed western blots showing the entire lane. Representative raw data of full western blots of (A) BCLAF1, (B) Caspase-3, (C) Caspase-9 (D) BAX, (E) p53, (F) p21, (G) EXO1 and (H) BCL2 proteins. Separate amplification of GAPDH served as a housekeeping gene to control for loading in each set of experiments. BCLAF1, BCL2 associated transcription factor 1; EXO1, exonuclease 1; siRNA, small interfering RNA.

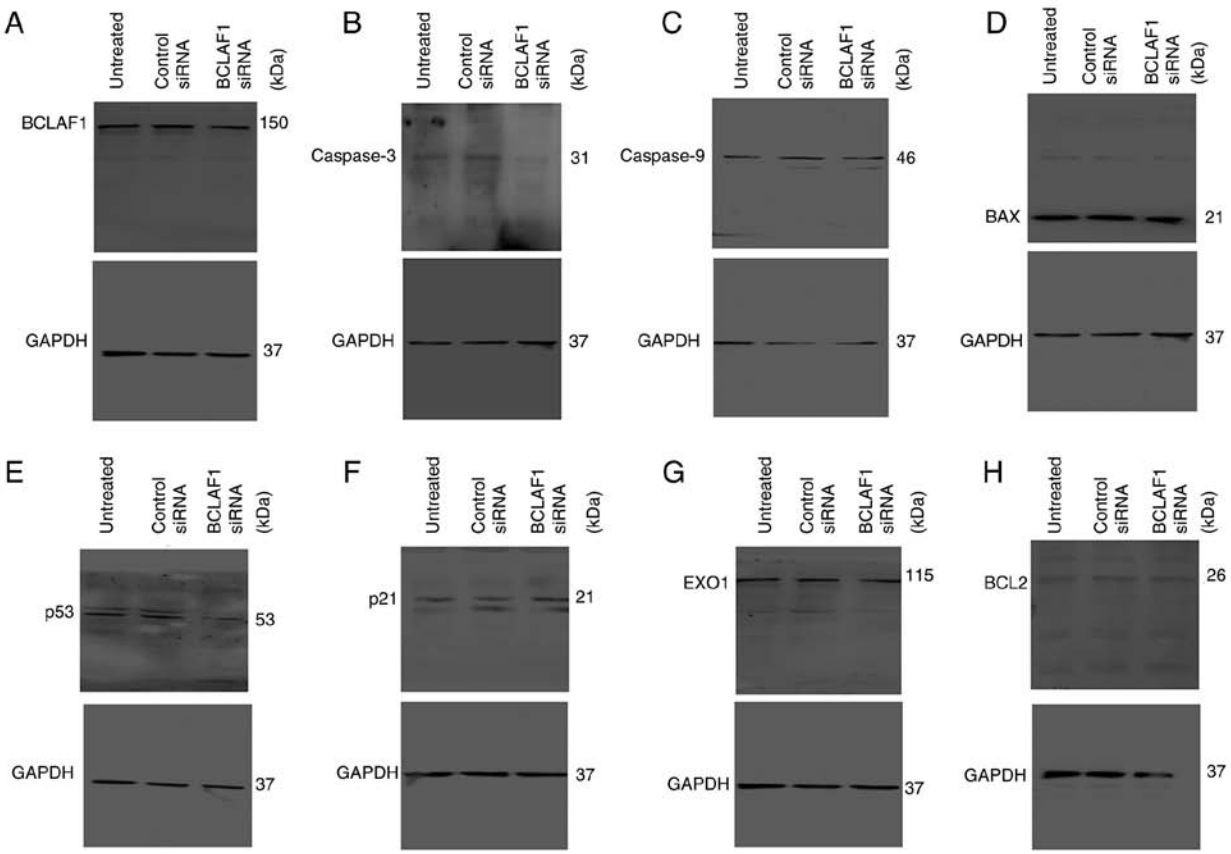


Table SI. Sequence coverage and quality indicators for whole genome sequencing of four tumour samples.

Sequence coverage/quality measures	B381	B450	M456	M478
Reference genome length	3,095,693,981	3,095,693,981	3,095,693,981	3,095,693,981
Proportion duplicate reads	0.02	0.02	0.02	0.02
Proportion unique reads	0.98	0.98	0.98	0.98
Mean depth of coverage	40.7	35.0	33.7	34.2
Median fragment length, bp	320	301	311	314
Fragment length standard deviation, bp	63	62	62	65

All four samples were aligned to the human reference genome (NCBI37) using ELAND and CASAVA software. Duplication rate of the reads was only 2%, while 98% were unique reads, thus allowing for a greater confidence in variant calling. Following paired end sequencing, all samples achieved a median targeted fragment length of >300 bp and fragment length standard deviation around the median of >60 bp.

Table SII. Sequences of the BCLAF siRNA duplexes used to knock down the expression of BCLAF1.

siRNA	Sequences (5'→3')
BCLAF-1	F: CAAGAAUUCCGAAUCCAUCU[dT][dT]
	R: AGAUGGAUCGGAAUUCUUG[dT][dT]
BCLAF-2	F: CGAUGAAUUUAAUAAGUCA[dT][dT]
	R: UGACUUAUUAAAUUCAUCG[dT][dT]
BCLAF-3	F: CAGUACAGUUCACUCUGCA[dT][dT]
	R: UGCAGAGUGAACUGUACUG[dT][dT]

BCLAF1, BCL2 associated transcription factor 1; siRNA, small interfering RNA; F, forward; R, reverse.

Table SIII. Primer sequences used in reverse transcription-quantitative PCR and annealing temperatures.

Primer	Sequences (5'→3')	Annealing temperature, ˚C
ATRIP	F: AGGCTGCTAACCTCTGTGGA	56
	R: CAGAGACTCCCAGCAAGGTC	
BACH1	F: CTGCCACCTCCCAACATAGT	59
	R: GAGATGCAGCACAGACCAAA	
BCL2	F: CTGCACCTGACGCCCTTCACC	61
	R: CACATGACCCCACCGAACTCAAAGA	
BCLAF1	F: CGCGTCGAAGGTAGCTCTAT	59
	R: TTGGAGCGACCCATTTCTTTT	
BCL-XL	F: GATCCCCATGGCAGCAGTAAAGCAAG	58
	R: CCCCATCCCGGAAGAGTTCATTCACT	
BRCA1	F: GGCTATCCTCTCAGAGTGACATTTTA	60
	R: GCTTTATCAGGTTATGTTGCATGGT	
Caspase-3	F: ACATGACTCAGCCTGTTCC	60
	R: GCCTCACCACCTTTAGAA	
Caspase-9	F: GTGAACTTCTGCCGTGAGTC	59
	R: GCAAAGCCAGCACCATTTTC	
EXO1	F: CTCAAGTGGGAGAGGCTTTG	62
	R: AACGCTGTCCTGGAAGAGAA	
GAPDH	F: GGCTCTCCAGAACATCATCC	59
	R: GCCTGCTTCACCACCTTC	
H2AX	F: TCCCTTCCAGCAAACTCA	60
	R: TCTAAAACTCCCCAAATGC	
Ku70	F: GGCTGTGGTGTTCTATGG	61
	R: CCCTTAAACTGGTCAAGC	
P21	F: ACCTCACCTGCTCTGCTGC	65
	R: ATTAGGGCTTCCTCTTGGAGA	
P53	F: CATCATCACACTGGAAGACTCC	63
	R: CAGTGCTCGCTTAGTGCTCC	

BCLAF1, BCL2 associated transcription factor 1; BACH1, transcription regulator protein BACH1; ATRIP, ATR-interacting protein; EXO1, exonuclease 1; F, forward; R, reverse.

Table SIV. Semi-quantification of western blotting results.

A, Western blot analysis presented in Fig. 3D

Protein	Untreated	Control siRNA	BCLAF1 siRNA
BCLAF1	1	0.8914±0.0059	0.6923±0.0045
BAX	1	0.8411±0.0011	0.7263±0.0024
Caspase-3	1	0.8231±0.0031	0.5203±0.0076
Caspase-9	1	0.9065±0.0076	0.8795±0.0008
GAPDH	1	0.9811±0.0006	0.9751±0.0036

B, Western blot analysis presented in Fig. 4D

Protein	Untreated	Control siRNA	BCLAF1 siRNA
BCLAF1	1	0.7953±0.0040	0.6357±0.0007
BCL2	1	0.9132±0.0037	0.8722±0.0099
P53	1	0.9731±0.0046	0.6721±0.0016
P21	1	0.7813±0.0009	0.8113±0.0021
GAPDH	1	0.9502±0.0005	0.9508±0.0018

C, Western blot analysis presented in Fig. 5F

Protein	Untreated	Control siRNA	BCLAF1 siRNA
BCLAF1	1	0.8107±0.0003	0.6105±0.0002
EXO1	1	0.9116±0.0091	0.8711±0.0016
H2AX	1	0.8714±0.0014	0.7688±0.0064
GAPDH	1	0.9636±0.0007	0.9735±0.0004

BCLAF1, BCL2 associated transcription factor 1; EXO1, exonuclease 1; siRNA, small interfering RNA. The table shows the semi-quantification of the western blot images for Figs. 3D, 4D and 5F generated using ImageJ software and normalized to 1 with the untreated sample. Data are expressed as the mean ± standard deviation (n=3).