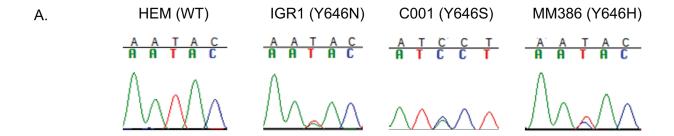
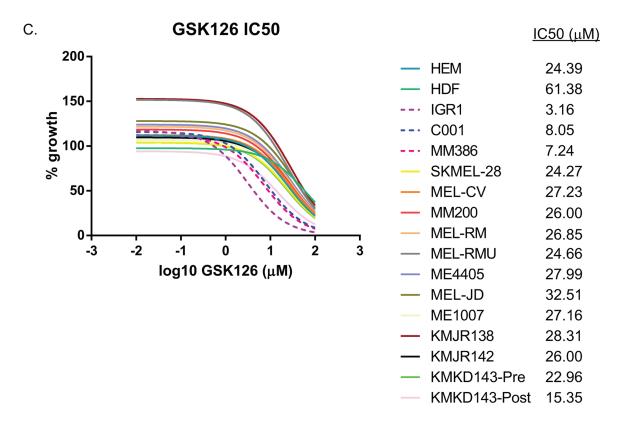
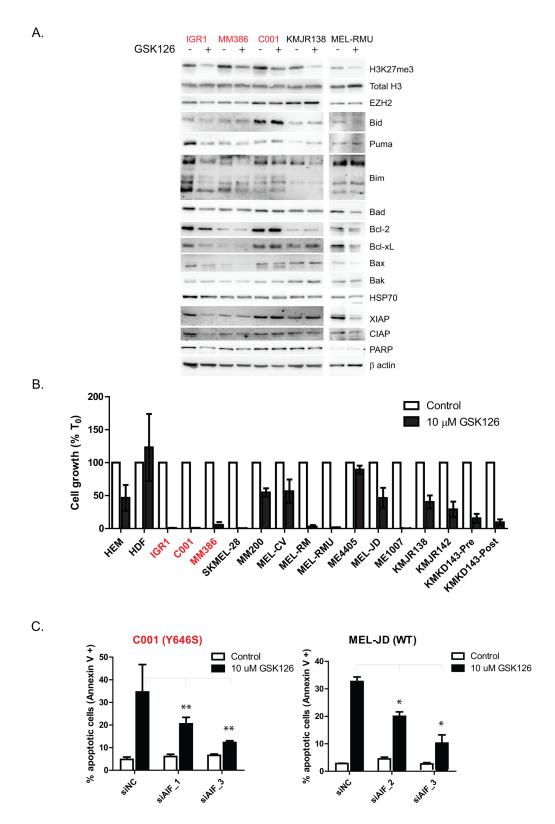
## SUPPLEMENTARY FIGURES AND TABLES



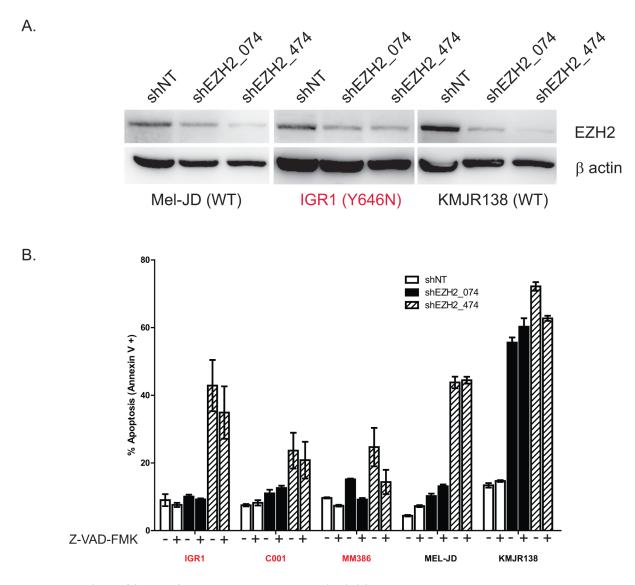
B.	Cell Line	Nucleotide change	Protein change	BRAF	CDKN2A	p14ARF	CDK4	NRAS	PTEN	p53
	IGR1	TAC>AAC	Y646N	V600E/M	-	-	-	-	-	-
	C001	TAC> TCC	Y646S	WT	WT	WT	WT	Q61K	WT	E258_S261del (EDSS), 771_782delGGAAGACTC CAG
	MM386	TAC> CAC	Y646H	V600E	WT(methylated)	WT	WT	WT	HD	WT



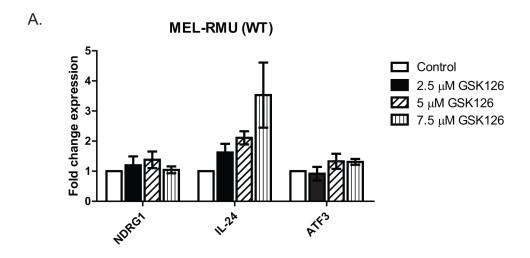
**Supplementary Figure S1: Mutation status and IC50 values of cell lines.** Sequencing traces of EZH2<sup>Y646</sup> mutant cell lines identified by Sanger sequencing. **A.** Mutational status of EZH2<sup>Y646</sup> cell lines **B.** IC50 values of GSK126 against the cell panel **C.** 

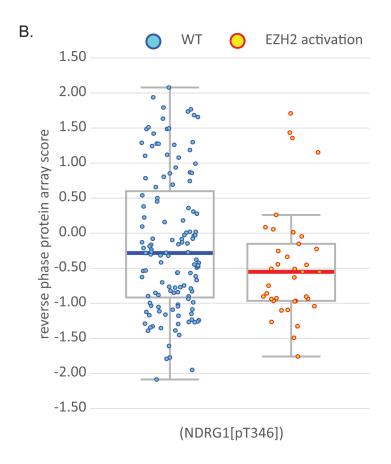


Supplementary Figure S2: Apoptosis screen, Day 8 proliferation values and AIFM1 knockdown in additional cell lines. Western blot of mutant EZH2 $^{Y646}$  cell lines (highlighted in red) and WT cells treated with 7.5  $\mu$ M GSK126 for 48 hr. **A.** Day 8 proliferation values in cell panel treated with GSK126 normalized to control values at 100% **B.** siRNA knockdown of AIFM1 in EZH2 $^{Y646}$  mutant (C001) or EZH2 WT (MEL-JD) was able to prevent GSK126 mediated apoptosis **C.** Mutants are indicated in red.



Supplementary Figure S3: EZH2 knockdown and caspase inhibition. Western blot showing knockdown of EZH2 in multiple cell lines using two individual shRNA lentiviral vectors 6 days after transfection including 4 days of puromycin selection. **A.** Pan caspase inhibition in EZH2 knockdown cells 24 hr after transduction was unable to prevent cell death **B.** as in drug treated cells (n = 2). Cells in (B) were not preselected with puromycin as Z-VAD-FMK is known to prevent puromycin cell death. Mutants are indicated in red.





**Supplementary Figure S4: Target validation in WT cells and NDRG1\_pT346 RPPA data.** RT-qPCR of microarray targets in EZH2 wildtype MEL-RMU. **A.** cells treated for 48 hr with different doses of GSK126. Reverse phase protein array (RPPA) data **B.** for NDRG1\_pT346 in melanoma patients from TCGA with WT or EZH2 activation (somatic mutations, amplification or mRNA upregulation).

## Supplementary Table S1: RT-PCR Primers used in this study

Gene of Interest	Forward Primer	Reverse Primer	Location relative to transcription start site
ATF3 (A)	CTACAGTCACCTTGCGGTGC	GAGGCTGGGAAGGGTAATGG	-10152 to -10041
ATF3 (B)	CCCTCCACTTCATGGCACTG	GTCTTTGCCACAGGAGAGTGATC	-2670 to -2539
ATF3 (C)	GACACCTCTAGTTTCTACCCCAAATT	ACGGTGAAGGGCAGAAACAC	-1453 to -1354
ATF3 (D)	CTTCCTCTTTCAGGACTGTTTG	GGATGATGTTTCAGGCTACTCTG	6018 to 6115
CCND2	TAGGATCCGTTTTGAAGAAGCC	CATTCTGTAGGTGTAGCACGCC	−337 to −273
CDC6	GATTCCCTCCCCGTTCA	CAATGAGAGAGCCCCAAGTCTT	60 to 124

NB ATF3 transcript NCBI refseq NM\_001674

## Supplementary Table S2: Antibodies used in this study

Catalogue number	Manufacturer
5246	Cell Signaling Technology
AC-74	Sigma
61017	Active Motif
ab1791	AbCam
sc-5586	Santa Cruz
3217	Cell Signaling Technology
sc-126	Santa Cruz
C34C5	Cell Signaling Technology
114C307.1	Imgenex
559027	BD Bioscience
2002S	Cell Signaling Technology
4976	Cell Signaling Technology
610392	BD Bioscience
C-2, sc-7382	Santa Cruz
H-5, sc-8392	Santa Cruz
2772	Cell Signaling Technology
G-23, sc-832	BD Bioscience
4872	Cell Signaling Technology
610716	BD Bioscience
AF 8181	R&D
F-2, sc-8007	Santa Cruz
H-221	Santa Cruz
	5246 AC-74 61017 ab1791 sc-5586 3217 sc-126 C34C5 114C307.1 559027 2002S 4976 610392 C-2, sc-7382 H-5, sc-8392 2772 G-23, sc-832 4872 610716 AF 8181 F-2, sc-8007