

CELL LINE	GENE	MUTATION	CODON	PROTEIN	ZYGOSITY
SK28	BRAF	V600E	c.1799T>A	p.Val600Glu	100%
	PTEN	T167A	c.499A>G	p.Thr167Ala	100%
	EGFR	P753S	c.2257C>T	p.Pro753Ser	100%
SK28 R	BRAF	V600E	c.1799T>A	p.Val600Glu	100%
	PTEN	T167A	c.499A>G	p.Thr167Ala	100%
	EGFR	P753S	c.2257C>T	p.Pro753Ser	100%
M14	BRAF	V600E	c.1799T>A	p.Val600Glu	100%
	PIK3CA	P539R	c.1616C>G	p.Pro539Arg	33%
	TP53	G266E	c.797G>A	p.Gly266Glu	76%
M14 R	BRAF	V600E	c.1799T>A	p.Val600Glu	100%
	PIK3CA	P539R	c.1616C>G	p.Pro539Arg	36%
	TP53	G266E	c.797G>A	p.Gly266Glu	69%

Additional file 2: Table S2: Genetic alterations in sensitive and resistant melanoma cell lines

NGS sequencing and Ion AmpliSeq™ Colon and Lung Cancer Research Panel (Life Technologies) was used to detect common mutations in hotspots and targeted regions for 22 known genes associated with tumor tissues.