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Supplemental Tables for:
Clinical Activity of Ipilimumab in Acral Melanoma: A Retrospective Review
Douglas Johnson et al.

Table S1: Mutations assessed at VICC[1]

Gene	Amino acid substitution	Nucleotide substitution
BRAF	V600E	c.1799T>A
	V600K	c.1798_1799GT>AA
	V600M	c.1798G>A
	V600D	c. 1799_1800TG>AT
	V600R	c. 1798_1799GT>AG
	V600G	c.1799T>G
	V600E'	c. 1799_1800TG>AA
NRAS	G12S	c.34G>A
	G12C	c.34G>T
	G12R	c.34G>C
	G12V	c.35G>A
	G12A	c.35G>C
	G12D	c.35G>A
	G13A	c.38G>C
	G13V	c.38G>T
	G13R	c.37G>C
	G13C	c.37G>T
	G13S	c.37G>A
	G13D	c.38G>A
	Q61E	c.181C>G
	Q61H	c.183A>T
	Q61H	c.183A>C
	Q61L	c.182A>T
	Q61L	c.182_183AA>TG
	Q61K	c.181C>A
	Q61P	c.182A>C
	Q61R	c.182A>G
	Q61R	c.182_183AA>GG
CKIT	W557R	c.1669T>C
	V559A	c.1669T>C
	V559D	c.1669T>A
	L576P	c.1727T>C
	K642E	c.1924A>G
	D816H	c.2446G>C
GNA11	Q209P	c.626A>C
	Q209L	c.626A>T
GNAQ	Q209P	c.626A>C
	Q209L	c.626A>T
	Q209R	c.626A>G
CTNNB1	S37F	c.110C>T

S37Y	c.110C>A
S45P	c.133T>C
S45F	c.134C>T
S45Y	c.134C>A

[1]Mutations assessed by SNaPshot testing, melanoma specific panel

Table S2: Mutations assessed at MSKCC[1]

Gene	Amino acid substitution	Nucleotide substitution	Gene	Amino acid substitution	Nucleotide substitution
BRAF	V600E	c.1799T>A	**KRAS**	G12S	c.34G>A
	V600M	c.1798G>A		G12R	c.34G>C
	V600A	c. 1799_T>C		G12C	c.34G>T
	V600G	c.1799T>G		G12D	c.35G>A
	G469A	c.1406G>C		G12A	c.35G>C
	G469E	c.1406G>A		G12V	c.35G>T
	G469V	c.1406G>T		G13S	c.37G>A
	D594G	c.1781A>G		G13R	c.37G>C
	D594V	c.1781A>T		G13C	c.37G>T
NRAS	G12S	c.34G>A		G13D	c.38G>A
	G12C	c.34G>T		G13A	c.38G>C
	G12R	c.34G>C		G13V	c.38G>T
	G12V	c.35G>A		Q61K	c.180-181TC>CA
	G12A	c.35G>C		Q61E	c.181C>G
	G12D	c.35G>A		Q61K	c.181C>A
	G13A	c.38G>C		Q61R	c.182A>G
	G13V	c.38G>T		Q61L	c.182A>T
	G13R	c.37G>C		Q61P	c.182A>C
	G13C	c.37G>T		Q61H	c.183A>C
	G13S	c.37G>A		Q61H	c.183A>T
	G13D	c.38G>A		K117N	c351A>C
	Q61E	c.181C>G		K117N	c351A>T

	Q61H	c.183A>T		A146P	c.436G>C
	Q61H	c.183A>C		A146T	c.436G>A
	Q61L	c.182A>T	**ERBB2**	L755S	c.2264T>C
	Q61K	c.181C>A		D769H	c.2305G>C
	Q61P	c.182A>C		V777L	c.2329G>T
	Q61R	c.182A>G		V777M	c.2329G>A
	Q61Q	c.183A>G	**EGFR**	E709K	c.2125G>A
PIK3CA	R88Q	c.263G>A		E709H	c.2125_2127GAA>CAT
	N345K	c.1035T>G		E709A	c.2126A>C
	N345K	c.1035T>A		E709G	c.2126A>G
	C420R	c.1258T>C		E709V	c.2126A>T
	E542K	c.1624G>A		G719C	c.2155G>T
	E542Q	c.1624G>C		G719S	c.2155G>A
	E545K	c.1633G>A		G719A	c.2156G>C
	E545Q	c.1633G>C		G719D	c.2156G>A
	E545A	c.1634A>C		D761Y	c.2281G>T
	E545G	c.1634A>G		D761N	c.2281G>A
	E545D	c.1635G>T		S768I	c.2303G>T
	M1043I	c.3129G>T		R776C	c.2326C>T
	H1047Y	c.3139C>T		R776H	c.2327G>A
	H1047L	c.3140A>T		T790M	c.2369C>T
	H1047R	c.3140A>G		T854A	c.2560A>G
MEK1	p.Q56P	c.167A>C		L858M	c.2572C>A
	p.K57N	c.171G>T		L858R	c.2573T>G
	p.D67N	c.199G>A		L861Q	c.2582T>A
AKT	p.E17K	c.49G>A		L861R	c.2582T>G

[1]Mutations assessed by Sequenome, cancer-specific panel