Supplementary Tables S7 and S8

Supplementary Table S7. Univariable regression of overall-survival (OS) using cutaneous or acral melanoma patients - only factors with a significant association with at least 1 subtype are displayed

Supplementary Table S8. Criteria for gene aberrations in pathway

Supplementary Table S7. Univariable regression of overall-survival (OS) using cutaneous or acral melanoma patients - only factors with a significant association with at least 1 subtype are displayed

	Cutaneous			Acral		
Variable	**Variable**	**HR**	**P-value**	**Variable**	**HR**	**P-value**
Ulceration						
No	157	1	<.001	36	1	0.048
Yes	81	2.4 (1.6, 3.7)		43	2.0 (1.0, 4.1)	
Mitotic rate						
0	22	1	<.001	4	1	0.191
1-5	106	1.5 (0.7, 3.4)		41	1.4 (0.3, 6.0)	
>=6	108	3.5 (1.6, 7.6)		35	2.4 (0.5, 11.0)	
Lymphovascular invasion						
No	188	1	0.003	56	1	0.882
Yes	26	2.5 (1.4, 4.7)		17	0.9 (0.4, 2.3)	
Measure of telomere length						
Lower median	142	1	0.001	42	1	0.318
Upper median	142	2.0 (1.3, 3.0)		41	1.4 (0.7, 2.7)	
TCGA category						
BRAF	113	1	0.374	19	1	0.021
NF1	69	1.2 (0.7, 2.0)		21	0.6 (0.2, 2.0)	
RAS	77	1.5 (0.9, 2.4)		18	3.2 (1.2, 8.6)	
triple-WT	25	1.1 (0.5, 2.5)		25	1.6 (0.6, 3.9)	

*the following parameters were non-significant (p≥0.05): gender, number of SNVs/indels; number of rearrangements; presence of WGD; presence of complex rearrangements; number of kataegis loci; presence of complex rearrangements on chromosomes 5,6,7,8,11,12, 17 or 22; presence of *TERT* promoter mutations, presence of *CDKN2A* aberrations, presence of *PTEN* aberrations, presence of *KIT* activating mutations, presence of aberrations in MAPK, PI3K, p53, p16 or telomere maintenance pathways; *CCND1*, *CDK4*, *PAK1*, *GAB2* amplifications (tested in AM only); presence of *SPRED1* aberrations (tested in AM only); presence of *TYRP1* aberrations (tested in AM only)

Supplementary Table S8. Criteria for gene aberrations in pathway

Pathway	Gene	Aberrations included
MAPK	BRAF	BRAF TCGA category: V600 missense,V601 missense,K597 missense, Fusion
MAPK	NRAS	RAS TCGA category: Q61,G12,G13 hotspot
MAPK	KRAS	RAS TCGA category: Q61,G12,G13 hotspot
MAPK	HRAS	RAS TCGA category: Q61,G12,G13 hotspot
MAPK	NF1	NF1 TCGA category: Missense, Nonsense, Nonstop, Splice Site, Frameshift indel, Inframe indel, LOH*, Homozygous deletion, SV
MAPK	SPRED1	Missense, Nonsense, Nonstop, Splice Site, Frameshift indel, Inframe indel, LOH*, Homozygous deletion, SV
MAPK	KIT	Missense or inframe indel
MAPK	MAP2K1	Codon 124, 125, 203 hotspot
MAPK	MAP2K2	Codon 124, 125, 203 hotspot - none found so not shown in figure
MAPK	RAF1	Fusion
MAPK	RAC1	P29S hotspot
MAPK	ROS1	Fusion
MAPK	ALK	Fusion
MAPK	MET	Fusion
PI3K	NRAS	RAS TCGA category: Q61,G12,G13 hotspot
PI3K	KRAS	RAS TCGA category: Q61,G12,G13 hotspot
PI3K	HRAS	RAS TCGA category: Q61,G12,G13 hotspot
PI3K	NF1	NF1 TCGA category: LOH*, Homozygous deletion, Missense, Nonsense, Nonstop, Splice Site, Frameshift indel, Inframe indel, SV
PI3K	SPRED1	LOH*, Homozygous deletion, Missense, Nonsense, Nonstop, Splice Site, Frameshift indel, Inframe indel, SV
PI3K	PTEN	LOH*, Homozygous deletion, Missense, Nonsense, Nonstop, Splice Site, Frameshift indel, Inframe indel, SV, Nonsense germline
PI3K	AKT1	E17 hotspot
PI3K	AKT2	E17 hotspot - none found so not shown in figure

PI3K	AKT3	E17 hotspot - none found so not shown in figure
PI3K	PIK3CA	All cooccur with BRAF/NRAS so not shown in figure
PI3K	KIT	Missense or inframe indel
PI3K	ROS1	Fusion
PI3K	ALK	Fusion
PI3K	MET	Fusion
p53	TP53	LOH*, Homozygous deletion, Missense, Nonsense, Nonstop, Splice Site, Frameshift indel, Inframe indel, SV
p53	MDM2	Amplification
p53	CDKN2A (p14)	Missense, Nonsense, Nonstop, Splice Site, Frameshift indel, Inframe indel, LOH*, Homozygous deletion, SV
p16/Cell cycle	CDKN2A (p16)	Missense, Nonsense, Nonstop, Splice Site, Frameshift indel, Inframe indel, LOH*, Homozygous deletion, SV, Methylation, Missense pathogenic germline
p16/Cell cycle	RB1	Missense, Nonsense, Nonstop, Splice Site, Frameshift indel, Inframe indel, LOH*, Homozygous deletion, SV, Methylation
p16/Cell cycle	CDK4	Amplification, Hotspot Missense codon 24
p16/Cell cycle	CCND1	Amplification
Telomere	TERT	Promoter, Amplification, SV within 20 upstream of start site, Germline promoter
Telomere	ATRX	LoF mutations: Nonsense, Nonstop, Splice Site, Frameshift indel, SV
Telomere	POT1	LoF mutations: Nonsense, Nonstop, Splice Site, Frameshift indel, Homozygous deletion, SV

*LOH for the tumour suppressor genes was included to consider the possibility of haploinsufficiency