SKCM - Skin Cutaneous Melanoma

Subtype (Prevalence)	Biology & Expression	Genomic Alterations	Clinical Features
BRAF (~50%)	Constitutive MAPK activation; MITF-driven melanocytic differentiation; moderate proliferative signature	BRAF hotspot mutations (V600E/K most common); occasional non-hotspot BRAF alterations	Sensitive to BRAF/MEK inhibitors; generally cutaneous superficial-spreading; intermediate prognosis
RAS (~28%)	MAPK activation via RAS; proliferative melanocytic program	NRAS (Q61) mutations (also KRAS/HRAS less common); mutually exclusive with BRAF	No approved RAS-specific inhibitors; MEK inhibitors sometimes used; intermediate prognosis
NF1 (~23%)	Loss of NF1 leads to RAS pathway activation; high overall mutational burden; UV-signature enriched	NF1 loss-of-function mutations; frequent TP53 and CDKN2A co-alterations	Higher immune infiltration; often good candidates for immunotherapy; intermediate–poor prognosis
Triple-WT (~8–15%)	Lower MAPK signaling; diverse lineage programs; often acral/mucosal transcriptional features	Wild-type for BRAF, RAS, NF1; enriched KIT mutations/amplifications and kinase fusions	Enriched in acral/mucosal melanomas; may respond to KIT inhibitors; variable prognosis