Conclusions

The melanoma tumor genome analysis performed here using CNA, mRNA expression, and IHC identified several targetable pathways in melanomas.

AM and CM had a similar age

AM were a majority female (61%) while CM were a majority male (64%) (P < 0.0001).

Given the UV light exposure in the CM, the GA tumor was significantly higher than in the AM as were the median TMB and frequency of TMB ≥ 10 and 20 mutations/Mb (P < 0.0001 for all comparisons)

AM and CM were MS-stable

The contrast in SFB1 mutations in AM and TERT in GA were significant (P < 0.0001).

AM featured significantly more KIT GA than CM (P < 0.0001), whereas CM featured significantly more BRAF GA (P < 0.0001). Only 11% of AM BRAF GA were V600E whereas 74% of CM BRAF GA were V600E (P < 0.0001).

mTOR pathway targets including NFI1 and PTEN were commonly altered in both tumor types.

Additional potentially targetable alteration in PDGFRα and ERBB2 kinases were seen in AM but not in CM.

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