Results

1. Patient Characteristics: A total of 12,788 CRC tumors were investigated

Methods

• Consensus Molecular Subtypes (CMS) of colorectal cancer (CRC) were first developed in 2015 using microarray-based assays but are not widely used clinically.
• We developed a Caris CMS classifier on whole transcriptome sequencing data (WTS) with high concordance with the previously established CMS pipeline (Guimoye et al 2015).
• We applied the Caris CMS classifier to a large clinic genomic database of CRC to investigate the utility of CMS classification in identifying patients that may respond well to therapies commonly used in CRC.

Results

2. Prognosis of CRC stratified by CMS

3. Outcome of Immune Checkpoint Inhibitors in CMS1-4

Conclusions

A Whole-Transcriptome-Sequencing based CMS classifier allows for investigation in a large real-world clinic-genomic database. We found that MSS CMS1 CRCs may derive benefit from immunotherapy. Additionally, CMS2 subgroup of right-sided tumors may derive benefit from cetuximab. Routine CMS subgrouping of CRC provides important treatment associations that should be further investigated.

References

• Guimoye 2015, Nat Med
• Heon 2022, ASCO Natle Cancer Inst
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