**Highlights**

* CMSN tumors with high TMB showed worse prognosis, unlike SCC and AC subtypes.
* *KIT* and *ROS1* mutations differed across HPV+ cervical cancer subtypes.
* *PIK3CA* hotspot mutations clustered in PI3Ka I domain across all CC subtypes.
* 3q26 amplification was a shared alteration with diagnostic and prognostic value.
* *KRAS* mutations were enriched in adenocarcinomas but absent in squamous tumors.