UCEC - Uterine Corpus Endometrial Carcinoma

| Subtype | Biology & Expression | Genomic Alterations | Clinical Features |
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| **POLE-ultramutated** | Very high neoantigen load; strong cytotoxic T-cell and interferon signatures | Hotspot exonuclease-domain mutations in POLE; ultramutator phenotype (≥100 mut/Mb) | Excellent prognosis; often younger patients; low recurrence rates even with high-grade histology |
| **MSI-hypermutated** | Upregulated immune/inflammatory pathways; high microsatellite instability | MLH1 promoter methylation (sporadic) or germline MMR mutations; MSI-H (20–30 mut/Mb) | Good–intermediate prognosis; often grade 2–3 endometrioid; responsive to immune checkpoint blockade |
| **Copy-number low (endometrioid-like)** | Hormone-driven, epithelial differentiation; moderate proliferation signatures | PTEN, PIK3CA, ARID1A and CTNNB1 mutations; low burden of copy-number alterations | Intermediate prognosis; typically low–intermediate grade endometrioid; hormone-sensitive |
| **Copy-number high (serous-like)** | TP53-driven proliferation; serous carcinoma–like expression profiles | TP53 mutations (ubiquitous); frequent amplifications (CCNE1, ERBB2, MYC); high CNAs | Poor prognosis; high-grade serous or mixed histology; early recurrence; benefit from aggressive therapy |