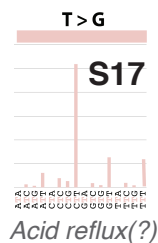


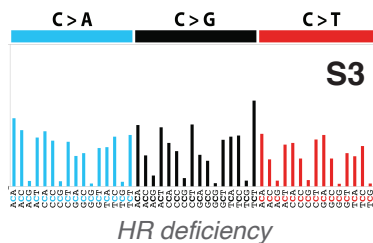
Mutagenic (53%)

High neoantigen burden
Increased CD8+ T cell infiltration



DDR impaired (18%)

Defects in homologous recombination
and chromosome segregation



C>A/T dominant (29%)

Reduced genomic instability

