LUSC - Lung squamous cell carcinoma

Subtype	Biology & Expression	Genomic Alterations	Clinical Features
Classical	Enriched xenobiotic-metabolism and oxidative-stress pathways; high expression of detoxification enzymes and NRF2 targets.	Frequent alterations in the NRF2 antioxidant-response pathway (NFE2L2, KEAP1, CUL3) and SOX2/TP63 amplifications.	Intermediate prognosis; strongly associated with heavy-smoking signature.
Basal	High expression of basal-cell markers (KRT5, KRT6, KRT14, TP63) and cell–cell adhesion genes.	SOX2 and TP63 amplifications; moderate involvement of NRF2 pathway genes.	Intermediate prognosis; corresponds to tumors with basal-cell differentiation.
Secretory	Enrichment for immune- and inflammation-related programs (e.g. cytokines, chemokines) and secretory-cell markers.	Moderate rates of TP53 mutations; intermediate burden of copy-number alterations.	Intermediate prognosis; "immune-hot" microenvironment suggests potential sensitivity to immunotherapy.
Primitive	Strong upregulation of proliferation and cell-cycle programs (MKI67, E2F targets).	Ubiquitous TP53 mutations; frequent cell-cycle gene amplifications (e.g. CCNE1, CDK6); high tumor mutational burden.	**Worst** overall survival among subtypes; high-grade, poorly differentiated tumors.