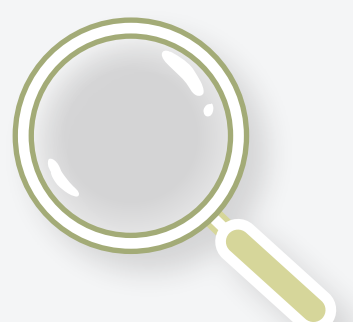


EBV genome-guided transcriptomic re-annotation reveals molecular subtypes of nasopharyngeal carcinoma (NPC), informing prognosis and treatment

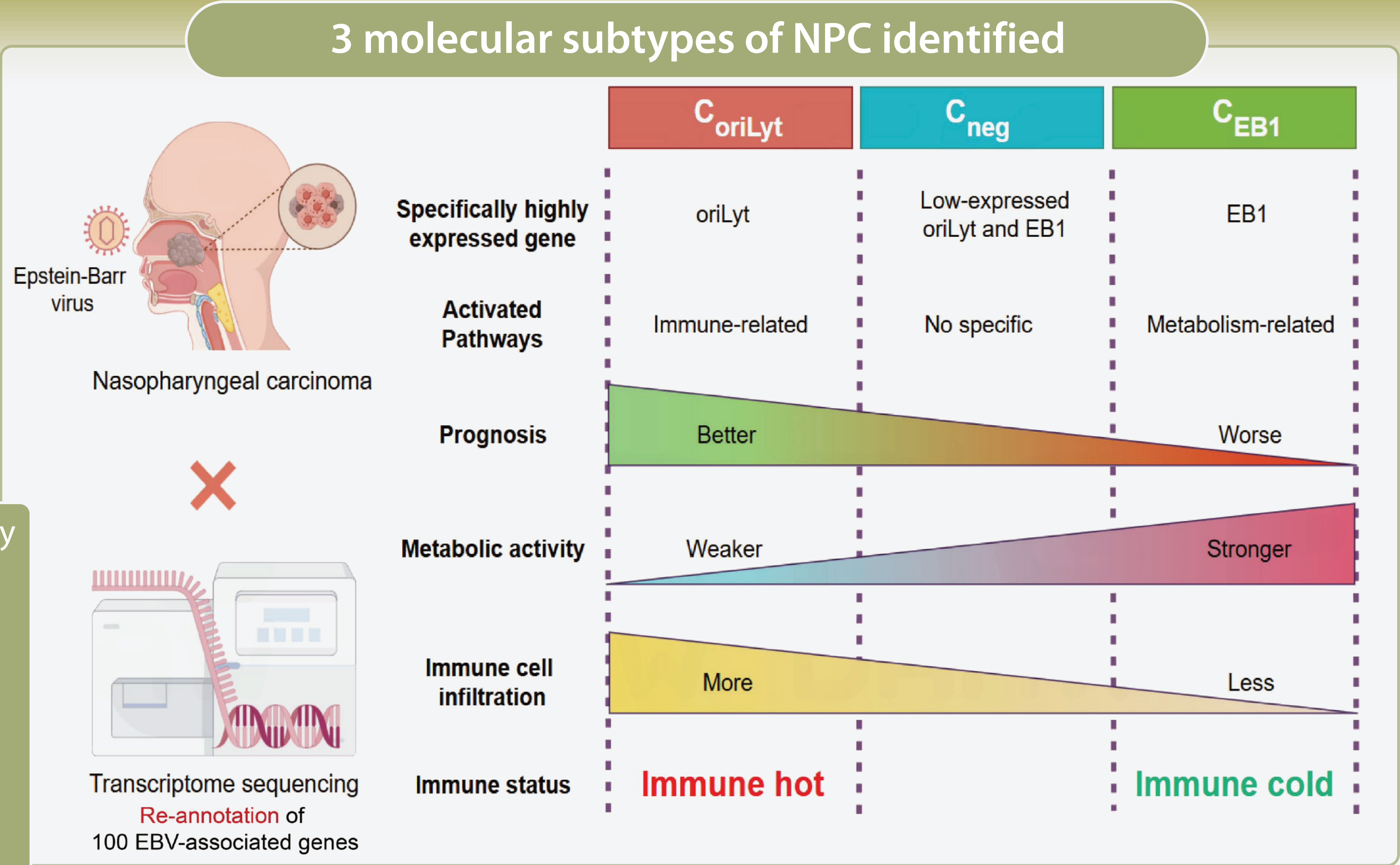
 Aim

- Identify molecular subgroups based on EBV involvement



- Refining personalized treatment strategies
- Improving treatment outcomes in NPC patients

- Hub-gene-based risk model strongly predicted disease free survival
- The CEB1 subtype showed heightened metabolic activity
- Results were replicated in the validated cohort
- M2-type macrophages exhibit a high-risk score profile and play a critical role in EBV infection



→ This study introduced a new EBV-related transcriptomics-based classification system for NPC

→ The risk model shows high predictive accuracy and stability