

Figure S1. Proteomics-based molecular subtypes by the random forest model in 2019 and 2020 CRC data-bases.

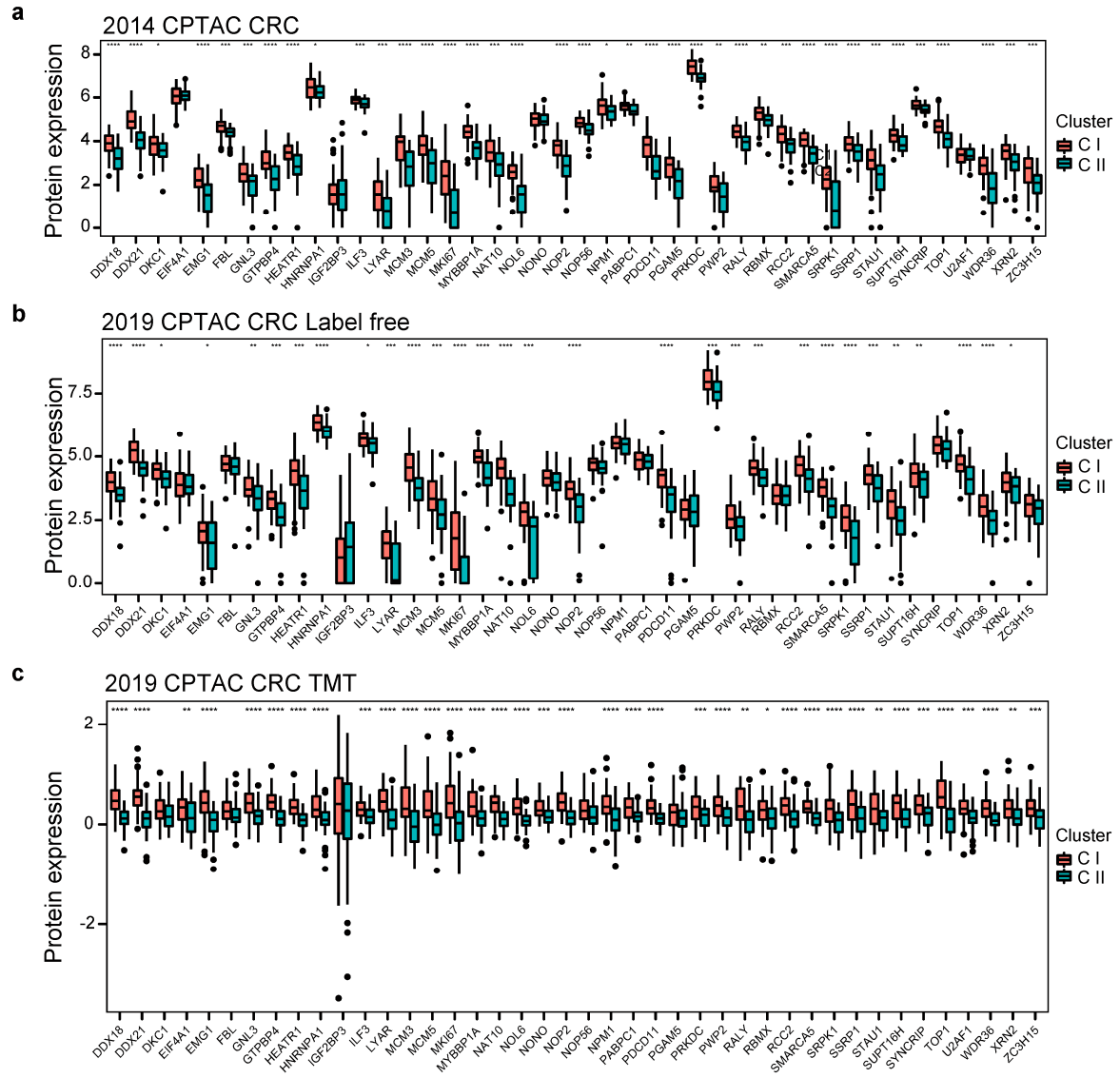


Figure S2. Proteomics-based clustering of RLBP's expression in CRC patients.

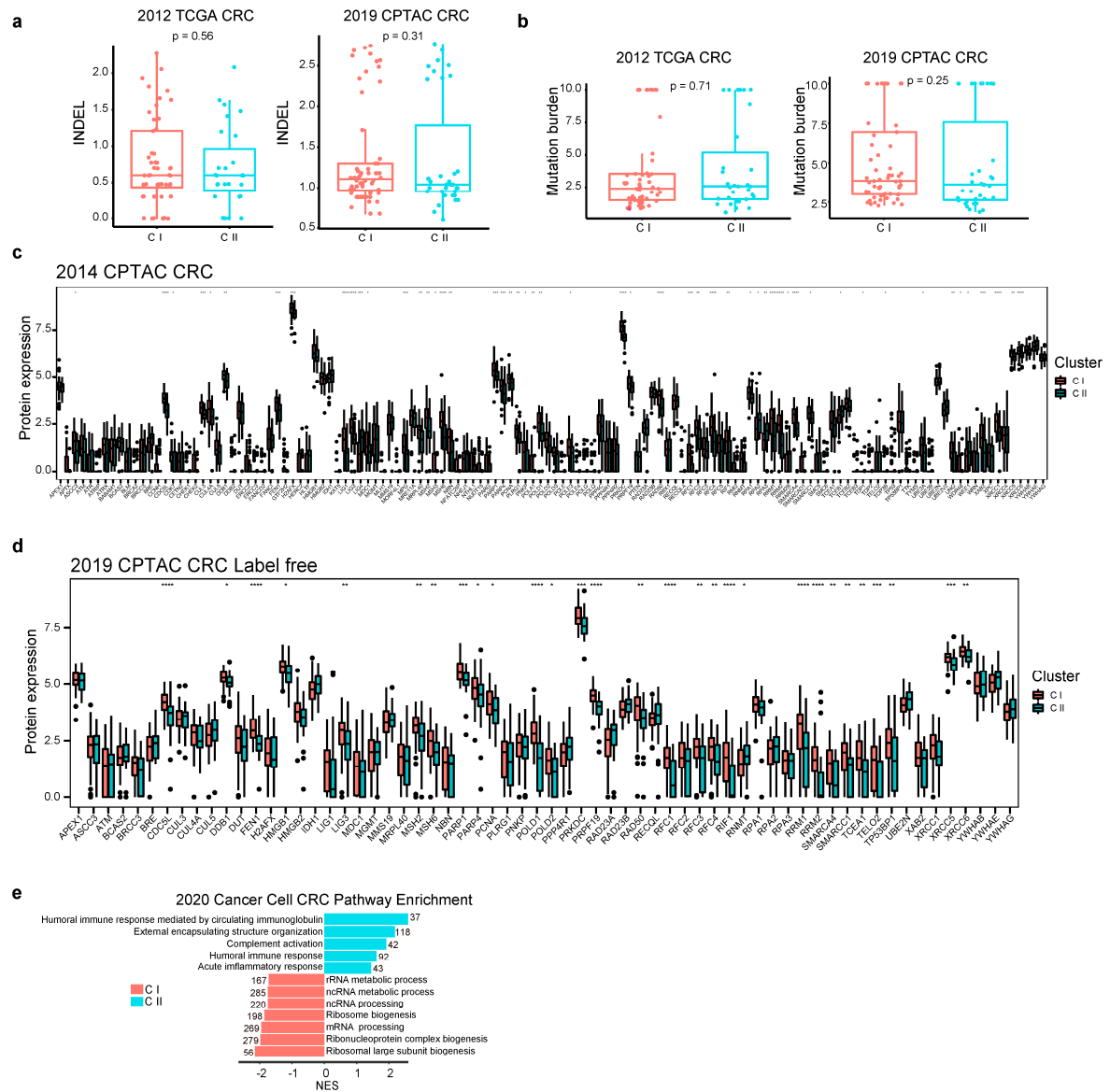


Figure S3. Landscape of pathway enrichment and DDR genes expression in two clusters.

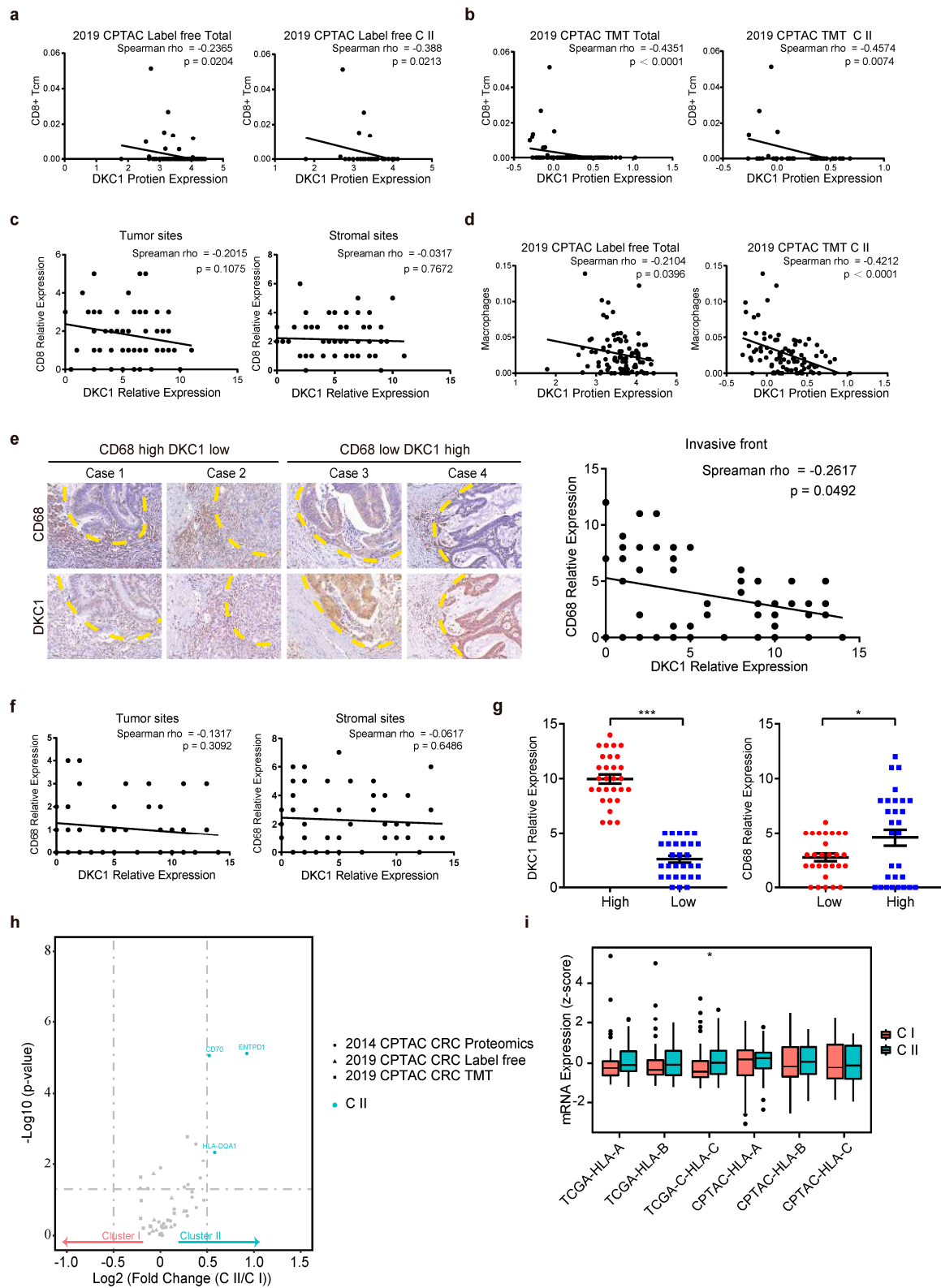


Figure S4. The correlation of RLBP with immunomodulatory factors.

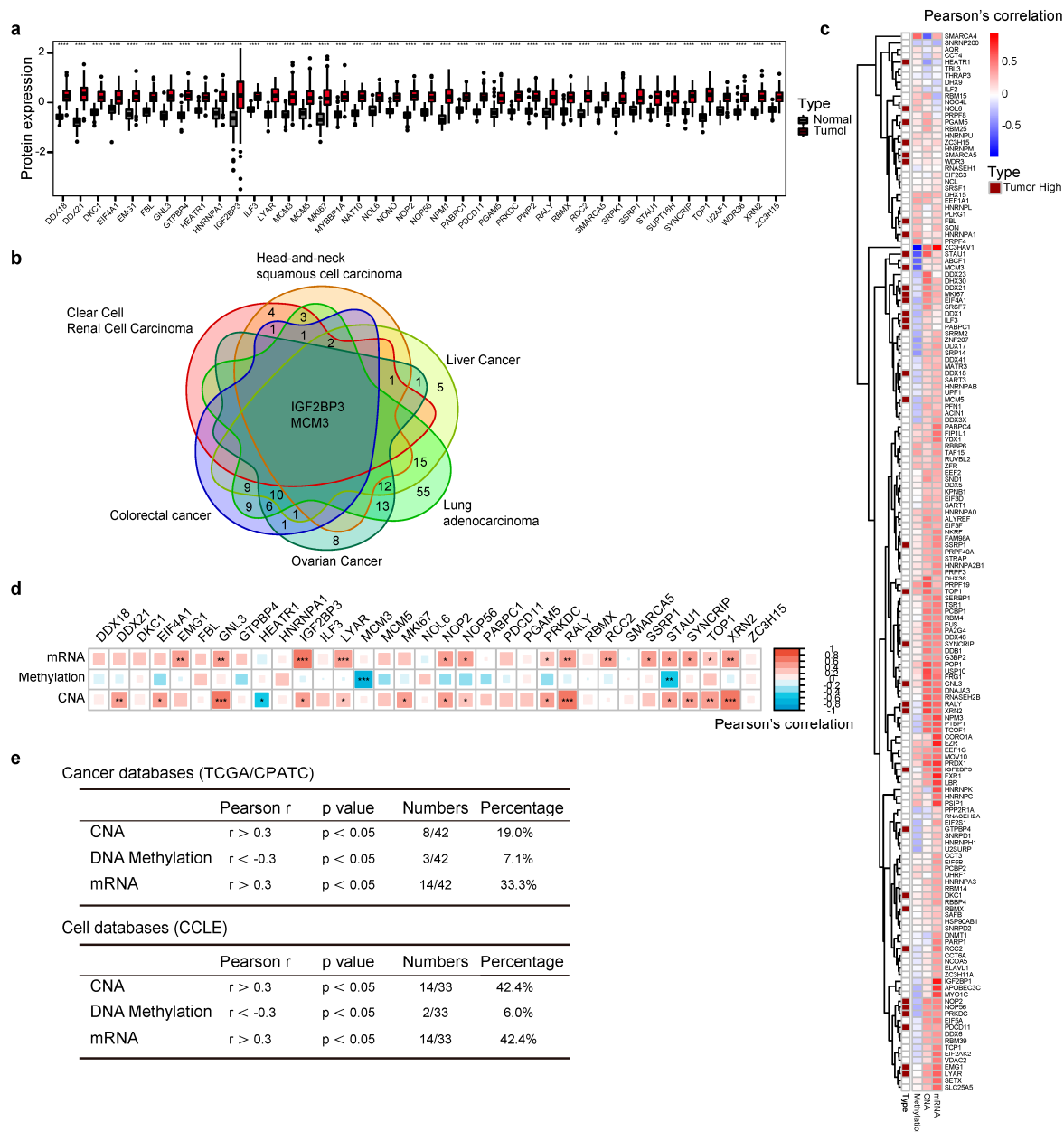


Figure S5. The RLBP are affected by CNA, DNA methylation (promoter CpG clusters) or transcriptional regulations.

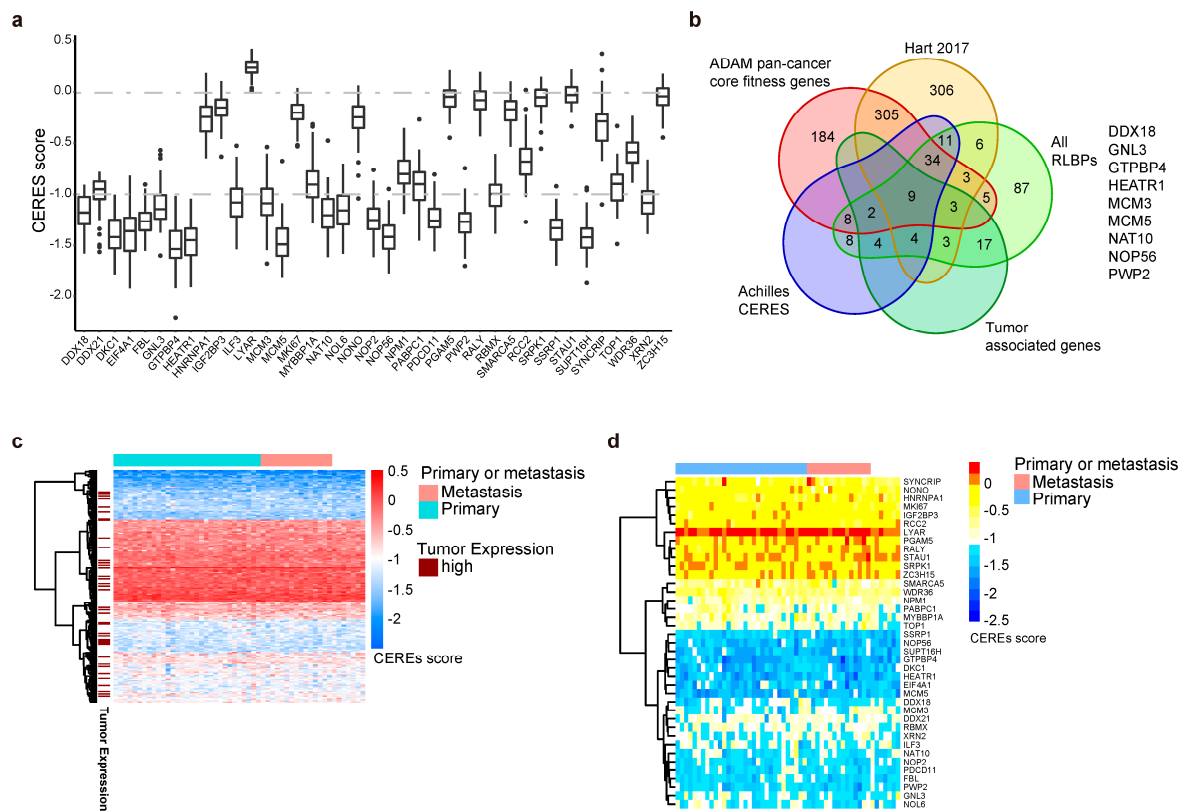


Figure S6. RLBP's serve as potential therapeutic targets.

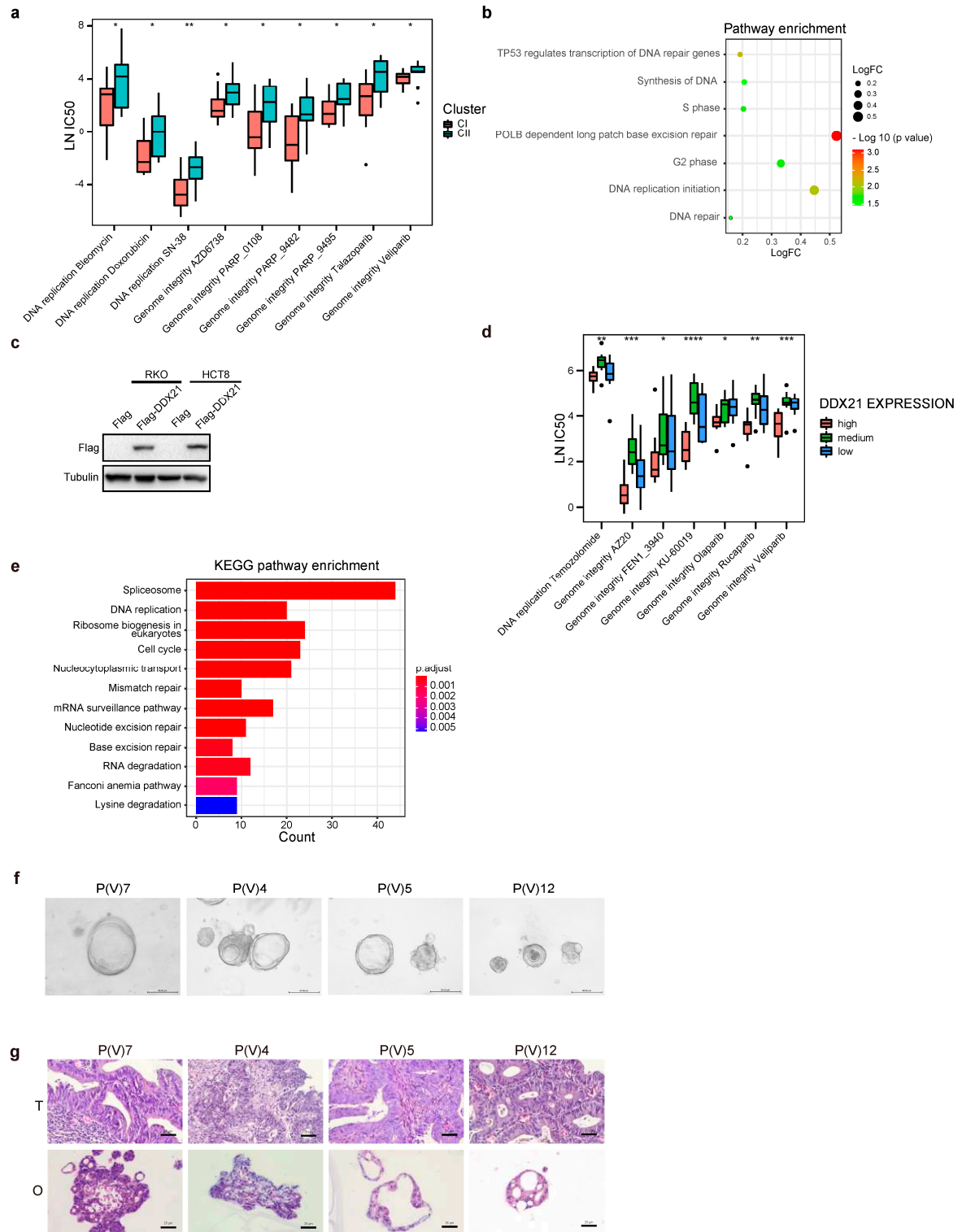


Figure S7. The Drug sensitivity analysis in cells with differential RLBP expression.