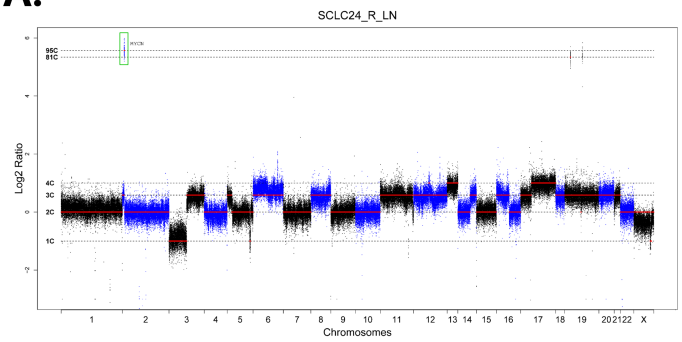
Supplementary Figure S14

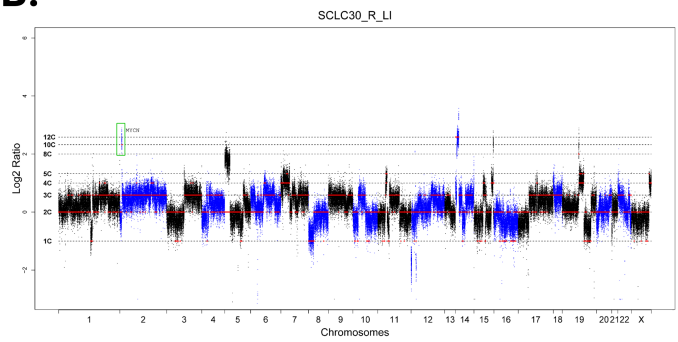
High-level focal amplifications detected by segmented CNA

WES: Wagner et al., *Nat. Comm.* 2018

A.



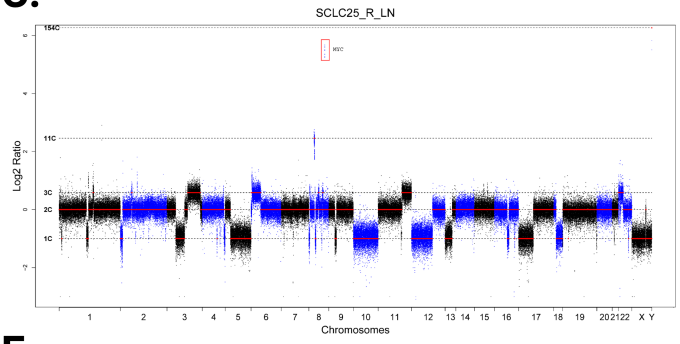
B.



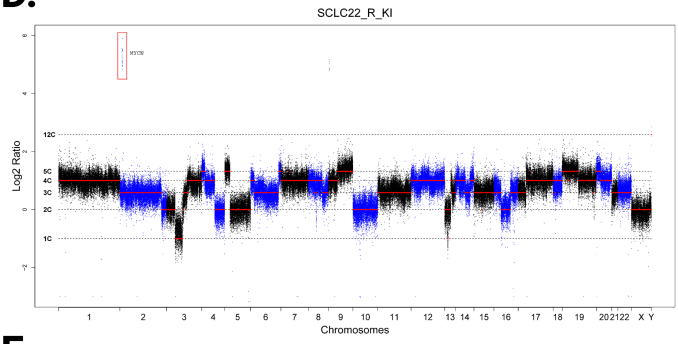
High-level focal amplifications not detected by segmented CNA

WES: Wagner et al., *Nat. Comm.* 2018

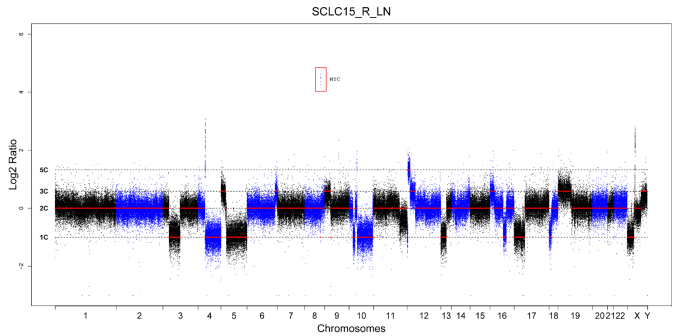
C.



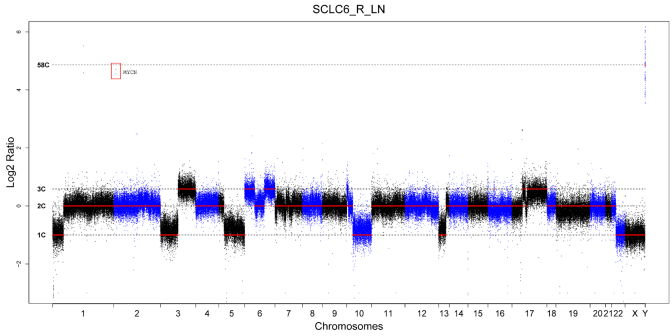
D.



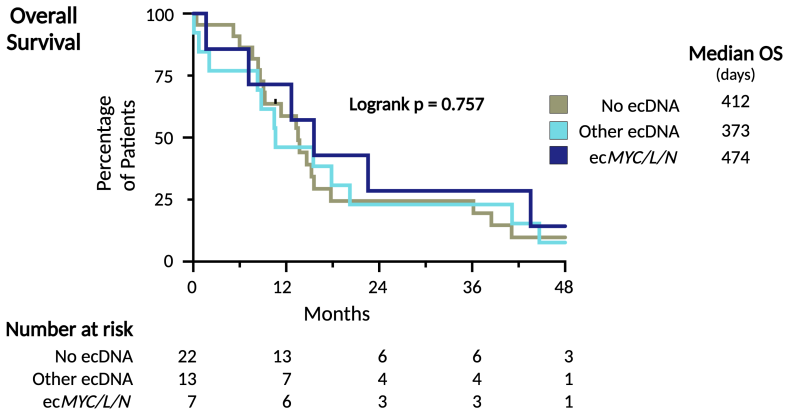
E.



F.



G.



Supplementary Figure S14. MYC paralog amplifications that were detected or omitted by segmented copy number analysis, and patient survival compared with ecDNA status of PDX models. (**A-F**) Copy number variation by exon across the genome for tumor samples from patients with relapsed SCLC, as reported in Wagner et al., 2018 (62). For these 6 patients, re-analysis of copy number detected focal *MYC* paralog amplifications. (**A-B**) *MYC* paralog amplifications detected by segmented copy number analysis, with amplified exons in green boxes. (**C-F**) *MYC* paralog amplifications detected only by unsegmented (raw) copy number analysis, with amplified exons in red boxes. (**G**) Analysis of overall survival of the 42 patients from whom PDX models were derived, categorized by ecDNA status of their models. Survival from diagnosis of SCLC to death, 4-year follow-up or loss to follow-up. For patients from whom multiple models were derived, category priority is ec*MYC/N/L* > Other ecDNA > No ecDNA. For example, patient MGH1518 categorized as ec*MYC/N/L*+ for model MGH1518-3A, even though model MGH1518-1BX lacked any ecDNA. (created with BioRender.com)