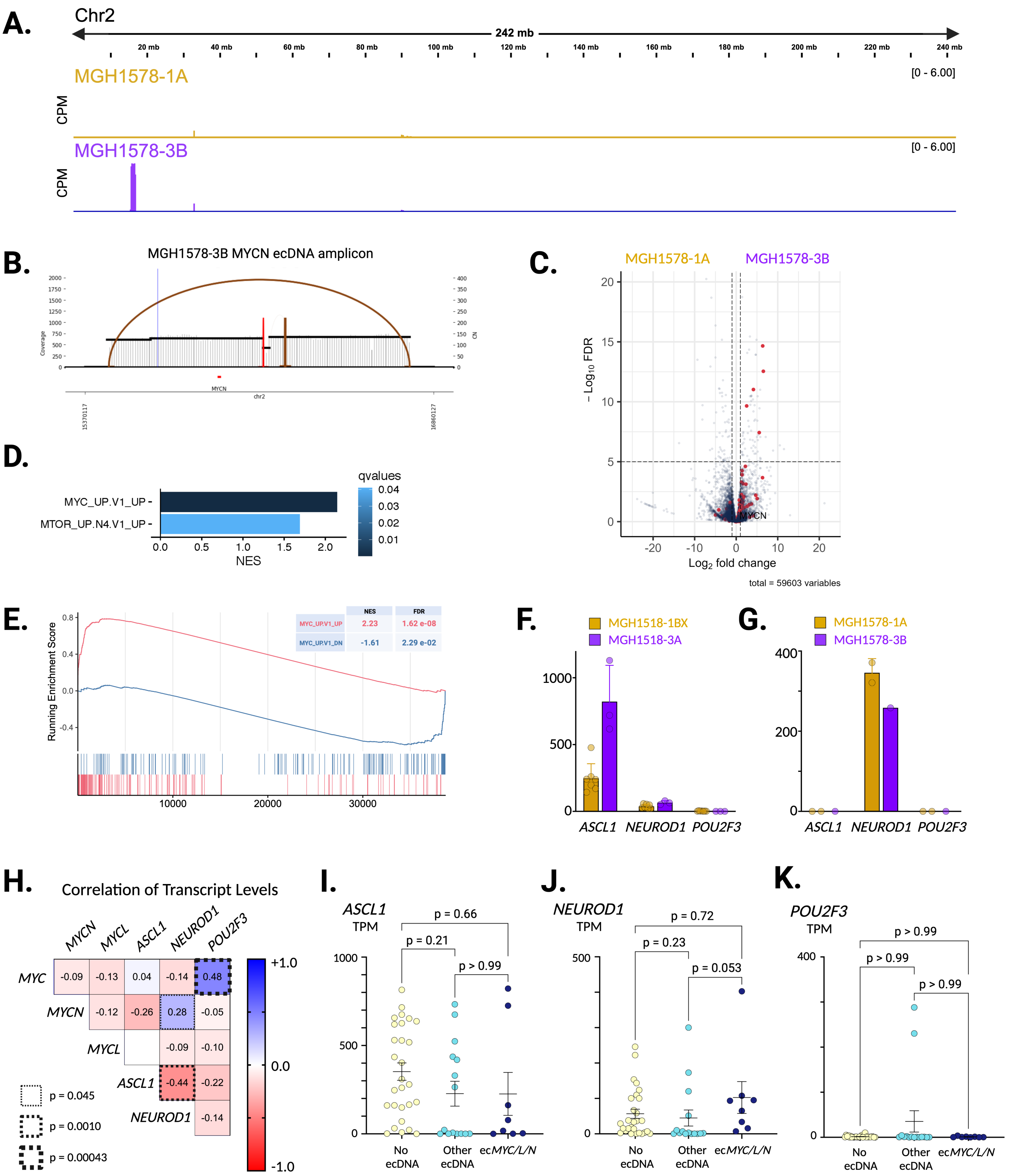
Supplementary Figure S12



	MYCN	*MYCL*	*ASCL1*	*NEUROD1*	*POU2F3*
MYC	-0.09	-0.13	0.04	-0.14	0.48
MYCN		-0.12	-0.26	0.28	-0.05
MYCL				-0.09	-0.10
ASCL1				-0.44	-0.22
NEUROD1					-0.14

Supplementary Figure S12. Acquired ec*MYCN* amplification in MGH1578 serial models and lineage oncogene expression compared with ecDNA status across the PDX panel. (**A**) Focal amplification of *MYCN* on chromosome 2 in MGH1578-3B but not MGH1578-1A. Peak heights = counts per million mapped reads (CPM). (**B**) AmpliconArchitect reconstruction of rearrangements to form ec*MYCN* in MGH1578-3B. (**C**) MGH1578 PDX differential gene expression. Red = genes upregulated upon overexpression of *MYC* in primary breast epithelial cells (MYC_UP.V1_UP) as in **Fig. 1E**. (**D**) Gene set enrichment analysis of differentially expressed genes in MGH1578-3B vs. MGH1578-1A. The MYC and MTOR gene sets were the only gene sets with significant differential expression. (**E**) Gene set enrichment plot in MGH1578-3B vs. MGH1578-1A for genes upregulated and downregulated with MYC overexpression, as in **Fig. 1F**. (**F-G**) Serial PDX expression of neuroendocrine lineage-specific transcription factors *ASCL1, NEUROD1,* and *POU2F3* transcripts per million (TPM). Circles = replicate xenografts. Error bars = mean and SEM. (**F**) MGH1518 serial models. (**G**) MGH1578 serial models. (**H**) Pearson correlation matrix of transcripts of *ASCL1, NEUROD1, POU2F3, MYC, MYCL,* and *MYCN* across the 51-model PDX panel. 2-tailed p = probability that correlation is due to random sampling. Only $p < 0.05$ is annotated. (**I-K**) Expression of neuroendocrine lineage-specific transcription factors (TPM) in models with ec*MYC/L/N* vs. models with other ecDNAs vs. models without ecDNAs. Kruskall-Wallis test p-values. (**I**) *ASCL1* expression. (**J**) *NEUROD1* expression. (**K**) *POU2F3* expression. (created with BioRender.com)