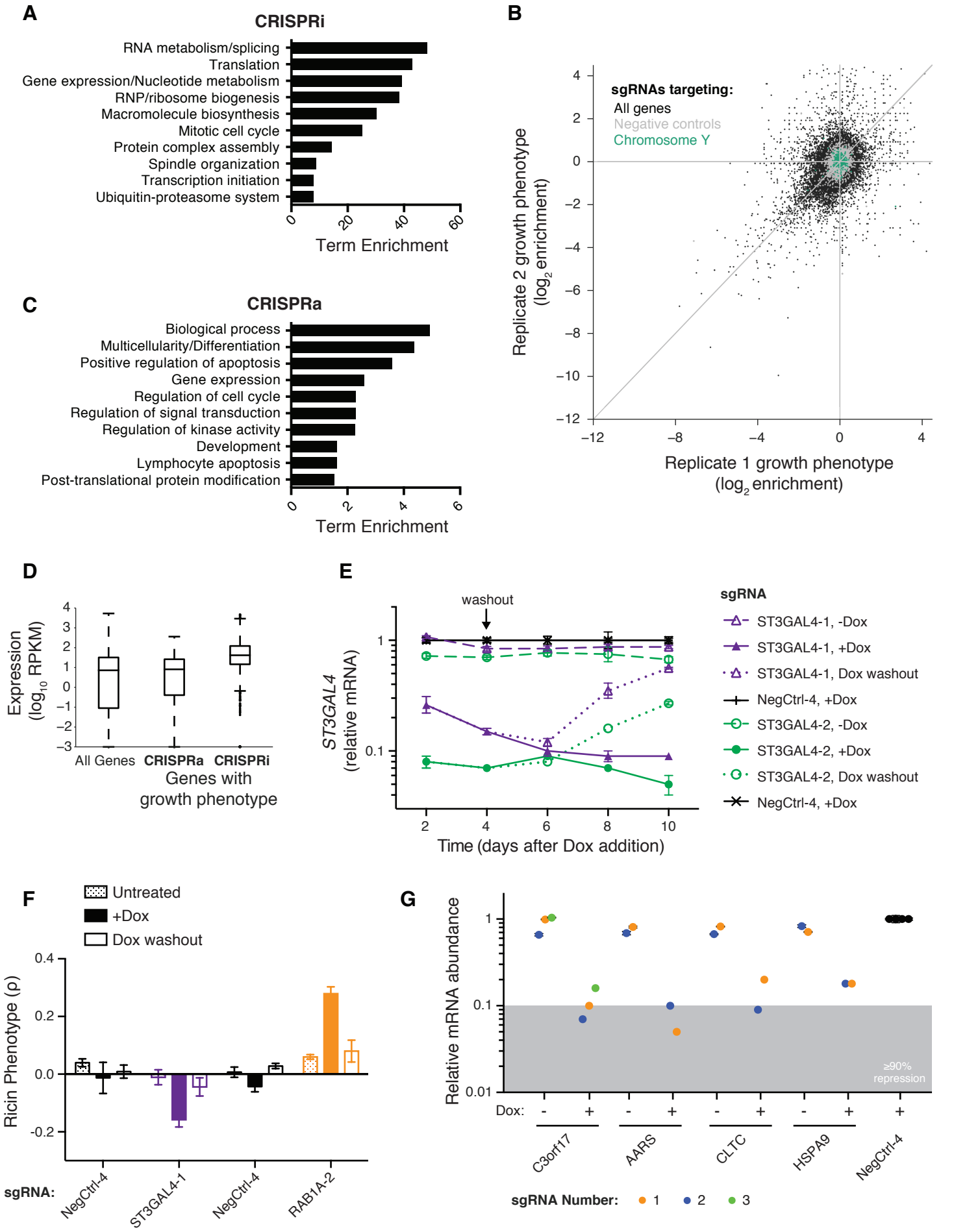
Figure S5


A
CRISPRi
RNA metabolism/splicing
Translation
Gene expression/Nucleotide metabolism
RNP/ribosome biogenesis
Macromolecule biosynthesis
Mitotic cell cycle
Protein complex assembly
Spindle organization
Transcription initiation
Ubiquitin-proteasome system
0
20
40
60
Term Enrichment
B
sgRNAs targeting:
All genes
Negative controls
Chromosome Y
Replicate 2 growth phenotype
(log2 enrichment)
Replicate 1 growth phenotype
(log2 enrichment)
C
CRISPRa
Biological process
Multicellularity/Differentiation
Positive regulation of apoptosis
Gene expression
Regulation of cell cycle
Regulation of signal transduction
Regulation of kinase activity
Development
Lymphocyte apoptosis
Post-translational protein modification
0
2
4
6
Term Enrichment
D
Expression
(log10 RPKM)
All Genes
CRISPRa
CRISPRi
Genes with
growth phenotype
E
washout
ST3GAL4
(relative mRNA)
Time (days after Dox addition)
sgRNA
ST3GAL4-1, -Dox
ST3GAL4-1, +Dox
ST3GAL4-1, Dox washout
NegCtrl-4, +Dox
ST3GAL4-2, -Dox
ST3GAL4-2, +Dox
ST3GAL4-2, Dox washout
NegCtrl-4, +Dox
F
Untreated
+Dox
Dox washout
Ricin Phenotype (ρ)
sgRNA:
NegCtrl-4
ST3GAL4-1
NegCtrl-4
RAB1A-2
G
Relative mRNA abundance
≥90%
repression
Dox:
C3orf17
AARS
CLTC
HSPA9
NegCtrl-4
sgRNA Number:
1
2
3