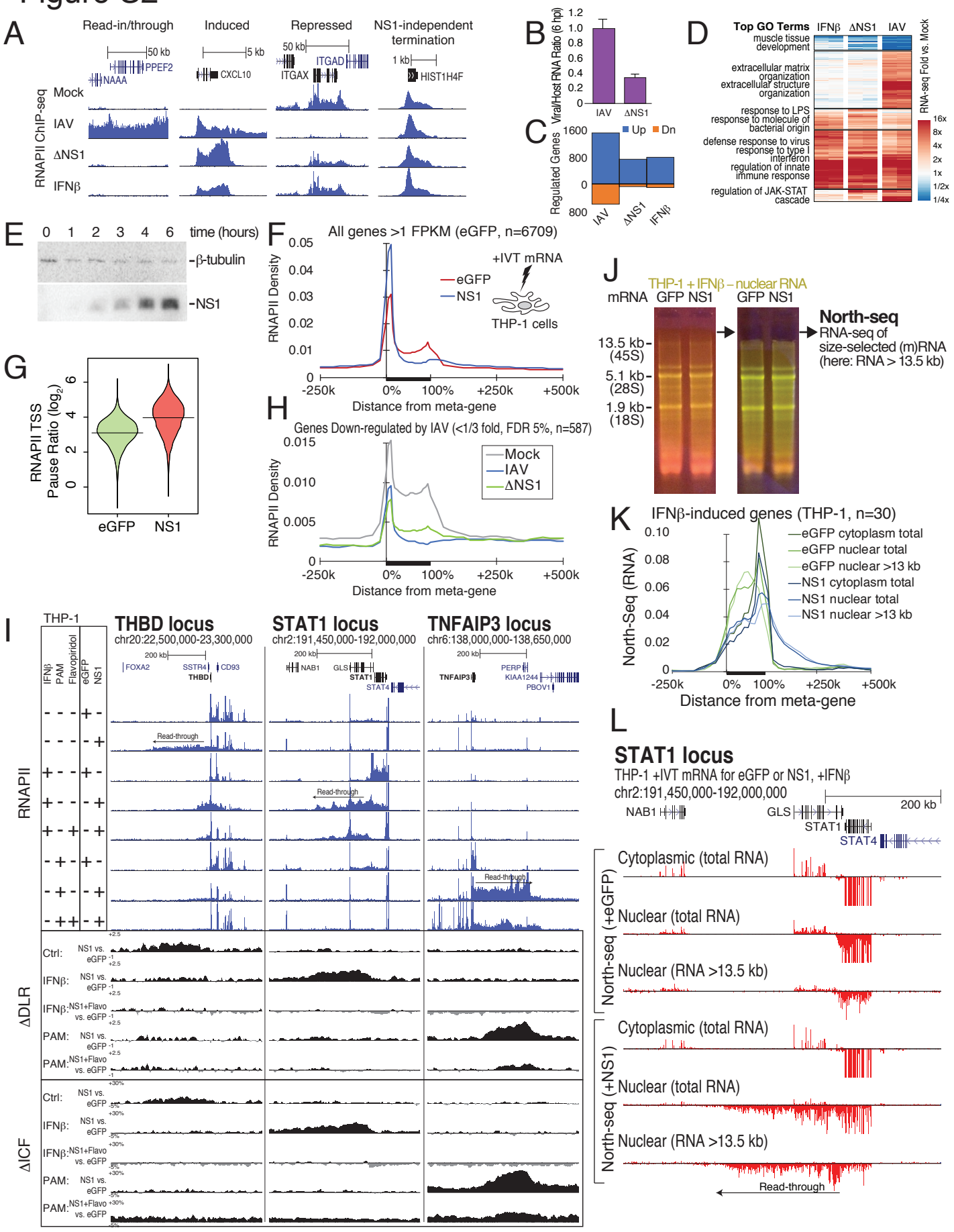
Figure S2


A
Read-in/through
Induced
Repressed
NS1-independent termination
50 kb
PPEF2
NAAA
5 kb
CXCL10
50 kb
ITGAD
ITGAX
1 kb
HIST1H4F
RNAPII ChIP-seq
Mock
IAV
ΔNS1
IFNβ
B
Viral/Host RNA Ratio (6 hpi)
IAV
ΔNS1
C
Regulated Genes
Up
Dn
IAV
ΔNS1
IFNβ
D
Top GO Terms
IFNβ
ΔNS1
IAV
muscle tissue development
extracellular matrix organization
extracellular structure organization
response to LPS
response to molecule of bacterial origin
defense response to virus
response to type I interferon
regulation of innate immune response
regulation of JAK-STAT cascade
RNA-seq Fold vs. Mock
16x
8x
4x
2x
1x
1/2x
1/4x
E
0 1 2 3 4 6 time (hours)
β-tubulin
NS1
F
All genes >1 FPKM (eGFP, n=6709)
RNAPII Density
+IVT mRNA
eGFP
NS1
THP-1 cells
-250k 0% 100% +250k +500k
Distance from meta-gene
G
RNAPII TSS Pause Ratio (log2)
eGFP
NS1
H
Genes Down-regulated by IAV (<1/3 fold, FDR 5%, n=587)
RNAPII Density
Mock
IAV
ΔNS1
-250k 0% 100% +250k +500k
Distance from meta-gene
J
THP-1 + IFNβ – nuclear RNA
mRNA GFP NS1 GFP NS1
13.5 kb (45S)
5.1 kb (28S)
1.9 kb (18S)
North-seq
RNA-seq of size-selected (m)RNA (here: RNA > 13.5 kb)
K
IFNβ-induced genes (THP-1, n=30)
North-Seq (RNA)
eGFP cytoplasm total
eGFP nuclear total
eGFP nuclear >13 kb
NS1 cytoplasm total
NS1 nuclear total
NS1 nuclear >13 kb
-250k 0% 100% +250k +500k
Distance from meta-gene
I
THP-1
IFNβ
PAM
Flavopiridol
eGFP
NS1
RNAPII
THBD locus
chr20:22,500,000-23,300,000
200 kb
FOXA2
SSTR4
CD93
THBD
Read-through
STAT1 locus
chr2:191,450,000-192,000,000
NAB1
GLS
STAT1
STAT4
TNFAIP3 locus
chr6:138,000,000-138,650,000
TNFAIP3
PERP
KIAA1244
PBOV1
ΔDLR
Ctrl: NS1 vs. eGFP
IFNβ: NS1 vs. eGFP
IFNβ: NS1+Flavo vs. eGFP
PAM: NS1 vs. eGFP
PAM: NS1+Flavo vs. eGFP
ΔICF
L
STAT1 locus
THP-1 +IVT mRNA for eGFP or NS1, +IFNβ
chr2:191,450,000-192,000,000
200 kb
NAB1
GLS
STAT1
STAT4
North-seq (+eGFP)
Cytoplasmic (total RNA)
Nuclear (total RNA)
Nuclear (RNA >13.5 kb)
North-seq (+NS1)
Cytoplasmic (total RNA)
Nuclear (total RNA)
Nuclear (RNA >13.5 kb)
Read-through