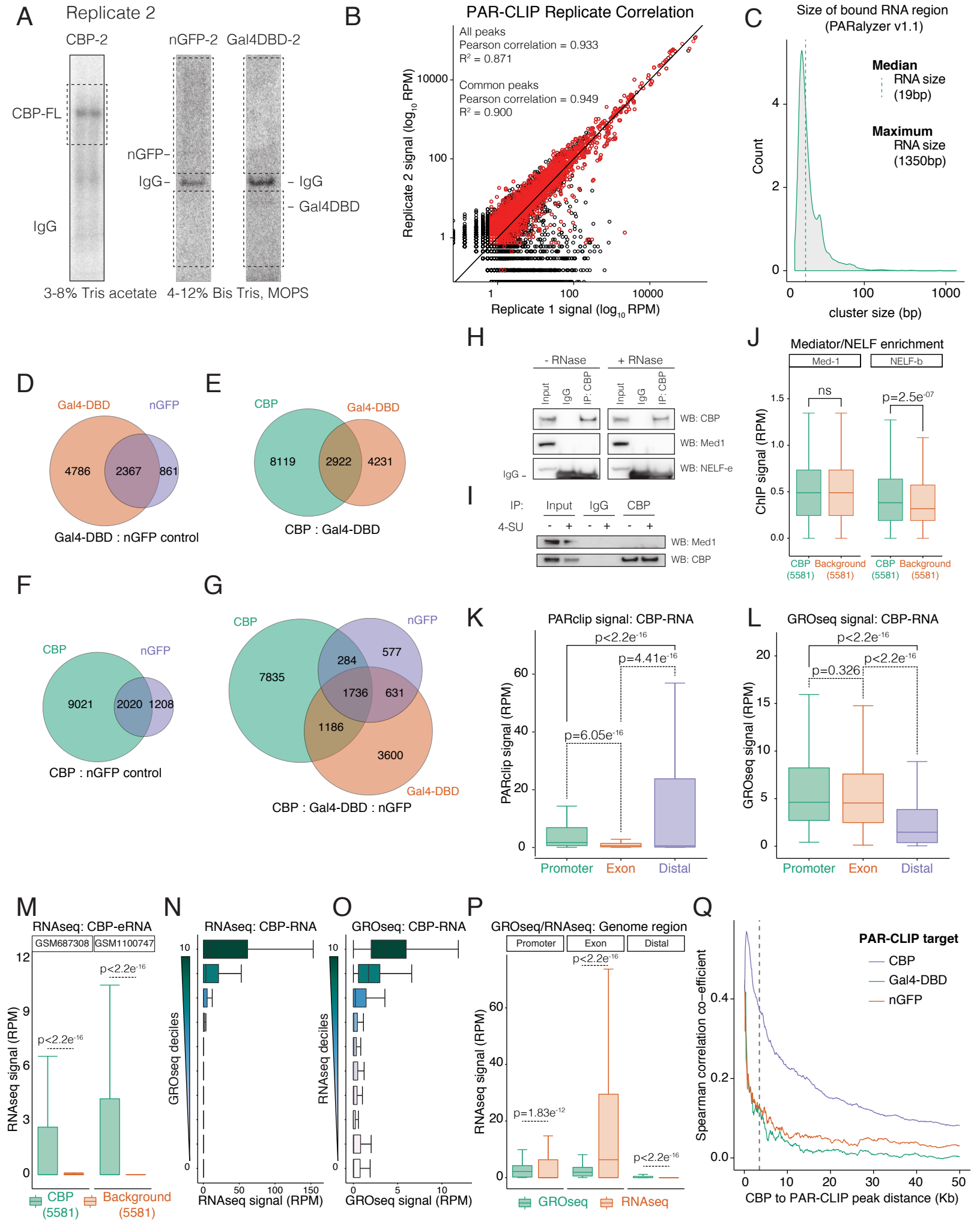
# Figure S2


A
Replicate 2
CBP-2
nGFP-2
Gal4DBD-2
CBP-FL
nGFP
IgG
IgG
IgG
Gal4DBD
3-8% Tris acetate
4-12% Bis Tris, MOPS
B
PAR-CLIP Replicate Correlation
All peaks
Pearson correlation = 0.933
R² = 0.871
Common peaks
Pearson correlation = 0.949
R² = 0.900
Replicate 2 signal (log10 RPM)
Replicate 1 signal (log10 RPM)
C
Size of bound RNA region
(PARalyzer v1.1)
Median
RNA size
(19bp)
Maximum
RNA size
(1350bp)
Count
cluster size (bp)
D
Gal4-DBD
nGFP
4786
2367
861
Gal4-DBD : nGFP control
E
CBP
Gal4-DBD
8119
2922
4231
CBP : Gal4-DBD
F
CBP
nGFP
9021
2020
1208
CBP : nGFP control
G
CBP
nGFP
Gal4-DBD
7835
284
577
1736
631
1186
3600
CBP : Gal4-DBD : nGFP
H
- RNase
+ RNase
Input
IgG
IP: CBP
WB: CBP
WB: Med1
WB: NELF-e
IgG
I
IP:
Input
IgG
CBP
4-SU
WB: Med1
WB: CBP
J
Mediator/NELF enrichment
Med-1
NELF-b
ns
p=2.5e-07
ChIP signal (RPM)
CBP (5581)
Background (5581)
K
PARclip signal: CBP-RNA
p<2.2e-16
p=4.41e-16
p=6.05e-16
PARclip signal (RPM)
Promoter
Exon
Distal
L
GROseq signal: CBP-RNA
p<2.2e-16
p<2.2e-16
p=0.326
GROseq signal (RPM)
Promoter
Exon
Distal
M
RNAseq: CBP-eRNA
GSM687308
GSM1100747
p<2.2e-16
p<2.2e-16
RNAseq signal (RPM)
CBP (5581)
Background (5581)
N
RNAseq: CBP-RNA
GROseq deciles
RNAseq signal (RPM)
O
GROseq: CBP-RNA
RNAseq deciles
GROseq signal (RPM)
P
GROseq/RNAseq: Genome region
Promoter
Exon
Distal
p<2.2e-16
p=1.83e-12
p<2.2e-16
RNAseq signal (RPM)
GROseq
RNAseq
Q
PAR-CLIP target
CBP
Gal4-DBD
nGFP
Spearman correlation co-efficient
CBP to PAR-CLIP peak distance (Kb)