

ENCODE DCC Antibody Validation Document

Date of Submission

Name:

Email:

Lab

Antibody Name:

Target:

Company/
Source:

Catalog Number, database ID, laboratory

Lot Number

Antibody
Description:

Target
Description:

Species Target

Species Host

Validation Method #1

Validation Method #2

Purification
Method

Polyclonal/
Monoclonal

Vendor URL:

Reference (PI/
Publication
Information)

Please complete the following for antibodies to histone modifications:
*if your specifications are not listed in the drop-down box,
please write-in the appropriate information*

Histone Name

AA modified

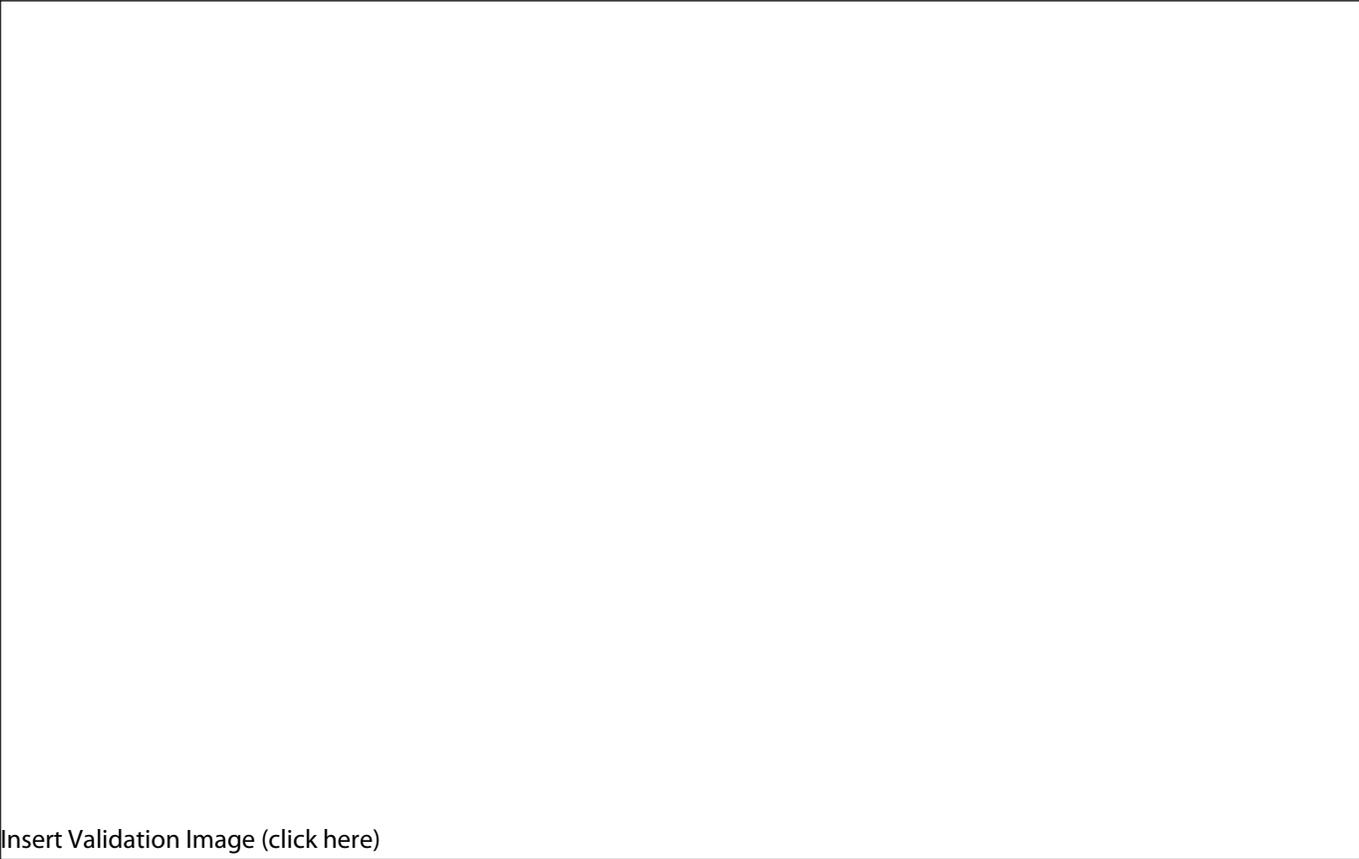
AA Position

Modification

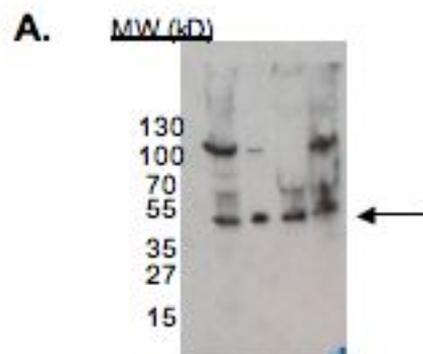
Validation #1
Analysis



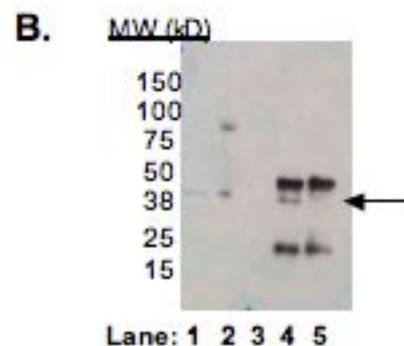
Insert Validation Image (click here)



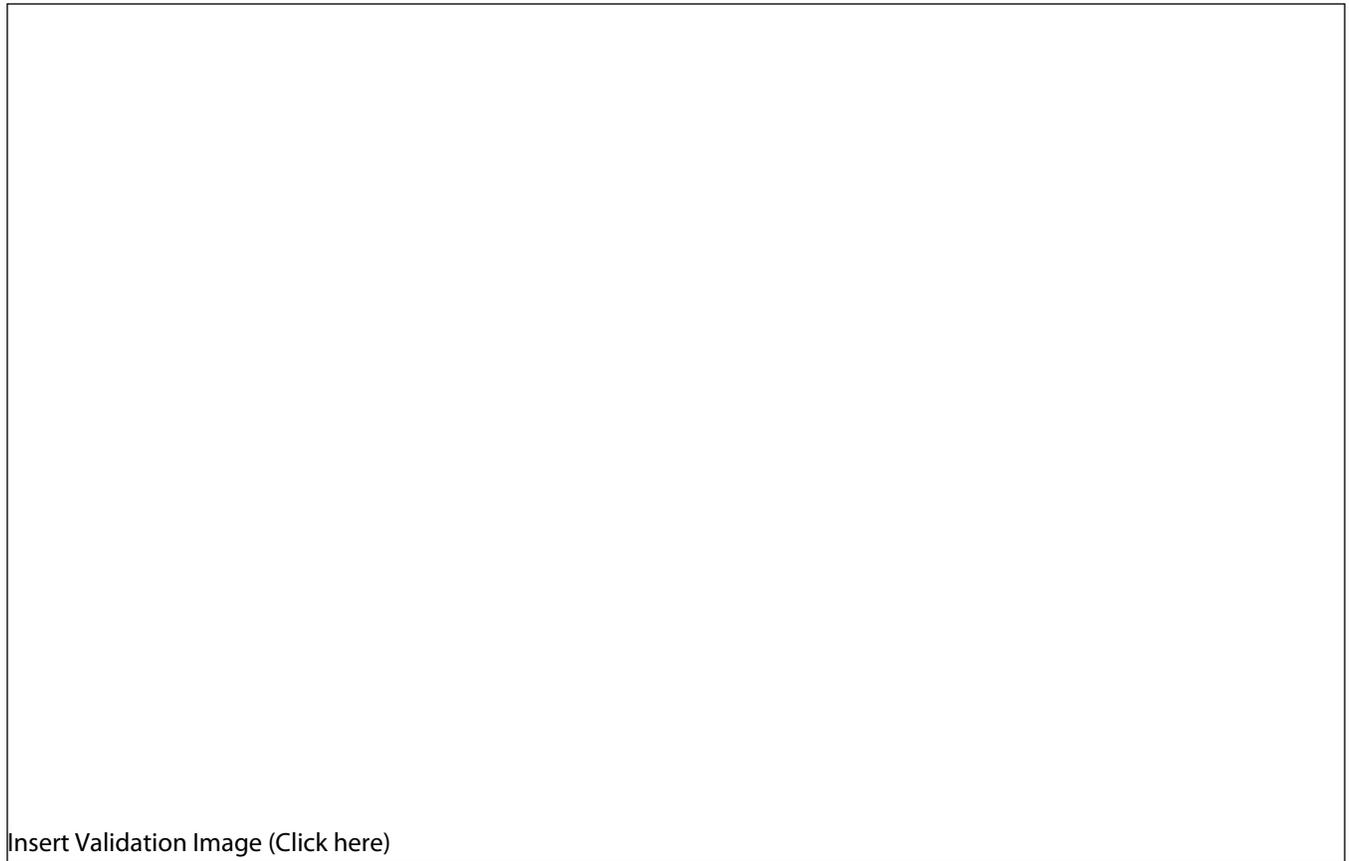
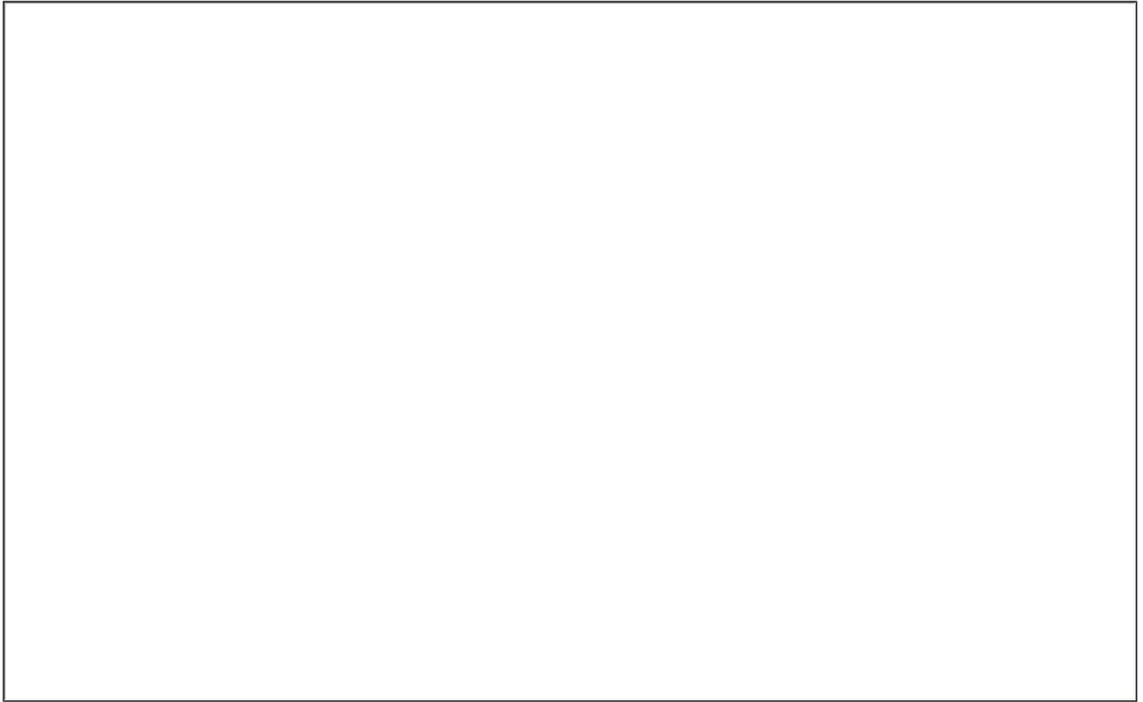
A. Arrow indicates band consistent with expected size (37kD) of USF2 in whole cell lysates from (left to right): K562, GM12878, HeLaS3, and HepG2 cell lines.



B. Arrow indicates immunoprecipitated band of expected size from K562 nuclear lysates. Lane 1= K562 nuclear lysate, Lane 2= K562 whole cell lysate, Lane 3= supernatant from K562 immunoprecipitation (IP), Lane 4= bound material from K562 IP, Lane 5= bound material from control IgG IP from K562.



Validation #2
Analysis



Insert Validation Image (Click here)

Table 1. USF2 motif enrichment.

Cell Line	Motif Enrichment (log2)	Enrichment p-value (-log10)	Fraction of peaks containing motif
GM12878	3.606 (Myc_known1)	1800.07 (Myc_known5)	0.505 (Myc_known5)
H1-hESC	3.532 (Myc_known9)	1978.91 (Myc_known5)	0.519 (Myc_known5)
HeLa-S3	3.238 (Myc_known9)	1440.64 (Myc_known5)	0.436 (Myc_known5)
HepG2	3.626 (Myc_known9)	1241 (Myc_known5)	0.591 (Myc_known5)
K562	3.764 (Myc_known9)	1637.89 (Myc_known5)	0.571 (Myc_known5)

Figure 1. Motif consensus sequences and position weight matrices for highly enriched USF2 motifs.

