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,
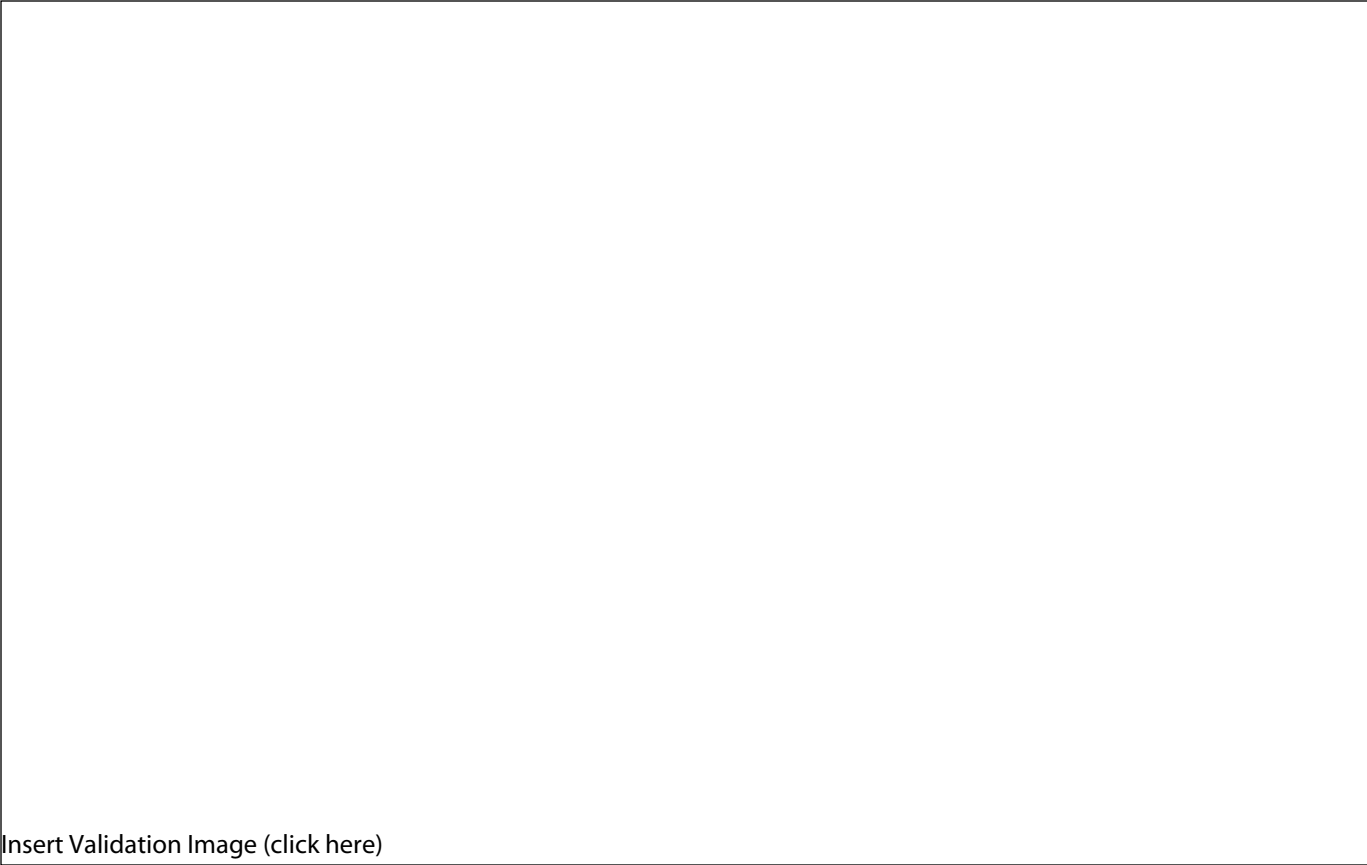*please write-in the appropriate information*

Histone Name [   ]   AA modified [   ]   AA Position [   ]   Modification [   ]
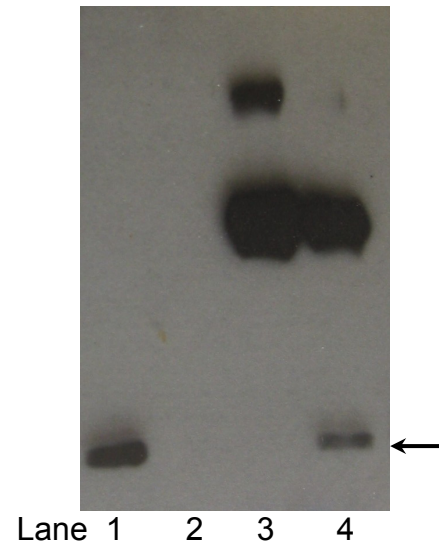
Validation #1
Analysis

Insert Validation Image (click here)

sc-197 (Max)
Immunoprecipitation

Lane 1   2   3   4

Immunoprecipitation of Max from K562 cells using sc-197. Lane 1: input nuclear lysate, Lane 2: unbound material from immunoprecipitation assay with sc-197 Lane 3: material immunoprecipitated with sc-197, Lane 4: material immunoprecipitated using control IgG.

Validation #2
Analysis
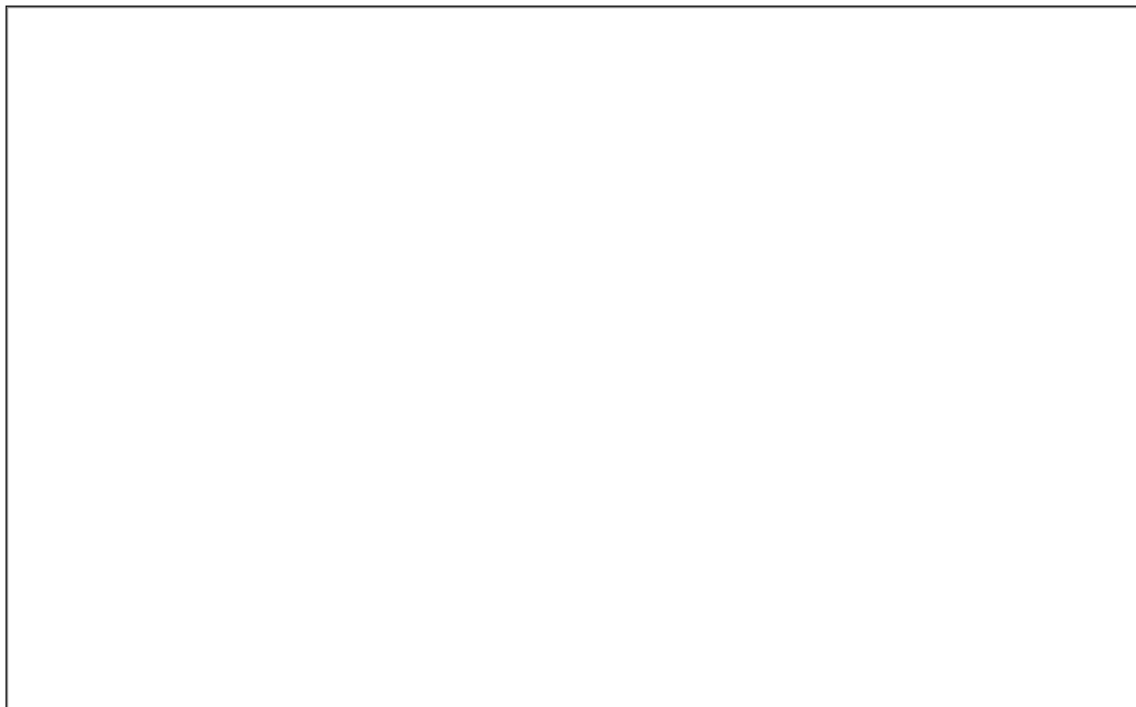
Insert Validation Image (Click here)

Table 1. Max motif enrichment.

Cell Line	Motif Enrichment (log2)	Enrichment p-value (-log10)	Fraction of peaks containing motif
HUVEC	3.84407 (Myc_known1)	1936.52 (Myc_known1)	0.410095 (Myc_known4)
K562	4.1347 (Myc_known1)	1095.32 (Myc_known1)	0.481899 (Myc_known4)
NB4	3.47161 (Myc_known1)	3018.99 (Myc_known1)	0.30184 (Myc_known4)

- **Figure 2.** Motif consensus sequences and position weight matrices for highly enriched Max motif.

Position/Consensus

Myc_known1

>Myc_known1 Max_bulyk_sc09-primary –

	A	C	G	T
D	0.234855	0.152539	0.301720	0.310886
D	0.199226	0.147959	0.439250	0.213565
M	0.582926	0.274768	0.075866	0.066440
S	0.138829	0.475428	0.305884	0.079859
C	0.024979	0.969690	0.001811	0.003520
A	0.966345	0.003728	0.022320	0.007607
C	0.000598	0.907006	0.008160	0.084236
G	0.084236	0.008160	0.907006	0.000598
T	0.007607	0.022320	0.003728	0.966345
G	0.003520	0.001811	0.969690	0.024979
B	0.149140	0.241218	0.389598	0.220044
K	0.066440	0.075866	0.274768	0.582926
N	0.186990	0.346199	0.250066	0.216745
N	0.273437	0.225889	0.300738	0.199936
K	0.160893	0.111177	0.477963	0.249968
D	0.171790	0.101256	0.424580	0.302375

Myc_known4

>Myc_known4 Myc_jaspar_MA0147.1 –

	A	C	G	T
D	0.224670	0.105727	0.471366	0.198238
C	0.118943	0.806167	0.074890	0.000000
C	0.039648	0.951541	0.008811	0.000000
R	0.766519	0.000000	0.193833	0.039648
C	0.008811	0.898678	0.008811	0.083700
G	0.052863	0.013216	0.933921	0.000000
T	0.004405	0.022026	0.017621	0.955948
G	0.000000	0.000000	0.964758	0.035242
S	0.044053	0.572687	0.233480	0.149780
K	0.123348	0.158590	0.422907	0.295154

Myc_known7

>Myc_known7 MYC::MAX_jaspar_MA0059.1 –

	A	C	G	T
R	0.619048	0.000000	0.238095	0.142857
C	0.047619	0.857143	0.047619	0.047619
C	0.000000	1.000000	0.000000	0.000000
A	0.952381	0.000000	0.047619	0.000000
C	0.000000	0.952381	0.000000	0.047619
G	0.047619	0.000000	0.952381	0.000000
T	0.000000	0.000000	0.000000	1.000000
G	0.000000	0.000000	0.952381	0.047619
S	0.047619	0.428571	0.428571	0.095238
Y	0.047619	0.190476	0.047619	0.714286
H	0.190476	0.428571	0.047619	0.333333