

APPENDIX I

Blots as presented in Figure 2

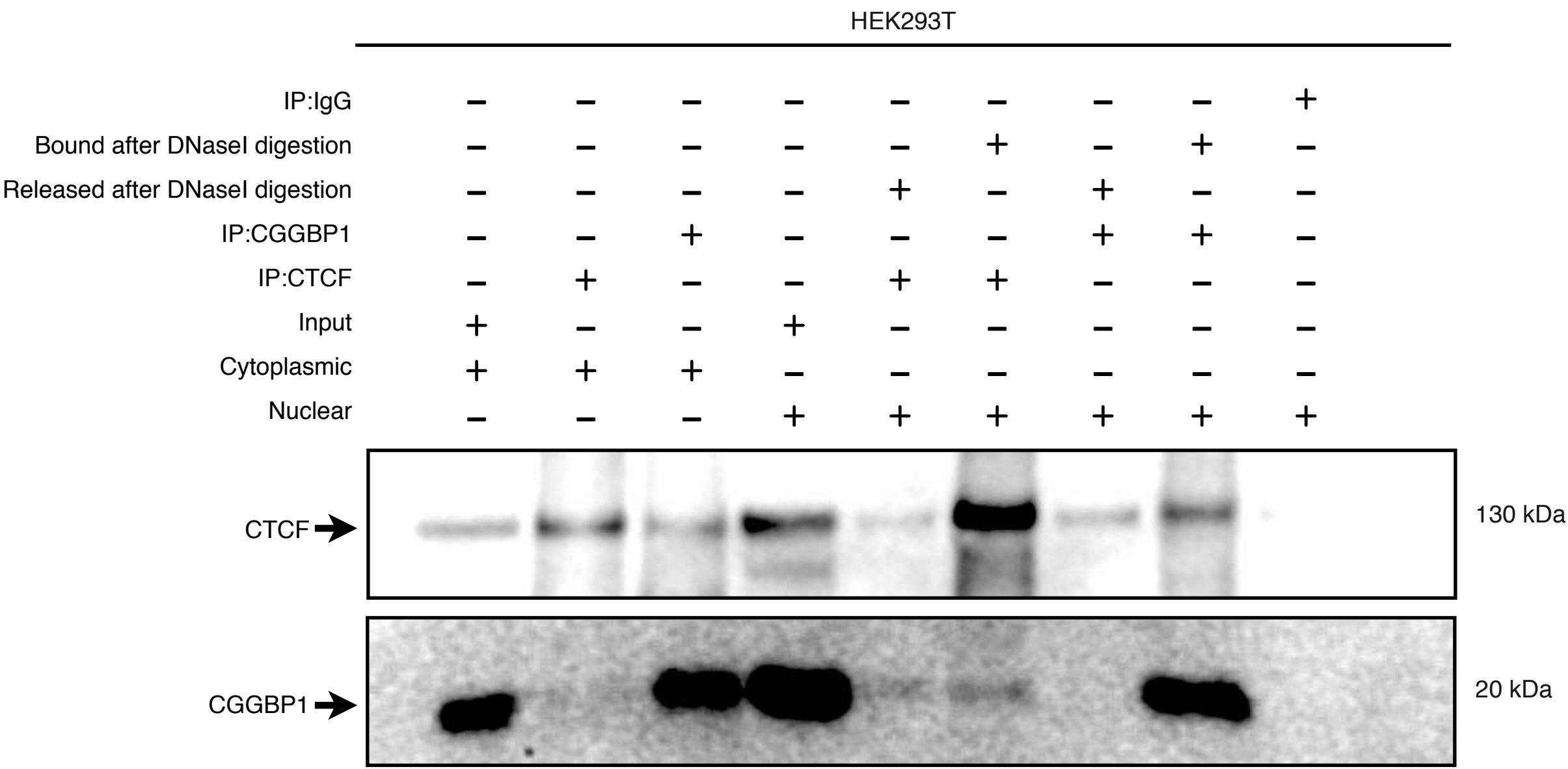
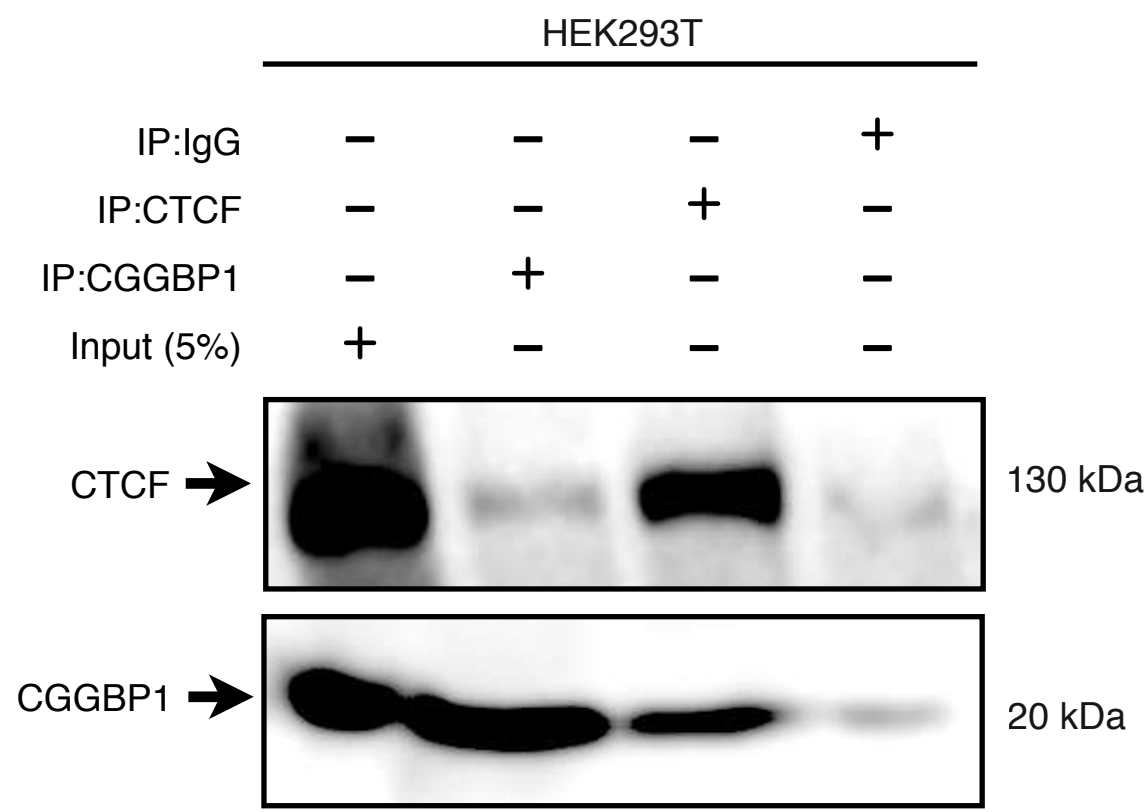
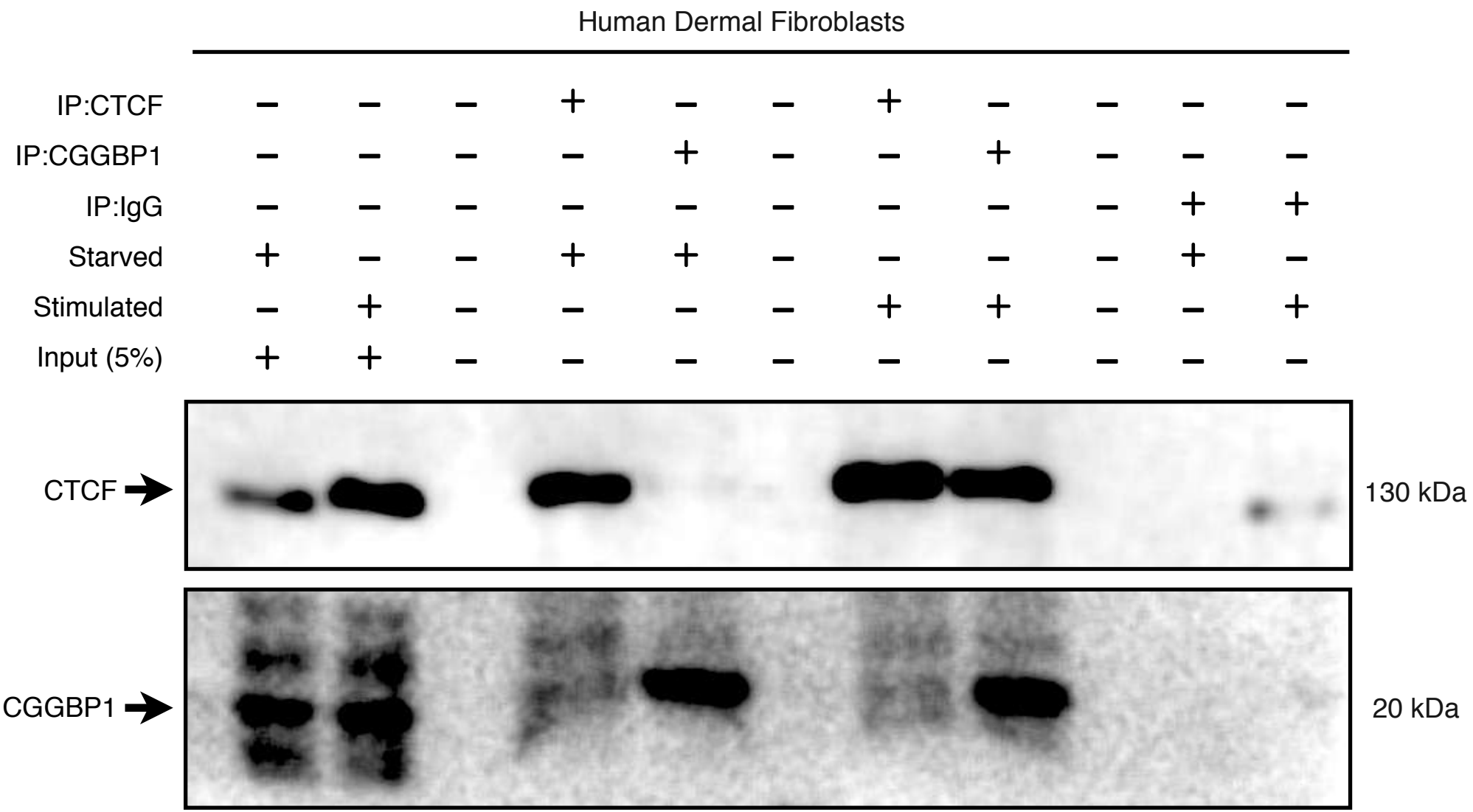
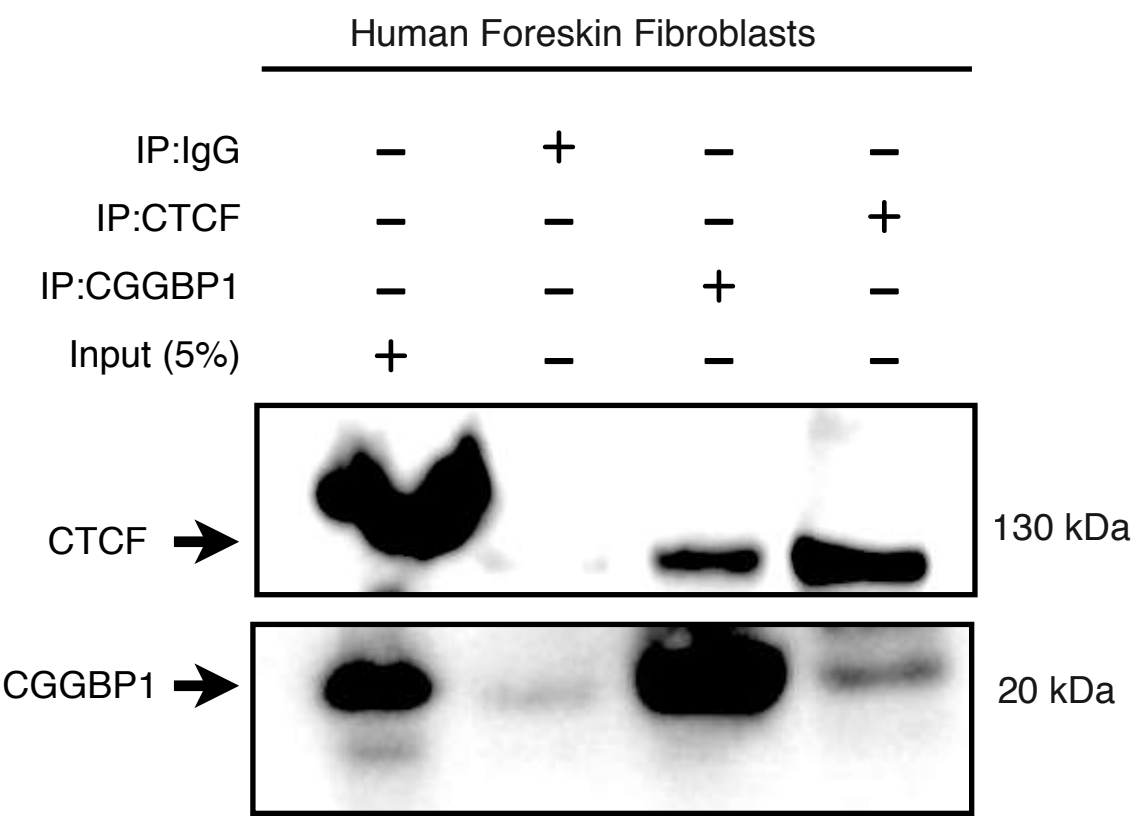


Figure 2A (CTCF)

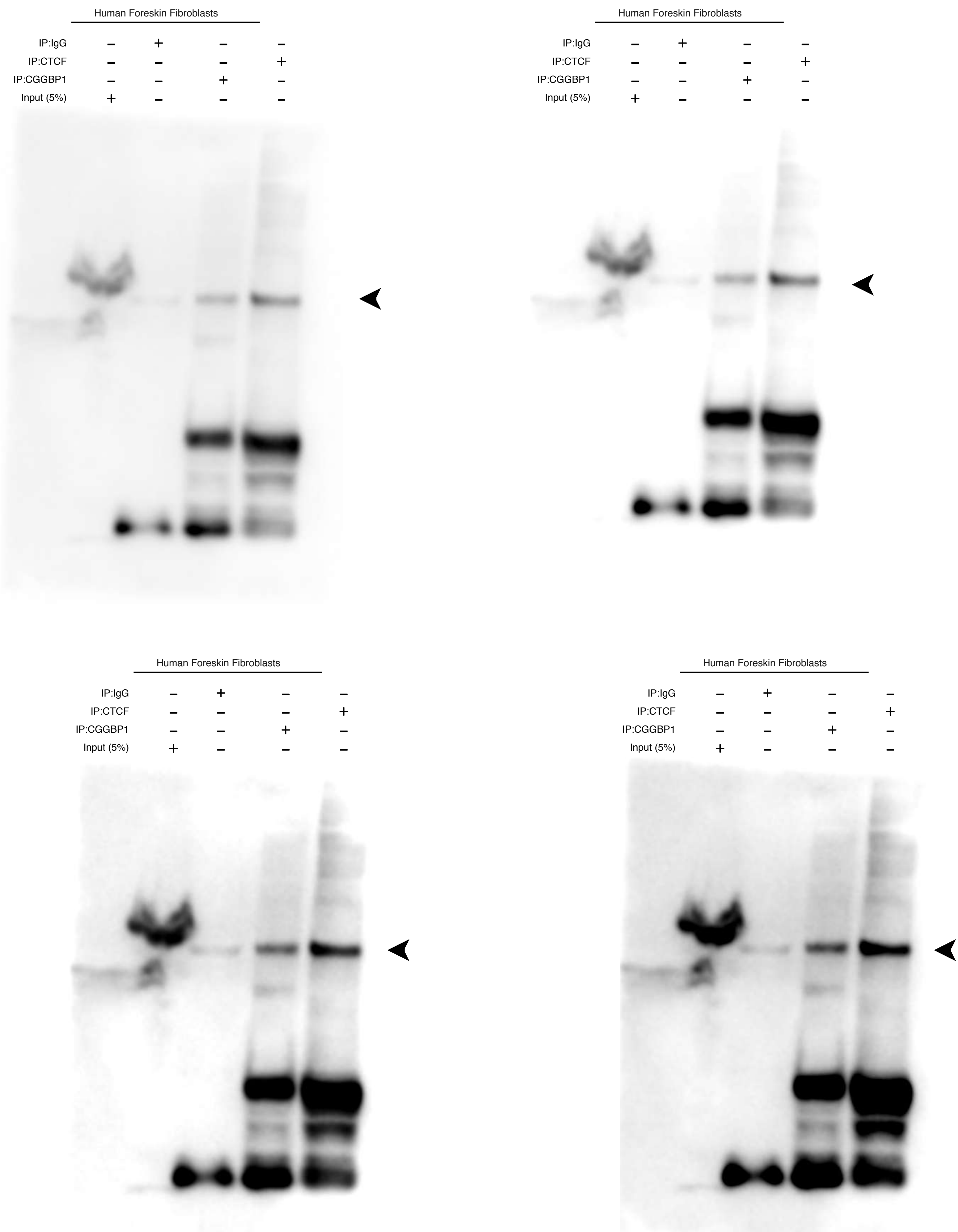


Figure 2A (CGGBP1)

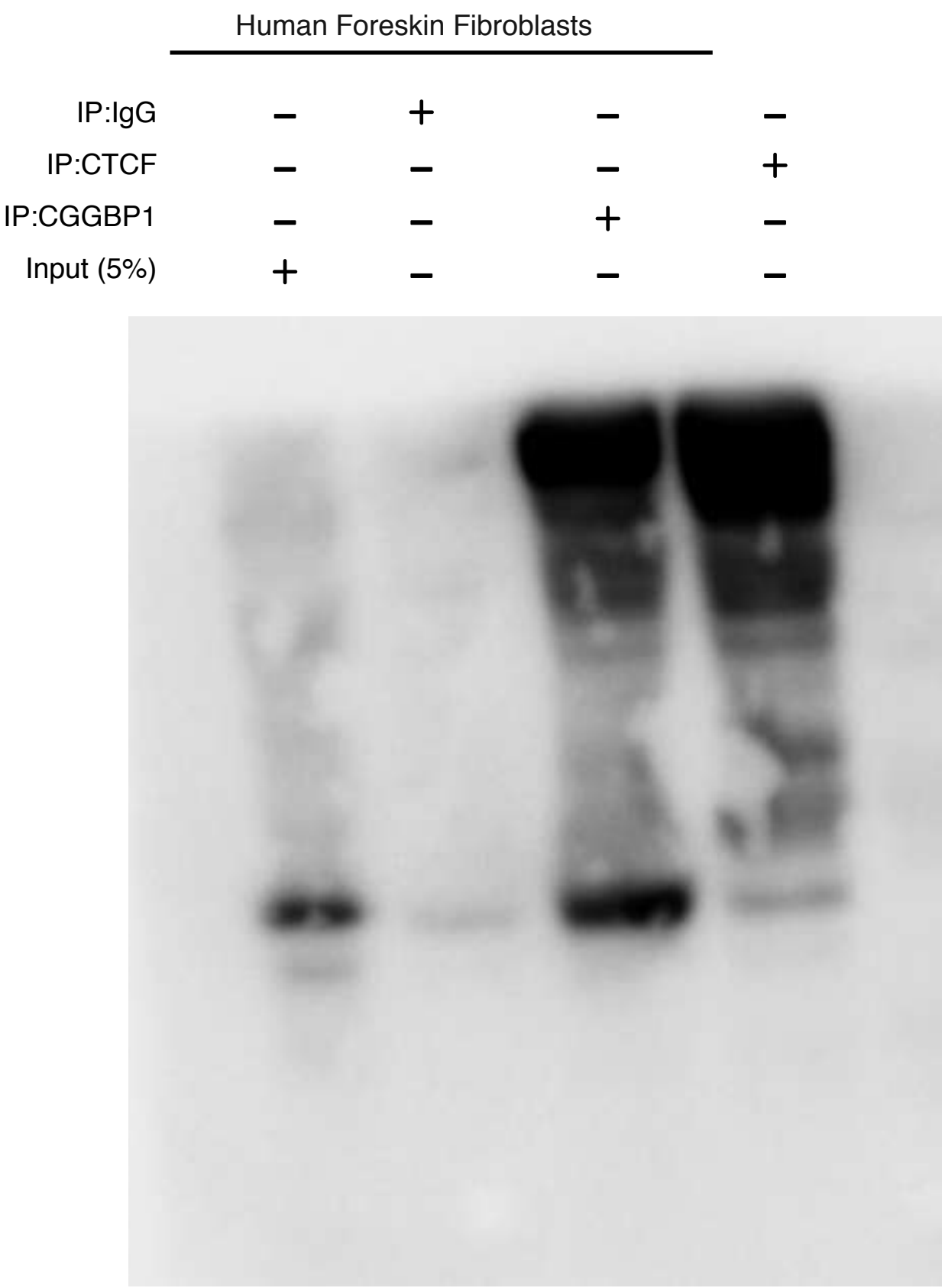
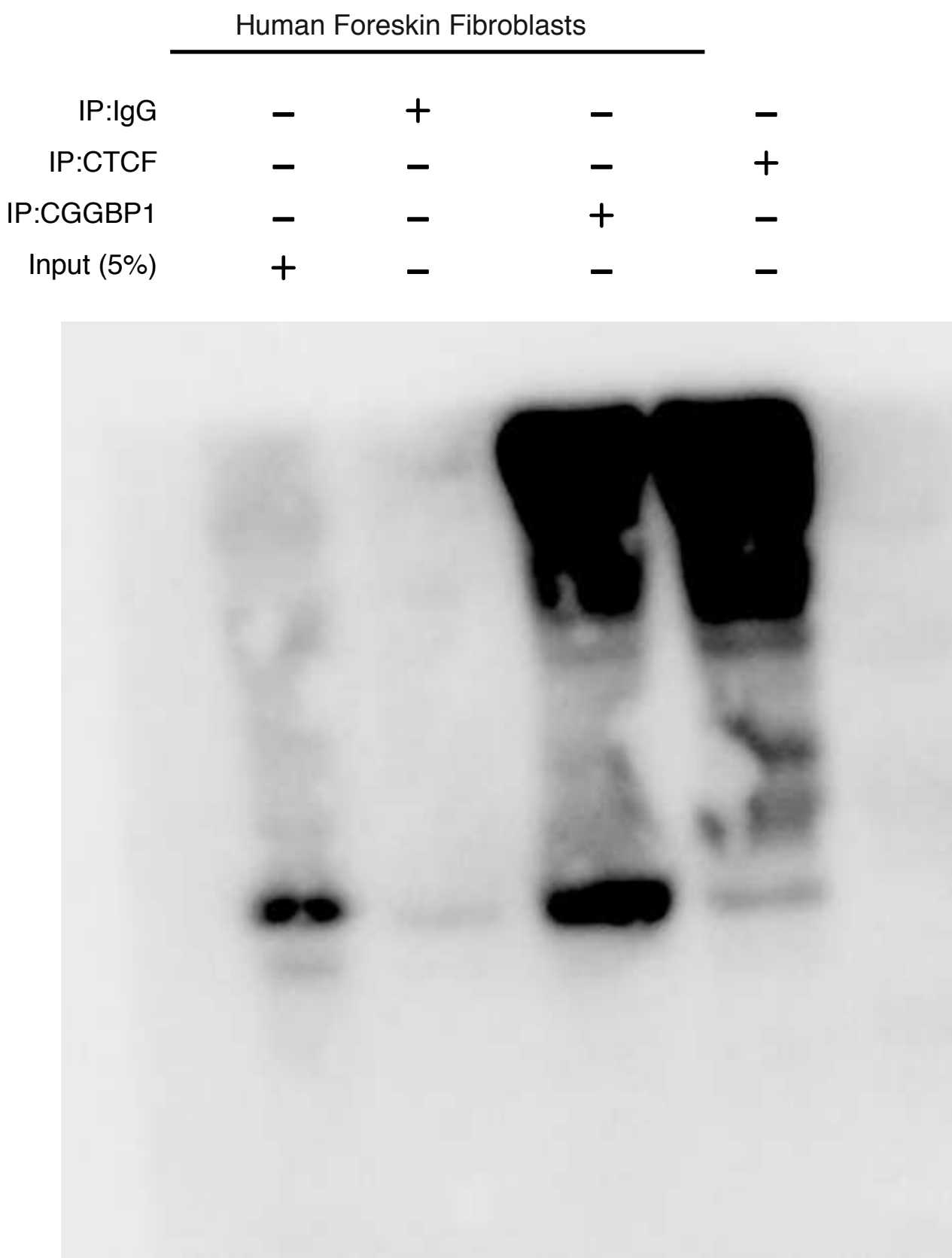
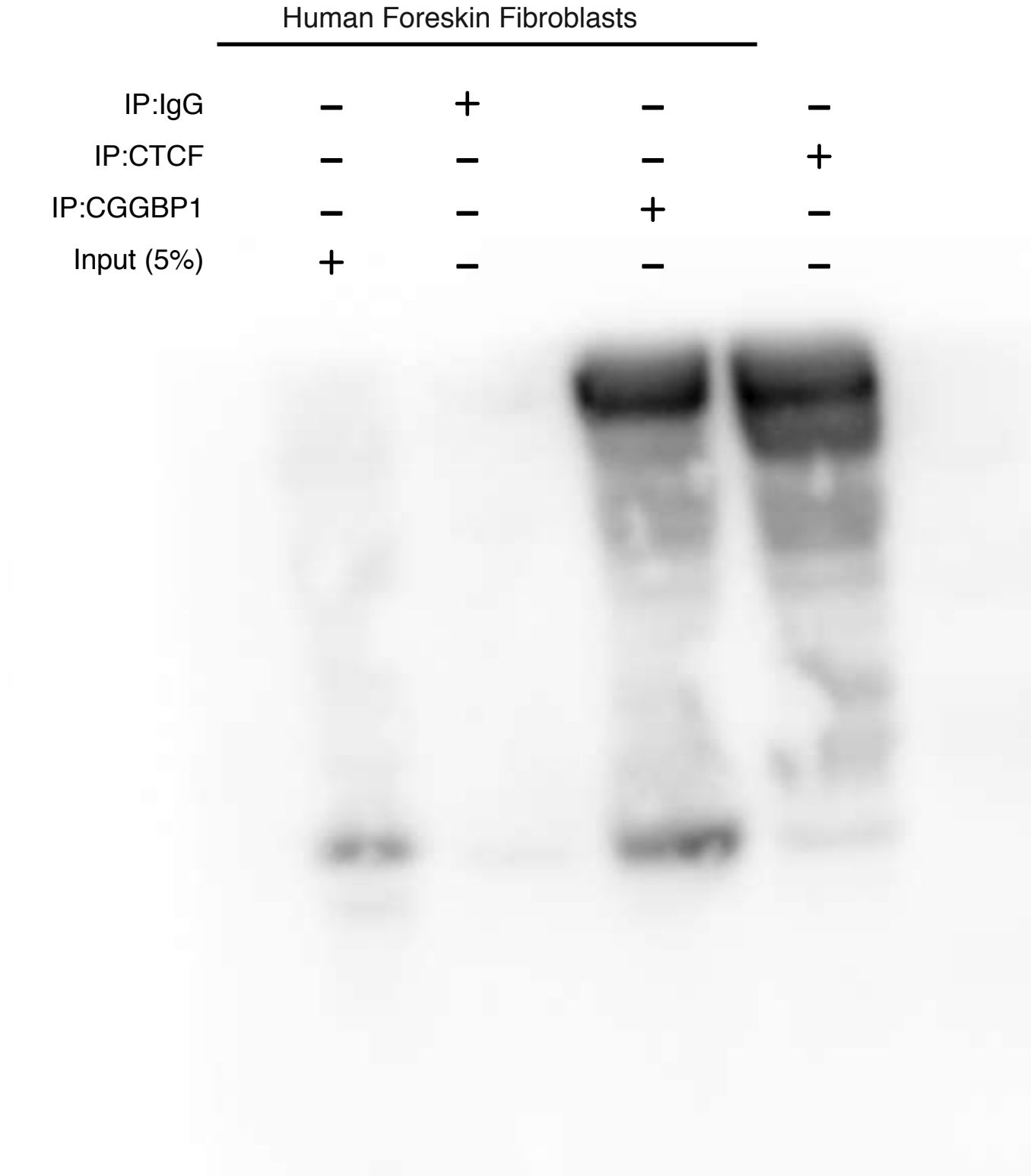
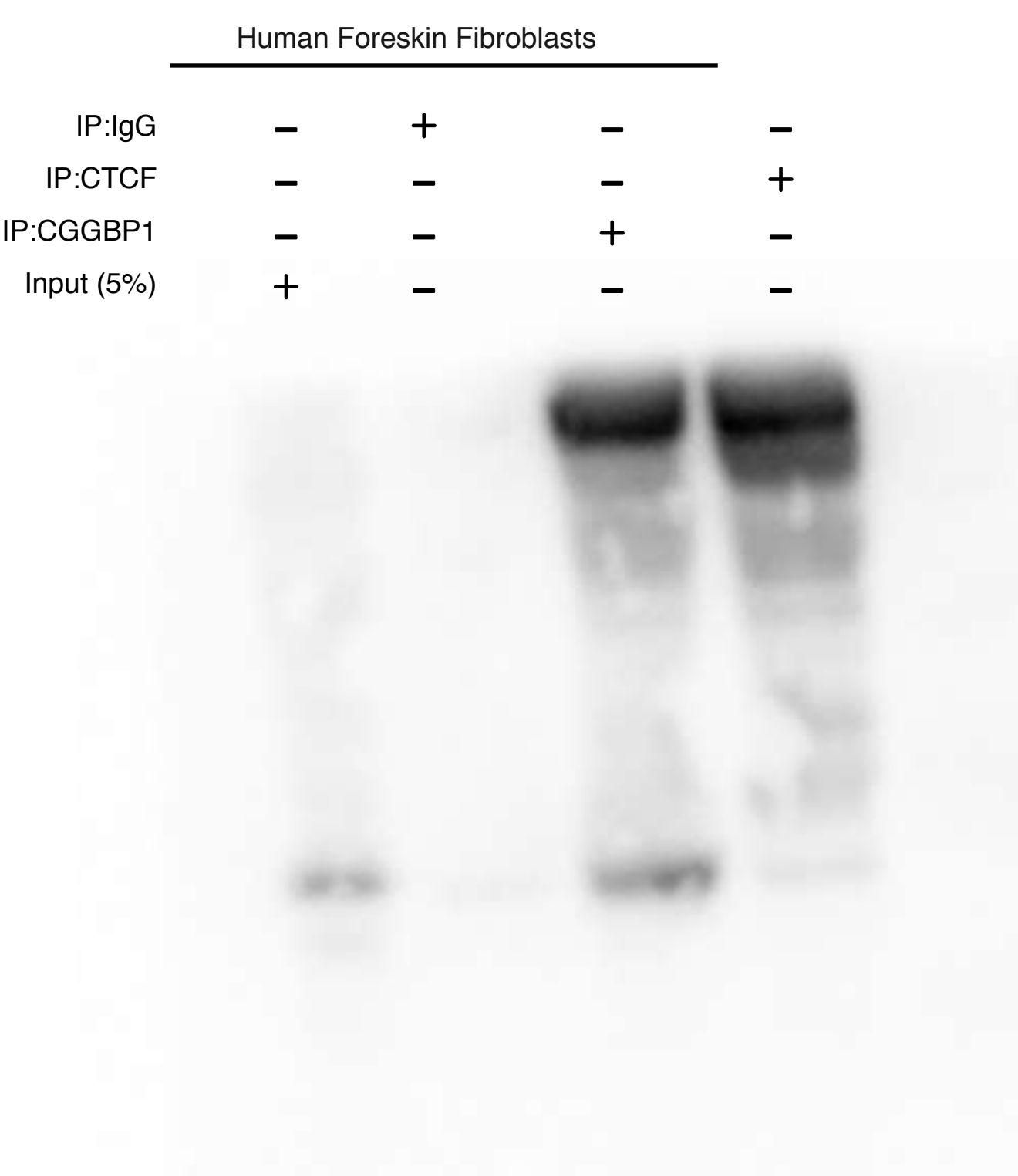
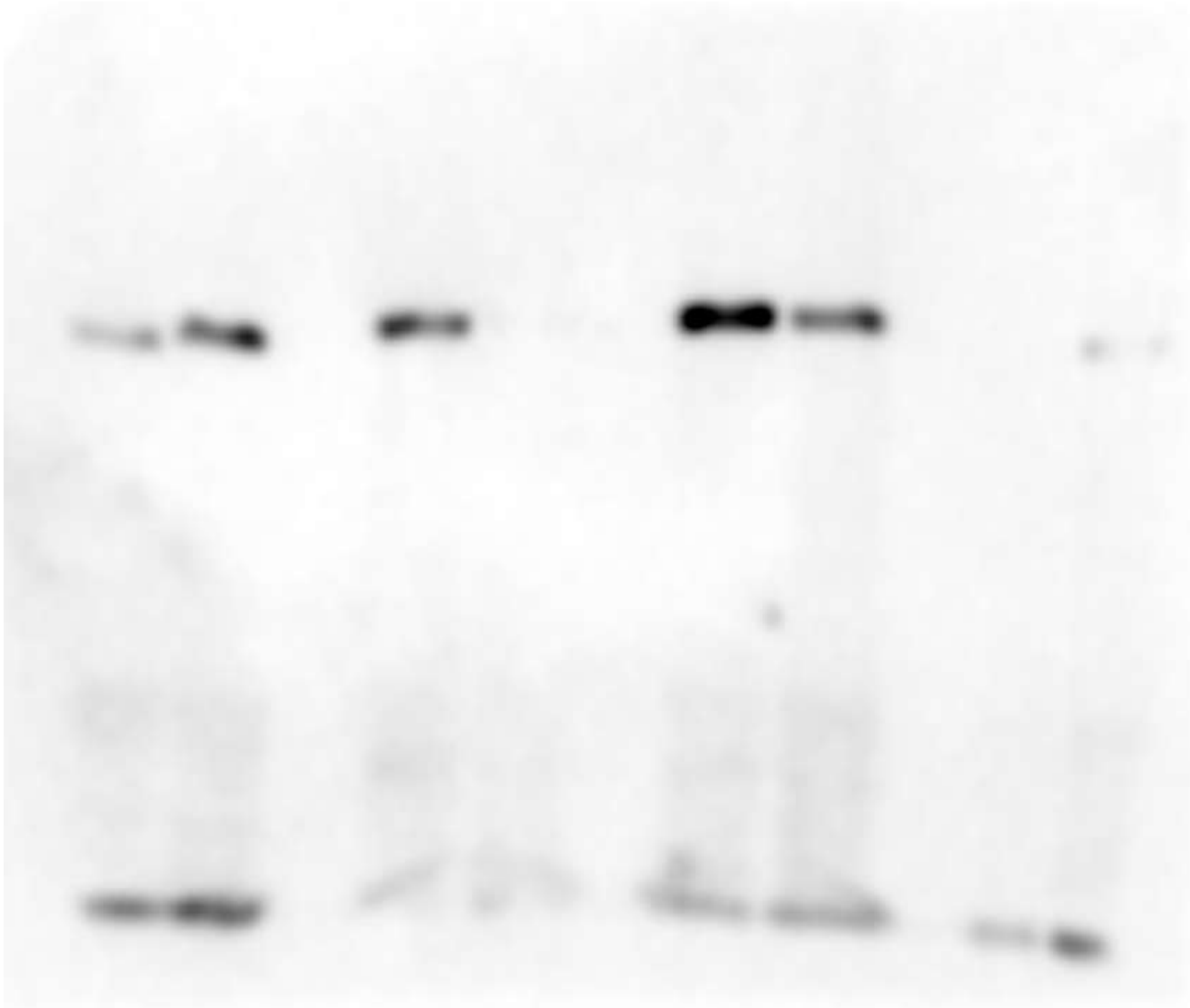
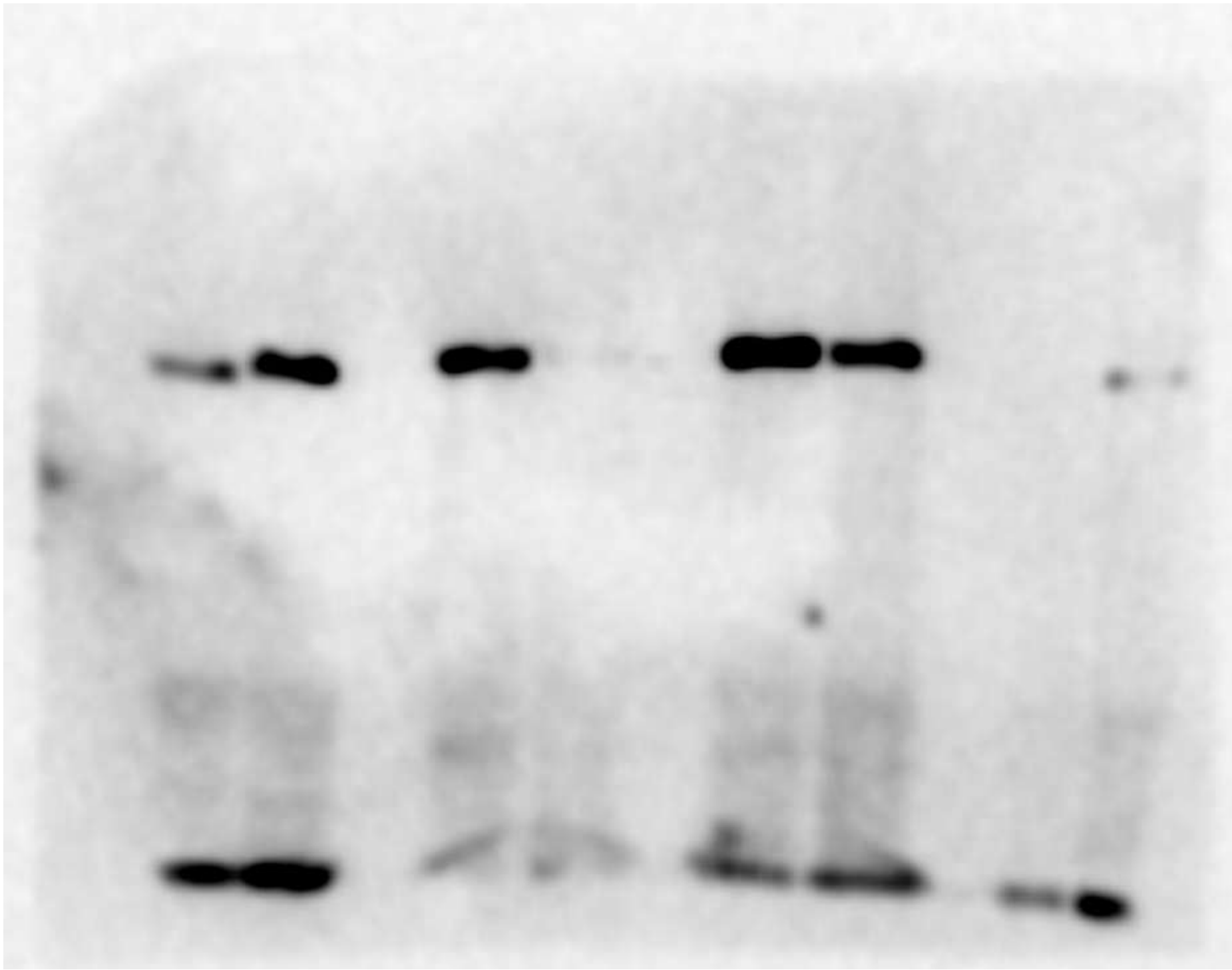


Figure 2B (CTCF)

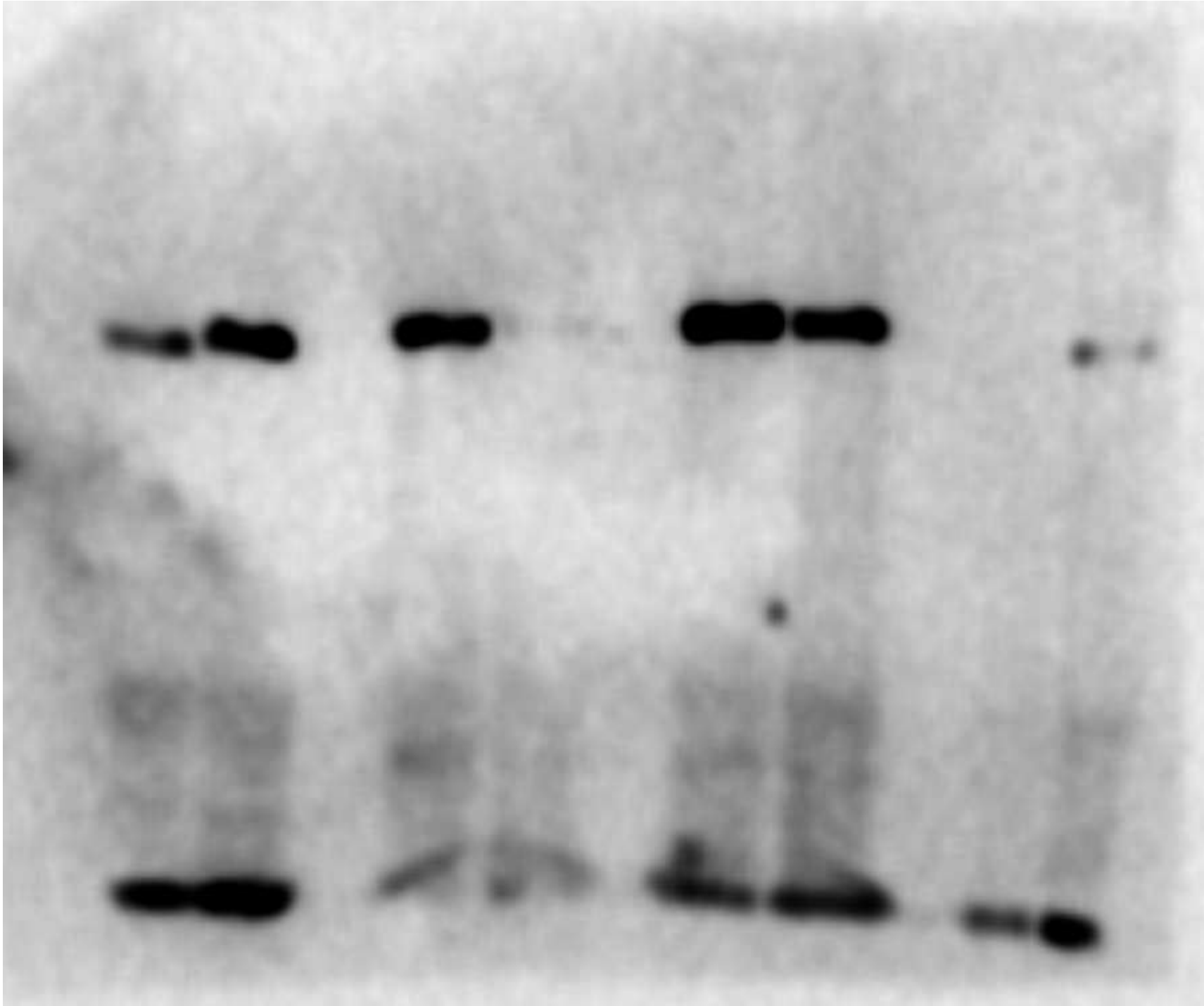
	Human Dermal Fibroblasts											
IP:CTCF	-	-	-	+	-	-	+	-	-	-	-	-
IP:CGGBP1	-	-	-	-	+	-	-	+	-	-	-	-
IP:IgG	-	-	-	-	-	-	-	-	-	+	+	-
Starved	+	-	-	+	+	-	-	-	-	+	-	-
Stimulated	-	+	-	-	-	-	+	+	-	-	+	-
Input (5%)	+	+	-	-	-	-	-	-	-	-	-	-



	Human Dermal Fibroblasts											
IP:CTCF	-	-	-	+	-	-	+	-	-	-	-	-
IP:CGGBP1	-	-	-	-	+	-	-	+	-	-	-	-
IP:IgG	-	-	-	-	-	-	-	-	-	+	+	-
Starved	+	-	-	+	+	-	-	-	-	+	-	-
Stimulated	-	+	-	-	-	-	+	+	-	-	+	-
Input (5%)	+	+	-	-	-	-	-	-	-	-	-	-



	Human Dermal Fibroblasts											
IP:CTCF	-	-	-	+	-	-	+	-	-	-	-	-
IP:CGGBP1	-	-	-	-	+	-	-	+	-	-	-	-
IP:IgG	-	-	-	-	-	-	-	-	-	+	+	-
Starved	+	-	-	+	+	-	-	-	-	+	-	-
Stimulated	-	+	-	-	-	-	+	+	-	-	+	-
Input (5%)	+	+	-	-	-	-	-	-	-	-	-	-



	Human Dermal Fibroblasts											
IP:CTCF	-	-	-	+	-	-	+	-	-	-	-	-
IP:CGGBP1	-	-	-	-	+	-	-	+	-	-	-	-
IP:IgG	-	-	-	-	-	-	-	-	-	+	+	-
Starved	+	-	-	+	+	-	-	-	-	+	-	-
Stimulated	-	+	-	-	-	-	+	+	-	-	+	-
Input (5%)	+	+	-	-	-	-	-	-	-	-	-	-

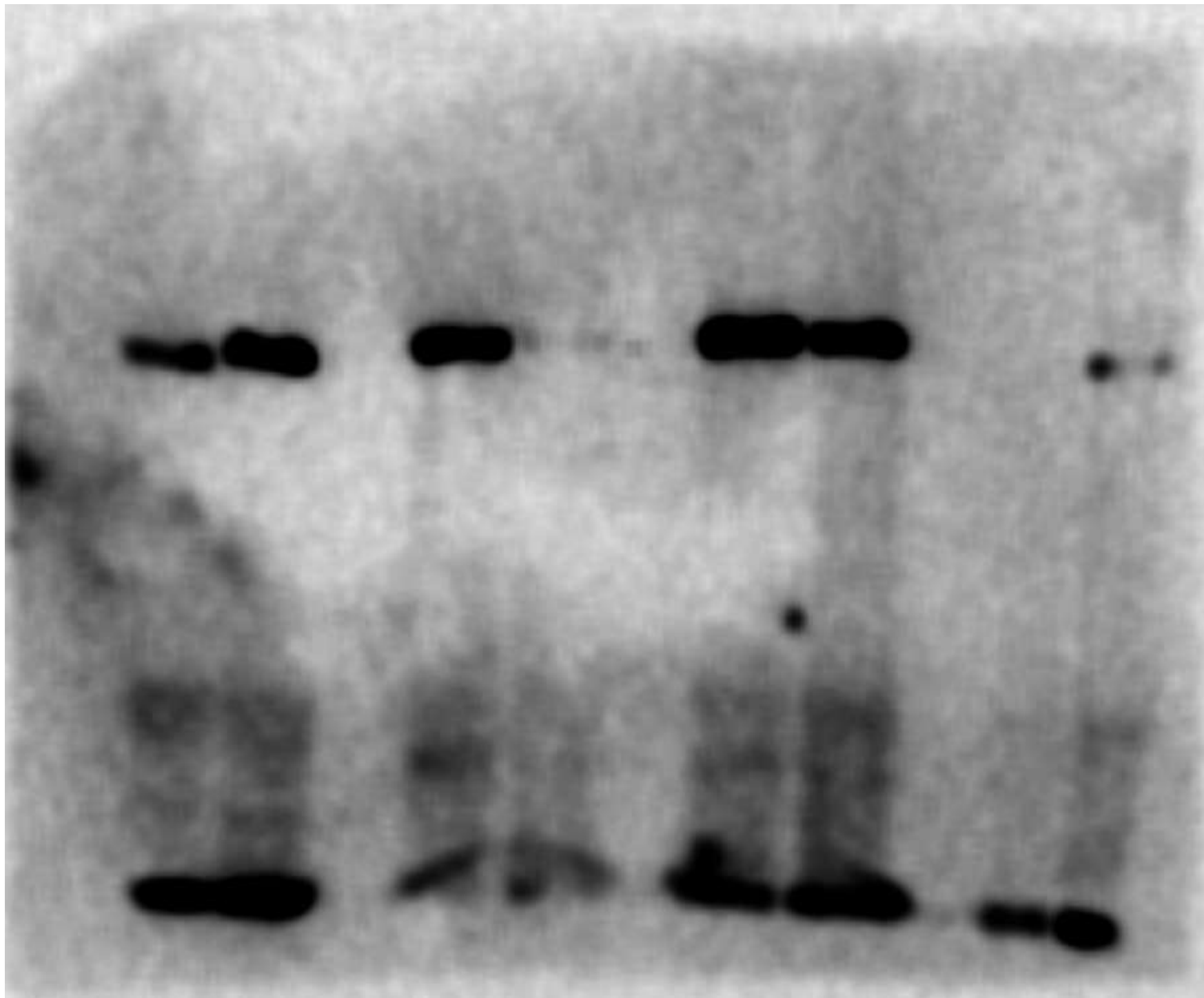
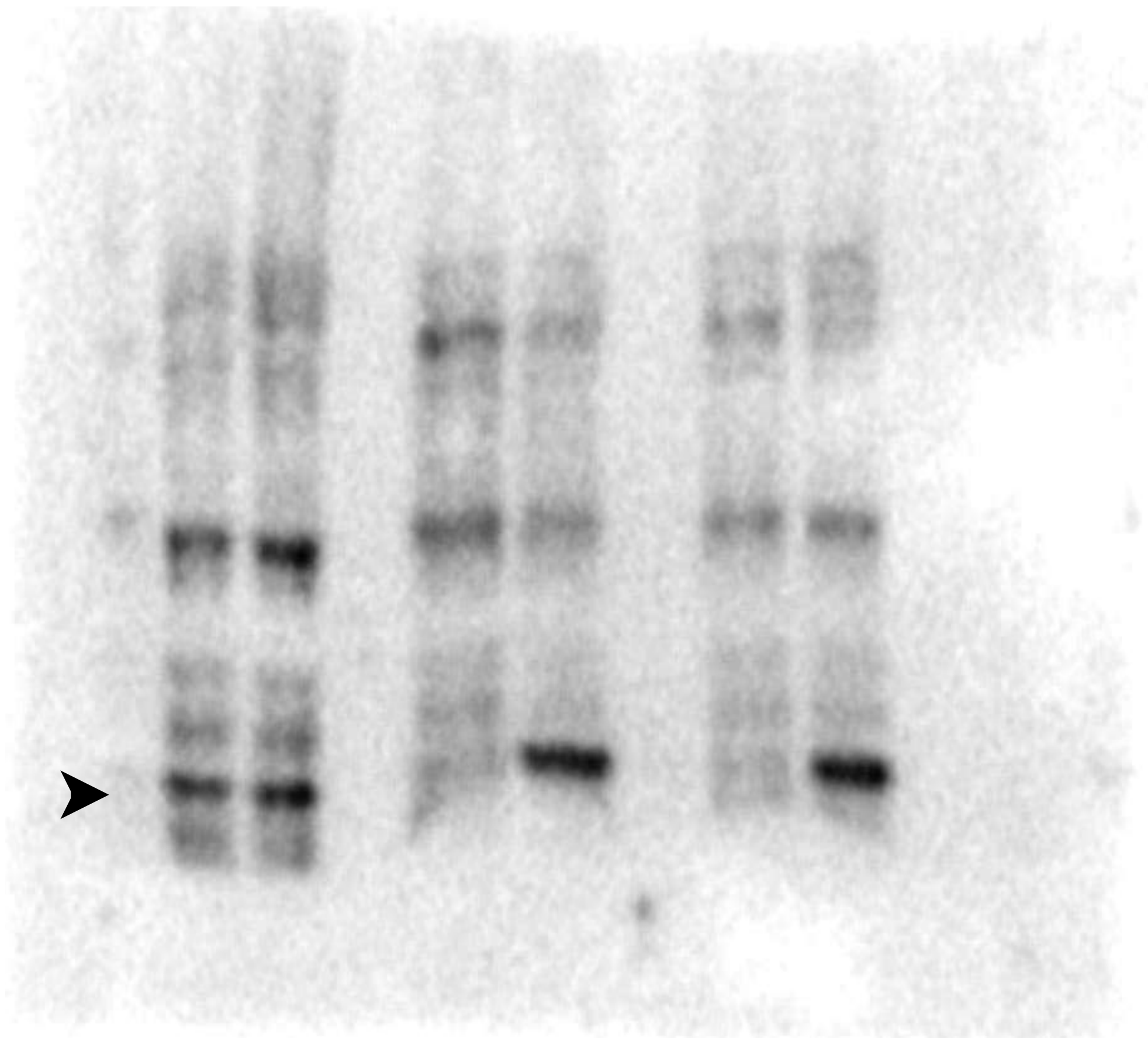
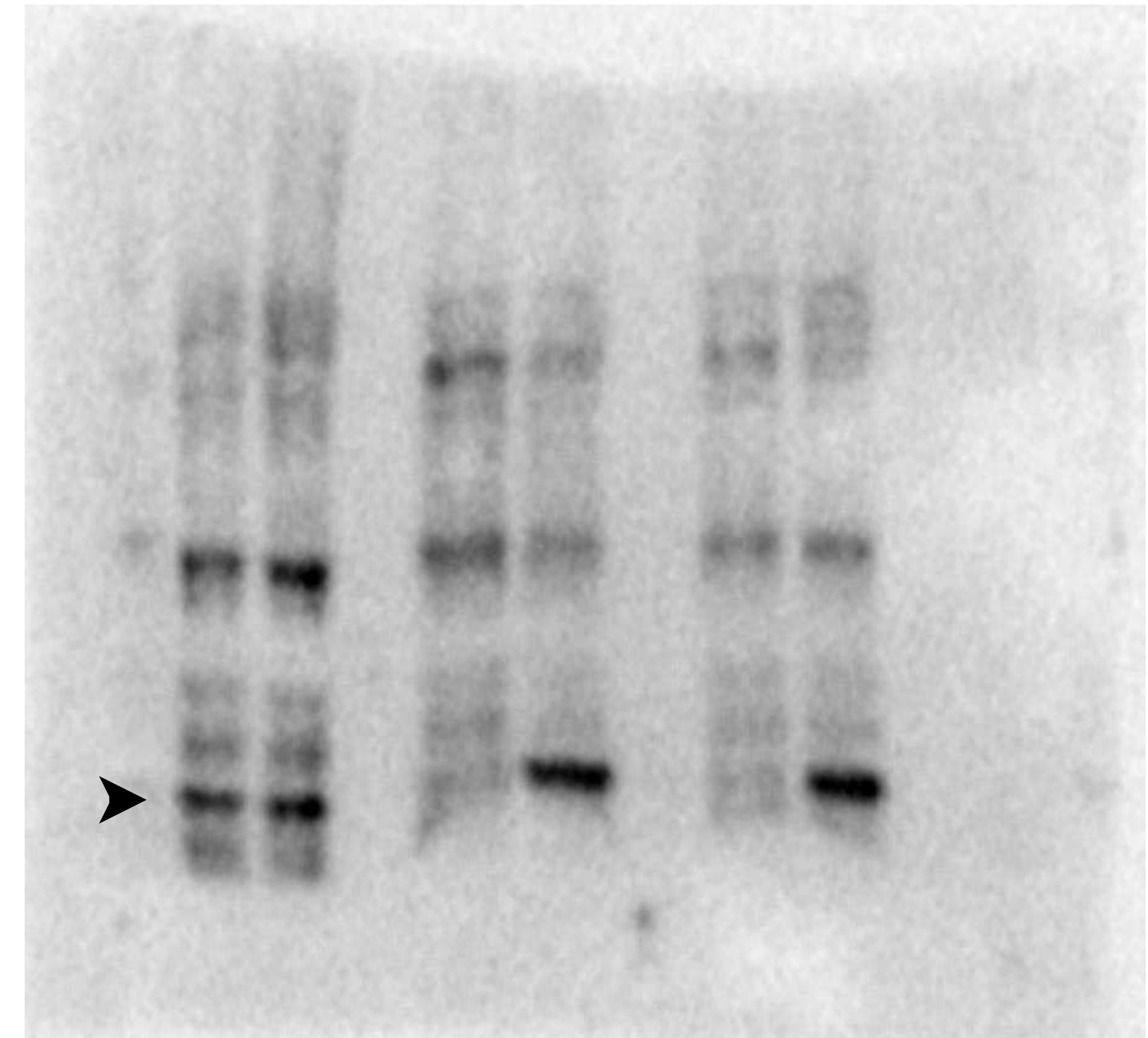


Figure 2B (CGGBP1)

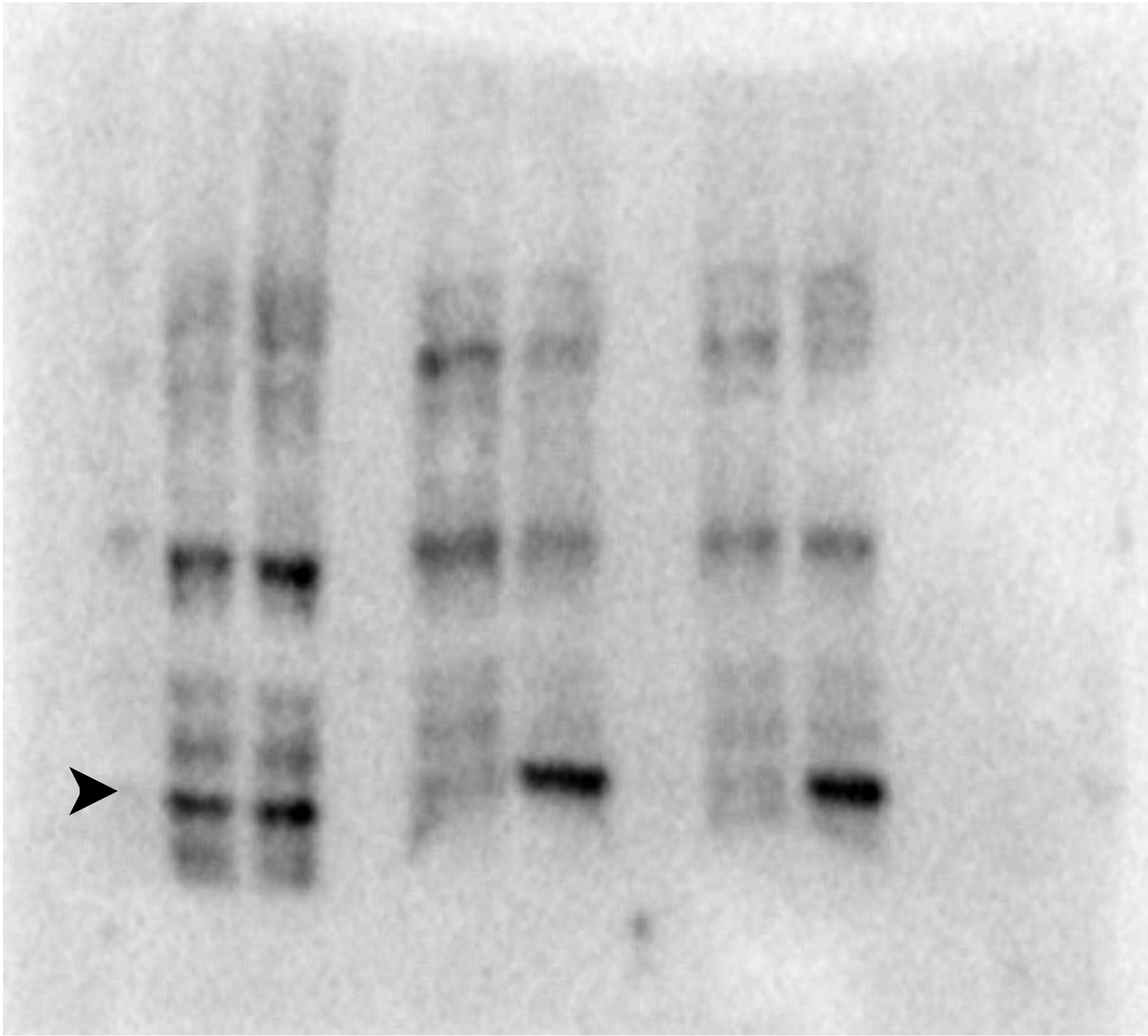
	Human Dermal Fibroblasts										
IP:CTCF	-	-	-	+	-	-	+	-	-	-	-
IP:CGGBP1	-	-	-	-	+	-	-	+	-	-	-
IP:IgG	-	-	-	-	-	-	-	-	-	+	+
Starved	+	-	-	+	+	-	-	-	-	+	-
Stimulated	-	+	-	-	-	-	+	+	-	-	+
Input (5%)	+	+	-	-	-	-	-	-	-	-	-



	Human Dermal Fibroblasts										
IP:CTCF	-	-	-	+	-	-	+	-	-	-	-
IP:CGGBP1	-	-	-	-	+	-	-	+	-	-	-
IP:IgG	-	-	-	-	-	-	-	-	-	+	+
Starved	+	-	-	+	+	-	-	-	-	+	-
Stimulated	-	+	-	-	-	-	+	+	-	-	+
Input (5%)	+	+	-	-	-	-	-	-	-	-	-



	Human Dermal Fibroblasts										
IP:CTCF	-	-	-	+	-	-	+	-	-	-	-
IP:CGGBP1	-	-	-	-	+	-	-	+	-	-	-
IP:IgG	-	-	-	-	-	-	-	-	-	+	+
Starved	+	-	-	+	+	-	-	-	-	+	-
Stimulated	-	+	-	-	-	-	+	+	-	-	+
Input (5%)	+	+	-	-	-	-	-	-	-	-	-



	Human Dermal Fibroblasts										
IP:CTCF	-	-	-	+	-	-	+	-	-	-	-
IP:CGGBP1	-	-	-	-	+	-	-	+	-	-	-
IP:IgG	-	-	-	-	-	-	-	-	-	+	+
Starved	+	-	-	+	+	-	-	-	-	+	-
Stimulated	-	+	-	-	-	-	+	+	-	-	+
Input (5%)	+	+	-	-	-	-	-	-	-	-	-

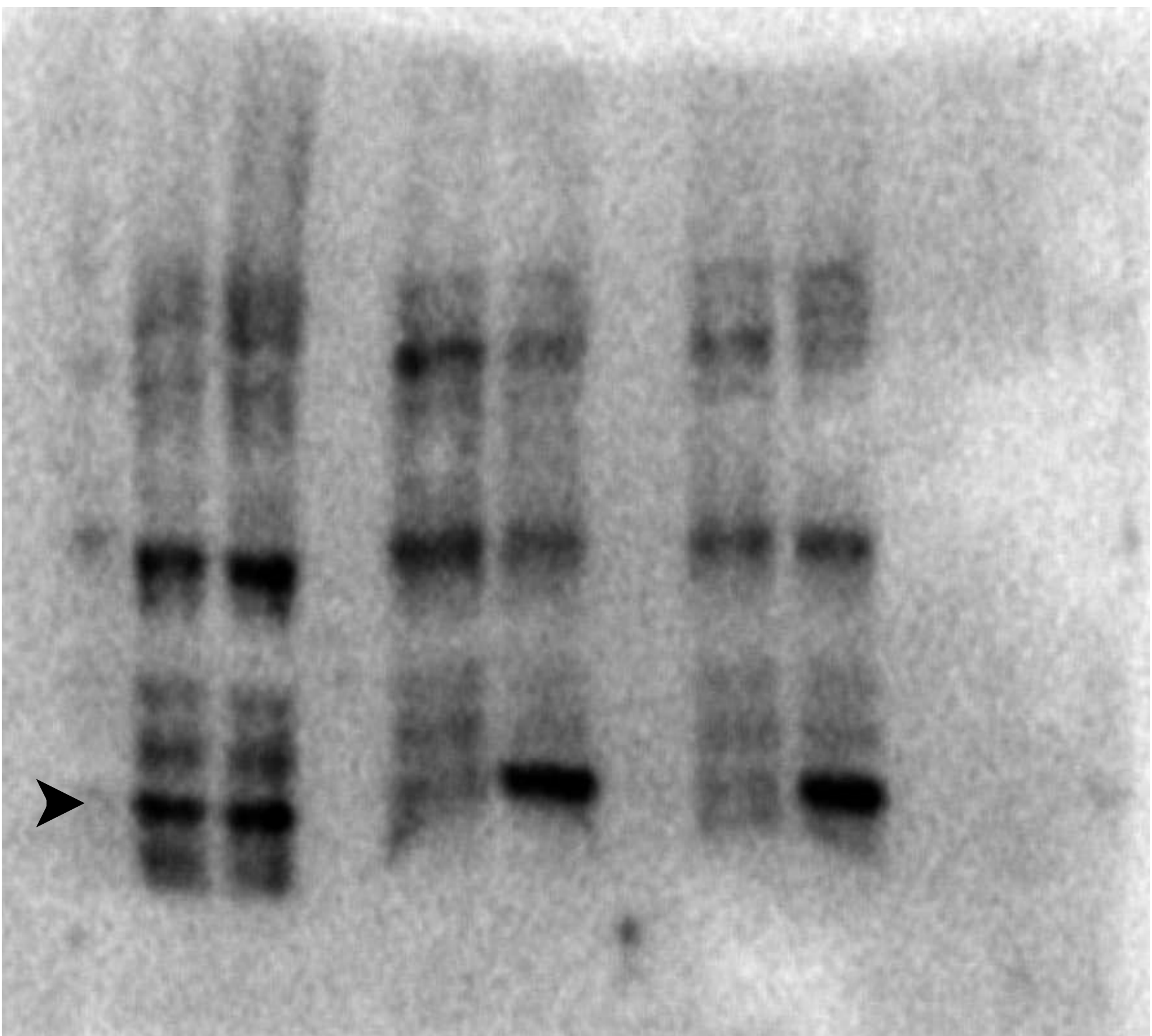


Figure 2C (CTCF)

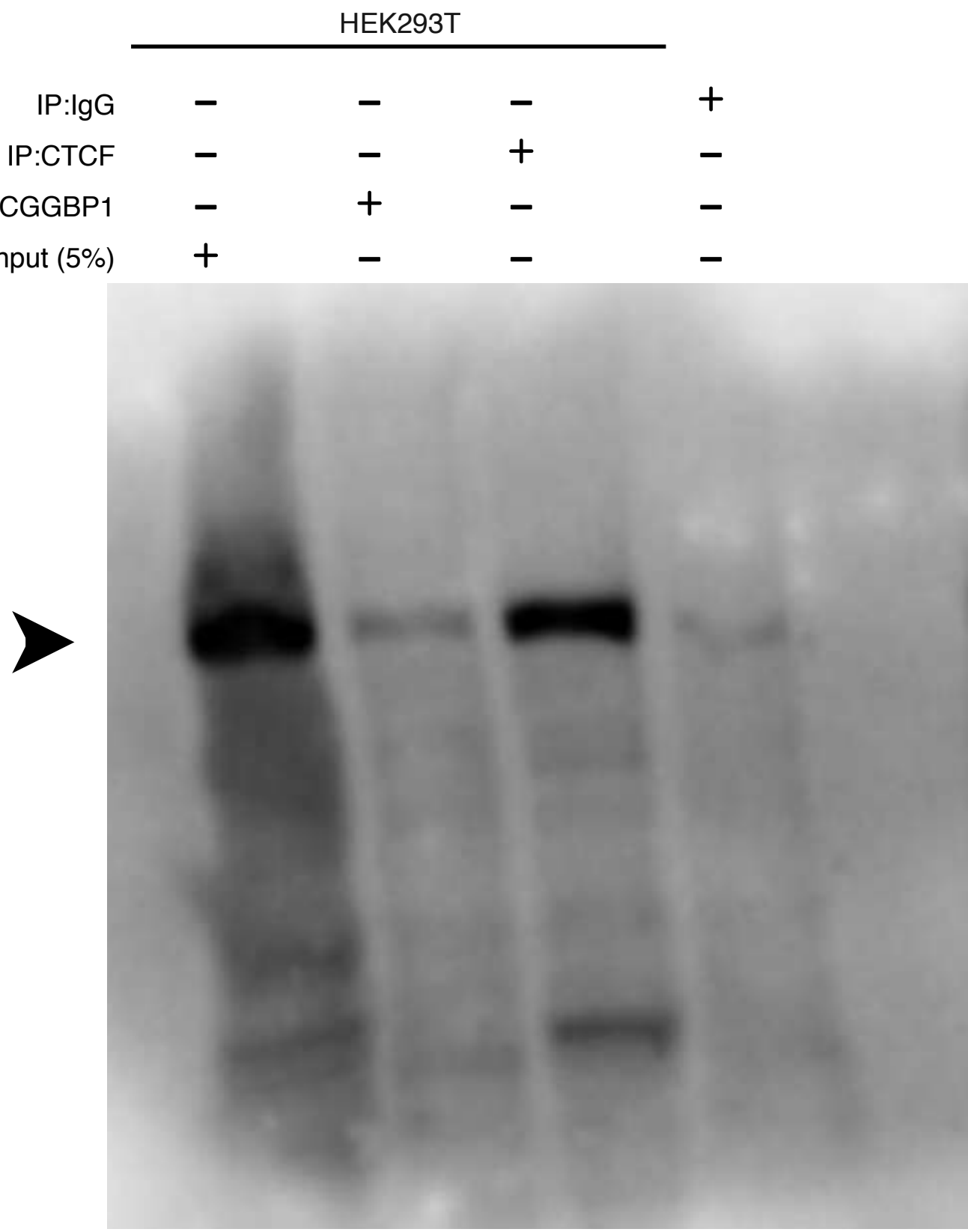
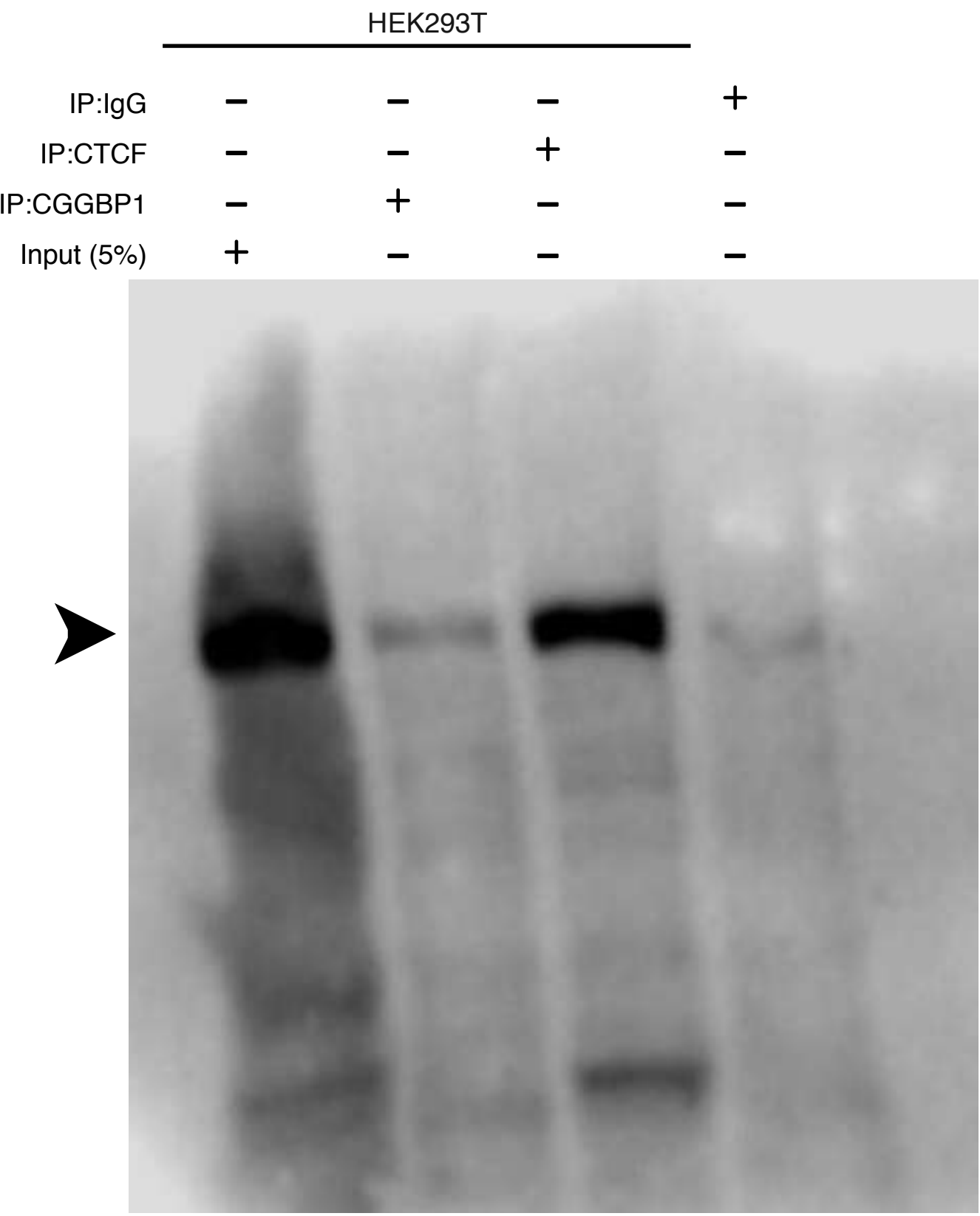
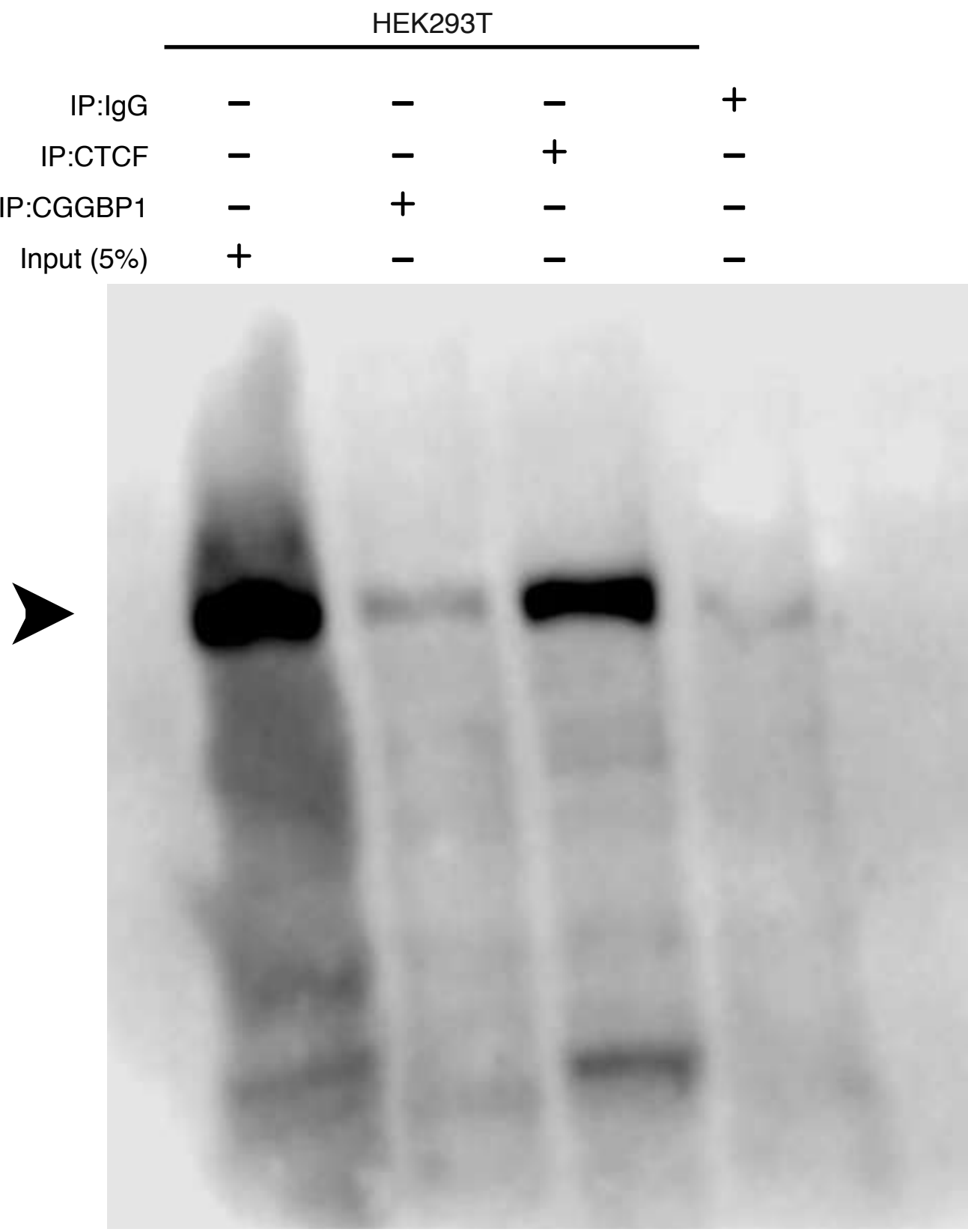
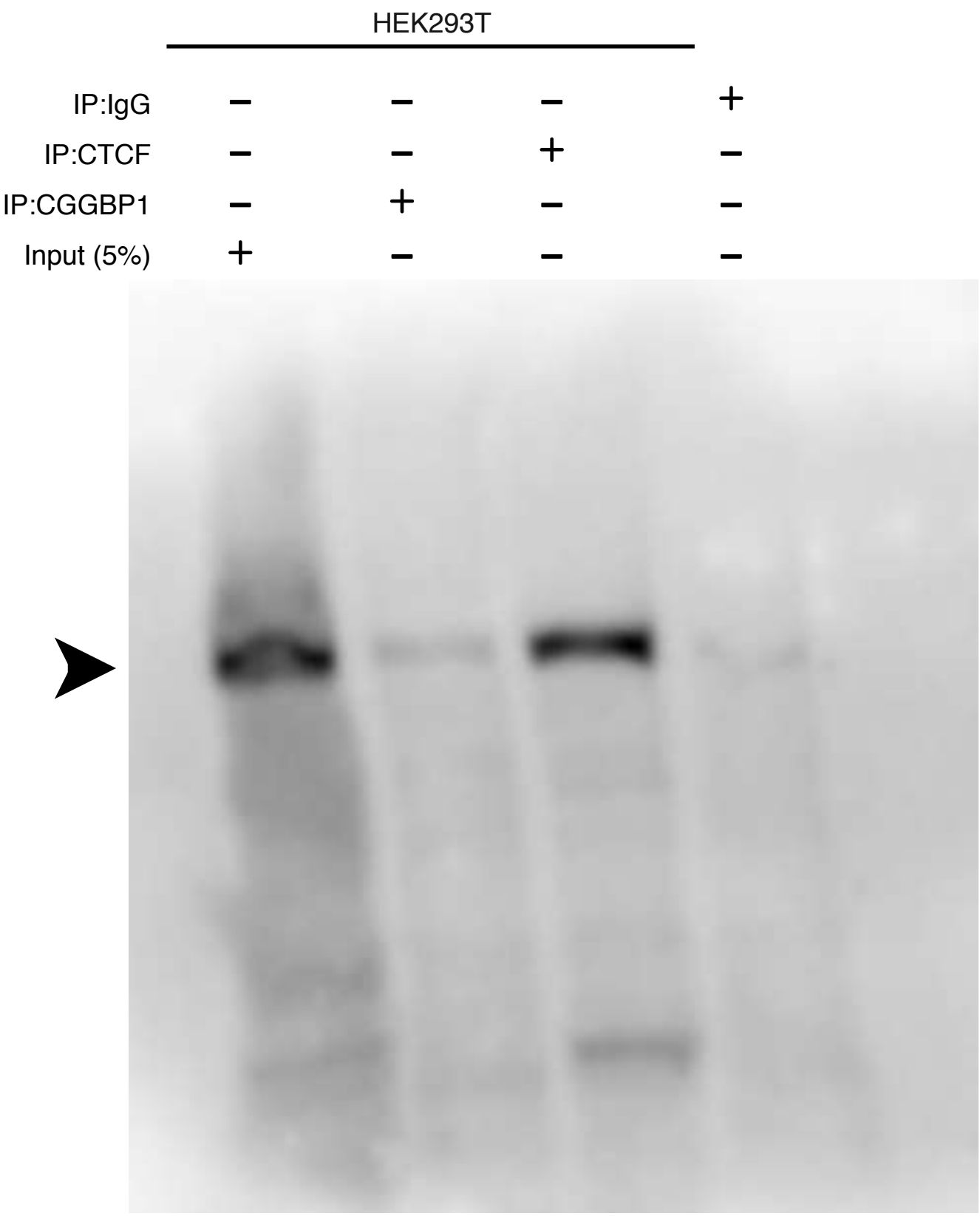
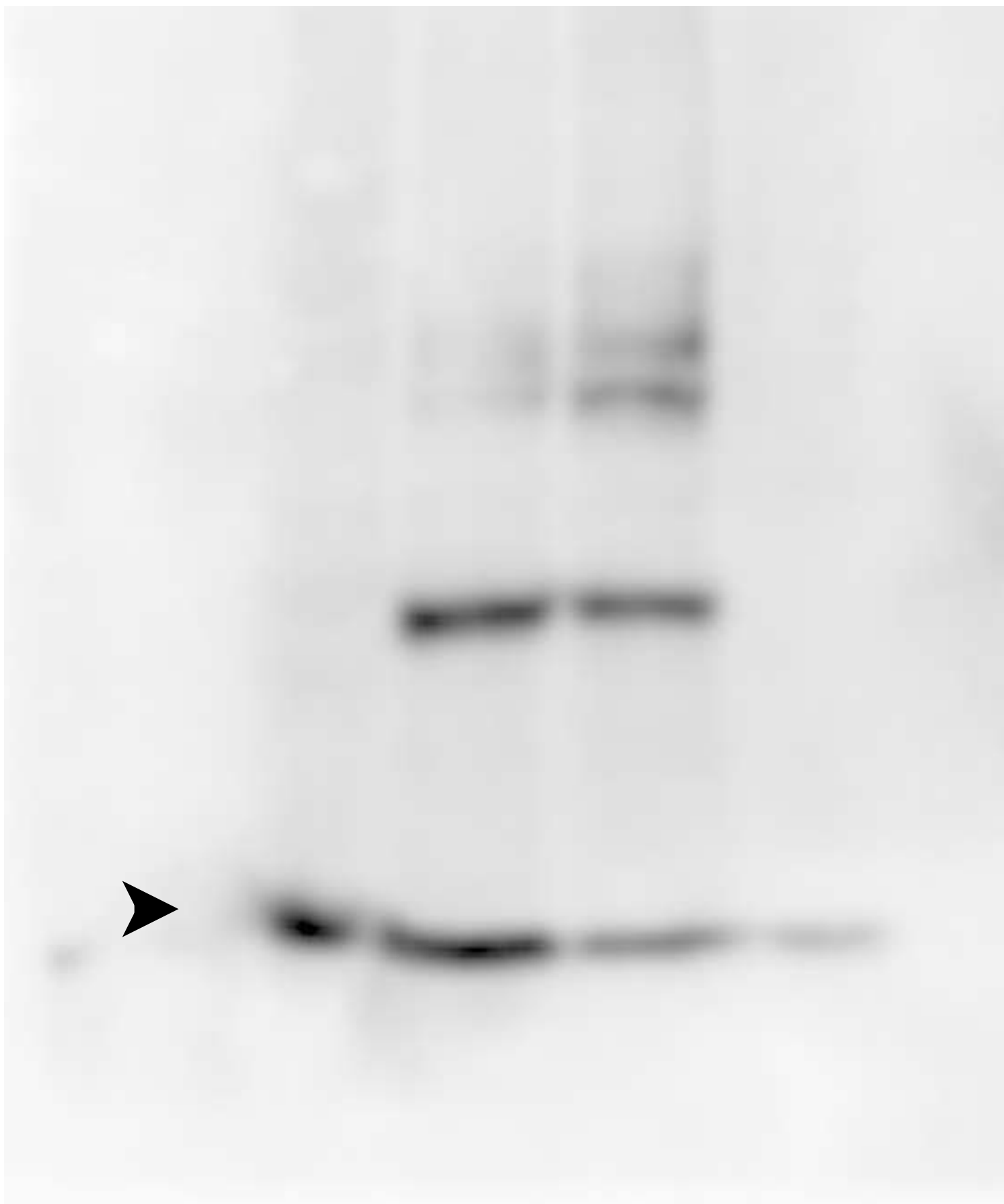
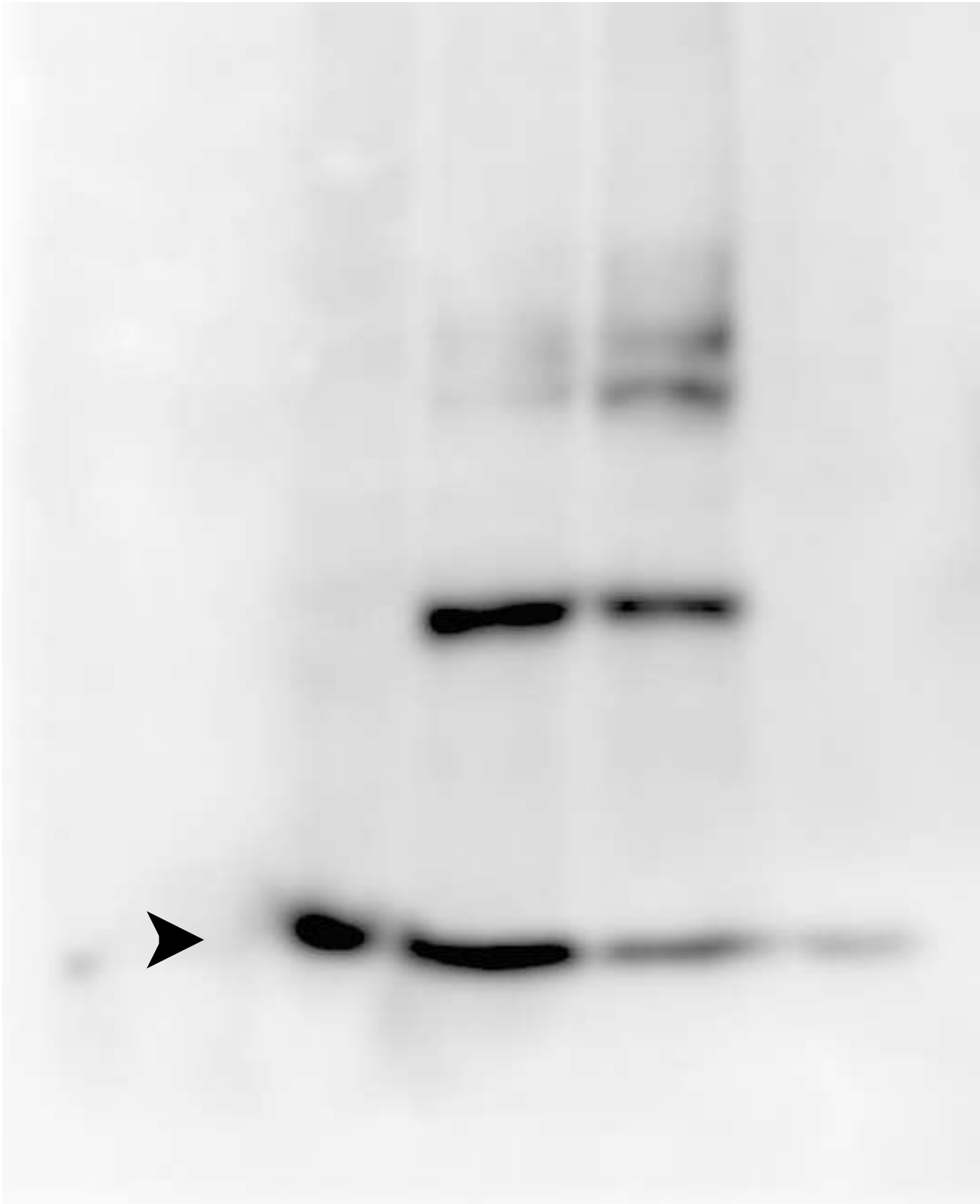


Figure 2C (CGGBP1)

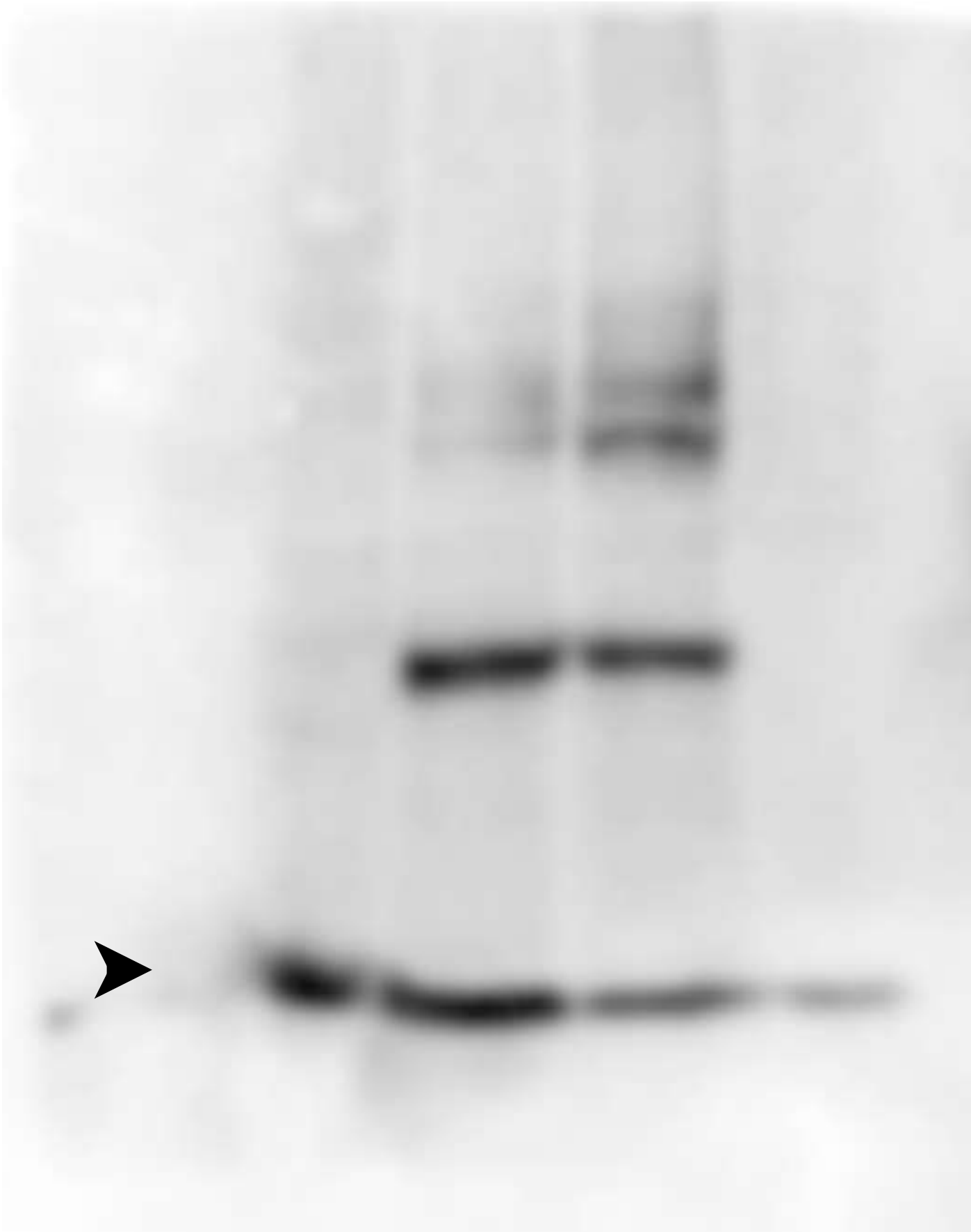
	HEK293T			
IP:IgG	-	-	-	+
IP:CTCF	-	-	+	-
IP:CGGBP1	-	+	-	-
Input (5%)	+	-	-	-



	HEK293T			
IP:IgG	-	-	-	+
IP:CTCF	-	-	+	-
IP:CGGBP1	-	+	-	-
Input (5%)	+	-	-	-



	HEK293T			
IP:IgG	-	-	-	+
IP:CTCF	-	-	+	-
IP:CGGBP1	-	+	-	-
Input (5%)	+	-	-	-



	HEK293T			
IP:IgG	-	-	-	+
IP:CTCF	-	-	+	-
IP:CGGBP1	-	+	-	-
Input (5%)	+	-	-	-

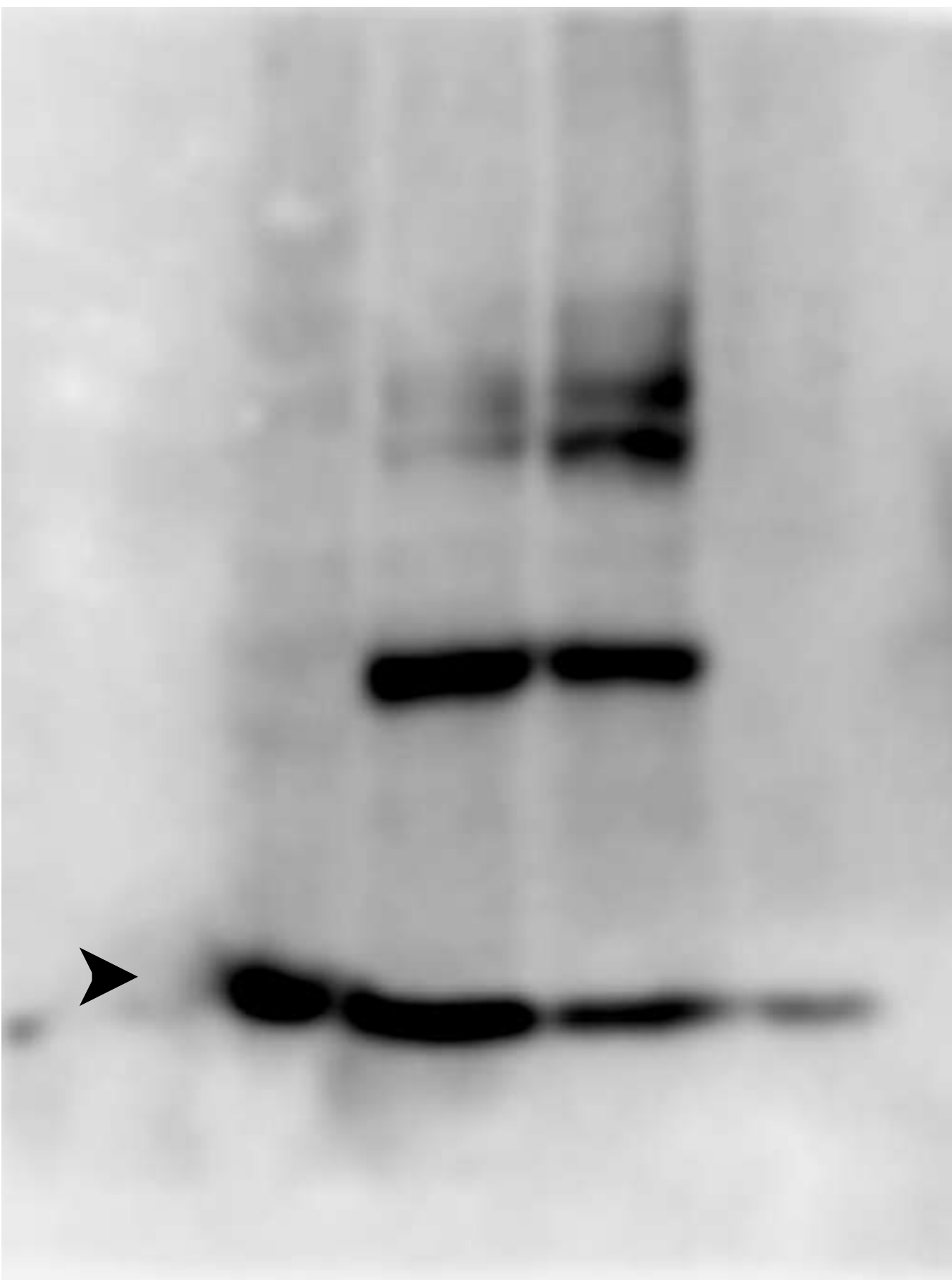


Figure 2D (CTCF)

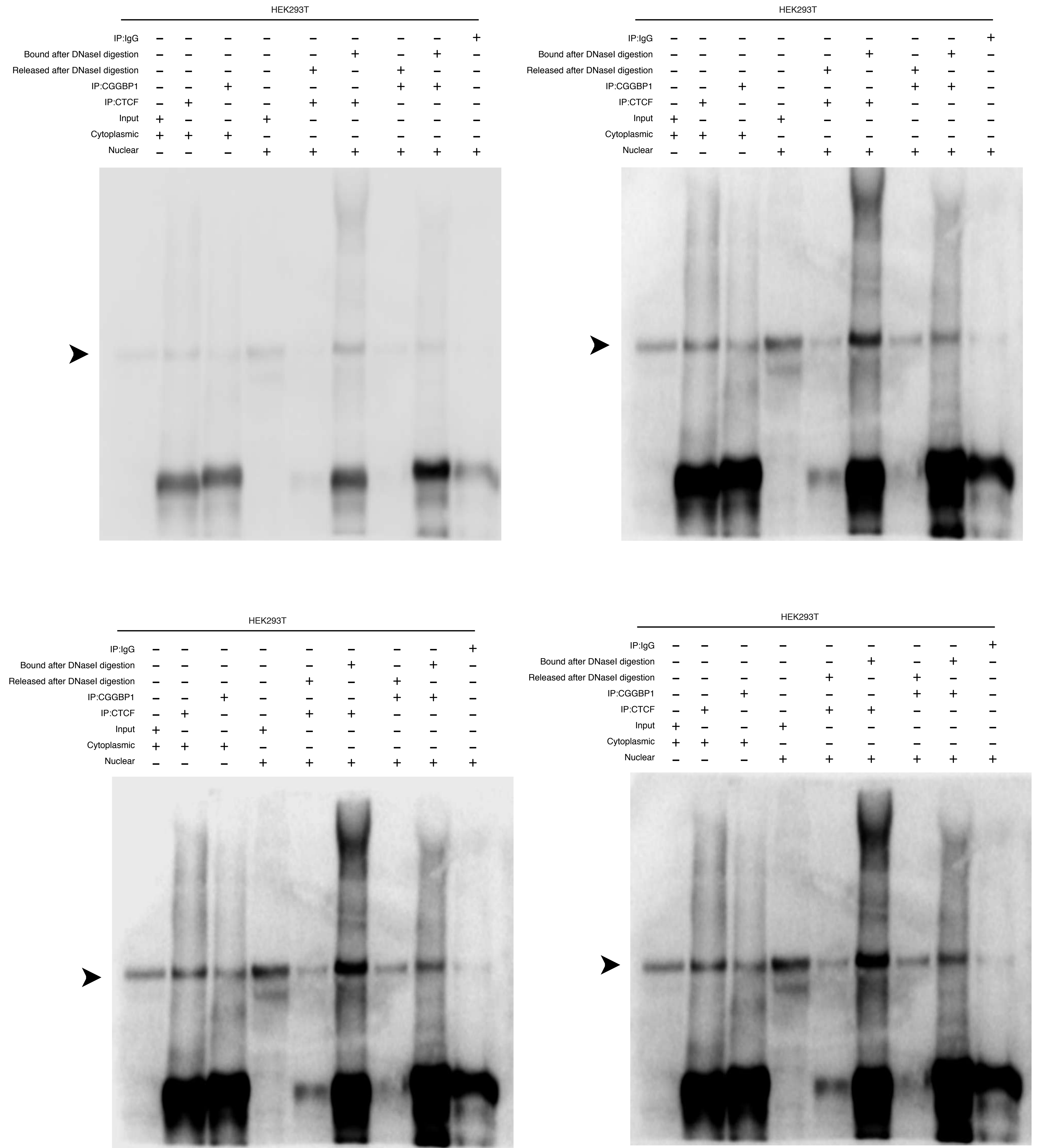
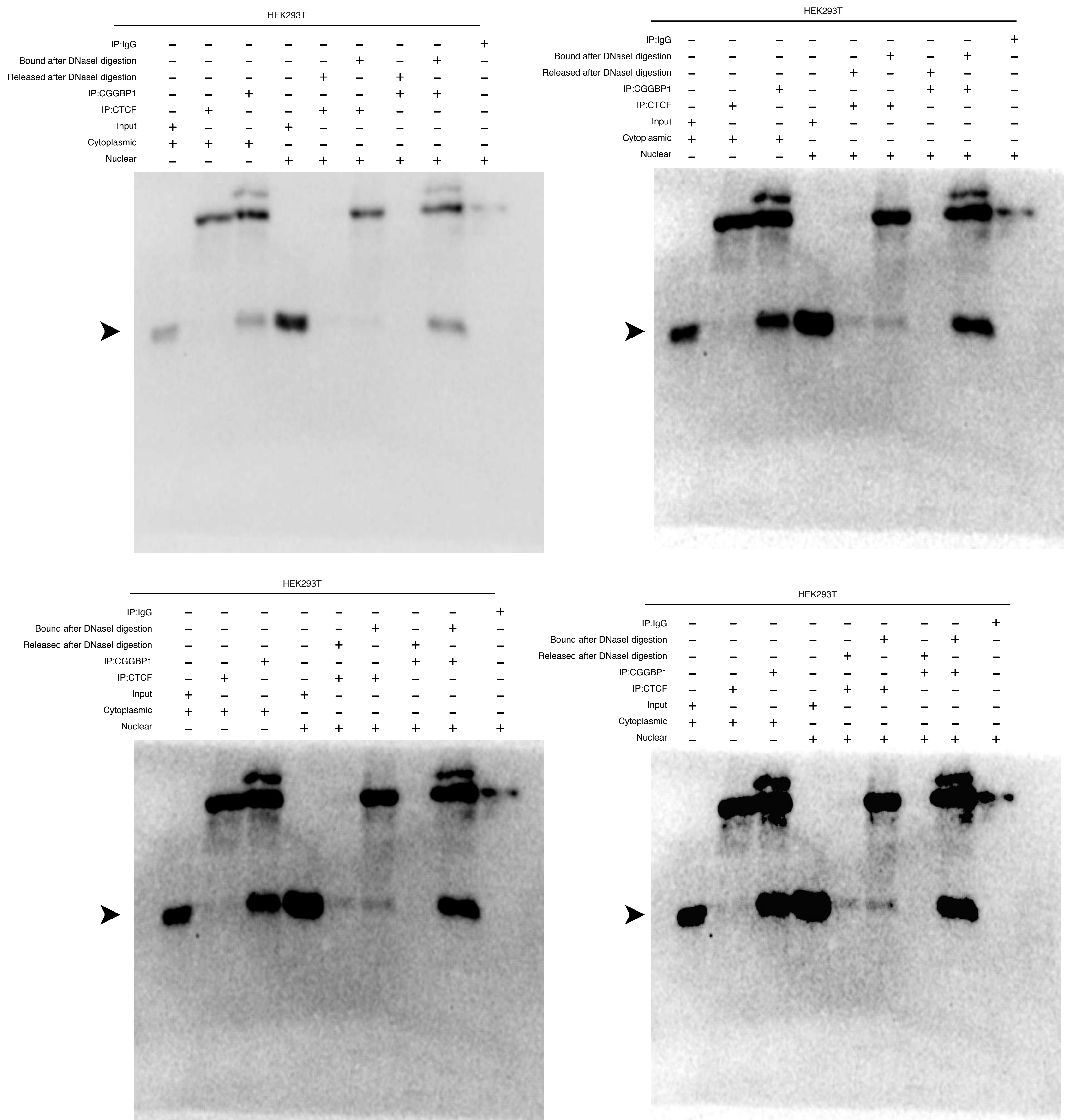


Figure 2D (CGGBP1)



APPENDIX II

Genome-browser views of CTCF ChIP-seq reads along with the published CTCF ChIP-seq datasets

A

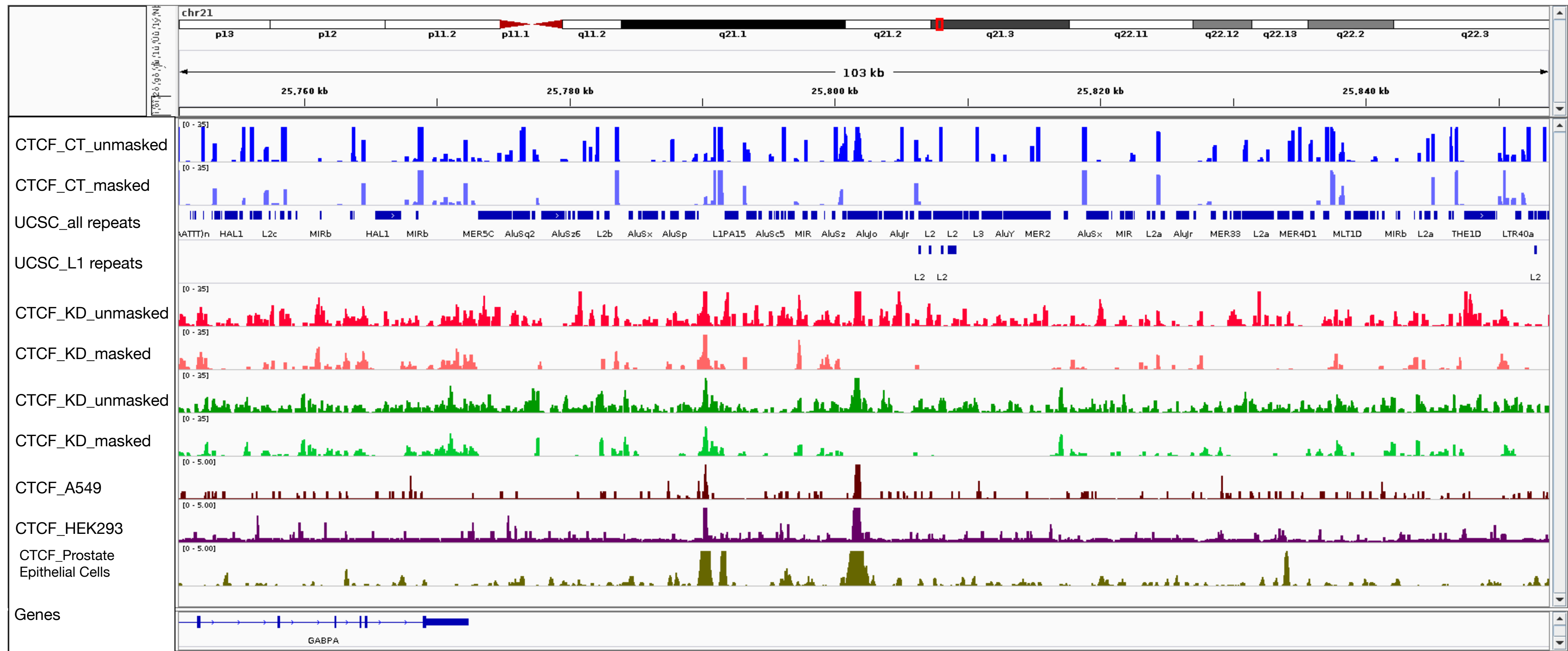


B

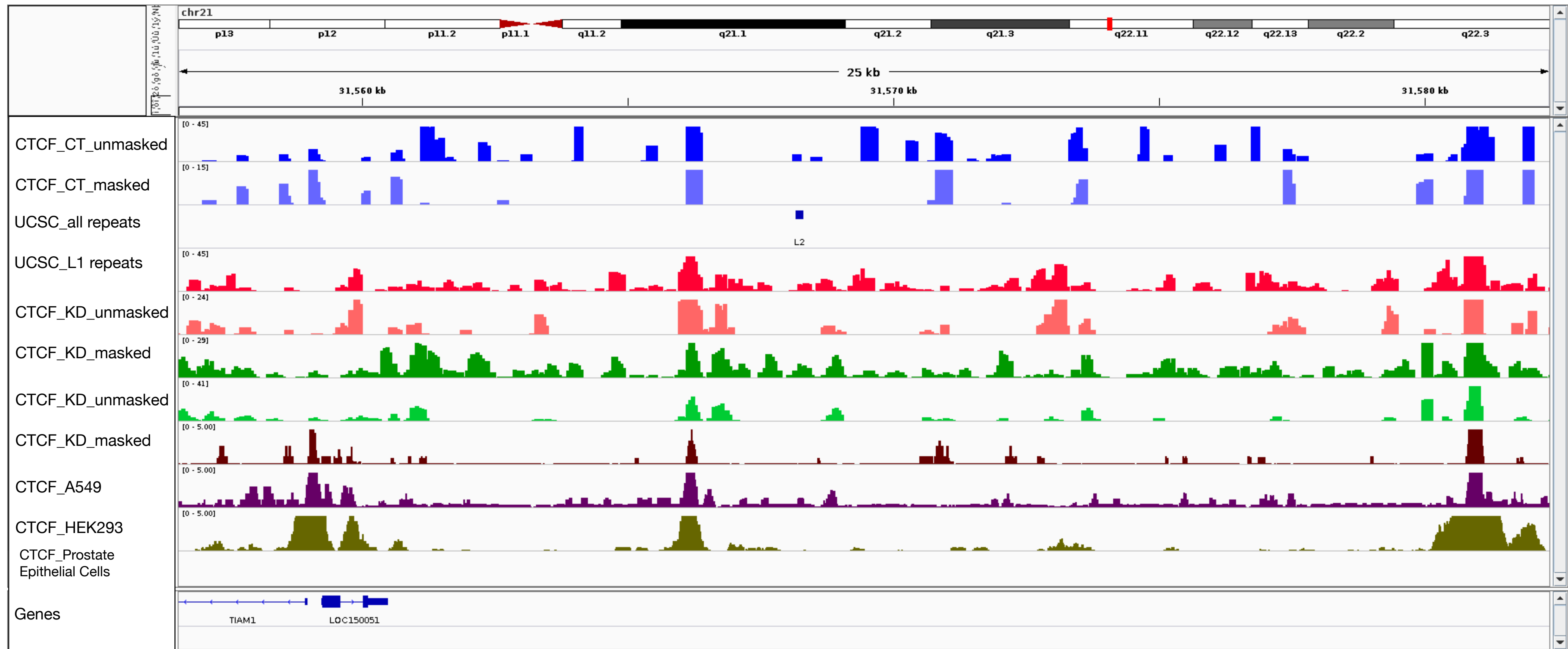


Genome-browser views of CTCF ChIP-seq reads along with the published CTCF ChIP-seq datasets

C

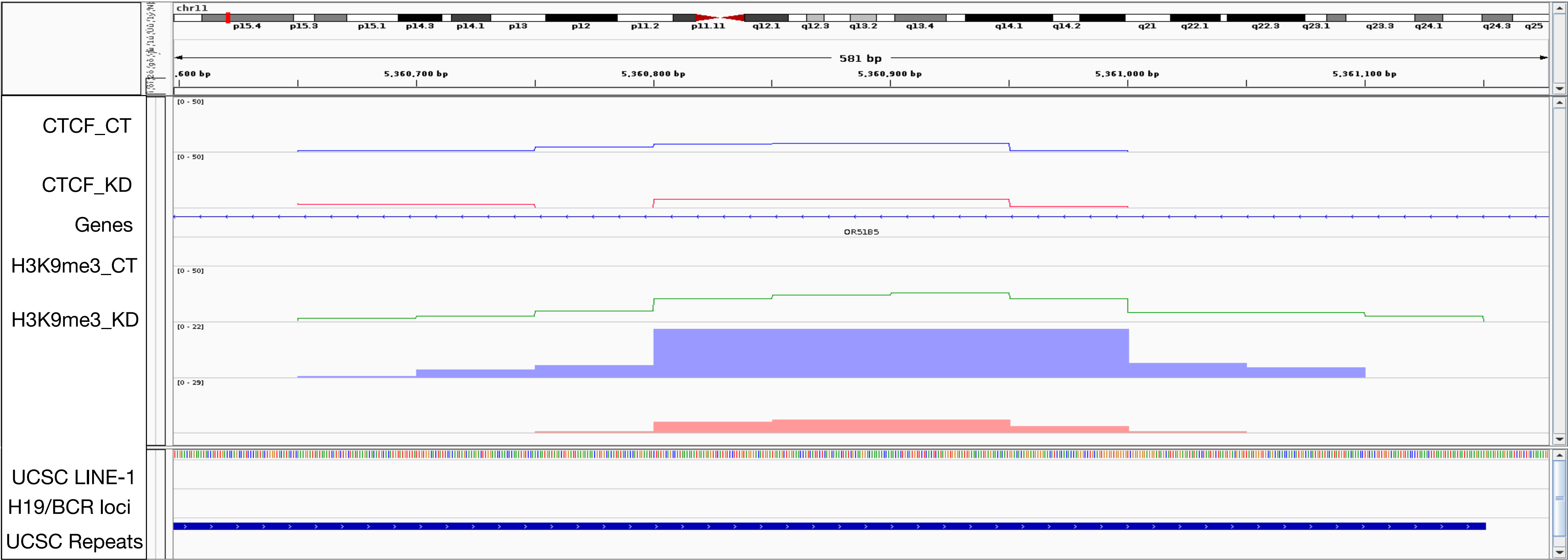
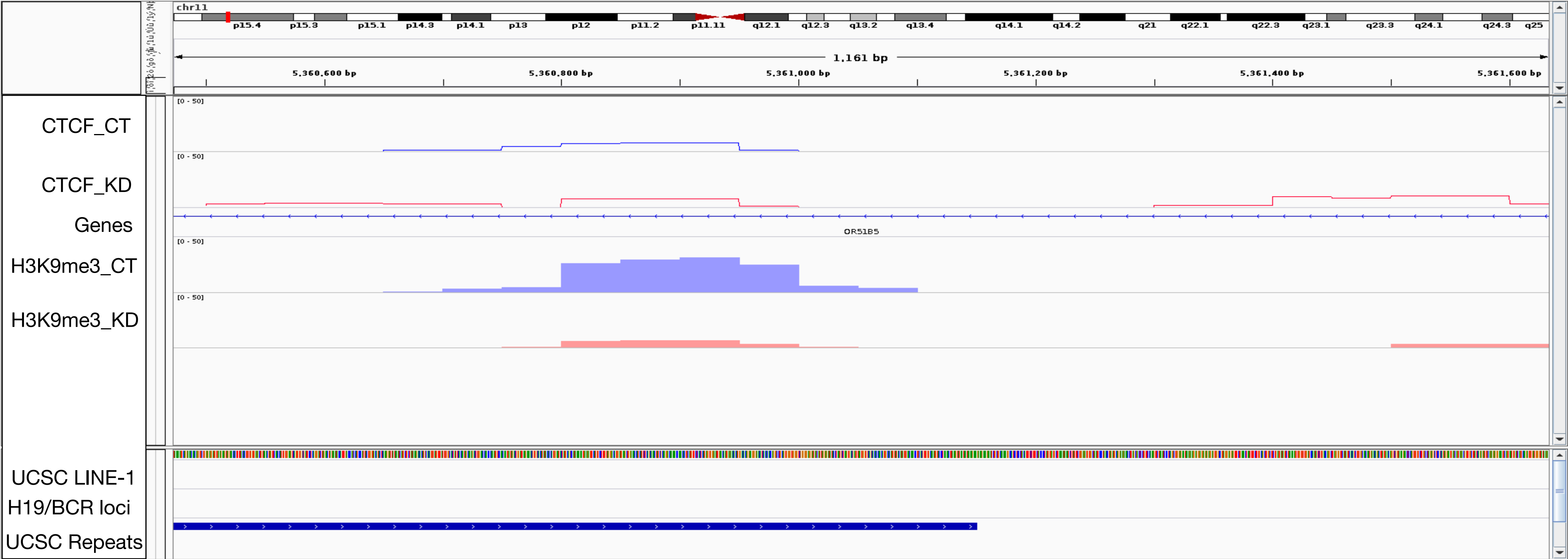
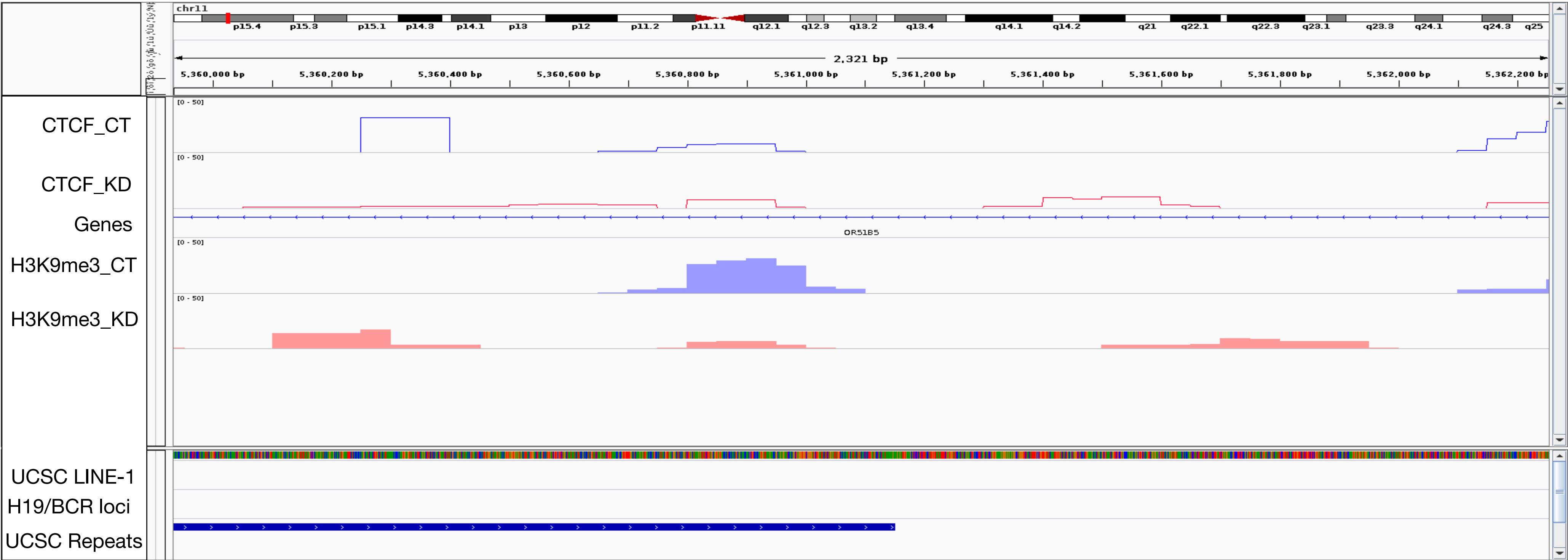


D

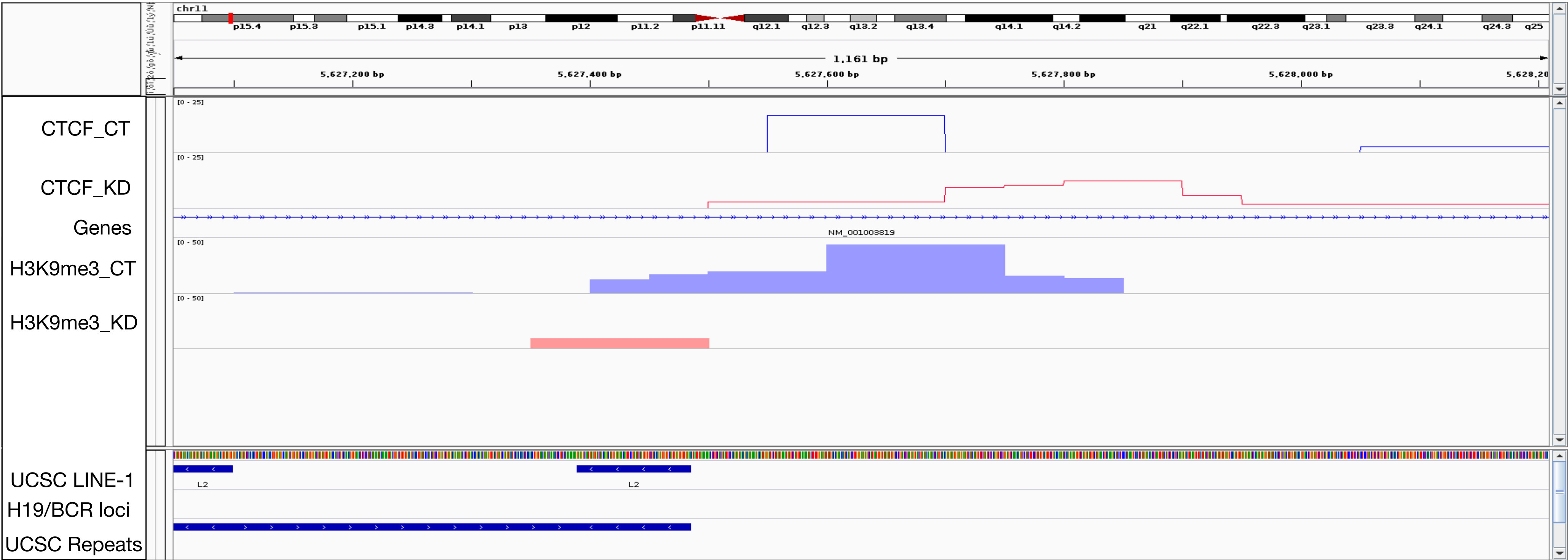


APPENDIX III

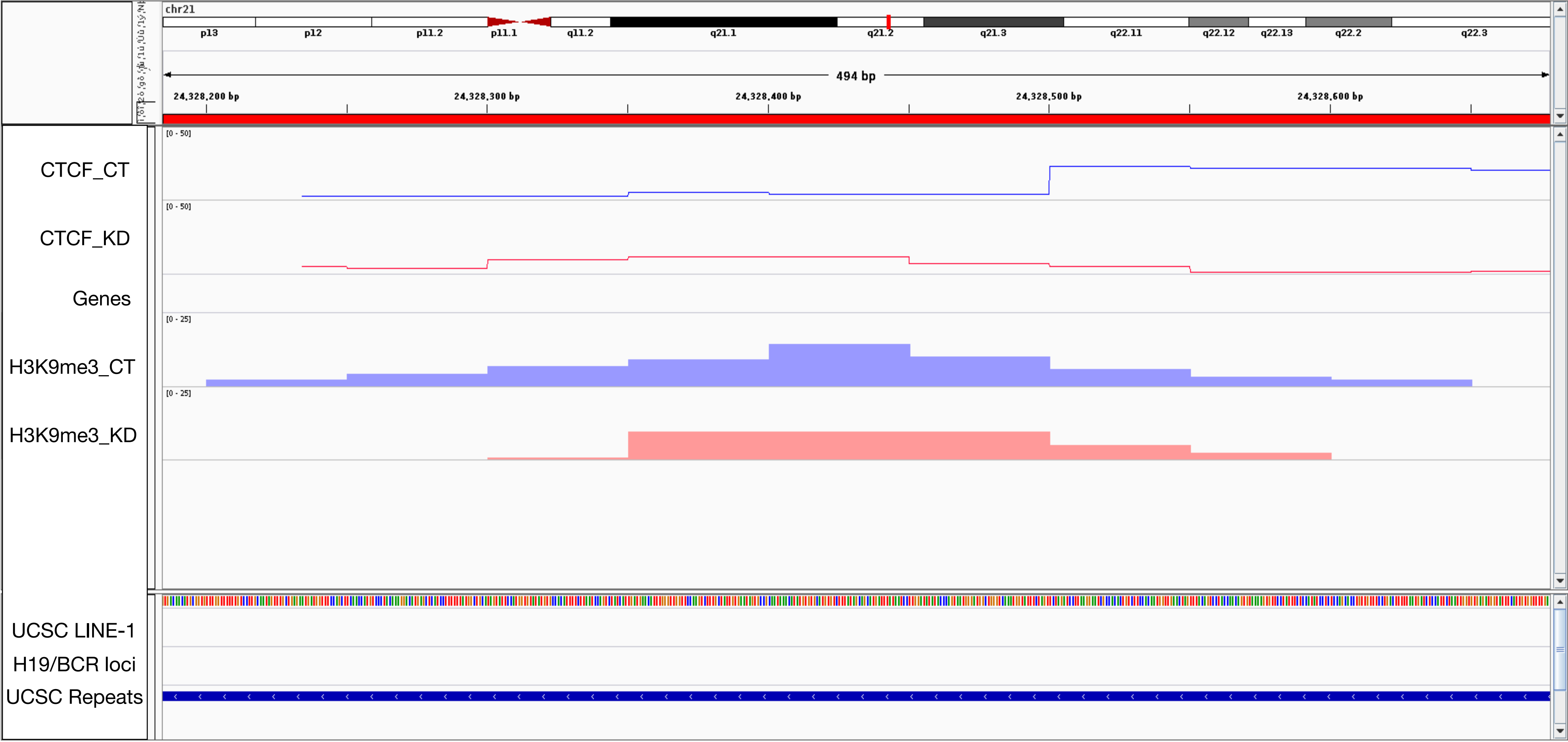
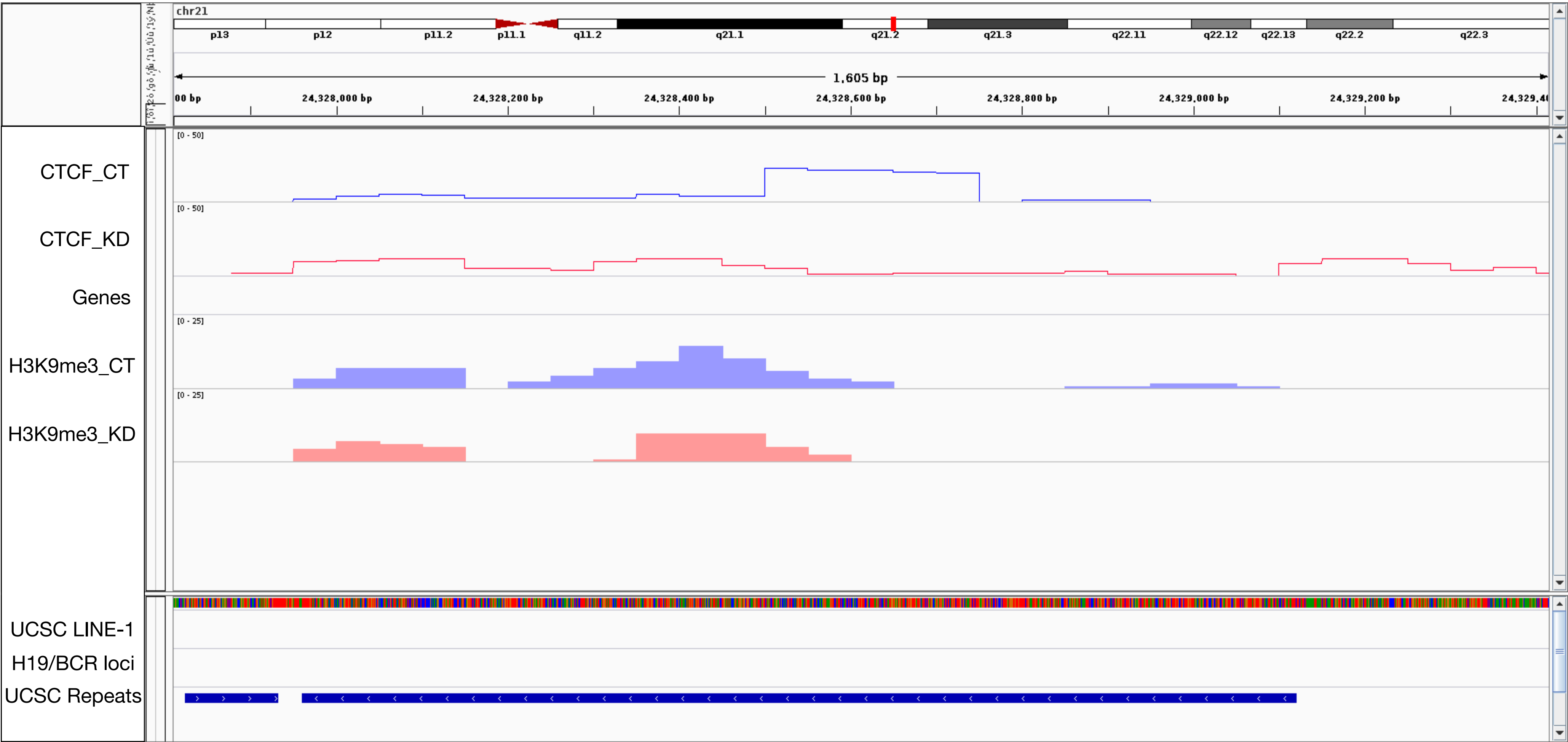
Genome-browser views displaying H3K9me3 read distribution patterns



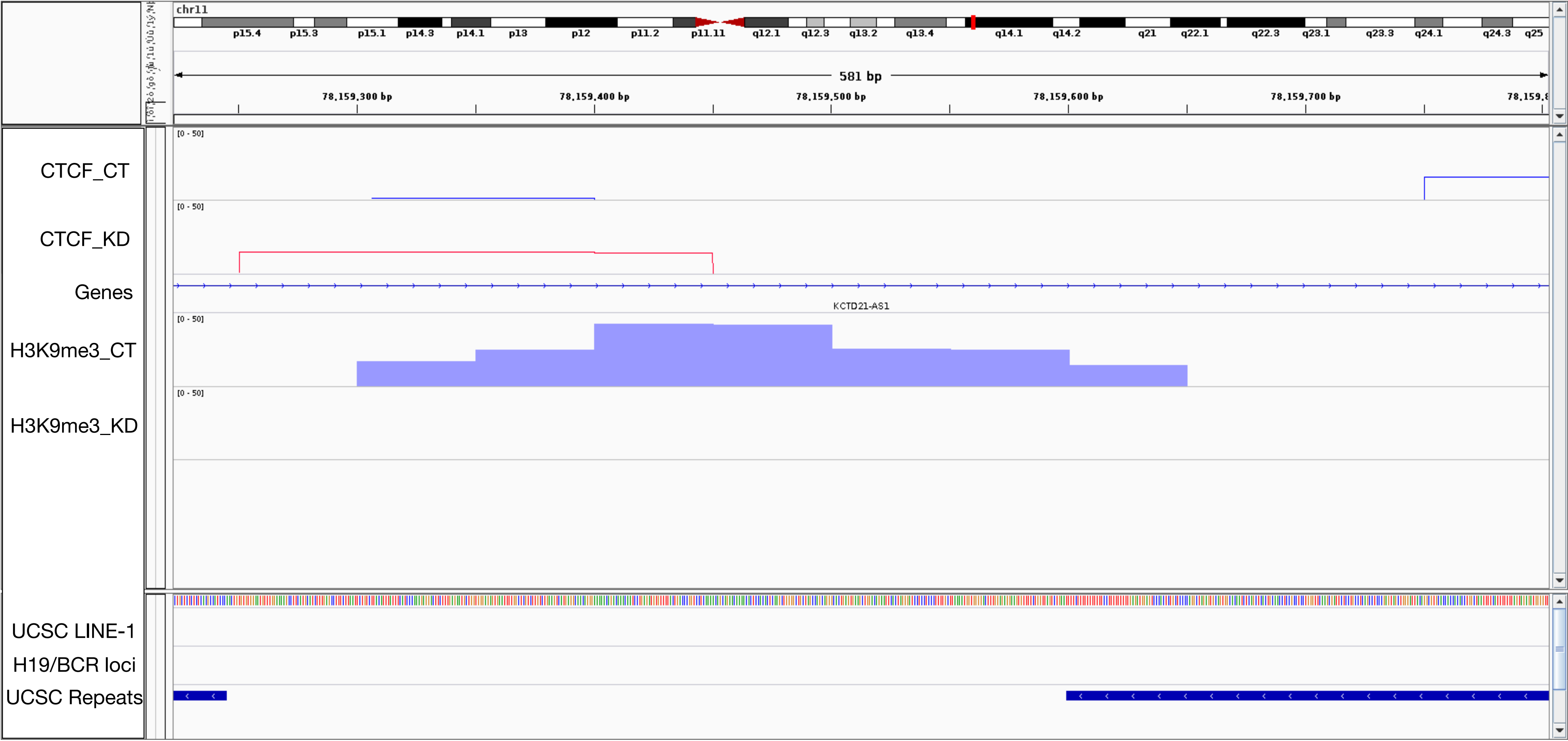
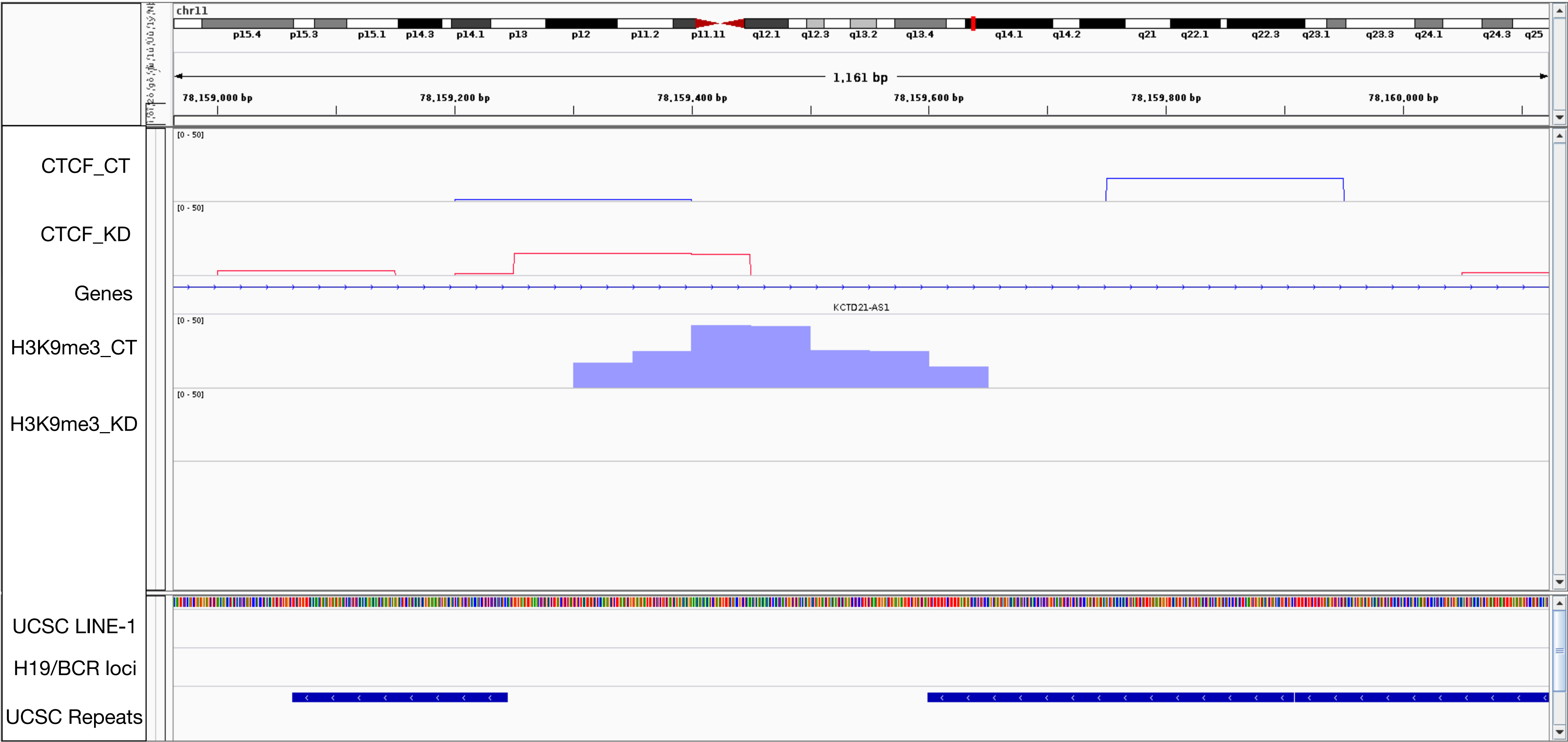
Genome-browser views displaying H3K9me3 read distribution patterns



Genome-browser views displaying H3K9me3 read distribution patterns



Genome-browser views displaying H3K9me3 read distribution patterns

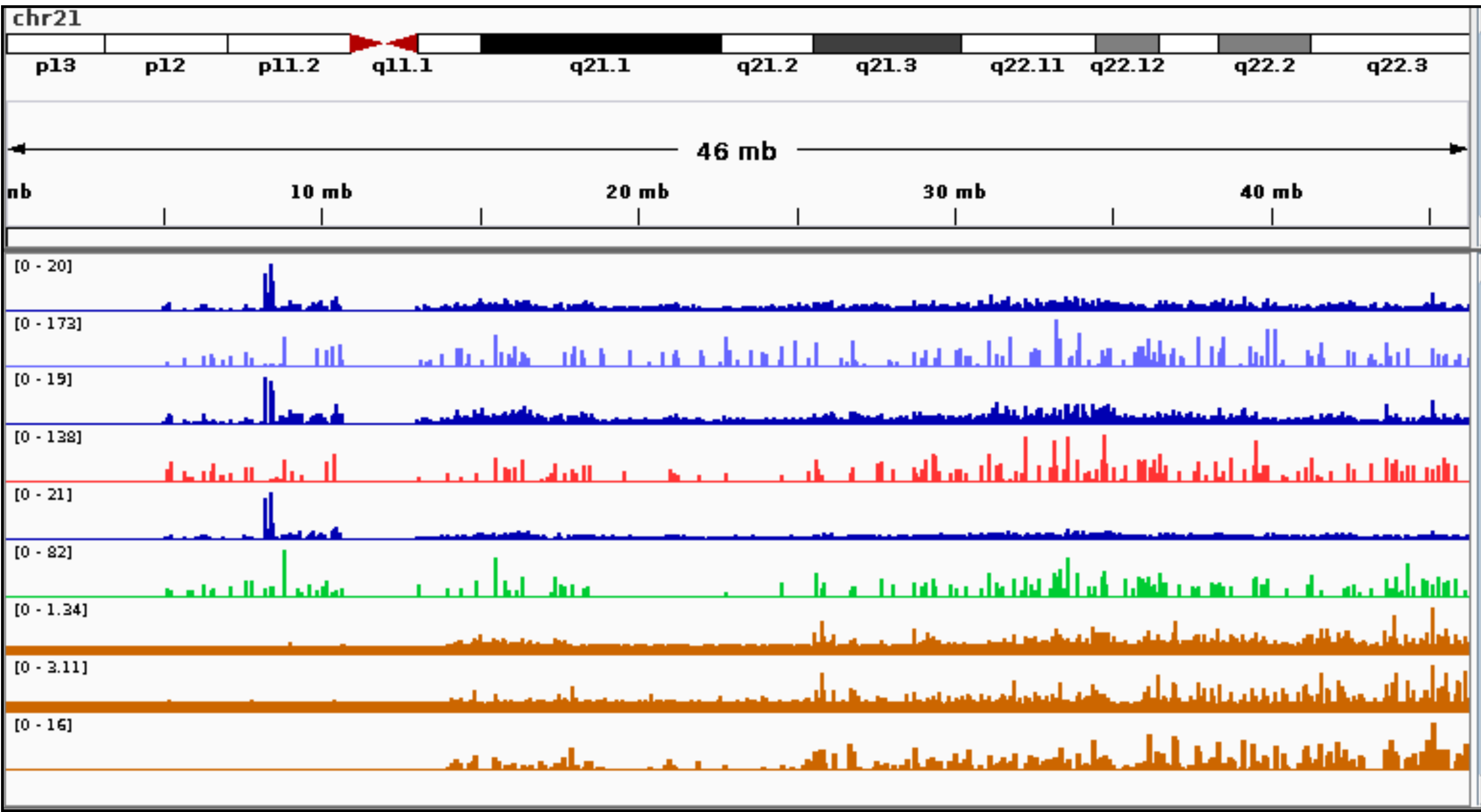


APPENDIX IV

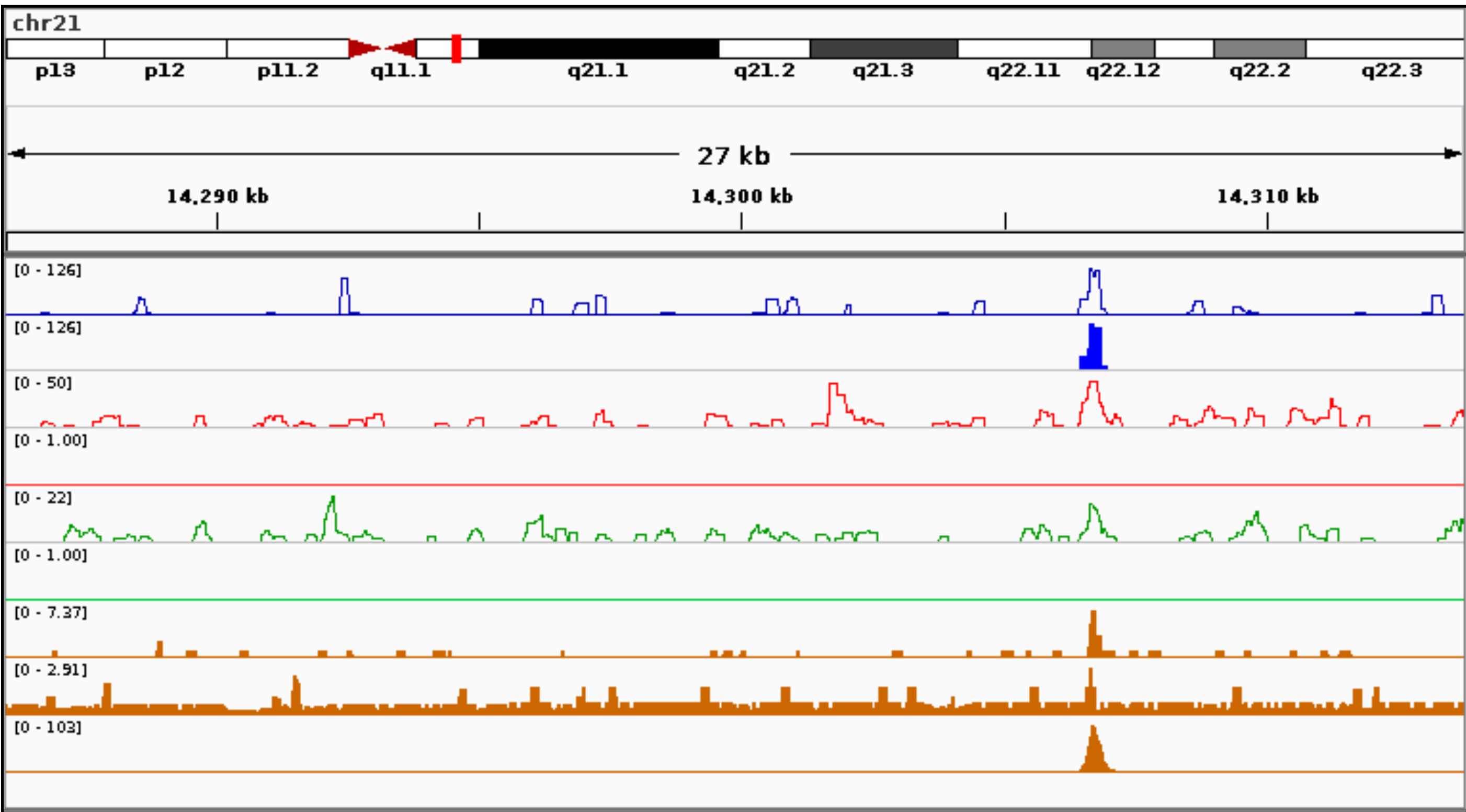
Genome-browser views displaying CTCF read distribution patterns in various regions of Chr21.

The Y-axis range is varying (Autoscale function of IGV). The peaks shown here are all from repeat-masked alignment of reads to hg38.

CT reads
CT peaks
KD reads
KD peaks
OE reads
OE peaks
A549
HEK293
Prostate Epithelial Cells



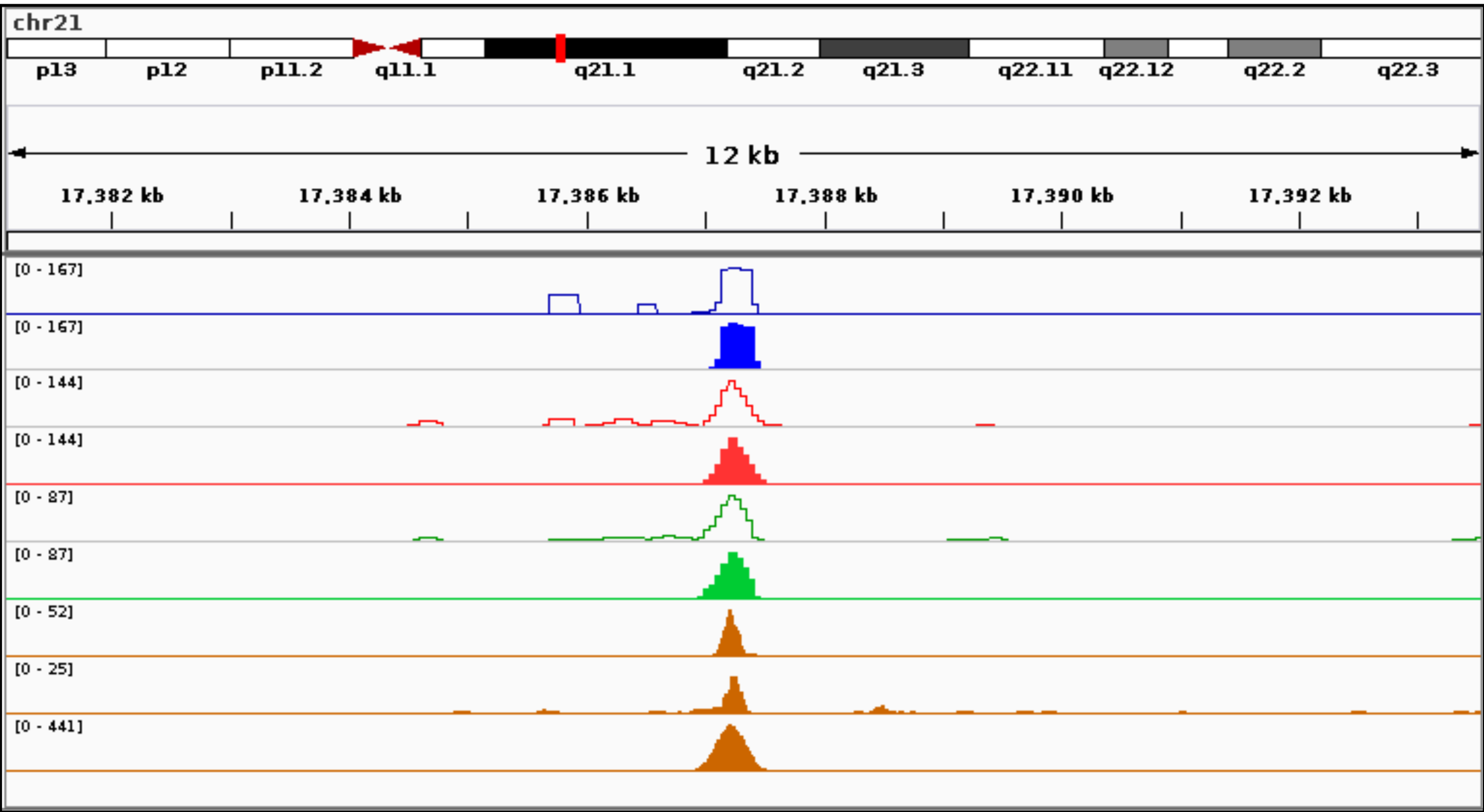
CT reads
CT peaks
KD reads
KD peaks
OE reads
OE peaks
A549
HEK293
Prostate Epithelial Cells



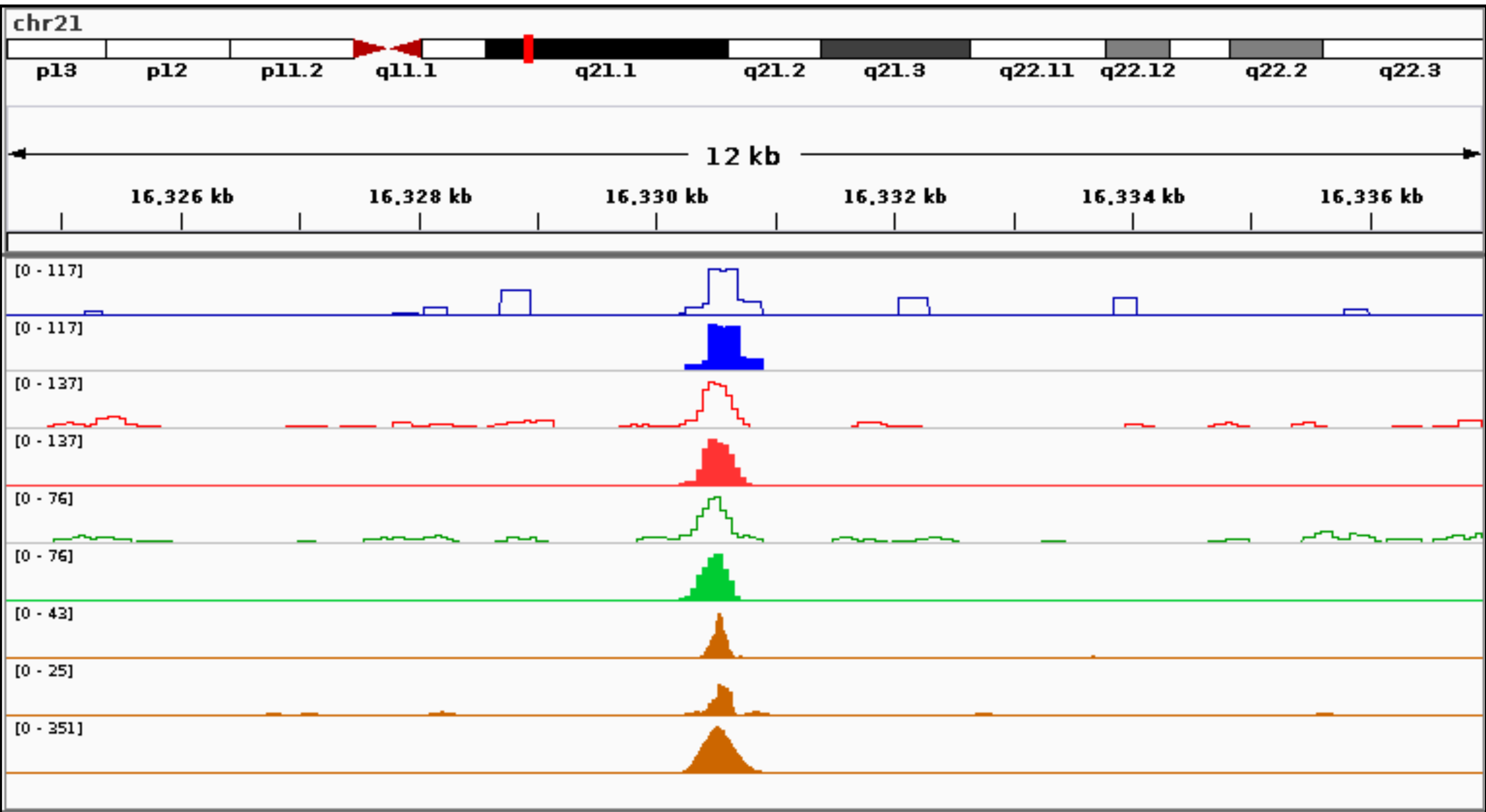
Genome-browser views displaying CTCF read distribution patterns in various regions of Chr21.

The Y-axis range is varying (Autoscale function of IGV). The peaks shown here are all from repeat-masked alignment of reads to hg38.

CT reads
CT peaks
KD reads
KD peaks
OE reads
OE peaks
A549
HEK293
Prostate Epithelial Cells



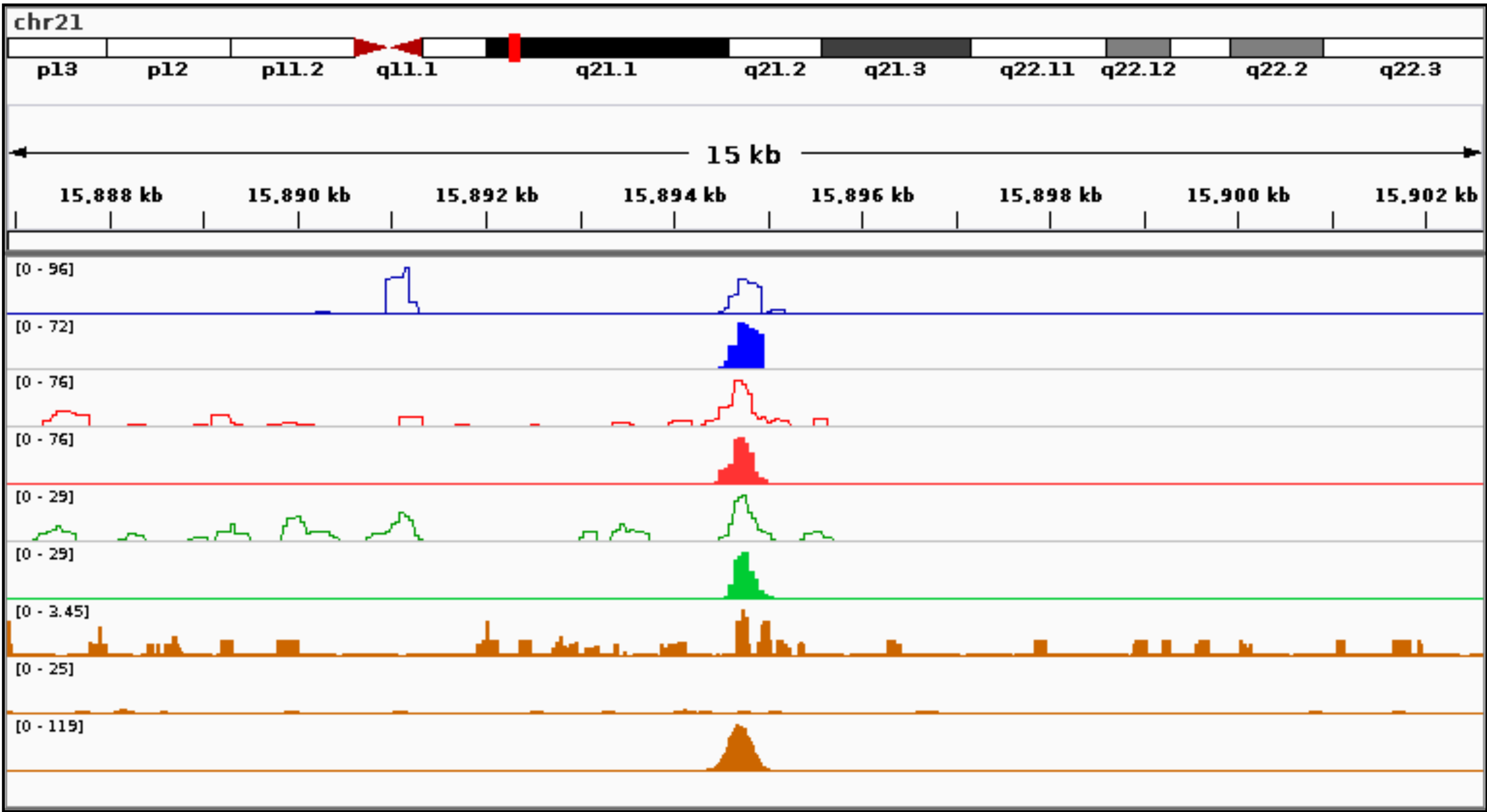
CT reads
CT peaks
KD reads
KD peaks
OE reads
OE peaks
A549
HEK293
Prostate Epithelial Cells



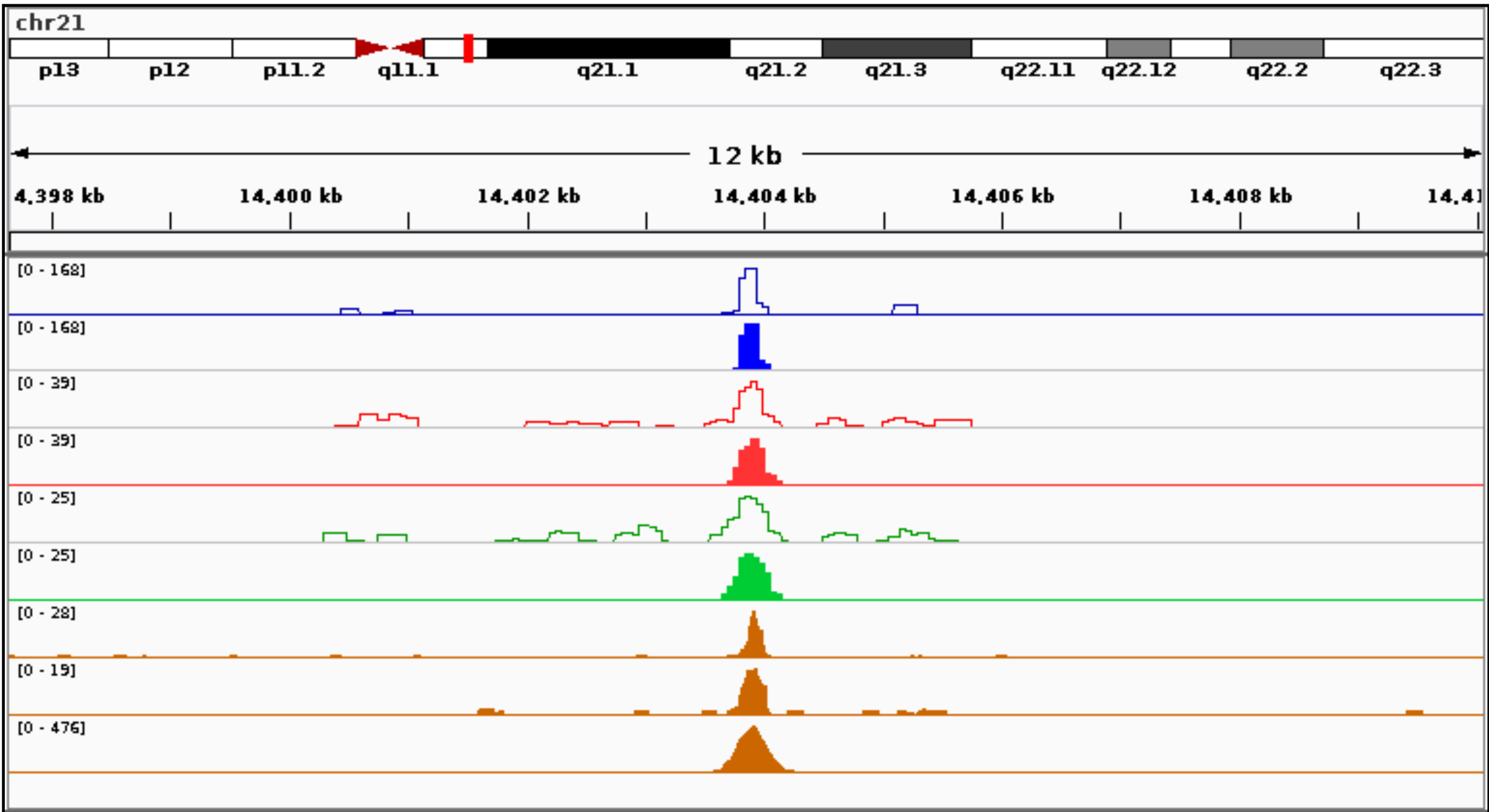
Genome-browser views displaying CTCF read distribution patterns in various regions of Chr21.

The Y-axis range is varying (Autoscale function of IGV). The peaks shown here are all from repeat-masked alignment of reads to hg38.

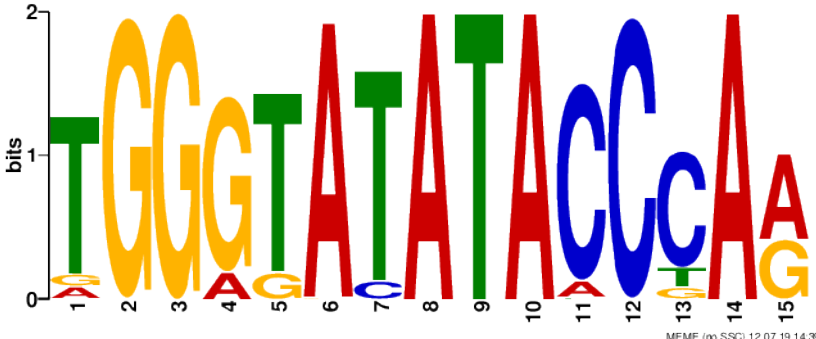
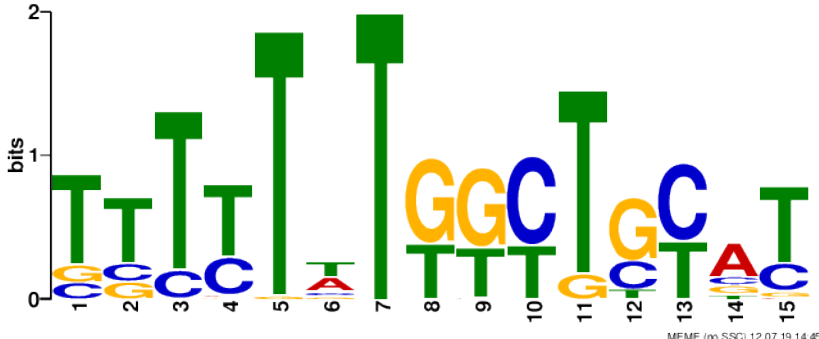
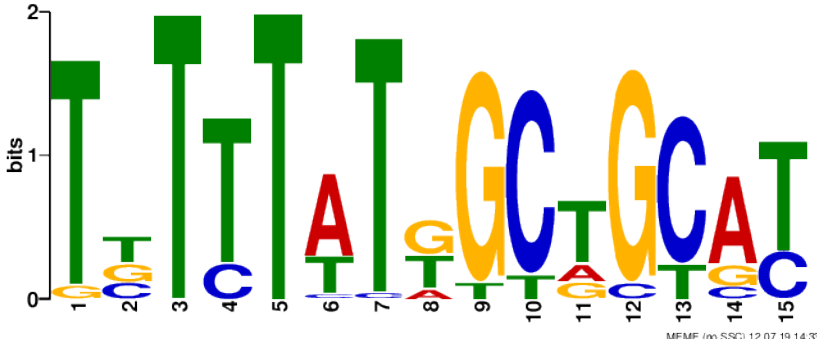
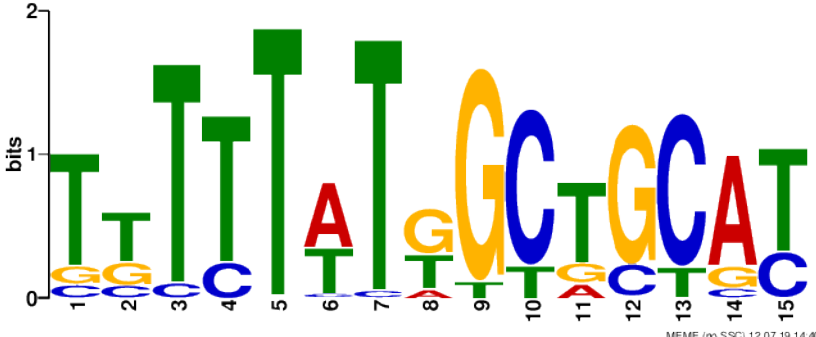
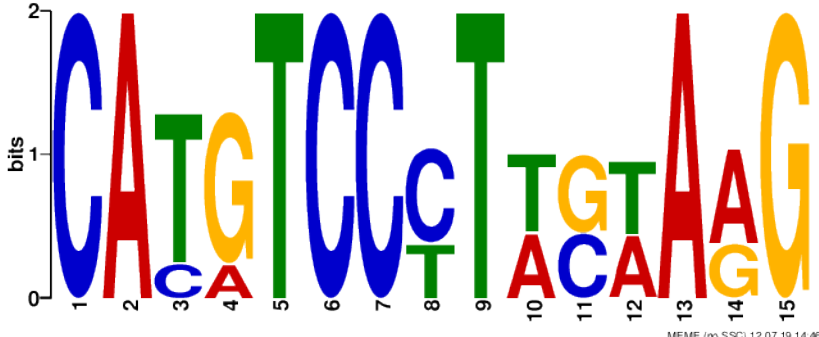
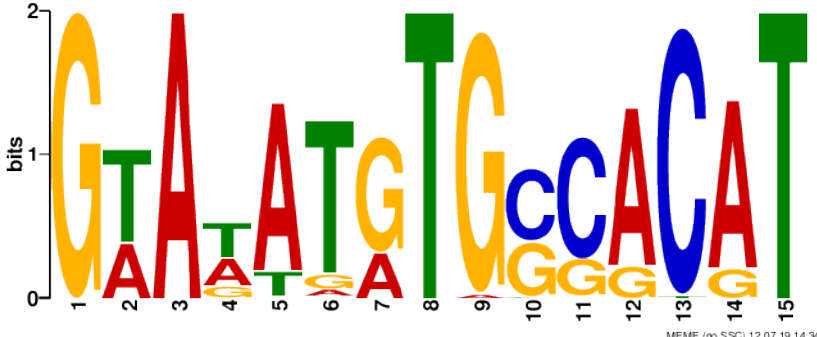
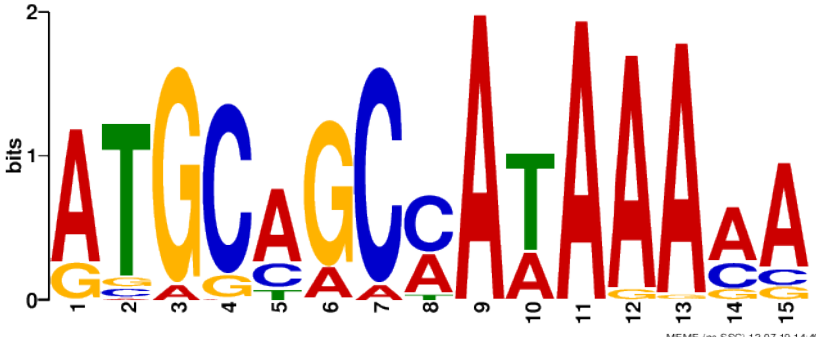
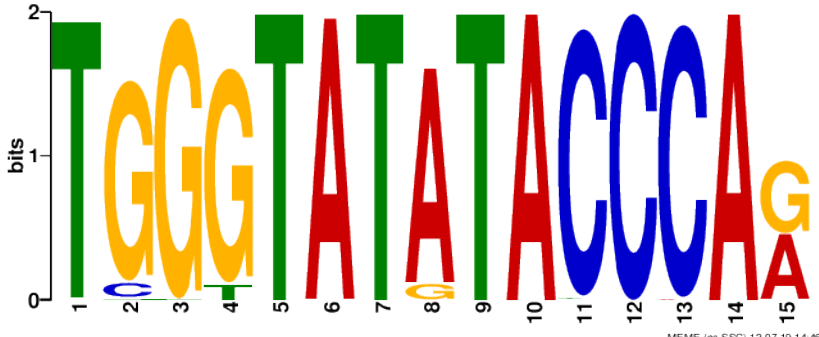
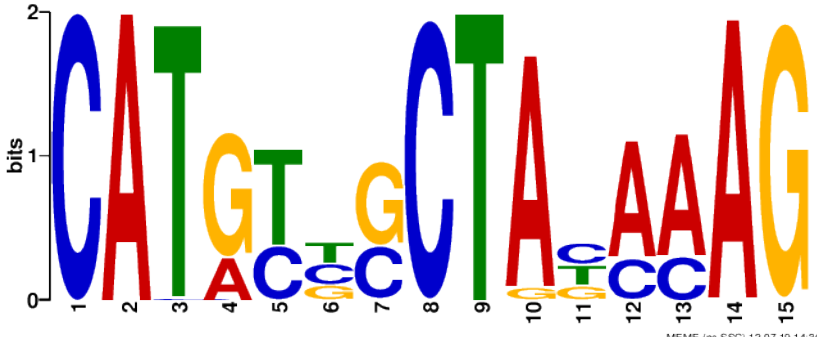
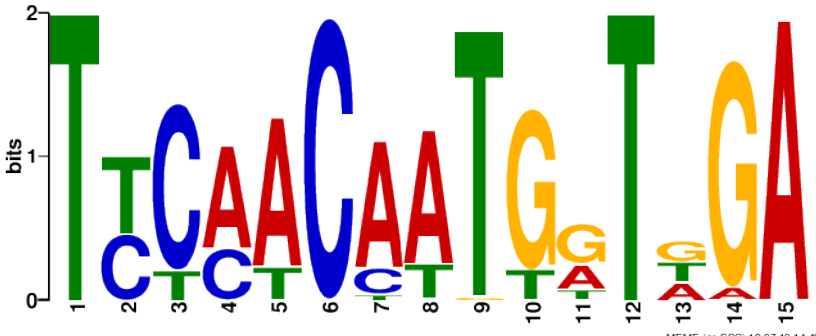
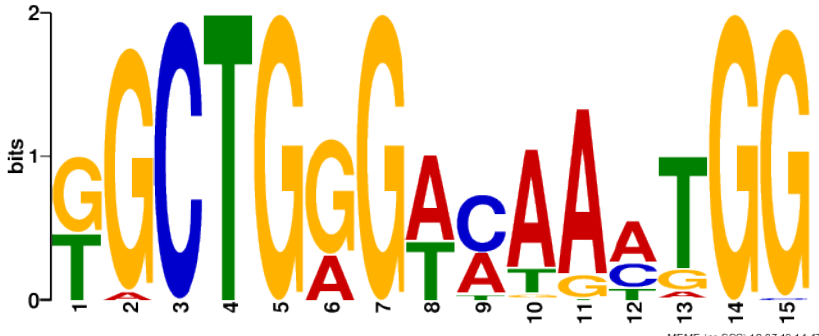
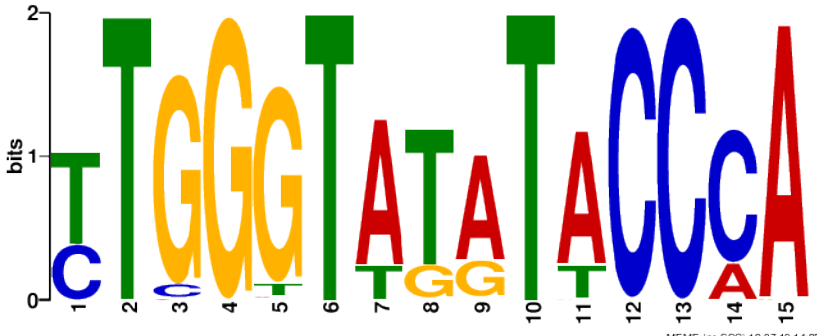
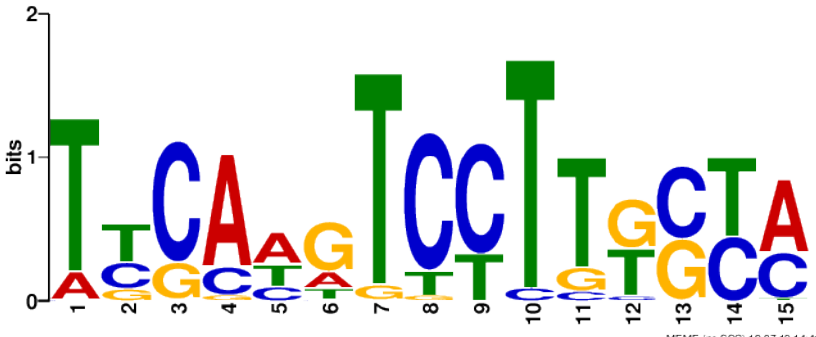
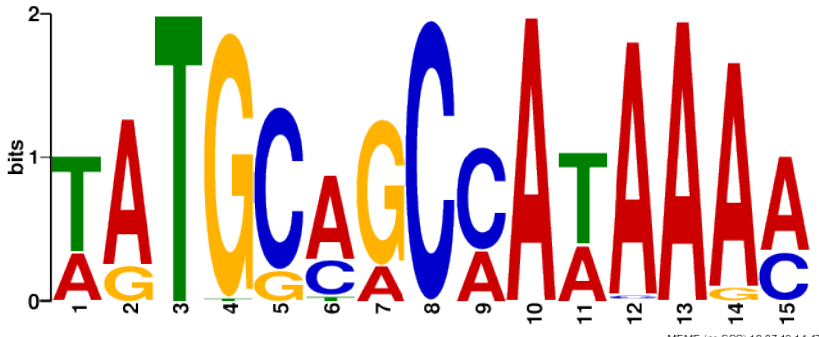
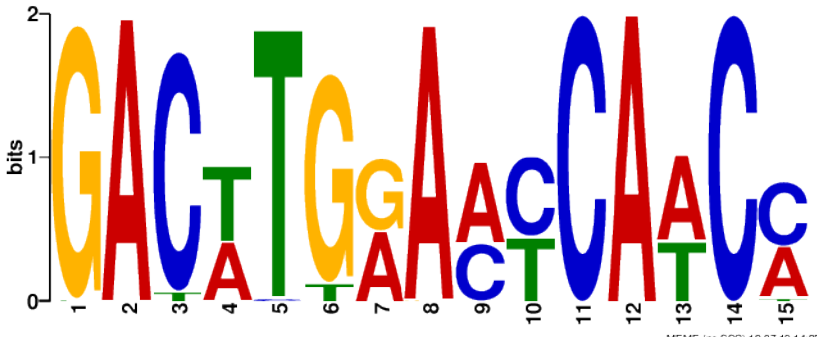
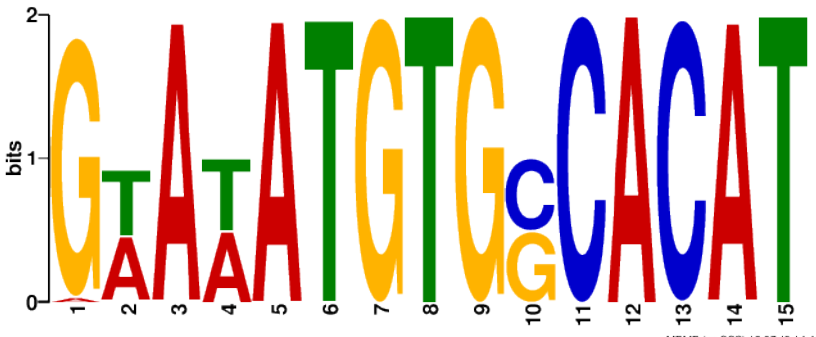
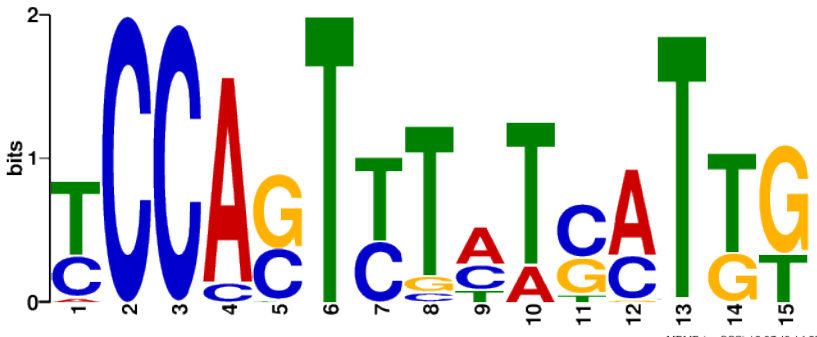
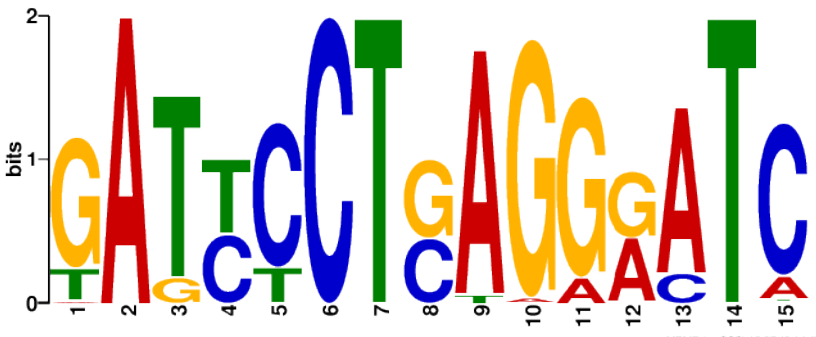
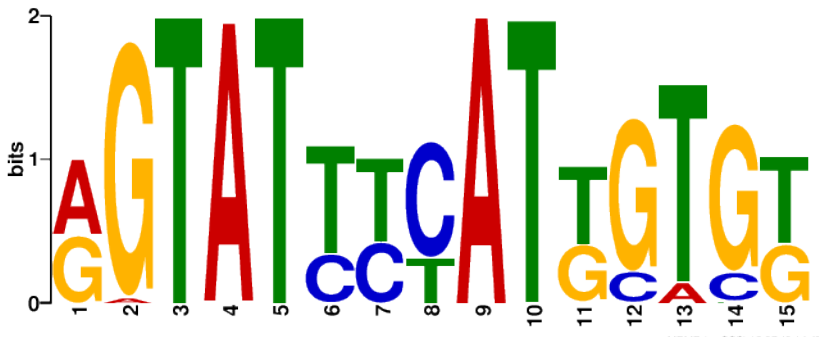
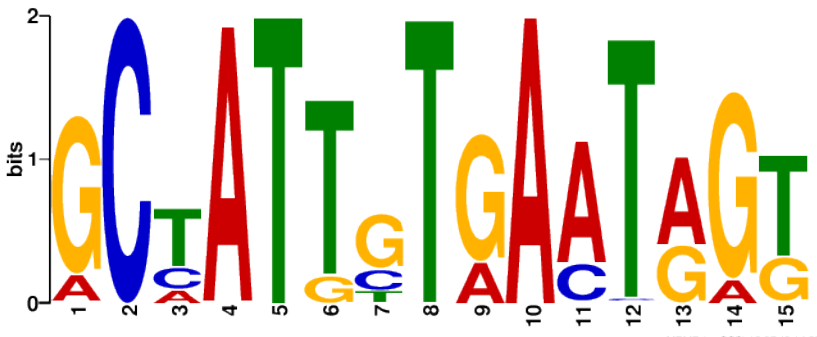
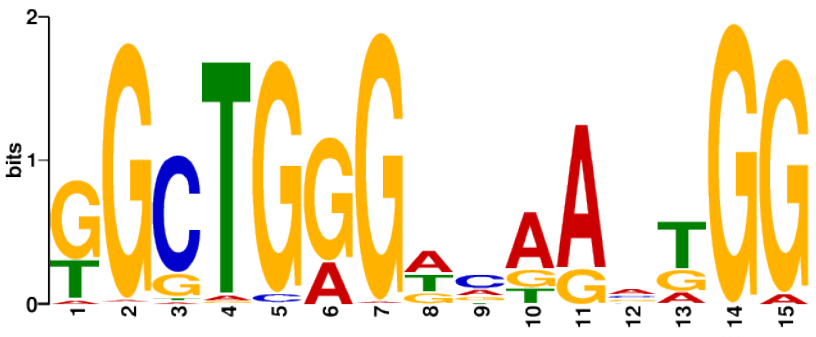
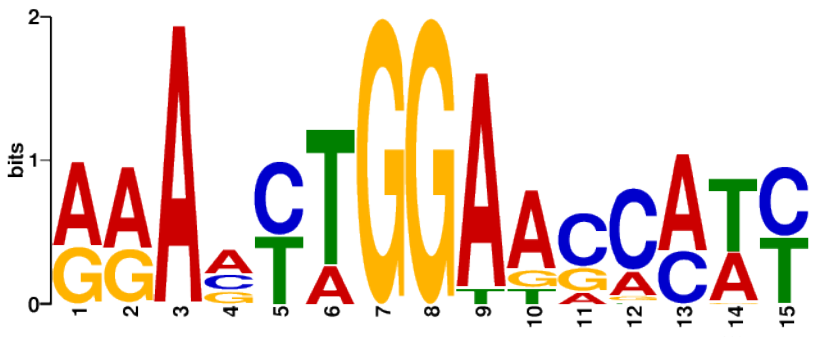
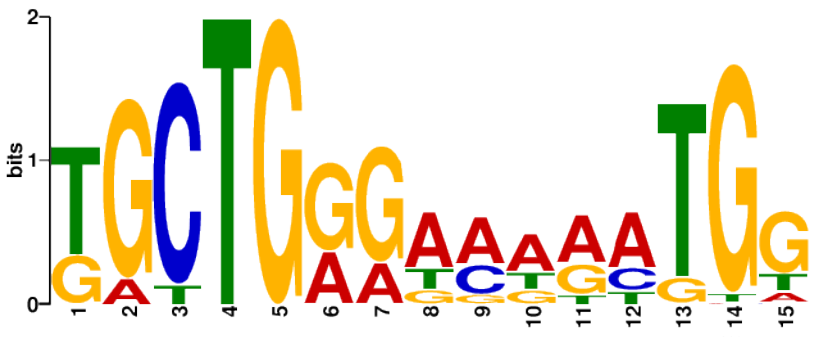
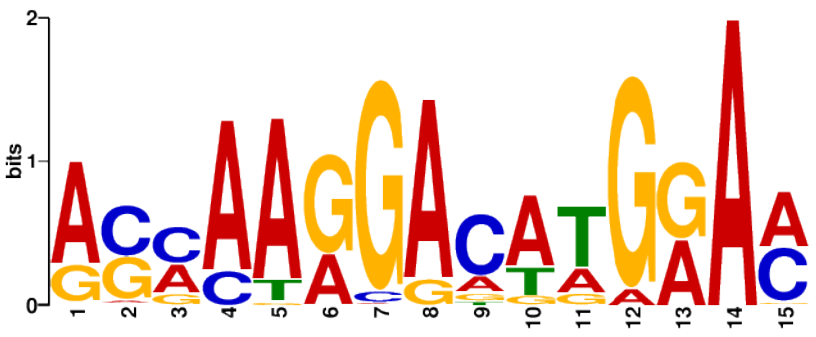
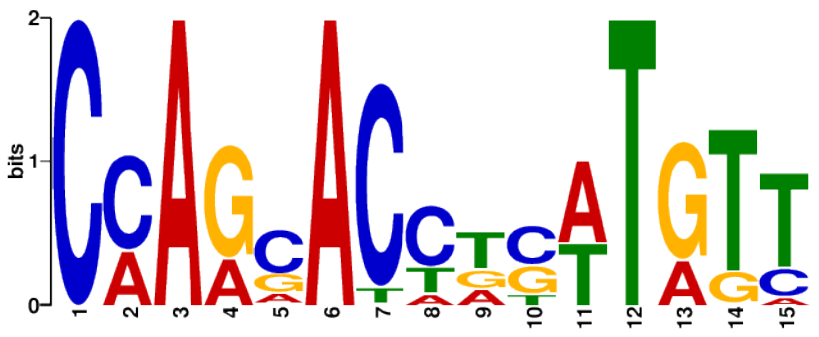
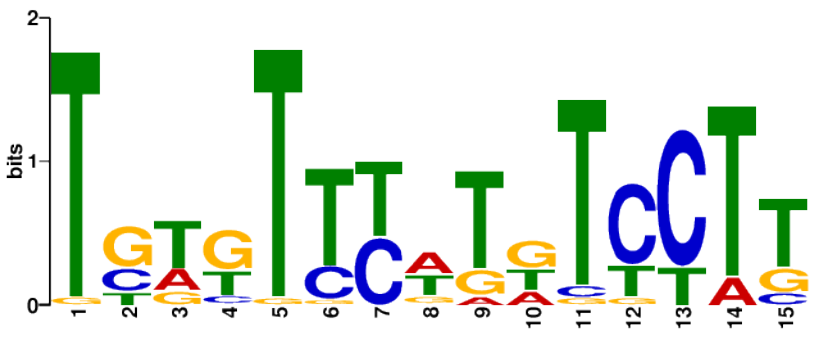
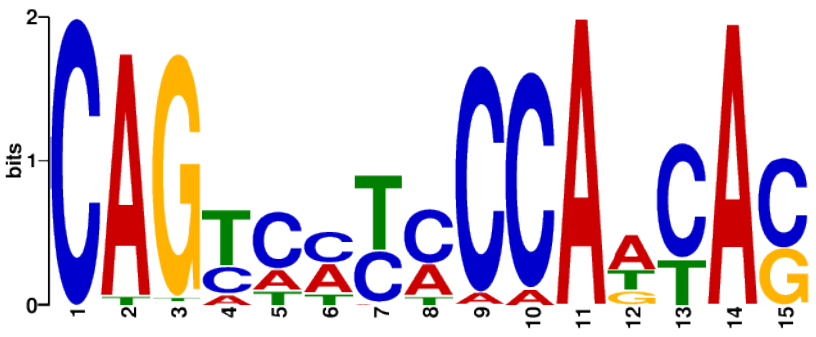
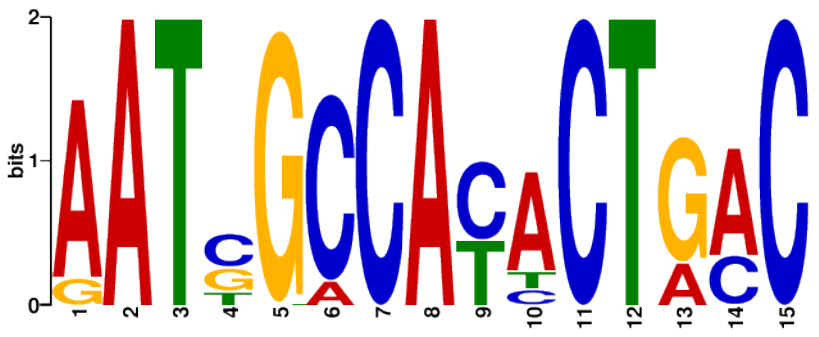
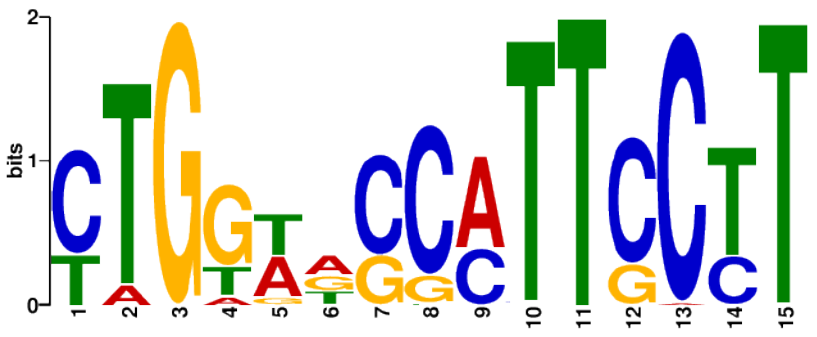
CT reads
CT peaks
KD reads
KD peaks
OE reads
OE peaks
A549
HEK293
Prostate Epithelial Cells



CT reads
CT peaks
KD reads
KD peaks
OE reads
OE peaks
A549
HEK293
Prostate Epithelial Cells



APPENDIX V

CT No. of peaks = 8765		KD No. of peaks = 4775		OE No. of peaks = 5250	
Motif	Count	Motif	Count	Motif	Count
	1078		1396		676
	2197		320		401
	1692		299		358
	1446		362		387
	2939		477		329
	910		301		471
	1209		387		389
	1520		633		679
	2129		571		1311
	1394		271		380

Motifs discovered in LINE-positive Motif-negative peaks for CT, KD and OE samples.

APPENDIX VI

"Table Analyzed" "Fig 3I"

"P value and statistical significance"

" Test" "Fisher's exact test"

" P value" <0.0001

" P value summary" ****

" One- or two-sided" Two-sided

" Statistically significant (P < 0.05)?" Yes

"Data analyzed" "deltaAUC (KD-CT) without motifs" "deltaAUC (KD-CT) with motifs" Total

" CT-KD peaks" 43386 24052 67438

" KD-CT peaks" 22801 17739 40540

" Total" 66187 41791 107978

"Percentage of row total" "deltaAUC (KD-CT) without motifs" "deltaAUC (KD-CT) with motifs"

" CT-KD peaks" 64.33% 35.67%

" KD-CT peaks" 56.24% 43.76%

"Percentage of column total" "deltaAUC (KD-CT) without motifs" "deltaAUC (KD-CT) with motifs"

" CT-KD peaks" 65.55% 57.55%

" KD-CT peaks" 34.45% 42.45%

"Percentage of grand total" "deltaAUC (KD-CT) without motifs" "deltaAUC (KD-CT) with motifs"

" CT-KD peaks" 40.18% 22.27%

" KD-CT peaks" 21.12% 16.43%

"Table Analyzed" "Fig 3J"

"P value and statistical significance"

" Test" "Fisher's exact test"

" P value" <0.0001

" P value summary" ****

" One- or two-sided" Two-sided

" Statistically significant (P < 0.05)?" Yes

"Data analyzed" "deltaAUC (OE-CT) without motifs" "deltaAUC (OE-CT) with motifs" Total

" CT-OE peaks" 45072 29337 74409

" OE-CT peaks" 12407 37 12444

" Total" 57479 29374 86853

"Percentage of row total" "deltaAUC (OE-CT) without motifs" "deltaAUC (OE-CT) with motifs"

" CT-OE peaks" 60.57% 39.43%

" OE-CT peaks" 99.70% 0.30%

"Percentage of column total" "deltaAUC (OE-CT) without motifs" "deltaAUC (OE-CT) with motifs"

" CT-OE peaks" 78.41% 99.87%

" OE-CT peaks" 21.59% 0.13%

"Percentage of grand total" "deltaAUC (OE-CT) without motifs" "deltaAUC (OE-CT) with motifs"

" CT-OE peaks" 51.89% 33.78%

" OE-CT peaks" 14.29% 0.04%

"Table Analyzed" "Fig 3K"

"P value and statistical significance"

" Test" "Fisher's exact test"

" P value" <0.0001

" P value summary" ****

" One- or two-sided" Two-sided

" Statistically significant (P < 0.05)?" Yes

"Data analyzed" "deltaAUC (KD-OE) without motifs" "deltaAUC (KD-OE) with motifs" Total

" KD-OE peaks" 25113 15337 40450

" OE-KD peaks" 19554 1390 20944

" Total" 44667 16727 61394

"Percentage of row total" "deltaAUC (KD-OE) without motifs" "deltaAUC (KD-OE) with motifs"

" KD-OE peaks" 62.08% 37.92%

" OE-KD peaks" 93.36% 6.64%

"Percentage of column total" "deltaAUC (KD-OE) without motifs" "deltaAUC (KD-OE) with motifs"

" KD-OE peaks" 56.22% 91.69%

" OE-KD peaks" 43.78% 8.31%

"Percentage of grand total" "deltaAUC (KD-OE) without motifs" "deltaAUC (KD-OE) with motifs"

" KD-OE peaks" 40.90% 24.98%

" OE-KD peaks" 31.85% 2.26%