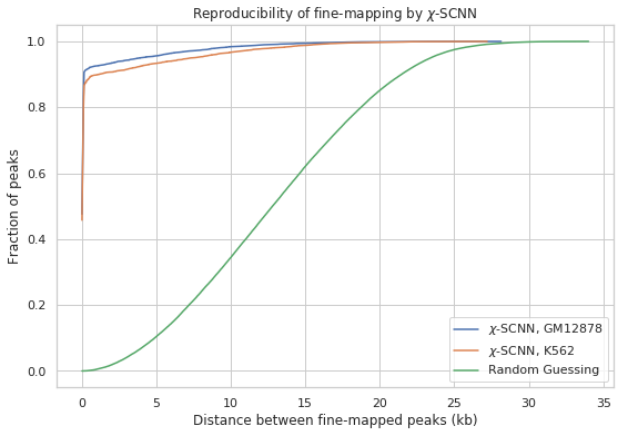
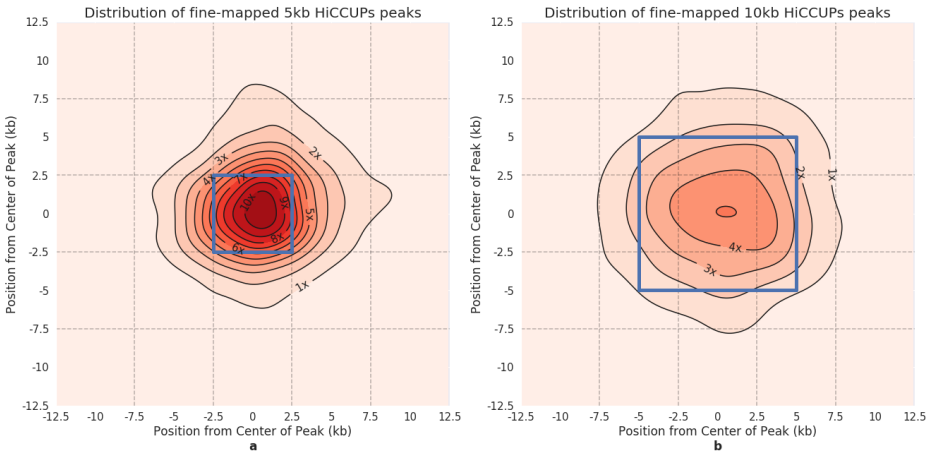
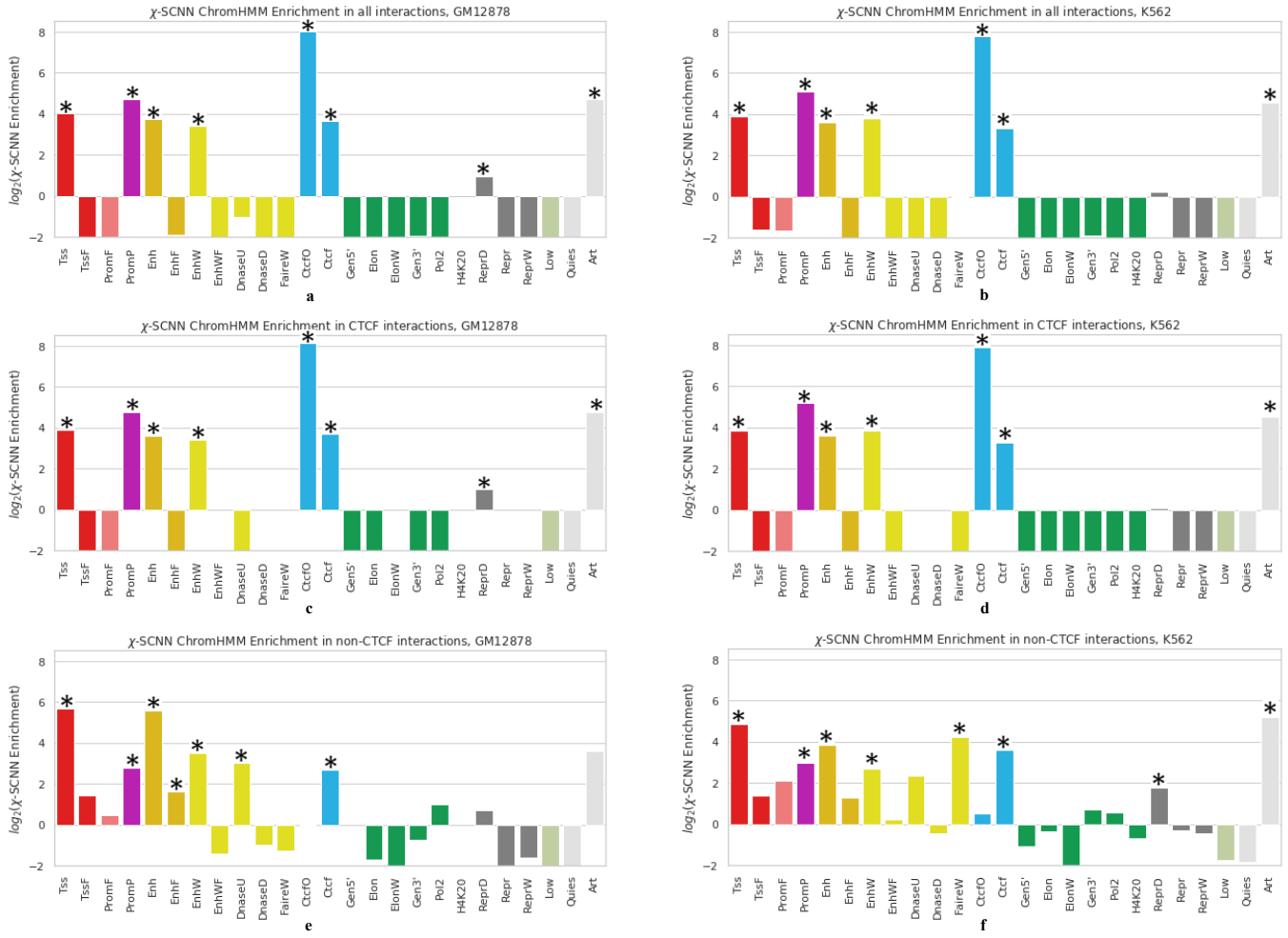


Supplementary Figure 1. Reproducibility of fine-mapped peaks. The plot shows as a function of Euclidean distance (x-axis) the fraction of fine mapped that fell within that distance (y-axis) from two different χ-SCNN models for both GM12878 and K562. 90% and 87% of fine-mappings fall within 100bp in either direction for GM12878 and K562, and 93% and 90% of peaks fall within 1kb. Also shown is a baseline of random guessing that is shared for the two cell types.



Supplementary Figure 2. Distribution of fine-mapping predictions for different size HiCCUPs peaks. Kernel Density Estimation (KDE) plots showing the distribution of χ-SCNN's fine-mapping predictions within GM12878 peaks after extending the original peak equally in both directions to form a 25kb peak. To generate plots, we used the 'jointplot' function with the KDE option in Python's Seaborn package. **(a)** For 5kb interaction peaks extended to 25kb, fine-mapped positions are strongly concentrated around the original 5kb peak (center blue bin). Enrichment in center 5kb bin is 8.9 fold compared to random guessing. **(b)** For 10kb peaks extended to 25kb, fine-mapped positions are concentrated in the original 10kb peak (center blue bin). Enrichment in center 5kb bin is 3.5 fold. There were no peaks called at 25kb for GM12878. The positive direction on the axes points toward the exterior of the interactions. The mode of the 5kb peak plot is shifted toward the positive direction, meaning that fine-mapped peaks are most likely to be approximately 1kb further out than the center of the called originally called peak.



Supplementary Figure 3. Enrichment of ChromHMM states of regions predicted by χ-SCNN. Log_2 fold enrichments of ChromHMM state for χ-SCNN fine-mapped positions in interactions for GM12878 and K562 across (**a**, **b**) all interactions, (**c**, **d**) CTCF-associated interactions, and (**e**, **f**) non-CTCF-associated interactions. Panel (a) is the same as **Fig. 5**, but shown again for direct comparison with the other panels. Any log_2 fold depletions less than -2 (1/4x) were truncated. Significant enrichments (adjusted p-value < 0.001, binomial test) are marked by an asterisk.

Metric		GM12878	K562
Maximum Matrix Resolution (kb)		1	5
Peak Resolution (kb)		5, 10	5, 10, 25
Training Resolution (kb)		25	25
Number of Peaks, 5kb		6316	1547
Number of Peaks, 10kb		3132	2343
Number of Peaks, 25kb		-	2167
Number of Peaks, total		9448	6057
Number of DNase and ChIP-seq Tracks		100	148
Hyperparameter Name	**Searched Values**	**Chosen Hyperparameter**	
# Encoder Kernels	K_{Enc} = 12:2:32	26	16
# Convolution Kernels	K_{Conv} = 12:2:32	16	28
Convolutional Width	C = 6:2:12	8	10
# Dense Kernels	K_{Dense} = 12:2:32	16	16
Regularization Type	L = {L1, L2, L1+L2}	L1+L2	L1+L2
Regularization Strength	S = {0, 10^{-6}, 10^{-5}, 10^{-4}}	0	10^{-6}
Dropout Magnitude	M = {0, 0.1, 0.25, 0.5}	0.25	0
χ-SCNN Classification Performance			
AUROC (validation)		0.973	0.974
AUROC (test)		0.959	0.977
AUPRC (validation)		0.977	0.974
AUPRC (test)		0.963	0.972

Supplementary Table 1. Detailed information on input data, hyperparameter search, and classification performance. (**top**) For each cell type, the number of peaks separated by size and the number of available features. (**middle**) The values of the hyperparameters considered and the values chosen for each cell type. We performed a random hyperparameter search and chose the combination of hyperparameter values that yielded the highest validation AUROC. (**bottom**) The validation and test AUROCs and AUPRCs for classification. Test performance was reported on a chromosome withheld from the training and hyperparameter optimization

5kb Peaks	**GM12878**			**K562**		
	#/6316	%	fold	#/1547	%	fold
χ-SCNN (all marks)	**2260**	**36%**	**8.9**	**507**	**33%**	**8.2**
χ-SCNN (primary marks only)	688	11%	2.6	148	10%	2.4
χ-SCNN (primary+secondary marks)	1913	30%	7.6	392	25%	6.3
χ-SCNN (primary+secondary marks+CTCF)	2129	34%	8.4	459	30%	7.4
CTCF	2073	33%	8.2	429	28%	7.0
RAD21	2165	34%	8.6	472	31%	7.6
SMC3	2183	35%	8.6	484	31%	7.8
Mean of all Signals	1631	26%	6.5	281	18%	4.5
Single Best Signal	2183	35%	8.6	484	31%	7.8
Logistic Regression on all data	2091	33%	8.3	442	29%	7.1
10kb Peaks	#/3132	%	fold	#/2343	%	fold
χ-SCNN	**1771**	**57%**	**3.5**	**1205**	**51%**	**3.2**
χ-SCNN (primary marks only)	856	27%	1.7	536	23%	1.4
χ-SCNN (primary+secondary marks)	1615	5.2%	3.2	1055	45%	2.8
χ-SCNN (primary+secondary marks+CTCF)	1720	55%	3.4	1172	50%	3.1
CTCF	1642	52%	3.3	1081	46%	2.8
RAD21	1673	53%	3.3	1149	49%	3.1
SMC3	1710	55%	3.4	1131	48%	3.0
Mean of all Signals	1472	47%	2.9	812	35%	2.2
Single Best Signal	1710	55%	3.4	1137	49%	3.0
Logistic Regression on all data	1666	53%	3.2	1109	47%	3.0

Supplementary Table 2. Peak recovery metrics for different size peaks, cell types, and methods. For each cell type, the three columns represent the number of correctly recovered peaks, the percentage of recovered peaks, and the fold enrichment over expected by chance. Enrichments for 10kb peaks are lower because the expected number by chance is larger; however, the percentage correctly recovered is higher. Across all methods, χ-SCNN on all marks performs the best (in bold). χ-SCNN applied to primary+secondary marks and CTCF consistently performs significantly better than CTCF alone (p-value < 0.05, two proportions z-test).