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Supplementary Figure 1. Performance of Domain Adaptation methods for cross-species prediction of histone marks in terms of (A) accuracy and (B) PR AUC scores.

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Supplementary Figure 2. Performance of Domain Adaptation methods for cross-species prediction of transcription factors in terms of (A) accuracy and (B) PR AUC scores.

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Supplementary Figure 3. Comparative performance of 9 DA models tested on TFs and HMs humanmouse and mouse-human cross-species predictions in terms of (A) accuracy and (B) PR AUC metrics.

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	AllCell	Blood	Breast	Cardiovascular	Liver	Lung	Neural	Pancreas	Pluripotent_stem_cell	Prostate
hg38 → mm10	0.05 0 0 0 0 0 0 0 0 0 0 0 0 0									
mm10 → hg38	0.02 0 ★ 0 0 ★ 0 0 ↓ 0 ↓ 0 ↓ 0 ↓ 0 ↓ 0 ↓ 0 ↓ 0 ↓ 0 ↓ 0					-				

		01000	Breast	Cardiovascular	Liver	Lung	Neural	Pancreas	Pluripotent_stem_cell	Prostate
0 -0.05 □ hg38 → mm100.1 -0.15 -0.2										
0 −0.05 mm10 → hg38 −0.1 −0.15 −0.2	◆ ★ 4 ※ ▷ 1 ⊕ ~		 							

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Supplementary Figure 4. Comparison of DA model performance across tissues for histone marks in terms of (A) accuracy and (B) PR AUC metrics.



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Supplementary Figure 5. Comparison of DA model performance across tissues for transcription factors in terms of (A) accuracy and (B) PR AUC metrics.



Supplementary Figure 6. Comparison of performance of different source DL models – CNN, LSTM or CNN+LSTM – used with DA approach for the H3K27ac histone mark in terms of (A) accuracy and (B) PR AUC metrics.



Supplementary Figure 7. Comparison of performance of different source DL models – CNN, LSTM or CNN+LSTM – used with DA approach for the TBX21 transcription factor in terms of (A) accuracy and (B) PR AUC metrics.

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