

S6 Table: 4conv2pool4norm recall for regulatory sequence prediction for different cell lines. Ten CNN models of the 4conv2pool4norm architecture were trained each on DHS datasets (positive) and corresponding negative sets of k-mer shuffled sequences (k=2, k=7) or genomic background sequences ($t_{GC}=0.02$) for A549 or MCF-7 cells. A549 and MCF-7 cell lines are represented in our data with two training datasets each, which are labeled as A and B, respectively. Model performance was evaluated based on recall for hold-out sets (chromosome 8). The table summarizes mean and standard deviation across ten trained models. There are seven different hold-out sets derived from different cell lines and we assess model generalization across cell-types. Datasets are named according to S1 Table. Respective results for the gkm-SVM models are available Table 1, results for CNN models of 2conv2norm architecture are available in S5 Table.

| | | Model | | | | | | | | | | | |
|-------------------|-----------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|--------------------------------------|----------------------|----------------------|----------------------|
| | | Shuffled ($k=2$) | | | | Shuffled ($k=7$) | | | | Genomic background ($t_{GC}=0.02$) | | | |
| | | A549 (A) | A549 (B) | MCF-7 (A) | MCF-7 (B) | A549 (A) | A549 (B) | MCF-7 (A) | MCF-7 (B) | A549 (A) | A549 (B) | MCF-7 (A) | MCF-7 (B) |
| Recall (test set) | A549 (A) | 0.887 ± 0.034 | 0.868 ± 0.032 | 0.869 ± 0.038 | 0.860 ± 0.030 | 0.667 ± 0.017 | 0.614 ± 0.022 | 0.639 ± 0.027 | 0.621 ± 0.025 | 0.840 ± 0.034 | 0.744 ± 0.035 | 0.795 ± 0.033 | 0.742 ± 0.055 |
| | A549 (A) | 0.867 ± 0.033 | 0.880 ± 0.031 | 0.856 ± 0.037 | 0.847 ± 0.032 | 0.581 ± 0.017 | 0.575 ± 0.016 | 0.557 ± 0.024 | 0.545 ± 0.022 | 0.813 ± 0.031 | 0.795 ± 0.029 | 0.784 ± 0.028 | 0.735 ± 0.051 |
| | HeLa-S3 | 0.858 ± 0.04 | 0.856 ± 0.038 | 0.849 ± 0.047 | 0.835 ± 0.025 | 0.611 ± 0.017 | 0.575 ± 0.021 | 0.598 ± 0.031 | 0.576 ± 0.024 | 0.773 ± 0.041 | 0.694 ± 0.033 | 0.756 ± 0.040 | 0.691 ± 0.060 |
| | HepG2 | 0.806 ± 0.046 | 0.818 ± 0.04 | 0.805 ± 0.044 | 0.800 ± 0.041 | 0.476 ± 0.024 | 0.493 ± 0.019 | 0.468 ± 0.030 | 0.465 ± 0.024 | 0.685 ± 0.040 | 0.626 ± 0.040 | 0.668 ± 0.038 | 0.617 ± 0.063 |
| | K562 | 0.848 ± 0.04 | 0.833 ± 0.038 | 0.825 ± 0.044 | 0.819 ± 0.041 | 0.648 ± 0.021 | 0.609 ± 0.025 | 0.609 ± 0.026 | 0.595 ± 0.026 | 0.729 ± 0.041 | 0.635 ± 0.044 | 0.674 ± 0.037 | 0.627 ± 0.065 |
| | MCF-7 (A) | 0.857 ± 0.04 | 0.845 ± 0.038 | 0.888 ± 0.038 | 0.875 ± 0.026 | 0.621 ± 0.017 | 0.577 ± 0.022 | 0.651 ± 0.025 | 0.631 ± 0.024 | 0.790 ± 0.038 | 0.700 ± 0.036 | 0.858 ± 0.029 | 0.801 ± 0.049 |
| | MCF-7 (B) | 0.864 ± 0.037 | 0.853 ± 0.035 | 0.894 ± 0.036 | 0.886 ± 0.026 | 0.628 ± 0.018 | 0.590 ± 0.022 | 0.666 ± 0.027 | 0.651 ± 0.025 | 0.816 ± 0.037 | 0.733 ± 0.035 | 0.876 ± 0.028 | 0.839 ± 0.043 |