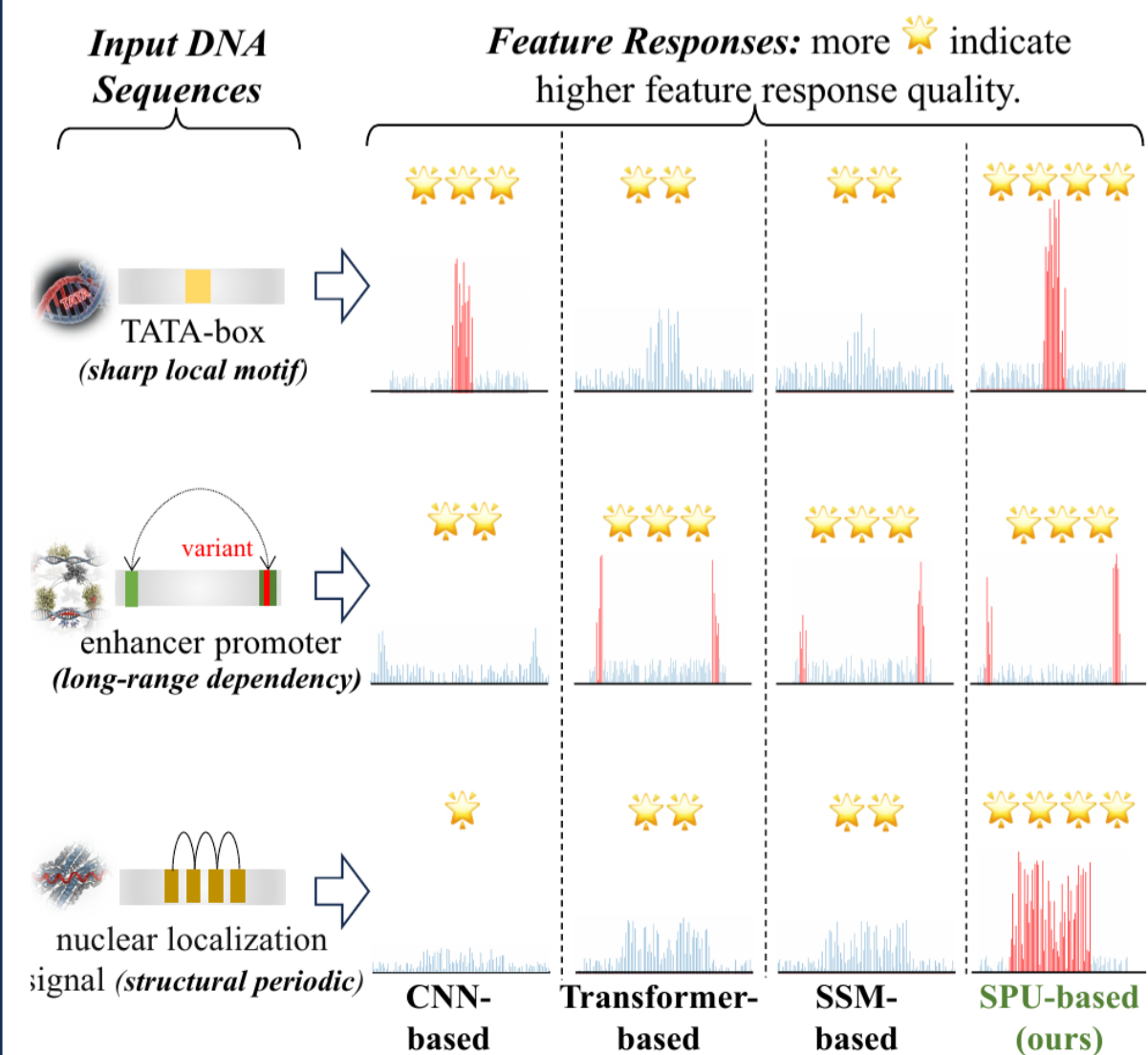


## Motivation

### Why DNA Needs a New Unit:

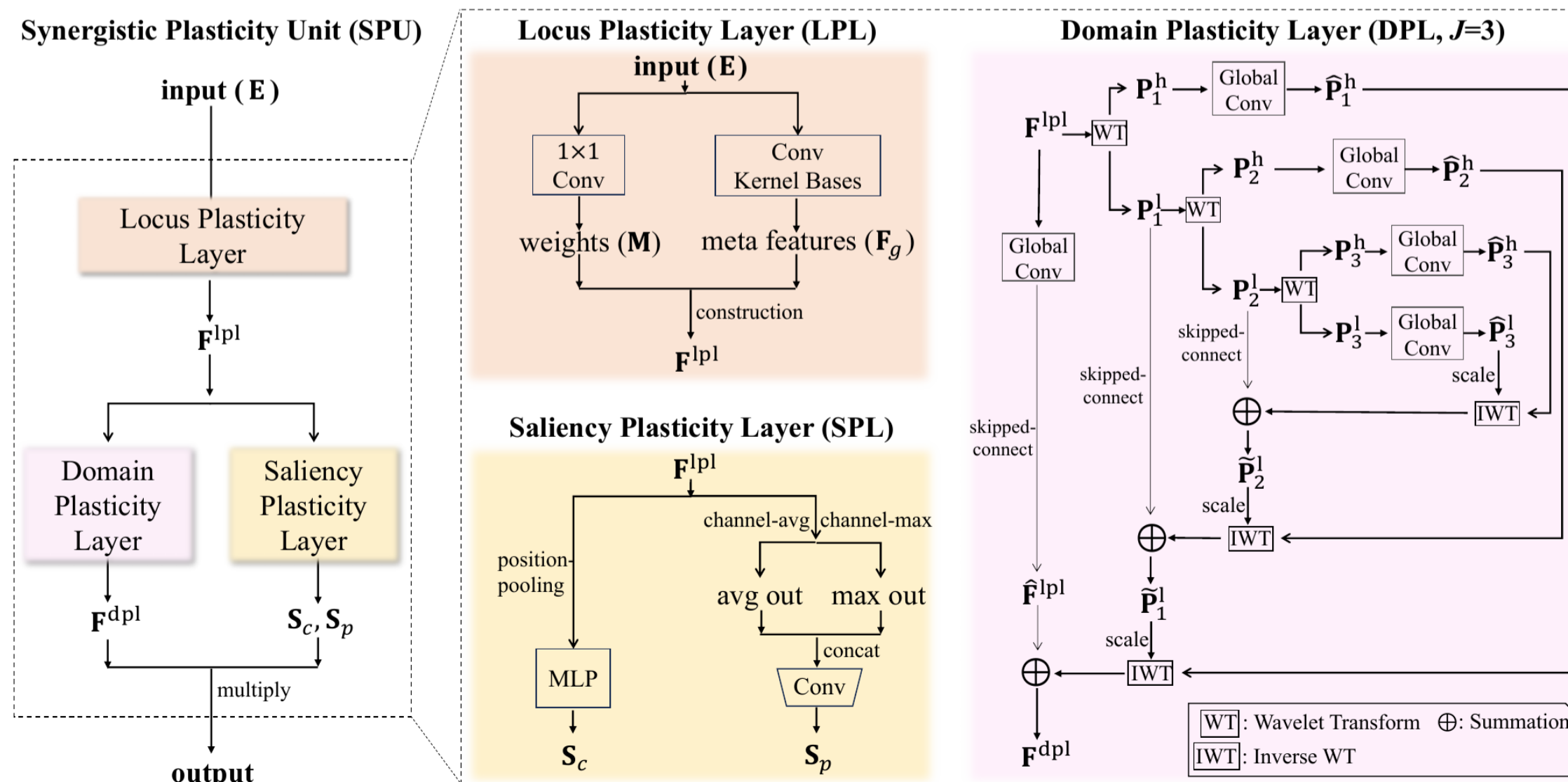
- Local motifs (e.g. TATA-box) — sharp, a few bp wide;
- Long-range deps (enhancer promoter) — up to  $10^5$  bp;
- Periodic signals (nucleosome, codon triplet) — frequency-domain.



## Methodology

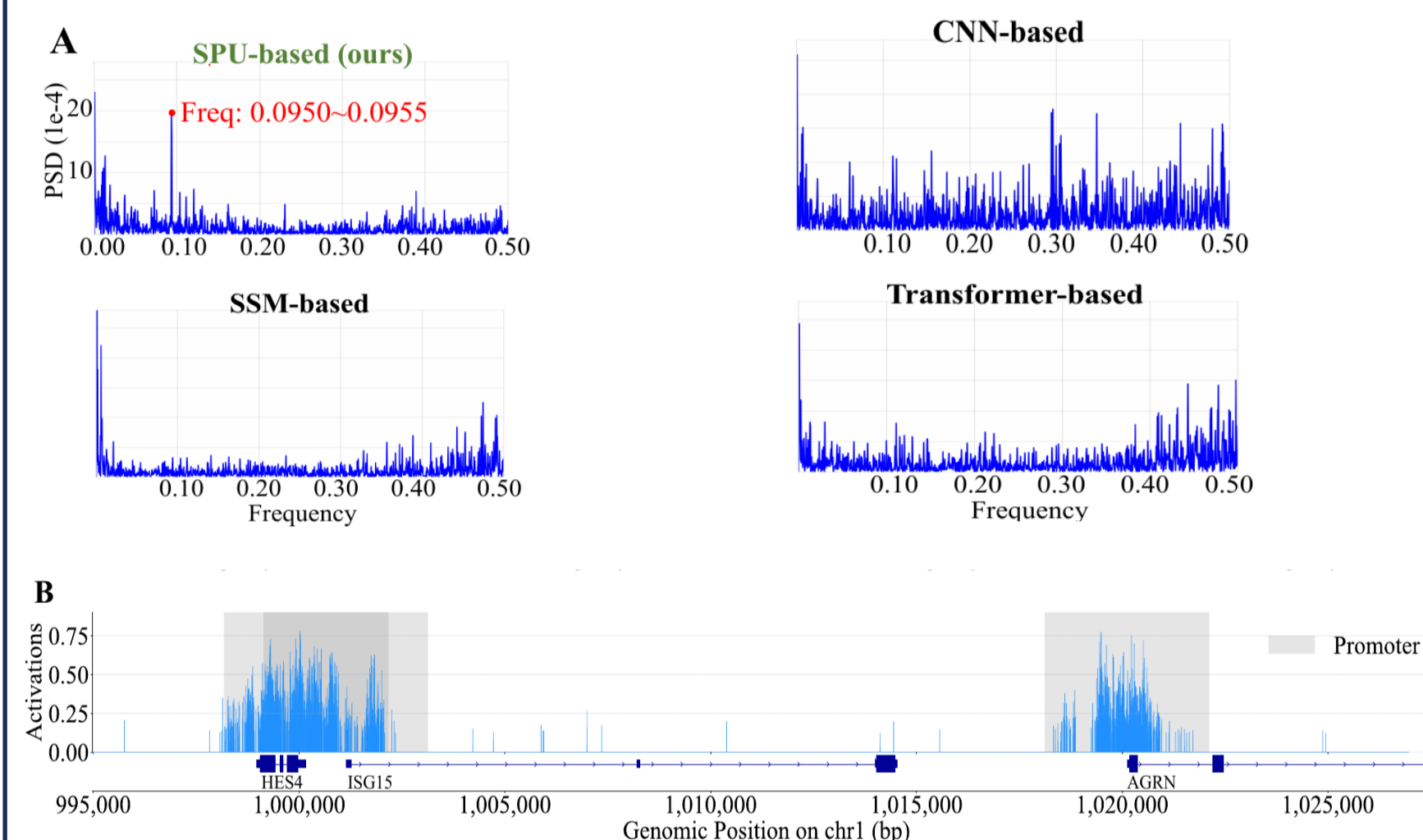
### SPU Architecture

- Locus Plasticity Layer (LPL): Token-specific dynamic convolution for local motif extraction;
- Domain Plasticity Layer (DPL): FFT-accelerated global long convolution +  $J$ -level wavelet decomposition capture complementary multi-resolution features;
- Saliency Plasticity Layer (SPL): Biologically motivated channel saliency ("what to look at") and position saliency ("where to look") jointly amplify signal and suppress noise.



## Results

### Biological Interpretability:



(A) Power spectrum on a nucleosome region. (B) An SAE feature of SPU's pretrained embedding aligns with promoter regions (HES4, ISG15, AGRN) without annotation supervision.

### Performance on Genomic Benchmark:

	HyenaDNA (436k)	CADUCEUS-PH (470k)	ConvNova (386k)	xLSTM-PH (500k)	SPU-DNA (ours) (490k)
Mouse Enhancers	78.03±0.19	78.60±1.32	79.17±0.87	78.48±0.94	<b>82.38±0.66</b>
Coding vs. Intergenic	90.43±0.05	91.86±0.28	93.35±1.52	93.11±1.38	<b>94.46±0.47</b>
Human vs. Worm	95.83±0.16	96.67±0.13	96.85±0.85	96.71±0.65	<b>97.19±0.75</b>
Human Enhancers Cohn	72.46±0.21	73.61±0.47	73.82±0.56	73.88±0.56	<b>74.96±0.35</b>
Human Enhancers Ensembl	89.43±0.02	90.11±0.32	90.10±0.16	90.42±1.04	<b>91.08±0.61</b>
Human Regulatory	88.45±0.08	87.82±0.46	88.21±1.03	87.67±0.31	<b>94.20±0.23</b>
Human Nontata Promoters	94.74±0.20	94.72±0.48	<b>95.21±1.26</b>	95.11±0.86	94.78±0.51
Human OCR Ensembl	78.14±2.01	80.17±0.15	79.61±0.42	81.72±1.16	<b>81.95±1.01</b>