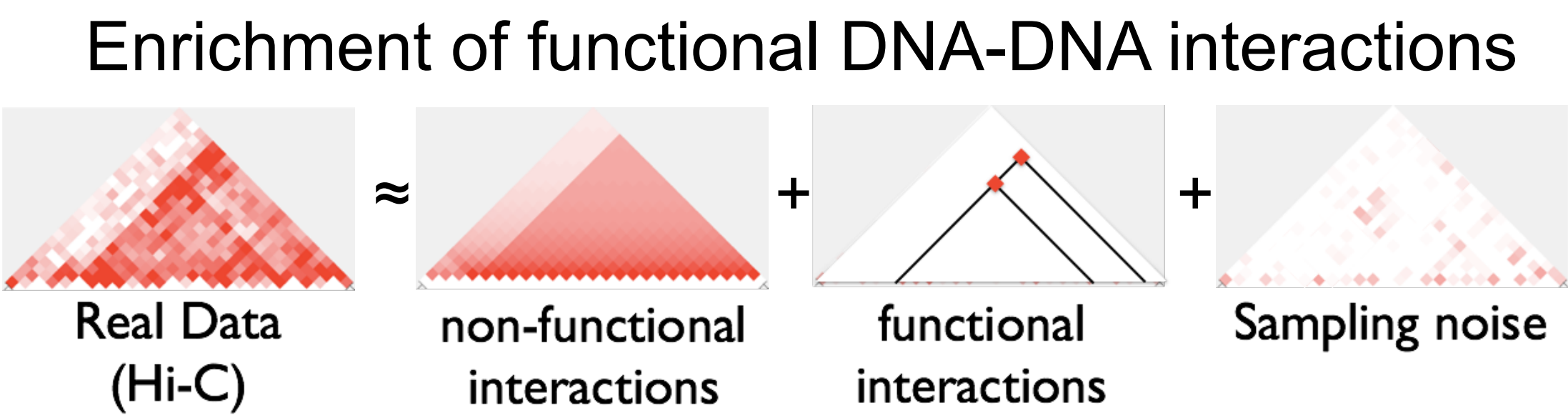


Promoter-Enhancer Interactions Identified from Hi-C Data

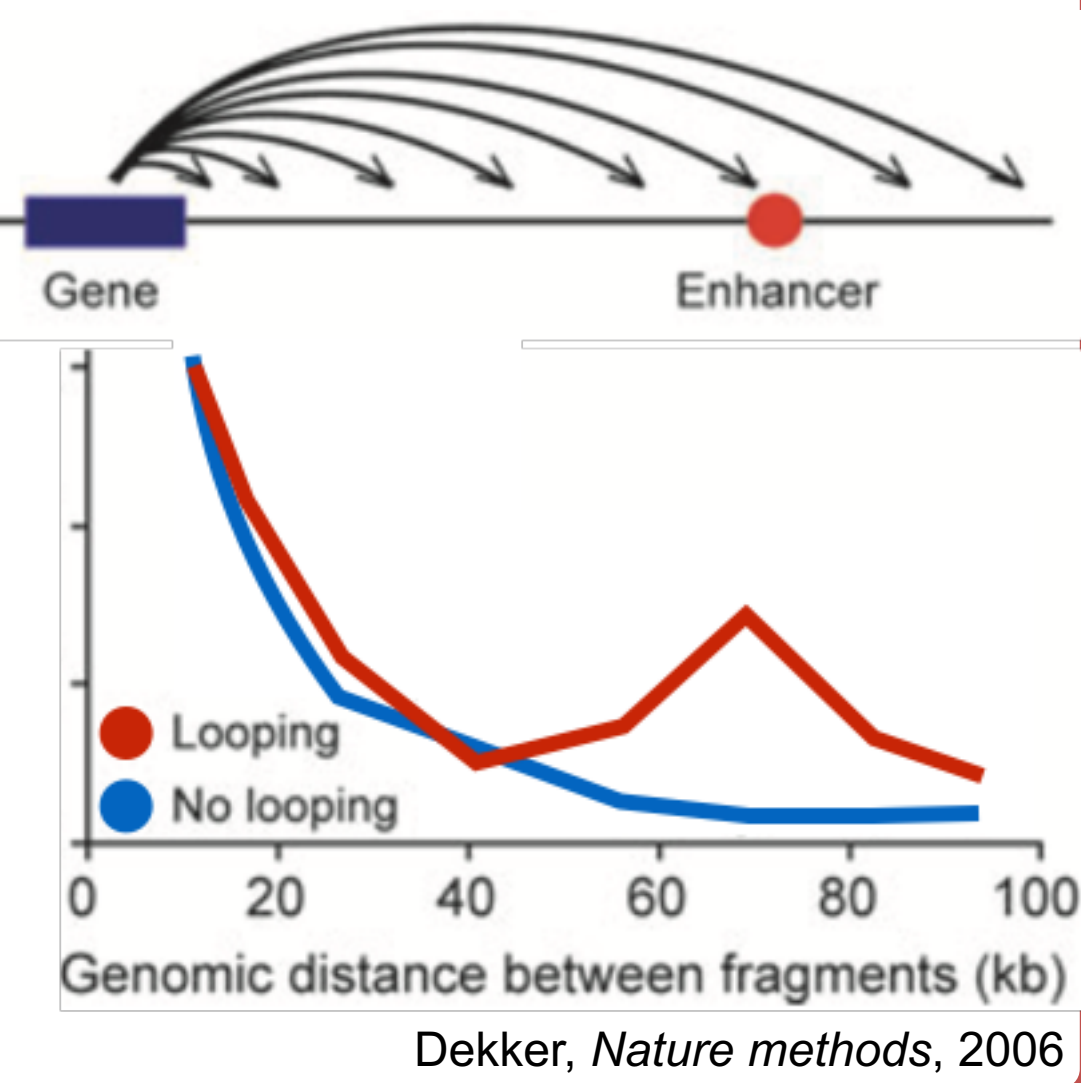
Gil Ron, Yuval Globerson, Dror Moran and Tommy Kaplan

School of Computer Science and Engineering
The Hebrew University, Israel. tommy@cs.huji.ac.il

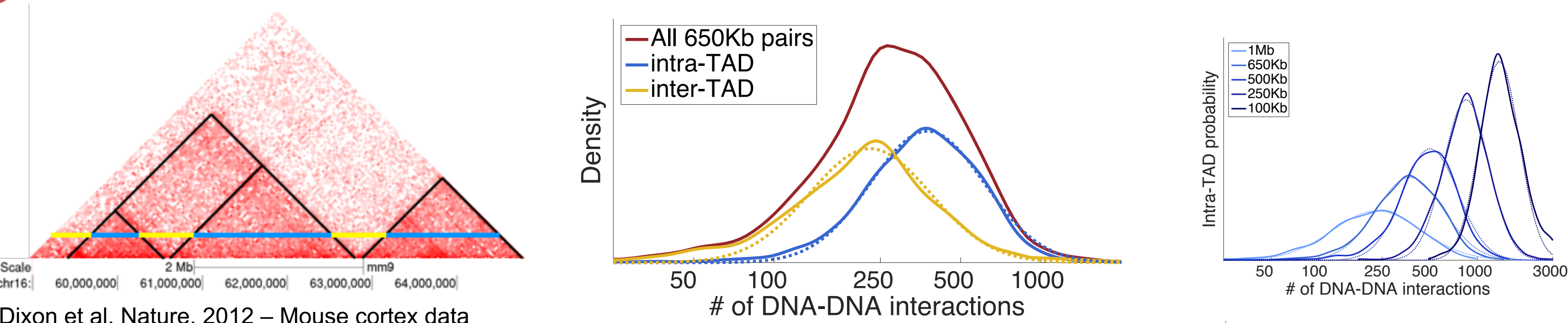
1 PSYCHIC



PSYCHIC segments the genome, fits a TAD-specific BG model, and identifies over-represented interactions



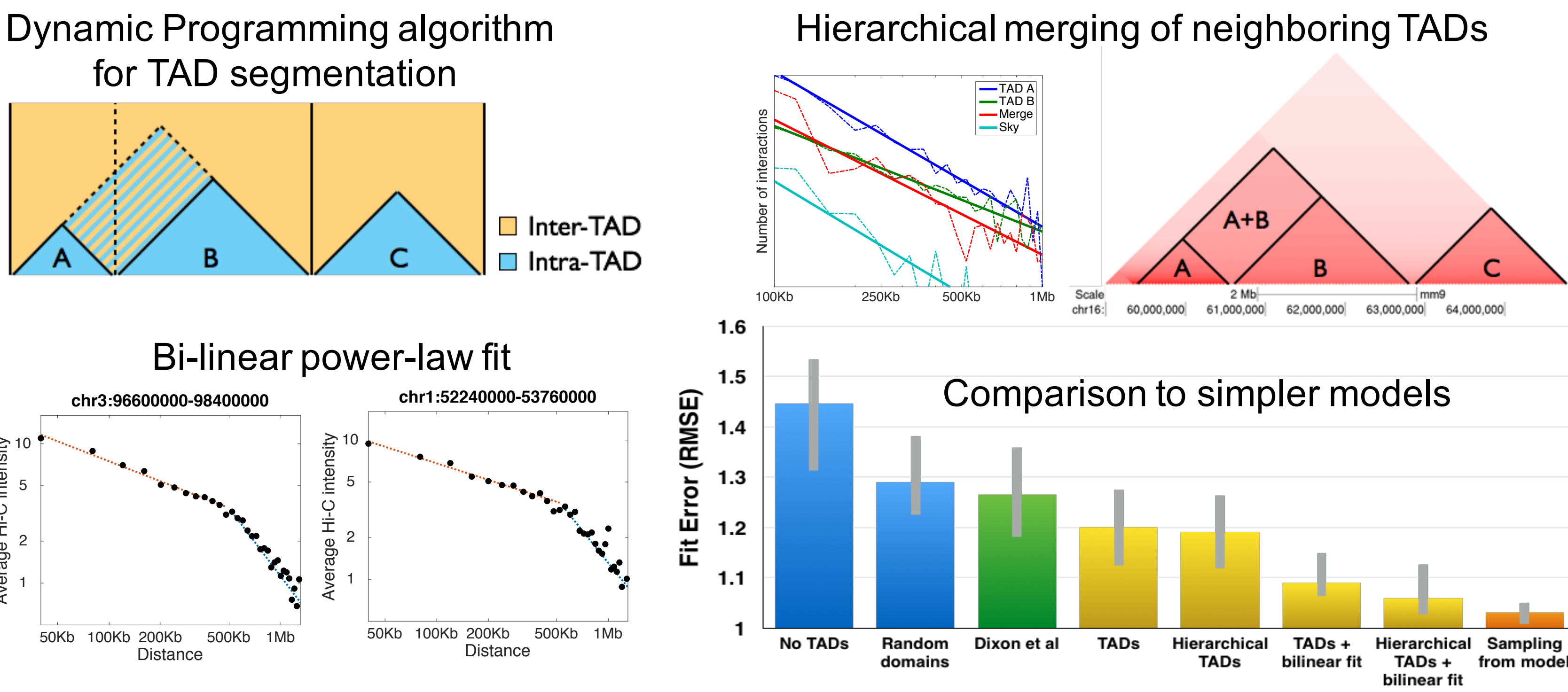
2 Probabilistic Mixture Model for Hi-C Data



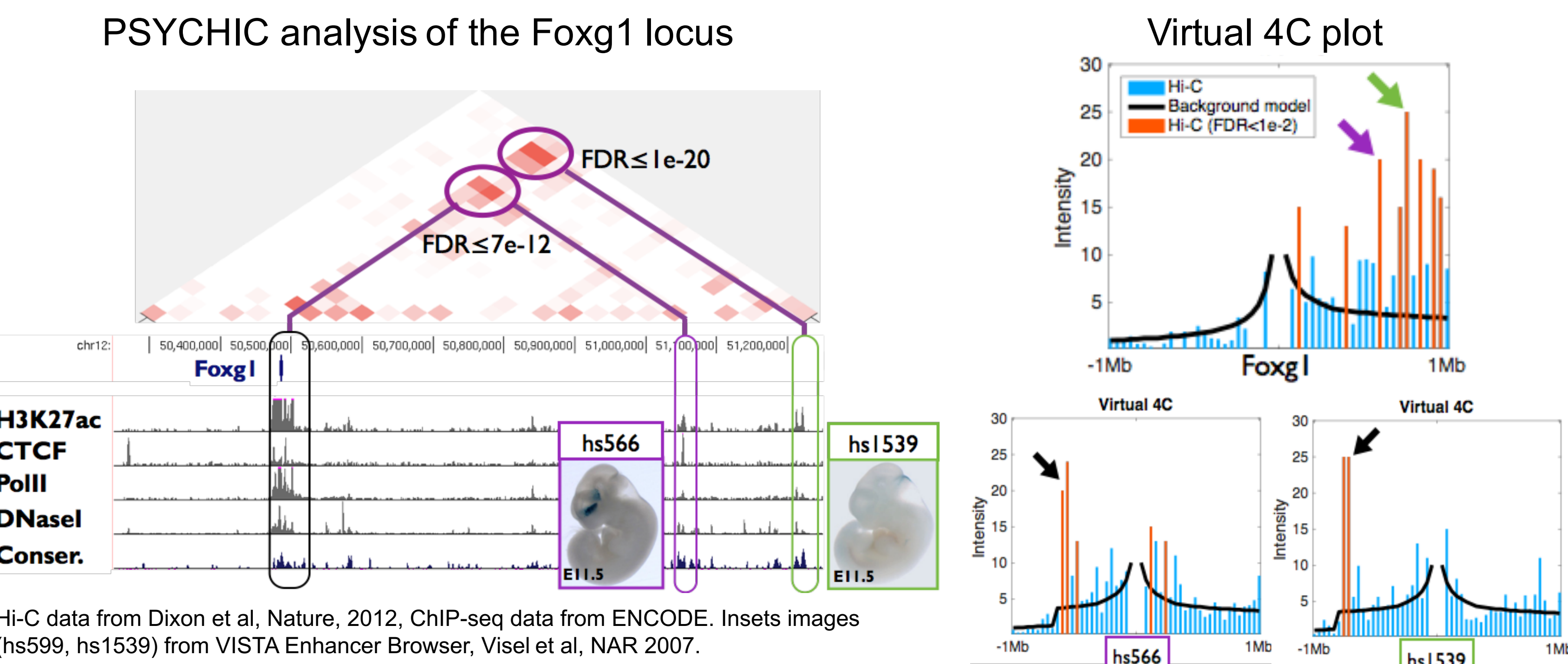
Segmentation uses log-posterior ratio between intra- and inter-TAD log-Normal models, using a Dynamic Programming algorithm

$$\text{Optimal segmentation} \triangleq \underset{\text{segmentation}}{\text{argmax}} \sum_{\text{in TADs}} \log \frac{P_{\Delta}(\text{TAD}|\text{Data})}{P_{\Delta}(\text{BG}|\text{Data})} + \sum_{\text{"skies"}} \log \frac{P_{\Delta}(\text{BG}|\text{Data})}{P_{\Delta}(\text{TAD}|\text{Data})}$$

3 Hierarchical Model of Topological Domains



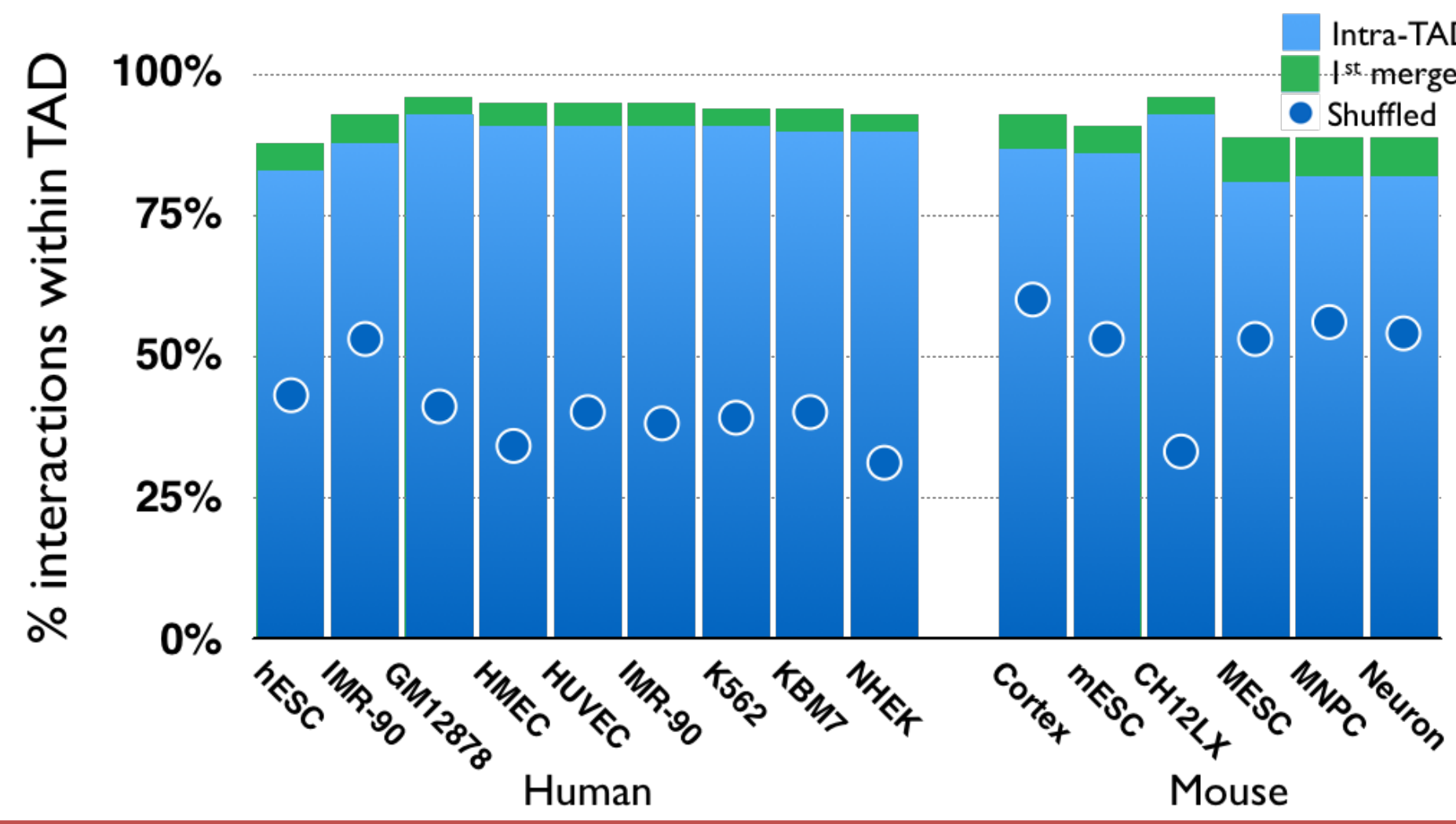
4 Identification of DNA-DNA interactions



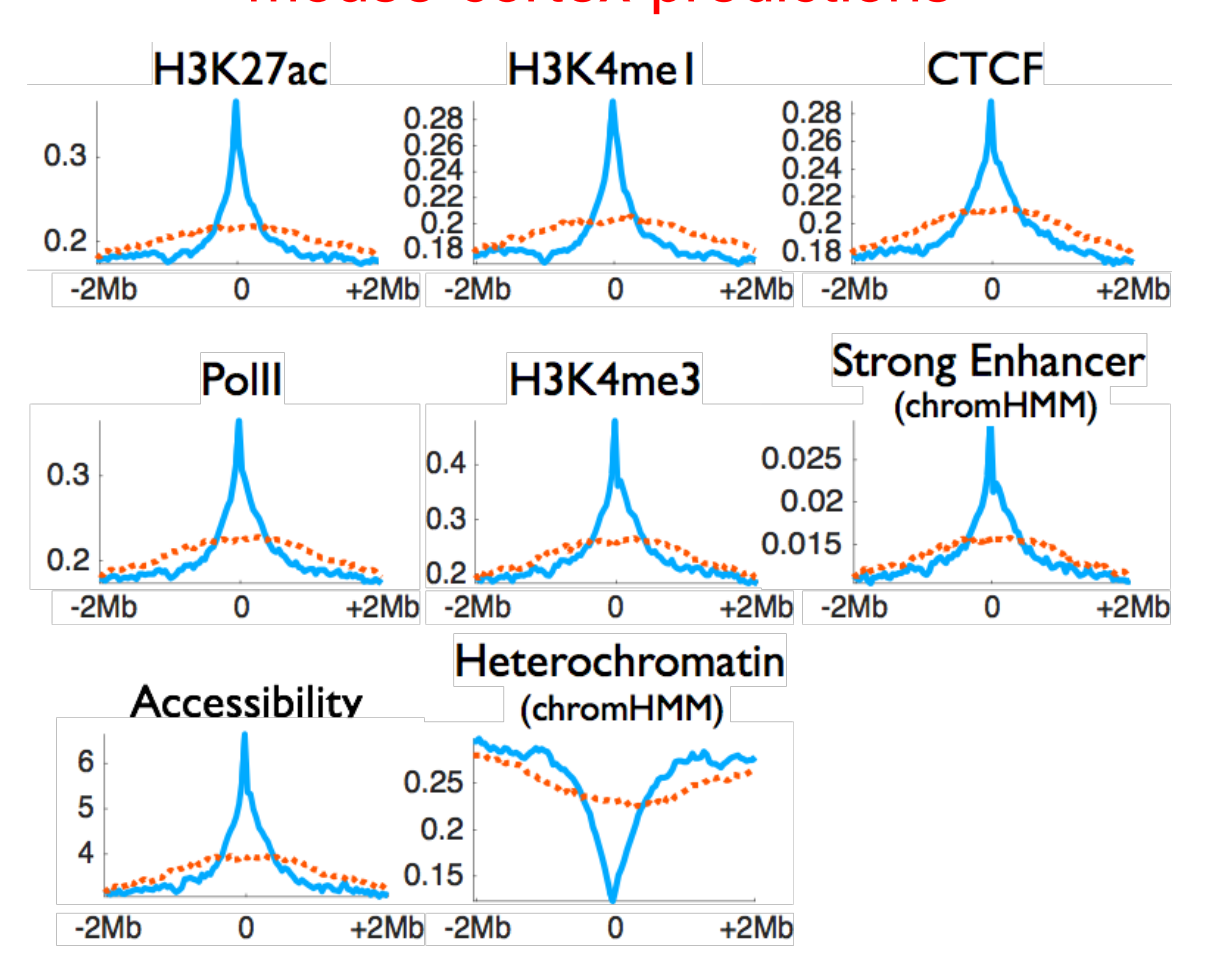
5 Genome-wide predictions

267,938 putative enhancer regions predicted using human and mouse Hi-C data

~90% of promoter-enhancer pairs fall within TAD



ChIP-seq enrichments for mouse cortex predictions

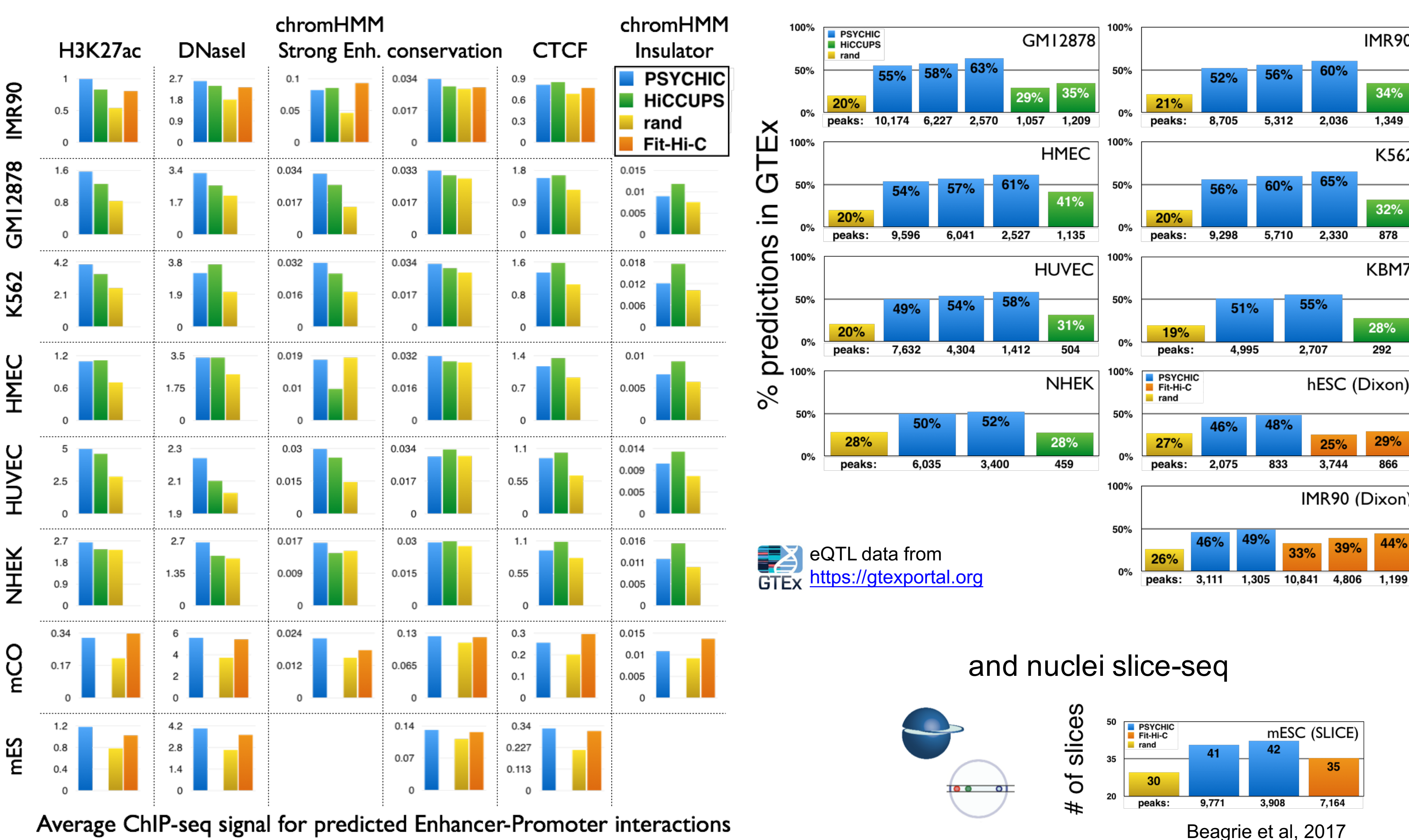


6 Validation by ChIP-seq, eQTLs and slicing

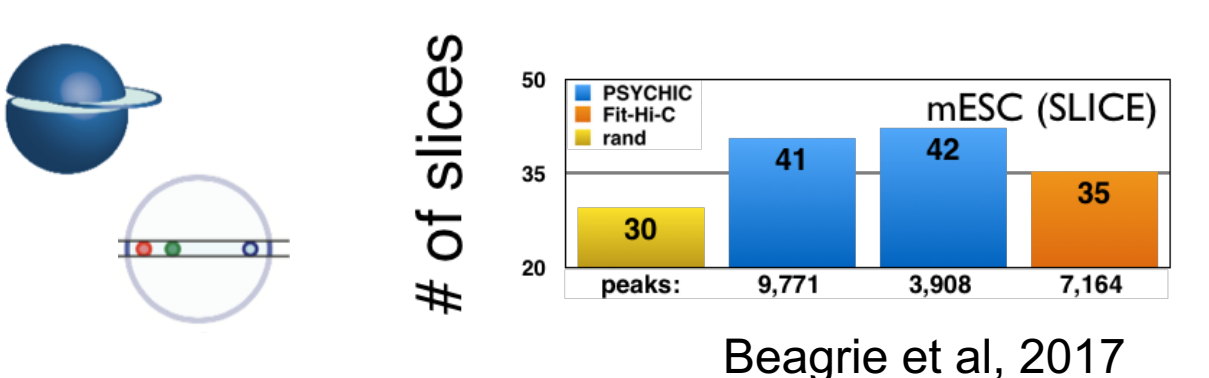
Enrichment of putative enhancer regions, compared to other methods

Chromatin, accessibility and conservation

Distal promoter-related eQTLs



and nuclei slice-seq



Summary

- PSYCHIC
- Ron et al, Nature Comm., 2017
- <https://github.com/dhkron/PSYCHIC>
- Accurate segmentation into TADs
- Hierarchical organization
- TAD specific background model
- Identification of putative interactions

