Mechanistic insights into transcription factor cooperativity and its impact on protein-phenotype interactions

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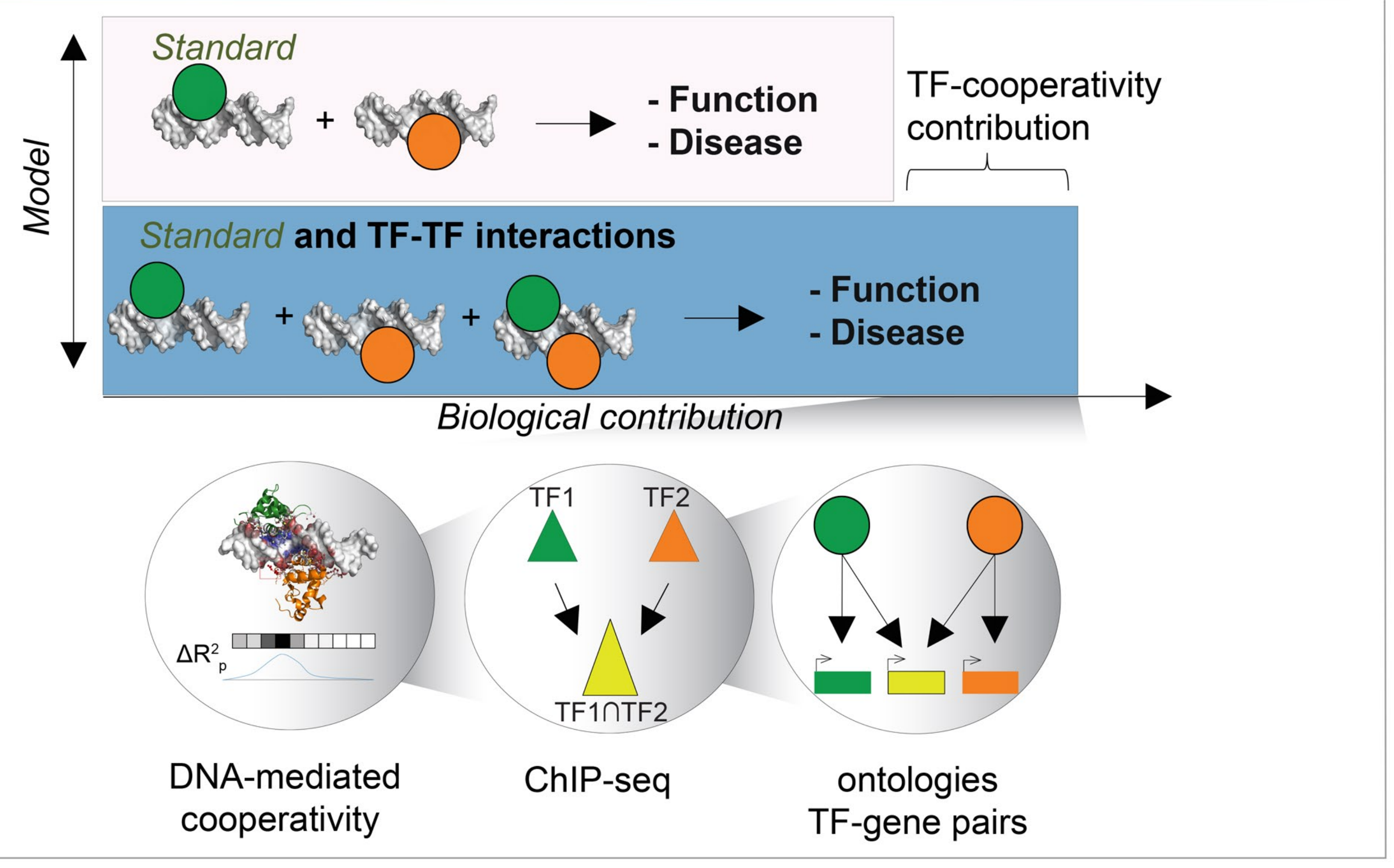
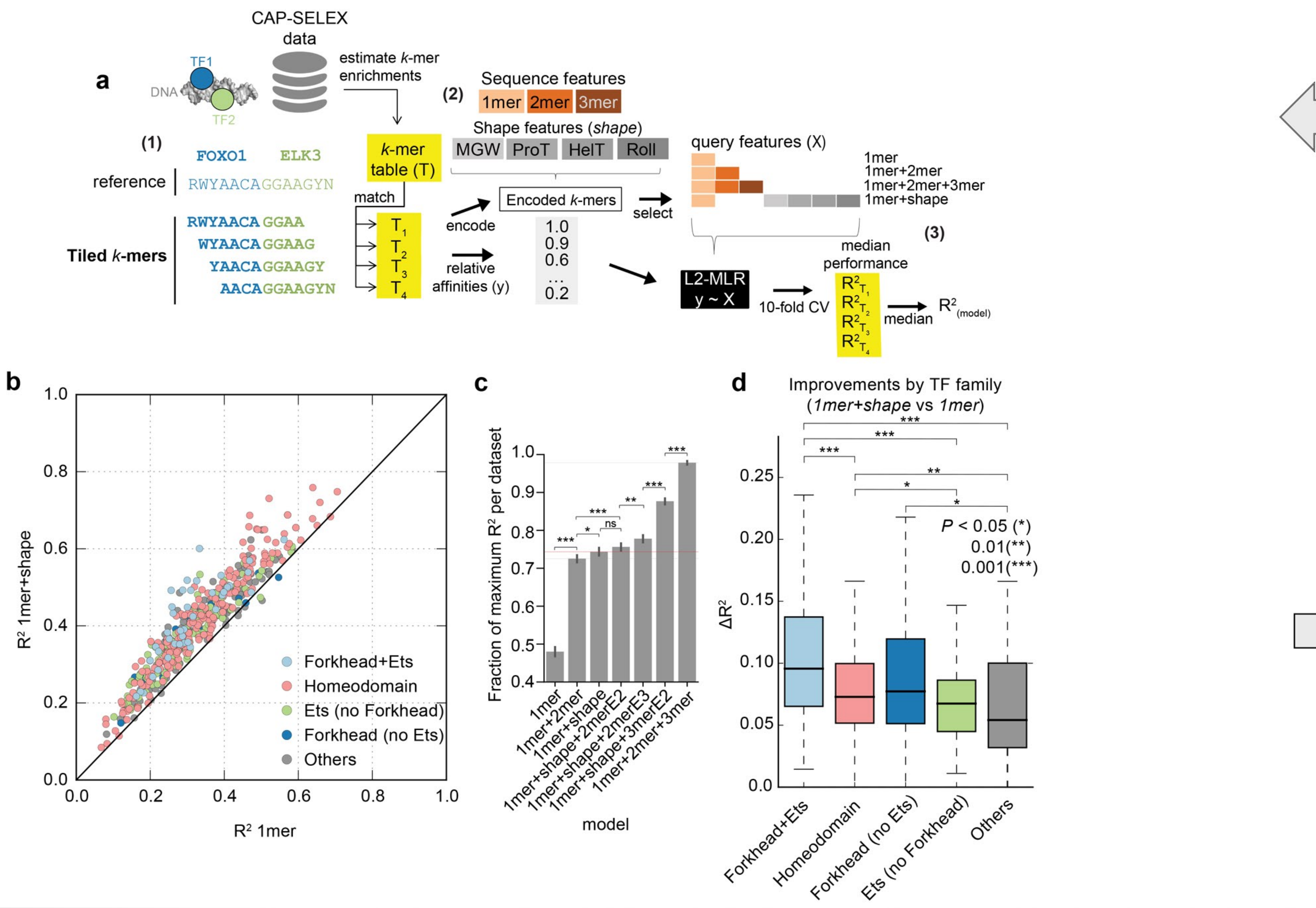
Highlights

- TF-cooperativity prediction through integration of in vitro human TF binding data.
- A link between Forkhead-Ets cooperativity and DNA-shape is inferred and experimentally validated.
- Integration of TF cooperativity and multi-omics data reveals novel TF-phenotype associations.

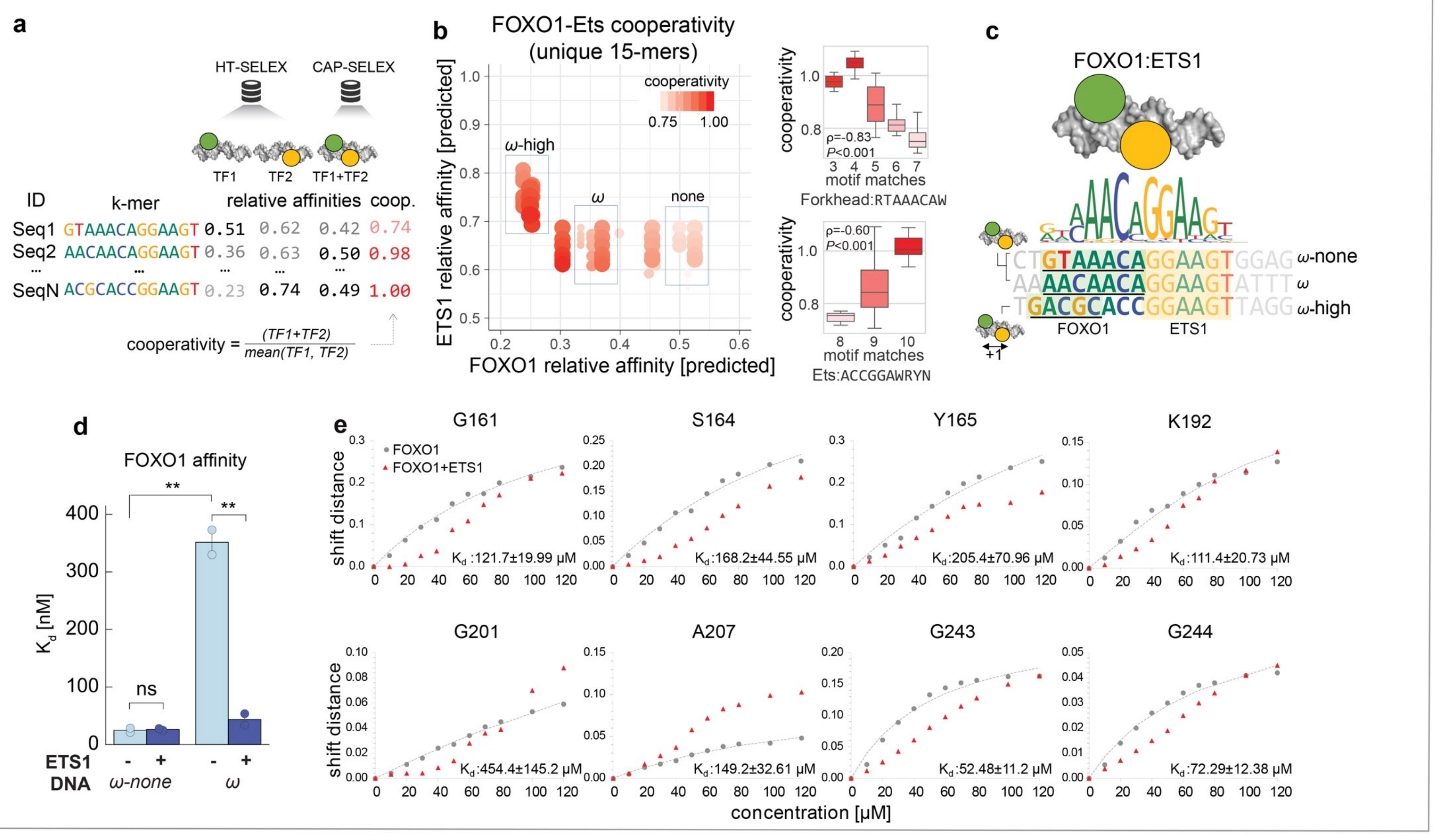
1 Model to estimate cooperative TF-binding contribution to TF-ontology associations.



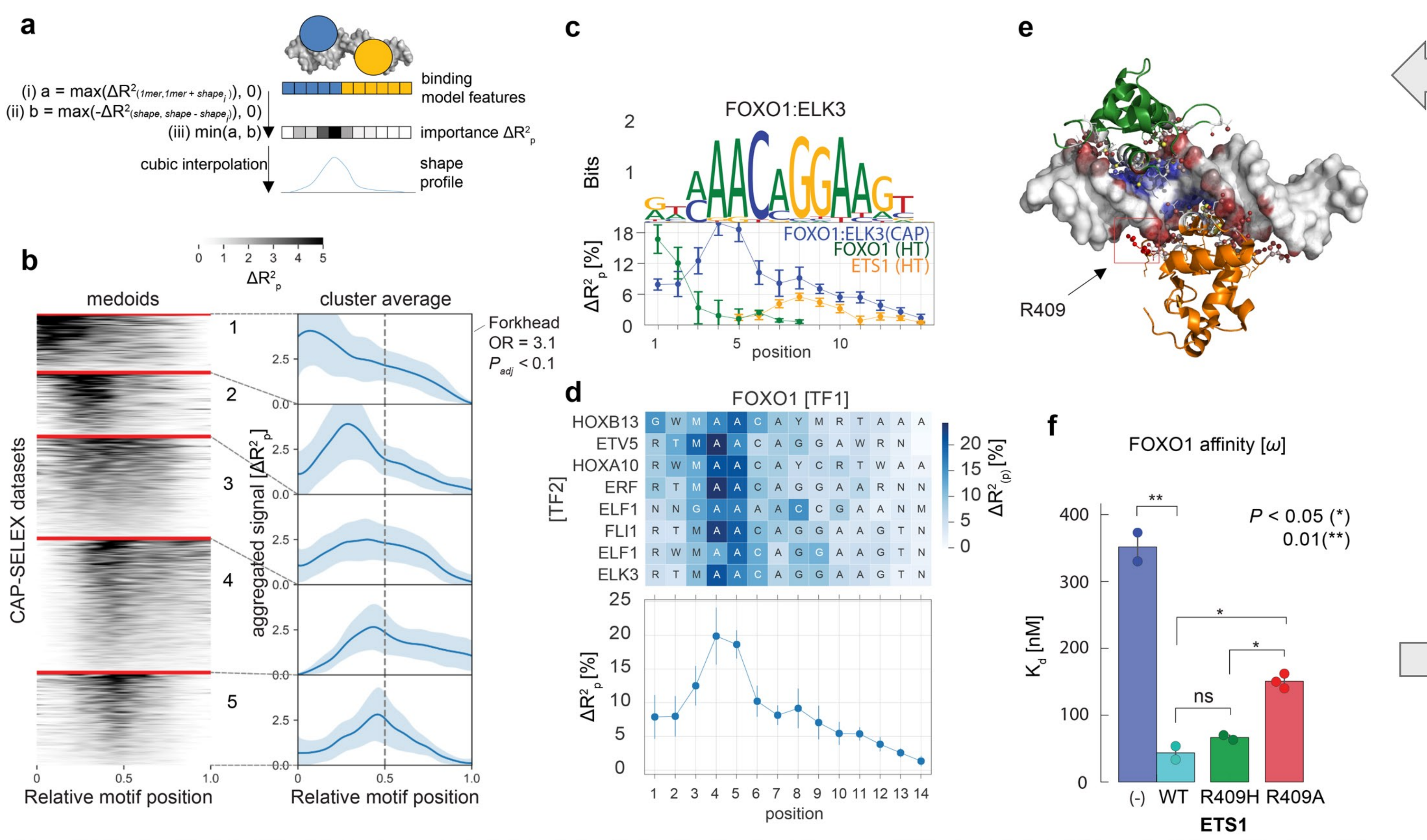
2 Addition of DNA-shape features improves combinatorial binding predictions in CAP-SELEX data.



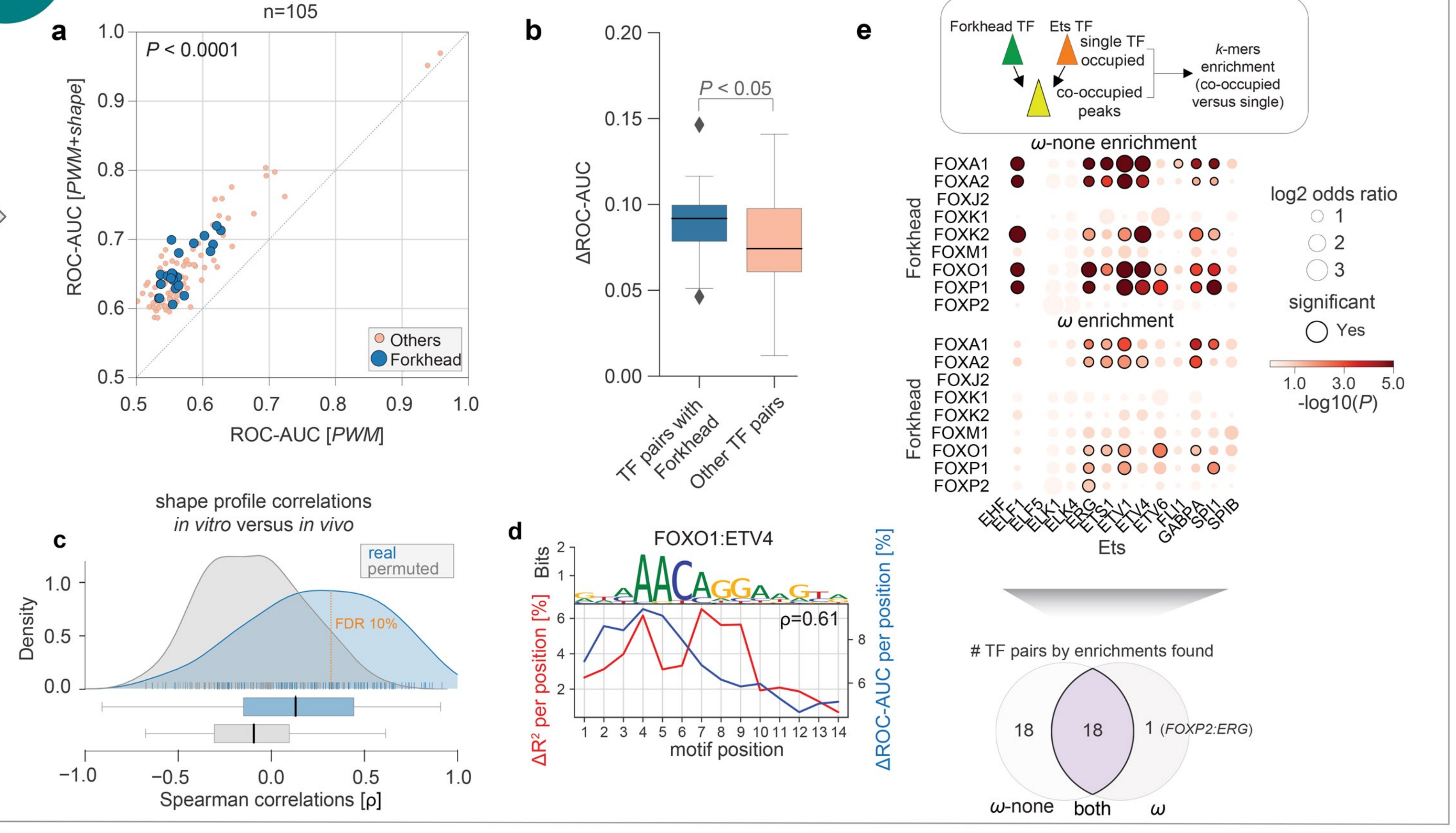
3 Prediction and validation of cooperative binding sites from SELEX data.



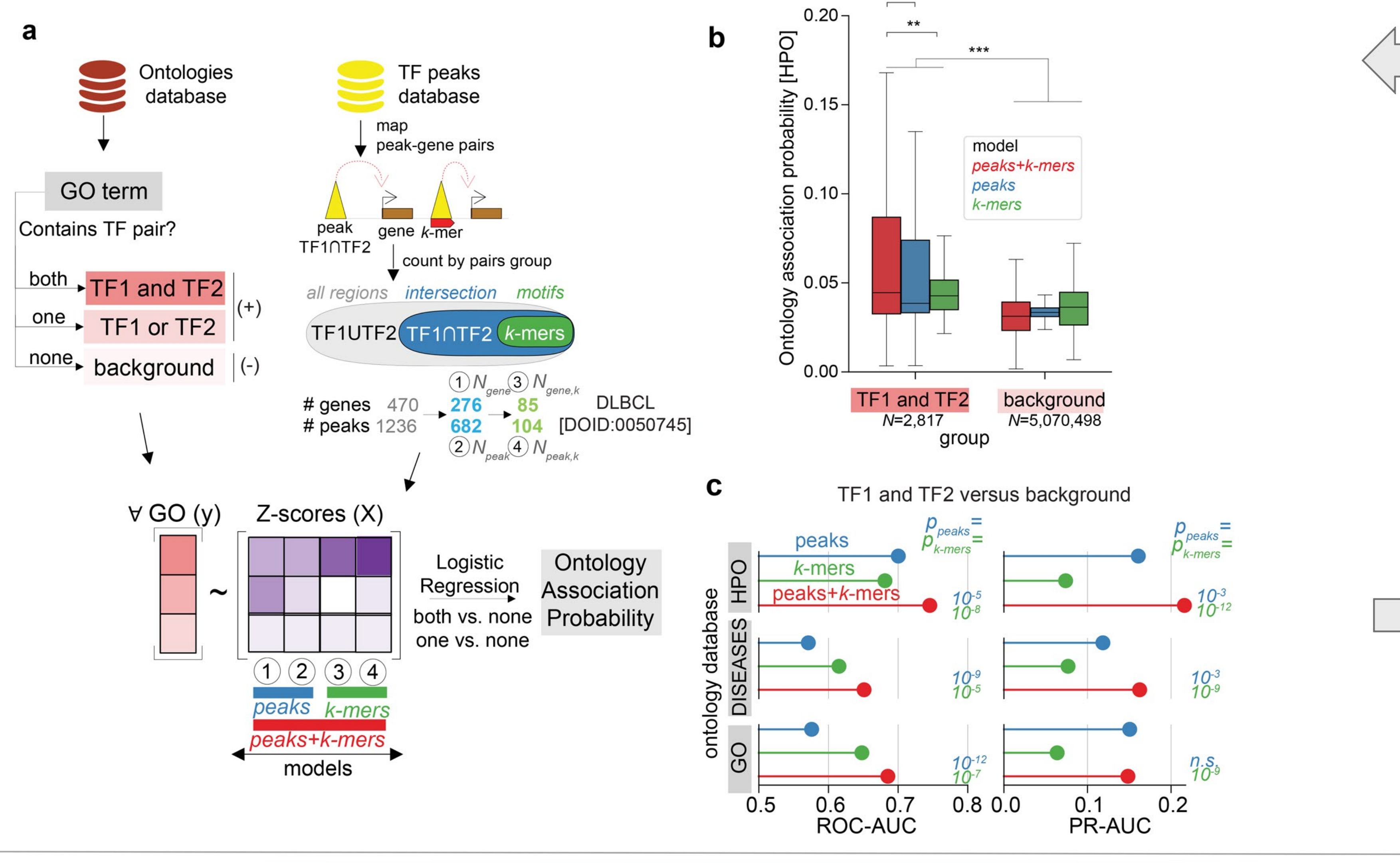
4 Clustering of shape improvements by position in CAP-SELEX data reveal shape-recognition biases in TF cooperative binding.



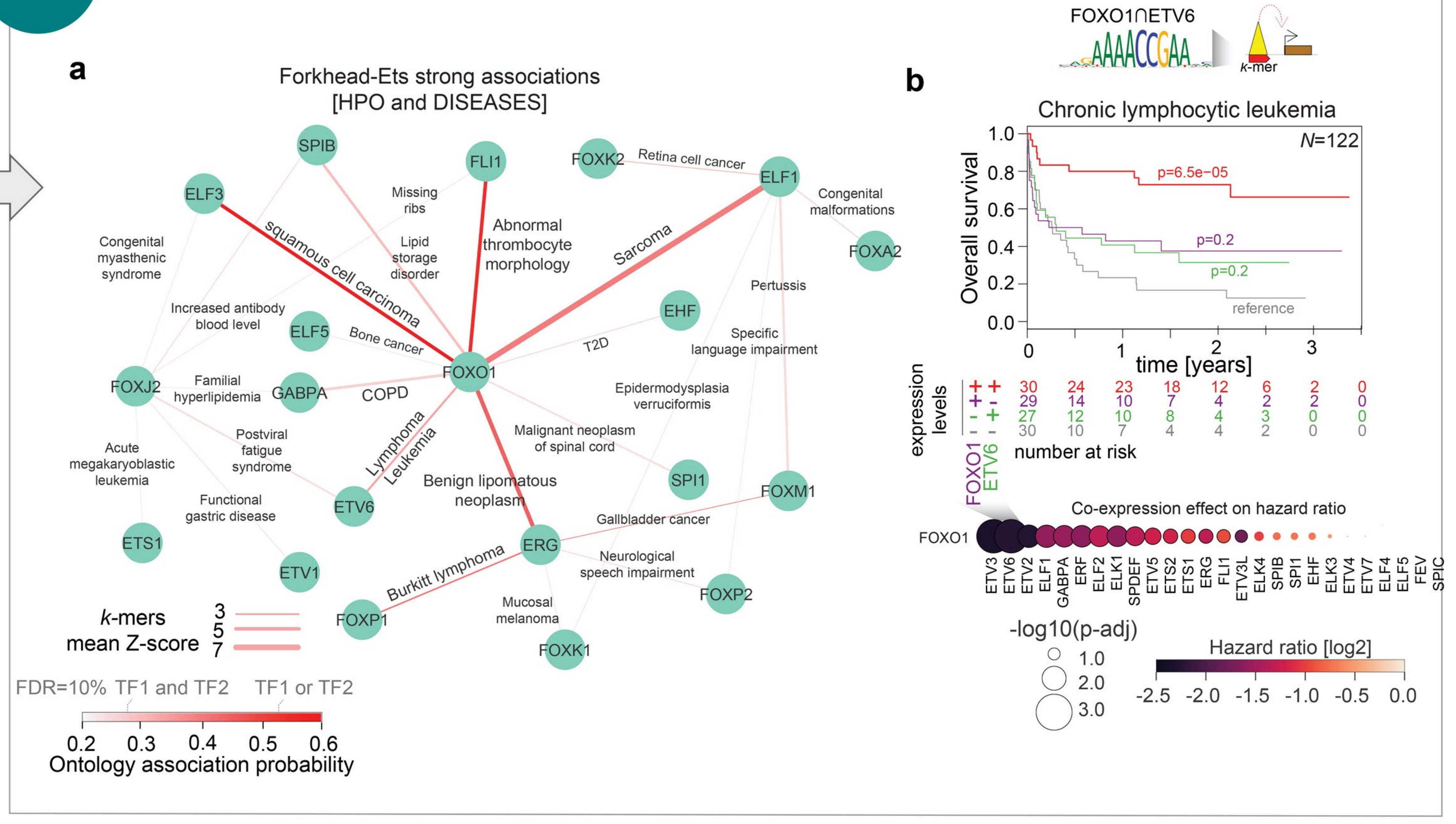
5 Cooperative TF binding agreement between SELEX and *in vivo* data.



6 Inference of TF-phenotype associations using TF-cooperative k-mers.



7 Forkhead-Ets cooperative associations to function and disease



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https://git.embl.de/rio/coop-tf-binding

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