

Supplementary Information

Genome-wide targets identification of “core” pluripotency transcription factors with integrated features in human embryonic stem cells

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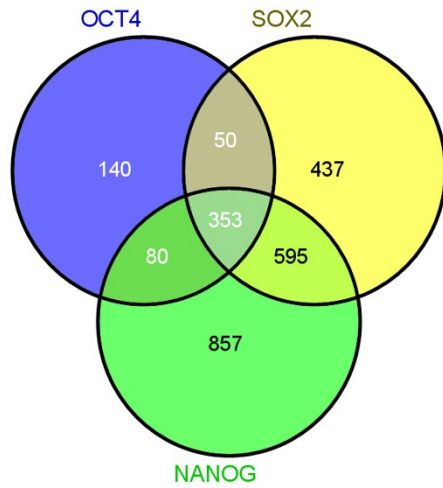
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Contribute equal to this study

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Figure S1 Comparison between original targets and prediction targets with Venn diagrams. (A) Primary data source about target genes of “core” TFs. (B) Prediction data about target genes of “core” TFs.

A



B

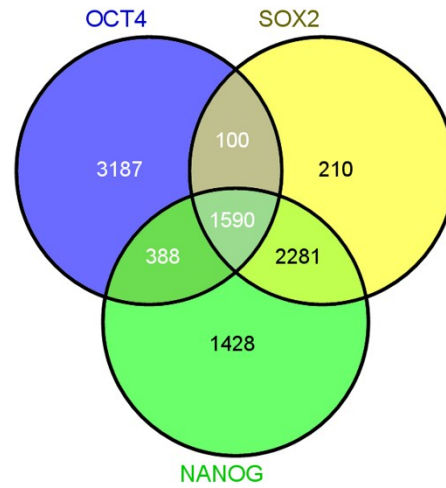


Figure S2 Comparison about M-C algorithm prediction results of three tests. It is a collection of predicted targets and verified targets in human.

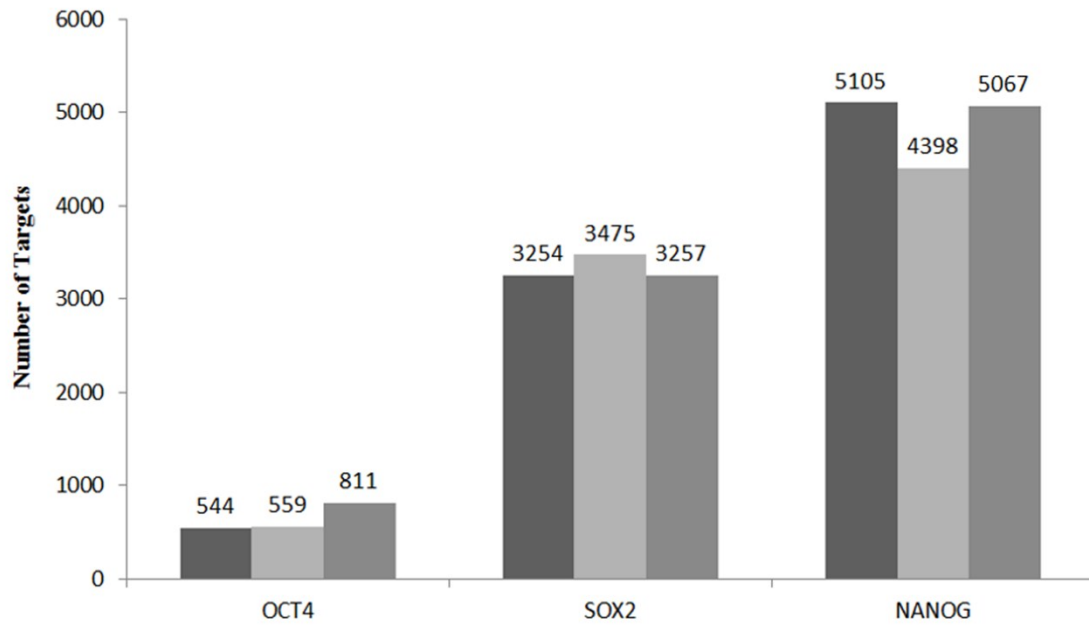
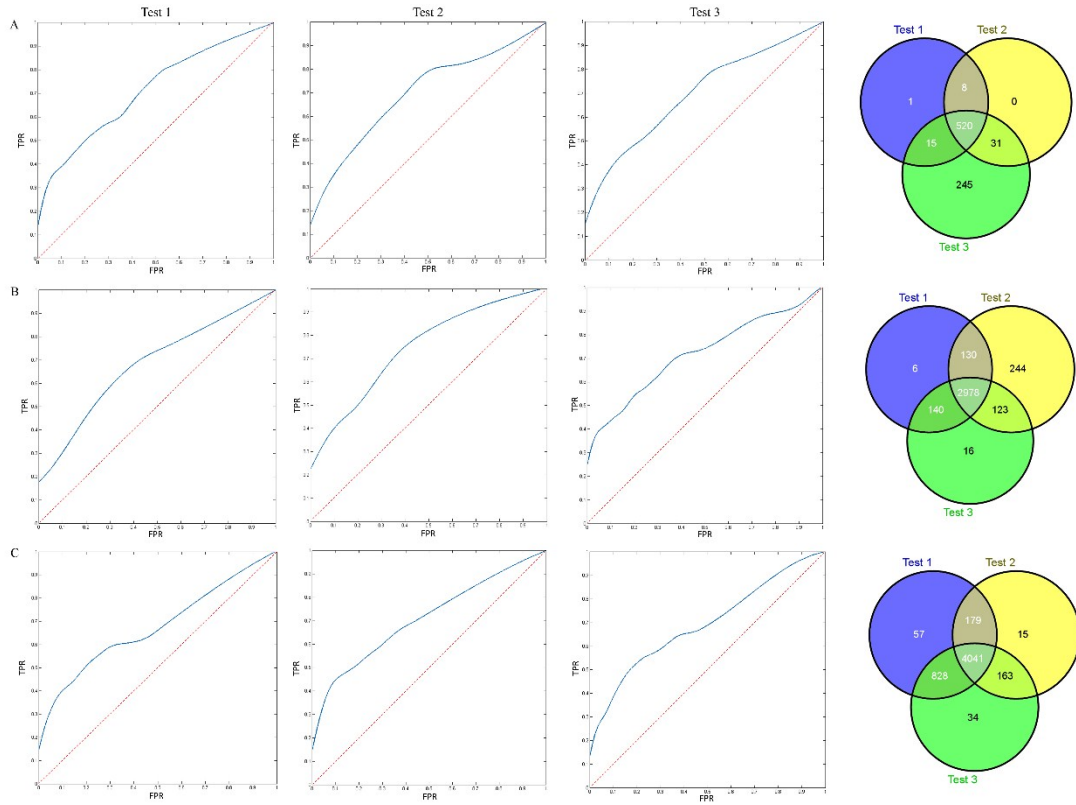


Figure S3 Details of M-C algorithm prediction results. Left are ROC curves of different tests. Right are the Venn diagrams for the result of three repeats. (A) (B) (C) Prediction results of OCT4, SOX2 and NANOG respectively.



Support data The features of “core” pluripotency transcription factors include 108 features for OCT4, 81 features for SOX2 and 36 features for NANOG.