Supplementary material for:

An unsupervised deep learning framework for predicting human essential genes from population and functional genomic data

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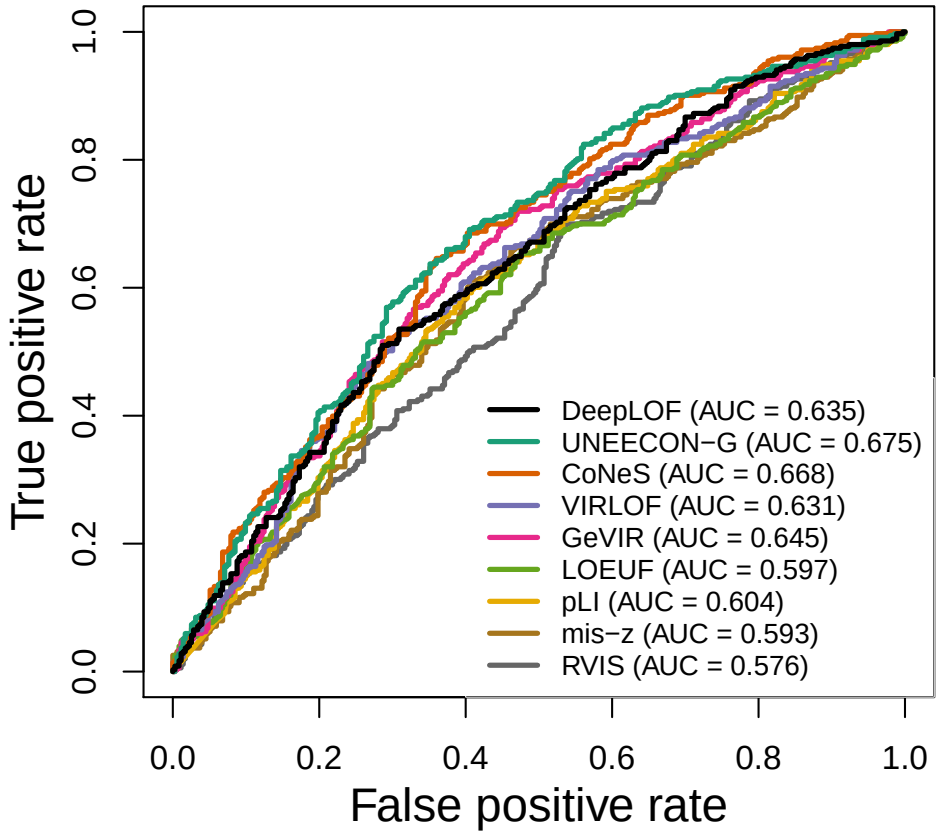

Supplementary Fig. 1: Performance of DeepLOF and alternative methods in predicting dominant negative genes.

Supplementary Table 1: Genomic features for model training.

Feature name	Feature type	Log transformation	Data source
H3K9ac signal	Continuous	Yes	[1]
H3K27me3 signal	Continuous	Yes	[1]
H3K4me3 signal	Continuous	Yes	[1]
H2A.Z signal	Continuous	Yes	[1]
Enhancer number	Continuous	Yes	[1]
GO embryo development	Binary	N/A	[2]
GO central nervous development	Binary	N/A	[2]
Reactome nervous system development	Binary	N/A	[2]
Reactome developmental biology	Binary	N/A	[2]
Transcription factor	Binary	N/A	[3]
Protein complex	Binary	N/A	[4]
Promoter CpG density	Continuous	No	[5]
Promoter phastCons score	Continuous	No	[5]
Exonic phastCons score	Continuous	No	[5]
Mean expression level	Continuous	Yes	[6]
Tissue specificity (tau)	Continuous	No	[6]
PPI degree	Continuous	Yes	[6]
UNEECON-G	Continuous	No	[7]

Supplementary Table 2: Statistical significance of the differences in AUC between DeepLOF and alternative methods in predicting essential genes. The numbers represent *P*-values from the DeLong test. *: $P < 0.05$; **: $P < 0.01$; ***: $P < 0.001$.

DeepLOF	ClinGen haploinsufficient genes	Human orthologs of mouse essential genes	Human essential genes in cell lines
vs. UNEECON-G	1.332e-05 ***	5.835e-04 ***	5.577e-10 ***
vs. CoNeS	8.679e-04 ***	3.688e-03 **	4.068e-21 ***
vs. VIRLOF	6.909e-07 ***	4.766e-06 ***	1.260e-02 *
vs. GeVIR	1.965e-08 ***	2.181e-05 ***	7.913e-05 ***
vs. LOEUF	6.601e-10 ***	1.073e-09 ***	3.151e-12 ***
vs. pLI	1.090e-09 ***	3.263e-10 ***	6.640e-50 ***
vs. mis-z	8.264e-22 ***	1.435e-14 ***	5.962e-09 ***
vs. RVIS	8.893e-23 ***	1.834e-16 ***	2.067e-15 ***

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