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The Journal of Biomedical Research, 2022 36(4): 1–3

JBR

Supplementary Data

Psychiatric risk gene transcription factor 4 preferentially regulates cortical interneuron neurogenesis during early brain development

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Supplementary Table 1 **Primers for real-time quantitative PCR analysis**

Human genes	Primer sequence (5′-3′)
SYPL1	Forward: CACTGTGGCTCCATTGTCTG
	Reverse: AAGCAGGGCTTTGTGTCACT
CHRNB4	Forward: CCCAGAAACAGGACTTGGAA
	Reverse: ACAGGACTCCCTGAGACGAG
OPRD1	Forward: CCTGCAGGACAGATGGAGAT
	Reverse: CAGGGAGGAATGGAAAATCA
RNU5F-1	Forward: TGTGTCACATTTGCCCTCAT
	Reverse: TGCAGATATCGGCTCAAGTG
SYT10	Forward: TAGAATGCACATCCTCTCCCAAT
	Reverse: GGCATGGAGAAGAGCCATTAAG
SEMA3E	Forward: TGATAACCACCATACTGCACCT
	Reverse: TATATGACAGCTATGCCCCCAG
CNTNAP2	Forward: TGTCCATAGGGGACAACCCT
	Reverse: TCATTTGAGATGTGAAGGAGCCA
BRINP3	Forward: AACATAGTCATGGAAGCGGC
	Reverse: GTGGTGTATCAAAGAGACACATCT

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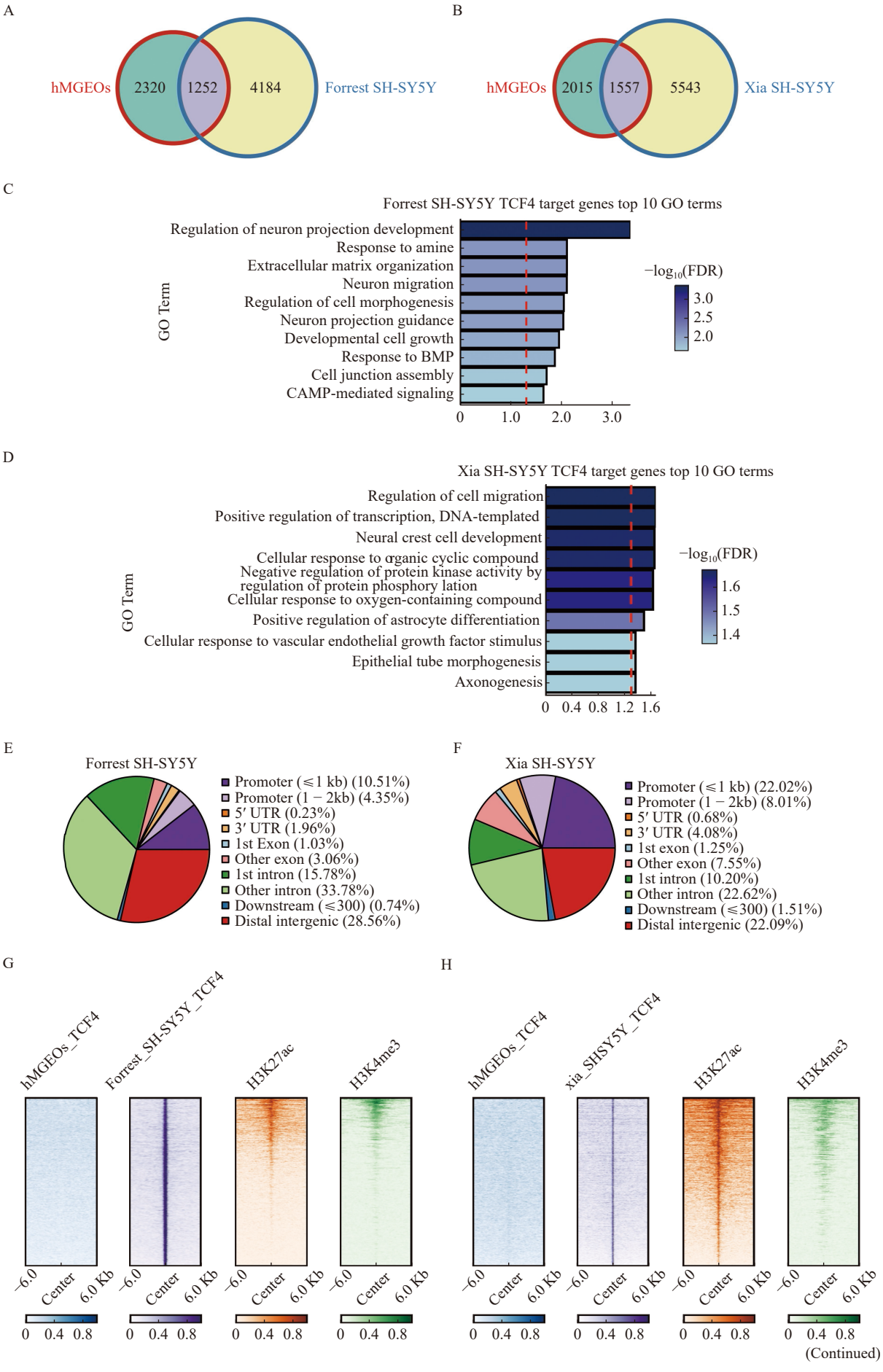
Received: 05 April 2022; Revised: 31 May 2022; Accepted: 01 June 2022; Published online: 28 July 2022

CLC number: R749.4, Document code: A

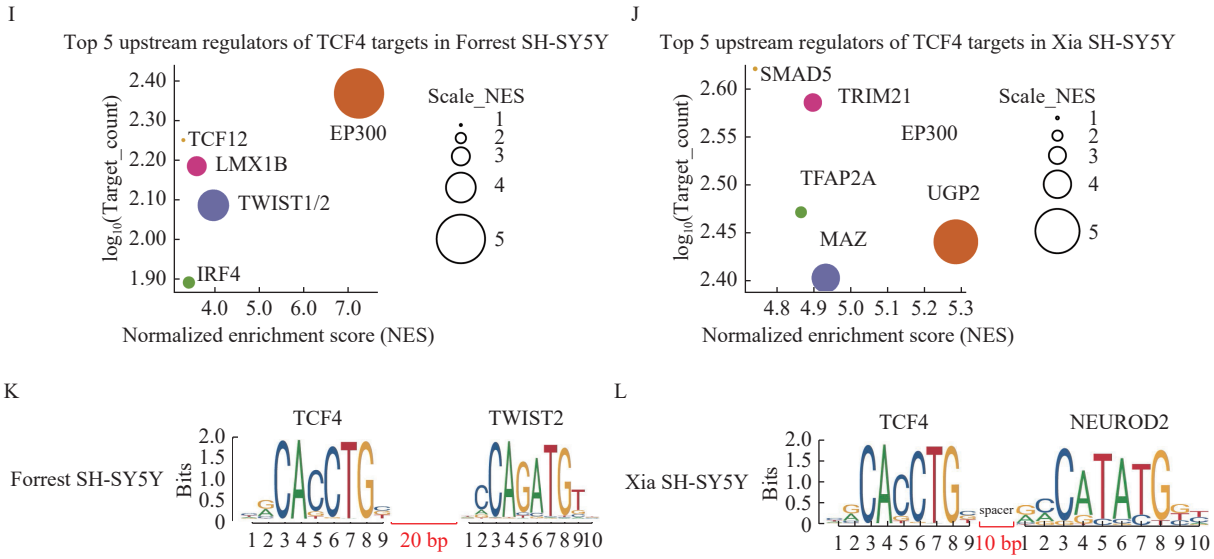
The authors reported no conflict of interests.

https://doi.org/10.7555/JBR.36.20220074


A
hMGEOs
2320
1252
4184
Forrest SH-SY5Y
B
hMGEOs
2015
1557
5543
Xia SH-SY5Y
C
Forrest SH-SY5Y TCF4 target genes top 10 GO terms
GO Term
Regulation of neuron projection development
Response to amine
Extracellular matrix organization
Neuron migration
Regulation of cell morphogenesis
Neuron projection guidance
Developmental cell growth
Response to BMP
Cell junction assembly
CAMP-mediated signaling
0 1.0 2.0 3.0
−log10(FDR)
3.0
2.5
2.0
D
Xia SH-SY5Y TCF4 target genes top 10 GO terms
GO Term
Regulation of cell migration
Positive regulation of transcription, DNA-templated
Neural crest cell development
Cellular response to organic cyclic compound
Negative regulation of protein kinase activity by regulation of protein phosphorylation
Cellular response to oxygen-containing compound
Positive regulation of astrocyte differentiation
Cellular response to vascular endothelial growth factor stimulus
Epithelial tube morphogenesis
Axonogenesis
0 0.4 0.8 1.2 1.6
−log10(FDR)
1.6
1.5
1.4
E
Forrest SH-SY5Y
Promoter (≤1 kb) (10.51%)
Promoter (1 − 2kb) (4.35%)
5′ UTR (0.23%)
3′ UTR (1.96%)
1st Exon (1.03%)
Other exon (3.06%)
1st intron (15.78%)
Other intron (33.78%)
Downstream (≤300) (0.74%)
Distal intergenic (28.56%)
F
Xia SH-SY5Y
Promoter (≤1 kb) (22.02%)
Promoter (1 − 2kb) (8.01%)
5′ UTR (0.68%)
3′ UTR (4.08%)
1st exon (1.25%)
Other exon (7.55%)
1st intron (10.20%)
Other intron (22.62%)
Downstream (≤300) (1.51%)
Distal intergenic (22.09%)
G
hMGEOs_TCF4
Forrest_SH-SY5Y_TCF4
H3K27ac
H3K4me3
−6.0 Center 6.0 Kb
0 0.4 0.8
H
hMGEOs_TCF4
xia_SHSY5Y_TCF4
H3K27ac
H3K4me3
−6.0 Center 6.0 Kb
0 0.4 0.8

(Continued)

(Continued)



Supplementary Fig. 1 **Difference in the predicted role of TCF4 in between hMGEOs and SH-SY5Y.** A: Venn diagram showing the intersection of TCF4 target genes identified in ihtc-03-derived hMGEOs with those identified in SH-SY5Y by Forrest *et al*.[1] Target genes were annotated by GREAT software. B: Venn diagram showing the intersection of TCF4 target genes identified in ihtc-03-derived hMGEOs with those identified in SH-SY5Y by Xia *et al*.[2] C: Barplot showing the top 10 enriched gene ontology among the top 500 target genes identified in SH-SY5Y by Forrest *et al.* The dotted line demarks false discovery rate (FDR) =0.05. D: Barplot showing the top 10 enriched gene ontology among the top 500 target genes identified in SH-SY5Y by Xia *et al.* The dotted line demarks false discovery rate (FDR) =0.05. E: Pie chart showing the genomic annotation of TCF4 binding sites identified in SH-SY5Y by Forrest *et al.* F: Pie chart showing the genomic annotation of TCF4 binding sites identified in SH-SY5Y by Xia *et al.* G: Heatmap showing the intensities of ChIP-seq signals of TCF4 in ihtc-03-derived hMGEOs, TCF4 in SH-SY5Y by Forrest *et al*, H3K27ac in fetal brain and H3K4me3 in fetal brain around TCF4 binding sites identified by Forrest *et al.* The signal intensity was measured in count-per-millon (CPM). The 12 000 bp flanking region of peak centers were shown, and each row represents a distinct peak. H: Heatmap showing the intensities of ChIP-seq signals of TCF4 in ihtc-03-derived hMGEOs, TCF4 in SH-SY5Y by Xia *et al*, H3K27ac in fetal brain and H3K4me3 in fetal brain around TCF4 binding sites identified by Xia *et al.* The signal intensity was measured in count-per-millon (CPM). The 12 000 bp flanking region of peak centers were shown, and each row represents a distinct peak. I: Scatter plot showing the normalized enrichment score of the potential upstream transcription factors and the corresponding number of downstream targets, predicted by iRegulon on the top 500 TCF4 target genes identified by Forrest *et al*. The sizes of the points were proportional to the scaled normalized enrichment score. J: Scatter plot showing the normalized enrichment score of the potential upstream transcription factors and the corresponding number of downstream targets, predicted by iRegulon on the top 500 TCF4 target genes identified by Xia *et al*. The sizes of the points were proportional to the scaled normalized enrichment score. K: Schematic showing the relative location of the top one co-occurring motif combination within TCF4 binding sites identified by Forrest *et al*, predicted by SIOMICS. L: Schematic showing the relative location of the top one co-occurring motif combination within TCF4 binding sites identified by Xia *et al*, predicted by SIOMICS.

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