Table S1. X-box motif sequences used for the bioinformatics search with the EMBOSS fuzznuc tool. All sequence information is shown 5' to 3'.

No.	Consensus	Organism	References
1	GTNRCC (0-3N) RGYAAC	*H sapiens*	Chen, L., et al.[1]
2	GTNRC(C/N)(0-3N) RGYAAC	*H sapiens*	Hsu, Y. C., *et al.*[2]
3	RYYNYY WW RRNRAC	*C elegans*	Efimenko, E., *et al.* [3]
4	RTHNYY WT RRNRAC	*C elegans*	Efimenko, E., *et al.* [3]
5	GTHNYY AT RRNAAC	*C elegans*	Efimenko, E., *et al.* [3]
6	GTTNCC NN(0-1N) GGHVAC	*H sapiens*	Internal
7	RBNNYY NH RGHAAC	*H sapiens*	Internal

[1] Chen, L., Smith, L., Johnson, M. R., Wang, K., Diasio, R. B., and Smith, J. B. (2000) Activation of protein kinase C induces nuclear translocation of RFX1 and down-regulates c-myc via an intron 1 X box in undifferentiated leukemia HL-60 cells. The Journal of biological chemistry 275, 32227-32233

[2] Hsu, Y. C., Liao, W. C., Kao, C. Y., and Chiu, I. M. (2010) Regulation of FGF1 gene promoter through transcription factor RFX1. The Journal of biological chemistry 285, 13885-13895

[3] .Efimenko, E., Bubb, K., Mak, H. Y., Holzman, T., Leroux, M. R., Ruvkun, G., Thomas, J. H., and Swoboda, P. (2005) Analysis of xbx genes in C. elegans. Development 132, 1923-1934

Table S2. Dyslexia candidate gene promoter construct cloning primers without restriction enzyme sequences and X-box wild type and mutant sequence information, respectively. All sequence information is shown 5' to 3'.

Gene	Forward primers	Reverse primers	X-box wild type[a]	X-box mutant
DYX1C1	TGAGTGTGCCCTATTTTGGG	CAGTCTTCGTCTGCTGCCAGC	GTCGCC GT GGTAAC	CACGAG GT TCCAAA
DCDC2[b]	CTCCCTCTTCCTCCAAACC and GTGTCGCCCAGGCTGGAGTG	CCGTGACTCATGCCTGTAAC and GAAACGAACGAGAAACTGACG	GCTTCC CT AGCAAC	ACTGGT AT GCAAAT
KIAA0319	GGATGTCCACTGAATGCTGA	ACAGGTGGAGCAAGGTTGCAC	GCTTCC CT AGCAAC	CATTGA CT CTCAAA

[a] For details of identification see Table S3.

[b] The *DCDC2* promoter construct was cloned by PCR sewing two regions together (chr6:24,359,852-24,360,507 and chr6:24,358,078-24,358,893) to avoid a TA-repeat region located at: chr6:24,358,894-24,359,851 in Hg19.