

Article

Increased Nuclear FOXP2 Is Related to Reduced Neural Stem Cell Number and Increased Neurogenesis in the Dorsal Telencephalon of Embryos of Diabetic Rats Through Histamine H1 Receptors

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Supplementary Material

Supplementary Tables

Table S1. Primer sequences, aligning temperatures, and size expected in the PCR reactions.

Target	Primer sequence Sense (5'-3') Antisense (5'-3')	Aligning temperature (°C)	Size bp*
<i>FoxP2</i>	GAA AGC GCG AGA CAC ATC G GAA GCC CCC GAA CAA CAC A	63°C	222
<i>β-III Tub</i>	GCC AAG TTC TGG GAG GTC ATC GTA GTA GAC ACT GAT GCG TTC CA	58°C	102
<i>Map2</i>	GAG AAG GAG GCC CAA CAC AA TCT TCG AGG CTT CTT CCA GTG	66°C	132
<i>PCKα</i>	GCC AAG TTC TGG GAG GTC ATC GTA GTA GAC ACT GAT GCG TTC CA	60°C	210
<i>PCKβ</i>	GAG AAG GAG GCC CAA CAC AA TCT TCG AGG CTT CTT CCA GTG-	60°C	203
<i>PCKγ</i>	AAA AGG CCA GCT CGT GAT CC CTG CTT TCC AAT GCC CCA GA	61°C	225
<i>Gapdh</i>	GGA CCT CAT GGC CTA CAT GG CCC CTC CTG TTG TTA TGG GG	58°C	198

*PCR product sizes were confirmed by visualizing the corresponding bands after end-point PCR and agarose gel electrophoresis stained with GelRed.

Table S2. Antibodies used in western blot and immunofluorescence assays.

Antibody	RRID (catalog #)	Dilution		MW (kDa) (μg)
		WB	IHF	
Nestin	AB_11175711 (GTx39577)	1:1000	1:100	~220 (40)
FOXP2	AB_2107107 (ab16046)	1:2000	1:500	~80 (40 ^{cy} or 20 ⁿ)
β-III TUB	AB_2210524 (MAB1637)	1:2000	1:100	~55 (60)
MAP2	AB_369978 (GTx11268)	1:5000	1:500	~280 ^{a/b} or ~70 ^c (80)
TBR2	AB_778267 (ab23345)		1:250	
Ki67	AB_10728990 (GTx84107)		1:250	
PKCα Total	AB_777294 (ab32376)	1:2500	1:1000	~77 (80)
PKCα phosphorilated (S657)	AB_2783796 (ab180848)	1:500	1:250	~77 (80)
TBP1	AB_945758 (ab51841)	1:2000		~38 (40 or 80)
GAPDH	AB_1080976 (GTx100118) AB_11174761 (GTx627408)	1:1000 1:5000		~37 (40 or 80)

*Amount of protein used for WB for cytoplasmic (^{cy}) or nuclear fraction (ⁿ).

^{a/b} and ^c, corresponding to the MAP2 isoforms.

WB, Western Blot and IHF, immunohistofluorescence.

Table S3. Secondary antibodies information.

Antibody	IRRID	Dilution
IRDye 680RD	AB_10954442	1:10000
IRDye 800CW	AB_621847	1:10000
Alexa Fluor 488	AB_2576217	1:1000
Alexa Fluor 568	AB_144696	1:1000

Table S4. Putative PKC phosphorylation sites for FoxP2.

Position	Amino acid	Sequence	Score GPS 3.0	Score NetPhos 3.1	RSA %	Disorder %
5	S	***MMQESATETISN	0.296	0.724	80	100
7	S	*MMQESATETISNSS	0.418	---	80	100
9	T	MQESATETISNSSMN	0.516	0.493	80	100
11	S	ESATETISNSSMNQN	0.401	---	78	100
13	S	ATETISNSSMNQNGM	0.292	---	79	100
14	S	TETISNSSMNQNGMS	0.309	0.731	79	100
24	S	QNGMSTLSSQLDAGS	0.253	---	77	100
71	S	QQQTSGLKS	---	0.586	76	98
79	S	GLKSPKSSDKQRPLQ	0.476	0.992	78	100
292	S	DLTTNNSSSTSSTT	0.248	0.596	77	100
294	T	TTNNSSSTSSTTSK	0.253	0.746	75	100
297	S	STTSSTTSK	---	0.673	76	100
298	T	TTSSTTSKA	---	0.784	76	100
299	T	SSTTSSTTSKASPI	0.424	0.893	75	100
336	T	GASHTLYGH	---	0.593	48	87
409	S	HMRPSEPKP	---	0.727	85	98
414	S	RPSEPKPSPKPLNLV	0.249	0.99	78	99
425	T	VSSVTMSKN	---	0.683	75	100
433	T	NMLETSPQS	---	0.719	77	100
443	T	PQTPTTPTA	---	0.524	79	100
446	T	PTTPTAPVT	---	0.598	79	100
463	S	ITPASVPNV	---	0.552	69	92
516	S	IMESSDRQL	---	0.518	64	1
532	T	WFT R TFAYF	---	0.618	37	0
		WFT H TFAYF	---	0.618	37	0
542	T	RNAATWKNA	---	0.842	35	1
580	S	VEYQ KRR SQKITGSP	0.368	0.997	76	33
		VEYQ AAA SQKITGSP	---	0.794	77	29
686	T	MSLVTTANH	---	0.609	64	98
706	S	EIEEEPLSEDLE***	0.275	---	77	100

Data was obtained with GPS 3.0-Species Specific (*R. norvegicus*) [1] and NetPhos-3.1 [2]. The percentage of relative Surface accessibility and disorder were obtained by NetSurfP-2.0 [3].

NLS2 mutation of “KRR” by “AAA” [4]

Mutation of WFT**R**⁵³¹TFAYF to WFT**H**⁵³¹TFAYF **548** corresponds to the R553H human mutation [4].

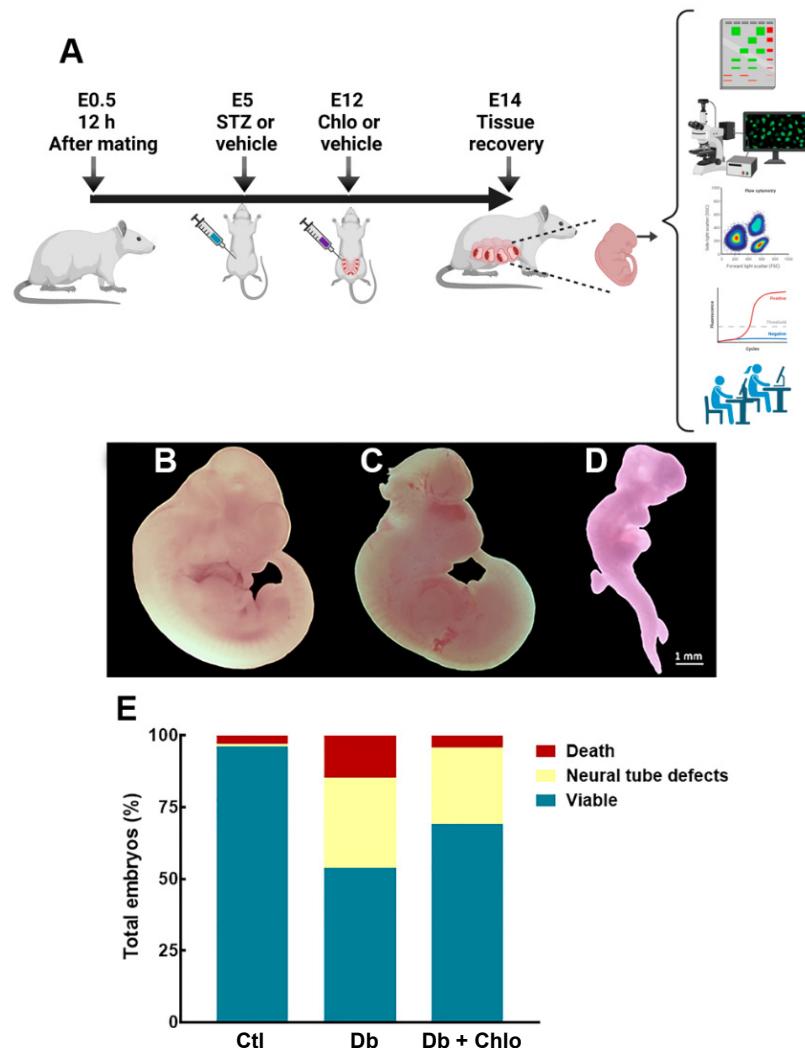


Figure S1. Working scheme and embryo morphology and viability. **A)** The scheme represents time point manipulation of pregnant rats, embryo recovery, and the methods used (from top to bottom: Western blot, immunofluorescence, flow cytometry, qRT-PCR, and bioinformatics analysis). E = embryo day. Created with BioRender.com (5 August 2022). **B-D)** Representative images of 14-day-old embryos obtained of diabetic rats showing viable (**B**, included in the study), neural tube defect (**C**, excluded), and death (**D**, excluded) embryos. **E)** Percentage of viable (blue), neural tube defect (yellow), and death (red) embryos obtained from control (Ctl), diabetic (Db), and diabetic chlorpheniramine-treated (Db+Chlo) pregnant rats. Data are expressed as a percentage of total embryos. n = 16 pregnant rats per group.

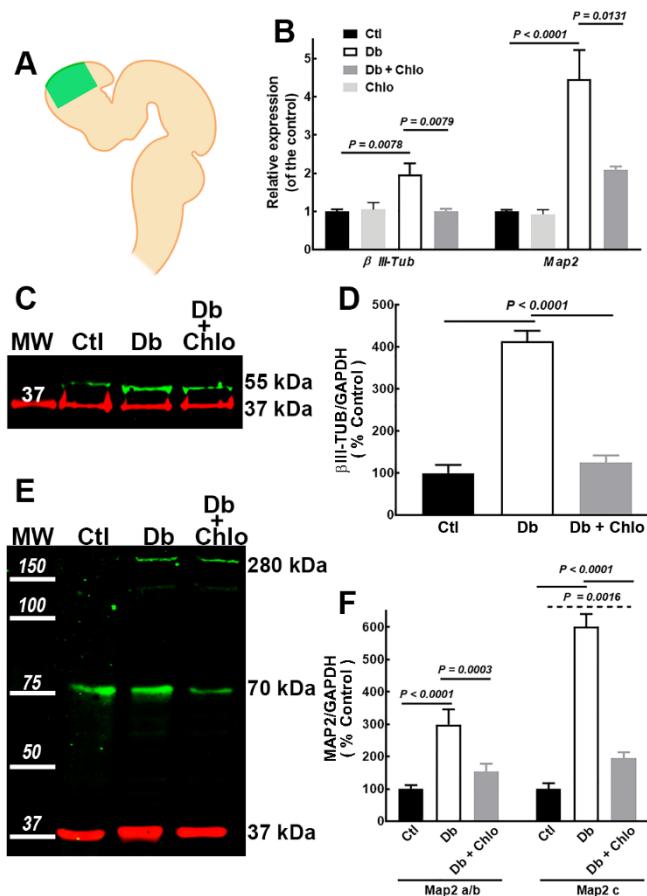


Figure S2. Neuron markers expression in the cortical neuroepithelium at 14-day-old embryos. **A)** Image showing the E14 neural tube. In green is highlighted the dorsal telencephalon dissected for qRT-PCR and Western blot analysis. Created with BioRender.com (1 January 2023). **B)** β III-Tubulin (β III-Tub) and Map2 mRNAs relative expression in E14 dorsal telencephalon of embryos from control (Ctl), Chlorpheniramine-treated, diabetic (Db) and chlorpheniramine-treated diabetic (Db+Chlo) groups using the $2^{-\Delta\Delta CT}$ method. The Gapdh amplification was used as an internal control. **C** and **E**) Representative Western Blots from E14 dorsal telencephalon from each experimental group for β III-TUB (C; green, ~55 kDa) and MAP2 (E, green, ~70 and ~280 kDa; light and heavy isoforms, respectively). GAPDH (red, 37 kDa) was used as a loading control. **D** and **F**) Quantitative fluorometry analysis for β III-TUB (D) and MAP2 (F). Values (means \pm S.E.M., n= 4) are expressed as a percentage of the control fluorescence ratio. The two-way ANOVA was performed, followed by Tukey's multiple comparisons test. Significant P values are shown in the graphs. MW = molecular weight ladder.

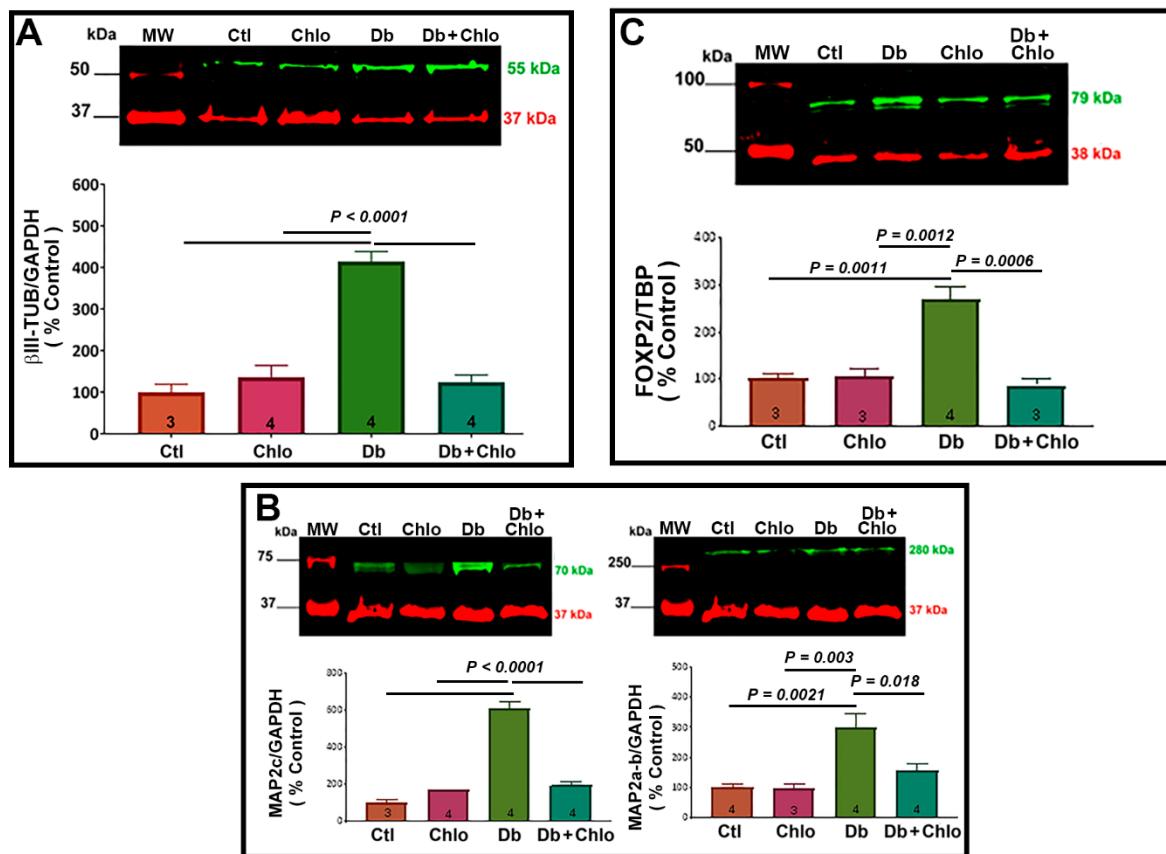


Figure S3. Chlorpheniramine alone does not affect nuclear neuronal markers and nuclear FOXP2. Top in **A, B, and C**) Representatives Western Blots from E14 dorsal telencephalon from control (Ctl) Chlorpheniramine-treated (Chlo), Diabetic (Db) and Chlorpheniramine-treated diabetic (Db+Chlo) groups for βIII-TUB (A; green, ~55 kDa), MAP2 (B; green, ~70 and ~280 kDa; light and heavy isoforms, respectively) and FOXP2 (C; green ~80 kDa). GAPDH (red, 37 kDa) and TBP (red, 38 kDa) were used as internal controls. **Down in A, B, and C)** Quantitative fluorometry analysis for βIII-TUB (A), MAP2 (B), and FOXP2 (C). Values (means ± S.E.M., n= are in each bar in the graphs) are expressed as a percentage of the control fluorescence ratio. The two-way ANOVA was performed, followed by Tukey's multiple comparisons test. Significant P values are shown in the graphs. MW = molecular weight ladder.

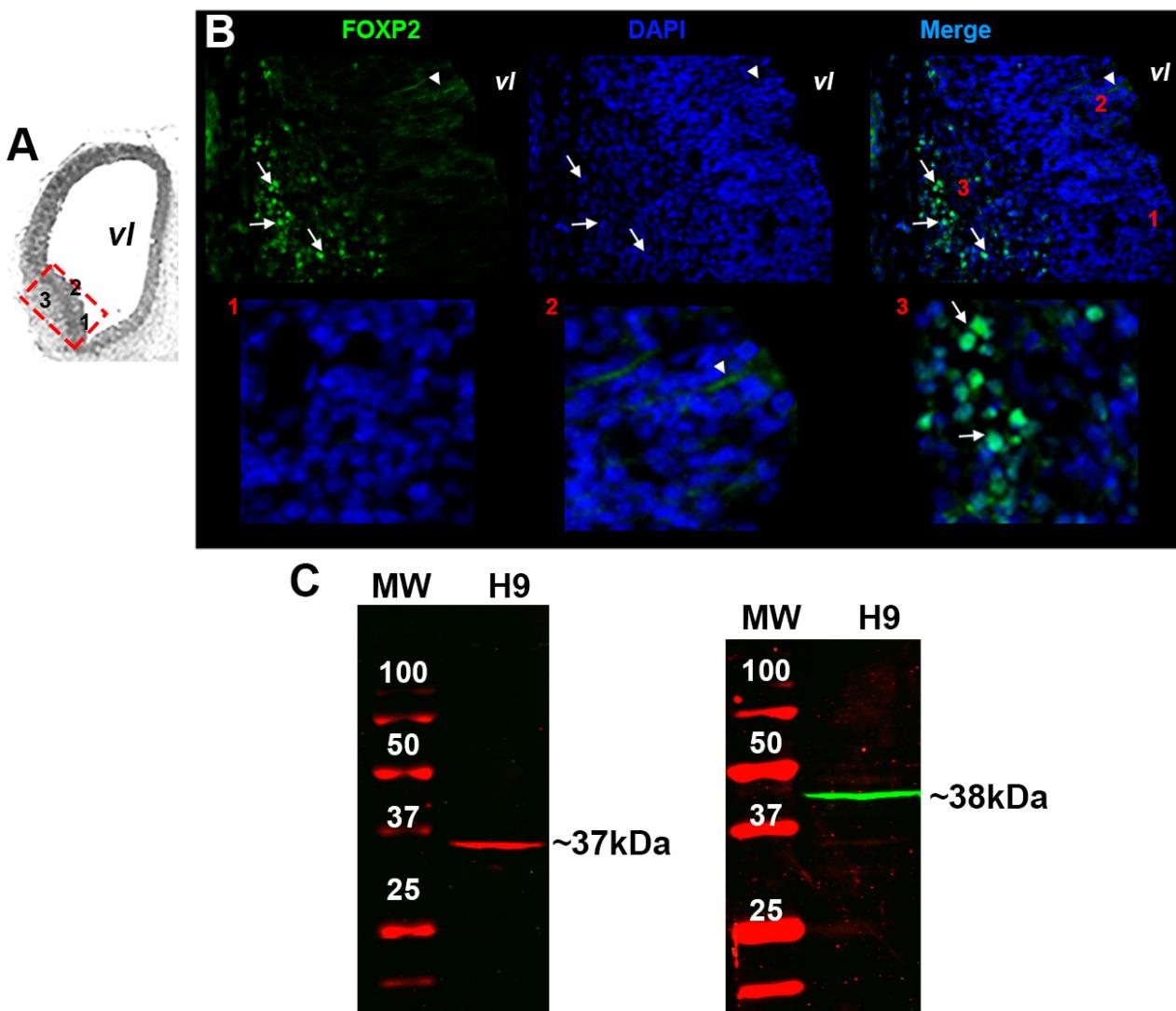


Figure S4. FOXP2 subcellular localization in the E14 ventral telencephalon. **A)** Hematoxylin-eosin-stained coronal section of E14 telencephalon used for the immunodetection in **B**. Numbers in black are 1 and 2 = pallidal neuroepithelium and 3 = subventricular zone of the pallidal neuroepithelium [5]. **B)** **Up:** from left to right: representative micrographs ($20\times$) of the immunofluorescence of FOXP2 (green) and the nuclei stained with DAPI (blue) per channel and merged channels in the ventral telencephalon. **Down:** from left to right are electronic zooms (300%) from the corresponding areas of the red numbers in red of the merged image in the upper panel. Numbers in red are the same as in **A**. Arrows are the FOXP2 mark in the nuclei, and arrowheads are cytoplasmic, which is absent in most ventral parts of the ventral telencephalon. **C)** FOXP2 negative control Western Blot of cytoplasmic (left, green) and nuclear (right, red) protein extracts obtained from the pluripotent cell line H9. GAPDH (in red on the left, ~37 kDa) and TBP1 (in green on the right, ~38 kDa) were used as internal controls for cytoplasm and nuclear fractions, respectively.

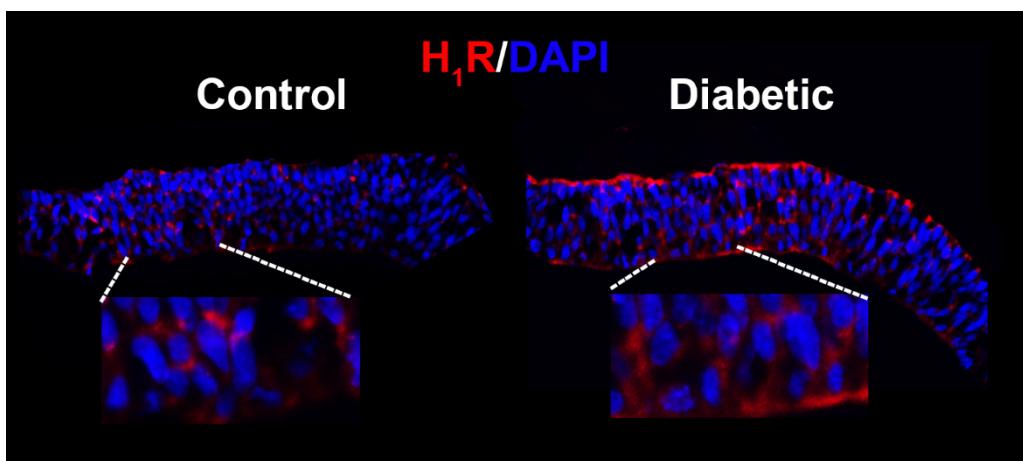


Figure S5. H₁R immunohistofluorescence in the 12-day-old cortical neuroepithelium of control and diabetic groups.

References

1. Xue, Y.; Liu, Z.; Cao, J.; Ma, Q.; Gao, X.; Wang, Q.; Jin, C.; Zhou, Y.; Wen, L.; Ren, J. GPS 2.1: Enhanced prediction of kinase-specific phosphorylation sites with an algorithm of motif length selection. *Protein Eng. Des. Sel.* **2011**, *24*, 255–260. <https://doi.org/10.1093/protein/gzq094>.
2. Blom, N.; Gammeltoft, S.; Brunak, S. Sequence and structure-based prediction of eukaryotic protein phosphorylation sites. *J. Mol. Biol.* **1999**, *294*, 1351–1362. <https://doi.org/10.1006/jmbi.1999.3310>.
3. Klausen, M.S.; Jespersen, M.C.; Nielsen, H.; Jensen, K.K.; Jurtz, V.I.; Sonderby, C.K.; Sommer, M.O.A.; Winther, O.; Nielsen, M.; Petersen, B.; et al. NetSurfP-2.0: Improved prediction of protein structural features by integrated deep learning. *Proteins* **2019**, *87*, 520–527. <https://doi.org/10.1002/prot.25674>.
4. Mizutani, A.; Matsuzaki, A.; Momoi, M.Y.; Fujita, E.; Tanabe, Y.; Momoi, T. Intracellular distribution of a speech/language disorder associated FOXP2 mutant. *Biochem. Biophys. Res. Commun.* **2007**, *353*, 869–874. <https://doi.org/10.1016/j.bbrc.2006.12.130>.