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<b>Title</b>	Host microbiota regulates central nervous system serotonin receptor 2C editing in rodents
<b>Author(s)</b>	van de Wouw, Marcel; Stilling, Roman M.; Peterson, Veronica L.; Ryan, Feargal J.; Hoban, Alan E.; Shanahan, Fergus; Clarke, Gerard; Claesson, Marcus J.; Dinan, Timothy G.; Cryan, John F.; Schellekens, Harriët
<b>Publication date</b>	2019-08-15
<b>Original citation</b>	van de Wouw, M., Stilling, R. M., Peterson, V. L., Ryan, F. J., Hoban, A. E., Shanahan, F., Clarke, G., Claesson, M. J., Dinan, T. G., Cryan, J. F. and Schellekens, H. (2019) 'Host Microbiota Regulates Central Nervous System Serotonin Receptor 2C Editing in Rodents', ACS Chemical Neuroscience, 10(9), pp. 3953-3960. doi: 10.1021/acscemneuro.9b00414
<b>Type of publication</b>	Article (peer-reviewed)
<b>Link to publisher's version</b>	<a href="https://pubs.acs.org/doi/10.1021/acscemneuro.9b00414">https://pubs.acs.org/doi/10.1021/acscemneuro.9b00414</a> <a href="http://dx.doi.org/10.1021/acscemneuro.9b00414">http://dx.doi.org/10.1021/acscemneuro.9b00414</a> Access to the full text of the published version may require a subscription.
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<b>Embargo lift date</b>	2020-08-15
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## Supporting information

### Host Microbiota Regulates Central Nervous System Serotonin Receptor 2C Editing in Rodents

Marcel van de Wouw<sup>1,2</sup>, Roman M Stilling<sup>1,2</sup>, Veronica L Peterson<sup>1,3</sup>, Feargal J Ryan<sup>1,4</sup>, Alan E Hoban<sup>1,2</sup>, Fergus Shanahan<sup>1</sup>, Gerard Clarke<sup>1,3</sup>, Marcus J Claesson<sup>1,4</sup>, Timothy G Dinan<sup>1,3</sup>, John F Cryan<sup>1-3</sup>, Harriët Schellekens<sup>1,2</sup>

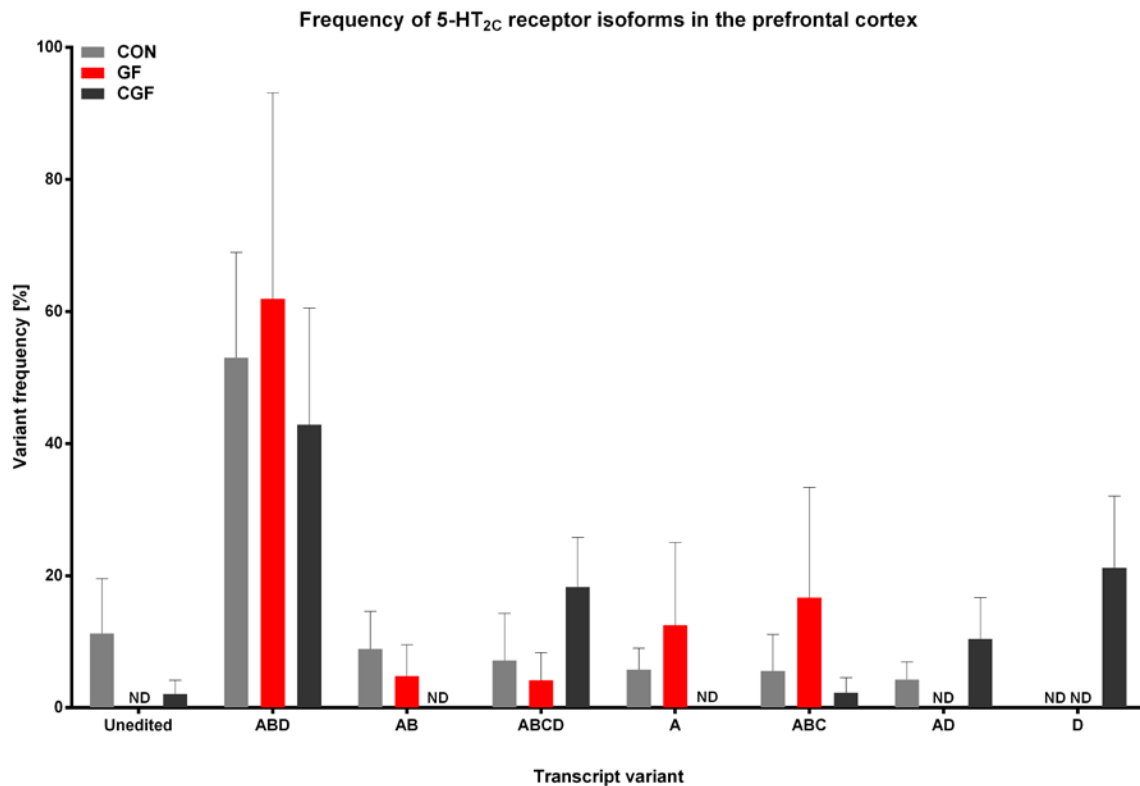
<sup>1</sup>*APC Microbiome Ireland, University College Cork, Cork, Ireland*

<sup>2</sup>*Department of Anatomy and Neuroscience, University College Cork, Cork, Ireland*

<sup>3</sup>*Department of Psychiatry and Neurobehavioral Science, University College Cork, Cork, Ireland*

<sup>4</sup>*Department of Microbiology, University College Cork, Cork, Ireland*

**Corresponding author:** Dr Harriët Schellekens, APC Microbiome Ireland, University College Cork, Cork; Department of Anatomy and Neuroscience, University College Cork, Cork. Email address: H.Schellekens@ucc.ie



**Figure 1. 5-HT<sub>2C</sub> receptor transcript variants in the prefrontal cortex.** The prefrontal cortex of mice with a conventional microbiota (CON), mice without a microbiota (GF) and mice of which the microbiota was colonized (CGF), were investigated using RNA sequencing, after which the relative frequency of 5-HT<sub>2C</sub> receptor transcript variants was assessed. Notably, the 5-HT<sub>2C</sub> receptor is not as highly expressed in the prefrontal cortex as the amygdala. As such, the sequencing depth of the 5-HT<sub>2C</sub> receptor and its isoforms was not as high, and these findings need to be interpreted with care. Only transcript variants are depicted of which relative frequency was higher than 1%. All data are expressed as mean  $\pm$  SEM (n = 3-4).

**sTable 1. Relative occurrence of 5-HT<sub>2C</sub> isoforms compared to previous work investigating 5-HT<sub>2C</sub> editing in the hypothalamus of C57Bl/6 mice showing similar editing patterns (Schellekens et al. 2012).**

Rank	Relative occurrence in CON, Amygdala, Swiss-Webster	Edited sites / Isoform	Sequence of edited cassette as seen in RNA-seq data	% Relative occurrence Schellekens et al. 2012
1	33.66%	ABD	GTGCGTAATCCTG	33.58%
2	13.81%	ABCD	GTGCGTAGTCCTG	11.32%
3	11.53%	AB	GTGCGTAATCCTA	19.31%
4	9.50%	ABC	GTGCGTAGTCCTA	8.82%
5	8.45%	(unedited)	ATACGTAATCCTA	6.24%
6	5.43%	A	GTACGTAATCCTA	8.68%
7	4.17%	AD	GTACGTAATCCTG	<1%
8	3.36%	D	ATACGTAATCCTG	2.66%
9	2.61%	ACD	GTACGTAGTCCTG	<1%
10	1.86%	CD	ATACGTAGTCCTG	<1%
11	<1%	AC	GTACGTAGTCCTA	1.11%
11	<1%	AE	GTACGTGATCCTA	<1%
11	<1%	C	ATACGTAGTCCTA	<1%
11	<1%	DE	ATACGTGATCCTG	<1%
11	<1%	ABCDE	GTGCGTGGTCCTG	<1%
11	<1%	ABCE	GTGCGTGGTCCTA	<1%
11	<1%	ABDE	GTGCGTGATCCTG	<1%
11	<1%	ABE	GTGCGTGATCCTA	<1%
11	<1%	ACDE	GTGCGTGGTCCTA	<1%
11	<1%	ACE	GTACGTGGTCCTA	<1%
11	<1%	ADE	GTACGTGATCCTG	<1%
11	<1%	B	ATGCGTAATCCTA	<1%
11	<1%	BC	ATGCGTAGTCCTA	<1%
11	<1%	BCD	ATGCGTAGTCCTG	<1%
11	<1%	BCDE	ATGCGTGGTCCTG	<1%
11	<1%	BD	ATGCGTAATCCTG	<1%
11	<1%	BDE	ATGCGTGATCCTG	<1%
11	<1%	BE	ATGCGTGATCCTA	<1%
11	<1%	BCE	ATGCGTGGTCCTA	<1%
11	<1%	CDE	ATACGTGGTCCTG	<1%
11	<1%	CE	ATACGTGGTCCTA	<1%
11	<1%	E	ATACGTGATCCTA	<1%